**Association study highlights the influence of *ELOVL fatty acid elongase 6* gene region on backfat fatty acid composition in Large White pig breed.**

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*animal* journal

Supplementary Table S1. The proportions of variance explained by the analysed 45 704 markers for the adjusted phenotypes of the traits and returned by GenSel software.

|  |  |
| --- | --- |
| Trait | Posterior mean of proportions of variance explained by the analysed markers |
| Backfat fatty acid composition (% on total fatty acids) |  |
| Palmitic acid | 0.60 |
| Palmitoleic acid | 0.36 |
| Stearic acid | 0.33 |
| Oleic acid | 0.56 |
| Linoleic acid | 0.46 |
| Linolenic acid | 0.45 |
| Arachidic acid | 0.35 |
| Arachidonic acid | 0.41 |
| Docosapentaenoic acid | 0.31 |
| Docosahexaenoic acid | 0.17 |
| Saturated fatty acids | 0.42 |
| Monounsaturated fatty acids | 0.54 |
| Polyunsaturated fatty acids | 0.43 |
| Unsaturated fatty acids | 0.42 |
| Omega-6 polyunsaturated fatty acids1 | 0.46 |
| Omega-3 polyunsaturated fatty acids2 | 0.27 |
| Short chain fatty acids3 | 0.19 |
| Medium chain fatty acids4 | 0.20 |
| Long chain fatty acids5 | 0.19 |
| Backfat thickness (mm) | 0.43 |

