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Estudis de Doctorat en Biologia i Biotecnologia Vegetal

PhD thesis

Fragaria vesca NIL collection: Development and Genetic Characterization of agronomical, Nutritional and Organoleptic traits.

Dissertation presented by María Urrutia Rosauro for the degree of Doctor of Biology and Plant Biotechnology by Universitat Autònoma de Barcelona (UAB)

This work was performed in Centre de Recerca en Agrigenòmica (CRAG), Bellaterra.

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Barcelona, July 2015

Chapter IV

Differential expression analysis of four NILs vs. their recurrent parental

Introduction

Wild strawberries (*Fragaria vesca spp.*) are close diploid relatives of the octoploid cultivated strawberries (*Fragaria x ananassa spp.*). Despite their outstanding organoleptic and nutritional characteristics are only minor crops due to their short post-harvest shelf-life. However they offer great advantages for being used as research model species for the *Fragaria* and *Rosaceae* breeding community. They have a small diploid genome (roughly 240 Mb) that has been shown to shear long synthenic regions with other species from distant *Rosaceae* genus like *Prunus persica* and *Malus domestica* (Vilanova *et al.* 2008, Illa *et al.* 2011) and that shows great co-linearity with the octploid *Fragaria x ananassa* genome (Rousseau-Geutin *et al.* 2008; Tennessen *et al.* 2014). Besides, their intergenerational period (4-5 months from seed to seed) is much shorter than that of fruit-trees and their small plant size and simple growing requirements make them ideal to be maintained in greenhouses and laboratory facilities.

Its interest as a model species persuaded strawberry scientific community to join efforts and sequence the genome of the *F. vesca* var. Hawaii 4 (Shulaev *et al.* 2011). The high quality *F. vesca* v1.1 reference genome and annotation (a1) has been a tool of great utility, extensively used by the strawberry research community but it is still being improved. In the last year, two big-impact independent up-dates have been disclosed. In first place, a new assembly version (v2.0) that presents 84 translocations, 39 inversions and 18 newly mapped scaffolds with respect to v1.1 came out in 2014 (Tennessen *et al.* 2014). This new assembly however does not report any improvements in gene prediction. In second place, a new annotation version based on whole transcriptome sequencing data was publicly available in 2015 (a2) (Darwish *et al.* 2015). It provides 2286 new gene models and 9139 new coding regions with respect to annotation version 1 (a1). However, this new annotation (a2) is anchored to the old assembly version 1.1.

The availability of a reference genome sequence has facilitated the implementation of new genomic high-throughput techniques in the last years. For instance an SNP array for in depth strawberry genotyping that was published recently (Bassil & Davis *et al.* 2015) and that was used for the NIL collection genotyping (see annex Chap. I). Whole transcriptome sequencing (RNAseq) experiments with diverse objectives have also been reported in *F. vesca* and *F. x ananassa*. Kang *et al.* (2013) and Hollender *et al.* (2014) in detail described changes in expression and expression networks along early fruit, flower receptacle and anthers development stages in *F. vesca* using RNAseq. This high-throughput technique has been also used in *F. x ananassa* to elucidate γ-decalactone synthesis (Chambers *et al.* 2014; Sanchez-Sevilla *et al.* 2014).

Studies with other *Rosaceae* species provide more examples of the wide range of applications that can be addressed with this technology. Apple (*Malus x domestica*), was the first sequenced genome among the *Rosaceae* family (Velasco *et al.* 2010) and several biological questions have been answered by RNAseq approach. It has been used to investigate responses to biotic and abiotic stress (Gusberti *et al.* 2013; Wang *et al.* 2014), developmental processes such as fruit abscission and columnar growth (Krost *et al.* 2013; Ferrero *et al.* 2015) and post-harvests quality such as flesh browning (Mellidou *et al.* 2014). Besides whole genome sequencing experiments have been implemented to improve genome annotation (Bai *et al.*

2014). Whole genome transcriptome studies have also been used to reveal complex mechanisms in genus *Prunus* were the reference genome belongs to *Prunus persica* (Verde *et al. 2013)*. Coloration of leafs in *P. persica* and fruits in *P. avium* (Wei *et al.* 2015; Ying *et al.* 2014), response to chill stress in *P. dulcis* and to root hypoxia in *Prunus* sp. (Mousavi *et al.* 2014; Arismendi *et al.* 2015). RNAseq has also been used in species without a sequenced reference genome like *Rubus* sp. to build a reference transcriptome (Hyun *et al.* 2014; Garcia-Seco *et al.* 2015) as a simpler approach for further genomic studies. Whole transcriptome sequencing is in expansion and new analysis tools and application examples are growing very fast. Therefore it is very likely that new strawberry RNAseq analysis exploring expression pattern of different *Fragaria* sp., different tissues or different growth conditions will come out in near future to broaden our knowledge of the species.

The *F. vesca* NIL collection (Urrutia *et al.* 2015) is a mapping population that has been extensively phenotyped for nutritional (Urrutia *et al.* accepted) and organoleptic traits and has shown its usefulness for detecting strong and stable metabolic quantitative trait loci (mQTL).

In order to take a closer look at the genetic control of the observed phenotypes, we performed a whole mRNA sequencing (RNAseq) analysis and evaluated differences in expression levels between a set of 4 NIL harboring interesting mQTL and the parental line *F. vesca* var. Reine des vallées (RV)

Materials and Methods

Plant material and phenotypes

The full near isogenic line (NIL) collection of *F. vesca* (see Urrutia *et al.* 2015 for details on the collection) was grown in shaded greenhouses in Caldes de Montbui (Barcelona) from March to September in 2013. Three biological replicates of fully ripe berries from a set of NIL Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10 and the recurrent parental *F. vesca* RV, were individually harvested, immediately frozen with liquid nitrogen, grinded to fine powder and stored at -80ºC until RNA isolation.

RNA isolation, library preparation and sequencing

Total RNA was isolated from the 15 samples (5 lines and 3 biological replicates) following the protocol described in (Liao *et al.* 2004). That basically consists in a cell lysis step with CTAB buffer modified with 3% PVP and 4% β-mercaptoethanol followed by 2-3 cleaning steps with chloroform-isoamyl alcohol (24:1 v/v), an overnight precipitation step with Lithium Chloride (8 M), followed by 1-2 additional cleaning steps with chloroform-isoamyl alcohol (24:1 v/v) and precipitation with cold absolute ethanol. RNA was quantified and checked for purity and integrity in a Bioanalyzer-2100 (Agilent Technologies, CA, USA). Concentration and quality threshold were set at 150 ng/μL and RNA integrity number (RIN) above 8.

Further steps in RNA quality control, library preparation and mRNA paired end (2 x 75bp) sequencing were performed by Centro de Análisis Genómico (CNAG), Spain in a HiSeq2000 sequencer (Illumina, CA, USA).

Mapping and assembly of reads

The general workflow outline is presented in Figure CIV. 4. Quality control and trimming for sequencing adaptors, low quality reads and short reads (<40bp) were performed using FASTQC v0.10.1 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc) and Trimmomatic v0.32 (Bolger *et al.* 2014) respectively. Trimmed reads were mapped against the *Fragaria vesca* reference genome v1.1 using Tophat v2.0.11 with recommended parameters (Kim *et al.* 2013) and taking as annotation reference version 1 (a1) and version 2 (a2) (genome and both annotations were downloaded from the *Fragaria* repository in the Genomic Rosaceae Database, GDR, https://www.rosaceae.org/species/fragaria/fragaria_vesca). Mapping quality was evaluated with *bamqc* and *rnaseq* functions from Qualimap v2.1 (García-Alcalde *et al.* 2012)

Differential gene expression analysis

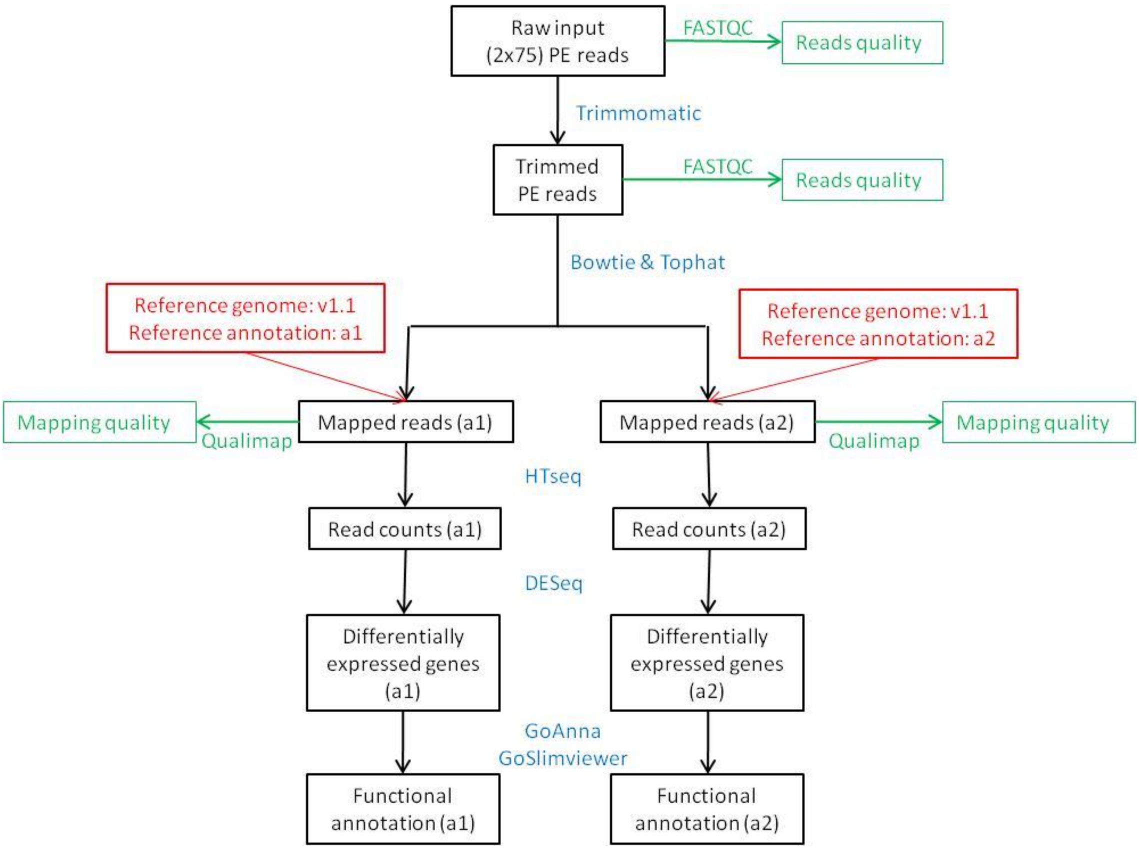
Differential expression analysis was first performed using annotations a1 and then complemented, using the same filters and parameters with a2. Firstly, independent tables of counts per gene were generated with *HTSeq-count* with mode *union* (Anders *et al.* 2015) considering all annotated genes from the reference annotation a1 and a2 respectively. These tables were provided as input to DESeq package in R (Anders & Huber 2010) using the function *newCountDataSetFromHTSeqCount*. DESeq counts all the reads-pairs mapped to a gene and normalizes the number of counts between samples correcting by the library size. We considered that a gene was expressed in a specific line if at least 2 of the 3 biological replicates had >=1 read-counts for the gene. Secondly, genes with low expression levels were filtered in order to maximize discovery rate (Supplemental Figure CIV. 1). Several filter parameters (mean, minimum, maximum and standard deviation of counts) and cutoffs (0-80%) were tested for a1 data (Supplemental Figure CIV. 2, Supplemental Figure CIV. 3) and finally, a common filter at 40% of the genes with lowest standard deviation was set. After filtering, the differential expression analyses contrasting each NIL against RV were computed with the *nbinomTest* function (Anders & Huber 2010). Multi-testing corrected p-values (p-adjust) were calculated by Benjamini & Hochberg method. The significance threshold for a differentially expressed gene (DEG) was fixed in p-adjust=0.1 (what is equivalent to p-values of 0.0065, 0.01, 0.005 and 0.01 for the contrast of Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10 respectively vs. *F. vesca* RV with a1) (Supplemental Figure CIV. 4). Lists of differential expressed genes obtained with a1 (Supplemental Table CIV..1) and a2 were compared for coincidence. Commonly DEGs were signaled in Supplemental Table CIV. 1 and removed from a2 DEGs list, that keeps those newly detected DEGs using a2 only (Supplemental Table CIV..2).

Functional annotation

Lists of differentially expressed genes (DEG) were inquired for predicted protein similarity with other proteins annotated in plant databases. For a1 list, predicted protein sequence was extracted from the rosaceae database (https://www.rosaceae.org/species/fragaria/fragaria_vesca/genome_v1.0). For a2 list, mRNA sequence was extracted from predicted exon coordinates, as protein predictions are not directly available. These proteins and mRNA sequences were inquired by *blastp* and *blastx* respectively with *GoAnna* tool from Agbase (McCarthy *et al.* 2006) against the manually annotated protein plant database with a significant threshold of 0.05. Annotated function and gene ontology terms (GO terms) of best blast hits were assumed as putative function by protein or mRNA query. In order to obtain a summarized view of the functional annotation results we used *GoSlimViewer* from AgBase (McCarthy *et al.* 2006). In addition, functional enrichment analysis to detect metabolic functions or biological processes that might be over-represented among the DEGs was carried out using MetGenMAP on-line platform with a1 data (Joung *et al.* 2009). Putatively affected metabolic pathways were also explored using MetGenMAP.

Candidate genes (CG) located in *cis* according to polyphenol mQTL were highlighted in chap II (Urrutia et al, submited). Those CG that were considered for NIL Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10 were re-evaluated with expression data. Differences between *F. vesca* allele (RV) and *F. bucharica* allele (NIL) were visually detected with IGV 2.3 (Thorvaldsdottir *et al.* 2013) and putative effects over protein function were evaluated using PROVEAN (http://provean.jcvi.org).

Figure CIV. 1 RNAseq general workflow. Data analysis workflow steps are presented as a diagram: Data analysis step (black), quality checking steps (green), analysis softwares (blue) and external data (red).



Results

Phenotypic variation between NILs

According to phenotypic criteria, a set of four NILs were selected for a differential expression analysis (NILs: Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10).

NILs Fb**5**:0-35 and Fb**7**:0-10 (with exotic introgression sizes of 6.51 and 14.20 Mb respectively) were selected because they harbor QTL linked to the accumulation of several volatile alcohols and esters, including five 'key compounds' for the strawberry aroma (methyl 2-aminobenzoate, myrtenyl acetate, methyl butanoate, butyl butanoate, methyl hexanoate) and also several QTL accounting for variability of flavan-3-ols. Fb**5**:50-76 (introgression size = 17.22 Mb) was chosen because it shows QTLs related with the accumulation of compounds derived from the lipoxigenase pathway associated to the "herbaceous-refreshing" scent ((*E*)-2-hexenal, (*Z*)-3-hexenal, (*E*)-2-hexenyl acetate, (*Z*)-3-hexenyl acetate) and derivatives of kaempferol. Finally Fb**6**:84-101 (introgression size = 6.60 Mb) was selected because it gathers QTLs related with the accumulation of volatile compounds derived from degradation of phenylalanine and phenolic glucosides.

Detection of differentially expressed genes that may relay behind the observed phenotypic differences among the NIL (Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10) and their recurrent parental (RV) was approached from a whole transcriptome sequencing-differential expression analysis strategy.

Whole transcriptome sequencing and reads mapping

The transcriptome of fully ripe fruits from the selected NILs (Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10) and the recurrent parental of the NIL collection *F. vesca* var. 'Reine des Vallées' (RV) with three biological replicates (a total of 15 samples) were sequenced with paired ends (2x75 bp) in an illumina HiSeq2000 platform (Illumina, CA, USA). A total of 673.11 millions of read-pairs were obtained with an average of 44.87 M read-pairs per sample (min. 33.03 M, max. 58.45 M) (Table CIV.1).

Quality of raw read pairs was assessed and sequencing adaptors and low quality reads were filtered using the software Trimmomatic v0.32 (Bolger *et al.* 2014). A total of 621.16 M (92%) passed the filter cutoff and were kept for further analysis (average of 41.41 M read-pairs per sample) (Table CIV.1).

High percentage of trimmed reads (88.5-91.0%) were mapped to the reference *F. vesca* genome v1.1 (Table CIV.1) using Tophat v2.0.11 (Kim *et al.* 2013). Attending to annotation version 1, 69 to 73% of mapped reads were located in exons, 7 to 8% in introns and the remaining 19-24% in intergenic regions. The new annotation version a2 improved the number of reads mapped in exonic regions by around 2% ranging between 70-75% of total mapped reads. It has also increased the number of reads mapped to intronic regions by 1-2% and decreased the percentage of reads mapping to intergenic regions by 3-4% ranging from 15-19% (Table CIV.1). These revealing that although a2 represents an improvement in comparison to a1, there might be still un-annotated expressed genes.

Table CIV. 1 Sequencing and mapping summary. Number of total, trimmed and mapped reads per sample (no pairs). Trimmed reads mapped to the *F. vesca* v1.1 genome percentage. Mapped reads in exonic, intronic or intergenic regions according to annotation versions 1 and 2 percentages.

						annotation a1			annotation a2		
genotype	replicate	Total reads	Total trimmed reads	Total mapped reads	% Mapped reads	% exonic	% intronic	% intergenic	% exonic	% intronic	% intergenic
RV	R1	109.092.822	100.158.704	93.029.027	93	71	8	21	73	9	17
RV	R2	81.510.370	74.155.530	68.147.534	92	72	8	20	74	9	17
RV	R3	83.497.832	76.431.248	70.982.845	93	72	7	20	74	9	17
Fb5:0-35	R1	116.903.324	108.432.126	99.900.726	92	73	7	19	75	8	16
Fb5:0-35	R2	70.369.654	65.137.888	59.690.856	92	72	7	20	74	9	17
Fb5:0-35	R3	66.055.216	59.123.378	54.566.189	92	71	7	21	73	9	17
Fb5:50-76	R1	95.206.004	87.903.890	82.076.075	93	73	7	19	75	8	16
Fb5:50-76	R2	81.773.036	75.782.254	70.820.016	93	72	8	20	74	9	16
Fb5:50-76	R3	86.408.734	80.156.848	74.175.077	93	72	8	19	74	9	16
Fb6:84-101	R1	95.017.216	88.087.320	81.514.383	93	73	7	19	75	9	16
Fb6:84-101	R2	71.666.526	66.397.372	59.744.191	90	69	8	23	70	10	19
Fb6:84-101	R3	101.873.898	94.426.026	87.468.242	93	71	8	21	73	9	17
Fb7:0-10	R1	102.796.206	95.517.746	87.309.247	91	71	7	21	73	9	18
Fb7:0-10	R2	80.766.218	74.683.082	69.002.192	92	72	7	20	74	9	17
Fb7:0-10	R3	103.283.744	95.931.722	88.863.699	93	71	7	21	74	9	17

Differential expression analysis and functional annotation

Differential expression analysis was first conducted using annotation version 1 and then complemented with version 2 in order to detect trancriptomic differences between the selected NILs and RV. The analysis was carried out using DESeq (Anders &Hubers 2010) unless otherwise is specified. From the 31213 genes anchored to the genome in the reference annotation a1, 19574 (62%) were expressed in all NILs and RV. Additionally 4286 genes were expressed in at least one of the lines resulting in 76% of the *F. vesca* a1 predicted genes present in the samples. A minimum of 215 and a maximum of 450 genes were uniquely expressed by one of the lines. While 7353 (23%) were not expressed in any of the NILs nor in RV (Figure CIV. 2A).

First we evaluated if the gene expression pattern was different between NIL and the recurrent parental *F. vesca* RV, to do so, we performed a principal component analysis of the samples taking into account the 500 most variable genes. Samples formed four clear groups according to their genotypes, this meaning that differences between lines are clearly higher than differences within samples. NILs Fb**5**:0-35, Fb**5**:50-76 and Fb**7**:0-10 form three independent clusters and *F. vesca* RV together with Fb**6**:84-101 form the forth cluster. Therefore we could expect different expression patterns between lines forming the different clusters, and a similar expression pattern between Fb**6**:84-101 and RV (Figure CIV. 3).

Filtering the less likely DEG, is a highly recommended step before DE analysis in order to maximize the number of rejections at a specific false discovery rate (FDR). Genes with low expression levels show little probability to be differentially expressed and act as a background noise diminishing the discovery rate of the contrast test. After considering several combinations of filtering parameters and cutoffs with our experimental data (see mat. and meth.), we applied a filter of 40% of genes with the lowest standard deviation. In this way we recover the maximum number of truly DEGs.

Figure CIV. 2 Venn diagrams. Venn diagram **A** depicts the number of annotated genes (a1) expressed by each line. Colored ellipses represent analyzed lines (Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101, Fb**7**:0-10 and RV). Venn diagram **B** depicts the number of differentially expressed genes detected between each NIL and the recurrent parental (RV). Colored ellipses represent comparisons (NIL vs. RV). Numbers in intersecting areas indicate that those genes are shared between the lines/comparisons meeting in the area. Non-intersecting areas indicate the number of genes that are specifically expressed/differentially expressed in a line.

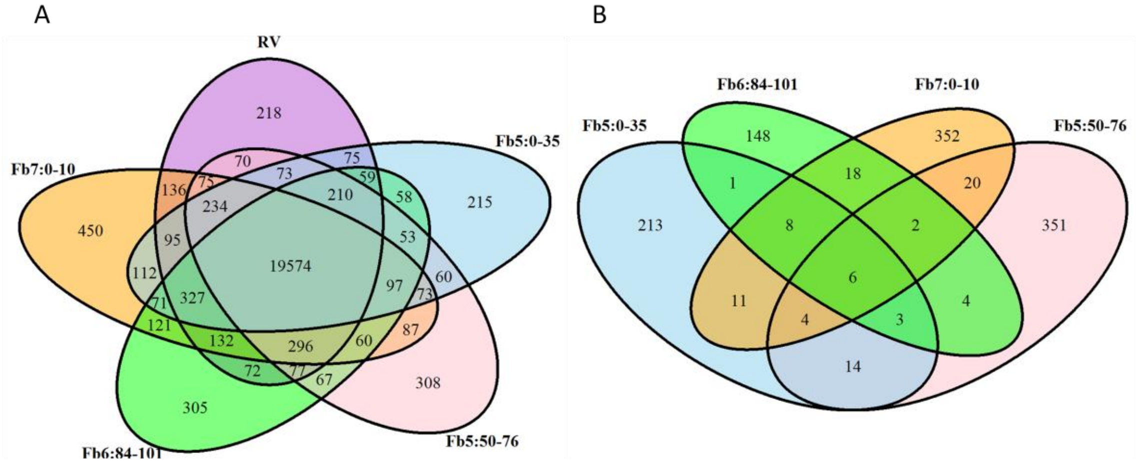
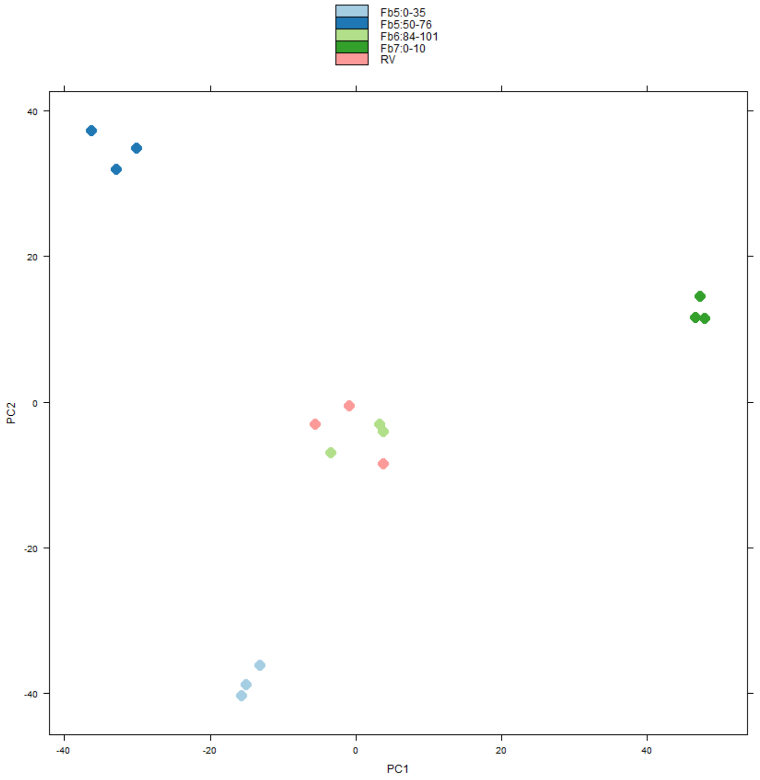


Figure CIV. 3 Differential expression patterns between lines. Principal component analysis (PCA) of the lines studied: Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101, Fb**7**:0-10 and RV using the three biological replicates. Samples are separated or clustered according to expression of the 500 most variable genes across the lines.



The differential expression analysis was performed contrasting each NIL against *F. vesca* RV using a negative binomial distribution-based method proposed in DESeq (Anders & Hubers 2010). The significance threshold was fixed after Benjamini & Hochberg correction in p-adjust=0.1. As a result we obtained four lists of 260, 404, 190 and 421 differentially expressed (DE) genes corresponding to the contrast of Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101, Fb**7**:0-10 respectively vs. RV using a1 (Table CIV.2, Supplemental Table CIV.1). Very similar values were detected using a2 (Table CIV.2), however only around half of the DEGs were commonly annotated between the two versions and roughly the other half (123, 178, 58,235 for Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10 respectively) were exclusive from a2 (Table CIV.2, Supplemental Table CIV.2).

Among the DEGs of NILs Fb**6**:84-101 and Fb**7**:0-10 there was not a tendency towards the up or down regulation, however in NILs Fb**5**:0-35 and Fb**5**:50-76 there were more down-regulated than up-regulated DEGs.

Great majority of the differentially expressed genes were altered only in one NIL with respect to *F. vesca* RV, this was expected as NILs do not share overlapping introgressions. However there were also 6 genes that were differentially expressed in all NILs when compared with *F. vesca* RV (Figure CIV. 2B).

High percentage of the differentially expressed genes in each NIL (54% in Fb**5**:0-35, 74% in Fb**5**:50-76, 52% in Fb**6**:84-101 and 59% in Fb**7**:0-10) are located within the boundaries of their introgressed region this meaning that they are regulated in *cis*.

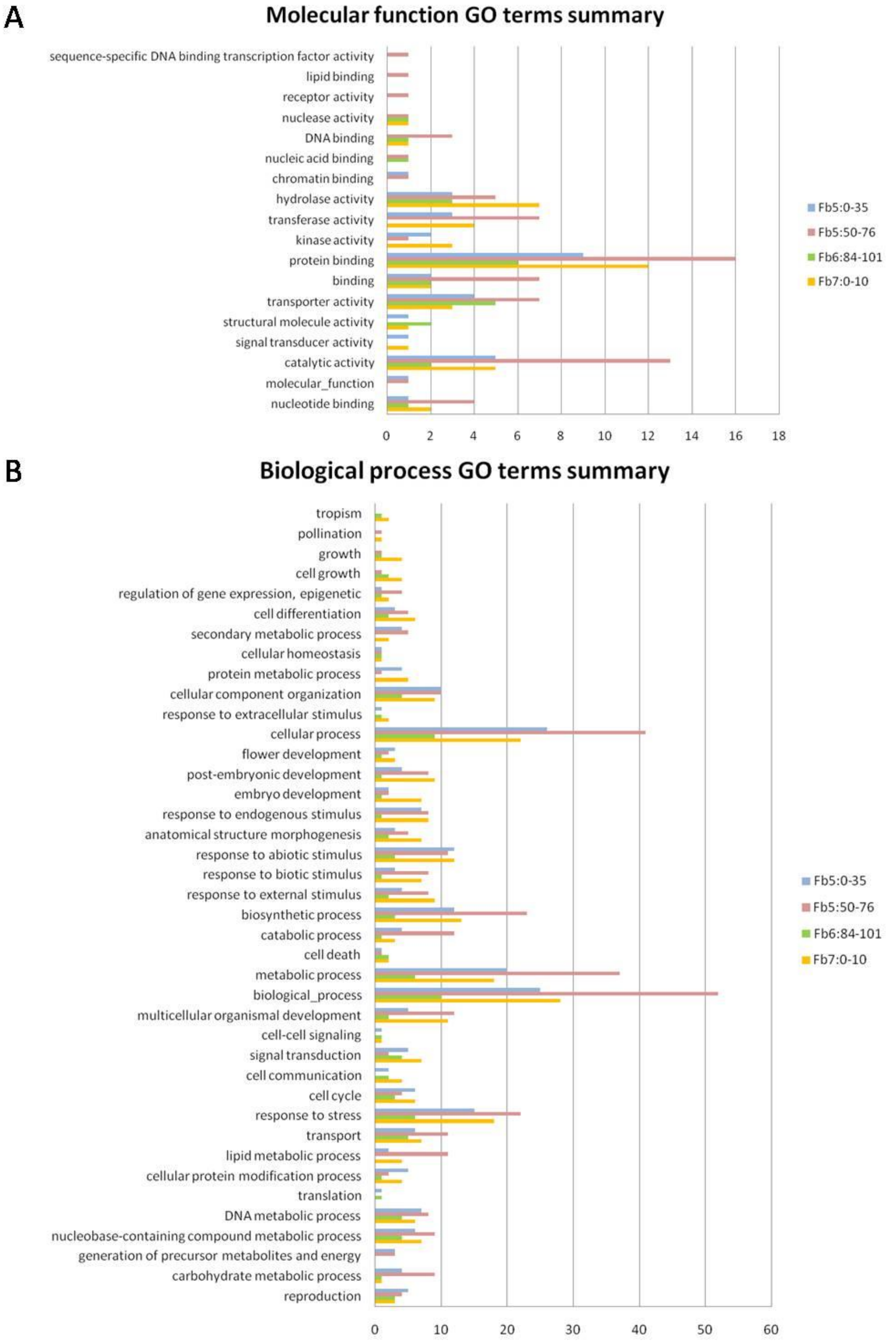
Functional annotation

Functional annotation of DEGs is crucial to determine which functions or biological pathways could be affected by the observed differences in expression. It was conducted for DEGs from a1 and those DEGs exclusively found in a2. Although predicted genes in annotation version 1 have a putative function assigned (Supplemental Table CIV.1), this information is not publicly available for a2. Therefore, these new functional annotation has the double objective of actualize and homogenize a1 and a2 DEGs functional annotations.

Table CIV.2 Differentially expressed genes (DEG) summary. Number total, up- and down-regulated DEG obtained with annotation version 1 (a1) and 2 (a2) for all four contrasting hypothesis (each NIL vs. RV). The number of common DEG between the two annotation versions and the number of DEG that were only detected with a2 and how many of them obtained significant blasts hits.

		a1				a2					
NIL vs. RV	**Introgression size (Mb)**	**DEG**	**blast homo logies**	**Up reg.**	**Down reg.**	**DEG**	**Up reg.**	**Down reg.**	**Comm. DEG**	**a2 specific DEG**	**a2 specific DEG blast homologies**
Fb5:0-35	6.51	260	234	109	151	257	106	151	134	123	102
Fb5:50-76	17.22	404	335	149	255	402	147	255	224	178	155
Fb6:84-101	6.60	190	159	100	90	167	82	85	109	58	49
Fb7:0-10	14.20	421	338	202	219	442	204	234	207	235	184

Figure CIV. 4 GO terms summary. Summary of GO terms associated with DEG, considering both a1 and a2 DEGs, in each NIL. **A:** GO terms summary for molecular function **B**: GO terms summary for biological process**.**



In first place, public plant-protein databases were inquired for predicted protein similarity using the *GoAnna* tool from Agbase (McCarthy *et al.* 2006). Significant blast hits were found for between 80 and 90% of the DEG detected using a1 and similar proportions (78-87%) were found for specific a2 DEGs. Therefore predicted functions and gene ontology terms (GO terms) were assigned to those genes.

In second place, GO terms were summarized in order to present a global view of DEGs predicted function (Figure CIV. 4) using *GoSlimViewer* from Agbase (McCarthy *et al.* 2006). GO terms summaries presented here belong to two main categories: molecular function and biological process. Some of the DEGs in the introgression lines were related with metabolic biological processes such as catabolic, biosynthetic and secondary metabolic processes and carbohydrate metabolic and lipid metabolic processes (Figure CIV. 4B). Along the same lines, several assigned GO terms for molecular function were related with metabolic functions such as catalytic, transferase, hydrolase and protein binding activity (Figure CIV. 4A). These suggesting that *F. bucharica* introgressions may have an effect over the metabolic machinery in *F. vesca* fruit. There were also an important number of DEGs related with responses to stress (biological process) and with transporter activity (molecular function).

In third place a GO term enrichment analysis for the up- and down-regulated DEG from each NIL was performed with MetGenMap (Joung *et al.* 2009) using a1 results. It revealed that our DEGs data sets had different numbers of GO enrichment terms (Table CIV.3). Up-regulated DEGs from the comparison between Fb**5**:0-35 and RV gave the higher number of enriched terms including among the most statistically relevant biological process related with phytoalexin metabolism (this includes (poly)-phenols synthesis), indole metabolism (derivated from anthranilate), ripening and defense response. It is also enriched in terpenoid metabolic process. Among the down regulated DEGs for Fb**5**:0-35 most enriched functions were related with (metal)ion-binding. Enriched GO terms for up regulated DEG in Fb**5**:50-76 are related with respiration and in Fb**6**:84-101 are related with glucosyl- glycosyl and glucuronsyltransferase activity and with the regulation of transcription factors. However DEG from Fb**7**:0-10 did not show any significant enrichment.

Finally, taken together all expression data, known metabolic *F. vesca* pathways that might be significantly affected by observed changes in expression levels were evaluated (Table CIV.4) using MetGenMap (Joung *et al.* 2009). This revealed that several pathways involved in volatile synthesis were probably affected by the differentially expressed genes in NIL. Instances of these affected pathways are: lipoxygenase pathway (13-LOX and 13-HPL pathway), terpene synthesis (farnesene, monoterpene and linalool synthesis pathways), amino acids biosynthesis (β-alanine and glutamine) and degradation (valine and asparagine) and sugars metabolism.

Table CIV. 3 GO terms enrichment. Significantly enriched GO terms for each set of DEG (one set for comparison NIL vs. RV)

Table CIV. 3

[a]BP= bioological process MF= molecular function

NIL vs. RV	DEGs reg.	GO term class[a]	GO term	GO term frequency in DEG	Genome frequency of use	p-value	adjusted p-value
Fb5:0-35	UP	BP	indole phytoalexin biosynthetic process	6,70%	0,50%	6,03E-07	0,00E+00
Fb5:0-35	UP	BP	indole metabolic process	6,70%	0,50%	6,03E-07	0,00E+00
Fb5:0-35	UP	BP	indole phytoalexin metabolic process	6,70%	0,50%	6,03E-07	0,00E+00
Fb5:0-35	UP	BP	phytoalexin biosynthetic process	6,70%	0,50%	1,75E-06	0,00E+00
Fb5:0-35	UP	BP	phytoalexin metabolic process	6,70%	0,60%	2,23E-06	0,00E+00
Fb5:0-35	UP	BP	camalexin biosynthetic process	5,80%	0,50%	9,30E-06	0,00E+00
Fb5:0-35	UP	BP	camalexin metabolic process	5,80%	0,50%	9,30E-06	0,00E+00
Fb5:0-35	UP	BP	ripening	7,70%	1,10%	1,93E-05	0,00E+00
Fb5:0-35	UP	BP	defense response	32,70%	16,20%	2,62E-05	0,00E+00
Fb5:0-35	UP	BP	indole derivative biosynthetic process	9,60%	1,90%	2,63E-05	0,00E+00
Fb5:0-35	UP	BP	response to biotic stimulus	32,70%	16,90%	5,85E-05	3,64E-03
Fb5:0-35	UP	BP	indole and derivative metabolic process	9,60%	2,10%	7,10E-05	5,00E-03
Fb5:0-35	UP	BP	indole derivative metabolic process	9,60%	2,10%	7,10E-05	4,62E-03
Fb5:0-35	UP	BP	response to other organism	28,80%	14,90%	2,00E-04	2,57E-02
Fb5:0-35	UP	BP	multi-organism process	33,70%	18,90%	2,60E-04	2,80E-02
Fb5:0-35	UP	BP	oxidation reduction	16,30%	6,30%	2,80E-04	2,63E-02
Fb5:0-35	UP	BP	response to fungus	14,40%	5,40%	4,60E-04	3,53E-02
Fb5:0-35	UP	BP	defense response to bacterium	16,30%	6,70%	5,50E-04	3,78E-02
Fb5:0-35	UP	BP	regulation of transcription from RNA polymerase II promoter	8,70%	2,20%	5,60E-04	3,58E-02
Fb5:0-35	UP	BP	terpenoid metabolic process	10,60%	3,30%	5,90E-04	3,70E-02
Fb5:0-35	UP	BP	heterocycle metabolic process	15,40%	6,30%	7,70E-04	4,95E-02
Fb5:0-35	DOWN	MF	hydroxyphenylacetonitrile 2-monooxygenase activity	3,60%	0,20%	7,74E-06	0,00E+00
Fb5:0-35	DOWN	MF	4-hydroxyphenylacetaldehyde oxime monooxygenase activity	3,60%	0,20%	7,74E-06	0,00E+00
Fb5:0-35	DOWN	MF	transition metal ion binding	24,30%	12,60%	1,10E-04	0,00E+00
Fb5:0-35	DOWN	MF	cation binding	27,10%	14,80%	1,10E-04	0,00E+00
Fb5:0-35	DOWN	MF	indoleacetaldoxime dehydratase activity	2,90%	0,20%	1,30E-04	0,00E+00
Fb5:0-35	DOWN	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	5,00%	0,90%	2,20E-04	3,33E-03
Fb5:0-35	DOWN	MF	metal ion binding	31,40%	18,80%	2,40E-04	5,71E-03
Fb5:0-35	DOWN	MF	ion binding	31,40%	19,50%	5,00E-04	2,25E-02
Fb5:0-35	UP	MF	hydroxyphenylacetonitrile 2-monooxygenase activity	6,70%	0,20%	1,29E-09	0,00E+00
Fb5:0-35	UP	MF	4-hydroxyphenylacetaldehyde oxime monooxygenase activity	6,70%	0,20%	1,29E-09	0,00E+00

Table CIV. 3

[a]BP= bioological process MF= molecular function

NIL vs. RV	DEGs reg.	GO term class[a]	GO term	GO term frequency in DEG	Genome frequency of use	p-value	adjusted p-value
Fb5:0-35	UP	MF	indoleacetaldoxime dehydratase activity	5,80%	0,20%	4,00E-08	0,00E+00
Fb5:0-35	UP	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	6,70%	0,90%	3,49E-05	5,00E-03
Fb5:0-35	UP	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	8,70%	2,10%	3,50E-04	4,80E-02
Fb5:0-35	UP	MF	tetrapyrrole binding	7,70%	1,80%	5,20E-04	4,57E-02
Fb5:0-35	UP	MF	lyase activity	9,60%	2,90%	8,90E-04	4,50E-02
Fb5:50-76	UP	BP	ATP synthesis coupled electron transport	6,30%	0,30%	1,26E-09	0,00E+00
Fb5:50-76	UP	BP	respiratory electron transport chain	7,10%	0,40%	1,49E-09	0,00E+00
Fb5:50-76	UP	BP	oxidative phosphorylation	6,30%	0,40%	4,23E-08	0,00E+00
Fb5:50-76	UP	BP	electron transport chain	7,90%	1,60%	4,10E-05	3,00E-02
Fb5:50-76	DOWN	MF	12-oxophytodienoate reductase activity	1,30%	0,00%	4,69E-05	0,00E+00
Fb5:50-76	UP	MF	glucose-6-phosphate dehydrogenase activity	2,40%	0,00%	1,32E-05	0,00E+00
Fb6:84-101	UP	BP	negative regulation of transcription factor activity	5,00%	0,40%	3,53E-05	0,00E+00
Fb6:84-101	UP	BP	negative regulation of DNA binding	5,00%	0,40%	5,06E-05	0,00E+00
Fb6:84-101	UP	BP	negative regulation of binding	5,00%	0,50%	9,90E-05	1,33E-02
Fb6:84-101	UP	MF	glucuronosyltransferase activity	4,00%	0,30%	1,30E-04	3,00E-02
Fb6:84-101	UP	MF	UDP-glucosyltransferase activity	6,00%	0,80%	1,50E-04	2,00E-02
Fb6:84-101	UP	MF	glucosyltransferase activity	6,00%	0,80%	1,70E-04	1,50E-02
Fb6:84-101	UP	MF	UDP-glycosyltransferase activity	7,00%	1,20%	2,60E-04	1,60E-02
Fb6:84-101	UP	MF	transcription cofactor activity	6,00%	1,10%	6,70E-04	4,67E-02

Table CIV. 4 Metabolic pathways affected. Metabolic pathways that are probably affected by the DEG detected in each NIL.

NIL vs. RV	pathway	p-value
Fb5:0-35	glutathione biosynthesis	1,51E-02
Fb5:0-35	ß-alanine biosynthesis I	1,58E-02
Fb5:0-35	farnesene biosynthesis	2,22E-02
Fb5:0-35	cis-zeatin biosynthesis	2,26E-02
Fb5:0-35	linalool biosynthesis	3,41E-02
Fb5:0-35	γ-glutamyl cycle	4,48E-02
Fb5:50-76	pentose phosphate pathway (oxidative branch)	6,05E-04
Fb5:50-76	jasmonic acid biosynthesis	1,66E-03
Fb5:50-76	pentose phosphate pathway	2,26E-03
Fb5:50-76	UDP-galactose biosynthesis (salvage pathway from galactose using UDP-glucose)	1,13E-02
Fb5:50-76	galactose degradation II	4,64E-02
Fb6:84-101	sucrose biosynthesis	3,69E-03
Fb6:84-101	DIMBOA-glucoside degradation	6,69E-03
Fb6:84-101	monoterpene biosynthesis	3,74E-02
Fb6:84-101	glutamine biosynthesis	4,20E-02
Fb6:84-101	alanine biosynthesis III	4,20E-02
Fb7:0-10	valine degradation I	7,67E-03
Fb7:0-10	divinyl ether biosynthesis II (13-LOX)	1,89E-02
Fb7:0-10	13-LOX and 13-HPL pathway	1,89E-02
Fb7:0-10	asparagine degradation I	3,38E-02
Fb7:0-10	homogalacturonan degradation	4,82E-02

Candidate genes

After the global functional characterization of the differentially expressed genes detected, a careful selection of candidate genes was addressed combining expression data with the metabolic QTL mapped in chap. II and III (Table CIV. 5).

Firstly it is noteworthy to mention that not all the specific a2 DEGs (Supplemental Table CIV. 2) are new gene models but re-annotations of genes present in a1. The majority of them are minor re-annotations that implied slight changes in coordinates or number of exons but with similar predicted functions with respect to the genes in annotation 1, but there are also major re-annotations that implied big changes in transcript size, position, fusion or separation of adjacent genes and/or transcript orientation. Minor re-annotations, although might have different names between the two annotations, are considered for the effects of this work as the same genes (Table CIV. 5). In many cases these minor re-annotations were similarly up- or down-regulated as their relatives in annotation a1 (Table CIV. 5A) but in other cases were differentially expressed only using annotation version 2 (Table CIV. 5B). There were also new gene models, and 16 of them were proposed as candidate genes (Table CIV. 5B).

Candidate genes for poly-phenols

mQTL related to (poly)phenolic compounds were in detail described in chap. II and several candidate genes (CG) located in *cis* were proposed as putatively involved in the observed phenotypes, in this section we will revise those candidate genes with the new RNA sequencing data (Supplemental Table CIV. 3) and will add other new putative candidate genes (Table CIV. 5).

Line with introgression at the beginning of LG5 (Fb**5**:0-35) harbors seven mQTL related with the under-accumulation of flavan-3-ols and one under accumulating p-coumaroyl-glucose ester. The genes *FaANS* (gene32347) and *FaANR* (gene24665) were highlighted as putative CG in Fb**5**:0-35 as their biochemically characterized function described by Almeida *et al.* (2007) may explain the mQTL diminishing flavan-3-ols accumulation in NILs with an introgression in this region. The RNAseq revealed that gene32347 was differentially up regulated in Fb**5**:0-35 compared with RV ($\log_2$(fold change) =1.75) (Table CIV. 5A) and harbors a total of six non-synonymous SNPs with respect to RV allele, two of them predicted as deleterious for protein fucntion (Supplemental Table CIV. 3) what supports its putative role as a CG. However the gene24665 did not present any significant difference in expression or sequence in Fb**5**:0-35 with respect to RV (Supplemental Table CIV. 3).

Fb**5**:50-76 gathers mQTL over-accumulating kaempferol- and kaempferol-coumaryl- glucosides and under accumulating anthocyanins, hydroxycinnamic acid derivatives and total (poly)phenols. In chap. II there were six genes highlighted as putative candidate genes. Four were predicted DFR (gene29344, gene31464, gene31465, gene02203), one was a predicted leucoanthocyanidin dioxygenase (gene22073) and another one was a predicted flavonol glucosyltransferase (gene13530). Among them, only the expression of gene31465 (also *in-silico* annotated as cinnamoyl-coA reductase), was strongly down regulated in Fb**5**:50-76 with respect to RV (log2 fold change =-6.25) (Table CIV. 5A). However the re-annotated gene in a2 (maker-LG5-augustus-gene-199.161-mRNA-1) is not differentially expressed. Looking carefully at this re-annotation, a2 merges gene31465 and gene31464 in one larger transcript. Our experimental data reveal that although some long-version transcripts were detected in RV, most of the transcripts correspond to the genes described in a1 alone, and Fb**5**:50-76 barely expressed few copies of the transcript corresponding to gene31465. Besides, *F. bucharica* allele presents an early stop codon that would produce a truncated protein of 200 aa instead the 321 aa of the *F. vesca* allele protein (Supplemental Table CIV. 3). These results maintain gene31465 as a good candidate gene for the observed mQTL. The rest of the evaluated genes in Fb**5**:50-76 were not differentially expressed with respect to RV but all of them had non-synonymous SNPs between the *F. bucharica* and the *F. vesca* alleles. Three of those changes derived into early stop codons that would produce truncated proteins in gene29344, gene31464 and gene22073. In addition one of the non-synonymous changes in gene02203 was predicted as potentially deleterious. In any case, further studies should be done in order to determine the effect of these mutations and maintain or discard those genes as CG (Supplmental Table CIV. 3).

(Poly)phenol mQTL in Fb**6**:84-101 are characterized for the under-accumulation of flavonoid glucosides, cinnamoyl-glucosides esters and total hydoxycinnamic acid derivatives. Two biochemically characterized glucosyltransferases were highlighted as putative candidate genes, gene26265 (FaGT2) and gene26344 (FaGT7), however none of them presented any evidence of difference in expression or sequence in Fb**6**:84-101 with respect to RV (Supplemental Table CIV. 3). Additionally, three genes that were associated to flavonoid glucosides accumulation in a previous study with an octoploid F_2 population (unpublished) were also proposed as candidate genes: gene24019, gene26403 (both *in-silico* annotated as GT) and gene28428 (putative DFR). From the three, only gene26403 was expressed, in small amounts, in the analyzed samples, and presented seven non-synonymous SNPs, four of them predicted as deleterious for protein function in the *F. bucharica* allele in comparison with RV allele (Supplemental Table CIV. 3). Finally three hypothetical cinnamyl alcohol dehydrogenases (gene24025, gene26301 and gene26302) were selected as putative CG. Gene26301 was not expressed in the analyzed samples and none of the other two was differentially expressed or presented differences in sequence between *F. bucharica* and *F. vesca* alleles. So, only one glycosyltransferase (gene26403) among the postulated CG in chap II for Fb**6**:84-101 mQTL seems to be a good candidate gene for the mapped mQTL and further studies should evaluate its real effect.

Several QTL for the under-accumulation of flavan-3-ols and flavanones were mapped in NIL Fb**7**:0-10. Attending to this phenotype, four biochemically characterized chalcone synthases (*FaCHS*, *FaCHS2*, *FaCHS3* and *FaCHS4*) that correspond to gene26825 and gene26826 were selected as candidate genes in Fb**7**:0-10. Although none of them were differentially expressed in Fb7:0-10 when compared with RV, both alleles of *F. bucharica* harbor non-synonymous SNPs predicted as deleterious for protein function (2 and 1 respectively) and one indel each in comparison with RV alleles (Supplemental Table CIV. 3), so they must be taken into account as candidate genes in future experiments.

The differential expression analysis revealed new candidate genes for (poly)phenolic mQTL not necessarily located in *cis*.

Interestingly, a putative 4-coumarate-CoA ligase (4CL) is down-regulated in Fb**7**:0-10 (gene12577), this enzyme acts very early in the phenylpropanoid pathway and may have important implications (Table CIV. 5). However there are not strong mQTL affecting (poly)phenol content in this NIL.

Three differentially expressed genes putatively involved in hydroxycinnamic acid derivatives metabolism were detected. Two of them in Fb**5**:50-76. The first one was an up-regulated probable cinnamyl alcohol dehydrogenase (gene08569) (Table CIV. 5A). The most similar protein in *A. thaliana* (CADH9_ARATH) catalyzes the final step for production of lignin monomers. The second one was a new gene model from a2 with a putative feruloyl-CoA hydroxylase function (snap_masked-LG5-processed-gene-250.75-mRNA-1) that was down-regulated in Fb**5**:50-76 (Table CIV. 5B). Both of them match with the general decrease in hydroxycinnamic acid derivatives in this NIL. Additionally, Fb**6**:84-101A presents a down-regulated caffeoyl-CoA O-methyltransferase (gene11384), whose more similar protein in *A. thaliana* (CAMT3_ARATH) is involved in methylation of caffeoyl-CoA to feruloyl-CoA.

Several differentially expressed genes probably involved in flavonoid modifications like glycosyltrasnferases and methyltransferases were detected (Table CIV. 5). Attending to flavonoid glycosyltransferases, the majority of them were detected in NIL Fb**6**:84-101 that was characterized by under-accumulating flavonoid glucosides. Surprisingly it presented four up-regulated putative glycosyltransferases, one detected by a1 (gene28196) two detected by a2 (maker-LG1-augustus-gene-184.198-mRNA-1 and maker-LG6-augustus-gene-376.214-mRNA-1) and one detected by both annotations and down-regulated in Fb**5**:0-35 (gene28200). There were also differentially expressed glycosyltransferases in other NIL: Two up-regulated in Fb**5**:0-35 (gene00094 and gene09619), two down-regulated in Fb**5**:50-76 (gene26881, maker-LG5-snap-gene-279.141-mRNA-1) and one down-regulated in Fb**7**.0-10 (augustus_masked-LG6-processed-gene-333.35-mRNA-1).

Regarding methyltransferases, a flavone methyltransferase (gene01858) and a flavonoid 3',5'-methyltransferase (gene12150) were down-regulated in Fb**5**:0-35 and Fb**5**:50-76 respectively (Table CIV. 5). In addition a down-regulated isoflavonoid malonyl transferase (snap_masked-LG7-processed-gene-78.70-mRNA-1) was detected in Fb**7**:0-10 using annotation version 2.

Candidate genes for volatile compounds

A hundred volatile compounds were identified in the *F. vesca* strawberry fruit in chap. III and many QTL explaining considerable percentages of their variability were mapped. The identified volatile compounds may arise from various metabolic pathways. The degradation of fatty acids through the lipoxygenase pathway or through α- or β- oxidation (Schwab & Schreier 2002) is the main source of plant volatile compounds including straight-chain alcohols, aldehydes, ketones, acids, esters and lactones. Terpenoids, which are important plant volatiles are synthesized from acetyl-coA and pyruvate by prenyl transferases and terpene synthases. Yet there are other sources of volatile compounds such as the degradation of branched-chain and aromatic amino acids and the carbohydrate-derived compounds.

All selected NIL (Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10) present QTL for fatty-acid derived volatiles. Main enzymes involved in the lipoxygenase pathway are lipoxygenase (LOX), hydroperoxydie lyase (HPL) that is an enzyme from the cytochrome P450 family CYP74B/C, 3Z, 2E-enal isomerase that has never been cloned and alcohol dehydrogenase (ADH)

Four differentially expressed lipoxygenases were consistently detected with both annotations. One of them, gene29184, was down-regulated in NIL Fb**5**:50-76 may explain the special under-accumulation of (*E*)-2- isomers of hexenal, nonenal and hexenyl acetate and the over accumulation of the (*Z*)-3-hexenal and (*Z*)-3-hexenyl acetate in this line. The remaining DE lipoxygenases were found in Fb**7**:0-10 and may be involved in the high number of volatile QTL mapped in this region. Two of them were down-regulated, gene23606 and gene26949, and one was up-regulated (gene32226) (Table CIV. 5).

Attending to other enzymes in the lipoxygenase pathway, twenty putative cytochrome P450 were differentially expressed (11 in Fb**5**:50-76, 9 in Fb**7**:0-10 and 1 in Fb**5**:50-76) but none of them were annotated as belonging to the CYP74B/C families (Supplemental Table CIV. 1). In addition no ADH or 3*Z*, 2*E*-enal isomerases were annotated among the differentially expressed genes.

The α- and β- oxidation of free fatty acids in plants is not completely understood. α-oxidation is mediated by a dual-function α-dioxygenase/peroxidise-NAD$^+$ oxidoreductase, that was not found among the differentially expressed genes. The β-oxidation liberates C_2 units (acetyl-coA) from the parent fatty acid to produce short- and medium-chain linear carboxylic acids by the action of an acyl-coA hydrolase. NIL Fb**7**:0-10 showed two down-regulated acyl-coA hydrolases, gene05329 and gene09200, whose more similar protein in *A. thaliana* (HIBC1_ARATH) is indirectly involved in benzoic acid biosynthesis (Table CIV. 5). Therefore they might be candidate genes for the observed QTL in Fb**7**:0-10 that under-accumulate methyl benzoate and methyl 2-aminobenzoate.

Acyltransferases are basic enzymes in the synthesis of esters and NIL Fb**5**:0-35 and Fb**7**:0-10 harbor several QTL related with ester accumulation. Fb**7**:0-10 showed three up-regulated (gene19411, gene23453 and gene34009) and three down-regulated (gene34011, gene19766 and maker-LG7-snap-gene-129.164-mRNA-1) acyl-transferases (Table CIV. 5). While, Fb**5**:0-35 showed only one down-regulated acyl-transferase (gene09934).

Additionally, there were two DEGs in Fb**7**:0-10 specific from a2 annotation involved in lipid metabolism (Table CIV. 5B). One of them is a new gene model, a probable carboxylesterase (augustus_masked-LG7-processed-gene-45.13-mRNA-1) whose closest protein in *A. thaliana* (CXE20_ARATH) acts on esters with a varying acyl chain length. The other one is a non-specific lipid-transfer protein (maker-LG6-augustus-gene-114.104-mRNA-1) whose more similar protein in *A. thaliana* (NLTP1_ARATH) transfers phospholipids and galactolipids across membranes.

Terpenoids are a big and diverse family of compounds. The majority of terpenoids produced are not volatiles, and are involved in important plant processes such as photosynthesis (carotenoids), growth regulation (brassinosteroids, gibberellins) or membrane structure (sterols). Volatile terpenoids identified include six monoterpenes (C_{10}) and two sesquiterpenes (C_{15}). Several QTL for terpenoids accumulation are harbored in NIL Fb**5**:0-35 (α-pinene), NIL Fb**5**:50-76 (myrtenol and nerol) and NIL Fb**7**:0-10 (limonene and myrtenol). Genes annotated as terpene or sesquiterpene synthases were also differentially expressed in all three NIL and could therefore be involved in the observed QTL. Fb**5**:0-35 gathers, two up-regulated (gene09971 and gene09977) and one down regulated (gene09972) putative sesquiterpene synthases. Fb**5**:50-76 join a down regulated sesquiterpene synthase (gene12094) and Fb**7**:0-10 harbors a terpene synthase (gene23886) that is up-regulated (Table CIV. 5A). Other re-annotated terpene synthases were detected as differentially expressed using a2. In NIL Fb**5**:0-35 we found one up-regulated putative monoterpene synthase (maker-LG4-augustus-gene-136.257-mRNA-1) whose more similar protein homologue is a monoterpene synthase from *Mentha piperita* (MFS_MENPI). In addition there was also a putative adenylate isopentenyltransferase (augustus_masked-LG2-processed-gene-150.11-mRNA-1) that was down-regulated in NIL Fb**5**:0-35 and Fb**7**:0-10 and one down-regulated diterpene synthase (maker-LG5-augustus-gene-136.110-mRNA-1) in Fb**5**:50-76 (Table CIV. 5B).

Although degradation of amino acids leads to production of high number of volatile compounds, their pathways are still largely unknown. In the analyzed samples we could identify five differentially expressed genes involved in amino acids metabolism. Two of them were putative arginosuccinate synthases, gene09887 under-regulated in Fb**5**:0-35 and gene11807 up-regultaed in Fb**5**:50-76. Other two were up-regulated tryptophan synthases, gene03800 in Fb**6**:84-101 and gene03242 in Fb**7**:0-10 that could be involved in the QTL for volatile compounds with a benzoic ring. Finally one annotated serine hydroxymethyltransferase (gene11045) down-regulated in Fb**5**:50-76 and Fb**7**:0-10 (Table CIV. 5A) that is probably involved in the interconversion of serine and glycine.

Additionally, attending to amino acids metabolism we also detected new differentially expressed genes specifically using a2. In NIL Fb**7**:0-10 we found a strongly up-regulated putative hydroxyisobutyryl-CoA hydrolase (augustus_masked-LG7-processed-gene-21.17-mRNA-1) probably involved in valine catabolism. Two putative amino acid permeases (maker-LG5-augustus-gene-177.104-mRNA-1 and maker-LG5-snap-gene-226.119-mRNA-1) are down-regulated in Fb**5**:50-76. Finally a putative Isoleucine monooxygenase (maker-LG6-est_gff_Cufflinks-gene-378.6-mRNA-1) was down-regulated in Fb**6**:84-101.

Furanones and pyrones are the main volatile compounds derived from carbohydrates. Only four furanones and no pyrones were detected in the metabolic analysis and only two QTL are mapped among the selected NIL for these comopounds. Fb**7**:0-10 has two QTL for the under-accumulation of 2,1-pentenyl furan and 2-pentylfuran. However, as no enzymes have been described in their synthesis pathway, no candidate genes were highlighted for their accumulation.

Transcription factors

Finally, several transcription factors (TF) were differentially expressed in NIL Fb**5**:0-35, Fb**5**:50-76 and Fb**7**:0-10 with respect to RV. As alterations in TF can have wide range effects, all of them are considered putative candidate genes.

Two of the differentially expressed TF might be involved in the (poly)-phenolic biosynthesis (Table CIV. 5). Gene32494, annotated as TF GLABRA 3, is up-regulated in Fb**5**:0-35 and its more similar protein in *A. thaliana,* (GL3_ARATH), plays a role in the activation of anthocyanin biosynthesis. Gene25060, annotated as transcription factor TT2 , is down-regulated in Fb**5**:50-76 and its closest protein in *A. thaliana* has shown to be involved in the control of flavonoid late metabolism and plays a key role in determining the tissue-specific activation of leucoanthocyanidin reductase.

Another TF might be related with terpenoid synthesis (Table CIV. 5B). It is a putative MYC2 TF in that is up-regulated in Fb**7**:0-10 (maker-LG7-snap-gene-91.103-mRNA-1) whose closets relative in *A. thaliana,* (MYC2_ARATH), has shown to be related with sesquiterpene biosynthesis among other functions.

Interestingly a putative transcription factor SAC51 (snap_masked-LG5-processed-gene-244.64-mRNA-1) that is up-regulated in Fb**5**:50-76 has been shown to be involved in stem elongation in *A. thaliana* (SAC51_ARATH), and close to this region there is a QTL for flowering shoots stem length (Urrutia *et al.* 2015).

Other differentially expressed transcription factors that are supposed to be related to general developmental or basic regulation function in the plant were detected with annotation version 1 (Supplemental Table CIV. 1). Transcription factors TFIID (gene06413), probably involved in regulation of RNA polymerase transcription and LEC2 (gene10539), probably involved in embryogenesis and germination are down regulated in Fb**5**:0-35. Finally transcription factors GTE11 (gene04933), bHLH91 (gene09222) and UNE10 (gene26073) are up-regulated in Fb**7**:0-10 (Supplemental Table CIV. 1).

Additional differentially expressed transcription factors were detected with annotation version 2. These were concentrated in Fb**7**:0-10 And were mainly down-regulated: two putative VRN1 TFs probably involved in vernalization, one transcription initiation factor TFIID, probably involved in negative regulation of cytokinin sensitivity, a putative REVEILLE TF and one NAC domain TF among others. There is also a putative transcription initiation factor IIF up-regulated in Fb**5**:50-76 and a putative TCP13 TF down-regulated in Fb**6**:84-101.

In addition it is noteworthy mention that there were 313 differentially expressed genes whose function could not be assigned by sequence similarity. Therefore we cannot discard these genes as having important functions involved with the observed phenotypes (Supplemental Table CIV. 1 and 3).

Table CIV. 5 DEG candidate genes. A: list of all DEG using a1 is provided for each contrasting hypothesis (NIL vs. RV). **B:** list of DEG specifically found using a2

Table CIV. 5A

	annotation a1							annotation a2				
comparison vs. RV	**gene id[a]**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**blast hit[c]**	**blast hit protein description**	**predicted function in reference annotation (a1)**	**equivalent in a2**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**common DEG a1 & a2**
Fb5:0-35	gene09934	-11,82	4,56E-44	8,49E-40	F4JBC7_ARATH	HXXXD-type acyl-transferase-like protein	Vinorine synthase (probable)	mrna09934.1	-11,81	1,33E-39	2,51E-34	YES
Fb5:0-35	gene09972	-4,35	4,06E-15	2,16E-12	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	maker-LG4-snap-gene-135.249-mRNA-1	-2,09	2,79E-05	3,74E-03	YES
Fb5:0-35	gene28200	-1,76	7,98E-05	9,25E-03	U87A1_ARATH	UDP-glycosyltransferase 87A1	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (probable)	maker-LG3-augustus-gene-206.156-mRNA-1	-1,78	5,27E-05	6,34E-03	YES
Fb5:0-35	gene32494	1,68	6,21E-04	5,20E-02	GL3_ARATH	Transcription factor GLABRA 3	Transcription factor GLABRA 3 (bHLH 1) (putative)	mrna32494.1	1,70	3,89E-04	3,48E-02	YES
Fb5:0-35	gene32347	1,75	5,82E-04	4,91E-02	LDOX_ARATH	Leucoanthocyanidin dioxygenase	Leucoanthocyanidin dioxygenase (LDOX) (putative)	mrna32347.1	1,79	3,26E-04	3,00E-02	YES
Fb5:0-35	gene00094	1,90	4,00E-04	3,58E-02	U73D1_ARATH	UDP-glycosyltransferase 73D1	Cytokinin-O-glucosyltransferase 3 (AtZOG3) (probable)	mrna00094.1	1,97	2,52E-04	2,43E-02	YES
Fb5:0-35	gene09887	-Inf	6,03E-06	9,29E-04	ASSY_ARATH	Argininosuccinate synthase, chloroplastic	Argininosuccinate synthase, chloroplastic, Precursor (similar to)	mrna09887.1	-Inf	5,66E+00	9,07E-04	YES
Fb5:50-76	gene11045	-Inf	9,07E-38	2,82E-34	GLYC7_ARATH	Serine hydroxymethyltransferase 7	Serine hydroxymethyltransferase 2 (SHMT 2) (probable)	maker-LG5-snap-gene-206.105-mRNA-1	-Inf	7,96E-39	3,77E-35	YES
Fb5:50-76	gene25060	-9,08	3,22E-19	1,40E-16	TT2_ARATH	Transcription factor TT2	Transcription factor TT2 (AtMYB123) (similar to)	augustus_masked-LG3-processed-gene-116.16-mRNA-1	-9,02	4,85E-21	2,78E-18	YES

Table CIV. 5A

	annotation a1							annotation a2				
comparison vs. RV	**gene id[a]**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**blast hit[c]**	**blast hit protein description**	**predicted function in reference annotation (a1)**	**equivalent in a2**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**common DEG a1 & a2**
Fb5:50-76	gene12150	-4,27	9,05E-12	1,67E-09	FAOMT_VITVI	Flavonoid 3',5'-methyltransferase	Putative caffeoyl-CoA O-methyltransferase At1g67980 (CCoAOMT)	mrna12150.1	-4,21	1,08E-05	2,04E-03	YES
Fb5:50-76	gene26881	-2,35	2,95E-06	2,80E-04	I7GT1_SOYBN	Isoflavone 7-O-glucosyltransferase 1	Anthocyanidin 5,3-O-glucosyltransferase (probable)	mrna26881.1	-2,35	2,34E+00	2,25E-04	YES
Fb5:50-76	gene08569	1,73	5,11E-04	2,85E-02	CADH9_ARATH	Probable cinnamyl alcohol dehydrogenase 9	Probable cinnamyl alcohol dehydrogenase 6 (OsCAD6) (putative)	maker-LG2-snap-gene-191.317-mRNA-1	1,73	4,16E-04	2,42E-02	YES
Fb5:50-76	gene11807	1,78	1,81E-04	1,17E-02	ASSY_ARATH	Argininosuccinate synthase, chloroplastic	Argininosuccinate synthase, chloroplastic, Precursor (putative)	genemark-LG5-processed-gene-215.72-mRNA-1	1,75	1,85E-04	1,20E-02	YES
Fb5:50-76	gene29184	-Inf	1,22E-04	8,37E-03	LOXC2_ORYSJ	Probable lipoxygenase 8, chloroplastic	Probable lipoxygenase 8, chloroplastic, Precursor (similar to)	maker-LG5-snap-gene-197.135-mRNA-1	-Inf	1,60E-04	1,05E-02	YES
Fb5:50-76	gene30007	-Inf	1,87E-23	1,20E-20	Q9STI1_ARATH	Putative flavonoid 3',5'-hydroxylase	Cytochrome P450 93A3 (probable)	maker-LG5-augustus-gene-275.181-mRNA-1	-3,94	1,50E-07	1,75E-05	YES
Fb6:84-101	gene28200	5,46	5,53E-22	7,37E-19	U87A1_ARATH	UDP-glycosyltransferase 87A1	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (probable)	maker-LG3-augustus-gene-206.156-mRNA-1	5,46	1,56E-22	2,10E-19	YES
Fb7:0-10	gene09200	-9,07	4,30E-32	1,34E-28	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (HIB-CoA hydrolase), Precursor (probable)	maker-LG7-augustus-gene-88.90-mRNA-1	-3,90	4,37E-13	9,30E-11	YES
Fb7:0-10	gene11045	-1,95	5,96E-05	4,35E-03	GLYC7_ARATH	Serine hydroxymethyltransferase 7	Serine hydroxymethyltransferase 2 (SHMT 2) (probable)	maker-LG5-snap-gene-206.105-mRNA-1	-1,97499478	3,70E-05	2,70E-03	YES
Fb7:0-10	gene23606	-6,85	1,24E-14	3,45E-12	LOX2_ORYSJ	Linoleate 9S-lipoxygenase 2	3-deoxy-manno-octulosonate cytidylyltransferase (CKS) (similar to)	mrna23606.1	-6,30	2,84E-11	8,55E-10	YES

Table CIV. 5A

	annotation a1							annotation a2				
comparison vs. RV	**gene id[a]**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**blast hit[c]**	**blast hit protein description**	**predicted function in reference annotation (a1)**	**equivalent in a2**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**common DEG a1 & a2**
Fb7:0-10	gene34011	-6,02	1,38E-25	1,52E-22	F4JBC7_ARATH	HXXXD-type acyl-transferase-like protein	BAHD acyltransferase At5g47980 (probable)	mrna34011.1	-6,01	4,06E-20	2,74E-17	YES
Fb7:0-10	gene05329	-5,23	3,51E-10	6,56E-08	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (HIB-CoA hydrolase), Precursor (probable)	maker-LG3-augustus-gene-99.141-mRNA-1	-5,22	2,93E-10	4,85E-08	YES
Fb7:0-10	gene26949	-3,94	3,76E-10	6,82E-08	LOXC2_ORYSJ	Probable lipoxygenase 8, chloroplastic	Probable lipoxygenase 8, chloroplastic, Precursor (similar to)	augustus_masked-LG7-processed-gene-56.12-mRNA-1	-4,02	1,56E-10	2,72E-08	YES
Fb7:0-10	gene26949	-3,94	3,76E-10	6,82E-08	LOXC2_ORYSJ	Probable lipoxygenase 8, chloroplastic	Probable lipoxygenase 8, chloroplastic, Precursor (similar to)	augustus_masked-LG7-processed-gene-56.13-mRNA-1	-3,51	6,02E-09	8,65E-07	YES
Fb7:0-10	gene12577	-1,56	1,82E-03	8,32E-02	4CL3_ARATH	4-coumarate--CoA ligase 3	4-coumarate--CoA ligase 2 (4CL 2) (putative)	mrna12577.1	-1,54	1,75E-03	7,71E-02	YES
Fb7:0-10	gene23886	1,87	1,86E-03	8,43E-02	TPS10_RICCO	Terpene synthase 10	Myrcene synthase, chloroplastic, Precursor (probable)	maker-LG6-augustus-gene-341.179-mRNA-1	1,86	1,53E-03	6,87E-02	YES
Fb7:0-10	gene19411	2,86	1,45E-03	6,95E-02	ZDH14_ARATH	Probable protein S-acyltransferase 14	Probable S-acyltransferase At3g60800 (putative)	augustus_masked-LG7-processed-gene-50.27-mRNA-1	2,83	1,59E-03	7,05E-02	YES
Fb7:0-10	gene32226	3,30	2,63E-04	1,60E-02	LOX2_ARATH	Lipoxygenase 2, chloroplastic	Lipoxygenase 2, chloroplastic (AtLOX2), Precursor (similar to)	maker-LG5-augustus-gene-34.145-mRNA-1	3,14	5,88E-04	3,12E-02	YES
Fb7:0-10	gene03242	8,83	6,85E-14	1,73E-11	O04225_ORYSA	Tryptophan synthase B	Zinc finger MYM-type protein 5 (probable)	mrna03242.1	8,82	5,44E-08	1,26E-05	YES
Fb7:0-10	gene23453	10,79	9,58E-26	1,12E-22	O23392_ARATH	HXXXD-type acyl-transferase family protein	Vinorine synthase (probable)	mrna23453.1	11,01	2,67E-20	2,02E-17	YES
Fb7:0-10	gene34009	13,10	9,76E-40	6,08E-36	F4JBC7_ARATH	HXXXD-type acyl-transferase-like protein	Vinorine synthase (probable)	mrna34009.1	13,29	3,28E-39	6,22E-35	YES

Table CIV. 5A

	annotation a1							annotation a2				
comparison vs. RV	**gene id[a]**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**blast hit[c]**	**blast hit protein description**	**predicted function in reference annotation (a1)**	**equivalent in a2**	**log$_2$(fold change)[b]**	**p-value**	**p-adjusted**	**common DEG a1 & a2**
Fb5:0-35	gene01858	-4,67	5,62E-18	4,19E-15	OMT1_ARATH	Flavone 3'-O-methyltransferase 1	Caffeic acid 3-O-methyltransferase (CAOMT) (putative)	snap_masked-LG5-processed-gene-55.125-mRNA-1	0.4944664	-1,02E+00	2,55E-01	NO
Fb5:0-35	gene09619	1,84	1,23E-03	9,05E-02	U86A1_ARATH	UDP-glycosyltransferase 86A1	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (probable)	maker-LG6-augustus-gene-90.165-mRNA-1	-0,08	9,20E-01	1,00E+00	NO
Fb5:0-35	gene09977	3,53	5,13E-10	1,59E-07	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	augustus_masked-LG4-processed-gene-136.60-mRNA-1	1,32	8,67E-03	3,64E-01	NO
Fb5:0-35	gene09971	8,07	4,86E-29	1,13E-25	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	maker-LG4-snap-gene-135.249-mRNA-1	-2,09	2,79E-05	3,74E-03	NO
Fb5:50-76	gene12094	-6,59	7,53E-12	1,41E-09	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	maker-LG5-snap-gene-245.175-mRNA-1	-1,83	3,66E-03	1,60E-01	NO
Fb5:50-76	gene31465	-6,25	1,22E-22	7,11E-20	O22809_ARATH	Putative cinnamoyl-CoA reductase	Dihydroflavonol-4-reductase (DFR) (probable)	maker-LG5-augustus-gene-199.161-mRNA-1	0,07	9,10E-01	1,00E+00	NO
Fb6:84-101	gene11384	-3,62	2,80E-10	1,11E-07	CAMT3_ARATH	Probable caffeoyl-CoA O-methyltransferase At4g26220	Probable caffeoyl-CoA O-methyltransferase At4g26220 (CCoAOMT) (similar to)	maker-LG1-snap-gene-46.193-mRNA-1	0,07	9,55E-01	1,00E+00	NO
Fb6:84-101	gene28196	2,23	1,29E-04	1,68E-02	U87A2_ARATH	UDP-glycosyltransferase 87A2	hypothetical protein	maker-LG3-snap-gene-206.210-mRNA-1	-0,53	4,96E-01	1,00E+00	NO
Fb6:84-101	gene03800	2,59	3,89E-07	9,32E-05	Q9FFW8_ARATH	Tryptophan synthase beta chain	Tryptophan synthase beta chain 2 (similar to)	maker-LG6-augustus-gene-323.219-mRNA-1	-0,05	9,35E-01	1,00E+00	NO

Table CIV. 5A

	annotation a1						annotation a2				
comparison vs. RV	gene id[a]	$\log_2$(fold change)[b]	p-value	p-adjusted	blast hit[c]	blast hit protein description	predicted function in reference annotation (a1)	equivalent in a2	$\log_2$(fold change)[b]	p-value	p-adjusted	common DEG a1 & a2
Fb7:0-10	gene19766	-3,99	1,39E-04	9,17E-03	ASAT1_ARATH	Acyl-CoA--sterol O-acyltransferase 1	Probable long-chain-alcohol O-fatty-acyltransferase 5	maker-LG3-augustus-gene-10.249-mRNA-1	0,44	3,61E-01	1,00E+00	NO

Table CIV. 5B

comparison	gene id[d]	$\log_2$(fold change)[b]	p-value	p-adjusted	blast hit[b]	blast hit protein description	equivalent a1
Fb7:0-10	augustus_masked-LG3-processed-gene-102.20-mRNA-1	-2,29879304	6,74E-06	5,72E-04	ERF61_ARATH	Ethylene-responsive transcription factor ERF061	NO
Fb7:0-10	augustus_masked-LG7-processed-gene-126.10-mRNA-1	-6,68703269	2,99E-05	2,20E-03	TA12B_ARATH	Transcription initiation factor TFIID subunit 12b	NO
Fb7:0-10	augustus_masked-LG7-processed-gene-21.17-mRNA-1	Inf	3,17E-05	2,33E-03	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1	NO
Fb7:0-10	augustus_masked-LG7-processed-gene-45.13-mRNA-1	-3,10444741	1,59E-05	1,27E-03	CXE20_ARATH	Probable carboxylesterase 120	NO
Fb7:0-10	genemark-LG7-processed-gene-22.65-mRNA-1	-1,75110007	1,91E-04	1,19E-02	F4JW79_ARATH	Kow domain-containing transcription factor 1	NO
Fb5:50-76	maker-LG1-snap-gene-199.180-mRNA-1	3,52222995	4,85E-04	2,79E-02	Q9LQZ4_ARATH	Transcription initiation factor IIF, beta subunit	NO
Fb5:0-35	maker-LG4-augustus-gene-138.110-mRNA-1	-Inf	1,76E-10	6,05E-08	PAT1_ARATH	Scarecrow-like transcription factor PAT1	NO
Fb5:50-76	maker-LG5-augustus-gene-177.104-mRNA-1	-2,7687312	7,92E-07	8,28E-05	AAP5_ARATH	Amino acid permease 5	NO
Fb5:50-76	maker-LG5-snap-gene-279.141-mRNA-1	-8,18975802	9,67E-18	3,81E-15	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	NO
Fb6:84-101	maker-LG6-est_gff_Cufflinks-gene-378.6-mRNA-1	-9,92773994	5,94E-27	1,25E-23	C79D4_LOTJA	Isoleucine N-monooxygenase 2	NO
Fb7:0-10	maker-LG7-augustus-gene-26.89-mRNA-1	-9,50450667	1,23E-38	5,84E-35	RVE6_ARATH	Protein REVEILLE 6	NO
Fb7:0-10	maker-LG7-augustus-gene-8.110-mRNA-1	6,4407235	4,87E-22	2,37E-19	NAC86_ARATH	NAC domain-containing protein 86	NO
Fb7:0-10	maker-LG7-snap-gene-1.135-mRNA-1	-Inf	5,34E-04	2,88E-02	F4KGA3_ARATH	Putative PHD finger transcription factor	NO

Table CIV. 5B

comparison	gene id[d]	$\log_2$(fold change)[b]	p-value	p-adjusted	blast hit[b]	blast hit protein description	equivalent a1
Fb5:50-76	snap_masked-LG5-processed-gene-244.64-mRNA-1	1,54127767	9,18E-04	4,94E-02	SAC51_ARATH	Transcription factor SAC51	NO
Fb5:50-76	snap_masked-LG5-processed-gene-250.75-mRNA-1	-Inf	2,01E-03	9,50E-02	F6H1_ARATH	Feruloyl CoA ortho-hydroxylase 1	NO
Fb7:0-10	snap_masked-LG7-processed-gene-42.93-mRNA-1	-7,15467096	2,77E-09	4,07E-07	VRN1_ARATH	B3 domain-containing transcription factor VRN1	NO
Fb7:0-10	snap_masked-LG7-processed-gene-78.70-mRNA-1	-3,48706127	1,16E-04	7,59E-03	B4Y0U0_MEDTR	Isoflavonoid malonyl transferase 1	gene29347
Fb5:50-76	augustus_masked-LG5-processed-gene-279.16-mRNA-1	-2,25057974	1,83E-05	1,51E-03	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	gene28678
Fb6:84-101	maker-LG6-augustus-gene-376.214-mRNA-1	7,23359433	1,01E-31	4,79E-28	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	gene28033
Fb7:0-10	augustus_masked-LG2-processed-gene-150.11-mRNA-1	-1,82545893	2,11E-03	9,13E-02	IPT3_ARATH	Adenylate isopentenyltransferase 3, chloroplastic	gene27842
Fb5:50-76	maker-LG5-augustus-gene-136.110-mRNA-1	-Inf	1,95E-28	1,67E-25	TPS4_SELML	Bifunctional diterpene synthase, chloroplastic	gene27679
Fb5:50-76	maker-LG5-snap-gene-226.119-mRNA-1	-2,25829565	3,28E-04	1,97E-02	AAP6_ARATH	Amino acid permease 6	gene26913
Fb5:0-35	augustus_masked-LG6-processed-gene-175.2-mRNA-1	1,61808236	5,65E-04	4,81E-02	EIF3C_ARATH	Eukaryotic translation initiation factor 3 subunit C	gene18007
Fb7:0-10	augustus_masked-LG6-processed-gene-175.2-mRNA-1	-1,56037683	1,31E-03	6,03E-02	EIF3C_ARATH	Eukaryotic translation initiation factor 3 subunit C	gene18007
Fb6:84-101	maker-LG1-augustus-gene-184.198-mRNA-1	7,14408087	2,35E-24	4,45E-21	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	gene16276
Fb7:0-10	maker-LG6-augustus-gene-114.104-mRNA-1	6,65451325	1,30E-14	3,27E-12	NLTP1_ARATH	Non-specific lipid-transfer protein 1	gene14445
Fb5:50-76	mrna13530.1	1,50727919	1,99E-03	9,46E-02	U73B3_ARATH	UDP-glycosyltransferase 73B3	gene13530
Fb5:0-35	maker-LG4-augustus-gene-136.257-mRNA-1	3,97052263	2,44E-12	9,39E-10	MFS_MENPI	(+)-menthofuran synthase	gene09988
Fb7:0-10	maker-LG7-snap-gene-91.103-mRNA-1	3,34759687	3,42E-05	2,50E-03	MYC2_ARATH	Transcription factor MYC2	gene09222
Fb7:0-10	maker-LG7-augustus-gene-95.135-mRNA-1	-1,78914326	2,12E-04	1,29E-02	VRN1_ARATH	B3 domain-containing transcription factor VRN1	gene07345
Fb7:0-10	augustus_masked-LG6-processed-gene-333.35-mRNA-1	-1,88054587	1,11E-04	7,30E-03	U88A1_ARATH	UDP-glycosyltransferase 88A1	gene04359

Table CIV. 5B

comparison	gene id[d]	$\log_2$(fold change)[b]	p-value	p-adjusted	blast hit[b]	blast hit protein description	equivalent a1
Fb6:84-101	maker-LG6-augustus-gene-328.155-mRNA-1	-1,9544496	5,64E-04	6,68E-02	TCP13_ARATH	Transcription factor TCP13	gene04255
Fb7:0-10	maker-LG7-snap-gene-129.164-mRNA-1	-Inf	7,03E-08	8,53E-06	ZDH22_ARATH	Protein S-acyltransferase 24	gene00424

Discussion

Differences between NIL

A set of four phenotypically different NILs in terms of volatile and (poly)-phenolic metabolite accumulation were selected for a transcriptomic analysis with the aim of finding out if those differences were also evident at transcript level. In a first approach, genes specifically expressed by one of the lines indicated that there were substancial differences in gene expression between the selected genotypes (Figure CIV. 1). Further exploratory analysis by principal components clustered samples from different genetic origins in different groups these highlighting that there were different expression patterns between the lines (Figure CIV. 2). However NIL Fb**6**:84-101 and RV clustered together. Line Fb**6**:84-101 has a relatively small introgression from F. bucharica and the QTL mapped in this line are less statistically significant among the NIL selected for the transcriptome analysis, these led us to think that the phenotypical differences it was chosen for might come from small differences in expression levels or from other more subtile changes that are undetectable with a whole transcriptomic differential expression analysis. Finally, the detection of specific differentially expressed genes in all NIL compared with RV indicates that the *F. bucharica* introgressions in the *F. vesca* genetic background has an effect over the levels and patterns of gene expression that might affect metabolic pathways resulting in phenotypic differences in terms of metabolite accumulation.

Mapping quality

Proportion of filtered reads mapped to the *F. vesca* v1.1 genome (88%-91% of filtered reads) was high in comparison of that published by other studies (79.6%) (Kang *et al.* 2013). In addition the proportion of reads mapping to coding sequences was also higher in our study (69-73%) when compared with that of Kang *et al.* (2013) (62.6%). Multiple reasons could be beneath these discrepancies, from the method to prepare and sequence the cDNA libraries, as they used 51 bp single-end reads and we used 75bp paired-ends, the different types of tissue sequenced, as they did not use ripe fruits, to the alignment software, as they used Bowtie v1.0 and we used Bowtie v2.0 and Tophat v2.0.11. In any case, the percentage of reads mapping in non coding sequences in both studies suggests that many genes are still un-annotated in the *F. vesca* reference genome. The publication of a new annotation version (a2) based in whole transcriptome sequencing data (Darwish *et al.* 2015) improved by 2% the percentage of reads mapping to exonic regions. As ripe fruit transcriptome was not included in the new annotation version, the small improvement rate in coding sequence mapping might indicate that there are genes specifically expressed in the ripe stage not present in other tissues or developmental stages. Besides the new version of the annotation was performed with the white-fruited variety of *F. vesca* 'Yellow Wonder' which may also express different set of genes. Therefore, we think that further insights in the transcriptomic data generated by this experiment may also contribute to improve *F. vesca* annotation.

The number of commonly expressed genes between all the analyzed lines in this study (19574) was similar to that found between different tissues and developmental stages by Kang *et al.* (2013) (19236) what may indicate that a high percentage of the genes are basally expressed.

Functional annotation and differentially expressed genes

Differences in expression levels between the NIL (Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101 and Fb**7**:0-10) and their recurrent parental *F. vesca* var. 'Reine des vallées' led to the proposal of four sets of differentially expressed genes. The study of the putative functions associated to these DEG in each NIL revealed that in many cases they were associated with metabolic processes and also with defense responses (Figure CIV. 4), both of these activities might be in agreement with the observed changes in volatile and (poly)-phenolic composition in the studied NIL as these compounds have a function in resistence to biotic and abiotic stress (Gould & Lister 2006). However as the introgressed regions in the selected NIL cover several Mb, there were also DEG with predicted functions no related with the studied phenotypes but that may have other effects in the plant machinery. The use of an integrative tool like MetGenMap allowed prediction of metabolic pathways that may be affected by the DEG detected. Interestingly several of this putatively affected pathways were involved in terpene biosynthesis, fatty acids degradation or sugar metabolism (Table CIV. 3) what suggests that DEG are truly related with the observed QTL.

From all DEG detected, around 50% of them matched between a1 and a2 (Supplemental Table CIV. 1). Although this may seem a low agreement rate, there are in fact "masked" common DEG, as in many cases predicted genes in a1 and a2 overlap in one or more exons but have slightly different coordinates. In addition we observed that some genes annotated with the same coordinates in both versions are only differentially expressed in one of them. This is due to the fact that we only consider annotated genes, and as a2 increases annotated regions respect a1, some reads are re-arranged in those new annotated regions.

Candidate genes

Expression data provided solid reasons to maintain or discard candidate genes proposed in chap. II as we could identify significant differences in expression (gene32347 and gene31465) and allelic variability including deleterious amino acid changes (gene32347, gene29344, gene31464, gene22073, gene02203, gene26403, gene26825 and gene26826). These narrows down the number of CG and give a starting point for future functional research.

New candidate genes for both polyphenols and volatile QTL were proposed attending to significant differences in expression levels between the analyzed NILs and the recurrent parental RV.

In some cases, differentially expressed gene predicted function suggest association with the observed mQTL. Clear relations can be presumed between a putative lipoxygenase (gene29184) down-regulated in Fb**5**:50-76 and four very strong QTL for fatty-acid derivatives ((*E*)-2-hexenal, (*E*)-2-hexenyl acetate, (*Z*)-3-hexenal and (*Z*)-3-hexenyl acetate) in this line. It seems also reasonable that the up-regulation of terpene synthase (gene23886), that is similar to *SamonoTPS1*, who produces α-terpineol and limonene in *Santalum album (Jones et al. 2008)* could be linked with the two QTL for limonene and myrtenol accumulation in this NIL. Data also suggest that the two down regulated and one up-regulated acyl-coA hydrolases in Fb**7**:0- 10 might be behind benzoates QTL and other ester-QTL in this NIL. They are similar to *CHY1* gene in *A. thaliana* that has been associated indirectly with fatty acid β-oxidation and benzoic acid biosynthesis (Zolman *et al.* 2001). In addition it seems likely that differentially expressed acyltransferases in Fb**7**:0-10 and Fb**5**:0-35 could be coupled with up and under accumulation of a variety of esters with different acyl and acid moieties. Finally DEG putatively related with hydroxycinnamic acid derivatives synthesis co-localize with general under-accumulation of those compounds in Fb**5**:50-76 and Fb**6**:84-101.Although the RNAseq experiment was done with the aim of revealing candidate genes for the metabolite QTL detected in the selected lines, the exhaustive characterization of the NIL collection allowed us to highlight a putative candidate gene for a completely different trait such as flowering stem length. Lines with *F. bucharica* introgressions at the final region of LG5 produce shorter stems for flowering shoots than for vegetative shoots, while the recurrent parental *F. vesca* var. 'Reine des vallées' produces similar stem length for both shoot classes. The up-regulation of the *F. bucharica* allele in Fb**5**:50-76 of a putative transcription factor SAC51 (Snap_masked-LG5-processed-gene-244.64-mRNA-1) that is involved in stem elongation in *A. thaliana* (Imai *et al.* 2006) could be behind this phenotype.

All those promising results should be further evaluated in additional studies to functionally characterize those candidate genes and estimate their real effect over the strawberry fruit phenotype.

However, there were also cases where links between DEG function and observed phenotypes are not evident or even contradictory. For instance the down-regulation of a putative 4CL in Fb**7**:0-10 is not reflected in any strong polyphenol mQTL in this NIL. It is also surprising that several glucosyltransferases are up-regulated in Fb**6**:84-101, when this NIL harbors mQTL under-accumulating polyphenolic glucosides. In addition, a clear down-regulation of *FaANS* ortholog (gene32347) was not associated to any strong anthocyanin or kaempferol QTL when it has been seen to produce anthocyanins and flavonols (mainly pelargonidin and kaempferol) in *F. x ananassa* (Almeida *et al.* 2007). These unexpected results could be due to many different reasons. First, functional annotation was performed *in-silico* from sequence similarity without experimental evidence, it could be therefore inaccurate. Second, the differences in transcript accumulation may not lead to differences in protein accumulation, or these differences may not have a significant effect in metabolite synthesis. Third, although we have quantified an important number of metabolites (see chap. II and III), identification of compounds is limited and many remain undetected. DEG might affect to those not quantified metabolites. And finally, excess or lack of functionality of a gene can be compensated by others with similar functions in biological systems.

Transcriptome sequencing has revealed as a useful tool to reveal new putative candidate genes and evaluate previous hypothesis. It has narrowed down the search of candidate genes and has also provided us useful information about expression patterns and differences between *F. vesca* and *F. bucharica* alleles. Further insights, such as SNP discovery between NIL and RV, with this data may still produce interesting results.

General discussion

F. vesca has been recognized by strawberry research community as a model species for the genus (Slovin & Mihael 2011). Many genetic tools, including dense genetic maps (Sargent *et al.* 2004, Sargent *et al.* 2006, Sargent *et al.* 2011), synteny studies within the *Fragaria* genus and the *Rosaceae* family (Rousseau-Guetin *et al.* 2008; Vilanova *et al.* 2008; Illa *et al.* 2011; Jung *et al.* 2012; Tennessen *et al.* 2014) and its genome sequence (Shulaev *et al.* 2011) including two genome up-dates (Tennessen *et al.* 2014; Darwish *et al.* 2015) have been released in the last decade. In addition detailed descriptions of morphological and trancriptomic developmental stages have been recently reported (Hollender *et al.* 2012; Hollender *et al.* 2014; Kang *et al.* 2013).

It is believed that *F. vesca* and other wild *Fragaria* species maintain genetic diversity of the genus that is not present in cultivated strawberry. Narrow genetic diversity among *F. x ananassa* commercial varieties is due to the use of few founder clones at the initial steps of strawberry breeding programs. As little as 7 clones account for 50% of nuclear genes in modern cultivars (reviewed by Stewart 2011). It is therefore very likely that many interesting alleles with potential to be introgressed into elite varieties remain unexploited in wild accessions. These could make the difference for determined breeders willing to overcome the obstacles posed by sterility and ploidy barriers in untested material.

Despite of *F. vesca* unstoppable emergence as a model species, most functional annotation and QTL mapping experiments are carried out in *F. x ananassa* (Hoffmann *et al.* 2006; Almeida *et al.* 2007; Hoffmann *et al.* 2011; Zorrilla-Fontanesi *et al.* 2011a; Zorrilla-Fontanesi *et al.* 2012; Chambers *et al.* 2014; Medina-Puche *et al.* 2014; Sanchez-Sevilla *et al.* 2014; Medina-Puche *et al.* 2015). Maybe scarcity of well characterized mapping population is behind this phenomenon. We really believe that making a wider use of *Fragaria vesca* resources for genetic and functional studies would have a positive impact in strawberry research in terms of time-saving, discovery of new variability and transferability among laboratories. Therefore, aiming to contribute to *F. vesca* development as a model species, we provide in this study a powerful genetic tool: A near isogenic line collection thoroughly characterized for agronomical, nutritional and organoleptic traits.

F. vesca NIL collection comes from an inter-specific cross (*F. vesca* cv. 'Reine des Vallées' x *F. bucharica* FDP601) and combines the genetic background of a well known European *F. vesca* accession with the exotic introgressions from a Himalayan species. This provides an interesting recovery of *Fragaria* genus variability and has allowed us to observe a wide range of phenotypic traits segregating among the NIL collection. We have set the focus in ripe strawberry fruit metabolites with a direct relation with nutritional and organoleptic parameters but also have described variability in other agronomical traits such as flowering time, fruit shape, runnering habit and floral stem length among others. All these encourage us to think that this collection might be effective in deciphering inheritance and environment interactions of many other interesting traits from pests resistance to developmental processes.

F. vesca genome sequence release was a milestone in strawberry research (Shulaev *et al.* 2011). In first place it allowed us to link our genetic maps to their physical positions. This gave us access to whole sequence and gene models predicted in our QTL intervals, what was extremely useful for candidate gene identification. In second place it allowed us to perform a whole transcriptome analysis that revealed important differences between *F. vesca* genetic background and the NILs harboring *F. bucharica* introgressions and in third place it allowed the use of dense genotyping methods like the IStraw90®(Bassil & Davis *et al.* 2015).

The NIL collection is a very well defined population by genetic markers. It has been conscientiously genotyped with SSRs throughout all steps during collection development and introgressions have been confirmed every season. To increase marker density, we chose the genotyping array IStraw90® that provided us 1510 polypmorphic SNPs. Discrepancies between the expected and the observed genotypes in the NIL collection, allowed us to discover miss-assembled regions in the *F. vesca* reference genome v1.1 that were confirmed by the new enhanced assembly version 2 (Tennessen *et al.* 2014).

The NILs collection covers 96% of the genome with overlapping introgressions in genetic distance (88% with homozygous introgressions), and there is a single gap of 1.5 Mb in LG1. It is a pity that we could not phenotype fruits from NILs harboring introgressions in the middle region of LG6. These plants took more than two years to flower and produced only few inflorescences that were self-fertilized in order to develop and maintain the collection. It would be interesting to get NILs with recombination points near (but not covering) the *SFL* in order to have everbearing plants that could be evaluated for fruit quality.

The detailed description of ripe berries' functional compounds reported here provides an interesting global insight in fruit composition. In addition, the phenotyping of a whole mapping population has allowed identification of QTL and major genes for more than a hundred traits and metabolic compounds. Specifically: 11 agronomical traits, 1 nutritional trait (total antioxidant capacity), 27 nutritional compounds (including 3 sugars, 22 polyphenols, citric acid and DMHF-glucose) and 81 organoleptic compounds (volatiles). Furthermore, it captures important differences between diploid and octoploid strawberries that could have an impact in fruits marketability. Most of the mapped QTL reported in this work have been described for the first time in *F. vesca*. However, we also report QTL that confirm those described in previous works validating the mapping resolution of the NIL collection. As an example runnering habit at LG2:39-45 cM (Sargent *et al.* 2004a), seasonal flowering at LG6:30-38 cM (Albani *et al.* 2004; Sargent *et al.* 2004) and mesifurano (at LG7:26-43 cM), methyl benzoate (at LG1:26-61), benzyl acetate (at LG7:0-10) and ethyl decanoate (at LG3:8-15 cM) accumulation (Zorrilla-Fontanesi *et al.* 2012)

In terms of aroma, we detected a total of 100 volatiles, including 19 'key' contributors to strawberry fruit smell segregating among the NIL collection. In total 50 major and 76 minor QTL were mapped. Among the detected volatiles, 13 were absent in commercial strawberries (Zorrilla-Fontanesi *et al.* 2012; Schwiterman *et al.* 2014). These included two important 'key' compounds for strawberry smell, methyl 2-aminobenzoate and methyl cinnamate, that provide interesting 'wild strawberry' and 'strawberry' notes to overall scent. In addition, linalool and nerolidol, both volatiles claimed to be present only in octoploid strawberries (Aharoni *et al.* 2004, Chambers *et al.* 2012) were found in NILs with introgressions in LG3:0-8, pointing to *F. bucharica* allele of *FaNES* ortholog as most probable causal gene for its synthesis (Table D. 1).

Attending to (poly)phenols, 22 metabolites were identified and 25 major QTL were mapped. Different balances of anthocyanins and flavonols between diploid and octoploid species were described (Thill *et al.* 2013; Ring *et al.* 2013; Aaby *et al.* 2012; Buendía *et al.* 2010). This could help to uncover different regulation pathways. Pelargonidin 3-glucoside is the only important anthocyanin in *F. x ananassa,* while *F. vesca* accumulates roughly equal proportions of cyanidin 3-glucoside and pelargonidin 3-glucoside (Figure D. 1A). In the NIL collection there are even lines where the most abundant anthocyanin is cyanidin 3-glucoside (QTL in LG2:45-63). This different anthocyanin composition was described by Thill *et al.* (2013), they propose a *F3'H* as a candidate gene for the lower perlargonidin derivatives accumulation in *F. vesca*. This gene co-locates with a major QTL under-accumulating pelargonidin-3-glucoside-malonate in the NIL collection. However, our QTL in LG2:46-63 cM may indicate that there are unexplored sources of variability for anthocyanin composition. Considering flavonols accumulation, differences between *F. vesca* and *F. x ananassa* are obvious, being kaempferol- and quercetin- glucuronide the most abundant flavonols respectively (Ring *et al.* 2013) (Figure D. 1B), and a major QTL in LG1:26-61 cM could help to elucidate at least partially their regulation.

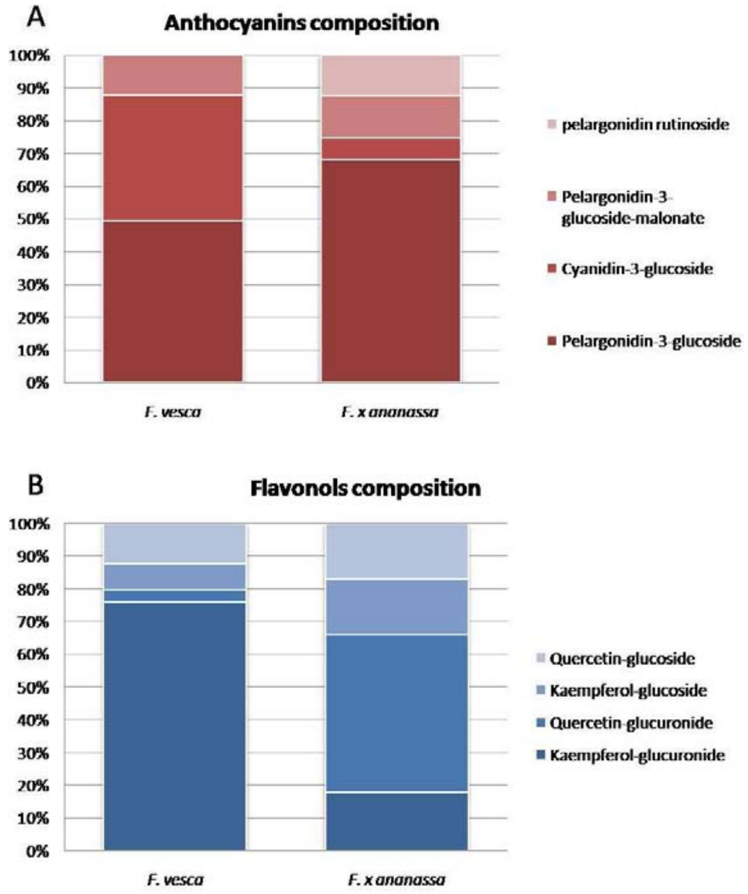


Figure D. 1 Anthocyanin and Flavonol comparison between *F. vesca* and *F. x ananassa*. Anthocyanin (A) and Flavonol (B) percentual composition in *F. vesca* and *F. x ananassa*. *F. x ananassa* data extracted from Ring *et al.* (2013)

From an organoleptic point of view, ‘key’ volatiles contributing to overall strawberyy aroma are the most interesting. A set of four NILs harboring several QTL for those important volatiles (and other QTL for nutritional metabolites) were selected for whole trancriptome analysis (Fb**5**:0-35, Fb**5**:50-76, Fb**6**:84-101, Fb**7**:0-10). This provided new insights in the understanding of phenotypic differences among NILs. In this report we detail a differential expression analysis that gave us further clues into genes that could be considered as candidate genes contributing to the observed QTL. These differentially expressed genes included one well-characterized gene (*FaANS*) and a large set of uncharacterized genes that should be investigated from a functional perspective in order to be confirmed as causal genes. Complementing the DE analysis with a SNP discovery approach in CG located in *cis* with the introgression, provided additional evidence of their probable implication in the observed phenotypes. The SNP discovery should be extended to all predicted genes in the introgressed regions in order to increase arguments both for and against CG.

Major QTL for polyphenolic and volatile compounds in strawberry fruit, together with a selection of candidate genes are summarized in Table D. 1. Non-previously described QTL with important implications in fruit quality could be good targets for marker assisted selection and positional cloning.

The initial region in LG5 between 0 and 35 cM is relatively small (only 6.5 Mb) and concentrates several major QTL for volatile and polyphenolic compounds. It includes QTL for ‘key’ aroma compounds like methyl 2-aminobenzoate and butyl butanoate, but also for a variety of esters and terpenoids. It also gathers QTL for flavan-3-ols family. Line Fb**5**:0-35, that covers the whole region with an exotic introgression from *F. bucharica*, was selected for a differential expression analysis with promising results. *FaANS* and several acyl transferases and terpene synthases were differentially expressed in Fb**5**:0-35 with respect the recurrent parental RV (Table D. 1). The disection of this region that is covered by overlapping introgressions in several NILs (Fb**5**:0-11, Fb**5**:0-20, Fb**5**:0-35, Fb**5**:11-76 and Fb**5**:20-76) with new phenotyping steps in different environments and at different developmental stages, complemented with expression analysis and the development of sub-NILs may contribute to uncover the genetic control of the detected QTL.

Attending to specific traits, the wild-strawberry scent provided by methy 2-aminobenzoate, absent in most commercial varieties, is definitely a desirable trait to increase fruit quality. The fine mapping of the two major QTL affecting methyl 2-aminobenzoate accumulation in LG5:0-35 cM and LG7:0-10 cM, together with the evaluation of the putative acyl-coA hydrolases that might be involved in fatty acid β-oxidation and benzoic acid biosynthesis (Zolman *et al.* 2001), and acyltransferases differentially expressed as candidate genes could elucidate its synthetic pathway.

“Green compounds” derived from the lipoxygenase pathway, (*E*)-2- and (*Z*)-3- hexenal and hexenyl acetates, are usually associated to unripe fruits and therefore not desired in commercial varieties. The major QTL regulating their accumulation and a differentially expressed lipoxygenase at region LG5:50-76 cM, might be a good starting point for further research on this trait.

In addition it would be interesting to see if an alternative allele from *F. bucharica* in *FaNES* gene is responsible for the linalool and nerolidol accumulation in lines harboring introgressions in LG3:0-8 cM (Aharoni *et al.* 2004, Chambers *et al.* 2012)

The work presented here sets an interesting starting point for genetic studies in woodland strawberry. It provides a powerful tool, the NIL collection, a deep phenotypic and metabolic study of all the lines and a transcriptomic analysis of four selected NILs. All taken together form an accurate picture of the effects of the exotic introgressed regions of *F. bucharica* over the *F. vesca* genetic background. From this point, many interesting biological questions can be considered and addressed. Novel traits can be mapped using the NIL collection; sub-NILs can be developed for fine-mapping of selected QTL and eventually end with positional cloning of causal genes; new bioinformatic approach to transcriptomic data could reveal new gene-models and splicing variants and could contribute to improve genome annotation.

Table D. 1 major QTL and candidate gene summary.

qtl location (cM)	compound	%expl. Var.		candidate genes
LG1:26-61	Kaempferol-glucoside	23-41%		*FaF3H* (g.14611)
	Ellagic acid	15-22%		*FaCAD1, FaCAD2 (g.20700)*
	Kaempferol-glucuronide	41-50%		p. gycosyltransferase: g.14947
	Flavonols	16-34%		p. monoxygenase: g.12513, g.12514, g.12515
	α-ionone	16-36%		
	β-ionone	18-30%		
	pentyl acetate	8-23%		
LG2:0-30	Cinnamoyl-glucose ester	37-52%		*FaFLS (g.11126)*
	Hydroxycinnamic.ac.deriv	40-58%		p. FLS: g.01063, g.01034, g.23698, g.11130
	methyl cinnamate	18-32%		p. 4CL: g.24683
	(epi)afzelechin-(epi)catechin dimers	8-22%		p. CHS: g.10965, g.10966
	2-pentylfuran	21-35%		p. CHI: g.27804
	hexyl hexanoate	27-38%		
	octyl butanoate	21-25%		
	octyl hexanoate	21-23%		
LG2:39-45	Citric acid	34%		
	3-methyl-2-butenyl acetate	5-49%		
LG2:45-63	Cyanidin-3-glucoside	25-69%		*FaDFR, FaDFR1 (g.15174)*
LG2:63-73	Quercetin-glucoside	4-52%		p. DFR: g.15176
	Quercetin-glucuronide	23-35%		p. LOX: g.15078
LG3:0-8	linalool	54-59%		FaNES2 (g.30669)
	nerolidol	76-95%		
LG3:54-94	3-methyl-2-butenyl acetate	11-24%		
	acetophenone	14-21%		
LG4:9-20	p-Coumaroyl-glucose ester	28-40%		*Fraa1A* (g.07080), *Fraa2* (g.07065), *Fraa3* (g.07082)
	p-Coumaroyl-glucoside ester	29-36%		
	Feruloyl-glucose ester	60-71%		
	Ellagic acid	29-50%		
	nerol	17-45%		
LG4:20-44	α-farnesene	10-26%		
LG5:0-11	Procyanidin B1	9-28%	**LG5:0-35**	FaANS (g.32347)*+
	Procyanidin B3	12-31%		p. flavonol glycosyltransferase: g.28200*,g.00094*, g.09619*
	Catechin	16-33%		p. acyltransferase: g.09934*
	(epi)catechin dimers iso1	12-31%		p. terpene synthases: g.09971*, g.09977*, g.09972*, m.LG4a.g.136.257*, a.ma.LG2pr.g.150.11*
	(epi)catechin dimers iso2	9-29%		p. aa-metabolism protein: g.09887*
	(epi)afzelechin-(epi)catechin dimers	3-22%		p. TF: g.32494*
	Flavan-3-ols	12-32%		
	1-decanol	16-22%		
	α-pinene	35-42%		
	butyl hexanoate	30-35%		
	methyl decanoate	24-28%		

	methyl octanoate	43-48%	
LG5:11-35	butyl butanoate	30-38%	
	methyl 2-aminobenzoate	33-60%	
	methyl butanoate	16-31%	
	methyl hexanoate	35-52%	
	myrtenyl acetate	45-47%	
	decyl acetate	20-22%	
	hexyl butanoate	34-46%	
	methyl 2-hexenoate	14-35%	
	octyl acetate	25-27%	
LG5:39-41	p-Coumaroyl-glucose ester	13-22%	
LG5:41-50	Pelargonidin-3-glucoside-malonate	9-27%	FaMYB1 (g.09407),
			F3'H (g.25801)
LG5:50-76	(Z)-3-hexenal	58-86%	p. DFR: g.31465*+, g.31464+, g.29344+,g.02203+
	(Z)-3-hexenyl acetate	44-53%	p. leucoanthocyanidin dioxigenase: g.22073+
	(E)-2-hexenal	74-88%	p. flavonol gycosyltransferase: m.-LG5-s.g.279.141-*, g.26881*
	(E)-2-hexenyl acetate	82-89%	p. cinnamyl alcohol dehydrogenase: g.08569*,
	(E)-2-heptenal	46-87%	p. feruloyl-coA hydroxylase: snap_ma.LG5pr.g.250.75*
	(E)-2-hexen-1-ol	63-88%	p. LOX: g.29184*
	eugenol	33-45%	p. terpene synthase: g.12094*, m.-LG5-a.-g.-136,110-*
	nerol	38-44%	p. aa-metabolism protein: g.11807*, g.11045*, m.LG5a.g.77.104*, m.LG5s.g.226.119*
			p. TF: g.25060*
LG7:0-10	methyl 2-aminobenzoate	8-29%	FaCHS FaCHS2 FaCHS3 (g.26825)+,FaCHS4 (g.26826)+
	(E)-2-pentenal	30-32%	p. 4CL: g.12577*
	2,1-pentenyl furan	36-45%	p. flavonol glycosyltransferase: a._ma.LG6pr.g.333.35*
	2,3-butanedioldiacetate	6-28%	p. LOX: g.23606*, g.26949*, g.32226*
	benzyl acetate	15-26%	p. acyl-coA hydrolases: g.05329*, g.09200*
	ethyl decanoate	10-38%	p. acyltransferases: g.19411*, g.23453*, g.34009*, g.19766*, g.34011, g.19766 and m.LG7s.g.129.164*
	ethyl dodecanoate	5-38%	p. carboxylesterase: a.ma. -LG7-pr.g.45.13*
	ethyl methylthioacetate	1-22%	p. lipid-transfer protein: m.LG6a.g.114.104*
	ethyl octanoate	10-35%	p. terpene synthase: g.23886*, a.ma.LG2pr.g.150.11*
	limonene	21-24%	p. aa-metabolism protein: g.03242*, g.11045*, a.ma.LG7pr.g.21.17*
	myrtenol	8-44%	p. TF: m.LG7s.g.91.103
	propyl butanoate	5-31%	
LG7:26-43	mesifurane	16-62%	*FaOMT* (g.12447)
LG7:43-59	Kaempferol-coumaryl-glucoside	18-38%	*FaFGT1* (g.12591)

* DEG; + SNP with deleterious effect or stop codon over predicted protein.

Abreviations Table D. 1: p. putative; m. maker; a. augustus; ma. Masked; pr. Processed; s. snap

Conclusions

- A *F. vesca* NIL collection consisting in 39 NILs and 2 pre-NILs covering 96.4% of the genetic background of *F. vesca* with overlapping introgressions of *F. bucharica* and with an average bin resolution of 14 cM (5 Mb) was developped.

- Eleven agronomical traits segregating among the collection were described and 16 QTL were mapped. These included some non-previously reported QTL in *F. vesca* like round, flat and elongated fruit shape and short floral stems.

- Three main sugars were identified and quantified in *F. vesca* ripe fruits and four QTL were mapped for glucose and fructose accumulation.

- Polyphenolic composition of ripe strawberry fruit was elucidated. A set of 22 polyphenols that segregated among the NIL collection were unambigously identified and quantified in *F. vesca* ripe fruit. Segregation rates between the NILs ranged from undetectable to 9 fold-change.

- Twenty-five major QTL were mapped for polyphenolic compounds. Including a QTL for cyanidin-3-glucoside accumulation (LG2:45-63), several overlapping QTL controlling flavan-3-ols accumulation (LG5:0-11) and QTL involved in the kaempferol derivatives balance (LG1:26-61).

- Disection of aroma composition allowed detection of 100 volatile compounds in the *F. vesca* ripe fruit segregating among the NIL collection. Of which 88 were unambigously and 12 were tentatively identified. These included 19 volatiles considered key contributors for the strawberry aroma percived by humans.

- Fifty major QTL were mapped for volatile compounds accumulation. Including 14 major QTL for 'key' compounds, most of them were mapped to LG5 and LG7.

- Two major QTL for methyl 2-aminobenzoate, responsible for the 'wild-strawberry-like' smell were mapped to LG5:11-35 and LG7:0-10.

- Differentially expressed genes in ripe fruits from NILs Fb**5**:0-35 (260 DEGs), Fb**5**:50-76 (404 DEGs), Fb**6**:84-101 (190 DEGs) and Fb**7**:0-10 (421 DEGs) with respect to *F. vesca* cv. 'Reine des Vallées' were detected.

- Candidate genes for major nutritional and organoleptic QTL in Fb**5**:0-35, Fb**5**:50-76 and Fb**7**:0-10 were selected attending to predicted function, differential expression and SNPs prediction. In total, 17 candidate genes for polyphenolic QTL, 33 candidate genes for volatile QTL and 3 transcription factors were highlighted.

- Candidate genes for major QTL located in regions not covered by NILs Fb**5**:0-35, Fb**5**:50-76 and Fb**7**:0-10 were selected attending to predicted function and *cis*-location. In total 24 candidate genes for polyphenolic QTL and 2 candidate genes for volatile QTL were highlighted.

