Table S1. Superconserved transcriptomic response to bPTH(7-34). For each specific transcript significantly regulated in each tissue the z ratio (bPTH(7-34) compared to vehicle control) is indicated.

Gene Symbol	**Aorta**	**Bone**	**Heart**	**Kidney**	**Liver**	**Lung**
Acadl	-3.42			-1.57		-2.09
Acads	-2.04			-1.77	-2.83	-2.41
Acot8		-1.65	-1.6		-1.56	-2.6
Acta2	6.32				2.51	4.72
Acvr2b				-2.66		-2.77
Add3	-2.2			-3.83		-2.63
Alkbh7				-1.81	-2.25	-2.43
Araf					-1.74	-1.5
Arhgap17				-2.06		-2.42
Atf4			4.26		3.59	2.04
Atpaf2	-2.32	-1.63				-2.17
Caprin1				1.75	4.58	
Casp6	-2.07					-1.74
Casp9		-1.77				-2.34
Cd151				1.78	1.64	2.31
Cd63			2.96		2.45	
Cd81		1.83	1.8			2.13
Cdkn1c	-1.71				-2.12	-1.73
Cdkn2b	2.89				2.45	
Cdv3			2.58	2.79	1.83	
Cnih			3.24		3.16	1.7
Col1a1	3.53	5.35			2.43	
Col4a1	2.28	2.78			1.96	1.99
Cox4nb		-1.85			-1.6	-2.45
Creld2			2.73	3.42	2.2	
Ctnna1				2.88	1.69	
Cyp4f13				-1.7	-3.44	-2.65
Dctn4		-1.96			-1.8	-1.62
Dnajb9				2.84	1.85	3.98
Dusp7				-4.39	-2.05	-1.55
Dynll1					1.97	2.28
Eef1b2	2.49		2.07		2.28	5.38
Eif4ebp1					1.77	1.91
Ep300				-2.47		-2.68
Etfa					2.03	3.45
Fadd					-2.44	-2.13

Fam207a		-2.87			-2.85	-3.6
Gbl		-2.8			-2.12	-2.2
Ghr					2.3	2.23
Gnb2					-2.8	-1.59
Gorasp2			2.41		3.41	2.02
Gpatch2	-2.58				-2.93	-1.51
Gpd2	-4.01			-1.85		
Gpr172b	-1.72	-1.67			-1.61	-1.75
Hbegf			2.9		3.18	
Hdgf	2.31	2.26			1.64	
Hsp90ab1			4.1	2.18	4.76	3.48
Hspa8			4.37		9.96	3.31
Hspb1	4.91				4.41	2.59
Icam1	2.79				3.41	
Ifngr1		2.53	2.77		2.43	
Ift172	-1.8				-1.91	-2.74
Ift20	1.53				2.23	2.4
Igfbp7					2.37	2.15
Ing4				-1.63	-2.11	-2.81
Irak3		-3.28			-1.59	
Irf2bp1		-2.36			-3.59	-2.25
Itgb5		2.55			2.34	1.53
Jmjd3		-1.97		-1.66	-1.92	
Kif3a		-2.59		-2.23	-1.88	
Klf2	-2.29		-8.79		-4.98	-2.36
Lass2				1.84	2.45	3.2
Lsm3		-2.17		-1.52		-1.52
Ltbp4	2.36			1.74	2.04	
Luc7l3	-2.07			-2.97	-2.19	
Lyrm2		-1.83		-3.59	-2.09	
Lysmd1	-1.83				-1.79	-2.52
Man2a1			2.98	2.59	1.68	1.56
Map2k3		2.55			1.82	
Mapbpip		-2.67			-1.83	1.82
Mark3	-1.72				-2.2	-1.58
Mmp2	1.8	4.37				
Mterf1b	-2.99		-1.77	-2.79	-2.82	
Mterfd2				-2.32	-2.58	
Myg1		-1.83		-2.4		-1.74
N4bp2l1	-1.95			-3.71		-3.94
Ncoa6		1.84			2.42	

Neo1		2.53	2.48		1.6	
Nsmce1				-2.08	-1.97	-1.81
Ogn		3.57		2.84	3.85	
Pdia3			2.85		3.12	
Pdpk1	-3.92	-2.77			-4.23	-3.16
Pex11a	-1.97			-2.04	-1.99	
Picalm				4.15	2.48	3.45
Pik3c3	-1.78					-2.68
Ppp1r10		-3.93			-2.4	-1.83
Ppp1r35		-1.55			-2.16	-2.04
Prkacb					-2.36	-1.83
Prkch		3.09			5.27	
Prkcz					-2.38	-3.01
Psmb7				1.61	3.9	1.74
Psmd10		-1.75		-2.38		-1.76
Psmg3		-2.12			-1.63	-3.42
Ptpn11	1.75		3.47	2.23	1.69	
Rasa1		-2.2			-2.02	-2.13
Rhot2					-1.68	-2.14
Rnasek	1.62		2.26		1.95	1.8
Rnf135	-1.53	-2.07				-4.32
Rps3			2.48		2.12	3.04
Rusc2			2.27	2.2		4.76
Sepp1		4.44			4.57	6
Sin3a					-1.65	-3.22
Snx2	-2.55			-2.31		-2.51
Sparc	3.09	5.16			5.3	1.73
Spsb2		-1.78		-2.21		-1.71
Tgfbr2		3.38		3.36	2.58	
Timm44	-1.96				-1.69	-1.7
Tmem53				-1.76	-2.22	-2.47
Tmem85			2.04		3.2	1.97
Tomm7	2.66				1.6	2.05
Trf				5.16	2.09	2.17
Txnl4b	-2.22	-1.56		-1.87	-1.83	
Utx	-1.81			-2.42	-2.68	-2.34
Vkorc1	2.84	2.81			1.82	
Yeats4		-1.85		-1.89	-2.32	-2.23
Ywhab				2.88		2.79
Ywhag				1.97		2.23

Table S2. Superconserved transcriptomic response to hPTH(1-34). For each specific transcript significantly regulated in each tissue the z ratio (hPTH(1-34) compared to vehicle control) is indicated.

Gene Symbol	Aorta	Bone	Heart	Kidney	Liver	Lung
2610507B11Rik	-1.75		-1.57			-1.54
9030025P20Rik		1.6				1.55
Acadl	-1.69					-2.12
Afg3l1					3.02	1.57
Aplp2		2.57	1.94			
Atp6v1h	-1.91					-4.19
Bace2	2.75				2.35	1.58
Bgn		3.15				2.75
Bnip3l	-2.31					-2.74
C1qtnf2	2.55		3.81		3.32	
Ccdc41					-3.37	-2.06
Cd163			-2.24			-1.55
Cnot11		-1.75				-1.78
Cox17	-3.2	-3.98				
Cpt1b	-2.83		-2.44			
Cutc					-2.07	-1.83
Cyb5r3	2.69				1.81	
D3Ucla1	-1.6				-3.03	-2.7
Dars		1.75				2.44
Ddx24		1.63				2.1
Dnajc15	-2.75	-2.48			-1.95	
Dnajc5			1.76		2.42	
Eftud2			2.08			1.98
Eif4e3	-2.42	-1.92			-2.15	
Ensa			-2.73			-1.55
Fcgrt		1.99			2.48	
Fnta	-1.77					-1.68
Fpgs	2.06					3.14
Hsd3b7		2.15				2.61
Igf2r					-3.51	-2
Ipmk					-2.12	-2.68
Itm2b					-3.02	-2.01
Ivns1abp	-1.92					-3.8
Klf2			-4.94			-4.34
Lims2	-1.86					-3.42
LOC100045617					-4.01	-2.03

LOC668492		-2.53	-2.08			-2.13
Mcee	-2.38	-2.84			-3.4	
Mmab				2.66		3.83
Mvd					2.07	6.71
Ndufb2		-4.86	-2.6			
Ndufb6	-3.67	-2.18				
Ndufs4	-2.07	-3.47			-3.1	
Nfatc4	1.72		1.97			
Nfkb1	1.95	1.95				
Pdha1	-3.78					-1.76
Plekhg3		-1.65				-2.65
Ppm1a	-1.67					-2.63
Prdx3	-3.21				-2.68	
Psen2					1.87	3.27
Psip1					-3.29	-1.68
Rab1		2.75				3.34
Rnps1					2.98	2.88
Rshl2a					-3.07	-1.96
Serf2		-2.64				-1.71
Slc22a5			-2.62			-2.93
Styx		-1.81				-2.05
Tm9sf4					-2.12	-1.63
Tmem223	-2.01					-1.68
Tmem38b	-1.56					-2.04
Xdh	-1.82					-3.04

Table S3. KEGG pathway enrichment for superconserved hPTH(1-34)-induced significant transcript regulation. For each described pathway the number of total whole murine genome background genes included in the pathway is indicated (C). The number of transcripts observed (O) in the input dataset that populated the specific KEGG pathway is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of KEGG pathway enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

KEGG Pathway	**C**	**O**	**E**	**R**	**P**	**H**
Metabolic pathways	1184	13	1.15	11.34	1.12E-09	101.5019
Oxidative phosphorylation	147	5	0.14	35.14	2.21E-06	198.7381
Alzheimer's disease	188	5	0.18	27.48	4.98E-06	145.7201
Parkinson's disease	148	3	0.14	20.94	0.0013	60.43403
Huntington's disease	197	3	0.19	15.73	0.0022	41.80369
Fatty acid metabolism	48	2	0.05	43.05	0.0022	114.4087
MAPK signaling pathway	268	3	0.26	11.57	0.0036	28.27358
PPAR signaling pathway	80	2	0.08	25.83	0.0036	63.12071
B cell receptor signaling pathway	76	2	0.07	27.19	0.0036	66.44414
Adipocytokine signaling pathway	68	2	0.07	30.39	0.0036	74.26397
T cell receptor signaling pathway	110	2	0.11	18.79	0.0061	41.61365
Lysosome	123	2	0.12	16.8	0.0069	36.30734
Neurotrophin signaling pathway	131	2	0.13	15.77	0.0072	33.78987

Table S4. KEGG pathway enrichment for superconserved bPTH(7-34)-induced significant transcript regulation. For each described pathway the number of total whole murine genome background genes included in the pathway is indicated (C). The number of transcripts observed (O) in the input dataset that populated the specific KEGG pathway is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of KEGG pathway enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

KEGG Pathway	**C**	**O**	**E**	**R**	**P**	**H**
Pathways in cancer	325	10	0.61	16.48	4.02E-08	121.8824
Prostate cancer	89	6	0.17	36.12	5.83E-07	225.1841
MAPK signaling pathway	268	8	0.5	15.99	9.30E-07	96.44396
Apoptosis	86	5	0.16	31.15	9.87E-06	155.927
GnRH signaling pathway	99	5	0.18	27.06	1.59E-05	129.8502
Endometrial cancer	52	4	0.1	41.21	3.00E-05	186.3878
Cell cycle	127	5	0.24	21.09	3.88E-05	93.03154
Neurotrophin signaling pathway	131	5	0.24	20.45	3.94E-05	90.0721
Insulin signaling pathway	137	5	0.26	19.55	4.37E-05	85.22859
Long-term potentiation	69	4	0.13	31.06	5.60E-05	132.0613
TGF-beta signaling pathway	85	4	0.16	25.21	0.0001	100.84
Vasopressin-regulated water reabsorption	43	3	0.08	37.38	0.0004	127.015
Amoebiasis	116	4	0.22	18.47	0.0004	62.75995
Leukocyte transendothelial migration	120	4	0.22	17.86	0.0004	60.68721
Vascular smooth muscle contraction	123	4	0.23	17.42	0.0004	59.19211
Natural killer cell mediated cytotoxicity	125	4	0.23	17.14	0.0004	58.24069
Toxoplasmosis	127	4	0.24	16.87	0.0004	57.32325
Non-small cell lung cancer	55	3	0.1	29.22	0.0007	92.18624
Jak-STAT signaling pathway	153	4	0.29	14.01	0.0007	44.20018
Colorectal cancer	65	3	0.12	24.73	0.0008	76.58658
Pancreatic cancer	71	3	0.13	22.64	0.0008	70.11404
Renal cell carcinoma	71	3	0.13	22.64	0.0008	70.11404
Protein processing in endoplasmic reticulum	169	4	0.32	12.68	0.0008	39.26882

Table S5. Wikipathways enrichment for superconserved hPTH(1-34)-induced significant transcript regulation. For each described pathway the number of transcripts observed (O) in the input dataset that populated the specific KEGG pathway is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of KEGG pathway enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

WikiPathway Description	**O**	**E**	**R**	**P**	**H**
Electron Transport Chain	4	0.1	40.52	3.12E-05	182.5769
Oxidative phosphorylation	3	0.06	51.66	0.0001	206.64
mRNA processing	5	0.47	10.7	0.0003	37.6948
Apoptosis	2	0.09	22.22	0.0053	50.56659
PPAR signaling pathway	2	0.09	22.22	0.0053	50.56659
Fatty Acid Beta Oxidation	2	0.07	29.95	0.0053	68.15794
IL-2 Signaling Pathway	2	0.09	22.46	0.0053	51.11276
MicroRNAs in cardiomyocyte hypertrophy	2	0.1	20.26	0.0056	45.62171
MAPK signaling pathway	2	0.16	12.52	0.0126	23.78336
PluriNetWork	2	0.28	7.08	0.0327	10.517

Table S6. Wikipathways enrichment for superconserved bPTH(7-34)-induced significant transcript regulation. For each described pathway the number of transcripts observed (O) in the input dataset that populated the specific KEGG pathway is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of KEGG pathway enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

WikiPathway Description	**O**	**E**	**R**	**P**	**H**
MAPK signaling pathway	10	0.31	32.47	4.19E-11	336.9667
Insulin Signaling	8	0.29	27.13	1.23E-08	214.6009
Myometrial Relaxation and Contraction Pathways	8	0.29	27.13	1.23E-08	214.6009
EGFR1 Signaling Pathway	8	0.41	19.75	1.12E-07	137.2779
Focal Adhesion	7	0.35	20.16	6.84E-07	124.2853
TNF-alpha NF-kB Signaling Pathway	7	0.4	17.44	1.53E-06	101.419
Calcium Regulation in the Cardiac Cell	6	0.28	21.15	3.33E-06	115.8503
Integrin-mediated cell adhesion	5	0.19	26.79	8.61E-06	135.6913
FAS pathway and Stress induction of HSP regulation	4	0.1	42.02	1.49E-05	202.8227
IL-6 signaling Pathway	5	0.22	22.9	1.49E-05	110.534
TGF-beta Receptor Signaling Pathway	6	0.45	13.39	2.98E-05	60.60024
Apoptosis Modulation by HSP70	3	0.04	69.88	4.63E-05	302.8892
IL-4 signaling Pathway	4	0.14	28.57	4.94E-05	123.0302
PluriNetWork	6	0.55	11.01	7.10E-05	45.67765
B Cell Receptor Signaling Pathway	5	0.38	13.26	0.0001	53.04
G Protein Signaling Pathways	4	0.18	22.8	0.0001	91.2
IL-3 Signaling Pathway	4	0.21	19.31	0.0002	71.42711
ESC Pluripotency Pathways	4	0.23	17.42	0.0002	64.43606
Senescence and Autophagy	4	0.2	19.66	0.0002	72.72175
ErbB signaling pathway	3	0.11	27.24	0.0005	89.92006
Fatty Acid Beta Oxidation	3	0.13	23.29	0.0007	73.47767
Kit Receptor Signaling Pathway	3	0.13	22.96	0.0007	72.43655
Endochondral Ossification	3	0.13	23.99	0.0007	75.6861
Mitochondrial LC-Fatty Acid Beta-Oxidation	2	0.03	66.97	0.0008	207.4001
Type II interferon signaling (IFNG)	3	0.14	21.72	0.0008	67.26489
IL-1 Signaling Pathway	3	0.15	19.6	0.001	58.8
Hypertrophy Model	2	0.04	53.58	0.0011	158.5222
IL-2 Signaling Pathway	3	0.17	17.47	0.0012	51.0267
Alpha6-Beta4 Integrin Signaling Pathway	3	0.17	17.86	0.0012	52.16582
Apoptosis	3	0.17	17.28	0.0012	50.47175
Wnt Signaling Pathway and Pluripotency	3	0.18	16.57	0.0013	47.82196
MAPK Cascade	2	0.06	35.72	0.0024	93.57885

Androgen Receptor Signaling Pathway	3	0.24	12.76	0.0026	32.98494
Toll Like Receptor signaling	2	0.07	28.96	0.0033	71.86384
Signaling of Hepatocyte Growth Factor Receptor	2	0.07	28.2	0.0034	69.61229
Translation Factors	2	0.09	21.43	0.0057	48.0916
Chemokine signaling pathway	3	0.35	8.64	0.0071	18.56513
Splicing factor NOVA regulated synpatic proteins	2	0.11	18.47	0.0071	39.68726
TGF Beta Signaling Pathway	2	0.11	18.16	0.0072	38.91084
Wnt Signaling Pathway	2	0.11	17.57	0.0073	37.54142
Proteasome Degradation	2	0.11	17.86	0.0073	38.16105
G1 to S cell cycle control	2	0.12	16.48	0.008	34.55708
Alzheimers Disease	2	0.14	13.92	0.0109	27.31902
IL-5 Signaling Pathway	2	0.15	13.39	0.0115	25.96726
estrogen signalling	2	0.16	12.32	0.0131	23.19522
PPAR signaling pathway	2	0.17	11.52	0.0146	21.14666
Cell cycle	2	0.18	11.05	0.0155	19.99683
MicroRNAs in cardiomyocyte hypertrophy	2	0.19	10.5	0.0167	18.66148
Delta-Notch Signaling Pathway	2	0.21	9.65	0.0189	16.63214
Toll-like receptor signaling pathway	2	0.21	9.74	0.0189	16.78726
T Cell Receptor Signaling Pathway	2	0.27	7.49	0.0295	11.46103

Table S7. Ingenuity Canonical signaling pathway enrichment for superconserved hPTH(1-34)-induced significant transcript regulation. For each described Canonical signaling pathway the –$\log_{10}$ transform of the enrichment probability is given. In addition the enrichment ratio is also given for each significantly-populated signaling pathway.

Ingenuity Canonical Pathway	**-log(p-value)**	**Ratio**
Mitochondrial Dysfunction	1.05E+01	5.85E-02
Oxidative Phosphorylation	3.65E+00	3.67E-02
April Mediated Signaling	2.31E+00	5.26E-02
B Cell Activating Factor Signaling	2.27E+00	5.00E-02
Amyloid Processing	2.07E+00	3.92E-02
Wnt/Ca+ pathway	1.99E+00	3.57E-02
PPARα/RXRα Activation	1.89E+00	1.68E-02
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	1.70E+00	2.53E-02
T Cell Receptor Signaling	1.54E+00	2.06E-02
Glucocorticoid Receptor Signaling	1.46E+00	1.15E-02
fMLP Signaling in Neutrophils	1.45E+00	1.85E-02
iCOS-iCOSL Signaling in T Helper Cells	1.45E+00	1.85E-02
CD28 Signaling in T Helper Cells	1.38E+00	1.69E-02
PKCθ Signaling in T Lymphocytes	1.38E+00	1.69E-02
PTEN Signaling	1.38E+00	1.69E-02
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	1.32E+00	1.57E-02
D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	1.32E+00	1.57E-02
PI3K Signaling in B Lymphocytes	1.32E+00	1.56E-02

Table S8. Ingenuity Canonical signaling pathway enrichment for superconserved bPTH(7-34)-induced significant transcript regulation. For each described Canonical signaling pathway the –$\log_{10}$ transform of the enrichment probability is given. In addition the enrichment ratio is also given for each significantly-populated signaling pathway.

Ingenuity Canonical Pathway	**-log(p-value)**	**Ratio**
Molecular Mechanisms of Cancer	1.03E+01	4.38E-02
IGF-1 Signaling	1.02E+01	1.03E-01
IL-8 Signaling	9.77E+00	6.56E-02
PPARα/RXRα Activation	8.70E+00	6.15E-02
Huntington's Disease Signaling	8.63E+00	5.22E-02
ERK/MAPK Signaling	7.37E+00	5.35E-02
Aldosterone Signaling in Epithelial Cells	7.06E+00	5.92E-02
Protein Kinase A Signaling	7.05E+00	3.37E-02
P2Y Purigenic Receptor Signaling Pathway	6.75E+00	6.72E-02
Prostate Cancer Signaling	6.68E+00	8.54E-02
NF-κB Signaling	6.58E+00	5.20E-02
Role of NFAT in Cardiac Hypertrophy	6.45E+00	5.03E-02
Myc Mediated Apoptosis Signaling	6.29E+00	1.03E-01
eNOS Signaling	6.19E+00	5.67E-02
ERK5 Signaling	6.08E+00	9.52E-02
Neurotrophin/TRK Signaling	5.92E+00	8.96E-02
Melatonin Signaling	5.80E+00	8.57E-02
Prolactin Signaling	5.70E+00	8.22E-02
FLT3 Signaling in Hematopoietic Progenitor Cells	5.66E+00	8.11E-02
Cardiac Hypertrophy Signaling	5.66E+00	4.04E-02
p38 MAPK Signaling	5.63E+00	5.98E-02
HER-2 Signaling in Breast Cancer	5.59E+00	7.89E-02
Synaptic Long Term Potentiation	5.58E+00	5.88E-02
p70S6K Signaling	5.58E+00	5.88E-02
CREB Signaling in Neurons	5.55E+00	4.68E-02
NRF2-mediated Oxidative Stress Response	5.39E+00	4.44E-02
ErbB Signaling	5.28E+00	6.98E-02
Insulin Receptor Signaling	5.23E+00	5.22E-02
Neuregulin Signaling	5.22E+00	6.82E-02
G Beta Gamma Signaling	5.22E+00	6.82E-02
Tumoricidal Function of Hepatic Natural Killer Cells	5.19E+00	1.67E-01
Leukocyte Extravasation Signaling	5.08E+00	4.04E-02
Tec Kinase Signaling	4.77E+00	4.43E-02
Pancreatic Adenocarcinoma Signaling	4.75E+00	5.66E-02
Germ Cell-Sertoli Cell Junction Signaling	4.73E+00	4.37E-02
NGF Signaling	4.73E+00	5.61E-02
Dopamine-DARPP32 Feedback in cAMP Signaling	4.71E+00	4.35E-02
Fc Epsilon RI Signaling	4.68E+00	5.50E-02
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	4.64E+00	3.02E-02
Growth Hormone Signaling	4.56E+00	7.25E-02

Endothelin-1 Signaling	4.55E+00	4.09E-02
Colorectal Cancer Metastasis Signaling	4.53E+00	3.39E-02
14-3-3-mediated Signaling	4.51E+00	5.13E-02
PI3K/AKT Signaling	4.39E+00	4.88E-02
ILK Signaling	4.31E+00	3.76E-02
mTOR Signaling	4.28E+00	3.72E-02
GNRH Signaling	4.27E+00	4.65E-02
Thrombin Signaling	4.24E+00	3.66E-02
Hepatic Fibrosis / Hepatic Stellate Cell Activation	4.15E+00	3.55E-02
Melanocyte Development and Pigmentation Signaling	4.14E+00	5.95E-02
FGF Signaling	4.12E+00	5.88E-02
Virus Entry via Endocytic Pathways	4.02E+00	5.62E-02
Death Receptor Signaling	3.96E+00	5.43E-02
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	3.94E+00	8.16E-02
Glioma Signaling	3.89E+00	5.26E-02
Endometrial Cancer Signaling	3.84E+00	7.69E-02
Gap Junction Signaling	3.83E+00	3.87E-02
Nitric Oxide Signaling in the Cardiovascular System	3.81E+00	5.05E-02
UVB-Induced MAPK Signaling	3.80E+00	7.55E-02
Neuropathic Pain Signaling In Dorsal Horn Neurons	3.78E+00	5.00E-02
Lymphotoxin β Receptor Signaling	3.77E+00	7.41E-02
Thrombopoietin Signaling	3.74E+00	7.27E-02
Glioma Invasiveness Signaling	3.68E+00	7.02E-02
Sphingosine-1-phosphate Signaling	3.61E+00	4.59E-02
Gαs Signaling	3.61E+00	4.59E-02
ErbB4 Signaling	3.59E+00	6.67E-02
Corticotropin Releasing Hormone Signaling	3.57E+00	4.50E-02
Androgen Signaling	3.57E+00	4.50E-02
B Cell Receptor Signaling	3.53E+00	3.41E-02
Dendritic Cell Maturation	3.49E+00	3.35E-02
IL-6 Signaling	3.48E+00	4.31E-02
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	3.48E+00	3.33E-02
Non-Small Cell Lung Cancer Signaling	3.46E+00	6.15E-02
PTEN Signaling	3.45E+00	4.24E-02
Angiopoietin Signaling	3.43E+00	6.06E-02
Regulation of the Epithelial-Mesenchymal Transition Pathway	3.43E+00	3.26E-02
Clathrin-mediated Endocytosis Signaling	3.42E+00	3.24E-02
HMGB1 Signaling	3.42E+00	4.17E-02
Axonal Guidance Signaling	3.41E+00	2.08E-02
Erythropoietin Signaling	3.41E+00	5.97E-02
Glucocorticoid Receptor Signaling	3.40E+00	2.68E-02
Macropinocytosis Signaling	3.38E+00	5.88E-02
Breast Cancer Regulation by Stathmin1	3.34E+00	3.14E-02
Small Cell Lung Cancer Signaling	3.31E+00	5.63E-02
PI3K Signaling in B Lymphocytes	3.29E+00	3.91E-02
LPS-stimulated MAPK Signaling	3.27E+00	5.48E-02
NF-κB Activation by Viruses	3.27E+00	5.48E-02
Leptin Signaling in Obesity	3.25E+00	5.41E-02

Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	3.23E+00	9.38E-02
AMPK Signaling	3.20E+00	3.73E-02
IL-12 Signaling and Production in Macrophages	3.18E+00	3.70E-02
Acute Myeloid Leukemia Signaling	3.18E+00	5.19E-02
TWEAK Signaling	3.16E+00	8.82E-02
GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells	3.04E+00	4.76E-02
Regulation of eIF4 and p70S6K Signaling	3.03E+00	3.42E-02
Gαq Signaling	3.02E+00	3.40E-02
HIPPO signaling	3.00E+00	4.65E-02
Docosahexaenoic Acid (DHA) Signaling	2.98E+00	7.69E-02
α-Adrenergic Signaling	2.98E+00	4.60E-02
TGF-β Signaling	2.98E+00	4.60E-02
CXCR4 Signaling	2.95E+00	3.29E-02
Role of PKR in Interferon Induction and Antiviral Response	2.95E+00	7.50E-02
Mechanisms of Viral Exit from Host Cells	2.92E+00	7.32E-02
IL-1 Signaling	2.91E+00	4.40E-02
Factors Promoting Cardiogenesis in Vertebrates	2.89E+00	4.35E-02
UVC-Induced MAPK Signaling	2.89E+00	7.14E-02
Chronic Myeloid Leukemia Signaling	2.87E+00	4.30E-02
Phospholipase C Signaling	2.84E+00	2.51E-02
MSP-RON Signaling Pathway	2.77E+00	6.52E-02
Tight Junction Signaling	2.77E+00	2.99E-02
Cholecystokinin/Gastrin-mediated Signaling	2.74E+00	3.96E-02
Protein Ubiquitination Pathway	2.70E+00	2.35E-02
TNFR1 Signaling	2.69E+00	6.12E-02
Ephrin Receptor Signaling	2.69E+00	2.87E-02
G-Protein Coupled Receptor Signaling	2.69E+00	2.34E-02
HGF Signaling	2.68E+00	3.81E-02
RAR Activation	2.67E+00	2.84E-02
fMLP Signaling in Neutrophils	2.63E+00	3.70E-02
Renin-Angiotensin Signaling	2.62E+00	3.67E-02
Natural Killer Cell Signaling	2.61E+00	3.64E-02
Type I Diabetes Mellitus Signaling	2.61E+00	3.64E-02
Role of Tissue Factor in Cancer	2.61E+00	3.64E-02
Unfolded protein response	2.57E+00	5.56E-02
Xenobiotic Metabolism Signaling	2.56E+00	2.21E-02
Wnt/Ca+ pathway	2.53E+00	5.36E-02
CCR3 Signaling in Eosinophils	2.51E+00	3.42E-02
Type II Diabetes Mellitus Signaling	2.51E+00	3.42E-02
Nur77 Signaling in T Lymphocytes	2.50E+00	5.26E-02
Sperm Motility	2.47E+00	3.33E-02
Estrogen-Dependent Breast Cancer Signaling	2.40E+00	4.84E-02
Antiproliferative Role of Somatostatin Receptor 2	2.38E+00	4.76E-02
Calcium-induced T Lymphocyte Apoptosis	2.36E+00	4.69E-02
Pyridoxal 5'-phosphate Salvage Pathway	2.36E+00	4.69E-02
CD40 Signaling	2.34E+00	4.62E-02
Hypoxia Signaling in the Cardiovascular System	2.34E+00	4.62E-02
Ovarian Cancer Signaling	2.33E+00	3.05E-02

Endoplasmic Reticulum Stress Pathway	2.29E+00	9.52E-02
Relaxin Signaling	2.29E+00	2.96E-02
CCR5 Signaling in Macrophages	2.27E+00	4.35E-02
IL-3 Signaling	2.24E+00	4.23E-02
Renal Cell Carcinoma Signaling	2.24E+00	4.23E-02
Epithelial Adherens Junction Signaling	2.17E+00	2.74E-02
VEGF Family Ligand-Receptor Interactions	2.15E+00	3.95E-02
Signaling by Rho Family GTPases	2.15E+00	2.14E-02
VDR/RXR Activation	2.12E+00	3.85E-02
Hepatic Cholestasis	2.01E+00	2.47E-02
FAK Signaling	1.99E+00	3.45E-02
UVA-Induced MAPK Signaling	1.98E+00	3.41E-02
Acute Phase Response Signaling	1.95E+00	2.37E-02
VEGF Signaling	1.94E+00	3.30E-02
Mitochondrial Dysfunction	1.93E+00	2.34E-02
RhoGDI Signaling	1.92E+00	2.31E-02
Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes	1.92E+00	3.23E-02
Circadian Rhythm Signaling	1.91E+00	6.06E-02
Salvage Pathways of Pyrimidine Ribonucleotides	1.89E+00	3.16E-02
Sertoli Cell-Sertoli Cell Junction Signaling	1.87E+00	2.25E-02
Calcium Signaling	1.87E+00	2.25E-02
Role of JAK2 in Hormone-like Cytokine Signaling	1.86E+00	5.71E-02
p53 Signaling	1.85E+00	3.06E-02
Telomerase Signaling	1.84E+00	3.03E-02
HIF1α Signaling	1.81E+00	2.94E-02
Paxillin Signaling	1.81E+00	2.94E-02
FcγRIIB Signaling in B Lymphocytes	1.73E+00	4.88E-02
Integrin Signaling	1.69E+00	1.98E-02
Role of IL-17F in Allergic Inflammatory Airway Diseases	1.67E+00	4.55E-02
iNOS Signaling	1.67E+00	4.55E-02
Role of RIG1-like Receptors in Antiviral Innate Immunity	1.65E+00	4.44E-02
CD28 Signaling in T Helper Cells	1.64E+00	2.54E-02
nNOS Signaling in Neurons	1.62E+00	4.26E-02
Ephrin A Signaling	1.60E+00	4.17E-02
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	1.58E+00	1.83E-02
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	1.56E+00	2.36E-02
Cellular Effects of Sildenafil (Viagra)	1.54E+00	2.33E-02
CD27 Signaling in Lymphocytes	1.53E+00	3.85E-02
CNTF Signaling	1.53E+00	3.85E-02
IL-2 Signaling	1.52E+00	3.77E-02
Cardiac β-adrenergic Signaling	1.51E+00	2.26E-02
Role of IL-17A in Arthritis	1.50E+00	3.70E-02
Human Embryonic Stem Cell Pluripotency	1.50E+00	2.24E-02
EGF Signaling	1.48E+00	3.57E-02
ErbB2-ErbB3 Signaling	1.46E+00	3.51E-02
Aryl Hydrocarbon Receptor Signaling	1.45E+00	2.14E-02
Synaptic Long Term Depression	1.44E+00	2.13E-02
ATM Signaling	1.43E+00	3.39E-02

Induction of Apoptosis by HIV1	1.42E+00	3.33E-02
Glioblastoma Multiforme Signaling	1.41E+00	2.05E-02
GM-CSF Signaling	1.39E+00	3.23E-02
Role of JAK1 and JAK3 in γc Cytokine Signaling	1.38E+00	3.17E-02
Retinoic acid Mediated Apoptosis Signaling	1.37E+00	3.12E-02
Cell Cycle: G1/S Checkpoint Regulation	1.37E+00	3.12E-02
Role of PI3K/AKT Signaling in the Pathogenesis of Influenza	1.35E+00	3.03E-02
3-phosphoinositide Biosynthesis	1.34E+00	1.94E-02
GDNF Family Ligand-Receptor Interactions	1.32E+00	2.94E-02
Remodeling of Epithelial Adherens Junctions	1.32E+00	2.94E-02

Table S9. Transcription Factor (TF) target enrichment for superconserved hPTH(1-34)-induced significant transcript regulation. For each described TF target (murine database) the number of total whole murine genome background TFs included in the target group is indicated (C). The number of targets observed (O) in the input dataset that populated the specific TF target group is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of TF target enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

Transcription Factor Target	**C**	**O**	**E**	**R**	**P**	**H**
mmu_CACGTG_V$MYC_Q2	949	7	0.92	7.62	0.002	20.56615
mmu_GGGCGGR_V$SP1_Q6	2704	11	2.62	4.2	0.002	11.33567
mmu_V$USF_Q6_01	217	4	0.21	19.05	0.002	51.41538
mmu_TGAYRTCA_V$ATF3_Q6	487	5	0.47	10.61	0.0024	27.79596
mmu_GGGAGGRR_V$MAZ_Q6	2104	9	2.04	4.42	0.0039	10.64749
mmu_RYTTCCTG_V$ETS2_B	990	6	0.96	6.26	0.0065	13.69116
mmu_CTTTAAR_UNKNOWN	883	5	0.85	5.85	0.0087	12.05381
mmu_V$SP1_Q6	235	3	0.23	13.19	0.0087	27.17774
mmu_V$CREBP1CJUN_01	241	3	0.23	12.86	0.0087	26.49778
mmu_V$ATF1_Q6	219	3	0.21	14.15	0.0087	29.1558
mmu_V$PAX4_01	244	3	0.24	12.7	0.0087	26.16811
mmu_TGACGTCA_V$ATF3_Q6	213	3	0.21	14.55	0.0087	29.97999
mmu_CTTTGA_V$LEF1_Q2	1107	6	1.07	5.6	0.0087	11.53869
mmu_V$CREB_02	231	3	0.22	13.42	0.0087	27.65165
mmu_AACTTT_UNKNOWN	1750	7	1.69	4.13	0.0087	8.509785
mmu_V$SP1_Q4_01	238	3	0.23	13.02	0.0087	26.82746
mmu_V$LMO2COM_01	241	3	0.23	12.86	0.0087	26.49778
mmu_V$CREB_01	242	3	0.23	12.81	0.0087	26.39476
mmu_GCANCTGNY_V$MYOD_Q6	854	5	0.83	6.05	0.0087	12.46591
mmu_V$CEBPB_01	247	3	0.24	12.55	0.0087	25.85903
mmu_V$IK2_01	255	3	0.25	12.16	0.0088	24.99509
mmu_V$USF_C	257	3	0.25	12.06	0.0088	24.78954
mmu_RYTGCNNRGNAAC_V$MIF1_01	73	2	0.07	28.31	0.0097	56.99449
mmu_GGCNRNWCTTYS_UNKNOWN	77	2	0.07	26.84	0.0105	53.11128
mmu_TGACATY_UNKNOWN	602	4	0.58	6.87	0.0109	13.48288
mmu_TGANTCA_V$AP1_C	1041	5	1.01	4.96	0.0123	9.474071
mmu_SCGGAAGY_V$ELK1_02	1070	5	1.04	4.83	0.0137	8.99964
mmu_AAAYRNCTG_UNKNOWN	337	3	0.33	9.2	0.0149	16.80669
mmu_MGGAAGTG_V$GABP_B	690	4	0.67	5.99	0.0151	10.90793
mmu_CAGGTG_V$E12_Q6	2292	7	2.22	3.16	0.02	5.368745
mmu_TGGAAA_V$NFAT_Q4_01	1718	6	1.66	3.61	0.02	6.133282

mmu_WWTAAGGC_UNKNOWN	131	2	0.13	15.77	0.0218	26.20254
mmu_V$STAT_Q6	242	2	0.23	8.54	0.029	13.13112
mmu_V$MYCMAX_B	240	2	0.23	8.61	0.029	13.23875
mmu_V$MZF1_02	220	2	0.21	9.39	0.029	14.43808
mmu_V$E2A_Q2	218	2	0.21	9.48	0.029	14.57647
mmu_V$LEF1_Q6	240	2	0.23	8.61	0.029	13.23875
mmu_V$NFAT_Q6	228	2	0.22	9.06	0.029	13.93067
mmu_V$ATF3_Q6	230	2	0.22	8.98	0.029	13.80767
mmu_V$AP4_Q5	251	2	0.24	8.23	0.029	12.65446
mmu_V$CREB_Q4_01	196	2	0.19	10.54	0.029	16.20633
mmu_V$SP1_Q6_01	226	2	0.22	9.14	0.029	14.05368
mmu_V$MYC_Q2	172	2	0.17	12.01	0.029	18.4666
mmu_V$AREB6_04	235	2	0.23	8.79	0.029	13.51552
mmu_V$E47_01	229	2	0.22	9.02	0.029	13.86917
mmu_V$CETS1P54_01	229	2	0.22	9.02	0.029	13.86917
mmu_V$GCM_Q2	219	2	0.21	9.44	0.029	14.51496
mmu_V$SP3_Q3	230	2	0.22	8.98	0.029	13.80767
mmu_V$MYCMAX_03	230	2	0.22	8.98	0.029	13.80767
mmu_V$AP1_Q6_01	246	2	0.24	8.4	0.029	12.91586
mmu_V$ETS1_B	236	2	0.23	8.76	0.029	13.46939
mmu_V$CREB_Q4	250	2	0.24	8.27	0.029	12.71597
mmu_V$NFY_C	221	2	0.21	9.35	0.029	14.37658
mmu_V$SREBP_Q3	235	2	0.23	8.79	0.029	13.51552
mmu_V$MEIS1_01	224	2	0.22	9.23	0.029	14.19207
mmu_GTGACGY_V$E4F1_Q6	595	3	0.58	5.21	0.029	8.010906
mmu_V$ATF_01	239	2	0.23	8.65	0.029	13.30026
mmu_V$CDX2_Q5	231	2	0.22	8.95	0.029	13.76154
mmu_V$CP2_01	247	2	0.24	8.37	0.029	12.86973
mmu_V$USF2_Q6	234	2	0.23	8.83	0.029	13.57703
mmu_V$E47_02	233	2	0.23	8.87	0.029	13.63853
mmu_V$AP4_Q6_01	237	2	0.23	8.72	0.029	13.40789
mmu_V$MIF1_01	162	2	0.16	12.76	0.029	19.6198
mmu_V$NFY_01	236	2	0.23	8.76	0.029	13.46939
mmu_V$ATF4_Q2	243	2	0.24	8.5	0.029	13.06962
mmu_V$CREB_Q2_01	205	2	0.2	10.08	0.029	15.49903
mmu_CAGCTG_V$AP4_Q5	1387	5	1.34	3.72	0.029	5.719879
mmu_V$RORA1_01	228	2	0.22	9.06	0.029	13.93067
mmu_V$MYCMAX_02	246	2	0.24	8.4	0.029	12.91586
mmu_GATTGGY_V$NFY_Q6_01	1059	4	1.02	3.9	0.029	5.996648
mmu_V$ARNT_02	230	2	0.22	8.98	0.029	13.80767
mmu_V$STAT6_02	241	2	0.23	8.57	0.029	13.17725

mmu_V$CEBPB_02	245	2	0.24	8.43	0.029	12.96198
mmu_V$MYOD_Q6_01	239	2	0.23	8.65	0.029	13.30026
mmu_V$NRF2_01	248	2	0.24	8.33	0.029	12.80822
mmu_V$CART1_01	203	2	0.2	10.18	0.029	15.65279
mmu_V$USF_01	235	2	0.23	8.79	0.029	13.51552
mmu_V$ER_Q6_01	240	2	0.23	8.61	0.029	13.23875
mmu_V$DR4_Q2	236	2	0.23	8.76	0.029	13.46939
mmu_V$MSX1_01	162	2	0.16	12.76	0.029	19.6198
mmu_V$ATF_B	176	2	0.17	11.74	0.029	18.05145
mmu_V$MYOD_01	242	2	0.23	8.54	0.029	13.13112
mmu_V$RFX1_01	227	2	0.22	9.1	0.029	13.99218
mmu_V$CEBP_Q2_01	256	2	0.25	8.07	0.0297	12.32486
mmu_V$E4F1_Q6	261	2	0.25	7.92	0.0301	12.04975
mmu_TGCCAAR_V$NF1_Q6	665	3	0.64	4.66	0.0301	7.08988
mmu_YGCGYRCGC_UNKNOWN	293	2	0.28	7.05	0.0367	10.1191
mmu_TTCYNRGAA_V$STAT5B_01	311	2	0.3	6.64	0.0405	9.246499
mmu_CATTGTYY_V$SOX9_B1	333	2	0.32	6.21	0.0452	8.35159

Table S10. Transcription Factor (TF) target enrichment for superconserved bPTH(7-34)-induced significant transcript regulation. For each described TF target (murine database) the number of total whole murine genome background TFs included in the target group is indicated (C). The number of targets observed (O) in the input dataset that populated the specific TF target group is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of TF target enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

Transcription Factor Target	**C**	**O**	**E**	**R**	**P**	**H**
mmu_GGGCGGR_V$SP1_Q6	2704	32	5.05	6.34	5.72E-15	90.29811
mmu_MGGAAGTG_V$GABP_B	690	12	1.29	9.32	1.14E-06	55.38965
mmu_GCCATNTTG_V$YY1_Q6	393	9	0.73	12.27	2.40E-06	68.95481
mmu_CTTTGT_V$LEF1_Q2	1814	17	3.39	5.02	2.40E-06	28.21134
mmu_GGGTGGRR_V$PAX4_03	1207	14	2.25	6.21	2.40E-06	34.89889
mmu_RCGCANGCGY_V$NRF1_Q6	835	12	1.56	7.7	2.40E-06	43.27237
mmu_CAGGTG_V$E12_Q6	2292	19	4.28	4.44	2.40E-06	24.95186
mmu_CACGTG_V$MYC_Q2	949	13	1.77	7.34	2.40E-06	41.24925
mmu_GGGAGGRR_V$MAZ_Q6	2104	18	3.93	4.58	2.44E-06	25.70575
mmu_SCGGAAGY_V$ELK1_02	1070	13	2	6.51	3.15E-06	35.816
mmu_TTCYRGAA_UNKNOWN	302	8	0.56	14.19	3.15E-06	78.06897
mmu_V$USF_02	250	7	0.47	15	1.28E-05	73.39185
mmu_CTTTAAR_UNKNOWN	883	11	1.65	6.67	1.98E-05	31.37124
mmu_GTGGGTGK_UNKNOWN	273	7	0.51	13.74	1.98E-05	64.62382
mmu_WGGAATGY_V$TEF1_Q6	345	7	0.64	10.87	8.65E-05	44.16463
mmu_V$USF_01	235	6	0.44	13.68	9.50E-05	55.02474
mmu_AACTTT_UNKNOWN	1750	14	3.27	4.29	9.50E-05	17.25557
mmu_V$MAX_01	236	6	0.44	13.62	9.50E-05	54.7834
mmu_V$TATA_01	236	6	0.44	13.62	9.50E-05	54.7834
mmu_RNGTGGGC_UNKNOWN	710	9	1.33	6.79	0.0001	27.16
mmu_V$SREBP1_01	161	5	0.3	16.64	0.0002	61.55086
mmu_TAATTA_V$CHX10_01	735	9	1.37	6.56	0.0002	24.26524
mmu_TGGAAA_V$NFAT_Q4_01	1718	13	3.21	4.05	0.0003	14.26766
mmu_TTGTTT_V$FOXO4_01	1879	13	3.51	3.71	0.0006	11.95306
mmu_V$VDR_Q3	206	5	0.38	13	0.0006	41.88403
mmu_V$IK1_01	258	5	0.48	10.38	0.0007	32.74788
mmu_V$GR_Q6_01	243	5	0.45	11.02	0.0007	34.76702
mmu_V$AR_Q6	228	5	0.43	11.75	0.0007	37.0701
mmu_RGAANNTTC_V$HSF1_01	408	6	0.76	7.88	0.0007	24.86063
mmu_V$ELK1_02	227	5	0.42	11.8	0.0007	37.22784
mmu_V$USF_Q6	242	5	0.45	11.07	0.0007	34.92476

mmu_V$USF_Q6_01	217	5	0.41	12.34	0.0007	38.93149
mmu_V$ARNT_01	232	5	0.43	11.55	0.0007	36.43912
mmu_RYTTCCTG_V$ETS2_B	990	9	1.85	4.87	0.0007	15.36437
mmu_V$TITF1_Q3	223	5	0.42	12.01	0.0007	37.89037
mmu_ATCMNTCCGY_UNKNOWN	48	3	0.09	33.48	0.0007	105.6261
mmu_V$OLF1_01	251	5	0.47	10.67	0.0007	33.6628
mmu_V$ARNT_02	230	5	0.43	11.65	0.0007	36.75461
mmu_V$ZIC1_01	238	5	0.44	11.26	0.0007	35.5242
mmu_V$NFMUE1_Q6	223	5	0.42	12.01	0.0007	37.89037
mmu_TATAAA_V$TATA_01	1166	10	2.18	4.59	0.0007	14.481
mmu_V$AML1_01	248	5	0.46	10.8	0.0007	34.07294
mmu_V$ALPHACP1_01	239	5	0.45	11.21	0.0007	35.36645
mmu_V$AML1_Q6	248	5	0.46	10.8	0.0007	34.07294
mmu_V$COUP_01	241	5	0.45	11.12	0.0007	35.08251
mmu_GATTGGY_V$NFY_Q6_01	1059	9	1.98	4.55	0.0013	13.13156
mmu_ACAWNRNSRCGG_UNKNOWN	57	3	0.11	28.2	0.0013	81.3868
mmu_STTTCRNTTT_V$IRF_Q6	176	4	0.33	12.18	0.0018	33.43078
mmu_WGTTNNNNNAAA_UNKNOWN	490	6	0.91	6.56	0.0018	18.00541
mmu_V$CREBP1_01	164	4	0.31	13.07	0.0018	35.87359
mmu_CCGNMNNTNACG_UNKNOWN	71	3	0.13	22.64	0.0018	62.14063
mmu_YTAATTAA_V$LHX3_01	173	4	0.32	12.39	0.0018	34.00717
mmu_V$PAX3_B	83	3	0.15	19.36	0.0029	49.12797
mmu_V$RREB1_01	191	4	0.36	11.22	0.0029	28.47189
mmu_V$E4BP4_01	205	4	0.38	10.45	0.0033	25.93153
mmu_V$SRF_Q5_01	204	4	0.38	10.5	0.0033	26.0556
mmu_V$CHX10_01	207	4	0.39	10.35	0.0033	25.68338
mmu_V$MTF1_Q4	227	4	0.42	9.44	0.0037	22.95618
mmu_V$E2F1_Q3_01	227	4	0.42	9.44	0.0037	22.95618
mmu_V$TEF_Q6	221	4	0.41	9.7	0.0037	23.58844
mmu_V$NFKB_Q6_01	223	4	0.42	9.61	0.0037	23.36958
mmu_V$CEBPDELTA_Q6	226	4	0.42	9.48	0.0037	23.05345
mmu_V$FOXJ2_02	213	4	0.4	10.06	0.0037	24.46389
mmu_V$SRF_Q6	227	4	0.42	9.44	0.0037	22.95618
mmu_GTGACGY_V$E4F1_Q6	595	6	1.11	5.4	0.0037	13.13171
mmu_V$CIZ_01	217	4	0.41	9.88	0.0037	24.02617
mmu_TGANTCA_V$AP1_C	1041	8	1.94	4.12	0.0037	10.01901
mmu_V$HP1SITEFACTOR_Q6	216	4	0.4	9.92	0.0037	24.12344
mmu_V$AP3_Q6	230	4	0.43	9.32	0.0037	22.66436
mmu_V$TEL2_Q6	219	4	0.41	9.79	0.0037	23.80731
mmu_V$IPF1_Q4	229	4	0.43	9.36	0.0037	22.76163
mmu_V$YY1_02	222	4	0.41	9.65	0.0037	23.46685

mmu_V$NFAT_Q6	228	4	0.43	9.4	0.0037	22.8589
mmu_V$YY1_Q6	225	4	0.42	9.52	0.0037	23.15072
mmu_V$MYCMAX_03	230	4	0.43	9.32	0.0037	22.66436
mmu_V$STAT_01	232	4	0.43	9.24	0.0038	22.3628
mmu_V$HNF4_01_B	232	4	0.43	9.24	0.0038	22.3628
mmu_V$DR1_Q3	236	4	0.44	9.08	0.0038	21.97556
mmu_V$CP2_02	236	4	0.44	9.08	0.0038	21.97556
mmu_V$SREBP_Q3	235	4	0.44	9.12	0.0038	22.07237
mmu_V$SP1_Q6	235	4	0.44	9.12	0.0038	22.07237
mmu_V$PAX_Q6	237	4	0.44	9.04	0.0039	21.77678
mmu_TTAYRTAA_V$E4BP4_01	240	4	0.45	8.93	0.0039	21.51179
mmu_V$HNF4_Q6	238	4	0.44	9	0.0039	21.68042
mmu_V$STAT6_01	239	4	0.45	8.97	0.0039	21.60815
mmu_RTAAACA_V$FREAC2_01	854	7	1.59	4.39	0.0039	10.57523
mmu_V$NFKB_Q6	240	4	0.45	8.93	0.0039	21.51179
mmu_V$FREAC2_01	239	4	0.45	8.97	0.0039	21.60815
mmu_V$HSF1_01	246	4	0.46	8.71	0.0041	20.79265
mmu_V$VDR_Q6	245	4	0.46	8.75	0.0041	20.88814
mmu_V$MYCMAX_02	246	4	0.46	8.71	0.0041	20.79265
mmu_V$AP2_Q6_01	250	4	0.47	8.57	0.0043	20.28118
mmu_V$MMEF2_Q6	253	4	0.47	8.47	0.0043	20.04452
mmu_V$CEBP_Q2_01	256	4	0.48	8.37	0.0046	19.56272
mmu_CYTAGCAAY_UNKNOWN	129	3	0.24	12.46	0.006	27.68424
mmu_WWTAAGGC_UNKNOWN	131	3	0.24	12.27	0.006	27.26208
mmu_V$AHRARNT_01	130	3	0.24	12.36	0.006	27.46205
mmu_RGAGGAARY_V$PU1_Q6	469	5	0.88	5.71	0.006	12.68676
mmu_CCCNNGGGAR_V$OLF1_01	292	4	0.55	7.34	0.0072	15.72718
mmu_TTCNRGNNNNTTC_V$HSF_Q6	140	3	0.26	11.48	0.0074	24.46122
mmu_V$PPARG_01	41	2	0.08	26.13	0.0083	54.37449
mmu_CRGAARNNNNCGA_UNKNOWN	43	2	0.08	24.92	0.0091	50.86069
mmu_WTGAAAT_UNKNOWN	548	5	1.02	4.89	0.0114	9.501735
mmu_V$ATF_B	176	3	0.33	9.13	0.0134	17.09953
mmu_V$HSF_Q6	180	3	0.34	8.93	0.014	16.55508
mmu_CCAATNNSNNNGCG_UNKNOWN	55	2	0.1	19.48	0.014	36.11343
mmu_V$AHR_01	60	2	0.11	17.86	0.0163	31.93033
mmu_TCCCRNNRTGC_UNKNOWN	192	3	0.36	8.37	0.0163	14.96399
mmu_YTCCCRNNAGGY_UNKNOWN	67	2	0.13	15.99	0.0201	27.1319
mmu_V$HIF1_Q3	210	3	0.39	7.65	0.0205	12.91508
mmu_TGACGTCA_V$ATF3_Q6	213	3	0.4	7.55	0.0212	12.63616
mmu_RYAAAKNNNNNNTTGW_UNKNOWN	77	2	0.14	13.92	0.0216	23.1844
mmu_V$STAT5A_01	233	3	0.43	6.9	0.0216	11.49227

mmu_V$E2F1_Q4_01	216	3	0.4	7.44	0.0216	12.39166
mmu_V$IRF1_Q6	241	3	0.45	6.67	0.0216	11.10919
mmu_TAANNYSGCG_UNKNOWN	76	2	0.14	14.1	0.0216	23.4842
mmu_V$PAX4_03	231	3	0.43	6.96	0.0216	11.5922
mmu_V$CREBP1CJUN_01	241	3	0.45	6.67	0.0216	11.10919
mmu_V$COUP_DR1_Q6	225	3	0.42	7.14	0.0216	11.892
mmu_V$AP2_Q6	237	3	0.44	6.78	0.0216	11.2924
mmu_TCANNTGAY_V$SREBP1_01	437	4	0.82	4.9	0.0216	8.161177
mmu_V$PEA3_Q6	236	3	0.44	6.81	0.0216	11.34237
mmu_V$E2F_Q3_01	221	3	0.41	7.27	0.0216	12.10852
mmu_V$AP4_01	244	3	0.46	6.59	0.0216	10.97595
mmu_V$TFIIA_Q6	235	3	0.44	6.84	0.0216	11.39234
mmu_V$ISRE_01	232	3	0.43	6.93	0.0216	11.54224
mmu_V$ZIC2_01	226	3	0.42	7.11	0.0216	11.84203
mmu_V$SP3_Q3	230	3	0.43	6.99	0.0216	11.64217
mmu_V$ELK1_01	243	3	0.45	6.61	0.0216	11.00926
mmu_V$DR4_Q2	236	3	0.44	6.81	0.0216	11.34237
mmu_V$MYOGENIN_Q6	235	3	0.44	6.84	0.0216	11.39234
mmu_V$P300_01	231	3	0.43	6.96	0.0216	11.5922
mmu_V$P53_DECAMER_Q2	235	3	0.44	6.84	0.0216	11.39234
mmu_GGGNRMNNYCAT_UNKNOWN	78	2	0.15	13.74	0.0216	22.88461
mmu_V$SP1_Q2_01	234	3	0.44	6.87	0.0216	11.4423
mmu_CTGCAGY_UNKNOWN	692	5	1.29	3.87	0.0216	6.445664
mmu_V$HMGIY_Q6	231	3	0.43	6.96	0.0216	11.5922
mmu_V$CREB_01	242	3	0.45	6.64	0.0216	11.05923
mmu_V$SOX9_B1	216	3	0.4	7.44	0.0216	12.39166
mmu_V$AP1_01	244	3	0.46	6.59	0.0216	10.97595
mmu_V$HNF4_DR1_Q3	241	3	0.45	6.67	0.0216	11.10919
mmu_V$FOXO1_02	230	3	0.43	6.99	0.0216	11.64217
mmu_V$NERF_Q2	228	3	0.43	7.05	0.0216	11.7421
mmu_V$ETS_Q4	230	3	0.43	6.99	0.0216	11.64217
mmu_V$NFY_Q6	234	3	0.44	6.87	0.0216	11.4423
mmu_V$ELF1_Q6	226	3	0.42	7.11	0.0216	11.84203
mmu_V$NFKB_C	243	3	0.45	6.61	0.0216	11.00926
mmu_V$YY1_01	221	3	0.41	7.27	0.0216	12.10852
mmu_V$PPAR_DR1_Q2	240	3	0.45	6.7	0.0216	11.15916
mmu_V$SP1_Q4_01	238	3	0.44	6.75	0.0216	11.24244
mmu_V$CEBPA_01	230	3	0.43	6.99	0.0216	11.64217
mmu_V$PR_Q2	238	3	0.44	6.75	0.0216	11.24244
mmu_V$NFY_01	236	3	0.44	6.81	0.0216	11.34237
mmu_TGACCTY_V$ERR1_Q2	954	6	1.78	3.37	0.0216	5.612891

mmu_V$NFY_Q6_01	244	3	0.46	6.59	0.0216	10.97595
mmu_V$CREB_Q3	226	3	0.42	7.11	0.0216	11.84203
mmu_V$HNF4_01	248	3	0.46	6.48	0.022	10.7411
mmu_V$NFAT_Q4_01	247	3	0.46	6.51	0.022	10.79083
mmu_V$HAND1E47_01	246	3	0.46	6.53	0.022	10.82398
mmu_V$NRF2_01	248	3	0.46	6.48	0.022	10.7411
mmu_V$EGR1_01	252	3	0.47	6.38	0.0228	10.47638
mmu_V$COREBINDINGFACTOR_Q6	253	3	0.47	6.35	0.0229	10.41504
mmu_WTTGKCTG_UNKNOWN	475	4	0.89	4.51	0.0233	7.363225
mmu_V$ER_Q6	256	3	0.48	6.28	0.0234	10.24132
mmu_V$USF_C	257	3	0.48	6.25	0.0236	10.1693
mmu_TGAYRTCA_V$ATF3_Q6	487	4	0.91	4.4	0.0249	7.056723
mmu_V$GATA1_05	265	3	0.49	6.07	0.0252	9.703499
mmu_TGCGCANK_UNKNOWN	500	4	0.93	4.29	0.0269	6.736363
mmu_GTTGNYNNRGNAAC_UNKNOWN	99	2	0.18	10.82	0.0272	16.93796
mmu_V$MEIS1AHOXA9_01	107	2	0.2	10.01	0.0313	15.0596
mmu_GCGNNANTTCC_UNKNOWN	110	2	0.21	9.74	0.0329	14.44251
mmu_V$AR_Q2	115	2	0.21	9.32	0.0354	13.52329
mmu_CCTNTMAGA_UNKNOWN	117	2	0.22	9.16	0.0364	13.18031
mmu_TTCYNRGAA_V$STAT5B_01	311	3	0.58	5.17	0.0368	7.414567
mmu_V$PPARA_02	120	2	0.22	8.93	0.0378	12.703
mmu_V$STAT5A_02	121	2	0.23	8.86	0.0381	12.573
mmu_V$PR_02	122	2	0.23	8.78	0.0384	12.42957
mmu_GCANCTGNY_V$MYOD_Q6	854	5	1.59	3.14	0.0387	4.434588
mmu_V$XBP1_01	124	2	0.23	8.64	0.0392	12.15401
mmu_CATTGTYY_V$SOX9_B1	333	3	0.62	4.83	0.0426	6.619952
mmu_YNGTTNNNATT_UNKNOWN	340	3	0.63	4.73	0.0446	6.388646
mmu_V$PAX5_01	139	2	0.26	7.71	0.0475	10.20269
mmu_GGGYGTGNY_UNKNOWN	618	4	1.15	3.47	0.0488	4.551183
mmu_V$OCT1_07	143	2	0.27	7.49	0.0495	9.777407

Table S11. microRNA target enrichment for superconserved hPTH(1-34)-induced significant transcript regulation. For each described microRNA target (murine database), the number of total whole murine genome background microRNAs included in the target group is indicated (C). The number of targets observed (O) in the input dataset that populated the specific microRNA target group is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of microRNA target enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

microRNA target	**C**	**O**	**E**	**R**	**P**	**H**
mmu_ATCATGA,MIR-433	104	3	0.1	29.8	0.0024	78.0697
mmu_ACTGTAG,MIR-139	118	3	0.11	26.27	0.0024	68.82185
mmu_TGTATGA,MIR-485-3P	141	3	0.14	21.98	0.0032	54.8368
mmu_GTATGAT,MIR-154,MIR-487	65	2	0.06	31.79	0.0108	62.51746
mmu_AGGAAGC,MIR-516-3P	114	2	0.11	18.13	0.0232	29.6337
mmu_ATGAAGG,MIR-205	143	2	0.14	14.45	0.0232	23.6187
mmu_GTGACTT,MIR-224	144	2	0.14	14.35	0.0232	23.45525
mmu_TCTCTCC,MIR-185	117	2	0.11	17.66	0.0232	28.86548
mmu_TCATCTC,MIR-143	140	2	0.14	14.76	0.0232	24.1254
mmu_GTGCCAT,MIR-183	164	2	0.16	12.6	0.0266	19.84649
mmu_AACTGGA,MIR-145	213	2	0.21	9.7	0.0312	14.6067
mmu_TTTTGAG,MIR-373	209	2	0.2	9.89	0.0312	14.89281
mmu_CACCAGC,MIR-138	199	2	0.19	10.38	0.0312	15.63068
mmu_TGCTGCT,MIR-15A,MIR-16,MIR-15B,MIR-195,MIR-424,MIR-497	560	3	0.54	5.54	0.0312	8.342384
mmu_CCTGCTG,MIR-214	223	2	0.22	9.27	0.0318	13.8825
mmu_ATTCTTT,MIR-186	252	2	0.24	8.2	0.0374	11.70245
mmu_CAGTGTT,MIR-141,MIR-200A	295	2	0.29	7	0.0444	9.468319
mmu_GTGCCAA,MIR-96	290	2	0.28	7.13	0.0444	9.644159

Table S12. microRNA target enrichment for superconserved bPTH(7-34)-induced significant transcript regulation. For each described microRNA target (murine database), the number of total whole murine genome background microRNAs included in the target group is indicated (C). The number of targets observed (O) in the input dataset that populated the specific microRNA target group is indicated, as well as the number expected by chance from the background expression frequency (E) in the genome. The degree of microRNA target enrichment (R) is then calculated from O/E. The probability of this enrichment is denoted by P. The hybrid score (H) is a combinatorial measure of both R and P (*i.e.* $-\log_{10}(P) * R$).

microRNA target	**C**	**O**	**E**	**R**	**P**	**H**
mmu_TATTATA,MIR-374	267	6	0.5	12.04	0.0005	39.7444
mmu_AAAGACA,MIR-511	185	5	0.35	14.48	0.0005	47.79891
mmu_CAGTGTT,MIR-141,MIR-200A	295	6	0.55	10.9	0.0005	35.98123
mmu_TTGCCAA,MIR-182	307	6	0.57	10.47	0.0005	34.56178
mmu_AAAGGGA,MIR-204,MIR-211	209	5	0.39	12.82	0.0008	39.70239
mmu_GTGCAAA,MIR-507	124	4	0.23	17.28	0.0012	50.47175
mmu_GACTGTT,MIR-212,MIR-132	149	4	0.28	14.38	0.0018	39.46918
mmu_CCAGGTT,MIR-490	61	3	0.11	26.35	0.0018	72.32357
mmu_CTAGGAA,MIR-384	62	3	0.12	25.92	0.0018	71.14334
mmu_ATACCTC,MIR-202	173	4	0.32	12.39	0.0022	32.92738
mmu_TGGTGCT,MIR-29A,MIR-29B,MIR-29C	478	6	0.89	6.72	0.0022	17.85892
mmu_TCTGATA,MIR-361	82	3	0.15	19.6	0.0033	48.63713
mmu_TAATAAT,MIR-126	208	4	0.39	10.3	0.0036	25.17008
mmu_AACTGGA,MIR-145	213	4	0.4	10.06	0.0037	24.46389
mmu_GGCAGTG,MIR-324-3P	92	3	0.17	17.47	0.0037	42.48352
mmu_ACTGTGA,MIR-27A,MIR-27B	438	5	0.82	6.12	0.0061	13.55378
mmu_CCTGTGA,MIR-513	116	3	0.22	13.86	0.0061	30.69533
mmu_CAGTATT,MIR-200B,MIR-200C,MIR-429	437	5	0.82	6.13	0.0061	13.57593
mmu_ACATTCC,MIR-1,MIR-206	275	4	0.51	7.79	0.0071	16.7387
mmu_ATGTAGC,MIR-221,MIR-222	130	3	0.24	12.36	0.0071	26.55845
mmu_TGCACTG,MIR-148A,MIR-152,MIR-148B	278	4	0.52	7.71	0.0071	16.5668
mmu_ACTACCT,MIR-196A,MIR-196B	134	3	0.25	11.99	0.0075	25.47802
mmu_GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367	290	4	0.54	7.39	0.0076	15.66079
mmu_ACCATTT,MIR-522	149	3	0.28	10.79	0.0088	22.17903
mmu_CACTGTG,MIR-128A,MIR-128B	306	4	0.57	7	0.0088	14.38862
mmu_TGCTGCT,MIR-15A,MIR-16,MIR-15B,MIR-195,MIR-424,MIR-497	560	5	1.05	4.78	0.0125	9.09677
mmu_CCATCCA,MIR-432	52	2	0.1	20.61	0.0126	39.15136
mmu_GGCACAT,MIR-455	56	2	0.1	19.13	0.0127	36.27423
mmu_GTACAGG,MIR-486	55	2	0.1	19.48	0.0127	36.9379
mmu_ACTGAAA,MIR-30A-3P,MIR-30E-3P	181	3	0.34	8.88	0.0127	16.83822
mmu_TGTGTGA,MIR-377	183	3	0.34	8.78	0.0127	16.6486

mmu_GTGTGAG,MIR-342	60	2	0.11	17.86	0.0136	33.335
mmu_AAGCACA,MIR-218	377	4	0.7	5.68	0.0136	10.6015
mmu_AATGTGA,MIR-23A,MIR-23B	391	4	0.73	5.48	0.0146	10.05935
mmu_GCAAGGA,MIR-502	65	2	0.12	16.48	0.0149	30.10589
mmu_GTGCCTT,MIR-506	666	5	1.24	4.02	0.0184	6.975432
mmu_ATGTTAA,MIR-302C	228	3	0.43	7.05	0.0191	12.11871
mmu_TCTATGA,MIR-376A,MIR-376B	77	2	0.14	13.92	0.0191	23.92802
mmu_GTTTGTT,MIR-495	238	3	0.44	6.75	0.0201	11.45343
mmu_AGGCACT,MIR-515-3P	81	2	0.15	13.23	0.0201	22.44872
mmu_AGGTGCA,MIR-500	86	2	0.16	12.46	0.0218	20.70283
mmu_AACTGAC,MIR-223	87	2	0.16	12.32	0.0218	20.47022
mmu_ATTACAT,MIR-380-3P	92	2	0.17	11.65	0.0239	18.89166
mmu_ATAGGAA,MIR-202	95	2	0.18	11.28	0.0242	18.23056
mmu_GTGTTGA,MIR-505	95	2	0.18	11.28	0.0242	18.23056
mmu_ACTTTAT,MIR-142-5P	274	3	0.51	5.87	0.0256	9.343631
mmu_ACTGCAG,MIR-17-3P	101	2	0.19	10.61	0.0261	16.79944
mmu_ATCATGA,MIR-433	104	2	0.19	10.3	0.0268	16.19021
mmu_ATGCAGT,MIR-217	106	2	0.2	10.11	0.0272	15.82651
mmu_GCACCTT,MIR-18A,MIR-18B	108	2	0.2	9.92	0.0277	15.4506
mmu_ATGTACA,MIR-493	296	3	0.55	5.43	0.0282	8.415147
mmu_AGGAAGC,MIR-516-3P	114	2	0.21	9.4	0.0295	14.38367
mmu_TGCTTTG,MIR-330	307	3	0.57	5.24	0.0297	8.002756
mmu_AGCATTA,MIR-155	118	2	0.22	9.08	0.0297	13.86737
mmu_ACTGTAG,MIR-139	118	2	0.22	9.08	0.0297	13.86737
mmu_TTGCACT,MIR-130A,MIR-301,MIR-130B	370	3	0.69	4.34	0.0452	5.836699
mmu_ATGTTTC,MIR-494	151	2	0.28	7.1	0.0452	9.548517
mmu_CATGTAA,MIR-496	160	2	0.3	6.7	0.0494	8.752029

Table S13. KEGG pathway-based keystone factor analysis for hPTH(1-34) and bPTH(7-34) superconserved transcript datasets. For both superconserved ligand-regulated datasets both 95th (p=0.05) and 99th (p=0.01) percentile cut-offs were employed to induce distinct levels of multidimensional keystone strength. Each identified transcript (denoted by the specific Gene Symbol) possesses at least a Cosine Similarity score of >0.1, indicating at least an implicit association with the input KEGG pathway interrogator term.

hPTH(1-34) p=0.01	**hPTH(1-34) p=0.05**	**bPTH(7-34) p=0.01**	**bPTH(7-34) p=0.05**
atg9a	atg9a	scg2	scg2
lpin2	lpin2	nts	nts
pank2	pank2	maged1	maged1
capn5	capn5	gpr55	gpr55
vps54	vps54	ssh1	ssh1
fabp3	fabp3	pea15	pea15
nhlrc1	nhlrc1	gper	gper
atg5	atg5	ptprs	ptprs
asmd	asmd	zfp36	zfp36
afg3l2	afg3l2	ptpn9	ptpn9
epm2a	epm2a	nr4a1	nr4a1
ppt1	ppt1	mtnr1a	mtnr1a
spast	spast	rap1gap	rap1gap
pabpn1	pabpn1	prex1	prex1
dars2	dars2	mok	mok
tor1a	tor1a	gdf15	gdf15
usp30	usp30	igfbp7	igfbp7
coq2	coq2	gipc1	gipc1
mrps27	mrps27	fgf7	fgf7
dnm1l	dnm1l	il11	il11
kiaa1549l	kiaa1549l	pdlim7	pdlim7
atg4a	atg4a	frk	frk
trappc5	trappc5	dok4	dok4
acyp2	acyp2	metrnl	metrnl
atg7	atg7	arhgap4	arhgap4
fxn	fxn	appl1	appl1
kiaa0226	kiaa0226	insrr	insrr
psmc4	psmc4	eef2	eef2
cln3	cln3	atf3	atf3
oit3	oit3	eef2k	eef2k
serf2	serf2	mzb1	mzb1

fastkd3	fastkd3	ptpro	ptpro
fastkd1	fastkd1	zhx2	zhx2
fastkd5	fastkd5	arhgdia	arhgdia
ppp2r4	ppp2r4	pla2g4c	pla2g4c
rcan1	rcan1	pik3r5	pik3r5
abcd4	abcd4	mmd2	mmd2
pex11b	pex11b	nuak2	nuak2
cyp4f22	cyp4f22	neu3	neu3
them5	them5	ptprh	ptprh
cisd1	cisd1	prkd3	prkd3
tfam	tfam	wisp2	wisp2
oxct1	oxct1	nisch	nisch
slc25a1	slc25a1	hspd1	hspd1
dgke	dgke	rgs16	rgs16
pnpla8	pnpla8	egfl6	egfl6
arhgap20	arhgap20	gpr68	gpr68
plin4	plin4	nuak1	nuak1
dgat1	dgat1	trib2	trib2
sc5d	sc5d	map4k4	map4k4
rarres2	rarres2	cdon	cdon
plin2	plin2	nupr1	nupr1
dgat2	dgat2	ptpn12	ptpn12
bscl2	bscl2	enpp2	enpp2
dync1h1	dync1h1	rmdn3	rmdn3
slc2a13	slc2a13	sgms1	sgms1
b3galt4	b3galt4	txnip	txnip
map1b	map1b	stk25	stk25
thtpa	thtpa	pik3c2a	pik3c2a
	ndufv2	ralgapa2	ralgapa2
	mfsd12	aebp1	aebp1
	nd6	camk2n2	camk2n2
	nat8l	ppm1f	ppm1f
	pdss1	gnb2l1	gnb2l1
	acadm	rit1	rit1
	gdf15	iqgap1	iqgap1
	bp3	trpm7	trpm7
	bp2	ndrg4	ndrg4
	mir5691	pggt1b	pggt1b
	bai3	fabp5	fabp5
	bp4	chn2	chn2
	bmnd2	clic4	clic4

	pee1	ddr2	ddr2
	capn10	tdgf1	tdgf1
	fabp2	tm4sf5	tm4sf5
	slc25a29	rasl11b	rasl11b
	scd	thsd1	thsd1
	mir605	npnt	npnt
	plin1	fhl3	fhl3
	pnpla3	has1	has1
	ffar1	naa15	naa15
	atg12	fnta	fnta
	atg14	foxq1	foxq1
	map1lc3a	nrep	nrep
	nbr1	stc1	stc1
	atg16l2	c1qtnf4	c1qtnf4
	hdac6	asb15	asb15
	becn1	il24	il24
	als7		map2k3
	sumf1		srcin1
	tbce		rin1
	ctns		mapk7
	tuba1b		tsc2
	gcdh		prkci
	rnaseh2a		alox15
	ndufs7		alox12
	pcmt1		grpr
	dhrs4l2		rps6ka2
	ndufa7		rps6ka3
	trni		acvr1c
	slc33a1		igfbp6
	ndufaf6		id1
	sdim1		klf10
	hexb		nmu
	b3galt1		ereg
	msrb2		prok1
	arfgap1		prokr1
	gigyf2		axl
	psma7		shc4
	slc25a18		vav2
	psmc1		cxcl14
	cnbp		rala
	thap1		csk

	enoph1		pik3cb
	snx33		ralbp1
	wars		prkch
	fig4		serpinf1
	coq7		arhgap5
	chchd4		pik3r2
	btd		retnlb
	msra		fer
	opa1		yes1
	galc		ralgds
	stard4		dusp6
	gba		crk
	klc1		tiam1
	mcoln1		rasgrp3
	hmgcl		akap12
	msrb1		stmn1
	ndufa1		lpar2
	psap		plce1
	alkbh7		ptn
	vdac1		rhob
	hgsnat		mdk
	znf334		lpar1
	naglu		btg2
	b3galt2		klf4
	c1orf85		lrrc4
	pus10		etv1
	gbe1		artn
	atp10d		fstl1
	ndufs2		dab2
	gaa		sulf1
	mtmr6		wisp1
	slc19a3		cyr61
	ccz1		sema7a
	scp2		tgfb1i1
	tst		znf580
	coa5		nedd9
	rab28		reck
	ccdc88b		wisp3
	fis1		pdgfd
	tspan11		rgcc
	ndnf		elf3

	bcs1l		fhl2
	slc30a10		areg
	cep112		has2
	galt		itga8
	ndufs3		tagln
	uqcrc1		ptk6
	c10orf2		bmx
	slc25a13		il20
	nucks1		ppm1a
	mfn2		sos2
	acy1		prkd1
	qpct		spry3
	lrch3		sgpp1
	col4a3bp		ptpra
	ppif		pik3c2g
	ppox		ptprf
	gimap2		mapk13
	gbap1		capn2
	mff		hipk3
	dguok		brsk2
	ndufv1		madd
	vps35		crtc1
	cpne7		gnrh2
	syn3		ranbp9
	ndufs4		nenf
	snord12c		traf4
	sbds		ptprr
	chchd7		prr5
	chchd6		agap2
	pex13		ralb
	mut		pik3ip1
	ahcy		ptpn21
	prdx4		sh2d3a
	tuba4a		grb7
	parl		pip4k2b
	mars2		cerk
	gne		clmp
	yme1l1		ptpn13
	polg		ksr1
	atp6		phip
	nd1		tbc1d3

	mrs2		pik3ap1
	suox		cnksr1
	rdh14		pak7
	mon1a		gmfb
	spg7		rasgrf2
	psma2		ntsr2
	dhrs4l1		ncam2
	tbc1d8b		numbl
	htn3		stk17b
	cpox		camk1d
	pygm		ptprk
	psmd11		erbb2ip
	rpn2		net1
	arsa		tob2
	psmc3		dynlrb1
	mocs1		stk16
	xk		tob1
	slc17a5		nbl1
	etfa		fam3c
	cox17		serpinb10
	c19orf12		crtc2
	aspa		rheb
	mccc2		smurf1
	cln6		lox
	rab5b		c1qtnf6
	cln5		mapk4
	gsap		ddit4
	oma1		rrad
	mgst1		mapk6
	trappc8		rps6
	prss3p2		ggps1
	gnptab		trib3
	cln8		ppp2r5a
	pmpcb		grb14
	vdac1p3		ogt
	epg5		chka
	dmwd		pim3
	kiaa1033		errfi1
	nudt14		klb
	ckmt1b		ddit4l
	ckb		rasd1

	blmh		pawr
	ppt2		bex1
	bace1-as		gpr39
	slc38a5		gprc6a
	dmpk		uchl3
	dhodh		nfatc4
	yipf6		sphkap
	kmo		thg1l
	ppp2r2b		klf14
	iscu		rasl10b
	ptbp2		ppap2a
	txnl4a		ptpn23
	cox6b1p3		cdk5rap3
	slc1a2		spred2
	zmat1		rgl2
	paaf1		rras
	pdxk		mzf1
	slc7a11		mapkapk5
	slc25a39		mir92a1
	atg9b		fgfbp1
	psme3		zc3h12c
	ddx24		dusp10
	atg12p1		brap
	atg4b		mir214
	rab33b		mst1
	gpr158		creg1
	tbc1d25		akap13
	stab2		mir190a
	dusp15		cxcl17
	oser1		cyp4z1
	gimap8		mir101-1
	ttpa		ccdc88a
	tmbim6		lmcd1
	phb		anxa2r
	slc25a15		hsp90aa2
	loc401131		metap2
	cdo1		ptp4a2
	cers5		dab2ip
	rnase3		ddr1
	mid1		eltd1
	zadh2		mir564

	hadhb		ociad1
	lrrc8c		lrrn3
	dbi		med28
	cpt2		cdcp1
	clps		rgs3
	lipa		tnfrsf12a
	decr1		bst1
	plin3		stk4
	atpaf1		tnfrsf25
	mospd1		ptprm
	glyat		aimp1
	slc44a1		wdr83
	abhd12		st3gal5
	mettl7b		sgpl1
	tysnd1		ptp4a1
	cox15		sh3rf3
	nt5m		trip6
	cers4		pxdn
	glyctk		rpsa
	acot7		ecscr
	aebp1		slk
	fabp5		chi3l2
	mat2a		pkn3
	elovl1		map3k6
	acadl		marcksl1
	gnpat		mtus1
	acot11		rnf181
	pank3		mgarp
	grhpr		plxnc1
	abhd5		lect2
	mfsd8		thoc5
	ifi27l2		phpt1
	eddm3b		kank1
	akap10		pgam1
	tor2a		phlda1
	ntan1		mir30c2
	eddm3a		icmt
	slc30a6		inpp5j
	c19orf59		inpp4b
	plin5		lamtor1
	pnpla2		gpld1

	echs1		sorbs2
	acsl1		cd68
	rnr2		pnck
	nus1		chl1
	sptlc1		clca1
	lppr4		mrvi1
	gpr12		cib1
	scarna17		limk1
	scarna7		dpysl3
	scarna9		bai1
	scarna12		rcan1
	scarna6		nrn1
	dars		loxl2
	c21orf62		scube3
	ift43		tmtc3
	bex5		spon1
	smpd2		fut8
	ppt2-egfl8		fndc3b
	tub		crtac1
			adam19
			lrg1
			serpinh1
			tnfaip6
			dpt
			bambi
			fap
			cdc42ep3
			fndc1
			fermt1
			slc39a9
			fntb
			fbln1
			rgmb
			vasn
			angptl7
			ltbp1
			bmp10
			ptpn14
			tnn
			col1ar
			rgma

			lrp12
			cthrc1
			socs6
			stap2
			ptpn2
			gadd45gip1
			gbp1
			ndufa13
			pdlim2

Table S14. Word occurrence scores for hPTH(1-34) and bPTH(7-34) keystone factors. Word occurrence scores were generated using Genes2Wordcloud with the input 99th percentile-ranked keystone factors derived from KEGG pathway analysis of the hPTH(1-34) and bPTH(7-34) superconserved datasets. hPTH(1-34) word scores are denoted in black, bPTH(7-34) word scores are denoted in blue.

hPTH(1-34)		**bPTH(7-34)**	
Word	***Occurrence Score***	***Word***	***Occurrence Score***
mitochondrial	85	receptor	134
regulate	76	regulate	126
mutated	74	transcript	117
autophagy	69	mrna	109
neuron	64	signal	93
cdna	56	cdna	92
transcript	55	cancer	90
clone	48	inhibit	88
cellular	48	kinase	86
site	47	differential	59
brain	47	clone	56
signal	47	growth	54
model	45	bind	54
cause	43	pathway	50
muscle	42	tumor	49
acid	42	full-length	48
mrna	42	overexpressed	47
target	40	diabetic	45
decrease	40	tissue	45
bind	39	decrease	42
rna	39	apoptosis	42
deficient	38	response	41
inhibit	38	rack1	39
fatty	37	genome	36
enzyme	37	suppress	35
tissue	37	new	35
structure	37	up-regulated	35
phosphorylate	37	neuron	35
general	37	treatment	35
reveal	34	phosphorylated	33
degraded	34	reduce	32
mutant	34	general	31

map	34	neurotensin	31
overexpress	34	secreted	31
reduce	33	reveal	31
provide	33	vitro	31

Table S15. Latent semantic indexing interrogator terms. The specific textual terms outlined below were employed to generate the respective implicit gene-association lists: each reported identified gene possesses a Cosine Similarity score of at least >0.1.

