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Genetic analysis of ocular tumour-associated genes using large genomic datasets: insights into selection constraints and variant representation in the population

Alexander Tanner [1,2] Mandeep S Sagoo [1,3,4] Omar A Mahroo [1,2] Jose S Pulido[1,2,5]

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[1]Institute of Ophthalmology, University College London, London, UK
[2]Retinal Genetics Service, Moorfields Eye Hospital NHS Foundation Trust, London, UK
[3]Retinoblastoma Service, The Royal London Hospital, London, UK
[4]Oncology Service, Moorfields Eye Hospital NHS Foundation Trust, London, UK
[5]Wills Eye Hospital, Philadelphia, Pennsylvania, USA

Correspondence to
Dr Jose S Pulido; jpulido@willseye.org

ABSTRACT

Background Large genomic databases enable genetic evaluation in terms of haploinsufficiency and prevalence of missense and synonymous variants. We explored these parameters in ocular tumour-associated genes.

Methods A curated list of ocular tumour-associated genes was assessed using the genomic databases Genome Aggregation Database (gnomAD) and DatabasE of genomiC varIation and Phenotype in Humans using Ensembl Resources (DECIPHER) and compared with breast and lung cancer-associated gene lists. Haploinsufficiency was determined based on specific criteria: probability of loss of function index ≥0.9 in gnomAD, upper CI O/E limit <0.35 for loss of function variants in gnomAD and/or a DECIPHER pHaplo ≥0.86. UniProt was used for further gene characterisation, and gene ontology Protein Analysis THrough Evolutionary Relationships was explored for common biological pathways. In addition, we identified genes with under-representation/over-representation of missense/synonymous variants.

Results Fifty-seven genes were identified in association with ocular and extraocular tumours.
Regarding haploinsufficiency, 41% of genes met the criteria for negative selection, with 57% categorised as tumour-suppressing and 39% as oncogenic. Most genes were involved in regulatory processes. Regarding triplosensitivity, 33% of genes reached significance and 83% of these were haploinsufficient. Analysis of variants revealed under-representation of missense variants in 23% of genes and over-representation of synonymous variants in 5% of genes. Ocular tumour-associated genes exhibited higher scores for haploinsufficiency and triplosensitivity compared with breast and lung cancer-associated genes. Pathway analysis revealed significant enrichment in cellular proliferation, differentiation and division. Encoded proteins of ocular tumour-associated genes were generally longer than the median of the UniProt database.

Conclusion Our findings highlight the importance of negative selection in ocular tumour genes, supporting cranial gene conservation. This study provides insights into ocular tumourigenesis and future research avenues.

WHAT IS ALREADY KNOWN ON THIS TOPIC

⇒ Large genomic databases enable the evaluation of genes based on parameters such as haploinsufficiency, triplosensitivity and the prevalence of missense or synonymous variants.

WHAT THIS STUDY ADDS

⇒ Using the above parameters for ocular tumour-associated genes: 23 genes were identified as haploinsufficient, 18 were triplosensitive, 13 showed under-representation of missense variants and 3 showed over-representation of synonymous variants.

HOW THIS STUDY MIGHT AFFECT RESEARCH, PRACTICE OR POLICY

⇒ These findings highlight the importance of negative selection in ocular tumourigenesis and can be used for comparison with future genetic studies.

BACKGROUND

Ocular tumours can manifest either as local, somatic mutations or as germline mutations in individuals with hereditary tumour predisposition syndromes.[1] Among these tumours are retinoblastoma and uveal melanoma, both of which are rare but can have devastating consequences. Retinoblastoma, a paediatric neoplasm, is the most prevalent primary intraocular tumour worldwide, with an estimated incidence of 7202–8102 children each year.[2] It arises from cells that harbour cancer-associated variants in both copies of their *RB1* genes. This can be inherited in an autosomal dominant pattern or can occur spontaneously. Despite advancements in diagnosis and treatment, the mortality rate for retinoblastoma remains high at 70% in low-income and middle-income countries.[3] In adults, uveal melanoma is the leading primary malignancy affecting the eye, impacting an estimated 7000 individuals worldwide each year.[4] *GNAQ* and *GNA11* are the most frequently mutated genes in uveal melanoma, with mutations occurring in 71%–93% of associated tumours.[5] Notably, the risk of treatment-resistant metastatic disease contributes to persistently high mortality rates, with some studies reporting long-term mortality rates exceeding 50% for this condition.[6]

Genetic studies enhance our understanding of the disease pathways underpinning ocular tumours. Moreover, the emergence of large genomic databases has facilitated the evaluation of genes based on parameters such as intolerance to loss of function ('haploinsufficiency') and the prevalence of missense or synonymous variants. Haploinsufficiency refers to a genetic condition wherein the presence of only one functional copy of a specific gene in a diploid organism is insufficient to maintain normal cellular function. In this context, the remaining single functional copy of the gene is incapable of producing the level of gene product required for proper biological functioning. This may lead to various developmental abnormalities, increased susceptibility to diseases or other medical conditions, depending on the specific gene and its role in cellular processes.

We used two databases, namely 'The Genome Aggregation Database' (gnomAD)[7] and 'DatabasE of genomiC varIation and Phenotype in Humans using Ensembl Resources' (DECIPHER),[8] to investigate these parameters in genes associated with ocular tumours. gnomAD incorporates data from over 141 456 individuals sequenced with 125 748 exomes and 15 708 genomes, aligned against the Genome Reference Consortium Human genome build 37.[7] DECIPHER, another extensive database, contains genomic data from 33 000 children with rare diseases from 250 centres.[8] By analysing these databases, we aimed to determine if the genes implicated in ocular tumours exhibit selection constraints and whether their variants are over-represented or underrepresented in the population.

METHODS

Overview

We used a similar, but updated methodology to our previously published investigation of inherited retinal disease (IRD)-associated genes.[9]

A list of intraocular and extraocular tumours, and their related genes, was generated using MalaCards: The human disease database (https://www.malacards.org/).[10] This was supplemented by two ocular oncologists querying the Online Mendelian Inheritance in Man (OMIM) genetic database (https://omim.org/about)[11] and by performing a systematic search for articles that listed pseudomelanomas, pseudogliomas and orbital tumours in PubMed.[12 13] This curation of tumours and related genes was performed in January 2021 and was updated in June 2023.

Evaluation of these genes for haploinsufficiency, triplosensitivity and the degree of missense and synonymous variation was conducted using the online databases (gnomAD and DECIPHER). This analysis was originally performed in January 2021 and was updated in June 2023.

Genome Aggregation Database

The constraint variables in gnomAD (https://gnomad.broadinstitute.org/) include pLI (probability of loss of function intolerance), O (observed, which is the frequency of the particular variant in the database), E (expected which is the expected frequency in the database assuming that the variant develops randomly), O/E (observed divided by expected, which is the ratio of observed variants to expected) and CI (the CI for the O/E). The pLI ranges from 0 to 1, and a pLI of 0.9 or greater is a strong indicator that loss of function variants in the gene are selected against. This is confirmed when the upper CI for loss of function is 0.35 or less.[7] The O/E for missense and synonymous variants can also be explored: for this study Z scores of 2.99 or greater, or −2.99 or less, were taken to indicate a significant over-representation or under-representation of missense and synonymous variants (a Z value of −2.99 means that the chance of variants occurring randomly with such low frequency in the population is only 0.14% (0.0014)).

DatabasE of genomiC varIation and Phenotype in Humans using Ensembl Resources

DECIPHER (https://decipher.sanger.ac.uk) comprises genomic data from 36 000 children with rare diseases from over 270 specialist centres.[8] Previously, a haploinsufficiency score was provided, where an index of less than 10% was taken to indicate that loss of function is significantly selected against.[14] This has now been replaced by the updated 'pHaplo' and 'pTriplo' scores which enable the evaluation of haploinsufficiency and triplosensitivity, respectively.[8] To ensure greater accuracy, a pHaplo of ≥0.86 and a pTriplo of ≥0.94 were adopted as per Collins *et al*.[15]

Combined selection criteria

Those ocular cancer genes that met the following criteria for haploinsufficiency: (1) a pLI in gnomAD of ≥0.9 and (2) an upper CI O/E limit for loss of function variants in gnomAD of <0.35 and/or a DECIPHER pHaplo of ≥0.86 were then further characterised, using UniProt and evaluated for the presence of common biological pathways using the online gene ontology resource gene ontology Protein Analysis THrough Evolutionary Relationships (GO PANTHER).[16]

Protein Analysis THrough Evolutionary Relationships

Identification of common biological pathways was achieved by inputting our list of haploinsufficient genes through the gene ontology PANTHER (http://pantherdb.org/) resource.[16]

UniProt

Amino acid lengths of the encoded proteins of all identified genes were obtained from the UniProt Database (

www.uniprot.org), a comprehensive resource that details protein sequence and functional information.[17]

Comparisons

This list of ocular tumour genes was then compared with two lists of genes generated by MalaCards and supplemented by a comprehensive search of OMIM and PubMed articles, one associated with breast cancer and the other with lung cancer.[10 11 18] The analysis was performed using gnomAD, DECIPHER, PANTHER and UniProt.[8 11 16 17]

RESULTS

Ocular tumour-associated genes

There were 57 genes identified in association with ocular and extraocular tumours (online supplemental table 1). For 56 of the ocular tumour-associated genes, excluding *DUX4* due to insufficient data, the median of the haploinsufficiency variables was as follows: pLI of 0.72, O/E of 0.19 and pHaplo 0.89. Of these 56 genes, 23/56 (41%) met our combined criteria for negative selection when haploinsufficient (table 1): (1) A pLI in gnomAD of ≥0.9 and (2) an upper CI O/E limit for loss of function variants in gnomAD of <0.35 and/or a DECIPHER pHaplo of ≥0.86.

Among these 23 haploinsufficient genes, 57% (13/23) were identified as tumour-suppressing, while 39% (9/23) exhibited oncogenic properties. Furthermore, most of these genes, 87% (20/23), were found to be involved in regulatory processes. A smaller subset, 9% (2/23), was associated with DNA repair, and 4% (1/23) were identified as mechanochemical.

Regarding triplosensitivity, the median score for these genes was 0.71 (pTriplo). Out of the 54 genes analysed, 33% (18/54) reached significance (pTriplo≥0.94), with exclusion of *EIF1AX* and *NDP* in addition to *DUX4,* due to insufficient data. 83% (15/18) of the triplosensitive genes also met our criteria for haploinsufficiency.

Thirteen of the 56 genes (23%) demonstrated under-representation of missense variants (Z score ≥2.99), of which 10/13 (77%) also met our criteria for haploinsufficiency. The median missense score of the 56 genes was 1.48 (Z score). No ocular tumour-associated genes demonstrated over-representation of missense variants. Three out of 56 genes (5%) demonstrated over-representation of synonymous variants: *MC1R*, *PTCH1* and *TSC2*. Incidentally, *PTCH1* and *TSC2* were also found to meet our criteria for haploinsufficiency. No ocular tumour-associated genes demonstrated under-representation of synonymous variants. The median synonymous score of the 56 genes was −0.08 (Z score).

Breast cancer-associated genes

A total of 29 breast cancer-associated genes were identified. Among these genes, 6 out of 29 (21%) met the study's criteria for haploinsufficiency (table 1). For these 29 breast cancer genes, the median of the haploinsufficiency variables was pLI 0, O/E 0.60 and pHaplo 0.68.

Table 1 Table depicting the haploinsufficient genes identified in ocular tumour-associated disease, breast cancer and lung cancer

Ocular tumour-associated genes	Breast cancer-associated genes	Lung cancer-associated genes
APC	AKT1	ABL1
BAP1	ESR1	AKT1
BRAF	MSH2	ARID1A
CDK6	PIK3CA	ARID2
CTNNB1	RET	BRAF
DICER1	STK11	CTNNB1
GNAQ		CTNND2
KIF11		FBXW7
MDM2		FGF10
MITF		GNAQ
MYC		IRF1
MSH2		KMT2C
NF1		KMT2D
NF2		MAP2K1
PLAG1		MAPK1
PTCH1		MET
RB1		PIK3CA
SF3B1		PPP2R1A
SUFU		RB1
TERT		RELN
TSC1		REV3L
TSC2		
U2AF1		
		SLC25A5
		SMARCA4
		STK11
		TERT
		ZEB2
		ZFHX3
		ZNF521

Regarding the haploinsufficient breast cancer-associated genes, 50% of the genes were identified as tumour suppressing, while the remaining 50% were classified as oncogenic. Additionally, 83% (5/6) of the genes were found to be involved in regulatory processes and 17% (1/6) were associated with DNA repair.

Out of the 29 genes analysed, 5 (17%) met the criteria for triplosensitivity, and the median triplosensitivity score for the breast cancer-associated genes was 0.43 (pTriplo). Out of the five triplosensitive genes identified, *AKT1* and *PIK3CA* (40%) also met our criteria for haploinsufficiency.

Regarding missense variants, 3/29 (10%) of the genes (*AKT1, PIK3CA* and *PTEN*) exhibited significantly fewer variants than would be expected. The median missense score of the 29 genes was 0.58 (Z score). No breast cancer genes demonstrated over-representation of missense variants. However, one genes, *MSH6*, demonstrated over-representation of synonymous variants. None of the breast cancer-associated genes showed under-representation of synonymous variants. The median synonymous score for the 29 genes was −0.13 (Z score).

Lung cancer-associated genes

Seventy-five lung cancer-associated genes were identified. Among these, 28/75 (37%) were observed to be negatively selected for when haploinsufficient (table 1). The median values of the haploinsufficiency variables for lung cancer were as follows: pLI 0.26, O/E 0.24 and pHaplo 0.78. Out of those haploinsufficient lung cancer-associated genes, 43% (12/28) were identified as oncogenic, while 46% (13/28) were categorised as tumour suppressing. 79% (22/28) of the genes were found to be involved in regulatory processes, 4% (1/28) in DNA repair and 11% (3/28) mechanochemical.

Twenty-five out of the 75 lung cancer-associated genes (33%) were found to meet our criteria for triplosensitivity and the median triplosensitivity score was 0.75 (pTriplo). 72% (18/25) of the triplosensitive genes also met our criteria for haploinsufficiency.

Sixteen of the 75 lung cancer-associated genes (21%) exhibited under-representation of missense variants. Additionally, two genes (MUC4 and MUC16) demonstrated over-representation of missense variants. Six out of the 75 lung cancer-associated genes were found to demonstrate under-representation of synonymous variants (8%). No genes showed over-representation of synonymous variants. The median synonymous score for the 75 genes was −0.52 (Z score).

Protein Analysis THrough Evolutionary Relationships

When performing PANTHER analysis on the 23/56, ocular tumour-associated, haploinsufficient genes >100 fold enrichment in 14 biological pathways were observed including, cellular proliferation, differentiation and division (online supplemental table 2).

PANTHER analysis of the 6/29 haploinsufficient breast cancer-associated genes and 28/75 lung cancer-associated genes demonstrated >100 fold enrichment in 33 (online supplemental table 3) and 15 (online supplemental table 4) biological pathways, respectively.

UniProt

Most encoded proteins were longer than the median length in the UniProt database.[19] The median amino acid length of the ocular tumour-associated genes was 605 (781 for the haploinsufficient group), 754 for breast cancer genes (764.5 for the haploinsufficient group) and 781 for lung cancer genes (1099 for the haploinsufficient group). While the median amino acid lengths for triplosensitive ocular tumour-associated genes, breast cancer-associated genes and lung cancer-associated genes were 667, 480 and 824, respectively.

DISCUSSION

Many ocular tumour-associated-genes, when haploinsufficient, are strongly associated with negative selection. In contrast, we have previously shown that for IRDs, relatively few genes were associated with negative selection for loss of function variants.[9] It should be noted that many of these ocular tumour-associated-genes develop their mutations as somatic mutations. This is consistent with the fact that genetic mutations are negatively selected for since they are involved in important cellular pathways that would affect the development of many organs in the body. Recently, it has been shown that in certain cells there is a temporal spectrum for mutations to occur, from early in the germline until late into adulthood.[20]

Compared with breast and lung cancer-associated genes, the ocular tumour-associated genes identified in our study exhibited higher scores for haploinsufficiency. Moreover, there was an equal proportion (compared with lung cancer) and greater proportion (compared with breast cancer) of negatively selected haploinsufficient ocular tumour-associated genes. This finding highlights the inherent importance of many cranial-associated genes and supports the notion that these tissues are evolutionarily conserved compared with other somatic tissues.[21 22]

In an attempt to characterise these haploinsufficient genes, we have found that most of them encode proteins involved in regulatory processes. This was the same for ocular tumour-associated, breast cancer-associated and lung cancer-associated genes. This supports the notion that these encoded proteins are likely to be 'structural', 'regulatory 'and/or 'mechanochemical'.[23] Moreover, our data present a similar finding to Niemitz, with a large proportion of haploinsufficient genes acting as tumour suppressors and a large proportion of triplosensitive genes acting as oncogenes.[24]

Collins *et al* demonstrated some interesting findings in relation to haploinsufficient genes.[15] These genes tended to be larger in size, located farther away from other genes and possessed a greater number of conserved enhancers in cis. These characteristics are considered classic indicators of precisely regulated, developmentally critical genes. On the other hand, triplosensitive genes were generally shorter, rich in G/C content and located in gene-dense, highly active regions, which were not particularly enriched for conserved enhancers.[15] Our data also show that the median size of the haploinsufficient genes is larger than the median of all the identified genes, per category. Additionally, the median size of the triplosensitive genes is smaller than that of the haploinsufficient genes, per category, but larger than the median size of all the identified genes, except for breast cancer-associated genes. It should be noted that pLI scores, for a given combination of selection parameters, can vary greatly with gene length.[25]

There are several limitations to this study that require mentioning. It is likely that there are other genes involved in the development of breast cancer, lung cancer and ocular tumours that this study has missed or that have not yet been discovered. Moreover, the gene lists include tumour suppressor genes, regulatory genes and oncogenes responsible for somatic tumours, as well as rare severe Mendelian disorders, some of which are lethal in the homozygous state. It should also be mentioned that the determinant of ‘haploinsufficiency’ that we use relies on scores derived from population genetics, such as ‘pLI’. These scores in fact reflect the strength of selection on heterozygotes and are not direct indicators of haploinsufficiency relative to phenotype,[25] making it challenging to draw firm conclusions from the data. The observed difference between our results in this paper and that of our previous paper on IRDs may reflect the variance in disease types and, consequently, differing selection pressures. It is also important to highlight that the interpretation of our findings may have been influenced by the cross-over of certain genes across the analysed categories: ocular tumour-associated, breast cancer-associated and lung cancer-associated genes. Nonetheless, this study lays a foundation for evaluating genes by a novel and potentially useful means. Additionally, a very stringent level of a Z value of ≤−2.99 or ≥2.99 was used that may have resulted in some genes being omitted from the study that would otherwise have been included, should the Z value have been less stringent. Finally, we included genes that are associated with intraocular, orbital and pseudogliomas in this study.