1 Omega-6 polyunsaturated fatty acids included linoleic and arachidonic acids.

2 Omega-3 polyunsaturated fatty acids included linolenic, docosapentaenoic and docosahexaenoic acids.

3 Short chain fatty acids included fatty acids with a chain length to 10 atoms of carbons.

4 Medium chain fatty acids included fatty acids with a chain length from 12 to 16 atoms of carbons.

5 Long chain fatty acids included fatty acids with a chain length from 17 atoms of carbons.

Supplementary Table S2. Comparison between the regions obtained from the present study and the quantitative trait loci (QTLs) reported in literature for the same regions or in nearby chromosomal regions.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genome-wide association study results | | |  | QTLs in literature1 | | |
| SSC2 | Region (Mb)3 | Trait |  | Trait | Region (Mb)3 | Literature |
| 1 | 18-194 | Linolenic acid |  | - | - | - |
|  | 75-80 | Stearic acid, saturated fatty acids, unsaturated fatty acids |  | Saturated fatty acid content | 81.4 | Ramayo-Caldas *et al.*, 2012 |
|  | 277-280 | Unsaturated fatty acids, palmitic acid |  | Oleic acid content | 280.5-280.6 | Sanchez *et al.*, 2007 |
| 2 | 107-1084 | Palmitoleic acid |  | - | - | - |
| 3 | 32-334 | Linolenic acid |  | - | - | - |
| 5 | 65-664 | Linolenic acid |  | - | - | - |
|  | 70-75 | Arachidic acid |  | Arachidic acid content | 69; 77 | Yang *et al.*, 2013 |
|  | 104-105 | Linoleic acid, polyunsaturated fatty acids, omega-6 polyunsaturated fatty acids |  | Average Feeding rate | 107.5 | Do *et al.*, 2013 |
| 7 | 5-6 | Stearic acid, unsaturated fatty acids |  | Linoleic acid content | 8.8-13.8 | Kim *et al.*, 2006 |
|  | 10-16 | Backfat thickness |  | Average backfat thickness | 9.7-14.8 | Paszek *et al.*, 2001 |
|  | 51-54 | Palmitic acid, stearic acid, arachidonic acid, saturated fatty acids, unsaturated fatty acids |  | Arachidonic acid content; Cis-11-Eicosenoic acid content | 50.8; 52.2 | Yang *et al.*, 2013 |
|  | 56-58 | Monounsaturated fatty acids, linoleic acid |  | Linoleic acid content | 49.2-49.4 | Guo *et al.*, 2009 |
|  | 122-123 | Backfat thickness |  | Average backfat thickness | 106.8-120.7 | Kim *et al.*, 2005 |
| 8 | 8-10 | Palmitic acid, unsaturated fatty acids |  | Palmitic acid content | 0.8-6.7 | Uemoto *et al.*, 2012 |
|  | 33-34 | Stearic acid |  | Average backfat thickness | 33-34 | Jiao *et al.*, 2014 |
|  | 119-122 | Palmitic acid, palmitoleic acid, oleic acid, medium chain fatty acids, long chain fatty acids |  | Palmitoleic acid content; Oleic acid content and Palmitic acid content | 114.2-122.3; 117.4 | Muñoz *et al.*, 2013; Revilla *et al.*, 2014 |
|  | 141-142 | Unsaturated fatty acids |  | Palmitoleic acid content | 72-139 | Clop *et al.*, 2003 |
| 9 | 22-234 | Arachidonic acid |  | - | - | - | |
|  | 26-27 | Linolenic acid |  | Palmitoleic acid content | 24.6-71.4 | Uemoto *et al.*, 2012 |
|  | 28-29 | Oleic acid, monounsaturated fatty acids |  | Palmitoleic acid content | 24.6-71.4 | Uemoto *et al.*, 2012 | |
| 10 | 10-11 | Palmitic acid |  | Palmitic acid content | 5.9-13.9 | Uemoto *et al.*, 2012 | |
|  | 55-56 | Linoleic acid, polyunsaturated fatty acids, omega-6 polyunsaturated fatty acids |  | Oleic acid content | 61.5 | Sanchez *et al.*, 2007 |
| 11 | 7-8 | Linolenic acid |  | Linoleic acid content | 7.8 | Ramayo-Caldas *et al.*, 2012 |
|  | 65-66 | Backfat thickness |  | Backfat at rump | 68.5 | Fontanesi *et al.*, 2012 |
| 13 | 167-174 | Short chain fatty acids |  | Cholesterol level | 185.4-206.7 | Yoo *et al.*, 2012 |
| 14 | 10-114 | Monounsaturated fatty acids |  | - | - | - |
|  | 46-52 | Short chain fatty acids, docosahexaenoic acid, omega-3 polyunsaturated fatty acids |  | [Homolonolenic acid content (C20:3)](http://www.animalgenome.org/cgi-bin/QTLdb/SS/qtrait?trait_ID=533) | 45 | Yang *et al.*, 2013 |
|  | 116-124 | Stearic acid, oleic acid, unsaturated fatty acids, monounsaturated fatty acids |  | Monounsaturated fatty acid content and Stearic acid content;  Oleic acid content | 116.6-116.7;  120.2 | Sanchez *et al.*, 2007;  Yang *et al.*, 2013 |
|  | 138-139 | Arachidic acid |  | Arachidic acid content | 121-121.5 | Zhang *et al.*, 2016 |
| 16 | 0-3 | Backfat thickness |  | Backfat above muscle dorsi | 0.3-67.6 | Liu *et al.*, 2008 |
|  | 36-37 | Arachidonic acid |  | Arachidic acid content | 38.8-38.9 | Guo *et al.*, 2009 |
| 17 | 17-18 | Linolenic acid |  | Eicosenoic acid to eicosanoic acid ratio | 22.5 | Ramayo-Caldas *et al.*, 2012 |
| 18 | 3-4 | Palmitic acid |  | Palmitic acid content | 5.7-22.9 | Uemoto *et al.*, 2012 |
|  | 41-42 | Oleic acid |  | Palmitic acid content | 46.7-47.7 | Quintanilla *et al.*, 2011 |

1 The reported QTLs were obtained from QTLdb (url: http://www.animalgenome.org/cgi-bin/QTLdb/index).

2 SSC stands for *Sus scrofa* chromosome.

3 Windows positions referred to *Sus scrofa* assembly Build 10.2, expressed in Mb.

4 For these regions there are not QTLs located in the neighbourhood or in the same genomic region reported in literature.

