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GENETIC DISSECTION OF GROWTH AND MEAT QUALITY TRAITS IN PIGS

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4. GENERAL DISCUSSION

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Consumer demand for healthy high quality pork products has grown fast during the last decades (Ngapo *et al.,* 2003; Grunert 2005). Economically important production traits in the pork industry such as growth, fatness and meat quality vary greatly among individuals and do not show simple Mendelian inheritance (Andersson & Georges 2004). The genetic basis lying behind these complex traits is believed to be determined by many *loci* with a small effect and few genes with moderate effects (Hayes & Goddard 2001). Over the years, all these traits have been systematically screened with traditional and novel technologies to unravel their genetic basis, contributing with new advances to both the scientific community and the pork industry. Approaches like candidate gene association analyses (Linville *et al.,* 2001) and QTL mapping (Rothschild *et al.,* 2007) provided new insights about the genetic architecture of pork complex traits. More recently, high-throughput genotyping platforms and gene expression microarrays (Tuggle *et al.,* 2007) provided massive results. Studies performed to date using many thousands of markers have greatly increased the information about the architecture of these traits with the identification of some *loci* accounting for large effects (Rothschild *et al.,* 2007). However, even with screening for many variants in the genome, a large portion of the heritability of complex traits is not explained (Hill 2010; Manolio *et al.,* 2009). This phenomenon is usually called the 'missing heritability' problem.

The development of high-throughput technologies to explore different layers of biologic information: the "omics" approaches including genomics, transcriptomics, epigenomics, proteomics, metabolomics and phenomics (Mackay *et al.,* 2009), along with the emerging systems biology approaches (Headon 2013), bring new opportunities to identify the complex architecture of quantitative traits. Moreover, bioinformatics and biostatistics have evolved to handle these massive amounts of data and to effectively analyze them, saving both time and efforts.

Particularly, in the IBMAP experimental population several *loci* have been described to be associated with growth, fatness and meat quality traits in pigs by using GWAS and QTL approaches. Within these *loci*, some functional strong candidate genes have

been studied, explaining some of them a large part of the phenotypic variability among animals. Nevertheless, the genetic basis determining the major part of the production traits remains unclear.

Hereby, with the aim to provide additional insight on the genetic basis of growth and meat quality traits in pigs, the present thesis exploited some of the new high-throughput and systems biology emerging approaches.

4.1. QTL, GWAS and candidate gene approaches in the IBMAP cross

The chromosome 4 FAT1 QTL region affecting fat deposition was identified in the first genome scan for pig QTLs (Andersson *et al.,* 1994) and since then has been replicated and validated in multiple pig populations (Marklund *et al.,* 1999), including the IBMAP cross (Pérez-Enciso *et al.,* 2000). In the same region, QTLs have been identified in the IBMAP F_2 cross for palmitoleic (C18:2(n-6)) and oleic (C18:1(n-9)) fatty acid content in backfat (Pérez-Enciso *et al.,* 2000) and for double-bound index and peroxidability indexes (Clop *et al.,* 2003). According to Mercadé *et al.* (2005a), two proximal SSC4 QTLs were segregating in the IBMAP cross for fatness and growth traits. The QTL with a largest effect on fatness was centered at 70 cM and the second QTL affecting growth was located at 95 cM. Concerning the first QTL, with a major effect on fatness related traits and located approximately at 60 Mb on SSC4 (*Sus scrofa* assembly 10.2), the *FABP4* and *FABP5* were the most likely candidate genes (Mercadé *et al.,* 2006b; Estellé *et al.,* 2006); whereas the second QTL was overlapping with the FAT1 QTL described by other authors. By the same year, the FAT1 QTL region was considerably refined to a 3.3 cM interval between the retinoic X receptor, gamma (*RXRG*) and succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa (*SDHC*) genes (aproximately at 93-97 Mb on SSC4, *Sus scrofa* assembly 10.2) (Berg *et al.,* 2006). This region harbored 20 genes in comparison with the human map (Berg *et al.,* 2006). Interestingly, the FAT1 region co-localizes with QTLs for intramuscular palmitic (C16:0), palmitoleic (C16:1(n-7)) and linoleic (C18:2(n-6)) fatty acid composition and octadecenoic/palmitoleic (C18:1(n-7)/C16:1(n-7)) ratio (Ramayo-Caldas *et al.,* 2012a; Muñoz *et al.,* 2013) and

backfat eicosatrienoic (C20:3(n-6)) fatty acid composition (Muñoz *et al.,* 2013) identified in the IBMAP cross.

The success on QTL identification depends largely in the recombination frequency and the number of samples used (Mackay *et al.,* 2009). The QTL approach is highly affected by incongruence in marker positions. Moreover, candidate genes identified within the QTLs relies on the correct mapping and annotation of genes. To date, the *Sus scrofa* reference sequence and annotation remains incomplete. Particularly, in the most recent version of the annotation (Ensembl release 80) of the *Sscrofa10.2* (Groenen *et al.,* 2012), *FABP5* is located on SSC4 at 60.3 Mb and *FABP4* remains unmapped. The efforts made to localize this gene using radiation hybrid and linkage mapping concluded that *FABP4* was positioned close to *FABP5* in agreement with the human comparative map (Moller *et al.,* 2004; Estellé *et al.,* 2006). In previous studies of our group, *FABP4* and *FABP5* genes were evaluated as candidate genes for the SSC4 QTL for growth and fatness in the IBMAP population (Estellé *et al.,* 2006; Mercadé *et al.,* 2006b). More recently, a GWAS study in the IBMAP BC1_LD identified eight SSC4 regions associated with intramuscular fatty acid composition, one of them co-localizing with the *FABP4* and *FABP5 locus* at 54.4-60.2 Mb for C16:1(n-7), C18:1(n-9) and C18:2(n-6) (Ramayo-Caldas *et al.,* 2012a). Muñoz *et al.* (2013) also reported associations in the *FABP4-FABP5* region for intramuscular content of C18:2(n-6) and C20:3(n-6) fatty acids in the same animal material. For this reason, and because the FABP gene family are involved in the intracellular transport of fatty acids, we decided to further evaluate them as candidate genes determining the backfat and intramuscular fatty acid composition.

Two polymorphisms of *FABP4* (*g.2634_2635insC*) and *FABP5* (*g.3000T>G*) genes previously described by our group in the IBMAP population (Estellé *et al.,* 2006; Mercadé *et al.,* 2006b) were genotyped in the BC1_LD backcross. We observed significant associations of polymorphism *FABP4*:*g.2634_2635insC* with the intramuscular fat content of C16:0, C16:1(n-7), C18:1(n-7), C18:2(n-6) and C20:3(n-6) fatty acids, MUFA and PUFA; and in backfat, with the percentages of C16:0, C18:2(n-6), C18:3(n-3), and C20:3(n-6) fatty acids and PUFA. Significant associations were also found between SNP *FABP5:g.3000T>G* and intramuscular fat content of C18:1(n-

9) and C18:2(n-6) fatty acids, MUFA and PUFA; and backfat content of C18:1(n-9) fatty acid and MUFA (Puig-Oliveras *et al.,* submitted).

A QTL scan analysis was performed assuming that alternative alleles are fixed in each parental population. *FABP4* and *FABP5* polymorphisms were included together with the 155 SNPs from the PorcineSNP60 BeadChip (*Illumina*) (Ramos *et al.,* 2009) mapping on SSC4. Furthermore, markers were also filtered for their correct position in the linkage map (Muñoz *et al.,* 2012) and for their informativity calculated by the Ron index (Ron *et al.,* 1995). A significant QTL on SSC4 spanning a maximum interval from 34 to 71 cM and harbouring 265 protein-coding genes (including genes with lipid-related functions such as *the nuclear receptor coactivator 2* or *NCOA2*; *cytochrome P450, family 7, subfamily A, polypeptide 1* or *CYP7A1;* and *peroxisomal biogenesis factor 2* or *PEX2*) was identified for C16:1(n-7), C18:1(n-9), C18:2(n-6) and C20:3(n-6) fatty acids, PUFA and MUFA intramuscular fat content and C18:2(n-6) fatty acid and PUFA backfat content. *FABP4* and *FABP5* were the strongest candidate genes mapping within this chromosome fragment at approximately 50 cM showing significant QTL effects for intramuscular and backfat fatty acid composition (Puig-Oliveras *et al.,* submitted). For the C18:2(n-6) fatty acid and PUFA content in backfat, the largest QTL effect was surrounding the 59-108 cM region (approximately from 73 to 129 Mb) discarding *FABP4* and *FABP5* genes as the main candidates for the backfat QTL (Puig-Oliveras *et al.,* submitted). This is a very large region harboring 738 genes (www.ensembl.org/biomart), which includes the FAT1 narrowed region described by Berg *et al.* (2006). In this region, two strong positional candidate genes were reported: *pre-B-cell leukemia homeobox 1* (*PBX1*) gene, essential for normal pancreatic development function, and *LIM homeobox transcription factor 1, alpha* (*LMX1A*) gene, a strong transcription factor that enhances insulin gene transcription. In addition, other strong candidate genes were described in this region in the IBMAP cross affecting intramuscular fatty acid composition (Ramayo-Caldas *et al.,* 2012a), such as the *apolipoprotein A-II* (*APOA2*) gene at 97 Mb and *CYP7A1* gene at 81 Mb involved in cholesterol metabolism. The *APOA2* and *CYP7A1* genes were identified as differentially-expressed in the liver of animals extreme for intramuscular fatty acid composition (Ramayo-Caldas *et al.,* 2012b). Variations within and nearby *APOA2* gene have been associated with free fatty acid levels in mice and humans (Warden

et al., 1993). Furthermore, polymorphisms on *APOA2* gene have been proposed to interact with SFA intake and to have an effect on body mass index and obesity in humans (Corella *et al.,* 2009; Basiri *et al.,* 2015). The *CYP7A1* gene deficiency in humans determines hypercholesterolemia (Pullinger *et al.,* 2002). Moreover, the *upstream transcription factor* 1 (*USF1*) gene located at 97 Mb encodes a transcription factor responsible for the regulation of many proteins of the glucose and lipid metabolism including *APOA5*, *APOC3* and *FAS*. Besides, variants within this gene have been associated with hyperlipidemia and cardiovascular diseases in humans (Johansen *et al.,* 2011). In addition, 20 genes mapping to this QTL region (*ADHFE1, ANKRD35, CD1E, COL11A1, CRABP2, F5, IQGAP3, METTL11B, MPC2, MPZ, PAQR6, PEAR1, PHGDH, PMVK, RGS4, S100A12, S100A4, S100A8, THEM5, VAV3*) were also detected as differentially-expressed in backfat tissue of animals with extreme phenotypes for intramuscular fatty acid composition (Corominas *et al.,* 2013b). Among them, the *regulator of G-protein signalling 4* (*RGS4*) gene was a strong candidate because it controls the balance between adipose tissue lipolysis and lipogenesis through the regulation of catecholamine secretion, which plays a major role stimulating the lipolysis in the adipose tissue (Iankova *et al.,* 2008). Finally, this region has been described to present a pleiotropic QTL for C16:0 fatty acid content in both muscle and backfat (94.0-99.0 Mb) where *RGS4* was proposed as the main candidate gene (Muñoz *et al.,* 2013).

FABP4 and *FABP5* gene expression of 114 BC1_LD animals was analyzed in muscle and backfat tissues. The analysis revealed that *FABP4* gene expression in backfat, but not in muscle, was associated with *FABP4:g.2634_2635insC* polymorphism. Animals homozygous for the *FABP4:g.2635insC* allele (fixed in the IBMAP Iberian boars and found at low frequency (0.23) in Landrace sows) showed a higher *FABP4* gene expression. In contrast, the SNP *FABP5:g.3000T>G* was not associated with *FABP5* gene expression levels. The expression genome-wide association studies (eGWAS) evidenced a different regulation for *FABP4* and *FABP5* genes transcription among tissues. Noteworthy, the eGWAS confirmed the *FABP4 g.2634_2635insC* polymorphism as the most associated with *FABP4* gene expression in backfat. For *FABP5* gene expression significant associated regions in *trans* were detected in

muscle, with positional candidate genes including *FCRL1* (SSC4), *E2F4* (SSC6), *CLMP* (SSC9), and *AZI2* (SSC13) (Puig-Oliveras *et al.,* submitted).

Interestingly, the *FABP4 g.2634_2635insC* polymorphism, located in intron 1, maps within a putative binding site for PPARG, a major regulator for fatness and growth traits (Puig-Oliveras *et al.,* 2014b). Hence, this polymorphism may alter the binding of PPARG, explaining the differential expression of *FABP4* gene in adipose tissue. Animals inheriting the most frequent Iberian allele *FABP4:g.2635insC* may have a positive regulation by PPARG enhancing *FABP4* gene expression in backfat. In agreement with our hypothesis, Nielsen *et al.* (2008) observed an increased *FABP4* mRNA level when adipocytes were treated with rosiglitazone, a PPARG agonist. In the same study the authors reported a higher number of PPARG:RXR binding sites located in introns in a chromatin-immunoprecipitation sequencing (ChIP-seq) experiment (Nielsen *et al.,* 2008).

FABP4 is a carrier protein involved in the transport of fatty acids for intracellular uptake and/or extracellular release from lipid droplets to the muscle for their utilization (Syamsunarno *et al.,* 2013; Furuhashi *et al.,* 2014). Animals inheriting *FABP4:g.2635insC,* the Iberian most frequent allele, showed a higher *FABP4* gene expression in backfat that may be regulated by PPARG transcription factor binding. The higher *FABP4* gene expression in adipocytes may positively impact the intracellular uptake of C16 and C18 fatty acids for *de novo* lipogenesis. These fatty acids may be stored as triacylglycerol or delivered to the muscle in order to fulfill the required energy.

In a previous study of our group, the *ELOVL fatty acid elongase 6* (*ELOVL6*) gene, involved in *de novo* lipogenesis, has been described as a major causative gene for the SSC8 QTL affecting palmitic and palmitoleic acid composition in the IBMAP cross (Corominas *et al.,* 2013a). In this regard, the *ELOVL6:c.-394G>A* SNP in the promoter may influence the expression of *ELOVL6* in adipose tissue through an epigenetic mechanism (Corominas *et al.,* 2015). The differential expression of *ELOVL6* was associated with the balance among C16:0, C16:1(n-7), stearic (C18:0), C18:1(n-7), and C18:1(n-9) fatty acids (Corominas *et al.,* 2013a). Animals inheriting the Iberian allele *ELOVL6:c.-394G* are associated with increased methylation levels of the

ELOVL6 promoter, which in turn may inhibit the *ELOVL6* gene expression and determine a decreased elongation activity of C16:0 to C18:0 and of C16:1(n-7) to C18:1(n-7) fatty acids (Corominas *et al.,* 2013a; Corominas *et al.,* 2015).

Altogether these results show that animals inheriting the Iberian *ELOVL6:c.-394G* and *FABP4:g. 2635insC* alleles had higher *FABP4* and lower *ELOVL6* gene expression levels in adipose tissue in comparison with animals with the Landrace alleles. In the Iberian genotype-like animals, PPARG may be up-regulating *FABP4* gene expression and, thus, determining a higher uptake of C16 and C18; whereas the decreased *ELOVL6* gene expression may affect the elongation activity of SFA and MUFA with C16 to C18 carbons, determining a higher accumulation of C16 fatty acids in Iberian animals.

On the other hand, PPARG may also enhance the *stearoyl-CoA desaturase (delta-9-desaturase)* (*SCD*) gene expression *via* binding to the gene promoter (Estany *et al.,* 2014). In agreement with that, we observed a high correlation (r=0.78; p-value<1.00×10^{-16}) between *PPARG* and *SCD* gene expression in BC1_LD animals (Puig-Oliveras *et al.,* in preparation). SCD may play a role in the desaturation of C16 and C18 to C16:1 and C18:1 fatty acids increasing the MUFA content.

In summary, in animals inheriting the *FABP4* and *ELOVL6* Iberian alleles there must be an enhanced uptake of C16 and C18 fatty acids in the adipocytes, an inhibited elongation activity to C18 fatty acids and enhanced desaturation to C16:1(n-7) and C18:1(n-9) fatty acids. Afterwards FABP4 may be also involved in the extracellular fatty acid transport to the muscle determining the higher muscle uptake of C16:1(n-7).

4.2. Studying the swine muscle transcriptome using RNA-Seq

Meat quality is influenced by many factors such as muscle structure, chemical composition and interaction of constituents, pre-slaughter stress, handling, processing, storage, microbiological content, and dietary intake of the animal (Joo *et al.,* 2013). Meat is composed by adipose, epithelial, connective and nervous tissues,

although the major component is muscle. The fatty acid composition and deposition in muscle are key factors in determining the aspect and the properties of the fresh and the cooked meat, affecting the final product. However, it is well known that differences in muscle fatty acid composition are not only influenced by dietary fatty acid intake, but also by genetics. For instance, Iberian and Landrace × Large White pigs raised under the same nutritional management show significant differences in their intramuscular fatty acid composition (Seiquer *et al.,* 2013).

Considering that muscle is the main component of the final meat product, the transcriptome of the *Longissimus dorsi* muscle was analyzed by RNA-Seq in BC1_LD animals. To discard diet, sex and environmental effects, all the animals analyzed were females fed with the same diet, slaughtered at the same age, raised in the same experimental farm with an identical management for all pigs (Ramayo-Caldas *et al.,* 2012a). However, the final fatty acid composition in muscle is also influenced by other tissues, such as the adipose and hepatic tissues. Hence, the RNA-Seq transcriptome profiling of backfat and liver was also performed in previous studies of our group using extreme animals for intramuscular fatty acid composition. Animals were classified in two groups, the L group showing higher levels of MUFA and SFA content in muscle, as observed in Iberian pigs, and the H group showing higher levels of intramuscular PUFA similar to Landrace animals. In the muscle transcriptome we identified a total of 131 genes differentially-expressed between the H and L group, which were mainly related to lipid metabolism pathways. Overall, the transcriptome results obtained in the three tissues showed a decreased fatty acid oxidation in liver (Ramayo-Caldas *et al.,* 2012b), an increased *de novo* lipogenesis in adipose tissue (Corominas *et al.,* 2013b) and an increased fatty acid and glucose uptake and enhanced lipogenesis in muscle (Puig-Oliveras *et al.,* 2014a) in the L group. In addition, in concordance with the high energy demand of muscle metabolism, we observed in general a cross-talk between glucose and lipid metabolism.

Within the overrepresented pathways identified in the functional analysis of the differentially expressed genes on each of the three tissues, we found the PPAR signalling pathway (Ramayo-Caldas *et al.*, 2012b; Corominas *et al.,* 2013b; Puig-Oliveras *et al.,* 2014a). PPARs are major regulators of fatty acid metabolism and are

expressed at high levels in tissues that are most active in lipid metabolism (Figure 4.2) (Poulsen *et al.,* 2012).

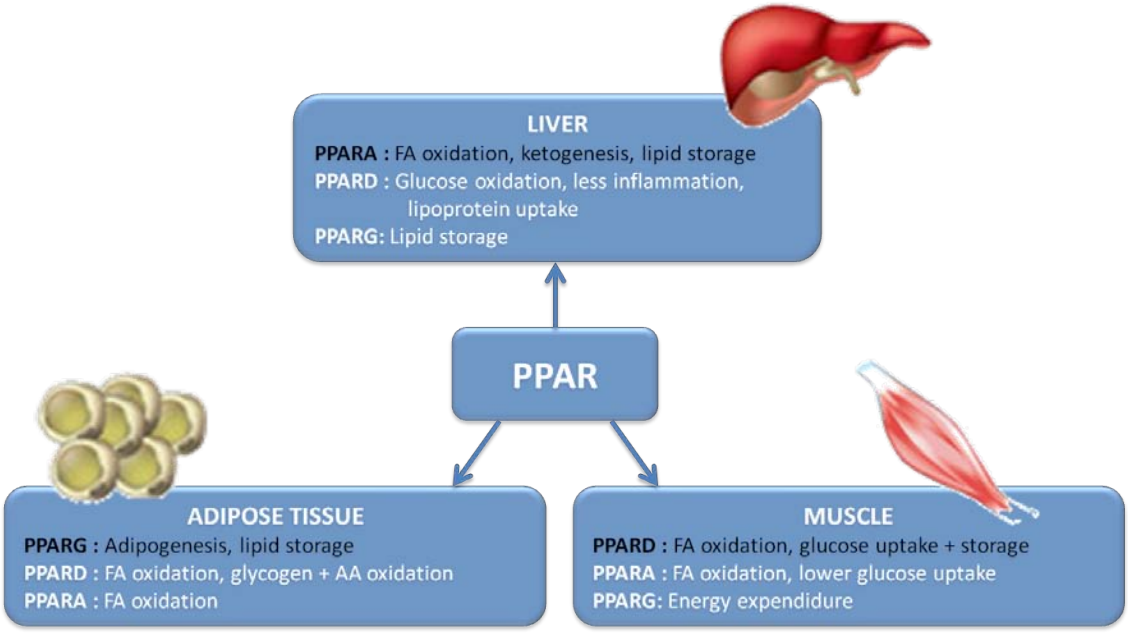

Figure 4.1. Distinct but overlapping distribution and function of the PPARs in the lipid metabolism key tissues. The most important PPAR subtypes expressed at the highest level in each tissue are indicated in black letters, while the subtypes expressed at lower levels are indicated in white (adapted from Poulsen *et al.,* 2012).

In skeletal muscle, the PPARD and the PPARA have overlapping functions for fatty acid oxidation. However, PPARA determines lower glucose uptake, whereas PPARD leads to high glycogen storage *via* solute carrier family 2 (facilitated glucose transporter), member 4 (SLC2A4, also called GLUT4). PPARG is found at lower levels in muscle; although the exact function of PPARG in this tissue remains unclear, mice treated with PPARG agonist have been shown to increase triacylglycerol content in skeletal muscle. In concordance, we observed that *PPARG* and *SLC2A4* genes were more expressed in the muscle of animals with a higher content of MUFA and SFA (Puig-Oliveras *et al.,* 2014a). We hypothesized that the insulin signalling pathway may be responsible for the changes in glycogen storage, facilitating the glucose diffusion into adipose and muscle cells via GLUT and the storage of triglycerides by the esterification of glycerol phosphate.

PPARG is highly expressed in adipose tissue switching on adipogenesis (Figure 4.2). In contrast, *PPARD* gene is expressed at low levels in this tissue and it is suggested to prime preadipocytes differentiation and increase oxidation of fatty acids, glucose and amino acids.

Finally, in liver, the most expressed PPAR gene family member is *PPARA* in response to fasting, enhancing the fatty acid catabolism and ketogenesis (Figure 4.2). Consistent with this, Corominas *et al.* (2013b) described higher levels of *PPARA* expression in the liver, as compared to adipose tissue, which suggests an important role of the liver in porcine β-oxidation. Noteworthy, although the *PPARA* gene was not identified as differentially-expressed in liver, animals belonging to the L group (having more MUFA and SFA content) showed a decreased expression of genes regulated by this transcription factor (Ramayo-Caldas *et al.,* 2012b). Besides, an overrepresentation of the RXR function which mediates the transcriptional activity of PPARs, was regulating several genes involved in cholesterol and bile acid homeostasis including the *CYP7A1* gene. The RXR function was also overrepresented in the liver transcriptome being the RXR regulated genes less expressed in the L group (Ramayo-Caldas *et al.* 2012b).

In order to validate our hypothesis, in which PPARs are the main regulators affecting fatty acid composition, we performed an *in-silico* identification of the transcription factor binding sites in the promoter region of the differentially expressed genes in the muscle of animals with extreme intramuscular fatty acid composition (Puig-Oliveras *et al.,* 2014a). For this analysis we used iRegulon (Janky *et al.,* 2014) which relies on the analysis of the motif enrichment for a transcription factor in the gene set using databases of nearly 10,000 transcription factor motifs and 1,000 ChIP-seq data sets or ‘‘tracks’’. We observed that the major regulator was the RXRA transcription factor, identifying putative transcription binding sites on the promoter of 68 out of 131 differentially expressed genes, with a maximum significant enrichment for this motif (Figure 4.3). However, the probability that the different PPARs subtypes bind to the same motif was very high (p-value $_{PPARA}$ = 1.39×10^{-6}; p-value $_{PPARD}$ = 1.39×10^{-6}; p-value $_{PPARG}$ = 4.05×10^{-11}). Noteworthy, when all the genes differentially-expressed in liver, adipose tissue and muscle (Ramayo-Caldas *et al.,* 2012b; Corominas *et al.,* 2013b; Puig-Oliveras *et al.,* 2014a) were analyzed (n=503),

the first transcription factor with 207 genes was the TATA box binding protein like 2 (TBPL2), followed by the E1A binding protein p300 (EP300) with 175 target genes. EP300 has also been described as a major regulator of fatty acid metabolism in our animal material using a network based on gene-by-gene co-association analysis (Ramayo-Caldas *et al.,* 2014a).

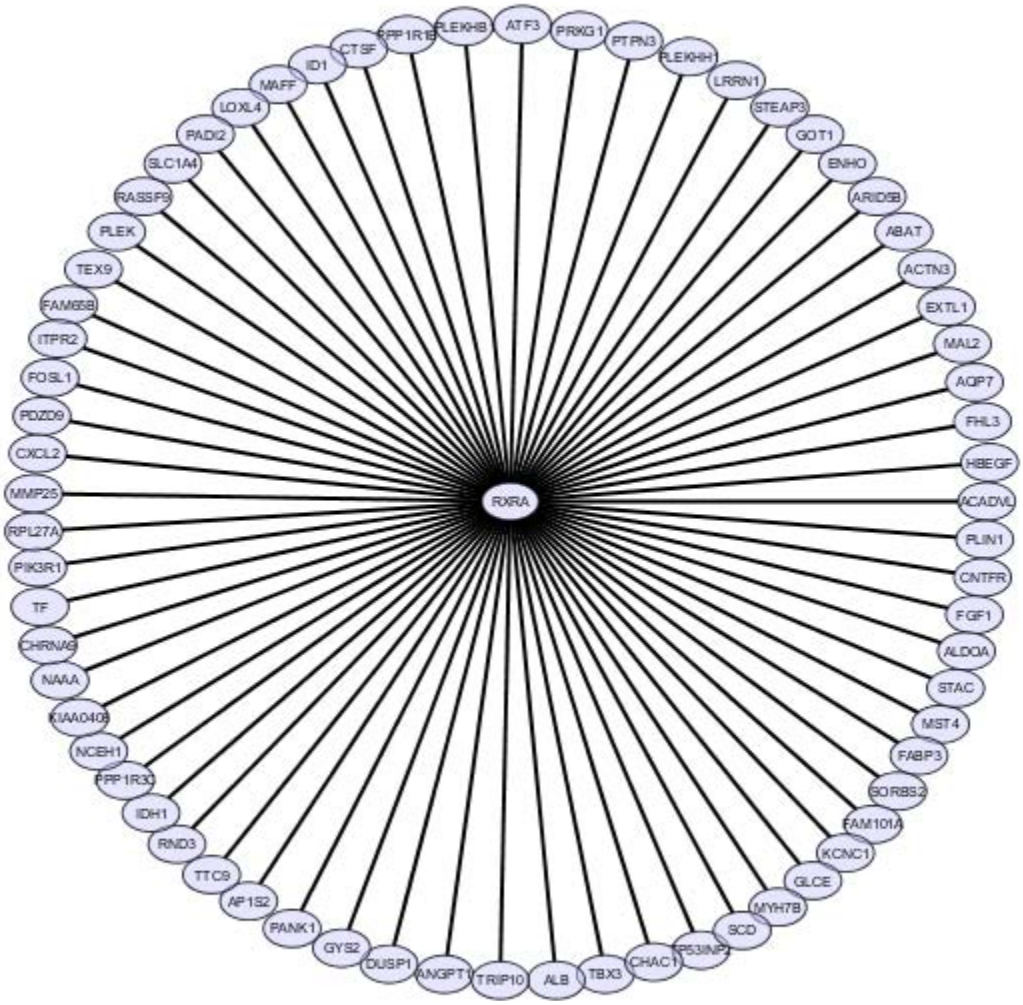

Figure 4.2. RXR targeting differentially expressed genes (n=68) identified in the muscle transcriptome for animals extreme in their intramuscular fatty acid composition (Puig-Oliveras *et al.,* 2014a) using iRegulon cytoscape plugin (Janky *et al.,* 2014).

Despite the high number of evidences supporting a key role of PPAR nuclear receptors in determining the differences in intramuscular fatty acid composition in the BC1_LD cross, we only identified the *PPARG* gene as differentially-expressed in the muscle transcriptome (Puig-Oliveras *et al.,* 2014a). *PPARG* gene was also identified as a major regulator for growth and fatness related traits in a co-

association network in muscle (Puig-Oliveras *et al.,* 2014b). We could not identify other PPAR subtypes differentially-expressed in muscle, neither in liver or adipose tissue (Ramayo-Caldas *et al.,* 2012b; Corominas *et al.,* 2013b). One possible explanation is that although having large effects most of the transcription-factor genes are expressed at lower levels than the non-transcription factor genes (Vaquerizas *et al.,* 2009). The mechanism proposed is that a single transcription factor molecule produces the transcription of many copies of the target gene. This hypothesis is in accordance with our results, in which the differential expression of target genes for PPARs was observed: *acyl-CoA oxidase 2, branched chain* (*ACOX2*), *aquoporin 7* (*AQP7*), *apolipoprotein A-II* (*APOA2*), *cytochrome P450, family 2, subfamily C, polypeptide 19* (*CYP2C19*), *cytochrome P450, family 2, subfamily C, polypeptide 9* (*CYP2C9*), *fatty acid binding protein 3* (*FABP3*) and *stearoyl-CoA desaturase* (*SCD*). Hereby, we suggest that the genetic variants inherited from the Iberian and Landrace parental breeds affect the gene expression of the PPAR gene family members, which, in turn, are the key regulators determining the differences in the intramuscular fatty acid composition. However, we cannot rule out that the phenotypic differences observed among individuals may be caused by the genetic variability in the intestinal absorption of essential fatty acids or in the following steps of fatty acid metabolism: transport, deposition, storage or degradation.

RNA-Seq is a powerful tool, with a lot of strengths, giving us a global view of gene transcription and, thus, a better understanding of the pathways and genes which are influencing the phenotypes. However, it has also some limitations, as its dependence on the quality of the genome reference sequence. Taking into account that the current pig reference sequence is not complete, we cannot identify non-annotated or/and unmapped genes that may be key in these pathways or functions. To overcome this problem, we performed a novel coding gene discovery which allowed the identification of 2,372 novel unannotated predicted proteins of which 1,406 shared similarities with known proteins in pigs, humans or cows. Among them, novel proteins with lipid, protein and nucleic acid binding activity were predicted. Furthermore, within the main metabolic represented pathways for the 1,406 predicted novel proteins there were the "phosphatidylinositol signalling system" and

the "inositol phosphate metabolism". Therefore, important genes affecting the lipid metabolism are not annotated in the current porcine reference sequence.

4.3. Networks to decipher conformation, growth and fatness related traits in pigs

As stated before, the processes regulating conformation, growth and fatness traits in pigs are complex and most of the genetic mechanisms remain unknown despite being of great interest for the pig industry. Reported QTLs for growth and fatness traits in the IBMAP F_2 animals were identified by linkage analyses using few microsatellite markers and resulting in large QTL intervals spanning several cM (Óvilo *et al.,* 2000; Pérez-Enciso *et al.,* 2000; Varona *et al.,* 2002; Mercadé *et al.,* 2005a). More recently, the use of the PorcineSNP60 BeadChip (Illumina, Ramos *et al.,* 2009) has allowed the detection of QTLs with narrow confidence intervals (Fernández *et al.,* 2012) and the identification of genomic associated regions by GWAS (Ramayo-Caldas *et al.,* 2012a; Muñoz *et al.,* 2013). Even so, the number of candidate genes inside the associated intervals is large (Fernández *et al.,* 2012; Ramayo-Caldas *et al.,* 2012a). In addition, GWAS and QTL approaches are single-trait analyses that ignore functional interactions. For instance, the QTL on SSC8 for C16:1(n-7) backfat content identified in the IBMAP cross spanning approximately 17 cM (Clop *et al.,* 2003) was narrowed by combining GWAS and haplotype based approaches. This result allowed the recent identification of the *ELOVL6* gene as a strong candidate explaining the SSC8 QTL for C16:1(n-7) fatty acid composition in backfat (Corominas *et al.,* 2013a).

The use of network approaches considering the interactions of multiple molecules and traits may provide useful insights into the molecular mechanisms of complex traits. For this reason, we decided to apply a network based methodology, named Association Weight Matrix (Fortes *et al.,* 2010; Reverter & Fortes 2013), to study gene interactions and pathways affecting pig conformation, growth and fatness traits. This approach not only considers gene-by-gene and trait-by-trait interactions but also takes advantage of biological information of regulators. It is well described that the perturbation in one gene (regulator) can affect many other genes and so on. This approach allows drawing a biological network, as a result of the analysis,

representing the relations between genes and their functional connections. Moreover, it has been described that it is more difficult to predict a single gene than a gene module function (Cho *et al.,* 2012).

The resulting network of co-association included 1,747 nodes representing genes and SNPs connected by 316,166 edges or interactions, which evidenced the high complexity of the molecular processes involved in growth, conformation and fatness traits. The network exploration highlighted three transcription factors, PPARG, E74-like factor 1 (ELF1), and PR domain containing 16 (PRDM16) involved in mesoderm tissue differentiation, connecting a total of 513 genes with a total of 639 interactions. An *in-silico* analysis was performed with iRegulon (Janky *et al.,* 2014) to detect enriched transcription factor binding sequence motifs within the 148 genes co-associated with *PPARG* on the network. Consistently, this analysis highlighted PPARG binding to the highest number of gene targets (n=56). Within the most enriched motifs for the *ELF1* gene set (n=238 genes), we identified the *forkhead box P3* (*FOXP3*), which interacts with *ELF1,* and was identified as a central transcription factor regulating intramuscular fat in cattle using the same methodology (Rudra *et al.,* 2012; Ramayo-Caldas *et al.,* 2014b). For the motif enrichment of *PRDM16* co-associated genes set, the most enriched motif was the *homeobox A2* (*HOXA2*) transcription factor. This is an interesting result because HOX genes are key regulators of development required to specify segmental identity in the embryo (Carroll 1995). Futhermore, *HOXA2* gene knockdown in mice affects skeletal elements such as ossification centers of the middle ear and clef centers (Mouse Genome Informatics, MGI; http://www.informatics.jax.org/). Both genes *PRDM16* and *HOXA2* were described as candidate genes that may be regulating adipogenesis (Tchoukalova *et al.,* 2014), and interestingly, HOX genes family members regulate *PRDM16* gene expression (Yu *et al.,* 2014).

Interestingly, the SNP represented by the *PPARG* gene (ISU10000701) was the most associated marker for seven of the 12 traits (body weights at three different ages, carcass weight, and primary cut weights) (Puig-Oliveras *et al.,* 2014b). Furthermore, *PPARG* gene was also identified as differentially-expressed in the muscle of animals with extreme fatty acid composition (Puig-Oliveras *et al.,* 2014a). Besides, this transcription factor has been also identified as a key regulator in a co-association

network for maturity in cattle (Fortes *et al.,* 2010). In the pre-mature phase, animals grow increasing their muscle mass, organ and bone formation; whereas in the mature phase, there is a switch towards fattening and intramuscular fat deposition. In agreement with this, the functional analysis considering the 513 co-associated genes related to the top trio of transcription factors, uncovered the lipid metabolism and the corticotropin and gonadotropin release hormone pathways among the most important pathways influencing these traits. All three key transcription factors (ELF1, PRDM16 and PPARG) are involved in cell fate switch in adipocytes, myocytes or osteocytes which may be determined by the hormonal changes depending on the mature stage. Remarkably, seven genes on the network (*COPS7B, EFEMP1, ETV6, FRS2, HSPG2, SH3PXD2A* and *TGS1*) have been associated with human height (Gudbjartsson *et al.,* 2008; Soranzo *et al.,* 2009). Highly concordant with our results, 46 out of 513 genes were also identified in a cattle study for growth traits with metabolomic data using the same methodology, and consistently they described the same overrepresented pathways: the gonadotropin hormone and the nitric oxide metabolism (Widmann *et al.,* 2013). The gonadotropin hormone pathway has also been identified affecting puberty traits in cattle (Fortes *et al.,* 2010).

In the network, we could also identify interesting known candidate genes such as the *FABP5* gene described in the IBMAP cross (Estellé *et al.,* 2006), the *calpastatin* (*CAST*) gene reported in the literature to determine meat quality traits (Ciobanu *et al.,* 2004), and *RYR1* gene causal for the malignant hyperthermia (Fujii *et al.,* 1991). Moreover, the network uncovered new candidate genes such as the 55 genes which have a growth-related function (Figure 4.4) (Mouse Genome Informatics, MGI; http://www.informatics.jax.org/). As we can clearly observe in Figure 4.4 for the 55 growth-related genes, the hierarchical cluster analysis evidenced a clear division of the additive effects of the SNPs for the 12 growth phenotypic traits, between animal weight-related and fat-related traits.

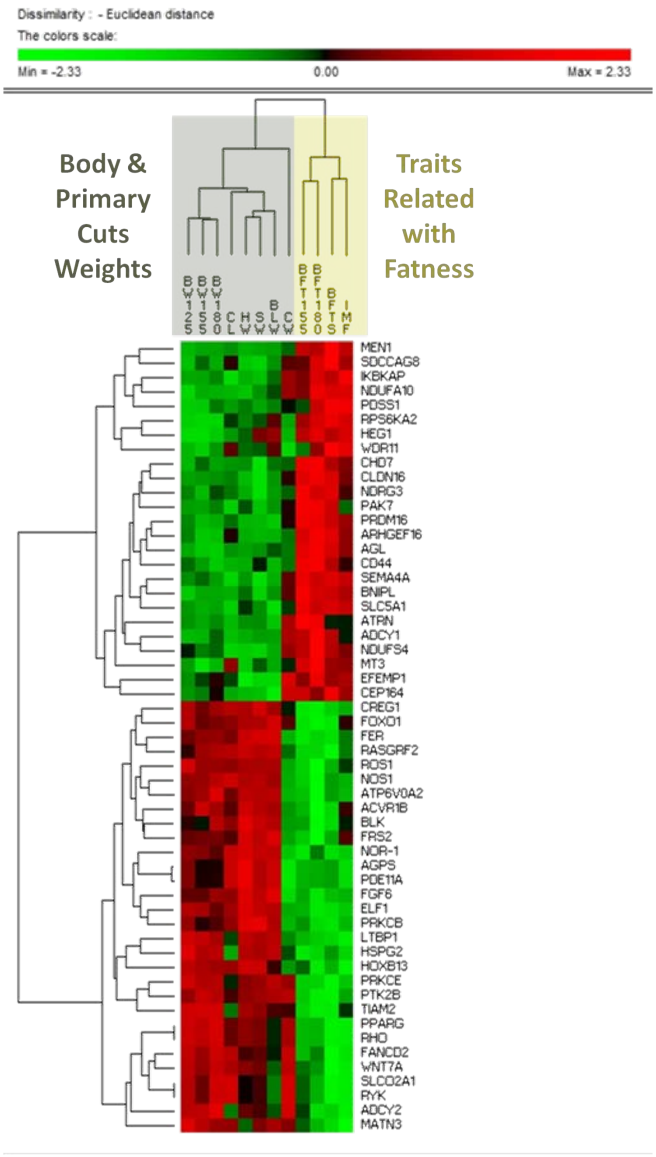

Figure 4.3. Hierarchical cluster analysis considering only those genes in the network related with growth among 12 phenotypic traits. The green colour in the figure corresponds to negative SNP additive effect values and red to positive SNP additive effect values (adapted from Puig-Oliveras *et al.,* 2014b).

Overall, the network suggests a key role for the transcription factors ELF1, PRDM16 and PPARG and their co-associated genes controlling growth, conformation and carcass traits in pigs. Moreover, the gonadotropin and the nitric oxide pathways may be relevant in the regulation of these traits. Despite the present methodology highly relies on the correct annotation of the SNPs and genes in the reference genome sequence and it is affected by linkage, we obtained consistent results with the published literature.

