SUPPLEMENTAL TABLE S5 GREAT ANALYSIS

GREAT version 2.0.2

Species assembly: mm9

Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 100000 bp max extension

ALL ESC CLUSTERS

Ontology	# Term Name	P-Value	Total Regions	Gene Hits
GO Molecular Function	regulatory region DNA binding	5.44E-223	2190	275
	transcription regulatory region DNA binding	3.83E-215	2118	266
	transcription factor binding	9.83E-203	2226	310
	kinase binding	1.68E-190	2055	304
	protein kinase binding	2.16E-166	1794	264
	transcription factor binding transcription factor activity	5.30E-163	1880	275
	transcription cofactor activity	8.29E-158	1817	265
	small GTPase regulator activity	7.66E-152	1730	233
	structure-specific DNA binding	9.29E-110	1257	184
	structural constituent of ribosome	5.66E-94	722	153
GO Biological Process	negative regulation of gene expression	0	5191	721
	chordate embryonic development	3.59591e-319	3586	500
	protein complex subunit organization	5.98E-213	2417	389
	in utero embryonic development	8.33E-213	2222	306
	protein complex biogenesis	4.08E-210	2367	379
	protein complex assembly	1.15E-208	2356	377
	chromatin modification	6.02E-194	2207	343
	posttranscriptional regulation of gene expression	3.92E-182	1668	262
	actin filament-based process	1.21E-149	1651	226
	actin cytoskeleton organization	2.83E-145	1584	214
Mouse Phenotype	prenatal lethality	0	11776	1770
	embryonic lethality	0	8939	1338
	embryonic lethality during organogenesis	0	5726	808
	abnormal embryonic tissue morphology	0	5919	801
	abnormal prenatal growth/weight/body size	0	6567	894
	complete embryonic lethality during organogenesis	0	4611	647
	abnormal embryonic growth/weight/body size	0	5586	753

	abnormal prenatal body size	0	4922	655
	abnormal neural tube morphology/development	0	3627	485
	abnormal embryo size	0	4056	534
MGI Expression	TS23_testis	0	10405	1608
	Theiler_stage_5	0	7656	1078
	Theiler_stage_4	0	7710	1094
	TS4_embryo	0	7670	1084
	TS4_extraembryonic component	0	7248	1032
	TS23_collecting duct	0	6193	964
	TS23_nephrogenic zone	0	6487	1003
	TS4_inner cell mass	0	6397	895
	TS3_second polar body	0	6366	904
	TS3_zona pellucida	0	6333	898
MSigDB Perturbation	Genes up-regulated in CD34+ [Gene ID=947] cells isolated from	0	8126	1343
	Genes constituting the BRCA1-PCC network of transcripts whose	0	8632	1514
	Genes up-regulated in brain from patients with Alzheimer's dise	0	10110	1534
	Genes whose promoters are bound by MYC [Gene ID=4609], acc	0	5290	986
	Genes up-regulated in liver tumor compared to the normal adja	0	4155	774
	Genes whose promoters contain E-box motifs and whose expres	0	4225	717
	Set 'Nanog targets': genes upregulated and identified by ChIP on	0	5605	897
	Set 'Sox2 targets': genes upregulated and identified by ChIP on c	0	4434	676
	Genes down-regulated in PC3 cells (prostate cancer) after knock	0	5220	721
	Set 'Myc targets2': targets of c-Myc [Gene ID=4609] and Max [G	0	3753	725

The test set of 74,577 genomic regions picked 16,773 genes (83%) of all 20,221 genes.

GO Molecular Function has 3,254 terms covering 15,499 (77%) of all 20,221 genes.

GO Biological Process has 8,583 terms covering 15,210 (75%) of all 20,221 genes.

Mouse Phenotype has 7,310 terms covering 6,642 (33%) of all 20,221 genes.

MGI Expression: Detected has 8,374 terms covering 12,066 (60%) of all 20,221 genes.

MSigDB Perturbation has 2,374 terms covering 15,669 (77%) of all 20,221 genes.

ALL EPISC CLUSTERS

GO Molecular Function	sequence-specific DNA binding	1.02E-261	2372	530
	sequence-specific DNA binding transcription factor activity	1.04E-260	2743	654
	nucleic acid binding transcription factor activity	1.05E-258	2745	655

