

SUPPLEMENTARY MATERIAL

Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs

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Figure S1. Evidence of interactions between *FABP1*, *FADS1*, *FADS2*, *PPAR α* and *SREBP1c* using GeneMANIA.

Figure S2. Plot of GWAS for *FADS1*, *FADS2* and *FADS3* gene expression in liver. Association analysis between the liver *FADS1* (A), *FADS2* (B) and *FADS3* (C) expression level and genotypes of markers included in the Porcine SNP60 Bead-Chip (Illumina). The X-axis represents the chromosomes, and the Y-axis shows the $-\log_{10}$ (p-value).

Table S1. Mean comparison of liver gene expression levels of 43 lipid-related genes between males and females.

Table S2. Topological mean parameters of male and female liver co-expression networks.

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Table S9. List of primers for the RT-qPCR analysis.

Figure S1. Evidence of interactions between *FABP1*, *FADS1*, *FADS2*, *PPAR α* and *SREBF1c* using GeneMANIA.

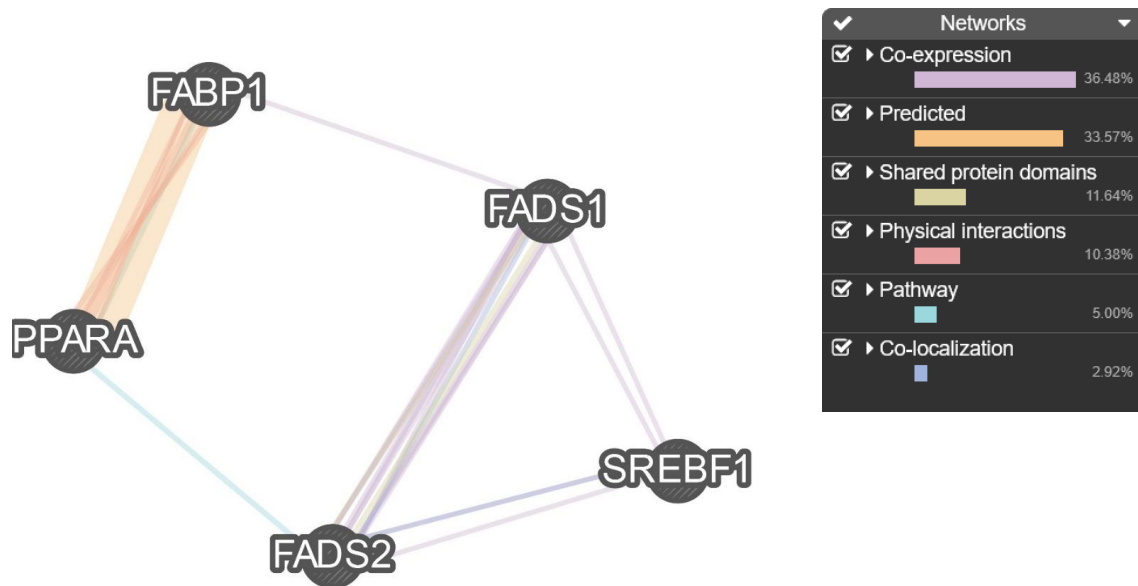
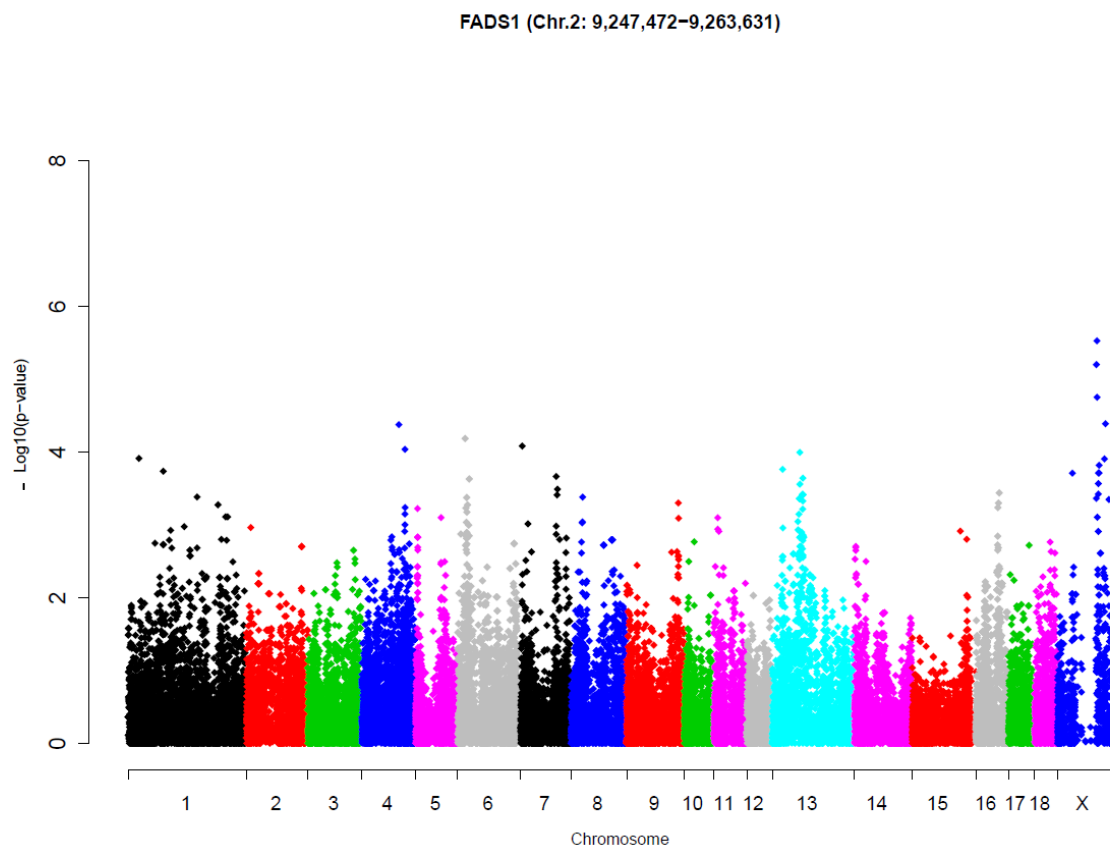