Arrestin	**G protein**	**Cell Signaling**
arrestin	G protein	signaling
arrestin 2	G alpha	cell signaling
arrestin-2	G beta	cellular signaling
arrestin 3	G gamma	signal transduction
arrestin-3	G beta gamma	intermediary cell metabolism
beta arrestin 1	Guanine-nucleotide binding protein	signalling
beta arrestin-1	Heterotrimeric	cell signalling
beta arrestin 2	G alpha beta gamma	cellular signalling
beta arrestin-2		

Table S16. Arrestin theoretical dataset. Latent semantic indexing generated list of implicitly-associated genes linked to arrest-related input terminology. For each gene the Gene Symbol and textual definition is denoted below.

Gene Symbol	Definition
1110020p15rik	ubiquinol-cytochrome c reductase, complex III subunit X
1110028a07rik	fat storage-inducing transmembrane protein 1
1200014j11rik	similar to RIKEN cDNA 1200014J11 gene; RIKEN cDNA 1200014J11 gene
1500005a01rik	family with sequence similarity 158, member A
1500010j02rik	RIKEN cDNA 1500010J02 gene
1700001g17rik	RIKEN cDNA 1700001G17 gene
2310079n02rik	RIKEN cDNA 2310079N02 gene
3222402p14rik	protein phosphatase 2, regulatory subunit B'', alpha
3300001g02rik	small nuclear ribonucleoprotein 25 (U11/U12)
3322402l07rik	retinal degeneration 3
5730449l18rik	tRNA splicing endonuclease 15 homolog (S. cerevisiae)
621968	T-cell receptor beta, variable 1
751864	predicted gene 9733
8430415e04rik	protein phosphatase 4, regulatory subunit 4
9230105e10rik	similar to tripartite motif protein TRIM5; RIKEN cDNA 9230105E10 gene
9930022n03rik	T cell-interacting, activating receptor on myeloid cells 1
a430107p09rik	similar to T-cell receptor alpha chain V region CTL-L17 precursor;
a630038e17rik	RIKEN cDNA A630038E17 gene; RIKEN cDNA A630098A13 gene
a630098a13rik	RIKEN cDNA A630038E17 gene; RIKEN cDNA A630098A13 gene
a730076h11rik	RIKEN cDNA A730076H11 gene
aak1	AP2 associated kinase 1
abca4	ATP-binding cassette, sub-family A (ABC1), member 4
abhd1	abhydrolase domain containing 1
abhd2	abhydrolase domain containing 2
abhd3	abhydrolase domain containing 3
abhd6	predicted gene 1833; abhydrolase domain containing 6
abpa	androgen binding protein alpha; hypothetical protein LOC100044256
abpb	androgen binding protein beta
abpd	predicted gene 6725; androgen binding protein delta; predicted gene 4684
abpe	androgen binding protein epsilon
abpg	androgen binding protein gamma
abpz	androgen binding protein zeta
abtb2	ankyrin repeat and BTB (POZ) domain containing 2
actl6b	actin-like 6B
acvr1b	activin A receptor, type 1B
acvr1c	activin A receptor, type IC
acvr2a	activin receptor IIA
acvr2b	activin receptor IIB
adam1a	a disintegrin and metallopeptidase domain 1a
adam1b	similar to a disintegrin and metalloproteinase domain 1b; a disintegrin and metallopeptidase domain 1b
adam2	a disintegrin and metallopeptidase domain 2
adam23	a disintegrin and metallopeptidase domain 23; similar to ADAM23
adam3	a disintegrin and metallopeptidase domain 3 (cyritestin)
adam4	predicted gene 5746; a disintegrin and metallopeptidase domain 4
adam5	a disintegrin and metallopeptidase domain 5
adamts16	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16
add2	adducin 2 (beta)

add3	adducin 3 (gamma)
adra1a	adrenergic receptor, alpha 1a
adra1b	adrenergic receptor, alpha 1b
adra1d	adrenergic receptor, alpha 1d
adra2a	adrenergic receptor, alpha 2a
adra2b	adrenergic receptor, alpha 2b
adra2c	similar to alpha-2 adrenergic receptor; adrenergic receptor, alpha 2c
adrb1	adrenergic receptor, beta 1
adrb2	adrenergic receptor, beta 2
adrbk1	adrenergic receptor kinase, beta 1
adrbk2	adrenergic receptor kinase, beta 2
ads4	anti dsDNA antibody 4
aftph	aftiphilin
ai324046	expressed sequence AI324046
ai607873	expressed sequence AI607873
aipl1	aryl hydrocarbon receptor-interacting protein-like 1
akap5	A kinase (PRKA) anchor protein 5
akr1c19	aldo-keto reductase family 1, member C19
aldr5	aldehyde reductase 5
alph1	alphaprotein 1
alph2	alphaprotein 2
als2cl	ALS2 C-terminal like
als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 homolog (human)
amd	autoimmune myocardial disease
ankrd44	ankyrin repeat domain 44
ankrd49	ankyrin repeat domain 49
ankrd52	ankyrin repeat domain 52
ap1b1	adaptor protein complex AP-1, beta 1 subunit
ap1m1	adaptor-related protein complex AP-1, mu subunit 1
ap1m2	adaptor protein complex AP-1, mu 2 subunit
ap1s1	adaptor protein complex AP-1, sigma 1
ap2a1	adaptor protein complex AP-2, alpha 1 subunit
ap2a2	hypothetical protein LOC100044229; adaptor protein complex AP-2, alpha 2 subunit
ap2b1	adaptor-related protein complex 2, beta 1 subunit
ap2m1	predicted gene 8717; adaptor protein complex AP-2, mu1
ap2s1	adaptor-related protein complex 2, sigma 1 subunit
ap3m1	adaptor-related protein complex 3, mu 1 subunit; similar to Adapter-related protein complex 3 mu 1 subunit (Mu-adaptin 3A) (AP-3 adapter complex mu3A subunit)
ap3s1	predicted gene 7603; adaptor-related protein complex 3, sigma 1 subunit; predicted gene 5610
ap3s2	adaptor-related protein complex 3, sigma 2 subunit
ap4b1	adaptor-related protein complex AP-4, beta 1
ap4e1	adaptor-related protein complex AP-4, epsilon 1
ap4m1	adaptor-related protein complex AP-4, mu 1
ap4s1	adaptor-related protein complex AP-4, sigma 1
apbh	androgen-binding protein eta
arcn1	similar to Archain 1; archain 1; similar to coat protein delta-cop; predicted gene 8752; predicted gene 8750; similar to archain
arf6	ADP-ribosylation factor 6
arl3	ADP-ribosylation factor-like 3
arr3	arrestin 3, retinal
arrb1	arrestin, beta 1
arrb2	arrestin, beta 2
arrdc2	arrestin domain containing 2
arrdc3	arrestin domain containing 3
arrdc4	arrestin domain containing 4
asa	anti-sarcolemmal autoantibodies

atp12a	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide
atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide
atp1a4	ATPase, Na+/K+ transporting, alpha 4 polypeptide
atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide
atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide
atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide
atp1b3-rs	ATPase, Na+/K+ transporting, beta 3 polypeptide, related sequence
atp1b3-rs2	ATPase, Na+/K+ transporting, beta 3 polypeptide, related sequence 2
atp1b4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide
atp4a	ATPase, H+/K+ exchanging, gastric, alpha polypeptide
atp4b	ATPase, H+/K+ exchanging, beta polypeptide
atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit
atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1; predicted gene 12231
atp5g2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F
atp5j2	predicted gene 6835; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2; predicted gene 6581
atp5k	predicted gene 2972; ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e
atp5l	ATP synthase, H+ transporting, mitochondrial FO complex, subunit G2, pseudogene;
atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s
atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C, pseudogene 2; ATPase, H+ transporting, lysosomal V0 subunit C
atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2
atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1
aup1	ancient ubiquitous protein 1
avpr2	arginine vasopressin receptor 2
b230339m05rik	Ral GTPase activating protein, beta subunit (non-catalytic)
b3galt4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4
b3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
b3galt6	similar to UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6; UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6
b3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)
b3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
b3gnt3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
b3gnt4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
b3gnt5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
b4galnt3	beta-1,4-N-acetyl-galactosaminyl transferase 3
b4galnt4	beta-1,4-N-acetyl-galactosaminyl transferase 4
b4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1
b4galt2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2
b4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3
b4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4
b4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
b4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6; similar to Beta-1,4-galactosyltransferase 6
bat4	predicted gene 5628; HLA-B associated transcript 4
bat5	HLA-B associated transcript 5
bc023829	cDNA sequence BC023829
bc023892	family with sequence similarity 46, member A
bcam	basal cell adhesion molecule
bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide
bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide; similar to 3-methyl-2-oxobutanoate dehydrogenase
blvrb	biliverdin reductase B (flavin reductase (NADPH))

bmp15	bone morphogenetic protein 15
bola1	bolA-like 1 (E. coli)
bola2	bolA-like 2 (E. coli)
bola3	bolA-like 3 (E. coli)
btf3	predicted gene 9308; basic transcription factor 3; predicted gene 3531; predicted gene 7973
c330016o10rik	RIKEN cDNA C330016O10 gene
c4bp-ps1	complement component 4 binding protein, pseudogene 1
c8a	complement component 8, alpha polypeptide
c8b	complement component 8, beta polypeptide
c8g	complement component 8, gamma polypeptide
cab39	calcium binding protein 39
cabp2	calcium binding protein 2
cabp4	calcium binding protein 4
cabp5	similar to CaBP5; calcium binding protein 5
cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit
cacna1d	calcium channel, voltage-dependent, L type, alpha 1D subunit
cacna1f	calcium channel, voltage-dependent, alpha 1F subunit
cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1
cacna2d2	calcium channel, voltage-dependent, alpha 2/delta subunit 2; similar to Cacna2d2 protein
cacna2d3	calcium channel, voltage-dependent, alpha2/delta subunit 3
cacna2d4	calcium channel, voltage-dependent, alpha 2/delta subunit 4
cacnb1	calcium channel, voltage-dependent, beta 1 subunit
cacnb2	calcium channel, voltage-dependent, beta 2 subunit
cacnb3	calcium channel, voltage-dependent, beta 3 subunit
cacnb4	calcium channel, voltage-dependent, beta 4 subunit
cacng1	calcium channel, voltage-dependent, gamma subunit 1
cacng3	calcium channel, voltage-dependent, gamma subunit 3
cacng4	calcium channel, voltage-dependent, gamma subunit 4
cacng5	calcium channel, voltage-dependent, gamma subunit 5
cacng6	calcium channel, voltage-dependent, gamma subunit 6
cacng7	calcium channel, voltage-dependent, gamma subunit 7
calr2	calreticulin 2
camk1g	calcium/calmodulin-dependent protein kinase I gamma
camk2b	calcium/calmodulin-dependent protein kinase II, beta
camkl	calcium/calmodulin dependent protein kinase-like
capns2	calpain, small subunit 2
capza1	capping protein (actin filament) muscle Z-line, alpha 1; similar to capping protein (actin filament) muscle Z-line, alpha 1; predicted gene 3608; predicted gene 5920
capza1-ps2	capping protein (actin filament) muscle Z-line, alpha 1, pseudogene 2
capza2	capping protein (actin filament) muscle Z-line, alpha 2
capzb	capping protein (actin filament) muscle Z-line, beta
cbl-ps1	Casitas B-lineage lymphoma, pseudogene 1
cbx3-ps1	chromobox homolog 3 (Drosophila HP1 gamma), pseudogene 1
cbx3-ps2	chromobox homolog 3 (Drosophila HP1 gamma), pseudogene 2
cbx3-ps3	chromobox homolog 3 (Drosophila HP1 gamma), pseudogene 3
ccdc85b	coiled-coil domain containing 85B
ccl19	predicted gene 2564; predicted gene 12407; predicted gene 2457; chemokine (C-C motif) ligand 19; predicted gene 2023
ccl21b	predicted gene 13304; similar to beta chemokine Exodus-2; predicted gene 10591; chemokine (C-C motif) ligand 21B; chemokine (C-C motif) ligand 21C (leucine)
ccl21c	predicted gene 13304; similar to beta chemokine Exodus-2; predicted gene 10591; chemokine (C-C motif) ligand 21B; chemokine (C-C motif) ligand 21C (leucine)
ccl25	chemokine (C-C motif) ligand 25
ccr1l1	chemokine (C-C motif) receptor 1-like 1
ccr7	chemokine (C-C motif) receptor 7
ccrl1	chemokine (C-C motif) receptor-like 1
ccrl2	chemokine (C-C motif) receptor-like 2

cct2	chaperonin containing Tcp1, subunit 2 (beta)
cct3	chaperonin containing Tcp1, subunit 3 (gamma)
cct3-ps1	chaperonin containing Tcp1, subunit 3 (gamma) pseudogene 1
cct5	chaperonin containing Tcp1, subunit 5 (epsilon)
cct6a	chaperonin containing Tcp1, subunit 6a (zeta)
cct7	chaperonin containing Tcp1, subunit 7 (eta)
cct8	chaperonin containing Tcp1, subunit 8 (theta)
cd3d	CD3 antigen, delta polypeptide
cd3g	CD3 antigen, gamma polypeptide
cd84	CD84 antigen
cd8b1	CD8 antigen, beta chain 1
cdc42bpb	CDC42 binding protein kinase beta
cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2
cebpg	CCAAT/enhancer binding protein (C/EBP), gamma
cep290	centrosomal protein 290
cerkl	ceramide kinase-like
cetn1	centrin 1
cetn3	centrin 3
cetn4	centrin 4; predicted gene 7094
cfhe	complement component factor h, electrophoretic variant
cga	glycoprotein hormones, alpha subunit
chkb	choline kinase beta
chm	similar to choroidermia; choroidermia
chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle); similar to acetylcholine receptor alpha-subunit
chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)
chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6
chrnb1	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)
chrnb3	cholinergic receptor, nicotinic, beta polypeptide 3
chrnb4	cholinergic receptor, nicotinic, beta polypeptide 4
chrnd	cholinergic receptor, nicotinic, delta polypeptide
chrne	cholinergic receptor, nicotinic, epsilon polypeptide
chrng	cholinergic receptor, nicotinic, gamma polypeptide
chst8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8
chst9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9
circp1	circadian photosensitivity 1
circp2	circadian photosensitivity 2
clta	clathrin, light polypeptide (Lca)
cltb	clathrin, light polypeptide (Lcb)
cltc	clathrin, heavy polypeptide (Hc)
cnga1	cyclic nucleotide gated channel alpha 1
cnga3	cyclic nucleotide gated channel alpha 3
cnga4	cyclic nucleotide gated channel alpha 4
cngb1	cyclic nucleotide gated channel beta 1
cngb3	cyclic nucleotide gated channel beta 3
col13a1	collagen, type XIII, alpha 1
col16a1	collagen, type XVI, alpha 1
col6a3	collagen, type VI, alpha 3
copa	coatomer protein complex subunit alpha
copb1	coatomer protein complex, subunit beta 1
copb2	coatomer protein complex, subunit beta 2 (beta prime)
cope	coatomer protein complex, subunit epsilon
copg	coatomer protein complex, subunit gamma
copg2	coatomer protein complex, subunit gamma 2
copz1	coatomer protein complex, subunit zeta 1
copz2	coatomer protein complex, subunit zeta 2

cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like; predicted gene 6969
cpn2	carboxypeptidase N, polypeptide 2
crb1	crumbs homolog 1 (Drosophila)
creb5	RIKEN cDNA 9430076C15 gene; cAMP responsive element binding protein 5
creld2	cysteine-rich with EGF-like domains 2
crsp	cryptorchidism with white spotting, deletion region
crx	cone-rod homeobox containing gene
cryba2	crystallin, beta A2
crygn	crystallin, gamma N
csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)
csn1s1	casein alpha s1
csn1s2a	casein alpha s2-like A
csn1s2b	casein alpha s2-like B
csn2	casein beta
csn3	casein kappa
csnk1g1	casein kinase 1, gamma 1
csnk1g3	casein kinase 1, gamma 3; similar to casein kinase 1, gamma 3
csnk2a1-ps1	casein kinase 2, alpha 1 polypeptide, pseudogene 1
csnk2a1-rs2	casein kinase 2, alpha 1, related sequence 2
csnk2a1-rs3	casein kinase 2, alpha 1, related sequence 3
cts	cataract and small eye
cx3cl1-rs1	chemokine (C-X3-C motif) ligand 1, related sequence 1
cxcl3	chemokine (C-X-C motif) ligand 3
cxcr4	chemokine (C-X-C motif) receptor 4
cxcr7	chemokine (C-X-C motif) receptor 7
cyp11d	cytochrome P450, 11d
cyp2a	cytochrome P450, family 2, subfamily a
cyp2b13	cytochrome P450, family 2, subfamily b, polypeptide 13
cyp2d	cytochrome P450, 2d region
cyp2d10	cytochrome P450, family 2, subfamily d, polypeptide 10
cyp2d11	cytochrome P450, family 2, subfamily d, polypeptide 11
cysltr1	cysteinyl leukotriene receptor 1
d10mit135	DNA segment, Chr 10, Massachusetts Institute of Technology 135
d10mit164	DNA segment, Chr 10, Massachusetts Institute of Technology 164
d10mit271	DNA Segment, Chr 10, Massachusetts Institute of Technology 271
d10mit70	DNA segment, Chr 10, Massachusetts Institute of Technology 70
d10mit96	DNA segment, Chr 10, Massachusetts Institute of Technology 96
d10nds2	DNA segment, Chr 10, Nuffield Department of Surgery 2
d11mit174	DNA segment, Chr 11, Massachusetts Institute of Technology 174
d11mit188	DNA segment, Chr 11, Massachusetts Institute of Technology 188
d11mit51	DNA segment, Chr 11, Massachusetts Institute of Technology 51
d11mit84	DNA segment, Chr 11, Massachusetts Institute of Technology 84
d13mit130	DNA segment, Chr 13, Massachusetts Institute of Technology 130
d13mit260	DNA segment, Chr 13, Massachusetts Institute of Technology 260
d13mit47	DNA segment, Chr 13, Massachusetts Institute of Technology 47
d14mit101	DNA segment, Chr 14, Massachusetts Institute of Technology 101
d14mit113	DNA segment, Chr 14, Massachusetts Institute of Technology 113
d14mit173	DNA segment, Chr 14, Massachusetts Institute of Technology 173
d14mit45	DNA segment, Chr 14, Massachusetts Institute of Technology 45
d14mit56	DNA segment, Chr 14, Massachusetts Institute of Technology 56
d14mit60	DNA segment, Chr 14, Massachusetts Institute of Technology 60
d14mit62	DNA segment, Chr 14, Massachusetts Institute of Technology 62
d17h6s53e	DNA segment, Chr 17, human D6S53E

d18ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed
d19mit1	DNA segment, Chr 19, Massachusetts Institute of Technology 1
d1mit538	DNA Segment, Chr 1, Massachusetts Institute of Technology 538
d1mit77	DNA segment, Chr 1, Massachusetts Institute of Technology 77
d1nds1	DNA segment, Chr 1, Nuffield Department of Surgery 1
d2mit19	DNA segment, Chr 2, Massachusetts Institute of Technology 19
d2mit65	DNA segment, Chr 2, Massachusetts Institute of Technology 65
d3mit116	DNA segment, Chr 3, Massachusetts Institute of Technology 116
d3mit121	DNA segment, Chr 3, Massachusetts Institute of Technology 121
d3mit147	DNA segment, Chr 3, Massachusetts Institute of Technology 147
d3mit19	DNA segment, Chr 3, Massachusetts Institute of Technology 19
d3mit277	DNA segment, Chr 3, Massachusetts Institute of Technology 277
d3mit293	DNA segment, Chr 3, Massachusetts Institute of Technology 293
d3mit44	DNA segment, Chr 3, Massachusetts Institute of Technology 44
d3mit89	DNA segment, Chr 3, Massachusetts Institute of Technology 89
d4mit116	DNA segment, Chr 4, Massachusetts Institute of Technology 116
d4mit152	DNA segment, Chr 4, Massachusetts Institute of Technology 152
d5mit405	DNA Segment, Chr 5 Massachusetts Institute of Technology 405
d5mit75	DNA segment, Chr 5, Massachusetts Institute of Technology 75
d6mit33	DNA segment, Chr 6, Massachusetts Institute of Technology 33
d6mit59	DNA segment, Chr 6, Massachusetts Institute of Technology 59
d7h19f11s1	DNA segment, Chr 7, human D19F11S1
d7mit133	DNA segment, Chr 7, Massachusetts Institute of Technology 133
d7mit151	DNA segment, Chr 7, Massachusetts Institute of Technology 151
d7mit177	DNA segment, Chr 7, Massachusetts Institute of Technology 177
d7mit242	DNA segment, Chr 7, Massachusetts Institute of Technology 242
d7mit357	DNA segment, Chr 7, Massachusetts Institute of Technology 357
d7mit362	DNA segment, Chr 7, Massachusetts Institute of Technology 362
d7mit72	DNA segment, Chr 7, Massachusetts Institute of Technology 72
d7mit98	DNA segment, Chr 7, Massachusetts Institute of Technology 98
d8ertd738e	DNA segment, Chr 8, ERATO Doi 738, expressed
d9mit150	DNA segment, Chr 9, Massachusetts Institute of Technology 150
d9mit227	DNA segment, Chr 9, Massachusetts Institute of Technology 227
d9mit247	DNA segment, Chr 9, Massachusetts Institute of Technology 247
d9mit260	DNA segment, Chr 9, Massachusetts Institute of Technology 260
d9mit263	DNA segment, Chr 9, Massachusetts Institute of Technology 263
d9mit264	DNA segment, Chr 9, Massachusetts Institute of Technology 264
d9mit286	DNA segment, Chr 9, Massachusetts Institute of Technology 286
d9mit289	DNA segment, Chr 9, Massachusetts Institute of Technology 289
d9mit304	DNA Segment, Chr 9, Massachusetts Institute of Technology 304
d9mit48	DNA segment, Chr 9, Massachusetts Institute of Technology 48
dak	dihydroxyacetone kinase 2 homolog (yeast)
dbt	dihydrolipoamide branched chain transacylase E2
ddx50	predicted gene 8228; DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
deb1	differentially expressed in B16F10 1
dgkb	diacylglycerol kinase, beta
dgkd	diacylglycerol kinase, delta
dgkg	diacylglycerol kinase, gamma
dgkh	diacylglycerol kinase, eta
dgkq	diacylglycerol kinase, theta
dhrs3	dehydrogenase/reductase (SDR family) member 3
dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8
dmkn	dermokine
dmxl2	Dmx-like 2
dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14

dnajc5b	DnaJ (Hsp40) homolog, subfamily C, member 5 beta
dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6
dnase1l3	deoxyribonuclease 1-like 3
drap1	Dr1 associated protein 1 (negative cofactor 2 alpha); similar to Dr1 associated protein 1 (negative cofactor 2 alpha)
drd2	dopamine receptor 2
dtnb	dystrobrevin, beta
dtwd2	DTW domain containing 2
dub1	deubiquitinating enzyme 1; similar to DUB-1
dub3	predicted gene 6596
dub4	deubiquitinating enzyme 4
dusp16	dual specificity phosphatase 16
dvb11-1	V11<+> T-cell deletion 1
dvb11-2	V11<+> T-cell deletion 2
dvb11-3	V11<+> T-cell deletion 3
dxcp3	dexamethasone induced cleft palate 3
dxhxs101	DNA segment, Chr X, human DXS101
dxhxs178	DNA segment, Chr X, human DXS178
dxmit103	DNA segment, Chr X, Massachusetts Institute of Technology 103
dxmit125	DNA segment, Chr X, Massachusetts Institute of Technology 125
dxmit139	DNA segment, Chr X, Massachusetts Institute of Technology 139
dxmit49	DNA segment, Chr X, Massachusetts Institute of Technology 49
dxmit52	DNA segment, Chr X, Massachusetts Institute of Technology 52
dxmit81	DNA segment, Chr X, Massachusetts Institute of Technology 81
dxmit85	DNA segment, Chr X, Massachusetts Institute of Technology 85
dxpas23	DNA segment, Chr X, Pasteur Institute 23
ea4	erythrocyte antigen 4
eae1	experimental allergic encephalomyelitis susceptibility1
ebi2	G protein-coupled receptor 183
edil3	EGF-like repeats and discoidin I-like domains 3
eef1b2	eukaryotic translation elongation factor 1 beta 2
eef1d	predicted gene 11675; eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
eef1g	eukaryotic translation elongation factor 1 gamma
eg622901	predicted gene 6368
eg627648	kelch-like 3 (Drosophila)
eg630061	T cell receptor alpha variable 7-5
eg630579	zinc finger protein 80
eg667604	predicted gene 8721
eg668389	immunoglobulin heavy variable V2-4
eg668723	amylase 2, pseudogene 1
eif2b1	eukaryotic translation initiation factor 2B, subunit 1 (alpha)
eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta
eif2b4	eukaryotic translation initiation factor 2B, subunit 4 delta
eif2s2	similar to Eif2s2 protein; eukaryotic translation initiation factor 2, subunit 2 (beta)
eif3b	hypothetical protein LOC100047993; eukaryotic translation initiation factor 3, subunit B
eif3i	eukaryotic translation initiation factor 3, subunit I
eif5	similar to Eukaryotic translation initiation factor 5; eukaryotic translation initiation factor 5
elmaz1	elevated maze behavior 1
elmaz2	elevated maze behavior 2
elovl4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
elp2	elongation protein 2 homolog (S. cerevisiae)
emv22	endogenous ecotropic MuLV 22
emv27	endogenous ecotropic MuLV 27
emv35	endogenous ecotropic MuLV 35
eno3	enolase 3, beta muscle
ensa	predicted gene 5224; endosulfine alpha; similar to endosulfine alpha isoform 1

ensmusg00000061310	predicted gene, ENSMUSG00000061310
ensmusg00000076783	T-cell receptor alpha, variable 8
epn1	epsin 1
eraf	alpha hemoglobin stabilizing protein
ermp1	endoplasmic reticulum metallopeptidase 1
etfa	predicted gene 2893; electron transferring flavoprotein, alpha polypeptide
etn1	early transposon element 1
etv2	similar to ETS related protein 71; ets variant gene 2
fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)
farsa	phenylalanyl-tRNA synthetase, alpha subunit
farsb	phenylalanyl-tRNA synthetase, beta subunit
fermt3	fermitin family homolog 3 (Drosophila)
ffar1	free fatty acid receptor 1
fgfr1op2	FGFR1 oncogene partner 2; similar to FGFR1 oncogene partner 2; predicted gene 12312
figla	folliculogenesis specific basic helix-loop-helix
fiz1	Flt3 interacting zinc finger protein 1
fnta	farnesyltransferase, CAAX box, alpha; similar to farnesyltransferase alpha subunit
fntb	similar to farnesyltransferase, CAAX box, beta; farnesyltransferase, CAAX box, beta
foxa3	forkhead box A3
fpr1	formyl peptide receptor 1
fpr2	formyl peptide receptor 2
fpr3	formyl peptide receptor 3
fpr-rs3	formyl peptide receptor, related sequence 3
fpr-rs4	formyl peptide receptor, related sequence 4
fpr-rs6	formyl peptide receptor, related sequence 6
fscn2	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)
fshb	follicle stimulating hormone beta
fshr	follicle stimulating hormone receptor
fut4-ps1	fucosyltransferase 4, pseudogene 1
fxyd2	FXYD domain-containing ion transport regulator 2
fxyd4	FXYD domain-containing ion transport regulator 4
fxyd7	FXYD domain-containing ion transport regulator 7
fyn	Fyn proto-oncogene
g6pc2	glucose-6-phosphatase, catalytic, 2
gabpa	GA repeat binding protein, alpha
gabpb1	GA repeat binding protein, beta 1
gabra2	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2
gabra3	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3
gabra4	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 4
gabra5	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 5
gabra6	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 6
gabrb1	gamma-aminobutyric acid (GABA) A receptor, subunit beta 1
gabrb2	gamma-aminobutyric acid (GABA) A receptor, subunit beta 2
gabrb3	gamma-aminobutyric acid (GABA) A receptor, subunit beta 3
gabrd	gamma-aminobutyric acid (GABA) A receptor, subunit delta
gabre	similar to gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon; gamma-aminobutyric acid (GABA) A receptor, subunit epsilon
gabrg1	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 1
gabrg2	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 2
gabrg3	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3
gabrp	gamma-aminobutyric acid (GABA) A receptor, pi
gabrq	gamma-aminobutyric acid (GABA) A receptor, subunit theta
gabrr2	gamma-aminobutyric acid (GABA) C receptor, subunit rho 2
gabrr3	gamma-aminobutyric acid (GABA) receptor, rho 3
gal3st2	predicted gene 9994; galactose-3-O-sulfotransferase 2

gal3st3	galactose-3-O-sulfotransferase 3
gal3st4	galactose-3-O-sulfotransferase 4
galm	galactose mutarotase
galnt11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11
ganab	alpha glucosidase 2 alpha neutral subunit
gcgr	glucagon receptor
gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2; similar to glucosaminyl (N-acetyl) transferase 1, core 2
gda	guanine deaminase
gdf9	growth differentiation factor 9
gdi2	predicted gene 4973; guanosine diphosphate (GDP) dissociation inhibitor 2
gipc3	GIPC PDZ domain containing family, member 3
gja6	gap junction protein, alpha 6
glra2	glycine receptor, alpha 2 subunit
glra3	glycine receptor, alpha 3 subunit
glra4	glycine receptor, alpha 4 subunit
glrb	glycine receptor, beta subunit
glt25d1	glycosyltransferase 25 domain containing 1
glt25d2	glycosyltransferase 25 domain containing 2
gluchos1	glucose homeostasis QTL 1
glycam1	glycosylation dependent cell adhesion molecule 1
gm1220	gene model 1220, (NCBI)
gm1848	predicted gene 1848
gm2a	GM2 ganglioside activator protein
gm75	epididymal protein 3B
gmppa	GDP-mannose pyrophosphorylase A
gmppb	GDP-mannose pyrophosphorylase B
gna14	guanine nucleotide binding protein, alpha 14
gna15	guanine nucleotide binding protein, alpha 15
gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type
gnat1	guanine nucleotide binding protein, alpha transducing 1
gnat2	guanine nucleotide binding protein, alpha transducing 2
gnat3	guanine nucleotide binding protein, alpha transducing 3
gnaz	guanine nucleotide binding protein, alpha z subunit
gnb1	guanine nucleotide binding protein (G protein), beta 1
gnb1-ps2	guanine nucleotide binding protein (G protein), beta 1, pseudogene 2
gnb1-ps3	guanine nucleotide binding protein (G protein), beta 1, pseudogene 3
gnb2	guanine nucleotide binding protein (G protein), beta 2
gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1
gnb3	guanine nucleotide binding protein (G protein), beta 3
gnb4	guanine nucleotide binding protein (G protein), beta 4
gnb5	guanine nucleotide binding protein (G protein), beta 5
gng10	guanine nucleotide binding protein (G protein), gamma 10
gng11	guanine nucleotide binding protein (G protein), gamma 11
gng12	guanine nucleotide binding protein (G protein), gamma 12
gng13	guanine nucleotide binding protein (G protein), gamma 13
gng2	guanine nucleotide binding protein (G protein), gamma 2
gng3	guanine nucleotide binding protein (G protein), gamma 3
gng4	guanine nucleotide binding protein (G protein), gamma 4
gng5	guanine nucleotide binding protein (G protein), gamma 5
gng7	guanine nucleotide binding protein (G protein), gamma 7
gng8	guanine nucleotide binding protein (G protein), gamma 8
gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
gnptab	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits
gnptg	similar to N-acetylglucosamine-1-phosphotransferase, gamma subunit; N-acetylglucosamine-1-phosphotransferase, gamma

	subunit
gnrhr	gonadotropin releasing hormone receptor
gpha2	glycoprotein hormone alpha 2
gphb5	glycoprotein hormone beta 5
gphn	gephyrin
gpr110	G protein-coupled receptor 110
gpr111	G protein-coupled receptor 111
gpr116	G protein-coupled receptor 116
gpr123	G protein-coupled receptor 123
gpr128	G protein-coupled receptor 128
gpr135	G protein-coupled receptor 135
gpr141	G protein-coupled receptor 141
gpr142	G protein-coupled receptor 142
gpr156	G protein-coupled receptor 156
gpr160	G protein-coupled receptor 160
gpr177	G protein-coupled receptor 177
gpr20	G protein-coupled receptor 20
gpr26	G protein-coupled receptor 26
gpr3	G-protein coupled receptor 3
gpr31c	predicted gene 8593; predicted gene 6553; predicted gene 6544; G protein-coupled receptor 31, D17Leh66c region
gpr33	G protein-coupled receptor 33
gpr34	G protein-coupled receptor 34
gpr45	G protein-coupled receptor 45
gpr61	G protein-coupled receptor 61
gpr63	G protein-coupled receptor 63
gpr75	G protein-coupled receptor 75
gprin2	G protein regulated inducer of neurite outgrowth 2
gprin3	GPRIN family member 3
gpsm3	G-protein signalling modulator 3 (AGS3-like, C. elegans)
grk1	similar to rhodopsin kinase; G protein-coupled receptor kinase 1
grk4	G protein-coupled receptor kinase 4
grk5	G protein-coupled receptor kinase 5
grk6	G protein-coupled receptor kinase 6
grm6	glutamate receptor, metabotropic 6
gsta	glutathione S-transferase cluster
gsta3	glutathione S-transferase, alpha 3
gtf2a1	predicted gene 5435; general transcription factor II A, 1
gtf2a2	similar to TFIIA small subunit; general transcription factor II A, 2
gtf3a	general transcription factor III A
gtf3c1	general transcription factor III C 1
gtf3c2	general transcription factor IIIC, polypeptide 2, beta; Mpv17 transgene, kidney disease mutant
gtf3c6	general transcription factor IIIC, polypeptide 6, alpha
guca1a	guanylate cyclase activator 1a (retina)
guca1b	guanylate cyclase activator 1B
gucy1a2	hypothetical protein LOC100044212; guanylate cyclase 1, soluble, alpha 2
gucy1a3	guanylate cyclase 1, soluble, alpha 3
gucy1b2	similar to guanylate cyclase 1, soluble, beta 2; guanylate cyclase 1, soluble, beta 2
gucy1b3	guanylate cyclase 1, soluble, beta 3
gucy2e	guanylate cyclase 2e
gucy2f	guanylate cyclase 2f
h2-dmb2	histocompatibility 2, class II, locus Mb2
h2-eb2	histocompatibility 2, class II antigen E beta2
h2-gs10	MHC class I like protein GS10
h2-i	H2 I region, includes H2-Aa, Ab, Bl, Ea, Eb, Eb2, Ob, Pb
h2-k2	histocompatibility 2, K region locus 2

h2-ob	histocompatibility 2, O region beta locus
h2-pb	histocompatibility 2, P region beta locus
h2-q11	histocompatibility 2, Q region locus 11
h2-q5	histocompatibility 2, Q region locus 5
h2-q9	histocompatibility 2, Q region locus 1; histocompatibility 2, Q region locus 9
h2-t10	histocompatibility 2, T region locus 10
h2-t18	histocompatibility 2, T region locus 18
h2-t22	histocompatibility 2, T region locus 22
h2-t3	histocompatibility 2, T region locus 3
h2-t9	histocompatibility 2, T region locus 9
h3	histocompatibility 3
h36	histocompatibility 36
h8	histocompatibility 8
hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit; predicted gene 9108
hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex
hbb-b2	hemoglobin, beta adult major chain; hemoglobin, beta adult minor chain
hbb-bh0	hemoglobin Z, beta-like embryonic chain; hypothetical protein LOC100044263; hemoglobin, beta, pseudogene bh0
hbb-bh1	hemoglobin Z, beta-like embryonic chain; hypothetical protein LOC100044263; hemoglobin, beta, pseudogene bh0
hbb-bh2	hemoglobin beta, pseudogene bh2
hbb-bh3	hemoglobin beta, pseudogene bh3
hbb-y	similar to beta-globin; hemoglobin Y, beta-like embryonic chain
hbq1	hemoglobin, theta 1
hc11	heterochromatin, Chr 11
hc8	heterochromatin, Chr 8
hebp1	heme binding protein 1
hectd3	HECT domain containing 3
hecw1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1
hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
herc5	hect domain and RLD 5
hexa	hexosaminidase A
hexb	hexosaminidase B
higd1a	HIG1 domain family, member 1A
hist1h2aj	histone cluster 1, H2aj
hist3h2ba	histone cluster 3, H2ba; histone cluster 3, H2bb
hivep1	human immunodeficiency virus type I enhancer binding protein 1
hnf4g	hepatocyte nuclear factor 4, gamma
hras1-ps1	Harvey rat sarcoma virus oncogene, pseudogene 1
hrdg1	hyperoxia-induced retinal degeneration 1
hsd3b2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2
hsd3b3	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3
hsd3b5	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5
htr1e	5-hydroxytryptamine (serotonin) receptor 1E
htr2a	5-hydroxytryptamine (serotonin) receptor 2A
htr2c	5-hydroxytryptamine (serotonin) receptor 2C
htr4	5 hydroxytryptamine (serotonin) receptor 4
htr5b	5-hydroxytryptamine (serotonin) receptor 5B
hug	hugger
icam4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group
ichs	immediate cutaneous hypersensitivity QTL
idd1	insulin dependent diabetes susceptibility 1
idd13	insulin dependent diabetes susceptibility 13
idh3a	isocitrate dehydrogenase 3 (NAD+) alpha
idh3b	isocitrate dehydrogenase 3 (NAD+) beta
idh3g	isocitrate dehydrogenase 3 (NAD+), gamma

if1	NDV-induced circulating interferon
ifi201	interferon activated gene 201
ifna1	interferon alpha 1
ifna10	interferon alpha 10
ifna2	interferon alpha 2
ifna3	interferon alpha 3
ifna4	interferon alpha 4
ifna5	interferon alpha 5
ifna6	interferon alpha 6
ifna7	interferon alpha 7
ifna9	interferon alpha 9
ifnab	interferon alpha B
ifna-ps1	interferon alpha gene, pseudogene 1
ifnar2	interferon (alpha and beta) receptor 2
ifnz	interferon zeta
ift122	intraflagellar transport 122 homolog (Chlamydomonas)
ift140	intraflagellar transport 140 homolog (Chlamydomonas)
igbl	immunoglobulin-associated beta-like complex
igbp1	immunoglobulin (CD79A) binding protein 1
igh-1b	similar to gamma-2a immunoglobulin heavy chain; immunoglobulin heavy chain 1a (serum IgG2a); immunoglobulin heavy chain 1b (serum IgG2c)
ighg	immunoglobulin heavy chain 3 (serum IgG2b); Immunoglobulin heavy chain (gamma polypeptide)
igh-ia	immunoglobulin heavy chain Ia
igh-sa1	immunoglobulin heavy chain Sa1
igk-v5	immunoglobulin kappa chain variable 5 (V5 family)
il11ra2	interleukin 11 receptor, alpha chain 2; predicted gene 13305; predicted gene, 100038993
il3ra	interleukin 3 receptor, alpha chain
il5ra	interleukin 5 receptor, alpha
il8ra	chemokine (C-X-C motif) receptor 2
il8rb	chemokine (C-X-C motif) receptor 2
iltifb	interleukin 10-related T cell-derived inducible factor beta; interleukin 22
impdh1	inosine 5'-phosphate dehydrogenase 1
impg1	interphotoreceptor matrix proteoglycan 1
impg2	interphotoreceptor matrix proteoglycan 2
in(4)56rk	inversion, Chr 4, Roderick 56
inhbb	inhibin beta-B
inhbc	inhibin beta-C
inhbe	inhibin beta E
inpp4b	inositol polyphosphate-4-phosphatase, type II
insl3	insulin-like 3
ipo13	importin 13
ipo4	importin 4
ipo5	hypothetical protein LOC100044315; importin 5
ipo7	importin 7
ipo8	importin 8
ipo9	importin 9
ir8	immune response 8
irf9	interferon regulatory factor 9
itch	itchy, E3 ubiquitin protein ligase
itga1	integrin alpha 1
itga10	integrin, alpha 10
itga11	integrin alpha 11
itga7	integrin alpha 7
itga8	integrin alpha 8
itga9	integrin alpha 9

itgad	integrin, alpha D
itgae	integrin alpha E, epithelial-associated
itgb1bp1	integrin beta 1 binding protein 1
itgb1bp2	integrin beta 1 binding protein 2
itgb1bp3	integrin beta 1 binding protein 3
itgb2l	integrin beta 2-like
itgb3bp	predicted gene 3507; integrin beta 3 binding protein (beta3-endonexin); similar to integrin beta 3 binding protein
itgb5	integrin beta 5
itgb6	integrin beta 6
itgb7	integrin beta 7
itgb8	integrin beta 8
itgbl1	integrin, beta-like 1
kbtbd8	kelch repeat and BTB (POZ) domain containing 8
kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1
kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2
kcnab3	potassium voltage-gated channel, shaker-related subfamily, beta member 3
kcng2	potassium voltage-gated channel, subfamily G, member 2
kcnmb2	potassium large conductance calcium-activated channel, subfamily M, beta member 2
kcnmb4	potassium large conductance calcium-activated channel, subfamily M, beta member 4
kcns1	K+ voltage-gated channel, subfamily S, 1
kcns2	K+ voltage-gated channel, subfamily S, 2
kcnu1	potassium channel, subfamily U, member 1
kcnv2	potassium channel, subfamily V, member 2
kctd13	potassium channel tetramerisation domain containing 13
kctd2	potassium channel tetramerisation domain containing 2
kif3a	kinesin family member 3A
kifc3	kinesin family member C3
klhl7	kelch-like 7 (Drosophila)
klk1b11	kallikrein 1-related peptidase b11
klk1b8	kallikrein 1-related peptidase b8
kpna1	karyopherin (importin) alpha 1
kpna2	karyopherin (importin) alpha 2
kpna3	karyopherin (importin) alpha 3
kpnb1	karyopherin (importin) beta 1
krtap8-1	keratin associated protein 8-1
l1md-a1	L1 repeat, A subfamily, member 1
lama4	laminin, alpha 4
lamb2	laminin, beta 2
lamc3	laminin gamma 3
lamr1-rs5	laminin receptor 1 (ribosomal protein SA), related sequence 5
lca5	Leber congenital amaurosis 5 (human)
lca5l	Leber congenital amaurosis 5-like
lcn13	lipocalin 13
leprel2	leprecan-like 2
lgr4	leucine-rich repeat-containing G protein-coupled receptor 4
lgr6	leucine-rich repeat-containing G protein-coupled receptor 6
lhb	luteinizing hormone beta
lhcgr	luteinizing hormone/choriogonadotropin receptor
loc100034726	predicted gene 15772
loc100042493	chemokine (C-C motif) ligand 21B (leucine)
loc100043207	amylase 2a1
loc381763	T-cell receptor beta chain V region
loc381765	similar to T cell antigen receptor
loc383420	predicted gene 5241
loc383650	proteasome (prosome, macropain) subunit, beta type 6, pseudogene 2

loc433466	jumonji domain containing 7
loc636017	immunglobulin heavy chain
loc641050	hypothetical protein LOC641050
loc665506	similar to T-cell receptor beta-2 chain C region
loc676689	similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor
lrat	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)
lrdg1	light induced retinal degeneration 1
lrdg2	light induced retinal degeneration 2
lrit1	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1
lsr	lipolysis stimulated lipoprotein receptor
ltb4r1	leukotriene B4 receptor 1
ltbp1	latent transforming growth factor beta binding protein 1
ltbp3	latent transforming growth factor beta binding protein 3
ly23	lymphocyte antigen 23
ly7	lymphocyte antigen 7
ly77	lymphocyte antigen 77
m-01983	DNA segment, M-01983
madcam1	mucosal vascular addressin cell adhesion molecule 1
mafa	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein A (avian)
man1a2	mannosidase, alpha, class 1A, member 2
man1b-rs	mannosidase 1, beta, related sequence
map2k4	mitogen-activated protein kinase kinase 4
map2k7	predicted gene 14378; similar to transforming growth factor, beta receptor III (betaglycan, 300kDa); mitogen-activated protein kinase kinase 7
map3k5	mitogen-activated protein kinase kinase kinase 5; similar to mitogen activated protein kinase kinase kinase 5
map3k6	mitogen-activated protein kinase kinase kinase 6
mapbpip	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2
mapk10	mitogen-activated protein kinase 10
mapk13	mitogen-activated protein kinase 13
mapk8ip1	mitogen-activated protein kinase 8 interacting protein 1
mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2
mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3
mat2a	methionine adenosyltransferase II, alpha
mat2b	methionine adenosyltransferase II, beta
mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
mcg_21548	brain expressed, associated with Nedd4, 1
mdm1	transformed mouse 3T3 cell double minute 1
mdm2	transformed mouse 3T3 cell double minute 2
mdm3	transformed mouse 3T3 cell double minute 3
med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
mep1a	meprin 1 alpha
mep1b	meprin 1 beta
mgat3	mannoside acetylglucosaminyltransferase 3
mgat4a	mannoside acetylglucosaminyltransferase 4, isoenzyme A
mgat5b	mannoside acetylglucosaminyltransferase 5, isoenzyme B
mirn30d	
mobkl2b	MOB1, Mps One Binder kinase activator-like 2B (yeast)
mord2	modifier of retinal degeneration 2
mord3	modifier of retinal degeneration 3
morn4	MORN repeat containing 4
moxd2	monooxygenase, DBH-like 2
mpmv14	modified polytropic murine leukemia virus 14
mpp4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
mr1	major histocompatibility complex, class I-related

mrgprb2	MAS-related GPR, member B2
mrgpre	MAS-related GPR, member E
mrps31	mitochondrial ribosomal protein S31
mrto4	predicted gene 9178; MRT4, mRNA turnover 4, homolog (S. cerevisiae); predicted gene 5633
ms15-9	minisatellite 15-9
ms4a3	membrane-spanning 4-domains, subfamily A, member 3
ms4a5	membrane-spanning 4-domains, subfamily A, member 5
mtv1	mammary tumor virus locus 1
mtv11	mammary tumor virus locus 11
mtv2	mammary tumor virus locus 2
mtv3	mammary tumor virus locus 3
mtv43	mammary tumor virus locus 43
mtv48	mammary tumor virus locus 48
mtv50	mammary tumor virus locus 50
mtv51	mammary tumor virus locus 51
mtv6	mammary tumor virus locus 6
mtv7	mammary tumor virus locus 7
mtv8	mammary tumor virus locus 8
mtv9	mammary tumor virus locus 9
mug1	murinoglobulin 1; predicted gene 7298
mug4	murinoglobulin 4
mug-ps1	murinoglobulin, pseudogene 1
mynf1	myeloid nuclear factor 1
myo3b	myosin IIIB
n4bp1	NEDD4 binding protein 1
naca	nascent polypeptide-associated complex alpha polypeptide
ncaph2	non-SMC condensin II complex, subunit H2
ncoa7	nuclear receptor coactivator 7
ndfip1	Nedd4 family interacting protein 1; similar to Nedd4 WW domain-binding protein 5
ndfip2	Nedd4 family interacting protein 2
ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4; predicted gene 3873; predicted gene 3244
ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5
ndufc1	predicted gene 4237; NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1
necap1	NECAP endocytosis associated 1
necap2	NECAP endocytosis associated 2
nedd4	neural precursor cell expressed, developmentally down-regulated 4
neurl2	neuralized-like 2 (Drosophila)
nfrkb	nuclear factor related to kappa B binding protein
ng23	Ng23 protein
nidd1n	non-insulin-dependent diabetes mellitus 1 in NSY
nkain1	Na+/K+ transporting ATPase interacting 1
nkain2	Na+/K+ transporting ATPase interacting 2
nkain3	Na+/K+ transporting ATPase interacting 3
nkain4	Na+/K+ transporting ATPase interacting 4
nme2	non-metastatic cells 2, protein (NM23B) expressed in; predicted gene 5566; predicted gene 5425; similar to Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (P18)
nme7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
npnt	nephronectin
nr	nervous
nr1d2	nuclear receptor subfamily 1, group D, member 2; predicted gene 5827
nr1d2-rs2	nuclear receptor subfamily 1, group D, member 2, related sequence 2
nr2e3	nuclear receptor subfamily 2, group E, member 3
nrl	neural retina leucine zipper gene
nub1	negative regulator of ubiquitin-like proteins 1
nup93	similar to nucleoporin 93; nucleoporin 93

nupl1	nucleoporin like 1
nus1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)
nutf2	nuclear transport factor 2
nxnl1	similar to Thioredoxin-like 6; nucleoredoxin-like 1
nxnl2	nucleoredoxin-like 2
nyx	nyctalopin
obfc1	oligonucleotide/oligosaccharide-binding fold containing 1
odc-rs9	ornithine decarboxylase, related sequence 9
olfr1310	olfactory receptor 1310
olfr1342	olfactory receptor 1342
olfr410	olfactory receptor 410
olfr412	olfactory receptor 412
olfr461	olfactory receptor 461
olfr553	olfactory receptor 553
olfr556	olfactory receptor 556
olfr557	olfactory receptor 557
olfr705	olfactory receptor 705
olfr71	olfactory receptor 71
olfr850	olfactory receptor 850
olfr937	olfactory receptor 937
olfr985	olfactory receptor 985
onecut1	one cut domain, family member 1
oog2	oogenesin 2
oog3	predicted gene 4350; oogenesin 3
oog4	oogenesin 4
opn1lw	opsin 1 (cone pigments), long-wave-sensitive
opn1mw	opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)
opn1sw	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)
opn3	opsin 3
opn4	opsin 4 (melanopsin)
opn5	opsin 5
oprd1	hypothetical protein LOC100044222; opioid receptor, delta 1
orf9	orosomucoid 3
orm3	orosomucoid 3
ottmusg00000000246	predicted gene 11212
ottmusg00000003947	predicted gene 11744
ottmusg00000010328	predicted gene 13084
ottmusg00000011275	predicted gene 13280
ottmusg00000011291	predicted gene 13290
ottmusg00000015025	predicted gene 13893
ottmusg00000015050	T cell receptor alpha variable 9D-4
ottmusg00000015102	predicted gene 16454
ottmusg00000015160	T cell receptor alpha variable 6-3
ottmusg00000015161	T cell receptor alpha variable 7-4
ottmusg00000015181	T cell receptor alpha variable 7D-4
ottmusg00000022462	amylase 2b
otud5	OTU domain containing 5
oua1	ouabain resistance 1
oxgr1	oxoglutarate (alpha-ketoglutarate) receptor 1
p2ry14	purinergic receptor P2Y, G-protein coupled, 14
p4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide
p4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide
p4ha3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III
pafah1b1-ps1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, pseudogene 1
pafah1b1-ps2	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, pseudogene 2

pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2
pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3
pank1	pantothenate kinase 1
paqr5	progestin and adipoQ receptor family member V
paqr7	progestin and adipoQ receptor family member VII
paqr8	progestin and adipoQ receptor family member VIII
pax4	paired box gene 4
pcbp3	poly(rC) binding protein 3
pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide
pccb	propionyl Coenzyme A carboxylase, beta polypeptide
pcdh21	cadherin-related family member 1
pcdhga1	protocadherin gamma subfamily A, 1
pcolce2	procollagen C-endopeptidase enhancer 2
pdc	phosducin
pdcl	phosducin-like
pde4d	phosphodiesterase 4D, cAMP specific
pde6a	phosphodiesterase 6A, cGMP-specific, rod, alpha
pde6b	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide
pde6c	phosphodiesterase 6C, cGMP specific, cone, alpha prime
pde6d	phosphodiesterase 6D, cGMP-specific, rod, delta
pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma
pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma
pdha2	pyruvate dehydrogenase E1 alpha 2
pdhb	predicted gene 6123; pyruvate dehydrogenase (lipoamide) beta
pdhx	pyruvate dehydrogenase complex, component X; similar to pyruvate dehydrogenase complex, component X
pggt1b	protein geranylgeranyltransferase type I, beta subunit
phka1	phosphorylase kinase alpha 1
phka2	phosphorylase kinase alpha 2
phkb	phosphorylase kinase beta
phkg1	phosphorylase kinase gamma 1
phkg2	phosphorylase kinase, gamma 2 (testis)
pigz	phosphatidylinositol glycan anchor biosynthesis, class Z
pik3r5	phosphoinositide-3-kinase, regulatory subunit 5, p101
pik3r6	phosphoinositide-3-kinase, regulatory subunit 6
pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha
pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma
pitpnb	phosphatidylinositol transfer protein, beta
pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2
pitpnm3	PITPNM family member 3
pkia	protein kinase inhibitor, alpha
pkib	protein kinase inhibitor beta, cAMP dependent, testis specific
pla2g4b	phospholipase A2, group IVB (cytosolic); jumonji domain containing 7
pla2g4d	phospholipase A2, group IVD
pla2g4e	phospholipase A2, group IVE
pla2g4f	phospholipase A2, group IVF
plcb1	phospholipase C, beta 1
plcb2	phospholipase C, beta 2
plcb3	phospholipase C, beta 3
plcd1	phospholipase C, delta 1
plch1	phospholipase C, eta 1
plcl1	phospholipase C-like 1
plcl2	phospholipase C-like 2
plek	pleckstrin
pltr3	polytropic long terminal repeat containing proviral locus 3

pmpca	peptidase (mitochondrial processing) alpha
pmpcb	peptidase (mitochondrial processing) beta
pmv11	polytropic murine leukemia virus 11
pmv27	polytropic murine leukemia virus 27
pnpla8	patatin-like phospholipase domain containing 8
pol	pol protein
pola2	polymerase (DNA directed), alpha 2
pold1	polymerase (DNA directed), delta 1, catalytic subunit
pold2	polymerase (DNA directed), delta 2, regulatory subunit
pold4	polymerase (DNA-directed), delta 4
pole	polymerase (DNA directed), epsilon
pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)
polg2	polymerase (DNA directed), gamma 2, accessory subunit
polr2h	predicted gene 7511; polymerase (RNA) II (DNA directed) polypeptide H
polr2i	similar to RNA Polymerase II subunit 14.5 kD; polymerase (RNA) II (DNA directed) polypeptide I
polr2k	polymerase (RNA) II (DNA directed) polypeptide K; similar to polymerase (RNA) II (DNA directed) polypeptide K
polr2l	similar to DNA-directed RNA polymerase II 7.6 kDa polypeptide (RPB10) (RPB7.6) (RPABC5); hypothetical protein LOC100044218
pomc-ps1	pro-opiomelanocortin, pseudogene 1
pomp	similar to proteasome maturation protein; proteasome maturation protein
ppap2b	phosphatidic acid phosphatase type 2B
ppef1	protein phosphatase with EF hand calcium-binding domain 1
ppef2	protein phosphatase, EF hand calcium-binding domain 2
ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1); similar to mKIAA1230 protein
ppm1b	similar to serine/threonine phosphatase; protein phosphatase 1B, magnesium dependent, beta isoform
ppm1e	protein phosphatase 1E (PP2C domain containing)
ppp1cc-ps1	protein phosphatase 1, catalytic subunit, gamma isoform, pseudogene 1
ppp1r9b	protein phosphatase 1, regulatory subunit 9B
ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
ppp2cb	similar to protein phosphatase 2a, catalytic subunit, beta isoform; protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform
ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform
ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform
ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; RIKEN cDNA 3222402P14 gene
ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)
ppp2r5a	similar to protein phosphatase 2, regulatory subunit B (B56), alpha isoform
ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform
ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform
ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
pramel1	preferentially expressed antigen in melanoma-like 1
prickle3	prickle homolog 3 (Drosophila)
prim1	DNA primase, p49 subunit
prim2	DNA primase, p58 subunit
prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit
prkacb	protein kinase, cAMP dependent, catalytic, beta
prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
prkag3	protein kinase, AMP-activated, gamma 3 non-catatlytic subunit
prkar1b	protein kinase, cAMP dependent regulatory, type I beta
prkcsh	protein kinase C substrate 80K-H
prpf3	PRP3 pre-mRNA processing factor 3 homolog (yeast)
prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)

prph2	peripherin 2
prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1
psat1	similar to Phosphoserine aminotransferase 1; phosphoserine aminotransferase 1
pscd1	cytohesin 1
psma2	proteasome (prosome, macropain) subunit, alpha type 2
psma3	proteasome (prosome, macropain) subunit, alpha type 3; predicted gene 5406
psma5	proteasome (prosome, macropain) subunit, alpha type 5
psma6	proteasome (prosome, macropain) subunit, alpha type 6
psma8	proteasome (prosome, macropain) subunit, alpha type, 8
psmb1	proteasome (prosome, macropain) subunit, beta type 1
psmb10	proteasome (prosome, macropain) subunit, beta type 10
psmb11	proteasome (prosome, macropain) subunit, beta type, 11
psmb2	proteasome (prosome, macropain) subunit, beta type 2
psmb3	proteasome (prosome, macropain) subunit, beta type 3
psmb4	proteasome (prosome, macropain) subunit, beta type 4
psmb5	predicted gene 3375; proteasome (prosome, macropain) subunit, beta type 5
psmb6	proteasome (prosome, macropain) subunit, beta type 6
psmb7	proteasome (prosome, macropain) subunit, beta type 7
psmb7-ps1	proteasome (prosome, macropain) subunit, beta type 7, pseudogene 1
psme1	predicted gene 7776; proteasome (prosome, macropain) 28 subunit, alpha
psme1-ps1	protease (prosome, macropain) 28 subunit, alpha, pseudogene 1
psme2	protease (prosome, macropain) 28 subunit beta B, pseudogene; similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b)
psme2b-ps	protease (prosome, macropain) 28 subunit beta B, pseudogene; similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b)
psme2-ps1	protease (prosome, macropain) 28 subunit, beta, b, pseudogene 1
psme2-ps2	protease (prosome, macropain) 28 subunit, beta, b, pseudogene 2
psme3	proteaseome (prosome, macropain) 28 subunit, 3
psme4	proteasome (prosome, macropain) activator subunit 4
psmg1	proteasome (prosome, macropain) assembly chaperone 1
psmg2	proteasome (prosome, macropain) assembly chaperone 2; similar to Clast3 protein
psmg3	proteasome (prosome, macropain) assembly chaperone 3
ptafr	platelet-activating factor receptor
ptcra	pre T-cell antigen receptor alpha
ptms	parathymosin
ptprb	protein tyrosine phosphatase, receptor type, B
ptrh1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)
purb	purine rich element binding protein B
qsm	Qa1 structure modifier
rabggta	Rab geranylgeranyl transferase, a subunit
rabggtb	RAB geranylgeranyl transferase, b subunit
raet1a	retinoic acid early transcript 1E; retinoic acid early transcript beta; retinoic acid early transcript 1, alpha; retinoic acid early transcript delta; retinoic acid early transcript gamma
raet1b	retinoic acid early transcript 1E; retinoic acid early transcript beta; retinoic acid early transcript 1, alpha; retinoic acid early transcript delta; retinoic acid early transcript gamma
raet1c	retinoic acid early transcript 1E; retinoic acid early transcript beta; retinoic acid early transcript 1, alpha; retinoic acid early transcript delta; retinoic acid early transcript gamma
raf1	v-raf-leukemia viral oncogene 1
ranbp17	RAN binding protein 17
rars	arginyl-tRNA synthetase
rbp3	retinol binding protein 3, interstitial
rcvrn	recoverin
rd4	retinal degeneration 4
rdh11	retinol dehydrogenase 11
rdh12	retinol dehydrogenase 12
rdh13	retinol dehydrogenase 13 (all-trans and 9-cis)
rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)
rdh5	retinol dehydrogenase 5

rdh8	retinol dehydrogenase 8
reg2	regenerating islet-derived 2
reg3a	regenerating islet-derived 3 alpha
reg3g	regenerating islet-derived 3 gamma
rem1	rad and gem related GTP binding protein 1
rem2	rad and gem related GTP binding protein 2
rexo4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)
rgr	retinal G protein coupled receptor
rgs11	regulator of G-protein signaling 11; similar to regulator of G-protein signaling 11
rgs7	regulator of G protein signaling 7
rgs7bp	regulator of G-protein signalling 7 binding protein
rgs9	regulator of G-protein signaling 9
rgs9bp	regulator of G-protein signalling 9 binding protein
rho	rhodopsin
rims3	regulating synaptic membrane exocytosis 3
ripr	repression of phenobarbitol-inducible P450
rlbp1	retinaldehyde binding protein 1
rmcs2	histocompatibility 2, class II antigen A, beta 1; response to metastatic cancers 2; similar to H-2 class II histocompatibility antigen, A-D beta chain precursor
rmcs5	response to metastatic cancers 5
rn7s6	7S RNA 6
rncr2	myocardial infarction associated transcript (non-protein coding)
rnf181	ring finger protein 181
rnf31	ring finger protein 31
rnu1-ps1	U1 small nuclear RNA pseudogene 1
rom1	rod outer segment membrane protein 1
rorb	hypothetical protein LOC100047843; RAR-related orphan receptor beta
rp1h	retinitis pigmentosa 1 homolog (human)-like 1
rp1l1	retinitis pigmentosa 1 homolog (human)-like 1
rp2h	retinitis pigmentosa 2 homolog (human)
rpain	RPA interacting protein
rpe65	retinal pigment epithelium 65
rpgr	sushi-repeat-containing protein; retinitis pigmentosa GTPase regulator
rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1
rpl14	predicted gene 9811; ribosomal protein L14
rpl23a	ribosomal protein L23a
rpl26	ribosomal protein L26
rpl27a	ribosomal protein L27a
rpl41	ribosomal protein L41; predicted gene 3699
rpl5	ribosomal protein L5
rplag	reduced platelet aggregation
rplp2	similar to LOC665931 protein; ribosomal protein, large P2; predicted gene 7852; WD repeat domain 89
rpo1-1	polymerase (RNA) I polypeptide C
rpo1-2	polymerase (RNA) I polypeptide B
rpo1-3	RNA polymerase 1-3
rpo1-4	polymerase (RNA) I polypeptide A
rps7	similar to 40S ribosomal protein S7 (S8)
rrh	retinal pigment epithelium derived rhodopsin homolog
rrm2-ps1	ribonucleotide reductase M2 pseudogene 1
rrt1	retinoic acid regulated transcript 1
rrt1os	retinoic acid regulated transcript 1 opposite strand transcription unit
rrt2	retinoic acid regulated transcript 2
rrt3	retinoic acid regulated transcript 3
rs1	retinoschisis (X-linked, juvenile) 1 (human)
rtp1	receptor transporter protein 1

rxfp1	relaxin/insulin-like family peptide receptor 1
rxfp2	relaxin/insulin-like family peptide receptor 2
rxfp3	relaxin family peptide receptor 3
rxfp4	relaxin family peptide receptor 4
sag	retinal S-antigen
samd11	sterile alpha motif domain containing 11
sap30bp	similar to transcriptional regulator protein; SAP30 binding protein
sarm1	sterile alpha and HEAT/Armadillo motif containing 1
sas2	serum antigenic substance 2
scn1b	sodium channel, voltage-gated, type I, beta
scn2b	sodium channel, voltage-gated, type II, beta
scn3b	sodium channel, voltage-gated, type III, beta
scn4b	sodium channel, type IV, beta
sctr	secretin receptor; similar to Sctr protein
sdf2l1	stromal cell-derived factor 2-like 1
sec1	secretory blood group 1
sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)
sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)
sec61b	Sec61 beta subunit; predicted gene 10320; predicted gene 5870; similar to protein translocation complex beta subunit
sec61g	predicted gene 11575; predicted gene 10177; predicted gene 4184; SEC61, gamma subunit; similar to Sec61-complex gamma-subunit
sgcz	sarcoglycan zeta
sh2d1a	similar to T cell signal transduction molecule1 SAP; SH2 domain protein 1A
sh2d1b1	SH2 domain protein 1B1
sh2d1b2	SH2 domain protein 1B2
slamf9	SLAM family member 9
slc24a1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1
slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
slc9a5	solute carrier family 9 (sodium/hydrogen exchanger), member 5
smap1	stromal membrane-associated protein 1
smap2	stromal membrane-associated GTPase-activating protein 2
snapc3	small nuclear RNA activating complex, polypeptide 3
snrp2a	U2 small nuclear ribonucleoprotein polypeptide 2A
snta1	syntrophin, acidic 1
sntb1	syntrophin, basic 1
sntb2	similar to beta-2-syntrophin; syntrophin, basic 2
sntg1	syntrophin, gamma 1
sntg2	syntrophin, gamma 2
snupn	snurportin 1
snx22	sorting nexin 22
spata7	spermatogenesis associated 7
spg21	spastic paraplegia 21 homolog (human); similar to spastic paraplegia 21 homolog
spi5l	serine protease inhibitor 5-like
spnb1	spectrin beta 1
spnb2	spectrin beta 2
spnb5	spectrin beta 5
srp14	signal recognition particle 14
srp19	signal recognition particle 19
srp54a	signal recognition particle 54b; signal recognition particle 54a; signal recognition particle 54C
srp54b	signal recognition particle 54b; signal recognition particle 54a; signal recognition particle 54C
srp9	signal recognition particle 9
srpr	signal recognition particle receptor ('docking protein')
srprb	signal recognition particle receptor, B subunit
ssr1	signal sequence receptor, alpha; similar to signal sequence receptor, alpha
ssr2	signal sequence receptor, beta

ssr3	signal sequence receptor, gamma
ssr4	signal sequence receptor, delta
st3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
st3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2
st3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
st3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
st6gal1	beta galactoside alpha 2,6 sialyltransferase 1
st6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
st8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
st8sia3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
stambpl1	STAM binding protein like 1
ston1	stonin 1
ston2	stonin 2
sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit
suclg1	succinate-CoA ligase, GDP-forming, alpha subunit
suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit
svs3a	seminal vesicle secretion 3A
svs3b	seminal vesicle secretory protein 3B
t(2;4)1go	reciprocal translocation, Chr 2 and 4, Gottingen 1
tbca	tubulin cofactor A; predicted gene 4374; predicted gene 6142; similar to cofactor A
tbcc	tubulin-specific chaperone C
tbcd	tubulin-specific chaperone d
tblvi1	thymotropic type B leukemogenic virus integration
tbxa2r	thromboxane A2 receptor
tceb1l-rs2	transcription elongation factor B (SIII), polypeptide 1-like, related sequence 2
tcfap2b	transcription factor AP-2 beta
tcfap2d	transcription factor AP-2, delta
tcfap2e	transcription factor AP-2, epsilon
tcra-c	T-cell receptor alpha, constant region
tcra-v	T-cell receptor alpha, variable region
tcra-v1	T-cell receptor alpha, variable 1
tcra-v11.1	T-cell receptor alpha, variable 11.1
tcra-v11.2	T-cell receptor alpha, variable 11.2
tcra-v11.3	T-cell receptor alpha, variable 11.3
tcra-v11.8	T-cell receptor alpha, variable 11.8
tcra-v13	T-cell receptor alpha, variable 13
tcra-v13.1	T-cell receptor alpha variable region family 13 subfamily 1
tcra-v13.2	T-cell receptor alpha variable region family 13 subfamily 2
tcra-v13.3	T-cell receptor alpha variable region family 13 subfamily 3
tcra-v13.4	T-cell receptor alpha variable region family 13 subfamily 4
tcra-v13.5	T-cell receptor alpha variable region family 13 subfamily 5
tcra-v14	T-cell receptor alpha, variable 14
tcra-v15	T-cell receptor alpha, variable 15
tcra-v16.1	T-cell receptor, alpha, variable 16.1
tcra-v19.1	T-cell receptor alpha, variable 19.1
tcra-v2	T-cell receptor alpha, variable 2
tcra-v2.4	T-cell receptor alpha, variable 2.4
tcra-v2.5	T-cell receptor alpha, variable 2.5
tcra-v2.6	T-cell receptor alpha, variable 2.6
tcra-v23.1	T-cell receptor alpha, variable 23.1
tcra-v3	T-cell receptor alpha, variable 3
tcra-v3.1	T-cell receptor alpha, variable 3.1
tcra-v4	T-cell receptor alpha, variable 4
tcra-v5	T-cell receptor alpha, variable 5
tcra-v6	T-cell receptor alpha, variable 6

tcra-v7	T-cell receptor alpha, variable 7
tcra-v9	T-cell receptor alpha, variable 9
tcra-va10	T-cell receptor alpha, variable A10
tcrb-c	T-cell receptor beta, constant region
tcrb-d	T-cell receptor beta, D region
tcrbe	T-cell receptor beta chain enhancer
tcrb-j	T-cell receptor beta, joining region
tcrb-v	T-cell receptor beta, variable region
tcrb-v1	T-cell receptor beta, variable 1
tcrb-v10	T-cell receptor beta, variable 10
tcrb-v11	T-cell receptor beta, variable 11
tcrb-v12	T-cell receptor beta, variable 12
tcrb-v13	T-cell receptor beta, variable 13
tcrb-v14	T-cell receptor beta, variable 14
tcrb-v15	T-cell receptor beta, variable 15
tcrb-v16	T-cell receptor beta, variable 16
tcrb-v17	T-cell receptor beta, variable 17
tcrb-v19	T-cell receptor beta, variable 19
tcrb-v2	T-cell receptor beta, variable 2
tcrb-v20	protease, serine, 3; predicted gene 10334; T-cell receptor beta, variable V20; similar to trypsinogen 15
tcrb-v3	T-cell receptor beta, variable 3
tcrb-v3.1	T-cell receptor beta, variable 3.1
tcrb-v3.2	T-cell receptor beta, variable 3.2
tcrb-v4	T-cell receptor beta, variable 4
tcrb-v5	T-cell receptor beta, variable 5
tcrb-v5.1	T-cell receptor beta, variable 5.1
tcrb-v5.2	T-cell receptor beta, variable 5.2
tcrb-v6	T-cell receptor beta, variable 6
tcrb-v7	T-cell receptor beta, variable 7
tcrb-v8	T-cell receptor beta, variable 8
tcrb-v8.2	T-cell receptor beta, variable 8.2
tcrb-v9	T-cell receptor beta, variable 9
tcrd-c	T-cell receptor delta, constant region
tcrd-d	T-cell receptor delta, D region
tcrd-j	T-cell receptor delta, joining region
tcrd-v1	T-cell receptor delta, variable 1
tcrd-v2	T-cell receptor delta, variable 2
tcrd-v3	T-cell receptor delta, variable 3
tcrd-v4	T-cell receptor delta, variable 4
tcrd-v5	T-cell receptor delta, variable 5
tcrd-v5t	T-cell receptor delta, variable 5T
tcrd-v6	T-cell receptor delta, variable 6
tcrd-v7	T-cell receptor delta, variable 7
tcrg	T-cell receptor gamma, variable 2; T-cell receptor gamma chain
tcrg-c	T-cell receptor gamma, constant region
tcrg-c1	T-cell receptor gamma, constant 1
tcrg-c2	T-cell receptor gamma, constant 2
tcrg-c4	T-cell receptor gamma, constant 4
tcrg-j	T-cell receptor gamma, joining region
tcrg-v	T-cell receptor gamma, variable region
tcrg-v1	T-cell receptor gamma, variable 1
tcrg-v2	T-cell receptor gamma, variable 2; T-cell receptor gamma chain
tcrg-v3	T-cell receptor gamma, variable 3
tcrg-v4	T-cell receptor gamma, variable 4
tcrg-v5	T-cell receptor gamma, variable 5

tcrg-v6	T-cell receptor gamma, variable 6
tg(il1a)1.1tsk	Transgene insertion 1.1, Thomas Kupper
tg(itga5)0844fmw	transgene insertion 0858, Fiona M Watt
tg(itgb1)0840fmw	transgene insertion 0840, Fiona M Watt
tg(tgfb1)1der	transgene insertion 1, Dennis R Roop
tgfb1i2	transforming growth factor beta 1 induced transcript 2
tgfb1i3	transforming growth factor beta 1 induced transcript 3
tgfbr3	transforming growth factor, beta receptor III
tgtp	T-cell specific GTPase 1
thrap3	thyroid hormone receptor associated protein 3; predicted gene 5898
tk	tail-kinks
tln1	talin 1
tln2	talin 2
tlsr4	thymic lymphoma suppressor region 4
tlsr5	thymic lymphoma suppressor region 5
tm2d1	TM2 domain containing 1
tm2d2	TM2 domain containing 2
tmed9	transmembrane emp24 protein transport domain containing 9
tmem11	transmembrane protein 11
tmem181	transmembrane protein 181
tmem185b	transmembrane protein 185B
tmem37	transmembrane protein 37
tmem66	transmembrane protein 66
tmevp1	heiler's murine encephalomyelitis virus persistence 1
tmsb10	predicted gene 3787; predicted gene 9844; predicted gene 8034; similar to thymosin, beta 10; thymosin, beta 10
tnpo1	predicted gene 6493; transportin 1
top2b	topoisomerase (DNA) II beta
tpml	tropomyosin-like
tram1	translocating chain-associating membrane protein 1
trappc6b	trafficking protein particle complex 6B
trappc9	trafficking protein particle complex 9
trav12n-1	T cell receptor alpha variable 12d-1;
trav16d/dv11	T cell receptor alpha variable 16D-DV11
trav7d-3	T cell receptor alpha chain V region 7D-3; similar to T cell receptor alpha
trbd1	T cell receptor beta diversity 1
trbd2	T cell receptor beta diversity 2
trdd1	T cell receptor delta diversity 1
trdd2	T cell receptor delta diversity 2
trdj2	T cell receptor delta joining 2
treh	trehalase (brush-border membrane glycoprotein)
trgj4	T cell receptor gamma joining 4
trhr	thyrotropin releasing hormone receptor
try5	trypsin 5
tse2	tissue specific extinction 2, of L-ADH
tshb	thyroid stimulating hormone, beta subunit
tshr	thyroid stimulating hormone receptor
tspan4	tetraspanin 4
tsri	T-cell subset ratio influence
ttyh3	tweety homolog 3 (Drosophila)
tuba-rs1	tubulin alpha, related sequence 1
tubb2c	tubulin, beta 2c, psuedogene 1; tubulin, beta 2C; tubulin, beta 2c, pseudogene 2
tug1	taurine upregulated gene 1
tulp1	tubby like protein 1
tulp2	tubby-like protein 2
tulp3	tubby-like protein 3

ubb	ubiquitin B
ubb3	ubiquitin 3
ubc	ubiquitin C
ube1y1-ps2	ubiquitin-activating enzyme E1, Chr Y-1, pseudogene 2
ubqln2	ubiquilin 2
umpk-ps	uridine monophosphate kinase, pseudogene
unc119	unc-119 homolog (C. elegans)
uqcrb	predicted gene 2962; ubiquinol-cytochrome c reductase binding protein
usp20	ubiquitin specific peptidase 20
usp3	ubiquitin specific peptidase 3
usp33	ubiquitin specific peptidase 33
usp38	ubiquitin specific peptidase 38
utp14b	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast)
v1rh13	vomeronasal 1 receptor 219
vars	valyl-tRNA synthetase
vhll	von Hippel-Lindau tumor suppressor-like, pseudogene 1
vit	vitrin
vsx1	visual system homeobox 1 homolog (zebrafish)
vsx2	visual system homeobox 2
wdr17	WD repeat domain 17
wdr61	WD repeat domain 61
wdr7	WD repeat domain 7
wwp2	WW domain containing E3 ubiquitin protein ligase 2
x76971	T cell receptor alpha variable 14N-3; cDNA sequence X76971; predicted gene, OTTMUSG00000015124
xcr1	chemokine (C motif) receptor 1
xmv12	xenotropic murine leukemia virus 12
xmv24	xenotropic murine leukemia virus 24
xmv26	xenotropic murine leukemia virus 26
xmv28	xenotropic murine leukemia virus 28
xmv33	xenotropic murine leukemia virus 33
xmv65	xenotropic murine leukemia virus 65
xmv66	xenotropic murine leukemia virus 66
xpo4	exportin 4
yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1
zbed4	predicted gene 8007; hypothetical protein LOC100045355; predicted gene 3711; zinc finger, BED domain containing 4; predicted gene 15583
zbtb43	zinc finger and BTB domain containing 43
zdhhc21	zinc finger, DHHC domain containing 21
zdhhc3	zinc finger, DHHC domain containing 3
zdhhc7	zinc finger, DHHC domain containing 7
zfp148-ps1	zinc finger protein 148, pseudogene 1
zfp414	zinc finger protein 414
zfyve9	zinc finger, FYVE domain containing 9
zswim6	zinc finger, SWIM domain containing 6

Table S17. G protein theoretical dataset. Latent semantic indexing generated list of implicitly-associated genes linked to arrest-related input terminology. For each gene the Gene Symbol and textual definition is denoted below.