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Supplementary Table S3. For the genomic regions associated with the analysed traits are reported the upper limits of the posterior type I error rate (PER).

|  |  |  |  |
| --- | --- | --- | --- |
| Trait | SSC1 | Nucleotide Position2 | PER3 |
| Palmitic acid | 8 | 119-120 | 0.01 |
|  | 8 | 9-10 | 0.42 |
|  | 7 | 52-53 | 0.43 |
| Palmitoleic acid | 8 | 119-120 | 0.63 |
| Stearic acid | 1 | 77-78 | 0.57 |
|  | 14 | 117-118 | 0.46 |
| Oleic acid | 8 | 119-120 | 0.26 |
|  | 14 | 122-123 | 0.49 |
| Linoleic acid | 5 | 104-105 | 0.41 |
|  | 10 | 55-56 | 0.55 |
|  | 7 | 57-58 | 0.48 |
| Linolenic acid | 17 | 17-18 | 0.48 |
|  | 9 | 26-27 | 0.41 |
|  | 5 | 65-66 | 0.52 |
| Arachidic acid | 5 | 72-73 | 0.62 |
|  | 14 | 138-139 | 0.66 |
| Arachidonic acid | 7 | 53-54 | 0.52 |
|  | 9 | 22-23 | 0.58 |
| Docosahexaenoic acid | 14 | 50-51 | 0.84 |
| Saturated fatty acids | 7 | 53-54 | 0.32 |
|  | 1 | 77-78 | 0.50 |
| Monounsaturated fatty acids | 7 | 56-57 | 0.38 |
|  | 14 | 122-123 | 0.47 |
| Polyunsaturated fatty acids | 5 | 104-105 | 0.41 |
|  | 10 | 55-56 | 0.55 |
| Unsaturated fatty acids | 7 | 53-54 | 0.32 |
|  | 1 | 77-78 | 0.51 |
|  | 1 | 277-278 | 0.61 |
|  | 14 | 117-118 | 0.44 |
| Omega-6 polyunsaturated fatty acids | 5 | 104-105 | 0.39 |
|  | 10 | 55-56 | 0.56 |
| Omega-3 polyunsaturated fatty acids | 14 | 50-51 | 0.78 |
| Short chain fatty acids | 14 | 50-52 | 0.81 |
| Medium chain fatty acids | 8 | 119-120 | 0.00 |
| Long chain fatty acids | 8 | 119-120 | 0.00 |
| Backfat thickness | 7 | 15-16 | 0.37 |
|  | 7 | 122-123 | 0.40 |
|  | 16 | 0-1 | 0.51 |
|  | 11 | 65-66 | 0.47 |

1 *Sus scrofa* chromosome.

2 Windows positions referred to *Sus scrofa* assembly Build 10.2, expressed in Mb.

3 The upper limit of the posterior type I error rate (PER) calculated as 1 – the posterior probability of inclusion of the markers in the model.

