Supplemental Information

Krüppel-like factor 9 (KLF9) promotes cytochrome P450 (CYP) 2D6 expression during pregnancy in CYP2D6-humanized mice

Kwihye Koh, Xian Pan, Wei Zhang, Alan Mclachlan, Raul Urrutia, Hyunyoung Jeong

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Table S1. Sequences of oligonucleotides used in the study

Cloning primers for luciferase vectors (mutated sites underlined)

Construct	Forward primer	Reverse primer
pGL3-CYP2D6 mK1	GGGCAAAGGCCATCATCAGCTTTGATTATAAGGGAAGGGTCACGCG	CGCGTGACCCTTCCCTTATAATCAAAGCTGATGATGGCCTTTGCCC
pGL3-CYP2D6 mK2	GGCCATCATCAGCTCCCTTTATAAGGGATTATTCACGCGCTCGGTGT	ACACCGAGCGCGTGAATAATCCCTTATAAAGGGAGCTGATGATGGCC
pGL3-CYP2D6 mK3	CGCTCGGTGTGCTGAGAGTGTAATGCCTGGTCCT	AGGACCAGGCATTACACTCTCAGCACACCGAGCG
pGL3-CYP2D6 mK4	CCTCTGTGCCTGGTTTGGTGGGGGTGCC	GGCACCCCCACCAAACCAGGCACAGAGG
pGL3-CYP2D6 mK5	CTCTGTGCCTGGTGGGGTTTATGTGCCAGGTGTGTCCAGA	TCTGGACACACCTGGCACATAAACCCCACCAGGCACAGAG

qRT-PCR probes

SYBR green probes			
Mouse gene	**Species**	**Forward primer**	**Reverse primer**
Atf5	Mouse	TGGGCTGGCTCGTAGACTAT	GTCATCCAATCAGAGAAGCCG
Egr1	Mouse	TCGGCTCCTTTCCTCACTCA	CTCATAGGGTTGTTCGCTCGG
Foxa3	Mouse	GCGGGCGAGGTGTATTCTC	GAGTGGGTTCAAGGTCATGTAG
Id3	Mouse	GACGACATGAACCACTGCTAC	CCTGGCTAAGCTGAGTGCC
Junb	Mouse	TCACGACGACTCTTACGCAG	CCTTGAGACCCCGATAGGGA
Klf9	Mouse	GCCGCCTACATGGACTTCG	GGTCACCGTGTTCCTTGGT
Klf10	Mouse	AGCTGCGACTGGAAGTCTCA	CGGAGGTATCAGACACTGGTG
Rev-erbα	Mouse	ACTTCCCACCATCACCTACTG	GGGGAGCTATCATCACTGAGA
β-actin	Mouse	GGCTGTATTCCCCTCCATCG	CCAGTTGGTAACAATGCCATGT
Gapdh	Mouse	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

Commercial Taqman probes			
Gene	**Species**	**Catalog number**	**Company**
CYP2D6	Human	Hs.PT.49a.205234723/ Hs02576167_m1	IDT/ABI
Klf9	Mouse	Mm.PT.49a.17256251	IDT
Gapdh	Mouse	Mm.PT.39a.1	IDT
β-actin	Mouse	Mm00607939_s1	ABI

qPCR probes for ChIP

Gene	Species	Forward primer	Reverse primer	Taqman probe
CYP2D6	Human	CAACACAGCAGGTTCACT	CTACCAAATGGGCTCCTCT	AGGCCATCATCAGCTCCCTTTA
Apoc2	Mouse	CCATGCGTAGGGCATTAGAAGA	GGCCCATCCTGTAACAGAGCTT	
Cyp1a1	Mouse	GTCGTTGCGCTTCTCACGCGA	CACTGAGGGAGGGGTTTGAGG	
Hes6	Mouse	GGAGTCCTGCCCGGCCTAAGTGC	ATTGGCTGTGCGTGGTCGGAGAG	
CYP2D6 distal	Human	AGGGAACGACACTCATCACC	GATACCCCTGCAAGACTCCA	

EMSA DNA probes

	Forward primer	Reverse primer
CYP2D6/K2	CCTTTATAAGGGAAGGGTCACGCG	CGCGTGACCCTTCCCTTATAAAGG
CYP2D6/mK2	CCTTTATAAGGGATTATTCACGCG	CGCGTGAATAATCCCTTATAAAGG
Consensus BTE	AGAGAAGGAGGCGTGGCCAACAGA	TCTGTTGGCCACGCCTCCTTCTCT

Table S2. Genes that are upregulated at G21 (compared to Virgin) and/or downregulated at PP7 (compared to G21) (* For negative fold change = down-regulated; positive fold change = up-regulated)

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
Genes that are updated at G21 and downregualted at PP7								
1	NM_001126318 /// NM_026419 /// XM_914439 /// XR_034091 /// XR_034282	Cela3b /// Gm13011 /// LOC638418	chymotrypsin-like elastase family, member 3B /// predicted gene 13011 /// simila	up G21 & down PP7	0.00002	92.52300	-95.23180	-1.02928
2	NM_026419 /// XM_914439	Cela3b /// LOC638418	chymotrypsin-like elastase family, member 3B /// similar to elastase 3B, pancrea	up G21 & down PP7	0.00005	44.43770	-42.91710	1.03543
3	NM_010915	Klk1b4	kallikrein 1-related pepidase b4	up G21 & down PP7	0.00017	32.62190	-12.46350	2.6174
4	NM_026419	Cela3b	chymotrypsin-like elastase family, member 3B	up G21 & down PP7	0.00002	20.87770	-17.09570	1.22123
5	NM_001083929 /// NM_008161	Gpx3	glutathione peroxidase 3	up G21 & down PP7	0.00070	15.76090	-10.15390	1.5522
6	NM_201640 /// XM_001475399	Cyp4a31	cytochrome P450, family 4, subfamily a, polypeptide 31	up G21 & down PP7	0.00349	12.16770	-2.93002	4.15277
7	NM_001111324 /// NM_017464	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	up G21 & down PP7	0.13121	6.92718	-2.74540	2.52319
8	NM_001159555 /// NM_001159556 /// NM_001159557 /// NM_001159558 /// NM_007643	Cd36	CD36 antigen	up G21 & down PP7	0.01105	6.56232	-1.97107	3.32932
9	NM_011704	Vnn1	vanin 1	up G21 & down PP7	0.02950	5.87271	-7.36795	-1.25461
10	NM_011267	Rgs16	regulator of G-protein signaling 16	up G21 & down PP7	0.03495	5.83684	-3.93322	1.48399
11	NM_007913	Egr1	early growth response 1	up G21 & down PP7	0.29081	5.75685	-2.37520	2.42374
12	NM_001160378 /// NM_001160379 /// XM_135029 /// XM_918327 /// XM_925654 /// XM_9	Fam46a	family with sequence similarity 46, member A	up G21 & down PP7	0.01853	5.68905	-1.74399	3.26208
13	NM_008730	Nptx1	neuronal pentraxin 1	up G21 & down PP7	0.14178	5.54993	-4.57742	1.21246
14	NM_007657	Cd9	CD9 antigen	up G21 & down PP7	0.00443	5.18752	-2.43438	2.13094
15	NM_008817	Peg3	paternally expressed 3	up G21 & down PP7	0.02317	5.03919	-2.79539	1.80267
16	NM_133185	Rogdi	rogdi homolog (Drosophila)	up G21 & down PP7	0.02092	5.01917	-3.20538	1.56586

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
17	NM_133903	Spon2	spondin 2, extracellular matrix protein	up G21 & down PP7	0.06749	4.98912	-1.69745	2.93919
18	NM_013602	Mt1	metallothionein 1	up G21 & down PP7	0.03101	4.96035	-5.54661	-1.11819
19	NM_007820	Cyp3a16	cytochrome P450, family 3, subfamily a, polypeptide 16	up G21 & down PP7	0.00085	4.68539	-1.49615	3.13163
20	NM_011169	Prlr	prolactin receptor	up G21 & down PP7	0.00115	4.36049	-3.25334	1.34031
21	NM_001029842 /// NM_134038	Slc16a6	solute carrier family 16 (monocarboxylic acid transporters), member 6	up G21 & down PP7	0.15879	4.33768	-1.91583	2.26413
22	NM_008681	Ndrg1	N-myc downstream regulated gene 1	up G21 & down PP7	0.06787	4.29101	-1.75641	2.44305
23	NM_010917	Nid1	nidogen 1	up G21 & down PP7	0.01294	4.28544	-3.50781	1.22169
24	NM_007618	Serpina6	serine (or cysteine) peptidase inhibitor, clade A, member 6	up G21 & down PP7	0.01277	4.16163	-2.57513	1.61609
25	NM_010114 /// NM_010116	Klk1b22 /// Klk1b9	kallikrein 1-related peptidase b22 /// kallikrein 1-related peptidase b9	up G21 & down PP7	0.00167	4.02512	-3.21485	1.25204
26	NM_177420	Psat1	phosphoserine aminotransferase 1	up G21 & down PP7	0.12595	4.00777	-2.21124	1.81246
27	NM_027237	2010003K11Rik	RIKEN cDNA 2010003K11 gene	up G21 & down PP7	0.01633	3.86839	-2.21298	1.74804
28	NM_007763	Crip1	cysteine-rich protein 1 (intestinal)	up G21 & down PP7	0.05363	3.72008	-3.29548	1.12884
29	NM_172053	Adamts16	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin ty	up G21 & down PP7	0.00951	3.57345	-3.35550	1.06495
30	NM_011921	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	up G21 & down PP7	0.00698	3.55899	-1.33821	2.65951
31	NM_008381 /// XM_001476835	Inhbb /// LOC100046802	inhibin beta-B /// similar to Inhbb protein	up G21 & down PP7	0.02972	3.53558	-6.18301	-1.7488
32	NM_009695	Apoc2	apolipoprotein C-II	up G21 & down PP7	0.00023	3.48893	-2.57256	1.35621
33	NM_011315	Saa3	serum amyloid A 3	up G21 & down PP7	0.02424	3.43185	-3.59394	-1.04723
34	NM_001163691 /// NM_021415	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	up G21 & down PP7	0.46018	3.36997	-3.50505	-1.04008
35	NM_001159650 /// NM_021352	Crybb3	crystallin, beta B3	up G21 & down PP7	0.16596	3.36294	-3.09776	1.0856
36	NM_178739	Dcaf12l1	DDB1 and CUL4 associated factor 12-like 1	up G21 & down PP7	0.03299	3.16895	-1.67979	1.88651
37	NM_144544	2210407C18Rik	RIKEN cDNA 2210407C18 gene	up G21 & down PP7	0.00057	3.16881	-3.27236	-1.03268
38	NM_013742	Cars	cysteinyl-tRNA synthetase	up G21 & down PP7	0.00138	3.12860	-1.70011	1.84023
39	NM_008489	Lbp	lipopolysaccharide binding protein	up G21 & down PP7	0.01310	3.12680	-2.09817	1.49025

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
40	NM_011242	Rasgrp2	RAS, guanyl releasing protein 2	up G21 & down PP7	0.03834	3.04398	-1.66493	1.8283
41	NM_001136181 /// XM_885191 /// XM_917141	Hsbp1l1	heat shock factor binding protein 1-like 1	up G21 & down PP7	0.06876	3.03098	-2.02392	1.49758
42	NM_010060	Dnahc11	dynein, axonemal, heavy chain 11	up G21 & down PP7	0.12670	3.01047	-2.33859	1.2873
43	NM_020013	Fgf21	fibroblast growth factor 21	up G21 & down PP7	0.00301	2.96893	-3.33099	-1.12195
44	NM_013851	Abca8b	ATP-binding cassette, sub-family A (ABC1), member 8b	up G21 & down PP7	0.01291	2.92594	-2.01993	1.44854
45	NM_008135	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	up G21 & down PP7	0.23899	2.90785	-2.21416	1.31329
46	NM_175138	Dnaic1	dynein, axonemal, intermediate chain 1	up G21 & down PP7	0.01048	2.90490	-2.89809	1.00235
47	NM_011979	Vnn3	vanin 3	up G21 & down PP7	0.00025	2.89108	-2.99114	-1.03461
48	NM_026095	Snrpd3	small nuclear ribonucleoprotein D3	up G21 & down PP7	0.00018	2.84673	-1.90584	1.49369
49	NM_010172	F7	coagulation factor VII	up G21 & down PP7	0.00951	2.83440	-1.61849	1.75126
50	NM_009416	Tpm2	tropomyosin 2, beta	up G21 & down PP7	0.03002	2.73555	-1.99933	1.36823
51	NM_013888	Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12	up G21 & down PP7	0.46708	2.68956	-3.12669	-1.16253
52	NM_013874	Dpf1	D4, zinc and double PHD fingers family 1	up G21 & down PP7	0.05596	2.68710	-2.03142	1.32277
53	NM_181401	Tmem64	transmembrane protein 64	up G21 & down PP7	0.23151	2.59980	-2.12031	1.22614
54	NM_001113386 /// NM_013584	Lifr	leukemia inhibitory factor receptor	up G21 & down PP7	0.02669	2.55655	-2.31969	1.10211
55	NM_024281 /// NM_133626	Rrbp1	ribosome binding protein 1	up G21 & down PP7	0.01786	2.54885	-1.72579	1.47692
56	NM_001077514 /// NM_001077515 /// NM_011393	Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	up G21 & down PP7	0.01516	2.53303	-2.00652	1.2624
57	NM_001170959 /// NM_033614	Pde6c	phosphodiesterase 6C, cGMP specific, cone, alpha prime	up G21 & down PP7	0.06381	2.52642	-2.50647	1.00796
58	NM_012055	Asns	asparagine synthetase	up G21 & down PP7	0.15433	2.47223	-2.23344	1.10692
59	NM_001136077 /// NM_015744	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	up G21 & down PP7	0.00060	2.38308	-4.77438	-2.00344
60	NM_133765	Fbxo31	F-box protein 31	up G21 & down PP7	0.00109	2.37834	-1.82990	1.29971
61	NM_001042611 /// NM_007752	Cp	ceruloplasmin	up G21 & down PP7	0.00981	2.37231	-2.41713	-1.01889
62	NM_013667	Slc22a2	solute carrier family 22 (organic cation transporter), member 2	up G21 & down PP7	0.27637	2.36115	-1.96743	1.20012
63	NM_028066	F11	coagulation factor XI	up G21 & down PP7	0.00001	2.35869	-2.11048	1.11761