Gene Symbol	Definition
621968	T-cell receptor beta, variable 1
100039796	T-cell specific GTPase 2
0610007p14rik	RIKEN cDNA 0610007P14 gene
0610031j06rik	RIKEN cDNA 0610031J06 gene
0610037d15rik	coiled-coil domain containing 163
0610038d11rik	tRNA methyltransferase 11-2 homolog (S. cerevisiae)
1100001e04rik	Rho GTPase activating protein 36
1110001d15rik	collagen, type VI, alpha 4
1110004f10rik	predicted gene 9169; RIKEN cDNA 1110004F10 gene; similar to small acidic protein
1110004o12rik	ankyrin repeat and KH domain containing 1
1110005a03rik	RIKEN cDNA 1110005A03 gene
1110007l15rik	predicted gene 14127; RIKEN cDNA 1110005A03 gene
1110017d15rik	RIKEN cDNA 1110017D15 gene
1110020p15rik	ubiquinol-cytochrome c reductase, complex III subunit X
1110028a07rik	fat storage-inducing transmembrane protein 1
1200014j11rik	similar to RIKEN cDNA 1200014J11 gene; RIKEN cDNA 1200014J11 gene
1500005a01rik	family with sequence similarity 158, member A
1500010j02rik	RIKEN cDNA 1500010J02 gene
1600002k03rik	RIKEN cDNA 1600002K03 gene
1700006a11rik	RIKEN cDNA 1700006A11 gene
1700007e06rik	RIKEN cDNA 1700007E06 gene
1700008g05rik	fatty acid binding protein 12
1700009n14rik	RIKEN cDNA 1700009N14 gene
1700011f03rik	RIKEN cDNA 1700011F03 gene
1700016k13rik	septin 14
1700016m24rik	RIKEN cDNA 1700016M24 gene
1700019h03rik	solute carrier family 17, member 9
1700021p22rik	family with sequence similarity 71, member E1
1700047i17rik1	RIKEN cDNA 1700047I17 gene 2; RIKEN cDNA 1700047I17 gene 1
1700047l15rik	SPANX family, member N4
1700054f22rik	nipsnap homolog 3A (C. elegans)
1700055m20rik	testis, prostate and placenta expressed
1700057k13rik	RIKEN cDNA 1700057K13 gene
1700126l10rik	RIKEN cDNA 1810014F10 gene
1810007m14rik	GC-rich sequence DNA-binding factor 1
1810014f10rik	RIKEN cDNA 1810014F10 gene
1810023f06rik	interferon, alpha-inducible protein 27 like 2B
1810048j11rik	RIKEN cDNA 1810048J11 gene
1810055g02rik	RIKEN cDNA 1810055G02 gene
2010002n04rik	RIKEN cDNA 2010002N04 gene
2300002d11rik	TMF1-regulated nuclear protein 1
2310001a20rik	RIKEN cDNA 2310001A20 gene
2310002b06rik	coiled-coil domain containing 75
2310003c23rik	predicted gene 5206; RIKEN cDNA 2310003C23 gene
2310033p09rik	RIKEN cDNA 2310033P09 gene
2310047d13rik	family with sequence similarity 57, member A
2310079n02rik	RIKEN cDNA 2310079N02 gene

2410015n17rik	dCTP pyrophosphatase 1
2410018c20rik	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)
2410018m08rik	RIKEN cDNA 2410018M08 gene
2500003m10rik	predicted gene 6365; RIKEN cDNA 2500003M10 gene
2610024e20rik	family with sequence similarity 13, member B
2610036l11rik	RIKEN cDNA 2610036L11 gene
2700078k21rik	RIKEN cDNA 2700078K21 gene
2810012g03rik	family with sequence similarity 53, member C
3110043j09rik	Rho GTPase activating protein 8
3222402p14rik	protein phosphatase 2, regulatory subunit B'', alpha
3300001g02rik	small nuclear ribonucleoprotein 25 (U11/U12)
4121402d02rik	male-specific lethal 1 homolog (Drosophila)
4432412l15rik	RIKEN cDNA 4432412L15 gene
4631416l12rik	RIKEN cDNA 4631416L12 gene
4632419k20rik	family with sequence similarity 160, member A2
4733401h18rik	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3
4833424o15rik	RIKEN cDNA 4833424O15 gene
4921509e07rik	family with sequence similarity 71, member D
4921537p18rik	POTE ankyrin domain family, member G
4922501c03rik	RIKEN cDNA 4922501C03 gene
4930420k17rik	RIKEN cDNA 4930420K17 gene
4930432k09rik	RIKEN cDNA 4930432K09 gene
4930455c21rik	RIKEN cDNA 4930455C21 gene
4930467e23rik	RIKEN cDNA 4930467E23 gene
4930481f22rik	synaptonemal complex central element protein 1 like
4930527e24rik	Slx-like 1
4930579c15rik	RIKEN cDNA 4930579C15 gene
4931433a01rik	ATP/GTP binding protein-like 4
4932425i24rik	RIKEN cDNA 4932425I24 gene
4932432k03rik	MU-2/AP1M2 domain containing, death-inducing
4932438h23rik	RIKEN cDNA 4932438H23 gene
4932442k08rik	family with sequence similarity 120, member B
4933406e20rik	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)
4933411k20rik	RIKEN cDNA 4933411K20 gene
4933417m04rik	family with sequence similarity 71, member A
4933424b01rik	RIKEN cDNA 4933424B01 gene
4933428g20rik	hypothetical LOC100141474
4933436h12rik	RIKEN cDNA 4933436H12 gene
5133400g04rik	spermatogenesis associated 24
5730427n09rik	NSA2 ribosome biogenesis homolog (S. cerevisiae)
5730449l18rik	RIKEN cDNA 6430548M08 gene
5730596k20rik	RIKEN cDNA 9430023L20 gene
5830417i10rik	RIKEN cDNA 5830417I10 gene
6330569m22rik	family with sequence similarity 40, member A
6430548m08rik	RIKEN cDNA 6430548M08 gene
6720467c03rik	family with sequence similarity 92, member A
8430415e04rik	protein phosphatase 4, regulatory subunit 4
9130227c08rik	KH and NYN domain containing
9430023l20rik	RIKEN cDNA 9430023L20 gene
9930111j21rik	RIKEN cDNA 9930111J21 gene 1
a130040m12rik	RIKEN cDNA A130040M12 gene
a130090k04rik	interaction protein for cytohesin exchange factors 1
a230067g21rik	Ral GTPase activating protein, alpha subunit 2 (catalytic)
a230083h22rik	prune homolog 2 (Drosophila)
a430041b07rik	family with sequence similarity 179, member B

a430107p09rik	similar to T-cell receptor alpha chain V region CTL-L17 precursor; RIKEN cDNA A430107P09 gene; T cell receptor alpha variable 6N-6
a430110n23rik	RIKEN cDNA A430110N23 gene
a630007b06rik	RIKEN cDNA A630007B06 gene
a630038e17rik	RIKEN cDNA A630038E17 gene; RIKEN cDNA A630098A13 gene
a630095e13rik	RIKEN cDNA A630095E13 gene
a630098a13rik	RIKEN cDNA A630038E17 gene; RIKEN cDNA A630098A13 gene
a730076h11rik	RIKEN cDNA A730076H11 gene
abca14	ATP-binding cassette, sub-family A (ABC1), member 14
abca15	ATP-binding cassette, sub-family A (ABC1), member 15
abca16	ATP-binding cassette, sub-family A (ABC1), member 16
abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10; similar to ABC transporter
abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6
abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8
abcb9	ATP-binding cassette, sub-family B (MDR/TAP), member 9
abcf1	ATP-binding cassette, sub-family F (GCN20), member 1
abhd1	abhydrolase domain containing 1
abhd14b	abhydrolase domain containing 14b
abhd2	abhydrolase domain containing 2
abhd3	abhydrolase domain containing 3
abhd6	predicted gene 1833; abhydrolase domain containing 6
ablim2	actin-binding LIM protein 2
abpa	androgen binding protein alpha; hypothetical protein LOC100044256
abpb	androgen binding protein beta
abpd	predicted gene 6725; androgen binding protein delta; predicted gene 4684
abpe	androgen binding protein epsilon
abpg	androgen binding protein gamma
abpz	androgen binding protein zeta
abr	active BCR-related gene
accn5	amiloride-sensitive cation channel 5, intestinal
actl6b	actin-like 6B
actr8	ARP8 actin-related protein 8 homolog (S. cerevisiae)
adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta); similar to metalloprotease-disintegrin meltrin beta
adam1a	a disintegrin and metallopeptidase domain 1a
adam1b	similar to a disintegrin and metalloproteinase domain 1b; a disintegrin and metallopeptidase domain 1b
adam2	a disintegrin and metallopeptidase domain 2
adam23	a disintegrin and metallopeptidase domain 23; similar to ADAM23
adam28	a disintegrin and metallopeptidase domain 28
adam3	a disintegrin and metallopeptidase domain 3 (cyritestin)
adam32	a disintegrin and metallopeptidase domain 32
adam4	predicted gene 5746; a disintegrin and metallopeptidase domain 4
adam5	a disintegrin and metallopeptidase domain 5
adcy2	adenylate cyclase 2
adcy4	adenylate cyclase 4
adcy5	adenylate cyclase 5; similar to adenylate cyclase 5
add3	adducin 3 (gamma)
adnp2	ADNP homeobox 2
adra1a	adrenergic receptor, alpha 1a
adra1b	adrenergic receptor, alpha 1b
adra1d	adrenergic receptor, alpha 1d
ads4	anti dsDNA antibody 4
agbl5	ATP/GTP binding protein-like 5
ai314180	expressed sequence AI314180
ai324046	expressed sequence AI324046

ai507611	family with sequence similarity 71, member F2
ai607873	expressed sequence AI607873
ai662250	vimentin-type intermediate filament associated coiled-coil protein
aig1	androgen-induced 1
aim1l	absent in melanoma 1-like
ak3l1	predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1
ak5	adenylate kinase 5
akap13	A kinase (PRKA) anchor protein 13
akr1c19	aldo-keto reductase family 1, member C19
akr1e1	aldo-keto reductase family 1, member E1
aldr5	aldehyde reductase 5
alph1	alphaprotein 1
alph2	alphaprotein 2
als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)
als2cl	ALS2 C-terminal like
als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 homolog (human)
ambp	alpha 1 microglobulin/bikunin
amd	autoimmune myocardial disease
amotl2	angiomotin-like 2
ankar	ankyrin and armadillo repeat containing
ankfy1	ankyrin repeat and FYVE domain containing 1
ankhd1	ankyrin repeat and KH domain containing 1; eukaryotic translation initiation factor 4E binding protein 3
ankrd27	ankyrin repeat domain 27 (VPS9 domain)
ankrd35	ankyrin repeat domain 35
ankrd42	ankyrin repeat domain 42
ankrd44	ankyrin repeat domain 44
ankrd49	ankyrin repeat domain 49
ankrd52	ankyrin repeat domain 52
ankrd7	ankyrin repeat domain 7
ap1b1	adaptor protein complex AP-1, beta 1 subunit
ap1g1	adaptor protein complex AP-1, gamma 1 subunit
ap1m1	adaptor-related protein complex AP-1, mu subunit 1
ap1s1	adaptor protein complex AP-1, sigma 1
ap2b1	adaptor-related protein complex 2, beta 1 subunit
ap2m1	predicted gene 8717; adaptor protein complex AP-2, mu1
ap2s1	adaptor-related protein complex 2, sigma 1 subunit
ap3m1	adaptor-related protein complex 3, mu 1 subunit; similar to Adapter-related protein complex 3 mu 1 subunit (Mu-adaptin 3A) (AP-3 adapter complex mu3A subunit)
ap3s1	predicted gene 7603; adaptor-related protein complex 3, sigma 1 subunit; predicted gene 5610
ap3s2	adaptor-related protein complex 3, sigma 2 subunit
ap4b1	adaptor-related protein complex AP-4, beta 1
ap4e1	adaptor-related protein complex AP-4, epsilon 1
ap4m1	adaptor-related protein complex AP-4, mu 1
ap4s1	adaptor-related protein complex AP-4, sigma 1
apbh	androgen-binding protein eta
arcn1	similar to Archain 1; archain 1; similar to coat protein delta-cop; predicted gene 8752; predicted gene 8750; similar to archain
ard1b	N(alpha)-acetyltransferase 11, NatA catalytic subunit
arf1	predicted gene 5823; ADP-ribosylation factor 1; predicted gene 8230
arf2	ADP-ribosylation factor 2
arf3	ADP-ribosylation factor 3
arf4	ADP-ribosylation factor 4
arf5	similar to ADP-ribosylation factor; ADP-ribosylation factor 5
arf6	ADP-ribosylation factor 6
arfgap1	ADP-ribosylation factor GTPase activating protein 1

arfgap2	ADP-ribosylation factor GTPase activating protein 2
arfgap3	ADP-ribosylation factor GTPase activating protein 3
arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)
arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
arfip1	ADP-ribosylation factor interacting protein 1
arfip2	ADP-ribosylation factor interacting protein 2
arfrp1	ADP-ribosylation factor related protein 1
arhgap1	Rho GTPase activating protein 1; predicted gene 8514
arhgap10	Rho GTPase activating protein 10
arhgap12	Rho GTPase activating protein 12
arhgap15	Rho GTPase activating protein 15
arhgap17	Rho GTPase activating protein 17
arhgap19	Rho GTPase activating protein 19
arhgap20	Rho GTPase activating protein 20
arhgap21	Rho GTPase activating protein 21
arhgap22	Rho GTPase activating protein 22
arhgap24	Rho GTPase activating protein 24
arhgap25	Rho GTPase activating protein 25
arhgap26	RIKEN cDNA 9630014M24 gene; Rho GTPase activating protein 26; predicted gene 5820
arhgap27	Rho GTPase activating protein 27; SH3 domain containing 20
arhgap29	Rho GTPase activating protein 29
arhgap4	Rho GTPase activating protein 4
arhgap5	Rho GTPase activating protein 5
arhgap6	Rho GTPase activating protein 6
arhgap9	Rho GTPase activating protein 9
arhgdia	Rho GDP dissociation inhibitor (GDI) alpha
arhgdib	Rho, GDP dissociation inhibitor (GDI) beta
arhgdig	Rho GDP dissociation inhibitor (GDI) gamma
arhgef1	Rho guanine nucleotide exchange factor (GEF) 1
arhgef10	Rho guanine nucleotide exchange factor (GEF) 10
arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like
arhgef11	Rho guanine nucleotide exchange factor (GEF) 11
arhgef12	predicted gene 7281; predicted gene 5831; similar to SP140 nuclear body protein (predicted); Rho guanine nucleotide exchange factor (GEF) 12
arhgef15	Rho guanine nucleotide exchange factor (GEF) 15
arhgef17	Rho guanine nucleotide exchange factor (GEF) 17
arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18
arhgef19	Rho guanine nucleotide exchange factor (GEF) 19
arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2
arhgef3	Rho guanine nucleotide exchange factor (GEF) 3
arhgef4	Rho guanine nucleotide exchange factor (GEF) 4
arhgef5	Rho guanine nucleotide exchange factor (GEF) 5
arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
arhgef7	Rho guanine nucleotide exchange factor (GEF7)
arhgef9	CDC42 guanine nucleotide exchange factor (GEF) 9
arid3c	AT rich interactive domain 3C (BRIGHT-like)
arid5a	AT rich interactive domain 5A (MRF1-like)
arl1	ADP-ribosylation factor-like 1
arl10	ADP-ribosylation factor-like 10
arl13b	ADP-ribosylation factor-like 13B
arl14	ADP-ribosylation factor-like 14
arl2	ADP-ribosylation factor-like 2
arl2bp	ADP-ribosylation factor-like 2 binding protein
arl3	ADP-ribosylation factor-like 3
arl4a	ADP-ribosylation factor-like 4A

arl4c	similar to ADP-ribosylation factor-like protein 7; ADP-ribosylation factor-like 4C
arl4d	ADP-ribosylation factor-like 4D; hypothetical protein LOC100044157
arl5a	ADP-ribosylation factor-like 5A
arl5b	ADP-ribosylation factor-like 5B
arl6	ADP-ribosylation factor-like 6
arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1
arl6ip2	atlastin GTPase 2
arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4; similar to SRp25 nuclear protein
arl6ip6	similar to ADP-ribosylation-like factor 6-interacting protein 6; ADP-ribosylation factor-like 6 interacting protein 6
arl8a	ADP-ribosylation factor-like 8A
arl8b	ADP-ribosylation factor-like 8B
arl9	ADP-ribosylation factor-like 9
armc6	armadillo repeat containing 6
armc8	armadillo repeat containing 8
arpm1	actin related protein M1
ars2	CG7843 gene product from transcript CG7843-RA
arsj	arylsulfatase J
arsk	similar to arylsulfatase K; arylsulfatase K
asa	anti-sarcolemmal autoantibodies
asb17	ankyrin repeat and SOCS box-containing 17
asb8	ankyrin repeat and SOCS box-containing 8
ascl4	achaete-scute complex homolog 4 (Drosophila)
asna1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)
astl	similar to Astacin-like metalloendopeptidase precursor (Oocyte astacin) (Ovastacin); astacin-like metalloendopeptidase (M12 family)
asxl3	additional sex combs like 3 (Drosophila)
atad3a	ATPase family, AAA domain containing 3A
atp12a	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
atp13a3	ATPase type 13A3
atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide
atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide
atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide
atp1a4	ATPase, Na+/K+ transporting, alpha 4 polypeptide
atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide
atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide
atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide
atp1b3-rs	ATPase, Na+/K+ transporting, beta 3 polypeptide, related sequence
atp1b3-rs2	ATPase, Na+/K+ transporting, beta 3 polypeptide, related sequence 2
atp1b4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide
atp4a	ATPase, H+/K+ exchanging, gastric, alpha polypeptide
atp4b	ATPase, H+/K+ exchanging, beta polypeptide
atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit
atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1; predicted gene 12231
atp5g2	predicted gene 10231; similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9); predicted gene 10175; predicted gene 5911; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F pseudogene; similar to ATP synthase coupling factor 6, mitochondrial precursor (ATPase subunit F6); ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F
atp5j2	predicted gene 6835; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2; predicted gene 6581
atp5k	predicted gene 2972; ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e

atp5l	predicted gene 10221; predicted gene 4602; predicted gene 9391; ATP synthase, H+ transporting, mitochondrial FO complex, subunit G2, pseudogene; predicted gene 11477; predicted gene 9712; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; predicted gene 4045
atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s
atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2
atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D
atp8b2	ATPase, class I, type 8B, member 2
atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1
aup1	ancient ubiquitous protein 1
aw125753	family with sequence similarity 84, member A
aw554918	expressed sequence AW554918
axud1	cysteine-serine-rich nuclear protein 1
aym1	activator of yeast meiotic promoters 1
b020018g12rik	RNA binding motif protein 8a; RIKEN cDNA B020018G12 gene
b230208h17rik	RIKEN cDNA B230208H17 gene
b230339m05rik	Ral GTPase activating protein, beta subunit (non-catalytic)
b3galt4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4
b3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
b3gnt3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
b3gnt4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
b3gntl1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1
b4galnt3	beta-1,4-N-acetyl-galactosaminyl transferase 3
b4galnt4	beta-1,4-N-acetyl-galactosaminyl transferase 4
b4galt2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2
b4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3
b4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4
b4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6; similar to Beta-1,4-galactosyltransferase 6 (Beta-1,4-GalTase 6) (Beta4Gal-T6) (b4Gal-T6) (UDP-galactose:beta-N-acetylglucosamine beta-1,4-galactosyltransferase 6) (UDP-Gal:beta-GlcNAc beta-1,4-galactosyltransferase 6)
baiap3	BAI1-associated protein 3
bas	BALB murine sarcoma oncogene
bat4	predicted gene 5628; HLA-B associated transcript 4
bc010304	family with sequence similarity 120, member A
bc013712	cDNA sequence BC013712
bc016423	cDNA sequence BC016423
bc017158	cDNA sequence BC017158
bc021395	regulation of nuclear pre-mRNA domain containing 1A
bc028663	BC028663
bc029169	family with sequence similarity 20, member A
bc048502	cDNA sequence BC048502
bc048679	cDNA sequence BC048679
bc065397	cDNA sequence BC065397
bc067047	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1
bcam	basal cell adhesion molecule
bcar3	breast cancer anti-estrogen resistance 3
bcas2	breast carcinoma amplified sequence 2
bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide
bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide; similar to 3-methyl-2-oxobutanoate dehydrogenase
bicd1	bicaudal D homolog 1 (Drosophila)
bin3	bridging integrator 3
bivm	basic, immunoglobulin-like variable motif containing
blvrb	biliverdin reductase B (flavin reductase (NADPH))
blzf1	basic leucine zipper nuclear factor 1
bnip2	BCL2/adenovirus E1B interacting protein 2

bnipl	BCL2/adenovirus E1B 19kD interacting protein like
bola1	bolA-like 1 (E. coli)
bola2	bolA-like 2 (E. coli)
bola3	bolA-like 3 (E. coli)
bpil2	bactericidal/permeability-increasing protein-like 2
bpil3	bactericidal/permeability-increasing protein-like 3
braf-rs1	Braf transforming gene, related sequence 1
brd1	bromodomain containing 1; similar to bromodomain containing 1
bri3bp	Bri3 binding protein
bspry	B-box and SPRY domain containing
btbd1	similar to BTB (POZ) domain containing 1 (predicted); BTB (POZ) domain containing 1; predicted gene 14121
btbd2	BTB (POZ) domain containing 2
btf3	predicted gene 9308; basic transcription factor 3; predicted gene 3531; predicted gene 7973
bud31	BUD31 homolog (yeast)
bves	blood vessel epicardial substance
bxdc1	ribosome production factor 2 homolog (S. cerevisiae)
bxdc2	brix domain containing 2
bxdc5	ribosome production factor 1 homolog (S. cerevisiae)
c1ql1	complement component 1, q subcomponent-like 1
c230097i24rik	zinc finger and SCAN domain containing 30
c2cd2l	C2 calcium-dependent domain containing 2-like
c4bp	complement component 4 binding protein
c4bp-ps1	complement component 4 binding protein, pseudogene 1
c77670	expressed sequence C77670
c80913	expressed sequence C80913
c8a	complement component 8, alpha polypeptide
c8b	complement component 8, beta polypeptide
c8g	complement component 8, gamma polypeptide
c9	complement component 9
cab39	calcium binding protein 39
cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit
cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1
cacna2d2	calcium channel, voltage-dependent, alpha 2/delta subunit 2; similar to Cacna2d2 protein
cacna2d3	calcium channel, voltage-dependent, alpha2/delta subunit 3
cacna2d4	calcium channel, voltage-dependent, alpha 2/delta subunit 4
cacnb1	calcium channel, voltage-dependent, beta 1 subunit
cacnb2	calcium channel, voltage-dependent, beta 2 subunit
cacnb3	calcium channel, voltage-dependent, beta 3 subunit
cacnb4	calcium channel, voltage-dependent, beta 4 subunit
cacng1	calcium channel, voltage-dependent, gamma subunit 1
cacng3	calcium channel, voltage-dependent, gamma subunit 3
cacng4	calcium channel, voltage-dependent, gamma subunit 4
cacng5	calcium channel, voltage-dependent, gamma subunit 5
cacng6	calcium channel, voltage-dependent, gamma subunit 6
cacng7	calcium channel, voltage-dependent, gamma subunit 7
cacng8	calcium channel, voltage-dependent, gamma subunit 8
camk1g	calcium/calmodulin-dependent protein kinase I gamma
camk2b	calcium/calmodulin-dependent protein kinase II, beta
camk2d	calcium/calmodulin-dependent protein kinase II, delta
camk2g	similar to Calcium/calmodulin-dependent protein kinase type II gamma chain (CaM-kinase II gamma chain) (CaM kinase II gamma subunit) (CaMK-II subunit gamma); calcium/calmodulin-dependent protein kinase II gamma
camkl	calcium/calmodulin dependent protein kinase-like
capns2	calpain, small subunit 2
capza1	capping protein (actin filament) muscle Z-line, alpha 1; similar to capping protein (actin filament) muscle Z-

	line, alpha 1; predicted gene 3608; predicted gene 5920
capza1-ps2	capping protein (actin filament) muscle Z-line, alpha 1, pseudogene 2
capza2	capping protein (actin filament) muscle Z-line, alpha 2
capzb	capping protein (actin filament) muscle Z-line, beta
card6	caspase recruitment domain family, member 6
cbl-ps1	Casitas B-lineage lymphoma, pseudogene 1
cbx3-ps1	chromobox homolog 3 (Drosophila HP1 gamma), pseudogene 1
cbx3-ps2	chromobox homolog 3 (Drosophila HP1 gamma), pseudogene 2
cbx3-ps3	chromobox homolog 3 (Drosophila HP1 gamma), pseudogene 3
ccdc135	coiled-coil domain containing 135
ccdc19	coiled-coil domain containing 19
ccdc62	coiled-coil domain containing 62
ccdc65	coiled-coil domain containing 65
ccdc67	coiled-coil domain containing 67
ccdc85b	coiled-coil domain containing 85B
ccdc88a	coiled coil domain containing 88A
ccdc88b	coiled-coil domain containing 88B
ccdc89	coiled-coil domain containing 89
ccdc91	coiled-coil domain containing 91
ccpg1	cell cycle progression 1
ccpn-ps	calcyphosine, pseudogene
ccr1l1	chemokine (C-C motif) receptor 1-like 1
ccrl2	chemokine (C-C motif) receptor-like 2
cct2	chaperonin containing Tcp1, subunit 2 (beta)
cct3	chaperonin containing Tcp1, subunit 3 (gamma)
cct3-ps1	chaperonin containing Tcp1, subunit 3 (gamma) pseudogene 1
cct6a	chaperonin containing Tcp1, subunit 6a (zeta)
cct6b	chaperonin containing Tcp1, subunit 6b (zeta)
cct7	chaperonin containing Tcp1, subunit 7 (eta)
cct8	chaperonin containing Tcp1, subunit 8 (theta)
cd247	CD247 antigen
cd3d	CD3 antigen, delta polypeptide
cd3e	CD3 antigen, epsilon polypeptide
cd3g	CD3 antigen, gamma polypeptide
cd8b1	CD8 antigen, beta chain 1
cdadc1	cytidine and dCMP deaminase domain containing 1
cdc34-ps	cell division cycle 34 homolog, pseudogene (S. cerevisiae)
cdc42bpa	CDC42 binding protein kinase alpha
cdc42bpb	CDC42 binding protein kinase beta
cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1
cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2
cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3
cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4
cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5
cdc42l1	cell division cycle 42 homolog (S. cerevisiae)-like 1
cdc42l2	cell division cycle 42 homolog (S. cerevisiae)-like 2
cdc42l3	cell division cycle 42 homolog (S. cerevisiae)-like 3
cdc42se1	CDC42 small effector 1
cdc42se2	similar to CDC42 small effector 2; CDC42 small effector 2
cdgap	Rho GTPase activating protein 31
cebpg	CCAAT/enhancer binding protein (C/EBP), gamma
cenpk	centromere protein K
centa1	centaurin, alpha 1
centb1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
centb2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2

centb5	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3
centd1	centaurin, delta 1
centd2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
centd3	centaurin, delta 3
centg1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2
centg2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1
centg3	centaurin, gamma 3
cep350	centrosomal protein 350
cep57	centrosomal protein 57
cfhe	complement component factor h, electrophoretic variant
cgnl1	cingulin-like 1
chchd1	coiled-coil-helix-coiled-coil-helix domain containing 1
chd6	chromodomain helicase DNA binding protein 6; predicted gene 8291
chic1	cysteine-rich hydrophobic domain 1
chid1	chitinase domain containing 1
chkb	choline kinase beta
chm	similar to choroidermia; choroidermia
chml	choroideremia-like
chn1	chimerin (chimaerin) 1
chn2	chimerin (chimaerin) 2
chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
chpst	chrondroprogenitor specific transcript
chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle); similar to acetylcholine receptor alpha-subunit
chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)
chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6
chrnb1	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)
chrnb3	cholinergic receptor, nicotinic, beta polypeptide 3
chrnb4	cholinergic receptor, nicotinic, beta polypeptide 4
chrnd	cholinergic receptor, nicotinic, delta polypeptide
chrne	cholinergic receptor, nicotinic, epsilon polypeptide
chrng	cholinergic receptor, nicotinic, gamma polypeptide
cib3	calcium and integrin binding family member 3
cirbp-rs1	cold inducible RNA binding protein, related sequence 1
cirbp-rs3	cold inducible RNA binding protein, related sequence 3
clec4b1	C-type lectin domain family 4, member b1
clmn	calmin
clp1	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)
clybl	citrate lyase beta like
cml1	N-acetyltransferase 8B; camello-like 1
cml2	camello-like 2
cml3	predicted gene 4477; camello-like 3
cml5	camello-like 5
cnbpl1	cellular nucleic acid binding protein-like 1
cnbpl2	cellular nucleic acid binding protein-like 2
cngb1	cyclic nucleotide gated channel beta 1
cnih	cornichon homolog (Drosophila)
cnksr1	connector enhancer of kinase suppressor of Ras 1
cnnm1	cyclin M1
cnnm2	cyclin M2
cnnm3	cyclin M3
cnot1	predicted gene 6158; CCR4-NOT transcription complex, subunit 1
cnot8	CCR4-NOT transcription complex, subunit 8
col12a1	collagen, type XII, alpha 1
col13a1	collagen, type XIII, alpha 1
col16a1	collagen, type XVI, alpha 1

col19a1	collagen, type XIX, alpha 1
col27a1	collagen, type XXVII, alpha 1
col4a2	collagen, type IV, alpha 2
col4a4	collagen, type IV, alpha 4
col4a5	collagen, type IV, alpha 5
col4a6	collagen, type IV, alpha 6
col5a1	collagen, type V, alpha 1
col5a2	collagen, type V, alpha 2
col5a3	collagen, type V, alpha 3
col6a1	collagen, type VI, alpha 1
col6a2	collagen, type VI, alpha 2
col6a3	collagen, type VI, alpha 3
col8a1	collagen, type VIII, alpha 1
col8a2	collagen, type VIII, alpha 2
comtd1	catechol-O-methyltransferase domain containing 1
copa	coatomer protein complex subunit alpha
copb1	coatomer protein complex, subunit beta 1
copb2	coatomer protein complex, subunit beta 2 (beta prime)
cope	coatomer protein complex, subunit epsilon
copg	coatomer protein complex, subunit gamma
copg2	coatomer protein complex, subunit gamma 2
cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)
copz1	coatomer protein complex, subunit zeta 1
copz2	coatomer protein complex, subunit zeta 2
coq4	coenzyme Q4 homolog (yeast)
coro2a	coronin, actin binding protein 2A
cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like; predicted gene 6969
cpn2	carboxypeptidase N, polypeptide 2
cpne3	copine III
cpne4	copine IV
cpne6	copine VI
cpne8	copine VIII
cpsf3l	cleavage and polyadenylation specific factor 3-like
cpxm2	carboxypeptidase X 2 (M14 family)
creb5	RIKEN cDNA 9430076C15 gene; cAMP responsive element binding protein 5
creg2	cellular repressor of E1A-stimulated genes 2
creld2	cysteine-rich with EGF-like domains 2
crlf2	cytokine receptor-like factor 2
cryba1	crystallin, beta A1
cryba2	crystallin, beta A2
cryba4	crystallin, beta A4
crybb1	crystallin, beta B1
crybb2	crystallin, beta B2
crybb3	crystallin, beta B3
cryg	crystallin gamma complex
cryga	crystallin, gamma A
crygb	crystallin, gamma B
crygc	crystallin, gamma C
crygd	crystallin, gamma D
cryge	crystallin, gamma E
crygf	crystallin, gamma F
crygn	crystallin, gamma N
crygs	crystallin, gamma S
cryzl1	crystallin, zeta (quinone reductase)-like 1
csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)

csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)
csmd2	CUB and Sushi multiple domains 2
csn1s1	casein alpha s1
csn1s2a	casein alpha s2-like A
csn1s2b	casein alpha s2-like B
csn2	casein beta
csn3	casein kappa
csnk1g1	casein kinase 1, gamma 1
csnk1g2	casein kinase 1, gamma 2
csnk1g3	casein kinase 1, gamma 3; similar to casein kinase 1, gamma 3
csnk2a1-ps1	casein kinase 2, alpha 1 polypeptide, pseudogene 1
csnk2a1-rs2	casein kinase 2, alpha 1, related sequence 2
csnk2a1-rs3	casein kinase 2, alpha 1, related sequence 3
csrnp2	cysteine-serine-rich nuclear protein 2
csrnp3	cysteine-serine-rich nuclear protein 3
csrp2bp	cysteine and glycine-rich protein 2 binding protein; similar to cysteine and glycine-rich protein 2 binding protein; similar to CSRP2BP; hypothetical protein LOC100048725
ctf2	cardiotrophin 2
ctla2b	cytotoxic T lymphocyte-associated protein 2 beta
ctps2	cytidine 5'-triphosphate synthase 2
ctrb1	chymotrypsinogen B1
ctrc	chymotrypsin C (caldecrin)
ctxn3	cortexin 3
cutc	cutC copper transporter homolog (E.coli)
cx3cl1-rs1	chemokine (C-X3-C motif) ligand 1, related sequence 1
cxx1a	CAAX box 1 homolog A (human); CAAX box 1 homolog B (human); similar to mammalian retrotransposon derived 8b
cxx1c	CAAX box 1 homolog C (human)
cycl	cyclin-like
cyp11d	cytochrome P450, 11d
cyp2a	cytochrome P450, family 2, subfamily a
cyp2a12	cytochrome P450, family 2, subfamily a, polypeptide 12; cytochrome P450, family 2, subfamily a, polypeptide 22
cyp2a5	cytochrome P450, family 2, subfamily a, polypeptide 21, pseudogene; cytochrome P450, family 2, subfamily a, polypeptide 5
cyp2b13	cytochrome P450, family 2, subfamily b, polypeptide 13
cyp2c40	cytochrome P450, family 2, subfamily c, polypeptide 40; similar to RIKEN cDNA C730004C24 gene; cytochrome P450, family 2, subfamily c, polypeptide 69; cytochrome P450, family 2, subfamily c, polypeptide 67
cyp2d	cytochrome P450, 2d region
cyp2d10	cytochrome P450, family 2, subfamily d, polypeptide 10
cyp2d11	cytochrome P450, family 2, subfamily d, polypeptide 11
cyp2d9	cytochrome P450, family 2, subfamily d, polypeptide 9
cyyr1	cysteine and tyrosine-rich protein 1
d030074e01rik	RIKEN cDNA D030074E01 gene
d0hxs9928e	family with sequence similarity 50, member A
d0kist4	DNA segment, KIST 4
d10ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed
d10mit116	DNA segment, Chr 10, Massachusetts Institute of Technology 116
d10mit260	DNA Segment, Chr 10, Massachusetts Institute of Technology 260
d11jkn1e	DNA segment, Chr 11, Ian Jackson-1, expressed
d11mit109	DNA segment, Chr 11, Massachusetts Institute of Technology 109
d11mit139	DNA segment, Chr 11, Massachusetts Institute of Technology 139
d11mit174	DNA segment, Chr 11, Massachusetts Institute of Technology 174
d11mit188	DNA segment, Chr 11, Massachusetts Institute of Technology 188
d11mit205	DNA segment, Chr 11, Massachusetts Institute of Technology 205
d11mit208	DNA segment, Chr 11, Massachusetts Institute of Technology 208

d11mit258	DNA segment, Chr 11, Massachusetts Institute of Technology 258
d11mit51	DNA segment, Chr 11, Massachusetts Institute of Technology 51
d11mit84	DNA segment, Chr 11, Massachusetts Institute of Technology 84
d12ertd673e	DNA segment, Chr 12, ERATO Doi 673, expressed
d12mit149	DNA segment, Chr 12, Massachusetts Institute of Technology 149
d12mit182	DNA segment, Chr 12, Massachusetts Institute of Technology 182
d12mit238	DNA segment, Chr 12, Massachusetts Institute of Technology 238
d13mit130	DNA segment, Chr 13, Massachusetts Institute of Technology 130
d13mit260	DNA segment, Chr 13, Massachusetts Institute of Technology 260
d13mit31	DNA segment, Chr 13, Massachusetts Institute of Technology 31
d13mit91	DNA segment, Chr 13, Massachusetts Institute of Technology 91
d14ertd574e	DNA segment, Chr 14, ERATO Doi 574, expressed
d14mit101	DNA segment, Chr 14, Massachusetts Institute of Technology 101
d14mit104	DNA segment, Chr 14, Massachusetts Institute of Technology 104
d14mit113	DNA segment, Chr 14, Massachusetts Institute of Technology 113
d14mit116	DNA segment, Chr 14, Massachusetts Institute of Technology 116
d14mit142	DNA segment, Chr 14, Massachusetts Institute of Technology 142
d14mit173	DNA segment, Chr 14, Massachusetts Institute of Technology 173
d14mit45	DNA segment, Chr 14, Massachusetts Institute of Technology 45
d14mit56	DNA segment, Chr 14, Massachusetts Institute of Technology 56
d14mit60	DNA segment, Chr 14, Massachusetts Institute of Technology 60
d14mit62	DNA segment, Chr 14, Massachusetts Institute of Technology 62
d15mit188a	DNA segment, Chr 15, Massachusetts Institute of Technology 188a
d15mit198	DNA segment, Chr 15, Massachusetts Institute of Technology 198
d15mit72	DNA segment, Chr 15, Massachusetts Institute of Technology 72
d16ertd6e	DNA segment, Chr 16, ERATO Doi 6, expressed
d16mit179	DNA segment, Chr 16, Massachusetts Institute of Technology 179
d16mit26	DNA segment, Chr 16, Massachusetts Institute of Technology 26
d16mit69	DNA segment, Chr 16, Massachusetts Institute of Technology 69
d17h6s53e	DNA segment, Chr 17, human D6S53E
d17mit196	DNA segment, Chr 17, Massachusetts Institute of Technology 196
d17mit7	DNA segment, Chr 17, Massachusetts Institute of Technology 7
d18ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed
d19mit24	DNA segment, Chr 19, Massachusetts Institute of Technology 24
d19mit66	DNA segment, Chr 19, Massachusetts Institute of Technology 66
d19mit75	DNA segment, Chr 19, Massachusetts Institute of Technology 75
d19rp19e	DNA segment, Chr 19, Roswell Park 19, expressed
d1ertd57e	DNA segment, Chr 1, ERATO Doi 57, expressed
d1mit213	DNA segment, Chr 1, Massachusetts Institute of Technology 213
d1mit330	DNA segment, Chr 1, Massachusetts Institute of Technology 330
d1mit388	DNA segment, Chr 1, Massachusetts Institute of Technology 388
d1mit488	DNA Segment, Chr 1 Massachusetts Institute of Technology 488
d2ertd337e	DNA segment, Chr 2, ERATO Doi 337, expressed
d2mit19	DNA segment, Chr 2, Massachusetts Institute of Technology 19
d2mit434	DNA Segment, Chr 2, Massachusetts Institute of Technology 434
d2mit496	DNA Segment, Chr 2 Massachusetts Institute of Technology 496
d2mit97	DNA segment, Chr 2, Massachusetts Institute of Technology 97
d330017j20rik	family with sequence similarity 40, member B
d3mit121	DNA segment, Chr 3, Massachusetts Institute of Technology 121
d3mit250	DNA segment, Chr 3, Massachusetts Institute of Technology 250
d3mit277	DNA segment, Chr 3, Massachusetts Institute of Technology 277
d4mit100	DNA segment, Chr 4, Massachusetts Institute of Technology 100
d4mit110	DNA segment, Chr 4, Massachusetts Institute of Technology 110
d4mit116	DNA segment, Chr 4, Massachusetts Institute of Technology 116
d4mit144	DNA segment, Chr 4, Massachusetts Institute of Technology 144

d4mit152	DNA segment, Chr 4, Massachusetts Institute of Technology 152
d4mit287	DNA segment, Chr 4, Massachusetts Institute of Technology 287
d4mit339	DNA segment, Chr 4, Massachusetts Institute of Technology 339
d530033c11rik	UTP23, small subunit (SSU) processome component, homolog (yeast)
d5mit193	DNA segment, Chr 5, Massachusetts Institute of Technology 193
d5mit202	DNA segment, Chr 5, Massachusetts Institute of Technology 202
d5mit317	DNA segment, Chr 5, Massachusetts Institute of Technology 317
d5mit318	DNA segment, Chr 5, Massachusetts Institute of Technology 318
d5pas1	DNA segment, Chr 5, Pasteur Institute 1
d6kcc1	DNA segment, Chr 6, Kimmel Cancer Center 1
d6mit118	DNA segment, Chr 6, Massachusetts Institute of Technology 118
d6mit252	DNA segment, Chr 6, Massachusetts Institute of Technology 252
d6mit33	DNA segment, Chr 6, Massachusetts Institute of Technology 33
d6mit59	DNA segment, Chr 6, Massachusetts Institute of Technology 59
d6mm5e	DNA segment, Chr 6, Miriam Meisler 5, expressed
d730040f13rik	RIKEN cDNA D730040F13 gene
d7h19f11s1	DNA segment, Chr 7, human D19F11S1
d7mit151	DNA segment, Chr 7, Massachusetts Institute of Technology 151
d7mit177	DNA segment, Chr 7, Massachusetts Institute of Technology 177
d7mit242	DNA segment, Chr 7, Massachusetts Institute of Technology 242
d7mit357	DNA segment, Chr 7, Massachusetts Institute of Technology 357
d7mit362	DNA segment, Chr 7, Massachusetts Institute of Technology 362
d7mit72	DNA segment, Chr 7, Massachusetts Institute of Technology 72
d7mit98	DNA segment, Chr 7, Massachusetts Institute of Technology 98
d8ertd738e	DNA segment, Chr 8, ERATO Doi 738, expressed
d8ertd82e	DNA segment, Chr 8, ERATO Doi 82, expressed
d8mit280	DNA segment, Chr 8, Massachusetts Institute of Technology 280
d8mit297	DNA Segment, Chr 8, Massachusetts Institute of Technology 297
d8mit336	DNA segment, Chr 8, Massachusetts Institute of Technology 336
d8mit96	DNA segment, Chr 8, Massachusetts Institute of Technology 96
d8mit98	DNA segment, Chr 8, Massachusetts Institute of Technology 98
d930005d10rik	Ras association and DIL domains
d930014e17rik	RIKEN cDNA D930014E17 gene
d9citb3	DNA segment, Chr 9, California Institute of Technology, Biology Department 3
d9mit133	DNA segment, Chr 9, Massachusetts Institute of Technology 133
d9mit150	DNA segment, Chr 9, Massachusetts Institute of Technology 150
d9mit215	DNA segment, Chr 9, Massachusetts Institute of Technology 215
d9mit223	DNA segment, Chr 9, Massachusetts Institute of Technology 223
d9mit245	DNA segment, Chr 9, Massachusetts Institute of Technology 245
d9mit259	DNA segment, Chr 9, Massachusetts Institute of Technology 259
d9mit260	DNA segment, Chr 9, Massachusetts Institute of Technology 260
d9mit261	DNA segment, Chr 9, Massachusetts Institute of Technology 261
d9mit263	DNA segment, Chr 9, Massachusetts Institute of Technology 263
d9mit270	DNA segment, Chr 9, Massachusetts Institute of Technology 270
d9mit289	DNA segment, Chr 9, Massachusetts Institute of Technology 289
d9mit304	DNA Segment, Chr 9, Massachusetts Institute of Technology 304
d9mit48	DNA segment, Chr 9, Massachusetts Institute of Technology 48
d9mit60	DNA segment, Chr 9, Massachusetts Institute of Technology 60
d9mit61	DNA segment, Chr 9, Massachusetts Institute of Technology 61
dak	dihydroxyacetone kinase 2 homolog (yeast)
dars	aspartyl-tRNA synthetase
dbt	dihydrolipoamide branched chain transacylase E2
dcdc2b	predicted gene 12964
dchs2	dachsous 2 (Drosophila)
dcpp2	demilune cell and parotid protein 2

dcpp3	demilune cell and parotid protein 3
ddef1	ArfGAP with SH3 domain, ankyrin repeat and PH domain1
ddef2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2
ddefl1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b
ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41
ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42
ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49
ddx50	predicted gene 8228; DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
ddx5-ps1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5, pseudogene 1
deb1	differentially expressed in B16F10 1
def6	differentially expressed in FDCP 6
def8	differentially expressed in FDCP 8
defb29	defensin beta 29
dennd4a	DENN/MADD domain containing 4A
dennd4b	DENN/MADD domain containing 4B
dennd4c	DENN/MADD domain containing 4C
depdc2	DEP domain containing 2
dgkb	diacylglycerol kinase, beta
dgkd	diacylglycerol kinase, delta
dgkg	diacylglycerol kinase, gamma
dgkh	diacylglycerol kinase, eta
dgkq	diacylglycerol kinase, theta
dhdds	dehydrodolichyl diphosphate synthase
dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16
dhx29	DEAH (Asp-Glu-Ala-His) box polypeptide 29
dhx35	predicted gene 4713; DEAH (Asp-Glu-Ala-His) box polypeptide 35; hypothetical protein LOC100046264
dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36
dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8
diap2	diaphanous homolog 2 (Drosophila)
dip2a	DIP2 disco-interacting protein 2 homolog A (Drosophila); similar to mKIAA0184 protein
diras1	DIRAS family, GTP-binding RAS-like 1
diras2	DIRAS family, GTP-binding RAS-like 2
dis3	DIS3 mitotic control homolog (S. cerevisiae)
dmkn	dermokine
dmrtc1a	DMRT-like family C1a
dmrtc1b	DMRT-like family C1b
dmrtc1c	DMRT-like family C1c2; DMRT-like family C1c
dmxl1	Dmx-like 1
dmxl2	Dmx-like 2
dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2
dnajb13	DnaJ (Hsp40) related, subfamily B, member 13
dnajb3	DnaJ (Hsp40) homolog, subfamily B, member 3
dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1
dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11
dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12
dnajc21	DnaJ (Hsp40) homolog, subfamily C, member 21
dnajc4	DnaJ (Hsp40) homolog, subfamily C, member 4
dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5
dnajc5b	DnaJ (Hsp40) homolog, subfamily C, member 5 beta
dnajc9	DnaJ (Hsp40) homolog, subfamily C, member 9

dnase1l1	deoxyribonuclease 1-like 1
dnase1l3	deoxyribonuclease 1-like 3
dnmlp1	dynamin-like protein 1
dntt	deoxynucleotidyltransferase, terminal
dock1	dedicator of cytokinesis 1
dock10	dedicator of cytokinesis 10
dock11	dedicator of cytokinesis 11
dock2	dedicator of cyto-kinesis 2
dock4	dedicator of cytokinesis 4
dock6	dedicator of cytokinesis 6
dock9	dedicator of cytokinesis 9
dolpp1	dolichyl pyrophosphate phosphatase 1
dopey1	dopey family member 1
dopey2	dopey family member 2
dpf2	D4, zinc and double PHD fingers family 2
dph2	DPH2 homolog (S. cerevisiae)
dph3	DPH3 homolog (KTI11, S. cerevisiae)
dph4	DnaJ (Hsp40) homolog, subfamily C, member 24
dpm3	dolichyl-phosphate mannosyltransferase polypeptide 3
dpy30	dpy-30 homolog (C. elegans); predicted gene 2059; similar to RIKEN cDNA 2810410M20 gene
dqx1	DEAQ RNA-dependent ATPase
drap1	Dr1 associated protein 1 (negative cofactor 2 alpha); similar to Dr1 associated protein 1 (negative cofactor 2 alpha)
drb1	dopamine receptor binding 1
drg1	developmentally regulated GTP binding protein 1
drg2	hypothetical protein LOC674305; predicted gene 8918; developmentally regulated GTP binding protein 2
dscr3	Down syndrome critical region gene 3
dsg1c	desmoglein 1 gamma
dtd1	similar to D-tyrosyl-tRNA deacylase 1; D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)
dtna	dystrobrevin alpha
dtwd2	DTW domain containing 2
dub2	ubiquitin specific peptidase 17-like 5
dub3	predicted gene 6596
dub4	deubiquitinating enzyme 4
dullard	similar to Dullard homolog (Xenopus laevis); Dullard homolog (Xenopus laevis)
dusp15	dual specificity phosphatase-like 15
dvb11-1	V11<+> T-cell deletion 1
dvb11-2	V11<+> T-cell deletion 2
dvb11-3	V11<+> T-cell deletion 3
dxcp3	dexamethasone induced cleft palate 3
dxhxs101	DNA segment, Chr X, human DXS101
dxhxs178	DNA segment, Chr X, human DXS178
dxmit39	DNA segment, Chr X, Massachusetts Institute of Technology 39
dxmit49	DNA segment, Chr X, Massachusetts Institute of Technology 49
dxmit85	DNA segment, Chr X, Massachusetts Institute of Technology 85
dxpas19	DNA segment, Chr X, Pasteur Institute 19
dxpas23	DNA segment, Chr X, Pasteur Institute 23
dzip1	DAZ interacting protein 1
e130112l23rik	RIKEN cDNA E130112L23 gene
e330026b02rik	collagen, type VI, alpha 6
ea4	erythrocyte antigen 4
eae1	experimental allergic encephalomyelitis susceptibility1
ect2	ect2 oncogene
edc3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)
edil3	EGF-like repeats and discoidin I-like domains 3

eef1a1	predicted gene 5869; predicted gene 7161; predicted gene 7105; predicted gene 5822; similar to eukaryotic translation elongation factor 1 alpha 1; predicted gene 6192; predicted gene 6392; predicted gene 6767; predicted gene 6170; predicted gene 6548; predicted gene 6789; eukaryotic translation elongation factor 1 alpha 1
eef1b2	eukaryotic translation elongation factor 1 beta 2
eef1d	predicted gene 11675; eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
eef1g	predicted gene 4462; similar to eukaryotic translation elongation factor 1 gamma; predicted gene 9276; predicted gene 5525; eukaryotic translation elongation factor 1 gamma; similar to Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma); predicted gene 4366
efhd1	EF hand domain containing 1
eg208426	IQ motif containing J
eg238217	ribosomal protein L10-like
eg382639	zinc finger and BTB domain containing 42
eg436240	forkhead box R2
eg622901	predicted gene 6368
eg627648	kelch-like 3 (Drosophila)
eg629860	immunoglobulin heavy variable V1-12
eg630061	T cell receptor alpha variable 7-5
eg630579	zinc finger protein 80
eg653016	predicted gene 7325
eg665033	collagen, type VI, alpha 5
eg665419	RAB11b, member RAS oncogene family, pseudogene 2
eg667604	predicted gene 8721
eg667683	immunoglobulin kappa variable 4-59
eg668389	immunoglobulin heavy variable V2-4
eg668723	amylase 2, pseudogene 1
egfl8	EGF-like domain 8
eif1ad	eukaryotic translation initiation factor 1A domain containing
eif1b	eukaryotic translation initiation factor 1B
eif2b1	eukaryotic translation initiation factor 2B, subunit 1 (alpha)
eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta
eif2b3	eukaryotic translation initiation factor 2B, subunit 3
eif2b4	eukaryotic translation initiation factor 2B, subunit 4 delta
eif2s2	similar to Eif2s2 protein; eukaryotic translation initiation factor 2, subunit 2 (beta)
eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked; similar to translation initiation factor eIF-2 gamma subunit; predicted gene 2223
eif3b	hypothetical protein LOC100047993; eukaryotic translation initiation factor 3, subunit B
eif3d	eukaryotic translation initiation factor 3, subunit D
eif3g	eukaryotic translation initiation factor 3, subunit G
eif3i	eukaryotic translation initiation factor 3, subunit I
eif4e2	eukaryotic translation initiation factor 4E member 2
eif4ebp1-ps1	eukaryotic translation initiation factor 4E binding protein 1, pseudogene 1
eif4ebp1-ps2	eukaryotic translation initiation factor 4E binding protein 1, pseudogene 2
eif5	similar to Eukaryotic translation initiation factor 5; eukaryotic translation initiation factor 5
eif5b	eukaryotic translation initiation factor 5B
ela1	elastase 1, pancreatic
elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)
elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)
elmo3	engulfment and cell motility 3, ced-12 homolog (C. elegans)
elmod1	ELMO domain containing 1
elmod2	ELMO domain containing 2
elp2	elongation protein 2 homolog (S. cerevisiae)
emb-rs4	embigin related sequence 4
emid2	EMI domain containing 2
emilin3	elastin microfibril interfacer 3
eml2	echinoderm microtubule associated protein like 2

eml3	echinoderm microtubule associated protein like 3
emv22	endogenous ecotropic MuLV 22
emv24	endogenous ecotropic MuLV 24
emv27	endogenous ecotropic MuLV 27
eno3	enolase 3, beta muscle
ensa	predicted gene 5224; endosulfine alpha; similar to endosulfine alpha isoform 1
ensmusg00000053178	predicted gene 9897
ensmusg00000061310	predicted gene, ENSMUSG00000061310
ensmusg00000067748	ribosomal protein L17, pseudogene 5
ensmusg00000076783	T-cell receptor alpha, variable 8
entpd6	ectonucleoside triphosphate diphosphohydrolase 6
entpd7	ectonucleoside triphosphate diphosphohydrolase 7
epb4.1l4a	erythrocyte protein band 4.1-like 4a
epb4.1l4b	erythrocyte protein band 4.1-like 4b
eps8	epidermal growth factor receptor pathway substrate 8
eps8l1	EPS8-like 1
eps8l2	EPS8-like 2
eps8l3	EPS8-like 3
eral1	Era (G-protein)-like 1 (E. coli)
erc1	ELKS/RAB6-interacting/CAST family member 1; similar to Rab6-interacting protein 2
erdr1	erythroid differentiation regulator 1
esrrg	estrogen-related receptor gamma
etaa1	Ewing's tumor-associated antigen 1
etf1	eukaryotic translation termination factor 1
etfa	predicted gene 2893; electron transferring flavoprotein, alpha polypeptide
etfb	similar to Electron transferring flavoprotein, beta polypeptide; electron transferring flavoprotein, beta polypeptide
etn1	early transposon element 1
etv2	similar to ETS related protein 71; ets variant gene 2
evi5l	ecotropic viral integration site 5 like
exoc1	exocyst complex component 1
exoc2	exocyst complex component 2
exoc3	exocyst complex component 3
exoc5	exocyst complex component 5
exoc6b	exocyst complex component 6B
exoc7	exocyst complex component 7
exoc8	exocyst complex component 8
exosc8	exosome component 8
f13b	coagulation factor XIII, beta subunit
f830045p16rik	RIKEN cDNA F830045P16 gene
f830116e18rik	RIKEN cDNA F830116E18 gene
farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived); similar to FERMRhoGEF (Arhgef) and pleckstrin domain protein 1
farp2	FERM, RhoGEF and pleckstrin domain protein 2
fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)
farsa	phenylalanyl-tRNA synthetase, alpha subunit
farsb	phenylalanyl-tRNA synthetase, beta subunit
fbxo10	F-box protein 10
fbxo16	F-box protein 16
fbxo17	F-box protein 17; hypothetical protein LOC100047462
fbxo27	F-box protein 27
fbxo44	similar to F-box protein 44; F-box protein 44
fbxo8	F-box protein 8

fbxw15	F-box and WD-40 domain protein 15
fcer1a	Fc receptor, IgE, high affinity I, alpha polypeptide
fcho2	FCH domain only 2
fdpsl8	farnesyl diphosphate synthetase-like 8
fer1l4	fer-1-like 4 (C. elegans)
fermt3	fermitin family homolog 3 (Drosophila)
fgd1	FYVE, RhoGEF and PH domain containing 1
fgd2	FYVE, RhoGEF and PH domain containing 2
fgd3	FYVE, RhoGEF and PH domain containing 3
fgd4	FYVE, RhoGEF and PH domain containing 4
fgfr1op2	FGFR1 oncogene partner 2; similar to FGFR1 oncogene partner 2; predicted gene 12312
fgg	fibrinogen gamma chain
ficd	FIC domain containing
fkbp2	FK506 binding protein 2
fkbp9	FK506 binding protein 9
fnbp1	formin binding protein 1
fndc1	fibronectin type III domain containing 1; similar to fibronectin type III domain containing 1
fndc4	fibronectin type III domain containing 4
fndc5	fibronectin type III domain containing 5
fnta	farnesyltransferase, CAAX box, alpha; similar to farnesyltransferase alpha subunit
fntb	similar to farnesyltransferase, CAAX box, beta; farnesyltransferase, CAAX box, beta
foxa3	forkhead box A3
fpgt	fucose-1-phosphate guanylyltransferase
frag1	post-GPI attachment to proteins 2
frmd4b	FERM domain containing 4B
frmpd1	FERM and PDZ domain containing 1
fsd1l	fibronectin type III and SPRY domain containing 1-like
ftsj2	FtsJ homolog 2 (E. coli)
fuk	fucokinase
fut4-ps1	fucosyltransferase 4, pseudogene 1
fxc1	fractured callus expressed transcript 1; dynein heavy chain domain 1
fxyd1	FXYD domain-containing ion transport regulator 1
fxyd2	FXYD domain-containing ion transport regulator 2
fxyd3	FXYD domain-containing ion transport regulator 3
fxyd4	FXYD domain-containing ion transport regulator 4
fxyd7	FXYD domain-containing ion transport regulator 7
g0s2	G0/G1 switch gene 2
gabarap	gamma-aminobutyric acid receptor associated protein
gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1
gabarapl2	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 2; predicted gene 3724
gabpa	GA repeat binding protein, alpha
gabpb1	GA repeat binding protein, beta 1
gabra1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1
gabra2	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2; similar to Gamma-aminobutyric-acid receptor subunit alpha-2 precursor (GABA(A) receptor subunit alpha-2)
gabra3	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3
gabra4	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 4
gabra5	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 5
gabra6	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 6
gabrb1	gamma-aminobutyric acid (GABA) A receptor, subunit beta 1
gabrb2	gamma-aminobutyric acid (GABA) A receptor, subunit beta 2
gabrb3	gamma-aminobutyric acid (GABA) A receptor, subunit beta 3
gabrd	gamma-aminobutyric acid (GABA) A receptor, subunit delta
gabre	similar to gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon; gamma-aminobutyric acid (GABA) A receptor, subunit epsilon

gabrg1	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 1
gabrg2	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 2
gabrg3	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3
gabrp	gamma-aminobutyric acid (GABA) A receptor, pi
gabrq	gamma-aminobutyric acid (GABA) A receptor, subunit theta
gabrr1	gamma-aminobutyric acid (GABA) C receptor, subunit rho 1
gabrr2	gamma-aminobutyric acid (GABA) C receptor, subunit rho 2
gabrr3	gamma-aminobutyric acid (GABA) receptor, rho 3
gal3st2	predicted gene 9994; galactose-3-O-sulfotransferase 2
gal3st3	galactose-3-O-sulfotransferase 3
gal3st4	galactose-3-O-sulfotransferase 4
ganab	alpha glucosidase 2 alpha neutral subunit
gapvd1	GTPase activating protein and VPS9 domains 1
garnl1	Ral GTPase activating protein, alpha subunit 1
garnl4	RAP1 GTPase activating protein 2
gas2l1	growth arrest-specific 2 like 1
gas2l2	growth arrest-specific 2 like 2
gas4	growth arrest specific 4
gatad1	GATA zinc finger domain containing 1
gbas	glioblastoma amplified sequence
gbf1	golgi-specific brefeldin A-resistance factor 1
gbp1	similar to guanylate nucleotide binding protein 1; guanylate binding protein 1
gbp2	guanylate binding protein 2
gbp3	guanylate binding protein 3
gbp4	guanylate binding protein 4
gbp5	guanylate binding protein 5
gcc1	golgi coiled coil 1
gcc2	GRIP and coiled-coil domain containing 2
gda	guanine deaminase
gde1	glycerophosphodiester phosphodiesterase 1
gdi1	guanosine diphosphate (GDP) dissociation inhibitor 1
gdi2	predicted gene 4973; guanosine diphosphate (GDP) dissociation inhibitor 2
gdpd1	glycerophosphodiester phosphodiesterase domain containing 1
gdpd4	glycerophosphodiester phosphodiesterase domain containing 4
gem	GTP binding protein (gene overexpressed in skeletal muscle)
gfm1	G elongation factor, mitochondrial 1
ggnbp1	gametogenetin binding protein 1; RIKEN cDNA 0610031G08 gene
ggnbp2	gametogenetin binding protein 2
ggps1	geranylgeranyl diphosphate synthase 1; similar to Ggps1 protein; predicted gene 5630
ggt7	gamma-glutamyltransferase 7
ggta1	glycoprotein galactosyltransferase alpha 1, 3
gimap1	GTPase, IMAP family member 1
gimap3	similar to immunity-associated nucleotide 4; GTPase, IMAP family member 3
gimap4	GTPase, IMAP family member 4
gimap6	GTPase, IMAP family member 6
gimap7	GTPase, IMAP family member 7
gimap8	GTPase, IMAP family member 8
gimap9	GTPase, IMAP family member 9
gins4	GINS complex subunit 4 (Sld5 homolog)
gipc2	GIPC PDZ domain containing family, member 2
gipc3	GIPC PDZ domain containing family, member 3
git1	G protein-coupled receptor kinase-interactor 1
git2	G protein-coupled receptor kinase-interactor 2
gja6	gap junction protein, alpha 6
glipr2	GLI pathogenesis-related 2

glod4	glyoxalase domain containing 4
glra2	glycine receptor, alpha 2 subunit
glra3	glycine receptor, alpha 3 subunit
glra4	glycine receptor, alpha 4 subunit
glrb	glycine receptor, beta subunit
glt25d1	glycosyltransferase 25 domain containing 1
glt25d2	glycosyltransferase 25 domain containing 2
gm1110	predicted gene 1110
gm1220	gene model 1220, (NCBI)
gm1423	gene model 1423, (NCBI)
gm1848	predicted gene 1848
gm312	keratin associated protein 24-1
gm347	predicted gene 347
gm459	predicted gene 459
gm75	epididymal protein 3B
gm885	predicted gene 885
gm900	predicted gene 5353; immunoglobulin heavy chain (J558 family); similar to Ig heavy chain V region 108A precursor; similar to Ig heavy chain V-I region V35 precursor; predicted gene 900; immunoglobulin heavy chain complex; similar to Ig H-chain V-JH1-region; immunoglobulin heavy variable V1-31; immunoglobulin heavy chain 2 (serum IgA)
gm98	predicted gene 98
gmip	Gem-interacting protein
gmppa	GDP-mannose pyrophosphorylase A
gmppb	GDP-mannose pyrophosphorylase B
gmpr	guanosine monophosphate reductase
gna11	guanine nucleotide binding protein, alpha 11
gna12	guanine nucleotide binding protein, alpha 12; similar to Guanine nucleotide-binding protein alpha-12 subunit (G alpha-12)
gna13	guanine nucleotide binding protein, alpha 13
gna14	guanine nucleotide binding protein, alpha 14
gna15	guanine nucleotide binding protein, alpha 15
gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1
gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting 2; similar to Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate cyclase-inhibiting G alpha protein)
gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting 3
gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type
gnao1	guanine nucleotide binding protein, alpha O
gna-rs1	guanine nucleotide binding protein-like 1
gnat2	guanine nucleotide binding protein, alpha transducing 2
gnaz	guanine nucleotide binding protein, alpha z subunit
gnb1	guanine nucleotide binding protein (G protein), beta 1
gnb1-ps2	guanine nucleotide binding protein (G protein), beta 1, pseudogene 2
gnb1-ps3	guanine nucleotide binding protein (G protein), beta 1, pseudogene 3
gnb2	guanine nucleotide binding protein (G protein), beta 2
gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1
gnb4	guanine nucleotide binding protein (G protein), beta 4
gnb5	guanine nucleotide binding protein (G protein), beta 5
gng10	guanine nucleotide binding protein (G protein), gamma 10
gng11	guanine nucleotide binding protein (G protein), gamma 11
gng12	guanine nucleotide binding protein (G protein), gamma 12
gng13	guanine nucleotide binding protein (G protein), gamma 13
gng2	guanine nucleotide binding protein (G protein), gamma 2
gng3	guanine nucleotide binding protein (G protein), gamma 3
gng4	guanine nucleotide binding protein (G protein), gamma 4
gng5	predicted gene 13342; predicted gene 3785; predicted gene 15776; predicted gene 6825; similar to G protein gamma-5 subunit; predicted gene 3150; predicted gene 4356; guanine nucleotide binding protein (G protein), gamma 5

gng7	guanine nucleotide binding protein (G protein), gamma 7
gng8	guanine nucleotide binding protein (G protein), gamma 8
gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
gnl2	guanine nucleotide binding protein-like 2 (nucleolar)
gnl3l	guanine nucleotide binding protein-like 3 (nucleolar)-like
gnptab	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits
gnptg	similar to N-acetylglucosamine-1-phosphotransferase, gamma subunit; N-acetylglucosamine-1-phosphotransferase, gamma subunit
golga4	golgi autoantigen, golgin subfamily a, 4
golga5	golgi autoantigen, golgin subfamily a, 5
golga7	predicted gene 6829; golgi autoantigen, golgin subfamily a, 7
golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1
golt1b	golgi transport 1 homolog B (S. cerevisiae)
gorasp2	golgi reassembly stacking protein 2
got1l1	glutamic-oxaloacetic transaminase 1-like 1
gpha2	glycoprotein hormone alpha 2
gphb5	glycoprotein hormone beta 5
gphn	gephyrin
gpr107	G protein-coupled receptor 107; hypothetical protein LOC100047589
gpr108	G protein-coupled receptor 108
gpr111	G protein-coupled receptor 111
gpr113	G protein-coupled receptor 113
gpr123	G protein-coupled receptor 123
gpr128	G protein-coupled receptor 128
gpr137b-ps	G protein-coupled receptor 137B, pseudogene
gpr142	G protein-coupled receptor 142
gpr156	G protein-coupled receptor 156
gpr160	G protein-coupled receptor 160
gpr173	G-protein coupled receptor 173
gpr176	G protein-coupled receptor 176
gpr177	G protein-coupled receptor 177
gpr20	G protein-coupled receptor 20
gpr26	G protein-coupled receptor 26
gpr27	G protein-coupled receptor 27
gpr3	G-protein coupled receptor 3
gpr31c	predicted gene 8593; predicted gene 6553; predicted gene 6544; G protein-coupled receptor 31, D17Leh66c region
gpr45	G protein-coupled receptor 45
gpr6	G protein-coupled receptor 6
gpr63	G protein-coupled receptor 63
gprin1	G protein-regulated inducer of neurite outgrowth 1
gprin2	G protein regulated inducer of neurite outgrowth 2
gprin3	GPRIN family member 3
gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)
gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)
gpsm3	G-protein signalling modulator 3 (AGS3-like, C. elegans)
grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein
grit	Rho GTPase activating protein 32
grlf1	glucocorticoid receptor DNA binding factor 1
grtp1	GH regulated TBC protein 1
grwd1	glutamate-rich WD repeat containing 1
gsdma1	gasdermin A
gsdmc2	gasdermin C2
gsdmc3	gasdermin C3

gsdmc4	gasdermin C4
gsg1	germ cell-specific gene 1
gspt2	G1 to S phase transition 2
gsta	glutathione S-transferase cluster
gsta1	glutathione S-transferase, alpha 1 (Ya)
gsta2	glutathione S-transferase, alpha 2 (Yc2)
gsta3	glutathione S-transferase, alpha 3
gtdc1	glycosyltransferase-like domain containing 1
gtf2a1	predicted gene 5435; general transcription factor II A, 1
gtf2a1l	general transcription factor IIA, 1-like
gtf2a2	similar to TFIIA small subunit; general transcription factor II A, 2
gtf3c1	general transcription factor III C 1
gtf3c2	general transcription factor IIIC, polypeptide 2, beta; Mpv17 transgene, kidney disease mutant
gtf3c3	general transcription factor IIIC, polypeptide 3
gtf3c6	general transcription factor IIIC, polypeptide 6, alpha
gtpbp1	GTP binding protein 1
gtpbp10	GTP-binding protein 10 (putative); predicted gene 6877
gtpbp2	GTP binding protein 2
gtpbp3	GTP binding protein 3
gtpbp4	GTP binding protein 4
gtpbp5	GTP binding protein 5
gtsf1l	zinc finger protein 850; gametocyte specific factor 1-like
gucy1a2	hypothetical protein LOC100044212; guanylate cyclase 1, soluble, alpha 2
gucy1a3	guanylate cyclase 1, soluble, alpha 3
gucy1b2	similar to guanylate cyclase 1, soluble, beta 2; guanylate cyclase 1, soluble, beta 2
gucy1b3	guanylate cyclase 1, soluble, beta 3
guf1	GUF1 GTPase homolog (S. cerevisiae)
gvin1	predicted gene 1966; predicted gene 8995; GTPase, very large interferon inducible 1
gykl1	glycerol kinase-like 1
h2-dmb2	histocompatibility 2, class II, locus Mb2
h2-eb2	histocompatibility 2, class II antigen E beta2
h2-gs10	MHC class I like protein GS10
h2-k2	histocompatibility 2, K region locus 2
h2-m2	histocompatibility 2, M region locus 2
h2-ob	histocompatibility 2, O region beta locus
h2-pb	histocompatibility 2, P region beta locus
h2-q11	histocompatibility 2, Q region locus 11
h2-q5	histocompatibility 2, Q region locus 5
h2-t10	histocompatibility 2, T region locus 9; hypothetical protein LOC100044191; histocompatibility 2, T region locus 10; hypothetical protein LOC100044190; histocompatibility 2, T region locus 22
h2-t18	MHC class I antigen; histocompatibility 2, T region locus 18; hypothetical protein LOC100044192; histocompatibility 2, T region locus 3; similar to histocompatibility 2, T region locus 3; similar to H-2 class I histocompatibility antigen, TLA(C) alpha chain precursor
h2-t22	histocompatibility 2, T region locus 9; hypothetical protein LOC100044191; histocompatibility 2, T region locus 10; hypothetical protein LOC100044190; histocompatibility 2, T region locus 22
h2-t3	MHC class I antigen; histocompatibility 2, T region locus 18; hypothetical protein LOC100044192; histocompatibility 2, T region locus 3; similar to histocompatibility 2, T region locus 3; similar to H-2 class I histocompatibility antigen, TLA(C) alpha chain precursor
h2-t9	histocompatibility 2, T region locus 9; hypothetical protein LOC100044191; histocompatibility 2, T region locus 10; hypothetical protein LOC100044190; histocompatibility 2, T region locus 22
h36	histocompatibility 36
h8	histocompatibility 8
hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
hadhb	predicted gene 13910; similar to Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit; hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit; predicted gene 9108

harbi1	harbinger transposase derived 1
hba-ps3	hemoglobin alpha, pseudogene 3
hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex
hbb-b2	hemoglobin, beta adult major chain; hemoglobin, beta adult minor chain
hbb-bh0	hemoglobin Z, beta-like embryonic chain; hypothetical protein LOC100044263; hemoglobin, beta, pseudogene bh0
hbb-bh1	hemoglobin Z, beta-like embryonic chain; hypothetical protein LOC100044263; hemoglobin, beta, pseudogene bh0
hbb-bh2	hemoglobin beta, pseudogene bh2
hbb-bh3	hemoglobin beta, pseudogene bh3
hbb-y	similar to beta-globin; hemoglobin Y, beta-like embryonic chain
hbq1	hemoglobin, theta 1
hc11	heterochromatin, Chr 11
hc8	heterochromatin, Chr 8
hcm	heterochromatin, multiple chromosomes
hdgfl1	hepatoma derived growth factor-like 1
hebp2	heme binding protein 2
hel308	helicase, POLQ-like
helb	helicase (DNA) B
helz	helicase with zinc finger domain
herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1
herc3	hect domain and RLD 3
herc5	hect domain and RLD 5
hfm1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)
hhat	hedgehog acyltransferase
hhatl	hedgehog acyltransferase-like
higd1a	HIG1 domain family, member 1A
hint1	histidine triad nucleotide binding protein 1
hint3	histidine triad nucleotide binding protein 3
hist1h2aj	histone cluster 1, H2aj
hist3h2ba	histone cluster 3, H2ba; histone cluster 3, H2bb
hivep1	human immunodeficiency virus type I enhancer binding protein 1
hmga2-ps1	high mobility group AT-hook 2, pseudogene 1
hmgn1-rs15	high mobility group nucleosomal binding domain 1, related sequence 15
hmgn1-rs5	high mobility group nucleosomal binding domain 1, related sequence 5
hmgn2-rs2	high mobility group nucleosomal binding domain 2, related sequence 2
hn1l	hematological and neurological expressed 1-like
hnf4g	hepatocyte nuclear factor 4, gamma
hnrnpul2	heterogeneous nuclear ribonucleoprotein U-like 2
homez	homeodomain leucine zipper-encoding gene
hormad1	HORMA domain containing 1; predicted gene 7167
hras1-ps1	Harvey rat sarcoma virus oncogene, pseudogene 1
hrasls	HRAS-like suppressor
hscb	HscB iron-sulfur cluster co-chaperone homolog (E. coli)
hsd3b2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2
hsd3b3	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3
hsd3b5	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5
hsdl1	hydroxysteroid dehydrogenase like 1
hsdl2	hydroxysteroid dehydrogenase like 2
hsfy2	heat shock transcription factor, Y linked 2
hspa9-ps1	heat shock protein 9, pseudogene 1
hspbap1	Hspb associated protein 1
htr1e	5-hydroxytryptamine (serotonin) receptor 1E
htr5b	5-hydroxytryptamine (serotonin) receptor 5B
iapls3-28	intracisternal A particle, lymphocyte specific 3-28