Supplementary Table S4. Markers most relevantly associated with pigs backfat fatty acids composition listed on the basis of their genomic position.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| SSC1 | Nucleotide Position2 | Marker | Trait | Genetic Variance3 | 4 | BF5 |
| 1 | 18 577 487 | ASGA0101644 | Linolenic acid | 1.21E-05 | 0.21 | 17.24 |
|  | 277 975 238 | MARC0053473 | Saturated fatty acids | 2.45E-03 | 0.23 | 19.36 |
|  | 277 975 238 | MARC0053473 | Unsaturated fatty acids | 1.96E-03 | 0.21 | 17.67 |
| 5 | 65 687 961 | MARC0035523 | Linolenic acid | 4.29E-06 | 0.13 | 10.13 |
|  | 71 056 487 | MARC0070351 | Arachidic acid | 3.24E-07 | 0.10 | 7.39 |
|  | 104 959 696 | DRGA0006379 | Linoleic acid | 4.18E-03 | 0.35 | 28.94 |
|  | 104 959 696 | DRGA0006379 | Polyunsaturated fatty acids | 4.23E-03 | 0.33 | 26.99 |
|  | 104 959 696 | DRGA0006379 | Omega-6 polyunsaturated fatty acids | 4.08E-03 | 0.34 | 28.34 |
| 7 | 5 620 893 | ALGA0038213 | Stearic acid | 6.66E-04 | 0.20 | 16.32 |
|  | 5 620 893 | ALGA0038213 | Saturated fatty acids | 2.27E-03 | 0.24 | 20.61 |
|  | 5 620 893 | ALGA0038213 | Unsaturated fatty acids | 2.49E-03 | 0.25 | 21.87 |
|  | 10 506 639 | ALGA0038542 | Backfat thickness | 2.05E-03 | 0.14 | 10.56 |
|  | 11 385 909 | ASGA0031202 | Backfat thickness | 2.83E-03 | 0.16 | 12.35 |
|  | 15 108 730 | H3GA0020080 | Backfat thickness | 3.41E-02 | 0.39 | 42.27 |
|  | 51 426 179 | ALGA0041370 | Saturated fatty acids | 8.84E-04 | 0.15 | 11.74 |
|  | 53 685 735 | ASGA0033717 | Stearic acid | 3.67E-04 | 0.14 | 10.83 |
|  | 53 685 735 | ASGA0033717 | Saturated fatty acids | 1.29E-03 | 0.16 | 12.90 |
|  | 53 685 735 | ASGA0033717 | Unsaturated fatty acids | 9.76E-04 | 0.15 | 11.82 |
|  | 122 615 348 | ALGA0045097 | Backfat thickness | 6.58E-03 | 0.21 | 17.67 |
|  | 122 628 410 | ASGA0036491 | Backfat thickness | 5.27E-03 | 0.20 | 16.07 |
| 8 | 8 826 922 | ASGA0037719 | Palmitic acid | 6.40E-04 | 0.21 | 17.61 |
|  |  |  | Saturated fatty acids | 7.62E-04 | 0.15 | 11.45 |
|  |  |  | Unsaturated fatty acids | 7.85E-04 | 0.15 | 11.72 |
|  | 9 494 068 | DRGA0008295 | Palmitic acid | 3.16E-04 | 0.16 | 12.34 |
|  | 33 282 771 | H3GA0024720 | Stearic acid | 7.43E-04 | 0.20 | 16.55 |
|  | 119 727 823 | SIRI0000509 | Palmitic acid | 2.48E-03 | 0.26 | 23.01 |
|  | 119 727 823 | SIRI0000509 | Oleic acid | 9.47E-04 | 0.21 | 14.62 |
|  | 119 851 261 | INRA0030422 | Palmitic acid | 7.93E-04 | 0.16 | 12.09 |