	regulatory region DNA binding	2.84E-123	1099	238
	transcription regulatory region DNA binding	1.91E-120	1067	230
	protein binding transcription factor activity	1.73E-94	972	249
	transcription factor binding transcription factor activity	5.66E-93	949	243
	chromatin binding	3.67E-92	883	204
	transcription cofactor activity	1.11E-87	910	233
	sequence-specific DNA binding RNA polymerase II transcription f	3.92E-65	571	116
GO Biological Process	embryo development	7.61E-278	2939	721
	negative regulation of gene expression	2.05E-229	2541	633
	negative regulation of transcription, DNA-dependent	7.10E-210	2525	629
	embryonic morphogenesis	2.35E-191	1800	405
	chordate embryonic development	5.61E-179	1804	440
	embryo development ending in birth or egg hatching	1.21E-178	1826	446
	epithelium development	8.60E-157	1779	404
	pattern specification process	1.16E-153	1503	344
	negative regulation of transcription from RNA polymerase II pro	4.64E-142	1532	355
	tissue morphogenesis	2.14E-141	1555	351
	negative regulation of developmental process	3.29E-137	1538	348
	embryonic organ development	3.08E-134	1251	281
	negative regulation of cell differentiation	7.58E-126	1288	290
	regionalization	1.24E-124	1098	251
Mouse Phenotype	abnormal embryonic tissue morphology	5.16E-287	2915	695
	embryonic lethality during organogenesis	1.08E-253	2755	691
	complete embryonic lethality during organogenesis	6.30E-205	2221	558
	abnormal neural tube morphology/development	8.58E-194	1828	419
	lethality throughout fetal growth and development	6.54E-160	1619	368
	abnormal neural tube closure	7.76E-129	1163	260
	abnormal neuron differentiation	1.93E-118	1254	259
	embryonic lethality between implantation and placentation	3.94E-116	1269	351
	partial embryonic lethality during organogenesis	6.19E-115	1087	232
	abnormal cell proliferation	4.65E-111	1184	311
	abnormal heart development	3.79E-108	1231	274
MGI Expression	TS23_male associated reproductive structure	3.50E-303	3287	876

	TS21_embryo; head	1.17E-283	2963	731
	TS23_early tubule	2.27E-275	3035	832
	TS17_limb	5.59E-272	2947	741
	TS17_brain	4.82E-266	2723	645
	Theiler_stage_3	3.39E-257	2841	782
	TS3_4-8 cell stage	1.26E-253	2767	758
	TS15_nervous system	1.67E-249	2356	517
	TS3_second polar body	6.82E-245	2727	755
	TS21_spinal cord	1.09E-243	2632	685
	TS3_zona pellucida	5.11E-243	2708	749
MSigDB Perturbation	Genes within amplicon 17q21-q25 identified in a copy number a	2.56E-239	934	291
	Genes with copy number losses in primary neuroblastoma tumo	5.21E-204	1886	632
	Genes with copy number gains in primary neuroblastoma tumor	5.30E-171	658	159
	Transcripts depleted from pseudopodia of NIH/3T3 cells (fibrobl	1.21E-165	1856	567
	Transcripts depleted in pseudopodia of NIH/3T3 cells (fibroblast)	5.63E-156	1432	399
	Housekeeping genes identified as expressed across 19 normal tis	1.36E-120	978	322
	Genes up-regulated in NHEK cells (normal epidermal keratinocyt	2.27E-119	1190	407
	Genes up-regulated in the MM1S cells (multiple myeloma) after	2.57E-114	1273	352
	The postradiation tumor escape signature: genes up-regulated i	1.70E-109	1179	340
	Genes up-regulated in lymphoblastoid cells from the European p	7.15E-105	1062	379

The test set of 36,000 genomic regions picked 13,645 genes (67%) of all 20,221 genes.

GO Molecular Function has 3,254 terms covering 15,499 (77%) of all 20,221 genes.

GO Biological Process has 8,583 terms covering 15,210 (75%) of all 20,221 genes.

Mouse Phenotype has 7,310 terms covering 6,642 (33%) of all 20,221 genes.

MGI Expression: Detected has 8,374 terms covering 12,066 (60%) of all 20,221 genes.

MSigDB Perturbation has 2,374 terms covering 15,669 (77%) of all 20,221 genes.

ALL NCS CLUSTERS

GO Molecular Function	beta-dystroglycan binding	2.28E-16	51	2
	transforming growth factor beta-activated receptor activity	1.01E-13	128	14
	semaphorin receptor activity	1.13E-13	85	5
	L-ascorbic acid binding	5.26E-13	119	16
	phosphatidylinositol-3,4,5-trisphosphate binding	8.08E-13	117	14
	histone kinase activity (H3-T6 specific)	2.98E-12	39	2