iapt15	intracisternal A particle, tumor specific 15
iapt8	intracisternal A particle, tumor specific 8
icam4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group
ichs	immediate cutaneous hypersensitivity QTL
icmt	isoprenylcysteine carboxyl methyltransferase
idh3a	isocitrate dehydrogenase 3 (NAD+) alpha
idh3b	isocitrate dehydrogenase 3 (NAD+) beta
idh3g	isocitrate dehydrogenase 3 (NAD+), gamma
ier3ip1	immediate early response 3 interacting protein 1; haloacid dehalogenase-like hydrolase domain containing 2; predicted gene 10784
if1	NDV-induced circulating interferon
if3	Sendai virus induced interferon 3
ifi201	interferon activated gene 201
ifna1	interferon alpha 1
ifna10	interferon alpha 10
ifna11	interferon alpha 11; hypothetical protein LOC100044216
ifna2	interferon alpha 2
ifna3	interferon alpha 3
ifna4	interferon alpha 4
ifna5	interferon alpha 5
ifna6	interferon alpha 6
ifna7	interferon alpha 7
ifna9	interferon alpha 9
ifnab	interferon alpha B
ifna-ps1	interferon alpha gene, pseudogene 1
ifnar2	interferon (alpha and beta) receptor 2
ifngr2	interferon gamma receptor 2
ifnz	interferon zeta
ift122	intraflagellar transport 122 homolog (Chlamydomonas)
ift52	intraflagellar transport 52 homolog (Chlamydomonas)
igbl	immunoglobulin-associated beta-like complex
igbp1	immunoglobulin (CD79A) binding protein 1
igh-1a	similar to gamma-2a immunoglobulin heavy chain; immunoglobulin heavy chain 1a (serum IgG2a); immunoglobulin heavy chain 1b (serum IgG2c)
igh-1b	similar to gamma-2a immunoglobulin heavy chain; immunoglobulin heavy chain 1a (serum IgG2a); immunoglobulin heavy chain 1b (serum IgG2c)
igh-2	predicted gene 5353; immunoglobulin heavy chain (J558 family); similar to Ig heavy chain V region 108A precursor; similar to Ig heavy chain V-I region V35 precursor; predicted gene 900; immunoglobulin heavy chain complex; similar to Ig H-chain V-JH1-region; immunoglobulin heavy variable V1-31; immunoglobulin heavy chain 2 (serum IgA)
igh-3	immunoglobulin heavy chain 3 (serum IgG2b); Immunoglobulin heavy chain (gamma polypeptide)
igh-5	immunoglobulin heavy chain 5 (delta-like heavy chain)
igh-7	immunoglobulin heavy chain 7 (heavy chain of IgE)
igh-8	immunoglobulin heavy chain 8 (heavy chain of IgG3)
ighg	immunoglobulin heavy chain 3 (serum IgG2b); Immunoglobulin heavy chain (gamma polypeptide)
ighg1	immunoglobulin heavy constant gamma 1 (G1m marker)
igh-ia	immunoglobulin heavy chain Ia
igh-pc	immunoglobulin heavy chain Pc
igh-sa1	immunoglobulin heavy chain Sa1
igh-vj558	predicted gene 5353; immunoglobulin heavy chain (J558 family); similar to Ig heavy chain V region 108A precursor; similar to Ig heavy chain V-I region V35 precursor; predicted gene 900; immunoglobulin heavy chain complex; similar to Ig H-chain V-JH1-region; immunoglobulin heavy variable V1-31; immunoglobulin heavy chain 2 (serum IgA)
igk-v	immunoglobulin kappa chain complex variable region
igkv1-110	immunoglobulin kappa chain variable 1-110
igkv1-135	immunoglobulin kappa variable 1-135
igk-v5	immunoglobulin kappa chain variable 5 (V5 family)

igkv6-25	immunoglobulin kappa chain variable 6-25
igl-c1	immunoglobulin lambda chain, constant region 2; immunoglobulin lambda chain, constant region 1; immunoglobulin lambda chain, variable 1
igl-c2	immunoglobulin lambda chain, constant region 2; immunoglobulin lambda chain, constant region 1; immunoglobulin lambda chain, variable 1
igl-j	immunoglobulin lambda chain, joining region
igsf11	immunoglobulin superfamily, member 11
ihpk1	interferon inducible GTPase 1; interferon-inducible GTPase-like
iigp1	interleukin 10 receptor, beta
iigp2	interleukin 11 receptor, alpha chain 2; predicted gene 13305; predicted gene, 100038993
il10rb	interleukin 15 receptor, alpha chain
il11ra2	interleukin 22 receptor, alpha 2
il15ra	interleukin 15 receptor, alpha chain
il22ra2	interleukin 22 receptor, alpha 2
il2rb	interleukin 2 receptor, beta chain
il2rg	predicted gene 614; interleukin 2 receptor, gamma chain
il3ra	interleukin 3 receptor, alpha chain
il7r	interleukin 7 receptor
il9r	similar to interleukin 9 receptor; interleukin 9 receptor
iltifb	interleukin 10-related T cell-derived inducible factor beta; interleukin 22
ilvbl	ilvB (bacterial acetolactate synthase)-like
inhbc	inhibin beta-C
inhbe	inhibin beta E
inpp4b	inositol polyphosphate-4-phosphatase, type II
ints4	integrator complex subunit 4
ints9	integrator complex subunit 9
ipo11	importin 11
ipo13	importin 13
ipo4	importin 4
ipo5	hypothetical protein LOC100044315; importin 5
ipo7	importin 7
iqcf4	IQ motif containing F4
iqgap2	IQ motif containing GTPase activating protein 2
iqgap3	IQ motif containing GTPase activating protein 3
iqsec1	IQ motif and Sec7 domain 1
iqsec2	IQ motif and Sec7 domain 2
iqsec3	IQ motif and Sec7 domain 3
ir8	immune response 8
irf9	interferon regulatory factor 9
islr	immunoglobulin superfamily containing leucine-rich repeat
islr2	immunoglobulin superfamily containing leucine-rich repeat 2
itga1	integrin alpha 1
itga10	integrin, alpha 10
itga11	integrin alpha 11
itga7	integrin alpha 7
itga8	integrin alpha 8
itga9	integrin alpha 9
itgad	integrin, alpha D
itgae	integrin alpha E, epithelial-associated
itgb1bp1	integrin beta 1 binding protein 1
itgb1bp2	integrin beta 1 binding protein 2
itgb1bp3	integrin beta 1 binding protein 3
itgb2l	integrin beta 2-like
itgb3bp	predicted gene 3507; integrin beta 3 binding protein (beta3-endonexin); similar to integrin beta 3 binding protein
itgb5	integrin beta 5

itgb6	integrin beta 6
itgb7	integrin beta 7
itgb8	integrin beta 8
itgbl1	integrin, beta-like 1
itih1	inter-alpha trypsin inhibitor, heavy chain 1
itih2	inter-alpha trypsin inhibitor, heavy chain 2
itih3	inter-alpha trypsin inhibitor, heavy chain 3
itm2c	integral membrane protein 2C
itpa-ps1	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) pseudogene 1
itpa-ps3	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) pseudogene 3
itsn1	intersectin 1 (SH3 domain protein 1A)
itsn2	intersectin 2
jmjd1b	lysine (K)-specific demethylase 3B
jrkl	jerky homolog-like (mouse)
kalrn	kalirin, RhoGEF kinase
kank1	KN motif and ankyrin repeat domains 1
kank2	KN motif and ankyrin repeat domains 2
kank3	KN motif and ankyrin repeat domains 3
kank4	KN motif and ankyrin repeat domains 4
kbtbd11	kelch repeat and BTB (POZ) domain containing 11
kbtbd7	kelch repeat and BTB (POZ) domain containing 7
kbtbd8	kelch repeat and BTB (POZ) domain containing 8
kcmf1	potassium channel modulatory factor 1
kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1
kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2
kcnab3	potassium voltage-gated channel, shaker-related subfamily, beta member 3
kcng2	potassium voltage-gated channel, subfamily G, member 2
kcnmb2	potassium large conductance calcium-activated channel, subfamily M, beta member 2
kcnmb4	potassium large conductance calcium-activated channel, subfamily M, beta member 4
kcns1	K+ voltage-gated channel, subfamily S, 1
kcns2	K+ voltage-gated channel, subfamily S, 2
kcnu1	potassium channel, subfamily U, member 1
kctd13	potassium channel tetramerisation domain containing 13
kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
kif13b	kinesin family member 13B
kif19a	kinesin family member 19A
kif20a	kinesin family member 20A
kif9	kinesin family member 9
kifl1-ps	kinesin-like 1, pseudogene
klhdc1	kelch domain containing 1
klhdc2	kelch domain containing 2
klhdc3	kelch domain containing 3
klhl20	kelch-like 20 (Drosophila)
klhl31	kelch-like 31 (Drosophila)
klhl5	kelch-like 5 (Drosophila)
klk1b11	kallikrein 1-related peptidase b11
klk1b8	kallikrein 1-related peptidase b8
kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1
kng2	kininogen 2
kpna1	karyopherin (importin) alpha 1
kpna3	karyopherin (importin) alpha 3
kpna4	karyopherin (importin) alpha 4
kpna6	karyopherin (importin) alpha 6
krtap12-1	keratin associated protein 12-1
ktelc1	KTEL (Lys-Tyr-Glu-Leu) containing 1

kti12	KTI12 homolog, chromatin associated (S. cerevisiae)
ktn1	kinectin 1
l1md-a1	L1 repeat, A subfamily, member 1
lama3	laminin, alpha 3
lama4	laminin, alpha 4
lama5	laminin, alpha 5
lamb1-1	laminin B1 subunit 1
lamb2	laminin, beta 2
lamb3	laminin, beta 3
lamc1	laminin, gamma 1
lamc2	laminin, gamma 2
lamc3	laminin gamma 3
lamr1-rs5	laminin receptor 1 (ribosomal protein SA), related sequence 5
lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1
lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2
lcn13	lipocalin 13
lcorl	ligand dependent nuclear receptor corepressor-like
lctl	lactase-like
len1	eye lens protein 1
leng9	leukocyte receptor cluster (LRC) member 9
leprel2	leprecan-like 2
lgi2	leucine-rich repeat LGI family, member 2
li	lined
loc100034726	predicted gene 15772
loc100043188	predicted gene 10696
loc100043207	amylase 2a1
loc100043989	similar to Ig heavy chain V region 7-39 precursor; similar to Ig heavy chain V region 345 precursor; similar to monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain; similar to Ig heavy chain V region RF precursor; V(H)76 segment leader peptide; similar to Ig heavy chain V region 5-84 precursor; similar to Immunogloblin heavy chain
loc16697	keratin associated protein LOC16697
loc381763	T-cell receptor beta chain V region
loc381765	similar to T cell antigen receptor
loc382653	immunoglobulin heavy chain variable region
loc383420	predicted gene 5241
loc383650	proteasome (prosome, macropain) subunit, beta type 6, pseudogene 2
loc432699	VH gene product
loc433466	jumonji domain containing 7
loc436194	predicted gene 5754
loc544903	similar to immunoglobulin mu-chain
loc621269	actin, gamma, pseudogene 1
loc630253	similar to Ig heavy chain V region 5-84 precursor
loc636017	immunglobulin heavy chain
loc641050	hypothetical protein LOC641050
loc641088	similar to Ig heavy chain V region RF precursor
loc665506	similar to T-cell receptor beta-2 chain C region
loc667655	predicted gene 8747
loc667882	ubiquitin specific peptidase, pseudogene (USP17 homolog)
loc676689	similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor
lphn1	latrophilin 1
lrba	LPS-responsive beige-like anchor
lrig2	leucine-rich repeats and immunoglobulin-like domains 2
lrrc18	leucine rich repeat containing 18
lrrc26	leucine rich repeat containing 26
lrrc59	leucine rich repeat containing 59

lrrc6	leucine rich repeat containing 6 (testis)
lrrc8a	leucine rich repeat containing 8A
lrrc8b	leucine rich repeat containing 8 family, member B
lrrc8c	leucine rich repeat containing 8 family, member C
lrrc8d	leucine rich repeat containing 8D
lrrc8e	similar to Leucine rich repeat containing 8 family, member E; leucine rich repeat containing 8 family, member E
lrrn2	leucine rich repeat protein 2, neuronal
lsg1	large subunit GTPase 1 homolog (S. cerevisiae)
lsm12	LSM12 homolog (S. cerevisiae)
lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)
lsr	lipolysis stimulated lipoprotein receptor
luc7l	Luc7 homolog (S. cerevisiae)-like
ly23	lymphocyte antigen 23
ly6f	lymphocyte antigen 6 complex, locus F
ly6g5c	lymphocyte antigen 6 complex, locus G5C
ly6h	similar to Lymphocyte antigen 6H precursor (Ly-6H); lymphocyte antigen 6 complex, locus H
ly77	lymphocyte antigen 77
lyzl1	lysozyme-like 1
lyzl4	lysozyme-like 4
lztr1	leucine-zipper-like transcriptional regulator, 1
mageb2	melanoma antigen, family B, 1; melanoma antigen, family B, 2
man1a2	mannosidase, alpha, class 1A, member 2
man1b-rs	mannosidase 1, beta, related sequence
mapk13	mitogen-activated protein kinase 13
mast4	microtubule associated serine/threonine kinase family member 4
mat2a	methionine adenosyltransferase II, alpha
mat2b	methionine adenosyltransferase II, beta
mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
mcf2	mcf.2 transforming sequence
mcf2l	mcf.2 transforming sequence-like
mdn1	midasin homolog (yeast)
mea1	male enhanced antigen 1
med16	mediator complex subunit 16
med29	mediator complex subunit 29; predicted gene 9450
med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
megf11	multiple EGF-like-domains 11
mep1a	meprin 1 alpha
mep1b	meprin 1 beta
mett10d	methyltransferase 10 domain containing
mett11d1	methyltransferase 11 domain containing 1
mettl1	methyltransferase like 1
mettl3	methyltransferase like 3
mfsd11	major facilitator superfamily domain containing 11
mgat3	mannoside acetylglucosaminyltransferase 3
mgat5b	mannoside acetylglucosaminyltransferase 5, isoenzyme B
mgll-rs2	monoglyceride lipase, related sequence 2
mical1	microtubule associated monoxygenase, calponin and LIM domain containing 1
mical3	microtubule associated monoxygenase, calponin and LIM domain containing 3
micalcl	MICAL C-terminal like
micall1	microtubule associated monoxygenase, calponin and LIM domain containing -like 1
midn	midnolin
mif4gd	MIF4G domain containing
mif-ps3	macrophage migration inhibitory factor, pseudogene 3

minta	Moloney MuLV integration site, EC cells, a
mkrn2	makorin, ring finger protein, 2
mmd	monocyte to macrophage differentiation-associated; similar to monocyte to macrophage differentiation-associated
mobkl2b	MOB1, Mps One Binder kinase activator-like 2B (yeast)
mon1b	MON1 homolog b (yeast)
mon2	MON2 homolog (yeast)
morc4	microrchidia 4
morn4	MORN repeat containing 4
mospd1	predicted gene 2147; motile sperm domain containing 1
mospd2	motile sperm domain containing 2
mov24	Moloney leukemia virus 24
moxd2	monooxygenase, DBH-like 2
mphosph8	M-phase phosphoprotein 8
mpmv14	modified polytropic murine leukemia virus 14
mpmv23	modified polytropic murine leukemia virus 23
mppe1	metallophosphoesterase 1
mpped1	metallophosphoesterase domain containing 1
mprip	myosin phosphatase Rho interacting protein; predicted gene 8086
mr1	major histocompatibility complex, class I-related
mras	muscle and microspikes RAS
mrgprf	MAS-related GPR, member F
mrpl12	mitochondrial ribosomal protein L12
mrpl15	mitochondrial ribosomal protein L15
mrpl2	mitochondrial ribosomal protein L2
mrpl3	mitochondrial ribosomal protein L3
mrpl37	mitochondrial ribosomal protein L37
mrpl39	mitochondrial ribosomal protein L39
mrpl46	mitochondrial ribosomal protein L46
mrps11	mitochondrial ribosomal protein S11
mrps25	mitochondrial ribosomal protein S25
mrps31	mitochondrial ribosomal protein S31
mrps34	mitochondrial ribosomal protein S34
mrps35	mitochondrial ribosomal protein S35
mrps9	mitochondrial ribosomal protein S9
mrrf	mitochondrial ribosome recycling factor; similar to mitochondrial ribosome recycling factor; predicted gene 6374
mrto4	predicted gene 9178; MRT4, mRNA turnover 4, homolog (S. cerevisiae); predicted gene 5633
ms4a14	membrane-spanning 4-domains, subfamily A, member 14
ms4a2	membrane-spanning 4-domains, subfamily A, member 2
ms4a3	membrane-spanning 4-domains, subfamily A, member 3
ms4a5	membrane-spanning 4-domains, subfamily A, member 5
ms4a7	membrane-spanning 4-domains, subfamily A, member 7
ms6-4	minisatellite-4 detected by probe 33.6
msto1	misato homolog 1 (Drosophila)
mterfd3	MTERF domain containing 3
mtmr7	myotubularin related protein 7
mtrf1	mitochondrial translational release factor 1
mtv1	mammary tumor virus locus 1
mtv11	mammary tumor virus locus 11
mtv37	mammary tumor virus locus 37
mtv43	mammary tumor virus locus 43
mtv48	mammary tumor virus locus 48
mtv50	mammary tumor virus locus 50
mtv51	mammary tumor virus locus 51

mtv54	mammary tumor virus locus 54
mtv6	mammary tumor virus locus 6
mtv7	mammary tumor virus locus 7
mtv8	mammary tumor virus locus 8
mtv9	mammary tumor virus locus 9
mtx2	metaxin 2
mtx3	metaxin 3
mug1	murinoglobulin 1; predicted gene 7298
mug2	murinoglobulin 2
mug4	murinoglobulin 4
mug-ps1	murinoglobulin, pseudogene 1
mycbpap	MYCBP associated protein
myef2	myelin basic protein expression factor 2, repressor
myg1	melanocyte proliferating gene 1
mynf1	myeloid nuclear factor 1
mynn	myoneurin
myo1f	myosin IF
myo9a	myosin IXa
myo9b	myosin IXb
n6amt1	N-6 adenine-specific DNA methyltransferase 1 (putative)
naif1	nuclear apoptosis inducing factor 1
narg2	NMDA receptor-regulated gene 2
nasp-ps1	nuclear autoantigenic sperm protein (histone-binding), pseudogene 1
nat14	N-acetyltransferase 14
nat5	N-acetyltransferase 5
nbea	neurobeachin
nbeal1	neurobeachin like 1
ncaph2	non-SMC condensin II complex, subunit H2
nckap1	NCK-associated protein 1
ncoa7	nuclear receptor coactivator 7
ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)
ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4; predicted gene 3873; predicted gene 3244
ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5
ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7
ndufc1	predicted gene 4237; NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1
nek3	NIMA (never in mitosis gene a)-related expressed kinase 3
net1	predicted gene 8990; neuroepithelial cell transforming gene 1
nfrkb	nuclear factor related to kappa B binding protein
nfu1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae); predicted gene 7859
nfxl1	nuclear transcription factor, X-box binding-like 1
ng23	Ng23 protein
ngef	neuronal guanine nucleotide exchange factor
ngrn	neugrin, neurite outgrowth associated
nicn1	nicolin 1
nif3l1	Ngg1 interacting factor 3-like 1 (S. pombe)
nip7	nuclear import 7 homolog (S. cerevisiae)
nisch	nischarin
nkain1	Na+/K+ transporting ATPase interacting 1
nkain2	Na+/K+ transporting ATPase interacting 2
nkain3	Na+/K+ transporting ATPase interacting 3
nkain4	Na+/K+ transporting ATPase interacting 4
nkg7	natural killer cell group 7 sequence
nkpd1	NTPase, KAP family P-loop domain containing 1
nlrc4	NLR family, CARD domain containing 4
nlrp10	NLR family, pyrin domain containing 10

nlrp12	NLR family, pyrin domain containing 12
nlrp1a	NLR family, pyrin domain containing 1A
nlrp1b	NLR family, pyrin domain containing 1B
nlrp2	NLR family, pyrin domain containing 2
nlrp4e	predicted gene 4541; predicted gene 8685; predicted gene 8567; NLR family, pyrin domain containing 4E; predicted gene 8486; predicted gene 16443; predicted gene 8728
nlrp6	NLR family, pyrin domain containing 6
nlrp9a	similar to NALP9A; NLR family, pyrin domain containing 9A
nlrp9c	NLR family, pyrin domain containing 9C
nme2	predicted gene 7730; non-metastatic cells 2, protein (NM23B) expressed in; predicted gene 5566; predicted gene 5425; similar to Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (P18)
nme4	non-metastatic cells 4, protein expressed in
nme6	similar to Nme6 protein; non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)
nme7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)
nol10	nucleolar protein 10
nol14	nucleolar protein 14
nol4	nucleolar protein 4
nol8	nucleolar protein 8
npdc1	neural proliferation, differentiation and control gene 1
npm3-ps1	nucleoplasmin 3; nucleoplasmin 3, pseudogene 1
npnt	nephronectin
nr1d2	nuclear receptor subfamily 1, group D, member 2; predicted gene 5827
nr1d2-rs2	nuclear receptor subfamily 1, group D, member 2, related sequence 2
nr2c1	nuclear receptor subfamily 2, group C, member 1
nrbf2	nuclear receptor binding factor 2
nrbp1	nuclear receptor binding protein 1
nrsn2	neurensin 2
nsbp1	high-mobility group nucleosome binding domain 5
nsg2	neuron specific gene family member 2
nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5
nutf2-ps1	nuclear transport factor 2, pseudogene 1
nvl	nuclear VCP-like
nxph2	neurexophilin 2
obfc1	oligonucleotide/oligosaccharide-binding fold containing 1
odc-rs9	ornithine decarboxylase, related sequence 9
odf3	outer dense fiber of sperm tails 3
odf4	outer dense fiber of sperm tails 4
oit3	oncoprotein induced transcript 3
ola1	Obg-like ATPase 1
olfml1	olfactomedin-like 1
olfml3	olfactomedin-like 3
olfr1310	olfactory receptor 1310
olfr1342	olfactory receptor 1342
olfr71	olfactory receptor 71
olfr937	olfactory receptor 937
olfr985	olfactory receptor 985
oog1	predicted gene 2042; predicted gene 10436; oogenesin 1; expressed sequence C87977
oog2	oogenesin 2
oog3	predicted gene 4350; oogenesin 3
oog4	oogenesin 4
oosp1	oocyte secreted protein 1
orf61	open reading frame 61
orm1	orosomucoid 1
orm3	orosomucoid 3

ormdl2	ORM1-like 2 (S. cerevisiae); predicted gene 5553
osbpl6	oxysterol binding protein-like 6
osbpl7	oxysterol binding protein-like 7
osgepl1	O-sialoglycoprotein endopeptidase-like 1
ottmusg00000000246	predicted gene 11212
ottmusg00000004461	predicted gene 11818
ottmusg00000005491	family with sequence similarity 71, member B
ottmusg00000010328	predicted gene 13084
ottmusg00000011275	predicted gene 13280
ottmusg00000011291	predicted gene 13290
ottmusg00000012291	predicted gene 13458
ottmusg00000015025	predicted gene 13893
ottmusg00000015050	T cell receptor alpha variable 9D-4
ottmusg00000015102	predicted gene 16454
ottmusg00000015160	T cell receptor alpha variable 6-3
ottmusg00000015161	T cell receptor alpha variable 7-4
ottmusg00000015181	T cell receptor alpha variable 7D-4
ottmusg00000020615	predicted gene 15352
ottmusg00000022462	amylase 2b
oua1	ouabain resistance 1
p42pop	Myb-related transcription factor, partner of profilin
p4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide
p4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide
p4ha3	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III
pabpc4	similar to Poly A binding protein, cytoplasmic 4; poly(A) binding protein, cytoplasmic 4; predicted gene 12623; predicted gene 5088; hypothetical protein LOC100044219
pabpc5	poly(A) binding protein, cytoplasmic 5
pabpnl1	poly(A)binding protein nuclear 1-like
pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2
pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3
pak1ip1	PAK1 interacting protein 1
pak3	p21 protein (Cdc42/Rac)-activated kinase 3
pak4	p21 protein (Cdc42/Rac)-activated kinase 4
pak6	p21 protein (Cdc42/Rac)-activated kinase 6
palmd	palmdelphin; similar to palmdelphin
pank1	pantothenate kinase 1
papolg	poly(A) polymerase gamma
paqr5	progestin and adipoQ receptor family member V
paqr6	progestin and adipoQ receptor family member VI; predicted gene 6821
paqr7	progestin and adipoQ receptor family member VII
paqr8	progestin and adipoQ receptor family member VIII
paqr9	progestin and adipoQ receptor family member IX
parp12	poly (ADP-ribose) polymerase family, member 12
parvb	parvin, beta; similar to parvin, beta
patl1	protein associated with topoisomerase II homolog 1 (yeast)
patl2	protein associated with topoisomerase II homolog 2 (yeast)

pcbp3	poly(rC) binding protein 3
pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide
pccb	propionyl Coenzyme A carboxylase, beta polypeptide
pcdh1	protocadherin 1
pcdh3	protocadherin 3
pcdha1	similar to protocadherin; protocadherin alpha 10; protocadherin alpha 9; protocadherin alpha 6; protocadherin alpha 12; similar to protocadherin alpha 11; protocadherin alpha 7; protocadherin alpha 11; protocadherin alpha 1; protocadherin alpha 5; protocadherin alpha 4; protocadherin alpha 2; protocadherin alpha subfamily C, 1; protocadherin alpha subfamily C, 2; protocadherin alpha cluster
pcdha4	similar to protocadherin; protocadherin alpha 10; protocadherin alpha 9; protocadherin alpha 6; protocadherin alpha 12; similar to protocadherin alpha 11; protocadherin alpha 7; protocadherin alpha 11; protocadherin alpha 1; protocadherin alpha 5; protocadherin alpha 4; protocadherin alpha 2; protocadherin alpha subfamily C, 1; protocadherin alpha subfamily C, 2; protocadherin alpha cluster
pcdhb12	protocadherin beta 12
pcdhga1	protocadherin gamma subfamily A, 1
pcp2	Purkinje cell protein 2 (L7)
pctk2	cyclin-dependent kinase 17
pdc	phosducin
pdcl	phosducin-like
pdcl2	phosducin-like 2
pdcl3	phosducin-like 3
pde6a	phosphodiesterase 6A, cGMP-specific, rod, alpha
pde6d	phosphodiesterase 6D, cGMP-specific, rod, delta
pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma
pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma
pdha2	pyruvate dehydrogenase E1 alpha 2
pdhb	predicted gene 6123; pyruvate dehydrogenase (lipoamide) beta
pdhx	pyruvate dehydrogenase complex, component X; similar to pyruvate dehydrogenase complex, component X
pdik1l	PDLIM1 interacting kinase 1 like
pdzd4	PDZ domain containing 4
pepb	peptidase B
pepc	peptidase C
pet112l	PET112-like (yeast)
pet2	plasmacytoma expressed transcript 2
pgbd1	piggyBac transposable element derived 1
pgbd5	piggyBac transposable element derived 5
pggt1b	protein geranylgeranyltransferase type I, beta subunit
pgls	6-phosphogluconolactonase
phactr3	phosphatase and actin regulator 3
phf7	PHD finger protein 7
phka1	phosphorylase kinase alpha 1
phka2	phosphorylase kinase alpha 2
phkb	phosphorylase kinase beta
phkg1	phosphorylase kinase gamma 1
phkg2	phosphorylase kinase, gamma 2 (testis)
phldb1	pleckstrin homology-like domain, family B, member 1
phtf2	putative homeodomain transcription factor 2
pigy	phosphatidylinositol glycan anchor biosynthesis, class Y
pigyl	phosphatidylinositol glycan anchor biosynthesis, class Y-like
pigz	phosphatidylinositol glycan anchor biosynthesis, class Z
pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)
pik3r5	phosphoinositide-3-kinase, regulatory subunit 5, p101
pik3r6	phosphoinositide-3-kinase, regulatory subunit 6
pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha
pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha

pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta; similar to phosphatidylinositol 4-phosphate 5-kinase type I-alpha
pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma
pitpna	phosphatidylinositol transfer protein, alpha
pitpnb	phosphatidylinositol transfer protein, beta
pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
pitpnm1	phosphatidylinositol transfer protein, membrane-associated 1
pitpnm3	PITPNM family member 3
pkia	protein kinase inhibitor, alpha
pkib	protein kinase inhibitor beta, cAMP dependent, testis specific
pkig	similar to protein kinase inhibitor gamma; protein kinase inhibitor, gamma; predicted gene 6334
pkn3	protein kinase N3
pla2g4b	phospholipase A2, group IVB (cytosolic); jumonji domain containing 7
pla2g4d	phospholipase A2, group IVD
pla2g4e	phospholipase A2, group IVE
pla2g4f	phospholipase A2, group IVF
plac9	placenta specific 9; predicted gene 10393; predicted gene 9780
plcb1	phospholipase C, beta 1
plcb2	phospholipase C, beta 2
plcb3	phospholipase C, beta 3
plcd1	phospholipase C, delta 1
plcd2	phospholipase C, delta 2
plce1	phospholipase C, epsilon 1
plcg2	phospholipase C, gamma 2
plch1	phospholipase C, eta 1
plch2	phospholipase C, eta 2
plcl1	phospholipase C-like 1
plcl2	phospholipase C-like 2
pld4	phospholipase D family, member 4
plek	pleckstrin
plek2	pleckstrin 2
plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3
plekha8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8
plekhb2	pleckstrin homology domain containing, family B (evectins) member 2
plekhg2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2
plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5
plekhg6	pleckstrin homology domain containing, family G (with RhoGef domain) member 6
plekhj1	pleckstrin homology domain containing, family J member 1
plk-ps1	polo-like kinase, pseudogene 1
pltr6	polytropic long terminal repeat containing proviral locus 6
plxnb1	plexin B1
plxnb2	plexin B2
plxnb3	plexin B3
pmpca	peptidase (mitochondrial processing) alpha
pmv11	polytropic murine leukemia virus 11
pmv23	polytropic murine leukemia virus 23
pmv39	polytropic murine leukemia virus 39
pnma5	paraneoplastic antigen family 5
pno1	partner of NOB1 homolog (S. cerevisiae)
pnpla8	patatin-like phospholipase domain containing 8
pol	pol protein
pola2	polymerase (DNA directed), alpha 2
pold1	polymerase (DNA directed), delta 1, catalytic subunit
pold2	polymerase (DNA directed), delta 2, regulatory subunit
pold3	polymerase (DNA-directed), delta 3, accessory subunit

pold4	polymerase (DNA-directed), delta 4
pole	polymerase (DNA directed), epsilon
pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)
pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)
pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)
polg2	polymerase (DNA directed), gamma 2, accessory subunit
polr2h	predicted gene 7511; polymerase (RNA) II (DNA directed) polypeptide H
polr2i	similar to RNA Polymerase II subunit 14.5 kD; polymerase (RNA) II (DNA directed) polypeptide I
polr2k	polymerase (RNA) II (DNA directed) polypeptide K; similar to polymerase (RNA) II (DNA directed) polypeptide K
polr2l	similar to DNA-directed RNA polymerase II 7.6 kDa polypeptide (RPB10) (RPB7.6) (RPABC5); hypothetical protein LOC100044218; predicted gene 13015; polymerase (RNA) II (DNA directed) polypeptide L; cytochrome P450, family 4, subfamily a, polypeptide 31; cytochrome P450, family 4, subfamily a, polypeptide 32; predicted gene 10774; cytochrome P450, family 4, subfamily a, polypeptide 10
polr3e	polymerase (RNA) III (DNA directed) polypeptide E
pomp	similar to proteasome maturation protein; proteasome maturation protein
pop1	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae)
pop5	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)
ppa2	pyrophosphatase (inorganic) 2
ppan	peter pan homolog (Drosophila)
ppap2b	phosphatidic acid phosphatase type 2B
ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta
ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1); similar to mKIAA1230 protein
ppfibp2	protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2
ppie	peptidylprolyl isomerase E (cyclophilin E)
ppil3	peptidylprolyl isomerase (cyclophilin)-like 3
ppil4	peptidylprolyl isomerase (cyclophilin)-like 4
ppi-ps1	peptidylprolyl isomerase, pseudogene 1
ppi-ps2	peptidylprolyl isomerase, pseudogene 2
ppi-ps3	peptidylprolyl isomerase, pseudogene 3
ppi-ps4	peptidylprolyl isomerase, pseudogene 4
ppi-ps5	peptidylprolyl isomerase, pseudogene 5
ppm1b	similar to serine/threonine phosphatase; protein phosphatase 1B, magnesium dependent, beta isoform
ppm1e	protein phosphatase 1E (PP2C domain containing)
ppm1f	protein phosphatase 1F (PP2C domain containing)
ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform
ppp1cc-ps1	protein phosphatase 1, catalytic subunit, gamma isoform, pseudogene 1
ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B
ppp1r14d	protein phosphatase 1, regulatory (inhibitor) subunit 14D
ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A
ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7
ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
ppp2cb	similar to protein phosphatase 2a, catalytic subunit, beta isoform; protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform
ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
ppp2r2b	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform
ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform
ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform
ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; RIKEN cDNA 3222402P14 gene
ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)
ppp2r5a	predicted gene 3353; predicted gene 13142; predicted gene 13169; similar to protein phosphatase 2, regulatory subunit B (B56), alpha isoform; predicted gene 13244; predicted gene 13233; protein phosphatase 2, regulatory subunit B (B56), alpha isoform
ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform
ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform

ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform
ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
ppp3cc	protein phosphatase 3, catalytic subunit, gamma isoform
ppp4r1	protein phosphatase 4, regulatory subunit 1
pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)
pramel1	preferentially expressed antigen in melanoma-like 1
preb	prolactin regulatory element binding
prim1	DNA primase, p49 subunit
prim2	DNA primase, p58 subunit
prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit
prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit
prkacb	protein kinase, cAMP dependent, catalytic, beta
prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
prkag3	protein kinase, AMP-activated, gamma 3 non-catatlytic subunit
prkar1b	protein kinase, cAMP dependent regulatory, type I beta
prkar1b-rs	protein kinase, cAMP dependent regulatory, type I beta, related sequence
prkch	protein kinase C, eta
prkcsh	protein kinase C substrate 80K-H
prkd3	protein kinase D3
prl8a6	prolactin family 8, subfamily a, member 6
prosc	proline synthetase co-transcribed
prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)
prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1
prpsap2	predicted gene 13651; phosphoribosyl pyrophosphate synthetase-associated protein 2
prr15	proline rich 15
prrg2	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2
prrg3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)
prss22	protease, serine, 22
psat1	similar to Phosphoserine aminotransferase 1; phosphoserine aminotransferase 1
pscd1	cytohesin 1
pscd2	cytohesin 2
pscd3	cytohesin 3
pscd4	cytohesin 4
pscdbp	cytohesin 1 interacting protein
psd	pleckstrin and Sec7 domain containing
psd2	pleckstrin and Sec7 domain containing 2
psd4	pleckstrin and Sec7 domain containing 4
psma1	proteasome (prosome, macropain) subunit, alpha type 1
psma2	proteasome (prosome, macropain) subunit, alpha type 2
psma3	proteasome (prosome, macropain) subunit, alpha type 3; predicted gene 5406
psma4	proteasome (prosome, macropain) subunit, alpha type 4; predicted gene 6542
psma5	proteasome (prosome, macropain) subunit, alpha type 5
psma8	proteasome (prosome, macropain) subunit, alpha type, 8
psmb10	proteasome (prosome, macropain) subunit, beta type 10
psmb11	proteasome (prosome, macropain) subunit, beta type, 11
psmb2	proteasome (prosome, macropain) subunit, beta type 2
psmb3	proteasome (prosome, macropain) subunit, beta type 3
psmb4	proteasome (prosome, macropain) subunit, beta type 4
psmb5	predicted gene 3375; proteasome (prosome, macropain) subunit, beta type 5
psmb6	proteasome (prosome, macropain) subunit, beta type 6
psmb7	proteasome (prosome, macropain) subunit, beta type 7
psmb7-ps1	proteasome (prosome, macropain) subunit, beta type 7, pseudogene 1
psmc1-rs1	protease (prosome, macropain) 26S subunit, ATPase 1, related sequence 1
psme1	predicted gene 7776; proteasome (prosome, macropain) 28 subunit, alpha

psme1-ps1	protease (prosome, macropain) 28 subunit, alpha, pseudogene 1
psme2	protease (prosome, macropain) 28 subunit beta B, pseudogene; similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta); proteasome (prosome, macropain) 28 subunit, beta; predicted gene 7928
psme2b-ps	protease (prosome, macropain) 28 subunit beta B, pseudogene; similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta); proteasome (prosome, macropain) 28 subunit, beta; predicted gene 7928
psme2-ps1	protease (prosome, macropain) 28 subunit, beta, b, pseudogene 1
psme2-ps2	protease (prosome, macropain) 28 subunit, beta, b, pseudogene 2
psme3	proteaseome (prosome, macropain) 28 subunit, 3
psme4	proteasome (prosome, macropain) activator subunit 4
psmg1	proteasome (prosome, macropain) assembly chaperone 1
psmg2	proteasome (prosome, macropain) assembly chaperone 2; similar to Clast3 protein
psmg3	proteasome (prosome, macropain) assembly chaperone 3
ptcd3	pentatricopeptide repeat domain 3
ptcra	pre T-cell antigen receptor alpha
ptgr2	prostaglandin reductase 2
ptms	parathymosin
ptplad1	protein tyrosine phosphatase-like A domain containing 1
ptplb	predicted gene 7908; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b
ptprb	protein tyrosine phosphatase, receptor type, B
ptprg	protein tyrosine phosphatase, receptor type, G; similar to protein tyrosine phosphatase, receptor type, G
ptrh1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)
purb	purine rich element binding protein B
pwp1	PWP1 homolog (S. cerevisiae)
pxmp4	peroxisomal membrane protein 4
pzp	pregnancy zone protein
qsm	Qa1 structure modifier
qtrt1	queuine tRNA-ribosyltransferase 1
qtrtd1	queuine tRNA-ribosyltransferase domain containing 1
rab1	RAB1, member RAS oncogene family
rab10	RAB10, member RAS oncogene family
rab11a	RAB11a, member RAS oncogene family
rab11b	RAB11B, member RAS oncogene family
rab11b-ps1	RAB11b, member RAS oncogene family, pseudogene 1
rab11fip1	RAB11 family interacting protein 1 (class I)
rab11fip2	RAB11 family interacting protein 2 (class I)
rab11fip3	RAB11 family interacting protein 3 (class II)
rab11fip4	RAB11 family interacting protein 4 (class II)
rab11fip5	RAB11 family interacting protein 5 (class I)
rab12	RAB12, member RAS oncogene family
rab13	RAB13, member RAS oncogene family
rab14	RAB14, member RAS oncogene family
rab15	RAB15, member RAS oncogene family
rab17	RAB17, member RAS oncogene family; similar to RAB17, member RAS oncogene family
rab18	RAB18, member RAS oncogene family
rab19	RAB19, member RAS oncogene family
rab1b	RAB1B, member RAS oncogene family
rab20	RAB20, member RAS oncogene family
rab21	RAB21, member RAS oncogene family
rab22a	RAB22A, member RAS oncogene family
rab24	RAB24, member RAS oncogene family
rab25	RAB25, member RAS oncogene family
rab26	RAB26, member RAS oncogene family

rab28	RAB28, member RAS oncogene family
rab2a	predicted gene 5865; RAB2A, member RAS oncogene family
rab2b	RAB2B, member RAS oncogene family
rab30	RAB30, member RAS oncogene family
rab31	RAB31, member RAS oncogene family
rab32	RAB32, member RAS oncogene family
rab33a	RAB33A, member of RAS oncogene family
rab33b	RAB33B, member of RAS oncogene family
rab34	RAB34, member of RAS oncogene family
rab35	RAB35, member RAS oncogene family
rab37	RAB37, member of RAS oncogene family
rab39b	RAB39B, member RAS oncogene family
rab3a	RAB3A, member RAS oncogene family
rab3b	RAB3B, member RAS oncogene family
rab3c	similar to RAB3C, member RAS oncogene family; RAB3C, member RAS oncogene family
rab3d	RAB3D, member RAS oncogene family
rab3gap1	RAB3 GTPase activating protein subunit 1
rab3gap2	RAB3 GTPase activating protein subunit 2
rab3il1	RAB3A interacting protein (rabin3)-like 1
rab3ip	RAB3A interacting protein
rab40c	Rab40c, member RAS oncogene family
rab43	RAB43, member RAS oncogene family
rab4a	RAB4A, member RAS oncogene family
rab5a	RAB5A, member RAS oncogene family; similar to small GTP-binding protein rab5
rab5b	RAB5B, member RAS oncogene family; predicted gene 13991; similar to RAB5B, member RAS oncogene family
rab5c	RAB5C, member RAS oncogene family
rab6	similar to Rab6 protein; predicted gene 13082; RAB6, member RAS oncogene family
rab6b	RAB6B, member RAS oncogene family
rab6ip1	DENN/MADD domain containing 5A
rab7	RAB7, member RAS oncogene family
rab7l1	RAB7, member RAS oncogene family-like 1
rab8a	RAB8A, member RAS oncogene family
rab8b	RAB8B, member RAS oncogene family
rab9	RAB9, member RAS oncogene family; predicted gene 9181
rab9b	RAB9B, member RAS oncogene family
rabac1	Rab acceptor 1 (prenylated)
rabep1	rabaptin, RAB GTPase binding effector protein 1
rabgap1	RAB GTPase activating protein 1
rabgef1	similar to Ras negative regulator Rabex-5/Rin2; RAB guanine nucleotide exchange factor (GEF) 1
rabggta	Rab geranylgeranyl transferase, a subunit
rabggtb	RAB geranylgeranyl transferase, b subunit
rabif	RAB interacting factor
rabl2a	RAB, member of RAS oncogene family-like 2A
rac2	RAS-related C3 botulinum substrate 2
rac3	RAS-related C3 botulinum substrate 3
racgap1	Rac GTPase-activating protein 1; predicted gene 1859
raet1a	retinoic acid early transcript 1E; retinoic acid early transcript beta; retinoic acid early transcript 1, alpha; retinoic acid early transcript delta; retinoic acid early transcript gamma
raet1b	retinoic acid early transcript 1E; retinoic acid early transcript beta; retinoic acid early transcript 1, alpha; retinoic acid early transcript delta; retinoic acid early transcript gamma
raet1c	retinoic acid early transcript 1E; retinoic acid early transcript beta; retinoic acid early transcript 1, alpha; retinoic acid early transcript delta; retinoic acid early transcript gamma
rai14	retinoic acid induced 14
rala	v-ral simian leukemia viral oncogene homolog A (ras related)
ralb	v-ral simian leukemia viral oncogene homolog B (ras related)

ralbp1	ralA binding protein 1
ralgds	ral guanine nucleotide dissociation stimulator
ralgps1	Ral GEF with PH domain and SH3 binding motif 1
ralgps2	Ral GEF with PH domain and SH3 binding motif 2
ralyl	RALY RNA binding protein-like
ranbp1	RAN binding protein 1
ranbp10	RAN binding protein 10
ranbp17	RAN binding protein 17
ranbp3	RAN binding protein 3
rangrf	predicted gene 7791; similar to Ran-interacting protein MOG1; predicted gene 15711; RAN guanine nucleotide release factor; predicted gene 4535; predicted gene 8572
rap1a	predicted gene 9392; similar to Raichu404X; RAS-related protein-1a
rap1b	RAS related protein 1b; similar to GTP-binding protein (smg p21B)
rap1gap	Rap1 GTPase-activating protein
rap1gds1	similar to RAP1, GTP-GDP dissociation stimulator 1; RAP1, GTP-GDP dissociation stimulator 1
rap2a	RAS related protein 2a
rap2b	RAP2B, member of RAS oncogene family
rap2c	similar to RAP2C, member of RAS oncogene family; RAP2C, member of RAS oncogene family
rapgef1	Rap guanine nucleotide exchange factor (GEF) 1
rapgef2	Rap guanine nucleotide exchange factor (GEF) 2
rapgef3	Rap guanine nucleotide exchange factor (GEF) 3
rapgef4	Rap guanine nucleotide exchange factor (GEF) 4
rapgef5	Rap guanine nucleotide exchange factor (GEF) 5
rapgef6	Rap guanine nucleotide exchange factor (GEF) 6
rapgefl1	Rap guanine nucleotide exchange factor (GEF)-like 1
rarg	retinoic acid receptor, gamma
rars	arginyl-tRNA synthetase
ras	resistance to audiogenic seizures
rasa2	RAS p21 protein activator 2
rasa3	RAS p21 protein activator 3
rasa4	RAS p21 protein activator 4
rasal1	RAS protein activator like 1 (GAP1 like)
rasal2	RAS protein activator like 2
rasd1	RAS, dexamethasone-induced 1
rasd2	RASD family, member 2
rasgef1b	RasGEF domain family, member 1B; hypothetical protein LOC100044232
rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1
rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2
rasgrp1	RAS guanyl releasing protein 1
rasgrp2	RAS, guanyl releasing protein 2
rasgrp3	RAS, guanyl releasing protein 3
rasgrp4	RAS guanyl releasing protein 4
rasl10a	RAS-like, family 10, member A
rasl10b	RAS-like, family 10, member B
rasl11a	RAS-like, family 11, member A
rasl11b	RAS-like, family 11, member B
rasl2-1	RAS-like, family 2, locus 1
rasl2-9	RAS-like, family 2, locus 9; RAN, member RAS oncogene family; similar to RAN, member RAS oncogene family
rassf5	Ras association (RalGDS/AF-6) domain family member 5
rbj	DnaJ (Hsp40) homolog, subfamily C, member 27
rbm12	RNA binding motif protein 12
rbm15b	RNA binding motif protein 15B
rbm22	RNA binding motif protein 22
rbm26	RNA binding motif protein 26

rbm27	RNA binding motif protein 27
rbms2	RNA binding motif, single stranded interacting protein 2
rbmy1a1-rs1	RNA binding motif protein, Y chromosome, family 1, member A1, related sequence 1
rc3h2	ring finger and CCCH-type zinc finger domains 2
rcbtb1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1
rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2
rcc1	regulator of chromosome condensation 1
rce1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)
rcl1	RNA terminal phosphate cyclase-like 1
rcn1	reticulocalbin 1
reg2	regenerating islet-derived 2
reg3a	regenerating islet-derived 3 alpha
reg3g	regenerating islet-derived 3 gamma
rell1	RELT-like 1
rell2	RELT-like 2
rem1	rad and gem related GTP binding protein 1
rem2	rad and gem related GTP binding protein 2
reps1	RalBP1 associated Eps domain containing protein
reps2	RALBP1 associated Eps domain containing protein 2
rerg	RAS-like, estrogen-regulated, growth-inhibitor
rexo1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)
rgl1	ral guanine nucleotide dissociation stimulator,-like 1
rgl2	ral guanine nucleotide dissociation stimulator-like 2
rgl3	ral guanine nucleotide dissociation stimulator-like 3
rgnef	Rho-guanine nucleotide exchange factor
rgs1	regulator of G-protein signaling 1
rgs10	regulator of G-protein signalling 10
rgs11	regulator of G-protein signaling 11; similar to regulator of G-protein signaling 11
rgs12	regulator of G-protein signaling 12
rgs13	regulator of G-protein signaling 13
rgs14	regulator of G-protein signaling 14
rgs16	regulator of G-protein signaling 16
rgs17	regulator of G-protein signaling 17
rgs18	regulator of G-protein signaling 18
rgs19	regulator of G-protein signaling 19; similar to Regulator of G-protein signaling 19
rgs2	regulator of G-protein signaling 2
rgs20	regulator of G-protein signaling 20
rgs22	regulator of G-protein signalling 22
rgs3	regulator of G-protein signaling 3
rgs4	regulator of G-protein signaling 4
rgs5	regulator of G-protein signaling 5
rgs6	regulator of G-protein signaling 6
rgs7	regulator of G protein signaling 7
rgs7bp	regulator of G-protein signalling 7 binding protein
rgs8	regulator of G-protein signaling 8
rgs9	regulator of G-protein signaling 9
rgs9bp	regulator of G-protein signalling 9 binding protein
rhbdl1	rhomboid, veinlet-like 1 (Drosophila)
rheb	Ras homolog enriched in brain; similar to RAS-homolog enriched in brain
rhebl1	Ras homolog enriched in brain like 1
rhob	ras homolog gene family, member B
rhobtb1	Rho-related BTB domain containing 1
rhobtb3	Rho-related BTB domain containing 3
rhoc	ras homolog gene family, member C
rhod	ras homolog gene family, member D

rhof	ras homolog gene family, member f
rhog	ras homolog gene family, member G
rhoh	ras homolog gene family, member H
rhoj	ras homolog gene family, member J
rhoq	ras homolog gene family, member Q
rhot1	ras homolog gene family, member T1
rhot2	ras homolog gene family, member T2
rhou	ras homolog gene family, member U
rhov	ras homolog gene family, member V
rhpn1	rhophilin, Rho GTPase binding protein 1
rhpn2	rhophilin, Rho GTPase binding protein 2
ribc2	RIB43A domain with coiled-coils 2
ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)
ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)
rimbp2	RIMS binding protein 2
rin1	Ras and Rab interactor 1
rin2	similar to Ras and Rab interactor 2; Ras and Rab interactor 2
rin3	Ras and Rab interactor 3
riok1	RIO kinase 1 (yeast)
riok2	RIO kinase 2 (yeast)
riok3	RIO kinase 3 (yeast)
rip	regulation of phenobarbitol-inducible P450
ripk4	receptor-interacting serine-threonine kinase 4
ripr	repression of phenobarbitol-inducible P450
rit1	Ras-like without CAAX 1
rit2	Ras-like without CAAX 2
rlbp1l1	rearranged L-myc fusion sequence
rlf	rearranged L-myc fusion sequence
rmcs2	histocompatibility 2, class II antigen A, beta 1; response to metastatic cancers 2; similar to H-2 class II histocompatibility antigen, A-D beta chain precursor
rmnd5a	similar to required for meiotic nuclear division 5 homolog A; required for meiotic nuclear division 5 homolog A (S. cerevisiae)
rn18s-rs4	18s RNA, related sequence 4
rnase10	ribonuclease, RNase A family, 10 (non-active)
rnase9	ribonuclease, RNase A family, 9 (non-active)
rnaset2b	ribonuclease T2B; ribonuclease T2A
rnd1	Rho family GTPase 1
rnd2	Rho family GTPase 2; predicted gene 4768
rnd3	Rho family GTPase 3
rnf10	ring finger protein 10
rnf112	ring finger protein 112
rnf113a2	ring finger protein 113A2
rnf114	ring finger protein 114
rnf122	ring finger protein 122
rnf141	predicted gene 10179; ring finger protein 141
rnf144a	ring finger protein 144A
rnf151	ring finger protein 151
rnf181	ring finger protein 181
rnf38	ring finger protein 38
rnpc3	RNA-binding region (RNP1, RRM) containing 3
rnu1-ps1	U1 small nuclear RNA pseudogene 1
rnu5g	RNA, U5G small nuclear
rod1	ROD1 regulator of differentiation 1 (S. pombe)
ropn1	ropporin, rhophilin associated protein 1
rorb	hypothetical protein LOC100047843; RAR-related orphan receptor beta

rorc	RAR-related orphan receptor gamma
rp23-433p19.11	serine incorporator 4
rpain	RPA interacting protein
rpl10a	predicted gene 13573; predicted gene 15451; ribosomal protein L10A; predicted gene 7695; similar to ribosomal protein L10a
rpl12	similar to ribosomal protein L12; predicted gene 7117; small nucleolar RNA, H/ACA box 65; predicted gene 11425; predicted gene 6285; predicted gene 5962; predicted gene 9396; similar to 60S ribosomal protein L12; ribosomal protein L12; predicted gene 6336
rpl14	predicted gene 9811; ribosomal protein L14
rpl17	predicted gene 8081; similar to Ribosomal protein L17; similar to Rpl17 protein; predicted gene 10164; similar to 60S ribosomal protein L17 (L23) (Amino acid starvation-induced protein) (ASI); predicted gene 3800; predicted gene 10294; predicted gene 10223; predicted gene 7299; predicted gene 10362; predicted gene 8358; predicted gene 8371; ribosomal protein L17; similar to hCG24487; predicted gene 8776
rpl23a	predicted gene 3174; predicted gene 8112; predicted gene 8158; ribosomal protein L23a; predicted gene 5384; predicted gene 8264; predicted gene 6233; similar to 60S ribosomal protein L23a; predicted gene 7413; predicted gene 5351; predicted gene 6177; similar to ribosomal protein L23a; predicted gene 7065; predicted gene 7755; predicted gene 10335; predicted gene 8137; predicted gene 3362; predicted gene 10132; predicted gene 6118
rpl26	ribosomal protein L26; predicted gene 15772; predicted gene 9197; predicted gene 13268; predicted gene 11826; predicted gene 8253; predicted gene 7606
rpl27a	predicted gene 14439; predicted gene 8213; predicted gene 13981; predicted gene 8451; predicted gene 6378; predicted gene 8667; predicted gene 4923; predicted gene 5908; ribosomal protein L27a; predicted gene 14044; predicted gene 7536; predicted gene 14407
rpl28	predicted gene 13226; predicted gene 15435; ribosomal protein L28; predicted gene 12938
rpl31	predicted gene 10191; predicted gene 7689; predicted gene 9401; similar to ribosomal protein L31; hypothetical protein LOC675768; predicted gene 13004; predicted gene 9228; predicted gene 10072; predicted gene 5437; predicted gene 9154; ribosomal protein L31; predicted gene 6670; predicted gene 8759
rpl32p	ribosomal protein L32 pseudogene
rpl32-ps	ribosomal protein L32, pseudogene
rpl35	ribosomal protein L35; predicted gene 10269; predicted gene 8444; predicted gene 2000; predicted gene 4342
rpl36al	predicted gene 8697; similar to large subunit ribosomal protein L36a; predicted gene 11970; predicted gene 10077; similar to ribosomal protein L36a; predicted gene 2718; predicted gene 10316; predicted gene 8001; predicted gene 6525; predicted gene 9409; ribosomal protein L36A; ribosomal protein L36A-like
rpl37	ribosomal protein L37
rpl37a	ribosomal protein L37a; predicted gene 4149; predicted gene 4613; predicted gene 14251; predicted gene 14173
rpl39	predicted gene 15148; ribosomal protein L39; predicted gene 12013
rpl41	ribosomal protein L41; predicted gene 3699
rpl8	ribosomal protein L8; similar to 60S ribosomal protein L8
rpl9	predicted gene 10117; similar to ribosomal protein L9; ribosomal protein L9; similar to 60S ribosomal protein L9; predicted gene 4600; predicted gene 6028; predicted gene 5451; predicted gene 14231; similar to Ribosomal protein L9; predicted gene 8662; predicted gene 10321; predicted gene 6450; predicted gene 8959
rplag	reduced platelet aggregation
rpo1-1	polymerase (RNA) I polypeptide C
rpo1-2	polymerase (RNA) I polypeptide B
rpo1-3	polymerase (RNA) I polypeptide D
rpo1-4	polymerase (RNA) I polypeptide A, 194kDa
rpp21	ribonuclease P 21 subunit (human)
rpp40	ribonuclease P 40 subunit (human)
rprl1	ribonuclease P RNA-like 1
rprl2	ribonuclease P RNA-like 3; ribonuclease P RNA component H1; ribonuclease P RNA-like 2; predicted gene 6093
rprl3	ribonuclease P RNA-like 3; ribonuclease P RNA component H1; ribonuclease P RNA-like 2; predicted gene 6093
rps10	ribosomal protein S10; predicted gene 9180
rps12	predicted gene 16422; predicted gene 6646; ribosomal protein S12; predicted gene 12334; predicted gene 5642; predicted gene 14059; predicted gene 5462; predicted gene 7698; predicted gene 7586; similar to ribosomal protein S12; predicted gene 14958; predicted gene 15887; predicted gene 10063; predicted gene 7601; predicted gene 9153; predicted gene 7671; predicted gene 9122; similar to 40S ribosomal protein S12; predicted gene 7711; predicted gene 7567; predicted gene 7643

rps13	similar to ribosomal protein S13; predicted gene 12270; predicted gene 6834; predicted gene 15483; predicted gene 6573; ribosomal protein S13; predicted gene 10159
rps15	similar to 40S ribosomal protein S15 (RIG protein); predicted gene 6921; similar to insulinoma protein (rig); predicted gene 8460; predicted gene 7121; predicted gene 5781; predicted gene 5508; predicted gene 6867; ribosomal protein S15
rps16-ps	ribosomal protein S16, pseudogene
rps21	predicted gene 5963; ribosomal protein S21
rps23	predicted gene 8624; predicted gene 9701; predicted gene 8467; predicted gene 15450; ribosomal protein S23; similar to yeast ribosomal protein S28 homologue; predicted gene 5148; similar to ribosomal protein S23; predicted gene 10054
rps25	similar to 40S ribosomal protein S25; predicted gene 6988; predicted gene 10206; ribosomal protein S25; predicted gene 6029; predicted gene 4963; predicted gene 7926; predicted gene 2225
rps28	similar to 40S ribosomal protein S28; predicted gene 10443; predicted gene 12943; predicted gene 13192; similar to ribosomal protein S28; predicted gene 10263; predicted gene 3511; ribosomal protein S28
rps29	predicted gene 7079; predicted gene 7618; predicted gene 10126; predicted gene 10059; predicted gene 5735; similar to 40S ribosomal protein S29; predicted gene 2581; predicted gene 6134; ribosomal protein S29; predicted gene 14303
rps6kc1	ribosomal protein S6 kinase polypeptide 1
rps7	similar to 40S ribosomal protein S7 (S8); predicted gene 6252; predicted gene 5055; predicted gene 4761; ribosomal protein S7; predicted gene 7351; predicted gene 6472
rps9	ribosomal protein S9; predicted gene 5905
rpsa	predicted gene 9323; predicted gene 7516; ribosomal protein SA pseudogene; predicted gene 9819; predicted gene 6339; predicted gene 9083; ribosomal protein SA; predicted gene 13374; predicted gene 12595; similar to laminin receptor 1 (ribosomal protein SA); predicted gene 13208; predicted gene 12113; predicted gene 5498; similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor); predicted gene 7549
rrad	Ras-related associated with diabetes
rraga	Ras-related GTP binding A
rragb	Ras-related GTP binding B
rragc	Ras-related GTP binding C
rragd	Ras-related GTP binding D
rras	Harvey rat sarcoma oncogene, subgroup R
rras2	related RAS viral (r-ras) oncogene homolog 2
rrm2-ps1	ribonucleotide reductase M2 pseudogene 1
rrp15	ribosomal RNA processing 15 homolog (S. cerevisiae)
rrt1	retinoic acid regulated transcript 1
rrt1os	retinoic acid regulated transcript 1 opposite strand transcription unit
rrt2	retinoic acid regulated transcript 2
rrt3	retinoic acid regulated transcript 3
rsu1	Ras suppressor protein 1
rtcd1	RNA terminal phosphate cyclase domain 1
rtkn	rhotekin
rufy1	RUN and FYVE domain containing 1
rufy2	RUN and FYVE domain-containing 2
rundc3a	RUN domain containing 3A
rusc2	RUN and SH3 domain containing 2
rwdd1	predicted gene 12693; RWD domain containing 1; predicted gene 13743
rxrb	retinoid X receptor beta
rxrg	retinoid X receptor gamma
s100a16	S100 calcium binding protein A16
s100z	S100 calcium binding protein, zeta
sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)
samd11	sterile alpha motif domain containing 11
samd9l	sterile alpha motif domain containing 9-like
sap30bp	similar to transcriptional regulator protein; SAP30 binding protein
saps1	SAPS domain family, member 1
saps3	SAPS domain family, member 3
sar1a	SAR1 gene homolog A (S. cerevisiae)
sar1b	SAR1 gene homolog B (S. cerevisiae)

sarb	SAR1b gene homolog (S. cerevisiae)
sas2	serum antigenic substance 2
sav1	similar to WW45 protein; salvador homolog 1 (Drosophila)
sbk1	SH3-binding kinase 1
sc4mol	sterol-C4-methyl oxidase-like
scamp4	secretory carrier membrane protein 4
scand1	SCAN domain-containing 1
scn1b	sodium channel, voltage-gated, type I, beta
scn2b	sodium channel, voltage-gated, type II, beta
scn3b	sodium channel, voltage-gated, type III, beta
scn4b	sodium channel, type IV, beta
scnn1d	sodium channel, nonvoltage-gated 1, delta
scoc	short coiled-coil protein
sdad1	SDA1 domain containing 1; similar to SDA1 domain containing 1
sdccag8	serologically defined colon cancer antigen 8
sdf2	stromal cell derived factor 2
sdf2l1	stromal cell-derived factor 2-like 1
sec1	secretory blood group 1
sec14l1	SEC14-like 1 (S. cerevisiae)
sec14l3	SEC14-like 3 (S. cerevisiae)
sec14l4	SEC14-like 4 (S. cerevisiae)
sec16b	SEC16 homolog B (S. cerevisiae)
sec23b	similar to SEC23B; SEC23B (S. cerevisiae)
sec24c	Sec24 related gene family, member C (S. cerevisiae)
sec31b	Sec31 homolog B (S. cerevisiae)
sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)
sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)
sec61b	Sec61 beta subunit; predicted gene 10320; predicted gene 5870; similar to protein translocation complex beta subunit
sec61g	predicted gene 11575; predicted gene 10177; predicted gene 4184; SEC61, gamma subunit; similar to Sec61-complex gamma-subunit
sec62	SEC62 homolog (S. cerevisiae)
sectm1a	secreted and transmembrane 1A
sectm1b	secreted and transmembrane 1B
sept10	septin 10
sept11	septin 11
sept12	septin 12
sept6	septin 6
sept7	septin 7
sept8	septin 8
sergef	secretion regulating guanine nucleotide exchange factor
serinc1	serine incorporator 1
serinc2	serine incorporator 2; hypothetical protein LOC100044221
serinc3	serine incorporator 3
serinc5	serine incorporator 5
serpina1a	serine (or cysteine) peptidase inhibitor, clade A, member 1A
serpina1b	serine (or cysteine) preptidase inhibitor, clade A, member 1B
serpina1c	serine (or cysteine) peptidase inhibitor, clade A, member 1C
serpina1d	serine (or cysteine) peptidase inhibitor, clade A, member 1D
serpina1f	serine (or cysteine) peptidase inhibitor, clade A, member 1F
serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K
serpina3kr	serine (or cysteine) peptidase inhibitor, clade A, member 3K regulator
serpina3m	serine (or cysteine) peptidase inhibitor, clade A, member 3M
sestd1	SEC14 and spectrin domains 1; predicted gene 9165
sf4	splicing factor 4

sfrs18	splicing factor, arginine/serine-rich 18
sfxn2	similar to Sideroflexin-2; sideroflexin 2
sfxn4	sideroflexin 4
sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)
sgcg	sarcoglycan, gamma (dystrophin-associated glycoprotein)
sgcz	sarcoglycan zeta
sgsm1	small G protein signaling modulator 1
sgsm2	small G protein signaling modulator 2
sgsm3	small G protein signaling modulator 3
sh2d3c	SH2 domain containing 3C
sh3bgrl	SH3-binding domain glutamic acid-rich protein like
sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2
sh3bp1	similar to SH3-domain binding protein 1; SH3-domain binding protein 1; similar to SH3 domain-binding protein 1 (3BP-1)
sh3yl1	Sh3 domain YSC-like 1
shoc2	soc-2 (suppressor of clear) homolog (C. elegans)
sidt1	SID1 transmembrane family, member 1
sig	sightless
sipa1	signal-induced proliferation associated gene 1
sirpb1	signal-regulatory protein beta 1
slc10a7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7
slc25a21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
slc25a41	solute carrier family 25, member 41
slc33a1	solute carrier family 33 (acetyl-CoA transporter), member 1
slc35a4	predicted gene 5866; solute carrier family 35, member A4
slc35b2	solute carrier family 35, member B2
slc39a12	solute carrier family 39 (zinc transporter), member 12
slc41a3	solute carrier family 41, member 3
slc44a3	solute carrier family 44, member 3
slfn4	schlafen 4
slfn9	similar to putative protein; schlafen 9; similar to schlafen 9
slitrk2	SLIT and NTRK-like family, member 2
slitrk4	SLIT and NTRK-like family, member 4
sltm	SAFB-like, transcription modulator
smad-ps1	MAD homolog, pseudogene 1 (Drosophila)
smap1	stromal membrane-associated protein 1
smap2	stromal membrane-associated GTPase-activating protein 2
smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A
smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)
snapc1	small nuclear RNA activating complex, polypeptide 1
snapc2	small nuclear RNA activating complex, polypeptide 2
snapc3	small nuclear RNA activating complex, polypeptide 3
snhg3	small nucleolar RNA host gene (non-protein coding) 3
snora74a	small nucleolar RNA, H/ACA box 74A
snrp1c-ps1	U1 small nuclear ribonucleoprotein 1C, pseudogene 1
snrp1c-ps2	U1 small nuclear ribonucleoprotein 1C, pseudogene 2
snrp2a	U2 small nuclear ribonucleoprotein polypeptide 2A
snrpe-ps1	small nuclear ribonucleoprotein E, pseudogene 1
snrpe-ps2	small nuclear ribonucleoprotein E, pseudogene 2
snta1	syntrophin, acidic 1
sntb1	syntrophin, basic 1
sntb2	similar to beta-2-syntrophin; syntrophin, basic 2
sntg1	syntrophin, gamma 1
sntg2	syntrophin, gamma 2
snx13	sorting nexin 13

snx21	sorting nexin family member 21
snx22	sorting nexin 22
snx26	Rho GTPase activating protein 33
solh	small optic lobes homolog (Drosophila)
sos1	son of sevenless homolog 1 (Drosophila)
sos2	son of sevenless homolog 2 (Drosophila)
spata13	spermatogenesis associated 13
spata16	spermatogenesis associated 16
spata17	spermatogenesis associated 17
spata19	spermatogenesis associated 19
spata20	spermatogenesis associated 20
spata21	spermatogenesis associated 21
spata22	spermatogenesis associated 22; olfactory receptor 20
spata3	spermatogenesis associated 3
spata4	spermatogenesis associated 4
spats2	spermatogenesis associated, serine-rich 2
specc1	sperm antigen with calponin homology and coiled-coil domains 1
spert	spermatid associated
spg21	spastic paraplegia 21 homolog (human); similar to spastic paraplegia 21 homolog
spi5l	serine protease inhibitor 5-like
spin2	spindlin family, member 2
spint4	serine protease inhibitor, Kunitz type 4
spire1	spire homolog 1 (Drosophila)
spire2	spire homolog 2 (Drosophila)
spnb1	spectrin beta 1
spnb5	spectrin beta 5
spryd4	SPRY domain containing 4
spsb4	splA/ryanodine receptor domain and SOCS box containing 4
srcrb4d	scavenger receptor cysteine rich domain containing, group B (4 domains)
srcs2	v-src suppressed transcript 2
srcs4	v-src suppressed transcript 4
srgap1	SLIT-ROBO Rho GTPase activating protein 1
srgap2	SLIT-ROBO Rho GTPase activating protein 2
srgap3	SLIT-ROBO Rho GTPase activating protein 3
srp14	signal recognition particle 14
srp54a	signal recognition particle 54b; signal recognition particle 54a; signal recognition particle 54C
srp54b	signal recognition particle 54b; signal recognition particle 54a; signal recognition particle 54C
srp68	signal recognition particle 68
srp9	signal recognition particle 9
srpr	signal recognition particle receptor ('docking protein')
srprb	signal recognition particle receptor, B subunit
srst	simple repeat sequence-containing transcript
ssbp3	single-stranded DNA binding protein 3
ssna1	Sjogren's syndrome nuclear autoantigen 1
ssr1	signal sequence receptor, alpha; similar to signal sequence receptor, alpha
ssr2	signal sequence receptor, beta
ssr3	signal sequence receptor, gamma
ssr4	signal sequence receptor, delta
st3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2
st3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
st3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
st5	suppression of tumorigenicity 5
st6gal2	beta galactoside alpha 2,6 sialyltransferase 2
st6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4

st8sia3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
stac	src homology three (SH3) and cysteine rich domain
stard10	START domain containing 10
stard13	StAR-related lipid transfer (START) domain containing 13; similar to serologically defined colon cancer antigen 13
stard7	START domain containing 7
stard8	START domain containing 8
stard9	START domain containing 9
stbd1	starch binding domain 1
stk33	serine/threonine kinase 33
stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)
suclg1	succinate-CoA ligase, GDP-forming, alpha subunit
suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit
supt4h2	suppressor of Ty 4 homolog 2 (S. cerevisiae)
sval1	seminal vesicle antigen-like 1
sval2	seminal vesicle antigen-like 2
svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
svs3a	seminal vesicle secretion 3A
svs3b	seminal vesicle secretory protein 3B
syap1	synapse associated protein 1
syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)
syngr2	synaptogyrin 2
syt13	synaptotagmin XIII
sytl5	synaptotagmin-like 5
sytr1	synaptotagmin related 1
syx1	similar sequence on Y and X 1
syx2	similar sequence on Y and X 2
tagap1	similar to T-cell activation Rho GTPase-activating protein; T-cell activation Rho GTPase-activating protein; T-cell activation GTPase activating protein 1
tbc1d10a	TBC1 domain family, member 10a
tbc1d15	TBC1 domain family, member 15
tbc1d2	TBC1 domain family, member 2
tbc1d20	TBC1 domain family, member 20
tbc1d25	TBC1 domain family, member 25
tbc1d30	TBC1 domain family, member 30
tbc1d5	TBC1 domain family, member 5
tbca	tubulin cofactor A; predicted gene 4374; predicted gene 6142; similar to cofactor A
tbcc	tubulin-specific chaperone C
tbcd	tubulin-specific chaperone d
tceal8	transcription elongation factor A (SII)-like 8; similar to transcription elongation factor A (SII)-like 8
tceb1l-rs2	transcription elongation factor B (SIII), polypeptide 1-like, related sequence 2
tceb2l	transcription elongation factor B (SIII), polypeptide 2 (elongin B),-like
tcf25	transcription factor 25 (basic helix-loop-helix)
tcfap2b	transcription factor AP-2 beta
tcfap2d	transcription factor AP-2, delta
tcfap2e	transcription factor AP-2, epsilon
tcra-c	T-cell receptor alpha, constant region
tcra-v	T-cell receptor alpha, variable region
tcra-v1	T-cell receptor alpha, variable 1
tcra-v11.1	T-cell receptor alpha, variable 11.1
tcra-v11.2	T-cell receptor alpha, variable 11.2
tcra-v11.3	T-cell receptor alpha, variable 11.3
tcra-v11.8	T-cell receptor alpha, variable 11.8
tcra-v13	T-cell receptor alpha, variable 13
tcra-v13.1	T-cell receptor alpha variable region family 13 subfamily 1

tcra-v13.2	T-cell receptor alpha variable region family 13 subfamily 2
tcra-v13.3	T-cell receptor alpha variable region family 13 subfamily 3
tcra-v13.4	T-cell receptor alpha variable region family 13 subfamily 4
tcra-v13.5	T-cell receptor alpha variable region family 13 subfamily 5
tcra-v14	T-cell receptor alpha, variable 14
tcra-v15	T-cell receptor alpha, variable 15
tcra-v16.1	T-cell receptor, alpha, variable 16.1
tcra-v19.1	T-cell receptor alpha, variable 19.1
tcra-v2	T-cell receptor alpha, variable 2
tcra-v2.4	T-cell receptor alpha, variable 2.4
tcra-v2.5	T-cell receptor alpha, variable 2.5
tcra-v2.6	T-cell receptor alpha, variable 2.6
tcra-v22.1	similar to TRAV10; T-cell receptor alpha, variable 22.4; T-cell receptor alpha, variable 22.1
tcra-v22.2	T-cell receptor alpha, variable 22.2
tcra-v22.3	T-cell receptor alpha, variable 22.3
tcra-v22.4	similar to TRAV10; T-cell receptor alpha, variable 22.4; T-cell receptor alpha, variable 22.1
tcra-v23.1	T-cell receptor alpha, variable 23.1
tcra-v3	T-cell receptor alpha, variable 3
tcra-v3.1	T-cell receptor alpha, variable 3.1
tcra-v4	T-cell receptor alpha, variable 4
tcra-v5	T-cell receptor alpha, variable 5
tcra-v6	T-cell receptor alpha, variable 6
tcra-v7	T-cell receptor alpha, variable 7
tcra-v9	T-cell receptor alpha, variable 9
tcra-va10	T-cell receptor alpha, variable A10
tcrb-c	T-cell receptor beta, constant region
tcrb-d	T-cell receptor beta, D region
tcrbe	T-cell receptor beta chain enhancer
tcrb-j	T-cell receptor beta, joining region
tcrb-v	T-cell receptor beta, variable region
tcrb-v1	T-cell receptor beta, variable 1
tcrb-v10	T-cell receptor beta, variable 10
tcrb-v11	T-cell receptor beta, variable 11
tcrb-v12	T-cell receptor beta, variable 12
tcrb-v13	T-cell receptor beta, variable 13
tcrb-v14	T-cell receptor beta, variable 14
tcrb-v15	T-cell receptor beta, variable 15
tcrb-v16	T-cell receptor beta, variable 16
tcrb-v17	T-cell receptor beta, variable 17
tcrb-v19	T-cell receptor beta, variable 19
tcrb-v2	T-cell receptor beta, variable 2
tcrb-v20	protease, serine, 3; predicted gene 10334; T-cell receptor beta, variable V20; similar to trypsinogen 15
tcrb-v3	T-cell receptor beta, variable 3
tcrb-v3.1	T-cell receptor beta, variable 3.1
tcrb-v3.2	T-cell receptor beta, variable 3.2
tcrb-v4	T-cell receptor beta, variable 4
tcrb-v5	T-cell receptor beta, variable 5
tcrb-v5.1	T-cell receptor beta, variable 5.1
tcrb-v5.2	T-cell receptor beta, variable 5.2
tcrb-v6	T-cell receptor beta, variable 6
tcrb-v7	T-cell receptor beta, variable 7
tcrb-v8	T-cell receptor beta, variable 8
tcrb-v8.2	T-cell receptor beta, variable 8.2
tcrb-v8.3	T-cell receptor beta, variable 8.3
tcrb-v9	T-cell receptor beta, variable 9

tcrd-c	T-cell receptor delta, constant region
tcrd-d	T-cell receptor delta, D region
tcrd-j	T-cell receptor delta, joining region
tcrd-v	T-cell receptor delta, variable region
tcrd-v1	T-cell receptor delta, variable 1
tcrd-v2	T-cell receptor delta, variable 2
tcrd-v3	T-cell receptor delta, variable 3
tcrd-v4	T-cell receptor delta, variable 4
tcrd-v5	T-cell receptor delta, variable 5
tcrd-v5t	T-cell receptor delta, variable 5T
tcrd-v6	T-cell receptor delta, variable 6
tcrd-v7	T-cell receptor delta, variable 7
tcrg	T-cell receptor gamma, variable 2; T-cell receptor gamma chain
tcrg-c	T-cell receptor gamma, constant region
tcrg-c1	T-cell receptor gamma, constant 1
tcrg-c2	T-cell receptor gamma, constant 2
tcrg-c4	T-cell receptor gamma, constant 4
tcrg-j	T-cell receptor gamma, joining region
tcrg-v	T-cell receptor gamma, variable region
tcrg-v1	T-cell receptor gamma, variable 1
tcrg-v2	T-cell receptor gamma, variable 2; T-cell receptor gamma chain
tcrg-v3	T-cell receptor gamma, variable 3
tcrg-v4	T-cell receptor gamma, variable 4
tcrg-v5	T-cell receptor gamma, variable 5
tcrg-v6	T-cell receptor gamma, variable 6
tdpoz1	TD and POZ domain containing 1; similar to TD and POZ domain-containing protein 1 (MAPP family protein 2); predicted gene 9117; predicted gene 9125
tdpoz2	TD and POZ domain containing 2; predicted gene 5773
tdpoz3	TD and POZ domain containing 3; predicted gene 4982
tdpoz4	predicted gene 5541; TD and POZ domain containing 4
tdpoz5	predicted gene 10697; predicted gene 5543; similar to Tdpoz5 protein; similar to TD and POZ domain containing 5; predicted gene 9107; TD and POZ domain containing 5
tekt1	tektin 1
tes3-ps	testis derived transcript 3, pseudogene
tex2	testis expressed gene 2
tex21	testis expressed gene 21
tex24	testis expressed gene 24; predicted gene 6853
tg(il1a)1.1tsk	Transgene insertion 1.1, Thomas Kupper
tg(itga5)0844fmw	transgene insertion 0858, Fiona M Watt
tg(itgb1)0840fmw	transgene insertion 0840, Fiona M Watt
tg(tgfb1)1der	transgene insertion 1, Dennis R Roop
tgfb1i2	transforming growth factor beta 1 induced transcript 2
tgfb1i3	transforming growth factor beta 1 induced transcript 3
tgtp	T-cell specific GTPase 1
thrap3	thyroid hormone receptor associated protein 3; predicted gene 5898
thumpd2	THUMP domain containing 2
tiam1	T-cell lymphoma invasion and metastasis 1
tiam2	T-cell lymphoma invasion and metastasis 2
timm44	translocase of inner mitochondrial membrane 44
tk	tail-kinks
tlk2	predicted gene 13161; tousled-like kinase 2 (Arabidopsis)
tlm	T lymphoma oncogene
tln2	talin 2
tm	tremulous
tm4sf5	transmembrane 4 superfamily member 5

