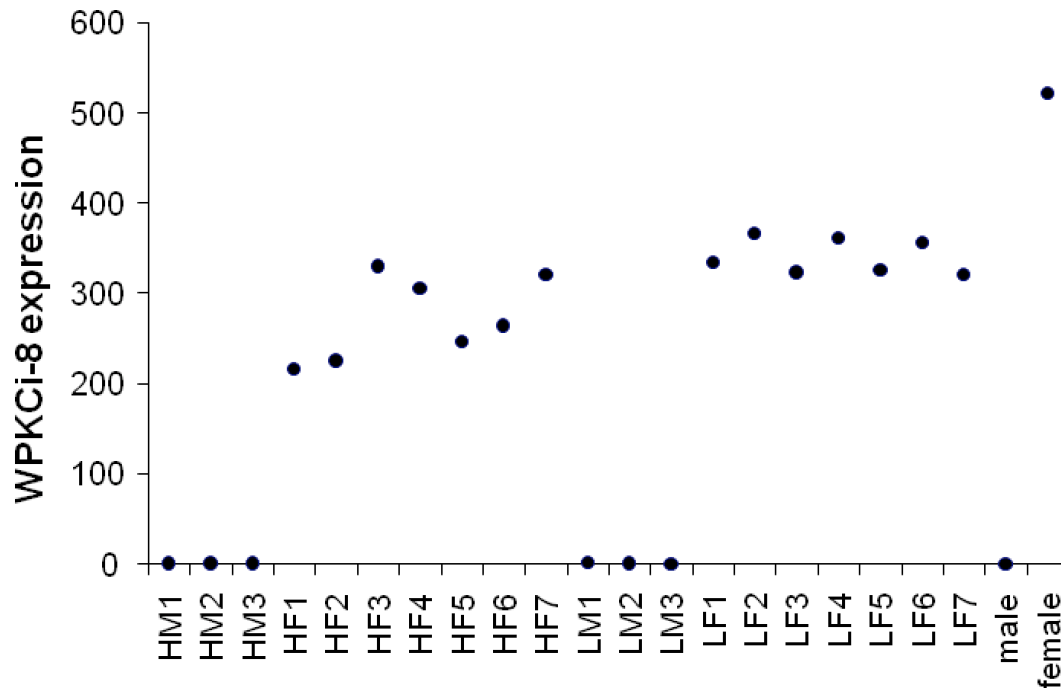


Supplementary information

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Title: Differential Gene Expression in the Hypothalamus of Two Chicken Lines with Different Feeding Behaviours Resulting from Divergent Selection for High or Low Body Weight.

Figures and tables



Supplementary Figure S1. Expression of WPKCi-8 mRNA and sex determination of 4 day old chickens.

Relative mRNA expression levels of female-specific WPKCi-8 were tested in male and female control chickens and the 4 day old chickens subjected to array analysis. HM, HWS male; HF, HWS female; LM, LWS male; LF, LWS female.

Supplementary material Table S1. Sojeong Ka et al

List with 383 differentially expressed probe sets with p<0.001 and fold change (fold change; FC) >1.5

List #	Probe ID	Gene Symbol	Gene Title	p-values	Fold Difference LWS/HWS	Alignments (genome version: WUSTL Feb. 2004 release)
1	Gga.4900.1.S1_s_at	17.5	lectin-like protein, type II transmembrane protein	7.034E-11	0.10	chrUn:147194872-147194872 (-) // 37.45 //
2	Gga.14876.1.S1_s_at	RPS6K3	ribosomal protein S6 kinase alpha 3	2.298E-11	0.12	chr1:113143163-113143163 (+) // 99.85 //
3	Gga.9083.1.S1_s_at	KCN2A	potassium voltage-gated channel, shaker-related subfamily, member 2	5.723E-09	0.14	chr28:139918-142216 (-) // 99.91 //
4	GgaAffx.12680.1.S1_s_at	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	5.941E-05	0.16	chr7:13465914-13479527 (+) // 93.95 //
5	Gga.19409.1.S1_s_at	LOC418752	similar to alpha 2 type IV collagen preproprotein; constant	1.228E-12	0.17	chr1:131080769-132050573 (+) // 93.03 //
6	Gga.12738.1.S1_s_at	LOC415802	similar to dynein, cytoplasmic, light chain 2B; dynein, cytoplasmic, light polypeptide 2B	1.882E-11	0.21	chr11:15786165-15790925 (+) // 99.55 //
7	Gga.7397.1.S1_s_at	PCP4	perlecan core protein 4	1.676E-06	0.21	chr1:10185210-101906499 (+) // 98.39 //
8	GgaAffx.3939.1.S1_s_at	LOC420440	similar to dipeptidyl aminopeptidase-like protein 6 (Dipeptidylpeptidase VI) (Dipeptidyl peptidase IV like protein) (Dipeptidyl aminopeptidase-related protein) (DPPX)	0.0032	0.26	chr2:7042359-7082740 (+) // 100.0 //
9	Gga.9621.1.S1_s_at	GIGYF2	glutamine rich protein, Grb10 interacting GYF protein 2	2.95E-07	0.27	chr9:487268-488554 (+) // 99.53 //
10	Gga.10041.Z1.A1_s_at	---	preproenkephalin	0.0060	0.29	chr3:103624409-103625647 (+) // 77.66 //
11	GgaAffx.5087.2.S1_s_at	ARL2BP	similar to binder of Arl Two; Arf-like 2 binding protein BART1 // ADP-ribosylation factor-like 2 binding protein	0.0019	0.30	chr11:737178-739520 (+) // 100.0 // chrUn:154379564-154381867 (-) // 99.43 //
12	GgaAffx.20528.1.S1_s_at	PROS1	vitamin K-dependent protein S precursor and stimulating fibrinolysis	4.18E-05	0.31	chr1:8359664-83597380 (-) // 99.46 //
13	Gga.18928.1.S1_s_at	LOC395978 // LOC424742 // LOC424743	glutamine rich protein // similar to tritrucoeloid repeat containing 15; Grb10 interacting GYF protein 2	1.07E-06	0.33	chr9:425725-488013 (+) // 94.69 //
14	Gga.16832.1.S1_s_at	---	finished cDNA, clone CHEST115n14	0.0055	0.34	chr5:654275-656218 (-) // 92.03 //
15	GgaAffx.8012.1.S1_s_at	PWP1	PWP1 homolog (S. cerevisiae)	9.81E-06	0.35	chr1:50058462-50072886 (-) // 98.0 //
16	GgaAffx.20534.1.S1_s_at	---	finished cDNA, clone CHEST835p19	3.58E-06	0.35	chr4:9193274-9194099 (-) // 82.75 //
17	Gga.4680.1.S2_s_at	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	1.03E-05	0.35	chr7:36381868-36387313 (+) // 87.37 //
18	Gga.19474.1.S1_s_at	LOC422242	similar to Mtap7 protein	4.12E-05	0.38	chr4:4034529-4035785 (+) // 99.13 //
19	Gga.14193.1.S1_s_at	CNTNAP5	contactin associated protein-like 5	1.80E-06	0.36	chr7:25124509-25140486 (+) // 97.08 //
20	GgaAffx.11874.1.S1_s_at	LOC421394	similar to hypothetical protein MGC29875; novel putative protein similar to YIL019C yeast hypothetical 84 kD protein from SGA1-KTR7	2.47E-05	0.38	chr7:19180152-19195117 (-) // 98.02 //
21	Gga.3447.1.S1_s_at	LOC420416	similar to Phospholipase C, delta 1	2.44E-10	0.38	chr2:4089904-4091636 (-) // 81.64 //
22	Gga.17201.1.S1_s_at	---	finished cDNA, clone CHEST4769	1.74E-07	0.38	chr4:85581588-85582806 (-) // 78.17 //
23	Gga.9825.2.S1_s_at	ARMC1	armadillo repeat containing 1	4.89E-07	0.39	chr2:11404871-11404936 (+) // 88.94 // chr2:114045833-114046424 (-) // 86.19 //
24	GgaAffx.10490.1.S1_s_at	LOC427996	similar to Membrane-bound transcription factor site 2 protease (S2P endopeptidase) (Site-2 protease) (Sterol-regulatory element-binding proteins intramembrane protease)	1.35E-08	0.39	chr1:112422369-112423395 (-) // 100.0 //
25	Gga.13233.1.S1_s_at	SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	0.0098	0.39	chr5:656412-660936 (-) // 99.18 //
26	GgaAffx.21577.1.S1_s_at	---	finished cDNA, clone CHEST567k4	5.79E-05	0.39	chr2:12745458-12746136 (+) // 57.16 //
27	Gga.9299.1.S1_s_at	---	carthagen palmitoyltransferase 1B isoform a, CPT1, muscle	1.20E-07	0.40	---
28	GgaAffx.3939.2.S1_s_at	LOC420440	similar to Dipeptidyl aminopeptidase-like protein 6 (Dipeptidylpeptidase VI) (Dipeptidyl peptidase IV like protein) (Dipeptidyl aminopeptidase-related protein) (DPPX)	0.0054	0.40	chr7:7036851-7053329 (+) // 100.0 //
29	Gga.7021.1.S1_s_at	---	similar to exosome component RRP41	9.42E-06	0.41	---
30	Gga.692.1.S2_s_at	LOC386173	GABA A receptor	7.02E-07	0.41	chr4:10607528-10640808 (+) // 97.88 //
31	GgaAffx.5084.1.S1_s_at	LOC421211	similar to hypothetical protein	5.48E-06	0.41	chr3:2269955-2331924 (+) // 100.0 //
32	GgaAffx.21211.1.S1_s_at	---	finished cDNA, clone CHEST527c8	1.23E-05	0.42	chr2:31576472-31577287 (+) // 87.72 //
33	Gga.18390.1.S1_s_at	---	finished cDNA, clone CHEST710a19	5.36E-05	0.42	chrUn:90296978-90299585 (+) // 96.14 //
34	GgaAffx.10490.2.S1_s_at	LOC427996	similar to Membrane-bound transcription factor site 2 protease (S2P endopeptidase) (Site-2 protease) (Sterol-regulatory element-binding proteins intramembrane protease)	1.94E-09	0.42	chr1:112422369-112421292 (-) // 100.0 //
35	Gga.4308.1.S1_s_at	LOC398507	M-CK	0.0017	0.42	---
36	Gga.16476.1.S1_s_at	---	finished cDNA, clone CHEST119114	6.92E-08	0.43	chr1:106811863-106814192 (+) // 97.56 //
37	GgaAffx.24672.1.S1_s_at	PROS1	protein S (alpha)	6.16E-05	0.43	chr1:8359750-83597842 (-) // 100.0 //
38	GgaAffx.21572.1.S1_s_at	LOC427552	similar to MGC64409 protein	0.0027	0.44	chr1:11801700-11802372 (-) // 96.19 // chr11:11802823-11803464 (-) // 62.27 //
39	Gga.1684.1.S1_s_at	LOC423531	similar to chromosome 14 open reading frame 149	0.0019	0.44	chr5:515124-5153725 (+) // 93.1 //
40	Gga.18202.1.S1_s_at	---	finished cDNA, clone CHEST1008q24	2.31E-08	0.45	chr14:2492671-2496878 (+) // 99.14 //
41	Gga.1622.1.S1_s_at	---	MANEA from homo sapiens gene	2.17E-05	0.45	chr3:71625440-71626214 (-) // 92.19 //
42	Gga.19198.1.S1_s_at	---	hypothetical protein, clone 12m23	1.43E-05	0.45	chr1:2801272-2803486 (+) // 98.38 //
43	Gga.19851.1.S1_s_at	RGMA	Repulsive guidance molecule A precursor (RGM domain family member A)	1.24E-05	0.45	chr10:15246749-15247768 (+) // 96.46 //
44	Gga.9574.1.S1_s_at	LOC419390	hairly and enhancer of split 5	0.0030	0.46	chr21:1312315-1313972 (-) // 98.78 //
45	Gga.4900.5.S1_s_at	17.5	lectin-like protein, type II transmembrane protein (17.5)	4.31E-08	0.46	chr1:2953439-29537807 (-) // 67.7 //
46	Gga.11811.1.S1_s_at	LOC422184	CXorf41 (Sarcoma antigen NY-SAR-97) from homo sapiens gene	0.00011	0.47	chr4:1754923-1763443 (+) // 99.85 //
47	GgaAffx.12011.1.S1_s_at	---	hypothetical protein, clone 12m23	1.00E-04	0.47	chr2:7623778-7623973 (+) // 96.46 //
48	Gga.11241.1.S1_s_at	HJES5	hairly and enhancer of split 5 (Drosophila)	0.0082	0.47	chr21:1330107-1331739 (+) // 98.52 //
49	GgaAffx.8131.1.S1_s_at	LOC418108	similar to zinc finger CCOH type domain containing 1	9.65E-06	0.47	chr1:53311766-53318124 (-) // 100.0 //
50	Gga.17631.1.S1_s_at	---	finished cDNA, clone CHEST1028e	0.00030	0.48	chr1:63054645-63059193 (-) // 98.51 //
51	GgaAffx.21722.1.S1_s_at	---	transcription factor IIRF (upstream binding factor)	0.0013	0.48	---
52	GgaAffx.26036.1.S1_s_at	HERC4	hect domain and RLD 4	1.74E-08	0.48	chr6:973557-9763142 (-) // 99.24 //
53	GgaAffx.20426.1.S1_s_at	---	similar to B-cell CLL/lymphoma 11A isoform 6	0.0026	0.48	chr3:578403-579676 (+) // 90.79 //
54	Gga.1865.1.S1_s_at	---	finished cDNA, clone CHEST293q4	0.002903	0.49	chr2:11751173-117512761 (+) // 97.21 //
55	Gga.18190.1.S1_s_at	---	finished cDNA, clone CHEST223q4	1.43E-05	0.49	chr11:87091-871820 (-) // 76.77 //
56	Gga.17542.1.S1_s_at	---	finished cDNA, clone CHEST199k16	1.30E-05	0.49	chr24:1635883-1640437 (-) // 98.98 //
57	Gga.13311.1.S1_s_at	LOC419738	similar to RIKEN cDNA 181001205	0.0071	0.49	chr24:2478871-2485682 (+) // 91.65 //
58	GgaAffx.1501.3.S1_s_at	LOC428222	similar to aragonate 1 protein	1.90E-06	0.49	chr23:3680289-3737379 (+) // 100.0 //
59	Gga.1327.1.S1_s_at	---	finished cDNA, clone CHEST1130d1	0.0057	0.49	chr5:9514211-9515375 (+) // 93.78 //
60	GgaAffx.12484.1.S1_s_at	LOC223346	similar to hypothetical protein SB30457H20	0.0024	0.49	chr5:34607614-34605034 (+) // 97.25 //
61	GgaAffx.12072.1.S1_s_at	ARL2BP	ADP-ribosylation factor-like 2 binding protein	7.00E-05	0.49	chrUn:15437345-154383905 (+) // 65.64 // chrUn:114691069-114694767 (-) // 45.33 //
62	Gga.18577.1.S1_s_at	LOC422887	hypothetical gene supported by CR390999	0.00015	0.49	chr4:8269586-82695704 (-) // 97.36 //
63	GgaAffx.9141.1.S1_s_at	LOC430962	similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1 (Phosphoinositide phospholipase C) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-1) (PLC-148)	1.71E-06	0.49	chr1:5668502-56689473 (-) // 100.0 //
64	GgaAffx.9875.1.S1_s_at	ARMC1	armadillo repeat containing 1	0.00019	0.50	chrUn:14159298-14163487 (+) // 100.0 //
65	Gga.1733.1.S1_s_at	GABAR9	GABA A receptor, beta-2 subunit	3.35E-05	0.50	chr3:2100828-2100913 (+) // 100.0 //
66	Gga.14326.1.S1_s_at	LOC416324	similar to KIA0837 protein	3.17E-05	0.50	chrUn:93113477-93116978 (+) // 57.37 // chr13:15682064-15690349 (-) // 92.55 //
67	Gga.2691.1.S1_s_at	CSK	c-src tyrosine kinase	0.0067	0.51	chr10:1394-8795 (-) // 87.7 //
68	GgaAffx.3861.1.S1_s_at	LOC428707	similar to 5-hydroxytryptamine 2C receptor (5-HT-2C) (Serotonin receptor 2C) (5HT-1C)	1.00E-04	0.51	chr4:2608572-2641285 (+) // 100.0 //
69	Gga.11386.1.S1_s_at	GLT1B1	glycyltransferase 28 domain containing 1	4.43E-08	0.51	chr1:1292587-12930024 (+) // 98.31 //
70	GgaAffx.8828.2.S1_s_at	LOC425424 // VPS45A	similar to vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45; vacuolar protein sorting 45B (yeast) // vacuolar protein sorting 45A (yeast)	5.50E-08	0.51	chr14:14111432-14114296 (+) // 100.0 //
71	Gga.8155.1.S1_s_at	---	finished cDNA, clone CHEST27b12	0.00037	0.51	---
72	GgaAffx.9513.1.S1_s_at	LOC428795	similar to dopamine receptor D1B - chicken	0.00033	0.51	chr4:7860461-7860604 (-) // 100.0 //
73	Gga.19329.1.S1_s_at	---	finished cDNA, clone CHEST739g15	9.01E-05	0.51	chr2:19844768-19859000 (+) // 97.99 //
74	Gga.2850.1.S1_s_at	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	5.49E-07	0.52	chr5:3032120-3033313 (+) // 54.31 //
75	GgaAffx.8023.1.S1_s_at	LOC420818	similar to aldehyde dehydrogenase 5A1 precursor isoform 2; mitochondrial succinate semialdehyde dehydrogenase; NAD(+)-dependent succinate semialdehyde dehydrogenase	0.00024	0.52	chr2:5763145-5763862 (-) // 100.0 //
76	Gga.4717.1.S1_s_at	PLDN	palldin homolog (mouse)	4.12E-05	0.53	chr10:11305155-113010789 (+) // 95.82 // chr10:11250843-11255975 (+) // 87.46 //
77	Gga.1145.2.S1_s_at	LOC415848	similar to RIKEN cDNA 4930470D19	0.0012	0.53	chr1:701740-733534 (+) // 94.81 //
78	GgaAffx.10717.1.S1_s_at	---	similar to Gamma-aminobutyric acid receptor alpha-5 subunit precursor (GABA(A) receptor)	0.00080	0.53	chr1:1242921-1243671 (+) // 100.0 //
79	GgaAffx.21977.1.S1_s_at	LOC425320	similar to chromosome 2 open reading frame 11	3.30E-05	0.53	chrUn:1493388-14939437 (+) // 100.0 // chr7:1217947-1218894 (+) // 98.43 //
80	Gga.18957.1.S1_s_at	Mk167	antigen identified by monoclonal antibody Ki-67	1.18E-05	0.53	chr1:93130851-93134829 (+) // 99.48 //
81	Gga.10335.1.S1_s_at	---	finished cDNA, clone CHEST68m22	1.31E-05	0.53	chr14:13894137-13895191 (+) // 99.36 //
82	Gga.19903.1.S1_s_at	---	finished cDNA, clone CHEST573k11	0.00032	0.54	chr4:84483-85468 (+) // 91.19 //
83	GgaAffx.11490.1.S1_s_at	LOC418410	similar to KIA1624 protein	6.65E-06	0.54	chr1:81572875-81599226 (-) // 99.04 //
84	Gga.7457.1.S1_s_at	---	finished cDNA, clone CHEST1172k15	0.00012	0.54	---
85	Gga.15024.1.S1_s_at	---	finished cDNA, clone CHEST1038k15	0.0006	0.55	chr2:30161020-30161720 (-) // 25.35 //
86	Gga.4680.1.S1_s_at	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	0.00024	0.55	chr7:36381868-36387313 (+) // 87.37 //
87	GgaAffx.21427.1.S1_s_at	---	finished cDNA, clone CHEST529g13	0.00063	0.55	chr14:12222465-1222356 (+) // 99.21 // chrUn:104274853-10427574 (-) // 99.33 //
88	Gga.15556.1.S1_s_at	---	transcribed locus	0.0017	0.55	chr3:1821224-1824598 (+) // 99.47 //
89	Gga.2847.1.S1_s_at	---	hypothetical protein, clone 23a22	0.00069	0.55	chr2:427E-05
90	GgaAffx.12082.1.S1_s_at	LOC417252 // ARRC1	LOC417252 // arrestin domain containing 1	2.47E-05	0.55	chr17:8900609-8926629 (-) // 97.6 //
91	Gga.14140.1.S1_s_at	---	finished cDNA, clone CHEST443k14	0.0032	0.55	chr12:15803980-15804885 (-) // 93.98 //
92	Gga.9765.1.S1_s_at	---	finished cDNA, clone CHEST12022	9.99E-05	0.56	chr1:5081538-5084584 (+) // 97.74 //
93	GgaAffx.22091.1.S1_s_at	LOC416323	similar to Long-chain-fatty-acyl-CoA ligase 6 (Long-chain acyl-CoA synthetase 6) (LACS 6)	0.00012	0.56	chr13:1567268-15690349 (+) // 98.95 //
94	GgaAffx.5055.2.S1_s_at	LOC417705	similar to HMG-box transcription factor 1; HMG-box containing protein 1	0.0016	0.56	chr1:9152578-9152925 (-) // 100.0 //
95	Gga.8213.1.S1_s_at	LOC431499	similar to hypothetical protein	0.0099	0.56	chrUn:10869103-109402009 (-) // 45.2 // chrUn:161673207-16167355 (-) // 56.23 //
96	GgaAffx.12497.1.S1_s_at	REC3	replication factor C (activator 1), 3, 38kDa	1.74E-05	0.57	chr1:16593165-16594573 (-) // 98.68 //
97	Gga.7226.1.S1_s_at	---	finished cDNA, clone CHEST140z2	0.0022	0.57	---