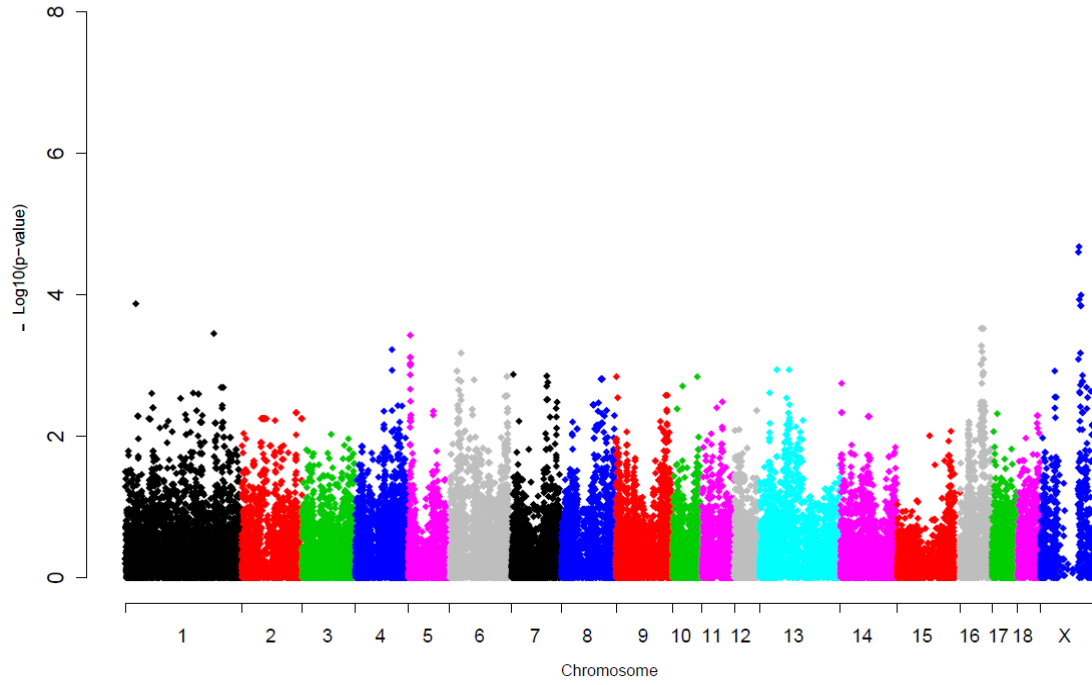
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(A)



(B)

FADS2 (Chr.2: 9,119,389-9,152,215)



(C)

FADS3 (Chr.2: 9,157,720-9,178,637)

