SI Appendix

Overrepresented and Underrepresented Gene Ontology (GO) Terms

To explore the biological functions of the sets of genes identified by our analysis we examined each gene set for overrepresented and underrepresented Gene Ontology (GO) terms using the Generic GO Term Finder at http://go.princeton.edu/cgi-bin/GOTermFinder. The results from this analysis are summarized in tables S1-S4 containing the enriched GO terms with the corresponding Bonferroni corrected p-values. The legend for the header of the tables is:

N Set – Number of genes in the our gene set with the corresponding GO term (first column)
N Tot – Number of genes in the genome with the corresponding GO term (first column)
p val – Bonferroni corrected probability for finding the observed **N Set** number or greater number of genes with the corresponding GO term if the genes were sampled from the genome randomly. The probability is computed from the hypergeometric distribution and corrected for multiple hypotheses testing.

The Swiss-Prot identifiers corresponding to the genes from each set can be found in the accompanying word document, Supp_Info_GO_GeneSets.doc. The genes are listed in accordance to the enriched GO terms in the default format of the

Generic GO Term Finder. The total number of Swiss-Prot identifiers used by the GO Term Finder for computing p-values is 38594.

1.1 Genes coupled more strongly in non-cancer cells, $\Delta C > 1$

The total number of Swiss-Prot identifiers corresponding to the gene set and used for computing the p-values is 846.

Table S1

GO ID	Term	p val	N Set	N Tot
GO:0032501	multicellular organismal process	8.E-24	200	4721
GO:0032502	developmental process	6.E-13	163	4393
GO:0048856	anatomical structure development	9.E-13	120	2822
GO:0009605	response to external stimulus	5.E-12	59	929
GO:0006936	muscle contraction	5.E-12	27	200
GO:0048731	system development	1.E-11	108	2497
GO:0003012	muscle system process	2.E-11	27	209
GO:0006941	striated muscle contraction	3.E-11	17	70
GO:0003008	system process	4.E-11	83	1701
GO:0048513	organ development	4.E-11	87	1832
GO:0007275	multicellular organismal development	5.E-11	126	3206
GO:0007267	cell-cell signaling	3.E-08	46	758
GO:0065008	regulation of biological quality	6.E-08	76	1720
GO:0007154	cell communication	1.E-07	190	6205
GO:0006952	defense response	1.E-07	43	712
GO:0051239	regulation of multicellular organismal process	3.E-07	43	732
GO:0051239	regulation of multicellular organismal process & multicellular organismal process	3.E-07	43	732
GO:0006935	chemotaxis	6.E-07	20	179
GO:0042330	taxis	6.E-07	20	179
GO:0050896	response to stimulus	1.E-06	138	4213
GO:0048518	positive regulation of biological process	3.E-06	74	1814
GO:0007155	cell adhesion	4.E-06	53	1103
GO:0022610	biological adhesion	4.E-06	53	1103
GO:0032103	positive regulation of response to external stimulus	4.E-06	11	50
GO:0007165	signal transduction	5.E-06	171	5693
GO:0006950	response to stress	3.E-05	74	1916
GO:0008283	cell proliferation	4.E-05	51	1118
GO:0048522	positive regulation of cellular process	4.E-05	66	1636
GO:0048869	cellular developmental process	5.E-05	74	1935
GO:0030154	cell differentiation	5.E-05	69	1753
GO:0042221	response to chemical stimulus	5.E-05	45	933
GO:0007626	locomotory behavior	6.E-05	22	279
GO:0040011	locomotion	7.E-05	33	576
GO:0009611	response to wounding	8.E-05	32	550
GO:0051704	multi-organism process	9.E-05	36	671
GO:0009653	anatomical structure morphogenesis	1.E-04	60	1461
GO:0007166	cell surface receptor linked signal transduction	1.E-04	94	2731

GO:0003013	circulatory system process	2.E-04	20	248
GO:0008015	blood circulation	2.E-04	20	248
GO:0003015	heart process	2.E-04	12	87
GO:0060047	heart contraction	2.E-04	12	87
GO:0032101	regulation of response to external stimulus	3.E-04	13	109
GO:0032101	regulation of response to external stimulus & response to external stimulus	3.E-04	13	109
GO:0006968	cellular defense response	3.E-04	10	60
GO:0007517	muscle development	6.E-04	21	295
GO:0003009	skeletal muscle contraction	9.E-04	5	10
GO:0050900	leukocyte migration	9.E-04	10	67
GO:0019932	second-messenger-mediated signaling	1.E-03	21	309
GO:0007610	behavior	1.E-03	27	476
GO:0050793	regulation of developmental process & developmental process	2.E-03	50	1228
GO:0048519	negative regulation of biological process	2.E-03	66	1813
GO:0050793	regulation of developmental process	2.E-03	50	1230
GO:0009887	organ morphogenesis	2.E-03	34	693
GO:0042592	homeostatic process	3.E-03	40	910
GO:0042127	regulation of cell proliferation	4.E-03	35	751
GO:0051707	response to other organism	4.E-03	18	252
GO:0006928	cell motion	4.E-03	31	626
GO:0051674	localization of cell	4.E-03	31	626
GO:0042127	regulation of cell proliferation & cell proliferation	5.E-03	33	696
GO:0030855	epithelial cell differentiation	5.E-03	10	80
GO:0006874	cellular calcium ion homeostasis	5.E-03	14	161
GO:0012501	programmed cell death	6.E-03	46	1144
GO:0002376	immune system process	6.E-03	63	1775
GO:0055074	calcium ion homeostasis	6.E-03	14	164
GO:0048584	positive regulation of response to stimulus	7.E-03	15	188
GO:0008219	cell death	1.E-02	47	1204