125	Gaa.8833.1.S1.at	---	transcribed locus	0.0065	0.59	chr3:25549356-25561486 (+) // 94.51 //
126	Gga.2242.1.S1.at	---	transcribed locus	0.0023	0.60	chr4:85272705-85273266 (-) // 97.38 // chrUn:29877281-29877894 (-) // 97.38 //
127	Gaa.14609.1.S1.at	HERC4	probable E3 ubiquitin-protein ligase HERC4	3.98E-07	0.60	chr5:97594.1 (-) // 98.86 //
128	Gaa.1925.1.S1.at	---	finished cDNA, clone CHEST23317	0.00010	0.60	chr4:16306479-16309446 (-) // 96.33 //
129	Gaa.17895.1.S1.at	---	finished cDNA, clone CHEST17718	0.00032	0.60	chr4:55549736-55586764 (-) // 98.98 //
130	Gaa.19633.1.S1.at	PHACTR1	phosphatase and actin regulator 1	0.00038	0.60	chr2:61988660-61988850 (-) // 98.68 //
131	GaaAffx.13010.1.S1.at	COCA1	cell division cycle associated 1	0.00064	0.60	chr6:56137.3-5629237 (-) // 98.19 //
132	GaaAffx.9143.2.S1.at	LOC430964	similar to Epitope holoprosencephaly candidate-1 protein (EHO-C-1) (Transmembrane protein 1) (GT33A) protein	0.00064	0.60	chrUn:15668214-156685823 (-) // 99.67 //
133	Gaa.16165.1.S1.at	---	finished cDNA, clone CHEST460a6	0.00038	0.60	chr23:4900885-4901530 (-) // 89.49 //
134	Gaa.16162.1.S1.at	ACSL6	fatty acid Coenzyme A ligase, long chain 6	2.32E-06	0.60	chr13:15661319-15662246 (+) // 77.04 // chr13:15670964-15672023 (-) // 75.97 //
135	GaaAffx.25188.1.S1.at	KBTBD3	kelch repeat and BTB (POZ) domain containing 3	0.00046	0.60	chr1:173064510-173088913 (+) // 100.0 //
136	Gaa.17397.1.S1.at	---	finished cDNA, clone CHEST1017121	6.61E-05	0.60	chr13:16413026-16414838 (-) // 98.95 //
137	GaaAffx.23748.1.S1.at	LOC418009	LOC418009	0.00113	0.61	chr1:46820138-4682636 (-) // 100.0 //
138	Gaa.13195.1.S1.at	---	finished cDNA, clone CHEST422h3	0.0023	0.61	chr2:12619197-12619257 (+) // 96.81 //
139	GaaAffx.3883.1.S1.at	LOC422242	similar to Mia97 protein	0.00090	0.61	chr4:4023080-4026220 (-) // 100.0 //
140	Gaa.19413.1.S1.at	LOC426058	similar to chronic myelogenous leukemia tumor antigen 66 // similar to chronic myelogenous leukemia tumor antigen 66 short form	0.0066002	0.61	chrUn:127294288-127295753 (+) // 79.79 // chr2:130972803-130974631 (-) // 96.74 //
141	GaaAffx.12496.1.S1.at	LOC426379	ectodermless A1 receptor associated death domain protein	7.06E-05	0.61	chr1:99572836-99574235 (-) // 99.57 //
142	GaaAffx.10777.1.S1.at	LOC418747	similar to Guanine nucleotide exchange factor DBS (DBS big sister) (MCF2 transforming sequence-like protein)	8.28E-06	0.61	chr1:130612304-130733913 (-) // 99.25 //
143	GaaAffx.494.1.S1.at	LOC415616	similar to Ras GTPase-activating-like protein IQGAP1 (P195)	0.00015	0.61	chr11:17210-87730 (-) // 100.0 //
144	GaaAffx.21167.1.S1.at	LOC426379	finished cDNA, clone CHEST1991c21	5.62E-05	0.61	chr1:99572836-99574235 (-) // 99.57 //
145	Gaa.19301.1.S1.at	LOC419603	hypothetical gene supported by CE386657	2.09E-06	0.61	chr23:5098944-5071385 (-) // 95.73 //
146	Gaa.14254.4.S1.a	LOC421928	similar to Intorin beta-1 binding protein 1 (Intorin cytoplasmic domain-associated protein 1) (ICAP-1)	0.00012	0.61	chr3:9445385-94452166 (-) // 98.08 //
147	Gaa.17375.1.S1.at	---	finished cDNA, clone CHEST709a8	3.90E-05	0.61	chr1:51357623-51359170 (+) // 99.32 //
148	Gaa.17285.1.S1.at	---	finished cDNA, clone CHEST1938c2	0.00014	0.61	chr1:17075498-170756709 (+) // 96.98 //
149	GaaAffx.875.1.S1.s	LOC421025	similar to downstream of tyrosine kinase 6	8.13E-05	0.61	chr2:8361643-8365970 (+) // 100.0 //
150	Gaa.893.1.S1.a	CYP2A1	cytochrome P450, family 2A, subfamily A, peptidyl 1 // hypothetical gene supported by NM_204979	3.48E-07	0.62	chrUn:281961-284413 (+) // 69.09 //
151	Gaa.12797.1.S1.at	---	reverse transcriptase/hypothetical protein	3.05E-06	0.62	chr4:25480419-25481592 (+) // 82.54 //
152	GaaAffx.1251.1.S1.at	---	finished cDNA, clone CHEST569i0	0.00017	0.62	chr2:14319125-14320268 (-) // 97.28 //
153	GaaAffx.25126.1.S1.s	LOC418805	CM007_HUMAN from homo sapiens gene	5.67E-08	0.62	chr1:150247494-150271948 (+) // 100.0 //
154	Gaa.13205.1.S1.at	LOC423358	similar to ribosomal protein S6 kinase-like 1	0.00076	0.62	chr5:34964979-34968042 (-) // 99.29 //
155	Gaa.9688.1.S1.at	C10orf7	D123 gene product	0.00038	0.62	chrUn:14603088-146050448 (-) // 99.67 //
156	Gaa.16352.1.S1.at	---	finished cDNA, clone CHEST533o2	3.69E-06	0.62	chr2:2673317-26734064 (+) // 99.17 //
157	Gaa.2930.2.S1.at	---	---	0.00079	0.62	chr5:31282997-31283984 (+) // 98.84 //
158	Gaa.734.1.S1.at	GABARB	GABA-A receptor, beta-2 subunit // similar to gamma-aminobutyric acid A receptor beta 2 chain precursor - chicken	0.00030	0.63	chr13:2100903-2233449 (-) // 93.04 //
159	GaaAffx.6756.1.S1.s	LOC431265	similar to p64 isoform of N-Src	0.00031	0.63	chrUn:3189802-3243209 (-) // 95.29 //
160	Gaa.12471.1.S1.at	LOC421984	similar to RIKEN cDNA B130052G07	0.00013	0.63	chr3:18084460-18104300 (-) // 85.58 //
161	Gaa.7458.1.S1.at	---	finished cDNA, clone CHEST128a14	0.00018	0.63	chr26:2370954-2372202 (-) // 99.2 //
162	Gaa.13577.1.S1.at	---	finished cDNA, clone CHEST60d14	0.00021	0.63	chr3:95422396-95442026 (+) // 95.45 //
163	Gaa.10360.1.S1.at	---	finished cDNA, clone CHEST45a1	0.00020	0.63	chr2:6650503-66508272 (+) // 96.56 //
164	Gaa.19822.1.S1.at	---	finished cDNA, clone CHEST1681f5	0.00016	0.63	chr3:58613077-58619215 (+) // 98.22 //
165	GaaAffx.12191.1.S1.s	CD200	CD200 antigen	0.00029	0.63	chr1:82709027-82722123 (+) // 99.13 //
166	GaaAffx.20559.1.S1.at	---	finished cDNA, clone CHEST582b19	0.00013	0.63	chr13:14601294-14602385 (-) // 99.91 //
167	Gaa.2971.2.S1.at	AER61	glycosyltransferase // similar to hypothetical protein	0.0001099	0.63	chrUn:3693287-36934567 (+) // 97.97 // chrUn:128134993-128136473 (-) // 87.25 //
168	Gaa.4168.1.S1.at	SERPINH4	serpin peptidase inhibitor, clade H (hepat shock protein 47), member 1 (collagen binding protein 1)	0.00073	0.63	chr5:4535960-45340170 (+) // 79.67 //
169	Gaa.18177.1.S1.a	---	finished cDNA, clone CHEST868a19	0.00070	0.63	chr1:179323919-179324811 (-) // 75.78 //
170	GaaAffx.6826.1.S1.at	---	finished cDNA, clone CHEST569i0	0.00020	0.63	chr8:2590220-25903748 (+) // 100.0 //
171	Gaa.888.1.S1.at	COL6A3	collagen, type VI, alpha 3	0.00026	0.63	chr7:4729217-4733180 (+) // 96.02 //
172	Gaa.13491.1.S1.at	LOC422439	similar to E74-like factor 2 (ets domain transcription factor) isoform 2; new Ets-related factor	2.12E-06	0.63	chr4:29742571-29744153 (-) // 97.0 //
173	Gaa.3670.1.S1.at	LOC385978	glutamine rich protein	1.60E-07	0.63	chr9:442050-487214 (+) // 91.53 //
174	Gaa.3293.1.S1.at	FN1	fibrinectin 1	8.47E-05	0.63	chr7:4308335-4329848 (-) // 98.85 //
175	Gaa.3310.1.S1.at	XPAC	XPC-hHR23 protein	2.75E-06	0.63	---
176	Gaa.13709.1.S1.x	---	finished cDNA, clone CHEST964m18	0.00029	0.63	chrUn:44678001-44678823 (+) // 44.54 //
177	Gaa.16308.1.S1.at	---	finished cDNA, clone CHEST552o18	0.00038	0.63	chr2:110176086-110184803 (+) // 96.25 // chr2:110177278-110178861 (+) // 54.96 //
178	Gaa.15586.1.S1.at	---	---	0.00081	0.63	chrUn:18355472-15863392 (+) // 98.3 //
179	Gaa.18579.1.S1.at	LOC417622	similar to RIKEN cDNA 3100002B05	1.45E-05	0.64	chr16:68001-6858876 (+) // 99.2 //
180	GaaAffx.11119.1.S1.at	---	finished cDNA, clone CHEST246i15	0.00032	0.64	chr3:43919559-43920756 (+) // 86.89 //
181	Gaa.12387.1.S1.at	LOC420238	plasma glutamate carboxypeptidase	8.85E-05	0.64	chr2:12631449-126509608 (+) // 97.86 //
182	Gaa.2790.1.S1.at	---	transcribed locus	0.00050	0.64	chr1:99330681-99330682 (+) // 85.74 //
183	Gaa.672.1.S1.at	CNGA3	cyclic nucleotide gated channel alpha 3	0.00037	0.64	chr1:124961889-124994803 (-) // 92.04 //
184	Gaa.14871.1.S1.at	---	finished cDNA, clone CHEST294b17	2.28E-05	0.64	chr11:8607408-8608517 (-) // 99.28 //
185	Gaa.1788.1.S1.at	LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.00018	0.64	chr2:510123-515720 (-) // 98.07 //
186	Gaa.673.1.S1.at	---	finished cDNA, clone CHEST125o15	3.62E-05	0.64	chr3:50675421-50677255 (+) // 99.03 //
187	Gaa.12890.1.S1.at	RA8409	RA8409, member RAS oncogene family	0.00060	0.64	chr6:769694-7699122 (+) // 98.71 //
188	Gaa.6390.3.S1.a	LOC419014	similar to Dipeptidyl-peptidase 1 precursor (DPP-1) (DPP1) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase)	0.00028	0.64	chr1:179942795-179949701 (+) // 93.77 //
189	Gaa.692.1.S1.at	LOC396173	GABA-A receptor	0.00088	0.64	chr4:10607526-10640008 (+) // 97.88 //
190	Gaa.7649.1.S1.at	GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	5.22E-05	0.64	chr15:920195-955107 (-) // 97.42 //
191	Gaa.18989.1.S1.at	---	finished cDNA, clone CHEST12916	0.00025	0.64	---
192	Gaa.6263.2.S1.a	LOC424014	similar to methyltransferase 24 (37.8 kD) (3D495)	0.00086	0.64	chr7:4485712-4490145 (+) // 98.79 //
193	Gaa.2506.1.S1.at	---	finished cDNA, clone CHEST173e69	0.00022	0.64	chr8:2599015-25993566 (-) // 94.93 //
194	GaaAffx.12101.1.S1.s	LOC418951	similar to RIKEN cDNA 2510005D08	0.00071	0.64	chr1:17076397-170768945 (+) // 94.95 //
195	Gaa.12890.1.S1.at	RA8409	RA8409, member RAS oncogene family	0.00060	0.64	chr6:769694-7699122 (+) // 98.71 //
196	GaaAffx.1673.2.S1.at	LOC416407	similar to mKIAA1924 protein	0.00023	0.65	chr14:1959196-1959652 (-) // 100.0 //
197	Gaa.12147.1.S1.at	---	finished cDNA, clone CHEST1016a8	0.00064	0.65	chrUn:39438252-39437672 (+) // 98.74 //
198	Gaa.2324.2.S1.at	LOC425159	similar to Cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Proline aminopeptidase)	0.00011	0.65	chrUn:53951524-53952941 (+) // 87.47 // chrUn:65383735-65385193 (-) // 86.74 //
199	Gaa.4318.1.S1.at	FABP7	fatty acid binding protein 7, brain	0.00024	0.65	chr3:59867635-59871341 (-) // 91.81 //
200	Gaa.6054.2.S1.s	LOC422583	similar to polycystin 2, polycystin // polycystic kidney disease 2 (autosomal dominant)	0.00013	0.65	chr4:46227756-46229771 (-) // 93.16 //
201	GaaAffx.23228.1.S1.at	PKD2	---	0.00074	0.65	chr9:23318450-23322914 (+) // 100.0 //
202	Gaa.5452.1.S1.at	---	finished cDNA, clone CHEST21818	0.00087	0.65	chr26:730902-739313 (-) // 97.82 //
203	Gaa.7709.1.S1.at	LOC427465	similar to Death-associated protein kinase 1 (DAP kinase 1)	0.00082	0.65	chrZ_random:13835360-13937414 (+) // 97.73 //
204	GaaAffx.24960.1.S1.at	LOC421941	similar to hypothetical protein MGC33602	0.00061	0.65	chr3:95414489-95422104 (+) // 100.0 //
205	GaaAffx.12328.1.S1.at	LOC418874	similar to FLJ11712 protein	0.00024	0.65	chr1:162004621-162048842 (+) // 98.81 //
206	GaaAffx.20265.1.S1.at	---	finished cDNA, clone CHEST11121	0.00035	0.65	chr6:28025876-28026268 (+) // 99.91 //
207	Gaa.9692.1.S1.at	---	finished cDNA, clone CHEST716a23	0.00057	0.65	---
208	GaaAffx.26882.1.S1.s	LOC423061	similar to TUBBY PROTEIN HOMOLOG	6.74E-06	0.65	chr5:7720620-7841077 (-) // 100.0 //
209	Gaa.16086.1.S1.at	---	XPG	0.00064	0.65	chr1:135443545-135450589 (-) // 96.87 //
210	GaaAffx.12429.1.S1.at	CRSP8	factor required for S1 transcriptional activation, subunit 8, 34kDa	0.00019	0.65	chr17:392657-4007491 (+) // 98.71 //
211	GaaAffx.13009.1.S1.at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	0.00044	0.65	chrZ_random:5223548-5226999 (-) // 98.95 //
212	Gaa.13514.1.S1.at	---	finished cDNA, clone CHEST324o15	0.00015	0.65	chr1:49387204-49388705 (-) // 94.63 //
213	GaaAffx.20450.1.S1.at	---	finished cDNA, clone CHEST1995a4	0.00091	0.65	chr15:8414073-8415589 (+) // 98.28 //
214	Gaa.14884.1.S1.at	LOC421020	similar to hypothetical protein LOC55580	0.00016	0.65	chr3:22131-233983 (-) // 96.71 //
215	Gaa.5236.1.S1.at	LOC418916	similar to hypothetical protein	0.00085	0.65	chr1:177279291-177294700 (-) // 91.7 //
216	Gaa.8814.1.S1.s	NANS	N-acetylneuraminic acid synthase (sialic acid synthase)	0.00040	0.65	chr2:24052174-24054356 (-) // 99.59 // chrZ:24069307-24070023 (-) // 68.48 //
217	GaaAffx.1143.1.S1.s	SDFR1	stromal cell derived factor receptor 1	0.00033	0.65	chr10:449032-494194 (+) // 98.81 //
218	Gaa.8935.2.S1.s	LOC417173	similar to C3G protein	0.00077	0.65	chr17:4078126-4100742 (+) // 94.5 //
219	GaaAffx.349.4.S1.s	Per3	circadian clock protein	0.00011	0.65	chr21:239082-241070 (-) // 100.0 //
220	GaaAffx.23684.1.S1.s	LOC419857	similar to plexin A2, plexin_A2 plexin-A2	0.00071	0.66	chr26:1336906-1425238 (-) // 100.0 //
221	Gaa.19520.1.S1.at	---	finished cDNA, clone CHEST1879h10	0.00021	0.66	chr21:1367340-1368817 (-) // 88.33 //
222	Gaa.8320.1.S1.at	WEE1	WEE1 homolog (S. pombe)	4.03E-05	0.66	chr5:6836956-6844648 (+) // 99.94 //
223	Gaa.19457.1.S1.at	---	finished cDNA, clone CHEST471m7	0.00019	0.66	chr2:84201944-84203216 (-) // 75.97 //
224	GaaAffx.11526.1.S1.s	LOC421804	similar to KIAA0776 protein	1.88E-05	0.66	chr3:7116601-71187606 (-) // 97.89 //
225	Gaa.19548.1.S1.at	---	finished cDNA, clone CHEST1911f15	0.00049	0.66	chr3:142451-51425903 (-) // 93.26 //