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64	NM_001048147 /// NM_001048178 /// NM_010284	Ghr	growth hormone receptor	up G21 & down PP7	0.00368	2.34216	-2.80673	-1.19835
65	NM_001033431 /// XM_001476888 /// XM_904112	Nlrp12	NLR family, pyrin domain containing 12	up G21 & down PP7	0.00450	2.26691	-3.17369	-1.40001
66	NM_175096	Stbd1	starch binding domain 1	up G21 & down PP7	0.04452	2.25060	-1.69099	1.33094
67	NM_008341	Igfbp1	insulin-like growth factor binding protein 1	up G21 & down PP7	0.19290	2.24286	-1.96212	1.14308
68	NM_028077	1810055G02Rik	RIKEN cDNA 1810055G02 gene	up G21 & down PP7	0.02453	2.23610	-2.17266	1.0292
69	NM_013692	Klf10	Kruppel-like factor 10	up G21 & down PP7	0.04238	2.22874	-2.29372	-1.02915
70	NM_025670	5730403B10Rik	RIKEN cDNA 5730403B10 gene	up G21 & down PP7	0.00780	2.22754	-1.74197	1.27874
71	NM_010638 /// XM_001479552	Klf9	Kruppel-like factor 9	up G21 & down PP7	0.03948	2.21838	-2.05764	1.07812
72	NR_002860	1200003I10Rik /// 1200015M12Rik /// A130040M12Rik /// E430024C06Rik	RIKEN cDNA 1200003I10 gene /// RIKEN cDNA 1200015M12 gene /// RIKEN cDNA A130040	up G21 & down PP7	0.00508	2.21466	-1.93114	1.14682
73	NR_002860	1200015M12Rik /// A130040M12Rik /// E430024C06Rik	RIKEN cDNA 1200015M12 gene /// RIKEN cDNA A130040M12 gene /// RIKEN cDNA E430024	up G21 & down PP7	0.00508	2.21466	-1.93114	1.14682
74	NR_002860	3930401B19Rik /// A130040M12Rik /// E430024C06Rik	RIKEN cDNA 3930401B19 gene /// RIKEN cDNA A130040M12 gene /// RIKEN cDNA E430024	up G21 & down PP7	0.00508	2.21466	-1.93114	1.14682
75	NR_002860	A130040M12Rik	RIKEN cDNA A130040M12 gene	up G21 & down PP7	0.00508	2.21466	-1.93114	1.14682
76	NM_080436	Rdh1	retinol dehydrogenase 1 (all trans)	up G21 & down PP7	0.39646	2.20551	-2.19098	1.00663
77	NM_178613	4933433P14Rik	RIKEN cDNA 4933433P14 gene	up G21 & down PP7	0.02544	2.14941	-1.87090	1.14887
78	NM_011338	Ccl9	chemokine (C-C motif) ligand 9	up G21 & down PP7	0.05841	2.11098	-1.51604	1.39243
79	NM_013834	Sfrp1	secreted frizzled-related protein 1	up G21 & down PP7	0.00953	2.07307	-2.00748	1.03267
80	NM_008260	Foxa3	forkhead box A3	up G21 & down PP7	0.00030	2.06809	-1.86595	1.10833

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81	NM_008630	Mt2	metallothionein 2	up G21 & down PP7	0.00377	2.05934	-6.93971	-3.36987
82	NM_177473 /// XM_358773 /// XM_910361	Tmem191c	transmembrane protein 191C	up G21 & down PP7	0.00496	2.05492	-2.22917	-1.0848
83	NM_007972	F10	coagulation factor X	up G21 & down PP7	0.00453	2.05186	-1.37178	1.49576
84	NM_013786	Hsd17b6	hydroxysteroid (17-beta) dehydrogenase 6	up G21 & down PP7	0.01123	2.05051	-2.20632	-1.07599
85	NM_008963	Ptgds	prostaglandin D2 synthase (brain)	up G21 & down PP7	0.02462	2.04987	-1.65761	1.23664
86	NM_173182	Fndc3b	fibronectin type III domain containing 3B	up G21 & down PP7	0.02357	2.04866	-1.87989	1.08978
87	NM_009252	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	up G21 & down PP7	0.00080	2.02468	-1.59811	1.26692
88	NM_153133	Rdh9	retinol dehydrogenase 9	up G21 & down PP7	0.01896	1.97806	-3.09008	-1.56218
89	NM_008491	Lcn2	lipocalin 2	up G21 & down PP7	0.28438	1.96715	-2.37391	-1.20678
90	NM_194336	Mpa2l	macrophage activation 2 like	up G21 & down PP7	0.09225	1.92768	-1.67737	1.14923
91	NM_029269	Spp2	secreted phosphoprotein 2	up G21 & down PP7	0.00110	1.91993	-1.61817	1.18648
92	NM_009014	Rad51l1	RAD51-like 1 (S. cerevisiae)	up G21 & down PP7	0.44521	1.91098	-1.63762	1.16692
93	NM_010559	Il6ra	interleukin 6 receptor, alpha	up G21 & down PP7	0.01501	1.85350	-2.01721	-1.08833
94	NM_020283	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	up G21 & down PP7	0.40889	1.79532	-1.66699	1.07698
95	NM_007930	Enc1	ectodermal-neural cortex 1	up G21 & down PP7	0.01250	1.79441	-1.97271	-1.09936
96	NM_007976	F5	coagulation factor V	up G21 & down PP7	0.01442	1.77481	-2.16489	-1.21978
97	NM_027147 /// XM_001473388 /// XM_001478385 /// XM_912979	Enho	energy homeostasis associated	up G21 & down PP7	0.00486	1.76593	-1.66080	1.0633
98	NR_033510 /// XM_001000061	1500017E21Rik	RIKEN cDNA 1500017E21 gene	up G21 & down PP7	0.20001	1.76134	-2.81523	-1.59834
99	NM_178111	Trp53inp2	transformation related protein 53 inducible nuclear protein 2	up G21 & down PP7	0.00728	1.75723	-1.98955	-1.13221
100	NM_001034851 /// NM_025459	Fam134b	family with sequence similarity 134, member B	up G21 & down PP7	0.03602	1.70980	-1.61888	1.05617
101	NM_001110505 /// NM_007446	Amy1	amylase 1, salivary	up G21 & down PP7	0.00408	1.68353	-1.51569	1.11073
102	NM_001166399 /// NM_009001	Rab3a	RAB3A, member RAS oncogene family	up G21 & down PP7	0.00194	1.67977	-1.68111	-1.0008
103	NM_025745	Erlec1	endoplasmic reticulum lectin 1	up G21 & down PP7	0.03408	1.66264	-1.80484	-1.08553
104	NM_010217	Ctgf	connective tissue growth factor	up G21 & down PP7	0.60125	1.63829	-1.65873	-1.01248

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105	NM_009754 /// NM_207680 /// NM_207681	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	up G21 & down PP7	0.03657	1.63708	-2.19813	-1.34271
106	NM_001159299 /// NM_018746	Itih4	inter alpha-trypsin inhibitor, heavy chain 4	up G21 & down PP7	0.00457	1.61601	-1.41561	1.14156
107	NM_027460	Slc25a33	solute carrier family 25, member 33	up G21 & down PP7	0.00332	1.59995	-2.70768	-1.69236
108	NM_001077184 /// NM_009768	Bsg	basigin	up G21 & down PP7	0.00323	1.59229	-1.51041	1.05421
109	NM_009243 /// NM_009244 /// NM_009245 /// NM_009246 /// NM_009247 /// XR_032407	LOC100046187 /// Serpina1a /// Serpina1b /// Serpina1c /// Serpina1d /// Serpina1e	similar to Alpha-1-antitrypsin 1-2 precursor (Serine protease inhibitor 1-2) (Al	up G21 & down PP7	0.00558	1.52777	-2.15334	-1.40947
110	NM_145594	Fgl1	fibrinogen-like protein 1	up G21 & down PP7	0.00090	1.51549	-1.47646	1.02643
111	NM_001166350 /// NM_199314	Serpina11	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antit	up G21 & down PP7	0.02369	1.50744	-2.12381	-1.40888
112	NM_001136069 /// NM_010699	Ldha	lactate dehydrogenase A	up G21 & down PP7	0.00375	1.43139	-1.42483	1.0046
113	NM_011707	Vtn	vitronectin	up G21 & down PP7	0.01048	1.39987	-1.51130	-1.0796
114	NM_009780	C4b	complement component 4B (Childo blood group)	up G21 & down PP7	0.02546	1.34978	-1.36072	-1.0081
115	NM_008407	Itih3	inter-alpha trypsin inhibitor, heavy chain 3	up G21 & down PP7	0.00676	1.32786	-1.47241	-1.10886
116	NM_010168	F2	coagulation factor II	up G21 & down PP7	0.00123	1.30022	-1.26214	1.03017
117	NM_027918	1300017J02Rik	RIKEN cDNA 1300017J02 gene	up G21 & down PP7	0.00021	1.27232	-1.30834	-1.02831
118	NM_017370	Hp	haptoglobin	up G21 & down PP7	0.02415	1.23552	-1.51509	-1.22628
119	NM_007686 /// XM_001478214	Cfi /// LOC100047470	complement component factor i /// similar to complement component factor i	up G21 & down PP7	0.00317	1.23494	-1.34630	-1.09017
120	NM_013465	Ahsg	alpha-2-HS-glycoprotein	up G21 & down PP7	0.00432	1.17124	-1.15545	1.01367

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
Genes that are updated at G21 or downregualted at PP7								
1	NM_007809	Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	up G21	0.00219	34.31100	-1.15121	29.8043
2	NM_008553	Ascl1	achaete-scute complex homolog 1 (Drosophila)	up G21	0.37963	7.08973	-1.33331	5.31737
3	NM_025696	Sorcs3	sortilin-related VPS10 domain containing receptor 3	up G21	0.12660	5.47537	-1.61730	3.3855
4	NM_178756	E130309F12Rik	RIKEN cDNA E130309F12 gene	up G21	0.00799	5.28544	-1.24634	4.24078
5	NM_177388	Slc41a2	solute carrier family 41, member 2	up G21	0.45403	4.37836	-1.36617	3.20484
6	NM_146260	Tmie	transmembrane inner ear	up G21	0.02064	4.15055	-1.48126	2.80205
7	NM_026637	Ggct	gamma-glutamyl cyclotransferase	up G21	0.02948	3.62265	-1.27787	2.83492
8	NM_021481	Treh	trehalase (brush-border membrane glycoprotein)	up G21	0.01070	3.43860	-1.90061	1.80921
9	NM_030693 /// NR_033136	Atf5	activating transcription factor 5	up G21	0.00270	3.42054	-1.33382	2.56446
10	NM_020577	As3mt	arsenic (+3 oxidation state) methyltransferase	up G21	0.02385	3.40189	-1.16070	2.93089
11	NM_177343	Camk1d	calcium/calmodulin-dependent protein kinase ID	up G21	0.00389	3.15692	1.76018	5.55674
12	NM_028270	Aldh1b1	aldehyde dehydrogenase 1 family, member B1	up G21	0.01700	2.90649	-1.34554	2.16008
13	NR_030738 /// XM_001479267 /// XM_001479728	2410006H16Rik	RIKEN cDNA 2410006H16 gene	up G21	0.01672	2.89543	-1.49321	1.93907
14	NM_001122736 /// NM_001122737 /// NM_010514	Igf2	insulin-like growth factor 2	up G21	0.04610	2.87389	-1.37557	2.08923
15	NM_153533	Tenc1	tensin like C1 domain-containing phosphatase	up G21	0.00013	2.84365	-1.15650	2.45884
16	NM_010368	Gusb	glucuronidase, beta	up G21	0.00748	2.78226	-1.32801	2.09506
17	NM_008655	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	up G21	0.12977	2.77714	-1.56250	1.77736
18	NM_019806	Vapb	vesicle-associated membrane protein, associated protein B and C	up G21	0.00007	2.76114	1.06677	2.94551
19	NM_007874	Reep5	receptor accessory protein 5	up G21	0.00049	2.74098	-1.05404	2.60046
20	NM_145434	Nr1d1	nuclear receptor subfamily 1, group D, member 1	up G21	0.05001	2.68653	-1.01826	2.63836
21	NM_009622	Adcy1	adenylate cyclase 1	up G21	0.00116	2.68446	-1.06091	2.53034
22	NM_001163028 /// NM_021486	Bcmo1	beta-carotene 15,15'-monooxygenase	up G21	0.01544	2.67299	-1.33237	2.00619

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
23	NM_019698 /// NM_153554	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	up G21	0.10631	2.67263	1.93570	5.17342
24	NM_183023	Rims4	regulating synaptic membrane exocytosis 4	up G21	0.06372	2.64593	1.76411	4.66771
25	NM_029942	Prelid2	PRELI domain containing 2	up G21	0.02593	2.64219	1.34153	3.54459
26	NM_029083	Ddit4	DNA-damage-inducible transcript 4	up G21	0.01590	2.62464	1.12220	2.94538
27	NM_011405	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	up G21	0.05861	2.62404	-1.60261	1.63735
28	NM_009469	Ulk1	Unc-51 like kinase 1 (C. elegans)	up G21	0.00408	2.62112	-1.51108	1.7346
29	NM_022325	Ctsz	cathepsin Z	up G21	0.00037	2.62061	-1.39030	1.88492
30	NM_007634	Ccnf	cyclin F	up G21	0.19855	2.55412	-1.05257	2.42656
31	NM_010299	Gm2a	GM2 ganglioside activator protein	up G21	0.00025	2.54886	-1.09916	2.31892
32	NM_145482	Setd4	SET domain containing 4	up G21	0.01988	2.51912	1.26582	3.18876
33	NM_013769	Tjp3	tight junction protein 3	up G21	0.01507	2.50233	2.06742	5.17338
34	NM_016966 /// XR_030810 /// XR_030923 /// XR_031967 /// XR_032429 /// XR_034648	Gm7669 /// Gm7901 /// Gm9347 /// Phgdh	3-phosphoglycerate dehydrogenase pseudogene /// 3-phosphoglycerate dehydrogenase	up G21	0.09869	2.49378	-1.69947	1.46738
35	NM_029413	Morc4	microrchidia 4	up G21	0.03695	2.48710	-1.17663	2.11375
36	NM_009205	Slc3a1	solute carrier family 3, member 1	up G21	0.00931	2.48500	1.04684	2.60139
37	NM_001037221 /// NM_001163433 /// NM_028966	Samd4	sterile alpha motif domain containing 4	up G21	0.00240	2.47160	-1.35118	1.82921
38	NM_007418	Adra2c	adrenergic receptor, alpha 2c	up G21	0.07824	2.46875	-1.72553	1.43072
39	NM_144855 /// NM_178224	Cbs	cystathionine beta-synthase	up G21	0.00933	2.45893	1.18839	2.92218
40	NM_133214	BC017612	cDNA sequence BC017612	up G21	0.06049	2.44607	-1.26590	1.93228
41	NM_010421	Hexa	hexosaminidase A	up G21	0.00464	2.43783	-1.36389	1.78741
42	NR_001463 /// NR_001570	Xist	inactive X specific transcripts	up G21	0.02508	2.40332	1.14853	2.76029
43	NM_001130184 /// NM_001130185 /// NM_001130186 /// NM_172303	Phf17	PHD finger protein 17	up G21	0.00417	2.38687	1.08975	2.6011
44	NM_024169	Fkbp11	FK506 binding protein 11	up G21	0.12502	2.37856	-1.37966	1.72402
45	NM_011415	Snai2	snail homolog 2 (Drosophila)	up G21	0.06160	2.36659	-1.33350	1.77471

