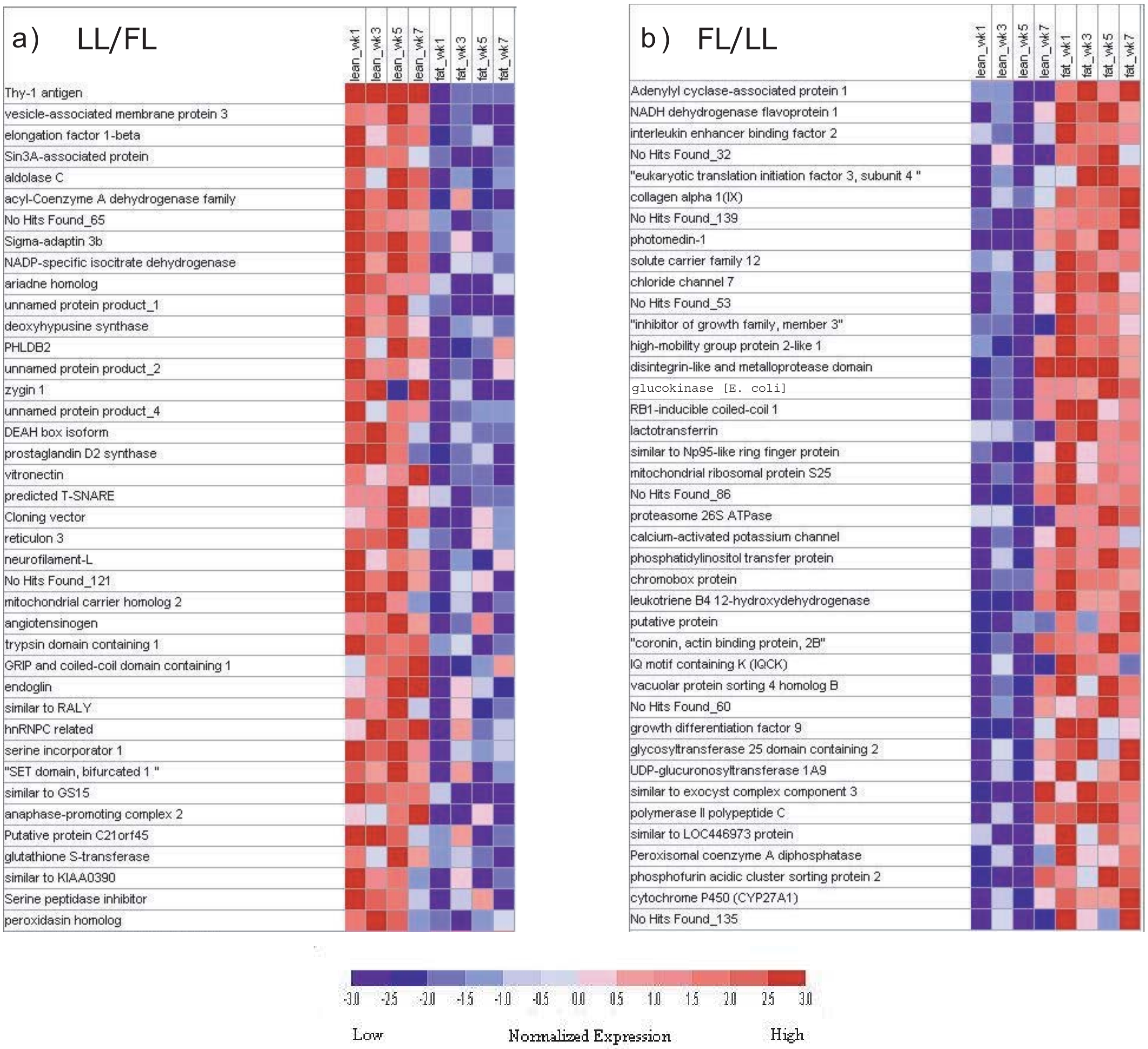

Supplemental Figure 1. Hypothalamic expression patterns that correlate with either the fat or lean phenotype. a) 40 genes up-regulated in LL relative to FL. b) 40 genes up-regulated in the FL relative to LL.
All genes are differentially expressed between lines (P<.05) and ranking is calculated based on the difference of the means for each line scaled by the sum of the standard deviations (x1-x2)/(x12+x22)1/2.
Genes in red represent high expression levels and genes in blue represent low expression levels.

Supplemental Table 1. Oligonucleotide primers used for qRT-PCR.

GENE	**Sense primer**	**Antisense primer**
CYTB	5’TTCACATCGGACGAGGCCTAT3’	5’CACAAAGGCGGTGGCTATGA3’
EEF1A	5’GTGTGTGGAGAGCTTCTCCCAGTAC3’	5’CGCTCTTCTTCTCCACGTTCTTG3’
PGAM1	5’CACCCCTTCTTCAGCACCAT3’	5’ATGGTGTCCTTCAGGCTCTCA3’
NAPB	5’AAGCCCACGAGGAGCAGAAC3’	5’GCGAAGCAACATGGTTGTGA3’
TPH1	5’AATCCGTATACTCAGAGTGTGCAGAT3’	5’AGGGCATCGCTGACAATGTC3’
ENO2	5’AGATGACCCAAGCCGCTACA3’	5’GGTCAAAGGGATCCTCAATGG3’
GPI	5’GCCCAACCAATTCCATCATG3’	5’CCAGACAACCCCCTGAACAA3’
CEBPZ	5’GGATGAAAATGCTGGGTCCAA3’	5’CGCCGCTCTAATTCCCACTTG3'
DPYSL2	5’TCTCTGCCAAGACCCACAACA’	5’CACGATCTTCCCTTGGCTGAT3’
TMEM120A	5’ACAACGCCGTCACCCTATTC3’	5’GTTCCCCAGGAAGAGGACGAA3’
GHRHR	5’CCTTGGCATTCGGCTTTATTTAG3’	5’TCAGGAAACAGTAGAGGAGTGCTACA3’
PITRM1	5’TCAGATGAAATGAAGCAGTCA3’	5’GTGCTCTTCCCAACTGCAAGA3’
GAPDH	5’AAGGAGTGAGCCAAGCACACA3’	5’TCACTGCAGGATGCAGAACTG3’
ACTB	5’CCCAAAGCCAACAGAGAGAAG3’	5’ACCATCACCAGAGTCCATCAC3’

Supplemental Table 2

cDNA Clone ID	Human Protein ID	HUGO Gene Symbol	Highest BlastX Hit	LL Wk1 mean	LL Wk3 mean	LL Wk5 mean	LL Wk7 mean	FL Wk1 mean	FL Wk3 mean	FL Wk5 mean	FL Wk7 mean	P-value (Line)	P-value (Age)	P-value (Line X Age)
pgp1n.pk010.e8			No Hits Found	0.561	0.248	0.814	0.535	-0.484	0.252	0.529	0.238	0.032	0.103	0.207
pgp1c.pk001.j21	NP_001377	DPYSL2	DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2)	0.000	0.032	0.384	0.366	-1.004	0.365	0.399	0.186	0.113	0.002	0.027
pgp1n.pk010.l21	NP_116226		No Hits Found	0.482	0.254	0.712	0.356	-0.481	0.187	0.630	0.121	0.040	0.048	0.175
pgp1n.pk012.k20	NP_004862	GOSR1	golgi SNAP receptor complex member 1 [Homosapiens]	0.180	-0.131	0.263	0.124	-0.761	-0.126	-0.097	-0.181	0.019	0.404	0.188
pgp1c.pk001.m22	NP_821133	TUBB4	tubulin, beta 5 [Mus musculus]	0.108	-0.011	0.141	-0.015	-0.785	0.178	0.073	-0.129	0.064	0.036	0.014
pgp1n.pk008.d3	NP_001684		adenosinetriphosphatase (EC 3.6.1.3) B chain - chicken	0.278	0.095	0.421	0.434	-0.614	0.422	0.307	0.364	0.063	0.001	0.001
pgp2n.pk003.c7	NP_003359		Ubiquitin carboxyl-terminal hydrolase 1 (Ubiquitin thiolesterase 1)	-0.163	-0.158	0.052	0.265	-1.054	0.113	0.142	0.033	0.164	0.002	0.025
pgp1n.pk010.f8	NP_689477		Unknown (protein for MGC:20695) [Homo sapiens]	0.588	0.063	0.697	0.424	-0.275	0.432	0.617	0.297	0.203	0.079	0.026
pnfb.pk0002.b12			No Hits Found	0.363	0.680	0.718	0.615	-0.467	0.177	0.570	-0.808	0.000	0.005	0.076
pgp1c.pk001.b7	NP_006077	TUBB3	Unknown (protein for IMAGE:2823044) [Homo sapiens]	0.205	0.123	0.216	0.079	-0.608	0.088	0.174	-0.135	0.020	0.082	0.055
pgp2n.pk010.a21	NP_065735		Supported by Human EST H08032.1 (NID:g872854)	0.069	-0.077	0.022	0.048	-0.730	0.045	0.042	-0.093	0.061	0.070	0.016
pgp1n.pk012.p19	NP_115667	SGIP1	unnamed protein product [Mus musculus]	-0.012	0.023	0.075	0.257	-0.802	0.274	0.202	0.127	0.078	0.000	0.000
pgp1n.pk001.j10	NP_057707	FAM49B	similar to hypothetical protein DKFZp566A1524 [Homo sapiens]	0.517	0.374	0.486	0.528	-0.244	0.301	0.528	0.069	0.026	0.161	0.074
pgp1n.pk006.h4	NP_001949	EEF1A2	eukaryotic translation elongation factor 1 alpha 2 [Homo sapiens]	0.153	-0.005	0.163	0.184	-0.606	0.103	0.026	-0.126	0.022	0.202	0.071
pgm1c.pk001.d14	XP_379905		extensin - Volvox carteri (fragment)	0.560	0.363	0.586	0.372	-0.171	0.351	0.329	0.272	0.044	0.568	0.217
pgp1n.pk007.n5	NP_055112		HSCO protein [Mus musculus]	0.333	0.318	0.327	0.609	-0.381	0.604	0.730	0.065	0.229	0.011	0.003
pgp1n.pk014.n20	NP_004334	CALR	calreticulin [Mus musculus]	0.487	0.261	0.202	0.394	-0.222	0.404	0.280	0.186	0.076	0.514	0.021
pgm2n.pk014.b17	NP_002857	RAB3A	RAB3A, member RAS oncogene family [Mus musculus]	0.459	0.392	0.425	0.200	-0.247	0.293	0.241	0.021	0.042	0.415	0.453
pgp1n.pk011.f12	NP_002816	PTN	pleiotrophin	0.353	0.065	0.419	0.178	-0.352	0.127	0.034	-0.043	0.037	0.743	0.238
pgp1n.pk010.o24	NP_001393		ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	0.037	0.107	0.097	0.026	-0.667	-0.049	0.069	-0.386	0.035	0.211	0.382
pgl1n.pk003.d1	NP_000567		interleukin-1beta [Gallus gallus]	0.337	0.148	0.137	0.145	-0.330	0.125	0.399	0.288	0.411	0.260	0.026
pgp1n.pk004.m13	NP_005554	STMN1	stathmin [Gallus gallus]	0.331	-0.029	-0.069	-0.178	-0.326	-0.103	-0.263	-0.306	0.026	0.437	0.256
pgp1n.pk005.l22	NP_002789	PSMB6	Similar to proteasome (prosome, macropain) subunit, beta type 6	0.110	-0.003	0.130	0.182	-0.547	0.279	0.169	0.062	0.236	0.026	0.011
pgp1n.pk005.b24	NP_542117	AP1GBP1	gamma-synergin [Rattus norvegicus]	-0.066	-0.071	0.111	0.189	-0.723	0.091	0.105	0.062	0.068	0.000	0.011
pgf2c.pk001.p22	NP_078994		unnamed protein product [Homo sapiens]	0.169	0.004	0.283	0.151	-0.486	0.211	0.163	0.039	0.099	0.073	0.040
pgp1n.pk011.n7	NP_065198		NDRG family member 4 [Homo sapiens]	-0.166	-0.171	0.187	0.297	-0.819	0.058	0.265	0.162	0.254	0.000	0.038
pgp1n.pk004.n4	NP_005701	PQBP1	PQBP-1b/c [Homo sapiens]	0.309	0.288	0.414	0.242	-0.337	0.124	0.356	0.104	0.036	0.164	0.299
pgm1c.pk003.a20	NP_008993	PWP1	nuclear phosphoprotein similar to S. cerevisiae PWP1	0.134	-0.072	0.316	0.141	-0.512	-0.328	0.203	-0.053	0.037	0.080	0.492
pgp1n.pk012.j21	NP_001966	ENO2	Gamma enolase (Neural enolase)	0.140	0.082	0.262	0.214	-0.498	0.114	0.192	-0.013	0.048	0.082	0.159
pgp1n.pk006.n22	NP_004786		klotho secreted isoform [Macaca fascicularis]	0.046	-0.032	0.135	0.158	-0.587	-0.057	0.071	-0.052	0.028	0.049	0.130
pgf1n.pk011.o18	NP_002733		protein kinase C, mu [Mus musculus]	0.437	0.340	0.478	0.632	-0.193	0.565	0.577	-0.072	0.030	0.068	0.009
pgm1c.pk002.d7	NP_055399		ERO1-like (S. cerevisiae) [Mus musculus]	0.153	0.080	0.244	0.378	-0.477	0.354	0.407	0.199	0.209	0.000	0.001
pgf2n.pk006.p11	NP_004147	PPP2CB	Serine/threonine protein phosphatase 2A, catalytic subunit, alpha	0.315	0.375	0.452	0.358	-0.314	0.299	0.381	0.188	0.046	0.083	0.256
pgp1c.pk003.a11	NP_006169		vesicular fusion protein NSF - Chinese hamster (fragment)	0.211	0.039	0.383	0.345	-0.414	0.296	0.379	0.270	0.262	0.011	0.032
pgf2c.pk001.a11	NP_958816		beta-amyloid precursor protein 751 isoform [Gallus gallus]	0.267	0.183	0.484	0.421	-0.358	0.349	0.409	0.267	0.064	0.004	0.031
pgp1n.pk013.j1	NP_071344		mitochondrial ribosomal protein L17 [Mus musculus]	0.513	0.292	0.665	0.337	-0.110	0.349	0.353	0.250	0.045	0.305	0.197
pgp1n.pk009.i17	NP_004951	FUS	fusion, derived from t(12;16) malignant liposarcoma [Homo sapiens]	0.111	0.095	0.142	0.189	-0.507	0.109	0.193	-0.046	0.036	0.043	0.056
pgp2n.pk007.f6	NP_068807	SPHK1	sphingosine kinase 1 [Mus musculus]	0.176	0.057	0.404	0.278	-0.441	0.209	0.272	0.437	0.239	0.011	0.031
pgp2n.pk008.k1	NP_003701		hepatocyte growth factor activator inhibitor precursor	0.448	0.367	0.296	0.071	-0.166	0.063	0.226	-0.174	0.012	0.304	0.364
pgf2c.pk001.h24	NP_004648		serum deprivation response protein [Homo sapiens]	0.311	0.386	0.436	0.216	-0.302	0.349	0.401	0.209	0.038	0.006	0.031
pgm2n.pk004.c7			No Hits Found	0.190	0.049	0.330	0.238	-0.419	-0.020	0.231	0.093	0.021	0.030	0.156
pgf1n.pk006.d19	NP_001737	CANX	calnexin [Homo sapiens]	0.237	-0.004	0.413	-0.040	-0.367	0.044	0.261	0.395	0.500	0.059	0.018
pgp1n.pk007.h11	NP_036611	YWHAG	tyrosine 3-monooxgenase/tryptophan 5-monooxgenase	0.397	0.193	0.455	0.185	-0.205	0.143	0.138	0.155	0.029	0.619	0.222
pgp1n.pk013.i12	NP_071363	NAPB	N-ethylmaleimide-sensitive factor attachment protein,beta	0.269	0.227	0.494	0.462	-0.334	0.235	0.465	0.488	0.079	0.001	0.020
pgp1n.pk013.f6	NP_036380		Selenide,water dikinase 2 (Selenophosphate synthetase 2)	0.030	0.031	0.039	0.296	-0.570	0.270	0.243	0.121	0.252	0.000	0.001
pgp1n.pk008.m24	NP_001139	ANK2	ankyrin 2, isoform 1 [Homo sapiens]	0.501	0.291	0.487	0.374	-0.097	0.440	0.365	0.162	0.013	0.164	0.010
pgp1n.pk004.l24	NP_002620	PGAM1	similar to phosphoglycerate mutase B chain - rat	0.010	-0.049	0.159	0.105	-0.582	-0.040	-0.110	-0.099	0.005	0.058	0.118
pgp1n.pk005.c24	XP_372887		cytochrome b [Gallus gallus]	0.267	0.015	0.362	0.030	-0.320	0.075	-0.058	-0.061	0.032	0.683	0.186
pgp1n.pk004.c21	NP_631961	FUS	RNA-binding protein FUS (Pigpen protein)	0.152	0.097	0.132	0.148	-0.430	0.044	0.089	-0.069	0.024	0.292	0.189
pgl1n.pk013.n12			POL-like	0.311	0.336	0.367	0.540	-0.271	0.440	0.492	0.202	0.046	0.006	0.013
pgf2c.pk001.p6	NP_000081	COL3A1	alpha 1 type III collagen [Homo sapiens]	0.188	0.036	0.282	0.223	-0.391	-0.001	0.082	-0.100	0.037	0.455	0.448
pgf1n.pk009.d13	NP_000964		ribosomal protein L8 [Homo sapiens]	0.396	0.122	0.095	0.063	-0.182	0.235	0.229	-0.034	0.232	0.509	0.041
pgl1n.pk014.h3	NP_006331	BAIAP2	Fas-ligand associated factor 3 [Homo sapiens]	0.159	0.016	0.015	0.055	-0.417	0.013	0.039	-0.098	0.022	0.435	0.030
pgp1n.pk007.n4	NP_570711		multiple endocrine neoplasia 1 [Rattus norvegicus]	0.458	0.321	0.427	0.509	-0.113	0.469	0.448	0.281	0.088	0.166	0.041
pgp1n.pk010.o12	NP_958833		reticulon 3 [Homo sapiens]	0.386	0.520	0.567	0.201	-0.172	0.189	0.748	-0.528	0.039	0.030	0.283
pgp1n.pk011.e23	NP_056530	PLA2G3	group III secreted phospholipase A2 [Homo sapiens]	0.226	-0.080	-0.164	-0.155	-0.331	-0.162	0.150	-0.192	0.315	0.581	0.019
pgp1n.pk004.h16	NP_009037	UBL3	ubiquitin-like 3 [Homo sapiens]	0.006	-0.116	0.119	0.098	-0.547	0.124	0.177	0.025	0.304	0.006	0.010
pgf1n.pk004.c4	NP_001686	ATP6V1C1	Vacuolar ATP synthase subunit C (V-ATPase C subunit)	0.365	0.246	0.410	0.445	-0.188	0.394	0.161	0.484	0.088	0.049	0.045
pgl1n.pk007.n4	NP_000987	RPL35A	60S RIBOSOMAL PROTEIN L35A (L32)	0.154	0.003	0.186	-0.164	-0.397	0.126	0.212	0.020	0.578	0.121	0.039
pgp1n.pk003.d3	NP_008819	CALM1	calmodulin 2 (phosphorylase kinase, delta) [Homo sapiens]	0.267	0.055	0.234	0.145	-0.283	0.127	0.101	0.120	0.050	0.423	0.043
pgp1c.pk002.i8			hypothetical protein [Rhodopseudomonas palustris]	0.215	-0.001	0.093	0.079	-0.334	0.081	0.090	0.065	0.098	0.433	0.015
pgf1n.pk006.m9	NP_000179	HK1	hexokinase1 [Gallus gallus]	0.013	-0.039	0.241	0.301	-0.532	0.130	0.185	0.111	0.077	0.002	0.046
pgp1n.pk012.f18	NP_064709	CIAPIN1	Unknown gene product [Homo sapiens]	0.379	0.224	0.251	0.321	-0.165	0.240	0.200	0.261	0.027	0.345	0.068
pgp1n.pk008.c18	NP_004037	ATP5A1	ATP synthase alpha subunit [Gallus gallus]	0.469	0.231	0.374	0.130	-0.075	0.341	0.275	0.341	0.318	0.690	0.022
pgp1n.pk001.n2	NP_000166	GPI	phosphoglucose isomerase [Boiga kraepelini]	0.212	0.085	0.311	0.317	-0.327	0.357	0.275	0.075	0.207	0.082	0.039
pgp1n.pk006.i9	NP_065185	ATP8B2	Unknown (protein for IMAGE:4111596) [Homo sapiens]	0.217	0.038	0.257	0.058	-0.320	0.028	0.016	0.006	0.028	0.542	0.176
pgl1n.pk005.d4			No Hits Found	0.280	0.212	0.366	0.445	-0.256	0.235	0.377	0.218	0.024	0.012	0.051
pgp1c.pk003.o18	NP_008818		butyrate response factor 2 [Homo sapiens]	0.065	0.020	0.224	0.260	-0.465	0.066	0.320	0.243	0.242	0.003	0.044
pgp1n.pk009.j20	NP_006149	NEFL	Neurofilament triplet L protein (Neurofilament light polypeptide)(NF-L)	0.329	0.084	0.221	0.141	-0.196	-0.050	-0.154	0.058	0.004	0.916	0.275
pgp1n.pk005.f1	NP_071746		unnamed protein product [Mus musculus]	-0.004	0.079	0.230	0.237	-0.528	0.089	0.383	0.069	0.098	0.000	0.031
pgp1n.pk012.p2	NP_003169	SYN2	synapsin IIb - human	0.185	0.093	0.189	0.196	-0.334	0.169	0.219	0.130	0.093	0.038	0.020
pgp2n.pk009.e21	NP_000085		hypothetical protein [Mycobacterium tuberculosis CDC1551]	-0.034	-0.080	0.079	-0.045	-0.548	-0.253	-0.172	-0.128	0.011	0.221	0.336
pgp1n.pk002.p23	NP_031389		Unknown (protein for MGC:19787) [Homo sapiens]	0.480	0.232	0.542	0.352	-0.034	0.248	0.423	0.228	0.022	0.114	0.080
pgm2n.pk012.f15	NP_060464		Similar to hypothetical protein FLJ10099 [Homo sapiens]	0.023	-0.050	0.141	-0.004	-0.488	0.181	0.206	-0.075	0.426	0.023	0.041
pgf1n.pk007.c22	NP_005511	HNRPH1	unnamed protein product [Mus musculus]	-0.007	0.222	0.248	0.241	-0.517	0.210	0.190	0.176	0.043	0.007	0.255
pgp1c.pk003.d9	NP_055582	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	0.026	-0.090	0.015	0.308	-0.479	-0.361	-0.024	-0.332	0.022	0.498	0.481
pgl1n.pk012.e8			No Hits Found	0.071	0.089	0.069	0.171	-0.431	0.171	0.253	0.191	0.437	0.004	0.010
pgl1n.pk003.d3	NP_001605	ACTB	ACTIN, CYTOPLASMIC TYPE 5	0.107	0.063	0.165	0.183	-0.393	0.167	0.164	-0.033	0.056	0.043	0.047
pgp1n.pk003.l19	NP_066959		chS-Rex-s	0.277	0.245	0.208	0.089	-0.222	0.137	0.022	0.046	0.015	0.519	0.217
pgp1n.pk006.j24	NP_001524	HNRPL	heterogeneous nuclear ribonucleoprotein L [Mus musculus]	0.015	-0.076	0.035	0.203	-0.482	0.081	0.202	0.072	0.272	0.002	0.006
pgp1n.pk009.b10	NP_060571		No Hits Found	0.219	0.317	0.131	0.261	-0.273	0.198	0.049	-0.122	0.009	0.244	0.353
pgm1n.pk001.d16	NP_003274	TNNT1	slow muscle troponin T - chicken	-0.030	0.181	0.086	0.119	-0.521	0.274	0.324	0.209	0.849	0.004	0.041
pgp1n.pk010.o10	NP_919228	TTLL11	unknown [Homo sapiens]	0.582	0.279	0.711	0.372	0.093	0.267	0.426	0.171	0.047	0.249	0.539
pgp2n.pk006.m23	NP_061917	CCDC93	hypothetical protein FLJ10996 [Homo sapiens]	0.275	0.136	0.265	0.125	-0.213	0.151	0.131	-0.057	0.035	0.461	0.267
pgp1n.pk012.i22			No Hits Found	0.400	0.121	0.090	0.017	-0.084	0.051	-0.019	-0.149	0.014	0.251	0.248
pgl1n.pk010.e19	NP_005715	TSPAN3	tetraspan 3 [Homo sapiens]	0.329	0.231	0.352	0.357	-0.152	0.426	0.405	0.224	0.284	0.102	0.045
pgf1n.pk001.o8	NP_036364		leucine zipper protein [Gallus gallus]	0.133	0.049	0.117	0.563	-0.348	0.153	0.244	-0.127	0.058	0.235	0.045
pgl1n.pk013.d12	NP_006614		unnamed protein product [Mus musculus]	-0.116	-0.020	-0.001	0.019	-0.595	0.066	-0.098	-0.284	0.007	0.011	0.037
pgp2n.pk005.i23	NP_689849	METT5D1	hypothetical protein FLJ33979 [Homo sapiens]	0.311	0.159	0.247	0.109	-0.160	0.138	0.077	-0.054	0.015	0.594	0.256
pgp1c.pk001.p2	NP_000362	TTR	Transthyretin precursor (Prealbumin) (TBPA)	0.363	0.124	0.158	0.177	-0.107	0.117	0.052	0.015	0.004	0.980	0.066
pgl1n.pk001.k20	NP_005989		chaperonin containing TCP-1 complex gamma chain	-0.008	-0.094	-0.127	0.024	-0.472	0.076	-0.037	-0.116	0.194	0.093	0.010
pgf1n.pk011.c3	NP_003747	EIF3S3	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa	0.358	0.271	0.195	0.229	-0.106	0.194	0.293	-0.086	0.020	0.323	0.054
pgp1n.pk011.o15	NP_653284	DHRS13	RIKEN cDNA 2610209N15 [Mus musculus]	0.380	0.346	0.366	0.211	-0.082	0.198	0.379	0.219	0.043	0.130	0.064
pgp1n.pk013.i20	NP_003002	SET	SET protein (HLA-DR associated protein II) (PHAPII)	0.159	0.034	0.191	0.172	-0.299	0.121	0.314	0.109	0.264	0.020	0.022
pgp1n.pk007.h15	NP_009057		valosin-containing protein [Rattus norvegicus]	0.305	0.234	0.393	0.445	-0.150	0.410	0.358	0.434	0.198	0.001	0.008
pgp2n.pk010.k5	NP_877496	ELMO2	KIAA1834 protein [Homo sapiens]	0.217	0.037	0.234	0.143	-0.235	0.238	0.170	0.250	0.496	0.180	0.033
pft1c.pk004.c9			No Hits Found	0.187	0.352	0.304	0.705	-0.264	0.451	0.590	0.094	0.159	0.022	0.034
pgp1c.pk003.c7	NP_006013	TSC22D1	Regulatory protein TSC-22 (TGFB stimulated clone 22 homolog)	0.319	0.204	0.326	0.271	-0.132	0.225	0.240	0.125	0.038	0.376	0.173
pgp1c.pk002.l18	NP_858059		UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase	0.365	0.234	0.151	0.257	-0.086	0.349	0.313	0.074	0.193	0.377	0.012
pgf1n.pk002.c11	NP_003246		tissue inhibitor of metalloproteinase-2 precursor [Gallus gallus]	0.047	0.029	-0.062	0.389	-0.392	0.186	0.184	-0.144	0.125	0.078	0.007
pgp2n.pk008.o10	NP_059990		Unknown (protein for IMAGE:3611719) [Homo sapiens]	-0.068	-0.246	0.085	0.203	-0.493	0.031	0.372	0.083	0.962	0.003	0.039
pgp1n.pk003.p1	NP_054749		p95-APP1 [Gallus gallus]	0.152	0.195	0.252	0.147	-0.270	0.169	0.197	0.280	0.061	0.001	0.005
pgl1n.pk006.j11	NP_055415	EHD3	EH-domain containing 3 [Homo sapiens]	0.063	-0.144	0.023	-0.111	-0.356	-0.116	-0.186	-0.347	0.040	0.763	0.430
pgf1n.pk012.o13	NP_000945	PTGDS	chondrogenesis associated lipocalin [Gallus gallus]	0.432	0.427	0.315	0.075	0.017	0.052	0.119	-0.024	0.012	0.394	0.641
pgp1n.pk006.d23	NP_000282	PGK1	Phosphoglycerate kinase	-0.051	-0.072	0.214	0.109	-0.462	-0.149	nd	-0.565	0.019	0.537	0.248
pgp1n.pk005.o11	NP_002734	PRKCSH	Similar to protein kinase C substrate 80K-H [Homo sapiens]	0.071	-0.038	0.049	-0.033	-0.339	-0.091	-0.107	-0.090	0.036	0.798	0.327
pgp2n.pk005.m21	NP_775098	APBB2	similar to Amyloid beta A4 precursor protein-binding family B member 2	0.153	0.080	0.163	0.068	-0.257	0.067	0.033	-0.021	0.043	0.519	0.290
pgp2n.pk006.p5	NP_078916	YRDC	hypothetical protein MGC38336 [Mus musculus]	-0.071	-0.108	-0.185	0.052	-0.476	-0.101	0.104	nd	0.577	0.024	0.004
pgp2n.pk009.a3	NP_004216	MFHAS1	Similar to MFH-amplified sequences with leucine-rich tandem repeats1	-0.116	-0.064	-0.053	0.070	-0.519	0.053	0.120	0.126	0.790	0.000	0.002
pgl1n.pk007.c1	NP_000020		angiotensinogen [Callithrix jacchus]	0.465	0.550	0.668	0.412	0.065	0.183	0.467	0.062	0.004	0.112	0.899
pgm2n.pk002.o6	NP_116203		retinoblastoma tumor suppressor [Gallus gallus]	0.257	0.188	0.274	0.364	-0.140	0.358	0.352	0.180	0.182	0.027	0.012
pgp1n.pk002.e6	NP_001266	CHGA	chromogranin A [Rana ridibunda]	0.043	-0.050	0.150	-0.014	-0.349	0.162	-0.061	0.032	0.214	0.135	0.021
pgm2n.pk011.k5			No Hits Found	0.088	0.034	0.122	0.087	-0.303	0.130	0.262	0.005	0.335	0.014	0.018
pnfb.pk0001.e4	NP_054797	MRPL13	mitochondrial ribosomal protein L13 [Homo sapiens]	0.057	0.105	0.014	0.055	-0.332	0.036	0.057	-0.007	0.029	0.057	0.063
pgp1n.pk003.k20	NP_001166	ARHGDIB	Rho GDP-dissociation inhibitor 2 (Rho GDI 2)	0.075	0.005	-0.001	0.208	-0.314	0.131	0.135	0.078	0.377	0.087	0.048
pgp2n.pk006.a21	NP_077000	ASB8	ankyrin repeat and SOCS box-containing protein 8 [Mus musculus]	0.095	0.012	0.127	0.220	-0.292	0.282	0.236	0.201	0.926	0.029	0.025
pgp1n.pk010.j22	NP_002891	RBP3	interphotoreceptor retinoid-binding protein N-terminal fragment	0.214	0.000	0.100	0.331	-0.172	0.023	0.160	0.181	0.044	0.033	0.014
pgp1n.pk013.k16	NP_055532		unnamed protein product [Mus musculus]	0.379	0.229	0.273	0.082	-0.006	0.158	0.000	0.057	0.030	0.689	0.379
pft1c.pk001.h12	NP_001091		alpha 1 actin precursor [Homo sapiens]	0.217	0.341	0.306	0.218	-0.165	0.109	0.371	0.055	0.046	0.097	0.347
pgp1n.pk004.b18	NP_057100	SLC25A39	hypothetical protein DKFZp434C119.1 - human	nd	-0.347	-0.288	0.094	-0.382	0.262	0.105	0.041	0.039	0.044	0.115