1.1 Genes

Receptors

nuclear receptor co-repressor 1	C20orf191
insulin-like growth factor 2 receptor	IGF2R
interferon gamma receptor 2 (interferon gamma transducer 1)	IFNGR2
epidermal growth factor receptor	EGFR
diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	DBI
protein tyrosine phosphatase, non-receptor type 1	PTPN1
integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ITGB2
tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B
sortilin-related receptor, L(DLR class) A repeats-containing	SORL1
Fc fragment of IgG, low affinity IIa, receptor (CD32)	FCGR2A
colony stimulating factor 3 receptor (granulocyte)	CSF3R

fibroblast growth factor receptor 2	FGFR2
Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	FCGR3A /// FCGR3B
Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	FCGR3B
Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	FCER1G
fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	FGFR3
folate receptor 1 (adult)	FOLR1
Fas (TNF receptor superfamily, member 6)	FAS
interferon (alpha, beta and omega) receptor 2	IFNAR2
toll-like receptor 2	TLR2
chemokine (C-C motif) receptor 1	CCR1
formyl peptide receptor 1	FPR1
interleukin 2 receptor, beta	IL2RB
adenosine A1 receptor	ADORA1
ryanodine receptor 1 (skeletal)	RYR1
protein tyrosine phosphatase, non-receptor type 14	PTPN14
integrin, alpha M (complement component 3 receptor 3 subunit)	ITGAM
interleukin 7 receptor	IL7R
chemokine (C-X3-C motif) receptor 1	CX3CR1
interleukin 6 receptor	IL6R
G protein-coupled receptor 64	GPR64
protein tyrosine phosphatase, receptor type, R	PTPRR
growth factor receptor-bound protein 14	GRB14
platelet-activating factor receptor	PTAFR
nuclear receptor subfamily 0, group B, member 1	NR0B1
tumor necrosis factor receptor superfamily, member 8	TNFRSF8
leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	LILRA3
anti-Mullerian hormone receptor, type II	AMHR2
protein tyrosine phosphatase, receptor type, alpha 2	PPFIA2
interleukin 8 receptor, beta	IL8RB
hepatitis A virus cellular receptor 1	HAVCR1
colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	CSF2RA
neuropeptide Y receptor Y5	NPY5R
leukocyte-associated immunoglobulin-like receptor 2	LAIR2
egf-like module containing, mucin-like, hormone receptor-like 2	EMR2
chemokine-like receptor 1	CMKLR1
cannabinoid receptor 1 (brain)	CNR1
angiotensin II receptor, type 1	AGTR1
arginine vasopressin receptor 1B	AVPR1B
killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	KIR2DL4
G protein-coupled receptor 15	GPR15
leukocyte receptor cluster (LRC) member 4	LENG4
interleukin 10 receptor, beta	IL10RB
G protein-coupled receptor kinase interactor 2	GIT2
integrin, alpha X (complement component 3 receptor 4 subunit)	ITGAX
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), alpha 1	PPFIA1
colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	CSF2RA

cholecystokinin B receptor	CCKBR
glutamate receptor, ionotropic, N-methyl D-aspartate 2C	GRIN2C
protein tyrosine phosphatase, receptor type, R	PTPRR
growth factor receptor-bound protein 7	GRB7
natural cytotoxicity triggering receptor 3	NCR3
T cell receptor beta variable 19	TRBV19
T cell receptor beta constant 1	TRBC1
aryl hydrocarbon receptor nuclear translocator-like	ARNTL
fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	FGFR1
Fc fragment of IgG, low affinity IIc, receptor for (CD32)	FCGR2C
leukocyte receptor cluster (LRC) member 4	LENG4
diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	DBI
leukocyte immunoglobulin-like receptor, subfamily B, member 3	LILRB3
killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	KIR2DL4
pre T-cell antigen receptor alpha	PTCRA
colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	CSF2RA
protein tyrosine phosphatase, receptor type, U	PTPRU
natural cytotoxicity triggering receptor 3	NCR3
met proto-oncogene (hepatocyte growth factor receptor)	MET
interferon gamma receptor 1	IFNGR1
EPH receptor B1	EPHB1
protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	PTPN18
killer cell lectin-like receptor subfamily B, member 1	KLRB1
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	PPFIA4
neurotrophic tyrosine kinase, receptor, type 3	NTRK3
G protein-coupled receptor 17	GPR17
5-hydroxytryptamine (serotonin) receptor 3A	HTR3A
T-cell receptor active beta-chain (V10-D-J-C) mRNA, clone PL3.9	
somatostatin receptor 2	SSTR2
similar to olfactory receptor, family 7, subfamily A, member 17	LOC441453
triggering receptor expressed on myeloid cells 1	TREM1
nuclear receptor interacting protein 3	NRIP3
purinergic receptor P2Y, G-protein coupled, 13	P2RY13
apolipoprotein B48 receptor	APOB48R
activin A receptor, type IIB	ACVR2B
complement component 5a receptor 1	C5AR1
CD244 molecule, natural killer cell receptor 2B4	CD244
G protein-coupled receptor 88	GPR88
chemokine (C-C motif) receptor 10	CCR10
cholinergic receptor, nicotinic, alpha 9	CHRNA9
free fatty acid receptor 2	FFAR2
purinergic receptor P2X, ligand-gated ion channel, 2	P2RX2
cholinergic receptor, muscarinic 4	CHRM4
melanocortin 4 receptor	MC4R
G protein-coupled receptor 137	GPR137

interleukin 27 receptor, alpha IL27RA
paired immunoglobin-like type 2 receptor alpha PILRA
cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) CELSR3