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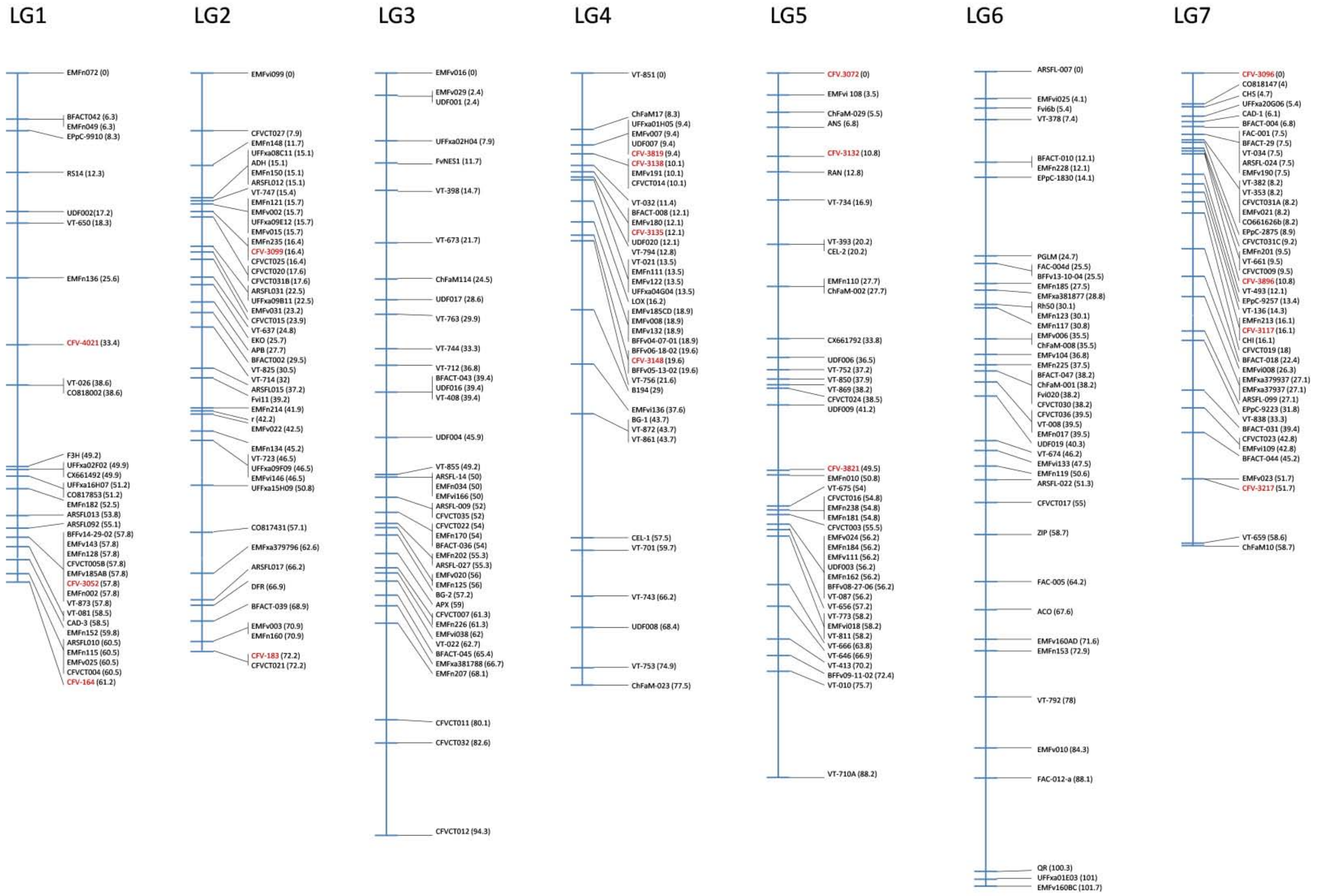
Supplementary Material

Chapter I

Supplementary Material

Suplemental Figure CI. 1. Fragaria map. Markers in red colour were developed in this paper. Nomenclature and description of other markers are as in previously published maps (Ruiz-Rojas et al. 2010; Sargent et al. 2011).



Supplementary Table CI. 1. Set of markers used in NIL selection

Supplemental Table CI. 1

Marker	LG	Map position	Genome position (pb)*	BC$_1$: 1st set of 7 markers	BC$_1$: 2nd set of 7 markers	BC$_1$: 3rd set of 28 markers	BC$_2$	Selfing generations	Source
EMFvi072	1	0.0	148772	X			X	X	Sargent et al. 2003
EMFn049	1	6.3	2324142			X	X	X	Sargent et al. 2006
UDF002	1	17.2	5396953			X	X	X	Cipriani & Testolin 2004, Cipriani et al. 2006
EMFn136	1	25.6	4167810			X	X	X	Sargent et al. 2006
CFV4021	1	33.4	6057666				X	X	This paper
CO818002	1	38.6	5707444					X	Spigler et al. 2008
UFFxa02F02	1	49.9	nf			X	X	X	Sargent et al. 2006
CFV-3052	1	57.8	12937099					X	This paper
EMFv025	1	60.5	20855820		X		X	X	James et al. 2003, Hadonou et al. 2004
CFV164	1	61.2	20571506				X	X	This paper
EMFvi099	2	0,0	nf	X			X	X	Sargent et al. 2003
CFVCT027	2	8,0	8605822					X	Monfort et al. 2006
EMFn148	2	11.7	6321835					X	Sargent et al. 2006
EMFv002	2	15.7	4557158			X	X	X	James et al. 2003, Hadonou et al. 2004
CFV3099	2	16.4	8583985					X	This paper
EMFv031	2	23.2	13547574			X	X	X	James et al. 2003, Hadonou et al. 2004
BFACT002	2	29.5	15627579					X	Denoyes-Rothan, Unpublished
ARSFL015	2	37.2	nf			X	X	X	Lewers et al. 2005
Fvi11	2	39,0	18266038					X	Ashlye et al. 2003
EMFn134	2	45.2	20825075			X	X	X	Sargent et al. 2006
EMFxa379796	2	62.6	22583781					X	Sargent et al. 2008
EMFv003	2	70.9	21834680		X		X	X	James et al. 2003, Hadonou et al. 2004
CFV183	2	72.2	21539118			X	X	X	This paper
EMFv016	3	0,0	1203384				X	X	James et al. 2003, Hadonou et al. 2004
EMFv029	3	2.4	1214623	X			X	X	James et al. 2003, Hadonou et al. 2004
UFFxa02H04	3	7.9	nf			X	X	X	Sargent et al. 2006
VT398	3	14.7	2958951					X	Ruiz-Rojas et al. 2010
UDF017	3	28.6	4427227			X	X	X	Cipriani & Testolin 2004, Cipriani et al. 2006
UDF004	3	45.9	25204787			X			Cipriani & Testolin 2004, Cipriani et al. 2006
CFVCT022	3	54,0	11500786				X	X	Monfort et al. 2006
BFACT045	3	65.4	29479405			X			Denoyes-Rothan, Unpublished
EMFn207	3	68.1	30571418		X		X	X	Sargent et al. 2006
CFVCT011	3	80.1	nf			X	X	X	Monfort et al. 2006
CFVCT032	3	82.6	31873578			X	X	X	Monfort et al. 2006
CFVCT012	3	94.3	nf			X	X	X	Monfort et al. 2006
VT851	4	0,0	nu				X	X	Ruiz-Rojas et al. 2010
EMFv007	4	9.4	1913209		X				James et al. 2003, Hadonou et al. 2004
UDF007	4	9.4	1708726						Cipriani & Testolin 2004, Cipriani et al. 2006
CFV3819	4	9.4	414322					X	This paper
CFV3135	4	12.1	12218379			X	X	X	This paper
CFV3148	4	19.6	22629816				X	X	This paper
FvH4091	4	31.2	24264539					X	Sargent et al. 2011
EMFvi136	4	37.6	25426304			X	X	X	Sargent et al. 2003
VT861	4	43.7	nf					X	Ruiz-Rojas et al. 2010
CEL1	4	57.5	nf	X			X	X	Sargent et al. 2008
ChFaM23	4	77.5	14064455			X	X	X	Gil-Ariza et al. 2006, Zorrilla Fontanesi et al. 2010
CFV3072	5	0,0	184102				X	X	This paper
EMFvi108	5	3.5	178094		X		X	X	Sargent et al. 2003

Supplemental Table CI. 1

Marker	LG	Map position	Genome position (pb)*	BC$_1$: 1st set of 7 markers	BC$_1$: 2nd set of 7 markers	BC$_1$: 3rd set of 28 markers	BC$_2$	Selfing generations	Source
CFV3132	5	10.8	1518272					X	This paper
CEL2	5	20.2	2730257			X	X	X	Sargent et al. 2008
EMFn110	5	27.7	4829209					X	Sargent et al. 2006
FvH4093	5	29.1	5102101					X	Sargent et al. 2011
UDF006	5	36.5	8189646					X	Cipriani & Testolin 2004, Cipriani et al. 2006
CFVCT024	5	38.5	7246484					X	Monfort et al. 2006
UDF009	5	41.2	6928955			X	X	X	Cipriani & Testolin 2004, Cipriani et al. 2006
CFV3821	5	49.5	9385738					X	This paper
EMFv024	5	56.2	22220809					X	James et al. 2003, Hadonou et al. 2004
EMFvi018	5	58,0	nf	X			X	X	Sargent et al. 2003
VT010	5	75.7	18317716				X	X	Ruiz-Rojas et al. 2010
ARSFL007	6	0,0	148649			X	X	X	Lewers et al. 2005
CFaCT107	6	6.7	13471604					X	Sargent et al. 2008
EMFn228	6	11.4	nu	X			X	X	Sargent et al. 2006
FvH4123	6	24.3	3617068					X	Sargent et al. 2011
EMFn117	6	30.1	4681055			X	X	X	Sargent et al. 2006
FvTFL	6		12837123					X	This paper
EMFn017	6	38.8	nf			X	X	X	Sargent et al. 2006
CFVCT017	6	54.3	30117701					X	Monfort et al. 2006
EMFv160AD	6	70.9	31606413				X	X	James et al. 2003, Hadonou et al. 2004
EMFv010	6	83.6	32525001					X	James et al. 2003, Hadonou et al. 2004
EMFv160BC	6	101,0	36914434		X		X	X	James et al. 2003, Hadonou et al. 2004
CFV3096	7	0,0	12787415			X	X	X	This paper
EMFv021	7	8.2	10613144	X			X	X	James et al. 2003, Hadonou et al. 2004
EMFn201	7	9.5	3520491				X	X	Sargent et al. 2006
CFV3896	7	10.8	3559634				X	X	This paper
CFV3117	7	16.1	15413904			X		X	This paper
EMFvi008	7	26,0	17678937			X	X	X	Sargent et al. 2003
ARSFL099	7	27.1	18153770					X	Lewers et al. 2005
CFVCT023	7	42.8	20963623			X	X	X	Monfort et al. 2006
BFACT44	7	44.82	20746759					X	Denoyes-Rothan, Unpublished
EMFv023	7	51.7	19993942		X		X	X	James et al. 2003, Hadonou et al. 2004
ChFaM010	7	58.7	nf				X	X	Gil-Ariza et al. 2006, Zorrilla Fontanesi et al. 2010

*nf means not found, and nu means not unique

Supplementary table CI. 2. Characterization of 14 new SSRs. Name of new locus, name of originally mapped locus (RFLP) close to the SSR, microsatellite motif, primer sequences, allele sizes, segregation data and marker location of new molecular markers developed in this investigation. Allele sizes in bold are those segregating in the selected F1 individual used for NIL development. Monogenic segregation data and chi-square values for goodness-of-fit to expected Mendelian segregation ratios 1:2:1 (aa:ab:bb), 3:1 (a_:bb) or 1:3 (aa:b_), where the a-allele is from F. vesca ´Reine des Vallées´ and the b-allele from F. bucharica. Segregation ratios deviating significantly from the expected ratios of P ≤ 0.05, 0.01 and 0.001 are indicated with one, two and three asterisks, respectively.

Marker name	Original locus	SSR motif	primer sequence(5' - 3')	F. vesca allele(s) size (bp)	F. bucharica allele(s) size (bp)	Classification	Expected segregation ratio	Observed segregation ratio	χ^2	Distorsion	Degrees of freedom	Fv x Fb linkage group	Position
CFV4021	TSA3	$[TAA]_{16}$	F: CTGGAATGGTGGAGAAACG R: AAAGCCCATCTAAACGTGAGAG	**240**-249	-	a_:bb	3:1	57:15	0.67	-	1	LG1	33.4
CFV3052	AC8	$[TG]_5$	F: GGGGTTAGGGTTTTGTCTCC R: AGTGGTTCAAACCCCATTCA	**277**-280	267	aa:ab:bb	1:2:1	22:39:14	1.83	-	2	LG1	57.8
CFV164	EMFv164	$[GA]_{12}$	F: AAGGCCACCTGATTTGTCC R: AGTTCGGTTCAACGGTTTTG	245	267	aa:ab:bb	1:2:1	20:37:11	2.91	-	2	LG1	61.2
CFV3099	PC101	$[CT]_6 + [CT]_{30}$	F: CCTACAAAATTAAGGGGATGGA R: ATCACCGATGGAGGAGTTTAGA	179	**153**-260	aa:ab:bb	1:2:1	1:35:39	38.84	***	2	LG2	16.4
CFV183	EMFv183	$[GT]_8$	F: GCGTCCTTGCCATGTATTTT R: GCACTTCTCGAATCACACGA	316	307	aa:ab:bb	1:2:1	20:33:16	0.59	-	2	LG2	72.2
CFV3135	AC32	$[CT]_{38}$	F: GCTTTAGCGGTTGACACATACA R: GTCCATGTGGGTTACTGGATTAA	**232**-289	236-**254**	aa:ab:bb	1:2:1	10:32:31	13.19	***	2	LG4	12.1
CFV3819	AG53	$[CT]_{12}$	F: CTCTCATGGCTTCATCGTCA R: ATTGTCGGTACCGGTTCATC	**256**-260	234-**251**	aa:ab:bb	1:2:1	9:33:33	16.44	***	2	LG4	9.4
CFV3138	AC24	$[AG]_6$	F: ACCCAGCCAACCATTACAA R: CTCTCGCCTCGAGTATCCTG	300	308	aa:ab:bb	1:2:1	10:32:26	7.76	**		LG4	10.1
CFV3148	PC78	$[GA]_{17}$	F: GGCCAAGACAACATCCTAAAAC R: TGTACGTCTGGTGTATCTTTGACA	174	**157**-174	aa:ab:bb	1:2:1	10:31:31	13.64	***	2	LG4	10.1
CFV3072	AC49	$[TAAAAAA]_5$	F: TTTGCCTTGGTTGAGCGTAT R: TTACGTTGTGGTCGTTCAGG	212	**204**-210	aa:ab:bb	1:2:1	16:32:24	2.67	-	2	LG5	0.0
CFV3132	PC14	$[CA]_{22}$	F: TTGTTTGCCGCATATCTCTC R: GGACACTCAAAAGCACTGCA	170	130-**139**	aa:ab:bb	1:2:1	18:29:27	5.65	*	2	LG5	10.8
CFV3821	AG33	$[TAA]_{13}$	F: TATGCGGTTGATTAGGAGTTCA R: GCTAGTTTTGGTGCAATGTCAA	175	**168**-161	aa:ab:bb	1:2:1	13:31:27	6.66	**	2	LG5	49.5
CFV3096	AC31	$[AT]_{21}$	F: TTCCGCTGATGGTTAGGATG R: GCAAATGGCAGAAACATGAAG	261-**267**	226	aa:ab:bb	1:2:1	14:23:39	28.29	***	2	LG7	0.0
CFV3896	AG35	$[AT]_{13} + [TTTTA]_9$	F: CCAGGCAATCAGGTGAAGAT R: ATGGCCACTATGATTGAGCA	206	-	a_:bb	3:1	42:33	14.44	***	1	LG7	10.8
CFV3117	MC045	$[AG]_{51}$	F: CTCACGGACGGCAAGAAA R: CCTCAATATGCCACTCCATCTC	207	228-**240**	aa:ab:bb	1:2:1	11:30:21	3.29	-	2	LG7	16.1
CFV3217	CoMET	$SNP_{145}[G/C]$	F: CGACATCAACGATGGATTTG R: TGCCATATGACTCAAGTAGCAG	203	203	aa:ab:bb	1:2:1	15:35:22	1.42	-	2	LG7	51.7

Supplementary Table CI. 3: Correlation index for fruit size, shape and weight. Abbreviations: L, length, Wi, width; I, index L/Wi; We, weight, following by a number indicating the year of harvest (11 = 2011; 12 = 2012) and by the month of harvest, May or July. The last capital letters indicate the location, C, Cabrils, TM, Torre Marimon. ns, not significant (P>0.05).

	L_11mayC	Wi_11mayC	I_11mayC	L_11julyC	W_i11julyC	I_11julyC	We_11julyC	L_11mayTM	Wi_11mayTM	I_11mayTM	L_12mayC	Wi_12mayC	I_12mayC	L_12julyC	Wi_12julyC	I_12julyC
L_11mayC	1.00															
Wi_11mayC	0.33	1.00														
I_11mayC	0.68	-0.51	1.00													
L_11julyC	0.61	0.21	0.43	1.00												
W_i11julyC	0.24	0.25	ns	0.35	1.00											
I_11julyC	0.39	ns	0.37	0.66	-0.45	1.00										
We_11julyC	0.44	0.38	0.14	0.65	0.72	ns	1.00									
L_11mayTM	0.29	-0.17	0.29	0.25	ns	0.27	ns	1.00								
Wi_11mayTM	ns	ns	ns	ns	ns	ns	ns	0.31	1.00							
I_11mayTM	0.19	-0.21	0.33	0.2	-0.14	0.32	ns	0.64	-0.49	1.00						
L_12mayC	0.42	-0.24	0.63	0.54	0.17	0.51	0.3	0.37	0.38	ns	1.00					
Wi_12mayC	0.29	0.54	ns	0.51	ns	ns	0.48	ns	ns	ns	ns	1.00				
I_12mayC	ns	-0.52	0.56	0.12	ns	0.16	0.26	0.26	ns	ns	0.75	-0.59	1.00			
L_12julyC	ns	ns	ns	0.25	0.17	ns	0.17	ns	ns	ns	0.55	-0.11	0.5	1.00		
Wi_12julyC	ns	0.14	-0.26	ns	ns	ns	ns	ns	ns	ns	-0.14	0.23	-0.18	0.27	1.00	
I_12julyC	0.14	ns	0.32	0.25	ns	ns	0.22	ns	ns	ns	0.51	-0.23	0.53	0.67	-0.51	1.00

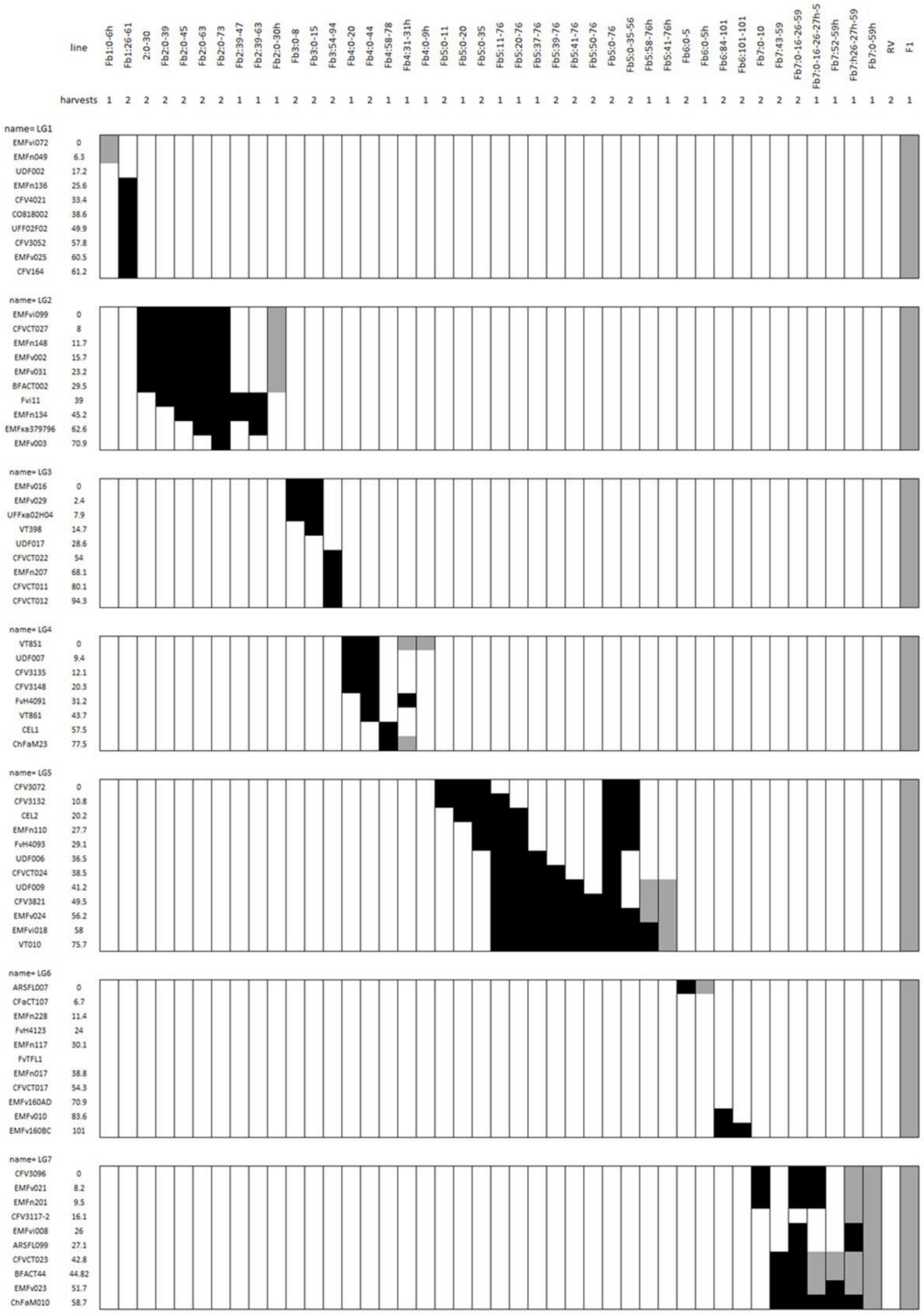
Supplementary Table CI. 4: Correlation index for nutritional traits. Abbreviations: Fru, fructose; Glu, glucose; Suc, sucrose; TotSug, total sugars content and TotPhe, total polyphenol content. The number following indicates the year of harvest: 11 = 2011; 12 = 2012; 13 = 2013. ns, not significant (P>0.05).

	Fru__11	**Glu_11**	**Suc_11**	**TotSug_11**	**TotPhe_11**	**Fru_12**	**Glu_12**	**Suc_12**	**TotSug_12**	**TotPhe_12**	**Fru_13**	**Glu_13**	**Suc_13**	**TotSug_13**	**TotPhe_13**
Fru__11	1.00														
Glu_11	0.92	1.00													
Suc_11	0.41	0.44	1.00												
TotSug_11	0.91	0.92	0.73	1.00											
TotPhe_11	ns	ns	ns	ns	1.00										
Fru_12	0.72	0.74	ns	0.66	ns	1.00									
Glu_12	0.58	0.63	ns	0.53	ns	0.91	1.00								
Suc_12	ns	ns	ns	ns	ns	ns	ns	1.00							
TotSug_12	0.65	0.7	ns	0.6	ns	0.94	0.97	0.31	1.00						
TotPhe_12	ns	ns	ns	ns	0.48	ns	ns	ns	ns	1.00					
Fru_13	0.48	0.58	ns	0.47	ns	ns	ns	ns	ns	ns	1.00				
Glu_13	0.6	0.67	ns	0.58	ns	ns	ns	ns	ns	ns	0.92	1.00			
Suc_13	0.51	0.52	ns	0.49	ns	ns	ns	ns	ns	ns	ns	0.31	1.00		
TotSug_13	0.58	0.66	ns	0.57	ns	ns	ns	ns	ns	ns	0.91	0.94	0.54	1.00	
TotPhe_13	ns	ns	ns	ns	0.75	ns	ns	ns	ns	0.42	0.38	0.3	0.41	0.45	1.00

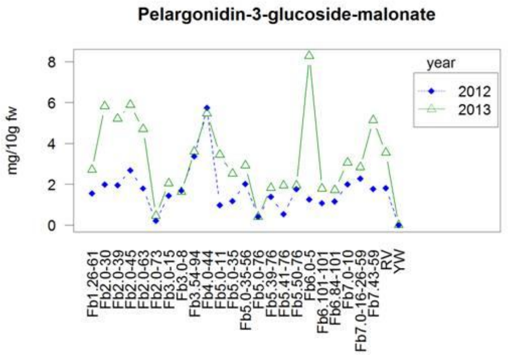
Chapter II

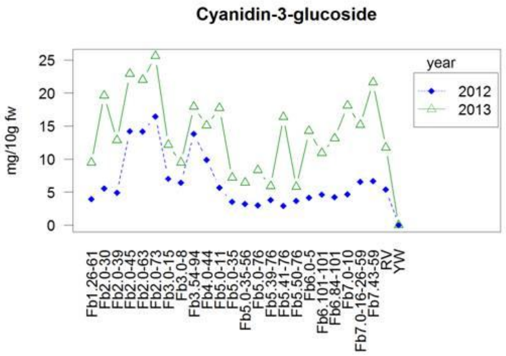
Supplementary material

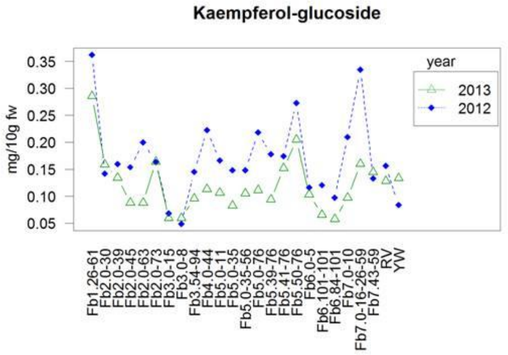
Supplemental figure CII. 1 NIL collection genotypes: Graphical representation of near isogenic lines (NILs) from *F. vesca* (recurrent parental) x *F. bucharica* (donor parental). Lines evaluated in the experiments and the number of harvests analyzed (1 or 2) are presented at the top. On the left, the microsatellites (SSRs) used for the genotyping and their position (in cM) are given. Colours representing the genotypes are: *F. vesca* RV alleles in homozygosity (genetic background) in white, *F. bucharica* alleles in homozygosity (donor introgressions) in black and heterozygous introgressions in grey.

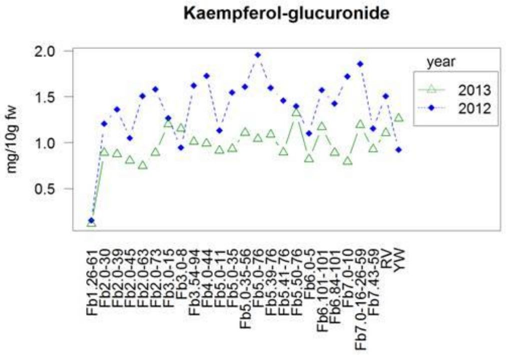


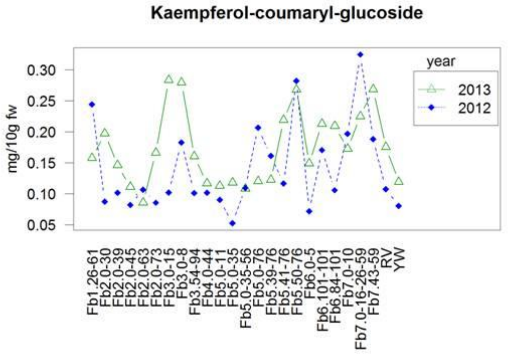
Supplemental figure CII. 2 Interaction plots: Individual plots for all detected compounds representing average values (mg/10g of fw) for each line in the NIL collection for both harvests (blue, 2012; green, 2013). Parallel lines indicate high effect of the genotype. Non parallel lines reflect the effect of the environment and crosses of the lines for specific genotypes reflect the effect of GxE interaction.

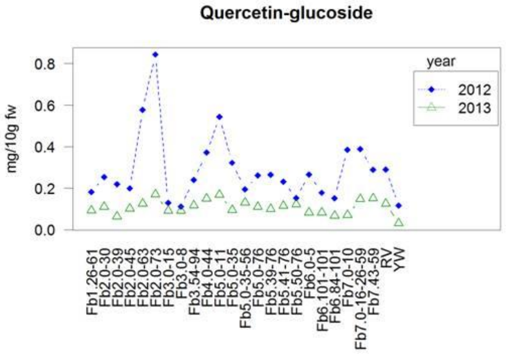


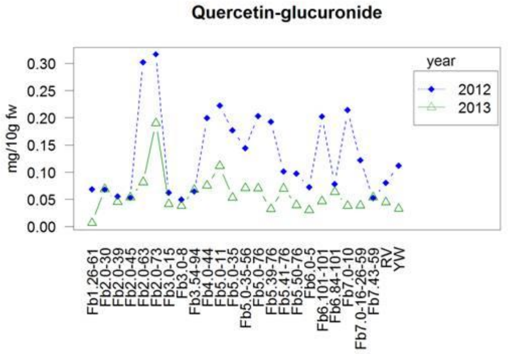


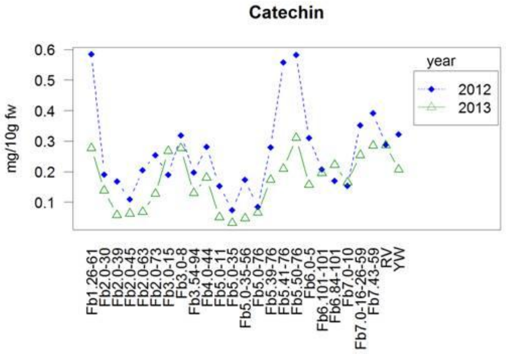




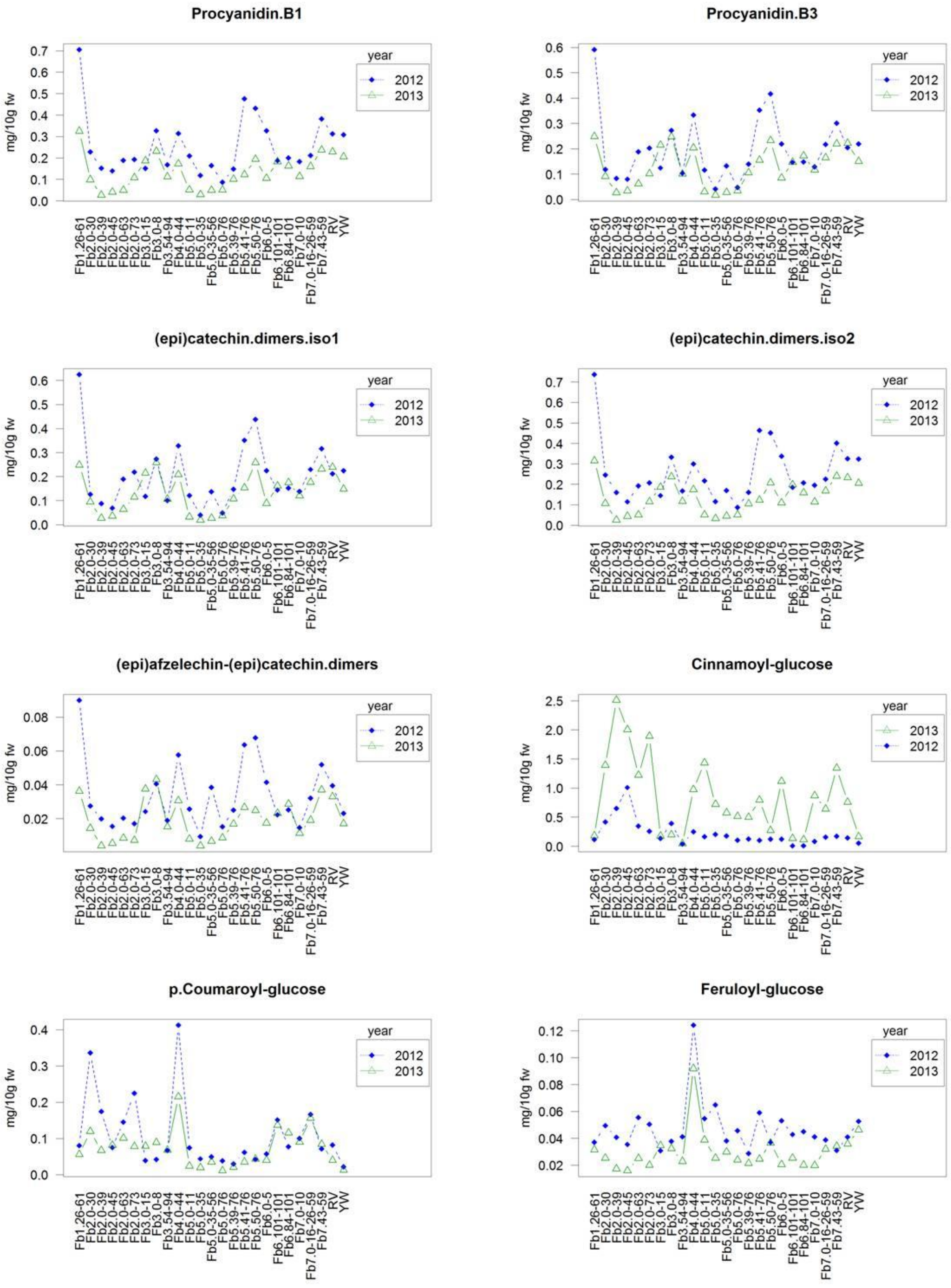




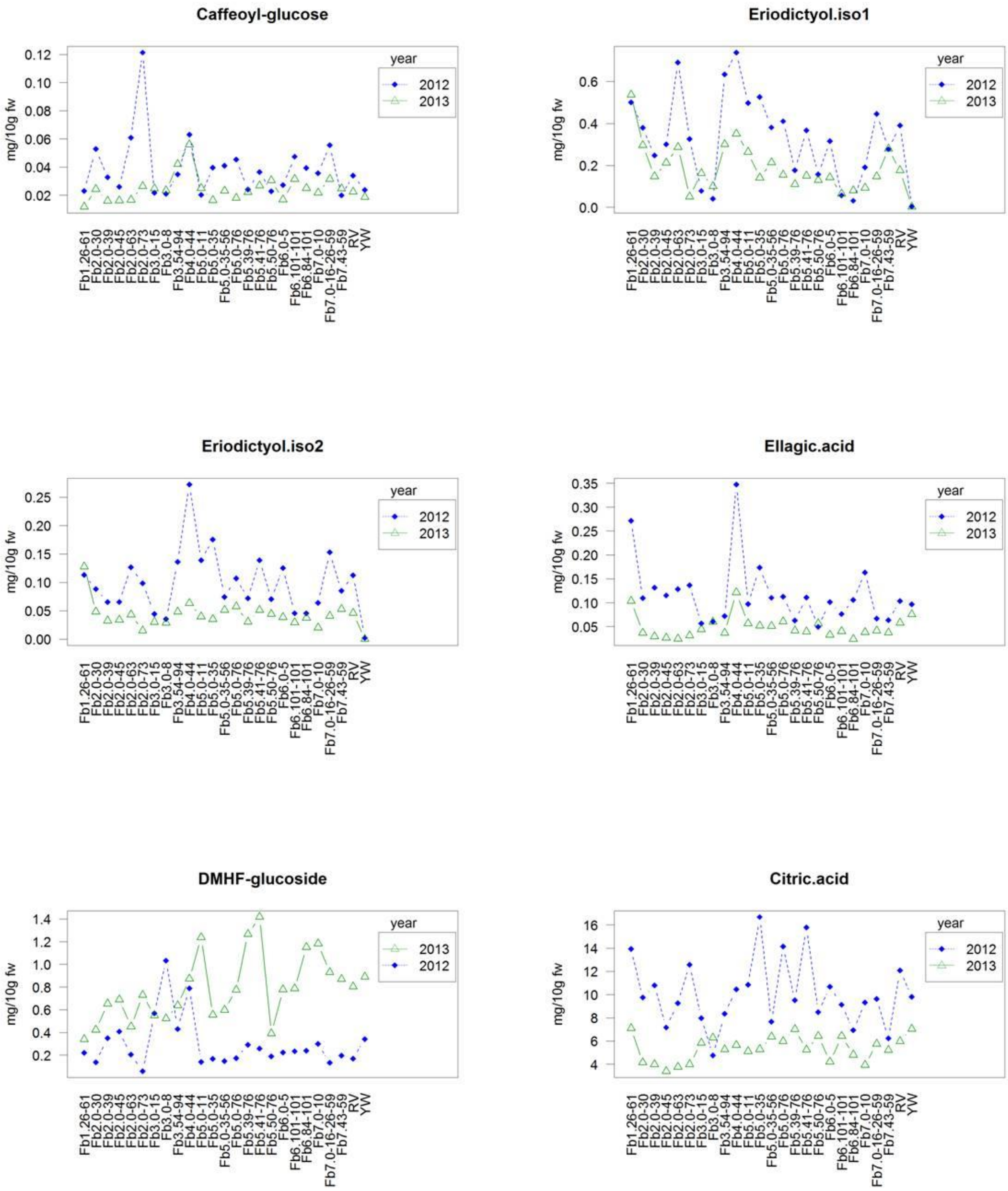




Supplemental figure CII. 2 continues



Supplemental figure CII. 2



Supplemental table CII. 1 Phenolic content summary per genotypes. Average (per genotype per harvest) concentration of the detected phenolic metabolites expressed as part per ten thousand (mg/10g) of fresh weight.

		Supplemental table CII. 1																													
		per ten thousand of fw																													
genotype	year	Pelargonidin-3-glucoside	Pelargonidin-3-glucoside-malonate	Cyanidin-3-glucoside	Kaempferol-glucoside	Kaempferol-glucuronide	Kaempferol-coumaryl-glucoside	Quercetin-glucoside	Quercetin-glucuronide	Procyanidin.B1	Procyanidin.B3	Catechin	(epi)catechin.dimers.iso1	(epi)catechin.dimers.iso2	(epi)afzelechin-(epi)catechin.dimers	Eriodictyol.iso1	Eriodictyol.iso2	p.Coumaroyl-glucose ester	p.Coumaroyl-glucoside	Cinnamoyl-glucose ester	Feruloyl-glucose ester	Caffeoyl-glucose ester	Ellagic acid	DMHF-glucoside	Citric acid	Anthocyanins	Flavonols	Flavan.3.ols	Flavanones	Hydroxycinnamic.ac.deriv	Total phenolics
Fb1.26-61	2012	7,89	1,55	3,94	0,36	0,15	0,24	0,18	0,07	0,71	0,59	0,58	0,62	0,74	0,09	0,50	0,11	0,08	0,01	0,12	0,04	0,02	0,27	0,22	13,92	13,38	1,01	3,33	0,61	0,26	18,88
Fb2.0-30	2012	8,31	1,98	5,54	0,14	1,21	0,09	0,25	0,07	0,23	0,12	0,19	0,13	0,25	0,03	0,38	0,09	0,34	0,06	0,42	0,05	0,05	0,11	0,14	9,75	15,84	1,76	0,94	0,47	0,91	20,02
Fb2.0-30h	2012	5,76	1,84	3,62	0,10	1,53	0,06	0,18	0,07	0,17	0,09	0,15	0,10	0,18	0,02	0,28	0,06	0,19	0,03	0,46	0,05	0,04	0,13	0,10	11,50	11,23	1,94	0,71	0,34	0,77	15,12
Fb2.0-39	2012	8,41	1,95	4,88	0,16	1,36	0,10	0,22	0,06	0,15	0,08	0,17	0,09	0,16	0,02	0,25	0,07	0,17	0,03	0,65	0,04	0,03	0,13	0,35	10,80	15,24	1,90	0,67	0,31	0,93	19,19
Fb2.0-45	2012	14,98	2,68	14,21	0,15	1,05	0,08	0,20	0,05	0,14	0,08	0,11	0,07	0,11	0,02	0,30	0,07	0,07	0,03	1,01	0,04	0,03	0,12	0,41	7,17	31,87	1,54	0,53	0,37	1,18	35,59
Fb2.0-63	2012	12,72	1,79	14,14	0,20	1,51	0,11	0,58	0,30	0,19	0,19	0,20	0,19	0,19	0,02	0,69	0,13	0,15	0,09	0,35	0,06	0,06	0,13	0,21	9,26	28,65	2,69	0,98	0,82	0,70	33,98
Fb2.0-73	2012	4,99	0,21	16,43	0,16	1,58	0,09	0,84	0,32	0,19	0,20	0,25	0,22	0,21	0,02	0,33	0,10	0,23	0,14	0,26	0,05	0,12	0,14	0,06	12,57	21,63	2,99	1,09	0,42	0,79	27,07
Fb3.0-15	2012	7,79	1,43	7,00	0,07	1,27	0,10	0,13	0,06	0,15	0,12	0,19	0,12	0,14	0,02	0,08	0,04	0,04	0,01	0,14	0,03	0,02	0,06	0,57	7,98	16,22	1,63	0,75	0,12	0,24	19,02
Fb3.0-8	2012	6,54	1,69	6,43	0,05	0,95	0,18	0,11	0,05	0,33	0,27	0,32	0,27	0,33	0,04	0,04	0,04	0,04	0,01	0,39	0,04	0,02	0,06	1,03	4,75	14,66	1,34	1,56	0,08	0,50	18,20
Fb3.54-94	2012	19,18	3,36	13,80	0,15	1,62	0,10	0,24	0,06	0,17	0,10	0,20	0,10	0,17	0,02	0,63	0,14	0,07	0,01	0,04	0,04	0,03	0,07	0,43	8,35	36,33	2,17	0,76	0,77	0,20	40,30
Fb4.0-44	2012	20,49	5,74	9,89	0,22	1,73	0,10	0,37	0,20	0,31	0,33	0,28	0,33	0,30	0,06	0,74	0,27	0,41	0,16	0,25	0,12	0,06	0,35	0,79	10,45	36,13	2,62	1,61	1,01	1,01	42,73
Fb4.0-9h	2012	8,37	1,63	4,34	0,15	1,34	0,13	0,30	0,09	0,24	0,18	0,25	0,18	0,24	0,03	0,39	0,14	0,06	0,00	0,14	0,04	0,03	0,08	0,17	13,14	14,33	2,00	1,13	0,52	0,27	18,34
Fb4.31-31h	2012	8,92	2,03	6,16	0,20	1,63	0,13	0,46	0,08	0,24	0,21	0,27	0,22	0,26	0,03	0,44	0,12	0,07	0,01	0,07	0,05	0,03	0,05	0,29	8,63	17,11	2,50	1,23	0,56	0,23	21,68
Fb5.0-11	2012	9,44	0,98	5,66	0,17	1,13	0,09	0,54	0,22	0,21	0,12	0,15	0,12	0,22	0,03	0,50	0,14	0,07	0,01	0,17	0,05	0,02	0,10	0,14	10,86	16,08	2,16	0,84	0,64	0,33	20,14

Supplemental table CII. 1

		per ten thousand of fw																													
genotype	year	Pelargonidin-3-glucoside	Pelargonidin-3-glucoside-malonate	Cyanidin-3-glucoside	Kaempferol-glucoside	Kaempferol-glucuronide	Kaempferol-coumaryl-glucoside	Quercetin-glucoside	Quercetin-glucuronide	Procyanidin.B1	Procyanidin.B3	Catechin	(epi)catechin.dimers.iso1	(epi)catechin.dimers.iso2	(epi)afzelechin-(epi)catechin.dimers	Eriodictyol.iso1	Eriodictyol.iso2	p.Coumaroyl-glucose ester	p.Coumaroyl-glucoside	Cinnamoyl-glucose ester	Feruloyl-glucose ester	Caffeoyl-glucose ester	Ellagic acid	DMHF-glucoside	Citric acid	Anthocyanins	Flavonols	Flavan.3.ols	Flavanones	Hydroxycinnamic.ac.deriv	Total phenolics
Fb5.0-35	2012	8,13	1,17	3,54	0,15	1,54	0,05	0,32	0,18	0,12	0,04	0,07	0,04	0,12	0,01	0,53	0,18	0,04	0,00	0,21	0,06	0,04	0,17	0,17	16,68	12,84	2,24	0,40	0,70	0,36	16,72
Fb5.0-35-56	2012	6,75	2,02	3,22	0,15	1,61	0,11	0,19	0,14	0,16	0,13	0,17	0,14	0,17	0,04	0,38	0,07	0,05	0,01	0,18	0,04	0,04	0,11	0,15	7,66	11,98	2,20	0,82	0,45	0,31	15,88
Fb5.0-76	2012	6,81	0,40	3,00	0,22	1,96	0,21	0,26	0,20	0,09	0,05	0,08	0,05	0,09	0,02	0,41	0,11	0,04	0,00	0,10	0,05	0,05	0,11	0,18	14,14	10,22	2,84	0,37	0,52	0,24	14,30
Fb5.39-76	2012	7,88	1,39	3,80	0,18	1,60	0,16	0,26	0,19	0,15	0,14	0,28	0,15	0,16	0,03	0,18	0,07	0,03	0,01	0,12	0,03	0,02	0,06	0,29	9,52	13,07	2,39	0,90	0,25	0,22	16,89
Fb5.41-76	2012	6,87	0,53	2,90	0,17	1,46	0,12	0,23	0,10	0,48	0,35	0,56	0,35	0,46	0,06	0,37	0,14	0,06	0,01	0,10	0,06	0,04	0,11	0,26	15,79	10,30	2,08	2,26	0,51	0,27	15,54
Fb5.41-76h	2012	10,13	2,40	6,59	0,25	1,98	0,22	0,38	0,17	0,22	0,18	0,30	0,18	0,23	0,03	0,66	0,14	0,09	0,03	0,07	0,05	0,06	0,11	0,15	13,89	19,11	2,99	1,13	0,80	0,30	24,45
Fb5.50-76	2012	6,35	1,76	3,66	0,27	1,39	0,28	0,15	0,10	0,43	0,42	0,58	0,44	0,45	0,07	0,16	0,07	0,04	0,00	0,12	0,04	0,02	0,05	0,19	8,48	11,77	2,20	2,39	0,23	0,23	16,87
Fb5.58-76h	2012	16,75	1,25	7,98	0,14	1,06	0,08	0,21	0,06	0,28	0,30	0,35	0,26	0,25	0,03	0,21	0,08	0,02	0,00	0,48	0,03	0,01	0,07	1,39	10,88	25,98	1,55	1,48	0,29	0,55	29,91
Fb6.0-5	2012	7,32	1,26	4,13	0,12	1,10	0,07	0,26	0,07	0,33	0,22	0,31	0,22	0,34	0,04	0,32	0,13	0,06	0,01	0,12	0,05	0,03	0,10	0,22	10,68	12,70	1,62	1,46	0,44	0,27	16,60
Fb6.0-5h	2012	7,98	2,41	4,53	0,16	1,20	0,14	0,20	0,07	0,31	0,24	0,38	0,25	0,32	0,04	0,17	0,09	0,05	0,01	0,18	0,04	0,03	0,07	0,21	8,40	14,92	1,77	1,54	0,26	0,31	18,87
Fb6.101-101	2012	4,19	1,07	4,61	0,12	1,57	0,17	0,18	0,20	0,19	0,15	0,21	0,14	0,19	0,02	0,06	0,05	0,15	0,03	0,01	0,04	0,05	0,08	0,24	9,13	9,87	2,24	0,89	0,10	0,28	13,47
Fb6.84-101	2012	2,82	1,16	4,21	0,10	1,43	0,11	0,15	0,08	0,20	0,15	0,17	0,15	0,21	0,03	0,03	0,05	0,08	0,01	0,01	0,04	0,04	0,11	0,24	6,93	8,19	1,86	0,90	0,08	0,18	11,31
Fb7.0-10	2012	7,18	1,99	4,64	0,21	1,72	0,20	0,38	0,21	0,18	0,13	0,15	0,14	0,20	0,01	0,19	0,06	0,10	0,03	0,08	0,04	0,04	0,16	0,30	9,31	13,81	2,72	0,81	0,26	0,29	18,06
Fb7.43-59	2012	10,05	1,77	6,64	0,13	1,15	0,19	0,29	0,05	0,38	0,30	0,39	0,32	0,40	0,05	0,28	0,09	0,07	0,01	0,17	0,03	0,02	0,06	0,20	6,23	18,46	1,82	1,84	0,36	0,30	22,85
Fb7.0-16-26-59	2012	9,76	2,27	6,53	0,33	1,85	0,32	0,39	0,12	0,21	0,22	0,35	0,23	0,23	0,03	0,45	0,15	0,17	0,08	0,16	0,04	0,06	0,07	0,13	9,64	18,56	3,02	1,27	0,60	0,50	24,02
Fb7-0-16-26-27h-59	2012	7,72	1,77	5,16	0,25	1,84	0,21	0,41	0,10	0,19	0,17	0,26	0,18	0,21	0,02	0,33	0,13	0,14	0,03	0,10	0,04	0,05	0,10	0,27	11,14	14,64	2,80	1,03	0,46	0,37	19,39
Fb7.0-59h	2012	6,04	1,63	3,31	0,15	1,59	0,20	0,20	0,05	0,51	0,35	0,47	0,36	0,53	0,05	0,34	0,09	0,11	0,01	0,12	0,04	0,03	0,09	0,15	11,46	10,99	2,20	2,26	0,42	0,31	16,28

Supplemental table CII. 1

		per ten thousand of fw																													
genotype	year	Pelargonidin-3-glucoside	Pelargonidin-3-glucoside-malonate	Cyanidin-3-glucoside	Kaempferol-glucoside	Kaempferol-glucuronide	Kaempferol-coumaryl-glucoside	Quercetin-glucoside	Quercetin-glucuronide	Procyanidin.B1	Procyanidin.B3	Catechin	(epi)catechin.dimers.iso1	(epi)catechin.dimers.iso2	(epi)afzelechin-(epi)catechin.dimers	Eriodictyol.iso1	Eriodictyol.iso2	p.Coumaroyl-glucose ester	p.Coumaroyl-glucoside	Cinnamoyl-glucose ester	Feruloyl-glucose ester	Caffeoyl-glucose ester	Ellagic acid	DMHF-glucoside	Citric acid	Anthocyanins	Flavonols	Flavan.3.ols	Flavanones	Hydroxycinnamic.ac.deriv	Total phenolics
Fb7.52-59h	2012	8,21	2,49	5,47	0,21	1,28	0,24	0,26	0,06	0,17	0,13	0,21	0,13	0,17	0,02	0,33	0,07	0,11	0,02	0,13	0,03	0,04	0,06	0,18	8,39	16,17	2,04	0,84	0,40	0,33	19,84
Fb7.h26-27h-59	2012	6,41	2,69	5,27	0,25	1,85	0,28	0,24	0,08	0,64	0,54	0,73	0,55	0,65	0,10	0,46	0,08	0,39	0,14	0,11	0,05	0,05	0,10	0,12	12,51	14,37	2,71	3,20	0,53	0,75	21,66
RV	2012	8,46	1,81	5,37	0,16	1,50	0,11	0,29	0,08	0,31	0,20	0,29	0,21	0,33	0,04	0,39	0,11	0,08	0,01	0,14	0,04	0,03	0,10	0,17	12,09	15,63	2,14	1,38	0,50	0,31	20,07
YW	2012	0,00	0,00	0,00	0,08	0,92	0,08	0,12	0,11	0,31	0,22	0,32	0,22	0,32	0,02	0,00	0,00	0,02	0,00	0,05	0,05	0,02	0,10	0,34	9,80	0,00	1,31	1,42	0,01	0,15	2,99
Fb1.0-6h	2013	15,96	3,72	14,40	0,13	0,88	0,12	0,14	0,05	0,11	0,09	0,13	0,09	0,11	0,01	0,12	0,06	0,03	0,00	0,21	0,01	0,02	0,03	1,04	4,68	34,08	1,32	0,53	0,18	0,28	36,42
Fb1.26-61	2013	20,29	2,71	9,46	0,29	0,12	0,16	0,09	0,01	0,33	0,25	0,28	0,25	0,32	0,04	0,54	0,13	0,06	0,01	0,18	0,03	0,01	0,10	0,34	7,11	32,46	0,66	1,45	0,66	0,29	35,62
Fb2.0-30	2013	20,52	5,81	19,60	0,16	0,89	0,20	0,11	0,07	0,10	0,09	0,14	0,09	0,11	0,01	0,30	0,05	0,12	0,08	1,39	0,03	0,02	0,04	0,42	4,16	45,94	1,43	0,54	0,34	1,64	49,93
Fb2.0-39	2013	19,47	5,20	12,84	0,13	0,87	0,15	0,06	0,05	0,03	0,03	0,06	0,03	0,03	0,00	0,15	0,03	0,07	0,02	2,51	0,02	0,02	0,03	0,65	3,97	37,50	1,26	0,17	0,18	2,63	41,77
Fb2.0-45	2013	23,27	5,89	22,88	0,09	0,80	0,11	0,10	0,05	0,04	0,03	0,06	0,04	0,04	0,01	0,21	0,03	0,08	0,05	2,00	0,02	0,02	0,03	0,69	3,39	52,04	1,16	0,22	0,25	2,17	55,87
Fb2.0-63	2013	21,80	4,69	21,97	0,09	0,75	0,09	0,13	0,08	0,05	0,06	0,07	0,06	0,05	0,01	0,29	0,04	0,10	0,06	1,22	0,03	0,02	0,02	0,45	3,76	48,46	1,13	0,30	0,33	1,42	51,66
Fb2.0-73	2013	6,28	0,46	25,58	0,16	0,89	0,17	0,17	0,19	0,11	0,10	0,13	0,12	0,12	0,01	0,05	0,01	0,08	0,02	1,89	0,02	0,03	0,03	0,73	4,00	32,31	1,58	0,58	0,07	2,04	36,61
Fb2.39-47	2013	17,76	4,63	11,61	0,10	1,04	0,14	0,08	0,03	0,13	0,12	0,17	0,12	0,13	0,02	0,21	0,06	0,04	0,01	1,08	0,02	0,02	0,04	0,97	5,07	34,00	1,40	0,69	0,27	1,16	37,55
Fb2.39-63	2013	8,05	1,19	23,06	0,10	0,90	0,16	0,11	0,03	0,20	0,21	0,25	0,22	0,20	0,02	0,09	0,02	0,02	0,01	0,87	0,01	0,02	0,03	0,58	4,50	32,30	1,30	1,09	0,10	0,93	35,76
Fb3.0-15	2013	9,19	2,05	12,18	0,06	1,20	0,28	0,09	0,04	0,19	0,22	0,27	0,22	0,19	0,04	0,16	0,03	0,08	0,05	0,18	0,03	0,02	0,04	0,55	5,83	23,42	1,67	1,11	0,19	0,37	26,80
Fb3.0-8	2013	7,15	1,63	9,48	0,06	1,15	0,28	0,09	0,04	0,23	0,25	0,28	0,26	0,24	0,04	0,10	0,03	0,09	0,04	0,20	0,03	0,02	0,06	0,52	6,27	18,25	1,62	1,29	0,13	0,39	21,74
Fb3.54-94	2013	20,60	3,60	17,94	0,10	1,01	0,16	0,12	0,07	0,11	0,10	0,13	0,11	0,12	0,02	0,30	0,05	0,07	0,03	0,05	0,02	0,04	0,04	0,64	5,28	42,13	1,45	0,58	0,35	0,21	44,76
Fb4.0-20	2013	16,69	4,30	17,28	0,11	1,03	0,17	0,13	0,06	0,26	0,33	0,38	0,34	0,28	0,04	0,22	0,06	0,17	0,10	0,47	0,07	0,07	0,07	0,58	5,40	38,27	1,50	1,62	0,28	0,88	42,63

Supplemental table CII. 1

		per ten thousand of fw																													
genotype	year	Pelargonidin-3-glucoside	Pelargonidin-3-glucoside-malonate	Cyanidin-3-glucoside	Kaempferol-glucoside	Kaempferol-glucuronide	Kaempferol-coumaryl-glucoside	Quercetin-glucoside	Quercetin-glucuronide	Procyanidin.B1	Procyanidin.B3	Catechin	(epi)catechin.dimers.iso1	(epi)catechin.dimers.iso2	(epi)afzelechin-(epi)catechin.dimers	Eriodictyol.iso1	Eriodictyol.iso2	p.Coumaroyl-glucose ester	p.Coumaroyl-glucoside	Cinnamoyl-glucose ester	Feruloyl-glucose ester	Caffeoyl-glucose ester	Ellagic acid	DMHF-glucoside	Citric acid	Anthocyanins	Flavonols	Flavan.3.ols	Flavanones	Hydroxycinnamic.ac.deriv	Total phenolics
Fb4.0-44	2013	20,23	5,46	15,05	0,11	0,99	0,12	0,15	0,08	0,17	0,20	0,18	0,21	0,17	0,03	0,35	0,06	0,22	0,10	0,97	0,09	0,06	0,12	0,87	5,64	40,75	1,44	0,97	0,41	1,44	45,14
Fb4.58-78	2013	16,18	3,83	13,46	0,15	0,78	0,16	0,14	0,11	0,13	0,09	0,09	0,09	0,14	0,02	0,22	0,03	0,06	0,02	1,36	0,02	0,03	0,02	0,90	4,91	33,47	1,33	0,56	0,25	1,49	37,12
Fb5.0-11	2013	21,28	3,44	17,71	0,11	0,91	0,11	0,17	0,11	0,05	0,03	0,05	0,03	0,05	0,01	0,26	0,04	0,02	0,01	1,43	0,04	0,03	0,06	1,24	5,10	42,43	1,41	0,22	0,30	1,53	45,95
Fb5.0-20	2013	28,48	6,17	21,78	0,09	0,83	0,10	0,12	0,12	0,03	0,02	0,05	0,02	0,03	0,01	0,16	0,05	0,03	0,01	2,23	0,03	0,03	0,04	1,16	4,05	56,43	1,26	0,16	0,21	2,32	60,42
Fb5.0-35	2013	12,44	2,51	7,20	0,08	0,93	0,12	0,09	0,05	0,03	0,02	0,03	0,02	0,03	0,00	0,14	0,04	0,02	0,01	0,72	0,03	0,02	0,05	0,55	5,29	22,15	1,28	0,13	0,18	0,79	24,57
Fb5.0-35-56	2013	13,43	2,92	6,44	0,11	1,10	0,11	0,13	0,07	0,05	0,03	0,05	0,03	0,05	0,01	0,21	0,05	0,03	0,01	0,58	0,03	0,02	0,05	0,60	6,36	22,79	1,52	0,20	0,26	0,67	25,49
Fb5.0-76	2013	13,83	0,40	8,30	0,11	1,04	0,12	0,11	0,07	0,05	0,03	0,07	0,04	0,05	0,01	0,16	0,06	0,01	0,00	0,52	0,02	0,02	0,06	0,78	5,98	22,54	1,45	0,25	0,21	0,57	25,08
Fb5.11-76	2013	11,63	0,67	11,03	0,14	0,74	0,18	0,07	0,07	0,13	0,15	0,15	0,17	0,15	0,02	0,05	0,01	0,01	0,00	0,99	0,03	0,01	0,05	1,21	4,55	23,34	1,20	0,78	0,06	1,05	26,46
Fb5.20-76	2013	12,17	0,91	12,88	0,12	1,09	0,16	0,09	0,07	0,14	0,17	0,17	0,18	0,16	0,02	0,07	0,02	0,02	0,00	1,36	0,04	0,02	0,07	1,16	6,81	25,97	1,55	0,85	0,10	1,44	29,97
Fb5.37-76	2013	16,32	1,87	14,78	0,11	1,17	0,09	0,11	0,03	0,08	0,07	0,16	0,07	0,07	0,02	0,13	0,06	0,03	0,01	0,41	0,02	0,02	0,04	1,10	7,26	32,98	1,51	0,47	0,20	0,48	35,66
Fb5.39-76	2013	13,33	1,82	5,91	0,09	1,09	0,12	0,10	0,03	0,10	0,11	0,17	0,11	0,10	0,02	0,11	0,03	0,02	0,00	0,50	0,02	0,02	0,04	1,27	7,02	21,06	1,43	0,61	0,14	0,57	23,85
Fb5.41-76	2013	18,33	1,94	16,35	0,15	0,89	0,22	0,12	0,07	0,12	0,15	0,21	0,15	0,12	0,03	0,15	0,05	0,04	0,01	0,80	0,02	0,03	0,04	1,42	5,23	36,62	1,45	0,79	0,20	0,90	39,99
Fb5.50-76	2013	8,38	1,94	5,79	0,20	1,32	0,27	0,12	0,04	0,19	0,23	0,31	0,26	0,21	0,02	0,13	0,04	0,04	0,01	0,27	0,04	0,03	0,06	0,39	6,44	16,10	1,95	1,23	0,17	0,39	19,91
Fb6.101-101	2013	8,87	1,78	10,89	0,07	1,17	0,21	0,08	0,05	0,18	0,15	0,20	0,16	0,20	0,02	0,06	0,03	0,14	0,05	0,13	0,03	0,03	0,04	0,79	6,42	21,54	1,58	0,91	0,09	0,37	24,53
Fb7.0-16-26-59	2013	8,00	1,72	13,15	0,06	0,89	0,21	0,07	0,06	0,16	0,17	0,22	0,17	0,16	0,03	0,08	0,04	0,11	0,04	0,11	0,02	0,02	0,02	1,15	4,81	22,86	1,29	0,92	0,12	0,32	25,53
Fb6.0-5	2013	19,69	8,27	14,24	0,10	0,82	0,15	0,08	0,03	0,11	0,08	0,16	0,09	0,11	0,02	0,14	0,04	0,04	0,02	1,11	0,02	0,02	0,03	0,78	4,21	42,20	1,19	0,56	0,18	1,21	45,37
Fb7.0-10	2013	16,63	3,06	18,09	0,10	0,79	0,17	0,07	0,04	0,11	0,12	0,16	0,12	0,11	0,01	0,09	0,02	0,09	0,06	0,87	0,02	0,02	0,04	1,18	3,93	37,79	1,17	0,64	0,11	1,06	40,80

Supplemental table CII. 1

		per ten thousand of fw																													
genotype	year	Pelargonidin-3-glucoside	Pelargonidin-3-glucoside-malonate	Cyanidin-3-glucoside	Kaempferol-glucoside	Kaempferol-glucuronide	Kaempferol-coumaryl-glucoside	Quercetin-glucoside	Quercetin-glucuronide	Procyanidin.B1	Procyanidin.B3	Catechin	(epi)catechin.dimers.iso1	(epi)catechin.dimers.iso2	(epi)afzelechin-(epi)catechin.dimers	Eriodictyol.iso1	Eriodictyol.iso2	p.Coumaroyl-glucose ester	p.Coumaroyl-glucoside	Cinnamoyl-glucose ester	Feruloyl-glucose ester	Caffeoyl-glucose ester	Ellagic acid	DMHF-glucoside	Citric acid	Anthocyanins	Flavonols	Flavan.3.ols	Flavanones	Hydroxycinnamic.ac.deriv	Total phenolics
Fb7.43-59	2013	21,40	5,14	21,61	0,14	0,93	0,27	0,15	0,05	0,24	0,22	0,29	0,23	0,24	0,04	0,28	0,05	0,08	0,05	1,34	0,03	0,02	0,04	0,87	5,22	48,15	1,55	1,25	0,33	1,53	52,85
Fb7.0-16-26-59	2013	14,60	2,83	15,16	0,16	1,19	0,22	0,15	0,04	0,16	0,16	0,25	0,18	0,17	0,02	0,15	0,04	0,16	0,07	0,64	0,03	0,03	0,04	0,93	5,75	32,59	1,76	0,94	0,19	0,93	36,45
RV	2013	13,24	3,54	11,72	0,13	1,10	0,18	0,13	0,04	0,23	0,22	0,29	0,24	0,23	0,03	0,18	0,05	0,04	0,01	0,76	0,04	0,02	0,06	0,80	5,97	28,50	1,58	1,24	0,22	0,87	32,47
F1	2013	5,58	0,59	12,56	0,13	0,72	0,26	0,06	0,05	0,04	0,04	0,04	0,04	0,04	0,00	0,02	0,01	0,08	0,03	1,11	0,02	0,04	0,04	1,17	4,62	18,73	1,23	0,20	0,03	1,28	21,51
YW	2013	0,00	0,00	0,00	0,13	1,26	0,12	0,03	0,03	0,21	0,15	0,21	0,15	0,20	0,02	0,00	0,00	0,01	0,00	0,17	0,05	0,02	0,08	0,89	7,04	0,00	1,58	0,93	0,00	0,25	2,84

Supplemental Table CII. 2 Analysis of variance (ANOVA) fitting G+E+GxE model. Shown for each compound are the degrees of freedom (Df), the sum of squares (SS) and the p value of the F-test from the ANOVA analysis.

		Pelargonidin-3-glucoside		Pelargonidin-3-glucoside-malonate		Cyanidin-3-glucoside		Kaempferol-glucoside		Kaempferol-glucuronide		Kaempferol-coumaryl-glucoside		Quercetin-glucoside		Quercetin-glucuronide	
	Df	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value
G	23	9815,500	< 2,20E-16	835,140	< 2,20E-16	10477,400	< 2,20E-16	0,813	< 2,20E-16	17,084	< 2,20E-16	0,958	< 2,20E-16	2,668	< 2,20E-16	1,044	< 2,20E-16
E	1	4300,600	< 2,20E-16	273,490	< 2,20E-16	5477,200	< 2,20E-16	0,168	1,01E-14	16,540	< 2,20E-16	0,195	1,09E-11	3,199	< 2,20E-16	0,486	< 2,20E-16
GxE	23	1756,400	0,0004891	259,470	1,57E-12	1605,500	0,0003252	0,185	3,18E-06	8,897	9,39E-08	0,348	2,31E-08	2,016	< 2,20E-16	0,443	1,36E-12
Error	374	12105,400		821,330		10774,900		0,969		40,058		1,486		2,193		1,398	

		Procyanidin.B1		Procyanidin.B3		Catechin		(epi)catechin.dimers.iso1		(epi)catechin.dimers.iso2		(epi)afzelechin-(epi)catechin.dimers		Eriodictyol.iso1		Eriodictyol.iso2	
	Df	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value
G	23	3,254	< 2,20E-16	3,047	< 2,20E-16	3,886	< 2,20E-16	3,332	< 2,20E-16	3,433	< 2,20E-16	0,070	< 2,20E-16	6,899	< 2,20E-16	0,266	< 2,20E-16
E	1	1,318	< 2,20E-16	0,338	1,14E-10	0,707	< 2,20E-16	0,325	1,76E-09	1,402	< 2,20E-16	0,015	< 2,20E-16	2,043	< 2,20E-16	0,292	< 2,20E-16
GxE	23	0,715	6,55E-10	0,611	2,74E-07	0,889	1,63E-09	0,690	1,79E-07	0,777	1,00E-09	0,018	3,60E-10	2,031	7,89E-13	0,188	< 2,20E-16
Error	374	2,702		2,870		3,459		3,187		2,977		0,068		6,312		0,471	

		p-Coumaroyl-glucose ester		p-Coumaroyl-glucoside		Cinnamoyl-glucose ester		Feruloyl-glucose ester		Caffeoyl-glucose ester		Ellagic acid		DMHF-glucoside		Citric acid	
	Df	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value
G	23	1,823	< 2,20E-16	0,319	< 2,20E-16	82,323	< 2,20E-16	0,077	< 2,20E-16	0,047	< 2,20E-16	0,391	< 2,20E-16	12,856	0,002564	672,550	1,76E-08
E	1	0,170	1,93E-13	0,001	0,3747	44,141	< 2,20E-16	0,030	< 2,20E-16	0,022	< 2,20E-16	0,448	< 2,20E-16	22,549	< 2,20E-16	2395,190	< 2,20E-16
GxE	23	0,469	< 2,20E-16	0,099	4,12E-15	28,341	9,47E-12	0,014	0,02876	0,041	< 2,20E-16	0,228	2,06E-13	12,680	0,003047	833,650	2,27E-11
Error	374	1,089		0,270		94,265		0,141		0,101		0,683		99,878		2843,210	

		Anthocyanins		Flavonols		Flavan-3-ols		Flavanones		Hydroxycinnamic.ac.deriv		Total phenolics	
	Df	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value	SS	p_value
G	23	39924,000	< 2,20E-16	24,401	7,60E-11	86,196	< 2.2e-16	9,483	< 2,20E-16	99,440	< 2,20E-16	38383,000	< 2,20E-16
E	1	24375,000	< 2,20E-16	42,525	< 2,20E-16	19,770	2,67E-05	3,880	< 2,20E-16	35,233	< 2,20E-16	10974,000	< 2,20E-16
GxE	23	7920,000	0,0001554	24,013	1,29E-10	18,160	5,43E-05	3,263	2,75E-08	22,309	6,48E-09	7642,000	0,0003253
Error	374	50771,000		86,239		72,590		9,279		91,027		51289,000	

Supplemental table CII. 3 Pearson correlation values (corr) between compounds for 2012 and 2013 independent harvests. Asterisks indicate significance of correlation coefficients as follows: p-value <0.05 '*', p-value <0.01 '**', p-value <0.001 '***'

		2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012	2012
		Pelargonidin-3-glucoside	Pelargonidin-3-glucoside-malonate	Cyanidin-3-glucoside	Kaempferol-glucoside	Kaempferol-glucuronide	Kaempferol-coumaryl-glucoside	Quercetin-glucoside	Quercetin-glucuronide	Procyanidin B1	Procyanidin B3	Catechin	(epi)catechin dimers iso1	(epi)catechin dimers iso2	(epi)afzelechin-(epi)catechin dimers	Eriodictyol iso1	Eriodictyol iso2	p-Coumaroyl-glucose ester	p-Coumaroyl-glucoside	Cinnamoyl-glucose ester	Feruloyl-glucose ester	Caffeoyl-glucose ester	Ellagic acid	DMHF-glucoside	Citric acid	Anthocyanins	Flavonols	Flavan-3-ols	Flavanones	Hydroxycinnamic.ac.deriv	Total phenolics
2012	Pelargonidin-3-glucoside	1																													
2012	Pelargonidin-3-glucoside-malonate	0.85***	1																												
2012	Cyanidin-3-glucoside	0.62**	0.38	1																											
2012	Kaempferol-glucoside	0.24	0.19	0	1																										
2012	Kaempferol-glucuronide	0.17	0.15	0.14	-0.12	1																									
2012	Kaempferol-coumaryl-glucoside	-0.16	-0.05	-0.27	0.55**	-0.13	1																								
2012	Quercetin-glucoside	0.18	-0.06	0.58**	0.19	0.29	-0.26	1																							
2012	Quercetin-glucuronide	-0.01	-0.13	0.29	0.23	0.5*	-0.07	0.78***	1																						
2012	Procyanidin B1	-0.08	0.01	-0.24	0.47*	-0.67***	0.46*	-0.2	-0.34	1																					
2012	Procyanidin B3	-0.02	0.1	-0.12	0.54**	-0.56**	0.54**	-0.11	-0.19	0.96***	1																				
2012	Catechin	-0.14	-0.07	-0.23	0.42*	-0.48*	0.53**	-0.2	-0.28	0.92***	0.93***	1																			
2012	(epi)catechindimers iso1	-0.05	0.08	-0.13	0.55**	-0.56**	0.56**	-0.1	-0.18	0.96***	1***	0.93***	1																		
2012	(epi)catechin dimers iso2	-0.12	-0.02	-0.26	0.48*	-0.67***	0.48*	-0.19	-0.33	1***	0.95***	0.91***	0.96***	1																	
2012	(epi)afzelechin-(epi)catechin dimers	0.05	0.19	-0.25	0.52**	-0.5*	0.51*	-0.26	-0.34	0.93***	0.94***	0.89***	0.93***	0.92***	1																
2012	Eriodictyol iso1	0.74***	0.5*	0.43*	0.49*	0.16	-0.23	0.47*	0.32	0.05	0.06	-0.08	0.06	0.03	0.12	1															
2012	Eriodictyol iso2	0.68***	0.55**	0.27	0.4*	0.25	-0.22	0.41*	0.29	0.11	0.15	0.02	0.13	0.09	0.23	0.86***	1														
2012	p-Coumaroyl-glucose	0.4	0.55**	0.37	0.16	0.18	-0.23	0.38	0.26	-0.03	0.05	-0.11	0.05	-0.04	0.04	0.4	0.48*	1													
2012	p-Coumaroyl-glucoside	0.42*	0.45*	0.64***	0.18	0.27	-0.25	0.66***	0.55**	-0.09	0.08	-0.09	0.07	-0.1	-0.04	0.45*	0.5*	0.85***	1												
2012	Cinnamoyl-glucose	0.35	0.27	0.44*	-0.05	-0.18	-0.26	0.05	-0.18	-0.22	-0.22	-0.27	-0.23	-0.24	-0.2	0.1	-0.04	0.25	0.23	1											
2012	Feruloyl-glucose	0.42*	0.51*	0.13	0.14	0.25	-0.34	0.29	0.34	0.05	0.12	-0.04	0.1	0.02	0.13	0.55**	0.78***	0.66***	0.66***	-0.03	1										
2012	Caffeoyl-glucose	0.05	0	0.55**	0.08	0.42*	-0.27	0.74***	0.66***	-0.24	-0.11	-0.2	-0.1	-0.24	-0.25	0.3	0.29	0.6**	0.8***	0.04	0.38	1									
2012	Ellagic acid	0.39	0.51*	0.11	0.56**	-0.09	-0.05	0.23	0.24	0.29	0.35	0.06	0.34	0.27	0.32	0.57**	0.67***	0.58**	0.57**	0.08	0.72***	0.31	1								
2012	DMHF-glucoside	0.34	0.5*	0.14	-0.31	-0.12	0.03	-0.35	-0.29	0.04	0.12	0.02	0.08	0.01	0.1	-0.13	0.04	0.12	0.13	0.22	0.25	-0.23	0.14	1							
2012	Citric acid	-0.09	-0.29	-0.21	0.44*	0.1	-0.13	0.29	0.31	0.16	0.08	0.1	0.08	0.15	0.09	0.42*	0.49*	0.05	0.07	-0.19	0.32	0.26	0.42*	-0.43*	1						
2012	Anthocyanins	0.93***	0.76***	0.86***	0.15	0.17	-0.22	0.37	0.12	-0.16	-0.06	-0.19	-0.08	-0.19	-0.07	0.66***	0.56**	0.46*	0.59**	0.43*	0.35	0.29	0.32	0.31	-0.18	1					
2012	Flavonols	0.19	0.09	0.31	0.21	0.87***	-0.01	0.66***	0.8***	-0.49*	-0.34	-0.34	-0.33	-0.48*	-0.37	0.36	0.39	0.29	0.5*	-0.18	0.31	0.63***	0.12	-0.28	0.26	0.26	1				
2012	Flavan-3-ols	-0.08	0.02	-0.21	0.5*	-0.6**	0.52**	-0.17	-0.28	0.99***	0.99***	0.96***	0.99***	0.98***	0.94***	0.02	0.1	-0.01	-0.03	-0.24	0.05	-0.18	0.27	0.06	0.12	-0.14	-0.41*	1			
2012	Flavanones	0.74***	0.52**	0.41*	0.48*	0.18	-0.23	0.47*	0.32	0.06	0.08	-0.06	0.07	0.04	0.15	0.99***	0.91***	0.42*	0.47*	0.07	0.61**	0.3	0.6**	-0.09	0.45*	0.65***	0.37	0.04	1		
2012	Hydroxycinnamic.ac.deriv	0.47*	0.47*	0.58**	0.05	0.01	-0.34	0.32	0.09	-0.19	-0.13	-0.26	-0.15	-0.22	-0.15	0.32	0.27	0.71***	0.68***	0.85***	0.37	0.43*	0.39	0.22	-0.07	0.59**	0.09	-0.2	0.31	1	
2012	Total phenolics	0.93***	0.76***	0.85***	0.21	0.17	-0.19	0.4	0.15	-0.11	0	-0.14	-0.02	-0.14	-0.01	0.69***	0.6**	0.5*	0.63**	0.41*	0.39	0.32	0.37	0.29	-0.14	1***	0.29	-0.08	0.69***	0.6**	1

	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013	2013
	Pelargonidin-3-glucoside	Pelargonidin-3-glucoside-malonate	Cyanidin-3-glucoside	Kaempferol-glucoside	Kaempferol-glucuronide	Kaempferol-coumaryl-glucoside	Quercetin-glucoside	Quercetin-glucuronide	Procyanidin B1	Procyanidin B3	Catechin	(epi)catechin dimers iso1	(epi)catechin dimers iso2	(epi)afzelechin-(epi)catechin dimers	Eriodictyol iso1	Eriodictyol iso2	p-Coumaroyl-glucose	p-Coumaroyl-glucoside	Cinnamoyl-glucose	Feruloyl-glucose	Caffeoyl-glucose	Ellagic acid	DMHF-glucoside	Citric acid	Anthocyanins	Flavonols	Flavan-3-ols	Flavanones	Hydroxycinnamic.ac.deriv	Total phenolics
Pelargonidin-3-glucoside	1																													
Pelargonidin-3-glucoside-malonate	0.77***	1																												
Cyanidin-3-glucoside	0.57**	0.47*	1																											
Kaempferol-glucoside	0.16	-0.01	-0.03	1																										
Kaempferol-glucuronide	-0.58**	-0.33	-0.38	-0.49*	1																									
Kaempferol-coumaryl-glucoside	-0.3	-0.17	0.01	0.04	0.28	1																								
Quercetin-glucoside	0.36	0.14	0.51*	0.18	-0.04	-0.04	1																							
Quercetin-glucuronide	-0.03	-0.16	0.57**	-0.04	0.04	-0.19	0.67***	1																						
Procyanidin B1	-0.3	-0.22	-0.24	0.4	-0.07	0.58**	-0.11	-0.39	1																					
Procyanidin B3	-0.3	-0.2	-0.17	0.29	0.07	0.71***	-0.03	-0.34	0.94***	1																				
Catechin	-0.34	-0.2	-0.21	0.29	0.13	0.76***	-0.12	-0.4	0.92***	0.97***	1																			
(epi)catechin dimers iso1	-0.31	-0.2	-0.16	0.29	0.1	0.72***	-0.01	-0.32	0.94***	1***	0.97***	1																		
(epi)catechin dimers iso2	-0.31	-0.22	-0.23	0.39	-0.03	0.61**	-0.1	-0.38	1***	0.95***	0.93***	0.94***	1																	
(epi)afzelechin-(epi)catechin dimers	-0.19	-0.1	-0.16	0.13	0.06	0.72***	-0.03	-0.4	0.88***	0.94***	0.91***	0.93***	0.88***	1																
Eriodictyol iso1	0.72***	0.45*	0.26	0.49*	-0.65***	-0.17	0.39	-0.11	0.2	0.12	0	0.1	0.17	0.18	1															
Eriodictyol iso2	0.51*	0.21	0	0.61**	-0.66***	-0.04	0.25	-0.25	0.35	0.26	0.17	0.24	0.32	0.32	0.86***	1														
p-Coumaroyl-glucose	0.18	0.32	0.42*	-0.18	-0.08	0.18	0.13	0.12	0.2	0.3	0.16	0.3	0.21	0.29	0.23	0.08	1													
p-Coumaroyl-glucoside	0.31	0.44*	0.52**	-0.24	-0.06	0.18	0.13	0.09	0.08	0.21	0.09	0.2	0.09	0.23	0.27	0.01	0.92***	1												
Cinnamoyl-glucose	0.5*	0.53**	0.62**	0.09	-0.27	-0.31	0.31	0.43*	-0.52**	-0.5*	-0.5*	-0.49*	-0.52**	-0.51*	0.07	-0.15	0.09	0.18	1											
Feruloyl-glucose	-0.03	0.05	-0.18	0.1	0.2	-0.05	0.27	-0.01	0.36	0.41*	0.26	0.4	0.35	0.38	0.29	0.19	0.45*	0.39	-0.16	1										
Caffeoyl-glucose	0.03	0.04	0.14	-0.14	0.36	0.15	0.39	0.25	0.15	0.29	0.18	0.3	0.17	0.26	0.12	0.01	0.61**	0.52**	-0.19	0.66***	1									
Ellagic acid	-0.06	-0.14	-0.43*	0.41*	-0.11	-0.13	0.09	-0.22	0.49*	0.42*	0.28	0.41*	0.47*	0.38	0.44*	0.5*	0.16	0.06	-0.33	0.81***	0.34	1								
DMHF-glucoside	0	-0.16	0.07	-0.27	0.1	-0.1	0.01	0.13	-0.14	-0.09	-0.02	-0.1	-0.15	-0.04	-0.35	-0.29	-0.11	-0.13	0.03	0.01	0.15	-0.14	1							
Citric acid	-0.49*	-0.56**	-0.8***	0.21	0.3	0.17	-0.14	-0.41*	0.57**	0.48*	0.48*	0.47*	0.56**	0.48*	0.02	0.25	-0.27	-0.41*	-0.74***	0.36	0.12	0.6**	-0.03	1						
Anthocyanins	0.9***	0.77***	0.86***	0.06	-0.53**	-0.17	0.46*	0.24	-0.3	-0.26	-0.31	-0.26	-0.3	-0.19	0.56**	0.28	0.35	0.49*	0.64***	-0.1	0.09	-0.26	0.01	-0.73***	1					
Flavonols	-0.55**	-0.36	-0.22	-0.23	0.92***	0.48*	0.22	0.22	0.09	0.24	0.3	0.28	0.13	0.19	-0.52**	-0.51*	-0.03	-0.03	-0.21	0.23	0.44*	-0.07	0.04	0.29	-0.44*	1				
Flavan-3-ols	-0.32	-0.21	-0.2	0.33	0.04	0.69***	-0.07	-0.38	0.98***	0.99***	0.98***	0.99***	0.98***	0.93***	0.12	0.27	0.24	0.14	-0.52**	0.36	0.22	0.42*	-0.1	0.52**	-0.29	0.21	1			
Flavanones	0.7***	0.42*	0.22	0.52**	-0.66***	-0.15	0.37	-0.14	0.23	0.15	0.03	0.13	0.2	0.2	1***	0.9***	0.21	0.23	0.03	0.28	0.1	0.46*	-0.35	0.06	0.52**	-0.53**	0.15	1		
Hydroxycinnamic.ac.deriv	0.51*	0.56**	0.66***	0.07	-0.26	-0.28	0.33	0.44*	-0.49*	-0.45*	-0.47*	-0.44*	-0.49*	-0.46*	0.1	-0.14	0.22	0.29	0.99***	-0.08	-0.1	-0.29	0.02	-0.76***	0.67***	-0.2	-0.48*	0.06	1	
Total phenolics	0.9***	0.77***	0.86***	0.07	-0.52**	-0.15	0.47*	0.25	-0.28	-0.24	-0.29	-0.24	-0.29	-0.18	0.56**	0.28	0.36	0.5*	0.66***	-0.08	0.1	-0.26	0	-0.73***	1***	-0.42*	-0.27	0.52**	0.69***	1

Supplemental Table CII. 3

Supplemental table CII. 4 Candidate genes located in mQTL. The mQTL intervals in cM are defined in the first column, followed by the gene id number and position in the reference genome in bp (LG, start, end and strand). It is followed by the predicted function and the evidence provided by the source (direct or indirect). The name of the gene and the characterized protein, if available, is in the last column.

Supplemental table CII. 4

mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG1:26-61	gene12966	1	6655681	6658248	-	softening-pectin degradation	direct/empirical	FaPE1	pectin methyl esterase
LG1:33-61	gene13071	1	7313368	7314345	+	-	direct/empirical	FaChi2-2	chitinase
LG1:26-61	gene12626	1	5465935	5470202	+	-	direct/empirical	FabGal3	beta-galactosidase
LG1:26-61	gene20700	1	17192737	17194207	+	firmness	direct/empirical	FaCAD1	cinnamyl alcohol dehydrogenase
LG1:26-61	gene20700	1	17192737	17194207	+	-	direct/empirical	FaCAD2	cinnamyl alcohol dehydrogenase
LG1:26-61	gene14611	1	7929548	7931288	-	pigment formation	direct/empirical	FaF3H	flavanone-3-hydroxylase
LG1:26-61	gene21106	1	16843349	16848956	+	ethylene receptor	direct/empirical	FaEtr1	ethylene resistant
LG1:26-61	gene13037	1	7119883	7125296	+	methylation of cytosine residues in DNA	direct/empirical	FaMet	DNA-methyltransferases
LG2:0-30	gene17555	2	12033155	12036938	+	softening-pectin degradation	direct/empirical	FaPLA	pectae lyase
LG2:0-30	gene17555	2	12033155	12036938	+	-	direct/empirical	FaPLB	pectae lyase
LG2:0-30	gene17555	2	12033155	12036938	+	-	direct/empirical	FcPL1	pectae lyase
LG2:0-30	gene30069	2	5674614	5677085	+	aroma	direct/empirical	FaADH	alcohol dehydrogenase
LG2:0-30	gene25195	2	3603750	3611662	-	starch biosynthesis	direct/empirical	FagpL1	ADP-glucose pyrophosphorylase-largesubunit
LG2:0-30	gene11126	2	16378605	16383661	-	pigment formation	direct/empirical	FaFLS	flavonol synthase
LG2:0-30	gene27415	2	216755	225190	-	photosynthesis	direct/empirical	FacpFBP	chloroplastic fructose diphosphatase
LG2:0-30	gene11090	2	16162075	16164668	-	ethylene receptor	direct/empirical	FaErs2	ethylene resistant
LG2:0-30	gene27729	2	15248702	15250161	-	auxin perception	direct/empirical	FaABP1	auxin-binding-protein
LG2:30-39	gene08518	2	18909782	18910279	-	arresting cell elongation	direct/empirical	FaGAST	small-prot-12cysteine-residues
LG2:45-63	gene15174	2	22421967	22423633	-	pigment formation	direct/empirical	FaDFR	dihydroflavonol-4-reductase
LG2:45-63	gene15174	2	22421967	22423633	-	-	direct/empirical	FaDFR1	dihydroflavonol-4-reductase
LG3:0-8	gene21638	3	3516364	3517987	-	softening-pectin degradation	direct/empirical	FcPG1	polygalacturonase
LG3:0-8	gene21638	3	3516364	3517987	-	-	direct/empirical	FaPG1	polygalacturonase
LG3:0-8	gene21638	3	3516364	3517987	-	-	direct/empirical	FaPG2	polygalacturonase
LG3:0-8	gene30669	3	3341450	3343617	-	aroma-mono and sesquiterpene formation	direct/empirical	FaNES2	S-nerolidol-linalool-synthase
LG3:0-8	gene30750	3	3079463	3081172	+	floral identity	direct/empirical	FvLFY	LEAFY
LG3:54-94	gene25391	3	19265955	19271166	-	gluthatione-ascorbate cycle	direct/empirical	FaAPX	citosolic ascorbate peroxidase
LG4:9-20	gene04817	4	21373037	21378764	+	-	direct/empirical	FabGal2	beta-galactosidase
LG4:9-20	gene00616	4	14923252	14925151	-	L-ascorbate biosynthesis	direct/empirical	FaGalUR	D-galacturonic-acid-reductase
LG4:9-20	gene33967	4	6894437	6896285	+	aroma-fruit ester formation	direct/empirical	SAAT	alcohol acyl-CoA transferase
LG4:9-20	gene33967	4	6894437	6896285	+	-	direct/empirical	FcAAT	alcohol acyl-CoA transferase
LG4:9-20	gene10008	4	13728629	13729661	+	repair of proteins and peptides	direct/empirical	Fapmsr	methionine-sulfoxide-reductase
LG4:9-20	gene32532	4	2854804	2857895	+	ethylene receptor	direct/empirical	FaEin1	ethylene insensitive_2
LG4:9-20	gene06814	4	19852304	19853663	-	fruit ripening	direct/empirical	FaTCTP	translationally conrolled tumor protein

Supplemental table CII. 4

mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG4:9-20	gene07080	4	20342785	20346343	-	flavonoid biosynthesis	direct/empirical	Fraa1A	allergen
LG4:9-20	gene07065	4	20239851	20240333	-	-	direct/empirical	Fraa2	allergen
LG4:9-20	gene07082	4	20349804	20350402	+	-	direct/empirical	Fraa3	allergen
LG4:20-44	gene05164	4	22696276	22705796	+	softening-hemicellulose degradation	direct/empirical	FaXyl	beta-xylosidase
LG4:20-44	gene23065	4	23347645	23354344	-	beta-galactosidase	direct/empirical	FabGal1	softening
LG4:20-44	gene03877	4	25703897	25706053	+	leucoanthocyanidin reductase	direct/empirical	FaLAR	pigment formation
LG5:0-11	gene32347	5	831406	832669	-	pigment formation	direct/empirical	FaANS	anthocyanidin synthase
LG5:0-11	gene24665	5	66912	68692	+	pigment formation	direct/empirical	FaANR	anthocyanidin reductase
LG5:0-11	gene31839	5	1983769	1985918	-	ethylene biosynthesis	direct/empirical	FaACS	aminocyclopropane-1-carboxylic-acid-synthase
LG5:0-11	gene32422	5	1254512	1255192	+	pathogenesis related-stress	direct/empirical	FaOLP	osmotin-like-protein
LG5:0-11	gene32421	5	1253296	1253985	+	-	direct/empirical	FaOLP2	osmotin-like-protein
LG5:11-35	gene32087	5	2725023	2731420	+	-	direct/empirical	FaEG3	endo-beta-1-4-glucanase
LG5:11-35	gene32087	5	2725023	2731420	+	-	direct/empirical	Facel2	endo-beta-1-4-glucanase
LG5:11-35	gene22676	5	5146799	5148667	+	aroma-monoterpene formation	direct/empirical	FaPINH	pinene hydroxylase
LG5:39-41	gene26030	5	7171678	7172921	-	-	direct/empirical	FaExp5	expansin cell wall proteins
LG5:41-50	gene08914	5	8949158	8954516	-	resistance	direct/empirical	FaRP7	tonoplast intrinsic protein
LG5:41-50	gene09178	5	9422265	9422765	+	polyphenol anchoring	direct/empirical	Fahyprp	hybrid-proline-rich-protein
LG5:41-50	gene09407	5	10192077	10193600	-	regulation of pigment biosynthesis	direct/empirical	FaMYB1	transcription factor
LG5:50-76	gene29267	5	18939272	18944184	-	pathogenesis related	direct/empirical	FaChi2-1	chitinase
LG5:50-76	gene02221	5	28194562	28196775	-	softening-cell wall disassembly	direct/empirical	FaExp1	expansin cell wall proteins
LG6:101-101	gene28406	6	36624320	36631108	+	aroma-furanone formation	direct/empirical	FaQR	quinone-oxidoreductase
LG6:101-101	gene26265	6	39240233	39241900	+	phenylpropanoid metabolism	direct/empirical	FaGT2	UDP-glucose-cinnamate-glucosyltransferase
LG6:101-101	gene26344	6	38765124	38766533	+	flavonoid metabolism	direct/empirical	FaGT7	flavonol glucosyltransferases
LG6:101-101	gene04420	6	33560589	33563775	-	methionine biosynthesis	direct/empirical	FvCGS	cystathionine-gamma-synthase
LG6:101-101	gene04435	6	33646384	33647707	+	-	direct/empirical	FaExp3	expansin cell wall proteins
LG7:0-10	gene34011	7	13781022	13782619	+	-	direct/empirical	FvAAT	alcohol acyl-CoA transferase
LG7:0-10	gene26825	7	6149732	6151108	-	pigment formation	direct/empirical	FaCHS	chalconse synthase
LG7:0-10	gene26825	7	6149732	6151108	-	-	direct/empirical	FaCHS2	chalconse synthase
LG7:0-10	gene26825	7	6149732	6151108	-	-	direct/empirical	FaCHS3	chalconse synthase
LG7:0-10	gene26826	7	6154395	6155736	-	-	direct/empirical	FaCH4	chalconse synthase
LG7:0-10	gene26820	7	6123363	6129719	-	lutein degradation	direct/empirical	FaCCD1	carotenoid cleavage dioxygenase
LG7:0-10	gene21476	7	8680369	8681607	+	cystein protease inhibitor-antifungal	direct/empirical	FaCyf1	phytocystatin
LG7:43-59	gene12447	7	19881382	19883765	+	aroma-furanone formation	direct/empirical	FaOMT	O-methyltransferase
LG7:43-59	gene13340	7	22062128	22064232	-	sugar metabolism	direct/empirical	FaSDH	sorbitol dehydrogenase
LG7:43-59	gene12591	7	19513486	19515049	-	pigment formation	direct/empirical	FaGT1	anthocyanidin glucosyltransferase
LG7:43-59	gene13329	7	22008955	22009644	+	cold acclimation response	direct/empirical	FaCBF1	cold-induced transcription factor
LG1:26-61	gene17840	1	12638073	12640631	+	Probable cinnamyl alcohol dehydrogenase 9 (AtCAD9)	indirect/*in-silico*	-	-
LG1:26-61	gene17846	1	12693952	12694738	+	Probable cinnamyl alcohol dehydrogenase 9 (AtCAD9) (similar to)	indirect/*in-silico*	-	-

Supplemental table CII. 4

mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG1:26-61	gene12684	1	5727293	5728827	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene12528	1	6267643	6268699	-	Glucans biosynthesis glucosyltransferase H	indirect/*in-silico*	-	-
LG1:26-61	gene14946	1	8406734	8407323	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene14947	1	8412049	8413613	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene30501	1	9515513	9516940	+	Anthocyanidin 5,3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene17891	1	13023716	13026317	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG1:26-61	gene20721	1	17280873	17283689	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene20725	1	17303938	17305752	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene20726	1	17308493	17314323	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene20728	1	17323512	17324199	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene16276	1	18388657	18390949	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG1:26-61	gene16278	1	18395948	18396445	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG1:26-61	gene16279	1	18397865	18401775	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG1:26-61	gene16456	1	19403840	19406724	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene16457	1	19410142	19411534	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG1:26-61	gene05783	1	15073494	15075524	+	Putative glycosyltransferase 7 (AtGT7)	indirect/*in-silico*	-	-
LG1:26-61	gene12513	1	6195774	6197721	-	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG1:26-61	gene12514	1	6198955	6201006	-	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG1:26-61	gene12515	1	6203459	6208201	-	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG2:0-30	gene24683	2	8235080	8239234	+	4-coumarate--CoA ligase-like 4	indirect/*in-silico*	-	-
LG2:0-30	gene08139	2	1859986	1869439	-	Sterol 3-beta-glucosyltransferase	indirect/*in-silico*	-	-
LG2:0-30	gene24693	2	8319915	8321365	-	Anthocyanidin 3-O-glucosyltransferase 2	indirect/*in-silico*	-	-
LG2:0-30	gene24695	2	8330371	8331823	+	Anthocyanidin 3-O-glucosyltransferase 6	indirect/*in-silico*	-	-
LG2:0-30	gene24696	2	8332542	8334486	-	Anthocyanidin 3-O-glucosyltransferase 2 (similar to)	indirect/*in-silico*	-	-
LG2:0-30	gene17551	2	12003929	12018194	+	Sterol 3-beta-glucosyltransferase	indirect/*in-silico*	-	-
LG2:0-30	gene02170	2	2725736	2730521	-	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit (Oligosaccharyl transferase 48 kDa subunit), Precursor	indirect/*in-silico*	-	-
LG2:0-30	gene01652	2	6855556	6856272	+	UDP-sugar-dependent glycosyltransferase 52	indirect/*in-silico*	-	-
LG2:0-30	gene17317	2	10064932	10069040	-	Uncharacterized glycosyltransferase At3g02350 (similar to)	indirect/*in-silico*	-	-
LG2:0-30	gene17431	2	11006864	11017723	+	Probable xyloglucan glycosyltransferase 6 (AtCslC6) (similar to)	indirect/*in-silico*	-	-
LG2:0-30	gene17381	2	11312216	11318161	-	Glycosyltransferase QUASIMODO1 (similar to)	indirect/*in-silico*	-	-

Supplemental table CII. 4

mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG2:0-30	gene08261	2	13069681	13076320	-	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (RPN-II), Precursor	indirect/*in-silico*	-	-
LG2:0-30	gene08365	2	13689735	13690685	+	Glycosyltransferase 8 domain-containing protein 4	indirect/*in-silico*	-	-
LG2:0-30	gene27629	2	15235143	15236210	-	Glycosyltransferase 8 domain-containing protein 1	indirect/*in-silico*	-	-
LG2:0-30	gene10573	2	15796943	15798295	-	Putative glycosyltransferase 2 (AtGT2)	indirect/*in-silico*	-	-
LG2:0-30	gene23696	2	3032571	3034316	+	Leucoanthocyanidin dioxygenase (LDOX)	indirect/*in-silico*	-	-
LG2:0-30	gene01063	2	2447358	2450036	-	Flavonol synthase/flavanone 3-hydroxylase (FLS)	indirect/*in-silico*	-	-
LG2:0-30	gene01064	2	2451132	2452479	-	Flavonol synthase/flavanone 3-hydroxylase (FLS)	indirect/*in-silico*	-	-
LG2:0-30	gene23698	2	3037049	3038084	+	Flavonol synthase/flavanone 3-hydroxylase (FLS)	indirect/*in-silico*	-	-
LG2:0-30	gene17126	2	10418449	10420283	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG2:0-30	gene11130	2	16404777	16406137	+	Flavonol synthase/flavanone 3-hydroxylase (FLS)	indirect/*in-silico*	-	-
LG2:0-30	gene01641	2	6687271	6688953	-	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG2:0-30	gene27804	2	14793549	14795640	+	Chalcone--flavonone isomerase (Chalcone isomerase)	indirect/*in-silico*	-	-
LG2:30-39	gene02631	2	18014905	18018397	-	Probable xyloglucan glycosyltransferase 12 (AtCslC12)	indirect/*in-silico*	-	-
LG2:30-39	gene10965	2	17267797	17269037	+	Chalcone synthase	indirect/*in-silico*	-	-
LG2:30-39	gene10966	2	17270120	17271389	+	Chalcone synthase 1	indirect/*in-silico*	-	-
LG2:39-45	gene08621	2	19372383	19375011	-	4-coumarate--CoA ligase-like 5 (At4CL9)	indirect/*in-silico*	-	-
LG2:39-45	gene08569	2	19157777	19160126	+	Probable cinnamyl alcohol dehydrogenase 6 (OsCAD6)	indirect/*in-silico*	-	-
LG2:39-45	gene08733	2	19946565	19952069	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG2:39-45	gene08808	2	20318920	20319431	-	Glucans biosynthesis glucosyltransferase H	indirect/*in-silico*	-	-
LG2:39-45	gene08735	2	19959218	19962208	-	Probable xyloglucan glycosyltransferase 5 (AtCslC5)	indirect/*in-silico*	-	-
LG2:39-45	gene34621	2	20710538	20711536	+	Flavonol sulfotransferase-like	indirect/*in-silico*	-	-
LG2:39-45	gene09081	2	21056505	21062647	+	Putative dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG2:45-63	gene15176	2	22426340	22430200	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR) (similar to)	indirect/*in-silico*	-	-
LG2:63-73	gene15107	2	22126470	22127909	+	Anthocyanidin 3-O-glucosyltransferase 5	indirect/*in-silico*	-	-
LG2:63-73	gene15079	2	22031932	22033053	-	Glycosyltransferase 8 domain-containing protein 1	indirect/*in-silico*	-	-
LG2:63-73	gene15078	2	22028092	22028933	+	Leucoanthocyanidin dioxygenase (LDOX)	indirect/*in-silico*	-	-
LG3:0-8	gene30556	3	1555677	1556122	-	Alpha-1,2 glucosyltransferase ALG10	indirect/*in-silico*	-	-

Supplemental table CII. 4

mQTL	**gene_id**	**LG**	**start**	**end**	**strand**	**predicted function**	**evidence**	**Gene**	**protein**
LG3:0-8	gene19556	3	195490	196509	+	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3	indirect/*in-silico*	-	-
LG3:0-8	gene19862	3	1420292	1423820	+	Glycosyltransferase QUASIMODO1 (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene28898	3	16680274	16692277	-	4-coumarate--CoA ligase-like 7 (At4CL6) (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene28093	3	20085452	20088614	+	Trans-cinnamate 4-monooxygenase (CA4H)	indirect/*in-silico*	-	-
LG3:54-94	gene00125	3	5820599	5823225	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT) (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene00126	3	5825999	5827432	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG3:54-94	gene28972	3	6340550	6342072	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG3:54-94	gene19906	3	6937739	6938402	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG3:54-94	gene19964	3	7233814	7235266	+	Anthocyanidin 3-O-glucosyltransferase 1	indirect/*in-silico*	-	-
LG3:54-94	gene19965	3	7235992	7237413	-	Anthocyanidin 3-O-glucosyltransferase 1	indirect/*in-silico*	-	-
LG3:54-94	gene20125	3	8254996	8257657	-	Cytokinin-N-glucosyltransferase 2	indirect/*in-silico*	-	-
LG3:54-94	gene20181	3	8538499	8539929	-	Anthocyanidin 3-O-glucosyltransferase 6 (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene03056	3	10134253	10145274	-	Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene28901	3	16716763	16717272	-	UGT74B1 (UDP-glucosyl transferase 74B1); UDP-glycosyltransferase/ thiohydroximate beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	indirect/*in-silico*	-	-
LG3:54-94	gene28059	3	19888955	19890389	-	Anthocyanidin 3-O-glucosyltransferase 5	indirect/*in-silico*	-	-
LG3:54-94	gene28169	3	20498812	20499195	+	Flavonol-3-O-glycoside-7-O-glucosyltransferase 1	indirect/*in-silico*	-	-
LG3:54-94	gene28200	3	20666199	20668385	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG3:54-94	gene07755	3	21638538	21643040	+	Cytokinin-N-glucosyltransferase 1	indirect/*in-silico*	-	-
LG3:54-94	gene07756	3	21644967	21646786	+	Cytokinin-N-glucosyltransferase 2	indirect/*in-silico*	-	-
LG3:54-94	gene07763	3	21697829	21699323	+	Cytokinin-N-glucosyltransferase 1	indirect/*in-silico*	-	-
LG3:54-94	gene07876	3	22412941	22414377	+	Anthocyanidin 3-O-glucosyltransferase 1	indirect/*in-silico*	-	-
LG3:54-94	gene30064	3	23050072	23050772	+	Anthocyanidin 5,3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG3:54-94	gene27158	3	23639081	23640454	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG3:54-94	gene34573	3	24553802	24555637	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene34574	3	24576164	24593631	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene27357	3	24593770	24594548	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG3:54-94	gene01472	3	29168538	29168939	+	Sterol 3-beta-glucosyltransferase	indirect/*in-silico*	-	-
LG3:54-94	gene10439	3	25421142	25421728	+	Glycosyltransferase 6 (AtGT6) (similar to)	indirect/*in-silico*	-	-

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mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG3:54-94	gene03288	3	12165896	12169351	+	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG3:54-94	gene28208	3	20709774	20715711	+	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG3:54-94	gene05317	3	9868794	9875012	-	Flavonoid 3',5'-hydroxylase (F3'5'H)	indirect/*in-silico*	-	-
LG3:54-94	gene03562	3	14564603	14568161	-	Flavonoid 3',5'-hydroxylase 2 (F3'5'H)	indirect/*in-silico*	-	-
LG3:54-94	gene14053	3	26438249	26442579	+	Flavonoid 3'-monooxygenase (AtF3'H)	indirect/*in-silico*	-	-
LG3:54-94	gene27138	3	24691710	24692520	-	Chalcone--flavonone isomerase 1B-2 (Chalcone isomerase 1B-2)	indirect/*in-silico*	-	-
LG4:0-9	gene22597	4	9163	10629	-	Anthocyanidin 3-O-glucosyltransferase 6 (similar to)	indirect/*in-silico*	-	-
LG4:0-9	gene22709	4	37917	39592	+	Anthocyanidin 3-O-glucosyltransferase 1	indirect/*in-silico*	-	-
LG4:0-9	gene22710	4	41004	42635	+	Anthocyanidin 3-O-glucosyltransferase 6	indirect/*in-silico*	-	-
LG4:9-20	gene29614	4	9199785	9201392	+	Flavonoid 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG4:9-20	gene22440	4	11872034	11882146	+	Zeatin O-glucosyltransferase	indirect/*in-silico*	-	-
LG4:9-20	gene22484	4	12118156	12119619	-	Cytokinin-O-glucosyltransferase 1 (AtZOG1)	indirect/*in-silico*	-	-
LG4:9-20	gene00622	4	14958770	14960800	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG4:9-20	gene33839	4	15008201	15008887	-	Dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	indirect/*in-silico*	-	-
LG4:9-20	gene06599	4	17320833	17322254	+	Indole-3-acetate beta-glucosyltransferase 1	indirect/*in-silico*	-	-
LG4:9-20	gene06600	4	17325026	17326453	-	Indole-3-acetate beta-glucosyltransferase 1	indirect/*in-silico*	-	-
LG4:9-20	gene06601	4	17328115	17329536	-	Indole-3-acetate beta-glucosyltransferase 1	indirect/*in-silico*	-	-
LG4:9-20	gene06602	4	17330686	17332236	-	Indole-3-acetate beta-glucosyltransferase 1	indirect/*in-silico*	-	-
LG4:9-20	gene28359	4	10231362	10239055	-	Xyloglucan glycosyltransferase 4 (AtCslC4) (similar to)	indirect/*in-silico*	-	-
LG4:9-20	gene09944	4	13438838	13441090	-	Glycosyltransferase-like protein LARGE2	indirect/*in-silico*	-	-
LG4:9-20	gene06069	4	16473747	16476581	-	Glycosyltransferase QUASIMODO1	indirect/*in-silico*	-	-
LG4:9-20	gene06514	4	16833116	16834818	-	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit (Oligosaccharyl transferase 48 kDa subunit), Precursor	indirect/*in-silico*	-	-
LG4:9-20	gene06894	4	19596357	19597715	+	Putative glycosyltransferase 2 (AtGT2)	indirect/*in-silico*	-	-
LG4:20-44	gene04524	4	26240883	26242301	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG4:20-44	gene04525	4	26244285	26245703	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG4:20-44	gene03747	4	25284728	25286736	+	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG4:20-44	gene34814	4	26353868	26354881	+	Flavonol sulfotransferase-like	indirect/*in-silico*	-	-
LG4:20-44	gene22145	4	24174474	24176874	+	NAD(P)H-dependent 6'-deoxychalcone synthase (similar to)	indirect/*in-silico*	-	-
LG4:20-44	gene22147	4	24182367	24183623	+	NAD(P)H-dependent 6'-deoxychalcone synthase	indirect/*in-silico*	-	-
LG5:0-11	gene31819	5	1889024	1891790	-	Beta-1,3-glucosyltransferase	indirect/*in-silico*	-	-

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mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
						(Beta3Glc-T)			
LG5:0-11	gene32333	5	767084	770337	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG5:0-11	gene32271	5	443367	449534	+	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG5:0-11	gene32272	5	450467	452119	+	Flavonoid 3',5'-hydroxylase (F3'5'H)	indirect/*in-silico*	-	-
LG5:0-11	gene32273	5	453434	455082	+	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG5:0-11	gene32278	5	475658	477351	-	Flavonoid 3',5'-hydroxylase (F3'5'H)	indirect/*in-silico*	-	-
LG5:0-11	gene32280	5	481843	486224	+	Flavonoid 3'-monooxygenase (AtF3'H)	indirect/*in-silico*	-	-
LG5:11-35	gene06385	5	5003524	5006850	+	4-coumarate--CoA ligase-like 9 (At4CL4) (similar to)	indirect/*in-silico*	-	-
LG5:11-35	gene01839	5	5394745	5396600	+	Probable cinnamyl alcohol dehydrogenase 1 (AtCAD1)	indirect/*in-silico*	-	-
LG5:11-35	gene32055	5	2562184	2563596	+	Hydroquinone glucosyltransferase	indirect/*in-silico*	-	-
LG5:11-35	gene32056	5	2567395	2574428	+	Hydroquinone glucosyltransferase (similar to)	indirect/*in-silico*	-	-
LG5:11-35	gene32061	5	2588575	2590074	+	Hydroquinone glucosyltransferase	indirect/*in-silico*	-	-
LG5:11-35	gene32062	5	2590387	2597749	+	Hydroquinone glucosyltransferase (similar to)	indirect/*in-silico*	-	-
LG5:11-35	gene32078	5	2670246	2671831	-	Cytokinin-N-glucosyltransferase 2	indirect/*in-silico*	-	-
LG5:11-35	gene06474	5	4458540	4460837	+	Sterol 3-beta-glucosyltransferase	indirect/*in-silico*	-	-
LG5:11-35	gene01827	5	5329222	5332878	+	Beta-1,3-glucosyltransferase (Beta3Glc-T)	indirect/*in-silico*	-	-
LG5:11-35	gene01913	5	5801107	5801573	-	UGT74B1 (UDP-glucosyl transferase 74B1); UDP-glycosyltransferase/ thiohydroximate beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	indirect/*in-silico*	-	-
LG5:11-35	gene32066	5	2624652	2626119	+	Leucoanthocyanidin reductase (LAR)	indirect/*in-silico*	-	-
LG5:11-35	gene32069	5	2633279	2639066	+	Leucoanthocyanidin reductase (LAR)	indirect/*in-silico*	-	-
LG5:41-50	gene09310	5	9635161	9635477	-	Trans-cinnamate 4-monooxygenase (CA4H)	indirect/*in-silico*	-	-
LG5:41-50	gene25804	5	7641390	7644028	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG5:41-50	gene26144	5	8034151	8035611	+	Cytokinin-O-glucosyltransferase 3 (AtZOG3)	indirect/*in-silico*	-	-
LG5:41-50	gene09479	5	10574959	10577123	-	N-hydroxythioamide S-beta-glucosyltransferase	indirect/*in-silico*	-	-
LG5:41-50	gene26058	5	7314255	7315625	+	Putative glycosyltransferase 5 (AtGT5)	indirect/*in-silico*	-	-
LG5:41-50	gene25812	5	7689307	7690320	+	Glycosyltransferase alg8	indirect/*in-silico*	-	-
LG5:41-50	gene26124	5	7941630	7944348	+	Glycosyltransferase QUASIMODO1	indirect/*in-silico*	-	-
LG5:41-50	gene09173	5	9400895	9404607	-	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 (Oligosaccharyl transferase subunit STT3)	indirect/*in-silico*	-	-
LG5:41-50	gene26127	5	7953723	7954671	-	Flavonol 4'-sulfotransferase (F4-ST)	indirect/*in-silico*	-	-
LG5:41-50	gene26129	5	7959776	7960751	-	Flavonol 4'-sulfotransferase (F4-ST)	indirect/*in-silico*	-	-

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mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG5:41-50	gene25801	5	7611467	7614828	+	Flavonoid 3'-monooxygenase (similar to)	indirect/*in-silico*	-	-
LG5:41-50	gene09319	5	9694595	9698069	-	NAD(P)H-dependent 6'-deoxychalcone synthase	indirect/*in-silico*	-	-
LG5:50-76	gene13673	5	15678176	15681122	+	4-coumarate--CoA ligase-like 6 (At4CL7)	indirect/*in-silico*	-	-
LG5:50-76	gene12222	5	25432738	25434523	+	Trans-cinnamate 4-monooxygenase (CA4H) (similar to)	indirect/*in-silico*	-	-
LG5:50-76	gene31141	5	14758574	14759621	+	Anthocyanidin 3-O-glucosyltransferase 6	indirect/*in-silico*	-	-
LG5:50-76	gene13529	5	15485873	15489175	-	Cytokinin-O-glucosyltransferase 3 (AtZOG3)	indirect/*in-silico*	-	-
LG5:50-76	gene13530	5	15489661	15491127	-	Flavonol-3-O-glycoside-7-O-glucosyltransferase 1	indirect/*in-silico*	-	-
LG5:50-76	gene13533	5	15498773	15500326	-	Cytokinin-O-glucosyltransferase 3 (AtZOG3)	indirect/*in-silico*	-	-
LG5:50-76	gene13733	5	16131690	16136960	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG5:50-76	gene13747	5	16283711	16285075	+	Anthocyanidin 3-O-glucosyltransferase 2	indirect/*in-silico*	-	-
LG5:50-76	gene29215	5	18081170	18089197	-	UDP-glucose:glycoprotein glucosyltransferase (UGT), Precursor	indirect/*in-silico*	-	-
LG5:50-76	gene11048	5	20646017	20666405	-	UDP-glucose:glycoprotein glucosyltransferase 1, Precursor	indirect/*in-silico*	-	-
LG5:50-76	gene11817	5	21547471	21549827	+	Probable dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase (similar to)	indirect/*in-silico*	-	-
LG5:50-76	gene11834	5	21623774	21632932	+	Sterol 3-beta-glucosyltransferase	indirect/*in-silico*	-	-
LG5:50-76	gene26881	5	22244850	22246286	-	Anthocyanidin 5,3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG5:50-76	gene11943	5	23627076	23628734	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG5:50-76	gene11944	5	23629744	23632598	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG5:50-76	gene11945	5	23633464	23636910	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG5:50-76	gene11947	5	23644095	23647095	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG5:50-76	gene28677	5	27927711	27929581	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG5:50-76	gene28678	5	27932031	27933732	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG5:50-76	gene31475	5	19986060	19994479	+	Glycosyltransferase 8 domain-containing protein 2	indirect/*in-silico*	-	-
LG5:50-76	gene31484	5	20059143	20064471	+	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (RPN-I), Precursor	indirect/*in-silico*	-	-
LG5:50-76	gene11885	5	21900856	21908985	-	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A (Oligosaccharyl transferase subunit STT3A)	indirect/*in-silico*	-	-
LG5:50-76	gene22073	5	26886694	26887761	-	Leucoanthocyanidin dioxygenase (LDOX)	indirect/*in-silico*	-	-
LG5:50-76	gene29275	5	19012889	19015988	+	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-