4.4. Gene expression study of 45 candidate genes for muscle lipid metabolism to explore gene interactions and identify key regulators

During these years, several studies have been performed on the experimental IBMAP population highlighting several strong candidate genes affecting the deposition of intramuscular fat and the fatty acid composition by QTL and GWAS, RNA-Seq and co-association network approaches (Fernández *et al.,* 2012; Ramayo-Caldas *et al.,* 2012a; Muñoz *et al.,* 2013; Pena *et al.,* 2013; Puig-Oliveras *et al.,* 2014a; Puig-Oliveras *et al.,* 2014b; Ramayo-Caldas *et al.,* 2014a). A large number of functional and positional genes were identified with these approaches and several candidate genes were more carefully evaluated: *ACACA, ACADM, ACSL4, CDS1, CDS2, DECR, DGAT1, ELOVL6, FABP2, FABP3, FABP4, FABP5, FASN, GIP, IGF2, LEPR, MTTP* and *SETD7* (Clop *et al.,* 2002; Óvilo *et al.,* 2002b; Óvilo *et al.,* 2005; Estellé *et al.,* 2005a; Mercadé *et al.,* 2005b; Estellé *et al.,* 2006; Kim *et al.,* 2006; Mercadé *et al.,* 2006a; Mercadé *et al.,* 2006b; Mercadé *et al.,* 2007; Muñoz *et al.,* 2007; Estellé *et al.,* 2009a; Estellé *et al.,* 2009b; Muñoz *et al.,* 2009; Corominas *et al.,* 2012; Corominas *et al.,* 2013a; Revilla *et al.,* 2014; Corominas *et al.,* 2015; Puig-Oliveras *et al.,* submitted). Besides, interesting genes showing differential expression among animals with extreme fatty acid composition in muscle by RNA-Seq (12 animals, 6 per group) need further evaluation. One recent proposed strategy to deepen into the study of the genetic architecture of complex traits is the detection of quantitative trait *loci* associated with gene expression levels named eQTL approach (Schadt *et al.,* 2003; Gilad *et al.,* 2008). This technique considers gene expression values as a quantitative trait allowing the identification of genetic variants associated with gene transcription levels and also to gain insight into the regulation mechanisms uncovering gene network interactions (Harm-Jan & Franke 2014). Such genomic positions can be either *cis*- or *trans*-acting modifiers of gene expression, depending on whether they are located in the vicinity of or far from the measured gene, respectively (Gilad *et al.,* 2008).

In the IBMAP cross, gene-specific eQTL analysis has been performed for some candidate genes (*ACSL4, ELOVL6, FABP4* and *FABP5*) in order to find potential genomic regions regulating their expression (Corominas *et al.,* 2012, Corominas *et*

al., 2013a, Puig-Oliveras *et al.,* submitted). Moreover, an eQTL analysis has been performed for genes that mapped within QTLs for fatty acid composition of the IBMAP cross by using microarray gene expression data in *Longissimus dorsi* samples (Muñoz *et al.,* 2013). The authors successfully detected eQTLs in SSC8, SSC11 and SSC17 for *MGST2, PTPN11, BGLAP, ELOVL6, SEC13, PNPLA2, SGMS1, PTGR2, THRB, AGPAT9, DPP4* and *RUNX1*; however, only *MGST2* passed the FDR correction cut-off (0.2). Microarrays are extremely powerful tools providing an overall picture of gene expression in a whole genome scale. However, results from microarrays are often noisy or ambiguous (Spurgeon *et al.,* 2008). In the present work, we decided to use the Fluidigm (Fluidigm; San Francisco, CA, USA), a high-throughput microfluidic system that analyze gene expression by multiple real-time quantitative PCRs (RT-qPCR). This technique allows the simultaneous analysis of gene expression of a flexible moderate number of genes in several animals. As it is based on RT-qPCR, it shows a high sensitivity, high reproducibility, and is able to detect a large dynamic range of expression values (Spurgeon *et al.,* 2008). Hence, 45 candidate genes related with lipid metabolism identified in previous studies of our group were selected for analyzing their gene expression values in 114 BC1_LD animals and performing an eGWAS. The eGWAS identified 241 eSNPs located in 18 genomic regions and associated with eleven genes, of which 215 could be succesfully annotated, being 54% located in intergenic regions and the remaining 56% within genes. Of the 18 eQTLs detected for *acyl-CoA synthetase medium-chain family member 5* (*ACSM5*), *carnitine O-octanoyltransferase* (*CROT*), *FABP3, FBJ murine osteosarcoma viral oncogene homolog* (*FOS*), *hypoxia in ducible factor 1, alpha subunit inhibitor* (*HIF1AN*), *phosphoinositide-3-kinase, regulatory subunit 1 (alpha)* (*PIK3R1*), *phospholipase A2, group XIIA* (*PLA2G12A*), *monoglyceride lipase* (*MGLL*), *insulin-like growth factor 2* (*IGF2*), *nuclear receptor coactivator 1* (*NCOA1*) and *PPARA* genes, only three were identified in *cis* (*ACSM5, IGF2* and *MGLL*). One of the major objectives for the eQTL studies is to identify potential transcription factors responsible for mediating the expression of these genes, which may in turn affect the trait (Sun *et al.,* 2007). The present eQTL analysis provided new knowledge about the regulation of lipid metabolism genes, for instance, we observed that PPARG may act as a potential regulator for *MGLL* gene expression, and *phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma* (*PIK3CG*)

for both, *PLA2G12A* and *HIF1AN* gene expression. Remarkably, in the top-network of functions obtained for the genes annotated within the genomic regions of the 18 eQTL we identified the serine/threonine kinase (Akt) complex, which is involved in glucose transport and lipogenesis. Noteworthy, the Akt complex was identified being a downstream affected pathway in the top network of functions obtained in the muscle and liver transcriptome analysis (Ramayo-Caldas *et al.,* 2012b; Puig-Oliveras *et al.,* 2014a). Furthermore, the results of the identification of key regulators with iRegulon (Janky *et al.,* 2014) for the 45 lipid-related analyzed genes pinpointed the *nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)* (*NR3C1*) gene as a key regulator. Noteworthy, the *NR3C1* gene is located within a *PPARA* *trans*-eQTL in SSC2 (Puig-Oliveras *et al.,* in preparation).

The present study allowed us to deepen into the study of candidate genes associated with intramuscular fatty acid composition affecting pork meat quality. The results obtained confirm the eQTL approach as a good strategy for identifying important variants and genes regulating these complex traits. Nonetheless, more studies are needed to validate the effect of the main genes and variants uncovered in the present work. Besides, since the porcine reference genome sequence and annotation is incomplete, this approach allowed the characterization of associated genomic regions with gene expression levels of non-annotated genes in swine which are known to be relevant for the analyzed traits (i.e.: *PPARGC1A* and *IGF2* genes).

4.5. Integrative view

In summary, all studies highlighted a key role of PPARs transcription factors as the main regulators of lipid metabolism genes determining fatness and fatty acid composition in the BC1_LD population. PPARs transcriptional activity is mediated by RXR, which binds co-activator proteins, including PPARGC1A, to recognize specific DNA sequence elements called PPAR responsive elements (Wahli & Michalik 2012; Diez *et al.,* 2012). The eQTL study performed with the strongest candidate genes identified in the RNA-Seq and co-association network studies pinpointed towards the effects of corticotropin and insulin hormones in activating NR3C1, which may be responsible for at least the *PPARA* gene expression regulation (Figure 4.5). Moreover, Chen *et al.* (1995) reported that the *NR3C1* gene may play a negative role in adipogenesis regulating the lipolytic and antilipogenic gene expression in pigs. Supporting our hypothesis, Diez *et al.* (2012) observed in a co-transcriptional network from microarray data that glucocorticoids activate the NR3C1 receptor, activating in turn the PPAR pathway *via RXRA* and *PPARGC1A* gene up-regulation.

In addition, the RNA-Seq analysis in muscle suggested that the C16:1(n-7) jointly with *PPARG* gene expression may affect the insulin signalling cascade, enhancing the glucose metabolism and resulting in a downstream effect on phosphoinositide 3-kinases (PI3 kinases) and Akt pathways (Figure 4.5). Moreover, the Akt pathway was also identified as being central and directly connected with the gonadotropin hormones (luteinizing hormone and follicle-stimulating hormone) in the principal enriched network (gathering the energy production, small molecule biochemistry and drug metabolism functions) obtained in the eQTL study of 45 lipid-related genes. Moreover, the gonadotropin releasing hormone pathway was also identified as overrepresented in the co-association network for fatness and growth traits. The gonadotropin hormones have been described to trigger sexual maturation, determining in the pre-mature phase an increased muscle mass, organ and bone formation, and in the mature phase a higher fat and intramuscular fat deposition (Owens *et al.,* 1993). The *PPARG* gene has been described to be regulating the gonadotropin releasing hormone pathway (Sharma *et al.,* 2011). In concordance, in the co-association network the PPARG was identified as a main regulator.

In conclusion, the different studies presented in this thesis suggested a key role of genes and variants within these genes such as *ELF1, NR3C1, PIK3CG, PRDM16, PPARA, PPARG, RXRG, SLC2A4* in determining growth, fatness and fatty acid composition traits. Moreover, we have studied in more detail the *FABP4* and *FABP5* genes, which play a role in the intracellular fatty acid transport, and also in the mobilization of fatty acids to the muscle to supply energy requirements. The results obtained suggest that *FABP4* is also regulated by PPARG (Figure 4.5). The *FABP4* gene plays a key role in the intracellular uptake of fatty acids in adipose tissue and in the delivery of fatty acids to muscle, therefore, affecting the meat quality traits.

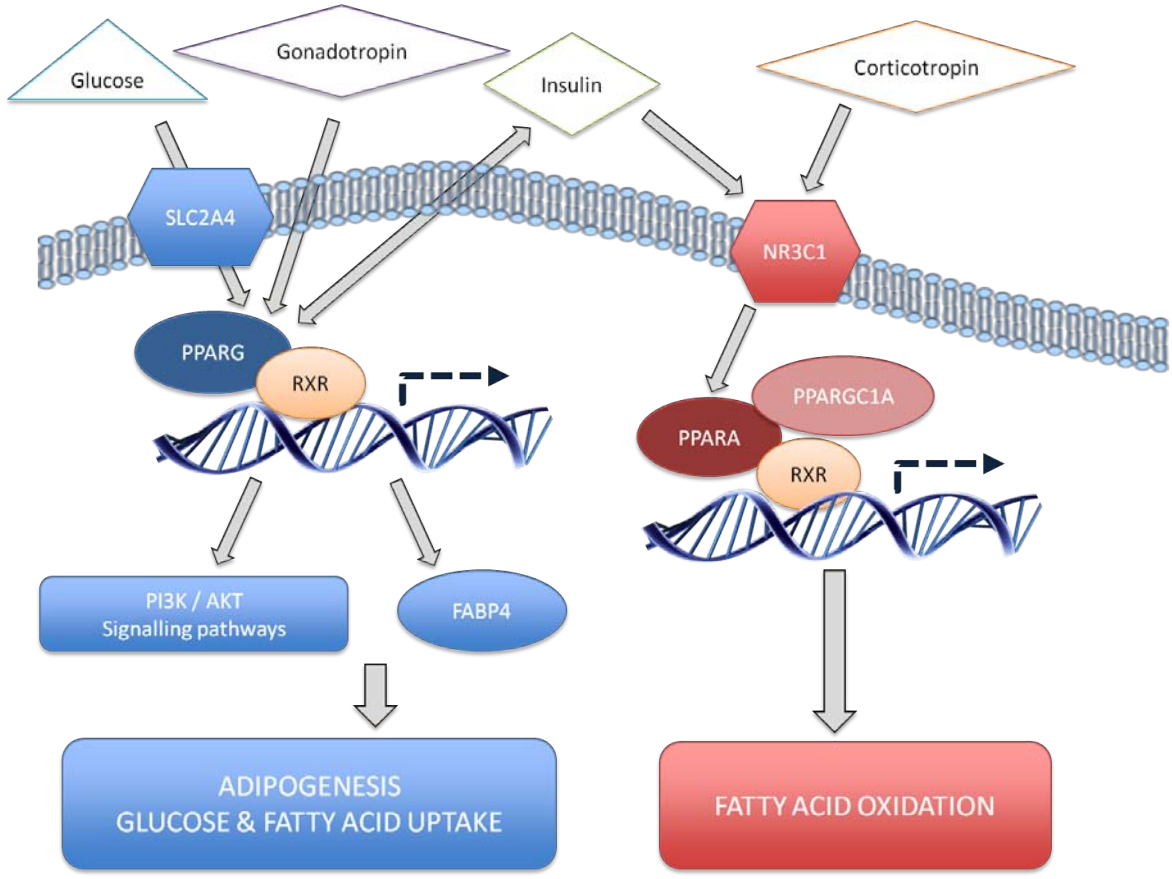

Figure 4.4. Integrative view of pathways and regulators playing a key role in determining fatness and fatty acid composition in the BC1_LD population highlighted in this thesis.

4.6. Future directions and challenges

In the past decade, animal breeding programs based on genetics have had a major impact on improving economic important traits for the pork meat production such as the carcass growth and composition, meat quality and efficiency (Andersson 2001). The availability of the pig genome sequence has enabled to perform high resolution QTL and GWAS analyses identifying major *loci* containing several candidate genes, and also variations such as SNPs, indels, and copy number variants underlying these economically important traits. Some of them have been already applied in the genomic selection conducted by the porcine industry (Andersson & Georges 2004). These models are typically limited to account for additive effects; while other known relevant effects such as epistasis or dominance are less explored, probably for its modeling complexity (Casellas *et al.,* 2014). However, despite the considerable efforts made by the scientific community to unravel the genetic basis of growth, conformation and fatness traits, the genes and variants behind these complex phenotypes are unclear. With the advent of the "omics" era, the analysis of the genome, transcriptome, proteome, epigenome, metagenome, metabolome and phenotypes in a high-resolution way provided new insights and revealed that many *loci* contribute to the genetic variation of these traits (Mackay *et al.,* 2009). The vast majority of the production important traits are quantitative traits which can be explained by many genes of small effect and few ones of large effect. The final phenotypes are affected by pathways controlled by many genes and enzymes. One can compare these pathways as a production chain, if one part of the chain slows down, it acts as a bottleneck affecting the whole production, and if one important part of this chain collapses, the production fails. Therefore, during the last years we have been focused entirely on finding genes and variants determining the crucial points where the pathways can fail and affect these phenotypes in a straightforward manner. Perhaps, a more realistic approach to understand the genetic basis is to take into account the whole pathway, not only accounting for a few specific genes. Network holistic approaches considering gene-gene interactions can help us to understand the biological processes under consideration in a more complete view. Besides, the integration of all the "omics" and traits in a system biology approach may be clue to analyze complex traits. These studies based on systems biology have a significant potential, but considerable research effort will be required before they

can effectively be utilized to enhance efficiency of pork production in the future. Henceforth, there is still a very long way to go before we can decipher the "black box" underlying the inheritance of the quantitative traits. The answer to the long-standing unanswered questions in quantitative genetics will require the efforts of a global multidisciplinary research community.

The IBMAP cross was well designed to perform GWAS and QTL analyses, however it has some limitations in terms of large linkage blocks present in the genome because of the close relationship between animals coming from the same founders. For this reason, a large number of animals should be analyzed in order to overcome the large genetic linkage blocks and genetic validation in different genomic backgrounds will be required. The steps followed during these years to unravel the genetic basis of growth, carcass, fatness, and meat quality traits in the IBMAP cross can be summarized as follows: (1) QTL and GWAS mapping experiments, (2) analysis of positional candidate genes, (3) identification of genomic variants (indels, SNPs and copy number variants), (4) identification of differentially expressed genes by microarray and RNA-Seq analysis, (5) network analyses to uncover key transcription factors, and (6) eQTL mapping experiments to identify expression regulatory regions. The existence of additional crosses, such as the Iberian × Pietrain and Iberian × Duroc, would bring us the opportunity to validate the results of QTLs and candidate genes identified in the Iberian × Landrace cross studied in this thesis.

Although bigger populations would be more appropriate for performing gene network analysis, the results obtained showed a high concordance with the literature and provide new insights on the genetic determination of the analyzed traits. In this context, and concerning to the continuity of the present work, the co-association network for growth and fatness traits allowed the identification of interesting SNPs, genes and gene interactions. These results should be carefully studied in future works, for example, by confirming the co-association interactions with gene expression correlation analyses or by chromatin-immunoprecipitation sequencing (CHIP-seq) analysis to validate gene interactions.

From the RNA-Seq analysis of the muscle transcriptome, some of the differentially expressed genes were validated and studied in a larger number of animals by RT-

qPCR. This study provided additional information about their interactions and the genomic regions which regulate their expression. Moreover, the RNA-Seq data brings the opportunity to explore other sources of genetic variation such as SNVs, transcript isoforms, and allelic specific expression in near future studies. Furthermore, each candidate gene obtained from the cross reference list of evidences among all the studies must be analyzed apart for an independent confirmation. For instance, in the present work, we analyzed the *FABP4* gene and promising results strongly suggests this gene as a key factor determining fatty acid composition. However, the hypothesis concerning the causality of PPARG binding to *FABP4 g.2634_2635insC* polymorphism should be proved and validated. On the other hand, to validate causal mutations in candidate genes a next step should be a functional confirmation (for example by experiments involving transfection of cell lines or the analysis of transgenic animals). In the future, studying other layers of phenotypic variance such as the epigenome, the metabolome or the metagenome would be of great interest in the IBMAP project context. For instance, exploring the metabolomic data may provide clues for understanding how the hormone pathways identified affect gene expression, or obtaining metagenomic data of the gut may help to understand how the microbiota affects the fatty acid absorption or the food digestibility. Finally, we hope that new molecular, bioinformatic and statistical tools will emerge with the aim to integrate the heterogeneous sources of information from the different biologic layers studied and provide a better understanding of the mechanisms behind the quantitative genetic variation.

5. CONCLUSIONS

5. CONCLUSIONS

1. The *FABP4:g.2634_2635insC* polymorphism was the most significant marker of the SSC4 QTL for palmitoleic and eicosatrienoic fatty acids and PUFA content in intramuscular fat. Moreover, this indel had the strongest statistical significance for *FABP4* gene expression, which may be regulated by the differential binding of PPARG in intron 1.

2. The *FABP5:g.3000T>G* polymorphism was the most associated marker for oleic and linoleic fatty acids and MUFA content in muscle. However, this variant was not associated with *FABP5* gene expression, which was influenced in muscle by eQTLs located on SSC4, SSC6, SSC9, and SSC13.

3. A global view of porcine muscle tissue transcriptome has been obtained by RNA-Seq analysis, allowing the identification of 2,372 putative unannotated protein coding sequences and a description of new transposable elements.

4. The transcriptome comparison between two groups of pigs with extreme phenotypes for intramuscular fatty acid composition allowed the identification of 131 differentially expressed genes in muscle. Fifty genes had a higher expression in animals with higher intramuscular content of PUFA, whereas the remaining 81 genes had a higher expression in the group showing more SFA and MUFA content.

5. Functional analysis of these differentially expressed genes revealed the enrichment of the glucose and lipid metabolism pathways, which may be controlled by insulin and PPAR effectors. Animals with more PUFA showed an increase in lipolisis activity and a lower glucose uptake in muscle.

6. A biological network analysis for growth, shape, and fatness traits in pigs showed a highly connected network with 1,747 genes and 316,166 interactions, identifying three transcription factors (*PPARG, PRDM16,* and *ELF1*) as key potential regulators. Functional analysis revealed the lipid metabolism and the corticotropin and gonadotropin release hormone among the most important pathways influencing these traits.

7. A Real-Time qPCR expression analysis of 45 candidate genes for fatty acid composition in muscle identified a total of 18 eQTLs for eleven genes; three of them were acting in *cis* on the *ACSM5, IGF2* and *MGLL* gene expression and 16 regulated in *trans* the expression of 11 genes (*ACSM5, CROT, FABP3, FOS, HIF1AN, IGF2, MGLL, NCOA1, PIK3R1, PLA2G12A,* and *PPARA*). The NR3C1 transcription factor was identified within a *trans*-eQTL for *PPARA* gene and was highlighted as a key regulator in the *in-silico* analysis of transcription factor binding sites of the 45 studied gene promoters.

6. REFERENCES

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Ai H, Fang X, Yang B, Huang Z, Chen H, Mao L, *et al.* (2015). Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. Nature Genetics 47:217-225.

Amaral AJ, Ferretti L, Megens H-J, Crooijmans RPMA, Nie H, Ramos-Onsins SE, *et al.* (2011). Genome-wide footprints of pig domestication and selection revealed through massive parallel sequencing of pooled DNA. Plos One 6(4):e14782.

Andersson L, Haley CS, Ellegren H, Knott SA, Johansson M, Andersson K, *et al.* (1994). Genetic mapping of quantitative trait loci for growth and fatness in pigs. Science 263:1771-1774.

Andersson L (2001). Genetic dissection of phenotypic diversity in farm animals. Nature Reviews Genetics 2(2):130-8.

Andersson L, Georges M (2004). Domestic-anima genomics: deciphering the genetics of complex traits. Nature Reviews Genetics 5:202-212.

Archibald A, Bolund L, Churcher C, Fredholm M, Groenen M, Harlizius B, *et al.* (2010). Pig genome sequence - analysis and publication strategy. BMC Genomics 11:438.

Basiri MG, Sotoudeh G, Alvandi E, Djalali M, Eshraghian MR, Noorshahi N, *et al.* (2015). APOA2 -256T>C polymorphism interacts with saturated fatty acids intake to affect anthropometric and hormonal variables in type 2 diabetic patients. Genes Nutr 10:15.

Berg F, Stern S, Andersson K, Andersson L, Moller M (2006). Refined localization of the FAT1 quantitative trait locus on pig chromosome 4 by marker-assisted backcrossing. BMC Genet 7:17.

Bianco E, Nevado B, Ramos-Onsins SE, Pérez-Enciso M (2015). Deep catalog of autosomal single nucleotide variation in the pig. Plos One 10(3):e0118867.

Bidanel JP, Milan D, Iannucelli N, Amigues Y, Boscher MY, Bourgeois F, *et al.* (2001). Detection of quantitative trait loci for growth and fatness in pigs. Genetics Selection Evolution 33:289-309.

Bijma P (2012). Long-term genomic improvement - new challenges for population genetics. Journal of Animal Breeding and Genetics 129:1-2.

Bolormaa S, Pryce JE, Reverter A, Zhang Y, Barendse W, Kemper K, *et al.* (2014). A multi-trait, meta-analysis for detecting pleiotropic polymorphisms for stature, fatness and reproduction in beef cattle. Plos Genetics 10(3):e1004198.

Bosse M, Megens HJ, Madsen O, Paudel Y, Frantz LAF, Lawrence B, *et al.* (2012). Regions of homozygosity in the porcine genome: consequence of demography and the recombination landscape. Plos Genetics 8:e1003100.

Cao H, Gerhold K, Mayers JR, Wiest MM, Watkins SM, Hotamisligil GS (2008). Identification of a lipokine, a lipid hormone linking adipose tissue to systemic metabolism. Cell 134(6):933-944.

Cánovas A, Quintanilla R, Amills, Pena RN (2010). Muscle transcriptomic profiles in pigs with divergent phenotypes for fatness traits. BMC Genomics 11,372.

Cánovas A, Pena RN, Gallardo D, Ramírez O, Amills M, Quintanilla R (2012). Segregation of regulatory polymorphisms with effects on the gluteus medius transcriptome in a purebred pig population. Plos One 7(4):e35583.

Carroll SB (1995). Homeotic genes and the evolution of arthropods and chordates. Nature 376,479-485.

Casellas J, Noguera JL, Reixach J, Díaz I, Amills M, Quintanilla R (2010). Bayes factor analysis of heritability for serum and muscle lipid traits in Duroc pigs. Journal of Animal Science 88:2246-54.

Casellas J, Gianola D, Medrano JF (2014). Bayesian analysis of additive epistasis arising from new mutations in mice. Genetics Research 96:e008.

Cepica S, Stratil A, Kopecny M, Blazkova P, Schröffel J, Davoli R, *et al.* (2003). Linkage and QTL mapping for Sus scrofa chromosome 4. Journal of Animal Breeding and Genetics 120(1):28-37.

Chen NX, White BD, Hausman GJ (1995). Glucocorticoid receptor binding in porcine preadipocytes during development. Journal of Animal Science 73:722-727.

Chen Y, Lübberstedt T (2010). Molecular basis of trait correlations. Trends in Plant Science 15(8):454-61.

Chen C, Ai H, Ren J, Li W, Li P, Qiao R, *et al.* (2011). A global view of porcine transcriptome in three tissues from a full-sib pair with extreme phenotypes in growth and fat deposition by paired-end RNA sequencing. BMC Genomics 12:448.

Chen C, Yang B, Zeng Z, Liu C, Ren J, Huang L (2013a). Genetic dissection of blood lipid traits by integrating genome-wide association study and gene expression profiling in a porcine model. BMC genomics 14:848.

Chen QM, Wang H, Zeng YQ, Chen W (2013b). Developmental changes and effect on intramuscular fat conent of H-FABP and A-FABP mRNA expression in pigs. Journal of Applied Genetics 54:119-123.

Cho DY, Kim YA, Przytycka TM (2012). Chapter 5: Network biology approach to complex diseases. Plos Comuptational Biology 8(12):e1002820.

Choi JW, Chung WH, Lee KT, Cho ES, Lee SW, Choi BH, *et al.* (2015). Whole-genome resequencing analysis of five pig breeds, including Korean wild and native, and three European origin breeds. DNA Research 22(4):259-267.

Ciobanu DC, Bastiaansen J, Lonergan SM, Thomsen H, Dekkers JCM, Plastow GS, *et al.* (2004). New alleles in calpastatin gene are associated with meat quality traits in pigs. Journal of Animal Science 82(10):2829:39.

Cisneros F, Ellis M, McKeith FK, McCaw J, Fernando RL (1996). Influence of slaughter weight on growth and carcass characteristics, commercial cutting and curing yields, and meat quality of barrows and gilts from two genotypes. Journal of Animal Science 74:925-933.

Civelek M, Lusis AJ (2014). Systems genetics approaches to understand complex traits. Nature Reviews Genetics 15(1):34-48.

Clop A, Cercos A, Tomas A, Perez-Enciso M, Varona L, Noguera JL, *et al.* (2002). Assignment of the 2,4-dienoyl-coa reductase (DECR) gene to porcine chromosome 4. Animal Genetics 33(2):164-165.

Clop A, Óvilo C, Pérez-Enciso M, Cercos A, Tomás A, Fernández AI, *et al.* (2003). Detection of QTL affecting fatty acid composition in the pig. Mammalian Genome 14: 650-656.

Corella D, Peloso G, Arnett DK, Demissie S, Cupples LA, Tucker K, *et al.* (2009). APOA2, dietary fat, and body mass index: replication of a gene-diet interaction in 3 independent populations. Archives of Internal Medicine 169(20):1897-906.

Corominas J, Ramayo-Caldas Y, Castelló A, Muñoz M, Ibáñez-Escriche N, Folch JM, *et al*. (2012). Evaluation of the porcine ACSL4 gene as a candidate gene for meat quality traits in pigs. Animal Genetics 43(6):714-20.

Corominas J, Ramayo-Caldas Y, Puig-Oliveras A, Pérez-Montarelo D, Noguera JL, Folch JM, *et al.* (2013a). Polymorphism in the ELOVL6 gene is associated with a major QTL effect on fatty acid composition in pigs. Plos One 8(1):e53687.

Corominas J, Ramayo-Caldas Y, Puig-Oliveras A, Estellé J, Castelló A, Alves E, *et al.* (2013b). Analysis of porcine adipose tissue transcriptome reveals differences in de novo fatty acid synthesis in pigs with divergent muscle fatty acid composition. BMC Genomics 14:843.

Corominas J, Marchesi JA, Puig-Oliveras A, Revilla M, Estellé J, Alves E, *et al.* (2015). Epigenetic regulation of the ELOVL6 gene is associated with a major QTL effect on fatty acid composition in pigs. Genetics Selection Evolution 47:20.

D'Andrea M, Dal Monego S, Pallavicini A, Modonut M, Dreos R, Stefanon B, *et al.* (2011). Muscle transcriptome profiling in divergent phenotype swine breeds during growth using microarray and RT-PCR tools. Animal Genetics 42:501-509.

Damon M, Wyszynska-Koko J, Vincent A, Hérault F, Lebret B (2012). Comparison of muscle transcriptome between pigs with divergent meat quality phenotypes identifies genes related to muscle metabolism and structure. Plos One 7(3):e33763.

Davies AS, Kallweit E (1979). The effect of body weight and maturity on the carcass composition of pig. J Anim Breed Genetics 96(1-4):6-17.

Davoli R, Braglia S (2007). Molecular approaches in pig breeding to improve meat quality. Briefings in Functional Genomics and Proteomics 6(4):313-21.

Dekkers JCM (2004). Commercial application of marker- and gene-assisted selection in livestock: Strategies and lessons. Journal of Animal Science 82(E. Suppl.):E313-328.

Dekkers JCM, Mathur PK, Knol EF (2011). Genetic improvement of the pig. In: The genetics of the pig. CAB International, UK 390-425.

Di Luca A, Elia G, Mullen AM, Hamill RH (2013). Monitoring post mortem changes in porcine muscle through 2-D DIGE proteome analysis of Longissimus muscle exudate. Proteome Science 11:9.

Diez D, Goto S, Fahy JV, Erle DJ, Woodruff PG, Wheelock AS, *et al.* (2012). Network analysis identifies a putative role for the PPAR and type 1 interferon pathways in glucocorticoid actions in asthmatics. BMC Medical Genomics 5:27.

Ducos A (1994). Paramètres génétiques des caractères de production chez le porc. Mis au point bibliographique, Techni-porc 17: 35-67.

Doss S, Schadt EE, Drake TA, Lusis AJ (2005). Cis-acting expression quantitative trait loci in mice. Genome Research 15(5):681-91.

Eggert JM, Grant AL, Schinckel (2007). Factors affecting fat distribution in pork carcasses. The Professional Animal Scientist 23: 42-53.

Estany J, Ros-Freixedes R, Tor M, Pena RN (2014). A functional variant in the stearoyl-coA desaturase gene promoter enhances fatty acid desaturation in pork. Plos One 9(1):e86177.

Estellé J, Mercadé A, Noguera JL, Pérez-Enciso M, Óvilo C, Sánchez A*, et al.* (2005a). Effect of the porcine IGF2-intron3-G3072A substitution in an outbred Large White population and in an Iberian x Landrace cross. Journal of Animal Science 83:2723-8.

Estellé J, Sánchez A, Folch JM (2005b). Assignment of the microsomial triglyceride transfer protein large subunit (MTP) gene to porcine chromosome 8. Animal Genetics 36:354-5.

Estellé J, Pérez-Enciso M, Mercadé A, Varona L, Alves E, Sánchez A, *et al.* (2006). Characterization of the porcine FABP5 gene and its association with the FAT1 QTL in an Iberian by Landrace cross. Animal Genetics 37:589–591.

Estellé J, Fernández AI, Pérez-Enciso M, Fernández A, Rodríguez C, Sánchez A, *et al.* (2009a). A non-synonymous mutation in a conserved site of the MTTP gene is

strongly associated with protein activity and fatty acid profile in pigs. Animal Genetics 40:813-20.

Estellé J, Mercadé A, Pérez-Enciso M, Pena RN, Silió L, Sánchez A, *et al.* (2009b). Evaluation of FABP2 as candidate gene for a fatty acid composition QTL in porcine chromosome 8. Journal of Animal Breeding and Genetics 126:52-8.

Esteve-Codina A, Kofler R, Palmieri N, Bussotti G, Notredame C, Pérez-Enciso M (2011). Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics 12:552.

Esteve-Codina A, Paudel Y, Ferretti L, Raineri E, Megens HJ, Silió L, *et al.* (2013). Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. BMC genomics 14:148.

Eynard SE, Windig JJ, Leroy G, van Binsbergen R, Calus MPL (2015). The effect of rare alleles on estimated genomic relationships from whole genome sequence data. BMC Genetics 16:24.

Farajzadeh L, Hornshøj H, Momeni J, Thomsen B, Larseb J, Hedegaard J, *et al.* (2013). Pairwise comparisons of ten porcine tissues identify differential transcriptional regulation at the gene, isoform, promoter and transcription start site level. Biochemical and Biophysical Research Communications 438(2):346-352.

Fernández A, García-Casco J, De Pedro E, Silió L, Rodríguez MC (2007). Genetic antagonism between intramuscular fat content and primal cuts in Iberian pigs ?. 5 International Symposium on the Mediterranean Pig. Zaragoza : CIHEAM, 2007. p.43-46 (Options Méditerranéennes: Série A. Séminaires Méditerranéens; n. 76).

Fernández AI, Pérez-Montarelo D, Barragán C, Ramayo-Caldas Y, Ibáñez-Escriche N, Castello A, *et al.* (2012). Genome-wide linkage analysis of QTL for growth and body composition employing the Porcine SNP60 BeadChip. BMC Genomics 13:41.

Fortes MRS, Reverter A, Zhang Y, Collis E, Nagaraj SH, Jonsson NN, *et al.* (2010) Association weight matrix for the genetic dissection of puberty in beef cattle. Proceedings of the National Academy of Sciences of the United States of America 107:13642–13647.

Fujii J, Otsu K, Zorzato F, de Leon S, Khanna VK, Weiler JE, *et al.* (1991). Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia. Science 253:448-451.

Furuhashi M, Saitoh S, Shimamoto K, Miura T (2014). Fatty acid-binding protein 4 (FABP4): pathophysiological insights and potential clinical biomarker of metabolic and cardiovascular diseases. Clin Med Insights Cardiol 8(3):23-33.

Gao Y, Zhang YH, Zhang S, Li F, Wang S, Dai L, *et al.* (2011). Association of A-FABP gene polymorphism in intron 1 with meat quality traits in Junmu No. 1 white swine. Gene 487:170-173.

García-Alcalde F, Okonechnikov K, Carbonell J, Cruz LM, Götz S, Tarazona S, *et al.* (2012). Qualimap: evaluating next-generation sequencing alignment data. Bioinformatics 28(20):2678-2679.

Gerbens F, Jansen A, van Erp AJM, Harders F, Meuwissen THE, Rettenberger G, *et al.* (1998). The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs. Mammalian Genome 9:1022-1026.

Gerbens F, de Koning DJ, Harders FL, Meuwissen TH, Janss LL, Groenen MA, *et al.* (2000). The effect of adipocyte and heart fatty acid-binding protein genes on intramuscular fat and backfat content in Meishan crossbred pigs. Journal of Animal Science 78:552–559.

Gerbens F, Verburg FJ, Van Moerkerk HT, Engel B, Buist W, Veerkamp JH, *et al.* (2001). Associations of heart and adipocyte fatty acid-binding protein gene expression with intramuscular fat content in pigs. Journal of Animal Science 79:347–354.

Ghosh M, Sodhi SS, Song KD, Kim JH, Mongre RK, Sharma N, *et al.* (2015). Evaluation of body growth and immunity-related differentially-expressed genes through deep RNA sequencing in piglets of Jeju native pig and Berkshire. Animal Genetics 46(3):255-64.

Gilad Y, Rifkin SA, Pritchard JK (2008). Revealing the architecture of gene regulation: the promise of eQTL studies. Trends in Genetics 24(8):408-415.

Glatz JFC, Luiken JJFP, Bonen A (2010). Membrane fatty acid transporters as regulators of lipid metabolism: Implications for metabolic disease. Physiological Reviews 90(1):367-417.

Groenen MAM, Archibald AL, Uenishi H, Tuggle CK, Takeuchi Y, Rothschild MF, *et al.* (2012). Analyses of pig genomes provide insight into porcine demography and evolution. Nature 491:393-398.

Grunert K (2005). Food quality and safety: consumer perception and demand. European Review of Agricultural Economics 32:369-391.

Gu Y, Schinckel AP and Martin TG (1992). Growth, development and carcass composition in five genotypes of swine. Journal of Animal Science 70:1719–1729.

Gudbjartsson DF, Walters GB, Thorleifsson G, Stefansson H, Halldorsson BV, Zusmanovich P, *et al.* (2008). Many sequence variants affecting diversity of adult human height. Nature Genetics 40:609–615.

Guillou H, Zadravec D, Martin PGP, Jacobsson A (2010). The key roles of elongases and desaturases in mammalian fatty acid metabolism: Insights from transgenic mice. Progress in Lipid Research 49(2):186-199.

Haley CS, Archibald AL, Andersson L, Bosma AA, Davies W, Fredholm M, *et al.* (1990). The pig gene mapping project - pigmap. In: 4th World Congress on Genetics Applied to Livestock Production, Edinburgh, p 67-70.

Hamill RM, Aslan O, Mullen AM, O'Doherty JV, McBryan J, Morris DG, *et al.* (2013). Transcriptome analysis of porcine M. semimembranosus divergent in intramuscularfat as a consequence of dietary protein restriction. BMC Genomics 14:453.

Harm-Jan W, Franke L (2014). From genome to function by studying eQTLs. Biochimica et Biophysica Acta 1842:1895-1902.

Hayes B, Goddard ME (2001). The distribution of the effects of genes affecting quantitative traits in livestock. Genetics Selection Evolution 33:209-229.

Headon D (2013). Systems biology and livestock production. Animal 7(12):1959-1963.

Heidt H, Cinar MU, Uddin MJ, Looft C, Jüngst H, Tesfaye D, *et al.* (2013). A genetical genomics approach reveals new candidates and confirms know candidate genes for drip loss in a porcine resource population. Mammalian Genome 24:416-426.

Hermesch S, Luxford BG, Graser HU (2000). Genetic parameters for lean meat yield, meat quality, reproduction and feed efficiency traits for Australian pigs. 3. Description of traits and heritability estimates. Livestock Production Science 65:239-248.

Hill WG (2010). Understanding and using quantitative genetic variation. Philosophical Transactions of the Royal Society B 365:73-85.

Hitzemann R, Bottomly D, Darakjian P, Walter N, Iancu O, Searles R, *et al.* (2013). Genes, behavior and next-generation RNA sequencing. Genes, Brain and Behavior 12:1-12.

Hoashi S, Hinenoya T, Tanaka A, Ohsaki H, Sasazaki S, Taniguchi M, *et al.* (2008). Association between fatty acid compositions and genotypes of FABP4 and LXR-alpha in Japanese Black cattle. BMC Genetics 9:84.

Huisman A, Charagu P (2013). A Genomic Future. London Swine Conference - Managing For Production, 27-28 march 2013. p.9-13.

Iankova I, Chavey C, Clapé C, Colomer C, Guérineau NC, Grillet N, *et al.* (2008) Regulator of G protein signaling-4 controls fatty acid and glucose homeostasis. Endocrinology 149(11):5706-5712.

IBMAP_Consortium (1996). An experiment to detect qtls affecting meat quality in Iberian and Landrace breeds. In: Proc. 6th World Congress of Genetics Applied to Livestock Production, Armidale, Australia. p 316-319.

Janky R, Verfaillie A, Imrichová H, Van de Sande B, Standaert L, Christiaens V, *et al.* (2014). iRegulon: From a Gene List to a Gene Regulatory Network Using Large Motif and Track Collections. Plos Computational Biology 10(7): e1003731.

Jiang S, Wei H, Song T, Yang Y, Peng J, Jiang S (2013). Transcriptome comparison between porcine subcutaneous and intramuscular stromal vascular cells during adipogenic differentiation. Plos One 8(10):e77094.

Johansen CT, Kathiresan S, Hegele RA (2011). Genetic determinants of plasma triglycerides. Journal of Lipid Research 52:189-206.

Johansson K, Andersson K, Sigvardsson J (1987). Evaluation of station testing of pigs III. Genetic parameters for carcass measurements of partially dissected pigs. Acta Agriculturae Scandinavica 37:120-129.

Joo ST, Kim GD, Hwang YH, Ryu YC (2013). Control of fresh meat quality through manipualtion of muscle fiber characteristics. Meat Science 95:828-836.

Jung WY, Kwon SG, Son M, Cho ES, Lee Y, Kim JH, *et al.* (2012). RNA-Seq approach for genetic improvement of meat quality in pig and evolutionary insight into the substrate specificity of aimla carbonyl reductases. Plos One 7(9):e42198.

Kadarmideen HN (2014). Genomics to systems biology in animal and veterinary sciences: progress, lessons and opportunities. Livestock Science 166:232-248.

Kanis E, De Greef KH, Hiemstra A, van Arendonk JAM (2005). Breeding for societally important traits in pigs. Journal of Animal Science 83:948-957.

Kiens B (2006). Skeletal muscle lipid metabolism in exercise and insulin resistance. Physiological Reviews 86:205-243.

Kim JH, Lim HT, Park EW, Rodríguez C, Silió L, Varona L, *et al.* (2006). Polymorphisms in the promoter region of the porcine acyl-coA dehydrogenase, medium-chain (ACADM) gene have no effect on fat deposition traits in a pig Iberian x Landrace cross. Animal Genetics 37:430-431.

Knott S, Marklund L, Haley C, Andersson K, Davies W, Ellegren H, *et al.* (1998). Multiple marker mapping of quantitative trait loci in a cross between outbred wild boar and Large White pigs. Genetics 149:1069-1080.

Li H, Homer N (2010). A survey of sequence alignment algorithms for next-generation sequencing. Briefings in bioinformatics 2(5):473-483.

Liaubet L, Lobjois V, Faraut T, Tircazes A, Benne F, Iannuccelli N, *et al.* (2011). Genetic variability of transcript abundance in pig peri-mortem skeletal muscle: eQTL localized genes involved in stress response, cell death, muscle disorders and metabolism. BMC Genomics 12:548.

Linville RC, Pomp D, Johnson RK, Rothschild MF (2001). Candidate gene analysis for loci affecting litter size and ovulation rate in swine. Journal of Animal Science 79:60-67.

Liu J, Damon M, Guitton N, Guisle I, Ecolan P, Vincent A, *et al.* (2009). Differentially-expressed genes in pig longissimus muscles with contrasting levels of fat, as identified by combined transcriptomic, reverse transcritpion PCR, and proteomic analyses. Journal of Agricultural and Food Chemistry 57:3808-3817.

Ma J, Yang J, Zhou L, Ren J, Liu X, Zhang H, *et al.* (2014). A splice mutation in the PHKG1 gene causes high glycogen content and low meat quality in pig skeletal muscle. Plos Genetics 10(10):e10004710.