pgp1n.pk014.o13		GAPDH	Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)	0.463	0.248	0.389	0.185	0.082	0.275	0.076	0.117	0.019	0.652	0.175
pgp1n.pk009.m9	NP_004772	VAMP3	vesicle-associated membrane protein 3 [Mus musculus]	0.456	0.433	0.615	0.401	0.075	0.159	0.101	0.101	0.027	0.966	0.951
pgp1n.pk002.o14	NP_733779	SKP1A	S-phase kinase-associated protein 1A isoform b [Homo sapiens]	0.228	0.186	0.424	0.294	-0.152	0.225	0.243	0.213	0.042	0.051	0.235
pgp1n.pk011.o19	NP_000133		Tyrosine kinase receptor CEK2 precursor	0.228	0.016	0.081	0.096	-0.145	0.035	-0.027	-0.057	0.016	0.994	0.136
pgp2n.pk002.n14	NP_003818	NAPA	N-ethylmaleimide sensitive fusion protein attachment protein alpha	0.079	-0.021	0.047	0.074	-0.289	-0.029	-0.026	-0.006	0.033	0.377	0.160
pgl1n.pk012.i21	NP_002626		phosphate carrier protein precursor, mitochodrial, splice form B	0.067	0.060	0.121	0.130	-0.297	0.082	0.084	0.151	0.089	0.010	0.041
pgp1n.pk006.g11	NP_055031		similar to inositol 1,3,4-triphosphate 5/6 kinase [Mus musculus]	0.364	0.309	0.034	0.414	nd	0.270	0.263	-0.153	0.283	0.478	0.042
pgf1n.pk010.c13	NP_003783		endothelial differentiation-related factor 1 isoform alpha	0.129	0.138	0.074	0.078	-0.231	-0.079	0.203	-0.350	0.012	0.136	0.114
pgp1n.pk011.d13			No Hits Found	0.309	0.207	0.272	0.276	-0.051	0.287	0.311	0.199	0.107	0.092	0.009
pgp1c.pk003.k3	NP_996737		RNA binding/signal transduction protein QkI-2 [Gallus gallus]	0.201	0.228	0.325	0.265	-0.151	0.344	0.366	0.274	0.403	0.003	0.032
pgm2n.pk002.p11			No Hits Found	0.301	0.201	0.317	0.254	-0.046	0.176	0.359	0.420	0.404	0.012	0.007
pgp2n.pk003.k15	NP_005008	PCYT1A	CTP:phosphocholine cytidylyltransferase	-0.092	-0.016	-0.101	0.347	-0.437	0.187	0.126	-0.088	0.287	0.016	0.016
pgp1n.pk013.m13	NP_115798		unnamed protein product [Mus musculus]	0.151	0.322	0.292	0.066	-0.189	0.155	0.084	0.136	0.049	0.119	0.333
pgp1n.pk004.n20	NP_443183	DNTTIP1	RIKEN cDNA 6430706C13 [Mus musculus]	0.167	0.201	0.100	0.097	-0.170	0.007	0.186	-0.155	0.035	0.338	0.278
pgp2n.pk004.p14	NP_149015		Piccolo protein (Aczonin)	0.191	0.096	0.145	0.102	-0.145	0.208	0.176	0.083	0.300	0.233	0.029
pgf2c.pk001.f22	NP_065164		unnamed protein product [Mus musculus]	0.189	0.244	0.155	0.063	-0.146	0.207	0.061	0.022	0.013	0.023	0.107
pgp1n.pk002.o19	NP_714543	GSTA1	GLUTATHIONE S-TRANSFERASE (CLASS-ALPHA)	0.314	0.085	0.435	0.175	-0.020	0.041	-0.030	-0.154	0.010	0.562	0.552
pgp1n.pk006.e3	NP_112604		heterogeneous nuclear ribonucleoprotein C (C1/C2)	-0.107	-0.278	-0.094	0.330	-0.436	-0.046	0.269	-0.044	0.785	0.017	0.023
pgp1n.pk014.m11	NP_001921	DHPS	deoxyhypusine synthase isoform a [Homo sapiens]	0.444	0.327	0.400	0.280	0.115	0.193	0.225	0.175	0.031	0.901	0.770
pgl1n.pk013.c6	NP_068832	TMSB10	Thymosin beta	0.509	0.205	0.228	0.106	0.183	-0.038	-0.091	-0.342	0.016	0.086	0.931
pgf1n.pk006.i24	NP_005608	RPS14	ribosomal protein S14 [Homo sapiens]	0.092	0.327	-0.238	0.214	-0.233	-0.038	-0.017	-0.064	0.039	0.111	0.080
pgp2n.pk003.o4			No Hits Found	0.405	0.100	0.171	0.011	0.086	0.013	-0.039	-0.023	0.027	0.078	0.459
pgl1n.pk011.b23	NP_006232	PPP1R2	unnamed protein product [Mus musculus]	0.001	-0.097	0.026	0.019	-0.317	0.122	0.201	0.010	0.753	0.011	0.006
pgp1n.pk013.o5	NP_000996		ribosomal protein S3 (AA 1-243) [Rattus rattus]	0.280	0.116	0.102	-0.104	-0.037	0.086	-0.051	0.022	0.073	0.110	0.029
pgr1n.pk002.p13			No Hits Found	0.171	0.177	0.173	0.169	-0.142	0.080	0.076	0.063	0.031	0.648	0.665
pgr1n.pk003.o24	NP_009096		No Hits Found	0.254	0.141	0.172	0.076	-0.057	0.065	0.123	0.032	0.021	0.620	0.178
pgp1n.pk004.e22	NP_005552	LAMP1	LEP100 protein precursor - chicken	0.076	0.043	0.144	0.165	-0.234	0.194	0.153	0.111	0.263	0.004	0.011
pgp2n.pk005.k21	NP_006279	THY1	Thy-1 membrane glycoprotein precursor (Thy-1 antigen)	0.100	0.101	0.093	0.105	-0.207	-0.124	-0.117	-0.119	0.000	0.895	0.890
pgf2c.pk001.h2	NP_002037	GAPDH	Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)	0.245	0.195	0.224	0.023	-0.058	0.110	-0.213	-0.102	0.031	0.532	0.568
pgp1c.pk003.f13	NP_060563		hypothetical protein FLJ10439 [Homo sapiens]	-0.210	-0.377	-0.401	0.121	-0.513	0.900	0.127	-0.091	0.007	0.009	0.001
pgr1c.pk001.p2	NP_001633	APLP2	Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II)	0.127	0.126	0.220	0.162	-0.174	0.046	0.090	0.036	0.008	0.171	0.522
pgp1c.pk003.b5	NP_006504	SARS	Seryl-tRNA synthetase (Serine--tRNA ligase) (SerRS)	0.045	0.105	0.496	0.474	-0.255	0.257	0.027	0.171	0.007	0.001	0.043
pgl1n.pk010.l1	XP_375261		NONHISTONE CHROMOSOMAL PROTEIN HMG-14A	0.322	0.094	0.119	0.049	0.027	0.158	0.092	0.035	0.149	0.271	0.048
pgl1n.pk005.c17	NP_006591		nuclear distribution gene C homolog (Aspergillus) [Mus musculus]	0.117	0.058	0.134	0.175	-0.178	0.206	0.196	0.081	0.444	0.086	0.045
pgp1n.pk013.e7	NP_056415		Unknown (protein for IMAGE:3484538) [Mus musculus]	0.169	0.201	0.443	0.581	-0.125	0.384	0.298	0.449	0.089	0.000	0.032
pgm2n.pk010.m18			No Hits Found	0.222	0.095	0.248	0.198	-0.071	-0.023	0.007	0.127	0.016	0.554	0.588
pgf1n.pk002.a12	NP_112190	CDT1	putative CDT1 protein [Xenopus laevis]	-0.104	-0.034	-0.060	0.263	-0.396	0.329	0.156	-0.220	0.607	0.050	0.012
pgl1n.pk012.k4	NP_036522		No Hits Found	0.163	0.059	0.027	0.004	-0.123	-0.249	-0.183	-0.136	0.023	0.836	0.925
pgf1n.pk007.j8			No Hits Found	0.255	0.119	0.180	0.279	-0.029	0.329	0.294	-0.018	0.301	0.318	0.017
pgp1n.pk003.j1	NP_004729	VAPB	VAMP (vesicle-associated membrane protein)-associated protein B	0.182	0.080	0.163	0.138	-0.102	0.108	0.076	0.021	0.007	0.547	0.066
pgm2n.pk002.f22	NP_003465	ADAM12	ADAM 12 [Coturnix coturnix]	0.211	0.147	0.208	0.245	-0.071	0.229	0.183	0.094	0.017	0.080	0.013
pgf1n.pk002.a14	NP_057103	LUC7L2	similar to CGI-74 protein [Homo sapiens]	-0.032	0.035	-0.002	0.336	-0.313	0.446	0.307	-0.166	0.891	0.056	0.016
pgm2n.pk013.c2	NP_036307	FBXO3	F-box only protein 3	0.163	0.115	0.155	0.170	-0.113	0.146	0.042	0.018	0.027	0.587	0.285
pgp2n.pk007.c3	NP_057295		vesicle associated protein [Rattus norvegicus]	0.287	0.271	0.310	0.325	0.012	0.300	0.286	0.158	0.024	0.114	0.099
pgl1n.pk006.b9	NP_055038		nuclear transcription factor Y, gamma [Homo sapiens]	0.009	0.042	0.057	0.113	-0.267	0.128	0.077	-0.147	0.046	0.036	0.043
pgp2n.pk006.g22	NP_005820	AP3S2	unnamed protein product [Mus musculus]	0.022	-0.003	0.042	-0.034	-0.250	-0.114	-0.378	-0.233	0.020	0.864	0.679
pgp1c.pk002.b23		ATP5A1	ATP synthase alpha subunit [Gallus gallus]	0.111	0.082	0.024	0.017	-0.160	0.038	-0.105	0.016	0.027	0.297	0.198
pgf2n.pk001.g21		RAB11FIP4	similar to Eferin [Homo sapiens]	0.067	0.054	0.094	0.125	-0.196	0.197	0.163	0.111	0.706	0.013	0.021
pgl1n.pk003.a5	NP_112186	ACSBG2	hypothetical protein PRTD-NY3 [Homo sapiens]	0.238	0.038	0.197	0.029	-0.024	-0.010	0.040	-0.037	0.039	0.377	0.605
pgf1n.pk003.l21	NP_001143		solute carrier family 25, member 5 [Homo sapiens]	0.154	0.011	0.029	0.073	-0.109	-0.021	-0.030	-0.154	0.036	0.916	0.501
pgf2n.pk005.g9		KIAA0247	No Hits Found	0.213	0.228	0.152	0.119	-0.048	0.215	0.158	-0.056	0.046	0.063	0.227
pgm2n.pk003.l17			No Hits Found	0.352	0.410	0.414	0.365	0.092	0.371	0.272	0.202	0.021	0.266	0.665
pgf1n.pk001.h12	NP_000629		vitronectin [Gallus gallus]	0.508	0.417	0.470	0.624	0.249	0.306	0.310	0.245	0.037	0.962	0.800
pgl1n.pk002.m19	NP_056109		KIAA0898 protein [Homo sapiens]	0.014	0.132	0.024	0.151	-0.243	0.041	0.037	0.031	0.039	0.048	0.310
pgm2n.pk011.p17			unknown [Gallus gallus]	-0.023	-0.109	-0.073	0.104	-0.279	-0.027	-0.023	-0.091	0.078	0.121	0.024
pgp1n.pk007.b4	NP_001485		Rab-GDP dissociation inhibitor [Gallus gallus]	0.126	0.104	0.107	0.232	-0.127	0.298	0.201	0.223	0.903	0.023	0.039
pgp1n.pk012.j20	NP_004323	BPHL	No Hits Found	0.259	0.099	0.082	0.058	0.006	0.088	0.108	0.004	0.045	0.268	0.045
pgp2n.pk005.i19	XP_291128	RBM26	Similar to cutaneous T-cell lymphoma tumor antigen se70-2	0.140	0.088	0.088	0.102	-0.112	0.160	0.133	0.077	0.293	0.190	0.022
pgp1n.pk002.n3	NP_002559		poly(A) binding protein, cytoplasmic 1 [Rattus norvegicus]	0.208	0.181	0.244	0.154	-0.041	0.214	0.126	0.126	0.024	0.156	0.072
pgm2n.pk004.e5	NP_005287	GPR23	unnamed protein product [Mus musculus]	0.278	0.244	0.297	0.233	0.030	0.257	0.139	0.117	0.044	0.683	0.519
pgp1n.pk011.a10	NP_004059	AP2M1	agCP3452 [Anopheles gambiae str. PEST]	0.182	0.226	0.253	0.198	-0.063	0.226	0.171	0.012	0.012	0.040	0.216
pgp1n.pk008.m17		HMGB1	No Hits Found	0.261	0.106	0.196	-0.022	0.019	0.001	nd	-0.259	0.011	0.012	0.674
pgf1n.pk009.o4	NP_005156	ALDOC	aldolase C	0.021	-0.088	0.061	0.022	-0.219	-0.147	-0.181	-0.144	0.036	0.943	0.831
pgr1n.pk002.i7	NP_003063	SMARCA4	BRG1 protein [Gallus gallus]	0.175	0.134	0.097	0.225	-0.063	0.383	0.396	0.211	0.203	0.063	0.009
pgp1n.pk007.f1	XP_371885	C5orf13	NEURONAL PROTEIN 3.1 (P311 PROTEIN)	0.298	0.139	0.190	0.098	0.059	0.236	0.085	0.048	0.062	0.141	0.035
pgm2n.pk003.e23			No Hits Found	0.277	0.199	0.308	0.162	0.040	0.147	0.147	0.083	0.049	0.714	0.726
pgm2n.pk002.b21	NP_055781		Unknown (protein for MGC:27662) [Mus musculus]	0.294	0.341	0.277	0.156	0.059	0.154	0.115	0.120	0.020	0.622	0.674
pgm2n.pk007.d10	NP_055378	TRAPPC2	RIKEN cDNA 1110066L09 [Mus musculus]	0.358	0.255	0.214	0.152	0.125	0.231	0.189	0.085	0.045	0.143	0.257
pgp1c.pk002.e9	NP_004453	FDFT1	farnesyl-diphosphate farnesyltransferase 1 [Homo sapiens]	0.083	0.123	-0.060	0.053	-0.146	0.170	0.101	-0.095	0.384	0.076	0.035
pgm2n.pk002.h21			No Hits Found	0.128	0.077	0.160	0.136	-0.097	0.226	0.073	0.146	0.295	0.072	0.015
pgf1n.pk001.d14	NP_115545	ACAD11	RIKEN cDNA 2410021P16 [Mus musculus]	0.152	0.108	0.156	0.106	-0.073	0.067	-0.077	-0.125	0.012	0.780	0.670
pgp1n.pk002.f8	NP_036289	FBXL2	F-box protein FBL2 [Homo sapiens]	0.132	0.002	-0.130	-0.207	-0.090	-0.085	-0.021	0.014	0.900	0.305	0.017
pgm2n.pk003.b15	NP_060901	DOK5	DOK5 protein [Homosapiens]	0.186	0.074	0.017	-0.061	-0.031	-0.027	-0.016	-0.006	0.028	0.108	0.034
pgr1n.pk003.f22	NP_110435	NDEL1	endooligopeptidase A protein [Oryctolagus cuniculus]	0.211	0.144	0.098	0.192	-0.004	0.276	0.263	0.052	0.774	0.401	0.026
pgp1n.pk002.j12	NP_002036	GAP43	Neuromodulin (Axonal membrane protein GAP-43)	0.065	0.040	-0.064	0.166	-0.147	0.153	0.038	0.066	0.554	0.024	0.015
pgf1n.pk003.b5	NP_653272		No Hits Found	-0.040	-0.086	0.033	-0.165	-0.248	0.061	-0.164	0.043	0.773	0.313	0.004
pgm2n.pk004.b6		FAM26B	No Hits Found	0.053	0.021	-0.032	0.045	-0.153	0.010	0.023	-0.003	0.094	0.327	0.044
pgp2n.pk003.a6			phosphotyrosyl phosphatase activator [Homo sapiens]	0.093	-0.003	-0.010	0.037	-0.110	0.080	0.038	-0.049	0.251	0.737	0.023
pgp1n.pk005.b7	NP_002991	SDHB	succinate dehydrogenase Ip subunit [Gallus gallus]	0.099	0.057	-0.012	0.070	-0.098	-0.128	nd	nd	0.024	0.672	0.931
pgp2n.pk006.a16	XP_370977		immunoglobulin alpha heavy chain [Gallus gallus]	0.168	0.081	0.094	0.039	-0.028	0.011	-0.010	0.040	0.036	0.950	0.419
pgp1n.pk009.e10	NP_065806	SERINC1	similar to hypothetical protein DKFZp566H033.1 - human [Homosapiens]	0.248	0.225	0.242	0.203	0.053	0.146	0.124	0.141	0.004	0.891	0.562
pgm2n.pk002.o2	NP_005124		prenyl protein protease RCE1 [Homo sapiens]	0.204	0.136	0.124	0.152	0.013	0.157	0.115	0.082	0.046	0.818	0.085
pgf2n.pk001.b5			unknown [Gallus gallus]	0.158	0.155	-0.043	0.266	-0.033	0.521	0.368	-0.054	0.486	0.278	0.033
pnlb.pk0008.g7			putative protein; protein id: At5g12470.1 [Arabidopsisthaliana]	-0.002	-0.072	-0.041	-0.106	-0.190	-0.168	-0.198	-0.103	0.037	0.982	0.550
pgl1n.pk012.k3	NP_006347		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	0.193	0.076	0.073	0.027	0.005	-0.117	-0.038	-0.068	0.025	0.498	0.908
pgp2n.pk002.m5	XP_373544		hypothetical protein XP_139227 [Mus musculus]	0.029	0.133	-0.116	0.313	-0.155	0.241	0.484	0.026	0.520	0.192	0.022
pgf1n.pk006.a8			No Hits Found	0.235	0.307	0.255	0.078	0.056	-0.009	0.086	0.143	0.048	0.912	0.279
pgm2n.pk004.h9	NP_112576	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3 [Homo sapiens]	0.079	0.036	0.078	0.084	-0.101	0.071	-0.025	-0.025	0.034	0.718	0.305
pgf1n.pk004.g24	XP_370601		hydroxyproline-rich glycoprotein DZ-HRGP [Volvox carteri f. nagariensis]	-0.002	-0.030	0.072	0.000	-0.181	-0.147	-0.123	0.018	0.004	0.165	0.158
pgp1n.pk011.c18			No Hits Found	-0.117	-0.071	0.110	-0.217	-0.295	-0.523	-0.386	-0.425	0.026	0.717	0.675
pgp2n.pk005.h6	NP_892116		eukaryotic initiation factor 5 (eIF-5) [Rattus norvegicus]	0.242	0.231	0.327	0.131	0.065	0.182	0.128	0.092	0.035	0.394	0.591
pnl1s.pk002.a11			No Hits Found	0.217	0.180	0.267	0.155	0.042	0.081	0.136	0.135	0.015	0.567	0.594
pgf2n.pk004.g13	NP_066952	PPA1	pyrophosphatase (inorganic) [Homosapiens]	0.163	0.220	0.284	0.113	-0.011	0.196	0.138	0.463	0.971	0.037	0.004
pgp2n.pk007.a9	XP_375511		No Hits Found	0.315	0.173	0.180	0.048	0.141	0.128	0.006	0.074	0.016	0.011	0.121
pgp1n.pk010.k7	NP_003109	SPARC	SPARC precursor (Secreted protein acidic and rich in cysteine)	0.141	0.145	0.115	0.004	-0.030	0.102	0.022	-0.117	0.034	0.097	0.786
pgm2n.pk002.e6	NP_055993	RHOBTB2	Rho-related BTB domain containing 2 [Homo sapiens]	0.124	0.114	0.116	0.064	-0.045	0.086	0.043	0.031	0.030	0.526	0.396
pgp1n.pk013.i16	NP_058632		No Hits Found	0.287	0.185	0.216	0.019	0.119	0.172	0.208	0.191	0.902	0.133	0.031
pgp2n.pk005.p6	NP_003234		TGF-beta receptor type III precursor (TGFR-3) (Betaglycan)	-0.001	0.036	0.105	0.098	-0.167	-0.004	-0.043	-0.128	0.003	0.279	0.506
pgp1n.pk004.p13	NP_789794	BBS7	hypothetical protein FLJ10715 [Homo sapiens]	0.085	0.069	-0.005	-0.137	-0.078	-0.129	nd	-0.068	0.029	0.250	0.053
pgp1c.pk003.o3	XP_371254		Ubiquitin carboxyl-terminal hydrolase 24 (Ubiquitin thiolesterase24)	0.050	0.073	0.047	0.182	-0.113	0.163	0.279	0.146	0.502	0.016	0.030
pgf2n.pk006.j18	NP_006089	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2	-0.158	-0.175	-0.134	0.096	-0.319	-0.018	0.171	-0.096	0.697	0.085	0.049
pgp2n.pk004.f16	NP_002602	PDK2	Unknown (protein for MGC:25519) [Mus musculus]	0.094	-0.044	0.004	-0.030	-0.065	-0.119	-0.081	-0.034	0.043	0.379	0.558
pgp1n.pk006.h24	NP_071286	FXYD6	FXYD domain-containing ion transport regulator 6 [Homo sapiens]	-0.123	-0.164	-0.182	0.132	-0.282	-0.024	0.117	-0.015	0.590	0.047	0.032
pgp1n.pk010.m24	NP_077310	TMEM43	RIKEN cDNA 1200015A22 [Mus musculus]	0.054	0.026	0.193	0.112	-0.104	-0.031	0.031	-0.038	0.005	0.142	0.797
pgp2n.pk004.n22	NP_006809	MLLT11	unknown protein [Gallus gallus]	0.094	0.044	0.112	0.044	-0.060	0.050	-0.077	-0.012	0.040	0.953	0.416
pgp1n.pk014.p13	NP_009107	C14orf1	HSPC288 [Homo sapiens]	0.247	0.239	0.152	0.125	0.094	0.159	0.143	0.328	0.792	0.457	0.012
pgp2n.pk005.j20	NP_006492	NEFH	neurofilament triplet H1 protein - rabbit (fragment)	0.189	0.096	0.111	0.089	0.036	-0.014	-0.105	0.132	0.032	0.264	0.262
pgm2n.pk003.l7	NP_079426	TARS2	hypothetical protein FLJ12528 [Homo sapiens]	0.131	0.047	0.100	0.077	-0.020	0.007	0.022	0.016	0.023	0.900	0.684
pgm2n.pk002.p1			No Hits Found	0.176	0.123	0.074	0.018	0.025	0.024	0.025	0.052	0.042	0.469	0.221
pgm2n.pk002.a13			No Hits Found	0.214	0.180	0.234	0.154	0.071	0.116	0.152	0.141	0.005	0.408	0.298
pgp1n.pk013.h11	NP_004503	IL11RA	interleukin 11 receptor, alpha chain 1 [Rattus norvegicus]	0.012	0.154	0.086	0.006	-0.129	0.082	nd	-0.025	0.035	0.005	0.509
pgm2n.pk005.g19	NP_054786	C20orf133	expressed sequence AI604841 [Mus musculus]	0.061	-0.064	-0.046	-0.073	-0.080	-0.134	-0.028	-0.166	0.003	0.006	0.064
pgp1n.pk013.i4	NP_005887	IDH1	ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC	0.201	0.206	0.196	0.075	0.060	0.232	0.103	0.162	0.307	0.086	0.041
pgf1n.pk005.h24	NP_878917		Unknown (protein for IMAGE:5149947) [Mus musculus]	0.196	0.194	0.170	0.019	0.056	0.072	0.055	0.050	0.041	0.223	0.334
pgp2n.pk005.k14	NP_037498	ANAPC2	anaphase-promoting complex subunit 2 [Homo sapiens]	0.101	0.066	0.189	0.272	-0.038	-0.041	0.099	-0.029	0.004	0.166	0.459
pgl1c.pk001.g4		MBNL1	No Hits Found	-0.040	-0.008	-0.051	-0.120	-0.175	0.003	-0.145	0.050	0.737	0.141	0.027
pgp2n.pk006.p11			No Hits Found	0.255	0.275	0.303	0.030	0.126	0.187	0.033	0.037	0.030	0.068	0.322
pgp2n.pk008.f16	NP_002798	PSMD1	unnamed protein product [Mus musculus]	-0.082	-0.057	0.006	-0.084	-0.207	-0.167	0.078	-0.024	0.366	0.001	0.031
pgp2n.pk010.p11	NP_116221		hypothetical protein FLJ14735 [Homo sapiens]	0.367	0.299	0.234	0.044	0.243	0.159	0.165	0.094	0.037	0.001	0.205
pgr1n.pk003.k12	NP_071929	TMEM168	RIKEN cDNA 8430437G11 [Mus musculus]	0.216	0.344	0.366	0.301	0.093	0.223	0.295	0.183	0.014	0.037	0.954
pgp2n.pk006.g5	NP_078795	FAM65A	hypothetical protein [Homo sapiens]	0.207	0.108	0.133	0.240	0.085	0.252	0.186	0.256	0.415	0.094	0.028
pgp2n.pk007.f24			No Hits Found	0.293	0.306	0.290	0.195	0.172	0.243	0.114	0.167	0.038	0.511	0.612
pgf1n.pk003.o16			No Hits Found	0.119	0.050	0.113	0.237	nd	0.056	0.061	0.040	0.022	0.183	0.043