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mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG5:50-76	gene29344	5	19884512	19886406	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG5:50-76	gene31464	5	19914309	19915955	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG5:50-76	gene31465	5	19917319	19920088	-	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG5:50-76	gene02203	5	28093974	28096041	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG5:50-76	gene30008	5	27489720	27490947	-	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG6:84-101	gene10343	6	32226895	32233796	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG6:101-101	gene24025	6	34889070	34891494	-	Probable cinnamyl alcohol dehydrogenase (CAD) (similar to)	indirect/*in-silico*	-	-
LG6:101-101	gene26301	6	39160060	39161314	-	Probable cinnamyl alcohol dehydrogenase 1 (CAD 1) (similar to)	indirect/*in-silico*	-	-
LG6:101-101	gene26302	6	39162911	39164900	-	Probable cinnamyl alcohol dehydrogenase 1 (CAD 1)	indirect/*in-silico*	-	-
LG6:101-101	gene04289	6	33010952	33013229	+	Cyanohydrin beta-glucosyltransferase	indirect/*in-silico*	-	-
LG6:101-101	gene04290	6	33014034	33015688	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG6:101-101	gene04291	6	33017153	33018790	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG6:101-101	gene04292	6	33019857	33021620	+	Cytokinin-O-glucosyltransferase 2 (AtZOG2)	indirect/*in-silico*	-	-
LG6:101-101	gene04355	6	33303576	33304701	+	Anthocyanidin 5,3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG6:101-101	gene04357	6	33308740	33309777	+	Anthocyanidin 5,3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG6:101-101	gene04359	6	33318204	33320142	+	Anthocyanidin 5,3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG6:101-101	gene24019	6	34860792	34864089	-	Limonoid UDP-glucosyltransferase (Limonoid glucosyltransferase)	indirect/*in-silico*	-	-
LG6:101-101	gene28389	6	36532229	36533635	-	Cytokinin-O-glucosyltransferase 3 (AtZOG3)	indirect/*in-silico*	-	-
LG6:101-101	gene28033	6	37614645	37616820	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG6:101-101	gene28034	6	37617576	37619755	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG6:101-101	gene26341	6	38750834	38752339	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26342	6	38763106	38764539	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26345	6	38768388	38769821	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26347	6	38777880	38779358	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26348	6	38780312	38780707	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26349	6	38783826	38785229	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26351	6	38794619	38796031	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26352	6	38797763	38799214	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-

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mQTL	gene_id	LG	start	end	strand	predicted function	evidence	Gene	protein
LG6:101-101	gene26353	6	38800535	38801989	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26354	6	38803996	38805453	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26355	6	38807030	38809431	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG6:101-101	gene26356	6	38811178	38819234	+	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT) (similar to)	indirect/*in-silico*	-	-
LG6:101-101	gene26249	6	39284637	39288591	+	Limonoid UDP-glucosyltransferase (Limonoid glucosyltransferase) (similar to)	indirect/*in-silico*	-	-
LG6:101-101	gene04333	6	33206350	33210643	+	Glycosyltransferase QUASIMODO1	indirect/*in-silico*	-	-
LG6:101-101	gene26403	6	38610217	38612483	-	Xyloglucan glycosyltransferase 4 (AtCslC4)	indirect/*in-silico*	-	-
LG6:101-101	gene26408	6	38624939	38630428	-	Xyloglucan glycosyltransferase 4 (AtCslC4) (similar to)	indirect/*in-silico*	-	-
LG6:101-101	gene28428	6	36739951	36741682	+	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG7:0-10	gene23553	7	11477291	11479264	-	4-coumarate--CoA ligase-like 5 (At4CL9)	indirect/*in-silico*	-	-
LG7:0-10	gene18900	7	2092087	2093508	-	Hydroquinone glucosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene18903	7	2108331	2109770	-	Hydroquinone glucosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene35022	7	2446172	2447593	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene35023	7	2458292	2459601	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene35024	7	2461471	2462901	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene19244	7	2829139	2834660	+	Beta-1,3-glucosyltransferase (Beta3Glc-T)	indirect/*in-silico*	-	-
LG7:0-10	gene21496	7	8297082	8299639	-	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	indirect/*in-silico*	-	-
LG7:0-10	gene09273	7	9429777	9431207	+	Cytokinin-O-glucosyltransferase 1 (AtZOG1)	indirect/*in-silico*	-	-
LG7:0-10	gene23575	7	11632829	11634896	-	Ecdysteroid UDP-glucosyltransferase, Precursor	indirect/*in-silico*	-	-
LG7:0-10	gene33947	7	11874469	11875418	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene19436	7	4461260	4466479	+	Glycosyltransferase QUASIMODO1 (similar to)	indirect/*in-silico*	-	-
LG7:0-10	gene19220	7	2057466	2064027	-	Leucoanthocyanidin reductase (LAR)	indirect/*in-silico*	-	-
LG7:0-10	gene19221	7	2064948	2066734	-	Leucoanthocyanidin reductase (LAR)	indirect/*in-silico*	-	-
LG7:0-10	gene35019	7	1592524	1595127	-	Flavonol 3-sulfotransferase (F3-ST)	indirect/*in-silico*	-	-
LG7:0-10	gene19117	7	3822546	3823244	-	Flavonol 4'-sulfotransferase (F4-ST) (similar to)	indirect/*in-silico*	-	-
LG7:0-10	gene35031	7	3827259	3828278	-	Flavonol sulfotransferase-like	indirect/*in-silico*	-	-
LG7:0-10	gene35032	7	3833953	3834948	-	Flavonol sulfotransferase-like	indirect/*in-silico*	-	-
LG7:0-10	gene35033	7	3844764	3845789	-	Flavonol sulfotransferase-like	indirect/*in-silico*	-	-
LG7:0-10	gene19406	7	5056311	5060903	-	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG7:0-10	gene19407	7	5063676	5065948	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG7:0-10	gene19409	7	5067860	5069593	-	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-

Supplemental table CII. 4

mQTL	**gene_id**	**LG**	**start**	**end**	**strand**	**predicted function**	**evidence**	**Gene**	**protein**
LG7:0-10	gene29478	7	8021952	8023702	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG7:0-10	gene29479	7	8025949	8029192	-	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG7:0-10	gene29482	7	8062959	8070326	-	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR)	indirect/*in-silico*	-	-
LG7:0-10	gene29483	7	8083902	8085471	-	Dihydroflavonol-4-reductase (DFR)	indirect/*in-silico*	-	-
LG7:0-10	gene34207	7	8348123	8349112	-	Flavonol sulfotransferase-like	indirect/*in-silico*	-	-
LG7:0-10	gene19153	7	1671560	1680195	+	Flavonoid 3'-monooxygenase	indirect/*in-silico*	-	-
LG7:0-10	gene35021	7	2436393	2437509	-	Flavanone 7-O-glucoside 2''-O-beta-L-rhamnosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene35028	7	2822823	2824136	-	Flavanone 7-O-glucoside 2''-O-beta-L-rhamnosyltransferase	indirect/*in-silico*	-	-
LG7:0-10	gene04837	7	11351422	11352892	-	Chalcone synthase 9	indirect/*in-silico*	-	-
LG7:10-26	gene26305	7	15258179	15259636	-	Anthocyanin 3'-O-beta-glucosyltransferase (3'GT)	indirect/*in-silico*	-	-
LG7:10-26	gene26479	7	15446094	15453554	+	Anthocyanin 5-O-glucosyltransferase	indirect/*in-silico*	-	-
LG7:10-26	gene26609	7	15702925	15706276	+	Dolichyl-phosphate beta-glucosyltransferase (DolP-glucosyltransferase)	indirect/*in-silico*	-	-
LG7:10-26	gene20878	7	16901710	16906834	+	Cytokinin-N-glucosyltransferase 2	indirect/*in-silico*	-	-
LG7:10-26	gene20879	7	16911499	16914768	+	Cytokinin-N-glucosyltransferase 2	indirect/*in-silico*	-	-
LG7:10-26	gene20880	7	16915363	16916180	+	Cytokinin-N-glucosyltransferase 2	indirect/*in-silico*	-	-
LG7:10-26	gene34102	7	16916235	16916839	+	Cytokinin-N-glucosyltransferase 1 (similar to)	indirect/*in-silico*	-	-
LG7:10-26	gene34103	7	16918278	16919764	+	Cytokinin-N-glucosyltransferase 2	indirect/*in-silico*	-	-
LG7:10-26	gene20881	7	16920819	16921328	+	Cytokinin-N-glucosyltransferase 2 (similar to)	indirect/*in-silico*	-	-
LG7:10-26	gene20882	7	16924079	16924564	+	Cytokinin-N-glucosyltransferase 2 (similar to)	indirect/*in-silico*	-	-
LG7:10-26	gene20936	7	17180219	17180566	-	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG7:10-26	gene20937	7	17180591	17181694	+	Anthocyanidin 3-O-glucosyltransferase	indirect/*in-silico*	-	-
LG7:10-26	gene23277	7	14207556	14213042	+	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (RPN-I), Precursor	indirect/*in-silico*	-	-
LG7:10-26	gene26457	7	16475327	16477296	+	Probable CPS biosynthesis glycosyltransferase	indirect/*in-silico*	-	-
LG7:10-26	gene20980	7	17411954	17414293	-	Leucoanthocyanidin dioxygenase (LDOX)	indirect/*in-silico*	-	-
LG7:10-26	gene23367	7	15113802	15115265	-	Chalcone--flavonone isomerase 1 (Chalcone isomerase 1)	indirect/*in-silico*	-	-

Suplemental table CII. 5. F. vesca NIL collection genotyping with IStraw90® (strawberry genome v1.1)

Supplemental table CII. 5

		introgression (cM)		introgression (bp)		introgression (bp)*	
NIL	**LG**	**start**	**end**	**start**	**end**	**start**	**end**
Fb1:0-6	1	0	6	0	4.386.861		
Fb1:0-6-26	1	0	6	0	4.386.861		
Fb1:26-61	1	26	61	3.315.998	20.747.404		
Fb1:33-61	1	33	61	4.386.861	20.747.404		
Fb1:50-61	1	50	61	6.590.214	20.747.404		
Fb1:58-61	1	58	61	4.492.657	20.747.404		
Fb2:0-30	2	0	30	0	16.919.611		
Fb2:0.39	2	0	39	0	18.950.307		
Fb2:0-45	2	0	45	0	21.299.464		
Fb2:0-63	2	0	63	0	21.299.464	22.329.904	22.663.853
Fb2:0-73	2	0	73	0	22.663.853		
Fb2:39-47	2	39	47	17.562.135	21.299.464		
Fb2:39-63	2	39	63	17.562.135	21.735.578	22.279.702	22.663.853
Fb3:0-8	3	0	8	0	3.885.527		
Fb3:0-15	3	0	15	0	3.885.527		
Fb3:29-94	3	29	94	1.632.631	31.977.233	47.000	315.550
Fb3:54-94	3	54	94	5.640.150	31.977.233		
Fb4:0-20	4	0	20	0	22.629.816		
Fb4:0-31	4	0	31	0	25.264.830		
Fb4:0-44	4	0	44	0	26.591.772		
Fb4:0-78	4	0	78	0	27.173.808		
Fb4:58-78	4	58	78	26.554.022	27.173.808		
Fb5:0-11	5	0	11	0	2.346.373		
Fb5:0-20	5	0	20	0	3.377.329		
Fb5:0-35	5	0	35	0	6.412.800		
Fb5:0-76	5	0	76	0	28.390.316		
Fb5:11-76	5	11	76	1.386.925	28.390.316		
Fb5:20-76	5	20	76	1.844.732	28.390.316		
Fb5:39-76	5	39	76	6.928.955	28.390.316		
Fb5:41-76	5	41	76	7.246.484	28.390.316		
Fb5:50-76	5	50	76	11.167.415	28.390.316		
Fb6:0-5	6	0	5	0	4.282.249		
Fb6:30-39	6	30	39	4.282.249	27.676.081		
Fb6:32-32	6	32	32	8.467.792	33.982.439		
Fb6:32-39	6	32	39	8.467.792	27.724.547		
Fb6:39-39	6	39	39	27.724.547	36.467.630		
Fb6:71-101	6	71	101	33.161.314	39.317.498		
Fb6:84-101	6	84	101	31.804.961	38.408.696		

Supplemental table CII. 5

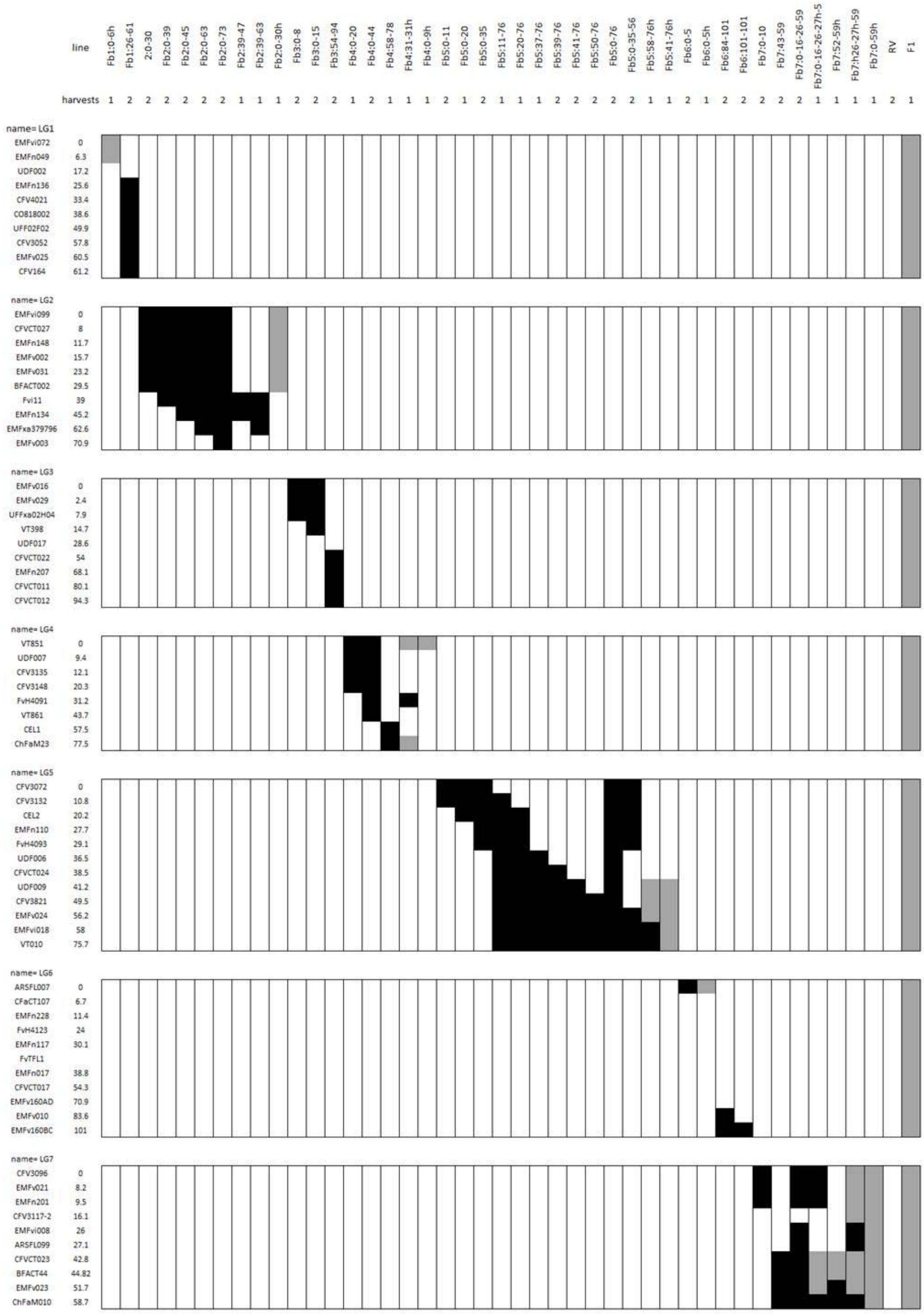
		introgression (cM)		introgression (bp)		introgression (bp)*	
NIL	**LG**	**start**	**end**	**start**	**end**	**start**	**end**
Fb6:101-101	6	101	101	32.816.413	39.317.498		
Fb7:0-10	7	0	10	0	14.169.385		
Fb7:0-27	7	0	27	0	19.258.489	21.331.516	22.511.020
Fb7:26-27	7	26	27	17.286.349	19.258.489	21.331.516	22.511.020
Fb7:26-45	7	26	45	17.286.349	19.258.489	20.175.347	22.511.020
Fb7:26-59	7	26	59	17.286.349	22.511.020		
Fb7:43-59	7	43	59	19.453.937	21.046.215		
Fb7:52-59	7	52	59	19.453.937	20.478.584		
Fb7:0-59	7	0	59	0	22.511.020		

* Double recombination events are resolved in the new *F. vesca* genome v2.0 with the reorientation of scf0513194a, scf0513171 and scf0513190 [10]

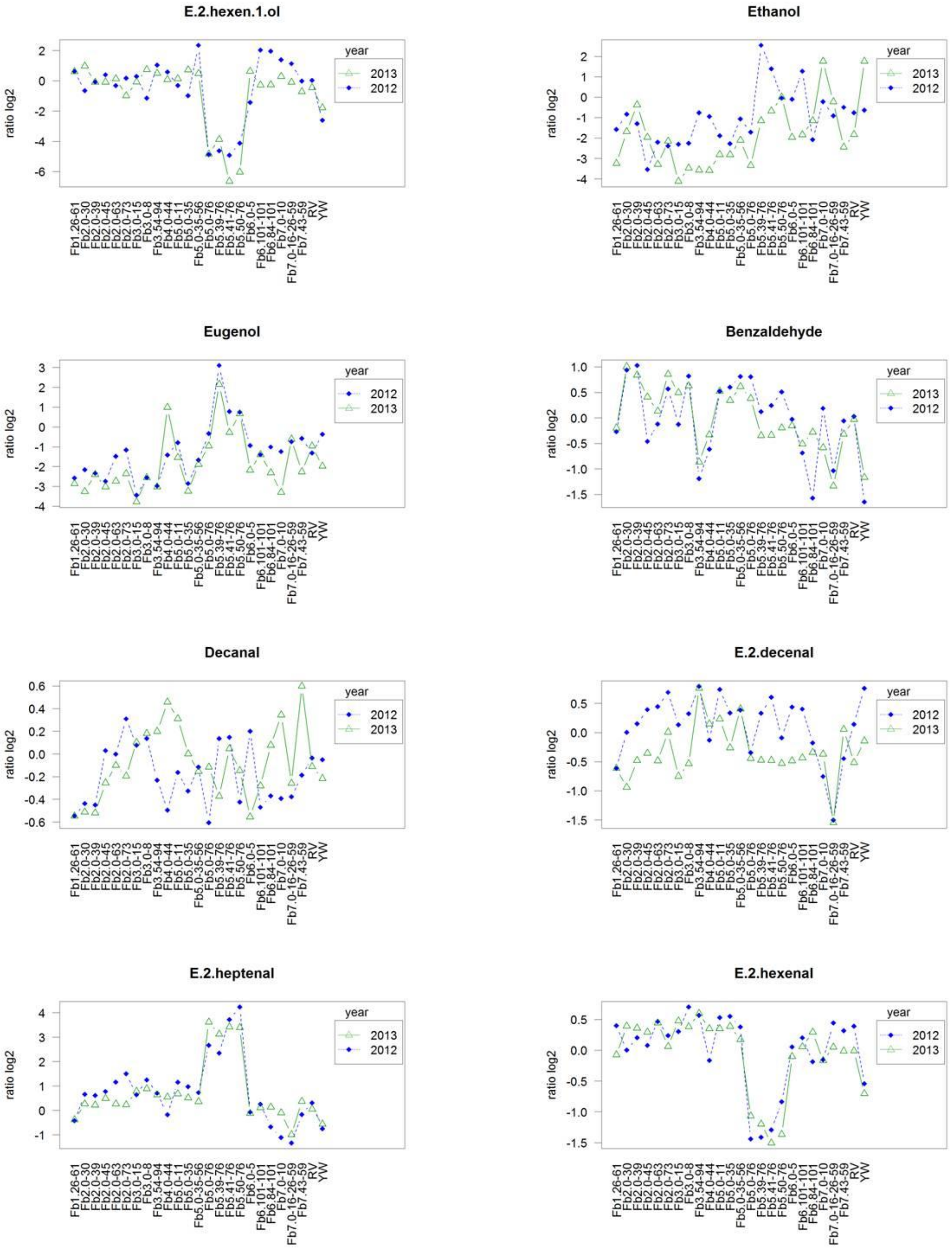
Chapter III

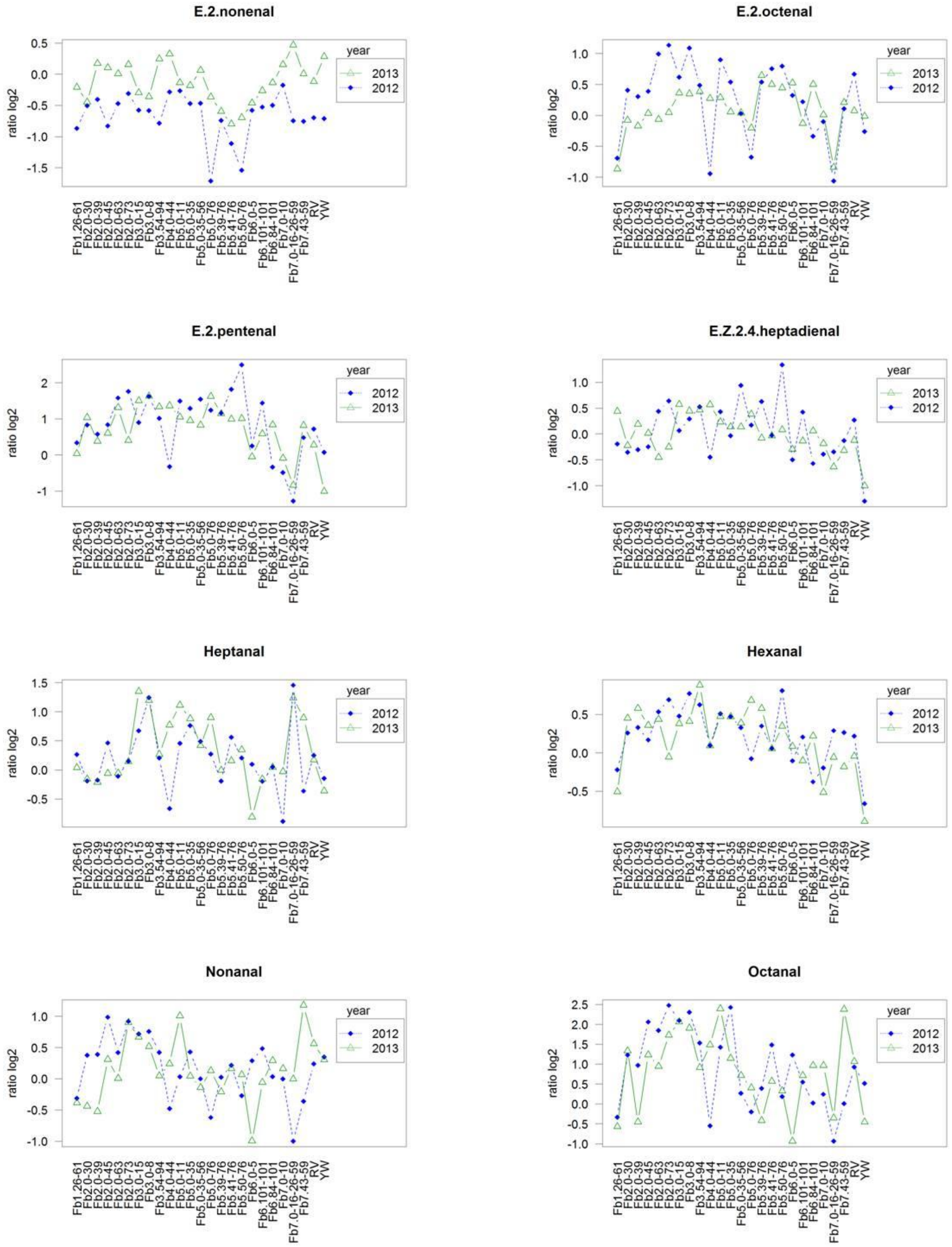
Supplementary material

Supplemental Figure CIII. 1 NIL collection genotypes: Graphical representation of near isogenic lines (NILs) from *F. vesca* (recurrent parental) x *F. bucharica* (donor parental). Lines that were evaluated in the experiments and the number of harvests that were analyzed (1 or 2) are presented on top side. At left side, the microsatellites (SSRs) used for the genotyping and their position (in cM) are presented. Color represent the genotypes codified as: *F. vesca* RV alleles in homozygosity (genetic background) in white, *F. bucharica* alleles in homozygosity (donor introgressions) in black and heterozygous introgressions in grey



Supplemental figure C.III 2 Interaction plots. Individual plots for all identified volatile





E.2.nonenal

E.2.octenal

E.2.pentenal

E.Z.2.4.heptadienal

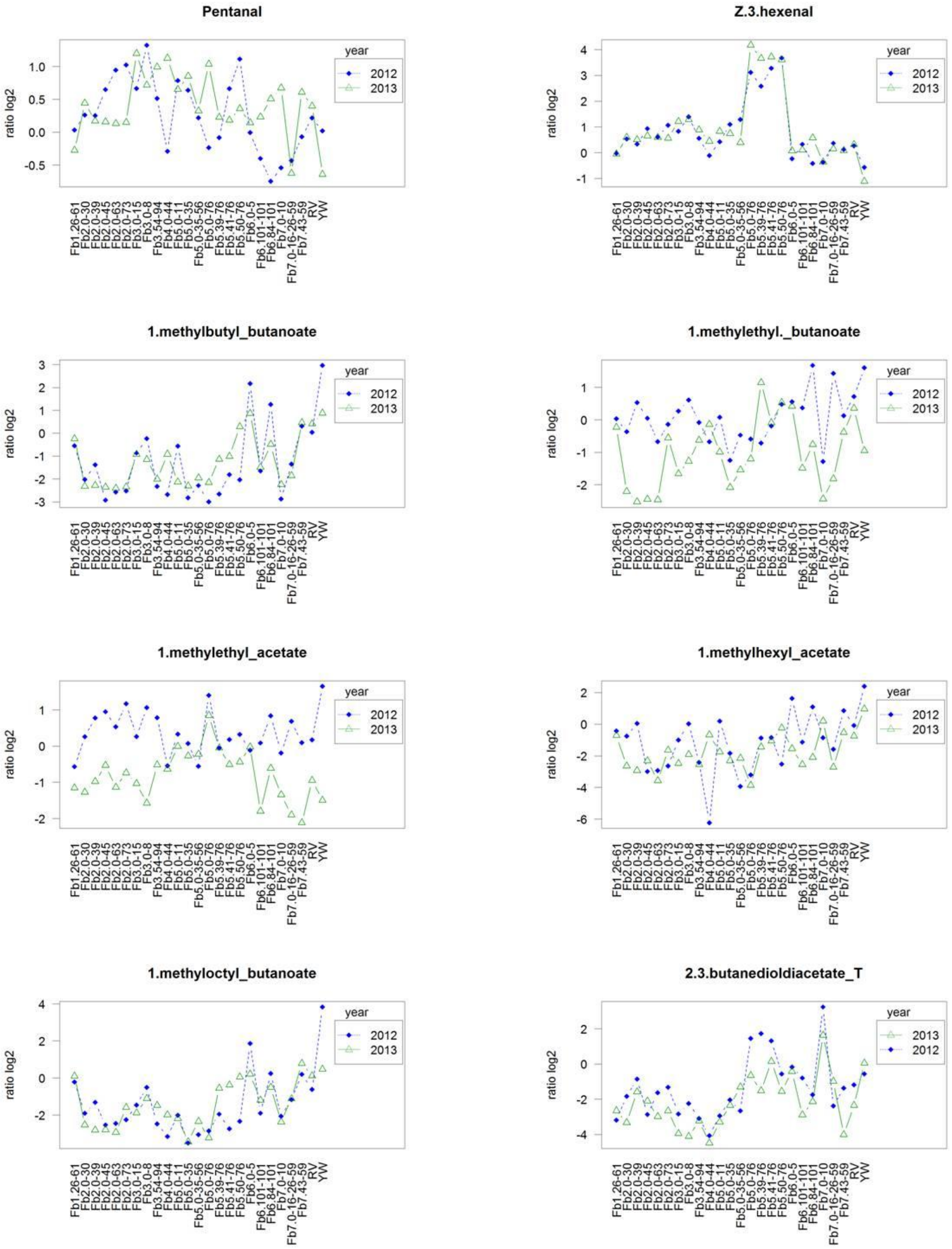
Heptanal

Hexanal

Nonanal

Octanal

Supplemental figure C.III 2 continues



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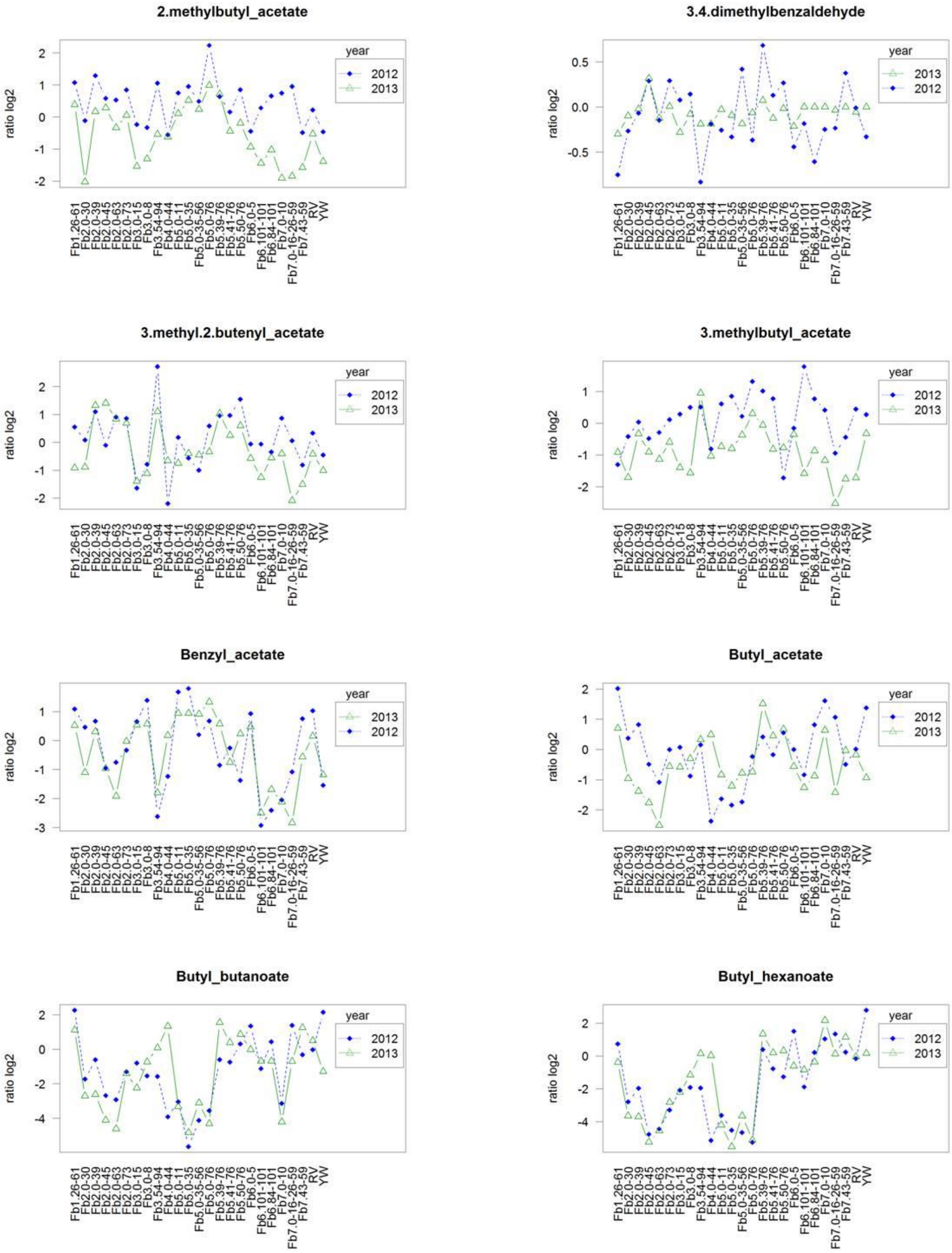

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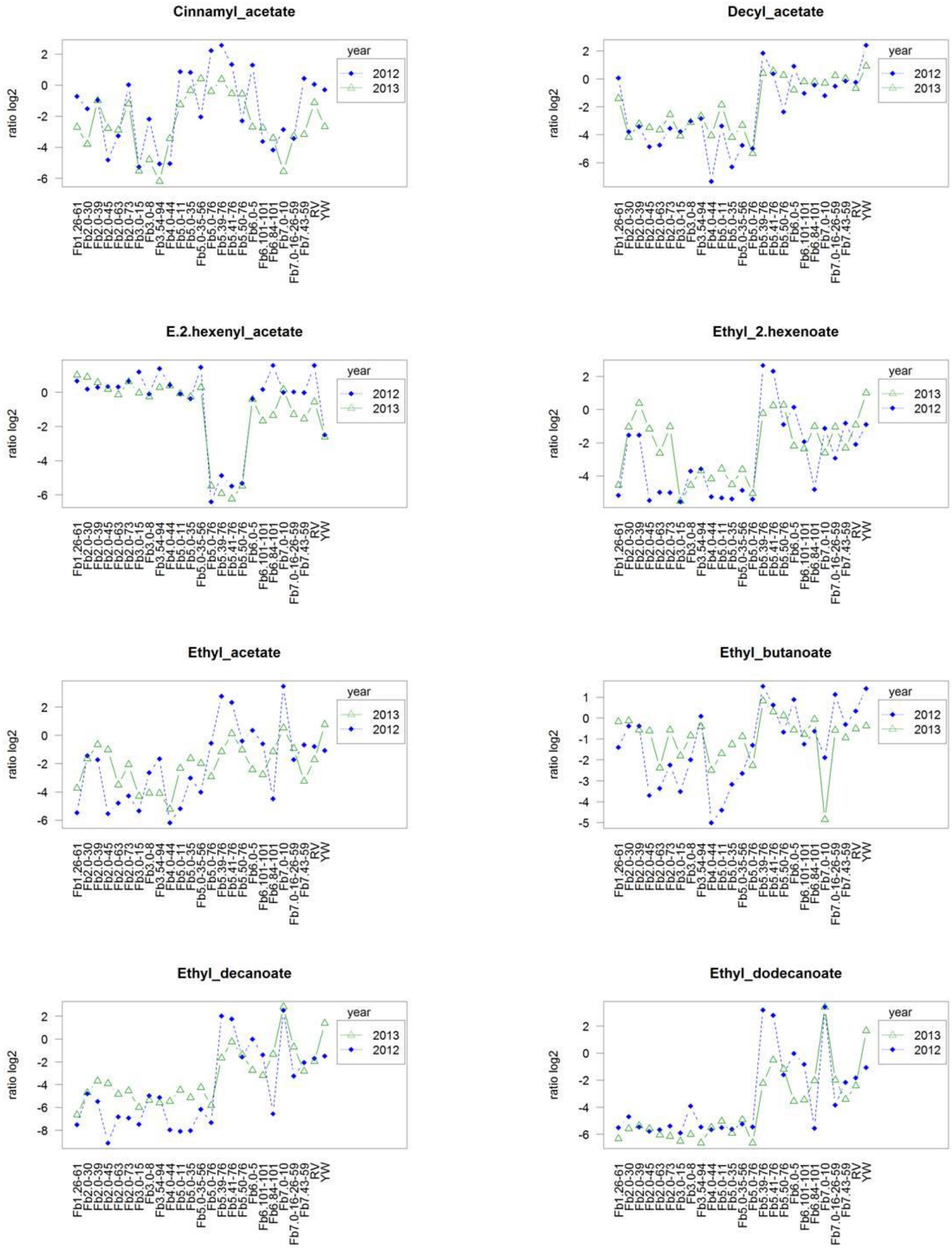

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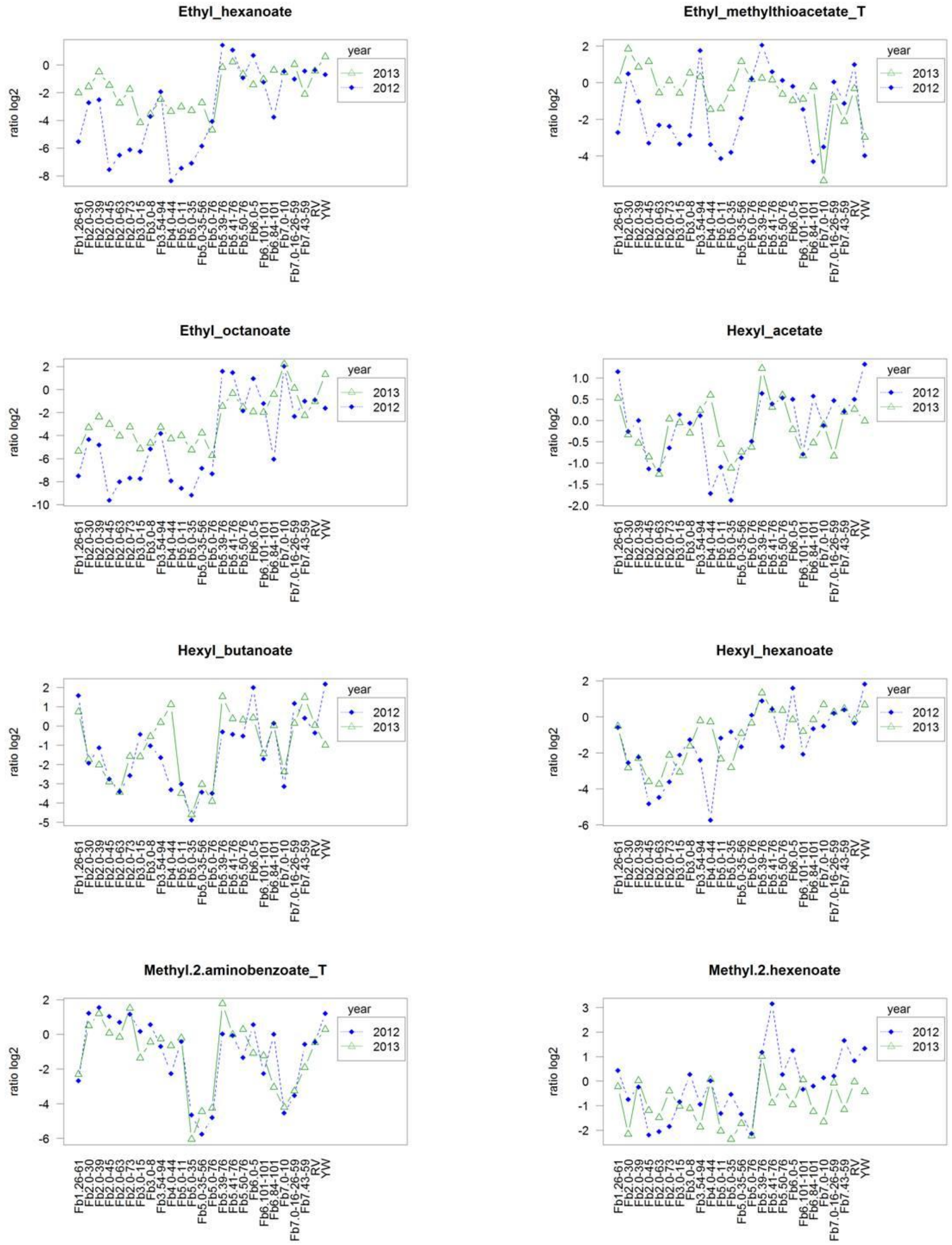

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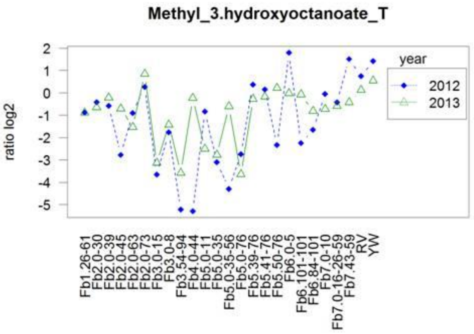

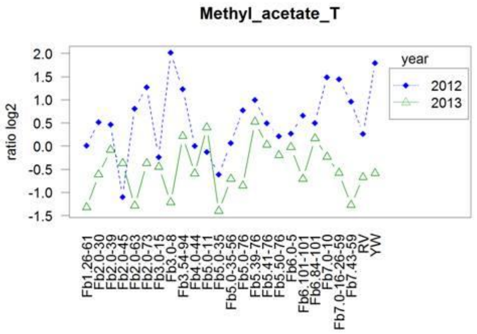

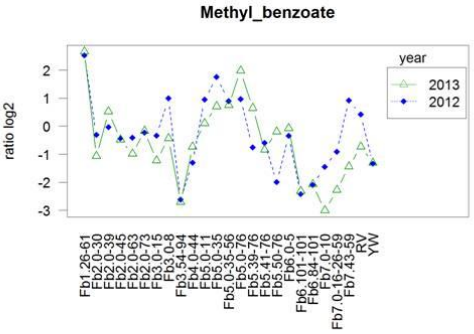

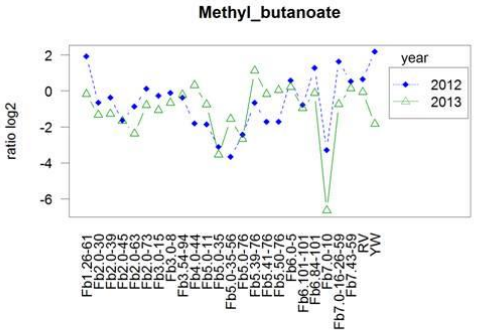

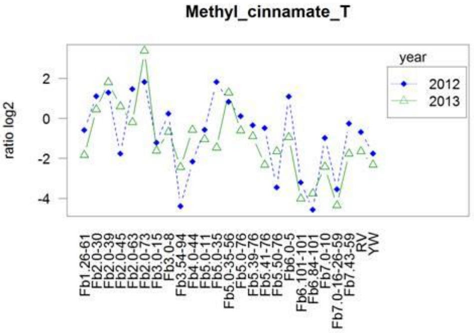

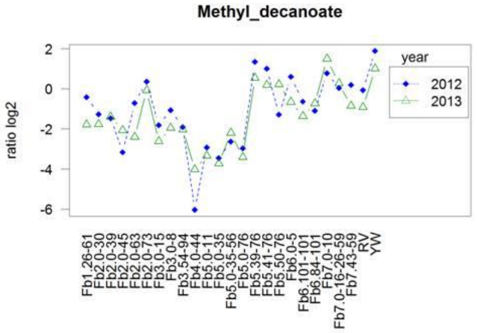

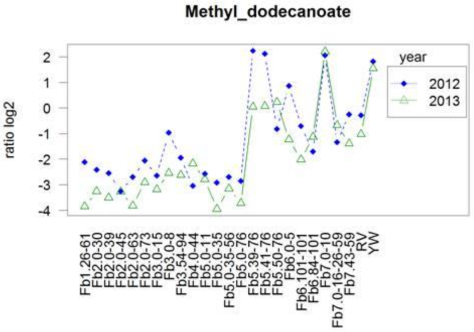

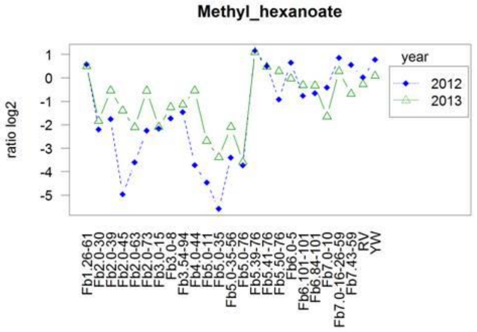

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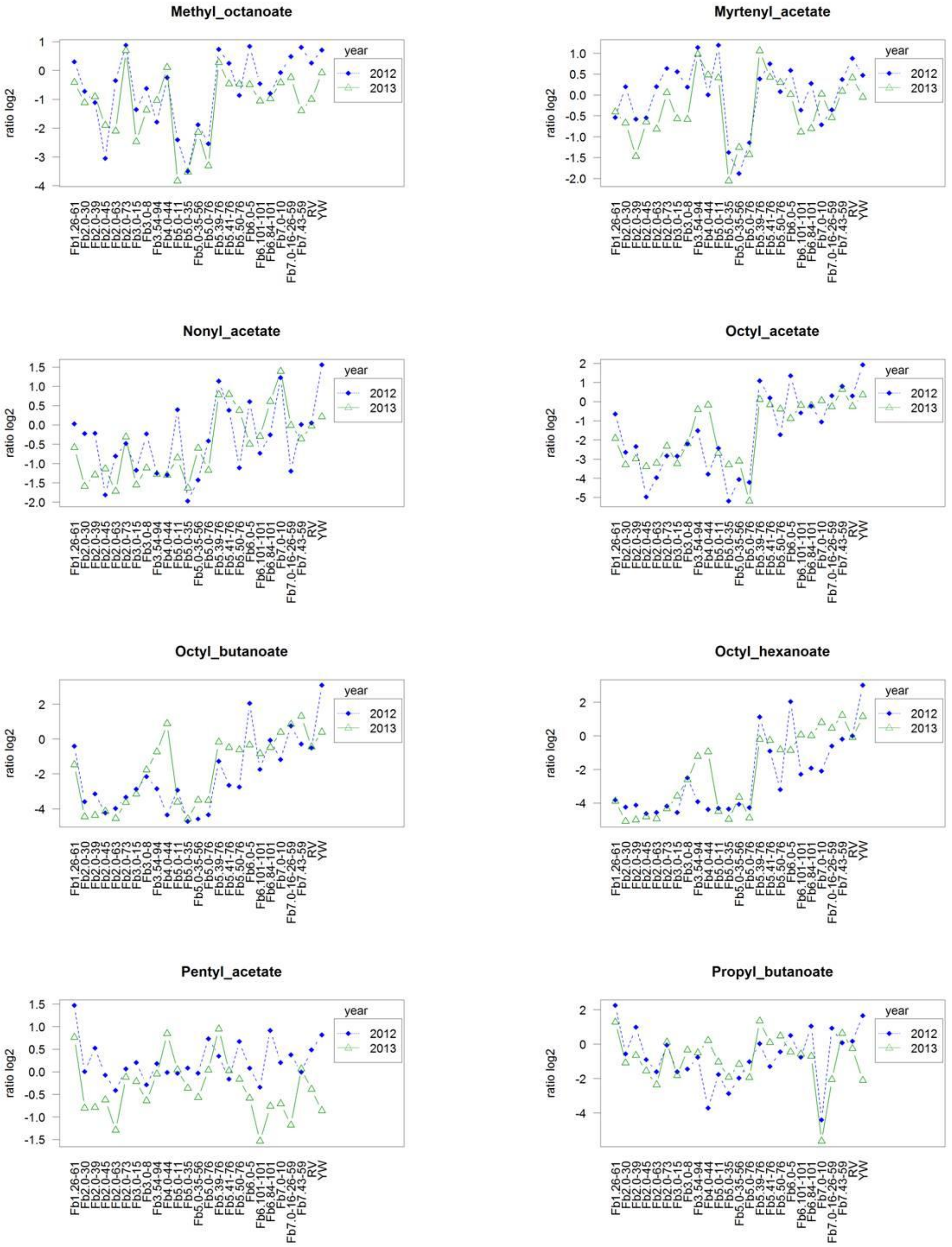

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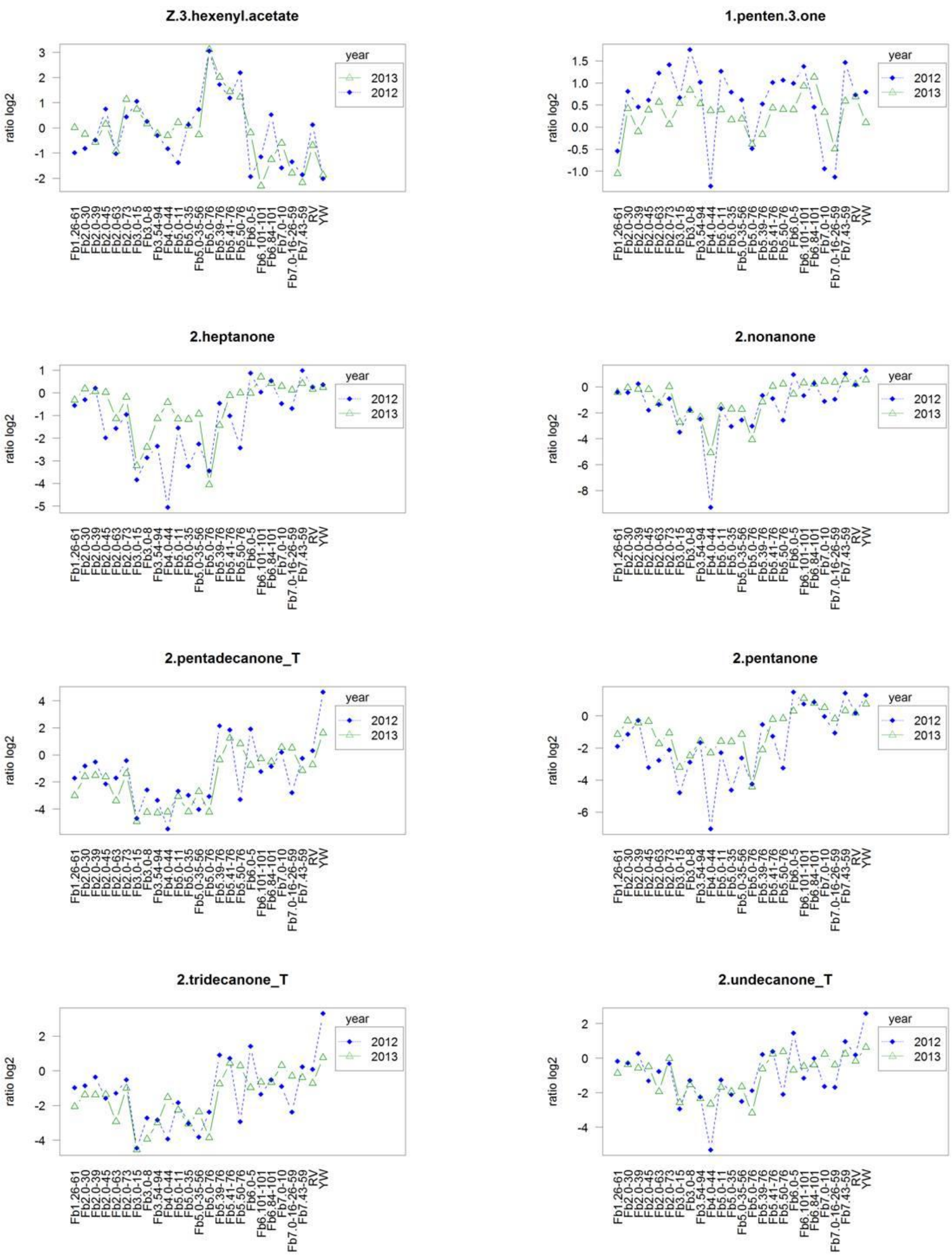

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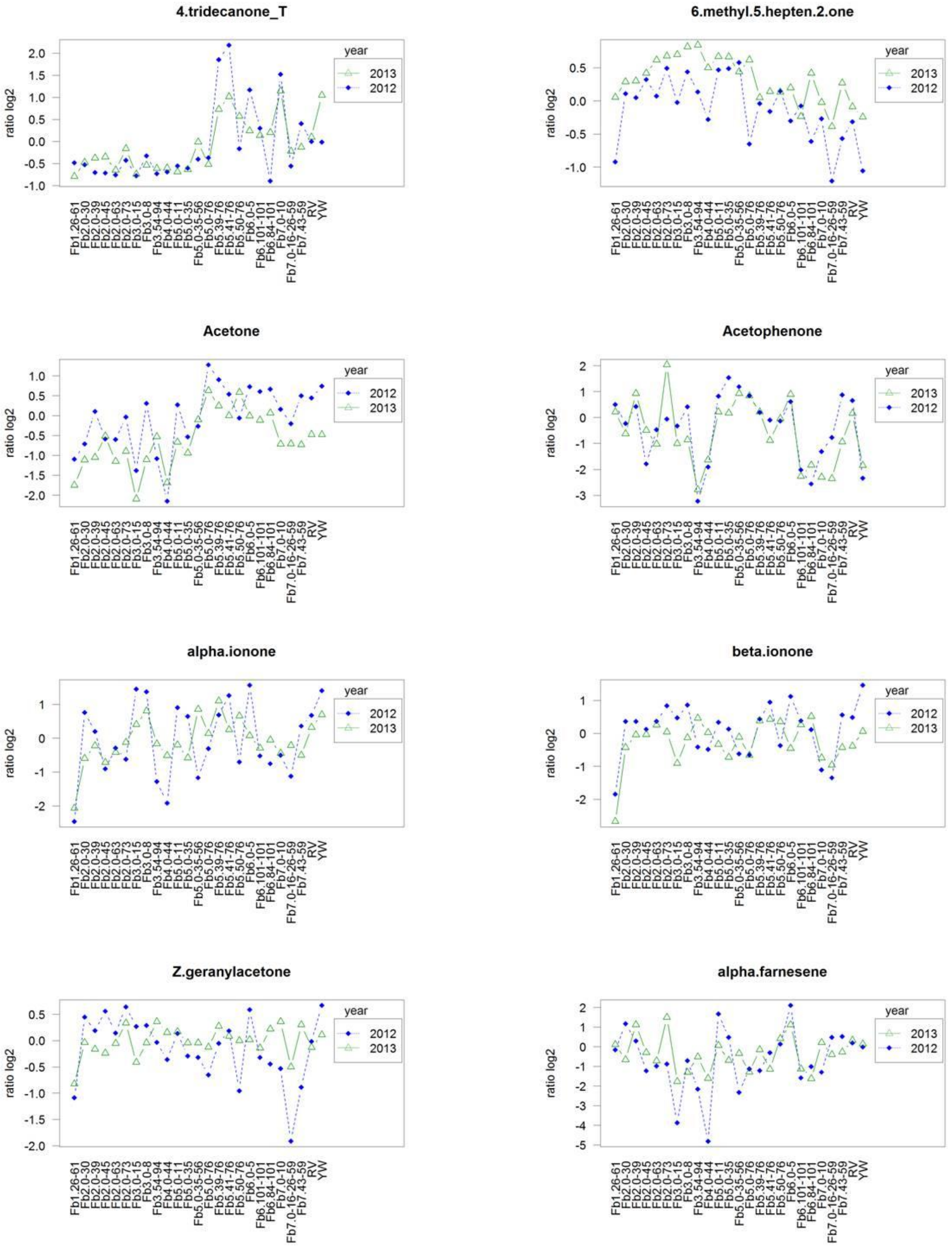

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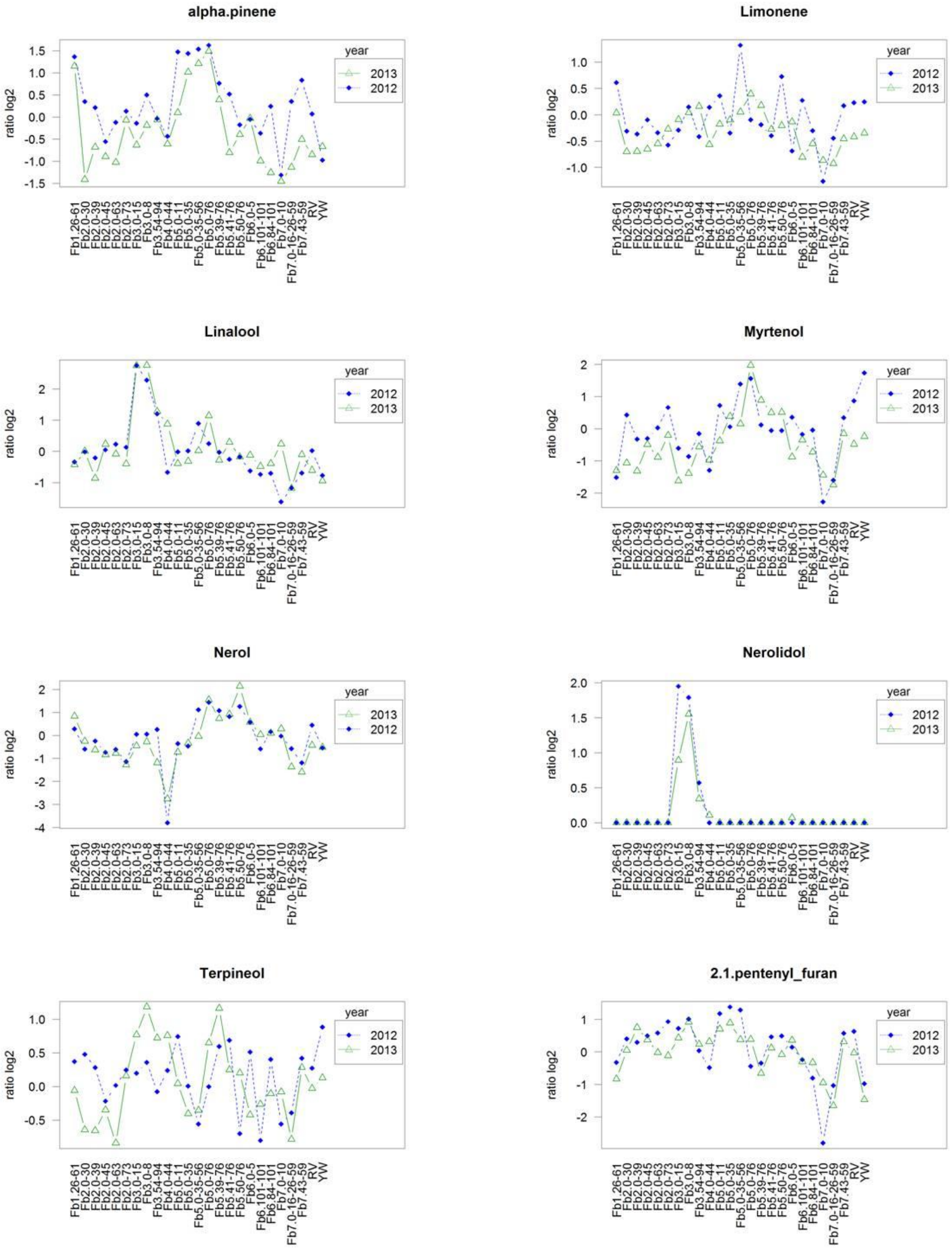

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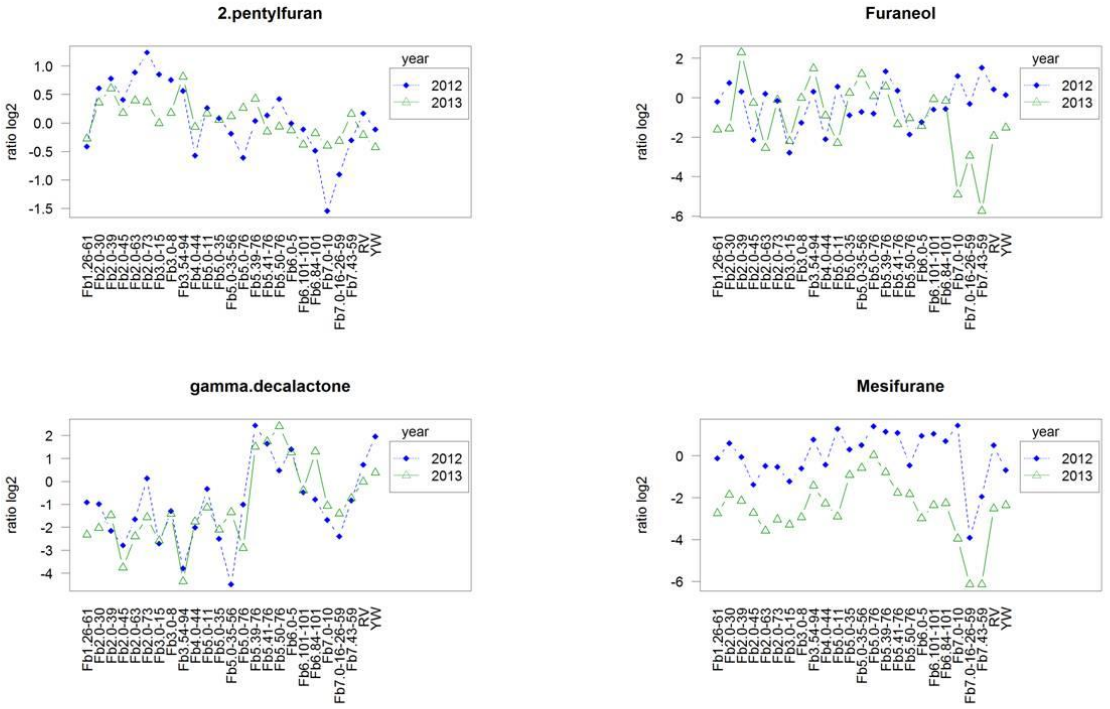


Supplemental figure C.III 2

Supplemental table CIII.1. Volatile compounds average values per genotype per year. Average values (per genotype per harvests) of all detected volatile compounds are provided. Data are expressed as the log2 ratio between the samples and a reference sample.

genotype	year	1-decanol	1-hexanol	1-octanol	1-penten-3-ol	2-heptanol	2-nonanol	2-tridecanol T	2-undecanol T	(E)-2-hexen-1-ol	Ethanol	Eugenol	3,4-dimethylbenzaldehyde	Benzaldehyde	Decanal	(E)-2-decenal	(E)-2-heptenal	(E)-2-hexenal	(E)-2-nonenal	(E)-2-octenal	(E)-2-pentenal
Fb1.26-61	2012	-1,40	-0,14	-1,68	0,23	-1,86	-1,34	-0,69	-0,76	0,62	-1,57	-2,58	-0,75	-0,27	-0,55	-0,61	-0,41	0,40	-0,87	-0,69	0,34
Fb2.0-30	2012	-3,65	-0,57	-1,42	-0,30	-1,82	-1,40	-0,60	-1,06	-0,66	-0,83	-2,16	-0,27	0,94	-0,44	0,00	0,66	0,00	-0,50	0,41	0,83
Fb2.0-30h	2012	-4,68	-0,46	-2,02	-1,05	-3,19	-1,98	-0,86	-1,27	-0,18	-2,59	-3,14	0,52	0,80	-0,16	0,49	1,26	0,00	-0,41	0,91	1,52
Fb2.0-39	2012	-3,70	-0,14	-1,32	-0,16	-1,48	-0,66	-0,11	-0,73	-0,07	-1,29	-2,34	-0,07	1,03	-0,45	0,15	0,62	0,21	-0,41	0,30	0,57
Fb2.0-45	2012	-4,82	0,66	-1,35	-0,28	-3,85	-2,86	-1,75	-2,68	0,40	-3,54	-2,74	0,29	-0,46	0,03	0,39	0,78	0,08	-0,83	0,39	0,84
Fb2.0-63	2012	-3,93	-0,34	-1,68	0,30	-3,72	-2,28	-1,64	-1,78	-0,32	-2,20	-1,48	-0,15	-0,12	0,00	0,45	1,17	0,47	-0,47	0,99	1,58
Fb2.0-73	2012	-3,16	-0,02	-0,96	0,50	-2,79	-1,67	-0,13	-0,94	0,17	-2,38	-1,16	0,29	0,57	0,31	0,69	1,51	0,24	-0,31	1,14	1,76
Fb3.0-15	2012	-4,44	0,28	-2,01	0,32	-3,48	-3,04	-3,97	-3,30	0,28	-2,31	-3,44	0,08	-0,13	0,08	0,13	0,65	0,30	-0,58	0,62	0,90
Fb3.0-8	2012	-2,93	0,09	-1,23	0,08	-1,44	-1,49	-1,43	-1,05	-1,15	-2,26	-2,56	0,14	0,82	0,14	0,32	1,26	0,70	-0,58	1,09	1,62
Fb3.54-94	2012	-3,76	0,64	-1,54	0,91	-3,87	-3,28	-2,45	-3,10	1,04	-0,76	-2,97	-0,83	-1,19	-0,23	0,79	0,72	0,57	-0,79	0,49	1,01
Fb4-0-9h	2012	0,54	-0,97	0,52	-0,50	0,46	0,68	0,98	0,86	-2,03	1,17	-1,31	-0,59	-0,45	-0,29	-0,25	-0,58	-0,41	-0,48	-0,26	-0,51
Fb4.0-44	2012	-6,25	-0,54	-3,03	0,14	-6,87	-9,62	-3,09	-4,28	0,59	-0,94	-1,42	-0,19	-0,62	-0,50	-0,13	-0,18	-0,17	-0,29	-0,95	-0,33
Fb4.31-31h	2012	1,15	0,15	1,12	0,35	0,30	0,24	0,50	0,48	0,27	0,05	-0,88	-0,32	-0,48	-0,16	0,49	0,13	0,03	-0,50	0,09	0,32
Fb5.0-11	2012	-3,80	-0,10	-1,65	0,37	-1,91	-1,50	-1,41	-1,45	-0,31	-1,89	-0,78	-0,26	0,52	-0,16	0,74	1,16	0,53	-0,27	0,90	1,49
Fb5.0-35	2012	-5,44	-0,99	-2,39	-0,71	-3,85	-3,59	-2,20	-3,00	-0,98	-2,27	-2,85	-0,33	0,60	-0,33	0,34	0,98	0,55	-0,47	0,54	1,29
Fb5.0-35-56	2012	-3,22	1,52	-1,86	1,26	-4,21	-4,23	-2,46	-3,07	2,35	-1,06	-1,67	0,42	0,81	-0,12	0,39	0,74	0,38	-0,47	0,03	1,55
Fb5.0-76	2012	-4,41	0,94	-2,27	0,64	-4,30	-3,93	-1,42	-2,68	-4,88	-1,71	-0,33	-0,37	0,80	-0,61	-0,34	2,67	-1,44	-1,71	-0,68	1,24
Fb5.39-76	2012	2,18	0,40	1,09	0,72	0,33	-0,42	1,32	0,67	-4,63	2,55	3,11	0,68	0,12	0,14	0,33	2,35	-1,41	-0,74	0,54	1,16
Fb5.41-76	2012	0,90	0,11	0,33	-0,40	-0,20	-0,42	0,85	0,44	-4,91	1,40	0,78	0,13	0,24	0,15	0,60	3,72	-1,29	-1,11	0,76	1,81
Fb5.41-76h	2012	0,01	1,23	0,25	0,02	-1,18	-0,52	-0,73	-0,70	1,51	0,19	-0,63	-0,02	-0,82	-0,19	-0,57	-0,81	-0,48	-0,70	-0,63	-0,56
Fb5.50-76	2012	-1,56	1,26	-0,51	1,67	-2,00	-2,11	-2,46	-1,69	-4,12	-0,04	0,75	0,27	0,51	-0,42	-0,09	4,24	-0,84	-1,54	0,80	2,49
Fb5.58-76h	2012	1,85	0,31	1,40	-0,83	1,15	1,17	1,46	2,10	-2,14	1,97	-0,96	-0,79	-0,57	-0,20	0,45	-0,18	-0,14	-0,16	0,78	0,19
Fb6.0-5h	2012	0,69	-0,63	0,27	-0,26	0,71	0,60	0,96	0,60	-1,16	0,79	-0,62	-0,03	-0,48	-0,41	-0,43	-0,37	-0,07	-1,31	-0,60	-0,47
Fb6.0-5	2012	1,19	-0,76	0,93	-0,48	1,45	1,23	1,80	1,60	-1,44	-0,09	-0,93	-0,44	-0,03	0,20	0,44	-0,07	0,06	-0,58	0,32	0,25
Fb6.101-101	2012	-0,57	0,73	0,18	1,40	-0,50	-1,32	-1,54	-1,47	2,03	1,27	-1,40	-0,18	-0,69	-0,47	0,40	0,26	0,20	-0,53	0,22	1,44
Fb6.84-101	2012	-0,70	1,23	0,16	-0,16	0,58	0,58	-1,04	-0,28	1,96	-2,08	-1,01	-0,61	-1,57	-0,37	-0,18	-0,67	-0,18	-0,50	-0,34	-0,33
Fb7-0-16-26-27h-59	2012	-0,15	0,68	0,20	-0,54	-0,47	-1,36	-0,30	-1,09	0,60	0,97	-0,45	-0,34	-0,95	-0,64	-1,45	-1,81	0,32	-0,62	-0,62	-1,11
Fb7-52-59h	2012	0,01	-0,35	0,22	0,09	0,82	0,49	0,15	0,40	-0,20	-1,19	0,00	-0,69	-0,77	-0,67	-1,23	-1,05	-0,25	-1,45	-1,09	-0,33
Fb7.0-10	2012	-1,34	0,82	0,07	-0,38	0,12	-0,93	-0,34	-0,64	1,40	-0,22	-1,24	-0,25	0,19	-0,39	-0,75	-1,11	-0,15	-0,18	-0,10	-0,48
Fb7.0-16-26-59	2012	-0,65	0,86	0,07	-0,13	-0,58	-1,11	-1,17	-1,00	1,14	-0,91	-0,74	-0,23	-1,03	-0,38	-1,50	-1,33	0,44	-0,75	-1,06	-1,28
Fb7.0-59h	2012	0,06	-0,21	-0,54	-0,74	-0,06	0,72	0,10	1,19	-0,29	-1,60	-0,95	-0,51	-0,92	-0,35	-0,57	-0,74	-0,04	-0,96	-0,69	-1,47
Fb7.43-59	2012	0,11	-0,06	0,55	0,17	0,92	1,01	0,77	1,03	-0,02	-0,49	-0,58	0,38	-0,06	-0,19	-0,45	-0,16	0,32	-0,76	0,11	0,48
Fb7.h26-27h-59	2012	-0,87	0,49	-0,85	0,53	-1,02	-0,95	-1,32	-0,61	1,37	-1,82	-1,45	-0,69	-0,93	-0,68	-1,04	-0,66	0,22	-1,84	-0,95	0,46
RV	2012	-0,29	0,02	0,56	0,19	0,04	0,10	-0,19	0,06	0,03	-0,76	-1,31	-0,01	0,03	-0,04	0,14	0,32	0,39	-0,70	0,67	0,72
YW	2012	1,97	0,16	1,02	-0,80	2,21	2,42	4,22	2,95	-2,61	-0,64	-0,37	-0,33	-1,65	-0,05	0,76	-0,74	-0,54	-0,71	-0,26	0,07
F1	2013	1,12	-0,26	1,16	-0,17	0,77	0,58	1,49	1,31	0,04	0,27	-1,39	0,01	-0,22	0,33	0,33	0,06	-0,17	0,27	0,39	0,41
Fb1.0-6h	2013	-1,06	0,39	-0,04	0,12	-1,05	-1,07	-1,78	-1,43	0,54	-1,40	-1,51	0,00	-0,98	-0,67	-1,19	-0,36	0,12	-0,36	-0,86	-0,26
Fb1.26-61	2013	-2,44	-0,04	-2,18	-0,12	-1,86	-1,77	-2,29	-1,61	0,60	-3,25	-2,86	-0,30	-0,20	-0,55	-0,61	-0,38	-0,07	-0,21	-0,87	0,03
Fb2.0-30	2013	-3,52	0,71	-2,23	0,55	-2,27	-1,62	-1,74	-1,48	0,96	-1,69	-3,25	-0,10	1,00	-0,51	-0,94	0,27	0,39	-0,45	-0,08	1,04
Fb2.0-39	2013	-3,34	-0,20	-2,28	-0,03	-2,74	-1,93	-1,10	-1,52	-0,09	-0,38	-2,40	-0,02	0,84	-0,52	-0,48	0,22	0,36	0,17	-0,17	0,38
Fb2.0-45	2013	-3,34	0,01	-1,94	0,02	-2,49	-1,62	-1,78	-1,78	-0,08	-1,97	-3,02	0,32	0,41	-0,26	-0,35	0,49	0,29	0,10	0,03	0,60
Fb2.0-63	2013	-3,58	0,20	-2,49	-0,05	-3,42	-2,95	-2,89	-2,81	0,14	-3,30	-2,74	-0,12	0,13	-0,10	-0,49	0,27	0,44	0,01	-0,07	1,31
Fb2.0-73	2013	-2,65	-0,43	-1,42	-0,40	-2,15	-1,19	-0,83	-0,72	-0,99	-2,15	-2,36	0,01	0,86	-0,20	0,01	0,24	0,06	0,16	0,05	0,41
Fb2.39-47	2013	0,94	-0,88	0,22	-0,39	-1,24	-0,46	0,35	0,32	-1,33	-2,56	-1,32	-0,10	-0,25	0,09	-0,04	0,15	0,09	0,15	0,02	0,44
Fb2.39-63	2013	0,52	0,01	-0,32	0,07	-2,24	-1,44	-0,86	-0,63	-0,20	-2,08	-2,41	-0,11	-0,03	0,13	0,08	0,55	0,24	0,13	0,18	1,04
Fb3.0-15	2013	-3,93	0,23	-1,97	0,12	-2,96	-2,48	-4,31	-3,04	-0,08	-4,12	-3,78	-0,28	0,49	0,10	-0,75	0,79	0,48	-0,30	0,36	1,50
Fb3.0-8	2013	-2,97	0,64	-1,35	0,28	-2,25	-1,56	-3,49	-2,16	0,74	-3,47	-2,55	-0,08	0,63	0,18	-0,54	0,90	0,39	-0,36	0,35	1,63
Fb3.54-94	2013	-3,01	0,37	-0,68	0,51	-3,35	-3,30	-2,71	-2,77	0,49	-3,58	-3,03	-0,19	-0,86	0,20	0,76	0,65	0,60	0,25	0,38	1,33
Fb4.0-20	2013	-0,11	0,45	0,84	0,25	-0,96	-0,34	-1,48	-1,27	0,22	-3,79	-0,32	-0,13	-0,63	1,00	-0,23	0,38	0,35	0,30	0,49	0,85
Fb4.0-44	2013	-3,77	0,03	-0,43	0,42	-1,41	-5,27	-1,45	-3,24	0,07	-3,58	0,99	-0,19	-0,33	0,46	0,15	0,55	0,35	0,32	0,27	1,36
Fb4.58-78	2013	-1,60	-0,03	-0,97	-0,01	-0,85	-0,28	-1,06	-0,40	-0,32	-1,95	-2,40	-0,11	0,94	0,10	0,02	0,51	0,38	0,10	0,18	0,97
Fb5.0-11	2013	-3,26	0,17	-1,38	0,17	-2,49	-2,12	-2,45	-2,54	0,13	-2,81	-1,54	-0,03	0,52	0,31	0,23	0,68	0,35	-0,13	0,29	1,05
Fb5.0-20	2013	-3,87	0,08	-1,88	0,55	-3,16	-2,49	-2,70	-2,75	0,03	-4,13	-1,69	0,00	0,48	-0,30	-0,15	0,46	0,49	-0,29	-0,10	0,99
Fb5.0-35	2013	-4,43	0,43	-2,09	0,24	-3,11	-3,03	-3,33	-3,14	0,73	-2,81	-3,24	-0,09	0,34	0,00	-0,26	0,51	0,39	-0,18	0,05	0,95
Fb5.0-35-56	2013	-3,23	0,18	-1,75	0,19	-2,93	-3,23	-2,18	-2,56	0,47	-2,10	-1,89	-0,18	0,61	-0,15	0,41	0,36	0,17	0,06	0,04	0,83
Fb5.0-76	2013	-5,09	0,15	-2,32	0,49	-4,52	-4,28	-2,80	-3,29	-4,84	-3,34	-0,95	-0,06	0,38	-0,12	-0,45	3,62	-1,07	-0,37	-0,20	1,62
Fb5.11-76	2013	-3,23	0,04	-1,13	0,08	-1,85	-1,67	-2,46	-2,85	-5,89	-4,21	-1,91	0,20	0,35	0,09	-0,88	3,65	-1,07	-0,84	0,19	1,43
Fb5.20-76	2013	-2,16	0,28	-0,91	0,37	-0,92	-1,06	-1,87	-2,25	-5,88	-1,72	-1,70	0,00	0,62	0,28	-0,34	4,04	-0,89	-0,34	0,24	1,95
Fb5.37-76	2013	-1,99	0,27	-1,60	0,02	-3,20	-3,01	-2,00	-2,47	-4,14	-3,71	1,10	0,07	-0,46	-1,00	-1,88	3,00	-1,25	-1,05	-0,69	0,64
Fb5.39-76	2013	0,29	0,70	-0,04	0,36	-1,67	-1,52	-0,31	-0,88	-3,87	-1,15	2,15	0,07	-0,35	-0,37	-0,47	3,13	-1,20	-0,60	0,65	1,14
Fb5.41-76	2013	0,62	-0,27	-0,02	0,04	-0,70	-0,49	0,77	0,00	-6,64	-0,67	-0,27	-0,12	-0,34	0,05	-0,48	3,42	-1,51	-0,80	0,50	0,99
Fb5.50-76	2013	0,35	0,07	-0,14	0,13	-0,01	0,19	0,77	0,26	-6,04	0,00	0,66	-0,01	-0,20	-0,15	-0,53	3,40	-1,36	-0,70	0,45	1,01
Fb6.0-5	2013	-0,63	0,44	-0,28	0,18	-1,03	-1,49	-0,68	-0,92	0,64	-1,97	-2,18	-0,21	-0,16	-0,55	-0,48	-0,12	-0,10	-0,46	0,53	-0,05
Fb6.101-101	2013	0,32	-0,35	0,32	-0,03	-0,80	-0,76	-0,39	-0,64	-0,29	-1,84	-1,39	0,00	-0,51	-0,28	-0,44	0,12	0,06	-0,26	-0,13	0,58
Fb6.84-101	2013	0,18	-0,37	0,13	0,07	-0,76	-0,57	-0,89	-0,63	-0,25	-1,15	-2,32	0,00	-0,28	0,08	-0,34	0,13	0,30	-0,13	0,50	0,83
Fb7.0-10	2013	-0,07	0,15	0,17	-0,88	-0,54	0,48	-1,77	-0,02	0,28	1,77	-3,29	0,00	-0,59	0,34	-0,37	-0,10	-0,17	0,15	0,01	-0,09
Fb7.0-16-26-59	2013	0,37	0,09	-0,12	-0,88	-1,17	-0,66	0,37	0,11	-0,09	-0,22	-0,61	-0,03	-1,33	-0,26	-1,55	-0,99	0,05	0,47	-0,84	-0,84
Fb7.43-59	2013	0,21	-0,25	0,85	0,17	-0,17	0,36	-0,66	-0,14	-0,72	-2,44	-2,26	0,00	-0,32	0,60	0,05	0,38	-0,01	0,01	0,21	0,82
H4	2013	-0,29	0,02	-0,33	0,08	-0,16	0,22	0,54	0,60	0,04	-3,41	3,13	-0,03	-0,77	-0,21	0,40	-0,06	0,03	0,14	-0,15	0,30
RV	2013	-0,54	-0,11	-0,16	-0,31	-0,57	-0,19	-0,68	-0,40	-0,45	-1,83	-0,97	-0,06	-0,03	-0,11	-0,51	0,06	-0,01	-0,12	0,07	0,27
YW	2013	1,27	-0,39	0,87	-1,05	1,09	1,27	1,11	0,87	-1,78	1,77	-1,98	0,00	-1,16	-0,22	-0,14	-0,56	-0,70	0,28	-0,01	-1,00

Supplemental table CIII. 1 continues

genotype	year	(E,Z)-2,4-heptadienal	Heptanal	Hexanal	Nonanal	Octanal	Pentanal	(Z)-3-hexenal	1-methylbutyl butanoate	1-methylethyl butanoate	1-methylethyl acetate	1-methylhexyl acetate	1-methyloctyl butanoate	2,3-butanedioldiacetate T	2 -methylbutyl acetate	3-methyl-2-butenyl acetate	3-methylbutyl acetate	Benzyl acetate	Butyl acetate	Butyl butanoate	Butyl hexanoate
Fb1.26-61	2012	-0,19	0,26	-0,22	-0,31	-0,33	0,03	-0,02	-0,54	0,03	-0,56	-0,42	-0,22	-3,19	1,07	0,55	-1,30	1,08	2,02	2,26	0,74
Fb2.0-30	2012	-0,35	-0,19	0,26	0,38	1,23	0,26	0,54	-2,02	-0,36	0,26	-0,75	-1,91	-1,84	-0,11	0,09	-0,42	0,46	0,37	-1,73	-2,80
Fb2.0-30h	2012	0,04	0,22	0,46	0,62	1,84	0,95	0,66	-2,44	0,36	1,05	-1,59	-2,17	-2,63	0,89	0,38	-0,52	0,69	0,73	-1,36	-2,95
Fb2.0-39	2012	-0,30	-0,17	0,33	0,39	0,97	0,25	0,34	-1,38	0,54	0,78	0,05	-1,32	-0,86	1,29	1,10	0,03	0,66	0,82	-0,61	-1,98
Fb2.0-45	2012	-0,25	0,46	0,17	0,99	2,06	0,65	0,93	-2,93	0,05	0,95	-2,98	-2,54	-2,87	0,58	-0,11	-0,48	-0,96	-0,49	-2,68	-4,77
Fb2.0-63	2012	0,44	-0,11	0,54	0,42	1,85	0,95	0,61	-2,57	-0,67	0,54	-2,92	-2,46	-1,64	0,53	0,91	-0,29	-0,75	-1,09	-2,92	-4,44
Fb2.0-73	2012	0,64	0,15	0,69	0,92	2,48	1,02	1,07	-2,51	-0,14	1,17	-2,64	-2,26	-1,32	0,85	0,86	0,11	-0,33	0,00	-1,30	-3,30
Fb3.0-15	2012	0,07	0,67	0,48	0,72	2,10	0,67	0,84	-0,86	0,27	0,27	-1,00	-1,47	-2,84	-0,23	-1,64	0,28	0,65	0,07	-0,79	-2,08
Fb3.0-8	2012	0,29	1,24	0,77	0,76	2,31	1,32	1,40	-0,23	0,61	1,06	0,03	-0,51	-2,24	-0,33	-0,78	0,50	1,39	-0,88	-1,55	-1,93
Fb3.54-94	2012	0,53	0,20	0,63	0,42	1,53	0,51	0,56	-2,32	-0,08	0,79	-2,42	-2,47	-3,09	1,06	2,72	0,51	-2,62	0,15	-1,57	-1,95
Fb4-0-9h	2012	-1,11	-0,37	-0,13	-0,04	0,00	-0,42	-0,48	-0,12	0,08	-0,09	0,78	-0,23	-1,03	0,18	0,18	0,02	0,03	-0,35	-0,95	0,12
Fb4.0-44	2012	-0,45	-0,67	0,10	-0,48	-0,55	-0,29	-0,11	-2,68	-0,67	-0,55	-6,23	-3,16	-4,07	-0,55	-2,20	-0,82	-1,24	-2,38	-3,91	-5,15
Fb4.31-31h	2012	0,19	-0,42	0,07	-0,07	0,09	-0,04	0,01	0,01	0,93	-0,10	0,34	0,38	-0,22	-0,45	-0,52	0,06	-1,65	-0,65	0,13	0,36
Fb5.0-11	2012	0,43	0,46	0,51	0,03	1,43	0,79	0,43	-0,57	0,08	0,33	0,20	-2,02	-2,94	0,75	0,18	0,61	1,68	-1,64	-3,04	-3,61
Fb5.0-35	2012	-0,03	0,76	0,47	0,43	2,43	0,64	1,10	-2,82	-1,24	0,07	-1,83	-3,51	-2,04	0,95	-0,56	0,84	1,79	-1,84	-5,64	-4,52
Fb5.0-35-56	2012	0,94	0,49	0,33	0,00	0,27	0,22	1,29	-2,29	-0,47	-0,56	-3,93	-3,07	-2,66	0,49	-1,00	0,22	0,20	-1,74	-4,12	-4,67
Fb5.0-76	2012	0,17	0,27	-0,08	-0,62	-0,20	-0,23	3,12	-3,00	-0,59	1,40	-3,20	-2,86	1,45	2,23	0,59	1,31	0,67	-0,24	-3,56	-5,26
Fb5.39-76	2012	0,63	-0,19	0,35	0,02	0,39	-0,08	2,58	-2,65	-0,71	-0,05	-0,87	-1,95	1,73	0,64	0,96	1,01	-0,85	0,41	-0,61	0,39
Fb5.41-76	2012	-0,02	0,56	0,06	0,22	1,48	0,66	3,28	-1,81	-0,19	0,18	-0,84	-2,74	1,32	0,15	0,97	0,77	-0,26	-0,17	-0,75	-0,78
Fb5.41-76h	2012	-0,93	-0,50	-0,32	-0,14	-0,17	0,00	-0,31	-1,94	-0,05	-0,05	-1,50	-1,01	-1,24	0,29	0,13	0,16	-1,24	0,04	0,12	-0,31
Fb5.50-76	2012	1,34	0,21	0,81	-0,27	0,19	1,11	3,68	-2,03	0,48	0,32	-2,52	-2,34	-0,56	0,85	1,55	-1,72	-1,37	0,56	0,31	-1,27
Fb5.58-76h	2012	-0,23	-0,78	-0,14	-0,04	0,32	-0,45	-0,34	-1,98	-1,31	-0,52	0,79	-1,36	1,09	-0,03	0,88	-0,04	0,07	-1,88	-3,17	-0,03
Fb6.0-5h	2012	-1,05	-0,59	-0,34	-0,29	-0,28	-1,09	-0,36	-0,54	0,19	0,02	0,33	0,31	-0,51	-0,15	-0,06	0,03	0,05	-0,36	-0,58	0,03
Fb6.0-5	2012	-0,50	0,10	-0,10	0,29	1,23	0,00	-0,24	2,17	0,56	-0,11	1,63	1,86	-0,17	-0,45	-0,06	-0,16	0,92	0,00	1,35	1,51
Fb6.101-101	2012	0,42	-0,20	0,21	0,48	0,55	-0,40	0,33	-1,65	0,37	0,09	-1,13	-1,90	-0,80	0,28	-0,06	1,78	-2,93	-0,84	-1,12	-1,89
Fb6.84-101	2012	-0,57	0,05	-0,38	0,03	0,02	-0,75	-0,42	1,26	1,68	0,84	1,09	0,24	-1,74	0,66	-0,35	0,76	-2,41	0,81	0,44	0,21
Fb7-0-16-26-27h-59	2012	-0,77	0,64	0,14	-0,73	-0,34	-0,57	0,15	-2,49	-0,29	0,62	-0,97	-2,38	0,56	-0,50	0,67	-0,57	-2,18	-0,80	-1,24	-0,74
Fb7-52-59h	2012	-0,46	-0,47	-0,17	-0,97	-1,43	-0,26	0,01	1,03	1,48	0,75	0,74	1,16	-2,51	-0,09	-0,40	0,02	0,24	0,51	0,75	0,61
Fb7.0-10	2012	-0,39	-0,89	-0,20	0,00	0,24	-0,54	-0,37	-2,87	-1,28	-0,19	-0,86	-2,07	3,24	0,75	0,87	0,41	-2,05	1,61	-3,14	1,03
Fb7.0-16-26-59	2012	-0,34	1,46	0,29	-1,00	-0,94	-0,43	0,37	-1,35	1,44	0,68	-1,57	-1,17	-2,38	0,95	0,06	-0,95	-1,08	1,07	1,39	1,33
Fb7.0-59h	2012	-0,92	1,33	-0,36	-0,92	-0,63	-0,81	-0,54	-0,65	0,24	0,81	0,72	0,67	-1,76	-0,68	-0,80	-0,87	-0,41	0,07	-0,39	1,18
Fb7.43-59	2012	-0,13	-0,36	0,27	-0,36	0,01	-0,07	0,13	0,31	0,13	0,10	0,85	0,20	-1,37	-0,48	-0,81	-0,44	0,75	-0,50	-0,32	0,22
Fb7.h26-27h-59	2012	-0,49	0,38	-0,04	-1,43	-1,07	-0,46	0,20	-1,49	0,56	1,24	-1,24	-0,79	-2,86	-0,30	-0,38	-0,61	-1,82	0,16	-0,17	1,16
RV	2012	0,27	0,25	0,22	0,24	0,93	0,22	0,26	0,04	0,72	0,17	-0,08	-0,62	-1,19	0,22	0,33	0,44	1,03	0,01	-0,03	-0,17
YW	2012	-1,30	-0,15	-0,66	0,35	0,52	0,02	-0,57	2,96	1,60	1,65	2,39	3,83	-0,57	-0,46	-0,45	0,27	-1,54	1,38	2,14	2,78
F1	2013	-0,27	0,34	0,04	0,49	0,83	0,21	-0,15	-0,76	0,02	0,41	0,76	0,28	-1,24	1,04	1,26	1,19	-1,16	0,30	0,12	0,22
Fb1.0-6h	2013	-0,64	-0,40	0,14	-0,43	-0,76	-0,17	0,22	-0,68	-0,16	-0,39	-1,17	-0,71	-2,67	-0,72	-1,52	-1,30	-0,82	0,03	0,11	-0,54
Fb1.26-61	2013	0,44	0,04	-0,51	-0,38	-0,57	-0,27	-0,05	-0,24	-0,23	-1,15	-0,71	0,10	-2,66	0,39	-0,92	-0,92	0,52	0,70	1,12	-0,39
Fb2.0-30	2013	-0,22	-0,16	0,45	-0,44	1,34	0,44	0,60	-2,31	-2,20	-1,27	-2,64	-2,54	-3,34	-2,03	-0,89	-1,71	-1,11	-0,97	-2,70	-3,65
Fb2.0-39	2013	0,19	-0,21	0,58	-0,52	-0,45	0,17	0,51	-2,28	-2,53	-0,98	-2,93	-2,82	-1,58	0,17	1,32	-0,34	0,31	-1,38	-2,62	-3,70
Fb2.0-45	2013	0,02	-0,06	0,36	0,31	1,24	0,16	0,65	-2,36	-2,45	-0,53	-2,32	-2,80	-2,10	0,28	1,41	-0,91	-0,97	-1,76	-4,11	-5,25
Fb2.0-63	2013	-0,45	-0,05	0,44	0,00	0,94	0,13	0,59	-2,41	-2,47	-1,14	-3,57	-2,94	-2,99	-0,34	0,83	-1,14	-1,92	-2,51	-4,61	-4,57
Fb2.0-73	2013	-0,25	0,14	-0,05	0,90	1,73	0,15	0,56	-2,34	-0,56	-0,74	-1,63	-1,59	-2,66	0,05	0,69	-0,59	-0,03	-0,56	-1,40	-2,82
Fb2.39-47	2013	0,00	-0,04	0,00	0,32	0,82	-0,05	0,06	-1,43	-0,95	-1,61	-1,99	0,16	-2,09	0,07	0,97	-0,71	-0,10	-1,15	0,14	0,33
Fb2.39-63	2013	0,33	-0,04	0,31	0,02	0,96	-0,03	0,27	-2,19	-1,32	-0,82	-3,28	-0,85	-3,54	0,68	1,59	-0,67	-0,64	-1,42	-0,16	-0,55
Fb3.0-15	2013	0,57	1,35	0,38	0,67	2,06	1,20	1,21	-0,93	-1,65	-1,04	-2,47	-1,88	-3,95	-1,54	-1,40	-1,40	0,54	-0,58	-2,24	-2,21
Fb3.0-8	2013	0,45	1,20	0,41	0,52	1,91	0,72	1,29	-1,15	-1,27	-1,57	-1,92	-1,11	-4,12	-1,30	-1,12	-1,56	0,57	-0,30	-0,73	-1,16
Fb3.54-94	2013	0,46	0,27	0,88	0,05	0,91	0,99	0,88	-2,01	-0,62	-0,51	-2,55	-1,48	-3,23	-0,54	1,10	0,94	-1,80	0,33	0,09	0,13
Fb4.0-20	2013	0,28	0,92	0,37	0,99	1,86	0,60	0,47	0,92	0,65	-0,87	-0,99	1,24	-4,50	-1,34	-1,62	-1,95	-1,63	0,22	1,37	0,88
Fb4.0-44	2013	0,57	0,77	0,09	0,24	1,49	1,13	0,45	-0,92	-0,14	-0,63	-0,67	-1,98	-4,49	-0,62	-0,66	-1,04	0,17	0,49	1,33	0,01
Fb4.58-78	2013	0,34	1,16	0,08	0,52	1,67	0,83	0,43	0,10	0,11	-1,30	-0,87	0,69	-3,94	-0,78	-1,52	-1,62	-0,54	-0,30	0,41	-0,04
Fb5.0-11	2013	0,23	1,11	0,48	1,01	2,39	0,65	0,83	-2,13	-0,99	0,00	-1,75	-2,20	-3,30	0,11	-0,75	-0,74	0,94	-0,84	-3,32	-4,21
Fb5.0-20	2013	0,19	0,72	0,62	0,17	0,77	0,70	1,01	-2,33	-1,43	-0,45	-2,49	-2,64	-3,39	-0,03	-0,78	-1,64	0,50	-0,61	-3,19	-4,89
Fb5.0-35	2013	0,14	0,88	0,47	0,04	1,15	0,85	0,75	-2,30	-2,08	-0,27	-2,30	-3,44	-2,35	0,52	-0,40	-0,80	0,94	-1,21	-4,82	-5,53
Fb5.0-35-56	2013	0,14	0,42	0,39	-0,14	0,71	0,32	0,39	-1,95	-1,54	-0,22	-2,16	-2,35	-1,31	0,24	-0,46	-0,37	0,91	-0,78	-3,11	-3,65
Fb5.0-76	2013	0,38	0,90	0,68	0,13	0,40	1,03	4,17	-2,16	-1,20	0,85	-3,86	-3,23	-0,66	0,99	-0,34	0,30	1,33	-0,74	-4,30	-5,13
Fb5.11-76	2013	0,86	0,89	0,34	-0,04	0,87	0,99	4,01	-1,91	-0,41	-0,30	-2,91	-1,84	-2,37	0,30	-0,62	-1,28	-0,35	0,44	-1,15	-2,90
Fb5.20-76	2013	0,74	1,08	0,54	0,22	1,30	1,13	4,26	-1,72	-0,83	-0,28	-1,79	-2,30	-2,12	0,47	-0,05	-0,87	0,24	0,69	-1,26	-2,80
Fb5.37-76	2013	0,09	-0,29	0,49	-0,30	-1,03	-0,05	3,54	-1,82	0,54	-0,56	-3,55	-1,32	-2,95	0,04	-0,37	-0,34	0,62	0,87	0,69	-0,53
Fb5.39-76	2013	-0,08	-0,01	0,58	-0,21	-0,42	0,23	3,66	-1,13	1,15	-0,05	-1,44	-0,55	-1,52	0,72	1,04	-0,06	0,57	1,51	1,54	1,33
Fb5.41-76	2013	-0,03	0,16	0,06	0,16	0,57	0,18	3,72	-1,00	-0,08	-0,51	-1,05	-0,38	0,15	-0,44	0,26	-0,82	-0,75	0,45	0,39	0,20
Fb5.50-76	2013	0,08	0,35	0,35	0,07	0,33	0,36	3,60	0,29	0,53	-0,44	-0,25	0,05	-1,55	-0,19	0,60	-0,77	0,23	0,68	0,87	0,32
Fb6.0-5	2013	-0,29	-0,81	0,08	-0,99	-0,93	0,14	0,07	0,87	0,42	-0,02	-1,54	0,21	-0,43	-0,93	-0,58	-0,35	0,47	-0,56	-0,01	-0,61
Fb6.101-101	2013	-0,13	-0,16	-0,10	-0,06	0,72	0,23	0,10	-1,49	-1,49	-1,79	-2,54	-1,20	-2,90	-1,44	-1,26	-1,58	-2,49	-1,26	-0,69	-0,85
Fb6.84-101	2013	0,06	0,04	0,22	0,29	0,97	0,51	0,57	-0,49	-0,76	-0,61	-2,09	-0,51	-2,15	-1,03	-0,56	-0,87	-1,69	-0,87	-0,68	-0,37
Fb7.0-10	2013	-0,18	-0,03	-0,52	0,16	0,97	0,67	-0,37	-2,24	-2,44	-1,34	0,20	-2,37	1,63	-1,91	-0,41	-1,17	-2,12	0,63	-4,21	2,15
Fb7.0-16-26-59	2013	-0,63	1,24	-0,06	-0,01	-0,35	-0,63	0,15	-1,86	-1,81	-1,90	-2,72	-1,12	-0,98	-1,84	-2,09	-2,53	-2,84	-1,42	-0,70	0,12
Fb7.43-59	2013	-0,32	0,90	-0,18	1,17	2,38	0,61	0,08	0,46	-0,38	-2,12	-0,53	0,78	-4,02	-1,57	-1,51	-1,76	-0,56	-0,04	1,25	1,13
H4	2013	-0,28	-0,21	0,17	-0,01	0,19	-0,15	0,05	0,73	0,64	-0,54	0,67	1,06	-3,51	-0,14	-1,93	0,35	0,08	0,12	0,17	-0,97
RV	2013	-0,12	0,17	-0,04	0,56	1,07	0,40	0,32	0,41	0,36	-0,95	-0,74	0,11	-2,36	-0,53	-0,42	-1,72	0,15	-0,18	0,50	-0,06
YW	2013	-1,00	-0,36	-0,89	0,31	-0,45	-0,64	-1,11	0,87	-0,95	-1,50	0,96	0,48	0,05	-1,39	-1,01	-0,32	-1,18	-0,93	-1,28	0,15

Supplemental table CIII. 1 continues

genotype	year	Cinnamyl acetate	Decyl acetate	(E)-2-hexenyl acetate	Ethyl 2-hexenoate	Ethyl acetate	Ethyl butanoate	Ethyl decanoate	Ethyl dodecanoate	Ethyl hexanoate	Ethyl methylthioacetate T	Ethyl octanoate	Hexyl acetate	Hexyl butanoate	Hexyl hexanoate	Methyl-2-aminobenzoate T	Methyl-2-hexenoate	Methyl 3-hydroxyoctanoate T	Methyl acetate T	Methyl benzoate	Methyl butanoate
Fb1.26-61	2012	-0,72	0,06	0,67	-5,17	-5,48	-1,40	-7,52	-5,51	-5,54	-2,72	-7,50	1,15	1,57	-0,58	-2,68	0,43	-0,88	0,01	2,53	1,93
Fb2.0-30	2012	-1,52	-3,79	0,19	-1,54	-1,45	-0,39	-4,79	-4,70	-2,73	0,50	-4,34	-0,26	-1,93	-2,55	1,22	-0,74	-0,42	0,52	-0,31	-0,65
Fb2.0-30h	2012	-1,49	-4,16	0,29	-3,92	-3,88	-1,96	-6,98	-5,82	-5,27	-1,08	-7,06	-0,45	-1,63	-2,93	1,85	-1,90	-0,76	0,23	0,03	-0,43
Fb2.0-39	2012	-0,97	-3,42	0,29	-1,53	-1,72	-0,38	-5,48	-5,45	-2,51	-1,02	-4,82	0,00	-1,13	-2,22	1,54	-0,24	-0,58	0,46	-0,03	-0,36
Fb2.0-45	2012	-4,82	-4,86	0,34	-5,47	-5,54	-3,70	-9,12	-5,78	-7,55	-3,30	-9,62	-1,14	-2,75	-4,83	1,03	-2,19	-2,77	-1,10	-0,43	-1,63
Fb2.0-63	2012	-3,27	-4,75	0,31	-4,99	-4,79	-3,37	-6,82	-5,66	-6,52	-2,32	-8,01	-1,17	-3,41	-4,47	0,70	-2,06	-0,90	0,81	-0,41	-0,86
Fb2.0-73	2012	0,03	-3,55	0,65	-5,01	-4,29	-2,25	-6,92	-5,38	-6,11	-2,38	-7,69	-0,65	-2,58	-3,61	1,16	-1,85	0,27	1,27	-0,23	0,13
Fb3.0-15	2012	-5,26	-3,77	1,19	-5,56	-5,35	-3,52	-7,47	-5,89	-6,24	-3,35	-7,74	0,14	-0,43	-2,12	0,17	-0,85	-3,65	-0,24	-0,33	-0,27
Fb3.0-8	2012	-2,19	-3,01	-0,09	-3,70	-2,63	-2,00	-4,97	-3,90	-3,72	-2,87	-5,15	-0,06	-1,02	-1,27	0,56	0,28	-1,76	2,02	1,00	-0,11
Fb3.54-94	2012	-5,07	-2,84	1,39	-3,57	-1,67	0,09	-5,13	-5,47	-1,93	1,76	-3,82	0,11	-1,64	-2,41	-0,69	-0,94	-5,22	1,23	-2,62	-0,37
Fb4-0-9h	2012	0,56	0,48	-0,36	-1,30	0,12	0,35	-0,61	-0,44	-0,10	-0,27	0,00	-0,02	-0,13	0,63	0,68	1,11	1,29	1,75	-0,56	-0,20
Fb4.0-44	2012	-5,06	-7,34	0,43	-5,26	-6,19	-5,01	-7,97	-5,65	-8,36	-3,37	-7,94	-1,72	-3,31	-5,74	-2,27	0,02	-5,29	0,00	-1,30	-1,80
Fb4.31-31h	2012	-1,62	0,96	0,15	-0,27	0,12	0,51	0,81	0,63	0,77	0,11	1,22	0,07	0,84	0,61	-0,32	-0,50	0,20	0,73	-1,02	0,26
Fb5.0-11	2012	0,86	-3,38	-0,10	-5,32	-5,19	-4,40	-8,08	-5,50	-7,44	-4,14	-8,58	-1,10	-3,01	-1,18	-0,42	-1,32	-0,83	-0,13	0,95	-1,85
Fb5.0-35	2012	0,82	-6,30	-0,38	-5,38	-3,02	-3,17	-8,03	-5,62	-7,09	-3,80	-9,18	-1,88	-4,89	-0,83	-4,65	-0,54	-3,10	-0,61	1,76	-3,11
Fb5.0-35-56	2012	-2,05	-4,76	1,46	-4,86	-4,02	-2,65	-6,17	-5,24	-5,86	-1,94	-6,86	-0,88	-3,45	-1,67	-5,76	-1,34	-4,30	0,07	0,90	-3,66
Fb5.0-76	2012	2,23	-4,99	-6,41	-5,40	-0,55	-1,30	-7,33	-5,46	-4,07	0,22	-7,32	-0,49	-3,50	0,10	-4,79	-2,13	-2,75	0,77	0,97	-2,43
Fb5.39-76	2012	2,57	1,85	-4,87	2,66	2,76	1,52	2,02	3,19	1,43	2,05	1,60	0,64	-0,31	0,90	0,02	1,17	0,37	1,00	-0,75	-0,65
Fb5.41-76	2012	1,33	0,36	-5,49	2,31	2,33	0,62	1,76	2,79	1,08	0,60	1,47	0,39	-0,44	0,43	-0,07	3,15	0,15	0,49	-0,59	-1,71
Fb5.41-76h	2012	-2,27	0,07	0,78	-0,97	-0,25	0,76	-1,41	-2,31	0,17	1,20	-0,63	0,41	-0,07	0,05	-0,26	0,77	-0,13	-0,74	-1,19	-0,32
Fb5.50-76	2012	-2,30	-2,36	-5,32	-0,90	-0,40	-0,68	-1,56	-1,60	-0,93	0,13	-1,84	0,53	-0,52	-1,66	-1,34	0,27	-2,34	0,21	-1,99	-1,70
Fb5.58-76h	2012	1,51	0,95	-1,40	3,73	2,32	0,86	2,38	3,51	1,51	0,17	2,08	0,45	-1,00	2,59	-0,46	2,88	0,96	0,90	0,46	-2,10
Fb6.0-5h	2012	0,38	0,83	-0,57	-0,18	0,36	0,70	-0,17	-0,88	0,60	-0,64	0,65	0,06	-0,07	0,98	0,26	0,91	0,93	1,22	-0,76	-0,17
Fb6.0-5	2012	1,29	0,90	-0,39	0,15	0,36	0,88	-0,01	-0,04	0,68	-0,19	0,96	0,50	1,99	1,61	0,56	1,25	1,80	0,27	-0,34	0,58
Fb6.101-101	2012	-3,63	-1,03	0,17	-1,93	-0,60	-1,25	-1,39	-0,83	-1,24	-1,45	-1,22	-0,79	-1,72	-2,07	-2,26	-0,33	-2,25	0,66	-2,42	-0,77
Fb6.84-101	2012	-4,17	-0,44	1,57	-4,81	-4,50	-0,63	-6,56	-5,55	-3,77	-4,30	-6,05	0,57	0,14	-0,66	0,00	-0,20	-1,65	0,50	-2,09	1,28
Fb7-0-16-26-27h-59	2012	-1,64	0,05	-0,50	0,74	1,87	1,52	-0,09	-1,45	1,17	1,56	1,02	-0,18	-0,84	0,11	-4,43	-0,15	-0,45	1,49	-1,86	-0,31
Fb7-52-59h	2012	-0,30	0,09	0,05	-2,37	-1,10	1,12	-2,79	-3,35	-0,67	-2,82	-2,22	0,22	0,83	0,70	-1,58	0,81	0,88	2,31	0,38	2,10
Fb7.0-10	2012	-2,87	-1,21	-0,01	-1,14	3,47	-1,89	2,52	3,40	-0,46	-3,50	2,02	-0,12	-3,14	-0,51	-4,54	0,14	-0,05	1,48	-1,45	-3,28
Fb7.0-16-26-59	2012	-3,44	-0,52	0,02	-2,93	-1,72	1,12	-3,25	-3,84	-1,02	0,04	-2,32	0,47	1,18	0,20	-3,53	0,21	-0,42	1,44	-0,90	1,64
Fb7.0-59h	2012	-2,52	0,77	-0,12	-2,80	-2,71	-1,74	-2,12	-2,17	-2,21	-3,74	-2,12	-0,28	0,19	0,01	-2,16	2,20	1,13	1,13	-0,79	0,08
Fb7.43-59	2012	0,43	-0,14	-0,02	-0,81	-0,68	-0,31	-2,07	-2,16	-0,44	-1,13	-1,00	0,21	0,41	0,39	-0,58	1,65	1,52	0,96	0,92	0,54
Fb7.h26-27h-59	2012	-4,87	-0,53	-0,12	-4,64	-4,08	-1,15	-2,54	-3,56	-3,36	-4,49	-2,64	-0,73	-0,15	-0,51	-4,95	0,55	-1,02	1,42	-2,13	-0,31
RV	2012	0,05	-0,24	1,57	-2,09	-0,79	0,33	-1,70	-1,84	-0,36	0,99	-0,90	0,50	-0,36	-0,35	-0,45	0,83	0,75	0,26	0,42	0,66
YW	2012	-0,30	2,41	-2,49	-0,90	-1,06	1,41	-1,49	-1,07	-0,70	-3,98	-1,61	1,32	2,18	1,82	1,21	1,33	1,42	1,80	-1,33	2,19
F1	2013	0,82	0,79	-1,20	0,04	-0,33	0,01	-0,99	-0,73	-0,43	-0,55	-0,43	-0,32	-0,11	0,07	-2,16	0,06	0,12	0,68	-0,62	-0,02
Fb1.0-6h	2013	-2,44	-1,25	-0,94	-3,14	-2,97	-0,72	-3,81	-5,14	-1,02	-1,53	-2,02	-0,25	-0,18	-0,37	0,18	-0,38	0,14	-1,26	-0,37	-0,48
Fb1.26-61	2013	-2,71	-1,40	1,01	-4,56	-3,74	-0,17	-6,64	-6,32	-2,02	0,10	-5,35	0,52	0,74	-0,52	-2,31	-0,23	-0,90	-1,33	2,66	-0,18
Fb2.0-30	2013	-3,81	-4,18	0,89	-1,05	-1,66	-0,13	-4,70	-5,58	-1,57	1,84	-3,31	-0,34	-1,75	-2,83	0,49	-2,17	-0,65	-0,61	-1,07	-1,32
Fb2.0-39	2013	-0,99	-3,22	0,57	0,37	-0,65	-0,57	-3,69	-5,37	-0,51	0,86	-2,39	-0,53	-2,02	-2,30	1,18	0,02	-0,21	-0,08	0,52	-1,28
Fb2.0-45	2013	-2,80	-3,49	0,18	-1,17	-1,03	-0,61	-3,90	-5,58	-1,47	1,16	-3,02	-0,86	-2,90	-3,60	0,06	-1,20	-0,70	-0,37	-0,48	-1,66
Fb2.0-63	2013	-2,89	-3,66	-0,14	-2,62	-3,52	-2,38	-4,85	-6,05	-2,75	-0,55	-4,03	-1,26	-3,44	-3,74	-0,17	-1,49	-1,53	-1,29	-0,99	-2,37
Fb2.0-73	2013	-1,21	-2,57	0,61	-1,03	-2,06	-0,58	-4,54	-6,14	-1,77	0,11	-3,27	0,04	-1,58	-2,13	1,50	-0,40	0,84	-0,37	-0,16	-0,79
Fb2.39-47	2013	-0,86	0,74	-1,58	-1,87	-3,61	-0,97	-2,04	-3,39	-0,97	-1,01	-1,20	-0,47	0,42	0,36	-0,02	0,24	0,58	-1,41	0,00	-0,59
Fb2.39-63	2013	-1,95	0,06	-1,31	-1,66	-3,19	-1,33	-2,31	-2,97	-1,34	-0,12	-1,78	-0,65	0,45	-0,60	-2,12	-0,29	0,25	-0,96	0,36	-0,40
Fb3.0-15	2013	-5,53	-4,09	-0,04	-5,53	-4,31	-1,81	-5,99	-6,52	-4,17	-0,57	-5,15	-0,05	-1,59	-3,07	-1,37	-1,02	-3,13	-0,45	-1,22	-1,07
Fb3.0-8	2013	-4,81	-3,12	-0,25	-4,55	-4,08	-0,84	-5,35	-6,00	-3,53	0,52	-4,66	-0,30	-0,55	-1,62	-0,45	-1,12	-1,42	-1,22	-0,44	-0,65
Fb3.54-94	2013	-6,20	-2,66	0,28	-3,68	-4,10	-0,40	-5,59	-6,64	-2,48	0,32	-3,27	0,24	0,18	-0,21	-0,27	-1,87	-3,58	0,21	-2,70	-0,20
Fb4.0-20	2013	-4,12	-0,02	-0,42	-4,34	-4,91	-2,10	-4,86	-4,98	-3,02	-2,07	-4,02	0,33	1,59	0,42	-1,11	-1,02	-1,06	-0,98	-1,14	0,06
Fb4.0-44	2013	-3,44	-4,07	0,38	-4,18	-5,23	-2,50	-5,46	-5,51	-3,35	-1,46	-4,28	0,59	1,12	-0,27	-0,66	0,06	-0,23	-0,60	-0,73	0,32
Fb4.58-78	2013	-2,66	-2,00	-0,35	-3,28	-3,83	-1,61	-4,29	-4,87	-2,06	-0,99	-3,72	0,05	0,75	-0,25	-1,22	0,28	-0,82	-1,21	0,38	0,13
Fb5.0-11	2013	-1,26	-1,86	-0,07	-3,57	-2,33	-1,70	-4,47	-5,03	-3,02	-1,42	-4,02	-0,56	-3,50	-2,35	-0,21	-2,04	-2,50	0,41	0,10	-0,74
Fb5.0-20	2013	-2,05	-3,53	-0,61	-5,38	-4,20	-2,79	-5,79	-6,44	-4,84	-2,79	-5,31	-0,92	-4,18	-3,19	-4,20	-2,19	-3,21	-0,21	0,20	-1,42
Fb5.0-35	2013	-0,34	-4,19	-0,25	-4,52	-1,65	-1,27	-5,14	-5,93	-3,30	-0,32	-5,25	-1,12	-4,61	-2,81	-6,06	-2,37	-2,77	-1,40	0,71	-3,55
Fb5.0-35-56	2013	0,42	-3,33	0,27	-3,62	-1,99	-0,88	-4,25	-4,92	-2,73	1,15	-3,77	-0,74	-3,04	-0,91	-4,45	-1,74	-0,60	-0,71	0,75	-1,56
Fb5.0-76	2013	-0,41	-5,34	-5,48	-5,06	-2,92	-2,26	-5,81	-6,64	-4,69	0,16	-5,73	-0,63	-3,91	-0,34	-4,25	-2,23	-3,65	-0,85	1,98	-2,68
Fb5.11-76	2013	-1,82	-3,37	-6,23	-4,11	-4,84	-2,21	-5,82	-6,64	-3,98	-0,77	-5,49	-0,41	-3,02	-2,90	-5,12	-2,26	-2,35	-1,44	0,09	-1,93
Fb5.20-76	2013	-2,34	-2,58	-6,26	-2,32	-1,15	-0,52	-3,57	-3,94	-1,96	-0,17	-3,62	-0,09	-2,77	-2,70	-5,83	-1,39	-1,93	-0,84	0,57	-2,16
Fb5.37-76	2013	-1,23	-1,45	-5,78	-3,99	-4,15	-0,68	-4,79	-5,78	-3,08	-0,61	-4,48	0,61	0,35	-0,67	1,54	-0,84	-1,54	-1,03	0,58	0,08
Fb5.39-76	2013	0,38	0,41	-5,93	-0,24	-1,15	0,82	-1,67	-2,23	-0,18	0,25	-1,46	1,23	1,52	1,33	1,76	1,02	-0,27	0,52	0,65	1,13
Fb5.41-76	2013	-0,56	0,56	-6,24	0,24	0,13	0,29	-0,26	-0,52	0,22	0,15	-0,34	0,31	0,38	0,38	-0,01	-0,89	-0,17	0,03	-0,84	-0,17
Fb5.50-76	2013	-0,58	0,25	-5,48	0,27	-1,03	0,11	-1,36	-1,18	-0,67	-0,63	-1,53	0,59	0,31	0,36	0,28	-0,26	0,23	-0,20	-0,19	0,05
Fb6.0-5	2013	-2,70	-0,79	-0,41	-2,18	-2,44	-0,57	-2,74	-3,57	-1,43	-0,98	-1,94	-0,22	0,42	-0,15	-1,08	-0,96	-0,02	-0,03	-0,07	0,22
Fb6.101-101	2013	-2,75	-0,20	-1,67	-2,36	-2,77	-0,77	-3,20	-3,46	-1,04	-0,89	-1,98	-0,83	-1,44	-0,80	-1,24	0,05	-0,07	-0,71	-2,30	-0,95
Fb6.84-101	2013	-3,42	-0,21	-1,35	-1,02	-1,14	-0,06	-1,34	-2,04	-0,39	-0,22	-0,41	-0,53	0,02	-0,15	-3,05	-1,25	-0,81	0,17	-2,07	-0,11
Fb7.0-10	2013	-5,56	-0,30	0,17	-2,60	0,52	-4,85	2,81	3,38	-0,55	-5,35	2,20	-0,10	-2,39	0,68	-4,22	-1,66	-0,73	-0,23	-3,00	-6,64
Fb7.0-16-26-59	2013	-3,29	0,24	-1,29	-1,05	-0,92	-0,59	-0,71	-2,00	0,04	-0,81	0,10	-0,84	0,13	0,26	-3,26	-0,07	-0,59	-0,58	-2,28	-0,74
Fb7.43-59	2013	-3,18	0,04	-1,56	-2,31	-3,25	-0,94	-2,83	-3,42	-2,12	-2,11	-2,25	0,20	1,49	0,46	-1,92	-1,16	-0,42	-1,27	-1,44	0,15
H4	2013	-0,42	0,06	-0,59	-4,75	-4,75	-1,48	-5,15	-5,79	-3,17	-1,02	-4,35	0,25	-0,15	-1,06	0,46	-1,21	0,03	-0,81	-0,41	0,28
RV	2013	-1,12	-0,69	-0,55	-0,92	-1,72	-0,51	-1,97	-2,43	-0,44	-0,32	-1,03	0,26	0,04	-0,17	-0,47	-0,02	0,12	-0,67	-0,73	-0,06
YW	2013	-2,67	0,91	-2,61	1,00	0,76	-0,37	1,37	1,64	0,59	-2,97	1,31	-0,01	-1,00	0,67	0,29	-0,44	0,55	-0,58	-1,30	-1,84