	stem cell factor receptor binding	5.29E-12	56	3
	histone kinase activity	6.65E-12	93	12
GO Biological Process	positive regulation of myoblast differentiation	6.09E-27	131	9
	peptidyl-threonine modification	1.24E-20	197	22
	negative regulation of epithelial cell migration	6.49E-20	54	3
	B cell receptor signaling pathway	2.90E-19	190	21
	peptidyl-threonine phosphorylation	6.08E-19	174	20
	histone phosphorylation	8.63E-18	131	15
	negative regulation of axon extension	1.18E-17	141	11
	regulation of neuron maturation	4.86E-17	62	3
	negative regulation of neuron maturation	3.12E-16	51	2
	axonal fasciculation	2.40E-15	133	13
Mouse Phenotype	synechia	7.12E-30	208	16
	dilated respiratory conducting tubes	9.53E-23	232	21
	abnormal foot pigmentation	7.25E-19	178	19
	increased wet-to-dry lung weight ratio	1.20E-17	66	4
	abnormal terminal bronchiole morphology	3.44E-17	141	12
	decreased circulating interferon-beta level	1.64E-16	72	6
	abnormal circulating interferon-beta level	5.74E-15	79	8
	corneal adhesion to iris	3.95E-13	100	8
MGI Expression	TS24_tooth; mesenchyme; dental papilla	8.76E-24	98	6
	TS26_upper jaw	3.33E-23	220	19
	TS19_gut; associated mesenchyme	1.14E-19	63	3
	TS20_arch of aorta	5.56E-19	73	7
	TS19_trunk mesenchyme; mesenchyme derived from neural cre	3.00E-18	135	10
	TS24_tooth; mesenchyme	3.84E-18	98	6
	TS23_endolymphatic duct	4.49E-18	139	11
	TS25_cerebral cortex; subventricular zone	1.47E-17	137	12
	TS15_trunk mesenchyme; mesenchyme derived from neural cre	4.49E-17	156	13
	TS23_epithelium of degenerating rest of paramesonephric duct	3.77E-16	55	4
MSigDB Perturbation	Genes down-regulated in glioblastoma cell lines displaying spher	2.77E-25	234	24
	Selected genes implicated in metastasis and epithelial-to-mesen	1.36E-22	169	12
	Genes down-regulated in Kasumi-1 cells (acute myeloid leukaem	1.01E-21	191	17
	Genes down-regulated in CD34+ [Gene ID=947] hematopoetic ce	1.22E-21	202	21

	EMT (epithelial-mesenchymal transition) genes up-regulated ger	2.04E-20	214	26
	Genes up-regulated in glioblastoma cell lines displaying spherica	2.38E-20	181	19
	Genes significantly mutated in 91 glioblastoma samples.	3.47E-19	95	7
	Examples of transcription factors whose activities are regulated	8.58E-19	100	7
	Genes up-regulated during prostate cancer progression in mice	1.81E-16	169	20
	Genes highly expressed in the neonatal hippocampus (clusters 4	2.37E-16	118	14

The test set of 81,248 genomic regions picked 14,656 genes (72%) of all 20,221 genes.
GO Molecular Function has 3,254 terms covering 15,499 (77%) of all 20,221 genes.
GO Biological Process has 8,583 terms covering 15,210 (75%) of all 20,221 genes.
Mouse Phenotype has 7,310 terms covering 6,642 (33%) of all 20,221 genes.
MGI Expression: Detected has 8,374 terms covering 12,066 (60%) of all 20,221 genes.
MSigDB Perturbation has 2,374 terms covering 15,669 (77%) of all 20,221 genes.

ALL MEF CLUSTERS

GO Molecular Function	growth factor binding	6.29E-47	484	83
	insulin-like growth factor binding	1.12E-34	169	23
	extracellular matrix structural constituent	9.16E-26	174	26
	lipase inhibitor activity	6.62E-14	55	7
	platelet-derived growth factor binding	1.48E-13	72	10
	histone acetyltransferase binding	1.34E-11	74	14
	phosphatidylinositol 3-kinase binding	3.10E-11	101	18
GO Biological Process	negative regulation of MAPKKK cascade	1.61E-21	230	44
	collagen fibril organization	3.83E-20	154	24
	positive regulation of vesicle fusion	3.29E-17	52	4
	regulation of epithelial cell proliferation involved in lung morphc	1.79E-16	67	6
	endothelial cell migration	1.85E-15	150	29
	mesenchymal-epithelial cell signaling	8.38E-15	80	9
	positive regulation of smooth muscle cell proliferation	1.56E-14	150	35
	regulation of vesicle fusion	2.37E-14	54	6
	negative regulation of endothelial cell proliferation	3.71E-14	85	15
	actin filament bundle assembly	1.04E-13	115	20
Mouse Phenotype	abnormal wound healing	7.09E-37	400	85
	abnormal cell adhesion	1.22E-27	250	44
	corneal thinning	4.05E-26	117	15

	abnormal pulmonary artery morphology	1.21E-24	185	32
	abnormal semilunar valve morphology	3.42E-23	247	49
	small placenta	1.02E-22	237	51
	abnormal bronchiole morphology	2.70E-22	229	35
	abnormal lung alveolus development	3.30E-22	219	39
	impaired lung alveolus development	3.53E-22	218	38
	impaired wound healing	8.53E-22	176	36
MGI Expression	TS22_pancreas; mesenchyme	3.65E-43	298	48
	TS28_tendon	1.47E-37	167	17
	TS28_tendo calcaneus	4.42E-30	117	12
	TS20_arterial system	3.70E-29	298	50
	TS26_upper jaw	6.74E-28	156	19
	TS20_dorsal aorta	4.64E-25	253	42
	TS21_inner ear; associated mesenchyme	5.38E-23	91	9
	TS13_trunk mesenchyme; paraxial mesenchyme; somite	1.19E-21	231	39
	TS20_lung; associated mesenchyme	4.25E-21	195	30
	TS21_otic capsule	5.73E-21	153	25
MSigDB Perturbation	Genes down-regulated in luminal-like breast cancer cell lines cor	2.10E-207	2124	379
	Genes commonly down-regulated in human alveolar rhabdomyc	1.80E-174	1704	341
	Up-regulated genes in angioimmunoblastic lymphoma (AILT) cor	6.99E-124	1013	159
	Genes down-regulated in UB27 cells (osteosarcoma) at 12 hr aft	1.66E-76	847	169
	Up-regulated genes distinguishing between two subtypes of gast	3.46E-75	799	133
	Genes whose expression positively correlated with sensitivity of	4.01E-67	460	58
	Genes down-regulated in primary fibroblast cell culture after inf	1.57E-66	666	126
	Genes down-regulated in NIH3T3 cells (fibroblasts) after treatme	3.05E-59	346	45
	Genes up-regulated in lobular carcinoma vs normal ductal breast	1.84E-56	390	57
	Down-regulated at 24 h following infection of primary human fo	1.49E-49	326	51

