**Table S6. Genes of acyl lipid metabolism, regulated in stem tissue of *fax1* knockout mutants.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **ko\_stem** | | |  |  |  |
| **AGI** | **Mu**  **signal** | **Wt signal** | **FCH** | **Pathway** | **Protein Family Name** | **Gene Name** |

**strongest change in ko\_stem**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| At1g57750 | 1911.17 | 193.67 | **9.87** | Fatty Acid Elongation & Wax Biosynthesis | Secondary Alcohol Dehydrogenase; Midchain Alkane Hydroxylase | CYP96A15/MAH1 |
| At4g33790 | 619.85 | 115.02 | **5.39** | Fatty Acid Elongation & Wax Biosynthesis;  Suberin Synthesis & Transport 1 | Alcohol-forming Fatty Acyl-CoA Reductase | AlcFAR3/CER4 |
| At2g13820 | 1074.19 | 225.61 | **4.76** | Fatty Acid Elongation & Wax Biosynthesis | Lipid Transfer Protein | (LTP type 5) |
| At1g06350 | 181.93 | 39.58 | **4.60** | Pathway, function or subcellular location uncertain | Acyl-CoA Desaturase-like / FAD5-like Desaturase |  |

**up-regulated**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| At3g48720 | 257.98 | 107.80 | **2.39** | Cutin Synthesis & Transport 1 | Feruloyl Transferase | DCF |
| At4g00400 | 90.57 | 41.28 | **2.19** | Cutin Synthesis & Transport 1 | Glycerol-3-Phosphate Acyltransferase | sn-2-GPAT8 |
| At2g26910 | 680.53 | 447.66 | **1.52** | Cutin Synthesis & Transport 1 | ABC Transporter | ABCG32/PEC1 |
| At3g03540 | 35.31 | 16.06 | **2.20** | Eukaryotic Galactolipid & Sulfolipid Synthesis | Phospholipase C (Non specific) | NPC5 |
| At3g18000 | 253.24 | 105.28 | **2.41** | Eukaryotic Phospholipid Synthesis & Editing | Phosphoethanolamine N-Methyltransferase | NMT1 |
| At3g05420 | 582.57 | 341.03 | **1.71** | Eukaryotic Phospholipid Synthesis & Editing | Acyl CoA Binding Protein | ACBP4 |
| At1g55260 | 94.84 | 22.00 | **4.31** | Fatty Acid Elongation & Wax Biosynthesis | Lipid Transfer Protein | (LTP type 5) |
| At1g62790 | 985.90 | 456.44 | **2.16** | Fatty Acid Elongation & Wax Biosynthesis | Lipid Transfer Protein | (LTP type 5) |
| At3g43720 | 764.16 | 371.95 | **2.05** | Fatty Acid Elongation & Wax Biosynthesis | Lipid Transfer Protein | (LTP type 5) |
| At2g27130 | 618.57 | 345.45 | **1.79** | Fatty Acid Elongation & Wax Biosynthesis | Lipid Transfer Protein | (LTP type 5) |
| At4g24510 | 389.75 | 204.92 | **1.90** | Fatty Acid Elongation & Wax Biosynthesis | CER2-like Protein | CER2 |
| At1g10670 | 3952.44 | 1453.62 | **2.72** | Fatty Acid Elongation & Wax Biosynthesis | ATP Citrate Lyase A subunit | ACLA-1 |
| At1g60810 | 1654.10 | 391.95 | **4.22** | Fatty Acid Elongation & Wax Biosynthesis | ATP Citrate Lyase A subunit | ACLA-2 |
| At3g06650 | 1761.47 | 1092.56 | **1.61** | Fatty Acid Elongation & Wax Biosynthesis | ATP Citrate Lyase B subunit | ACLB-1 |
| At5g49460 | 2327.85 | 622.54 | **3.74** | Fatty Acid Elongation & Wax Biosynthesis | ATP Citrate Lyase B subunit | ACLB-2 |
| At2g47240 | 230.37 | 74.51 | **3.09** | Fatty Acid Elongation & Wax Biosynthesis;  Cutin/Suberin Synthesis & Transport 1 | Long-Chain Acyl-CoA Synthetase | LACS1 |
| At1g64400 | 1221.43 | 556.37 | **2.20** | Fatty Acid Elongation & Wax Biosynthesis;  Cutin/Suberin Synthesis & Transport 1 | Long-Chain Acyl-CoA Synthetase | LACS3 |
| At5g25390 | 178.10 | 101.40 | **1.76** | Fatty Acid Elongation & Wax Biosynthesis;  Cutin/Suberin Synthesis & Transport 1 | SHN Transcription Factors | SHN3 |
| At1g19440 | 316.09 | 201.47 | **1.57** | Fatty Acid Elongation & Wax Biosynthesis;  Suberin Synthesis & Transport 1 | Ketoacyl-CoA Synthase | KCS4 |
| At5g16230 | 54.86 | 34.83 | **1.58** | Fatty Acid Elongation, Desaturation & Export From Plastid;  Fatty Acid Synthesis;  Pro. Galactolipid, Sulfolipid, & Phospholipid Synthesis 1 | Stearoyl-ACP Desaturase | DES3 |
| At4g16155 | 224.24 | 125.69 | **1.78** | Fatty Acid Synthesis | Dihydrolipoamide Dehydrogenase,  E3 component of Pyruvate Dehydrogenase Complex | LPD2 (E3) |
| At1g63430 | 493.58 | 339.81 | **1.45** | Mitochondrial Phospholipid Synthesis | CDP-DAG Synthase | CDS1; CDP-DAGS |
| At3g63200 | 208.03 | 68.92 | **3.02** | Oxylipin Metabolism 1 | Acyl-Hydrolase (Patatin-like) |  |
| At3g08510 | 1643.86 | 1189.24 | **1.38** | Phospholipid Signaling | Phosphoinositide-specific Phospholipase C |  |
| At4g00240 | 95.21 | 72.07 | **1.32** | Phospholipid Signaling | Phospholipase D beta |  |
| At4g20870 | 656.25 | 337.76 | **1.94** | Sphingolipid Biosynthesis 1 | Fatty Acid 2-hydroxylase | FAH2 |
| At3g06060 | 444.72 | 301.83 | **1.47** | Sphingolipid Biosynthesis 1 | Ketosphinganine Reductase | TSC10A |
| At2g40890 | 3124.42 | 1307.77 | **2.39** | Suberin Synthesis & Transport 2 | Coumaroyl 3-Hydroxylase | CYP98A3 |
| At2g30490 | 8521.15 | 3903.89 | **2.18** | Suberin Synthesis & Transport 2 | Cinnamate 4-Hydroxylase | CYP73A5 |
| At4g34050 | 15751.28 | 7257.13 | **2.17** | Suberin Synthesis & Transport 2 | Caffeoyl-CoA O-Methyltransferase |  |
| At4g14440 | 390.23 | 176.59 | **2.21** | Triacylglycerol & Fatty Acid Degradation | Enoyl CoA isomerase | ECI3 |
| At4g32010 | 814.61 | 472.90 | **1.72** | Triacylglycerol Biosynthesis | a member of a novel family of B3 domain proteins | HSL1/VAL2 |
| At2g29980 | 1486.81 | 535.98 | **2.77** | Triacylglycerol Biosynthesis; Euk. Phospholipid Synthesis & Editing | Linoleate Desaturase | FAD3 |
| At3g18850 | 195.48 | 73.54 | **2.66** | Triacylglycerol Biosynthesis; Euk. Phospholipid Synthesis & Editing | 1-Acylglycerol-3-Phosphate Acyltransferase | LPAAT5 |
| At5g47730 | 844.73 | 444.99 | **1.90** | Pathway, function or subcellular location uncertain | Sec14-like Protein |  |