Cancer related

melanoma antigen family B, 1 MAGEB1
melanoma antigen family A, 8 MAGEA8
melanoma antigen family A, 10 MAGEA10
melanoma antigen family A, 11 MAGEA11
melanoma antigen family A, 4 MAGEA4
v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian) MYCL1
breast carcinoma amplified sequence 3 BCAS3
palate, lung and nasal epithelium carcinoma associated PLUNC
amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) AMPH
cancer susceptibility candidate 3CASC3
synuclein, gamma (breast cancer-specific protein 1) SNCG
similar to cervical cancer suppressor-1 LOC400410
tumor necrosis factor, alpha-induced protein 2 TNFAIP2
tumor necrosis factor receptor superfamily, member 1B TNFRSF1B
tumor necrosis factor receptor superfamily, member 8 TNFRSF8
tumor necrosis factor (ligand) superfamily, member 14 TNFSF14
deleted in malignant brain tumors 1 DMBT1
tumor protein D52-like 1 TPD52L1
tumor protein p73-like TP73L
fibroblast growth factor 3 oncogene homolog) FGF3
RAS-like, family 10, member A RASL10A

2.1 Genes whose correlation vectors in cancer and non-cancer are least correlated, $\rho_{i(s1,s2)} < 0.2$

The total number of Swiss-Prot identifiers corresponding to the gene set and used for computing the p-values is 1552.

Table S2

GO ID	**Term**	**p val**	**N Set**	**N Tot**
GO:0032502	developmental process	4.E-17	257	4393
GO:0007275	multicellular organismal development	2.E-11	187	3206
GO:0048856	anatomical structure development	3.E-11	170	2822
GO:0032501	multicellular organismal process	9.E-11	248	4721
GO:0048513	organ development	1.E-10	123	1832
GO:0048522	positive regulation of cellular process	1.E-09	111	1636
GO:0048518	positive regulation of biological process	2.E-09	119	1814
GO:0048519	negative regulation of biological process	4.E-09	118	1813
GO:0050793	regulation of developmental process & developmental process	4.E-09	90	1228
GO:0050793	regulation of developmental process	4.E-09	90	1230
GO:0048731	system development	1.E-08	147	2497
GO:0048523	negative regulation of cellular process	3.E-08	109	1675
GO:0008283	cell proliferation	8.E-08	81	1118
GO:0006091	generation of precursor metabolites and energy	1.E-06	48	537
GO:0012501	programmed cell death	1.E-06	79	1144
GO:0006915	apoptosis	2.E-06	78	1135
GO:0009653	anatomical structure morphogenesis	3.E-06	93	1461
GO:0008219	cell death	3.E-06	81	1204
GO:0016265	death	3.E-06	81	1208
GO:0051093	negative regulation of developmental process	3.E-06	48	555
GO:0007507	heart development	4.E-06	28	227
GO:0009887	organ morphogenesis	1.E-05	54	693
GO:XXXXXXX	unannotated	3.E-05	468	11418
GO:0042127	regulation of cell proliferation & cell proliferation	4.E-05	53	696
GO:0042127	regulation of cell proliferation	8.E-05	55	751
GO:0031325	positive regulation of cellular metabolic process	1.E-04	54	738
GO:0042981	regulation of apoptosis	1.E-04	58	819
GO:0043067	regulation of programmed cell death	1.E-04	58	828
GO:0043067	regulation of programmed cell death & programmed cell death	1.E-04	58	828
GO:0009893	positive regulation of metabolic process	3.E-04	54	762
GO:0010604	positive regulation of macromolecule metabolic process	3.E-04	52	722
GO:0010604	positive regulation of macromolecule	3.E-04	52	722

	metabolic process & macromolecule metabolic process			
GO:0007167	enzyme linked receptor protein signaling pathway	3.E-04	38	451
GO:0051094	positive regulation of developmental process	6.E-04	44	579
GO:0051239	regulation of multicellular organismal process	1.E-03	51	732
GO:0051239	regulation of multicellular organismal process & multicellular organismal process	1.E-03	51	732
GO:0043066	negative regulation of apoptosis	1.E-03	31	349
GO:0015980	energy derivation by oxidation of organic compounds	1.E-03	18	139
GO:0006936	muscle contraction	2.E-03	22	200
GO:0043069	negative regulation of programmed cell death	2.E-03	31	354
GO:0001501	skeletal system development	2.E-03	31	355
GO:0065008	regulation of biological quality	2.E-03	94	1720
GO:0005977	glycogen metabolic process	3.E-03	11	55
GO:0006073	glucan metabolic process	3.E-03	11	56
GO:0003012	muscle system process	3.E-03	22	209
GO:0007243	protein kinase cascade	5.E-03	39	528
GO:0010557	positive regulation of macromolecule biosynthetic process	6.E-03	43	611
GO:0010557	positive regulation of macromolecule biosynthetic process & macromolecule biosynthetic process	6.E-03	43	611
GO:0007267	cell-cell signaling	6.E-03	50	758
GO:0031328	positive regulation of cellular biosynthetic process	6.E-03	44	633
GO:0032879	regulation of localization	8.E-03	29	344
GO:0032879	regulation of localization & localization	8.E-03	29	344
GO:0009891	positive regulation of biosynthetic process	8.E-03	44	639
GO:0006916	anti-apoptosis	9.E-03	22	222
GO:0006112	energy reserve metabolic process	9.E-03	11	62
GO:0005976	polysaccharide metabolic process	9.E-03	14	100

2.2 Genes

Oncogenes

CDC42 effector protein (Rho GTPase binding) 2	CDC42EP2
Rho-related BTB domain containing 2	RHOBTB2
CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3
Rho-related BTB domain containing 3	RHOBTB3
myosin phosphatase-Rho interacting protein	M-RIP
Rho GTPase activating protein 8 /// PRR5-ARHGAP8 fusion	ARHGAP8 /// LOC553158
FYVE, RhoGEF and PH domain containing 6	FGD6
Rho-related BTB domain containing 3	RHOBTB3
ras homolog gene family, member Q	RHOQ
Rho-related BTB domain containing 2	RHOBTB2
ras homolog gene family, member T1	RHOT1
Rab acceptor 1 (prenylated)	RABAC1
RAN binding protein 5	RANBP5

