Table 1 Genes with expression altered by ≥ 2.5 fold ($p \leq 0.05$) in HNF4α null embryonic livers

GENES DOWNREGULATED ≥2.5 FOLD ($p \leq 0.05$) in HNF4α NULL EMBRYONIC LIVERS

GENE	GENE SYMBOL	GENE ONTOLOGY BIOLOGICAL PROCESS	GENE ID	FOLD CHANGE	P VALUE
4-hydroxyphenylpyruvic acid dioxygenase	Hpd	amino acid metabolism	15445	-29.23	0.001108
amidohydrolase domain containing 1	Amdhd1	amino acid metabolism	71761	-39.82	0.007207
aminoadipate-semialdehyde synthase	Aass	amino acid metabolism	30956	-7.52	0.003453
arginase 1, liver	Arg1	amino acid metabolism	11846	-3.23	0.003236
argininosuccinate lyase	Asl	amino acid metabolism	109900	-7.46	0.000187
argininosuccinate synthetase 1	Ass1	amino acid metabolism	11898	-4.33	0.015563
betaine-homocysteine methyltransferase	Bhmt	amino acid metabolism	12116	-17.46	0
betaine-homocysteine methyltransferase 2	Bhmt2	amino acid metabolism	64918	-12.19	0.000429
branched chain ketoacid dehydrogenase E1, beta polypeptide	Bckdhb	amino acid metabolism	12040	-2.69	0.006287
cystathionase (cystathionine gamma-lyase)	Cth	amino acid metabolism	107869	-6.85	0.011846
cysteine conjugate-beta lyase	Ccbl1	amino acid metabolism	70266	-6.29	0.008984
cysteine dioxygenase 1, cytosolic	Cdo1	amino acid metabolism	12583	-8.45	0.000371
cysteine sulfinic acid decarboxylase	Csad	amino acid metabolism	246277	-3.32	0.004894
dimethylglycine dehydrogenase precursor	Dmgdh	amino acid metabolism	74129	-8.9	0.000059
formiminotransferase cyclodeaminase	Ftcd	amino acid metabolism	14317	-31.2	0.001548
fumarylacetoacetate hydrolase	Fah	amino acid metabolism	14085	-13.59	0.003263
glutamate oxaloacetate transaminase 1, soluble	Got1	amino acid metabolism	14718	-2.73	0.000706
glutamate oxaloacetate transaminase 2, mitochondrial	Got2	amino acid metabolism	14719	-2.77	0.000574
glutamate-ammonia ligase (glutamine synthase)	Glul	amino acid metabolism	14645	-2.52	0.014339
glutaminase 2 (liver, mitochondrial)	Gls2	amino acid metabolism	216456	-4.89	0.001456
glutathione transferase zeta 1 (maleylacetoacetate isomerase)	Gstz1	amino acid metabolism	14874	-3.46	0.000285
glycine decarboxylase	Gldc	amino acid metabolism	104174	-25.02	0.000172
histidine ammonia lyase	Hal	amino acid metabolism	15109	-14.6	0.001689
homogentisate 1, 2-dioxygenase	Hgd	amino acid metabolism	15233	-7.9	0.000178
kynureninase (L-kynurenine hydrolase)	Kynu	amino acid metabolism	70789	-4.35	0.007292
lysosomal membrane glycoprotein 2	Lamp2	amino acid metabolism	16784	-2.67	0.001169
methionine adenosyltransferase I, alpha	Mat1a	amino acid metabolism	11720	-7.93	0.000121
ornithine transcarbamylase	Otc	amino acid metabolism	18416	-1055.36	0.007811
proline dehydrogenase (oxidase) 2	Prodh2	amino acid metabolism	56189	-7.19	0.005565
RIKEN cDNA 0610012D14 gene	0610012D14Rik	amino acid metabolism	68352	-27.24	0.002423
sarcosine dehydrogenase	Sardh	amino acid metabolism	192166	-4.49	0.000868
serine hydroxymethyl transferase 1 (soluble)	Shmt1	amino acid metabolism	20425	-3.58	0.00462
tyrosine aminotransferase	Tat	amino acid metabolism	234724	-4.18	0.015757
urocanase domain containing 1	Uroc1	amino acid metabolism	243537	-26.86	0.003172

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6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	Pfkfb1	carbohydrate metabolism	18639	-3.21	0.00056
aldolase 2, B isoform	Aldob	carbohydrate metabolism	230163	-145.42	0.000114
dicarbonyl L-xylulose reductase	Dcxr	carbohydrate metabolism	67880	-3.53	0.004723
fructose bisphosphatase 1	Fbp1	carbohydrate metabolism	14121	-18.64	0.003536
galactokinase 1	Galk1	carbohydrate metabolism	14635	-5.02	0.000132
galactose mutarotase	Galm	carbohydrate metabolism	319625	-2.86	0.008453
glucokinase regulatory protein	Gckr	carbohydrate metabolism	231103	-5.19	0.000719
glucose-6-phosphatase, catalytic	G6pc	carbohydrate metabolism	14377	-16.33	0.016574
glycerol kinase	Gyk	carbohydrate metabolism	14933	-6.78	0.031386
glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	carbohydrate metabolism	14555	-28.98	0.000351
glycogen synthase 2	Gys2	carbohydrate metabolism	232493	-11.43	0.000226
hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	H6pd	carbohydrate metabolism	100198	-4.18	0.005553
liver glycogen phosphorylase	Pygl	carbohydrate metabolism	110095	-2.99	0.000503
maltase-glucoamylase	Mgam	carbohydrate metabolism	232714	-6.1	0.00039
protein phosphatase 1, regulatory (inhibitor) subunit 3B	Ppp1r3b	carbohydrate metabolism	244416	-3.88	0.024111
protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	carbohydrate metabolism	53412	-2.6	0.046223
pyruvate carboxylase	Pcx	carbohydrate metabolism	18563	-9.16	0.000909
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	carbohydrate metabolism	27273	-2.68	0.008193
succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	carbohydrate metabolism	56451	-2.51	0.004354
UDP-glucose pyrophosphorylase 2	Ugp2	carbohydrate metabolism	216558	-2.81	0.007562
xylulokinase homolog	Xylb	carbohydrate metabolism	102448	-17.35	0.016977
cadherin 1	Cdh1	cell adhesion	12550	-17.73	0.004391
CEA-related cell adhesion molecule 1	Ceacam1	cell adhesion	26365	-5.05	0.010441
CEA-related cell adhesion molecule 2	Ceacam2	cell adhesion	26367	-4.99	0.000645
claudin 1	Cldn1	cell adhesion	12737	-24.41	0.001018
coxsackievirus and adenovirus receptor	Cxadr	cell adhesion	13052	-3.42	0.017047
crumbs homolog 3 (Drosophila)	Crb3	cell adhesion	224912	-10.08	0.012988
desmocollin 2	Dsc2	cell adhesion	13506	-55.3	0.005931
epiplakin 1	Eppk1	cell adhesion	223650	-3.94	0.0327
epithelial V-like antigen 1	Eva1	cell adhesion	14012	-6.24	0.000276
F11 receptor	F11r	cell adhesion	16456	-2.58	0.006942
gap junction membrane channel protein beta 1	Gjb1	cell adhesion	14618	-7.4	0.003246
gelsolin	Gsn	cell adhesion	227753	-8.8	0.002249
glycosylphosphatidylinositol specific phospholipase D1	Gpld1	cell adhesion	14756	-8.9	0.000075
lectin, galactose binding, soluble 9	Lgals9	cell adhesion	16859	-2.91	0.004381
mannose binding lectin, serum (C)	Mbl2	cell adhesion	17195	-52.32	0.035122
nephronectin	Npnt	cell adhesion	114249	-3.98	0.00802
occludin	Ocln	cell adhesion	18260	-4.86	0.000244
plakophilin 2	Pkp2	cell adhesion	67451	-4.59	0.000413
rhophilin, Rho GTPase binding protein 2	Rhpn2	cell adhesion	52428	-2.64	0.007374