Supplemental table CIII. 1 continues

genotype	year	Methyl cinnamate T	Methyl decanoate	Methyl dodecanoate	Methyl hexanoate	Methyl octanoate	Myrtenyl acetate	Nonyl acetate	Octyl acetate	Octyl butanoate	Octyl hexanoate	Pentyl acetate	Propyl butanoate	(Z)-3-hexenyl acetate	2,1-pentenyl_furan	2-pentylfuran	Furaneol	Mesifurane	1-penten-3-one	2-heptanone	2-nonanone
Fb1.26-61	2012	-0,59	-0,42	-2,12	0,57	0,30	-0,54	0,03	-0,64	-0,41	-3,81	1,47	2,25	-0,99	-0,33	-0,42	-0,21	-0,12	-0,54	-0,56	-0,40
Fb2.0-30	2012	1,10	-1,27	-2,41	-2,20	-0,72	0,20	-0,22	-2,65	-3,60	-4,24	0,01	-0,57	-0,82	0,40	0,61	0,75	0,61	0,81	-0,31	-0,43
Fb2.0-30h	2012	0,80	-1,64	-2,64	-3,55	-1,41	-0,20	-0,13	-3,51	-4,14	-4,45	0,30	-0,07	-0,20	0,96	1,30	0,34	0,01	1,34	-0,85	-0,57
Fb2.0-39	2012	1,28	-1,48	-2,55	-1,76	-1,12	-0,58	-0,22	-2,34	-3,15	-4,12	0,52	0,98	-0,48	0,29	0,78	0,30	-0,05	0,45	0,21	0,25
Fb2.0-45	2012	-1,77	-3,17	-3,26	-4,97	-3,05	-0,55	-1,81	-4,97	-4,24	-4,62	-0,07	-0,90	0,75	0,49	0,41	-2,14	-1,38	0,61	-1,99	-1,79
Fb2.0-63	2012	1,47	-0,71	-2,70	-3,61	-0,35	0,20	-0,81	-3,97	-3,99	-4,56	-0,41	-1,61	-1,03	0,58	0,89	0,19	-0,49	1,22	-1,57	-1,34
Fb2.0-73	2012	1,83	0,35	-2,06	-2,25	0,88	0,64	-0,48	-2,83	-3,33	-4,19	0,07	-0,06	0,44	0,93	1,24	-0,16	-0,53	1,41	-0,96	-0,91
Fb3.0-15	2012	-1,22	-1,81	-2,64	-2,17	-1,36	0,56	-1,18	-2,84	-2,88	-4,56	0,21	-1,60	1,05	0,72	0,85	-2,79	-1,22	0,67	-3,84	-3,50
Fb3.0-8	2012	0,24	-1,07	-0,96	-1,73	-0,63	0,19	-0,23	-2,21	-2,15	-2,49	-0,29	-1,45	0,26	1,01	0,75	-1,27	-0,61	1,75	-2,87	-1,79
Fb3.54-94	2012	-4,38	-1,90	-1,94	-1,47	-1,79	1,14	-1,25	-1,52	-2,85	-3,92	0,18	-0,77	-0,30	0,04	0,56	0,31	0,77	1,02	-2,36	-2,48
Fb4-0-9h	2012	0,10	0,74	0,99	0,24	0,58	0,39	0,58	1,12	-0,21	0,75	-0,37	0,20	-2,02	-0,95	-0,32	0,53	0,36	0,74	0,69	0,78
Fb4.0-44	2012	-2,17	-6,04	-3,04	-3,73	-0,25	0,01	-1,30	-3,78	-4,36	-4,38	-0,02	-3,72	-0,83	-0,49	-0,58	-2,11	-0,43	-1,34	-5,06	-9,30
Fb4.31-31h	2012	-2,19	0,80	1,03	0,24	0,81	0,18	-0,01	1,09	0,86	1,59	-0,29	-0,19	-1,72	-0,31	-0,08	-0,62	-0,27	0,29	0,22	0,18
Fb5.0-11	2012	-0,57	-2,93	-2,58	-4,47	-2,40	1,19	0,39	-2,44	-2,93	-4,31	-0,03	-1,76	-1,38	1,17	0,26	0,56	1,28	1,26	-1,55	-1,67
Fb5.0-35	2012	1,81	-3,46	-2,92	-5,59	-3,50	-1,38	-1,97	-5,19	-4,73	-4,35	0,08	-2,88	0,13	1,38	0,08	-0,88	0,30	0,79	-3,24	-3,05
Fb5.0-35-56	2012	0,83	-2,64	-2,69	-3,40	-1,88	-1,89	-1,43	-4,06	-4,59	-4,07	-0,03	-1,98	0,74	1,29	-0,19	-0,72	0,51	0,62	-2,27	-2,55
Fb5.0-76	2012	0,11	-2,97	-2,85	-3,73	-2,54	-1,14	-0,41	-4,22	-4,34	-4,27	0,73	-1,03	3,05	-0,44	-0,61	-0,80	1,41	-0,48	-3,45	-3,02
Fb5.39-76	2012	-0,35	1,35	2,24	1,16	0,73	0,38	1,14	1,09	-1,27	1,12	0,35	0,02	1,72	-0,35	0,04	1,34	1,15	0,53	-0,47	-0,66
Fb5.41-76	2012	-0,48	1,00	2,12	0,50	0,25	0,75	0,38	0,20	-2,65	-0,90	-0,16	-1,30	1,19	0,46	0,13	0,35	1,09	1,01	-1,02	-0,90
Fb5.41-76h	2012	-1,09	-0,15	-0,82	0,60	0,11	-0,35	-0,42	0,35	-0,63	-0,42	0,25	0,28	-0,08	-0,86	-0,40	-0,89	-0,10	-0,13	-0,29	-0,31
Fb5.50-76	2012	-3,44	-1,29	-0,82	-0,93	-0,86	0,08	-1,11	-1,72	-2,75	-3,20	0,67	-0,45	2,19	0,49	0,42	-1,87	-0,45	1,06	-2,43	-2,56
Fb5.58-76h	2012	0,45	1,83	3,35	0,49	0,23	0,23	0,38	0,98	-1,23	1,62	-0,97	-2,67	-1,91	0,42	-0,57	0,93	1,25	0,29	-1,17	-0,57
Fb6.0-5h	2012	-0,22	0,28	0,17	0,80	0,42	-0,12	0,29	0,92	-0,01	1,55	-0,41	-0,08	-2,04	-0,38	-0,40	-0,55	-0,17	0,70	0,85	0,69
Fb6.0-5	2012	1,08	0,60	0,87	0,65	0,84	0,59	0,60	1,35	2,05	2,03	0,08	0,50	-1,94	0,15	-0,01	-1,24	0,96	0,99	0,86	0,96
Fb6.101-101	2012	-3,20	-0,64	-0,71	-0,77	-0,46	-0,36	-0,73	-0,59	-1,74	-2,29	-0,34	-0,76	-1,15	-0,24	-0,11	-0,59	1,05	1,37	0,03	-0,66
Fb6.84-101	2012	-4,57	-1,11	-1,70	-0,66	-0,80	0,28	-0,26	-0,23	-0,07	-1,93	0,92	1,05	0,52	-0,81	-0,49	-0,57	0,71	0,45	0,53	0,27
Fb7-0-16-26-27h-59	2012	-3,46	-0,12	-0,92	0,60	0,00	-0,78	-0,15	0,39	-0,88	-0,95	-1,25	-1,50	-1,68	-2,30	-1,12	0,51	-2,60	-0,98	-0,50	-1,03
Fb7-52-59h	2012	-0,64	-0,27	-0,65	0,79	0,10	-0,15	-0,71	0,29	0,85	0,41	0,57	1,36	-1,73	-1,90	-1,05	-0,46	-2,60	0,16	0,57	0,55
Fb7.0-10	2012	-0,98	0,78	2,06	-0,41	-0,08	-0,71	1,22	-1,06	-1,18	-2,10	0,20	-4,40	-1,58	-2,80	-1,55	1,10	1,45	-0,94	-0,47	-1,11
Fb7.0-16-26-59	2012	-3,55	0,04	-1,34	0,86	0,48	-0,36	-1,19	0,30	0,75	-0,60	0,37	0,92	-1,34	-1,03	-0,90	-0,32	-3,91	-1,13	-0,69	-0,94
Fb7.0-59h	2012	-1,84	1,68	1,33	1,35	1,58	0,54	0,80	0,25	1,76	0,04	-0,14	-1,13	-1,93	-1,66	-1,21	0,03	-1,77	-0,47	0,21	0,72
Fb7.43-59	2012	-0,26	0,18	-0,25	0,55	0,81	0,37	0,01	0,80	-0,29	-0,20	0,00	0,07	-1,86	0,57	-0,31	1,52	-1,95	1,46	0,98	1,01
Fb7.h26-27h-59	2012	-3,25	0,21	-0,56	0,67	0,35	-0,07	-0,53	-0,59	0,99	0,02	-0,12	-0,57	-1,30	-0,61	-0,62	-1,93	-2,97	-0,26	-0,47	-0,45
RV	2012	-0,68	-0,08	-0,28	0,02	0,27	0,88	0,05	0,30	-0,50	-0,01	0,48	0,17	0,13	0,63	0,17	0,43	0,50	0,73	0,25	0,16
YW	2012	-1,76	1,88	1,83	0,77	0,71	0,47	1,56	1,92	3,09	3,01	0,81	1,66	-2,01	-0,98	-0,11	0,13	-0,69	0,80	0,35	1,27
F1	2013	0,40	1,05	1,22	-0,05	0,96	0,82	1,39	0,94	1,46	0,47	-0,08	0,36	-1,74	-0,24	0,13	0,83	2,02	0,25	-0,12	0,05
Fb1.0-6h	2013	-1,81	-1,14	-2,43	0,03	-0,48	0,04	-1,39	-0,35	-0,01	-1,02	-0,30	0,38	-1,07	0,01	-0,06	-0,42	-1,18	-0,19	-0,02	-0,27
Fb1.26-61	2013	-1,84	-1,79	-3,85	0,49	-0,41	-0,41	-0,58	-1,92	-1,47	-3,90	0,76	1,27	0,01	-0,83	-0,28	-1,62	-2,74	-1,06	-0,32	-0,41
Fb2.0-30	2013	0,45	-1,77	-3,26	-1,85	-1,12	-0,68	-1,60	-3,30	-4,46	-5,09	-0,80	-1,10	-0,25	0,05	0,36	-1,57	-1,86	0,42	0,17	-0,07
Fb2.0-39	2013	1,79	-1,40	-3,51	-0,55	-0,91	-1,47	-1,29	-2,99	-4,38	-5,01	-0,78	-0,66	-0,56	0,75	0,60	2,30	-2,15	-0,10	0,06	-0,16
Fb2.0-45	2013	0,59	-2,07	-3,27	-1,39	-1,90	-0,65	-1,14	-3,40	-4,16	-4,81	-0,62	-1,56	0,15	0,37	0,18	-0,27	-2,72	0,39	0,02	-0,20
Fb2.0-63	2013	-0,19	-2,41	-3,82	-2,11	-2,10	-0,82	-1,72	-3,22	-4,57	-4,93	-1,29	-2,37	-0,93	-0,02	0,39	-2,55	-3,58	0,56	-1,15	-1,27
Fb2.0-73	2013	3,37	-0,07	-2,90	-0,55	0,69	0,06	-0,31	-2,33	-3,64	-4,34	-0,12	0,11	1,13	-0,12	0,37	-0,11	-3,04	0,06	-0,20	0,02
Fb2.39-47	2013	0,75	0,33	-0,80	0,31	0,23	0,05	0,62	0,30	0,93	0,85	-0,72	0,44	-2,55	-0,21	0,23	0,08	-2,82	0,24	0,25	0,42
Fb2.39-63	2013	1,20	0,59	-0,78	0,13	0,72	0,13	-0,02	-0,48	-0,34	-0,51	-0,68	0,57	-2,29	0,44	0,24	-2,48	-3,97	0,34	-0,51	-0,31
Fb3.0-15	2013	-1,62	-2,63	-3,18	-2,09	-2,47	-0,57	-1,55	-3,24	-3,16	-3,59	-0,22	-1,82	0,75	0,43	-0,01	-2,19	-3,28	0,53	-3,22	-2,72
Fb3.0-8	2013	-0,67	-1,96	-2,54	-1,26	-1,37	-0,58	-1,12	-2,19	-1,77	-2,61	-0,64	-0,34	0,16	0,91	0,18	0,00	-2,94	0,83	-2,40	-1,79
Fb3.54-94	2013	-2,44	-2,03	-2,62	-1,15	-1,04	0,97	-1,28	-0,41	-0,73	-1,23	-0,05	-0,51	-0,23	0,24	0,81	1,48	-1,43	0,53	-1,14	-2,33
Fb4.0-20	2013	-3,76	-1,25	-1,66	-0,79	-1,46	-0,30	-0,45	0,40	1,79	1,28	0,53	0,45	-0,70	-0,67	0,12	-3,76	-4,60	0,41	-0,36	-0,35
Fb4.0-44	2013	-0,59	-4,03	-2,18	-0,55	0,11	0,48	-1,30	-0,17	0,89	-0,95	0,85	0,21	-0,31	0,32	-0,07	-0,90	-2,28	0,37	-0,43	-5,07
Fb4.58-78	2013	1,20	-1,35	-2,30	-0,38	-1,08	-0,37	-1,34	-1,42	-0,22	-1,65	0,38	0,31	-1,28	0,18	-0,13	-5,00	-3,31	0,37	-0,18	-0,13
Fb5.0-11	2013	-1,05	-3,34	-2,79	-2,69	-3,84	0,41	-0,86	-2,71	-3,63	-4,49	0,04	-1,05	0,21	0,70	0,16	-2,30	-2,90	0,39	-1,16	-1,51
Fb5.0-20	2013	-1,34	-3,64	-3,61	-3,73	-4,11	-0,13	-1,03	-3,24	-3,85	-5,18	-0,09	-1,05	-0,26	0,14	0,07	-4,36	-2,93	0,11	-1,29	-1,58
Fb5.0-35	2013	-1,48	-3,72	-3,95	-3,39	-3,52	-2,06	-1,64	-3,31	-4,58	-4,98	-0,36	-1,92	0,09	0,89	0,05	0,26	-0,92	0,16	-1,17	-1,71
Fb5.0-35-56	2013	1,28	-2,20	-3,15	-2,10	-2,14	-1,26	-0,60	-3,10	-3,51	-3,65	-0,57	-1,18	-0,27	0,38	0,12	1,21	-0,58	0,18	-0,94	-1,73
Fb5.0-76	2013	-0,61	-3,40	-3,71	-3,59	-3,31	-1,43	-1,18	-5,19	-3,52	-4,89	0,04	-1,95	3,11	0,38	0,26	0,08	0,02	-0,39	-4,06	-4,08
Fb5.11-76	2013	-1,87	-3,12	-3,66	-1,98	-2,96	-2,21	-0,76	-3,24	-2,59	-3,96	0,03	-0,50	2,02	-0,13	-0,48	-6,00	-1,64	0,20	-1,49	-1,48
Fb5.20-76	2013	-0,38	-2,34	-2,37	-0,98	-2,30	-2,75	-0,97	-2,43	-3,26	-3,27	0,28	-0,27	1,49	-0,52	-0,14	-3,79	-1,13	0,73	-0,97	-0,75
Fb5.37-76	2013	-1,29	-0,85	-2,32	0,19	-0,65	0,01	-0,45	-1,93	-2,19	-3,71	0,54	1,01	2,78	-0,39	0,36	-0,86	-1,46	-1,17	-1,99	-1,74
Fb5.39-76	2013	-0,90	0,53	0,05	1,09	0,27	1,06	0,78	0,10	-0,18	-0,22	0,94	1,34	2,01	-0,66	0,42	0,57	-0,79	-0,17	-1,43	-1,15
Fb5.41-76	2013	-2,32	0,18	0,07	0,46	-0,47	0,42	0,79	-0,17	-0,48	-0,27	0,02	0,08	1,44	0,12	-0,15	-1,34	-1,76	0,43	-0,12	0,06
Fb5.50-76	2013	-1,65	0,21	0,24	0,28	-0,47	0,30	0,38	-0,39	-0,61	-0,83	-0,17	0,48	1,22	-0,08	-0,06	-1,04	-1,84	0,40	-0,01	0,23
Fb6.0-5	2013	-0,95	-0,66	-1,23	-0,03	-0,49	0,02	-0,50	-0,88	-0,34	-0,86	-0,59	-0,46	-0,19	0,36	-0,13	-1,44	-2,99	0,39	-0,01	-0,56
Fb6.101-101	2013	-4,02	-1,37	-2,02	-0,32	-1,06	-0,89	-0,30	-0,19	-0,83	0,06	-1,54	-0,58	-2,31	-0,30	-0,38	-0,08	-2,36	0,93	0,70	0,32
Fb6.84-101	2013	-3,76	-0,74	-1,12	-0,33	-0,98	-0,80	0,60	-0,20	-0,49	0,01	-0,76	-0,71	-1,26	-0,33	-0,19	-0,16	-2,27	1,13	0,41	0,24
Fb7.0-10	2013	-2,43	1,48	2,21	-1,66	-0,42	0,02	1,39	0,04	0,40	0,80	-0,71	-5,64	-0,60	-0,95	-0,40	-4,92	-3,96	0,34	0,29	0,43
Fb7.0-16-26-59	2013	-4,35	0,27	-0,68	0,28	-0,24	-0,54	-0,01	-0,26	0,86	0,45	-1,18	-2,06	-1,80	-1,66	-0,32	-2,94	-6,14	-0,50	0,12	0,36
Fb7.43-59	2013	-1,77	-0,86	-1,39	-0,68	-1,40	0,09	-0,37	0,64	1,31	1,23	0,06	0,62	-2,17	0,32	0,16	-5,75	-6,14	0,59	0,41	0,59
H4	2013	-1,70	-0,37	-1,39	-0,79	-0,12	0,73	-0,08	0,04	-0,01	-1,50	0,76	0,37	-1,46	0,30	0,34	0,95	-1,62	-0,24	-0,87	0,05
RV	2013	-1,66	-0,92	-1,02	-0,28	-1,00	0,41	-0,03	-0,26	-0,45	-0,09	-0,39	-0,27	-0,69	-0,03	-0,21	-1,94	-2,53	0,69	0,17	0,20
YW	2013	-2,32	1,00	1,55	0,08	-0,08	-0,05	0,21	0,34	0,40	1,15	-0,86	-2,11	-1,87	-1,47	-0,43	-1,52	-2,36	0,10	0,23	0,54

Supplemental table CIII. 1

genotype	year	2-pentadecanone T	2-pentanone	2-tridecanone T	2-undecanone T	4-tridecanone T	6-methyl-5-hepten-2-one	Acetone	Acetophenone	α-ionone	β-ionone	(Z)-geranyl acetone	γ-decalactone	α-farnesene	α-pinene	Limonene	Linalool	Myrtenol	Nerol	Nerolidol	Terpineol
Fb1.26-61	2012	-1,71	-1,90	-0,97	-0,18	-0,48	-0,92	-1,09	0,51	-2,46	-1,84	-1,09	-0,91	-0,16	1,36	0,61	-0,34	-1,51	0,29	0,00	0,37
Fb2.0-30	2012	-0,83	-1,15	-0,86	-0,29	-0,53	0,11	-0,71	-0,23	0,76	0,36	0,45	-0,99	1,17	0,35	-0,31	-0,02	0,43	-0,60	0,00	0,48
Fb2.0-30h	2012	-0,20	-2,03	-0,56	-0,15	-0,91	0,59	-0,77	0,02	1,14	0,74	1,07	-0,92	1,43	0,49	0,39	0,15	-0,46	-0,78	0,00	0,51
Fb2.0-39	2012	-0,53	-0,29	-0,37	0,27	-0,70	0,05	0,10	0,43	0,20	0,37	0,19	-2,16	0,29	0,21	-0,37	-0,21	-0,32	-0,25	0,00	0,28
Fb2.0-45	2012	-2,15	-3,22	-1,59	-1,31	-0,71	0,32	-0,59	-1,79	-0,90	0,12	0,56	-2,79	-1,23	-0,56	-0,10	0,05	-0,30	-0,73	0,00	-0,22
Fb2.0-63	2012	-1,70	-2,78	-1,29	-0,77	-0,76	0,07	-0,60	-0,47	-0,29	0,37	0,14	-1,66	-0,99	-0,12	-0,34	0,23	0,03	-0,61	0,00	0,02
Fb2.0-73	2012	-0,42	-2,12	-0,52	-0,31	-0,43	0,49	-0,04	-0,06	-0,62	0,83	0,64	0,14	-0,88	0,13	-0,57	0,13	0,66	-1,14	0,00	0,24
Fb3.0-15	2012	-4,69	-4,79	-4,46	-2,94	-0,78	-0,02	-1,38	-0,32	1,45	0,47	0,27	-2,71	-3,87	-0,14	-0,29	2,75	-0,61	0,05	1,95	0,20
Fb3.0-8	2012	-2,59	-2,89	-2,72	-1,30	-0,33	0,44	0,31	0,42	1,37	0,86	0,29	-1,29	-0,71	0,50	0,15	2,28	-0,86	0,06	1,79	0,36
Fb3.54-94	2012	-3,35	-1,67	-2,83	-2,24	-0,73	0,14	-1,08	-3,22	-1,28	-0,41	-0,03	-3,79	-2,16	-0,04	-0,42	1,21	-0,15	0,26	0,57	-0,08
Fb4-0-9h	2012	1,14	1,05	1,11	1,21	1,38	-1,06	0,73	0,10	0,85	0,36	-0,23	0,98	0,56	0,15	-0,75	-1,13	0,13	-0,66	0,00	0,16
Fb4.0-44	2012	-5,47	-7,05	-3,93	-5,31	-0,69	-0,28	-2,15	-1,91	-1,92	-0,49	-0,36	-2,02	-4,81	-0,44	0,14	-0,67	-1,29	-3,80	0,00	0,24
Fb4.31-31h	2012	1,28	0,42	0,95	0,46	0,86	-0,76	0,44	-1,21	-0,04	0,10	-0,36	0,55	-0,14	-0,63	-0,79	-0,64	0,18	-0,51	0,00	-0,65
Fb5.0-11	2012	-2,68	-2,30	-1,83	-1,27	-0,56	0,47	0,27	0,83	0,90	0,34	0,14	-0,33	1,67	1,47	0,36	-0,02	0,72	-0,35	0,00	0,74
Fb5.0-35	2012	-2,99	-4,63	-3,04	-2,11	-0,60	0,49	-0,53	1,54	0,65	0,13	-0,29	-2,50	0,47	1,44	-0,34	0,02	0,06	-0,46	0,00	0,01
Fb5.0-35-56	2012	-4,04	-2,64	-3,82	-2,51	-0,40	0,58	-0,27	1,19	-1,17	-0,62	-0,32	-4,49	-2,32	1,53	1,32	0,90	1,39	1,12	0,00	-0,56
Fb5.0-76	2012	-3,07	-4,25	-2,38	-1,88	-0,37	-0,65	1,28	0,84	-0,31	-0,66	-0,65	-1,01	-1,13	1,62	-0,10	0,25	1,56	1,45	0,00	0,00
Fb5.39-76	2012	2,15	-0,53	0,90	0,21	1,85	-0,04	0,91	0,19	0,69	0,43	-0,05	2,43	-1,21	0,76	-0,19	-0,03	0,12	1,07	0,00	0,60
Fb5.41-76	2012	1,85	-1,27	0,71	0,39	2,18	-0,16	0,54	-0,09	1,26	0,94	0,19	1,64	-0,31	0,52	-0,40	-0,25	-0,06	0,82	0,00	0,69
Fb5.41-76h	2012	-1,18	-0,53	-0,87	-0,46	-0,12	-0,67	0,26	-0,38	-0,89	-0,48	-0,92	-0,85	-0,59	0,50	-0,18	-0,38	-0,22	0,52	0,00	-0,14
Fb5.50-76	2012	-3,29	-3,24	-2,94	-2,09	-0,17	0,15	-0,06	-0,13	-0,70	-0,37	-0,96	0,48	0,13	-0,18	0,73	-0,18	-0,06	1,26	0,00	-0,70
Fb5.58-76h	2012	2,14	-1,85	1,29	0,96	2,28	-0,38	-0,01	0,04	1,68	0,97	0,56	1,64	1,55	-0,42	-1,04	-1,08	0,59	0,79	0,00	1,13
Fb6.0-5h	2012	0,75	1,59	0,62	0,61	0,15	-1,04	0,83	0,12	-0,02	0,05	-0,82	-0,21	0,63	-0,74	-0,45	-0,53	0,01	0,39	0,00	-0,12
Fb6.0-5	2012	1,91	1,48	1,41	1,45	1,17	-0,30	0,73	0,61	1,57	1,12	0,59	1,40	2,10	-0,06	-0,69	-0,63	0,36	0,57	0,00	0,51
Fb6.101-101	2012	-1,23	0,74	-1,36	-1,16	0,30	-0,08	0,61	-2,02	-0,52	0,38	-0,32	-0,48	-1,59	-0,37	0,27	-0,74	-0,18	-0,59	0,00	-0,80
Fb6.84-101	2012	-0,84	0,86	-0,53	-0,01	-0,90	-0,61	0,67	-2,56	-0,75	0,11	-0,44	-0,79	-1,01	0,24	-0,30	-0,70	-0,04	0,17	0,00	0,40
Fb7-0-16-26-27h-59	2012	-1,39	-0,60	-1,90	-1,87	-0,20	-1,35	-0,26	-1,41	-0,90	-1,58	-1,66	-2,46	-1,02	-1,59	-0,98	-1,86	-1,42	0,09	0,00	-1,16
Fb7-52-59h	2012	-0,81	1,20	-0,13	0,24	-0,54	-1,28	0,81	0,33	-0,47	-0,69	-1,54	-0,69	0,40	0,00	0,04	-1,33	-0,36	-1,15	0,00	-0,44
Fb7.0-10	2012	0,19	-0,03	-0,90	-1,64	1,52	-0,27	0,16	-1,32	-0,50	-1,11	-0,53	-1,68	-1,30	-1,31	-1,26	-1,62	-2,27	-0,03	0,00	-0,56
Fb7.0-16-26-59	2012	-2,79	-1,07	-2,38	-1,69	-0,56	-1,21	-0,20	-0,76	-1,13	-1,35	-1,91	-2,39	0,47	0,35	-0,44	-1,17	-1,60	-0,57	0,00	-0,39
Fb7.0-59h	2012	0,52	-0,19	1,20	1,36	-0,73	-1,22	0,71	-0,42	-0,41	-0,67	-1,23	-0,31	-0,78	-0,16	-0,86	-0,85	-0,82	0,04	0,00	0,22
Fb7.43-59	2012	-0,24	1,41	0,23	0,97	0,40	-0,57	0,50	0,87	0,36	0,56	-0,89	-0,83	0,52	0,83	0,17	-0,70	0,34	-1,19	0,00	0,42
Fb7.h26-27h-59	2012	-0,94	-0,52	-0,45	-0,29	-0,37	-1,23	0,15	-1,35	-1,07	-0,80	-1,21	-1,49	-1,87	-0,61	-1,17	-0,47	-2,20	-0,87	0,00	-1,00
RV	2012	0,31	0,17	0,08	0,18	-0,01	-0,32	0,44	0,65	0,68	0,48	-0,02	0,72	0,20	0,07	0,23	0,02	0,87	0,44	0,00	0,27
YW	2012	4,64	1,29	3,31	2,59	-0,01	-1,06	0,74	-2,34	1,41	1,46	0,67	1,96	-0,01	-0,97	0,25	-0,77	1,74	-0,54	0,00	0,88
F1	2013	1,29	-0,32	1,08	0,68	0,37	-0,09	0,92	-1,65	-0,51	0,38	0,26	2,23	-1,12	-0,23	-0,48	0,79	0,08	-0,85	1,66	0,58
Fb1.0-6h	2013	-1,97	-0,19	-1,65	-1,05	-0,16	-0,40	-0,39	-0,87	-0,37	-0,43	-1,12	-1,95	0,36	-0,46	-0,61	-1,30	-0,85	-1,26	0,00	-0,08
Fb1.26-61	2013	-3,00	-1,15	-2,06	-0,88	-0,79	0,05	-1,75	0,22	-2,07	-2,67	-0,82	-2,32	0,10	1,15	0,04	-0,43	-1,29	0,84	0,00	-0,06
Fb2.0-30	2013	-1,61	-0,32	-1,39	-0,37	-0,48	0,29	-1,12	-0,63	-0,60	-0,43	-0,03	-2,03	-0,66	-1,42	-0,70	0,00	-1,06	-0,25	0,00	-0,64
Fb2.0-39	2013	-1,52	-0,44	-1,38	-0,58	-0,38	0,30	-1,05	0,93	-0,22	-0,05	-0,16	-1,48	1,12	-0,68	-0,70	-0,86	-1,31	-0,63	0,00	-0,66
Fb2.0-45	2013	-1,62	-0,35	-1,36	-0,50	-0,35	0,42	-0,51	-0,50	-0,72	-0,03	-0,24	-3,75	-0,30	-0,89	-0,65	0,23	-0,49	-0,84	0,00	-0,35
Fb2.0-63	2013	-3,40	-1,73	-2,94	-1,94	-0,65	0,62	-1,15	-1,03	-0,42	0,25	-0,05	-2,40	-0,72	-1,02	-0,55	-0,09	-0,88	-0,78	0,00	-0,84
Fb2.0-73	2013	-1,39	-1,06	-1,00	-0,02	-0,16	0,68	-0,90	2,03	-0,12	0,04	0,33	-1,57	1,50	-0,07	-0,27	-0,40	-0,21	-1,28	0,00	0,16
Fb2.39-47	2013	-0,13	0,20	0,04	0,37	-0,22	0,17	0,68	1,11	0,69	0,33	0,32	1,29	0,38	-0,29	-0,13	0,37	-0,53	-0,69	0,00	0,28
Fb2.39-63	2013	-0,96	-0,84	-0,56	-0,28	-0,25	0,51	0,52	1,32	-0,22	-0,02	0,21	1,18	0,18	-0,28	-0,09	0,47	-0,32	-0,18	0,00	0,16
Fb3.0-15	2013	-4,93	-3,21	-4,56	-2,57	-0,74	0,70	-2,10	-1,01	0,41	-0,91	-0,42	-2,59	-1,78	-0,63	-0,09	2,75	-1,62	-0,46	0,89	0,77
Fb3.0-8	2013	-4,24	-2,50	-3,94	-1,54	-0,54	0,82	-1,11	-0,86	0,81	-0,13	-0,04	-1,42	-1,30	-0,19	0,04	2,76	-1,39	-0,27	1,55	1,18
Fb3.54-94	2013	-4,29	-1,57	-3,00	-2,35	-0,61	0,84	-0,53	-2,78	-0,17	0,46	0,36	-4,36	-0,52	-0,07	0,16	1,28	-0,57	-1,18	0,34	0,72
Fb4.0-20	2013	-2,10	-0,46	-1,57	-1,03	-0,19	0,23	-0,54	-2,52	-0,16	0,05	0,25	-0,55	-0,20	-0,92	-0,62	-0,26	-0,69	-0,80	0,00	0,09
Fb4.0-44	2013	-4,22	-2,31	-1,54	-2,66	-0,60	0,50	-1,69	-1,63	-0,51	0,03	0,15	-1,76	-1,61	-0,61	-0,56	0,88	-0,97	-2,75	0,11	0,76
Fb4.58-78	2013	-1,07	-0,30	-1,05	-0,50	-0,52	0,53	-0,68	1,41	0,19	-0,38	0,01	-0,28	0,05	-1,06	-0,41	0,06	-0,63	-0,66	0,00	-0,38
Fb5.0-11	2013	-3,07	-1,58	-2,27	-1,70	-0,69	0,67	-0,67	0,22	-0,20	-0,33	0,17	-1,15	0,06	0,10	-0,18	-0,39	-0,38	-0,73	0,00	0,04
Fb5.0-20	2013	-3,95	-1,97	-2,98	-1,75	-0,66	0,54	-0,54	0,02	-0,42	-0,51	-0,54	-2,18	0,23	-0,13	-0,30	-0,68	-0,52	-0,48	0,00	-0,45
Fb5.0-35	2013	-4,21	-1,60	-3,07	-1,95	-0,64	0,66	-0,94	0,18	-0,58	-0,72	-0,04	-2,10	-0,70	1,01	-0,09	-0,31	0,39	-0,33	0,00	-0,40
Fb5.0-35-56	2013	-2,71	-1,15	-2,36	-1,66	-0,02	0,44	-0,10	0,93	0,86	-0,11	-0,04	-1,34	-0,34	1,21	0,05	0,03	0,15	-0,04	0,00	-0,35
Fb5.0-76	2013	-4,22	-4,44	-3,86	-3,18	-0,52	0,62	0,63	0,84	0,14	-0,66	-0,12	-2,91	-1,29	1,48	0,39	1,15	1,97	1,55	0,00	0,65
Fb5.11-76	2013	-2,59	-1,52	-2,38	-1,81	-0,14	0,50	-0,20	-0,13	-0,22	-0,20	-0,11	-2,18	-1,80	-0,53	-0,32	0,18	2,53	1,24	0,00	0,24
Fb5.20-76	2013	-1,70	-1,17	-1,98	-1,28	-0,13	0,61	0,54	0,21	-0,05	0,37	0,26	-1,74	-0,76	-0,32	-0,28	0,39	1,66	0,85	0,00	0,38
Fb5.37-76	2013	-2,40	-2,82	-2,42	-1,67	-0,64	-0,31	0,29	0,80	0,02	-1,24	-0,88	-0,33	-0,21	0,66	0,07	-0,64	-0,27	0,24	0,00	-0,29
Fb5.39-76	2013	-0,35	-2,10	-0,76	-0,63	0,73	0,05	0,25	0,22	1,10	0,38	0,28	1,50	-0,16	0,39	0,18	-0,28	0,88	0,73	0,00	1,16
Fb5.41-76	2013	1,23	-0,23	0,45	0,24	1,01	0,14	0,00	-0,88	0,25	0,43	0,08	1,73	-1,14	-0,80	-0,28	0,30	0,50	0,92	0,00	0,25
Fb5.50-76	2013	0,84	-0,16	0,28	0,37	0,57	0,13	0,59	-0,04	0,66	0,35	0,00	2,40	0,42	-0,39	-0,21	-0,18	0,51	2,14	0,00	0,20
Fb6.0-5	2013	-0,76	0,31	-0,97	-0,69	0,24	0,20	-0,01	0,89	0,07	-0,45	0,02	1,26	1,12	-0,03	-0,13	-0,12	-0,87	0,58	0,07	-0,42
Fb6.101-101	2013	-0,28	1,09	-0,65	-0,48	0,13	-0,23	-0,11	-2,26	-0,29	0,26	-0,14	-0,40	-1,13	-0,99	-0,80	-0,48	-0,35	0,03	0,00	-0,27
Fb6.84-101	2013	-0,51	0,80	-0,67	-0,39	0,20	0,42	0,07	-1,83	-0,05	0,51	0,22	1,30	-1,63	-1,26	-0,55	-0,39	-0,72	0,10	0,00	-0,11
Fb7.0-10	2013	0,55	0,52	0,31	0,23	1,14	-0,02	-0,72	-2,30	-0,45	-0,74	0,36	-1,07	0,21	-1,45	-0,87	0,24	-1,44	0,28	0,00	-0,08
Fb7.0-16-26-59	2013	0,50	-0,18	-0,31	-0,38	-0,22	-0,39	-0,71	-2,36	-0,21	-0,96	-0,50	-1,41	-0,40	-1,14	-0,93	-1,18	-1,74	-1,37	0,00	-0,78
Fb7.43-59	2013	-1,16	0,33	-0,39	0,24	-0,13	0,27	-0,73	-0,94	-0,50	-0,43	0,30	-0,73	-0,27	-0,50	-0,46	-0,11	-0,15	-1,59	0,00	0,28
H4	2013	-0,48	-0,66	0,32	0,97	-0,62	0,43	-0,43	-1,45	1,28	0,77	0,74	-5,01	0,91	0,42	0,10	0,04	-0,40	-0,49	0,00	0,27
RV	2013	-0,72	0,17	-0,72	-0,17	0,10	-0,09	-0,47	0,16	0,32	-0,39	-0,13	-0,01	0,32	-0,85	-0,42	-0,61	-0,48	-0,42	0,00	-0,03
YW	2013	1,63	0,73	0,76	0,63	1,05	-0,24	-0,48	-1,85	0,69	0,06	0,11	0,38	0,14	-0,67	-0,35	-0,95	-0,24	-0,51	0,00	0,13

Supplemental table CIII. 2. Pearson correlation values between volatile compounds for 2012 and 2013 independent harvests. Asterisk after the values indicate significance at different thresholds: p-value <0.05 '*', p-value <0.01 '**', p-value <0.001 '***'

		2012 1-decanol	2012 1-hexanol	2012 1-octanol	2012 1-penten-3-ol	2012 2-heptanol	2012 2-nonanol	2012 2-tridecanol T	2012 2-undecanol T	2012 (E)-2-hexen-1-ol	2012 Ethanol	2012 Eugenol	2012 3,4-dimethylbenzaldehyde	2012 Benzaldehyde	2012 Decanal	2012 (E)-2-decenal	2012 (E)-2-heptenal	2012 (E)-2-hexenal	2012 (E)-2-nonenal	2012 (E)-2-octenal	2012 (E)-2-pentenal	2012 (E,Z)-2,4-heptadienal	2012 Heptanal	2012 Hexanal	2012 Nonanal	2012 Octanal	2012 Pentanal	2012 (Z)-3-hexenal
2012	1-decanol	1																										
2012	1-hexanol	0.15	1																									
2012	1-octanol	0.95***	0.16	1																								
2012	1-penten-3-ol	-0.09	0.54**	-0.14	1																							
2012	2-heptanol	0.9***	0.03	0.92***	-0.3	1																						
2012	2-nonanol	0.79***	0.01	0.82***	-0.3	0.93***	1																					
2012	2-tridecanol T	0.78***	-0.22	0.75***	-0.46*	0.79***	0.76***	1																				
2012	2-undecanol T	0.88***	-0.14	0.87***	-0.38	0.93***	0.9***	0.94***	1																			
2012	(E)-2-hexen-1-ol	-0.29	0.1	-0.2	0.03	-0.16	-0.16	-0.37	-0.3	1																		
2012	Ethanol	0.69***	0.11	0.61**	0.24	0.48*	0.26	0.42*	0.43*	-0.37	1																	
2012	Eugenol	0.65***	0.22	0.59**	0.19	0.43*	0.29	0.49*	0.49*	-0.64***	0.71***	1																
2012	3,4-dimethylbenzaldehyde	0.13	0.17	0.19	0.27	0.01	0	0.04	0.06	-0.27	0.21	0.42*	1															
2012	Benzaldehyde	-0.32	-0.21	-0.33	0.14	-0.25	-0.16	-0.16	-0.19	-0.29	-0.06	0	0.42*	1														
2012	Decanal	0.27	-0.19	0.32	-0.15	0.22	0.3	0.31	0.32	-0.19	0	0.15	0.49*	0.06	1													
2012	(E)-2-decenal	-0.06	-0.24	-0.04	0.09	-0.08	0.04	0.13	0.04	-0.19	0	-0.03	0.14	0.09	0.56**	1												
2012	(E)-2-heptenal	-0.07	0.11	-0.12	0.43*	-0.23	-0.15	-0.14	-0.15	-0.74***	0.22	0.42*	0.44*	0.52**	0.21	0.38	1											
2012	(E)-2-hexenal	-0.37	-0.27	-0.29	-0.07	-0.17	-0.07	-0.34	-0.25	0.78***	-0.54**	-0.76***	-0.24	-0.04	0.04	0.01	-0.55**	1										
2012	(E)-2-nonenal	-0.17	-0.36	-0.07	-0.3	0.01	-0.04	-0.02	-0.03	0.67***	-0.17	-0.35	-0.05	-0.05	0.18	0.15	-0.6**	0.61**	1									
2012	(E)-2-octenal	-0.05	-0.22	0.05	0.16	0.03	0.2	-0.03	0.05	-0.21	-0.04	-0.01	0.41*	0.44*	0.64***	0.68***	0.53**	0.15	0.12	1								
2012	(E)-2-pentenal	-0.17	0.03	-0.21	0.53**	-0.26	-0.1	-0.21	-0.2	-0.41*	0.04	0.12	0.41*	0.55**	0.31	0.63***	0.84***	-0.14	-0.31	0.75***	1							
2012	(E,Z)-2,4-heptadienal	-0.18	0.34	-0.2	0.84***	-0.35	-0.27	-0.48*	-0.4*	-0.12	0.12	0.18	0.44*	0.45*	0.14	0.23	0.65***	0	-0.24	0.52**	0.76***	1						
2012	Heptanal	-0.11	0.11	-0.15	-0.02	-0.11	0	-0.26	-0.18	-0.06	-0.33	-0.21	0.04	0.09	0.25	-0.04	0.17	0.26	-0.24	0.14	0.16	0.19	1					
2012	Hexanal	-0.42*	-0.05	-0.35	0.5*	-0.43*	-0.32	-0.54**	-0.46*	-0.01	-0.14	-0.13	0.41*	0.49*	0.24	0.23	0.48*	0.33	0.02	0.65***	0.61**	0.77***	0.36	1				
2012	Nonanal	-0.18	-0.24	-0.05	-0.14	-0.04	0.14	0.01	-0.01	0.12	-0.29	-0.41*	0.17	0.12	0.59**	0.73***	0.11	0.29	0.34	0.72***	0.42*	0.06	0.04	0.26	1			
2012	Octanal	-0.32	-0.4*	-0.21	-0.18	-0.17	0.04	-0.11	-0.13	-0.05	-0.38	-0.39	0.16	0.31	0.63***	0.69***	0.29	0.32	0.25	0.83***	0.54**	0.19	0.27	0.49*	0.88***	1		
2012	Pentanal	-0.34	-0.24	-0.32	0.15	-0.31	-0.1	-0.23	-0.21	-0.27	-0.34	-0.2	0.32	0.46*	0.5*	0.54**	0.59**	0.22	-0.09	0.8***	0.75***	0.51**	0.42*	0.72***	0.55**	0.76***	1	
2012	(Z)-3-hexenal	-0.02	0.29	-0.09	0.44*	-0.22	-0.18	-0.17	-0.19	-0.74***	0.26	0.48*	0.48*	0.48*	0.11	0.13	0.93***	-0.62***	-0.71***	0.32	0.69***	0.63***	0.3	0.42*	-0.08	0.1	0.43*	1
2012	1-methylbutyl butanoate	0.57**	-0.14	0.54**	-0.36	0.69***	0.66***	0.57**	0.7***	0.03	0.03	0.03	-0.26	-0.41*	0.21	0.08	-0.41*	0.13	0.08	-0.09	-0.32	-0.51**	0.04	-0.48*	0.01	-0.11	-0.19	-0.48*
2012	1-methylethyl butanoate	0.44*	0.24	0.47*	-0.11	0.53**	0.53**	0.3	0.46*	0.12	-0.06	0.02	-0.17	-0.52**	0.07	-0.09	-0.29	0.11	-0.11	-0.16	-0.31	-0.32	0.31	-0.25	-0.05	-0.2	-0.14	-0.28
2012	1-methylethyl acetate	-0.02	0.16	0.08	-0.17	0.12	0.29	0.24	0.18	-0.25	-0.37	-0.03	-0.08	-0.17	0.17	0.21	0.11	-0.12	-0.27	0.14	0.07	-0.18	0.25	-0.01	0.28	0.27	0.22	0.1
2012	1-methylhexyl acetate	0.66***	-0.17	0.67***	-0.43*	0.88***	0.91***	0.68***	0.82***	-0.09	0.17	0.11	-0.18	-0.17	0.21	0.06	-0.28	0.05	0.09	0.13	-0.21	-0.44*	0.02	-0.38	0.14	0.06	-0.14	-0.34
2012	1-methyloctyl butanoate	0.64***	-0.13	0.61**	-0.4*	0.74***	0.72***	0.71***	0.79***	-0.02	0.07	0.08	-0.23	-0.45*	0.19	-0.01	-0.47*	0.05	0.04	-0.17	-0.41*	-0.59**	-0.07	-0.56**	0.01	-0.17	-0.25	-0.5*
2012	2,3-butanedioldiacetate T	0.53**	0.19	0.55**	-0.08	0.5*	0.43*	0.51**	0.48*	-0.53**	0.57**	0.62***	0.2	0.21	0.07	-0.09	0.28	-0.68***	-0.27	0.06	0.06	-0.02	-0.35	-0.29	-0.1	-0.13	-0.26	0.35
2012	2 -methylbutyl acetate	-0.26	0.37	-0.29	0.27	-0.28	-0.14	-0.24	-0.31	-0.11	-0.16	0.04	-0.22	0.21	-0.42*	-0.21	0.26	-0.18	-0.37	-0.14	0.14	0.32	0.15	0.1	-0.24	-0.13	-0.05	0.36
2012	3-methyl-2-butenyl acetate	0.2	0.19	0.21	0.25	0.15	0.28	0.17	0.16	-0.27	0.26	0.24	-0.17	0.07	-0.03	0.13	0.38	-0.21	-0.33	0.29	0.29	0.35	-0.08	0.2	0.04	0.09	0.18	0.32
2012	3-methylbutyl acetate	0.1	0.1	0.14	0.02	0.14	0.13	0.11	0.05	-0.08	0.22	0.1	-0.02	0.02	0.15	0.41*	0.09	-0.18	0.11	0.2	0.2	0.04	-0.02	-0.11	0.3	0.26	-0.17	0.08
2012	Benzyl acetate	-0.21	-0.54**	-0.29	-0.25	-0.09	0.02	0.01	0.01	-0.21	-0.32	-0.2	0.13	0.66***	0.18	0.05	0.15	0.23	0	0.24	0.22	0.04	0.38	0.22	0.04	0.31	0.39	0.11
2012	Butyl acetate	0.53**	0.24	0.49*	-0.19	0.57**	0.6**	0.45*	0.53**	-0.08	0.18	0.14	-0.26	-0.27	-0.14	-0.4*	-0.23	-0.22	-0.22	-0.26	-0.39	-0.33	-0.11	-0.43*	-0.14	-0.31	-0.31	-0.14
2012	Butyl butanoate	0.72***	0.07	0.65***	-0.09	0.69***	0.68***	0.54**	0.69***	-0.1	0.28	0.24	-0.15	-0.44*	0.11	-0.2	-0.21	-0.1	-0.23	-0.17	-0.3	-0.29	0.07	-0.34	-0.14	-0.31	-0.2	-0.19
2012	Butyl hexanoate	0.86***	0.07	0.82***	-0.28	0.88***	0.77***	0.67***	0.81***	-0.07	0.47*	0.33	-0.15	-0.44*	0.1	-0.29	-0.37	-0.12	-0.03	-0.2	-0.47*	-0.41*	-0.09	-0.47*	-0.21	-0.35	-0.39	-0.3
2012	Cinnamyl acetate	0.41*	-0.31	0.31	-0.15	0.38	0.4*	0.6**	0.53**	-0.64***	0.34	0.54**	0.19	0.46*	0.2	0.15	0.36	-0.41*	-0.26	0.17	0.26	0.05	0	-0.12	-0.15	0.02	0.05	0.34
2012	Decyl acetate	0.97***	0.13	0.91***	-0.14	0.91***	0.83***	0.76***	0.88***	-0.22	0.6**	0.52**	-0.01	-0.39	0.23	-0.09	-0.16	-0.28	-0.15	-0.07	-0.25	-0.26	-0.08	-0.45*	-0.14	-0.3	-0.34	-0.12
2012	(E)-2-hexenyl acetate	-0.31	-0.17	-0.21	-0.13	-0.14	-0.09	-0.3	-0.23	0.92***	-0.48*	-0.73***	-0.26	-0.22	0.02	-0.02	-0.71***	0.88***	0.74***	-0.01	-0.35	-0.17	0	0.08	0.3	0.19	-0.07	-0.78***
2012	Ethyl 2-hexenoate	0.78***	-0.03	0.78***	-0.09	0.69***	0.56**	0.66***	0.7***	-0.5*	0.85***	0.67***	0.3	0.03	0.22	0.04	0.22	-0.52**	-0.18	0.14	0.01	-0.07	-0.27	-0.16	-0.09	-0.17	-0.16	0.23
2012	Ethyl acetate	0.65***	0.14	0.67***	-0.04	0.6**	0.47*	0.53**	0.54**	-0.48*	0.77***	0.59**	0.17	0.12	0.05	-0.11	0.22	-0.55**	-0.28	0.06	0	0	-0.24	-0.17	-0.17	-0.19	-0.26	0.3
2012	Ethyl butanoate	0.81***	0.14	0.78***	-0.1	0.75***	0.7***	0.69***	0.73***	-0.36	0.61**	0.49*	-0.04	-0.23	0.08	-0.13	0	-0.38	-0.35	-0.12	-0.2	-0.19	0	-0.3	-0.21	-0.3	-0.31	0.09
2012	Ethyl decanoate	0.82***	0.13	0.83***	-0.03	0.72***	0.55**	0.59**	0.66***	-0.35	0.85***	0.63***	0.23	-0.07	0.19	-0.08	0.08	-0.45*	-0.12	0.07	-0.08	-0.04	-0.28	-0.22	-0.15	-0.24	-0.27	0.14
2012	Ethyl dodecanoate	0.77***	0.1	0.77***	-0.07	0.66***	0.47*	0.58**	0.61**	-0.41*	0.82***	0.67***	0.29	-0.03	0.24	-0.03	0.14	-0.53**	-0.11	0.09	-0.03	-0.04	-0.3	-0.26	-0.1	-0.19	-0.25	0.2
2012	Ethyl hexanoate	0.84***	0.17	0.85***	-0.02	0.78***	0.66***	0.62***	0.71***	-0.37	0.78***	0.57**	0.1	-0.13	0.1	-0.14	0.07	-0.42*	-0.3	0	-0.12	-0.08	-0.16	-0.23	-0.2	-0.29	-0.31	0.14
2012	Ethyl methylthioacetate T	0.34	0.1	0.32	0.33	0.15	0.13	0.16	0.16	-0.42*	0.6**	0.42*	0.16	0.17	0.04	-0.04	0.41*	-0.37	-0.49*	0.1	0.19	0.35	0.03	0.23	-0.22	-0.16	-0.03	0.47*
2012	Ethyl octanoate	0.83***	0.13	0.84***	-0.03	0.75***	0.57**	0.59**	0.67***	-0.3	0.84***	0.59**	0.15	-0.12	0.14	-0.13	0.01	-0.4*	-0.14	0	-0.16	-0.09	-0.27	-0.24	-0.2	-0.3	-0.34	0.07
2012	Hexyl acetate	0.77***	0.22	0.67***	-0.08	0.72***	0.7***	0.57**	0.71***	-0.26	0.38	0.33	-0.11	-0.32	0.09	-0.22	-0.09	-0.28	-0.35	-0.15	-0.25	-0.23	0.03	-0.38	-0.2	-0.34	-0.22	-0.02
2012	Hexyl butanoate	0.76***	0.02	0.67***	-0.18	0.72***	0.67***	0.57**	0.72***	-0.13	0.33	0.25	-0.12	-0.45*	0.16	-0.2	-0.25	-0.11	-0.21	-0.21	-0.36	-0.37	0.1	-0.39	-0.18	-0.32	-0.24	-0.21
2012	Hexyl hexanoate	0.77***	0.08	0.67***	-0.23	0.77***	0.7***	0.65***	0.72***	-0.4*	0.47*	0.46*	-0.08	-0.08	0.09	-0.16	-0.05	-0.33	-0.3	-0.16	-0.19	-0.24	0.14	-0.43*	-0.33	-0.28	-0.32	0.06
2012	Methyl-2-aminobenzoate T	0.18	-0.35	0.28	-0.24	0.3	0.42*	0.37	0.42*	-0.16	-0.07	0.02	0.14	-0.11	0.52**	0.47*	0.1	0.03	0.14	0.51**	0.13	-0.18	-0.09	0.1	0.57**	0.47*	0.38	-0.13
2012	Methyl-2-hexenoate	0.75***	-0.17	0.67***	-0.28	0.67***	0.48*	0.58**	0.67***	-0.35	0.67***	0.46*	0.09	-0.18	0.15	-0.11	0	-0.32	-0.13	-0.09	-0.2	-0.3	-0.08	-0.33	-0.24	-0.27	-0.22	0.03
2012	Methyl 3-hydroxyoctanoate T	0.73***	-0.28	0.75***	-0.42*	0.83***	0.84***	0.84***	0.91***	-0.27	0.3	0.44*	0.14	0.04	0.34	-0.08	-0.13	-0.15	0.05	0.14	-0.17	-0.32	-0.15	-0.31	-0.01	-0.04	-0.11	-0.17
2012	Methyl acetate T	0.43*	0.16	0.42*	-0.01	0.44*	0.38	0.44*	0.46*	-0.1	0.29	0.27	-0.04	-0.16	0.11	-0.12	-0.15	-0.09	0.02	-0.04	-0.17	-0.1	-0.07	-0.05	-0.11	-0.16	-0.12	-0.08
2012	Methyl benzoate	-0.21	-0.4	-0.34	-0.2	-0.15	-0.03	0	-0.03	-0.09	-0.37	-0.22	0.09	0.55**	0.05	-0.09	0.03	0.24	-0.02	0.04	0.15	0.03	0.34	0.07	-0.06	0.15	0.25	0.06
2012	Methyl butanoate	0.5*	-0.15	0.46*	-0.24	0.54**	0.57**	0.46*	0.58**	0.09	0	0	-0.27	-0.55**	0.13	-0.15	-0.42*	0.17	-0.01	-0.19	-0.42*	-0.43*	0.11	-0.29	-0.04	-0.17	-0.18	-0.43*
2012	Methyl cinnamate T	-0.18	-0.58**	-0.21	-0.27	-0.1	0.03	0.2	0.09	-0.2	-0.17	-0.09	0.29	0.74***	0.33	0.24	0.18	0.1	0.23	0.38	0.32	0.06	-0.02	0.18	0.29	0.45*	0.36	0.09
2012	Methyl decanoate	0.86***	0.06	0.85***	-0.17	0.85***	0.86***	0.76***	0.86***	-0.24	0.49*	0.45*	0.13	-0.16	0.4*	-0.03	-0.06	-0.22	-0.06	0.17	-0.08	-0.14	-0.08	-0.26	0.07	-0.03	-0.11	-0.04
2012	Methyl dodecanoate	0.87***	0.07	0.85***	-0.19	0.78***	0.62***	0.73***	0.77***	-0.4*	0.75***	0.64***	0.19	-0.18	0.32	0.01	0.03	-0.47*	-0.09	0.06	-0.12	-0.19	-0.25	-0.36	-0.07	-0.17	-0.24	0.07
2012	Methyl hexanoate	0.89***	0.14	0.82***	-0.05	0.8***	0.67***	0.62***	0.75***	-0.15	0.65***	0.47*	-0.01	-0.35	0.11	-0.29	-0.19	-0.26	-0.16	-0.19	-0.34	-0.22	-0.13	-0.36	-0.28	-0.43*	-0.39	-0.1
2012	Methyl octanoate	0.72***	-0.13	0.67***	-0.09	0.61**	0.47*	0.61**	0.69***	-0.08	0.51**	0.45*	0.13	-0.25	0.27	-0.2	-0.22	-0.15	0.1	-0.1	-0.3	-0.21	-0.29	-0.25	-0.19	-0.32	-0.25	-0.21
2012	Myrtenyl acetate	0.31	-0.26	0.36	-0.06	0.34	0.34	0.27	0.38	-0.17	0.17	0.2	-0.06	-0.29	0.46*	0.36	0.09	0.01	0.08	0.42*	0.07	-0.02	-0.06	0.14	0.23	0.26	0.25	-0.1
2012	Nonyl acetate	0.71***	-0.11	0.66***	-0.3	0.75***	0.67***	0.81***	0.82***	-0.34	0.49*	0.52**	-0.02	-0.05	0.2	0.05	-0.11	-0.38	0.07	0.01	-0.19	-0.34	-0.4*	-0.5*	-0.07	-0.18	-0.27	-0.15
2012	Octyl acetate	0.93***	0.05	0.89***	-0.14	0.88***	0.74***	0.72***	0.84***	-0.16	0.64***	0.51**	-0.06	-0.44*	0.17	-0.14	-0.24	-0.23	-0.07	-0.14	-0.35	-0.3	-0.15	-0.42*	-0.24	-0.38	-0.4*	-0.21
2012	Octyl butanoate	0.82***	0.01	0.79***	-0.32	0.85***	0.75***	0.71***	0.82***	-0.01	0.33	0.28	-0.23	-0.55**	0.14	-0.22	-0.48*	-0.04	0.01	-0.28	-0.53**	-0.51**	-0.05	-0.56**	-0.21	-0.36	-0.43*	-0.44*
2012	Octyl hexanoate	0.91***	-0.02	0.89***	-0.29	0.84***	0.69***	0.81***	0.86***	-0.3	0.58**	0.56**	0.09	-0.38	0.33	-0.03	-0.21	-0.31	-0.09	-0.13	-0.33	-0.37	-0.09	-0.47*	-0.17	-0.28	-0.36	-0.15
2012	Pentyl acetate	0.25	0.22	0.11	-0.05	0.22	0.24	0.22	0.24	-0.13	-0.03	0.11	-0.38	-0.25	-0.41*	-0.39	-0.15	-0.26	-0.38	-0.5*	-0.33	-0.25	-0.04	-0.49*	-0.41*	-0.51**	-0.36	-0.06
2012	Propyl butanoate	0.53**	0.05	0.46*	-0.05	0.53**	0.63***	0.51**	0.59**	-0.09	0.07	0.15	-0.15	-0.31	0.04	-0.08	-0.13	-0.04	-0.28	-0.15	-0.16	-0.21	0.16	-0.27	-0.08	-0.22	-0.14	-0.13
2012	(Z)-3-hexenyl acetate	-0.19	0.43*	-0.23	0.42*	-0.36	-0.29	-0.35	-0.36	-0.51**	-0.01	0.26	0.37	0.34	0.05	0.1	0.75***	-0.55**	-0.62***	0.19	0.53**	0.53**	0.27	0.29	0.02	0.1	0.27	0.84***
2012	2,1-pentenyl_furan	-0.35	-0.3	-0.36	0.21	-0.34	-0.15	-0.29	-0.26	-0.08	-0.31	-0.23	0.35	0.48*	0.39	0.54**	0.46*	0.33	-0.01	0.63***	0.69***	0.49*	0.45*	0.64***	0.41*	0.61**	0.73***	0.31
2012	2-pentylfuran	-0.28	-0.31	-0.23	0.16	-0.22	0.01	-0.13	-0.11	-0.13	-0.28	-0.25	0.26	0.31	0.51**	0.66***	0.44*	0.24	0.06	0.78***	0.65***	0.38	0.23	0.63***	0.71***	0.77***	0.81***	0.22
2012	Furaneol	0.46*	-0.1	0.45*	-0.12	0.5*	0.51**	0.56**	0.54**	-0.07	0.43*	0.38	0	0.07	-0.01	-0.04	-0.11	-0.08	0.17	0.08	-0.1	-0.06	-0.36	-0.14	-0.16	-0.16	-0.23	-0.14
2012	Mesifurane	0.06	-0.02	0.01	0.14	0.04	0	0.1	0.03	-0.22	0.33	0.19	-0.2	0.27	-0.07	0.44*	0.3	-0.34	0.02	0.22	0.34	0.18	-0.4*	-0.17	0.17	0.12	-0.09	0.17
2012	1-penten-3-one	0.14	-0.15	0.21	0.18	0.23	0.4*	0.15	0.25	-0.13	-0.01	-0.01	0.3	0.2	0.56**	0.71***	0.38	0.2	0.03	0.83***	0.69***	0.37	0.15	0.45*	0.65***	0.67***	0.62***	0.17
2012	2-heptanone	0.75***	-0.02	0.8***	-0.24	0.86***	0.87***	0.74***	0.83***	0.1	0.35	0.28	-0.05	-0.2	0.11	-0.07	-0.34	0.01	0.14	0.01	-0.27	-0.31	-0.27	-0.4*	0.01	-0.18	-0.36	-0.38
2012	2-nonanone	0.69***	0.02	0.73***	-0.24	0.84***	0.96***	0.71***	0.81***	-0.05	0.19	0.19	-0.02	-0.08	0.24	0.03	-0.17	0.03	-0.02	0.19	-0.06	-0.21	0	-0.28	0.17	0.06	-0.11	-0.2
2012	2-pentadecanone T	0.81***	-0.17	0.82***	-0.43*	0.83***	0.81***	0.95***	0.93***	-0.36	0.47*	0.49*	0.07	-0.17	0.37	0.21	-0.07	-0.37	0.01	0.12	-0.12	-0.41*	-0.3	-0.51**	0.17	0.01	-0.2	-0.13
2012	2-pentanone	0.8***	0.09	0.86***	-0.18	0.9***	0.89***	0.74***	0.84***	0.09	0.43*	0.29	-0.08	-0.28	0.13	-0.02	-0.34	-0.02	0.11	0.01	-0.27	-0.3	-0.25	-0.41*	0.02	-0.18	-0.4	-0.36
2012	2-tridecanone T	0.77***	-0.23	0.78***	-0.44*	0.8***	0.8***	0.96***	0.93***	-0.32	0.4*	0.47*	0	-0.22	0.31	0.19	-0.12	-0.32	0	0.05	-0.17	-0.46*	-0.34	-0.55**	0.1	-0.05	-0.23	-0.21
2012	2-undecanone T	0.74***	-0.19	0.74***	-0.38	0.83***	0.92***	0.89***	0.92***	-0.27	0.25	0.32	0.01	-0.11	0.34	0.19	-0.09	-0.15	-0.06	0.18	-0.05	-0.35	-0.12	-0.4*	0.18	0.07	-0.08	-0.17
2012	4-tridecanone T	0.7***	-0.01	0.66***	-0.1	0.56**	0.4*	0.56**	0.56**	-0.47*	0.79***	0.66***	0.31	0.1	0.32	0.04	0.23	-0.55**	-0.12	0.12	0.05	-0.02	-0.26	-0.24	-0.08	-0.1	-0.2	0.27
2012	6-methyl-5-hepten-2-one	-0.5*	-0.1	-0.41*	0.29	-0.45*	-0.33	-0.43*	-0.46*	0.06	-0.21	-0.23	0.4*	0.58**	0.35	0.61**	0.46*	0.25	0.29	0.75***	0.7***	0.61**	0.1	0.71***	0.62***	0.71***	0.68***	0.3
2012	Acetone	0.65***	0.25	0.68***	-0.02	0.69***	0.69***	0.62***	0.66***	-0.43*	0.37	0.59**	0.18	0.1	0.18	0.08	0.2	-0.44*	-0.3	0.12	0.12	0	0	-0.27	-0.07	-0.1	-0.2	0.23
2012	Acetophenone	-0.05	-0.31	-0.14	0.01	-0.02	0.06	0.02	0.05	-0.3	-0.05	0.1	0.36	0.79***	0.14	-0.06	0.32	0.04	-0.11	0.25	0.36	0.32	0.29	0.3	-0.13	0.14	0.31	0.34
2012	α-ionone	0.31	-0.37	0.37	-0.38	0.47*	0.5*	0.43*	0.48*	-0.45*	0.16	0.16	0.24	0.26	0.54**	0.41*	0.2	-0.13	0.05	0.52**	0.22	-0.16	0.15	0.04	0.39	0.49*	0.29	0.11
2012	β-ionone	0.27	-0.38	0.37	-0.26	0.37	0.42*	0.47*	0.47*	-0.31	0.1	0.15	0.31	0.05	0.67***	0.7***	0.21	-0.08	0.15	0.61**	0.33	-0.12	-0.04	0.06	0.62***	0.58**	0.35	0.01
2012	(Z)-geranyl acetone	-0.08	-0.39	0	-0.27	0.02	0.13	0.27	0.16	-0.14	-0.15	-0.16	0.14	0.15	0.63***	0.83***	0.16	0.02	0.31	0.61**	0.34	-0.11	-0.15	0.04	0.84***	0.74***	0.44*	-0.08
2012	γ-decalactone	0.73***	-0.21	0.69***	-0.13	0.66***	0.58**	0.73***	0.77***	-0.64***	0.55**	0.72***	0.16	-0.05	0.32	0.2	0.29	-0.57**	-0.23	0.19	0.13	-0.11	-0.21	-0.29	-0.02	-0.06	-0.04	0.2
2012	α-farnesene	0.4*	-0.3	0.42*	-0.33	0.59**	0.68***	0.54**	0.61**	-0.25	0.07	0.19	-0.12	0.24	0.06	-0.02	0.03	0.07	-0.1	0.21	0.04	-0.13	0.17	-0.06	-0.06	0.08	0.1	-0.04
2012	α-pinene	-0.16	-0.06	-0.33	0.18	-0.21	-0.12	-0.16	-0.17	-0.18	-0.1	0.06	0.03	0.46*	-0.12	-0.03	0.29	0.02	-0.23	-0.02	0.31	0.33	0.42*	0.21	-0.3	-0.05	0.12	0.35
2012	Limonene	-0.03	0.27	-0.18	0.54**	-0.18	-0.18	-0.18	-0.15	0.02	0	0.05	0.23	0.08	-0.15	0.12	0.19	0.06	-0.25	-0.06	0.36	0.39	0.17	0.11	-0.19	-0.26	0.16	0.19
2012	Linalool	-0.41*	0.01	-0.45*	0.26	-0.41*	-0.26	-0.47*	-0.42*	-0.04	-0.36	-0.41*	0.19	0.28	0.38	0.39	0.32	0.25	-0.07	0.48*	0.49*	0.41*	0.48*	0.55**	0.48*	0.57**	0.63***	0.29
2012	Myrtenol	0.12	0.02	0.1	0.14	0.08	0.22	0.32	0.22	-0.34	0	0.24	0.17	0.15	0.25	0.56**	0.33	-0.23	-0.25	0.25	0.44*	0.16	0.01	-0.05	0.17	0.18	0.17	0.22
2012	Nerol	0.37	0.46*	0.28	0.28	0.3	0.4*	0.13	0.22	-0.42*	0.25	0.29	0.07	0.26	0.12	0.06	0.46*	-0.36	-0.55**	0.22	0.38	0.39	0.3	0.02	-0.03	0.02	0.11	0.54**
2012	Nerolidol	-0.23	0	-0.24	0.05	-0.15	-0.11	-0.37	-0.25	0.06	-0.27	-0.42*	0.08	0.07	0.32	0.11	0.04	0.28	0.05	0.3	0.15	0.1	0.43*	0.37	0.38	0.43*	0.41*	0.06
2012	Terpineol	0.25	-0.57**	0.17	-0.54**	0.32	0.35	0.55**	0.51**	-0.36	0	0.17	-0.08	-0.03	0.38	0.32	-0.01	-0.14	0.12	0.13	-0.08	-0.44*	-0.04	-0.27	0.13	0.19	0.09	-0.15

		2012 1-methylbutyl butanoate	2012 1-methylethyl butanoate	2012 1-methylethyl acetate	2012 1-methylhexyl acetate	2012 1-methyloctyl butanoate	2012 2,3-butanedioldiacetate T	2012 2 -methylbutyl acetate	2012 3-methyl-2-butenyl acetate	2012 3-methylbutyl acetate	2012 Benzyl acetate	2012 Butyl acetate	2012 Butyl butanoate	2012 Butyl hexanoate	2012 Cinnamyl acetate	2012 Decyl acetate	2012 (E)-2-hexenyl acetate	2012 Ethyl 2-hexenoate	2012 Ethyl acetate	2012 Ethyl butanoate	2012 Ethyl decanoate
2012	1-methylbutyl butanoate	1																			
2012	1-methylethyl butanoate	0.76***	1																		
2012	1-methylethyl acetate	0.18	0.45*	1																	
2012	1-methylhexyl acetate	0.81***	0.56**	0.22	1																
2012	1-methyloctyl butanoate	0.94***	0.71***	0.27	0.8***	1															
2012	2,3-butanedioldiacetate T	-0.07	-0.21	0.08	0.26	0.06	1														
2012	2 -methylbutyl acetate	-0.5*	-0.21	0.23	-0.27	-0.45*	0.2	1													
2012	3-methyl-2-butenyl acetate	-0.25	-0.09	0.23	0.06	-0.15	0.39	0.59**	1												
2012	3-methylbutyl acetate	-0.03	-0.13	0.21	0.18	-0.09	0.38	0.14	0.03	1											
2012	Benzyl acetate	0.12	-0.17	-0.13	0.18	0.01	-0.17	-0.03	-0.27	-0.07	1										
2012	Butyl acetate	0.31	0.39	0.21	0.51**	0.5*	0.38	0.21	0.44*	-0.22	-0.25	1									
2012	Butyl butanoate	0.69***	0.76***	0.15	0.63***	0.76***	0.07	-0.21	0.17	-0.31	-0.14	0.73***	1								
2012	Butyl hexanoate	0.67***	0.54**	-0.01	0.75***	0.76***	0.36	-0.27	0.16	-0.11	-0.2	0.75***	0.83***	1							
2012	Cinnamyl acetate	0.15	-0.17	0.01	0.36	0.16	0.51**	0.16	0.19	0.26	0.55**	0.04	0.08	0.17	1						
2012	Decyl acetate	0.63***	0.51**	0.03	0.75***	0.71***	0.45*	-0.22	0.25	0.08	-0.2	0.65***	0.81***	0.92***	0.35	1					
2012	(E)-2-hexenyl acetate	0.16	0.14	-0.2	0.03	0.09	-0.63***	-0.25	-0.3	-0.12	0.01	-0.12	-0.06	-0.06	-0.55**	-0.22	1				
2012	Ethyl 2-hexenoate	0.21	0.09	-0.13	0.44*	0.29	0.66***	-0.27	0.32	0.08	-0.17	0.36	0.43*	0.62***	0.43*	0.71***	-0.49*	1			
2012	Ethyl acetate	0.02	-0.1	-0.03	0.34	0.13	0.87***	0.03	0.43*	0.3	-0.19	0.38	0.2	0.52**	0.46*	0.58**	-0.55**	0.86***	1		
2012	Ethyl butanoate	0.42*	0.45*	0.19	0.56**	0.53**	0.48*	-0.01	0.43*	0.07	-0.19	0.63***	0.7***	0.76***	0.38	0.81***	-0.35	0.76***	0.71***	1	
2012	Ethyl decanoate	0.21	0.06	-0.18	0.41*	0.3	0.75***	-0.25	0.3	0.15	-0.29	0.4*	0.39	0.69***	0.33	0.74***	-0.41*	0.92***	0.91***	0.71***	1
2012	Ethyl dodecanoate	0.12	-0.07	-0.22	0.35	0.21	0.79***	-0.24	0.23	0.22	-0.26	0.32	0.28	0.61**	0.38	0.69***	-0.48*	0.87***	0.88***	0.56**	0.96***
2012	Ethyl hexanoate	0.33	0.28	0.01	0.53**	0.42*	0.67***	-0.13	0.4*	0.14	-0.25	0.53**	0.57**	0.75***	0.35	0.8***	-0.4*	0.9***	0.89***	0.9***	0.92***
2012	Ethyl methylthioacetate T	-0.19	-0.05	-0.06	-0.05	-0.14	0.33	0.18	0.55**	0.02	-0.06	0.19	0.23	0.17	0.3	0.29	-0.4*	0.59**	0.59**	0.65***	0.48*
2012	Ethyl octanoate	0.28	0.16	-0.16	0.45*	0.36	0.69***	-0.26	0.3	0.12	-0.29	0.44*	0.47*	0.74***	0.29	0.77***	-0.35	0.92***	0.9***	0.77***	0.98***
2012	Hexyl acetate	0.61**	0.59**	0.15	0.65***	0.69***	0.3	-0.1	0.28	-0.17	-0.12	0.82***	0.89***	0.87***	0.19	0.85***	-0.22	0.54**	0.43*	0.8***	0.54**
2012	Hexyl butanoate	0.77***	0.73***	0.08	0.68***	0.81***	0.06	-0.34	0.03	-0.28	-0.06	0.65***	0.96***	0.86***	0.12	0.83***	-0.07	0.48*	0.24	0.71***	0.44*
2012	Hexyl hexanoate	0.57**	0.32	0.05	0.71***	0.58**	0.53**	-0.01	0.11	0.25	0.18	0.45*	0.5*	0.73***	0.63***	0.77***	-0.4*	0.56**	0.63***	0.72***	0.61**
2012	Methyl-2-aminobenzoate T	0.39	0.4*	0.41*	0.42*	0.41*	-0.1	-0.4*	0.13	-0.09	0.01	0.17	0.42*	0.19	-0.01	0.25	0.08	0.25	-0.08	0.19	0.04
2012	Methyl-2-hexenoate	0.48*	0.26	-0.27	0.52**	0.47*	0.35	-0.47*	-0.03	-0.05	0.01	0.3	0.54**	0.73***	0.35	0.72***	-0.31	0.78***	0.59**	0.63***	0.74***
2012	Methyl 3-hydroxyoctanoate T	0.52**	0.29	0.13	0.73***	0.61**	0.5*	-0.22	0.17	-0.03	0.2	0.47*	0.56**	0.66***	0.6**	0.72***	-0.17	0.6**	0.48*	0.58**	0.57**
2012	Methyl acetate T	0.22	0.24	0.41*	0.29	0.37	0.38	-0.07	0.25	0.16	-0.3	0.37	0.32	0.47*	0.09	0.43*	-0.14	0.35	0.46*	0.5*	0.47*
2012	Methyl benzoate	0.01	-0.26	-0.18	0.07	-0.04	-0.18	0.13	-0.26	-0.08	0.9***	-0.19	-0.18	-0.22	0.51**	-0.19	0.05	-0.3	-0.27	-0.25	-0.37
2012	Methyl butanoate	0.71***	0.76***	0.3	0.59**	0.77***	-0.21	-0.26	0.01	-0.24	-0.06	0.55**	0.87***	0.66***	-0.02	0.62**	0.22	0.14	-0.09	0.52**	0.09
2012	Methyl cinnamate T	-0.14	-0.48*	-0.1	0.02	-0.11	0.15	-0.02	-0.1	0.07	0.72***	-0.25	-0.33	-0.3	0.57**	-0.25	-0.02	-0.01	0	-0.18	-0.11
2012	Methyl decanoate	0.44*	0.32	0.16	0.67***	0.57**	0.58**	-0.16	0.37	0.09	-0.15	0.66***	0.67***	0.81***	0.37	0.87***	-0.21	0.69***	0.63***	0.75***	0.74***
2012	Methyl dodecanoate	0.36	0.13	-0.06	0.53**	0.45*	0.72***	-0.31	0.22	0.2	-0.25	0.43*	0.45*	0.76***	0.39	0.82***	-0.42*	0.86***	0.82***	0.67***	0.94***
2012	Methyl hexanoate	0.52**	0.47*	-0.08	0.58**	0.61**	0.41*	-0.25	0.22	-0.09	-0.25	0.69***	0.84***	0.92***	0.2	0.92***	-0.18	0.72***	0.59**	0.83***	0.77***
2012	Methyl octanoate	0.42*	0.31	-0.12	0.36	0.54**	0.29	-0.44*	0.04	-0.22	-0.18	0.45*	0.68***	0.7***	0.19	0.69***	-0.05	0.58**	0.38	0.56**	0.62***
2012	Myrtenyl acetate	0.41*	0.35	0.2	0.38	0.34	-0.06	-0.4*	0.22	0	-0.08	0.11	0.43*	0.33	0.03	0.39	0.03	0.29	0.07	0.24	0.23
2012	Nonyl acetate	0.5*	0.15	0.06	0.67***	0.6**	0.63***	-0.2	0.18	0.21	0.01	0.49*	0.45*	0.67***	0.53**	0.74***	-0.3	0.62***	0.58**	0.52**	0.65***
2012	Octyl acetate	0.67***	0.54**	-0.02	0.71***	0.72***	0.37	-0.34	0.16	0.03	-0.22	0.57**	0.81***	0.93***	0.28	0.96***	-0.15	0.72***	0.57**	0.81***	0.75***
2012	Octyl butanoate	0.82***	0.66***	0.1	0.76***	0.9***	0.23	-0.34	-0.01	-0.08	-0.16	0.6**	0.82***	0.93***	0.17	0.88***	0.01	0.47*	0.35	0.68***	0.55**
2012	Octyl hexanoate	0.67***	0.46*	0.06	0.65***	0.74***	0.45*	-0.42*	-0.01	0.11	-0.13	0.37	0.63***	0.82***	0.4*	0.86***	-0.26	0.72***	0.6**	0.76***	0.75***
2012	Pentyl acetate	0.32	0.36	0.1	0.27	0.39	0.07	0.39	0.18	-0.25	-0.01	0.69***	0.54**	0.44*	0.16	0.36	-0.16	-0.03	-0.01	0.35	-0.04
2012	Propyl butanoate	0.58**	0.72***	0.32	0.56**	0.65***	-0.08	0.07	0.23	-0.21	0.02	0.6**	0.84***	0.55**	0.23	0.62**	-0.03	0.22	0	0.64***	0.07
2012	(Z)-3-hexenyl acetate	-0.45*	-0.19	0.18	-0.4	-0.49*	0.21	0.45*	0.17	0.19	0.05	-0.09	-0.24	-0.39	0.13	-0.25	-0.54**	-0.07	0.05	-0.05	-0.13
2012	2,1-pentenyl_furan	-0.07	-0.09	-0.01	-0.13	-0.26	-0.48*	-0.11	-0.13	0	0.6**	-0.6**	-0.27	-0.53**	0.18	-0.4	0.12	-0.25	-0.42*	-0.32	-0.44*
2012	2-pentylfuran	-0.05	0.05	0.32	-0.02	-0.11	-0.32	-0.11	0.18	-0.02	0.26	-0.22	-0.03	-0.35	-0.02	-0.26	0.12	-0.11	-0.32	-0.15	-0.32
2012	Furaneol	0.05	-0.13	-0.03	0.39	0.14	0.43*	0.11	0.45*	0.22	-0.01	0.29	0.12	0.37	0.48*	0.47*	-0.06	0.49*	0.51**	0.47*	0.47*
2012	Mesifurane	-0.11	-0.4*	-0.2	0.06	-0.18	0.44*	0.2	0.3	0.58**	-0.01	-0.1	-0.3	-0.13	0.36	0.03	-0.23	0.19	0.34	0	0.21
2012	1-penten-3-one	0.24	0.14	0.26	0.35	0.14	-0.06	-0.28	0.15	0.26	0.18	-0.26	0.04	-0.07	0.19	0.11	0.03	0.16	0.02	0.07	0.05
2012	2-heptanone	0.55**	0.44*	0.05	0.75***	0.62**	0.35	-0.13	0.27	0.05	-0.11	0.54**	0.62***	0.7***	0.32	0.77***	0.11	0.55**	0.43*	0.67***	0.53**
2012	2-nonanone	0.55**	0.45*	0.26	0.82***	0.62***	0.37	-0.01	0.35	0.13	0.05	0.58**	0.6**	0.65***	0.4*	0.74***	0.01	0.47*	0.41*	0.66***	0.44*
2012	2-pentadecanone T	0.51**	0.26	0.21	0.7***	0.63***	0.6**	-0.23	0.26	0.22	-0.09	0.49*	0.52**	0.67***	0.54**	0.79***	-0.28	0.72***	0.6**	0.69***	0.67***
2012	2-pentanone	0.6**	0.48*	0.1	0.78***	0.66***	0.41*	-0.17	0.28	0.19	-0.22	0.53**	0.61**	0.76***	0.27	0.82***	0.07	0.61**	0.53**	0.73***	0.63***
2012	2-tridecanone T	0.56**	0.32	0.22	0.7***	0.68***	0.5*	-0.22	0.24	0.13	-0.07	0.47*	0.56**	0.65***	0.53**	0.77***	-0.23	0.65***	0.49*	0.66***	0.57**
2012	2-undecanone T	0.64***	0.43*	0.3	0.82***	0.72***	0.39	-0.16	0.26	0.11	0.11	0.5*	0.62***	0.64***	0.55**	0.76***	-0.15	0.55**	0.4*	0.68***	0.45*
2012	4-tridecanone T	0.05	-0.22	-0.3	0.29	0.11	0.78***	-0.2	0.21	0.27	-0.1	0.2	0.18	0.48*	0.5*	0.61**	-0.51**	0.83***	0.83***	0.49*	0.88***
2012	6-methyl-5-hepten-2-one	-0.46*	-0.47*	-0.1	-0.34	-0.57**	-0.17	0.02	0.07	0.19	0.22	-0.59**	-0.64***	-0.65***	-0.05	-0.56**	0.15	-0.2	-0.2	-0.52**	-0.27
2012	Acetone	0.35	0.28	0.36	0.56**	0.37	0.69***	0.16	0.24	0.51**	0.02	0.22	0.25	0.38	0.64***	0.57**	-0.48*	0.5*	0.62**	0.56**	0.53**
2012	Acetophenone	-0.07	-0.3	-0.28	0.07	-0.15	0.11	0.13	-0.12	-0.04	0.87***	-0.23	-0.18	-0.17	0.68***	-0.11	-0.19	0.03	0.06	-0.07	-0.05
2012	α-ionone	0.42*	0.14	0.24	0.6**	0.36	0.33	-0.42*	-0.13	0.39	0.42*	-0.07	0.09	0.22	0.46*	0.28	-0.24	0.43*	0.37	0.26	0.35
2012	β-ionone	0.43*	0.24	0.37	0.45*	0.38	0.14	-0.54**	-0.13	0.36	0.15	-0.22	0.11	0.08	0.29	0.21	-0.1	0.35	0.14	0.17	0.21
2012	(Z)-geranyl acetone	0.16	-0.06	0.29	0.19	0.15	0.02	-0.36	-0.02	0.31	0.14	-0.2	-0.13	-0.19	0.1	-0.08	0.09	0.07	-0.08	-0.12	-0.06
2012	γ-decalactone	0.43*	0.24	0.11	0.51**	0.47*	0.54**	-0.24	0.17	0.12	0.02	0.29	0.51**	0.53**	0.63***	0.69***	-0.55**	0.66***	0.51*	0.53**	0.6**
2012	α-farnesene	0.4*	0.26	0.14	0.64***	0.39	0.21	0.08	0.31	-0.11	0.41*	0.26	0.34	0.37	0.6**	0.41*	-0.15	0.35	0.31	0.44*	0.25
2012	α-pinene	-0.13	-0.21	-0.17	-0.06	-0.27	-0.17	0.39	-0.04	0.14	0.64***	-0.3	-0.23	-0.31	0.53**	-0.18	-0.15	-0.23	-0.18	-0.09	-0.35
2012	Limonene	0.11	0.16	-0.22	-0.16	0	-0.42*	-0.07	-0.26	-0.2	0.17	-0.29	0.03	-0.2	0.02	-0.08	-0.03	-0.2	-0.34	-0.16	-0.24
2012	Linalool	-0.1	-0.06	0.16	-0.15	-0.2	-0.37	-0.08	-0.13	0.15	0.34	-0.29	-0.2	-0.39	-0.19	-0.36	0.14	-0.35	-0.35	-0.3	-0.4*
2012	Myrtenol	0.24	0.12	0.36	0.15	0.18	0.07	0.02	0.02	0.34	0.22	-0.25	-0.06	-0.19	0.49*	0.04	-0.26	0.03	0.02	0.17	-0.07
2012	Nerol	0.05	0.06	0.08	0.28	0.04	0.47*	0.43*	0.48*	0.25	0.13	0.35	0.2	0.23	0.39	0.37	-0.44*	0.3	0.45*	0.45*	0.33
2012	Nerolidol	0.1	0.12	0.16	0.08	0.05	-0.26	-0.29	-0.28	0.11	0.2	-0.07	0.01	-0.04	-0.35	-0.14	0.19	-0.22	-0.21	-0.21	-0.18
2012	Terpineol	0.52**	0.19	0.18	0.51**	0.48*	-0.03	-0.34	-0.13	0.09	0.43*	0.07	0.29	0.24	0.48*	0.31	-0.1	0.21	-0.04	0.2	0

		2012 Ethyl dodecanoate	2012 Ethyl hexanoate	2012 Ethyl methylthioacetate T	2012 Ethyl octanoate	2012 Hexyl acetate	2012 Hexyl butanoate	2012 Hexyl hexanoate	2012 Methyl-2-aminobenzoate T	2012 Methyl-2-hexenoate	2012 Methyl 3-hydroxyoctanoate T	2012 Methyl acetate T	2012 Methyl benzoate	2012 Methyl butanoate	2012 Methyl cinnamate T	2012 Methyl decanoate
2012	Ethyl dodecanoate	1														
2012	Ethyl hexanoate	0.81***	1													
2012	Ethyl methylthioacetate T	0.36	0.65***	1												
2012	Ethyl octanoate	0.91***	0.96***	0.54**	1											
2012	Hexyl acetate	0.43*	0.7***	0.34	0.6**	1										
2012	Hexyl butanoate	0.33	0.6**	0.22	0.52**	0.89***	1									
2012	Hexyl hexanoate	0.57**	0.7***	0.26	0.63***	0.67***	0.6**	1								
2012	Methyl-2-aminobenzoate T	0	0.13	0.05	0.07	0.27	0.37	-0.13	1							
2012	Methyl-2-hexenoate	0.71***	0.73***	0.28	0.76***	0.61**	0.66***	0.64***	0.13	1						
2012	Methyl 3-hydroxyoctanoate T	0.54**	0.58**	0.15	0.57**	0.53**	0.55**	0.59**	0.4*	0.52**	1					
2012	Methyl acetate T	0.35	0.51**	0.2	0.48*	0.43*	0.3	0.35	0.1	0.26	0.36	1				
2012	Methyl benzoate	-0.3	-0.36	-0.18	-0.39	-0.14	-0.12	0.15	-0.21	-0.07	0.14	-0.27	1			
2012	Methyl butanoate	-0.04	0.3	0.06	0.18	0.69***	0.84***	0.31	0.51**	0.34	0.48*	0.35	-0.07	1		
2012	Methyl cinnamate T	-0.06	-0.19	-0.04	-0.18	-0.3	-0.31	0	0.08	-0.12	0.32	-0.09	0.68***	-0.25	1	
2012	Methyl decanoate	0.68***	0.76***	0.3	0.73***	0.74***	0.65***	0.64***	0.31	0.56**	0.81***	0.59**	-0.15	0.51**	0.05	1
2012	Methyl dodecanoate	0.95***	0.84***	0.29	0.91***	0.61**	0.52**	0.68***	0.12	0.79***	0.63***	0.5*	-0.29	0.2	-0.1	0.8***
2012	Methyl hexanoate	0.66***	0.84***	0.42*	0.82***	0.88***	0.85***	0.65***	0.18	0.77***	0.61**	0.53**	-0.26	0.64***	-0.29	0.82***
2012	Methyl octanoate	0.54**	0.59**	0.25	0.64***	0.6**	0.67***	0.34	0.3	0.63***	0.67***	0.56**	-0.19	0.61**	-0.01	0.73***
2012	Myrtenyl acetate	0.18	0.27	0.2	0.27	0.35	0.41*	0.08	0.71***	0.31	0.34	0.23	-0.32	0.48*	-0.22	0.33
2012	Nonyl acetate	0.67***	0.59**	0.09	0.63***	0.59**	0.48*	0.64***	0.28	0.55**	0.75***	0.5*	-0.03	0.32	0.13	0.71***
2012	Octyl acetate	0.66***	0.82***	0.33	0.81***	0.82***	0.85***	0.72***	0.26	0.79***	0.68***	0.49*	-0.28	0.65***	-0.31	0.79***
2012	Octyl butanoate	0.46*	0.63***	0.04	0.61**	0.78***	0.87***	0.71***	0.21	0.62**	0.67***	0.44*	-0.18	0.75***	-0.29	0.71***
2012	Octyl hexanoate	0.71***	0.78***	0.27	0.78***	0.66***	0.72***	0.77***	0.2	0.75***	0.69***	0.44*	-0.2	0.5*	-0.14	0.73***
2012	Pentyl acetate	-0.07	0.13	0	0.01	0.62***	0.48*	0.39	-0.13	0.15	0.13	0	0.12	0.44*	-0.27	0.17
2012	Propyl butanoate	-0.05	0.35	0.25	0.16	0.72***	0.78***	0.41*	0.41*	0.25	0.48*	0.17	0.05	0.83***	-0.14	0.5*
2012	(Z)-3-hexenyl acetate	-0.06	-0.08	0.29	-0.17	-0.05	-0.27	-0.07	-0.14	-0.21	-0.38	-0.22	0.03	-0.38	-0.02	-0.22
2012	2,1-pentenyl_furan	-0.44*	-0.39	0.03	-0.45*	-0.37	-0.25	-0.25	0.23	-0.22	-0.17	-0.42*	0.46*	-0.16	0.45*	-0.31
2012	2-pentylfuran	-0.36	-0.24	0.1	-0.33	-0.14	-0.1	-0.4*	0.67***	-0.28	-0.05	-0.12	0.06	0.09	0.34	-0.04
2012	Furaneol	0.41*	0.49*	0.33	0.47*	0.26	0.1	0.39	0.07	0.3	0.58**	0.46*	0.06	0.13	0.19	0.55**
2012	Mesifurane	0.3	0.13	0.13	0.17	-0.1	-0.3	0.14	-0.11	0	-0.04	-0.09	-0.05	-0.43*	0.17	-0.02
2012	1-penten-3-one	0.02	0.1	0.07	0.03	-0.01	0.03	0.03	0.54**	0.02	0.21	0.05	0.02	0.07	0.24	0.24
2012	2-heptanone	0.44*	0.63***	0.19	0.58**	0.57**	0.58**	0.52**	0.34	0.43*	0.81***	0.29	-0.1	0.54**	0.02	0.76***
2012	2-nonanone	0.35	0.58**	0.18	0.47*	0.61**	0.56**	0.6**	0.37	0.32	0.79***	0.32	0.06	0.52**	0.13	0.8***
2012	2-pentadecanone T	0.67***	0.68***	0.18	0.66***	0.57**	0.53**	0.61**	0.43*	0.58**	0.84***	0.39	-0.12	0.41*	0.17	0.83***
2012	2-pentanone	0.52**	0.73***	0.23	0.68***	0.61**	0.61**	0.6**	0.29	0.48*	0.74***	0.42*	-0.23	0.51**	-0.1	0.78***
2012	2-tridecanone T	0.56**	0.61**	0.16	0.58**	0.55**	0.56**	0.56**	0.48*	0.54**	0.85***	0.34	-0.08	0.5*	0.15	0.76***
2012	2-undecanone T	0.4*	0.57**	0.16	0.47*	0.62**	0.62**	0.62**	0.51**	0.46*	0.86***	0.31	0.08	0.57**	0.22	0.79***
2012	4-tridecanone T	0.95***	0.72***	0.38	0.82***	0.34	0.26	0.55**	-0.02	0.69***	0.52**	0.25	-0.13	-0.12	0.11	0.61**
2012	6-methyl-5-hepten-2-one	-0.2	-0.4*	-0.08	-0.34	-0.61**	-0.66***	-0.5*	0.11	-0.43*	-0.36	-0.31	0.1	-0.62***	0.39	-0.37
2012	Acetone	0.52**	0.6**	0.24	0.52**	0.37	0.26	0.7***	0.06	0.3	0.61**	0.38	-0.01	0.1	0.08	0.57**
2012	Acetophenone	-0.02	-0.06	0.13	-0.09	-0.11	-0.12	0.28	-0.21	0.06	0.26	-0.23	0.82***	-0.24	0.74***	-0.01
2012	α-ionone	0.35	0.35	0.07	0.32	0.17	0.2	0.46*	0.45*	0.36	0.48*	0.14	0.12	0.06	0.38	0.37
2012	β-ionone	0.21	0.21	-0.01	0.19	0.04	0.16	0.14	0.7***	0.25	0.41*	0.12	-0.11	0.18	0.3	0.31
2012	(Z)-geranyl acetone	0	-0.12	-0.13	-0.1	-0.15	-0.12	-0.19	0.66***	-0.12	0.13	-0.07	-0.05	-0.04	0.41*	0.07
2012	γ-decalactone	0.65***	0.58**	0.25	0.57**	0.5*	0.5*	0.54**	0.41*	0.6**	0.72***	0.25	-0.1	0.36	0.07	0.63***
2012	α-farnesene	0.19	0.37	0.18	0.27	0.29	0.32	0.53**	0.22	0.26	0.71***	0.07	0.3	0.26	0.3	0.43*
2012	α-pinene	-0.32	-0.24	0.13	-0.34	-0.15	-0.18	0.23	-0.36	-0.11	-0.1	-0.24	0.72***	-0.17	0.36	-0.25
2012	Limonene	-0.25	-0.22	-0.06	-0.25	0	0.04	-0.04	-0.21	-0.03	-0.27	-0.25	0.29	-0.04	-0.09	-0.27
2012	Linalool	-0.41*	-0.34	0	-0.41*	-0.11	-0.16	-0.24	0.18	-0.31	-0.45*	-0.08	0.23	-0.1	0.17	-0.26
2012	Myrtenol	-0.1	0.04	0.16	-0.08	-0.01	-0.05	0.23	0.16	-0.13	0.15	-0.04	0.14	-0.03	0.28	0.05
2012	Nerol	0.3	0.44*	0.43*	0.31	0.46*	0.2	0.56**	-0.15	0.1	0.14	0.05	0.11	-0.1	0.03	0.38
2012	Nerolidol	-0.19	-0.15	-0.16	-0.17	0.08	0.08	-0.08	0.2	-0.06	-0.3	0.15	0.06	0.09	-0.04	-0.08
2012	Terpineol	0.04	0.06	-0.05	0.02	0.3	0.37	0.31	0.58**	0.38	0.47*	0.09	0.3	0.43*	0.3	0.23

		2012 Methyl dodecanoate	2012 Methyl hexanoate	2012 Methyl octanoate	2012 Myrtenyl acetate	2012 Nonyl acetate	2012 Octyl acetate	2012 Octyl butanoate	2012 Octyl hexanoate	2012 Pentyl acetate	2012 Propyl butanoate	2012 (Z)-3-hexenyl acetate	2012 2,1-pentenyl_furan	2012 2-pentylfuran	2012 Furaneol	2012 Mesifurane	2012 1-penten-3-one	2012 2-heptanone
2012	Methyl dodecanoate	1																
2012	Methyl hexanoate	0.77***	1															
2012	Methyl octanoate	0.65***	0.83***	1														
2012	Myrtenyl acetate	0.31	0.35	0.42*	1													
2012	Nonyl acetate	0.78***	0.63***	0.6**	0.38	1												
2012	Octyl acetate	0.81***	0.94***	0.77***	0.48*	0.71***	1											
2012	Octyl butanoate	0.66***	0.82***	0.67***	0.35	0.64***	0.9***	1										
2012	Octyl hexanoate	0.84***	0.78***	0.67***	0.32	0.68***	0.89***	0.87***	1									
2012	Pentyl acetate	0.06	0.37	0.13	-0.1	0.25	0.31	0.41*	0.17	1								
2012	Propyl butanoate	0.13	0.57**	0.41*	0.24	0.27	0.56**	0.6**	0.43*	0.59**	1							
2012	(Z)-3-hexenyl acetate	-0.16	-0.24	-0.38	-0.19	-0.29	-0.36	-0.5*	-0.3	0.15	-0.1	1						
2012	2,1-pentenyl_furan	-0.46*	-0.46*	-0.36	0.09	-0.45*	-0.41*	-0.47*	-0.35	-0.38	-0.01	0.25	1					
2012	2-pentylfuran	-0.32	-0.29	-0.13	0.39	-0.25	-0.29	-0.35	-0.31	-0.32	0.15	0.21	0.74***	1				
2012	Furaneol	0.45*	0.4*	0.38	0.21	0.61**	0.45*	0.26	0.34	0.03	0.18	-0.34	-0.22	-0.17	1			
2012	Mesifurane	0.21	-0.1	-0.19	0.02	0.36	-0.02	-0.18	-0.04	0	-0.26	0.21	-0.05	-0.06	0.25	1		
2012	1-penten-3-one	0.07	-0.05	-0.03	0.41*	0.03	0.06	-0.04	0.07	-0.43*	0.15	0.03	0.67***	0.72***	0.11	0.13	1	
2012	2-heptanone	0.53**	0.67***	0.57**	0.24	0.61**	0.73***	0.69***	0.63***	0.2	0.62***	-0.47*	-0.26	-0.13	0.63***	0.05	0.22	1
2012	2-nonanone	0.47*	0.57**	0.39	0.21	0.56**	0.62***	0.63***	0.56**	0.21	0.67***	-0.29	-0.08	0.06	0.56**	0.02	0.41*	0.91***
2012	2-pentadecanone T	0.79***	0.63***	0.59**	0.32	0.81***	0.72***	0.66***	0.79***	0.15	0.45*	-0.27	-0.29	-0.06	0.57**	0.21	0.23	0.78***
2012	2-pentanone	0.63***	0.72***	0.54**	0.27	0.64***	0.8***	0.75***	0.71***	0.15	0.56**	-0.45*	-0.32	-0.18	0.61**	0.11	0.27	0.96***
2012	2-tridecanone T	0.69***	0.61**	0.6**	0.36	0.79***	0.72***	0.68***	0.76***	0.21	0.54**	-0.34	-0.27	-0.06	0.57**	0.16	0.21	0.81***
2012	2-undecanone T	0.56**	0.58**	0.5*	0.32	0.69***	0.67***	0.67***	0.68***	0.23	0.68***	-0.29	-0.06	0.1	0.54**	0.07	0.41*	0.86***
2012	4-tridecanone T	0.88***	0.57**	0.49*	0.16	0.64***	0.57**	0.34	0.62***	-0.14	-0.09	0	-0.31	-0.31	0.42*	0.37	0.04	0.37
2012	6-methyl-5-hepten-2-one	-0.33	-0.63***	-0.5*	-0.04	-0.37	-0.61**	-0.7***	-0.54**	-0.6**	-0.51**	0.28	0.66***	0.61**	-0.16	0.3	0.54**	-0.37
2012	Acetone	0.56**	0.39	0.21	0.05	0.59**	0.49*	0.43*	0.59**	0.1	0.32	0.13	-0.14	-0.18	0.41*	0.31	0.3	0.57**
2012	Acetophenone	-0.09	-0.14	-0.08	-0.26	0.03	-0.17	-0.2	-0.07	-0.03	-0.03	0.19	0.53**	0.13	0.11	0.06	0.16	-0.02
2012	α-ionone	0.42*	0.13	0.09	0.39	0.44*	0.27	0.24	0.44*	-0.29	0.01	-0.03	0.28	0.33	0.13	0.16	0.54**	0.21
2012	β-ionone	0.3	0.06	0.19	0.51**	0.31	0.23	0.17	0.39	-0.41*	0.12	-0.07	0.4	0.56**	0.06	0.12	0.74***	0.26
2012	(Z)-geranyl acetone	0.05	-0.24	-0.07	0.37	0.21	-0.12	-0.11	0.02	-0.37	-0.07	-0.02	0.35	0.63***	-0.06	0.34	0.55**	0.04
2012	γ-decalactone	0.71***	0.57**	0.6**	0.5*	0.73***	0.66***	0.54**	0.69***	0.19	0.38	0.01	-0.13	0.01	0.31	0.26	0.24	0.48*
2012	α-farnesene	0.24	0.24	0.13	0.16	0.37	0.35	0.4*	0.36	0.12	0.44*	-0.3	0.15	0.05	0.44*	0.03	0.32	0.62***
2012	α-pinene	-0.34	-0.24	-0.33	-0.28	-0.17	-0.23	-0.3	-0.25	0.13	0.1	0.31	0.51**	0.03	0.13	0.14	0.08	-0.15
2012	Limonene	-0.25	-0.11	-0.15	-0.21	-0.21	-0.1	-0.11	-0.1	0.16	0.17	0.17	0.43*	0.06	-0.2	-0.06	0.16	-0.17
2012	Linalool	-0.37	-0.33	-0.36	0.12	-0.35	-0.39	-0.4*	-0.39	-0.22	-0.14	0.43*	0.59**	0.64***	-0.41*	-0.03	0.41*	-0.53**
2012	Myrtenol	-0.03	-0.16	-0.15	0.09	0.12	-0.01	-0.03	0.18	-0.01	0.24	0.24	0.45*	0.32	0.13	0.27	0.49*	0.13
2012	Nerol	0.3	0.26	-0.12	-0.11	0.22	0.2	0.11	0.19	0.31	0.25	0.52**	0.06	0.01	0.12	0.38	0.21	0.18
2012	Nerolidol	-0.12	-0.06	-0.12	0.21	-0.16	-0.13	-0.08	-0.17	-0.18	-0.16	0.18	0.23	0.38	-0.43*	-0.19	0.24	-0.42*
2012	Terpineol	0.22	0.19	0.28	0.56**	0.55**	0.34	0.31	0.35	0.15	0.34	-0.17	0.16	0.23	0.29	0.12	0.2	0.24