Ras protein-specific guanine nucleotide-releasing factor 1	RASGRF1
Ras-related associated with diabetes	RRAD
Ras-related GTP binding D	RRAGD
RAB14, member RAS oncogene family	RAB14
RAB21, member RAS oncogene family	RAB21
Ras protein-specific guanine nucleotide-releasing factor 1	RASGRF1
RAB31, member RAS oncogene family	RAB31
RAB3B, member RAS oncogene family	RAB3B
RAS guanyl releasing protein 3 (calcium and DAG-regulated)	RASGRP3
RAB27B, member RAS oncogene family	RAB27B
golgi reassembly stacking protein 2, 55kDa	GORASP2
related RAS viral (r-ras) oncogene homolog 2	RRAS2
RAB7A, member RAS oncogene family	RAB7A
RAB22A, member RAS oncogene family	RAB22A
RAS p21 protein activator 4 /// hypothetical protein FLJ21767	FLJ21767 /// RASA4
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS
RAP2B, member of RAS oncogene family	RAP2B
v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	RALB
RAB14, member RAS oncogene family	RAB14
translocated promoter region (to activated MET oncogene)	TPR
ret proto-oncogene	RET
v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	KIT
RAB31, member RAS oncogene family	RAB31
vav 3 oncogene	VAV3
fibroblast growth factor 3 (oncogene homolog)	FGF3
RAB27B, member RAS oncogene family	RAB27B
v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	MYCN
myeloproliferative leukemia virus oncogene	MPL
related RAS viral (r-ras) oncogene homolog 2	RRAS2
runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	RUNX1
epidermal growth factor receptor (erythroblastic leukemia viral oncogene homolog, avian)	EGFR
BMI1 polycomb ring finger oncogene	BMI1
RAB7A, member RAS oncogene family	RAB7A
RAB22A, member RAS oncogene family	RAB22A
v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS
SKI-like oncogene	SKIL
vav 3 oncogene	VAV3
v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	MAF
RAP2B, member of RAS oncogene family	RAP2B
lipocalin 2 (oncogene 24p3)	LCN2
mitogen-activated protein kinase 12	MAPK12
mitogen-activated protein kinase 7	MAPK7
mitogen-activated protein kinase 1	MAPK1
mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2
tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A
fibroblast growth factor 3 (murine mammary tumor virus integration oncogene homolog)	FGF3
tumor necrosis factor receptor superfamily, member 8	TNFRSF8

tumor necrosis factor receptor superfamily, member 10b	TNFRSF10B
tumor necrosis factor receptor superfamily, member 10d	TNFRSF10D
tumor necrosis factor, alpha-induced protein 6	TNFAIP6
rhabdoid tumor deletion region gene 1	RTDR1
tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	TNFRSF11B
tumor necrosis factor, alpha-induced protein 6	TNFAIP6
ADAM metallopeptidase domain 17 (tumor necrosis factor, alpha)	ADAM17
arginine-rich, mutated in early stage tumors	ARMET
tumor protein p53 inducible protein 11	TP53I11
cancer/testis antigen 1B /// cancer/testis antigen 1A	CTAG1A /// CTAG1B
synuclein, gamma (breast cancer-specific protein 1)	SNCG
leucine zipper, down-regulated in cancer 1	LDOC1
cancer/testis antigen 2	CTAG2

Dehydrogenases

NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	NDUFA1
aldehyde dehydrogenase 1 family, member A1	ALDH1A1
isocitrate dehydrogenase 2 (NADP+), mitochondrial	IDH2
aldehyde dehydrogenase 1 family, member A2	ALDH1A2
NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	NDUFS7
NAD(P)H dehydrogenase, quinone 2	NQO2
aldehyde dehydrogenase 5 family, member A1	ALDH5A1
pyruvate dehydrogenase kinase, isozyme 2	PDK2
hydroxyacyl-Coenzyme A dehydrogenase	HADH
dehydrogenase/reductase (SDR family) member 9	DHRS9
dehydrogenase E1 and transketolase domain containing 1	DHTKD1
succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1	SDHALP1
hydroxysteroid (17-beta) dehydrogenase 8	HSD17B8
aldehyde dehydrogenase 3 family, memberA1	ALDH3A1
isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A
acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	ACADM
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	NDUFA3
isocitrate dehydrogenase 2 (NADP+), mitochondrial	IDH2
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	NDUFA4
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NDUFB8
NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NDUFV2
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	NDUFB11
dehydrogenase/reductase (SDR family) member 7	DHRS7
hydroxysteroid (11-beta) dehydrogenase 1	HSD11B1
hydroxysteroid (17-beta) dehydrogenase 1	HSD17B1

3.1 Genes whose correlation vectors in cancer and non-cancer are most separated (in Euclidian sense) in the space of genes, $D_{i(s1,s2)} > 30$

The total number of Swiss-Prot identifiers corresponding to the gene set and used for computing the p-values is 1641.