|  | 119 851 261 | INRA0030422 | Oleic acid | 3.35E-03 | 0.34 | 28.15 |
|  | 119 887 465 | H3GA0025321 | Palmitic acid | 3.59E-02 | 0.72 | 166.13 |
|  | 119 887 465 | H3GA0025321 | Palmitoleic acid | 7.96E-05 | 0.18 | 12.02 |
|  | 119 887 465 | H3GA0025321 | Oleic acid | 4.59E-04 | 0.16 | 10.05 |
|  | 119 887 465 | H3GA0025321 | Medium chain fatty acids | 1.61E-01 | 1.00 | > 1 000 |
|  | 119 887 465 | H3GA0025321 | Long chain fatty acids | 1.55E-01 | 1.00 | > 1 000 |
|  | 121 743 169 | ALGA0049269 | Palmitic acid | 8.69E-04 | 0.22 | 18.39 |
|  | 121 829 267 | ASGA0039683 | Palmitic acid | 3.12E-04 | 0.14 | 10.73 |
|  | 140 400 180 | ASGA0102346 | Backfat thickness | 4.41E-03 | 0.17 | 13.84 |
| 9 | 22 748 295 | ASGA0099198 | Arachidonic acid | 9.83E-07 | 0.17 | 13.84 |
|  | 26 225 411 | H3GA0026788 | Linolenic acid | 4.45E-06 | 0.14 | 10.76 |
| 10 | 10 036 337 | MARC0022071 | Palmitic acid | 3.02E-04 | 0.17 | 13.01 |
|  | 54 960 156 | ALGA0105237 | Palmitic acid | 1.79E-04 | 0.14 | 10.32 |
|  | 55 858 372 | H3GA0030320 | Linoleic acid | 1.03E-03 | 0.20 | 13.24 |
|  | 55 858 372 | H3GA0030320 | Polyunsaturated fatty acids | 1.03E-03 | 0.19 | 12.57 |
|  | 55 858 372 | H3GA0030320 | Unsaturated fatty acids | 5.50E-04 | 0.14 | 10.51 |
|  | 55 858 372 | H3GA0030320 | Omega-6 polyunsaturated fatty acids | 1.00E-03 | 0.19 | 13.02 |
| 11 | 7 320 581 | ASGA0049556 | Linolenic acid | 7.33E-06 | 0.18 | 13.98 |
|  | 63 662 080 | M1GA0015159 | Linolenic acid | 6.28E-06 | 0.16 | 12.85 |
|  | 65 750 596 | INRA0036865 | Backfat thickness | 7.18E-03 | 0.20 | 16.79 |
| 14 | 123 733 166 | MARC0006531 | Stearic acid | 4.50E-04 | 0.15 | 11.71 |
| 16 | 665 251 | ASGA0071831 | Backfat thickness | 1.98E-03 | 0.14 | 10.43 |
|  | 864 816 | ASGA0071832 | Backfat thickness | 7.03E-03 | 0.22 | 18.35 |
|  | 81 266 338 | MARC0078879 | Saturated fatty acids | 1.87E-03 | 0.22 | 18.35 |
|  | 81 266 338 | MARC0078879 | Monounsaturated fatty acids | 3.66E-04 | 0.15 | 9.55 |
|  | 81 266 338 | MARC0078879 | Unsaturated fatty acids | 5.85E-04 | 0.14 | 11.12 |
| 17 | 17 548 504 | INRA0052808 | Linolenic acid | 1.36E-05 | 0.21 | 17.63 |
|  | 17 686 439 | MARC0013253 | Linolenic acid | 1.50E-05 | 0.23 | 19.38 |
| 18 | 13 833 809 | ASGA0078689 | Palmitic acid | 1.79E-04 | 0.15 | 11.28 |
|  | 13 900 864 | ASGA0088995 | Palmitic acid | 2.46E-04 | 0.16 | 12.89 |
|  | 141 909 500 | ASGA0102347 | Oleic acid | 6.46E-04 | 0.18 | 11.93 |