ESC SPECIFIC CLUSTERS

GO Molecular Function	regulatory region DNA binding	2.34E-130	1342	246
	transcription regulatory region DNA binding	7.50E-125	1295	237
	small GTPase regulator activity	1.64E-100	1099	208
	protein C-terminus binding	6.33E-60	529	108
	phosphatidylinositol binding	3.14E-58	576	107

	kinase regulator activity	1.40E-47	454	93
	beta-catenin binding	7.06E-36	298	46
GO Biological Process	protein complex subunit organization	2.90E-134	1515	333
	in utero embryonic development	3.00E-134	1393	271
	protein complex assembly	6.66E-133	1481	323
	protein complex biogenesis	2.78E-132	1483	325
	lipid biosynthetic process	3.15E-123	1342	295
	posttranscriptional regulation of gene expression	1.74E-105	1018	227
	histone modification	7.74E-92	864	181
	covalent chromatin modification	9.23E-78	874	183
	homeostasis of number of cells	4.41E-77	623	119
	stem cell maintenance	9.40E-69	396	53
Mouse Phenotype	prenatal growth retardation	1.96E-224	2338	441
	decreased embryo size	1.04E-215	2448	470
	lethality throughout fetal growth and development	1.53E-199	2080	375
	embryonic growth retardation	2.70E-198	2067	390
	abnormal erythrocyte morphology	3.40E-182	1990	407
	embryonic lethality between implantation and placentation	1.09E-176	1729	342
	abnormal placenta morphology	1.85E-146	1585	314
	abnormal cell proliferation	6.06E-146	1545	313
	abnormal neural tube closure	6.41E-146	1450	262
	embryonic lethality before somite formation	1.93E-141	1281	250
MGI Expression	Theiler_stage_4	0	4783	949
	TS4_embryo	0	4756	939
	Theiler_stage_5	0	4784	932
	TS4_extraembryonic component	0	4465	890
	TS28_female germ cell	0	4408	910
	Theiler_stage_2	0	4077	838
	TS4_inner cell mass	0	3965	774
	TS4_compacted morula	0	3461	680
	TS5_embryo	0	3459	639
	TS3_4-8 cell stage	0	3957	780
MSigDB Perturbation	Genes constituting the BRCA1-PCC network of transcripts whose	0	5328	1277
	Genes down-regulated in PC3 cells (prostate cancer) after knock	0	3201	638

	Genes up-regulated in brain from patients with Alzheimer's disea	0	6171	1301
	Transcripts depleted from pseudopodia of NIH/3T3 cells (fibrobla	0	2822	583
	Genes up-regulated in HeLa cells (cervical cancer) after simultan	2.27E-288	2844	660
	Genes up-regulated in T24 (bladder cancer) cells in response to t	1.03E-285	3224	657
	Set 'Sox2 targets': genes upregulated and identified by ChIP on c	7.22E-268	2729	557
	Up-regulated genes in colon carcinoma tumors compared to the	3.66E-264	2259	538
	Genes constituting the CHEK2-PCC network of transcripts whose	2.01E-250	2585	612
	Genes down-regulated in HL-60 cells (acute promyelocytic leuke	3.43E-249	2736	665

The test set of 52,148 genomic regions picked 14,749 genes (73%) of all 20,221 genes.
GO Molecular Function has 3,254 terms covering 15,499 (77%) of all 20,221 genes.
GO Biological Process has 8,583 terms covering 15,210 (75%) of all 20,221 genes.
Mouse Phenotype has 7,310 terms covering 6,642 (33%) of all 20,221 genes.
MGI Expression: Detected has 8,374 terms covering 12,066 (60%) of all 20,221 genes.
MSigDB Perturbation has 2,374 terms covering 15,669 (77%) of all 20,221 genes.