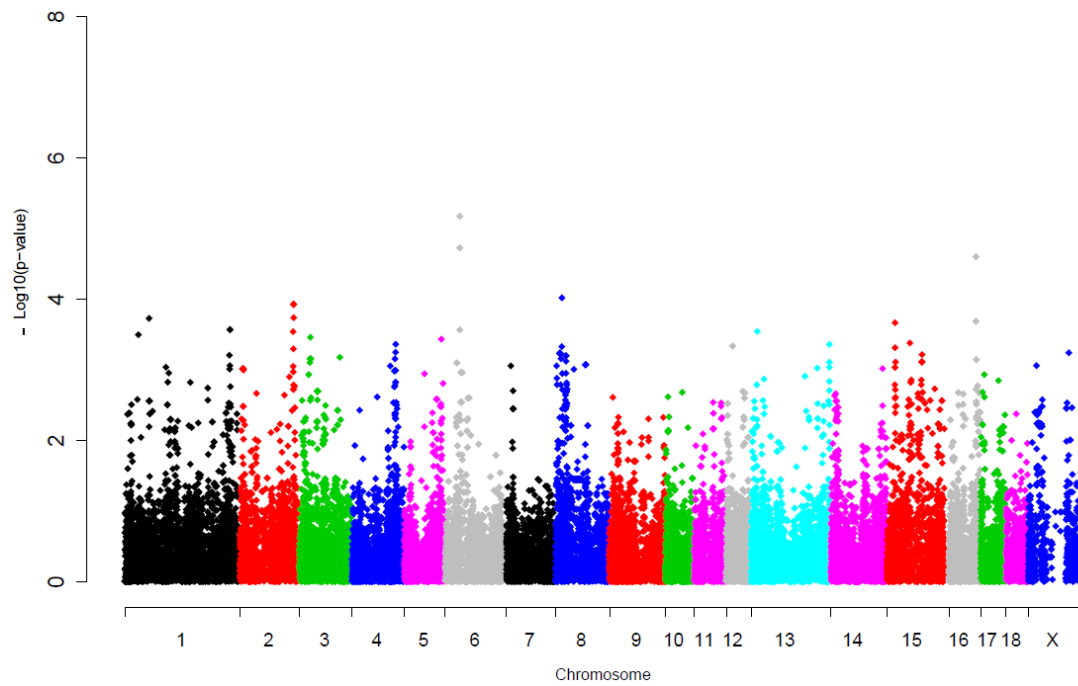


Table S1. Mean comparison of liver gene expression levels of 43 lipid-related genes between males and females.

| Gene | Mean in Male | Mean in Female | P-value |
|-------------|---------------------|-----------------------|----------------|
| ABCG8 | 1.10638507 | 1.32735359 | 4.05E-004 |
| ACSM5 | 0.79516155 | 1.1851219 | 2.22E-010 |
| AGPAT2 | 1.19071574 | 1.38563175 | 5.07E-003 |
| APOA2 | 0.20550265 | 0.02713742 | 2.41E-001 |
| APOB | -0.02306437 | 0.11954847 | 1.32E-002 |
| ARNT | 0.79698145 | 1.05437107 | 3.40E-006 |
| CPT1A | 0.29427247 | 0.16898876 | 3.37E-001 |
| CROT | 0.26698294 | -0.66364779 | 1.47E-008 |
| CYP2U1 | 0.82864276 | 1.03923552 | 8.59E-003 |
| CYP7A1 | -2.44494517 | -0.05319579 | 4.03E-009 |
| DGAT1 | -0.41921145 | 0.36465435 | 1.30E-015 |
| EGF | -1.22717633 | -0.85612796 | 3.78E-004 |
| ELOVL5 | 1.06074307 | 1.23407169 | 1.00E-002 |
| ELOVL6 | 0.73797252 | 0.84591396 | 5.52E-002 |
| ESRRA | 0.34666028 | 0.30251565 | 3.73E-001 |
| FABP1 | -0.59242455 | -0.57381859 | 9.66E-001 |
| FABP5 | -0.92984332 | -0.72534364 | 2.05E-001 |
| FADS1 | -1.72876913 | -0.72295389 | 2.02E-006 |
| FADS2 | -1.47984864 | -0.29575868 | 1.75E-008 |
| FADS3 | -0.10099681 | 0.17610714 | 1.28E-004 |
| FOXA1 | 0.22632908 | 0.4291075 | 2.08E-002 |
| HADH | 0.06495191 | 0.22201133 | 4.85E-002 |
| HNF4A | 1.09180931 | 1.17050052 | 1.65E-001 |
| HNF4G | 0.7645411 | 0.83374403 | 1.63E-001 |
| KLF10 | 0.03005835 | 0.13973121 | 2.20E-001 |
| LIPC | 0.86223939 | 1.08434376 | 1.88E-006 |
| LPIN1 | -0.56350028 | 0.17233961 | 2.53E-006 |