1 SSC stands for *Sus scrofa* chromosome.

2 Marker positions referred to *Sus scrofa* assembly Build 10.2.

3 Proportion of the genetic variance explained by the marker on the total genetic variance of the trait.

4 Posterior probability of the marker inclusion in the model iterations.

5 BF stands for the Bayes Factor of the marker.

Docosapentaenoic acid, docosahexaenoic acid, omega-3 polyunsaturated fatty acids and short chain fatty acids are not reported in the table because no marker showed relevant associations with these fatty acids (Bayes Factors were less than or equal to 3.2).

Supplementary Table S5. List of the pathways in which are involved the genes located in the regions relevantly associated with the traits*:* for each pathway, the summary statistics (adjusted P value, Z-score and combined score) obtained from Enrichr online tool and the list of candidate genes involved in those pathways are reported.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Traits | Pathways | Adjusted *P* value | Z-score | Combined score | Genes |
| Palmitic acid | Acetylcholine Binding And Downstream Events1 | 4.52E-05 | -2.32 | 13.88 | *CHRNA3;CHRNB; CHRNA5* |
|  | Regulation of cholesterol biosynthesis by SREBP (SREBF)1 | 1.82E-03 | -1.90 | 5.14 | *SEC24B; INSIG1;ELOVL6* |
|  | Synthesis of very long-chain fatty acyl-CoAs1 | 4.14E-03 | -2.05 | 4.25 | *ACSBG1; ELOVL6* |
| Palmitoleic acid | Metabolism of lipids and lipoproteins1 | 2.08E-02 | -2.18 | 3.47 | *SEC24B; ELOVL6; PLA2G12A; ETNPPL* |
|  | Regulation of cholesterol biosynthesis by SREBP (SREBF)1 | 3.94E-03 | -1.97 | 3.13 | *SEC24B; ELOVL6* |
| Stearic acid | Biosynthesis of amino acids2 | 2.01E-03 | -1.77 | 2.83 | *GOT1; PGAM1; ALDH18A1; IDH3A* |
|  | Arginine and proline metabolism2 | 5.77E-03 | -1.86 | 2.56 | *GOT1; ALDH18A1; HOGA1* |
|  | B cell receptor signaling pathway2 | 1.55E-02 | -1.83 | 2.46 | *CHUK; BLNK; PIK3AP1* |
|  | PPAR signaling pathway2 | 1.34E-02 | -1.59 | 2.14 | *SCD; ACSBG1; SORBS1* |
|  | Fatty acid metabolism2 | 4.68E-02 | -1.41 | 1.19 | *SCD; ACSBG1* |
| Oleic acid | Biosynthesis of unsaturated fatty acids2 | 8.26E-03 | -1.59 | 1.62 | *SCD; ELOVL6* |
|  | Fatty acid elongation2 | 9.60E-03 | -1.41 | 1.44 | *ELOVL3; ELOVL6* |
| Linoleic acid | Myogenesis1 | 6.22E-04 | -2.41 | 7.83 | *MYF6; MYF5* |
|  | CDO in myogenesis1 | 6.22E-04 | -2.40 | 7.78 | *MYF6; MYF5* |
|  | Neurotransmitter Release Cycle1 | 1.82E-03 | -1.97 | 5.08 | *GAD2; LIN7A* |
|  | Developmental Biology1 | 6.53E-02 | -2.21 | 2.23 | *APBB1IP; MYF6; MYF5* |
| Linolenic acid | Cytokine Signaling in Immune system1 | 1.32E-02 | -2.38 | 2.57 | *GRIN2A; CIITA; SOCS1; TNFRSF17; TAB2; NUP43* |
|  | Amino acid synthesis and interconversion (transamination) 1 | 3.35E-03 | -2.26 | 2.45 | *FOLH1B; NAALAD2* |
|  | Cellular responses to stress1 | 2.99E-02 | -2.26 | 2.45 | *PHC1; HSPH1; NOX4; NUP43* |
|  | Metabolism of amino acids and derivatives1 | 2.23E-02 | -2.23 | 2.41 | *IYD; FOLH1B; NAALAD2; TYR* |
|  | Immune System1 | 1.95E-02 | -2.20 | 2.38 | *CIITA; GRIN2A; SOCS1; KLRB1; TNFRSF17; TAB2; NUP43; CLEC2D; ULBP1; KLRG1* |
| Arachidic acid | Digestion of dietary lipid1 | 6.59E-08 | -1.94 | 22.68 | *PNLIPRP1; PNLIPRP2; PNLIPRP3; PNLIP* |
|  | Lipid digestion, mobilization, and transport | 1.25E-05 | -1.82 | 12.98 | *PNLIPRP1; PNLIPRP2; PNLIPRP3; PNLIP* |
|  | NCAM1 interactions1 | 2.68E-03 | -2.03 | 4.41 | *GFRA1; CACNA1C* |
|  | Metabolism of lipids and lipoproteins1 | 3.91E-02 | -2.13 | 2.41 | *PNLIPRP1; PNLIPRP2; PNLIP; PNLIPRP3* |