Table S3

GO ID	***Term***	***p val***	***N Set***	***N Tot***
GO:0048518	positive regulation of biological process	6.E-22	177	1814
GO:0048522	positive regulation of cellular process	8.E-22	165	1636
GO:0048523	negative regulation of cellular process	7.E-20	163	1675
GO:0050793	regulation of developmental process & developmental process	8.E-20	133	1228
GO:0050793	regulation of developmental process	1.E-19	133	1230
GO:0012501	programmed cell death	9.E-19	125	1144
GO:0048519	negative regulation of biological process	1.E-18	169	1813
GO:0006915	apoptosis	1.E-18	124	1135
GO:0043067	regulation of programmed cell death	4.E-17	99	828
GO:0043067	regulation of programmed cell death & programmed cell death	4.E-17	99	828
GO:0042981	regulation of apoptosis	6.E-17	98	819
GO:0008219	cell death	6.E-17	125	1204
GO:0016265	death	8.E-17	125	1208
GO:0032502	developmental process	1.E-12	295	4393
GO:0043069	negative regulation of programmed cell death	1.E-11	52	354
GO:0008380	RNA splicing	2.E-11	43	256
GO:0043066	negative regulation of apoptosis	3.E-11	51	349
GO:0006396	RNA processing	2.E-10	70	616
GO:0016043	cellular component organization	5.E-10	207	2933
GO:0006091	generation of precursor metabolites and energy	3.E-09	62	537
GO:0051094	positive regulation of developmental process	3.E-09	65	579
GO:0051093	negative regulation of developmental process	4.E-09	63	555
GO:XXXXXXX	unannotated	2.E-08	610	11418
GO:0043065	positive regulation of apoptosis	5.E-08	47	370
GO:0043068	positive regulation of programmed cell death	7.E-08	47	374
GO:0031325	positive regulation of cellular metabolic process	1.E-07	72	738
GO:0051128	regulation of cellular component organization	1.E-07	47	381
GO:0006366	transcription from RNA polymerase II promoter	1.E-07	83	912
GO:0032268	regulation of cellular protein metabolic process	3.E-07	46	376
GO:0015980	energy derivation by oxidation of organic compounds	3.E-07	26	139
GO:0006917	induction of apoptosis	4.E-07	40	302

GO:0012502	induction of programmed cell death	5.E-07	40	303
GO:0044419	interspecies interaction between organisms	5.E-07	40	303
GO:0009893	positive regulation of metabolic process	5.E-07	72	762
GO:0008283	cell proliferation	6.E-07	94	1118
GO:0043933	macromolecular complex subunit organization	6.E-07	88	1020
GO:0010604	positive regulation of macromolecule metabolic process	8.E-07	69	722
GO:0010604	positive regulation of macromolecule metabolic process & macromolecule metabolic process	8.E-07	69	722
GO:0006916	anti-apoptosis	8.E-07	33	222
GO:0042274	ribosomal small subunit biogenesis	8.E-07	8	10
GO:0031328	positive regulation of cellular biosynthetic process	9.E-07	63	633
GO:0022613	ribonucleoprotein complex biogenesis and assembly	1.E-06	39	298
GO:0031324	negative regulation of cellular metabolic process	1.E-06	67	698
GO:0009891	positive regulation of biosynthetic process	1.E-06	63	639
GO:0009892	negative regulation of metabolic process	1.E-06	69	733
GO:0065008	regulation of biological quality	2.E-06	127	1720
GO:0010605	negative regulation of macromolecule metabolic process	2.E-06	66	694
GO:0022900	electron transport chain	3.E-06	25	143
GO:0051246	regulation of protein metabolic process	3.E-06	53	505
GO:0000375	RNA splicing, via transesterification reactions	3.E-06	19	84
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	3.E-06	19	84
GO:0000398	nuclear mRNA splicing, via spliceosome	3.E-06	19	84
GO:0006357	regulation of transcription from RNA polymerase II promoter	9.E-06	66	719
GO:0010557	positive regulation of macromolecule biosynthetic process	1.E-05	59	611
GO:0010557	positive regulation of macromolecule biosynthetic process & macromolecule biosynthetic process	1.E-05	59	611
GO:0033036	macromolecule localization	1.E-05	102	1320
GO:0007242	intracellular signaling cascade	1.E-05	156	2306
GO:0045941	positive regulation of transcription	1.E-05	54	539
GO:0034621	cellular macromolecular complex subunit organization	2.E-05	71	810
GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.E-05	56	575
GO:0010628	positive regulation of gene expression	2.E-05	54	548
GO:0010628	positive regulation of gene expression & gene expression	2.E-05	54	548
GO:0042127	regulation of cell proliferation	2.E-05	67	751
GO:0006913	nucleocytoplasmic transport	3.E-05	30	219
GO:0051169	nuclear transport	4.E-05	30	221
GO:0051170	nuclear import	4.E-05	23	139
GO:0015031	protein transport	5.E-05	89	1135

GO:0046907	intracellular transport	5.E-05	89	1135
GO:0008104	protein localization	5.E-05	96	1259
GO:0045184	establishment of protein localization	6.E-05	89	1139
GO:0006996	organelle organization	6.E-05	100	1334
GO:0006605	protein targeting	6.E-05	36	304
GO:0065003	macromolecular complex assembly	7.E-05	77	938
GO:0045893	positive regulation of transcription, DNA-dependent	7.E-05	47	461
GO:0022607	cellular component assembly	8.E-05	81	1010
GO:0051254	positive regulation of RNA metabolic process	8.E-05	47	464
GO:0045333	cellular respiration	8.E-05	16	72
GO:0007243	protein kinase cascade	1.E-04	51	528
GO:0022618	ribonucleoprotein complex assembly	1.E-04	24	157
GO:0048856	anatomical structure development	1.E-04	178	2822
GO:0006606	protein import into nucleus	2.E-04	22	137
GO:0051649	establishment of localization in cell	2.E-04	102	1402
GO:0016071	mRNA metabolic process	2.E-04	37	334
GO:0048513	organ development	3.E-04	125	1832
GO:0050794	regulation of cellular process	3.E-04	539	10504
GO:0051641	cellular localization	4.E-04	104	1457
GO:0030029	actin filament-based process	4.E-04	40	384
GO:0046637	regulation of alpha-beta T cell differentiation	6.E-04	8	18
GO:0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	6.E-04	49	527
GO:0006119	oxidative phosphorylation	6.E-04	25	185
GO:0017038	protein import	7.E-04	24	173
GO:0030036	actin cytoskeleton organization	7.E-04	38	363
GO:0006397	mRNA processing	7.E-04	32	279
GO:0010608	posttranscriptional regulation of gene expression	8.E-04	25	187
GO:0006886	intracellular protein transport	8.E-04	58	678
GO:0042127	regulation of cell proliferation & cell proliferation	9.E-04	59	696
GO:0046649	lymphocyte activation	9.E-04	34	310
GO:0022904	respiratory electron transport chain	1.E-03	16	85
GO:0008154	actin polymerization or depolymerization	1.E-03	17	96
GO:0007015	actin filament organization	1.E-03	22	153
GO:0009060	aerobic respiration	1.E-03	13	57
GO:0052548	regulation of endopeptidase activity	1.E-03	16	86
GO:0042775	mitochondrial ATP synthesis coupled electron transport	1.E-03	14	67
GO:0050789	regulation of biological process	2.E-03	547	10828
GO:0065007	biological regulation	2.E-03	573	11416
GO:0008064	regulation of actin polymerization or depolymerization	2.E-03	15	79
GO:0052547	regulation of peptidase activity	2.E-03	16	90
GO:0042773	ATP synthesis coupled electron transport	2.E-03	14	70
GO:0016192	vesicle-mediated transport	3.E-03	62	770
GO:0045321	leukocyte activation	3.E-03	36	355
GO:0042306	regulation of protein import into nucleus	3.E-03	10	36