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syndecan 1	Sdc1	cell adhesion	20969	-2.63	0.006026
T-cell immunoglobulin and mucin domain containing 2	Timd2	cell adhesion	171284	-22.49	0.006035
vitronectin	Vtn	cell adhesion	22370	-2.86	0.002887
clusterin	Clu	cell death	12759	-3.09	0.019155
angiopoietin-like 4	Angptl4	cell death	57875	-4.73	0.000839
cell death-inducing DNA fragmentation factor, alpha subunit-like effector B12684	Cideb	cell death	12684	-9.68	0.000063
serine incorporator 3	Serinc3	cell death	26943	-4.96	0.001471
thrombopoietin	Thpo	cell proliferation	21832	-2.59	0.024386
leukocyte cell-derived chemotaxin 2	Lect2	chemotaxis	16841	-2.52	0.000234
apolipoprotein H	Apoh	coagulation	11818	-2.5	0.00106
coagulation factor II	F2	coagulation	14061	-2.89	0.000121
coagulation factor IX	F9	coagulation	14071	-22.75	0.00205
coagulation factor V	F5	coagulation	14067	-8.07	0.004506
coagulation factor VII	F7	coagulation	14068	-6.51	0.006378
coagulation factor X	F10	coagulation	14058	-43.85	0.000786
coagulation factor XI	F11	coagulation	109821	-2.75	0.003407
coagulation factor XII (Hageman factor)	F12	coagulation	58992	-1198.94	0.000589
coagulation factor XIII, beta subunit	F13b	coagulation	14060	-230.01	0.000574
kininogen 1	Kng1	coagulation	16644	-10.33	0.000148
macrophage stimulating 1 (hepatocyte growth factor-like)	Mst1	coagulation	15235	-3.84	0.000235
protein C	Proc	coagulation	19123	-3.03	0.000342
protein Z, vitamin K-dependent plasma glycoprotein	Proz	coagulation	66901	-405.03	0.0024
serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1	Serpinc1	coagulation	11905	-7.11	0.000181
tissue factor pathway inhibitor 2	Tfpi2	coagulation	21789	-16.89	0.003257
vitamin K epoxide reductase complex, subunit 1	Vkorc1	coagulation	27973	-3.12	0.000861
myosin Vb	Myo5b	cytoskeletal organization	17919	-4.14	0.001391
Wiskott-Aldrich syndrome protein interacting protein	Waspip	cytoskeletal organization	215280	-5.13	0.003413
erythrocyte protein band 4.1-like 5	Epb4.1l5	development	226352	-2.91	0.000352
N-myc downstream regulated gene 2	Ndrg2	development	29811	-4.93	0.021283
acyl-Coenzyme A dehydrogenase family, member 11	Acad11	electron transport	102632	-14.65	0.005618
aldehyde oxidase 3	Aox3	electron transport	71724	-21.13	0.03362
arachidonate 12-lipoxygenase	Alox12	electron transport	11684	-2.51	0.031662
cytochrome P450, family 2, subfamily b, polypeptide 9	Cyp2b9	electron transport	13094	-3.44	0.046149
cytochrome P450, family 2, subfamily c, polypeptide 40	Cyp2c40	electron transport	13099	-2.64	0.002811
cytochrome P450, family 2, subfamily c, polypeptide 70	Cyp2c70	electron transport	226105	-12.2	0.000042
cytochrome p450, family 2, subfamily c, pp44	Cyp2c44	electron transport	226143	-11.94	0.021312

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cytochrome P450, family 2, subfamily d, polypeptide 10	Cyp2d10	electron transport	13101	-1023.6	0.000136
cytochrome P450, family 2, subfamily d, polypeptide 26	Cyp2d26	electron transport	76279	-3014.9	0.000197
cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	electron transport	13106	-52.68	0.023257
cytochrome P450, family 2, subfamily j, polypeptide 5	Cyp2j5	electron transport	13109	-35.17	0.002812
cytochrome P450, family 3, subfamily a, polypeptide 11	Cyp3a11	electron transport	13112	-56.22	0.030333
cytochrome P450, family 3, subfamily a, polypeptide 16	Cyp3a16	electron transport	13114	-28.64	0.029809
cytochrome P450, family 3, subfamily a, polypeptide 25	Cyp3a25	electron transport	56388	-274.97	0.037079
cytochrome P450, family 3, subfamily a, polypeptide 41	Cyp3a41	electron transport	53973	-444.84	0.017532
cytochrome P450, family 39, subfamily a, polypeptide 1	Cyp39a1	electron transport	56050	-4.6	0.032146
cytochrome P450, family 4, subfamily a, polypeptide 12	Cyp4a12	electron transport	277753	-24.51	0.044568
cytochrome P450, family 4, subfamily f, polypeptide 15	Cyp4f15	electron transport	106648	-4	0.0351
cytochrome P450, family 4, subfamily v, polypeptide 3	Cyp4v3	electron transport	102294	-2.64	0.003125
cytochrome P450, family 7, subfamily a, polypeptide 1	Cyp7a1	electron transport	13122	-3.56	0.032412
cytochrome P450, family 8, subfamily b, polypeptide 1	Cyp8b1	electron transport	13124	-67.42	0.000566
dihydropyrimidine dehydrogenase	Dpyd	electron transport	99586	-12.57	0.016779
electron transferring flavoprotein, dehydrogenase	Etfdh	electron transport	66841	-2.61	0.000427
ferredoxin 1	Fdx1	electron transport	14148	-3.22	0.000714
flavin containing monooxygenase 1	Fmo1	electron transport	14261	-9.58	0.000028
flavin containing monooxygenase 5	Fmo5	electron transport	14263	-13.15	0.008679
glutaryl-Coenzyme A dehydrogenase	Gcdh	electron transport	270076	-2.63	0.00956
gulonolactone (L-) oxidase	Gulo	electron transport	268756	-3.3	0.00957
hydroxyacid oxidase (glycolate oxidase) 3	Hao3	electron transport	56185	-29.12	0.002192
hydroxyacid oxidase 1, liver	Hao1	electron transport	15112	-29.8	0.007848
monoamine oxidase B	Maob	electron transport	109731	-2.6	0.001342
P450 (cytochrome) oxidoreductase	Por	electron transport	18984	-5.29	0.009756
pipecolic acid oxidase	Pipox	electron transport	19193	-6.4	0.000168
quiescin Q6	Qscn6	electron transport	104009	-3.95	0.001024
asialoglycoprotein receptor 1	Asgr1	endocytosis	11889	-682.84	0.002778
asialoglycoprotein receptor 2	Asgr2	endocytosis	11890	-24.23	0.017185
alpha-2-glycoprotein 1, zinc	Azgp1	immune response	12007	-17.96	0.011914
CD1d1 antigen	Cd1d1	immune response	12479	-3.88	0.01432
chemokine (C-C motif) ligand 9	Ccl9	immune response	20308	-9.05	0.004004