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
46	NM_010359	Gstm3	glutathione S-transferase, mu 3	up G21	0.00306	2.35131	1.77158	4.16553
47	NM_026947	1810022C23Rik	RIKEN cDNA 1810022C23 gene	up G21	0.00186	2.34569	3.01165	7.06441
48	NM_001139511 /// NM_001139512 /// NM_001139513 /// NM_023130	Raly	hnRNP-associated with lethal yellow	up G21	0.00330	2.33438	1.14290	2.66796
49	NM_172442	Dtx4	deltex 4 homolog (Drosophila)	up G21	0.02195	2.33039	-1.12260	2.07588
50	NM_009434	Phlda2	pleckstrin homology-like domain, family A, member 2	up G21	0.02810	2.32677	-1.11575	2.08537
51	NM_001033178 /// NM_001045538 /// NR_028305 /// NR_028306 /// NR_033520 /// XR_0	Tmem181a /// Tmem181b /// Tmem181c-ps /// Tmem181d-ps	transmembrane protein 181A /// transmembrane protein 181B /// transmembrane prot	up G21	0.01751	2.31343	-1.18707	1.94886
52	NM_144893	Slc35c2	solute carrier family 35, member C2	up G21	0.00430	2.30759	1.01229	2.33596
53	NM_009731	Akr1b7	aldo-keto reductase family 1, member B7	up G21	0.01097	2.29611	2.30690	5.29689
54	NM_183257	Hamp2	hepcidin antimicrobial peptide 2	up G21	0.01084	2.28888	-1.13791	2.01147
55	NM_029310	Fabp12	fatty acid binding protein 12	up G21	0.00199	2.28327	1.60160	3.65689
56	NM_029021	4833422F24Rik	RIKEN cDNA 4833422F24 gene	up G21	0.00117	2.27708	-1.62093	1.4048
57	NM_172301	Ccnb1	cyclin B1	up G21	0.14712	2.27617	2.47508	5.63371
58	NM_001039509 /// NM_019999 /// NM_025580	Pnkd	paroxysmal nonkinesiogenic dyskinesia	up G21	0.11143	2.27035	1.22223	2.7749
59	NM_144795	Pycr1	pyrroline-5-carboxylate reductase 1	up G21	0.07057	2.26069	-1.63020	1.38675
60	NM_001001179	BC048546	cDNA sequence BC048546	up G21	0.01015	2.24105	-1.26455	1.77221
61	NM_177855 /// XM_887994	Med12l	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	up G21	0.00798	2.23595	-1.20267	1.85915
62	NM_013476	Ar	androgen receptor	up G21	0.00960	2.23455	1.54817	3.45947
63	NM_016974	Dbp	D site albumin promoter binding protein	up G21	0.25884	2.22934	-1.16722	1.90996
64	NM_001142968 /// XR_035100 /// XR_035103	BC024139	cDNA sequence BC024139	up G21	0.01430	2.21896	-1.39086	1.59539
65	NM_011708	Vwf	Von Willebrand factor homolog	up G21	0.28282	2.21303	-1.60086	1.3824
66	NM_026501 /// NM_028933	Fam134c	family with sequence similarity 134, member C	up G21	0.01316	2.20685	-1.29460	1.70466

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
67	NM_001162492 /// NM_001162493 /// NM_138670	Mpst	mercaptopyruvate sulfurtransferase	up G21	0.00264	2.20389	1.31178	2.89103
68	NM_001038492 /// NM_008906	Ctsa	cathepsin A	up G21	0.00400	2.20202	-1.36174	1.61706
69	NM_175687	A230050P20Rik	RIKEN cDNA A230050P20 gene	up G21	0.00401	2.20070	1.07904	2.37465
70	NM_007630	Ccnb2	cyclin B2	up G21	0.12097	2.19798	3.63989	8.00039
71	NM_030187 /// XM_911194 /// XM_994344	Ak7	adenylate kinase 7	up G21	0.04714	2.19468	-1.05200	2.08621
72	NM_146093	Ubxn1	UBX domain protein 1	up G21	0.02851	2.18945	-1.13681	1.92596
73	NM_177900	Hapln4	hyaluronan and proteoglycan link protein 4	up G21	0.10389	2.18821	1.05681	2.31251
74	NM_001081196 /// XM_001477687	Hnrnpul2	heterogeneous nuclear ribonucleoprotein U-like 2	up G21	0.00128	2.18760	1.12406	2.45899
75	NM_029809	2310014L17Rik	RIKEN cDNA 2310014L17 gene	up G21	0.00030	2.18614	-1.42014	1.53938
76	NM_053014	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	up G21	0.00045	2.18573	-1.12832	1.93716
77	NM_001081212	Irs2	insulin receptor substrate 2	up G21	0.06887	2.18144	-1.09428	1.99349
78	NM_001039655 /// NM_011245	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	up G21	0.05917	2.16895	-1.28690	1.6854
79	NM_181748	Gpr120	G protein-coupled receptor 120	up G21	0.00271	2.16299	-1.39695	1.54837
80	NM_134188	Acot2	acyl-CoA thioesterase 2	up G21	0.12962	2.16181	-1.32086	1.63666
81	NM_009331	Tcf7	transcription factor 7, T-cell specific	up G21	0.00901	2.15566	-1.10324	1.95393
82	NM_026959	Stx18	syntaxin 18	up G21	0.25839	2.14405	-1.25599	1.70706
83	NM_133779	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	up G21	0.02190	2.14321	1.10662	2.37172
84	NM_016966 /// XR_001608 /// XR_001935 /// XR_030502 /// XR_030672 /// XR_030810	Gm13337 /// Gm5847 /// Gm6756 /// Gm7669 /// Gm7901 /// Gm8341 /// Gm9210 /// Gm9347 /// LOC630896 /// Phgdh	3-phosphoglycerate dehydrogenase pseudogene /// 3-phosphoglycerate dehydrogenase	up G21	0.17286	2.12909	-1.78443	1.19315
85	NM_008509	Lpl	lipoprotein lipase	up G21	0.01919	2.12785	1.10837	2.35845
86	NM_133191	Eps8l2	EPS8-like 2	up G21	0.10031	2.12409	1.04302	2.21547

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87	NM_178661	Creb3l2	cAMP responsive element binding protein 3-like 2	up G21	0.18516	2.12212	-1.01489	2.09098
88	NM_024223	Crip2	cysteine rich protein 2	up G21	0.00966	2.10320	-1.00331	2.09625
89	NM_133979	Ano10	anoctamin 10	up G21	0.00533	2.10016	-1.27184	1.65128
90	NM_001161746 /// NM_013749	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	up G21	0.07555	2.09746	-1.15762	1.81187
91	NM_029609	Lhpp	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	up G21	0.04597	2.09697	-1.24277	1.68734
92	NM_021319	Pglyrp2	peptidoglycan recognition protein 2	up G21	0.00305	2.09666	-1.11643	1.87801
93	NM_008416	Junb	Jun-B oncogene	up G21	0.19129	2.08824	-1.55102	1.34637
94	NM_178924	Upk1b	uroplakin 1B	up G21	0.12215	2.08510	-1.48126	1.40766
95	NM_001161667 /// NM_053115	Acox2	acyl-Coenzyme A oxidase 2, branched chain	up G21	0.02188	2.08360	-1.49454	1.39414
96	NM_001081756 /// NM_172484 /// NM_176957	Nckap5	NCK-associated protein 5	up G21	0.09429	2.07546	1.14321	2.37268
97	NM_145447	Mfsd7c	major facilitator superfamily domain containing 7C	up G21	0.21157	2.06855	-1.34216	1.54121
98	NM_145564	Fbxo21	F-box protein 21	up G21	0.02687	2.06051	-1.30761	1.57579
99	NM_010687	Large	like-glycosyltransferase	up G21	0.00358	2.05313	-1.26513	1.62286
100	NM_025563	2010012O05Rik	RIKEN cDNA 2010012O05 gene	up G21	0.00297	2.04939	-1.04852	1.95455
101	NM_010422	Hexb	hexosaminidase B	up G21	0.01573	2.04766	-1.18079	1.73415
102	NR_030703	Snord104	small nucleolar RNA, C/D box 104	up G21	0.02791	2.04349	-1.46803	1.392
103	NM_025662 /// NM_178016	Pigk	phosphatidylinositol glycan anchor biosynthesis, class K	up G21	0.00158	2.04241	1.05450	2.15372
104	NM_010012	Cyp8b1	cytochrome P450, family 8, subfamily b, polypeptide 1	up G21	0.01404	2.03097	1.35499	2.75196
105	NM_019447	Hgfac	hepatocyte growth factor activator	up G21	0.00280	2.03002	-1.20248	1.68819
106	NM_001025613 /// NM_001025614	Otud7b	OTU domain containing 7B	up G21	0.00473	2.02824	1.10718	2.24562
107	NM_010198	Fgf11	fibroblast growth factor 11	up G21	0.33070	2.02673	-1.75364	1.15573
108	NM_009698	Aprt	adenine phosphoribosyl transferase	up G21	0.12120	2.01681	-1.21857	1.65506
109	NM_025638	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	up G21	0.00459	2.01572	-1.13703	1.7728
110	NM_001039701 /// NM_001159562 /// NM_031167	Il1rn	interleukin 1 receptor antagonist	up G21	0.23924	2.01343	-1.91438	1.05174

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
111	NM_001081213	Ermp1	endoplasmic reticulum metallopeptidase 1	up G21	0.03548	2.01229	-1.65669	1.21464
112	NM_175093	Trib3	tribbles homolog 3 (Drosophila)	up G21	0.26904	1.99986	-1.39706	1.43148
113	NM_133974	Cdcp1	CUB domain containing protein 1	up G21	0.06060	1.99475	-1.15527	1.72664
114	NM_153782	Fam20a	family with sequence similarity 20, member A	up G21	0.00331	1.99167	-1.13348	1.75712
115	NM_010271	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	up G21	0.00288	1.99079	1.02092	2.03244
116	NM_053195	Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	up G21	0.12727	1.98960	-1.63757	1.21497
117	NM_145384	Pqlc2	PQ loop repeat containing 2	up G21	0.01618	1.98356	-1.37834	1.43909
118	NM_001177833 /// NM_001177834 /// NM_001177835 /// NM_001177836 /// NM_001177837	Smox	spermine oxidase	up G21	0.08675	1.98237	-1.31404	1.50861
119	NM_018887	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	up G21	0.00529	1.97605	1.54703	3.057
120	NM_172702	Serinc2	serine incorporator 2	up G21	0.08231	1.97517	-1.05132	1.87876
121	NM_177380	Cyp3a44	cytochrome P450, family 3, subfamily a, polypeptide 44	up G21	0.00018	1.97401	1.18540	2.33999
122	NM_001080940	Gm6484	predicted gene 6484	up G21	0.26611	1.97367	1.21712	2.4022
123	NM_001163704 /// NM_001163705 /// NM_001163706 /// NM_001163707 /// NM_015797	Fbxo6	F-box protein 6	up G21	0.04972	1.97294	-1.37983	1.42984
124	NM_013731	Sgk2	serum/glucocorticoid regulated kinase 2	up G21	0.01661	1.97111	1.83175	3.61058
125	NM_001163440 /// NM_001163441 /// NM_008619	Mov10	Moloney leukemia virus 10	up G21	0.00077	1.97024	-1.09507	1.79919
126	NM_018861	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	up G21	0.00313	1.96254	-1.12785	1.74007
127	NM_001159324 /// NM_008064	Gaa	glucosidase, alpha, acid	up G21	0.01154	1.95792	1.05040	2.0566
128	NM_001035854 /// NM_027915	Ap2b1	adaptor-related protein complex 2, beta 1 subunit	up G21	0.00094	1.95476	1.15562	2.25896
129	NM_001166177 /// NM_028710	Arsg	arylsulfatase G	up G21	0.08032	1.95421	-1.30422	1.49838
130	NM_008608	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	up G21	0.00889	1.95081	-1.17779	1.65633

