

Supplemental Table

Supplement. Composite list of differentially regulated genes based on either fold-change greater than 2 or significant statistical analysis using parametric tests adjusting for multiple comparisons. Upregulated genes on day 12 of gestation are denoted by positive fold-change and downregulated genes on day 12 are represented by negative fold-change values. Standard deviations (SD) are not shown for probe sets with only two expression values.

Entrez Gene ID	Gene Title	Fold Change	SD	p value
<i>Transport functions</i>				
12870	ceruloplasmin	2.38	1.73	0.092
56774	solute carrier family 6 (neurotransmitter transporter), member 14	2.21	2.95	0.184
23844	chloride channel calcium activated 3	2.19	0.89	0.027
18438	purinergic receptor P2X, ligand-gated ion channel 4	1.66	0.16	0.010
16517	potassium inwardly-rectifying channel, subfamily J, member 16	1.53	0.48	0.017
18806	phospholipase D2	1.48	0.31	0.030
52150	potassium inwardly-rectifying channel, subfamily K, member 6	1.41	0.11	0.004
22134	trans-golgi network protein 2	1.36	0.10	0.014
269966	nucleoporin 98	1.25	0.04	0.005
21452	transcobalamin 2	1.24	0.07	0.001
71240	oxysterol binding protein-like 7	1.23		0.020
70568	copine III	1.19	0.09	0.029
72844	potassium channel tetramerisation domain containing 17	1.13	0.05	0.016
224742	ATP-binding cassette, sub-family F (GCN20), member 1	-1.15	0.05	0.025
58244	syntaxin 6	-1.17	0.05	0.003
77040	autophagy-related 16-like (yeast)	-1.21	0.06	0.018
215436	solute carrier family 35, member E3	-1.23	0.03	0.004
20531	solute carrier family 34 (sodium phosphate), member 2	-1.42	0.21	0.019
227059	solute carrier family 39 (zinc transporter), member 10	-1.47	0.08	0.000
320982	ADP-ribosylation factor-like 7	-1.57	0.31	0.017
108052	solute carrier family 14 (urea transporter), member 1	-2.07	0.69	0.013
11576	alpha fetoprotein	-7.63	5.98	0.348
<i>Cytoskeletal components</i>				
19240	thymosin, beta 10	4.59	5.13	0.132
16660	keratin complex 1, acidic, gene 1	2.68		0.296
16687	keratin complex 2, basic, gene 6a	2.33	1.67	0.211
18472	Platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	2.16	1.41	0.471

20753	small proline-rich protein 1A	1.75	0.44	0.018
66695	asporin	1.64	0.25	0.030
16667	keratin complex 1, acidic, gene 17	1.54	0.20	0.014
94190	oligophrenin 1	1.20	0.12	0.017
74006	dynamamin 1-like	-1.14	0.02	0.029
68041	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	-1.36	0.23	0.029
15529	syndecan 2	-1.41	0.12	0.015
58187	Claudin 10	-2.36	1.59	0.295
245049	myosin VIIA and Rab interacting protein	-2.41	1.54	0.229
16561	Kinesin family member 1B	-2.62		0.518
11459	actin, alpha 1, skeletal muscle	-2.62	2.03	0.429
<i>DNA repair/RNA associated</i>				
75560	E1A binding protein p400	1.79	0.02	0.002
68048	interferon stimulated exonuclease gene 20-like 1	1.52	0.36	0.018
14156	flap structure specific endonuclease 1	1.51	0.37	0.017
67204	eukaryotic translation initiation factor 2, subunit 2 (beta)	1.21	0.04	0.007
66085	eukaryotic translation initiation factor 3, subunit 5 (epsilon)	1.19	0.05	0.012
18970	polymerase (DNA directed), beta	1.19	0.12	0.026
19933	ribosomal protein L21	1.14	0.04	0.017
19823	ring finger protein 7	1.12	0.07	0.012
59054	mitochondrial ribosomal protein S30	1.10	0.04	0.022
71807	threonyl-tRNA synthetase-like 1	1.10	0.06	0.023
13002	DnaJ (Hsp40) homolog, subfamily C, member 5	1.09	0.02	0.019
70560	tryptophanyl tRNA synthetase 2 (mitochondrial)	-1.08	0.02	0.008
14000	ribonuclease III, nuclear	-1.22	0.07	0.012
15499	heat shock factor 1	-1.25	0.06	0.016
17193	methyl-CpG binding domain protein 4	-1.36	0.05	0.014
15505	heat shock protein 105	-1.44	0.21	0.027
70359	GTP binding protein 3	-1.49	0.18	0.023
28113	Terf1 (TRF1)-interacting nuclear factor 2	-1.55	0.21	0.005
19366	RAD54 like (<i>S. cerevisiae</i>)	-1.90	0.85	0.025
109113	Ubiquitin-like, containing PHD and RING finger domains 2	-2.69	0.85	0.050
<i>Enzymes</i>				
241230	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	3.02	1.89	0.126
14933	glycerol kinase	2.46	1.30	0.070
68631	crystallin, lamda 1	2.21		0.422
14538	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	2.08	0.89	0.316
78753	lipase-like, ab-hydrolase domain containing 3	1.69	0.36	0.029
11846	arginase 1, liver	1.69	0.24	0.007