| | | | |
|----------|-------------|------------|-----------|
| MLXIPL | 1.00207993 | 1.51263934 | 5.10E-007 |
| MTTP | 0.71398821 | 0.74801256 | 1.22E-001 |
| NFKB1 | 0.87144002 | 0.97034133 | 2.84E-005 |
| NR1H3 | 0.32850425 | 0.49924015 | 3.74E-003 |
| PLA2G12A | 0.94732107 | 0.97141924 | 3.61E-001 |
| PLCB2 | -0.02181955 | 0.32819592 | 9.73E-006 |
| POU2F1 | 0.08581884 | 0.22957523 | 3.26E-002 |
| PPAP2A | -0.19031833 | 0.0091592 | 1.51E-004 |
| PPARA | 0.87208797 | 1.08429168 | 7.95E-005 |
| PPARD | 0.41621572 | 0.26473171 | 1.91E-001 |
| PPARGC1A | -0.14427855 | 0.01644963 | 1.71E-002 |
| PEX2 | -0.07879949 | 0.30253662 | 1.34E-005 |
| SCAP | 0.34398852 | 0.64865395 | 2.06E-005 |
| SCD1 | -0.34087252 | 0.32686898 | 5.34E-005 |
| SREBF1 | -0.72304021 | 0.36053337 | 3.08E-012 |
| USF1 | 1.11536894 | 1.16965193 | 9.58E-002 |

Table S2. Topological mean parameters of male and female liver co-expression networks.

| Topological parameters | Female | Male |
|-------------------------------|---------------|-------------|
| Average Distance | 1.76655052 | 1.45876887 |
| Centroid mean value | -12.5952381 | -11.5 |
| Closeness mean value unDir | 0.01406093 | 0.01705652 |
| Degree mean value | 14.2380952 | 22.9047619 |
| Eccentricity mean value | 0.34126984 | 0.4484127 |
| Radiality mean value | 3.23344948 | 2.54123113 |
| Stress mean value | 251.380952 | 201.666667 |

Table S4. List of genes annotated in the seven chromosomal regions associated with gene expression phenotypes.

| Gene list | | | | |
|------------------|----------|----------|----------|--------|
| ABCC5 | DGKG | LARP7 | POU4F2 | VPS8 |
| ABCE1 | DIAPH1 | LEF1 | PPA2 | VWA5B2 |
| ABCF3 | DKK2 | LIPH | PPP1R42 | XKR9 |
| ACTL6A | DNAJB11 | LRIT3 | PRDM14 | YEATS2 |
| ADHFE1 | DNAJC19 | LSM6 | PREX2 | ZMAT3 |
| AHSG | DNAJC5B | MAGEF1 | PRMT9 | ZNF827 |
| AIMP1 | DVL3 | MAP3K13 | PSMD2 | |
| ALG3 | ECE2 | MASP1 | RELL2 | |
| ALPK1 | EDNRA | MCCC1 | RFC4 | |
| ANAPC10 | EIF2B5 | MCF2L2 | RNF14 | |
| ANK2 | EIF4A2 | MCMDC2 | RPL34 | |
| AP1AR | EIF4G1 | MMAA | RRH | |
| AP2M1 | ELOVL6 | MRPL47 | RRS1 | |
| ARAP3 | ENPEP | MSC | RTP1 | |
| ARFGEF1 | EPHB3 | MTFR1 | RTP2 | |
| ARHGAP10 | ETNPPL | MYBL1 | SEC24B | |
| ARHGAP26 | EYA1 | NAALADL2 | SENP2 | |
| ARHGEF38 | FAM131A | NCOA2 | SGK3 | |
| ARMC1 | FCHSD1 | NDFIP1 | SGMS2 | |
| ARSJ | FETUB | NDUFB5 | SLC10A7 | |
| ATP11B | FGF1 | NLGN1 | SLCO5A1 | |
| B3GNT5 | FXR1 | NPNT | SOX2 | |
| BCL6 | GAR1 | NR3C1 | SPRY4 | |
| C8orf34 | GNPDA1 | NR3C2 | SST | |
| C8orf46 | GSTCD | OSTC | SULF1 | |
| CALM1 | HADH | OTUD4 | TAF7 | |
| CAMK2D | HDAC3 | PARL | TBCCD1 | |
| CAMK2N2 | HHIP | PCDH1 | TBCK | |
| CASP6 | HRG | PCDH12 | TBL1XR1 | |
| CCDC109B | HTR3C | PCDHB16 | THPO | |
| CCDC39 | HTR3D | PCDHGA12 | TIFA | |
| CFI | IGF2BP2 | PCDHGA8 | TMEM184C | |
| CHRD | INTS12 | PCDHGA9 | TMEM41A | |
| CLCN2 | KCNMB2 | PCDHGB5 | TRAM1 | |
| COPS5 | KCNMB3 | PCDHGC5 | TRIM55 | |
| CPA6 | KIAA0141 | PDE7A | TRPA1 | |
| CRH | KLHL24 | PEX5L | TTC14 | |
| CRYGS | KLHL6 | PIK3CA | TTC29 | |
| CSPP1 | KNG1 | PITX2 | UGT8 | |
| CYP2U1 | LACTB2 | PLA2G12A | USP13 | |
| DCUN1D1 | LAMP3 | POLR2H | VCPIP1 | |