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complement component 1, r subcomponent	C1r	immune response	50909	-5.46	0.008999
complement component 2 (within H-2S)	C2	immune response	12263	-5.55	0.001273
complement component 4 (within H-2S)	C4	immune response	12268	-14.36	0.004076
complement component 8, alpha polypeptide	C8a	immune response	230558	-50.17	
complement component 8, beta subunit	C8b	immune response	110382	-6.62	0.013077
complement component factor h	Cfh	immune response	12628	-21.42	0.004866
complement component factor h-like 1	Cfhl1	immune response	50702	-168.63	0.005419
complement component factor i	Cfi	immune response	12630	-13.49	0.000304
C-reactive protein, petaxin related	Crp	immune response	12944	-4.2	0.001386
defensin beta 1	Defb1	immune response	13214	-81.46	0.031347
haptoglobin	Hp	immune response	15439	-8.49	0.002222
hemolytic complement	Hc	immune response	15139	-10.95	0.013873
histocompatibility 2, complement component factor B	H2-Bf	immune response	14962	-28.11	0.000219
histocompatibility 2, Q region locus 10	H2-Q10	immune response	15007	-21.52	0.008922
interleukin 1 receptor antagonist	Il1rn	immune response	16181	-4.67	0.024091
lipopolysaccharide binding protein	Lbp	immune response	16803	-2.64	0.003103
liver-expressed antimicrobial peptide 2	Leap2	immune response	259301	-18.72	0.001578
macrophage activation 2 like	Mpa2l	immune response	100702	-7.1	0.007472
mannan-binding lectin serine protease 1	Masp1	immune response	17174	-7.65	0.004163
peptidoglycan recognition protein 2	Pglyrp2	immune response	57757	-258.57	0.012178
retinoic acid receptor responder (tazarotene induced) 2	Rarres2	immune response	71660	-5.27	0.020174
serine (or cysteine) proteinase inhibitor, clade A, member 1a	Serpina1a	immune response	20700	-6.99	0.00008
serine (or cysteine) proteinase inhibitor, clade A, member 1b	Serpina1b	immune response	20701	-3.9	0.000154
serine (or cysteine) proteinase inhibitor, clade A, member 1b /// serine (or cysteine) proteinase inhibitor, clade A, member 1d /// serine (or cysteine) proteinase inhibitor, clade A, member 1a /// serine (or cysteine) proteinase inhibitor, clade A, member 1e	Serpina1a///Serpina1b///Serpina1d///Serpina1e	immune response	20700 /// 20701 /// 20703 /// 20704	-6.43	0.010918
serine (or cysteine) proteinase inhibitor, clade A, member 3N	Serpina3n	immune response	20716	-35.79	0.000457
serine (or cysteine) proteinase inhibitor, clade G, member 1	Serping1	immune response	12258	-2.97	0.000061
serum amyloid A 4	Saa4	immune response	20211	-6.33	0.00665
serum amyloid P-component	Apcs	immune response	20219	-14.35	0.004519
T-cell receptor gamma, variable 4	Tcrg-V4	immune response	21638	-3.22	0.004577
T-cell specific GTPase	Tgtp	immune response	21822	-8.73	0.033472
trefoil factor 3, intestinal	Tff3	immune response	21786	-31.43	0.016602
1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	Agpat2	lipid metabolism	67512	-3.66	0.005536
1-acylglycerol-3-phosphate O-acyltransferase 3	Agpat3	lipid metabolism	28169	-2.98	0.000137

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7-dehydrocholesterol reductase	Dhcr7	lipid metabolism	13360	-2.56	0.004445
acetyl-Coenzyme A acyltransferase 1 /// acetyl-Coenzyme A acyltransferase 1B	Acaa1///Acaa1b	lipid metabolism	113868 /// 235674	-4.44	0.003672
acetyl-Coenzyme A acyltransferase 1B	Acaa1b	lipid metabolism	235674	-71.44	0.010596
acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	lipid metabolism	52538	-3.54	0.008544
acyl-CoA thioesterase 12	Acot12	lipid metabolism	74156	-69	0.015363
acyl-CoA synthetase long-chain family member 1	Acsl1	lipid metabolism	14081	-3.56	0.001591
acyl-CoA synthetase medium-chain family member 3	Acsm3	lipid metabolism	20216	-5.45	0.00339
acyl-CoA thioesterase 4	Acot4	lipid metabolism	171282	-2.93	0.009887
acyl-Coenzyme A binding domain containing 3	Acbd3	lipid metabolism	170760	-3.25	0.010533
acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	lipid metabolism	11430	-13.1	0.021528
acyl-Coenzyme A oxidase 2, branched chain	Acox2	lipid metabolism	93732	-17.7	0.000695
aldo-keto reductase family 1, member C20	Akr1c20	lipid metabolism	116852	-8.64	0.041331
aldo-keto reductase family 1, member C6	Akr1c6	lipid metabolism	83702	-28.03	0.027685
apolipoprotein A-I	Apoa1	lipid metabolism	11806	-4.95	0.002297
apolipoprotein A-II	Apoa2	lipid metabolism	11807	-5.3	0.000834
apolipoprotein B	Apob	lipid metabolism	238055	-421.14	0.048419
apolipoprotein C-II	Apoc2	lipid metabolism	11813	-14.72	0.008305
apolipoprotein C-III	Apoc3	lipid metabolism	11814	-26.11	0.022446
apolipoprotein C-IV	Apoc4	lipid metabolism	11425	-3.48	0.002002
apolipoprotein E	Apoe	lipid metabolism	11816	-2.55	0.001165
apolipoprotein M	Apom	lipid metabolism	55938	-3.55	0.000101
ATPase, class I, type 8B, member 1	Atp8b1	lipid metabolism	54670	-2.76	0.007388
carnitine O-octanoyltransferase	Crot	lipid metabolism	74114	-5.67	0.011524
carnitine palmitoyltransferase 1a, liver	Cpt1a	lipid metabolism	12894	-2.94	0.044126
dehydrogenase/reductase (SDR family) member 8	Dhrs8	lipid metabolism	114664	-5.33	0.017881
diacylglycerol O-acyltransferase 2	Dgat2	lipid metabolism	67800	-2.83	0.003301
elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	Elovl2	lipid metabolism	54326	-18.34	0.007799
emopamil binding protein-like	Ebpl	lipid metabolism	68177	-4.24	0.0109
enoyl coenzyme A hydratase 1, peroxisomal	Ech1	lipid metabolism	51798	-3.43	0.008925
enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Ehhadh	lipid metabolism	74147	-13.37	0.029944
fatty acid binding protein 1, liver	Fabp1	lipid metabolism	14080	-8.34	0.0012
fatty acid desaturase 1	Fads1	lipid metabolism	76267	-2.66	0.014768
fatty acid desaturase 2	Fads2	lipid metabolism	56473	-5.83	0.04425
high density lipoprotein (HDL) binding protein	Hdlbp	lipid metabolism	110611	-2.67	0.005459
hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	Hsd3b7	lipid metabolism	101502	-13.81	0.00279
hydroxysteroid (17-beta) dehydrogenase 2	Hsd17b2	lipid metabolism	15486	-41.68	0.005435
hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	lipid metabolism	15488	-2.89	0.002972
hydroxysteroid (17-beta) dehydrogenase 7	Hsd17b7	lipid metabolism	15490	-4.58	0.001267