14571	glycerol phosphate dehydrogenase 2, mitochondrial	1.57	0.43	0.018
100727	UDP glucuronosyltransferase 2 family, polypeptide B34	1.56	0.32	0.006
53897	galactose-3-O-sulfotransferase 1	1.55	0.23	0.007
100727	UDP glucuronosyltransferase 2 family, polypeptide B34	1.51	0.27	0.010
14426	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4	1.39	0.23	0.017
14629	glutamate-cysteine ligase, catalytic subunit	1.34	0.25	0.027
67880	dicarbonyl L-xylulose reductase	1.30	0.14	0.014
14860	glutathione S-transferase, alpha 4	1.29	0.12	0.028
59010	sulfide quinone reductase-like (yeast)	1.27	0.06	0.006
269437	phospholipase C-like 3	1.26	0.05	0.006
110208	phosphogluconate dehydrogenase	1.25	0.16	0.023
54128	phosphomannomutase 2	1.24	0.02	0.004
14873	glutathione S-transferase omega 1	1.24	0.12	0.009
12409	carbonyl reductase 2	1.21	0.08	0.021
107652	UDP-N-acetylglucosamine pyrophosphorylase 1	1.21	0.04	0.023
69051	pyrroline-5-carboxylate reductase family, member 2	1.19	0.06	0.005
70152	AAM-B protein	1.15	0.05	0.014
11674	aldolase 1, A isoform	1.13	0.04	0.025
69663	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	1.12	0.02	0.020
64292	prostaglandin E synthase	-1.24	0.03	0.012
78038	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	-1.27	0.06	0.012
106248	queuine tRNA-ribosyltransferase domain containing 1	-1.32	0.18	0.023
12934	dihydropyrimidinase-like 2	-1.32	0.09	0.024
170439	ELOVL family member 6, elongation of long chain fatty acids (yeast)	-1.48	0.26	0.015
60525	acetyl-Coenzyme A synthetase 2 (ADP forming)	-1.54	0.18	0.019
14137	farnesyl diphosphate farnesyl transferase 1	-1.58	0.43	0.026
76267	fatty acid desaturase 1	-1.59	0.10	0.000
56473	fatty acid desaturase 2	-1.63	0.26	0.006
22169	thymidylate kinase family LPS-inducible member	-1.99	0.04	0.016
12411	cystathionine beta-synthase	-2.01	0.79	0.056
52815	lactate dehydrogenase D	-2.04	1.25	0.163
20249	stearoyl-Coenzyme A desaturase 1	-2.08	0.59	0.036
16891	lipase, endothelial	-2.09	0.71	0.008
77219	zinc binding alcohol dehydrogenase, domain containing 1	-2.16	1.16	0.204
11676	aldolase 3, C isoform	-2.18	0.35	0.088
11687	arachidonate 15-lipoxygenase	-2.26	1.21	0.031
17523	myeloperoxidase	-2.47		0.354

Cellular growth and differentiation

21784	trefoil factor 1	2.19	0.68	0.040
21946	peptidoglycan recognition protein 1	2.03	0.37	0.061
16970	lymphoid-restricted membrane protein	1.48	0.06	0.009
56018	START domain containing 10	1.47	0.11	0.003
72433	Rab38, member of RAS oncogene family	1.37	0.18	0.008
12223	betacellulin, epidermal growth factor family member	1.36	0.18	0.011
171388	BCL2/adenovirus E1B 19kD interacting protein like	1.33	0.10	0.025
72400	PIN2/TRF1-interacting protein	1.32	0.12	0.012
20853	staufer (RNA binding protein) homolog 1 (Drosophila)	1.27	0.02	0.008
12055	B-cell CLL/lymphoma 7C	1.26	0.10	0.005
19055	protein phosphatase 3, catalytic subunit, alpha isoform	1.26	0.11	0.012
64058	PERP, TP53 apoptosis effector	1.21	0.06	0.002
223775	proviral integration site 3	1.20	0.07	0.007
20256	C-type lectin domain family 11, member a	1.12	0.03	0.020
100604	factor for adipocyte differentiation 158	-1.22		0.017
18952	septin 4	-1.26	0.09	0.023
29811	N-myc downstream regulated gene 2	-1.27	0.12	0.004
16651	sarcospan	-1.30	0.15	0.010
18003	neural precursor cell expressed, developmentally down-regulated gene 9	-1.36	0.14	0.021
17863	myeloblastosis oncogene	-1.39	0.27	0.024
12759	clusterin	-1.51	0.33	0.027
268977	latent transforming growth factor beta binding protein 1	-1.53	0.21	0.021
22612	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	-1.60	0.23	0.022
12759	clusterin	-1.80	0.36	0.019