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Contributors All authors contributed to data collection, analysis and interpretation. AT, OAM and JSP contributed to the drafting of the manuscript. All authors contributed to the revision of manuscript and approval of the final version. JSP and OAM contributed to supervision. Guarantor: JSP.

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ORCID iDs

Alexander Tanner http://orcid.org/0000-0002-7194-0978
Mandeep S Sagoo http://orcid.org/0000-0003-1530-3824
Omar A Mahroo http://orcid.org/0000-0003-1254-0832

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Supplementary Table 1: Table depicting the ocular tumour-associated genes, their location, function, and associated diseases.

Gene:	**Location:**	**Function:**	**Disease:**
ABCG2	4q22.1	ATP Binding Cassette Subfamily G Member 2	Retinoblastoma
APC	5q22.2	Tumour suppressor gene. Regulator of Wnt Signalling Pathway.	Congenital hypertrophy of retinal pigment epithelium, Gardner syndrome, ocular surface squamous cell neoplasia.
BAP1	3p21.1	Tumour suppressor gene. A deubiquitylase, thought to be a key regulator of cell cycle, growth, response to DNA damage and chromatin dynamics.	Uveal melanoma, conjunctival melanoma
BRAF	7q34	Proto-oncogene. Raf family of serine/threonine kinases. Key regulator MAP kinase/ ERK signalling pathway, affecting cell division, differentiation, and secretion.	Conjunctival melanoma, cutaneous melanoma, uveal melanoma
BRCA2	13q13.1	Tumour suppressor gene. DNA Repair Associated.	Uveal melanoma
CCND1	11q13.3	Proto-oncogene. Regulatory protein in G1/S transition of cell cycle.	Von Hippel-Lindau Syndrome, Uveal melanoma
CDK4	12q14.1	Proto-oncogene. Serine/threonine kinase involved in cell cycle regulation and repair of damage caused by UV radiation.	Uveal melanoma, conjunctival melanoma
CDK6	7q21.2	Proto-oncogene. Serine/threonine kinase involved in cell cycle and differentiation; promotes G1/S transition.	Uveal melanoma, conjunctival melanoma

CDKN2A	9p21.3	Tumour suppressor gene. Capable of inducing cell cycle arrest in G1 and G2 phases.	Uveal melanoma, neurofibromatosis
CTC1	17p13.1	Putative tumour suppressor gene. Component *CST* complex believed to play a role in promoting DNA replication.	Cerebroretinal microangiopathy with calcifications and cysts
CTNNB1	3p22.1	Proto-oncogene. Key downstream component of canonical Wnt signalling pathway.	Teratocarcinosarcoma of the eye
CYSLTR2	13q14.2	Proto-oncogene. Involved in the production and activity of inflammatory mediators.	Uveal melanoma
DICER1	14q32.13	Haploinsufficient tumour suppressor gene with loss of one allele leading to tumour progression but loss of both alleles having an inhibitory effect on tumour development. Endoribonuclease involved in post-transcriptional gene silencing.	Ciliary body medulloepithelioma, rhabdomyosarcoma
DMPK	19q13.32	Mediator of tumour suppressor genes. Various functions including maintenance of skeletal/ cardiac muscle structure and function, synaptic plasticity and regulation of chloride currents.	Uveal melanoma
DUX4	4q35.2	Tumour suppressor/ proto-oncogene. Transcription factor involved in embryogenesis, physiology & disease.	Coats-like syndrome, exudative retinopathy
EIF1AX	Xp22.12	Proto-oncogene. Encodes an essential eukaryotic	Uveal melanoma

		translation initiation factor. Required for binding of *43S* complex to the 5' end of capped RNA.	
ERCC2	19q13.32	DNA repair gene involved in separating the double helix via the 5'-3' helicase activity.	Xeroderma pigmentosum, ocular squamous cell carcinoma
FHIT	3p14.2	Tumour suppressor gene. Important in regulation of apoptosis. Involved in purine metabolism.	Uveal melanoma
FLCN	17p11.2	Tumour suppressor gene. Multi-functional protein, involved in both the cellular response to amino acid availability and in the regulation of glycolysis.	Birt-Hogg-Dubé syndrome, choroidal melanoma, uveal melanoma, lid folliculoma
GNA11	19p13.3	Proto-oncogene. G Protein Subunit Alpha 11	Uveal melanoma, choroidal
GNAQ	9q21.2	Proto-oncogene. G Protein Subunit Alpha Q	Sturge weber syndrome, uveal melanoma, nevus of ota
KDM4C	9p24.1	Regulator of oncogenes and tumour suppressor genes. Nuclear protein involved in histone modification and a regulator of several transcription factors.	Uveal melanoma
KIF11	10q23.33	Proto-oncogene. Protein involved in spindle dynamics during mitosis. Also involved in retinal vascular development.	Familial exudative vitreoretinopathy
LRP5	11q13.2	This gene encodes a transmembrane low-density lipoprotein receptor that binds and internalises ligands in the process of receptor-mediated endocytosis	Osteoporosis-pseudoglioma syndrome

MAPKAPK5	12q24.12-q24.13	Tumour suppressor gene. Serine/threonine kinase involved in cellular stress and inflammatory response.	Uveal melanoma
MC1R	16q24.3	Tumour suppressor gene. Encodes melanocortin one receptor.	Uveal melanoma
MDM2	12q15	Important negative regulator of *p53* tumour suppressor.	Uveal melanoma, retinoblastoma
MITF	3p13	Tumour suppressor gene. Regulates differentiation and development of melanocytes and retinal pigment epithelium.	Uveal melanoma
MLANA	9p24.1	Protein antigen found on the surface of melanocytes.	Uveal melanoma, conjunctival melanoma, malignant spindle cell melanoma
MLH1	3p22.2	Tumour suppressor gene. Involved in post-replicative DNA mismatch repair.	Keratocanthoma, Muir-Torre syndrome, sebaceous adenoma, cutaneous melanoma
MYC	8p24.21	Proto-oncogene. Multifunctional, nuclear phosphoprotein involved in cell cycle, cell growth, apoptosis, metabolism, biosynthesis, adhesion, and mitochondrial biogenesis.	Uveal melanoma
MSH2	2p21-p16	Tumour suppressor gene. Protein involved in post-replicative DNA mismatch repair system.	Sebaceous adenoma, cutaneous melanoma, uveal melanoma
MYD88	3p22.2	Proto-oncogene. Adapter protein involved in *Toll-like* receptor and *IL-1* receptor signalling pathway in innate immune response.	Vitreoretinal lymphoma

NDP	Xp11.3	Activates the canonical Wnt signalling pathway through *FZD4* and *LRP5* coreceptor. Involved in retinal vascularisation.	Coats, familial exudative vitreoretinopathy, persistent foetal vasculature, Norrie disease
NF1	17q11.2	Tumour suppressor gene. Appears to be a negative regulator of the ras signal transduction pathway.	Multiple including, Lisch nodules, optic gliomas, capillary haemangiomas
NF2	22q12.2	Tumour suppressor gene. Involved in regulation of contact-dependent inhibition of cell proliferation and functions in cell-cell adhesion and transmembrane signalling.	Hamartomas
NRAS	1p13.2	Proto-oncogene. Regulatory protein in cell division.	Conjunctival melanoma, uveal melanoma, cutaneous melanoma
PDCD1	2q37.3	Tumour suppressor gene. Immune-inhibitory receptor expressed in activated T cells; involved in regulation T cell function.	Conjunctival squamous cell carcinoma, uveal melanoma
PLAG1	8q12.1	Proto-oncogene. Involved in cell proliferation by regulating a wide array of target genes.	Pleomorphic adenoma lacrimal gland
PLCB4	20p12.3-p12.2	Proto-oncogene. Encoding form of *phospholipase C* involved in *phosphoinositide cycle*.	Uveal melanoma
POT1	7q31.33	Encodes a protein involved in telomere maintenance.	Uveal melanoma
PRDX3	10q26.11	Mitochondrial protein with antioxidant function.	Uveal melanoma
PTCH1	9q22.32	Tumour suppressor gene. Acts as a receptor for Sonic Hedgehog (*SHH*).	Ocular surface squamous cell neoplasia, retinoblastoma, basal cell

			carcinoma, Gorlin-Goltz syndrome, orbital teratoma
PTCH2	1q34.1	Tumour suppressor gene. Role in control of cellular growth may be a receptor for *SHH*.	Gorlin-Goltz syndrome,
PTEN	10q23.31	Tumour suppressor gene. Acts as a dual-specificity protein phosphatase, dephosphorylating tyrosine-, serine- and threonine-phosphorylated proteins.	Cowden syndrome, retinoblastoma, conjunctival melanoma, uveal melanoma, PTEN hamartoma tumour syndrome, choroidal schwannoma
RB1	13q14.2	Tumour suppressor gene. Key regulator of G1/S transition of cell cycle.	Retinoblastoma, ocular sebaceous carcinoma
RBL1	20q11.23	Likely to be a tumour suppressor gene. Key regulator of entry into cell division.	Retinoblastoma
SF3B1	2q33.1	Proto-oncogene. Involved in pre-mRNA splicing as a component of the splicing factor *SF3B* complex.	Uveal melanoma, conjunctival melanoma
SRSF2	17q25.1	Proto-oncogene. Necessary for the regulation of gene transcription, pre-mRNA splicing, mRNA transport and stability.	Uveal melanoma, iris and ciliary melanocytoma
SUFU	10q24.32	Tumour suppressor gene. Negative regulator in the hedgehog/smoothened signalling pathway.	Retinoblastoma, conjunctival melanoma
TERT	5p15.33	Tumour suppressor gene. Encodes telomerase a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes.	Uveal melanoma, conjunctival melanoma

TP53	17p13.1	Tumour suppressor gene implicated in many tumour types; induces growth arrest or apoptosis depending on physiological circumstances and cell type.	Ocular surface squamous cell neoplasia, Li-Fraumeni syndrome, orbital rhabdomyosarcoma, uveal melanoma
TSC1	9q34.13	Tumour suppressor gene. Encodes growth inhibitory protein hamartin.	Tuberous sclerosis
TSC2	16p13.3	Tumour suppressor gene. Encodes growth inhibitory protein tuberin.	Tuberous sclerosis
U2AF1	21q22.3	Encodes an RNA-binding protein involved in the recognition of the 3’ splice site required for recruitment of U2 snRNP during pre-mRNA splicing.	Uveal melanoma
VHL	3p25.3	Tumour suppressor gene. Involved in ubiquitination and subsequent proteasomal degradation via von Hippel-Lindau ubiquitination complex.	Von Hippel-Lindau, Hemangioblastoma
XPA	9q22.33	Involved in DNA excision repair.	Ocular squamous cell carcinoma, pterygium, pinguecula, conjunctival melanoma

Supplementary Table 2: PANTHER Overrepresentation Test (Haploinsufficient Ocular Tumour-Associated Genes)

Analysis Type:				PANTHER Overrepresentation Test (Released 20221013)			
Annotation Version and Release Date:				GO Ontology database DOI: 10.5281/zenodo.7942786 Released 2023-05-10			
Analyzed List:				Client Text Box Input (Homo sapiens)			
Reference List:				Homo sapiens (all genes in database)			
Test Type:				FISHER			
Correction:				FDR			
GO biological process complete	Homo sapiens - REFLIST (20589)	Client Text Box Input (23)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
Schwann cell proliferation (GO:0014010)	3	2	.00	+	> 100	1.19E-05	1.14E-03
negative regulation of Schwann cell proliferation (GO:0010626)	8	3	.01	+	> 100	1.99E-07	5.24E-05
regulation of Schwann cell proliferation (GO:0010624)	9	3	.01	+	> 100	2.65E-07	6.34E-05
negative regulation of monocyte differentiation (GO:0045656)	7	2	.01	+	> 100	4.27E-05	3.08E-03
negative regulation of glial cell proliferation (GO:0060253)	16	4	.02	+	> 100	5.64E-09	2.92E-06
siRNA processing (GO:0030422)	8	2	.01	+	> 100	5.33E-05	3.70E-03
neural plate development (GO:0001840)	10	2	.01	+	> 100	7.81E-05	4.99E-03
negative regulation of oligodendrocyte differentiation (GO:0048715)	14	2	.02	+	> 100	1.42E-04	8.14E-03

regulation of glial cell proliferation (GO:0060251)	35	5	.04	+	> 100	6.97E-10	7.73E-07
negative regulation of protein import into nucleus (GO:0042308)	15	2	.02	+	> 100	1.60E-04	8.80E-03
negative regulation of cell division (GO:0051782)	16	2	.02	+	> 100	1.80E-04	9.72E-03
myeloid cell apoptotic process (GO:0033028)	16	2	.02	+	> 100	1.80E-04	9.69E-03
negative regulation of gliogenesis (GO:0014014)	42	5	.05	+	> 100	1.62E-09	1.39E-06
dorsal/ventral neural tube patterning (GO:0021904)	17	2	.02	+	> 100	2.01E-04	1.07E-02
regulation of monocyte differentiation (GO:0045655)	19	2	.02	+	94.23	2.47E-04	1.26E-02
ectoderm development (GO:0007398)	19	2	.02	+	94.23	2.47E-04	1.26E-02
glial cell proliferation (GO:0014009)	30	3	.03	+	89.52	6.48E-06	6.89E-04
negative regulation of stem cell proliferation (GO:2000647)	22	2	.02	+	81.38	3.24E-04	1.59E-02
sympathetic nervous system development (GO:0048485)	22	2	.02	+	81.38	3.24E-04	1.59E-02
negative regulation of cellular senescence (GO:2000773)	23	2	.03	+	77.84	3.52E-04	1.70E-02
smooth muscle tissue development (GO:0048745)	23	2	.03	+	77.84	3.52E-04	1.69E-02

negative regulation of nucleocytoplasmic transport (GO:0046823)	24	2	.03	+	74.60	3.81E-04	1.80E-02
negative regulation of smoothened signaling pathway (GO:0045879)	36	3	.04	+	74.60	1.08E-05	1.05E-03
positive regulation of mesenchymal cell proliferation (GO:0002053)	25	2	.03	+	71.61	4.11E-04	1.92E-02
regulation of vascular associated smooth muscle cell migration (GO:1904752)	25	2	.03	+	71.61	4.11E-04	1.91E-02
negative regulation of glial cell differentiation (GO:0045686)	26	2	.03	+	68.86	4.42E-04	2.03E-02
positive regulation of transcription regulatory region DNA binding (GO:2000679)	26	2	.03	+	68.86	4.42E-04	2.03E-02
negative regulation of myeloid leukocyte differentiation (GO:0002762)	53	4	.06	+	67.56	4.47E-07	8.58E-05
myelination in peripheral nervous system (GO:0022011)	29	2	.03	+	61.74	5.43E-04	2.40E-02
peripheral nervous system axon ensheathment (GO:0032292)	29	2	.03	+	61.74	5.43E-04	2.40E-02
spinal cord motor neuron differentiation (GO:0021522)	30	2	.03	+	59.68	5.79E-04	2.53E-02
negative regulation of endothelial cell	30	2	.03	+	59.68	5.79E-04	2.52E-02

apoptotic process (GO:2000352)							
branching involved in ureteric bud morphogenesis (GO:0001658)	46	3	.05	+	58.38	2.16E-05	1.82E-03
prostate gland development (GO:0030850)	46	3	.05	+	58.38	2.16E-05	1.81E-03
negative regulation of osteoblast differentiation (GO:0045668)	48	3	.05	+	55.95	2.44E-05	1.94E-03
regulation of stem cell proliferation (GO:0072091)	80	5	.09	+	55.95	3.36E-08	1.27E-05
Schwann cell development (GO:0014044)	32	2	.04	+	55.95	6.54E-04	2.83E-02
negative regulation of macroautophagy (GO:0016242)	32	2	.04	+	55.95	6.54E-04	2.82E-02
regulation of mesenchymal cell proliferation (GO:0010464)	32	2	.04	+	55.95	6.54E-04	2.81E-02
negative regulation of osteoclast differentiation (GO:0045671)	33	2	.04	+	54.25	6.93E-04	2.97E-02
neural tube patterning (GO:0021532)	33	2	.04	+	54.25	6.93E-04	2.96E-02
positive regulation of telomerase activity (GO:0051973)	34	2	.04	+	52.66	7.33E-04	3.11E-02
regulation of intrinsic apoptotic signaling pathway by p53 class mediator (GO:1902253)	34	2	.04	+	52.66	7.33E-04	3.10E-02
negative regulation of fibroblast	34	2	.04	+	52.66	7.33E-04	3.09E-02

proliferation (GO:0048147)							
regulation of gliogenesis (GO:0014013)	102	6	.11	+	52.66	1.69E-09	1.38E-06
hindlimb morphogenesis (GO:0035137)	35	2	.04	+	51.15	7.75E-04	3.26E-02
positive regulation of stress fiber assembly (GO:0051496)	53	3	.06	+	50.67	3.24E-05	2.45E-03
negative regulation of cell-matrix adhesion (GO:0001953)	36	2	.04	+	49.73	8.17E-04	3.41E-02
astrocyte development (GO:0014002)	36	2	.04	+	49.73	8.17E-04	3.40E-02
osteoclast differentiation (GO:0030316)	55	3	.06	+	48.83	3.60E-05	2.70E-03
Schwann cell differentiation (GO:0014037)	37	2	.04	+	48.39	8.61E-04	3.53E-02
positive regulation of vascular associated smooth muscle cell proliferation (GO:1904707)	37	2	.04	+	48.39	8.61E-04	3.52E-02
ureteric bud morphogenesis (GO:0060675)	57	3	.06	+	47.11	3.98E-05	2.95E-03
mesonephric tubule morphogenesis (GO:0072171)	58	3	.06	+	46.30	4.19E-05	3.05E-03
negative regulation of protein localization to nucleus (GO:1900181)	39	2	.04	+	45.91	9.51E-04	3.83E-02
negative regulation of epithelial cell apoptotic process (GO:1904036)	59	3	.07	+	45.52	4.40E-05	3.15E-03
endocardial cushion	40	2	.04	+	44.76	9.98E-04	3.96E-02