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hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	lipid metabolism	15483	-5.81	0.001914
hydroxysteroid dehydrogenase-1, delta<5>-3-beta	Hsd3b1	lipid metabolism	15492	-34.67	0.000105
hydroxysteroid dehydrogenase-2, delta<5>-3-beta	Hsd3b2	lipid metabolism	15493	-4.66	0.020024
hydroxysteroid dehydrogenase-2, delta<5>-3-beta /// hydroxysteroid dehydrogenase-6, delta<5>-3-beta	Hsd3b2///Hsd3b6	lipid metabolism	15493 /// 15497	-3.15	0.001761
hydroxysteroid dehydrogenase-3, delta<5>-3-beta	Hsd3b3	lipid metabolism	15494	-6.93	0.002647
insulin induced gene 1	Insig1	lipid metabolism	231070	-4.28	0.049651
lanosterol synthase	Lss	lipid metabolism	16987	-2.95	0.031145
lecithin cholesterol acyltransferase	Lcat	lipid metabolism	16816	-8.01	0.00349
lipase, hepatic	Lipc	lipid metabolism	15450	-28.7	0.000926
lipin 1	Lpin1	lipid metabolism	14245	-8.4	0.0004
lysosomal acid lipase 1	Lip1	lipid metabolism	16889	-3.24	0.000431
microsomal triglyceride transfer protein	Mttp	lipid metabolism	17777	-4.69	0.000012
paraoxonase 1	Pon1	lipid metabolism	18979	-5.29	0.000162
peroxisomal trans-2-enoyl-CoA reductase	Pecr	lipid metabolism	111175	-3.42	0.000164
phosphate cytidylyltransferase 2, ethanolamine	Pcyt2	lipid metabolism	68671	-3.13	0.000352
phosphatidic acid phosphatase type 2B	Ppap2b	lipid metabolism	67916	-4.4	0.000563
phosphatidylethanolamine N-methyltransferase	Pemt	lipid metabolism	18618	-5.97	0.001015
phospholipase A1 member A	Pla1a	lipid metabolism	85031	-3.29	0.002231
phospholipase A2, group XIIB	Pla2g12b	lipid metabolism	69836	-21.55	0.000089
phytanoyl-CoA 2-hydroxylase 2	Phyh2	lipid metabolism	56794	-59.61	0.003495
phytanoyl-CoA hydroxylase	Phyh	lipid metabolism	16922	-7.88	0.003034
solute carrier family 27 (fatty acid transporter), member 2	Slc27a2	lipid metabolism	26458	-9.1	0.001764
solute carrier family 27 (fatty acid transporter), member 5	Slc27a5	lipid metabolism	26459	-15.6	0.001544
sulfotransferase family 1A, phenol-preferring, member 1	Sult1a1	lipid metabolism	20887	-32.67	0.003685
transmembrane 7 superfamily member 2	Tm7sf2	lipid metabolism	73166	-4.43	0.000154
UDP-glucuronosyltransferase 2 familypolypeptide B36	Ugt2b36	metabolism	231396	-3.72	0.009493
2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	metabolism	67460	-2.75	0.000184
2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	metabolism	26378	-6.25	0.000026
3-hydroxyanthranilate 3,4-dioxygenase	Haao	metabolism	107766	-10.23	0.002294
3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	Bdh	metabolism	71911	-6.83	0.000351
3-hydroxyisobutyryl-Coenzyme A hydrolase	Hibch	metabolism	227095	-2.55	0.003566
4-aminobutyrate aminotransferase	Abat	metabolism	268860	-9.24	0.027017
aconitase 1	Aco1	metabolism	11428	-2.54	0.009206
alanine-glyoxylate aminotransferase	Agxt	metabolism	11611	-18.59	0.006058

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alcohol dehydrogenase 1 (class I)	Adh1	metabolism	11522	-8.83	0.000205
alcohol dehydrogenase, iron containing, 1	Adhfe1	metabolism	76187	-3.4	0.001274
aldehyde dehydrogenase 8 family, member A1	Aldh8a1	metabolism	237320	-59.12	0.019353
aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	metabolism	11671	-5.82	0.002932
aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	metabolism	104776	-3.04	0.00156
aldo-keto reductase family 1, member C12, C13	Akr1C12 ///Akr1C13	metabolism	622402 /// 27384	-2.65	0.009834
aldo-keto reductase family 1, member C13	Akr1c13	metabolism	27384	-3.05	0.006718
aminoadipate aminotransferase	Aadat	metabolism	23923	-66.41	0.000221
arylacetamide deacetylase (esterase)	Aadac	metabolism	67758	-49.59	0.00437
biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	metabolism	68021	-2.75	0.000137
butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	Bbox1	metabolism	170442	-8.72	0.001218
butyryl Coenzyme A synthetase 1	Bucs1	metabolism	117147	-23.87	0.000276
carbonic anhydrase 8	Car8	metabolism	12319	-2.52	0.015332
carbonyl reductase 1	Cbr1	metabolism	12408	-3.07	0.001259
carboxylesterase 3	Ces3	metabolism	104158	-144.97	0.017646
carboxylesterase 6	Ces6	metabolism	102022	-29.66	0.001164
D-dopachrome tautomerase	Ddt	metabolism	13202	-2.89	0.003294
dehydrogenase/reductase (SDR family) member 4	Dhrs4	metabolism	28200	-2.8	0.0026
dimethylarginine dimethylaminohydrolase 1	Ddah1	metabolism	69219	-3.02	0.005823
dopachrome tautomerase	Dct	metabolism	13190	-2.77	0.008795
enoyl Coenzyme A hydratase domain containing 2	Echdc2	metabolism	52430	-3.5	0.00184
enoyl Coenzyme A hydratase domain containing 3	Echdc3	metabolism	67856	-4.54	0.000663
epoxide hydrolase 2, cytoplasmic	Ephx2	metabolism	13850	-15.25	0.000828
folylpolyglutamyl synthetase	Fpgs	metabolism	14287	-2.65	0.00236
formyltetrahydrofolate dehydrogenase	Fthfd	metabolism	107747	-8.24	0.000459
gamma-glutamyltransferase 1	Ggt1	metabolism	14598	-13.97	0.002255
glucosamine	Gne	metabolism	50798	-2.71	0.013356
glutathione S-transferase kappa 1	Gstk1	metabolism	76263	-3.01	0.022781
glutathione S-transferase, alpha 3	Gsta3	metabolism	14859	-16.55	0.005145
glutathione S-transferase, alpha 4	Gsta4	metabolism	14860	-2.81	0.000133
glutathione S-transferase, mu 7	Gstm7	metabolism	68312	-3.28	0.02711
glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	Gcat	metabolism	26912	-3.96	0.001756
glycine N-methyltransferase	Gnmt	metabolism	14711	-18.54	0.016978
guanidinoacetate methyltransferase	Gamt	metabolism	14431	-3.03	0.001798
hydroxysteroid (17-beta) dehydrogenase 13	Hsd17b13	metabolism	243168	-1766.89	0.002961
lipoma HMGIC fusion partner-like 2	Lhfpl2	metabolism	218454	-3.59	0.003239
microsomal glutathione S-transferase 1	Mgst1	metabolism	56615	-3.29	0.002702