Hormones

57262	resistin like alpha	2.24	1.19	0.612
18776	chorionic somatomammotropin hormone 2	-3.51	2.43	0.338

Immune function

20311	chemokine (C-X-C motif) ligand 5	3.92	3.11	0.147
12654	chitinase 3-like 1	3.34	8.43	0.359
26388	interferon activated gene 202B	1.86	0.43	0.021
13136	decay accelerating factor 1	1.51	0.30	0.019
15944	interferon inducible protein 1	-1.27	0.10	0.015
14129	Fc receptor, IgG, high affinity I	-1.31	0.07	0.004
20293	chemokine (C-C motif) ligand 12	-1.34	0.03	0.014
76933	interferon, alpha-inducible protein 27	-2.13	1.03	0.213

Matrix molecules/cellular adhesion

21922	C-type lectin domain family 3, member b	2.38	0.27	0.141
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12805	contactin 1	1.77	0.49	0.013
50706	periostin, osteoblast specific factor	1.68	0.49	0.018
11658	activated leukocyte cell adhesion molecule	1.54	0.07	0.027
230801	phosphatidylinositol glycan, class V	1.13	0.05	0.017
93893	protocadherin beta 22	-1.33	0.03	0.014
66996	CEA-related cell adhesion molecule 11	-8.72	9.18	0.355

Undefined function

328660	brain expressed, X-linked 6	2.48	1.54	0.218
17141	melanoma antigen, family A, 5	2.47		0.225
68718	Ring finger protein 166	2.25	0.64	0.390
170654	keratin associated protein 16-4	2.04	1.08	0.389
52305	DNA segment, Chr 1, ERATO Doi 259, expressed	1.83		0.022
67729	MANSC domain containing 1	1.68	0.39	0.024
238896	similar to CDC20-like protein form 2	1.56	0.24	0.017
67501	Ymer protein	1.54	0.15	0.018
223473	NIPA-like domain containing 2	1.50	0.39	0.026
14675	guanine nucleotide binding protein, alpha 14	1.46	0.27	0.016
66805	tetraspan 1	1.43	0.22	0.010
226971	pleckstrin homology domain containing, family B (evectins) member 2	1.36	0.12	0.004
68421	liver regeneration p-53 related protein	1.35	0.17	0.021
66109	tetraspanin 13	1.31	0.13	0.017
238257	transmembrane protein 30B	1.25	0.10	0.016
19707	RalBP1 associated Eps domain containing protein	1.20	0.09	0.014
230584	Yip1 domain family, member 1	1.20	0.05	0.011
74213	cutaneous T-cell lymphoma tumor antigen se70-2	1.18	0.05	0.017
22378	WW domain binding protein 2	1.18	0.12	0.020
219249	tudor domain containing 3	1.17	0.05	0.008
67860	S100 calcium binding protein A16	1.16	0.04	0.013
68151	putative NFkB activating protein 373	1.16	0.02	0.010
20196	S100 calcium binding protein A13	1.08	0.04	0.015
235542	protein phosphatase 2	1.08	0.02	0.019
26961	ribosomal protein L8	1.05	0.01	0.007
50850	spastic paraplegia 4 homolog (human)	1.03	0.01	0.014
117198	influenza virus NS1A binding protein	-1.16	0.10	0.017
66978	Luc7 homolog (S. cerevisiae)-like	-1.17	0.01	0.020
74998	RAB11 family interacting protein 2	-1.23	0.05	0.015
83675	Bicaudal C homolog 1 (Drosophila)	-1.30	0.03	0.010
117198	influenza virus NS1A binding protein	-1.30	0.22	0.029
386612	WD repeat domain 58	-1.31	0.12	0.022
225266	kelch-like 14 (Drosophila)	-1.93	0.66	0.021
545422	similar to low density lipoprotein receptor-related protein 2	-2.22	1.39	0.142
327959	F-box protein 39	-2.28	1.42	0.444
21984	trophoblast specific protein alpha	-6.70	4.57	0.329