Supplemental table CIII. 2

		2013 1-decanol	2013 1-hexanol	2013 1-octanol	2013 1-penten-3-ol	2013 2-heptanol	2013 2-nonanol	2013 2-tridecanol T	2013 2-undecanol T	2013 (E)-2-hexen-1-ol	2013 Ethanol	2013 Eugenol	2013 3,4-dimethylbenzaldehyde	2013 Benzaldehyde	2013 Decanal	2013 (E)-2-decenal	2013 (E)-2-heptenal	2013 (E)-2-hexenal	2013 (E)-2-nonenal	2013 (E)-2-octenal	2013 (E)-2-pentenal	2013 (E,Z)-2,4-heptadienal	2013 Heptanal	2013 Hexanal	2013 Nonanal	2013 Octanal	2013 Pentanal	2013 (Z)-3-hexenal	2013 1-methylbutyl butanoate	2013 1-methylethyl butanoate	2013 1-methylethyl acetate	2013 1-methylhexyl acetate	2013 1-methyloctyl butanoate	2013 2,3-butanedioldiacetate T	2013 2 -methylbutyl acetate	2013 3-methyl-2-butenyl acetate	2013 3-methylbutyl acetate	2013 Benzyl acetate	2013 Butyl acetate	2013 Butyl butanoate	2013 Butyl hexanoate	2013 Cinnamyl acetate	2013 Decyl acetate	2013 (E)-2-hexenyl acetate	2013 Ethyl 2-hexenoate	2013 Ethyl acetate	2013 Ethyl butanoate	2013 Ethyl decanoate	2013 Ethyl dodecanoate	2013 Ethyl hexanoate	2013 Ethyl methylthioacetate T	2013 Ethyl octanoate	2013 Hexyl acetate	2013 Hexyl butanoate	2013 Hexyl hexanoate	2013 Methyl-2-aminobenzoate T	2013 Methyl-2-hexenoate	2013 Methyl 3-hydroxyoctanoate T	2013 Methyl acetate T	2013 Methyl benzoate	2013 Methyl butanoate	2013 Methyl cinnamate T	2013 Methyl decanoate	2013 Methyl dodecanoate	2013 Methyl hexanoate	2013 Methyl octanoate	2013 Myrtenyl acetate	2013 Nonyl acetate	2013 Octyl acetate	2013 Octyl butanoate	2013 Octyl hexanoate	2013 Pentyl acetate	2013 Propyl butanoate	2013 (Z)-3-hexenyl acetate	2013 2,1-pentenyl_furan	2013 2-pentylfuran	2013 Furaneol	2013 Mesifurane	2013 1-penten-3-one	2013 2-heptanone	2013 2-nonanone	2013 2-pentadecanone T	2013 2-pentanone	2013 2-tridecanone T	2013 2-undecanone T	2013 4-tridecanone T	2013 6-methyl-5-hepten-2-one	2013 Acetone	2013 Acetophenone	2013 α-ionone	2013 β-ionone	2013 (Z)-geranyl acetone	2013 γ-decalactone	2013 α-farnesene	2013 α-pinene	2013 Limonene	2013 Linalool	2013 Myrtenol	2013 Nerol	2013 Nerolidol	2013 Terpineol
2013	1-decanol	1																																																																																																				
2013	1-hexanol	-0.38	1																																																																																																			
2013	1-octanol	0.89***	-0.36	1																																																																																																		
2013	1-penten-3-ol	-0.52**	0.49*	-0.38	1																																																																																																	
2013	2-heptanol	0.89***	-0.44*	0.86***	-0.54**	1																																																																																																
2013	2-nonanol	0.83***	-0.39	0.63***	-0.64***	0.81***	1																																																																																															
2013	2-tridecanol T	0.83***	-0.49*	0.72***	-0.44*	0.79***	0.65***	1																																																																																														
2013	2-undecanol T	0.92***	-0.45*	0.74***	-0.64***	0.87***	0.93***	0.86***	1																																																																																													
2013	(E)-2-hexen-1-ol	-0.35	0.19	-0.27	-0.06	-0.21	-0.2	-0.5*	-0.33	1																																																																																												
2013	Ethanol	0.7***	-0.31	0.54**	-0.69***	0.67***	0.74***	0.73***	0.81***	-0.29	1																																																																																											
2013	Eugenol	0.38	-0.02	0.42*	0.11	0.3	-0.02	0.56**	0.23	-0.64***	0.18	1																																																																																										
2013	3,4-dimethylbenzaldehyde	0.26	-0.22	0.21	-0.23	0.21	0.39	0.35	0.37	-0.19	0.43*	0.15	1																																																																																									
2013	Benzaldehyde	-0.69***	0.24	-0.75***	0.47*	-0.59**	-0.37	-0.53**	-0.5*	0.17	-0.42*	-0.32	-0.01	1																																																																																								
2013	Decanal	-0.03	-0.1	0.31	0.08	0.08	-0.08	-0.23	-0.17	0.02	-0.19	0	-0.02	-0.16	1																																																																																							
2013	(E)-2-decenal	-0.21	-0.13	0.08	0.29	-0.14	-0.29	-0.18	-0.31	0.1	-0.24	-0.06	-0.06	0.06	0.47*	1																																																																																						
2013	(E)-2-heptenal	-0.02	0.19	-0.02	0.48*	-0.16	-0.15	0.09	-0.09	-0.86***	-0.07	0.56**	0.09	0.14	0.07	0.04	1																																																																																					
2013	(E)-2-hexenal	-0.51**	0.13	-0.38	0.1	-0.38	-0.34	-0.6**	-0.49*	0.93***	-0.45*	-0.65***	-0.16	0.3	0.16	0.17	-0.73***	1																																																																																				
2013	(E)-2-nonenal	-0.13	-0.31	0.03	-0.48*	-0.03	-0.1	-0.05	-0.06	0.56**	0.09	-0.26	0.12	-0.25	0.21	0.24	-0.7***	0.55**	1																																																																																			
2013	(E)-2-octenal	0.14	0.2	0.31	0.44*	0.13	0.01	0.03	-0.02	-0.29	-0.06	0.24	0.07	0.1	0.37	0.41*	0.46*	-0.18	-0.44*	1																																																																																		
2013	(E)-2-pentenal	-0.56**	0.4*	-0.4*	0.85***	-0.59**	-0.61**	-0.58**	-0.68***	-0.16	-0.69***	0.07	-0.17	0.5*	0.37	0.29	0.58**	0.09	-0.42*	0.49*	1																																																																																	
2013	(E,Z)-2,4-heptadienal	-0.6**	0.27	-0.45*	0.66***	-0.55**	-0.65***	-0.63***	-0.7***	0.05	-0.65***	-0.03	-0.37	0.4*	0.25	0.28	0.33	0.21	-0.21	0.19	0.7***	1																																																																																
2013	Heptanal	-0.34	0.17	-0.16	0.17	-0.31	-0.31	-0.44*	-0.41*	0.01	-0.44*	0.05	-0.16	0.1	0.58**	-0.03	0.15	0.17	0.09	-0.06	0.4*	0.42*	1																																																																															
2013	Hexanal	-0.59**	0.54**	-0.53**	0.77***	-0.75***	-0.63***	-0.48*	-0.65***	-0.05	-0.52**	0.05	-0.01	0.49*	0	0.16	0.45*	0.18	-0.25	0.35	0.75***	0.54**	0.26	1																																																																														
2013	Nonanal	0	-0.35	0.19	-0.13	0.1	0.17	-0.11	0.02	-0.06	-0.17	-0.05	0.26	0.06	0.72***	0.3	0.03	0.1	0.2	0.18	0.2	0.05	0.58**	-0.12	1																																																																													
2013	Octanal	-0.35	0.01	-0.12	0.28	-0.2	-0.15	-0.47*	-0.34	0.23	-0.45*	-0.28	0.08	0.41*	0.72***	0.33	-0.02	0.43*	0.07	0.29	0.54**	0.31	0.56**	0.2	0.79***	1																																																																												
2013	Pentanal	-0.53**	0.33	-0.22	0.65***	-0.45*	-0.55**	-0.64***	-0.64***	0.06	-0.56**	-0.11	-0.23	0.36	0.6**	0.39	0.33	0.25	-0.16	0.48*	0.79***	0.72***	0.46*	0.54**	0.29	0.63***	1																																																																											
2013	(Z)-3-hexenal	-0.06	0.25	-0.11	0.49*	-0.25	-0.2	0.05	-0.12	-0.82***	-0.12	0.55**	0.07	0.15	-0.02	-0.1	0.97***	-0.68***	-0.69***	0.37	0.58**	0.35	0.21	0.53**	-0.02	-0.06	0.29	1																																																																										
2013	1-methylbutyl butanoate	0.6**	-0.24	0.61**	-0.15	0.72***	0.47*	0.47*	0.5*	-0.21	0.19	0.26	-0.19	-0.42*	0.01	-0.05	-0.01	-0.35	-0.24	0.25	-0.3	-0.21	-0.19	-0.5*	0.02	-0.26	-0.22	-0.09	1																																																																									
2013	1-methylethyl butanoate	0.45*	-0.04	0.51**	0.19	0.42*	0.15	0.44*	0.3	-0.47*	-0.03	0.65***	-0.17	-0.3	0.02	0.17	0.4*	-0.54**	-0.42*	0.44*	0.04	0.07	-0.1	-0.11	0.04	-0.21	-0.03	0.37	0.68***	1																																																																								
2013	1-methylethyl acetate	-0.39	0.26	-0.33	0.49*	-0.47*	-0.52**	-0.19	-0.45*	-0.36	-0.24	0.27	-0.05	0.31	-0.11	0.31	0.58**	-0.3	-0.35	0.37	0.4*	0.41*	-0.03	0.54**	-0.19	-0.14	0.35	0.58**	-0.17	0.27	1																																																																							
2013	1-methylhexyl acetate	0.6**	-0.29	0.65***	-0.45*	0.81***	0.58**	0.51**	0.61**	-0.18	0.52**	0.23	0.04	-0.43*	0.24	0.17	-0.08	-0.37	0.02	0.18	-0.44*	-0.27	-0.2	-0.73***	0.21	-0.07	-0.23	-0.22	0.65***	0.48*	-0.25	1																																																																						
2013	1-methyloctyl butanoate	0.78***	-0.3	0.73***	-0.24	0.78***	0.64***	0.62**	0.69***	-0.26	0.27	0.31	-0.09	-0.53**	-0.02	-0.06	-0.02	-0.4*	-0.22	0.18	-0.38	-0.31	-0.21	-0.54**	0.08	-0.26	-0.4*	-0.06	0.89***	0.74***	-0.31	0.65***	1																																																																					
2013	2,3-butanedioldiacetate T	0.45*	-0.15	0.28	-0.54**	0.3	0.41*	0.46*	0.51**	-0.4*	0.76***	0.12	0.2	-0.35	-0.28	-0.2	0.15	-0.58**	-0.07	-0.09	-0.55**	-0.45*	-0.43*	-0.34	-0.37	-0.62**	-0.42*	0.12	0.05	-0.02	0.21	0.27	0.07	1																																																																				
2013	2 -methylbutyl acetate	-0.42*	0.04	-0.47*	0.35	-0.5*	-0.47*	-0.17	-0.42*	-0.31	-0.29	0.27	0.09	0.34	-0.23	0.31	0.47*	-0.25	-0.17	0.02	0.3	0.37	-0.02	0.42*	-0.1	-0.19	0.08	0.48*	-0.24	0.2	0.75***	-0.24	-0.29	0.04	1																																																																			
2013	3-methyl-2-butenyl acetate	-0.19	0.03	-0.27	0.22	-0.3	-0.18	0.02	-0.13	-0.28	0.04	0.11	0.34	0.25	-0.21	0.32	0.38	-0.15	-0.07	0.3	0.25	0.13	-0.43*	0.45*	-0.19	-0.16	0.04	0.36	-0.33	0.03	0.46*	-0.16	-0.28	0.14	0.6**	1																																																																		
2013	3-methylbutyl acetate	-0.23	0.09	-0.15	0.32	-0.34	-0.35	-0.1	-0.29	-0.26	-0.08	0.07	-0.07	0.04	-0.1	0.62***	0.39	-0.23	-0.07	0.34	0.22	0.27	-0.29	0.37	-0.24	-0.29	0.2	0.33	-0.09	0.23	0.71***	-0.08	-0.14	0.23	0.61**	0.62**	1																																																																	
2013	Benzyl acetate	-0.46*	0.28	-0.41*	0.47*	-0.35	-0.4*	-0.34	-0.44*	-0.16	-0.4*	0.16	-0.25	0.58**	-0.05	0.21	0.4*	-0.15	-0.38	0.23	0.39	0.52**	0.26	0.31	0.04	0.08	0.36	0.38	0.12	0.33	0.6**	0.01	-0.09	-0.17	0.62***	0.1	0.34	1																																																																
2013	Butyl acetate	0.33	0.15	0.41*	0.15	0.32	0.12	0.21	0.22	-0.39	0.1	0.48*	-0.21	-0.27	0.22	0.19	0.43*	-0.49*	-0.34	0.34	0.12	0.32	0.02	-0.14	0.02	-0.09	0.21	0.37	0.38	0.72***	0.15	0.59**	0.48*	0.11	0.08	0.05	0.23	0.26	1																																																															
2013	Butyl butanoate	0.56**	-0.15	0.6**	0.07	0.56**	0.26	0.52**	0.42*	-0.26	0.02	0.55**	-0.2	-0.45*	0.03	0.01	0.12	-0.32	-0.2	0.22	-0.09	0.04	-0.08	-0.25	0	-0.2	-0.16	0.11	0.69***	0.82***	-0.21	0.48*	0.83***	-0.19	-0.15	-0.14	-0.07	0	0.66***	1																																																														
2013	Butyl hexanoate	0.78***	-0.15	0.83***	-0.32	0.74***	0.53**	0.53**	0.64***	-0.2	0.42*	0.38	-0.1	-0.72***	0.23	-0.04	-0.01	-0.35	-0.03	0.19	-0.32	-0.19	-0.14	-0.51**	0.03	-0.22	-0.16	-0.06	0.6**	0.57**	-0.39	0.68***	0.76***	0.21	-0.47*	-0.24	-0.14	-0.34	0.7***	0.76***	1																																																													
2013	Cinnamyl acetate	0.03	-0.14	-0.11	0.11	-0.05	-0.05	0.33	0.07	-0.51**	0.12	0.52**	0.2	0.25	-0.34	0.03	0.45*	-0.52**	-0.33	0.02	0	-0.1	-0.1	0.14	-0.11	-0.28	-0.24	0.45*	0	0.29	0.51**	-0.03	-0.03	0.26	0.71***	0.29	0.23	0.51**	0.01	-0.03	-0.3	1																																																												
2013	Decyl acetate	0.97***	-0.37	0.85***	-0.52**	0.86***	0.81***	0.79***	0.88***	-0.34	0.66***	0.38	0.22	-0.69***	-0.02	-0.15	-0.02	-0.5*	-0.12	0.11	-0.57**	-0.54**	-0.3	-0.58**	0.03	-0.35	-0.55**	-0.06	0.59**	0.5*	-0.34	0.63***	0.8***	0.43*	-0.32	-0.17	-0.18	-0.39	0.38	0.58**	0.77***	0.07	1																																																											
2013	(E)-2-hexenyl acetate	-0.45*	0.06	-0.39	-0.08	-0.25	-0.23	-0.5*	-0.35	0.94***	-0.3	-0.68***	-0.22	0.31	0.02	0.16	-0.82***	0.92***	0.58**	-0.32	-0.13	0.14	-0.01	-0.06	0	0.3	0.08	-0.79***	-0.27	-0.49*	-0.32	-0.14	-0.31	-0.41*	-0.23	-0.13	-0.22	-0.09	-0.37	-0.28	-0.27	-0.47*	-0.43*	1																																																										
2013	Ethyl 2-hexenoate	0.66***	-0.37	0.45*	-0.41*	0.6**	0.66***	0.85***	0.79***	-0.4*	0.76***	0.34	0.53**	-0.24	-0.36	-0.22	0.06	-0.44*	-0.05	0.11	-0.49*	-0.66***	-0.57**	-0.26	-0.14	-0.4*	-0.63***	0.04	0.24	0.19	-0.18	0.33	0.39	0.43*	-0.11	0.33	-0.04	-0.35	0	0.25	0.29	0.31	0.62**	-0.36	1																																																									
2013	Ethyl acetate	0.55**	-0.26	0.32	-0.57**	0.46*	0.66***	0.62**	0.69***	-0.35	0.9***	0.1	0.53**	-0.2	-0.28	-0.25	0.05	-0.47*	-0.04	-0.03	-0.58**	-0.6**	-0.42*	-0.32	-0.14	-0.39	-0.53**	0.03	0.02	-0.11	-0.01	0.32	0.1	0.79***	-0.05	0.19	0.01	-0.26	-0.04	-0.18	0.13	0.34	0.52**	-0.35	0.76***	1																																																								
2013	Ethyl butanoate	0.32	-0.05	0.14	0.2	0.21	0.25	0.45*	0.32	-0.28	0.04	0.29	0.1	-0.03	-0.5*	-0.12	0.18	-0.27	-0.36	0.13	-0.08	-0.12	-0.24	0.13	-0.2	-0.33	-0.43*	0.24	0.34	0.48*	0.03	0.01	0.5*	-0.11	0.18	0.16	0.11	0.09	0.12	0.54**	0.1	0.36	0.34	-0.31	0.5*	0.16	1																																																							
2013	Ethyl decanoate	0.83***	-0.3	0.74***	-0.67***	0.76***	0.77***	0.72***	0.83***	-0.33	0.92***	0.25	0.4*	-0.57**	0.05	-0.2	-0.02	-0.48*	0.03	0.12	-0.6**	-0.65***	-0.34	-0.55**	-0.01	-0.32	-0.44*	-0.08	0.31	0.11	-0.25	0.58**	0.4*	0.74***	-0.39	-0.06	-0.16	-0.47*	0.19	0.13	0.59**	0.03	0.78***	-0.39	0.68***	0.81***	-0.04	1																																																						
2013	Ethyl dodecanoate	0.84***	-0.29	0.76***	-0.65***	0.8***	0.76***	0.68***	0.81***	-0.35	0.89***	0.28	0.29	-0.61**	0.1	-0.17	0.01	-0.52**	-0.02	0.13	-0.57**	-0.58**	-0.31	-0.61**	0	-0.3	-0.38	-0.07	0.39	0.18	-0.25	0.68***	0.46*	0.71***	-0.4*	-0.14	-0.16	-0.41*	0.3	0.19	0.66***	0	0.8***	-0.41*	0.59**	0.74***	-0.08	0.98***	1																																																					
2013	Ethyl hexanoate	0.83***	-0.38	0.61**	-0.58**	0.74***	0.76***	0.85***	0.88***	-0.26	0.84***	0.28	0.4*	-0.5*	-0.34	-0.29	-0.12	-0.39	0.01	-0.03	-0.68***	-0.65***	-0.58**	-0.47*	-0.23	-0.52**	-0.7***	-0.13	0.32	0.21	-0.32	0.46*	0.51**	0.55**	-0.25	0.13	-0.14	-0.5*	0.14	0.35	0.53**	0.14	0.81***	-0.28	0.89***	0.77***	0.42*	0.81***	0.75***	1																																																				
2013	Ethyl methylthioacetate T	-0.45*	0.26	-0.58**	0.59**	-0.54**	-0.41*	-0.21	-0.38	-0.02	-0.46*	0	-0.04	0.55**	-0.48*	-0.08	0.23	0.13	-0.29	-0.02	0.41*	0.34	0	0.64***	-0.27	-0.04	0.01	0.35	-0.28	-0.01	0.3	-0.61**	-0.23	-0.37	0.42*	0.33	0.15	0.3	-0.21	0	-0.52**	0.31	-0.46*	0.03	-0.01	-0.22	0.62***	-0.61**	-0.68***	-0.2	1																																																			
2013	Ethyl octanoate	0.85***	-0.35	0.77***	-0.68***	0.78***	0.78***	0.75***	0.86***	-0.22	0.9***	0.21	0.38	-0.62***	0	-0.18	-0.14	-0.36	0.13	0.09	-0.65***	-0.67***	-0.42*	-0.54**	-0.04	-0.34	-0.48*	-0.19	0.31	0.12	-0.34	0.54**	0.45*	0.65***	-0.47*	-0.03	-0.16	-0.59**	0.16	0.22	0.64***	-0.08	0.8***	-0.28	0.73***	0.76***	0.04	0.97***	0.93***	0.88***	-0.54**	1																																																		
2013	Hexyl acetate	0.37	0.03	0.43*	0.09	0.41*	0.18	0.34	0.3	-0.41*	0.1	0.52**	-0.16	-0.26	0.09	0.14	0.37	-0.48*	-0.28	0.35	0.04	0.17	-0.09	-0.19	0.06	-0.13	0.06	0.31	0.52**	0.79***	0.06	0.62***	0.61**	-0.02	0.05	0.12	0.2	0.24	0.91***	0.78***	0.7***	0.02	0.4*	-0.35	0.2	-0.05	0.29	0.17	0.25	0.25	-0.12	0.19	1																																																	
2013	Hexyl butanoate	0.6**	-0.11	0.63***	0	0.59**	0.32	0.52**	0.48*	-0.2	0.11	0.47*	-0.16	-0.51**	0.05	-0.08	0.05	-0.28	-0.13	0.22	-0.15	-0.04	-0.12	-0.28	-0.05	-0.23	-0.19	0.06	0.67***	0.73***	-0.29	0.49*	0.82***	-0.11	-0.29	-0.14	-0.13	-0.14	0.64***	0.96***	0.83***	-0.18	0.6**	-0.24	0.3	-0.12	0.46*	0.23	0.28	0.42*	-0.07	0.34	0.77***	1																																																
2013	Hexyl hexanoate	0.73***	-0.17	0.79***	-0.24	0.62***	0.39	0.62***	0.58**	-0.45*	0.47*	0.58**	-0.04	-0.72***	0.13	0.05	0.23	-0.62***	-0.09	0.13	-0.33	-0.21	-0.13	-0.41*	-0.08	-0.42*	-0.19	0.17	0.56**	0.65***	-0.03	0.58**	0.67***	0.46*	-0.14	-0.2	0.13	-0.12	0.69***	0.65***	0.83***	0.08	0.72***	-0.55**	0.29	0.27	0.15	0.6**	0.66***	0.48*	-0.43*	0.59**	0.61**	0.67***	1																																															
2013	Methyl-2-aminobenzoate T	0.15	-0.05	0.08	0.07	0.18	0.18	0.33	0.23	-0.21	0.07	0.27	0.23	0.12	-0.23	0.03	0.16	-0.13	-0.15	0.31	0.06	-0.13	-0.35	0.09	0.05	-0.02	-0.22	0.14	0.13	0.31	-0.09	0.13	0.26	-0.23	0.01	0.45*	0.11	-0.02	0.12	0.37	0.13	0.02	0.16	-0.1	0.53**	0.02	0.44*	0	-0.04	0.32	0.24	0.11	0.43*	0.36	-0.09	1																																														
2013	Methyl-2-hexenoate	0.51**	-0.3	0.41*	-0.29	0.49*	0.29	0.58**	0.47*	-0.24	0.27	0.6**	0.13	-0.34	-0.3	-0.28	0.01	-0.31	0.01	-0.05	-0.34	-0.17	-0.22	-0.33	-0.12	-0.43*	-0.45*	0.03	0.41*	0.49*	-0.27	0.34	0.52**	0.02	0	0.07	-0.17	-0.07	0.34	0.67***	0.53**	0.19	0.51**	-0.24	0.47*	0.09	0.39	0.26	0.26	0.53**	-0.04	0.33	0.54**	0.65***	0.41*	0.49*	1																																													
2013	Methyl 3-hydroxyoctanoate T	0.63***	-0.43*	0.48*	-0.44*	0.73***	0.58**	0.78***	0.74***	-0.14	0.58**	0.35	0.3	-0.16	-0.31	-0.17	-0.18	-0.28	0.03	-0.02	-0.55**	-0.55**	-0.54**	-0.58**	-0.12	-0.31	-0.62***	-0.23	0.41*	0.3	-0.36	0.54**	0.51**	0.25	-0.2	0.04	-0.3	-0.2	0.13	0.44*	0.42*	0.26	0.57**	-0.08	0.73***	0.44*	0.33	0.53**	0.5*	0.72***	-0.12	0.58**	0.3	0.45*	0.33	0.41*	0.65***	1																																												
2013	Methyl acetate T	0.29	0.01	0.3	0.05	0.14	0.13	0.33	0.22	-0.28	0.32	0.34	0.23	-0.13	-0.05	0.18	0.27	-0.24	-0.14	0.52**	-0.02	0.04	-0.26	0.24	-0.09	-0.16	0.02	0.28	-0.02	0.32	0.4*	0.08	0.11	0.29	0.08	0.39	0.42*	-0.06	0.31	0.19	0.25	0.06	0.33	-0.27	0.42*	0.36	0.23	0.35	0.3	0.41*	-0.01	0.41*	0.34	0.22	0.27	0.42*	0.19	0.09	1																																											
2013	Methyl benzoate	-0.44*	0.17	-0.56**	0.34	-0.41*	-0.39	-0.22	-0.37	-0.19	-0.33	0.16	-0.18	0.49*	-0.4*	0	0.33	-0.24	-0.33	-0.19	0.18	0.35	0.04	0.2	-0.22	-0.25	-0.03	0.35	0	0.21	0.54**	-0.13	-0.13	-0.03	0.78***	0.18	0.33	0.82***	0.1	-0.07	-0.45*	0.65***	-0.35	-0.12	-0.23	-0.15	0.21	-0.49*	-0.45*	-0.35	0.44*	-0.6**	0.09	-0.19	-0.16	-0.05	0.02	-0.1	-0.23	1																																										
2013	Methyl butanoate	0.22	-0.05	0.23	0.38	0.19	-0.03	0.32	0.1	-0.2	-0.3	0.49*	-0.13	-0.08	-0.14	0.04	0.18	-0.13	-0.26	0.29	0.15	0.14	0.01	0.17	0.01	-0.09	-0.12	0.23	0.48*	0.71***	0.04	0.04	0.58**	-0.45*	0.11	0.01	0.02	0.19	0.28	0.79***	0.27	0.17	0.26	-0.21	0.21	-0.33	0.75***	-0.24	-0.24	0.13	0.45*	-0.13	0.49*	0.71***	0.23	0.53**	0.52**	0.26	0.26	0.15	1																																									
2013	Methyl cinnamate T	-0.57**	0.12	-0.6**	0.25	-0.46*	-0.35	-0.25	-0.34	0.09	-0.22	-0.13	0.09	0.78***	-0.23	0.26	0.08	0.16	0.06	0.06	0.24	0.15	-0.13	0.31	-0.01	0.16	0.09	0.06	-0.36	-0.15	0.31	-0.2	-0.42*	-0.16	0.45*	0.51**	0.28	0.51**	-0.16	-0.31	-0.55**	0.34	-0.57**	0.29	0.01	-0.09	0	-0.41*	-0.48*	-0.29	0.43*	-0.42*	-0.04	-0.34	-0.51**	0.35	-0.09	0.13	-0.04	0.49*	-0.03	1																																								
2013	Methyl decanoate	0.85***	-0.27	0.65***	-0.65***	0.71***	0.84***	0.73***	0.92***	-0.34	0.82***	0.2	0.31	-0.49*	-0.2	-0.28	-0.01	-0.51**	-0.06	0.05	-0.62***	-0.64***	-0.44*	-0.54**	-0.08	-0.42*	-0.59**	-0.04	0.35	0.26	-0.34	0.54**	0.58**	0.63***	-0.36	0.04	-0.11	-0.44*	0.32	0.34	0.67***	-0.01	0.82***	-0.35	0.73***	0.7***	0.23	0.85***	0.81***	0.84***	-0.39	0.87***	0.37	0.44*	0.59**	0.24	0.44*	0.64***	0.34	-0.38	-0.02	-0.24	1																																							
2013	Methyl dodecanoate	0.86***	-0.2	0.85***	-0.56**	0.82***	0.71***	0.69***	0.79***	-0.4*	0.8***	0.39	0.25	-0.67***	0.17	-0.11	0.09	-0.56**	-0.06	0.27	-0.48*	-0.51**	-0.25	-0.55**	0.05	-0.27	-0.3	0.01	0.48*	0.36	-0.22	0.72***	0.57**	0.61**	-0.42*	-0.12	-0.09	-0.36	0.46*	0.37	0.79***	-0.07	0.82***	-0.47*	0.56**	0.61**	-0.02	0.93***	0.96***	0.71***	-0.66***	0.9***	0.44*	0.46*	0.76***	0.09	0.35	0.49*	0.39	-0.48*	-0.07	-0.48*	0.83***	1																																						
2013	Methyl hexanoate	0.76***	-0.31	0.61**	-0.31	0.7***	0.52**	0.76***	0.71***	-0.28	0.42*	0.49*	0.08	-0.52**	-0.29	-0.22	-0.02	-0.4*	-0.1	0.05	-0.46*	-0.31	-0.41*	-0.44*	-0.21	-0.51**	-0.58**	-0.01	0.57**	0.6**	-0.32	0.5*	0.78***	0.17	-0.17	0.05	-0.12	-0.26	0.45*	0.82***	0.73***	0.05	0.76***	-0.29	0.63***	0.25	0.57**	0.45*	0.45*	0.75***	-0.06	0.55**	0.62***	0.85***	0.6**	0.48*	0.83***	0.72***	0.31	-0.14	0.59**	-0.26	0.68***	0.55**	1																																					
2013	Methyl octanoate	0.6**	-0.25	0.52**	-0.38	0.61**	0.41*	0.66***	0.64***	-0.16	0.47*	0.36	0.05	-0.43*	-0.23	-0.15	-0.11	-0.29	0.11	0	-0.46*	-0.34	-0.47*	-0.48*	-0.22	-0.42*	-0.47*	-0.12	0.36	0.43*	-0.35	0.51**	0.56**	0.22	-0.28	0.1	-0.07	-0.34	0.45*	0.66***	0.71***	-0.12	0.55**	-0.11	0.57**	0.23	0.3	0.45*	0.44*	0.66***	-0.16	0.56**	0.6**	0.73***	0.54**	0.45*	0.72***	0.75***	0.24	-0.25	0.32	-0.04	0.7***	0.55**	0.86***	1																																				
2013	Myrtenyl acetate	0.45*	0.02	0.56**	-0.03	0.44*	0.25	0.38	0.34	-0.27	0.12	0.46*	0.01	-0.42*	0.27	0.26	0.2	-0.31	-0.09	0.44*	-0.03	-0.06	-0.11	-0.16	0.23	0.04	-0.01	0.14	0.39	0.7***	0	0.55**	0.57**	-0.02	-0.13	0.15	0.14	-0.1	0.67***	0.66***	0.68***	-0.16	0.51**	-0.24	0.27	-0.03	0.17	0.29	0.33	0.31	-0.27	0.36	0.78***	0.67***	0.52**	0.55**	0.39	0.25	0.53**	-0.28	0.46*	-0.16	0.4*	0.53**	0.55**	0.52**	1																																			
2013	Nonyl acetate	0.86***	-0.34	0.75***	-0.51**	0.72***	0.71***	0.69***	0.8***	-0.46*	0.73***	0.42*	0.28	-0.54**	0.05	-0.11	0.17	-0.62***	-0.16	0.17	-0.45*	-0.39	-0.28	-0.52**	0.05	-0.3	-0.37	0.12	0.38	0.44*	-0.1	0.62**	0.57**	0.64***	-0.18	-0.04	-0.05	-0.28	0.51**	0.39	0.72***	0.15	0.86***	-0.5*	0.54**	0.64***	0.11	0.85***	0.87***	0.73***	-0.48*	0.82***	0.44*	0.44*	0.77***	0	0.4*	0.53**	0.42*	-0.27	0	-0.41*	0.84***	0.87***	0.6**	0.54**	0.45*	1																																		
2013	Octyl acetate	0.86***	-0.3	0.93***	-0.36	0.84***	0.58**	0.68***	0.7***	-0.16	0.48*	0.41*	0.07	-0.78***	0.26	0.06	-0.11	-0.28	0.07	0.24	-0.41*	-0.36	-0.22	-0.53**	0.08	-0.18	-0.26	-0.18	0.6**	0.54**	-0.42*	0.68***	0.76***	0.18	-0.45*	-0.18	-0.17	-0.45*	0.51**	0.73***	0.92***	-0.19	0.85***	-0.25	0.45*	0.23	0.19	0.66***	0.69***	0.65***	-0.52**	0.73***	0.55**	0.77***	0.77***	0.17	0.53**	0.52**	0.28	-0.55**	0.32	-0.58**	0.64***	0.79***	0.75***	0.67***	0.65***	0.71***	1																																	
2013	Octyl butanoate	0.77***	-0.23	0.9***	-0.32	0.76***	0.45*	0.58**	0.59**	-0.21	0.37	0.46*	-0.04	-0.82***	0.31	-0.02	-0.04	-0.35	0.08	0.14	-0.37	-0.24	-0.04	-0.54**	0.08	-0.22	-0.17	-0.09	0.65***	0.57**	-0.34	0.64***	0.75***	0.21	-0.45*	-0.36	-0.17	-0.34	0.57**	0.74***	0.93***	-0.25	0.75***	-0.32	0.23	0.09	0.06	0.57**	0.64***	0.46*	-0.56**	0.61**	0.56**	0.79***	0.87***	-0.01	0.48*	0.38	0.17	-0.44*	0.29	-0.64***	0.54**	0.76***	0.66***	0.6**	0.6**	0.66***	0.92***	1																																
2013	Octyl hexanoate	0.88***	-0.29	0.97***	-0.4*	0.82***	0.59**	0.65***	0.7***	-0.23	0.51**	0.4*	0.09	-0.82***	0.29	-0.02	-0.05	-0.36	0.05	0.23	-0.41*	-0.4	-0.13	-0.53**	0.1	-0.2	-0.21	-0.11	0.62***	0.48*	-0.38	0.62***	0.73***	0.3	-0.52**	-0.32	-0.19	-0.45*	0.45*	0.63***	0.9***	-0.21	0.83***	-0.37	0.37	0.26	0.09	0.73***	0.76***	0.59**	-0.58**	0.76***	0.45*	0.69***	0.84***	0	0.44*	0.42*	0.23	-0.58**	0.2	-0.68***	0.65***	0.85***	0.63***	0.55**	0.54**	0.74***	0.94***	0.95***	1																															
2013	Pentyl acetate	-0.15	0.15	-0.01	0.4	-0.08	-0.32	-0.08	-0.23	-0.31	-0.32	0.43*	-0.23	0.03	0.22	0.32	0.45*	-0.31	-0.22	0.24	0.33	0.51**	0.22	0.1	0.15	0.06	0.32	0.42*	0.2	0.63***	0.43*	0.31	0.19	-0.19	0.48*	0.16	0.36	0.59**	0.75***	0.46*	0.22	0.22	-0.05	-0.23	-0.24	-0.31	0.12	-0.27	-0.18	-0.24	0.06	-0.32	0.75***	0.4*	0.3	0.13	0.2	-0.12	0.17	0.5*	0.39	0.16	-0.18	-0.04	0.16	0.12	0.49*	0.06	0.09	0.19	-0.01	1																														
2013	Propyl butanoate	0.12	-0.07	0.1	0.46*	0.12	-0.06	0.26	0.05	-0.25	-0.34	0.46*	-0.13	0.08	-0.18	0.13	0.29	-0.21	-0.37	0.21	0.23	0.25	-0.04	0.15	-0.01	-0.08	-0.07	0.3	0.41*	0.71***	0.1	0.1	0.52**	-0.46*	0.33	0.13	0.11	0.37	0.4*	0.75***	0.19	0.34	0.17	-0.22	0.14	-0.33	0.74***	-0.35	-0.32	0.05	0.5*	-0.28	0.56**	0.63***	0.2	0.47*	0.49*	0.28	0.08	0.4*	0.9***	0.13	-0.07	-0.18	0.54**	0.3	0.35	-0.02	0.21	0.17	0.05	0.55**	1																													
2013	(Z)-3-hexenyl acetate	-0.38	0.35	-0.4*	0.44*	-0.47*	-0.38	-0.22	-0.34	-0.58**	-0.25	0.3	-0.05	0.41*	-0.11	0.02	0.8***	-0.49*	-0.55**	0.28	0.51**	0.47*	0.16	0.48*	-0.04	-0.03	0.35	0.82***	-0.22	0.29	0.76***	-0.19	-0.25	0.13	0.63***	0.43*	0.49*	0.63***	0.38	-0.09	-0.26	0.4*	-0.34	-0.46*	-0.17	-0.05	0.06	-0.28	-0.26	-0.34	0.35	-0.39	0.31	-0.15	-0.04	0.11	-0.1	-0.31	0.25	0.58**	0.05	0.4*	-0.17	-0.17	-0.2	-0.15	0.1	-0.04	-0.45*	-0.33	-0.41*	0.57**	0.18	1																												
2013	2,1-pentenyl_furan	-0.65***	0.27	-0.49*	0.73***	-0.55**	-0.53**	-0.56**	-0.65***	0.12	-0.62***	-0.21	-0.12	0.72***	0.24	0.38	0.26	0.32	-0.27	0.43*	0.72***	0.61**	0.26	0.66***	0.13	0.5*	0.68***	0.24	-0.23	-0.11	0.39	-0.4	-0.41*	-0.47*	0.34	0.25	0.21	0.58**	-0.15	-0.25	-0.55**	0.13	-0.63***	0.19	-0.42*	-0.44*	-0.06	-0.61**	-0.63***	-0.64***	0.43*	-0.65***	-0.21	-0.34	-0.53**	0.02	-0.43*	-0.41*	-0.08	0.3	0.08	0.47*	-0.69***	-0.61**	-0.54**	-0.58**	-0.26	-0.61**	-0.53**	-0.54**	-0.55**	0.14	0.18	0.31	1																											
2013	2-pentylfuran	-0.56**	0.38	-0.51**	0.59**	-0.68***	-0.49*	-0.39	-0.51**	0.05	-0.43*	-0.1	0.05	0.49*	-0.02	0.36	0.26	0.24	0.02	0.23	0.56**	0.32	0.05	0.78***	-0.01	0.2	0.34	0.29	-0.5*	-0.12	0.32	-0.54**	-0.43*	-0.38	0.4*	0.62**	0.49*	0.24	-0.09	-0.18	-0.43*	0.06	-0.54**	0.12	-0.09	-0.3	0.15	-0.53**	-0.62***	-0.36	0.55**	-0.47*	-0.02	-0.18	-0.4*	0.37	-0.24	-0.37	0.17	0.19	0.16	0.6**	-0.35	-0.54**	-0.3	-0.21	0.01	-0.53**	-0.44*	-0.52**	-0.54**	0.19	0.22	0.36	0.53**	1																										
2013	Furaneol	-0.36	0.11	-0.37	0.4*	-0.44*	-0.45*	-0.12	-0.37	-0.06	-0.19	0.12	0.01	0.31	-0.42*	0.25	0.23	0.04	-0.08	0.14	0.27	0.39	-0.18	0.55**	-0.38	-0.28	0.08	0.27	-0.29	0.01	0.48*	-0.42*	-0.31	-0.07	0.56**	0.51**	0.59**	0.3	-0.08	-0.06	-0.38	0.34	-0.36	-0.04	0.02	-0.05	0.43*	-0.38	-0.42*	-0.09	0.67***	-0.33	-0.07	-0.17	-0.18	0.17	0.09	-0.12	0.24	0.36	0.22	0.35	-0.28	-0.4*	-0.03	-0.03	-0.25	-0.28	-0.34	-0.41*	-0.39	0.05	0.31	0.34	0.34	0.46*	1																									
2013	Mesifurane	-0.34	0.24	-0.32	0.5*	-0.38	-0.44*	-0.16	-0.39	-0.32	-0.14	0.21	-0.09	0.31	-0.27	0.32	0.53**	-0.28	-0.4*	0.29	0.42*	0.41*	-0.21	0.46*	-0.34	-0.21	0.29	0.49*	-0.18	0.15	0.73***	-0.19	-0.31	0.12	0.62***	0.44*	0.68***	0.47*	0.17	-0.16	-0.34	0.46*	-0.35	-0.3	-0.08	0.04	0.21	-0.26	-0.22	-0.19	0.45*	-0.31	0.09	-0.28	-0.03	-0.01	-0.16	-0.24	0.21	0.48*	0	0.27	-0.3	-0.22	-0.23	-0.21	-0.16	-0.13	-0.36	-0.38	-0.35	0.26	0.16	0.59**	0.33	0.29	0.75***	1																								
2013	1-penten-3-one	0.15	-0.06	0.31	0.21	0.21	0.16	-0.04	0.03	0.13	-0.07	-0.15	0.16	0.07	0.45*	0.25	-0.03	0.27	-0.14	0.65***	0.35	0.01	-0.04	0.16	0.32	0.54**	0.4*	-0.1	0.12	-0.04	-0.17	0	0.07	-0.29	-0.43*	-0.02	-0.18	-0.27	-0.17	0	0.08	-0.32	0.06	0.07	0.06	-0.1	-0.06	0.13	0.11	-0.01	-0.08	0.17	-0.16	0.02	-0.14	0.13	-0.2	0.03	0.14	-0.61**	0.06	-0.17	-0.04	0.14	-0.11	-0.13	0.11	0.01	0.23	0.08	0.25	-0.38	-0.08	-0.31	0.36	-0.01	-0.07	-0.06	1																							
2013	2-heptanone	0.62**	-0.47*	0.52**	-0.43*	0.7***	0.6**	0.68***	0.69***	0.14	0.58**	0.03	0.3	-0.35	-0.15	-0.04	-0.46*	0.03	0.23	-0.12	-0.62***	-0.54**	-0.56**	-0.53**	-0.14	-0.2	-0.54**	-0.5*	0.26	0.06	-0.47*	0.46*	0.41*	0.2	-0.36	0	-0.32	-0.54**	-0.02	0.3	0.39	-0.01	0.6**	0.18	0.66***	0.46*	0.23	0.54**	0.51**	0.76***	-0.23	0.65***	0.07	0.35	0.24	0.18	0.33	0.75***	0.13	-0.4*	0.09	-0.18	0.52**	0.42*	0.57**	0.55**	0.2	0.44*	0.61**	0.38	0.45*	-0.28	0.09	-0.64***	-0.4*	-0.37	-0.23	-0.37	0.16	1																						
2013	2-nonanone	0.7***	-0.39	0.41*	-0.57**	0.63***	0.9***	0.6**	0.85***	-0.04	0.67***	-0.15	0.41*	-0.22	-0.31	-0.32	-0.29	-0.17	-0.04	-0.16	-0.64***	-0.67***	-0.47*	-0.5*	-0.03	-0.23	-0.67***	-0.29	0.25	-0.02	-0.51**	0.34	0.47*	0.37	-0.35	-0.02	-0.36	-0.47*	-0.1	0.13	0.31	0.05	0.7***	-0.04	0.71***	0.67***	0.35	0.63***	0.57**	0.79***	-0.17	0.68***	-0.03	0.19	0.18	0.18	0.23	0.61**	0.09	-0.31	-0.03	-0.2	0.75***	0.46*	0.49*	0.37	0.07	0.56**	0.42*	0.2	0.36	-0.45*	-0.03	-0.45*	-0.46*	-0.33	-0.31	-0.42*	0.08	0.74***	1																					
2013	2-pentadecanone T	0.88***	-0.42*	0.69***	-0.6**	0.81***	0.83***	0.91***	0.95***	-0.41*	0.88***	0.33	0.44*	-0.48*	-0.25	-0.3	0.01	-0.56**	-0.1	0.01	-0.66***	-0.72***	-0.51**	-0.56**	-0.12	-0.44*	-0.66***	-0.03	0.38	0.23	-0.28	0.52**	0.54**	0.64***	-0.3	0	-0.2	-0.45*	0.15	0.3	0.53**	0.21	0.84***	-0.43*	0.86***	0.81***	0.3	0.88***	0.85***	0.93***	-0.33	0.9***	0.21	0.35	0.55**	0.22	0.43*	0.74***	0.34	-0.33	0.04	-0.3	0.88***	0.8***	0.66***	0.58**	0.29	0.81***	0.63***	0.5*	0.64***	-0.27	-0.03	-0.26	-0.63***	-0.49*	-0.26	-0.23	0.02	0.71***	0.8***	1																				
2013	2-pentanone	0.74***	-0.47*	0.6**	-0.51**	0.76***	0.76***	0.68***	0.79***	0.1	0.67***	-0.08	0.32	-0.39	-0.16	-0.1	-0.44*	-0.03	0.12	-0.05	-0.67***	-0.62***	-0.57**	-0.57**	-0.12	-0.23	-0.55**	-0.49*	0.36	0.02	-0.49*	0.45*	0.48*	0.33	-0.47*	-0.1	-0.31	-0.58**	-0.08	0.23	0.42*	-0.06	0.7***	0.08	0.66***	0.57**	0.23	0.67***	0.63***	0.8***	-0.31	0.75***	-0.03	0.28	0.29	0.09	0.23	0.68***	0.15	-0.49*	0	-0.33	0.63***	0.53**	0.51**	0.44*	0.12	0.54**	0.61**	0.4*	0.55**	-0.47*	-0.05	-0.68***	-0.42*	-0.47*	-0.27	-0.37	0.29	0.93***	0.85***	0.79***	1																			
2013	2-tridecanone T	0.84***	-0.48*	0.73***	-0.54**	0.85***	0.74***	0.92***	0.9***	-0.33	0.82***	0.38	0.41*	-0.51**	-0.11	-0.13	-0.06	-0.48*	0.03	0.02	-0.64***	-0.65***	-0.51**	-0.61**	-0.07	-0.35	-0.58**	-0.13	0.4*	0.3	-0.29	0.64***	0.54**	0.52**	-0.28	0.02	-0.18	-0.44*	0.24	0.39	0.58**	0.18	0.81***	-0.32	0.82***	0.7***	0.23	0.83***	0.81***	0.89***	-0.4*	0.86***	0.32	0.44*	0.58**	0.23	0.46*	0.8***	0.32	-0.34	0.08	-0.26	0.79***	0.77***	0.68***	0.65***	0.39	0.77***	0.73***	0.58**	0.67***	-0.11	0.05	-0.33	-0.59**	-0.48*	-0.31	-0.26	0.02	0.83***	0.71***	0.94***	0.82***	1																		
2013	2-undecanone T	0.8***	-0.43*	0.58**	-0.57**	0.8***	0.92***	0.78***	0.95***	-0.22	0.78***	0.1	0.45*	-0.29	-0.22	-0.25	-0.14	-0.37	-0.08	-0.02	-0.64***	-0.67***	-0.49*	-0.6**	0.01	-0.25	-0.64***	-0.19	0.39	0.18	-0.45*	0.59**	0.58**	0.43*	-0.34	0.01	-0.31	-0.38	0.14	0.31	0.48*	0.11	0.77***	-0.19	0.82***	0.72***	0.35	0.75***	0.71***	0.87***	-0.26	0.78***	0.24	0.37	0.38	0.29	0.39	0.79***	0.18	-0.29	0.06	-0.14	0.85***	0.65***	0.64***	0.59**	0.26	0.7***	0.58**	0.39	0.51**	-0.24	0.08	-0.34	-0.51**	-0.4*	-0.32	-0.36	0.06	0.78***	0.92***	0.91***	0.84***	0.88***	1																	
2013	4-tridecanone T	0.81***	-0.27	0.72***	-0.48*	0.73***	0.69***	0.73***	0.79***	-0.52**	0.83***	0.37	0.32	-0.48*	-0.04	-0.06	0.23	-0.68***	-0.22	0.31	-0.44*	-0.53**	-0.47*	-0.48*	-0.09	-0.37	-0.36	0.13	0.39	0.32	-0.06	0.62**	0.47*	0.74***	-0.21	0.08	0.07	-0.27	0.38	0.25	0.6**	0.19	0.76***	-0.56**	0.66***	0.75***	0.1	0.91***	0.92***	0.75***	-0.47*	0.86***	0.35	0.3	0.67***	0.11	0.32	0.58**	0.4*	-0.31	-0.11	-0.28	0.84***	0.9***	0.51**	0.51**	0.36	0.88***	0.63***	0.55**	0.69***	-0.09	-0.14	-0.04	-0.51**	-0.46*	-0.19	0.03	0.13	0.44*	0.53**	0.86***	0.57**	0.79***	0.71***	1																
2013	6-methyl-5-hepten-2-one	-0.77***	0.32	-0.59**	0.62***	-0.72***	-0.65***	-0.75***	-0.78***	0.2	-0.71***	-0.35	-0.2	0.61**	0.36	0.48*	0.19	0.42*	-0.03	0.37	0.75***	0.62**	0.38	0.66***	0.28	0.58**	0.69***	0.2	-0.41*	-0.18	0.42*	-0.44*	-0.51**	-0.52**	0.33	0.3	0.38	0.43*	-0.13	-0.35	-0.54**	-0.14	-0.74***	0.28	-0.58**	-0.56**	-0.2	-0.7***	-0.71***	-0.78***	0.35	-0.72***	-0.18	-0.38	-0.57**	-0.01	-0.57**	-0.62***	-0.06	0.21	-0.03	0.48*	-0.67***	-0.64***	-0.63***	-0.51**	-0.16	-0.63***	-0.59**	-0.57**	-0.62***	0.23	0.03	0.41*	0.76***	0.67***	0.32	0.29	0.23	-0.61**	-0.62***	-0.81***	-0.66***	-0.77***	-0.68***	-0.62***	1															
2013	Acetone	0.44*	-0.08	0.39	0.07	0.2	0.25	0.5*	0.37	-0.62***	0.38	0.47*	0.4*	-0.22	-0.15	0.08	0.54**	-0.66***	-0.39	0.31	-0.02	-0.24	-0.28	0.15	-0.16	-0.34	-0.13	0.51**	0.16	0.36	0.46*	0.01	0.21	0.54**	0.26	0.25	0.37	-0.01	0.13	0.08	0.12	0.5*	0.4*	-0.71***	0.42*	0.47*	0.3	0.43*	0.39	0.35	0.04	0.38	0.04	0.04	0.5*	-0.05	0.01	0.15	0.4*	0.03	0.09	-0.17	0.36	0.4*	0.15	0.02	0.11	0.51**	0.19	0.2	0.32	-0.08	0.08	0.26	-0.1	-0.04	0.22	0.38	0.11	0.07	0.22	0.49*	0.22	0.39	0.27	0.57**	-0.25	1														
2013	Acetophenone	-0.36	0.07	-0.48*	0.24	-0.33	-0.2	-0.1	-0.18	-0.15	-0.2	0.07	-0.02	0.69***	-0.4*	0.06	0.26	-0.16	-0.3	0.03	0.12	0.15	-0.09	0.23	-0.09	-0.08	-0.02	0.27	-0.05	0.2	0.53**	-0.14	-0.13	0.02	0.66***	0.31	0.27	0.77***	-0.01	-0.14	-0.48*	0.7***	-0.3	-0.02	0	0.01	0.21	-0.34	-0.38	-0.21	0.42*	-0.42*	0.04	-0.25	-0.26	0.12	0.01	0.12	-0.03	0.8***	0.14	0.75***	-0.17	-0.4*	-0.14	-0.15	-0.2	-0.18	-0.52**	-0.52**	-0.56**	0.3	0.34	0.55**	0.42*	0.31	0.31	0.35	-0.35	-0.22	-0.07	-0.16	-0.28	-0.19	-0.06	-0.17	0.26	0.13	1													
2013	α-ionone	0.26	0.17	0.3	0.03	0.14	0.15	0.22	0.16	-0.43*	0.22	0.42*	0.12	-0.01	0.07	0.08	0.43*	-0.39	-0.27	0.59**	0.16	-0.12	0.1	0.23	0.11	-0.04	0.08	0.41*	0.2	0.3	0.23	0.07	0.17	0.2	-0.01	0.09	0.2	0.21	0.15	0.11	0.16	0.26	0.2	-0.51**	0.26	0.23	0.21	0.31	0.28	0.12	0.04	0.25	0.18	0.08	0.29	0.21	0.16	0.1	0.36	-0.1	0.18	0.05	0.28	0.39	0.1	0.05	0.2	0.28	0.15	0.14	0.28	-0.07	0.03	0.26	0.06	0.08	0.26	0.29	0.31	-0.29	-0.07	0.2	-0.13	0.04	0.04	0.45*	0.01	0.49*	0.09	1												
2013	β-ionone	0.22	-0.11	0.33	0.19	0.13	0.06	0.33	0.13	-0.33	0.19	0.33	0.4*	-0.04	0.19	0.35	0.33	-0.15	-0.08	0.67***	0.29	-0.16	-0.22	0.34	0.12	0.14	0.12	0.27	-0.06	0.12	0.15	-0.07	-0.01	0.01	0	0.47*	0.28	-0.23	-0.08	0.06	0.05	0.13	0.14	-0.34	0.47*	0.2	0.21	0.26	0.18	0.25	0.1	0.3	0.01	0.05	0.07	0.43*	0.08	0.2	0.47*	-0.42*	0.2	0.08	0.16	0.25	0.12	0.14	0.25	0.16	0.25	0.06	0.23	-0.21	0.08	0	0.18	0.31	0.34	0.26	0.64***	0.14	0.03	0.25	0.17	0.24	0.12	0.36	0.15	0.48*	-0.16	0.59**	1											
2013	(Z)-geranyl acetone	0.21	-0.01	0.44*	0.11	0.19	0.12	0.19	0.15	-0.15	0.21	0.17	0.27	-0.07	0.5*	0.6**	0.2	-0.11	0.04	0.68***	0.2	-0.16	-0.15	0.1	0.3	0.32	0.32	0.08	-0.03	0.22	0.17	0.26	0.04	0.09	-0.08	0.3	0.36	-0.1	0.26	0.05	0.25	-0.02	0.18	-0.17	0.23	0.17	-0.14	0.34	0.31	0.12	-0.32	0.34	0.23	0.08	0.28	0.19	-0.17	0.1	0.43*	-0.39	-0.06	0.12	0.23	0.4*	-0.04	0.16	0.44*	0.31	0.36	0.22	0.32	0.11	-0.06	0.03	0.13	0.28	-0.03	0.11	0.49*	0.14	0	0.18	0.14	0.28	0.15	0.41*	0.24	0.35	-0.1	0.38	0.69***	1										
2013	γ-decalactone	0.77***	-0.2	0.64***	-0.17	0.72***	0.58**	0.72***	0.68***	-0.53**	0.55**	0.56**	0.1	-0.28	-0.11	-0.19	0.3	-0.63***	-0.51**	0.43*	-0.23	-0.36	-0.31	-0.3	-0.11	-0.33	-0.31	0.26	0.61**	0.6**	0.03	0.51**	0.64***	0.39	-0.11	-0.07	-0.09	0.03	0.36	0.49*	0.53**	0.4*	0.75***	-0.59**	0.6**	0.48*	0.38	0.64***	0.66***	0.62***	-0.22	0.58**	0.39	0.47*	0.58**	0.19	0.45*	0.61**	0.36	-0.05	0.34	-0.28	0.61**	0.68***	0.6**	0.42*	0.32	0.73***	0.59**	0.5*	0.59**	0.03	0.3	0	-0.26	-0.44*	-0.12	0.02	0.2	0.39	0.45*	0.72***	0.48*	0.66***	0.61**	0.74***	-0.51**	0.54**	0.08	0.47*	0.33	0.26	1									
2013	α-farnesene	0.2	-0.15	0.04	-0.37	0.21	0.37	0.37	0.41*	0.04	0.4*	-0.03	0.19	0.08	-0.42*	0.07	-0.21	-0.11	0.15	-0.13	-0.55**	-0.38	-0.48*	-0.23	-0.17	-0.36	-0.47*	-0.23	0.11	0.16	0.03	0.3	0.2	0.34	0.2	0.34	0.19	0.13	0.05	0.05	0.05	0.31	0.27	0.16	0.46*	0.39	0.15	0.24	0.18	0.41*	-0.1	0.27	0.15	0.03	0.08	0.32	0.25	0.48*	0.21	0.2	-0.01	0.43*	0.44*	0.16	0.29	0.34	0.19	0.22	0.09	-0.05	-0.04	-0.01	0.09	-0.02	-0.14	0.11	0	-0.14	-0.33	0.42*	0.49*	0.39	0.37	0.41*	0.5*	0.24	-0.25	0.13	0.52**	-0.05	-0.09	0.11	0.19	1								
2013	α-pinene	-0.42*	0.24	-0.39	0.37	-0.48*	-0.48*	-0.35	-0.47*	-0.12	-0.43*	0.1	-0.31	0.24	-0.13	0.33	0.31	-0.18	-0.18	-0.09	0.24	0.41*	0.23	0.26	-0.11	-0.16	0.16	0.31	-0.05	0.25	0.59**	-0.14	-0.12	-0.02	0.73***	0.06	0.53**	0.73***	0.21	-0.06	-0.32	0.5*	-0.33	-0.13	-0.5*	-0.29	0.1	-0.5*	-0.44*	-0.51**	0.28	-0.61**	0.07	-0.21	0.04	-0.34	-0.19	-0.38	-0.21	0.8***	0.06	0.27	-0.41*	-0.42*	-0.29	-0.36	-0.21	-0.24	-0.42*	-0.27	-0.39	0.51**	0.29	0.52**	0.29	0.23	0.39	0.52**	-0.53**	-0.55**	-0.47*	-0.47*	-0.57**	-0.48*	-0.48*	-0.3	0.34	0.15	0.58**	0.03	-0.34	-0.17	-0.18	0.08	1							
2013	Limonene	-0.32	0.37	-0.26	0.49*	-0.42*	-0.39	-0.36	-0.43*	-0.29	-0.47*	0.12	-0.37	0.2	0	0.37	0.52**	-0.28	-0.41*	0.3	0.45*	0.47*	0.23	0.38	0.01	-0.05	0.32	0.51**	0.12	0.45*	0.62***	-0.09	0.06	-0.08	0.58**	0.15	0.64***	0.7***	0.38	0.11	-0.13	0.28	-0.24	-0.3	-0.43*	-0.34	0.22	-0.44*	-0.38	-0.5*	0.3	-0.53**	0.3	-0.01	0.11	-0.07	-0.19	-0.48*	0.02	0.6**	0.24	0.19	-0.29	-0.26	-0.2	-0.28	0.1	-0.17	-0.29	-0.16	-0.25	0.57**	0.36	0.67***	0.34	0.34	0.38	0.57**	-0.25	-0.71***	-0.5*	-0.47*	-0.65***	-0.53**	-0.49*	-0.18	0.48*	0.21	0.43*	0.32	-0.1	0.03	-0.06	-0.07	0.83***	1						
2013	Linalool	-0.46*	0.42*	-0.27	0.46*	-0.41*	-0.42*	-0.65***	-0.54**	0.04	-0.56**	-0.21	-0.33	0.27	0.41*	0.13	0.29	0.17	-0.22	0.36	0.67***	0.64***	0.47*	0.38	0.22	0.46*	0.7***	0.28	-0.1	-0.06	0.11	-0.21	-0.21	-0.38	-0.11	-0.07	0.09	0.27	0.18	-0.05	-0.06	-0.48*	-0.49*	0.05	-0.63***	-0.58**	-0.27	-0.44*	-0.39	-0.67***	0.13	-0.48*	0.1	-0.03	-0.21	-0.04	-0.3	-0.56**	-0.11	-0.04	-0.02	0.07	-0.4*	-0.25	-0.37	-0.27	0.03	-0.37	-0.29	-0.11	-0.18	0.2	-0.06	0.38	0.48*	0.25	0.08	0.14	0.28	-0.71***	-0.62**	-0.63***	-0.65***	-0.68***	-0.59**	-0.33	0.63***	-0.28	-0.14	0.22	0	0.01	-0.37	-0.56**	0.12	0.43*	1					
2013	Myrtenol	0.01	-0.04	0.05	0.33	-0.12	-0.12	0.19	-0.04	-0.71***	-0.01	0.47*	0.24	0.06	0	0.29	0.75***	-0.66***	-0.43*	0.28	0.31	0.02	0	0.26	0.08	-0.08	0.15	0.68***	0.01	0.37	0.63***	-0.04	-0.02	0.24	0.62**	0.31	0.51**	0.39	0.2	-0.03	-0.18	0.7***	0	-0.72***	0.09	0.17	0.21	0.01	0.02	-0.09	0.16	-0.12	0.13	-0.16	0.26	-0.08	-0.12	-0.11	0.09	0.42*	0.07	0.11	-0.06	0.03	-0.16	-0.23	0.01	0.16	-0.13	-0.09	-0.04	0.33	0.23	0.57**	0.17	0.17	0.28	0.61**	-0.1	-0.29	-0.18	0.07	-0.26	0.04	-0.09	0.25	0.09	0.72***	0.38	0.35	0.31	0.3	0.24	-0.03	0.54**	0.54**	-0.09	1				
2013	Nerol	0.22	0.14	-0.03	0.1	0.05	0.24	0.15	0.22	-0.59**	0.25	0.18	-0.04	0.04	-0.4*	-0.27	0.59**	-0.68***	-0.76***	0.1	0.06	0.07	-0.25	0.06	-0.38	-0.44*	-0.1	0.59**	0.19	0.26	0.4*	0.04	0.17	0.52**	0.28	0.14	0.26	0.25	0.29	0	0.05	0.37	0.23	-0.61**	0.13	0.34	0.21	0.2	0.26	0.16	0.1	0.09	0.15	-0.05	0.27	-0.12	-0.03	-0.03	0.14	0.38	-0.08	-0.15	0.28	0.21	0.08	-0.07	-0.09	0.38	-0.1	-0.05	-0.01	0.05	0.05	0.51**	-0.08	-0.19	0.13	0.46*	-0.17	-0.19	0.19	0.28	-0.01	0.09	0.18	0.4*	-0.2	0.59**	0.28	0.23	-0.09	-0.17	0.46*	0.07	0.31	0.4*	-0.01	0.47*	1			
2013	Nerolidol	-0.25	0.39	-0.16	0.21	-0.2	-0.13	-0.51**	-0.3	0.21	-0.4*	-0.25	-0.26	0.21	0.26	-0.06	0.02	0.28	-0.13	0.25	0.4*	0.43*	0.46*	0.22	0.22	0.35	0.37	0.05	0.03	-0.07	-0.2	-0.11	0	-0.41*	-0.27	-0.23	-0.14	0.19	0.07	0.06	0.04	-0.49*	-0.27	0.16	-0.45*	-0.46*	-0.06	-0.32	-0.29	-0.44*	0.13	-0.33	0.04	0.08	-0.2	0.08	-0.08	-0.33	-0.18	-0.09	0.09	0	-0.2	-0.16	-0.14	-0.12	-0.01	-0.29	-0.14	-0.04	-0.08	-0.02	0.02	0.11	0.35	0.13	0.1	-0.07	0.29	-0.53**	-0.32	-0.47*	-0.42*	-0.57**	-0.34	-0.29	0.45*	-0.37	-0.15	0.31	-0.03	-0.11	-0.2	-0.38	0.01	0.3	0.83***	-0.35	-0.08	1		
2013	Terpineol	-0.02	0.2	0.21	0.34	-0.02	-0.16	-0.17	-0.17	-0.34	-0.29	0.35	-0.11	-0.07	0.44*	0.31	0.52**	-0.29	-0.26	0.51**	0.49*	0.49*	0.38	0.16	0.38	0.26	0.5*	0.47*	0.22	0.52**	0.21	0.23	0.24	-0.25	0.12	0.02	0.31	0.38	0.67***	0.43*	0.36	-0.13	-0.01	-0.37	-0.29	-0.37	0.04	-0.15	-0.07	-0.31	-0.05	-0.19	0.64***	0.38	0.35	0.2	0.17	-0.25	0.18	0.08	0.31	-0.05	-0.06	0.16	0.09	0.1	0.49*	0.11	0.18	0.32	0.22	0.64***	0.34	0.48*	0.16	0.16	0.12	0.25	0.09	-0.54**	-0.49*	-0.28	-0.53**	-0.26	-0.29	0.05	0.32	0.03	-0.06	0.42*	0.15	0.3	0.05	-0.33	0.28	0.6**	0.66***	0.28	0.06	0.55**	1

Supplemental table CIII. 3. Analysis of variance (ANOVA) fitting the model G+E+GxE and ω2 values. ANOVA was calculated for all volatile compounds independently considering two factors, genotype (G) and environment (E), and their interaction (GxE). The resulting parameters of the ANOVA test Sum of squares (SS), degrees of freedom (df) and p-values are provided. Omega squared values (ω^2) were calculated from the ANOVA parameters for G, E and GxE and reflect the percentage of variability accounted by each one of them. The error is 1 minus the percentual variability accounted by G, E and GxE.

Supplemental table CIII. 3

		G			E			GxE						
Family	**Compound**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**ω^2G**	**ω^2E**	**ω^2GxE**	**error**
alcohol	1-decanol	850,07	24	0,0000	3,59	1	0,1349	44,58	24	0,2796	0,70	0,00	0,01	0,30
alcohol	1-hexanol	17,09	24	0,0334	0,36	1	0,3582	30,46	24	0,0000	0,06	0,00	0,17	0,77
alcohol	1-octanol	224,83	24	0,0000	2,59	1	0,0398	25,19	24	0,0233	0,60	0,01	0,03	0,37
alcohol	1-penten-3-ol	31,26	24	0,0000	1,31	1	0,0529	19,34	24	0,0010	0,21	0,01	0,10	0,68
alcohol	2-heptanol	451,76	24	0,0000	1,29	1	0,4659	94,32	24	0,0399	0,41	0,00	0,04	0,55
alcohol	2-nonanol	547,81	24	0,0000	0,03	1	0,9036	75,57	24	0,0417	0,53	0,00	0,03	0,44
alcohol	2-tridecanol T	369,01	24	0,0000	20,43	1	0,0011	83,38	24	0,0111	0,42	0,02	0,05	0,51
alcohol	2-undecanol T	342,71	24	0,0000	5,43	1	0,0583	48,55	24	0,1367	0,48	0,01	0,02	0,50
alcohol	(E)-2-hexen-1-ol	784,09	24	0,0000	1,59	1	0,1504	76,18	24	0,0000	0,77	0,00	0,06	0,17
alcohol	Ethanol	296,51	24	0,0000	32,35	1	0,0010	114,69	24	0,0339	0,25	0,03	0,05	0,67
alcohol	Eugenol	376,49	24	0,0000	14,68	1	0,0009	34,10	24	0,3427	0,54	0,02	0,01	0,43
aldehyde	3,4-dimethylbenzaldehyde	6,83	24	0,0560	0,06	1	0,5712	4,81	24	0,3522	0,06	0,00	0,01	0,93
aldehyde	Benzaldehyde	86,85	24	0,0000	0,00	1	0,9631	10,16	24	0,0024	0,63	0,00	0,04	0,33
aldehyde	Decanal	9,24	24	0,0014	0,29	1	0,1936	7,21	24	0,0209	0,11	0,00	0,07	0,81
aldehyde	(E)-2-decenal	34,70	24	0,0000	13,86	1	0,0000	9,51	24	0,5727	0,19	0,10	0,00	0,71
aldehyde	(E)-2-heptenal	302,52	24	0,0000	0,50	1	0,2552	16,06	24	0,0210	0,77	0,00	0,02	0,21
aldehyde	(E)-2-hexenal	70,14	24	0,0000	0,12	1	0,2994	4,36	24	0,0311	0,73	0,00	0,02	0,25
aldehyde	(E)-2-nonenal	16,29	24	0,0001	14,02	1	0,0000	5,97	24	0,5051	0,13	0,17	0,00	0,70
aldehyde	(E)-2-octenal	28,67	24	0,0000	2,63	1	0,0030	12,82	24	0,0134	0,24	0,03	0,06	0,68
aldehyde	(E)-2-pentenal	84,83	24	0,0000	1,17	1	0,1896	22,18	24	0,1288	0,31	0,00	0,03	0,66

Supplemental table CIII. 3

		G			E			GxE						
Family	**Compound**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**ω^2G**	**ω^2E**	**ω^2GxE**	**error**
aldehyde	(E,Z)-2,4-heptadienal	26,57	24	0,0000	0,28	1	0,2931	14,07	24	0,0011	0,25	0,00	0,10	0,66
aldehyde	Heptanal	45,41	24	0,0000	0,62	1	0,1560	11,36	24	0,0568	0,35	0,00	0,04	0,61
aldehyde	Hexanal	22,63	24	0,0000	0,09	1	0,4078	5,33	24	0,0246	0,39	0,00	0,05	0,56
aldehyde	Nonanal	21,54	24	0,0035	0,17	1	0,5338	20,50	24	0,0061	0,10	0,00	0,09	0,81
aldehyde	Octanal	115,14	24	0,0000	1,06	1	0,3455	48,08	24	0,0303	0,24	0,00	0,05	0,71
aldehyde	Pentanal	27,27	24	0,0009	0,50	1	0,3091	20,40	24	0,0217	0,12	0,00	0,07	0,81
aldehyde	(Z)-3-hexenal	305,00	24	0,0000	0,54	1	0,1637	9,95	24	0,0725	0,83	0,00	0,01	0,16
ester	1-methylbutyl butanoate	306,52	24	0,0000	0,05	1	0,8529	50,35	24	0,0828	0,46	0,00	0,03	0,52
ester	1-methylethyl butanoate	111,99	24	0,0000	69,31	1	0,0000	70,18	24	0,0000	0,26	0,19	0,14	0,41
ester	1-methylethyl acetate	41,79	24	0,0000	79,77	1	0,0000	35,44	24	0,0002	0,11	0,32	0,09	0,48
ester	1-methylhexyl acetate	256,60	24	0,0000	25,71	1	0,0019	149,15	24	0,0006	0,23	0,03	0,10	0,64
ester	1-methyloctyl butanoate	317,41	24	0,0000	0,01	1	0,9431	71,72	24	0,0012	0,47	0,00	0,07	0,46
ester	2,3-butanedioldiacetate T	408,15	24	0,0000	40,18	1	0,0007	58,34	24	0,8226	0,31	0,03	0,00	0,66
ester	2 -methylbutyl acetate	102,12	24	0,0000	56,40	1	0,0000	23,01	24	0,0000	0,42	0,25	0,07	0,25
ester	3-methyl-2-butenyl acetate	146,00	24	0,0000	10,74	1	0,0000	32,33	24	0,0000	0,52	0,04	0,08	0,35
ester	3-methylbutyl acetate	72,39	24	0,0000	59,50	1	0,0000	39,92	24	0,0000	0,23	0,22	0,10	0,45
ester	Benzyl acetate	270,64	24	0,0000	2,67	1	0,0390	42,49	24	0,0000	0,61	0,00	0,07	0,32
ester	Butyl acetate	113,53	24	0,0000	12,02	1	0,0001	69,59	24	0,0000	0,29	0,03	0,16	0,52
ester	Butyl butanoate	659,76	24	0,0000	2,51	1	0,2515	134,56	24	0,0000	0,55	0,00	0,08	0,37
ester	Butyl hexanoate	938,13	24	0,0000	0,05	1	0,8787	103,21	24	0,0039	0,64	0,00	0,04	0,32
ester	Cinnamyl acetate	702,04	24	0,0000	48,13	1	0,0008	139,85	24	0,1101	0,38	0,03	0,03	0,57
ester	Decyl acetate	868,08	24	0,0000	5,69	1	0,1176	67,85	24	0,2236	0,61	0,00	0,01	0,37
ester	(E)-2-hexenyl acetate	962,40	24	0,0000	15,92	1	0,0000	46,55	24	0,0025	0,80	0,01	0,02	0,17
ester	Ethyl 2-hexenoate	733,74	24	0,0000	29,36	1	0,0150	160,40	24	0,1263	0,36	0,01	0,03	0,61
ester	Ethyl acetate	587,29	24	0,0000	0,03	1	0,9342	228,92	24	0,0068	0,29	0,00	0,07	0,64

Supplemental table CIII. 3

		G			E			GxE						
Family	**Compound**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**ω^2G**	**ω^2E**	**ω^2GxE**	**error**
ester	Ethyl butanoate	310,02	24	0,0000	3,43	1	0,2781	104,71	24	0,0711	0,27	0,00	0,04	0,69
ester	Ethyl decanoate	1.337,70	24	0,0000	44,48	1	0,0010	227,88	24	0,0006	0,55	0,02	0,06	0,38
ester	Ethyl dodecanoate	1.363,81	24	0,0000	19,05	1	0,0143	155,05	24	0,0040	0,63	0,01	0,04	0,33
ester	Ethyl hexanoate	733,60	24	0,0000	102,84	1	0,0000	236,51	24	0,0073	0,32	0,05	0,06	0,57
ester	Ethyl methylthioacetate T	390,44	24	0,0000	49,09	1	0,0001	185,66	24	0,0001	0,29	0,04	0,11	0,56
ester	Ethyl octanoate	1.293,51	24	0,0000	133,70	1	0,0000	294,44	24	0,0006	0,46	0,05	0,07	0,43
ester	Hexyl acetate	74,55	24	0,0000	0,34	1	0,3922	21,72	24	0,0067	0,37	0,00	0,06	0,57
ester	Hexyl butanoate	560,05	24	0,0000	1,05	1	0,4369	80,19	24	0,0085	0,56	0,00	0,04	0,40
ester	Hexyl hexanoate	464,48	24	0,0000	4,43	1	0,1668	90,31	24	0,0382	0,43	0,00	0,04	0,53
ester	Methyl-2-aminobenzoate T	791,35	24	0,0000	2,37	1	0,2205	59,19	24	0,0518	0,68	0,00	0,02	0,30
ester	Methyl-2-hexenoate	166,99	24	0,0000	29,33	1	0,0002	67,83	24	0,1010	0,20	0,05	0,03	0,72
ester	Methyl 3-hydroxyoctanoate T	364,31	24	0,0000	3,00	1	0,3023	114,78	24	0,0274	0,31	0,00	0,05	0,64
ester	Methyl acetate T	33,44	24	0,0403	55,91	1	0,0000	38,83	24	0,0108	0,05	0,20	0,07	0,68
ester	Methyl benzoate	258,24	24	0,0000	4,89	1	0,0081	43,08	24	0,0002	0,58	0,01	0,06	0,35
ester	Methyl butanoate	336,13	24	0,0000	11,43	1	0,0028	105,01	24	0,0000	0,46	0,02	0,11	0,41
ester	Methyl cinnamate T	557,37	24	0,0000	8,28	1	0,0244	88,23	24	0,0012	0,56	0,01	0,05	0,38
ester	Methyl decanoate	431,44	24	0,0000	5,76	1	0,0675	35,50	24	0,6431	0,52	0,01	0,00	0,48
ester	Methyl dodecanoate	554,17	24	0,0000	26,38	1	0,0000	33,94	24	0,3568	0,63	0,03	0,00	0,34
ester	Methyl hexanoate	423,03	24	0,0000	16,39	1	0,0051	67,44	24	0,1237	0,44	0,02	0,02	0,52
ester	Methyl octanoate	252,56	24	0,0000	16,01	1	0,0015	28,93	24	0,7521	0,39	0,03	0,00	0,58
ester	Myrtenyl acetate	105,76	24	0,0000	8,40	1	0,0000	13,74	24	0,0040	0,57	0,05	0,04	0,34
ester	Nonyl acetate	116,59	24	0,0000	2,99	1	0,0426	32,35	24	0,0115	0,37	0,01	0,06	0,57
ester	Octyl acetate	590,04	24	0,0000	0,03	1	0,9091	65,51	24	0,1301	0,55	0,00	0,02	0,44
ester	Octyl butanoate	705,25	24	0,0000	2,47	1	0,2390	113,10	24	0,0001	0,59	0,00	0,06	0,34
ester	Octyl hexanoate	963,87	24	0,0000	3,19	1	0,2321	107,55	24	0,0053	0,63	0,00	0,04	0,33

Supplemental table CIII. 3

		G			E			GxE						
Family	**Compound**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**ω^2G**	**ω^2E**	**ω^2GxE**	**error**
ester	Pentyl acetate	38,58	24	0,0000	20,76	1	0,0000	18,15	24	0,0019	0,23	0,15	0,07	0,55
ester	Propyl butanoate	295,89	24	0,0000	3,80	1	0,1107	100,31	24	0,0001	0,40	0,00	0,10	0,49
ester	(Z)-3-hexenyl acetate	287,83	24	0,0000	0,02	1	0,8705	30,78	24	0,0091	0,63	0,00	0,03	0,34
furan	2,1-pentenyl furan	91,34	24	0,0000	1,32	1	0,1337	17,96	24	0,1803	0,37	0,00	0,02	0,60
furan	2-pentylfuran	34,80	24	0,0000	0,26	1	0,2141	11,44	24	0,0000	0,41	0,00	0,10	0,48
furan	Furaneol	195,41	24	0,0504	34,07	1	0,0110	263,04	24	0,0030	0,05	0,02	0,10	0,82
furan	Mesifurane	284,27	24	0,0000	330,52	1	0,0000	49,07	24	0,0226	0,30	0,38	0,02	0,29
ketone	1-penten-3-one	47,69	24	0,0000	5,07	1	0,0001	19,66	24	0,0004	0,31	0,04	0,09	0,56
ketone	2-heptanone	298,33	24	0,0000	16,60	1	0,0018	58,44	24	0,0815	0,40	0,02	0,03	0,55
ketone	2-nonanone	477,51	24	0,0000	10,03	1	0,0222	60,97	24	0,1406	0,50	0,01	0,02	0,47
ketone	2-pentadecanone T	720,61	24	0,0000	13,03	1	0,0277	121,85	24	0,0092	0,51	0,01	0,05	0,44
ketone	2-pentanone	466,94	24	0,0000	25,14	1	0,0022	88,29	24	0,1068	0,40	0,02	0,03	0,55
ketone	2-tridecanone T	398,92	24	0,0000	5,54	1	0,1001	87,59	24	0,0170	0,42	0,00	0,05	0,53
ketone	2-undecanone T	250,94	24	0,0000	0,38	1	0,6340	61,87	24	0,0575	0,36	0,00	0,04	0,61
ketone	4-tridecanone T	83,94	24	0,0000	0,01	1	0,8704	13,92	24	0,1591	0,43	0,00	0,02	0,55
ketone	6-methyl-5-hepten-2-one	25,58	24	0,0000	8,58	1	0,0000	6,39	24	0,2634	0,26	0,11	0,01	0,62
ketone	Acetone	87,44	24	0,0000	17,75	1	0,0000	13,61	24	0,3600	0,36	0,08	0,01	0,55
ketone	Acetophenone	258,43	24	0,0000	2,35	1	0,0164	34,78	24	0,0000	0,69	0,01	0,07	0,24
ketone	α-ionone	90,92	24	0,0000	0,88	1	0,2399	40,93	24	0,0001	0,32	0,00	0,11	0,57
ketone	β-ionone	57,72	24	0,0000	8,01	1	0,0000	21,74	24	0,0000	0,36	0,05	0,10	0,49
ketone	(Z)-geranyl acetone	21,85	24	0,0008	0,25	1	0,4259	16,21	24	0,0226	0,12	0,00	0,07	0,81
lactone	γ-decalactone	519,04	24	0,0000	1,38	1	0,5301	63,29	24	0,7854	0,37	0,00	0,00	0,63
terpenoid	α-farnesene	192,16	24	0,0000	2,15	1	0,0742	77,65	24	0,0000	0,46	0,00	0,16	0,38
terpenoid	α-pinene	100,59	24	0,0000	24,45	1	0,0000	16,02	24	0,1574	0,39	0,11	0,02	0,48
terpenoid	Limonene	20,96	24	0,0000	3,23	1	0,0013	12,15	24	0,0303	0,16	0,03	0,06	0,75

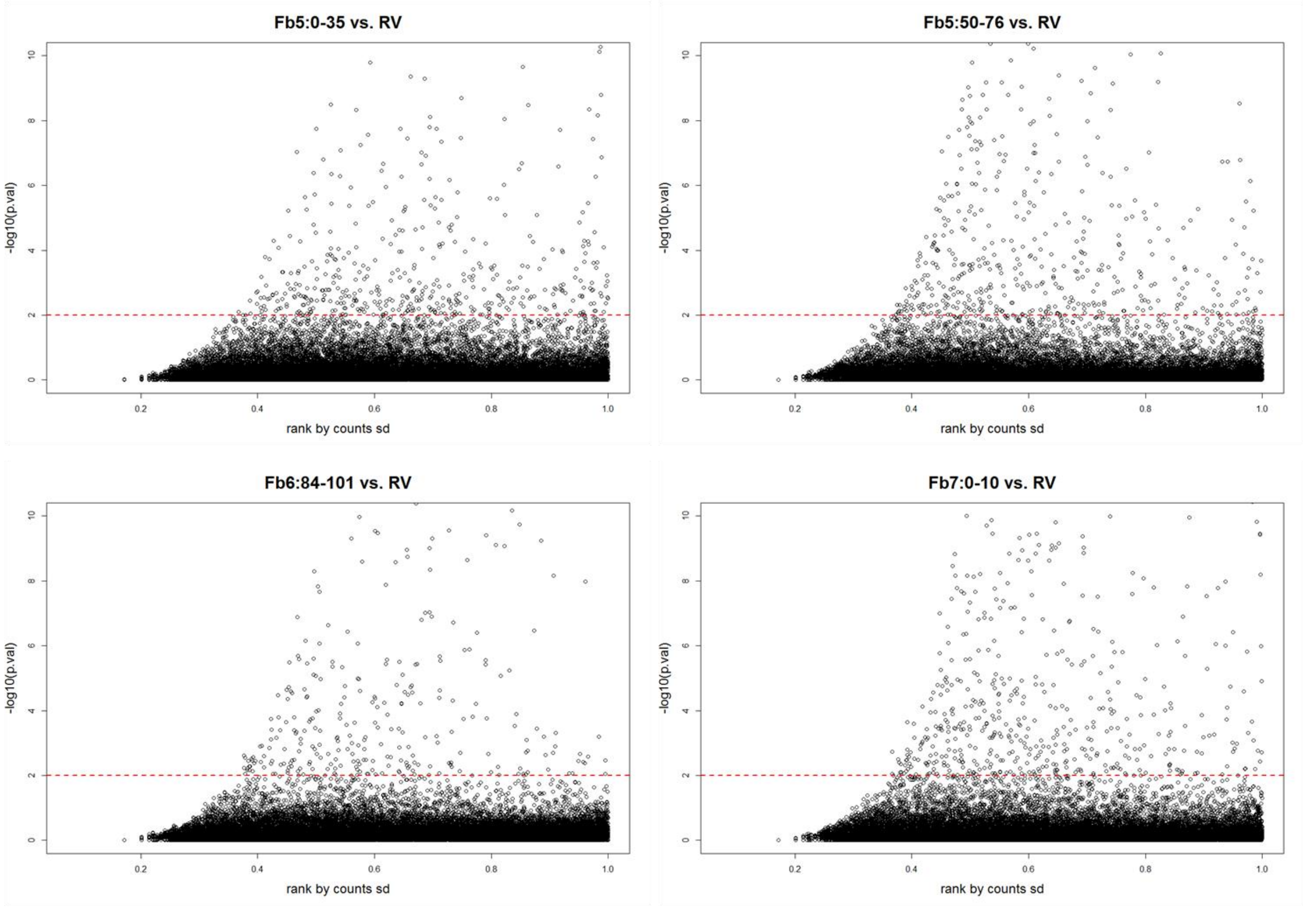
Supplemental table CIII. 3

		G			E			GxE						
Family	**Compound**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**SS**	**df**	**p-value**	**ω^2G**	**ω^2E**	**ω^2GxE**	**error**
terpenoid	Linalool	162,01	24	0,0000	0,10	1	0,5014	18,73	24	0,0000	0,72	0,00	0,06	0,22
terpenoid	Myrtenol	126,77	24	0,0000	14,98	1	0,0000	30,31	24	0,0000	0,56	0,07	0,11	0,26
terpenoid	Nerol	176,29	24	0,0000	1,30	1	0,1315	15,70	24	0,2890	0,57	0,00	0,01	0,42
terpenoid	Nerolidol	32,94	24	0,0000	0,13	1	0,1853	2,19	24	0,2232	0,65	0,00	0,01	0,34
terpenoid	Terpineol	33,16	24	0,0000	1,39	1	0,0114	20,81	24	0,0000	0,31	0,01	0,17	0,51

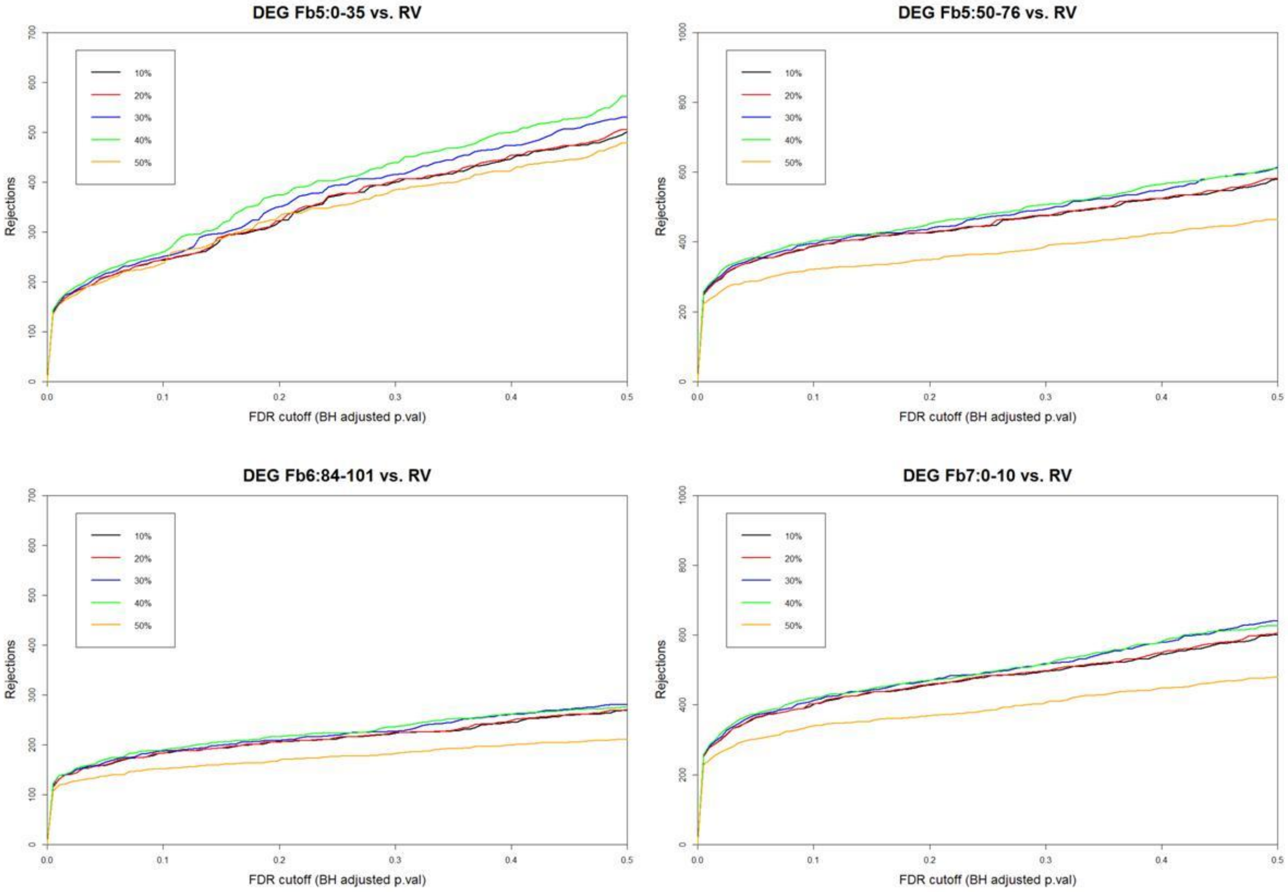
Chapter IV

Supplementary material

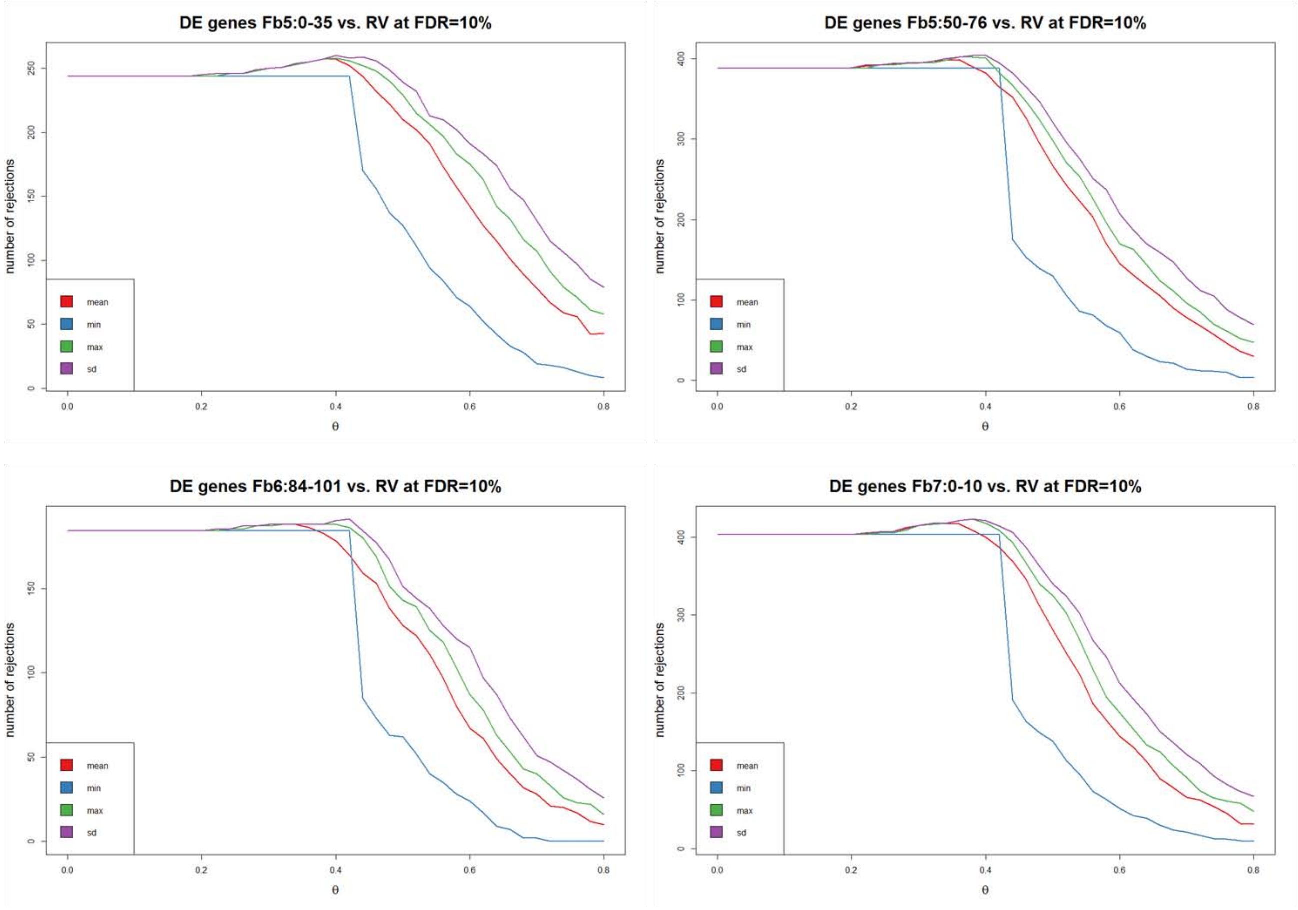
Supplemental Figure CIV. 1 Low expressed transcripts effect. Graphics represent all four contrasting hypothesis (each NIL vs. RV) for the differential expression analysis. Expressed genes (empty dots) are ranked according to their standard deviation (SD) across the samples from the minimum SD (0) to the maximum SD (1) in the x-axis and confronted to the observed p-value (expressed in a $-\log_{10}$) of the contrast hypothesis in the y-axis. The red-dashed line is the significant threshold fixed at p-value<0.01 ($-\log_{10}$p-value=2). The graphics reveal that genes with lower SD rarely reject the null hypothesis.



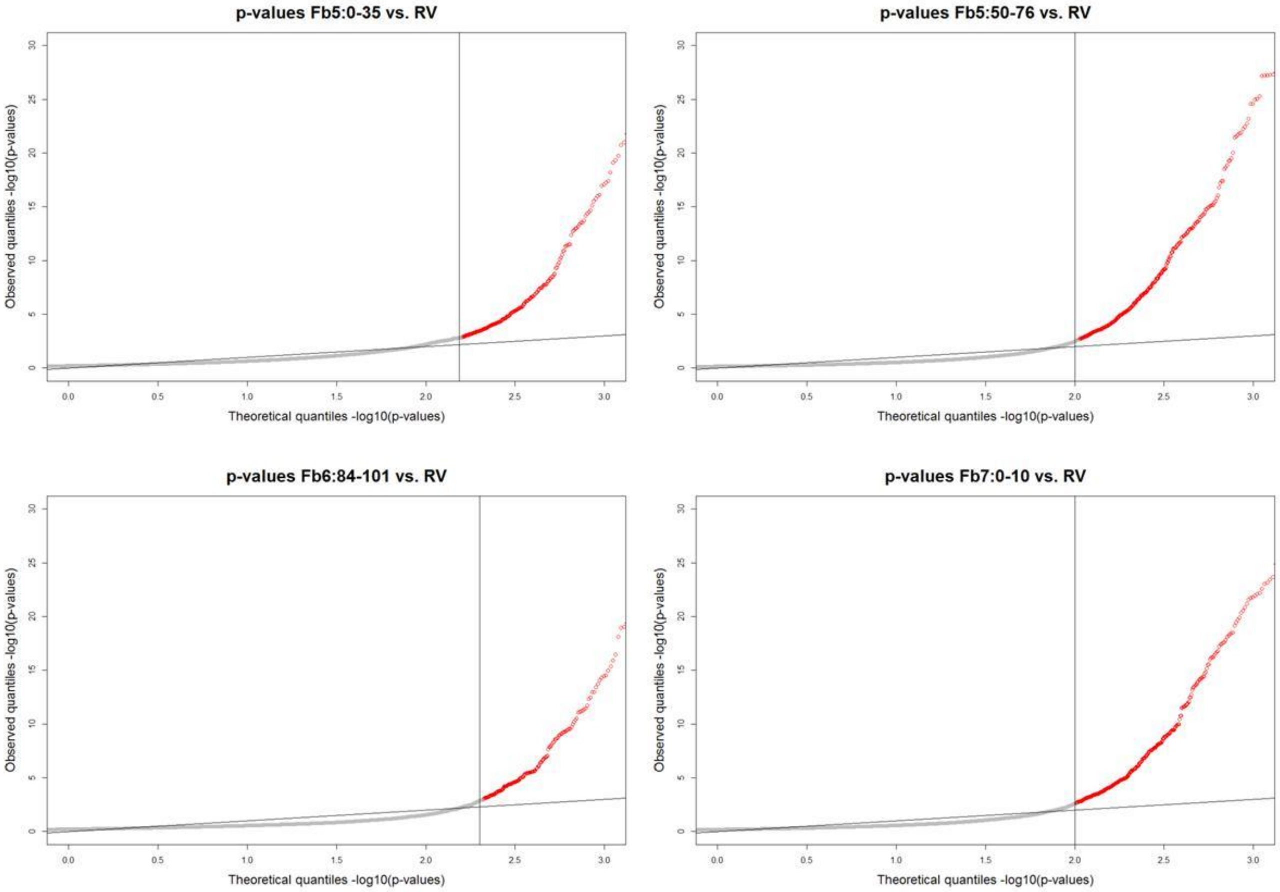
Supplemental Figure CIV. 2 Filtering effect over discovery rate. Graphics represent all four contrasting hypothesis (each NIL vs. RV) for the differential expression analysis. Colored lines represent different filtering cutoffs ranging from 10% filtering (10% of genes removed) to 50% filtering (50% of the lower SD genes removed). Depending on the false discovery rate (adjusted p-value) chosen (x-axis) the number of rejections to the null hypothesis (differentially expressed genes) varies.



Supplemental Figure CIV. 3 Filtering parameter choices. Graphics represent all four contrasting hypothesis (each NIL vs. RV) for the differential expression analysis. For a fix FDR=0.1, the number of rejections to the null hypothesis (differentially expressed genes) is presented in y-axis considering different filtering cutoffs ranging from 0% to 80% in x-axix and different ranking parameters (colored lines): minimum, maximum or mean number of counts and standard deviation.



Supplemental Figure CIV. 4 Distribution of p-values. Q-Q plots of all four contrasting hypothesis (each NIL vs. RV) for the differential expression analysis. Q-Q plot represents the expected quantiles vs. the observed quantiles for p-value distribution. P-values are expressed as - log10(p-value). Experimental p-values are depicted as grey circles that turn to red when the associated p-adjust is <0.1. The point where the observed p-values detach from expected p-values is depicted as the intersection between the expected p-value distribution (sloping black line) and the significance threshold (vertical black line).



Supplemental Table CIV. 1 List of DEG using annotation a1. A list of all DEG using a1 is provided for each contrasting hypothesis (NIL vs. RV). Genes that were also differentially expressed using a2 are indicated in the last column. DEG for each NIL are presented in ascending order of log$_2$(fold change).

Supplemental Table CIV. 1

[a] gene id is according to *F. vesca* annotation 1 nomenclature

[b] log$_2$(fold change) values use as reference RV, so negative values indicate down-regulation in NIL vs. RV and positive values up-regulation in NIL vs. RV

[c] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb5:0-35	gene01807	-Inf	4,67E-26	7,91E-23	CIP8_ARATH	E3 ubiquitin-protein ligase CIP8	E3 ubiquitin-protein ligase CIP8 (probable)	NO
Fb5:0-35	gene01866	-Inf	5,05E-04	4,35E-02	B0M1H3_ARATH	ZIP4-like protein	Leiomodin-1 (SM-Lmod) (probable)	YES
Fb5:0-35	gene04512	-Inf	9,69E-22	1,00E-18	B8AFR4_ORYSI	Putative uncharacterized protein	hypothetical protein	YES
Fb5:0-35	gene06414	-Inf	8,29E-05	9,54E-03	Q8VZ20_ARATH	Putative uncharacterized protein At2g33550	U1 small nuclear ribonucleoprotein component SNU71 (probable)	YES
Fb5:0-35	gene06472	-Inf	3,06E-14	1,46E-11	-	-	Formin-like protein 1 (AtFH1), Precursor (probable)	NO
Fb5:0-35	gene09886	-Inf	1,84E-04	1,91E-02	B8B6E8_ORYSI	Putative uncharacterized protein	Integrase (probable)	NO
Fb5:0-35	gene09887	-Inf	6,03E-06	9,29E-04	ASSY_ARATH	Argininosuccinate synthase, chloroplastic	Argininosuccinate synthase, chloroplastic, Precursor (similar to)	YES
Fb5:0-35	gene09907	-Inf	6,36E-27	1,19E-23	B8BCB0_ORYSI	Putative uncharacterized protein	Beta-glucosidase 16 (AtBGLU16), Precursor (probable)	YES
Fb5:0-35	gene09933	-Inf	1,69E-22	1,86E-19	A2WZX6_ORYSI	Putative uncharacterized protein	Ribosomal protein S12 methylthiotransferase rimO (S12 methylthiotransferase) (probable)	YES
Fb5:0-35	gene10539	-Inf	2,20E-07	4,61E-05	LEC2_ARATH	B3 domain-containing transcription factor LEC2	B3 domain-containing transcription factor LEC2 (similar to)	YES
Fb5:0-35	gene11307	-Inf	1,33E-04	1,42E-02	-	-	hypothetical protein	NO
Fb5:0-35	gene11802	-Inf	2,98E-04	2,86E-02	O23864_9ORYZ	Polyprotein	Endonuclease (probable)	YES
Fb5:0-35	gene11803	-Inf	2,29E-27	4,75E-24	KEULE_ARATH	SNARE-interacting protein KEULE	SNARE-interacting protein KEULE (similar to)	NO
Fb5:0-35	gene12674	-Inf	5,88E-04	4,94E-02	RH21_ARATH	DEAD-box ATP-dependent RNA helicase 21	DEAD-box ATP-dependent RNA helicase 21 (similar to)	NO
Fb5:0-35	gene18184	-Inf	5,01E-05	6,36E-03	Q8S6N1_ORYSJ	Putative gag-pol polyprotein	Protein P200 (probable)	YES
Fb5:0-35	gene24473	-Inf	4,10E-07	8,22E-05	-	-	ATP synthase gamma chain (similar to)	YES
Fb5:0-35	gene27274	-Inf	8,80E-05	1,01E-02	Q8H957_ORYSJ	A protein	hypothetical protein	YES
Fb5:0-35	gene30985	-Inf	1,62E-05	2,29E-03	PID2_ARATH	Protein kinase PINOID 2	Protein kinase G11A (probable)	YES
Fb5:0-35	gene31982	-Inf	9,12E-08	2,07E-05	HR3_ARATH	RPW8-like protein 3	Probable disease resistance protein At5g66910	YES

Supplemental Table CIV. 1

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[c] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb5:0-35	gene32220	-Inf	1,18E-29	3,15E-26	APY7_ARATH	Probable apyrase 7	Guanosine-diphosphatase (GDPase) (probable)	YES
Fb5:0-35	gene32361	-Inf	3,73E-12	1,42E-09	PLDG2_ARATH	Phospholipase D gamma 2	Phospholipase D gamma 2 (AtPLDgamma2) (similar to)	NO
Fb5:0-35	gene32394	-Inf	1,62E-04	1,70E-02	Q8W494_ARATH	Uncharacterized protein	Protein catecholamines up (probable)	NO
Fb5:0-35	gene09906	-12,19	2,16E-32	2,01E-28	TIM13_ORYSJ	Mitochondrial import inner membrane translocase subunit Tim13	Mitochondrial import inner membrane translocase subunit Tim13 (similar to)	YES
Fb5:0-35	gene09934	-11,82	4,56E-44	8,49E-40	F4JBC7_ARATH	HXXXD-type acyl-transferase-like protein	Vinorine synthase (probable)	YES
Fb5:0-35	gene22683	-11,03	1,67E-20	1,56E-17	CINV2_ARATH	Alkaline/neutral invertase CINV2	2',3'-cyclic-nucleotide 2'-phosphodiesterase (probable)	YES
Fb5:0-35	gene32194	-8,87	9,75E-31	4,54E-27	RPS2_ARATH	Disease resistance protein RPS2	Disease resistance protein At4g27190 (probable)	NO
Fb5:0-35	gene25025	-8,69	1,87E-13	7,76E-11	Q94H40_ORYSJ	Putative reverse transcriptase	Putative ribonuclease H protein At1g65750 (probable)	YES
Fb5:0-35	gene09993	-8,46	2,23E-30	8,30E-27	Q0E0X9_ORYSJ	Os02g0513700 protein	Ankyrin repeat domain-containing protein 34A (probable)	NO
Fb5:0-35	gene06475	-8,33	4,68E-20	4,15E-17	FB285_ARATH	F-box protein At5g46170	Transactivator/viroplasmin protein (Tav) (probable)	NO
Fb5:0-35	gene27067	-8,21	2,88E-15	1,58E-12	FBK67_ARATH	F-box/kelch-repeat protein At3g23880	F-box/kelch-repeat protein At3g06240 (probable)	NO
Fb5:0-35	gene28808	-8,10	2,85E-14	1,40E-11	Q93Z72_ARATH	Zinc-binding dehydrogenase family protein	Probable NADP-dependent oxidoreductase P1	YES
Fb5:0-35	gene06473	-7,76	1,75E-21	1,72E-18	Q9FW98_ORYSJ	Putative non-LTR retroelement reverse transcriptase	Putative ribonuclease H protein At1g65750 (probable)	YES
Fb5:0-35	gene34199	-7,65	4,19E-14	1,96E-11	C71AQ_ARATH	Cytochrome P450 71A26	Cytochrome P450 71A4 (probable)	NO
Fb5:0-35	gene16771	-7,16	7,72E-17	5,14E-14	Q9SYP1_ARATH	Putative U5 small nuclear ribonucleoprotein helicase	U5 small nuclear ribonucleoprotein 200 kDa helicase (U5-200KD) (putative)	YES
Fb5:0-35	gene31818	-6,76	3,96E-13	1,61E-10	Q9SSN4_ARATH	Toll-Interleukin-Resistance domain-containing protein	TMV resistance protein N (probable)	NO
Fb5:0-35	gene09891	-6,75	2,39E-25	3,42E-22	B8BP56_ORYSI	Putative uncharacterized protein	Probable Ufm1-specific protease (UfSP)	YES
Fb5:0-35	gene09885	-6,64	6,88E-09	1,91E-06	B8BLZ3_ORYSI	Putative uncharacterized protein	RING finger protein 165 (probable)	NO
Fb5:0-35	gene05008	-6,37	1,23E-07	2,74E-05	C71AM_ARATH	Cytochrome P450 71A22	Cytochrome P450 71A22 (probable)	NO
Fb5:0-35	gene31829	-6,20	7,82E-16	4,56E-13	F4JEP8_ARATH	Uncharacterized protein	Glucose-6-phosphate isomerase, cytosolic 2 (GPI) (similar to)	NO

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[c] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb5:0-35	gene06340	-5,93	4,08E-18	3,17E-15	Q9SNB6_ARATH	Putative uncharacterized protein F12A12.140	RING finger protein 122 (probable)	YES
Fb5:0-35	gene25316	-5,82	1,42E-13	6,00E-11	B9G602_ORYSJ	Putative uncharacterized protein	Copia protease (probable)	NO
Fb5:0-35	gene32459	-5,72	2,34E-06	4,12E-04	A2Y9C9_ORYSI	Putative uncharacterized protein	Putative F-box protein At4g22660 (probable)	NO
Fb5:0-35	gene34729	-5,62	2,18E-10	7,02E-08	-	-	Protein FAM83H (probable)	YES
Fb5:0-35	gene22708	-5,59	5,37E-11	1,82E-08	C71AL_ARATH	Cytochrome P450 71A21	Cytochrome P450 71A26 (similar to)	NO
Fb5:0-35	gene32312	-5,58	1,63E-16	1,01E-13	SC31B_ARATH	Protein transport protein SEC31 homolog B	Probable protease htpX homolog	NO
Fb5:0-35	gene22680	-5,49	6,18E-19	5,01E-16	CPR30_ARATH	F-box protein CPR30	F-box/kelch-repeat protein At3g06240 (probable)	YES
Fb5:0-35	gene32402	-5,25	6,72E-14	3,06E-11	B8AGG3_ORYSI	Putative uncharacterized protein	Cytochrome P450 87A3 (similar to)	NO
Fb5:0-35	gene09884	-4,97	5,60E-06	8,70E-04	-	-	FAD-dependent cmnm(5)s(2)U34 oxidoreductase (probable)	NO
Fb5:0-35	gene29473	-4,89	4,97E-04	4,33E-02	B9F6L9_ORYSJ	Putative uncharacterized protein	Trichothecene 3-O-acetyltransferase (probable)	YES
Fb5:0-35	gene01867	-4,84	2,94E-16	1,77E-13	Q0DY33_ORYSJ	cDNA clone:J033045A20, full insert sequence	ADP,ATP carrier protein, mitochondrial (ANT), Precursor (similar to)	YES
Fb5:0-35	gene35185	-4,81	1,09E-03	8,20E-02	-	-	Ribosome-binding protein 1 (mRRp) (probable)	NO
Fb5:0-35	gene01858	-4,67	5,62E-18	4,19E-15	OMT1_ARATH	Flavone 3'-O-methyltransferase 1	Caffeic acid 3-O-methyltransferase (CAOMT) (putative)	NO
Fb5:0-35	gene33939	-4,57	5,55E-08	1,29E-05	Q9FE41_ORYSJ	Similar to Arabidopsis thaliana chromosome II BAC F26H6	Protein ycf2 (probable)	YES
Fb5:0-35	gene32467	-4,53	1,10E-04	1,21E-02	A2WZX6_ORYSI	Putative uncharacterized protein	Polyamine-modulated factor 1-binding protein 1 (PMF-1-binding protein) (probable)	NO
Fb5:0-35	gene22681	-4,53	1,93E-06	3,47E-04	Q6ESS0_ORYSJ	Putative pseudouridine synthase 1	tRNA pseudouridine synthase 1 (similar to)	NO
Fb5:0-35	gene01616	-4,42	2,50E-05	3,38E-03	F4IBR2_ARATH	Uncharacterized protein	Proteasome subunit alpha type-7-B (similar to)	YES
Fb5:0-35	gene32466	-4,41	4,07E-06	6,66E-04	Q9SUE9_ARATH	Uncharacterized protein	Probable DNA repair protein Amir_3417	NO
Fb5:0-35	gene09972	-4,35	4,06E-15	2,16E-12	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	NO

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[c] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	**gene id[a]**	**$\log_2$(FCh)[b]**	**p-val.**	**p-adj.**	**blast hit[c]**	**blast hit protein description**	**predicted function (a1)**	**a1 & a2 comm.**
Fb5:0-35	gene32023	-4,34	6,71E-04	5,51E-02	Q93Z72_ARATH	Zinc-binding dehydrogenase family protein	Probable NADP-dependent oxidoreductase P1 (putative)	YES
Fb5:0-35	gene22676	-4,30	6,73E-15	3,48E-12	C71AQ_ARATH	Cytochrome P450 71A26	Cytochrome P450 71A26 (putative)	YES
Fb5:0-35	gene32187	-4,27	1,20E-03	8,91E-02	DOF56_ARATH	Dof zinc finger protein DOF5.6	Dof zinc finger protein DOF5.6 (AtDOF5.6) (probable)	NO
Fb5:0-35	gene32368	-4,13	4,78E-09	1,35E-06	Q6Z226_ORYSJ	Putative uncharacterized protein P0690E03.30	F-box/FBD/LRR-repeat protein At1g13570 (probable)	YES
Fb5:0-35	gene32398	-4,11	2,56E-07	5,30E-05	B8AGG3_ORYSI	Putative uncharacterized protein	Cytochrome P450 87A3 (similar to)	NO
Fb5:0-35	gene06474	-4,10	1,61E-10	5,27E-08	-	-	Sterol 3-beta-glucosyltransferase (probable)	YES
Fb5:0-35	gene20699	-4,04	1,12E-03	8,38E-02	A3AB76_ORYSJ	Putative uncharacterized protein	Metalloendoproteinase 1, Precursor (probable)	NO
Fb5:0-35	gene06294	-3,97	3,32E-09	9,68E-07	Q8S6P1_ORYSJ	Putative reverse transcriptase	Putative ribonuclease H protein At1g65750 (probable)	YES
Fb5:0-35	gene32141	-3,94	4,25E-12	1,58E-09	Q0JH95_ORYSJ	Os01g0876400 protein	hypothetical protein	NO
Fb5:0-35	gene31842	-3,80	2,74E-08	6,81E-06	SPO12_ARATH	Meiotic recombination protein SPO11-2	Meiotic recombination protein SPO11-2 (AtSPO11-2) (putative)	NO
Fb5:0-35	gene34943	-3,71	5,42E-04	4,64E-02	-	-	Probable nitrile hydratase (Nitrilase)	YES
Fb5:0-35	gene32238	-3,70	2,83E-12	1,12E-09	F4I5Q5_ARATH	Uncharacterized protein	Pentatricopeptide repeat-containing protein At4g18975, chloroplastic, Precursor (probable)	NO
Fb5:0-35	gene09905	-3,67	1,24E-11	4,38E-09	Q94BR1_ARATH	Putative topoisomerase	Programmed cell death protein 4 (probable)	YES
Fb5:0-35	gene01808	-3,63	1,22E-11	4,37E-09	HS901_ARATH	Heat shock protein 90-1	Heat shock protein 83 (similar to)	YES
Fb5:0-35	gene13651	-3,49	1,16E-06	2,13E-04	Q058J9_ARATH	Molecular chaperone Hsp40/DnaJ family protein	Chaperone protein dnaJ (probable)	NO
Fb5:0-35	gene31867	-3,47	3,69E-08	8,81E-06	O82354_ARATH	Putative uncharacterized protein At2g46150/T3F17.20	Anthranilate phosphoribosyltransferase (probable)	YES
Fb5:0-35	gene31820	-3,47	2,66E-05	3,57E-03	MUB3_ARATH	Membrane-anchored ubiquitin-fold protein 3	Cullin-7 (CUL-7) (probable)	NO
Fb5:0-35	gene06413	-3,46	5,28E-07	1,04E-04	TAF8_ARATH	Transcription initiation factor TFIID subunit 8	hypothetical protein	YES
Fb5:0-35	gene17416	-3,44	3,94E-04	3,55E-02	C82C2_ARATH	Cytochrome P450 82C2	Cytochrome P450 82A3 (probable)	NO
Fb5:0-35	gene31994	-3,36	1,80E-08	4,64E-06	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (similar to)	NO
Fb5:0-35	gene32499	-3,35	3,70E-04	3,38E-02	O80829_ARATH	Putative uncharacterized protein At2g45900	Protein MSB2 (probable)	NO

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[c] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	**gene id[a]**	**log$_2$(FCh)[b]**	**p-val.**	**p-adj.**	**blast hit[c]**	**blast hit protein description**	**predicted function (a1)**	**a1 & a2 comm.**
Fb5:0-35	gene16766	-3,30	9,06E-09	2,45E-06	-	-	Tegument protein BRRF2 (probable)	YES
Fb5:0-35	gene31819	-3,29	1,98E-05	2,76E-03	F4HU33_ARATH	Uncharacterized protein	Beta-1,3-glucosyltransferase (Beta3Glc-T) (probable)	YES
Fb5:0-35	gene10136	-3,25	3,49E-06	5,81E-04	U74E2_ARATH	UDP-glycosyltransferase 74E2	hypothetical protein	NO
Fb5:0-35	gene23505	-3,21	8,02E-06	1,21E-03	Q10RH2_ORYSJ	cDNA clone:001-023-C08, full insert sequence	Hornerin (probable)	YES
Fb5:0-35	gene32117	-3,13	3,63E-06	5,99E-04	Q6YTR3_ORYSJ	cDNA clone:J013091B08, full insert sequence	Pentatricopeptide repeat-containing protein At5g25630 (probable)	YES
Fb5:0-35	gene32242	-3,12	3,51E-08	8,51E-06	Q9SUV9_ARATH	Uncharacterized protein	Transcription factor TGA2 (AHBP-1b) (probable)	YES
Fb5:0-35	gene18953	-3,12	2,22E-04	2,23E-02	Q8H374_ORYSJ	Putative uncharacterized protein OSJNBa0061L20.120	hypothetical protein	NO
Fb5:0-35	gene09501	-3,11	2,81E-06	4,78E-04	ARR5_ARATH	Two-component response regulator ARR5	Two-component response regulator ARR5 (similar to)	NO
Fb5:0-35	gene34612	-3,11	4,27E-06	6,92E-04	Q75IS6_ORYSJ	Putative Mutator-like transposase	Protein FAR1-RELATED SEQUENCE 5 (probable)	NO
Fb5:0-35	gene31823	-3,11	1,82E-08	4,64E-06	A3BAA3_ORYSJ	Putative uncharacterized protein	Pentatricopeptide repeat-containing protein At3g61520, mitochondrial, Precursor (probable)	NO
Fb5:0-35	gene01871	-3,11	2,00E-09	6,02E-07	ATPO_ARATH	ATP synthase subunit O, mitochondrial	ATP synthase subunit O, mitochondrial (OSCP), Precursor (probable)	YES
Fb5:0-35	gene32358	-3,06	4,07E-04	3,63E-02	PLDB1_ARATH	Phospholipase D beta 1	Phospholipase D beta 1 (AtPLDbeta1) (similar to)	NO
Fb5:0-35	gene15934	-2,91	2,45E-06	4,26E-04	Q9LEU3_ARATH	Zinc finger-like protein	Zinc finger protein 1 (probable)	YES
Fb5:0-35	gene32196	-2,89	6,77E-06	1,03E-03	Q2QNH0_ORYSJ	cDNA clone:J023062N03, full insert sequence	Putative boron transporter 2	NO
Fb5:0-35	gene18203	-2,88	1,39E-03	9,99E-02	Q0WQJ7_ARATH	Kinesin-like protein	125 kDa kinesin-related protein (probable)	NO
Fb5:0-35	gene15712	-2,87	1,36E-03	9,83E-02	A2X1L7_ORYSI	Putative uncharacterized protein	hypothetical protein	YES
Fb5:0-35	gene26292	-2,83	8,91E-05	1,01E-02	Q5QLG8_ORYSJ	Putative uncharacterized protein B1147B04.15	Mucin-5AC (TBM), Precursor (probable)	YES
Fb5:0-35	gene04367	-2,80	2,34E-05	3,21E-03	DSLE_ARATH	Zinc finger BED domain-containing protein DAYSLEEPER	Putative AC9 transposase (probable)	NO
Fb5:0-35	gene34961	-2,80	1,51E-05	2,16E-03	FAR1_ARATH	Protein FAR-RED IMPAIRED RESPONSE 1	Protein FAR1-RELATED SEQUENCE 5 (probable)	YES
Fb5:0-35	gene18559	-2,73	1,61E-06	2,91E-04	B9FFZ6_ORYSJ	Putative uncharacterized protein	Serine/threonine-protein phosphatase PP1 (probable)	YES