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
131	NM_001081454 /// NM_011046	Furin	furin (paired basic amino acid cleaving enzyme)	up G21	0.01460	1.94845	-1.41774	1.37433
132	NM_019578	Extl1	exostoses (multiple)-like 1	up G21	0.02346	1.94829	-1.24380	1.5664
133	NM_001042674 /// NM_001042675 /// NM_019733	Rbpms	RNA binding protein gene with multiple splicing	up G21	0.02239	1.94166	-1.40532	1.38164
134	NM_001110162 /// NM_175384	Cdca2	cell division cycle associated 2	up G21	0.07835	1.93883	-1.08959	1.77941
135	NM_028733 /// NM_030880	Pacsin3	protein kinase C and casein kinase substrate in neurons 3	up G21	0.00425	1.93856	-1.23324	1.57192
136	NM_008638	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofola	up G21	0.15148	1.93172	-2.02939	-1.05056
137	NM_008486	Anpep	alanyl (membrane) aminopeptidase	up G21	0.01147	1.92961	-1.52522	1.26513
138	NM_009539	Zap70	zeta-chain (TCR) associated protein kinase	up G21	0.04931	1.92796	-1.40298	1.37419
139	NM_011832	Insrr	insulin receptor-related receptor	up G21	0.09336	1.92739	-2.04082	-1.05885
140	NM_001114339 /// NM_023792	Pank1	pantothenate kinase 1	up G21	0.17114	1.92736	-1.71474	1.124
141	NM_146125	Itpka	inositol 1,4,5-trisphosphate 3-kinase A	up G21	0.00412	1.91875	1.02917	1.97472
142	NM_001177576 /// NM_026646	Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	up G21	0.02690	1.91627	-1.02025	1.87824
143	NM_001033178 /// NM_001045538 /// NR_033520	Tmem181a /// Tmem181b	transmembrane protein 181A /// transmembrane protein 181B	up G21	0.04596	1.91057	-1.07597	1.77567
144	NM_172785	Zc3h12d	zinc finger CCCH type containing 12D	up G21	0.10786	1.90660	-1.52751	1.24818
145	NM_213729	Inca1	inhibitor of CDK, cyclin A1 interacting protein 1	up G21	0.03173	1.90540	-1.21562	1.56744
146	NM_172884	2900026A02Rik	RIKEN cDNA 2900026A02 gene	up G21	0.02029	1.90373	1.11259	2.11808
147	NM_012052	Rps3	ribosomal protein S3	up G21	0.12050	1.90279	-1.95418	-1.02701
148	NM_026609	Leprotl1	leptin receptor overlapping transcript-like 1	up G21	0.02877	1.89780	-1.28397	1.47807
149	NM_011565	Tead2	TEA domain family member 2	up G21	0.00061	1.89426	-1.43175	1.32304
150	NM_153136	Nudt18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	up G21	0.01635	1.89294	-1.24059	1.52584
151	NM_145449	Ifi27l2b	interferon, alpha-inducible protein 27 like 2B	up G21	0.00451	1.89207	-1.29179	1.46469
152	NM_133994	Gstt3	glutathione S-transferase, theta 3	up G21	0.03217	1.89028	1.00609	1.9018
153	NM_001043228 /// NM_009345	Dntt	deoxynucleotidyltransferase, terminal	up G21	0.01076	1.88888	2.26456	4.27749

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
154	NR_002853 /// NR_027772 /// NR_027773 /// NR_027784	Airn	antisense Igf2r RNA	up G21	0.04034	1.88654	1.12681	2.12577
155	NM_146190	Tubgcp5	Tubulin, gamma complex associated protein 5	up G21	0.18723	1.88130	-1.61204	1.16703
156	NM_009180	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	up G21	0.04812	1.88033	-1.44717	1.29931
157	NM_009932	Col4a2	collagen, type IV, alpha 2	up G21	0.01327	1.87561	-1.53372	1.22292
158	NM_146173	Tspan33	tetraspanin 33	up G21	0.11177	1.87476	-1.24296	1.50831
159	NM_019781	Pex14	peroxisomal biogenesis factor 14	up G21	0.00255	1.87219	-1.26271	1.48268
160	NM_172397	Limd2	LIM domain containing 2	up G21	0.02630	1.87215	1.12129	2.09922
161	NM_001166406 /// NM_001166407 /// NM_009004	Kif20a	kinesin family member 20A	up G21	0.14704	1.86994	2.26109	4.22809
162	NM_145940	Wipi1	WD repeat domain, phosphoinositide interacting 1	up G21	0.00945	1.86928	-1.05130	1.77805
163	NM_173371	H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	up G21	0.00111	1.86562	-1.32540	1.40759
164	NM_001081349 /// NM_001083809 /// NM_024497	Slc43a1	solute carrier family 43, member 1	up G21	0.23686	1.86519	-1.50298	1.24099
165	NM_172404	Ccbl1	cysteine conjugate-beta lyase 1	up G21	0.03311	1.86255	-1.06734	1.74504
166	NM_023627	Isyna1	myo-inositol 1-phosphate synthase A1	up G21	0.00721	1.86145	1.17200	2.18162
167	NM_001003955 /// NM_177466	Rab11fip5	RAB11 family interacting protein 5 (class I)	up G21	0.04668	1.86004	-1.08294	1.71758
168	NM_030706	Trim2	tripartite motif-containing 2	up G21	0.02128	1.85941	1.37228	2.55164
169	NM_025833	Baiap2l1	BAI1-associated protein 2-like 1	up G21	0.00634	1.85034	-1.31859	1.40327
170	NM_020009	Mtor	mechanistic target of rapamycin (serine/threonine kinase)	up G21	0.00918	1.85014	-1.18144	1.56601
171	NM_008140	Gnat1	guanine nucleotide binding protein, alpha transducing 1	up G21	0.11870	1.84778	-1.00376	1.84086
172	NM_145516	Plekhb2	pleckstrin homology domain containing, family B (evectins) member 2	up G21	0.03427	1.84765	-1.74755	1.05728
173	NM_011163	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	up G21	0.00460	1.84711	1.50816	2.78575
174	NM_001177713 /// NM_175475	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	up G21	0.16824	1.84596	2.20623	4.07261
175	NM_011803	Klf6	Kruppel-like factor 6	up G21	0.01916	1.84330	-1.28447	1.43506

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
176	NM_001025566 /// NM_013490	Chka	choline kinase alpha	up G21	0.16147	1.84168	1.33092	2.45113
177	NM_007623	Cbx2	chromobox homolog 2 (Drosophila Pc class)	up G21	0.00056	1.84155	-1.27220	1.44753
178	NM_001081420	BC026590	cDNA sequence BC026590	up G21	0.00722	1.83765	-1.39177	1.32037
179	NM_013541	Gstp1	glutathione S-transferase, pi 1	up G21	0.00064	1.83750	-1.04211	1.76325
180	NM_033314	Slco2a1	solute carrier organic anion transporter family, member 2a1	up G21	0.01163	1.83496	1.12202	2.05887
181	NM_020027	Bat2	HLA-B associated transcript 2	up G21	0.00085	1.83181	1.38315	2.53367
182	NM_009931	Col4a1	collagen, type IV, alpha 1	up G21	0.00469	1.83035	-1.59097	1.15046
183	NM_029787	Cyb5r3	cytochrome b5 reductase 3	up G21	0.00721	1.82998	-1.08488	1.6868
184	NM_025735	Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	up G21	0.00025	1.82820	-1.01881	1.79446
185	NM_019699	Fads2	fatty acid desaturase 2	up G21	0.01319	1.82497	-1.50357	1.21376
186	NM_026878	Rasl11b	RAS-like, family 11, member B	up G21	0.04136	1.81840	-1.31167	1.38632
187	NM_010011 /// NM_201640 /// XM_001475399	Cyp4a10 /// Cyp4a31	cytochrome P450, family 4, subfamily a, polypeptide 10 /// cytochrome P450, fami	up G21	0.14430	1.81232	1.02387	1.85559
188	NM_133962	Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	up G21	0.00606	1.81037	-1.58656	1.14107
189	NM_001012402	Hs3st6	heparan sulfate (glucosamine) 3-O-sulfotransferase 6	up G21	0.04775	1.80567	-1.16961	1.54383
190	NM_144919	Hdac11	histone deacetylase 11	up G21	0.03468	1.80231	-1.03483	1.74165
191	NM_010799	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	up G21	0.03305	1.80215	-1.32662	1.35845
192	NM_011318	Apcs	serum amyloid P-component	up G21	0.00151	1.80120	-1.12212	1.60518
193	NM_001164036 /// NM_001164037 /// NM_001164038 /// NM_001164039 /// NM_001164040	Ly6e	lymphocyte antigen 6 complex, locus E	up G21	0.00550	1.80045	-1.02582	1.75514
194	NM_029357	Pcdh1	protocadherin 1	up G21	0.12880	1.79988	-1.10082	1.63503
195	NR_027828 /// XM_001480596 /// XM_919114	Ncrna00081	non-protein coding RNA 81	up G21	0.03901	1.79914	-1.08414	1.65951
196	NM_172580	Acot6	acyl-CoA thioesterase 6	up G21	0.03405	1.79868	1.09022	1.96095
197	NM_011851	Nt5e	5' nucleotidase, ecto	up G21	0.03963	1.79854	-1.13056	1.59083
198	NM_010956 /// XM_001478677	Ogdh	oxoglutarate dehydrogenase (lipoamide)	up G21	0.03867	1.79606	-1.00901	1.78003
199	NM_010442	Hmox1	heme oxygenase (decycling) 1	up G21	0.00644	1.79490	-1.01370	1.77064

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200	NM_001130458 /// NM_001130459 /// NM_015749	Tcn2	transcobalamin 2	up G21	0.01533	1.79278	-1.17862	1.52108
201	NM_016722	Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	up G21	0.00362	1.78982	-1.03121	1.73565
202	XM_001476664 /// XM_001476679 /// XM_001476703	2010205A11Rik /// Gm10883 /// Gm1420 /// Gm7202 /// Igk /// Igk-C /// Igk-J1 /// Igk-V28 /// LOC100047628	RIKEN cDNA 2010205A11 gene /// predicted gene 10883 /// predicted gene 1420 ///	up G21	0.04751	1.78693	1.22345	2.18622
203	XM_001476664 /// XM_001476679 /// XM_001476703	Gm10883 /// Gm1420 /// Gm7202 /// Igk /// Igk-C /// Igk-J1 /// Igk-V28 /// LOC100047628	predicted gene 10883 /// predicted gene 1420 /// predicted gene 7202 /// immunog	up G21	0.04751	1.78693	1.22345	2.18622
204	NM_010736	Ltbr	lymphotoxin B receptor	up G21	0.00179	1.78613	-1.15847	1.5418
205	NM_001168469 /// NM_145578	Ube2m	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	up G21	0.02602	1.78492	-1.32202	1.35015
206	NM_011319	Sars	seryl-aminoacyl-tRNA synthetase	up G21	0.00381	1.77995	-1.23642	1.43961
207	NM_138595	Gldc	glycine decarboxylase	up G21	0.03021	1.77953	-1.04945	1.69568
208	NR_003368	Pvt1	plasmacytoma variant translocation 1	up G21	0.00686	1.77929	1.64016	2.91832
209	NM_146073	Zdhhc14	zinc finger, DHHC domain containing 14	up G21	0.52474	1.77906	-1.41514	1.25715
210	NM_053090	Fam126a	family with sequence similarity 126, member A	up G21	0.01542	1.77783	1.15601	2.05518
211	NM_007760	Crat	carnitine acetyltransferase	up G21	0.02694	1.77302	-1.13534	1.56167
212	NM_133664	Lad1	ladinin	up G21	0.03909	1.77164	1.25939	2.23119
213	NM_001145937 /// NM_011857	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	up G21	0.04563	1.77069	-1.32869	1.33266
214	NM_001146217 /// NM_022316	Smoc1	SPARC related modular calcium binding 1	up G21	0.00033	1.77059	1.05798	1.87325
215	NM_008621	Mpp1	membrane protein, palmitoylated	up G21	0.00440	1.77047	-1.29439	1.3678
216	NM_021567	Pcbp4	poly(rC) binding protein 4	up G21	0.03416	1.76655	1.04967	1.85429

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
217	NM_144847	Nrbp2	nuclear receptor binding protein 2	up G21	0.02331	1.76473	-1.53987	1.14602
218	NM_007493	Asgr2	asialoglycoprotein receptor 2	up G21	0.06124	1.76397	-1.44732	1.21879
219	NM_198411	Inf2	inverted formin, FH2 and WH2 domain containing	up G21	0.07664	1.76186	-1.01084	1.74297
220	NM_008046	Fst	follistatin	up G21	0.32576	1.76124	1.04342	1.83771
221	NM_001161774 /// NM_009176	St3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	up G21	0.01670	1.76119	-1.24314	1.41673
222	NM_175478	Lrfn3	leucine rich repeat and fibronectin type III domain containing 3	up G21	0.13265	1.75705	-1.20550	1.45753
223	NM_008467	9630025H16Rik /// Kpna4	RIKEN cDNA 9630025H16 gene /// karyopherin (importin) alpha 4	up G21	0.00082	1.75265	-1.14851	1.52602
224	NM_030251	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	up G21	0.00075	1.75143	-1.20666	1.45146
225	NM_008723 /// NR_002702 /// XM_916150	LOC639633 /// Npm3 /// Npm3-ps1	similar to Nucleoplasmin-3 /// nucleoplasmin 3 /// nucleoplasmin 3, pseudogene 1	up G21	0.05296	1.74749	1.40415	2.45374
226	NM_001042592 /// NM_025549	Arrdc4	arrestin domain containing 4	up G21	0.11673	1.74568	-1.09867	1.58891
227	NM_001002011 /// NM_001111102 /// NM_019390	Lmna	lamin A	up G21	0.01111	1.74399	1.61426	2.81525
228	NM_012032	Serinc3	serine incorporator 3	up G21	0.00057	1.74282	-1.30090	1.3397
229	NM_008538	Marcks	myristoylated alanine rich protein kinase C substrate	up G21	0.20359	1.73997	1.12105	1.9506
230	NM_001136066 /// NM_010443	Hmox2	heme oxygenase (decycling) 2	up G21	0.00212	1.73766	-1.42802	1.21684
231	NM_019972	Sort1	sortilin 1	up G21	0.00242	1.73702	-1.42848	1.21599
232	NM_172752	Sorbs2	sorbin and SH3 domain containing 2	up G21	0.02682	1.73628	-1.16406	1.49157
233	NM_001130529 /// NM_172941	Zkscan17	zinc finger with KRAB and SCAN domains 17	up G21	0.03746	1.73403	-1.23263	1.40678
234	NM_001081205	Nipal1	NIPA-like domain containing 1	up G21	0.08931	1.73087	-1.14343	1.51375
235	NM_153081	Slc16a11	solute carrier family 16 (monocarboxylic acid transporters), member 11	up G21	0.00137	1.73007	-1.21200	1.42745
236	NM_001163689 /// NM_025802 /// NR_028142	Pnpla2	patatin-like phospholipase domain containing 2	up G21	0.00116	1.72841	-1.18364	1.46025
237	NM_153069	Leap2	liver-expressed antimicrobial peptide 2	up G21	0.01929	1.72801	1.02624	1.77336
238	NM_139149	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	up G21	0.04608	1.72383	-1.30770	1.31821