morphogenesis (GO:0003203)							
regulation of myeloid leukocyte differentiation (GO:0002761)	125	6	.14	+	42.97	5.43E-09	2.91E-06
negative regulation of myeloid cell differentiation (GO:0045638)	84	4	.09	+	42.63	2.58E-06	3.46E-04
positive regulation of G1/S transition of mitotic cell cycle (GO:1900087)	42	2	.05	+	42.63	1.10E-03	4.28E-02
T cell differentiation in thymus (GO:0033077)	63	3	.07	+	42.63	5.30E-05	3.71E-03
positive regulation of actin filament bundle assembly (GO:0032233)	63	3	.07	+	42.63	5.30E-05	3.69E-03
urogenital system development (GO:0001655)	64	3	.07	+	41.96	5.55E-05	3.83E-03
embryonic axis specification (GO:0000578)	43	2	.05	+	41.64	1.15E-03	4.45E-02
positive regulation of glucose transmembrane transport (GO:0010828)	43	2	.05	+	41.64	1.15E-03	4.44E-02
cell fate determination (GO:0001709)	44	2	.05	+	40.69	1.20E-03	4.59E-02
cell fate specification (GO:0001708)	88	4	.10	+	40.69	3.08E-06	3.99E-04
negative regulation of intracellular protein transport (GO:0090317)	44	2	.05	+	40.69	1.20E-03	4.58E-02
regulation of oligodendrocyte differentiation (GO:0048713)	44	2	.05	+	40.69	1.20E-03	4.57E-02

bone remodeling (GO:0046849)	44	2	.05	+	40.69	1.20E-03	4.55E-02
regulation of fibroblast proliferation (GO:0048145)	89	4	.10	+	40.23	3.22E-06	4.10E-04
regulation of cellular senescence (GO:2000772)	45	2	.05	+	39.79	1.25E-03	4.74E-02
autonomic nervous system development (GO:0048483)	45	2	.05	+	39.79	1.25E-03	4.73E-02
nephron tubule morphogenesis (GO:0072078)	68	3	.08	+	39.49	6.60E-05	4.36E-03
regulation of extrinsic apoptotic signaling pathway in absence of ligand (GO:2001239)	46	2	.05	+	38.92	1.30E-03	4.91E-02
ventral spinal cord development (GO:0021517)	46	2	.05	+	38.92	1.30E-03	4.90E-02
positive regulation of stem cell proliferation (GO:2000648)	46	2	.05	+	38.92	1.30E-03	4.88E-02
neural tube closure (GO:0001843)	93	4	.10	+	38.50	3.81E-06	4.59E-04
nephron epithelium morphogenesis (GO:0072088)	70	3	.08	+	38.36	7.17E-05	4.70E-03
tube closure (GO:0060606)	94	4	.11	+	38.09	3.97E-06	4.71E-04
regulation of osteoclast differentiation (GO:0045670)	72	3	.08	+	37.30	7.78E-05	5.05E-03
stem cell proliferation (GO:0072089)	72	3	.08	+	37.30	7.78E-05	5.03E-03
renal tubule morphogenesis (GO:0061333)	72	3	.08	+	37.30	7.78E-05	5.01E-03

heart valve development (GO:0003170)	72	3	.08	+	37.30	7.78E-05	4.99E-03
limbic system development (GO:0021761)	121	5	.14	+	36.99	2.43E-07	5.89E-05
nephron morphogenesis (GO:0072028)	73	3	.08	+	36.79	8.09E-05	5.11E-03
negative regulation of G1/S transition of mitotic cell cycle (GO:2000134)	74	3	.08	+	36.29	8.41E-05	5.29E-03
primary neural tube formation (GO:0014020)	99	4	.11	+	36.17	4.84E-06	5.37E-04
regulation of glial cell differentiation (GO:0045685)	75	3	.08	+	35.81	8.74E-05	5.47E-03
embryonic epithelial tube formation (GO:0001838)	127	5	.14	+	35.24	3.06E-07	6.89E-05
neural tube formation (GO:0001841)	106	4	.12	+	33.78	6.29E-06	6.73E-04
epithelial tube formation (GO:0072175)	135	5	.15	+	33.15	4.10E-07	8.28E-05
protein localization to chromosome (GO:0034502)	81	3	.09	+	33.15	1.09E-04	6.67E-03
negative regulation of leukocyte differentiation (GO:1902106)	109	4	.12	+	32.85	7.00E-06	7.29E-04
negative regulation of cell cycle G1/S phase transition (GO:1902807)	82	3	.09	+	32.75	1.13E-04	6.88E-03
dorsal/ventral pattern formation (GO:0009953)	84	3	.09	+	31.97	1.21E-04	7.26E-03
G1/S transition of mitotic cell cycle (GO:0000082)	84	3	.09	+	31.97	1.21E-04	7.23E-03

negative regulation of hemopoiesis (GO:1903707)	113	4	.13	+	31.69	8.03E-06	8.10E-04
nephron tubule development (GO:0072080)	86	3	.10	+	31.23	1.29E-04	7.64E-03
cell cycle G1/S phase transition (GO:0044843)	86	3	.10	+	31.23	1.29E-04	7.62E-03
ureteric bud development (GO:0001657)	88	3	.10	+	30.52	1.38E-04	8.04E-03
metanephros development (GO:0001656)	88	3	.10	+	30.52	1.38E-04	8.01E-03
associative learning (GO:0008306)	88	3	.10	+	30.52	1.38E-04	7.98E-03
negative regulation of neurogenesis (GO:0050768)	148	5	.17	+	30.24	6.38E-07	1.09E-04
mesonephric tubule development (GO:0072164)	89	3	.10	+	30.17	1.43E-04	8.16E-03
mesonephric epithelium development (GO:0072163)	89	3	.10	+	30.17	1.43E-04	8.13E-03
regulation of smoothened signaling pathway (GO:0008589)	89	3	.10	+	30.17	1.43E-04	8.10E-03
morphogenesis of embryonic epithelium (GO:0016331)	150	5	.17	+	29.84	6.80E-07	1.14E-04
tube formation (GO:0035148)	150	5	.17	+	29.84	6.80E-07	1.12E-04
positive regulation of mitotic cell cycle phase transition (GO:1901992)	90	3	.10	+	29.84	1.47E-04	8.30E-03
kidney morphogenesis (GO:0060993)	90	3	.10	+	29.84	1.47E-04	8.27E-03

smoothened signaling pathway (GO:0007224)	91	3	.10	+	29.51	1.52E-04	8.47E-03
renal tubule development (GO:0061326)	91	3	.10	+	29.51	1.52E-04	8.44E-03
hippocampus development (GO:0021766)	92	3	.10	+	29.19	1.57E-04	8.68E-03
regulation of stress fiber assembly (GO:0051492)	92	3	.10	+	29.19	1.57E-04	8.65E-03
regulation of cell-matrix adhesion (GO:0001952)	123	4	.14	+	29.11	1.11E-05	1.07E-03
mesonephros development (GO:0001823)	93	3	.10	+	28.88	1.62E-04	8.86E-03
negative regulation of nervous system development (GO:0051961)	155	5	.17	+	28.88	7.96E-07	1.26E-04
regulation of osteoblast differentiation (GO:0045667)	127	4	.14	+	28.19	1.26E-05	1.20E-03
neural tube development (GO:0021915)	163	5	.18	+	27.46	1.01E-06	1.59E-04
regulation of epithelial cell apoptotic process (GO:1904035)	99	3	.11	+	27.13	1.94E-04	1.03E-02
negative regulation of protein kinase activity (GO:0006469)	200	6	.22	+	26.86	8.12E-08	2.57E-05
cellular response to decreased oxygen levels (GO:0036294)	134	4	.15	+	26.72	1.54E-05	1.42E-03
regulation of myeloid cell differentiation (GO:0045637)	202	6	.23	+	26.59	8.59E-08	2.62E-05
regulation of actomyosin structure	101	3	.11	+	26.59	2.05E-04	1.08E-02

organization (GO:0110020)							
regulation of neural precursor cell proliferation (GO:2000177)	101	3	.11	+	26.59	2.05E-04	1.08E-02
spinal cord development (GO:0021510)	102	3	.11	+	26.33	2.11E-04	1.11E-02
tissue remodeling (GO:0048771)	104	3	.12	+	25.82	2.23E-04	1.16E-02
negative regulation of epithelial cell proliferation (GO:0050680)	140	4	.16	+	25.58	1.82E-05	1.62E-03
regulation of actin filament bundle assembly (GO:0032231)	105	3	.12	+	25.58	2.30E-04	1.18E-02
nephron epithelium development (GO:0072009)	109	3	.12	+	24.64	2.56E-04	1.29E-02
negative regulation of protein serine/threonine kinase activity (GO:0071901)	110	3	.12	+	24.41	2.62E-04	1.32E-02
negative regulation of kinase activity (GO:0033673)	222	6	.25	+	24.19	1.48E-07	4.33E-05
regulation of protein localization to nucleus (GO:1900180)	148	4	.17	+	24.19	2.26E-05	1.86E-03
myeloid leukocyte differentiation (GO:0002573)	150	4	.17	+	23.87	2.38E-05	1.92E-03
cellular response to oxygen levels (GO:0071453)	150	4	.17	+	23.87	2.38E-05	1.91E-03
positive regulation of cell cycle phase transition (GO:1901989)	113	3	.13	+	23.77	2.83E-04	1.42E-02

glial cell development (GO:0021782)	114	3	.13	+	23.56	2.91E-04	1.45E-02
myelination (GO:0042552)	115	3	.13	+	23.35	2.98E-04	1.48E-02
pallium development (GO:0021543)	193	5	.22	+	23.19	2.27E-06	3.10E-04
ensheathment of neurons (GO:0007272)	117	3	.13	+	22.95	3.13E-04	1.55E-02
axon ensheathment (GO:0008366)	117	3	.13	+	22.95	3.13E-04	1.54E-02
negative regulation of neuron apoptotic process (GO:0043524)	158	4	.18	+	22.66	2.90E-05	2.25E-03
negative regulation of cell development (GO:0010721)	279	7	.31	+	22.46	1.87E-08	7.62E-06
positive regulation of mitotic cell cycle (GO:0045931)	120	3	.13	+	22.38	3.37E-04	1.63E-02
regulation of G1/S transition of mitotic cell cycle (GO:2000045)	164	4	.18	+	21.83	3.34E-05	2.52E-03
cellular response to hypoxia (GO:0071456)	125	3	.14	+	21.48	3.78E-04	1.80E-02
mitotic cell cycle checkpoint signaling (GO:0007093)	127	3	.14	+	21.15	3.96E-04	1.85E-02
negative regulation of mitotic cell cycle (GO:0045930)	214	5	.24	+	20.92	3.72E-06	4.59E-04
cell fate commitment (GO:0045165)	258	6	.29	+	20.82	3.51E-07	7.56E-05
positive regulation of cell-substrate adhesion (GO:0010811)	129	3	.14	+	20.82	4.14E-04	1.92E-02
MAPK cascade (GO:0000165)	216	5	.24	+	20.72	3.89E-06	4.65E-04

cerebral cortex development (GO:0021987)	130	3	.15	+	20.66	4.23E-04	1.96E-02
epithelial cell proliferation (GO:0050673)	174	4	.19	+	20.58	4.19E-05	3.04E-03
endocrine system development (GO:0035270)	131	3	.15	+	20.50	4.33E-04	1.99E-02
positive regulation of supramolecular fiber organization (GO:1902905)	175	4	.20	+	20.46	4.28E-05	3.08E-03
regulation of cell-substrate adhesion (GO:0010810)	219	5	.24	+	20.44	4.16E-06	4.82E-04
negative regulation of transferase activity (GO:0051348)	266	6	.30	+	20.19	4.18E-07	8.32E-05
gliogenesis (GO:0042063)	266	6	.30	+	20.19	4.18E-07	8.21E-05
regulation of neuron apoptotic process (GO:0043523)	226	5	.25	+	19.80	4.83E-06	5.40E-04
T cell differentiation (GO:0030217)	181	4	.20	+	19.78	4.87E-05	3.42E-03
myeloid cell homeostasis (GO:0002262)	136	3	.15	+	19.75	4.81E-04	2.19E-02
branching morphogenesis of an epithelial tube (GO:0048754)	137	3	.15	+	19.60	4.92E-04	2.22E-02
regulation of leukocyte differentiation (GO:1902105)	321	7	.36	+	19.52	4.77E-08	1.58E-05
nephron development (GO:0072006)	138	3	.15	+	19.46	5.02E-04	2.26E-02
kidney epithelium development (GO:0072073)	140	3	.16	+	19.18	5.23E-04	2.33E-02
regulation of smooth muscle	142	3	.16	+	18.91	5.45E-04	2.40E-02

cell proliferation (GO:0048660)							
response to ionizing radiation (GO:0010212)	143	3	.16	+	18.78	5.56E-04	2.43E-02
regulation of cell cycle G1/S phase transition (GO:1902806)	191	4	.21	+	18.75	5.97E-05	4.02E-03
regulation of neuron death (GO:1901214)	292	6	.33	+	18.39	7.13E-07	1.15E-04
negative regulation of neuron death (GO:1901215)	195	4	.22	+	18.36	6.46E-05	4.31E-03
glial cell differentiation (GO:0010001)	206	4	.23	+	17.38	7.96E-05	5.07E-03
learning (GO:0007612)	156	3	.17	+	17.21	7.12E-04	3.03E-02
epithelial tube morphogenesis (GO:0060562)	316	6	.35	+	17.00	1.12E-06	1.72E-04
leukocyte differentiation (GO:0002521)	424	8	.47	+	16.89	1.30E-08	5.45E-06
negative regulation of protein phosphorylation (GO:0001933)	318	6	.36	+	16.89	1.16E-06	1.75E-04
cell cycle checkpoint signaling (GO:0000075)	161	3	.18	+	16.68	7.79E-04	3.26E-02
immune system development (GO:0002520)	165	3	.18	+	16.28	8.35E-04	3.46E-02
mitotic cell cycle phase transition (GO:0044772)	165	3	.18	+	16.28	8.35E-04	3.45E-02
morphogenesis of a branching epithelium (GO:0061138)	165	3	.18	+	16.28	8.35E-04	3.44E-02
regulation of neurogenesis (GO:0050767)	386	7	.43	+	16.23	1.64E-07	4.54E-05
negative regulation of	167	3	.19	+	16.08	8.65E-04	3.52E-02

mitotic cell cycle phase transition (GO:1901991)							
anatomical structure maturation (GO:0071695)	223	4	.25	+	16.06	1.08E-04	6.61E-03
telencephalon development (GO:0021537)	279	5	.31	+	16.04	1.32E-05	1.25E-03
negative regulation of MAPK cascade (GO:0043409)	171	3	.19	+	15.70	9.25E-04	3.74E-02
negative regulation of cell cycle phase transition (GO:1901988)	228	4	.25	+	15.70	1.17E-04	7.07E-03
response to decreased oxygen levels (GO:0036293)	286	5	.32	+	15.65	1.48E-05	1.38E-03
myeloid cell differentiation (GO:0030099)	286	5	.32	+	15.65	1.48E-05	1.37E-03
negative regulation of apoptotic signaling pathway (GO:2001234)	229	4	.26	+	15.64	1.19E-04	7.16E-03
negative regulation of Wnt signaling pathway (GO:0030178)	172	3	.19	+	15.61	9.40E-04	3.79E-02
regulation of hemopoiesis (GO:1903706)	403	7	.45	+	15.55	2.18E-07	5.55E-05
negative regulation of phosphorylation (GO:0042326)	348	6	.39	+	15.43	1.94E-06	2.71E-04
lymphocyte differentiation (GO:0030098)	290	5	.32	+	15.43	1.58E-05	1.44E-03
morphogenesis of a branching structure (GO:0001763)	175	3	.20	+	15.35	9.88E-04	3.94E-02
cell maturation (GO:0048469)	175	3	.20	+	15.35	9.88E-04	3.93E-02

cell cycle phase transition (GO:0044770)	176	3	.20	+	15.26	1.00E-03	3.98E-02
negative regulation of DNA-binding transcription factor activity (GO:0043433)	176	3	.20	+	15.26	1.00E-03	3.97E-02
negative regulation of cell population proliferation (GO:0008285)	708	12	.79	+	15.17	2.86E-12	7.41E-09
positive regulation of binding (GO:0051099)	179	3	.20	+	15.00	1.05E-03	4.14E-02
positive regulation of neurogenesis (GO:0050769)	240	4	.27	+	14.92	1.42E-04	8.14E-03
negative regulation of cell cycle (GO:0045786)	361	6	.40	+	14.88	2.39E-06	3.23E-04
kidney development (GO:0001822)	303	5	.34	+	14.77	1.95E-05	1.69E-03
cell-cell junction organization (GO:0045216)	182	3	.20	+	14.76	1.10E-03	4.30E-02
cell-substrate adhesion (GO:0031589)	185	3	.21	+	14.52	1.16E-03	4.47E-02
regulation of mitotic cell cycle (GO:0007346)	494	8	.55	+	14.50	4.16E-08	1.47E-05
positive regulation of cytoskeleton organization (GO:0051495)	186	3	.21	+	14.44	1.17E-03	4.52E-02
regulation of epithelial cell proliferation (GO:0050678)	372	6	.42	+	14.44	2.83E-06	3.76E-04
regulation of apoptotic signaling pathway (GO:2001233)	375	6	.42	+	14.32	2.97E-06	3.90E-04
regulation of chromosome	250	4	.28	+	14.32	1.66E-04	9.00E-03