EPISC SPECIFIC CLUSTERS

GO Molecular Function	sequence-specific DNA binding	8.95E-94	849	360
	regulatory region DNA binding	1.31E-35	366	155
	transcription regulatory region DNA binding	2.04E-34	354	150
	transcription regulatory region sequence-specific DNA binding	8.39E-24	153	53
	sequence-specific DNA binding RNA polymerase II transcription f	5.18E-21	195	81
	sequence-specific distal enhancer binding RNA polymerase II trai	4.13E-13	118	50
	DNA bending activity	1.60E-12	83	36
GO Biological Process	embryonic morphogenesis	1.05E-64	632	264
	pattern specification process	4.20E-62	557	232
	regionalization	3.64E-54	417	162
	negative regulation of developmental process	1.14E-52	560	238
	negative regulation of cell differentiation	2.41E-46	463	198
	anterior/posterior pattern specification	4.55E-45	304	114
	embryonic organ development	1.63E-39	420	182
	embryonic organ morphogenesis	8.59E-33	303	123
	cell fate commitment	2.68E-32	297	120
	axon guidance	3.36E-31	244	85

Mouse Phenotype	abnormal neuron differentiation	9.96E-45	454	177
	partial neonatal lethality	5.78E-40	430	179
	abnormal nervous system tract	7.09E-38	282	96
	complete perinatal lethality	4.56E-36	375	152
	abnormal forebrain development	4.12E-34	299	111
	abnormal diencephalon morphology	6.18E-34	348	132
	abnormal eye development	2.39E-32	326	136
	abnormal brain white matter morphology	8.91E-31	269	98
	abnormal olfactory lobe morphology	4.89E-30	246	84
	abnormal brain commissure morphology	5.68E-30	231	81
MGI Expression	TS17_brain	2.36E-91	963	431
	TS15_nervous system	6.65E-76	803	328
	TS15_central nervous system	5.60E-70	766	314
	TS28_head	6.66E-69	701	289
	TS21_diencephalon	1.68E-67	657	256
	TS15_embryo; mesenchyme	3.33E-63	651	268
	TS15_future brain	2.91E-62	622	247
	Theiler_stage_12	8.24E-59	589	250
	TS12_embryo	1.68E-57	565	240
	TS17_midbrain	7.73E-57	498	184
	TS21_thalamus	3.07E-56	540	214
	TS15_trunk mesenchyme	9.36E-53	538	222
	TS17_hindbrain	1.25E-52	520	201
	TS21_midbrain	1.81E-51	537	216
	TS21_hypothalamus	3.66E-50	465	179
	TS15_future spinal cord	1.32E-49	442	174
	TS15_eye	3.92E-47	377	149
	TS15_future spinal cord; neural tube	7.22E-46	392	153
	TS13_future brain	9.11E-27	286	113
	TS15_1st arch; maxillary component	9.95E-27	255	109
	TS14_embryo; mesenchyme	9.93E-26	225	81
	Theiler_stage_8	2.17E-24	201	77
	TS8_embryo	5.77E-23	1.61E+02	61

MSigDB Perturbation	Set 'PRC2 targets': Polycomb Repression Complex 2 (PRC) target	7.86E-86	848	353
	Genes within amplicon 17q21-q25 identified in a copy number a	2.86E-61	288	183
	Genes with copy number gains in primary neuroblastoma tumor	3.91E-26	164	89
	Genes bearing H3K27me3 mark or whose promoters are bound	4.80E-19	135	51
	Genes with high histone H3 trimethylation mark at K27 (H3K27n	1.58E-15	128	50
	Genes down-regulated in SCC12B2 cells (squamous cell carcinon	1.76E-14	133	56
	Genes within amplicon 17q11-q21 identified in a copy number a	2.95E-14	76	56
	Genes down-regulated in primary fibroblast cell culture after inf	5.39E-14	137	53
	The 'stemnes' signature: genes up-regulated and common to 6 h	1.16E-08	76	38

The test set of 12,966 genomic regions picked 7,419 genes (37%) of all 20,221 genes.

GO Molecular Function has 3,254 terms 3,254 ontology terms were tested (100%) using an annotation count range of [1, Inf].

GO Biological Process has 8,583 terms c 8,583 ontology terms were tested (100%) using an annotation count range of [1, Inf].

Mouse Phenotype has 7,310 terms cove 7,310 ontology terms were tested (100%) using an annotation count range of [1, Inf].

MGI Expression: Detected has 8,374 ter 8,374 ontology terms were tested (100%) using an annotation count range of [1, Inf].

MSigDB Perturbation has 2,374 terms c 2,374 ontology terms were tested (100%) using an annotation count range of [1, Inf].

ESC EPISC SHARED CLUSTERS

GO Molecular Function	nucleic acid binding	6.34E-228	2019	1143
	DNA binding	1.93E-204	1489	785
	sequence-specific DNA binding	6.54E-143	746	345
	sequence-specific DNA binding transcription factor activity	2.32E-135	832	396
	nucleic acid binding transcription factor activity	2.21E-134	832	396
	regulatory region DNA binding	1.34E-70	353	152
	transcription regulatory region DNA binding	5.39E-69	343	148
	protein domain specific binding	1.14E-46	413	214
	transcription factor binding	6.57E-45	309	154
	transcription regulatory region sequence-specific DNA binding	4.48E-43	153	57
	sequence-specific DNA binding RNA polymerase II transcription f	8.48E-42	192	78
GO Biological Process	regulation of cellular metabolic process	3.43E-288	2658	1528
	regulation of macromolecule metabolic process	2.09E-272	2499	1426
	regulation of nitrogen compound metabolic process	1.65E-257	2290	1273
	regulation of nucleobase-containing compound metabolic proce	5.85E-256	2275	1264
	nitrogen compound metabolic process	4.79E-246	2359	1447
	regulation of cellular biosynthetic process	9.02E-245	2165	1207