Table S5. Top-five associated networks and molecules from the list of genes annotated in the seven eQTLs based on IPA.

| ID | Molecules in Network | Score | Focus Molecules | Top Diseases and Functions |
|----|--|-------|-----------------|--|
| 1 | Akt,ARAP3,ARFGEF1,C8orf44-SGK3/SGK3,CASP6,caspase,CPA6,DIAPH1,DNAJB11,DNAJC19,DNAJC5B,EIF2B5,EPHB3,EYA1,FABP1,GTPase,Hdac,HSP,Hsp70,Hsp90,Hsp22/Hsp40/Hsp90,KIAA0141,LSM6,Mlc,MSC,NDFIP1,PITX2,PP2A,PRDM14,PREX2,SEC24B,SOX2,TRIM55,trypsin,USP13 | 45 | 24 | Cellular Development, Digestive System Development and Function, Auditory and Vestibular System Development and Function |
| 2 | AHSG,ANK2,C/ebp,CAMK2N2,Cbp/p300,Creb,CRH,Cyclin A,DKK2,ELOVL6,ERK1/2,estrogen receptor,FGF1,Fgfr,HDAC3,HDL,histone deacetylase,Histone h4,LEF1,LIPH,N-cor,NCOA2,NCoR/SMRT corepressor,NLGN1,Nr1h,NR3C2,PCDH1,Pias,RNF14,SPRY4,SULF1,TB L1XR1,TTC29,UGT8,Wnt | 35 | 20 | Organismal Development, Endocrine System Disorders, Gastrointestinal Disease |
| 3 | AIMP1,Alpha Actinin,Ap1,ATP11B,B3GNT5,CAMK2D,Caspase 3/7,CD3,CHRD,DVL3,ENPEP,FABP5,FETUB,Fibrinogen,HRG,IgG,IKK (complex),IL1,KNG1,MAP3K13,Mapk,Mek,MYBL1,NFkB (complex),p70 S6k,p85 (pik3r),PDGF BB,PIK3CA,Ras,SENP2,Sos,Tgf beta,THPO,TIFA,TRPA1 | 31 | 18 | Post-Translational Modification, Cellular Growth and Proliferation, Hematological System Development and Function |
| 4 | 26s Proteasome,Actin,ACTL6A,ADCY,ARMC1,CALM1 (includes others),Calmodulin,Cg,CLCN2,EIF4A2,EIF4G1,ERK,FXR1,GNRH,HADH ,HISTONE,Histone h3,Insulin,MEF2,NR3C1,PI3K (complex),Pka,Pka catalytic subunit,PLC,POLR2H,Proinsulin,PSMD2,RFC4,RNA polymerase II,RRS1,SST,STAT5a/b,TAF7,voltage-gated calcium channel,YEATS2 | 26 | 16 | Drug Metabolism, Endocrine System Development and Function, Lipid Metabolism |
| 5 | ANKRD39,APP,Aspartyl Protease,CALML4,CCDC39,CFDP1,CUL3,DNAJC4,ETNPPL,HTT,INTS1 2,KCNC4,KCNMA1,KCNMB2,KCNMB3,KCNMB4,KCNU1,KCTD18,L ARP7,MASP1,MTFR1,NAALADL2,ODF2L,PEX5L,PIN1,PPA2,PRPF40B ,PRRC1,Rbfox3,RPL34,RPL3L,TBCK,WDR91,ZMAT4,ZNF706 | 20 | 13 | Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Cardiac Arrythmia |

Table S6. Description of the 17 significant *cis*-eSNPs at chromosome level.