organization (GO:0033044)							
heart development (GO:0007507)	563	9	.63	+	14.31	5.30E-09	2.94E-06
renal system development (GO:0072001)	313	5	.35	+	14.30	2.27E-05	1.86E-03
response to oxygen levels (GO:0070482)	314	5	.35	+	14.25	2.30E-05	1.88E-03
response to light stimulus (GO:0009416)	316	5	.35	+	14.16	2.37E-05	1.93E-03
tissue morphogenesis (GO:0048729)	570	9	.64	+	14.13	5.89E-09	2.95E-06
cellular response to xenobiotic stimulus (GO:0071466)	191	3	.21	+	14.06	1.27E-03	4.78E-02
heart morphogenesis (GO:0003007)	255	4	.28	+	14.04	1.79E-04	9.67E-03
protein localization to nucleus (GO:0034504)	193	3	.22	+	13.91	1.30E-03	4.88E-02
negative regulation of protein modification process (GO:0031400)	462	7	.52	+	13.56	5.40E-07	9.98E-05
regulation of nervous system development (GO:0051960)	466	7	.52	+	13.45	5.72E-07	1.02E-04
regulation of mitotic cell cycle phase transition (GO:1901990)	333	5	.37	+	13.44	3.04E-05	2.35E-03
regulation of Wnt signaling pathway (GO:0030111)	334	5	.37	+	13.40	3.08E-05	2.37E-03
mononuclear cell differentiation (GO:1903131)	335	5	.37	+	13.36	3.12E-05	2.39E-03
regulation of protein stability (GO:0031647)	335	5	.37	+	13.36	3.12E-05	2.38E-03

negative regulation of phosphate metabolic process (GO:0045936)	404	6	.45	+	13.29	4.53E-06	5.13E-04
negative regulation of phosphorus metabolic process (GO:0010563)	405	6	.45	+	13.26	4.59E-06	5.16E-04
response to hypoxia (GO:0001666)	272	4	.30	+	13.16	2.28E-04	1.18E-02
negative regulation of cell cycle process (GO:0010948)	274	4	.31	+	13.07	2.34E-04	1.20E-02
developmental maturation (GO:0021700)	278	4	.31	+	12.88	2.47E-04	1.26E-02
negative regulation of cell migration (GO:0030336)	286	4	.32	+	12.52	2.75E-04	1.38E-02
positive regulation of nervous system development (GO:0051962)	289	4	.32	+	12.39	2.86E-04	1.43E-02
regulation of cell cycle phase transition (GO:1901987)	434	6	.48	+	12.38	6.78E-06	7.12E-04
response to radiation (GO:0009314)	445	6	.50	+	12.07	7.81E-06	7.98E-04
negative regulation of cell differentiation (GO:0045596)	670	9	.75	+	12.02	2.34E-08	9.32E-06
mitotic cell cycle process (GO:1903047)	522	7	.58	+	12.00	1.21E-06	1.79E-04
negative regulation of cell motility (GO:2000146)	301	4	.34	+	11.90	3.33E-04	1.63E-02
reproductive structure development (GO:0048608)	301	4	.34	+	11.90	3.33E-04	1.62E-02

hemopoiesis (GO:0030097)	685	9	.77	+	11.76	2.83E-08	1.10E-05
regulation of supramolecular fiber organization (GO:1902903)	381	5	.43	+	11.75	5.72E-05	3.93E-03
reproductive system development (GO:0061458)	305	4	.34	+	11.74	3.50E-04	1.69E-02
morphogenesis of an epithelium (GO:0002009)	458	6	.51	+	11.73	9.19E-06	9.09E-04
mitotic cell cycle (GO:0000278)	616	8	.69	+	11.63	2.21E-07	5.45E-05
T cell activation (GO:0042110)	315	4	.35	+	11.37	3.95E-04	1.85E-02
regulation of cell cycle (GO:0051726)	1120	14	1.25	+	11.19	1.10E-12	3.43E-09
regulation of cell cycle process (GO:0010564)	725	9	.81	+	11.11	4.58E-08	1.55E-05
forebrain development (GO:0030900)	409	5	.46	+	10.94	7.96E-05	5.05E-03
chordate embryonic development (GO:0043009)	661	8	.74	+	10.83	3.76E-07	7.68E-05
regulation of cell development (GO:0060284)	829	10	.93	+	10.80	8.36E-09	3.61E-06
muscle tissue development (GO:0060537)	334	4	.37	+	10.72	4.92E-04	2.23E-02
camera-type eye development (GO:0043010)	337	4	.38	+	10.63	5.08E-04	2.28E-02
negative regulation of locomotion (GO:0040013)	338	4	.38	+	10.59	5.14E-04	2.30E-02
gland development (GO:0048732)	425	5	.47	+	10.53	9.52E-05	5.92E-03
regulation of intracellular transport (GO:0032386)	340	4	.38	+	10.53	5.25E-04	2.33E-02

embryo development ending in birth or egg hatching (GO:0009792)	683	8	.76	+	10.49	4.81E-07	9.10E-05
response to xenobiotic stimulus (GO:0009410)	433	5	.48	+	10.34	1.04E-04	6.40E-03
negative regulation of intracellular signal transduction (GO:1902532)	524	6	.59	+	10.25	1.95E-05	1.69E-03
regulation of protein kinase activity (GO:0045859)	615	7	.69	+	10.19	3.54E-06	4.44E-04
positive regulation of cell development (GO:0010720)	441	5	.49	+	10.15	1.13E-04	6.86E-03
negative regulation of catalytic activity (GO:0043086)	630	7	.70	+	9.95	4.15E-06	4.84E-04
chromosome organization (GO:0051276)	456	5	.51	+	9.82	1.32E-04	7.74E-03
regulation of transferase activity (GO:0051338)	847	9	.95	+	9.51	1.70E-07	4.64E-05
apoptotic process (GO:0006915)	1047	11	1.17	+	9.40	4.74E-09	2.94E-06
positive regulation of cell differentiation (GO:0045597)	857	9	.96	+	9.40	1.88E-07	5.03E-05
lymphocyte activation (GO:0046649)	478	5	.53	+	9.36	1.64E-04	8.95E-03
eye development (GO:0001654)	385	4	.43	+	9.30	8.32E-04	3.46E-02
visual system development (GO:0150063)	389	4	.43	+	9.20	8.65E-04	3.52E-02
tube morphogenesis (GO:0035239)	684	7	.76	+	9.16	7.08E-06	7.28E-04

regulation of cell population proliferation (GO:0042127)	1674	17	1.87	+	9.09	2.01E-14	3.12E-10
embryonic morphogenesis (GO:0048598)	591	6	.66	+	9.09	3.82E-05	2.85E-03
sensory system development (GO:0048880)	395	4	.44	+	9.07	9.15E-04	3.71E-02
animal organ morphogenesis (GO:0009887)	991	10	1.11	+	9.03	4.48E-08	1.55E-05
programmed cell death (GO:0012501)	1093	11	1.22	+	9.01	7.39E-09	3.48E-06
in utero embryonic development (GO:0001701)	401	4	.45	+	8.93	9.67E-04	3.88E-02
cell death (GO:0008219)	1105	11	1.23	+	8.91	8.27E-09	3.67E-06
regulation of kinase activity (GO:0043549)	709	7	.79	+	8.84	8.93E-06	8.89E-04
positive regulation of organelle organization (GO:0010638)	508	5	.57	+	8.81	2.17E-04	1.13E-02
negative regulation of developmental process (GO:0051093)	919	9	1.03	+	8.77	3.38E-07	7.39E-05
circulatory system development (GO:0072359)	926	9	1.03	+	8.70	3.60E-07	7.66E-05
regulation of cell differentiation (GO:0045595)	1558	15	1.74	+	8.62	4.44E-12	9.85E-09
cell population proliferation (GO:0008283)	729	7	.81	+	8.60	1.07E-05	1.04E-03
negative regulation of signal transduction (GO:0009968)	1266	12	1.41	+	8.49	2.19E-09	1.62E-06
negative regulation of molecular	975	9	1.09	+	8.26	5.54E-07	1.00E-04

function (GO:0044092)							
regulation of protein localization (GO:0032880)	874	8	.98	+	8.19	3.01E-06	3.93E-04
negative regulation of transcription by RNA polymerase II (GO:0000122)	985	9	1.10	+	8.18	6.03E-07	1.06E-04
negative regulation of protein metabolic process (GO:0051248)	986	9	1.10	+	8.17	6.08E-07	1.06E-04
cell cycle process (GO:0022402)	881	8	.98	+	8.13	3.19E-06	4.10E-04
negative regulation of apoptotic process (GO:0043066)	892	8	1.00	+	8.03	3.50E-06	4.42E-04
response to abiotic stimulus (GO:0009628)	1118	10	1.25	+	8.01	1.38E-07	4.11E-05
tube development (GO:0035295)	900	8	1.01	+	7.96	3.73E-06	4.57E-04
negative regulation of cell communication (GO:0010648)	1361	12	1.52	+	7.89	4.94E-09	2.95E-06
negative regulation of signaling (GO:0023057)	1362	12	1.52	+	7.89	4.98E-09	2.87E-06
positive regulation of hydrolase activity (GO:0051345)	571	5	.64	+	7.84	3.71E-04	1.77E-02
cell morphogenesis (GO:0000902)	687	6	.77	+	7.82	8.74E-05	5.45E-03
negative regulation of programmed cell death (GO:0043069)	920	8	1.03	+	7.78	4.39E-06	5.05E-04
regulation of multicellular organismal	1401	12	1.57	+	7.67	6.84E-09	3.32E-06

development (GO:2000026)							
embryo development (GO:0009790)	1054	9	1.18	+	7.64	1.06E-06	1.64E-04
positive regulation of developmental process (GO:0051094)	1319	11	1.47	+	7.47	5.09E-08	1.65E-05
anatomical structure formation involved in morphogenesis (GO:0048646)	961	8	1.07	+	7.45	6.04E-06	6.52E-04
leukocyte activation (GO:0045321)	601	5	.67	+	7.45	4.68E-04	2.13E-02
head development (GO:0060322)	847	7	.95	+	7.40	2.80E-05	2.18E-03
protein localization to organelle (GO:0033365)	731	6	.82	+	7.35	1.23E-04	7.27E-03
epithelium development (GO:0060429)	1103	9	1.23	+	7.30	1.54E-06	2.19E-04
regulation of cellular localization (GO:0060341)	981	8	1.10	+	7.30	7.03E-06	7.27E-04
negative regulation of cellular metabolic process (GO:0031324)	2217	18	2.48	+	7.27	7.94E-14	6.16E-10
negative regulation of DNA-templated transcription (GO:0045892)	1327	10	1.48	+	6.75	6.69E-07	1.13E-04
brain development (GO:0007420)	798	6	.89	+	6.73	1.97E-04	1.05E-02
regulation of apoptotic process (GO:0042981)	1471	11	1.64	+	6.69	1.54E-07	4.35E-05
regulation of protein	1071	8	1.20	+	6.69	1.33E-05	1.25E-03

phosphorylation (GO:0001932)							
negative regulation of RNA biosynthetic process (GO:1902679)	1341	10	1.50	+	6.68	7.36E-07	1.18E-04
regulation of MAPK cascade (GO:0043408)	672	5	.75	+	6.66	7.75E-04	3.25E-02
positive regulation of cell population proliferation (GO:0008284)	950	7	1.06	+	6.60	5.80E-05	3.95E-03
negative regulation of response to stimulus (GO:0048585)	1637	12	1.83	+	6.56	3.88E-08	1.40E-05
regulation of programmed cell death (GO:0043067)	1521	11	1.70	+	6.47	2.16E-07	5.60E-05
positive regulation of catalytic activity (GO:0043085)	1112	8	1.24	+	6.44	1.75E-05	1.59E-03
negative regulation of nitrogen compound metabolic process (GO:0051172)	2376	17	2.65	+	6.40	6.08E-12	1.18E-08
negative regulation of multicellular organismal process (GO:0051241)	1125	8	1.26	+	6.37	1.90E-05	1.67E-03
cell cycle (GO:0007049)	1270	9	1.42	+	6.34	4.90E-06	5.39E-04
regulation of cell motility (GO:2000145)	991	7	1.11	+	6.32	7.56E-05	4.93E-03
intracellular signal transduction (GO:0035556)	1558	11	1.74	+	6.32	2.75E-07	6.48E-05
negative regulation of macromolecule biosynthetic	1560	11	1.74	+	6.31	2.79E-07	6.47E-05

process (GO:0010558)							
negative regulation of nucleobase-containing compound metabolic process (GO:0045934)	1568	11	1.75	+	6.28	2.94E-07	6.71E-05
regulation of protein modification process (GO:0031399)	1443	10	1.61	+	6.20	1.44E-06	2.08E-04
cell activation (GO:0001775)	724	5	.81	+	6.18	1.08E-03	4.24E-02
negative regulation of macromolecule metabolic process (GO:0010605)	2755	19	3.08	+	6.17	1.38E-13	7.12E-10
negative regulation of RNA metabolic process (GO:0051253)	1451	10	1.62	+	6.17	1.51E-06	2.17E-04
negative regulation of cellular biosynthetic process (GO:0031327)	1601	11	1.79	+	6.15	3.62E-07	7.60E-05
tissue development (GO:0009888)	1753	12	1.96	+	6.13	8.28E-08	2.57E-05
regulation of phosphorylation (GO:0042325)	1170	8	1.31	+	6.12	2.52E-05	2.00E-03
regulation of organelle organization (GO:0033043)	1175	8	1.31	+	6.09	2.60E-05	2.04E-03
regulation of locomotion (GO:0040012)	1036	7	1.16	+	6.05	9.99E-05	6.18E-03
anatomical structure morphogenesis (GO:0009653)	2244	15	2.51	+	5.98	7.86E-10	8.14E-07
negative regulation of biosynthetic	1650	11	1.84	+	5.97	4.90E-07	9.17E-05

process (GO:0009890)							
central nervous system development (GO:0007417)	1069	7	1.19	+	5.86	1.21E-04	7.22E-03
regulation of developmental process (GO:0050793)	2462	16	2.75	+	5.82	1.94E-10	3.02E-07
regulation of cell migration (GO:0030334)	933	6	1.04	+	5.76	4.55E-04	2.08E-02
negative regulation of metabolic process (GO:0009892)	2985	19	3.33	+	5.70	5.98E-13	2.32E-09
negative regulation of gene expression (GO:0010629)	955	6	1.07	+	5.62	5.15E-04	2.30E-02
regulation of cellular component biogenesis (GO:0044087)	968	6	1.08	+	5.55	5.53E-04	2.43E-02
regulation of phosphate metabolic process (GO:0019220)	1315	8	1.47	+	5.45	5.79E-05	3.96E-03
generation of neurons (GO:0048699)	1151	7	1.29	+	5.44	1.92E-04	1.03E-02
regulation of phosphorus metabolic process (GO:0051174)	1316	8	1.47	+	5.44	5.82E-05	3.95E-03
neurogenesis (GO:0022008)	1321	8	1.48	+	5.42	5.98E-05	4.01E-03
regulation of catalytic activity (GO:0050790)	1827	11	2.04	+	5.39	1.35E-06	1.98E-04
positive regulation of gene expression (GO:0010628)	1173	7	1.31	+	5.34	2.16E-04	1.13E-02
positive regulation of molecular function (GO:0044093)	1519	9	1.70	+	5.30	2.08E-05	1.75E-03

regulation of multicellular organismal process (GO:0051239)	2983	17	3.33	+	5.10	2.37E-10	3.07E-07
cell-cell signaling (GO:0007267)	1092	6	1.22	+	4.92	1.04E-03	4.10E-02
animal organ development (GO:0048513)	2925	16	3.27	+	4.90	2.56E-09	1.73E-06
positive regulation of multicellular organismal process (GO:0051240)	1654	9	1.85	+	4.87	4.08E-05	2.99E-03
regulation of immune system process (GO:0002682)	1488	8	1.66	+	4.81	1.38E-04	8.06E-03
positive regulation of cellular component organization (GO:0051130)	1118	6	1.25	+	4.80	1.17E-03	4.51E-02
regulation of protein metabolic process (GO:0051246)	2462	13	2.75	+	4.73	3.71E-07	7.69E-05
cell surface receptor signaling pathway (GO:0007166)	2093	11	2.34	+	4.70	5.15E-06	5.63E-04
cellular response to oxygen-containing compound (GO:1901701)	1146	6	1.28	+	4.69	1.33E-03	4.97E-02
protein localization (GO:0008104)	1936	10	2.16	+	4.62	1.99E-05	1.70E-03
cellular macromolecule localization (GO:0070727)	1942	10	2.17	+	4.61	2.04E-05	1.73E-03
regulation of transport (GO:0051049)	1776	9	1.98	+	4.54	7.14E-05	4.70E-03
regulation of molecular function (GO:0065009)	2569	13	2.87	+	4.53	6.11E-07	1.05E-04

cell development (GO:0048468)	2185	11	2.44	+	4.51	7.82E-06	7.94E-04
nervous system development (GO:0007399)	2233	11	2.49	+	4.41	9.65E-06	9.48E-04
system development (GO:0048731)	3553	17	3.97	+	4.28	3.83E-09	2.48E-06
regulation of localization (GO:0032879)	2131	10	2.38	+	4.20	4.58E-05	3.25E-03
regulation of signal transduction (GO:0009966)	2992	14	3.34	+	4.19	4.24E-07	8.23E-05
positive regulation of DNA-templated transcription (GO:0045893)	1716	8	1.92	+	4.17	3.68E-04	1.76E-02
positive regulation of RNA biosynthetic process (GO:1902680)	1723	8	1.92	+	4.16	3.78E-04	1.79E-02
regulation of intracellular signal transduction (GO:1902531)	1727	8	1.93	+	4.15	3.84E-04	1.81E-02
macromolecule localization (GO:0033036)	2377	11	2.66	+	4.14	1.76E-05	1.58E-03
multicellular organism development (GO:0007275)	3966	18	4.43	+	4.06	1.69E-09	1.31E-06
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	2052	9	2.29	+	3.93	2.18E-04	1.13E-02
positive regulation of RNA metabolic process (GO:0051254)	1856	8	2.07	+	3.86	6.25E-04	2.71E-02
regulation of transcription by RNA polymerase II (GO:0006357)	2594	11	2.90	+	3.80	4.03E-05	2.97E-03