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molybdenum cofactor synthesis 2	Mocs2	metabolism	17434	-3.42	0.000569
nitrilase 1	Nit1	metabolism	27045	-3.53	0.010424
nudix (nucleoside diphosphate linked moiety X)-type motif 12 p	Nudt12	metabolism	67993	-2.78	0.000825
pantothenate kinase 1	Pank1	metabolism	75735	-3.86	0.000533
phosphotriesterase related	Pter	metabolism	19212	-3.45	0.01784
propionyl-Coenzyme A carboxylase, alpha polypeptide	Pcca	metabolism	110821	-2.56	0.002951
pyridoxal (pyridoxine, vitamin b6) kinase	Pdxk	metabolism	216134	-2.98	0.000456
retinol dehydrogenase 5	Rdh5	metabolism	19682	-3.05	0.0059
retinol dehydrogenase 7	Rdh7	metabolism	54150	-68.31	0.000191
RIKEN cDNA 2310016A09 gene	2310016A09Rik	metabolism	69574	-9.14	0.001582
RIKEN cDNA A530016O06 gene	A530016O06Rik	metabolism	319660	-27.18	0.01509
S-adenosylhomocysteine hydrolase	Ahcy	metabolism	269378	-2.66	0.000441
sulfotransferase family 1D, member 1	Sult1d1	metabolism	53315	-259.05	0.007114
transferrin receptor 2	Trfr2	metabolism	50765	-7.29	0.00445
UDP glucuronosyltransferase 2 family, polypeptide B1	Ugt2b1	metabolism	71773	-3.08	0.003075
UDP glycosyltransferase 1 family, polypeptide A10; polypeptide A5; polypeptide A6; polypeptide A12; polypeptide A9 ;polypeptide A13; member1; member2	Ugt1a2///Ugt1a10///Ugt1a5///Ugt1a9///Ugt1a6b///Ugt1a1///Ugt1a6a	metabolism	22236 /// 394430 /// 394432 /// 394433 /// 394434 /// 394435 /// 394436 /// 94284	-12.96	0.008605
UDP-glucuronosyltransferase 2 family, member 5	Ugt2b5	metabolism	22238	-5.92	0.000349
ureidopropionase, beta	Upb1	metabolism	103149	-50.73	0.005637
vanin 1	Vnn1	metabolism	22361	-7.87	0.027252
5' nucleotidase, ecto	Nt5e	nucleic acid metabolism	23959	-5.39	0.008492
adenosine kinase	Adk	nucleic acid metabolism	11534	-5.53	0.040911
adenylate kinase 3 alpha-like 1	Ak3l1	nucleic acid metabolism	56248	-8.22	0.000765
deoxyribonuclease II alpha	Dnase2a	nucleic acid metabolism	13423	-3.59	0.000859
ectonucleotide pyrophosphatase/phosphodiesterase 2	Enpp2	nucleic acid metabolism	18606	-7.21	0.001725
methyltransferase-like 3	Mettl3	nucleic acid metabolism	56335	-4.99	0.002823
quinolinate phosphoribosyltransferase	Qprt	nucleic acid metabolism	67375	-12.14	0.00768
urate oxidase	Uox	nucleic acid metabolism	22262	-8.97	0.007131
uridine phosphorylase 2	Upp2	nucleic acid metabolism	76654	-109.58	0.033834
peroxisomal membrane protein 2	Pxmp2	peroxisome organization	19301	-2.62	0.000737
alpha-2-macroglobulin	A2m	protease inhibitor	232345	-87.66	0.010845
caseinolytic protease X (E.coli)	Clpx	protein folding/ modification	270166	-4.8	0.005327
CDC14 cell division cycle 14 homolog B (S. cerevisiae)	Cdc14b	protein folding/ modification	218294	-3.31	0.002106
chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1	protein folding/ modification	67426	-2.6	0.001195
dual specificity phosphatase 9	Dusp9	protein folding/ modification	75590	-2.75	0.003992
F-box protein 42	Fbxo42	protein folding/ modification	213499	-4.86	0.001714
FK506 binding protein 5	Fkbp5	protein folding/ modification	14229	-2.83	0.006351

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homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Herpud1	protein folding/ modification	64209	-2.63	0.000053
neural precursor cell expressed, developmentally down-regulated gene 4-like	Nedd4l	protein folding/ modification	83814	-2.95	0.002322
protein phosphatase 1K (PP2C domain containing)	Ppm1k	protein folding/ modification	243382	-3.24	0.000092
protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	Ptplb	protein folding/ modification	70757	-2.52	0.00346
RIKEN cDNA 2810451A06 gene	2810451A06Rik	protein folding/ modification	72778	-26.55	0.008463
ubiquitin specific protease 8	Usp8	protein folding/ modification	84092	-3.69	0.004792
ubiquitin-conjugating enzyme E2D 2	Ube2d2	protein folding/ modification	56550	-2.53	0.00616
calpain 10	Capn10	proteolysis	23830	-3.15	0.001895
cathepsin H	Ctsh	proteolysis	13036	-2.92	0.001147
cathepsin L	Ctsl	proteolysis	13039	-2.95	0.000396
expressed sequence AI317395	AI317395	proteolysis	215929	-3.87	0.022797
hepsin	Hpn	proteolysis	15451	-3.45	0.007188
inter alpha-trypsin inhibitor, heavy chain 4	Itih4	proteolysis	16427	-95.83	0.000673
inter-alpha trypsin inhibitor, heavy chain 1	Itih1	proteolysis	16424	-4.14	0.000952
RIKEN cDNA 1300002A08 gene	1300002A08Rik	proteolysis	66887	-2.67	0.000209
RIKEN cDNA 4732466D17 gene	4732466D17Rik	proteolysis	212933	-2.88	0.013522
ring finger protein 128	Rnf128	proteolysis	66889	-2.78	0.002135
ring finger protein 13	Rnf13	proteolysis	24017	-2.65	0.015319
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11	Serpina11	proteolysis	380780	-2.98	0.002215
transmembrane serine protease 6	Tmprss6	proteolysis	71753	-3.99	0.001486
small nuclear ribonucleoprotein D3	Snrpd3	RNA splicing	67332	-3.53	0.007265
adenosine A1 receptor	Adora1	signal transduction	11539	-3.52	0.01152
ankyrin repeat and SOCS box-containing protein 13	Asb13	signal transduction	142688	-3.24	0.018409
bone morphogenetic protein 1	Bmp1	signal transduction	12153	-4.83	0.019181
breast cancer anti-estrogen resistance 3	Bcar3	signal transduction	29815	-2.84	0.018055
DEP domain containing 6	Depdc6	signal transduction	97998	-2.57	0.00523
epidermal growth factor receptor	Egfr	signal transduction	13649	-17.09	0.013761
G protein-coupled receptor 120	Gpr120	signal transduction	107221	-2.9	0.036845
G protein-coupled receptor 64	Gpr64	signal transduction	237175	-4.84	0.0231
growth factor receptor bound protein 10	Grb10	signal transduction	14783	-2.74	0.042944
growth factor receptor bound protein 7	Grb7	signal transduction	14786	-2.58	0.001092
growth hormone receptor	Ghr	signal transduction	14600	-3.67	0.005965
insulin-like growth factor binding protein 2	Igfbp2	signal transduction	16008	-55.7	0.002748
insulin-like growth factor binding protein 4	Igfbp4	signal transduction	16010	-2.57	0.0313
interleukin 1 receptor accessory protein	Il1rap	signal transduction	16180	-6.94	0.005212
membrane-spanning 4-domains, subfamily A, member 1	Ms4a1	signal transduction	12482	-2.66	0.020135
mitogen activated protein kinase kinase kinase kinase 1	Map4k1	signal transduction	26411	-7.54	0.004925