	regulation of biosynthetic process	3.33E-244	2175	1213
	cellular nitrogen compound metabolic process	1.27E-242	2313	1408
	regulation of gene expression	8.98E-242	2135	1186
	regulation of cellular macromolecule biosynthetic process	2.71E-238	2062	1133
	regulation of macromolecule biosynthetic process	7.30E-238	2084	1149
Mouse Phenotype	abnormal nervous system morphology	1.08E-165	1653	898
	lethality during fetal growth through weaning	3.68E-157	1614	878
	prenatal lethality	6.49E-155	1411	791
	abnormal embryogenesis/ development	1.92E-143	1221	648
	abnormal nervous system development	8.79E-117	946	458
	abnormal embryonic tissue morphology	1.45E-113	806	390
	embryonic lethality	6.52E-111	1049	574
	no abnormal phenotype detected	1.50E-107	1132	618
	normal phenotype	3.75E-107	1135	620
	abnormal brain morphology	3.18E-105	1068	568
	perinatal lethality	3.21E-102	1012	513
MGI Expression	Theiler_stage_17	1.93E-298	2480	1379
	TS19_embryo	6.48E-254	2403	1381
	TS23_metanephros	3.87E-240	2182	1262
	Theiler_stage_15	1.49E-234	1796	950
	TS15_embryo	5.43E-229	1757	933
	TS17_nervous system	1.33E-228	1640	866
	TS23_reproductive system; male	8.88E-184	1639	909
	TS28_spinal cord	7.00E-177	1765	1031
	Theiler_stage_13	2.54E-163	1221	613
	TS21_nervous system	6.86E-147	1631	928
	TS21_central nervous system	4.21E-145	1254	647
	TS19_future spinal cord	7.10E-138	1306	735
	TS28_gastrointestinal system	7.40E-127	1299	752
	TS21_brain	2.93E-124	1134	584
	TS22_gut	4.76E-124	1182	646
	TS21_embryo; head	3.68E-123	844	429
	Theiler_stage_18	2.27E-117	1168	641
	TS18_embryo	9.34E-116	1160	637

	TS19_midbrain	1.14E-114	1175	661
	TS15_nervous system	1.39E-114	691	318
	TS20_nervous system	1.60E-114	1000	524
	TS22_sensory organ	7.63E-113	1125	616
	TS4_embryo	9.29E-108	878	471
	Theiler_stage_4	1.65E-106	879	472
MSigDB Perturbation	Set 'H3K27 bound': genes posessing the trimethylated H3K27 (H3	8.48E-126	1005	497
	Genes up-regulated in brain from patients with Alzheimer's disea	1.12E-123	1150	656
	Set 'Eed targets': genes identified by ChIP on chip as targets of th	2.17E-106	909	451
	Set 'Suz12 targets': genes identified by ChIP on chip as targets of	1.75E-101	920	455
	Genes up-regulated in the HMEC cells (primary mammary epithe	2.20E-99	817	450
	Set 'PRC2 targets': Polycomb Repression Complex 2 (PRC) targets	4.03E-97	662	314
	Genes with copy number losses in primary neuroblastoma tumo	2.75E-58	469	309
	Set 'Sox2 targets': genes upregulated and identified by ChIP on c	1.95E-56	514	272
	Genes up-regulated in luminal-like breast cancer cell lines compa	6.11E-50	325	173
	Set 'ES exp1': genes overexpressed in human embryonic stem ce	1.00E-49	332	175

The test set of 8,508 genomic regions picked 6,503 genes (32%) of all 20,221 genes.
GO Molecular Function has 3,254 terms 3,254 ontology terms were tested (100%) using an annotation count range of [1, Inf].
GO Biological Process has 8,583 terms co 8,583 ontology terms were tested (100%) using an annotation count range of [1, Inf].
Mouse Phenotype has 7,310 terms cove 7,310 ontology terms were tested (100%) using an annotation count range of [1, Inf].
MGI Expression: Detected has 8,374 term 8,374 ontology terms were tested (100%) using an annotation count range of [1, Inf].
MSigDB Perturbation has 2,374 terms co 2,374 ontology terms were tested (100%) using an annotation count range of [1, Inf].