pgp2n.pk002.a16			No Hits Found	0.294	0.291	0.306	0.281	0.179	0.039	0.270	0.268	0.009	0.132	0.148
pnlb.pk0005.g7	NP_057303	MAN1B1	Chain A, Crystal Structure Of Human Class I Alpha1,2-Mannosidase	0.147	0.116	0.220	0.080	0.035	0.089	0.056	0.036	0.022	0.466	0.507
pgf1n.pk011.g1	NP_078799		No Hits Found	-0.153	-0.079	-0.065	-0.029	-0.265	-0.231	-0.190	-0.119	0.025	0.297	0.978
pft1c.pk002.g12			No Hits Found	-0.067	-0.044	-0.046	0.219	-0.178	0.167	0.195	-0.082	0.888	0.149	0.029
pgm2n.pk002.k9	NP_005799	CTDSPL	NLI-interacting factor isoform T2 [Gallus gallus]	-0.038	-0.030	-0.070	0.020	-0.148	0.071	0.031	-0.074	0.982	0.157	0.039
pgm2n.pk002.d12	NP_004627		Similar to sema domain, immunoglobulin domain (Ig)	0.095	0.111	0.055	0.011	-0.015	0.000	0.052	0.104	0.254	0.970	0.049
pgp2n.pk008.h16	NP_056118		hypothetical protein [Homo sapiens]	0.137	0.184	0.175	0.195	0.028	0.144	0.068	0.097	0.023	0.444	0.906
pgf1n.pk007.l13	NP_689497		No Hits Found	0.081	0.184	0.101	0.102	-0.025	0.098	-0.036	0.037	0.017	0.150	0.897
pgm2n.pk003.l3	NP_940983		unnamed protein product [Homo sapiens]	0.010	0.017	0.048	0.096	-0.097	0.030	0.036	-0.014	0.048	0.086	0.232
pgp1n.pk005.h1	NP_000405	HSD17B4	17-beta-hydroxysteroid dehydrogenase type IV [Gallus gallus]	-0.015	0.040	-0.096	-0.102	-0.119	-0.046	-0.048	-0.053	0.273	0.059	0.019
pgp1n.pk012.b5		SPOCK1	No Hits Found	0.158	0.197	0.094	0.090	0.054	0.012	0.070	0.044	0.003	0.699	0.152
pgm2n.pk007.g19	NP_872617	PLTP	dJ337O18.1.2 (Phospholipid Transfer Protein (Lipid Transfer ProteinII)	0.345	0.322	0.390	0.236	0.250	0.153	0.171	0.308	0.045	0.836	0.172
pco1c.pk001.e22			No Hits Found	0.148	0.175	0.203	0.024	0.056	0.153	-0.017	0.119	0.116	0.343	0.040
pgp1n.pk007.a12		CACNA2D2	No Hits Found	-0.007	-0.061	-0.132	0.154	-0.099	0.130	0.181	0.048	0.143	0.240	0.015
pgm2n.pk003.c19			ACRC protein [Homo sapiens]	0.170	0.142	0.187	0.104	0.088	0.071	0.074	0.076	0.038	0.802	0.843
pgm2n.pk002.j11	NP_055951		No Hits Found	0.094	0.134	0.104	0.047	0.014	-0.003	0.063	0.071	0.024	0.835	0.145
pgm2n.pk002.e4	NP_057951		RNA-binding protein Raly	0.085	0.069	0.100	0.035	0.006	0.052	0.016	0.025	0.028	0.704	0.439
pgm2n.pk003.f20	NP_006343	ZNF238	zinc finger protein C2H2-171 - human	0.100	0.061	0.069	-0.035	0.022	0.043	-0.102	-0.056	0.006	0.010	0.112
pgm2n.pk006.g5			No Hits Found	0.176	0.166	0.158	0.164	0.105	0.119	0.062	0.085	0.030	0.875	0.959
pgf2n.pk006.a8	NP_653324	ZMAT2	RIKEN cDNA 2610510D14 [Mus musculus]	-0.045	-0.038	0.000	-0.110	-0.114	-0.165	-0.082	0.015	0.162	0.353	0.016
pgr1n.pk002.n5	NP_036579		stromal antigen 3 [Homo sapiens]	0.262	0.251	0.235	0.239	0.194	0.148	0.152	0.157	0.046	0.899	0.989
pgl1n.pk014.b14	NP_077024		hypothetical protein FLJ11354 [Homo sapiens]	-0.031	0.050	0.181	-0.020	-0.099	-0.029	-0.240	-0.045	0.026	0.866	0.120
pgp1c.pk003.h23	NP_006612	AHCYL1	S-adenosylhomocysteine hydrolase-like 1 [Homo sapiens]	0.083	-0.160	-0.038	0.009	0.016	0.117	-0.077	-0.065	0.580	0.373	0.020
pft1c.pk003.a10	NP_055594		TSC22-related inducible leucine zipper 4c [Homo sapiens]	0.124	0.098	0.163	-0.119	0.059	0.048	-0.026	0.053	0.427	0.156	0.034
pgp1n.pk002.c16	NP_055701		unnamed protein product [Mus musculus]	-0.108	-0.054	-0.077	-0.163	-0.168	-0.115	-0.227	-0.047	0.215	0.405	0.036
pgm2n.pk004.e6	NP_005112	THRAP1	thyroid hormone receptor-associated protein	0.209	0.208	0.124	0.047	0.151	0.111	0.028	0.006	0.020	0.003	0.874
pgm2n.pk002.b6		CYB5B	cytochrome b5 outer mitochondrial membrane precursor [Homo sapiens]	0.195	0.195	0.161	0.017	0.140	0.101	-0.026	0.003	0.050	0.053	0.526
pgm2n.pk004.f24	NP_689940	CPNE2	copine II [Homo sapiens]	0.169	0.157	0.193	0.041	0.114	0.066	0.030	0.023	0.044	0.241	0.589
pgf1n.pk001.e8		CIRBP	No Hits Found	-0.041	0.013	-0.117	0.022	-0.093	0.043	0.113	-0.052	0.384	0.367	0.035
pgp1n.pk013.e10	NP_005861	SAP18	SAP18 [Gallus gallus]	0.009	-0.151	-0.189	-0.275	-0.043	-0.242	-0.334	0.067	0.781	0.019	0.020
pgp2n.pk007.g15	NP_057154	MRPS23	mitochondrial ribosomal protein S23 [Homo sapiens]	0.173	0.159	0.165	0.012	0.123	0.141	-0.034	0.123	0.267	0.148	0.038
pgp1n.pk001.j15	NP_620407	MAPK1	extracellular signal-regulated kinase 2 [Gallus gallus]	0.029	0.032	-0.024	0.158	-0.013	0.157	0.172	0.184	0.007	0.002	0.017
pgf1n.pk003.n17	NP_031388	NCBP2	nuclear cap binding protein subunit 2, 20kDa [Homo sapiens]	0.000	0.006	-0.015	0.407	-0.040	-0.077	0.165	-0.359	0.066	0.705	0.045
pgl1n.pk008.l14	NP_620124	RHOT2	hypothetical protein MGC31216 [Mus musculus]	-0.121	-0.083	-0.109	0.000	-0.161	-0.213	-0.145	-0.107	0.028	0.193	0.681
pgm2n.pk003.f8			No Hits Found	0.110	0.098	0.111	-0.051	0.071	0.050	0.011	0.104	0.793	0.468	0.037
pgl1n.pk014.e11			No Hits Found	0.071	0.199	0.143	0.016	0.036	0.075	-0.100	0.055	0.047	0.258	0.158
pgp2n.pk004.o16	NP_005476		Unknown (protein for MGC:11997) [Mus musculus]	0.090	0.022	0.031	-0.008	0.060	0.049	-0.087	0.105	0.928	0.021	0.014
pgr1n.pk001.o10	XP_291064		similar to LPS-responsive beige-like anchor [Homo sapiens]	0.243	0.211	0.252	0.096	0.218	0.177	0.139	0.190	0.406	0.087	0.033
pgp2n.pk010.k9			No Hits Found	0.009	0.052	0.020	-0.035	-0.016	-0.080	-0.247	-0.030	0.037	0.365	0.195
pgp2n.pk003.k24	NP_004791	TM9SF2	transmembrane 9 superfamily member 2 [Homo sapiens]	0.115	0.089	0.099	-0.113	0.092	0.095	0.082	0.319	0.003	0.975	0.001
pgp1n.pk004.g17	NP_002796	PSMC5	similar to proteasome (prosome, macropain) 26S subunit, ATPase, 5	-0.163	-0.016	-0.172	-0.212	-0.186	-0.258	-0.289	-0.196	0.043	0.469	0.177
pnfb.pk0010.d5	NP_002942	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	0.110	0.138	0.080	-0.034	0.087	-0.058	-0.012	0.120	0.353	0.730	0.031
pgp1n.pk002.o6	NP_001687	ATP6V1E1	Vacuolar ATP synthase subunit E (V-ATPase E subunit)	0.028	0.072	-0.006	0.125	0.007	0.278	0.120	-0.012	0.240	0.028	0.011
pgm2n.pk013.o12	NP_078811	CORO7	hypothetical protein FLJ22021 [Homo sapiens]	-0.015	0.008	-0.086	0.014	-0.034	-0.123	-0.145	-0.083	0.006	0.067	0.459
pgp1n.pk012.i15	NP_055799	AZI1	similar to 5-azacytidine induced gene 1 [Homo sapiens]	-0.010	0.129	-0.013	-0.075	-0.026	-0.069	-0.190	0.056	0.123	0.176	0.033
pgp1n.pk002.g4	NP_110378	ZEB1	deltaEF1 [Gallus gallus]	-0.037	-0.085	-0.203	0.025	-0.046	-0.045	0.064	-0.066	0.197	0.752	0.036
pgm2n.pk004.g11			No Hits Found	0.073	0.032	0.113	-0.012	0.065	0.062	0.003	0.043	0.665	0.245	0.025
pgp2n.pk009.a17			No Hits Found	0.135	0.156	0.158	0.050	0.128	-0.005	-0.087	0.064	0.039	0.505	0.174
pgp2n.pk004.m24	NP_000700	BCKDHA	branched-chain alpha-keto acid dehydrogenase E1-alpha subunit	0.001	0.067	-0.027	-0.233	-0.006	0.022	-0.206	0.034	0.838	0.052	0.028
pgm2n.pk013.c19			No Hits Found	-0.127	-0.086	-0.133	0.016	-0.131	-0.026	0.028	0.039	0.016	0.001	0.129
pgp1n.pk011.o12	NP_054909		adducin 1 (alpha) [Mus musculus]	-0.002	-0.037	-0.046	0.120	-0.003	0.078	0.133	0.036	0.086	0.250	0.025
pgp2n.pk005.k22		PKP4	plakophilin 4 [Homo sapiens]	0.137	0.180	0.057	0.067	0.138	0.033	-0.017	0.014	0.018	0.011	0.184
pgp1n.pk012.g16	XP_034872		Septin-like protein KIAA0202	0.038	0.033	-0.021	0.065	0.039	-0.031	0.178	0.042	0.164	0.060	0.001
pgp1c.pk002.m24	NP_075063		expressed sequence AW558420 [Mus musculus]	-0.204	-0.165	-0.358	-0.132	-0.198	-0.013	0.041	0.062	0.004	0.227	0.130
pgp1n.pk008.n6	NP_006536	TUSC4	G21 protein [Mus musculus]	-0.017	-0.137	-0.149	-0.316	-0.008	0.020	-0.145	0.575	0.000	0.046	0.001
pgp1n.pk006.d21	NP_149035		Similar to rhotekin [Homo sapiens]	-0.090	0.086	0.135	0.530	-0.080	0.011	0.227	-0.179	0.052	0.128	0.029
pgp1n.pk009.l2	NP_000963		60S RIBOSOMAL PROTEIN L7A	nd	-0.416	-0.336	-0.405	0.012	-0.137	-0.102	0.290	0.041	0.724	0.505
pgf2c.pk001.f15	NP_000080	COL1A2	alpha-2 type I collagen [Gallus gallus]	0.230	0.303	0.150	0.020	0.245	0.165	-0.051	0.133	0.185	0.004	0.035
pgm2n.pk004.f18	NP_036250	CCRN4L	CCR4 carbon catabolite repression 4-like	0.160	0.398	0.135	0.009	0.176	0.049	0.001	0.010	0.028	0.029	0.064
pgr1n.pk006.e8	NP_004707	PCSK7	proprotein convertase subtilisin/kexin type 7 preproprotein [Homo sapiens]	0.078	0.153	0.137	-0.088	0.095	-0.101	0.012	0.077	0.190	0.217	0.007
pgp2n.pk008.h19	NP_001312		Cysteine-rich protein 2 (CRP2) (Beta-cysteine-rich protein)(Beta-CRP)	0.024	0.101	0.088	-0.116	0.045	0.005	-0.209	0.033	0.308	0.384	0.041
pgp1n.pk011.l5	NP_001476	GBX2	HOMEOBOX PROTEIN GBX-2	-0.010	-0.031	0.058	-0.003	0.012	0.017	-0.131	-0.038	0.240	0.799	0.037
pgf2n.pk002.l2	NP_003863	NRP2	neuropilin-2a2 receptor [Gallus gallus]	-0.250	-0.264	-0.296	-0.067	-0.226	-0.224	-0.079	-0.167	0.220	0.079	0.047
pgp2n.pk004.d17	NP_258412		similar to inosine triphosphatase [Mus musculus]	-0.037	-0.028	-0.217	0.014	-0.010	-0.013	0.032	-0.067	0.155	0.407	0.022
pgp1n.pk010.h11	NP_003160	SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae) [Homo sapiens]	-0.129	-0.144	-0.134	-0.030	-0.101	-0.114	0.076	-0.098	0.124	0.132	0.047
pft1c.pk003.b7			No Hits Found	-0.090	-0.177	-0.118	0.010	-0.060	-0.027	0.094	0.109	0.048	0.261	0.724
pgp1n.pk003.h15	NP_005722		Chain D, Crystal Structure Of Arp23 COMPLEX	-0.248	-0.332	-0.345	-0.052	-0.217	-0.117	-0.201	-0.295	0.468	0.576	0.017
pgp2n.pk006.p20	NP_065855	PACSIN1	KIAA1379 protein [Homo sapiens]	0.202	0.237	0.266	0.093	0.234	0.085	0.164	0.269	0.775	0.689	0.032
pnlb.pk0005.g9	NP_056290	FAM98A	unnamed protein product [Homo sapiens]	0.040	0.086	0.147	-0.028	0.076	-0.040	-0.099	-0.025	0.043	0.515	0.066
pgp1n.pk005.o24	NP_000399	GPD2	glycerol-3-phosphate dehydrogenase	-0.206	-0.257	-0.148	-0.018	-0.168	-0.093	0.045	0.037	0.048	0.042	0.677
pnl1s.pk001.f3			No Hits Found	-0.178	-0.117	-0.136	-0.008	-0.137	-0.055	-0.002	-0.035	0.049	0.011	0.195
pgm2n.pk002.d5	NP_005331	FHIT	fragile histidine triad gene [Homo sapiens]	0.195	0.272	0.079	-0.081	0.239	0.001	-0.060	0.077	0.201	0.001	0.005
pgr1c.pk001.c20	NP_079130		hypothetical protein FLJ22028 [Homo sapiens]	-0.185	-0.166	-0.201	-0.003	-0.139	-0.180	-0.031	-0.191	0.933	0.552	0.038
pnl1s.pk003.a6			No Hits Found	0.018	0.035	0.075	-0.121	0.066	0.003	-0.184	0.008	0.530	0.285	0.031
pgm2n.pk007.k15	NP_076990	ATG9A	similar to hypothetical protein FLJ22169 [Homo sapiens] [Mus musculus]	-0.034	-0.067	-0.057	0.086	0.014	-0.121	0.070	-0.138	0.519	0.302	0.034
pft1c.pk004.e10	NP_291024		myosin regulatory light chain, cellular - chicken	0.179	0.231	0.276	0.215	0.227	0.246	0.436	0.330	0.037	0.092	0.549
pgp2n.pk007.c15	NP_079202	TTC26	unnamed protein product [Mus musculus]	0.120	0.052	0.121	-0.044	0.170	0.004	-0.089	0.037	0.398	0.040	0.045
pgp1c.pk003.i15	NP_065682		KIAA0720 protein [Homo sapiens]	-0.062	0.045	0.097	-0.145	-0.012	0.004	-0.143	0.025	0.723	0.570	0.020
pgm2n.pk009.e2			No Hits Found	0.148	0.187	0.101	-0.058	0.201	0.011	-0.062	0.053	0.264	0.013	0.026
pgp1n.pk008.c5	NP_113655	SLC4A9	solute carrier family 4, sodium bicarbonate cotransporter	0.039	0.029	0.081	-0.068	0.092	-0.014	-0.100	0.008	0.449	0.202	0.038
pgf1n.pk008.o24	NP_005145	USP8	ubiquitin specific protease 8 [Homo sapiens]	-0.081	-0.073	-0.006	0.050	-0.025	0.028	0.100	0.183	0.009	0.010	0.894
pgp2n.pk002.l9	NP_005140		brachyury	-0.033	-0.019	0.003	-0.194	0.028	-0.124	-0.208	0.193	0.383	0.161	0.000
pgm2n.pk006.m14			No Hits Found	0.312	0.230	0.336	0.195	0.374	0.244	0.090	0.239	0.401	0.072	0.019
pgp2n.pk009.f8	NP_006850	LIAS	Lipoic acid synthetase, mitochondrial (Lip-syn) (Lipoate synthase)	0.143	0.147	0.188	0.042	0.205	0.135	0.046	0.131	0.970	0.185	0.034
pgp1n.pk003.e15			No Hits Found	-0.228	-0.146	-0.153	-0.251	-0.165	-0.169	-0.391	-0.126	0.692	0.338	0.045
pgl1n.pk010.h4	NP_005315	HIST2H3D	agCP12107 [Anopheles gambiae str. PEST]	-0.138	-0.206	-0.300	-0.263	-0.074	-0.238	-0.156	-0.078	0.034	0.166	0.251
pgl1n.pk002.o3		PSMC4	proteasome 26S ATPase subunit 4 isoform 1 [Homosapiens]	-0.008	0.011	-0.095	-0.132	0.057	0.065	0.122	0.086	0.003	0.746	0.325
pgp1n.pk014.f13	NP_055390	SCHIP1	schwannomin interacting protein 1 [Homo sapiens]	-0.075	-0.030	0.058	-0.079	-0.009	0.073	-0.067	0.077	0.132	0.461	0.047
pgm1n.pk001.k11		ATP2A2	Ca2+-transporting ATPase (EC 3.6.3.8) SERCA2a - chicken	0.133	0.211	0.178	0.111	0.200	0.090	0.070	0.156	0.320	0.736	0.050
pgp2n.pk004.m16	NP_064632	CABC1	unnamed protein product [Mus musculus]	0.089	0.060	0.099	-0.010	0.157	0.032	0.003	0.133	0.452	0.226	0.035
pgp1n.pk004.k13	NP_002065	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1	-0.208	0.006	0.044	0.082	-0.139	0.136	0.174	0.150	0.047	0.001	0.910
pgp1c.pk002.k20	NP_057098	FAM108B1	Similar to CGI-67 protein [Homo sapiens]	-0.210	-0.184	-0.208	-0.037	-0.142	-0.103	0.004	-0.070	0.034	0.124	0.155
pgp2n.pk008.h24			No Hits Found	0.047	0.102	0.110	-0.091	0.115	0.036	-0.126	0.044	0.540	0.172	0.014
pnlb.pk0008.g8			No Hits Found	-0.177	-0.163	-0.142	-0.019	-0.109	0.095	0.014	0.005	0.032	0.360	0.477
pgf2n.pk004.o23			No Hits Found	0.013	0.003	-0.031	-0.039	0.085	-0.049	-0.100	0.025	0.862	0.004	0.028
pgl1n.pk002.o8			No Hits Found	-0.039	-0.041	-0.013	-0.025	0.034	-0.028	0.117	-0.018	0.035	0.100	0.282
pgf1n.pk001.a5	NP_114404	RNF26	ring finger protein 26 [Homo sapiens]	0.223	0.175	0.156	0.041	0.299	0.067	-0.042	0.101	0.243	0.002	0.031
pgm2n.pk003.e17	NP_065714	RHOJ	TC10-like Rho GTPase [Homosapiens]	0.099	0.166	0.211	0.030	0.176	0.013	0.008	0.041	0.065	0.230	0.027
pgm2n.pk010.n5	NP_079066		hypothetical protein FLJ22490 [Homo sapiens]	-0.004	0.079	0.266	0.078	0.074	0.032	-0.070	0.165	0.336	0.687	0.040
pgp1c.pk003.m18	NP_002329	LSAMP	Limbic system-associated membrane protein precursor (E19S)	-0.150	-0.199	-0.192	0.117	-0.070	-0.135	0.045	-0.092	0.387	0.098	0.037
pnl1s.pk003.d12			Putative protein, with 2 coiled coil-4 domains, nematode specific	-0.226	-0.177	-0.199	-0.103	-0.145	-0.146	-0.129	-0.039	0.039	0.035	0.940
pgp1n.pk005.a21	NP_060751	ECHDC2	Similar to RIKEN cDNA 1300017C12 gene [Mus musculus]	-0.189	nd	-0.216	0.152	-0.107	-0.213	-0.065	-0.146	0.745	0.180	0.029
pgp1n.pk003.l20			No Hits Found	-0.201	-0.108	-0.102	-0.065	-0.118	-0.097	-0.007	0.068	0.050	0.046	0.740
pgm2n.pk006.k6	NP_006436		splicing factor Prp8 [Homo sapiens]	0.037	-0.048	-0.080	0.023	0.122	-0.024	0.073	-0.068	0.106	0.017	0.017
pgp2n.pk002.k22	NP_848591	C3orf59	Unknown (protein for IMAGE:5267040) [Homo sapiens]	-0.027	0.109	0.032	-0.065	0.058	-0.089	-0.100	0.014	0.322	0.780	0.048
pgp1n.pk014.l6	NP_002731		protein kinase C, iota [Homo sapiens]	0.181	0.208	0.190	0.049	0.266	0.068	0.059	0.202	0.811	0.152	0.009
pgf2n.pk005.o18	NP_060836	CNO	hypothetical protein FLJ11230 [Homo sapiens]	-0.111	0.020	0.027	-0.112	-0.023	-0.027	-0.149	0.018	0.975	0.674	0.044
pgp2n.pk007.n14		FOXI2	No Hits Found	-0.045	-0.072	-0.064	-0.019	0.043	0.003	-0.053	-0.013	0.012	0.110	0.200
pgp2n.pk010.f3	NP_054752		DKFZP586A0522 protein [Homo sapiens]	-0.097	0.018	-0.140	-0.042	-0.007	-0.173	-0.082	0.012	0.930	0.321	0.025
pgl1n.pk009.f10	NP_150279	BOC	unnamed protein product [Homo sapiens]	-0.105	-0.050	-0.004	-0.195	-0.014	-0.058	-0.168	0.005	0.449	0.852	0.022
pgp1n.pk013.a17	NP_006126		F-ACTIN CAPPING PROTEIN ALPHA-1 SUBUNIT (CAPZ 36/32)	-0.171	-0.107	-0.149	0.044	-0.077	-0.053	0.024	0.063	0.023	0.010	0.437
pgm2n.pk013.g16	NP_004271	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1 [Homo sapiens]	-0.293	-0.279	-0.251	-0.051	-0.199	-0.155	0.021	-0.047	0.011	0.017	0.233
pgp1n.pk012.l13	NP_003461		ubiquitin specific protease 7 (herpes virus-associated)	0.047	0.064	0.100	-0.011	0.143	0.012	0.498	0.060	0.031	0.023	0.072
pgr1n.pk007.l23	NP_000319	RPGR	RPGR protein [Homo sapiens]	0.124	0.098	0.157	-0.046	0.220	0.133	0.201	0.168	0.028	0.203	0.443
pgp2n.pk006.n22	XP_376947	SURF5	surfeit gene 5 [Mus musculus]	-0.008	0.050	-0.062	-0.076	0.088	-0.047	-0.101	0.078	0.397	0.089	0.043
pgr1n.pk006.a16			hypothetical protein XP_062490 [Homo sapiens]	0.048	0.080	0.148	0.015	0.146	0.034	-0.014	0.061	0.592	0.569	0.022
pgp2n.pk007.f3	NP_057416		Selenoprotein X 1 (Protein HSPC270)	0.049	-0.034	-0.013	0.000	0.147	0.034	0.009	0.053	0.036	0.043	0.773
pgm2n.pk008.p11	NP_037392	SAP30BP	HCNGP [Homo sapiens]	-0.084	-0.040	-0.122	-0.151	0.015	0.409	-0.188	-0.152	0.045	0.005	0.038
pgp2n.pk008.o5			No Hits Found	0.076	0.095	0.103	-0.043	0.176	-0.024	-0.100	0.088	0.526	0.088	0.005
pgf2n.pk004.f5			No Hits Found	-0.118	-0.027	-0.020	-0.150	-0.018	-0.041	-0.101	-0.062	0.333	0.227	0.038
pgm2n.pk004.c15	NP_037415	MAT2B	expressed sequence AI182287 [Mus musculus]	-0.157	-0.140	-0.161	-0.088	-0.057	-0.253	-0.088	-0.109	0.716	0.079	0.048
pgp2n.pk008.p23	NP_005478		hypothetical protein [Homo sapiens]	-0.058	-0.094	-0.120	-0.015	0.043	0.013	0.025	-0.009	0.009	0.738	0.431
pgr1n.pk002.l6	NP_113640	FAM103A1	hypothetical protein MGC2560 [Homo sapiens]	0.241	-0.040	0.077	0.140	0.343	0.142	0.496	0.106	0.020	0.044	0.116