tm6sf1	transmembrane 6 superfamily member 1
tm6sf2	transmembrane 6 superfamily member 2
tm9sf1	transmembrane 9 superfamily member 1
tm9sf2	transmembrane 9 superfamily member 2
tm9sf3	transmembrane 9 superfamily member 3
tmed2	transmembrane emp24 domain trafficking protein 2; predicted gene 10698; predicted gene 7318
tmed9	transmembrane emp24 protein transport domain containing 9
tmem11	transmembrane protein 11
tmem115	transmembrane protein 115
tmem135	transmembrane protein 135
tmem150	transmembrane protein 150
tmem159	transmembrane protein 159
tmem16d	anoctamin 4
tmem16e	transmembrane protein 16E
tmem16f	anoctamin 6
tmem22	transmembrane protein 22
tmem30a	transmembrane protein 30A
tmem30b	transmembrane protein 30B
tmem30c	transmembrane protein 30C
tmem33	transmembrane protein 33
tmem37	transmembrane protein 37
tmem57	transmembrane protein 57
tmem59l	transmembrane protein 59-like
tmem8	transmembrane protein 8 (five membrane-spanning domains)
tmem85	transmembrane protein 85
tmem90a	transmembrane protein 90a
tmevd5	Theiler's murine encephalomyelitis virus induced demyelinating disease susceptibility 5
tmevp1	heiler's murine encephalomyelitis virus persistence 1
tnik	TRAF2 and NCK interacting kinase
tnk1	tyrosine kinase, non-receptor, 1
tnk2	tyrosine kinase, non-receptor, 2
tnrc6c	trinucleotide repeat containing 6C
tob2	transducer of ERBB2, 2
tomm7	similar to translocase of outer mitochondrial membrane 7 homolog; translocase of outer mitochondrial membrane 7 homolog (yeast)
top1-rs1	topoisomerase (DNA) I, related sequence 1
top2b	topoisomerase (DNA) II beta
tor3a	torsin family 3, member A
tox2	TOX high mobility group box family member 2
tox4	TOX high mobility group box family member 4; predicted gene 5828
tpd52-ps	tumor protein D52, pseudogene
tpi-rs4	triosephosphate isomerase related sequence 4
tpml	tropomyosin-like
tpt1p	predicted gene 1974; tumor protein, translationally-controlled 1 pseudogene; tumor protein, translationally-controlled 1; predicted gene 14456
tpt1-ps1	tumor protein, translationally-controlled, pseudogene 1
tram1	translocating chain-associating membrane protein 1
trappc1	trafficking protein particle complex 1
trappc3	trafficking protein particle complex 3
trappc5	trafficking protein particle complex 5
trappc6b	trafficking protein particle complex 6B
trappc9	trafficking protein particle complex 9
trav12n-1	predicted gene, EG667677; T cell receptor alpha variable 12d-1; predicted gene 11046; T-cell receptor alpha, variable 8; predicted gene, ENSMUSG00000076785; similar to T cell receptor V alpha 8.5; similar to OTTMUSG00000015204 protein; T cell receptor alpha variable 12N-1; predicted gene, ENSMUSG00000076783; T cell receptor alpha variable 12N-2; similar to T-cell receptor alpha chain V

	region CTL-F3 precursor; predicted gene 8758
trav16d/dv11	T cell receptor alpha variable 16D-DV11
trav7d-3	T cell receptor alpha chain V region 7D-3; similar to T cell receptor alpha
trbd1	T cell receptor beta diversity 1
trbd2	T cell receptor beta diversity 2
trcg1	taste receptor protein 1
trdd1	T cell receptor delta diversity 1
trdd2	T cell receptor delta diversity 2
trdj2	T cell receptor delta joining 2
trgj4	T cell receptor gamma joining 4
trim14	tripartite motif-containing 14
trim17	tripartite motif-containing 17
trim23	tripartite motif-containing 23
trim36	tripartite motif-containing 36
trim45	tripartite motif-containing 45
trim46	tripartite motif-containing 46
trim47	tripartite motif-containing 47
trim59	similar to mouse RING finger 1; tripartite motif-containing 59
trim67	tripartite motif-containing 67
trim69	tripartite motif-containing 69
trim7	tripartite motif-containing 7
triml1	tripartite motif family-like 1
trio	triple functional domain (PTPRF interacting)
triobp	TRIO and F-actin binding protein
trmt1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)
trp53i13	transformation related protein 53 inducible protein 13
trpd52l3	tumor protein D52-like 3
trpt1	tRNA phosphotransferase 1
trub1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)
trub2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)
try5	trypsin 5
tse2	tissue specific extinction 2, of L-ADH
tsfm	Ts translation elongation factor, mitochondrial
tsga8	testis specific gene A8
tsnaxip1	translin-associated factor X (Tsnax) interacting protein 1
tspan4	tetraspanin 4
tspyl-ps	testis-specific protein, Y-encoded-like, pseudogene
tsri	T-cell subset ratio influence
tssk3	testis-specific serine kinase 3
ttc1	tetratricopeptide repeat domain 1
ttc3	tetratricopeptide repeat domain 3
ttc35	tetratricopeptide repeat domain 35; predicted gene 5333
ttc4	tetratricopeptide repeat domain 4
ttll1	tubulin tyrosine ligase-like 1
ttll3	tubulin tyrosine ligase-like family, member 3
ttll4	tubulin tyrosine ligase-like family, member 4
tuba1b	predicted gene 3756; tubulin, alpha 1B; predicted gene 5620; similar to alpha-tubulin isotype M-alpha-2; predicted gene 14150; predicted gene 3226
tuba-rs1	tubulin alpha, related sequence 1
tubb2b	tubulin, beta 2a, pseudogene 2; tubulin, beta 2B
tubb2c	tubulin, beta 2c, psuedogene 1; tubulin, beta 2C; tubulin, beta 2c, pseudogene 2
tulp3	tubby-like protein 3
tulp4	similar to mKIAA1397 protein; tubby like protein 4
twf1	twinfilin, actin-binding protein, homolog 1 (Drosophila); predicted gene 4887
twf2	twinfilin, actin-binding protein, homolog 2 (Drosophila)

txndc1	thioredoxin-related transmembrane protein 1
txndc14	thioredoxin domain containing 14
txndc9	predicted gene 8774; predicted gene 7868; thioredoxin domain containing 9
txnl1	thioredoxin-like 1
ube1y1-ps2	ubiquitin-activating enzyme E1, Chr Y-1, pseudogene 2
ube2w	ubiquitin-conjugating enzyme E2W (putative)
ubl3	ubiquitin-like 3
ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)
ubqln3	ubiquilin 3
ubtd2	ubiquitin domain containing 2
ubxd5	UBX domain containing 5
ubxd6	UBX domain protein 8
uchl4	ubiquitin carboxyl-terminal esterase L4
uck1	uridine-cytidine kinase 1; predicted gene 4482
umpk-ps	uridine monophosphate kinase, pseudogene
unc50	unc-50 homolog (C. elegans)
uqcrb	predicted gene 2962; ubiquinol-cytochrome c reductase binding protein
usmg5	upregulated during skeletal muscle growth 5
uso1	USO1 homolog, vesicle docking protein (yeast)
usp12	ubiquitin specific peptidase 12; predicted gene 8902
usp38	ubiquitin specific peptidase 38
usp6nl	USP6 N-terminal like
v1rh13	vomeronasal 1 receptor 219
vars	valyl-tRNA synthetase
vav1	vav 1 oncogene
vav2	vav 2 oncogene
vav3	vav 3 oncogene
vgll1	vestigial like 1 homolog (Drosophila)
vh7183.a28.48	Ig heavy chain V region VH7183.a28.48
vhll	von Hippel-Lindau tumor suppressor-like, pseudogene 1
vit	vitrin
vps13c	vacuolar protein sorting 13C (yeast)
vps13d	vacuolar protein sorting 13 D (yeast)
vps26b	vacuolar protein sorting 26 homolog B (yeast)
vrk3	vaccinia related kinase 3
wd	waddler
wdfy3	WD repeat and FYVE domain containing 3
wdr12	WD repeat domain 12; predicted gene 4879
wdr13	WD repeat domain 13
wdr16	WD repeat domain 16
wdr25	WD repeat domain 25
wdr3	WD repeat domain 3
wdr31	WD repeat domain 31
wdr33	WD repeat domain 33
wdr4	WD repeat domain 4
wdr44	WD repeat domain 44
wdr45	WD repeat domain 45
wdr6	WD repeat domain 6
wdr61	WD repeat domain 61
wdr7	WD repeat domain 7
wdr8	WD repeat domain 8
wfdc15b	WAP four-disulfide core domain 15B
wfdc3	WAP four-disulfide core domain 3
x76971	T cell receptor alpha variable 14N-3; cDNA sequence X76971; predicted gene, OTTMUSG00000015124
xcr1	chemokine (C motif) receptor 1

xkrx	X Kell blood group precursor related X linked
xm_359419	zygote arrest 1-like
xmv12	xenotropic murine leukemia virus 12
xmv24	xenotropic murine leukemia virus 24
xmv26	xenotropic murine leukemia virus 26
xmv28	xenotropic murine leukemia virus 28
xmv33	xenotropic murine leukemia virus 33
xmv45	xenotropic murine leukemia virus 45
xmv65	xenotropic murine leukemia virus 65
xmv66	xenotropic murine leukemia virus 66
xrra1	X-ray radiation resistance associated 1
yif1a	Yip1 interacting factor homolog A (S. cerevisiae)
yipf1	Yip1 domain family, member 1
yipf5	Yip1 domain family, member 5; predicted gene 5738
yme1l1	YME1-like 1 (S. cerevisiae)
ypel1	yippee-like 1 (Drosophila)
ypel3	yippee-like 3 (Drosophila)
ypel4	yippee-like 4 (Drosophila)
ypel5	yippee-like 5 (Drosophila)
zbed4	predicted gene 8007; hypothetical protein LOC100045355; predicted gene 3711; zinc finger, BED domain containing 4; predicted gene 15583
zbtb12	zinc finger and BTB domain containing 12
zbtb25	zinc finger and BTB domain containing 25
zbtb34	zinc finger and BTB domain containing 34
zbtb43	zinc finger and BTB domain containing 43
zbtb6	RIKEN cDNA A930039A15 gene; zinc finger and BTB domain containing 6
zc3h14	zinc finger CCCH type containing 14
zc3h7a	zinc finger CCCH type containing 7 A
zcchc17	zinc finger, CCHC domain containing 17
zcchc4	zinc finger, CCHC domain containing 4
zcrb1	predicted gene 9202; zinc finger CCHC-type and RNA binding motif 1
zdhhc1	zinc finger, DHHC domain containing 1
zdhhc16	zinc finger, DHHC domain containing 16
zdhhc21	zinc finger, DHHC domain containing 21
zdhhc3	zinc finger, DHHC domain containing 3
zdhhc7	zinc finger, DHHC domain containing 7
zer1	zer-1 homolog (C. elegans)
zfand2a	zinc finger, AN1-type domain 2A
zfand3	zinc finger, AN1-type domain 3; similar to Zfand3 protein
zfand6	zinc finger, AN1-type domain 6
zfml	zinc finger, matrin-like
zfp1	zinc finger protein 1
zfp105	zinc finger protein 105
zfp111	zinc finger protein 111
zfp113	zinc finger protein 113
zfp119	zinc finger protein 119
zfp12	zinc finger protein 12
zfp120	zinc finger protein 120
zfp125	zinc finger protein 125
zfp161-rs1	zinc finger protein 161, related sequence 1
zfp207	zinc finger protein 207
zfp212	Zinc finger protein 212
zfp239	zinc finger protein 239
zfp263	zinc finger protein 263
zfp27	zinc finger protein 27

zfp28	zinc finger protein 28; predicted gene 3203
zfp30	zinc finger protein 30
zfp300	zinc finger protein 300
zfp317	zinc finger protein 317
zfp319	zinc finger protein 319
zfp322a	zinc finger protein 322A
zfp326	zinc finger protein 326
zfp330	zinc finger protein 330
zfp354b	zinc finger protein 354B
zfp367	zinc finger protein 367
zfp37	zinc finger protein 37
zfp382	zinc finger protein 382
zfp383	zinc finger protein 383
zfp386	zinc finger protein 386 (Kruppel-like)
zfp414	zinc finger protein 414
zfp418	zinc finger protein 418
zfp438	zinc finger protein 438
zfp445	zinc finger protein 445
zfp446	zinc finger protein 446
zfp449	zinc finger protein 449
zfp457	zinc finger protein 457
zfp458	zinc finger protein 458
zfp472	zinc finger protein 472
zfp51	hypothetical protein LOC100044272; zinc finger protein 51
zfp54	hypothetical protein LOC100044271; zinc finger protein 54
zfp58	zinc finger protein 58
zfp59	zinc finger protein 59; predicted gene 7452
zfp60	similar to Zinc finger protein 60; zinc finger protein 60
zfp606	zinc finger protein 606
zfp61	zinc finger protein 61
zfp612	zinc finger protein 612
zfp622	zinc finger protein 622
zfp637	zinc finger protein 637
zfp641	zinc finger protein 641
zfp655	zinc finger protein 655
zfp661	zinc finger protein 661
zfp689	zinc finger protein 689
zfp7	zinc finger protein 7
zfp74	zinc finger protein 74; hypothetical protein LOC100044255
zfp825	zinc finger protein 825
zfp87	zinc finger protein 87
zfp93	zinc finger protein 93; predicted gene 11677
zfp94	zinc finger protein 94
zfp97	zinc finger protein 97; cDNA sequence BC018101
zfpl1	zinc finger like protein 1
zfyve1	zinc finger, FYVE domain containing 1
zfyve20	zinc finger, FYVE domain containing 20
zfyve27	zinc finger, FYVE domain containing 27
zkscan14	zinc finger with KRAB and SCAN domains 14
zkscan5	zinc finger with KRAB and SCAN domains 5
zkscan6	zinc finger with KRAB and SCAN domains 6
zmym5	zinc finger, MYM-type 5
znrf4	zinc and ring finger 4
zscan12	zinc finger and SCAN domain containing 12
zscan2	zinc finger and SCAN domain containing 2

zscan22	zinc finger and SCAN domain containing 22

Table S18. G protein signaling theoretical dataset. The G protein signaling dataset represents the intersection between the cellular signaling and G protein theoretical datasets.

Gene Symbol	**Gene Definition**
LOC139796	LOC139796
0610007p14rik	RIKEN cDNA 0610007P14 gene
0610031j06rik	RIKEN cDNA 0610031J06 gene
1600002k03rik	RIKEN cDNA 1600002K03 gene
1700009n14rik	RIKEN cDNA 1700009N14 gene
1700057k13rik	RIKEN cDNA 1700057K13 gene
1810014f10rik	RIKEN cDNA 1810014F10 gene
2310001a20rik	RIKEN cDNA 2310001A20 gene
2410018m08rik	RIKEN cDNA 2410018M08 gene
2500003m10rik	RIKEN cDNA 2500003M10 gene
2700078k21rik	RIKEN cDNA 2700078K21 gene
4833424o15rik	RIKEN cDNA 4833424O15 gene
4930420k17rik	RIKEN cDNA 4930420K17 gene
4930455c21rik	RIKEN cDNA 4930455C21 gene
4933424b01rik	RIKEN cDNA 4933424B01 gene
4933436h12rik	RIKEN cDNA 4933436H12 gene
6430548m08rik	RIKEN cDNA 6430548M08 gene
9430023l20rik	RIKEN cDNA 9430023L20 gene
A130040m12rik	RIKEN cDNA A130040M12 gene
Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6
Actr8	ARP8 actin-related protein 8 homolog (S. cerevisiae)
Adcy2	adenylate cyclase 2
Adcy4	adenylate cyclase 4
Adcy5	adenylate cyclase 5; similar to adenylate cyclase 5
Adnp2	ADNP homeobox 2
Aig1	androgen-induced 1
Ak3l1	predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1
Ak5	adenylate kinase 5
Akap13	A kinase (PRKA) anchor protein 13
Akr1e1	aldo-keto reductase family 1, member E1
Als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 homolog (human)
Ankrd7	ankyrin repeat domain 7
Ard1b	N(alpha)-acetyltransferase 11, NatA catalytic subunit
Arhgap1	Rho GTPase activating protein 1; predicted gene 8514
Arhgap10	Rho GTPase activating protein 10
Arhgap21	Rho GTPase activating protein 21
Arhgap22	Rho GTPase activating protein 22
Arhgap26	RIKEN cDNA 9630014M24 gene; Rho GTPase activating protein 26; predicted gene 5820
Arhgap29	Rho GTPase activating protein 29
Arhgap36	Rho GTPase activating protein 36
Arhgap4	Rho GTPase activating protein 4

Arhgap5	Rho GTPase activating protein 5
Arhgap8	Rho GTPase activating protein 8
Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1
Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11
Arhgef12	predicted gene 7281; predicted gene 5831; similar to SP140 nuclear body protein (predicted); Rho guanine nucleotide exchange factor (GEF) 12
Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15
Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17
Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2
Arhgef4	Rho guanine nucleotide exchange factor (GEF) 4
Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
Arid3c	AT rich interactive domain 3C (BRIGHT-like)
Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1
Arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4; similar to SRp25 nuclear protein
Arl8b	ADP-ribosylation factor-like 8B
Ars2	serrate RNA effector molecule homolog (Arabidopsis)
Arsj	arylsulfatase J
Arsk	similar to arylsulfatase K; arylsulfatase K
Astl	similar to Astacin-like metalloendopeptidase precursor (Oocyte astacin) (Ovastacin); astacin-like metalloendopeptidase (M12 family)
Asxl3	additional sex combs like 3 (Drosophila)
Atad3a	ATPase family, AAA domain containing 3A
Atp13a3	ATPase type 13A3
Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1; predicted gene 12231
Atp5k	predicted gene 2972; ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1
Aup1	ancient ubiquitous protein 1
Aw125753	Fam84a family with sequence similarity 84, member A
Axud1	cysteine-serine-rich nuclear protein 1
B020018g12rik	RNA binding motif protein 8a; RIKEN cDNA B020018G12 gene
B230208h17rik	RIKEN cDNA B230208H17 gene
Bc010304	Fam120a family with sequence similarity 120, member A
Bc017158	cDNA sequence BC017158
Bc021395	Bc021395
Bc028663	Bc028663
Bc029169	Bc029169
Bcar3	breast cancer anti-estrogen resistance 3
Bcas2	breast carcinoma amplified sequence 2
Bin3	bridging integrator 3
Bnip2	BCL2/adenovirus E1B interacting protein 2
Bnipl	BCL2/adenovirus E1B 19kD interacting protein like
Brd1	bromodomain containing 1; similar to bromodomain containing 1
Bri3bp	Bri3 binding protein
Bspry	B-box and SPRY domain containing
Cab39	calcium binding protein 39
Camk1g	calcium/calmodulin-dependent protein kinase I gamma
Card6	caspase recruitment domain family, member 6
Ccdc88a	coiled coil domain containing 88A
Ccdc88b	coiled-coil domain containing 88B

Ccpg1	cell cycle progression 1
Ccpn-ps	calcyphosine, pseudogene
Cd247	CD247 antigen
Cd3g	CD3 antigen, gamma polypeptide
Cdc42bpb	CDC42 binding protein kinase beta
Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2
Cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5
Cdc42se1	CDC42 small effector 1
Cdgap	Rho GTPase activating protein 31
Cenpw	centromere protein W
Centa1	ArfGAP with dual PH domains 1
Centd2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
Centd3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3
Centg1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2
Centg2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1
Centg3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3
Cep57	centrosomal protein 57
Chn1	chimerin (chimaerin) 1
Chn2	chimerin (chimaerin) 2
Chpst	chrondroprogenitor specific transcript
Cirbp-rs1	cold inducible RNA binding protein, related sequence 1
Cirbp-rs3	cold inducible RNA binding protein, related sequence 3
Clec4b1	C-type lectin domain family 4, member b1
Clybl	citrate lyase beta like
Cml1	N-acetyltransferase 8B; camello-like 1
Cml2	camello-like 2
Cml3	predicted gene 4477; camello-like 3
Cml5	camello-like 5
Cnbpl2	cellular nucleic acid binding protein-like 2
Cnih	cornichon homolog (Drosophila)
Cnksr1	connector enhancer of kinase suppressor of Ras 1
Cnnm1	cyclin M1
Cnnm2	cyclin M2
Cnnm3	cyclin M3
Cnot1	predicted gene 6158; CCR4-NOT transcription complex, subunit 1
Cnot8	CCR4-NOT transcription complex, subunit 8
Cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)
Coq4	coenzyme Q4 homolog (yeast)
Coro2a	coronin, actin binding protein 2A
Cpne3	copine III
Creg2	cellular repressor of E1A-stimulated genes 2
Cryzl1	crystallin, zeta (quinone reductase)-like 1
Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)
Csmd2	CUB and Sushi multiple domains 2
Csnk1g1	casein kinase 1, gamma 1
Csnk1g2	casein kinase 1, gamma 2
Csnk1g3	casein kinase 1, gamma 3; similar to casein kinase 1, gamma 3

Csrnp2	cysteine-serine-rich nuclear protein 2
Csrnp3	cysteine-serine-rich nuclear protein 3
Ctf2	cardiotrophin 2
Ctps2	cytidine 5'-triphosphate synthase 2
Cutc	cutC copper transporter homolog (E.coli)
D10ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed
D11mit109	DNA segment, Chr 11, Massachusetts Institute of Technology 109
D11mit205	DNA segment, Chr 11, Massachusetts Institute of Technology 205
D13mit91	DNA segment, Chr 13, Massachusetts Institute of Technology 91
D14mit116	DNA segment, Chr 14, Massachusetts Institute of Technology 116
D14mit173	DNA segment, Chr 14, Massachusetts Institute of Technology 173
D14mit56	DNA segment, Chr 14, Massachusetts Institute of Technology 56
D15mit198	DNA segment, Chr 15, Massachusetts Institute of Technology 198
D17mit7	DNA segment, Chr 17, Massachusetts Institute of Technology 7
D19mit24	DNA segment, Chr 19, Massachusetts Institute of Technology 24
D19mit66	DNA segment, Chr 19, Massachusetts Institute of Technology 66
D19mit75	DNA segment, Chr 19, Massachusetts Institute of Technology 75
D330017j20rik	Fam40b family with sequence similarity 40, member B
D5mit317	DNA segment, Chr 5, Massachusetts Institute of Technology 317
D6mit252	DNA segment, Chr 6, Massachusetts Institute of Technology 252
D8ertd82e	DNA segment, Chr 8, ERATO Doi 82, expressed
D930005d10rik	Radil Ras association and DIL domains
D9mit60	DNA segment, Chr 9, Massachusetts Institute of Technology 60
D9mit61	DNA segment, Chr 9, Massachusetts Institute of Technology 61
Dak	dihydroxyacetone kinase 2 homolog (yeast)
Dchs2	dachsous 2 (Drosophila)
Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41
Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
Ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
Def6	differentially expressed in FDCP 6
Def8	differentially expressed in FDCP 8
Defb29	defensin beta 29
Dennd4c	DENN/MADD domain containing 4C
Depdc2	DEP domain containing 2
Dgkb	diacylglycerol kinase, beta
Dgkd	diacylglycerol kinase, delta
Dgkg	diacylglycerol kinase, gamma
Dgkq	diacylglycerol kinase, theta
Dhdds	dehydrodolichyl diphosphate synthase
Dhx35	predicted gene 4713; DEAH (Asp-Glu-Ala-His) box polypeptide 35
Diras1	DIRAS family, GTP-binding RAS-like 1
Diras2	DIRAS family, GTP-binding RAS-like 2
Dock1	dedicator of cytokinesis 1
Dock10	dedicator of cytokinesis 10
Dock2	dedicator of cyto-kinesis 2
Dock4	dedicator of cytokinesis 4
Dock9	dedicator of cytokinesis 9

Dolpp1	dolichyl pyrophosphate phosphatase 1
Dpf2	D4, zinc and double PHD fingers family 2
Dph2	DPH2 homolog (S. cerevisiae)
Dph3	DPH3 homolog (KTI11, S. cerevisiae)
Dqx1	DEAQ RNA-dependent ATPase
Dtd1	similar to D-tyrosyl-tRNA deacylase 1; D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)
Dub2	ubiquitin specific peptidase 17-like 5
Dub3	predicted gene 6596
Dub4	deubiquitinating enzyme 4
Dullard	similar to Dullard homolog (Xenopus laevis); Dullard homolog (Xenopus laevis)
E130112l23rik	RIKEN cDNA E130112L23 gene
Efhd1	EF hand domain containing 1
Egfl8	EGF-like domain 8
Eif3i	eukaryotic translation initiation factor 3, subunit I
Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)
Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)
Emilin3	elastin microfibril interfacer 3
Eml3	echinoderm microtubule associated protein like 3
Ensmusg00000053178	Gm9897 predicted gene 9897
Ensmusg00000067748	Rpl17-ps5 ribosomal protein L17, pseudogene 5
Epb4.1l4a	erythrocyte protein band 4.1-like 4a
Epb4.1l4b	erythrocyte protein band 4.1-like 4b
Eps8	epidermal growth factor receptor pathway substrate 8
Eps8l1	EPS8-like 1
Eps8l2	EPS8-like 2
Eps8l3	EPS8-like 3
Eral1	Era (G-protein)-like 1 (E. coli)
Erdr1	erythroid differentiation regulator 1
Etaa1	Ewing's tumor-associated antigen 1
Etv2	similar to ETS related protein 71; ets variant gene 2
Exoc2	exocyst complex component 2
Exosc8	exosome component 8
F830045p16rik	RIKEN cDNA F830045P16 gene
Fam177a	Fam177a family with sequence similarity 177, member A
Fam40a	family with sequence similarity 40, member A
Fam57a	Fam57a family with sequence similarity 57, member A
Fam92a	family with sequence similarity 92, member A
Farp2	FERM, RhoGEF and pleckstrin domain protein 2
Fbxo10	F-box protein 10
Ficd	FIC domain containing
Fitm1	fat storage-inducing transmembrane protein 1
Fndc1	fibronectin type III domain containing 1; similar to fibronectin type III domain containing 1
Fndc4	fibronectin type III domain containing 4
Fndc5	fibronectin type III domain containing 5
Fpgt	fucose-1-phosphate guanylyltransferase
Frag1	post-GPI attachment to proteins 2
Frmd4b	FERM domain containing 4B
Ftsj2	FtsJ homolog 2 (E. coli)

Fuk	fucokinase
Gas2l1	growth arrest-specific 2 like 1
Gas2l2	growth arrest-specific 2 like 2
Gas4	growth arrest specific 4
Gde1	glycerophosphodiester phosphodiesterase 1
Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1
Gdpd4	glycerophosphodiester phosphodiesterase domain containing 4
Gem	GTP binding protein (gene overexpressed in skeletal muscle)
Get4	golgi to ER traffic protein 4 homolog (S. cerevisiae)
Gfm1	G elongation factor, mitochondrial 1
Ggps1	geranylgeranyl diphosphate synthase 1; similar to Ggps1 protein; predicted gene 5630
Ggt7	gamma-glutamyltransferase 7
Gimap1	GTPase, IMAP family member 1
Gimap6	GTPase, IMAP family member 6
Gimap7	GTPase, IMAP family member 7
Gimap8	GTPase, IMAP family member 8
Gimap9	GTPase, IMAP family member 9
Gipc2	GIPC PDZ domain containing family, member 2
Gipc3	GIPC PDZ domain containing family, member 3
Glipr2	GLI pathogenesis-related 2
Glod4	glyoxalase domain containing 4
Gm11818	Gm11818 predicted gene 11818
Gm13290	Gm13290 predicted gene 13290
Gm13458	Gm13458 predicted gene 13458
Gm15352	Gm15352 predicted gene 15352
Gm347	predicted gene 347
Gm7325	Gm7325 predicted gene 7325
Gm885	predicted gene 885
Gmpr	guanosine monophosphate reductase
Gna11	guanine nucleotide binding protein, alpha 11
Gna12	guanine nucleotide binding protein, alpha 12; similar to Guanine nucleotide-binding protein alpha-12 subunit (G alpha-12)
Gna13	guanine nucleotide binding protein, alpha 13
Gna14	guanine nucleotide binding protein, alpha 14
Gna15	guanine nucleotide binding protein, alpha 15
Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1
Gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting 3
Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type
Gnao1	guanine nucleotide binding protein, alpha O
Gnaz	guanine nucleotide binding protein, alpha z subunit
Gnb1	guanine nucleotide binding protein (G protein), beta 1
Gnb2	guanine nucleotide binding protein (G protein), beta 2
Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1
Gnb4	guanine nucleotide binding protein (G protein), beta 4
Gnb5	guanine nucleotide binding protein (G protein), beta 5
Gng11	guanine nucleotide binding protein (G protein), gamma 11
Gng12	guanine nucleotide binding protein (G protein), gamma 12
Gng13	guanine nucleotide binding protein (G protein), gamma 13
Gng2	guanine nucleotide binding protein (G protein), gamma 2

Gng3	guanine nucleotide binding protein (G protein), gamma 3
Gng4	guanine nucleotide binding protein (G protein), gamma 4
Gng7	guanine nucleotide binding protein (G protein), gamma 7
Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
Got1l1	glutamic-oxaloacetic transaminase 1-like 1
Gpr107	G protein-coupled receptor 107; hypothetical protein LOC100047589
Gpr108	G protein-coupled receptor 108
Gpr111	G protein-coupled receptor 111
Gpr113	G protein-coupled receptor 113
Gpr128	G protein-coupled receptor 128
Gpr142	G protein-coupled receptor 142
Gpr156	G protein-coupled receptor 156
Gpr176	G protein-coupled receptor 176
Gpr177	G protein-coupled receptor 177
Gpr20	G protein-coupled receptor 20
Gpr3	G-protein coupled receptor 3
Gpr6	G protein-coupled receptor 6
Gprin1	G protein-regulated inducer of neurite outgrowth 1
Gprin2	G protein regulated inducer of neurite outgrowth 2
Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)
Gpsm3	G-protein signalling modulator 3 (AGS3-like, C. elegans)
Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein
Grit	Rho GTPase activating protein 32
Grlf1	glucocorticoid receptor DNA binding factor 1
Grtp1	GH regulated TBC protein 1
Grwd1	glutamate-rich WD repeat containing 1
Gsdma1	gasdermin A
Gtpbp1	GTP binding protein 1
Gtpbp10	GTP-binding protein 10 (putative); predicted gene 6877
Gtpbp2	GTP binding protein 2
Gtpbp3	GTP binding protein 3
Gtpbp5	GTP binding protein 5
Hdgfl1	hepatoma derived growth factor-like 1
Helz	helicase with zinc finger domain
Hhat	hedgehog acyltransferase
Higd1a	HIG1 domain family, member 1A
Hrasls	HRAS-like suppressor
Hsdl1	hydroxysteroid dehydrogenase like 1
Hsdl2	hydroxysteroid dehydrogenase like 2
Hspa9-ps1	heat shock protein 9, pseudogene 1
Htr1e	5-hydroxytryptamine (serotonin) receptor 1E
Iapls3-28	intracisternal A particle, lymphocyte specific 3-28
Icmt	isoprenylcysteine carboxyl methyltransferase
Ier3ip1	immediate early response 3 interacting protein 1; haloacid dehalogenase-like hydrolase domain containing 2; predicted gene 10784
If3	Sendai virus induced interferon 3
Ifnar2	interferon (alpha and beta) receptor 2
Ifnz	interferon zeta

Igsf11	immunoglobulin superfamily, member 11
Il22ra2	interleukin 22 receptor, alpha 2
Il2rb	interleukin 2 receptor, beta chain
Il3ra	interleukin 3 receptor, alpha chain
Il9r	similar to interleukin 9 receptor; interleukin 9 receptor
Inpp4b	inositol polyphosphate-4-phosphatase, type II
Ints4	integrator complex subunit 4
Ipo11	importin 11
Iqgap2	IQ motif containing GTPase activating protein 2
Iqgap3	IQ motif containing GTPase activating protein 3
Irf9	interferon regulatory factor 9
Itgb1bp1	integrin beta 1 binding protein 1
Itgb1bp2	integrin beta 1 binding protein 2
Itgb1bp3	integrin beta 1 binding protein 3
Itgb3bp	predicted gene 3507; integrin beta 3 binding protein (beta3-endonexin); similar to integrin beta 3 binding protein
Itm2c	integral membrane protein 2C
Kank1	KN motif and ankyrin repeat domains 1
Kank2	KN motif and ankyrin repeat domains 2
Kank3	KN motif and ankyrin repeat domains 3
Kank4	KN motif and ankyrin repeat domains 4
Kbtbd7	kelch repeat and BTB (POZ) domain containing 7
Kcmf1	potassium channel modulatory factor 1
Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
Kif13b	kinesin family member 13B
Klhdc1	kelch domain containing 1
Klhdc2	kelch domain containing 2
Klhl31	Klhl3 kelch-like 3 (Drosophila)
Klhl31	kelch-like 31 (Drosophila)
Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1
Ktelc1	KTEL (Lys-Tyr-Glu-Leu) containing 1
Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1
Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2
Li	lined
Loc436194	Gm5754 predicted gene 5754
Lphn1	latrophilin 1
Lrig2	leucine-rich repeats and immunoglobulin-like domains 2
Lrrc26	leucine rich repeat containing 26
Lrrc8a	leucine rich repeat containing 8A
Lrrc8b	leucine rich repeat containing 8 family, member B
Lrrc8c	leucine rich repeat containing 8 family, member C
Lrrc8d	leucine rich repeat containing 8D
Lrrc8e	similar to Leucine rich repeat containing 8 family, member E; leucine rich repeat containing 8 family, member E
Ly6h	similar to Lymphocyte antigen 6H precursor (Ly-6H); lymphocyte antigen 6 complex, locus H
Mageb2	melanoma antigen, family B, 1; melanoma antigen, family B, 2
Mapk13	mitogen-activated protein kinase 13
Mat2a	methionine adenosyltransferase II, alpha
Mat2b	methionine adenosyltransferase II, beta
Mcf2l	mcf.2 transforming sequence-like

Med29	mediator complex subunit 29; predicted gene 9450
Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
Megf11	multiple EGF-like-domains 11
Mett11d1	methyltransferase 11 domain containing 1
Mettl3	methyltransferase like 3
Mical1	microtubule associated monoxygenase, calponin and LIM domain containing 1
Micalcl	MICAL C-terminal like
Midn	midnolin
Mmd	monocyte to macrophage differentiation-associated; similar to monocyte to macrophage differentiation-associated
Mon1b	MON1 homolog b (yeast)
Mprip	myosin phosphatase Rho interacting protein; predicted gene 8086
Mras	muscle and microspikes RAS
Mrpl12	mitochondrial ribosomal protein L12
Mrpl15	mitochondrial ribosomal protein L15
Mrpl2	mitochondrial ribosomal protein L2
Mrpl3	mitochondrial ribosomal protein L3
Mrpl46	mitochondrial ribosomal protein L46
Mrps25	mitochondrial ribosomal protein S25
Mrps35	mitochondrial ribosomal protein S35
Mrrf	mitochondrial ribosome recycling factor
Ms4a3	membrane-spanning 4-domains, subfamily A, member 3
Ms4a5	membrane-spanning 4-domains, subfamily A, member 5
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7
Msto1	misato homolog 1 (Drosophila)
Mterfd3	MTERF domain containing 3
Mtx2	metaxin 2
Mudeng	MU-2/AP1M2 domain containing, death-inducing
Mycbpap	MYCBP associated protein
Myg1	melanocyte proliferating gene 1
N6amt1	N-6 adenine-specific DNA methyltransferase 1 (putative)
Naif1	nuclear apoptosis inducing factor 1
Narg2	NMDA receptor-regulated gene 2
Nckap1	NCK-associated protein 1
Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3
Net1	predicted gene 8990; neuroepithelial cell transforming gene 1
Ngef	neuronal guanine nucleotide exchange factor
Ngrn	neugrin, neurite outgrowth associated
Nicn1	nicolin 1
Nip7	nuclear import 7 homolog (S. cerevisiae)
Nipsnap3a	nipsnap homolog 3A (C. elegans)
Nisch	nischarin
Nkg7	natural killer cell group 7 sequence
Nlrp12	NLR family, pyrin domain containing 12
Nlrp4e	NLR family, pyrin domain containing 4E
Nme2	non-metastatic cells 2, protein (NM23B)
Nme6	similar to Nme6 protein; non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)
Nme7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)

Nol8	nucleolar protein 8
Npdc1	neural proliferation, differentiation and control gene 1
Nrbp1	nuclear receptor binding protein 1
Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5
Nxph2	neurexophilin 2
Odc-rs9	ornithine decarboxylase, related sequence 9
Ola1	Obg-like ATPase 1
Olfml1	olfactomedin-like 1
Olfml3	olfactomedin-like 3
Olfr1310	olfactory receptor 1310
Olfr1342	olfactory receptor 1342
Olfr71	olfactory receptor 71
Olfr937	olfactory receptor 937
Olfr985	olfactory receptor 985
Oosp1	oocyte secreted protein 1
Osbpl6	oxysterol binding protein-like 6
Osbpl7	oxysterol binding protein-like 7
Pak1ip1	PAK1 interacting protein 1
Pak4	p21 protein (Cdc42/Rac)-activated kinase 4
Pak6	p21 protein (Cdc42/Rac)-activated kinase 6
Pank1	pantothenate kinase 1
Paqr5	progestin and adipoQ receptor family member V
Paqr6	progestin and adipoQ receptor family member VI; predicted gene 6821
Paqr7	progestin and adipoQ receptor family member VII
Paqr8	progestin and adipoQ receptor family member VIII
Paqr9	progestin and adipoQ receptor family member IX
Patl1	protein associated with topoisomerase II homolog 1 (yeast)
Patl2	protein associated with topoisomerase II homolog 2 (yeast)
Pcdhga1	protocadherin gamma subfamily A, 1
Pdc	phosducin
Pdcl	phosducin-like
Pdcl3	phosducin-like 3
Pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma
Pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma
Pdik1l	PDLIM1 interacting kinase 1 like
Pdzd4	PDZ domain containing 4
Pet2	plasmacytoma expressed transcript 2
Pgls	6-phosphogluconolactonase
Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y
Pigyl	phosphatidylinositol glycan anchor biosynthesis, class Y-like
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)
Pik3r5	phosphoinositide-3-kinase, regulatory subunit 5, p101
Pik3r6	phosphoinositide-3-kinase, regulatory subunit 6
Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha
Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha
Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta; similar to phosphatidylinositol 4-phosphate 5-kinase type I-alpha
Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma

Pitpna	phosphatidylinositol transfer protein, alpha
Pitpnb	phosphatidylinositol transfer protein, beta
Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
Pitpnm1	phosphatidylinositol transfer protein, membrane-associated 1
Pitpnm3	PITPNM family member 3
Pkn3	protein kinase N3
Plcb1	phospholipase C, beta 1
Plcb2	phospholipase C, beta 2
Plcb3	phospholipase C, beta 3
Plcd1	phospholipase C, delta 1
Plce1	phospholipase C, epsilon 1
Plcg2	phospholipase C, gamma 2
Plch1	phospholipase C, eta 1
Plch2	phospholipase C, eta 2
Plcl2	phospholipase C-like 2
Plek	pleckstrin
Plek2	pleckstrin 2
Plekha8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8
Plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5
Plk-ps1	polo-like kinase, pseudogene 1
Plxnb1	plexin B1
Plxnb2	plexin B2
Plxnb3	plexin B3
Pno1	partner of NOB1 homolog (S. cerevisiae)
Pnpla8	patatin-like phospholipase domain containing 8
Ppa2	pyrophosphatase (inorganic) 2
Ppan	peter pan homolog (Drosophila)
Ppap2b	phosphatidic acid phosphatase type 2B
Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1); similar to mKIAA1230 protein
Ppfibp2	protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2
Ppil3	peptidylprolyl isomerase (cyclophilin)-like 3
Ppm1b	similar to serine/threonine phosphatase; protein phosphatase 1B, magnesium dependent, beta isoform
Ppm1e	protein phosphatase 1E (PP2C domain containing)
Ppm1f	protein phosphatase 1F (PP2C domain containing)
Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A
Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform
Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform
Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; RIKEN cDNA 3222402P14 gene
Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)
Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
Ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform
Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)
Prex1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1
Prkch	protein kinase C, eta
Prkd3	protein kinase D3

Psat1	similar to Phosphoserine aminotransferase 1; phosphoserine aminotransferase 1
Pscd3	cytohesin 3
Pscdbp	cytohesin 1 interacting protein
Psd	pleckstrin and Sec7 domain containing
Psd4	pleckstrin and Sec7 domain containing 4
Psmg1	proteasome (prosome, macropain) assembly chaperone 1
Ptcd3	pentatricopeptide repeat domain 3
Ptgr2	prostaglandin reductase 2
Ptplad1	protein tyrosine phosphatase-like A domain containing 1
Ptplb	predicted gene 7908; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b
Ptprb	protein tyrosine phosphatase, receptor type, B
Pwp1	PWP1 homolog (S. cerevisiae)
Rab37	RAB37, member of RAS oncogene family
Rab7l1	RAB7, member RAS oncogene family-like 1
Rabgef1	similar to Ras negative regulator Rabex-5/Rin2; RAB guanine nucleotide exchange factor (GEF) 1
Rac3	RAS-related C3 botulinum substrate 3
Racgap1	Rac GTPase-activating protein 1; predicted gene 1859
Rala	v-ral simian leukemia viral oncogene homolog A (ras related)
Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)
Ralbp1	ralA binding protein 1
Ralgapa2	Ral GTPase activating protein, alpha subunit 2 (catalytic)
Ralgapb	Ralgapb Ral GTPase activating protein, beta subunit (non-catalytic)
Ralgds	ral guanine nucleotide dissociation stimulator
Ralgps1	Ral GEF with PH domain and SH3 binding motif 1
Ralgps2	Ral GEF with PH domain and SH3 binding motif 2
Ranbp10	RAN binding protein 10
Ranbp3	RAN binding protein 3
Rap1b	RAS related protein 1b; similar to GTP-binding protein (smg p21B)
Rap1gap	Rap1 GTPase-activating protein
Rap1gds1	similar to RAP1, GTP-GDP dissociation stimulator 1; RAP1, GTP-GDP dissociation stimulator 1
Rap2a	RAS related protein 2a
Rap2b	RAP2B, member of RAS oncogene family
Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1
Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2
Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3
Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4
Rapgefl1	Rap guanine nucleotide exchange factor (GEF)-like 1
Rarg	retinoic acid receptor, gamma
Rasa2	RAS p21 protein activator 2
Rasa3	RAS p21 protein activator 3
Rasa4	RAS p21 protein activator 4
Rasal1	RAS protein activator like 1 (GAP1 like)
Rasd1	RAS, dexamethasone-induced 1
Rasd2	RASD family, member 2
Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1
Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2
Rasgrp1	RAS guanyl releasing protein 1
Rasgrp2	RAS, guanyl releasing protein 2

Rasgrp3	RAS, guanyl releasing protein 3
Rasgrp4	RAS guanyl releasing protein 4
Rasl11b	RAS-like, family 11, member B
Rbj	DnaJ (Hsp40) homolog, subfamily C, member 27
Rbm27	RNA binding motif protein 27
Rcl1	RNA terminal phosphate cyclase-like 1
Rell1	RELT-like 1
Rell2	RELT-like 2
Rem1	rad and gem related GTP binding protein 1
Reps1	RalBP1 associated Eps domain containing protein
Reps2	RALBP1 associated Eps domain containing protein 2
Rgnef	Rho-guanine nucleotide exchange factor
Rgs1	regulator of G-protein signaling 1
Rgs10	regulator of G-protein signalling 10
Rgs11	regulator of G-protein signaling 11; similar to regulator of G-protein signaling 11
Rgs12	regulator of G-protein signaling 12
Rgs13	regulator of G-protein signaling 13
Rgs14	regulator of G-protein signaling 14
Rgs16	regulator of G-protein signaling 16
Rgs17	regulator of G-protein signaling 17
Rgs18	regulator of G-protein signaling 18
Rgs19	regulator of G-protein signaling 19; similar to Regulator of G-protein signaling 19
Rgs2	regulator of G-protein signaling 2
Rgs20	regulator of G-protein signaling 20
Rgs22	regulator of G-protein signalling 22
Rgs3	regulator of G-protein signaling 3
Rgs4	regulator of G-protein signaling 4
Rgs5	regulator of G-protein signaling 5
Rgs6	regulator of G-protein signaling 6
Rgs7	regulator of G protein signaling 7
Rgs7bp	regulator of G-protein signalling 7 binding protein
Rgs8	regulator of G-protein signaling 8
Rgs9	regulator of G-protein signaling 9
Rgs9bp	regulator of G-protein signalling 9 binding protein
Rhbdl1	rhomboid, veinlet-like 1 (Drosophila)
Rheb	Ras homolog enriched in brain; similar to RAS-homolog enriched in brain
Rhebl1	Ras homolog enriched in brain like 1
Rhod	ras homolog gene family, member D
Rhog	ras homolog gene family, member G
Rhoh	ras homolog gene family, member H
Rhoj	ras homolog gene family, member J
Rhoq	ras homolog gene family, member Q
Rhot1	ras homolog gene family, member T1
Rhot2	ras homolog gene family, member T2
Rhou	ras homolog gene family, member U
Rhov	ras homolog gene family, member V
Rhpn2	rhophilin, Rho GTPase binding protein 2
Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)

Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)
Rin1	Ras and Rab interactor 1
Riok1	RIO kinase 1 (yeast)
Riok2	RIO kinase 2 (yeast)
Riok3	RIO kinase 3 (yeast)
Ripk4	receptor-interacting serine-threonine kinase 4
Rit1	Ras-like without CAAX 1
Rit2	Ras-like without CAAX 2
Rnd1	Rho family GTPase 1
Rnd3	Rho family GTPase 3
Rnu5g	RNA, U5G small nuclear
Rod1	ROD1 regulator of differentiation 1 (S. pombe)
Ropn1	ropporin, rhophilin associated protein 1
Rpl28	predicted gene 13226; predicted gene 15435; ribosomal protein L28; predicted gene 12938
Rpl35	ribosomal protein L35; predicted gene 10269; predicted gene 8444; predicted gene 2000; predicted gene 4342
Rpl36al	ribosomal protein L36A-like
Rpl37	ribosomal protein L37
Rpl37a	ribosomal protein L37a; predicted gene 4149; predicted gene 4613; predicted gene 14251; predicted gene 14173
Rpl8	ribosomal protein L8; similar to 60S ribosomal protein L8
Rps28	ribosomal protein S28
Rps29	ribosomal protein S29
Rps6kc1	ribosomal protein S6 kinase polypeptide 1
Rras	Harvey rat sarcoma oncogene, subgroup R
Rras2	related RAS viral (r-ras) oncogene homolog 2
Rrp15	ribosomal RNA processing 15 homolog (S. cerevisiae)
Rsu1	Ras suppressor protein 1
Rtcd1	RNA terminal phosphate cyclase domain 1
Rtkn	rhotekin
Rufy2	RUN and FYVE domain-containing 2
Rwdd1	predicted gene 12693; RWD domain containing 1; predicted gene 13743
S100a16	S100 calcium binding protein A16
Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)
Samd9l	sterile alpha motif domain containing 9-like
Sap30bp	similar to transcriptional regulator protein; SAP30 binding protein
Saps3	SAPS domain family, member 3
Sav1	similar to WW45 protein; salvador homolog 1 (Drosophila)
Sbk1	SH3-binding kinase 1
Sc4mol	sterol-C4-methyl oxidase-like
Scand1	SCAN domain-containing 1
Sdad1	SDA1 domain containing 1; similar to SDA1 domain containing 1
Sec14l3	SEC14-like 3 (S. cerevisiae)
Sec14l4	SEC14-like 4 (S. cerevisiae)
Sec16b	SEC16 homolog B (S. cerevisiae)
Sectm1a	secreted and transmembrane 1A
Sectm1b	secreted and transmembrane 1B
Sept14	septin 14
Serinc1	serine incorporator 1
Serinc2	serine incorporator 2; hypothetical protein LOC100044221

Serinc3	serine incorporator 3
Serinc4	Serinc4 serine incorporator 4
Serinc5	serine incorporator 5
Sfxn4	sideroflexin 4
Sgsm1	small G protein signaling modulator 1
Sgsm2	small G protein signaling modulator 2
Sgsm3	small G protein signaling modulator 3
Sh2d3c	SH2 domain containing 3C
Sh3bgrl	SH3-binding domain glutamic acid-rich protein like
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)
Sidt1	SID1 transmembrane family, member 1
Sirpb1	signal-regulatory protein beta 1
Slc10a7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7
Slc25a21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
Slc25a41	solute carrier family 25, member 41
Slc33a1	solute carrier family 33 (acetyl-CoA transporter), member 1
Slc35a4	predicted gene 5866; solute carrier family 35, member A4
Slc35b2	solute carrier family 35, member B2
Slc41a3	solute carrier family 41, member 3
Slfn4	schlafen 4
Slfn9	similar to putative protein; schlafen 9; similar to schlafen 9
Slitrk2	SLIT and NTRK-like family, member 2
Slitrk4	SLIT and NTRK-like family, member 4
Sltm	SAFB-like, transcription modulator
Smad-ps1	MAD homolog, pseudogene 1 (Drosophila)
Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A
Snx13	sorting nexin 13
Snx21	sorting nexin family member 21
Snx26	sorting nexin family member 26
Sos1	son of sevenless homolog 1 (Drosophila)
Sos2	son of sevenless homolog 2 (Drosophila)
Spata17	spermatogenesis associated 17
Spata3	spermatogenesis associated 3
Specc1	sperm antigen with calponin homology and coiled-coil domains 1
Spg21	spastic paraplegia 21 homolog (human); similar to spastic paraplegia 21 homolog
Spin2	spindlin family, member 2
Spire2	spire homolog 2 (Drosophila)
Spnb5	spectrin beta 5
Spryd4	SPRY domain containing 4
Srgap1	SLIT-ROBO Rho GTPase activating protein 1
Srgap2	SLIT-ROBO Rho GTPase activating protein 2
Srgap3	SLIT-ROBO Rho GTPase activating protein 3
St5	suppression of tumorigenicity 5
Stard10	START domain containing 10
Stard9	START domain containing 9
Stk33	serine/threonine kinase 33
Suclg1	succinate-CoA ligase, GDP-forming, alpha subunit
Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1

Syap1	synapse associated protein 1
Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)
Tbc1d2	TBC1 domain family, member 2
Tcf25	transcription factor 25 (basic helix-loop-helix)
Tex2	testis expressed gene 2
Tg(tgfb1)1der	transgene insertion 1, Dennis R Roop
Tiam2	T-cell lymphoma invasion and metastasis 2
Timm44	translocase of inner mitochondrial membrane 44
Tlk2	predicted gene 13161; tousled-like kinase 2 (Arabidopsis)
Tln2	talin 2
Tm4sf5	transmembrane 4 superfamily member 5
Tm9sf1	transmembrane 9 superfamily member 1
Tm9sf3	transmembrane 9 superfamily member 3
Tmem11	transmembrane protein 11
Tmem150	transmembrane protein 150
Tmem159	transmembrane protein 159
Tmem16e	transmembrane protein 16e
Tmem16f	transmembrane protein 16f
Tmem22	transmembrane protein 22
Tmem30b	transmembrane protein 30B
Tmem30c	transmembrane protein 30C
Tmem33	transmembrane protein 33
Tmem8	transmembrane protein 8 (five membrane-spanning domains)
Tmem85	transmembrane protein 85
Tnik	TRAF2 and NCK interacting kinase
Tnk1	tyrosine kinase, non-receptor, 1
Tnk2	tyrosine kinase, non-receptor, 2
Tob2	transducer of ERBB2, 2
Tomm7	similar to translocase of outer mitochondrial membrane 7 homolog; translocase of outer mitochondrial membrane 7 homolog (yeast)
Tpd52-ps	tumor protein D52, pseudogene
Tpt1p	predicted gene 1974; tumor protein, translationally-controlled 1 pseudogene; tumor protein, translationally-controlled 1; predicted gene 14456
Tpt1-ps1	tumor protein, translationally-controlled, pseudogene 1
Trappc9	trafficking protein particle complex 9
Trcg1	taste receptor protein 1
Trim14	tripartite motif-containing 14
Trim45	tripartite motif-containing 45
Trim47	tripartite motif-containing 47
Trim69	tripartite motif-containing 69
Trio	triple functional domain (PTPRF interacting)
Trnp1	TMF1-regulated nuclear protein 1
Trp53i13	transformation related protein 53 inducible protein 13
Trp53tg5	transformation related protein 53 target 5
Trpd52l3	tumor protein D52-like 3
Trpt1	tRNA phosphotransferase 1
Tssk3	testis-specific serine kinase 3
Ttc1	tetratricopeptide repeat domain 1
Tulp3	tubby-like protein 3
Twf2	twinfilin, actin-binding protein, homolog 2 (Drosophila)

Ube2w	ubiquitin-conjugating enzyme E2W (putative)
Ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)
Ubtd2	ubiquitin domain containing 2
Ubxd5	UBX domain protein 11
Umpk-ps	uridine monophosphate kinase, pseudogene
Unc50	unc-50 homolog (C. elegans)
Usmg5	upregulated during skeletal muscle growth 5
Usp6nl	USP6 N-terminal like
Usp-ps	ubiquitin specific peptidase, pseudogene (USP17 homolog)
Vav1	vav 1 oncogene
Vav2	vav 2 oncogene
Vrk3	vaccinia related kinase 3
Wdr12	WD repeat domain 12; predicted gene 4879
Wdr13	WD repeat domain 13
Wdr16	WD repeat domain 16
Wdr25	WD repeat domain 25
Wdr3	WD repeat domain 3
Wdr45	WD repeat domain 45
Wdr6	WD repeat domain 6
Xrra1	X-ray radiation resistance associated 1
Yme1l1	YME1-like 1 (S. cerevisiae)
Ypel1	yippee-like 1 (Drosophila)
Ypel3	yippee-like 3 (Drosophila)
Zdhhc16	zinc finger, DHHC domain containing 16
Zdhhc7	zinc finger, DHHC domain containing 7
Zfand2a	zinc finger, AN1-type domain 2A
Zfand6	zinc finger, AN1-type domain 6
Zfp113	zinc finger protein 113
Zfp12	zinc finger protein 12
Zfp212	Zinc finger protein 212
Zfp263	zinc finger protein 263
Zfp319	zinc finger protein 319
Zfp322a	zinc finger protein 322A
Zfp326	zinc finger protein 326
Zfp383	zinc finger protein 383
Zfp414	zinc finger protein 414
Zfp418	zinc finger protein 418
Zfp445	zinc finger protein 445
Zfp449	zinc finger protein 449
Zfp458	zinc finger protein 458
Zfp58	zinc finger protein 58
Zfp612	zinc finger protein 612
Zfp622	zinc finger protein 622
Zfp641	zinc finger protein 641
Zfp689	zinc finger protein 689
Zfp74	zinc finger protein 74; hypothetical protein LOC100044255
Zfp97	zinc finger protein 97; cDNA sequence BC018101
Zfyve27	zinc finger, FYVE domain containing 27

Table S19. Arrestin signaling theoretical dataset. The Arrestin signaling dataset represents the intersection between the cellular signaling and Arrestin theoretical datasets.

Gene Symbol	Gene Definition
751864	Gm9733 predicted gene 9733
Acvr1b	activin A receptor, type IB
Acvr1c	activin A receptor, type IC
Acvr2a	activin A receptor, type IIA
Acvr2b	activin A receptor, type IIB
Akap5	A kinase (PRKA) anchor protein 5
Als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2
Arrdc2	arrestin domain containing 2
Arrdc3	arrestin domain containing 3
Atp5f1	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1
Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1
Aup1	ancient ubiquitous protein 1
B230339m05rik	B230339m05rik
Bc023829	cDNA sequence BC023829
Cab39	calcium binding protein 39
Camk1g	calcium/calmodulin dependent protein kinase IG
Cd3g	CD3 antigen, gamma polypeptide
Cd84	CD84 molecule
Cdc42bpb	CDC42 binding protein kinase beta (DMPK like)
Cds2	CDP diacylglycerol synthase (phosphatidate cytidylyltransferase) 2
Cetn4	centrin 4
Cnga4	cyclic nucleotide gated channel alpha 4
Csf2ra	colony stimulating factor 2 receptor, alpha, low affinity (granulocyte macrophage)
Csf2rb	colony stimulating factor 2 receptor, beta, low affinity (granulocyte macrophage)
Csf2rb2	colony stimulating factor 2 receptor, beta 2, low affinity (granulocyte macrophage)
Csnk1g1	casein kinase 1, gamma 1
Csnk1g3	casein kinase 1, gamma 3
D10mit271	DNA Segment, Chr 10, Massachusetts Institute of Technology 271
D14mit173	DNA segment, Chr 14, Massachusetts Institute of Technology 173
D14mit56	DNA segment, Chr 14, Massachusetts Institute of Technology 56
Dak	dihydroxyacetone kinase 2 homolog (S. cerevisiae)
Dgkb	diacylglycerol kinase, beta
Dgkd	diacylglycerol kinase, delta
Dgkg	diacylglycerol kinase, gamma
Dgkq	diacylglycerol kinase, theta
Dhrs3	dehydrogenase/reductase (SDR family) member 3
Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14
Dub1	deubiquitinating enzyme 1; similar to DUB
Dub3	deubiquitinating enzyme 3
Dub4	deubiquitinating enzyme 4

Dusp16	dual specificity phosphatase 16
Ebi2	Epstein-Barr virus induced gene 2 (lymphocyte specific G protein)
Eg627648	Eg627648
Eif3i	eukaryotic translation initiation factor 3, subunit I
Etv2	similar to ETS related protein 71; ets variant gene 2
Fitm1	fat storage-inducing transmembrane protein 1
Fiz1	FLT3 interacting zinc finger 1
Galm	galactose mutarotase
Gipc3	GIPC PDZ domain containing family, member 3
Gluchos1	glucose homeostasis QTL 1
Gna14	guanine nucleotide binding protein, alpha 14
Gna15	guanine nucleotide binding protein, alpha 15
Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type
Gnat3	guanine nucleotide binding protein, alpha transducing 3
Gnaz	guanine nucleotide binding protein, alpha z subunit
Gnb1	guanine nucleotide binding protein (G protein), beta 1
Gnb2	guanine nucleotide binding protein (G protein), beta 2
Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1
Gnb4	guanine nucleotide binding protein (G protein), beta 4
Gnb5	guanine nucleotide binding protein (G protein), beta 5
Gng11	guanine nucleotide binding protein (G protein), gamma 11
Gng12	guanine nucleotide binding protein (G protein), gamma 12
Gng13	guanine nucleotide binding protein (G protein), gamma 13
Gng2	guanine nucleotide binding protein (G protein), gamma 2
Gng3	guanine nucleotide binding protein (G protein), gamma 3
Gng4	guanine nucleotide binding protein (G protein), gamma 4
Gng7	guanine nucleotide binding protein (G protein), gamma 7
Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
Gpr111	G protein coupled receptor 111
Gpr128	G protein coupled receptor 128
Gpr142	G protein coupled receptor 142
Gpr156	G protein coupled receptor 156
Gpr177	G protein coupled receptor 177
Gpr20	G protein coupled receptor 20
Gpr3	G protein coupled receptor 3
Gpr61	G protein coupled receptor 61
Gprin2	G protein regulated inducer of neurite outgrowth 2
Gpsm3	G protein signaling modulator 3 (AGS3 like, C. elegans)
Gucy2f	guanylate cyclase 2f
Higd1a	HIG1 domain family, member 1A
Htr1e	5 hydroxytryptamine (serotonin) receptor 1E
Ifnar2	interferon (alpha and beta) receptor 2
Ifnz	interferon zeta
Il3ra	interleukin 3 receptor, alpha chain
Il5ra	interleukin 5 receptor, alpha
Inpp4b	inositol polyphosphate 4, type II
Irf9	interferon regulatory factor 9

Itgb1bp1	integrin beta 1 binding protein 1
Itgb1bp2	integrin beta 1 binding protein 2
Itgb1bp3	integrin beta 1 binding protein 3
Itgb3bp	integrin beta 3 binding protein (beta3 endonexin)
Kif3a	kinesin family member 3A
Lgr6	leucine rich repeat containing G protein
Map2k7	mitogen activated protein kinase kinase 7
Map3k5	mitogen activated protein kinase kinase kinase 5
Map3k6	mitogen activated protein kinase kinase kinase 6
Mapbpip	similar to Late endosomal/lysosomal Mp1 interacting protein (p14)
Mapk13	mitogen activated protein kinase 13
Mapk8ip1	mitogen activated protein kinase 8 interacting protein 1
Mapk8ip2	mitogen activated protein kinase 8 interacting protein 2
Mapk8ip3	mitogen activated protein kinase 8 interacting protein 3
Mat2a	methionine adenosyltransferase II, alpha
Mat2b	methionine adenosyltransferase II, beta
Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
Mrgprb2	MAS related GPR, member B2
Mrgpre	MAS related GPR, member E
Ms4a3	membrane spanning 4 domains, subfamily A, member 3
Ms4a5	membrane spanning 4 domains, subfamily A, member 5
Nme2	non metastatic cells 2
Nme7	non metastatic cells 7
Odc-rs9	ornithine decarboxylase, related sequence 9
Olfr1310	olfactory receptor 1310
Olfr1342	olfactory receptor 1342
Olfr410	olfactory receptor 410
Olfr412	olfactory receptor 412
Olfr705	olfactory receptor 705
Olfr71	olfactory receptor 71
Olfr937	olfactory receptor 937
Olfr985	olfactory receptor 985
Ottmusg00000011291	Ottmusg00000011291
Otud5	OTU domain containing 5
Pank1	pantothenate kinase 1
Paqr5	progestin and adipoQ receptor family member V
Paqr7	progestin and adipoQ receptor family member VII
Paqr8	progestin and adipoQ receptor family member VIII
Pcdhga1	protocadherin gamma subfamily A, 1
Pdc	phosducin
Pdcl	phosducin-like
Pde4d	phosphodiesterase 4D, cAMP specific (phosphodiesterase E3 dunce homolog, Drosophila)
Pde6g	phosphodiesterase 6G, cGMP specific, rod, gamma
Pde6h	phosphodiesterase 6H, cGMP specific, cone, gamma
Pik3r5	phosphoinositide 3 kinase, regulatory subunit 5, p101
Pik3r6	phosphoinositide 3 kinase, regulatory subunit 6
Pip5k1a	phosphatidylinositol 4 phosphate 5-kinase, type I, alpha
Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma

Pitpnb	phosphatidylinositol transfer protein, beta
Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
Pitpnm2	phosphatidylinositol transfer protein, membrane associated 2
Pitpnm3	PITPNM family member 3
Plcb1	phospholipase C, beta 1 (phosphoinositide specific)
Plcb2	phospholipase C, beta 2 (phosphatidylinositol specific)
Plcb3	phospholipase C, beta 3 (phosphatidylinositol specific)
Plcd1	phospholipase C, delta 1
Plch1	phospholipase C, eta 1
Plcl2	phospholipase C-like 2
Plek	pleckstrin
Pnpla8	patatin like phospholipase domain containing 8
Ppap2b	phosphatidic acid phosphatase type 2B
Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)
Ppm1b	protein phosphatase 1B (formerly 2C), magnesium dependent, beta isoform
Ppm1e	protein phosphatase 1E (PP2C domain containing)
Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform
Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform
Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform
Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; RIKEN cDNA 3222402P14 gene
Ppp2r4	protein phosphatase 2A activator, regulatory subunit 4
Ppp2r5a	protein phosphatase 2, regulatory subunit B', alpha isoform
Ppp2r5b	protein phosphatase 2, regulatory subunit B', beta isoform
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform
Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
Psat1	phosphoserine aminotransferase 1
Psmg1	proteasome (prosome, macropain) assembly chaperone 1
Ptprb	protein tyrosine phosphatase, receptor type, B
Rdh11	retinol dehydrogenase 11
Rem1	rad and gem related GTP binding protein 1
Rgs11	regulator of G protein signaling 11
Rgs7	regulator of G protein signaling 7
Rgs7bp	regulator of G protein signaling 7 binding protein
Rgs9	regulator of G protein signaling 9
Rgs9bp	regulator of G protein signaling 9 binding protein
Rtp1	receptor (chemosensory) transporter protein 1
Rxfp4	relaxin/insulin like family peptide receptor 4
Sap30bp	similar to transcriptional regulator protein; SAP30 binding protein
Sarm1	sterile alpha and TIR motif containing 1
Sctr	secretin receptor
Sh2d1b1	SH2 domain protein 1B1
Sh2d1b2	SH2 domain protein 1B2
Slamf9	SLAM family member 9
Spg21	spastic paraplegia 21 homolog (human); similar to spastic paraplegia 21 homolog
Spnb5	spectrin beta 5
Stambpl1	STAM binding protein like 1
Sucla2	succinate CoA ligase, ADP forming, beta subunit
Suclg1	succinate CoA ligase, alpha subunit

Tg(tgfb1)1der	transgene insertion 1, Dennis R Roop
Tln2	talin 2
Tmem11	transmembrane protein 11
Tmem181	transmembrane protein 181
Tmem185b	transmembrane protein 185b
Trappc9	trafficking protein particle complex 9
Treh	trehalase (brush border membrane glycoprotein)
Tulp3	tubby like protein 3
Umpk-ps	uridine monophosphate kinase, pseudogene
Unc119	unc 119 homolog (C. elegans)
Xpo4	exportin 4
Yes1	v-yes 1 Yamaguchi sarcoma viral oncogene homolog 1
Zdhhc7	zinc finger, DHHC domain containing 7
Zfp414	zinc finger protein 414
Zfyve9	zinc finger, FYVE domain containing 9

Table S20. G protein signaling theoretical dataset. The G protein signaling dataset represents the intersection between the cellular signaling and G protein theoretical datasets.