266	GgaAfx.8187.1.S1_at	LOC418135 // GET	similar to 672043521Rlx protein // gonad expressed transcript	5.63E-05	1.58	chr1:55978768-55980087 (-) // 100.0 //
267	Gga.7842.1.S1_at	---	finished cDNA, clone CHEST534m23	0.0047	1.58	chr26:3344937-3345952 (-) // 95.14 //
268	Gga.2858.1.S1_at	LOC423675	similar to Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN (Mutated in multiple advanced cancers 1)	9.82E-06	1.58	chr6:8896743-8901294 (-) // 99.17 //
269	GgaAfx.25913.1.S1_at	LOC423675	similar to Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN (Mutated in multiple advanced cancers 1)	2.63E-05	1.58	chr6:8900086-8941657 (-) // 100.0 //
270	Gga.18371.1.S1_s_at	LARP6	La ribonucleoprotein domain family, member 6	0.0065	1.59	chr10:7024023-7025867 (-) // 99.1 //
271	Gga.1347.1.S1_at	MRP533	mitochondrial ribosomal protein S33	8.24E-07	1.59	chr1:53700891-53706422 (-) // 93.85 //
272	Gga.13559.1.S1_at	---	finished cDNA, clone CHEST219m12	3.74E-07	1.60	chr1:180684099-180684846 (+) // 46.25 //
273	Gga.1185.3.S1_a_at	NTHL1	nth endonuclease III-like 1 (E. coli)	0.0024	1.61	chr14:8304909-8307405 (-) // 99.9 //
274	GgaAfx.2169.1.S1_at	---	finished cDNA, clone CHEST897r18	0.00029	1.61	chr10:74611526-74615181 (+) // 98.95 //
275	Gga.1809.1.S1_at	HSPB1	heat shock 27kDa protein 1	0.0018	1.61	chr19:3987372-3988804 (-) // 97.73 //
276	Gga.1739.1.S1_s_at	LOC428256	similar to zinc finger protein 259, zinc finger protein ZPR1	6.37E-05	1.62	chr24:4790367-4793732 (-) // 74.23 //
277	Gga.19123.1.S1_at	---	finished cDNA, clone CHEST17644	2.61E-06	1.63	chrUn:131884994-131888358 (-) // 98.22 //
278	Gga.16760.1.S1_at	LOC416710	similar to RNA polymerase I polypeptide B, DNA-directed RNA polymerase I 135kDa polypeptide, RNA polymerase I subunit 2	0.0010	1.64	chr14:16219529-16220709 (-) // 67.0 //
279	Gga.1901.1.S1_at	LOC423718	similar to cadherin-related 23 protein	1.79E-07	1.65	chr6:11069632-11067698 (+) // 99.21 //
280	Gga.10365.1.S1_at	---	finished cDNA, clone CHEST1662h4	1.38E-05	1.65	chr1:126893923-126898058 (+) // 81.59 //
281	Gga.12201.1.S1_at	LOC420784	similar to chromosome 7, open reading frame 36, GK003 protein	0.0031	1.66	chr2:49514534-49524056 (+) // 91.27 //
282	GgaAfx.10743.1.S1_at	LOC418716	similar to interleukin 1 receptor, type 1	0.0021	1.66	chr1:126892244-126903475 (+) // 100.0 //
283	Gga.768.1.S1_at	TGIF	TGF-beta-induced factor (TAL1 family homeobox)	5.43E-05	1.66	chr2:99554053-99567291 (+) // 89.82 //
284	Gga.8006.1.S1_at	---	transcribed locus, strongly similar to XP_430006.1 PREDICTED: hypothetical protein XP_430006 (Gallus gallus)	1.68E-05	1.67	chr4:89736430-89737380 (+) // 99.05 //
285	Gga.19285.1.S1_at	LOC427259	similar to RIN1c cDNA D610038L10 gene	1.39E-05	1.68	chr2:17818499-17824324 (-) // 85.86 //
286	GgaAfx.10224.1.S1_at	LOC418913	similar to Protein C210r6	0.0019	1.68	chr1:10036272-100383058 (+) // 100.0 //
287	GgaAfx.5549.1.S1_at	LOC427854	similar to glycoprotein	6.35E-06	1.68	chr1:19314772-19386040 (+) // 100.0 //
288	GgaAfx.25884.1.S1_at	LOC420130	similar to KIAA0561 protein	0.00096	1.68	chr28:3345744-3350345 (+) // 100.0 //
289	Gga.14438.1.S1_at	---	finished cDNA, clone CHEST35k24	0.0028	1.68	chr1:12526901-12528780 (-) // 47.75 //
290	Gga.12599.1.S1_at	RHOJ	Ras homolog gene family, member J	6.82E-06	1.69	chr5:50176682-50221383 (-) // 96.83 //
291	Gga.739.1.S1_at	P20K	pucescens-specific protein	0.0013	1.69	---
292	Gga.16760.1.S1_s_at	LOC416710	similar to RNA polymerase I polypeptide B, DNA-directed RNA polymerase I 135kDa polypeptide; RNA polymerase I subunit 2	0.00089	1.70	chr14:16219529-16220709 (-) // 67.0 //
293	Gga.11055.1.S1_at	---	finished cDNA, clone CHEST720m16	0.0047	1.70	chr1:52148489-52149480 (+) // 85.65 //
294	Gga.4579.1.S1_at	TUBB	tubulin, beta polypeptide	0.00070	1.70	chrUn:15018291-15018375 (+) // 44.75 //
295	Gga.2324.1.S1_s_at	LAP3 // LOC425351 // LOC439694	leucine aminopeptidase 3 // similar to Cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Proline aminopeptidase) (Prolyl aminopeptidase) // similar to Cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Prolyl aminopeptidase) (Prolyl aminopeptidase)	6.18E-07	1.71	chrUn:53940747-53955822 (+) // 47.34 // chrUn:65380877-65386998 (-) // 51.33 //
296	Gga.11319.1.S1_at	LOC439648	similar to aminopeptidase 1 (Prolyl aminopeptidase)	0.0067	1.71	---
297	Gga.6363.1.S1_at	LOC421593	similar to JH5M6.4 (novel 58.3 kDa protein)	0.0040	1.72	chr3:42140519-42148825 (+) // 99.82 //
298	Gga.17989.1.S1_at	---	finished cDNA, clone CHEST276h23	0.0013	1.72	chr1:63055700-63057963 (-) // 99.46 //
299	Gga.15298.1.S1_at	---	finished cDNA, clone CHEST53e19	1.57E-06	1.72	chr3:42163480-42165073 (+) // 96.93 //
300	Gga.5544.1.S1_at	LOC395100	cytochrome 4	0.00018	1.72	chr2:31434-42710 (+) // 95.49 //
301	Gga.1714.1.S1_at	LOC427874	similar to Alpha-2-macroglobulin precursor (Alpha-2-M)	0.0047	1.72	chr1:40285150-40291047 (-) // 99.61 //
302	Gga.17956.1.S1_at	---	finished cDNA, clone CHEST28k22	0.0063	1.73	chr4:23936437-23937288 (+) // 65.8 //
303	Gga.12888.1.S1_at	HIPK2	homeodomain interacting protein kinase 2	6.80E-06	1.73	chr1:52753898-52817234 (+) // 99.45 //
304	GgaAfx.22248.1.S1_at	LOC418648	similar to CR36.1 (3-methyl-adenine DNA glycosylase)	0.00139	1.73	chr14:13984373-13991455 (+) // 100.0 //
305	Gga.714.1.S1_at	FMN	formin	0.0043	1.73	chr5:27313397-27422165 (+) // 89.04 //
306	Gga.1806.1.S1_at	SQJL	SQJL protein	0.00030	1.74	chr5:55448066-55458995 (+) // 99.19 //
307	GgaAfx.2588.1.S1_x_at	LOC417588	similar to hypothetical protein DKFZ0434K1421	0.0010	1.74	chr19:576554-5776189 (+) // 100.0 //
308	GgaAfx.1974.1.S1_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.00057	1.74	chr6:3392593-3393504 (+) // 99.81 //
309	GgaAfx.1974.1.S1_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.00057	1.75	chr6:8243332-8407124 (+) // 99.04 //
310	Gga.3551.1.S1_at	LOC395210	osteopontin	0.0057	1.75	chr4:46242098-46245154 (-) // 95.29 //
311	Gga.4579.1.S1_x_at	TUBB	tubulin, beta polypeptide	0.00088	1.76	chrUn:15018291-15018375 (+) // 44.75 //
312	Gga.20015.1.S1_at	---	finished cDNA, clone CHEST53b24	8.41E-06	1.76	---
313	Gga.10533.1.S1_at	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif 1)	0.0042	1.77	chr2:18946818-18963993 (-) // 93.83 //
314	GgaAfx.13119.1.S1_s_at	RPS14	ribosomal protein S14	0.0096	1.77	chr13:12081746-12086248 (+) // 98.72 //
315	Gga.7262.4.S1_s_at	MRRF	mitochondrial ribosome recycling factor	0.00011	1.79	chr17:1678602-1682826 (-) // 99.42 //
316	Gga.5448.1.S1_s_at	---	finished cDNA, clone CHEST53b24	0.00019	1.79	chr14:18514129-18535054 (+) // 96.61 //
317	Gga.17281.1.S1_at	---	finished cDNA, clone CHEST257h20	1.17E-05	1.80	chr2:84532519-84533765 (-) // 89.53 //
318	GgaAfx.22766.1.S1_at	MKKS	McKusick-Kaufman syndrome	1.47E-06	1.81	chr14:18616344-18618677 (-) // 100.0 //
319	GgaAfx.24101.1.S1_at	LOC428502	similar to methionine synthase reductase isoform 2	0.00080	1.82	chr2:79181094-79210068 (-) // 100.0 //
320	Gga.1727.1.S1_s_at	PP1F	protein phosphatase 1 (cytosolic F)	0.00051	1.83	chr6:11498988-11506763 (-) // 98.16 //
321	Gga.13364.1.S1_at	---	finished cDNA, clone CHEST52i97	3.96E-10	1.83	---
322	Gga.11966.1.S1_a_at	LOC422057	similar to calcineurin inhibitor ZAK1-4 beta splice variant 1	1.21E-05	1.83	chr3:10758814-107663468 (-) // 88.82 //
323	Gga.15891.1.S1_at	LOC426592 // LOC429375 // LOC439616	similar to nucleoporin 98k isoform 1; Nup98-Nup96 precursor; GLFG-repeat containing nucleoporin; nucleoporin 98k // similar to nucleoporin 98k isoform 1; Nup98-Nup96 precursor; GLFG-repeat containing nucleoporin; nucleoporin 98k // similar to nucleoporin 98k isoform 1; Nup98-Nup96 precursor; GLFG-repeat containing nucleoporin; nucleoporin 98k	0.00041	1.84	chrUn:13405362-134074317 (+) // 97.16 //
324	GgaAfx.3403.1.S1_at	LOC427354	similar to hypothetical protein FLI33868	6.31E-06	1.84	chrZ_random:1421170-1448671 (+) // 94.84 //
325	Gga.11763.1.S1_at	LOC423009	gene model G31_INCB1	2.45E-05	1.85	chr5:257982-2655145 (+) // 88.84 //
326	Gga.19630.1.S1_s_at	TREM2	Toll-like receptor expressed on myeloid cells 2	0.0002196	1.85	chr26:3285584-3290127 (-) // 97.11 //
327	Gga.1404.2.S1_at	MCFD2	multiple coagulation factor deficiency 2	6.85E-06	1.87	chr3:23263129-23264812 (-) // 86.57 //
328	Gga.16608.1.S1_at	---	transcribed locus	3.42E-07	1.88	chr13:15645962-15646988 (-) // 99.42 //
329	GgaAfx.13149.1.S1_at	LOC422344	similar to AW547198 protein	0.0034	1.88	chr4:13446085-13449246 (-) // 98.37 //
330	Gga.1815.2.S1_at	---	ankyrin 3, node of Ranvier (ankyrin G)	0.00037	1.88	chr6:840313-8401786 (+) // 99.81 //
331	GgaAfx.6199.1.S1_at	LOC421384	similar to hypothetical protein MGC29875; novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7	0.00097	1.88	chr3:19180152-19195117 (-) // 99.97 //
332	Gga.1594.2.S1_a_at	---	finished cDNA, clone CHEST1753i1	0.0019	1.89	chr15:7866755-7868773 (+) // 64.27 //
333	Gga.1790.1.S1_at	ZC3HAV1	zinc finger CCHC-type, antiviral 1	6.00E-05	1.89	chrUn:142641976-142643135 (+) // 94.29 //
334	GgaAfx.12194.1.S1_at	DUT (mouse)	hypothetical protein, clone 1048	2.95E-06	1.91	chr10:10702976-10713811 (+) // 98.19 //
335	Gga.5161.1.S1_s_at	CHANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.00028	1.91	chr6:8372224-8407119 (+) // 94.15 //
336	GgaAfx.3400.1.S1_s_at	LOC416539	similar to hypothetical protein MGC35212	0.0076	1.92	chr14:8093737-8100073 (-) // 100.0 //
337	Gga.5295.1.S1_at	---	transcribed locus	0.00012	1.93	chr15:8574467-8575831 (+) // 83.93 //
338	GgaAfx.2588.1.S1_at	LOC417588	similar to hypothetical protein DKFZ0434K1421	8.07E-05	1.96	chr19:576554-5776189 (+) // 100.0 //
339	Gga.7484.1.S1_at	---	transcribed locus, weakly similar to XP_425603.1 PREDICTED: similar to ORF2 (Gallus gallus)	3.25E-09	1.96	chr3:315971-316736 (-) // 59.62 //
340	GgaAfx.26361.1.S1_s_at	LOC422188	similar to Alpha-galactosidase A precursor (Melibiase) (Alpha-D-galactoside galactohydrolase) (Alpha-D-galactosidase A) (Alpha-D-galactosidase)	0.0012	1.96	chr4:1848393-1853423 (+) // 100.0 //
341	Gga.14050.1.S1_at	LOC410570	(Arabidopsis thaliana)	0.0065	1.97	chr13:16812776-16813999 (+) // 98.46 //
342	Gga.10674.1.S1_at	MAP3K2	mitogen-activated protein kinase kinase kinase2	0.00046	2.01	chr7:24306003-24307429 (+) // 98.32 //
343	Gga.7457.2.S1_a_at	---	finished cDNA, clone CHEST172k15	0.0017	2.01	---
344	Gga.5137.1.S1_x_at	---	major histocompatibility class I antigen B-L beta mRNA, partial cds, beta 1 domain	0.00015	2.10	chr16:1750811-1764881 (-) // 84.4 //
345	GgaAfx.2851.1.S1_at	LOC424441	similar to beta-2-microglobulin protein 2, putative beta-binding protein	0.00052	2.11	chr8:7445252-7425794 (+) // 100.0 //
346	GgaAfx.26094.1.S1_at	LARP6	La ribonucleoprotein domain family, member 6	0.0077	2.12	chr10:7023437-7025779 (-) // 100.0 //
347	GgaAfx.7834.1.S1_at	LOC429049	similar to neuroxophilin	0.00053	2.13	chr7:32104615-32135161 (-) // 100.0 //
348	Gga.6508.1A1_at	LOC422188	similar to Alpha-galactosidase A precursor (Melibiase) (Alpha-D-galactoside galactohydrolase) (Alpha-D-galactosidase A) (Alpha-D-galactosidase)	0.00019	2.15	chr4:1853299-1853829 (+) // 99.24 //
349	Gga.4604.1.S1_at	LOC423925	similar to DNA segment, Chr 19, ERATO D01 73, expressed	0.00024	2.23	chr6:2864047-28701148 (-) // 95.49 //
350	GgaAfx.25213.1.S1_at	LOC419020	similar to RAB30	7.93E-07	2.31	chr1:180754146-180762406 (-) // 100.0 //
351	GgaAfx.4393.3.S1_s_at	---	---	2.77E-06	2.37	chr4:8529298-8549458 (-) // 100.0 //
352	Gga.2481.1.S1_at	---	transcribed locus	0.00037	2.45	chr13:8321304-8322395 (+) // 94.07 //
353	Gga.4536.2.S1_a_at	AKR1D1	alko-steroid reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	8.52E-08	2.45	chr1:5328040-53267287 (+) // 97.33 //
354	Gga.15862.1.S1_at	LOC418241	similar to CG9646-PA	0.000286	2.48	chr1:66809031-66820016 (-) // 98.76 //
355	Gga.20011.1.S1_at	LOC419787	RNF19 from homo sapiens gene	0.00080	2.50	chr2:127537199-127546083 (-) // 54.9 //
356	GgaAfx.1940.1.S1_at	LOC416208	similar to stannocalcin	0.0016	2.52	chr13:8324348-8329988 (+) // 100.0 //
357	Gga.46.1.S1_a_at	LOC396351	ca-d4	0.0026	2.53	chr5:23815899-23904897 (+) // 97.18 //
358	GgaAfx.25213.2.S1_s_at	LOC419020 // LOC430100	similar to RAB30 // similar to RAB30	1.79E-05	2.56	chr1:180757159-180762400 (-) // 99.48 // chrUn:102992765-102992737 (-) // 100.0 //
359	Gga.8227.1.S1_s_at	ISG12-1	putative ISG12L protein	3.52E-05	2.65	chr23:3860194-3851214 (+) // 75.82 //
360	Gga.12484.1.S1_at	---	finished cDNA, clone CHEST122b1	0.0082	2.66	chr2:97898534-9790381 (+) // 89.4 //
361	Gga.12364.1.S1_at	ZNF330	zinc finger protein 330	4.76E-05	2.87	chr4:30413474-30424562 (+) // 90.82 //
362	GgaAfx.11956.1.S1_at	LOC418729	similar to PINCH-1	3.16E-06	2.98	chr1:129327744-129392199 (+) // 96.65 // chr1:129410765-129421418 (+) // 73.78 //
363	Gga.6010.1.S1_at	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	2.59E-08	3.03	chr26:3296170-3302489 (+) // 99.23 //
364	GgaAfx.1849.2.S1_s_at	LOC416208	similar to stannocalcin	0.00057	3.09	chr13:8324356-8329988 (+) // 100.0 //

Supplementary material Table S2. Ka et al.

List with 585 differentially expressed genes with $p < 0.01$. G1- G13 indicates that gene is located in QTL regions for growth and altered body weights (Jacobsson et al 2005).