| Chr | SNP | bp | fA1 | fA2 | p-value | q-value | Associated_Gene | Consequence | Ensembl_GeneId | GeneId |
|-----|-------------|-----------|------|------|----------|----------|-----------------|-----------------------|--------------------|------------------|
| 3 | ALGA0020228 | 102155060 | 0.79 | 0.21 | 2.82E-05 | 1.52E-02 | ABCG8 | intergenic_variant | | |
| 3 | ASGA0015479 | 102763903 | 0.79 | 0.21 | 2.82E-05 | 1.52E-02 | ABCG8 | intron_variant | ENSSSCG00000008453 | ABCG8 |
| 3 | M1GA0004530 | 103046883 | 0.79 | 0.21 | 2.82E-05 | 1.52E-02 | ABCG8 | intron_variant | ENSSSCG00000028599 | orthologue THADA |
| 3 | MARC0037203 | 102111329 | 0.87 | 0.13 | 6.62E-05 | 2.04E-02 | ABCG8 | intergenic_variant | | |
| 3 | H3GA0010157 | 102401629 | 0.87 | 0.13 | 6.62E-05 | 2.04E-02 | ABCG8 | intron_variant | ENSSSCT00000009253 | PPM1B |
| 3 | H3GA0010212 | 104427661 | 0.72 | 0.28 | 1.49E-04 | 4.02E-02 | ABCG8 | intergenic_variant | | |
| 3 | ALGA0020335 | 104692463 | 0.71 | 0.29 | 1.96E-04 | 4.70E-02 | ABCG8 | intergenic_variant | | |
| 4 | ASGA0020802 | 97973034 | 0.74 | 0.26 | 8.20E-06 | 2.07E-02 | USF1 | upstream_gene_variant | ENSSSCG00000006383 | VANGL2 |
| 8 | ALGA0049276 | 122249328 | 0.93 | 0.07 | 3.83E-06 | 3.72E-03 | CYP2U1 | intron_variant | ENSSSCG00000009150 | HADH |
| 8 | ALGA0110177 | 122654894 | 0.41 | 0.59 | 6.02E-05 | 1.58E-02 | HADH | intergenic_variant | | |
| 8 | ASGA0106126 | 122655115 | 0.41 | 0.59 | 6.02E-05 | 1.58E-02 | HADH | intergenic_variant | | |
| 8 | ASGA0103857 | 122655547 | 0.41 | 0.59 | 6.02E-05 | 1.58E-02 | HADH | intergenic_variant | | |
| 8 | MARC0003202 | 122664524 | 0.41 | 0.59 | 6.02E-05 | 1.58E-02 | HADH | intergenic_variant | | |
| 8 | ALGA0108851 | 122072309 | 0.42 | 0.58 | 9.28E-05 | 1.95E-02 | HADH | intergenic_variant | | |
| 8 | ASGA0089440 | 124212852 | 0.46 | 0.54 | 1.73E-04 | 2.98E-02 | HADH | intron_variant | ENSSSCG00000020821 | NPNT |
| 8 | ALGA0049269 | 121743168 | 0.42 | 0.58 | 2.48E-04 | 3.62E-02 | HADH | intergenic_variant | | |
| 8 | MARC0037703 | 122288920 | 0.61 | 0.39 | 2.88E-04 | 3.78E-02 | HADH | intron_variant | ENSSSCG00000009151 | CYP2U1 |

Table S7. Significant co-expression values among genes regulated by the hotspots on SSC8.

| From | To | Weight | sign |
|-------------|-----------|---------------|-------------|
| APOB | HADH | 0.77372545 | + |
| AGPAT2 | PPARA | 0.75664717 | + |
| AGPAT2 | HADH | 0.73869884 | + |
| DGAT1 | APOB | 0.724836052 | + |
| CYP2U1 | HADH | 0.716647029 | + |
| DGAT1 | PPARA | 0.71526891 | + |
| DGAT1 | HADH | 0.711374998 | + |
| PPARA | HADH | 0.69495374 | + |
| AGPAT2 | DGAT1 | 0.688199759 | + |
| PPARA | APOB | 0.654403329 | + |
| AGPAT2 | ESRRA | 0.635816097 | + |
| AGPAT2 | APOB | 0.59262836 | + |
| CYP2U1 | APOB | 0.580422282 | + |
| CYP2U1 | DGAT1 | 0.57343328 | + |
| ESRRA | APOB | 0.559513271 | + |
| ESRRA | PPARA | 0.530570805 | + |
| ESRRA | HADH | 0.50790447 | + |
| CYP2U1 | PPARA | 0.499788463 | + |
| CYP2U1 | AGPAT2 | 0.484627783 | + |
| DGAT1 | EGF | 0.365692794 | + |
| AGPAT2 | EGF | 0.325705379 | + |
| EGF | PPARA | 0.309143394 | + |
| EGF | APOB | 0.240296617 | + |
| EGF | HADH | 0.240153566 | + |

Table S9. List of primers for the RT-qPCR analysis.