Gene Symbol	**Gene Definition**
LOC139796	LOC139796
0610007p14rik	RIKEN cDNA 0610007P14 gene
0610031j06rik	RIKEN cDNA 0610031J06 gene
1600002k03rik	RIKEN cDNA 1600002K03 gene
1700009n14rik	RIKEN cDNA 1700009N14 gene
1700057k13rik	RIKEN cDNA 1700057K13 gene
1810014f10rik	RIKEN cDNA 1810014F10 gene
2310001a20rik	RIKEN cDNA 2310001A20 gene
2410018m08rik	RIKEN cDNA 2410018M08 gene
2500003m10rik	RIKEN cDNA 2500003M10 gene
2700078k21rik	RIKEN cDNA 2700078K21 gene
4833424o15rik	RIKEN cDNA 4833424O15 gene
4930420k17rik	RIKEN cDNA 4930420K17 gene
4930455c21rik	RIKEN cDNA 4930455C21 gene
4933424b01rik	RIKEN cDNA 4933424B01 gene
4933436h12rik	RIKEN cDNA 4933436H12 gene
6430548m08rik	RIKEN cDNA 6430548M08 gene
9430023l20rik	RIKEN cDNA 9430023L20 gene
A130040m12rik	RIKEN cDNA A130040M12 gene
Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6
Actr8	ARP8 actin-related protein 8 homolog (S. cerevisiae)
Adcy2	adenylate cyclase 2
Adcy4	adenylate cyclase 4
Adcy5	adenylate cyclase 5; similar to adenylate cyclase 5
Adnp2	ADNP homeobox 2
Aig1	androgen-induced 1
Ak3l1	predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1
Ak5	adenylate kinase 5
Akap13	A kinase (PRKA) anchor protein 13
Akr1e1	aldo-keto reductase family 1, member E1
Als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 homolog (human)
Ankrd7	ankyrin repeat domain 7
Ard1b	N(alpha)-acetyltransferase 11, NatA catalytic subunit
Arhgap1	Rho GTPase activating protein 1; predicted gene 8514
Arhgap10	Rho GTPase activating protein 10
Arhgap21	Rho GTPase activating protein 21
Arhgap22	Rho GTPase activating protein 22
Arhgap26	RIKEN cDNA 9630014M24 gene; Rho GTPase activating protein 26; predicted gene 5820
Arhgap29	Rho GTPase activating protein 29
Arhgap36	Rho GTPase activating protein 36
Arhgap4	Rho GTPase activating protein 4

Arhgap5	Rho GTPase activating protein 5
Arhgap8	Rho GTPase activating protein 8
Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1
Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11
Arhgef12	predicted gene 7281; predicted gene 5831; similar to SP140 nuclear body protein (predicted); Rho guanine nucleotide exchange factor (GEF) 12
Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15
Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17
Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2
Arhgef4	Rho guanine nucleotide exchange factor (GEF) 4
Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
Arid3c	AT rich interactive domain 3C (BRIGHT-like)
Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1
Arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4; similar to SRp25 nuclear protein
Arl8b	ADP-ribosylation factor-like 8B
Ars2	serrate RNA effector molecule homolog (Arabidopsis)
Arsj	arylsulfatase J
Arsk	similar to arylsulfatase K; arylsulfatase K
Astl	similar to Astacin-like metalloendopeptidase precursor (Oocyte astacin) (Ovastacin); astacin-like metalloendopeptidase (M12 family)
Asxl3	additional sex combs like 3 (Drosophila)
Atad3a	ATPase family, AAA domain containing 3A
Atp13a3	ATPase type 13A3
Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1; predicted gene 12231
Atp5k	predicted gene 2972; ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1
Aup1	ancient ubiquitous protein 1
Aw125753	Fam84a family with sequence similarity 84, member A
Axud1	cysteine-serine-rich nuclear protein 1
B020018g12rik	RNA binding motif protein 8a; RIKEN cDNA B020018G12 gene
B230208h17rik	RIKEN cDNA B230208H17 gene
Bc010304	Fam120a family with sequence similarity 120, member A
Bc017158	cDNA sequence BC017158
Bc021395	Bc021395
Bc028663	Bc028663
Bc029169	Bc029169
Bcar3	breast cancer anti-estrogen resistance 3
Bcas2	breast carcinoma amplified sequence 2
Bin3	bridging integrator 3
Bnip2	BCL2/adenovirus E1B interacting protein 2
Bnipl	BCL2/adenovirus E1B 19kD interacting protein like
Brd1	bromodomain containing 1; similar to bromodomain containing 1
Bri3bp	Bri3 binding protein
Bspry	B-box and SPRY domain containing
Cab39	calcium binding protein 39
Camk1g	calcium/calmodulin-dependent protein kinase I gamma
Card6	caspase recruitment domain family, member 6
Ccdc88a	coiled coil domain containing 88A
Ccdc88b	coiled-coil domain containing 88B

Ccpg1	cell cycle progression 1
Ccpn-ps	calcyphosine, pseudogene
Cd247	CD247 antigen
Cd3g	CD3 antigen, gamma polypeptide
Cdc42bpb	CDC42 binding protein kinase beta
Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2
Cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5
Cdc42se1	CDC42 small effector 1
Cdgap	Rho GTPase activating protein 31
Cenpw	centromere protein W
Centa1	ArfGAP with dual PH domains 1
Centd2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
Centd3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3
Centg1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2
Centg2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1
Centg3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3
Cep57	centrosomal protein 57
Chn1	chimerin (chimaerin) 1
Chn2	chimerin (chimaerin) 2
Chpst	chrondroprogenitor specific transcript
Cirbp-rs1	cold inducible RNA binding protein, related sequence 1
Cirbp-rs3	cold inducible RNA binding protein, related sequence 3
Clec4b1	C-type lectin domain family 4, member b1
Clybl	citrate lyase beta like
Cml1	N-acetyltransferase 8B; camello-like 1
Cml2	camello-like 2
Cml3	predicted gene 4477; camello-like 3
Cml5	camello-like 5
Cnbpl2	cellular nucleic acid binding protein-like 2
Cnih	cornichon homolog (Drosophila)
Cnksr1	connector enhancer of kinase suppressor of Ras 1
Cnnm1	cyclin M1
Cnnm2	cyclin M2
Cnnm3	cyclin M3
Cnot1	predicted gene 6158; CCR4-NOT transcription complex, subunit 1
Cnot8	CCR4-NOT transcription complex, subunit 8
Cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)
Coq4	coenzyme Q4 homolog (yeast)
Coro2a	coronin, actin binding protein 2A
Cpne3	copine III
Creg2	cellular repressor of E1A-stimulated genes 2
Cryzl1	crystallin, zeta (quinone reductase)-like 1
Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)
Csmd2	CUB and Sushi multiple domains 2
Csnk1g1	casein kinase 1, gamma 1
Csnk1g2	casein kinase 1, gamma 2
Csnk1g3	casein kinase 1, gamma 3; similar to casein kinase 1, gamma 3

Csrnp2	cysteine-serine-rich nuclear protein 2
Csrnp3	cysteine-serine-rich nuclear protein 3
Ctf2	cardiotrophin 2
Ctps2	cytidine 5'-triphosphate synthase 2
Cutc	cutC copper transporter homolog (E.coli)
D10ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed
D11mit109	DNA segment, Chr 11, Massachusetts Institute of Technology 109
D11mit205	DNA segment, Chr 11, Massachusetts Institute of Technology 205
D13mit91	DNA segment, Chr 13, Massachusetts Institute of Technology 91
D14mit116	DNA segment, Chr 14, Massachusetts Institute of Technology 116
D14mit173	DNA segment, Chr 14, Massachusetts Institute of Technology 173
D14mit56	DNA segment, Chr 14, Massachusetts Institute of Technology 56
D15mit198	DNA segment, Chr 15, Massachusetts Institute of Technology 198
D17mit7	DNA segment, Chr 17, Massachusetts Institute of Technology 7
D19mit24	DNA segment, Chr 19, Massachusetts Institute of Technology 24
D19mit66	DNA segment, Chr 19, Massachusetts Institute of Technology 66
D19mit75	DNA segment, Chr 19, Massachusetts Institute of Technology 75
D330017j20rik	Fam40b family with sequence similarity 40, member B
D5mit317	DNA segment, Chr 5, Massachusetts Institute of Technology 317
D6mit252	DNA segment, Chr 6, Massachusetts Institute of Technology 252
D8ertd82e	DNA segment, Chr 8, ERATO Doi 82, expressed
D930005d10rik	Radil Ras association and DIL domains
D9mit60	DNA segment, Chr 9, Massachusetts Institute of Technology 60
D9mit61	DNA segment, Chr 9, Massachusetts Institute of Technology 61
Dak	dihydroxyacetone kinase 2 homolog (yeast)
Dchs2	dachsous 2 (Drosophila)
Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41
Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54
Ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
Def6	differentially expressed in FDCP 6
Def8	differentially expressed in FDCP 8
Defb29	defensin beta 29
Dennd4c	DENN/MADD domain containing 4C
Depdc2	DEP domain containing 2
Dgkb	diacylglycerol kinase, beta
Dgkd	diacylglycerol kinase, delta
Dgkg	diacylglycerol kinase, gamma
Dgkq	diacylglycerol kinase, theta
Dhdds	dehydrodolichyl diphosphate synthase
Dhx35	predicted gene 4713; DEAH (Asp-Glu-Ala-His) box polypeptide 35
Diras1	DIRAS family, GTP-binding RAS-like 1
Diras2	DIRAS family, GTP-binding RAS-like 2
Dock1	dedicator of cytokinesis 1
Dock10	dedicator of cytokinesis 10
Dock2	dedicator of cyto-kinesis 2
Dock4	dedicator of cytokinesis 4
Dock9	dedicator of cytokinesis 9

Dolpp1	dolichyl pyrophosphate phosphatase 1
Dpf2	D4, zinc and double PHD fingers family 2
Dph2	DPH2 homolog (S. cerevisiae)
Dph3	DPH3 homolog (KTI11, S. cerevisiae)
Dqx1	DEAQ RNA-dependent ATPase
Dtd1	similar to D-tyrosyl-tRNA deacylase 1; D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)
Dub2	ubiquitin specific peptidase 17-like 5
Dub3	predicted gene 6596
Dub4	deubiquitinating enzyme 4
Dullard	similar to Dullard homolog (Xenopus laevis); Dullard homolog (Xenopus laevis)
E130112l23rik	RIKEN cDNA E130112L23 gene
Efhd1	EF hand domain containing 1
Egfl8	EGF-like domain 8
Eif3i	eukaryotic translation initiation factor 3, subunit I
Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)
Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)
Emilin3	elastin microfibril interfacer 3
Eml3	echinoderm microtubule associated protein like 3
Ensmusg00000053178	Gm9897 predicted gene 9897
Ensmusg00000067748	Rpl17-ps5 ribosomal protein L17, pseudogene 5
Epb4.1l4a	erythrocyte protein band 4.1-like 4a
Epb4.1l4b	erythrocyte protein band 4.1-like 4b
Eps8	epidermal growth factor receptor pathway substrate 8
Eps8l1	EPS8-like 1
Eps8l2	EPS8-like 2
Eps8l3	EPS8-like 3
Eral1	Era (G-protein)-like 1 (E. coli)
Erdr1	erythroid differentiation regulator 1
Etaa1	Ewing's tumor-associated antigen 1
Etv2	similar to ETS related protein 71; ets variant gene 2
Exoc2	exocyst complex component 2
Exosc8	exosome component 8
F830045p16rik	RIKEN cDNA F830045P16 gene
Fam177a	Fam177a family with sequence similarity 177, member A
Fam40a	family with sequence similarity 40, member A
Fam57a	Fam57a family with sequence similarity 57, member A
Fam92a	family with sequence similarity 92, member A
Farp2	FERM, RhoGEF and pleckstrin domain protein 2
Fbxo10	F-box protein 10
Ficd	FIC domain containing
Fitm1	fat storage-inducing transmembrane protein 1
Fndc1	fibronectin type III domain containing 1; similar to fibronectin type III domain containing 1
Fndc4	fibronectin type III domain containing 4
Fndc5	fibronectin type III domain containing 5
Fpgt	fucose-1-phosphate guanylyltransferase
Frag1	post-GPI attachment to proteins 2
Frmd4b	FERM domain containing 4B
Ftsj2	FtsJ homolog 2 (E. coli)

Fuk	fucokinase
Gas2l1	growth arrest-specific 2 like 1
Gas2l2	growth arrest-specific 2 like 2
Gas4	growth arrest specific 4
Gde1	glycerophosphodiester phosphodiesterase 1
Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1
Gdpd4	glycerophosphodiester phosphodiesterase domain containing 4
Gem	GTP binding protein (gene overexpressed in skeletal muscle)
Get4	golgi to ER traffic protein 4 homolog (S. cerevisiae)
Gfm1	G elongation factor, mitochondrial 1
Ggps1	geranylgeranyl diphosphate synthase 1; similar to Ggps1 protein; predicted gene 5630
Ggt7	gamma-glutamyltransferase 7
Gimap1	GTPase, IMAP family member 1
Gimap6	GTPase, IMAP family member 6
Gimap7	GTPase, IMAP family member 7
Gimap8	GTPase, IMAP family member 8
Gimap9	GTPase, IMAP family member 9
Gipc2	GIPC PDZ domain containing family, member 2
Gipc3	GIPC PDZ domain containing family, member 3
Glipr2	GLI pathogenesis-related 2
Glod4	glyoxalase domain containing 4
Gm11818	Gm11818 predicted gene 11818
Gm13290	Gm13290 predicted gene 13290
Gm13458	Gm13458 predicted gene 13458
Gm15352	Gm15352 predicted gene 15352
Gm347	predicted gene 347
Gm7325	Gm7325 predicted gene 7325
Gm885	predicted gene 885
Gmpr	guanosine monophosphate reductase
Gna11	guanine nucleotide binding protein, alpha 11
Gna12	guanine nucleotide binding protein, alpha 12; similar to Guanine nucleotide-binding protein alpha-12 subunit (G alpha-12)
Gna13	guanine nucleotide binding protein, alpha 13
Gna14	guanine nucleotide binding protein, alpha 14
Gna15	guanine nucleotide binding protein, alpha 15
Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1
Gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting 3
Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type
Gnao1	guanine nucleotide binding protein, alpha O
Gnaz	guanine nucleotide binding protein, alpha z subunit
Gnb1	guanine nucleotide binding protein (G protein), beta 1
Gnb2	guanine nucleotide binding protein (G protein), beta 2
Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1
Gnb4	guanine nucleotide binding protein (G protein), beta 4
Gnb5	guanine nucleotide binding protein (G protein), beta 5
Gng11	guanine nucleotide binding protein (G protein), gamma 11
Gng12	guanine nucleotide binding protein (G protein), gamma 12
Gng13	guanine nucleotide binding protein (G protein), gamma 13
Gng2	guanine nucleotide binding protein (G protein), gamma 2

Gng3	guanine nucleotide binding protein (G protein), gamma 3
Gng4	guanine nucleotide binding protein (G protein), gamma 4
Gng7	guanine nucleotide binding protein (G protein), gamma 7
Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
Got1l1	glutamic-oxaloacetic transaminase 1-like 1
Gpr107	G protein-coupled receptor 107; hypothetical protein LOC100047589
Gpr108	G protein-coupled receptor 108
Gpr111	G protein-coupled receptor 111
Gpr113	G protein-coupled receptor 113
Gpr128	G protein-coupled receptor 128
Gpr142	G protein-coupled receptor 142
Gpr156	G protein-coupled receptor 156
Gpr176	G protein-coupled receptor 176
Gpr177	G protein-coupled receptor 177
Gpr20	G protein-coupled receptor 20
Gpr3	G-protein coupled receptor 3
Gpr6	G protein-coupled receptor 6
Gprin1	G protein-regulated inducer of neurite outgrowth 1
Gprin2	G protein regulated inducer of neurite outgrowth 2
Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)
Gpsm3	G-protein signalling modulator 3 (AGS3-like, C. elegans)
Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein
Grit	Rho GTPase activating protein 32
Grlf1	glucocorticoid receptor DNA binding factor 1
Grtp1	GH regulated TBC protein 1
Grwd1	glutamate-rich WD repeat containing 1
Gsdma1	gasdermin A
Gtpbp1	GTP binding protein 1
Gtpbp10	GTP-binding protein 10 (putative); predicted gene 6877
Gtpbp2	GTP binding protein 2
Gtpbp3	GTP binding protein 3
Gtpbp5	GTP binding protein 5
Hdgfl1	hepatoma derived growth factor-like 1
Helz	helicase with zinc finger domain
Hhat	hedgehog acyltransferase
Higd1a	HIG1 domain family, member 1A
Hrasls	HRAS-like suppressor
Hsdl1	hydroxysteroid dehydrogenase like 1
Hsdl2	hydroxysteroid dehydrogenase like 2
Hspa9-ps1	heat shock protein 9, pseudogene 1
Htr1e	5-hydroxytryptamine (serotonin) receptor 1E
Iapls3-28	intracisternal A particle, lymphocyte specific 3-28
Icmt	isoprenylcysteine carboxyl methyltransferase
Ier3ip1	immediate early response 3 interacting protein 1; haloacid dehalogenase-like hydrolase domain containing 2; predicted gene 10784
If3	Sendai virus induced interferon 3
Ifnar2	interferon (alpha and beta) receptor 2
Ifnz	interferon zeta

Igsf11	immunoglobulin superfamily, member 11
Il22ra2	interleukin 22 receptor, alpha 2
Il2rb	interleukin 2 receptor, beta chain
Il3ra	interleukin 3 receptor, alpha chain
Il9r	similar to interleukin 9 receptor; interleukin 9 receptor
Inpp4b	inositol polyphosphate-4-phosphatase, type II
Ints4	integrator complex subunit 4
Ipo11	importin 11
Iqgap2	IQ motif containing GTPase activating protein 2
Iqgap3	IQ motif containing GTPase activating protein 3
Irf9	interferon regulatory factor 9
Itgb1bp1	integrin beta 1 binding protein 1
Itgb1bp2	integrin beta 1 binding protein 2
Itgb1bp3	integrin beta 1 binding protein 3
Itgb3bp	predicted gene 3507; integrin beta 3 binding protein (beta3-endonexin); similar to integrin beta 3 binding protein
Itm2c	integral membrane protein 2C
Kank1	KN motif and ankyrin repeat domains 1
Kank2	KN motif and ankyrin repeat domains 2
Kank3	KN motif and ankyrin repeat domains 3
Kank4	KN motif and ankyrin repeat domains 4
Kbtbd7	kelch repeat and BTB (POZ) domain containing 7
Kcmf1	potassium channel modulatory factor 1
Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
Kif13b	kinesin family member 13B
Klhdc1	kelch domain containing 1
Klhdc2	kelch domain containing 2
Klhl31	Klhl3 kelch-like 3 (Drosophila)
Klhl31	kelch-like 31 (Drosophila)
Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1
Ktelc1	KTEL (Lys-Tyr-Glu-Leu) containing 1
Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1
Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2
Li	lined
Loc436194	Gm5754 predicted gene 5754
Lphn1	latrophilin 1
Lrig2	leucine-rich repeats and immunoglobulin-like domains 2
Lrrc26	leucine rich repeat containing 26
Lrrc8a	leucine rich repeat containing 8A
Lrrc8b	leucine rich repeat containing 8 family, member B
Lrrc8c	leucine rich repeat containing 8 family, member C
Lrrc8d	leucine rich repeat containing 8D
Lrrc8e	similar to Leucine rich repeat containing 8 family, member E; leucine rich repeat containing 8 family, member E
Ly6h	similar to Lymphocyte antigen 6H precursor (Ly-6H); lymphocyte antigen 6 complex, locus H
Mageb2	melanoma antigen, family B, 1; melanoma antigen, family B, 2
Mapk13	mitogen-activated protein kinase 13
Mat2a	methionine adenosyltransferase II, alpha
Mat2b	methionine adenosyltransferase II, beta
Mcf2l	mcf.2 transforming sequence-like

Med29	mediator complex subunit 29; predicted gene 9450
Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
Megf11	multiple EGF-like-domains 11
Mett11d1	methyltransferase 11 domain containing 1
Mettl3	methyltransferase like 3
Mical1	microtubule associated monoxygenase, calponin and LIM domain containing 1
Micalcl	MICAL C-terminal like
Midn	midnolin
Mmd	monocyte to macrophage differentiation-associated; similar to monocyte to macrophage differentiation-associated
Mon1b	MON1 homolog b (yeast)
Mprip	myosin phosphatase Rho interacting protein; predicted gene 8086
Mras	muscle and microspikes RAS
Mrpl12	mitochondrial ribosomal protein L12
Mrpl15	mitochondrial ribosomal protein L15
Mrpl2	mitochondrial ribosomal protein L2
Mrpl3	mitochondrial ribosomal protein L3
Mrpl46	mitochondrial ribosomal protein L46
Mrps25	mitochondrial ribosomal protein S25
Mrps35	mitochondrial ribosomal protein S35
Mrrf	mitochondrial ribosome recycling factor
Ms4a3	membrane-spanning 4-domains, subfamily A, member 3
Ms4a5	membrane-spanning 4-domains, subfamily A, member 5
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7
Msto1	misato homolog 1 (Drosophila)
Mterfd3	MTERF domain containing 3
Mtx2	metaxin 2
Mudeng	MU-2/AP1M2 domain containing, death-inducing
Mycbpap	MYCBP associated protein
Myg1	melanocyte proliferating gene 1
N6amt1	N-6 adenine-specific DNA methyltransferase 1 (putative)
Naif1	nuclear apoptosis inducing factor 1
Narg2	NMDA receptor-regulated gene 2
Nckap1	NCK-associated protein 1
Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3
Net1	predicted gene 8990; neuroepithelial cell transforming gene 1
Ngef	neuronal guanine nucleotide exchange factor
Ngrn	neugrin, neurite outgrowth associated
Nicn1	nicolin 1
Nip7	nuclear import 7 homolog (S. cerevisiae)
Nipsnap3a	nipsnap homolog 3A (C. elegans)
Nisch	nischarin
Nkg7	natural killer cell group 7 sequence
Nlrp12	NLR family, pyrin domain containing 12
Nlrp4e	NLR family, pyrin domain containing 4E
Nme2	non-metastatic cells 2, protein (NM23B)
Nme6	similar to Nme6 protein; non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)
Nme7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)

Nol8	nucleolar protein 8
Npdc1	neural proliferation, differentiation and control gene 1
Nrbp1	nuclear receptor binding protein 1
Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5
Nxph2	neurexophilin 2
Odc-rs9	ornithine decarboxylase, related sequence 9
Ola1	Obg-like ATPase 1
Olfml1	olfactomedin-like 1
Olfml3	olfactomedin-like 3
Olfr1310	olfactory receptor 1310
Olfr1342	olfactory receptor 1342
Olfr71	olfactory receptor 71
Olfr937	olfactory receptor 937
Olfr985	olfactory receptor 985
Oosp1	oocyte secreted protein 1
Osbpl6	oxysterol binding protein-like 6
Osbpl7	oxysterol binding protein-like 7
Pak1ip1	PAK1 interacting protein 1
Pak4	p21 protein (Cdc42/Rac)-activated kinase 4
Pak6	p21 protein (Cdc42/Rac)-activated kinase 6
Pank1	pantothenate kinase 1
Paqr5	progestin and adipoQ receptor family member V
Paqr6	progestin and adipoQ receptor family member VI; predicted gene 6821
Paqr7	progestin and adipoQ receptor family member VII
Paqr8	progestin and adipoQ receptor family member VIII
Paqr9	progestin and adipoQ receptor family member IX
Patl1	protein associated with topoisomerase II homolog 1 (yeast)
Patl2	protein associated with topoisomerase II homolog 2 (yeast)
Pcdhga1	protocadherin gamma subfamily A, 1
Pdc	phosducin
Pdcl	phosducin-like
Pdcl3	phosducin-like 3
Pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma
Pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma
Pdik1l	PDLIM1 interacting kinase 1 like
Pdzd4	PDZ domain containing 4
Pet2	plasmacytoma expressed transcript 2
Pgls	6-phosphogluconolactonase
Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y
Pigyl	phosphatidylinositol glycan anchor biosynthesis, class Y-like
Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide
Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)
Pik3r5	phosphoinositide-3-kinase, regulatory subunit 5, p101
Pik3r6	phosphoinositide-3-kinase, regulatory subunit 6
Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha
Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha
Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta; similar to phosphatidylinositol 4-phosphate 5-kinase type I-alpha
Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma

Pitpna	phosphatidylinositol transfer protein, alpha
Pitpnb	phosphatidylinositol transfer protein, beta
Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
Pitpnm1	phosphatidylinositol transfer protein, membrane-associated 1
Pitpnm3	PITPNM family member 3
Pkn3	protein kinase N3
Plcb1	phospholipase C, beta 1
Plcb2	phospholipase C, beta 2
Plcb3	phospholipase C, beta 3
Plcd1	phospholipase C, delta 1
Plce1	phospholipase C, epsilon 1
Plcg2	phospholipase C, gamma 2
Plch1	phospholipase C, eta 1
Plch2	phospholipase C, eta 2
Plcl2	phospholipase C-like 2
Plek	pleckstrin
Plek2	pleckstrin 2
Plekha8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8
Plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5
Plk-ps1	polo-like kinase, pseudogene 1
Plxnb1	plexin B1
Plxnb2	plexin B2
Plxnb3	plexin B3
Pno1	partner of NOB1 homolog (S. cerevisiae)
Pnpla8	patatin-like phospholipase domain containing 8
Ppa2	pyrophosphatase (inorganic) 2
Ppan	peter pan homolog (Drosophila)
Ppap2b	phosphatidic acid phosphatase type 2B
Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1); similar to mKIAA1230 protein
Ppfibp2	protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2
Ppil3	peptidylprolyl isomerase (cyclophilin)-like 3
Ppm1b	similar to serine/threonine phosphatase; protein phosphatase 1B, magnesium dependent, beta isoform
Ppm1e	protein phosphatase 1E (PP2C domain containing)
Ppm1f	protein phosphatase 1F (PP2C domain containing)
Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A
Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform
Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform
Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; RIKEN cDNA 3222402P14 gene
Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)
Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
Ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform
Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)
Prex1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1
Prkch	protein kinase C, eta
Prkd3	protein kinase D3

Psat1	similar to Phosphoserine aminotransferase 1; phosphoserine aminotransferase 1
Pscd3	cytohesin 3
Pscdbp	cytohesin 1 interacting protein
Psd	pleckstrin and Sec7 domain containing
Psd4	pleckstrin and Sec7 domain containing 4
Psmg1	proteasome (prosome, macropain) assembly chaperone 1
Ptcd3	pentatricopeptide repeat domain 3
Ptgr2	prostaglandin reductase 2
Ptplad1	protein tyrosine phosphatase-like A domain containing 1
Ptplb	predicted gene 7908; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b
Ptprb	protein tyrosine phosphatase, receptor type, B
Pwp1	PWP1 homolog (S. cerevisiae)
Rab37	RAB37, member of RAS oncogene family
Rab7l1	RAB7, member RAS oncogene family-like 1
Rabgef1	similar to Ras negative regulator Rabex-5/Rin2; RAB guanine nucleotide exchange factor (GEF) 1
Rac3	RAS-related C3 botulinum substrate 3
Racgap1	Rac GTPase-activating protein 1; predicted gene 1859
Rala	v-ral simian leukemia viral oncogene homolog A (ras related)
Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)
Ralbp1	ralA binding protein 1
Ralgapa2	Ral GTPase activating protein, alpha subunit 2 (catalytic)
Ralgapb	Ralgapb Ral GTPase activating protein, beta subunit (non-catalytic)
Ralgds	ral guanine nucleotide dissociation stimulator
Ralgps1	Ral GEF with PH domain and SH3 binding motif 1
Ralgps2	Ral GEF with PH domain and SH3 binding motif 2
Ranbp10	RAN binding protein 10
Ranbp3	RAN binding protein 3
Rap1b	RAS related protein 1b; similar to GTP-binding protein (smg p21B)
Rap1gap	Rap1 GTPase-activating protein
Rap1gds1	similar to RAP1, GTP-GDP dissociation stimulator 1; RAP1, GTP-GDP dissociation stimulator 1
Rap2a	RAS related protein 2a
Rap2b	RAP2B, member of RAS oncogene family
Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1
Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2
Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3
Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4
Rapgefl1	Rap guanine nucleotide exchange factor (GEF)-like 1
Rarg	retinoic acid receptor, gamma
Rasa2	RAS p21 protein activator 2
Rasa3	RAS p21 protein activator 3
Rasa4	RAS p21 protein activator 4
Rasal1	RAS protein activator like 1 (GAP1 like)
Rasd1	RAS, dexamethasone-induced 1
Rasd2	RASD family, member 2
Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1
Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2
Rasgrp1	RAS guanyl releasing protein 1
Rasgrp2	RAS, guanyl releasing protein 2

Rasgrp3	RAS, guanyl releasing protein 3
Rasgrp4	RAS guanyl releasing protein 4
Rasl11b	RAS-like, family 11, member B
Rbj	DnaJ (Hsp40) homolog, subfamily C, member 27
Rbm27	RNA binding motif protein 27
Rcl1	RNA terminal phosphate cyclase-like 1
Rell1	RELT-like 1
Rell2	RELT-like 2
Rem1	rad and gem related GTP binding protein 1
Reps1	RalBP1 associated Eps domain containing protein
Reps2	RALBP1 associated Eps domain containing protein 2
Rgnef	Rho-guanine nucleotide exchange factor
Rgs1	regulator of G-protein signaling 1
Rgs10	regulator of G-protein signalling 10
Rgs11	regulator of G-protein signaling 11; similar to regulator of G-protein signaling 11
Rgs12	regulator of G-protein signaling 12
Rgs13	regulator of G-protein signaling 13
Rgs14	regulator of G-protein signaling 14
Rgs16	regulator of G-protein signaling 16
Rgs17	regulator of G-protein signaling 17
Rgs18	regulator of G-protein signaling 18
Rgs19	regulator of G-protein signaling 19; similar to Regulator of G-protein signaling 19
Rgs2	regulator of G-protein signaling 2
Rgs20	regulator of G-protein signaling 20
Rgs22	regulator of G-protein signalling 22
Rgs3	regulator of G-protein signaling 3
Rgs4	regulator of G-protein signaling 4
Rgs5	regulator of G-protein signaling 5
Rgs6	regulator of G-protein signaling 6
Rgs7	regulator of G protein signaling 7
Rgs7bp	regulator of G-protein signalling 7 binding protein
Rgs8	regulator of G-protein signaling 8
Rgs9	regulator of G-protein signaling 9
Rgs9bp	regulator of G-protein signalling 9 binding protein
Rhbdl1	rhomboid, veinlet-like 1 (Drosophila)
Rheb	Ras homolog enriched in brain; similar to RAS-homolog enriched in brain
Rhebl1	Ras homolog enriched in brain like 1
Rhod	ras homolog gene family, member D
Rhog	ras homolog gene family, member G
Rhoh	ras homolog gene family, member H
Rhoj	ras homolog gene family, member J
Rhoq	ras homolog gene family, member Q
Rhot1	ras homolog gene family, member T1
Rhot2	ras homolog gene family, member T2
Rhou	ras homolog gene family, member U
Rhov	ras homolog gene family, member V
Rhpn2	rhophilin, Rho GTPase binding protein 2
Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)

Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)
Rin1	Ras and Rab interactor 1
Riok1	RIO kinase 1 (yeast)
Riok2	RIO kinase 2 (yeast)
Riok3	RIO kinase 3 (yeast)
Ripk4	receptor-interacting serine-threonine kinase 4
Rit1	Ras-like without CAAX 1
Rit2	Ras-like without CAAX 2
Rnd1	Rho family GTPase 1
Rnd3	Rho family GTPase 3
Rnu5g	RNA, U5G small nuclear
Rod1	ROD1 regulator of differentiation 1 (S. pombe)
Ropn1	ropporin, rhophilin associated protein 1
Rpl28	predicted gene 13226; predicted gene 15435; ribosomal protein L28; predicted gene 12938
Rpl35	ribosomal protein L35; predicted gene 10269; predicted gene 8444; predicted gene 2000; predicted gene 4342
Rpl36al	ribosomal protein L36A-like
Rpl37	ribosomal protein L37
Rpl37a	ribosomal protein L37a; predicted gene 4149; predicted gene 4613; predicted gene 14251; predicted gene 14173
Rpl8	ribosomal protein L8; similar to 60S ribosomal protein L8
Rps28	ribosomal protein S28
Rps29	ribosomal protein S29
Rps6kc1	ribosomal protein S6 kinase polypeptide 1
Rras	Harvey rat sarcoma oncogene, subgroup R
Rras2	related RAS viral (r-ras) oncogene homolog 2
Rrp15	ribosomal RNA processing 15 homolog (S. cerevisiae)
Rsu1	Ras suppressor protein 1
Rtcd1	RNA terminal phosphate cyclase domain 1
Rtkn	rhotekin
Rufy2	RUN and FYVE domain-containing 2
Rwdd1	predicted gene 12693; RWD domain containing 1; predicted gene 13743
S100a16	S100 calcium binding protein A16
Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)
Samd9l	sterile alpha motif domain containing 9-like
Sap30bp	similar to transcriptional regulator protein; SAP30 binding protein
Saps3	SAPS domain family, member 3
Sav1	similar to WW45 protein; salvador homolog 1 (Drosophila)
Sbk1	SH3-binding kinase 1
Sc4mol	sterol-C4-methyl oxidase-like
Scand1	SCAN domain-containing 1
Sdad1	SDA1 domain containing 1; similar to SDA1 domain containing 1
Sec14l3	SEC14-like 3 (S. cerevisiae)
Sec14l4	SEC14-like 4 (S. cerevisiae)
Sec16b	SEC16 homolog B (S. cerevisiae)
Sectm1a	secreted and transmembrane 1A
Sectm1b	secreted and transmembrane 1B
Sept14	septin 14
Serinc1	serine incorporator 1
Serinc2	serine incorporator 2; hypothetical protein LOC100044221

Serinc3	serine incorporator 3
Serinc4	Serinc4 serine incorporator 4
Serinc5	serine incorporator 5
Sfxn4	sideroflexin 4
Sgsm1	small G protein signaling modulator 1
Sgsm2	small G protein signaling modulator 2
Sgsm3	small G protein signaling modulator 3
Sh2d3c	SH2 domain containing 3C
Sh3bgrl	SH3-binding domain glutamic acid-rich protein like
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)
Sidt1	SID1 transmembrane family, member 1
Sirpb1	signal-regulatory protein beta 1
Slc10a7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7
Slc25a21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
Slc25a41	solute carrier family 25, member 41
Slc33a1	solute carrier family 33 (acetyl-CoA transporter), member 1
Slc35a4	predicted gene 5866; solute carrier family 35, member A4
Slc35b2	solute carrier family 35, member B2
Slc41a3	solute carrier family 41, member 3
Slfn4	schlafen 4
Slfn9	similar to putative protein; schlafen 9; similar to schlafen 9
Slitrk2	SLIT and NTRK-like family, member 2
Slitrk4	SLIT and NTRK-like family, member 4
Sltm	SAFB-like, transcription modulator
Smad-ps1	MAD homolog, pseudogene 1 (Drosophila)
Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A
Snx13	sorting nexin 13
Snx21	sorting nexin family member 21
Snx26	sorting nexin family member 26
Sos1	son of sevenless homolog 1 (Drosophila)
Sos2	son of sevenless homolog 2 (Drosophila)
Spata17	spermatogenesis associated 17
Spata3	spermatogenesis associated 3
Specc1	sperm antigen with calponin homology and coiled-coil domains 1
Spg21	spastic paraplegia 21 homolog (human); similar to spastic paraplegia 21 homolog
Spin2	spindlin family, member 2
Spire2	spire homolog 2 (Drosophila)
Spnb5	spectrin beta 5
Spryd4	SPRY domain containing 4
Srgap1	SLIT-ROBO Rho GTPase activating protein 1
Srgap2	SLIT-ROBO Rho GTPase activating protein 2
Srgap3	SLIT-ROBO Rho GTPase activating protein 3
St5	suppression of tumorigenicity 5
Stard10	START domain containing 10
Stard9	START domain containing 9
Stk33	serine/threonine kinase 33
Suclg1	succinate-CoA ligase, GDP-forming, alpha subunit
Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1

Syap1	synapse associated protein 1
Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)
Tbc1d2	TBC1 domain family, member 2
Tcf25	transcription factor 25 (basic helix-loop-helix)
Tex2	testis expressed gene 2
Tg(tgfb1)1der	transgene insertion 1, Dennis R Roop
Tiam2	T-cell lymphoma invasion and metastasis 2
Timm44	translocase of inner mitochondrial membrane 44
Tlk2	predicted gene 13161; tousled-like kinase 2 (Arabidopsis)
Tln2	talin 2
Tm4sf5	transmembrane 4 superfamily member 5
Tm9sf1	transmembrane 9 superfamily member 1
Tm9sf3	transmembrane 9 superfamily member 3
Tmem11	transmembrane protein 11
Tmem150	transmembrane protein 150
Tmem159	transmembrane protein 159
Tmem16e	transmembrane protein 16e
Tmem16f	transmembrane protein 16f
Tmem22	transmembrane protein 22
Tmem30b	transmembrane protein 30B
Tmem30c	transmembrane protein 30C
Tmem33	transmembrane protein 33
Tmem8	transmembrane protein 8 (five membrane-spanning domains)
Tmem85	transmembrane protein 85
Tnik	TRAF2 and NCK interacting kinase
Tnk1	tyrosine kinase, non-receptor, 1
Tnk2	tyrosine kinase, non-receptor, 2
Tob2	transducer of ERBB2, 2
Tomm7	similar to translocase of outer mitochondrial membrane 7 homolog; translocase of outer mitochondrial membrane 7 homolog (yeast)
Tpd52-ps	tumor protein D52, pseudogene
Tpt1p	predicted gene 1974; tumor protein, translationally-controlled 1 pseudogene; tumor protein, translationally-controlled 1; predicted gene 14456
Tpt1-ps1	tumor protein, translationally-controlled, pseudogene 1
Trappc9	trafficking protein particle complex 9
Trcg1	taste receptor protein 1
Trim14	tripartite motif-containing 14
Trim45	tripartite motif-containing 45
Trim47	tripartite motif-containing 47
Trim69	tripartite motif-containing 69
Trio	triple functional domain (PTPRF interacting)
Trnp1	TMF1-regulated nuclear protein 1
Trp53i13	transformation related protein 53 inducible protein 13
Trp53tg5	transformation related protein 53 target 5
Trpd52l3	tumor protein D52-like 3
Trpt1	tRNA phosphotransferase 1
Tssk3	testis-specific serine kinase 3
Ttc1	tetratricopeptide repeat domain 1
Tulp3	tubby-like protein 3
Twf2	twinfilin, actin-binding protein, homolog 2 (Drosophila)

Ube2w	ubiquitin-conjugating enzyme E2W (putative)
Ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)
Ubtd2	ubiquitin domain containing 2
Ubxd5	UBX domain protein 11
Umpk-ps	uridine monophosphate kinase, pseudogene
Unc50	unc-50 homolog (C. elegans)
Usmg5	upregulated during skeletal muscle growth 5
Usp6nl	USP6 N-terminal like
Usp-ps	ubiquitin specific peptidase, pseudogene (USP17 homolog)
Vav1	vav 1 oncogene
Vav2	vav 2 oncogene
Vrk3	vaccinia related kinase 3
Wdr12	WD repeat domain 12; predicted gene 4879
Wdr13	WD repeat domain 13
Wdr16	WD repeat domain 16
Wdr25	WD repeat domain 25
Wdr3	WD repeat domain 3
Wdr45	WD repeat domain 45
Wdr6	WD repeat domain 6
Xrra1	X-ray radiation resistance associated 1
Yme1l1	YME1-like 1 (S. cerevisiae)
Ypel1	yippee-like 1 (Drosophila)
Ypel3	yippee-like 3 (Drosophila)
Zdhhc16	zinc finger, DHHC domain containing 16
Zdhhc7	zinc finger, DHHC domain containing 7
Zfand2a	zinc finger, AN1-type domain 2A
Zfand6	zinc finger, AN1-type domain 6
Zfp113	zinc finger protein 113
Zfp12	zinc finger protein 12
Zfp212	Zinc finger protein 212
Zfp263	zinc finger protein 263
Zfp319	zinc finger protein 319
Zfp322a	zinc finger protein 322A
Zfp326	zinc finger protein 326
Zfp383	zinc finger protein 383
Zfp414	zinc finger protein 414
Zfp418	zinc finger protein 418
Zfp445	zinc finger protein 445
Zfp449	zinc finger protein 449
Zfp458	zinc finger protein 458
Zfp58	zinc finger protein 58
Zfp612	zinc finger protein 612
Zfp622	zinc finger protein 622
Zfp641	zinc finger protein 641
Zfp689	zinc finger protein 689
Zfp74	zinc finger protein 74; hypothetical protein LOC100044255
Zfp97	zinc finger protein 97; cDNA sequence BC018101
Zfyve27	zinc finger, FYVE domain containing 27

Table S21. *Textrous!*-mediated Collective mode analysis of bPTH(7-34) superconserved dataset. For each identified word the Cosine Similarity, Z score and P value are given.

Word	Cosine Similarity	Z score	P value
creb-binding	0.459745268	2.016553221	0.021847757
protein-binding	0.449445286	1.97336052	0.024247781
acetyltransferases	0.444120311	1.951030381	0.025528523
acetylated	0.436610839	1.919539608	0.02742895
coactivators	0.43261819	1.902796541	0.028520273
acetylation	0.431672402	1.898830404	0.028782238
trans-activation	0.428811772	1.886834429	0.029580163
acetyltransferase	0.425936906	1.874778755	0.030396362
quercetin	0.423964122	1.866505938	0.030950794
coactivator	0.420383922	1.851492464	0.032084777
adenovirus	0.415617483	1.83150453	0.03347571
transactivation	0.415567477	1.831294832	0.033550272
smad	0.413212156	1.821417853	0.034303428
nonhistone	0.410089164	1.808321671	0.03530325
acetylase	0.410013788	1.808005581	0.03530325
transactivators	0.407318747	1.796704	0.03616781
sclera	0.403944073	1.782552394	0.037293152
scleroderma	0.403068556	1.778880937	0.037619881
staurosporine	0.401880926	1.773900642	0.038031575
tad	0.400530617	1.768238159	0.038530452
anti-apoptotic	0.397999305	1.757623167	0.039373755
non-histone	0.394498279	1.742941707	0.040666807
hdac	0.392242588	1.733482529	0.041547834
amp-responsive	0.388605941	1.718232345	0.042898308
hydroxamic	0.385954824	1.707114956	0.043911026
deacetylase	0.376771575	1.668605246	0.04755869
vpr	0.376519156	1.667546732	0.047657863
collagen	0.37413997	1.657569682	0.048658733
transactivator	0.371999701	1.64859452	0.049573817
connective	0.368116069	1.63230861	0.051339743
jurkat	0.364922136	1.618914939	0.052723632
procollagen	0.363385396	1.612470662	0.05348097
activation	0.360721361	1.601299101	0.05468846
nucleosomal	0.357752231	1.588848133	0.056030196
element-binding	0.355503802	1.579419407	0.057168029
imperfecta	0.353969212	1.572984144	0.057859409

histones	0.352819634	1.568163419	0.058440566
apoptosome	0.348169941	1.548665054	0.06069086
cofactors	0.347410836	1.545481769	0.061173132
histone	0.346418258	1.541319418	0.061658393
pro	0.341666567	1.52139333	0.064129919
osteogenesis	0.340984912	1.518534827	0.064381248
t-lymphotropic	0.337888258	1.505549092	0.066033587
collagens	0.336931199	1.501535689	0.066548554
dermal	0.332460284	1.482787025	0.069037205
chloromethyl	0.329871973	1.471933013	0.070510439
phosphorylation	0.329835078	1.471778292	0.070510439
end-labeling	0.329669832	1.47108534	0.070645558
oncoproteins	0.329383449	1.469884398	0.070780877
intrinsic	0.329274214	1.469426325	0.070916395
heat-shock	0.326947039	1.45966738	0.072145037
pkc-delta	0.326056935	1.455934753	0.07269631
fibroblasts	0.325368727	1.453048771	0.073111877
deacetylases	0.323401838	1.444800674	0.074228943
protease-activating	0.323162783	1.443798201	0.074369488
ccaat	0.323146509	1.443729957	0.074369488
decorin	0.32304198	1.443291616	0.074510236
caspases	0.321265962	1.435843932	0.075501171
col	0.320407968	1.432245959	0.076071911
tendon	0.319946234	1.430309689	0.07635851
tendons	0.319265119	1.427453452	0.076789947
shock	0.316056957	1.414000109	0.078680951
ehlers-danlos	0.315559619	1.411914536	0.078974981
camp-responsive	0.315224272	1.410508269	0.079122307
heat	0.315166091	1.410264287	0.079269841
alpha-crystallin	0.314969832	1.409441279	0.079417584
hsp	0.31455087	1.407684374	0.079565535
caspase	0.314333853	1.406774321	0.079713694
apoptosis	0.313570236	1.40357211	0.080159425
initiator	0.312559165	1.399332211	0.080906492
trimerization	0.309336399	1.385817627	0.082873452
chaperone	0.308470571	1.382186801	0.083485851
apoptotic	0.307902806	1.379805896	0.083793322
pro-apoptotic	0.30767495	1.378850387	0.083947377
inhibited	0.306252859	1.372886887	0.084876173
trans-activator	0.30548752	1.369677457	0.085343451
gabp	0.304073525	1.363747905	0.086283783

remodeling	0.3020365	1.355205694	0.087708779
c-myb	0.300593016	1.349152484	0.088668483
phosphopeptides	0.29991948	1.34632803	0.089151258
templates	0.299888151	1.346196652	0.089151258
factor-beta	0.299763899	1.345675605	0.089151258
unfolding	0.299551254	1.344783881	0.089312617
antagonist-killer	0.298446462	1.340150965	0.090122672
collagenase	0.295642567	1.328392906	0.092089053
acetyl	0.294708821	1.324477268	0.092751522
fractures	0.294061833	1.321764143	0.093084075
palpebral	0.293551128	1.319622514	0.093417509
inhibition	0.293049129	1.317517396	0.093751824
s-nitroso-n-acetylpenicillamine	0.292534647	1.31535993	0.094254951
myofibroblast	0.291493468	1.310993772	0.094928882
potentiated	0.289268678	1.301664172	0.096458193
heteroduplexes	0.289024752	1.300641278	0.096629227
fracture	0.288873762	1.300008106	0.096800485
translocated	0.288856721	1.299936643	0.096800485
chondrocyte-specific	0.287413027	1.293882551	0.09783271
antihuman	0.286477873	1.289961006	0.098525329
zap	0.285949531	1.28774542	0.098872982
transforming	0.285533483	1.286000734	0.099221531
bromide	0.285149076	1.284388732	0.099570978

Table S22. Textrous!-based noun extraction from theoretical and empirically-derived transcriptomic datasets. The *Textrous!*-extracted nouns associated with the input transcript terms from the LSI-derived 'arrestin signaling' theoretical dataset and the superconserved datasets from hPTH(1-34)- and bPTH(7-34)-treated mice are denoted in each column. Nouns in standard type were extracted using the Collective *Textrous!* processing module and the nouns in italics were extracted using the Individual *Textrous!* processing module.

LSI-derived 'arrestin signaling'	hPTH(1-34) superconserved	bPTH(7-34) superconserved
phosphorylation	presenilin	creb-binding
kinase	presenilins	protein-binding
serine-threonine	gamma-secretase	acetyltransferases
phosphorylating	beta-peptide	acetylated
rapamycin	beta-protein	coactivators
amp-dependent	fad	acetylation
camp-dependent	amyloid	trans-activation
pka	paraparesis	acetyltransferase
pkc-alpha	aspartyl	quercetin
transduction	beta-amyloid	coactivator
phosphopeptides	amyloidogenic	adenovirus
catalytic	precursor	transactivation
c-akt	early-onset	smad
phosphoamino	alzheimer's	nonhistone
cascades	nf-kappab	acetylase
c-alpha	beta-secretase	transactivators
forskolin	nf-kappa	sclera
cgmp-dependent	dysarthria	scleroderma
c-beta	spastic	staurosporine
a-kinase	kappab	tad
downstream	alzheimer	anti-apoptotic
beta-galactoside	ikappabalpha	non-histone
activation	ikappab	hdac
phosphopeptide	ikk	amp-responsive
phosphoserine	c-rel	hydroxamic
kinases	gsk	deacetylase
amp-activated	senile	vpr
phosphospecific	familial	collagen
phosphatidylinositol	nf-kb	transactivator
cyclic	sulfide	connective
galphaq	knock-in	jurkat
anchor	hydrophilic	procollagen
cascade	impairments	activation
photons	late-onset	nucleosomal
serine	cleavages	element-binding
pkc-delta	factor-kappab	imperfecta
holoenzymes	angiopathy	histones
phosphorylations	single-photon	apoptosome

cenocepacia	phenethyl	cofactors
pumping	deficits	histone
rhodopsin	neuritic	pro
receptor-mediated	hemorrhages	osteogenesis
gmp-dependent	lanthanum	t-lymphotropic
gs	onset	collagens
monophosphate	caffeic	dermal
cross-talk	inulin	phosphorylation
sector	age-related	chloromethyl
methanobacterium	neurogenesis	end-labeling
bleaching	myoclonus	oncoproteins
diacylglycerol	emission-computed	intrinsic
phosphatidylinositide	deposits	heat-shock
dbcamp	dantrolene	pkc-delta
sialyltransferase	presymptomatic	fibroblasts
phosphoinositide	sulfonamides	deacetylases
activated	proteolytic	protease-activating
heterotrimeric	nf	ccaat
aicar	neurotoxic	decorin
phorbol	plaques	caspases
pkc-epsilon	cleavage	col
okadaic	b-dna	tendon
arrestin	pharynx	tendons
beta-adrenergic	kikuchi	shock
stimulation	jejuni	ehlers-danlos
biosensors	co-immunoprecipitations	camp-responsive
dag	comment	heat
raft	mercury	alpha-crystallin
beta-ar	deposit	hsp
alpha-subunit	hsu	caspase
signaling	congo	apoptosis
riboside	deoxycholate	initiator
pdgfr	stearic	trimerization
phototransduction	curcumin	chaperone
hormone-sensitive	synaptosomal	apoptotic
particulate	brains	pro-apoptotic
lipofuscin	ki	inhibited
subunit	disruptions	trans-activator
cyclase	mini	gabp
methanothermobacter	cutting	remodeling
couple	fragments	c-myb
rafts	herb	phosphopeptides
pigment	cleaving	templates
rii	mexico	factor-beta
opsin	proteolysis	unfolding
peutz-jeghers	cyclo-oxygenase	antagonist-killer
phosphatidyl	pre-clinical	collagenase
gtp-binding	pathology	acetyl

lamellipodia	emsa	fractures
adenyl	flippase	palpebral
esters	photolysis	inhibition
tyrosyl	neprilysin	s-nitroso-n-acetylpenicillamine
pathways	spheroid	myofibroblast
calmodulin-dependent	sulindac	potentiated
opsins	subiculum	heteroduplexes
cone	brdu	fracture
beta-subunit	myoclonic	translocated
nak	high-molecular-weight	chondrocyte-specific
isoproterenol	headache	antihuman
ceramide	confusion	zap
cones	account	transforming
cats	channel-interacting	bromide
opsins	*oxidation*	*phosphorylation*
pigment	*clone*	*phosphopeptide*
rhodopsin	*exons*	*kinase*
opsin	*sequence*	*phosphorylating*
visual	*introns*	*serine-threonine*
vision	*exon*	*activation*
photons	*amino*	*amp-activated*
camp-dependent	*clones*	*phosphopeptides*
bleaching	*cdna*	*pkc-delta*
catalytic	*lectin*	*aicar*
cgmp-dependent	*mitochondrial*	*a-kinase*
lipofuscin	*ophthalmoplegia*	*c-akt*
kinase	*oxidants*	*cenocepacia*
degeneration	*chromatographies*	*downstream*
beta-galactoside	*purified*	*phosphoamino*
retina	*encoded*	*cgmp-dependent*
rods	*structural*	*rapamycin*
cone	*coding*	*dbcamp*
g-protein	*isolated*	*mitochondrial*
retinitis	*congenital*	*gtpase*
cones	*alpha-aminoadipate*	*gtpase-activating*
photoreceptors	*conservation*	*amp-dependent*
photoreceptor	*geobacillus*	*ribonucleoside*
photosensitive	*adipocytes*	*pka*
esters	*formylated*	*transduction*
electroretinography	*homology*	*camp-dependent*
pigmentosa	*reading*	*gtp-binding*
degenerations	*cytosolic*	*pkc-alpha*
rod	*pseudogene*	*okadaic*
amaurosis	*mitochondria*	*kinases*
retinal	*bird*	*gastrocnemius*
retinas	*transcripts*	*hormone-sensitive*
photopic	*identical*	*phosphorylations*
scotopic	*fatty*	*coiled-coil*

degenerative	*analysis*	*lamellipodia*
pupillary	*alternative*	*c-alpha*
phosphodiesterase	*amplified*	*biosensors*
amp-dependent	*isolation*	*gtp-dependent*
receptors	*transcript*	*forskolin*
leber	*identification*	*mitochondria*
phototransduction	*sequences*	*anchor*
arrestin	*habitats*	*catalytic*
beta-subunit	*mutational*	*gelsolin*
g-protein-coupled	*fingers*	*riboside*
rod-cone	*early-onset*	*phosphatidylinositol*
illumination	*genomics*	*pkc-epsilon*
blind	*autosomal*	*oligomycin*
methanobacterium	*amyloid*	*guanine*
blindness	*counseling*	*cytoskeleton*
pka	*hot*	*exchange*

Table S23. ***Textrous!*****-mediated Collective mode noun-phrase analysis of bPTH(7-34) superconserved dataset**. For each identified noun-phrase the Cosine Similarity score is given.

Collective: noun-phrases	**Cosine Similarity**
aberrant chromatin acetylation	0.396099471
abnormal apoptotic response	0.261078909
abnormal collagenase	0.206897569
abnormal histone acetylation	0.405230509
abnormal histone acetylation	0.405230509
abnormal tubulin acetylation	0.389735145
absent deep tendon	0.184642253
absent deep tendon reflexes	0.165766921
absent phosphorylation	0.32413618
accelerated apoptotic death	0.271510356
acetyl	0.294695351
acetyl group	0.163036767
acetyl groups	0.172034786
acetylase	0.410012973
acetylated	0.436594697
acetylated actin	0.135882134
acetylated alpha-tubulin	0.414708313
acetylated bovine serum albumin	0.190951071
acetylated chromatin	0.349610414
acetylated histone	0.380570676
acetylated histone	0.380570676
acetylated histone binding	0.384968165
acetylated histone binding	0.384968165
acetylated histone levels	0.367981875
acetylated histone levels	0.367981875
acetylated histones	0.423136915
acetylated histones	0.423136915
acetylated low density lipoprotein	0.114103766
acetylated low-density lipoprotein	
acetylated lysine	0.390013511
acetylated n-terminal alanine	0.380599283
acetylated nucleosomes	0.418477984
acetylated residues	0.383716106
acetylated substrates	0.421835814
acetylated tubulin peptide	0.16778485
acetylation	0.431650017

acetylation carcinogenic amines	0.400130634
acetylation defects	0.4001759
acetylation polymorphism	0.343522778
acetylation state	0.430887876
acetylation status	0.426927946
acetyl-coa acetyltransferases	0.438572418
acetyltransferase	0.425934545
acetyltransferase activity	0.441590817
acetyltransferase domain	0.389401658
acetyltransferases	0.444106332
acidic activation	0.361541431
acidic activation domain	0.358800912
acidic transactivator domain	0.174728427
actin remodeling	0.032291199
actin skeleton remodeling machinery	0.036624943
activated acetyl residues	0.229941449
activated caspases	0.357196744
activated fibroblasts	0.385954899
activated heat shock loci	0.315290693
activated heat shock loci	0.315290693
activated heat-shock factor transcription factors	0.33801528
activated histone marks	0.377619041
activated smad	0.466231727
activating heat-shock genes	0.284113609
activation	0.360768213
activation assay	0.377901875
activation cascade	0.358063939
activation contraction	0.36441909
activation curves	0.360244811
activation domain	0.361175696
activation energies	0.360373595
activation energy	0.363151478
activation factors	0.366309911
activation mechanism	0.3598018
activation programs	0.3600776
activation reaction	0.360880066
activation segment phosphorylation	0.403910359
activation segment phosphorylation	0.403910359
activation sites	0.363686456
activation state	0.358868743
activation states	0.360235646

active caspases	0.329055311
active collagenase	0.310872931
active histone deacetylase complex	0.355299093
active histone deacetylase complex	0.355299093
active histone marks	0.350790074
active remodeling	0.308737627
acute septic shock	0.277959643
acute transforming retroviruses	0.230883491
additive inhibition	0.2794893
adenovirus	0.415612797
adenovirus biology	0.392747452
adenovirus dna replication	
adenovirus dna-binding protein	0.187454477
adenovirus infection	0.062340214
adenovirus lacz	0.169625734
adenovirus late infection	0.04343772
adenovirus life cycle	0.058481091
adenovirus major late promoter	0.210490854
adenovirus particles	0.297730462
adenovirus protein	0.235655398
adenovirus replication	-0.010630327
adenovirus trafficking	0.072938056
adenovirus transfer	0.201467247
adenovirus vector	0.413672218
adenovirus vectors	0.375124044
adult bone remodeling	0.098635787
adult fibroblasts	0.243316147
adventitial fibroblasts	0.330730879
aging stromal fibroblasts	0.240708117
airway collagen deposition	0.368984986
ala partially inhibited transport activity	0.089791641
allergen activation	0.358170494
alpha-amanitin inhibition	0.289322164
alpha-crystallin	0.31493555
alpha-crystallin domain	0.199434952
alpha-crystallin domain characteristic	0.18273001
alpha-crystallin expression	
alpha-tubulin acetylation	0.426918014
alveolar remodeling	0.145452159
alveolar remodeling response	0.138469208
amelogenesis imperfecta	0.364336504

amelogenesis imperfecta type iii	0.323246803
amino-terminal activation domain	0.360715612
amino-terminal caspase recruitment domain	0.352882155
amino-terminal transactivation domain	0.375198032
amnion fibroblasts	0.315221557
amp-responsive	0.388555037
angiogenic remodeling	0.213059045
angiogenic vascular remodeling	0.142235604
ankyrin repeat-containing cofactors	0.016953871
antagonist-killer	0.298482878
antiangiogenic collagen fragments	0.371183699
anti-apoptotic	0.39798591
anti-apoptotic agent	0.375892248
anti-apoptotic effects	0.289351002
anti-apoptotic genes	
anti-apoptotic mechanisms	0.331636432
antibiotic staurosporine	0.290806038
antibody inhibition	0.243469534
antigen presentation coactivators	
antihuman	0.286414077
antisense inhibition	0.263149497
antisense inhibition experiments	0.232622316
antisense oligonucleotide inhibition	0.249490818
aortic wall collagen	0.371634589
apical caspase	0.292515739
apoptosis	0.313576191
apoptosis assay	0.323136455
apoptosis concomitant	0.31231047
apoptosis factor aif	0.323454591
apoptosis induction	0.311170814
apoptosis inhibition	0.345251127
apoptosis inhibition	0.345251127
apoptosis inhibitor	0.351669821
apoptosis mediated	0.323576053
apoptosis protein	0.321948176
apoptosis protein binding motif	0.342275422
apoptosis rates	0.309583242
apoptosis reduction	0.309081608
apoptosis regulator	0.308056019
apoptosis repeat	0.305158083
apoptosis required interaction	0.327357067

apoptosis resistance	0.306879861
apoptosis signal	0.313598589
apoptosis signal-regulating kinase	0.339115412
apoptosis substrates	0.314717213
apoptosome	0.34817123
apoptosome complex	
apoptosome formation	0.260292205
apoptotic	0.307900989
apoptotic activities	0.317662967
apoptotic activity	0.367642438
apoptotic bodies	0.285988762
apoptotic body formation	0.256882892
apoptotic cardiac myocytes	0.23403684
apoptotic cardiomyocyte death	0.310808667
apoptotic cardiomyocytes	0.308742167
apoptotic cascades	0.311939609
apoptotic cell death	0.240677466
apoptotic cell feeding	0.218125465
apoptotic challenge	0.292510953
apoptotic chromatin	0.379598928
apoptotic competence	0.30569955
apoptotic conditions	0.30806602
apoptotic control	0.2922081
apoptotic corpses	0.307580007
apoptotic death	0.295393754
apoptotic defects	0.226182861
apoptotic degeneration	0.212971776
apoptotic destruction	0.291702207
apoptotic domains	0.304329542
apoptotic effect	0.313912448
apoptotic effects	0.305259288
apoptotic elimination	0.294800832
apoptotic events	0.300971567
apoptotic fraction	0.298231274
apoptotic hepatocyte cell death	0.244794758
apoptotic hepatocytes	0.28539229
apoptotic inducer	0.313806897
apoptotic inducers	0.309157496
apoptotic induction	0.291286199
apoptotic initiator caspase	0.331940591
apoptotic initiator caspase	0.331940591

apoptotic initiator caspase	0.331940591
apoptotic injury	0.269172476
apoptotic keratinocytes	0.248086809
apoptotic kinetics	0.280833163
apoptotic leukocytes	0.311462566
apoptotic loss	0.237370334
apoptotic machinery	0.306597843
apoptotic markers	0.294755566
apoptotic mechanism	0.323818286
apoptotic mechanisms	0.298262957
apoptotic mimicry	0.30838689
apoptotic muscle degeneration	0.232949227
apoptotic neutrophils	0.255563633
apoptotic nuclei	0.289849927
apoptotic outcome	0.303480034
apoptotic pathway	0.257041565
apoptotic pathways	0.288908273
apoptotic process	0.297217585
apoptotic processes	0.303081898
apoptotic program	0.305754446
apoptotic programs	0.30817811
apoptotic proteases	0.285914668
apoptotic proteins	0.258489327
apoptotic reagent staurosporine	0.324488828
apoptotic reagent staurosporine	0.324488828
apoptotic regression	0.282200737
apoptotic regulators	0.278819107
apoptotic response	0.286822781
apoptotic responses	0.220077225
apoptotic retardation	0.279662593
apoptotic selective pressure	0.278433345
apoptotic sensitivity	0.270258341
apoptotic signal	0.297206593
apoptotic signals	0.293338059
apoptotic stimulus	0.305541569
apoptotic stress	0.310801284
apoptotic targets	0.295091878
arch artery remodeling	0.225242591
arterial remodeling	0.238970688
arterial wall remodeling	0.197649351
astrocyte activation	0.37221367

asymmetric remodeling	0.225558896
atp-dependent chromatin remodeling activity	0.316937997
atp-dependent chromatin remodeling mechanisms	0.284149592
atp-dependent nucleosome remodeling	0.336203736
atp-dependent nucleosome remodeling activities	0.33607256
atp-dependent phosphorylation	0.341982419
attenuated apoptosis	0.318361737
atypical collagen complexes	0.376803683
autonomic activation	
autonomous transactivation domain	0.383269989
autosomal dominant hsp	0.233583788
autosomal dominant hypoplastic amelogenesis imperfecta	0.255524358
average fibroblasts	0.328446101
avian fibroblasts	0.30913025
baby hamster fibroblasts	0.304480407
baby hamster kidney fibroblasts	
bacterial chaperone dnaj	0.26609469
bacterial chloramphenicol acetyltransferase	0.374038652
bacterial collagenase	0.172161935
bacterial septic shock	0.280704989
baculoviral caspase inhibitor	0.359890355
basal apoptosis	0.317187876
basal phosphorylation	0.326242602
baseline microvascular endothelial apoptosis	0.30972618
basement membrane collagens	0.136627293
beta-catenin transactivation	
bind acetyl groups	0.219184932
bind collagen	0.381006518
bind phosphopeptides	0.230731995
binding inhibition	0.274342666
blocking apoptosis	0.31947844
blocks apoptosis	0.315275688
blue sclera	0.187322452
bone fracture	0.099248776
bone fracture repair	-0.005509085
bone fractures	0.091891496
bone remodeling	0.124952513
bone remodeling factor	0.133300688
bound collagen	0.377313693
brain-specific chromatin remodeling complexes	0.243053937
brain-specific membrane-bound collagen	0.36795334

broad caspase inhibitor	0.36135948
bromide	0.285129605
bulk histone preparation	0.343058436
calcium-dependent inhibition	0.264378143
calf thymus core histones	0.177198348
calnexin chaperone system	0.268918841
camp-dependent activation	0.384744686
camp-dependent inhibition	0.306514733
camp-dependent phosphorylation	0.323827224
camp-responsive	0.315228826
camp-responsive calcium currents	-0.095067407
camp-responsive element-binding protein phosphorylation	0.376180503
camp-responsive element-binding protein phosphorylation	0.376180503
camp-responsive element-binding protein phosphorylation	0.376180503
camp-responsive genes	
camp-responsive luciferase reporter plasmid	0.117418035
camp-responsive promoter	0.183589626
camp-responsive promoter elements	0.15822255
camp-responsive promoters	0.239060416
camp-responsive region	0.072200623
camp-responsive signaling complex	0.062020426
candidate caspase cleavage site	0.307501562
canonical initiator elements	0.05884172
capsular fibroblasts	0.329349157
carbohydrate response element-binding protein	0.215539183
carboxy-terminal activation helix	0.397403887
carboxy-terminal phosphorylation sites	0.329401881
cardiac myocyte apoptosis	0.325178839
cardiac remodeling	0.153753803
cardiomyocyte apoptosis	0.320751932
cardiovascular remodeling	0.190399652
carnitine acetyltransferase	0.34179356
cartilage collagen	0.372135737
cartilage collagen ii	0.372926683
cartilage-specific collagen	0.37306067
cartilaginous templates	0.335454671
caspase	0.314343755
caspase activation	0.393165646
caspase activation	0.393165646
caspase activation program	0.392539074
caspase activation program	0.392539074

caspase activity	0.343183493
caspase cascade	0.318236297
caspase cascade amplification	0.318951641
caspase cleavage	0.311053765
caspase cleavage fragments	0.311855987
caspase cleavage site	0.316816617
caspase consensus sequence	0.310304589
caspase consensus site	0.325882615
caspase independent	0.312457858
caspase inhibition	0.350710771
caspase inhibition	0.350710771
caspase inhibitor	0.360617495
caspase inhibitor analysis	0.353455905
caspase inhibitors	0.341330158
caspase pathway	0.304583771
caspase processing	0.304270058
caspase production	0.31141313
caspase recruitment domain	0.348794596
caspase sequences	0.303984639
caspase substrate	0.32272679
caspase substrates	0.312335193
caspase zymogen	0.311407911
caspases	0.32127955
catalytic activation	0.362090611
catalytic phosphorylation site	0.328626564
caucasian septic shock patients	
ccaat	0.32315294
ccaat box	0.051865676
ccaat box consensus	0.086360551
ccaat box consensus sequence	0.02542766
ccaat boxes	0.244014539
ccaat displacement protein	0.160254719
ccaat element	0.156669574
ccaat elements	0.097788641
ccaat enhancer-binding protein-binding sites	
ccaat enhancer-binding protein-binding sites	0.237496041
ccaat motif	0.117627318
ccaat sequence	0.055874576
ccaat sequences	0.027039545
cdna templates	-0.017361055
cell intrinsic	0.064374693

cell-specific inhibition	0.235380489
cellular activation	0.371007365
cellular apoptosis	0.326452322
cellular apoptosis machinery	0.326044086
cellular apoptotic response	0.306404939
cellular cofactors binding	0.219808956
cellular heat production	0.328480021
cellular transforming genes	0.185878028
central acetyltransferase domain	0.376097967
central collagen domain	0.380989581
central tendon	0.226277022
cervical carcinoma cells inhibited tumor growth	0.060056106
cgmp-dependent phosphorylation	0.329741348
chaperone	0.30843813
chaperone activities	0.317910081
chaperone activity	0.362098378
chaperone characteristics	0.298630626
chaperone cofactors	0.333277768
chaperone cofactors	0.333277768
chaperone complexes	0.278599317
chaperone diseases	0.300102696
chaperone efficiency	0.296386924
chaperone folding environment	0.304858092
chaperone levels	0.25088189
chaperone protein	0.288401891
chaperone protein substrates	0.276615906
chaperone system	0.280764874
chemical activation	0.364251993
chemical chaperone	0.310988865
chemical hdac inhibitors	0.443055711
chemical inhibition	0.294602085
chemical templates	0.276665542
chicken collagen	0.370636294
chicken histones	0.252015721
chicken type ii procollagen	0.303640056
chimeric transforming oncogenes	0.243067691
chinese hamster fibroblasts	0.304624926
chloramphenicol acetyltransferase	0.430091231
chloramphenicol acetyltransferase activity	0.443921233
chloramphenicol acetyltransferase assay	0.446093554
chloramphenicol acetyltransferase reporter fusions	0.393094256

chloromethyl	0.329889141
choline acetyltransferase	0.38505022
choline acetyltransferase activity	0.406661047
choline acetyltransferase mrna	
chondrocyte-specific	0.287423189
chondrocyte-specific activation	0.378843192
chondrocyte-specific activation	0.378843192
chondrocyte-specific enhancers	0.069238304
chondrocyte-specific expression	0.071414233
chorionic villus fibroblasts	0.300303013
chromatin acetylation	0.406063046
chromatin activation	0.396888343
chromatin remodeling	0.285388938
chromatin remodeling activities	0.287380746
chromatin remodeling complexes	0.251071756
chromatin remodeling enzymes	0.232927283
chromatin remodeling factors	0.268663435
chromatin remodeling protein	0.281334331
chromatin remodeling proteins	0.237304153
chromatin templates	0.222649689
chromatin templates results	0.207816693
chromosome remodeling	0.01697407
chronic inhibition	0.252721011
chronic initiator	0.179987059
c-jun transactivation domain	0.246661853
class ii hdac	0.093652842
class ii hdac activity	0.161165323
class ii hdac deficiency	
class ii hdac kinase	0.206994826
class ii hdac phosphorylation	0.332195679
class ii hdac phosphorylation	0.332195679
class ii histone deacetylases	0.294086772
classic activation	0.361941106
c-myb	0.30059469
c-myb oncogene	
coactivator	0.420384339
coactivator access	0.419663247
coactivator activity	0.434136073
coactivator binding	0.412087714
coactivator binding domain	0.389861167
coactivator complexes	0.40277616

coactivator motif	0.407938605
coactivator peptides	0.393752859
coactivator protein	0.427830814
coactivator proteins	0.399423885
coactivator recognition groove	0.40405431
coactivator recruitment	0.410866589
coactivator release	0.413882095
coactivators	0.432614301
cofactors	0.347400967
cognate histone modifications	0.344016981
col	0.320400649
cold shock domain	0.331875536
collagen	0.374138699
collagen assembly factor decorin	0.387632326
collagen assembly factor decorin	0.387632326
collagen binding	0.395782953
collagen binding reaction	0.393056147
collagen bundles	0.369164177
collagen chains	0.367830962
collagen content	0.373214898
collagen crosslinking	0.37236796
collagen c-terminal domain	0.384540736
collagen deposition	0.374259034
collagen digestion	0.373674208
collagen domain	0.384120698
collagen domains	0.373425199
collagen fiber assembly	0.36944035
collagen fibers	0.371427081
collagen fibril	0.371826318
collagen fibril architecture	0.369796767
collagen fibril arrangement	0.370674996
collagen fibril diameters	0.37163205
collagen folding	0.388172156
collagen gel	0.378719961
collagen gel matrix	0.416545057
collagen glycation	0.373329231
collagen helical modification	0.378951759
collagen helix	0.376620311
collagen helix formation	0.369573908
collagen iib	0.37070256
collagen iii	0.369393099

collagen iii anomaly	0.369986366
collagen iii expression	0.368858924
collagen ix	0.373676939
collagen lattices	0.374288341
collagen maps	0.369817372
collagen matrices	0.375313205
collagen matrix	0.413185363
collagen melting temperature	0.37250423
collagen motif	0.372576953
collagen polypeptides	0.373389984
collagen production	0.370497845
collagen prolyl	0.377282426
collagen promoter	0.400180689
collagen protein	0.388741747
collagen proteins	0.371319496
collagen stimulation	0.38609482
collagen studies	0.371342463
collagen synthesis	0.372325015
collagen triple helices	0.371374129
collagen triple helix	0.372878039
collagen triple helix stability	0.371298995
collagen types	0.37203557
collagen types ii	0.372071049
collagen types ix	0.371718922
collagen xi	0.371916335
collagen xiv	0.372360162
collagen xv	0.369941425
collagen xviii	0.367658962
collagenase	0.295674263
collagenase analysis	0.231625214
collagenase digestion	0.304874142
collagenase inhibition	0.387002425
collagenase inhibition	0.387002425
collagenase inhibitor	0.321801507
collagens	0.336914304
collagens inhibited degranulation	0.400636283
collagens inhibited degranulation	0.400636283
collateral remodeling	0.282508975
colon cancer cells inhibited expression	0.063233592
combined inhibition	0.256576148
common smad	0.374665839

common smad protein	0.302842471
compensatory alternative apoptotic pathways	0.264947977
competitive inhibition	0.286411662
competitive inhibition mechanism	0.276231955
complete inhibition	0.262754324
complete unfolding	0.044759546
concomitant activation	0.361094962
concomitant inhibition	0.280892079
concomitant phosphorylation	0.329194612
concurrent activation	0.357988418
conformational activation	0.394206403
connective	0.368049093
connective tissue	0.149159154
connective tissue abnormalities	0.076226418
connective tissue bed	0.145714363
connective tissue biopsies	0.160247408
connective tissue cells	0.03904405
connective tissue components	0.112162843
connective tissue defects	0.013977811
connective tissue development	0.045039811
connective tissue diseases	0.132043282
connective tissue disorders	0.096478094
connective tissue elements	0.12245687
connective tissue glycoprotein	0.064417144
connective tissue growth factor	0.121116218
connective tissue manifestations	0.133816789
connective tissue matrices	0.173277052
connective tissue metabolism	0.07277148
connective tissue patterning	0.045582868
connective tissue sheath	0.12546997
connective tissue sheet	0.154257476
connective tissue sites	0.161435171
connective tissues	0.14904827
connective tissue-type mast cells	0.011532545
consensus caspase cleavage recognition motif	0.299459299
consensus ccaat boxes	0.226741561
consensus initiator sequences	0.089036002
consensus phosphorylation sites	0.327840919
conserved acetyltransferase activity	0.386837626
conserved aspirin acetylation site	0.408237158
constitutive phosphorylation	0.325819821

contact inhibition	0.280176469
contact inhibition signal	0.230268277
control adenovirus	0.262673056
control adenovirus vector	0.26911987
control fibroblasts	0.292936256
controls tgf-beta activation	0.368286212
cooperative activation	0.36701485
cooperative cofactors	0.33668377
cooperative transactivation	0.413812996
coordinating apoptosis	0.313868165
copper chaperone	0.178816389
core apoptotic pathway	0.273701761
core histone	0.354239571
core histone acetylation	0.414441471
core histone acetylation	0.414441471
core histone mixtures	0.353302751
core histones	0.306441613
corneal fibroblasts	0.292831528
corneal stromal fibroblasts	0.2475993
couples apoptotic signals	0.296640322
creb-binding	0.459747978
creb-binding domain	
creb-binding protein	
creb-binding protein histone acetyltransferase	
creb-binding protein histone acetyltransferase	0.416106378
creb-binding protein histone acetyltransferase	0.416106378
creb-binding regions	
creb-binding sites	
critical acetylation sites	0.429793639
critical apoptotic cell	0.225760044
critical caspase substrate	0.322703565
critical coactivator	0.415201143
critical intrinsic dopamine neuron determinants	-0.026231638
critical phosphorylation site	0.331750312
critical positive coactivator	0.415522245
critical transactivator	0.220226716
cryptic site activation	0.37016447
c-terminal acetyltransferase domain	0.344728565
c-terminal apoptotic domain	0.307200613
c-terminal coactivator interaction domain	0.367828205
c-terminal hdac domain	0.238367972

c-terminal phosphorylation site	0.330888195
c-terminal transactivation	0.378557449
c-terminal transactivation domain	0.337488058
c-terminal transactivation inhibitory domain	0.318381166
cultured chicken fibroblasts	0.319870698
cultured chondrocyte-specific expression	0.123680884
cultured dermal fibroblasts	0.38371691
cultured dermal fibroblasts	0.38371691
cultured dermal sheath cells	0.065607248
cultured fibroblasts	0.355563847
cultured human dermal fibroblasts	0.322199282
cultured human dermal fibroblasts	0.322199282
cultured human dermal lymphatic endothelial cells	0.095958029
cultured human diploid fibroblasts	0.279612149
cultured human fibroblasts	0.288341439
cultured patient fibroblasts	0.345594327
cultured rodent fibroblasts	0.329783374
cultured skin fibroblasts	0.244573403
cultured tendon cells	0.063412361
cyanogen bromide	0.283804033
cyanogen bromide fragments	0.192635549
cyanogen bromide treatment	0.259497477
cyclic amp-dependent inhibition	0.252429293
cyclic phosphorylation	0.336102591
cysteine-rich protein-binding domains	
cytokine-induced activation	0.358302274
cytokine-induced phosphorylation	0.330642857
cytoskeletal remodeling	0.189451751
cytoskeletal remodeling mechanisms	0.18150222
cytosolic chaperone	0.287028873
cytosolic iron chaperone	
cytosolic lipid chaperone	0.21940067
cytosolic phosphorylation	0.334809363
deacetylase	0.37677819
deacetylase activity	0.397786653
deacetylase activity accounts	0.392074687
deacetylase complexes	0.316177763
deacetylases	0.323444767
death receptor-mediated apoptosis	0.311317151
decidual fibroblasts	0.319882644
decorin	0.323069173

decreased activation	0.363984771
decreased apoptosis	0.319611776
decreased apoptotic response	0.292231617
decreased caspase activity	0.351595414
decreased fracture risk	0.058418996
decreased histone acetylation	0.417741325
decreased histone acetylation	0.417741325
decreased inhibition	0.249533668
decreased interstitial collagen deposition	0.379950265
decreased phosphorylation	0.3351596
defective histone acetylation	0.399241468
defective histone acetylation	0.399241468
defective transactivation	0.368718004
deficient decorin expression	
degenerative tendon	0.248739333
dendritic cell intrinsic defect	-0.06525168
dense connective tissue	0.131040099
deprivation-induced apoptosis	0.314669047
dermal	0.332464988
dermal area	0.303269066
dermal biopsies	0.28567316
dermal blood vessels	0.191741343
dermal capillaries	0.325399621
dermal cells	0.035884307
dermal collagen fibrils	0.370467902
dermal collagen fibrils	0.370467902
dermal collagens	0.368281228
dermal collagens	0.368281228
dermal cysts	0.228650162
dermal dendritic cells	-0.027864222
dermal eccrine sweat glands	0.087348412
dermal extracellular matrix	0.290571552
dermal fibroblast cdna libraries	-0.020608782
dermal fibroblasts	0.359781998
dermal fibroblasts	0.359781998
dermal inflammation	0.061094443
dermal layers	0.245123659
dermal leprosy lesions	0.047216694
dermal mast cells	0.019358371
dermal matrix	0.295599092
dermal microvascular endothelial cell cdna library	0.076723841

dermal mosaicism	0.289640009
dermal neovascularization	0.274001694
dermal papilla	0.261991497
dermal papilla cell cdna library	0.020526117
dermal papillae	0.250684845
dermal papillae cells	0.029519272
dermal papillae maturation	0.111712137
dermal ridge pattern	0.149090723
dermal ridges	0.336547165
dermal sinus	0.23388436
dermal substrates	0.238761374
dermal tissue	0.157521997
dermal wounds	0.357392847
descending inhibition	0.285760993
developing sclera	
dids inhibition	0.292086064
differential inhibition	0.245731553
differentiated fibroblasts	0.30559735
diffuse collagen deposition	0.376520977
dihydrolipoamide acetyltransferase	0.423736246
dimethyl histone	0.34669255
diminished apoptotic cell death	0.240994588
diminished histone	0.349773256
diploid fibroblasts	0.313060756
diploid human fibroblasts	0.258315008
direct coactivator target	0.39996829
direct inhibition	0.282654805
direct phosphorylation	0.329600915
disordered collagen fibril orientation	0.370504998
distal ccaat box	
distal fibroblasts	0.310653476
divergent n-terminal coactivator domain	0.388622501
divergent receptor-regulated smad downstream	0.430623481
dna templates	-0.104660621
dna-binding transactivator	0.112809911
dnase activation	0.362863973
dominant inhibition	0.259858937
dominant transactivator	0.186682788
downstream activation	0.362293632
downstream caspase activation	0.398189977
downstream caspase activation	0.398189977

downstream caspases	0.343338662
downstream effector caspases	0.298029137
downstream initiator	0.348829133
downstream remodeling	0.361536101
drug-induced apoptosis	0.319303635
drug-induced inhibition	0.289386277
dual inhibition	0.241890405
dual phosphorylation	0.322397508
dynamic phosphorylation	0.326758152
dynamic phosphorylation mark	0.327377308
dynamic remodeling	0.288425938
early apoptotic events	0.278592241
early passage fibroblasts	0.291150673
early remodeling	0.245447664
early remodeling process	0.218047878
early-onset bone fractures	0.065759782
ebv protein-binding sequence	
ec collagen	0.373835548
effector caspase activation	0.372183619
effector caspase activation	0.372183619
effector caspase activity	0.320759086
effector caspase inhibition	0.329233973
effector caspase inhibition	0.329233973
effector caspases	
ehlers-danlos	0.315556421
ehlers-danlos syndrome	
ehlers-danlos syndrome ii	0.033287619
ehlers-danlos syndrome type	0.104978639
ehlers-danlos syndrome type ii	0.108106442
ehlers-danlos syndrome type vi	0.113942769
ehlers-danlos variant	0.153406644
elastase inhibition	0.24393592
electric activation	0.361059956
electric foot shock	0.313908879
electric shock	0.316705666
electroconvulsive shock	0.316719003
element-binding	0.355503705
elevated apoptosis	0.309724097
elevated histone	0.34349025
elevated phosphorylation	0.32389167
embryo fibroblasts	0.255799068

embryonic blood vascular remodeling	0.109282444
empty adenovirus	0.416225472
end-labeling	0.329684584
endogenous beta-amyloid chaperone	0.253992805
endogenous mouse type ii procollagen	
endogenous phosphorylation	0.324576433
endometrial fibroblasts	0.303567455
endoplasmic reticulum chaperone calreticulin	0.25379896
endoplasmic reticulum chaperone protein	0.246798633
endothelial apoptosis	0.311308889
endothelial remodeling	0.136182729
endotoxic shock	0.311460514
enhanced acetylation	0.437530547
enhanced apoptosis	0.322169564
enhanced basal apoptotic activity	0.364447381
enhanced collagen deposition	0.382398453
enhanced dermal fibroblast infiltration	0.003444996
enhanced myocyte apoptosis	0.34002848
enhanced osteogenesis	0.374118751
enhanced phosphorylation	0.335623572
enhanced smad signaling	0.154615402
enhanced transactivation	0.415297541
enterocyte apoptosis	0.3146722
environmental cofactors	0.164149026
eosinophil apoptosis	0.315806094
epidermal remodeling	0.1732025
epstein-barr virus transforming protein	0.174494777
erythropoietin receptor-mediated activation	0.361025818
essential coactivator	0.399618716
essential coactivators	0.398748776
essential cofactors	0.020606704
essential intrinsic determinant	0.036979183
estrogen receptor-alpha coactivator	
ethidium bromide	0.214490384
excess apoptosis	0.310653958
excessive activation	0.359862489
excessive apoptosis	0.31410673
excessive apoptotic cell death	0.24206096
experimental inhibition	0.262639075
expressed collagenase	0.122388692
expressed decorin	0.049051712

extended histone	0.345509276
extensor tendons	0.339516053
extracellular collagen	0.385112198
extracellular matrix collagen fibrils	0.406512467
extracellular matrix collagens	0.321310871
extracellular matrix remodeling	0.287360493
extraskeletal connective tissues	0.153420347
extremely severe osteogenesis imperfecta	0.329403806
extremely severe osteogenesis imperfecta	0.329403806
factor-beta	0.299759662
fanconi anemia fibroblasts	0.254450015
feedback inhibition	0.23292782
fetal fibroblasts	0.255046923
fibrillar collagen	0.369083728
fibrillar collagens	0.306538599
fibroblast collagenase	0.009093509
fibroblasts	0.32538294
fluoride inhibition	0.294023183
focal dermal hypoplasia	0.084621208
foot fibroblasts	0.321317435
force activation	0.365636102
forced activation	0.362271492
foreskin fibroblasts	0.321357337
fracture	0.288873187
fracture callus	0.253893285
fracture callus formation	0.150993284
fracture energy	0.308526191
fracture healing	0.318830432
fracture history	0.268368662
fracture repair	
fracture risk	0.037472635
fracture site	0.294779897
fracture wound	0.331831543
fractures	0.294068602
free core histones	0.297271854
free histone	0.344683878
free histones	0.340662871
free radical initiator	0.252088338
freeze fracture	0.290471575
full activation	0.359696395
full collagen vi protein	0.378272457

full t-lymphocyte activation	0.360462615
functional acetyltransferase	0.361884058
functional caspase cascades	0.296799404
functional transactivation	0.34593434
gabp	0.30408108
gabp complex	0.034163307
gabp transcription factor complex	0.141619418
gastric intrinsic factor	0.081115841
general apoptotic pathway	0.255327807
general caspase	0.313598
general coactivator	0.417439053
general connective tissue weakness	0.139547913
general inhibition	0.289384337
gene-specific phosphorylation	0.329886601
gingival fibroblasts	0.309478942
global coactivator	0.42036217
global histone acetylation	0.408992041
global histone acetylation	0.408992041
global histone acetylation levels	0.402970315
global histone acetylation levels	0.402970315
glomerular apoptosis	0.312615923
glomerular apoptotic bodies	0.273836793
glucocorticoid activation	0.379205728
glucocorticoid-induced apoptosis	0.308836354
glucokinase inhibition	0.261301047
glycinergic inhibition	0.260989329
goat inhibition	0.29152941
gorilla fibroblasts	0.320253452
gram-negative septic shock	0.288884583
gram-negative shock	0.296673232
greater apoptotic response	0.277715641
greater inhibition	0.26972039
growth factor-beta	0.211901082
growth factor-beta expression	0.19367329
growth factor-beta families	0.20292197
growth factor-beta mrna	0.135414483
growth factor-beta signaling	0.155582203
growth factor-beta superfamily signaling	0.139321772
growth factor-beta treatment	0.236002581
hair follicle dermal sheath	
hamster fibroblasts	0.305646249

harmful heat	0.315616711
hcv entry cofactors	0.121299839
hdac	0.392265499
hdac activity	0.398734188
hdac binding	0.283325601
hdac binding domain	0.253714335
hdac catalytic activity	0.356807041
hdac domain	0.299870907
hdac enzymatic activity	0.346661997
hdac expression	0.204370335
hdac inhibition	0.45321484
hdac inhibition	0.45321484
hdac inhibitor	0.398266676
hdac inhibitors	0.438209585
heart remodeling	0.215612606
heat	0.315117297
heat activation	0.479689454
heat activation	0.479689454
heat avoidance	0.310603746
heat denaturation	0.321254997
heat exposure	0.290966226
heat loss	0.268371742
heat nociception	0.298823927
heat production	0.302410466
heat repeat	0.287832194
heat repeat clusters	0.275926666
heat repeat segments	0.271401292
heat repeats	0.275982584
heat sensitivity	0.284343443
heat shock	0.315806368
heat shock	0.315806368
heat shock cognate protein	0.310078805
heat shock cognate protein	0.310078805
heat shock protein	0.311370149
heat shock protein	0.311370149
heat shock protein expression	0.29930795
heat shock protein expression	0.29930795
heat shock proteins	0.294888562
heat shock proteins	0.294888562
heat shock response	0.309603914
heat shock response	0.309603914