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neuronal guanine nucleotide exchange factor	Ngef	signal transduction	53972	-3.8	0.018865
PDZ domain containing 1	Pdzk1	signal transduction	59020	-4.08	0.013372
prolactin receptor	Prlr	signal transduction	19116	-4.27	0.028751
Ras association (RalGDS/AF-6) domain family	Rassf8	signal transduction	101333	-2.78	0.001329
RAS protein activator like 2	Rasal2	signal transduction	320357	-300.11	0.000214
regulator of G-protein signaling 16	Rgs16	signal transduction	19734	-9.39	0.01129
sorbin and SH3 domain containing 2	Sorbs2	signal transduction	234214	-7.66	0.013841
suppressor of cytokine signaling 2	Socs2	signal transduction	216233	-3.82	0.002603
V-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	Erbb3	signal transduction	13867	-10.6	0.000269
wnt inhibitory factor 1	Wif1	signal transduction	24117	-16.51	0.038749
activating transcription factor 5	Atf5	transcription	107503	-4.25	0.000344
ankyrin repeat and KH domain containing 1	Ankhd1	transcription	108857	-10.78	0.021281
CCAAT/enhancer binding protein (C/EBP), alpha	Cebpa	transcription	12606	-3.38	0.000558
forkhead box Q1	Foxq1	transcription	15220	-4.67	0.005571
interferon regulatory factor 6	Irf6	transcription	54139	-3.08	0.002615
kruppel-like factor 15	Klf15	transcription	66277	-3.78	0.000369
kuppel-like factor 12	Klf12	transcription	16597	-3.02	0.031582
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	Nfatc3	transcription	18021	-3.72	0.000618
nuclear factor, interleukin 3, regulated	Nfil3	transcription	18030	-3.01	0.027745
nuclear receptor subfamily 1, group H, member 4	Nr1h4	transcription	20186	-3.43	0.013871
nuclear receptor subfamily 1, group I, member 2	Nr1i2	transcription	18171	-2.85	0.008637
one cut domain, family member 1	Onecut1	transcription	15379	-5	0.000049
RAR-related orphan receptor alpha	Rora	transcription	19883	-4.46	0.005403
Sal-like 1	Sall1	transcription	58198	-10.4	0.000616
SEC14-like 2 (S. cerevisiae)	Sec14l2	transcription	67815	-7.37	0.015111
sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae)	Sirt3	transcription	64384	-5.18	0.00497
aquaporin 11	Aqp11	transport	66333	-4.38	0.002865
aquaporin 9	Aqp9	transport	64008	-5.85	0.00198
ATP-binding cassette, sub-family A (ABC1), member 1	Abca1	transport	11303	-3.3	0.019625
ATP-binding cassette, sub-family B (MDR/TAP), member 11	Abcb11	transport	27413	-1480.96	0.014353
ATP-binding cassette, sub-family D (ALD), member 2	Abcd2	transport	26874	-7.1	0.019279
cDNA sequence BC011209	BC011209	transport	217721	-3.04	0.006628
ceruloplasmin	Cp	transport	12870	-10.8	0.029816
copper chaperone for superoxide dismutase	Ccs	transport	12460	-3.92	0.00014
diazepam binding inhibitor	Dbi	transport	13167	-3.02	0.001436
expressed sequence AI132487	AI132487	transport	104910	-9.83	0.002087
hemopexin	Hpxn	transport	15458	-12.38	0.001066

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MOCO sulphurase C-terminal domain containing 2	Mosc2	transport	67247	-2.93	0.000605
phosphatidylcholine transfer protein	Pctp	transport	18559	-4.8	0.049555
purinergic receptor P2X, ligand-gated ion channel, 1	P2rx1	transport	18436	-3.11	0.007825
RAB4A, member RAS oncogene family	Rab4a	transport	19341	-3.9	0.000218
retinol binding protein 1, cellular	Rbp1	transport	19659	-2.74	0.005107
ribosome binding protein 1	Rrbp1	transport	81910	-3.1	0.003225
RIKEN cDNA 1300017J02 gene	1300017J02Rik	transport	71775	-3.3	0.000021
RIKEN cDNA 1700013L23 gene	1700013L23Rik	transport	69379	-3.36	0.004144
RIKEN cDNA C730036D15 gene	C730036D15Rik	transport	209186	-3.96	0.037848
sideroflexin 2	Sfxn2	transport	94279	-3.24	0.011657
solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Slc10a1	transport	20493	-73.11	0.000742
solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	Slc13a3	transport	114644	-2.68	0.028604
solute carrier family 16 (monocarboxylic acid transporters), member 7	Slc16a7	transport	20503	-3.45	0.002648
solute carrier family 17 (sodium phosphate), member 2	Slc17a2	transport	218103	-10.02	0.008077
solute carrier family 20, member 2	Slc20a2	transport	20516	-2.9	0.00102
solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	Slc25a15	transport	18408	-2.71	0.029054
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Slc25a13	transport	50799	-4.11	0.00008
solute carrier family 26 (sulfate transporter), member 1	Slc26a1	transport	231583	-3.86	0.004514
solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	Slc35d1	transport	242585	-2.95	0.000379
solute carrier family 37 (glycerol-6-phosphate transporter), member 4	Slc37a4	transport	14385	-4.96	0.007984
solute carrier family 38, member 3	Slc38a3	transport	76257	-11.75	0.002344
solute carrier family 39 (metal ion transporter), member 5	Slc39a5	transport	72002	-3.96	0.002831
solute carrier family 39 (zinc transporter), member 14	Slc39a14	transport	213053	-5.68	0.000898
solute carrier family 39 (zinc transporter), member 4	Slc39a4	transport	72027	-11.42	0.022058
Solute carrier family 4 (anion exchanger), member 4	Slc4a4	transport	54403	-2.65	0.008333
solute carrier family 6 (neurotransmitter transporter, GABA), member 13	Slc6a13	transport	14412	-11.3	0.000205
solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	Slc7a2	transport	11988	-2.79	0.001054
solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Slc9a3r1	transport	26941	-2.74	0.003454

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solute carrier organic anion transporter family, member 1b2	Slco1b2	transport	28253	-71	0.018046
solute carrier organic anion transporter family, member 2a1	Slco2a1	transport	24059	-3.67	0.000763
StAR-related lipid transfer (START) domain containing 5	Stard5	transport	170460	-6.68	0.000261
sterol carrier protein 2, liver	Scp2	transport	20280	-6.09	0.000004
syntaxin binding protein 6 (amisyn)	Stxbp6	transport	217517	-5.04	0.0016
thiosulfate sulfurtransferase, mitochondrial	Tst	transport	22117	-3.04	0.019938
tocopherol (alpha) transfer protein	Ttpa	transport	50500	-14.54	0.0025
Insulin receptor substrate2///Riken cDNA 3930402G23 gene	Irs2///3930402G23Rik	unknown	384783///74027	-3.25	0.010227
0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632424N07		unknown		-2.55	0.006627
3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	unknown	15356	-2.86	0.024109
4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	Nipsnap1	unknown	18082	-4.42	0.000069
A kinase (PRKA) anchor protein 1	Akap1	unknown	11640	-6.12	0.000973
abhydrolase domain containing 1	Abhd1	unknown	57742	-3.59	0.001746
abhydrolase domain containing 14b	Abhd14b	unknown	76491	-2.62	0.004136
abhydrolase domain containing 3	Abhd3	unknown	106861	-15.26	0.002883
acetyl-Coenzyme A acetyltransferase 1	Acat1	unknown	110446	-3.68	0.000018
agmatine ureohydrolase (agmatinase)	Agmat	unknown	75986	-11.22	0.000552
alanine-glyoxylate aminotransferase 2	Agxt2	unknown	268782	-6.98	0.011308
ankyrin repeat and BTB (POZ) domain containing 2	Abtb2	unknown	99382	-3.53	0.000417
apolipoprotein N	Apon	unknown	28194	-4.88	0.000395
ATP-binding cassette, sub-family A (ABC1), member 6	Abca6	unknown	76184	-3.61	0.002918
brain protein 44-like	Brp44l	unknown	55951	-3.2	0.000649
butyrylcholinesterase	Bche	unknown	12038	-2.58	0.000446
calmodulin-like 4	Calml4	unknown	75600	-2.7	0.026569
camello-like 1	Cml1	unknown	66116	-113.71	0.000005
carboxypeptidase N, polypeptide 2	Cpn2	unknown	71756	-38.09	0.000804
CD302 antigen	Cd302	unknown	66205	-3.29	0.000704
cDNA sequence BC004004	BC004004	unknown	80748	-2.81	0.030755
cDNA sequence BC006662		unknown	223267	-5.34	0.000199
cDNA sequence BC010787	BC010787	unknown	235043	-4.25	0.000088
cDNA sequence BC014685	BC014685	unknown	232086	-12.25	0.00006
cDNA sequence BC014699	BC014699	unknown	232146	-7.31	0.001648
cDNA sequence BC021608	BC021608	unknown	192653	-8.27	0.000223
cDNA sequence BC021614	BC021614	unknown	225884	-5.41	0.000968
cDNA sequence BC040756	BC040756	unknown	414073	-7.05	0.006582
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	unknown	228889	-2.97	0.003745
dihydropyrimidinase	Dpys	unknown	64705	-14.07	0.000147