| Gene | Full name | Type | Primer sequence | |
|-----------------|--|------------|-----------------------------|------------------------------|
| | | | Forward | Reverse |
| <i>ABCG8</i> | ATP binding cassette subfamily G member 8 | Target | ATGTCCGCCCTCTTGTTCAT | TCCGAGTGGCATTGGAGAT |
| <i>ACSM5</i> | acyl-CoA synthetase medium-chain family member 5 | Target | TGTAATCTGTGCCAATCCCAAA | CATCATCTACGATCTGCACCTCAT |
| <i>ACTB</i> | actin beta | Endogenous | CAAGGACCTCTACGCCAACAC | TGGAGGCGCGATGATCTT |
| <i>AGPAT2</i> | 1-acylglycerol-3-phosphate O-acyltransferase 2 | Target | CATGGTCAGGGAGAAGCTCAA | GCCAGGTAGAAGGCACCTTTC |
| <i>APOA2</i> | apolipoprotein A2 | Target | AACTTCAAACCTCAGGCCAAGACTTA | GGCCAATGAAACTGCTCAAGA |
| <i>APOB</i> | apolipoprotein B | Target | CCACCAAGATCAACTGCAAGGT | GGAGCAGTGGCTGGTCTTCA |
| <i>ARNT</i> | aryl hydrocarbon receptor nuclear translocator | Target | TCTAATGATAAGGAGCGGTTTGC | TATGATTTTCCCTGGCGAGTCT |
| <i>B2M</i> | beta-2-microglobulin | Endogenous | ACCTTCTGGTCCACACTGAGTTC | GGTCTCGATCCCCTTAACCTATCTTG |
| <i>MLXIPL</i> | MLX interacting protein like | Target | CCCAAGTGGAGAATTTCAAAGG | CTTCTCCGCTCCACATACTG |
| <i>CPT1A</i> | carnitine palmitoyltransferase 1A | Target | CCTGAAGGTGCTGCTCTCCTA | CTCACCATCATCATCCAGATCTTG |
| <i>CROT</i> | carnitine O-octanoyltransferase | Target | GGGAAACGAAAATTGGTTGGA | CGCAAAGTTGACATTCAGTTGTG |
| <i>CYP2U1</i> | cytochrome P450 family 2 subfamily U member 1 | Target | AGAGAAAACAGTGCTCCAAGGGTAT | TGGCTGGGTCTCTGTGTACTGA |
| <i>CYP7A1</i> | cytochrome P450 family 7 subfamily A member 1 | Target | TGACGCAGAGAAAAGCCAAGTC | TTCAGAAGCTGCTTTCATTGCT |
| <i>DGAT1</i> | diacylglycerol O-acyltransferase 1 | Target | CCTGAATTGGTGTGTGGTCATG | GATGCCGTACTIONTGTAGAGTTCTC |
| <i>EGF</i> | epidermal growth factor | Target | AACGGGAATGCCACTTGTGT | CCTTCCAAGTCAATCCTAAAGATACTG |
| <i>ELOVL5</i> | ELOVL fatty acid elongase 5 | Target | CCTCTCGGCTGGCTGTACTT | CCTTCTTGTTGAGGTCTGGATGTAG |
| <i>ELOVL6</i> | ELOVL fatty acid elongase 6 | Target | AGCAGTTCACGAGAACGAAGCC | TGCCGACCGCCAAAGATAAAG |
| <i>ESRRA</i> | estrogen related receptor alpha | Target | CAAGAGCATCCCAGGCTTCTC | CACCCAACACCAATACCTCCAT |
| <i>FABP1</i> | fatty acid binding protein 1 | Target | AAGGTCGTCCAGAATGAGTTCAC | TTCCAACGAACCACTGTCTTGA |
| <i>FABP5</i> | fatty acid binding protein 5 (psoriasis-associated) | Target | CCAATGGAGAATTGGTCAACA | GTTCATGACGCATACCACCACTA |
| <i>FADS1</i> | fatty acid desaturase 1 | Target | CCTTGTGAGGAAGTATATGAGCTCTCT | TCATCTGTGAGCTCTTTATTCTTAGTCG |
| <i>FADS2</i> | fatty acid desaturase 2 | Target | TCCACCGCGACCTTGATTTA | TCGGTGTATCTCAGAGTTCTTGGT |
| <i>FADS3</i> | fatty acid desaturase 3 | Target | CCAGCACCTCTACTTCTTCTGAT | CATGTATGCCAGATTTTCCACTTC |
| <i>FOXA1</i> | forkhead box A1 | Target | ACAGTACTACGCGGACACACA | ATGGTGCTCAGACCCGAGTT |
| <i>HADH</i> | hydroxyacyl-CoA dehydrogenase | Target | AGCTCTTCAAGAGGCTGGACAA | TTGTGATCTGCAAAGAGGAAGTG |
| <i>HNF4A</i> | hepatocyte nuclear factor 4 alpha | Target | GACCATGGGCAATGACACATC | GCACACAAGGCGCTGACA |
| <i>HNF4G</i> | hepatocyte nuclear factor 4 gamma | Target | GTCTTGGTGGAAATGGGCTAAAT | CTCTCAACAGTGCCACCTGATC |
| <i>HPRT1</i> | hypoxanthine phosphoribosyltransferase 1 | Endogenous | TCATTATGCCGAGGATTTGGA | CTCTTTCATCAGATCTCGAGCAA |
| <i>KLF10</i> | Kruppel like factor 10 | Target | ACGATCCCAGCATTTTGTGTTG | TGGTGCCATCAGATTTGACACT |
| <i>LIPC</i> | lipase C, hepatic type | Target | CGTTACAGCAGTGTGGCTTCA | CCAGCAAGCCATCCATCAA |
| <i>LPIN1</i> | lipin 1 | Target | CCGAGAGAAGGTGGTGGACAT | CTCTCCATTGTCTCCAGTTTCA |
| <i>MTTP</i> | microsomal triglyceride transfer protein | Target | GAGGTCCAGGTTGGTCTAGCTATT | AGTTATTACCACGGTTACCCGATTT |
| <i>NFKB1</i> | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 | Target | CCCACAGACGTTTATAGACAATTT | GAGGCTGGTTTTGTAATGTTGACA |
| <i>NR1H3</i> | nuclear receptor subfamily 1, group H, member 3 | Target | CTGGGCATGATCGAGAAGCT | TGGGCCAAGGCGTGACT |
| <i>NR2E1</i> | nuclear receptor subfamily 2 group E member 1 | Target | GGAATAGCACAAATGGGCCATT | TTGTCACCATTTCATGCCAGATA |
| <i>PEX2</i> | peroxisomal biogenesis factor 2 | Target | CTCAGACTCCTAAGAAACCTTCAGAGA | ACTGATCTGAGCACTCTGTTTGC |
| <i>PLA2G12A</i> | phospholipase A2, group XIIA | Target | CCCCTCTTTGGTGTTCATCTTAA | ATAGCACCTGTCTGTCTGGTT |
| <i>PLCB2</i> | phospholipase C beta 2 | Target | AGATCTTCACTTCTACCCTCCAA | GCGCTGTTCTGTGTTGATGA |
| <i>POU2F1</i> | POU class 2 homeobox 1 | Target | CCCATACAGATCGCACAGGAT | GATGATAAACTGTGCTGGTTGCA |
| <i>PPAP2A</i> | phosphatidic acid phosphatase type 2A | Target | GGCCACTTCTATTCTCCATGTAC | AGGCCACGTAATGGATACAG |