Mackay TFC, Stone EA, Ayroles JF (2009). The genetics of quantitative traits: challenges and prospects. Nature Review Genetics 10:565-577.

Manolio TA, Collins FS, Cox NJ, Goldstein DB, Hindorff LA, Hunter DJ, *et al.* (2009) Finding the missing heritability of complex diseases. Nature 461, 747–753.

Marklund S, Kijas J, Rodríguez-Martínez H, Rönnstrand L, Funa K, Moller M, *et al.* (1998). Molecular basis for the dominant white phenotype in the domestic pig. Genome Research 8(8):826-33.

Marklund L, Nyström P, Stern S, Andersson-Eklund L, Andersson L (1999). Confirmed quantitative trait loci for fatness and growth on pig chromosome 4. Heredity 82:134-141.

Martin J, Sykes S, Young S, Kota K, Sanka R, Sheth N, *et al.* (2012). Optimizing read mapping to reference genomes to determine composition and species prevalence in microbial communities. Plos One 7(6):e36427.

Mercadé A, Estellé J, Noguera J, Folch JM, Varlona L, Silió L, *et al.* (2005a). On growth, fatness, and form: A further look at porcine Chromosome 4 in an Iberian x Landrace cross. Mammalian Genome 16:374-82.

Mercadé A, Sánchez A, Folch JM (2005b). Exclusion of the acyl CoA: diacylglycerol acyltransferase 1 gene (DGAT1) as a candidate for a fatty acid composition QTL on porcine chromosome 4. Journal of Animal Breeding and Genetics, 122:161-164.

Mercadé A, Sánchez A, Folch JM (2005c). Assignment of the acyl-CoA synthetase long-chain family member 4 (ACSL4) gene to porcine chromosome X. Animal Genetics 36(1):76.

Mercadé A, Estellé J, Pérez-Enciso M, Varona L, Silió L, Noguera JL, *et al.* (2006a). Characterization of the porcine acyl-CoA synthetase long-chain 4 (ACSL4) gene and its association with growth and meat quality traits. Animal Genetics 3:219-24.

Mercadé A, Pérez-Enciso M, Varona L, Alves E, Noguera JL, Sánchez A, *et al.* (2006b). Adipocyte fatty-acid binding protein is closely associated to the porcine FAT1 locus on chromosome 4. Journal of Animal Science 84:2907–2913.

Mercadé A, Sánchez A, Folch JM (2007). Characterization and physical mapping of the porcine CDS1 and CDS2 genes. Animal Biotechnology 18(1):23-35.

Merks JWM, Mathur PK, Knol EF (2012). New phenotypes for new breeding goals in pigs. Animal 6(4):535-543.

Meuwissen HTE, Hayes BJ, Goddard ME (2001). Prediction of total genetic value using genome-wide dense marker maps. Genetics 157:1819-1829.

Miar Y, Plastow G, Bruce H, Moore S, Manifiazar G, Kemp R, *et al.* (2014). Genetic and phenotypic correlations between performance traits with meat quality and carcass characteristics in commercial crossbred pigs. Plos One 9(10): e110105.

Miar Y, Plastow G, Wang Z (2015). Genomic selection, a new era for pork quality improvement. Springer Science Reviews 3:27-37.

Mohrmann M, Roehe R, Knap PW, Looft H, Plastow GS, Kalm E (2006). Quantitative trait loci associated with AutoFOM grading characteristics, carcass cuts and chemical body composition during growth of Sus scrofa. Animal Genetics 37:435-443.

Moller M, Berg F, Riquet J, Pomp D, Archibald A, Anderson S, *et al.* (2004). High-resolution comparative mapping of pig Chromosome 4 emphasizing the FAT1 region. Mammalian Genome 2004, 15:717–731.

Moon S, Kim TH, Lee KT, Kwak W, Lee T, Lee SW, *et al.* (2015). A genome-wide scan for signatures of directional selection in domesticated pigs. BMC Genomics 16:130.

Morozova O, Marra MA (2008). Applications of next-generation technologies in functional genomics. Genomics 92:255-264.

Muñoz G, Alves E, Fernández A, Óvilo C, Barragán C, Estellé J, *et al.* (2007). QTL detection on porcine chromosome 12 for fatty-acid composition and association analyses of the fatty acid synthase, gastric inhibitory polypeptide and acetyl-coenzyme A carboxylase alpha genes. Animal Genetics 38:639-46.

Muñoz G, Ovilo C, Silió L, Tomás A, Noguera JL, Rodríguez MC (2009). Single- and joint-population analyses of two experimental pig crosses to confirm quantitative trait loci of Sus scrofa chromosome 6 and leptin receptor effects on fatness and growth traits. Journal of Animal Science 87(2):459-68.

Muñoz M, Alves E, Ramayo-Caldas Y, Casellas J, Rodríguez C, Folch JM, *et al*. (2012). Recombination rates across porcine autosomes inferred from high-density linkage maps. Animal Genetics 43(5):620-3.

Muñoz M, Rodríguez MC, Alves E, Folch JM, Ibañez-Escriche N, Silió L, *et al.* (2013). Genome-wide analysis of porcine backfat and intramuscular fat fatty acid composition using high-density genotyping and expression data. BMC genomics 14:845.

Nagamine Y, Pong-Wong R, Visscher PM, Haley CS (2009). Detection of multiple quantitative trait loci and their pleiotropic effects in outbred pig populations. Genetics Selection Evolution 6:41-44.

Ngapo T, Dransfield E, Martina J, Magnusson M, Bredahl L, Nuted G (2003). Consumer perceptions: pork and pig production. Insights from France, England, Sweden and Denmark. Meat Science 66, 125-134.

Ntawubizi M, Colman E, Janssens S, Raes K, Buys N, De Smet S (2010). Genetic parameters for intramuscular fatty acid composition and metabolism in pigs. Journal of Animal Science 88:1286-1294.

Ohashi H, Hasegawa M, Wakimoto K, Miyamoto-Sato E (2015). Next-generation technologies for multiomics approaches including interactome sequencing. BioMed Research International 104209. doi:10.1155/2015/104209.

Óvilo C, Pérez-Enciso M, Barragán C, Clop A, Rodríguez C, Oliver MA, *et al.* (2000). A QTL for intramuscular fat and backfat thickness is located on porcine chromosome 6. Mammalian Genome 11(4):344-6.

Óvilo C, Clop A, Noguera JL, Oliver MA, Barragán C, Rodríguez C, *et al.* (2002a). Quantitative trait locus mapping for meat quality traits in an Iberian x Landrace F2 pig population. Journal of Animal Science 80:2801-2808.

Óvilo C, Oliver A, Noguera J, Clop A, Barragán C, Varona L, *et al.* (2002b). Test for positional candidate genes for body composition on pig chromosome 6. Genetics Selection Evolution 34:465-79.

Óvilo C, Fernández A, Noguera JL, Barragán C, Letón R, Rodríguez C, *et al.* (2005). Fine mapping of porcine chromosome 6 QTL and LEPR effects on body composition in multiple generations of an Iberian by Landrace intercross. Genetics Research 85:47-67.

Óvilo C, Benítez R, Fernández A, Isabel B, Núñez Y, Fernández AI, *et al*. (2014). Dietary energy source largely affects tissue fatty acid composition but has minor influence on gene transcription in Iberian pigs. Journal of Animal Science 92(3):939-54.

Orcutt MW, Forrest JC, Judge MD, Schinckel AP, Kuey CH (1990). Practical means for estimating pork carcass composition. Journal of Animal Science 68:3987-3997.

Ollivier L (1998). Genetic improvement of the pig. In MF Rothschild and A Ruvinsky (eds.) The genetics of the pig. p 511-540. CAB International, Oxon.

Owens FN, Dubeski P, Hanson CF (1993). Factors that alter the growth and development of rumiants. Journal of Animal Science 71:3138-3150.

Pabinger S, Dander A, Fischer M, Snajder R, Sperk M, Efremova M, *et al.* (2013). A survey of tools for variant analysis of next-generation genome sequencing data. Briefings in Bioninformatics Advance doi.10.1093/bib/bbs086.

Paudel Y, Madsen O, Megens HJ, Frantz LAF, Bosse M, Crooijmans RPMA, *et al.* (2015). Copy number ariation in the speciation of pigs: a posible prominent role for olfactory receptors. BMC genomics 16:330.

Pena R, Noguera JL, Casellas J, Díaz I, Fernández AI, Folch JM, *et al.* (2013). Transcriptional analysis of intramuscular fatty acid composition in the Longissimus thoracis muscle of Iberian × Landrace back-crossed pigs. Animal Genetics 44:648-660.

Pena RM, Quintanilla R, Manunza A, Gallardo D, Casellas J, Amills M (2014). Application of the microarray technology to the transcriptional analysis of muscle phenotypes in pigs. Animal Genetics 45:311-321.

Paredi G, Sentandreu MA, Mozzarelli A, Fadda S, Hollung K, de Almeida AM (2013). Muscle and meat: New horizons and applications for proteomics on a farm to fork perspective. Journal of Proteomics 88:58-82.

Pérez-Enciso M, Clop A, Noguera JL, Ovilo C, Coll A, Folch JM, *et al.* (2000). A QTL on pig chromosome 4 affects fatty acid metabolism: evidence from an Iberian by Landrace intercross. Journal of Animal Science 78:2525–2531.

Pérez-Enciso M, Clop A, Folch JM, Sánchez A, Oliver MA, Óvilo C, *et al.* (2002). Exploring alternative models for sex-linked quantitative trait loci in outbred populations: application to an Iberian x Landrace pig intercross. Genetics 161:1625-1632.

Pérez-Enciso M, Mercadé A, Bidanel JP, Geldermann H, Cepica S, Bartenschlager H, *et al.* (2005). Large-scale, multibreed, multitrait analyses of quantitative trait loci experiments: The case of porcine X chromosome. Journal of Animal Science 83:2289-96.

Pérez-Enciso M, Rincón JC, Legarra A (2015). Squence- vs. chip-assisted genomic selection: accurate biological information is adviced. Genetics Selection Evolution 47:43.

Pérez-Montarelo D, Hudson N, Fernández AI, Ramayo-Caldas Y, Dalrymple BP, Reverter A, *et al.* (2012). Porcine tissue-specific regulatory networks derived from meta-analysis of the transcriptome. Plos One 7(9):e46159.

Ponsuksili S, Jonas E, Murani E, Phatsara C, Srikanchai T, Walz C, *et al.* (2008). Trait correlated expression combined with expression QTL analysis reveals biological pathways and candidate genes affecting water holding capacity of muscle. BMC Genomics 9:367.

Ponsuksili S, Murani E, Schwerin M, Schellander K, Wimmers K (2010). Identification of expression QTL (eQTL) of genes expressed in porcine M. longissimus dorsi and associated with meat quality traits. BMC Genomics 11:572.

Ponsuksili S, Du Y, Murani E, Schwerin M, Wimmers K (2012). Elucidating molecular networks that either affect or respond to plasma cortisol concentration in target tissues of liver and muscle. Genetics 192(3):1109-22.

Ponsuksili S, Murani E, Trakooljul N, Schwerin M, Wimmers K (2014). Discovery of candidate genes for muscle traits based on GWAS supported by eQTL-analysis. International Journal of Biological Sciences 10(3):327-337.

Poulsen LI, Siersbæk M, Mandrup S (2012). PPARs: fatty acid sensors controlling metabolism. Seminars in Cell & Developmental Biology 23(6):631-9.

Puig-Oliveras A, Ramayo-Caldas Y, Corominas J, Estellé J, Pérez-Montarelo D, Hudson NJ, *et al.* (2014a). Differences in muscle transcriptome among pigs phenotipically extreme for fatty acid composition. Plos One 9(7):e103668.

Puig-Oliveras A, Ballester M, Corominas J, Revilla M, Estellé J, Fernández AI, *et al.* (2014b). A co-association network analysis of the genetic determination of pig conformation growth and fatness. Plos One 9(12):e114862.

Pugliese C, Sirtori F (2012). Quality of meat and meat products produced from southern European pig breeds. Meat Science 90:511-518.

Pullinger CR, Eng C, Salen G, Shefer S, Batta AK, Erickson SK, *et al.* (2002). Human cholesterol 7alpha-hydroxylase (CYP7A1) deficiency has a hypercholesterolemic phenotype. The Journal of Clinical Investigation 110(1):109-117.

Qiao R, Gao J, Zhang Z, Li L, Xie X, Fan Y, *et al.* (2015). Genome-wide association analyses reveal significant loci and strong candidate genes for growth and fatness traits in two pig populations. Genetics Selection Evolution 47:17.

Ramayo-Caldas Y, Mercadé A, Castelló A, Yang B, Rodríguez C, Alves E, *et al.* (2012a). Genome-wide association study for intramuscular fatty acid composition in an Iberian × Landrace cross. Journal of Animal Science 90:2883–2893.

Ramayo-Caldas Y, Mach N, Esteve-Codina A, Corominas J, Castelló A, Ballester M, *et al.* (2012b). Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. BMC Genomics 13:547.

Ramayo-Caldas Y, Ballester M, Fortes MRS, Esteve-Codina A, Castelló A, Noguera JL, *et al.* (2014a). From SNP co-association to RNA co-expression: Novel insights into

gene networks for intramuscular fatty acid composition in porcine. BMC genomics 15:232.

Ramayo-Caldas Y, Fortes MR, Hudson NJ, Porto-Neto LR, Bolormaa S, Barendse W, *et al.* (2014b). A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle. Journal of Animal Science 92(7):2832-45.

Ramírez O, Burgos-Paz W, Casas E, Ballester M, Bianco E, Olalde I, et al. (2015). Genome data from a sixteenth century pig illuminate modern breed relationships. Heredity 114:175-184.

Ramos AM, Crooijmans RPMA, Affara NA, Amaral AJ, Archibald AL, Beever JE, *et al.* (2009). Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. Plos One 4:e6524.

Rao DC (2008). An Overview of the Genetic Dissection of Complex Traits. Advances in Genetics 60:3–34.

Reiner G, Dreher F, Drungowski M, Hoeltig D, Bertsch N, Selke M, *et al.* (2014). Pathway deregulation and expression QTLs in response to Actinobacillus pleuropneumoniae infection in swine. Mammalian Genome 25(11-12):660-617.

Reverter A, Chan EK (2008). Combining partial correlation and an information theory approach to the reversed engineering of gene co-expression networks. Bioinformatics 24(21):2491-7.

Reverter A, Fortes MS (2013). Association Weight Matrix: A Network-Based Approach Towards Functional Genome-Wide Association Studies. In: Gondro C, van der Werf J, Hayes B editors. Genome-Wide Association Studies and Genomic Prediction. Methods in Molecular Biology. Humana Press Vol. 1019. pp.437–447.

Revilla M, Ramayo-Caldas Y, Castelló A, Corominas J, Puig-Oliveras A, Ibáñez-Escriche N, *et al*. (2014). New insight into the SSC8 genetic determination of fatty acid composition in pigs. Genetics Selection Evolution 46:28.

Ron M, Lwein H, Da Y, Band M, Yanai A, Blank Y, *et al.* (1995). Prediction of informativeness for microsatellite markers among progeny of sires used for detection of economic trait loci in dairy cattle. Animal Genetics 26:439-441.

Rothschild MF (2003). Advances in pig genomics and functional gene discovery. Comparative and Functional Genomics 4:266-270.

Rothschild MF, Hu Z, Jiang Z (2007). Advances in QTL mapping in pigs. International Journal of Biological Science 3(3):192-197.

Rubin CJ, Megens HJ, Barrio AM, Maqbool K, Sayyab S, Schwochow D, *et al.* (2012). Strong signatures of selection in the domestic pig genome. Proceedings of the National Academy of Sciences of the United States of America 109:19529-19536.

Rudra D, deRoos P, Chaudhry A, Niec RE, Arvey A, Samstein R, *et al.* (2012). Transcription factor Foxp3 and its protein partners form a complex regulatory network. Nature Immunology 13:1010–1019.

Schadt EE, Monks SA, Drake TA, Lusis AJ, Che N, Colinayo V, *et al.* (2003). Genetics of gene expression surveyed in maize, human and man. Nature 422(6929):297-302.

Seiquer I, Haro A, Aguilera JF, Nieto R (2013). Changes in fatty acid composition of intramuscular fat in growing Iberian and Landrace × Large White pigs under identical nutritional management. Energy and Protein Metabolism and Nutrition Insustainable Animal Production 134:431-432.

Serra X, Gil F, Pérez-Enciso M, Oliver MA, Vazquez JM, Gispert M, *et al.* (1998). A comparison of carcass, meat quality and histochemical characteristics of Iberian (Guadyerbas line) and landrace pigs. Livestock Production Science 56:215-223.

Sharma S, Sharma PM, Mistry DS, Chang RJ, Olefsky JM, Mellon PL, *et al.* (2011). PPARG regulates gonadotropin-releasing hormone signaling in Lbeta T2 cells in vitro and pituitary gonadotroph function in vivo in mice. Biology of Reproduction 84(3):466-75.

Shi Y, Burn P (2004). Lipid metabolic enzymes: emerging drug targets for the treatment of obesity. Nature Reviews Drug Discovery 3:695-710.

Smathers RL, Petersen DR (2011). The human fatty acid-binding protein family: evolutionary divergences and functions. Human Genomics 5(3): 170-191.

Sodhi SS, Song KD, Ghosh M, Sharma N, Lee SJ, Kim N, *et al.* (2014). Comparative transcriptomic analysis by RNA-Seq to discern differential expression of genes in liver and muscle tissues of adult Berkshire and Jeju Native pig. Gene 546(2):233-42.

Solovieff N, Cotsapas C, Lee PH, Purcell SM, Smoller JW (2013). Pleiotropy in complex traits: challenges and strategies. Nature Reviews Genetics 14:483-495.

Soneson C, Delorenzi M (2013). Acomparison of methods for differential expression analysis of RNA-seq data. BMC Bioinformatics 14:91.

Soranzo N, Rivadeneira F, Chinappen-Horsley U, Malkina I, Richards JB, *et al.* (2009) Meta-Analysis of Genome-Wide Scans for Human Adult Stature Identifies Novel Loci and Associations with Measures of Skeletal Frame Size. Plos Genetics 5(4):e1000445.

Spurgeon SL, Jones RC, Ramakrishnan R (2008). High throughput gene expression measurement with real time PCR in microfluidic dynamic array. Plos One 3(2):e1662.

Steibel JP, Bates RO, Rosa GJ, Tempelman RJ, Rilington VD, Ragavendran A, *et al.* (2011). Genome-wide linkage analysis of global gene expression in loin muscle tissue identifies candidate genes in pigs. Plos One 6(2):e16766.

Sun W, Yu T, Li KC (2007). Detection of eQTL modules mediated by activity levels of transcription factors. Bioinformatics 23(17):2290-2297.

Sun WX, Wang HH, Jiang BC, Zhao YY, Xie ZR, Xiong K, *et al.* (2013). Global comparison of gene expression between subcutaneous and intramuscular adipose tissue of mature Erhualian pig. Genetics and Molecular Research 12(4):5085-5101.

Syamsunarno MRAA, Iso T, Hanaoka H, Yamaguchi A, Obokata M, Koitabashi N, *et al.* (2013). A critical role of fatty acid binding protein 4 and 5 (FABP4/5) in the systemic response to fasting. Plos One 8(11):e79386.

Sławińska A, Siwek M, Knol EF, Roelofs-Prins DT, Wijk HJ, Dibbits B, *et al.* (2009). Validation of the QTL on SSC4 for meat and carcass quality traits in a commercial crossbred pig population. Journal of Animal Breeding and Genetics 126:43-51.

Tchoukalova YD, Krishnapuram R, White UA, Burk D, Fang X, Nijland MJ, *et al.* (2014). Fetal baboon sex specific outcomes in adipocyte differentiation at 0.9 gestation in response to moderate maternal nutrient reduction. Int J Obes (Lond) 38(2):224-230.

Toro MA, Silió L (1992). La mejora de la selección porcina. Porci 7:69-79.

Toro MA, Rodrigañez J, Silió L, Rodríguez C (2000). Genealogical analysis of a closed herd of black hairless Iberian pigs. Conservation biology 14:1843-1851.

Tuggle CK, Wang Y, Couture O (2007). Advances in swine transcriptomics. International Journal of Biological Sciences 3:132-152.

Van Laere AS, Nguyen M, Braunschweig M, Nezer C, Collete C, Moreau L, *et al.* (2003). A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. Nature 425:832-836.

Vaquerizas JM, Kummerfeld SK, Teichmann SA, Luscombe NM (2009). A census of human transcription factors: function, expression and evolution. Nature Reviews Genetics 10(4):252-63.

Varona L, Óvilo C, Clop A, Noguera JL, Pérez-Enciso M, Coll A, *et al.* (2002). QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects. Genetical Research 80:145-154.

Verdugo RA, Farber CR, Warden CH, Medrano JF (2010). Serious limitations of the QTL/Microarray approach for QTL gene discovery. BMC Biology 8:96.

Veroneze R, Lopes PS, Guimarães SE, Silva FF, Lopes MS, Harlizius B, *et al.* (2013). Linkage disequilibrium and haplotype block structure in six commercial pig lines. Journal of Animal Science 91(8):3493-501.

Wagner GP, Zhang J (2011). The pleiotropic structure of the genotype-phenotype map: the evolvability of complex organisms. Nature Reviews Genetics 12:204-213.

Wahly W, Michalik L (2012). PPARs at the crossroads of lipid signaling and inflammation. Trens in Endocrinology and Metabolism 23(7):351-363.

Walling G, Visscher P, Andersson L, Rothschield M, Wang L, Moser G, *et al.* (2000). Combined analyses of data from quantitative trait loci mapping studies. Chromosome 4 effects on porcine growth and fatness. Genetics 155:1369-1378.

Wang Z, Gerstein M, Snyder M (2009a). RNA-Seq: a revolutionary tool for transcriptomics. Nature Reviews Genetics 10:57-63.

Wang Q, Guan T, Li H, Bernlohr DA (2009b). A novel polymorphism in the chicken adipocyte fatty acid binding protein gene (FABP4) that alters ligand-binding and

correlates with fatness. Comparative Biochemistry and Physiology Part B: Biochemistry and Molecular Biology 154(3):298-302.

Warden CH, Daluiski A, Bu X, Purcel-Huynh DA, De Mester C, Shieh BH, *et al.* (1993). Evidence for linkage of the apolipoprotein A-II locus to plasma apolipoprotein A-II and free fatty acid levels in mice and humans. Proceedings of the National Academy of Sciences of the United States of America 90(22):10886-10890.

Whittaker AD, Park B, Thane BR, Miller RK, Savell JW (1992). Principles of ultrasound and measurement of intramuscular fat. Journal of Animal Science 70:942-952.

Widmann P, Reverter A, Fortes MRS, Weikard R, Suhre K, Hammon H, *et al.* (2013). A systems biology approach using metabolic data reveals genes and pathways interacting to modulate divergent growth in cattle. BMC Genomics 14:798.

Wimmers K, Murani E, Ponsuksili S (2010). Functional genomics and genetical genomics approaches towards elucidating networks of genes affecting meat performance in pigs. Briefings in Functional Genomics 9(3):251-8.

Wood JD, Enser M (1997). Factors influencing fatty acids in meat and the role of antioxidants in improving meat quality. British Journal of Nutrition 78(1):S49-60.

Wood JD, Richardson RI, Nute GR, Fisher AV, Campo MM, Kasapidou E, *et al.* (2004). Effects of fatty acids on meat quality: a review. Meat Science 66(1):21-32.

Wood J, Whittemore C (2007). Pig Meat and Carcass Quality. In: Whittemore's Science and Practice of Pig Production (pp.4-64). Blackwell Publishing Ltd.

Wu H, Gaur U, Mekchay S, Peng X, Li L, Sun H, *et al.* (2015). Genome-wide identification of allele-specific expression in response to Streptococcus suis 2 infection in two differnetially susceptible pig breeds. Journal of Applied Genetics doi.10.1007/s13353-015-0275-8.

Xing K, Zhu F, Zhai L, Liu H, Wang Z, Hou Z, *et al.* (2014). The liver transcriptome of two full-sibling Songliao black pigs with extreme differences in backfat thickness. Journal of Animal Science and Biotechnology 5(1):32.

Xu QL, Tang GW, Zhang QL, Huang YK, Liu YX, *et al.* (2011). The FABP4 gene polymorphism is associated with meat tenderness in three Chinese native sheep breeds. Czech Journal of Animal Science 56:1–6.

Yang B, Bassols A, Saco Y, Pérez-Enciso M (2011). Association between plasma metabolites and gene expression profiles in five porcine endocrine tissues. Genetics Selection Evolution 43:28.

Yang Y, Xie B, Yan J (2014). Application of next-generation sequencing technology in forensic science. Genomics, Proteomics and Bioinformatics 12(5):190-197.

Yu K, Shu G, Yuan F, Zhu X, Gao P, Wang S, *et al.* (2013). Fatty acid and transcriptome profiling of Longissimus dorsi muscles between pig breeds differing in meat quality. International Journal of Biological Sciences 9(1):108-118.

Yu H, Neale G, Zhang H, Lee HM, Ma Z, Zhou S, *et al.* (2014). Downregulation of Prdm16 mRNA is a specific antileukemic mechanism during HOXB4-mediated HSC expansion in vivo. Blood 124(11):1737-1747.

Zhao M, Wang Q, Wang Q, Jia P, Zhao Z (2013). Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. BMC Bioinformatics 14(11):S1.

7. ANNEXES

7. ANNEXES

7.1. Supplementary material of paper I: "Analysis of *FABP4* and *FABP5* gene expression and polymorphisms affecting pig fatty acid composition"

7.1.1. Supplementary Tables Paper I

Table S1. Markers in SSC4 for QTL scan analysis and their position in the linkage map (cM) and in the physical map (bp).

Marker	Physical position (bp)	Position in the linkage map (cM)
H3GA0011286	2876120	0.000
M1GA0005355	3457261	1.144
ALGA0022251	4040391	6.863
ASGA0017570	5863845	7.281
ASGA0017810	7367321	9.032
ASGA0017939	8511137	12.256
ASGA0017978	8756650	13.306
ASGA0018040	9005118	14.273
ALGA0022983	9946393	16.545
H3GA0011974	11887853	19.162
ALGA0023289	13259972	22.711
ASGA0018522	14945584	24.914
M1GA0005738	15395576	25.691
ALGA0023572	16449950	27.290
DRGA0004508	17887210	29.368
DRGA0004577	21990523	34.767
ALGA0024027	22978568	35.321
ASGA0019110	30926557	38.001
M1GA0005832	33879368	38.577
ALGA0024435	34631401	39.676
DIAS0003601	36472579	40.516
INRA0013802	41613692	43.562
MARC0043520	42123722	44.130
ASGA0019472	42766642	45.576
H3GA0012605	43156266	45.634
ASGA0019517	43983124	45.916
MARC0005194	44103011	46.039
ASGA0019540	44528721	46.114
ALGA0024892	46858772	46.300
INRA0014337	59098323	48.253
ALGA0025092	59777178	49.870
FABP4:g.2634_2635insC	NA	49.000
FABP5:g.3000T>G	60309543	50.367

ASGA0019785	62754567	52.122
ASGA0019801	64397825	52.683
DRGA0004818	64678175	52.892
ALGA0025326	64983207	52.994
DRGA0004850	65243711	55.035
ALGA0025401	68181201	56.678
H3GA0012847	69896058	57.731
ASGA0019960	71246232	58.257
DRGA0004852	73017408	58.652
ASGA0020455	77270738	63.283
ASGA0020148	78641029	65.080
MARC0093868	81685224	66.364
ALGA0026060	83279186	68.161
ASGA0020384	83846382	69.985
ALGA0026224	88832904	72.301
ALGA0026359	93118487	74.742
H3GA0013324	95397347	76.010
MARC0019710	98113610	77.362
ASGA0020851	98609935	78.231
ALGA0026743	99632094	79.253
ALGA0026828	101428842	80.088
ASGA0021398	109905911	83.992
ALGA0027343	109952275	84.433
M1GA0006285	113759229	86.669
ALGA0027672	114969990	88.523
DBNP0001666	116772432	90.040
M1GA0006350	117287160	91.426
MARC0081739	118719770	92.643
ASGA0021963	119233824	94.482
ALGA0028034	119763345	95.100
DRGA0005119	123202552	102.304
ALGA0028470	125919689	104.295
ASGA0022402	127645367	105.414
WUR10000042	128846322	107.175
MARC0037052	129339835	109.131
ALGA0028692	129807416	109.674
H3GA0014433	130336597	111.180
MARC0040414	130652161	113.690
H3GA0014484	131855695	115.603
MARC0047995	133799979	118.365
ASGA0023026	135296413	121.020
ASGA0023017	135600323	121.584
MARC0014258	137337942	122.397
ALGA0029474	138575812	125.271
ALGA0029732	142739989	128.931

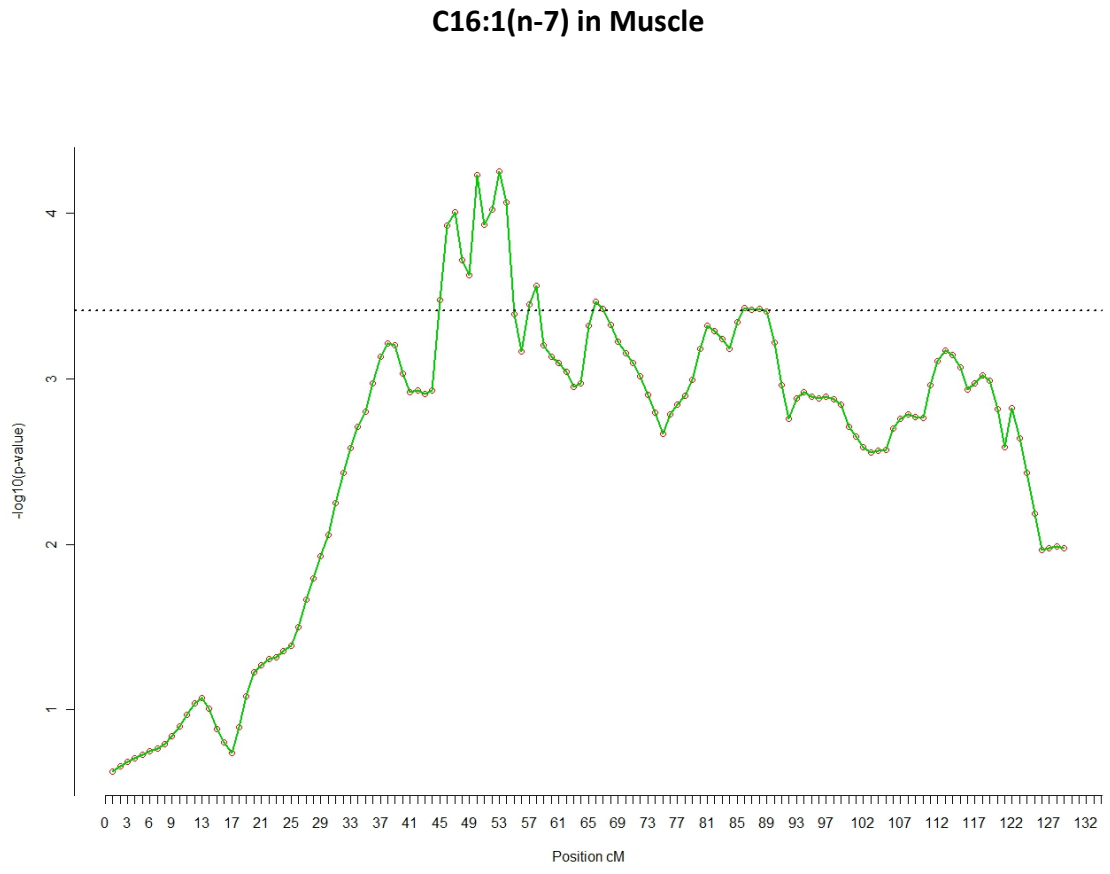
Table S2. Primers used for *FABP4* and *FABP5* gene expression quantification by RT-qPCR.

Primer Name	Description	Sequence [1]	Amplicon length	Tm	[$MgCl_2$]
FABP4-RT-Fw	RT-qPCR	5'- TAA GTT GGT GGT GGA ATG TAT CAT G -3'	106 bp	60 ºC	5 mM
FABP4-RT-Rv		5'- AGA GTG TTG TAG AGT TCG ATC CAA AC -3'			
FABP5-RT-Fw	RT-qPCR	5'- CCA ATG GAG AAT TGG TTC AAC A -3'	101 bp	60 ºC	5 mM
FABP5-RT-Rv		5'- GTT CAT GAC GCA TAC CAC CAC TA -3'			
HPRT1-RT-Fw	RT-qPCR	5'-TCA TTA TGC CGA GGA TTT GGA -3'	91 bp	60 ºC	5 mM
HPRT1-RT-Rv		5'-CTC TTT CAT CAC ATC TCG AGC AA -3'			
β2M-RT-Fw	RT-qPCR	5'-ACC TTC TGG TCC ACA CTG AGT TC -3'	100 bp	60 ºC	5 mM
β2M -RT-Rv		5'-GGT CTC GAT CCC ACT TAA CTA TCT TG -3'			

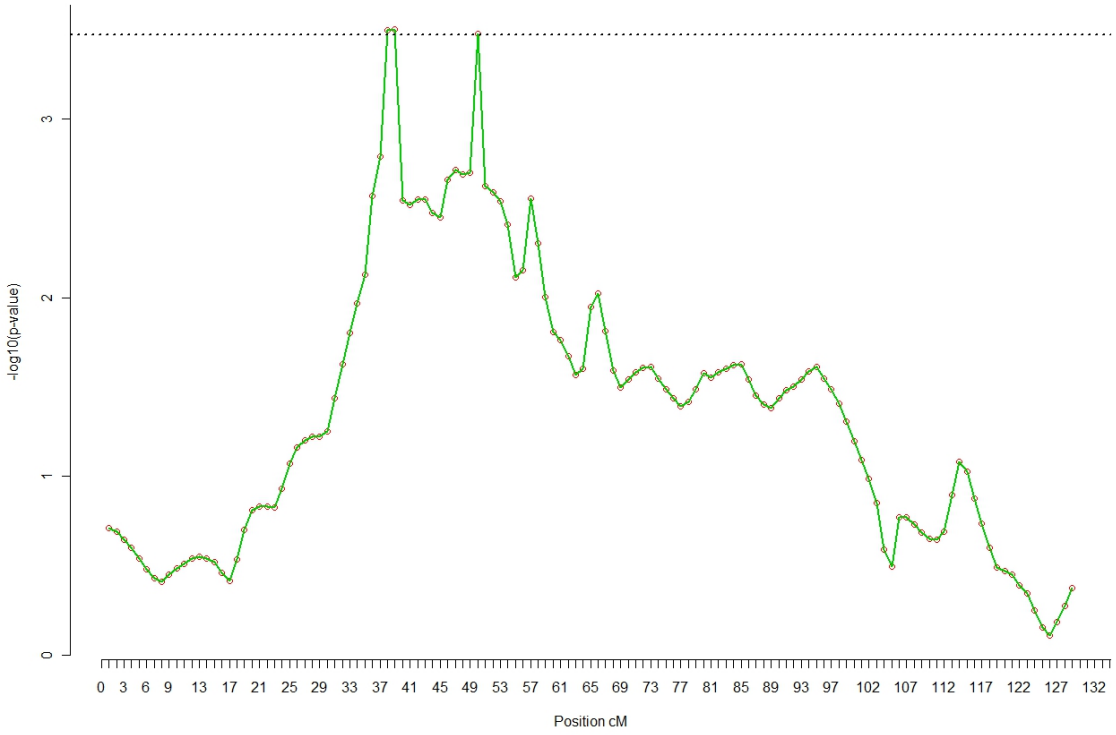
[1] Primers were designed from the GenBank Y16039 sequence

7.1.2. Supplementary Figures Paper I

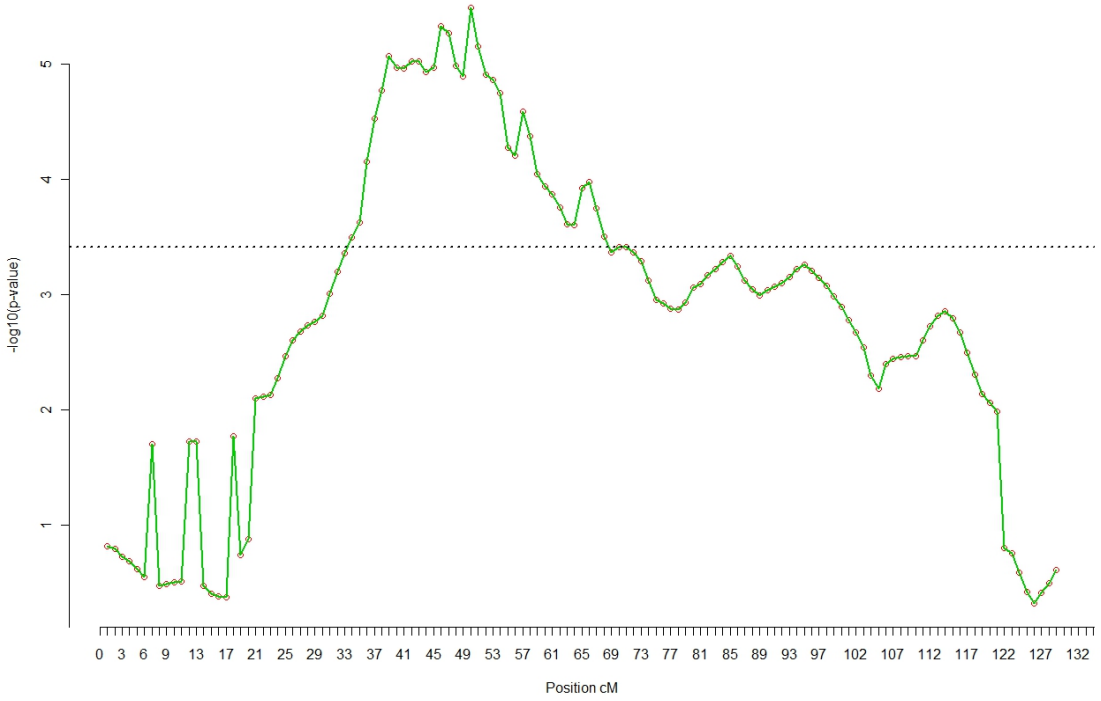
Figure S1. QTL scan with significant QTL regions. QTL scan for C16:1(n-7), C18:1(n-9), C18:2(n-6) and C20:3(n-6) FAs, PUFA and MUFA IMF content and C18:2(n-6) FA and PUFA backfat content.