GO:0030097	hemopoiesis	4.E-03	33	314
GO:0010629	negative regulation of gene expression	4.E-03	45	497
GO:0043281	regulation of caspase activity	4.E-03	15	83
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	4.E-03	11	45
GO:0010558	negative regulation of macromolecule biosynthetic process	4.E-03	48	549
GO:0008632	apoptotic program	5.E-03	18	118
GO:0006417	regulation of translation	5.E-03	19	130
GO:0016481	negative regulation of transcription	6.E-03	43	476
GO:0008064	regulation of actin polymerization or depolymerization & actin polymerization or depolymerization	6.E-03	14	76
GO:0050871	positive regulation of B cell activation	7.E-03	9	31
GO:0046634	regulation of alpha-beta T cell activation	8.E-03	8	24
GO:0051129	negative regulation of cellular component organization	8.E-03	18	122
GO:0034622	cellular macromolecular complex assembly	8.E-03	58	729
GO:0051253	negative regulation of RNA metabolic process	8.E-03	36	372
GO:0022411	cellular component disassembly	8.E-03	17	111
GO:0030832	regulation of actin filament length	9.E-03	14	78
GO:0031327	negative regulation of cellular biosynthetic process	9.E-03	48	564
GO:0046632	alpha-beta T cell differentiation	9.E-03	9	32

3.2 Genes

Ras Super Family

Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA
Rho GDP dissociation inhibitor (GDI)	LOC728908
Rho GDP dissociation inhibitor (GDI) beta	ARHGDIB
Rho guanine nucleotide exchange factor (GEF) 11	ARHGEF11
Rho-related BTB domain containing 3	RHOBTB3
Rho GTPase activating protein 4	ARHGAP4
Rho GTPase activating protein 25	ARHGAP25
Rho GTPase activating protein 26	ARHGAP26
Rho guanine nucleotide exchange factor (GEF) 15	ARHGEF15
Rho GTPase activating protein 8 /// PRR5-ARHGAP8 fusion	ARHGAP8 /// LOC553158
Rho GTPase-activating protein	RICS
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA
Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4
Rho-related BTB domain containing 1	RHOBTB1
Rho-related BTB domain containing 3	RHOBTB3
CDC42 effector protein (Rho GTPase binding) 4	CDC42EP4
Rho GTPase activating protein 15	ARHGAP15
Rho guanine nucleotide exchange factor (GEF) 10-like	ARHGEF10L
Rho GTPase activating protein 8 /// PRR5-ARHGAP8 fusion	ARHGAP8 /// LOC553158

Rho GTPase activating protein 25	ARHGAP25
Ras and Rab interactor 3	RIN3
Ras association (RalGDS/AF-6) domain family 2	RASSF2
Ras association (RalGDS/AF-6) domain family 1	RASSF1
connector enhancer of kinase suppressor of Ras 1	CNKSR1
Ras-related GTP binding D	RRAGD
Ras association (RalGDS/AF-6) domain family 7	RASSF7
RAN, member RAS oncogene family	RAN
RAB13, member RAS oncogene family	RAB13
neuroblastoma RAS viral (v-ras) oncogene homolog	NRAS
Ras association (RalGDS/AF-6) domain family 2	RASSF2
RAB21, member RAS oncogene family	RAB21
RAB30, member RAS oncogene family	RAB30
RAS guanyl releasing protein 2 (calcium and DAG-regulated)	RASGRP2
RAB27A, member RAS oncogene family	RAB27A
RAB14, member RAS oncogene family	RAB14
RAB7A, member RAS oncogene family	RAB7A
RAB, member of RAS oncogene family-like 4	RABL4
RAP2B, member of RAS oncogene family	RAP2B
RAB31, member RAS oncogene family	RAB31
RAB22A, member RAS oncogene family	RAB22A
Ras association (RalGDS/AF-6) domain family 7	RASSF7
RAB26, member RAS oncogene family	RAB26

MAPK

mitogen-activated protein kinase 1	MAPK1
mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2
mitogen-activated protein kinase-activated protein kinase 5	MAPKAPK5
mitogen-activated protein kinase 11	MAPK11
mitogen-activated protein kinase 14	MAPK14

TNF

tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A
tumor necrosis factor receptor superfamily, member 1B	TNFRSF1B
tumor necrosis factor, alpha-induced protein 2	TNFAIP2
tumor necrosis factor, alpha-induced protein 3	TNFAIP3
tumor necrosis factor, alpha-induced protein 8	TNFAIP8
tumor necrosis factor (ligand) superfamily, member 10	TNFSF10
tumor necrosis factor receptor superfamily, member 10c	MGC31957 /// TNFRSF10C
tumor necrosis factor receptor superfamily, member 10d,	TNFRSF10D
tumor necrosis factor receptor superfamily, member 13B	TNFRSF13B
tumor necrosis factor (ligand) superfamily, member 14	TNFSF14