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Fb5:0-35	gene06344	-2,72	3,13E-07	6,42E-05	-	-	Transcription factor Sox-7 (probable)	NO
Fb5:0-35	gene32240	-2,70	1,34E-07	2,94E-05	FABH_ARATH	3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplastic	3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplastic (KAS III), Precursor (putative)	NO
Fb5:0-35	gene31651	-2,70	2,16E-04	2,17E-02	-	-	Angiomotin (probable)	YES
Fb5:0-35	gene32068	-2,67	3,58E-04	3,32E-02	B9EYI9_ORYSJ	Serine/threonine-protein kinase	Putative receptor protein kinase ZmPK1, Precursor (probable)	NO
Fb5:0-35	gene09927	-2,61	8,58E-04	6,70E-02	FRO8_ARATH	Ferric reduction oxidase 8, mitochondrial	Superoxide-generating NADPH oxidase heavy chain subunit B (probable)	NO
Fb5:0-35	gene31864	-2,59	5,12E-05	6,45E-03	O82354_ARATH	Putative uncharacterized protein At2g46150/T3F17.20	Anthranilate phosphoribosyltransferase (probable)	YES
Fb5:0-35	gene30450	-2,59	3,29E-06	5,53E-04	A2WXJ8_ORYSI	Putative uncharacterized protein	hypothetical protein	YES
Fb5:0-35	gene27842	-2,57	3,59E-05	4,65E-03	IPT3_ARATH	Adenylate isopentenyltransferase 3, chloroplastic	tRNA Delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (probable)	NO
Fb5:0-35	gene32300	-2,57	1,91E-04	1,94E-02	PHR_ARATH	Deoxyribodipyrimidine photo-lyase	Deoxyribodipyrimidine photo-lyase (similar to)	NO
Fb5:0-35	gene11116	-2,56	1,38E-04	1,47E-02	Q84VX4_ARATH	Serine/threonine-protein kinase TTK/MPS1-like protein	Probable serine/threonine-protein kinase mps1	NO
Fb5:0-35	gene32257	-2,55	2,28E-06	4,04E-04	Q9SI77_ARATH	Isoprenoid biosynthesis enzyme domain-containing protein	UPF0551 protein C8orf38 homolog, mitochondrial, Precursor (probable)	YES
Fb5:0-35	gene32319	-2,50	1,73E-04	1,80E-02	BASS6_ARATH	Probable sodium/metabolite cotransporter BASS6, chloroplastic	hypothetical protein	NO
Fb5:0-35	gene13665	-2,49	9,53E-05	1,07E-02	Q8SAW7_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Structural protein ORF567 (probable)	YES
Fb5:0-35	gene06310	-2,46	1,88E-04	1,93E-02	TL1Y_ARATH	Thylakoid lumenal 17.9 kDa protein, chloroplastic	Thylakoid lumenal 17.9 kDa protein, chloroplastic, Precursor (putative)	NO
Fb5:0-35	gene31783	-2,43	5,14E-06	8,13E-04	Q93VK9_ARATH	Putative uncharacterized protein At3g48210	Kinetochore protein spc25 (probable)	YES
Fb5:0-35	gene12135	-2,42	2,89E-04	2,81E-02	-	-	Polyadenylate-binding protein 1-B (Poly(A)-binding protein, cytoplasmic 1-B) (probable)	YES
Fb5:0-35	gene32442	-2,41	3,31E-04	3,12E-02	Q7G2C6_ORYSJ	Os10g0504600 protein	Myosin-3 (probable)	NO
Fb5:0-35	gene06309	-2,40	6,79E-05	8,06E-03	B9GB87_ORYSJ	Putative uncharacterized protein	Phytosulfokine receptor 1 (DcPSKR1), Precursor (probable)	NO

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Fb5:0-35	gene33425	-2,35	2,62E-06	4,52E-04	Q0IWU5_ORYSJ	Os10g0487400 protein	RING-H2 zinc finger protein RHA1a (probable)	NO
Fb5:0-35	gene31252	-2,31	1,47E-04	1,56E-02	Q10IC1_ORYSJ	Transposon protein, putative, Mutator sub-class	Beta-amyloid protein, Precursor (probable)	YES
Fb5:0-35	gene00428	-2,30	3,68E-04	3,38E-02	-	-	WD repeat-containing protein 48 homolog (probable)	YES
Fb5:0-35	gene06490	-2,28	3,80E-04	3,44E-02	Q2QRE6_ORYSJ	Oxidoreductase, short chain dehydrogenase/reductase family protein, expressed	Hydroxysteroid 11-beta-dehydrogenase 1-like protein (11-beta-HSD3), Precursor (probable)	YES
Fb5:0-35	gene06467	-2,27	1,60E-05	2,27E-03	Q9LST0_ARATH	Zn-dependent exopeptidases superfamily protein	Aspartyl aminopeptidase (DAP) (probable)	NO
Fb5:0-35	gene27115	-2,27	4,76E-04	4,17E-02	SYCP1_ARATH	Synaptonemal complex protein 1	Synaptonemal complex protein 1 (probable)	NO
Fb5:0-35	gene32261	-2,24	1,26E-03	9,18E-02	Q9LVA4_ARATH	Ripening-related protein-like contains similarity to pectinesterase	21 kDa protein, Precursor (probable)	YES
Fb5:0-35	gene16108	-2,22	8,66E-04	6,73E-02	Q8VZ10_ARATH	Putative uncharacterized protein At1g56500	Transcription factor unc-86 (probable)	YES
Fb5:0-35	gene13448	-2,15	1,31E-03	9,50E-02	F4IYK4_ARATH	Armadillo/beta-catenin-like repeat-containing protein	Importin subunit beta-1 (PTAC97) (probable)	YES
Fb5:0-35	gene32088	-2,02	5,55E-05	6,81E-03	P2C56_ARATH	Protein phosphatase 2C 56	Probable protein phosphatase 2C 8 (OsPP2C08)	NO
Fb5:0-35	gene32373	-2,01	1,72E-04	1,80E-02	NRPD1_ARATH	DNA-directed RNA polymerase IV subunit 1	DNA-directed RNA polymerase II subunit RPB1-B (RNA polymerase II subunit B1-B) (probable)	NO
Fb5:0-35	gene01833	-1,98	1,85E-04	1,91E-02	RAE1_ARATH	Protein RAE1	Rae1-like protein At1g80670 (putative)	NO
Fb5:0-35	gene32289	-1,98	1,01E-04	1,13E-02	O49654_ARATH	Leucine-rich repeat receptor-like protein kinase	LRR receptor-like serine/threonine-protein kinase GSO2, Precursor (probable)	NO
Fb5:0-35	gene05794	-1,97	6,29E-04	5,24E-02	PUB30_ARATH	U-box domain-containing protein 30	U-box domain-containing protein 30 (putative)	NO
Fb5:0-35	gene06447	-1,95	6,18E-05	7,49E-03	Q9M300_ARATH	Putative uncharacterized protein T21J18_100	Poly(A) polymerase (PAP) (probable)	YES
Fb5:0-35	gene21470	-1,94	6,98E-04	5,64E-02	Q94HN3_ORYSJ	Putative retroelement	DNA-directed RNA polymerase subunit beta'' (RNA polymerase subunit beta'') (probable)	YES
Fb5:0-35	gene20865	-1,90	2,23E-04	2,23E-02	BLH9_ARATH	BEL1-like homeodomain protein 9	BEL1-like homeodomain protein 9 (BEL1-like protein 9) (probable)	NO

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Fb5:0-35	gene03953	-1,87	5,06E-04	4,35E-02	SKA1_ARATH	Spindle and kinetochore-associated protein 1 homolog	Spindle and kinetochore-associated protein 1 homolog (putative)	NO
Fb5:0-35	gene06305	-1,81	7,57E-04	6,09E-02	NPC3_ARATH	Non-specific phospholipase C3	Phospholipase C 3, Precursor (probable)	YES
Fb5:0-35	gene06308	-1,81	5,70E-04	4,83E-02	A2WS87_ORYSI	Putative uncharacterized protein	Serine/threonine-protein kinase BRI1-like 2, Precursor (probable)	NO
Fb5:0-35	gene28659	-1,79	3,24E-04	3,07E-02	14310_ARATH	14-3-3-like protein GF14 epsilon	14-3-3 protein 7 (similar to)	NO
Fb5:0-35	gene19238	-1,79	8,80E-04	6,81E-02	MPK4_ARATH	Mitogen-activated protein kinase 4	Mitogen-activated protein kinase homolog MMK2 (putative)	NO
Fb5:0-35	gene12820	-1,78	5,06E-04	4,35E-02	ATXR6_ARATH	Histone-lysine N-methyltransferase ATXR6	Histone-lysine N-methyltransferase ATXR6 (TRX-related protein 6) (putative)	YES
Fb5:0-35	gene11511	-1,77	8,33E-04	6,58E-02	F4JUQ2_ARATH	Transducin/WD40 domain-containing protein-like protein	Nuclease sbcCD subunit C (probable)	YES
Fb5:0-35	gene28200	-1,76	7,98E-05	9,25E-03	U87A1_ARATH	UDP-glycosyltransferase 87A1	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (probable)	NO
Fb5:0-35	gene22014	-1,76	2,44E-04	2,41E-02	GSTFD_ARATH	Glutathione S-transferase F13	Probable glutathione S-transferase GSTF1 (putative)	YES
Fb5:0-35	gene12199	-1,72	1,02E-03	7,71E-02	F4IK92_ARATH	ARM repeat superfamily protein	Microtubule-associated protein TORTIFOLIA1 (probable)	NO
Fb5:0-35	gene09950	-1,71	6,97E-04	5,64E-02	PCH2_ORYSJ	Pachytene checkpoint protein 2 homolog	Thyroid receptor-interacting protein 13 (TRIP-13) (probable)	NO
Fb5:0-35	gene20350	-1,70	5,56E-04	4,73E-02	MPK2_ARATH	Mitogen-activated protein kinase 2	Chloride anion exchanger (Protein DRA) (probable)	YES
Fb5:0-35	gene15126	-1,69	8,51E-04	6,67E-02	SMC4_ARATH	Structural maintenance of chromosomes protein 4	Structural maintenance of chromosomes protein 4 (AtSMC4) (putative)	NO
Fb5:0-35	gene24485	-1,62	1,36E-03	9,83E-02	Q0WR66_ARATH	Putative uncharacterized protein At2g46980	Muscle M-line assembly protein unc-89 (probable)	NO
Fb5:0-35	gene29484	-1,61	9,13E-04	7,03E-02	Q29Q34_ARATH	At5g19440	LRR receptor-like serine/threonine-protein kinase FLS2, Precursor (probable)	NO
Fb5:0-35	gene05907	-1,53	1,23E-03	9,03E-02	UGPI4_ARATH	Uncharacterized GPI-anchored protein At3g06035	Uncharacterized GPI-anchored protein At3g06035, Precursor (similar to)	YES
Fb5:0-35	gene32186	-1,51	1,00E-03	7,64E-02	SRO5_ARATH	Probable inactive poly [ADP-ribose] polymerase SRO5	Poly [ADP-ribose] polymerase 14 (PARP-14) (probable)	NO

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Fb5:0-35	gene22918	1,59	8,41E-04	6,61E-02	Q3E6S9_ARATH	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	Isopenicillin N epimerase (probable)	YES
Fb5:0-35	gene18007	1,61	6,97E-04	5,64E-02	EIF3C_ARATH	Eukaryotic translation initiation factor 3 subunit C	Eukaryotic translation initiation factor 3 subunit C (eIF3c) (putative)	NO
Fb5:0-35	gene18181	1,66	1,13E-03	8,46E-02	O80625_ARATH	Putative uncharacterized protein At2g39380	Exocyst complex component 7 (probable)	YES
Fb5:0-35	gene32494	1,68	6,21E-04	5,20E-02	GL3_ARATH	Transcription factor GLABRA 3	Transcription factor GLABRA 3 (bHLH 1) (putative)	YES
Fb5:0-35	gene06430	1,72	2,91E-04	2,81E-02	Q6YS36_ORYSJ	Putative fertility restorer homologue	Pentatricopeptide repeat-containing protein At5g61990, mitochondrial, Precursor (probable)	YES
Fb5:0-35	gene09980	1,74	3,45E-04	3,22E-02	AFC2_ARATH	Serine/threonine-protein kinase AFC2	Serine/threonine-protein kinase AFC2 (putative)	YES
Fb5:0-35	gene12765	1,75	6,77E-04	5,53E-02	ATHB7_ARATH	Homeobox-leucine zipper protein ATHB-7	Homeobox-leucine zipper protein ATHB-12 (probable)	NO
Fb5:0-35	gene32347	1,75	5,82E-04	4,91E-02	LDOX_ARATH	Leucoanthocyanidin dioxygenase	Leucoanthocyanidin dioxygenase (LDOX) (putative)	YES
Fb5:0-35	gene06325	1,76	2,53E-04	2,48E-02	PPA27_ARATH	Probable inactive purple acid phosphatase 27	Probable inactive purple acid phosphatase 27, Precursor (putative)	NO
Fb5:0-35	gene09962	1,81	1,31E-03	9,50E-02	NRT31_ARATH	High-affinity nitrate transporter 3.1	Ephrin type-A receptor 2, Precursor (probable)	NO
Fb5:0-35	gene09619	1,84	1,23E-03	9,05E-02	U86A1_ARATH	UDP-glycosyltransferase 86A1	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (probable)	NO
Fb5:0-35	gene32478	1,86	2,39E-04	2,37E-02	GSH1_ARATH	Glutamate--cysteine ligase, chloroplastic	Glutamate--cysteine ligase, chloroplastic (GCS), Precursor (putative)	YES
Fb5:0-35	gene09848	1,88	1,16E-04	1,26E-02	Q8L866_ARATH	Putative copper amine oxidase	Primary amine oxidase, Precursor (probable)	NO
Fb5:0-35	gene20954	1,89	3,65E-04	3,37E-02	Q9FF29_ARATH	Receptor serine/threonine kinase	Receptor-like protein kinase At3g21340, Precursor (similar to)	NO
Fb5:0-35	gene00094	1,90	4,00E-04	3,58E-02	U73D1_ARATH	UDP-glycosyltransferase 73D1	Cytokinin-O-glucosyltransferase 3 (AtZOG3) (probable)	YES
Fb5:0-35	gene14383	1,92	1,21E-04	1,30E-02	Q9ZUY4_ARATH	Uncharacterized protein	hypothetical protein	YES
Fb5:0-35	gene01371	1,94	9,22E-04	7,07E-02	CSPLO_ARATH	CASP-like protein 1E1	UPF0497 membrane protein 7 (probable)	YES
Fb5:0-35	gene08194	1,96	6,79E-05	8,06E-03	IAA16_ARATH	Auxin-responsive protein IAA16	Auxin-induced protein AUX28 (putative)	YES

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Fb5:0-35	gene09948	1,97	4,61E-05	5,89E-03	-	-	WUSCHEL-related homeobox 3B (similar to)	YES
Fb5:0-35	gene01830	1,98	2,81E-05	3,75E-03	Q94GX1_ORYSJ	cDNA clone:J033005B11, full insert sequence	Phthiotriol/phenolphthiotriol dimycocerosates methyltransferase (probable)	YES
Fb5:0-35	gene12033	2,00	1,11E-04	1,22E-02	CAP16_ARATH	Putative clathrin assembly protein At4g40080	Putative clathrin assembly protein At4g40080 (probable)	YES
Fb5:0-35	gene01819	2,01	9,11E-05	1,03E-02	NIP51_ARATH	Probable aquaporin NIP5-1	Probable aquaporin NIP5-1 (AtNIP5) (similar to)	YES
Fb5:0-35	gene16699	2,03	5,29E-05	6,61E-03	A2ZNL8_ORYSJ	Uncharacterized protein	Probable serine/threonine-protein kinase At1g18390, Precursor	NO
Fb5:0-35	gene03102	2,03	7,62E-05	8,93E-03	Q93YW3_ARATH	Putative uncharacterized protein At1g01830	hypothetical protein	YES
Fb5:0-35	gene14357	2,06	2,58E-04	2,52E-02	UBC24_ARATH	Probable ubiquitin-conjugating enzyme E2 24	Probable ubiquitin-conjugating enzyme E2 24	YES
Fb5:0-35	gene16431	2,06	5,48E-05	6,77E-03	-	-	UPF0467 protein At2g41420 (similar to)	YES
Fb5:0-35	gene18571	2,09	2,45E-05	3,33E-03	Y3550_ARATH	REF/SRPP-like protein At3g05500	REF/SRPP-like protein At3g05500 (probable)	NO
Fb5:0-35	gene16897	2,11	2,28E-05	3,15E-03	H32_ARATH	Histone H3.2	Thyroid receptor-interacting protein 11 (TRIP-11) (probable)	YES
Fb5:0-35	gene18550	2,12	6,41E-05	7,71E-03	PTR2_ARATH	Protein NRT1/ PTR FAMILY 8.3	Peptide transporter PTR2 (putative)	NO
Fb5:0-35	gene16045	2,19	1,37E-05	1,99E-03	FB95_ARATH	F-box protein At2g02240	F-box protein PP2-B1 (AtPP2-B1) (probable)	NO
Fb5:0-35	gene05293	2,19	9,88E-04	7,55E-02	Q53JL7_ORYSJ	Receptor-like protein kinase	Probably inactive leucine-rich repeat receptor-like protein kinase At5g48380, Precursor (probable)	YES
Fb5:0-35	gene06509	2,22	1,98E-05	2,76E-03	F4JJL8_ARATH	Subtilase family protein	Holliday junction ATP-dependent DNA helicase ruvB (probable)	NO
Fb5:0-35	gene05871	2,22	9,39E-06	1,39E-03	FBX6_ARATH	F-box only protein 6	Protein UNUSUAL FLORAL ORGANS (AtFBX1) (probable)	YES
Fb5:0-35	gene32135	2,25	6,70E-04	5,51E-02	RNG1L_ARATH	E3 ubiquitin-protein ligase RING1-like	hypothetical protein	YES
Fb5:0-35	gene28609	2,27	1,99E-04	2,02E-02	Q7XZF8_ORYSJ	Putative DNA binding protein	50S ribosomal protein L9 (probable)	YES
Fb5:0-35	gene01820	2,36	1,19E-05	1,75E-03	A2XWP4_ORYSI	Putative uncharacterized protein	WAS/WASL-interacting protein family member 1 (WASP-interacting protein) (probable)	NO
Fb5:0-35	gene00803	2,37	6,66E-04	5,51E-02	-	-	Isochorismatase (probable)	NO

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Fb5:0-35	gene16048	2,38	6,26E-06	9,57E-04	O22813_ARATH	Putative steroid dehydrogenase	Myosin heavy chain, clone 203 (probable)	NO
Fb5:0-35	gene32413	2,46	3,00E-04	2,87E-02	BAP2_ARATH	BON1-associated protein 2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (PLC) (similar to)	NO
Fb5:0-35	gene32163	2,48	2,82E-06	4,78E-04	A2XUF5_ORYSI	Putative uncharacterized protein	hypothetical protein	NO
Fb5:0-35	gene24866	2,49	4,37E-05	5,63E-03	SRG1_ARATH	Protein SRG1	Protein SRG1 (AtSRG1) (putative)	NO
Fb5:0-35	gene32144	2,59	6,76E-07	1,27E-04	Q8RWI0_ARATH	Uncharacterized protein	Probable serine/threonine-protein kinase mkcB	NO
Fb5:0-35	gene19278	2,63	6,09E-05	7,42E-03	RD22_ARATH	Dehydration-responsive protein RD22	Dehydration-responsive protein RD22, Precursor (probable)	NO
Fb5:0-35	gene31838	2,64	8,14E-06	1,21E-03	Q9LTE3_ARATH	Emb|CAA71173.1	Putative late blight resistance protein homolog R1A-3 (probable)	YES
Fb5:0-35	gene09983	2,66	2,05E-07	4,39E-05	C71AP_ARATH	Cytochrome P450 71A25	Cytochrome P450 71A8 (similar to)	YES
Fb5:0-35	gene29726	2,70	3,15E-04	3,00E-02	SPL3_ARATH	Squamosa promoter-binding-like protein 3	Squamosa promoter-binding protein 1 (similar to)	YES
Fb5:0-35	gene32051	2,78	1,11E-06	2,04E-04	GAT2_ARATH	Probable GABA transporter 2	Lysine histidine transporter-like 3 (probable)	NO
Fb5:0-35	gene09832	2,81	7,62E-04	6,10E-02	F4IHU8_ARATH	NUC173 domain-containing protein	Putative ubiquitin thioesterase 232R (probable)	YES
Fb5:0-35	gene08784	2,81	5,39E-07	1,05E-04	C71AJ_AMMMJ	Psoralen synthase	Cytochrome P450 71A8 (probable)	NO
Fb5:0-35	gene11555	2,82	5,59E-06	8,70E-04	Q9FVQ7_ARATH	Uncharacterized protein	SH3 and multiple ankyrin repeat domains protein 1 (Shank1) (probable)	NO
Fb5:0-35	gene09981	2,85	1,93E-08	4,85E-06	C71AQ_ARATH	Cytochrome P450 71A26	Cytochrome P450 71A26 (probable)	NO
Fb5:0-35	gene31179	2,87	3,45E-04	3,22E-02	A2X685_ORYSI	Putative uncharacterized protein	Probable beta-1,3-galactosyltransferase 8 (putative)	YES
Fb5:0-35	gene06817	2,90	2,91E-05	3,85E-03	-	-	Forkhead box protein G1 (FoxG1) (probable)	YES
Fb5:0-35	gene07037	2,95	1,62E-08	4,32E-06	-	-	Probable exocyst complex component 6	YES
Fb5:0-35	gene32252	2,95	3,37E-08	8,28E-06	TL225_ARATH	Thylakoid lumenal protein At1g12250, chloroplastic	Thylakoid lumenal protein At1g12250, chloroplastic, Precursor (putative)	NO
Fb5:0-35	gene32052	2,96	4,52E-08	1,07E-05	GAT2_ARATH	Probable GABA transporter 2	Lysine histidine transporter-like 1 (probable)	NO
Fb5:0-35	gene20417	2,96	7,63E-09	2,09E-06	NPS11_ARATH	Novel plant SNARE 11	Mesoderm induction early response protein 2 (Mi-er2) (probable)	YES

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Fb5:0-35	gene28404	2,97	3,51E-07	7,10E-05	B8BLZ3_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RLIM (R-LIM) (probable)	YES
Fb5:0-35	gene20289	2,97	3,34E-05	4,38E-03	CDPKO_ARATH	Calcium-dependent protein kinase 24	Protein transport protein sec31 (probable)	YES
Fb5:0-35	gene32224	2,99	4,51E-06	7,18E-04	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At5g61990, mitochondrial, Precursor (probable)	YES
Fb5:0-35	gene32353	3,03	4,60E-09	1,32E-06	SGRW_PEA	Protein STAY-GREEN, chloroplastic	UPF0251 protein Hore_18270 (probable)	YES
Fb5:0-35	gene32128	3,03	2,19E-07	4,61E-05	P4KG2_ARATH	Phosphatidylinositol 4-kinase gamma 2	Phosphatidylinositol 4-kinase type 2-beta (probable)	NO
Fb5:0-35	gene04487	3,23	1,10E-03	8,26E-02	Q9LFQ8_ARATH	Uncharacterized protein	Uridylate kinase (UK) (probable)	NO
Fb5:0-35	gene33416	3,32	7,55E-11	2,51E-08	Q9M198_ARATH	Rossmann-fold NAD(P)-binding domain-containing protein	Carbonyl reductase [NADPH] 1 (probable)	YES
Fb5:0-35	gene14442	3,37	1,17E-03	8,69E-02	Q6ESG7_ORYSJ	Putative uncharacterized protein P0461B08.33	30S ribosomal protein S16 (probable)	YES
Fb5:0-35	gene28405	3,37	6,20E-07	1,18E-04	ARP4_ARATH	Actin-related protein 4	Actin-related protein 4 (similar to)	YES
Fb5:0-35	gene05185	3,39	7,96E-05	9,25E-03	ADA68331	pathogenesis-related protein 10	Major allergen Mal d 1 (putative)	NO
Fb5:0-35	gene16043	3,39	5,32E-05	6,61E-03	HR3_ARATH	RPW8-like protein 3	Probable disease resistance protein At5g66910	NO
Fb5:0-35	gene13930	3,40	4,31E-04	3,83E-02	IF4G2_ARATH	Eukaryotic translation initiation factor isoform 4G-2	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1) (probable)	NO
Fb5:0-35	gene29922	3,40	4,71E-04	4,15E-02	TBA6_ARATH	Tubulin alpha-6 chain	Tubulin alpha chain (similar to)	NO
Fb5:0-35	gene32017	3,51	4,72E-04	4,15E-02	-	-	2',3'-cyclic-nucleotide 2'-phosphodiesterase (probable)	NO
Fb5:0-35	gene09977	3,53	5,13E-10	1,59E-07	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	NO
Fb5:0-35	gene32283	3,72	9,49E-08	2,13E-05	Q8L742_ARATH	Amine oxidase	Primary amine oxidase, Precursor (similar to)	NO
Fb5:0-35	gene28403	3,75	1,09E-04	1,21E-02	B8BLZ3_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RLIM (R-LIM) (probable)	YES
Fb5:0-35	gene23021	3,93	7,72E-04	6,15E-02	-	-	hypothetical protein	YES
Fb5:0-35	gene09988	3,96	4,59E-12	1,68E-09	C83B1_ARATH	Cytochrome P450 83B1	Cytochrome P450 71A9 (putative)	NO
Fb5:0-35	gene25323	4,01	2,75E-11	9,51E-09	B8A7Y9_ORYSI	Putative uncharacterized protein	RNA polymerase-associated protein rapA (probable)	YES

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Fb5:0-35	gene01817	4,06	8,25E-08	1,90E-05	NAP1B_ARATH	Nucleosome assembly protein 12	Putative nucleosome assembly protein C364.06 (probable)	NO
Fb5:0-35	gene12208	4,29	4,39E-07	8,71E-05	RFL1_ARATH	Disease resistance protein RFL1	Probable disease resistance protein At1g51480	YES
Fb5:0-35	gene09917	4,61	1,17E-04	1,27E-02	Y3622_ARATH	B3 domain-containing protein At3g06220	B3 domain-containing protein Os02g0598200 (probable)	YES
Fb5:0-35	gene00622	4,73	8,22E-18	5,89E-15	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (probable)	NO
Fb5:0-35	gene09984	4,76	5,48E-07	1,05E-04	C71AP_ARATH	Cytochrome P450 71A25	Cytochrome P450 71A25 (similar to)	NO
Fb5:0-35	gene32510	4,98	1,60E-07	3,46E-05	Q2V4G0_ARATH	Probable disease resistance protein	Probable disease resistance protein At1g61190	YES
Fb5:0-35	gene32228	5,04	1,60E-09	4,90E-07	PTR7_ARATH	Protein NRT1/ PTR FAMILY 6.3	Nitrate/chlorate transporter (putative)	YES
Fb5:0-35	gene14572	5,36	1,04E-13	4,52E-11	-	-	Protein sip5 (probable)	YES
Fb5:0-35	gene27080	5,70	1,88E-14	9,46E-12	DEF06_ARATH	Defensin-like protein 6	Defensin-like protein, Precursor (similar to)	NO
Fb5:0-35	gene32505	5,71	7,37E-05	8,69E-03	TIC32_ARATH	Short-chain dehydrogenase TIC 32, chloroplastic	Retinol dehydrogenase 14 (probable)	YES
Fb5:0-35	gene10205	5,90	3,17E-09	9,37E-07	A3ALU8_ORYSJ	Putative uncharacterized protein	Beta-glucosidase 44 (AtBGLU44), Precursor (similar to)	NO
Fb5:0-35	gene32471	6,04	7,74E-24	1,03E-20	FBL63_ARATH	F-box/LRR-repeat protein At3g59190	F-box/LRR-repeat protein At4g14096 (probable)	NO
Fb5:0-35	gene32131	6,11	2,05E-15	1,16E-12	Q0IWU5_ORYSJ	Os10g0487400 protein	E3 ubiquitin-protein ligase CIP8 (probable)	YES
Fb5:0-35	gene08374	6,16	3,55E-05	4,62E-03	Q8RZ67_ORYSJ	Putative rice retrotransposon retrofit gag/pol polyprotein	Isoleucyl-tRNA synthetase (IleRS) (probable)	YES
Fb5:0-35	gene32130	6,17	3,63E-23	4,24E-20	CNBL3_ARATH	Calcineurin B-like protein 3	Calcineurin B-like protein 2 (similar to)	NO
Fb5:0-35	gene34513	6,29	1,17E-23	1,46E-20	-	-	Methenyltetrahydrofolate cyclohydrolase (probable)	YES
Fb5:0-35	gene31849	6,39	4,47E-10	1,41E-07	-	-	Peptide chain release factor 3 (RF-3) (probable)	NO
Fb5:0-35	gene12282	6,44	8,06E-04	6,40E-02	Q9C5N3_ARATH	Serine/threonine-protein phosphatase 2A activator	Putative AC9 transposase (similar to)	YES
Fb5:0-35	gene04519	6,90	9,62E-07	1,79E-04	Q0IZG6_ORYSJ	cDNA clone:006-310-E10, full insert sequence	Retinol dehydrogenase 14 (probable)	YES
Fb5:0-35	gene32030	6,95	1,38E-05	1,99E-03	Q9LJU1_ARATH	Predicted GPI-anchored protein	Early nodulin-like protein 1, Precursor (probable)	YES
Fb5:0-35	gene09979	7,28	4,31E-06	6,92E-04	C71AN_ARATH	Cytochrome P450 71A23	Cytochrome P450 71A24 (probable)	NO

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Fb5:0-35	gene09971	8,07	4,86E-29	1,13E-25	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	NO
Fb5:0-35	gene31380	8,40	3,73E-04	3,39E-02	Q9ARZ4_ORYSJ	Putative polyprotein	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase trmFO (probable)	YES
Fb5:0-35	gene06485	8,56	1,07E-17	7,39E-15	B8A7Y9_ORYSI	Putative uncharacterized protein	Enhancer of mRNA-decapping protein 3 (probable)	YES
Fb5:0-35	gene05002	8,58	1,13E-29	3,15E-26	Q7X670_ORYSJ	OSJNBa0093P23.9 protein	Endonuclease (probable)	YES
Fb5:0-35	gene06426	8,79	1,00E-16	6,44E-14	-	-	Signal recognition particle 68 kDa protein (SRP68) (similar to)	YES
Fb5:0-35	gene10011	9,14	9,45E-14	4,20E-11	Q2QM44_ORYSJ	F-box domain containing protein	F-box protein At4g19940 (probable)	YES
Fb5:0-35	gene31775	9,50	8,30E-20	7,04E-17	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At5g61990, mitochondrial, Precursor (probable)	YES
Fb5:0-35	gene09982	10,34	3,28E-12	1,27E-09	C71AK_ARATH	Cytochrome P450 71A20	Cytochrome P450 71A4 (probable)	YES
Fb5:0-35	gene09849	Inf	2,14E-31	1,33E-27	-	-	Parasporal crystal protein cry18Ca (probable)	YES
Fb5:0-35	gene09923	Inf	1,43E-25	2,23E-22	-	-	Probable RNA 3'-terminal phosphate cyclase (RNA-3'-phosphate cyclase)	YES
Fb5:0-35	gene32071	Inf	1,81E-08	4,64E-06	A2ZWE1_ORYSJ	Serine/threonine-protein kinase	Putative receptor protein kinase ZmPK1, Precursor (similar to)	YES
Fb5:50-76	gene02052	-Inf	4,24E-11	7,54E-09	B6IDH6_ARATH	Uncharacterized protein	GP2, Precursor (probable)	NO
Fb5:50-76	gene02210	-Inf	1,94E-08	2,57E-06	-	-	Glutamate-rich WD repeat-containing protein 1 (probable)	YES
Fb5:50-76	gene07728	-Inf	2,05E-04	1,30E-02	Q9SYP1_ARATH	Putative U5 small nuclear ribonucleoprotein helicase	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase (probable)	YES
Fb5:50-76	gene07734	-Inf	3,52E-04	2,07E-02	Q25AF6_ORYSA	H0512B01.8 protein	Endonuclease (probable)	NO
Fb5:50-76	gene07800	-Inf	2,35E-05	1,85E-03	Q0DY33_ORYSJ	cDNA clone:J033045A20, full insert sequence	ADP,ATP carrier protein, mitochondrial (ANT), Precursor (similar to)	YES
Fb5:50-76	gene07802	-Inf	1,31E-03	6,51E-02	-	-	Biotin--[acetyl-CoA-carboxylase] ligase (probable)	YES
Fb5:50-76	gene08904	-Inf	2,14E-36	5,72E-33	RK5_ARATH	50S ribosomal protein L5, chloroplastic	50S ribosomal protein L5, chloroplastic (similar to)	YES
Fb5:50-76	gene08905	-Inf	4,76E-28	4,93E-25	Q9LZ83_ARATH	Putative uncharacterized protein T32M21_20	Zinc finger protein 764 (probable)	YES

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Fb5:50-76	gene08907	-Inf	5,74E-28	5,10E-25	-	-	Protein zerknuellt 1 (ZEN-1) (probable)	NO
Fb5:50-76	gene08927	-Inf	3,10E-16	1,16E-13	-	-	D-arabinono-1,4-lactone oxidase (ALO) (probable)	YES
Fb5:50-76	gene10513	-Inf	2,43E-06	2,32E-04	KCS21_ARATH	3-ketoacyl-CoA synthase 21	Protein bassoon (probable)	YES
Fb5:50-76	gene10664	-Inf	8,95E-08	1,09E-05	-	-	hypothetical protein	YES
Fb5:50-76	gene10700	-Inf	1,07E-25	8,02E-23	AFP1_ARATH	Ninja-family protein AFP1	Villidin (probable)	NO
Fb5:50-76	gene10830	-Inf	8,06E-09	1,13E-06	RL122_ARATH	60S ribosomal protein L12-2	60S ribosomal protein L12 (similar to)	NO
Fb5:50-76	gene10903	-Inf	1,57E-17	6,25E-15	CPR30_ARATH	F-box protein CPR30	UDP-sugar pyrophospharylase (UGGPase) (similar to)	NO
Fb5:50-76	gene10922	-Inf	3,75E-18	1,56E-15	MPK12_ARATH	Mitogen-activated protein kinase 12	Mitogen-activated protein kinase 12 (MAP kinase 12) (probable)	YES
Fb5:50-76	gene11045	-Inf	9,07E-38	2,82E-34	GLYC7_ARATH	Serine hydroxymethyltransferase 7	Serine hydroxymethyltransferase 2 (SHMT 2) (probable)	NO
Fb5:50-76	gene11307	-Inf	8,56E-05	6,10E-03	-	-	hypothetical protein	NO
Fb5:50-76	gene11777	-Inf	1,62E-10	2,72E-08	-	-	Peroxidase 42 (Atperox P42), Precursor (probable)	NO
Fb5:50-76	gene11792	-Inf	2,32E-09	3,43E-07	Q2V359_ARATH	SAUR-like auxin-responsive protein	Auxin-induced protein 6B (similar to)	YES
Fb5:50-76	gene11802	-Inf	1,86E-04	1,20E-02	O23864_9ORYZ	Polyprotein	Endonuclease (probable)	YES
Fb5:50-76	gene11803	-Inf	4,03E-29	5,38E-26	KEULE_ARATH	SNARE-interacting protein KEULE	SNARE-interacting protein KEULE (similar to)	NO
Fb5:50-76	gene11818	-Inf	1,94E-22	1,06E-19	Q9SAJ2_ARATH	T8K14.1 protein	Tyrosine-protein kinase receptor Tie-1, Precursor (probable)	YES
Fb5:50-76	gene11923	-Inf	1,54E-04	1,02E-02	-	-	Protein sidekick homolog, Precursor (probable)	YES
Fb5:50-76	gene11929	-Inf	1,07E-08	1,46E-06	A2Z676_ORYSI	MATE efflux family protein	Protein TRANSPARENT TESTA 12 (probable)	NO
Fb5:50-76	gene11949	-Inf	3,89E-05	2,98E-03	-	-	Tubulin polyglutamylase TTLL4 (probable)	YES
Fb5:50-76	gene12041	-Inf	6,08E-06	5,41E-04	-	-	hypothetical protein	YES
Fb5:50-76	gene12674	-Inf	3,92E-04	2,26E-02	RH21_ARATH	DEAD-box ATP-dependent RNA helicase 21	DEAD-box ATP-dependent RNA helicase 21 (similar to)	NO
Fb5:50-76	gene13497	-Inf	4,48E-09	6,53E-07	A8HWI3_CHLRE	Bardet-biedl syndrome 5 protein	Peripherin (probable)	YES
Fb5:50-76	gene13542	-Inf	3,04E-04	1,83E-02	Q94H40_ORYSJ	Putative reverse transcriptase	hypothetical protein	YES
Fb5:50-76	gene13667	-Inf	1,81E-39	1,13E-35	-	-	Rhophilin-2 (probable)	NO

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Fb5:50-76	gene13740	-Inf	3,55E-05	2,72E-03	Q8S7B7_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Copia protease (probable)	YES
Fb5:50-76	gene16005	-Inf	2,62E-05	2,05E-03	-	-	Phosphatase and actin regulator 4 (probable)	YES
Fb5:50-76	gene16818	-Inf	5,92E-04	3,25E-02	Q9M8R6_ARATH	Putative aspartyl protease	Aspartic proteinase-like protein 2, Precursor (probable)	NO
Fb5:50-76	gene22021	-Inf	2,56E-14	6,92E-12	-	-	Putative adhesin P1-like protein MPN_144 (probable)	YES
Fb5:50-76	gene22102	-Inf	9,19E-05	6,53E-03	EBF2_ARATH	EIN3-binding F-box protein 2	Putative F-box protein At1g47800 (probable)	YES
Fb5:50-76	gene22103	-Inf	1,68E-11	3,07E-09	-	-	Fibulin-2 (FIBL-2), Precursor (probable)	YES
Fb5:50-76	gene22135	-Inf	2,17E-13	5,06E-11	TVP23_ARATH	Golgi apparatus membrane protein-like protein ECHIDNA	hypothetical protein	YES
Fb5:50-76	gene23295	-Inf	2,91E-06	2,78E-04	-	-	227 kDa spindle- and centromere-associated protein (probable)	YES
Fb5:50-76	gene25883	-Inf	1,97E-03	9,20E-02	RPE1_ORYSJ	Ribulose-phosphate 3-epimerase, cytoplasmic isoform	Ribulose-phosphate 3-epimerase, cytoplasmic isoform (PPE) (similar to)	YES
Fb5:50-76	gene26510	-Inf	5,53E-28	5,10E-25	Q94J89_ORYSJ	Uncharacterized protein	Putative disease resistance RPP13-like protein 1 (probable)	NO
Fb5:50-76	gene26523	-Inf	9,32E-10	1,45E-07	-	-	Thermolabile hemolysin (TL), Precursor (probable)	NO
Fb5:50-76	gene26526	-Inf	8,56E-17	3,33E-14	Q656H7_ORYSJ	Putative uncharacterized protein B1012D10.29	Ribosome biogenesis protein ERB1 (probable)	YES
Fb5:50-76	gene26578	-Inf	3,63E-04	2,12E-02	B8BN73_ORYSI	Putative uncharacterized protein	Cell division cycle 5-related protein (probable)	YES
Fb5:50-76	gene26902	-Inf	4,26E-08	5,38E-06	B9GBH0_ORYSJ	Putative uncharacterized protein	Parvalbumin beta (similar to)	NO
Fb5:50-76	gene26930	-Inf	3,14E-08	4,04E-06	-	-	L-fucose isomerase (probable)	YES
Fb5:50-76	gene27071	-Inf	1,02E-05	8,63E-04	Q53N93_ORYSJ	NB-ARC domain, putative	Putative disease resistance protein At1g59780 (probable)	YES
Fb5:50-76	gene27679	-Inf	6,60E-28	5,60E-25	-	-	BEACH domain-containing protein lvsC (probable)	NO
Fb5:50-76	gene27686	-Inf	1,17E-07	1,37E-05	-	-	3-oxo-5-alpha-steroid 4-dehydrogenase 1 (probable)	NO
Fb5:50-76	gene27694	-Inf	3,43E-05	2,65E-03	F4K0G5_ARATH	Uncharacterized protein	WD repeat-containing protein 55 homolog (probable)	NO
Fb5:50-76	gene29153	-Inf	1,06E-07	1,26E-05	-	-	XK-related protein 6 (probable)	NO

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NIL vs. RV	gene id[a]	log$_2$(F Ch)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb5:50-76	gene29184	-Inf	1,22E-04	8,37E-03	LOXC2_ORYSJ	Probable lipoxygenase 8, chloroplastic	Probable lipoxygenase 8, chloroplastic, Precursor (similar to)	NO
Fb5:50-76	gene29258	-Inf	1,33E-19	6,05E-17	Q7X8D0_ORYSJ	OSJNBb0015N08.13 protein	60S ribosomal protein L7 (similar to)	NO
Fb5:50-76	gene29293	-Inf	7,60E-08	9,27E-06	-	-	Transforming acidic coiled-coil-containing protein 3 (probable)	YES
Fb5:50-76	gene29303	-Inf	8,64E-04	4,54E-02	-	-	Cell division control protein 6 homolog (HsCDC6) (probable)	YES
Fb5:50-76	gene29305	-Inf	2,37E-10	3,96E-08	AHK3_ARATH	Histidine kinase 3	Eukaryotic translation initiation factor 3 subunit G-2 (eIF3g-2) (probable)	YES
Fb5:50-76	gene29473	-Inf	1,70E-05	1,37E-03	B9F6L9_ORYSJ	Putative uncharacterized protein	Trichothecene 3-O-acetyltransferase (probable)	YES
Fb5:50-76	gene29943	-Inf	1,77E-09	2,66E-07	Q6K4C3_ORYSJ	Hydroxyproline-rich glycoprotein-like	Coiled-coil domain-containing protein 34 (probable)	YES
Fb5:50-76	gene29944	-Inf	5,32E-06	4,82E-04	Q53MC6_ORYSJ	Transposon protein, putative, CACTA, En/Spm sub-class	Ribulose-phosphate 3-epimerase (PPE) (probable)	YES
Fb5:50-76	gene30007	-Inf	1,87E-23	1,20E-20	Q9STI1_ARATH	Putative flavonoid 3',5'-hydroxylase	Cytochrome P450 93A3 (probable)	NO
Fb5:50-76	gene31496	-Inf	7,07E-13	1,50E-10	-	-	Uptake hydrogenase small subunit, Precursor (probable)	YES
Fb5:50-76	gene34512	-Inf	2,74E-04	1,68E-02	B8AMS6_ORYSI	Putative uncharacterized protein	Protein FAR1-RELATED SEQUENCE 6 (probable)	YES
Fb5:50-76	gene29302	-12,93	1,67E-38	6,23E-35	F4J8C7_ARATH	Phosphoglycerate mutase-like protein	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase (similar to)	NO
Fb5:50-76	gene27680	-11,85	3,12E-48	5,82E-44	-	-	Non-capsid protein NS-1 (probable)	NO
Fb5:50-76	gene25023	-11,67	1,09E-28	1,36E-25	A2Y618_ORYSI	Putative uncharacterized protein	Putative disease resistance RPP13-like protein 1 (probable)	NO
Fb5:50-76	gene26516	-10,38	2,49E-31	3,87E-28	Q25A54_ORYSA	H0613A10.7 protein	Putative F-box/kelch-repeat protein At4g11750 (probable)	YES
Fb5:50-76	gene35152	-10,31	1,11E-38	5,18E-35	-	-	Spidroin-1 (probable)	YES
Fb5:50-76	gene22019	-9,88	6,44E-18	2,61E-15	-	-	Mucin-6 (MUC-6), Precursor (probable)	NO
Fb5:50-76	gene11942	-9,59	1,10E-34	2,57E-31	ISPD_MENPI	(-)-isopiperitenol/(-)-carveol dehydrogenase, mitochondrial	Sex determination protein tasselseed-2 (probable)	NO
Fb5:50-76	gene10882	-9,43	3,60E-44	3,36E-40	Q9LQQ3_ARATH	Putative globulin protein	Glutelin type-A 2 basic chain, Precursor (probable)	YES
Fb5:50-76	gene07791	-9,33	3,01E-33	5,86E-30	-	-	Pentatricopeptide repeat-containing protein At2g31400, chloroplastic, Precursor (probable)	YES

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Fb5:50-76	gene29216	-9,28	6,80E-24	4,54E-21	Q84PX0_ORYSJ	Putative tyrosyl-tRNA synthetase	Tyrosyl-tRNA synthetase, cytoplasmic (TyrRS) (probable)	NO
Fb5:50-76	gene25060	-9,08	3,22E-19	1,40E-16	TT2_ARATH	Transcription factor TT2	Transcription factor TT2 (AtMYB123) (similar to)	NO
Fb5:50-76	gene12017	-8,88	1,80E-29	2,58E-26	CPR30_ARATH	F-box protein CPR30	F-box/kelch-repeat protein At3g23880 (probable)	YES
Fb5:50-76	gene16016	-8,68	1,23E-15	4,04E-13	Q9FKB9_ARATH	TIR-NBS-LRR class disease resistance protein	Ethanolamine utilization protein eutQ (probable)	YES
Fb5:50-76	gene13720	-8,64	5,73E-20	2,67E-17	Q2QWB7_ORYSJ	Transposon protein, putative, CACTA, En/Spm sub-class	Pentatricopeptide repeat-containing protein At1g69290 (similar to)	YES
Fb5:50-76	gene16049	-8,63	5,63E-28	5,10E-25	Q9AYI0_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Copia protease (probable)	YES
Fb5:50-76	gene10500	-8,48	3,71E-12	7,36E-10	-	-	Splicing factor, arginine/serine-rich 19 (SR-A1) (probable)	YES
Fb5:50-76	gene26809	-8,45	2,26E-12	4,59E-10	B9G0A3_ORYSJ	Putative uncharacterized protein	Cytochrome b (probable)	NO
Fb5:50-76	gene10832	-8,40	2,15E-19	9,58E-17	-	-	GTP-binding protein lepA (probable)	YES
Fb5:50-76	gene31303	-8,10	1,68E-14	4,76E-12	-	-	Serine/threonine-protein kinase unc-51 (probable)	NO
Fb5:50-76	gene08975	-7,96	2,52E-25	1,81E-22	C7254_GLYUR	11-oxo-beta-amyrin 30-oxidase	Secologanin synthase (SLS) (probable)	NO
Fb5:50-76	gene25083	-7,53	7,78E-04	4,13E-02	F4I403_ARATH	12-oxophytodienoate reductase 1	12-oxophytodienoate reductase 1 (OPDA-reductase 1) (similar to)	NO
Fb5:50-76	gene10887	-7,30	8,51E-14	2,18E-11	-	-	Retrotransposable element SLACS 45 kDa protein (probable)	NO
Fb5:50-76	gene31523	-7,30	9,36E-26	7,28E-23	B8A6W1_ORYSI	Putative uncharacterized protein	Glutathione S-transferase P (probable)	NO
Fb5:50-76	gene10852	-7,29	3,82E-12	7,51E-10	-	-	Probable monogalactosyldiacylglycerol synthase 3, chloroplastic (OsMGD3), Precursor	YES
Fb5:50-76	gene26517	-7,25	3,28E-28	3,60E-25	-	-	D-alanine--D-alanine ligase (probable)	NO
Fb5:50-76	gene26581	-7,22	4,18E-06	3,85E-04	Q9STV1_ARATH	Rhamnogalacturonate lyase family protein	Rhamnogalacturonate lyase (Rhamnogalacturonase), Precursor (probable)	NO
Fb5:50-76	gene16007	-7,21	6,85E-13	1,47E-10	F4IBR2_ARATH	Uncharacterized protein	hypothetical protein	YES
Fb5:50-76	gene26927	-7,11	2,35E-14	6,53E-12	Q9T069_ARATH	Uncharacterized protein	Cytospin-A-A (probable)	NO
Fb5:50-76	gene26901	-7,11	2,64E-25	1,82E-22	TBA6_ARATH	Tubulin alpha-6 chain	Tubulin alpha-1 chain (similar to)	NO
Fb5:50-76	gene34685	-7,03	6,73E-06	5,90E-04	Q7XVK6_ORYSJ	OSJNBa0069D17.8 protein	Probable disease resistance protein At5g66900	NO

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Fb5:50-76	gene13668	-6,99	2,42E-28	2,83E-25	B8B1L2_ORYSI	Putative uncharacterized protein	5'-AMP-activated protein kinase subunit gamma-3 (AMPK gamma-3 chain) (probable)	YES
Fb5:50-76	gene08915	-6,80	3,30E-15	1,03E-12	B8B1U9_ORYSI	Putative uncharacterized protein	Shugoshin-2 (probable)	NO
Fb5:50-76	gene10831	-6,65	1,03E-08	1,42E-06	-	-	Myb-like protein X (probable)	YES
3886	gene12094	-6,59	7,53E-12	1,41E-09	STPS1_SANAL	Sesquiterpene synthase	(+)-delta-cadinene synthase isozyme A (D-cadinene synthase A) (probable)	NO
Fb5:50-76	gene01616	-6,52	2,61E-08	3,43E-06	F4IBR2_ARATH	Uncharacterized protein	Proteasome subunit alpha type-7-B (similar to)	YES
Fb5:50-76	gene30030	-6,50	4,03E-07	4,35E-05	Q53JM7_ORYSJ	Os11g0251200 protein	Ankyrin repeat-containing protein At3g12360 (probable)	YES
Fb5:50-76	gene28678	-6,36	3,71E-16	1,36E-13	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	NO
Fb5:50-76	gene29117	-6,33	4,97E-05	3,73E-03	Q8S6P1_ORYSJ	Putative reverse transcriptase	Putative ribonuclease H protein At1g65750 (probable)	YES
Fb5:50-76	gene16053	-6,31	4,56E-15	1,40E-12	F4HR53_ARATH	Transmembrane receptors / ATP binding protein	TMV resistance protein N (probable)	NO
Fb5:50-76	gene15264	-6,31	4,53E-09	6,55E-07	Q0IR45_ORYSJ	Os11g0681400 protein	Protein FAR-RED IMPAIRED RESPONSE 1 (probable)	NO
Fb5:50-76	gene31465	-6,25	1,22E-22	7,11E-20	O22809_ARATH	Putative cinnamoyl-CoA reductase	Dihydroflavonol-4-reductase (DFR) (probable)	NO
Fb5:50-76	gene11010	-6,19	6,31E-06	5,55E-04	Q84R17_ARATH	Uncharacterized protein	DNA-binding protein REB1 (probable)	NO
Fb5:50-76	gene11941	-6,10	1,24E-08	1,68E-06	GSXL2_ARATH	Flavin-containing monooxygenase FMO GS-OX-like 2	Flavin-containing monooxygenase FMO GS-OX5 (similar to)	NO
Fb5:50-76	gene26444	-6,00	5,35E-07	5,61E-05	FBK67_ARATH	F-box/kelch-repeat protein At3g23880	F-box/kelch-repeat protein At3g23880 (probable)	NO
Fb5:50-76	gene27274	-5,93	2,56E-04	1,60E-02	Q8H957_ORYSJ	A protein	hypothetical protein	YES
Fb5:50-76	gene16022	-5,83	8,51E-21	4,30E-18	Q5SN79_ORYSJ	cDNA clone:J013158F22, full insert sequence	4'-phosphopantetheinyl transferase hetI (probable)	YES
Fb5:50-76	gene02293	-5,61	3,07E-07	3,35E-05	B8ACK0_ORYSI	Putative uncharacterized protein	Probable anion transporter 1, chloroplastic, Precursor (similar to)	YES
Fb5:50-76	gene22124	-5,53	9,13E-11	1,56E-08	Q9C9S1_ARATH	Uncharacterized protein	NADH-ubiquinone oxidoreductase 75 kDa subunit (CI-75kD) (probable)	YES
Fb5:50-76	gene27676	-5,49	5,84E-05	4,29E-03	Q9AV68_ORYSJ	Putative gag-pol	UPF0374 protein GK0468 (probable)	YES

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Fb5:50-76	gene25089	-5,36	5,75E-08	7,11E-06	F4I403_ARATH	12-oxophytodienoate reductase 1	12-oxophytodienoate reductase 1 (OPDA-reductase 1) (similar to)	NO
Fb5:50-76	gene29257	-5,33	8,08E-09	1,13E-06	Q9LQP1_ARATH	Putative uncharacterized protein At1g07645/F24B9_23	Apolipoprotein B-48, Precursor (probable)	YES
Fb5:50-76	gene13678	-5,26	3,07E-20	1,51E-17	-	-	Casein kinase I isoform delta-like (CKI-delta) (similar to)	NO
Fb5:50-76	gene29306	-5,24	1,05E-13	2,60E-11	B8ARQ3_ORYSI	Putative uncharacterized protein	Spermidine synthase (PAPT) (probable)	YES
Fb5:50-76	gene29307	-5,19	3,30E-13	7,52E-11	Q9AT60_ARATH	TLD-domain containing nucleolar protein	Putative vacuolar protein sorting-associated protein 13F (probable)	YES
Fb5:50-76	gene29146	-5,14	1,95E-03	9,13E-02	O22807_ARATH	Uncharacterized protein	Keratin-associated protein 10-7 (probable)	NO
Fb5:50-76	gene16021	-5,14	6,88E-16	2,42E-13	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (probable)	NO
Fb5:50-76	gene25316	-5,13	4,81E-13	1,07E-10	B9G602_ORYSJ	Putative uncharacterized protein	Copia protease (probable)	NO
Fb5:50-76	gene10712	-5,07	1,85E-12	3,87E-10	LOL1_ARATH	Protein LOL1	Metacaspase-1 (AtMCP1b) (probable)	YES
Fb5:50-76	gene13722	-5,07	9,98E-05	6,93E-03	Q8LDS7_ARATH	Protein B-cell receptor-associated 31-like protein	VHS domain-containing protein At3g16270 (similar to)	YES
Fb5:50-76	gene22134	-5,03	4,56E-05	3,46E-03	CCR4A_ARATH	Carbon catabolite repressor protein 4 homolog 1	Carbon catabolite repressor protein 4 homolog 1 (CCR4 homolog 1) (probable)	YES
Fb5:50-76	gene22140	-4,90	1,11E-07	1,30E-05	Y4885_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g08850	Probable leucine-rich repeat receptor-like protein kinase At1g35710, Precursor	NO
Fb5:50-76	gene08926	-4,85	7,53E-08	9,25E-06	RPS2_ARATH	Disease resistance protein RPS2	Probable disease resistance protein At1g61190	YES
Fb5:50-76	gene11943	-4,82	1,13E-15	3,76E-13	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	NO
Fb5:50-76	gene12166	-4,79	4,30E-11	7,57E-09	-	-	E3 ubiquitin-protein ligase UPL2 (Ubiquitin-protein ligase 2) (probable)	YES
Fb5:50-76	gene13511	-4,69	9,90E-08	1,18E-05	B9FQJ3_ORYSJ	Putative uncharacterized protein	Putative ribonuclease H protein At1g65750 (probable)	YES
Fb5:50-76	gene10669	-4,64	1,71E-11	3,09E-09	FRS1_ARATH	Protein FAR1-RELATED SEQUENCE 1	Protein FAR1-RELATED SEQUENCE 11 (probable)	YES
Fb5:50-76	gene16004	-4,59	9,12E-10	1,43E-07	BXL4_ARATH	Beta-D-xylosidase 4	Beta-D-xylosidase 4 (AtBXL4), Precursor (similar to)	NO
Fb5:50-76	gene22017	-4,54	1,18E-05	9,72E-04	Q8VYB9_ARATH	Transcription factor jumonji (JmjC) domain-containing protein	Lysine-specific demethylase 3B (probable)	YES

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Fb5:50-76	gene11069	-4,54	1,70E-15	5,37E-13	B8AXS8_ORYSI	Putative uncharacterized protein	ABC transporter G family member 23 (ABC transporter ABCG.23) (similar to)	NO
Fb5:50-76	gene20480	-4,50	9,16E-07	9,30E-05	A2WV77_ORYSI	Putative uncharacterized protein	Protein HPH1 (probable)	NO
Fb5:50-76	gene02308	-4,49	1,10E-03	5,61E-02	Q93W91_ARATH	Putative uncharacterized protein At3g62550	Universal stress protein A-like protein (similar to)	YES
Fb5:50-76	gene00485	-4,45	1,00E-14	2,88E-12	Q0J8E8_ORYSJ	Os08g0116400 protein	Calcium-transporting ATPase 10, plasma membrane-type (similar to)	NO
Fb5:50-76	gene03924	-4,45	4,17E-04	2,38E-02	B8A748_ORYSI	Pectinesterase	Pectinesterase 36 (PE 36), Precursor (similar to)	NO
Fb5:50-76	gene12100	-4,44	6,25E-14	1,62E-11	REN1_ARATH	Rho GTPase-activating protein REN1	Rho GTPase-activating protein 15 (probable)	YES
Fb5:50-76	gene28675	-4,41	4,06E-04	2,33E-02	F4I2E4_ARATH	RNA recognition motif-containing protein	RNA-binding protein 24 (similar to)	YES
Fb5:50-76	gene33866	-4,41	7,81E-04	4,13E-02	B8A6T5_ORYSI	Putative uncharacterized protein	Pre-mRNA-splicing factor SYF1 (probable)	NO
Fb5:50-76	gene29267	-4,40	1,29E-13	3,10E-11	Q9FZ25_ARATH	Putative chitinase	Chitinase 10, Precursor (similar to)	NO
Fb5:50-76	gene11780	-4,38	4,07E-07	4,37E-05	Q67Z40_ARATH	Putative uncharacterized protein At1g54330	NAC domain-containing protein 74 (ONAC074) (probable)	YES
Fb5:50-76	gene22092	-4,36	2,98E-07	3,29E-05	NAC2_ARATH	NAC domain-containing protein 2	NAC domain-containing protein 2 (ANAC002) (probable)	YES
Fb5:50-76	gene20479	-4,28	1,40E-10	2,38E-08	B8B2V5_ORYSI	Putative uncharacterized protein	Histidine-rich glycoprotein, Precursor (probable)	NO
Fb5:50-76	gene12150	-4,27	9,05E-12	1,67E-09	FAOMT_VITVI	Flavonoid 3',5'-methyltransferase	Putative caffeoyl-CoA O-methyltransferase At1g67980 (CCoAOMT)	YES
Fb5:50-76	gene12163	-4,25	5,39E-15	1,62E-12	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At2g32630 (probable)	YES
Fb5:50-76	gene28669	-4,25	5,72E-05	4,22E-03	Q53JM7_ORYSJ	Os11g0251200 protein	Ankyrin repeat-containing protein At3g12360 (probable)	YES
Fb5:50-76	gene35104	-4,23	8,96E-06	7,71E-04	-	-	Lysyl-tRNA synthetase (LysRS) (probable)	NO
Fb5:50-76	gene02270	-4,21	2,11E-05	1,67E-03	-	-	Ribonucleoside-diphosphate reductase subunit alpha (probable)	YES
Fb5:50-76	gene28659	-4,18	3,63E-14	9,68E-12	14310_ARATH	14-3-3-like protein GF14 epsilon	14-3-3 protein 7 (similar to)	NO
Fb5:50-76	gene31419	-4,17	5,39E-05	3,99E-03	-	-	rRNA-processing protein EFG1 (probable)	YES

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Fb5:50-76	gene26895	-4,14	2,70E-04	1,67E-02	BH093_ARATH	Transcription factor bHLH93	Transcription factor bHLH93 (bHLH 93) (similar to)	YES
Fb5:50-76	gene18184	-4,11	6,00E-04	3,28E-02	Q8S6N1_ORYSJ	Putative gag-pol polyprotein	Protein P200 (probable)	YES
Fb5:50-76	gene13541	-4,10	5,32E-13	1,15E-10	PILR1_FORIN	Bifunctional pinoresinol-lariciresinol reductase	Isoflavone reductase homolog (similar to)	NO
Fb5:50-76	gene10492	-4,10	3,70E-14	9,72E-12	CLPB1_ORYSJ	Chaperone protein ClpB1	Heat shock protein 101 (probable)	NO
Fb5:50-76	gene29221	-4,10	4,37E-05	3,33E-03	A2Y2W3_ORYSI	Putative uncharacterized protein	30S ribosomal protein S4 (probable)	YES
Fb5:50-76	gene03790	-4,05	1,63E-09	2,48E-07	Q5XVE2_ARATH	Minichromosome maintenance protein 10	Protein MCM10 homolog (probable)	YES
Fb5:50-76	gene11812	-4,04	4,01E-08	5,09E-06	Q9SYP1_ARATH	Putative U5 small nuclear ribonucleoprotein helicase	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase (probable)	NO
Fb5:50-76	gene30005	-3,95	1,27E-04	8,62E-03	Y4885_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g08850	Probable LRR receptor-like serine/threonine-protein kinase At4g08850, Precursor	NO
Fb5:50-76	gene11050	-3,95	1,10E-13	2,70E-11	Q9SII1_ARATH	Putative uncharacterized protein At2g38800	Mitochondrial intermembrane space import and assembly protein 40, Precursor (probable)	YES
Fb5:50-76	gene26445	-3,90	3,04E-08	3,94E-06	Q8H1R1_ARATH	Rossmann-fold NAD(P)-binding domain-containing protein	Dihydroflavonol-4-reductase (DFR) (probable)	NO
Fb5:50-76	gene11786	-3,87	5,06E-12	9,83E-10	PPA15_ARATH	Purple acid phosphatase 15	Purple acid phosphatase 23, Precursor (similar to)	NO
Fb5:50-76	gene12172	-3,87	4,51E-07	4,78E-05	WEX_ARATH	Werner Syndrome-like exonuclease	Probable exonuclease mut-7 homolog	YES
Fb5:50-76	gene12161	-3,81	3,12E-13	7,18E-11	Q9SVY0_ARATH	DNA-directed RNA polymerase	DNA-directed RNA polymerase I subunit rpa1 (RNA polymerase I subunit A1) (probable)	YES
Fb5:50-76	gene29298	-3,70	8,92E-07	9,10E-05	SKIP1_ARATH	F-box protein SKIP1	F-box protein SKIP1 (probable)	YES
Fb5:50-76	gene11025	-3,68	4,01E-10	6,62E-08	CPSF3_ARATH	Cleavage and polyadenylation specificity factor subunit 3-I	Cleavage and polyadenylation specificity factor subunit 3 (CPSF 73 kDa subunit) (probable)	NO
Fb5:50-76	gene28658	-3,67	1,14E-05	9,44E-04	Q9LTW4_ARATH	Chloroplast nucleoid DNA binding protein-like	Aspartic proteinase nepenthesin-2, Precursor (probable)	NO
Fb5:50-76	gene13917	-3,53	7,54E-12	1,41E-09	Q9T0J2_ARATH	SAUR-like auxin-responsive protein	Indole-3-acetic acid-induced protein ARG7 (similar to)	NO
Fb5:50-76	gene22138	-3,52	3,65E-04	2,13E-02	ANXD1_ARATH	Annexin D1	Annexin D1 (similar to)	NO

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NIL vs. RV	gene id[a]	log$_2$(F Ch)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb5:50-76	gene31457	-3,50	6,14E-06	5,43E-04	NFYB3_ARATH	Nuclear transcription factor Y subunit B-3	Nuclear transcription factor Y subunit B-3 (AtNF-YB-3) (similar to)	YES
Fb5:50-76	gene12164	-3,47	2,10E-09	3,13E-07	F4IBK8_ARATH	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Lupus brain antigen 1 homolog (probable)	YES
Fb5:50-76	gene10539	-3,46	4,37E-04	2,47E-02	LEC2_ARATH	B3 domain-containing transcription factor LEC2	B3 domain-containing transcription factor LEC2 (similar to)	YES
Fb5:50-76	gene10916	-3,43	1,42E-03	7,02E-02	Q0D8G3_ORYSJ	Serine/threonine-protein kinase RIO1	Serine/threonine-protein kinase RIO1 (RIO kinase 1) (probable)	YES
Fb5:50-76	gene08874	-3,42	2,45E-04	1,53E-02	-	-	RNA-binding protein 27 (probable)	NO
Fb5:50-76	gene27093	-3,40	1,65E-05	1,34E-03	GXM2_ARATH	Glucuronoxylan 4-O-methyltransferase 2	UvrABC system protein C (Protein uvrC) (probable)	NO
Fb5:50-76	gene29217	-3,40	1,94E-03	9,13E-02	Q6AUI1_ORYSJ	cDNA clone:J033023F07, full insert sequence	Cytochrome b mRNA maturase bI3 (probable)	NO
Fb5:50-76	gene13914	-3,39	6,04E-10	9,89E-08	Q9SKP3_ARATH	SAUR-like auxin-responsive protein	Indole-3-acetic acid-induced protein ARG7 (putative)	NO
Fb5:50-76	gene16057	-3,35	1,04E-08	1,42E-06	ARFQ_ARATH	Auxin response factor 17	Auxin response factor 17 (probable)	NO
Fb5:50-76	gene29337	-3,25	7,33E-10	1,16E-07	F4HWD0_ARATH	Uncharacterized protein	F-box/kelch-repeat protein At3g24760 (probable)	NO
Fb5:50-76	gene27697	-3,24	3,19E-06	3,00E-04	Q6YVK6_ORYSJ	cDNA clone:J013158P10, full insert sequence	Protein notum homolog, Precursor (probable)	NO
Fb5:50-76	gene25080	-3,16	7,69E-05	5,52E-03	F4I403_ARATH	12-oxophytodienoate reductase 1	12-oxophytodienoate reductase 1 (OPDA-reductase 1) (similar to)	NO
Fb5:50-76	gene11808	-3,11	4,66E-09	6,64E-07	ARF5_ARATH	ADP-ribosylation factor-like protein 2	Probable ADP-ribosylation factor At2g18390 (similar to)	YES
Fb5:50-76	gene16017	-3,09	1,73E-05	1,39E-03	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (similar to)	NO
Fb5:50-76	gene11984	-3,06	2,93E-04	1,77E-02	B8ALJ7_ORYSI	Putative uncharacterized protein	Nucleocapsid protein p15-gag (similar to)	NO
Fb5:50-76	gene10863	-3,04	1,11E-03	5,64E-02	C7A14_ARATH	Cytochrome P450 72A14	Secologanin synthase (SLS) (putative)	YES
Fb5:50-76	gene10881	-3,01	3,01E-09	4,43E-07	A2XJZ9_ORYSI	Putative uncharacterized protein	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P (similar to)	NO
Fb5:50-76	gene29276	-2,92	1,84E-04	1,19E-02	ATB14_ARATH	Homeobox-leucine zipper protein ATHB-14	StAR-related lipid transfer protein 5 (StARD5) (probable)	NO
Fb5:50-76	gene26561	-2,90	7,22E-07	7,53E-05	Q75HV1_ORYSJ	Kinesin-like protein	Kinesin-4 (probable)	NO

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb5:50-76	gene31421	-2,87	1,01E-03	5,20E-02	Y5537_ARATH	G-type lectin S-receptor-like serine/threonine-protein kinase At5g35370	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 (LH3), Precursor (probable)	NO
Fb5:50-76	gene12155	-2,87	3,25E-08	4,15E-06	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At5g61990, mitochondrial, Precursor (probable)	NO
Fb5:50-76	gene25664	-2,84	3,50E-06	3,27E-04	Q7EZJ0_ORYSJ	Putative ubiquitin-specific protease	Ubiquitin carboxyl-terminal hydrolase 12 (AtUBP12) (probable)	YES
Fb5:50-76	gene26576	-2,84	1,98E-06	1,92E-04	GWD2_ARATH	Alpha-glucan water dikinase 2	Alpha-glucan water dikinase 2, Precursor (probable)	NO
Fb5:50-76	gene16479	-2,83	1,44E-03	7,07E-02	B9RYP6_RICCO	Heat shock protein, putative	Luminal-binding protein 3 (BiP3), Precursor (probable)	YES
Fb5:50-76	gene13918	-2,83	1,81E-07	2,06E-05	Q9T0J2_ARATH	SAUR-like auxin-responsive protein	Indole-3-acetic acid-induced protein ARG7 (similar to)	NO
Fb5:50-76	gene12086	-2,82	1,25E-05	1,02E-03	LAC9_ORYSJ	Putative laccase-9	Putative laccase-9, Precursor (probable)	NO
Fb5:50-76	gene26432	-2,81	1,56E-06	1,54E-04	AGL16_ARATH	Agamous-like MADS-box protein AGL16	MADS-box transcription factor 27 (similar to)	YES
Fb5:50-76	gene07742	-2,80	3,12E-04	1,87E-02	Y4361_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g36180	Probable LRR receptor-like serine/threonine-protein kinase At4g36180, Precursor (putative)	YES
Fb5:50-76	gene11770	-2,79	1,12E-05	9,36E-04	A2X8V6_ORYSI	Putative uncharacterized protein	Chromosomal replication initiator protein dnaA (probable)	NO
Fb5:50-76	gene13498	-2,76	1,32E-07	1,53E-05	PHSB_ARATH	Probable polyamine transporter At1g31830	hypothetical protein	NO
Fb5:50-76	gene10535	-2,70	9,78E-08	1,18E-05	RAH1B_ARATH	Ras-related protein RABH1b	Ras-related protein RABH1B (similar to)	YES
Fb5:50-76	gene29203	-2,69	2,33E-07	2,59E-05	B9GBH0_ORYSJ	Putative uncharacterized protein	Putative ribonuclease H protein At1g65750 (probable)	NO
Fb5:50-76	gene11036	-2,68	3,03E-07	3,33E-05	F4IK92_ARATH	ARM repeat superfamily protein	Glucoamylase GLA1, Precursor (probable)	YES
Fb5:50-76	gene12167	-2,67	1,78E-04	1,16E-02	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At2g26790, mitochondrial, Precursor (probable)	NO
Fb5:50-76	gene30014	-2,60	1,68E-07	1,93E-05	Q0JCR9_ORYSJ	Os04g0452700 protein	Sugar transport protein 5 (putative)	NO
Fb5:50-76	gene08930	-2,59	1,66E-06	1,63E-04	A2ZKN4_ORYSI	Putative uncharacterized protein	Probable disease resistance protein At4g27220	YES
Fb5:50-76	gene27193	-2,59	6,31E-04	3,45E-02	FB135_ARATH	F-box protein At3g07870	F-box protein At3g07870 (probable)	YES

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Fb5:50-76	gene30073	-2,57	7,41E-04	3,95E-02	Q9LIZ8_ORYSJ	Uncharacterized protein	Probable glutamyl-tRNA synthetase, cytoplasmic (GluRS)	YES
Fb5:50-76	gene17765	-2,57	6,04E-05	4,42E-03	IDD8_ARATH	Zinc finger protein NUTCRACKER	Zinc finger protein NUTCRACKER (putative)	YES
Fb5:50-76	gene10508	-2,56	7,74E-04	4,12E-02	PYR1_ARATH	Abscisic acid receptor PYR1	Ribulose bisphosphate carboxylase (RuBisCO) (probable)	YES
Fb5:50-76	gene30023	-2,54	3,13E-04	1,87E-02	Q7XI45_ORYSJ	cDNA clone:006-211-F03, full insert sequence	Protein piccolo (probable)	NO
Fb5:50-76	gene13545	-2,51	1,52E-06	1,51E-04	F4KEK2_ARATH	Homeodomain-like superfamily protein	Myb family transcription factor APL (AtAPL) (probable)	YES
Fb5:50-76	gene18559	-2,47	4,16E-06	3,85E-04	B9FFZ6_ORYSJ	Putative uncharacterized protein	Serine/threonine-protein phosphatase PP1 (probable)	YES
Fb5:50-76	gene08940	-2,47	1,30E-04	8,80E-03	B8ASV0_ORYSI	Putative uncharacterized protein	Glycogenin-2 (GN-2) (probable)	NO
Fb5:50-76	gene08860	-2,47	3,95E-06	3,67E-04	-	-	Serine/threonine-protein phosphatase 1 regulatory subunit 10 (Protein PNUTS) (probable)	NO
Fb5:50-76	gene10530	-2,44	1,08E-03	5,56E-02	F4KIF3_ARATH	TIR-NBS-LRR class disease resistance protein	Probable WRKY transcription factor 19	YES
Fb5:50-76	gene02207	-2,41	2,88E-04	1,75E-02	A2ZAJ4_ORYSI	Uncharacterized protein	Adenosine monophosphate-protein transferase FICD homolog (probable)	NO
Fb5:50-76	gene11788	-2,39	3,66E-04	2,13E-02	ESP1_ARATH	Separase	Separin (probable)	YES
Fb5:50-76	gene26881	-2,35	2,95E-06	2,80E-04	I7GT1_SOYBN	Isoflavone 7-O-glucosyltransferase 1	Anthocyanidin 5,3-O-glucosyltransferase (probable)	YES
Fb5:50-76	gene13515	-2,32	1,89E-03	8,92E-02	PMTK_ARATH	Probable methyltransferase PMT20	Sterol 24-C-methyltransferase (probable)	YES
Fb5:50-76	gene11901	-2,32	4,21E-06	3,85E-04	Q8RWT8_ARATH	Seryl-tRNA synthetase	Seryl-tRNA synthetase (SerRS) (probable)	NO
Fb5:50-76	gene13915	-2,31	1,94E-04	1,24E-02	Q9T0J2_ARATH	SAUR-like auxin-responsive protein	Indole-3-acetic acid-induced protein ARG7 (similar to)	YES
Fb5:50-76	gene26880	-2,29	1,71E-04	1,12E-02	BH080_ARATH	Transcription factor bHLH80	Transcription factor bHLH80 (bHLH 80) (probable)	YES
Fb5:50-76	gene26542	-2,26	5,16E-05	3,86E-03	Q9LVA1_ARATH	No apical meristem family protein	NAC domain-containing protein 7 (ANAC007) (probable)	YES
Fb5:50-76	gene30102	-2,24	1,66E-04	1,10E-02	Q9SJQ1_ARATH	Putative receptor-like protein kinase	Probable inactive receptor kinase At2g26730, Precursor	NO

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Fb5:50-76	gene16081	-2,23	9,19E-06	7,87E-04	F4JK17_ARATH	Cofactor-independent phosphoglycerate mutase	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 (Phosphoglyceromutase 1) (probable)	NO
Fb5:50-76	gene08889	-2,22	2,96E-04	1,78E-02	ACCH1_ARATH	1-aminocyclopropane-1-carboxylate oxidase homolog 1	Deacetoxyvindoline 4-hydroxylase (similar to)	NO
Fb5:50-76	gene12020	-2,21	6,82E-06	5,95E-04	-	-	Lateral signaling target protein 2 homolog (probable)	YES
Fb5:50-76	gene10735	-2,20	1,07E-05	8,99E-04	SPZX_ARATH	Serpin-ZX	Serpin-ZX (probable)	NO
Fb5:50-76	gene26913	-2,18	3,34E-04	1,97E-02	AAP6_ARATH	Amino acid permease 6	Amino acid permease 6 (putative)	NO
Fb5:50-76	gene04502	-2,16	2,40E-04	1,52E-02	A2XE87_ORYSI	Putative uncharacterized protein	Phytosulfokine-beta, Precursor (similar to)	NO
Fb5:50-76	gene10883	-2,12	3,42E-05	2,65E-03	3HID1_ARATH	Probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial	hypothetical protein	NO
Fb5:50-76	gene34480	-2,07	1,46E-03	7,11E-02	Q940I0_ARATH	Putative uncharacterized protein At4g17950 T6K21.130	Transcription factor IIIB 70 kDa subunit (TFIIIB) (probable)	NO
Fb5:50-76	gene29334	-2,07	6,94E-04	3,73E-02	Q9FXB0_ARATH	Protein SMALLER WITH VARIABLE BRANCHES	hypothetical protein	NO
Fb5:50-76	gene26550	-2,07	2,07E-05	1,65E-03	Q655G6_ORYSJ	Putative uncharacterized protein P0009H10.11	Translation initiation factor IF-2 (probable)	YES
Fb5:50-76	gene12033	-2,04	7,05E-05	5,08E-03	CAP16_ARATH	Putative clathrin assembly protein At4g40080	Putative clathrin assembly protein At4g40080 (probable)	YES
Fb5:50-76	gene31424	-2,04	5,28E-05	3,93E-03	F4JCS8_ARATH	BAH and TFIIS domain-containing protein	Protein SCD5 (probable)	YES
Fb5:50-76	gene26830	-2,03	6,53E-05	4,76E-03	IAA8_ARATH	Auxin-responsive protein IAA8	Auxin-responsive protein IAA8 (similar to)	YES
Fb5:50-76	gene25321	-1,95	1,52E-03	7,36E-02	REF6_ARATH	Lysine-specific demethylase REF6	Lysine-specific demethylase 5D (similar to)	YES
Fb5:50-76	gene31325	-1,93	1,44E-03	7,07E-02	CYP59_ARATH	Peptidyl-prolyl cis-trans isomerase CYP59	Protein translocase subunit secA 1 (probable)	YES
Fb5:50-76	gene31320	-1,90	1,19E-03	6,01E-02	-	-	Acidic leucine-rich nuclear phosphoprotein 32 family member E (probable)	NO
Fb5:50-76	gene13105	-1,88	5,23E-04	2,90E-02	A2X344_ORYSI	Putative uncharacterized protein	General transcription factor IIF subunit 1 (TFIIF-alpha) (probable)	YES
Fb5:50-76	gene26938	-1,88	1,31E-04	8,82E-03	Q84JG6_ARATH	TPX2 (Targeting protein for Xklp2) family protein	LisH domain-containing protein C1711.05 (probable)	NO

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Fb5:50-76	gene13768	-1,87	1,23E-04	8,41E-03	Q9SKP3_ARATH	SAUR-like auxin-responsive protein	Indole-3-acetic acid-induced protein ARG7 (similar to)	NO
Fb5:50-76	gene05292	-1,83	4,48E-04	2,52E-02	A3B881_ORYSJ	Putative uncharacterized protein	Putative tetratricopeptide repeat protein 3-like (probable)	YES
Fb5:50-76	gene30450	-1,83	9,88E-04	5,14E-02	A2WXJ8_ORYSI	Putative uncharacterized protein	hypothetical protein	YES
Fb5:50-76	gene02296	-1,82	1,26E-04	8,61E-03	F4I4Y6_ARATH	P-loop containing nucleoside triphosphate hydrolases superfamily protein	ATPase family AAA domain-containing protein 1-B (probable)	NO
Fb5:50-76	gene02288	-1,78	2,88E-04	1,75E-02	Q7XC13_ORYSJ	Putative uncharacterized protein OSJNBa0057L21.4	Putative F-box protein At1g47790 (probable)	YES
Fb5:50-76	gene02234	-1,75	1,28E-03	6,39E-02	ARFQ_ARATH	Auxin response factor 17	Auxin response factor 17 (probable)	NO
Fb5:50-76	gene13770	-1,72	3,81E-04	2,21E-02	Q9T0J2_ARATH	SAUR-like auxin-responsive protein	Indole-3-acetic acid-induced protein ARG7 (similar to)	NO
Fb5:50-76	gene31420	-1,71	6,73E-04	3,64E-02	AB26B_ARATH	ABC transporter B family member 26, chloroplastic	ABC transporter B family member 26, chloroplastic (ABC transporter ABCB.26), Precursor (similar to)	NO
Fb5:50-76	gene29099	-1,69	6,49E-04	3,52E-02	Q8GWG0_ARATH	Putative uncharacterized protein At5g60620/mup24_30	Glycerol-3-phosphate acyltransferase 3 (GPAT3) (probable)	NO
Fb5:50-76	gene10417	-1,65	1,14E-03	5,78E-02	DHE1_ARATH	Glutamate dehydrogenase 1	Glutamate dehydrogenase 1 (GDH 1) (putative)	YES
Fb5:50-76	gene01234	-1,56	1,72E-03	8,20E-02	GUN7_ORYSJ	Endoglucanase 7	Endoglucanase 11, Precursor (similar to)	NO
Fb5:50-76	gene22106	-1,56	1,04E-03	5,37E-02	A8MQN4_ARATH	Calcineurin-like metallo-phosphoesterase superfamily protein	Metallophosphoesterase 1 (probable)	YES
Fb5:50-76	gene07812	-1,55	1,49E-03	7,24E-02	MAP22_ARATH	Methionine aminopeptidase 2B	Methionine aminopeptidase 2B (MetAP 2B) (similar to)	NO
Fb5:50-76	gene10716	-1,49	1,21E-03	6,06E-02	PIRL5_ORYSJ	Plant intracellular Ras-group-related LRR protein 5	Leucine-rich repeat-containing protein 1 (probable)	NO
Fb5:50-76	gene20865	-1,46	2,12E-03	9,79E-02	BLH9_ARATH	BEL1-like homeodomain protein 9	BEL1-like homeodomain protein 9 (BEL1-like protein 9) (probable)	NO
Fb5:50-76	gene03607	1,46	2,11E-03	9,78E-02	Q9SIS4_ARATH	Putative inositol polyphosphate-5-phosphatase	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (similar to)	NO
Fb5:50-76	gene12079	1,48	1,62E-03	7,78E-02	BH145_ARATH	Transcription factor bHLH145	Transcription factor bHLH143 (bHLH 143) (probable)	NO
Fb5:50-76	gene10518	1,51	1,87E-03	8,85E-02	F4KHI7_ARATH	Uncharacterized protein	Inner nuclear membrane protein HEH2 (probable)	NO

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Fb5:50-76	gene26838	1,51	1,68E-03	8,02E-02	HEM11_ARATH	Glutamyl-tRNA reductase 1, chloroplastic	Glutamyl-tRNA reductase 1, chloroplastic (GluTR), Precursor (putative)	YES
Fb5:50-76	gene29243	1,52	1,86E-03	8,83E-02	O80456_ARATH	Uncharacterized protein	Conserved oligomeric Golgi complex subunit 7 (COG complex subunit 7) (probable)	YES
Fb5:50-76	gene22136	1,52	1,34E-03	6,62E-02	Q9SMR7_ARATH	Uncharacterized protein	FACT complex subunit SSRP1-A (probable)	YES
Fb5:50-76	gene31596	1,57	1,08E-03	5,53E-02	Q94D04_ORYSJ	Putative p40	Rab9 effector protein with Kelch motifs (probable)	YES
Fb5:50-76	gene13534	1,59	2,09E-03	9,69E-02	Q94F50_ARATH	Uncharacterized protein	Glyceraldehyde-3-phosphate dehydrogenase, chloroplastic, Precursor (probable)	NO
Fb5:50-76	gene26876	1,61	9,38E-04	4,92E-02	Q93XY9_ARATH	Uncharacterized protein	hypothetical protein	YES
Fb5:50-76	gene25306	1,64	5,84E-04	3,22E-02	Q0WL81_ARATH	tRNA ligase	DNA ligase (probable)	YES
Fb5:50-76	gene12078	1,69	4,13E-04	2,37E-02	-	-	Myosin-binding protein C, fast-type (probable)	NO
Fb5:50-76	gene04481	1,72	1,24E-03	6,23E-02	NUP85_ARATH	Nuclear pore complex protein NUP85	LOB domain-containing protein 13 (AS2-like protein 10) (probable)	YES
Fb5:50-76	gene10800	1,73	4,46E-04	2,51E-02	VAP21_ARATH	Vesicle-associated protein 2-1, N-terminally processed	Vesicle-associated membrane protein-associated protein C16G5.05c (VAMP-associated protein C16G5.05c) (probable)	NO
Fb5:50-76	gene08569	1,73	5,11E-04	2,85E-02	CADH9_ARATH	Probable cinnamyl alcohol dehydrogenase 9	Probable cinnamyl alcohol dehydrogenase 6 (OsCAD6) (putative)	NO
Fb5:50-76	gene26528	1,74	3,32E-04	1,97E-02	CTR1_ARATH	Serine/threonine-protein kinase CTR1	Serine/threonine-protein kinase CTR1 (similar to)	YES
Fb5:50-76	gene10799	1,74	6,47E-04	3,52E-02	-	-	Probable pectate lyase 8, Precursor	NO
Fb5:50-76	gene04367	1,75	7,08E-04	3,80E-02	DSLE_ARATH	Zinc finger BED domain-containing protein DAYSLEEPER	Putative AC9 transposase (probable)	NO
Fb5:50-76	gene29295	1,77	1,32E-03	6,57E-02	A8MR59_ARATH	Uncharacterized protein	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic, Precursor (probable)	NO
Fb5:50-76	gene11807	1,78	1,81E-04	1,17E-02	ASSY_ARATH	Argininosuccinate synthase, chloroplastic	Argininosuccinate synthase, chloroplastic, Precursor (putative)	NO

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Fb5:50-76	gene29299	1,84	1,73E-04	1,13E-02	Y1796_ARATH	Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic	Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic, Precursor (similar to)	NO
Fb5:50-76	gene29289	1,84	1,71E-04	1,12E-02	Q8L641_ARATH	Putative uncharacterized protein At3g52170	Transcriptional regulator ATRX homolog (probable)	YES
Fb5:50-76	gene16482	1,85	9,78E-04	5,10E-02	A2Y0K9_ORYSI	Putative uncharacterized protein	DnaJ homolog subfamily B member 11, Precursor (probable)	NO
Fb5:50-76	gene16579	1,87	1,58E-03	7,63E-02	-	-	UPF0737 protein Os03g0419100 (probable)	NO
Fb5:50-76	gene16771	1,88	6,75E-04	3,64E-02	Q9SYP1_ARATH	Putative U5 small nuclear ribonucleoprotein helicase	U5 small nuclear ribonucleoprotein 200 kDa helicase (U5-200KD) (putative)	YES
Fb5:50-76	gene24633	1,91	1,75E-03	8,31E-02	SKI25_ARATH	F-box/kelch-repeat protein SKIP25	F-box/kelch-repeat protein SKIP25 (probable)	NO
Fb5:50-76	gene03601	1,93	6,70E-05	4,84E-03	-	-	hypothetical protein	YES
Fb5:50-76	gene08949	1,95	5,16E-04	2,86E-02	ANM16_ARATH	Protein arginine N-methyltransferase 1.6	Protein arginine N-methyltransferase 7 (probable)	NO
Fb5:50-76	gene17652	1,96	1,97E-03	9,20E-02	RS232_ARATH	40S ribosomal protein S23-2	40S ribosomal protein S23 (similar to)	NO
Fb5:50-76	gene11555	1,96	1,43E-03	7,02E-02	Q9FVQ7_ARATH	Uncharacterized protein	SH3 and multiple ankyrin repeat domains protein 1 (Shank1) (probable)	NO
Fb5:50-76	gene26808	1,99	4,93E-05	3,71E-03	MLH1_ARATH	DNA mismatch repair protein MLH1	DNA mismatch repair protein Mlh1 (probable)	NO
Fb5:50-76	gene25876	2,00	1,34E-04	9,01E-03	Q5JMD7_ORYSJ	Peptidase M48-like	Probable protease htpX homolog	NO
Fb5:50-76	gene32385	2,01	2,87E-04	1,75E-02	BAG1_ARATH	BAG family molecular chaperone regulator 1	BAG family molecular chaperone regulator 1A (BAG-1A) (probable)	YES
Fb5:50-76	gene07790	2,03	1,11E-04	7,65E-03	-	-	Cytochrome P450 11B1, mitochondrial, Precursor (probable)	YES
Fb5:50-76	gene25880	2,03	1,43E-04	9,53E-03	Q5JMD7_ORYSJ	Peptidase M48-like	Probable protease htpX homolog	NO
Fb5:50-76	gene07037	2,07	2,62E-05	2,05E-03	-	-	Probable exocyst complex component 6	YES
Fb5:50-76	gene12119	2,08	1,18E-04	8,14E-03	SVP_ARATH	MADS-box protein SVP	MADS-box protein JOINTLESS (similar to)	YES
Fb5:50-76	gene21218	2,09	1,87E-04	1,20E-02	HS23M_ARATH	23.6 kDa heat shock protein, mitochondrial	23.6 kDa heat shock protein, mitochondrial (AtHsp23.6), Precursor (probable)	NO
Fb5:50-76	gene34018	2,15	2,74E-04	1,68E-02	-	-	Reticulon-2 (xRTN2) (probable)	YES

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Fb5:50-76	gene11963	2,15	6,03E-06	5,39E-04	Q10KC0_ORYSJ	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast, putative, expressed	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic, Precursor (putative)	YES
Fb5:50-76	gene20417	2,19	9,86E-06	8,40E-04	NPS11_ARATH	Novel plant SNARE 11	Mesoderm induction early response protein 2 (Mi-er2) (probable)	YES
Fb5:50-76	gene27711	2,21	5,35E-06	4,83E-04	Q9C863_ARATH	Uncharacterized protein	Serine/threonine-protein kinase STE20 (probable)	YES
Fb5:50-76	gene22918	2,24	1,07E-05	8,99E-04	Q3E6S9_ARATH	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	Isopenicillin N epimerase (probable)	YES
Fb5:50-76	gene08895	2,31	7,57E-06	6,57E-04	BRC2A_ARATH	Protein BREAST CANCER SUSCEPTIBILITY 2 homolog A	Rho guanine nucleotide exchange factor 7 (probable)	YES
Fb5:50-76	gene11046	2,33	9,67E-04	5,06E-02	AKT2_ARATH	Potassium channel AKT2/3	Potassium channel AKT2/3 (putative)	NO
Fb5:50-76	gene03547	2,33	1,39E-04	9,30E-03	WNK11_ARATH	Probable serine/threonine-protein kinase WNK11	Probable serine/threonine-protein kinase WNK11 (AtWNK11) (similar to)	YES
Fb5:50-76	gene31469	2,34	9,32E-05	6,59E-03	-	-	Ornithine carbamoyltransferase (OTCase) (probable)	YES
Fb5:50-76	gene06817	2,49	4,24E-04	2,41E-02	-	-	Forkhead box protein G1 (FoxG1) (probable)	YES
Fb5:50-76	gene29226	2,52	1,24E-03	6,23E-02	GXM1_ARATH	Glucuronoxylan 4-O-methyltransferase 1	S-adenosyl-L-methionine-dependent methyltransferase mraW (probable)	NO
Fb5:50-76	gene16052	2,57	2,67E-04	1,66E-02	SUVH8_ARATH	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH8	ATP-dependent DNA helicase MPH1 (probable)	YES
Fb5:50-76	gene13537	2,60	4,01E-04	2,31E-02	A8MQW3_ARATH	Ubiquitin fusion degradation 1	Ubiquitin fusion degradation protein 1 homolog (probable)	YES
Fb5:50-76	gene29168	2,61	1,14E-05	9,44E-04	Q9C9K5_ARATH	Putative uncharacterized protein F14G6.12	hypothetical protein	YES
Fb5:50-76	gene19196	2,63	2,69E-04	1,67E-02	ATX5_ARATH	Histone-lysine N-methyltransferase ATX5	Histone-lysine N-methyltransferase ATX3 (TRX-homolog protein 3) (similar to)	NO
Fb5:50-76	gene29207	2,63	5,52E-04	3,05E-02	PSD2B_ARATH	26S proteasome non-ATPase regulatory subunit 2 homolog B	26S proteasome non-ATPase regulatory subunit 2 (probable)	YES
Fb5:50-76	gene22095	2,70	3,40E-06	3,19E-04	Q9LVA1_ARATH	No apical meristem family protein	NAC domain-containing protein 68 (ONAC068) (probable)	YES
Fb5:50-76	gene07810	2,71	5,07E-04	2,83E-02	HPPD_ARATH	4-hydroxyphenylpyruvate dioxygenase	4-hydroxyphenylpyruvate dioxygenase (HPPDase) (probable)	YES

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Fb5:50-76	gene12135	2,73	1,41E-05	1,15E-03	-	-	Polyadenylate-binding protein 1-B (Poly(A)-binding protein, cytoplasmic 1-B) (probable)	YES
Fb5:50-76	gene10659	2,77	7,39E-07	7,67E-05	O82174_ARATH	Histone H3 K4-specific methyltransferase SET7/9-like protein	Phosphatidylinositol-4-phosphate 5-kinase 5 (AtPIP5K5) (probable)	YES
Fb5:50-76	gene29715	2,79	5,34E-07	5,61E-05	Q9FE41_ORYSJ	Similar to Arabidopsis thaliana chromosome II BAC F26H6	Short transient receptor potential channel 3 (TrpC3) (probable)	YES
Fb5:50-76	gene12132	2,83	1,87E-07	2,10E-05	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At1g06710, mitochondrial, Precursor (probable)	YES
Fb5:50-76	gene24562	2,85	4,19E-04	2,38E-02	BGAL7_ARATH	Beta-galactosidase 7	Beta-galactosidase (Lactase), Precursor (similar to)	YES
Fb5:50-76	gene10660	3,14	1,93E-05	1,55E-03	Q94I65_ORYSJ	Putative retroelement	Catalase-peroxidase (CP), Precursor (probable)	YES
Fb5:50-76	gene29193	3,23	6,40E-10	1,04E-07	C3H46_ARATH	Zinc finger CCCH domain-containing protein 46	Zinc finger CCCH domain-containing protein 53 (OsC3H53) (similar to)	YES
Fb5:50-76	gene13437	3,26	3,24E-04	1,92E-02	AP4S_ARATH	AP-4 complex subunit sigma	AP-4 complex subunit sigma-1 (similar to)	YES
Fb5:50-76	gene02437	3,32	5,83E-06	5,23E-04	O22813_ARATH	Putative steroid dehydrogenase	m15 protein (probable)	YES
Fb5:50-76	gene29108	3,36	1,19E-05	9,78E-04	Q8W3F6_ORYSJ	Putative epoxide hydrolase	Epoxide hydrolase 2 (SEH) (probable)	NO
Fb5:50-76	gene11912	3,37	2,07E-04	1,31E-02	ISOA3_ARATH	Isoamylase 3, chloroplastic	Isoamylase 3, chloroplastic (AtISA3), Precursor (putative)	NO
Fb5:50-76	gene31474	3,39	8,37E-11	1,45E-08	NAC31_ARATH	Protein CUP-SHAPED COTYLEDON 3	Protein CUP-SHAPED COTYLEDON 3 (ANAC031) (similar to)	YES
Fb5:50-76	gene27080	3,42	4,14E-07	4,41E-05	DEF06_ARATH	Defensin-like protein 6	Defensin-like protein, Precursor (similar to)	NO
Fb5:50-76	gene10243	3,47	2,88E-04	1,75E-02	B8B1I4_ORYSI	Putative uncharacterized protein	LysM domain-containing GPI-anchored protein 2, Precursor (probable)	YES
Fb5:50-76	gene10835	3,49	2,06E-05	1,64E-03	O48787_ARATH	Putative phytocyanin	Mavicyanin (similar to)	YES
Fb5:50-76	gene24441	3,53	1,28E-08	1,72E-06	G6PD2_ARATH	Glucose-6-phosphate 1-dehydrogenase 2, chloroplastic	Glucose-6-phosphate 1-dehydrogenase, chloroplastic (G6PD), Precursor (similar to)	YES
Fb5:50-76	gene24640	3,60	1,53E-04	1,02E-02	DUR3_ARATH	Urea-proton symporter DUR3	Probable urea active transporter 1	NO
Fb5:50-76	gene29192	3,68	4,41E-06	4,02E-04	Q69L11_ORYSJ	Glutamate receptor	Splicing factor, arginine/serine-rich 12 (SRrp86) (probable)	NO
Fb5:50-76	gene01567	3,74	1,53E-03	7,39E-02	Q9LFQ0_ARATH	Putative uncharacterized protein F2G14_170	Xylosyltransferase 2 (probable)	NO

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Fb5:50-76	gene31314	3,78	3,76E-07	4,08E-05	-	-	Putative E3 ubiquitin-protein ligase protein PFF1365c (probable)	YES
Fb5:50-76	gene10743	3,87	2,03E-03	9,44E-02	Q8RV84_ORYSJ	Putative 5-3 exoribonuclease	5'-3' exoribonuclease 3 (similar to)	NO
Fb5:50-76	gene29497	3,88	7,32E-04	3,92E-02	A2YQE2_ORYSI	Putative uncharacterized protein	Protein BPS1, chloroplastic, Precursor (probable)	NO
Fb5:50-76	gene02712	3,90	1,80E-11	3,23E-09	Q10I88_ORYSJ	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed	Paramyosin (probable)	YES
Fb5:50-76	gene22139	3,93	7,98E-06	6,89E-04	Y1571_ARATH	Probable leucine-rich repeat receptor-like protein kinase At1g35710	Probable leucine-rich repeat receptor-like protein kinase At1g35710, Precursor	NO
Fb5:50-76	gene31287	4,00	4,56E-09	6,55E-07	SUT21_ARATH	Sulfate transporter 2.1	Low affinity sulfate transporter 3 (putative)	YES
Fb5:50-76	gene07735	4,28	8,94E-15	2,61E-12	Q9C7T7_ARATH	Leucine-rich repeat receptor-like protein kinase	Receptor-like protein kinase HSL1, Precursor (probable)	NO
Fb5:50-76	gene02336	4,33	5,20E-13	1,14E-10	Q9SIF2_ARATH	Putative heat shock protein	Chaperone protein htpG (probable)	YES
Fb5:50-76	gene27639	4,40	1,48E-03	7,21E-02	Q68K27_CHLRE	Intraflagellar transport particle protein 140	Putative DNA helicase ino80 (probable)	YES
Fb5:50-76	gene10516	4,49	2,02E-07	2,25E-05	-	-	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (probable)	YES
Fb5:50-76	gene20289	4,49	7,26E-09	1,03E-06	CDPKO_ARATH	Calcium-dependent protein kinase 24	Protein transport protein sec31 (probable)	YES
Fb5:50-76	gene07744	4,50	6,87E-15	2,04E-12	EME1B_ARATH	Crossover junction endonuclease EME1B	Probable serine/threonine-protein kinase fnkE	NO
Fb5:50-76	gene26565	4,53	1,10E-03	5,61E-02	A2Z903_ORYSI	Uncharacterized protein	Protein lingerer (probable)	NO
Fb5:50-76	gene28845	4,63	9,73E-05	6,83E-03	Q2R8I1_ORYSJ	Retrotransposon protein, putative, Ty3-gypsy subclass	Integrase p58 (probable)	YES
Fb5:50-76	gene00473	4,75	3,39E-04	2,00E-02	A2YY35_ORYSI	Putative uncharacterized protein	Cyclase, Precursor (similar to)	YES
Fb5:50-76	gene13539	4,75	6,70E-10	1,08E-07	Q8L7G1_ARATH	Uncharacterized protein	Phosphoribosylaminoimidazole-succinocarboxamide synthase (probable)	YES
Fb5:50-76	gene31431	4,83	9,60E-05	6,76E-03	-	-	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (probable)	YES
Fb5:50-76	gene24546	4,85	4,63E-05	3,50E-03	-	-	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- carboxylate synthase (SEPHCHC synthase) (probable)	YES

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Fb5:50-76	gene30476	4,89	1,61E-15	5,17E-13	BGAL8_ARATH	Beta-galactosidase 8	Beta-galactosidase 8 (Lactase 8), Precursor (putative)	YES
Fb5:50-76	gene30017	4,92	6,78E-12	1,30E-09	F4IJR9_ARATH	ATP binding / aminoacyl-tRNA ligase/ nucleotide binding protein	Retrotransposon-derived protein PEG10 (MEF3-like protein 1) (similar to)	YES
Fb5:50-76	gene02295	4,95	9,83E-08	1,18E-05	-	-	hypothetical protein	YES
Fb5:50-76	gene13905	4,95	9,78E-05	6,84E-03	RPM1_ARATH	Disease resistance protein RPM1	Disease resistance protein RPM1 (probable)	YES
Fb5:50-76	gene16023	5,18	3,77E-18	1,56E-15	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (similar to)	NO
Fb5:50-76	gene20454	5,33	7,93E-04	4,18E-02	-	-	hypothetical protein	NO
Fb5:50-76	gene28812	5,35	3,42E-12	6,86E-10	Q7XLX2_ORYSJ	OSJNBa0042I15.19 protein	Endonuclease (probable)	YES
Fb5:50-76	gene12154	5,37	1,93E-12	4,00E-10	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At1g62590 (probable)	YES
Fb5:50-76	gene12130	5,38	5,56E-08	6,92E-06	PP407_ARATH	Pentatricopeptide repeat-containing protein At5g39710	Pentatricopeptide repeat-containing protein At5g39710 (probable)	NO
Fb5:50-76	gene07821	5,49	1,73E-06	1,69E-04	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At1g09900 (probable)	YES
Fb5:50-76	gene10652	5,51	1,41E-06	1,41E-04	Q8S1D2_ORYSJ	Uncharacterized protein	LRR receptor-like serine/threonine-protein kinase FLS2, Precursor (probable)	YES
Fb5:50-76	gene26840	5,63	2,79E-22	1,49E-19	SR543_ARATH	Signal recognition particle 54 kDa protein 3	Signal recognition particle 54 kDa protein 2 (SRP54) (putative)	NO
Fb5:50-76	gene13665	5,65	1,37E-22	7,74E-20	Q8SAW7_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Structural protein ORF567 (probable)	YES
Fb5:50-76	gene12127	5,77	9,97E-05	6,93E-03	PPR96_ARATH	Pentatricopeptide repeat-containing protein At1g62930, chloroplastic	Pentatricopeptide repeat-containing protein At1g05665, mitochondrial, Precursor (probable)	YES
Fb5:50-76	gene14572	5,89	1,52E-16	5,79E-14	-	-	Protein sip5 (probable)	YES
Fb5:50-76	gene12139	5,99	2,43E-04	1,53E-02	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At5g65560 (probable)	NO
Fb5:50-76	gene16029	6,21	2,12E-06	2,05E-04	F4JMQ8_ARATH	Calcineurin-like metallo-phosphoesterase family protein	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (probable)	YES
Fb5:50-76	gene24566	6,33	6,76E-10	1,08E-07	Q8L3P4_ARATH	Putative uncharacterized protein At2g43650	Phosphoglycerate kinase (probable)	YES
Fb5:50-76	gene27016	6,41	3,12E-05	2,43E-03	SYV_ARATH	Valine--tRNA ligase	Valyl-tRNA synthetase (ValRS) (similar to)	YES

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Fb5:50-76	gene02297	6,43	3,58E-13	8,05E-11	A2XXJ7_ORYSI	Putative uncharacterized protein	Protein FAR1-RELATED SEQUENCE 6 (probable)	YES
Fb5:50-76	gene08964	6,49	8,76E-07	9,02E-05	F4IAA0_ARATH	Type I inositol-1,4,5-trisphosphate 5-phosphatase 13	Type I inositol-1,4,5-trisphosphate 5-phosphatase 12 (At5PTase12) (similar to)	NO
Fb5:50-76	gene03139	6,76	9,33E-07	9,41E-05	-	-	Glucose-6-phosphate 1-dehydrogenase, chloroplastic (G6PD), Precursor (probable)	YES
Fb5:50-76	gene30074	6,83	1,82E-07	2,06E-05	B8BE99_ORYSI	Putative uncharacterized protein	Ankyrin repeat-containing protein At3g12360 (probable)	YES
Fb5:50-76	gene10796	7,11	3,51E-23	2,18E-20	GLPT4_ARATH	Putative glycerol-3-phosphate transporter 4	Sugar phosphate exchanger 2 (probable)	NO
Fb5:50-76	gene14835	7,16	1,61E-09	2,47E-07	Q7XME3_ORYSJ	OSJNBa0061G20.16 protein	hypothetical protein	YES
Fb5:50-76	gene07718	7,95	3,41E-22	1,77E-19	-	-	Elongation factor 1-alpha (EF-1-alpha) (probable)	YES
Fb5:50-76	gene10671	8,25	8,67E-16	2,94E-13	B9FZX0_ORYSJ	Putative uncharacterized protein	Keratin-associated protein 5-6 (probable)	YES
Fb5:50-76	gene07785	8,25	5,23E-26	4,24E-23	FB135_ARATH	F-box protein At3g07870	F-box protein At3g07870 (probable)	YES
Fb5:50-76	gene13721	9,01	3,14E-33	5,86E-30	CSLD3_ARATH	Cellulose synthase-like protein D3	Cellulose synthase-like protein D3 (AtCslD3) (similar to)	YES
Fb5:50-76	gene07805	10,40	5,50E-23	3,31E-20	SUVR4_ARATH	Histone-lysine N-methyltransferase SUVR4	Histone-lysine N-methyltransferase SUVR4 (Su(var)3-9-related protein 4) (similar to)	YES
Fb5:50-76	gene02280	Inf	1,74E-07	2,00E-05	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (probable)	NO
Fb5:50-76	gene02298	Inf	1,12E-13	2,71E-11	O24438_ORYLO	Retrofit	Uncharacterized mitochondrial protein AtMg00810 (similar to)	YES
Fb5:50-76	gene02335	Inf	6,65E-05	4,83E-03	Q6ATE2_ORYSJ	Uncharacterized protein	Probable transporter MCH1	NO
Fb5:50-76	gene10478	Inf	1,36E-06	1,37E-04	-	-	Agrin, Precursor (probable)	YES
Fb5:50-76	gene10480	Inf	7,79E-05	5,57E-03	RAB1B_ARATH	Ras-related protein RABB1b	Ras-related protein Rab-2-B (similar to)	NO
Fb5:50-76	gene10672	Inf	2,47E-14	6,78E-12	FBL13_ARATH	F-box/LRR-repeat protein 13	FBD-associated F-box protein At4g13985 (probable)	YES
Fb5:50-76	gene10891	Inf	9,00E-14	2,27E-11	CMTA5_ARATH	Calmodulin-binding transcription activator 5	Calmodulin-binding transcription activator 5 (EICBP.f) (similar to)	NO
Fb5:50-76	gene11052	Inf	1,64E-03	7,84E-02	-	-	Putative protein FAM47C (probable)	YES
Fb5:50-76	gene11824	Inf	3,77E-32	6,39E-29	B9G5Y1_ORYSJ	Putative uncharacterized protein	Undecaprenyl-diphosphatase (probable)	YES

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Fb5:50-76	gene11836	Inf	6,52E-16	2,34E-13	TRXB1_ARATH	Thioredoxin reductase 1	Phosphopentomutase (probable)	NO
Fb5:50-76	gene12128	Inf	2,03E-13	4,81E-11	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At5g65560 (probable)	YES
Fb5:50-76	gene12138	Inf	2,41E-04	1,52E-02	A3BB28_ORYSJ	Ribosomal protein L15	Pentatricopeptide repeat-containing protein At5g46100 (probable)	NO
Fb5:50-76	gene12292	Inf	8,80E-07	9,02E-05	-	-	Extensin, Precursor (probable)	YES
Fb5:50-76	gene13717	Inf	7,91E-16	2,74E-13	AAE5_ARATH	Probable acyl-activating enzyme 5, peroxisomal	Putative ankyrin repeat protein FPV022 (probable)	YES
Fb5:50-76	gene24075	Inf	2,17E-06	2,09E-04	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (similar to)	NO
Fb5:50-76	gene25657	Inf	2,20E-12	4,52E-10	-	-	D-tyrosyl-tRNA(Tyr) deacylase (probable)	YES
Fb5:50-76	gene25853	Inf	5,06E-04	2,83E-02	-	-	Peroxidase 55 (Atperox P55), Precursor (similar to)	NO
Fb5:50-76	gene26868	Inf	1,57E-08	2,10E-06	FB135_ARATH	F-box protein At3g07870	F-box protein At3g07870 (probable)	YES
Fb5:50-76	gene27017	Inf	5,25E-20	2,51E-17	ERF21_ARATH	Ethylene-responsive transcription factor ERF021	Ethylene-responsive transcription factor ERF022 (similar to)	NO
Fb5:50-76	gene29002	Inf	5,93E-11	1,03E-08	Q9FE41_ORYSJ	Similar to Arabidopsis thaliana chromosome II BAC F26H6	RNA-binding protein sym-2 (probable)	YES
Fb5:50-76	gene29091	Inf	1,60E-03	7,72E-02	-	-	tRNA-specific 2-thiouridylase mnmA 1 (probable)	YES
Fb5:50-76	gene29173	Inf	2,96E-08	3,87E-06	DET2_SOLLC	Steroid 5-alpha-reductase DET2	Methionyl-tRNA synthetase (MetRS) (probable)	YES
Fb5:50-76	gene29297	Inf	1,46E-09	2,25E-07	SKIP1_ARATH	F-box protein SKIP1	F-box protein SKIP1 (similar to)	YES
Fb5:50-76	gene29300	Inf	6,84E-12	1,30E-09	B8A913_ORYSI	Putative uncharacterized protein	DNA polymerase III subunit gamma/tau (probable)	YES
Fb5:50-76	gene30076	Inf	1,14E-03	5,78E-02	Q53JM5_ORYSJ	cDNA clone:J013147L18, full insert sequence	Ankyrin repeat-containing protein At3g12360 (probable)	YES
Fb5:50-76	gene33934	Inf	1,00E-03	5,19E-02	-	-	Nuclear pore complex protein Nup96, Precursor (probable)	YES
Fb5:50-76	gene34070	Inf	4,43E-08	5,54E-06	G6PD3_ARATH	Glucose-6-phosphate 1-dehydrogenase 3, chloroplastic	Glucose-6-phosphate 1-dehydrogenase, chloroplastic (G6PD), Precursor (similar to)	YES
Fb6:84-101	gene04177	-Inf	6,95E-07	1,64E-04	DOR_ARATH	F-box protein DOR	F-box protein At3g28330 (probable)	YES
Fb6:84-101	gene04209	-Inf	8,66E-12	3,95E-09	-	-	Integrase (probable)	YES
Fb6:84-101	gene05059	-Inf	1,15E-19	1,13E-16	-	-	Torsin-1A-interacting protein 2 (probable)	YES

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Fb6:84-101	gene06510	-Inf	1,94E-21	2,41E-18	F4JTS8_ARATH	Nuclear factor NO VEIN	UPF0102 protein RPC_0320 (probable)	YES
Fb6:84-101	gene06615	-Inf	4,15E-20	4,56E-17	GUF1_ORYSI	Translation factor GUF1 homolog, mitochondrial	GTP-binding protein GUF1 homolog (similar to)	YES
Fb6:84-101	gene10539	-Inf	1,61E-07	4,13E-05	LEC2_ARATH	B3 domain-containing transcription factor LEC2	B3 domain-containing transcription factor LEC2 (similar to)	YES
Fb6:84-101	gene16880	-Inf	1,32E-07	3,43E-05	B9G5C7_ORYSJ	Putative uncharacterized protein	Piwi-like protein 4 (probable)	YES
Fb6:84-101	gene26394	-Inf	9,94E-05	1,33E-02	-	-	Chaperone protein dnaJ 1 (probable)	NO
Fb6:84-101	gene26407	-Inf	4,48E-21	5,23E-18	-	-	F-box protein At2g07140 (probable)	YES
Fb6:84-101	gene27957	-Inf	7,86E-19	7,34E-16	F4IDJ0_ARATH	Nucleolar complex-associated protein domain-containing protein	ATP-dependent RNA helicase DDX51 (probable)	YES
Fb6:84-101	gene27974	-Inf	1,64E-22	2,35E-19	ILVD_ARATH	Dihydroxy-acid dehydratase, chloroplastic	Protein single-minded (probable)	NO
Fb6:84-101	gene27985	-Inf	7,16E-12	3,35E-09	Q9AYH7_ORYSJ	Putative uncharacterized protein OSJNBa0087H07.7	F-box/LRR-repeat protein At2g43260 (probable)	YES
Fb6:84-101	gene28363	-Inf	4,16E-04	4,60E-02	DRL29_ARATH	Probable disease resistance protein At4g33300	Probable disease resistance protein At5g66900	NO
Fb6:84-101	gene28382	-Inf	2,94E-27	6,86E-24	FK131_ARATH	F-box/kelch-repeat protein At5g39560	Kelch repeat-containing protein At1g19470 (probable)	YES
Fb6:84-101	gene29473	-Inf	2,58E-05	4,08E-03	B9F6L9_ORYSJ	Putative uncharacterized protein	Trichothecene 3-O-acetyltransferase (probable)	YES
Fb6:84-101	gene04210	-12,52	3,84E-41	3,59E-37	CPR30_ARATH	F-box protein CPR30	Putative F-box/kelch-repeat protein At1g15680 (probable)	YES
Fb6:84-101	gene10294	-11,24	6,09E-52	1,14E-47	7OMT_PAPSO	(R,S)-reticuline 7-O-methyltransferase	(RS)-norcoclaurine 6-O-methyltransferase (6-OMT) (probable)	YES
Fb6:84-101	gene28502	-9,70	6,27E-25	1,30E-21	F4ICB5_ARATH	Zinc finger (C3HC4-type RING finger) family protein	E3 ubiquitin-protein ligase PRT1 (similar to)	NO
Fb6:84-101	gene27983	-8,27	7,48E-29	2,79E-25	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	YES
Fb6:84-101	gene10350	-7,20	5,57E-05	7,89E-03	Q10LG3_ORYSJ	cDNA clone:J023049J20, full insert sequence	E3 ubiquitin-protein ligase CIP8 (probable)	YES
Fb6:84-101	gene04348	-7,02	1,16E-22	1,80E-19	CNGC2_ARATH	Cyclic nucleotide-gated ion channel 2	Cyclic nucleotide-gated ion channel 2 (AtCNGC2) (similar to)	NO
Fb6:84-101	gene01249	-6,99	5,65E-28	1,51E-24	CML38_ARATH	Calcium-binding protein CML38	Glycophorin-binding protein (probable)	YES
Fb6:84-101	gene04446	-6,40	1,09E-15	8,47E-13	-	-	Ena/VASP-like protein (probable)	NO
Fb6:84-101	gene24473	-6,08	2,51E-06	5,44E-04	-	-	ATP synthase gamma chain (similar to)	YES