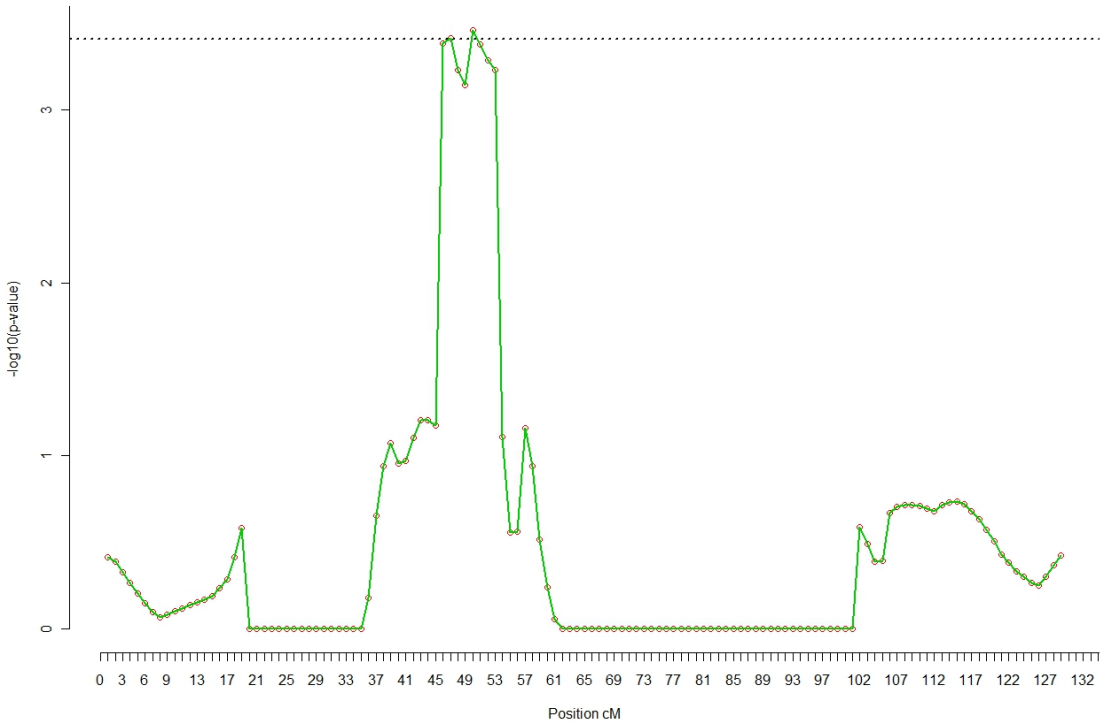
C18:1(n-9) in Muscle



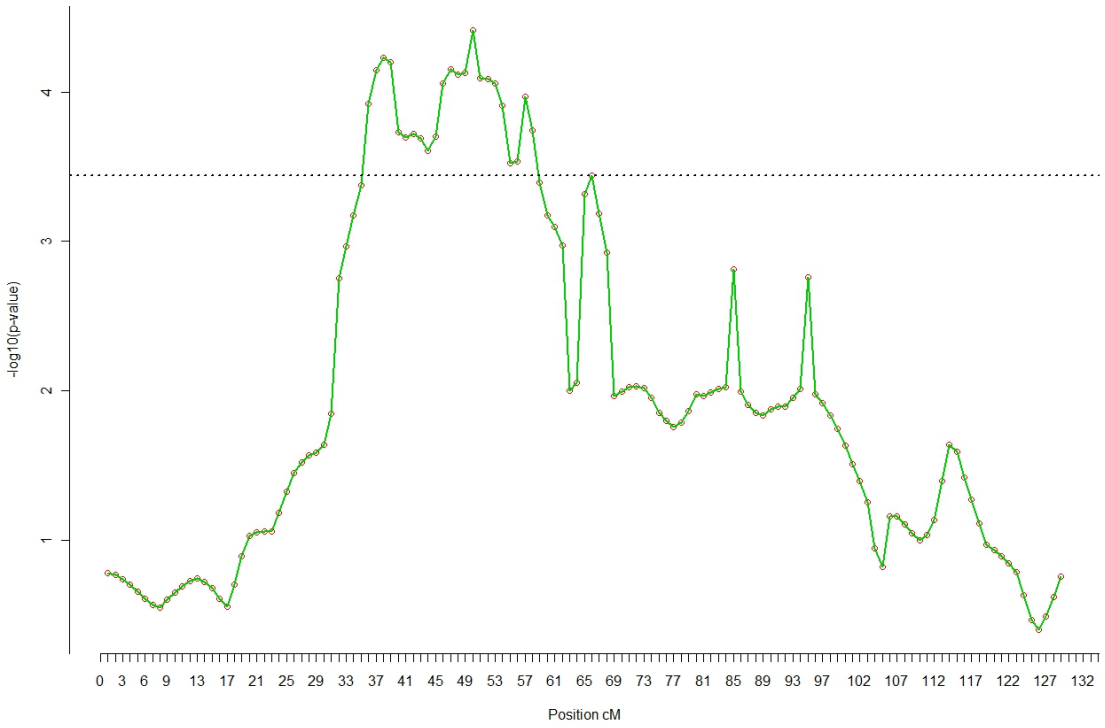
C18:2(n-6) in Muscle



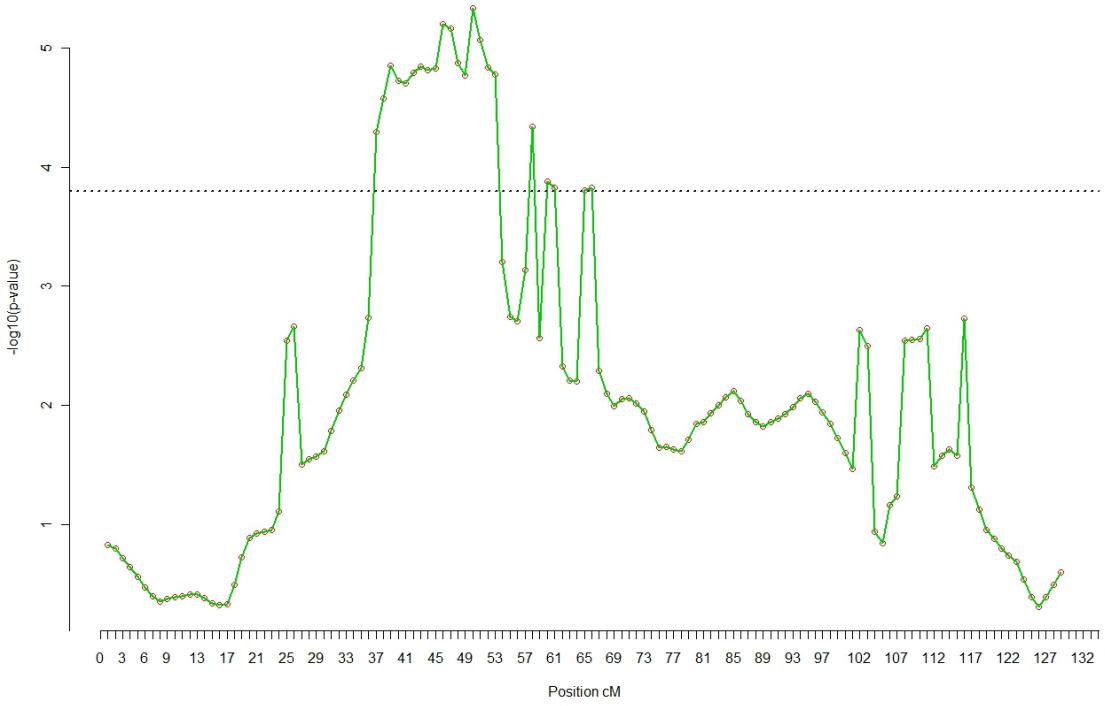
C20:3(n-6) in Muscle



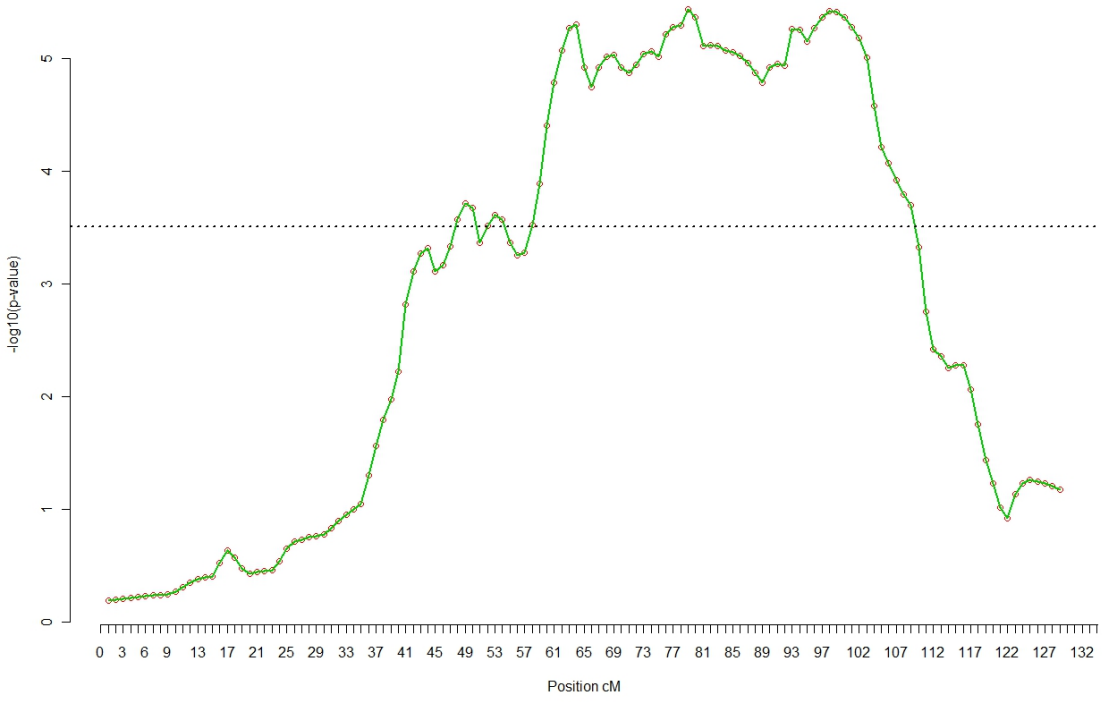
MUFA in Muscle



PUFA in Muscle



C18:2(n-6) in Backfat



PUFA in Backfat

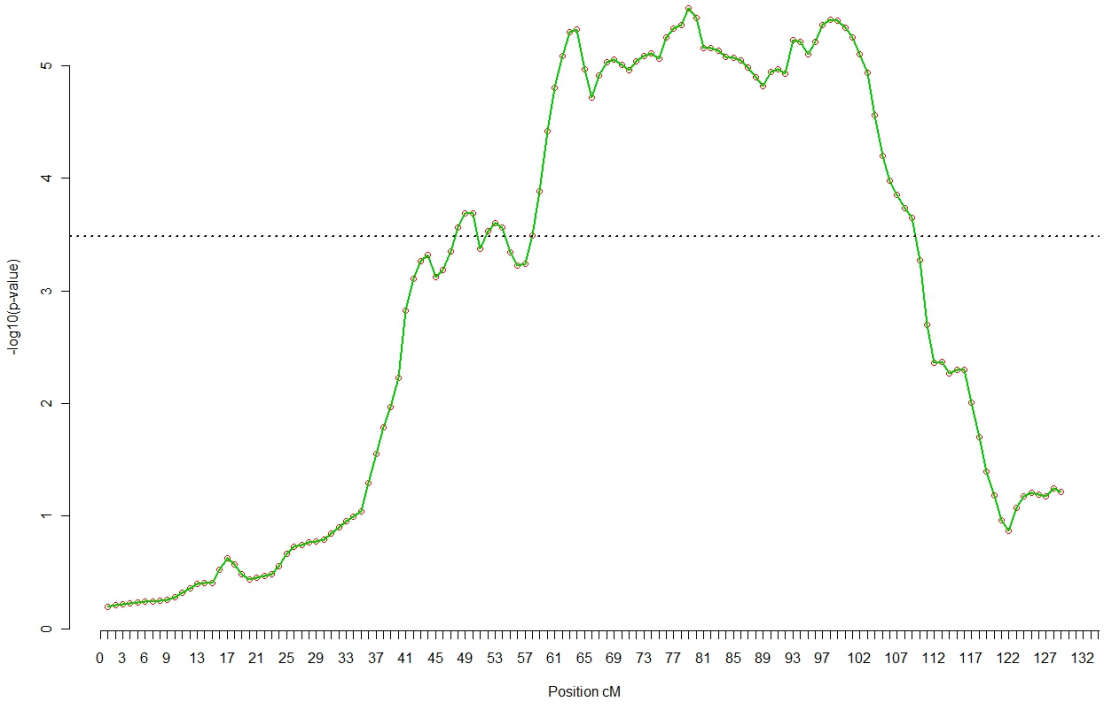
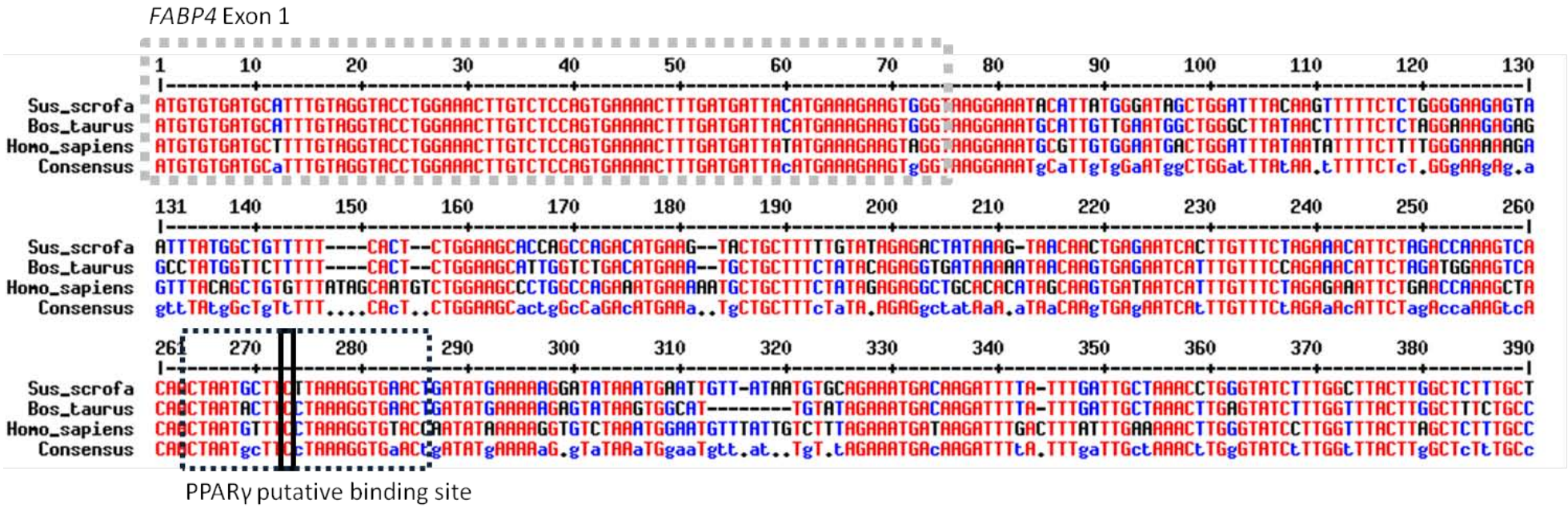


Figure S2. Multi-alignmentof porcine, cattle, and human *FABP4* gene sequence of exon 1 and proximal intron 1. This region harbours *FABP4:g.2634_2635insC* polymorphism and PPARG putative transcription factor binding site affected by this polymorphism. The grey dotted box indicates *FABP4* exon 1 region, the black dotted box indicates the PPARG putative transcription binding site, and the black continuous box *FABP4:g.2634_2635insC* polymorphism in intron 1.



7.2. Supplementary material of paper II: "Differences in muscle transcriptome among pigs phenotypically extreme for fatty acid composition"

7.2.1. Supplementary Tables Paper II

Table S1. Percentage of reads mapped for each sample and their localization (exonic, intronic or intergenic) regarding the pig reference genome sequence (Sscrofa10.2 genome assembly).

Sample	Mapped Reads (%)	Exonic Reads (%)	Intronic Reads (%)	Intergenic Reads (%)
H1	84.70	78.74	6.14	15.12
H2	85.21	80.87	5.29	13.84
H3	85.80	79.69	5.94	14.37
H4	85.09	77.51	6.77	15.71
H5	86.11	84.01	3.61	12.37
H6	86.65	80.03	5.67	14.31
L1	76.48	78.16	6.58	15.26
L2	86.64	79.22	5.80	14.98
L3	85.53	78.14	6.47	15.38
L4	85.14	77.70	6.84	15.45
L5	85.63	77.87	6.17	15.97
L6	85.49	77.91	6.19	15.90
Average	84.87	79.15	5.96	14.89

Table S2. Total number of assembled transcripts with cufflinks.

Animal	L1		L2		L3		L4		L5		L6		H1		H2		H3		H4		H5		H6		Total	Mean
	TA	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*	*TA*	*%*		
=	25,990	61	25,989	60	26,136	66	25,998	60	25,957	59	25,958	56	25,955	57	25,875	53	26,029	69	25,976	61	25,994	59	26,028	65	311,885	25,990
c	3	0	6	0	7	0	5	0	6	0	5	0	5	0	2	0	4	0	3	0	2	0	4	0	52	4
e	724	2	741	2	582	1	778	2	778	2	945	2	911	2	938	2	258	1	722	2	792	2	522	1	8,691	724
i	1,452	3	1,594	4	1,021	3	1,735	4	1,647	4	2,295	5	2,144	5	2,660	5	490	1	1,281	3	1,902	4	1,013	3	19,234	1,602
j	8,756	21	9,114	21	7,960	20	9,058	21	9,095	21	9,683	21	9,471	21	9,875	20	7,234	19	9,059	22	9,403	21	7,962	20	106,670	8,889
o	501	1	526	1	380	1	500	1	563	1	614	1	549	1	670	1	398	1	507	1	542	1	468	1	6,218	518
p	836	2	881	2	806	2	1,073	2	913	2	1,015	2	998	2	1,195	2	686	2	801	2	984	2	781	2	10,969	914
s	3	0	7	0	2	0	4	0	7	0	6	0	7	0	8	0	4	0	6	0	7	0	6	0	67	5
u	4,221	10	4,276	10	2,849	7	4,375	10	4,784	11	5,443	12	5,233	12	7,583	16	2,724	7	3,872	9	4,558	10	3,367	8	53,285	4,440
x	161	0	164	0	107	0	143	0	198	0	215	1	207	0	254	1	114	0	150	0	149	1	132	0	1,994	166
Total	**42,647**		**43,298**		**39,850**		**43,669**		**43,948**		**46,179**		**45,480**		**49,060**		**37,941**		**42,377**		**44,333**		**40,283**		**519,065**	**43,255**

= Exactly equal to the reference annotation
c Contained in the reference annotation
e Possible pre-mRNA molecule
i An exon falling into an intron of the reference
j New isoforms
o Unknown, generic overlap with reference
p Possible polymerase run-on fragment
s An intron of the transfag overlapping a reference intron on the opposite strand
u Unknown, intergenic transcript
x Exonic overlap with reference on the opposite strand
TA Transcript Assembly

Table S3. Description of the repetitive elements identified in the intergenic transcripts of the swine muscle transcriptome.

		Number of elements	Length occupied (bp)	Percentage sequence
SINEs:		54,081	10,653,056	14.12
	Alu/B1	0	0	0.00
	MIRs	10,755	1,520,033	2.01
LINEs:		24,147	11,260,471	14.92
	LINE1	17,049	9,425,600	12.49
	LINE2	6,161	1,607,095	2.13
	L3/CR1	752	181,472	0.24
	RTE	182	45,909	0.06
LTR elements:		7,062	2,567,345	3.40
	ERVL	1,695	695,439	0.92
	ERVL-MaLRs	3,462	1,143,189	1.51
	ERV_classI	1,581	631,945	0.84
	ERV_classII	87	41,151	0.05
DNA elements:		7,275	1,531,597	2.03
	hAT-Charlie	4,583	873,939	1.16
	TcMar-Tigger	1,307	389,915	0.52
Unclassified:		39	8,158	0.01
Total interespersed repeats			26,020,627	34.48
Small RNA:		113	10,536	0.01
Satellites:		8	5,395	0.01
Simple repeats:		12,310	497,650	0.66
Low complexity:		10,336	400,389	0.53

Total length: 75,471,156 bp

GC level: 43.88 %

Bases masked: 26,929,199 bp (35.68%)

Table S4. New predicted novel proteins with Augustus which have orthologous known genes identified with BLASTP option of Blast2GO. (too large to be attached, please visit the link below:

http://journals.plos.org/plosone/article/asset?unique&id=info:doi/10.1371/journal.pone.0099720.s005)

Table S5. Differentially-expressed genes identified between extreme groups (High and Low) for fatty acid composition in muscle.

Overlapping DE genes from DESeq and EdgeR analyses	Associated ID	Fold Change	*P*-value	*Q*-value	Mean Reads Low	Mean Reads High
ENSSSCG00000026478	*PADI2*	-11.89	3.60E-27	4.76E-24	326.7	27.5
ENSSSCG00000006932	*CLCA4*	-5.26	1.09E-06	1.15E-04	29.8	5.7
ENSSSCG00000006035	*ANGPT1*	-3.38	4.36E-04	1.39E-02	46.0	13.6
ENSSSCG00000020756	*FAM101A*	-3.26	5.64E-05	3.39E-03	78.7	24.2
ENSSSCG00000013513	*PLIN5*	-3.13	1.27E-09	2.58E-07	284.9	91.1
ENSSSCG00000000577	*GYS2*	-3.11	7.39E-05	4.16E-03	19.6	6.3
ENSSSCG00000010554	*SCD*	-3.08	1.29E-12	4.27E-10	660.0	214.3
ENSSSCG00000024306	*UBCH5B*	-2.89	9.46E-04	2.28E-02	37.2	12.9
ENSSSCG00000024342	*AQP4*	-2.86	1.02E-09	2.25E-07	368.1	128.7
ENSSSCG00000029099	*ERGIC3*	-2.69	2.12E-04	9.51E-03	19.7	7.3
ENSSSCG00000002292	*PLEKHH1*	-2.68	6.41E-04	1.77E-02	41.9	15.6
ENSSSCG00000006245	*SDR16C5*	-2.60	6.13E-05	3.60E-03	38.5	14.8
ENSSSCG00000017947	*ACADVL*	-2.33	5.32E-05	3.27E-03	512.5	219.8
ENSSSCG00000017501	*PNMT*	-2.27	1.19E-03	2.77E-02	79.5	35.1
ENSSSCG00000010635	*ZDHHC6*	-2.26	4.43E-03	6.97E-02	39.3	17.4
ENSSSCG00000011848	*TFRC*	-2.24	1.05E-06	1.15E-04	2848.1	1269.2
ENSSSCG00000008959	*CXCL2*	-2.21	2.73E-05	2.12E-03	186.8	84.4
ENSSSCG00000016958	*PIK3R1*	-2.19	2.25E-05	1.80E-03	77.9	35.6
ENSSSCG00000009079	*INTU*	-2.16	8.64E-03	1.14E-01	30.4	14.1
ENSSSCG00000010348	*CDHR1*	-2.13	6.16E-03	8.93E-02	75.0	35.2
ENSSSCG00000023287	*MYL6B*	-2.10	2.57E-03	4.90E-02	1224.3	583.3
ENSSSCG00000006003	*MAL2*	-2.08	5.05E-04	1.53E-02	43.0	20.7
ENSSSCG00000011755	*NCEH1*	-2.08	8.57E-05	4.72E-03	166.8	80.2
ENSSSCG00000007288	*MYH7B*	-2.07	1.05E-04	5.33E-03	3034.6	1468.2
ENSSSCG00000029304	*STEAP3*	-2.03	2.58E-04	1.10E-02	225.8	111.4
ENSSSCG00000029558	*EXTL1*	-1.99	3.18E-03	5.57E-02	202.3	101.6
ENSSSCG00000004248	*PLN*	-1.97	9.52E-05	5.04E-03	4710.5	2385.2
ENSSSCG00000007909	*ABAT*	-1.97	3.48E-03	5.82E-02	36.8	18.7
ENSSSCG00000009074	*C4ORF29*	-1.94	1.43E-04	7.01E-03	411.3	212.1
ENSSSCG00000024681	*TECRL*	-1.92	1.19E-03	2.77E-02	496.8	258.6
ENSSSCG00000023806	*LRRN1*	-1.89	2.63E-03	4.97E-02	108.8	57.5
ENSSSCG00000025527	*FABP3*	-1.87	5.23E-04	1.57E-02	589.7	315.8
ENSSSCG00000005449	*PTPN3*	-1.86	1.67E-03	3.51E-02	282.7	152.2
ENSSSCG00000029058	*C14H10orf116*	-1.85	8.75E-04	2.12E-02	173.7	93.6
ENSSSCG00000023548	*GSTCD*	-1.83	1.12E-03	2.65E-02	135.5	74.2
ENSSSCG00000002383	*FOS*	-1.81	2.63E-07	3.48E-05	4424.6	2441.5
ENSSSCG00000010992	*AQP7*	-1.80	4.42E-03	6.97E-02	162.3	90.0
ENSSSCG00000003546	*FABP3*	-1.77	1.48E-03	3.16E-02	703.8	397.4
ENSSSCG00000017498	*PPP1R1B*	-1.77	1.37E-03	3.02E-02	83.9	47.5
ENSSSCG00000007227	*ID1*	-1.76	6.32E-03	8.96E-02	155.7	88.5
ENSSSCG00000024954	*FGF1*	-1.75	4.15E-04	1.39E-02	519.5	297.0

ENSSSCG00000010537	*GOT1*	-1.73	2.88E-04	1.16E-02	5639.9	3259.7
ENSSSCG00000007094	*ENSSSCG00000007094*	-1.73	9.07E-03	1.18E-01	172.2	99.7
ENSSSCG00000010456	*PANK1*	-1.73	8.85E-03	1.16E-01	137.2	79.5
ENSSSCG00000015886	*ITGB6*	-1.72	1.48E-03	3.16E-02	619.4	360.1
ENSSSCG00000010631	*GPAT*	-1.72	2.23E-03	4.50E-02	1032.8	600.5
ENSSSCG00000004602	*TEX9*	-1.71	2.30E-04	1.01E-02	593.0	346.1
ENSSSCG00000005437	*KLF2*	-1.71	4.29E-05	2.88E-03	504.3	295.0
ENSSSCG00000011218	*SLC4A7*	-1.71	1.37E-03	3.02E-02	659.9	386.7
ENSSSCG00000009534	*BIVM*	-1.71	2.68E-04	1.13E-02	1372.1	804.4
ENSSSCG00000026078	*GLCE*	-1.67	4.35E-04	1.39E-02	568.7	339.6
ENSSSCG00000009865	*TBX3*	-1.67	3.77E-03	6.19E-02	330.4	197.6
ENSSSCG00000011557	*CIDE-C*	-1.67	6.17E-04	1.74E-02	128.3	77.0
ENSSSCG00000001844	*PLIN1*	-1.65	8.36E-06	7.13E-04	183.2	111.1
ENSSSCG00000021281	*TRIP10*	-1.65	5.57E-04	1.60E-02	165.0	100.0
ENSSSCG00000006769	*MCT1*	-1.65	3.79E-04	1.33E-02	1607.4	975.4
ENSSSCG00000027030	*BDKRB2*	-1.65	9.97E-03	1.27E-01	45.2	27.4
ENSSSCG00000027344	*ATP2A2*	-1.64	3.44E-04	1.25E-02	5961.3	3633.3
ENSSSCG00000030197	*CD2AP*	-1.62	6.39E-03	8.99E-02	357.1	219.8
ENSSSCG00000007077	*ESF1*	-1.62	6.56E-03	9.13E-02	617.1	380.3
ENSSSCG00000004215	*KIAA0408*	-1.60	2.76E-03	5.11E-02	632.9	395.4
ENSSSCG00000014827	*PLEKHB1*	-1.59	2.93E-03	5.28E-02	203.7	127.8
ENSSSCG00000006682	*POLR3GL*	-1.59	4.92E-03	7.48E-02	1105.2	693.7
ENSSSCG00000002831	*IRX3*	-1.59	2.06E-03	4.26E-02	427.3	268.5
ENSSSCG00000011477	*ACOX2*	-1.59	4.61E-03	7.17E-02	427.5	268.7
ENSSSCG00000017759	*ALDOA*	-1.58	4.53E-05	2.92E-03	230.8	145.9
ENSSSCG00000016991	*DUSP1*	-1.57	6.99E-05	4.02E-03	5735.8	3657.6
ENSSSCG00000010893	*FH*	-1.57	5.69E-03	8.36E-02	360.5	230.1
ENSSSCG00000006857	*COL11A1*	-1.56	3.14E-03	5.54E-02	95.6	61.2
ENSSSCG00000010429	*PRKG1*	-1.56	4.71E-03	7.25E-02	552.3	353.8
ENSSSCG00000023264	*IDH1*	-1.55	3.44E-03	5.80E-02	426.0	274.3
ENSSSCG00000001723	*PAF-AH*	-1.55	6.02E-04	1.71E-02	1600.8	1031.9
ENSSSCG00000000555	*ITPR2*	-1.54	6.26E-03	8.94E-02	290.2	187.9
ENSSSCG00000014889	*NDUFC2*	-1.53	3.72E-03	6.15E-02	211.3	138.2
ENSSSCG00000008504	*CRIM1*	-1.50	2.72E-03	5.07E-02	652.4	434.1
ENSSSCG00000022099	*TP53INP2*	-1.49	5.63E-03	8.31E-02	4778.1	3200.2
ENSSSCG00000029683	*ENSSSCG00000029683*	-1.48	8.05E-04	2.03E-02	425.6	287.0
ENSSSCG00000006866	*DBT*	-1.45	6.03E-03	8.81E-02	783.1	539.1
ENSSSCG00000003909	*PIK3R3*	-1.44	9.10E-03	1.18E-01	722.9	500.3
ENSSSCG00000008237	*RETSAT*	-1.43	4.04E-03	6.56E-02	843.3	591.4
ENSSSCG00000010532	*LOXL4*	-1.36	8.23E-04	2.05E-02	224.7	165.4
ENSSSCG00000010678	*NANOS1*	1.78	4.54E-06	4.41E-04	249.7	443.5
ENSSSCG00000015854	*OCA2*	1.79	5.21E-03	7.78E-02	40.8	73.0
ENSSSCG00000010850	*ENAH*	1.80	3.14E-07	3.96E-05	1645.3	2961.6
ENSSSCG00000016983	*STC2*	1.80	8.05E-04	2.03E-02	291.6	525.9
ENSSSCG00000015986	*HOXD1*	1.81	1.86E-04	8.63E-03	98.5	178.3
ENSSSCG00000012142	*AP1S2*	1.83	5.36E-04	1.58E-02	44.7	81.6

ENSSSCG00000021205	*MST4*	1.87	2.04E-04	9.29E-03	92.1	172.2
ENSSSCG00000002279	*GPX2*	1.92	3.44E-03	5.80E-02	19.0	36.4
ENSSSCG00000001097	*FAM65B*	1.93	3.19E-05	2.41E-03	297.0	571.9
ENSSSCG00000010464	*PPP1R3C*	1.94	3.73E-05	2.74E-03	4374.7	8479.0
ENSSSCG00000014362	*HBEGF*	1.95	1.85E-07	2.72E-05	1155.8	2258.5
ENSSSCG00000011265	*CMYA1*	1.96	2.37E-03	4.71E-02	62973.1	123374.9
ENSSSCG00000013374	*KCNC1*	1.96	7.69E-04	2.01E-02	98.1	192.3
ENSSSCG00000027428	*ENHO*	1.96	9.45E-06	7.81E-04	618.6	1215.5
ENSSSCG00000030165	*MAFF*	2.00	3.83E-04	1.33E-02	427.6	854.5
ENSSSCG00000010974	*CNTFR*	2.02	4.84E-06	4.41E-04	738.2	1494.8
ENSSSCG00000021104	*Pseudogene*	2.08	3.35E-03	5.80E-02	66.6	138.2
ENSSSCG00000028384	*RND3*	2.08	1.11E-08	2.10E-06	720.8	1498.2
ENSSSCG00000017251	*SOX9*	2.10	7.57E-03	1.02E-01	42.6	89.2
ENSSSCG00000020701	*TTC9*	2.11	2.87E-08	4.47E-06	1191.0	2512.7
ENSSSCG00000010219	*ARID5B*	2.12	6.90E-06	6.08E-04	2323.1	4936.4
ENSSSCG00000008973	*NAAA*	2.14	7.61E-04	2.01E-02	58.0	124.1
ENSSSCG00000015331	*PON2*	2.15	6.23E-03	8.94E-02	51.9	111.4
ENSSSCG00000023085	*STAC*	2.26	1.01E-04	5.26E-03	52.8	119.3
ENSSSCG00000015340	*ASNS*	2.32	2.75E-10	7.27E-08	401.2	931.5
ENSSSCG00000012967	*FOSL1*	2.35	3.01E-04	1.16E-02	74.9	176.2
ENSSSCG00000008348	*PLEK*	2.38	4.18E-05	2.88E-03	82.6	196.7
ENSSSCG00000028282	*SLC1A4*	2.47	4.98E-03	7.53E-02	9.9	24.5
ENSSSCG00000022913	*SLPI*	2.49	9.95E-07	1.14E-04	86.7	216.1
ENSSSCG00000024428	*CHRNA9*	2.57	1.48E-03	3.16E-02	33.9	87.2
ENSSSCG00000021569	*MMP25*	2.62	1.46E-03	3.16E-02	11.2	29.4
ENSSSCG00000015589	*VASH2*	2.63	9.13E-07	1.10E-04	47.5	124.8
ENSSSCG00000015595	*ATF3*	2.66	2.24E-13	8.46E-11	1718.3	4566.1
ENSSSCG00000029066	*IDI1*	2.71	2.97E-04	1.16E-02	31.9	86.4
ENSSSCG00000010555	*HIF1AN*	2.77	2.07E-11	6.08E-09	80.2	221.8
ENSSSCG00000004302	*C6ORF165*	2.77	7.25E-04	1.96E-02	20.3	56.3
ENSSSCG00000026686	*PDZD9*	2.78	1.92E-08	3.17E-06	161.3	447.8
ENSSSCG00000022060	*RASSF9*	2.78	9.25E-03	1.19E-01	16.3	45.2
ENSSSCG00000025136	*ACTN3*	2.83	4.79E-10	1.15E-07	10044.0	28453.2
ENSSSCG00000022059	*RPL27A*	2.84	4.96E-04	1.53E-02	17.0	48.1
ENSSSCG00000015797	*SORBS2*	3.13	4.78E-05	3.01E-03	51.8	162.4
ENSSSCG00000028568	*HSPB1*	3.35	1.87E-14	8.24E-12	231.4	775.3
ENSSSCG00000027368	*CTSF*	3.49	2.49E-07	3.47E-05	30.4	105.9
ENSSSCG00000004754	*CHAC1*	3.52	8.53E-04	2.09E-02	10.7	37.5
ENSSSCG00000003647	*FHL3*	3.79	4.35E-05	2.88E-03	15.8	59.9
ENSSSCG00000011640	*TF*	3.99	2.45E-03	4.79E-02	8.9	35.3
ENSSSCG00000024482	*HSPB1*	4.25	7.64E-24	6.74E-21	218.9	929.3
ENSSSCG00000005385	*NOR-1*	8.04	1.65E-44	4.36E-41	266.6	2144.1
ENSSSCG00000008948	*ALB*	8.69	1.13E-18	7.47E-16	32.0	278.0
ENSSSCG00000012961	*BANF1*	11.15	7.87E-16	4.16E-13	9.3	103.5

Table S6. Overrepresented categories identified with Babelomics and IPA for the differentially-expressed genes between the High and Low group.

Category	Program	*P*-value	Molecules
Lipid Metabolism	IPA	1.04×10^{-6} - 1.35×10^{-2}	*SCD, PLIN1, IDI1, PPP1R3C, PIK3R1, ATP2A2, IDH1, NCEH1, BDKRB2, NAAA, PLIN5, GOT1, FABP3, AQP7, PON2, ATF3, ACOX2, SDR16C5, CNTFR, RETSAT, FGF1, PANK1, FOS, ALB, ACADVL, DUSP1, HIF1AN, PLEK, FH, EXTL1*
Molecular Transport	IPA	1.04×10^{-6} - 1.34×10^{-2}	*SCD, SLC1A4, PLIN1, PIK3R1, PPP1R3C, AQP4, ATP2A2, IDH1, NCEH1, BDKRB2, CLCA4, KCNC1, FABP3, AQP7, ATF3, PON2, PLN, ITPR2, CHRNA9, RETSAT, FGF1, PANK1, FOS, ALB, PRKG1, ACADVL, TF, DUSP1, HIF1AN, ALDOA, TFRC, CXCL2, FH, STEAP3, EXTL1*
Small Molecule Biochemistry	IPA	1.04×10^{-6} - 1.45×10^{-2}	*SCD, PLIN1, SLC1A4, IDI1, PIK3R1, PPP1R3C, ASNS, ATP2A2, IDH1, NCEH1, BDKRB2, SOX9, NAAA, STC2, KCNC1, PLIN5, GOT1, FOSL1, FABP3, OCA2, AQP7, ATF3, PON2, ANGPT1, ITPR2, PPP1R1B, ACOX2, SDR16C5, CNTFR, HBEGF, GLCE, RETSAT, PNMT, FGF1, PANK1, FOS, ALB, PRKG1, TF, ACADVL, DUSP1, HIF1AN, TFRC, PLEK, FH, STEAP3, EXTL1*
Cell Death and Survival	IPA	1.55×10^{-6} - 1.45×10^{-2}	*SCD, TRIP10, PIK3R1, SLPI, CDHR1, ASNS, ATP2A2, BDKRB2, ID1, SOX9, CD2AP, FOSL1, SORBS2, KLF2, AQP7, PON2, ATF3, ANGPT1, ITPR2, TBX3, PPP1R1B, CNTFR, SLC4A7, HBEGF, FGF1, MST4, FOS, ALB, PRKG1, RND3, TF, DUSP1, GPX2, TFRC, ALDOA, CXCL2, STEAP3, HSPB1*
Carbohydrate Metabolism	IPA	2.25×10^{-6} - 1.31×10^{-2}	*SCD, PLIN1, PIK3R1, PPP1R3C, ATP2A2, IDH1, NCEH1, BDKRB2, KCNC1, GOT1, FABP3, AQP7, ATF3, ANGPT1, ITPR2, HBEGF, GLCE, FGF1, GYS2, PANK1, ALB, PRKG1, ACADVL, DUSP1, HIF1AN, ALDOA, COL11A1, PLEK, FH, STEAP3*
Energy Production	IPA	5.8×10^{-5} - 6.57×10^{-3}	*SCD, ALB, PON2, PRKG1, PLIN1, ACADVL, ACOX2, PLIN5, FABP3, FGF1*
Drug Metabolism	IPA	1.28×10^{-4} - 1.31×10^{-2}	*ALB, ANGPT1, PPP1R1B, GLCE, PNMT*
Skeletal and Muscular System Development and Function	IPA	2.47×10^{-4} - 1.42×10^{-2}	*ARID5B, PLN, TBX3, PIK3R1, HBEGF, FHL3, ATP2A2, MYL6B, FGF1, FOS, ID1, ALB, SOX9, PRKG1, TF, DUSP1, HIF1AN, XIRP1, ALDOA, TFRC, FOSL1, COL11A1, KLF2*
Response to organic substance	Babelomics	3.86×10^{-7}	*ANGPT1, GYS2, TFRC,PIK3R1, ABAT, FABP3, FOS, ID1, GOT1, DUSP1, IDH1, PIK3R3, SOX9, ASNS, FOSL1, HSPB1, TF, ALB*
Muscle organ development	Babelomics	3.89×10^{-5}	*PIK3R1, MYL6B, PLN, TBX3, COL11A1, FAM65B, HBEGF, ARID5B, FHL3*
Energy derivation by oxidation of organic compounds	Babelomics	1.06×10^{-4}	*GYS2, ACADVL, GOT1, FH, IDH1, NDUFC2, PPP1R3C*
Response to hormone stimulus	Babelomics	2.65×10^{-4}	*ANGPT1,PIK3R1,FABP3,FOS,GOT1,DUSP1,IDH1,PIK3R3,FOSL1*

Table S7. Specific functions identified with IPA for the differentially-expressed genes. (too large to be attached, please visit the link below: http://journals.plos.org/plosone/article/asset?unique&id=info:doi/10.1371/journal.pone.0099720.s008)

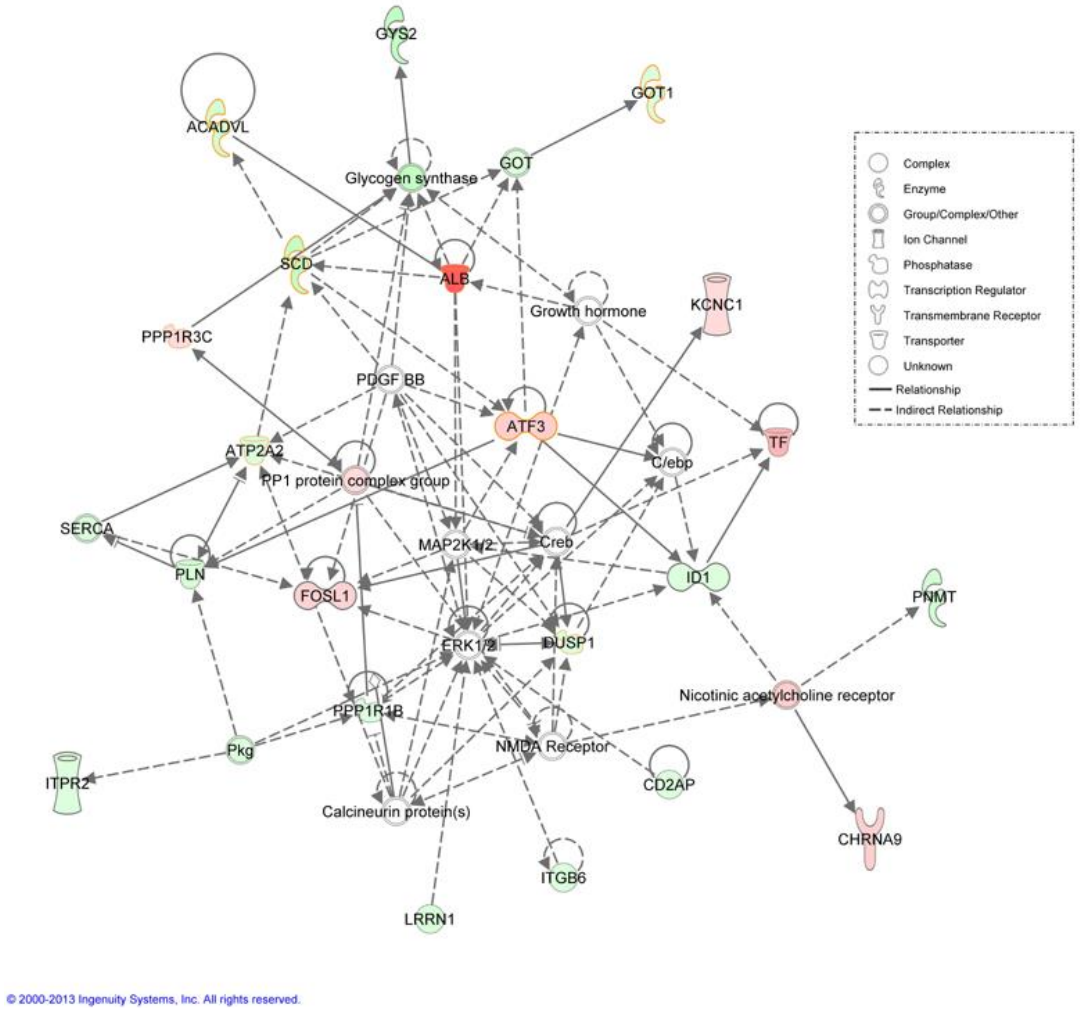
Table S8. Top networks identified with IPA from the differential expressed genes between High and Low animals.