**down-regulated**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| At4g01950 | 50.04 | 106.16 | **0.47** | Cutin Synthesis & Transport 1 | Glycerol-3-Phosphate Acyltransferase | GPAT3 |
| At3g05630 | 51.79 | 84.00 | **0.62** | Eukaryotic Galactolipid & Sulfolipid Synthesis | Phospholipase D zeta | PLD zeta2 |
| At5g06530 | 3735.37 | 6032.49 | **0.62** | Fatty Acid Elongation & Wax Biosynthesis | ABC Transporter | WBC23 / ABCG22 |
| At4g34250 | 21.08 | 31.52 | **0.67** | Fatty Acid Elongation & Wax Biosynthesis | Ketoacyl-CoA Synthase | KCS16 |
| At2g26560 | 34.20 | 97.29 | **0.35** | Oxylipin Metabolism 1 | Acyl-Hydrolase (Patatin-like) |  |
| At1g76690 | 885.61 | 1542.35 | **0.57** | Oxylipin Metabolism 1 | Oxo-Phytodienoic Acid Reductase |  |
| At5g24210 | 389.27 | 942.16 | **0.41** | Oxylipin Metabolism 1; Oxylipin Metabolism 2 | Lipid Acylhydrolase-like |  |
| At5g42650 | 923.39 | 1430.32 | **0.65** | Oxylipin Metabolism 1; Oxylipin Metabolism 2 | Allene Oxide Synthase |  |
| At1g73680 | 573.59 | 873.55 | **0.66** | Oxylipin Metabolism 2 | alpha-Dioxygenase-Peroxidase (involved in fatty acid alpha-oxidation) |  |
| At5g39400 | 19.42 | 29.38 | **0.66** | Phospholipid Signaling | Phosphoinositide 3-Phosphatase | PTEN1 |
| At3g18220 | 25.02 | 34.65 | **0.72** | Pro. Galactolipid, Sulfolipid, & Phospholipid Synthesis 1;  Euk. Galactolipid & Sulfolipid Synthesis;  Phospholipid Signaling | Phosphatidate Phosphatase /  Diacylglycerol-Pyrophosphate Phosphatase | LPP4 |
| At5g01220 | 285.43 | 486.91 | **0.59** | Pro. Galactolipid, Sulfolipid, & Phospholipid Synthesis 2;  Euk. Galactolipid & Sulfolipid Synthesis | UDP-sulfoquinovose:DAG sulfoquinovosyltransferase | SQD2 |
| At1g69640 | 483.29 | 815.40 | **0.59** | Sphingolipid Biosynthesis 1 | Sphingobase C4-Hydroxylase | SBH1 |
| At4g04930 | 21.34 | 33.43 | **0.64** | Sphingolipid Biosynthesis 1 | Dihydrosphingosine Delta-4 Desaturase | DSD1 |
| At1g73480 | 692.89 | 1867.35 | **0.37** | Triacylglycerol & Fatty Acid Degradation | Monoacylglycerol Lipase (MAGL) |  |
| At1g23330 | 261.05 | 461.22 | **0.57** | Triacylglycerol & Fatty Acid Degradation | Triacylglycerol Lipase (TAGL) |  |
| At5g14930 | 68.61 | 110.41 | **0.62** | Triacylglycerol & Fatty Acid Degradation | Triacylglycerol Lipase (TAGL) | SAG101 |
| At1g76150 | 1060.49 | 1440.39 | **0.74** | Triacylglycerol & Fatty Acid Degradation | Peroxisomal Enoyl-CoA Hydratase 2 | ECH2 |
| At3g51970 | 53.00 | 102.58 | **0.52** | Pathway, function or subcellular location uncertain | Membrane-bound O-acyltransferase | ACAT1 |