pgr1n.pk002.p16	NP_056012	PACS2	hypothetical protein KIAA0602 - human (fragment)	-0.036	-0.054	-0.041	0.099	0.066	0.035	0.121	0.100	0.026	0.242	0.539
pgm2n.pk011.n14	NP_444281	TADA1L	SPT3-associated factor 42 [Homo sapiens]	-0.344	-0.216	-0.423	-0.069	-0.242	-0.139	-0.005	-0.128	0.037	0.186	0.067
pgp2n.pk007.k19			No Hits Found	-0.153	-0.161	-0.271	-0.001	-0.050	-0.091	0.054	-0.010	0.035	0.366	0.211
pgr1n.pk006.g22	NP_000017	ADSL	Adenylosuccinate lyase (Adenylosuccinase) (ASL) (ASASE)	0.102	0.142	0.109	-0.036	0.206	0.053	0.100	0.162	0.151	0.390	0.035
pgp1n.pk004.p6			No Hits Found	-0.202	-0.135	-0.192	-0.069	-0.097	-0.051	-0.001	-0.051	0.030	0.522	0.556
pgp1n.pk007.n9	NP_004374	CSK	Tyrosine-protein kinase CSK (C-SRC kinase)	-0.233	-0.210	-0.200	-0.035	-0.128	0.010	-0.035	-0.055	0.010	0.185	0.243
pgm2n.pk008.d4	NP_057094		Similar to CGI-62 protein [Homo sapiens]	0.035	-0.052	-0.073	-0.152	0.140	-0.067	-0.041	-0.020	0.043	0.001	0.328
pgp2n.pk004.j3	NP_006159	NKX6-2	homeodomain protein [Gallus gallus]	0.016	0.035	0.061	0.026	0.122	0.004	-0.001	0.043	0.704	0.316	0.033
pgp1n.pk014.j22	NP_006689	BLCAP	bladder cancer associated protein [Homo sapiens]	-0.171	-0.128	-0.134	0.085	-0.063	0.131	0.085	0.012	0.000	0.004	0.003
pgf1n.pk003.n3	NP_116236		No Hits Found	0.040	0.151	0.074	-0.071	0.147	0.042	-0.051	0.065	0.948	0.165	0.042
pgp1c.pk002.e5		SCAP	Sterol regulatory element binding protein cleavage-activating protein	-0.238	-0.184	-0.258	-0.340	-0.128	-0.234	-0.178	-0.104	0.041	0.890	0.130
pgp1n.pk004.o2	NP_000588	IGFBP2	Insulin-like growth factor binding protein 2 precursor (IGFBP-2)	-0.429	-0.421	-0.335	-0.051	-0.318	-0.021	-0.047	-0.081	0.009	0.020	0.152
pgm2n.pk003.l4			No Hits Found	-0.031	-0.040	-0.062	-0.022	0.081	-0.100	0.004	-0.039	0.214	0.024	0.024
pgf1n.pk007.f7	NP_057175		eukaryotic translation initiation factor 3, subunit 6 interacting protein	-0.131	-0.082	-0.124	-0.003	-0.019	-0.002	-0.011	-0.021	0.047	0.571	0.499
pgp1n.pk011.e7	NP_689676	LRRC59	ribosome-binding protein p34 - rat	-0.145	-0.125	-0.191	-0.033	-0.030	-0.093	-0.028	-0.024	0.025	0.313	0.369
pgr1n.pk002.m3	NP_055509	ADAMTSL2	KIAA0605 gene product [Homo sapiens]	0.123	0.085	0.028	0.039	0.238	0.104	-0.039	-0.040	0.898	0.000	0.039
pgp2n.pk008.f18	NP_003161	SUPT6H	similar to emb-5 protein of C.elegans. [Homo sapiens]	0.012	-0.001	-0.066	-0.094	0.127	-0.170	-0.032	-0.067	0.953	0.005	0.022
pgr1n.pk008.h7	NP_003280	TPM2	beta-tropomyosin	-0.095	-0.128	-0.194	0.138	0.020	0.158	0.087	0.065	0.017	0.210	0.090
pgf2n.pk004.d6			No Hits Found	-0.009	-0.063	-0.071	-0.049	0.109	-0.088	-0.012	-0.038	0.037	0.000	0.060
pgm2n.pk009.d24	NP_065802	COG6	similar to CG1968 gene product [Homo sapiens]	-0.090	-0.126	-0.151	-0.047	0.030	-0.093	-0.001	-0.074	0.020	0.252	0.119
pgp2n.pk007.j18		NUDT4	No Hits Found	0.072	0.180	0.130	0.015	0.192	0.044	0.002	0.088	0.637	0.395	0.043
pgp1n.pk001.n7	NP_002334	TF	Ovotransferrin precursor (Conalbumin) (Allergen Gal d 3) (Gal d III)	-0.161	-0.203	-0.264	-0.372	-0.040	-0.015	-0.085	-0.082	0.000	0.096	0.466
pgp1n.pk009.j4	NP_056207	NPDC1	Similar to neural proliferation, differentiation and control gene 1	-0.015	-0.069	-0.057	0.015	0.106	0.000	0.077	0.035	0.020	0.462	0.575
pgp2n.pk008.g10	NP_116120	TXNL5	No Hits Found	0.042	0.155	0.269	-0.006	0.164	0.062	-0.090	0.091	0.177	0.648	0.003
pgf1n.pk001.l15	NP_848611	EXOC3L	unnamed protein product [Mus musculus]	-0.273	-0.306	-0.302	-0.027	-0.151	-0.046	-0.060	-0.080	0.036	0.336	0.312
pgp2n.pk004.c1			No Hits Found	-0.035	-0.186	-0.194	-0.102	0.087	-0.123	-0.061	-0.073	0.018	0.005	0.660
pgf2n.pk001.i6		ING3	RIKEN cDNA 1300013A07 gene [Mus musculus]	-0.200	-0.206	-0.231	-0.215	-0.077	-0.099	-0.116	-0.157	0.017	0.829	0.935
pgp2n.pk004.b23	NP_006658		Membrane associated progesterone receptor component 1	-0.145	-0.060	-0.110	0.031	-0.021	-0.029	0.079	0.012	0.032	0.228	0.191
pgr1n.pk003.b21	NP_149014		unnamed protein product [Mus musculus]	-0.144	-0.039	-0.180	-0.024	-0.019	-0.102	0.032	-0.008	0.027	0.324	0.030
pgf2n.pk006.k5	NP_114131		transmembrane protein induced by tumor necrosis factor alpha	-0.330	-0.242	-0.382	-0.014	-0.204	0.001	-0.028	-0.172	0.048	0.271	0.056
pgp2n.pk006.e11	NP_036549	PITPNC1	retinal degeneration B beta [Mus musculus]	-0.168	-0.104	-0.154	-0.060	-0.042	-0.064	-0.027	-0.046	0.016	0.650	0.420
pgf1n.pk010.j21	NP_004069	CSRP1	LIM-domain protein CRP1 [Coturnix japonica]	-0.257	-0.273	-0.228	-0.005	-0.131	-0.049	-0.011	-0.059	0.037	0.250	0.319
pgf1n.pk008.d22	NP_001822	CLU	clusterin [Gallus gallus]	-0.523	-0.181	-0.166	0.045	-0.395	-0.380	-0.167	-0.047	0.291	0.000	0.043
pgm2n.pk010.b15	NP_006082	CORO2B	KIAA0925 protein [Homo sapiens]	-0.139	-0.115	-0.161	-0.002	-0.009	-0.017	0.021	-0.012	0.005	0.400	0.196
pgr1n.pk006.j22			unnamed protein product [Mus musculus]	0.094	0.152	0.141	-0.128	0.225	0.048	0.058	0.168	0.117	0.118	0.004
pgp1n.pk003.e14	NP_937994		hypothetical protein FLJ11021 similar to splicing factor, argini	-0.400	-0.296	-0.243	0.046	-0.270	-0.062	0.152	0.043	0.014	0.006	0.276
pnlb.pk0007.d3			Apolipoprotein A-I precursor (Apo-AI)	-0.594	-0.799	-0.624	-0.253	-0.463	-0.265	-0.313	-0.263	0.037	0.248	0.351
pgp2n.pk003.g3	NP_008938		No Hits Found	-0.044	0.032	-0.049	-0.156	0.087	-0.119	-0.083	0.027	0.340	0.252	0.011
pgf1n.pk008.i2	NP_055916	GLT25D2	similar to chromosome 1 open reading frame 17 [Homo sapiens]	-0.092	-0.023	-0.073	0.002	0.040	0.044	-0.031	0.055	0.048	0.377	0.793
pgm2n.pk005.l4	NP_061138	VPS33B	similar to vacuolar protein sorting homolog r-vps33b [Rattus norvegicus] [Mus mu	-0.009	-0.114	-0.189	-0.139	0.122	-0.166	-0.145	0.011	0.039	0.000	0.122
pgp2n.pk010.f24	NP_005975		mitochondrial citrate transport protein [Homo sapiens]	-0.097	-0.217	-0.634	-0.738	0.036	-0.498	-0.470	-0.028	0.113	0.030	0.044
pgp2n.pk007.h9	NP_004852	GAL3ST1	Similar to cerebroside sulfotransferase [Homo sapiens]	-0.065	0.069	0.222	-0.064	0.068	-0.081	-0.102	0.027	0.279	0.766	0.028
pgf2c.pk001.n9	NP_000129	FBN1	similar to fibrillin [Homo sapiens]	0.101	0.152	0.186	0.031	0.234	-0.058	0.003	0.184	0.590	0.447	0.018
pgf1n.pk007.l1	NP_115785	PINK1	PTEN induced putative kinase 1 [Mus musculus]	-0.196	-0.181	-0.192	-0.018	-0.062	-0.102	-0.055	-0.048	0.028	0.121	0.295
pgf1n.pk001.f16	NP_008963	GCAT	KIAA1662 protein [Homo sapiens]	-0.156	-0.100	-0.094	-0.213	-0.022	-0.224	-0.269	-0.136	0.568	0.293	0.019
pgp2n.pk002.m20	NP_663747		cell division cycle associated 4 [Homo sapiens]	-0.144	-0.125	-0.148	0.022	-0.010	-0.029	0.027	-0.012	0.001	0.104	0.052
pgr1n.pk003.m11	NP_114155	TTLL2	NYD-TSPG protein [Homo sapiens]	0.129	0.101	0.342	-0.119	0.263	0.115	nd	0.199	0.020	0.049	0.164
pgm2n.pk011.e18	NP_002472		M21 chain - chicken	-0.200	-0.140	-0.168	-0.109	-0.065	-0.173	-0.001	-0.040	0.016	0.251	0.163
pgm2n.pk009.h1	NP_055617	KIAA0528	hypothetical protein KIAA0528 - human	0.030	0.045	0.047	-0.069	0.166	-0.073	-0.088	-0.066	0.409	0.015	0.035
pgp1n.pk004.f20	NP_115696	BTBD10	RIKEN cDNA 1110056N09 [Mus musculus]	-0.269	-0.146	-0.206	-0.123	-0.134	-0.133	-0.043	-0.028	0.021	0.218	0.589
pgf1n.pk003.e11	NP_005040	PWP2	PWP2 protein [Homo sapiens]	0.250	0.201	0.239	-0.041	0.388	0.068	-0.006	0.157	0.832	0.019	0.018
pgf2n.pk001.p20			No Hits Found	-0.073	-0.065	-0.097	0.109	0.064	-0.132	0.133	-0.067	0.490	0.157	0.022
pgm2n.pk003.p22	NP_002201	ITGAV	Integrin alpha-V precursor (Vitronectin receptor alpha subunit)	0.033	0.025	0.007	-0.054	0.170	-0.077	-0.108	-0.026	0.690	0.011	0.036
pgp2n.pk009.n5			No Hits Found	0.025	0.085	0.022	-0.021	0.164	-0.117	0.048	0.122	0.563	0.417	0.044
pgf2n.pk005.b5	XP_035527	KIAA1370	similar to KIAA1370 protein [Homo sapiens]	-0.208	-0.409	-0.257	-0.109	-0.068	-0.024	-0.088	-0.209	0.003	0.686	0.006
pgr1n.pk002.b14		KBTBD3	No Hits Found	-0.054	0.020	0.009	0.150	0.086	0.051	0.169	0.015	0.143	0.316	0.013
pgp2n.pk008.l16	NP_004242	RAB9A	RAB9A, member RAS oncogene family [Homo sapiens]	0.114	0.118	0.079	-0.116	0.254	-0.040	-0.070	0.071	0.920	0.021	0.030
pgp1n.pk008.g16	NP_085046	ITIH5	unnamed protein product [Mus musculus]	-0.210	-0.151	-0.089	0.055	-0.070	-0.031	0.030	0.034	0.037	0.022	0.462
pgl1n.pk013.n11	NP_002323	C10orf54	FLJ00041 protein [Homo sapiens]	-0.071	-0.022	0.018	-0.253	0.070	-0.099	-0.128	0.152	0.163	0.845	0.031
pgm1c.pk003.a3	NP_003273	TNNI2	TROPONIN I, FAST SKELETAL MUSCLE	-0.282	-0.201	-0.222	-0.073	-0.141	-0.121	-0.019	-0.084	0.031	0.220	0.402
pgp2n.pk002.b18	NP_002563	PAFAH1B2	platelet-activating factor acetylhydrolase alpha 2 subunit	0.032	0.001	0.080	0.070	0.174	-0.003	0.065	0.019	0.449	0.032	0.040
pgf1n.pk001.n6	NP_075526	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2 [Homo sapiens]	-0.136	-0.120	-0.151	-0.100	0.007	-0.119	-0.031	-0.086	0.005	0.400	0.077
pgr1n.pk006.f16	NP_620156		BLOCK 25 [Homo sapiens]	-0.230	-0.278	-0.293	-0.002	-0.086	-0.172	0.023	-0.157	0.056	0.274	0.028
pgp2n.pk006.o8	NP_663324		SREC-4 [Homo sapiens]	-0.425	-0.221	-0.314	0.070	-0.281	-0.014	0.111	0.027	0.016	0.005	0.174
pgm1c.pk002.b11	XP_036942		No Hits Found	-0.149	-0.168	-0.206	-0.039	-0.004	-0.131	-0.131	-0.137	0.184	0.089	0.044
pgp2n.pk010.c15	NP_002283	LAMB2	laminin beta 2-like chain [Gallus gallus]	0.043	0.076	-0.020	0.004	0.187	-0.050	0.068	-0.037	0.634	0.066	0.041
pgr1n.pk004.i8	NP_036450	LETM2	leucine zipper-EF-hand containing transmembrane protein 1	0.182	0.219	0.176	0.039	0.328	0.089	0.160	0.274	0.137	0.174	0.017
pgm2n.pk006.p18			unnamed protein product [Homo sapiens]	0.095	0.089	0.101	0.024	0.241	0.042	-0.066	0.036	0.696	0.021	0.035
pnlb.pk0008.b3	NP_072093		No Hits Found	-0.177	-0.226	-0.168	-0.124	-0.031	-0.133	-0.055	-0.136	0.019	0.419	0.365
pgr1n.pk005.h17	NP_037389	SGK3	unnamed protein product [Mus musculus]	-0.028	0.009	0.058	-0.064	0.120	-0.010	-0.019	0.013	0.239	0.280	0.027
pgp2n.pk004.j1	NP_065389	PCBP3	unnamed protein product [Homo sapiens]	0.010	0.041	0.048	-0.027	0.157	-0.059	-0.033	0.063	0.678	0.274	0.036
pgf1n.pk001.i14	NP_003000	SEPW1	Selenoprotein W	-0.239	-0.274	-0.190	0.037	-0.091	-0.051	0.072	-0.024	0.033	0.182	0.299
pgf2n.pk001.m15		EFCAB1	No Hits Found	-0.212	-0.170	-0.141	-0.053	-0.064	-0.107	-0.067	-0.042	0.045	0.233	0.590
pgp1n.pk008.k12	NP_878899		RIKEN cDNA 4933422M21 [Mus musculus]	-0.221	-0.179	-0.222	-0.071	-0.073	-0.087	-0.009	-0.041	0.015	0.491	0.535
pgp1n.pk002.l9	NP_115602	ZCCHC7	FLJ22611-like protein [Danio rerio]	-0.398	-0.287	-0.340	-0.047	-0.249	-0.140	0.011	-0.065	0.034	0.082	0.369
pgp1n.pk005.k16	NP_115825	CC2D1B	unnamed protein product [Mus musculus]	-0.236	-0.232	-0.225	0.008	-0.087	-0.270	0.023	-0.155	0.361	0.106	0.044
pco1c.pk001.p24	NP_001534		N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-0.166	-0.089	-0.155	-0.065	-0.017	-0.054	-0.092	-0.100	0.039	0.487	0.090
pgf1n.pk005.h11			No Hits Found	0.029	0.030	0.045	-0.108	0.179	0.061	-0.093	0.087	0.157	0.105	0.049
pgm2n.pk004.d15			No Hits Found	-0.130	-0.101	-0.115	-0.053	0.020	-0.076	-0.080	-0.015	0.038	0.358	0.402
pgp2n.pk002.p1	NP_116027	GATA2	GATA binding factor-2 (Transcription factor NF-E1B) (GATA-2)	-0.282	-0.227	-0.223	0.000	-0.130	-0.086	0.036	-0.095	0.030	0.146	0.106
pgf2n.pk001.l21	XP_371953		pol polyprotein - chicken EAV element (fragment)	0.134	0.211	0.255	-0.018	0.286	0.060	-0.009	0.162	0.659	0.269	0.014
pgf2n.pk006.i10	NP_057006	NSDHL	NAD(P) dependent steroid dehydrogenase-like [Homo sapiens]	-0.215	-0.260	-0.234	0.052	-0.063	-0.098	0.026	-0.060	0.031	0.107	0.070
pgr1n.pk003.i19			No Hits Found	-0.013	0.077	0.050	-0.035	0.140	-0.003	-0.103	0.051	0.959	0.276	0.011
pgr1n.pk002.m1			No Hits Found	0.067	0.134	0.007	0.159	0.221	-0.075	0.152	0.029	0.829	0.376	0.016
pgp2n.pk008.c6	NP_149044	HIAT1	unnamed protein product [Mus musculus]	-0.078	-0.067	-0.041	-0.066	0.075	-0.092	0.019	-0.028	0.027	0.112	0.098
pgr1n.pk007.a19	XP_370768	ACYP2	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYME	-0.187	-0.116	-0.208	-0.045	-0.033	-0.116	-0.040	-0.053	0.017	0.315	0.093
pgr1n.pk007.h10			No Hits Found	-0.153	-0.171	-0.168	-0.138	0.002	-0.137	-0.135	-0.014	0.035	0.272	0.570
pgm1n.pk001.d9			No Hits Found	-0.224	-0.139	-0.165	-0.106	-0.069	-0.243	-0.184	-0.112	0.775	0.079	0.004
pgf1n.pk004.h12			No Hits Found	-0.136	-0.012	-0.024	0.070	0.019	-0.012	0.037	-0.026	0.333	0.262	0.043
pgr1c.pk001.k14	XP_371755		unnamed protein product [Homo sapiens]	-0.121	-0.071	-0.105	0.071	0.034	0.001	-0.081	0.059	0.028	0.002	0.113
pgp1n.pk014.c9	NP_757367		infertility-related sperm protein [Homo sapiens]	-0.109	-0.122	-0.139	-0.035	0.046	-0.007	-0.099	-0.006	0.002	0.033	0.232
pgp2n.pk006.l4	NP_112184		hypothetical protein [Takifugu rubripes]	0.001	0.082	-0.002	-0.073	0.157	-0.021	-0.061	0.027	0.433	0.053	0.013
pgp2n.pk002.m19			No Hits Found	0.006	-0.056	-0.128	-0.150	0.163	0.106	-0.026	-0.028	0.012	0.073	0.967
pgf1n.pk002.n2	NP_055558		KIAA0232 protein [Homo sapiens]	-0.192	-0.218	-0.223	-0.090	-0.035	-0.150	-0.087	-0.111	0.019	0.300	0.240
pgm2n.pk007.g10	NP_000062	CBS	cystathionine beta synthase [Rattus norvegicus]	-0.092	-0.097	-0.114	-0.003	0.066	-0.042	0.008	-0.006	0.037	0.561	0.450
pgl1n.pk015.h22	NP_113637	ZMIZ2	FLJ00315 protein [Homo sapiens]	-0.297	-0.199	-0.215	-0.072	-0.138	-0.088	-0.075	-0.062	0.002	0.019	0.343
pgf1n.pk002.h24	NP_689742	GPR155	hypothetical protein FLJ31819 [Homo sapiens]	-0.240	-0.354	-0.190	-0.108	-0.080	-0.021	-0.145	-0.242	0.078	0.983	0.050
pgp1n.pk012.i23	NP_904355	RNF19	hypothetical protein DKFZp434M1115.1 - human (fragment)	-0.062	-0.136	-0.138	-0.133	0.098	-0.069	-0.075	-0.131	0.035	0.016	0.400
pgf1n.pk002.j24	XP_049068	ARID5A	modulator recognition factor 1 - human (fragment)	0.069	0.091	0.027	0.045	0.229	-0.039	0.043	0.038	0.740	0.031	0.022
pgm2n.pk004.i18			No Hits Found	0.041	0.058	0.030	-0.067	0.202	-0.038	-0.014	0.068	0.289	0.127	0.047
pnlb.pk0005.h7	XP_372417		RIBONUCLEASE CL2 (POLY C PREFERENTIAL RIBONUCLEASE)	-0.326	-0.270	-0.313	-0.030	-0.165	-0.127	-0.052	-0.072	0.014	0.058	0.207
pgm2n.pk004.p2	NP_060684	LRRC1	LAP (leucine-rich repeats and PDZ) and no PDZ protein [Homo sapiens]	-0.216	-0.165	-0.313	-0.131	-0.054	-0.319	-0.126	-0.191	0.480	0.358	0.044
pgp1n.pk010.o5			No Hits Found	-0.196	-0.192	-0.192	-0.026	-0.034	-0.066	0.031	-0.081	0.038	0.725	0.274
pgp2n.pk008.j3	NP_005026		No Hits Found	0.004	-0.028	-0.046	-0.021	0.166	-0.009	0.017	0.000	0.016	0.029	0.204
pgl1n.pk010.j22	XP_371352		ENOD2 [Styphnolobium japonicum]	-0.185	0.060	0.042	-0.070	-0.023	-0.131	-0.147	-0.030	0.318	0.708	0.018
pgr1n.pk006.f8			No Hits Found	-0.125	-0.006	-0.079	-0.123	0.038	-0.131	-0.129	-0.048	0.616	0.567	0.014
pgl1n.pk008.n13	NP_690856		unnamed protein product [Mus musculus]	-0.200	-0.246	-0.215	-0.141	-0.037	-0.138	-0.096	-0.105	0.001	0.249	0.471
pgf2n.pk005.d4	NP_036344	LTB4DH	15-oxoprostaglandin 13-reductase [Sus scrofa]	-0.139	-0.144	-0.176	-0.013	0.024	-0.037	-0.039	0.009	0.046	0.486	0.761
pgp1n.pk001.i19	NP_004346	CD74	MHC class II-associated invariant chain [Gallus gallus]	-0.354	-0.173	-0.140	-0.135	-0.191	-0.035	-0.043	0.012	0.015	0.036	0.969
pgp2n.pk008.o23	NP_078986		similar to hypothetical protein FLJ23469	-0.610	-0.353	-0.370	0.077	-0.446	-0.072	0.092	-0.049	0.050	0.004	0.193
pgf1n.pk010.i21	NP_077275	C20orf149	chromosome 20 open reading frame 149 [Homo sapiens]	-0.168	-0.101	-0.207	-0.044	-0.004	-0.161	-0.112	-0.107	0.302	0.234	0.041
pgp2n.pk003.j16	NP_001528		No Hits Found	-0.075	-0.086	-0.080	0.062	0.090	-0.292	-0.040	-0.054	0.467	0.007	0.018
pgf1n.pk002.i6			No Hits Found	-0.088	-0.002	-0.076	-0.027	0.077	-0.051	-0.037	-0.019	0.090	0.478	0.021
pgp2n.pk009.n2	NP_038462	KCNIP3	unnamed protein product [Mus musculus]	0.087	0.043	0.144	0.114	0.252	0.078	-0.043	0.042	0.672	0.086	0.016
pgm2n.pk011.l19			No Hits Found	-0.249	-0.299	-0.326	-0.107	-0.083	-0.060	-0.059	-0.007	0.008	0.296	0.677
pgf1n.pk002.c4	NP_001278	CLCN7	chloride channel 7 [Mus musculus]	-0.239	-0.184	-0.224	-0.120	-0.071	-0.093	-0.071	-0.130	0.035	0.965	0.481
pgf2n.pk002.l9	NP_003452		Zyxin	-0.428	-0.315	-0.142	0.109	-0.259	0.028	0.107	0.035	0.011	0.002	0.114
pgm2n.pk007.o13			type V preprocollagen alpha 2 chain [Homo sapiens]	-0.297	-0.170	-0.227	0.038	-0.129	-0.035	0.004	-0.018	0.049	0.074	0.329
pgr1n.pk003.i12	NP_660202		similar to CG3714-PA [Drosophila melanogaster] [Mus musculus]	-0.117	-0.056	-0.123	0.039	0.052	-0.013	-0.005	0.041	0.027	0.225	0.361
pgl1n.pk011.k19			No Hits Found	-0.177	-0.051	-0.013	-0.207	-0.008	-0.107	-0.178	0.132	0.156	0.843	0.009
pnlb.pk0008.h11			putative protein; protein id: At5g56470.1 [Arabidopsis thaliana]	-0.195	-0.216	-0.168	-0.177	-0.026	-0.160	-0.063	0.028	0.012	0.457	0.705
pgp1n.pk009.h1	NP_064618		x 006 protein [Homo sapiens]	-0.016	-0.078	-0.027	-0.016	0.154	-0.083	-0.092	-0.038	0.486	0.006	0.035
pgp1n.pk006.d20			No Hits Found	-0.336	-0.156	-0.238	-0.020	-0.166	0.203	0.065	-0.099	0.020	0.095	0.187