ID	Network type	Molecules in Network
1	Direct	*Akt, Alpha tubulin, ANGPT1, Ap1, ASNS, ATF3, ATP2A2, CD2AP, Creb, CXCL2, DBT, DUSP1, ESF1, FOS, FOSL1, HSPB1, ID1, KCNC1, KLF2, NFkB (complex), OCA2, PIK3R1, PIK3R3, PLN, PPP1R1B, PRKG1, RNA polymerase II, RND3, SCD, SLPI, SORBS2, SOX9, TF, TFRC, TRIP10*
2	Direct	*ABAT, ACADVL, ACE, ALB, BDKRB2, CTSF, D-glucose, DENR, EEF2K, EIF4A3, FABP3, fatty acid, glutathione peroxidase, GPX2, HBEGF, IDH1, Insulin, KRAS, LGALS3, METAP2, miR-30c-5p (and other miRNAs w/seed GUAAACA), MRAS, NCEH1, PADI2, palmitic acid, PLEK, PLEKHB1, RASSF9, SLC4A7, sphingosine-1-phosphate, TBX3, TGFBR1, TP53, UIMC1, Zn2+*
3	Direct	*ANO1, ARID5B, BNIP3L, CHAC1, CLCA1, CLCA2, CLCA4, Clca1/Clca2, CRIM1, EIF4G1, ERGIC1, ERGIC3, GABARAPL2, GLCE, GMEB1, GOT2, GSPT1, GYS2, HPRT1, KHSRP, LRRN1, MLX, NIPSNAP1, PKMYT1, POLR3GL, PON2, PPP1R3C, RETSAT, SETD7, SSBP3, STEAP3, TP53INP2, TPT1, UBC, ZDHHC6*
4	Direct	*ACAD9, AP1G2, AP1M2, AP1S2, AP2M1, AP3M1, AQP2, AQP4, ARHGEF40, ASB9, CARHSP1, CEP57L1, EGFL7, EIF2B3, ENAH, FAT1, FGFR1OP2, FH, GOT1, HIF1AN, IDH1, IDI1, INVS, ITPR2, KIAA0408, LOXL4, MST4, MYH7B, MYL6B, NUP155, RAPH1, RRP12, STC2, UBC, XPO6*
5	Direct	*ABCC4, ABHD5, ACOX2, Acox, AHR, AQP3, AQP7, ASNS, CDHR1, CHI3L1, CHRNA9, COL11A1, COL16A1, COL6A3, ENHO, fatty acid, G6PD, GSTCD, HNF4A, LPCAT3, MAFF, MAL2, MOGS, NRF1, PKM, PLIN1, PLIN5, PNMT, PPARA, PPP1R3C, PROM1, SLC1A4, SP1, SUB1, TEF*
6	Direct	*Actin, ACTN3, ALDOA, Alpha Actinin, BANF1, CMIP, CNTFR, DUSP15, FAM101A/ZNF664-FAM101A, FAM65B, FHL3, FLNA, FYN, HIST1H1D, HOXA9, Integrin, Integrinα, Integrinβ, IRX3, ITGA7, ITGB6, MMP25, MYOZ2, NUMA1, PANK1, PARVG, PSIP1, PTPN3, RPL27A, STAC, SUB1, TMPO, TRA2B, YWHAE, YWHAZ*
7	Direct	*ARHGEF11, ASAP2, AXL, BIVM, BRPF3, CAST, CD164, CTLA4, DTX1, DUSP15, ELAVL1, EXTL1, FGF1, FGF5, GRB2, GRB10, HCST, HNRNPC, HNRNPD, HOXD1, KHSRP, NANOS1, ND4, NDUFC2, NLK, PARP1, PHACTR2, PUM2, RBPJ, SDR16C5, SERBP1, SH3D19, SMARCC2, SNX3, SPEN*
8	Direct	*CCDC112, TEX9*
9	Direct	*ceramidase, NAAA*
10	Indirect	*ACADVL, ALB, ATF3, ATP2A2, C/ebp, Calcineurin protein(s), CD2AP, CHRNA9, Creb, DUSP1, ERK1/2, FOSL1, Glycogen synthase, GOT1, GOT, Growth hormone, GYS2, ID1, ITGB6, ITPR2, KCNC1, LRRN1, MAP2K1/2, Nicotinic acetylcholine receptor, NMDA Receptor, PDGF BB, Pkg, PLN, PNMT, PP1 protein complex group, PPP1R1B, PPP1R3C, SCD, SERCA, TF*

11	Indirect	*ACTN3, Alp, Alpha Actinin, ANGPT1, AP1S2, DBT, FGF1, Hdac, HDL, Histone h4, Iga, IRX3, KLF2, LDL, Mek, N-cor, NFkB (complex), Notch, p70 S6k, Pdgf (complex), Pdgf Ab, PIK3R1, PIK3R3, PLIN1, PRKG1, RETSAT, RND3, Rock, SLPI, SORBS2, Sos, SOX9, TBX3, TFRC, Tgf beta*
12	Indirect	*ANO1, CHAC1, CLCA1, CLCA2, CLCA4, Clca1/Clca2, CRIM1, DICER1, EGFL7, ENAH, ERGIC1, ERGIC3, FAT1, GMEB1, GNE, GSTCD, KIAA0408, LOXL4, MYH3, MYH7B, MYL6B, NANOS1, NPHS2, PELI2, PFDN1, POLR3GL, PUM2, RAPH1, SLC4A7, STEAP3, TES, UBC, UFC1, XPO6, ZDHHC6*
13	Indirect	*ADAMTS5, AHR, ATP5J, BLVRB, C9orf156, COL11A1, COL16A1, CTSF, DDB2, ENHO, FAM101B, FH, GPX2, HOXD1, HPRT1, IDI1, KRT16, L-carnitine, MAN1A2, MYH7B, MYL6B, NEUROD6, OSMR, PCSK6, PLEKHB1, PON2, RPL27A, SLC1A4, SNRPD3, SNX8, STAC, SYNPO, TNF, tretinoin, UBC*
14	Indirect	*ACOX2, ALDOA, ARID5B, ATP5J, BANF1, beta-estradiol, CCND1, CD2BP2, CDK5RAP3, CHAF1B, D-glucose, dehydroepiandrosterone sulfate, DPY30, FAM101A/ZNF664-FAM101A, FAM65B, fatty acid, FLNA, KRAS, KRT16, L-phenylalanine, L-proline, LMNB2, MAPK1, MGAT4A, NCEH1, PANK1, Proinsulin, PTPN3, RASSF9, RHOA, SUB1, TMPO, TP53INP2, TRA2B, TTC9*
15	Indirect	*ADCY, Ap1, ASNS, BDKRB2, CNTFR, ESF1, Focal adhesion kinase, FOS, FSH, G protein alpha, G protein beta gamma, GNRH, Gpcr, Gsk3, HBEGF, HIF1AN, IDH1, IL1, Jnk, Lh, MMP25, Mmp, OCA2, Pka, Pkc(s), PLC, PLIN5, Rac, Ras, Ras homolog, Sapk, STC2, TCR, Vegf, voltage-gated calcium channel*
16	Indirect	*ABAT, ADAM10, anandamide, ARID5B, BIVM, BRPF3, CD164, CDHR1, Ck2, CXCL2, DDB2, DUSP15, ELAVL1, EXTL1, FURIN, GLCE, GRB2, HCST, Histone h3, HPRT1, MAL2, Mapk, NAAA, NDUFC2, PCSK7, PHACTR2, RNA polymerase II, SDR16C5, SH3D19, SMOC2, SNRPD3, SUB1, TGFB1, TUFM, WDR44*
17	Indirect	*26s Proteasome, Actin, Akt, Alpha tubulin, AQP4, AQP7, calpain, CD3, Cyclin A, Cyclin E, ERK, estrogen receptor, FABP3, Fcer1, FHL3, Hsp27, HSPB1, Ige, IgG, IL12 (complex), Immunoglobulin, Insulin, Integrin, MAFF, MST4, P38 MAPK, p85 (pik3r), PADI2, PI3K (complex), PLEK, Rb, Rsk, TRIP10, tyrosine kinase, Ubiquitin*
18	Indirect	*CCDC112, TEX9*

7.2.2. Supplementary Figures Paper II

Figure S1. Network (indirect, score 36) generated by IPA of 35 focus genes corresponding to metabolic disease, lipid metabolism and molecular transport. Node colours indicate gene expression, being the red nodes higher-expressed genes and the green nodes lower-expressed genes in the H group relative to the L group. Colour intensity is related to the degree of expression. Node shapes indicate the biological function of the protein.



7.3. Supplementary material of paper III: "A Co-Association Network Analysis of the Genetic Determination of Pig Conformation, Growth and Fatness"

7.3.1. Supplementary Tables Paper III

Table S1. List of 54 growth-related genes in the network.

ACVR1B, ADCY1, ADCY2, AGL, AGPS, ARHGEF16, ATP6V0A2, ATRN, BLK, BNIPL, CD44, CEP164, CHD7, CLDN16, CREG1, EFEMP1, FANCD2, FER, FGF6, FOXO1, FRS2, HEG1, HOXB13, HSPG2, IKBKAP, LTBP1, MATN3, MEN1, MT3, NDRG3, NDUFA10, NDUFS4, NOR-1, NOS1, PAK7, PDE11A, PDSS1, PPARG, PRDM16, PRKCB, PRKCE, PTK2B, RASGRF2, RHO, ROS1, RPS6KA2, RYK, SDCCAG8, SEMA4A, SLC5A1, SLCO2A1, TIAM2, WDR11, WNT7A

Table S2. List of 142 regulators (transcription factors and miRNAs) identified within the list of associated-genes.

AKNA, ARNT, ARNTL, ARNTL2, ASXL2, ATF6, ATF6B, BAZ1A, BCL9, BHLHE22, BMAL1, BMPR1A, BRPF1, BTAF1, CERS2, CERS5, CHCHD3, CHD1, CITED2, CNOT1, CREB3, CREB3L1, CREB5, CREG1, CSDA, CUX1, CUX2, DBX1, DDX20, DDX21, DDX54, DMRT1, E2F6, E2F7, EHMT2, ELF1, ELF5, ELL2, ENSSSCG00000003361, ENSSSCG00000018341, ENSSSCG00000018468, ENSSSCG00000018614, ENSSSCG00000018662, ENSSSCG00000018677, ENSSSCG00000018904, ENSSSCG00000019021, ENSSSCG00000019760, ENSSSCG00000019806, ENSSSCG00000023641, ENSSSCG00000024457, ENSSSCG00000025509, ENSSSCG00000027780, ENSSSCG00000029632, ENSSSCG00000030555, EP300, EPAS1, ERCC3, ERG, ESRRG, ETV6, FOXN3, FOXO1, GABPB2, GATA4, GLIS3, GRAP2, GTF2H3, GTF3C5, HEYL, HMBOX1, HMGA2, HNF1A, HOXB13, HTATIP2, JHDM1D, JMJD1C, KCNIP3, KDM5B, L3MBTL3, LHX6, MAFF, MDFIC, MECOM, MED19, MED28, MEF2D, MEN1, MTF2, MYB, NCOA7, NCOR1, NOR-1, NPAS2, NPAS3, NPAS4, NR1H4, NR2C2, NR2F2, NRBF2, OTX2, PARP1, PHC3, PPARG, PRDM15, PRDM16, PTGER3, PTH, RB1, RFX4, RFX5, RLF, RORC, SF-1, SMARCA5, SNAPC3, sscmir196a1, ST18, TADA3, TAF2, TBPL2, TCEA1, TCEB3, TCERG1, TCF23, TCF7L2, TEAD1, TFAP2D, TFEC, TLX1, TOX, TP63, TRERF1, TRRAP, UHRF1, WWTR1, YBX1, ZBTB48, ZFP42, ZFPM2, ZNF192, ZNF367, ZNF488

Table S3. Top networks of molecular functions identified with IPA for the 513 genes.

ID	Molecules in Network	Score	Focus Molecules	Top Functions
1	*ADCY, ADCY1, ADCY2, ADORA3, ADRB, ARHGAP32, CaMKII, CCDC6, CD6, CRAT, Ctbp, ELF1, ERK1/2, ETV6, G protein beta gamma, GALNT2, HSD17B7, KCNMA1, KCNN2, KCNN3, KLRB1, KLRD1, MATN3, MYCBP2, OSMR, potassium channel, Proinsulin, RAB7L1, RASGRF2, SH2B3, SPRY4, STAT5a/b, TCF, Wnt, WNT7A*	*38*	*24*	Cell Signaling, Nucleic Acid Metabolism, Cell-To-Cell Signaling and Interaction
2	*ABCB10, BRPF1, BTAF1, CACNA1G, CHD1, CYB5A, CYP7A1, Dynamin, EAF1, ELL2, ELP4, FABP5, hemoglobin, Histone h3, Histone h4, HMMR, Holo RNA polymerase II, IKBKAP, INCENP, ITM2B, JINK1/2, KDM5B, MDN1, MED19, mediator, PEPCK, PI3K (complex), PRKDC, RNA polymerase II, Rxr, RYK, TADA3, TF, TRRAP, YTHDC2*	*38*	*24*	Organismal Development, DNA Replication, Recombination, and Repair, Lipid Metabolism
3	*BOLA1, Cg, CHD7, Collagen type IV, DNAH11, EFEMP1, estrogen receptor, FANCD2, FOXO1, FSH, Growth hormone, HSD17B12, Lh, Mapk, Mitochondrial complex 1, MME, NDUFA10, NDUFS4, NR2C2, PLXND1, PSMD4, RGS7, RGS20, S100A10, SCN10A, SCN11A, SCN8A, SEMA4A, ST8SIA4, STIP1, THBS2, TXNIP, Ubiquitin, voltage-gated sodium channel, WRAP73*	*38*	*25*	Hereditary Disorder, Neurological Disease, Developmental Disorder
4	*ADAMTS12, Alpha catenin, BCR (complex), BLK, c-Src, CADPS, CDCP1, CHKA, DPYSL2, E2F7, Erm, ESRRG, F Actin, GLRX, Ige, Igm, KDM2A, KSR2, MAVS, MLLT4, MT3, NFkB (complex), NRXN2, PIP5K1A, PIP5K1C, PLC gamma, RNF5, Rock, SH3PXD2A, SNAP25, Snare, SYK/ZAP, SYT1, tubulin (family), WIPF1*	*33*	*22*	Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Cellular Assembly and Organization
5	*26s Proteasome, ACOT7, Actin, BHLHE22, Calmodulin, caspase, Ck2, CLTB, Cyclin A, DNAJC13, E2f, E2F6, EIF4A3, ENSA, EPB41L2, Hsp70, Insulin, KIF17, KIF1B, MHC Class II (complex), MYB, NMDA Receptor, PAM, Pde, PDE11A, PDE9A, Pka, PLC, POT1, PPARG, RHO, SUGT1, TBXAS1, tubulin (complex), YBX1*	*29*	*20*	Cellular Development, Nervous System Development and Function, Behavior
6	*Akt, Collagen Alpha1, Collagen type II, Collagen type III, Collagen type VI, CREG1, DCN, Fcer1, FCGR1A/2A/3A, FER, Fgf, FGF6, Fgfr, FRS2, FYB, HSPG2, I kappa b kinase, Integrin, ITGA1, ITGA2, KMO, LCP1, Lfa-1, LNPEP, MGLL, N-Cadherin, PRDM16, RAB21, RRBP1, Talin, TBC1D4, TGFBR, TIAM2, TLX1, Vla-4*	*27*	*19*	Cell Morphology, Nervous System Development and Function, Inflammatory Disease

7	*AIDA, ALB, AMPK, ATG7, ATP2B2, CAB39, CACNA1I, Calcineurin protein(s), calpain, CAST, CIT, CTSL, cytochrome C, HDL, HDL-cholesterol, Jnk, KHDRBS3, LDL-cholesterol, MECOM, MEF2D, NADPH oxidase, NFAT (complex), Nfat (family), NOS1, PCSK9, PKC (α, β, γ, δ, ε, ι), PLCB4, PLXNA1, Pmca, PRKCB, RLF, RYR1, Sod, TAOK3, WDR26*	*26*	*21*	Cell Death and Survival, Cell Morphology, Cellular Assembly and Organization
8	*Alp, CDO1, CLEC7A, Cofilin, Collagen type I, Creb, CREB5, CSRP2, Cyclin E, DLL1, DOCK3, EIF2B5, ERK, FOXN3, Laminin, LTBP1, MAGI3, Mek, MEN1, OBFC1, p70 S6k, PDGF BB, PINK1, PP1 protein complex group, PP2A, Ppp2c, PPP2R2B, Rap1, Rb, RPS6KA2, sphingomyelinase, STRIP1, thymidine kinase, TPM1, ZC3H12D*	*25*	*18*	Cancer, Tissue Development, Cellular Compromise
9	*ACO1, AGPS, CD44, DEGS1, DOCK8, FBLIM1, FCER1G, Fibrinogen, Gsk3, HISTONE, HRH1, IgG, IgG1, Igg3, IgG2a, IL12 (family), Immunoglobulin, LDL, LHX6, MCL1, NDFIP2, Pdgf (complex), Pkc(s), Pld, PTK2B, PTPN22, PTPRC, RORC, SEC13, SELENBP1, Shc, Smad, Sos, SRC (family), Tgf beta*	*22*	*17*	Cell Death and Survival, Hematological System Development and Function, Cellular Function and Maintenance
10	*ANKRD17, ATG9A, BNIP1, CEP164, CMIP, FCHO2, FGFR1OP, FIG4, FLG2, GGH, HCN1, ITPRIP, MTMR1, MTMR14, NDNL2, NSMCE1, NSMCE2, NSMCE4A, PLCD3, PLCH1, PLD4, PPP2R3C, RSF1, SACM1L, SEC23IP, SMC5, SMC6, STX18, SUCLG2, TGS1, TMEM109, TTBK2, TUFT1, UBC, USE1*	*21*	*16*	Carbohydrate Metabolism, Lipid Metabolism, Small Molecule Biochemistry
11	*ACVR1B, AGL, ATL2, ATP5E, ATP5G3, ATPAF1, CC2D2A, Copb2, COPG1, COPG2, COPZ2, CRCP, ERGIC2, FOXRED2, JPH1, KCTD10, MAN1B1, MYO1D, POLR3B, POLR3C, POLR3G, POLR3H, RPN1, SEPT1, Sept9, SEPT9, SEPT10, STAMBP, STT3B, UBC, VPS9D1, WDR20, XRCC3, ZFP42, ZSWIM7*	*21*	*16*	Post-Translational Modification, Developmental Disorder, Hereditary Disorder
12	*ACAD9, ACSF2, AKNA, ARL6IP1, ASRGL1, CAPZA1, CLN3, CREB3, DESI1, EXPH5, FXN, GABARAPL1, GIGYF2, KIF11, LPGAT1, LRRC16A, MAPK8IP2, MARK3, NDRG3, NEK10, NOL10, PDSS1, PIWIL1, PMPCB, RAB27A, SBDS, SFT2D1, SMAD9, ST8SIA6, SYT12, TDRKH, UBC, UBXN7, UNC93B1, WDR11*	*21*	*16*	Cellular Assembly and Organization, Cellular Function and Maintenance, Hereditary Disorder
13	*ANO5, ANO10, AP1S3, CA10, CCDC138, CNTLN, CPNE9, DCBLD1, DEPDC5, GARNL3, GK5, HDDC2, HEG1, KDELC2, KMT2D, MARVELD1, NT5DC1, RABL3, RANGRF, RELL1, RIMKLB, SAMD8, SEC22C, SLC22A23, SLC35F5, SPEF2, SYPL2, SZT2, TFAP2D, TMEM159, TRMT2B, UBC, YDJC, ZFP62, ZNF347*	*19*	*15*	Developmental Disorder, Hereditary Disorder, Neurological Disease
14	*ASUN, BTAF1, CBX5, CFTR, CHAMP1, CLP1, EME1, FAM175A, FOXA1, HELZ, HIST3H2BB, INTS3, INTS4, INTS12, IWS1, KIAA1958, MS4A5, NELFA, NVL, OXCT1, PCF11, POLR2A, PRDM15, SCAF8, SCAI, SENP7,*	*18*	*14*	RNA Post-Transcriptional Modification, Developmental Disorder, Neurological

	SSRP1, SUMO2, TMTC1, TSEN2, TSEN15, TSEN34, TSEN54, ZNF687, ZNF829			Disease
15	*APITD1, APP, C17orf70, C19orf40, CAPSL, CCDC40, CCDC60, CHRM3, CINP, CLDN16, CLDN20, CLUAP1, CPA6, DPCD, endocannabinoid, EPB41L4A, FZD3, GAPDHS, GPR3, GPR6, GPR12, GPR61, GPR78, KIAA0825, LPAR3, NALCN, RXFP3, SPZ1, SUPT4H1, TAF7L, TSKS, TSSK6, TTLL6, VPS45, ZNF322*	*17*	*14*	Organismal Injury and Abnormalities, Reproductive System Disease, Nervous System Development and Function
16	*ADCYAP1, ALKBH5, ANGEL2, ATP6V0A2, ATRN, C12orf49, CEPT1, COPS7B, CTBS, DRG1, ELAVL1, Gas1, HECW2, HOXB13, INPP4B, KAZN, METAP1, MITF, MUM1, MYC, PIGM, RNF17, SAMD1, SELT, SEZ6L, SLC45A2, SLCO4C1, SNX10, SRBD1, SYT15, TBC1D16, UBL3, UST, ZBTB14, ZXDB*	*16*	*13*	Cell Morphology, Developmental Disorder, Organismal Injury and Abnormalities
17	*AATK, ABCC3, ALAD, ARRDC3, AZU1, CABP4, CCDC22, CORO1B, CPEB3, CUL1, EFCC1, FBXL17, FBXL18, FBXO45, GSTA2, KIF20A, MAEA, OLFML2B, PDK3, PPP1CA, PREX2, PRKCZ, PSMG1, PXR ligand-PXR-Retinoic acid-RXRα, RAPGEF5, RFTN1, SFI1, SLC7A14, SNX29, taurochenodeoxycholate, TNF, TPP2, UBD, ZBTB11, ZDHHC8*	*14*	*12*	Embryonic Development, Hair and Skin Development and Function, Cell-mediated Immune Response
18	*ALDH5A1, ARHGEF26, ARNT2, AS3MT, BCL9, BFSP2, CRISP2, DAGLA, DEFB104A/DEFB104B, DPP7, ELMOD1, ethanol, GCNT2, GPR65, H1FOO, H2-K2/H2-Q9, HAO2, IFNG, IL12 (complex), KLRB1, LIX1, MX2, NAPEPLD, NR3C1, NUPR1, Phb, PI4KB, RAB20, RDH11, TLR3, TLR3/4, TRIL, TXNRD3, ZNF483, ZNF488*	*14*	*12*	Endocrine System Development and Function, Cell-To-Cell Signaling and Interaction, Inflammatory Response
19	*ALX1, ARHGEF9, ARHGEF16, BAI2, BNIP2, BNIPL, CDC42, CDC42BPB, CELSR3, DDX20, DICER1, EPO, FMR1, GNRHR2, GPR45, GPRIN1, GRB2, HHIPL2, KIF25, LPAR3, mir-138, mir-194, miR-138-5p (miRNAs w/seed GCUGGUG), miR-218-5p (and other miRNAs w/seed UGUGCUU), PDLIM2, PNMA2, RASGEF1A, Rasgrf, RTN1, SH3D19, SLC24A1, SLCO2A1, SRGAP1, STRADB, WIPF2*	*14*	*12*	Cell Signaling, Cell Cycle, Embryonic Development
20	*ANKH, BMS1, CACNA2D3, CACNG4, CATSPER, CATSPER1, CDC37, DUPD1, GABRD, GRK5, HTT, HUNK, IL17RE, IP6K1, MCOLN2, NGF, Ntrk1 dimer, PLIN4, PPIP5K1, progesterone, PRPSAP1, RAB3IL1, RBMS1, REM1, RUSC1, SDCCAG8, SEMA6C, SHE, SORCS3, SPP1, STRADB, TRAF6, voltage-gated calcium channel, ZNF334, ZNF675*	*14*	*12*	Cellular Development, Neurological Disease, Cell Signaling
21	*ACAD11, Adaptor protein 2, alcohol group acceptor phosphotransferase, ALKBH3, Ap1, ASGR2, BLVRA, CD3, chemokine, Collagen(s), DHX36, F5, FAT1, Focal adhesion kinase, Gpcr, Hsp90, IL1, Interferon alpha, MAP2K1/2, Mmp, P2RX4, P38 MAPK, p85 (pik3r), PAK7, PRKCE, Pro-inflammatory*	*13*	*12*	Cell-To-Cell Signaling and Interaction, Cellular Assembly and Organization, Nervous System Development and Function

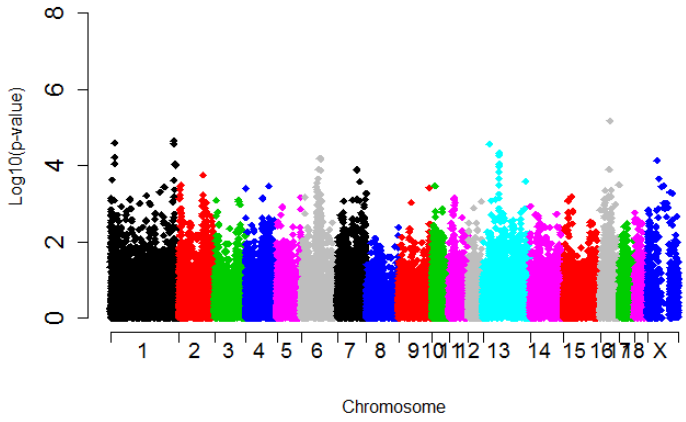
	Cytokine, Rac, Ras, Ras homolog, Sfk, SLC5A1, SRPRB, TCR, Tlr, Vegf			
22	*AR, ATXN1, BICC1, CD109, CHST5, CHST13, CUX2, DZIP3, EGFR, Gpcr, GPR62, GPR75, GPR82, GPR97, GPR111, GPR112, GPR128, GPR144, GPR149, GPR150, GPR152, GPR157, GPR162, GPR174, GPR176, GPRC5D, MAS1L, ROS1, SLC6A13, sulfotransferase, Sult4a1, TGFB1, UST, VN1R2, ZMIZ1*	*13*	*11*	Post-Translational Modification, Organ Morphology, Reproductive System Development and Function
23	*ARHGEF39, CARD9, CLDN4, CNKSR1, DIXDC1, DMD, DVL2, ENKD1, GJA5, HTR2B, MAP3K9, MAPK8, MDFIC, MEF2C, MYCBPAP, MYLK2, MYOZ1, NQO2, PLA2G12A, PRDX5, PROK1, RAB35, RBPMS, SCIN, SLC24A5, SOCS4, THEM5, TIFA, TMEM108, TRAFD1, UFC1, VANGL2, VHL, ZBTB48, ZBTB8A*	*7*	*7*	Cardiovascular System Development and Function, Embryonic Development, Organ Development

Table S4. Top pathways identified with IPA for the 513 genes. (too large to be attached, please visit the link below: http://journals.plos.org/plosone/article/asset?unique&id=info:doi/10.1371/journal.pone.0114862.s007)

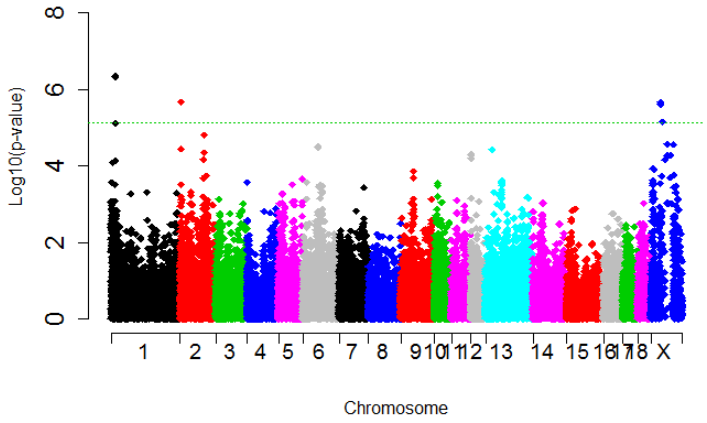
7.3.2. Supplementary Figures Paper III

Figure S1. GWAS plot of the 12 traits: body weight measured at 125, 155 and 180 days (BW125, BW155, and BW180, respectively), backfat thickness measured at 155 and 180 days (BFT155 and BFT180) and measured at slaughter (BFTS), carcass length and weight (CL and CW), weight of the hams, shoulders and belly (HW, SW and BLW) and intramuscular fat (IMF) content. The horizontal green line represents the statistical significance (false discovery rate; set at q-value ≤ 0.05) calculated with the q-value library [85] implemented in R program (http://www.r-project.org/).

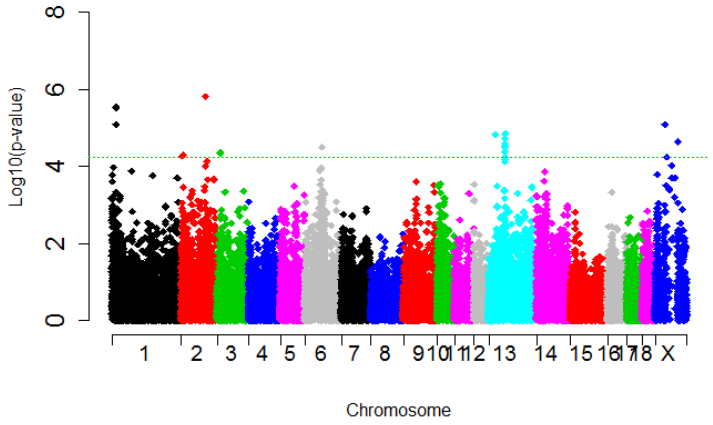
A) BW125



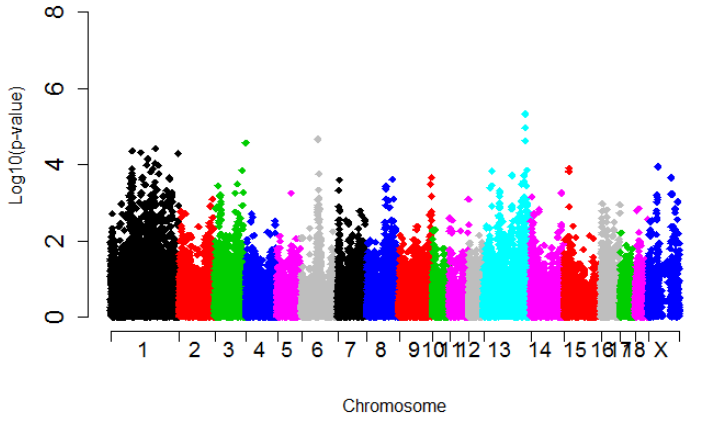
B) BW155



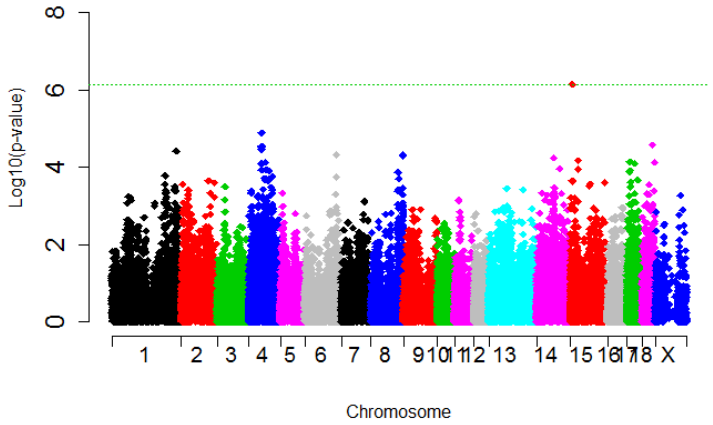
C) BW180



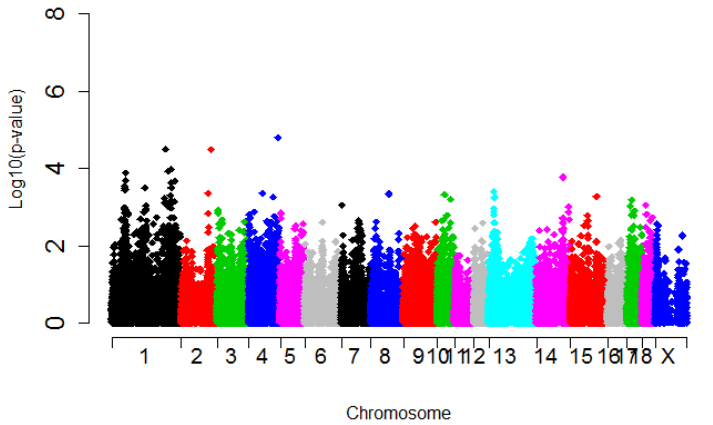
D) CW



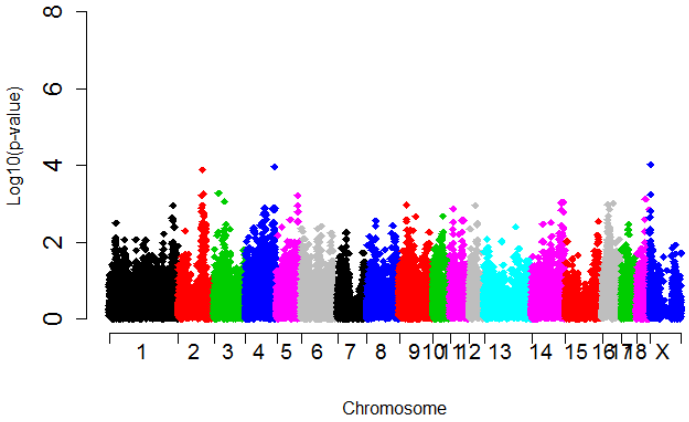
E) CL



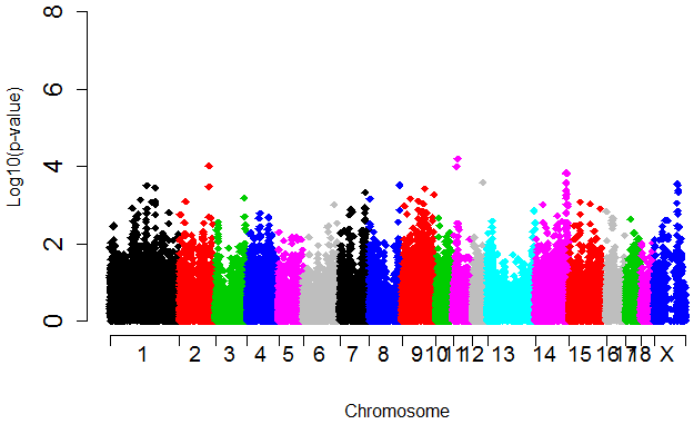
F) BFT155



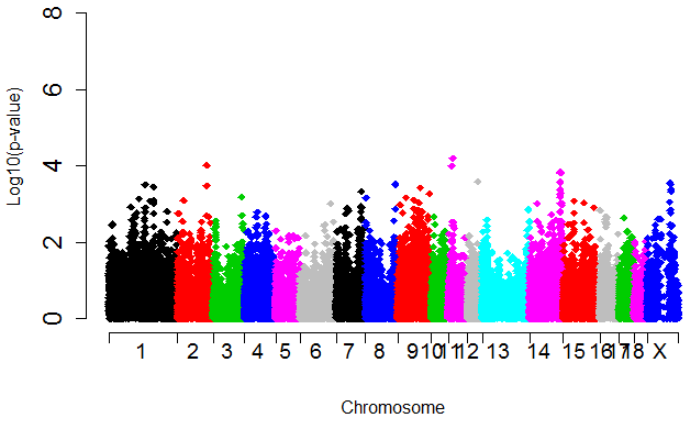
G) BFT180



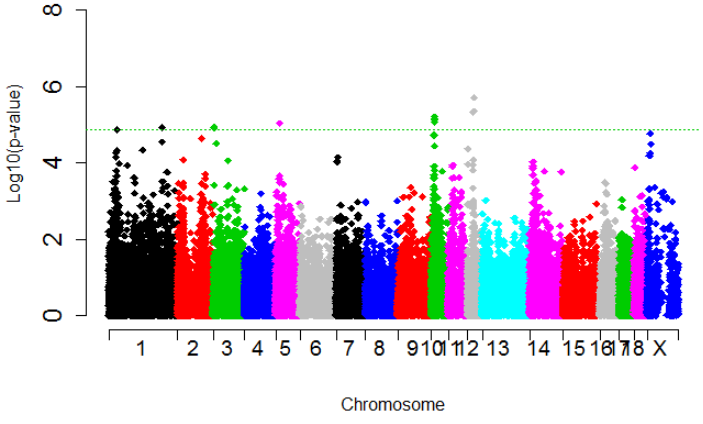
H) BFTS



I) IMF



J) HW



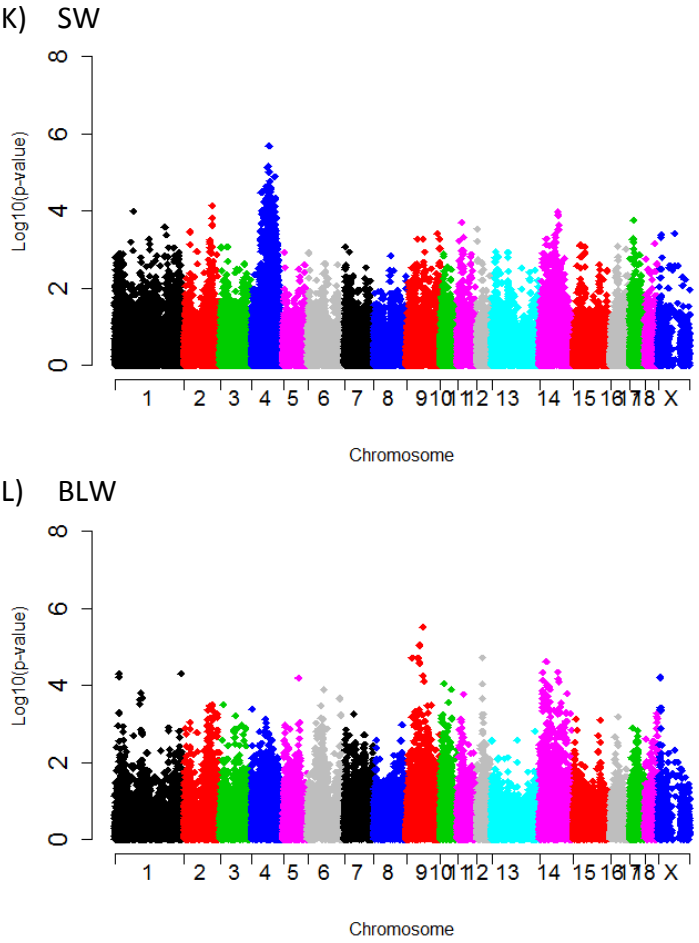
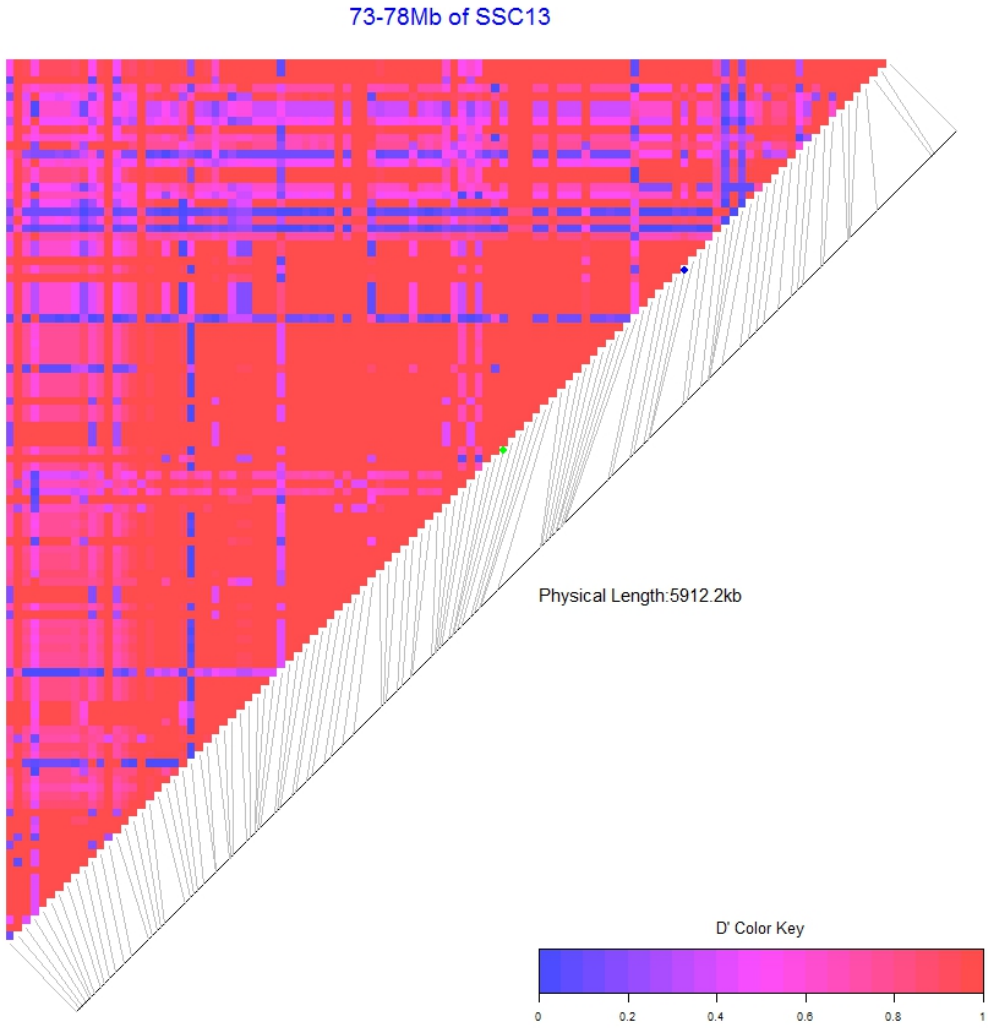


Figure S2. Hierarchical cluster analysis among 12 phenotypic traits: body weight measured at 125, 155 and 180 days (BW125, BW155, and BW180, respectively), backfat thickness measured at 155 and 180 days (BFT155 and BFT180) and measured at slaughter (BFTS), carcass length and weight (CL and CW), weight of the hams, shoulders and belly (HW, SW and BLW) and the intramuscular fat (IMF) content. (too large to be attached, please visit the link below: http://journals.plos.org/plosone/article/asset?unique&id=info:doi/10.1371/journal.pone.0114862.s002)

Figure S3. Linkage disequilibrium among the *PPARG* and *NR2C2* SNPs. Pattern of linkage disequilibrium analysis around ±2Mb of the SNPs in *PPARG* and *NR2C2*. Figure colored from blue to red according to LD strength between consecutive markers. The green diamond-shape corresponds to the SNP in *PPARG* gene and the blue diamond-shape the SNP in *NR2C2* gene.