Protease and protease inhibitors

72432	serine protease inhibitor, Kazal type 5	4.36	3.46	0.140
70574	carboxypeptidase M	3.01	1.37	0.153
69814	protease, serine, 32	1.85	0.73	0.027
20724	serine (or cysteine) proteinase inhibitor, clade B, member 5	1.57	0.20	0.029
15925	insulin degrading enzyme	1.29	0.10	0.018
20733	serine protease inhibitor, Kunitz type 2	1.18	0.06	0.025
213760	prolyl endopeptidase-like	-1.12	0.02	0.026
13032	cathepsin C	-1.24	0.12	0.025
17230	mast cell protease 7	-3.46	5.87	0.297

Cell surface receptors

12638	cystic fibrosis transmembrane conductance regulator homolog	2.61	0.84	0.151
21942	tumor necrosis factor receptor superfamily, member 9	2.50	2.09	0.161
14600	growth hormone receptor	1.55	0.13	0.004
19775	xenotropic and polytropic retrovirus receptor 1	1.18	0.01	0.006
192656	receptor (TNFRSF)-interacting serine-threonine kinase 2	1.16	0.11	0.021
15976	interferon (alpha and beta) receptor 2	-1.19	0.05	0.014
19116	prolactin receptor	-1.25	0.11	0.018
239849	Cd200 receptor 4	-2.00	0.72	0.407
26563	receptor tyrosine kinase-like orphan receptor 1	-2.15	1.43	0.113

Signaling cascade

76757	triadin	2.63	0.16	0.081
243659	serine/threonine/tyrosine kinase 1	2.51		0.252
14609	gap junction membrane channel protein alpha 1	2.43	2.12	0.121
100986	A kinase (PRKA) anchor protein (yotiao) 9	2.27	3.12	0.215
252837	Chemokine (C-C motif) receptor-like 1	2.02	0.88	0.138
17207	mcf.2 transforming sequence-like	1.69	0.14	0.000
16147	Indian hedgehog	1.49	0.31	0.025
217944	Rap guanine nucleotide exchange factor (GEF) 5	1.38	0.09	0.009
76142	protein phosphatase 1, regulatory (inhibitor) subunit 14c	1.31	0.06	0.019
21873	tight junction protein 2	1.28	0.12	0.010
54720	Down syndrome critical region homolog 1 (human)	1.26	0.07	0.025
57912	CDC42 small effector 1	1.22	0.14	0.028
117589	ankyrin repeat and SOCS box-containing protein 7	-1.14	0.04	0.020
71323	Ras association (RalGDS/AF-6) domain family 8	-1.17	0.09	0.008
78255	Ral GEF with PH domain and SH3 binding motif 2	-1.20	0.09	0.019

50780	regulator of G-protein signaling 3	-1.24	0.04	0.017
58523	signal transducer and activator of transcription interacting protein 1	-1.31	0.04	0.010
211577	MAS-related GPR, member F	-2.01		0.287
18546	Purkinje cell protein 4	-3.80	2.64	0.269

Transcription factors

20861	stefin A1	3.00	1.62	0.242
268885	stefin A2 like 1	2.83		0.561
268903	nuclear receptor interacting protein 1	2.44		0.335
19655	RNA binding motif protein, X chromosome	2.13	0.75	0.065
80913	Pumilio 2 (Drosophila)	2.06	1.45	0.506
15220	Forkhead box Q1	2.02	1.15	0.043
57438	membrane-associated ring finger (C3HC4) 7	1.44	0.28	0.028
18035	Nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	1.39	0.14	0.018
211586	transcription factor Dp 2	1.38	0.11	0.024
68585	reticulon 4	1.35	0.16	0.019
18035	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	1.27	0.10	0.023
17122	Max dimerization protein 4	1.27	0.10	0.025
13800	enabled homolog (Drosophila)	1.23	0.09	0.013
13661	ets homologous factor	1.20	0.07	0.026
12387	catenin (cadherin associated protein), beta 1, 88kDa	1.14	0.04	0.022
21856	translocator of inner mitochondrial membrane 44	1.07	0.05	0.012
228829	PHD finger protein 20	-1.18	0.08	0.028
22764	zinc finger protein X-linked	-1.19	0.05	0.002
20589	immunoglobulin mu binding protein 2	-1.26	0.01	0.015
59092	poly(rC) binding protein 4	-1.30	0.09	0.025
57230	transcriptional regulator protein	-1.35	0.10	0.018
54123	interferon regulatory factor 7	-1.36	0.13	0.020
50781	dickkopf homolog 3 (Xenopus laevis)	-1.37	0.21	0.029
245688	retinoblastoma binding protein 7	-1.52	0.09	0.018
104156	ets variant gene 5	-1.70	0.29	0.006
17877	myogenic factor 5	-2.06		0.923
353187	Nuclear receptor subfamily 1, group D, member 2	-2.08	1.28	0.202
69188	myeloid/lymphoid or mixed-lineage leukemia 5	-2.18		0.916