pgm1n.pk001.k12	NP_065107	C12orf4	chromosome 12 open reading frame 4 [Homo sapiens]	-0.085	-0.106	-0.037	-0.202	0.086	0.091	-0.096	-0.002	0.015	0.371	0.088
pgf1n.pk008.a8	NP_057568		hypothetical protein LOC51248 [Homo sapiens]	-0.246	-0.291	-0.346	0.023	-0.075	-0.120	0.023	-0.120	0.013	0.197	0.016
pnlb.pk0001.b11	NP_941961		No Hits Found	0.009	0.034	-0.032	-0.087	0.181	-0.128	-0.278	-0.005	0.429	0.011	0.016
pgf1n.pk005.o1	NP_006761	COL4A2	putative scavenger receptor MARCO [Gallus gallus]	-0.253	-0.344	-0.248	-0.122	-0.080	-0.133	-0.137	-0.076	0.030	0.389	0.755
pgm1c.pk001.e20	NP_000357		Tropomyosin 1 alpha chain (Alpha-tropomyosin)	-0.212	-0.125	-0.201	-0.015	-0.038	-0.028	-0.045	-0.040	0.006	0.157	0.171
pgp1n.pk006.d14	NP_006565	CSPG5	CALEB isoform b [Gallus gallus]	-0.389	-0.229	-0.109	0.031	-0.214	-0.061	0.043	-0.053	0.033	0.002	0.117
pgp2n.pk006.c6	NP_055886	ARHGAP26	Graf protein [Homo sapiens]	-0.236	-0.213	-0.217	-0.037	-0.061	-0.091	-0.038	-0.088	0.033	0.522	0.291
pgm2n.pk006.o16	NP_563616	ASB15	ankyrin and SOCS box-containing protein 15 [Bos taurus]	0.247	0.335	0.257	0.178	0.422	0.235	0.168	0.221	0.828	0.036	0.034
pgf1n.pk007.d11	NP_057097	NDUFAF1	CGI-65 protein [Homo sapiens]	-0.290	-0.189	-0.242	0.047	-0.114	-0.012	0.100	0.008	0.047	0.256	0.413
pgf1n.pk008.k5	NP_005012	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-0.359	-0.348	-0.429	-0.071	-0.182	-0.174	-0.046	-0.080	0.019	0.215	0.323
pco1c.pk001.o14	NP_002309		lysyl oxidase-like 2 [Homo sapiens]	-0.170	-0.099	-0.099	-0.202	0.006	-0.184	-0.293	-0.131	0.835	0.199	0.009
pgp1n.pk010.e16	NP_000143	GAA	acid alpha glucosidase [Coturnix japonica]	-0.197	-0.184	-0.191	-0.020	-0.020	-0.134	-0.079	-0.079	0.047	0.143	0.107
pco1c.pk001.j9	NP_077296		hypothetical protein MGC11242 [Homo sapiens]	-0.005	0.066	0.098	0.005	0.173	-0.004	0.021	0.031	0.597	0.336	0.012
pgl1n.pk004.a12	NP_612454		hypothetical protein BC014241 [Homo sapiens]	-0.203	-0.129	-0.127	-0.084	-0.024	-0.125	-0.153	-0.072	0.058	0.221	0.010
pgl1n.pk003.c2	NP_000775	CYP27A1	cytochrome P450, subfamily XXVIIA, polypeptide 1 precursor	-0.283	-0.193	-0.248	-0.173	-0.101	-0.153	-0.159	-0.086	0.016	0.536	0.627
pgm2n.pk003.d19	NP_036430	CAND2	hypothetical protein KIAA0667 - human (fragment)	-0.072	-0.011	-0.039	-0.153	0.109	-0.043	-0.031	0.070	0.012	0.611	0.039
pgf2n.pk005.d6	NP_036223	ADAT1	adenosine deaminase, tRNA-specific 1 [Homo sapiens]	-0.085	-0.164	-0.176	-0.170	0.097	-0.028	-0.189	-0.065	0.036	0.049	0.380
pgf2n.pk005.l7	NP_057299	EGFL7	Estrogen-regulated protein CBL20, 20.4kD [Rattus norvegicus]	-0.095	-0.030	-0.139	-0.059	0.088	-0.027	-0.070	-0.012	0.010	0.076	0.146
pgm1c.pk003.i21	NP_065698	JPH1	junctophilin 1 [Homo sapiens]	-0.249	-0.087	-0.219	-0.223	-0.066	-0.279	-0.275	-0.113	0.805	0.438	0.041
pgp2n.pk010.m13	NP_055157	MTCH2	mitochondrial carrier homolog 2 [Gallus gallus]	0.049	0.135	0.140	-0.025	0.233	-0.014	-0.072	0.044	0.530	0.165	0.011
pgf1n.pk010.k1	NP_055704	PITRM1	Similar to metalloprotease 1 (pitrilysin family) [Homo sapiens]	-0.096	0.034	-0.133	0.075	0.087	-0.080	-0.101	-0.053	0.843	0.033	0.010
pgp1n.pk003.h20	NP_004506	ILF2	transcription factor NF-AT 45K chain - human	-0.179	-0.226	-0.284	-0.175	0.006	-0.059	-0.062	-0.076	0.039	0.859	0.948
pgm2n.pk007.g5		HERC4	No Hits Found	-0.248	-0.198	-0.237	-0.012	-0.062	-0.171	-0.106	-0.128	0.068	0.051	0.008
pgf1n.pk003.i10	NP_055438	MEA1	unnamed protein product [Mus musculus]	-0.287	-0.121	-0.136	-0.067	-0.101	-0.085	-0.181	-0.150	0.419	0.096	0.013
pgf1n.pk011.b23	NP_055596	RB1CC1	Rb1-inducible coiled coil protein [Homo sapiens]	-0.204	-0.163	-0.212	-0.061	-0.017	-0.001	-0.085	-0.068	0.044	0.724	0.613
pgf1n.pk006.b7			No Hits Found	-0.150	-0.195	-0.209	0.010	0.039	-0.067	0.074	-0.054	0.037	0.626	0.256
pgp1n.pk014.o4	NP_008858	ST3GAL2	similar to sialyltransferase 4B	0.181	0.252	0.207	0.325	0.371	0.126	0.265	0.334	0.375	0.066	0.039
pgp2n.pk008.j1	NP_057685	KCNK9	potassium channel, subfamily K, member 9 [Homo sapiens]	0.064	0.090	0.093	0.034	0.254	0.066	-0.007	0.067	0.377	0.029	0.010
pnl1s.pk001.b11		VPS26A	No Hits Found	-0.261	-0.254	-0.196	-0.095	-0.072	-0.201	-0.051	-0.121	0.038	0.196	0.278
pgp1n.pk010.l3	NP_000044	ATP7B	ORF	-0.188	-0.063	-0.145	-0.095	0.001	-0.075	-0.129	0.023	0.040	0.261	0.201
pgr1c.pk001.h17	NP_055491	PUM1	pumilio-like protein 1 [Xenopus laevis]	-0.265	-0.096	-0.200	0.005	-0.075	0.079	0.001	0.012	0.034	0.191	0.674
pgp2n.pk002.i6			vesicle-associated membrane protein 1 [Mus musculus]	-0.371	-0.310	-0.248	0.021	-0.181	0.011	0.061	-0.095	0.007	0.046	0.048
pco1c.pk001.e8			Chain A, Ovotransferrin, N-Terminal Lobe, Apo Form	-0.072	-0.014	-0.045	-0.070	0.119	-0.061	-0.101	0.035	0.120	0.182	0.024
pgf1n.pk001.c19	NP_003583	CUL1	similar to cullin protein [Homo sapiens]	-0.266	-0.160	-0.168	-0.098	-0.075	-0.242	-0.239	-0.165	0.820	0.342	0.018
pgp1n.pk010.f6			homologous to FPV ORF4	-0.337	-0.305	-0.297	-0.060	-0.146	-0.240	0.022	-0.105	0.019	0.060	0.111
pgf1n.pk006.c11	NP_061850	NLGN3	KIAA1480 protein [Homo sapiens]	-0.125	0.008	0.045	-0.087	0.067	-0.022	-0.207	0.065	0.763	0.678	0.025
pgr1n.pk008.o20	NP_003464	STAM	signal transducing adaptor molecule 1 [Homo sapiens]	-0.117	-0.004	-0.143	0.066	0.076	0.050	0.008	0.055	0.034	0.180	0.343
pgr1n.pk005.i24			No Hits Found	-0.095	-0.037	-0.143	-0.018	0.097	-0.068	0.036	-0.113	0.059	0.465	0.005
pgr1n.pk006.l9	NP_005751		CCAAT-box-binding transcription factor (CCAAT-binding factor) (CBF)	-0.174	-0.094	-0.225	-0.077	0.019	0.035	-0.051	-0.120	0.002	0.161	0.037
pgp2n.pk009.j1	NP_659440		Unknown (protein for IMAGE:5756168) [Homo sapiens]	-0.127	-0.183	-0.270	-0.142	0.066	-0.019	-0.148	-0.149	0.021	0.076	0.422
pgr1n.pk001.j10			No Hits Found	-0.195	-0.197	-0.149	0.034	-0.001	-0.056	0.024	-0.040	0.050	0.393	0.270
pgr1n.pk005.a6	NP_001093		actinin [Gallus gallus]	-0.112	-0.062	-0.048	-0.040	0.081	-0.019	0.009	0.029	0.027	0.932	0.501
pgp2n.pk002.h11			No Hits Found	-0.165	-0.038	-0.147	-0.156	0.029	0.037	0.081	-0.056	0.050	0.759	0.848
pnlb.pk0005.d8			No Hits Found	-0.115	-0.174	-0.138	-0.158	0.079	-0.207	-0.162	-0.211	0.527	0.003	0.045
pgm2n.pk007.l13			No Hits Found	0.002	0.079	0.092	0.091	0.196	0.094	0.188	0.129	0.044	0.827	0.384
pgm2n.pk006.p12	NP_001185		No Hits Found	0.154	0.195	0.135	-0.054	0.349	0.056	-0.023	0.025	0.899	0.003	0.029
pgp2n.pk006.n15	NP_073741	TYSND1	RIKEN cDNA 1300019N10 [Mus musculus]	-0.047	0.011	-0.008	-0.147	0.147	-0.052	-0.154	0.040	0.235	0.098	0.005
pgp1n.pk011.e9	XP_044434		KIAA1458 protein [Homo sapiens]	-0.107	-0.051	-0.085	-0.026	0.088	-0.064	0.005	0.067	0.008	0.335	0.183
pgm2n.pk011.d8	NP_001837	COL4A2	Unknown (protein for MGC:7371) [Mus musculus]	-0.253	-0.104	-0.200	-0.118	-0.057	-0.113	-0.067	-0.013	0.025	0.533	0.443
pgp2n.pk003.b5	NP_694940	IQCK	hypothetical protein XP_058777 [Homo sapiens]	-0.130	-0.067	-0.132	-0.116	0.067	0.009	-0.004	-0.108	0.039	0.605	0.551
pgp2n.pk003.j3	NP_872384	ANKRD9	RIKEN cDNA 1110038F21 [Mus musculus]	-0.690	-0.313	-0.493	0.134	-0.491	-0.104	0.245	-0.066	0.024	0.002	0.016
pgp1n.pk010.h24	NP_054883		No Hits Found	-0.278	-0.308	-0.238	-0.087	-0.079	-0.186	-0.135	-0.096	0.031	0.086	0.339
pgr1n.pk002.a19	NP_037414		ubiquitin-like, containing PHD and RING finger domains, 1	-0.201	-0.068	-0.086	-0.128	-0.002	-0.194	-0.197	-0.071	0.910	0.826	0.021
pgf2n.pk001.a5	NP_005063	SLC12A4	solute carrier family 12, member 4 [Rattus norvegicus]	-0.057	-0.025	-0.148	-0.028	0.142	0.102	0.065	0.085	0.001	0.500	0.801
pgp2n.pk007.p22	NP_056034	EXOC7	Unknown (protein for MGC:9876) [Homo sapiens]	-0.072	-0.129	-0.250	-0.183	0.128	-0.036	-0.126	0.054	0.046	0.302	0.884
pgf2n.pk002.o16			No Hits Found	-0.213	-0.185	-0.202	-0.194	-0.013	-0.175	-0.192	-0.115	0.031	0.315	0.158
pgm2n.pk012.j13	NP_000811	GAS6	growth-arrest-specific protein	-0.227	-0.132	-0.087	-0.169	-0.026	-0.134	-0.107	-0.054	0.046	0.873	0.118
pgm2n.pk006.k14	XP_370537		No Hits Found	0.020	0.046	-0.013	-0.227	0.221	nd	-0.050	0.071	0.020	0.027	0.108
pgp2n.pk002.l18	NP_057431		putative N-acetyltransferase Camello 4 [Rattus norvegicus]	-0.372	-0.183	-0.285	0.107	-0.171	-0.003	0.143	0.102	0.035	0.055	0.422
pgp2n.pk009.j18	NP_056422	C1orf77	unnamed protein product [Mus musculus]	-0.152	-0.152	-0.191	0.045	0.050	-0.062	-0.017	-0.007	0.033	0.217	0.249
pgm2n.pk008.a22	NP_001842		collagen alpha 1(IX) chain long form precursor - chicken	-0.123	-0.028	-0.063	0.015	0.079	0.076	0.085	0.106	0.045	0.838	0.928
pgm2n.pk005.l8	NP_002685	POLR2C	Similar to polymerase (RNA) II (DNA directed) polypeptide C	-0.218	-0.112	-0.197	-0.012	-0.015	0.000	0.007	-0.041	0.015	0.524	0.243
pgf1n.pk004.p10	NP_061489	EFEMP1	extracellular protein - human	-0.334	-0.141	-0.279	-0.288	-0.132	-0.313	-0.313	-0.071	0.282	0.374	0.033
pgf2c.pk001.f6	NP_064706	MNT	max binding protein [Mus musculus]	-0.457	-0.219	-0.233	-0.063	-0.254	-0.284	-0.053	-0.065	0.031	0.000	0.030
pgp1n.pk002.i13	NP_006822	CLP1	ATP/GTP-binding protein [Homo sapiens]	-0.278	-0.281	-0.199	-0.023	-0.075	-0.102	0.012	-0.076	0.019	0.216	0.267
pgp1n.pk014.l5			No Hits Found	-0.154	-0.108	-0.109	-0.099	0.049	-0.120	-0.118	0.007	0.040	0.303	0.085
pgr1n.pk003.l11			No Hits Found	0.008	0.056	-0.026	0.034	0.211	0.023	0.041	0.192	0.007	0.085	0.080
pgp1n.pk004.m9			No Hits Found	-0.268	-0.131	-0.285	0.031	-0.063	0.009	-0.041	-0.008	0.038	0.158	0.407
pgp2n.pk003.k10	NP_077719	NOTCH2	Notch2 [Gallus gallus]	-0.001	0.072	0.021	-0.021	0.205	0.058	-0.025	0.073	0.072	0.131	0.039
pgp2n.pk005.f15	NP_003350		UDP-glucose dehydrogenase [Mus musculus]	0.023	0.090	-0.143	-0.100	0.229	0.016	-0.047	0.067	0.044	0.037	0.099
pgl1n.pk008.k21			HMG CoA synthase	-0.154	-0.027	0.031	-0.109	0.051	-0.126	-0.183	-0.020	0.926	0.980	0.022
pgp2n.pk008.o15			No Hits Found	0.061	-0.085	0.004	0.053	0.269	-0.122	-0.011	0.014	0.424	0.000	0.039
pgp1c.pk002.i13	NP_078863	TMEM53	hypothetical protein FLJ22353 [Homo sapiens]	-0.341	-0.530	-0.395	-0.176	-0.132	-0.281	-0.031	-0.088	0.044	0.382	0.776
pgf2n.pk001.g10	NP_004070	CTSS	cathepsin S [Homo sapiens]	-0.041	0.039	0.019	-0.053	0.168	0.016	-0.005	-0.012	0.072	0.154	0.033
pgf1n.pk007.p20	NP_006107	MAP3K7IP1	transforming growth factor beta-activated kinase-binding protein 1	-0.226	-0.041	-0.271	-0.021	-0.016	0.032	0.114	0.056	0.009	0.379	0.342
pgm2n.pk007.n5	NP_057211	TMEM66	similar to FOAP-7 [Homo sapiens]	-0.197	-0.178	-0.158	0.025	0.013	-0.120	0.047	-0.020	0.045	0.222	0.248
pgr1n.pk008.b8			No Hits Found	0.010	-0.009	0.015	0.032	0.221	0.017	0.151	0.075	0.042	0.393	0.484
pgr1n.pk004.l23			No Hits Found	-0.035	0.023	-0.051	0.086	0.177	0.119	0.140	0.098	0.034	0.949	0.577
pgp1n.pk004.j21			No Hits Found	-0.057	0.044	0.012	0.017	0.155	-0.043	-0.083	-0.006	0.959	0.551	0.033
pgp1n.pk008.e8			No Hits Found	-0.118	-0.068	-0.107	0.036	0.094	-0.009	0.058	-0.006	0.037	0.847	0.191
pgf1n.pk002.f3	NP_079511		RIKEN cDNA 5430432P15 [Mus musculus]	-0.100	-0.006	-0.134	-0.075	0.112	-0.210	-0.135	-0.213	0.307	0.009	0.000
pgp1n.pk003.p24	NP_002822	PTPN6	protein tyrosine phosphatase, non-receptor type 6, isoform 1	-0.231	-0.199	-0.239	-0.108	-0.017	-0.175	-0.087	-0.106	0.010	0.384	0.120
pnfb.pk0003.h9			No Hits Found	-0.560	-0.864	-0.204	0.035	-0.346	-0.011	0.025	-0.351	0.063	0.076	0.022
pgf2n.pk006.l16	NP_001107	ADCY9	Adenylate cyclase, type IX (ATP pyrophosphate-lyase)	-0.373	-0.291	-0.270	-0.246	-0.157	-0.160	-0.074	0.042	0.015	0.405	0.892
pgf2n.pk001.n17	NP_009034		NADH dehydrogenase (ubiquinone) flavoprotein 1 [Mus musculus]	-0.253	-0.181	-0.267	-0.136	-0.037	-0.057	-0.048	-0.109	0.024	0.963	0.627
pgr1n.pk005.k6	NP_001354	DKC1	dyskerin [Homo sapiens]	-0.060	-0.053	-0.047	-0.114	0.156	-0.166	-0.063	-0.066	0.304	0.009	0.011
pgf1n.pk012.a22			No Hits Found	-0.159	-0.189	-0.186	0.072	0.057	-0.104	0.059	-0.179	0.110	0.318	0.006
pgr1n.pk001.f21		MAPRE2	unnamed protein product [Mus musculus]	0.168	0.354	0.234	0.091	0.385	0.088	0.200	0.204	0.847	0.178	0.002
pgp1n.pk013.k19	NP_004408	DUSP1	MAP kinase phosphatase-1 [Gallus gallus]	-0.188	-0.158	-0.204	-0.107	0.029	-0.173	-0.095	-0.088	0.013	0.170	0.056
pgp1n.pk005.i6	NP_060242	TBC1D22B	TBC1 domain family protein C22orf4-like (QtsA-20424)	-0.236	-0.239	-0.243	0.064	-0.018	-0.090	0.046	-0.014	0.019	0.120	0.137
pgp2n.pk002.o9	NP_001919	CFD	Complement factor D precursor (C3 convertase activator)	-0.160	-0.021	-0.011	-0.090	0.058	0.035	-0.008	0.070	0.041	0.816	0.312
pgm2n.pk005.p22		RKHD3	hypothetical protein XP_145925 [Mus musculus]	-0.108	-0.077	-0.129	-0.061	0.110	-0.141	-0.094	-0.091	0.215	0.060	0.018
pgm2n.pk006.e7			No Hits Found	0.089	0.030	0.054	0.088	0.308	0.088	0.057	0.017	0.145	0.015	0.044
pgr1n.pk005.j19	NP_005634	TAF11	TBP-associated factor 11	-0.003	-0.049	-0.029	-0.193	0.216	-0.036	-0.122	-0.094	0.103	0.000	0.030
pgm2n.pk008.d7	NP_036398		No Hits Found	-0.342	-0.432	-0.250	-0.008	-0.123	-0.079	-0.148	-0.061	0.028	0.076	0.162
pgm2n.pk014.m13	NP_037485	TMOD4	Sk-tropomodulin [Gallus gallus]	-0.228	-0.211	-0.283	-0.122	-0.008	-0.218	-0.056	-0.136	0.012	0.308	0.050
pgf1n.pk009.l11	NP_000079		COLLAGEN ALPHA 1(I) CHAIN PRECURSOR	-0.326	-0.251	-0.248	0.039	-0.107	-0.005	0.043	0.001	0.020	0.172	0.390
pgp1n.pk014.k15		YES1	No Hits Found	-0.026	-0.049	nd	-0.192	0.194	-0.042	-0.157	0.302	0.002	0.013	0.021
pgm2n.pk007.p8			No Hits Found	-0.194	-0.071	-0.119	-0.133	0.027	-0.159	-0.030	0.231	0.007	0.138	0.023
pgp1n.pk009.k12			No Hits Found	-0.234	-0.130	-0.098	0.177	-0.013	0.346	0.286	0.017	0.040	0.477	0.134
pgr1n.pk003.a21	NP_000263	NPHP1	Nephrocystin	0.009	0.000	0.002	-0.052	0.230	-0.064	-0.076	-0.080	0.667	0.003	0.008
pgl1n.pk001.b17			Wiscott-Aldrich Syndrome protein homolog	-0.383	-0.191	-0.271	-0.028	-0.161	-0.022	0.051	0.029	0.002	0.015	0.395
pgp1n.pk011.n4	NP_777569	TMEM167	Similar to RIKEN cDNA 0610041E09 gene [Homo sapiens]	-0.130	-0.268	-0.379	-0.190	0.093	-0.138	-0.230	-0.136	0.048	0.049	0.850
pgm2n.pk007.f2	NP_005087	ZMYM3	zinc finger protein 261 [Homo sapiens]	-0.104	-0.138	-0.251	-0.150	0.119	-0.224	-0.102	-0.168	0.087	0.006	0.029
pgp1n.pk005.g15	NP_005178		MTGR1-like protein [Xenopus laevis]	-0.282	-0.108	-0.175	-0.164	-0.059	-0.224	-0.156	-0.095	0.142	0.752	0.018
pgr1n.pk003.h4			No Hits Found	0.070	0.042	0.009	0.174	0.295	0.043	0.055	0.025	0.457	0.054	0.031
pgf2n.pk006.e20	NP_065385		hypothetical protein MGC38361 [Mus musculus]	-0.228	-0.113	-0.210	-0.043	-0.002	-0.169	-0.031	-0.034	0.031	0.316	0.053
pgf2n.pk001.k15	NP_000468		Serum albumin precursor	-0.093	0.053	0.008	-0.118	0.135	-0.158	-0.104	0.178	0.398	0.615	0.022
pgp2n.pk004.p2	NP_006793	SF3A3	Similar to splicing factor 3a, subunit 3, 60kD [Homo sapiens]	-0.274	-0.055	-0.163	0.091	-0.047	0.007	0.133	0.154	0.018	0.037	0.472
pgr1n.pk004.c19			No Hits Found	-0.062	0.040	0.011	0.163	0.165	0.057	0.180	0.099	0.032	0.389	0.048
pgp2n.pk004.a7	NP_001937	DUSP6	dual specificity phosphatase 6 [Rattus norvegicus]	-0.116	-0.141	-0.117	-0.086	0.112	-0.125	-0.037	-0.028	0.014	0.107	0.205
pgf2n.pk006.n19	NP_057447	LILRA2	immunoglobulin-like receptor CHIR-A [Gallus gallus]	-0.225	-0.186	-0.245	-0.054	0.004	-0.131	-0.129	-0.075	0.018	0.127	0.150
pgf2n.pk004.a9	NP_003746	EIF3S4	Eukaryotic translation initiation factor 3 subunit 4 (eIF-3 delta)	-0.345	-0.195	-0.351	-0.141	-0.116	0.123	0.136	0.031	0.008	0.478	0.701
pgf2n.pk006.i1	NP_006358	CAP1	adenylyl cyclase-associated protein (CAP) homolog MCH1 - rat	-0.224	-0.207	-0.352	-0.321	0.006	0.108	-0.036	0.118	0.034	0.880	0.964
pgm2n.pk002.d1	NP_006518	SLBP	stem-loop binding protein [Mus musculus]	0.102	0.185	0.145	-0.103	0.332	0.000	-0.088	0.012	0.711	0.009	0.009
pco1c.pk001.j7	NP_060286		Ly1 antibody reactive clone [Mus musculus]	0.071	0.050	-0.027	-0.069	0.301	-0.046	-0.082	-0.019	0.416	0.001	0.031
pgf2n.pk006.l7	NP_113651	HSDL1	steroid dehydrogenase-like [Homo sapiens]	-0.333	-0.313	-0.215	0.059	-0.101	-0.153	0.047	0.198	0.025	0.022	0.928
pgp1n.pk002.g5			polymerase [simian type D virus 1]	-0.256	-0.161	-0.229	-0.127	-0.023	-0.144	-0.100	-0.041	0.003	0.363	0.198
pgf2n.pk006.b9	NP_002212	ITPKB	No Hits Found	-0.081	-0.008	-0.108	-0.083	0.151	-0.073	-0.076	-0.085	0.142	0.060	0.039
pgm1c.pk002.p13	XP_084376		Unknown (protein for MGC:13522) [Homo sapiens]	-0.243	-0.156	-0.197	-0.160	-0.010	-0.165	-0.156	-0.062	0.013	0.497	0.097
pgf1n.pk002.o9	NP_056969	PCF11	Pre-mRNA cleavage complex II protein Pcf11	-0.284	-0.217	-0.226	0.030	-0.051	-0.173	0.064	-0.009	0.027	0.087	0.168
pgr1n.pk006.f22	NP_872293		FLJ00237 protein [Homo sapiens]	-0.237	-0.226	-0.226	-0.063	-0.002	-0.060	0.047	-0.050	0.036	0.861	0.617
pgf1n.pk008.o23	NP_057376	TRAP1	tumor necrosis factor type 1 receptor associated protein [Homo sapiens]	-0.215	-0.181	-0.236	-0.101	0.021	-0.198	-0.120	-0.063	0.005	0.038	0.038