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Fb6:84-101	gene25929	-6,04	4,18E-16	3,39E-13	BGL12_ARATH	Beta-glucosidase 12	Non-cyanogenic beta-glucosidase, Precursor (probable)	NO
Fb6:84-101	gene06730	-5,95	3,52E-15	2,53E-12	-	-	Voltage-dependent R-type calcium channel subunit alpha-1E (BII) (probable)	YES
Fb6:84-101	gene16384	-5,89	2,05E-06	4,56E-04	B8B1V5_ORYSI	Putative uncharacterized protein	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (probable)	NO
Fb6:84-101	gene27961	-5,66	1,23E-16	1,04E-13	A2ZBE2_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase rnf181 (probable)	NO
Fb6:84-101	gene25861	-5,61	4,59E-15	3,18E-12	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	NO
Fb6:84-101	gene26395	-5,36	4,93E-10	1,77E-07	Y3037_ARATH	Probable inactive leucine-rich repeat receptor-like protein kinase At3g03770	Probable LRR receptor-like serine/threonine-protein kinase At1g14390, Precursor	YES
Fb6:84-101	gene04436	-5,22	4,42E-06	8,34E-04	RPS5_ARATH	Disease resistance protein RPS5	Probable disease resistance protein At5g63020	NO
Fb6:84-101	gene16771	-5,10	6,06E-12	2,98E-09	Q9SYP1_ARATH	Putative U5 small nuclear ribonucleoprotein helicase	U5 small nuclear ribonucleoprotein 200 kDa helicase (U5-200KD) (putative)	YES
Fb6:84-101	gene21241	-5,09	3,46E-06	6,88E-04	Q9S7W4_ARATH	Putative uncharacterized protein At3g07720	Glucose-6-phosphate isomerase (GPI) (probable)	YES
Fb6:84-101	gene34749	-5,00	1,05E-10	4,36E-08	Q9FJE3_ARATH	Ta11-like non-LTR retroelement protein-like	RAF proto-oncogene serine/threonine-protein kinase (probable)	NO
Fb6:84-101	gene01616	-4,80	7,89E-06	1,43E-03	F4IBR2_ARATH	Uncharacterized protein	Proteasome subunit alpha type-7-B (similar to)	YES
Fb6:84-101	gene25930	-4,63	1,10E-13	6,39E-11	Q01KB3_ORYSA	OSIGBa0135C13.6 protein	Beta-glucosidase 16 (AtBGLU16), Precursor (probable)	NO
Fb6:84-101	gene19366	-4,46	2,30E-04	2,77E-02	RFA1A_ARATH	Replication protein A 70 kDa DNA-binding subunit A	Kielin/chordin-like protein (KCP), Precursor (probable)	NO
Fb6:84-101	gene25902	-4,39	3,39E-05	5,15E-03	A2WS95_ORYSI	Putative uncharacterized protein	Polygalacturonase inhibitor (PGIG), Precursor (probable)	NO
Fb6:84-101	gene25854	-4,37	3,97E-12	2,00E-09	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	YES
Fb6:84-101	gene01244	-4,28	1,93E-12	1,03E-09	Q94CF9_ORYSA	RSSG8	Ankyrin repeat domain-containing protein 1 (probable)	NO
Fb6:84-101	gene23639	-4,25	2,92E-10	1,14E-07	Q84J94_ARATH	Putative uncharacterized protein At2g43280	Putative membrane protein ycf1 (RF1) (probable)	YES
Fb6:84-101	gene04317	-4,21	1,61E-04	2,06E-02	FBL38_ARATH	F-box/LRR-repeat protein At2g42720	Putative FBD-associated F-box protein At5g22720 (probable)	YES

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Fb6:84-101	gene01286	-4,21	4,16E-04	4,60E-02	LBD27_ARATH	LOB domain-containing protein 27	LOB domain-containing protein 27 (AS2-like protein 29) (probable)	NO
Fb6:84-101	gene05626	-4,17	1,62E-04	2,06E-02	RL122_ARATH	60S ribosomal protein L12-2	60S ribosomal protein L12-2 (similar to)	YES
Fb6:84-101	gene27956	-4,14	4,70E-13	2,58E-10	RNG1L_ARATH	E3 ubiquitin-protein ligase RING1-like	E3 ubiquitin-protein ligase rnf181 (probable)	NO
Fb6:84-101	gene10295	-4,03	6,81E-09	1,99E-06	A2RVK8_ARATH	ELMO/CED-12 family protein	ELMO domain-containing protein A (probable)	NO
Fb6:84-101	gene27986	-3,97	4,05E-11	1,76E-08	Q6AT20_ORYSJ	Putative uncharacterized protein OSJNBa0029B02.9	F-box protein At5g07610 (probable)	YES
Fb6:84-101	gene05057	-3,95	2,88E-05	4,45E-03	-	-	Death domain-associated protein 6 (probable)	YES
Fb6:84-101	gene04243	-3,88	1,33E-06	2,99E-04	-	-	5-aminolevulinate synthase, erythroid-specific, mitochondrial (ALAS-E), Precursor (probable)	NO
Fb6:84-101	gene28446	-3,79	3,87E-05	5,68E-03	Q0JQB6_ORYSJ	cDNA clone:J013121I24, full insert sequence	Electrogenic sodium bicarbonate cotransporter 4 (probable)	NO
Fb6:84-101	gene04248	-3,76	8,61E-07	2,00E-04	-	-	Glutamate-ammonia-ligase adenylyltransferase (ATase) (probable)	YES
Fb6:84-101	gene04229	-3,68	6,44E-12	3,09E-09	Q5XXN7_ARATH	SEPALLATA1	Developmental protein SEPALLATA 1 (putative)	NO
Fb6:84-101	gene28345	-3,66	3,64E-07	8,82E-05	PUB40_ARATH	U-box domain-containing protein 40	U-box domain-containing protein 40 (similar to)	NO
Fb6:84-101	gene11384	-3,62	2,80E-10	1,11E-07	CAMT3_ARATH	Probable caffeoyl-CoA O-methyltransferase At4g26220	Probable caffeoyl-CoA O-methyltransferase At4g26220 (CCoAOMT) (similar to)	NO
Fb6:84-101	gene04445	-3,60	3,87E-10	1,45E-07	Q01K44_ORYSA	OSIGBa0158F13.3 protein	E3 ubiquitin-protein ligase RNF181 (probable)	YES
Fb6:84-101	gene16766	-3,56	8,48E-10	2,88E-07	-	-	Tegument protein BRRF2 (probable)	YES
Fb6:84-101	gene23125	-3,50	6,66E-11	2,83E-08	B9FKI4_ORYSJ	Putative uncharacterized protein	Agglutinin (probable)	NO
Fb6:84-101	gene04430	-3,29	7,80E-10	2,70E-07	A2Y618_ORYSI	Putative uncharacterized protein	Putative disease resistance protein RGA3 (probable)	YES
Fb6:84-101	gene10313	-3,20	1,85E-10	7,52E-08	A2YM66_ORYSI	Putative uncharacterized protein	hypothetical protein	NO
Fb6:84-101	gene26411	-3,17	8,08E-04	8,07E-02	Q2R147_ORYSJ	Protein kinase domain containing protein, expressed	F-box/kelch-repeat protein At3g23880 (probable)	NO
Fb6:84-101	gene28461	-3,17	1,04E-08	2,99E-06	NRT27_ARATH	High affinity nitrate transporter 2.7	Nitrate transporter (probable)	YES

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Fb6:84-101	gene02712	-3,16	2,92E-06	6,05E-04	Q10I88_ORYSJ	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed	Paramyosin (probable)	YES
Fb6:84-101	gene25906	-3,10	2,24E-09	7,08E-07	Q0WMJ7_ARATH	Uncharacterized protein	hypothetical protein	YES
Fb6:84-101	gene15453	-3,03	7,21E-04	7,35E-02	F4IAX1_ARATH	Putative copper amine oxidase	Primary amine oxidase, Precursor (putative)	NO
Fb6:84-101	gene06681	-2,85	4,62E-06	8,63E-04	-	-	Coatomer subunit beta-2 (Beta-COP 2) (similar to)	YES
Fb6:84-101	gene10319	-2,77	2,77E-04	3,27E-02	Q6K7Q7_ORYSJ	Putative splicing factor 3B subunit 2	Splicing factor 3B subunit 2 (SF3b145) (probable)	NO
Fb6:84-101	gene26409	-2,76	1,95E-07	4,93E-05	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	NO
Fb6:84-101	gene30046	-2,76	1,81E-04	2,22E-02	LBD4_ARATH	LOB domain-containing protein 4	LOB domain-containing protein 4 (AS2-like protein 6) (putative)	YES
Fb6:84-101	gene19443	-2,74	4,20E-05	6,08E-03	T14H_TAXCU	Taxoid 14-beta-hydroxylase	Cytochrome P450 716B1 (probable)	NO
Fb6:84-101	gene15215	-2,74	3,63E-06	7,08E-04	T14H_TAXCU	Taxoid 14-beta-hydroxylase	Cytochrome P450 716B1 (probable)	YES
Fb6:84-101	gene28321	-2,61	4,56E-04	4,98E-02	Y3885_ARATH	Uncharacterized protein At3g28850	hypothetical protein	YES
Fb6:84-101	gene28322	-2,59	6,09E-05	8,37E-03	Q8S1E8_ORYSJ	cDNA clone:J033117E11, full insert sequence	Protein kinase APK1A, chloroplastic, Precursor (similar to)	NO
Fb6:84-101	gene28407	-2,55	3,40E-07	8,35E-05	QORL_ARATH	Quinone oxidoreductase-like protein At1g23740, chloroplastic	Quinone oxidoreductase-like protein At1g23740, chloroplastic, Precursor (probable)	NO
Fb6:84-101	gene31457	-2,51	3,39E-04	3,93E-02	NFYB3_ARATH	Nuclear transcription factor Y subunit B-3	Nuclear transcription factor Y subunit B-3 (AtNF-YB-3) (similar to)	YES
Fb6:84-101	gene04208	-2,49	2,46E-05	3,92E-03	Q94GB9_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Collagen-like protein 7 (probable)	YES
Fb6:84-101	gene25897	-2,47	1,59E-05	2,73E-03	CLCB_ARATH	Chloride channel protein CLC-b	Chloride channel protein CLC-b (AtCLC-b) (putative)	NO
Fb6:84-101	gene28332	-2,43	2,65E-05	4,15E-03	DRL4_ARATH	Putative disease resistance protein At1g50180	Probable disease resistance RPP8-like protein 2	NO
Fb6:84-101	gene04429	-2,43	2,77E-06	5,80E-04	SPSA3_ARATH	Probable sucrose-phosphate synthase 3	Sucrose-phosphate synthase 2 (similar to)	NO
Fb6:84-101	gene09375	-2,40	3,64E-06	7,08E-04	-	-	Autophagy-related protein 3 (probable)	YES
Fb6:84-101	gene04409	-2,36	8,51E-06	1,51E-03	B7F9W6_ORYSJ	cDNA, clone: J100005E18, full insert sequence	Putative disease resistance protein RGA3 (probable)	NO
Fb6:84-101	gene16753	-2,36	8,56E-04	8,51E-02	P2B10_ARATH	F-box protein PP2-B10	F-box protein At2g02240 (probable)	NO
Fb6:84-101	gene25882	-2,30	2,15E-06	4,73E-04	SUOX_ARATH	Sulfite oxidase	Sulfite oxidase (At-SO) (similar to)	NO

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Fb6:84-101	gene04174	-2,28	6,29E-05	8,52E-03	-	-	Synapsin-1 (probable)	NO
Fb6:84-101	gene01338	-2,24	6,39E-04	6,74E-02	SP13B_ARATH	Squamosa promoter-binding-like protein 13B	Squamosa promoter-binding-like protein 13 (probable)	YES
Fb6:84-101	gene24293	-2,20	5,96E-05	8,25E-03	Q7XK10_ORYSJ	Photosystem I P700 chlorophyll a apoprotein A1, putative, expressed	Probable aquaporin TIP1-1 (OsTIP1) (similar to)	NO
Fb6:84-101	gene04207	-2,17	4,84E-05	6,90E-03	Q8GZ81_ARATH	Putative auxin-independent growth promoter protein	DUF246 domain-containing protein At1g04910 (probable)	YES
Fb6:84-101	gene24721	-2,00	6,00E-04	6,41E-02	Q9AYI0_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Probable LRR receptor-like serine/threonine-protein kinase At1g07650, Precursor	NO
Fb6:84-101	gene22887	-1,96	1,01E-03	9,96E-02	YAB2_ARATH	Putative axial regulator YABBY 2	Putative axial regulator YABBY 2 (similar to)	NO
Fb6:84-101	gene04222	-1,82	3,60E-04	4,15E-02	Q9FMB4_ARATH	Uncharacterized protein	Major pollen allergen Lig v 1 (probable)	NO
Fb6:84-101	gene01281	-1,78	4,87E-04	5,26E-02	PMA11_ARATH	ATPase 11, plasma membrane-type	Plasma membrane ATPase 1 (putative)	YES
Fb6:84-101	gene03846	1,79	4,73E-04	5,14E-02	Q8S7U7_ORYSJ	Putative pentatricopeptide repeat containing protein	Pentatricopeptide repeat-containing protein At5g15280 (probable)	NO
Fb6:84-101	gene20622	1,80	7,96E-04	8,00E-02	BH122_ARATH	Transcription factor bHLH122	Transcription factor bHLH122 (bHLH 122) (probable)	YES
Fb6:84-101	gene13105	1,81	1,73E-04	2,17E-02	A2X344_ORYSI	Putative uncharacterized protein	General transcription factor IIF subunit 1 (TFIIF-alpha) (probable)	YES
Fb6:84-101	gene15008	1,88	1,55E-04	2,00E-02	-	-	Phospholipase D Y (PLD 3), Precursor (probable)	NO
Fb6:84-101	gene28188	1,91	3,30E-04	3,85E-02	F4HNW0_ARATH	Shewenella-like protein phosphatase 1	hypothetical protein	NO
Fb6:84-101	gene20386	1,94	2,99E-04	3,51E-02	B8BLS7_ORYSI	Putative uncharacterized protein	Probable E3 ubiquitin-protein ligase rbrA	YES
Fb6:84-101	gene28358	2,02	6,71E-04	6,92E-02	GASAE_ARATH	Gibberellin-regulated protein 14	Snakin-2, Precursor (similar to)	YES
Fb6:84-101	gene15023	2,08	3,98E-05	5,81E-03	REM9_ARATH	B3 domain-containing protein REM9	B3 domain-containing protein Os01g0723500 (probable)	NO
Fb6:84-101	gene20390	2,11	3,21E-05	4,91E-03	-	-	50S ribosomal protein L18 (probable)	YES
Fb6:84-101	gene04355	2,18	3,63E-04	4,16E-02	A3BAU1_ORYSJ	Putative uncharacterized protein	Anthocyanidin 5,3-O-glucosyltransferase (probable)	YES
Fb6:84-101	gene27953	2,20	6,59E-04	6,84E-02	A2ZBE2_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RNF181 (probable)	NO

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Fb6:84-101	gene27942	2,21	7,80E-05	1,05E-02	Q9SS93_ARATH	Putative uncharacterized protein At3g01620	Beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase (N-acetylglucosaminyltransferase III) (probable)	YES
Fb6:84-101	gene28196	2,23	1,29E-04	1,68E-02	U87A2_ARATH	UDP-glycosyltransferase 87A2	hypothetical protein	NO
Fb6:84-101	gene03102	2,23	2,36E-05	3,80E-03	Q93YW3_ARATH	Putative uncharacterized protein At1g01830	hypothetical protein	YES
Fb6:84-101	gene29201	2,32	1,70E-05	2,88E-03	RL102_ARATH	60S ribosomal protein L10-2	60S ribosomal protein L10 (similar to)	NO
Fb6:84-101	gene20580	2,37	3,76E-05	5,61E-03	Q9C6L2_ARATH	Regulator of Vps4 activity in the MVB pathway protein	Epidermal growth factor receptor kinase substrate 8-like protein 3 (probable)	YES
Fb6:84-101	gene28609	2,37	2,38E-04	2,83E-02	Q7XZF8_ORYSJ	Putative DNA binding protein	50S ribosomal protein L9 (probable)	YES
Fb6:84-101	gene16897	2,40	3,79E-06	7,22E-04	H32_ARATH	Histone H3.2	Thyroid receptor-interacting protein 11 (TRIP-11) (probable)	YES
Fb6:84-101	gene28326	2,40	1,74E-04	2,17E-02	Q94CF9_ORYSA	RSSG8	Tankyrase-2 (TANK2) (probable)	YES
Fb6:84-101	gene27952	2,49	1,28E-06	2,92E-04	A2XQC6_ORYSI	Putative uncharacterized protein	GATA zinc finger domain-containing protein 10 (probable)	NO
Fb6:84-101	gene04367	2,49	3,09E-06	6,35E-04	DSLE_ARATH	Zinc finger BED domain-containing protein DAYSLEEPER	Putative AC9 transposase (probable)	NO
Fb6:84-101	gene03547	2,57	1,24E-04	1,64E-02	WNK11_ARATH	Probable serine/threonine-protein kinase WNK11	Probable serine/threonine-protein kinase WNK11 (AtWNK11) (similar to)	YES
Fb6:84-101	gene03800	2,59	3,89E-07	9,32E-05	Q9FFW8_ARATH	Tryptophan synthase beta chain	Tryptophan synthase beta chain 2 (similar to)	NO
Fb6:84-101	gene01170	2,63	7,30E-04	7,41E-02	FB135_ARATH	F-box protein At3g07870	F-box/kelch-repeat protein At3g06240 (probable)	NO
Fb6:84-101	gene28506	2,71	1,85E-05	3,09E-03	RST1_ARATH	Protein RST1	mRNA guanylyltransferase (probable)	NO
Fb6:84-101	gene03797	2,73	1,01E-05	1,78E-03	A2YV87_ORYSI	Putative uncharacterized protein	Protein KIAA1199, Precursor (probable)	YES
Fb6:84-101	gene04180	2,85	1,74E-05	2,93E-03	GDU1_ARATH	Protein GLUTAMINE DUMPER 1	Translation initiation factor IF-2 (probable)	NO
Fb6:84-101	gene22796	2,93	3,77E-06	7,22E-04	A2WNQ5_ORYSI	Putative uncharacterized protein	ABC transporter B family member 4 (ABC transporter ABCB.4) (similar to)	NO
Fb6:84-101	gene04320	2,99	9,71E-08	2,59E-05	Q9FZE5_ARATH	T1K7.2 protein	Zinc finger protein 569 (Zfp-74) (probable)	YES
Fb6:84-101	gene34871	3,13	1,04E-04	1,38E-02	-	-	Protein FAM117A (probable)	YES

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Fb6:84-101	gene06817	3,15	8,33E-06	1,50E-03	-	-	Forkhead box protein G1 (FoxG1) (probable)	YES
Fb6:84-101	gene28037	3,19	5,82E-10	2,05E-07	Q33B34_ORYSJ	Os10g0145200 protein	Elongation factor G (EF-G) (probable)	YES
Fb6:84-101	gene20417	3,19	4,57E-09	1,38E-06	NPS11_ARATH	Novel plant SNARE 11	Mesoderm induction early response protein 2 (Mi-er2) (probable)	YES
Fb6:84-101	gene22795	3,28	7,71E-06	1,41E-03	AB11B_ARATH	ABC transporter B family member 11	ABC transporter B family member 11 (ABC transporter ABCB.11) (similar to)	NO
Fb6:84-101	gene07037	3,28	9,89E-10	3,30E-07	-	-	Probable exocyst complex component 6	YES
Fb6:84-101	gene34934	3,39	3,60E-05	5,43E-03	B9FZN5_ORYSJ	Putative uncharacterized protein	Putative disease resistance protein RGA3 (probable)	YES
Fb6:84-101	gene03788	3,39	2,81E-05	4,37E-03	Q9LXF8_ARATH	Transmembrane amino acid transporter family protein	Vacuolar amino acid transporter 4 (probable)	NO
Fb6:84-101	gene03842	3,46	5,78E-05	8,11E-03	NRP2_ARATH	NAP1-related protein 2	Putative adenylate cyclase regulatory protein (probable)	YES
Fb6:84-101	gene13437	3,60	1,34E-04	1,74E-02	AP4S_ARATH	AP-4 complex subunit sigma	AP-4 complex subunit sigma-1 (similar to)	YES
Fb6:84-101	gene28465	3,63	3,83E-05	5,68E-03	A2ZBE2_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RNF181 (probable)	NO
Fb6:84-101	gene01582	3,69	3,78E-04	4,31E-02	-	-	Slender lobes-like protein (probable)	YES
Fb6:84-101	gene28405	3,71	9,19E-08	2,49E-05	ARP4_ARATH	Actin-related protein 4	Actin-related protein 4 (similar to)	YES
Fb6:84-101	gene11308	3,74	4,46E-04	4,90E-02	AUR3_ARATH	Serine/threonine-protein kinase Aurora-3	Serine/threonine-protein kinase Aurora-3 (AtAur3) (similar to)	NO
Fb6:84-101	gene27944	3,85	6,06E-04	6,43E-02	-	-	tRNA modification GTPase mss1, mitochondrial, Precursor (probable)	NO
Fb6:84-101	gene31310	3,99	5,01E-04	5,38E-02	-	-	DAZ-associated protein 1 (probable)	YES
Fb6:84-101	gene28403	4,02	5,93E-05	8,25E-03	B8BLZ3_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RLIM (R-LIM) (probable)	YES
Fb6:84-101	gene28404	4,09	3,01E-11	1,34E-08	B8BLZ3_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RLIM (R-LIM) (probable)	YES
Fb6:84-101	gene32418	4,23	1,74E-04	2,17E-02	Q2QV96_ORYSJ	Os12g0238000 protein	Myb-related protein 3R-1 (Protein PC-MYB1) (similar to)	YES
Fb6:84-101	gene04404	4,26	2,59E-09	8,07E-07	EXPA9_ARATH	Expansin-A9	Expansin-A25 (AtEXPA25), Precursor (similar to)	YES
Fb6:84-101	gene27945	4,34	3,04E-15	2,27E-12	RNG1L_ARATH	E3 ubiquitin-protein ligase RING1-like	E3 ubiquitin-protein ligase rnf181 (probable)	YES

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Fb6:84-101	gene04372	4,40	3,91E-12	2,00E-09	SCPDL_ARATH	Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410	Probable mitochondrial saccharopine dehydrogenase At5g39410 (SDH) (similar to)	NO
Fb6:84-101	gene20289	4,82	2,66E-09	8,15E-07	CDPKO_ARATH	Calcium-dependent protein kinase 24	Protein transport protein sec31 (probable)	YES
Fb6:84-101	gene06749	4,97	4,93E-10	1,77E-07	A2XYK1_ORYSI	Putative uncharacterized protein	hypothetical protein	YES
Fb6:84-101	gene20633	5,13	6,58E-04	6,84E-02	H32_ARATH	Histone H3.2	Histone H3.2 (putative)	NO
Fb6:84-101	gene28200	5,46	5,53E-22	7,37E-19	U87A1_ARATH	UDP-glycosyltransferase 87A1	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (probable)	NO
Fb6:84-101	gene16302	5,49	2,35E-04	2,81E-02	-	-	Autophagy-related protein 7 (probable)	YES
Fb6:84-101	gene03841	5,60	2,73E-06	5,79E-04	SPSA3_ARATH	Probable sucrose-phosphate synthase 3	Sucrose-phosphate synthase 2 (similar to)	YES
Fb6:84-101	gene27937	5,68	6,78E-04	6,96E-02	Q93Z83_ARATH	TRAF-like family protein	Putative pentatricopeptide repeat-containing protein At3g01580 (probable)	NO
Fb6:84-101	gene26869	5,74	9,86E-04	9,74E-02	VDAC1_ARATH	Mitochondrial outer membrane protein porin 1	Mitochondrial outer membrane protein porin of 36 kDa (VDAC) (similar to)	YES
Fb6:84-101	gene24583	6,01	1,88E-05	3,11E-03	-	-	Mucin-7 (MUC-7), Precursor (probable)	YES
Fb6:84-101	gene24771	6,27	3,30E-06	6,63E-04	Q8LEJ7_ARATH	Uncharacterized protein	Protein tolB, Precursor (probable)	YES
Fb6:84-101	gene04360	6,59	8,74E-20	9,07E-17	SCPDL_ARATH	Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410	Probable mitochondrial saccharopine dehydrogenase At5g39410 (SDH) (similar to)	YES
Fb6:84-101	gene04364	6,59	3,37E-28	1,05E-24	SCPDL_ARATH	Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410	Probable mitochondrial saccharopine dehydrogenase At5g39410 (SDH) (similar to)	YES
Fb6:84-101	gene10249	6,64	2,23E-05	3,66E-03	B9GA75_ORYSJ	Putative uncharacterized protein	Ankyrin repeat-containing protein At3g12360 (probable)	YES
Fb6:84-101	gene20941	6,74	1,05E-05	1,84E-03	Q5VPA8_ORYSJ	cDNA clone:J013099M07, full insert sequence	Probable LRR receptor-like serine/threonine-protein kinase At3g47570, Precursor	NO
Fb6:84-101	gene25852	6,79	1,80E-09	5,81E-07	PER51_ARATH	Peroxidase 51	Peroxidase 55 (Atperox P55), Precursor (similar to)	NO
Fb6:84-101	gene34902	7,01	2,32E-07	5,79E-05	Q8S6X7_ORYSJ	Zinc knuckle family protein	Probable amino-acid ABC transporter permease protein patM (similar to)	YES

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Fb6:84-101	gene16276	7,18	6,72E-24	1,25E-20	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	NO
Fb6:84-101	gene28033	7,24	5,48E-31	2,56E-27	UGT2_GARJA	7-deoxyloganetin glucosyltransferase	Cytokinin-O-glucosyltransferase 2 (AtZOG2) (similar to)	NO
Fb6:84-101	gene28014	7,26	6,44E-04	6,75E-02	CTNS_ARATH	Cystinosin homolog	Cystinosin homolog (putative)	YES
Fb6:84-101	gene26396	7,29	2,01E-23	3,41E-20	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	YES
Fb6:84-101	gene03794	7,63	1,89E-14	1,22E-11	TBL20_ARATH	Protein trichome birefringence-like 20	hypothetical protein	YES
Fb6:84-101	gene01388	7,64	3,16E-06	6,41E-04	-	-	Probable RNA-directed RNA polymerase	YES
Fb6:84-101	gene10389	8,43	1,10E-09	3,61E-07	Q5W741_ORYSJ	Uncharacterized protein	hypothetical protein	YES
Fb6:84-101	gene16462	8,59	8,11E-15	5,41E-12	B8BL95_ORYSI	Putative uncharacterized protein	Anoctamin-8 (probable)	YES
Fb6:84-101	gene31661	8,63	1,28E-07	3,38E-05	B9G5C7_ORYSJ	Putative uncharacterized protein	hypothetical protein	NO
Fb6:84-101	gene03840	9,17	1,30E-08	3,68E-06	B8AA50_ORYSI	Putative uncharacterized protein	Kinesin-like protein KIF20B (MPP1) (probable)	YES
Fb6:84-101	gene28036	9,26	3,10E-34	1,93E-30	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	YES
Fb6:84-101	gene24757	9,68	1,04E-13	6,27E-11	F4I082_ARATH	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	Non-specific lipid-transfer protein-like protein At5g64080, Precursor (probable)	NO
Fb6:84-101	gene28452	9,92	6,16E-05	8,40E-03	Q9SI97_ARATH	Putative C2H2-type zinc finger protein	Zinc finger protein 1 (probable)	NO
Fb6:84-101	gene01305	Inf	1,87E-04	2,28E-02	A2X9A6_ORYSI	Putative uncharacterized protein	Cytoplasmic dynein 2 heavy chain 1 (probable)	NO
Fb6:84-101	gene03792	Inf	5,76E-06	1,07E-03	TPS2_LOTJA	Tricyclene synthase EBOS, chloroplastic	Myrcene synthase, chloroplastic, Precursor (probable)	YES
Fb6:84-101	gene04181	Inf	2,57E-06	5,52E-04	-	-	hypothetical protein	YES
Fb6:84-101	gene04343	Inf	1,79E-04	2,22E-02	-	-	Protein strawberry notch (probable)	YES
Fb6:84-101	gene06086	Inf	4,06E-04	4,54E-02	B7E5U7_ORYSJ	cDNA clone:J033084E14, full insert sequence	UvrABC system protein B (Protein uvrB) (probable)	NO
Fb6:84-101	gene10316	Inf	5,03E-09	1,49E-06	Q94LL1_ORYSA	Putative 40S ribosomal protein contains C-terminal domain	40S ribosomal protein S3-2 (similar to)	YES
Fb6:84-101	gene13894	Inf	4,44E-05	6,38E-03	-	-	Merozoite surface protein CMZ-8 (probable)	YES
Fb6:84-101	gene16028	Inf	7,65E-04	7,73E-02	Q0J5Y3_ORYSJ	Os08g0389500 protein	Endonuclease (probable)	YES
Fb6:84-101	gene18333	Inf	2,28E-05	3,70E-03	Q7XC13_ORYSJ	Putative uncharacterized protein OSJNBa0057L21.4	F-box only protein 8 (probable)	YES

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Fb6:84-101	gene24780	Inf	2,20E-04	2,67E-02	-	-	300 kDa antigen AG231 (probable)	YES
Fb6:84-101	gene25853	Inf	3,62E-14	2,26E-11	-	-	Peroxidase 55 (Atperox P55), Precursor (similar to)	NO
Fb6:84-101	gene25855	Inf	8,66E-07	2,00E-04	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	YES
Fb6:84-101	gene26371	Inf	3,82E-04	4,33E-02	F4JHK5_ARATH	Uncharacterized protein	HBS1-like protein (probable)	YES
Fb6:84-101	gene26405	Inf	3,45E-17	3,07E-14	A2X7H1_ORYSI	Putative uncharacterized protein	F-box protein At5g07610 (probable)	YES
Fb6:84-101	gene28013	Inf	1,08E-05	1,87E-03	B8BLZ3_ORYSI	Putative uncharacterized protein	RING finger protein 126 (probable)	YES
Fb6:84-101	gene28324	Inf	3,35E-10	1,28E-07	PP351_ARATH	Pentatricopeptide repeat-containing protein At4g35850, mitochondrial	Pentatricopeptide repeat-containing protein At4g35850, mitochondrial, Precursor (similar to)	YES
Fb6:84-101	gene28495	Inf	3,49E-13	1,97E-10	B8BJX4_ORYSI	Putative uncharacterized protein	Putative ankyrin repeat protein L93 (probable)	NO
Fb6:84-101	gene28897	Inf	1,48E-08	4,12E-06	MMSA_ARATH	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial (MMSDH), Precursor (similar to)	NO
Fb6:84-101	gene29333	Inf	3,96E-04	4,46E-02	-	-	ATP-dependent RNA helicase DED1 (probable)	NO
Fb6:84-101	gene30171	Inf	2,21E-08	6,06E-06	F4IE28_ARATH	TTF-type zinc finger protein with HAT dimerization domain	L-seryl-tRNA(Sec) selenium transferase (Sec synthase) (probable)	NO
Fb7:0-10	gene03065	-Inf	2,34E-05	1,87E-03	Q0E2T2_ORYSJ	Os02g0215900 protein	Probable LRR receptor-like serine/threonine-protein kinase At3g47570, Precursor	YES
Fb7:0-10	gene03916	-Inf	1,84E-15	5,72E-13	-	-	Capsid polyprotein (probable)	YES
Fb7:0-10	gene03979	-Inf	1,50E-09	2,41E-07	PR1B5_ARATH	PRA1 family protein B5	3-hydroxyacyl-CoA dehydrogenase (similar to)	NO
Fb7:0-10	gene05012	-Inf	6,97E-04	3,60E-02	-	-	UDP-N-acetylmuramoylalanine--D-glutamate ligase (probable)	YES
Fb7:0-10	gene05059	-Inf	4,71E-21	2,75E-18	-	-	Torsin-1A-interacting protein 2 (probable)	YES
Fb7:0-10	gene06510	-Inf	6,06E-23	4,92E-20	F4JTS8_ARATH	Nuclear factor NO VEIN	UPF0102 protein RPC_0320 (probable)	YES
Fb7:0-10	gene07457	-Inf	2,81E-18	1,19E-15	B9FEV7_ORYSJ	Putative uncharacterized protein	B3 domain-containing protein Os04g0386900 (probable)	YES
Fb7:0-10	gene07754	-Inf	1,58E-11	3,29E-09	-	-	Acylamino-acid-releasing enzyme (AARE) (probable)	YES

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Fb7:0-10	gene09194	-Inf	1,68E-08	2,32E-06	ARFJ_ARATH	Auxin response factor 10	Pre-rRNA-processing protein ipi1 (probable)	NO
Fb7:0-10	gene14179	-Inf	1,14E-27	1,78E-24	Q84VE6_ORYSJ	Putative uncharacterized protein	Probable receptor-like protein kinase At1g30570, Precursor	NO
Fb7:0-10	gene14247	-Inf	2,52E-12	5,53E-10	B0M1H3_ARATH	ZIP4-like protein	2-hydroxyacylsphingosine 1-beta-galactosyltransferase, Precursor (probable)	NO
Fb7:0-10	gene14337	-Inf	1,54E-07	1,78E-05	DNM1A_ORYSJ	DNA (cytosine-5)-methyltransferase 1A	Dihydroxy-acid dehydratase (DAD) (probable)	YES
Fb7:0-10	gene14448	-Inf	6,76E-09	9,97E-07	TCP18_ARATH	Transcription factor TCP18	Cyclic AMP-responsive element-binding protein 5 (cAMP-responsive element-binding protein 5) (probable)	NO
Fb7:0-10	gene16005	-Inf	1,62E-05	1,35E-03	-	-	Phosphatase and actin regulator 4 (probable)	YES
Fb7:0-10	gene16880	-Inf	3,62E-08	4,62E-06	B9G5C7_ORYSJ	Putative uncharacterized protein	Piwi-like protein 4 (probable)	YES
Fb7:0-10	gene17036	-Inf	2,57E-07	2,93E-05	B9FZS7_ORYSJ	Putative uncharacterized protein	HAUS augmin-like complex subunit 1 (probable)	YES
Fb7:0-10	gene18702	-Inf	3,45E-09	5,37E-07	Q8S6P1_ORYSJ	Putative reverse transcriptase	hypothetical protein	NO
Fb7:0-10	gene18954	-Inf	2,53E-04	1,56E-02	-	-	Os09g0462300 (probable)	NO
Fb7:0-10	gene18955	-Inf	1,38E-07	1,64E-05	FRS3_ARATH	Protein FAR1-RELATED SEQUENCE 3	Protein FAR-RED ELONGATED HYPOCOTYL 3 (probable)	NO
Fb7:0-10	gene19071	-Inf	9,84E-08	1,19E-05	-	-	Intestinal mucin-like protein (MLP) (probable)	NO
Fb7:0-10	gene19073	-Inf	2,85E-17	1,06E-14	-	-	Ferrochelatase (probable)	NO
Fb7:0-10	gene19074	-Inf	1,20E-20	6,76E-18	Q7FA54_ORYSJ	OSJNBa0018J19.2 protein	Homeobox protein MSX-1 (probable)	NO
Fb7:0-10	gene19246	-Inf	7,28E-05	5,21E-03	O23072_ARATH	Fringe-related protein	Probable receptor-like protein kinase At5g24010, Precursor	NO
Fb7:0-10	gene19400	-Inf	7,10E-05	5,12E-03	GSTZ1_ARATH	Glutathione S-transferase Z1	Glutathione S-transferase zeta class (similar to)	NO
Fb7:0-10	gene19430	-Inf	2,71E-16	9,04E-14	-	-	Glutamate--cysteine ligase (GCS) (probable)	NO
Fb7:0-10	gene19454	-Inf	6,46E-15	1,86E-12	Q2QRP3_ORYSJ	Plastocyanin-like domain containing protein, expressed	Blue copper protein, Precursor (probable)	NO
Fb7:0-10	gene21241	-Inf	2,10E-08	2,84E-06	Q9S7W4_ARATH	Putative uncharacterized protein At3g07720	Glucose-6-phosphate isomerase (GPI) (probable)	YES
Fb7:0-10	gene21480	-Inf	1,62E-28	2,75E-25	-	-	Malate dehydrogenase, peroxisomal (probable)	YES

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NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb7:0-10	gene23432	-Inf	1,67E-06	1,68E-04	H4_ARATH	Histone H4	Histone H4.3 (similar to)	NO
Fb7:0-10	gene24473	-Inf	8,97E-08	1,09E-05	-	-	ATP synthase gamma chain (similar to)	YES
Fb7:0-10	gene26755	-Inf	4,43E-05	3,34E-03	A2XWM0_ORYSI	Putative uncharacterized protein	Probable cellulose synthase A catalytic subunit 1 [UDP-forming]	NO
Fb7:0-10	gene26795	-Inf	3,56E-10	6,58E-08	-	-	AP-1 complex subunit gamma-1 (similar to)	YES
Fb7:0-10	gene26902	-Inf	2,15E-08	2,89E-06	B9GBH0_ORYSJ	Putative uncharacterized protein	Parvalbumin beta (similar to)	NO
Fb7:0-10	gene26950	-Inf	3,41E-04	2,00E-02	B9G4W2_ORYSJ	MATE efflux family protein	Phosphate import ATP-binding protein pstB 1 (probable)	YES
Fb7:0-10	gene28609	-Inf	3,75E-10	6,82E-08	Q7XZF8_ORYSJ	Putative DNA binding protein	50S ribosomal protein L9 (probable)	YES
Fb7:0-10	gene29473	-Inf	1,10E-05	9,70E-04	B9F6L9_ORYSJ	Putative uncharacterized protein	Trichothecene 3-O-acetyltransferase (probable)	YES
Fb7:0-10	gene34018	-Inf	4,80E-10	8,54E-08	-	-	Reticulon-2 (xRTN2) (probable)	YES
Fb7:0-10	gene35032	-Inf	1,49E-21	9,30E-19	SOT15_ARATH	Cytosolic sulfotransferase 15	Flavonol sulfotransferase-like (probable)	NO
Fb7:0-10	gene35119	-Inf	9,97E-11	2,02E-08	Q2QMW8_ORYSJ	Transposon protein, putative, CACTA, En/Spm sub-class	Histidine-rich glycoprotein, Precursor (probable)	YES
Fb7:0-10	gene35125	-Inf	3,83E-04	2,18E-02	Q259H7_ORYSA	H0103C06.10 protein	N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase (probable)	YES
Fb7:0-10	gene21489	-10,88	6,43E-19	3,00E-16	Q2R258_ORYSJ	Putative uncharacterized protein	Pleckstrin homology domain-containing family M member 1 (probable)	YES
Fb7:0-10	gene19696	-10,18	2,48E-18	1,08E-15	PLT5_ARATH	Polyol transporter 5	hypothetical protein	NO
Fb7:0-10	gene19154	-9,58	1,63E-33	7,60E-30	F4JH46_ARATH	MATE efflux family protein	Protein TRANSPARENT TESTA 12 (probable)	NO
Fb7:0-10	gene05315	-9,22	1,11E-28	2,08E-25	DRL36_ARATH	Probable disease resistance protein At5g45510	Transaldolase 2 (probable)	NO
Fb7:0-10	gene09200	-9,07	4,30E-32	1,34E-28	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (HIB-CoA hydrolase), Precursor (probable)	NO
Fb7:0-10	gene04804	-9,03	1,81E-22	1,25E-19	-	-	Colicin-E7 (probable)	NO
Fb7:0-10	gene00398	-8,80	2,70E-21	1,63E-18	C3H11_ORYSJ	Zinc finger CCCH domain-containing protein 11	Zinc finger CCCH domain-containing protein 11 (OsC3H11) (similar to)	NO
Fb7:0-10	gene08320	-8,80	2,05E-06	2,01E-04	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (similar to)	NO

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Fb7:0-10	gene23479	-8,43	9,26E-24	8,24E-21	AROD2_ARATH	Arogenate dehydratase/prephenate dehydratase 2, chloroplastic	Arogenate dehydratase/prephenate dehydratase 2, chloroplastic (AtADT2), Precursor (similar to)	NO
Fb7:0-10	gene03915	-8,26	4,02E-18	1,63E-15	B8A7H7_ORYSI	Putative uncharacterized protein	hypothetical protein	YES
Fb7:0-10	gene14190	-8,26	5,69E-31	1,18E-27	C79D2_MANES	Valine N-monooxygenase 2	Ethylene-responsive transcription factor ABI4 (ERF ABI4) (probable)	NO
Fb7:0-10	gene07458	-8,21	4,04E-17	1,48E-14	B9FEV7_ORYSJ	Putative uncharacterized protein	B3 domain-containing protein Os04g0386900 (probable)	NO
Fb7:0-10	gene18628	-8,18	3,82E-06	3,63E-04	Q9FLV1_ARATH	Putative 60S acidic ribosomal protein P1	60S acidic ribosomal protein P1 (probable)	NO
Fb7:0-10	gene19077	-8,08	6,25E-22	4,02E-19	A2XTE7_ORYSI	Putative uncharacterized protein	Protein FAR-RED IMPAIRED RESPONSE 1 (probable)	NO
Fb7:0-10	gene09158	-8,06	5,85E-17	2,10E-14	Q0DWY2_ORYSJ	Os02g0787500 protein	CCHC-type zinc finger protein CG3800 (probable)	YES
Fb7:0-10	gene35127	-8,02	2,56E-08	3,40E-06	-	-	Trigger factor (TF) (probable)	YES
Fb7:0-10	gene26753	-7,88	2,78E-12	5,97E-10	Q60DP5_ORYSJ	Expressed protein	hypothetical protein	YES
Fb7:0-10	gene35015	-7,87	2,68E-06	2,58E-04	-	-	Capsid protein (probable)	NO
Fb7:0-10	gene14245	-7,71	7,00E-20	3,63E-17	-	-	Endophilin-A2 (probable)	YES
Fb7:0-10	gene19027	-7,69	1,32E-14	3,61E-12	Q2R101_ORYSJ	Retrotransposon protein, putative, unclassified	MAP1 light chain LC2 (probable)	NO
Fb7:0-10	gene08906	-7,66	8,40E-23	6,53E-20	AP4E_ARATH	AP-4 complex subunit epsilon	AP-4 complex subunit epsilon-1 (probable)	YES
Fb7:0-10	gene19176	-7,52	4,62E-05	3,47E-03	RA51B_ARATH	DNA repair protein RAD51 homolog 2	Acetylglutamate kinase, Precursor (probable)	NO
Fb7:0-10	gene21443	-7,52	1,19E-22	8,88E-20	Q9LUD3_ARATH	Cytochrome P450, family 72, subfamily A, polypeptide 7	Secologanin synthase (SLS) (similar to)	YES
Fb7:0-10	gene07451	-7,42	2,25E-09	3,59E-07	-	-	Ribose-5-phosphate isomerase A (PRI) (probable)	YES
Fb7:0-10	gene19072	-7,34	1,51E-17	5,88E-15	A2YS34_ORYSI	Putative uncharacterized protein	F-box protein SKIP19 (probable)	YES
Fb7:0-10	gene04796	-7,32	1,09E-12	2,57E-10	TMVRN_NICGU	TMV resistance protein N	TMV resistance protein N (probable)	NO
Fb7:0-10	gene19024	-7,17	3,66E-24	3,60E-21	Q0JBG2_ORYSJ	Os04g0533900 protein	Putative late blight resistance protein homolog R1A-3 (probable)	NO
Fb7:0-10	gene19372	-6,98	2,10E-24	2,18E-21	PSA2A_ARATH	Proteasome subunit alpha type-2-A	Proteasome subunit alpha type-2-A (similar to)	NO
Fb7:0-10	gene09266	-6,91	6,78E-09	9,97E-07	Q6K4E4_ORYSJ	Putative CRS1	Tripartite motif-containing protein 45 (probable)	NO

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Fb7:0-10	gene23606	-6,85	1,24E-14	3,45E-12	LOX2_ORYSJ	Linoleate 9S-lipoxygenase 2	3-deoxy-manno-octulosonate cytidylyltransferase (CKS) (similar to)	YES
Fb7:0-10	gene26798	-6,84	2,51E-22	1,68E-19	VICHY_VICSN	Vicianin hydrolase	Beta-glucosidase 17 (AtBGLU17), Precursor (similar to)	YES
Fb7:0-10	gene16479	-6,74	1,49E-07	1,75E-05	B9RYP6_RICCO	Heat shock protein, putative	Luminal-binding protein 3 (BiP3), Precursor (probable)	YES
Fb7:0-10	gene23450	-6,72	1,99E-20	1,09E-17	A2WZX6_ORYSI	Putative uncharacterized protein	Tyrosine-protein kinase receptor TYRO3, Precursor (probable)	NO
Fb7:0-10	gene00374	-6,72	1,81E-05	1,49E-03	A2ZDW3_ORYSI	Putative uncharacterized protein	Cytosolic carboxypeptidase-like protein 5 (probable)	NO
Fb7:0-10	gene15215	-6,67	2,98E-19	1,50E-16	T14H_TAXCU	Taxoid 14-beta-hydroxylase	Cytochrome P450 716B1 (probable)	YES
Fb7:0-10	gene35026	-6,64	8,70E-26	1,08E-22	Q94GT7_ORYSJ	Transposon protein, putative, CACTA, En/Spm sub-class	Protein translocase subunit secA (probable)	NO
Fb7:0-10	gene23605	-6,59	4,15E-19	1,99E-16	Q6Z0P0_ORYSJ	Putative tyrosine-tRNA ligase	Tyrosyl-tRNA synthetase (TyrRS) (probable)	YES
Fb7:0-10	gene33856	-6,57	2,37E-26	3,16E-23	-	-	tRNA-processing ribonuclease BN (RNase BN) (probable)	YES
Fb7:0-10	gene03952	-6,55	3,26E-04	1,92E-02	Q9SZ66_ARATH	TIR-NBS-LRR class disease resistance protein	TMV resistance protein N (probable)	NO
Fb7:0-10	gene19028	-6,53	2,68E-23	2,28E-20	B8AF64_ORYSI	Putative uncharacterized protein	Keratin, high-sulfur matrix protein, IIIA3 (probable)	YES
Fb7:0-10	gene03102	-6,20	6,64E-16	2,14E-13	Q93YW3_ARATH	Putative uncharacterized protein At1g01830	hypothetical protein	YES
Fb7:0-10	gene14295	-6,19	6,06E-18	2,41E-15	PTR25_ARATH	Protein NRT1/ PTR FAMILY 5.12	Peptide transporter PTR1 (probable)	NO
Fb7:0-10	gene34011	-6,02	1,38E-25	1,52E-22	F4JBC7_ARATH	HXXXD-type acyl-transferase-like protein	BAHD acyltransferase At5g47980 (probable)	YES
Fb7:0-10	gene00399	-5,90	3,89E-15	1,19E-12	UBP12_ARATH	Ubiquitin carboxyl-terminal hydrolase 12	Ubiquitin carboxyl-terminal hydrolase 12 (AtUBP12) (similar to)	NO
Fb7:0-10	gene29481	-5,90	1,55E-22	1,11E-19	B9G602_ORYSJ	Putative uncharacterized protein	LOB domain-containing protein 16 (AS2-like protein 18) (probable)	NO
Fb7:0-10	gene14422	-5,61	1,59E-05	1,33E-03	B9GCH3_ORYSJ	Putative uncharacterized protein	E3 ubiquitin-protein ligase RNF8 (probable)	YES
Fb7:0-10	gene03028	-5,42	7,42E-19	3,38E-16	C14C2_ORYSJ	Cytochrome P450 714C2	Secologanin synthase (SLS) (probable)	NO
Fb7:0-10	gene29500	-5,36	3,45E-13	8,40E-11	Q9C9M1_ARATH	Putative S locus-linked protein	Methyltransferase-like protein 13 (probable)	YES
Fb7:0-10	gene26960	-5,34	3,46E-13	8,40E-11	Q9ZSB8_ARATH	Putative uncharacterized protein At4g10620	hypothetical protein	NO

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Fb7:0-10	gene19078	-5,28	7,38E-05	5,26E-03	-	-	Proliferating cell nuclear antigen (PCNA) (probable)	NO
Fb7:0-10	gene19222	-5,27	2,55E-12	5,53E-10	DRL4_ARATH	Putative disease resistance protein At1g50180	Putative disease resistance protein At1g50180 (probable)	NO
Fb7:0-10	gene19081	-5,27	1,93E-10	3,68E-08	IF4G1_ARATH	Eukaryotic translation initiation factor isoform 4G-1	Eukaryotic initiation factor iso-4F subunit p82-34 (eIF-(iso)4F p82-34) (probable)	NO
Fb7:0-10	gene18953	-5,26	4,29E-07	4,72E-05	Q8H374_ORYSJ	Putative uncharacterized protein OSJNBa0061L20.120	hypothetical protein	NO
Fb7:0-10	gene23615	-5,23	6,91E-08	8,49E-06	Q947Z9_ORYSJ	Putative retroelement	Ammonium transporter 1 member 2 (OsAMT1) (probable)	NO
Fb7:0-10	gene05329	-5,23	3,51E-10	6,56E-08	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (HIB-CoA hydrolase), Precursor (probable)	NO
Fb7:0-10	gene06730	-5,21	2,42E-14	6,47E-12	-	-	Voltage-dependent R-type calcium channel subunit alpha-1E (BII) (probable)	YES
Fb7:0-10	gene17958	-5,15	8,33E-07	8,89E-05	-	-	Endothelial transcription factor GATA-2 (probable)	YES
Fb7:0-10	gene23598	-5,12	1,34E-10	2,63E-08	Q9C637_ARATH	Receptor like protein 6	LRR receptor-like serine/threonine-protein kinase EFR (EF-Tu receptor), Precursor (probable)	YES
Fb7:0-10	gene23586	-5,06	3,74E-04	2,15E-02	-	-	DNA repair protein RAD5 (probable)	YES
Fb7:0-10	gene34943	-5,05	1,25E-05	1,08E-03	-	-	Probable nitrile hydratase (Nitrilase)	YES
Fb7:0-10	gene00421	-5,00	4,66E-15	1,38E-12	B9FN37_ORYSJ	Endoglucanase	Internalin-I, Precursor (probable)	NO
Fb7:0-10	gene19240	-4,94	1,55E-15	4,90E-13	F4J9K9_ARATH	Neurofilament protein-related protein	hypothetical protein	NO
Fb7:0-10	gene26780	-4,94	3,63E-04	2,10E-02	-	-	Kinase and exchange factor for Rac A (probable)	YES
Fb7:0-10	gene23609	-4,88	1,46E-12	3,37E-10	CPR30_ARATH	F-box protein CPR30	F-box protein At4g12560 (probable)	YES
Fb7:0-10	gene02778	-4,84	5,59E-06	5,19E-04	Q5W771_ORYSJ	Putative polyprotein	4F2 cell-surface antigen heavy chain (4F2hc) (probable)	YES
Fb7:0-10	gene14794	-4,75	4,41E-07	4,81E-05	A2X9Y9_ORYSI	Putative uncharacterized protein	Latent-transforming growth factor beta-binding protein 1 (LTBP-1), Precursor (probable)	YES
Fb7:0-10	gene21464	-4,73	1,84E-05	1,50E-03	Q10NU5_ORYSJ	cDNA clone:J023136E13, full insert sequence	Probable gibberellin receptor GID1L3	YES

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Fb7:0-10	gene29367	-4,72	2,45E-08	3,27E-06	F4ILW4_ARATH	Uncharacterized protein	Protein EFR3 homolog B (probable)	YES
Fb7:0-10	gene34293	-4,62	2,77E-05	2,17E-03	-	-	Replication factor C large subunit (RFC large subunit) (probable)	YES
Fb7:0-10	gene03038	-4,55	6,28E-17	2,21E-14	A2WU16_ORYSI	Putative uncharacterized protein	Wall-associated receptor kinase-like 14, Precursor (probable)	NO
Fb7:0-10	gene19079	-4,47	6,12E-09	9,22E-07	KEA1_ARATH	K(+) efflux antiporter 1, chloroplastic	Endonuclease (probable)	NO
Fb7:0-10	gene14941	-4,40	2,00E-14	5,42E-12	MSI3_ARATH	WD-40 repeat-containing protein MSI3	hypothetical protein	YES
Fb7:0-10	gene05057	-4,40	9,49E-06	8,56E-04	-	-	Death domain-associated protein 6 (probable)	YES
Fb7:0-10	gene34210	-4,22	8,46E-13	2,03E-10	Q10GE7_ORYSJ	Retrotransposon protein, putative, unclassified	Protein piccolo (probable)	YES
Fb7:0-10	gene18933	-4,16	1,56E-11	3,28E-09	C71AP_ARATH	Cytochrome P450 71A25	Cytochrome P450 71A25 (probable)	NO
Fb7:0-10	gene13852	-4,14	1,53E-05	1,29E-03	-	-	mRNA cap guanine-N7 methyltransferase (probable)	YES
Fb7:0-10	gene09224	-4,03	3,78E-04	2,16E-02	Q6ZAM7_ORYSJ	Putative uncharacterized protein P0031C02.3	Methyltransferase/helicase/RNA-directed RNA polymerase (probable)	YES
Fb7:0-10	gene19766	-3,99	1,39E-04	9,17E-03	ASAT1_ARATH	Acyl-CoA--sterol O-acyltransferase 1	Probable long-chain-alcohol O-fatty-acyltransferase 5	NO
Fb7:0-10	gene21507	-3,99	4,44E-14	1,14E-11	F4JK84_ARATH	Monooxygenase 1	Putative oxidoreductase yetM, Precursor (probable)	YES
Fb7:0-10	gene19121	-3,99	2,42E-12	5,39E-10	Q9FW98_ORYSJ	Putative non-LTR retroelement reverse transcriptase	Putative pentatricopeptide repeat-containing protein At5g09950 (probable)	NO
Fb7:0-10	gene04905	-3,97	2,17E-04	1,37E-02	Q9C699_ARATH	Receptor like protein 7	Probable LRR receptor-like serine/threonine-protein kinase At4g36180, Precursor	YES
Fb7:0-10	gene26949	-3,94	3,76E-10	6,82E-08	LOXC2_ORYSJ	Probable lipoxygenase 8, chloroplastic	Probable lipoxygenase 8, chloroplastic, Precursor (similar to)	NO
Fb7:0-10	gene19135	-3,91	3,30E-12	7,00E-10	F4JPR7_ARATH	Protein SAY1	FAS-associated factor 2 (probable)	NO
Fb7:0-10	gene35104	-3,89	2,12E-05	1,71E-03	-	-	Lysyl-tRNA synthetase (LysRS) (probable)	NO
Fb7:0-10	gene34612	-3,84	4,15E-08	5,24E-06	Q75IS6_ORYSJ	Putative Mutator-like transposase	Protein FAR1-RELATED SEQUENCE 5 (probable)	NO
Fb7:0-10	gene16496	-3,78	1,25E-05	1,08E-03	B8ADE3_ORYSI	Putative uncharacterized protein	Probable leucine-rich repeat receptor-like protein kinase At1g35710, Precursor	NO

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Fb7:0-10	gene03025	-3,77	1,58E-06	1,61E-04	RAC2_ARATH	Rac-like GTP-binding protein ARAC2	Rac-like GTP-binding protein RAC2, Precursor (similar to)	NO
Fb7:0-10	gene05626	-3,76	3,14E-04	1,87E-02	RL122_ARATH	60S ribosomal protein L12-2	60S ribosomal protein L12-2 (similar to)	YES
Fb7:0-10	gene00425	-3,75	1,24E-12	2,91E-10	NFS2_ARATH	Cysteine desulfurase 2, chloroplastic	Cysteine desulfurase 2, chloroplastic, Precursor (similar to)	YES
Fb7:0-10	gene19120	-3,70	2,17E-12	4,87E-10	Q2R147_ORYSJ	Protein kinase domain containing protein, expressed	DNA replication complex GINS protein psf2 (probable)	NO
Fb7:0-10	gene18674	-3,68	1,70E-08	2,32E-06	Q9SZ66_ARATH	TIR-NBS-LRR class disease resistance protein	TMV resistance protein N (probable)	NO
Fb7:0-10	gene14253	-3,67	2,46E-04	1,53E-02	-	-	Z-DNA-binding protein 1 (probable)	YES
Fb7:0-10	gene19370	-3,63	7,72E-10	1,35E-07	O64631_ARATH	Putative cytochrome P450	Cytochrome P450 704C1 (probable)	NO
Fb7:0-10	gene04436	-3,55	2,53E-04	1,56E-02	RPS5_ARATH	Disease resistance protein RPS5	Probable disease resistance protein At5g63020	NO
Fb7:0-10	gene27363	-3,48	2,99E-04	1,81E-02	-	-	Leucine-rich repeat-containing protein 26, Precursor (probable)	YES
Fb7:0-10	gene18897	-3,48	9,27E-10	1,59E-07	O65090_ARATH	Ribosomal RNA adenine dimethylase family protein	Dimethyladenosine transferase (probable)	NO
Fb7:0-10	gene19178	-3,43	6,86E-08	8,48E-06	-	-	DNA double-strand break repair rad50 ATPase (probable)	NO
Fb7:0-10	gene23449	-3,43	1,10E-10	2,18E-08	Q8GVR2_ORYSJ	cDNA clone:001-115-C06, full insert sequence	Cysteine proteinase 15A, Precursor (probable)	NO
Fb7:0-10	gene19373	-3,37	7,04E-10	1,24E-07	FLA21_ARATH	Fasciclin-like arabinogalactan protein 21	Putative fasciclin-like arabinogalactan protein 20 (probable)	NO
Fb7:0-10	gene29347	-3,37	1,86E-04	1,19E-02	PMAT2_ARATH	Phenolic glucoside malonyltransferase 2	Anthocyanin 5-aromatic acyltransferase (5AT) (probable)	NO
Fb7:0-10	gene16004	-3,36	3,77E-07	4,20E-05	BXL4_ARATH	Beta-D-xylosidase 4	Beta-D-xylosidase 4 (AtBXL4), Precursor (similar to)	NO
Fb7:0-10	gene12000	-3,29	9,72E-05	6,68E-03	Y3622_ARATH	B3 domain-containing protein At3g06220	B3 domain-containing protein REM5 (probable)	YES
Fb7:0-10	gene23640	-3,23	1,92E-04	1,22E-02	Q7XS05_ORYSJ	OSJNBa0095H06.14 protein	GDSL esterase/lipase At5g03610, Precursor (similar to)	NO
Fb7:0-10	gene19088	-3,22	7,10E-07	7,71E-05	FOLD4_ARATH	Methenyltetrahydrofolate cyclohydrolase	Methenyltetrahydrofolate cyclohydrolase (similar to)	NO
Fb7:0-10	gene23576	-3,21	8,84E-05	6,14E-03	Q94DE5_ORYSJ	Putative betaine/proline transporter	Lysine histidine transporter-like 1 (probable)	NO
Fb7:0-10	gene02775	-3,21	3,97E-04	2,25E-02	O82593_ARATH	Putative NAM-like protein	NAC domain-containing protein 68 (ANAC068) (probable)	YES
Fb7:0-10	gene04856	-3,18	3,13E-	1,87E-	TMVRN_NIC	TMV resistance protein N	TMV resistance protein N	YES

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			04	02	GU		(probable)	
Fb7:0-10	gene03943	-3,17	2,28E-04	1,42E-02	Q9FWI2_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Regulatory protein recX (probable)	YES
Fb7:0-10	gene00342	-3,12	1,22E-08	1,73E-06	Q9LPN6_ARATH	Putative uncharacterized protein At3g10630	Protein FYV10 (probable)	NO
Fb7:0-10	gene19447	-3,11	1,27E-04	8,48E-03	Q9LK11_ARATH	O-Glycosyl hydrolases family 17 protein	Glucan endo-1,3-beta-glucosidase 14 ((1->3)-beta-glucanase 14), Precursor (probable)	NO
Fb7:0-10	gene16503	-3,00	7,41E-05	5,26E-03	Q5VR20_ORYSJ	Putative verticillium wilt disease resistance protein	LRR receptor-like serine/threonine-protein kinase GSO1, Precursor (probable)	YES
Fb7:0-10	gene23480	-2,98	6,78E-06	6,27E-04	NUP1_ARATH	Nuclear pore complex protein NUP1	Nascent polypeptide-associated complex subunit alpha (probable)	YES
Fb7:0-10	gene35143	-2,96	2,84E-08	3,71E-06	R13L1_ARATH	Putative disease resistance RPP13-like protein 1	Putative disease resistance RPP13-like protein 1 (probable)	NO
Fb7:0-10	gene19287	-2,93	3,63E-04	2,10E-02	CNGC1_ARATH	Cyclic nucleotide-gated ion channel 1	Cyclic nucleotide-gated ion channel 1 (AtCNGC1) (probable)	NO
Fb7:0-10	gene03933	-2,90	3,80E-07	4,20E-05	Q8S7I2_ORYSJ	Putative transposase	Coiled-coil domain-containing protein 115 (probable)	YES
Fb7:0-10	gene02085	-2,88	1,04E-08	1,49E-06	Q93YS8_ARATH	Serinc-domain containing serine and sphingolipid biosynthesis protein	Probable serine incorporator	NO
Fb7:0-10	gene09217	-2,86	2,17E-03	9,66E-02	Q2R147_ORYSJ	Protein kinase domain containing protein, expressed	Protein SDS24 (probable)	NO
Fb7:0-10	gene19365	-2,84	1,45E-08	2,04E-06	A2WWS8_ORYSI	Putative uncharacterized protein	RNA-binding protein 28 (probable)	NO
Fb7:0-10	gene23635	-2,83	7,42E-06	6,79E-04	PSD2B_ARATH	26S proteasome non-ATPase regulatory subunit 2 homolog B	26S proteasome non-ATPase regulatory subunit 2 (probable)	NO
Fb7:0-10	gene11982	-2,80	3,43E-07	3,85E-05	-	-	Methyl-CpG-binding protein 2 (MeCP-2 protein) (probable)	NO
Fb7:0-10	gene03125	-2,80	6,14E-04	3,26E-02	Q10CE5_ORYSJ	Expressed protein	Translation initiation factor IF-2 (probable)	NO
Fb7:0-10	gene24189	-2,78	1,36E-03	6,56E-02	TBL20_ARATH	Protein trichome birefringence-like 20	Trehalose-phosphate synthase (TPS) (probable)	NO
Fb7:0-10	gene29363	-2,72	1,67E-03	7,78E-02	KCO1_ORYSJ	Two pore potassium channel a	Probable calcium-activated outward-rectifying potassium channel 6 (AtKCO6)	NO
Fb7:0-10	gene23652	-2,71	4,98E-05	3,69E-03	TBL36_ARATH	Protein trichome birefringence-like 36	Tryptophanyl-tRNA synthetase (TrpRS) (probable)	YES
Fb7:0-10	gene03970	-2,69	1,02E-	9,13E-	ZAT9_ARAT	Zinc finger protein ZAT9	Zinc finger protein 1	NO

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			05	04	H		(probable)	
Fb7:0-10	gene23448	-2,69	5,53E-04	2,99E-02	Q8GU81_ORYSJ	Uncharacterized protein	Sulfate/thiosulfate import ATP-binding protein cysA (probable)	YES
Fb7:0-10	gene25323	-2,66	5,33E-04	2,92E-02	B8A7Y9_ORYSI	Putative uncharacterized protein	RNA polymerase-associated protein rapA (probable)	YES
Fb7:0-10	gene19111	-2,66	1,96E-03	8,86E-02	Q9M2T2_ARATH	Putative elicitor responsive/phloem	Elicitor-responsive protein 3 (similar to)	NO
Fb7:0-10	gene14338	-2,62	3,64E-07	4,07E-05	RPE5C_ARATH	DNA-directed RNA polymerase V subunit 5C	DNA-directed RNA polymerases I, II, and III subunit RPABC1 (RNA polymerases I, II, and III subunit ABC1) (probable)	NO
Fb7:0-10	gene18597	-2,55	1,79E-06	1,79E-04	-	-	Secologanin synthase (SLS) (similar to)	NO
Fb7:0-10	gene19167	-2,55	6,26E-05	4,55E-03	-	-	Putative ubiquitin thioesterase L96 (probable)	NO
Fb7:0-10	gene30046	-2,46	3,49E-04	2,04E-02	LBD4_ARATH	LOB domain-containing protein 4	LOB domain-containing protein 4 (AS2-like protein 6) (putative)	YES
Fb7:0-10	gene29943	-2,45	1,23E-03	6,02E-02	Q6K4C3_ORYSJ	Hydroxyproline-rich glycoprotein-like	Coiled-coil domain-containing protein 34 (probable)	YES
Fb7:0-10	gene19399	-2,44	9,49E-07	1,00E-04	FKB43_ARATH	Peptidyl-prolyl cis-trans isomerase FKBP43	46 kDa FK506-binding nuclear protein (PPIase) (probable)	NO
Fb7:0-10	gene00348	-2,43	8,94E-07	9,49E-05	DNAJ2_ARATH	Chaperone protein dnaJ 2	DnaJ protein homolog (putative)	YES
Fb7:0-10	gene26977	-2,43	4,29E-04	2,40E-02	Q7X5Z0_ORYSJ	OSJNBb0071D01.3 protein	Endonuclease (probable)	YES
Fb7:0-10	gene34961	-2,41	4,91E-05	3,66E-03	FAR1_ARATH	Protein FAR-RED IMPAIRED RESPONSE 1	Protein FAR1-RELATED SEQUENCE 5 (probable)	YES
Fb7:0-10	gene03055	-2,39	7,93E-05	5,61E-03	Q7XP55_ORYSJ	cDNA clone:006-312-B04, full insert sequence	Mating-type protein A-alpha Y1 (probable)	YES
Fb7:0-10	gene14939	-2,38	3,04E-04	1,83E-02	O82230_ARATH	Uncharacterized protein	Cyclin-dependent kinase inhibitor 4 (probable)	NO
Fb7:0-10	gene18704	-2,36	5,09E-04	2,80E-02	B9V0R6_9ORYZ	F-box family-4	tRNA wybutosine synthesizing protein 2 homolog (probable)	NO
Fb7:0-10	gene18700	-2,35	9,06E-06	8,21E-04	FBL71_ARATH	Putative F-box/LRR-repeat protein At4g00320	F-box/LRR-repeat protein At3g58930 (probable)	NO
Fb7:0-10	gene18992	-2,34	2,42E-05	1,94E-03	F4JH46_ARATH	MATE efflux family protein	Protein TRANSPARENT TESTA 12 (probable)	NO
Fb7:0-10	gene04805	-2,33	4,43E-06	4,15E-04	B8AFY4_ORYSI	Putative uncharacterized protein	DNA-directed RNA polymerase II subunit RPB2 (RNA polymerase II subunit B2) (probable)	NO

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Fb7:0-10	gene30302	-2,28	1,53E-06	1,56E-04	CDR1_ARATH	Aspartic proteinase CDR1	Aspartic proteinase nepenthesin-1, Precursor (probable)	NO
Fb7:0-10	gene03216	-2,28	6,93E-06	6,37E-04	B9G2Z1_ORYSJ	Putative uncharacterized protein	Ankyrin repeat-containing protein At3g12360 (probable)	NO
Fb7:0-10	gene14303	-2,21	1,64E-04	1,07E-02	-	-	Formin-like protein 12 (probable)	YES
Fb7:0-10	gene29467	-2,18	1,06E-05	9,44E-04	B8B3E9_ORYSI	Putative uncharacterized protein	Pentatricopeptide repeat-containing protein At3g53170 (similar to)	YES
Fb7:0-10	gene23637	-2,14	2,02E-04	1,28E-02	A2Y2W3_ORYSI	Putative uncharacterized protein	Structure-specific endonuclease subunit SLX1 homolog (probable)	NO
Fb7:0-10	gene28626	-2,13	4,10E-05	3,10E-03	Q7XME3_ORYSJ	OSJNBa0061G20.16 protein	Putative ribonuclease H protein At1g65750 (probable)	YES
Fb7:0-10	gene24649	-2,12	8,34E-05	5,86E-03	CRK29_ARATH	Cysteine-rich receptor-like protein kinase 29	Cysteine-rich receptor-like protein kinase 29 (Cysteine-rich RLK29), Precursor (probable)	YES
Fb7:0-10	gene14306	-2,02	3,34E-05	2,57E-03	Q9S7P3_ARATH	Kinesin-like protein	Centromere-associated protein E (CENP-E) (probable)	YES
Fb7:0-10	gene28351	-2,01	4,87E-04	2,69E-02	SG101_ARATH	Senescence-associated carboxylesterase 101	Protein teflon (probable)	NO
Fb7:0-10	gene32196	-1,97	1,06E-03	5,23E-02	Q2QNH0_ORYSJ	cDNA clone:J023062N03, full insert sequence	Putative boron transporter 2	NO
Fb7:0-10	gene11808	-1,95	8,91E-05	6,17E-03	ARF5_ARATH	ADP-ribosylation factor-like protein 2	Probable ADP-ribosylation factor At2g18390 (similar to)	YES
Fb7:0-10	gene11045	-1,95	5,96E-05	4,35E-03	GLYC7_ARATH	Serine hydroxymethyltransferase 7	Serine hydroxymethyltransferase 2 (SHMT 2) (probable)	NO
Fb7:0-10	gene03005	-1,89	1,97E-04	1,25E-02	Q9FN84_ARATH	Putative uncharacterized protein MVA3.2	Protein Wnt-1 (probable)	NO
Fb7:0-10	gene13961	-1,89	3,63E-04	2,10E-02	-	-	Kappa-casein (probable)	NO
Fb7:0-10	gene04359	-1,88	1,32E-04	8,75E-03	A3BAU1_ORYSJ	Putative uncharacterized protein	Anthocyanidin 5,3-O-glucosyltransferase (probable)	NO
Fb7:0-10	gene02094	-1,88	2,86E-04	1,74E-02	Q8GZ31_ARATH	Putative uncharacterized protein At5g27920/F14I23_80	F-box/LRR-repeat protein 3 (probable)	NO
Fb7:0-10	gene27842	-1,88	1,72E-03	7,96E-02	IPT3_ARATH	Adenylate isopentenyltransferase 3, chloroplastic	tRNA Delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (probable)	NO
Fb7:0-10	gene27008	-1,86	1,04E-04	7,03E-03	-	-	UPF0493 protein KIAA1632 homolog (probable)	NO
Fb7:0-10	gene14349	-1,85	3,18E-04	1,89E-02	PAC_ARATH	Protein PALE CRESS, chloroplastic	Voltage-dependent T-type calcium channel subunit alpha-1G	YES

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							(probable)	
Fb7:0-10	gene29942	-1,83	1,30E-03	6,27E-02	B8BE99_ORYSI	Putative uncharacterized protein	Ankyrin repeat-containing protein At3g12360 (probable)	NO
Fb7:0-10	gene00397	-1,79	1,89E-04	1,21E-02	Q8RWT5_ARATH	Putative phosphoribosylaminoimidazolecarboxamide formyltransferase	IMP cyclohydrolase (probable)	YES
Fb7:0-10	gene11414	-1,77	3,00E-04	1,81E-02	SAT5_ARATH	Serine acetyltransferase 5	Serine acetyltransferase 5 (AtSAT-5) (similar to)	YES
Fb7:0-10	gene04803	-1,75	8,98E-04	4,51E-02	-	-	Prenyl transferase (probable)	NO
Fb7:0-10	gene00344	-1,74	6,97E-04	3,60E-02	B8AWT0_ORYSI	Putative uncharacterized protein	Putative protease Do-like 14 (similar to)	NO
Fb7:0-10	gene07345	-1,71	4,45E-04	2,48E-02	VRN1_ARATH	B3 domain-containing transcription factor VRN1	B3 domain-containing transcription factor VRN1 (probable)	NO
Fb7:0-10	gene03224	-1,65	5,83E-04	3,13E-02	Q6Z6J3_ORYSJ	Putative pentatricopeptide (PPR) repeat-containing protein	Pentatricopeptide repeat-containing protein At4g04790, mitochondrial, Precursor (probable)	NO
Fb7:0-10	gene09230	-1,64	5,40E-04	2,95E-02	AEE19_ARATH	Putative acyl-activating enzyme 19	Acyl-CoA synthetase family member 4 (probable)	NO
Fb7:0-10	gene12020	-1,63	1,18E-03	5,80E-02	-	-	Lateral signaling target protein 2 homolog (probable)	YES
Fb7:0-10	gene09216	-1,61	1,86E-03	8,43E-02	Q9FMN8_ARATH	Uncharacterized protein	ATP-dependent helicase/deoxyribonuclease subunit B (probable)	NO
Fb7:0-10	gene00385	-1,57	1,57E-03	7,33E-02	-	-	Protein BEAN (probable)	NO
Fb7:0-10	gene12577	-1,56	1,82E-03	8,32E-02	4CL3_ARATH	4-coumarate--CoA ligase 3	4-coumarate--CoA ligase 2 (4CL 2) (putative)	YES
Fb7:0-10	gene18007	-1,55	1,56E-03	7,30E-02	EIF3C_ARATH	Eukaryotic translation initiation factor 3 subunit C	Eukaryotic translation initiation factor 3 subunit C (eIF3c) (putative)	NO
Fb7:0-10	gene23447	-1,55	1,51E-03	7,17E-02	Q8GVR2_ORYSJ	cDNA clone:001-115-C06, full insert sequence	Cysteine proteinase 15A, Precursor (probable)	NO
Fb7:0-10	gene01896	-1,54	8,29E-04	4,21E-02	C78A6_ARATH	Cytochrome P450 78A6	Cytochrome P450 78A3 (putative)	YES
Fb7:0-10	gene00726	-1,53	2,07E-03	9,31E-02	ARR3_ARATH	Two-component response regulator ARR3	Two-component response regulator ARR4 (similar to)	YES
Fb7:0-10	gene18646	-1,48	2,08E-03	9,32E-02	CIPK9_ARATH	CBL-interacting serine/threonine-protein kinase 9	CBL-interacting serine/threonine-protein kinase 9 (putative)	NO

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Fb7:0-10	gene23289	1,48	1,82E-03	8,32E-02	O48986_ORYSA	NBS-LRR type resistance protein	Transcription elongation factor B polypeptide 3 (EloA) (probable)	NO
Fb7:0-10	gene19063	1,48	1,84E-03	8,40E-02	Q7XPV6_ORYSJ	OSJNBa0032F06.25 protein	tRNA-specific adenosine deaminase 1 (probable)	NO
Fb7:0-10	gene09239	1,54	1,53E-03	7,24E-02	Q9M1F3_ARATH	RING/U-box protein with C6HC-type zinc finger	Probable E3 ubiquitin-protein ligase RNF144A	NO
Fb7:0-10	gene13450	1,54	1,72E-03	7,96E-02	Q84J81_ARATH	Putative uncharacterized protein At3g09350	Hsp70 nucleotide exchange factor fes1 (probable)	NO
Fb7:0-10	gene28398	1,56	1,53E-03	7,23E-02	Q9M3C6_ARATH	Uncharacterized protein	Nuclear pore complex protein Nup214 (probable)	YES
Fb7:0-10	gene03959	1,57	1,79E-03	8,24E-02	O81315_ARATH	Putative uncharacterized protein AT4g00140	Centrin-1 (probable)	NO
Fb7:0-10	gene25088	1,57	1,96E-03	8,86E-02	B8ASP9_ORYSI	Putative uncharacterized protein	Disease resistance protein RPM1 (probable)	NO
Fb7:0-10	gene28922	1,58	1,49E-03	7,12E-02	Q2R147_ORYSJ	Protein kinase domain containing protein, expressed	NADH-ubiquinone oxidoreductase chain 2 (similar to)	YES
Fb7:0-10	gene00188	1,61	9,64E-04	4,82E-02	ASPGB_ARATH	Isoaspartyl peptidase/L-asparaginase 2 subunit beta	Isoaspartyl peptidase/L-asparaginase 2 subunit beta, Precursor (putative)	YES
Fb7:0-10	gene16766	1,63	5,20E-04	2,86E-02	-	-	Tegument protein BRRF2 (probable)	YES
Fb7:0-10	gene03097	1,65	1,09E-03	5,41E-02	A2X8G7_ORYSI	Putative uncharacterized protein	50S ribosomal protein L18 (probable)	NO
Fb7:0-10	gene04933	1,65	8,60E-04	4,33E-02	GTE11_ARATH	Transcription factor GTE11	Alanyl-tRNA synthetase (AlaRS) (probable)	YES
Fb7:0-10	gene20386	1,66	5,96E-04	3,18E-02	B8BLS7_ORYSI	Putative uncharacterized protein	Probable E3 ubiquitin-protein ligase rbrA	YES
Fb7:0-10	gene26073	1,68	1,24E-03	6,04E-02	UNE10_ARATH	Transcription factor UNE10	Transcription factor PIF7 (bHLH 72) (probable)	NO
Fb7:0-10	gene19110	1,68	8,10E-04	4,13E-02	MBD9_ARATH	Methyl-CpG-binding domain-containing protein 9	PH and SEC7 domain-containing protein 4 (probable)	NO
Fb7:0-10	gene23412	1,69	1,12E-03	5,51E-02	Q5QNJ3_ORYSJ	Uncharacterized protein	hypothetical protein	YES
Fb7:0-10	gene14289	1,69	1,28E-03	6,18E-02	PTR25_ARATH	Protein NRT1/ PTR FAMILY 5.12	Peptide transporter PTR5 (probable)	NO
Fb7:0-10	gene23610	1,74	2,05E-03	9,22E-02	B8ACY0_ORYSI	Putative uncharacterized protein	Probable receptor-like protein kinase At5g39030, Precursor (similar to)	NO
Fb7:0-10	gene26789	1,75	8,21E-04	4,18E-02	-	-	Translation initiation factor IF-2 (probable)	YES
Fb7:0-10	gene24380	1,78	5,53E-04	2,99E-02	C7102_ARATH	Cytochrome P450 710A2	ABC transporter F family member 3 (ABC transporter ABCF.3) (probable)	YES

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Fb7:0-10	gene19132	1,79	3,41E-04	2,00E-02	CSN1_ARATH	COP9 signalosome complex subunit 1	COP9 signalosome complex subunit 1 (CSN complex subunit 1) (putative)	NO
Fb7:0-10	gene26952	1,79	1,51E-03	7,17E-02	-	-	[Protein-PII] uridylyltransferase (PII uridylyl-transferase) (probable)	YES
Fb7:0-10	gene13216	1,80	3,16E-04	1,88E-02	F4JH46_ARATH	MATE efflux family protein	Protein TRANSPARENT TESTA 12 (probable)	NO
Fb7:0-10	gene14345	1,81	3,99E-04	2,25E-02	ANXD3_ARATH	Annexin D3	Annexin D3 (similar to)	YES
Fb7:0-10	gene15008	1,81	1,83E-04	1,18E-02	-	-	Phospholipase D Y (PLD 3), Precursor (probable)	NO
Fb7:0-10	gene03085	1,82	2,20E-03	9,78E-02	A2XJZ9_ORYSI	Putative uncharacterized protein	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P (similar to)	NO
Fb7:0-10	gene22796	1,82	1,54E-03	7,24E-02	A2WNQ5_ORYSI	Putative uncharacterized protein	ABC transporter B family member 4 (ABC transporter ABCB.4) (similar to)	NO
Fb7:0-10	gene15023	1,83	2,26E-04	1,41E-02	REM9_ARATH	B3 domain-containing protein REM9	B3 domain-containing protein Os01g0723500 (probable)	NO
Fb7:0-10	gene13105	1,83	1,40E-04	9,19E-03	A2X344_ORYSI	Putative uncharacterized protein	General transcription factor IIF subunit 1 (TFIIF-alpha) (probable)	YES
Fb7:0-10	gene23886	1,87	1,86E-03	8,43E-02	TPS10_RICCO	Terpene synthase 10	Myrcene synthase, chloroplastic, Precursor (probable)	NO
Fb7:0-10	gene23625	1,89	6,26E-04	3,31E-02	BASS4_ORYSI	Probable sodium/metabolite cotransporter BASS4, chloroplastic	hypothetical protein	YES
Fb7:0-10	gene14178	1,89	6,53E-04	3,42E-02	DEK1_ARATH	Calpain-type cysteine protease DEK1	Ribosomal RNA large subunit methyltransferase L (probable)	YES
Fb7:0-10	gene05316	1,90	2,13E-03	9,50E-02	DRL4_ARATH	Putative disease resistance protein At1g50180	Probable disease resistance RPP8-like protein 2	NO
Fb7:0-10	gene23234	1,90	8,41E-04	4,26E-02	VCS_ARATH	Enhancer of mRNA-decapping protein 4	Micronuclear linker histone-gamma (probable)	YES
Fb7:0-10	gene14447	1,92	9,78E-05	6,69E-03	F4JFL8_ARATH	Glycerol-3-phosphate dehydrogenase [NAD(+)]	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (probable)	NO
Fb7:0-10	gene04932	1,94	5,83E-04	3,13E-02	-	-	Chorismate synthase (probable)	YES
Fb7:0-10	gene18559	1,95	1,21E-04	8,11E-03	B9FFZ6_ORYSJ	Putative uncharacterized protein	Serine/threonine-protein phosphatase PP1 (probable)	YES
Fb7:0-10	gene09232	1,96	8,35E-05	5,86E-03	ATL51_ARATH	RING-H2 finger protein ATL51	Probable RING-H2 finger protein ATL5G	YES
Fb7:0-10	gene05307	2,00	8,54E-	5,95E-	FB135_ARAT	F-box protein At3g07870	F-box protein At3g07870	YES

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			05	03	H		(probable)	
Fb7:0-10	gene32503	2,03	6,80E-04	3,54E-02	PIP14_ARATH	Probable aquaporin PIP1-4	Aquaporin PIP1-3 (AtPIP1) (putative)	YES
Fb7:0-10	gene04445	2,03	3,83E-05	2,91E-03	Q01K44_ORYSA	OSIGBa0158F13.3 protein	E3 ubiquitin-protein ligase RNF181 (probable)	YES
Fb7:0-10	gene00270	2,03	2,52E-05	2,00E-03	PAPS1_ARATH	Nuclear poly(A) polymerase 1	Poly(A) polymerase (PAP) (probable)	NO
Fb7:0-10	gene21581	2,04	2,62E-04	1,60E-02	B9FYJ3_ORYSJ	Putative uncharacterized protein	30S ribosomal protein S3, chloroplastic (probable)	YES
Fb7:0-10	gene23641	2,07	4,01E-04	2,26E-02	Q8L440_ARATH	RNA recognition motif-containing protein	DAG protein, chloroplastic, Precursor (probable)	NO
Fb7:0-10	gene20416	2,08	4,20E-04	2,35E-02	A2Y6Y4_ORYSI	Putative uncharacterized protein	F-box/FBD/LRR-repeat protein At1g13570 (probable)	YES
Fb7:0-10	gene16567	2,11	1,66E-04	1,08E-02	B9F6U0_ORYSJ	Putative uncharacterized protein	Disease resistance protein At4g27190 (probable)	YES
Fb7:0-10	gene14186	2,12	1,41E-03	6,77E-02	DEK1_ARATH	Calpain-type cysteine protease DEK1	Calpain clp-1 (probable)	YES
Fb7:0-10	gene03366	2,12	2,68E-05	2,11E-03	APY1_ARATH	Apyrase 1	Nucleoside-triphosphatase (NTPase) (similar to)	YES
Fb7:0-10	gene03547	2,14	5,49E-04	2,99E-02	WNK11_ARATH	Probable serine/threonine-protein kinase WNK11	Probable serine/threonine-protein kinase WNK11 (AtWNK11) (similar to)	YES
Fb7:0-10	gene03126	2,17	5,98E-04	3,18E-02	Q2R4C6_ORYSJ	NB-ARC domain containing protein, expressed	hypothetical protein	YES
Fb7:0-10	gene04367	2,23	1,63E-05	1,35E-03	DSLE_ARATH	Zinc finger BED domain-containing protein DAYSLEEPER	Putative AC9 transposase (probable)	NO
Fb7:0-10	gene06586	2,23	1,80E-03	8,26E-02	DCL3_ARATH	Endoribonuclease Dicer homolog 3	hypothetical protein	NO
Fb7:0-10	gene22019	2,24	6,59E-04	3,45E-02	-	-	Mucin-6 (MUC-6), Precursor (probable)	NO
Fb7:0-10	gene07468	2,26	4,68E-04	2,59E-02	GLR14_ARATH	Glutamate receptor 1.4	Glutamate receptor 1.4, Precursor (probable)	NO
Fb7:0-10	gene33949	2,32	5,96E-05	4,35E-03	-	-	Probable tRNA pseudouridine synthase B (Psi55 synthase)	NO
Fb7:0-10	gene20417	2,34	3,05E-06	2,91E-04	NPS11_ARATH	Novel plant SNARE 11	Mesoderm induction early response protein 2 (Mi-er2) (probable)	YES
Fb7:0-10	gene04502	2,38	3,86E-06	3,64E-04	A2XE87_ORYSI	Putative uncharacterized protein	Phytosulfokine-beta, Precursor (similar to)	NO
Fb7:0-10	gene30887	2,41	7,18E-07	7,75E-05	PLT5_ARATH	Polyol transporter 5	Polyol transporter 5 (AtPLT5) (similar to)	NO
Fb7:0-10	gene29483	2,42	1,04E-06	1,09E-04	Q29Q34_ARATH	At5g19440	Dihydroflavonol-4-reductase (DFR) (probable)	YES

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Fb7:0-10	gene00429	2,43	9,96E-07	1,05E-04	-	-	IMP-specific 5'-nucleotidase 1 (probable)	NO
Fb7:0-10	gene29484	2,43	1,25E-05	1,08E-03	Q29Q34_ARATH	At5g19440	LRR receptor-like serine/threonine-protein kinase FLS2, Precursor (probable)	NO
Fb7:0-10	gene04444	2,43	2,04E-06	2,01E-04	A2Y618_ORYSI	Putative uncharacterized protein	Putative disease resistance protein RGA3 (probable)	YES
Fb7:0-10	gene20390	2,46	1,46E-06	1,50E-04	-	-	50S ribosomal protein L18 (probable)	YES
Fb7:0-10	gene07453	2,49	1,60E-06	1,61E-04	XPT_ARATH	Xylulose 5-phosphate/phosphate translocator, chloroplastic	Glucose-6-phosphate/phosphate translocator 1, chloroplastic, Precursor (probable)	YES
Fb7:0-10	gene11307	2,51	3,20E-04	1,89E-02	-	-	hypothetical protein	NO
Fb7:0-10	gene04372	2,54	2,62E-05	2,07E-03	SCPDL_ARATH	Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410	Probable mitochondrial saccharopine dehydrogenase At5g39410 (SDH) (similar to)	NO
Fb7:0-10	gene19094	2,56	7,62E-07	8,18E-05	Q94K30_ARATH	Rossmann-fold NAD(P)-binding domain-containing protein	(+)-neomenthol dehydrogenase (AtSDR1) (putative)	NO
Fb7:0-10	gene35014	2,62	1,55E-03	7,27E-02	Q9SRZ8_ARATH	NAC domain containing protein 28	NAC domain-containing protein 18 (ANAC018) (probable)	NO
Fb7:0-10	gene34577	2,64	3,01E-05	2,34E-03	AUR1_ARATH	Serine/threonine-protein kinase Aurora-1	Serine/threonine-protein kinase Aurora-1 (AtAur1) (probable)	NO
Fb7:0-10	gene19352	2,65	5,60E-04	3,02E-02	B8A960_ORYSI	Putative uncharacterized protein	Probable calcium-binding protein CML23	NO
Fb7:0-10	gene16897	2,65	1,73E-07	1,99E-05	H32_ARATH	Histone H3.2	Thyroid receptor-interacting protein 11 (TRIP-11) (probable)	YES
Fb7:0-10	gene31685	2,65	1,26E-07	1,50E-05	A2XYU1_ORYSI	Putative uncharacterized protein	Intracellular protease 1 (probable)	YES
Fb7:0-10	gene10824	2,66	3,06E-07	3,46E-05	PLA14_ARATH	Phospholipase A1-Ibeta2, chloroplastic	Lipase (ROL), Precursor (probable)	YES
Fb7:0-10	gene34945	2,67	3,18E-05	2,47E-03	BGA12_ARATH	Beta-galactosidase 12	Beta-galactosidase 12 (Lactase 12), Precursor (similar to)	YES
Fb7:0-10	gene03128	2,67	1,19E-05	1,04E-03	Q0WVR3_ARATH	Transducin family protein / WD-40 repeat family protein	Chaperone protein dnaK (probable)	YES
Fb7:0-10	gene10565	2,70	1,03E-04	7,03E-03	A2XGL9_ORYSI	Putative uncharacterized protein	Desiccation-related protein PCC13-62, Precursor (probable)	YES
Fb7:0-10	gene11803	2,71	1,69E-08	2,32E-06	KEULE_ARATH	SNARE-interacting protein KEULE	SNARE-interacting protein KEULE (similar to)	NO

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Fb7:0-10	gene25904	2,72	1,90E-04	1,21E-02	Q8VY59_ARATH	Plastocyanin-like domain-containing protein	Blue copper protein, Precursor (probable)	NO
Fb7:0-10	gene23593	2,73	1,72E-04	1,11E-02	BASS4_ARATH	Probable sodium/metabolite cotransporter BASS4, chloroplastic	Vacuolar proton translocating ATPase 100 kDa subunit (similar to)	YES
Fb7:0-10	gene11310	2,77	1,67E-04	1,08E-02	3HID1_ARATH	Probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial	hypothetical protein	NO
Fb7:0-10	gene13665	2,79	3,00E-08	3,89E-06	Q8SAW7_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Structural protein ORF567 (probable)	YES
Fb7:0-10	gene07810	2,85	2,23E-04	1,39E-02	HPPD_ARATH	4-hydroxyphenylpyruvate dioxygenase	4-hydroxyphenylpyruvate dioxygenase (HPPDase) (probable)	YES
Fb7:0-10	gene19411	2,86	1,45E-03	6,95E-02	ZDH14_ARATH	Probable protein S-acyltransferase 14	Probable S-acyltransferase At3g60800 (putative)	NO
Fb7:0-10	gene05821	2,92	1,59E-08	2,22E-06	PSAD2_ARATH	Photosystem I reaction center subunit II-2, chloroplastic	Photosystem I reaction center subunit II, chloroplastic (PSI-D), Precursor (similar to)	NO
Fb7:0-10	gene10539	2,92	3,80E-04	2,17E-02	LEC2_ARATH	B3 domain-containing transcription factor LEC2	B3 domain-containing transcription factor LEC2 (similar to)	YES
Fb7:0-10	gene23580	2,92	6,42E-09	9,59E-07	OTU_ARATH	OTU domain-containing protein At3g57810	OTU domain-containing protein 4 (probable)	NO
Fb7:0-10	gene11309	2,93	5,91E-05	4,34E-03	B9FSJ0_ORYSJ	Putative uncharacterized protein	hypothetical protein	NO
Fb7:0-10	gene22480	2,93	6,79E-04	3,54E-02	-	-	RNA-binding protein with serine-rich domain 1 (probable)	NO
Fb7:0-10	gene27067	2,94	5,76E-09	8,75E-07	FBK67_ARATH	F-box/kelch-repeat protein At3g23880	F-box/kelch-repeat protein At3g06240 (probable)	NO
Fb7:0-10	gene14335	2,94	3,09E-08	3,98E-06	PTC52_ARATH	Protochlorophyllide-dependent translocon component 52, chloroplastic	Pheophorbide a oxygenase, chloroplastic (Pheide a oxygenase), Precursor (probable)	YES
Fb7:0-10	gene14937	2,95	1,54E-05	1,29E-03	O81816_ARATH	Monooxygenase 2 (MO2)	30S ribosomal protein S5 (probable)	YES
Fb7:0-10	gene03053	2,96	1,48E-05	1,25E-03	SWT17_ARATH	Bidirectional sugar transporter SWEET17	Protein RUPTURED POLLEN GRAIN 1 (probable)	YES
Fb7:0-10	gene34552	2,96	6,44E-05	4,66E-03	R13L1_ARATH	Putative disease resistance RPP13-like protein 1	Putative disease resistance RPP13-like protein 1 (probable)	YES
Fb7:0-10	gene31606	2,99	3,01E-05	2,34E-03	-	-	60S ribosomal protein L27 (similar to)	YES
Fb7:0-10	gene00341	2,99	3,36E-05	2,58E-03	-	-	Serine-rich adhesin for platelets, Precursor (probable)	YES

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Fb7:0-10	gene26941	2,99	8,49E-04	4,29E-02	R13L1_ARATH	Putative disease resistance RPP13-like protein 1	Putative disease resistance RPP13-like protein 1 (probable)	YES
Fb7:0-10	gene19183	3,01	1,07E-04	7,21E-03	F4JKW8_ARATH	Uncharacterized protein	hypothetical protein	NO
Fb7:0-10	gene18592	3,02	8,49E-09	1,23E-06	Q66GJ1_ARATH	Cytochrome P450, family 706, subfamily A, polypeptide 6	Licodione synthase (probable)	NO
Fb7:0-10	gene19424	3,05	1,24E-03	6,04E-02	-	-	Nuclear envelope pore membrane protein POM 121 (probable)	NO
Fb7:0-10	gene16482	3,06	1,52E-07	1,78E-05	A2Y0K9_ORYSI	Putative uncharacterized protein	DnaJ homolog subfamily B member 11, Precursor (probable)	NO
Fb7:0-10	gene07037	3,15	9,41E-10	1,60E-07	-	-	Probable exocyst complex component 6	YES
Fb7:0-10	gene29872	3,18	2,07E-05	1,68E-03	-	-	Diaminopimelate decarboxylase (DAP decarboxylase) (probable)	NO
Fb7:0-10	gene16579	3,23	1,48E-07	1,75E-05	-	-	UPF0737 protein Os03g0419100 (probable)	NO
Fb7:0-10	gene09157	3,29	2,05E-06	2,01E-04	B9G3L3_ORYSJ	Putative uncharacterized protein	Carbamoyl-phosphate synthase small chain (probable)	YES
Fb7:0-10	gene32226	3,30	2,63E-04	1,60E-02	LOX2_ARATH	Lipoxygenase 2, chloroplastic	Lipoxygenase 2, chloroplastic (AtLOX2), Precursor (similar to)	NO
Fb7:0-10	gene09222	3,31	5,27E-05	3,89E-03	BH091_ARATH	Transcription factor bHLH91	Transcription factor bHLH91 (bHLH 91) (probable)	NO
Fb7:0-10	gene06817	3,32	2,57E-06	2,50E-04	-	-	Forkhead box protein G1 (FoxG1) (probable)	YES
Fb7:0-10	gene31483	3,35	1,31E-05	1,13E-03	-	-	G-protein coupled receptor 98, Precursor (probable)	NO
Fb7:0-10	gene18590	3,39	1,44E-04	9,41E-03	O81790_ARATH	NAM / CUC2-like protein	Protein CUP-SHAPED COTYLEDON 1 (ANAC054) (probable)	NO
Fb7:0-10	gene29876	3,42	6,45E-04	3,41E-02	A2ZD31_ORYSI	Putative uncharacterized protein	UDP-N-acetylmuramate--L-alanine ligase (probable)	YES
Fb7:0-10	gene30057	3,48	1,04E-10	2,08E-08	RPB9B_ARATH	DNA-directed RNA polymerases II, IV and V subunit 9B	DNA-directed RNA polymerase II subunit RPB9 (similar to)	YES
Fb7:0-10	gene19144	3,52	1,89E-06	1,88E-04	-	-	Ubiquitin-like domain-containing CTD phosphatase (probable)	NO
Fb7:0-10	gene31123	3,52	3,64E-04	2,10E-02	Q9CAM1_ARATH	Transcription elongation factor SPT6	Transcription elongation factor SPT6 (probable)	YES
Fb7:0-10	gene28404	3,57	1,45E-09	2,35E-07	B8BLZ3_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RLIM (R-LIM) (probable)	YES
Fb7:0-10	gene21475	3,57	4,23E-	7,59E-	C81F1_ARAT	Cytochrome P450 81F1	Probable cytochrome	NO

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NIL vs. RV	gene id[a]	log$_2$(F Ch)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
			10	08	H		P450 514A1	
Fb7:0-10	gene29198	3,60	1,33E-06	1,38E-04	LPAH1_ARATH	P-loop NTPase domain-containing protein LPA1 homolog 1	Cytochrome c biogenesis protein ccsB (probable)	NO
Fb7:0-10	gene04802	3,67	1,00E-03	4,99E-02	Q9LTQ5_ARATH	TRAF-like family protein	Ubiquitin carboxyl-terminal hydrolase 12 (AtUBP12) (probable)	YES
Fb7:0-10	gene28403	3,79	8,37E-05	5,86E-03	B8BLZ3_ORYSI	Putative uncharacterized protein	E3 ubiquitin-protein ligase RLIM (R-LIM) (probable)	YES
Fb7:0-10	gene02165	3,83	8,22E-10	1,42E-07	Q7XS07_ORYSJ	OSJNBa0095H06.12 protein	Replication protein A 70 kDa DNA-binding subunit (RP-A p70) (probable)	YES
Fb7:0-10	gene34006	3,83	5,01E-09	7,73E-07	Q9SRZ8_ARATH	NAC domain containing protein 28	NAC domain-containing protein 18 (ANAC018) (probable)	NO
Fb7:0-10	gene21218	3,85	3,69E-11	7,58E-09	HS23M_ARATH	23.6 kDa heat shock protein, mitochondrial	23.6 kDa heat shock protein, mitochondrial (AtHsp23.6), Precursor (probable)	NO
Fb7:0-10	gene10516	3,87	7,97E-06	7,26E-04	-	-	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (probable)	YES
Fb7:0-10	gene28399	3,89	7,74E-04	3,96E-02	Q9XIJ0_ARATH	T10O24.24	Uncharacterized protein At4g28440 (similar to)	NO
Fb7:0-10	gene35011	4,10	9,17E-05	6,32E-03	Q9LS24_ARATH	Putative uncharacterized protein At5g46590	NAC domain-containing protein 74 (ONAC074) (probable)	YES
Fb7:0-10	gene14283	4,12	3,09E-04	1,86E-02	-	-	Neurofilament heavy polypeptide (NF-H) (probable)	YES
Fb7:0-10	gene18891	4,17	3,44E-10	6,48E-08	B9F269_ORYSJ	Putative uncharacterized protein	Arginine/serine-rich-splicing factor RSP41 (similar to)	NO
Fb7:0-10	gene14282	4,19	1,14E-09	1,91E-07	Q9FVQ7_ARATH	Uncharacterized protein	Serine/threonine protein phosphatase 7 long form homolog (probable)	YES
Fb7:0-10	gene11322	4,19	1,28E-04	8,52E-03	RR5_ARATH	30S ribosomal protein S5, chloroplastic	30S ribosomal protein S5, chloroplastic, Precursor (probable)	YES
Fb7:0-10	gene28405	4,22	1,38E-09	2,28E-07	ARP4_ARATH	Actin-related protein 4	Actin-related protein 4 (similar to)	YES
Fb7:0-10	gene19438	4,24	7,11E-15	2,01E-12	GAOX1_ARATH	Gibberellin 20 oxidase 1	Gibberellin 20 oxidase 1 (AtGA20ox) (putative)	NO
Fb7:0-10	gene14344	4,35	7,45E-04	3,82E-02	ANXD4_ARATH	Annexin D4	Annexin D4 (similar to)	NO
Fb7:0-10	gene07718	4,38	1,85E-07	2,12E-05	-	-	Elongation factor 1-alpha (EF-1-alpha) (probable)	YES
Fb7:0-10	gene19339	4,44	2,34E-09	3,70E-07	F4KFY5_ARATH	TIR-NBS-LRR class disease resistance protein	Probable WRKY transcription factor 19	NO
Fb7:0-10	gene03922	4,46	1,18E-08	1,69E-06	PME18_ARATH	Bifunctional pectinesterase 18/rRNA N-glycosylase	Pectinesterase 36 (PE 36), Precursor (probable)	YES

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NIL vs. RV	gene id[a]	$\log_2$(F Ch)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb7:0-10	gene21655	4,50	3,64E-08	4,62E-06	NDUA9_ARATH	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	hypothetical protein	YES
Fb7:0-10	gene23595	4,73	1,42E-09	2,33E-07	CPR1_ARATH	Probable cysteine proteinase At3g19400	Probable cysteine proteinase At3g19400, Precursor (similar to)	YES
Fb7:0-10	gene00670	4,84	5,65E-09	8,66E-07	Q9ZV49_ARATH	Uncharacterized protein	UPF0118 membrane protein RP630 (probable)	NO
Fb7:0-10	gene19068	4,85	2,78E-14	7,30E-12	-	-	Septin homolog spn6 (probable)	NO
Fb7:0-10	gene19149	5,03	2,12E-03	9,48E-02	B8B8J7_ORYSI	Putative uncharacterized protein	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 (Brefeldin A-inhibited GEP 2) (probable)	NO
Fb7:0-10	gene23676	5,05	2,65E-06	2,56E-04	Q8L7K1_ARATH	Putative uncharacterized protein At4g32610	Protein sprT-like (probable)	NO
Fb7:0-10	gene22359	5,06	4,72E-05	3,53E-03	-	-	CYP98A8 (cytochrome P450, family 98, subfamily A, polypeptide 8); oxygen binding (probable)	YES
Fb7:0-10	gene34207	5,19	1,51E-10	2,93E-08	SOT15_ARATH	Cytosolic sulfotransferase 15	Flavonol sulfotransferase-like (probable)	YES
Fb7:0-10	gene23588	5,19	1,68E-03	7,81E-02	Q0WVQ3_ARATH	Putative transcription factor	Transcription factor IIIB 90 kDa subunit (TFIIIB90) (similar to)	YES
Fb7:0-10	gene06806	5,22	1,54E-03	7,24E-02	F4JKW9_ARATH	ARM repeat superfamily protein	Protein FAM179B (probable)	YES
Fb7:0-10	gene12802	5,25	1,10E-05	9,72E-04	Q6ATN2_ORYSJ	Retrotransposon protein, putative, Ty3-gypsy subclass	ABC transporter B family member 10 (ABC transporter ABCB.10) (similar to)	NO
Fb7:0-10	gene29842	5,28	1,27E-03	6,16E-02	Q93VC6_ORYSJ	cDNA clone:J033028P14, full insert sequence	40S ribosomal protein S5-1 (similar to)	YES
Fb7:0-10	gene14694	5,37	9,78E-08	1,19E-05	Q2R147_ORYSJ	Protein kinase domain containing protein, expressed	Putative ribonuclease H protein At1g65750 (probable)	YES
Fb7:0-10	gene24445	5,38	1,16E-05	1,02E-03	-	-	Homeobox protein Hox-B9 (probable)	YES
Fb7:0-10	gene33962	5,51	9,14E-04	4,58E-02	B8AMS6_ORYSI	Putative uncharacterized protein	Probable LRR receptor-like serine/threonine-protein kinase At1g53440, Precursor	YES
Fb7:0-10	gene03924	5,59	3,33E-18	1,38E-15	B8A748_ORYSI	Pectinesterase	Pectinesterase 36 (PE 36), Precursor (similar to)	NO
Fb7:0-10	gene11993	5,67	2,75E-08	3,62E-06	Q9SKM8_ARATH	Lactoylglutathione lyase / glyoxalase I-like protein	Lactoylglutathione lyase (Glx I) (probable)	YES

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NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb7:0-10	gene03925	5,78	5,13E-15	1,50E-12	PME18_ARATH	Bifunctional pectinesterase 18/rRNA N-glycosylase	Pectinesterase 36 (PE 36), Precursor (probable)	NO
Fb7:0-10	gene02129	5,81	5,92E-04	3,17E-02	-	-	Ankyrin repeat domain-containing protein 35 (probable)	YES
Fb7:0-10	gene18589	6,24	3,34E-19	1,64E-16	Q9LVA1_ARATH	No apical meristem family protein	Protein CUP-SHAPED COTYLEDON 1 (ANAC054) (probable)	YES
Fb7:0-10	gene00428	6,47	1,53E-26	2,21E-23	-	-	WD repeat-containing protein 48 homolog (probable)	YES
Fb7:0-10	gene14445	6,48	1,98E-13	4,93E-11	A2WW14_ORYSI	Putative uncharacterized protein	Protein 108, Precursor (probable)	NO
Fb7:0-10	gene01693	6,49	1,09E-09	1,84E-07	Q9T0J2_ARATH	SAUR-like auxin-responsive protein	Auxin-induced protein X10A (similar to)	YES
Fb7:0-10	gene05317	6,69	1,58E-12	3,60E-10	Q69P77_ORYSJ	cDNA clone:002-130-E07, full insert sequence	Flavonoid 3',5'-hydroxylase (F3'5'H) (probable)	NO
Fb7:0-10	gene12801	6,78	5,20E-06	4,86E-04	A3BD30_ORYSJ	Putative uncharacterized protein	Dynein-1-beta heavy chain, flagellar inner arm I1 complex (probable)	NO
Fb7:0-10	gene34410	7,04	1,55E-10	2,99E-08	Q10RD3_ORYSJ	Expressed protein	Phenylalanyl-tRNA synthetase alpha chain (PheRS) (probable)	YES
Fb7:0-10	gene19414	7,58	7,40E-24	6,91E-21	CPR30_ARATH	F-box protein CPR30	F-box protein At4g12560 (probable)	NO
Fb7:0-10	gene14372	7,68	2,36E-09	3,70E-07	-	-	Transcription factor SOX-5 (probable)	YES
Fb7:0-10	gene13935	7,80	7,27E-05	5,21E-03	-	-	Molybdenum cofactor biosynthesis protein C (probable)	YES
Fb7:0-10	gene29914	8,35	3,23E-14	8,37E-12	-	-	Histidine-rich glycoprotein, Precursor (probable)	YES
Fb7:0-10	gene23400	8,77	6,82E-17	2,36E-14	Q9M125_ARATH	Ribosomal RNA processing brix domain-containing protein	Ribosome production factor 1 (probable)	YES
Fb7:0-10	gene03242	8,83	6,85E-14	1,73E-11	O04225_ORYSA	Tryptophan synthase B	Zinc finger MYM-type protein 5 (probable)	YES
Fb7:0-10	gene35013	10,01	1,94E-42	3,63E-38	Q9SRZ8_ARATH	NAC domain containing protein 28	NAC domain-containing protein 68 (ONAC068) (probable)	YES
Fb7:0-10	gene18875	10,70	3,36E-20	1,79E-17	CNGC1_ARATH	Cyclic nucleotide-gated ion channel 1	Cyclic nucleotide-gated ion channel 1 (AtCNGC1) (probable)	NO
Fb7:0-10	gene23453	10,79	9,58E-26	1,12E-22	O23392_ARATH	HXXXD-type acyl-transferase family protein	Vinorine synthase (probable)	YES
Fb7:0-10	gene31970	10,94	2,40E-33	8,96E-30	-	-	Potassium-transporting ATPase C chain (probable)	YES
Fb7:0-10	gene18560	11,36	5,79E-42	5,40E-38	AKRCA_ARATH	Aldo-keto reductase family 4 member C10	Alcohol dehydrogenase [NADP+] (similar to)	YES

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Fb7:0-10	gene34009	13,10	9,76E-40	6,08E-36	F4JBC7_ARATH	HXXXD-type acyl-transferase-like protein	Vinorine synthase (probable)	YES
Fb7:0-10	gene00911	Inf	1,53E-05	1,29E-03	Q9FVQ7_ARATH	Uncharacterized protein	Hepatoma-derived growth factor-related protein 2 (HRP-2) (probable)	YES
Fb7:0-10	gene01199	Inf	1,11E-04	7,46E-03	F4I5H4_ARATH	Uncharacterized protein	Lead, cadmium, zinc and mercury-transporting ATPase (probable)	YES
Fb7:0-10	gene03928	Inf	3,26E-05	2,51E-03	PME32_ARATH	Pectinesterase 32	Pectinesterase 36 (PE 36), Precursor (probable)	YES
Fb7:0-10	gene03949	Inf	1,02E-03	5,08E-02	Q42044_ARATH	Putative proline-rich protein	14 kDa proline-rich protein DC2.15, Precursor (putative)	YES
Fb7:0-10	gene04834	Inf	2,96E-31	6,92E-28	GAUTA_ARATH	Probable galacturonosyltransferase 10	Putative TRAF4-associated factor 1 (probable)	YES
Fb7:0-10	gene04836	Inf	1,01E-16	3,41E-14	Q01LY2_ORYSA	H0825G02.10 protein	Actinidain (Actinidin), Precursor (probable)	NO
Fb7:0-10	gene08182	Inf	1,14E-04	7,65E-03	-	-	Transcriptional activator protein rdp1 (probable)	NO
Fb7:0-10	gene09590	Inf	1,11E-03	5,49E-02	-	-	DNA polymerase I (POL I) (probable)	YES
Fb7:0-10	gene11978	Inf	4,71E-08	5,90E-06	O49471_ARATH	TMV resistance protein N-like	GTPase obg (probable)	YES
Fb7:0-10	gene12159	Inf	3,85E-04	2,18E-02	B8BCG8_ORYSI	Putative uncharacterized protein	Solute carrier family 25 member 40 (probable)	YES
Fb7:0-10	gene14060	Inf	2,75E-06	2,64E-04	Q94GB9_ORYSJ	Retrotransposon protein, putative, Ty1-copia subclass	Formin-like protein 6 (probable)	YES
Fb7:0-10	gene17917	Inf	1,34E-05	1,14E-03	-	-	Hematopoietically-expressed homeobox protein hhex (Homeobox protein hex) (probable)	YES
Fb7:0-10	gene18591	Inf	1,73E-05	1,43E-03	RHS3_ARATH	Serine/threonine-protein kinase RHS3	hypothetical protein	YES
Fb7:0-10	gene18909	Inf	1,56E-03	7,30E-02	-	-	Elongation factor Ts (EF-Ts) (probable)	NO
Fb7:0-10	gene18935	Inf	2,49E-04	1,54E-02	CNGC1_ARATH	Cyclic nucleotide-gated ion channel 1	Cyclic nucleotide-gated ion channel 1 (AtCNGC1) (probable)	NO
Fb7:0-10	gene19153	Inf	1,52E-18	6,76E-16	C70A2_ARATH	Cytochrome P450 703A2	Flavonoid 3'-monooxygenase (probable)	NO
Fb7:0-10	gene19404	Inf	3,20E-16	1,05E-13	Q93ZN5_ARATH	Transducin/WD40 domain-containing protein	Transducin beta-like protein 2 (WS-betaTRP) (probable)	NO
Fb7:0-10	gene20688	Inf	6,96E-04	3,60E-02	Q38957_ARATH	Orf 05 protein	1-deoxy-D-xylulose-5-phosphate synthase (DXP synthase) (probable)	YES
Fb7:0-10	gene21462	Inf	7,45E-09	1,09E-06	TMVRN_NICGU	TMV resistance protein N	Probable WRKY transcription factor 19	NO

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NIL vs. RV	gene id[a]	$\log_2$(F Ch)[b]	p-val.	p-adj.	blast hit[c]	blast hit protein description	predicted function (a1)	a1 & a2 comm.
Fb7:0-10	gene22882	Inf	1,38E-06	1,42E-04	A2YQF1_ORYSI	Putative uncharacterized protein	Cytochrome P450 71A1 (probable)	NO
Fb7:0-10	gene23205	Inf	7,43E-04	3,82E-02	-	-	Copper-specific metallothionein-2 (probable)	YES
Fb7:0-10	gene26796	Inf	6,52E-04	3,42E-02	-	-	UDP-N-acetylmuramate--L-alanine ligase (probable)	YES
Fb7:0-10	gene26821	Inf	1,25E-31	3,32E-28	-	-	Arginine-glutamic acid dipeptide repeats protein (probable)	YES
Fb7:0-10	gene26822	Inf	1,88E-17	7,18E-15	O23864_9ORYZ	Polyprotein	RING1 and YY1-binding protein (DED-associated factor) (probable)	YES
Fb7:0-10	gene26970	Inf	2,17E-05	1,75E-03	-	-	GP2, Precursor (probable)	YES
Fb7:0-10	gene26975	Inf	1,02E-05	9,13E-04	RL311_ARATH	60S ribosomal protein L31-1	60S ribosomal protein L31 (putative)	YES
Fb7:0-10	gene27017	Inf	3,95E-15	1,19E-12	ERF21_ARATH	Ethylene-responsive transcription factor ERF021	Ethylene-responsive transcription factor ERF022 (similar to)	NO
Fb7:0-10	gene29333	Inf	4,57E-04	2,54E-02	-	-	ATP-dependent RNA helicase DED1 (probable)	NO
Fb7:0-10	gene34072	Inf	3,78E-05	2,88E-03	-	-	Dosage compensation regulator (probable)	NO
Fb7:0-10	gene35024	Inf	6,58E-08	8,19E-06	U91C1_ARATH	UDP-glycosyltransferase 91C1	Anthocyanidin 3-O-glucosyltransferase (probable)	YES