7.4. Supplementary material of paper IV: "Expression-based GWAS identify variants, gene interactions and potential key regulators affecting the intramuscular content and fatty acid composition in porcine meat"

7.4.1. Supplementary Tables Paper IV

Table S1. Descriptive statistics including mean and standard deviation (SD) of intramuscular fat (IMF), fatty acid (FA) composition and fatty acid indices of the BC1_LD animals analyzed.

Carcass quality	Abbreviation	Mean	SD
Meat quality (n=98)			
Intramuscular fat (%)	IMF	2.1	0.07
Fatty acids (n=114)			
Saturated FA*			
Myristic acid	C14:0	1.18	0.01
Palmitic acid	C16:0	22.55	0.12
Heptadecenoic acid	C17:0	0.26	0.01
Stearic acid	C18:0	14.19	0.09
Arachidic acid	C20:0	0.26	0.01
Monounsaturated FA*			
Palmitoleic acid	C16:1(n-7)	2.49	0.04
cis-7 hexadecenoic acid	C16:1(n-9)	0.39	0.01
Heptadecenoic acid	C17:1	0.26	0.01
Oleic acid	C18:1(n-9)	40.09	0.28
Octadecenoic acid	C18:1(n-7)	3.88	0.03
Eicosenoic acid	C20:1(n-9)	0.85	0.01
Polyunsaturated FA*			
Linoleic acid	C18:2(n-6)	10.38	0.24
α-Linolenic acid	C18:3(n-3)	0.66	0.03
Eicosadienoic acid	C20:2(n-6)	0.54	0.01
Eicosatrienoic acid	C20:3(n-6)	0.27	0.01
Arachidonic acid	C20:4(n-6)	1.54	0.07

*The percentage of each FA, relative to the total FA.

Table S2. Description of the 241 eSNPs identified as significantly associated with gene expression.

SNP	Inter-val	Chr	SNP position*	Analyzed Gene	Type of eQTL	F(A1)	F(A2)	N§	Ortho-logous	Annotated Gene	Consequence
ALGA0123977	1	3	16,487,448	*ACSM5*	*cis*	0.77	0.23	114			
H3GA0053939	1	3	18,724,340	*ACSM5*	*cis*	0.90	0.10	114	SH2B1	ENSSSCG00000007804	INTRONIC
ASGA0101457	1	3	18,742,778	*ACSM5*	*cis*	0.90	0.10	114	ATP2A1	ENSSSCG00000007805	INTRONIC
ALGA0017974	1	3	21,309,417	*ACSM5*	*cis*	0.77	0.23	114	-	-	INTERGENIC
ALGA0123606	1	3	21,777,886	*ACSM5*	*cis*	0.63	0.37	114	-	-	INTERGENIC
ALGA0018040	1	3	23,224,453	*ACSM5*	*cis*	0.66	0.34	114	-	-	INTERGENIC
DRGA0003820	1	3	23,241,425	*ACSM5*	*cis*	0.66	0.34	114	-	-	INTERGENIC
ASGA0098738	1	3	23,442,184	*ACSM5, PLA2G12A*	*Cis /trans*	0.73	0.27	114	SCNN1G	ENSSSCG00000007836	DOWNSTREAM
ALGA0103397	1	3	23,522,898	*ACSM5*	*cis*	0.73	0.27	113	USP31	ENSSSCG00000030424	UPSTREAM
MARC0041570	1	3	23,603,118	*ACSM5*	*cis*	0.73	0.27	114	USP31	ENSSSCG00000026544	DOWNSTREAM
ASGA0093175	1	3	23,778,733	*ACSM5*	*cis*	0.80	0.20	112	HS3ST2	ENSSSCG00000007837	INTRONIC
MARC0003844	1	3	23,802,761	*ACSM5*	*cis*	0.80	0.20	114	HS3ST2	ENSSSCG00000007837	INTRONIC
MARC0047020	1	3	23,961,903	*ACSM5*	*cis*	0.73	0.27	114	-	-	INTERGENIC
ASGA0103399	1	3	24,010,664	*ACSM5*	*cis*	0.75	0.25	114	OTOA	ENSSSCG00000007838	DOWNSTREAM
ALGA0123020	1	3	24,042,892	*ACSM5*	*cis*	0.78	0.22	114	OTOA	ENSSSCG00000007838	INTRONIC
ASGA0094620	1	3	24,288,043	*ACSM5*	*cis*	0.71	0.29	114	EEF2K	ENSSSCG00000007839	3'UTR
ASGA0089883	1	3	24,297,157	*ACSM5*	*cis*	0.71	0.29	114	EEF2K	ENSSSCG00000007839	INTRONIC
ASGA0099261	1	3	24,299,990	*ACSM5*	*cis*	0.85	0.15	114	EEF2K	ENSSSCG00000007839	INTRONIC
DRGA0017484	1	3	24,300,956	*ACSM5*	*cis*	0.71	0.29	114			
ASGA0101242	1	3	24,418,411	*ACSM5*	*cis*	0.78	0.22	114	SDR42E2	ENSSSCG00000007842	DOWNSTREAM
MARC0110831	1	3	25,162,049	*ACSM5*	*cis*	0.85	0.15	114	ABCA3	ENSSSCG00000007847	INTRONIC
ASGA0085542	1	3	25,695,049	*ACSM5*	*cis*	0.73	0.27	114	-	-	INTERGENIC
ASGA0013904	1	3	25,862,724	*ACSM5*	*cis*	0.74	0.26	114	-	-	INTERGENIC
ASGA0013906	1	3	25,939,787	*ACSM5*	*cis*	0.73	0.27	114	LYRM1	ENSSSCG00000007853	UPSTREAM
ALGA0018079	1	3	25,957,412	*ACSM5*	*cis*	0.73	0.27	114	-	-	INTERGENIC
ASGA0095840	1	3	25,990,903	*ACSM5*	*cis*	0.74	0.26	114	-	ENSSSCG00000007855	INTRONIC
MARC0108510	1	3	26,002,460	*ACSM5*	*cis*	0.74	0.26	114	-	ENSSSCG00000007855	INTRONIC
ALGA0108097	1	3	26,045,382	*ACSM5*	*cis*	0.74	0.26	114	ACSM3	ENSSSCG00000007857	INTRONIC
ASGA0085560	1	3	26,316,304	*ACSM5*	*cis*	0.76	0.24	114	-	-	INTERGENIC
H3GA0053928	1	3	26,392,557	*ACSM5*	*cis*	0.71	0.29	114	-	-	INTERGENIC
MARC0101263	1	3	26,425,965	*ACSM5*	*cis*	0.83	0.17	114	-	-	INTERGENIC
MARC0050331	1	3	26,428,824	*ACSM5*	*cis*	0.79	0.21	114	-	-	INTERGENIC
MARC0052941	1	3	26,537,702	*ACSM5*	*cis*	0.74	0.26	114	GPR139	ENSSSCG00000007862	DOWNSTREAM
MARC0001269	1	3	26,822,485	*ACSM5*	*cis*	0.72	0.28	114	-	-	INTERGENIC
CASI0010189	1	3	26,899,862	*ACSM5*	*cis*	0.72	0.28	114			
ALGA0121590	1	3	26,978,899	*ACSM5*	*cis*	0.52	0.48	114	TMC7 ; TMC5	ENSSSCG00000007866 ENSSSCG00000007868	INTRONIC
ASGA0090088	1	3	27,058,670	*ACSM5*	*cis*	0.77	0.23	114	TMC5	ENSSSCG00000007868	INTRONIC
ASGA0105223	1	3	27,200,658	*ACSM5*	*cis*	0.77	0.23	114	SYT17	ENSSSCG00000022200	INTRONIC
SIRI0001454	1	3	27,254,477	*ACSM5*	*cis*	0.77	0.23	114			
MARC0006897	1	3	27,719,357	*ACSM5*	*cis*	0.67	0.33	114			
ALGA0018138	1	3	27,839,633	*ACSM5*	*cis*	0.71	0.29	114	XYLT1	ENSSSCG00000007872	INTRONIC
MARC0046257	1	3	27,878,993	*ACSM5*	*cis*	0.79	0.21	112	XYLT1	ENSSSCG00000007872	INTRONIC
ASGA0013982	1	3	27,941,321	*ACSM5*	*cis*	0.71	0.29	114	-	-	INTERGENIC

ALGA0020170	2	3	100,347,076	*ACSM5*	*trans*	0.49	0.51	114	-	-	INTERGENIC
ASGA0090778	3	10	175,359	*ACSM5*	*trans*	0.76	0.24	114	COG7	ENSSSCG00000010799	INTRONIC
ALGA0046587	4	8	15,870,120	*CROT*	*trans*	0.69	0.31	114	-	-	INTERGENIC
DRGA0008346	4	8	15,886,903	*CROT*	*trans*	0.69	0.31	114	-	-	INTERGENIC
ALGA0046590	4	8	15,912,410	*CROT*	*trans*	0.63	0.37	114	-	-	INTERGENIC
ALGA0063896	5	11	81,364,018	*FABP3*	*trans*	0.54	0.46	113	-	-	INTERGENIC
H3GA0032639	5	11	82,160,789	*FABP3*	*trans*	0.65	0.35	113	-	-	INTERGENIC
MARC0042088	**6**	11	6,736,568	*FOS*	*trans*	0.15	0.85	114			
ALGA0060679	**6**	11	6,877,318	*FOS*	*trans*	0.87	0.13	113			
H3GA0031293	6	11	10,324,482	*FOS*	*trans*	0.88	0.12	114	-	-	INTERGENIC
MARC0011099	6	11	10,343,852	*FOS*	*trans*	0.76	0.24	114	-	-	INTERGENIC
ASGA0049736	6	11	10,355,880	*FOS*	*trans*	0.88	0.12	114	-	-	INTERGENIC
H3GA0031340	6	11	11,968,518	*FOS*	*trans*	0.75	0.25	113	-	-	INTERGENIC
H3GA0028012	7_17	9	117,742,788	*HIF1AN; PLA2G12A*	*trans*	0.93	0.07	114	-	-	INTERGENIC
ASGA0044215	7_18	9	117,750,464	*HIF1AN; PLA2G12A*	*trans*	0.93	0.07	114	-	-	INTERGENIC
ALGA0117195	7_19	9	117,851,340	*HIF1AN; PLA2G12A*	*trans*	0.93	0.07	114	-	-	INTERGENIC
ASGA0084177	8	2	16,416	*IGF2*	*cis*	0.75	0.25	114	-	-	INTERGENIC
H3GA0005551	8	2	356,856	*IGF2*	*cis*	0.89	0.11	114			
MARC0008125	8	2	1,264,220	*IGF2*	*cis*	0.75	0.25	114	-	-	INTERGENIC
ASGA0082213	8	2	1,457,259	*IGF2*	*cis*	0.75	0.25	114	-	-	INTERGENIC
ASGA0083230	8	2	1,460,039	*IGF2*	*cis*	0.81	0.19	114	-	-	INTERGENIC
ALGA0112642	8	2	1,505,302	*IGF2*	*cis*	0.75	0.25	114	PPFIA1	ENSSSCG00000021469	UPSTREAM
ASGA0101159	8	2	2,224,107	*IGF2*	*cis*	0.93	0.07	114	-	-	INTERGENIC
H3GA0005515	8	2	2,546,707	*IGF2*	*cis*	0.69	0.31	114	-	-	INTERGENIC
ALGA0011357	8	2	2,610,043	*IGF2*	*cis*	0.87	0.13	113	-	-	INTERGENIC
ALGA0109310	8	2	3,166,230	*IGF2*	*cis*	0.63	0.37	113	LRP5	ENSSSCG00000012885	DOWNSTREAM
ALGA0011460	8	2	3,606,836	*IGF2*	*cis*	0.80	0.20	114	NDUFV1	ENSSSCG00000012896	UPSTREAM
H3GA0005630	8	2	3,788,156	*IGF2*	*cis*	0.79	0.21	114	CABP4	ENSSSCG00000012906	INTRONIC
ASGA0008604	8	2	5,148,429	*IGF2*	*cis*	0.80	0.20	114	CD248	ENSSSCG00000029949	MISSENSE
DIAS0000846	8	2	6,201,646	*IGF2*	*cis*	0.87	0.13	114			
H3GA0005759	8	2	6,667,399	*IGF2*	*cis*	0.85	0.15	114	NRXN2	ENSSSCG00000013024	INTRONIC
ASGA0102529	8	2	8,596,505	*IGF2*	*cis*	0.76	0.24	114	-	-	INTERGENIC
M1GA0025098	8	2	11,175,095	*IGF2*	*cis*	0.86	0.14	114	Olfactory receptor	ENSSSCG00000013121	SYNONYMOUS
ASGA0106410	9	2	162,088,043	*IGF2*	*trans*	0.51	0.49	114	-	-	INTERGENIC
ASGA0085784	9	2	162,298,086	*IGF2*	*trans*	0.75	0.25	114	ANO9	ENSSSCG00000024569	INTRONIC
ASGA0057854	10	1	287,348,708	*MGLL*	*trans*	0.52	0.48	114			
H3GA0035933	11	13	27,954,256	*MGLL*	*cis*	0.66	0.34	114	-	ENSSSCG00000027268	INTRONIC
ASGA0057098	11	13	34,430,646	*MGLL*	*cis*	0.54	0.46	114	-	ENSSSCG00000011352	DOWNSTREAM
H3GA0036121	11	13	34,526,276	*MGLL*	*cis*	0.36	0.64	114	COL7A1	ENSSSCG00000011355	INTRONIC
ASGA0057858	11	13	40,676,887	*MGLL*	*cis*	0.80	0.20	114			
H3GA0036642	11	13	40,721,880	*MGLL*	*cis*	0.80	0.20	114			
INRA0040170	11	13	53,023,515	*MGLL*	*cis*	0.60	0.40	114			
MARC0021368	11	13	55,473,962	*MGLL*	*cis*	0.63	0.37	114	EOGT	ENSSSCG00000011504	DOWNSTREAM
DIAS0004227	11	13	55,667,971	*MGLL*	*cis*	0.63	0.37	114			
ALGA0070102	11	13	55,965,833	*MGLL*	*cis*	0.52	0.48	114	-	-	INTERGENIC
ALGA0070129	11	13	56,472,948	*MGLL*	*cis*	0.50	0.50	114	MITF	ENSSSCG00000011512	INTRONIC
M1GA0017549	11	13	59,816,021	*MGLL*	*cis*	0.68	0.32	114	SHQ1	ENSSSCG00000011518	INTRONIC

MARC0094430	11	13	59,852,917	*MGLL*	*cis*	0.68	0.32	114	SHQ1	ENSSSCG00000011518	INTRONIC
ALGA0070362	11	13	60,439,469	*MGLL*	*cis*	0.58	0.42	114	PDZRN3	ENSSSCG00000011521	INTRONIC
H3GA0036571	11	13	60,609,657	*MGLL*	*cis*	0.61	0.39	114	-	-	INTERGENIC
ALGA0070372	11	13	60,676,911	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ALGA0070387	11	13	60,801,744	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC
ALGA0070388	11	13	60,807,418	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC
ALGA0070390	11	13	61,014,675	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC
H3GA0036584	11	13	61,069,055	*MGLL*	*cis*	0.58	0.42	114	-	-	INTERGENIC
DRGA0012453	11	13	61,190,858	*MGLL*	*cis*	0.79	0.21	114	-	-	INTERGENIC
MARC0009388	11	13	61,263,202	*MGLL*	*cis*	0.79	0.21	114	-	-	INTERGENIC
ASGA0057792	11	13	61,833,288	*MGLL*	*cis*	0.79	0.21	114	-	-	INTERGENIC
H3GA0036592	11	13	61,883,698	*MGLL*	*cis*	0.80	0.20	111	-	-	INTERGENIC
ASGA0057789	11	13	61,953,632	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ASGA0088181	11	13	61,982,576	*MGLL*	*cis*	0.81	0.19	113	-	-	INTERGENIC
ASGA0094034	11	13	62,566,678	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC
INRA0040299	11	13	62,729,066	*MGLL*	*cis*	0.80	0.20	114			
CASI0004415	11	13	63,368,471	*MGLL*	*cis*	0.80	0.20	114			
ALGA0112091	11	13	63,470,641	*MGLL*	*cis*	0.79	0.21	114	-	-	INTERGENIC
ALGA0070440	11	13	63,588,824	*MGLL*	*cis*	0.79	0.21	114	-	-	INTERGENIC
MARC0058763	11	13	63,665,779	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ALGA0070472	11	13	64,137,647	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ALGA0070493	11	13	64,933,643	*MGLL*	*cis*	0.61	0.39	114	-	-	INTERGENIC
DRGA0012487	11	13	64,999,793	*MGLL*	*cis*	0.57	0.43	114	-	-	INTERGENIC
ASGA0057820	11	13	65,041,227	*MGLL*	*cis*	0.57	0.43	111	-	-	INTERGENIC
ALGA0070505	11	13	65,648,865	*MGLL*	*cis*	0.79	0.21	114	-	-	INTERGENIC
H3GA0036622	11	13	65,952,730	*MGLL*	*cis*	0.50	0.50	114	IL5RA	ENSSSCG00000011528	INTRONIC
ALGA0115138	11	13	66,145,615	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
MARC0096215	11	13	66,268,000	*MGLL*	*cis*	0.57	0.43	114	-	-	INTERGENIC
MARC0077830	11	13	66,315,906	*MGLL*	*cis*	0.57	0.43	114	-	-	INTERGENIC
ALGA0070545	11	13	66,348,482	*MGLL*	*cis*	0.57	0.43	114	-	-	INTERGENIC
ALGA0070557	11	13	66,460,974	*MGLL*	*cis*	0.52	0.48	114	-	-	INTERGENIC
MARC0110081	11	13	66,717,995	*MGLL*	*cis*	0.57	0.43	114	LRRN1	ENSSSCG00000023806	DOWNSTREAM
ALGA0115612	11	13	67,066,590	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
H3GA0036633	11	13	67,214,834	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
MARC0094085	11	13	67,289,917	*MGLL*	*cis*	0.80	0.20	114	SUMF1	ENSSSCG00000011532	INTRONIC
ALGA0070565	11	13	67,303,732	*MGLL*	*cis*	0.80	0.20	114	SUMF1	ENSSSCG00000011532	INTRONIC
H3GA0036644	11	13	67,397,487	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ASGA0057864	11	13	67,439,574	*MGLL*	*cis*	0.52	0.48	114	-	-	INTERGENIC
ALGA0070577	11	13	67,677,342	*MGLL*	*cis*	0.51	0.49	114	-	-	INTERGENIC
ALGA0070579	11	13	67,764,217	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ALGA0070583	11	13	67,822,598	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
DRGA0012516	11	13	67,918,828	*MGLL*	*cis*	0.80	0.20	114	ARL8B	ENSSSCG00000011535	INTRONIC
MARC0016713	11	13	68,100,531	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ALGA0070595	11	13	68,151,441	*MGLL*	*cis*	0.80	0.20	114	EDEM1	ENSSSCG00000020679	INTRONIC
ALGA0070608	11	13	68,207,174	*MGLL*	*cis*	0.80	0.20	114	-	-	INTERGENIC
ALGA0070612	11	13	68,279,611	*MGLL*	*cis*	0.58	0.42	114	-	-	INTERGENIC
DRGA0012520	11	13	68,402,608	*MGLL*	*cis*	0.52	0.48	114	-	-	INTERGENIC
ALGA0070619	11	13	68,529,027	*MGLL*	*cis*	0.60	0.40	114	-	-	INTERGENIC
ALGA0109826	11	13	68,552,642	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC
DRGA0012530	11	13	69,671,505	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC

MARC0080856	11	13	70,349,883	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC
ALGA0070645	11	13	70,563,982	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
DRGA0012562	11	13	71,601,046	*MGLL*	*cis*	0.54	0.46	114	-	-	INTERGENIC
ASGA0057937	11	13	71,634,446	*MGLL*	*cis*	0.55	0.45	114	-	-	INTERGENIC
ASGA0057936	11	13	71,661,735	*MGLL*	*cis*	0.69	0.31	114	-	-	INTERGENIC
ALGA0070705	11	13	72,217,472	*MGLL*	*cis*	0.51	0.49	114	LMCD1	ENSSSCG00000011538	INTRONIC
ASGA0057964	11	13	72,277,882	*MGLL*	*cis*	0.51	0.49	114	LMCD1	ENSSSCG00000011538	DOWNSTREAM
MARC0052393	11	13	72,320,984	*MGLL*	*cis*	0.51	0.49	114	SSUH2	ENSSSCG00000023082	3'UTR
MARC0015967	11	13	72,517,319	*MGLL*	*cis*	0.58	0.42	114	-	-	INTERGENIC
ALGA0115717	11	13	72,572,816	*MGLL*	*cis*	0.58	0.42	114	-	-	INTERGENIC
MARC0033394	11	13	72,574,306	*MGLL*	*cis*	0.52	0.48	114	-	-	INTERGENIC
H3GA0036693	11	13	72,895,609	*MGLL*	*cis*	0.52	0.48	114	SETD5	ENSSSCG00000011540	INTRONIC
ALGA0070709	11	13	72,975,884	*MGLL*	*cis*	0.52	0.48	114	LHFPL4	ENSSSCG00000011543	INTRONIC
ALGA0070717	11	13	73,058,596	*MGLL*	*cis*	0.66	0.34	114	MTMR 14	ENSSSCG00000011546	INTRONIC
ASGA0057975	11	13	73,107,395	*MGLL*	*cis*	0.66	0.34	114	OGG1	ENSSSCG00000011549	INTRONIC
MARC0037089	11	13	73,121,216	*MGLL*	*cis*	0.66	0.34	114	BRPF1	ENSSSCG00000011548	INTRONIC
DIAS0000744	11	13	73,139,546	*MGLL*	*cis*	0.66	0.34	114			
ALGA0070727	11	13	73,179,575	*MGLL*	*cis*	0.66	0.34	114	TTLL3	ENSSSCG00000011553	INTRONIC
ALGA0070736	11	13	73,342,777	*MGLL*	*cis*	0.66	0.34	114	FANCD 2	ENSSSCG00000011563	INTRONIC
ALGA0070746	11	13	73,529,988	*MGLL*	*cis*	0.66	0.34	114	-	ENSSSCG00000020719	UPSTREAM
DBKK0000291	11	13	73,562,335	*MGLL*	*cis*	0.66	0.34	114	SEC13	ENSSSCG00000011572	SYNONYMOUS
MARC0008575	11	13	73,609,814	*MGLL*	*cis*	0.69	0.31	114	ATP2B2	ENSSSCG00000023084	INTRONIC
ASGA0057995	11	13	73,749,480	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
H3GA0036725	11	13	73,807,719	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0111894	11	13	73,955,342	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0095999	11	13	73,959,641	*MGLL*	*cis*	0.69	0.31	114	-	-	INTERGENIC
H3GA0055439	11	13	74,216,361	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0002358	11	13	74,223,192	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0031633	11	13	74,237,321	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0070780	11	13	74,352,053	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0070777	11	13	74,364,519	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0046095	11	13	74,382,805	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ASGA0058022	11	13	74,464,820	*MGLL*	*cis*	0.68	0.32	114	HRH1	ENSSSCG00000011576	UPSTREAM
ASGA0058016	11	13	74,494,405	*MGLL*	*cis*	0.68	0.32	114	HRH1	ENSSSCG00000011576	INTRONIC
ALGA0070775	11	13	74,564,714	*MGLL*	*cis*	0.68	0.32	114	HRH1	ENSSSCG00000011576	INTRONIC
SIRI0000901	11	13	74,679,000	*MGLL*	*cis*	0.68	0.32	114			
ASGA0058032	11	13	75,066,887	*MGLL*	*cis*	0.69	0.31	114	-	-	INTERGENIC
ALGA0070790	11	13	75,084,617	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0019179	11	13	75,098,682	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0070793	11	13	75,170,684	*MGLL*	*cis*	0.68	0.32	114	TAMM 41	ENSSSCG00000011578	INTRONIC
ASGA0058030	11	13	75,263,496	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0070795	11	13	75,275,986	*MGLL*	*cis*	0.68	0.32	114	5_8S_r RNA	ENSSSCG00000019373	UPSTREAM
MARC0026104	11	13	75,400,094	*MGLL*	*cis*	0.68	0.32	114	SYN2	ENSSSCG00000023225	INTRONIC
ASGA0058041	11	13	75,539,907	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ISU10000701	11	13	75,577,805	*MGLL*	*cis*	0.68	0.32	114	PPARG	ENSSSCG00000011579	UPSTREAM
MARC0023801	11	13	75,723,927	*MGLL*	*cis*	0.68	0.32	114	TSEN2	ENSSSCG00000011580	INTRONIC
ASGA0058043	11	13	75,736,488	*MGLL*	*cis*	0.68	0.32	114	MKRN2 OS ; TSEN2	ENSSSCG00000011581 ENSSSCG00000011580	DOWNSTREAM
CASI0006992	11	13	76,136,374	*MGLL*	*cis*	0.68	0.32	114			

ASGA0058053	11	13	76,143,725	*MGLL*	*cis*	0.68	0.32	114	RHO	ENSSSCG00000011590	DOWNSTREAM
ASGA0058055	11	13	76,172,438	*MGLL*	*cis*	0.68	0.32	114	H1FOO	ENSSSCG00000011591	INTRONIC
ASGA0058060	11	13	76,212,117	*MGLL*	*cis*	0.68	0.32	114	PLXND 1	ENSSSCG00000011592	INTRONIC
ASGA0058062	11	13	76,230,975	*MGLL*	*cis*	0.68	0.32	114	PLXND 1	ENSSSCG00000011592	UPSTREAM
ALGA0070818	11	13	76,244,239	*MGLL*	*cis*	0.68	0.32	110	-	-	INTERGENIC
H3GA0036764	11	13	76,264,936	*MGLL*	*cis*	0.68	0.32	114	TMCC1	ENSSSCG00000011593	DOWNSTREAM
ALGA0070819	11	13	76,282,048	*MGLL*	*cis*	0.68	0.32	114	TMCC1	ENSSSCG00000011593	INTRONIC
INRA0040425	11	13	76,856,743	*MGLL*	*cis*	0.68	0.32	114			
ASGA0058079	11	13	77,581,700	*MGLL*	*cis*	0.68	0.32	114	SLC6A6	ENSSSCG00000011600	INTRONIC
ASGA0058083	11	13	77,635,903	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0124516	11	13	78,016,930	*MGLL*	*cis*	0.68	0.32	114	WNT7A	ENSSSCG00000011606	INTRONIC
MARC0069372	11	13	78,780,192	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0014783	11	13	78,935,288	*MGLL*	*cis*	0.68	0.32	114	ACAD9	ENSSSCG00000020690	INTRONIC
ASGA0096000	11	13	79,044,236	*MGLL*	*cis*	0.68	0.32	114	-	ENSSSCG00000024552	INTRONIC
ASGA0083811	11	13	79,111,100	*MGLL*	*cis*	0.68	0.32	114	EFCC1	ENSSSCG00000024000	INTRONIC
DIAS0001919	11	13	79,276,382	*MGLL*	*cis*	0.68	0.32	114			
MARC0093666	11	13	79,410,199	*MGLL*	*cis*	0.68	0.32	114	COPG1	ENSSSCG00000011616	3'UTR
ASGA0103932	11	13	80,063,897	*MGLL*	*cis*	0.65	0.35	114	MGLL	ENSSSCG00000024134	INTRONIC
MARC0054666	11	13	80,581,543	*MGLL*	*cis*	0.65	0.35	114	PLXNA 1	ENSSSCG00000024001	INTRONIC
ASGA0102308	11	13	80,715,219	*MGLL*	*cis*	0.65	0.35	114	TXNRD 3	ENSSSCG00000023929	INTRONIC
ASGA0093606	11	13	80,777,873	*MGLL*	*cis*	0.69	0.31	107	-	-	INTERGENIC
DRGA0012597	11	13	80,943,982	*MGLL*	*cis*	0.65	0.35	114	CHST13	ENSSSCG00000011625	UPSTREAM
ALGA0070897	11	13	81,083,948	*MGLL*	*cis*	0.59	0.41	114	-	-	INTERGENIC
ALGA0070915	11	13	81,338,092	*MGLL*	*cis*	0.65	0.35	111	ACAD1 1	ENSSSCG00000011629	INTRONIC
ALGA0070916	11	13	81,362,489	*MGLL*	*cis*	0.65	0.35	114	ACAD1 1	ENSSSCG00000011629	INTRONIC
INRA0040470	11	13	81,391,337	*MGLL*	*cis*	0.65	0.35	114			
MARC0047938	11	13	81,636,410	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0007815	11	13	81,649,116	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ASGA0090344	11	13	81,743,576	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
MARC0042047	11	13	81,902,962	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0070918	11	13	82,003,709	*MGLL*	*cis*	0.68	0.32	114	TMEM 108	ENSSSCG00000011635	INTRONIC
DRGA0012606	11	13	82,031,954	*MGLL*	*cis*	0.68	0.32	114	BFSP2	ENSSSCG00000011636	INTRONIC
ALGA0070925	11	13	82,085,380	*MGLL*	*cis*	0.68	0.32	114	BFSP2	ENSSSCG00000011636	INTRONIC
INRA0040493	11	13	82,450,638	*MGLL*	*cis*	0.68	0.32	114			
DRGA0012610	11	13	82,496,275	*MGLL*	*cis*	0.68	0.32	114	SRPRB	ENSSSCG00000011639	INTRONIC
ASGA0058169	11	13	82,550,213	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0070938	11	13	82,572,552	*MGLL*	*cis*	0.68	0.32	114	-	-	INTERGENIC
ALGA0070937	11	13	82,589,660	*MGLL*	*cis*	0.68	0.32	113	-	-	INTERGENIC
ALGA0016576	12	2	146,195,530	*NCOA1*	*trans*	0.91	0.09	114	ETF1	ENSSSCG00000014337	INTRONIC
MARC0045025	12	2	146,604,847	*NCOA1*	*trans*	0.91	0.09	114	CTNNA 1	ENSSSCG00000014339	INTRONIC
MARC0087200	12	2	146,722,998	*NCOA1*	*trans*	0.91	0.09	114	-	-	INTERGENIC
MARC0016562	**13**	6	143,952,619	*PIK3R1*	*trans*	0.62	0.38	114	-	-	INTERGENIC
ASGA0029993	13	6	143,976,085	*PIK3R1*	*trans*	0.61	0.39	114	-	-	INTERGENIC
ALGA0117336	13	6	145,605,378	*PIK3R1*	*trans*	0.54	0.46	114	C1orf1 77	ENSSSCG00000027362	INTRONIC
ALGA0113789	14	6	10,020,702	*PLA2G12A*	*trans*	0.81	0.19	114	VAT1L	ENSSSCG00000002696	INTRONIC
ALGA0103867	15	6	79,924,228	*PLA2G12A*	*trans*	0.66	0.34	114	-	-	INTERGENIC

ASGA0039774	16	8	128,899,782	*PLA2G12A*	*trans*	0.77	0.23	114	-	-	INTERGENIC
MARC0031261	16	8	134,024,195	*PLA2G12A*	*trans*	0.41	0.59	114	BMPR1B	ENSSSCG00000029621	INTRONIC
ALGA0108906	16	8	136,113,975	*PLA2G12A*	*trans*	0.54	0.46	114			
M1GA0003328	18	2	150,634,202	*PPARA*	*trans*	0.53	0.47	113	ARHGAP26	ENSSSCG00000014399	INTRONIC
MARC0074986	19	6	89,986,075	*PPARA*	*trans*	0.55	0.45	114	CEP192	ENSSSCG00000003673	INTRONIC
DIAS0004325	19	6	90,305,912	*PPARA*	*trans*	0.55	0.45	114			
CASI0006620	19	6	90,352,248	*PPARA*	*trans*	0.55	0.45	114			

* eSNP chromosomal location is given according to the Sscrofa10.2 assembly coordinates. Lengths are given in base pairs.

§ Number of animals considered to calculate allele frequencies.

Table S3. Gene annotation within the eQTL intervals. Annotation was performed by considering for *trans*-eQTLs the eQTL interval ±1Mb; whereas for *cis*-eQTLs only the studied gene was selected (*ACSM5, IGF2,* and *MGLL*).

Ensembl Gene ID	Associated Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Gene type	Description	Number of eQTLs	Gene	Orthologous
ENSSSCG00000026453	ACSM5	3	26172262	26260371	protein_coding	acyl-CoA synthetase medium-chain family member 5 [Source:HGNC Symbol;Acc:HGNC:26060]	1	ACSM5-cis	ACSM5
ENSSSCG00000008432	C2orf61	3	99516479	99563892	protein_coding	chromosome 2 open reading frame 61 [Source:HGNC Symbol;Acc:HGNC:26850]	2	ACSM5-trans	C2orf61
ENSSSCG00000008433	CALM1	3	99567552	99581893	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F2Z5G3]	2	ACSM5-trans	CALM1
ENSSSCG00000008434	TTC7A	3	99602190	99646256	protein_coding	tetratricopeptide repeat domain 7A [Source:HGNC Symbol;Acc:HGNC:19750]	2	ACSM5-trans	TTC7A
ENSSSCG00000021325	MCFD2	3	99714046	99719396	protein_coding	multiple coagulation factor deficiency 2 [Source:HGNC Symbol;Acc:HGNC:18451]	2	ACSM5-trans	MCFD2
ENSSSCG00000008436		3	99774207	99774661	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S5M3]	2	ACSM5-trans	
ENSSSCG00000008437	SOCS5	3	99871903	99939833	protein_coding	Sus scrofa suppressor of cytokine signaling 5 (SOCS5), mRNA. [Source:RefSeq mRNA;Acc:NM_001162890]	2	ACSM5-trans	SOCS5
ENSSSCG00000008440	PIGF	3	100009942	100014286	protein_coding	phosphatidylinositol glycan anchor biosynthesis, class F [Source:HGNC Symbol;Acc:HGNC:8962]	2	ACSM5-trans	PIGF
ENSSSCG00000008439	RHOQ	3	100058022	100097054	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F2Z5G1]	2	ACSM5-trans	RHOQ
ENSSSCG00000025420	U6	3	100065521	100065627	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	2	ACSM5-trans	U6
ENSSSCG00000008441	ATP6V1E2	3	100117152	100117832	protein_coding	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2 [Source:HGNC Symbol;Acc:HGNC:18125]	2	ACSM5-trans	ATP6V1E2
ENSSSCG00000008442	TMEM247	3	100146888	100151357	protein_coding	transmembrane protein 247 [Source:HGNC Symbol;Acc:HGNC:42967]	2	ACSM5-trans	TMEM247
ENSSSCG00000008443	EPAS1	3	100173612	100213334	protein_coding	Sus scrofa endothelial PAS domain protein 1 (EPAS1), mRNA. [Source:RefSeq mRNA;Acc:NM_001097420]	2	ACSM5-trans	EPAS1
ENSSSCG00000008444	PRKCE	3	100427913	100615864	protein_coding	protein kinase C, epsilon [Source:HGNC Symbol;Acc:HGNC:9401]	2	ACSM5-trans	PRKCE
ENSSSCG00000008445	SRBD1	3	101017493	101209095	protein_coding	S1 RNA binding domain 1 [Source:HGNC Symbol;Acc:HGNC:25521]	2	ACSM5-trans	SRBD1
ENSSSCG00000010793	DCTN5	10	2661	17242	protein_coding	dynactin 5 (p25) [Source:HGNC Symbol;Acc:HGNC:24594]	3	ACSM5-trans	DCTN5
ENSSSCG00000010794	PALB2	10	17295	43957	protein_coding	partner and localizer of BRCA2 [Source:HGNC Symbol;Acc:HGNC:26144]	3	ACSM5-trans	PALB2
ENSSSCG00000010795	NDUFAB1	10	50589	62614	protein_coding	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa [Source:HGNC Symbol;Acc:HGNC:7694]	3	ACSM5-trans	NDUFAB1
ENSSSCG00000010796	UBFD1	10	74434	86228	protein_coding	ubiquitin family domain containing 1 [Source:HGNC Symbol;Acc:HGNC:30565]	3	ACSM5-trans	UBFD1
ENSSSCG00000010797	EARS2	10	86465	115567	protein_coding	glutamyl-tRNA synthetase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:29419]	3	ACSM5-trans	EARS2
ENSSSCG00000010798	GGA2	10	135679	165446	protein_coding	golgi-associated, gamma adaptin ear containing, ARF binding protein 2 [Source:HGNC Symbol;Acc:HGNC:16064]	3	ACSM5-trans	GGA2
ENSSSCG00000010799	COG7	10	171589	254079	protein_coding	component of oligomeric golgi complex 7 [Source:HGNC Symbol;Acc:HGNC:18622]	3	ACSM5-trans	COG7
ENSSSCG00000028923		10	309239	337906	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LGX7]	3	ACSM5-trans	SCNN1B
ENSSSCG00000023093		10	328476	328570	miRNA		3	ACSM5-trans	

ENSSSCG00000029791		8	14998877	15018730	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LTN3]	4	CROT	
ENSSSCG00000008749	SLIT2	8	15355493	15443176	protein_coding	slit homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:11086]	4	CROT	SLIT2
ENSSSCG00000023893	ssc-mir-218-1	8	15443762	15443845	miRNA	ssc-mir-218-1 [Source:miRBase;Acc:MI0015924]	4	CROT	ssc-mir-218-1
ENSSSCG00000008750	PACRGL	8	15450655	15470225	protein_coding	PARK2 co-regulated-like [Source:HGNC Symbol;Acc:HGNC:28442]	4	CROT	PACRGL
ENSSSCG00000023934	KCNIP4	8	15471132	15609158	protein_coding	Kv channel interacting protein 4 [Source:HGNC Symbol;Acc:HGNC:30083]	4	CROT	KCNIP4
ENSSSCG00000028224		8	15579229	15580803	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LB18]	4	CROT	
ENSSSCG00000008753	ADGRA3	8	16905166	16910788	protein_coding	adhesion G protein-coupled receptor A3 [Source:HGNC Symbol;Acc:HGNC:13839]	4	CROT	ADGRA3
ENSSSCG00000009535	EFNB2	11	81565082	81610206	protein_coding	Sus scrofa ephrin-B2 (EFNB2), mRNA. [Source:RefSeq mRNA;Acc:NM_001114286]	5	FABP3	EFNB2
ENSSSCG00000009536	ARGLU1	11	81616020	81643873	protein_coding	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:HGNC:25482]	5	FABP3	ARGLU1
ENSSSCG00000027392	U6	11	81826840	81826946	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	5	FABP3	U6
ENSSSCG00000016840		11	81827710	81828106	pseudogene		5	FABP3	
ENSSSCG00000009537	FAM155A	11	82190417	82226221	protein_coding	family with sequence similarity 155, member A [Source:HGNC Symbol;Acc:HGNC:33877]	5	FABP3	FAM155A
ENSSSCG00000009539		11	82924144	82925148	protein_coding		5	FABP3	Rpl5
ENSSSCG00000020247	U6	11	82933949	82934054	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	5	FABP3	U6
ENSSSCG00000009540	LIG4	11	82953471	82956203	protein_coding	ligase IV, DNA, ATP-dependent [Source:HGNC Symbol;Acc:HGNC:6601]	5	FABP3	LIG4
ENSSSCG00000009541	ABHD13	11	82962703	82981428	protein_coding	abhydrolase domain containing 13 [Source:HGNC Symbol;Acc:HGNC:20293]	5	FABP3	ABHD13
ENSSSCG00000009542	TNFSF13B	11	83014418	83046597	protein_coding	Sus scrofa tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. [Source:RefSeq mRNA;Acc:NM_001097498]	5	FABP3	TNFSF13B
ENSSSCG00000029470	POMP	11	5755487	5758255	protein_coding	proteasome maturation protein [Source:HGNC Symbol;Acc:HGNC:20330]	6	FOS	POMP
ENSSSCG00000025996		11	5849650	5934897	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LU86]	6	FOS	
ENSSSCG00000009323	MTUS2	11	6139104	6174042	protein_coding	microtubule associated tumor suppressor candidate 2 [Source:HGNC Symbol;Acc:HGNC:20595]	6	FOS	MTUS2
ENSSSCG00000029456	SLC7A1	11	6181362	6188211	protein_coding	Sus scrofa solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. [Source:RefSeq mRNA;Acc:NM_001012613]	6	FOS	SLC7A1
ENSSSCG00000022344		11	6284506	6298410	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RST9]	6	FOS	UBL3
ENSSSCG00000009324		11	6317524	6359908	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSU0]	6	FOS	SLC7A1
ENSSSCG00000023265		11	6456359	6470262	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RST9]	6	FOS	UBL3
ENSSSCG00000009326	KATNAL1	11	6760617	6803995	protein_coding	katanin p60 subunit A-like 1 [Source:HGNC Symbol;Acc:HGNC:28361]	6	FOS	KATNAL1
ENSSSCG00000009328		11	6990311	7005937	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RST7]	6	FOS	
ENSSSCG00000009327	HMGB1	11	7125533	7133000	protein_coding	high mobility group box 1 [Source:HGNC Symbol;Acc:HGNC:4983]	6	FOS	HMGB1
ENSSSCG00000028065	USPL1	11	7207278	7213789	protein_coding	ubiquitin specific peptidase like 1 [Source:HGNC Symbol;Acc:HGNC:20294]	6	FOS	USPL1
ENSSSCG00000009330	ALOX5AP	11	7261120	7287563	protein_coding	Sus scrofa arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA. [Source:RefSeq mRNA;Acc:NM_001164001]	6	FOS	ALOX5AP
ENSSSCG00000009331	MEDAG	11	7396534	7414732	protein_coding	mesenteric estrogen-dependent adipogenesis [Source:HGNC Symbol;Acc:HGNC:25926]	6	FOS	MEDAG