List #	Ensemble Gene ID	p-values	Fold Difference LWS/HWS	Chr	Start	QTL	Description, Ensemble
1	ENSGALG00000014326	0.00445576	0.36	11	743991		ADP-ribosylation factor-like protein 2-binding protein (ARF-like 2-binding protein) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZKW5]
2	ENSGALG00000016382	2.7749E-10	0.38	1	122526313		Hypothetical protein with similarities to ZINC_PROTEASE IBI 00583043
3	ENSGALG00000006314	0.00495205	0.40	2	7139733		SIMILAR TO DIPEPTIDYL AMINOPEPTIDASE LIKE PROTEIN
4	ENSGALG00000012011	0.00483026	0.42	5	57377972		SIMILAR TO CHROMOSOME 14 OPEN READING FRAME 149, Pro_racemase; 1
5	ENSGALG000000012663	0.00026445	0.44	2	58961391	G2	SIMILAR TO SUCCINIC SEMIALDEHYDE DEHYDROGENASE
6	ENSGALG00000004870	0.00014799	0.46	4	1880366		SIMILAR TO PHOSPHOPANTETHEINE
7	ENSGALG000000003861	2.8756E-08	0.48	6	11530886		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5F401]
8	ENSGALG00000005853	0.00940071	0.50	4	2779925		Weakly SIMILAR TO 5-HYDROXYTRYPTAMINE 2C RECEPTOR.
9	ENSGALG000000012842	9.9392E-05	0.50	1	58688000		26 KDA PROTEIN, similarities to Poly(ADP-ribose) polymerase, catalytic region
10	ENSGALG000000014975	0.00387606	0.51	4	81452321		Dopa 1A/1B recpt. G. PROTEIN RECEPTOR F1 2; 1
11	ENSGALG000000016000	1.8717E-05	0.53	2	131923424	G3	Parial seq - similar to plasma glutamate carboxypeptidase
12	ENSGALG00000001797	0.00432084	0.54	17	8610999		Hypothetical protein with a tetra-trico peptide repeat (TPR) G-protein signaling modulator 1
13	ENSGALG000000030113	1.4858E-07	0.54	6	9524380		Uncharacterized protein C10orf107 [Source:UniProtKB/Swiss-Prot;Acc:Q8VU9]
14	ENSGALG00000016202	5.1383E-05	0.54	1	113445490		SIMILAR TO HSF2BP, PARTIAL
15	ENSGALG000000012537	0.00060192	0.55	7	37363230		G protein-activated inward rectifier potassium channel 1 (GIRK1)(Potassium channel, inwardly rectifying subfamily J member 3)(Inward rectifier)
16	ENSGALG000000023387	1.8303E-05	0.55	6	35379101		SIMILAR TO CHMADRIN , with FHA (Forkhead-associated) domain, phosphopeptide binding motif
17	ENSGALG000000000062	1.0943E-05	0.55	2	119063539	G3	Armaddillo repeat-containing protein 1 [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMQ0]
18	ENSGALG000000013925	0.00420563	0.56	4	67140610		Mast/stem cell growth factor receptor Precursor (SCFR)(EC 2.7.10.1)(Proto-oncogene tyrosine-protein kinase Kit)(c-kit) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZK11]
19	ENSGALG00000008532	7.5477E-07	0.56	17	2302407		similar to cofactor of BRCA1; negative elongation factor protein B [Source:RefSeq peptide;Acc:NP_001006202]
20	ENSGALG000000000444	0.00015858	0.56	26	1268577		
21	ENSGALG000000015360	0.00011108	0.56	1	90843676		Protein CIP2A homolog [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMJ7]
22	ENSGALG000000017064	7.4562E-05	0.57	1	178159176	G1	replication factor C (activator 1) 3, 38kDa [Source:RefSeq peptide;Acc:NP_001006276]
23	ENSGALG000000010294	0.00205157	0.58	5	40520686	G8	Ribosomal protein S6 kinase-like 1
24	ENSGALG000000017025	3.4591E-05	0.58	1	174680950	G1	cytoskeleton associated protein 2 [Source:RefSeq peptide;Acc:NP_001006274]
25	ENSGALG000000016890	0.00016004	0.59	13	7101357		GABA-A receptor beta 2 subunit Precursor; Fragment [Source:UniProtKB/TrEMBL;Acc:Q90590]
26	ENSGALG000000015409	0.000595	0.59	1	92894377		
27	ENSGALG000000013464	0.00304185	0.60	25	25979		Acidic leucine-rich nuclear phosphoprotein 32 family member E [Source:UniProtKB/Swiss-Prot;Acc:Q5F4A3]
28	ENSGALG000000000060	0.00251722	0.60	1	15505338		
29	ENSGALG000000015685	0.00017168	0.60	4	85606595		
30	ENSGALG000000020909	1.481E-07	0.60	20	11227253	G12	
31	ENSGALG000000016049	0.00020637	0.60	2	134426713		
32	ENSGALG000000012732	0.00571277	0.61	2	63373559		Phosphatase and actin regulator 1 [Source:UniProtKB/Swiss-Prot;Acc:Q801X6]
33	ENSGALG000000020292	0.00075463	0.61	4	10924256	G6	Gamma-aminobutyric acid receptor subunit gamma-4 Precursor (GABA(A) receptor subunit gamma-4) [Source:UniProtKB/Swiss-Prot;Acc:P345]
34	ENSGALG000000015396	0.00055841	0.62	1	92004787		CD200 antigen [Source:RefSeq peptide;Acc:NP_001025958]
35	ENSGALG000000014369	0.00021358	0.62	3	39222930	G4	ectodysplasin A1 receptor associated death domain protein [Source:RefSeq peptide;Acc:NP_001012405]
36	ENSGALG000000012946	0.0002851	0.63	1	61674910		Protein FAM60A [Source:UniProtKB/Swiss-Prot;Acc:Q5ZJ7]
37	ENSGALG000000012631	0.0006747	0.63	1	55381604		BTB (POZ) domain containing 11 [Source:RefSeq peptide;Acc:NP_001025932]
38	ENSGALG000000013753	0.00054972	0.63	2	96181508		
39	ENSGALG000000010562	0.00016848	0.64	5	43157795	G8	Similar to chromosome 14 open reading frame 145
40	ENSGALG00000004829	0.00054729	0.64	12	4060351		
41	ENSGALG00000001968	0.00163726	0.64	26	3638054		
42	ENSGALG000000017013	0.00335067	0.64	1	173732828	G1	
43	ENSGALG00000008682	0.00284715	0.64	4	16697566	G6	SIMILAR TO SOLUTE CARRIER FAMILY 25, MEMBER 43 - Mitochondrial carrier protein
44	ENSGALG000000016448	0.00596777	0.64	3	99891589	G5	Potassium voltage-gated channel, subfamily F, member 1
45	ENSGALG000000016442	0.00218714	0.64	3	99396972	G5	Ribonucleotide reductase M2 polypeptide
46	ENSGALG000000001741	0.00364605	0.65	10	1562925		
47	ENSGALG000000010592	0.00021959	0.65	4	40198184		
48	ENSGALG000000002117	0.00134948	0.65	6	3791555		
49	ENSGALG000000014866	0.00188903	0.66	3	63843220		Fatty acid-binding protein, brain (B-FABP)(Fatty acid-binding protein 7)(Fatty acid-binding protein, retina)(R-FABP) [Source:UniProtKB/Swiss-Prot;Acc:Q8QGX]
50	ENSGALG000000017175	0.00690442	0.66	1	185441867	G1	Hypothetical protein Kelch repeat and BTB (POZ) domain containing 3
51	ENSGALG000000015156	0.00075109	0.66	2	36390251		
52	ENSGALG000000012867	0.00084257	0.66	1	59082544		
53	ENSGALG00000006644	0.00025438	0.66	13	17175433		Fatty acid Coenzyme A ligase, long chain 6 Fragment [Source:UniProtKB/TrEMBL;Acc:Q5W453]
54	ENSGALG000000015838	0.00442196	0.66	3	80242895		
55	ENSGALG000000005769	0.00025193	0.66	5	10277283		wee1 tyrosine kinase [Source:RefSeq peptide;Acc:NP_001026352]
56	ENSGALG000000010638	5.0226E-05	0.66	4	40901629		caspase 3 [Source:RefSeq peptide;Acc:NP_990056]
57	ENSGALG000000016792	0.00021006	0.66	1	138271747		
58	ENSGALG000000016141	4.8688E-05	0.66	2	154502939		
59	ENSGALG000000013955	0.00625969	0.67	4	67857505		
60	ENSGALG000000012914	0.00015914	0.67	2	111118345	G3	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit)(DNA-PKcs)(EC 2.7.11.1) [Source:UniProtKB/Swiss-Prot;Acc:Q8QGX]
61	ENSGALG000000019036	0.00148933	0.67	1	200657050		Signal peptidase complex subunit 2 (EC 3.4.-.-)(Microsomal signal peptidase 25 kDa subunit)(SPase 25 kDa subunit) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZK11]
62	ENSGALG000000014234	0.00134096	0.67	1	72753975		
63	ENSGALG000000017133	0.00939344	0.67	1	183095166	G1	N(6)-adenine-specific DNA methyltransferase 2 (EC 2.1.1.-) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZK16]
64	ENSGALG000000012717	0.00112796	0.67	1	56680674		Nuclear transcription factor Y subunit beta (Nuclear transcription factor Y subunit B)(NF-YB)(CAAT-box DNA-binding protein subunit B) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZK11]
65	ENSGALG000000012116	0.00370375	0.68	2	46847660	G2	Endonuclease/exonuclease/phosphatase family domain containing 1
66	ENSGALG000000011497	2.2335E-06	0.68	7	25110164	G9	peroxisomal trans-2-enoyl-CoA reductase [Source:RefSeq peptide;Acc:NP_001006522]
67	ENSGALG000000019891	0.00043913	0.68	3	93821690	G5	CLN8 protein [Source:RefSeq peptide;Acc:NP_001026258]
68	ENSGALG00000001956	0.00042413	0.68	26	3629508		Olfactomedin-like protein 3 Precursor (Olfactomedin-Noelin-Tiarin factor 1) [Source:UniProtKB/Swiss-Prot;Acc:Q5C36]
69	ENSGALG000000022744	2.9981E-05	0.68	1	157605240		
70	ENSGALG000000016259	0.00276297	0.69	1	116702731		
71	ENSGALG000000023440	3.8797E-07	0.69	10	12548799		GA binding protein transcription factor, beta subunit 2 isoform 2 [Source:RefSeq peptide;Acc:NP_001005816]
72	ENSGALG000000010921	0.00177086	0.69	4	47092907	G7	polycystin 2 [Source:RefSeq peptide;Acc:NP_001026311]
73	ENSGALG000000017241	0.00050063	0.69	1	192825846		
74	ENSGALG000000008118	0.00581978	0.69	7	11272217		
75	ENSGALG00000008658	0.00817183	0.69	8	16869679		
76	ENSGALG000000000529	0.00076368	0.69	27	2678993		LIM domain containing 2 [Source:RefSeq peptide;Acc:NP_001006330]
77	ENSGALG000000007313	0.00918346	0.69	14	10211446		
78	ENSGALG000000007967	4.5793E-05	0.69	24	6374957		
79	ENSGALG00000001506	0.00059538	0.69	13	7577984		Pituitary tumor-transforming 1, Securin sister-chromatid separation inhibitor
80	ENSGALG000000023364	0.00404799	0.70	17	8539963		
81	ENSGALG000000010431	0.00485465	0.70	9	25465184		
82	ENSGALG000000023815	0.005283	0.70	7	4361947		
83	ENSGALG000000007182	0.00149703	0.70	12	13401575		
84	ENSGALG00000002546	0.00955655	0.70	17	8014025		alpha 1 (V) collagen [Source:RefSeq peptide;Acc:NP_990121]
85	ENSGALG000000008821	7.3981E-07	0.71	1	24083188		
86	ENSGALG000000019716	0.00522798	0.71	27	4169346		
87	ENSGALG000000007879	0.00978954	0.71	3	891596		Fanconi anemia, complementation group L [Source:RefSeq peptide;Acc:NP_001029113]
88	ENSGALG00000004622	0.00032456	0.71	17	5907955		
89	ENSGALG000000016973	0.0028893	0.71	1	171909504	G1	hypothetical protein LOC418842 [Source:RefSeq peptide;Acc:NP_001006270]
90	ENSGALG00000001079	0.0021376	0.71	5	48537539		glutaredoxin 5 homolog [Source:RefSeq peptide;Acc:NP_001008472]
91	ENSGALG000000016578	0.00475112	0.71	1	126388987		trafficking protein particle complex 2 [Source:RefSeq peptide;Acc:NP_001006263]
92	ENSGALG000000006020	9.2267E-05	0.71	10	12878743		BTB (POZ) domain containing 1 [Source:RefSeq peptide;Acc:NP_001005819]
93	ENSGALG000000007170	0.00112543	0.72	10	19764376		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZK11]
94	ENSGALG000000011842	0.00213825	0.72	2	42833516	G2	
95	ENSGALG000000023435	0.00594553	0.72	10	12588264		glycine amidinotransferase (L-arginine:glycine amidinotransferase) [Source:RefSeq peptide;Acc:NP_990076]
96	ENSGALG000000005986	6.5739E-05	0.72	5	11170610		
97	ENSGALG000000007493	0.0034003	0.72	4	11367738	G6	NAD(P) dependent steroid dehydrogenase-like
98	ENSGALG000000007438	0.00695946	0.72	24	5629899		
99	ENSGALG000000011906	0.00953755	0.72	2	43535863	G2	31 KDA PROTEIN

100	ENSGALG00000008104	0.00289207	0.72	3	34484		Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q5ZJE8]
101	ENSGALG00000024486	0.00385199	0.72	4	86131356		Hypothetical gene supported by CR352470
102	ENSGALG00000010014	0.00117444	0.72	3	27956254		Cysteine-rich PDZ-binding protein (Cysteine-rich interactor of PDZ three)[Cysteine-rich interactor of PDZ3] [Source:UniProtKB/Swiss-Prot;Acc:G3
103	ENSGALG00000022891	0.00488295	0.72	1	83954415		
104	ENSGALG00000016872	0.00022892	0.72	1	148194890		
105	ENSGALG00000016775	0.00289002	0.72	1	137505154		
106	ENSGALG00000016603	0.00652919	0.72	1	128243953		midline 1 [Source:RefSeq peptide;Acc:NP_989460]
107	ENSGALG00000003004	0.00068763	0.72	2	119107130	G3	chondrocyte protein with a poly-proline region [Source:RefSeq peptide;Acc:NP_989874]
108	ENSGALG00000011798	0.00704881	0.73	1	50117981		Heme-binding protein 1 [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMB2]
109	ENSGALG00000001482	7.7218E-05	0.73	9	1946276		Glutamine rich protein Fragment [Source:UniProtKB/TrEMBL;Acc:O42489]
110	ENSGALG00000004686	0.00506363	0.73	5	789726		
111	ENSGALG00000016636	0.00561659	0.73	1	132548048		arylsulfatase H [Source:RefSeq peptide;Acc:NP_989703]
112	ENSGALG00000015775	0.00082796	0.73	3	78396237		ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast) [Source:RefSeq peptide;Acc:NP_990094]
113	ENSGALG00000003249	0.00266773	0.73	6	10395166		
114	ENSGALG00000003584	0.00241299	0.73	18	6990203		karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source:RefSeq peptide;Acc:NP_001006209]
115	ENSGALG00000008128	0.00012287	0.73	7	11240055		Mps one binder kinase activator-like 3 (Preimplantation protein 3)(Mob1 homolog 3)(Mob3) [Source:UniProtKB/Swiss-Prot;Acc:Q5F495]
116	ENSGALG00000009296	0.00113332	0.73	3	18369190		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZHT7]
117	ENSGALG00000010674	0.0001786	0.73	4	41410071		dCMP deaminase [Source:RefSeq peptide;Acc:NP_001006444]
118	ENSGALG00000004483	0.00011526	0.74	3	2166476		
119	ENSGALG00000008963	2.6181E-05	0.74	2	20768433		
120	ENSGALG00000001925	0.0002807	0.74	15	949694		guanine nucleotide binding protein (G protein), beta polypeptide 1-like [Source:RefSeq peptide;Acc:NP_001012811]
121	ENSGALG00000016010	0.00052726	0.74	1	109304879		
122	ENSGALG00000010688	0.0052662	0.74	2	42730715		
123	ENSGALG00000009562	0.00751605	0.74	5	31243612	G8	SIMILAR TO PLEK2 PROTEIN, Pleckstrin 2, PH domain Rho/Rac interactor
124	ENSGALG00000005478	0.00466762	0.74	8	13071093		
125	ENSGALG00000014166	0.0002278	0.74	1	70697760		
126	ENSGALG00000016896	0.00351746	0.74	1	150346328		ATP-binding cassette, sub-family C, member 4 [Source:RefSeq peptide;Acc:NP_001025990]
127	ENSGALG00000011720	6.7455E-05	0.74	7	28967796	G9	Coiled-coil domain containing 14 CCDC14
128	ENSGALG00000016070	5.8521E-05	0.74	1	111455657		Putative uncharacterized proteinTryptophan rich basic protein ; [Source:UniProtKB/TrEMBL;Acc:Q5ZIM2]
129	ENSGALG00000002055	0.0016088	0.74	21	2786579		Transcription factor HES-1 (Hairy and enhancer of split 1)(C-HAIRY1) [Source:UniProtKB/Swiss-Prot;Acc:O57337]
130	ENSGALG00000014681	0.0001876	0.74	2	55049254		Phosphorylated adapter RNA export protein (RNA U small nuclear RNA export adapter protein) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZLY0]
131	ENSGALG00000016582	0.00406049	0.74	3	107960326		
132	ENSGALG00000014749	0.00017302	0.74	1	81087980		Ephrin type-B receptor 5 Precursor (EC 2.7.10.1)(Tyrosine-protein kinase CEK9) [Source:UniProtKB/Swiss-Prot;Acc:Q07497]
133	ENSGALG00000015958	0.0003573	0.74	4	89302740		
134	ENSGALG00000006830	7.2245E-05	0.74	5	16201189		
135	ENSGALG00000008603	0.00285731	0.75	5	26826566	G8	inositol 1,4,5-trisphosphate 3-kinase A [Source:RefSeq peptide;Acc:NP_990212]
136	ENSGALG00000021027	0.00541367	0.75	10	19898179		PREDICTED: Gallus gallus hypothetical LOC415528 (LOC415528), mRNA. [Source:RefSeq DNA;Acc:XR_026904]
137	ENSGALG00000008475	0.00715441	0.76	17	2361839		arrestin domain containing 1 [Source:RefSeq peptide;Acc:NP_001026646]
138	ENSGALG00000012523	0.00091236	0.76	1	53623713		
139	ENSGALG00000008295	0.00132557	0.76	1	13802183		
140	ENSGALG00000012687	0.00089579	0.76	2	61484818		
141	ENSGALG00000003570	0.00117888	0.76	7	4341051		Bifunctional purine biosynthesis protein PURH [Includes Phosphoribosylaminoimidazolecarboxamide formyltransferase(EC 2.1.2.3)(5-aminoim
142	ENSGALG00000010618	0.00019531	0.76	3	34858807		CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZIH3]
143	ENSGALG00000002679	0.00085296	0.76	15	3741937		glycosyltransferase 1 domain containing 1 [Source:RefSeq peptide;Acc:NP_001025827]
144	ENSGALG00000009054	0.00015456	0.76	17	794600		
145	ENSGALG00000003727	1.0274E-05	0.76	28	3757065		
146	ENSGALG00000009488	0.00398525	0.76	1	29286410		
147	ENSGALG00000012863	0.00014829	0.76	1	58958365		
148	ENSGALG00000007437	0.00064807	0.76	10	20177733		
149	ENSGALG00000009687	0.00658863	0.76	3	21980117		
150	ENSGALG00000011101	0.00220755	0.76	3	41970660	G4	similar to URB2 ribosome biogenesis 2 homolog
151	ENSGALG000000023732	0.00018296	0.77	4	8766371	G6	Hypothetical LOC422270
152	ENSGALG00000010282	0.00595843	0.77	3	31566038		
153	ENSGALG00000002663	0.00076309	0.77	9	11538990		
154	ENSGALG00000009410	0.00120963	0.77	2	22601837		
155	ENSGALG00000015678	0.00787349	0.77	2	124294436	G3	peroxisomal membrane protein 3 [Source:RefSeq peptide;Acc:NP_001008454]
156	ENSGALG00000017022	0.00528113	0.77	1	174638010	G1	Asparagine-linked glycosylation 11 homolog
157	ENSGALG00000009615	0.00683664	0.77	3	20551130		
158	ENSGALG00000011311	8.6276E-05	0.77	8	29827096		
159	ENSGALG00000016024	0.00312034	0.77	1	110017662		SET domain containing 4 [Source:RefSeq peptide;Acc:NP_001025965]
160	ENSGALG00000003652	7.728E-05	0.77	6	10721253		
161	ENSGALG00000004838	0.00363954	0.77	5	562246		BUB1 budding uninhibited by benzimidazoles 1 homolog beta [Source:RefSeq peptide;Acc:NP_989734]
162	ENSGALG00000016856	0.00481261	0.77	1	145254086		ephrin-B2 [Source:RefSeq peptide;Acc:NP_990155]
163	ENSGALG00000009254	0.0002058	0.77	6	30441505		
164	ENSGALG00000004794	0.0007465	0.77	6	13070352		
165	ENSGALG00000000408	0.00140698	0.77	28	540993		LSM7 homolog, U6 small nuclear RNA associated [Source:RefSeq peptide;Acc:NP_001006337]
166	ENSGALG00000016847	0.00034923	0.77	1	143425069		
167	ENSGALG00000015210	0.00010725	0.77	2	43555228		hypothetical protein LOC427269 [Source:RefSeq peptide;Acc:NP_001026600]
168	ENSGALG00000014908	0.00541112	0.77	2	15391867		Follistatin Precursor (FS)(Activin-binding protein) [Source:UniProtKB/Swiss-Prot;Acc:Q90844]
169	ENSGALG00000000573	0.00023556	0.77	21	265014		Circadian clock protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q8JH31]
170	ENSGALG00000014140	0.00459736	0.78	1	70535309		ADP-ribosylation factor GTPase activating protein 3 [Source:RefSeq peptide;Acc:NP_001012557]
171	ENSGALG00000004594	0.00552176	0.78	13	13225790		CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) [Source:RefSeq peptide;Acc:NP_001001
172	ENSGALG00000010804	0.00051991	0.78	2	28465051		Ankyrin repeat and MYND domain-containing protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMD2]
173	ENSGALG00000009890	1.8523E-05	0.78	3	24009443		
174	ENSGALG00000006808	0.00107268	0.78	4	5197934	G6	Tetraspanin 6
175	ENSGALG00000007168	1.3317E-05	0.78	12	12161250		
176	ENSGALG00000008312	0.00337037	0.78	1	13645222		Protein pigeon homolog [Source:UniProtKB/Swiss-Prot;Acc:A4D1B5]
177	ENSGALG00000019231	0.00106814	0.78	1	86766497		Cell surface glycoprotein CD200 receptor 1-A Precursor (Cell surface glycoprotein OX2 receptor 1-A)(CD200 cell surface glycoprotein receptor
178	ENSGALG00000001937	0.00016859	0.78	10	994572		hypothetical protein LOC415320 [Source:RefSeq peptide;Acc:NP_001025561]
179	ENSGALG00000014298	0.00125142	0.78	4	71317529		replication factor C (activator 1) 1, 145kDa [Source:RefSeq peptide;Acc:NP_001006456]
180	ENSGALG00000017158	0.00782761	0.78	1	184541610	G1	
181	ENSGALG000000004110	0.00256648	0.78	20	5188868	G11	
182	ENSGALG00000007038	0.0079289	0.78	17	3664189		PREDICTED: Gallus gallus similar to astrotactin 2 (LOC417242), mRNA. [Source:RefSeq DNA;Acc:XR_027091]
183	ENSGALG00000010798	0.00382738	0.79	8	26011325		24-dehydrocholesterol reductase [Source:RefSeq peptide;Acc:NP_001026459]
184	ENSGALG00000010992	0.00950903	0.79	1	43502527		
185	ENSGALG00000003286	0.00239163	0.79	10	4686281		
186	ENSGALG00000012405	0.00048447	0.79	2	55394439	G2	
187	ENSGALG00000002985	2.3356E-06	0.79	18	5094707		PREDICTED: Gallus gallus similar to CGI-48 protein (LOC417388), mRNA. [Source:RefSeq DNA;Acc:XR_027044]
188	ENSGALG00000007355	0.00200757	0.79	4	11053298	G6	
189	ENSGALG00000014779	0.00281261	0.79	1	82190807		
190	ENSGALG00000017180	0.00286535	0.79	1	186539287	G1	
191	ENSGALG00000006264	0.00196369	0.79	2	6484829		
192	ENSGALG00000014870	0.00973501	0.79	3	63957844		Heat shock factor protein 2 (HSF 2)(Heat shock transcription factor 2)(HSF 2)(HSF 3B)(HSF 3B) [Source:UniProtKB/Swiss-Prot;Acc:P38530]
193	ENSGALG00000004874	3.5074E-06	0.79	21	6606381		
194	ENSGALG00000006869	0.00191972	0.79	24	4456827		Ubiquitin carboxyl-terminal hydrolase 28 (EC 3.1.2.15)(Ubiquitin thioesterase 28)(Ubiquitin-specific-processing protease 28)(Deubiquitinating
195	ENSGALG00000009633	0.00533803	0.79	5	32325752	G8	hypothetical protein LOC423287 [Source:RefSeq peptide;Acc:NP_001026369]
196	ENSGALG00000015611	0.00014113	0.79	3	78136932		
197	ENSGALG00000005328	9.6781E-05	0.80	2	2196449		hypothetical protein LOC420396 [Source:RefSeq peptide;Acc:NP_001026129]
198	ENSGALG00000013383	0.00165391	0.80	23	5678687		
199	ENSGALG000000021573	0.00091128	0.80	18	1938528		Phosphoinositide 3-kinase regulatory subunit 5 (PI3-kinase regulatory subunit 5) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZIB8]
200	ENSGALG00000003438	0.00608447	0.80	8	5723320		Kinetochore protein Nuf2 (Cell division cycle-associated protein 1) [Source:UniProtKB/Swiss-Prot;Acc:Q76I90]
201	ENSGALG00000015645	0.00331134	0.80	4	85225812		G protein-coupled receptor kinase 4 [Source:RefSeq peptide;Acc:NP_001006459]
202	ENSGALG00000001220	0.00032164	0.80	11	603529		
203	ENSGALG00000005056	0.00683537	0.80	2	740225		
204	ENSGALG00000016581	0.00359714	0.80	1	126408830		
205	ENSGALG00000000510	0.00211204	0.80	27	2612006		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZT11]
206	ENSGALG00000011689	0.00828261	0.80	7	28411741	G9	Protein disulfide isomerase family A, member 5