|  | Glycerolipid metabolism2 | 5.50E-06 | -1.97 | 15.81 | *PNLIPRP1; PNLIPRP2; PNLIPRP3; PNLIP* |
|  | Fat digestion and absorption2 | 7.96E-05 | -1.82 | 11.01 | *PNLIPRP1; PNLIPRP2; PNLIP* |
|  | Pancreatic secretion2 | 8.83E-04 | -1.67 | 6.78 | *PNLIPRP1; PNLIPRP2; PNLIP* |
| Arachidonic acid | Cholinergic synapse2 | 3.67E-02 | -1.98 | 2.77 | *CHRNB4; CHRNA3* |
|  | Neuroactive ligand-receptor interaction2 | 6.02E-03 | -1.89 | 2.74 | *CHRNB4; CHRNA3; CHRNA5; GZMA* |
|  | Carbon metabolism2 | 3.79E-02 | -1.58 | 2.22 | *ME3; IDH3A* |
|  | Fatty acid degradation2 | 1.15E-01 | -1.33 | 1.55 | *ACSBG1* |
|  | Arachidonic acid metabolism2 | 1.57E-01 | -1.29 | 1.50 | *GPX8* |
| Docosahexaenoic acid | Phospholipid metabolism1 | 1.28E-04 | -1.95 | 8.58 | *MTMR3; INPP5J; PLA2G3;PISD* |
|  | Metabolism of lipids and lipoproteins1 | 2.08E-02 | -2.13 | 4.21 | *MTMR3;INPP5J; PLA2G3; PISD* |
| Saturated fatty acids | Neuroactive ligand-receptor interaction2 | 5.59E-04 | -1.89 | 7.68 | *CHRNB4; CHRNA3; CHRNA5; GRIK2; MCHR2* |
|  | Fatty acid degradation2 | 1.09E-01 | -1.38 | 1.75 | *ACSBG1* |
|  | Fatty acid biosynthesis2 | 3.53E-02 | -1.19 | 1.61 | *ACSBG1* |
| Monounsaturated fatty acids | Dectin-1 mediated noncanonical NF-kB signaling1 | 1.97E-02 | -2.24 | 2.79 | *BTRC; NFKB2* |
|  | Organelle biogenesis and maintenance1 | 2.55E-02 | -2.15 | 2.68 | *ACTR1A; GBF1; PPRC1; MRPL43* |
|  | Fatty acid and ketone body metabolism1 | 1.74E-01 | -1.37 | 1.04 | *ELOVL3; MED17* |
|  | Linoleic acid (LA) metabolism1 | 3.06E-02 | -0.82 | 1.02 | *ELOVL3* |
|  | Metabolism of lipids and lipoproteins1 | 1.91E-01 | -1.33 | 0.97 | *STARD5; ELOVL3; MED17; CYP17A1* |
| Polyunsaturated fatty acidsand omega-6 polyunsaturated fatty acids | Myogenesis1 | 2.40E-04 | -2.41 | 11.09 | *MYF6; MYF5* |
| CDO in myogenesis1 | 2.40E-04 | -2.40 | 11.02 | *MYF6; MYF5* |
| Insulin receptor signalling cascade1 | 2.04E-01 | -2.14 | 2.49 | *APBB1IP* |
|  | Gastrin-CREB signalling pathway via PKC and MAPK1 | 2.93E-01 | -1.93 | 2.07 | *APBB1IP* |
| Unsaturated fatty acids | Acetylcholine Binding And Downstream Events1 | 9.12E-05 | -2.32 | 12.14 | *CHRNA3; CHRNB4; CHRNA5* |
|  | Presynaptic nicotinic acetylcholine receptors1 | 6.15E-05 | -2.27 | 11.89 | *CHRNA3; CHRNB4; CHRNA5* |
|  | Fatty Acyl-CoA Biosynthesis1 | 2.05E-01 | -0.90 | 0.46 | *ACSBG1* |
|  | Synthesis of very long-chain fatty acyl-CoAs1 | 1.11E-01 | -0.84 | 0.43 | *ACSBG1* |
| Omega-3 polyunsaturated fatty acids | Phospholipid metabolism1 | 7.49E-06 | -1.95 | 14.13 | *MTMR3; PITPNB; INPP5J; PLA2G3; PISD* |
|  | Glycerophospholipid biosynthesis1 | 7.76E-04 | -1.87 | 7.42 | *PITPNB; PLA2G3; PISD* |
|  | Metabolism of lipids and lipoproteins1 | 4.76E-03 | -2.18 | 5.93 | *MTMR3; PITPNB; INPP5J; PLA2G3; PISD* |
|  | Metabolism of lipids and lipoproteins1 | 4.76E-03 | -2.18 | 5.93 | *MTMR3;PITPNB;INPP5J;PLA2G3;PISD* |
| Short chain fatty acids | Phospholipid metabolism1 | 7.93E-05 | -1.95 | 9.07 | *MTMR3; PITPNB; INPP5J; PLA2G3; PISD* |
|  | Glycerophospholipid biosynthesis1 | 2.95E-03 | -1.86 | 4.89 | *PITPNB; PLA2G3; PISD* |
|  | Metabolism of lipids and lipoproteins1 | 3.33E-02 | -2.13 | 2.83 | *MTMR3; PITPNB; INPP5J; PLA2G3; PISD* |
|  | Metabolism of carbohydrates1 | 5.51E-01 | -1.41 | 0.64 | *SLC5A1* |
| Backfat thickness | MicroRNA (miRNA) biogenesis1 | 2.38E-02 | -2.23 | 3.90 | *DICER1* |
|  | Hemostasis1 | 1.49E-02 | -2.12 | 3.71 | *SERPINA1; ITPK1; SERPINA5* |