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239	NM_145575	Cald1	caldesmon 1	up G21	0.02877	1.72236	-1.21374	1.41905
240	NM_020586	Herpud2	HERPUD family member 2	up G21	0.00659	1.72177	-1.65922	1.03769
241	NM_026364 /// XM_001481297 /// XM_181343	Prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1	up G21	0.02788	1.72118	-1.05471	1.6319
242	NM_001024945 /// NM_023268	Qsox1	quiescin Q6 sulfhydryl oxidase 1	up G21	0.01305	1.72059	-1.01955	1.68759
243	NM_001161823 /// NM_172382	Kdm4a	lysine (K)-specific demethylase 4A	up G21	0.01198	1.71814	-1.03691	1.65699
244	NM_027985	Mad2l2	MAD2 mitotic arrest deficient-like 2 (yeast)	up G21	0.31659	1.71806	1.04225	1.79065
245	NM_011327	Scp2	Sterol carrier protein 2, liver	up G21	0.00644	1.71734	-1.07880	1.5919
246	NM_001033929 /// NM_178413	Thnsl2	threonine synthase-like 2 (bacterial)	up G21	0.00733	1.71444	1.32227	2.26695
247	NM_198001	1110008P14Rik	RIKEN cDNA 1110008P14 gene	up G21	0.01747	1.71180	-1.19458	1.43297
248	NM_001034962 /// NM_001034963 /// NM_001034964 /// NM_009166 /// NM_178362	Sorbs1	sorbin and SH3 domain containing 1	up G21	0.01938	1.71110	-1.23213	1.38873
249	NM_028043	D1Bwg0212e	DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed	up G21	0.00214	1.70933	1.18179	2.02008
250	NM_001081005	1500012F01Rik	RIKEN cDNA 1500012F01 gene	up G21	0.05729	1.70917	-1.34886	1.26712
251	NM_001102404 /// NM_001102405 /// NM_007388	Acp5	acid phosphatase 5, tartrate resistant	up G21	0.00804	1.70542	-1.37796	1.23764
252	NM_025613	Eid1	EP300 interacting inhibitor of differentiation 1	up G21	0.09077	1.70525	-1.31283	1.29891
253	XM_001001707 /// XM_001479244	D630033O11Rik	RIKEN cDNA D630033O11 gene	up G21	0.06467	1.70480	-1.12532	1.51495
254	NM_001025427 /// NM_001039356 /// NM_001166476 /// NM_001166477 /// NM_001166535	Hmga1 /// Hmga1-rs1	high mobility group AT-hook 1 /// high mobility group AT-hook I, related sequenc	up G21	0.00113	1.70296	-1.15062	1.48004
255	NM_015786	Hist1h1c	histone cluster 1, H1c	up G21	0.11810	1.70235	-1.18448	1.43722
256	NM_001146049 /// NM_001146050 /// NM_001146052 /// NM_001146053 /// NM_016865	Htatip2	HIV-1 tat interactive protein 2, homolog (human)	up G21	0.00165	1.70162	1.38305	2.35343

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257	NM_008562 /// XR_031152	Mcl1	myeloid cell leukemia sequence 1	up G21	0.00180	1.69806	-1.11378	1.5246
258	NM_144839	Ube2e2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	up G21	0.01759	1.69710	-1.26228	1.34447
259	NM_017462	Polg	polymerase (DNA directed), gamma	up G21	0.01116	1.69706	-1.09194	1.55417
260	NM_007468	Apoa4	apolipoprotein A-IV	up G21	0.05130	1.69511	-1.17769	1.43935
261	NM_153112	Cadm4	cell adhesion molecule 4	up G21	0.15114	1.69408	-1.35340	1.25172
262	NM_007837	Ddit3	DNA-damage inducible transcript 3	up G21	0.05214	1.69067	-1.18012	1.43263
263	NM_001146120 /// NM_001146121 /// NM_001146122 /// NM_001146123 /// NM_001146124	Psap	prosaposin	up G21	0.02413	1.69054	-1.01799	1.66067
264	NM_001081400 /// XM_001480138 /// XM_907664	1810013L24Rik	RIKEN cDNA 1810013L24 gene	up G21	0.00253	1.69045	-1.18632	1.42495
265	NM_008194 /// NM_212444	Gyk	glycerol kinase	up G21	0.06429	1.68598	-1.75029	-1.03815
266	NM_001164197 /// NM_021412	Mmp19	matrix metallopeptidase 19	up G21	0.00025	1.67841	1.34888	2.26397
267	NM_133900	Psph	phosphoserine phosphatase	up G21	0.08524	1.67824	-1.20710	1.39031
268	NM_011149	Ppib	peptidylprolyl isomerase B	up G21	0.02960	1.67740	-1.35448	1.23841
269	NM_138950 /// XM_001002633 /// XM_911699	Wdr81	WD repeat domain 81	up G21	0.06250	1.67717	-1.10359	1.51974
270	NM_030703	Cpn1	carboxypeptidase N, polypeptide 1	up G21	0.00163	1.67426	-1.18531	1.41251
271	NM_001040398	Setd1b	SET domain containing 1B	up G21	0.00492	1.67404	1.09971	1.84095
272	NM_001127355 /// NM_001127356 /// NM_010122	Eif2b4	eukaryotic translation initiation factor 2B, subunit 4 delta	up G21	0.20049	1.67346	-1.04102	1.60752
273	NM_173744	2610019F03Rik	RIKEN cDNA 2610019F03 gene	up G21	0.19742	1.67185	-1.44725	1.15519
274	NM_026791	Fbxw9	F-box and WD-40 domain protein 9	up G21	0.01343	1.67144	-1.42450	1.17335
275	NM_008878	Serpinf2	serine (or cysteine) peptidase inhibitor, clade F, member 2	up G21	0.00939	1.66751	-1.24715	1.33705
276	NM_010664	Krt18	keratin 18	up G21	0.00801	1.66749	-1.07779	1.54714
277	NM_194342	Sun2	Sad1 and UNC84 domain containing 2	up G21	0.05305	1.66498	-1.54914	1.07477
278	NM_001081292	Map3k10	mitogen-activated protein kinase kinase kinase 10	up G21	0.00513	1.66253	1.09921	1.82747

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
279	NM_001163540 /// NM_001163542 /// NM_001163549 /// NM_001164203 /// NM_011117 //	Plec	plectin	up G21	0.04961	1.66206	1.12953	1.87735
280	NM_134129	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	up G21	0.00347	1.65984	1.09799	1.82248
281	NM_026211	Tmed9	transmembrane emp24 protein transport domain containing 9	up G21	0.01836	1.65934	1.25633	2.08468
282	NM_001008550	Zfyve26	zinc finger, FYVE domain containing 26	up G21	0.01606	1.65841	1.17704	1.95201
283	NM_001048227 /// NM_001048228 /// NM_001048229 /// NM_026797	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	up G21	0.01994	1.65703	-1.00345	1.65133
284	NM_010757	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	up G21	0.01587	1.65573	-1.04899	1.57841
285	NM_028440 /// XM_001473245 /// XM_912949	3110003A17Rik	RIKEN cDNA 3110003A17 gene	up G21	0.02358	1.65352	1.14952	1.90074
286	NM_029537	Tmem98	transmembrane protein 98	up G21	0.00371	1.65343	1.63159	2.69773
287	NM_030238	Dync1h1	dynein cytoplasmic 1 heavy chain 1	up G21	0.01697	1.65295	-1.00369	1.64687
288	NM_001136260 /// NM_018760	Slc4a4	solute carrier family 4 (anion exchanger), member 4	up G21	0.40719	1.65106	-1.11137	1.48561
289	NM_175406	Atp6v0d2	ATPase, H+ transporting, lysosomal V0 subunit D2	up G21	0.10063	1.65002	-1.06369	1.55123
290	NM_001048008 /// NM_023328	Agtpbp1	ATP/GTP binding protein 1	up G21	0.14858	1.64892	-1.16603	1.41414
291	NM_007383	Acads	acyl-Coenzyme A dehydrogenase, short chain	up G21	0.00438	1.64734	-1.00362	1.64141
292	NM_001085515 /// XM_001476939 /// XM_283952	AI464131	expressed sequence AI464131	up G21	0.05029	1.64369	-1.05459	1.5586
293	NM_153103	Kif1c	kinesin family member 1C	up G21	0.00359	1.64366	-1.00198	1.64042
294	NM_001004468 /// NM_021314 /// NM_206856	Tacc2	transforming, acidic coiled-coil containing protein 2	up G21	0.05527	1.64265	-1.10762	1.48305
295	NM_022993	Lrp10	low-density lipoprotein receptor-related protein 10	up G21	0.01636	1.64207	-1.08093	1.51912
296	NM_023580	Epha1	Eph receptor A1	up G21	0.00849	1.64002	-1.17659	1.39388
297	NM_010515	Igf2r	insulin-like growth factor 2 receptor	up G21	0.09792	1.63886	-1.17349	1.39657

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
298	NM_008796	Pctp	phosphatidylcholine transfer protein	up G21	0.29772	1.63880	1.83933	3.01429
299	NM_181540	Tm6sf2	transmembrane 6 superfamily member 2	up G21	0.04343	1.63849	1.22346	2.00464
300	NM_009738	Bche	butyrylcholinesterase	up G21	0.00057	1.63843	-1.19527	1.37076
301	NM_194348	Atg2a	ATG2 autophagy related 2 homolog A (S. cerevisiae)	up G21	0.10253	1.63833	-1.27398	1.286
302	NM_011014	Sigmar1	sigma non-opioid intracellular receptor 1	up G21	0.13549	1.63721	1.02869	1.68419
303	NM_001177812 /// NM_001177813 /// NM_146099	D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	up G21	0.01122	1.63686	-1.09597	1.49352
304	NM_133858	Fam63a	family with sequence similarity 63, member A	up G21	0.01895	1.63285	-1.21173	1.34754
305	NM_001135577 /// XM_001472442 /// XM_001473940	BC024659	cDNA sequence BC024659	up G21	0.02086	1.63110	-1.06587	1.5303
306	NM_011026	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	up G21	0.01664	1.63065	-1.15419	1.41282
307	NM_010478	Hspa1b	heat shock protein 1B	up G21	0.17994	1.62772	1.33975	2.18074
308	NM_001081274	Pgd	phosphogluconate dehydrogenase	up G21	0.05831	1.62624	1.62651	2.6451
309	NM_001039194 /// NM_153779 /// NM_178058	Aifm2	apoptosis-inducing factor, mitochondrion-associated 2	up G21	0.07841	1.62546	-1.36954	1.18686
310	NM_029364	Gns	glucosamine (N-acetyl)-6-sulfatase	up G21	0.00667	1.62146	-1.22298	1.32583
311	NM_007962	Mpzl2	myelin protein zero-like 2	up G21	0.00171	1.62017	-1.31377	1.23323
312	NM_008492	Ldhb	lactate dehydrogenase B	up G21	0.01591	1.61999	-1.17845	1.37468
313	NM_013581	Cog1	component of oligomeric golgi complex 1	up G21	0.01976	1.61990	-1.33837	1.21036
314	NM_001102455 /// NM_001102456 /// NM_009691	Aplp2	amyloid beta (A4) precursor-like protein 2	up G21	0.03650	1.61911	-1.24807	1.29729
315	NM_001136064 /// NM_008144	Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	up G21	0.00090	1.60948	-1.14298	1.40814
316	NM_010893	Neu1	neuraminidase 1	up G21	0.00178	1.60926	-1.34794	1.19387
317	NM_007527	Bax	BCL2-associated X protein	up G21	0.04783	1.60815	1.32533	2.13133
318	NM_001048061 /// NM_010448	Hnrnpab	heterogeneous nuclear ribonucleoprotein A/B	up G21	0.01959	1.60652	-1.12406	1.42921
319	NM_020507	Tob2	transducer of ERBB2, 2	up G21	0.28201	1.60589	-1.42600	1.12615
320	NM_011609	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	up G21	0.02475	1.60141	-1.19795	1.3368
321	NM_001039581 /// NM_013855	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	up G21	0.01916	1.60113	-1.03003	1.55444

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
322	NM_023530	Pla2g12b	phospholipase A2, group XIIB	up G21	0.00231	1.59962	-1.26074	1.26879
323	NM_001083904 /// NM_001083905 /// NM_021564	Fetub	fetuin beta	up G21	0.01471	1.59917	-1.35035	1.18427
324	NM_001039520	Dnm2	dynamin 2	up G21	0.04160	1.59842	-1.02711	1.55623
325	NM_009450	Tubb2a	tubulin, beta 2A	up G21	0.01817	1.59827	2.45196	3.91888
326	NM_009443 /// XM_001471628	Tgoln1	trans-golgi network protein	up G21	0.40378	1.59474	-1.31240	1.21514
327	NM_021456	Ces1	carboxylesterase 1	up G21	0.06000	1.59473	-1.13836	1.40089
328	NM_016905	Galk1	galactokinase 1	up G21	0.02574	1.59158	-1.36574	1.16536
329	NM_008256	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	up G21	0.04512	1.59070	-1.39848	1.13745
330	NM_181072	Myo1e	myosin IE	up G21	0.12397	1.58989	-1.19953	1.32542
331	NM_001077411 /// NM_008094	Gba	glucosidase, beta, acid	up G21	0.00032	1.58185	-1.54552	1.02351
332	NM_001142681 /// NM_026522	Chid1	chitinase domain containing 1	up G21	0.01069	1.57735	-1.19360	1.32151
333	NM_194334	Tbc1d2b	TBC1 domain family, member 2B	up G21	0.01811	1.57601	-1.18775	1.32689
334	NM_138677	Edem1	ER degradation enhancer, mannosidase alpha-like 1	up G21	0.00955	1.57367	-1.14289	1.37691
335	NM_031165	Hspa8	heat shock protein 8	up G21	0.26086	1.57290	1.03329	1.62527
336	NM_146251	Pnpla7	patatin-like phospholipase domain containing 7	up G21	0.02130	1.57162	1.02001	1.60307
337	NM_173011	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	up G21	0.01519	1.57099	-1.11197	1.41279
338	NM_013772	Tcl1b3	T-cell leukemia/lymphoma 1B, 3	up G21	0.01682	1.57077	-1.19450	1.31499
339	NM_001001144 /// NM_001103162	Scap	SREBF chaperone	up G21	0.03723	1.56906	1.18167	1.85411
340	NM_145987	Tmem82	transmembrane protein 82	up G21	0.01279	1.56570	-1.11150	1.40864
341	NM_008175	Grn	granulin	up G21	0.05892	1.56532	-1.31054	1.19441
342	NM_010688	Lasp1	LIM and SH3 protein 1	up G21	0.01447	1.56180	-1.03136	1.51431
343	NM_144880 /// XM_001476699	Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	up G21	0.05618	1.55467	-1.14327	1.35984
344	NM_018816	Apom	apolipoprotein M	up G21	0.00428	1.54765	-1.20182	1.28776
345	NM_145424	BC089597	cDNA sequence BC089597	up G21	0.00156	1.53677	-1.13677	1.35188
346	NM_007471	App	amyloid beta (A4) precursor protein	up G21	0.05091	1.52264	-1.51936	1.00216
347	NM_145146	Afm	afamin	up G21	0.00228	1.50776	-1.28152	1.17654