207	ENSGALG00000011238	0.00027933	0.80	8	29518977		Integral membrane protein GPR177 Precursor (Protein wntless homolog) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZLR1]
208	ENSGALG00000009733	0.00623339	0.80	2	24284953		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZJW7]
209	ENSGALG00000017296	0.00678031	0.80	1	74680694		
210	ENSGALG00000011738	0.00988491	0.80	1	49861152		
211	ENSGALG00000016854	0.00910645	0.80	1	144394049		DNA ligase 4 [EC 6.5.1.1](DNA ligase IV)[Polydeoxyribonucleotide synthase [ATP] 4] [Source:UniProtKB/Swiss-Prot;Acc:Q90VB1]
212	ENSGALG00000002745	0.00018618	0.80	11	1779838		Golgi apparatus protein 1 Precursor (Cysteine-rich fibroblast growth factor receptor) [Source:UniProtKB/Swiss-Prot;Acc:Q02391]
213	ENSGALG00000016280	0.00429541	0.80	3	89558215		
214	ENSGALG00000008569	0.00184445	0.80	13	16937180		
215	ENSGALG00000004472	0.00188394	0.80	8	7040839		
216	ENSGALG00000005849	0.00179011	0.80	20	9010484	G11	Exocrine differentiation and proliferation factor [Source:UniProtKB/Swiss-Prot;Acc:Q9H3Y8]
217	ENSGALG00000014719	0.00749891	0.80	2	16675929		Uncharacterized protein C5orf35 [Source:UniProtKB/Swiss-Prot;Acc:Q8NE22]
218	ENSGALG00000011554	0.00091691	0.80	5	53092245		
219	ENSGALG00000023093	9.4002E-05	0.80	5	43101477	G8	
220	ENSGALG00000015580	0.00033644	0.80	3	75492430		UPF0555 protein KIAA0776 homolog [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMG1]
221	ENSGALG00000014513	0.00023225	0.81	1	80411783		
222	ENSGALG00000012206	0.00052072	0.81	5	59027191		
223	ENSGALG00000015414	0.00907942	0.81	1	92978287		
224	ENSGALG00000006790	0.00415756	0.81	6	21800392		hypothetical protein LOC423809 [Source:RefSeq peptide;Acc:NP_001026401]
225	ENSGALG00000000550	0.00041084	0.81	27	2696787		STE20-related kinase adapter protein alpha (STRAD alpha)[STE20-related adapter protein] [Source:UniProtKB/Swiss-Prot;Acc:Q5ZK47]
226	ENSGALG00000005890	5.1174E-05	0.81	13	13541658		
227	ENSGALG00000014769	0.00499729	0.81	2	20068956		
228	ENSGALG00000001637	0.00477799	0.81	17	8970662		proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 [Source:RefSeq peptide;Acc:NP_001012815]
229	ENSGALG00000003578	0.00032348	0.81	7	4362118		Fibronectin Fragments (FN) [Source:UniProtKB/Swiss-Prot;Acc:P11722]
230	ENSGALG00000000226	0.00053253	0.81	26	893584		
231	ENSGALG00000010047	0.00094474	0.81	3	28994971		
232	ENSGALG00000012546	0.00041256	0.81	1	54126111		MCMS minichromosome maintenance deficient 5, cell division cycle 46 [Source:RefSeq peptide;Acc:NP_001006243]
233	ENSGALG00000006539	0.00380669	0.81	9	5418476		hypothetical protein LOC424866 [Source:RefSeq peptide;Acc:NP_001006544]
234	ENSGALG00000015066	0.00948473	0.81	3	69351597		
235	ENSGALG00000006974	0.00586159	0.82	20	10704399	G12	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 [Source:RefSeq peptide;Acc:NP_001006293]
236	ENSGALG00000004885	0.00129711	0.82	10	11522508		Solute carrier family 24 member 5 [Source:UniProtKB/TrEMBL;Acc:856557]
237	ENSGALG00000015236	0.00056636	0.82	2	111281452	G3	Ubiquitin-conjugating enzyme E2 variant 2 [Source:UniProtKB/Swiss-Prot;Acc:Q5F3Z3]
238	ENSGALG00000001976	0.00903716	0.82	26	3674324		
239	ENSGALG00000004891	0.00891579	0.82	17	5624063		Rolly protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q6BD17]
240	ENSGALG00000000267	0.00072958	0.82	20	9990131	G11	Targeting protein for Xklp2 (Restricted expression proliferation-associated protein 100)[p100](Differentially expressed in cancerous and non-c)
241	ENSGALG00000011015	0.00421179	0.82	3	40764731	G4	hypothetical protein LOC428588 [Source:RefSeq peptide;Acc:NP_001026694]
242	ENSGALG00000001711	0.00735338	0.82	10	1741896		
243	ENSGALG00000015939	0.00166106	0.82	4	89168677		
244	ENSGALG00000014542	0.00077239	0.82	19	73356		Williams Beuren syndrome chromosome region 22 [Source:RefSeq peptide;Acc:NP_001034421]
245	ENSGALG00000001056	0.00765167	0.82	19	650872		
246	ENSGALG00000002773	0.00625351	0.82	26	4138328		
247	ENSGALG00000005272	0.00949846	0.82	11	12423012		cadherin 5, type 2, VE-cadherin (vascular epithelium) [Source:RefSeq peptide;Acc:NP_989558]
248	ENSGALG00000023043	0.00757648	0.82	4	67821252		
249	ENSGALG00000015739	9.6571E-05	0.82	2	125525240	G3	Mitochondrial ribosomal protein S28
250	ENSGALG00000020599	0.00434204	0.82	19	4306639		Rhomboid domain-containing protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q6NTF9]
251	ENSGALG00000007417	0.00628581	0.83	2	15520221		
252	ENSGALG00000009934	0.00521743	0.83	1	37122935		
253	ENSGALG00000013647	0.00134863	0.83	3	52493295		
254	ENSGALG00000014060	0.00073942	0.83	1	195039424		Polycomb protein EED [Source:UniProtKB/Swiss-Prot;Acc:Q5ZKH3]
255	ENSGALG00000010620	0.00731145	0.83	3	34877937		Spastin (EC 3.6.1.3) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZK92]
256	ENSGALG00000002519	0.00176515	0.83	21	3385629		
257	ENSGALG00000013851	0.00027109	0.83	15	6939064		Ubiquitin protein ligase Fragment [Source:UniProtKB/TrEMBL;Acc:Q98SE8]
258	ENSGALG00000011116	0.00398019	0.83	5	49088185		vaccinia related kinase 1 [Source:RefSeq peptide;Acc:NP_001006485]
259	ENSGALG00000008416	0.00102117	0.83	3	3751585	G4	Uncharacterized protein C2orf26 [Source:UniProtKB/Swiss-Prot;Acc:Q8NHU2]
260	ENSGALG00000011947	0.00335915	0.83	1	51484204		
261	ENSGALG00000011666	0.00401511	0.83	19	3393424		
262	ENSGALG00000015949	0.000903	0.83	3	85054894		
263	ENSGALG00000010720	0.00629023	0.83	2	26557233		hypothetical protein LOC420586 [Source:RefSeq peptide;Acc:NP_001012576]
264	ENSGALG00000005499	0.00119314	0.83	12	8786154		Interleukin-17 receptor D Precursor (IL-17 receptor D)[IL-17RD][Sef homolog][cSEF] [Source:UniProtKB/Swiss-Prot;Acc:Q72L7]
265	ENSGALG00000012655	0.00108466	0.83	1	55854406		
266	ENSGALG00000012304	0.00689925	0.84	4	62616899		Nuclear factor NF-kappa-B p105 subunit [Contains Nuclear factor NF-kappa-B p50 subunit] [Source:UniProtKB/Swiss-Prot;Acc:Q04861]
267	ENSGALG000000003312	0.00301102	0.84	10	4733403		
268	ENSGALG00000013899	0.00184442	0.84	25	90724		vacuolar protein sorting 45A [Source:RefSeq peptide;Acc:NP_001026764]
269	ENSGALG000000006960	0.00127249	0.84	15	9342122		RING finger protein 185 [Source:UniProtKB/Swiss-Prot;Acc:P18861]
270	ENSGALG00000000997	0.00973065	0.84	27	1228980		Gap junction gamma-1 protein (Gap junction alpha-7 protein)[Connexin-45](Cx45) [Source:UniProtKB/Swiss-Prot;Acc:P18861]
271	ENSGALG00000001103	2.0592E-05	0.84	17	10091673		proteasome (prosome, macropain) subunit, beta type, 7 [Source:RefSeq peptide;Acc:NP_989728]
272	ENSGALG00000015368	0.00724736	0.84	2	52350486		Transmembrane protein 175 [Source:UniProtKB/Swiss-Prot;Acc:Q5ZKY0]
273	ENSGALG00000002388	0.00068892	0.84	19	4818142		hypothetical protein LOC417539 [Source:RefSeq peptide;Acc:NP_001025884]
274	ENSGALG00000007905	0.00541853	0.84	1	15859501		Laminin subunit beta-1 Fragment (Laminin beta-1-1 chain) [Source:UniProtKB/Swiss-Prot;Acc:Q01635]
275	ENSGALG00000008095	0.00069874	0.84	10	21512885		kinesin family member 23 [Source:RefSeq peptide;Acc:NP_001025725]
276	ENSGALG00000015618	0.00971015	0.84	2	62004120		
277	ENSGALG00000009325	0.0035035	0.84	7	18153750	G9	Obg-like ATPase 1 (EC 3.6.3.-) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZM25]
278	ENSGALG00000010138	0.00427619	0.84	4	35294883		Protein kinase-like protein Sgk196 [Sugen kinase 196] [Source:UniProtKB/Swiss-Prot;Acc:Q5F349]
279	ENSGALG00000010097	0.00025719	0.84	4	34567467		
280	ENSGALG00000007266	0.00964245	0.84	2	14538580		
281	ENSGALG00000004701	0.00446282	0.84	17	5834726		SET translocation (myeloid leukemia-associated) [Source:RefSeq peptide;Acc:NP_001025862]
282	ENSGALG00000011944	0.00172347	0.84	1	51466743		
283	ENSGALG00000011968	0.00683621	0.84	2	44453433	G2	galactosidase, beta 1 [Source:RefSeq peptide;Acc:NP_001026163]
284	ENSGALG000000004195	0.0067131	0.84	4	1250810		Chromosome-associated kinesin KIF4 (Chromokinesin) [Source:UniProtKB/Swiss-Prot;Acc:Q90640]
285	ENSGALG00000013907	0.00179263	0.85	4	67056278		kinase insert domain receptor (a type III receptor tyrosine kinase) [Source:RefSeq peptide;Acc:NP_001004368]
286	ENSGALG00000015960	0.00552065	0.85	4	89350452		ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) [Source:RefSeq peptide;Acc:NP_001026341]
287	ENSGALG00000003484	0.00173346	0.85	7	4181051		BRC1 associated RING domain 1 [Source:RefSeq peptide;Acc:NP_001026417]
288	ENSGALG000000021041	0.00656313	0.85	8	5252301		SCY1-like 3 [Source:RefSeq peptide;Acc:NP_001012613]
289	ENSGALG00000009348	0.0088958	0.85	2	22366098		A-kinase anchor protein 9 [Source:RefSeq peptide;Acc:NP_997062]
290	ENSGALG00000011088	0.00514401	0.85	5	48927532		GSK3-beta interaction protein (GSKIP) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMC6]
291	ENSGALG00000008162	0.00100447	0.85	1	891223		F-box helicase [Source:UniProtKB/TrEMBL;Acc:A1YKW0]
292	ENSGALG00000014238	0.00341615	0.85	1	73513798		UPF0595 protein C2orf40 homolog [Source:UniProtKB/Swiss-Prot;Acc:Q5ZKB8]
293	ENSGALG00000009843	0.00247903	0.85	3	23195862		Integrator complex subunit 7 (Int7) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZL91]
294	ENSGALG00000002421	0.003058	0.85	6	5460901		PREDICTED: Gallus gallus similar to chromosome 10 open reading frame 58 (LOC423625), misc RNA. [Source:RefSeq DNA;Acc:XR_026656]
295	ENSGALG000000008152	0.00656313	0.85	7	12154097	G9	hypothetical protein LOC424067 [Source:RefSeq peptide;Acc:NP_001008474]
296	ENSGALG00000000384	0.00139573	0.85	26	591508		Leucine-zipper-like transcriptional regulator 1 (LZTR-1) [Source:UniProtKB/Swiss-Prot;Acc:Q8N653]
297	ENSGALG00000019976	0.00795568	0.85	3	54272577		
298	ENSGALG00000003664	0.0013323	0.85	14	2125382		
299	ENSGALG00000008045	0.0030868	0.85	20	13879568		solute carrier family 9 (sodium/hydrogen exchanger), member 8 [Source:RefSeq peptide;Acc:NP_001034364]
300	ENSGALG00000011226	0.00959206	0.85	2	33986387		
301	ENSGALG00000004802	0.0019063	0.85	15	6360834		TRAF-type zinc finger domain containing 1 [Source:RefSeq peptide;Acc:NP_001006191]
302	ENSGALG00000008372	0.00064295	0.85	3	3462639		5'-3' exoribonuclease 2 [EC 3.1.13.-] [Source:UniProtKB/Swiss-Prot;Acc:Q5ZJP4]
303	ENSGALG00000004798	0.00069264	0.86	14	4703152		
304	ENSGALG000000020415	0.00267676	0.86	5	40917809	G8	Uncharacterized protein C14orf179 [Source:UniProtKB/Swiss-Prot;Acc:Q96FT9]
305	ENSGALG00000005487	0.0068916	0.86	2	3737755		coiled-coil domain containing 12 [Source:RefSeq peptide;Acc:NP_001006353]
306	ENSGALG00000002968	0.00304879	0.86	20	2135304		hypothetical protein LOC419152 [Source:RefSeq peptide;Acc:NP_001026020]
307	ENSGALG00000011704	0.0002946	0.86	7	28739236	G9	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b [Source:RefSeq peptide;Acc:NP_001012938]
308	ENSGALG00000015299	0.00616921	0.86	1	88310414		
309	ENSGALG00000001630	0.00714083	0.86	19	3380574		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZHS8]
310	ENSGALG00000003072	0.00055228	0.86	19	5395396		Replication protein A 70 kDa DNA-binding subunit (RP-A p70)(Replication factor A protein 1)(RF-A protein 1) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZKX2]
311	ENSGALG00000002042	0.00494897	0.86	14	15504755		
312	ENSGALG00000005976	0.00117687	0.86	20	9348338	G11	SIMILAR TO TRANSCRIPTION ELONGATION FACTOR S-II, HS-II-T1.
313	ENSGALG00000012944	0.00751688	0.86	1	61550458		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZKV2]