1 Pathways obtained from Reactome pathway database on Enrichr online tool (url: http://amp.pharm.mssm.edu/Enrichr/).

2 Pathways obtained from KEGG pathway database on Enrichr online tool (url: http://amp.pharm.mssm.edu/Enrichr/).

Medium chain fatty acids and long chain fatty acid categories are not reported in this table as their amounts in backfat showed to be associated exclusively to three markers already indicated in previous studies to be in linkage disequilibrium with mutations in the promoter region of the *ELOVL Fatty Acid Elongase 6* gene*.*

Docosapentaenoic acid is not reported in the table because no marker window explained at least 0.5% of the genetic variance and none of the markers showed bayes factors indicating suggestive or consistent associations with this fatty acid.

Supplementary Table S6**.** List of the microRNAs (miRNAs) mapped in the region on Sus scrofa chromosome (SSC) 11 associated with backfat thickness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Region on SSC11 included between 64 and 67 Mb associated with backfat thickness | | | | |
| miRNAs | Ensembl Gene ID | Ensembl Transcript ID | miRNA predicted target genes related to lipid metabolism | PicTar score |
| ssc-mir-20a | ENSSSCG00000019883 | ENSSSCT00000021478 | Very low density lipoprotein receptor (VLDLR) | 7.35 |
|  |  |  | Monoglyceride lipase (MGLL) | 2.58 |
|  |  |  | Factor for adipocyte differentiation 104 (FAD104) | 1.14 |
| ssc-mir-19a | ENSSSCG00000019897 | ENSSSCT00000021492 | Acyl-CoA synthetase long-chain family member 4 (ACSL4) | 10.95 |
|  |  |  | Low density lipoprotein-related protein 2 (LRP2) | 7.44 |
|  |  |  | Lysocardiolipin acyltransferase (LYCAT) | 1.62 |
| ssc-mir-18a1 | ENSSSCG00000019535 | ENSSSCT00000021130 | Estrogen receptor 1 (ESR1) | 6.03 |
|  |  |  | Prostaglandin F2 receptor negative regulator (PTGFRN) | 4.18 |
| ssc-mir-19b-12 | ENSSSCG00000019902 | ENSSSCT00000021497 | Low density lipoprotein-related protein 2 (LRP2) | 7.44 |
|  |  |  | Adiponectin receptor 2 (ADIPOR2) | 2.61 |
|  |  |  | Lysocardiolipin acyltransferase (LYCAT) | 1.62 |
|  |  |  | Factor for adipocyte differentiation 104 (FAD104) | 1.49 |
| ssc-mir-173 | ENSSSCG00000018617 | ENSSSCT00000020212 | Very low density lipoprotein receptor (VLDLR) | 7.35 |
|  |  |  | Factor for adipocyte differentiation 104 (FAD104) | 1.26 |
| ssc-mir-92a-14 | ENSSSCG00000018681 | ENSSSCT00000020276 | Factor for adipocyte differentiation 104 (FAD104) | 4.83 |
|  |  |  | Monoglyceride lipase (MGLL) | 3.53 |

All the predicted sites were obtained using the corresponding human microRNA (hsa-mir), and using on PicTar the algorithm for the predictions in vertebrates and choosing the dataset “target predictions for all human microRNAs based on conservation in mammals”.

1 Results are referred to human microRNA hsa-mir-18.

2 Results are referred to human microRNA hsa-mir-19b.

3 Results are referred to human microRNA hsa-mir-17-5p, previously known as hsa-mir-17.

4 Results are referred to human microRNA hsa-mir-92.