regulation of signaling (GO:0023051)	3396	14	3.79	+	3.69	2.05E-06	2.85E-04
positive regulation of macromolecule biosynthetic process (GO:0010557)	1942	8	2.17	+	3.69	8.45E-04	3.47E-02
regulation of cell communication (GO:0010646)	3405	14	3.80	+	3.68	2.12E-06	2.92E-04
regulation of cellular component organization (GO:0051128)	2439	10	2.72	+	3.67	1.45E-04	8.19E-03
cellular localization (GO:0051641)	2700	11	3.02	+	3.65	5.88E-05	3.97E-03
regulation of response to stimulus (GO:0048583)	3960	16	4.42	+	3.62	2.18E-07	5.46E-05
negative regulation of cellular process (GO:0048523)	4705	19	5.26	+	3.61	2.26E-09	1.60E-06
protein-containing complex organization (GO:0043933)	1984	8	2.22	+	3.61	9.74E-04	3.90E-02
positive regulation of cellular metabolic process (GO:0031325)	2976	12	3.32	+	3.61	2.39E-05	1.91E-03
positive regulation of cellular biosynthetic process (GO:0031328)	2022	8	2.26	+	3.54	1.10E-03	4.31E-02
positive regulation of metabolic process (GO:0009893)	3825	15	4.27	+	3.51	1.18E-06	1.76E-04
cell differentiation (GO:0030154)	3590	14	4.01	+	3.49	4.07E-06	4.78E-04
cellular developmental process (GO:0048869)	3614	14	4.04	+	3.47	4.41E-06	5.04E-04

positive regulation of nitrogen compound metabolic process (GO:0051173)	3121	12	3.49	+	3.44	3.89E-05	2.89E-03
positive regulation of biosynthetic process (GO:0009891)	2081	8	2.32	+	3.44	1.33E-03	4.98E-02
regulation of cellular metabolic process (GO:0031323)	5482	21	6.12	+	3.43	1.24E-10	2.13E-07
regulation of DNA-templated transcription (GO:0006355)	3450	13	3.85	+	3.37	1.77E-05	1.58E-03
negative regulation of biological process (GO:0048519)	5320	20	5.94	+	3.37	1.37E-09	1.33E-06
cellular response to chemical stimulus (GO:0070887)	2397	9	2.68	+	3.36	6.99E-04	2.98E-02
regulation of RNA biosynthetic process (GO:2001141)	3473	13	3.88	+	3.35	1.91E-05	1.67E-03
regulation of nitrogen compound metabolic process (GO:0051171)	5646	21	6.31	+	3.33	2.25E-10	3.17E-07
positive regulation of macromolecule metabolic process (GO:0010604)	3514	13	3.93	+	3.31	2.18E-05	1.81E-03
regulation of primary metabolic process (GO:0080090)	5825	21	6.51	+	3.23	4.23E-10	5.05E-07
regulation of macromolecule biosynthetic process (GO:0010556)	3961	14	4.42	+	3.16	1.34E-05	1.25E-03
regulation of gene expression (GO:0010468)	4888	17	5.46	+	3.11	5.45E-07	9.95E-05

anatomical structure development (GO:0048856)	5201	18	5.81	+	3.10	1.54E-07	4.43E-05
regulation of nucleobase-containing compound metabolic process (GO:0019219)	4051	14	4.53	+	3.09	1.76E-05	1.59E-03
regulation of RNA metabolic process (GO:0051252)	3766	13	4.21	+	3.09	4.67E-05	3.30E-03
positive regulation of cellular process (GO:0048522)	5511	19	6.16	+	3.09	3.73E-08	1.38E-05
regulation of cellular biosynthetic process (GO:0031326)	4068	14	4.54	+	3.08	1.85E-05	1.63E-03
regulation of macromolecule metabolic process (GO:0060255)	6188	21	6.91	+	3.04	1.43E-09	1.31E-06
regulation of biosynthetic process (GO:0009889)	4177	14	4.67	+	3.00	2.53E-05	2.00E-03
signal transduction (GO:0007165)	4819	16	5.38	+	2.97	3.56E-06	4.43E-04
cell communication (GO:0007154)	5278	17	5.90	+	2.88	1.74E-06	2.46E-04
developmental process (GO:0032502)	5702	18	6.37	+	2.83	6.89E-07	1.13E-04
signaling (GO:0023052)	5119	16	5.72	+	2.80	8.27E-06	8.28E-04
regulation of metabolic process (GO:0019222)	6719	21	7.51	+	2.80	7.50E-09	3.43E-06
response to chemical (GO:0042221)	3899	12	4.36	+	2.76	3.57E-04	1.71E-02
cellular component organization (GO:0016043)	5560	17	6.21	+	2.74	3.81E-06	4.62E-04

positive regulation of biological process (GO:0048518)	6219	19	6.95	+	2.73	3.09E-07	6.86E-05
cellular component organization or biogenesis (GO:0071840)	5774	17	6.45	+	2.64	6.68E-06	7.05E-04
multicellular organismal process (GO:0032501)	6713	19	7.50	+	2.53	1.16E-06	1.76E-04
cellular response to stimulus (GO:0051716)	6472	18	7.23	+	2.49	5.26E-06	5.71E-04
response to stimulus (GO:0050896)	8243	19	9.21	+	2.06	4.47E-05	3.18E-03
regulation of cellular process (GO:0050794)	11039	22	12.33	+	1.78	2.01E-05	1.71E-03
regulation of biological process (GO:0050789)	11806	22	13.19	+	1.67	6.52E-05	4.33E-03
biological regulation (GO:0065007)	12228	22	13.66	+	1.61	1.51E-04	8.41E-03

Supplementary Table 3: PANTHER Overrepresentation Test (Haploinsufficient Breast Cancer-Associated Genes)

Analysis Type: PANTHER Overrepresentation Test (Released 20221013)
Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.7942786 Released 2023-05-10
Analyzed List: Client Text Box Input (Homo sapiens)
Reference List: Homo sapiens (all genes in database)
Test Type: FISHER
Correction: FDR

GO biological process complete	Homo sapiens - REFLIST (20589)	Client Text Box Input (6)	Client Text Box Input (expected)	Client Text Box Input (over/under)	Client Text Box Input (fold Enrichment)	Client Text Box Input (raw P-value)	Client Text Box Input (FDR)
anoikis (GO:0043276)	12	3	.00	+	> 100	6.24E-09	9.70E-05
response to UV-B (GO:0010224)	21	2	.01	+	> 100	1.78E-05	1.11E-02
positive regulation of nitric-oxide synthase activity (GO:0051000)	22	2	.01	+	> 100	1.95E-05	1.04E-02
insulin-like growth factor receptor signaling pathway (GO:0048009)	31	2	.01	+	> 100	3.72E-05	1.44E-02
positive regulation of monooxygenase activity (GO:0032770)	32	2	.01	+	> 100	3.95E-05	1.50E-02
negative regulation of macroautophagy (GO:0016242)	32	2	.01	+	> 100	3.95E-05	1.46E-02
response to pain (GO:0048265)	34	2	.01	+	> 100	4.44E-05	1.50E-02
protein localization to chromatin (GO:0071168)	35	2	.01	+	> 100	4.69E-05	1.55E-02
regulation of nitric-oxide synthase activity (GO:0050999)	38	2	.01	+	> 100	5.49E-05	1.61E-02
T cell costimulation (GO:0031295)	40	2	.01	+	> 100	6.06E-05	1.65E-02
lymphocyte costimulation (GO:0031294)	42	2	.01	+	> 100	6.65E-05	1.72E-02

positive regulation of glucose metabolic process (GO:0010907)	42	2	.01	+	> 100	6.65E-05	1.69E-02
positive regulation of nitric oxide biosynthetic process (GO:0045429)	43	2	.01	+	> 100	6.96E-05	1.72E-02
phosphatidylinositol 3-kinase signaling (GO:0014065)	43	2	.01	+	> 100	6.96E-05	1.69E-02
cellular response to vascular endothelial growth factor stimulus (GO:0035924)	45	2	.01	+	> 100	7.60E-05	1.74E-02
positive regulation of nitric oxide metabolic process (GO:1904407)	45	2	.01	+	> 100	7.60E-05	1.71E-02
regulation of extrinsic apoptotic signaling pathway in absence of ligand (GO:2001239)	46	2	.01	+	> 100	7.93E-05	1.73E-02
prostate gland development (GO:0030850)	46	2	.01	+	> 100	7.93E-05	1.71E-02
regulation of monooxygenase activity (GO:0032768)	51	2	.01	+	> 100	9.68E-05	1.95E-02
epidermal growth factor receptor signaling pathway (GO:0007173)	52	2	.02	+	> 100	1.01E-04	1.95E-02
positive regulation of TOR signaling (GO:0032008)	52	2	.02	+	> 100	1.01E-04	1.93E-02
protein kinase B signaling (GO:0043491)	52	2	.02	+	> 100	1.01E-04	1.90E-02
regulation of TORC1 signaling (GO:1903432)	52	2	.02	+	> 100	1.01E-04	1.88E-02
intrinsic apoptotic signaling pathway by p53 class mediator (GO:0072332)	57	2	.02	+	> 100	1.20E-04	2.12E-02
regulation of nitric oxide biosynthetic	58	2	.02	+	> 100	1.24E-04	2.12E-02

process (GO:0045428)							
maternal process involved in female pregnancy (GO:0060135)	61	2	.02	+	> 100	1.37E-04	2.29E-02
mammary gland epithelium development (GO:0061180)	62	2	.02	+	> 100	1.41E-04	2.31E-02
positive regulation of oxidoreductase activity (GO:0051353)	63	2	.02	+	> 100	1.46E-04	2.31E-02
regulation of nitric oxide metabolic process (GO:0080164)	63	2	.02	+	> 100	1.46E-04	2.29E-02
ERBB signaling pathway (GO:0038127)	64	2	.02	+	> 100	1.50E-04	2.34E-02
urogenital system development (GO:0001655)	64	2	.02	+	> 100	1.50E-04	2.31E-02
peptidyl-threonine phosphorylation (GO:0018107)	68	2	.02	+	> 100	1.69E-04	2.50E-02
insulin receptor signaling pathway (GO:0008286)	68	2	.02	+	> 100	1.69E-04	2.48E-02
response to activity (GO:0014823)	70	2	.02	+	98.04	1.79E-04	2.55E-02
positive regulation of peptidyl-serine phosphorylation (GO:0033138)	108	3	.03	+	95.32	3.01E-06	6.68E-03
endothelial cell migration (GO:0043542)	72	2	.02	+	95.32	1.89E-04	2.67E-02
phosphatidylinositol-mediated signaling (GO:0048015)	76	2	.02	+	90.30	2.10E-04	2.87E-02
regulation of TOR signaling (GO:0032006)	116	3	.03	+	88.75	3.71E-06	7.21E-03
peptidyl-threonine modification (GO:0018210)	78	2	.02	+	87.99	2.21E-04	2.99E-02
positive regulation of carbohydrate	78	2	.02	+	87.99	2.21E-04	2.96E-02

metabolic process (GO:0045913)							
inositol lipid-mediated signaling (GO:0048017)	80	2	.02	+	85.79	2.32E-04	3.01E-02
protein localization to chromosome (GO:0034502)	81	2	.02	+	84.73	2.38E-04	3.03E-02
multicellular organismal response to stress (GO:0033555)	83	2	.02	+	82.69	2.50E-04	3.15E-02
positive regulation of smooth muscle cell proliferation (GO:0048661)	85	2	.02	+	80.74	2.62E-04	3.23E-02
negative regulation of autophagy (GO:0010507)	87	2	.03	+	78.89	2.74E-04	3.35E-02
signal transduction by p53 class mediator (GO:0072331)	91	2	.03	+	75.42	2.99E-04	3.55E-02
regulation of peptidyl-serine phosphorylation (GO:0033135)	140	3	.04	+	73.53	6.46E-06	1.11E-02
positive regulation of protein localization to nucleus (GO:1900182)	94	2	.03	+	73.01	3.19E-04	3.67E-02
regulation of carbohydrate biosynthetic process (GO:0043255)	98	2	.03	+	70.03	3.46E-04	3.75E-02
response to UV (GO:0009411)	153	3	.04	+	67.28	8.39E-06	1.18E-02
regulation of glucose metabolic process (GO:0010906)	102	2	.03	+	67.28	3.74E-04	3.95E-02
epithelial cell migration (GO:0010631)	102	2	.03	+	67.28	3.74E-04	3.92E-02
regulation of oxidoreductase activity (GO:0051341)	103	2	.03	+	66.63	3.81E-04	3.97E-02
regulation of generation of precursor	104	2	.03	+	65.99	3.88E-04	4.02E-02

metabolites and energy (GO:0043467)							
epithelium migration (GO:0090132)	105	2	.03	+	65.36	3.96E-04	4.04E-02
regulation of signal transduction by p53 class mediator (GO:1901796)	107	2	.03	+	64.14	4.11E-04	4.14E-02
regulation of protein kinase B signaling (GO:0051896)	167	3	.05	+	61.64	1.09E-05	1.12E-02
tissue migration (GO:0090130)	112	2	.03	+	61.28	4.49E-04	4.44E-02
positive regulation of protein kinase B signaling (GO:0051897)	113	2	.03	+	60.73	4.57E-04	4.43E-02
T cell receptor signaling pathway (GO:0050852)	113	2	.03	+	60.73	4.57E-04	4.41E-02
glucose metabolic process (GO:0006006)	120	2	.03	+	57.19	5.14E-04	4.84E-02
negative regulation of neuron death (GO:1901215)	195	3	.06	+	52.79	1.71E-05	1.16E-02
ameboidal-type cell migration (GO:0001667)	200	3	.06	+	51.47	1.85E-05	1.10E-02
glucose homeostasis (GO:0042593)	203	3	.06	+	50.71	1.93E-05	1.07E-02
carbohydrate homeostasis (GO:0033500)	204	3	.06	+	50.46	1.96E-05	1.01E-02
regulation of neuron death (GO:1901214)	292	3	.09	+	35.26	5.64E-05	1.62E-02
reproductive structure development (GO:0048608)	301	3	.09	+	34.20	6.16E-05	1.65E-02
reproductive system development (GO:0061458)	305	3	.09	+	33.75	6.41E-05	1.69E-02
response to light stimulus (GO:0009416)	316	3	.09	+	32.58	7.11E-05	1.67E-02
gland development (GO:0048732)	425	4	.12	+	32.30	2.69E-06	8.37E-03
positive regulation of lymphocyte	330	3	.10	+	31.20	8.08E-05	1.72E-02

activation (GO:0051251)							
regulation of autophagy (GO:0010506)	352	3	.10	+	29.25	9.77E-05	1.95E-02
positive regulation of cell projection organization (GO:0031346)	354	3	.10	+	29.08	9.94E-05	1.95E-02
response to peptide hormone (GO:0043434)	373	3	.11	+	27.60	1.16E-04	2.07E-02
positive regulation of leukocyte activation (GO:0002696)	379	3	.11	+	27.16	1.21E-04	2.10E-02
positive regulation of cell activation (GO:0050867)	396	3	.12	+	26.00	1.38E-04	2.28E-02
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	423	3	.12	+	24.34	1.68E-04	2.51E-02
positive regulation of kinase activity (GO:0033674)	430	3	.13	+	23.94	1.76E-04	2.53E-02
response to radiation (GO:0009314)	445	3	.13	+	23.13	1.95E-04	2.72E-02
regulation of neuron projection development (GO:0010975)	450	3	.13	+	22.88	2.01E-04	2.79E-02
response to peptide (GO:1901652)	454	3	.13	+	22.68	2.07E-04	2.84E-02
regulation of plasma membrane bounded cell projection organization (GO:0120035)	643	4	.19	+	21.35	1.38E-05	1.07E-02
positive regulation of cell adhesion (GO:0045785)	486	3	.14	+	21.18	2.52E-04	3.16E-02
regulation of cell projection organization (GO:0031344)	657	4	.19	+	20.89	1.50E-05	1.06E-02
regulation of lymphocyte	504	3	.15	+	20.43	2.81E-04	3.40E-02

activation (GO:0051249)							
cellular response to hormone stimulus (GO:0032870)	510	3	.15	+	20.19	2.91E-04	3.47E-02
response to lipid (GO:0033993)	854	5	.25	+	20.09	7.23E-07	5.61E-03
tube morphogenesis (GO:0035239)	684	4	.20	+	20.07	1.76E-05	1.14E-02
positive regulation of transferase activity (GO:0051347)	523	3	.15	+	19.68	3.13E-04	3.65E-02
negative regulation of intracellular signal transduction (GO:1902532)	524	3	.15	+	19.65	3.15E-04	3.65E-02
cellular response to lipid (GO:0071396)	527	3	.15	+	19.53	3.20E-04	3.65E-02
positive regulation of protein phosphorylation (GO:0001934)	711	4	.21	+	19.31	2.04E-05	1.02E-02
regulation of immune response (GO:0050776)	889	5	.26	+	19.30	8.82E-07	4.57E-03
vasculature development (GO:0001944)	546	3	.16	+	18.85	3.55E-04	3.83E-02
protein localization to organelle (GO:0033365)	731	4	.21	+	18.78	2.28E-05	1.07E-02
positive regulation of hydrolase activity (GO:0051345)	571	3	.17	+	18.03	4.05E-04	4.11E-02
positive regulation of phosphorylation (GO:0042327)	771	4	.22	+	17.80	2.81E-05	1.18E-02
response to hormone (GO:0009725)	791	4	.23	+	17.35	3.11E-05	1.24E-02
multicellular organismal-level homeostasis (GO:0048871)	594	3	.17	+	17.33	4.54E-04	4.43E-02
regulation of leukocyte activation (GO:0002694)	596	3	.17	+	17.27	4.59E-04	4.40E-02
regulation of growth (GO:0040008)	624	3	.18	+	16.50	5.24E-04	4.85E-02