pgf1n.pk010.o17			No Hits Found	-0.429	-0.310	-0.200	0.133	-0.193	-0.130	-0.060	-0.020	0.046	0.000	0.035
pgp1n.pk001.h20	XP_370993		similar to coenzyme A diphosphatase [Homo sapiens]	-0.234	-0.185	-0.259	-0.198	0.003	-0.131	-0.149	-0.049	0.023	0.668	0.705
pgm2n.pk003.d8	NP_932342		RIKEN cDNA 2310005N03 [Mus musculus]	0.095	0.145	0.087	-0.018	0.332	-0.005	-0.045	0.041	0.940	0.034	0.037
pgf2n.pk001.k6	NP_055835	PHLPPL	similar to hypothetical protein [Macaca fascicularis] [Mus musculus]	-0.132	-0.145	-0.094	-0.150	0.105	-0.193	-0.164	-0.132	0.286	0.009	0.008
pgf1n.pk010.a6	NP_056049		similar to dJ365O12.1 (KIAA0758 protein) [Homo sapiens]	-0.090	-0.038	-0.121	-0.021	0.147	0.046	-0.035	0.061	0.045	0.538	0.664
pgp1n.pk007.c21	NP_000023	ALAS2	5-AMINOLEVULINIC ACID SYNTHASE, ERYTHROID-SPECIFIC	-0.141	-0.111	-0.193	-0.036	0.099	-0.154	0.005	-0.023	0.049	0.340	0.144
pgp2n.pk002.n11			No Hits Found	-0.443	-0.229	-0.259	-0.015	-0.203	-0.147	0.093	-0.066	0.016	0.020	0.104
pgp1n.pk003.p8	NP_001677	ATP5B	ATP synthase beta chain, mitochondrial precursor	-0.313	-0.202	-0.341	-0.141	-0.072	-0.019	-0.182	-0.133	0.016	0.211	0.558
pnfb.pk0003.c1	NP_004346		MHC class II-associated invariant chain [Gallus gallus]	-0.285	-0.127	0.022	0.169	-0.042	0.019	0.080	0.001	0.063	0.000	0.003
pgp1n.pk003.h2	NP_056195	SAMM50	Protein CGI-51	-0.348	-0.027	0.037	0.268	-0.103	0.264	0.546	0.281	0.018	0.009	0.445
pgm2n.pk007.e15			No Hits Found	-0.242	-0.151	-0.216	-0.051	0.004	-0.133	-0.097	-0.127	0.013	0.371	0.003
pgm2n.pk006.n15	NP_055680	NCAPD2	chromosome condensation-related SMC-associated protein 1	0.114	0.166	0.084	-0.012	0.361	-0.017	-0.052	0.088	0.901	0.036	0.040
pgm2n.pk010.n12			No Hits Found	-0.133	-0.087	-0.120	-0.052	0.114	-0.036	-0.063	-0.022	0.010	0.345	0.092
pgr1n.pk002.j12			No Hits Found	-0.253	-0.138	-0.190	-0.145	-0.006	-0.232	-0.206	-0.133	0.173	0.222	0.002
pgp1n.pk014.j24	NP_006328		target of Jun 3 [Coturnix coturnix]	-0.381	-0.231	-0.420	-0.175	-0.133	-0.180	-0.245	-0.129	0.049	0.254	0.590
pgp2n.pk002.c19	NP_057055	MRPS7	mitchondrial ribosomal protein S7 [Mus musculus]	-0.094	-0.041	-0.075	-0.417	0.154	-0.063	-0.146	-0.020	0.048	0.073	0.078
pgf2n.pk006.b16	NP_036513	ORC3L	origin recognition complex, subunit 3 (yeast homolog)-like	-0.341	-0.151	-0.371	-0.076	-0.093	-0.149	-0.048	-0.156	0.036	0.445	0.042
pgf1n.pk007.c23	NP_002957	S100A10	Calpactin I light chain (P10 protein) (P11)	-0.734	-0.588	-0.375	-0.047	-0.485	-0.152	-0.096	-0.093	0.027	0.008	0.317
pgm2n.pk005.p24	NP_060853	C1orf212	hypothetical protein BC011880 [Homo sapiens]	-0.222	-0.258	-0.354	-0.304	0.029	-0.165	-0.199	-0.176	0.002	0.039	0.624
pgp1c.pk003.g7			No Hits Found	-0.402	-0.413	-0.322	-0.098	-0.150	-0.213	-0.054	-0.156	0.017	0.200	0.275
pgf2n.pk002.b3	NP_002399		alpha-1,6-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	-0.121	0.017	-0.132	0.198	0.132	0.087	0.112	0.112	0.047	0.207	0.148
pgp2n.pk004.a23	NP_000814	VIPR1	Growth hormone-releasing hormone receptor precursor (GHRH receptor)	-0.197	-0.194	-0.187	-0.101	0.058	-0.171	0.011	-0.087	0.013	0.302	0.164
pgf2n.pk001.o17	NP_006639		similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens]	-0.243	-0.325	-0.370	-0.161	0.012	-0.221	-0.187	-0.034	0.018	0.090	0.737
pgm2n.pk011.l14	XP_032181	ADAMTSL3	similar to thrombospondin like [Homo sapiens]	-0.354	-0.321	-0.388	-0.110	-0.097	-0.095	-0.095	-0.175	0.003	0.564	0.086
pgf2n.pk002.h3	NP_055976	ARL6IP1	ADP-ribosylation-like factor 6 interacting protein [Mus musculus]	-0.197	-0.226	-0.284	-0.050	0.060	-0.055	-0.092	-0.019	0.030	0.434	0.744
pco1c.pk001.p9	NP_892009		helicase [Homo sapiens]	-0.182	-0.179	-0.162	0.038	0.075	-0.058	0.085	-0.046	0.033	0.594	0.183
pgp2n.pk003.d14	NP_061847	UNC93A	BcDNA:GH10120 gene product [Drosophila melanogaster]	-0.160	-0.120	-0.102	-0.126	0.100	-0.173	-0.079	-0.029	0.017	0.114	0.014
pgp1n.pk006.f7	NP_003370	VIL2	ezrin [Gallus gallus]	-0.221	-0.237	-0.297	-0.164	0.039	-0.255	-0.180	0.007	0.016	0.042	0.264
pgl1n.pk012.d17	NP_659494	JUND	proline-rich protein - mouse (fragment)	-0.173	-0.157	-0.149	-0.003	0.088	-0.205	-0.135	-0.087	0.327	0.027	0.020
pgr1n.pk007.n6			No Hits Found	-0.013	0.075	0.033	0.218	0.248	0.147	0.148	0.089	0.064	0.747	0.023
pgm2n.pk012.p16	NP_064695	AKR1B10	aldo-keto reductase [Gallus gallus]	-0.327	-0.328	-0.367	-0.193	-0.064	-0.296	-0.136	0.061	0.014	0.125	0.663
pgf2n.pk001.e22	NP_835227	FAM134C	similar to RIKEN cDNA 1300010M03 [Homo sapiens]	-0.069	0.023	-0.036	0.043	0.194	-0.042	-0.014	-0.153	0.894	0.414	0.030
pgf2n.pk005.g6	NP_004721	ETF1	eukaryotic translation termination factor 1 [Homo sapiens]	-0.066	-0.030	-0.087	-0.089	0.198	-0.097	-0.124	-0.045	0.196	0.021	0.023
pgf1n.pk012.c5			No Hits Found	-0.269	-0.234	-0.248	-0.058	-0.001	-0.063	-0.083	-0.060	0.003	0.351	0.181
pgp1n.pk005.a17	NP_870988		hypothetical protein XP_110476 [Mus musculus]	-0.549	-0.206	-0.228	0.130	-0.280	0.060	0.198	0.124	0.039	0.013	0.574
pgm2n.pk012.e21			No Hits Found	-0.292	-0.210	-0.424	-0.130	-0.022	-0.232	-0.191	-0.283	0.148	0.260	0.033
pgp2n.pk002.j13	NP_055984		KIAA0112 [Homo sapiens]	-0.486	-0.179	-0.361	-0.132	-0.215	0.073	-0.045	0.100	0.029	0.179	0.995
pgp1n.pk006.c7	NP_006463	TXNIP	VDUP1 [Homo sapiens]	-0.070	0.016	0.033	-0.049	0.202	0.092	-0.030	0.041	0.016	0.392	0.026
pgf1n.pk009.c24	XP_370782		Ig gamma chain (clone 36) - chicken (fragment)	-0.222	-0.116	-0.126	-0.029	0.050	-0.174	-0.107	-0.113	0.389	0.621	0.027
pgp1n.pk002.h9	NP_037366	EIF3S12	muscle specific gene [Homo sapiens]	-0.417	-0.268	-0.383	0.015	-0.145	-0.067	0.090	-0.027	0.013	0.179	0.196
pgm1c.pk001.f22	NP_803883		putative sweet taste receptor T1R1 [Mus musculus]	-0.281	-0.171	-0.254	-0.144	-0.008	-0.277	-0.210	-0.220	0.386	0.354	0.007
pgm2n.pk011.p9	NP_077728		NADPH:adrenodoxin oxidoreductase, mitochondrial precursor	-0.324	-0.139	-0.326	-0.101	-0.051	-0.071	0.013	-0.072	0.002	0.416	0.104
pgf2n.pk004.p11	XP_374604		T cell receptor gamma	-0.032	0.086	0.128	-0.079	0.241	0.002	-0.059	0.075	0.414	0.468	0.008
pgf1n.pk004.i16	NP_004860	VPS4B	SKD1 [Mus musculus]	-0.322	-0.258	-0.273	-0.100	-0.048	-0.190	-0.059	-0.109	0.012	0.371	0.180
pgf2n.pk004.g15	NP_001815	CKM	CREATINE KINASE, M CHAIN (M-CK)	-0.307	-0.197	-0.379	-0.080	-0.032	-0.129	-0.099	-0.129	0.029	0.493	0.179
pgr1n.pk002.h16	NP_055026	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi [Homo sapiens]	-0.099	-0.054	-0.086	0.091	0.178	0.048	0.049	-0.045	0.035	0.761	0.015
pft1c.pk002.b4	NP_055944		septin 6 isoform B [Homo sapiens]	-0.176	-0.021	-0.107	-0.140	0.101	-0.146	-0.149	-0.065	0.295	0.540	0.027
pgm2n.pk013.f23		EMP1	No Hits Found	-0.465	-0.296	-0.150	-0.118	-0.186	-0.251	-0.464	-0.083	0.858	0.104	0.036
pgr1n.pk003.d9	NP_705842		heat shock protein 40 [Ciona intestinalis]	-0.296	-0.147	-0.289	-0.033	-0.017	-0.074	-0.046	-0.106	0.022	0.526	0.093
pgf2n.pk004.l17	NP_005868		splicing factor 3a, subunit 1, 120kDa [Homo sapiens]	-0.553	-0.452	-0.410	0.043	-0.271	0.018	0.065	-0.157	0.035	0.217	0.131
pft1c.pk002.f5	XP_371707		No Hits Found	-0.183	-0.188	-0.178	-0.044	0.098	-0.150	-0.086	-0.047	0.009	0.047	0.049
pgf2n.pk001.c14	NP_387448	UTP15	unnamed protein product [Homo sapiens]	-0.033	-0.191	-0.190	-0.395	0.249	0.010	-0.093	-0.114	0.003	0.007	0.649
pgf1n.pk010.o14	NP_115825	CC2D1B	KIAA1836 protein [Homo sapiens]	-0.552	-0.331	-0.229	-0.078	-0.270	-0.084	-0.005	-0.037	0.001	0.001	0.263
pgp2n.pk008.p5	NP_006202	PENK	proenkephalin [Homo sapiens]	-0.226	-0.416	-0.245	-0.039	0.059	0.153	nd	-0.027	0.049	0.943	0.276
pgr1n.pk003.n11	NP_620132	MRRF	RIKEN cDNA 2400002D02 [Mus musculus]	0.112	0.151	0.157	0.057	0.397	0.129	0.114	0.167	0.044	0.095	0.033
pgp2n.pk005.c11	NP_073624	NMNAT1	NMN adenylyltransferase [Mus musculus]	-0.062	-0.465	-0.726	-0.315	0.223	-0.180	-0.175	-0.162	0.003	0.003	0.431
pgm2n.pk006.o12	NP_001157	BIRC2	IAP homolog [Gallus gallus]	-0.022	0.109	-0.017	0.171	0.264	0.147	0.244	0.150	0.039	0.954	0.246
pgf1n.pk009.l5	NP_079104	C9orf82	hypothetical protein FLJ13657 [Homo sapiens]	-0.265	0.013	-0.195	0.049	0.023	-0.034	0.065	0.039	0.034	0.189	0.073
pgf1n.pk003.p2	NP_004459	FHL3	Similar to four and a half LIM domains 3 [Homo sapiens]	-0.266	-0.185	-0.270	-0.030	0.023	-0.129	-0.075	-0.063	0.027	0.368	0.169
pgm2n.pk006.a3			No Hits Found	-0.268	-0.144	-0.238	-0.044	0.021	-0.160	-0.195	-0.149	0.235	0.231	0.025
pgf1n.pk001.a12	NP_064530	SH3GLB2	SH3-containing protein SH3GLB2 [Mus musculus]	-0.156	-0.053	-0.162	0.053	0.133	0.149	0.001	0.006	0.027	0.458	0.334
pgm2n.pk008.b13	NP_071942	MRPS25	FLJ00023 protein [Homo sapiens]	-0.281	-0.226	-0.298	-0.095	0.010	-0.119	-0.054	-0.079	0.027	0.792	0.480
pnfb.pk0002.d5			lacZ alpha peptide	-0.459	-0.245	-0.058	0.026	-0.165	-0.109	-0.092	-0.027	0.072	0.002	0.049
pgr1n.pk008.j23	NP_787103	ZADH2	similar to NADPH oxidoreductase homolog [Homo sapiens]	0.001	0.020	-0.040	0.049	0.298	0.035	0.114	0.054	0.007	0.148	0.052
pgm2n.pk014.e16	NP_055467	IPO13	importin 13 [Homosapiens]	-0.384	-0.071	-0.273	-0.093	-0.084	-0.003	-0.075	-0.030	0.046	0.227	0.625
pgf1n.pk008.i10	NP_001859	CPA1	preprocarboxypeptidase A [Gallus gallus]	-0.355	-0.316	-0.415	-0.181	-0.054	-0.300	-0.233	-0.155	0.006	0.041	0.095
pgm2n.pk005.p14	NP_003272	TNNI1	troponin I slow skeletal muscle isoform	-0.058	-0.005	0.011	0.110	0.245	0.079	0.064	0.089	0.046	0.691	0.143
pgf2n.pk005.e12	NP_008964	RER1	RIKEN cDNA 1110060F11 [Mus musculus]	0.134	0.146	0.024	-0.002	0.437	-0.014	-0.024	0.028	0.567	0.007	0.040
pgf2n.pk001.l3	NP_005915	MEOX2	MOX-2 protein [Gallus gallus]	-0.138	0.021	-0.175	-0.036	0.166	-0.039	-0.115	0.003	0.069	0.091	0.048
pgp2n.pk005.a17			No Hits Found	-0.133	-0.111	-0.178	-0.289	0.174	0.196	-0.124	-0.148	0.033	0.136	0.669
pgm2n.pk011.n24	NP_892118		Unknown (protein for MGC:37636) [Mus musculus]	-0.304	-0.294	-0.499	-0.154	0.004	-0.230	-0.066	-0.173	0.025	0.543	0.176
pgr1n.pk004.p14		ANKAR	SI:dZ72B14.6 (novel glycoprotease) [Danio rerio]	-0.230	-0.099	-0.183	-0.017	0.079	-0.037	-0.024	-0.026	0.001	0.477	0.028
pgr1n.pk005.n15	NP_067627		small-conductance calcium-activated potassium channel [Gallus gallus]	0.002	0.059	0.003	0.152	0.313	0.212	0.213	0.106	0.011	0.948	0.168
pgm2n.pk012.e5	NP_036453		glycine-rich protein [Homo sapiens]	-0.369	-0.213	-0.300	0.010	-0.057	-0.102	-0.052	0.102	0.029	0.115	0.739
pgf1n.pk002.f12	NP_002191		interferon regulatory factor 5 isoform b [Homo sapiens]	-0.234	-0.122	-0.160	-0.108	0.078	-0.150	-0.269	-0.118	0.376	0.194	0.015
pgp2n.pk007.o4	NP_849196	SERINC2	Unknown (protein for MGC:25877) [Mus musculus]	-0.062	-0.067	-0.062	-0.164	0.257	-0.084	-0.116	0.075	0.025	0.043	0.029
pgp1n.pk002.o23	NP_038463	RAX	homeobox transcription factor RAX1 [Gallus gallus]	-0.519	-0.277	-0.395	0.112	-0.199	-0.089	0.166	0.060	0.024	0.048	0.246
pgr1n.pk008.p16			No Hits Found	-0.184	-0.159	-0.140	-0.021	0.138	-0.074	-0.175	-0.075	0.081	0.164	0.030
pgf2n.pk001.n16	NP_005497	SCARB2	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2	-0.170	-0.116	0.004	0.087	0.151	0.068	0.073	0.115	0.003	0.261	0.135
pnlb.pk0001.d5	NP_000761	CYP2C8	cytochrome P-450 [Gallus gallus]	-0.315	-0.264	-0.531	-0.348	0.013	-0.231	nd	-0.120	0.044	0.252	0.322
pgm2n.pk007.i8	NP_057671		chromobox protein (CHCB2) [Gallus gallus]	-0.204	-0.134	-0.112	0.057	0.130	0.064	0.074	0.034	0.019	0.815	0.354
pgf2n.pk005.c6	NP_037528	USP25	unnamed protein product [Homo sapiens]	-0.068	0.022	0.026	-0.146	0.271	-0.169	-0.134	-0.027	0.620	0.078	0.006
pgm2n.pk011.b11	NP_060829	C4orf20	hypothetical protein FLJ11200 [Homo sapiens]	-0.421	-0.219	-0.315	-0.070	-0.081	-0.132	-0.030	-0.122	0.028	0.505	0.203
pgm1n.pk001.a19	NP_005954	MYH1	fast myosin heavy chain isoform 2 [Gallus gallus]	-0.209	-0.240	-0.266	-0.048	0.131	-0.239	-0.026	-0.118	0.047	0.137	0.081
pgm2n.pk006.p4	NP_006166	NRAP	hypothetical protein [Homo sapiens]	0.012	0.040	-0.024	-0.182	0.354	-0.092	-0.145	-0.027	0.232	0.002	0.006
pgf2n.pk002.p2	NP_001389	ECH1	Unknown (protein for MGC:19561) [Homo sapiens]	-0.422	-0.157	-0.395	-0.005	-0.079	0.041	-0.013	-0.079	0.038	0.337	0.334
pgr1n.pk001.f24	NP_005251	GDF9	growth differentiation factor 9 precursor [Homo sapiens]	0.131	0.127	0.086	0.237	0.474	0.437	0.222	0.259	0.016	0.456	0.384
pgf2n.pk005.o4	NP_004170	TPH1	Tryptophan 5-monooxygenase (Tryptophan 5-hydroxylase)	-0.301	-0.269	-0.272	-0.115	0.043	-0.145	-0.115	-0.105	0.007	0.509	0.207
pgf2n.pk004.i19			ORF2 [Platemys spixii]	-0.137	-0.155	-0.112	-0.108	0.218	-0.161	-0.091	-0.136	0.039	0.009	0.006
pgp2n.pk007.h12	NP_061720	DNAH1	dynein heavy chain isotype 6 - sea urchin (Tripneustes gratilla)	0.027	0.071	0.022	-0.046	0.392	-0.056	-0.064	0.070	0.233	0.036	0.024
pgp1n.pk007.e22	NP_002056		GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)	-0.359	-0.214	-0.182	-0.219	0.007	-0.112	-0.158	-0.004	0.034	0.884	0.400
pgp1c.pk002.l20	NP_066961	TRAF2	Tnf receptor-associated factor 2 [Mus musculus]	-0.358	0.085	-0.453	0.143	0.018	0.040	-0.105	-0.166	0.267	0.046	0.015
pgm2n.pk007.o17	NP_056212	WDR40A	KIAA1892 protein [Homo sapiens]	-0.333	-0.123	-0.347	-0.136	0.044	-0.054	-0.049	-0.075	0.006	0.670	0.239
pgf1n.pk003.d3	NP_776194	SCARA5	RIKEN cDNA 4933425F03 [Mus musculus]	-0.491	-0.348	-0.528	-0.244	-0.108	-0.106	-0.274	-0.270	0.008	0.379	0.236
pgf2n.pk002.l24	NP_005713	ACTR2	ACTIN-LIKE PROTEIN 2 (ACTIN-LIKE PROTEIN ACTL)	-0.398	-0.277	-0.215	-0.129	-0.014	-0.190	-0.075	-0.036	0.024	0.366	0.557
pgp2n.pk009.i6			No Hits Found	-0.216	-0.026	-0.106	-0.100	0.174	-0.309	-0.218	-0.040	0.855	0.435	0.036
pgp1n.pk001.p5			No Hits Found	-0.432	-0.295	-0.408	-0.403	-0.026	-0.239	-0.347	-0.051	0.017	0.599	0.207
pgp2n.pk002.e6	NP_002862	RABIF	guanine-nucleotide-releasing protein Mss4 - human	-0.654	-0.398	-0.285	-0.047	-0.238	-0.019	-0.041	0.096	0.017	0.090	0.829
pgf1n.pk006.d13	NP_006222	POLE	DNA-directed DNA polymerase epsilon catalytic chain A	-0.001	-0.058	-0.238	-0.098	0.424	-0.194	-0.149	-0.080	0.167	0.004	0.040
pgr1c.pk001.c8	NP_065965	RNF213	FLJ00039 protein [Homo sapiens]	-0.354	-0.164	-0.162	-0.062	0.074	-0.139	-0.248	-0.177	0.350	0.743	0.037
pgp1n.pk004.b14	NP_000465	TWIST1	cTwist [Gallus gallus]	-0.350	-0.309	-0.200	-0.128	0.084	-0.129	-0.143	-0.128	0.016	0.699	0.141
pgm2n.pk007.o18	NP_061978		No Hits Found	-0.313	-0.187	-0.164	-0.194	0.162	-0.268	-0.209	0.096	0.005	0.051	0.003
pgp1c.pk003.c1	NP_000343	ABCC8	Sulfonylurea receptor 1	-0.738	-0.587	-0.580	0.198	-0.127	0.121	0.271	0.023	0.033	0.445	0.395