Bcl-2 Family

myeloid cell leukemia sequence 1 (BCL2-related)	MCL1
BCL2-associated transcription factor 1	BCLAF1
BCL2-associated athanogene 5	BAG5
BCL2-antagonist/killer 1	BAK1

BCL2/adenovirus E1B 19kDa interacting protein 1	BNIP1
BCL2/adenovirus E1B 19kDa interacting protein 2	BNIP2
BCL2-associated athanogene 2	BAG2
BCL2-associated transcription factor 1	BCLAF1
BCL2-associated athanogene 3	BAG3
BCL2/adenovirus E1B 19kDa interacting protein 3-like	BNIP3L

Caspases

caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1
caspase 4, apoptosis-related cysteine peptidase	CASP4
caspase 6, apoptosis-related cysteine peptidase	CASP6
caspase 8, apoptosis-related cysteine peptidase	CASP8
caspase 9, apoptosis-related cysteine peptidase	CASP9
caspase 10, apoptosis-related cysteine peptidase	CASP10
apoptosis, caspase activation inhibitor	AVEN

Other apoptosis related genes

SIVA1, apoptosis-inducing factor	SIVA1
NLR family, apoptosis inhibitory protein	LOC728519 /// NAIP
apoptosis inhibitor	FKSG2
nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3
tumor protein p53 binding protein, 2	TP53BP2

Dehydrogenases

malate dehydrogenase 1, NAD (soluble)	MDH1
pyruvate dehydrogenase (lipoamide) alpha 1	PDHA1
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	HADHB
lactate dehydrogenase B	LDHB
hydroxyacyl-Coenzyme A dehydrogenase	HADH
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NDUFB8
NADH dehydrogenase (ubiquinone) Fe-S protein 3, (NADH-coenzyme Q reductase)	NDUFS3
isocitrate dehydrogenase 3 (NAD+) alpha	IDH3A
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	NDUFA1
acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	ACADM
succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	SDHB
NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NDUFV2
NADH dehydrogenase (ubiquinone) Fe-S protein 1, (NADH-coenzyme Q reductase)	NDUFS1
pyruvate dehydrogenase complex, component X	PDHX
UDP-glucose dehydrogenase	UGDH
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	NDUFB3
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	NDUFB5
isovaleryl Coenzyme A dehydrogenase	IVD
dihydropyrimidine dehydrogenase	DPYD
aldehyde dehydrogenase 7 family, member A1	ALDH7A1
malate dehydrogenase 2, NAD (mitochondrial)	MDH2
hydroxysteroid dehydrogenase like 2	HSDL2
isocitrate dehydrogenase 3 (NAD+) beta	IDH3B
pyruvate dehydrogenase (lipoamide) beta	PDHB
hydroxyacyl-Coenzyme A dehydrogenase	HADH
NADH dehydrogenase (ubiquinone) Fe-S protein 7, (NADH-coenzyme Q reductase)	NDUFS7
glycerol-3-phosphate dehydrogenase 1-like	GPD1L
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	DLAT

glyceraldehyde-3-phosphate dehydrogenase	GAPDH
malate dehydrogenase 2, NAD (mitochondrial)	MDH2
glyceraldehyde-3-phosphate dehydrogenase	GAPDH
hydroxysteroid (17-beta) dehydrogenase 8	HSD17B8
lactate dehydrogenase B	LDHB
glyceraldehyde-3-phosphate dehydrogenase	GAPDH
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	NDUFA4
hydroxysteroid (17-beta) dehydrogenase 11	HSD17B11
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	NDUFA8
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	NDUFB11
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	NDUFA13
succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1	SDHALP1
glyceraldehyde-3-phosphate dehydrogenase	GAPDH

Cytochrome c

cytochrome c oxidase subunit Va	COX5A
cytochrome c oxidase subunit Vb	COX5B
cytochrome c oxidase subunit VIc	COX6C
cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	COX7A2
cytochrome c oxidase subunit VIIb	COX7B
cytochrome c oxidase subunit VIIc	COX7C
COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase	COX10
ubiquinol-cytochrome c reductase binding protein	UQCRB
ubiquinol-cytochrome c reductase core protein I	UQCRC1
cytochrome c, somatic	CYCS
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UQCRFS1
ubiquinol-cytochrome c reductase complex (7.2 kD)	UCRC

4. Genes from the biggest cluster of correlation vectors

The total number of Swiss-Prot identifiers corresponding to the gene set and used for computing the p-values is 5198.