positive regulation of phosphorus metabolic process (GO:0010562)	845	4	.25	+	16.24	4.02E-05	1.45E-02
positive regulation of phosphate metabolic process (GO:0045937)	845	4	.25	+	16.24	4.02E-05	1.42E-02
phosphorylation (GO:0016310)	884	4	.26	+	15.53	4.80E-05	1.55E-02
multicellular organismal reproductive process (GO:0048609)	887	4	.26	+	15.47	4.87E-05	1.54E-02
positive regulation of catalytic activity (GO:0043085)	1112	5	.32	+	15.43	2.67E-06	1.04E-02
tube development (GO:0035295)	900	4	.26	+	15.25	5.15E-05	1.54E-02
multicellular organism reproduction (GO:0032504)	930	4	.27	+	14.76	5.86E-05	1.65E-02
positive regulation of protein modification process (GO:0031401)	935	4	.27	+	14.68	5.98E-05	1.66E-02
developmental process involved in reproduction (GO:0003006)	967	4	.28	+	14.19	6.83E-05	1.71E-02
positive regulation of immune system process (GO:0002684)	977	4	.28	+	14.05	7.11E-05	1.70E-02
apoptotic process (GO:0006915)	1047	4	.31	+	13.11	9.31E-05	1.90E-02
regulation of protein phosphorylation (GO:0001932)	1071	4	.31	+	12.82	1.02E-04	1.88E-02
programmed cell death (GO:0012501)	1093	4	.32	+	12.56	1.10E-04	2.01E-02
cell death (GO:0008219)	1105	4	.32	+	12.42	1.15E-04	2.08E-02
response to abiotic stimulus (GO:0009628)	1118	4	.33	+	12.28	1.20E-04	2.10E-02
cellular response to oxygen-containing compound (GO:1901701)	1146	4	.33	+	11.98	1.32E-04	2.24E-02

regulation of phosphorylation (GO:0042325)	1170	4	.34	+	11.73	1.44E-04	2.32E-02
positive regulation of gene expression (GO:0010628)	1173	4	.34	+	11.70	1.45E-04	2.32E-02
regulation of apoptotic process (GO:0042981)	1471	5	.43	+	11.66	1.06E-05	1.18E-02
regulation of immune system process (GO:0002682)	1488	5	.43	+	11.53	1.12E-05	1.09E-02
positive regulation of molecular function (GO:0044093)	1519	5	.44	+	11.30	1.24E-05	1.07E-02
regulation of programmed cell death (GO:0043067)	1521	5	.44	+	11.28	1.25E-05	1.02E-02
intracellular signal transduction (GO:0035556)	1558	5	.45	+	11.01	1.41E-05	1.04E-02
regulation of phosphate metabolic process (GO:0019220)	1315	4	.38	+	10.44	2.26E-04	3.00E-02
regulation of phosphorus metabolic process (GO:0051174)	1316	4	.38	+	10.43	2.27E-04	2.99E-02
positive regulation of developmental process (GO:0051094)	1319	4	.38	+	10.41	2.29E-04	2.99E-02
positive regulation of multicellular organismal process (GO:0051240)	1654	5	.48	+	10.37	1.89E-05	1.09E-02
response to oxygen-containing compound (GO:1901700)	1681	5	.49	+	10.21	2.04E-05	9.92E-03
regulation of intracellular signal transduction (GO:1902531)	1727	5	.50	+	9.93	2.34E-05	1.07E-02
positive regulation of protein metabolic process (GO:0051247)	1425	4	.42	+	9.63	3.09E-04	3.64E-02

regulation of protein modification process (GO:0031399)	1443	4	.42	+	9.51	3.24E-04	3.68E-02
reproductive process (GO:0022414)	1448	4	.42	+	9.48	3.29E-04	3.70E-02
reproduction (GO:0000003)	1458	4	.42	+	9.41	3.38E-04	3.77E-02
regulation of catalytic activity (GO:0050790)	1827	5	.53	+	9.39	3.08E-05	1.26E-02
response to endogenous stimulus (GO:0009719)	1464	4	.43	+	9.38	3.43E-04	3.75E-02
positive regulation of signal transduction (GO:0009967)	1549	4	.45	+	8.86	4.27E-04	4.25E-02
cellular response to stress (GO:0033554)	1603	4	.47	+	8.56	4.87E-04	4.64E-02
regulation of developmental process (GO:0050793)	2462	6	.72	+	8.36	2.95E-06	7.62E-03
cell development (GO:0048468)	2185	5	.64	+	7.85	7.41E-05	1.72E-02
positive regulation of response to stimulus (GO:0048584)	2203	5	.64	+	7.79	7.71E-05	1.71E-02
anatomical structure morphogenesis (GO:0009653)	2244	5	.65	+	7.65	8.44E-05	1.77E-02
immune system process (GO:0002376)	2277	5	.66	+	7.54	9.06E-05	1.88E-02
animal organ development (GO:0048513)	2925	6	.85	+	7.04	8.27E-06	1.28E-02
positive regulation of cellular metabolic process (GO:0031325)	2976	6	.87	+	6.92	9.17E-06	1.19E-02
regulation of multicellular organismal process (GO:0051239)	2983	6	.87	+	6.90	9.31E-06	1.11E-02
regulation of molecular function (GO:0065009)	2569	5	.75	+	6.68	1.63E-04	2.49E-02

response to organic substance (GO:0010033)	2592	5	.76	+	6.62	1.71E-04	2.48E-02
positive regulation of nitrogen compound metabolic process (GO:0051173)	3121	6	.91	+	6.60	1.22E-05	1.11E-02
positive regulation of macromolecule metabolic process (GO:0010604)	3514	6	1.02	+	5.86	2.48E-05	1.10E-02
system development (GO:0048731)	3553	6	1.04	+	5.79	2.65E-05	1.14E-02
negative regulation of metabolic process (GO:0009892)	2985	5	.87	+	5.75	3.39E-04	3.76E-02
regulation of signal transduction (GO:0009966)	2992	5	.87	+	5.73	3.43E-04	3.78E-02
positive regulation of metabolic process (GO:0009893)	3825	6	1.11	+	5.38	4.13E-05	1.43E-02
regulation of response to stimulus (GO:0048583)	3960	6	1.15	+	5.20	5.08E-05	1.58E-02
multicellular organism development (GO:0007275)	3966	6	1.16	+	5.19	5.13E-05	1.56E-02
signal transduction (GO:0007165)	4819	6	1.40	+	4.27	1.65E-04	2.49E-02
signaling (GO:0023052)	5119	6	1.49	+	4.02	2.37E-04	3.04E-02
anatomical structure development (GO:0048856)	5201	6	1.52	+	3.96	2.61E-04	3.24E-02
cell communication (GO:0007154)	5278	6	1.54	+	3.90	2.85E-04	3.43E-02
regulation of cellular metabolic process (GO:0031323)	5482	6	1.60	+	3.76	3.57E-04	3.83E-02
positive regulation of cellular process (GO:0048522)	5511	6	1.61	+	3.74	3.69E-04	3.92E-02
cellular component organization (GO:0016043)	5560	6	1.62	+	3.70	3.89E-04	4.00E-02
regulation of nitrogen compound	5646	6	1.65	+	3.65	4.26E-04	4.27E-02

metabolic process (GO:0051171)							
developmental process (GO:0032502)	5702	6	1.66	+	3.61	4.52E-04	4.45E-02
cellular component organization or biogenesis (GO:0071840)	5774	6	1.68	+	3.57	4.88E-04	4.62E-02
regulation of primary metabolic process (GO:0080090)	5825	6	1.70	+	3.53	5.14E-04	4.81E-02
cellular metabolic process (GO:0044237)	5828	6	1.70	+	3.53	5.16E-04	4.80E-02

Supplementary Table 4: PANTHER Overrepresentation Test (Haploinsufficient Lung Cancer-Associated Genes)

<table>
<tr><td colspan="4">Analysis Type:</td><td colspan="4">PANTHER Overrepresentation Test (Released 20231017)</td></tr>
<tr><td colspan="4">Annotation Version and Release Date:</td><td colspan="4">GO Ontology database DOI: 10.5281/zenodo.10536401 Released 2024-01-17</td></tr>
<tr><td colspan="4">Analyzed List:</td><td colspan="4">Client Text Box Input (Homo sapiens)</td></tr>
<tr><td colspan="4">Reference List:</td><td colspan="4">Homo sapiens (all genes in database)</td></tr>
<tr><td colspan="4">Test Type:</td><td colspan="4">FISHER</td></tr>
<tr><td colspan="4">Correction:</td><td colspan="4">FDR</td></tr>
<tr><td>GO biological process complete</td><td>Homo sapiens - REFLIST (20592)</td><td>Client Text Box Input (28)</td><td>Client Text Box Input (expected)</td><td>Client Text Box Input (over/under)</td><td>Client Text Box Input (fold Enrichment)</td><td>Client Text Box Input (raw P-value)</td><td>Client Text Box Input (FDR)</td></tr>
<tr><td>regulation of Golgi inheritance (GO:0090170)</td><td>4</td><td>2</td><td>.01</td><td>+</td><td>> 100</td><td>2.66E-05</td><td>1.45E-03</td></tr>
<tr><td>trachea formation (GO:0060440)</td><td>7</td><td>3</td><td>.01</td><td>+</td><td>> 100</td><td>2.67E-07</td><td>2.81E-05</td></tr>
<tr><td>trachea morphogenesis (GO:0060439)</td><td>11</td><td>3</td><td>.01</td><td>+</td><td>> 100</td><td>8.08E-07</td><td>7.33E-05</td></tr>
<tr><td>Bergmann glial cell differentiation (GO:0060020)</td><td>11</td><td>3</td><td>.01</td><td>+</td><td>> 100</td><td>8.08E-07</td><td>7.29E-05</td></tr>
<tr><td>anoikis (GO:0043276)</td><td>12</td><td>3</td><td>.02</td><td>+</td><td>> 100</td><td>1.01E-06</td><td>8.94E-05</td></tr>
<tr><td>ERBB2-ERBB3 signaling pathway (GO:0038133)</td><td>9</td><td>2</td><td>.01</td><td>+</td><td>> 100</td><td>9.71E-05</td><td>4.11E-03</td></tr>
<tr><td>ERBB3 signaling pathway (GO:0038129)</td><td>9</td><td>2</td><td>.01</td><td>+</td><td>> 100</td><td>9.71E-05</td><td>4.10E-03</td></tr>
<tr><td>epithelial cell proliferation involved in prostate gland development (GO:0060767)</td><td>9</td><td>2</td><td>.01</td><td>+</td><td>> 100</td><td>9.71E-05</td><td>4.09E-03</td></tr>
<tr><td>regulation of epithelial cell proliferation involved in prostate gland development (GO:0060768)</td><td>10</td><td>2</td><td>.01</td><td>+</td><td>> 100</td><td>1.16E-04</td><td>4.81E-03</td></tr>
<tr><td>negative regulation of fibroblast</td><td>11</td><td>2</td><td>.01</td><td>+</td><td>> 100</td><td>1.37E-04</td><td>5.48E-03</td></tr>
</table>

migration (GO:0010764)							
genitalia morphogenesis (GO:0035112)	12	2	.02	+	> 100	1.60E-04	6.26E-03
trachea development (GO:0060438)	19	3	.03	+	> 100	3.39E-06	2.59E-04
nucleosome disassembly (GO:0006337)	19	3	.03	+	> 100	3.39E-06	2.57E-04
myoblast proliferation (GO:0051450)	13	2	.02	+	> 100	1.85E-04	7.09E-03
protein-DNA complex disassembly (GO:0032986)	21	3	.03	+	> 100	4.45E-06	3.23E-04
layer formation in cerebral cortex (GO:0021819)	15	2	.02	+	98.06	2.39E-04	8.92E-03
thyroid gland development (GO:0030878)	31	4	.04	+	94.89	1.38E-07	1.62E-05
insulin-like growth factor receptor signaling pathway (GO:0048009)	32	4	.04	+	91.93	1.55E-07	1.74E-05
regulation of Golgi organization (GO:1903358)	16	2	.02	+	91.93	2.68E-04	9.70E-03
thymus development (GO:0048538)	50	6	.07	+	88.25	1.10E-10	4.07E-08
positive regulation of nitric-oxide synthase activity (GO:0051000)	17	2	.02	+	86.52	3.00E-04	1.07E-02
regulation of nucleotide-excision repair (GO:2000819)	28	3	.04	+	78.80	9.83E-06	6.43E-04
regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (GO:1903376)	19	2	.03	+	77.41	3.67E-04	1.25E-02
ERK1 and ERK2 cascade (GO:0070371)	49	5	.07	+	75.04	9.56E-09	1.68E-06
regulation of early endosome to late	20	2	.03	+	73.54	4.04E-04	1.34E-02

endosome transport (GO:2000641)							
animal organ formation (GO:0048645)	40	4	.05	+	73.54	3.56E -07	3.64E -05
stress fiber assembly (GO:0043149)	20	2	.03	+	73.54	4.04E -04	1.34E -02
labyrinthine layer blood vessel development (GO:0060716)	20	2	.03	+	73.54	4.04E -04	1.34E -02
contractile actin filament bundle assembly (GO:0030038)	20	2	.03	+	73.54	4.04E -04	1.33E -02
negative regulation of endothelial cell apoptotic process (GO:2000352)	31	3	.04	+	71.17	1.30E -05	8.15E -04
placenta blood vessel development (GO:0060674)	31	3	.04	+	71.17	1.30E -05	8.12E -04
ERBB signaling pathway (GO:0038127)	65	6	.09	+	67.89	4.77E -10	1.30E -07
positive regulation of myoblast differentiation (GO:0045663)	44	4	.06	+	66.86	5.08E -07	4.93E -05
organ induction (GO:0001759)	22	2	.03	+	66.86	4.82E -04	1.55E -02
regulation of extrinsic apoptotic signaling pathway in absence of ligand (GO:2001239)	46	4	.06	+	63.95	6.00E -07	5.72E -05
ERBB2 signaling pathway (GO:0038128)	23	2	.03	+	63.95	5.23E -04	1.66E -02
negative regulation of cellular senescence (GO:2000773)	24	2	.03	+	61.29	5.66E -04	1.77E -02
male genitalia development (GO:0030539)	24	2	.03	+	61.29	5.66E -04	1.76E -02
negative regulation of extrinsic apoptotic signaling pathway in absence of ligand (GO:2001240)	36	3	.05	+	61.29	1.98E -05	1.15E -03

regulation of G0 to G1 transition (GO:0070316)	36	3	.05	+	61.29	1.98E-05	1.15E-03
negative regulation of signal transduction in absence of ligand (GO:1901099)	36	3	.05	+	61.29	1.98E-05	1.15E-03
epidermal growth factor receptor signaling pathway (GO:0007173)	49	4	.07	+	60.03	7.61E-07	6.94E-05
lung morphogenesis (GO:0060425)	50	4	.07	+	58.83	8.21E-07	7.36E-05
cardiac muscle cell proliferation (GO:0060038)	25	2	.03	+	58.83	6.11E-04	1.87E-02
response to muscle stretch (GO:0035994)	25	2	.03	+	58.83	6.11E-04	1.86E-02
androgen receptor signaling pathway (GO:0030521)	25	2	.03	+	58.83	6.11E-04	1.86E-02
regulation of fibroblast migration (GO:0010762)	38	3	.05	+	58.06	2.31E-05	1.28E-03
lung epithelium development (GO:0060428)	39	3	.05	+	56.57	2.48E-05	1.37E-03
lung epithelial cell differentiation (GO:0060487)	26	2	.04	+	56.57	6.58E-04	1.98E-02
lung cell differentiation (GO:0060479)	26	2	.04	+	56.57	6.58E-04	1.97E-02
regulation of nitric-oxide synthase activity (GO:0050999)	26	2	.04	+	56.57	6.58E-04	1.97E-02
metanephros morphogenesis (GO:0003338)	26	2	.04	+	56.57	6.58E-04	1.97E-02
epithelial tube branching involved in lung morphogenesis (GO:0060441)	27	2	.04	+	54.48	7.06E-04	2.09E-02
regulation of oxidative stress-induced intrinsic apoptotic signaling	42	3	.06	+	52.53	3.06E-05	1.64E-03

pathway (GO:1902175)							
telencephalon glial cell migration (GO:0022030)	28	2	.04	+	52.53	7.56E-04	2.20E-02
positive regulation of monooxygenase activity (GO:0032770)	28	2	.04	+	52.53	7.56E-04	2.20E-02
positive regulation of protein tyrosine kinase activity (GO:0061098)	28	2	.04	+	52.53	7.56E-04	2.19E-02
cerebral cortex radial glia-guided migration (GO:0021801)	28	2	.04	+	52.53	7.56E-04	2.19E-02
Schwann cell development (GO:0014044)	43	3	.06	+	51.31	3.27E-05	1.71E-03
positive regulation of oxidoreductase activity (GO:0051353)	43	3	.06	+	51.31	3.27E-05	1.71E-03
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (GO:1902176)	29	2	.04	+	50.72	8.07E-04	2.29E-02
regulation of axon regeneration (GO:0048679)	29	2	.04	+	50.72	8.07E-04	2.29E-02
regulation of animal organ formation (GO:0003156)	29	2	.04	+	50.72	8.07E-04	2.29E-02
positive regulation of G1/S transition of mitotic cell cycle (GO:1900087)	44	3	.06	+	50.14	3.49E-05	1.78E-03
positive regulation of glucose transmembrane transport (GO:0010828)	44	3	.06	+	50.14	3.49E-05	1.77E-03
sister chromatid cohesion (GO:0007062)	45	3	.06	+	49.03	3.72E-05	1.89E-03
positive regulation of extracellular	30	2	.04	+	49.03	8.60E-04	2.42E-02