314	ENSGALG00000008831	0.00713062	0.87	3	9642946		Galectin-related protein [Source:UniProtKB/Swiss-Prot;Acc:Q5ZHQ2]
315	ENSGALG00000011904	0.00288658	0.87	5	56815878		
316	ENSGALG00000005997	0.00410233	0.87	4	3284702		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZLT9]
317	ENSGALG00000013783	0.00048294	0.87	4	66919894		
318	ENSGALG00000011305	0.00448107	0.87	8	29803863		splicing factor, arginine/serine-rich 11 [Source:RefSeq peptide;Acc:NP_001026467]
319	ENSGALG00000010441	0.00316608	0.87	11	483523		katanin p80 WD40-containing subunit B1 (Katanin p80 subunit B1)[p80 katanin] [Source:UniProtKB/Swiss-Prot;Acc:Q5ZIU8]
320	ENSGALG00000015808	0.00806792	0.87	3	79169256		solute carrier family 35 (CMP-sialic acid transporter), member A1 [Source:RefSeq peptide;Acc:NP_989844]
321	ENSGALG00000009373	0.00481226	0.87	4	21969342		cathepsin O [Source:RefSeq peptide;Acc:NP_001026300]
322	ENSGALG00000011794	0.00612491	0.87	1	50074589		DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 [Source:RefSeq peptide;Acc:NP_001007854]
323	ENSGALG00000009264	0.00373333	0.87	7	17314962	G9	Metaxin 2, Outer mitochondrial membrane transport complex protein
324	ENSGALG00000009576	0.00074223	0.87	3	19933970		3'(2'), 5'-bisphosphate nucleotidase 1 [Source:RefSeq peptide;Acc:NP_001012892]
325	ENSGALG00000002379	0.00056991	0.88	19	4815142		
326	ENSGALG00000005028	0.00960858	0.88	14	5099951		topoisomerase (DNA) III alpha [Source:RefSeq peptide;Acc:NP_001025807]
327	ENSGALG00000002703	0.00162897	0.88	6	6292551		transcription factor A, mitochondrial [Source:RefSeq peptide;Acc:NP_989431]
328	ENSGALG00000011910	0.00624982	0.88	5	56822189		
329	ENSGALG00000010622	0.00444986	0.88	5	45577799		Zinc finger CCHC domain-containing protein 14 [Source:UniProtKB/Swiss-Prot;Acc:Q5F3Z9]
330	ENSGALG00000004416	0.00030841	0.88	19	6400388		
331	ENSGALG00000017174	0.00404796	0.88	1	185409823	G1	Aminoacidate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
332	ENSGALG00000005878	0.00621023	0.88	14	6524841		
333	ENSGALG00000017324	0.00805923	0.88	1	200270749		
334	ENSGALG00000016317	0.00397966	0.88	2	144339724		
335	ENSGALG00000009331	0.00609373	0.88	3	18734765		
336	ENSGALG00000015328	0.00840893	0.88	1	88656138		
337	ENSGALG00000015765	0.00539127	0.88	4	88669031		
338	ENSGALG00000007494	0.00292192	0.88	13	18388260		
339	ENSGALG00000010504	0.00195639	0.88	5	41801154	G8	Uncharacterized aarf domain-containing protein kinase 1 Precursor (EC 2.7.11.-) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMT7]
340	ENSGALG00000012355	0.00875978	0.89	7	32297226		aspartyl-tRNA synthetase [Source:RefSeq peptide;Acc:NP_001006528]
341	ENSGALG00000003485	0.00510735	0.89	26	4838550		cyclin D3 [Source:RefSeq peptide;Acc:NP_001008453]
342	ENSGALG00000006056	0.00976171	0.89	13	16499858		hypothetical protein LOC416321 [Source:RefSeq peptide;Acc:NP_001006154]
343	ENSGALG00000001538	0.00032485	0.89	26	3338844		Suppressor of tumorigenicity protein 7-like protein (Protein HELG) [Source:UniProtKB/Swiss-Prot;Acc:Q90VH8]
344	ENSGALG00000005684	0.00520163	0.89	2	4262073		glycyl-tRNA synthetase [Source:RefSeq peptide;Acc:NP_001026681]
345	ENSGALG00000001503	0.00191188	0.89	18	3204948		Tubulin-specific chaperone D (Tubulin-folding cofactor D)[Beta-tubulin cofactor D] [Source:UniProtKB/Swiss-Prot;Acc:Q5Z187]
346	ENSGALG00000016931	0.00340724	0.89	1	160346466		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5F351]
347	ENSGALG00000008421	0.00597485	0.89	5	26079856	G8	SIMILAR TO PEROXISOMAL BIOGENESIS FACTOR 16.
348	ENSGALG00000004442	0.00414772	0.89	6	12583454		
349	ENSGALG00000011953	0.00289051	0.89	1	51512448		
350	ENSGALG00000001381	0.00026944	0.89	10	1891946		Actin, cytoplasmic type 5 [Source:UniProtKB/Swiss-Prot;Acc:P53478]
351	ENSGALG00000011387	0.00292805	0.89	4	50651535	G7	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa [Source:RefSeq peptide;Acc:NP_001006448]
352	ENSGALG00000014023	0.00439576	0.89	4	61795242	G7	Histone H2A.Z (H2A/z) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMD6]
353	ENSGALG00000012009	0.00037316	0.90	5	57373453		
354	ENSGALG00000007096	0.00546804	0.90	13	17654109		
355	ENSGALG00000001485	0.00538604	0.90	15	453426		topoisomerase (DNA) III beta [Source:RefSeq peptide;Acc:NP_001006181]
356	ENSGALG00000004212	0.00431703	0.90	10	7909392		ADAM metallopeptidase domain 10 [Source:RefSeq peptide;Acc:NP_989592]
357	ENSGALG00000004294	0.00031536	0.90	10	8313671		
358	ENSGALG00000012408	0.00603561	0.90	5	60799872		proteasome (prosome, macropain) 26S subunit, ATPase, 6 [Source:RefSeq peptide;Acc:NP_001006494]
359	ENSGALG00000006904	0.00953806	0.90	5	17266720		ribonuclease/angiogenesis inhibitor 1 [Source:RefSeq peptide;Acc:NP_001006473]
360	ENSGALG00000008330	0.00201917	0.90	1	13471876		
361	ENSGALG00000005464	0.00380358	0.90	4	2201431		
362	ENSGALG00000015105	0.00551492	0.90	2	31672108		Lens epithelium-derived growth factor [Source:UniProtKB/Swiss-Prot;Acc:Q5XXA9]
363	ENSGALG00000007810	0.00671823	0.90	12	17132529		Serine/threonine-protein phosphatase 4 regulatory subunit 2 [Source:UniProtKB/Swiss-Prot;Acc:Q5ZMU6]
364	ENSGALG00000014555	0.00684331	0.91	1	80485024		
365	ENSGALG00000015355	0.00277324	0.91	1	90709489		CD47 antigen [Source:RefSeq peptide;Acc:NP_001004388]
366	ENSGALG00000010884	0.00183239	0.91	5	47880296		ATP-dependent RNA helicase DDX24 (EC 3.6.1.-)[DEAD box protein 24] [Source:UniProtKB/Swiss-Prot;Acc:Q9GZ77]
367	ENSGALG00000013880	0.00736296	0.91	2	99222826		
368	ENSGALG00000014747	0.00060139	0.91	2	19606970		
369	ENSGALG00000008707	0.00068799	0.91	3	16333571		
370	ENSGALG00000007070	0.00091217	0.91	14	8971162		
371	ENSGALG00000003664	0.00619584	0.91	8	5893272		ribonuclease L [Source:RefSeq peptide;Acc:NP_001026438]
372	ENSGALG00000002943	0.00723374	0.92	19	5315758		
373	ENSGALG00000000085	0.00726383	0.92	22	113818		glucosamine-fructose-6-phosphate aminotransferase [Source:RefSeq peptide;Acc:NP_001026053]
374	ENSGALG00000014697	0.00916262	0.92	2	1290952		Sma- and Mad-related protein 2 [Source:RefSeq peptide;Acc:NP_989892]
375	ENSGALG00000011472	0.00826363	0.92	7	24873612	G9	60S ribosomal protein L37a [Source:UniProtKB/Swiss-Prot;Acc:P32046]
376	ENSGALG00000014526	0.00021603	0.92	1	80431223		Triosephosphate isomerase (TIM)[EC 5.3.1.1][Triose-phosphate isomerase] [Source:UniProtKB/Swiss-Prot;Acc:P00940]
377	ENSGALG00000016405	0.00248814	0.93	2	142510932		
378	ENSGALG00000019201	0.00614448	0.93	1	101477585		stress 70 protein chaperone, microsome-associated, 60kDa [Source:RefSeq peptide;Acc:NP_001025964]
379	ENSGALG00000004796	2.3822E-06	0.93	21	6541984		Cell division control protein 42 homolog Precursor (G25K GTP-binding protein) [Source:UniProtKB/Swiss-Prot;Acc:Q90694]
380	ENSGALG00000009246	0.00655051	0.94	3	18227128		acyl-Coenzyme A binding domain containing 3 [Source:RefSeq peptide;Acc:NP_001026214]
381	ENSGALG00000013293	0.00304504	0.95	10	10606416		Gliomedin [Source:UniProtKB/Swiss-Prot;Acc:Q6ZM13]
382	ENSGALG00000007480	0.00437659	1.07	14	12791882		Axin-1 (Axin inhibition protein 1) [Source:UniProtKB/Swiss-Prot;Acc:O42400]
383	ENSGALG00000021827	0.00379226	1.07	2	113872085	G3	SIMILAR TO LYSOPHOSPHOLIPASE I, phospholipases and carboxylesterases
384	ENSGALG00000010281	0.00781517	1.08	4	35816799		
385	ENSGALG00000009703	0.00598132	1.08	28	2519800		
386	ENSGALG00000010735	0.0087433	1.09	8	25836620		
387	ENSGALG00000003909	0.00486058	1.09	20	5056893	G11	Phosphatidylinositol glycan anchor biosynthesis, class T
388	ENSGALG00000011695	0.00538273	1.09	5	5898036		
389	ENSGALG00000008239	0.00386663	1.09	7	12453044	G9	
390	ENSGALG00000004328	0.0011904	1.10	5	1469270		DNA-binding protein SMUBP-2 (EC 3.6.1.-)[ATP-dependent helicase IGHMBP2][Immunoglobulin mu-binding protein 2][Glia factor 1][GF-1] [So
391	ENSGALG00000011290	0.00581121	1.10	2	37176605		60S ribosomal protein L15 Fragment (L10) [Source:UniProtKB/Swiss-Prot;Acc:P51417]
392	ENSGALG00000005706	0.00267244	1.10	15	7935467		
393	ENSGALG00000003042	0.00401981	1.11	20	2155460		
394	ENSGALG00000008435	0.00180188	1.11	7	12824476	G9	Small ubiquitin-related modifier 1 Precursor (SUMO-1) [Source:UniProtKB/Swiss-Prot;Acc:Q8QGH2]
395	ENSGALG00000004249	0.00413131	1.11	23	5984422		
396	ENSGALG00000003994	0.00907831	1.11	7	5152776		
397	ENSGALG00000011464	0.0025757	1.12	5	52729308		eukaryotic translation initiation factor 5 [Source:RefSeq peptide;Acc:NP_001006488]
398	ENSGALG00000004930	0.00025272	1.12	12	4579578		Histamine H1 receptor Fragment [Source:UniProtKB/TrEMBL;Acc:A2ICM7]
399	ENSGALG00000008202	0.00844334	1.12	5	25261738	G8	nuclear receptor subfamily 1, group H, member 3 [Source:RefSeq peptide;Acc:NP_989873]
400	ENSGALG00000011297	0.00891509	1.12	1	46794800		hypothetical protein LOC417900 [Source:RefSeq peptide;Acc:NP_001025919]
401	ENSGALG00000014978	0.00135849	1.12	2	22920786		
402	ENSGALG00000007220	0.0050503	1.12	5	18042629		Ferritin heavy chain (Ferritin H subunit)[EC 1.16.3.1] [Source:UniProtKB/Swiss-Prot;Acc:P08267]
403	ENSGALG00000004162	0.00487778	1.13	18	7810042		
404	ENSGALG00000000040	0.00010314	1.13	14	14328696		
405	ENSGALG00000011239	0.00088859	1.13	2	34251703		
406	ENSGALG00000006338	0.00208718	1.13	15	8341158		
407	ENSGALG00000004410	0.00786661	1.14	6	12538258		
408	ENSGALG00000001716	0.00904009	1.14	10	1651993		
409	ENSGALG00000016380	0.0020808	1.14	2	143590853		
410	ENSGALG00000006430	0.0071811	1.14	15	8547990		Mediator of RNA polymerase II transcription subunit 15 (Mediator complex subunit 15)[Positive cofactor 2 glutamine/Q-rich-associated protei
411	ENSGALG00000012696	0.00443163	1.14	2	61637216		
412	ENSGALG00000002993	0.00599583	1.14	18	5152411		
413	ENSGALG00000001005	0.00480794	1.15	24	389639		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZLA7]
414	ENSGALG00000016146	0.00493328	1.15	2	154082817		topoisomerase (DNA) I, mitochondrial [Source:RefSeq peptide;Acc:NP_001001300]
415	ENSGALG00000003140	0.00417792	1.15	15	4865511		
416	ENSGALG00000019552	0.00075481	1.15	2	68889359		
417	ENSGALG00000008159	0.00646385	1.15	3	2805164		Acylphosphatase-2 (EC 3.6.1.7)[Acylphosphate phosphohydrolase 2][Acylphosphatase, muscle type isozyme][Acylphosphatase isozyme CH1] [
418	ENSGALG00000009547	0.00750252	1.15	1	31361499		periphilin 1 [Source:RefSeq peptide;Acc:NP_001025908]
419	ENSGALG00000011974	0.00460667	1.16	4	56083849	G7	ribosomal protein L7-like 1 [Source:RefSeq peptide;Acc:NP_001006452]

420	ENSGALG00000007439	0.00211007	1.16	20	10824109	G12	hypothetical protein LOC419310 [Source:RefSeq peptide;Acc:NP_001026037]
421	ENSGALG00000002988	0.00581648	1.16	8	4275692		
422	ENSGALG00000016136	0.00646244	1.16	2	154520767		
423	ENSGALG00000003400	0.00871103	1.17	14	973578		
424	ENSGALG00000008689	0.00733442	1.17	4	16734642	G6	Hypothetical gene supported by CR387161
425	ENSGALG00000011304	0.003556983	1.17	2	37908744		Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase (PNGase)[EC 3.5.1.52](Peptide-N-glycanase)[N-glycanase 1] [Source:UniProtKB/
426	ENSGALG00000001843	0.00024069	1.17	2	1560802		protein inhibitor of activated STAT X [Source:RefSeq peptide;Acc:NP_001025797]
427	ENSGALG00000020449	0.00372755	1.17	5	29837078	G8	
428	ENSGALG00000019171	0.00764422	1.17	1	113827940		hypothetical protein LOC418552 [Source:RefSeq peptide;Acc:NP_001025969]
429	ENSGALG00000009445	0.00144811	1.18	6	31804042		
430	ENSGALG00000007240	0.00560384	1.18	4	9669318	G6	TNF-related apoptosis inducing ligand-like protein [Source:RefSeq peptide;Acc:NP_989922]
431	ENSGALG00000015055	0.00981666	1.18	3	69172102		
432	ENSGALG00000017283	0.00934963	1.18	1	75501156		G1/S-specific cyclin-D2 [Source:UniProtKB/Swiss-Prot;Acc:P49706]
433	ENSGALG00000022861	0.00957906	1.19	3	106942553		
434	ENSGALG00000003920	0.00265735	1.19	4	1636260		
435	ENSGALG00000005085	0.00665306	1.19	5	524103		DRD4 [Source:UniProtKB/TrEMBL;Acc:R6UVA0]
436	ENSGALG00000006200	0.00098997	1.19	2	6194139		
437	ENSGALG00000010744	0.00946878	1.19	4	44695671	G7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)
438	ENSGALG00000016820	0.00292232	1.19	1	141415378		
439	ENSGALG00000017050	0.0083159	1.19	1	176679640	G1	MAD, mothers against decapentaplegic homolog 9 [Source:RefSeq peptide;Acc:NP_001019997]
440	ENSGALG00000001407	0.00543075	1.19	24	1705401		
441	ENSGALG00000001437	0.0047707	1.20	24	1827157		Protein CEPU-1 Precursor [Source:UniProtKB/Swiss-Prot;Acc:Q90773]
442	ENSGALG00000000712	0.00250614	1.20	26	2086175		
443	ENSGALG000000011227	0.0052905	1.20	4	48266556	G7	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1
444	ENSGALG00000000870	0.00461257	1.21	27	1290262		Dephospho-CoA kinase domain-containing protein [Source:UniProtKB/Swiss-Prot;Acc:Q8WVC6]
445	ENSGALG00000016369	0.00792464	1.21	2	143695682		F-box only protein 32 [Source:RefSeq peptide;Acc:NP_001026127]
446	ENSGALG00000011186	0.00338675	1.21	3	42991843	G4	
447	ENSGALG00000001529	0.00720375	1.21	24	2587749		Thymocyte nuclear protein 1 (Thymocyte protein Thy28)[cThy28] [Source:UniProtKB/Swiss-Prot;Acc:Q90679]
448	ENSGALG00000001939	0.00717196	1.21	26	3606173		
449	ENSGALG00000007132	1.3458E-07	1.21	12	12111993		
450	ENSGALG00000008182	0.0016685	1.22	3	2968684		Cation transport regulator-like protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q5Z166]
451	ENSGALG00000015258	0.00768936	1.22	1	87868803		discoidin, CUB and LCCL domain containing 2 [Source:RefSeq peptide;Acc:NP_001025954]
452	ENSGALG00000024167	1.6012E-05	1.22	25	862668		
453	ENSGALG00000011894	0.00197773	1.22	1	51291826		
454	ENSGALG00000013732	0.0041558	1.23	3	53764850		
455	ENSGALG00000006045	0.0018388	1.23	10	13102065		Endophilin-A3 (Endophilin-3)[SH3 domain-containing GRB2-like protein 3][SH3p13] [Source:UniProtKB/Swiss-Prot;Acc:Q8AXU9]
456	ENSGALG00000000181	0.00367151	1.23	16	41987		Transporter associated with antigen processing 2 [Source:UniProtKB/TrEMBL;Acc:A5HUM1]
457	ENSGALG00000010679	0.00054684	1.23	5	43305362	G8	Similar to Stonin 2, clathrin adaptor complex
458	ENSGALG00000002046	0.00025744	1.23	6	3719933		
459	ENSGALG00000012479	0.00357844	1.24	7	36725337		
460	ENSGALG00000009546	0.00947996	1.24	6	32807070		
461	ENSGALG00000011255	0.00629271	1.25	8	29563271		hypothetical protein LOC429115 [Source:RefSeq peptide;Acc:NP_001026736]
462	ENSGALG00000001567	0.00805275	1.25	12	642508		
463	ENSGALG00000009386	0.00192663	1.25	4	21936332		
464	ENSGALG00000004954	0.00178845	1.25	10	11635337		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZKJ3]
465	ENSGALG00000013002	0.00164946	1.25	2	80172659		death-associated protein [Source:RefSeq peptide;Acc:NP_001026174]
466	ENSGALG00000011436	0.00667618	1.25	7	24106575	G9	Transmembrane BAX inhibitor motif containing 1
467	ENSGALG00000008572	0.00773345	1.25	4	16551769	G6	Lysosome-associated membrane glycoprotein 2 Precursor (LAMP-2) [Source:UniProtKB/Swiss-Prot;Acc:Q90617]
468	ENSGALG00000013331	0.0014288	1.25	24	1599282		
469	ENSGALG00000016191	0.00145001	1.26	1	113058139		
470	ENSGALG00000013793	0.00019452	1.26	4	66928282		Circadian locomotor output cycles protein kaput [Source:UniProtKB/Swiss-Prot;Acc:Q80GQ6]
471	ENSGALG00000004339	0.00594821	1.26	2	22658894		
472	ENSGALG00000012117	0.00167932	1.26	7	30000506		
473	ENSGALG00000002062	0.00173359	1.26	18	4528117		signal recognition particle 68kDa [Source:RefSeq peptide;Acc:NP_001006204]
474	ENSGALG00000014708	0.00898706	1.26	1	80901800		
475	ENSGALG00000001728	0.00792703	1.26	17	8780039		BTB (POZ) domain containing 14A [Source:RefSeq peptide;Acc:NP_001025852]
476	ENSGALG00000013878	0.00018092	1.26	22	2888525		
477	ENSGALG00000008823	0.00298394	1.27	1	24090450		
478	ENSGALG00000010647	0.00656664	1.27	8	25277247		
479	ENSGALG00000017321	0.00268942	1.27	1	200431518		pleckstrin homology domain containing, family B (evectins) member 1 [Source:RefSeq peptide;Acc:NP_001012564]
480	ENSGALG00000014314	0.0025592	1.27	1	74297978		
481	ENSGALG00000003799	2.7626E-05	1.27	12	2637926		ubiquitin specific protease, proto-oncogene [Source:RefSeq peptide;Acc:NP_001006134]
482	ENSGALG00000001861	0.00128409	1.27	19	4133303		
483	ENSGALG00000008408	0.00382363	1.27	4	14367598	G6	GRB2-associated-binding protein 3 (Growth factor receptor bound protein 2-associated protein 3)[GRB2-associated binder 3] [Source:UniProt
484	ENSGALG00000010142	0.00646482	1.27	4	35304494		
485	ENSGALG00000004749	0.00014346	1.27	14	4547527		Transmembrane protein 11 [Source:UniProtKB/Swiss-Prot;Acc:Q5ZLD4]
486	ENSGALG00000017186	5.7115E-05	1.27	1	186919506	G1	Inhibitor of apoptosis protein (IAP)[Inhibitor of T-cell apoptosis protein] [Source:UniProtKB/Swiss-Prot;Acc:Q90660]
487	ENSGALG00000005465	0.0064674	1.28	14	6169906		
488	ENSGALG000000023498	0.0002476	1.28	9	25174969		
489	ENSGALG00000014241	0.00225689	1.29	1	76856978		cyclin-dependent kinase inhibitor 18 (p27, Kip1) [Source:RefSeq peptide;Acc:NP_989587]
490	ENSGALG00000011926	0.00859629	1.29	1	79369735		
491	ENSGALG00000009705	0.00549493	1.30	5	32471904	G8	ryanodine receptor 3 [Source:RefSeq peptide;Acc:NP_996757]
492	ENSGALG00000021314	0.00197507	1.31	14	833727		
493	ENSGALG00000011168	0.00469471	1.31	1	44668513		
494	ENSGALG00000009096	0.00126448	1.31	6	24612158		suppressor of fused homolog [Source:RefSeq peptide;Acc:NP_989595]
495	ENSGALG00000013911	4.1012E-05	1.31	1	73640877		zinc finger CCH-type, antiviral 1 [Source:RefSeq peptide;Acc:NP_001012956]
496	ENSGALG00000003028	0.00433071	1.32	17	7589987		
497	ENSGALG00000010601	8.8656E-05	1.32	4	40643754		Ufm1-specific protease 2 (UfSP2)[EC 3.4.22.-] [Source:UniProtKB/Swiss-Prot;Acc:Q5ZIF3]
498	ENSGALG000000024483	0.00020327	1.33	2	57311158	G2	Similar to Heat shock factor binding protein 1
499	ENSGALG00000016733	0.00076737	1.33	3	113633659		
500	ENSGALG00000012909	0.00220394	1.33	2	70369275		
501	ENSGALG00000022964	0.00550827	1.33	1	79334998		
502	ENSGALG00000007051	0.0073643	1.33	9	13850619		Uncharacterized protein C3orf21 [Source:UniProtKB/Swiss-Prot;Acc:Q8NBI6]
503	ENSGALG00000016631	0.00143306	1.33	3	108814040		Integrator complex subunit 9 (Int9) [Source:UniProtKB/Swiss-Prot;Acc:Q5ZKK2]
504	ENSGALG00000003079	0.0070693	1.33	9	10508034		
505	ENSGALG00000006147	0.00468919	1.34	5	12804220		nucleobindin 2 [Source:RefSeq peptide;Acc:NP_001006468]
506	ENSGALG00000005682	0.00275065	1.34	10	12301798		
507	ENSGALG00000010911	0.0009288	1.34	8	27474340		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5ZHU7]
508	ENSGALG00000016403	0.00511579	1.34	3	98711720	G5	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
509	ENSGALG00000008531	0.00749887	1.34	1	20079121		
510	ENSGALG00000012515	0.00510233	1.35	2	56762874	G2	SIMILAR TO TPPP PROTEIN ISOFORM 1, Tubulin polymerization promoting protein
511	ENSGALG00000008903	0.00878324	1.35	7	15248571	G9	139 KDA PROTEIN
512	ENSGALG00000003549	0.00458156	1.36	6	10499190		
513	ENSGALG00000007927	0.00052807	1.36	12	18180749		
514	ENSGALG00000002373	3.4737E-05	1.36	23	4589272		
515	ENSGALG00000002463	0.00083863	1.36	19	4858449		
516	ENSGALG00000009687	0.00426279	1.36	4	26359668		
517	ENSGALG00000007750	0.00226772	1.37	4	12438000	G6	ring finger protein 12 [Source:RefSeq peptide;Acc:NP_990159]
518	ENSGALG00000004521	0.00323861	1.37	13	13133782		
519	ENSGALG00000016372	0.00274774	1.37	2	143673960		
520	ENSGALG00000004272	0.00180824	1.37	7	5967467		
521	ENSGALG00000012647	0.00717917	1.38	1	55755290		
522	ENSGALG00000013043	0.00147629	1.38	2	80506041		Protein FAM173B [Source:UniProtKB/Swiss-Prot;Acc:Q6P4H8]
523	ENSGALG00000011772	0.00047442	1.38	1	50027275		Putative uncharacterized protein H1.01 [Source:UniProtKB/TrEMBL;Acc:Q7L259]
524	ENSGALG00000016094	0.00629807	1.39	4	93326253		
525	ENSGALG00000009981	0.00037731	1.39	3	26686985		Prolyl endopeptidase-like (EC 3.4.21.-)[Prolylendopeptidase-like] [Source:UniProtKB/Swiss-Prot;Acc:Q5ZKL5]
526	ENSGALG00000007717	0.00192745	1.40	20	11943466	G12	Similar to Glucosaminyl (N-acetyl) transferase family member 7