Supplemental Table CIV. 2 List of DEG specific from annotation a2. A list of all DEG specifically found using a2 is provided for each contrasting hypothesis (NIL). DEG for each NIL are presented in ascending order of log$_2$(fold change)

Supplemental Table CIV. 2

[a] gene id is according to F. vesca annotation 2 nomenclature

[b] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb5:0-35	augustus_masked-LG5-processed-gene-44.57-mRNA-1	-Inf	1,20E-25	1,62E-22	ZIP4L_ARATH	TPR repeat-containing protein ZIP4
Fb5:0-35	genemark-LG5-processed-gene-214.50-mRNA-1	-Inf	4,01E-08	8,91E-06	-	-
Fb5:0-35	maker-LG4-augustus-gene-138.110-mRNA-1	-Inf	1,76E-10	6,05E-08	PAT1_ARATH	Scarecrow-like transcription factor PAT1
Fb5:0-35	maker-LG4-snap-gene-134.201-mRNA-1	-Inf	9,52E-14	4,39E-11	RZP23_ORYSJ	Serine/arginine-rich splicing factor RSZ23
Fb5:0-35	maker-LG5-augustus-gene-214.101-mRNA-1	-Inf	2,44E-27	3,85E-24	KEULE_ARATH	SNARE-interacting protein KEULE
Fb5:0-35	maker-LG5-augustus-gene-44.131-mRNA-1	-Inf	6,13E-10	2,00E-07	AHK3_ARATH	Histidine kinase 3
Fb5:0-35	maker-LG5-augustus-gene-52.163-mRNA-1	-Inf	7,32E-33	6,92E-29	CIP8_ARATH	E3 ubiquitin-protein ligase CIP8
Fb5:0-35	mrna06408.1-v1.0-hybrid	-Inf	2,53E-05	3,42E-03	-	-
Fb5:0-35	mrna15215.1-v1.0-hybrid	-Inf	5,45E-19	4,12E-16	T14H_TAXCU	Taxoid 14-beta-hydroxylase
Fb5:0-35	mrna29117.1-v1.0-hybrid	-Inf	2,01E-04	2,02E-02	-	-
Fb5:0-35	mrna32401.1-v1.0-hybrid	-Inf	2,16E-05	3,02E-03	HAP2_ARATH	Protein HAPLESS 2
Fb5:0-35	snap_masked-LG5-processed-gene-156.75-mRNA-1	-Inf	5,11E-07	9,94E-05	-	-
Fb5:0-35	maker-LG5-est_gff_Cufflinks-gene-21.7-mRNA-1	-10,09	6,19E-31	1,46E-27	-	-
Fb5:0-35	maker-LG5-augustus-gene-33.144-mRNA-1	-9,74	3,06E-13	1,35E-10	BRL1_ARATH	Serine/threonine-protein kinase BRI1-like 1
Fb5:0-35	genemark-LG5-processed-gene-32.40-mRNA-1	-9,44	3,78E-32	2,38E-28	RPS2_ARATH	Disease resistance protein RPS2
Fb5:0-35	maker-LG5-augustus-gene-19.193-mRNA-1	-9,12	5,31E-28	1,00E-24	Q9SLX1_MAIZE	Uncharacterized protein
Fb5:0-35	augustus_masked-LG4-processed-gene-136.67-mRNA-1	-8,72	1,73E-31	5,45E-28	Q9LIE1_ARATH	Transposase-like protein
Fb5:0-35	maker-LG5-augustus-gene-44.106-mRNA-1	-8,71	1,61E-22	1,68E-19	-	-
Fb5:0-35	maker-LG5-augustus-gene-229.145-mRNA-1	-8,21	4,38E-15	2,51E-12	FBK67_ARATH	F-box/kelch-repeat protein At3g23880
Fb5:0-35	augustus_masked-LG5-processed-gene-42.19-mRNA-1	-7,69	1,72E-12	6,93E-10	FBK83_ARATH	Putative F-box/kelch-repeat protein At4g19330
Fb5:0-35	genemark-LG5-processed-gene-18.83-mRNA-1	-6,75	4,08E-13	1,75E-10	TMVRN_NICGU	TMV resistance protein N
Fb5:0-35	maker-LG4-augustus-gene-138.112-mRNA-1	-6,64	3,64E-09	9,83E-07	RING1_GOSHI	E3 ubiquitin-protein ligase RING1
Fb5:0-35	maker-LG5-augustus-gene-51.151-mRNA-1	-6,63	5,02E-13	2,11E-10	C71AP_ARATH	Cytochrome P450 71A25
Fb5:0-35	genemark-LG7-processed-gene-45.73-mRNA-1	-6,01	2,00E-09	5,82E-07	-	-
Fb5:0-35	maker-LG5-augustus-gene-11.129-mRNA-1	-5,09	2,34E-06	4,09E-04	F4K051_ARATH	Cytochrome P450 708A2
Fb5:0-35	augustus_masked-LG5-processed-gene-32.35-mRNA-1	-4,87	5,24E-10	1,74E-07	ISU1_ARATH	Iron-sulfur cluster assembly protein 1
Fb5:0-35	augustus_masked-LG1-processed-gene-67.30-mRNA-1	-4,79	1,10E-03	8,52E-02	-	-
Fb5:0-35	maker-LG5-augustus-gene-	-4,63	2,21E-08	5,22E-06	F4K051_ARATH	Cytochrome P450 708A2

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
	11.128-mRNA-1					
Fb5:0-35	augustus_masked-LG4-processed-gene-133.16-mRNA-1	-4,53	6,25E-17	3,94E-14	PUB51_ARATH	Serine/threonine-protein kinase
Fb5:0-35	maker-LG6-augustus-gene-326.101-mRNA-1	-4,34	3,57E-10	1,20E-07	Q9LXB8_ARATH	Periaxin-like protein
Fb5:0-35	maker-LG5-augustus-gene-6.146-mRNA-1	-4,29	5,04E-12	1,91E-09	SC31B_ARATH	Protein transport protein SEC31 homolog B
Fb5:0-35	maker-LG5-augustus-gene-32.120-mRNA-1	-4,26	1,05E-03	8,16E-02	DOF56_ARATH	Dof zinc finger protein DOF5.6
Fb5:0-35	maker-LG5-snap-gene-30.226-mRNA-1	-4,06	1,80E-12	7,07E-10	F4I8I0_ARATH	Galactose-binding protein
Fb5:0-35	maker-LG4-snap-gene-140.146-mRNA-1	-4,00	9,45E-12	3,43E-09	IDD10_ARATH	Zinc finger protein JACKDAW
Fb5:0-35	augustus_masked-LG5-processed-gene-14.31-mRNA-1	-3,76	4,13E-05	5,31E-03	-	-
Fb5:0-35	maker-LG6-augustus-gene-82.245-mRNA-1	-3,68	1,81E-07	3,71E-05	Q058J9_ARATH	Molecular chaperone Hsp40/DnaJ family protein
Fb5:0-35	maker-LG5-augustus-gene-156.138-mRNA-1	-3,61	1,39E-05	2,01E-03	BGAL8_ARATH	Beta-galactosidase 8
Fb5:0-35	augustus_masked-LG5-processed-gene-11.14-mRNA-1	-3,51	1,70E-04	1,74E-02	F4K051_ARATH	Cytochrome P450 708A2
Fb5:0-35	maker-LG5-augustus-gene-22.183-mRNA-1	-3,43	7,01E-10	2,25E-07	TMVRN_NICGU	TMV resistance protein N
Fb5:0-35	maker-LG3-augustus-gene-188.133-mRNA-1	-3,36	1,85E-04	1,88E-02	RZP23_ORYSJ	Serine/arginine-rich splicing factor RSZ23
Fb5:0-35	maker-LG5-augustus-gene-26.265-mRNA-1	-3,31	3,28E-06	5,58E-04	SD18_ARATH	Receptor-like serine/threonine-protein kinase SD1-8
Fb5:0-35	genemark-LG5-processed-gene-16.66-mRNA-1	-3,27	4,13E-04	3,63E-02	Q9M2C6_ARATH	Putative uncharacterized protein T20K12.280
Fb5:0-35	maker-LG5-augustus-gene-32.136-mRNA-1	-3,10	8,50E-06	1,31E-03	BOR2_ARATH	Probable boron transporter 2
Fb5:0-35	augustus_masked-LG5-processed-gene-19.23-mRNA-1	-3,10	1,33E-08	3,35E-06	PP407_ARATH	Pentatricopeptide repeat-containing protein At5g39710
Fb5:0-35	augustus_masked-LG5-processed-gene-2.48-mRNA-1	-3,09	1,34E-09	4,08E-07	-	-
Fb5:0-35	maker-LG5-augustus-gene-106.186-mRNA-1	-2,92	9,85E-06	1,49E-03	ARR5_ARATH	Two-component response regulator ARR5
Fb5:0-35	snap_masked-LG5-processed-gene-48.98-mRNA-1	-2,90	3,72E-08	8,46E-06	-	-
Fb5:0-35	snap_masked-LG5-processed-gene-5.116-mRNA-1	-2,68	9,95E-05	1,09E-02	PHR_ARATH	Deoxyribodipyrimidine photo-lyase
Fb5:0-35	maker-LG5-snap-gene-3.160-mRNA-1	-2,66	1,44E-07	3,02E-05	FABH_ARATH	3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplastic
Fb5:0-35	augustus_masked-LG6-processed-gene-369.37-mRNA-1	-2,65	4,27E-04	3,72E-02	ATPBO_ARATH	ATP synthase subunit beta-3, mitochondrial
Fb5:0-35	maker-LG4-augustus-gene-112.104-mRNA-1	-2,61	5,20E-06	8,46E-04	FPGS3_ARATH	Folylpolyglutamate synthase
Fb5:0-35	augustus_masked-LG2-processed-gene-150.11-mRNA-1	-2,48	5,54E-05	6,54E-03	IPT3_ARATH	Adenylate isopentenyltransferase 3, chloroplastic
Fb5:0-35	maker-LG1-augustus-gene-23.210-mRNA-1	-2,48	7,71E-04	6,33E-02	CPR30_ARATH	F-box protein CPR30

Supplemental Table CIV. 2

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NIL vs. RV	**gene id[a]**	**log$_2$(FCh)[b]**	**p-val.**	**p-adj.**	**blast hit[b]**	**blast hit protein description**
Fb5:0-35	maker-LG5-augustus-gene-6.164-mRNA-1	-2,45	2,77E-04	2,63E-02	BASS6_ARATH	Probable sodium/metabolite cotransporter BASS6, chloroplastic
Fb5:0-35	genemark-LG5-processed-gene-13.75-mRNA-1	-2,42	3,68E-04	3,32E-02	Q9FHD1_ARATH	Myosin heavy chain-related protein
Fb5:0-35	maker-LG5-augustus-gene-59.178-mRNA-1	-2,37	1,77E-06	3,19E-04	Q9SNB6_ARATH	Putative uncharacterized protein F12A12.140
Fb5:0-35	maker-LG6-augustus-gene-193.116-mRNA-1	-2,34	5,74E-04	4,86E-02	-	-
Fb5:0-35	mrna06429.1-v1.0-hybrid	-2,29	5,34E-04	4,59E-02	PHYK1_ARATH	Phytol kinase 1, chloroplastic
Fb5:0-35	maker-LG7-augustus-gene-81.137-mRNA-1	-2,18	2,33E-05	3,22E-03	Q29Q34_ARATH	At5g19440
Fb5:0-35	maker-LG4-snap-gene-135.249-mRNA-1	-2,09	2,79E-05	3,74E-03	STPS1_SANAL	Sesquiterpene synthase
Fb5:0-35	maker-LG1-est_gff_Cufflinks-gene-106.3-mRNA-1	-2,06	5,30E-05	6,34E-03	F4JIK9_ARATH	Galactosyltransferase family protein
Fb5:0-35	maker-LG5-augustus-gene-10.232-mRNA-1	-2,03	1,21E-04	1,29E-02	NRPD1_ARATH	DNA-directed RNA polymerase IV subunit 1
Fb5:0-35	maker-LG1-snap-gene-106.166-mRNA-1	-2,03	4,10E-04	3,62E-02	RGLG2_ARATH	E3 ubiquitin-protein ligase RGLG2
Fb5:0-35	maker-LG1-augustus-gene-151.165-mRNA-1	-2,02	2,52E-04	2,43E-02	PUB30_ARATH	U-box domain-containing protein 30
Fb5:0-35	snap_masked-LG5-processed-gene-27.99-mRNA-1	-2,02	4,35E-05	5,45E-03	P2C56_ARATH	Protein phosphatase 2C 56
Fb5:0-35	genemark-LG6-processed-gene-315.64-mRNA-1	-2,00	1,51E-04	1,58E-02	RH53_ARATH	DEAD-box ATP-dependent RNA helicase 53
Fb5:0-35	maker-LG4-augustus-gene-167.112-mRNA-1	-1,96	7,88E-04	6,41E-02	Q8VYS9_ARATH	Putative uncharacterized protein At5g35730
Fb5:0-35	maker-LG5-augustus-gene-5.212-mRNA-1	-1,95	9,43E-05	1,04E-02	O49654_ARATH	Leucine-rich repeat receptor-like protein kinase
Fb5:0-35	maker-LG5-snap-gene-30.224-mRNA-1	-1,87	8,46E-04	6,80E-02	O22993_ARATH	FtsH extracellular protease
Fb5:0-35	maker-LG5-augustus-gene-53.141-mRNA-1	-1,86	3,11E-04	2,88E-02	RAE1_ARATH	Protein RAE1
Fb5:0-35	maker-LG7-augustus-gene-168.216-mRNA-1	-1,84	2,29E-04	2,26E-02	PTR45_ARATH	Protein NRT1/ PTR FAMILY 5.7
Fb5:0-35	genemark-LG7-processed-gene-65.63-mRNA-1	-1,79	2,37E-04	2,32E-02	PPR85_ARATH	Pentatricopeptide repeat-containing protein At1g59720, mitochondrial
Fb5:0-35	maker-LG3-augustus-gene-206.156-mRNA-1	-1,78	5,27E-05	6,34E-03	U87A2_ARATH	UDP-glycosyltransferase 87A2
Fb5:0-35	maker-LG4-augustus-gene-111.102-mRNA-1	-1,76	1,19E-03	8,92E-02	ASHR3_ARATH	Histone-lysine N-methyltransferase ASHR3
Fb5:0-35	maker-LG5-augustus-gene-278.140-mRNA-1	-1,76	3,09E-04	2,87E-02	B6REZ8_GOSHI	14-3-3a protein
Fb5:0-35	genemark-LG3-processed-gene-290.52-mRNA-1	-1,74	2,92E-04	2,75E-02	-	-
Fb5:0-35	maker-LG4-augustus-gene-134.176-mRNA-1	-1,71	5,96E-04	5,03E-02	CD48D_ARATH	Cell division control protein 48 homolog D
Fb5:0-35	maker-LG3-augustus-gene-224.181-mRNA-1	-1,67	9,11E-04	7,17E-02	Q94CM2_ARATH	Putative CDC6
Fb5:0-35	augustus_masked-LG6-processed-gene-336.123-mRNA-1	-1,58	9,26E-04	7,26E-02	GLYM1_ARATH	Serine hydroxymethyltransferase 1, mitochondrial
Fb5:0-35	maker-LG5-augustus-gene-32.141-mRNA-1	-1,50	9,92E-04	7,74E-02	SRO5_ARATH	Probable inactive poly [ADP-ribose] polymerase SRO5
Fb5:0-35	mrna06332.1-v1.0-hybrid	1,60	1,24E-03	9,17E-02	HDG12_ARATH	Homeobox-leucine zipper protein HDG12
Fb5:0-35	mrna01281.1-v1.0-hybrid	1,60	1,31E-03	9,65E-02	-	-

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NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb5:0-35	augustus_masked-LG6-processed-gene-175.2-mRNA-1	1,62	5,65E-04	4,81E-02	EIF3C_ARATH	Eukaryotic translation initiation factor 3 subunit C
Fb5:0-35	mrna17054.1-v1.0-hybrid	1,70	1,16E-03	8,77E-02	RS173_ARATH	40S ribosomal protein S17-3
Fb5:0-35	mrna20390.1-v1.0-hybrid	1,76	4,05E-04	3,59E-02	EGC2_ARATH	EG45-like domain containing protein 2
Fb5:0-35	genemark-LG4-processed-gene-133.82-mRNA-1	1,77	2,58E-04	2,47E-02	Q8L866_ARATH	Putative copper amine oxidase
Fb5:0-35	augustus_masked-LG4-processed-gene-135.2-mRNA-1	1,82	1,06E-03	8,22E-02	NRT31_ARATH	High-affinity nitrate transporter 3.1
Fb5:0-35	maker-LG4-augustus-gene-254.184-mRNA-1	1,83	1,75E-04	1,79E-02	Q9FX63_ARATH	Unknown protein
Fb5:0-35	maker-LG5-augustus-gene-15.152-mRNA-1	1,99	3,79E-05	4,91E-03	FBL71_ARATH	Putative F-box/LRR-repeat protein At4g00320
Fb5:0-35	maker-LG6-augustus-gene-383.200-mRNA-1	2,03	1,62E-04	1,67E-02	-	-
Fb5:0-35	maker-LG6-augustus-gene-9.173-mRNA-1	2,03	4,20E-05	5,32E-03	Q9FF29_ARATH	Receptor serine/threonine kinase
Fb5:0-35	maker-LG5-snap-gene-5.242-mRNA-1	2,10	3,05E-05	4,03E-03	Q8L742_ARATH	Copper amine oxidase family protein
Fb5:0-35	maker-LG4-snap-gene-168.135-mRNA-1	2,13	5,74E-05	6,74E-03	-	-
Fb5:0-35	augustus_masked-LG7-processed-gene-6.37-mRNA-1	2,13	5,04E-05	6,22E-03	PTR2_ARATH	Protein NRT1/ PTR FAMILY 8.3
Fb5:0-35	snap_masked-LG5-processed-gene-180.81-mRNA-1	2,16	1,46E-04	1,54E-02	SMG7_ARATH	Protein SMG7
Fb5:0-35	mrna16044.1-v1.0-hybrid-2	2,17	1,31E-05	1,93E-03	-	-
Fb5:0-35	snap_masked-LG6-processed-gene-195.60-mRNA-1	2,19	9,01E-05	1,01E-02	Q9FRZ0_MAIZE	Response regulator 5
Fb5:0-35	maker-LG5-augustus-gene-53.155-mRNA-1	2,35	9,57E-06	1,46E-03	-	-
Fb5:0-35	augustus_masked-LG5-processed-gene-12.2-mRNA-1	2,36	4,22E-04	3,69E-02	F4I5P7_ARATH	Calcium-dependent lipid-binding domain-containing protein
Fb5:0-35	maker-LG3-augustus-gene-40.152-mRNA-1	2,42	4,33E-05	5,45E-03	SRG1_ARATH	Protein SRG1
Fb5:0-35	maker-LG5-augustus-gene-30.213-mRNA-1	2,47	2,19E-06	3,87E-04	Q8RWI0_ARATH	Uncharacterized protein
Fb5:0-35	augustus_masked-LG5-processed-gene-30.68-mRNA-1	2,54	2,17E-06	3,86E-04	-	-
Fb5:0-35	snap_masked-LG5-processed-gene-61.110-mRNA-1	2,57	8,93E-07	1,67E-04	O22813_ARATH	Putative steroid dehydrogenase
Fb5:0-35	augustus_masked-LG6-processed-gene-308.15-mRNA-1	2,66	3,69E-04	3,32E-02	O23035_ARATH	YUP8H12.4 protein
Fb5:0-35	augustus_masked-LG4-processed-gene-136.31-mRNA-1	2,66	8,97E-08	1,90E-05	C71AP_ARATH	Cytochrome P450 71A25
Fb5:0-35	mrna31810.1-v1.0-hybrid	2,75	8,23E-05	9,37E-03	-	-
Fb5:0-35	maker-LG4-augustus-gene-36.145-mRNA-1	2,77	8,35E-06	1,29E-03	Q9SIF2_ARATH	Putative heat shock protein
Fb5:0-35	maker-LG5-augustus-gene-25.139-mRNA-1	2,81	4,34E-08	9,54E-06	GAT2_ARATH	Probable GABA transporter 2
Fb5:0-35	maker-LG6-augustus-gene-117.94-mRNA-1	2,87	3,75E-06	6,33E-04	RSZ33_ARATH	Serine/arginine-rich splicing factor RS2Z33
Fb5:0-35	maker-LG5-augustus-gene-3.174-mRNA-1	2,88	1,21E-06	2,22E-04	TL225_ARATH	Thylakoid lumenal protein At1g12250, chloroplastic

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Fb5:0-35	augustus_masked-LG4-processed-gene-228.10-mRNA-1	3,39	8,52E-05	9,64E-03	E9M219_PANGI	PR10-1
Fb5:0-35	maker-LG4-augustus-gene-136.232-mRNA-1	3,88	4,85E-06	8,04E-04	C71AP_ARATH	Cytochrome P450 71A25
Fb5:0-35	maker-LG4-augustus-gene-136.257-mRNA-1	3,97	2,44E-12	9,39E-10	MFS_MENPI	(+)-menthofuran synthase
Fb5:0-35	maker-LG5-augustus-gene-19.163-mRNA-1	4,01	1,16E-03	8,77E-02	Q9C9I5_ARATH	Putative uncharacterized protein F26A9.14
Fb5:0-35	maker-LG5-augustus-gene-52.160-mRNA-1	4,25	3,88E-08	8,73E-06	NAP1B_ARATH	Nucleosome assembly protein 12
Fb5:0-35	snap_masked-LG7-processed-gene-30.94-mRNA-1	4,43	2,53E-06	4,39E-04	C71AP_ARATH	Cytochrome P450 71A25
Fb5:0-35	maker-LG4-augustus-gene-149.198-mRNA-1	4,74	2,77E-18	2,01E-15	UGT2_GARJA	7-deoxyloganetin glucosyltransferase
Fb5:0-35	maker-LG1-augustus-gene-13.136-mRNA-1	4,78	1,89E-08	4,58E-06	BGL26_ORYSJ	Beta-glucosidase 26
Fb5:0-35	snap_masked-LG4-processed-gene-18.68-mRNA-1	5,07	1,36E-19	1,07E-16	-	-
Fb5:0-35	genemark-LG5-processed-gene-230.60-mRNA-1	5,70	2,10E-14	1,04E-11	DEF02_ARATH	Defensin-like protein 2
Fb5:0-35	augustus_masked-LG5-processed-gene-20.29-mRNA-1	6,03	2,60E-09	7,44E-07	RH14_ARATH	DEAD-box ATP-dependent RNA helicase 14
Fb5:0-35	maker-LG5-snap-gene-29.215-mRNA-1	6,18	1,02E-23	1,13E-20	Q9SNB6_ARATH	Putative uncharacterized protein F12A12.140
Fb5:0-35	maker-LG4-snap-gene-136.274-mRNA-1	7,66	2,93E-09	8,15E-07	C71AN_ARATH	Cytochrome P450 71A23
Fb5:50-76	augustus_masked-LG1-processed-gene-33.54-mRNA-1	-Inf	8,81E-28	6,95E-25	R13L1_ARATH	Putative disease resistance RPP13-like protein 1
Fb5:50-76	augustus_masked-LG5-processed-gene-136.11-mRNA-1	-Inf	2,09E-06	2,03E-04	GRV2_ARATH	DnaJ homolog subfamily C GRV2
Fb5:50-76	augustus_masked-LG5-processed-gene-225.25-mRNA-1	-Inf	1,94E-10	3,33E-08	Q949W8_ARATH	Xylulose kinase-2
Fb5:50-76	augustus_masked-LG5-processed-gene-270.19-mRNA-1	-Inf	2,37E-18	1,07E-15	Q9FZH9_ARATH	Uncharacterized protein
Fb5:50-76	augustus_masked-LG5-processed-gene-62.62-mRNA-1	-Inf	8,40E-09	1,19E-06	F4HR53_ARATH	Transmembrane receptors / ATP binding protein
Fb5:50-76	genemark-LG5-processed-gene-137.53-mRNA-1	-Inf	9,99E-08	1,20E-05	FHY3_ARATH	Protein FAR-RED ELONGATED HYPOCOTYL 3
Fb5:50-76	genemark-LG5-processed-gene-168.62-mRNA-1	-Inf	3,17E-04	1,94E-02	-	-
Fb5:50-76	genemark-LG5-processed-gene-214.50-mRNA-1	-Inf	1,63E-08	2,24E-06	-	-
Fb5:50-76	genemark-LG5-processed-gene-220.37-mRNA-1	-Inf	4,88E-18	2,05E-15	NSF_ARATH	Vesicle-fusing ATPase
Fb5:50-76	maker-LG1-augustus-gene-35.110-mRNA-1	-Inf	9,35E-08	1,13E-05	MSL3_ARATH	Mechanosensitive ion channel protein 3, chloroplastic
Fb5:50-76	maker-LG2-augustus-gene-229.130-mRNA-1	-Inf	6,11E-10	9,89E-08	FRS3_ARATH	Protein FAR1-RELATED SEQUENCE 3
Fb5:50-76	maker-LG4-snap-gene-134.201-mRNA-1	-Inf	1,56E-14	4,36E-12	RZP23_ORYSJ	Serine/arginine-rich splicing factor RSZ23
Fb5:50-76	maker-LG5-augustus-gene-136.110-mRNA-1	-Inf	1,95E-28	1,67E-25	TPS4_SELML	Bifunctional diterpene synthase, chloroplastic
Fb5:50-76	maker-LG5-augustus-gene-136.134-mRNA-1	-Inf	1,39E-03	6,96E-02	Y4885_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g08850

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb5:50-76	maker-LG5-augustus-gene-142.132-mRNA-1	-Inf	1,12E-33	1,63E-30	Q9LZ83_ARATH	Putative uncharacterized protein T32M21_20
Fb5:50-76	maker-LG5-augustus-gene-184.97-mRNA-1	-Inf	1,69E-21	1,03E-18	DCL1_ORYSJ	Endoribonuclease Dicer homolog 1
Fb5:50-76	maker-LG5-augustus-gene-191.165-mRNA-1	-Inf	5,65E-12	1,14E-09	HSPR2_ARATH	Nematode resistance protein-like HSPRO2
Fb5:50-76	maker-LG5-augustus-gene-209.153-mRNA-1	-Inf	6,96E-18	2,80E-15	USP_ARATH	UDP-sugar pyrophosphorylase
Fb5:50-76	maker-LG5-augustus-gene-214.101-mRNA-1	-Inf	4,11E-29	3,88E-26	KEULE_ARATH	SNARE-interacting protein KEULE
Fb5:50-76	maker-LG5-augustus-gene-240.125-mRNA-1	-Inf	8,68E-09	1,22E-06	Q9FHB6_ARATH	Putative uncharacterized protein At5g52450
Fb5:50-76	maker-LG5-augustus-gene-250.85-mRNA-1	-Inf	8,74E-15	2,47E-12	-	-
Fb5:50-76	maker-LG5-augustus-gene-89.109-mRNA-1	-Inf	7,14E-30	7,50E-27	ILV5_ARATH	Ketol-acid reductoisomerase, chloroplastic
Fb5:50-76	maker-LG5-est_gff_Cufflinks-gene-114.12-mRNA-1	-Inf	2,84E-05	2,23E-03	USP_ARATH	Isoleucine N-monooxygenase 1
Fb5:50-76	maker-LG5-snap-gene-137.127-mRNA-1	-Inf	1,81E-17	6,98E-15	A4FVS4_ARATH	DNA-binding bromodomain-containing protein
Fb5:50-76	maker-LG5-snap-gene-188.102-mRNA-1	-Inf	5,64E-11	9,97E-09	RL72_ARATH	60S ribosomal protein L7-2
Fb5:50-76	maker-LG5-snap-gene-188.103-mRNA-1	-Inf	9,07E-19	4,29E-16	RL71_ARATH	60S ribosomal protein L7-1
Fb5:50-76	maker-LG5-snap-gene-197.135-mRNA-1	-Inf	1,60E-04	1,05E-02	-	-
Fb5:50-76	maker-LG5-snap-gene-206.105-mRNA-1	-Inf	7,96E-39	3,77E-35	GLYC7_ARATH	Serine hydroxymethyltransferase 7
Fb5:50-76	maker-LG5-snap-gene-232.125-mRNA-1	-Inf	1,09E-34	2,58E-31	G0X3E3_GOSHI	Fiber-specific MADS protein
Fb5:50-76	maker-LG5-snap-gene-281.161-mRNA-1	-Inf	3,45E-20	1,76E-17	-	-
Fb5:50-76	mrna27724.1-v1.0-hybrid	-Inf	4,48E-05	3,39E-03	HLTT_LUPAL	13-hydroxylupanine O-tigloyltransferase
Fb5:50-76	mrna28664.1-v1.0-hybrid	-Inf	9,49E-04	5,03E-02	Q6NQB8_ARATH	Ubiquitin carboxyl-terminal hydrolase family protein
Fb5:50-76	mrna31304.1-v1.0-hybrid	-Inf	1,06E-04	7,25E-03	-	-
Fb5:50-76	mrna35073.1-v1.0-hybrid	-Inf	9,31E-04	4,97E-02	-	-
Fb5:50-76	snap_masked-LG5-processed-gene-156.75-mRNA-1	-Inf	2,47E-07	2,78E-05	-	-
Fb5:50-76	snap_masked-LG5-processed-gene-250.75-mRNA-1	-Inf	2,01E-03	9,50E-02	F6H1_ARATH	Feruloyl CoA ortho-hydroxylase 1
Fb5:50-76	augustus_masked-LG5-processed-gene-136.12-mRNA-1	-11,85	2,81E-49	5,31E-45	-	-
Fb5:50-76	mrna16039.1-v1.0-hybrid	-11,38	5,52E-37	1,74E-33	PUX10_ARATH	Plant UBX domain-containing protein 10
Fb5:50-76	maker-LG5-augustus-gene-203.102-mRNA-1	-10,02	1,95E-30	2,30E-27	AB2D_ARATH	ABC transporter D family member 2, chloroplastic
Fb5:50-76	maker-LG5-snap-gene-157.111-mRNA-1	-9,56	1,88E-34	3,96E-31	NUP88_ARATH	Nuclear pore complex protein NUP88
Fb5:50-76	maker-LG5-augustus-gene-239.187-mRNA-1	-9,19	6,89E-35	1,86E-31	ISPD_MENPI	(-)-isopiperitenol/(-)-carveol dehydrogenase, mitochondrial
Fb5:50-76	augustus_masked-LG3-processed-gene-116.16-mRNA-1	-9,02	4,85E-21	2,78E-18	Q66Q66_GOSAR	Transcription factor WER-like protein

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NIL vs. RV	**gene id[a]**	**$\log_2$(FCh)[b]**	**p-val.**	**p-adj.**	**blast hit[b]**	**blast hit protein description**
Fb5:50-76	maker-LG5-est_gff_Cufflinks-gene-133.10-mRNA-1	-8,96	3,51E-21	2,07E-18	-	-
Fb5:50-76	maker-LG5-snap-gene-279.141-mRNA-1	-8,19	9,67E-18	3,81E-15	UGT2_GARJA	7-deoxyloganetin glucosyltransferase
Fb5:50-76	maker-LG5-augustus-gene-93.132-mRNA-1	-7,97	7,58E-26	5,31E-23	C7254_GLYUR	11-oxo-beta-amyrin 30-oxidase
Fb5:50-76	maker-LG3-augustus-gene-118.116-mRNA-1	-7,41	5,68E-07	6,10E-05	OPR2_ARATH	12-oxophytodienoate reductase 2
Fb5:50-76	mrna10668.1-v1.0-hybrid	-7,35	4,55E-18	2,00E-15	Q9LU44_ARATH	Splicing factor 1-like protein
Fb5:50-76	augustus_masked-LG1-processed-gene-39.16-mRNA-1	-7,21	4,38E-06	4,04E-04	Q9STV1_ARATH	Rhamnogalacturonate lyase family protein
Fb5:50-76	maker-LG5-augustus-gene-225.166-mRNA-1	-7,14	5,08E-26	3,70E-23	A9PL21_GOSHI	Alpha-tubulin
Fb5:50-76	augustus_masked-LG5-processed-gene-204.28-mRNA-1	-6,18	6,69E-06	5,86E-04	Q84R17_ARATH	Uncharacterized protein
Fb5:50-76	snap_masked-LG5-processed-gene-227.100-mRNA-1	-6,10	2,74E-13	6,24E-11	Q9T069_ARATH	Uncharacterized protein
Fb5:50-76	augustus_masked-LG3-processed-gene-116.25-mRNA-1	-5,85	5,04E-19	2,44E-16	R13L1_ARATH	Putative disease resistance RPP13-like protein 1
Fb5:50-76	snap_masked-LG5-processed-gene-157.82-mRNA-1	-5,81	1,66E-20	8,97E-18	KC1D_ARATH	Casein kinase I isoform delta-like
Fb5:50-76	maker-LG5-augustus-gene-212.146-mRNA-1	-5,36	3,26E-16	1,10E-13	CTF64_ARATH	Cleavage stimulating factor 64
Fb5:50-76	augustus_masked-LG6-processed-gene-197.36-mRNA-1	-5,24	1,06E-20	5,87E-18	LDL2_ARATH	Lysine-specific histone demethylase 1 homolog 2
Fb5:50-76	maker-LG5-augustus-gene-59.163-mRNA-1	-5,16	2,70E-16	9,30E-14	TMVRN_NICGU	TMV resistance protein N
Fb5:50-76	maker-LG5-augustus-gene-249.114-mRNA-1	-5,10	6,82E-18	2,80E-15	RL131_ARATH	60S ribosomal protein L13-1
Fb5:50-76	maker-LG7-snap-gene-99.185-mRNA-1	-5,09	9,04E-06	7,77E-04	PME17_ARATH	Pectinesterase 17
Fb5:50-76	maker-LG5-augustus-gene-273.100-mRNA-1	-4,91	1,01E-07	1,20E-05	Y4885_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g08850
Fb5:50-76	maker-LG5-augustus-gene-149.121-mRNA-1	-4,82	3,80E-10	6,36E-08	BXL4_ARATH	Beta-D-xylosidase 4
Fb5:50-76	augustus_masked-LG5-processed-gene-177.6-mRNA-1	-4,50	1,08E-06	1,10E-04	Y1720_ARATH	UPF0392 protein At1g27200
Fb5:50-76	augustus_masked-LG5-processed-gene-187.20-mRNA-1	-4,46	2,17E-08	2,91E-06	ISPD_ARATH	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, chloroplastic
Fb5:50-76	augustus_masked-LG5-processed-gene-189.17-mRNA-1	-4,43	5,31E-14	1,34E-11	Q9FZ25_ARATH	Putative chitinase
Fb5:50-76	maker-LG5-augustus-gene-278.140-mRNA-1	-4,14	1,90E-14	5,05E-12	B6REZ8_GOSHI	14-3-3a protein
Fb5:50-76	maker-LG5-snap-gene-111.147-mRNA-1	-4,10	1,61E-14	4,41E-12	CLPB3_ARATH	Chaperone protein ClpB3, chloroplastic
Fb5:50-76	maker-LG5-est_gff_Cufflinks-gene-166.5-mRNA-1	-4,06	5,61E-14	1,40E-11	F8H_ARATH	Probable glucuronoxylan glucuronosyltransferase F8H
Fb5:50-76	maker-LG5-augustus-gene-275.181-mRNA-1	-3,94	1,50E-07	1,75E-05	Q66GJ1_ARATH	Cytochrome P450, family 706, subfamily A, polypeptide 6
Fb5:50-76	genemark-LG5-processed-gene-213.81-mRNA-1	-3,79	3,58E-12	7,36E-10	PPA15_ARATH	Purple acid phosphatase 15

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb5:50-76	maker-LG5-augustus-gene-207.222-mRNA-1	-3,75	2,31E-12	4,92E-10	AB16G_ARATH	ABC transporter G family member 16
Fb5:50-76	maker-LG5-snap-gene-272.274-mRNA-1	-3,70	1,94E-03	9,26E-02	FB303_ARATH	F-box protein At1g22220
Fb5:50-76	maker-LG5-snap-gene-204.143-mRNA-1	-3,68	2,71E-10	4,58E-08	CPSF3_ARATH	Cleavage and polyadenylation specificity factor subunit 3-I
Fb5:50-76	maker-LG5-augustus-gene-273.120-mRNA-1	-3,54	3,17E-04	1,94E-02	O82090_GOSHI	Annexin
Fb5:50-76	maker-LG5-snap-gene-268.119-mRNA-1	-3,53	7,99E-12	1,56E-09	Q9LU44_ARATH	Splicing factor 1-like protein
Fb5:50-76	maker-LG5-snap-gene-193.154-mRNA-1	-3,50	2,51E-11	4,71E-09	F4HWD0_ARATH	Uncharacterized protein
Fb5:50-76	maker-LG1-augustus-gene-50.164-mRNA-1	-3,49	6,65E-12	1,31E-09	-	-
Fb5:50-76	maker-LG5-snap-gene-164.89-mRNA-1	-3,40	3,52E-11	6,40E-09	GEX1_ARATH	Protein GAMETE EXPRESSED 1
Fb5:50-76	augustus_masked-LG5-processed-gene-165.22-mRNA-1	-3,38	4,06E-10	6,73E-08	Q9T0J2_ARATH	SAUR-like auxin-responsive protein
Fb5:50-76	maker-LG5-snap-gene-251.134-mRNA-1	-3,37	3,54E-05	2,75E-03	RH32_ARATH	DEAD-box ATP-dependent RNA helicase 32
Fb5:50-76	augustus_masked-LG5-processed-gene-238.9-mRNA-1	-3,37	5,72E-09	8,21E-07	TL29_ARATH	Thylakoid lumenal 29 kDa protein, chloroplastic
Fb5:50-76	genemark-LG5-processed-gene-249.56-mRNA-1	-3,33	5,73E-09	8,21E-07	Y2349_ARATH	Uncharacterized protein At2g33490
Fb5:50-76	snap_masked-LG5-processed-gene-62.83-mRNA-1	-3,31	5,31E-09	7,73E-07	ARFJ_ARATH	Auxin response factor 10
Fb5:50-76	maker-LG5-snap-gene-137.136-mRNA-1	-3,23	3,62E-06	3,39E-04	PAE11_ARATH	Pectin acetylesterase 11
Fb5:50-76	genemark-LG5-processed-gene-140.51-mRNA-1	-3,09	9,38E-05	6,63E-03	PAPS4_ARATH	Nuclear poly(A) polymerase 4
Fb5:50-76	maker-LG5-augustus-gene-220.95-mRNA-1	-3,09	4,07E-05	3,12E-03	-	-
Fb5:50-76	augustus_masked-LG5-processed-gene-251.19-mRNA-1	-3,02	7,58E-04	4,16E-02	PPR87_ARATH	Pentatricopeptide repeat-containing protein At1g61870, mitochondrial
Fb5:50-76	augustus_masked-LG5-processed-gene-59.32-mRNA-1	-3,02	2,57E-05	2,04E-03	TMVRN_NICGU	TMV resistance protein N
Fb5:50-76	maker-LG6-augustus-gene-117.94-mRNA-1	-2,99	2,61E-04	1,65E-02	RSZ33_ARATH	Serine/arginine-rich splicing factor RS2Z33
Fb5:50-76	maker-LG5-snap-gene-155.194-mRNA-1	-2,94	7,17E-09	1,02E-06	PILR1_LINPE	Bifunctional pinoresinol-lariciresinol reductase
Fb5:50-76	maker-LG1-augustus-gene-38.125-mRNA-1	-2,91	4,83E-07	5,22E-05	A4GU96_GOSHI	Kinesin-like protein
Fb5:50-76	augustus_masked-LG5-processed-gene-208.18-mRNA-1	-2,88	1,99E-08	2,69E-06	F4JYE9_ARATH	Folylpolyglutamate synthase
Fb5:50-76	maker-LG5-augustus-gene-250.80-mRNA-1	-2,87	2,32E-08	3,09E-06	PP124_ARATH	Pentatricopeptide repeat-containing protein At1g74850, chloroplastic
Fb5:50-76	maker-LG5-augustus-gene-231.147-mRNA-1	-2,85	3,52E-08	4,57E-06	MAX2_ARATH	F-box protein MAX2
Fb5:50-76	augustus_masked-LG3-processed-gene-117.22-mRNA-1	-2,82	1,30E-04	8,65E-03	Q8H6F8_GOSHI	MADS-box protein MADS6
Fb5:50-76	augustus_masked-LG5-processed-gene-245.54-mRNA-1	-2,82	1,33E-05	1,12E-03	LAC15_ARATH	Laccase-15
Fb5:50-76	snap_masked-LG5-processed-gene-198.92-	-2,79	1,17E-07	1,39E-05	-	-

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NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
	mRNA-1					
Fb5:50-76	maker-LG5-augustus-gene-177.104-mRNA-1	-2,77	7,92E-07	8,28E-05	AAP5_ARATH	Amino acid permease 5
Fb5:50-76	mrna01818.1-v1.0-hybrid	-2,72	2,07E-03	9,75E-02	NAP1C_ARATH	Nucleosome assembly protein 13
Fb5:50-76	augustus_masked-LG5-processed-gene-152.17-mRNA-1	-2,68	1,79E-07	2,06E-05	PHSB_ARATH	Probable polyamine transporter At1g31830
Fb5:50-76	maker-LG5-augustus-gene-275.171-mRNA-1	-2,64	7,42E-08	9,17E-06	STP13_ARATH	Sugar transport protein 13
Fb5:50-76	maker-LG5-augustus-gene-190.175-mRNA-1	-2,62	8,78E-06	7,59E-04	-	-
Fb5:50-76	genemark-LG5-processed-gene-164.33-mRNA-1	-2,56	5,41E-04	3,08E-02	ANTR2_ARATH	Ascorbate transporter, chloroplastic
Fb5:50-76	maker-LG5-augustus-gene-91.138-mRNA-1	-2,54	9,68E-05	6,76E-03	GUX5_ARATH	Putative UDP-glucuronate:xylan alpha-glucuronosyltransferase 5
Fb5:50-76	maker-LG5-snap-gene-251.135-mRNA-1	-2,52	1,54E-05	1,28E-03	RH32_ARATH	DEAD-box ATP-dependent RNA helicase 32
Fb5:50-76	maker-LG3-augustus-gene-188.133-mRNA-1	-2,41	1,34E-03	6,79E-02	RZP23_ORYSJ	Serine/arginine-rich splicing factor RSZ23
Fb5:50-76	augustus_masked-LG5-processed-gene-276.48-mRNA-1	-2,40	5,10E-05	3,80E-03	-	-
Fb5:50-76	maker-LG5-snap-gene-150.181-mRNA-1	-2,38	1,93E-06	1,88E-04	F4JK17_ARATH	Cofactor-independent phosphoglycerate mutase
Fb5:50-76	maker-LG3-snap-gene-190.135-mRNA-1	-2,35	8,02E-05	5,79E-03	-	-
Fb5:50-76	maker-LG5-augustus-gene-117.178-mRNA-1	-2,34	1,91E-06	1,87E-04	SPZX_ARATH	Serpin-ZX
Fb5:50-76	maker-LG5-snap-gene-238.102-mRNA-1	-2,33	2,91E-06	2,74E-04	Q8RWT8_ARATH	Seryl-tRNA synthetase
Fb5:50-76	maker-LG5-snap-gene-226.119-mRNA-1	-2,26	3,28E-04	1,97E-02	AAP6_ARATH	Amino acid permease 6
Fb5:50-76	augustus_masked-LG5-processed-gene-279.16-mRNA-1	-2,25	1,83E-05	1,51E-03	UGT2_GARJA	7-deoxyloganetin glucosyltransferase
Fb5:50-76	maker-LG6-augustus-gene-326.101-mRNA-1	-2,22	1,08E-04	7,36E-03	Q9LXB8_ARATH	Periaxin-like protein
Fb5:50-76	maker-LG5-augustus-gene-236.224-mRNA-1	-2,16	1,43E-05	1,20E-03	UGT2_GARJA	7-deoxyloganetin glucosyltransferase
Fb5:50-76	augustus_masked-LG4-processed-gene-261.31-mRNA-1	-2,10	2,88E-04	1,78E-02	FAR1_ARATH	Protein FAR-RED IMPAIRED RESPONSE 1
Fb5:50-76	maker-LG1-augustus-gene-39.132-mRNA-1	-2,10	1,43E-03	7,09E-02	TMVRN_NICGU	TMV resistance protein N
Fb5:50-76	maker-LG5-est_gff_Cufflinks-gene-237.4-mRNA-1	-1,95	1,48E-03	7,27E-02	Q9FXA0_ARATH	Putative uncharacterized protein At1g49740
Fb5:50-76	maker-LG5-augustus-gene-227.181-mRNA-1	-1,92	7,50E-05	5,44E-03	Q84JG6_ARATH	TPX2 (Targeting protein for Xklp2) family protein
Fb5:50-76	genemark-LG5-processed-gene-262.72-mRNA-1	-1,76	1,04E-03	5,50E-02	ARFQ_ARATH	Auxin response factor 17
Fb5:50-76	mrna02292.1-v1.0-hybrid	-1,73	1,12E-03	5,84E-02	-	-
Fb5:50-76	maker-LG5-snap-gene-186.154-mRNA-1	-1,72	4,19E-04	2,43E-02	Q8GWG0_ARATH	Putative uncharacterized protein At5g60620/mup24_30
Fb5:50-76	augustus_masked-LG5-processed-gene-164.15-mRNA-1	-1,72	3,32E-04	2,00E-02	Q9T0J2_ARATH	SAUR-like auxin-responsive protein
Fb5:50-76	augustus_masked-LG5-processed-gene-157.11-mRNA-1	-1,68	1,01E-03	5,33E-02	KPPR_ARATH	Phosphoribulokinase, chloroplastic

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb5:50-76	maker-LG5-snap-gene-233.145-mRNA-1	-1,68	7,38E-04	4,10E-02	AB26B_ARATH	ABC transporter B family member 26, chloroplastic
Fb5:50-76	maker-LG5-augustus-gene-115.189-mRNA-1	-1,45	1,40E-03	6,98E-02	PIRL5_ORYSJ	Plant intracellular Ras-group-related LRR protein 5
Fb5:50-76	maker-LG4-augustus-gene-245.165-mRNA-1	1,46	1,89E-03	9,07E-02	Q9SIS4_ARATH	Putative inositol polyphosphate-5-phosphatase
Fb5:50-76	mrna13530.1-v1.0-hybrid	1,51	1,99E-03	9,46E-02	U73B3_ARATH	UDP-glycosyltransferase 73B3
Fb5:50-76	snap_masked-LG5-processed-gene-244.64-mRNA-1	1,54	9,18E-04	4,94E-02	SAC51_ARATH	Transcription factor SAC51
Fb5:50-76	maker-LG5-augustus-gene-195.127-mRNA-1	1,62	1,36E-03	6,84E-02	LUP1_ARATH	Lupeol synthase 1
Fb5:50-76	maker-LG5-snap-gene-155.198-mRNA-1	1,62	1,46E-03	7,18E-02	Q94F50_ARATH	Uncharacterized protein
Fb5:50-76	mrna20390.1-v1.0-hybrid	1,69	7,44E-04	4,10E-02	EGC2_ARATH	EG45-like domain containing protein 2
Fb5:50-76	maker-LG2-snap-gene-191.317-mRNA-1	1,73	4,16E-04	2,42E-02	CADH9_ARATH	Probable cinnamyl alcohol dehydrogenase 9
Fb5:50-76	mrna16020.1-v1.0-hybrid	1,74	5,73E-04	3,24E-02	TMVRN_NICGU	TMV resistance protein N
Fb5:50-76	genemark-LG5-processed-gene-215.72-mRNA-1	1,75	1,85E-04	1,20E-02	ASSY_ARATH	Argininosuccinate synthase, chloroplastic
Fb5:50-76	augustus_masked-LG5-processed-gene-127.22-mRNA-1	1,75	3,21E-04	1,94E-02	VAP21_ARATH	Vesicle-associated protein 2-1, N-terminally processed
Fb5:50-76	maker-LG5-augustus-gene-191.137-mRNA-1	1,79	2,01E-04	1,29E-02	Y1796_ARATH	Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic
Fb5:50-76	genemark-LG5-processed-gene-219.56-mRNA-1	1,87	1,05E-04	7,23E-03	MLH1_ARATH	DNA mismatch repair protein MLH1
Fb5:50-76	augustus_masked-LG5-processed-gene-283.8-mRNA-1	1,91	1,53E-03	7,47E-02	SKI25_ARATH	F-box/kelch-repeat protein SKIP25
Fb5:50-76	maker-LG5-augustus-gene-91.215-mRNA-1	1,95	4,32E-04	2,50E-02	ANM12_ARATH	Probable protein arginine N-methyltransferase 1.2
Fb5:50-76	augustus_masked-LG5-processed-gene-276.41-mRNA-1	2,00	5,39E-04	3,07E-02	Y3236_ARATH	Ankyrin repeat-containing protein At3g12360
Fb5:50-76	mrna34513.1-v1.0-hybrid	2,03	1,79E-03	8,57E-02	FAB1A_ARATH	1-phosphatidylinositol-3-phosphate 5-kinase FAB1A
Fb5:50-76	maker-LG6-snap-gene-383.224-mRNA-1	2,04	1,16E-04	7,84E-03	Q3LUM1_GOSHI	Elongation factor 1-alpha
Fb5:50-76	maker-LG6-augustus-gene-317.202-mRNA-1	2,15	2,60E-04	1,64E-02	C71DI_MENSP	Cytochrome P450 71D18
Fb5:50-76	maker-LG5-snap-gene-206.113-mRNA-1	2,29	1,18E-03	6,08E-02	AKT2_ARATH	Potassium channel AKT2/3
Fb5:50-76	genemark-LG5-processed-gene-233.50-mRNA-1	2,52	6,97E-04	3,88E-02	TMVRN_NICGU	TMV resistance protein N
Fb5:50-76	augustus_masked-LG5-processed-gene-181.17-mRNA-1	2,63	5,16E-04	2,95E-02	GXM1_ARATH	Glucuronoxylan 4-O-methyltransferase 1
Fb5:50-76	maker-LG6-augustus-gene-383.200-mRNA-1	2,66	1,33E-06	1,33E-04	-	-
Fb5:50-76	maker-LG5-est_gff_Cufflinks-gene-169.1-mRNA-1	2,71	1,26E-06	1,29E-04	HMGCL_ARATH	Hydroxymethylglutaryl-CoA lyase, mitochondrial
Fb5:50-76	maker-LG5-snap-gene-186.158-mRNA-1	2,93	6,38E-06	5,64E-04	Q9SD45_ARATH	Epoxide hydrolase-like protein

Supplemental Table CIV. 2

[a] gene id is according to F. vesca annotation 2 nomenclature

[b] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb5:50-76	maker-LG1-snap-gene-199.182-mRNA-1	3,13	2,68E-07	3,00E-05	F4JLM5_ARATH	Isoleucyl-tRNA synthetase
Fb5:50-76	maker-LG5-augustus-gene-239.182-mRNA-1	3,36	2,02E-04	1,29E-02	ISOA3_ARATH	Isoamylase 3, chloroplastic
Fb5:50-76	genemark-LG5-processed-gene-230.60-mRNA-1	3,43	4,12E-07	4,50E-05	DEF02_ARATH	Defensin-like protein 2
Fb5:50-76	snap_masked-LG4-processed-gene-193.96-mRNA-1	3,45	1,98E-04	1,28E-02	CSP1_ARATH	Cold shock protein 1
Fb5:50-76	maker-LG1-snap-gene-199.180-mRNA-1	3,52	4,85E-04	2,79E-02	Q9LQZ4_ARATH	Transcription initiation factor IIF, beta subunit
Fb5:50-76	maker-LG5-augustus-gene-283.170-mRNA-1	3,54	1,65E-04	1,08E-02	DUR3_ARATH	Urea-proton symporter DUR3
Fb5:50-76	maker-LG7-augustus-gene-81.148-mRNA-1	3,67	7,42E-04	4,10E-02	BPS1_ARATH	Protein BPS1, chloroplastic
Fb5:50-76	augustus_masked-LG5-processed-gene-117.12-mRNA-1	3,87	2,07E-03	9,75E-02	XRN3_ARATH	5'-3' exoribonuclease 3
Fb5:50-76	mrna00253.1-v1.0-hybrid	3,89	1,27E-03	6,50E-02	-	-
Fb5:50-76	maker-LG5-augustus-gene-273.97-mRNA-1	3,93	6,65E-06	5,85E-04	Y4885_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g08850
Fb5:50-76	augustus_masked-LG5-processed-gene-87.28-mRNA-1	4,22	3,84E-15	1,14E-12	CDKA1_ARATH	Cyclin-dependent kinase A-1
Fb5:50-76	maker-LG5-est_gff_Cufflinks-gene-128.6-mRNA-1	4,32	1,17E-09	1,85E-07	BKI1_ARATH	BRI1 kinase inhibitor 1
Fb5:50-76	augustus_masked-LG1-processed-gene-199.28-mRNA-1	4,39	1,98E-05	1,62E-03	F4JLM5_ARATH	Isoleucyl-tRNA synthetase
Fb5:50-76	augustus_masked-LG5-processed-gene-168.7-mRNA-1	4,46	4,33E-16	1,44E-13	Q9C7T7_ARATH	Leucine-rich repeat receptor-like protein kinase
Fb5:50-76	augustus_masked-LG5-processed-gene-169.11-mRNA-1	4,48	3,85E-15	1,14E-12	EME1B_ARATH	Crossover junction endonuclease EME1B
Fb5:50-76	genemark-LG5-processed-gene-60.55-mRNA-1	4,60	2,35E-16	8,22E-14	TMVRN_NICGU	TMV resistance protein N
Fb5:50-76	maker-LG5-augustus-gene-223.69-mRNA-1	5,15	3,72E-05	2,86E-03	RNS1_ARATH	Ribonuclease 1
Fb5:50-76	mrna26564.1-v1.0-hybrid	5,18	1,96E-05	1,61E-03	-	-
Fb5:50-76	mrna26879.1-v1.0-hybrid	5,29	1,40E-03	6,98E-02	-	-
Fb5:50-76	maker-LG5-augustus-gene-248.140-mRNA-1	5,36	3,95E-09	5,84E-07	PP407_ARATH	Pentatricopeptide repeat-containing protein At5g39710
Fb5:50-76	mrna03041.1-v1.0-hybrid	5,62	2,35E-04	1,49E-02	H2AXA_ARATH	Probable histone H2AXa
Fb5:50-76	augustus_masked-LG5-processed-gene-248.27-mRNA-1	6,94	2,20E-07	2,49E-05	PP124_ARATH	Pentatricopeptide repeat-containing protein At1g74850, chloroplastic
Fb5:50-76	maker-LG5-snap-gene-224.152-mRNA-1	7,50	3,82E-32	4,82E-29	SR543_ARATH	Signal recognition particle 54 kDa protein 3
Fb5:50-76	augustus_masked-LG6-processed-gene-357.19-mRNA-1	Inf	6,85E-05	5,02E-03	TMVRN_NICGU	TMV resistance protein N
Fb5:50-76	maker-LG5-est_gff_Cufflinks-gene-281.0-mRNA-1	Inf	1,38E-03	6,93E-02	O82219_ARATH	Rossmann-fold NAD(P)-binding domain-containing protein
Fb5:50-76	maker-LG5-snap-gene-132.128-mRNA-1	Inf	2,98E-05	2,33E-03	RAB1B_ARATH	Ras-related protein RABB1b
Fb5:50-76	mrna10415.1-v1.0-hybrid	Inf	8,77E-05	6,26E-03	-	-

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NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb5:50-76	mrna15838.1-v1.0-hybrid	Inf	1,45E-03	7,16E-02	CGS1_ARATH	Cystathionine gamma-synthase 1, chloroplastic
Fb5:50-76	mrna26047.1-v1.0-hybrid	Inf	3,81E-06	3,55E-04	FUT1_ARATH	Galactoside 2-alpha-L-fucosyltransferase
Fb5:50-76	snap_masked-LG5-processed-gene-60.85-mRNA-1	Inf	1,35E-03	6,84E-02	-	-
Fb6:84-101	genemark-LG7-processed-gene-45.73-mRNA-1	-Inf	1,04E-10	5,06E-08	-	-
Fb6:84-101	maker-LG2-snap-gene-87.121-mRNA-1	-Inf	1,31E-09	4,79E-07	Q8LCC1_ARATH	Uncharacterized protein
Fb6:84-101	maker-LG6-augustus-gene-18.133-mRNA-1	-Inf	1,33E-10	6,07E-08	-	-
Fb6:84-101	maker-LG6-snap-gene-337.172-mRNA-1	-Inf	2,36E-20	2,35E-17	EME1_ORYSJ	Crossover junction endonuclease EME1
Fb6:84-101	maker-LG6-snap-gene-364.151-mRNA-1	-Inf	4,38E-06	8,56E-04	DRL30_ARATH	Probable disease resistance protein At5g04720
Fb6:84-101	maker-LG6-snap-gene-374.212-mRNA-1	-Inf	4,20E-22	4,98E-19	ILVD_ARATH	Dihydroxy-acid dehydratase, chloroplastic
Fb6:84-101	maker-LG6-snap-gene-387.156-mRNA-1	-Inf	4,71E-06	9,11E-04	Q8L7T4_ARATH	Uncharacterized protein
Fb6:84-101	snap_masked-LG3-processed-gene-241.118-mRNA-1	-Inf	1,59E-09	5,46E-07	H32_ARATH	Histone H3.2
Fb6:84-101	maker-LG6-est_gff_Cufflinks-gene-378.6-mRNA-1	-9,93	5,94E-27	1,25E-23	C79D4_LOTJA	Isoleucine N-monooxygenase 2
Fb6:84-101	maker-LG6-augustus-gene-326.101-mRNA-1	-8,57	3,98E-22	4,98E-19	Q9LXB8_ARATH	Periaxin-like protein
Fb6:84-101	augustus_masked-LG6-processed-gene-332.35-mRNA-1	-7,02	8,43E-23	1,23E-19	CNGC2_ARATH	Cyclic nucleotide-gated ion channel 2
Fb6:84-101	maker-LG6-snap-gene-371.119-mRNA-1	-5,98	3,07E-18	2,64E-15	TIC32_ARATH	Short-chain dehydrogenase TIC 32, chloroplastic
Fb6:84-101	augustus_masked-LG6-processed-gene-382.34-mRNA-1	-5,60	2,30E-15	1,56E-12	C71DD_MENPI	Cytochrome P450 71D13
Fb6:84-101	augustus_masked-LG6-processed-gene-336.11-mRNA-1	-5,23	4,26E-06	8,41E-04	RPS5_ARATH	Disease resistance protein RPS5
Fb6:84-101	maker-LG6-augustus-gene-383.200-mRNA-1	-5,06	2,91E-07	7,55E-05	-	-
Fb6:84-101	maker-LG6-augustus-gene-385.145-mRNA-1	-4,89	8,26E-16	6,26E-13	BGL14_ARATH	Beta-glucosidase 14
Fb6:84-101	snap_masked-LG6-processed-gene-382.99-mRNA-1	-4,41	3,69E-08	1,11E-05	DR102_ARATH	DNA-damage-repair/toleration protein DRT102
Fb6:84-101	maker-LG6-augustus-gene-15.182-mRNA-1	-4,29	9,58E-13	5,67E-10	Q8GZ22_ARATH	Putative ankyrin
Fb6:84-101	genemark-LG6-processed-gene-17.80-mRNA-1	-4,20	3,97E-04	4,91E-02	LBD27_ARATH	LOB domain-containing protein 27
Fb6:84-101	maker-LG6-augustus-gene-319.147-mRNA-1	-4,04	6,54E-09	2,06E-06	EPF1_ARATH	MEPF1
Fb6:84-101	augustus_masked-LG6-processed-gene-327.20-mRNA-1	-3,88	1,48E-06	3,30E-04	-	-
Fb6:84-101	maker-LG4-augustus-gene-221.152-mRNA-1	-3,44	7,80E-09	2,38E-06	-	-
Fb6:84-101	augustus_masked-LG4-processed-gene-101.13-mRNA-1	-3,41	3,76E-06	7,49E-04	PUB38_ARATH	U-box domain-containing protein 38
Fb6:84-101	maker-LG6-augustus-gene-327.200-mRNA-1	-3,33	1,77E-10	7,63E-08	D2T2F8_GERHY	GRCD4 protein
Fb6:84-	maker-LG6-snap-gene-	-3,15	1,77E-10	7,63E-08	EBF2_ARATH	EIN3-binding F-box protein 2

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NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
101	32044.142-mRNA-1					
Fb6:84-101	augustus_masked-LG6-processed-gene-324.28-mRNA-1	-3,03	1,12E-07	3,04E-05	AB7I_ARATH	Protein ABCI7, chloroplastic
Fb6:84-101	maker-LG4-snap-gene-100.166-mRNA-1	-2,70	1,97E-05	3,31E-03	Y5158_ARATH	Probable receptor-like protein kinase At5g15080
Fb6:84-101	maker-LG4-est_gff_Cufflinks-gene-237.3-mRNA-1	-2,62	1,73E-04	2,34E-02	JAL20_ARATH	Jacalin-related lectin 20
Fb6:84-101	genemark-LG4-processed-gene-113.46-mRNA-1	-2,60	2,06E-06	4,49E-04	-	-
Fb6:84-101	maker-LG6-snap-gene-387.160-mRNA-1	-2,54	6,74E-07	1,66E-04	F4JPL6_ARATH	Sec1/munc18-like (SM) family protein
Fb6:84-101	maker-LG6-snap-gene-336.492-mRNA-1	-2,32	8,27E-06	1,46E-03	R13L1_ARATH	Putative disease resistance RPP13-like protein 1
Fb6:84-101	snap_masked-LG1-processed-gene-159.101-mRNA-1	-2,31	3,44E-04	4,35E-02	-	-
Fb6:84-101	maker-LG6-augustus-gene-386.153-mRNA-1	-2,27	1,07E-05	1,88E-03	CSLC4_ARATH	Xyloglucan glycosyltransferase 4
Fb6:84-101	maker-LG6-augustus-gene-383.177-mRNA-1	-2,14	6,55E-06	1,23E-03	SUOX_ARATH	Sulfite oxidase
Fb6:84-101	snap_masked-LG4-processed-gene-101.96-mRNA-1	-2,07	6,46E-05	9,79E-03	Q9FVQ7_ARATH	Uncharacterized protein
Fb6:84-101	maker-LG7-augustus-gene-47.110-mRNA-1	-2,05	2,15E-04	2,84E-02	FAR1_ARATH	Protein FAR-RED IMPAIRED RESPONSE 1
Fb6:84-101	maker-LG6-augustus-gene-328.155-mRNA-1	-1,95	5,64E-04	6,68E-02	TCP13_ARATH	Transcription factor TCP13
Fb6:84-101	maker-LG6-snap-gene-373.220-mRNA-1	-1,93	1,31E-04	1,88E-02	RING1_GOSHI	E3 ubiquitin-protein ligase RING1
Fb6:84-101	maker-LG6-snap-gene-336.482-mRNA-1	-1,91	1,10E-04	1,62E-02	SPSA3_ARATH	Probable sucrose-phosphate synthase 3
Fb6:84-101	augustus_masked-LG2-processed-gene-216.11-mRNA-1	1,86	1,45E-04	2,05E-02	-	-
Fb6:84-101	maker-LG3-augustus-gene-281.141-mRNA-1	2,69	1,90E-07	5,00E-05	Q7XA63_ARATH	Uncharacterized protein
Fb6:84-101	maker-LG4-augustus-gene-206.150-mRNA-1	2,93	1,29E-06	2,92E-04	AB4B_ARATH	ABC transporter B family member 4
Fb6:84-101	maker-LG6-snap-gene-338.136-mRNA-1	3,21	5,00E-05	7,95E-03	DHX8_ARATH	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase
Fb6:84-101	augustus_masked-LG6-processed-gene-369.37-mRNA-1	3,45	3,97E-07	1,00E-04	ATPBO_ARATH	ATP synthase subunit beta-3, mitochondrial
Fb6:84-101	maker-LG6-snap-gene-334.192-mRNA-1	3,71	5,81E-10	2,29E-07	SCPDL_ARATH	Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410
Fb6:84-101	maker-LG4-snap-gene-12.198-mRNA-1	4,18	1,39E-05	2,42E-03	-	-
Fb6:84-101	mrna28225.1-v1.0-hybrid	4,68	6,28E-11	3,13E-08	MRH1_ARATH	Probable LRR receptor-like serine/threonine-protein kinase MRH1
Fb6:84-101	mrna01177.1-v1.0-hybrid	5,45	7,63E-04	8,76E-02	F4KEV7_ARATH	Fragile histidine triad protein
Fb6:84-101	maker-LG3-augustus-gene-206.156-mRNA-1	5,46	1,56E-22	2,10E-19	U87A2_ARATH	UDP-glycosyltransferase 87A2
Fb6:84-101	augustus_masked-LG3-processed-gene-288.59-mRNA-1	5,50	6,21E-04	7,26E-02	PPR93_ARATH	Pentatricopeptide repeat-containing protein At1g62720

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb6:84-101	maker-LG6-augustus-gene-372.172-mRNA-1	6,16	2,30E-05	3,79E-03	Q9FI14_ARATH	Target of AVRB operation1 protein
Fb6:84-101	maker-LG6-augustus-gene-381.155-mRNA-1	6,56	1,35E-10	6,07E-08	PER51_ARATH	Peroxidase 51
Fb6:84-101	maker-LG7-snap-gene-172.205-mRNA-1	6,66	1,48E-04	2,07E-02	Y3475_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At3g47570
Fb6:84-101	maker-LG1-augustus-gene-184.198-mRNA-1	7,14	2,35E-24	4,45E-21	UGT2_GARJA	7-deoxyloganetin glucosyltransferase
Fb6:84-101	maker-LG6-augustus-gene-376.214-mRNA-1	7,23	1,01E-31	4,79E-28	UGT2_GARJA	7-deoxyloganetin glucosyltransferase
Fb6:84-101	augustus_masked-LG6-processed-gene-368.15-mRNA-1	9,91	5,90E-05	9,07E-03	ZAT11_ARATH	Zinc finger protein ZAT11
Fb6:84-101	maker-LG5-augustus-gene-193.132-mRNA-1	Inf	3,51E-04	4,41E-02	AP4S_ARATH	AP-4 complex subunit sigma
Fb6:84-101	maker-LG6-augustus-gene-370.158-mRNA-1	Inf	6,44E-15	4,21E-12	Y3236_ARATH	Ankyrin repeat-containing protein At3g12360
Fb7:0-10	augustus_masked-LG7-processed-gene-102.17-mRNA-1	-Inf	1,73E-06	1,68E-04	Q8GXW8_ARATH	Putative uncharacterized protein At1g04780/F13M7_20
Fb7:0-10	augustus_masked-LG7-processed-gene-112.38-mRNA-1	-Inf	2,81E-19	1,02E-16	Q8RY11_ARATH	Metallopeptidase M24 family protein
Fb7:0-10	augustus_masked-LG7-processed-gene-128.4-mRNA-1	-Inf	2,66E-28	2,65E-25	CIPK2_ARATH	CBL-interacting serine/threonine-protein kinase 2
Fb7:0-10	augustus_masked-LG7-processed-gene-27.22-mRNA-1	-Inf	2,71E-06	2,54E-04	RPP8_ARATH	Disease resistance protein RPP8
Fb7:0-10	augustus_masked-LG7-processed-gene-31.15-mRNA-1	-Inf	6,53E-16	1,77E-13	ENO2_ARATH	Bifunctional enolase 2/transcriptional activator
Fb7:0-10	augustus_masked-LG7-processed-gene-31.28-mRNA-1	-Inf	3,58E-18	1,17E-15	RST1_ARATH	Protein RST1
Fb7:0-10	augustus_masked-LG7-processed-gene-36.45-mRNA-1	-Inf	6,10E-06	5,23E-04	EFGM1_ARATH	Elongation factor G-1, mitochondrial
Fb7:0-10	augustus_masked-LG7-processed-gene-45.27-mRNA-1	-Inf	1,06E-19	4,08E-17	O81629_ARATH	Tetratricopeptide repeat domain-containing protein
Fb7:0-10	augustus_masked-LG7-processed-gene-50.13-mRNA-1	-Inf	9,31E-05	6,21E-03	SAP10_ARATH	Zinc finger A20 and AN1 domain-containing stress-associated protein 10
Fb7:0-10	augustus_masked-LG7-processed-gene-54.36-mRNA-1	-Inf	1,74E-15	4,54E-13	PLY13_ARATH	Probable pectate lyase 13
Fb7:0-10	augustus_masked-LG7-processed-gene-60.13-mRNA-1	-Inf	1,13E-31	1,53E-28	-	-
Fb7:0-10	augustus_masked-LG7-processed-gene-68.0-mRNA-1	-Inf	4,16E-10	6,74E-08	ZIP4L_ARATH	TPR repeat-containing protein ZIP4
Fb7:0-10	genemark-LG3-processed-gene-102.82-mRNA-1	-Inf	7,60E-08	9,00E-06	Y3475_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At3g47570
Fb7:0-10	genemark-LG7-processed-gene-102.79-mRNA-1	-Inf	1,67E-04	1,06E-02	PR1B5_ARATH	PRA1 family protein B5
Fb7:0-10	genemark-LG7-processed-gene-14.53-mRNA-1	-Inf	1,85E-16	5,14E-14	-	-
Fb7:0-10	genemark-LG7-processed-gene-15.63-mRNA-1	-Inf	6,02E-29	6,70E-26	-	-
Fb7:0-10	genemark-LG7-processed-gene-35.77-mRNA-1	-Inf	4,86E-26	3,18E-23	-	-

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NIL vs. RV	**gene id[a]**	**log$_2$(FCh)[b]**	**p-val.**	**p-adj.**	**blast hit[b]**	**blast hit protein description**
Fb7:0-10	maker-LG2-snap-gene-87.121-mRNA-1	-Inf	2,89E-10	4,84E-08	Q8LCC1_ARATH	Uncharacterized protein
Fb7:0-10	maker-LG5-augustus-gene-178.144-mRNA-1	-Inf	4,34E-04	2,41E-02	-	-
Fb7:0-10	maker-LG7-augustus-gene-124.109-mRNA-1	-Inf	1,51E-16	4,26E-14	-	-
Fb7:0-10	maker-LG7-augustus-gene-36.129-mRNA-1	-Inf	3,90E-10	6,36E-08	STSYN_PEA	Stachyose synthase
Fb7:0-10	maker-LG7-augustus-gene-80.131-mRNA-1	-Inf	1,71E-22	8,51E-20	Q9FIH8_ARATH	Putative pitrilysin
Fb7:0-10	maker-LG7-augustus-gene-88.88-mRNA-1	-Inf	1,26E-10	2,20E-08	Q9SAJ2_ARATH	T8K14.1 protein
Fb7:0-10	maker-LG7-exonerate_protein2genome-gene-88.76-mRNA-1	-Inf	5,07E-06	4,47E-04	TMVRN_NICGU	TMV resistance protein N
Fb7:0-10	maker-LG7-snap-gene-1.135-mRNA-1	-Inf	5,34E-04	2,88E-02	F4KGA3_ARATH	Putative PHD finger transcription factor
Fb7:0-10	maker-LG7-snap-gene-129.164-mRNA-1	-Inf	7,03E-08	8,53E-06	ZDH22_ARATH	Protein S-acyltransferase 24
Fb7:0-10	maker-LG7-snap-gene-36.148-mRNA-1	-Inf	1,81E-12	3,61E-10	Q0WWX4_ARATH	RanGAP1 interacting protein
Fb7:0-10	maker-LG7-snap-gene-45.196-mRNA-1	-Inf	4,97E-08	6,08E-06	T14H_TAXCU	Taxoid 14-beta-hydroxylase
Fb7:0-10	maker-LG7-snap-gene-64.82-mRNA-1	-Inf	1,94E-35	7,33E-32	ASD1_ARATH	Alpha-L-arabinofuranosidase 1
Fb7:0-10	mrna03066.1-v1.0-hybrid	-Inf	1,58E-03	7,05E-02	Y3475_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At3g47570
Fb7:0-10	mrna04929.1-v1.0-hybrid	-Inf	2,09E-04	1,27E-02	-	-
Fb7:0-10	mrna21706.1-v1.0-hybrid	-Inf	1,04E-05	8,59E-04	-	-
Fb7:0-10	mrna35027.1-v1.0-hybrid	-Inf	1,36E-17	4,24E-15	-	-
Fb7:0-10	snap_masked-LG3-processed-gene-241.118-mRNA-1	-Inf	2,94E-10	4,85E-08	H32_ARATH	Histone H3.2
Fb7:0-10	snap_masked-LG7-processed-gene-47.94-mRNA-1	-Inf	5,60E-25	3,31E-22	SPL14_ARATH	Squamosa promoter-binding-like protein 14
Fb7:0-10	XS:temp666	-Inf	1,88E-21	8,48E-19	-	-
Fb7:0-10	snap_masked-LG6-processed-gene-117.94-mRNA-1	-10,89	2,84E-34	8,98E-31	Q9FIH8_ARATH	Putative pitrilysin
Fb7:0-10	maker-LG7-augustus-gene-47.101-mRNA-1	-9,65	4,99E-32	8,61E-29	CPL2_ARATH	RNA polymerase II C-terminal domain phosphatase-like 2
Fb7:0-10	maker-LG7-snap-gene-36.146-mRNA-1	-9,63	1,25E-26	9,84E-24	SUS6_ARATH	Sucrose synthase 6
Fb7:0-10	maker-LG7-augustus-gene-26.89-mRNA-1	-9,50	1,23E-38	5,84E-35	RVE6_ARATH	Protein REVEILLE 6
Fb7:0-10	maker-LG7-snap-gene-47.121-mRNA-1	-9,49	6,68E-26	4,22E-23	MTP11_ARATH	Metal tolerance protein 11
Fb7:0-10	genemark-LG7-processed-gene-26.46-mRNA-1	-9,35	4,96E-25	3,03E-22	ERL1_ARATH	LRR receptor-like serine/threonine-protein kinase ERL1
Fb7:0-10	genemark-LG7-processed-gene-38.65-mRNA-1	-8,94	1,83E-27	1,57E-24	-	-
Fb7:0-10	maker-LG7-augustus-gene-26.93-mRNA-1	-8,63	1,86E-28	1,96E-25	-	-
Fb7:0-10	augustus_masked-LG7-processed-gene-44.4-mRNA-1	-8,57	5,35E-34	1,43E-30	-	-
Fb7:0-10	maker-LG7-augustus-gene-14.132-mRNA-1	-8,51	8,70E-28	8,24E-25	PUB32_ARATH	U-box domain-containing protein 32

Supplemental Table CIV. 2

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb7:0-10	maker-LG7-augustus-gene-10.167-mRNA-1	-8,33	6,33E-07	6,59E-05	Q9M1S3_ARATH	RNA binding protein-like
Fb7:0-10	maker-LG7-augustus-gene-40.145-mRNA-1	-8,17	1,86E-17	5,69E-15	TMVRN_NICGU	TMV resistance protein N
Fb7:0-10	maker-LG7-augustus-gene-65.133-mRNA-1	-8,12	8,94E-32	1,30E-28	-	-
Fb7:0-10	maker-LG7-snap-gene-68.128-mRNA-1	-7,62	5,00E-32	8,61E-29	ESD4_ARATH	Ubiquitin-like-specific protease ESD4
Fb7:0-10	augustus_masked-LG7-processed-gene-137.18-mRNA-1	-7,46	4,31E-29	5,44E-26	-	-
Fb7:0-10	augustus_masked-LG7-processed-gene-103.14-mRNA-1	-7,31	9,40E-13	1,94E-10	TMVRN_NICGU	TMV resistance protein N
Fb7:0-10	snap_masked-LG7-processed-gene-42.93-mRNA-1	-7,15	2,77E-09	4,07E-07	VRN1_ARATH	B3 domain-containing transcription factor VRN1
Fb7:0-10	augustus_masked-LG7-processed-gene-51.37-mRNA-1	-7,09	7,36E-12	1,41E-09	GPDL2_ARATH	Glycerophosphodiester phosphodiesterase protein kinase domain-containing GDPDL2
Fb7:0-10	maker-LG7-augustus-gene-36.137-mRNA-1	-6,86	1,75E-15	4,54E-13	IF4G1_ARATH	Eukaryotic translation initiation factor isoform 4G-1
Fb7:0-10	maker-LG7-snap-gene-44.140-mRNA-1	-6,76	6,94E-11	1,29E-08	Q93VS8_ARATH	Putative uncharacterized protein At5g19820
Fb7:0-10	mrna32485.1-v1.0-hybrid	-6,70	2,95E-08	3,80E-06	-	-
Fb7:0-10	augustus_masked-LG7-processed-gene-126.10-mRNA-1	-6,69	2,99E-05	2,20E-03	TA12B_ARATH	Transcription initiation factor TFIID subunit 12b
Fb7:0-10	maker-LG7-snap-gene-137.155-mRNA-1	-6,45	6,34E-20	2,50E-17	-	-
Fb7:0-10	snap_masked-LG7-processed-gene-113.89-mRNA-1	-6,37	1,17E-19	4,45E-17	PLP2_ARATH	Patatin-like protein 2
Fb7:0-10	maker-LG7-augustus-gene-71.127-mRNA-1	-6,21	2,23E-18	7,42E-16	PTR1_ARATH	Protein NRT1/ PTR FAMILY 8.1
Fb7:0-10	maker-LG7-augustus-gene-28.262-mRNA-1	-5,84	1,70E-04	1,07E-02	FRO2_ARATH	Ferric reduction oxidase 2
Fb7:0-10	maker-LG7-augustus-gene-9.167-mRNA-1	-5,72	6,05E-20	2,44E-17	IPYR4_ARATH	Soluble inorganic pyrophosphatase 4
Fb7:0-10	snap_masked-LG7-processed-gene-80.98-mRNA-1	-5,52	1,68E-20	7,23E-18	-	-
Fb7:0-10	maker-LG3-snap-gene-106.199-mRNA-1	-5,44	1,36E-05	1,10E-03	ERECT_ARATH	LRR receptor-like serine/threonine-protein kinase ERECTA
Fb7:0-10	augustus_masked-LG5-processed-gene-225.25-mRNA-1	-5,30	4,26E-08	5,28E-06	Q949W8_ARATH	Xylulose kinase-2
Fb7:0-10	maker-LG3-augustus-gene-99.141-mRNA-1	-5,22	2,93E-10	4,85E-08	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1
Fb7:0-10	maker-LG7-augustus-gene-129.144-mRNA-1	-5,18	4,84E-17	1,43E-14	Q9FHL8_ARATH	Putative uncharacterized protein At5g23400
Fb7:0-10	mrna03003.1-v1.0-hybrid	-4,98	1,97E-03	8,58E-02	-	-
Fb7:0-10	maker-LG3-augustus-gene-65.227-mRNA-1	-4,96	3,18E-08	4,01E-06	Y4885_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g08850
Fb7:0-10	maker-LG3-est_gff_Cufflinks-gene-104.6-mRNA-1	-4,94	1,55E-09	2,31E-07	-	-
Fb7:0-10	genemark-LG7-processed-gene-17.79-mRNA-1	-4,83	1,23E-10	2,17E-08	-	-
Fb7:0-10	genemark-LG4-processed-gene-113.46-mRNA-1	-4,80	8,58E-16	2,29E-13	-	-

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb7:0-10	maker-LG4-est_gff_Cufflinks-gene-102.0-mRNA-1	-4,74	8,15E-04	4,10E-02	-	-
Fb7:0-10	mrna27419.1-v1.0-hybrid	-4,69	2,98E-07	3,24E-05	UMPS_ARATH	Orotidine 5'-phosphate decarboxylase
Fb7:0-10	maker-LG7-snap-gene-50.180-mRNA-1	-4,39	4,51E-07	4,80E-05	KEULE_ARATH	SNARE-interacting protein KEULE
Fb7:0-10	maker-LG4-augustus-gene-221.152-mRNA-1	-4,30	2,02E-11	3,83E-09	-	-
Fb7:0-10	augustus_masked-LG3-processed-gene-100.26-mRNA-1	-4,30	6,10E-16	1,67E-13	Y3475_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At3g47570
Fb7:0-10	augustus_masked-LG7-processed-gene-56.12-mRNA-1	-4,02	1,56E-10	2,72E-08	LOX21_SOLTU	Linoleate 13S-lipoxygenase 2-1, chloroplastic
Fb7:0-10	maker-LG7-augustus-gene-88.90-mRNA-1	-3,90	4,37E-13	9,30E-11	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1
Fb7:0-10	maker-LG7-augustus-gene-38.137-mRNA-1	-3,82	1,72E-13	3,88E-11	CFTSY_ARATH	Cell division protein FtsY homolog, chloroplastic
Fb7:0-10	augustus_masked-LG3-processed-gene-99.24-mRNA-1	-3,67	2,96E-06	2,77E-04	RAC9_ARATH	Rac-like GTP-binding protein ARAC9
Fb7:0-10	maker-LG7-snap-gene-72.117-mRNA-1	-3,58	2,36E-11	4,43E-09	-	-
Fb7:0-10	augustus_masked-LG6-processed-gene-336.11-mRNA-1	-3,55	2,47E-04	1,49E-02	RPS5_ARATH	Disease resistance protein RPS5
Fb7:0-10	augustus_masked-LG7-processed-gene-56.13-mRNA-1	-3,51	6,02E-09	8,65E-07	LOX21_SOLTU	Linoleate 13S-lipoxygenase 2-1, chloroplastic
Fb7:0-10	snap_masked-LG7-processed-gene-78.70-mRNA-1	-3,49	1,16E-04	7,59E-03	B4Y0U0_MEDTR	Isoflavonoid malonyl transferase 1
Fb7:0-10	maker-LG5-augustus-gene-149.121-mRNA-1	-3,39	2,84E-07	3,10E-05	BXL4_ARATH	Beta-D-xylosidase 4
Fb7:0-10	maker-LG7-snap-gene-48.181-mRNA-1	-3,37	7,69E-09	1,09E-06	REM9_ARATH	B3 domain-containing protein REM9
Fb7:0-10	maker-LG7-augustus-gene-137.165-mRNA-1	-3,29	1,07E-10	1,93E-08	Q9SUL1_ARATH	Putative cysteine proteinase
Fb7:0-10	maker-LG7-augustus-gene-126.117-mRNA-1	-3,22	9,67E-10	1,49E-07	Q9LZ26_ARATH	Zn-dependent exopeptidases superfamily protein
Fb7:0-10	maker-LG7-snap-gene-13.208-mRNA-1	-3,17	9,30E-06	7,72E-04	MD37C_ARATH	Probable mediator of RNA polymerase II transcription subunit 37c
Fb7:0-10	augustus_masked-LG7-processed-gene-45.13-mRNA-1	-3,10	1,59E-05	1,27E-03	CXE20_ARATH	Probable carboxylesterase 120
Fb7:0-10	genemark-LG6-processed-gene-315.64-mRNA-1	-3,07	4,94E-08	6,08E-06	RH53_ARATH	DEAD-box ATP-dependent RNA helicase 53
Fb7:0-10	augustus_masked-LG7-processed-gene-31.29-mRNA-1	-3,00	7,37E-07	7,59E-05	Y3475_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At3g47570
Fb7:0-10	genemark-LG7-processed-gene-38.66-mRNA-1	-2,98	4,89E-04	2,66E-02	-	-
Fb7:0-10	maker-LG1-augustus-gene-53.303-mRNA-1	-2,85	8,24E-09	1,14E-06	Q93YS8_ARATH	Serinc-domain containing serine and sphingolipid biosynthesis protein
Fb7:0-10	genemark-LG7-processed-gene-77.56-mRNA-1	-2,85	3,22E-04	1,86E-02	KCO1_ORYSJ	Two pore potassium channel a
Fb7:0-10	maker-LG3-snap-gene-104.133-mRNA-1	-2,81	5,15E-06	4,52E-04	-	-
Fb7:0-10	maker-LG7-augustus-gene-120.122-mRNA-1	-2,75	9,86E-06	8,16E-04	PSD2B_ARATH	26S proteasome non-ATPase regulatory subunit 2 homolog B

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NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb7:0-10	maker-LG7-augustus-gene-11.186-mRNA-1	-2,70	4,94E-06	4,37E-04	Q9ASV2_ARATH	PfkB-type carbohydrate kinase-like protein
Fb7:0-10	genemark-LG7-processed-gene-74.51-mRNA-1	-2,68	1,16E-07	1,35E-05	RPE5C_ARATH	DNA-directed RNA polymerase V subunit 5C
Fb7:0-10	genemark-LG3-processed-gene-174.43-mRNA-1	-2,64	8,61E-07	8,77E-05	-	-
Fb7:0-10	maker-LG6-augustus-gene-116.135-mRNA-1	-2,56	1,45E-06	1,43E-04	-	-
Fb7:0-10	maker-LG3-snap-gene-106.198-mRNA-1	-2,54	4,49E-04	2,47E-02	PEX13_ARATH	Peroxisomal membrane protein 13
Fb7:0-10	mrna27193.1-v1.0-hybrid	-2,50	1,00E-03	4,86E-02	FB135_ARATH	F-box protein At3g07870
Fb7:0-10	snap_masked-LG4-processed-gene-113.61-mRNA-1	-2,50	4,64E-05	3,28E-03	-	-
Fb7:0-10	maker-LG7-augustus-gene-50.162-mRNA-1	-2,47	5,42E-07	5,74E-05	GSTZ1_ARATH	Glutathione S-transferase Z1
Fb7:0-10	maker-LG7-snap-gene-47.128-mRNA-1	-2,38	4,45E-04	2,46E-02	MYO5_ARATH	Myosin-5
Fb7:0-10	genemark-LG5-processed-gene-140.51-mRNA-1	-2,38	1,13E-03	5,29E-02	PAPS4_ARATH	Nuclear poly(A) polymerase 4
Fb7:0-10	maker-LG7-snap-gene-202.168-mRNA-1	-2,37	4,26E-05	3,04E-03	AB19B_ARATH	ABC transporter B family member 19
Fb7:0-10	augustus_masked-LG7-processed-gene-41.35-mRNA-1	-2,36	6,84E-06	5,78E-04	YC22_ARATH	Uncharacterized calcium-binding protein At1g02270
Fb7:0-10	maker-LG3-augustus-gene-107.125-mRNA-1	-2,31	3,98E-06	3,60E-04	Y3236_ARATH	Ankyrin repeat-containing protein At3g12360
Fb7:0-10	augustus_masked-LG3-processed-gene-102.20-mRNA-1	-2,30	6,74E-06	5,72E-04	ERF61_ARATH	Ethylene-responsive transcription factor ERF061
Fb7:0-10	augustus_masked-LG6-processed-gene-129.21-mRNA-1	-2,29	1,09E-06	1,10E-04	CDR1_ARATH	Aspartic proteinase CDR1
Fb7:0-10	augustus_masked-LG7-processed-gene-112.37-mRNA-1	-2,16	3,89E-05	2,79E-03	BUP1_ARATH	Beta-ureidopropionase
Fb7:0-10	genemark-LG7-processed-gene-120.65-mRNA-1	-2,08	6,66E-04	3,47E-02	Q8VWI7_ARATH	Phragmoplast-associated kinesin-related protein 2
Fb7:0-10	maker-LG5-augustus-gene-32.136-mRNA-1	-2,04	1,39E-03	6,28E-02	BOR2_ARATH	Probable boron transporter 2
Fb7:0-10	augustus_masked-LG2-processed-gene-6.1-mRNA-1	-2,04	1,09E-03	5,15E-02	Q1KPV0_ARATH	FZO-like protein
Fb7:0-10	maker-LG5-snap-gene-206.105-mRNA-1	-1,97	3,70E-05	2,70E-03	GLYC7_ARATH	Serine hydroxymethyltransferase 7
Fb7:0-10	augustus_masked-LG7-processed-gene-40.39-mRNA-1	-1,95	2,05E-04	1,26E-02	ATL59_ARATH	E3 ubiquitin-protein ligase ATL59
Fb7:0-10	augustus_masked-LG5-processed-gene-276.41-mRNA-1	-1,94	1,53E-03	6,87E-02	Y3236_ARATH	Ankyrin repeat-containing protein At3g12360
Fb7:0-10	augustus_masked-LG1-processed-gene-53.46-mRNA-1	-1,92	1,81E-04	1,14E-02	SKP2B_ARATH	F-box protein SKP2B
Fb7:0-10	augustus_masked-LG6-processed-gene-333.35-mRNA-1	-1,88	1,11E-04	7,30E-03	U88A1_ARATH	UDP-glycosyltransferase 88A1
Fb7:0-10	maker-LG7-augustus-gene-124.119-mRNA-1	-1,87	2,31E-04	1,39E-02	DEGP1_ARATH	Protease Do-like 1, chloroplastic
Fb7:0-10	augustus_masked-LG3-processed-gene-105.42-mRNA-1	-1,87	1,92E-04	1,19E-02	Q9FN84_ARATH	Putative uncharacterized protein MVA3.2
Fb7:0-10	genemark-LG3-processed-gene-108.47-mRNA-1	-1,84	1,17E-04	7,61E-03	Q9C685_ARATH	Uncharacterized protein

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NIL vs. RV	**gene id**[a]	**log$_2$(FCh)**[b]	**p-val.**	**p-adj.**	**blast hit**[b]	**blast hit protein description**
Fb7:0-10	augustus_masked-LG2-processed-gene-150.11-mRNA-1	-1,83	2,11E-03	9,13E-02	IPT3_ARATH	Adenylate isopentenyltransferase 3, chloroplastic
Fb7:0-10	snap_masked-LG7-processed-gene-121.101-mRNA-1	-1,81	4,41E-04	2,44E-02	-	-
Fb7:0-10	maker-LG7-est_gff_Cufflinks-gene-45.3-mRNA-1	-1,79	1,07E-03	5,10E-02	Q9LYL0_ARATH	N2,N2-dimethylguanosine tRNA methyltransferase
Fb7:0-10	maker-LG7-augustus-gene-95.135-mRNA-1	-1,79	2,12E-04	1,29E-02	VRN1_ARATH	B3 domain-containing transcription factor VRN1
Fb7:0-10	maker-LG7-augustus-gene-10.158-mRNA-1	-1,78	1,94E-03	8,47E-02	F4HQH8_ARATH	RNA-binding (RRM/RBD/RNP motifs) family protein
Fb7:0-10	augustus_masked-LG7-processed-gene-11.24-mRNA-1	-1,76	2,52E-04	1,51E-02	-	-
Fb7:0-10	genemark-LG7-processed-gene-22.65-mRNA-1	-1,75	1,91E-04	1,19E-02	F4JW79_ARATH	Kow domain-containing transcription factor 1
Fb7:0-10	snap_masked-LG3-processed-gene-221.94-mRNA-1	-1,72	1,27E-03	5,87E-02	Q9ZW37_ARATH	Thioesterase-like protein
Fb7:0-10	maker-LG6-augustus-gene-113.193-mRNA-1	-1,71	5,21E-04	2,82E-02	R13L1_ARATH	Putative disease resistance RPP13-like protein 1
Fb7:0-10	maker-LG7-snap-gene-143.78-mRNA-1	-1,69	3,73E-04	2,10E-02	-	-
Fb7:0-10	maker-LG4-snap-gene-125.176-mRNA-1	-1,67	2,29E-03	9,84E-02	-	-
Fb7:0-10	snap_masked-LG7-processed-gene-89.107-mRNA-1	-1,65	1,58E-03	7,04E-02	Q9FMN8_ARATH	Uncharacterized protein
Fb7:0-10	maker-LG7-augustus-gene-91.124-mRNA-1	-1,64	4,51E-04	2,48E-02	AAE13_ARATH	Malonate--CoA ligase
Fb7:0-10	maker-LG7-augustus-gene-39.150-mRNA-1	-1,63	6,52E-04	3,43E-02	PMTF_ARATH	Probable methyltransferase PMT15
Fb7:0-10	maker-LG7-snap-gene-137.177-mRNA-1	-1,60	8,85E-04	4,37E-02	RD19A_ARATH	Cysteine proteinase RD19a
Fb7:0-10	mrna10851.1-v1.0-hybrid	-1,58	2,31E-03	9,91E-02	-	-
Fb7:0-10	augustus_masked-LG6-processed-gene-175.2-mRNA-1	-1,56	1,31E-03	6,03E-02	EIF3C_ARATH	Eukaryotic translation initiation factor 3 subunit C
Fb7:0-10	genemark-LG7-processed-gene-29.69-mRNA-1	-1,51	1,38E-03	6,24E-02	UBC5_ARATH	Ubiquitin-conjugating enzyme E2 5
Fb7:0-10	maker-LG1-snap-gene-42.219-mRNA-1	1,49	2,12E-03	9,15E-02	Q9XGZ2_ARATH	T1N24.22 protein
Fb7:0-10	maker-LG7-snap-gene-71.132-mRNA-1	1,51	1,70E-03	7,54E-02	PTR25_ARATH	Protein NRT1/ PTR FAMILY 5.12
Fb7:0-10	augustus_masked-LG6-processed-gene-68.10-mRNA-1	1,54	1,55E-03	6,92E-02	Q84J81_ARATH	Putative uncharacterized protein At3g09350
Fb7:0-10	augustus_masked-LG7-processed-gene-85.4-mRNA-1	1,58	2,25E-03	9,71E-02	-	-
Fb7:0-10	maker-LG7-snap-gene-41.171-mRNA-1	1,68	6,93E-04	3,59E-02	GENL1_ORYSJ	Flap endonuclease GEN-like 1
Fb7:0-10	maker-LG7-snap-gene-101.129-mRNA-1	1,71	1,18E-03	5,50E-02	O81315_ARATH	Putative uncharacterized protein AT4g00140
Fb7:0-10	maker-LG7-augustus-gene-119.346-mRNA-1	1,74	1,92E-03	8,42E-02	Q9FF29_ARATH	Receptor serine/threonine kinase
Fb7:0-10	augustus_masked-LG2-processed-gene-216.11-mRNA-1	1,80	1,66E-04	1,06E-02	-	-

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NIL vs. RV	**gene id[a]**	**log$_2$(FCh)[b]**	**p-val.**	**p-adj.**	**blast hit[b]**	**blast hit protein description**
Fb7:0-10	maker-LG4-augustus-gene-206.150-mRNA-1	1,81	1,01E-03	4,90E-02	AB4B_ARATH	ABC transporter B family member 4
Fb7:0-10	maker-LG6-augustus-gene-114.139-mRNA-1	1,82	1,67E-04	1,06E-02	F4JFL8_ARATH	Glycerol-3-phosphate dehydrogenase [NAD(+)]
Fb7:0-10	maker-LG6-augustus-gene-341.179-mRNA-1	1,86	1,53E-03	6,87E-02	MTPS1_SANAL	(+)-alpha-terpineol synthase
Fb7:0-10	maker-LG5-augustus-gene-156.138-mRNA-1	1,87	7,55E-04	3,83E-02	BGAL8_ARATH	Beta-galactosidase 8
Fb7:0-10	maker-LG6-snap-gene-334.192-mRNA-1	1,90	9,35E-04	4,58E-02	SCPDL_ARATH	Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410
Fb7:0-10	genemark-LG7-processed-gene-29.64-mRNA-1	1,96	1,41E-04	9,11E-03	CRCK2_ARATH	Calmodulin-binding receptor-like cytoplasmic kinase 2
Fb7:0-10	maker-LG3-snap-gene-103.127-mRNA-1	2,01	8,46E-05	5,71E-03	-	-
Fb7:0-10	maker-LG5-snap-gene-179.89-mRNA-1	2,03	4,00E-04	2,23E-02	AUR1_ARATH	Serine/threonine-protein kinase Aurora-1
Fb7:0-10	augustus_masked-LG7-processed-gene-131.12-mRNA-1	2,03	2,07E-05	1,59E-03	PAPS1_ARATH	Nuclear poly(A) polymerase 1
Fb7:0-10	genemark-LG7-processed-gene-45.73-mRNA-1	2,03	1,24E-04	8,03E-03	-	-
Fb7:0-10	maker-LG1-augustus-gene-57.210-mRNA-1	2,06	1,95E-04	1,20E-02	RH21_ARATH	DEAD-box ATP-dependent RNA helicase 21
Fb7:0-10	genemark-LG3-processed-gene-98.67-mRNA-1	2,07	1,17E-03	5,49E-02	DRL4_ARATH	Putative disease resistance protein At1g50180
Fb7:0-10	maker-LG5-est_gff_Cufflinks-gene-133.10-mRNA-1	2,18	2,58E-05	1,94E-03	-	-
Fb7:0-10	maker-LG1-augustus-gene-15.190-mRNA-1	2,35	8,47E-07	8,68E-05	PLT5_ARATH	Polyol transporter 5
Fb7:0-10	augustus_masked-LG4-processed-gene-261.31-mRNA-1	2,39	2,65E-06	2,51E-04	FAR1_ARATH	Protein FAR-RED IMPAIRED RESPONSE 1
Fb7:0-10	maker-LG7-augustus-gene-81.137-mRNA-1	2,41	2,70E-05	2,01E-03	Q29Q34_ARATH	At5g19440
Fb7:0-10	augustus_masked-LG7-processed-gene-44.6-mRNA-1	2,42	8,48E-04	4,21E-02	Q8VYY8_ARATH	Uncharacterized protein
Fb7:0-10	genemark-LG5-processed-gene-214.50-mRNA-1	2,42	2,00E-05	1,55E-03	-	-
Fb7:0-10	maker-LG7-augustus-gene-130.144-mRNA-1	2,43	7,15E-07	7,41E-05	-	-
Fb7:0-10	maker-LG6-augustus-gene-383.200-mRNA-1	2,50	4,07E-06	3,68E-04	-	-
Fb7:0-10	augustus_masked-LG7-processed-gene-8.26-mRNA-1	2,50	1,21E-03	5,60E-02	Q5MK24_ARATH	Arv1-like protein
Fb7:0-10	maker-LG7-augustus-gene-37.152-mRNA-1	2,68	9,41E-07	9,53E-05	Q94K30_ARATH	Rossmann-fold NAD(P)-binding domain-containing protein
Fb7:0-10	maker-LG5-augustus-gene-214.101-mRNA-1	2,72	9,75E-09	1,33E-06	KEULE_ARATH	SNARE-interacting protein KEULE
Fb7:0-10	maker-LG7-augustus-gene-12.142-mRNA-1	2,75	6,65E-04	3,47E-02	Y1686_ARATH	Uncharacterized membrane protein At1g16860
Fb7:0-10	maker-LG7-snap-gene-50.196-mRNA-1	2,77	3,77E-05	2,73E-03	O22133_ARATH	Putative flavonol reductase
Fb7:0-10	maker-LG2-snap-gene-5.118-mRNA-1	2,78	2,68E-05	2,01E-03	AUR1_ARATH	Serine/threonine-protein kinase Aurora-1
Fb7:0-10	maker-LG4-snap-gene-12.198-mRNA-1	2,82	1,00E-03	4,86E-02	-	-
Fb7:0-10	augustus_masked-LG7-processed-gene-50.27-	2,83	1,59E-03	7,05E-02	Q940N4_ARATH	Putative uncharacterized protein At4g22740

Supplemental Table CIV. 2

[a] gene id is according to F. vesca annotation 2 nomenclature

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NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
	mRNA-1					
Fb7:0-10	maker-LG6-snap-gene-51.109-mRNA-1	2,86	1,84E-04	1,15E-02	CNGC1_ARATH	Cyclic nucleotide-gated ion channel 1
Fb7:0-10	maker-LG7-augustus-gene-174.173-mRNA-1	2,87	1,05E-03	5,05E-02	-	-
Fb7:0-10	maker-LG7-augustus-gene-81.140-mRNA-1	2,87	3,34E-08	4,19E-06	Q29Q34_ARATH	At5g19440
Fb7:0-10	maker-LG4-snap-gene-151.161-mRNA-1	2,91	1,09E-08	1,47E-06	PSAD_SPIOL	Photosystem I reaction center subunit II, chloroplastic
Fb7:0-10	augustus_masked-LG7-processed-gene-116.27-mRNA-1	2,92	4,21E-09	6,08E-07	OTU_ARATH	OTU domain-containing protein At3g57810
Fb7:0-10	maker-LG7-snap-gene-86.129-mRNA-1	2,92	1,23E-06	1,22E-04	C83A1_ARATH	Cytochrome P450 83A1
Fb7:0-10	maker-LG5-augustus-gene-229.145-mRNA-1	2,94	7,78E-09	1,09E-06	FBK67_ARATH	F-box/kelch-repeat protein At3g23880
Fb7:0-10	augustus_masked-LG7-processed-gene-137.19-mRNA-1	3,04	2,68E-07	2,95E-05	-	-
Fb7:0-10	augustus_masked-LG1-processed-gene-55.54-mRNA-1	3,05	2,12E-03	9,15E-02	TI172_ARATH	Mitochondrial import inner membrane translocase subunit TIM17-2
Fb7:0-10	mrna03036.1-v1.0-hybrid	3,07	3,92E-07	4,24E-05	O64745_ARATH	Putative berberine bridge enzyme
Fb7:0-10	maker-LG5-augustus-gene-34.145-mRNA-1	3,14	5,88E-04	3,12E-02	LOX21_SOLTU	Linoleate 13S-lipoxygenase 2-1, chloroplastic
Fb7:0-10	snap_masked-LG7-processed-gene-43.96-mRNA-1	3,15	8,74E-04	4,32E-02	Q9ATE9_PETHY	MADS-box transcription factor FBP20
Fb7:0-10	genemark-LG2-processed-gene-6.38-mRNA-1	3,17	4,85E-04	2,65E-02	NFYA1_ARATH	Nuclear transcription factor Y subunit A-1
Fb7:0-10	augustus_masked-LG7-processed-gene-15.38-mRNA-1	3,32	1,92E-03	8,42E-02	DREB3_ARATH	Dehydration-responsive element-binding protein 3
Fb7:0-10	maker-LG5-snap-gene-200.130-mRNA-1	3,33	6,86E-05	4,74E-03	-	-
Fb7:0-10	maker-LG7-snap-gene-91.103-mRNA-1	3,35	3,42E-05	2,50E-03	MYC2_ARATH	Transcription factor MYC2
Fb7:0-10	snap_masked-LG5-processed-gene-156.75-mRNA-1	3,45	3,21E-09	4,68E-07	-	-
Fb7:0-10	maker-LG7-augustus-gene-45.185-mRNA-1	3,51	5,63E-12	1,09E-09	HPR3_ARATH	Glyoxylate/hydroxypyruvate reductase HPR3
Fb7:0-10	augustus_masked-LG7-processed-gene-51.22-mRNA-1	3,54	3,62E-06	3,31E-04	MAP21_ARATH	Methionine aminopeptidase 2A
Fb7:0-10	maker-LG7-snap-gene-16.116-mRNA-1	3,59	1,39E-07	1,59E-05	DMS3_ARATH	Protein DEFECTIVE IN MERISTEM SILENCING 3
Fb7:0-10	maker-LG2-snap-gene-122.229-mRNA-1	3,63	1,20E-03	5,57E-02	Q9LJ87_ARATH	Putative uncharacterized protein At3g22590
Fb7:0-10	mrna03980.1-v1.0-hybrid	3,83	1,23E-03	5,68E-02	F4HUN4_ARATH	RAD3-like DNA-binding helicase protein
Fb7:0-10	genemark-LG6-processed-gene-366.74-mRNA-1	3,89	7,31E-04	3,73E-02	Q9XIJ0_ARATH	T10O24.24
Fb7:0-10	augustus_masked-LG1-processed-gene-199.26-mRNA-1	3,95	5,79E-06	5,01E-04	Q9LK77_ARATH	Thioesterase family protein
Fb7:0-10	maker-LG7-snap-gene-202.177-mRNA-1	4,06	5,58E-05	3,91E-03	AB10B_ARATH	ABC transporter B family member 10
Fb7:0-10	maker-LG7-augustus-gene-93.231-mRNA-1	4,27	9,34E-04	4,58E-02	Q9SD64_ARATH	Receptor kinase-like protein
Fb7:0-10	maker-LG7-snap-gene-35.172-mRNA-1	4,87	6,47E-15	1,66E-12	ACCA_ARATH	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha,

Supplemental Table CIV. 2

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[b] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	gene id[a]	log$_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
						chloroplastic
Fb7:0-10	maker-LG7-augustus-gene-121.129-mRNA-1	4,93	1,28E-07	1,48E-05	-	-
Fb7:0-10	genemark-LG7-processed-gene-8.56-mRNA-1	5,10	6,70E-14	1,53E-11	MYOB2_ARATH	Myosin-binding protein 2
Fb7:0-10	augustus_masked-LG7-processed-gene-49.21-mRNA-1	5,46	7,83E-09	1,09E-06	CML25_ARATH	Probable calcium-binding protein CML25
Fb7:0-10	maker-LG7-snap-gene-99.185-mRNA-1	5,62	2,12E-20	8,92E-18	PME17_ARATH	Pectinesterase 17
Fb7:0-10	maker-LG7-snap-gene-27.152-mRNA-1	5,76	4,37E-07	4,68E-05	PP438_ARATH	Pentatricopeptide repeat-containing protein PNM1, mitochondrial
Fb7:0-10	augustus_masked-LG7-processed-gene-123.13-mRNA-1	5,98	3,10E-08	3,94E-06	Q8L7K1_ARATH	Putative uncharacterized protein At4g32610
Fb7:0-10	maker-LG4-augustus-gene-152.155-mRNA-1	6,37	3,03E-04	1,77E-02	ZIP4L_ARATH	TPR repeat-containing protein ZIP4
Fb7:0-10	maker-LG7-augustus-gene-8.110-mRNA-1	6,44	4,87E-22	2,37E-19	NAC86_ARATH	NAC domain-containing protein 86
Fb7:0-10	maker-LG6-augustus-gene-114.104-mRNA-1	6,65	1,30E-14	3,27E-12	NLTP1_ARATH	Non-specific lipid-transfer protein 1
Fb7:0-10	snap_masked-LG7-processed-gene-75.77-mRNA-1	6,70	8,51E-05	5,71E-03	ANXD4_ARATH	Annexin D4
Fb7:0-10	maker-LG7-augustus-gene-39.149-mRNA-1	7,29	2,79E-13	6,01E-11	CNGC1_ARATH	Cyclic nucleotide-gated ion channel 1
Fb7:0-10	maker-LG7-augustus-gene-15.117-mRNA-1	7,77	6,04E-23	3,18E-20	PABN1_ARATH	Polyadenylate-binding protein 1
Fb7:0-10	maker-LG7-augustus-gene-59.155-mRNA-1	8,39	1,03E-03	4,95E-02	SHS1_ASTTA	Shionone synthase
Fb7:0-10	maker-LG3-augustus-gene-98.134-mRNA-1	8,78	3,05E-26	2,14E-23	C84A1_ARATH	Cytochrome P450 84A1
Fb7:0-10	maker-LG7-augustus-gene-37.143-mRNA-1	9,34	8,47E-19	2,97E-16	-	-
Fb7:0-10	augustus_masked-LG7-processed-gene-21.17-mRNA-1	Inf	3,17E-05	2,33E-03	HIBC1_ARATH	3-hydroxyisobutyryl-CoA hydrolase 1
Fb7:0-10	maker-LG3-snap-gene-159.90-mRNA-1	Inf	1,29E-06	1,28E-04	C71AK_ARATH	Cytochrome P450 71A20
Fb7:0-10	maker-LG5-augustus-gene-193.132-mRNA-1	Inf	4,08E-04	2,27E-02	AP4S_ARATH	AP-4 complex subunit sigma
Fb7:0-10	maker-LG7-augustus-gene-113.138-mRNA-1	Inf	1,06E-21	4,91E-19	SAG39_ORYSJ	Senescence-specific cysteine protease SAG39
Fb7:0-10	maker-LG7-augustus-gene-33.139-mRNA-1	Inf	1,33E-03	6,06E-02	G3OX4_ARATH	Gibberellin 3-beta-dioxygenase 4
Fb7:0-10	maker-LG7-snap-gene-85.114-mRNA-1	Inf	3,05E-14	7,21E-12	TMVRN_NICGU	TMV resistance protein N
Fb7:0-10	mrna05334.1-v1.0-hybrid	Inf	2,32E-08	3,05E-06	ZIP4L_ARATH	TPR repeat-containing protein ZIP4
Fb7:0-10	mrna15753.1-v1.0-hybrid	Inf	8,95E-04	4,40E-02	FBL70_ARATH	F-box/LRR-repeat protein At3g62440
Fb7:0-10	mrna17065.1-v1.0-hybrid	Inf	8,09E-04	4,07E-02	MD26C_ARATH	Probable mediator of RNA polymerase II transcription subunit 26c
Fb7:0-10	mrna23619.1-v1.0-hybrid	Inf	1,32E-03	6,03E-02	-	-
Fb7:0-10	snap_masked-LG7-processed-gene-31.92-mRNA-1	Inf	1,31E-03	6,02E-02	Q9SD64_ARATH	Receptor kinase-like protein
Fb7:0-10	snap_masked-LG7-processed-gene-31.96-mRNA-1	Inf	3,96E-04	2,22E-02	AHL18_ARATH	AT-hook motif nuclear-localized protein 18

Supplemental Table CIV. 2

[a] gene id is according to F. vesca annotation 2 nomenclature

[b] best blast hit found for the DEG predicted proteins. Codes are according to UniProtUK entries

NIL vs. RV	gene id[a]	$\log_2$(FCh)[b]	p-val.	p-adj.	blast hit[b]	blast hit protein description
Fb7:0-10	snap_masked-LG7-processed-gene-38.117-mRNA-1	Inf	3,67E-04	2,07E-02	SOT15_ARATH	Cytosolic sulfotransferase 15

Supplemental Table CIV. 3 Revision of candidate genes for (poly)-phenol content. Genes highlighted as putative candidate genes in chap. II revised with RNA sequencing data in terms of differential expression and/or differences in sequence (SNP/indel)

NIL	CG[a]	log2(FC)[b]	p-value (adjusted)	SNPs[c]	non-synonymous	early STOP	indel	frame shift
Fb5:0-35	gene32347	1,75	0,049	14	6	0	0	-
Fb5:0-35	gene24665	0,34	1	0	-	-	0	-
Fb5:50-76	gene29344	-1,59	0,322	3	3	1	0	-
Fb5:50-76	gene31464	1,16	1	3	1	1	0	-
Fb5:50-76	gene31465	-6,25	7,10E-15	3	2	1	0	-
Fb5:50-76	gene02203	0,36	1	17	5	0	0	-
Fb5:50-76	gene13530	1,5	0,108	7	4	0	0	-
Fb5:50-76	gene22073	1,41	1	6	2	1	0	-
Fb6:84-101	gene26265	-0,07	1	0	-	-	0	-
Fb6:84-101	gene26344	0,065	1	0	-	-	0	-
Fb6:84-101	gene24019	ne	-	-	-	-	-	-
Fb6:84-101	gene28428	ne	-	-	-	-	-	-
Fb6:84-101	gene26403	2,24	1	9	7	0	0	-
Fb6:84-101	gene24025	0,96	1	0	-	-	0	-
Fb6:84-101	gene26301	ne	-	-	-	-	-	-
Fb6:84-101	gene26302	0,62	1	0	-	-	0	-
Fb7:0-10	gene26825	-0,67	1	11	2	0	1	0
Fb7:0-10	gene26826	0,44	1	8	1	0	1	0

[a] Candidate genes described in Chapter II extracted from *F. vesca* reference genome v1.1a1

[b] $\log_2$ (fold change) of the NIL expression ratio. ne = not expressed.

[c] Number of SNPs between the RNA sequence in the NIL . An SNP is taken into account only if there is a minimum coverage of 4.