NSC SPECIFIC CLUSTERS

GO Molecular Function	beta-dystroglycan binding	2.91E-14	38	2
	endothelin-B receptor activity	8.73E-14	27	1
	glyceryl-ether monooxygenase activity	3.59E-12	25	1
	3',5'-cyclic-AMP phosphodiesterase activity	7.50E-12	80	7
	endothelin receptor activity	2.08E-11	34	2
	calcium channel regulator activity	4.65E-11	77	8
	semaphorin receptor activity	1.76E-10	58	5
	cytoskeletal regulatory protein binding	3.43E-10	32	1
	histone kinase activity (H3-T6 specific)	4.37E-10	28	2

	stem cell factor receptor binding	4.70E-10	40	3
GO Biological Process	positive regulation of myoblast differentiation	7.87E-19	87	8
	neurotransmitter-gated ion channel clustering	1.44E-17	45	2
	receptor localization to synapse	1.44E-17	45	2
	regulation of neuron maturation	1.77E-17	50	3
	neuron cell-cell adhesion	8.35E-17	63	4
	B cell receptor signaling pathway	2.05E-16	134	16
	peptidyl-threonine modification	4.09E-16	135	17
	presynaptic membrane assembly	3.78E-15	45	2
	peptidyl-threonine phosphorylation	4.57E-15	120	15
	calcium-dependent cell-cell adhesion	6.23E-15	82	9
Mouse Phenotype	synechia	6.48E-19	133	16
	abnormal vertical vestibuloocular reflex	4.38E-18	32	1
	dilated respiratory conducting tubes	8.45E-17	156	17
	abnormal cochlear IHC efferent innervation pattern	1.08E-12	62	6
	decreased maxillary shelf size	1.08E-12	77	7
	decreased circulating interferon-beta level	2.51E-12	49	5
	abnormal iridocorneal angle	7.45E-12	116	16
	abnormal foot pigmentation	8.63E-12	113	15
	optic nerve cupping	9.57E-12	41	3
MGI Expression	TS25_thalamus	1.33E-18	156	17
	TS19_trunk mesenchyme; mesenchyme derived from neural cre	1.72E-18	103	9
	TS23_endolymphatic duct	2.10E-18	106	10
	TS19_embryo; mesenchyme; mesenchyme derived from neural	7.03E-17	85	7
	TS15_trunk mesenchyme; mesenchyme derived from neural cre	9.83E-17	116	13
	TS25_cerebral cortex; subventricular zone	1.83E-16	101	10
	TS25_spinal cord; lateral wall; mantle layer	1.59E-14	47	3
MSigDB Perturbation	Genes up-regulated in glioblastoma cell lines displaying spherica	6.48E-17	127	15
	Examples of transcription factors whose activities are regulated	4.84E-14	68	7
	Genes down-regulated in CD34+ [Gene ID=947] hematopoetic ce	5.16E-14	130	19
	Selected genes implicated in metastasis and epithelial-to-mesen	2.59E-13	105	11
	Genes down-regulated in Kasumi-1 cells (acute myeloid leukaem	3.70E-12	117	15
	Genes significantly mutated in 91 glioblastoma samples.	1.20E-11	59	6
	Examples of transcription factors whose activities are regulated	4.68E-11	64	7

	Examples of transcription factors whose activities are regulated	1.93E-10	46	4
	Genes highly expressed in the neonatal hippocampus (clusters 4	1.05E-09	73	13
	Genes specifically down-regulated in pediatric acute lymphoblas	2.38E-09	85	14

MEF SPECIFIC CLUSTERS

GO Molecular Function	growth factor binding	5.11E-25	259	65
	extracellular matrix structural constituent	5.15E-21	109	23
	insulin-like growth factor binding	2.57E-13	78	15
	platelet-derived growth factor binding	6.87E-11	45	8
	hepatocyte growth factor-activated receptor activity	1.02E-09	19	2
	protein-lysine 6-oxidase activity	7.27E-09	18	2
	collagen V binding	4.69E-08	18	2
	phospholipase inhibitor activity	1.22E-07	28	5
	calcium-dependent phospholipid binding	1.82E-07	56	12
	Roundabout binding	2.57E-07	21	4
GO Biological Process	collagen fibril organization	8.87E-16	94	17
	luteolysis	2.96E-13	32	3
	myoblast proliferation	1.72E-12	33	5
	positive regulation of vesicle fusion	7.20E-12	31	4
	regulation of branching involved in salivary gland morphogenesi	8.39E-12	39	6
	hepatocyte growth factor receptor signaling pathway	1.28E-10	28	4
	mesenchymal-epithelial cell signaling	2.14E-10	47	9
	regulation of branching involved in salivary gland morphogenesi	1.56E-09	44	8
	regulation of vesicle fusion	1.94E-09	31	4
	regulation of epithelial cell proliferation involved in lung morpho	6.21E-09	35	6
Mouse Phenotype	decreased corneal stroma thickness	6.72E-17	49	8
	abnormal cutaneous collagen fibril morphology	8.34E-17	75	11
	corneal thinning	3.63E-15	64	13
	thin diaphragm muscle	5.24E-15	88	16
	herniated diaphragm	6.03E-14	68	12
	abnormal skin tensile strength	3.85E-13	74	14
	abnormal miniature inhibitory postsynaptic currents	8.55E-13	60	11
	abnormal kidney corticomedullary boundary morphology	1.24E-12	38	6
	abnormal motor neuron innervation	5.00E-12	105	23