Supplemental Table 3a. The number of up-regulated and down-regulated genes in the FL and LL at week 1 or week 3, according to GO biological process

Line	Up-regulated		Down-regulated	
	Wk 1	Wk 3	Wk 1	Wk 3
FL *vs*. LL	427	321	325	144
Transcription – DNA dependent	31	22	19	12
signal transduction	29	18	15	6
transcription	24	17	15	11
protein biosynthesis	12	12	17	2
transport	15	9	15	10
biological process unknown	17	4	11	9
metabolism	9	4	10	2
carbohydrate metabolism	4	5	4	1
lipid metabolism	5	4	4	2
glycolysis	0	4	5	0

*Gene numbers represent genes obtained using a P-value < 0.05.

Supplemental Table 3b. The number of up-regulated and down-regulated genes in the FL and LL at week 5 or week 7, according to GO biological process

Line	Up-regulated		Down-regulated	
	Wk 5	Wk 7	Wk 5	Wk 7
FL *vs*. LL	372	160	266	223
Transcription – DNA dependent	23	11	17	15
signal transduction	24	7	10	11
protein biosynthesis	8	3	11	12
transport	14	10	13	9
biological process unknown	12	9	10	9
metabolism	5	5	10	4
carbohydrate metabolism	6	4	3	3
lipid metabolism	5	4	3	2
glycolysis	2	0	3	4

*Gene numbers represent genes obtained using a P-value < 0.05.

Supplemental Table 4. Differentially expressed genes specifically expressed in neurons, astrocytes or oligodendrocytes.

Neuron	**Atrocyte**	**Oligo**
PPA1	TM9SF2	ERO1L
NEFL	SLC12A4	SEPT8
MAPK1	PPIG	TPM1
ATP1A3	PVGB	TIMP2
VSNL1	SPAG1	ZYX
CDC42	FDXR	YIF1A
EGFL7	AGT	TXNL1
STMN1	ANAPC2	CYP27A1
ATP10A	AIFM1	PKP4
TUBB5	SEC14L2	ADH1
SULT4A1	PITRM1	ENPP3
GAP43	CFLAR	CDYL
HN1	ANK2	
PCBP2	SRC	
TPM3	OGT	
GLE1	DUSP1	
TUBB3	DUSP6	
CHGB	FGFR3	
ATP1A3	PLA2G3	
SPOCK2	HSD17B4	
	HSPA4	
	AHCYL1	
	ARID5A	
	AGFBP2	

Supplemental Table 5. Gene Ontology (GO) analysis for cluster 17

Biological Process	# of Genes	Gene Name
Protein Biosynthesis	5	Seryl-tRNA synthetase **Eukaryotic translation EF1α** Ribosomal protein L17 Ribosomal protein L35A Ribosomal protein L26
Regulation of transcription DNA dependent	5	non-POU domain containing Calreticulin multiple endocrine neoplasia 1 PQBP-1b/c TSC-22
G-protein receptor Signaling	3	G protein-coupled receptor 123 Amyloid-like protein 2 precursor tubulin beta 3
Proteolysis	2	*ADAM 12* F-box only protein 3
Protein Polymerization	3	tubulin alpha 1 tubulin beta 3 tubulin beta 5
Protein Folding	2	Calreticulin Calnexin
Glycolysis	2	**Phosphoglycerate mutase 1** **Neural enolase**
Carbohydrate Metabolism	1	*Klotho secreted isoform*
Metabolism	3	**Phosphoglycerate mutase 1** Phospholipid-transporting ATPase Retinol dehydrogenase 11
Intracellular protein transport	3	Golgi SNAP receptor complex **Soluble NSF-attchment protein alpha** adaptor-related protein complex 2
Cell adhesion	3	*ADAM 12* Beta-amyloid precursor protein Glucose Regulated Protein, 95-KD (Grp94)
Microtubule-based movement	3	tubulin alpha 1 tubulin beta 3 tubulin beta 5

Bold denotes qPCR verification for microarray data. *Italic* denotes a homologues gene associated with the development of obesity.

Supplemental Table 6

Pathway Name	Gene Name	Accession
KEGG		
Glycolysis / Gluconeogenesis		
	ENO2	NP_001966
	PGK1	NP_000282
	HK1	NP_000179
	GPI	NP_000166
	PGAM1	NP_002620
ATP synthesis		
	ATP6V1B2	NP_001684
	ATP6V1C1	NP_001686
Starch and sucrose metabolism		
	HK1	NP_000179
	GPI	NP_000166
Oxidative phosphorylation		
	ATP6V1B2	NP_001684
	ATP6V1C1	NP_001686
Glycine, serine and threonine metabolism		
	SARS	NP_006504
	PHGDH	NP_006614
Nicotinate and nicotinamide metabolism		
	NMNAT1	NP_073624
Pyrimidine metabolism		
	POLE	NP_006222
Metabolism of xenobiotics by cytochrome P450		
	GSTA5	NP_714543
Glycerophospholipid metabolism		
	PCYT1A	NP_005008
Carbon fixation		
	PGK1	NP_000282
Aminosugars metabolism		
	HK1	NP_000179
Pentose phosphate pathway		
	GPI	NP_000166
Aminophosphonate metabolism		
	PCYT1A	NP_005008
Phenylalanine, tyrosine and tryptophan biosynthesis		
	ENO2	NP_001966
Glycosphingolipid metabolism		
	SPHK1	NP_068807
Selenoamino acid metabolism		
	SEPHS2	NP_036380
Galactose metabolism		
	HK1	NP_000179
Fructose and mannose metabolism		
	HK1	NP_000179
Streptomycin biosynthesis		
	HK1	NP_000179
Purine metabolism		

	POLE	NP_006222
Glutathione metabolism		
	GSTA5	NP_714543
Cholera - Infection		
	ATP6V1C1	NP_001686
	ERO1L	NP_055399
Wnt signaling pathway		
	FBXW11	NP_387448
	PPP2CB	NP_004147
Antigen processing and presentation		
	CALR	NP_004334
	CANX	NP_001737
MAPK signaling pathway		
	STMN1	NP_005554
	IL1B	NP_000567
Gap junction		
	TUBB	NP_821133
	TUBB3	NP_006077
Toll-like receptor signaling pathway		
	IL1B	NP_000567
Axon guidance		
	DPYSL2	NP_001377
Cell cycle		
	YWHAG	NP_036611
Focal adhesion		
	COL3A1	NP_000081
Neurodegenerative Disorders		
	APP	NP_958816
TGF-beta signaling pathway		
	PPP2CB	NP_004147
VEGF signaling pathway		
	SPHK1	NP_068807
Ubiquitin mediated proteolysis		
	FBXW11	NP_387448
Ribosome		
	RPL7A	NP_000963
Hematopoietic cell lineage		
	IL1B	NP_000567
DNA polymerase		
	POLE	NP_006222
Type II diabetes mellitus		
	ABCC8	NP_000343
SNARE interactions in vesicular transport		
	GOSR1	NP_004862
Long-term depression		
	PPP2CB	NP_004147
Proteasome		
	PSMB6	NP_002789
Tight junction		
	PPP2CB	NP_004147
ABC transporters - General		
	ABCC8	NP_000343

Cytokine-cytokine receptor interaction		
	IL1B	NP_000567
Apoptosis		
	IL1B	NP_000567
Aminoacyl-tRNA biosynthesis		
	SARS	NP_006504
ECM-receptor interaction		
	COL3A1	NP_000081
Alzheimer's disease		
	APP	NP_958816
Type I diabetes mellitus		
	IL1B	NP_000567
Hedgehog signaling pathway		
	FBXW11	NP_387448
Calcium signaling pathway		
	SPHK1	NP_068807
Cell Communication		
	COL3A1	NP_000081
BIOCARTA		
Glycolysis Pathway		
	PGK1	NP_000282
	HK1	NP_000179
	GPI	NP_000166
	PGAM1	NP_002620
Feeder Pathways for Glycolysis		
	HK1	NP_000179
Biosynthesis of Cysteine in mammals		
	PHGDH	NP_006614
Malate-aspartate shuttle		
	SLC25A1	NP_005975
Phosphatidylcholine Biosynthesis Pathway		
	PCYT1A	NP_005008
Shuttle for transfer of acetyl groups from mitochondria to the cytosol		
	SLC25A1	NP_005975
Biosynthesis of Glycine and Serine		
	PHGDH	NP_006614
NFAT and Hypertrophy of the heart (Transcription in the broken heart)		
	CALR	NP_004334
	AGT	NP_000020
Inhibition of Matrix Metalloproteinases		
	TIMP2	NP_003246
Msp/Ron Receptor Signaling Pathway		
	IL1B	NP_000567
Bioactive Peptide Induced Signaling Pathway		
	AGT	NP_000020
Phospholipids as signalling intermediaries		
	SPHK1	NP_068807
Generation of amyloid b-peptide by PS1		
	APP	NP_958816

Angiotensin-converting enzyme 2 regulates heart function		
	AGT	NP_000020
Rab GTPases Mark Targets In The Endocytotic Machinery		
	RAB3A	NP_002857
Platelet Amyloid Precursor Protein Pathway		
	APP	NP_958816
Deregulation of CDK5 in Alzheimers Disease		
	APP	NP_958816
Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy		
	AGT	NP_000020
IL 5 Signaling Pathway		
	IL1B	NP_000567
Proteasome Complex		
	PSMB6	NP_002789
Stathmin and breast cancer resistance to antimicrotubule agents		
	STMN1	NP_005554
CDK Regulation of DNA Replication		
	CDT1	NP_112190
IL 4 signaling pathway		
	IL1B	NP_000567
Antigen Processing and Presentation		
	PSMB6	NP_002789
NFkB activation by Nontypeable Hemophilus influenzae		
	IL1B	NP_000567
Gamma-aminobutyric Acid Receptor Life Cycle		
	NSF	NP_006169
Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling		
	AGT	NP_000020
ERassociated degradation (ERAD) Pathway		
	CANX	NP_001737
Signal transduction through IL1R		
	IL1B	NP_000567
GENMAPP		
Hs_Glycolysis_and_Gluconeogenesis		
	ENO2	NP_001966
	HK1	NP_000179
	GPI	NP_000166
Hs_Acetylcholine_Synthesis		
	PCYT1A	NP_005008
Hs_Glycogen_Metabolism		
	PPP2CB	NP_004147
Hs_Prostaglandin_synthesis_regulation		
	S100A10	NP_002957
Hs_Cell_cycle_KEGG		
	CALR	NP_004334
	YWHAG	NP_036611
	PRKD1	NP_002733

Hs_Smooth_muscle_contraction		
	IL1B	NP_000567
	YWHAG	NP_036611
	PRKD1	NP_002733
Hs_Nuclear_Receptors		
	FUS	NP_004951
	HNRPC	NP_112604
	SF3A1	NP_005868
Hs_DNA_replication_Reactome		
	POLE	NP_006222
	CDT1	NP_112190
Hs_Circadian_Exercise		
	TUBB3	NP_006077
	PPP2CB	NP_004147
Hs_GPCRDB_Class_A_Rhodopsin-like		
	RTKN	NP_149035
Hs_Translation_Factors		
	EEF1A2	NP_001949
Hs_Ribosomal_Proteins		
	NSF	NP_006169
Hs_Inflammatory_Response_Pathway		
	COL3A1	NP_000081
Hs_ACE-Inhibitor_pathway_PharmGKB		
	AGT	NP_000020
Hs_Wnt_signaling		
	PRKD1	NP_002733
Hs_Proteasome_Degradation		
	PSMB6	NP_002789
Hs_G_Protein_Signaling		
	PRKD1	NP_002733
Hs_S1P_Signaling		
	SPHK1	NP_068807
Hs_G1_to_S_cell_cycle_Reactome		
	POLE	NP_006222

Supplemental Table 7. Annotations for network predicted by Ingenuity Pathway Analysis presented in Figure 4.