527	ENSGALG00000007072	8.1365E-05	1.40	15	9436940		acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain [Source:RefSeq peptide;Acc:NP_001006193]
528	ENSGALG00000001399	0.00124065	1.40	28	2214540		ring finger protein 126 [Source:RefSeq peptide;Acc:NP_001006338]
529	ENSGALG00000016724	0.00050842	1.40	1	134230907		Regucalcin (RC) [Source:UniProtKB/Swiss-Prot;Acc:Q9I923]
530	ENSGALG00000006775	0.00203679	1.40	20	10324566	G12	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13)[Tissue transglutaminase](TGase C)(TGC)(TG(C))(Transglutaminase-2) [Source:Un
531	ENSGALG00000012658	0.00056041	1.41	1	55925408		putative t-complex protein 11 [Source:RefSeq peptide;Acc:NP_001001897]
532	ENSGALG00000016794	0.0014492	1.41	1	138039834		
533	ENSGALG00000010934	0.0013334	1.41	8	28103057		
534	ENSGALG00000006507	0.00642287	1.41	24	3068439		
535	ENSGALG00000002863	0.00846004	1.42	13	8996068	G10	Sillimar to Endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1
536	ENSGALG00000012936	0.00013761	1.43	1	61438862		Gonad expressed transcript Fragment [Source:UniProtKB/TrEMBL;Acc:Q5BMR5]
537	ENSGALG00000010857	0.00082009	1.43	8	26623165		disabled homolog 1 [Source:RefSeq peptide;Acc:NP_989569]
538	ENSGALG00000004186	0.00060904	1.44	19	6128639		
539	ENSGALG00000007689	0.00052649	1.46	24	5778800		
540	ENSGALG00000017285	0.00655641	1.46	1	75468823		
541	ENSGALG00000015675	0.00095753	1.47	1	101440726		
542	ENSGALG00000008896	0.00032061	1.47	7	15197760	G9	Similar to Protein phosphatase 1, regulatory (inhibitor) subunit 1C
543	ENSGALG00000005617	0.00190989	1.47	14	6298133		Escherichia coli endonuclease III-like 1 [Source:UniProtKB/TrEMBL;Acc:A7M7B9]
544	ENSGALG00000008875	0.00407542	1.48	3	16951662		
545	ENSGALG00000014278	0.00395711	1.49	1	79059526		
546	ENSGALG00000005674	0.00261047	1.49	11	18779565		ubiquitin specific protease 10 [Source:RefSeq peptide;Acc:NP_001006130]
547	ENSGALG00000003135	0.00171969	1.52	6	9980221		Ankyrin 3 Fragment [Source:UniProtKB/TrEMBL;Acc:Q90717]
548	ENSGALG00000015955	0.0002241	1.53	2	130826456	G3	DNA repair and recombination protein RAD54B (EC 3.6.1.-)[RAD54 homolog B] [Source:UniProtKB/Swiss-Prot;Acc:Q9D6G7]
549	ENSGALG00000011198	0.00060084	1.53	1	44737389		
550	ENSGALG00000014795	0.00073489	1.54	2	103921071	G3	Homeobox protein AKR (Avian knotted-related protein) [Source:UniProtKB/Swiss-Prot;Acc:Q90655]
551	ENSGALG00000003689	0.00518135	1.55	6	10736848		
552	ENSGALG00000002693	1.5813E-05	1.55	6	6274634		
553	ENSGALG00000003634	2.0169E-05	1.56	6	10670550		
554	ENSGALG00000014340	0.00143511	1.56	20	5455656	G11	Hypothetical protein LOC770857
555	ENSGALG000000022663	0.00357698	1.57	12	668355		
556	ENSGALG00000001333	0.00020345	1.57	17	9455298		
557	ENSGALG00000003527	0.00330321	1.58	28	3596444		
558	ENSGALG00000013053	0.00203763	1.61	2	81428975		
559	ENSGALG00000008076	0.00566745	1.66	4	13801069	G6	hypothetical protein LOC422344 [Source:RefSeq peptide;Acc:NP_001012904]
560	ENSGALG00000007445	0.00140652	1.66	14	12643118		
561	ENSGALG00000003196	0.0059108	1.67	6	10376970		Angiogenin Precursor (EC 3.1.27.-)(Ribonuclease A) [Source:UniProtKB/Swiss-Prot;Acc:P27043]
562	ENSGALG00000016040	0.00139592	1.71	1	110089174		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q5F3X3]
563	ENSGALG000000021855	8.523E-05	1.72	5	55954460		
564	ENSGALG00000004046	0.00762353	1.74	10	7217201		
565	ENSGALG00000008836	6.9602E-05	1.75	1	24119259		ATPase, H+ transporting, lysosomal accessory protein 1, vacuolar ATP synthase subunit S1 proteins
566	ENSGALG000000024011	0.00357879	1.76	17	881078		
567	ENSGALG00000016709	1.7682E-05	1.77	3	112530572		
568	ENSGALG00000012464	0.00018525	1.77	5	61370747		SOUL protein [Source:RefSeq peptide;Acc:NP_990120]
569	ENSGALG00000000104	0.00057591	1.78	26	1073277		cryptochrome 4 [Source:RefSeq peptide;Acc:NP_001034685]
570	ENSGALG00000007101	9.7999E-05	1.81	24	5224757		hypothetical protein LOC428256 [Source:RefSeq peptide;Acc:NP_001026668]
571	ENSGALG00000009013	5.202E-06	1.83	3	14518618		MKKS - member in TCP-1/cpn60 chaperonin family, McKusick-Kaufman syndrome
572	ENSGALG00000006962	0.00021319	1.84	14	6610074		
573	ENSGALG00000005416	4.7815E-08	1.90	2	31531947		Chromosome 9 open reading frame 52 - Deme6 fam. Putative RNP-1 motif and a candidate anchoring transmembrane domain
574	ENSGALG00000004936	0.00105132	2.13	4	1990373		SIMILAR TO GLYCINE RECEPTOR ALPHA4 SUBUNIT.
575	ENSGALG00000004807	0.00493897	2.16	8	7735996		SOUL heme-binding protein
576	ENSGALG00000012381	0.00065749	2.18	7	33042646		SIMILAR TO NEUREXOPHILIN , may function as neuropeptides that may signal via alpha-neurexins
577	ENSGALG00000007028	2.2144E-06	2.28	4	8805689	G6	115 KDA PROTEIN with Pleckstrin homology
578	ENSGALG00000009352	0.00584675	2.35	5	28669152	G8	Zinc finger protein DPF3 (cer-d4) [Source:UniProtKB/Swiss-Prot;Acc:P58270]
579	ENSGALG00000017248	1.2112E-05	2.51	1	193425881		RAB30, member RAS oncogene family, small GTPases
580	ENSGALG00000014226	0.00135264	2.51	1	72411997		C22orf9, conserved motifs including a CVLxxxD motif.The function is unknown.
581	ENSGALG00000012834	2.2777E-08	2.57	1	58612890		Aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase), oxidoreductase activity
582	ENSGALG00000002893	0.00302292	2.93	13	9169405	G10	Stanniocalcin 2, potential calcium- and phosphate-regulating hormone
583	ENSGALG00000009869	0.00039867	2.94	4	31054139		SIMILAR TO CYSTEINE-RICH PROTEIN ISOFORM 1. The function of this protein is unknown, Zn ion binding protein
584	ENSGALG00000006425	0.00142712	5.27	12	11251619		Similar to solute carrier family 6 (neurotransmitter transporter, taurine), member 6

Supplementary Table S3. Primers for qRT-PCR

Gene	mRNA sequence identifier	Forward	Reverse
D1B	ENSGALT00000024157	CCTCAAGTCCTCCATCAGGAAA	AGACAAAGACACCCATGATGATTG
Actin	NM_205518.1	AGGTCATCACCATTGGCAATG	GTTCCCTGTGTCGCTTGC
GAPDH	NM_204305	TGATGCCCCCATGTTTGTG	TGGTGCACGATGCATTGC
Leptin receptor	NM_204323	CTGAATGAGACATCTTCGAGTCCTT	TCCATGCTCCCTCCTCCA
MRAP2	ENSGALT00000025538	TGTTCTTTGTCCTGACCCCTGCT	TTTCTTGATGTGGTGCTCCTGT
WPKCI-8	AB026677.1	AGATTGTGGCGCACCTCTTC	CACTTCTCGCCAACAATCATCA
Casp-3	AF083029.1	TCTCGTTCAGGCACGGATGCAG	TCATCGCCATGGCTTAGCAACAC
SYT6	XM_425830	TGGGGGTCAATGCAGAAGGACTGG	CTTGCCACTGCTCCACCAATGGATG
GBRG4	X73533.1	ATGAAGATGACGACCCTGGCT	TGCAGCAGAAGAACCTCTCACAA
ARHGAP17	XM_414864.2	TGTGAGCACTGCCCAAACCAG	AGAGCTTTGGCTTCTGGTCTGC
GABRB2	XM_001232377.1	CTTCGTTTTTCATGGCTCTGCTA	GCTTTCTTTTGACGCTGAGGTC
Q90591_CHICK	XM_414492.2		
CKAP2	NP_001006274.1	TCCTGTTGTTCCCAAGTGGCAAGC	AAGCACAGATGTAGGCGGCC
IRK3_CHICK	L35555.1	TCCGCTGCAAGCTGTCAAGTC	ACAGGTGCTAGAAGGGGCTCTTGG
HTR2C	XM_426265.2	TTCTGATGTCCTTGGCGGTGG	TGAAGCGGCTGTGCTCAATGGG
RHOJ	XM_001234863.1	CAACAGCACCTGCTGGGACT	GCCTCATACCACAATGTCCAG
MBTPS2	ENSGALT00000026423	ACAACCTGGGGGAGGTGGAAACC	AGGCCACCATTGCCTCTACTGC
AR2BP	AJ719969	TTGGTGTAGCCGTCTCCTCC	ACCCAACGACAGCGTCAAA
RA54B	AF178529.1	AGCAGTGGCAGGTGTTTCAGGC	TGACGAGGTTTGACGCTCTGAGG
PTEN	XM_421555.2	TGGCGGAACTTGCAATCCTCAG	CACCGCATACCGGCAAAGGTTG
GLRA4	XM_001232994.1	ACGCCGCCGTCAACTTTGTCTC	TGGCACGGTCGACATAACGC
NXPH2	XM_426606.2	TCGCACGAACTAAACGCAGACC	TGAAGGTGCCGTTGCCGTGATC
RAB30	XM_417213.2	TGCGGGAAATCGAGCAGTACGC	TTCACCAGGGTGTCTGCCGTG
STC2	XM_414534.2	AATGCCGGCGATGTGGGATGTG	AATGGCTGGGCATTACGGCTG
CNKS2 Chick	ENSGALT00000011371 (ENSGALG00000007028)	ACCAGCCCAACAAGCAGTTCCAC	ACAGGGTGGCCTTACCACCTTC
TBP	NM_205103.1	TAGCCCGATGATGCCGTAT	GTTCCCTGTGTCGCTTGC

Primer design and identification of genes for normalization purpose see Ring et al. 2010.

Supplementary Table S4. Permutation test and calculation of false discovery rate (FDR) for the differentially expressed annotated genes.

Cut-off p-value	Observed DE genes	Permutation p-value ^a	Expected DE genes ^b	FDR (Expected/Observed)
0.00075	173	0.004	1	0.006
0.0010	195	0.004	2	0.010
0.0050	415	0.006	13	0.031
0.010	585	0.006	33	0.056
0.020	866	0.007	80	0.092
0.030	1060	0.007	134	0.12
0.040	1245	0.007	193	0.15
0.050	1385	0.010	252	0.18

a Significance was calculated using 1000 permutations and counting the number of times where the same or more than the observed number of significant probe sets at the given significance level was obtained.

b The median value of significant DE genes in the described permutation. At 5% FDR, the cut-off p-value was 0.008 with 546 significant DE genes.

DE; differentially expressed,

Supplementary material Table S5 (Ka et al)

Validation of array data using qRT-PCR

ENSEMBL ID	Gene	Description	p-value	Females FD; LWS/HWS	
				Array	qRT PCR ^{a)}
ENSGALG00000010638	NP_990056.1	caspase 3	5.02E-05	0.66	0.56
ENSGALG00000015838	MRAP2	Melanocortin-2 receptor accessory protein 2	0.0044	0.66	0.55
ENSGALG00000001968	SYT6	Synaptotagmin-6 (Synaptotagmin VI)(SytVI)	0.0016	0.64	0.53
ENSGALG00000020292	GBRG4_CHICK	GABA-A receptor gamma-4 subunit precursor (GABA(A) receptor subur	0.00075	0.61	0.6
ENSGALG00000005962	ARHGAP17	Rho GTPase-activating protein 17 (Rho-type GTPase-activating protein 1	0.00021	0.61	0.49
ENSGALG00000001690	Q90591_CHICK	GABA-A receptor beta 2 subunit precursor	0.00016	0.59	0.55
ENSGALG00000017025	NP_001006274.1	cytoskeleton associated protein 2, CKAP2	3.46E-05	0.58	0.43
ENSGALG00000012537	IRK3_CHICK	G protein-activated inward rectifier potassium channel 1 (GIRK1) (Potas	0.00060	0.55	0.42
ENSGALG00000014975	Q7LZ74_CHICK	DRD5, D(1B) dopamine receptor	0.0039	0.51	0.52
ENSGALG00000005853	HTR2C	5-hydroxytryptamine receptor 2C (5-HTR2C)(5-HT-2C)(5-HT2C)(5HT-1C)(0.0094	0.50	0.42
ENSGALG00000011855	RHOJ	Rho-related GTP-binding protein RhoJ Precursor (Tc10-like GTP-binding	8.52E-05	0.45	0.37
ENSGALG00000016382	MBTPS2	Membrane-bound transcription factor site-2 protease (Site-2 protease)(2.77E-10	0.38	0.41
ENSGALG00000014326	AR2BP_CHICK	ADP-ribosylation factor-like protein 2-binding protein (ARF-like 2- bindir	0.0045	0.36	0.45
ENSGALG00000015955	RA54B_CHICK	DNA repair and recombination protein RAD54B (EC 3.6.1.-) (RAD54 horr	0.00022	1.53	1.57
ENSGALG00000003634	PTEN	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-speci	2.02E-05	1.56	1.57
ENSGALG00000004936	GLRA4	Glycine receptor subunit alpha-4 Precursor	0.0011	2.13	3.9
ENSGALG00000012381	NXPH2	Neurexophilin-2 Precursor, potential neuropeptide	0.00066	2.18	2.05
ENSGALG00000007028	novel (CNKSR2)	Zebrafish_CNKSR2. Connector enhancer of kinase suppressor of ras 2	2.21E-06	2.28	3.39
ENSGALG00000017248	RAB30	Ras-related protein Rab-30, small GTPase	1.21E-05	2.51	4.37
ENSGALG00000002893	STC2	Stanniocalcin-2 Precursor (STC-2)(Ca regl factor)(STCRP)(STC-related prc	0.0030	2.93	1.24

a) pools of hypothalami from 7 individuals were analysed

Supplementary material Table S6 (Ka et al)

Functional classification of top 97 differential expressed genes, their chromosomal location in relation to QTLs for growth ^{a)} and to genome wide regions with significantly different allele frequencies in the genome of HWS and LWS line ^{b)}