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
348	NM_009693	Apob	apolipoprotein B	up G21	0.00082	1.49565	-1.03038	1.45156
349	NM_007428	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	up G21	0.02483	1.48221	-1.12761	1.31447
350	NM_011254 /// XM_001473622	Rbp1	retinol binding protein 1, cellular	up G21	0.03134	1.48155	-1.23642	1.19826
351	NM_008254	Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	up G21	0.00255	1.47797	-1.33762	1.10493
352	NM_001110252 /// NM_008281	Hpn	hepsin	up G21	0.03250	1.47282	-1.06922	1.37747
353	NM_008342	Igfbp2	insulin-like growth factor binding protein 2	up G21	0.07757	1.46066	-1.06637	1.36975
354	NM_001109991 /// NM_009929	Col18a1	collagen, type XVIII, alpha 1	up G21	0.01373	1.44220	-1.22406	1.1782
355	NM_008490	Lcat	lecithin cholesterol acyltransferase	up G21	0.01498	1.43032	-1.36014	1.05159
356	NM_016764	Prdx4	peroxiredoxin 4	up G21	0.00900	1.40454	-1.39621	1.00597
357	NM_008406	Itih1	inter-alpha trypsin inhibitor, heavy chain 1	up G21	0.00487	1.39020	-1.24881	1.11322
358	NM_146094	Fads1	fatty acid desaturase 1	up G21	0.02085	1.36623	-1.11768	1.22238
359	NM_016668	Bhmt	betaine-homocysteine methyltransferase	up G21	0.00682	1.34528	-1.01703	1.32276
360	NM_001102411 /// NM_001102412 /// NM_023125	Kng1	kininogen 1	up G21	0.00187	1.33829	-1.20637	1.10935
361	NM_172476	Tmc7	transmembrane channel-like gene family 7	down PP7	0.00356	1.72541	-2.21442	-1.28342
362	NM_001042671 /// NM_001042672 /// NM_028802	Gpcpd1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	down PP7	0.18571	1.71036	-2.32423	-1.35892
363	NM_001171004 /// NM_001171005 /// NM_029239	Prkd3	protein kinase D3	down PP7	0.17700	1.63202	-2.00531	-1.22873
364	NM_009700	Aqp4	aquaporin 4	down PP7	0.03030	1.60723	-2.52791	-1.57284
365	NM_178617	Necab1	N-terminal EF-hand calcium binding protein 1	down PP7	0.27107	1.58888	-2.08408	-1.31167
366	NM_153078	Ehbp1	EH domain binding protein 1	down PP7	0.01316	1.58673	-1.83817	-1.15846
367	NM_001009935 /// NM_023719	Txnip	thioredoxin interacting protein	down PP7	0.02025	1.53791	-2.38637	-1.5517
368	NM_001159367 /// NM_011065	Per1	period homolog 1 (Drosophila)	down PP7	0.13721	1.52416	-1.71536	-1.12545
369	NM_012006 /// NM_134188 /// XR_031056	Acot1 /// Acot2 /// LOC100044830	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2 /// similar to acyl-CoA thio	down PP7	0.54251	1.52226	-1.72954	-1.13616

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
370	NM_013562	Ifrd1	interferon-related developmental regulator 1	down PP7	0.15086	1.51278	-1.68601	-1.11452
371	NM_080289	Grhpr	glyoxylate reductase/hydroxypyruvate reductase	down PP7	0.09776	1.50673	-1.58673	-1.0531
372	NM_027455	Qpct	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	down PP7	0.05964	1.48176	-2.38308	-1.60827
373	NM_029796	Lrg1	leucine-rich alpha-2-glycoprotein 1	down PP7	0.10021	1.43682	-1.78615	-1.24313
374	NM_010220	Fkbp5	FK506 binding protein 5	down PP7	0.00110	1.40973	-2.25242	-1.59777
375	NM_020581	Angptl4	angiopoietin-like 4	down PP7	0.01265	1.39349	-3.35199	-2.40546
376	NM_133748 /// NM_178082	Insig2	insulin induced gene 2	down PP7	0.33685	1.38282	-1.58377	-1.14532
377	NM_001083958 /// NM_028298	Zfp655	zinc finger protein 655	down PP7	0.06234	1.35393	-1.94384	-1.4357
378	NM_001042591	Arrdc3	arrestin domain containing 3	down PP7	0.01794	1.34245	-2.51066	-1.87021
379	NM_008176	Cxcl1	chemokine (C-X-C motif) ligand 1	down PP7	0.42572	1.33282	-1.80377	-1.35335
380	NM_009117	Saa1	serum amyloid A 1	down PP7	0.30682	1.33245	-2.08859	-1.56749
381	NM_007981	Acsl1	acyl-CoA synthetase long-chain family member 1	down PP7	0.05402	1.31930	-1.98101	-1.50157
382	NM_011521	Sdc4	syndecan 4	down PP7	0.00270	1.31410	-1.43031	-1.08843
383	NM_019410	Pfn2	profilin 2	down PP7	0.00701	1.27710	-1.97534	-1.54673
384	NM_146011	Arhgap9	Rho GTPase activating protein 9	down PP7	0.02365	1.25386	-1.80317	-1.43809
385	NM_133898	N4bp2l1	NEDD4 binding protein 2-like 1	down PP7	0.05488	1.25295	-2.27207	-1.81337
386	NM_029562	Cyp2d26	cytochrome P450, family 2, subfamily d, polypeptide 26	down PP7	0.00418	1.24773	-1.39952	-1.12165
387	NM_011200	Ptp4a1	protein tyrosine phosphatase 4a1	down PP7	0.00195	1.23015	-1.58524	-1.28865
388	NM_030732	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	down PP7	0.03726	1.22322	-1.85493	-1.51643
389	NM_145365	Creb3l3	cAMP responsive element binding protein 3-like 3	down PP7	0.03989	1.19125	-1.62734	-1.36608
390	NM_177054 /// NM_199038	Casc4	cancer susceptibility candidate 4	down PP7	0.10835	1.17645	-2.06374	-1.75421
391	NM_011825	Grem2	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	down PP7	0.27867	1.16525	-1.65024	-1.41622
392	NM_054055	Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	down PP7	0.12568	1.15232	-1.64744	-1.42968
393	NM_010517	Igfbp4	insulin-like growth factor binding protein 4	down PP7	0.16362	1.15021	-1.23270	-1.07171
394	NM_007980	Fabp2	fatty acid binding protein 2, intestinal	down PP7	0.06783	1.13925	-1.95251	-1.71385

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
395	NM_015767	Ttpa	tocopherol (alpha) transfer protein	down PP7	0.04229	1.13351	-1.29058	-1.13857
396	NM_026819	Dhrs1	dehydrogenase/reductase (SDR family) member 1	down PP7	0.15318	1.13016	-1.63870	-1.44997
397	NM_001033324	Zbtb16	zinc finger and BTB domain containing 16	down PP7	0.06494	1.12881	-2.19763	-1.94686
398	NM_007376	Pzp	pregnancy zone protein	down PP7	0.02746	1.12414	-1.14949	-1.02255
399	NM_033037	Cdo1	cysteine dioxygenase 1, cytosolic	down PP7	0.00738	1.12053	-1.28181	-1.14393
400	NM_134114 /// XM_001471593	Sft2d1	SFT2 domain containing 1	down PP7	0.05451	1.10663	-1.63968	-1.48169
401	NM_009243	Serpina1a	serine (or cysteine) peptidase inhibitor, clade A, member 1A	down PP7	0.08364	1.10211	-1.13588	-1.03064
402	NM_010565	Inhbc	inhibin beta-C	down PP7	0.03213	1.10004	-2.51739	-2.28846
403	NM_029494	Rab30	RAB30, member RAS oncogene family	down PP7	0.00992	1.09324	-2.07150	-1.89483
404	NM_172715	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase 9	down PP7	0.05455	1.09261	-1.76358	-1.61409
405	NM_001012310	AI132487	expressed sequence AI132487	down PP7	0.03958	1.07919	-1.70079	-1.57599
406	NM_022331	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like d	down PP7	0.00783	1.05061	-1.96883	-1.874
407	NM_008058	Fzd8	frizzled homolog 8 (Drosophila)	down PP7	0.27499	1.04177	-1.92541	-1.84822
408	NM_008382	Inhbe	inhibin beta E	down PP7	0.19421	1.03269	-2.41437	-2.33795
409	NM_011044	Pck1	phosphoenolpyruvate carboxykinase 1, cytosolic	down PP7	0.15013	1.02190	-1.65432	-1.61887
410	NM_133753	Errfi1	ERBB receptor feedback inhibitor 1	down PP7	0.06449	1.01166	-1.49806	-1.4808
411	XM_001480564	Gm4586	predicted gene 4586	down PP7	0.13202	1.00142	-1.68608	-1.68369
412	NM_146008	Tcp11l2	t-complex 11 (mouse) like 2	down PP7	0.30692	-1.00233	-1.70868	-1.71266
413	NM_026232	Slc25a30	solute carrier family 25, member 30	down PP7	0.02607	-1.01312	-2.78431	-2.82083
414	NM_026821	D4Bwg0951e	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	down PP7	0.04153	-1.02092	-1.92877	-1.96911
415	NM_144784	Acat1	acetyl-Coenzyme A acetyltransferase 1	down PP7	0.00464	-1.02116	-2.02742	-2.07033
416	NM_175523	Ppm1k	protein phosphatase 1K (PP2C domain containing)	down PP7	0.26560	-1.02383	-1.64150	-1.68063
417	NM_001130412 /// NM_015763 /// NM_172950	Lpin1	lipin 1	down PP7	0.08664	-1.02461	-2.07209	-2.12308
418	NM_029870	A930001N09Rik	RIKEN cDNA A930001N09 gene	down PP7	0.11818	-1.05003	-1.67265	-1.75633
419	NM_013797	Slco1a1	solute carrier organic anion transporter family, member 1a1	down PP7	0.00861	-1.09402	-1.59588	-1.74591

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	Pattern	p-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
420	NM_145572	Gys2	glycogen synthase 2	down PP7	0.02585	-1.10010	-1.69188	-1.86124
421	NM_007811	Cyp26a1	cytochrome P450, family 26, subfamily a, polypeptide 1	down PP7	0.28371	-1.10919	-1.63840	-1.8173
422	NM_008358 /// NM_133836	Il15ra	interleukin 15 receptor, alpha chain	down PP7	0.01636	-1.11896	-1.72439	-1.92953
423	NM_026929	Chac1	ChaC, cation transport regulator-like 1 (E. coli)	down PP7	0.11977	-1.12374	-2.77952	-3.12344
424	NM_138654	5033411D12Rik	RIKEN cDNA 5033411D12 gene	down PP7	0.00099	-1.18452	-2.28268	-2.70387
425	NM_022026 /// XM_001003981 /// XM_980183	Aqp9	aquaporin 9	down PP7	0.03147	-1.19058	-1.91949	-2.28531
426	NM_026931	1810011O10Rik	RIKEN cDNA 1810011O10 gene	down PP7	0.21838	-1.22871	-1.63621	-2.01043
427	NM_001166409 /// NM_001166410 /// NM_001166411 /// NM_016809	Rbm3	RNA binding motif protein 3	down PP7	0.11298	-1.24188	-1.60406	-1.99205
428	NM_001039090 /// NM_011386	Skil	SKI-like	down PP7	0.00137	-1.36158	-1.73089	-2.35675
429	NM_146148	C8a	complement component 8, alpha polypeptide	down PP7	0.01174	-1.41739	-1.90548	-2.7008
430	NM_153198 /// NM_177993	Hbp1	high mobility group box transcription factor 1	down PP7	0.02364	-1.43526	-1.79978	-2.58316
431	NM_007606	Car3	carbonic anhydrase 3	down PP7	0.00987	-1.51882	-1.49412	-2.26929
432	NM_011316	Saa4	serum amyloid A 4	down PP7	0.00389	-1.98992	-1.89984	-3.78053
433	NM_007813	Cyp2b13	cytochrome P450, family 2, subfamily b, polypeptide 13	down PP7	0.02031	-3.31558	-2.15548	-7.14665
434	NM_020495 /// NM_178235	Slco1b2	solute carrier organic anion transporter family, member 1b2	down PP7	0.01657	-4.05104	-1.97889	-8.01658
435	NM_011458	Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	down PP7	0.00450	-4.14506	-1.74651	-7.2394

Table S3. Genes downregulated at term (compared to virgin) and upregulated at PP7 (compared to G21) (* For negative fold change = down-regulated; positive fold change = up-regulated)