MGI Expression	TS28_tendon	2.27E-22	93	16
	TS22_pancreas; mesenchyme	6.54E-22	156	37
	TS28_tendo calcaneus	2.39E-17	64	11
	TS21_perioptic mesenchyme	4.24E-15	40	6
	TS28_corpus luteum	8.41E-13	56	10
	TS23_forelimb; skeleton	5.51E-12	46	9
	TS26_lower jaw; skeleton	2.62E-10	65	18
	TS28_ovary secondary follicle	4.86E-10	65	12
	TS26_cornea	4.99E-10	84	24
	TS28_chondrocranium	9.71E-10	94	20
MSigDB Perturbation	Up-regulated genes distinguishing between two subtypes of gast	8.29E-47	450	114
	Up-regulated genes in angioimmunoblastic lymphoma (AILT) cor	4.52E-43	477	128
	Genes down-regulated in primary fibroblast cell culture after inf	4.03E-33	350	86
	Genes up-regulated in lobular carcinoma vs normal ductal breas	1.63E-31	212	46
	Selected genes down-regulated during invasion of lymphatic ves	1.38E-30	156	30
	Down-regulated at 24 h following infection of primary human fo	2.44E-29	181	35
	Genes down-regulated in lobular carcinoma vs normal lobular br	3.21E-29	200	48
	Down-regulated at any timepoint following infection of primary	3.16E-26	209	45
	Cluster 5: selected 17q21_23 amplicon genes clustered together	3.14E-25	96	13
	Genes whose expression positively correlated with sensitivity of	1.63E-24	216	52

The test set of 23,864 genomic regions picked 7,624 genes (38%) of all 20,221 genes.
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COMMON TO ALL

GO Molecular Function	nucleic acid binding	1.71E-148	1164	1012
	nucleotide binding	1.82E-87	869	750
	DNA binding	4.64E-81	736	613
	zinc ion binding	1.26E-67	665	549
	RNA binding	3.93E-61	343	298
	enzyme binding	2.50E-37	346	275

	transferase activity, transferring phosphorus-containing groups	1.33E-36	373	306
	hydrolase activity, acting on acid anhydrides	4.48E-28	275	233
	phosphotransferase activity, alcohol group as acceptor	1.09E-27	290	232
	pyrophosphatase activity	1.91E-27	270	228
GO Biological Process	cellular metabolic process	0	2316	2142
	primary metabolic process	0	2291	2109
	metabolic process	0	2501	2347
	cellular macromolecule metabolic process	5.32E-301	1881	1684
	macromolecule metabolic process	5.60E-298	1989	1792
	nitrogen compound metabolic process	1.27E-211	1475	1281
	cellular nitrogen compound metabolic process	6.82E-211	1452	1258
	nucleobase-containing compound metabolic process	1.45E-202	1360	1179
	nucleic acid metabolic process	4.37E-179	1171	1015
	regulation of cellular metabolic process	1.08E-162	1468	1239
Mouse Phenotype	preweaning lethality	1.20E-125	1218	1001
	prenatal lethality	2.75E-118	856	704
	embryonic lethality	3.94E-104	682	551
	abnormal embryogenesis/ development	2.45E-80	672	536
	cellular phenotype	5.08E-77	635	532
	abnormal cell physiology	4.68E-70	584	492
	abnormal blood cell morphology/development	3.53E-62	634	504
	abnormal hematopoiesis	3.40E-60	624	499
	embryonic lethality during organogenesis	2.44E-54	412	326
	abnormal prenatal growth/weight/body size	4.50E-52	449	350
MGI Expression	TS23_metanephros	1.02E-123	1174	965
	TS23_reproductive system	2.76E-107	1053	860
	TS23_urethra	1.63E-96	735	583
	TS23_early tubule	5.74E-90	526	415
	TS4_embryo	6.46E-88	549	438
	Theiler_stage_4	1.10E-87	551	440
	Theiler_stage_5	3.20E-87	548	436
	TS23_cap mesenchyme	1.31E-86	492	381
	TS4_extraembryonic component	8.98E-85	525	421
	TS23_renal cortex	1.09E-84	610	485

	TS23_renal interstitium	3.55E-83	535	413
MSigDB	Genes constituting the BRCA1-PCC network of transcripts whose	5.17E-123	711	617
Perturbation	Genes up-regulated in brain from patients with Alzheimer's disea	1.22E-111	738	587
	Genes whose promoters are bound by MYC [Gene ID=4609], acc	9.11E-99	482	415
	Genes up-regulated in CD34+ [Gene ID=947] cells isolated from b	1.58E-90	620	530
	Genes constituting the CHEK2-PCC network of transcripts whose	6.33E-80	382	322
	Genes down-regulated in nasopharyngeal carcinoma (NPC) comp	4.63E-76	545	475
	Set 'Myc targets2': targets of c-Myc [Gene ID=4609] and Max [Ge	3.05E-75	359	317
	Genes constituting the ATM-PCC network of transcripts whose e	8.55E-73	569	490
	Genes with copy number losses in primary neuroblastoma tumo	1.72E-71	344	317

The test set of 4,671 genomic regions picked 4,902 genes (24%) of all 20,221 genes.

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