ENSEMBL ID	Gene	Description	their chromosomal location in relation to QTLs for growth and to regions with significantly different allele frequencies ^{b)}		cell adhesion/signaling/phosphorylation	cell cycle/DNA repair/replication	transcription/translation	protein modification	metabolism; cofactor; DNA, lipid	channel/transport	RNA processing/RNA binding	others	neural plasticity	growth/size-rel. phenot's in transgen. mice	Position i region with significantly different allele frequency ^{b)}	
			p-value ^{c)}	LWS/HWS ^{d)}											Start Ch:Pos(Mb) ^{e)}	QTL ^{f)}
ENSGALG00000016141	novel (PLC3)	C.elegans_plc-3. Phospholipase C family member (plc-3)	4.87E-05	0.66											2:154.503	x
ENSGALG00000015838	MRAP2	Melanocortin-2 receptor accessory protein 2	0.0044	0.66											3:0.080243	x
ENSGALG00000001741	NPTN	Neuroplastin Precursor (Stromal cell-derived receptor 1)(SDR-1)	0.0036	0.65											10:1.563	
ENSGALG00000013753	DOK6	Docking protein 6 (Downstream of tyrosine kinase 6)	0.0005	0.63											2:96.182	
ENSGALG00000014369	EDARADD	Ectodysplasin-A receptor-associated adapter protein (EDAR-associated death domain protein)(Crikled homolog)	0.0002	0.62											3:39.23	G4
ENSGALG00000012732	PHAR1_CHICK	Phosphatase and actin regulator 1.	0.0057	0.61											2:63.38	
ENSGALG00000013464	AN32E_CHICK	Acidic leucine-rich nuclear phosphoprotein 32 family member E. Human_ANP32E	0.0030	0.60											25:0.026	
ENSGALG00000010294	RPS6KL1	Ribosomal protein S6 kinase-like 1	0.0021	0.58											5:40.52	G8
ENSGALG00000013925	KIT_CHICK	Mast/stem cell growth factor receptor precursor (EC 2.7.10.1) (SCFR) (Proto-oncogene tyrosine-protein kinase Kit)	0.0042	0.56											4:67.14	
ENSGALG00000001797	GPSM1	G-protein-signaling modulator 1 (Activator of G-protein signaling 3)	0.0043	0.54											17:8.61	
ENSGALG00000014975	Q7L274_CHICK	DRD5, D(1B) dopamine receptor	0.0039	0.51											4:81.452	x
ENSGALG00000005853	HTR2C	5-hydroxytryptamine receptor 2C (5-HT2C)(5-HT2C)(5HT-1C)(Serotonin receptor 2C)	0.0094	0.50											4:2.780	
ENSGALG00000011855	RHOJ	Rho-related GTP-binding protein RhoJ Precursor (Tc10-like GTP-binding protein TCL)(Ras-like protein family membl)	8.52E-05	0.45											5:55.955	x
ENSGALG00000003135	Q90717_CHICK	Ankyrin 3	0.0017	1.52											6:9.981	x
ENSGALG00000016709	DSCR11	Calcipressin-2 (Regulator of calcineurin 2)(Down syndrome candidate region 1-like 1)(Thyroid hormone-responsib)	1.77E-05	1.77											3:112.531	G5
ENSGALG00000007101	NP_001026668.1	hypothetical protein LOC428256. Human_ZNF259. Zinc finger protein ZPR1 (Zinc finger protein 259)	9.80E-05	1.81											24:5.225	
ENSGALG00000012381	NXPH2	Neurexophilin-2 Precursor, potential neuropeptide	0.0066	2.18											7:33.043	
ENSGALG00000007028	novel	CNKS2. Connector enhancer of kinase suppressor of ras 2	2.21E-06	2.28											4:8.81	G6
ENSGALG00000017248	RAB30	Ras-related protein Rab-30, small GTPase	1.21E-05	2.51											1:193.43	
ENSGALG00000002893	STC2	Stanniocalcin-2 Precursor (STC-2)(Ca regl factor)(STCRP)(STC-related protein)	0.0030	2.93											13:9.17	G10
ENSGALG00000005769	NP_001026352.1	wee1 tyrosine kinase	0.0003	0.66											5:10.277	
ENSGALG00000005962	ARHGAP17	Rho GTPase-activating protein 17 (Rho-type GTPase-activating protein 17)(RhoGAP interacting with CIP4 homolo	0.0002	0.61											14:6.61	x
ENSGALG00000015360	K1524_CHICK	Protein KIAA1524 homolog. Human_Protein CIP2A (Cancerous inhibitor of PP2A)(p90 autoantigen)	0.0001	0.56											1:90.84	
ENSGALG00000014326	AR2BP_CHICK	ADP-ribosylation factor-like protein 2-binding protein (ARF-like 2- binding protein).	0.0045	0.36											11:0.744	
ENSGALG00000003634	PTEN	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (EC 3.1.3	2.02E-05	1.56											6:10.671	x
ENSGALG00000002117	PARG	Poly(ADP-ribose) glycohydrolase	0.0013	0.65											6:3.792	x
ENSGALG00000016049	RRM2B	Ribonucleoside-diphosphate reductase subunit M2 B (EC 1.17.4.1)(TP53-inducible ribonucleotide reductase M2 I	0.0002	0.60											2:134.43	
ENSGALG00000017025	NP_001006274.1	cytoskeleton associated protein 2	3.46E-05	0.58											1:174.68	G1
ENSGALG00000015955	RA54B_CHICK	DNA repair and recombination protein RAD54B (EC 3.6.1.-) (RAD54 homolog B)	0.0002	1.53											2:130.827	G3
ENSGALG00000007445	MPG	DNA-3-methyladenine glycosylase (EC 3.2.2.21)(3-methyladenine DNA glycosidase)(ADPG)(3-alkyladenine DNA g	0.0014	1.66											14:12.644	
ENSGALG00000000104	NP_001034685.1	cryptochrome 4	0.0006	1.78											26:1.074	
ENSGALG00000008532	NP_001006202.1	similar to cofactor of BRCA1; negative elongation factor protein B	7.55E-07	0.56											17:2.30	x
ENSGALG00000014795	AKR_CHICK	Homeobox protein AKR (Avian knotted-related protein).	0.0007	1.54											2:103.922	G3
ENSGALG00000012631	NP_001025932.1	BTB (POZ) domain containing 11 / Human_PWP1. Periodic tryptophan protein 1 homolog (Keratinocyte protein II	0.0007	0.63											1:55.382	
ENSGALG00000017064	NP_001006276.1	replication factor C (activator 1) 3, 38kDa	7.46E-05	0.57											1:178.16	G1
ENSGALG00000001333	MRRF	Ribosome-recycling factor, mitochondrial Precursor (RRF)(Ribosome-releasing factor, mitochondrial)	0.0002	1.57											17:9.456	
ENSGALG00000009352	DPF3_CHICK	Zinc finger protein DPF3 (cer-d4).	0.0058	2.35											5:28.67	G8
ENSGALG00000016202	HSF2BP	Heat shock (transcription) factor 2-binding protein	5.14E-05	0.54											1:113.446	x
ENSGALG00000016000	novel	Human_Plasma glutamate carboxypeptidase Precursor (EC 3.4.17.-)	1.87E-05	0.53											2:131.924	x
ENSGALG00000003861	Q5F401_CHICK	Human_HERC4 Probable E3 ubiquitin-protein ligase HERC4	2.88E-08	0.48											6:11.53	x
ENSGALG00000012011	C14orf149	Probable proline racemase	0.0048	0.42											5:57.378	
ENSGALG00000006314	DPP6	Dipeptidyl aminopeptidase-like protein 6 (Dipeptidylpeptidase VI)(Dipeptidylpeptidase 6)(Dipeptidyl peptidase I	0.0050	0.40											2:7.14	x
ENSGALG00000009013	MKKS	McKusick-Kaufman/Bardet-Biedl syndromes putative chaperonin (Bardet-Biedl syndrome 6 protein)	5.20E-06	1.83											3:14.519	
ENSGALG00000010638	NP_990056.1	caspase 3	5.02E-05	0.66											4:40.902	x
ENSGALG00000016382	MBTPS2	Membrane-bound transcription factor site-2 protease (Site-2 protease)(EC 3.4.24.85)(S2P endopeptidase)(Sterol	2.77E-10	0.38											1:122.53	x
ENSGALG00000008060	PRKAR2B	cAMP-dependent protein kinase type II-beta regulatory subunit	0.00252	0.60											1:15.50	

ENSGALG00000003689	PAPSS2	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2 (PAPS synthetase 2)(PAPSS 2)(Sulfurylase kina:	0.00518	1.55			6:10.737		x
ENSGALG00000013053	MTRR	Methionine synthase reductase, mitochondrial Precursor (MSR)(EC 1.16.1.8)	0.00204	1.61			2:81.429		
ENSGALG00000012663	ALDH5A1	Succinate-semialdehyde dehydrogenase, mitochondrial Precursor (EC 1.2.1.24)(NAD(+)-dependent succinic semi	0.00026	0.44			2:58.962	G2	
ENSGALG00000006644	Q5W453_CHICK	Fatty acid Coenzyme A ligase, long chain 6 (Fragment).	0.00025	0.66			13:17.176		
ENSGALG00000016442	RRM2	Ribonucleoside-diphosphate reductase subunit M2 (EC 1.17.4.1)(Ribonucleotide reductase small subunit)(Ribon	0.00219	0.64			3:99.397	G5	
ENSGALG00000015156	C9orf95	Nicotinamide riboside kinase 1 (NMR-K 1)(NRK 1)(EC 2.7.1.22)(Ribosylnicotinamide kinase 1)(RNK 1)(Nicotinic aci	0.00075	0.66			2:36.391		
ENSGALG00000012834	AKR1D1	3-oxo-5-beta-steroid 4-dehydrogenase (EC 1.3.1.3)(Delta(4)-3-ketosteroid 5-beta-reductase)(Delta(4)-3-oxosteroi	2.28E-08	2.57			1:58.613		x
ENSGALG00000014866	FABPR_CHICK	Fatty acid-binding protein, retina (R-FABP).	0.00189	0.66			3:63.844		
ENSGALG00000016792	MFSD9	Major facilitator superfamily domain-containing protein 9	0.00021	0.66			1:138.272		
ENSGALG00000016448	KCNF1	Potassium voltage-gated channel subfamily F member 1 (Voltage-gated potassium channel subunit Kv5.1)(KH1)	0.00597	0.64			3:99.892	G5	
ENSGALG00000008682	SLC25A43	Solute carrier family 25 member 43, mitochondria	0.00285	0.64			4:16.70	G6	x
ENSGALG00000001968	SYT6	Synaptotagmin-6 (Synaptotagmin VI)(SytVI)	0.00164	0.64			26:3.64		
ENSGALG000000004829	ATP2B2	Plasma membrane calcium-transporting ATPase 2 (PMCA2)(EC 3.6.3.8)(Plasma membrane calcium ATPase isoform	0.00055	0.64			12:4.06		
ENSGALG00000020292	GBRG4_CHICK	GABA-A receptor gamma-4 subunit precursor (GABA(A) receptor subunit gamma-4).	0.00075	0.61			4:10.93	G6	x
ENSGALG00000001690	Q90591_CHICK	GABA-A receptor beta 2 subunit precursor	0.00016	0.59			13:7.10		x
ENSGALG000000000062	ARMC1_CHICK	Armadillo repeat-containing protein 1, metal ion binding, mitochondrion	1.09E-05	0.55			2:119.06	G3	x
ENSGALG00000004936	GLRA4	Glycine receptor subunit alpha-4 Precursor	0.00105	2.13			4:1.991		
ENSGALG000000006425	NP_001025771.1	hypothetical protein LOC416041. Human_SLC6A6.	0.00143	5.27			12:11.252		x
ENSGALG00000012537	IRK3_CHICK	G protein-activated inward rectifier potassium channel 1 (GIRK1) (Potassium channel, inwardly rectifying subfam	0.00060	0.55			7:37.36		x
ENSGALG000000012867	MRPS33	28S ribosomal protein S33, mitochondrial (S33mt)(MRP-S33)	0.00084	0.66			1:59.083		
ENSGALG00000022663	novel	mouse_Snhg8. small nucleolar RNA host gene (non-protein coding) 8 Gene	0.00358	1.57			12:0.6684		
ENSGALG000000003196	RSFR_CHICK	Angiogenin precursor (EC 3.1.27.-) (Ribonuclease A).	0.00591	1.67			6:10.377		
ENSGALG000000004046	LARP6	La-related protein 6 (La ribonucleoprotein domain family member 6)(Acheron)(Achn)	0.00762	1.74			10:7.218		x
ENSGALG00000012842	Novel	Human_ZC3HAV1. zinc finger CCCH type, antiviral 1. Novel protein coding in chicken.	9.94E-05	0.50			1:58.688		x
ENSGALG00000015396	NP_001025958.1	CD200 antigen	0.00056	0.62			1:92.01		x
ENSGALG00000015409	PROS1	Vitamin K-dependent protein S Precursor	0.00060	0.59			1:92.895		
ENSGALG00000012464	NP_990120.1	SOUL protein. Zebra fish_HEBP1. Heme-binding protein 1 (p22HBP)	0.00019	1.77			5:61.371		
ENSGALG00000009868	ZNF330	Zinc finger protein 330 (Nucleolar cysteine-rich protein)(Nucleolar autoantigen 36)	0.00040	2.94			4:31.06		
ENSGALG00000013955	novel	no description	0.00626	0.67	Function: uncharacterized		4:67.858		
ENSGALG000000017175	KBTBD3	Kelch repeat and BTB domain-containing protein 3 (BTB and kelch domain-containing protein 3)	0.00690	0.66			1:185.442	G1	x
ENSGALG00000010592	novel	no description	0.00022	0.65			4:40.198		x
ENSGALG00000017013	novel	no description	0.00335	0.64			1:173.733	G1	x
ENSGALG00000010562	novel	C14orf145, Phosphorylated upon DNA damage, CC-domain, PTM	0.00017	0.64			5:43.158	G8	x
ENSGALG00000012946	FAM60A_CHICK	Protein FAM60A	0.00029	0.63			1:61.675		x
ENSGALG00000020909	C20orf85	Uncharacterized protein C20orf85	1.48E-07	0.60			20:11.228	G12	
ENSGALG00000015685	novel	no description	0.00017	0.60			4:85.607		x
ENSGALG00000000444	novel	no description	0.00016	0.56			26:1.269		
ENSGALG00000023387	novel	no description	1.83E-05	0.55			6:35.379		
ENSGALG00000003013	C10orf107	Uncharacterized protein C10orf107	1.49E-07	0.54			6:9.525		
ENSGALG000000004870	CXorf41	Uncharacterized protein CXorf41 (Sarcoma antigen NY-SAR-97)	0.00015	0.46			4:1.881		
ENSGALG00000011198	TMTC3	Transmembrane and TPR repeat-containing protein 3 (Protein SMILE)	0.00060	1.53			1:44.74		
ENSGALG00000002693	FAM149B1	Protein FAM149B1	1.58E-05	1.55			6:6.275		
ENSGALG00000014340	novel	no description, uncharacterized	0.00144	1.56			20:5.456	G11	
ENSGALG00000003527	ARRDC2	Arrestin domain-containing protein 2	0.00330	1.58			28:3.597		
ENSGALG00000008076	NP_001012904.1	hypothetical protein LOC422344. Human_TMEM164. transmembrane protein 164	0.00567	1.66			4:13.801	G6	
ENSGALG00000016040	Q5F3X3_CHICK	Hypothetical protein. Human_MORC3. MORC family CW-type zinc finger protein 3 (Zinc finger CW-type coiled-co	0.00140	1.71			1:110.09		x
ENSGALG00000008836	novel	no description.	6.96E-05	1.75			1:24.120		x
ENSGALG00000024011	novel	no description.	0.00358	1.76			17:0.881		x
ENSGALG00000005416	TTC39B	Tetratricopeptide repeat protein 39B (TPR repeat protein 39B)	4.78E-08	1.90			2:31.532		x
ENSGALG00000004607	HEBP2	Hypothetical Heme-binding protein 2 (Placental protein 23)(PP23)(Protein SOUL)	0.00494	2.16			8:7.736		
ENSGALG00000014226	C22orf9	Uncharacterized protein C22orf9	0.00135	2.51			1:72.412		

- The list is sorted based on the functional characterization; fold change
- FD; fold difference
- p-value; one-way ANOVA
- L/H; ratio between hybridization signal from HWS / LWS
- Ch:Pos (Mb) Chick chromosome: position in Mega basepair from start of the p-arm
- QTL; quantitative trait locus, G1- G12 are the QTL regions for body weight (Jacobsson et al. 2005; Park et al. 2006; Wahlström et al. 2009)

Supplementary Table S7. Differentially expressed genes that have been reported to produce a phenotype in transgenic- or knock-out mice, which is related to that of the chicken lines.

ENSEMBL ID	Gene	Description	Fold difference LWS/HWS	MGI ID/ Reference	Phenotype	
					✓	✓
					Fatness/Body composition/Body weight	✓
					Feeding	✓
					Growth/Skeletal, visceral size	✓
					Heart rate/Blood pressure	✓
					Reproduction	✓
					Development of neuronal system/Neurophysiology/Neurological behaviour	✓
ENSGALG0000001797	GPSM1	G-protein-signaling modulator 1	0.54	MGI:1915089	✓	✓
ENSGALG00000012663	ALDH5A1	Succinate-semialdehyde dehydrogenase,	0.44	MGI:2441982	✓	✓
ENSGALG00000004829	ATP2B2	Plasma membrane calcium-transporting ATPase 2	0.64	MGI:105368	✓	✓
ENSGALG00000008060	PRKAR2B	Cyclic AMP-dependent protein kinase type II-beta regulatory subunit	0.60	MGI:97760	✓	✓
ENSGALG00000005853	HTR2C	5-hydroxytryptamine receptor 2C	0.50	MGI:96281	✓	✓
ENSGALG00000013053	MTRR	Methionine synthase reductase, mitochondrial Precursor	1.61	MGI:1891037	✓	
ENSGALG00000009013	MKKS	McKusick-Kaufman/Bardet-Biedl syndromes putative chaperonin	1.83	MGI:1891836	✓	
ENSGALG00000013925	KIT_CHICK	Mast/stem cell growth factor receptor precursor	0.56	MGI:96677	✓	✓
ENSGALG00000002893	STC2	Stanniocalcin-2 Precursor	2.93	MGI:1316731		✓
ENSGALG00000003689	PAPSS2	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2	1.55	MGI:1330223		✓
ENSGALG00000016049	RRM2B	Ribonucleoside-diphosphate reductase subunit M2 B	0.60	MGI:2155865		✓
ENSGALG00000010638	NP_990056.1	Caspase 3	0.66	MGI:107739		✓
ENSGALG00000006425	NP_001025771.1	Hypothetical protein LOC416041. Human_SLC6A6.	5.27	MGI:98488	✓	✓
ENSGALG00000016709	DSCR1L1	Calcipressin-2 (Regulator of calcineurin 2)	1.77	MGI:1858219		✓
ENSGALG00000014975	Q7LZ74_CHICK	Human_DRD5, D(1B) dopamine receptor	0.51	MGI:94927		✓
ENSGALG00000012537	IRK3_CHICK	G protein-activated inward rectifier potassium channel 1 (Inward rectifier K(+) channel Kir3.1)	0.55	MGI:104742		✓
ENSGALG00000003861	Q5F401_CHICK	Probable E3 ubiquitin-protein ligase HERC4	0.48	MGI:1914595		✓
ENSGALG00000016202	HSF2BP	Heat shock (transcription) factor 2-binding protein	0.54	MGI:96239	✓	✓
ENSGALG00000014369	EDARADD	Ectodysplasin-A receptor-associated adapter protein	0.62	MGI:1931001	✓	✓
ENSGALG00000003135	Q90717_CHICK	Ankyrin 3	1.52	MGI:88026		✓
ENSGALG00000003634	PTEN	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase	1.56	MGI:109583		✓
ENSGALG00000002117	PARG	Poly(ADP-ribose) glycohydrolase	0.65	MGI:1347094		✓
ENSGALG00000014866	FABPR_CHICK	Fatty acid-binding protein 7 (R-FABP).	0.66	MGI:101916		✓
ENSGALG00000001690	Q90591_CHICK	GABA-A receptor beta 2 subunit precursor	0.59	MGI:95620		✓
ENSGALG00000015396	NP_001025958.1	CD200 antigen	0.62	MGI:1196990		✓
ENSGALG00000007445	MPG	DNA-3-methyladenine glycosylase	1.66	MGI:97073		✓
ENSGALG00000014795	AKR_CHICK	Homeobox protein AKR	1.54	MGI:1194497		✓
ENSGALG00000015838	MRAP2	Melanocortin-2 receptor accessory protein 2	0.66	[Chan, 2009 #90]		