heat shock treatment	0.327185647
heat shock treatment	0.327185647
heat stability	0.314546167
heat stable	0.307736507
heat stimulus	0.314955519
heat stress	0.275665417
heat treatment	0.335140437
heat-shock	0.326904617
heat-shock chaperone components	0.321232825
heat-shock chaperone components	0.321232825
heat-shock cognate protein	0.321681221
heat-shock cognate proteins	0.306105774
heat-shock domains	0.328220435
heat-shock element	0.328903382
heat-shock genes	0.286354093
heat-shock loci	0.298199249
heat-shock promoter	0.354901812
heat-shock protein	0.322967523
heat-shock protein genes	0.28225856
heat-shock proteins	0.307204106
heat-shock response	0.322490903
heat-shock response element	0.323609764
heat-shock response genes	
heat-shock transcription factors	0.346113354
heat-shock treatment	0.337858699
hela cell native core histones	0.190966709
hela cells inhibited cell cycle progression	0.036452124
hela cells inhibited cell proliferation	0.051249385
hemorrhagic shock	0.310761688
hepatocellular apoptosis	0.312863995
hepatocyte apoptosis	0.316393206
heritable connective tissue disorder	0.075284081
herpes simplex virus transactivator	
heteroduplexes	0.289071227
high heat	0.306398759
high intrinsic ability	0.220622896
high transactivation ability	0.404176959
high transforming activity	0.343927428
highly conserved nucleosomal protein	0.080567553
highly conserved transforming growth factor-beta superfamily	0.212971889
highly conserved transforming growth factor-beta superfamily	0.212971889

hip fracture	0.283424142
histidine phosphorylation	0.322110899
histone	0.34642055
histone acetyl transferase activity	0.362019357
histone acetyl transferase activity	0.362019357
histone acetylase	0.357761226
histone acetylase	0.357761226
histone acetylase complex	
histone acetylase complex	
histone acetylation	0.409975217
histone acetylation	0.409975217
histone acetylation defects	0.394874632
histone acetylation defects	0.394874632
histone acetylation levels	0.404042834
histone acetylation levels	0.404042834
histone acetylation patterns	0.404356094
histone acetylation patterns	0.404356094
histone acetylation profiles	0.40807761
histone acetylation profiles	0.40807761
histone acetyltransferase	0.385356126
histone acetyltransferase	0.385356126
histone acetyltransferase activities	0.386122455
histone acetyltransferase activities	0.386122455
histone acetyltransferase activity	0.398720948
histone acetyltransferase activity	0.398720948
histone acetyltransferase complex	0.369146225
histone acetyltransferase complex	0.369146225
histone acetyltransferase complexes	0.370830518
histone acetyltransferase complexes	0.370830518
histone acetyltransferase domain	0.381378417
histone acetyltransferase domain	0.381378417
histone acetyltransferase domains	0.377707384
histone acetyltransferase domains	0.377707384
histone acetyltransferase repeat	0.374604497
histone acetyltransferase repeat	0.374604497
histone acetyltransferases	0.369707986
histone acetyltransferases	0.369707986
histone binding	0.3524592
histone biotinylation	0.348452924
histone chaperone	0.447555801
histone chaperone	0.447555801

histone chaperone activity	0.461537029
histone chaperone activity	0.461537029
histone chaperones	0.406561988
histone code	0.344687577
histone code mediator protein	0.351181068
histone deacetylase	0.367181466
histone deacetylase	0.367181466
histone deacetylase activity	0.382040312
histone deacetylase activity	0.382040312
histone deacetylase binding	0.370831429
histone deacetylase binding	0.370831429
histone deacetylase complex	0.349984567
histone deacetylase complex	0.349984567
histone deacetylase complexes	0.350985418
histone deacetylase complexes	0.350985418
histone deacetylase domain	0.363701169
histone deacetylase domain	0.363701169
histone deacetylase inhibition	0.407820443
histone deacetylase inhibition	0.407820443
histone deacetylase inhibition	0.407820443
histone deacetylase inhibitor	0.424165674
histone deacetylase inhibitor	0.424165674
histone deacetylase inhibitors	0.395420316
histone deacetylase inhibitors	0.395420316
histone deacetylases	0.349664731
histone deacetylases	0.349664731
histone demethylases	0.340753676
histone displacement	0.344906883
histone domain	0.343384143
histone exchange	0.343003711
histone fold	0.347228028
histone fold domain	0.343024365
histone fold motif	0.3378387
histone mark	0.343956087
histone markers	0.339460245
histone marks	0.343404301
histone methylase activity	0.365690421
histone modification	0.339245369
histone modifications	0.341072361
histone modifiers	0.33983961
histone nomenclature	0.345437063

histone n-terminal tails	0.34133511
histone octamer	0.344186505
histone polypeptides	0.345054021
histone protein production	0.345816806
histone replacement	0.343936831
histone storage	0.339464123
histone substrate	0.35574259
histone substrates	0.341151097
histone supply	0.345221308
histone tails	0.345094724
histone target	0.341992391
histone translation	0.358028092
histones	0.35281179
hiv activation	0.375939168
hiv inhibition	0.302196679
hormone response element-binding protein	0.163126635
hormone response element-binding proteins	0.12315852
hormone-dependent activation	0.364333368
hormone-dependent trans-activator	
host cofactors	0.063030587
hsp	0.314497525
hsp expression	0.273273315
hsp genes	
hsp proteins	0.258163554
human acetylation polymorphism	0.340560815
human amniotic fibroblasts	0.259524705
human autosomal recessive osteogenesis imperfecta	
human autosomal recessive osteogenesis imperfecta	
human carnitine acetyltransferase	0.321490494
human cells inhibited dna replication	-0.063326906
human choline acetyltransferase	0.360231337
human choline acetyltransferase genomic sequence	0.262213927
human collagenase	0.214267694
human collagenase inhibitor	0.307006338
human collagens	0.247836093
human connective tissue disorders	0.077393904
human dermal fibroblast cdna	-0.015421861
human dermal fibroblasts	0.308566995
human dermal fibroblasts	0.308566995
human dermal microvascular endothelial cells	0.085590297
human dermal microvasculature	0.163712449

human dermal vascular endothelial cell cdna	0.075614115
human diploid fibroblasts	0.258315008
human ehlers-danlos syndrome	0.020530194
human female fibroblasts	0.226673682
human fibroblast collagenase	0.012083342
human fibroblasts	0.269886195
human foreskin dermal fibroblasts	0.303726335
human foreskin dermal fibroblasts	0.303726335
human foreskin fibroblasts	0.264779614
human gastric intrinsic factor cdna clone	0.041863703
human gingival fibroblasts	0.259674458
human heat-shock protein	0.316659084
human jurkat cdna library	0.072926841
human jurkat cell cdna	0.073380565
human jurkat cell cdna libraries	0.068180591
human jurkat cells	0.091656312
human jurkat t-cell cdna expression library	0.016053597
human jurkat t-cell cdna library	0.010730018
human jurkat t-cell leukemia	0.044030685
human jurkat t-cell leukemia cells	0.026983371
human melanoma cells inhibited tumor growth	0.045892239
human mps iiic fibroblasts	0.229017756
human neutrophil collagenase	0.084894603
human pkc-delta	
human plantar fibroblasts	0.267110542
human primary fibroblasts	0.249606946
human sclera	0.056133831
human septic shock	0.299182806
human skin fibroblast collagenase	
human transforming growth factor-beta	0.256285375
human transforming growth factor-beta	0.256285375
hydroxamic	0.385942192
hypertrophic chondrocyte apoptosis	0.343118495
hypertrophic chondrocyte-specific genes	
ii collagen	0.374113153
ii collagens	0.249599111
ii histone deacetylases	0.346651731
ii histone deacetylases	0.346651731
iii collagen	0.369393099
iii collagens	0.290732094
immobilized collagen	0.375550538

impaired apoptosis	0.305582025
impaired chondrocyte apoptosis	0.319170361
impaired coactivator binding	0.39638617
impaired coactivator recruitment	0.395023196
impaired collagen folding	0.381780052
impaired transactivation	0.381592512
imperfecta	0.354002257
inactivating serine phosphorylation	0.328552752
inactive chromatin remodeling	0.291514647
inappropriate apoptosis	0.31138616
increased acetylation	0.444417855
increased activation	0.368659593
increased ameloblast apoptosis	0.325242357
increased apoptosis	0.321230904
increased apoptotic activity	0.361216978
increased apoptotic cell death	0.253117345
increased apoptotic resistance	0.289309433
increased basal phosphorylation	0.332367323
increased bronchiolar subepithelial collagen deposition	0.382412392
increased chromatin acetylation	0.416977558
increased collagen	0.384215983
increased collagen deposition	0.383470451
increased collagen staining	0.389893188
increased dermal melanin	0.190775408
increased fracture risk	0.063837642
increased glucocorticoid transactivation	0.409936299
increased lymphocyte apoptosis	0.312413469
increased mucosal remodeling	0.198664862
increased nad-dependent deacetylase activity	0.379452392
increased neuroepithelial apoptosis	0.316817678
increased phosphorylation	0.338039424
increased stromal cell apoptosis	0.324457432
increased threonine phosphorylation	0.324998126
increased tonic inhibition	0.226328997
increased transactivation	0.418912635
increased transactivation potential	0.406517218
increased type iii collagen expression	
increased vertebral fracture risk	0.07063468
indirect inhibition	0.269471412
individual human lysine deacetylase	0.322007191
individual lysine deacetylases	

indomethacin inhibition	0.281424765
induced apoptosis	0.31785655
induced human fibroblasts	0.28995131
induced phosphorylation	0.348814131
inducible phosphorylation	0.34563242
inducible phosphorylation site	0.348258191
inducible transactivation	0.413679899
inducing apoptosis	0.316494783
inflammatory caspase subfamily	
inflammatory heat hyperalgesia	
inherited connective tissue disorders	0.072747379
inherited nonlethal caspase abnormalities	0.300701386
inhibited	0.306248386
inhibited ability	0.292424702
inhibited activation	0.377266784
inhibited activation	0.377266784
inhibited adhesion	0.023161157
inhibited amyloid formation	0.040960302
inhibited apoptosis	0.336266906
inhibited apoptosis	0.336266906
inhibited bone formation	0.086785418
inhibited bone growth	0.132387506
inhibited cell death	0.155408957
inhibited cell division	0.063578614
inhibited cell growth	0.12874974
inhibited cell transformation	0.101232008
inhibited contraction	0.286627793
inhibited degradation	0.061555478
inhibited differentiation	0.044624233
inhibited dna replication	-0.08057056
inhibited dna synthesis	-0.035775978
inhibited dynein	0.14328693
inhibited entry	0.188109662
inhibited epidermal growth factor induction	0.134214742
inhibited erythroblast binding	0.226292911
inhibited erythrocyte invasion	0.235375417
inhibited expression	0.125591405
inhibited extension	0.246731235
inhibited extracts	0.273588545
inhibited formation	0.16653808
inhibited golgi fragmentation	0.096688288

inhibited growth	0.166975838
inhibited hela cell growth	0.145623452
inhibited homologous recombination	
inhibited induction	0.198621956
inhibited infection	0.063387242
inhibited interaction	0.27879014
inhibited intestinal adhesion	-0.006802246
inhibited iron release	0.037571855
inhibited muscle differentiation	0.090305314
inhibited packaging	0.296894822
inhibited phosphorylation	0.35558216
inhibited phosphorylation	0.35558216
inhibited process outgrowth	0.147674843
inhibited processing	0.214877502
inhibited production	0.160820458
inhibited proliferation	0.141871114
inhibited proteolysis	0.17131165
inhibited random migration	0.200832125
inhibited secretion	0.09886251
inhibited sleep	0.165692351
inhibited spindle formation	-0.07357699
inhibited splicing	0.080511484
inhibited transcription	0.194004905
inhibited transport	0.023698606
inhibited tumor angiogenesis	0.030771419
inhibited tumor growth	0.042842351
inhibited ubiquitination	0.004713831
inhibiting phosphorylation	0.339050046
inhibition	0.293106631
inhibition constant	0.263489662
inhibition experiments	0.26046143
inhibition mechanism	0.282256686
inhibition properties	0.253716013
inhibition results	0.23887318
inhibition studies	0.251909919
inhibitory cofactors	0.085839749
inhibitory smad	0.295372487
initiator	0.312554768
initiator assembly	0.163220859
initiator caspases	0.322062826
initiator caspases	0.322062826

initiator codon	0.124149669
initiator codon recognition	0.054095045
initiator element	0.213510588
initiator elements	0.151397515
initiator methionine	0.132682006
initiator methionine codon	0.066909337
initiator methionine mutation	
initiator methionine residue	0.147180761
initiator protein	0.198860294
initiator region	0.167496841
initiator sequence	0.113128491
insoluble apoptotic bodies	0.278087074
insulin control element-binding transcription factor	0.163748631
interfacial activation	0.36216506
interferon-gamma activation site element	0.363164197
interlobular connective tissue	0.153491851
interstitial collagen	0.375167353
interstitial collagen deposition	0.375200466
interstitial collagen expression	0.37461524
interstitial collagenase	0.270653336
interstitial collagens	0.336547665
interstitial connective tissue cells	0.047970816
interstitial fibrillar collagens	0.312619404
intracellular caspase activity	0.3329976
intracellular metal ion chaperone	0.229774391
intrinsic	0.329296081
intrinsic acetyltransferase activity	0.451873854
intrinsic acetyltransferase activity	0.451873854
intrinsic activity	0.313691287
intrinsic adhesiveness	0.327862666
intrinsic adjuvant activity	0.286942793
intrinsic androgenic activity	0.301682273
intrinsic apoptosis pathway	0.306959415
intrinsic apoptosis pathway	0.306959415
intrinsic atopic dermatitis	0.028967914
intrinsic attribute	0.322789366
intrinsic auxiliary subunits	-0.061056671
intrinsic b-cell defect	0.007837889
intrinsic b-cell signaling	0.078305015
intrinsic blood coagulation cascade	0.186372968
intrinsic catabolism	0.117446239

intrinsic catalytic activity	0.255880087
intrinsic cell defect	0.001908584
intrinsic channel properties	-0.073552171
intrinsic chloride channel activity	-0.017592375
intrinsic circadian period	-0.021659152
intrinsic clearance	0.028103738
intrinsic component	0.108255875
intrinsic congenital testicular abnormality	0.010707302
intrinsic deacetylase activity	0.417474156
intrinsic deacetylase activity	0.417474156
intrinsic defect	-0.042957796
intrinsic difference	0.19847556
intrinsic differences	0.14564613
intrinsic electrophysiologic properties	0.147337222
intrinsic enhancement	0.354284214
intrinsic enzymatic activity	0.246247935
intrinsic factor	0.109103939
intrinsic factor deficiency	0.030259896
intrinsic feedback inhibitor	0.27728574
intrinsic feedback mechanism	0.157746682
intrinsic gap activity	0.065444788
intrinsic glutamatergic connections	0.002132813
intrinsic glycoprotein	0.03959501
intrinsic gtpase activity	0.119911765
intrinsic histone acetyltransferase activity	0.405475285
intrinsic histone acetyltransferase activity	0.405475285
intrinsic histone acetyltransferase activity	0.405475285
intrinsic histone chaperone activity	0.470128138
intrinsic histone chaperone activity	0.470128138
intrinsic histone chaperone activity	0.470128138
intrinsic instability	0.035706129
intrinsic kinase activity	0.219757084
intrinsic light response	0.038153925
intrinsic lipid kinase activity	0.203995282
intrinsic low maturation efficiency	0.011232693
intrinsic mechanism	0.276380849
intrinsic mechanisms	0.197606679
intrinsic membrane glycoprotein	-0.017038238
intrinsic membrane molecule	-0.021646013
intrinsic membrane protein	0.041331405
intrinsic membrane-bound form	0.090207289

intrinsic negative modulator	0.113599214
intrinsic negative regulator	0.062939697
intrinsic neural differentiation	-0.072154943
intrinsic nonlinear behavior	0.014209122
intrinsic ocular structures	0.102509769
intrinsic parp activity	0.086963718
intrinsic part	0.277213844
intrinsic passive properties	0.159726962
intrinsic pathway	0.105659261
intrinsic pathways	0.161958479
intrinsic phosphatase activity	-0.001454175
intrinsic photosensitivity	0.23670997
intrinsic plasma membrane protein	-0.025984091
intrinsic polarity	0.013671917
intrinsic proliferation	0.104896394
intrinsic propensity	0.281298324
intrinsic properties	0.176063183
intrinsic property	0.33221398
intrinsic protein kinase activity	0.220616356
intrinsic protein-tyrosine phosphatase activity	0.037008169
intrinsic qualitative differences	0.1419621
intrinsic regulator	0.101435123
intrinsic renal abnormality	0.028401408
intrinsic renal cells	0.007291405
intrinsic resistance	0.097109908
intrinsic role	0.141026646
intrinsic substrate	0.201620336
intrinsic sulfate transport properties	-0.014812296
intrinsic susceptibility	-0.031672043
intrinsic transactivation domain	0.403262913
intrinsic transactivation domain	0.403262913
intrinsic transcription activity	0.205036755
intrinsic tyrosine kinase activity	0.191521349
intrinsic ubiquitin ligase activities	
intrinsic ubiquitin ligase activity	-0.064064132
intrinsic ubiquitin-protein ligase activity	-0.027802679
intrinsic variation	0.151752475
invertebrate collagens	0.328773692
inverted ccaat box	0.042712061
inverted ccaat element	0.136536159
irf activation	0.378087446

iron regulatory element-binding activities	0.06776173
iron-responsive element-binding activity	0.350977184
irradiated fibroblasts	0.278364562
irradiation-induced apoptosis	0.312027864
isolated dermal fibroblasts	0.325612946
isolated dermal fibroblasts	0.325612946
isolated fibroblasts	0.284880712
isolated transactivation domains	0.356680526
isoniazid acetylation	0.411811356
jurkat	0.364886162
jurkat cdna	0.088172984
jurkat cdna libraries	0.079832979
jurkat cdna library	0.075526738
jurkat cell cdna	0.078727911
jurkat cell cdna library	0.070073248
jurkat cell cytosol	0.182387381
jurkat cell messages	0.166061162
jurkat cells	0.099634252
jurkat human t-cell	0.034698007
jurkat human t-cell cdna library	0.010730018
jurkat human t-cell library	0.031705292
jurkat human t-cell nuclear extracts	0.056761009
jurkat lymphoblastoid cell cdna library	0.071828233
jurkat lymphocytes	0.150077061
jurkat t-cell	0.031382334
jurkat t-cell cdna	0.010481932
jurkat t-cell cdna libraries	
jurkat t-cell cdna library	0.007673567
jurkat t-cell expression library	0.034799657
jurkat t-cell extracts	0.032756964
jurkat t-cell leukemia cell lines	0.041700354
jurkat t-cell leukemia cells	0.025129634
jurkat t-cells	0.301662449
jurkat t-lymphocyte cdna library	0.076571153
jurkat t-lymphocyte expression library	0.195650674
jurkat t-lymphocytes	0.34781959
kidney fibroblasts	0.241384524
kinase inhibitor staurosporine	
labeled procollagen substrate	0.369335559
late apoptosis	0.309530043
latent inhibition	0.315315231

latent transforming growth factor-beta	0.26118712
latent transforming growth factor-beta	0.26118712
lateral inhibition	
left ventricular remodeling	0.10008923
lens apoptosis	0.305201655
lethal osteogenesis imperfecta congenita	0.313682575
lethal osteogenesis imperfecta congenita	0.313682575
light-induced apoptosis	0.308386191
linker histone	0.348151549
linker histones	0.314112264
lipid remodeling	0.097220571
lithium inhibition	0.271918439
local activation	0.361350377
local feedback inhibition	0.229929408
local helix unfolding map	0.064245389
local histone	0.345105781
local inhibition	0.289018753
local nucleosomal domain	0.216199633
localized inhibition	0.22717049
long bone fracture	0.097703245
loose connective tissue	0.147873729
loose connective tissues	0.147474543
lovastatin induced apoptosis	0.317875684
low intrinsic gtpase activity	0.101186888
low-affinity inhibition sites	0.269312977
lower acetylation capacity	0.432676313
lower intrinsic clearance	0.022024874
lower intrinsic gtpase activity	0.114814422
lymphatic dermal human microvascular endothelial cells	0.085554675
lymphatic remodeling	0.29970483
lysine acetylation	0.4196166
lysine acetyltransferases	
main phosphorylation domain	0.339580282
major acetyltransferase	0.420161908
major carboxy-terminal transactivation domains	0.373139819
major collagen	0.372081027
major intrinsic protein	0.165061666
major phosphorylation site	0.328625559
mammalian apoptosis	0.307251467
mammalian cells inhibited cell growth	0.064169005
mammalian cells potentiated activation	0.228635339

mammalian fibroblasts	0.273966941
mammalian histone deacetylase	0.353960213
mammalian histone deacetylase	0.353960213
manganese inhibited activity	0.294952728
massive apoptosis	0.308540767
massive apoptotic cell death	0.233120899
massive apoptotic death	0.28436224
massive remodeling	0.278620502
maternal inhibition	0.234279495
matrix remodeling	0.285262034
matrix-associated deacetylase bodies	0.33710598
mature caspase molecule	0.293044139
mature type iii procollagen molecules	0.274059927
maximal activation	0.36344955
maximal apoptosis	0.318325017
maximal inhibition	0.285724833
maximal phosphorylation	0.332592141
maximum transactivation	0.413061922
mediated transactivation	0.409439312
medullary connective tissue	0.096015686
membrane phospholipid remodeling	0.051496486
membrane remodeling	0.080824762
meningeal basement membrane remodeling	0.132809991
meningeal fibroblasts	0.322330039
mesangial cell apoptosis	0.308431132
metal cofactors	0.141408289
metalloproteinase inhibition	0.24190722
methionine initiator codon	0.066909337
methyl bromide	
methylated histones	
microtubule remodeling	0.002775267
microtubule-associated deacetylase	
migrating fibroblasts	0.314846657
mild heat shock	0.318012165
mild heat shock	0.318012165
mild osteogenesis imperfecta	0.352584331
mild osteogenesis imperfecta	0.352584331
minimal activation	0.363814194
minor collagens	0.314778727
mitochondrial acetyl-coa acetyltransferase	0.367679046
mitochondrial apoptotic pathway	0.219241164

mitochondrial deacetylase	0.290466631
mitogen activation induced recruitment	0.37219221
mitogenic activation	0.360200901
moderate heat shock	0.315138432
moderate heat shock	0.315138432
moderate inhibition	0.285549952
modified histone	0.340574322
modified histones	0.318333939
modulated apoptosis	0.314841373
monkey fibroblasts	0.321769097
morpholino inhibition	0.283436123
morpholino oligonucleotide inhibition	0.271203262
mouse creb-binding protein	
mouse embryonic stem cells inhibited cell growth	-0.032389665
mps iiia fibroblasts	0.269712096
mps vii fibroblasts	0.228276828
mucosal remodeling	0.199384319
multiple collagens	0.298675288
multiple fractures	0.223101697
multiple histone deacetylases	0.341640188
multiple histone deacetylases	0.341640188
multiple phosphorylation	0.322481224
multiple smad partners	0.353621572
multiple spontaneous bone fractures	
multiprotein coactivator	0.418332056
multiprotein coactivator complex	0.394597889
mutant collagens	
mutant inhibited basal	-0.09169528
mutant procollagen	0.167308225
mutant templates	
mycobacterial heat-shock proteins	0.30347146
myoblasts inhibited expression	0.11670056
myocardial apoptosis	0.32758361
myocyte activation	0.386679054
myocyte apoptosis	0.331949561
myofibroblast	0.291474339
myofibroblast activation	0.382359633
myofibroblast activation	0.382359633
myofibroblast cell phenotype	-0.05710842
myofibroblast differentiation	-0.010045351
myofibroblast phenotype	

myofibroblast transdifferentiation	0.206261289
myofibroblast transformation	0.129500401
myofibroblast viability	0.119596971
nad cofactors	0.082889312
nad-dependent histone deacetylases	0.349189063
nad-dependent histone deacetylases	0.349189063
naked dna templates	-0.105109136
naked templates	0.169003175
narrow palpebral fissures	0.186651584
native intrinsic factor	0.109749348
n-ethylmaleimide inhibition	0.284087239
neurofilament phosphorylation	
neuroimmune activation	0.360232786
neutrophil collagenase	0.089334416
nicotinamide adenine dinucleotide cofactors	0.073035699
nk-cell apoptosis	0.315831141
nociceptor activation	0.358910351
nocturnal activation	0.358813502
nonhistone	0.41007249
non-histone	0.394494553
nonhistone chromosomal	
nonhistone chromosomal protein	0.04580562
nonhistone chromosomal proteins	-0.047468768
nonhistone dna	-0.09510681
nonhistone modifier factors	0.094544247
nonhistone protein	0.160308333
nonhistone proteins	0.046626779
nonhistone region	0.101190698
nonhistone substrate	0.181701645
nonhistone substrates	0.143800269
nonlethal osteogenesis imperfecta	0.348094501
nonlethal osteogenesis imperfecta	0.348094501
nonspecific connective tissue disorder	0.054120345
normal apoptosis	0.306475212
normal collagen folding	0.378165628
normal fibroblasts	0.256463107
normal remodeling	0.206667108
normal senescent fibroblasts	0.250453384
normal tendon	0.103074569
normal transactivation	0.381482671
normal transactivation activity	0.398409652

normal valve remodeling	0.213733633
noxious heat	0.31171552
noxious heat sensor	0.306192843
noxious thermal heat	0.315441699
n-terminal acetylated form	0.371493483
n-terminal acetylation	0.425280899
n-terminal apoptotic domain	0.298576244
n-terminal caspase recruitment domain	0.341410055
n-terminal caspase recruitment domains	0.333202165
n-terminal histone tails	0.34133511
n-terminal minimal transactivation domain	0.343192888
n-terminal protein acetylation	0.421602501
n-terminal protein acetyltransferase activity	0.370461853
n-terminal protein-binding domain	
n-terminal transactivation domain	0.345694502
nuclear apoptosis	0.326675975
nuclear chaperone phosphoproteins	0.306101566
nuclear coactivators	0.372861225
nuclear histones	0.232930197
nuclear hormone receptor-mediated transactivation	0.252040411
nuclear nonhistone protein	0.153053937
nuclear response element-binding protein	0.204010512
nucleosomal	0.35775997
nucleosomal antigens	0.008719229
nucleosomal arrays	0.290337035
nucleosomal binding domain	0.202590268
nucleosomal core histones	0.336817216
nucleosomal core histones	0.336817216
nucleosomal dna	
nucleosomal dna fragmentation	-0.048944404
nucleosomal fragmentation	0.433137626
nucleosomal fragments	0.298388191
nucleosomal histone	0.34913547
nucleosomal histone	0.34913547
nucleosomal histones	0.360426168
nucleosomal histones	0.360426168
nucleosomal organization	0.238270058
nucleosomal response	0.151707677
nucleosomal substrates	0.204001653
nucleosomal targeting	0.084210661
nucleosomal units	0.328910211

nucleosome remodeling	0.348764778
nucleosome remodeling activities	0.347117182
nucleosome remodeling complex	0.27264522
nucleosome remodeling factor	0.208544163
n-wasp activation	0.358563433
observed cellular activation	0.3586404
oligodendrocyte apoptosis	0.31076441
oncoproteins	0.329395817
opsin phosphorylation	0.331814046
orderly activation	0.362675152
osmotic shock	0.298100698
osteoblast apoptosis	0.304692942
osteogenesis	0.341014187
osteogenesis imperfecta	0.350625256
osteogenesis imperfecta	0.350625256
osteogenesis imperfecta type ix	0.358672273
osteogenesis imperfecta type ix	0.358672273
osteogenesis imperfecta type vi	0.345907558
osteogenesis imperfecta type vi	0.345907558
osteogenesis imperfecta type vii	0.326819796
osteogenesis imperfecta type vii	0.326819796
osteoporotic fracture	0.272210824
osteoporotic fracture risk	0.077518936
osteoporotic fractures	0.268964287
osteoporotic vertebral fractures	0.245745599
ouabain inhibition	0.276164063
painful heat	0.314078066
palpebral	0.293559002
palpebral fissures	0.295243035
paradoxical activation	0.360082598
parallel apoptotic pathways	0.282254681
partial inhibition	0.26974183
partial transactivation domain	0.377051685
partial unfolding	0.103318962
partially inhibited conversion	0.157505069
pathologic fractures	0.311581432
pathologic phosphorylation	0.329920261
pathologic vascular remodeling	0.180633605
patient fibroblasts	0.320677884
pdgfr activation	0.370536436
pelvic fracture	0.268871198

pericyte apoptosis	0.317362791
periodic inhibition	0.240149129
permanent activation	0.360896761
persistent phosphorylation	0.324687908
pharmacologic inhibition	0.268945826
pharmacologic inhibition studies	0.233805289
phorbol ester activation	0.373195419
phorbol myristate acetate activation	0.372003251
phospholipid remodeling	0.208064797
phosphopeptides	0.299943772
phosphorylation	0.329901243
phosphorylation activity	0.352092174
phosphorylation cascade	0.342198255
phosphorylation events	0.325292559
phosphorylation increase	0.32657687
phosphorylation induced huvec migration	0.359091433
phosphorylation level	0.325598499
phosphorylation loop	0.327484658
phosphorylation motifs	0.323263375
phosphorylation reaction	0.33082876
phosphorylation reactions	0.328406322
phosphorylation response	0.326054838
phosphorylation sink	0.328026354
phosphorylation site	0.333313726
phosphorylation sites	0.324106503
phosphorylation state	0.327769689
phosphorylation states	0.329531685
phosphorylation status	0.326578403
phosphorylation target	0.330125889
phosphorylation targets	0.32252649
physiologic activation	0.35928297
pkc-delta	0.326099207
pkc-delta activation	0.39905839
pkc-delta activation	0.39905839
pkc-epsilon phosphorylation site	0.340414783
placental collagen	0.374265891
platelet cdna templates	-0.010100201
platelet-derived growth factor-beta	0.22420534
pluripotent hematopoietic progenitor cells inhibited colony formation	0.015047142
polymorphonuclear activation	0.360252811
poor acetyl acceptors	

poor phosphorylation	0.325109872
poor transactivator	0.124182426
portal fibroblasts	0.332216736
positive coactivators	0.42919732
positive cofactors	0.148501438
postmenopausal osteoporotic fracture	0.210161345
posttranslational histone modifications	0.346009516
posttranslational phosphorylation	0.341833619
potential activation loop phosphorylation motif	0.39509917
potential activation loop phosphorylation motif	0.39509917
potential c-terminal phosphorylation site	0.329522113
potential initiator methionine	0.120822123
potential phosphorylation domain	0.339359911
potential phosphorylation site	0.33303626
potential phosphorylation sites	0.323796896
potential serine phosphorylation sites	0.327639234
potentiated	0.289333548
potentiated activation	0.375084215
potentiated activation	0.375084215
potentiated apoptosis	0.325400522
potentiated apoptosis	0.325400522
potentiated interaction	0.233759385
potentiated parathyroid hormone	0.007421993
potentiated responses	
predominant caspase	0.3141823
preferred cofactors	0.299666055
preferred nucleosomal substrates	0.185743555
preferred remodeling mechanism	0.309807522
primary adult fibroblasts	0.232227078
primary cultured embryo fibroblasts	0.278524193
primary cultured fibroblasts	0.336431828
primary dermal fibroblasts	0.346695759
primary dermal fibroblasts	0.346695759
primary embryo fibroblasts	0.247452077
primary fibroblasts	0.312237643
primary foreskin fibroblasts	0.307452389
primary human dermal fibroblasts	0.288848566
primary human dermal fibroblasts	0.288848566
primary human diploid fibroblasts	0.23949008
primary human fibroblasts	0.249606946
primary human foreskin fibroblasts	0.244794029

primary human histone deacetylases	0.335946252
primary phosphorylation	0.327609973
primary synovial fibroblasts	0.327769201
primary transforming activity	0.348683307
primed dna templates	-0.112245556
primed phosphorylation	0.324507245
pro	0.341663025
pro domain	0.238182467
pro residue	0.286394803
pro residues	0.193446918
pro segment	
pro-apoptotic	0.307690047
procollagen	0.363400915
procollagen chain	0.333465421
procollagen genes	0.222635261
procollagen iia	0.353360729
procollagen suicide	0.36695829
procollagen synthesis	0.350748117
product inhibition	0.238086822
programmed remodeling	0.357844691
progressive apoptosis	0.311342225
progressive connective tissue nevi	0.12483443
prokaryotic chloramphenicol acetyltransferase	0.424799777
proliferating fibroblasts	0.28094417
prolonged collagenase digestion	0.282080053
prolonged pharmacologic inhibition	0.241441394
prolonged phosphorylation	0.325547835
promoter activation	0.381756986
promoter transactivation	0.341809624
promoting apoptosis	0.314208987
proper angiogenic remodeling	0.189777685
protease-activating	0.323171775
protein acetylation	0.437744012
protein acetyltransferase	0.411537866
protein chaperone	0.288401891
protein kinase inhibitor staurosporine	0.240095884
protein unfolding	0.138632623
protein-binding	0.449430708
protein-binding assays	
protein-binding domain	
protein-binding domains	

protein-binding experiments	
protein-binding oligonucleotides	
protein-binding properties	
protein-binding signal	
protein-binding site	
protein-binding sites	
protein-tyrosine phosphorylation	0.335079385
proteoglycans decorin	0.23097166
proteolytic activation	0.360407243
proteolytic activation site	0.36658698
pulmonary arterial remodeling	0.14750894
pulmonary vascular remodeling	0.132544594
purified gabp	0.116075925
purified histone	0.346365419
purified histones	0.302209303
quail fibroblasts	0.322897146
quercetin	0.423925121
rabbit antihuman serum	
rabbit synovial fibroblasts	0.291794249
rapamycin activation	0.385796945
rapid acetylation	0.41963479
rapid apoptosis	0.312777776
rapid phosphorylation	0.328378869
rapid serine phosphorylation	0.333577442
rapid versus slow acetylation	0.369836391
rat decorin	0.05468424
rat gabp beta subunits	
rat gastric intrinsic factor	0.066303073
rat zap	
rb protein-binding motif	
receptor-mediated apoptosis	0.316022286
receptor-mediated phosphorylation	0.330942975
receptor-mediated smad activation	0.442403302
receptor-mediated smad activation	0.442403302
receptor-regulated smad proteins	0.255750345
reciprocal protein-binding	
recombinant adenovirus	0.243223386
recombinant adenovirus vector	0.236143026
recurrent fractures	0.220168288
redox cofactors	0.04355087
reduced acetylation	0.42989834

reduced acetylation activity	0.441483343
reduced apoptosis	0.309690798
reduced downstream phosphorylation	0.328596392
reduced histone	0.342676514
reduced procollagen processing	0.33500842
reduced transactivation potential	0.387438388
reductive activation	0.361868358
regional activation	0.358506268
regional specific apoptosis	0.315213858
regular nucleosomal arrays	0.282366391
regulated apoptosis	0.314892181
regulated histone acetylation	0.406994002
regulated histone acetylation	0.406994002
regulating apoptosis	0.317047706
regulatory element-binding proteins	0.127613283
related cofactors	0.150666715
related fibrillar collagens	0.283904771
remodeling	0.30205543
remodeling atrioventricular endocardial cushions	0.239327083
remodeling capillaries	0.297939442
remodeling pathway	0.203341305
remodeling proteins	0.171321282
replacement histones	0.3305012
response element-binding protein	0.232865257
response element-binding proteins	0.178505259
resting fibroblasts	0.325736356
retinal remodeling	0.091945236
retinoic acid release histone deacetylase activity	0.246043052
reverse ccaat box	0.049273181
reversible acetylation	0.432246306
reversible inhibition	0.305965864
reversible phosphorylation	0.33287412
reversible protein phosphorylation	0.323516452
rhesus fibroblasts	0.313034054
rhodopsin phosphorylation	0.323543723
rhythmic acetylation	0.425300627
ribosomal chaperone	0.261453438
rodent fibroblasts	0.301196158
salicylate inhibition	0.310076509
sarcomere remodeling	0.2571142
sclera	0.403947414

scleroderma	0.40312337
scleroderma autoimmune disease	
scleroderma fibroblasts	0.358332419
scleroderma fibroblasts	0.358332419
scleroderma lesions	0.021294819
scleroderma patient	0.197150632
scleroderma patient sera	0.172091254
scleroderma skin	0.041970783
scleroderma status	0.165433764
secondary connective tissue manifestations	0.108632348
selective apoptosis	0.30715512
selective phosphorylation	0.323842563
senescent cultured fibroblasts	0.344940561
senescent diploid fibroblasts	0.301720123
senescent fibroblasts	0.313617819
senescent human fibroblasts	0.26206519
septic shock	0.309521036
septic shock patients	0.204473335
sequential activation	0.362831758
sequential phosphorylation	0.331658483
sequential remodeling	0.31763548
serial activation	0.360426128
serial histone modification	0.338752013
serine phosphorylation	0.334975168
severe apoptotic cell death	0.223910575
severe apoptotic defect	
severe inhibition	0.237423245
severe osteogenesis imperfecta	0.333795772
severe osteogenesis imperfecta	0.333795772
severe osteogenesis imperfecta type iii	0.321568355
severe osteogenesis imperfecta type iii	0.321568355
severe septic shock	0.290104655
severe systemic connective tissue abnormalities	
shared coactivators	0.426224198
sharp inhibition	0.289396807
shock	0.31601145
shock elements	0.301547518
short collagen domain	0.381765854
short collagen triple helix	0.370843566
short palpebral fissures	
short-chain collagen domain	0.382886329

short-chain collagen polypeptides	0.37208508
short-chain minor collagen	0.370433973
signature apoptotic fragments	0.308883805
simple inhibition	0.271806622
single intrinsic immune effector	-0.045622723
single serine phosphorylation site	0.322047046
sirna inhibition	0.304713174
sirna reduced phosphorylation	0.342835938
sirna treatment induced apoptosis	0.341288964
skeletal remodeling	0.249236058
slit inhibition	0.245983557
slow acetylation genotype	
slow intrinsic rate	0.068952245
smad	0.413200682
smad activation	0.457504988
smad activation	0.457504988
smad anchor	0.425498748
smad localization	0.199850485
smad nuclear translocation	0.330409767
smad pathway	0.252141027
smad phosphatase	
smad protein complexes	0.274890462
smad protein expression vectors	0.223767325
smad proteins	0.249099511
smad signaling	0.144320952
smad signaling pathway	0.127332956
smad signaling proteins	0.128588293
smad substrate	0.391388703
smad target genes	0.094263012
smad target promoter	0.275443419
smad transcription factor pathway	0.199527524
small acetylated peptides	0.340041571
small diameter collagen fibrils	0.368073475
small heat-shock protein	0.321388597
small heat-shock proteins	0.305822586
small hsp	0.312090533
small nonhistone chromatin	0.235858012
small palpebral fissures	0.165709289
smooth muscle cell apoptosis	0.31739226
s-nitroso-n-acetylpenicillamine	0.292581333
snornp chaperone	0.302788594

soft connective tissue matrix	0.251978179
soft connective tissues	0.143465175
soluble collagens	0.218519548
soluble transforming growth factor-alpha	0.156631244
somatic apoptosis	
somatic histones	0.233309988
specialized chaperone	0.30454996
specialized connective tissues	0.134233418
specific antihuman antibody	0.069988698
specific caspase cleavage site	0.316827148
specific chaperone	0.309789512
specific coactivator complexes	0.400953371
specific inhibition	0.286273495
specific interferon inhibition	0.246337049
specific nad-dependent deacetylase activity	0.374679181
specific oncoproteins	0.217141165
specific phosphorylation	0.329827869
specific phosphorylation events	0.324901485
specific protein-binding interface	
specific transforming genes	0.142411948
spermatocyte apoptosis	0.314058478
spiral artery remodeling	0.229225603
splicing coactivators	0.34533728
spontaneously transformed chinese hamster fibroblasts	0.261794458
srebp activation	0.37633012
stabilized tibia fractures	0.249850024
stable heteroduplexes	
stage-specific inhibition	0.280922475
staurosporine	0.401907333
staurosporine treatment	0.262797129
sterol regulatory element-binding proteins	0.072930551
sterol response element-binding protein genes	
stimulated fibroblasts	0.352720792
stimulated jurkat cells	0.119632293
stimulated jurkat library	0.375026631
stimulated sapk phosphorylation	0.339563874
stimulation induced phosphorylation	0.343680374
stress activation	0.367287811
stress apoptotic responses	0.237800104
stress fiber inhibition	0.255413765
stromal cell apoptosis	0.319116739

stromal fibroblasts	0.248673709
structural remodeling	0.249447347
substrate inhibition	0.260114034
substrate phosphorylation	0.324953363
suppressing activation	0.357956543
suppressing apoptosis	0.310489101
suppressing transactivation	0.411082368
sustained phosphorylation	0.329236314
synaptic remodeling	
synchronous remodeling	0.292445233
synovial cell collagenase	0.150063676
synovial fibroblasts	0.344554303
synthetic glucocorticoid inhibited expression	0.142298557
synthetic histone substrate	0.34823511
synthetic mapk phosphopeptides	
systemic sclerosis patient dermal fibroblasts	0.268409055
systemic sclerosis patient dermal fibroblasts	0.268409055
tad	0.400551292
target protein-binding regions	
targeted inhibition	0.250157258
targeted pharmacologic inhibition	0.230559383
targeting apoptotic programs	0.273377784
t-cell lymphoma jurkat cells	0.026648577
templates	0.299866466
tendon	0.319938272
tendon fiber bundles	0.109956853
tendon fibroblast mrna	-0.02275211
tendon maturation	0.100435267
tendon phenotype	
tendon progenitors	0.02082447
tendon reflexes	0.295548338
tendon stiffness	0.281062394
tendon strength	0.29376399
tendon tissue	0.130381072
tendon tissues	0.11791171
tendon weakness	0.275395989
tendons	0.319284989
tensin phosphorylation	0.333899987
term apoptosis	0.312753083
terminal transactivation domain	0.367928232
tgf-beta activation	0.375496602

tgf-beta inhibition	0.307696591
tgf-beta transcription activation	0.403330788
therapeutic inhibition	0.253313063
thermal heat	0.319146173
thymocyte apoptosis	0.309607078
thyroid hormone-dependent transactivation system	0.272793647
tibialis anterior tendons	
tissue remodeling	0.199109155
t-lymphocyte activation	0.361547834
t-lymphotropic	0.337876423
tonic inhibition	0.243542477
total protein acetylation	0.43726975
toxic shock	0.309545224
toxic shock syndrome	0.226687181
trail apoptotic activity	0.308784744
transactivation	0.415571113
trans-activation	0.428778429
transactivation abilities	0.413379179
transactivation ability	0.410800889
transactivation activities	0.413233705
transactivation activity	0.429163457
transactivation assay	0.419246987
transactivation assays	0.383190756
transactivation capacity	0.412820876
transactivation domain	0.385202586
trans-activation domain	
transactivation domains	0.384288573
transactivation functions	0.375589381
transactivation inhibitory domain	0.354910249
transactivation potential	0.409079914
transactivation properties	0.403852288
transactivation studies	0.397706935
transactivation thresholds	0.406414043
transactivation variants	0.353895173
transactivator	0.372009386
trans-activator	0.305480878
transactivator activity	0.31079546
transactivator protein	0.173863307
transactivators	0.407312215
transcription factor creb-binding protein	
transcription transactivation domain	0.26619476

transformed fibroblasts	0.312229977
transforming	0.285527075
transforming abilities	0.285278785
transforming ability	0.298955691
transforming activities	0.295894227
transforming activity	0.355953645
transforming agent	0.282156882
transforming allele	0.125949475
transforming capacity	0.286567149
transforming component	0.260571884
transforming dna sequence	0.074393628
transforming effects	0.283403224
transforming foci	0.266481744
transforming form	0.283586178
transforming genes	0.141100248
transforming growth factor beta superfamily	0.143046946
transforming growth factor beta superfamily cytokines	0.132520797
transforming growth factor-alpha locus	0.110634841
transforming growth factor-beta	0.25867449
transforming growth factor-beta	0.25867449
transforming growth factor-beta receptors	0.113156945
transforming growth factor-beta receptors	0.113156945
transforming growth factor-beta signaling pathway	0.199744009
transforming growth factor-beta signaling pathway	0.199744009
transforming growth factor-beta superfamily	0.23872887
transforming growth factor-beta superfamily	0.23872887
transforming mutants	
transforming oncogene	0.260057431
transforming potential	0.286826789
transforming properties	0.273755097
transforming sequence	0.257700651
transforming signal	0.273146763
transforming viruses	0.255324558
transforms fibroblasts	0.324389281
transient activation	0.358815371
transient inhibition	0.281030514
transient phosphorylation	0.337465658
transient topoisomerase inhibition	0.239302233
translation inhibition	0.28879025
translation inhibition activity	0.308059835
translation initiator codon	0.142246755

translation initiator downstream	0.299177471
translational inhibition	0.258395711
translocated	0.288840179
translocated allele	-0.035490355
translocated chromosome	
translocated chromosomes	-0.098310891
translocated c-myc genes	-0.059907465
translocated derivatives	0.049784924
translocated part	0.172308035
translocated segment	0.028806651
transmembrane collagens	0.180990698
treatment inhibited secretion	0.140800974
trigger apoptosis	0.311176006
triggering apoptosis	0.313060629
trimerization	0.309287908
triple helical collagen	0.371739177
triple helical collagen folding	0.384671186
tubulin acetylation	0.401458973
tubulin cofactors	
tubulin deacetylase	0.257795643
tumor necrosis factor-beta	
tumor-associated fibroblasts	0.302605441
tumor-associated tissue remodeling	0.181683069
type ii apoptosis signaling	0.331075783
type ii chick embryo collagens	0.198566875
type ii procollagen	0.315542281
type iii procollagen	0.320964392
type vi ehlers-danlos syndrome	0.113942769
typical apoptotic program	0.299356875
typical ccaat box	0.030519765
typical heat-shock elements	0.318735006
tyrosine kinase transforming protein	0.221689496
ubiquitous small heat-shock proteins	0.305603551
unfolding	0.299526016
unfolding behavior	
unfolding protein toxicity	0.11946317
unfolding rate	0.064317052
unique connective tissue disorder	0.059364332
unique inhibition	0.276937162
universal activation	0.358817153
universal inhibition	0.287046342

unrelated transactivators	
upper dermal atrophy	0.097103348
upstream caspases	0.321296955
uterine stromal remodeling	0.221679285
v-abl transforming activity	0.356349515
vascular ehlers-danlos syndrome	0.050239993
vascular remodeling	0.172289057
ventricular end-systolic remodeling	0.113711671
ventricular remodeling	0.116623198
vero fibroblasts	0.319861347
vertebral compression fractures	0.246689199
vertebral fracture	0.249071861
vertebral fracture cases	0.197875659
vertebral fracture risk	0.045140372
vertebral fractures	0.243452189
vessel remodeling	0.282886636
viral oncoproteins	
viral transforming genes	0.170166305
viral transforming proteins	0.240216312
virus-induced apoptosis	0.311537404
vitro acetyltransferase	0.431494323
vitro acetyltransferase activity	0.431145815
vitro acetyltransferase assay	0.435355324
vitro caspase cleavage	0.330841462
vitro inhibition	0.299309257
vitro phosphorylation	0.338363936
vitro phosphorylation sites	0.330540666
vitro phosphorylation studies	0.330357381
vitro protein-binding	
vitro protein-binding assay	
vitro transactivation	0.422650717
vitro transforming	0.334543014
vivo acetylation capacities	0.419927192
vivo acetylation capacity	0.417387684
vivo apoptosis program	0.319384423
vivo endothelial cell-specific apoptosis	0.306400365
vivo inhibited virus binding	0.139798291
vpr	0.376548218
wide palpebral fissures	0.16293985
widespread apoptosis	0.311390522
widespread apoptotic cell death	0.236597336

widespread inhibition	0.280180857
xi collagens	0.317813698
x-linked amelogenesis imperfecta	0.259163596
x-linked recessive hsp	0.20698574
yeast histone deacetylase	0.268266077
yeast transactivation assay	0.164527624
young human diploid fibroblasts	0.255947827
young versus senescent fibroblasts	0.306929284
zap	0.285908049
zap expression library	0.055066784

Table S24. *Textrous!*-mediated Individual mode noun-phrase analysis of bPTH(7-34) superconserved dataset. For each identified noun-phrase the Cosine Similarity score is given.

Individual: noun-phrases	**Cosine Similarity**
insulin resistance	0.059422944
abdominal subcutaneous adipocytes	0.01992443
abnormal mitochondria	0.049410181
absent phosphorylation	0.32413618
acidic activation	0.361541431
acidic activation domain	0.358800912
actin filaments anchor	-0.042020972
activated extracellular signal-regulated kinases	0.142371474
activated protein tyrosine kinases	0.099834759
activation assay	0.377901875
activation cascade	0.358063939
activation contraction	0.36441909
activation curves	0.360244811
activation domain	0.361175696
activation energies	0.360373595
activation energy	0.363151478
activation factors	0.366309911
activation mechanism	0.3598018
activation programs	0.3600776
activation reaction	0.360880066
activation segment phosphorylation	0.403910359
activation segment phosphorylation	0.403910359
activation sites	0.363686456
activation state	0.358868743
activation states	0.360235646
active catalytic domain	0.160998043
active chitinase catalytic domain	0.161041896
active kinase domain	0.207315246
active protein kinases	0.118024917
active serine hydrolase motif	0.121524268
active site catalytic triad	0.122479286
active site serine	0.220191323
active site serine residue	0.203517934
acute insulin response	0.051739534
adenylate kinases	0.02395248
adipocyte insulin action	0.05024067

adult mitochondria	0.017858804
aggregated mitochondria	0.111617633
a-kinase anchor	0.128325617
a-kinase anchor	0.128325617
a-kinase anchor protein	0.154166931
a-kinase anchor protein	0.154166931
a-kinase anchor proteins	
a-kinase anchor proteins	0.074730251
allergen activation	0.358170494
allosteric kinase inhibitor	0.231872302
altered signal transduction	0.039702702
aminoglycoside kinases	0.085080774
amino-terminal activation domain	0.360715612
amp-activated protein kinase	0.216809404
amp-activated protein kinase	
amp-activated protein kinase cascade	0.2222763
amp-activated protein kinase cascade	0.2222763
anchor loci	
anchor pcr	0.050945521
anchor point	0.083249652
anchor points	0.112808018
antibiotic staurosporine	0.290806038
antiviral signal transduction	0.039779322
apoptosis signal transduction pathway	0.297223445
apoptosis signal-regulating kinase	0.339115412
apoptosome complex	
apoptosome formation	0.260292205
apoptotic reagent staurosporine	0.324488828
aps kinases	0.048943717
aqueous cytosol	0.12933018
arterial endothelial signal transduction	0.102847574
astrocyte activation	0.37221367
atp-dependent kinases	0.102732181
atp-dependent phosphorylation	0.341982419
autonomic activation	0.357893773
autophagic vacuole formation	-0.148239088
autophagic vacuole fraction	-0.165525272
average transduction length	0.063062592
basal body temperatures	-0.018409591
basal insulin promoter activity	0.12583624
basal insulin release	0.055881022

basal kinase activity	0.207275671
basal phosphorylation	0.326242602
basic amino acid anchor	-0.055965539
bcr-abl signal transduction	0.046264874
bind phosphopeptides	0.230731995
bitter transduction	0.090720924
bitter transduction pathways	0.082732536
body temperatures	
bovine brain cytosol	-0.068254319
bovine cytosol	0.039516218
bovine heart mitochondria	0.078202427
bovine liver mitochondria	-0.001119366
brain mitochondria	-0.025261535
broad catalytic cleft	0.140007394
broad protein kinase inhibitor	0.233127757
brown adipocytes	0.005381375
calcium-dependent catalytic activity	0.188718268
calcium-dependent serine proteases	0.175061378
calmodulin-dependent serine kinase	0.204901964
camp-dependent activation	0.384744686
camp-dependent activation	0.384744686
camp-dependent attenuation	0.178110716
camp-dependent expression	0.117810478
camp-dependent inhibition	0.306514733
camp-dependent kinase	0.195767585
camp-dependent pathway	0.129839678
camp-dependent phosphorylation	0.323827224
camp-dependent phosphorylation	0.323827224
camp-dependent pka	0.142501083
camp-dependent pka	0.142501083
camp-dependent protein kinase	0.199135318
camp-dependent protein kinase activity	0.216690966
camp-dependent protein kinase activity	0.216690966
camp-dependent protein kinase catalytic subunit	0.176684667
camp-dependent protein kinase catalytic subunit	0.176684667
camp-dependent protein kinase pathway	0.194998199
camp-dependent protein kinase phosphorylation sites	0.266664441
camp-dependent protein kinase phosphorylation sites	0.266664441
camp-dependent protein kinase serine phosphorylation site	0.27603149
camp-dependent protein kinase serine phosphorylation site	0.27603149
camp-dependent protein kinase serine phosphorylation site	0.27603149

camp-dependent protein kinase substrates	0.198689955
camp-dependent protein kinase system	0.192103219
camp-dependent protein kinases	0.150460061
camp-dependent protein kinases	0.150460061
camp-dependent protein phosphorylation events	0.31390834
camp-dependent regulation	0.076939174
camp-dependent reporter system	0.102279578
camp-dependent serine-threonine protein kinases	0.193746632
camp-dependent serine-threonine protein kinases	0.193746632
camp-dependent serine-threonine protein kinases	0.193746632
camp-dependent signal transduction	0.130690344
camp-dependent signal transduction	0.130690344
camp-dependent signal transduction pathway	0.111099185
camp-dependent signal transduction pathway	0.111099185
camp-dependent signaling	0.096338347
camp-dependent signaling pathway	0.088731081
camp-dependent thyroid hormone	
camp-responsive element-binding protein phosphorylation	0.376180503
canonical protein-tyrosine kinase catalytic domain	0.219241003
canonical protein-tyrosine kinase catalytic domain	0.219241003
carbohydrate kinases	0.0734768
carboxypeptidase catalytic domain	0.10915666
carboxy-terminal activation helix	0.397403887
carboxy-terminal kinase domain	0.207288717
carboxy-terminal phosphorylation sites	0.329401881
carboxy-terminal serine cluster	0.165148722
cardiac mitochondria	0.113257668
cardiac mitochondrial ultrastructure	0.120367512
casein kinase ii consensus phosphorylation sites	0.269831022
casein kinase ii phosphorylation site	0.270131379
casein kinase ii phosphorylation sites	0.267646767
casein kinase phosphorylation sites	0.264586679
casein kinase type ii	0.220888359
caspase activation	0.393165646
caspase activation program	0.392539074
catalytic activation	0.362090611
catalytic activation	0.362090611
catalytic activities	0.121533088
catalytic activity	0.204946972
catalytic asparagine	0.105778847
catalytic cleavage site	0.171210493

catalytic cleft	0.13463826
catalytic competence	
catalytic core	0.135549567
catalytic core domain	0.164784249
catalytic core regions	0.130323108
catalytic cores	0.103628752
catalytic cysteine domain	0.12567042
catalytic domain	0.15451321
catalytic domain fragment	0.133032109
catalytic domain motifs	0.131674146
catalytic engine	0.104964313
catalytic kinase domain	0.207624671
catalytic kinase domain	0.207624671
catalytic lys	0.117474643
catalytic lysine	0.232248183
catalytic mechanism	0.158679915
catalytic metalloprotease domain	0.162435148
catalytic phosphorylation site	0.328626564
catalytic phosphorylation site	0.328626564
catalytic regions	0.104502779
catalytic residue	0.121059808
catalytic residues	0.10523032
catalytic serine	0.202327956
catalytic serine	0.202327956
catalytic site	0.123991185
catalytic transduction core	0.152520415
catalytic transduction core	0.152520415
catalytic tyrosine kinase domain	0.180793626
catalytic utilization	0.106185381
cell cytosol	0.041076114
cell division kinases	0.047851588
cellular activation	0.371007365
cellular ceramide content	0.222262201
cellular protein kinases	0.138765228
cellular signal transduction	0.125925581
cellular signal transduction pathways	0.115044858
central catalytic core domain	0.148747362
central catalytic domain	0.134799722
central insulin	
central serine residue	0.190082765
centromeric kinases	0.045790267

ceramide catabolism	0.070378297
ceramide composition	0.112803636
ceramide content	0.149842289
ceramide directly induced dna fragmentation	-0.004712564
ceramide generation	0.068748316
ceramide homolog	-0.017474359
ceramide hydrolysis	0.111043212
ceramide kinases	0.114078223
ceramide kinases	0.114078223
ceramide metabolism	0.033167101
ceramide production	0.083769932
ceramide release	0.108846099
ceramide storage	0.097387706
ceramide substrates	0.133470641
ceramide synthase	0.026988065
ceramide synthase activity	0.075183449
ceramide synthases	0.113163549
ceramide transport	
cgmp-dependent cation channels	
cgmp-dependent phosphodiesterase	0.070007978
cgmp-dependent phosphorylation	0.329741348
cgmp-dependent phosphorylation	0.329741348
cgmp-dependent protein kinase	0.190829091
cgmp-dependent protein kinase phosphorylation site	0.266852669
cgmp-dependent protein kinase phosphorylation site	0.266852669
cgmp-dependent protein kinase phosphorylation sites	0.264447899
cgmp-dependent protein kinase phosphorylation sites	0.264447899
characteristic n-terminal mitochondrial targeting domain	0.104285176
checkpoint kinases	-0.069816237
chemical activation	0.364251993
chemoattractant signal transduction	0.033780919
choline kinases	0.076844262
chondrocyte-specific activation	0.378843192
chromatin activation	0.396888343
chromatin immunoprecipitation	0.243554426
chromatin immunoprecipitation analyses	0.215730817
chromatin immunoprecipitation analysis	0.226187577
chromatin immunoprecipitation assay	0.25084355
chromatin immunoprecipitation assays	0.235718613
chromatin immunoprecipitation experiments	0.229003136
chromatin immunoprecipitation sequence analysis	0.199244905

chromatin immunoprecipitation sequencing	0.248343637
chromatin immunoprecipitation studies	0.229256793
chromosome immunoprecipitation experiments	
chymotrypsin-like serine proteases	0.180418026
circulating insulin	0.051265923
c-jun amino-terminal kinases	0.097295733
c-jun kinases	0.088989962
c-jun n-terminal kinase activation	0.24960332
c-jun n-terminal kinases	0.096743688
class ii hdac kinase	0.206994826
class ii hdac phosphorylation	0.332195679
class iii receptor-type tyrosine kinases	0.045067364
classic activation	0.361941106
clearing mitochondria	0.099163691
cold temperatures	-0.027749377
combined kinase inhibition	0.212393318
commercial insulin stocks	0.051339242
common catalytic domain	0.130157694
competitive chromatin immunoprecipitation	0.241181193
complex signal transduction pathways	0.050129199
concomitant activation	0.361094962
concomitant phosphorylation	0.329194612
concurrent activation	0.357988418
conformational activation	0.394206403
consensus map kinase phosphorylation site	0.256611427
consensus phosphorylation sites	0.327840919
consensus pka site	0.153429711
consensus tyrosyl kinase phosphorylation site	0.271454283
conserved camp-dependent protein kinase phosphorylation site	0.260581588
conserved camp-dependent protein kinase phosphorylation site	0.260581588
conserved kinase catalytic domains	0.1794931
conserved n-terminal serine	0.099178493
conserved protein kinase catalytic domain	0.194233136
conserved serine phosphorylation site	0.314993805
conserved serine phosphorylation sites	0.307092252
conserved tyrosine kinase phosphorylation site	0.231913191
constitutive phosphorylation	0.325819821
control cytosol	0.042866214
controls tgf-beta activation	0.368286212
cooperative activation	0.36701485
core body temperatures	0.054834482

core catalytic domain	0.164784249
creatine kinase inhibitor	0.231148418
creatine kinases	0.084618752
critical catalytic residue	0.120881373
critical catalytic residues	0.106744816
critical interacting	0.149238335
critical phosphorylation site	0.331750312
critical phosphoserine residue	0.128262055
critical serine	0.223300204
critical serine residues	0.17326872
critical transduction event	0.096218827
crosslinking immunoprecipitation	0.219034312
cryptic site activation	0.37016447
c-terminal catalytic core	0.128261682
c-terminal catalytic domain	0.132740745
c-terminal glycosylphosphatidylinositol membrane anchor	-0.026260604
c-terminal hydrophobic tail anchor characteristic	0.062116573
c-terminal kinase catalytic domain	0.20970278
c-terminal kinase catalytic domain	0.20970278
c-terminal membrane anchor	-0.013870822
c-terminal phosphorylation site	0.330888195
c-terminal phosphoserine residues	0.093185458
c-terminal protein tyrosine kinase catalytic domain	0.185520467
c-terminal serine	0.184214263
c-terminal serine-threonine kinase domain	0.22297692
c-terminal serine-threonine kinase domain	0.22297692
cultured adipocytes	0.089558201
cultured human adipocytes	0.08281749
cultured mouse adipocytes	-0.116834091
cyclic amp-dependent inhibition	0.252429293
cyclic amp-dependent protein kinase	0.207632466
cyclic amp-dependent protein kinase	
cyclic amp-dependent protein kinase phosphorylation site	0.270967781
cyclic amp-dependent protein kinase phosphorylation site	0.270967781
cyclic phosphorylation	0.336102591
cyclin d-dependent kinases	0.012500723
cyclin-dependent kinase activation	0.247248959
cyclin-dependent kinase inhibitor	0.20718667
cyclin-dependent kinase phosphorylation	0.244302826
cyclin-dependent kinases	0.045562612
cyclin-dependent protein kinases	0.073883829

cytokine-induced activation	0.358302274
cytokine-induced phosphorylation	0.330642857
cytoplasmic anchor protein	0.092171521
cytoplasmic kinases	0.074655885
cytoplasmic protein-tyrosine kinases	0.119378639
cytoplasmic signal transduction apparatus	0.042334929
cytoplasmic signal transduction pathways	0.05803164
cytoplasmic tyrosine kinases	0.063472169
cytosol extracts	0.098849654
cytosol independent	0.08143766
cytosolic catalytic domain	0.158694689
cytosolic phosphorylation	0.334809363
de novo ceramide synthesis	0.062632305
decreased activation	0.363984771
decreased catalytic activity	0.209006086
decreased fasting insulin	0.054206777
decreased mitochondrial nucleoside diphosphate kinase activity	0.22530763
decreased mitochondrial nucleoside diphosphate kinase activity	0.22530763
decreased phosphorylation	0.3351596
decreased pyruvate kinase activity	0.211897317
defective catalytic activity	0.128997234
defective mitochondria	0.01490871
deficient map kinase activation	0.232143984
diacylglycerol kinase catalytic site	0.19329823
diacylglycerol kinases	0.079397951
differentiated adipocytes	0.015766428
differentiated mouse adipocytes	-0.156700724
differentiated mouse brown adipocytes	-0.159600344
direct insulin action	0.0514925
direct phosphorylation	0.329600915
direct signal transduction pathway	0.063102756
discrete signal transduction pathways	0.062599685
divergent signal transduction cascade	0.097657078
dna interacting elements	-0.093516779
dna-dependent protein kinase catalytic subunit	0.166546787
dna-dependent protein kinase catalytic subunit activity	0.1831325
dna-dependent protein kinases	0.099229788
dnase activation	0.362863973
downstream activation	0.362293632
downstream caspase activation	0.398189977
downstream insulin signaling proteins	0.074445632

downstream insulin targets	0.064210557
downstream regulatory kinases	0.100333482
downstream signal transduction	0.109694966
drosophila anchor protein	-0.000951782
drosophila mitochondria	-0.010333585
dual phosphorylation	0.322397508
dual-specificity kinases	0.059470499
dynamic insulin release measurements	0.055810551
dynamic phosphorylation	0.326758152
dynamic phosphorylation mark	0.327377308
edema factor catalytic core	0.1368684
effect signal transduction	0.087635249
effector caspase activation	0.372183619
electric activation	0.361059956
elevated amp-activated protein kinase activity	0.231292186
elevated amp-activated protein kinase activity	0.231292186
elevated ceramide levels	0.016442207
elevated core temperatures	0.081855611
elevated phosphorylation	0.32389167
endogenous ceramide production	0.067814273
endogenous muscle creatine kinase promoter	0.237425231
endogenous phosphorylation	0.324576433
energy transduction	0.118486641
enhanced catalytic activity	0.22344991
enhanced insulin action	0.060535106
enhanced insulin secretion	0.050221976
enhanced insulin sensitivity	0.051975273
enhanced insulin signaling	0.075999544
enhanced kinase activity	0.214235205
enhanced phosphorylation	0.335623572
enhanced pka activity	0.184097314
enhanced signal transduction	0.096097717
enos catalytic activity	0.250823733
equivalent serine residue	0.200823228
erbb protein tyrosine kinases	0.078255063
erythrocyte cytosol	0.047668176
erythropoietin receptor-mediated activation	0.361025818
eukaryotic cell mitochondria	0.0549796
eukaryotic protein kinases	0.101361489
eukaryotic signal transduction	0.05851057
excess cellular ceramide	0.218094701

excessive activation	0.359862489
excessive insulin release	0.055828684
exogenous insulin	0.054504247
extended catalytic site	0.117414305
extra serine residue	0.198652265
extracellular c-terminal catalytic domain	0.199601854
extracellular regulated kinases	0.139466835
extracellular signal-regulated kinase activation	0.250981402
extracellular signal-regulated kinase mitogen-activated protein kinases	0.114444583
extracellular signal-regulated kinases	0.112904519
extreme insulin resistance	0.049376583
fetal adipocytes	-0.005249937
fibroblast mitochondria	-0.013612981
focal adhesion kinases	0.018837268
force activation	0.365636102
force transduction	0.108149008
forced activation	0.362271492
full activation	0.359696395
full kinase activity	0.206872151
full t-lymphocyte activation	0.360462615
functional adipocytes	-0.040469005
functional nerve growth factor signal transduction	0.05464456
functionally critical c-terminal membrane anchor region	-0.031461939
functionally interacting proteins	0.013695234
gastrocnemius muscle	0.095717828
gene-specific phosphorylation	0.329886601
germinal center kinases	0.049738723
glucocorticoid activation	0.379205728
glucosyl ceramide	0.185460757
glucosyl ceramide synthesis	0.121506457
glycosylphosphatidylinositol anchor	0.018733364
glycosylphosphatidylinositol anchor addition	0.012227978
glycosylphosphatidylinositol anchor biosynthesis	-0.105272154
glycosylphosphatidylinositol anchor sequences	-0.035092712
glycosylphosphatidylinositol anchor signal sequence	-0.009062671
glycosylphosphatidylinositol membrane anchor	-0.064433618
granule serine proteases	0.098962518
growth factor signal transduction	0.104451267
guanylate kinases	0.073769921
hdac catalytic activity	0.356807041
heat activation	0.479689454

hela cell cytosol	0.069168692
hela cell mitochondria	0.086738396
hela cell mitochondrial	0.10192545
hela cell mitochondrial fractions	0.102553712
herpesvirus thymidine kinase promoter	0.225877445
heterologous signal transduction pathways	0.048590841
high insulin demand	0.049751015
high mitochondrial activity	0.14711122
high phase separation temperatures	-0.079175096
high serine	0.195368039
high temperatures	0.001971171
higher temperatures	0.006914863
highly conserved serine	0.072385608
highly specific protein kinases rhodopsin kinase	0.174110619
histidine phosphorylation	0.322110899
hiv activation	0.375939168
hormone-dependent activation	0.364333368
hosphopeptide binding	0.178483358
human adenylate kinases	0.028258488
human adipocytes	0.030068
human bone marrow cell mitochondria	0.053052905
human cyclin-dependent kinases	0.049618142
human deoxyribonucleoside kinases	0.08395067
human fibroblast cytosol	-0.018288524
human hepatocyte mitochondria	0.10953561
human insulin	0.05522994
human insulin promoter	0.102723698
human insulin promoter region	0.097995122
human insulin resistance	0.052278377
human liver cytosol	-0.00715547
human liver mitochondria	0.012900292
human liver serine dehydratase	0.045426317
human mitochondria	0.081084224
human mitochondrial promoters	0.126313274
human pkc-delta	
human platelet cytosol	0.011725416
human primary adipocytes	0.028685128
human protein kinases	0.104817086
hydrophobic signal anchor sequence	0.039823705
hypertrophic adipocytes	0.100082408
immunoprecipitation analyses	0.167974065

immunoprecipitation analysis	0.198158446
immunoprecipitation assay	0.258932293
immunoprecipitation assays	0.222972784
immunoprecipitation experiments	0.221597473
immunoprecipitation studies	0.21311684
immunoprecipitation techniques	0.257460553
immunoreactive insulin	0.050584507
immunosuppressive drug rapamycin	0.174273871
impaired insulin signaling	0.060872342
impaired mitochondria	0.043861095
inactivating serine phosphorylation	0.328552752
inactivating serine phosphorylation	0.328552752
inactive camp-dependent protein kinase	0.201032412
inactive catalytic domain	0.159081309
increase kinase activity	0.208021746
increased activation	0.368659593
increased basal phosphorylation	0.332367323
increased basal pka activity	0.186331111
increased fasting insulin	0.058490126
increased insulin content	0.065076713
increased insulin release	0.067804758
increased insulin resistance	0.062526363
increased insulin secretion	0.053447351
increased insulin sensitivity	0.055273553
increased insulin signal transduction	0.077782459
increased insulin signal transduction	0.077782459
increased kinase activity	0.217330461
increased mitochondria	0.148264462
increased mitochondrial	0.123012201
increased phosphorylation	0.338039424
increased pka activity	0.18838084
increased serine pathway flux	0.184288778
increased temperatures	0.142165744
increased threonine phosphorylation	0.324998126
increased whole-body insulin sensitivity	0.053365262
incubation temperatures	0.162164978
individual adipocytes	0.015322843
individual insulin signaling components	0.062770846
individual pka isoforms	0.129440083
individual protein kinases	0.103004435
induced phosphorylation	0.348814131

inducible phosphorylation	0.34563242
inducible phosphorylation site	0.348258191
inhibited activation	0.377266784
inhibited phosphorylation	0.35558216
inhibiting phosphorylation	0.339050046
insufficient mitochondrial respiration activity	0.145713601
insufficient signal transduction	0.065804996
insulin action	0.050189033
insulin activator factor	0.065398282
insulin antibodies	0.049925492
insulin assay	0.066306481
insulin binding	0.087220651
insulin chicago	0.051924299
insulin content	0.051824072
insulin control element-binding transcription factor	0.163748631
insulin curve	0.049653096
insulin demand	0.051912199
insulin dependency	0.054280451
insulin dependent	0.052888286
insulin exposure	0.053028328
insulin expression	0.055902399
insulin granules	0.048672055
insulin hypersecretion	0.05004812
insulin hypoglycemia	0.04961877
insulin induction	0.064212932
insulin intolerance	0.050856091
insulin level	0.050082067
insulin los angeles	0.050833907
insulin mimetic	0.054585914
insulin minisatellite	0.050680637
insulin molecule	0.049147462
insulin processing	0.049481371
insulin production	0.050213621
insulin promoter	0.100363399
insulin promoter activity	0.126436247
insulin promoter variant	0.099097467
insulin release	0.054532069
insulin resistance	0.04941253
insulin resistant	0.053598665
insulin response	0.057193933
insulin response sequence	0.050691869

insulin sensitization	0.052927161
insulin signal transduction	0.065160223
insulin signal transduction	0.065160223
insulin signaling	0.068454749
insulin signaling pathway	0.070026091
insulin signals	0.04967227
insulin stimulation	0.070505634
insulin target tissues	0.051777206
insulin transcription	0.130452618
insulin treatment	0.067381966
insulin treatments	0.053552157
interacting cells	0.006210023
interacting dna sequences	-0.100149561
interacting domain	0.160876844
interacting domains	0.095744272
interacting effects	0.134032958
interacting molecules	0.0511492
interacting partner	0.160920435
interacting partners	0.158735758
interacting pathways	0.119286306
interacting protein	0.144125401
interacting proteins	0.040072108
interacting regions	0.137639592
interacting species	0.086268899
interacting splicing regulator	-0.014414606
intercellular signal transduction	0.037067471
interfacial activation	0.36216506
interfacial membrane anchor	-0.049854648
interferon-gamma activation site element	0.363164197
intracellular catalytic domain	0.109664415
intracellular ceramide	0.061045485
intracellular kinases	0.066817389
intracellular protein kinases	0.09176426
intracellular protein tyrosine kinases	0.074584964
intracellular serine levels	0.072195718
intracellular serine proteinase inhibitors	0.184453005
intracellular signal transduction	0.040799127
intracellular signal transduction domain	0.085235429
intracellular signal transduction pathway	0.04701928
intracellular signal transduction pathways	0.048142404
intracellular transduction	0.045241047

intracellular tyrosine kinase catalytic domain	0.176053105
intrinsic catalytic activity	0.255880087
intrinsic kinase activity	0.219757084
intrinsic protein kinase activity	0.220616356
invariant catalytic lysine	0.184506307
irf activation	0.378087446
isolated adipocytes	-0.001704594
isolated brain cell mitochondria	-0.019799248
isolated human mitochondria	0.048879052
isolated interacting peptide	0.000481085
isolated mitochondria	0.054602697
isolated muscle mitochondria	0.101413778
isolated n-terminal interacting peptide	0.021087247
isolated rat adipocytes	-0.010021023
isolated rat heart mitochondria	0.025498232
jak kinase activation	0.267639493
jak kinases	0.093815115
jak tyrosine kinases	0.068522394
janus kinases	0.085137813
janus protein kinases	0.110223
jurkat cell cytosol	0.182387381
keratinocyte mitochondria	0.082406882
kidney mitochondria	0.02815856
kinase activation	0.264876384
kinase activity	0.206957375
kinase anchor proteins	0.183865088
kinase catalytic domain	0.207624671
kinase catalytic domain	0.207624671
kinase catalytic domains	0.192611179
kinase consensus domain ix	0.226171788
kinase core domain	0.212242623
kinase domain induced osteopetrosis	0.212495683
kinase ii phosphorylation	0.268289825
kinase ii phosphorylation sites	0.268432768
kinase inhibition	0.216016711
kinase inhibitor	0.231226584
kinase inhibitor segment	0.228020532
kinase inhibitor staurosporine	0.239775114
kinase inhibitor staurosporine	
kinase pka	0.202570809
knockout adipocytes	-0.050503398

knockout altered serine	
latent mitochondrial dysfunction	0.09674029
leukocyte protein-tyrosine kinase	0.213217361
ligand interacting	0.000350326
lipid kinase catalytic domain	0.191913124
lipid kinases	0.037188279
liver cytosol	-0.018778772
liver mitochondria	0.006353501
local activation	0.361350377
long catalytic domain	0.147795885
long extracellular catalytic domain	0.22232244
long n-terminal serine	0.176429493
long serine	0.218888622
long-chain ceramide	0.103115866
low temperatures	-0.028593091
lower catalytic activity	0.192669834
lower insulin content	0.051187455
lower insulin response	0.056439592
lower kinase activity	0.206628514
lower temperatures	0.035750264
macrophage cytosol	-0.072919583
main phosphorylation domain	0.339580282
main pka subunits	
major camp-dependent protein kinase site	0.201063162
major cellular a-kinase substrate	0.202764095
major cellular interacting partner	0.194400911
major interacting proteins	0.031964641
major phosphorylation site	0.328625559
major pka phosphorylation site	0.271146047
major pka site	0.144928727
major signal transduction systems	0.049030384
mammalian mitochondria	0.054099593
mammalian signal transduction	0.043216499
map kinase activation	0.246001912
map kinase kinases	0.152569268
map kinase pathway activation	0.235637647
map kinase signal transduction pathway	0.162617705
map kinases	0.036160469
mapk kinases	-0.063872068
mass spectrometry phosphopeptide mapping	
mast kinases	0.056862179

mature adipocytes	-0.028452852
mature cultured mouse white fat adipocytes	-0.142524588
maximal activation	0.36344955
maximal catalytic activity	0.20702456
maximal phosphorylation	0.332592141
mechanical transduction	0.109869689
membrane anchor	-0.052721454
membrane anchor domain	0.026652756
membrane-associated guanylate kinases	0.062398135
membrane-associated serine hydrolase	0.098896109
membrane-bound vacuole	-0.182889278
mild insulin resistance	0.052592801
mild mitochondrial injury	0.105682295
minimal activation	0.363814194
minimal catalytic domain	0.15810575
mitochondria biogenesis	-0.015095757
mitochondria fragmentation	0.135204802
mitochondria localization signal	-0.002254789
mitochondria marker	0.052084906
mitochondria membrane potential	-0.010007979
mitochondria mouse cortical neurons	-0.194395228
mitochondria movements	0.088870629
mitochondria number	0.068424971
mitochondria results	0.090112922
mitochondria targeting signal	0.034231489
mitochondria transport	-0.013773437
mitochondrial acetyl-coa acetyltransferase	0.367679046
mitochondrial activity	0.154005537
mitochondrial activity assay	0.176541339
mitochondrial antibody	0.110286783
mitochondrial apoptosis	0.302562211
mitochondrial apoptotic pathway	0.219241164
mitochondrial binding site	0.163896513
mitochondrial calcium-binding protein	0.110732674
mitochondrial camp-dependent protein kinase	0.218559086
mitochondrial camp-dependent protein kinase	0.218559086
mitochondrial camp-dependent protein kinase	0.218559086
mitochondrial carbonic anhydrase	0.104415898
mitochondrial cardiomyopathy	0.096606777
mitochondrial carrier protein	0.10669319
mitochondrial chaperones	0.201365849