Table S4

GO ID	Term	p val	N Set	N Tot
GO:XXXXXXX	unannotated	4.E-83	1795	11418
GO:0032501	multicellular organismal process	7.E-51	839	4721
GO:0007267	cell-cell signaling	1.E-34	208	758
GO:0003008	system process	1.E-24	333	1701
GO:0007275	multicellular organismal development	3.E-24	540	3206
GO:0048856	anatomical structure development	1.E-23	486	2822
GO:0048731	system development	2.E-23	441	2497
GO:0050877	neurological system process	4.E-22	272	1338
GO:0032502	developmental process	7.E-21	679	4393
GO:0019935	cyclic-nucleotide-mediated signaling	8.E-20	56	120
GO:0007187	G-protein signaling, coupled to cyclic nucleotide second messenger	3.E-19	53	111
GO:0007601	visual perception	2.E-17	79	237
GO:0050953	sensory perception of light stimulus	3.E-17	79	238
GO:0019932	second-messenger-mediated signaling	1.E-16	92	309
GO:0048513	organ development	2.E-15	320	1832
GO:0019226	transmission of nerve impulse	1.E-14	111	437
GO:0007268	synaptic transmission	9.E-14	99	379
GO:0007399	nervous system development	2.E-13	207	1079
GO:0048518	positive regulation of biological process	2.E-12	306	1814
GO:0048522	positive regulation of cellular process	3.E-12	281	1636
GO:0007166	cell surface receptor linked signal transduction	8.E-12	423	2731
GO:0009887	organ morphogenesis	4.E-11	143	693
GO:0050890	cognition	7.E-11	181	955
GO:0030154	cell differentiation	4.E-10	288	1753
GO:0009653	anatomical structure morphogenesis	6.E-10	248	1461
GO:0007154	cell communication	1.E-09	833	6205
GO:0006366	transcription from RNA polymerase II promoter	2.E-09	170	912
GO:0008283	cell proliferation	3.E-09	198	1118
GO:0031279	regulation of cyclase activity	8.E-09	36	94
GO:0001501	skeletal system development	8.E-09	84	355
GO:0045761	regulation of adenylate cyclase activity	1.E-08	35	91
GO:0051339	regulation of lyase activity	2.E-08	36	96
GO:0007600	sensory perception	2.E-08	160	865
GO:0048869	cellular developmental process	2.E-08	304	1935
GO:0003002	regionalization	6.E-08	56	203
GO:0019933	cAMP-mediated signaling	1.E-07	32	83

GO:0007188	G-protein signaling, coupled to cAMP nucleotide second messenger	1.E-07	31	79
GO:0007389	pattern specification process	3.E-07	68	280
GO:0007167	enzyme linked receptor protein signaling pathway	3.E-07	95	451
GO:0007165	signal transduction	4.E-07	754	5693
GO:0042127	regulation of cell proliferation & cell proliferation	8.E-07	130	696
GO:0048523	negative regulation of cellular process	8.E-07	262	1675
GO:0042127	regulation of cell proliferation	1.E-06	137	751
GO:0000003	reproduction	2.E-06	139	766
GO:0006357	regulation of transcription from RNA polymerase II promoter	2.E-06	132	719
GO:0048519	negative regulation of biological process	3.E-06	277	1813
GO:0007610	behavior	3.E-06	96	476
GO:0022414	reproductive process	3.E-06	137	761
GO:0009952	anterior/posterior pattern formation	9.E-06	40	138
GO:0045762	positive regulation of adenylate cyclase activity	9.E-06	22	51
GO:0009891	positive regulation of biosynthetic process	1.E-05	118	639
GO:0031281	positive regulation of cyclase activity	1.E-05	22	52
GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.E-05	108	575
GO:0010557	positive regulation of macromolecule biosynthetic process	2.E-05	113	611
GO:0010557	positive regulation of macromolecule biosynthetic process & macromolecule biosynthetic process	2.E-05	113	611
GO:0051239	regulation of multicellular organismal process	2.E-05	130	732
GO:0051239	regulation of multicellular organismal process & multicellular organismal process	2.E-05	130	732
GO:0031328	positive regulation of cellular biosynthetic process	2.E-05	116	633
GO:0051349	positive regulation of lyase activity	3.E-05	22	54
GO:0048598	embryonic morphogenesis	6.E-05	66	303
GO:0048705	skeletal system morphogenesis	7.E-05	29	89
GO:0009790	embryonic development	8.E-05	109	597
GO:0035270	endocrine system development	8.E-05	25	70
GO:0030182	neuron differentiation	1.E-04	88	456
GO:0009893	positive regulation of metabolic process	1.E-04	131	762
GO:0007190	activation of adenylate cyclase activity	1.E-04	13	22
GO:0009628	response to abiotic stimulus	2.E-04	69	334
GO:0051254	positive regulation of RNA metabolic process	3.E-04	88	464
GO:0010604	positive regulation of macromolecule metabolic process	3.E-04	124	722
GO:0010604	positive regulation of macromolecule metabolic process & macromolecule metabolic process	3.E-04	124	722
GO:0031325	positive regulation of cellular metabolic process	4.E-04	126	738
GO:0050906	detection of stimulus involved in sensory	4.E-04	23	65

	perception			
GO:0007215	glutamate signaling pathway	4.E-04	14	27
GO:0045893	positive regulation of transcription, DNA-dependent	4.E-04	87	461
GO:0009605	response to external stimulus	5.E-04	151	929
GO:0010628	positive regulation of gene expression	5.E-04	99	548
GO:0010628	positive regulation of gene expression & gene expression	5.E-04	99	548
GO:0048732	gland development	8.E-04	33	120
GO:0045941	positive regulation of transcription	9.E-04	97	539
GO:0010646	regulation of cell communication	1.E-03	130	784
GO:0010646	regulation of cell communication & cell communication	1.E-03	130	784
GO:0051094	positive regulation of developmental process	1.E-03	102	579
GO:0009888	tissue development	1.E-03	79	417
GO:0048699	generation of neurons	1.E-03	93	516
GO:0048468	cell development	2.E-03	137	842
GO:0065008	regulation of biological quality	2.E-03	249	1720
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	2.E-03	18	47
GO:0009416	response to light stimulus	2.E-03	37	148
GO:0003013	circulatory system process	2.E-03	53	248
GO:0008015	blood circulation	2.E-03	53	248
GO:0007186	G-protein coupled receptor protein signaling pathway	3.E-03	250	1734
GO:0045165	cell fate commitment	3.E-03	38	155
GO:0007631	feeding behavior	3.E-03	20	57
GO:0022008	neurogenesis	3.E-03	97	553
GO:0008285	negative regulation of cell proliferation	4.E-03	68	351
GO:0007586	digestion	5.E-03	28	101
GO:0031324	negative regulation of cellular metabolic process	7.E-03	115	698