ENSSSCG00000009332	TEX26	11	7419907	7445573	protein_coding	testis expressed 26 [Source:HGNC Symbol;Acc:HGNC:28622]	6	FOS	TEX26
ENSSSCG00000026489	U6	11	7510599	7510702	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	6	FOS	U6
ENSSSCG00000009333		11	7528247	7566264	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RST2]	6	FOS	Wdr95
ENSSSCG00000009334	HSPH1	11	7585525	7661067	protein_coding	Sus scrofa heat shock 105kDa/110kDa protein 1 (HSPH1), mRNA. [Source:RefSeq mRNA;Acc:NM_001097504]	6	FOS	HSPH1
ENSSSCG00000026013	U6	11	7686855	7686958	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	6	FOS	U6
ENSSSCG00000029562		11	7754092	7754191	miRNA		6	FOS	
ENSSSCG00000009335	B3GALTL	11	7775851	7875184	protein_coding	beta 1,3-galactosyltransferase-like [Source:HGNC Symbol;Acc:HGNC:20207]	6	FOS	B3GALTL
ENSSSCG00000009336		11	8312524	8336889	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSS8]	6	FOS	RXFP2
ENSSSCG00000009338	FRY	11	8441468	8505378	protein_coding	furry homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:20367]	6	FOS	FRY
ENSSSCG00000009337		11	8547656	8586898	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSS6]	6	FOS	FRY
ENSSSCG00000023699		11	8592391	8596779	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSS7]	6	FOS	
ENSSSCG00000024888		11	8635383	8643423	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LBU1]	6	FOS	
ENSSSCG00000009346		11	8713904	8738650	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSR7]	6	FOS	N4bp2l2
ENSSSCG00000028932		11	8859998	8881844	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L5Z6]	6	FOS	
ENSSSCG00000021725	PDS5B	11	8911211	8915009	protein_coding	PDS5 cohesin associated factor B [Source:HGNC Symbol;Acc:HGNC:20418]	6	FOS	PDS5B
ENSSSCG00000009345		11	9020844	9044196	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSR8]	6	FOS	
ENSSSCG00000020174	U6	11	9076065	9076168	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	6	FOS	U6
ENSSSCG00000009347	KL	11	9345005	9392395	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSR6]	6	FOS	KL
ENSSSCG00000009348		11	9429665	9467656	protein_coding		6	FOS	STARD13
ENSSSCG00000009349	RFC3	11	10050846	10218454	protein_coding	replication factor C (activator 1) 3, 38kDa [Source:HGNC Symbol;Acc:HGNC:9971]	6	FOS	RFC3
ENSSSCG00000021829		11	11141413	11236840	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LML0]	6	FOS	
ENSSSCG00000021980		11	11291633	11293597	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L915]	6	FOS	
ENSSSCG00000029214		11	11325529	11327563	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L6R4]	6	FOS	
ENSSSCG00000030057		11	11349791	11353706	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L8B6]	6	FOS	
ENSSSCG00000020699		11	11355261	11378042	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LCS0]	6	FOS	
ENSSSCG00000009350		11	11439456	11659219	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSR3]	6	FOS	
ENSSSCG00000009351	MAB21L1	11	11568959	11570038	protein_coding	mab-21-like 1 (C. elegans) [Source:HGNC Symbol;Acc:HGNC:6757]	6	FOS	MAB21L1
ENSSSCG00000028213	U4	11	11627450	11627577	snRNA	U4 spliceosomal RNA [Source:RFAM;Acc:RF00015]	6	FOS	U4
ENSSSCG00000021381	NBEA	11	11684216	11750222	protein_coding	neurobeachin [Source:HGNC Symbol;Acc:HGNC:7648]	6	FOS	NBEA
ENSSSCG00000009352		11	11813459	11857640	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSR2]	6	FOS	DCLK1
ENSSSCG00000030111		11	11871940	11933177	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LJW1]	6	FOS	DCLK1
ENSSSCG00000029956		11	12116307	12116708	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L5C8]	6	FOS	DCLK1
ENSSSCG00000026164		11	12153276	12196294	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LBW9]	6	FOS	SOHLH2
ENSSSCG00000009353		11	12231552	12255683	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RSR1]	6	FOS	SPG20
ENSSSCG00000024635		11	12264417	12281396	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LMW6]	6	FOS	SPG20

ENSSSCG00000026564		11	12284861	12327375	protein_coding		6	FOS	
ENSSSCG00000009354	CCNA1	11	12355646	12364743	protein_coding	cyclin A1 [Source:HGNC Symbol;Acc:HGNC:1577]	6	FOS	CCNA1
ENSSSCG00000009355	SERTM1	11	12544491	12544814	protein_coding	serine-rich and transmembrane domain containing 1 [Source:HGNC Symbol;Acc:HGNC:33792]	6	FOS	SERTM1
ENSSSCG00000009356	RFXAP	11	12636923	12641834	protein_coding	regulatory factor X-associated protein [Source:HGNC Symbol;Acc:HGNC:9988]	6	FOS	RFXAP
ENSSSCG00000009357	SMAD9	11	12649696	12713009	protein_coding	Sus scrofa SMAD family member 9 (SMAD9), mRNA. [Source:RefSeq mRNA;Acc:NM_001195510]	6	FOS	SMAD9
ENSSSCG00000025521		11	12724510	12736276	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LGL3]	6	FOS	ALG5
ENSSSCG00000026613		11	12772405	12776621	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LPG2]	6	FOS	
ENSSSCG00000009358	EXOSC8	11	12778571	12784006	protein_coding	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17035]	6	FOS	EXOSC8
ENSSSCG00000009360	ALG5	11	12785056	12798122	protein_coding	dolichyl-phosphate beta-glucosyltransferase [Source:RefSeq peptide;Acc:NP_001231249]	6	FOS	ALG5
ENSSSCG00000009359	SUPT20H	11	12818502	12827481	protein_coding	suppressor of Ty 20 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:20596]	6	FOS	SUPT20H
IGF2	IGF2	2			protein_coding		8	IGF2-cis	IGF2
ENSSSCG00000024767		2	161099733	161100671	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:I3LDD7]	9	IGF2-trans	OR2T8
ENSSSCG00000021614		2	161166325	161167254	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:I3LLM2]	9	IGF2-trans	Olfr315
ENSSSCG00000027633		2	161223288	161224690	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RH05]	9	IGF2-trans	OR14C36
ENSSSCG00000021127		2	161253405	161254349	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:I3LCG0]	9	IGF2-trans	Olfr165
ENSSSCG00000024040		2	161382814	161383755	protein_coding		9	IGF2-trans	
ENSSSCG00000020815		2	161437708	161438670	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:I3L6S7]	9	IGF2-trans	OR2T29
ENSSSCG00000025019		2	161452575	161453537	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:I3LE37]	9	IGF2-trans	OR2T29
ENSSSCG00000029373	OR2T1	2	161501749	161502693	protein_coding	olfactory receptor, family 2, subfamily T, member 1 [Source:HGNC Symbol;Acc:HGNC:8277]	9	IGF2-trans	OR2T1
ENSSSCG00000028636		2	161635323	161636276	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:I3L9D2]	9	IGF2-trans	OR2T11
ENSSSCG00000027925		2	161685648	161686601	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:I3LI88]	9	IGF2-trans	OR2T11
ENSSSCG00000014553		2	161868269	161869222	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:F1RGZ9]	9	IGF2-trans	OR2T3
ENSSSCG00000014552		2	161918284	161919216	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:F1RH00]	9	IGF2-trans	OR2T3
ENSSSCG00000014551		2	161930185	161931129	protein_coding	Olfactory receptor [Source:UniProtKB/TrEMBL;Acc:F1RH01]	9	IGF2-trans	OR2T29
ENSSSCG00000021366		2	161971025	161972318	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LUD3]	9	IGF2-trans	OR2T29
ENSSSCG00000021903		2	162076800	162077818	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGC3]	9	IGF2-trans	IFITM3
ENSSSCG00000014565		2	162095326	162097509	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGC4]	9	IGF2-trans	IFITM3
ENSSSCG00000014564	IFITM1	2	162099157	162210447	protein_coding	Sus scrofa interferon induced transmembrane protein 2 (IFITM2), mRNA. [Source:RefSeq mRNA;Acc:NM_001246214]	9	IGF2-trans	IFITM1
ENSSSCG00000024218		2	162116301	162117384	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGC6]	9	IGF2-trans	IFITM5
ENSSSCG00000014562		2	162119619	162125406	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGC7]	9	IGF2-trans	ATHL1
ENSSSCG00000014561	NLRP6	2	162127965	162133634	protein_coding	NLR family, pyrin domain containing 6 [Source:HGNC Symbol;Acc:HGNC:22944]	9	IGF2-trans	NLRP6
ENSSSCG00000014560	COX8H	2	162153945	162155478	protein_coding	Sus scrofa COX8H protein (COX8H), mRNA. [Source:RefSeq mRNA;Acc:NM_001097500]	9	IGF2-trans	COX8H

ENSSSCG00000014559	PSMD13	2	162155823	162169535	protein_coding	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 [Source:HGNC Symbol;Acc:HGNC:9558]	9	IGF2-trans	PSMD13
ENSSSCG00000014558	SIRT3	2	162170117	162186215	protein_coding	Sus scrofa sirtuin 3 (SIRT3), mRNA. [Source:RefSeq mRNA;Acc:NM_001110057]	9	IGF2-trans	SIRT3
ENSSSCG00000014557	RIC8A	2	162186807	162192534	protein_coding	RIC8 guanine nucleotide exchange factor A [Source:HGNC Symbol;Acc:HGNC:29550]	9	IGF2-trans	RIC8A
ENSSSCG00000014556	BET1L	2	162193997	162195837	protein_coding	Bet1 golgi vesicular membrane trafficking protein-like [Source:HGNC Symbol;Acc:HGNC:19348]	9	IGF2-trans	BET1L
ENSSSCG00000014555	ODF3	2	162199735	162202834	protein_coding	outer dense fiber of sperm tails 3 [Source:HGNC Symbol;Acc:HGNC:19905]	9	IGF2-trans	ODF3
ENSSSCG00000014554		2	162203934	162205246	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGZ8]	9	IGF2-trans	SCGB1C2
ENSSSCG00000027302	PKP3	2	162275727	162284660	protein_coding	plakophilin 3 [Source:HGNC Symbol;Acc:HGNC:9025]	9	IGF2-trans	PKP3
ENSSSCG00000024389		2	162285371	162291360	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LD75]	9	IGF2-trans	SIGIRR
ENSSSCG00000024569		2	162294063	162307380	protein_coding	Anoctamin [Source:UniProtKB/TrEMBL;Acc:I3LGT9]	9	IGF2-trans	ANO9
ENSSSCG00000025023		2	162310113	162315342	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LIX6]	9	IGF2-trans	ATHL1
ENSSSCG00000027871		2	162318139	162319222	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGC6]	9	IGF2-trans	IFITM5
ENSSSCG00000028736		2	162339842	162340860	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LUQ7]	9	IGF2-trans	IFITM3
ENSSSCG00000020784	TNFSF15	1	286440638	286461441	protein_coding	Sus scrofa tumor necrosis factor (ligand) superfamily, member 15 (TNFSF15), mRNA. [Source:RefSeq mRNA;Acc:NM_001244555]	10	MGLL-trans	TNFSF15
ENSSSCG00000026633	TNFRSF8	1	286544943	286571421	protein_coding	Sus scrofa tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), mRNA. [Source:RefSeq mRNA;Acc:NM_001025219]	10	MGLL-trans	TNFRSF8
ENSSSCG00000026492		1	286604311	286608866	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1SMI6]	10	MGLL-trans	
ENSSSCG00000025956		1	286640943	286648888	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LUI4]	10	MGLL-trans	
ENSSSCG00000005494	TNC	1	286732772	286813962	protein_coding	tenascin precursor [Source:RefSeq peptide;Acc:NP_999395]	10	MGLL-trans	TNC
ENSSSCG00000005498	PAPPA	1	287904367	288136642	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1SMI4]	10	MGLL-trans	PAPPA
ENSSSCG00000030322		1	288324350	288434321	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LL19]	10	MGLL-trans	
ENSSSCG00000024134	MGLL	13	79998364	80086913	protein_coding	Sus scrofa monoglyceride lipase (MGLL), mRNA. [Source:RefSeq mRNA;Acc:NM_001143718]	11	MGLL-cis	MGLL
ENSSSCG00000014321	KLHL3	2	145357374	145464551	protein_coding	kelch-like family member 3 [Source:HGNC Symbol;Acc:HGNC:6354]	12	NCOA1	KLHL3
ENSSSCG00000018618	ssc-mir-874	2	145381099	145381176	miRNA	ssc-mir-874 [Source:miRBase;Acc:MI0022157]	12	NCOA1	ssc-mir-874
ENSSSCG00000014322	HNRNPA0	2	145502990	145503956	protein_coding	heterogeneous nuclear ribonucleoprotein A0 [Source:HGNC Symbol;Acc:HGNC:5030]	12	NCOA1	HNRNPA0
ENSSSCG00000014323		2	145543965	145546116	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RH93]	12	NCOA1	Npy6r
ENSSSCG00000014324	MYOT	2	145621370	145642089	protein_coding	myotilin [Source:HGNC Symbol;Acc:HGNC:12399]	12	NCOA1	MYOT
ENSSSCG00000026421	PKD2L2	2	145644303	145652786	protein_coding	polycystic kidney disease 2-like 2 [Source:HGNC Symbol;Acc:HGNC:9012]	12	NCOA1	PKD2L2
ENSSSCG00000021604		2	145674704	145681954	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LVQ4]	12	NCOA1	
ENSSSCG00000029125	FAM13B	2	145684311	145752899	protein_coding	family with sequence similarity 13, member B [Source:HGNC Symbol;Acc:HGNC:1335]	12	NCOA1	FAM13B
ENSSSCG00000023647	WNT8A	2	145778004	145783391	protein_coding	wingless-type MMTV integration site family, member 8A [Source:HGNC Symbol;Acc:HGNC:12788]	12	NCOA1	WNT8A
ENSSSCG00000027997	NME5	2	145831079	145865569	protein_coding	NME/NM23 family member 5 [Source:HGNC Symbol;Acc:HGNC:7853]	12	NCOA1	NME5
ENSSSCG00000021426		2	145866784	145879056	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LCW6]	12	NCOA1	4933408B17Rik

ENSSSCG00000014327	BRD8	2	145880841	145900801	protein_coding	bromodomain containing 8 [Source:HGNC Symbol;Acc:HGNC:19874]	12	NCOA1	BRD8
ENSSSCG00000014326	KIF20A	2	145901081	145910004	protein_coding	kinesin family member 20A [Source:HGNC Symbol;Acc:HGNC:9787]	12	NCOA1	KIF20A
ENSSSCG00000014325	CDC23	2	145910226	145929682	protein_coding	Sus scrofa cell division cycle 23 homolog (S. cerevisiae) (CDC23), mRNA. [Source:RefSeq mRNA;Acc:NM_001267826]	12	NCOA1	CDC23
ENSSSCG00000014328	GFRA3	2	145962126	145982576	protein_coding	GDNF family receptor alpha 3 [Source:HGNC Symbol;Acc:HGNC:4245]	12	NCOA1	GFRA3
ENSSSCG00000014329	CDC25C	2	145988074	146023662	protein_coding	Sus scrofa cell division cycle 25 homolog C (S. pombe) (CDC25C), mRNA. [Source:RefSeq mRNA;Acc:NM_001123095]	12	NCOA1	CDC25C
ENSSSCG00000023691		2	146024185	146027368	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LHJ1]	12	NCOA1	SLBP2
ENSSSCG00000028823		2	146024826	146024925	miRNA		12	NCOA1	AL596330.1
ENSSSCG00000026880		2	146030416	146030485	miRNA		12	NCOA1	
ENSSSCG00000021092	FAM53C	2	146033753	146039799	protein_coding	family with sequence similarity 53, member C [Source:HGNC Symbol;Acc:HGNC:1336]	12	NCOA1	FAM53C
ENSSSCG00000014331	KDM3B	2	146045349	146114676	protein_coding	lysine (K)-specific demethylase 3B [Source:HGNC Symbol;Acc:HGNC:1337]	12	NCOA1	KDM3B
ENSSSCG00000028081		2	146124809	146127019	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LGL0]	12	NCOA1	Fam53c
ENSSSCG00000014335	REEP2	2	146132308	146137792	protein_coding	receptor accessory protein 2 [Source:HGNC Symbol;Acc:HGNC:17975]	12	NCOA1	REEP2
ENSSSCG00000014336	EGR1	2	146156065	146160020	protein_coding	early growth response 1 [Source:HGNC Symbol;Acc:HGNC:3238]	12	NCOA1	EGR1
ENSSSCG00000014337	ETF1	2	146186428	146219318	protein_coding	eukaryotic translation termination factor 1 [Source:HGNC Symbol;Acc:HGNC:3477]	12	NCOA1	ETF1
ENSSSCG00000014338	HSPA9	2	146229842	146246784	protein_coding	Stress-70 protein, mitochondrial [Source:UniProtKB/TrEMBL;Acc:F1RGJ3]	12	NCOA1	HSPA9
ENSSSCG00000019602	SNORD63	2	146235153	146235223	snoRNA	Small nucleolar RNA SNORD63 [Source:RFAM;Acc:RF00154]	12	NCOA1	SNORD63
ENSSSCG00000014339	CTNNA1	2	146440622	146624740	protein_coding	catenin (cadherin-associated protein), alpha 1, 102kDa [Source:HGNC Symbol;Acc:HGNC:2509]	12	NCOA1	CTNNA1
ENSSSCG00000022546		2	146564096	146565646	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGJ0]	12	NCOA1	LRRTM2
ENSSSCG00000024543		2	146701916	146703466	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGJ0]	12	NCOA1	LRRTM2
ENSSSCG00000024189	SIL1	2	146842295	146859268	protein_coding	SIL1 nucleotide exchange factor [Source:HGNC Symbol;Acc:HGNC:24624]	12	NCOA1	SIL1
ENSSSCG00000014342		2	146889128	146952329	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGI9]	12	NCOA1	
ENSSSCG00000020188	SNORA74	2	147011745	147011885	snoRNA	Small nucleolar RNA SNORA74 [Source:RFAM;Acc:RF00090]	12	NCOA1	SNORA74
ENSSSCG00000018891	SNORA74	2	147014072	147014271	snoRNA	Small nucleolar RNA SNORA74 [Source:RFAM;Acc:RF00090]	12	NCOA1	SNORA74
ENSSSCG00000014343		2	147027901	147059819	protein_coding		12	NCOA1	MATR3
ENSSSCG00000026606	PAIP2	2	147068043	147090813	protein_coding	poly(A) binding protein interacting protein 2 [Source:HGNC Symbol;Acc:HGNC:17970]	12	NCOA1	PAIP2
ENSSSCG00000026423	SLC23A1	2	147088755	147107049	protein_coding	solute carrier family 23 (ascorbic acid transporter), member 1 [Source:HGNC Symbol;Acc:HGNC:10974]	12	NCOA1	SLC23A1
ENSSSCG00000029239	MZB1	2	147107912	147110247	protein_coding	marginal zone B and B1 cell-specific protein [Source:HGNC Symbol;Acc:HGNC:30125]	12	NCOA1	MZB1
ENSSSCG00000014347	PROB1	2	147112697	147115756	protein_coding	proline-rich basic protein 1 [Source:HGNC Symbol;Acc:HGNC:41906]	12	NCOA1	PROB1
ENSSSCG00000014348	SPATA24	2	147117507	147123827	protein_coding	Sus scrofa spermatogenesis associated 24 (SPATA24), mRNA. [Source:RefSeq mRNA;Acc:NM_001177922]	12	NCOA1	SPATA24
ENSSSCG00000024934		2	147137156	147147197	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LDN3]	12	NCOA1	
ENSSSCG00000014351		2	147153616	147162665	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGG9]	12	NCOA1	ECSCR

ENSSSCG00000014350		2	147165660	147166058	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RGH1]	12	NCOA1	1700066B19Rik
ENSSSCG00000014349	TMEM173	2	147169469	147177252	protein_coding	transmembrane protein 173 [Source:HGNC Symbol;Acc:HGNC:27962]	12	NCOA1	TMEM173
ENSSSCG00000014356	DNAJC18	2	147196150	147212221	protein_coding	DnaJ (Hsp40) homolog, subfamily C, member 18 [Source:HGNC Symbol;Acc:HGNC:28429]	12	NCOA1	DNAJC18
ENSSSCG00000014359	PSD2	2	147280801	147307996	protein_coding	pleckstrin and Sec7 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:19092]	12	NCOA1	PSD2
ENSSSCG00000014357	CXXC5	2	147317594	147321676	protein_coding	CXXC finger protein 5 [Source:HGNC Symbol;Acc:HGNC:26943]	12	NCOA1	CXXC5
ENSSSCG00000026374		2	147424679	147434964	protein_coding		12	NCOA1	
ENSSSCG00000026470		2	147508741	147512727	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LGU5]	12	NCOA1	
ENSSSCG00000029541		2	147515778	147546602	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LAZ5]	12	NCOA1	PSD2
ENSSSCG00000021082		2	147550519	147554780	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LS05]	12	NCOA1	NRG2
ENSSSCG00000025040	NRG2	2	147648534	147653247	protein_coding	neuregulin 2 [Source:HGNC Symbol;Acc:HGNC:7998]	12	NCOA1	NRG2
ENSSSCG00000003833	DAB1	6	142972837	143127238	protein_coding	Sus scrofa disabled homolog 1 (Drosophila) (DAB1), mRNA. [Source:RefSeq mRNA;Acc:NM_001097442]	13	PIK3R1	DAB1
ENSSSCG00000003834	C8B	6	143164815	143205954	protein_coding	Sus scrofa complement component 8, beta polypeptide (C8B), mRNA. [Source:RefSeq mRNA;Acc:NM_001097451]	13	PIK3R1	C8B
ENSSSCG00000003835	C8A	6	143217660	143266610	protein_coding	complement component C8 alpha chain precursor [Source:RefSeq peptide;Acc:NP_001090919]	13	PIK3R1	C8A
ENSSSCG00000003836		6	143478850	143485480	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S787]	13	PIK3R1	1700024P16Rik
ENSSSCG00000003838		6	143517368	143517922	pseudogene		13	PIK3R1	
ENSSSCG00000003837	PRKAA2	6	143547628	143573947	protein_coding	5'-AMP-activated protein kinase catalytic subunit alpha-2 [Source:RefSeq peptide;Acc:NP_999431]	13	PIK3R1	PRKAA2
ENSSSCG00000026682	C1orf168	6	143581803	143591161	protein_coding	chromosome 1 open reading frame 168 [Source:HGNC Symbol;Acc:HGNC:27295]	13	PIK3R1	C1orf168
ENSSSCG00000003839	PPAP2B	6	143689175	143732390	protein_coding	phosphatidic acid phosphatase type 2B [Source:HGNC Symbol;Acc:HGNC:9229]	13	PIK3R1	PPAP2B
ENSSSCG00000024345		6	145266837	145273453	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L9M0]	13	PIK3R1	
ENSSSCG00000029633	USP24	6	145323643	145450640	protein_coding	ubiquitin specific peptidase 24 [Source:HGNC Symbol;Acc:HGNC:12623]	13	PIK3R1	USP24
ENSSSCG00000025020	PCSK9	6	145451967	145473280	protein_coding	proprotein convertase subtilisin/kexin type 9 [Source:HGNC Symbol;Acc:HGNC:20001]	13	PIK3R1	PCSK9
ENSSSCG00000020989	BSND	6	145489573	145496027	protein_coding	barttin CLCNK-type chloride channel accessory beta subunit [Source:HGNC Symbol;Acc:HGNC:16512]	13	PIK3R1	BSND
ENSSSCG00000025097	TMEM61	6	145505144	145514876	protein_coding	Sus scrofa transmembrane protein 61 (TMEM61), mRNA. [Source:RefSeq mRNA;Acc:NM_001243365]	13	PIK3R1	TMEM61
ENSSSCG00000027525	DHCR24	6	145547688	145582947	protein_coding	Sus scrofa 24-dehydrocholesterol reductase (DHCR24), mRNA. [Source:RefSeq mRNA;Acc:NM_001243354]	13	PIK3R1	DHCR24
ENSSSCG00000027362	C1orf177	6	145596736	145617162	protein_coding	chromosome 1 open reading frame 177 [Source:HGNC Symbol;Acc:HGNC:26854]	13	PIK3R1	C1orf177
ENSSSCG00000003842	TTC22	6	145620012	145643859	protein_coding	tetratricopeptide repeat domain 22 [Source:HGNC Symbol;Acc:HGNC:26067]	13	PIK3R1	TTC22
ENSSSCG00000003843	PARS2	6	145656431	145657849	protein_coding	prolyl-tRNA synthetase 2, mitochondrial (putative) [Source:HGNC Symbol;Acc:HGNC:30563]	13	PIK3R1	PARS2
ENSSSCG00000003844	TTC4	6	145679556	145715195	protein_coding	tetratricopeptide repeat domain 4 [Source:HGNC Symbol;Acc:HGNC:12394]	13	PIK3R1	TTC4
ENSSSCG00000003845		6	145721149	145778826	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S770]	13	PIK3R1	MROH7-TTC4
ENSSSCG00000029698	LRRC42	6	145862151	145879058	protein_coding	leucine rich repeat containing 42 [Source:HGNC	13	PIK3R1	LRRC42

						Symbol;Acc:HGNC:28792]			
ENSSSCG00000027641	LDLRAD1	6	145893272	145902399	protein_coding	low density lipoprotein receptor class A domain containing 1 [Source:HGNC Symbol;Acc:HGNC:32069]	13	PIK3R1	LDLRAD1
ENSSSCG00000022494	TMEM59	6	145909244	145933295	protein_coding	Sus scrofa transmembrane protein 59 (TMEM59), mRNA. [Source:RefSeq mRNA;Acc:NM_001044558]	13	PIK3R1	TMEM59
ENSSSCG00000021216	TCEANC2	6	145933529	145975394	protein_coding	transcription elongation factor A (SII) N-terminal and central domain containing 2 [Source:HGNC Symbol;Acc:HGNC:26494]	13	PIK3R1	TCEANC2
ENSSSCG00000030538		6	145986151	145997731	protein_coding		13	PIK3R1	CDCP2
ENSSSCG00000028521		6	146029516	146036736	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LB37]	13	PIK3R1	RP11-446E24.4
ENSSSCG00000026264	HSPB11	6	146038998	146066626	protein_coding	heat shock protein family B (small), member 11 [Source:HGNC Symbol;Acc:HGNC:25019]	13	PIK3R1	HSPB11
ENSSSCG00000028896	DIO1	6	146076209	146094289	protein_coding	Sus scrofa deiodinase, iodothyronine, type I (DIO1), mRNA. [Source:RefSeq mRNA;Acc:NM_001001627]	13	PIK3R1	DIO1
ENSSSCG00000028506	YIPF1	6	146104657	146147322	protein_coding	Yip1 domain family, member 1 [Source:HGNC Symbol;Acc:HGNC:25231]	13	PIK3R1	YIPF1
ENSSSCG00000028748	NDC1	6	146160490	146215022	protein_coding	NDC1 transmembrane nucleoporin [Source:HGNC Symbol;Acc:HGNC:25525]	13	PIK3R1	NDC1
ENSSSCG00000003846	GLIS1	6	146376667	146465958	protein_coding	GLIS family zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:29525]	13	PIK3R1	GLIS1
ENSSSCG00000003847	DMRTB1	6	146498267	146506176	protein_coding	DMRT-like family B with proline-rich C-terminal, 1 [Source:HGNC Symbol;Acc:HGNC:13913]	13	PIK3R1	DMRTB1
ENSSSCG00000003848	APOER2	6	146567981	146649171	protein_coding	Sus scrofa low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), mRNA. [Source:RefSeq mRNA;Acc:NM_001199891]	13	PIK3R1	APOER2
ENSSSCG00000020519	5S_rRNA	6	9222444	9222549	rRNA	5S ribosomal RNA [Source:RFAM;Acc:RF00001]	14	PLA2G12A	5S_rRNA
ENSSSCG00000002694	CLEC3A	6	9640139	9647945	protein_coding	C-type lectin domain family 3, member A [Source:HGNC Symbol;Acc:HGNC:2052]	14	PLA2G12A	CLEC3A
ENSSSCG00000027415	WWOX	6	9684708	9744573	protein_coding	WW domain containing oxidoreductase [Source:HGNC Symbol;Acc:HGNC:12799]	14	PLA2G12A	WWOX
ENSSSCG00000020481	U6	6	9875118	9875207	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	14	PLA2G12A	U6
ENSSSCG00000002696	VAT1L	6	9896814	10062187	protein_coding	vesicle amine transport 1-like [Source:HGNC Symbol;Acc:HGNC:29315]	14	PLA2G12A	VAT1L
ENSSSCG00000020141	SNORA15	6	10031373	10031521	snoRNA	Small nucleolar RNA SNORA15 [Source:RFAM;Acc:RF00398]	14	PLA2G12A	SNORA15
ENSSSCG00000002697		6	10102289	10111860	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S465]	14	PLA2G12A	NUDT7
ENSSSCG00000018836	7SK	6	10126195	10126525	misc_RNA	7SK RNA [Source:RFAM;Acc:RF00100]	14	PLA2G12A	7SK
ENSSSCG00000019476	5S_rRNA	6	10678802	10678937	rRNA	5S ribosomal RNA [Source:RFAM;Acc:RF00001]	14	PLA2G12A	5S_rRNA
ENSSSCG00000002699		6	10685335	10687109	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S463]	14	PLA2G12A	
ENSSSCG00000002701	MON1B	6	10723002	10730291	protein_coding	MON1 secretory trafficking family member B [Source:HGNC Symbol;Acc:HGNC:25020]	14	PLA2G12A	MON1B
ENSSSCG00000002700	SYCE1L	6	10740186	10746905	protein_coding	synaptonemal complex central element protein 1-like [Source:HGNC Symbol;Acc:HGNC:37236]	14	PLA2G12A	SYCE1L
ENSSSCG00000028809		6	79016673	79043802	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LBP7]	15	PLA2G12A	DNAJC8
ENSSSCG00000029682	5S_rRNA	6	79031109	79031224	rRNA	5S ribosomal RNA [Source:RFAM;Acc:RF00001]	15	PLA2G12A	5S_rRNA
ENSSSCG00000027072	ATPIF1	6	79045745	79047942	protein_coding	Sus scrofa ATPase inhibitory factor 1 (ATPIF1), mRNA. [Source:RefSeq mRNA;Acc:NM_001097486]	15	PLA2G12A	ATPIF1
ENSSSCG00000029438		6	79067103	79087543	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LRB8]	15	PLA2G12A	SESN2
ENSSSCG00000028973	MED18	6	79123550	79156847	protein_coding	mediator complex subunit 18 [Source:HGNC Symbol;Acc:HGNC:25944]	15	PLA2G12A	MED18

ENSSSCG00000030650	U1	6	79148195	79148358	snRNA	U1 spliceosomal RNA [Source:RFAM;Acc:RF00003]	15	PLA2G12A	U1
ENSSSCG00000027532	PHACTR4	6	79274083	79343494	protein_coding	phosphatase and actin regulator 4 [Source:HGNC Symbol;Acc:HGNC:25793]	15	PLA2G12A	PHACTR4
ENSSSCG00000025419	SNORA73	6	79348530	79348733	snoRNA	Small nucleolar RNA SNORA73 family [Source:RFAM;Acc:RF00045]	15	PLA2G12A	SNORA73
ENSSSCG00000022489	SNORA73	6	79349750	79349953	snoRNA	Small nucleolar RNA SNORA73 family [Source:RFAM;Acc:RF00045]	15	PLA2G12A	SNORA73
ENSSSCG00000029097	RCC1	6	79360235	79380216	protein_coding	regulator of chromosome condensation 1 [Source:HGNC Symbol;Acc:HGNC:1913]	15	PLA2G12A	RCC1
ENSSSCG00000030284	TRNAU1AP	6	79381682	79406931	protein_coding	tRNA selenocysteine 1 associated protein 1 [Source:HGNC Symbol;Acc:HGNC:30813]	15	PLA2G12A	TRNAU1AP
ENSSSCG00000027280	SNORD99	6	79408210	79408283	snoRNA	Small nucleolar RNA SNORD99 [Source:RFAM;Acc:RF00608]	15	PLA2G12A	SNORD99
ENSSSCG00000030477	SNORA61	6	79408844	79408976	snoRNA	Small nucleolar RNA SNORA61 [Source:RFAM;Acc:RF00420]	15	PLA2G12A	SNORA61
ENSSSCG00000023086	SNORA44	6	79409980	79410110	snoRNA	Small nucleolar RNA SNORA44 [Source:RFAM;Acc:RF00405]	15	PLA2G12A	SNORA44
ENSSSCG00000028807	SNORA16	6	79410562	79410696	snoRNA	Small nucleolar RNA SNORA16B/SNORA16A family [Source:RFAM;Acc:RF00190]	15	PLA2G12A	SNORA16
ENSSSCG00000030432	RAB42	6	79417344	79420332	protein_coding	RAB42, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:28702]	15	PLA2G12A	RAB42
ENSSSCG00000027530	TAF12	6	79432404	79441052	protein_coding	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa [Source:HGNC Symbol;Acc:HGNC:11545]	15	PLA2G12A	TAF12
ENSSSCG00000028890		6	79439152	79439252	miRNA		15	PLA2G12A	
ENSSSCG00000027686	YTHDF2	6	79553079	79560103	protein_coding	YTH N(6)-methyladenosine RNA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:31675]	15	PLA2G12A	YTHDF2
ENSSSCG00000027401	OPRD1	6	79621534	79658663	protein_coding	Delta-type opioid receptor [Source:UniProtKB/Swiss-Prot;Acc:P79291]	15	PLA2G12A	OPRD1
ENSSSCG00000003586	EPB41	6	79677219	79876085	protein_coding	erythrocyte membrane protein band 4.1 [Source:HGNC Symbol;Acc:HGNC:3377]	15	PLA2G12A	EPB41
ENSSSCG00000027163		6	79774912	79775084	miRNA		15	PLA2G12A	
ENSSSCG00000026263		6	79899322	79913209	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LE55]	15	PLA2G12A	
ENSSSCG00000003587	TMEM200B	6	79917691	79918614	protein_coding	transmembrane protein 200B [Source:HGNC Symbol;Acc:HGNC:33785]	15	PLA2G12A	TMEM200B
ENSSSCG00000003588	SRSF4	6	79952183	79980058	protein_coding	Sus scrofa serine/arginine-rich splicing factor 4 (SRSF4), mRNA. [Source:RefSeq mRNA;Acc:NM_001077216]	15	PLA2G12A	SRSF4
ENSSSCG00000003589	MECR	6	79984219	80018092	protein_coding	trans-2-enoyl-CoA reductase, mitochondrial [Source:RefSeq peptide;Acc:NP_001231011]	15	PLA2G12A	MECR
ENSSSCG00000023182	U6	6	80016571	80016677	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	15	PLA2G12A	U6
ENSSSCG00000003590	PTPRU	6	80024322	80106273	protein_coding	protein tyrosine phosphatase, receptor type, U [Source:HGNC Symbol;Acc:HGNC:9683]	15	PLA2G12A	PTPRU
ENSSSCG00000009170		8	128097096	128129034	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S102]	16	PLA2G12A	BANK1
ENSSSCG00000009171		8	128229409	128321167	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S101]	16	PLA2G12A	BANK1
ENSSSCG00000009172		8	128461097	128798143	protein_coding		16	PLA2G12A	PPP3CA
ENSSSCG00000022835		8	128883086	128886400	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LQC2]	16	PLA2G12A	PPP3CA
ENSSSCG00000009173	EMCN	8	129169078	129176677	protein_coding	endomucin [Source:HGNC Symbol;Acc:HGNC:16041]	16	PLA2G12A	EMCN
ENSSSCG00000018455	U1	8	129190210	129190377	snRNA	U1 spliceosomal RNA [Source:RFAM;Acc:RF00003]	16	PLA2G12A	U1
ENSSSCG00000025240	DDIT4L	8	129550397	129555105	protein_coding	DNA-damage-inducible transcript 4-like [Source:HGNC Symbol;Acc:HGNC:30555]	16	PLA2G12A	DDIT4L
ENSSSCG00000030133		8	129615441	129615958	pseudogene		16	PLA2G12A	
ENSSSCG00000009178	H2AFZ	8	129743691	129745568	protein_coding	H2A histone family, member Z [Source:HGNC Symbol;Acc:HGNC:4741]	16	PLA2G12A	H2AFZ