mitochondrial chaperonin	0.11739141
mitochondrial cleavage site	0.148919484
mitochondrial contact sites	0.102402988
mitochondrial creatine kinase	0.20844492
mitochondrial creatine kinase	0.20844492
mitochondrial cytochrome	0.110615685
mitochondrial cytosolic face	0.104331817
mitochondrial deacetylase	0.290466631
mitochondrial death pathway	0.132304201
mitochondrial death signaling pathway	0.112636917
mitochondrial elongation factor ef-tu	0.108503899
mitochondrial elongation factor tu	0.106242772
mitochondrial energy production	0.097614809
mitochondrial energy signature	0.103400457
mitochondrial fractions	0.096633874
mitochondrial fragmentation	0.112032177
mitochondrial fragmentation activity	0.166911779
mitochondrial fusion factors	0.097339089
mitochondrial glycine cleavage system	0.154098446
mitochondrial leakage	0.099045224
mitochondrial light strand promoter	0.122087017
mitochondrial marker protein	0.105270428
mitochondrial mass	0.09703432
mitochondrial matrix	0.253510445
mitochondrial matrix enzyme	0.196139686
mitochondrial matrix protein	0.26128765
mitochondrial matrix soluble fraction	0.229864807
mitochondrial matrix space	0.253534397
mitochondrial mechanisms	0.096940099
mitochondrial metalloproteinases	0.187564294
mitochondrial myopathy	0.100418167
mitochondrial oxidative phosphorylation	0.284558847
mitochondrial oxidative phosphorylation activities	0.285998465
mitochondrial oxidative phosphorylation system	0.274234939
mitochondrial permeability transition	0.107902895
mitochondrial permeability transition induction	0.122758679
mitochondrial permeability transition process	0.102327904
mitochondrial phosphoprotein profile	0.100987653
mitochondrial processing proteases	0.102426395
mitochondrial products	0.097189042
mitochondrial proliferation	0.105509474

mitochondrial proteases	0.114907431
mitochondrial protein	0.121670082
mitochondrial protein import	0.096775919
mitochondrial protein quality control	0.107747013
mitochondrial protein synthesis	0.11631877
mitochondrial protein translation	0.127545062
mitochondrial release factor	0.117067372
mitochondrial respiratory activity	0.132480968
mitochondrial response	0.099213544
mitochondrial retention	0.101791263
mitochondrial rhodanese	0.102771077
mitochondrial ribosome release factor	0.109984643
mitochondrial rupture	0.116960104
mitochondrial staining pattern	0.100905266
mitochondrial transcription	0.177485593
mitochondrial transcription factor	0.165553291
mitochondrial transcription termination factor	0.162178598
mitochondrial translation	0.106206365
mitochondrial translation apparatus	0.09742239
mitochondrial translation elongation factor	0.111303963
mitochondrial translation elongation factor ts	0.103789985
mitochondrial translation factor	0.124449184
mitochondrial translation release factor	0.122846314
mitochondrial translation systems	0.099732997
mitochondrial translational activity	0.149544838
mitochondrial velocity	0.097455435
mitogen activation induced recruitment	0.37219221
mitogen-activated protein kinase kinases	0.107714232
mitogen-activated protein kinases	-0.002369226
mitogenic activation	0.360200901
mitogenic signal transduction	0.090825573
mitotic cytosol	-0.077953979
mixed-lineage kinases	0.08841034
monocyte serine esterase variants	0.03139781
mouse adipocytes	
mouse brain cytosol	
mouse cardiac mitochondria	-0.028983499
mouse gastrocnemius muscle	
mouse kidney mitochondria	-0.161452714
mouse liver cytosol	-0.169549063
mouse liver mitochondria	-0.146487145

mouse mitochondria	-0.158379603
mouse ptdins kinases	
m-phase cytosol	0.097261853
m-phase kinases	0.07975015
multifunctional protein serine kinase	0.208447633
multifunctional protein serine kinase	0.208447633
multiple interacting loci	
multiple map kinases	0.028136688
multiple phosphorylation	0.322481224
multiple potential serine phosphorylation sites	0.319541819
multiple protein kinases	0.098077931
multiple serine residues	0.149354648
multiple signal transduction pathways	0.054994908
multiple upstream kinases	0.077745471
murine adipocytes	-0.113619718
muscle creatine kinase e-box enhancer	0.216750646
muscle creatine kinase promoter	0.241056385
muscle insulin resistance	0.069579043
muscle mitochondria	0.12251445
mutant mitochondria	-0.135359862
mutant mouse liver mitochondria	-0.19967968
mutant yeast mitochondria	-0.214476792
mutated kinases	0.084084365
myocardial mitochondria	0.157145487
myocyte activation	0.386679054
myofibroblast activation	0.382359633
nak kinase activity	0.208823728
neurofilament phosphorylation	0.322039749
neuroimmune activation	0.360232786
neuromuscular signal transduction	
neuron-specific signal transduction pathway	0.048288731
neutral serine proteases	0.160836285
neutrophil cytosol	-0.016144651
neutrophil-derived serine proteases	0.189606302
nicotinamide riboside kinases	0.09051185
nociceptor activation	0.358910351
nocturnal activation	0.358813502
nonreceptor protein tyrosine kinases	0.073283267
nonreceptor type kinases	0.160174215
nonreceptor tyrosine kinases	0.059714488
nonspecific kinases	0.071449432

normal catalytic activity	0.162379641
normal human heart mitochondria	0.065221826
normal human insulin	0.05058681
normal mitochondria	0.064164576
normal pka activity	0.166944449
novo ceramide synthesis	0.076872844
novo glucosyl ceramide synthesis	0.075536657
n-terminal catalytic domain	0.138209087
n-terminal catalytic domain characteristic	0.130398403
n-terminal membrane anchor	-0.006766954
n-terminal mitochondria localization sequence	0.004648726
n-terminal mitochondrial leader sequence cleavage site	0.126579924
n-terminal mitochondrial presequence	0.097666679
n-terminal mitochondrial translocation signal	0.143408702
n-terminal serine	0.183268315
n-terminal serine-threonine domain	0.200697664
n-terminal signal anchor sequence	0.049292728
nucleoside diphosphate kinases	0.061540287
nucleoside monophosphate kinases	0.076521033
n-wasp activation	0.358563433
observed cellular activation	0.3586404
odorant signal transduction	0.044986908
odorant signal transduction cascade	0.085577977
omental adipocytes	0.040036812
opsin phosphorylation	0.331814046
optimum catalytic activity	0.194639711
orderly activation	0.362675152
pancreatic beta cell-specific rat insulin promoter	0.063088521
pancreatic mitochondria	0.017433748
paradoxical activation	0.360082598
paraoxonase catalytic activity	0.132082197
parasite cytosol	0.055362266
pathologic phosphorylation	0.329920261
pdgfr activation	0.370536436
permanent activation	0.360896761
persistent phosphorylation	0.324687908
phagocytic vacuole	-0.190055107
phorbol ester activation	0.373195419
phorbol myristate acetate activation	0.372003251
phosphatidylinositol kinase domain	0.225160275
phosphoamino acid analysis	

phosphoamino acids	-0.055474292
phosphoinositide signal transduction cascades	0.103163213
phosphoinositide signal transduction pathway	0.084702559
phospholipase catalytic activity	0.113691272
phosphopeptide analogs	0.092667189
phosphorylating rb	
phosphorylating tyrosine residues	0.06321375
phosphorylation activity	0.352092174
phosphorylation cascade	0.342198255
phosphorylation events	0.325292559
phosphorylation increase	0.32657687
phosphorylation induced huvec migration	0.359091433
phosphorylation level	0.325598499
phosphorylation loop	0.327484658
phosphorylation motifs	0.323263375
phosphorylation reaction	0.33082876
phosphorylation reactions	0.328406322
phosphorylation response	0.326054838
phosphorylation sink	0.328026354
phosphorylation site	0.333313726
phosphorylation sites	0.324106503
phosphorylation state	0.327769689
phosphorylation states	0.329531685
phosphorylation status	0.326578403
phosphorylation target	0.330125889
phosphorylation targets	0.32252649
phosphoserine motif	0.010250014
phosphoserine motifs	0.010297743
phosphoserine phosphatase	-0.053943932
phosphoserine phosphatase activity	-0.016445995
phosphoserine phosphatase deficiency	
phosphoserine residues	0.095081929
phospho-specific antibodies	
photochemical transduction	0.088941848
physically remote catalytic sites	0.137233652
physiologic activation	0.35928297
physiologic temperatures	0.104397863
pka activity	0.17309041
pka cascade	0.156350171
pka catalytic subunit	0.102527921
pka catalytic subunit	0.102527921

pka inhibition	0.199706979
pka pathway	0.147982903
pka phosphorylation	0.270560859
pka priming	0.12710136
pka scaffolding	0.133044533
pka site	0.147859409
pka substrate	0.154157676
pka substrates	0.141599869
pka type ii regulatory probe	0.176313497
pka type ii regulatory subunit	0.134343848
pkc-delta activation	0.39905839
pkc-delta activation	0.39905839
pkc-epsilon agonist	
pkc-epsilon phosphorylation site	0.340414783
pkc-epsilon phosphorylation site	0.340414783
placental nuclear protein interacting	0.133790364
plasmodium falciparum glycosylphosphatidylinositol anchor	-0.013344125
polymorphonuclear activation	0.360252811
poor insulin response	0.058730976
poor phosphorylation	0.325109872
porcine liver cytosol	-0.020113396
positive signal transduction	0.066006741
posttranslational phosphorylation	0.341833619
potential activation loop phosphorylation motif	0.39509917
potential activation loop phosphorylation motif	0.39509917
potential c-terminal phosphorylation site	0.329522113
potential cyclin-dependent kinase phosphorylation site	0.247764356
potential interacting partner	0.123569907
potential interacting partners	0.119616087
potential membrane anchor segment	-0.051336322
potential n-terminal casein kinase ii phosphorylation site	0.272555891
potential phosphorylation domain	0.339359911
potential phosphorylation site	0.33303626
potential phosphorylation sites	0.323796896
potential serine	0.208501272
potential serine phosphorylation sites	0.327639234
potential serine phosphorylation sites	0.327639234
potential signal anchor sequence	0.019754622
potential tyrosine kinase phosphorylation site	0.238861795
potential tyrosine kinase phosphorylation sites	0.23722874
potentiated activation	0.375084215

predominant glucose phosphorylating activity	0.095597955
predominant glucose phosphorylating enzyme	0.009089396
predominant interacting proteins	0.038076603
preferred signal transduction mechanism	0.098125284
presumed mitochondrial translocation signal	0.136989718
presynaptic pka activation	0.259911142
primary adipocytes	0.023396547
primary domain interacting	0.154309435
primary mouse adipocytes	-0.158601048
primary phosphorylation	0.327609973
primary signal transduction mechanism	0.095195219
primed phosphorylation	0.324507245
principal mitochondrial factor	0.117495907
prokaryotic serine beta-lactamases	0.201249911
proliferative signal transduction pathways	0.061344284
prolonged phosphorylation	0.325547835
promoter activation	0.381756986
protein complex interacting	0.094878222
protein interacting	0.144125401
protein kinase activation	0.264832159
protein kinase activity	0.208751492
protein kinase catalytic	0.194113783
protein kinase catalytic domain	0.207733793
protein kinase catalytic domain	0.207733793
protein kinase catalytic domains	0.19449281
protein kinase catalytic subunit	0.168680441
protein kinase inhibitor	0.232087711
protein kinase inhibitor staurosporine	0.240095884
protein kinase inhibitor staurosporine	0.240095884
protein kinase inhibitors	0.210278144
protein kinase phosphorylation site	0.266597386
protein kinases	0.107696923
protein transduction domain	0.150830628
protein tyrosine kinases	0.078736962
protein-tyrosine kinase	0.206889048
protein-tyrosine kinase activity	0.22703415
protein-tyrosine kinases	0.126130861
protein-tyrosine phosphorylation	0.335079385
proteolytic activation	0.360407243
proteolytic activation site	0.36658698
proximal signal transduction	0.091076786

ptk activity	
ptp catalytic domain	0.128150984
punctate mitochondria	0.076393917
purified mitochondria	0.103021568
purified rabbit brain cytosol aspartyl	-0.022784102
radiolabeled insulin	0.049954792
radiolabeled regulatory ii subunit pka	0.094945787
radiolabeled serine	0.208391323
rapamycin activation	0.385796945
rapamycin activation	0.385796945
rapamycin administration	0.226672475
rapamycin analog	0.233445105
rapamycin derivative	0.237826712
rapamycin functions	0.194205663
rapamycin inhibitor	0.313453642
rapamycin signaling	
rapamycin treatment	0.277112998
rapid phosphorylation	0.328378869
rapid serine phosphorylation	0.333577442
rapid serine phosphorylation	0.333577442
rat brain cytosol	-0.0392286
rat brown adipose tissue mitochondria	0.005688418
rat cerebral cytosol	0.024772043
rat insulin ii promoter	0.096694915
rat insulin promoter	0.090406794
rat liver cytosol	-0.01808657
rat liver mitochondria	-0.003392475
rat pancreatic beta-cell insulin promoter enhancer	0.067695252
rat testis cytosol	-0.002717237
receptor-mediated phosphorylation	0.330942975
receptor-mediated signal transduction	0.081289296
receptor-mediated smad activation	0.442403302
reciprocal immunoprecipitation	0.248694311
reciprocal immunoprecipitation analysis	0.174163155
recombinant catalytic domain	0.131320282
recombinant c-terminal catalytic domain	0.119868874
recombinant pka	0.140808999
reduced downstream phosphorylation	0.328596392
reduced insulin	0.049379462
reduced insulin release	0.051642919
reduced insulin signaling	0.066039279

reduced mitochondrial translational activity	0.1362134
reduced rhodopsin transduction activity	0.164068445
reduced transduction	0.067277629
reductive activation	0.361868358
regional activation	0.358506268
regulating protein-tyrosine kinases	0.140060867
regulatory type ii pka	0.178049739
related kinases	0.071604377
related serine proteases	0.163508558
related stress-activated protein kinases	0.089011253
residual catalytic activity	0.182375849
retinal signal transduction	0.050631894
retroviral transduction	0.04961783
reverse signal anchor	0.061252898
reversed insulin resistance	0.053398461
reversible phosphorylation	0.33287412
reversible protein phosphorylation	0.323516452
rhodopsin phosphorylation	0.323543723
ribonucleoside diphosphate reductases	
ribonucleoside diphosphates	0.095080023
ribonucleoside monophosphates	0.098857867
rii pka	0.14004004
rod signal transduction cascade	0.090593258
screening rat brain cytosol	-0.047022422
selective phosphorylation	0.323842563
self-antigens insulin	0.049449603
sequential activation	0.362831758
sequential immunoprecipitation	0.294108466
sequential phosphorylation	0.331658483
serial activation	0.360426128
serine alleles	0.047864601
serine base exchange	0.167852105
serine biosynthesis	0.057114154
serine biosynthesis pathway	0.06591655
serine carboxypeptidases	0.223226858
serine catalytic site	0.198064886
serine catalytic site	0.198064886
serine cluster	0.143651244
serine codon	0.146185941
serine dehydratase	0.182090815
serine esterase	0.172393903

serine esterase inhibitor	0.280172491
serine esterases	0.23178112
serine exchange	0.195892158
serine exchange activity	0.264474735
serine hydrolase superfamily	0.054751691
serine hydrolases	0.195536438
serine hydroxymethyltransferase	0.221068985
serine kinase	0.204422552
serine kinase irak	0.198772674
serine kinase receptors	0.125776046
serine kinases	0.146562933
serine kinases	0.146562933
serine palmitoyltransferase	0.211096359
serine peptidases	0.215456031
serine phosphorylation	0.334975168
serine phosphorylation	0.334975168
serine proteases	0.185755766
serine proteinase	0.166436294
serine proteinase inhibitor	0.251088333
serine proteinase inhibitors	0.220694576
serine proteinase plasmin	0.02909518
serine proteinases	0.171463699
serine racemase	0.211667089
serine recognition site	0.156960833
serine residue	0.215396582
serine residues	0.173433552
serine rich	0.220642766
serine stretch	0.231536487
serine strip	0.233472304
serine substitutions	0.242701484
serine synthesis	0.182741843
serine synthesis flux	0.184009983
serine synthesis pathway	0.140361255
serine transmembrane protein	0.120384802
serine uptake	0.060317161
serine-threonine kinase	0.202977791
serine-threonine kinase activity	0.223461643
serine-threonine kinase activity	0.223461643
serine-threonine kinase domain	0.220253862
serine-threonine kinase domain	0.220253862
serine-threonine kinases	0.144104206

serine-threonine kinases	
serine-threonine protein kinase	0.206278475
serine-threonine protein kinases	0.157799847
serine-threonine protein kinases	0.157799847
signal anchor	0.062197097
signal transduction	0.066605488
signal transduction adaptor downstream	0.07963101
signal transduction analysis	0.045974334
signal transduction assays	0.106715642
signal transduction cascade	0.105632013
signal transduction cascades	0.073570131
signal transduction component	0.035166222
signal transduction components	0.043724738
signal transduction downstream	0.109694966
signal transduction events	0.063589709
signal transduction machinery	0.068029789
signal transduction mechanisms	0.070689265
signal transduction molecules	0.044985602
signal transduction motifs	0.056066158
signal transduction pathway	0.061733137
signal transduction pathway downstream	0.088636441
signal transduction pathways	0.06878697
signal transduction processes	0.060756663
signal transduction protein	0.105175692
signal transduction repressor	0.056182368
single catalytic domain	0.103559313
single potential serine phosphorylation site	0.321045751
single serine phosphorylation site	0.322047046
single serine phosphorylation site	0.322047046
single serine residue	0.144957442
sirna reduced phosphorylation	0.342835938
sirtuin catalytic domain	0.151588603
skeletal muscle insulin action	0.08301788
skeletal muscle mitochondria	0.124952215
skeletal muscle transduction	0.12361429
smad activation	0.457504988
smad anchor	0.425498748
soluble catalytic domain	0.104311461
specific immunoprecipitation	0.253782757
specific mapk kinases	-0.061287128
specific phosphorylation	0.329827869

specific phosphorylation events	0.324901485
specific phosphoserine	0.097820509
specific protein kinase inhibitors	0.210246292
specific protein tyrosine kinases	0.07997907
specific serine residue	0.204098488
specific serine residues	0.168368445
sperm mitochondria	0.019109621
s-phase checkpoint kinases	-0.080652553
sphingolipid metabolite ceramide	0.04899983
sphingosine kinases	0.091272254
spinal cord mitochondria	-0.04469896
spinal mitochondria	-0.020208317
split catalytic domain	0.149784569
srebp activation	0.37633012
stabilizing anchor	0.091939677
staurosporine treatment	0.262797129
steroid hormone signal transduction	0.043566847
stimulated sapk phosphorylation	0.339563874
stimulation induced phosphorylation	0.343680374
stress activation	0.367287811
stress-activated protein kinases	0.097397269
stress-activated signal transduction pathways	0.063789822
structural abnormal mitochondria	0.026575135
subcutaneous adipocytes	0.021478338
subfragment cdna probes	
substituted serine	0.225909588
substrate phosphorylation	0.324953363
subtilisin-like catalytic domain	0.150002787
sugar kinases	0.076256465
suppressing activation	0.357956543
sustained phosphorylation	0.329236314
synaptic cytosol	-0.13318146
synthetic mapk phosphopeptides	
taste transduction	0.03928497
telomerase anchor site	-0.028633793
tensin phosphorylation	0.333899987
tgf-beta activation	0.375496602
tgf-beta signal transduction	0.284529045
tgf-beta transcription activation	0.403330788
thymidine kinase promoter	0.224336179
t-lymphocyte activation	0.361547834

t-lymphocyte signal transduction	0.068143776
total cellular pantothenate kinase activity	0.215964041
total serine exchange activity	0.252973357
transduction apparatus	0.072335413
transduction efficiency	0.069901376
transduction elements	0.071460615
transduction pathway	0.069841368
transduction pathways	0.08443221
transduction processes	0.081407503
transduction region	0.060965074
transduction studies	0.067913685
transient activation	0.358815371
transient phosphorylation	0.337465658
translational control couples insulin synthesis	0.049493637
transmembrane anchor	-0.025765649
triggered mitochondrial swelling	0.104536969
tumor cytosol	-0.012829007
type ii camp-dependent protein kinase	0.230601629
type ii camp-dependent protein kinase	0.230601629
type ii pka anchor	0.189998822
type ii pka anchor	0.189998822
type ii serine proteinases	0.2182492
typical catalytic activity	0.189835594
typical mitochondria targeting presequence	0.001430764
typical mitochondria targeting sequence	-0.013642051
typical serine proteinase	0.151995335
tyrosine kinase catalytic domain	0.180793626
tyrosine kinase domain activation loop	0.24193171
tyrosine kinase phosphorylation motif	0.234256084
tyrosine kinase phosphorylation site	0.238563878
tyrosine kinase transforming protein	0.221689496
tyrosine kinases	0.064889708
tyrosine protein kinases	0.078736962
tyrosine-specific protein kinase activity	0.207731717
tyrosine-specific protein kinases	0.104540518
ubiquitous mitochondrial	0.096618412
udp-galactose ceramide galactosyltransferase	0.176012847
udp-glucose ceramide glucosyltransferase	0.137307903
unique serine residue	0.188289719
unique signal transduction pathways	0.061222237
unique t-cell tyrosine kinases	0.032203066

universal activation	0.358817153
upstream kinases	0.087966448
usual serine residue	0.209858501
v-abl transforming activity	
vacuole characteristics	-0.230258347
vacuole development	
vacuole formation	-0.17005906
vacuole membranes	-0.169854141
vacuole sorting protein	-0.047676012
variant insulin	0.051184329
vertebrate mitochondria	0.055048763
visual signal transduction	0.064944916
vitro catalytic activities	0.187593873
vitro immunoprecipitation studies	0.234361136
vitro kinase activity	0.222593306
vitro kinase assay	0.212908873
vitro kinase assay results	0.211307919
vitro mitochondrial import experiments	0.110712486
vitro mitochondrial transcription reaction	0.195661649
vitro phosphorylation	0.338363936
vitro phosphorylation sites	0.330540666
vitro phosphorylation studies	0.330357381
vitro protein kinase activity	0.221898912
vivo ceramide metabolism	0.078840721
vivo immunoprecipitation	0.19029879
vivo immunoprecipitation experiments	0.166337324
vivo insulin action	0.066524353
white adipocytes	0.006995644
yeast mitochondria	-0.135938456
yeast mitogen-activated protein kinase kinase kinases	0.116580179

Table S25. Word counts of Individual mode ‘dismantled’ noun-phrases from the bPTH(7-34) superconserved dataset. For each identified word the number of times the specific word occurred in the list of dismantled noun-phrases from *Textrous!* Individual processing is given. Word count scores were generated from the Wordle-sourced cloud.

Individual: Dismantled	**Word Count**
kinase	174
phosphorylation	151
protein	128
serine	124
activation	117
catalytic	112
transduction	105
mitochondrial	104
kinases	102
insulin	102
signal	95
dependent	80
domain	70
activity	66
mitochondria	65
site	54
camp	49
anchor	42
terminal	40
tyrosine	36
pka	33
ceramide	33
interacting	30
cytosol	30
immunoprecipitation	26
adipocytes	26
human	24
pathway	23
sites	21
c	21
potential	20
increased	20
ii	19
n	18

threonine	17
specific	17
promoter	16
mouse	16
factor	16
activated	15
pathways	14
inhibitor	14
temperatures	13
rat	13
membrane	13
intracellular	13
cell	13
residue	12
liver	12
core	12
vitro	11
type	11
signaling	11
muscle	11
chromatin	11
amp	11
release	10
rapamycin	10
downstream	10
cellular	10
vacuole	9
synthesis	9
subunit	9
sequence	9
residues	9
proteases	9
phosphoserine	9
isolated	9
enhanced	9
critical	9
conserved	9
cgmp	9
cascade	9
translation	8
resistance	8

reduced	8
proteins	8
multiple	8
map	8
major	8
induced	8
glycosylphosphatidylinositol	8
cyclin	8
active	8
transcription	7
staurosporine	7
response	7
extracellular	7
decreased	7
creatine	7
brain	7
beta	7
basal	7
assay	7
a	7
proteinase	6
primary	6
pkc	6
dna	6
cytoplasmic	6
cyclic	6
consensus	6
casein	6
binding	6
analysis	6
action	6
studies	5
single	5
regulatory	5
regulated	5
receptor	5
normal	5
motif	5
mitogen	5
matrix	5
lower	5

long	5
inhibition	5
high	5
experiments	5
elevated	5
content	5
vivo	4
typical	4
tgf	4
targeting	4
t	4
system	4
stress	4
segment	4
production	4
phosphorylating	4
phase	4
nucleoside	4
motifs	4
mediated	4
mechanism	4
loop	4
jun	4
inhibitors	4
individual	4
hela	4
fragmentation	4
exchange	4
events	4
energy	4
elongation	4
domains	4
diphosphate	4
cultured	4
control	4
cleavage	4
central	4
caspase	4
carboxy	4
bovine	4
body	4

yeast	3
unique	3
treatment	3
translational	3
transition	3
substrates	3
substrate	3
smad	3
skeletal	3
sequential	3
sensitivity	3
ribonucleoside	3
rhodopsin	3
related	3
regions	3
region	3
recombinant	3
reaction	3
rapid	3
radiolabeled	3
predominant	3
phosphatase	3
permeability	3
partner	3
pancreatic	3
oxidative	3
novo	3
nonreceptor	3
mutant	3
maximal	3
mapk	3
lymphocyte	3
jak	3
intrinsic	3
hydrolase	3
hormone	3
heart	3
hdac	3
glucosyl	3
glucose	3
full	3

formation	3
eukaryotic	3
esterase	3
epsilon	3
endogenous	3
element	3
dynamic	3
direct	3
differentiated	3
delta	3
cytosolic	3
complex	3
class	3
characteristic	3
cardiac	3
calcium	3
brown	3
biosynthesis	3
assays	3
apparatus	3
apoptosis	3
amino	3
activities	3
white	2
variant	2
upstream	2
udp	2
tu	2
transport	2
transmembrane	2
translocation	2
transient	2
transforming	2
total	2
thymidine	2
targets	2
target	2
systems	2
synthase	2
subcutaneous	2
stimulation	2

states	2
state	2
spinal	2
soluble	2
sequences	2
secretion	2
reversible	2
results	2
regulating	2
reciprocal	2
purified	2
proteolytic	2
proteinases	2
processing	2
processes	2
presequence	2
poor	2
physiologic	2
phosphopeptides	2
phosphopeptide	2
phosphoinositide	2
phosphoamino	2
phorbol	2
peptide	2
partners	2
odorant	2
neutrophil	2
multifunctional	2
molecules	2
mitogenic	2
minimal	2
mild	2
metabolism	2
mechanisms	2
mature	2
mass	2
marker	2
mammalian	2
main	2
m	2
lysine	2

loci	2
localization	2
lipid	2
like	2
levels	2
level	2
knockout	2
kidney	2
janus	2
interfacial	2
insufficient	2
inhibited	2
induction	2
inducible	2
increase	2
inactive	2
inactivating	2
import	2
impaired	2
hydrophobic	2
highly	2
guanylate	2
growth	2
gastrocnemius	2
functionally	2
functional	2
fractions	2
fraction	2
force	2
flux	2
fibroblast	2
fasting	2
factors	2
expression	2
excessive	2
enzyme	2
enhancer	2
elements	2
dual	2
drosophila	2
diacylglycerol	2

demand	2
dehydratase	2
defective	2
death	2
cytokine	2
concomitant	2
components	2
cluster	2
cleft	2
checkpoint	2
cascades	2
canonical	2
broad	2
bitter	2
autophagic	2
atp	2
associated	2
apoptotic	2
apoptosome	2
antibodies	2
analyses	2
altered	2
adenylate	2
acidic	2
acid	2
abnormal	2
abl	2
whole	1
wasp	1
visual	1
vertebrate	1
velocity	1
variants	1
v	1
utilization	1
usual	1
uptake	1
universal	1
ultrastructure	1
ubiquitous	1
tyrosyl	1

tumor	1
ts	1
triggered	1
triad	1
treatments	1
tissues	1
tissue	1
thyroid	1
testis	1
termination	1
tensin	1
telomerase	1
techniques	1
taste	1
tail	1
synthetic	1
synthases	1
synaptic	1
swelling	1
sustained	1
suppressing	1
superfamily	1
sugar	1
subunits	1
subtilisin	1
substitutions	1
substituted	1
subfragment	1
structural	1
strip	1
stretch	1
strand	1
storage	1
stocks	1
stimulated	1
steroid	1
status	1
staining	1
stabilizing	1
srebp	1
split	1

splicing	1
sphingosine	1
sphingolipid	1
sperm	1
spectrometry	1
specificity	1
species	1
space	1
sorting	1
sirtuin	1
sirna	1
sink	1
signature	1
signals	1
serial	1
sequencing	1
separation	1
sensitization	1
self	1
selective	1
screening	1
scaffolding	1
sapk	1
s	1
rupture	1
rod	1
rii	1
rich	1
ribosome	1
riboside	1
rhodanese	1
reversed	1
reverse	1
retroviral	1
retinal	1
retention	1
responsive	1
respiratory	1
respiration	1
resistant	1
residual	1

repressor	1
reporter	1
remote	1
regulator	1
regulation	1
regional	1
reductive	1
reductases	1
recruitment	1
recognition	1
receptors	1
reagent	1
reactions	1
rb	1
racemase	1
rabbit	1
quality	1
pyruvate	1
punctate	1
ptp	1
ptk	1
ptdins	1
proximal	1
promoters	1
prolonged	1
proliferative	1
proliferation	1
prokaryotic	1
programs	1
program	1
profile	1
products	1
process	1
probes	1
probe	1
principal	1
priming	1
primed	1
presynaptic	1
presumed	1
preferred	1

potentiated	1
posttranslational	1
positive	1
porcine	1
polymorphonuclear	1
points	1
point	1
platelet	1
plasmodium	1
plasmin	1
placental	1
physically	1
photochemical	1
phosphoprotein	1
phospholipase	1
phosphodiesterase	1
phospho	1
phosphatidylinositol	1
phagocytic	1
persistent	1
permanent	1
peptidases	1
pdgfr	1
pcr	1
pattern	1
pathologic	1
parasite	1
paraoxonase	1
paradoxical	1
pantothenate	1
palmitoyltransferase	1
osteopetrosis	1
orderly	1
optimum	1
opsin	1
omental	1
observed	1
number	1
nuclear	1
nonspecific	1
nocturnal	1

nociceptor	1
nicotinamide	1
neutral	1
neurons	1
neuron	1
neuromuscular	1
neuroimmune	1
neurofilament	1
nerve	1
nak	1
myristate	1
myopathy	1
myofibroblast	1
myocyte	1
myocardial	1
mutated	1
murine	1
movements	1
monophosphates	1
monophosphate	1
monocyte	1
molecule	1
mixed	1
mitotic	1
minisatellite	1
mimetic	1
migration	1
metalloproteinases	1
metalloprotease	1
metabolite	1
membranes	1
mechanical	1
measurements	1
mast	1
marrow	1
mark	1
mapping	1
macrophage	1
machinery	1
lys	1
low	1

los	1
local	1
lineage	1
light	1
ligand	1
leukocyte	1
length	1
leakage	1
leader	1
latent	1
lactamases	1
keratinocyte	1
jurkat	1
ix	1
isoforms	1
irf	1
irak	1
invariant	1
intolerance	1
interferon	1
intercellular	1
injury	1
inhibiting	1
independent	1
incubation	1
immunosuppressive	1
immunoreactive	1
iii	1
hypoglycemia	1
hypertrophic	1
hypersecretion	1
hydroxymethyltransferase	1
hydrolysis	1
hydrolases	1
huvec	1
hosphopeptide	1
homolog	1
hiv	1
histidine	1
higher	1
heterologous	1

herpesvirus	1
hepatocyte	1
helix	1
heat	1
granules	1
granule	1
glycine	1
glucosyltransferase	1
glucocorticoid	1
germinal	1
generation	1
gene	1
gamma	1
galactosyltransferase	1
galactose	1
fusion	1
functions	1
fragment	1
forced	1
focal	1
filaments	1
fetal	1
fat	1
falciparum	1
face	1
extreme	1
extracts	1
extra	1
extended	1
exposure	1
exogenous	1
excess	1
event	1
esterases	1
ester	1
erythropoietin	1
erythrocyte	1
erbb	1
equivalent	1
enos	1
engine	1

energies	1
endothelial	1
electric	1
efficiency	1
effects	1
effector	1
effect	1
ef	1
edema	1
e	1
dysfunction	1
drug	1
dnase	1
division	1
divergent	1
discrete	1
directly	1
diphosphates	1
development	1
derived	1
derivative	1
dependency	1
deoxyribonucleoside	1
deficient	1
deficiency	1
deacetylase	1
de	1
d	1
cytochrome	1
cysteine	1
curves	1
curve	1
cryptic	1
crosslinking	1
couples	1
cortical	1
cores	1
cord	1
cooperative	1
controls	1
contraction	1

contact	1
constitutive	1
conformational	1
concurrent	1
composition	1
component	1
competitive	1
competence	1
common	1
commercial	1
combined	1
cold	1
codon	1
coa	1
clearing	1
classic	1
circulating	1
chymotrypsin	1
chromosome	1
chondrocyte	1
choline	1
chitinase	1
chicago	1
chemoattractant	1
chemical	1
characteristics	1
chaperonin	1
chaperones	1
channels	1
chain	1
cerebral	1
centromeric	1
center	1
cells	1
cdna	1
cation	1
catabolism	1
carrier	1
cardiomyopathy	1
carboxypeptidases	1
carboxypeptidase	1

carbonic	1
carbohydrate	1
calmodulin	1
box	1
bound	1
bone	1
biogenesis	1
bind	1
bcr	1
basic	1
base	1
average	1
autonomic	1
attenuation	1
astrocyte	1
aspartyl	1
asparagine	1
arterial	1
aqueous	1
aps	1
antiviral	1
antigens	1
antibody	1
antibiotic	1
anhydrase	1
angeles	1
analogs	1
analog	1
aminoglycoside	1
allosteric	1
allergen	1
alleles	1
agonist	1
aggregated	1
adult	1
administration	1
adipose	1
adipocyte	1
adhesion	1
addition	1
adaptor	1

acute	1
activator	1
actin	1
acids	1
acetyltransferase	1
acetyl	1
acetate	1
absent	1
abdominal	1

Table S26. Word counts of Collective mode 'dismantled' noun-phrases from the bPTH(7-34) superconserved dataset. For each identified word the number of times the specific word occurred in the list of dismantled noun-phrases from *Textrous!* Individual processing is given. Word count scores were generated from the Wordle-sourced cloud.

Collective: Dismantled	**Word Count**
histone	156
activation	116
fibroblasts	110
intrinsic	108
inhibition	107
apoptotic	107
phosphorylation	106
apoptosis	104
collagen	102
protein	87
remodeling	85
activity	79
inhibited	74
heat	72
human	69
binding	66
shock	64
dermal	63
cell	63
acetylation	56
domain	55
caspase	55
transactivation	53
acetyltransferase	51
transforming	50
factor	45
connective	41
tissue	40
growth	40
chaperone	39
jurkat	37
deacetylase	37
cells	32
beta	32

terminal	31
increased	28
smad	27
specific	26
initiator	26
imperfecta	26
coactivator	26
cdna	25
fracture	24
t	23
proteins	23
osteogenesis	23
type	22
nucleosomal	22
acetylated	22
response	21
expression	21
element	21
collagens	21
site	20
ii	20
chromatin	20
adenovirus	20
histones	19
hdac	19
collagenase	19
primary	18
library	18
dependent	18
cultured	18
cofactors	18
ccaat	18
tendon	17
induced	17
n	16
genes	16
sites	14
pathway	14
death	14
complex	14
camp	14

procollagen	13
inhibitor	13
dna	13
c	13
vitro	12
responsive	12
potential	12
nonhistone	12
complexes	12
templates	11
signaling	11
severe	11
iii	11
fractures	11
domains	11
deacetylases	11
core	11
bone	11
activities	11
transcription	10
substrate	10
receptor	10
membrane	10
matrix	10
formation	10
enhanced	10
downstream	10
decreased	10
treatment	9
syndrome	9
superfamily	9
substrates	9
properties	9
nuclear	9
normal	9
motif	9
mediated	9
kinase	9
endothelial	9
ehlers	9
danlos	9

creb	9
alpha	9
acetyl	9
transactivator	8
small	8
sequence	8
septic	8
scleroderma	8
reduced	8
promoter	8
potentiated	8
myofibroblast	8
interstitial	8
effector	8
deposition	8
critical	8
consensus	8
chondrocyte	8
cellular	8
caspases	8
activated	8
vertebral	7
vascular	7
unfolding	7
tumor	7
tubulin	7
translocated	7
repeat	7
recruitment	7
multiple	7
mechanism	7
levels	7
hormone	7
helix	7
fibroblast	7
elements	7
diploid	7
cleavage	7
class	7
box	7
assay	7

triple	6
tissues	6
target	6
stromal	6
staurosporine	6
signal	6
short	6
senescent	6
risk	6
production	6
patient	6
nucleosome	6
methionine	6
mammalian	6
major	6
local	6
impaired	6
hsp	6
foreskin	6
decorin	6
coactivators	6
chloramphenicol	6
active	6
vivo	5
vi	5
translation	5
studies	5
stress	5
serine	5
regulated	5
rapid	5
program	5
palpebral	5
osteoporotic	5
nad	5
mechanisms	5
lysine	5
lymphocyte	5
low	5
inhibitors	5
hamster	5

global	5
general	5
fragments	5
folding	5
fissures	5
fibril	5
factors	5
extracellular	5
early	5
defects	5
defect	5
control	5
conserved	5
cognate	5
codon	5
choline	5
chemical	5
cascade	5
bromide	5
basal	5
atp	5
abnormal	5
ability	5
virus	4
tyrosine	4
transient	4
tgf	4
synovial	4
stimulated	4
segment	4
reversible	4
replication	4
rat	4
pro	4
pkc	4
pharmacologic	4
pathways	4
negative	4
myocyte	4
mutant	4
mild	4

microvascular	4
maximal	4
massive	4
libraries	4
leukemia	4
ix	4
isolated	4
iron	4
interaction	4
inhibitory	4
induction	4
high	4
hela	4
glucocorticoid	4
gabp	4
free	4
fibrils	4
fibrillar	4
feedback	4
events	4
essential	4
embryo	4
dominant	4
differentiation	4
cytosolic	4
concomitant	4
chicken	4
chain	4
catalytic	4
capacity	4
bodies	4
bacterial	4
autosomal	4
associated	4
assembly	4
anti	4
amelogenesis	4
acetyltransferases	4
acetylase	4
widespread	3
viral	3

vii	3
ventricular	3
vector	3
ubiquitin	3
typical	3
types	3
transport	3
tails	3
systemic	3
system	3
synthetic	3
synthesis	3
suppressing	3
status	3
state	3
slow	3
skin	3
sirna	3
sheath	3
sequential	3
sequences	3
selective	3
sclera	3
responses	3
resistance	3
residues	3
release	3
regulatory	3
regulator	3
region	3
recognition	3
recessive	3
reaction	3
purified	3
prolonged	3
proliferation	3
programs	3
processing	3
process	3
preferred	3
positive	3

poor	3
polypeptides	3
phosphatase	3
phenotype	3
pathologic	3
partial	3
papillae	3
noxious	3
nonlethal	3
muscle	3
mrna	3
mps	3
mouse	3
modifications	3
modification	3
moderate	3
mitochondrial	3
maturation	3
marks	3
machinery	3
lymphatic	3
lower	3
loop	3
loci	3
lipid	3
ligase	3
latent	3
late	3
infection	3
inducible	3
highly	3
helical	3
gtpase	3
glycoprotein	3
gastric	3
functional	3
full	3
fragmentation	3
form	3
fold	3
fiber	3

extracts	3
experiments	3
excessive	3
endogenous	3
elevated	3
electric	3
effects	3
dynamic	3
disorders	3
disorder	3
direct	3
digestion	3
delta	3
defective	3
cyanogen	3
crystallin	3
cooperative	3
components	3
chromosomal	3
central	3
cartilage	3
cardiac	3
carboxy	3
bound	3
blood	3
bind	3
arterial	3
antisense	3
angiogenic	3
amino	3
adult	3
actin	3
acidic	3
absent	3
abnormalities	3
zap	2
young	2
yeast	2
xi	2
x	2
weakness	2

wall	2
versus	2
vectors	2
universal	2
unique	2
transformed	2
transformation	2
transferase	2
trans	2
toxic	2
tonic	2
thermal	2
tendons	2
targets	2
targeting	2
targeted	2
subunits	2
stimulus	2
stimulation	2
sterol	2
states	2
stable	2
stability	2
splicing	2
specialized	2
somatic	2
soluble	2
soft	2
single	2
signals	2
serum	2
serial	2
sensitivity	2
secretion	2
sclerosis	2
rodent	2
reticulum	2
results	2
residue	2
reporter	2
replacement	2

repair	2
renal	2
related	2
regulating	2
regions	2
regional	2
reflexes	2
recombinant	2
receptors	2
reagent	2
rate	2
rabbit	2
pulmonary	2
proteolytic	2
progressive	2
progression	2
profiles	2
primed	2
posttranslational	2
polymorphism	2
platelet	2
phosphopeptides	2
phospholipid	2
phorbol	2
peptides	2
patterns	2
patients	2
partially	2
part	2
papilla	2
oncoproteins	2
oncogene	2
oligonucleotide	2
neutrophil	2
native	2
naked	2
multiprotein	2
mucosal	2
morpholino	2
molecule	2
modified	2

minor	2
minimal	2
migration	2
microtubule	2
metal	2
meningeal	2
mature	2
matrices	2
mast	2
markers	2
mark	2
manifestations	2
lymphocytes	2
loss	2
loose	2
lipoprotein	2
linker	2
linked	2
light	2
lethal	2
lesions	2
kidney	2
inverted	2
intracellular	2
interferon	2
inherited	2
inflammatory	2
individual	2
hypertrophic	2
hiv	2
hepatocyte	2
groups	2
greater	2
gram	2
glomerular	2
gingival	2
gel	2
foot	2
extremely	2
expressed	2
epidermal	2

enzymatic	2
entry	2
enhancer	2
energy	2
endoplasmic	2
embryonic	2
efficiency	2
dual	2
drug	2
divergent	2
distal	2
displacement	2
diseases	2
diminished	2
differences	2
density	2
dendritic	2
degranulation	2
degeneration	2
deficiency	2
deep	2
cytoskeletal	2
cytokines	2
cytokine	2
cyclic	2
cycle	2
corneal	2
contraction	2
contact	2
congenita	2
component	2
complete	2
competitive	2
common	2
colony	2
code	2
coa	2
clone	2
clearance	2
chronic	2
chromosome	2

chinese	2
channel	2
cascades	2
carnitine	2
cardiomyocyte	2
capillaries	2
callus	2
calcium	2
bundles	2
brain	2
boxes	2
biopsies	2
behavior	2
basement	2
baby	2
b	2
assays	2
artery	2
arrays	2
apoptosome	2
antihuman	2
antibody	2
analysis	2
amyloid	2
alveolar	2
allele	2
agent	2
adhesion	2
acute	2
abnormality	2
abilities	2
zymogen	1
xviii	1
xv	1
xiv	1
wounds	1
wound	1
wide	1
wasp	1
viruses	1
villus	1

viability	1
vessels	1
vessel	1
vero	1
variation	1
variants	1
variant	1
valve	1
v	1
uterine	1
upstream	1
upper	1
unrelated	1
units	1
ubiquitous	1
ubiquitination	1
triggering	1
trigger	1
transmembrane	1
translocation	1
translational	1
transforms	1
transfer	1
transdifferentiation	1
transactivators	1
trail	1
trafficking	1
toxicity	1
total	1
topoisomerase	1
tibialis	1
tibia	1
thyroid	1
thymus	1
thymocyte	1
thresholds	1
threonine	1
therapeutic	1
testicular	1
term	1
tensin	1

temperature	1
systolic	1
synchronous	1
synaptic	1
sweat	1
sustained	1
susceptibility	1
supply	1
sulfate	1
suicide	1
subfamily	1
subepithelial	1
structures	1
structural	1
strength	1
storage	1
stiffness	1
stem	1
staining	1
stage	1
stabilized	1
srebp	1
spontaneously	1
spontaneous	1
spiral	1
spindle	1
spermatocyte	1
snornp	1
smooth	1
slit	1
sleep	1
skeleton	1
skeletal	1
sinus	1
sink	1
simplex	1
simple	1
signature	1
sheet	1
sharp	1
shared	1

sera	1
sensor	1
segments	1
secondary	1
sarcomere	1
sapk	1
salicylate	1
role	1
ridges	1
ridge	1
rich	1
ribosomal	1
rhythmic	1
rhodopsin	1
rhesus	1
reverse	1
retroviruses	1
retinoic	1
retinal	1
retardation	1
resting	1
required	1
repeats	1
regulators	1
regular	1
regression	1
reductive	1
reduction	1
redox	1
recurrent	1
recombination	1
reciprocal	1
reactions	1
rb	1
rates	1
rapamycin	1
random	1
radical	1
qualitative	1
quail	1
proteolysis	1

proteoglycans	1
proteases	1
property	1
proper	1
propensity	1
promoting	1
promoters	1
prolyl	1
proliferating	1
prokaryotic	1
programmed	1
progenitors	1
progenitor	1
product	1
processes	1
pressure	1
presentation	1
preparation	1
predominant	1
postmenopausal	1
portal	1
polymorphonuclear	1
polarity	1
pluripotent	1
plasmid	1
plasma	1
plantar	1
placental	1
physiologic	1
photosensitivity	1
phosphoproteins	1
persistent	1
permanent	1
periodic	1
period	1
pericyte	1
peptide	1
pelvic	1
pdgfr	1
patterning	1
pattern	1

passive	1
passage	1
partners	1
particles	1
parp	1
parathyroid	1
parallel	1
paradoxical	1
painful	1
packaging	1
outgrowth	1
outcome	1
ouabain	1
osteoblast	1
osmotic	1
orientation	1
organization	1
orderly	1
opsin	1
onset	1
oncogenes	1
oligonucleotides	1
oligodendrocyte	1
ocular	1
octamer	1
observed	1
nucleosomes	1
nuclei	1
nonspecific	1
nonlinear	1
nomenclature	1
nocturnal	1
nociceptor	1
nociception	1
nk	1
nicotinamide	1
nevi	1
neutrophils	1
neuron	1
neuroimmune	1
neurofilament	1

neuroepithelial	1
neural	1
neovascularization	1
necrosis	1
narrow	1
myristate	1
myocytes	1
myocardial	1
myoblasts	1
mycobacterial	1
myc	1
myb	1
mutation	1
mutants	1
motifs	1
mosaicism	1
monkey	1
molecules	1
modulator	1
modulated	1
modifiers	1
modifier	1
mixtures	1
mitogenic	1
mitogen	1
mimicry	1
migrating	1
microvasculature	1
methylated	1
methylase	1
methyl	1
metalloproteinase	1
metabolism	1
messages	1
mesangial	1
melting	1
melanoma	1
melanin	1
medullary	1
mediator	1
maximum	1

maternal	1
maps	1
mapk	1
map	1
manganese	1
main	1
lymphoma	1
lymphoblastoid	1
luciferase	1
lovastatin	1
long	1
locus	1
localized	1
localization	1
lithium	1
lines	1
life	1
level	1
leukocytes	1
leprosy	1
lens	1
left	1
layers	1
lattices	1
lateral	1
lacz	1
labeled	1
kinetics	1
keratinocytes	1
jun	1
isoniazid	1
irradiation	1
irradiated	1
irf	1
ion	1
invertebrate	1
invasion	1
intestinal	1
interlobular	1
interfacial	1
interface	1

insulin	1
instability	1
insoluble	1
injury	1
inhibiting	1
inflammation	1
infiltration	1
inducing	1
inducers	1
inducer	1
indomethacin	1
indirect	1
independent	1
increase	1
inappropriate	1
inactive	1
inactivating	1
immune	1
immobilized	1
iiic	1
iiia	1
iib	1
iia	1
hypoplastic	1
hypoplasia	1
hyperalgesia	1
huvec	1
host	1
homologous	1
history	1
histidine	1
hip	1
heteroduplexes	1
herpes	1
heritable	1
hepatocytes	1
hepatocellular	1
hemorrhagic	1
hematopoietic	1
helices	1
heart	1

healing	1
hcv	1
harmful	1
hair	1
group	1
groove	1
gorilla	1
golgi	1
goat	1
glycinergic	1
glycation	1
glutamatergic	1
glucokinase	1
glands	1
genotype	1
genomic	1
gene	1
gap	1
gamma	1
fusions	1
functions	1
freeze	1
fraction	1
forced	1
force	1
follicle	1
foci	1
focal	1
fluoride	1
fibers	1
fetal	1
female	1
feeding	1
fanconi	1
families	1
extraskeletal	1
extensor	1
extension	1
extended	1
exposure	1
experimental	1

exchange	1
excess	1
ethylmaleimide	1
ethidium	1
estrogen	1
ester	1
erythropoietin	1
erythrocyte	1
erythroblast	1
epstein	1
epsilon	1
eosinophil	1
enzymes	1
environmental	1
environment	1
enterocyte	1
enhancers	1
enhancement	1
energies	1
endotoxic	1
endometrial	1
endocardial	1
end	1
empty	1
elimination	1
electrophysiologic	1
electroconvulsive	1
elastase	1
effect	1
eccrine	1
ec	1
ebv	1
dynein	1
dopamine	1
dnase	1
dnaj	1
division	1
disordered	1
disease	1
dinucleotide	1
dimethyl	1

dihydrolipoamide	1
diffuse	1
differentiated	1
differential	1
difference	1
dids	1
diameters	1
diameter	1
development	1
developing	1
determinants	1
determinant	1
destruction	1
descending	1
dermatitis	1
derived	1
derivatives	1
deprivation	1
dense	1
denaturation	1
demethylases	1
degradation	1
degenerative	1
deficient	1
decidual	1
cytosol	1
cysts	1
cysteine	1
cushions	1
curves	1
currents	1
cryptic	1
crosslinking	1
couples	1
corpses	1
copper	1
coordinating	1
conversion	1
controls	1
content	1
containing	1

constitutive	1
constant	1
connections	1
congenital	1
conformational	1
conditions	1
concurrent	1
compression	1
competence	1
compensatory	1
combined	1
colon	1
collateral	1
cold	1
coagulation	1
clusters	1
classic	1
circadian	1
chromosomes	1
chorionic	1
chloride	1
chimeric	1
chick	1
characteristics	1
characteristic	1
chaperones	1
challenge	1
chains	1
cgmp	1
cervical	1
caucasian	1
catenin	1
catabolism	1
cases	1
cartilaginous	1
cardiovascular	1
cardiomyocytes	1
carcinoma	1
carcinogenic	1
carbohydrate	1
capsular	1

capacities	1
canonical	1
candidate	1
cancer	1
calreticulin	1
calnexin	1
calf	1
bulk	1
bronchiolar	1
broad	1
bovine	1
body	1
blue	1
blocks	1
blocking	1
biotinylation	1
biology	1
bed	1
baseline	1
barr	1
baculoviral	1
avoidance	1
avian	1
average	1
auxiliary	1
autonomous	1
autonomic	1
autoimmune	1
atypical	1
attribute	1
attenuated	1
atrophy	1
atrioventricular	1
atopic	1
asymmetric	1
astrocyte	1
aspirin	1
arrangement	1
area	1
architecture	1
arch	1

apical	1
aortic	1
antigens	1
antigen	1
antibiotic	1
antiangiogenic	1
anterior	1
anomaly	1
ankyrin	1
angiogenesis	1
anemia	1
androgenic	1
anchor	1
amplification	1
amp	1
amniotic	1
amnion	1
amines	1
ameloblast	1
amanitin	1
alternative	1
allergen	1
albumin	1
alanine	1
ala	1
airway	1
aif	1
aging	1
affinity	1
adventitial	1
adjuvant	1
adhesiveness	1
adenine	1
additive	1
activator	1
activating	1
acid	1
acetate	1
accounts	1
access	1
acceptors	1

accelerated	1
abl	1
aberrant	1

Table S27. Word counts of Collective + Individual mode 'dismantled' noun-phrases from the bPTH(7-34) superconserved dataset. For each identified word the number of times the specific word occurred in the list of dismantled noun-phrases from *Textrous!* Individual processing is given. Word count scores were generated from the Wordle-sourced cloud using WriteWords (http://www.writewords.org.uk/word_count.asp).

Collective + Individual Words	**Count**
phosphorylation	257
activation	233
protein	215
kinase	183
histone	156
activity	145
serine	129
domain	125
catalytic	116
inhibition	112
intrinsic	111
fibroblasts	110
apoptotic	109
mitochondrial	107
apoptosis	107
transduction	105
insulin	103
kinases	102
collagen	102
signal	101
dependent	98
human	93
remodeling	85
inhibited	76
cell	76
site	74
heat	73
binding	72
terminal	71
mitochondria	65
shock	64
dermal	63
camp	63

factor	61
caspase	59
acetylation	56
transactivation	53
transforming	52
acetyltransferase	52
increased	48
specific	43
anchor	43
growth	42
tissue	41
connective	41
tyrosine	40
ii	39
chaperone	39
beta	39
jurkat	38
deacetylase	38
pathway	37
sites	35
n	34
c	34
type	33
pka	33
ceramide	33
cells	33
potential	32
proteins	31
cytosol	31
chromatin	31
smad	30
interacting	30
response	28
t	27
inhibitor	27
initiator	26
imperfecta	26
immunoprecipitation	26
coactivator	26
cdna	26
adipocytes	26

induced	25
promoter	24
primary	24
fracture	24
element	24
vitro	23
osteogenesis	23
membrane	23
expression	23
core	23
activated	23
signaling	22
nucleosomal	22
hdac	22
cultured	22
acetylated	22
collagens	21
downstream	20
adenovirus	20
mouse	19
histones	19
enhanced	19
dna	19
collagenase	19
threonine	18
pathways	18
library	18
cofactors	18
cellular	18
ccaat	18
transcription	17
tendon	17
sequence	17
rat	17
decreased	17
critical	17
complex	17
reduced	16
genes	16
death	16
receptor	15

multiple	15
matrix	15
intracellular	15
domains	15
residue	14
normal	14
muscle	14
motif	14
major	14
conserved	14
consensus	14
cascade	14
assay	14
activities	14
active	14
translation	13
temperatures	13
substrate	13
staurosporine	13
responsive	13
release	13
procollagen	13
mediated	13
isolated	13
formation	13
treatment	12
synthesis	12
substrates	12
residues	12
nonhistone	12
liver	12
iii	12
extracellular	12
complexes	12
bone	12
basal	12
amp	12
templates	11
severe	11
resistance	11
rapamycin	11

mechanism	11
fractures	11
deacetylases	11
cleavage	11
superfamily	10
studies	10
regulated	10
proteases	10
production	10
pkc	10
nuclear	10
hormone	10
endothelial	10
class	10
cgmp	10
acetyl	10
vivo	9
vacuole	9
syndrome	9
subunit	9
stress	9
properties	9
potentiated	9
phosphoserine	9
myofibroblast	9
map	9
levels	9
inhibitors	9
high	9
fibroblast	9
elements	9
ehlers	9
effector	9
danlos	9
creb	9
control	9
chondrocyte	9
brain	9
alpha	9
tumor	8
transactivator	8

tgf	8
target	8
small	8
septic	8
segment	8
scleroderma	8
regulatory	8
recruitment	8
rapid	8
mammalian	8
lymphocyte	8
lower	8
interstitial	8
impaired	8
helix	8
hela	8
glycosylphosphatidylinositol	8
experiments	8
events	8
elevated	8
deposition	8
cyclin	8
cyclic	8
caspases	8
box	8
analysis	8
vertebral	7
vascular	7
unfolding	7
typical	7
tubulin	7
translocated	7
tissues	7
system	7
single	7
repeat	7
mutant	7
mechanisms	7
maximal	7
lysine	7
loop	7

local	7
fragmentation	7
factors	7
diploid	7
cytosolic	7
creatine	7
central	7
carboxy	7
atp	7
abnormal	7
a	7
triple	6
transient	6
targeting	6
stromal	6
short	6
sequential	6
senescent	6
risk	6
reversible	6
region	6
reaction	6
proteinase	6
program	6
phosphatase	6
patient	6
nucleosome	6
mitogen	6
mild	6
methionine	6
low	6
long	6
induction	6
individual	6
hsp	6
full	6
foreskin	6
energy	6
endogenous	6
dynamic	6
direct	6

delta	6
decorin	6
cytoplasmic	6
content	6
concomitant	6
codon	6
coactivators	6
choline	6
chloramphenicol	6
chemical	6
casein	6
cardiac	6
associated	6
amino	6
action	6
yeast	5
vi	5
unique	5
transport	5
stimulated	5
state	5
sequences	5
sensitivity	5
related	5
regions	5
recombinant	5
purified	5
processing	5
poor	5
palpebral	5
osteoporotic	5
nad	5
myocyte	5
motifs	5
loci	5
lipid	5
jun	5
ix	5
inducible	5
highly	5
hamster	5

glucocorticoid	5
global	5
general	5
functional	5
fragments	5
folding	5
fissures	5
fibril	5
exchange	5
excessive	5
early	5
defects	5
defective	5
defect	5
components	5
cognate	5
chain	5
calcium	5
bromide	5
bovine	5
body	5
assays	5
acidic	5
ability	5
virus	4
translational	4
targets	4
synthetic	4
synovial	4
suppressing	4
stimulation	4
status	4
states	4
soluble	4
skeletal	4
sirna	4
selective	4
secretion	4
rhodopsin	4
results	4
replication	4

regulator	4
regulating	4
recognition	4
proteolytic	4
prolonged	4
proliferation	4
programs	4
process	4
pro	4
preferred	4
predominant	4
positive	4
phosphorylating	4
phosphopeptides	4
phorbol	4
phase	4
pharmacologic	4
pathologic	4
nucleoside	4
neutrophil	4
negative	4
minimal	4
microvascular	4
mature	4
massive	4
mapk	4
machinery	4
libraries	4
leukemia	4
latent	4
kidney	4
iron	4
interaction	4
inhibitory	4
heart	4
gabp	4
free	4
fibrils	4
fibrillar	4
feedback	4
extracts	4

essential	4
epsilon	4
enhancer	4
embryo	4
elongation	4
electric	4
effects	4
dual	4
dominant	4
diphosphate	4
differentiation	4
differentiated	4
cytokine	4
cooperative	4
chicken	4
characteristic	4
cascades	4
capacity	4
bound	4
bodies	4
bind	4
bacterial	4
autosomal	4
assembly	4
arterial	4
apoptosome	4
anti	4
amelogenesis	4
adult	4
actin	4
acetyltransferases	4
acetylase	4
absent	4
widespread	3
viral	3
vii	3
ventricular	3
vector	3
variant	3
upstream	3
universal	3

ubiquitin	3
types	3
transmembrane	3
translocation	3
transition	3
total	3
tails	3
systemic	3
subunits	3
splicing	3
slow	3
skin	3
signals	3
sheath	3
serial	3
sclera	3
ribonucleoside	3
responses	3
reporter	3
regional	3
reciprocal	3
recessive	3
receptors	3
reagent	3
radiolabeled	3
rabbit	3
processes	3
primed	3
posttranslational	3
polypeptides	3
platelet	3
physiologic	3
phenotype	3
permeability	3
peptide	3
partners	3
partner	3
partial	3
papillae	3
pancreatic	3
oxidative	3

noxious	3
novo	3
nonreceptor	3
nonlethal	3
mrna	3
mps	3
molecules	3
molecule	3
modifications	3
modification	3
moderate	3
mitogenic	3
migration	3
metabolism	3
maturation	3
mast	3
marks	3
mark	3
main	3
lymphatic	3
localization	3
light	3
ligase	3
level	3
late	3
jak	3
interferon	3
interfacial	3
infection	3
increase	3
inactive	3
inactivating	3
hypertrophic	3
hydrolase	3
hiv	3
hepatocyte	3
helical	3
gtpase	3
glycoprotein	3
glucosyl	3
glucose	3

gastric	3
fraction	3
form	3
force	3
fold	3
fiber	3
eukaryotic	3
esterase	3
efficiency	3
drug	3
divergent	3
disorders	3
disorder	3
digestion	3
deficiency	3
cyanogen	3
crystallin	3
contraction	3
contact	3
component	3
competitive	3
common	3
coa	3
chromosome	3
chromosomal	3
cartilage	3
canonical	3
brown	3
broad	3
blood	3
biosynthesis	3
apparatus	3
antisense	3
antibody	3
angiogenic	3
adhesion	3
acute	3
acid	3
abnormalities	3
abl	3
zap	2

young	2
xi	2
x	2
white	2
weakness	2
wasp	2
wall	2
versus	2
vectors	2
variants	2
v	2
udp	2
ubiquitous	2
tu	2
transformed	2
transformation	2
transferase	2
trans	2
toxic	2
tonic	2
thyroid	2
thymidine	2
thermal	2
tensin	2
tendons	2
targeted	2
systems	2
synthase	2
synaptic	2
sustained	2
subcutaneous	2
structural	2
storage	2
stimulus	2
sterol	2
staining	2
stable	2
stability	2
srebp	2
spinal	2
specialized	2

somatic	2
soft	2
sink	2
signature	2
serum	2
sclerosis	2
sapk	2
rodent	2
rich	2
reverse	2
retinal	2
reticulum	2
replacement	2
repair	2
renal	2
reflexes	2
reductive	2
reactions	2
rb	2
rate	2
pulmonary	2
proteinases	2
promoters	2
prokaryotic	2
progressive	2
progression	2
profiles	2
presequence	2
polymorphonuclear	2
polymorphism	2
placental	2
phosphopeptide	2
phospholipid	2
phosphoinositide	2
phosphoamino	2
persistent	2
permanent	2
peptides	2
pdgfr	2
patterns	2
pattern	2

patients	2
partially	2
part	2
paradoxical	2
papilla	2
orderly	2
opsin	2
oncoproteins	2
oncogene	2
oligonucleotide	2
odorant	2
observed	2
nonspecific	2
nocturnal	2
nociceptor	2
nicotinamide	2
neuron	2
neuroimmune	2
neurofilament	2
native	2
naked	2
myristate	2
myocardial	2
multiprotein	2
multifunctional	2
mucosal	2
morpholino	2
modified	2
minor	2
microtubule	2
metal	2
meningeal	2
matrices	2
mass	2
markers	2
marker	2
manifestations	2
m	2
lymphocytes	2
loss	2
loose	2

lipoprotein	2
linker	2
linked	2
like	2
lethal	2
lesions	2
knockout	2
janus	2
irf	2
inverted	2
insufficient	2
injury	2
inhibiting	2
inherited	2
inflammatory	2
independent	2
import	2
hydrophobic	2
huvec	2
histidine	2
guanylate	2
groups	2
greater	2
gram	2
glomerular	2
gingival	2
gene	2
gel	2
gastrocnemius	2
gamma	2
functions	2
functionally	2
fractions	2
forced	2
foot	2
focal	2
flux	2
fetal	2
fasting	2
extremely	2
extended	2

expressed	2
exposure	2
excess	2
ester	2
erythropoietin	2
erythrocyte	2
epidermal	2
enzyme	2
enzymatic	2
entry	2
energies	2
endoplasmic	2
embryonic	2
effect	2
drosophila	2
dnase	2
division	2
distal	2
displacement	2
diseases	2
diminished	2
differences	2
diacylglycerol	2
development	2
derived	2
density	2
dendritic	2
demand	2
dehydratase	2
degranulation	2
degeneration	2
deficient	2
deep	2
cytoskeletal	2
cytokines	2
cysteine	2
cycle	2
curves	2
cryptic	2
crosslinking	2
couples	2

corneal	2
controls	2
constitutive	2
congenita	2
conformational	2
concurrent	2
complete	2
competence	2
combined	2
colony	2
cold	2
code	2
cluster	2
clone	2
cleft	2
clearance	2
classic	2
chronic	2
chinese	2
checkpoint	2
characteristics	2
chaperones	2
channel	2
catabolism	2
carnitine	2
cardiomyocyte	2
carbohydrate	2
capillaries	2
callus	2
bundles	2
boxes	2
bitter	2
biopsies	2
behavior	2
basement	2
baby	2
b	2
average	2
autophagic	2
autonomic	2
astrocyte	2

artery	2
arrays	2
antihuman	2
antigens	2
antibodies	2
antibiotic	2
analyses	2
amyloid	2
alveolar	2
altered	2
allergen	2
allele	2
agent	2
adenylate	2
activator	2
acetate	2
abnormality	2
abilities	2
zymogen	1
xviii	1
xv	1
xiv	1
wounds	1
wound	1
wide	1
whole	1
visual	1
viruses	1
villus	1
viability	1
vessels	1
vessel	1
vertebrate	1
vero	1
velocity	1
variation	1
valve	1
utilization	1
uterine	1
usual	1
uptake	1

upper	1
unrelated	1
units	1
ultrastructure	1
ubiquitination	1
tyrosyl	1
ts	1
triggering	1
triggered	1
trigger	1
triad	1
treatments	1
transforms	1
transfer	1
transdifferentiation	1
transactivators	1
trail	1
trafficking	1
toxicity	1
topoisomerase	1
tibialis	1
tibia	1
thymus	1
thymocyte	1
thresholds	1
therapeutic	1
testis	1
testicular	1
termination	1
term	1
temperature	1
telomerase	1
techniques	1
taste	1
tail	1
systolic	1
synthases	1
synchronous	1
swelling	1
sweat	1
susceptibility	1

supply	1
sulfate	1
suicide	1
sugar	1
subtilisin	1
substitutions	1
substituted	1
subfragment	1
subfamily	1
subepithelial	1
structures	1
strip	1
stretch	1
strength	1
strand	1
stocks	1
stiffness	1
steroid	1
stem	1
stage	1
stabilizing	1
stabilized	1
spontaneously	1
spontaneous	1
split	1
spiral	1
spindle	1
sphingosine	1
sphingolipid	1
spermatocyte	1
sperm	1
spectrometry	1
specificity	1
species	1
space	1
sorting	1
snornp	1
smooth	1
slit	1
sleep	1
skeleton	1

sirtuin	1
sinus	1
simplex	1
simple	1
sheet	1
sharp	1
shared	1
sera	1
sequencing	1
separation	1
sensor	1
sensitization	1
self	1
segments	1
secondary	1
screening	1
scaffolding	1
sarcomere	1
salicylate	1
s	1
rupture	1
role	1
rod	1
rii	1
ridges	1
ridge	1
ribosome	1
ribosomal	1
riboside	1
rhythmic	1
rhodanese	1
rhesus	1
reversed	1
retroviruses	1
retroviral	1
retinoic	1
retention	1
retardation	1
resting	1
respiratory	1
respiration	1

resistant	1
residual	1
required	1
repressor	1
repeats	1
remote	1
regulators	1
regulation	1
regular	1
regression	1
reduction	1
reductases	1
redox	1
recurrent	1
recombination	1
rates	1
random	1
radical	1
racemase	1
quality	1
qualitative	1
quail	1
pyruvate	1
punctate	1
ptp	1
ptk	1
ptdins	1
proximal	1
proteolysis	1
proteoglycans	1
property	1
proper	1
propensity	1
promoting	1
prolyl	1
proliferative	1
proliferating	1
programmed	1
progenitors	1
progenitor	1
profile	1

products	1
product	1
probes	1
probe	1
principal	1
priming	1
presynaptic	1
presumed	1
pressure	1
presentation	1
preparation	1
postmenopausal	1
portal	1
porcine	1
polarity	1
points	1
point	1
pluripotent	1
plasmodium	1
plasmin	1
plasmid	1
plasma	1
plantar	1
physically	1
photosensitivity	1
photochemical	1
phosphoproteins	1
phosphoprotein	1
phospholipase	1
phosphodiesterase	1
phospho	1
phosphatidylinositol	1
phagocytic	1
periodic	1
period	1
pericyte	1
peptidases	1
pelvic	1
pcr	1
patterning	1
passive	1

passage	1
particles	1
parp	1
parathyroid	1
parasite	1
paraoxonase	1
parallel	1
pantothenate	1
palmitoyltransferase	1
painful	1
packaging	1
outgrowth	1
outcome	1
ouabain	1
osteopetrosis	1
osteoblast	1
osmotic	1
orientation	1
organization	1
optimum	1
onset	1
oncogenes	1
omental	1
oligonucleotides	1
oligodendrocyte	1
ocular	1
octamer	1
number	1
nucleosomes	1
nuclei	1
nonlinear	1
nomenclature	1
nociception	1
nk	1
nevi	1
neutrophils	1
neutral	1
neurons	1
neuromuscular	1
neuroepithelial	1
neural	1

nerve	1
neovascularization	1
necrosis	1
narrow	1
nak	1
myopathy	1
myocytes	1
myoblasts	1
mycobacterial	1
myc	1
myb	1
mutation	1
mutated	1
mutants	1
murine	1
movements	1
mosaicism	1
monophosphates	1
monophosphate	1
monocyte	1
monkey	1
modulator	1
modulated	1
modifiers	1
modifier	1
mixtures	1
mixed	1
mitotic	1
minisatellite	1
mimicry	1
mimetic	1
migrating	1
microvasculature	1
methylated	1
methylase	1
methyl	1
metalloproteinases	1
metalloproteinase	1
metalloprotease	1
metabolite	1
messages	1

mesangial	1
membranes	1
melting	1
melanoma	1
melanin	1
medullary	1
mediator	1
mechanical	1
measurements	1
maximum	1
maternal	1
marrow	1
maps	1
mapping	1
manganese	1
macrophage	1
lys	1
lymphoma	1
lymphoblastoid	1
luciferase	1
lovastatin	1
los	1
locus	1
localized	1
lithium	1
lines	1
lineage	1
ligand	1
life	1
leukocytes	1
leukocyte	1
leprosy	1
lens	1
length	1
left	1
leakage	1
leader	1
layers	1
lattices	1
lateral	1
lacz	1

lactamases	1
labeled	1
kinetics	1
keratinocytes	1
keratinocyte	1
isoniazid	1
isoforms	1
irradiation	1
irradiated	1
irak	1
ion	1
invertebrate	1
invasion	1
invariant	1
intolerance	1
intestinal	1
interlobular	1
interface	1
intercellular	1
instability	1
insoluble	1
inflammation	1
infiltration	1
inducing	1
inducers	1
inducer	1
indomethacin	1
indirect	1
incubation	1
inappropriate	1
immunosuppressive	1
immunoreactive	1
immune	1
immobilized	1
iiic	1
iiia	1
iib	1
iia	1
hypoplastic	1
hypoplasia	1
hypoglycemia	1

hypersecretion	1
hyperalgesia	1
hydroxymethyltransferase	1
hydrolysis	1
hydrolases	1
host	1
hosphopeptide	1
homologous	1
homolog	1
history	1
hip	1
higher	1
heterologous	1
heteroduplexes	1
herpesvirus	1
herpes	1
heritable	1
hepatocytes	1
hepatocellular	1
hemorrhagic	1
hematopoietic	1
helices	1
healing	1
hcv	1
harmful	1
hair	1
group	1
groove	1
granules	1
granule	1
gorilla	1
golgi	1
goat	1
glycinergic	1
glycine	1
glycation	1
glutamatergic	1
glucosyltransferase	1
glucokinase	1
glands	1
germinal	1

genotype	1
genomic	1
generation	1
gap	1
galactosyltransferase	1
galactose	1
fusions	1
fusion	1
freeze	1
fragment	1
follicle	1
foci	1
fluoride	1
filaments	1
fibers	1
female	1
feeding	1
fat	1
fanconi	1
families	1
falciparum	1
face	1
extreme	1
extraskeletal	1
extra	1
extensor	1
extension	1
experimental	1
exogenous	1
event	1
ethylmaleimide	1
ethidium	1
estrogen	1
esterases	1
erythroblast	1
erbb	1
equivalent	1
epstein	1
eosinophil	1
enzymes	1
environmental	1

environment	1
enterocyte	1
enos	1
enhancers	1
enhancement	1
engine	1
endotoxic	1
endometrial	1
endocardial	1
end	1
empty	1
elimination	1
electrophysiologic	1
electroconvulsive	1
elastase	1
ef	1
edema	1
eccrine	1
ec	1
ebv	1
e	1
dysfunction	1
dynein	1
dopamine	1
dnaj	1
disordered	1
disease	1
discrete	1
directly	1
diphosphates	1
dinucleotide	1
dimethyl	1
dihydrolipoamide	1
diffuse	1
differential	1
difference	1
dids	1
diameters	1
diameter	1
developing	1
determinants	1

determinant	1
destruction	1
descending	1
dermatitis	1
derivatives	1
derivative	1
deprivation	1
dependency	1
deoxyribonucleoside	1
dense	1
denaturation	1
demethylases	1
degradation	1
degenerative	1
decidual	1
de	1
d	1
cytochrome	1
cysts	1
cushions	1
curve	1
currents	1
cortical	1
corpses	1
cores	1
cord	1
copper	1
coordinating	1
conversion	1
containing	1
constant	1
connections	1
congenital	1
conditions	1
compression	1
composition	1
compensatory	1
commercial	1
colon	1
collateral	1
coagulation	1

clusters	1
clearing	1
circulating	1
circadian	1
chymotrypsin	1
chromosomes	1
chorionic	1
chloride	1
chitinase	1
chimeric	1
chick	1
chicago	1
chemoattractant	1
chaperonin	1
channels	1
challenge	1
chains	1
cervical	1
cerebral	1
centromeric	1
center	1
caucasian	1
cation	1
catenin	1
cases	1
cartilaginous	1
carrier	1
cardiovascular	1
cardiomyopathy	1
cardiomyocytes	1
carcinoma	1
carcinogenic	1
carboxypeptidases	1
carboxypeptidase	1
carbonic	1
capsular	1
capacities	1
candidate	1
cancer	1
calreticulin	1
calnexin	1

calmodulin	1
calf	1
bulk	1
bronchiolar	1
blue	1
blocks	1
blocking	1
biotinylation	1
biology	1
biogenesis	1
bed	1
bcr	1
basic	1
baseline	1
base	1
barr	1
baculoviral	1
avoidance	1
avian	1
auxiliary	1
autonomous	1
autoimmune	1
atypical	1
attribute	1
attenuation	1
attenuated	1
atrophy	1
atrioventricular	1
atopic	1
asymmetric	1
aspirin	1
aspartyl	1
asparagine	1
arrangement	1
area	1
architecture	1
arch	1
aqueous	1
aps	1
apical	1
aortic	1

antiviral	1
antigen	1
antiangiogenic	1
anterior	1
anomaly	1
ankyrin	1
anhydrase	1
angiogenesis	1
angeles	1
anemia	1
androgenic	1
analogs	1
analog	1
amplification	1
amniotic	1
amnion	1
aminoglycoside	1
amines	1
ameloblast	1
amanitin	1
alternative	1
allosteric	1
alleles	1
albumin	1
alanine	1
ala	1
airway	1
aif	1
agonist	1
aging	1
aggregated	1
affinity	1
adventitial	1
administration	1
adjuvant	1
adipose	1
adipocyte	1
adhesiveness	1
adenine	1
additive	1
addition	1

adaptor	1
activating	1
acids	1
accounts	1
access	1
acceptors	1
accelerated	1
aberrant	1
abdominal	1

Table S28. Syntactic nature and associated word counts of Collective + Individual mode 'dismantled' noun-phrases from the bPTH(7-34) superconserved dataset. For each identified word the number of times the specific word occurred in the list of dismantled noun-phrases from *Textrous!* Individual processing is given. Word count scores were generated from the Wordle-sourced cloud using WriteWords (http://www.writewords.org.uk/word_count.asp). The words are sorted according to functional syntactic type.

FUNCTION	**Count**	**ADJECTIVE**	**Count**	**NOUN**	**Count**	**PROPER-NOUN**	**Count**
phosphorylation	257	catalytic	116	protein	183	histone	156
activation	232	intrinsic	111	kinase	176	serine	113
activity	145	mitochondrial	107	domain	125	fibroblasts	110
inhibition	112	dermal	63	kinases	102	insulin	103
apoptosis	107	camp-dependent	51	human	93	collagen	102
apoptotic	105	connective	41	site	74	mitochondria	65
transduction	105	chaperone	39	cell	51	caspase	59
signal	95	potential	32	tissue	40	acetyltransferase	52
remodeling	85	type	31	pathway	37	jurkat	38
inhibited	76	inhibitor	27	factor	36	deacetylase	38
acetylation	56	primary	24	sites	35	pka	33
transactivation	53	core	23	cells	32	ceramide	33
transforming	52	specific	23	proteins	31	chromatin	31
increased	48	nucleosomal	22	cytosol	31	smad	30
anchor	43	acetylated	22	n-terminal	31	tyrosine	27
growth	42	binding	21	c-terminal	27	cdna	26
heat	48	protein-binding	20	coactivator	26	adipocytes	26
shock	39	downstream	20	promoter	24	imperfecta	26
interacting	30	enhanced	19	fracture	24	factor-beta	23
response	28	cellular	18	pathways	18	osteogenesis	23
immunoprecipitation	26	element-binding	17	library	18	vitro	23
initiator	26			cofactors	18	hdac	22
heat-shock	25			membrane	18	collagens	21
expression	23					adenovirus	20
signaling	22					mouse	19
cultured	22					histones	19
						collagenase	19
						ccaat	18
						t-cell	18
						rat	17