matrix organization (GO:1903055)							
positive regulation of signaling receptor activity (GO:2000273)	30	2	.04	+	49.03	8.60E-04	2.41E-02
negative regulation of epithelial cell apoptotic process (GO:1904036)	61	4	.08	+	48.22	1.74E-06	1.45E-04
positive regulation of transforming growth factor beta receptor signaling pathway (GO:0030511)	31	2	.04	+	47.45	9.15E-04	2.54E-02
positive regulation of cellular response to transforming growth factor beta stimulus (GO:1903846)	31	2	.04	+	47.45	9.15E-04	2.54E-02
prostate gland development (GO:0030850)	47	3	.06	+	46.94	4.21E-05	2.08E-03
labyrinthine layer development (GO:0060711)	47	3	.06	+	46.94	4.21E-05	2.08E-03
positive regulation of stem cell proliferation (GO:2000648)	48	3	.07	+	45.96	4.47E-05	2.18E-03
Schwann cell differentiation (GO:0014037)	48	3	.07	+	45.96	4.47E-05	2.17E-03
T cell differentiation in thymus (GO:0033077)	64	4	.09	+	45.96	2.09E-06	1.69E-04
regulation of neuron projection regeneration (GO:0070570)	32	2	.04	+	45.96	9.71E-04	2.66E-02
protein localization to cell surface (GO:0034394)	32	2	.04	+	45.96	9.71E-04	2.65E-02
regulation of mitophagy (GO:1901524)	33	2	.04	+	44.57	1.03E-03	2.80E-02
astrocyte differentiation (GO:0048708)	66	4	.09	+	44.57	2.34E-06	1.87E-04

developmental induction (GO:0031128)	33	2	.04	+	44.57	1.03E-03	2.79E-02
hair follicle morphogenesis (GO:0031069)	33	2	.04	+	44.57	1.03E-03	2.79E-02
negative regulation of macroautophagy (GO:0016242)	33	2	.04	+	44.57	1.03E-03	2.78E-02
long-term synaptic potentiation (GO:0060291)	50	3	.07	+	44.13	5.02E-05	2.41E-03
hematopoietic or lymphoid organ development (GO:0048534)	100	6	.14	+	44.13	5.50E-09	1.06E-06
negative regulation of osteoclast differentiation (GO:0045671)	34	2	.05	+	43.26	1.09E-03	2.91E-02
lipopolysaccharide-mediated signaling pathway (GO:0031663)	34	2	.05	+	43.26	1.09E-03	2.90E-02
cardiac muscle tissue growth (GO:0055017)	34	2	.05	+	43.26	1.09E-03	2.90E-02
regulation of endothelial cell apoptotic process (GO:2000351)	52	3	.07	+	42.43	5.61E-05	2.64E-03
regulation of stress-activated MAPK cascade (GO:0032872)	35	2	.05	+	42.02	1.15E-03	3.01E-02
proximal/distal pattern formation (GO:0009954)	35	2	.05	+	42.02	1.15E-03	3.01E-02
positive regulation of telomere maintenance via telomerase (GO:0032212)	35	2	.05	+	42.02	1.15E-03	3.00E-02
positive T cell selection (GO:0043368)	35	2	.05	+	42.02	1.15E-03	3.00E-02
face development (GO:0060324)	53	3	.07	+	41.63	5.92E-05	2.76E-03
regulation of morphogenesis of a	54	3	.07	+	40.86	6.25E-05	2.88E-03

branching structure (GO:0060688)							
heart growth (GO:0060419)	36	2	.05	+	40.86	1.21E-03	3.11E-02
positive regulation of animal organ morphogenesis (GO:0110110)	36	2	.05	+	40.86	1.21E-03	3.11E-02
smooth muscle cell differentiation (GO:0051145)	36	2	.05	+	40.86	1.21E-03	3.10E-02
response to pain (GO:0048265)	36	2	.05	+	40.86	1.21E-03	3.10E-02
regulation of phospholipase C activity (GO:1900274)	36	2	.05	+	40.86	1.21E-03	3.09E-02
striated muscle cell proliferation (GO:0014855)	36	2	.05	+	40.86	1.21E-03	3.09E-02
positive regulation of glucose import (GO:0046326)	36	2	.05	+	40.86	1.21E-03	3.08E-02
endothelial cell migration (GO:0043542)	73	4	.10	+	40.30	3.44E-06	2.58E-04
peptidyl-threonine phosphorylation (GO:0018107)	55	3	.07	+	40.11	6.58E-05	3.02E-03
cerebral cortex radially oriented cell migration (GO:0021799)	37	2	.05	+	39.75	1.28E-03	3.23E-02
epidermis morphogenesis (GO:0048730)	37	2	.05	+	39.75	1.28E-03	3.23E-02
positive regulation of morphogenesis of an epithelium (GO:1905332)	37	2	.05	+	39.75	1.28E-03	3.22E-02
regulation of myoblast differentiation (GO:0045661)	75	4	.10	+	39.22	3.81E-06	2.81E-04
epithelial cell apoptotic process (GO:1904019)	57	3	.08	+	38.71	7.29E-05	3.25E-03
endothelial cell proliferation (GO:0001935)	38	2	.05	+	38.71	1.34E-03	3.36E-02

cellular response to cadmium ion (GO:0071276)	38	2	.05	+	38.71	1.34E-03	3.36E-02
regulation of ubiquitin-protein transferase activity (GO:0051438)	38	2	.05	+	38.71	1.34E-03	3.35E-02
spleen development (GO:0048536)	38	2	.05	+	38.71	1.34E-03	3.35E-02
positive regulation of telomere maintenance via telomere lengthening (GO:1904358)	38	2	.05	+	38.71	1.34E-03	3.34E-02
transcription initiation-coupled chromatin remodeling (GO:0045815)	38	2	.05	+	38.71	1.34E-03	3.34E-02
negative regulation of Notch signaling pathway (GO:0045746)	39	2	.05	+	37.71	1.41E-03	3.47E-02
regulation of monooxygenase activity (GO:0032768)	39	2	.05	+	37.71	1.41E-03	3.47E-02
regulation of cell migration involved in sprouting angiogenesis (GO:0090049)	39	2	.05	+	37.71	1.41E-03	3.46E-02
regulation of stress-activated protein kinase signaling cascade (GO:0070302)	39	2	.05	+	37.71	1.41E-03	3.46E-02
positive regulation of cell cycle G1/S phase transition (GO:1902808)	59	3	.08	+	37.39	8.04E-05	3.52E-03
positive regulation of gene expression, epigenetic (GO:0141137)	40	2	.05	+	36.77	1.48E-03	3.61E-02
response to cadmium ion (GO:0046686)	61	3	.08	+	36.17	8.84E-05	3.81E-03
mammary gland epithelium	61	3	.08	+	36.17	8.84E-05	3.79E-03

development (GO:0061180)							
regulation of autophagy of mitochondrion (GO:1903146)	41	2	.06	+	35.87	1.55E-03	3.75E-02
regulation of protein localization to cell surface (GO:2000008)	41	2	.06	+	35.87	1.55E-03	3.75E-02
positive regulation of glucose metabolic process (GO:0010907)	41	2	.06	+	35.87	1.55E-03	3.74E-02
negative regulation of gliogenesis (GO:0014014)	42	2	.06	+	35.02	1.62E-03	3.91E-02
urogenital system development (GO:0001655)	64	3	.09	+	34.47	1.01E-04	4.24E-03
T cell costimulation (GO:0031295)	43	2	.06	+	34.21	1.70E-03	4.08E-02
positive regulation of substrate adhesion-dependent cell spreading (GO:1900026)	43	2	.06	+	34.21	1.70E-03	4.07E-02
peptidyl-threonine modification (GO:0018210)	65	3	.09	+	33.94	1.06E-04	4.42E-03
regulation of morphogenesis of an epithelium (GO:1905330)	65	3	.09	+	33.94	1.06E-04	4.41E-03
muscle cell proliferation (GO:0033002)	44	2	.06	+	33.43	1.77E-03	4.24E-02
lymphocyte costimulation (GO:0031294)	44	2	.06	+	33.43	1.77E-03	4.23E-02
T cell homeostasis (GO:0043029)	44	2	.06	+	33.43	1.77E-03	4.22E-02
cerebellum morphogenesis (GO:0021587)	45	2	.06	+	32.69	1.85E-03	4.39E-02
cellular response to vascular endothelial growth factor stimulus (GO:0035924)	45	2	.06	+	32.69	1.85E-03	4.38E-02

regulation of mitotic metaphase/anaphase transition (GO:0030071)	90	4	.12	+	32.69	7.62E-06	5.21E-04
positive regulation of mitotic cell cycle phase transition (GO:1901992)	91	4	.12	+	32.33	7.95E-06	5.39E-04
regulation of oxidoreductase activity (GO:0051341)	69	3	.09	+	31.98	1.26E-04	5.16E-03
positive regulation of neuron apoptotic process (GO:0043525)	69	3	.09	+	31.98	1.26E-04	5.15E-03
insulin receptor signaling pathway (GO:0008286)	69	3	.09	+	31.98	1.26E-04	5.13E-03
regulation of cellular senescence (GO:2000772)	46	2	.06	+	31.98	1.93E-03	4.55E-02
response to epidermal growth factor (GO:0070849)	46	2	.06	+	31.98	1.93E-03	4.55E-02
regulation of myelination (GO:0031641)	46	2	.06	+	31.98	1.93E-03	4.54E-02
endodermal cell differentiation (GO:0035987)	46	2	.06	+	31.98	1.93E-03	4.53E-02
regulation of long-term synaptic potentiation (GO:1900271)	46	2	.06	+	31.98	1.93E-03	4.53E-02
substrate adhesion-dependent cell spreading (GO:0034446)	46	2	.06	+	31.98	1.93E-03	4.52E-02
cellular response to dopamine (GO:1903351)	46	2	.06	+	31.98	1.93E-03	4.51E-02
T cell receptor signaling pathway (GO:0050852)	116	5	.16	+	31.70	5.65E-07	5.41E-05
regulation of metaphase/anaphase transition of cell cycle (GO:1902099)	93	4	.13	+	31.63	8.64E-06	5.78E-04

lymphocyte homeostasis (GO:0002260)	70	3	.10	+	31.52	1.31E-04	5.25E-03
pancreas development (GO:0031016)	70	3	.10	+	31.52	1.31E-04	5.24E-03
regulation of G1/S transition of mitotic cell cycle (GO:2000045)	164	7	.22	+	31.39	2.44E-09	5.55E-07
regulation of cell cycle G1/S phase transition (GO:1902806)	191	8	.26	+	30.80	1.72E-10	5.70E-08
hindbrain morphogenesis (GO:0021575)	48	2	.07	+	30.64	2.09E-03	4.85E-02
positive regulation of stem cell population maintenance (GO:1902459)	48	2	.07	+	30.64	2.09E-03	4.85E-02
T cell selection (GO:0045058)	48	2	.07	+	30.64	2.09E-03	4.84E-02
genitalia development (GO:0048806)	48	2	.07	+	30.64	2.09E-03	4.83E-02
negative regulation of cold-induced thermogenesis (GO:0120163)	48	2	.07	+	30.64	2.09E-03	4.82E-02
cellular response to nerve growth factor stimulus (GO:1990090)	48	2	.07	+	30.64	2.09E-03	4.82E-02
glial cell migration (GO:0008347)	48	2	.07	+	30.64	2.09E-03	4.81E-02
response to dopamine (GO:1903350)	48	2	.07	+	30.64	2.09E-03	4.80E-02
positive regulation of TOR signaling (GO:0032008)	72	3	.10	+	30.64	1.42E-04	5.64E-03
positive regulation of mitotic cell cycle (GO:0045931)	122	5	.17	+	30.14	7.18E-07	6.64E-05
cerebral cortex cell migration (GO:0021795)	49	2	.07	+	30.02	2.18E-03	4.97E-02
cellular response to catecholamine	49	2	.07	+	30.02	2.18E-03	4.96E-02

stimulus (GO:0071870)							
cellular response to monoamine stimulus (GO:0071868)	49	2	.07	+	30.02	2.18E-03	4.96E-02
canonical NF-kappaB signal transduction (GO:0007249)	49	2	.07	+	30.02	2.18E-03	4.95E-02
digestive tract morphogenesis (GO:0048546)	49	2	.07	+	30.02	2.18E-03	4.94E-02
negative regulation of epithelial cell differentiation (GO:0030857)	49	2	.07	+	30.02	2.18E-03	4.94E-02
regulation of glucose transmembrane transport (GO:0010827)	75	3	.10	+	29.42	1.59E-04	6.24E-03
epithelial cell proliferation (GO:0050673)	178	7	.24	+	28.92	4.22E-09	8.69E-07
regulation of epithelial cell apoptotic process (GO:1904035)	103	4	.14	+	28.56	1.27E-05	8.00E-04
epithelial cell migration (GO:0010631)	104	4	.14	+	28.29	1.32E-05	8.16E-04
regulation of sister chromatid segregation (GO:0033045)	105	4	.14	+	28.02	1.37E-05	8.43E-04
alpha-beta T cell differentiation (GO:0046632)	79	3	.11	+	27.93	1.85E-04	7.08E-03
positive regulation of axonogenesis (GO:0050772)	80	3	.11	+	27.58	1.92E-04	7.32E-03
epithelium migration (GO:0090132)	107	4	.15	+	27.49	1.47E-05	8.99E-04
glial cell differentiation (GO:0010001)	218	8	.30	+	26.99	4.73E-10	1.31E-07
regulation of stem cell proliferation (GO:0072091)	83	3	.11	+	26.58	2.13E-04	8.03E-03
positive regulation of cell cycle phase transition (GO:1901989)	111	4	.15	+	26.50	1.70E-05	1.01E-03

immune system development (GO:0002520)	167	6	.23	+	26.42	1.03E-07	1.29E-05
positive regulation of smooth muscle cell proliferation (GO:0048661)	85	3	.12	+	25.96	2.28E-04	8.55E-03
positive regulation of Wnt signaling pathway (GO:0030177)	142	5	.19	+	25.90	1.48E-06	1.25E-04
tissue migration (GO:0090130)	114	4	.16	+	25.80	1.88E-05	1.10E-03
positive regulation of double-strand break repair (GO:2000781)	86	3	.12	+	25.65	2.35E-04	8.82E-03
embryonic placenta development (GO:0001892)	87	3	.12	+	25.36	2.43E-04	9.01E-03
associative learning (GO:0008306)	88	3	.12	+	25.07	2.51E-04	9.28E-03
negative regulation of protein modification by small protein conjugation or removal (GO:1903321)	88	3	.12	+	25.07	2.51E-04	9.26E-03
positive regulation of binding (GO:0051099)	118	4	.16	+	24.93	2.14E-05	1.22E-03
negative regulation of protein serine/threonine kinase activity (GO:0071901)	89	3	.12	+	24.79	2.60E-04	9.49E-03
peripheral nervous system development (GO:0007422)	90	3	.12	+	24.51	2.68E-04	9.73E-03
negative regulation of autophagy (GO:0010507)	90	3	.12	+	24.51	2.68E-04	9.71E-03
regulation of fibroblast proliferation (GO:0048145)	91	3	.12	+	24.24	2.77E-04	9.97E-03
regulation of T cell differentiation (GO:0045580)	183	6	.25	+	24.11	1.74E-07	1.93E-05

negative regulation of post-translational protein modification (GO:1901874)	92	3	.13	+	23.98	2.85E-04	1.03E-02
regulation of stress fiber assembly (GO:0051492)	92	3	.13	+	23.98	2.85E-04	1.02E-02
regulation of blood vessel endothelial cell migration (GO:0043535)	92	3	.13	+	23.98	2.85E-04	1.02E-02
gliogenesis (GO:0042063)	277	9	.38	+	23.89	9.19E-11	3.59E-08
glial cell development (GO:0021782)	128	4	.17	+	22.98	2.92E-05	1.58E-03
negative regulation of extrinsic apoptotic signaling pathway (GO:2001237)	97	3	.13	+	22.75	3.32E-04	1.17E-02
leukocyte homeostasis (GO:0001776)	97	3	.13	+	22.75	3.32E-04	1.17E-02
positive regulation of protein localization to nucleus (GO:1900182)	97	3	.13	+	22.75	3.32E-04	1.16E-02
antigen receptor-mediated signaling pathway (GO:0050851)	162	5	.22	+	22.70	2.77E-06	2.17E-04
positive regulation of DNA repair (GO:0045739)	130	4	.18	+	22.63	3.09E-05	1.65E-03
regulation of Notch signaling pathway (GO:0008593)	98	3	.13	+	22.51	3.42E-04	1.19E-02
regulation of chromosome segregation (GO:0051983)	131	4	.18	+	22.46	3.18E-05	1.69E-03
regulation of double-strand break repair (GO:2000779)	132	4	.18	+	22.29	3.28E-05	1.71E-03
endocrine system development (GO:0035270)	132	4	.18	+	22.29	3.28E-05	1.70E-03
regulation of dendrite	99	3	.13	+	22.29	3.52E-04	1.21E-02

development (GO:0050773)							
regulation of Wnt signaling pathway (GO:0030111)	336	10	.46	+	21.89	1.56E-11	1.19E-08
regulation of actomyosin structure organization (GO:0110020)	102	3	.14	+	21.63	3.83E-04	1.30E-02
organ growth (GO:0035265)	102	3	.14	+	21.63	3.83E-04	1.30E-02
regulation of actin filament bundle assembly (GO:0032231)	104	3	.14	+	21.21	4.05E-04	1.33E-02
oogenesis (GO:0048477)	104	3	.14	+	21.21	4.05E-04	1.33E-02
regulation of smooth muscle cell proliferation (GO:0048660)	139	4	.19	+	21.16	3.99E-05	1.99E-03
positive regulation of endothelial cell migration (GO:0010595)	106	3	.14	+	20.81	4.28E-04	1.40E-02
MAPK cascade (GO:0000165)	213	6	.29	+	20.72	4.15E-07	4.17E-05
regulation of TOR signaling (GO:0032006)	143	4	.19	+	20.57	4.44E-05	2.17E-03
regulation of lymphocyte differentiation (GO:0045619)	215	6	.29	+	20.52	4.38E-07	4.34E-05
nucleosome organization (GO:0034728)	108	3	.15	+	20.43	4.51E-04	1.46E-02
regulation of leukocyte differentiation (GO:1902105)	327	9	.44	+	20.24	3.83E-10	1.08E-07
alpha-beta T cell activation (GO:0046631)	109	3	.15	+	20.24	4.63E-04	1.49E-02
T cell differentiation (GO:0030217)	184	5	.25	+	19.98	5.08E-06	3.64E-04
cellular response to insulin stimulus (GO:0032869)	149	4	.20	+	19.74	5.19E-05	2.48E-03
negative regulation of leukocyte	112	3	.15	+	19.70	5.00E-04	1.60E-02