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DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	D4Bwg0951e	unknown	52829	-4	0.000333
ectonucleoside triphosphate diphosphohydrolase 8	Entpd8	unknown	72090	-5.46	0.001689
ELOVL family member 5, elongation of long chain fatty acids (yeast)	Elovl5	unknown	68801	-2.68	0.021813
esterase 1	Es1	unknown	13884	-170.12	0.029798
esterase 31-like	LOC13909	unknown	13909	-13.71	0.043801
expressed sequence AI195470	AI195470	unknown	107131	-8.85	0.027605
expressed sequence AI467657	AI467657	unknown	102538	-4.52	0.002902
expressed sequence AI852444	AI852444	unknown	101188	-4.52	0.001962
expressed sequence AV216087	AV216087	unknown	211896	-3.98	0.00276
expressed sequence AW061290	AW061290	unknown	381110	-3.34	0.006713
expressed sequence AW111920		unknown		-4	0.014099
expressed sequence AW112010	AW112010	unknown	107350	-5.36	0.028053
expressed sequence AW112037	AW112037	unknown	98667	-2.98	0.000435
expressed sequence BB229969		unknown		-10.22	0.011684
expressed sequence BE946605		unknown		-2.96	0.022754
expressed sequence BI647951		unknown		-2.75	0.000711
fetuin beta	Fetub	unknown	59083	-19.37	0.00446
fibrinogen-like protein 1	Fgl1	unknown	234199	-2.6	0.007985
forkhead-associated (FHA) phosphopeptide binding domain 1	Fhad1	unknown	329977	-4.01	0.001629
GLE1 RNA export mediator-like (yeast	Gle1l	unknown	74412	-2.73	0.014293
GRAM domain containing 1C	Gramd1c	unknown	207798	-3.2	0.009814
heat-responsive protein 12	Hrsp12	unknown	15473	-5.85	0.00564
helicase with zinc finger domain	Helz	unknown	78455	-2.98	0.001839
histidine-rich glycoprotein	Hrg	unknown	94175	-2724.57	0.003962
hypothetical protein C630010N09	C630010N09	unknown	330403	-3.33	0.021988
leucine rich repeat containing 8	Lrrc8	unknown	241296	-3.36	0.00109
leucine zipper transcription regulator 2	Lztr2	unknown	89867	-10.6	0.006058
leucine-rich alpha-2-glycoprotein 1	Lrg1	unknown	76905	-4.46	0.003238
LOC434338		unknown	434338	-3.17	0.028861
mal, T-cell differentiation protein 2	Mal2	unknown	105853	-4.75	0.003557
MARVEL (membrane-associating) domain containing 2	Marveld2	unknown	218518	-2.96	0.002399
microrchidia 4	Morc4	unknown	75746	-4.95	0.033557
MOCO sulphurase C-terminal domain containing 1	Mosc1	unknown	66112	-57.09	0.007271
NACHT, leucine rich repeat and PYD containing 6	Nalp6	unknown	101613	-5.38	0.00058
NIPA-like domain containing 1	Npal1	unknown	70701	-4.96	0.001263
nur77 downstream gene 2	Ndg2	unknown	103172	-2.75	0.000082
peroxisomal biogenesis factor 6	Pex6	unknown	224824	-3.11	0.003715
phosphatidic acid phosphatase type 2c	Ppap2c	unknown	50784	-3.08	0.000369
phosphodiesterase 4D interacting protein	Pde4dip	unknown	83679	-2.52	0.002412
pregnancy zone protein	Pzp	unknown	11287	-4.75	0.000029

GENE	GENE SYMBOL	GENE ONTOLOGY BIOLOGICAL PROCESS	GENE ID	FOLD CHANGE	P VALUE
progesterone receptor membrane component	Pgrmc1	unknown	53328	-2.66	0.0003
receptor accessory protein 6	Reep6	unknown	70335	-7.56	0.002824
regucalcin	Rgn	unknown	19733	-2.5	0.007288
RGM domain family, member C	Hfe2	unknown	69585	-142.52	0.001977
RIKEN cDNA 0610009A07	0610009A07Rik	unknown	70337	-15.49	0.00005
RIKEN cDNA 0610011I04 gene	0610011I04Rik	unknown	66058	-3.16	0.005842
RIKEN cDNA 0610039N19 gene	0610039N19Rik	unknown	67442	-3.75	0.00425
RIKEN cDNA 1110014J01 gene	1110014J01Rik	unknown	74778	-3.2	0.001753
RIKEN cDNA 1190003J15 gene	1190003J15Rik	unknown	76974	-21.39	0.000414
RIKEN cDNA 1200015M12 gene	1200015M12Rik	unknown	71739	-4.85	0.000133
RIKEN cDNA 1200016E24 gene /// RIKEN cDNA 1200015M12 gene /// RIKEN cDNA 1200003I10 gene	1200016E24Rik///1200015M12Rik///1200003I10Rik	unknown	319202 /// 71719 /// 71739	-2.93	0.003282
RIKEN cDNA 1300002K09 gene	1300002K09Rik	unknown	74152	-3.47	0.001163
RIKEN cDNA 1300011L04 gene	1300011L04Rik	unknown	71763	-8.58	0.000088
RIKEN cDNA 1300013J15 gene	1300013J15Rik	unknown	67473	-3.66	0.002803
RIKEN cDNA 1500019G21 gene	1500019G21Rik	unknown	66245	-2.53	0.004487
RIKEN cDNA 1600014C10 gene	1600014C10Rik	unknown	72244	-8.06	0.000108
RIKEN cDNA 1810005K13 gene	1810005K13Rik	unknown	66255	-5.5	0.041545
RIKEN cDNA 1810008I18 gene	1810008I18Rik	unknown	73625	-7.34	0.015094
RIKEN cDNA 1810010H24 gene	1810010H24Rik	unknown	69066	-4.82	0.003097
RIKEN cDNA 1810011O10 gene	1810011O10Rik	unknown	69068	-7.57	0.00315
RIKEN cDNA 1810015C04 gene	1810015C04Rik	unknown	66270	-3.26	0.000562
RIKEN cDNA 2010003K15 gene	2010003K15Rik	unknown	75606	-12.86	0.00231
RIKEN cDNA 2210010A19	2210010A19Rik	unknown	94184	-3.13	0.001141
RIKEN cDNA 2310033P09 gene	2310033P09Rik	unknown	67862	-3.39	0.000605
RIKEN cDNA 2310076L09 gene	2310076L09Rik	unknown	66968	-12.91	0.010097
RIKEN cDNA 2510049J12 gene	2510049J12Rik	unknown	70291	-3.49	0.00179
RIKEN cDNA 2610528J11 gene	2610528J11Rik	unknown	66451	-15.24	0.014138
RIKEN cDNA 2810459M11 gene	2810459M11Rik	unknown	72792	-4.3	0.002546
RIKEN cDNA 3930402G23 gene	3930402G23Rik	unknown	74027	-2.61	0.00473
RIKEN cDNA 4833422F24 gene	4833422F24Rik	unknown	74614	-3.34	0.023144
RIKEN cDNA 4930506M07 gene	4930506M07Rik	unknown	71653	-3.38	0.019352
RIKEN cDNA 4931406C07 gene	4931406C07Rik	unknown	70984	-3.57	0.000141
RIKEN cDNA 4932439K10 gene	4932439K10Rik	unknown	74392	-6.9	0.012059
RIKEN cDNA 4933429D07 gene	4933429D07Rik	unknown	399624	-10.37	0.000101
RIKEN cDNA 5730403B10 gene	5730403B10Rik	unknown	66626	-4.75	0.002861
RIKEN cDNA 5730469M10 gene	5730469M10Rik	unknown	70564	-2.71	0.009692
RIKEN cDNA 5730472N09 gene	5730472N09Rik	unknown	108958	-4	0.002882
RIKEN cDNA 6230410P16 gene	6230410P16Rik	unknown	235582	-18.58	0.000359
RIKEN cDNA 8430408G22 gene	8430408G22Rik	unknown	213393	-53.88	0.021514
RIKEN cDNA 8430418G19 gene	8430418G19Rik	unknown		-10.58	0.000064
RIKEN cDNA 8430436F23 gene	8430436F23Rik	unknown	71559	-4.03	0.011907
RIKEN cDNA 9030611N15 gene	9030611N15Rik	unknown	105387	-14.8	0.046773
RIKEN cDNA 9030623C06 gene	9030623C06Rik	unknown	66809	-2.86	0.018736
RIKEN cDNA 9130022K13 gene	9130022K13Rik	unknown	75761	-21.21	0.004064
RIKEN cDNA 9530008L14 gene	9530008L14Rik	unknown	109254	-8.85	0.00089