| | | | | |
|-----------------|---|------------|---------------------------|--------------------------|
| <i>PPARA</i> | peroxisome proliferator activated receptor alpha | Target | GGCACTGAACATCGAATGTAGAATC | CCGAAAGAAGCCCTTGCAA |
| <i>PPARD</i> | peroxisome proliferator activated receptor delta | Target | GCATGTCTCACAACGCCATT | GCTGACTCCCCTCGTTTGC |
| <i>PPARGCIA</i> | peroxisome proliferator-activated receptor gamma, coactivator 1 alpha | Target | CTCTGGAAGTGCAGGCCTAA | TGGAGAAGCCCTAAAAGGGTTAT |
| <i>SCAP</i> | SREBF chaperone | Target | AGATATCTCAGGCCTTCTACAACCA | AGTTTCAACAGTGGGTAGCAGC |
| <i>SCD1</i> | stearoyl-CoA desaturase (delta-9-desaturase) | Target | GGTGATGTTCCAGAGGAGGTACTAC | CAGCAATACCAGGGCACGAT |
| <i>SREBF1</i> | sterol regulatory element binding transcription factor 1 | Target | CACGGAGGCGAAGCTGAATA | GCTTCTGGTTGCTCTGCTGAA |
| <i>TBP</i> | TATA box binding protein | Endogenous | CAGAAATGATCAAACCGAGAATTGT | CTGCTCTGACTTTAGCACCTGTAA |
| <i>USF1</i> | upstream transcription factor 1 | Target | CCCTTATCCCCGAAGTCAGA | GCGGCGTTCCACTTCATTAT |