Symbol	Entrez Gene Name	Entrez Protein ID (human)	Log Ratio (FL/LL)
AAK1	AP2 associated kinase 1		
ALDOC	aldolase C, fructose-bisphosphate	NP_005156	-0.24
Androgen-AR			
ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	NP_075526	0.14
AP2A1	adaptor-related protein complex 2, alpha 1 subunit		
AP2B1	adaptor-related protein complex 2, beta 1 subunit		
AP2M1	adaptor-related protein complex 2, mu 1 subunit	NP_004059	-0.24
BID	BH3 interacting domain death agonist		
CAPN1	calpain 1, (mu/I) large subunit		
CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	NP_005178	0.22
CBS	cystathionine-beta-synthase	NP_000062	0.16
CLINT1	clathrin interactor 1		
Creb			
DLG4	discs, large homolog 4 (Drosophila)		
DPYSL2	dihydropyrimidinase-like 2	NP_001377	-1.00
EDF1	endothelial differentiation-related factor 1	NP_003783	-0.36
ENO2	enolase 2 (gamma, neuronal)	NP_001966	-0.64
ENSA	endosulfine alpha		
EPN2	epsin 2		
EPS15	epidermal growth factor receptor pathway substrate 15		
FXYD5	FXYD domain containing ion transport regulator 5	NP_054883	0.20
GCC1	GRIP and coiled-coil domain containing 1	NP_078799	-0.11
GPI	glucose phosphate isomerase	NP_000166	-0.54
Gsk3			
HISTONE			
HK1	hexokinase 1	NP_000179	-0.54
Hsp70			
HTT	huntingtin		
IL12			
Insulin			
Interferon alpha			
IRF5	interferon regulatory factor 5	NP_002191	0.31
L-glutamic acid			
LSAMP	limbic system-associated membrane protein	NP_002329	0.08
MARCO	macrophage receptor with collagenous structure	NP_006761	0.17
MCRS1	microspherule protein 1	NP_006328	0.25
MEA1	male-enhanced antigen 1	NP_055438	0.19
MEN1	multiple endocrine neoplasia I	NP_570711	-0.57
MYBPC2	myosin binding protein C, fast type		
NAPB	N-ethylmaleimide-sensitive factor attachment protein, beta	NP_071363	-0.60
NLGN3	neuroligin 3	NP_061850	0.19
NMNAT1	nicotinamide nucleotide adenylyltransferase 1	NP_073624	0.29
PACS2	phosphofurin acidic cluster sorting protein 2	NP_056012	0.10
PDGF BB			
Phosphocreatine			
Pka			
Pka catalytic subunit			
Pkc(s)			
Proteasome			
PTRF	polymerase I and transcript release factor	NP_036364	-0.48
RNF213	ring finger protein 213	NP_065965	0.43
SDH			
SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	NP_002991	-0.20
SET	SET nuclear oncogene	NP_003002	-0.46
SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1	NP_115667	-0.79
SLBP	stem-loop binding protein	NP_006518	0.23
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3		
SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	NP_005975	0.13
SLC25A22	solute carrier family 25 (mitochondrial carrier: glutamate), member 22		
SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	NP_002626	-0.36
ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	NP_008858	0.19
STON1-GTF2A1L	STON1-GTF2A1L readthrough transcript		
STON2	stonin 2		
SYN2	synapsin II	NP_003169	-0.52
TAS1R1	taste receptor, type 1, member 1	NP_803883	0.27
TAS1R3	taste receptor, type 1, member 3		
TRIM37	tripartite motif-containing 37	NP_056109	-0.26
TRIOBP	TRIO and F-actin binding protein	NP_008963	0.13
UFSP2	UFM1-specific peptidase 2	NP_060829	0.34
VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	NP_004729	-0.28

Supplemental Table 8. Genes identified in the microarray with related genes in knockout or transgenic mice leading to obesity.

Clone ID	**GenBank Accession #**	**Microarray Gene (chicken)**	**Microarray Expression (chicken)**	**Knockout/ Transgenic Gene (mouse)**	**Phenotype (mouse)**
pgf2n.pk006.k5	BM427410	Transmembrane protein induced by TNFα (*TMEM120A*)	FL ↑	TNFα over-expression	obese
pgp2n.pk004.a23	BM490642	GHRH-Receptor (*GHRH-R*)	LL ↓	GHRH knockout	obese
pgf1n.pk010.k1	BI067093	Metalo-peptidase 1 (*PITRM1*)	LL ↓	ADAMS TS knockout	lean
pgr1n.pk006.l9	CD218118	CEBP zeta (*CEBPZ*)	LL ↓	CEBP alpha knockout	lean

Supplemental Table 9. Marker analysis for similarities in gene expression profiles of selected genes. Expression profiles for genes denoted in bold were confirmed by qRT-PCR.

Marker selection analysis for Neural Enolase

Gene Name	Spot	Score
Neural enolase	13011	0
malignant liposarcoma	6875	0.01
klotho secreted isoform	3653	0.02
PP2A-alpha	3986	0.02
ACTIN, CYTOPLASMIC TYPE 5	4161	0.02
No Hits Found_20	15371	0.02
Sodium pump 3_1	2045	0.02
RNA-binding protein FUS	16410	0.03
beta-amyloid precursor	3906	0.03
eukaryotic translation elongation factor 1_1	16106	0.03
Regulatory protein TSC-22	5214	0.03
unnamed protein product	3853	0.03
synapsin Iib	14818	0.03
EST H08032.1	13326	0.03
tubulin, beta 5	2954	0.03
Unknown protein_3	17661	0.03
endocrine neoplasia 1	12899	0.03
vesicle associated protein	5128	0.03
No Hits Found_116	14562	0.04
No Hits Found_56	12987	0.04
transcription elongation factor B	1676	0.04
PQBP-1b/c	3258	0.04
similar to phosphoglycerate mutase	6482	0.04
tubulin, beta	9603	0.05
ADAM 12	17139	0.05
POL-like	15506	0.05
phosphoglucose isomerase	73	0.05
tetraspan 3	17122	0.05
No Hits Found_68	7604	0.05
beta-amyloid precursor	9607	0.05
Amyloid-like protein 2	12582	0.05
Dihydropyrimidinase related protein-2	12821	0.05
alpha 1 type III collagen	5511	0.06
similar to hypothetical protein_1	8410	0.06
gamma-synergin	14853	0.06
No Hits Found_47	5021	0.06
hexokinase1	10230	0.06
retinoblastoma tumor suppressor	9201	0.06
ubiquitin-like 3	18010	0.06
SNARE	10056	0.06
similar to Amyloid beta A4	1900	0.06
serum deprivation response protein	13473	0.06
unnamed protein product _6	16147	0.07
vesicular fusion protein NSF	9664	0.07
SET protein	11620	0.07
KIAA0605 gene product	13929	0.07
Similar to macropain	13235	0.07
Sodium pump 3	8105	0.07
fusion protein attachment protein	8244	0.07
Fas-ligand associated factor 3	7452	0.07

Marker selection analysis for hexokinase 1

Gene Name	Spot	Score
hexokinase1	10230	0
gamma-synergin	14853	0.01
beta-amyloid precursor	3906	0.02
Ubiquitin thiolesterase 1	13281	0.02
NDRG	4966	0.02
vesicular fusion protein NSF	9664	0.02
Dihydropyrimidinase related protein-2	12821	0.02
No Hits Found_20	15371	0.03
adenosinetriphosphatase	13232	0.03
valosin-containing protein	1746	0.03
tubulin, beta 5	2954	0.03
LEP100 protein	14458	0.03
ubiquitin-like 3	18010	0.04
ERO1-like	9129	0.04
nuclear ribonucleoprotein L	11670	0.04
EGF-response factor 2	16446	0.04
SNAP-beta	16210	0.04
Sodium pump 3_1	2045	0.05
klotho secreted isoform	3653	0.05
Dynactin	16239	0.05
unnamed protein product_17	6569	0.05
synapsin Iib	14818	0.05
phosphate carrier protein	12265	0.06
unnamed protein product _6	16147	0.06
transcription elongation factor B	1676	0.06
Neural enolase	13011	0.06
Unknown protein_5	1831	0.06
retinoblastoma tumor suppressor	9201	0.06
phosphoglucose isomerase	73	0.07
Similar to macropain	13235	0.07
nuclear distribution gene C	17031	0.07
QkI-2	16051	0.07
Selenophosphate synthetase 2	13258	0.07
unnamed protein product	3853	0.07
sphingosine kinase 1	3703	0.07
ACTIN, CYTOPLASMIC TYPE 5	4161	0.07
unnamed protein product _12	2170	0.07
POL-like	15506	0.07
unnamed protein product	15622	0.07
endocrine neoplasia 1	12899	0.08
ankyrin repeat and SOCS box protein	14767	0.08
Sodium pump 3	8105	0.08
SET protein	11620	0.08
KIAA0605 gene product	13929	0.08
EST H08032.1	13326	0.08
tetraspan 3	17122	0.08
malignant liposarcoma	6875	0.08
similar to phosphoglycerate mutase	6482	0.09
No Hits Found_68	7604	0.09
similar to Eferin	15094	0.09

Marker selection analysis for phosphoglucose isomerase

Gene Name	Spot	Score
phosphoglucose isomerase	73	0
tetraspan 3	17122	0.01
retinoblastoma tumor suppressor	9201	0.02
ACTIN, CYTOPLASMIC TYPE 5	4161	0.02
nuclear distribution gene C	17031	0.02
endocrine neoplasia 1	12899	0.02
ADAM 12	17139	0.02
tubulin, beta 5	2954	0.03
Similar to macropain	13235	0.03
unnamed protein product	3853	0.03
LEP100 protein	14458	0.04
beta-amyloid precursor	3906	0.04
ubiquitin-like 3	18010	0.04
No Hits Found_116	14562	0.04
eukaryotic translation elongation factor 1_1	16106	0.05
ERO1-like	9129	0.05
POL-like	15506	0.05
Neural enolase	13011	0.05
EST H08032.1	13326	0.05
vesicle associated protein	5128	0.05
Similar to hypothetical protein	14095	0.05
Dihydropyrimidinase related protein-2	12821	0.05
tubulin, beta	9603	0.05
KIAA0605 gene product	13929	0.05
malignant liposarcoma	6875	0.06
synapsin Iib	14818	0.06
vesicular fusion protein NSF	9664	0.06
adenosinetriphosphatase	13232	0.06
hexokinase1	10230	0.07
gamma-synergin	14853	0.07
Ubiquitin thiolesterase 1	13281	0.07
unnamed protein product _13	2687	0.07
similar to Eferin	15094	0.07
pre-mRNA splicing factor_1	14854	0.07
unnamed protein product_17	6569	0.07
No Hits Found_20	15371	0.07
Piccolo protein	6717	0.07
ankyrin 2	17734	0.07
nuclear transcription factor Y	4189	0.08
chaperonin containing TCP-1	17165	0.08
T-cell lymphoma tumor antigen	9876	0.08
QkI-2	16051	0.08
No Hits Found_71	6082	0.08
Regulatory protein TSC-22	5214	0.08
HSCO protein	12939	0.08
pre-mRNA splicing factor_2	14844	0.08
Selenophosphate synthetase 2	13258	0.08
Sodium pump 3_1	2045	0.09
klotho secreted isoform	3653	0.09
unnamed protein product	15622	0.09

Marker selection analysis for phosphoglycerate mutase

Gene Name	Spot	Score
phosphoglycerate mutase	6482	0
Sodium pump 3_1	2045	0.02
Sodium pump 3	8105	0.02
Amyloid-like protein 2	12582	0.03
SNARE	10056	0.03
transcription elongation factor B	1676	0.03
beta-amyloid precursor	9607	0.03
eukaryotic translation elongation factor 1_1	16106	0.04
Sodium pump 3_2	11249	0.04
klotho secreted isoform	3653	0.04
eukaryotic translation elongation factor 1	16149	0.04
fusion protein attachment protein	8244	0.04
pre-mRNA splicing factor	9696	0.04
Neural enolase	13011	0.04
Regulatory protein TSC-22	5214	0.05
alpha 1 type III collagen	5511	0.05
similar to Amyloid beta A4	1900	0.05
No Hits Found_128	4568	0.05
hypothetical protein _8	487	0.06
RNA-binding protein FUS	16410	0.06
extensin	17131	0.06
PP2A-alpha	3986	0.06
pre-mRNA splicing factor_2	14844	0.06
unnamed protein product	3853	0.06
No Hits Found_56	12987	0.06
Na/K ATPase_1	2049	0.06
beta-amyloid precursor	3906	0.07
calmodulin 2	14543	0.07
Similar to protein kinase C	6549	0.07
No Hits Found_20	15371	0.07
F-box only protein 3	1309	0.07
VAMP	8081	0.07
Unknown protein	14486	0.08
poly(A) binding protein	1670	0.08
ADAM 12	17139	0.08
ACTIN, CYTOPLASMIC TYPE 5	4161	0.08
EST H08032.1	13326	0.08
No Hits Found_68	7604	0.08
vesicle associated protein	5128	0.08
adenosinetriphosphatase	13232	0.08
malignant liposarcoma	6875	0.08
Na/K ATPase_3	4949	0.08
endocrine neoplasia 1	12899	0.08
hexokinase1	10230	0.09
agCP3452	8686	0.09
synapsin Iib	14818	0.09
Na/K ATPase	1902	0.09
Pleiotrophin	8479	0.09
Unknown gene product	17829	0.09
phosphate carrier protein	12265	0.09

Marker selection analysis for Isocitrate Dehydrogenase

Gene Name	Spot	Score
Isocitrate dehydrogenase	16230	0
Putative protein C21orf45	346	0.03
visinin-like 1	11435	0.04
No Hits Found_67	14042	0.04
unnamed protein product_9	5958	0.05
poly(A) binding protein	1670	0.05
eukaryotic initiation factor 5	11520	0.05
No Hits Found_130	16172	0.05
similar to LPS-responsive	11025	0.05
No Hits Found_5	17423	0.05
RIKEN cDNA 1110066L09	17279	0.05
serine incorporator 1	9694	0.05
ATP synthase alpha subunit_1	8133	0.06
DEAH box isoform	2736	0.06
No Hits Found_84	4336	0.06
ATP synthase alpha subunit	13508	0.06
prenyl protein protease	9139	0.06
NEURONAL PROTEIN 3.1	4912	0.06
HSPC288	13041	0.06
GAPDH	14661	0.07
deoxyhypusine synthase	16197	0.07
similar to RALY	1194	0.07
trypsin domain containing 1	10806	0.07
No Hits Found_34	2861	0.07
vesicle associated protein	5128	0.07
agCP3452	8686	0.08
hnRNPC related	6730	0.08
Lipid Transfer ProteinII	12459	0.08
unnamed protein product_1	4379	0.08
RIKEN cDNA _1	7775	0.08
similar to GS15	7790	0.08
No Hits Found_25	7453	0.08
mitochondrial ribosomal prtn S23	17989	0.09
No Hits Found_116	14562	0.09
No Hits Found_15	11568	0.09
ankyrin 2	17734	0.09
Nesprin-2	843	0.09
pre-mRNA splicing factor_2	14844	0.09
extensin	17131	0.09
Alpha1,2-Mannosidase	13854	0.09

Marker selection analysis for Aldolase C

Gene Name	Spot	Score
aldolase C	3836	0
PHLDB2	1283	0.07
NADP-specific isocitrate dehydrogenase	5860	0.07
unnamed protein product_4	15664	0.07
vesicle-associated membrane protein 3	1740	0.07
neurofilament-L	4896	0.09
Thy-1 antigen	5098	0.09
elongation factor 1-beta	2131	0.09

Marker selection analysis for Induced by TNF alpha (TNF AP)

Gene Name	Spot	Score
induced by tumor necrosis factor alpha	10372	0
c-src tyrosine kinase	10037	0.03
SPT3-associated factor	2884	0.03
similar to exocyst complex component 3	6894	0.03
splicing factor 3a	10344	0.04
No Hits Found_60	1724	0.04
Ribonuclease CL2	13900	0.04
GATA-2	5044	0.05
LIM-domain protein CRP1	13465	0.05
disintegrin-like and metalloprotease domain	4482	0.05
IGF-binding protein 2	3240	0.05
Tropomyosin 1 alpha chain	17149	0.05
eukaryotic translation initiation factor 3, s6	628	0.05
Similar to CGI-67 protein	14406	0.05
FLJ22611-like protein	3250	0.05
vesicle-associated membrane protein	16240	0.05
No Hits Found_33	10679	0.05
nucleotide pyrophosphatase 3	593	0.06
type V preprocollagen alpha	4453	0.06
Unknown protein_1	3921	0.06
Rho GTPase activating protein 26	11565	0.06
TROPONIN I	2751	0.06
FLJ00315 protein	17077	0.06
muscle specific gene	8010	0.06
hypothetical protein _3	10193	0.06
origin recognition complex	2327	0.06
polymerase II polypeptide C	2825	0.07
No Hits Found_7	4878	0.07
glucokinase	1753	0.07
hypothetical protein FLJ11200	15682	0.07
heat shock protein 40	17417	0.07
Tcf-3 co-repressor CtBP	161	0.07
phosphatidylinositol transfer protein	9927	0.07
RB1-inducible coiled-coil 1	7105	0.08
Ferredoxin-NADP(+)reductase	1322	0.08
PTEN induced putative kinase 1	15035	0.08
NADH dehydrogenase flavoprotein 1	5452	0.08
Collagen alpha 1	5378	0.08
chloride channel 7	530	0.08
Creatine kinase	15098	0.08
Arp23	9681	0.08
ATP synthase beta chain	1743	0.08
coronin, actin binding protein, 2B	14087	0.09
eukaryotic translation elongation factor 1_2	15734	0.09
BLOCK 25	7848	0.09
hypothetical protein	16484	0.09
Apolipoprotein A-I	12316	0.09
Calpactin I light chain	2210	0.09
No Hits Found_72	1662	0.09
ATP/GTP-binding protein	8012	0.09

Marker selection analysis for TNF receptor associated factor 1

Gene Name	Spot	Score
tumor necrosis factor type 1	15016	0
MAP kinase phosphatase-1	14632	0
preprocarboxypeptidase A	2215	0.01
protein tyrosine phosphatase	1679	0.01
No Hits Found_49	5980	0.02
immunoglobulin-like receptor	5532	0.02
ezrin	17732	0.02
UDP-glucuronosyltransferase 1A9	9610	0.02
similar to Heat shock protein HSP 90-alpha	5677	0.02
Sk-tropomodulin	13748	0.02
Unknown protein_4	2775	0.02
Tryptophan 5-monooxygenase	7185	0.03
Cytochrome P450	17362	0.03
KIAA0232 protein	8499	0.03
chromosome 20 open reading frame 149	13481	0.03
No Hits Found_99	4689	0.03
ankyrin repeat	5336	0.03
acid alpha glucosidase	12981	0.03
No Hits Found_85	15679	0.03
Peroxisomal coenzyme A diphosphatase	4869	0.03
No Hits Found_80	11711	0.04
vacuolar protein sorting 4 homolog B	498	0.04
Similar to LIM domains	16825	0.04
Serum albumin precursor	13896	0.04
similar to Np95-like ring finger protein	10599	0.04
Acylphosphatephosphohydrolase	14313	0.04
hypothetical protein MGC38361	13731	0.04
No Hits Found_58	16838	0.04
No Hits Found_88	14208	0.04
aldo-keto reductase	2889	0.04
mitochondrial ribosomal protein S25	2875	0.04
Unknown protein _3	2888	0.04
putative sweet taste receptor T1R1	17155	0.04
No Hits Found_129	9825	0.04
hypothetical protein_3	12224	0.04
No Hits Found_3	10789	0.05
LAP	12407	0.05
No Hits Found_64	17248	0.05
ribosome-binding protein	14626	0.05
No Hits Found_46	16241	0.05
cytochrome P450 (CYP27A1)	5763	0.05
No Hits Found_29	12453	0.05
Creatine kinase	15098	0.05
target of Jun 3	474	0.05
No Hits Found_6	10653	0.05
No Hits Found_54	15755	0.05
No Hits Found_31	12392	0.06
GHRH receptor	11448	0.06
Ig gamma chain	11778	0.06
AI182287	7560	0.06

Marker selection analysis for CEBPζ

Gene Name	Spot	Score
CEBPζ	19069	0
RB1-inducible coiled-coil 1	7105	0.05
ATP synthase beta chain	1743	0.05
KIAA1892 protein	4417	0.05
NADH dehydrogenase flavoprotein 1	5452	0.06
RIKEN cDNA _4	3763	0.06
IQ motif containing K (IQCK)	244	0.07
heat shock protein 40	17417	0.07
N-deacetylase/N-sulfotransferase	10917	0.07
Unknown protein _5	357	0.07
CREATINE KINASE	15098	0.08
disintegrin-like and metalloprotease domain	4482	0.08
polymerase II polypeptide C	2825	0.09
Ferredoxin-NADP(+)reductase\	1322	0.09
interleukin enhancer binding factor 2	9723	0.09
Tropomyosin 1 alpha chain	17149	0.09
Unknown protein_1	3921	0.09
eukaryotic translation initiation factor 3, s6	628	0.1
mitochondrial ribosomal protein S25	2875	0.1
No Hits Found_86	4050	0.1
chloride channel 7	530	0.1
origin recognition complex	2327	0.1
Unknown protein _3	2888	0.11
phosphatidylinositol transfer protein	9927	0.11
No Hits Found_54	15755	0.11
induced by tumor necrosis factor alpha	10372	0.12
No Hits Found_85	15679	0.12
ADP-ribosylation-like factor 6	13499	0.12
Tryptophan 5-monooxygenase	7185	0.12