GENE	GENE SYMBOL	GENE ONTOLOGY BIOLOGICAL PROCESS	GENE ID	FOLD CHANGE	P VALUE
RIKEN cDNA A130072N09 gene	A130072N09Rik	unknown	319271	-7.45	0.006254
RIKEN cDNA A230097K15	A230097K15Rik	unknown	231510	-2.87	0.045954
RIKEN cDNA A630076J17 gene	A630076J17Rik	unknown	319929	-44.89	0.002475
RIKEN cDNA C630028N24	C630028N24Rik	unknown	235386	-3.21	0.006651
RIKEN cDNA C730049O14 gene	C730049O14Rik	unknown	320117	-2.9	0.007448
RIKEN cDNA D630014A15 gene	D630014A15Rik	unknown	319666	-2.83	0.00427
ropporin 1-like	Ropn1l	unknown	252967	-3.72	0.018453
secreted phosphoprotein 2	Spp2	unknown	75396	-4.09	0.0076
selenium binding protein 1	Selenbp1	unknown	20341	-3.09	0.03298
selenophosphate synthetase 2	Sephs2	unknown	20768	-3.85	0.004798
taxilin beta	Txlnb	unknown	378431	-3.34	0.038045
TBC1 domain family, member 23	Tbc1d23	unknown	67581	-2.67	0.00421
transmembrane 4 superfamily member 12	Tspan12	unknown	269831	-3.61	0.000126
transmembrane protein 30B	Tmem30b	unknown	238257	-51.73	0.002795
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11	Galnt11	unknown	231050	-2.58	0.019243
von Willebrand factor C and EGF domains	Vwce	unknown	71768	-12.08	0.000377
WD repeat domain 40B	Wdr40b	unknown	245404	-2.58	0.004364
weakly similar to RIKEN cDNA 5730493B19 (Mus musculus)		unknown		-3.74	0.025572
zinc finger, DHHC domain containing 9	Zdhhc9	unknown	208884	-3.34	0.001578

GENES UPREGULATED ≥2.5 FOLD (p ≤ 0.05) in HNF4α NULL EMBRYONIC LIVERS

GENE	GENE SYMBOL	GENE ONTOLOGY BIOLOGICAL PROCESS	GENE ID	FOLD CHANGE	P VALUE
amylase 2, pancreatic	Amy2	carbohydrate metabolism	11723	20.87	0.011063
lactate dehydrogenase 2, B chain	Ldh2	carbohydrate metabolism	16832	9.27	0.000489
hexokinase 2	Hk2	carbohydrate metabolism	15277	2.63	0.019608
procollagen, type IV, alpha 5	Col4a5	cell adhesion	12830	2.81	0.003176
pleiotrophin	Ptn	cell proliferation	19242	4.02	0.00826
tubulin, beta 6	Tubb6	cytoskeletal organization	67951	2.54	0.00518
neuronatin	Nnat	development	18111	38.09	0.01651
annexin A13	Anxa13	development	69787	3.73	0.019489
roundabout homolog 1 (Drosophila)	Robo1	development	19876	2.86	0.027951
angiopoietin-like 6	Angptl6	development	70726	2.85	0.001405
delta-like 1 homolog (Drosophila)	Dlk1	development	13386	2.51	0.029544
interferon, alpha inducible protein 27	Ifi27	immune response	76933	3.26	0.028314
pancreatic lipase related protein 1	Pnliprp1	lipid metabolism	18946	4.41	0.004753
very low density lipoprotein receptor	Vldlr	lipid metabolism	22359	3.09	0.010095
fucosyltransferase 9	Fut9	protein folding/modification	14348	4.57	0.017847
RIKEN cDNA E430002G05	E430002G05Rik	proteolysis	210622	3.85	0.039976
protease, serine, 23	Prss23	proteolysis	76453	3.36	0.006548

GENE	GENE SYMBOL	GENE ONTOLOGY BIOLOGICAL PROCESS	GENE ID	FOLD CHANGE	P VALUE
platelet-derived growth factor, C polypeptide	Pdgfc	signal transduction	54635	3.51	0.009533
arginine vasopressin receptor 1A	Avpr1a	signal transduction	54140	2.7	0.006894
THO complex 1	Thoc1	signal transduction	225160	3.65	0.027801
transcription factor 4	Tcf4	transcription	21413	311.37	0.002505
high mobility group AT-hook 2	Hmga2	transcription	15364	4.16	0.020603
pre B-cell leukemia transcription factor 3	Pbx3	transcription	18516	2.74	0.001862
serine (or cysteine) proteinase inhibitor, clade A	Serpina6	transport	12401	30.2	0.018743
calcium channel, voltage-dependent, T type, alp	Cacna1h	transport	58226	2.63	0.036147
RIKEN cDNA 1110032A04 gene	1110032A04Rik	unknown	66183	126.87	0.009429
fidgetin	Fign	unknown	60344	5.5	0.023706
DnaJ (Hsp40) homolog, subfamily C, member 1	Dnajc12	unknown	30045	4.95	0.01253
RIKEN cDNA 9130213B05 gene	9130213B05Rik	unknown	231440	4.43	0.031931
brain expressed gene 1	Bex1	unknown	19716	2.88	0.017552
RNA imprinted and accumulated in nucleus	Rian	unknown	75745	2.67	0.0069
RIKEN cDNA 2310037P21 gene	2310037P21Rik	unknown	72309	2.56	0.00327
RIKEN cDNA 5033414K04	5033414K04Rik	unknown	98496	2.56	0.013487
RIKEN cDNA 6030405A18	6030405A18Rik	unknown	329641	2.52	0.001739