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
1	NM_008567	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	0.0003	-23.85	5.49	-4.34
2	NM_010701	Lect1	leukocyte cell derived chemotaxin 1	0.0008	-18.07	5.20	-3.48
3	NM_008234	Hells	helicase, lymphoid specific	0.0037	-17.10	3.64	-4.70
4	NM_007691	Chek1	checkpoint kinase 1 homolog (S. pombe)	0.0043	-13.71	2.76	-4.96
5	NM_013485	C9	complement component 9	0.0094	-13.71	3.81	-3.60
6	NM_008565	Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	0.0007	-13.30	4.91	-2.71
7	NM_008566	Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	0.0022	-12.97	3.76	-3.45
8	NM_001163359 /// NM_001163360 /// NM_021891	Fignl1	fidgetin-like 1	0.0025	-10.98	3.01	-3.64
9	NM_030210	Aacs	acetoacetyl-CoA synthetase	0.0146	-7.43	6.55	-1.13
10	NM_008564	Mcm2	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	0.0072	-7.41	2.37	-3.12
11	NM_008295	Hsd3b5	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5	0.0977	-6.30	4.44	-1.42
12	NM_001081642 /// NM_021365 /// NM_183094 /// XM_001471888	Xlr4a /// Xlr4b /// Xlr4c	x-linked lymphocyte-regulated protein 3A-like /// X-linked lymphocyte-regulated 4A /// X-linked lymphocyte-regulated 4B /// X-linked lymphocyte-regulated 4C	0.1953	-6.29	2.26	-2.79
13	NM_008255	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0.1123	-5.90	4.14	-1.43
14	NM_008921	Prim1	DNA primase, p49 subunit	0.0019	-5.65	2.04	-2.77
15	NM_008280	Lipc	lipase, hepatic	0.0375	-5.65	4.51	-1.25
16	NM_026993	Ddah1	dimethylarginine dimethylaminohydrolase 1	0.0064	-5.41	3.89	-1.39

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
17	NM_130450	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	0.0335	-5.41	9.28	1.71
18	NM_029600	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.0076	-5.14	4.42	-1.16
19	NM_172776 /// NM_177002	C730048C13 Rik /// D630002G06 Rik	RIKEN cDNA C730048C13 gene /// RIKEN cDNA D630002G06 gene	0.0304	-5.06	2.18	-2.33
20	NM_175283	Srd5a1	steroid 5 alpha-reductase 1	0.0077	-5.02	1.72	-2.92
21	NM_001163763 /// NM_001163764 /// NM_025674	Tcf19	transcription factor 19	0.0023	-5.02	2.58	-1.95
22	NM_029766	Dtl	denticleless homolog (Drosophila)	0.0033	-4.99	2.27	-2.20
23	NM_029662	Mfsd2a	major facilitator superfamily domain containing 2A	0.0030	-4.80	1.81	-2.65
24	NM_008087	Gas2	growth arrest specific 2	0.0078	-4.77	1.83	-2.61
25	NM_001013785	Akr1c19	aldo-keto reductase family 1, member C19	0.0015	-4.67	6.73	1.44
26	NM_134037	Acly	ATP citrate lyase	0.0295	-4.66	4.54	-1.03
27	NM_010720	Lipg	lipase, endothelial	0.0004	-4.61	4.51	-1.02
28	NM_007999	Fen1	flap structure specific endonuclease 1	0.0065	-4.49	2.34	-1.92
29	NM_009982	Ctsc	cathepsin C	0.0008	-4.43	1.50	-2.96
30	NM_144836	Slc17a2	solute carrier family 17 (sodium phosphate), member 2	0.0253	-4.38	2.63	-1.66
31	NM_009013	Rad51ap1	RAD51 associated protein 1	0.0332	-4.30	2.09	-2.06
32	NM_010518	Igfbp5	insulin-like growth factor binding protein 5	0.0160	-4.25	1.93	-2.21
33	NM_011284	Rpa2	replication protein A2	0.0066	-4.22	2.05	-2.06
34	NM_024437 /// NM_024446	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	0.0033	-4.05	1.92	-2.11
35	NM_026014	Cdt1	chromatin licensing and DNA replication factor 1	0.0015	-3.92	2.87	-1.36
36	NM_027435	Atad2	ATPase family, AAA domain containing 2	0.0053	-3.90	2.12	-1.84
37	NM_008262	Onecut1	one cut domain, family member 1	0.0628	-3.77	2.22	-1.70
38	NM_001081051	D130043K22 Rik	RIKEN cDNA D130043K22 gene	0.0584	-3.46	3.82	1.10

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
39	NM_001162883 /// NM_001168660 /// NM_173743 /// NM_173786 /// XM_128064 /// XM_9	Apol9a /// Apol9b	apolipoprotein L 9a /// apolipoprotein L 9b	0.0168	-3.44	2.54	-1.35
40	NM_008017	Smc2	structural maintenance of chromosomes 2	0.0787	-3.37	2.18	-1.54
41	NM_016904	Cks1b	CDC28 protein kinase 1b	0.0303	-3.29	2.21	-1.49
42	NM_175217	Mmd2	monocyte to macrophage differentiation-associated 2	0.1168	-3.29	2.16	-1.52
43	NM_008086	Gas1	growth arrest specific 1	0.0066	-3.23	2.12	-1.52
44	NM_009349	Inmt	indolethylamine N-methyltransferase	0.0238	-3.22	1.89	-1.70
45	NM_009381	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	0.4187	-3.21	2.92	-1.10
46	NM_001033123 /// XM_194572	Gm14288	ethanol induced 1 /// predicted gene 14288	0.0028	-3.19	1.79	-1.78
47	NM_001081643 /// NM_001110784 /// NM_011726 /// NM_011727 /// XM_001471591 /// X	Xlr3a /// Xlr3b /// Xlr3c	x-linked lymphocyte-regulated protein 3B-like /// X-linked lymphocyte-regulated 3A /// X-linked lymphocyte-regulated 3B /// X-linked lymphocyte-regulated 3C	0.2732	-3.18	2.24	-1.42
48	NM_146006	Lss	lanosterol synthase	0.0630	-3.14	3.36	1.07
49	NM_054088	Pnpla3	patatin-like phospholipase domain containing 3	0.2341	-3.12	11.35	3.63
50	NM_029720	Creld2	cysteine-rich with EGF-like domains 2	0.1151	-3.07	1.69	-1.82
51	NM_026282	Spc24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.0368	-3.06	3.00	-1.02
52	NM_008568	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	0.0009	-3.05	1.68	-1.82
53	NM_020010	Cyp51	cytochrome P450, family 51	0.1061	-3.02	2.89	-1.04
54	NM_178214	Hist2h2be	histone cluster 2, H2be	0.0129	-3.01	2.78	-1.08
55	NM_001161763 /// NM_001161765 /// NM_010232	Fmo5	flavin containing monooxygenase 5	0.0216	-2.98	1.76	-1.69

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
56	NM_001039720	9030619P08Rik	RIKEN cDNA 9030619P08 gene	0.0019	-2.97	2.27	-1.30
57	NM_010476	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	0.0154	-2.95	1.40	-2.11
58	NM_008321	Id3	inhibitor of DNA binding 3	0.0306	-2.94	1.73	-1.70
59	---	BC024137	cDNA sequence BC024137	0.0013	-2.93	1.75	-1.68
60	NM_001033331 /// NM_001079876	Gas2l3	growth arrest-specific 2 like 3	0.0643	-2.91	3.49	1.20
61	NM_019811	Acss2	acyl-CoA synthetase short-chain family member 2	0.0114	-2.90	4.82	1.66
62	NM_172769	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	0.0052	-2.85	1.60	-1.78
63	NM_183278	2200001I15Rik	RIKEN cDNA 2200001I15 gene	0.0316	-2.81	2.15	-1.30
64	NM_011172	Prodh	proline dehydrogenase	0.0078	-2.80	2.18	-1.28
65	NM_019778 /// NM_181058	Zbtb20	zinc finger and BTB domain containing 20	0.0050	-2.75	1.61	-1.70
66	NM_134469	Fdps	farnesyl diphosphate synthetase	0.1083	-2.74	3.18	1.16
67	NM_025408	Acer3	alkaline ceramidase 3	0.0830	-2.73	2.04	-1.34
68	NM_013831	Pstpip2	proline-serine-threonine phosphatase-interacting protein 2	0.0223	-2.72	1.75	-1.55
69	NM_027852	Rarres2	retinoic acid receptor responder (tazarotene induced) 2	0.0059	-2.70	1.77	-1.52
70	NM_172776	D630002G06Rik	RIKEN cDNA D630002G06 gene	0.0407	-2.66	1.77	-1.50
71	NM_009127	Scd1	stearoyl-Coenzyme A desaturase 1	0.0602	-2.66	6.30	2.37
72	NM_028372	Mblac2	metallo-beta-lactamase domain containing 2	0.0212	-2.65	2.11	-1.26
73	NM_018738	Igtp	interferon gamma induced GTPase	0.0310	-2.65	1.74	-1.53
74	NM_172653	Slc39a10	solute carrier family 39 (zinc transporter), member 10	0.0164	-2.59	2.33	-1.11
75	NM_019499	Mad2l1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.1882	-2.58	2.08	-1.24
76	NM_001177625 /// NM_001177626 /// NM_007900	Ect2	ect2 oncogene	0.0832	-2.58	4.69	1.82

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
77	NM_001033606 /// NM_001136222 /// NM_028817	Acsl3	acyl-CoA synthetase long-chain family member 3	0.0777	-2.57	2.23	-1.15
78	NM_001077410 /// NM_212486	Gimap8	GTPase, IMAP family member 8	0.0037	-2.55	2.13	-1.20
79	NM_001172055 /// NM_027208	Bdh2	3-hydroxybutyrate dehydrogenase, type 2	0.0059	-2.53	1.89	-1.34
80	NM_011369	Shcbp1	Shc SH2-domain binding protein 1	0.1350	-2.53	2.70	1.07
81	NM_179203	Atad3a	ATPase family, AAA domain containing 3A	0.0015	-2.53	3.38	1.34
82	NM_030598 /// NM_207649	Rcan2	regulator of calcineurin 2	0.0282	-2.52	2.56	1.01
83	NM_146245	Lrit1	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	0.0108	-2.51	2.54	1.01
84	NM_025901	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	0.0055	-2.49	2.08	-1.20
85	NM_021557	Rdh11	retinol dehydrogenase 11	0.0208	-2.48	4.00	1.61
86	---	AU015263	expressed sequence AU015263	0.0088	-2.48	3.10	1.25
87	NM_009193	Slbp	stem-loop binding protein	0.0009	-2.47	1.62	-1.52
88	NM_145360 /// NM_177960	Idi1	isopentenyl-diphosphate delta isomerase	0.1317	-2.47	2.35	-1.05
89	NM_025569	Mgst3	microsomal glutathione S-transferase 3	0.0196	-2.47	2.67	1.08
90	NM_172616	C330027C09 Rik	RIKEN cDNA C330027C09 gene	0.2565	-2.47	3.25	1.32
91	NM_001163587 /// NM_027907	Agxt2l1	alanine-glyoxylate aminotransferase 2-like 1	0.0058	-2.46	3.92	1.59
92	NM_001077353 /// NM_010356	Gsta3	glutathione S-transferase, alpha 3	0.0508	-2.45	1.72	-1.42
93	NM_001159543 /// NM_010074	Dpp4	dipeptidylpeptidase 4	0.0011	-2.44	1.96	-1.25
94	NM_145523	Gca	grancalcin	0.0244	-2.44	2.21	-1.10
95	NM_026904	Anapc10	anaphase promoting complex subunit 10	0.0414	-2.43	1.82	-1.33

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
96	NM_009834 /// XM_001477322	Ccrn4l /// LOC100047134	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	0.3758	-2.42	2.45	1.02
97	NM_008303	Hspe1	heat shock protein 1 (chaperonin 10)	0.0007	-2.41	1.87	-1.28
98	NM_010924	Nnmt	nicotinamide N-methyltransferase	0.0895	-2.41	2.32	-1.04
99	NM_008615 /// XM_001004685	LOC677317 /// Me1	malic enzyme 1, NADP(+)-dependent, cytosolic	0.0326	-2.38	3.25	1.37
100	NM_026708	Tlcd1	TLC domain containing 1	0.0535	-2.37	2.00	-1.18
101	NM_024473	BC005537	cDNA sequence BC005537	0.0145	-2.37	1.94	-1.22
102	NM_172734	Stk38l	serine/threonine kinase 38 like	0.0022	-2.36	1.95	-1.21
103	NM_009831	Ccng1	cyclin G1	0.0385	-2.36	1.64	-1.44
104	NM_009846	Cd24a	CD24a antigen	0.2108	-2.36	1.73	-1.36
105	NM_001083312 /// NM_145545	Gbp6	guanylate binding protein 6	0.0090	-2.35	1.70	-1.38
106	NM_008317 /// NM_019750	Hyal1 /// Nat6	hyaluronoglucosaminidase 1 /// N-acetyltransferase 6	0.0666	-2.34	1.79	-1.31
107	NM_009810	Casp3	caspase 3	0.1110	-2.33	1.34	-1.74
108	NM_010480	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	0.0146	-2.33	1.39	-1.67
109	NM_007792	Csrp2	cysteine and glycine-rich protein 2	0.0060	-2.31	1.84	-1.26
110	NM_028984	8430406I07Rik	RIKEN cDNA 8430406I07 gene	0.0423	-2.29	1.81	-1.26
111	NM_025436	Sc4mol	sterol-C4-methyl oxidase-like	0.2360	-2.29	1.90	-1.20
112	NM_009460	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	0.0037	-2.29	1.69	-1.35
113	NM_023523	Pecr	peroxisomal trans-2-enoyl-CoA reductase	0.0076	-2.28	2.53	1.11
114	NM_001164190 /// NM_001164191 /// NM_001164192 /// NM_001164193 /// NM_019926	Mtm1	X-linked myotubular myopathy gene 1	0.0000	-2.26	2.37	1.05
115	NM_019405	Cetn2	centrin 2	0.0159	-2.25	1.94	-1.16
116	NM_025429	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	0.0012	-2.25	5.21	2.32