ENSSSCG00000019455		8	129759865	129759961	miRNA		16	PLA2G12A	AC190387.2
ENSSSCG00000009177	DNAJB14	8	129770314	129798212	protein_coding	DnaJ (Hsp40) homolog, subfamily B, member 14 [Source:HGNC Symbol;Acc:HGNC:25881]	16	PLA2G12A	DNAJB14
ENSSSCG00000009176	LAMTOR3	8	129804996	129822001	protein_coding	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3 [Source:HGNC Symbol;Acc:HGNC:15606]	16	PLA2G12A	LAMTOR3
ENSSSCG00000028367		8	129822230	129850879	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LKE0]	16	PLA2G12A	DAPP1
ENSSSCG00000026779		8	129881481	129908979	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L5N1]	16	PLA2G12A	DAPP1
ENSSSCG00000009179	MTTP	8	130036414	130087547	protein_coding	Sus scrofa microsomal triglyceride transfer protein (MTTP), mRNA. [Source:RefSeq mRNA;Acc:NM_214185]	16	PLA2G12A	MTTP
ENSSSCG00000009180		8	130101784	130133413	protein_coding	Sus scrofa tRNA methyltransferase 10 homolog A (S. cerevisiae) (RG9MTD2), mRNA. [Source:RefSeq mRNA;Acc:NM_001244146]	16	PLA2G12A	TRMT10A
ENSSSCG00000009182	ADH7	8	130165209	130185018	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LFH9]	16	PLA2G12A	ADH7
ENSSSCG00000009181	C4orf17	8	130219448	130222743	protein_coding	chromosome 4 open reading frame 17 [Source:HGNC Symbol;Acc:HGNC:25274]	16	PLA2G12A	C4orf17
ENSSSCG00000030522		8	130231027	130242783	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LDJ8]	16	PLA2G12A	ADH1A
ENSSSCG00000009184	ADH4	8	130410138	130427879	protein_coding	alcohol dehydrogenase 4 (class II), pi polypeptide [Source:HGNC Symbol;Acc:HGNC:252]	16	PLA2G12A	ADH4
ENSSSCG00000009185	ADH5	8	130451260	130466903	protein_coding	Sus scrofa alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5), mRNA. [Source:RefSeq mRNA;Acc:NM_001244833]	16	PLA2G12A	ADH5
ENSSSCG00000009186	METAP1	8	130478288	130537719	protein_coding	methionyl aminopeptidase 1 [Source:HGNC Symbol;Acc:HGNC:15789]	16	PLA2G12A	METAP1
ENSSSCG00000021690		8	130593998	130594060	miRNA		16	PLA2G12A	
ENSSSCG00000028420	EIF4E	8	130594675	130649857	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1S0B9]	16	PLA2G12A	EIF4E
ENSSSCG00000029813	TSPAN5	8	130843387	131031868	protein_coding	tetraspanin 5 [Source:HGNC Symbol;Acc:HGNC:17753]	16	PLA2G12A	TSPAN5
ENSSSCG00000022353	RAP1GDS1	8	131053514	131106151	protein_coding	RAP1, GTP-GDP dissociation stimulator 1 [Source:HGNC Symbol;Acc:HGNC:9859]	16	PLA2G12A	RAP1GDS1
ENSSSCG00000029318		8	131057572	131057652	miRNA		16	PLA2G12A	
ENSSSCG00000009188	STPG2	8	131181709	131215185	protein_coding	sperm-tail PG-rich repeat containing 2 [Source:HGNC Symbol;Acc:HGNC:28712]	16	PLA2G12A	STPG2
ENSSSCG00000019720	U6	8	131260737	131260839	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	16	PLA2G12A	U6
ENSSSCG00000020116	U6	8	131429023	131429118	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	16	PLA2G12A	U6
ENSSSCG00000025773	U6	8	131561992	131562098	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	16	PLA2G12A	U6
ENSSSCG00000019832		8	131865409	131865496	miRNA		16	PLA2G12A	
ENSSSCG00000018598	SNORA50	8	133590839	133590973	snoRNA	Small nucleolar RNA SNORA50 [Source:RFAM;Acc:RF00407]	16	PLA2G12A	SNORA50
ENSSSCG00000029621	BMPR1B	8	133740991	134040905	protein_coding	bone morphogenetic protein receptor, type IB [Source:HGNC Symbol;Acc:HGNC:1077]	16	PLA2G12A	BMPR1B
ENSSSCG00000021874		8	133775432	133794041	protein_coding		16	PLA2G12A	
ENSSSCG00000028240	UNC5C	8	133842099	133844723	protein_coding	unc-5 homolog C (C. elegans) [Source:HGNC Symbol;Acc:HGNC:12569]	16	PLA2G12A	UNC5C
ENSSSCG00000009192	PDLIM5	8	134331169	134558588	protein_coding	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:17468]	16	PLA2G12A	PDLIM5
ENSSSCG00000009194	HPGDS	8	134669308	134692062	protein_coding	hematopoietic prostaglandin D synthase [Source:HGNC Symbol;Acc:HGNC:17890]	16	PLA2G12A	HPGDS
ENSSSCG00000009193	SMARCAD1	8	134696174	134777513	protein_coding	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 [Source:HGNC Symbol;Acc:HGNC:18398]	16	PLA2G12A	SMARCAD1
ENSSSCG00000018676		8	134860853	134860936	miRNA		16	PLA2G12A	

ENSSSCG00000009196	ATOH1	8	135104480	135105541	protein_coding	atonal homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:797]	16	PLA2G12A	ATOH1
ENSSSCG00000009197		8	135156732	135160822	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RWW0]	16	PLA2G12A	GRID2
ENSSSCG00000009199		8	135272060	135273409	pseudogene		16	PLA2G12A	
ENSSSCG00000023621		8	135417163	135568985	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L5L4]	16	PLA2G12A	GRID2
ENSSSCG00000019664	U6	8	135469370	135469475	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	16	PLA2G12A	U6
ENSSSCG00000009200		8	136033869	136034021	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RWV7]	16	PLA2G12A	
ENSSSCG00000022289	PCDH1	2	149690657	149696708	protein_coding	protocadherin 1 [Source:HGNC Symbol;Acc:HGNC:8655]	18	PPARA	PCDH1
ENSSSCG00000014396	KIAA0141	2	149731441	149747404	protein_coding	KIAA0141 [Source:HGNC Symbol;Acc:HGNC:28969]	18	PPARA	KIAA0141
ENSSSCG00000014395	PCDH12	2	149752166	149765761	protein_coding	protocadherin 12 [Source:HGNC Symbol;Acc:HGNC:8657]	18	PPARA	PCDH12
ENSSSCG00000014394	RNF14	2	149776430	149797096	protein_coding	ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:10058]	18	PPARA	RNF14
ENSSSCG00000014393	GNPDA1	2	149805752	149817596	protein_coding	Sus scrofa glucosamine-6-phosphate deaminase 1 (GNPDA1), mRNA. [Source:RefSeq mRNA;Acc:NM_001244093]	18	PPARA	GNPDA1
ENSSSCG00000014392		2	149914990	149924225	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RM53]	18	PPARA	NDFIP1
ENSSSCG00000014397	SPRY4	2	150066068	150066967	protein_coding	sprouty homolog 4 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:15533]	18	PPARA	SPRY4
ENSSSCG00000020485	U5	2	150153326	150153437	snRNA	U5 spliceosomal RNA [Source:RFAM;Acc:RF00020]	18	PPARA	U5
ENSSSCG00000024954	FGF1	2	150317384	150418060	protein_coding	Fibroblast growth factor 1 [Source:UniProtKB/Swiss-Prot;Acc:P20002]	18	PPARA	FGF1
ENSSSCG00000019432	SNORA36	2	150360414	150360541	snoRNA	Small nucleolar RNA SNORA36 family [Source:RFAM;Acc:RF00340]	18	PPARA	SNORA36
ENSSSCG00000014399	ARHGAP26	2	150495712	150918983	protein_coding	Rho GTPase activating protein 26 [Source:HGNC Symbol;Acc:HGNC:17073]	18	PPARA	ARHGAP26
ENSSSCG00000014400		2	150664569	150665149	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1RM36]	18	PPARA	BTF3
ENSSSCG00000014401	NR3C1	2	151054873	151158579	protein_coding	Sus scrofa nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. [Source:RefSeq mRNA;Acc:NM_001008481]	18	PPARA	NR3C1
ENSSSCG00000026857		6	89021503	89024892	protein_coding	Adenylyl cyclase-associated protein [Source:UniProtKB/TrEMBL;Acc:I3LVT1]	19	PPARA	
ENSSSCG00000003671		6	89101261	89120974	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1SMC1]	19	PPARA	PPT1
ENSSSCG00000027902	ZMPSTE24	6	89129878	89133484	protein_coding	zinc metallopeptidase STE24 [Source:HGNC Symbol;Acc:HGNC:12877]	19	PPARA	ZMPSTE24
ENSSSCG00000003670	RLF	6	89147722	89241759	protein_coding	rearranged L-myc fusion [Source:HGNC Symbol;Acc:HGNC:10025]	19	PPARA	RLF
ENSSSCG00000021567		6	89280559	89299207	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LEP6]	19	PPARA	PPT1
ENSSSCG00000003672	CAP1	6	89300803	89309905	protein_coding	CAP, adenylate cyclase-associated protein 1 (yeast) [Source:HGNC Symbol;Acc:HGNC:20040]	19	PPARA	CAP1
ENSSSCG00000023322	COL9A2	6	89419701	89434966	protein_coding	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:HGNC:2218]	19	PPARA	COL9A2
ENSSSCG00000027908	MC2R	6	89575890	89602023	protein_coding	Adrenocorticotropic hormone receptor [Source:UniProtKB/Swiss-Prot;Acc:Q8HYN8]	19	PPARA	MC2R
ENSSSCG00000027352		6	89653370	89668558	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L679]	19	PPARA	RNMT
ENSSSCG00000028411	MC5R	6	89672861	89673781	protein_coding	melanocortin 5 receptor [Source:HGNC Symbol;Acc:HGNC:6933]	19	PPARA	MC5R
ENSSSCG00000030438		6	89688246	89700389	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LPD1]	19	PPARA	FAM210A
ENSSSCG00000027417	LDLRAD4	6	89712706	89832876	protein_coding	low density lipoprotein receptor class A domain containing 4 [Source:HGNC Symbol;Acc:HGNC:1224]	19	PPARA	LDLRAD4
ENSSSCG00000003673	CEP192	6	89917876	89998073	protein_coding	centrosomal protein 192kDa [Source:HGNC Symbol;Acc:HGNC:25515]	19	PPARA	CEP192
ENSSSCG00000027473		6	90006898	90010610	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LHB6]	19	PPARA	

ENSSSCG00000021738	PTPN2	6	90126978	90263311	protein_coding	protein tyrosine phosphatase, non-receptor type 2 [Source:HGNC Symbol;Acc:HGNC:9650]	19	PPARA	PTPN2
ENSSSCG00000020995		6	90134254	90158229	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LH55]	19	PPARA	
ENSSSCG00000030252	SEH1L	6	90192180	90207246	protein_coding	SEH1-like (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:30379]	19	PPARA	SEH1L
ENSSSCG00000021827		6	90303818	90308192	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LHD2]	19	PPARA	PSMG2
ENSSSCG00000029671		6	90315474	90318709	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L5V5]	19	PPARA	PSMG2
ENSSSCG00000027007	CEP76	6	90319065	90337712	protein_coding	centrosomal protein 76kDa [Source:HGNC Symbol;Acc:HGNC:25727]	19	PPARA	CEP76
ENSSSCG00000027584		6	90359287	90435186	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LIP3]	19	PPARA	
ENSSSCG00000024151	SPIRE1	6	90571462	90592504	protein_coding	spire-type actin nucleation factor 1 [Source:HGNC Symbol;Acc:HGNC:30622]	19	PPARA	SPIRE1
ENSSSCG00000022163	GNAL	6	90674122	90703000	protein_coding	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type [Source:HGNC Symbol;Acc:HGNC:4388]	19	PPARA	GNAL
ENSSSCG00000026285		6	90689593	90690203	pseudogene		19	PPARA	
ENSSSCG00000028126	MPPE1	6	90704267	90714316	protein_coding	metallophosphoesterase 1 [Source:HGNC Symbol;Acc:HGNC:15988]	19	PPARA	MPPE1
ENSSSCG00000024162	IMPA2	6	90749827	90770377	protein_coding	inositol(myo)-1(or 4)-monophosphatase 2 [Source:HGNC Symbol;Acc:HGNC:6051]	19	PPARA	IMPA2
ENSSSCG00000024644	CIDEA	6	90781633	90795956	protein_coding	Sus scrofa cell death-inducing DFFA-like effector a (CIDEA), mRNA. [Source:RefSeq mRNA;Acc:NM_001112696]	19	PPARA	CIDEA
ENSSSCG00000026022		6	90808417	90814582	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LBV1]	19	PPARA	TUBB6
ENSSSCG00000022947	AFG3L2	6	90816096	90833719	protein_coding	AFG3-like AAA ATPase 2 [Source:HGNC Symbol;Acc:HGNC:315]	19	PPARA	AFG3L2
ENSSSCG00000024963		6	90910224	90911756	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LK93]	19	PPARA	
ENSSSCG00000015433		9	116718488	116747666	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1SB34]	7_17	HIF1AN PLA2G12A	CDHR3
ENSSSCG00000020297	U6	9	116849823	116849927	snRNA	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]	7_17	HIF1AN PLA2G12A	U6
ENSSSCG00000015435	PBEF1	9	116890800	116931198	protein_coding	Sus scrofa nicotinamide phosphoribosyltransferase (NAMPT), mRNA. [Source:RefSeq mRNA;Acc:NM_001031793]	7_17	HIF1AN PLA2G12A	PBEF1
ENSSSCG00000015436	CCDC71L	9	117342025	117342987	protein_coding	coiled-coil domain containing 71-like [Source:HGNC Symbol;Acc:HGNC:26685]	7_17	HIF1AN PLA2G12A	CCDC71L
ENSSSCG00000027272	PIK3CG	9	117537646	117576054	protein_coding	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform [Source:UniProtKB/Swiss-Prot;Acc:O02697]	7_17	HIF1AN PLA2G12A	PIK3CG
ENSSSCG00000015437	PIK3CG	9	117551880	117556657	protein_coding	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma [Source:HGNC Symbol;Acc:HGNC:8978]	7_17	HIF1AN PLA2G12A	PIK3CG
ENSSSCG00000026563		9	117761872	117769187	protein_coding		7_17	HIF1AN PLA2G12A	
ENSSSCG00000015441		9	117795865	117840904	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F1SAF2]	7_17	HIF1AN PLA2G12A	COG5
ENSSSCG00000015442	GPR22	9	117964302	117965809	protein_coding	G protein-coupled receptor 22 [Source:HGNC Symbol;Acc:HGNC:4477]	7_17	HIF1AN PLA2G12A	GPR22
ENSSSCG00000023193		9	117986641	118028877	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3L872]	7_17	HIF1AN PLA2G12A	COG5
ENSSSCG00000028433	DUS4L	9	118032152	118044547	protein_coding	dihydrouridine synthase 4-like (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:21517]	7_17	HIF1AN PLA2G12A	DUS4L

ENSSSCG00000022869	BCAP29	9	118047025	118084880	protein_coding	B-cell receptor-associated protein 29 [Source:HGNC Symbol;Acc:HGNC:24131]	7_17	HIF1AN PLA2G12A	BCAP29
ENSSSCG00000023509	snoU109	9	118070879	118070999	snoRNA	Small nucleolar RNA U109 [Source:RFAM;Acc:RF01233]	7_17	HIF1AN PLA2G12A	snoU109
ENSSSCG00000028969	SLC26A4	9	118120578	118178767	protein_coding	solute carrier family 26 (anion exchanger), member 4 [Source:HGNC Symbol;Acc:HGNC:8818]	7_17	HIF1AN PLA2G12A	SLC26A4
ENSSSCG00000021813	SLC26A3	9	118190326	118322545	protein_coding	Sus scrofa solute carrier family 26, member 3 (SLC26A3), mRNA. [Source:RefSeq mRNA;Acc:NM_001130248]	7_17	HIF1AN PLA2G12A	SLC26A3
ENSSSCG00000028585	CBLL1	9	118217376	118236706	protein_coding	Cbl proto-oncogene-like 1, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:21225]	7_17	HIF1AN PLA2G12A	CBLL1
ENSSSCG00000025267		9	118242687	118270357	protein_coding	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:I3LCH4]	7_17	HIF1AN PLA2G12A	SLC26A3
ENSSSCG00000022995		9	118345199	118345884	pseudogene		7_17	HIF1AN PLA2G12A	
ENSSSCG00000015443	DLD	9	118410807	118437645	protein_coding	Sus scrofa dihydrolipoamide dehydrogenase (DLD), mRNA. [Source:RefSeq mRNA;Acc:NM_214062]	7_17	HIF1AN PLA2G12A	DLD
ENSSSCG00000015444	LAMB1	9	118439608	118514521	protein_coding	laminin, beta 1 [Source:HGNC Symbol;Acc:HGNC:6486]	7_17	HIF1AN PLA2G12A	LAMB1
ENSSSCG00000015445	NRCAM	9	118730305	118785977	protein_coding	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:7994]	7_17	HIF1AN PLA2G12A	NRCAM

Table S4. Top functional networks identified with IPA based on the list of annotated genes mapping within the 18 eQTLs.

ID	Top Diseases and Functions	Score	Focus Molecules	Molecules in Network
1	Energy Production, Small Molecule Biochemistry, Drug Metabolism	44	25	ADH4,ADH5,ADH7,ADH1A,Akt,alcohol dehydrogenase,ATPIF1,BANK1,caspase,Cg,Cyclin A,cytochrome C,DHCR24,ECSCR,EIF4E,FSH,GRID2,KIAA0141,LAMTOR3,Lh,MAP2K1/2,MGLL,NDFIP1,PALB2,PDS5B,PPAP2B,PPT1,PTPase,PTPN2,PTPRU,SIRT3,SLIT2,STARD13,USPL1,YTHDF2
2	Organismal Injury and Abnormalities, Cancer, Hematological Disease	42	24	Dynein,EFNB2,EMCN,ENaC,EPB41,ERK1/2,Fgfr,IFITM3,Ige,KL,LDL-cholesterol,MED18,mediator,MHC Class II (complex),MTTP,NAMPT,NRG2,PCSK9,PIGF,PLC gamma,PSMD13,RFXAP,RIC8A,SCNN1B,SLC26A4,Smad1/5/8,SPG20,SPRY4,SUPT20H,TNFRSF8,TNFSF15,TNFSF13B,TUBB6,Ubiquitin,UNC5C
3	Connective Tissue Disorders, Inflammatory Disease, Skeletal and Muscular Disorders	37	22	BRD8,BTF3,Cbp/p300,CDC25C,CEP76,CIDEA,Ck2,DNAJB14,DNAJC8,DNAJC18,Growth hormone,Histone h4,HMGB1,HSP,Hsp70,Hsp22/Hsp40/Hsp90,HSPA9,HSPB11,HSPH1,IL12 (complex),Interferon alpha,Jnk,KLHL3,NME5,NR3C1,PDLIM5,phosphatase,POMP,PPP3CA,PRKCE,Proinsulin,PSMG2,RHOQ,SESN2,STAT5a/b
4	Connective Tissue Disorders, Dermatological Diseases and Conditions, Developmental Disorder	26	17	ALOX5AP,Alp,Ap1,CXXC5,DIO1,FGF1,HDL,IFITM1,Ifn,IFN Beta,IL1,LAMB1,LDL,MAB21L1,Mek,METAP1,NADPH oxidase,NFkB (complex),Nos,Nr1h,PAPPA,Pdgf (complex),PDGF BB,Pro-inflammatory Cytokine,RAP1GDS1,SIGIRR,SIL1,SLC7A1,SMAD9,SOCS5,Tgf beta,Tlr,TMEM173,TSH,ZMPSTE24
5	Cell-To-Cell Signaling and Interaction, Cellular Assembly and Organization, Cellular Function and Maintenance	26	17	Actin,ALG5,Alpha Actinin,Alpha catenin,ATOH1,BCR (complex),CAP1,CBLL1,CCNA1,COL9A2,Collagen type I,CTNNA1,Cyclin E,DAPP1,E2f,EGR1,ERK,estrogen receptor,EXOSC8,F Actin,FRY,IGF2,IgG,IgG2a,Igm,Immunoglobulin,MZB1,Nfat (family),NRCAM,p70 S6k,PCDH1,PI3K (complex),SLC26A3,TCF,TNC
6	Gene Expression, Protein Synthesis, Cancer	24	16	AFG3L2,APP,ATL3,BET1L,BMPR1B,BSND,CIART,COG5,COG7,CREB1,DDIT4L,FAM212B,FAM3A,GGA2,HRASLS,IGSF10,KCNC4,MEDAG,MPI,MPV17L,MYOT,NLN,OCIAD2,PACRGL,PKP3,POMZP3,PPARG,SEH1L,SERTM1,TCEANC2,TP53,UBL3,WARS2,ZDHHC23,ZNF35
7	Nervous System Development and Function, Lipid Metabolism, Nucleic Acid Metabolism	22	15	ARGLU1,ARTN,AUH,DCTN3,DCTN5,DCTN6,DECR2,EPHA5,GFRA3,IMPA1,IMPA2,IMPAD1,KATNAL1,MCFD2,MECR,MON1B,N4BP2L2,NAA38,NBEA,NDC1,REEP6,RET,RNF19A,SCARA3,SDK1,SRBD1,TMEM59,TSPAN3,TSPAN4,TSPAN5,TSPAN6,TT

				C4,UBC,VPS16,VPS41
8	Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function	22	15	ARHGAP19,BCAP29,CASC4,CDH9,CTNNB1,DIP2B,DMRTB1,ELAVL1,FAM110B,FAM13B,FAM53C,GNB1,HHAT,HIF1A,HPGDS,IFITM5,KCNIP4,MPV17L,NEDD9,NUDT7,ODF3,PANK1,PSD2,RLF,SAMD1,SPIRE1,SUMO2,TAF12,TBCB,TGFB1,TMEM19,TTC22,Wnt,WNT8A,YWHAQ
9	Cardiovascular Disease, Hereditary Disorder, Metabolic Disease	20	14	ANKEF1,ATHL1,ATP6V1E2,C4orf17,C9orf114,CACUL1,CEP192,DENND5B,DENND6A,DEPDC5,DLD,GLT8D2,GTPase,HNRNPA0,KDM1A,MPPE1,MRPL33,MTO1,NDUFAB1,PAXIP1,RCC1,RGP1,RIC1,RNF14,RPL5,SPATA24,SRSF4,SYDE1,UBC,USP24,USP35,USP40,USP27X,WBSCR27,ZNF480
10	Cell Signaling, Nucleic Acid Metabolism, Small Molecule Biochemistry	18	13	ADCY,ADGRA3,AMPK,ARHGAP26,Calmodulin,CD3,Collagen(s),Creb,DAB1,EPAS1,Focal adhesion kinase,GNAL,GNPDA1,GNRH,Gpcr,GPR22,Histone h3,IL12 (family),Mapk,MC2R,MC5R,OPRD1,p85 (pik3r),PAIP2,PIK3CG,Pka,Pkc(s),Rac,Ras,Ras homolog,RXFP2,SRC (family),TCR,tubulin (complex),Vegf
11	Developmental Disorder, Hereditary Disorder, Ophthalmic Disease	18	13	ANO10,B3GALTL,C1orf168,CCDC138,CCDC71L,CNTLN,DUS4L,EARS2,FANCA,FDFT1,GK5,HDDC2,KDELC2,KMT2D,LDLRAD4,MARVELD1,NT5DC1,RAB42,RANGRF,REEP2,RELL1,RIMKLB,SLC35F5,SOHLH2,SYPL2,TFAP2D,TRIQK,TRMT2B,TRNAU1AP,TRPV2,TTC7A,UBC,UBFD1,UBL3,ZNF761
12	Organismal Injury and Abnormalities, Digestive System Development and Function, Organ Morphology	14	11	C5,C5-C6-C7-C8,C5-C6-C7-C8-C9,C8A,C8B,C8G,CCND1,CEP95,CLEC6A,CXCL11,DDIAS,DONSON,ENDOD1,FAM210A,Fcr,GLIS1,IDO2,IFNG,IL22RA2,KIF20A,LRRC42,LRRTM2,MTUS2,NLRP6,NXF1,PGLYRP2,PGLYRP3,PGLYRP4,PRELP,RAB20,SETD5,SLC16A9,SLC23A1,YIPF1,ZNF324
13	RNA Post-Transcriptional Modification, Cellular Assembly and Organization, Cancer	14	11	ANAPC1,ANAPC2,ANAPC5,ANAPC7,CALM1 (includes others),CDC16,CDC23,CPSF1,CPSF2,CPSF3,CYFIP2,DCLK1,DMAP1,H2AFB3 (includes others),H2AFZ,HNRNPR,INCENP,KDM3B,MATR3,NCKAP1,PAICS,PDCD7,PHACTR4,RAB6B,RFC2,RFC3,RFC4,RFC5,RYR1,SMARCAD1,SYMPK,USP20,VAT1L,WDR33,WWOX
14	Organismal Development, Organismal Functions, Carbohydrate Metabolism	11	9	26s Proteasome,AACS,ACSM5,ADIPOQ,Adipor,ANO9,Anti-inflammatory Cytokine,ATP5G2,C1QTNF5,C2orf61,Cyp2j9,DLG1,DUOX1,ETF1,FITM2,GPR39,GYS2,Il15r,Insulin,LBX1,LDLRAD1,LIG4,MAL,mir-375,NNAT,P38 MAPK,PARS2,POU5F1,PRKAA2,RNA polymerase II,RNMT,SCAF8,Tnf (family),TRPM2,ZNF462
15	Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Cardiac Arrythmia	2	1	MYBPC2,PCDH12

Table S5. Positional concordance among the 241 eSNPs associated with gene expression and the QTLs described in the pig QTL database for fatness and fat composition related traits. (too large to be attached, not included in the present thesis).

Table S6. Primers used for the analyses gene expression analysis of the 48 genes by RT-qPCR.

Gene	Full name	Type	Primer sequence	
			Forward	Reverse
ACAA2	acetyl-CoA acyltransferase 2	Target	TGGATTGGATCTCAAGCTAGAAGA	CCATCGGGATTTGGATATGCT
ACSM5	acyl-CoA synthetase medium-chain family member 5	Target	TGTAATCTGTGCCAATCCCAAA	CATCATCTACGATCTGCACCTCAT
ACSS1	acyl-CoA synthetase short-chain family member 1	Target	TCAAGGGAGAAGCTGCGTTT	CCGACCGGAGCTCTTTCAC
ACSS2	acyl-CoA synthetase short-chain family member 2	Target	TGAAGCTGAAGGTTATCTGGTGTTC	CGTTCATGGTTCCCGTAGA
ACTB	actin, beta	Endogenous	CAAGGACCTCTACGCCAACAC	TGGAGGCGCGATGATCTT
ALB	albumin	Target	TCGTCGAGATACATACAAGAGTGAAA	AGCACTAGGCCTTTGAAATATTGTTC
ANGPT1	angiopoietin 1	Target	ACCAGCCTCCTCTCTCAAACC	GTTTGATTTAGTACCTGGGTCTCAACA
AQP7	aquaporin 7	Target	TTCAGCAGACATCTAACAATCTCAAAG	GACCTGGTAGACCGCCTCTTC
ATF3	activating transcription factor 3	Target	TCAGTCACGAAAGCCGAGGTA	GGCGGCAATCTTATTTCTTTCC
CPT1B	carnitine palmitoyltransferase 1B (muscle)	Target	ACATATCTACCTGTCCGGGATCA	CCCTGAGGATGCCATTCTTG
CREG1	cellular repressor of E1A-stimulated genes 1	Target	TAGGCAACTTGCAGGATAATCCA	ATCCATATTTCCTGCAGAAACTAGTCT
CROT	carnitine O-octanoyltransferase	Target	GGGAAACGAAATTGGTTGGA	CGCAAAGTTGACATTCAGTTGTG
DGAT1	diacylglycerol O-acyltransferase 1	Target	CCTGAATTGGTGTGTGGTCATG	GATGCCGTACTTGATGAGGTTCTC
DGAT2	diacylglycerol O-acyltransferase 2	Target	CTCATCACCGCGCTCTACTTC	ACCTCCGGCCACCTTTCTT
ELF1	E74-like factor 1 (ets domain transcription factor)	Target	GATGACATCACCCTGACAGTTGA	TCCGCAGCCTCGATGGT
ETS1	v-ets avian erythroblastosis virus E26 oncogene homolog 1	Target	CCTGGGAATCCCAAAAGATCC	ACTCATTGACAGCCCACATCAC
FABP3	fatty acid binding protein 3, muscle and heart	Target	CGGGCACCTGGAAGCTAGT	GGCAAAACCCACACCAATTG
FABP5	fatty acid binding protein 5 (psoriasis-associated)	Target	CCAATGGAGAATTGGTTCAACA	GTTCATGACGCATACCACCACTA
FOS	FBJ murine osteosarcoma viral oncogene homolog	Target	CCGTCAATGCGCAGGACT	TCTGGGCTGGTCGAGATAGC
HIF1AN	hypoxia inducible factor 1, alpha subunit inhibitor	Target	TTGGCATGGAAGGAAATGTG	GCCTTTTATCTGAGCAAAGAAGTTCT
HPRT1	hypoxanthine phosphoribosyltransferase 1	Endogenous	TCATTATGCCGAGGATTTGGA	CTCTTTCATCACATCTCGAGCAA
IGF2	insulin-like growth factor 2	Target	GACCGTGCTTCCGGACAA	CGTTGGGCGGACTGCTT
LPIN1	lipin 1	Target	CCGAGAGAAGGTGGTGGACAT	CTCTCCATTGTCTCCCAGTTTCA
MGLL	monoglyceride lipase	Target	GTGTTCGCCCACGACCAT	CCTGACGAACACCTGGAAGTC
MLXIPL	MLX interacting protein-like	Target	CCCAAGTGGAAGAATTTCAAAGG	CTTCCTCCGCTCCACATACTG

NCOA1	nuclear receptor coactivator 1	Target	AAGGAACAGATGGATCCTTGTAACA	TGGTCAAGGTCAGCTGTAAACTG
NCOA2	nuclear receptor coactivator 2	Target	CGTACCCACACAGGCACCTAT	CTGTCGAAGGTGCTGGTTCA
NCOA6	nuclear receptor coactivator 6	Target	TTACATCCAGGCCTAGGAGGAAT	TTGCATAAAGTTCGGATTGGC
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	Target	CCCACAGACGTTCATAGACAATTT	GAGGCTGGTTTTGTAATGTTGACA
NR1H3	nuclear receptor subfamily 1, group H, member 3	Target	CTGGGCATGATCGAGAAGCT	TGGGCCAAGGCGTGACT
PDHX	pyruvate dehydrogenase complex, component X	Target	AGCTGTGGTTACCTTAGATGCAAGT	TTTTAGATCCTTCGGCAACCACTA
PEX2	peroxisomal biogenesis factor 2	Target	CTCAGACTCCTAAGAAACCTTCAGAGA	ACTGATTCTGAGCACTCTGTTTGC
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	Target	TGGGGAGATATCTCGAGGGAA	TTTTAGTAGATGCGTCTCGTACCAA
PLA2G12A	phospholipase A2, group XIIA	Target	CCCACTCTTTGGTGTTCATCTTAA	ATAGCACCTGTCGTGCTGGTT
PLIN5	perilipin 5	Target	CTCAAACGATCCATGAGCCA	TGCCAGTGCCGCGAG
PPAP2A	phosphatidic acid phosphatase type 2A	Target	GGCCACTCTTCATTCTCCATGTAC	AGGCCCACGTAAATGGATACAG
PPARA	peroxisome proliferator-activated receptor alpha	Target	GGCACTGAACATCGAATGTAGAATC	CCGAAAGAAGCCCTTGCAA
PPARD	peroxisome proliferator-activated receptor delta	Target	GCATGTCTCA CAACGCCATT	GCTGACTCCCCTCGTTTGC
PPARG	peroxisome proliferator-activated receptor gamma	Target	TTGTGAAGGATGCAAGGGTTT	ATCCGACAGTTAAGATCGCACCTA
PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	Target	CTCTGGAACTGCAGGCCTAA	TGGAGAAGCCCTAAAAGGGTTAT
PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	Target	GTAAAAATGGAAGGCTGGATGAA	TGTGACAATAATCCACACCAGAAAG
RXRG	retinoid X receptor, gamma	Target	GAGGATTCTGGAAGCTGAACTTG	TCATTCGTCGAATTCTCCATGT
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	Target	GGTGATGTTCCAGAGGAGGTACTAC	CAGCAATACCAGGGCACGAT
SETD7	SET domain containing (lysine methyltransferase) 7	Target	TGCTGGATATACTACCCAGATGGA	TCTCCTGTCATCTCCCCATCTT
SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	Target	TCTGTGGGTGGCATGTTCTC	GAACAGCATTGCCTTCTTCCTT
SP1	Sp1 transcription factor	Target	CCACCATGAGCGACCAAGA	GCCACCAACTCCTTTTTCAATC
SREBF1	sterol regulatory element binding transcription factor 1	Target	CACGGAGGCGAAGCTGAATA	GCTTCTGGTTGCTCTGCTGAA
TBP	TATA box binding protein	Endogenous	CAGAATGATCAAACCGAGAATTGT	CTGCTCTGACTTTAGCACCTGTTAA

7.4.2. Supplementary Figures Paper IV

Figure S1. Comparison between males and females of muscle gene expression levels of 45 lipid-related genes. Data represents means ± SEM.

Significant differences between sexes are indicated as * P ≤ 0.05, ** P ≤ 0.01, ** P ≤ 0.001.

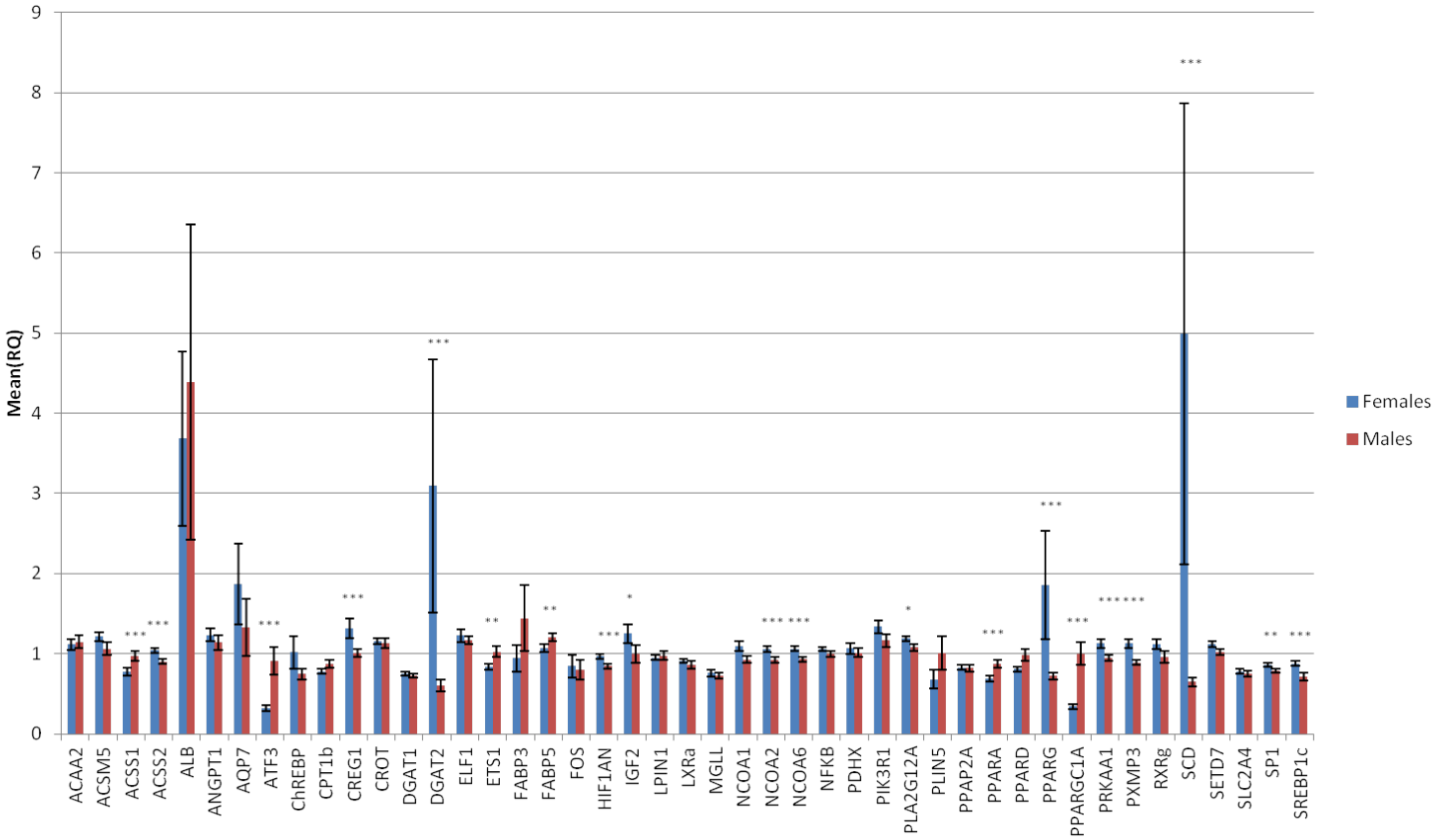


Figure S2. Network of the lipid metabolic process function obtained by Genomatix.

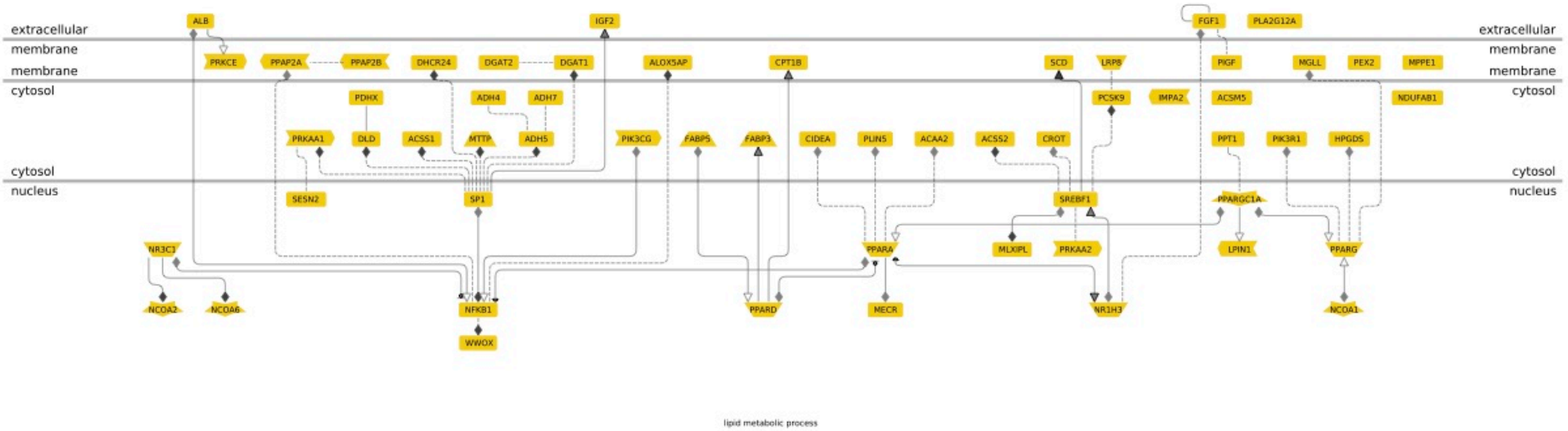
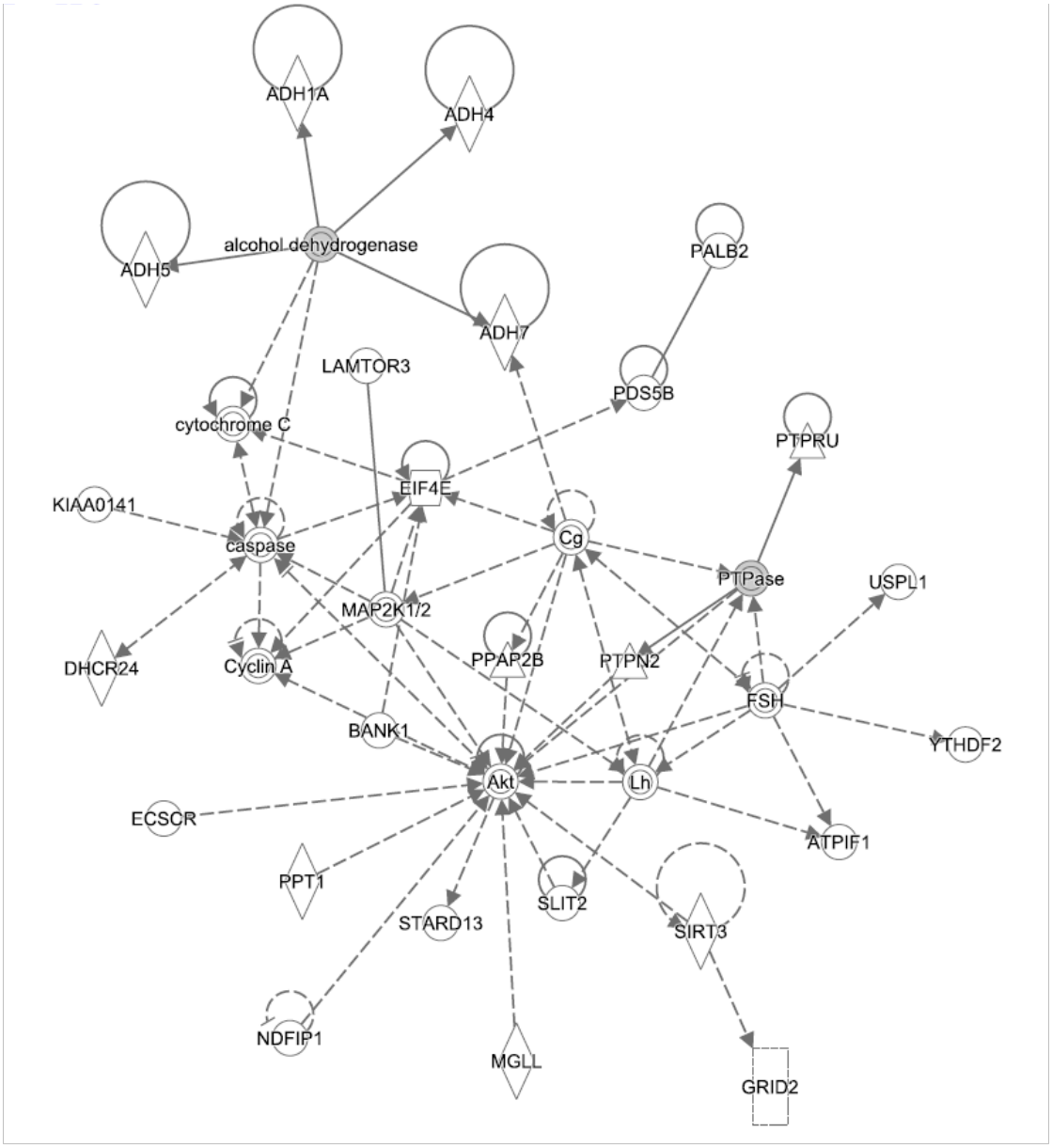


Figure S3. Network (score 44) generated by IPA of 25 focus genes corresponding to the energy production, small molecule biochemistry and drug metabolism functions.



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Colophon

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