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
117	---	4921509J17Rik	RIKEN cDNA 4921509J17 gene /// heat shock protein 4 like	0.0102	-2.25	2.19	-1.03
118	NM_178890	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	0.0080	-2.23	2.23	1.00
119	NM_001166635 /// NM_026524	Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	0.0322	-2.22	2.84	1.28
120	NM_007934	Enpep	glutamyl aminopeptidase	0.0306	-2.22	2.29	1.03
121	NM_001105667 /// NM_023136	Dtymk	deoxythymidylate kinase	0.0020	-2.22	1.73	-1.28
122	NM_007631	Ccnd1	cyclin D1	0.0153	-2.22	2.00	-1.11
123	NM_001160345 /// NR_027704	Svip	small VCP/p97-interacting protein	0.0095	-2.20	1.98	-1.11
124	NM_008894	Pold2	polymerase (DNA directed), delta 2, regulatory subunit	0.0075	-2.17	2.13	-1.02
125	NM_153526	Insig1	insulin induced gene 1	0.0578	-2.16	2.42	1.12
126	NM_177741	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	0.0399	-2.16	1.83	-1.18
127	NM_026784 /// NM_027348	Pmvk	phosphomevalonate kinase	0.0069	-2.16	3.00	1.39
128	NM_001081195	Arid4a	AT rich interactive domain 4A (RBP1-like)	0.0177	-2.15	1.94	-1.11
129	NM_145392	Bag2	BCL2-associated athanogene 2	0.0016	-2.15	2.27	1.06
130	NM_013663	Sfrs3	serine/arginine-rich splicing factor 3	0.0123	-2.15	1.43	-1.50
131	NM_011623	Top2a	topoisomerase (DNA) II alpha	0.1417	-2.13	2.27	1.06
132	NM_001009949	Mcart1	mitochondrial carrier triple repeat 1	0.0168	-2.13	1.91	-1.11
133	NM_145462	Haus4	HAUS augmin-like complex, subunit 4	0.1042	-2.12	1.70	-1.25
134	NM_026928	1810014F10Rik	RIKEN cDNA 1810014F10 gene	0.0128	-2.11	1.85	-1.14
135	NM_153565	Pcsk9	proprotein convertase subtilisin/kexin type 9	0.3386	-2.11	2.68	1.27
136	NM_019521	Gas6	growth arrest specific 6	0.0488	-2.10	2.00	-1.05
137	NM_134256 /// XM_922697 /// XM_984546	AB056442	cDNA sequence AB056442	0.0680	-2.10	1.67	-1.26
138	NM_009657	Aldoc	aldolase C, fructose-bisphosphate	0.0234	-2.10	2.22	1.06

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
139	NM_009104	Rrm2	ribonucleotide reductase M2	0.0595	-2.09	1.84	-1.13
140	NM_027052	Slc38a4	solute carrier family 38, member 4	0.0669	-2.08	1.55	-1.34
141	NM_001177544 /// NM_178185 /// NM_178188 /// XM_978341	Gm11276 /// Hist1h2ad /// Hist1h2ao	predicted gene 11276 /// histone cluster 1, H2ao	0.0930	-2.08	1.67	-1.25
142	NM_011020	Hspa4l	heat shock protein 4 like	0.0288	-2.07	1.82	-1.14
143	NM_133815	Lbr	lamin B receptor	0.0253	-2.07	1.90	-1.09
144	NM_001002012 /// NM_008301	Hspa2	heat shock protein 2	0.0377	-2.06	2.63	1.28
145	NM_027819	Ggt6	gamma-glutamyltransferase 6	0.0075	-2.05	3.82	1.86
146	NM_178639	Sfxn5	sideroflexin 5	0.0180	-2.04	1.94	-1.05
147	NM_021398	Slc43a3	solute carrier family 43, member 3	0.0586	-2.04	2.18	1.07
148	NM_009900	Clcn2	chloride channel 2	0.0171	-2.04	1.76	-1.16
149	NM_007824	Cyp7a1	cytochrome P450, family 7, subfamily a, polypeptide 1	0.5335	-2.03	1.96	-1.04
150	NM_145942	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	0.0586	-2.02	1.80	-1.12
151	NM_023525	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	0.0485	-2.02	1.90	-1.07
152	NM_009338	Acat2	acetyl-Coenzyme A acetyltransferase 2	0.0435	-2.02	2.97	1.47
153	NM_138656 /// NR_028354	Mvd	mevalonate (diphospho) decarboxylase	0.1616	-2.02	5.87	2.91
154	NM_001164223 /// NM_026653	Rpa1	replication protein A1	0.0024	-2.01	1.64	-1.23
155	NM_027249	Tlcd2	TLC domain containing 2	0.0121	-1.99	1.81	-1.10
156	NM_175382	Fam72a	family with sequence similarity 72, member A	0.2023	-1.98	2.11	1.07
157	NM_153525	Tmem41b	transmembrane protein 41B	0.0397	-1.98	1.51	-1.31
158	NM_009320	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0.0648	-1.97	1.94	-1.01
159	NM_153573	Fkbp14	FK506 binding protein 14	0.0046	-1.96	2.32	1.18

No.	RefSeq Transcript ID	Gene Symbol	Gene Title	*p*-value (group)	Fold-Change* (G21/Virgin)	Fold-Change* (PP7/G21)	Fold-Change* (PP7/Virgin)
160	NM_008395	Itch	itchy, E3 ubiquitin protein ligase	0.1157	-1.96	2.05	1.04
161	NM_025558	Cyb5b	cytochrome b5 type B	0.0555	-1.96	2.22	1.14
162	NM_138651	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.0029	-1.95	2.01	1.03
163	NM_009270	Sqle	squalene epoxidase	0.2242	-1.95	2.84	1.46
164	NM_001145831 /// NM_001145832 /// NM_010631	Kifc3	kinesin family member C3	0.0058	-1.95	1.79	-1.09
165	NM_027406	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	0.0030	-1.95	2.16	1.11
166	NM_010219	Fkbp4	FK506 binding protein 4	0.0451	-1.92	1.60	-1.20
167	NM_009425	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	0.0414	-1.92	2.00	1.04
168	NM_001122647 /// XM_001472055	Mup10	major urinary protein 10	0.0188	-1.91	1.66	-1.15
169	NM_001113326 /// NM_031195	Msr1	macrophage scavenger receptor 1	0.1168	-1.91	1.27	-1.51
170	NM_016672	Ddc	dopa decarboxylase	0.0086	-1.90	3.25	1.71
171	NM_009801	Car2	carbonic anhydrase 2	0.0219	-1.90	1.95	1.03
172	NM_001163239 /// NM_001163241 /// NM_001163242 /// NM_020282	Nqo2	NAD(P)H dehydrogenase, quinone 2	0.0829	-1.90	1.74	-1.09
173	NM_007988	Fasn	fatty acid synthase	0.0369	-1.88	4.29	2.28
174	NM_001043322 /// NM_010230	Fmn1	formin 1	0.0212	-1.88	2.31	1.23
175	NM_133786	Smc4	structural maintenance of chromosomes 4	0.3404	-1.88	1.38	-1.37
176	NM_011480	Srebf1	sterol regulatory element binding transcription factor 1	0.0781	-1.88	1.94	1.03
177	XM_895068	Gdap10	ganglioside-induced differentiation-associated-protein 10	0.2736	-1.87	1.83	-1.02
178	NM_007659	Cdk1	cyclin-dependent kinase 1	0.3055	-1.86	2.00	1.07

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179	NM_001033166 /// NM_001037279	2700094K13Rik	RIKEN cDNA 2700094K13 gene	0.1394	-1.85	2.07	1.11
180	NM_011638	Tfrc	transferrin receptor	0.0736	-1.84	4.02	2.18
181	NM_023665	D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	0.0860	-1.84	1.90	1.03
182	NM_001163577 /// NM_001163578 /// NM_001163581 /// NM_001163582 /// NM_001163583	Prom1	prominin 1	0.0118	-1.83	5.80	3.16
183	NM_016750 /// XR_031328 /// XR_033615	Gm6722 /// H2afz	H2A histone family, member Z /// hypothetical LOC100504949	0.0113	-1.83	2.10	1.15
184	NM_007780	Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0.0114	-1.83	2.35	1.28
185	NM_008379	Kpnb1	karyopherin (importin) beta 1	0.0133	-1.83	-1.03	-1.88
186	NM_029103	Manf	mesencephalic astrocyte-derived neurotrophic factor	0.1484	-1.83	1.66	-1.10
187	NM_001080129 /// NM_001080130 /// NM_001080131 /// NM_001080132 /// NM_001080134	Tmpo	thymopoietin	0.0300	-1.82	1.72	-1.06
188	NM_001033264	Gls2	glutaminase 2 (liver, mitochondrial)	0.0042	-1.82	2.15	1.18
189	NM_011796	Capn10	calpain 10	0.0047	-1.82	2.16	1.18
190	NM_001113560 /// NM_025374	Glo1	glyoxalase 1	0.0149	-1.82	1.63	-1.12
191	NM_145614	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	0.0143	-1.81	1.90	1.05
192	NM_133933	Rpn1	ribophorin I	0.0555	-1.81	1.75	-1.04

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193	NM_001103177 /// NM_001103178 /// NM_178688	Ablim1	actin-binding LIM protein 1	0.0065	-1.80	1.92	1.06
194	NM_026845	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	0.0001	-1.79	2.14	1.19
195	NM_177382	Cyp2r1	cytochrome P450, family 2, subfamily r, polypeptide 1	0.0136	-1.78	1.99	1.12
196	NM_172951	Sntg2	syntrophin, gamma 2	0.0184	-1.78	1.76	-1.01
197	NM_153557	BC029214	cDNA sequence BC029214	0.0069	-1.78	2.66	1.49
198	NM_133774	Stard4	StAR-related lipid transfer (START) domain containing 4	0.0737	-1.78	1.58	-1.13
199	NM_028179	2200002D01Rik	RIKEN cDNA 2200002D01 gene	0.0155	-1.78	2.26	1.27
200	NM_001164572 /// NM_133741	Snrk	SNF related kinase	0.0146	-1.78	1.66	-1.07
201	NM_001145947 /// NM_011792	Bace1	beta-site APP cleaving enzyme 1	0.3426	-1.77	1.74	-1.02
202	NM_133362	Erdr1	erythroid differentiation regulator 1	0.0497	-1.76	1.89	1.07
203	NM_025522	Dhrs7	dehydrogenase/reductase (SDR family) member 7	0.0040	-1.76	1.73	-1.02
204	NM_001081176	Polr3g	polymerase (RNA) III (DNA directed) polypeptide G	0.0219	-1.75	1.82	1.04
205	NM_017477 /// NM_201244	Copg	coatomer protein complex, subunit gamma	0.0049	-1.75	1.72	-1.02
206	NM_172772	Fam63b	family with sequence similarity 63, member B	0.0576	-1.74	1.79	1.03
207	NM_025868	Tmx2	thioredoxin-related transmembrane protein 2	0.0024	-1.74	1.99	1.14
208	NM_134147	Macrod1	MACRO domain containing 1	0.0082	-1.72	1.65	-1.04
209	NM_172665	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	0.0402	-1.72	1.83	1.07
210	NM_198937	Hn1l	hematological and neurological expressed 1-like	0.0003	-1.71	1.78	1.04
211	NM_178758	Acsm5	acyl-CoA synthetase medium-chain family member 5	0.0267	-1.70	1.94	1.15
212	NM_011542	Tcea3	transcription elongation factor A (SII), 3	0.0019	-1.69	2.07	1.22
213	NM_133960	Ces6	carboxylesterase 6	0.0033	-1.69	2.21	1.31

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214	NM_001164441 /// NM_026153 /// NM_027496	Ankrd33b	ankyrin repeat domain 33B	0.0410	-1.68	1.94	1.16
215	NM_011850	Nr0b2	nuclear receptor subfamily 0, group B, member 2	0.6932	-1.68	1.65	-1.02
216	NM_133806 /// XM_917484	LOC640502 /// Uap1	UDP-N-acetylhexosamine pyrophosphorylase-like /// UDP-N-acetylglucosamine pyrophosphorylase 1	0.0180	-1.68	1.52	-1.10
217	NM_010191	Fdft1	farnesyl diphosphate farnesyl transferase 1	0.1275	-1.67	2.18	1.30
218	NM_009466	Ugdh	UDP-glucose dehydrogenase	0.0042	-1.67	3.53	2.11
219	NM_027570	Ldhd	lactate dehydrogenase D	0.0152	-1.67	1.82	1.09
220	NM_019479	Hes6	hairy and enhancer of split 6 (Drosophila)	0.1347	-1.66	2.66	1.60
221	NM_011805 /// NM_175551 /// NM_177852	Dido1	death inducer-obliterator 1	0.0333	-1.66	1.64	-1.01
222	NM_009113	S100a13	S100 calcium binding protein A13	0.0740	-1.65	1.81	1.09
223	NM_019787 /// XM_001481049	LOC100048726 /// Sec23b	SEC23B (S. cerevisiae)	0.0603	-1.65	1.72	1.05
224	NM_001163290 /// NM_023341	Cabc1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	0.1030	-1.64	2.13	1.30
225	NM_153783 /// XR_033107 /// XR_035669	Gm10307 /// Paox	polyamine oxidase (exo-N4-amino)	0.0079	-1.62	1.86	1.14
226	NM_009721	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	0.0109	-1.61	1.87	1.16
227	NM_001033536	Rfx7	regulatory factor X, 7	0.0303	-1.61	1.69	1.05
228	NM_139269	Pla2g16	phospholipase A2, group XVI	0.0026	-1.61	1.62	1.01
229	NM_146230	Acaa1b	acetyl-Coenzyme A acyltransferase 1B	0.2947	-1.61	1.61	-1.00
230	NM_021455	Mlxipl	MLX interacting protein-like	0.0054	-1.61	2.48	1.54

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231	NM_001080127 /// NM_001080128 /// NM_009070	Rnps1	ribonucleic acid binding protein S1	0.0046	-1.60	1.81	1.13
232	NM_001168475 /// NM_001168476 /// NM_001168477 /// NM_025905	Ttc23	tetratricopeptide repeat domain 23	0.1676	-1.60	1.64	1.03
233	NM_010941	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	0.1839	-1.59	1.83	1.15
234	NM_007856	Dhcr7	7-dehydrocholesterol reductase	0.0272	-1.58	2.57	1.63
235	NM_013778	Akr1c13	aldo-keto reductase family 1, member C13	0.0027	-1.58	1.66	1.05
236	NM_001081169	Aspg	asparaginase homolog (S. cerevisiae)	0.0266	-1.56	2.04	1.30
237	NM_133768	Asl	argininosuccinate lyase	0.0180	-1.56	1.67	1.07
238	NM_007494	Ass1	argininosuccinate synthetase 1	0.0498	-1.55	1.57	1.01
239	NM_008439	Khk	ketohexokinase	0.0358	-1.52	1.85	1.22