differentiation (GO:1902106)							
developmental cell growth (GO:0048588)	112	3	.15	+	19.70	5.00E-04	1.60E-02
positive regulation of epithelial cell migration (GO:0010634)	151	4	.21	+	19.48	5.46E-05	2.59E-03
lung development (GO:0030324)	189	5	.26	+	19.46	5.77E-06	4.11E-04
regulation of circadian rhythm (GO:0042752)	114	3	.16	+	19.35	5.26E-04	1.67E-02
cell growth (GO:0016049)	114	3	.16	+	19.35	5.26E-04	1.66E-02
epigenetic regulation of gene expression (GO:0040029)	192	5	.26	+	19.15	6.22E-06	4.39E-04
respiratory tube development (GO:0030323)	193	5	.26	+	19.05	6.37E-06	4.48E-04
regulation of extrinsic apoptotic signaling pathway (GO:2001236)	155	4	.21	+	18.98	6.03E-05	2.80E-03
negative regulation of apoptotic signaling pathway (GO:2001234)	234	6	.32	+	18.86	7.10E-07	6.60E-05
negative regulation of hemopoiesis (GO:1903707)	117	3	.16	+	18.86	5.66E-04	1.77E-02
stem cell population maintenance (GO:0019827)	117	3	.16	+	18.86	5.66E-04	1.77E-02
positive regulation of T cell differentiation (GO:0045582)	119	3	.16	+	18.54	5.94E-04	1.82E-02
female gamete generation (GO:0007292)	159	4	.22	+	18.50	6.65E-05	3.04E-03
skin epidermis development (GO:0098773)	120	3	.16	+	18.39	6.08E-04	1.86E-02
maintenance of cell number (GO:0098727)	121	3	.16	+	18.23	6.23E-04	1.88E-02

regulation of neuron apoptotic process (GO:0043523)	243	6	.33	+	18.16	8.80E-07	7.85E-05
negative regulation of neuron apoptotic process (GO:0043524)	162	4	.22	+	18.16	7.13E-05	3.19E-03
negative regulation of protein kinase activity (GO:0006469)	164	4	.22	+	17.94	7.47E-05	3.30E-03
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	164	4	.22	+	17.94	7.47E-05	3.29E-03
regulation of mononuclear cell migration (GO:0071675)	124	3	.17	+	17.79	6.68E-04	1.99E-02
regulation of chromosome organization (GO:0033044)	249	6	.34	+	17.72	1.01E-06	8.91E-05
regulation of endothelial cell migration (GO:0010594)	168	4	.23	+	17.51	8.19E-05	3.58E-03
positive regulation of T cell activation (GO:0050870)	253	6	.34	+	17.44	1.11E-06	9.59E-05
positive regulation of ERK1 and ERK2 cascade (GO:0070374)	211	5	.29	+	17.43	9.72E-06	6.39E-04
regulation of T cell activation (GO:0050863)	380	9	.52	+	17.42	1.39E-09	3.31E-07
positive regulation of transmembrane transport (GO:0034764)	213	5	.29	+	17.26	1.02E-05	6.62E-04
mammary gland development (GO:0030879)	128	3	.17	+	17.24	7.31E-04	2.15E-02
myelination (GO:0042552)	128	3	.17	+	17.24	7.31E-04	2.15E-02
regulation of myeloid leukocyte differentiation (GO:0002761)	128	3	.17	+	17.24	7.31E-04	2.15E-02

regulation of DNA repair (GO:0006282)	214	5	.29	+	17.18	1.04E-05	6.74E-04
positive regulation of protein kinase activity (GO:0045860)	257	6	.35	+	17.17	1.21E-06	1.04E-04
gland development (GO:0048732)	430	10	.58	+	17.10	1.65E-10	5.57E-08
regulation of protein binding (GO:0043393)	129	3	.18	+	17.10	7.47E-04	2.18E-02
regulation of canonical Wnt signaling pathway (GO:0060828)	259	6	.35	+	17.04	1.27E-06	1.08E-04
respiratory system development (GO:0060541)	216	5	.29	+	17.02	1.09E-05	7.02E-04
regulation of macroautophagy (GO:0016241)	173	4	.24	+	17.00	9.15E-05	3.91E-03
positive regulation of DNA metabolic process (GO:0051054)	303	7	.41	+	16.99	1.46E-07	1.68E-05
ensheathment of neurons (GO:0007272)	130	3	.18	+	16.97	7.64E-04	2.21E-02
cellular response to reactive oxygen species (GO:0034614)	130	3	.18	+	16.97	7.64E-04	2.20E-02
axon ensheathment (GO:0008366)	130	3	.18	+	16.97	7.64E-04	2.20E-02
positive regulation of kinase activity (GO:0033674)	304	7	.41	+	16.93	1.50E-07	1.69E-05
negative regulation of kinase activity (GO:0033673)	175	4	.24	+	16.81	9.55E-05	4.07E-03
positive regulation of supramolecular fiber organization (GO:1902905)	175	4	.24	+	16.81	9.55E-05	4.06E-03
digestive tract development (GO:0048565)	133	3	.18	+	16.59	8.15E-04	2.30E-02
regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	222	5	.30	+	16.56	1.24E-05	7.85E-04

positive regulation of lymphocyte differentiation (GO:0045621)	134	3	.18	+	16.46	8.32E-04	2.35E-02
epithelial tube formation (GO:0072175)	134	3	.18	+	16.46	8.32E-04	2.34E-02
negative regulation of epithelial cell proliferation (GO:0050680)	136	3	.18	+	16.22	8.68E-04	2.43E-02
regulation of hemopoiesis (GO:1903706)	409	9	.56	+	16.18	2.61E-09	5.84E-07
branching morphogenesis of an epithelial tube (GO:0048754)	137	3	.19	+	16.10	8.86E-04	2.47E-02
regulation of epithelial cell migration (GO:0010632)	229	5	.31	+	16.06	1.43E-05	8.77E-04
positive regulation of leukocyte cell-cell adhesion (GO:1903039)	276	6	.38	+	15.99	1.81E-06	1.50E-04
positive regulation of lymphocyte activation (GO:0051251)	328	7	.45	+	15.70	2.48E-07	2.62E-05
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	422	9	.57	+	15.68	3.40E-09	7.21E-07
positive regulation of transferase activity (GO:0051347)	376	8	.51	+	15.65	3.02E-08	4.38E-06
positive regulation of synaptic transmission (GO:0050806)	141	3	.19	+	15.65	9.61E-04	2.65E-02
developmental growth involved in morphogenesis (GO:0060560)	141	3	.19	+	15.65	9.61E-04	2.64E-02
positive regulation of leukocyte differentiation (GO:1902107)	189	4	.26	+	15.56	1.28E-04	5.19E-03

negative regulation of cell growth (GO:0030308)	189	4	.26	+	15.56	1.28E-04	5.18E-03
positive regulation of hemopoiesis (GO:1903708)	189	4	.26	+	15.56	1.28E-04	5.17E-03
regulation of apoptotic signaling pathway (GO:2001233)	381	8	.52	+	15.44	3.34E-08	4.75E-06
regulation of mitotic cell cycle phase transition (GO:1901990)	334	7	.45	+	15.41	2.79E-07	2.90E-05
regulation of binding (GO:0051098)	240	5	.33	+	15.32	1.79E-05	1.05E-03
digestive system development (GO:0055123)	145	3	.20	+	15.22	1.04E-03	2.81E-02
protein-containing complex disassembly (GO:0032984)	146	3	.20	+	15.11	1.06E-03	2.85E-02
positive regulation of chemotaxis (GO:0050921)	146	3	.20	+	15.11	1.06E-03	2.85E-02
tube formation (GO:0035148)	147	3	.20	+	15.01	1.08E-03	2.89E-02
positive regulation of neurogenesis (GO:0050769)	246	5	.33	+	14.95	2.01E-05	1.15E-03
lymphocyte differentiation (GO:0030098)	296	6	.40	+	14.91	2.70E-06	2.12E-04
regulation of protein ubiquitination (GO:0031396)	198	4	.27	+	14.86	1.52E-04	6.01E-03
morphogenesis of embryonic epithelium (GO:0016331)	149	3	.20	+	14.81	1.12E-03	2.97E-02
ameboidal-type cell migration (GO:0001667)	200	4	.27	+	14.71	1.58E-04	6.23E-03
regulation of protein localization to nucleus (GO:1900180)	150	3	.20	+	14.71	1.15E-03	3.01E-02
regulation of mitochondrion organization (GO:0010821)	150	3	.20	+	14.71	1.15E-03	3.00E-02

immune response-activating cell surface receptor signaling pathway (GO:0002429)	250	5	.34	+	14.71	2.17E-05	1.23E-03
regulation of lymphocyte activation (GO:0051249)	502	10	.68	+	14.65	7.17E-10	1.82E-07
placenta development (GO:0001890)	151	3	.21	+	14.61	1.17E-03	3.03E-02
regulation of cold-induced thermogenesis (GO:0120161)	151	3	.21	+	14.61	1.17E-03	3.02E-02
positive regulation of cell development (GO:0010720)	453	9	.62	+	14.61	6.23E-09	1.17E-06
regulation of synaptic plasticity (GO:0048167)	203	4	.28	+	14.49	1.67E-04	6.49E-03
regulation of autophagy (GO:0010506)	357	7	.49	+	14.42	4.34E-07	4.32E-05
positive regulation of leukocyte activation (GO:0002696)	360	7	.49	+	14.30	4.58E-07	4.51E-05
response to UV (GO:0009411)	156	3	.21	+	14.14	1.28E-03	3.22E-02
protein autophosphorylation (GO:0046777)	156	3	.21	+	14.14	1.28E-03	3.22E-02
learning (GO:0007612)	156	3	.21	+	14.14	1.28E-03	3.21E-02
regulation of axonogenesis (GO:0050770)	158	3	.21	+	13.96	1.33E-03	3.32E-02
phagocytosis (GO:0006909)	159	3	.22	+	13.88	1.35E-03	3.35E-02
positive regulation of neuron projection development (GO:0010976)	159	3	.22	+	13.88	1.35E-03	3.34E-02
regulation of leukocyte cell-cell adhesion (GO:1903037)	371	7	.50	+	13.88	5.59E-07	5.39E-05
negative regulation of transferase	214	4	.29	+	13.75	2.04E-04	7.73E-03

activity (GO:0051348)							
hindbrain development (GO:0030902)	161	3	.22	+	13.70	1.40E-03	3.45E-02
positive regulation of cell activation (GO:0050867)	378	7	.51	+	13.62	6.32E-07	5.99E-05
positive regulation of cell-cell adhesion (GO:0022409)	325	6	.44	+	13.58	4.57E-06	3.29E-04
regulation of cell cycle phase transition (GO:1901987)	434	8	.59	+	13.56	8.93E-08	1.13E-05
response to insulin (GO:0032868)	217	4	.30	+	13.56	2.15E-04	8.09E-03
regulation of mitotic cell cycle (GO:0007346)	498	9	.68	+	13.29	1.39E-08	2.34E-06
morphogenesis of a branching epithelium (GO:0061138)	166	3	.23	+	13.29	1.52E-03	3.69E-02
anatomical structure homeostasis (GO:0060249)	224	4	.30	+	13.13	2.42E-04	9.00E-03
tissue homeostasis (GO:0001894)	224	4	.30	+	13.13	2.42E-04	8.97E-03
homeostasis of number of cells (GO:0048872)	282	5	.38	+	13.04	3.81E-05	1.92E-03
mononuclear cell differentiation (GO:1903131)	339	6	.46	+	13.02	5.80E-06	4.11E-04
immune response-regulating cell surface receptor signaling pathway (GO:0002768)	283	5	.38	+	12.99	3.88E-05	1.94E-03
regulation of leukocyte activation (GO:0002694)	566	10	.77	+	12.99	2.23E-09	5.16E-07
regulation of cell activation (GO:0050865)	623	11	.85	+	12.99	2.84E-10	8.18E-08
regulation of cellular response to stress (GO:0080135)	511	9	.69	+	12.95	1.74E-08	2.78E-06
negative regulation of protein	284	5	.39	+	12.95	3.94E-05	1.97E-03

phosphorylation (GO:0001933)							
mesenchymal cell differentiation (GO:0048762)	172	3	.23	+	12.83	1.68E-03	4.05E-02
regulation of DNA metabolic process (GO:0051052)	522	9	.71	+	12.68	2.08E-08	3.27E-06
regulation of protein kinase activity (GO:0045859)	464	8	.63	+	12.68	1.48E-07	1.68E-05
regulation of kinase activity (GO:0043549)	527	9	.72	+	12.56	2.25E-08	3.51E-06
positive regulation of nervous system development (GO:0051962)	294	5	.40	+	12.51	4.63E-05	2.24E-03
morphogenesis of a branching structure (GO:0001763)	177	3	.24	+	12.46	1.83E-03	4.34E-02
response to reactive oxygen species (GO:0000302)	177	3	.24	+	12.46	1.83E-03	4.33E-02
regulation of ERK1 and ERK2 cascade (GO:0070372)	296	5	.40	+	12.42	4.78E-05	2.31E-03
positive regulation of cell projection organization (GO:0031346)	358	6	.49	+	12.33	7.88E-06	5.36E-04
regulation of epithelial cell proliferation (GO:0050678)	361	6	.49	+	12.22	8.25E-06	5.57E-04
regulation of protein modification by small protein conjugation or removal (GO:1903320)	241	4	.33	+	12.21	3.18E-04	1.13E-02
regulation of synapse organization (GO:0050807)	242	4	.33	+	12.16	3.23E-04	1.14E-02
regulation of intrinsic apoptotic signaling pathway (GO:2001242)	182	3	.25	+	12.12	1.97E-03	4.60E-02
positive regulation of cell adhesion (GO:0045785)	486	8	.66	+	12.11	2.09E-07	2.26E-05

negative regulation of phosphorylation (GO:0042326)	304	5	.41	+	12.10	5.42E-05	2.58E-03
negative regulation of growth (GO:0045926)	244	4	.33	+	12.06	3.33E-04	1.16E-02
vasculature development (GO:0001944)	551	9	.75	+	12.01	3.28E-08	4.72E-06
regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction (GO:0051896)	245	4	.33	+	12.01	3.38E-04	1.18E-02
positive regulation of cytoskeleton organization (GO:0051495)	184	3	.25	+	11.99	2.03E-03	4.74E-02
regulation of post-translational protein modification (GO:1901873)	246	4	.33	+	11.96	3.44E-04	1.19E-02
cell-substrate adhesion (GO:0031589)	185	3	.25	+	11.93	2.07E-03	4.80E-02
cellular response to peptide hormone stimulus (GO:0071375)	248	4	.34	+	11.86	3.54E-04	1.22E-02
regulation of synapse structure or activity (GO:0050803)	248	4	.34	+	11.86	3.54E-04	1.22E-02
positive regulation of phosphorylation (GO:0042327)	622	10	.85	+	11.82	5.43E-09	1.06E-06
response to growth factor (GO:0070848)	506	8	.69	+	11.63	2.83E-07	2.91E-05
response to peptide hormone (GO:0043434)	380	6	.52	+	11.61	1.10E-05	7.05E-04
response to light stimulus (GO:0009416)	318	5	.43	+	11.56	6.68E-05	3.05E-03
positive regulation of cell cycle process (GO:0090068)	255	4	.35	+	11.54	3.93E-04	1.32E-02
regulation of cellular response to growth	319	5	.43	+	11.53	6.78E-05	3.09E-03

factor stimulus (GO:0090287)							
positive regulation of protein phosphorylation (GO:0001934)	576	9	.78	+	11.49	4.78E-08	6.56E-06
cell fate commitment (GO:0045165)	256	4	.35	+	11.49	3.98E-04	1.33E-02
regulation of transferase activity (GO:0051338)	640	10	.87	+	11.49	7.10E-09	1.32E-06
immune response-activating signaling pathway (GO:0002757)	321	5	.44	+	11.46	6.98E-05	3.15E-03
regulation of cell development (GO:0060284)	836	13	1.14	+	11.44	1.88E-11	1.31E-08
T cell activation (GO:0042110)	322	5	.44	+	11.42	7.08E-05	3.19E-03
positive regulation of cell cycle (GO:0045787)	324	5	.44	+	11.35	7.29E-05	3.24E-03
regulation of neurogenesis (GO:0050767)	389	6	.53	+	11.34	1.25E-05	7.93E-04
regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090092)	263	4	.36	+	11.19	4.41E-04	1.43E-02
regulation of protein serine/threonine kinase activity (GO:0071900)	264	4	.36	+	11.14	4.47E-04	1.45E-02
blood vessel development (GO:0001568)	530	8	.72	+	11.10	4.00E-07	4.06E-05
regulation of nervous system development (GO:0051960)	464	7	.63	+	11.09	2.42E-06	1.92E-04
regulation of leukocyte proliferation (GO:0070663)	266	4	.36	+	11.06	4.60E-04	1.48E-02

positive regulation of cell differentiation (GO:0045597)	871	13	1.18	+	10.98	3.12E-11	1.76E-08
regulation of actin filament organization (GO:0110053)	271	4	.37	+	10.86	4.92E-04	1.58E-02
multicellular organismal-level homeostasis (GO:0048871)	611	9	.83	+	10.83	7.85E-08	1.01E-05
enzyme-linked receptor protein signaling pathway (GO:0007167)	614	9	.83	+	10.78	8.18E-08	1.05E-05
negative regulation of protein modification process (GO:0031400)	412	6	.56	+	10.71	1.73E-05	1.02E-03
cellular response to chemical stress (GO:0062197)	278	4	.38	+	10.58	5.41E-04	1.71E-02
regulation of cell-cell adhesion (GO:0022407)	487	7	.66	+	10.57	3.32E-06	2.54E-04
positive regulation of phosphorus metabolic process (GO:0010562)	700	10	.95	+	10.51	1.65E-08	2.73E-06
positive regulation of phosphate metabolic process (GO:0045937)	700	10	.95	+	10.51	1.65E-08	2.70E-06
learning or memory (GO:0007611)	280	4	.38	+	10.51	5.56E-04	1.75E-02
regulation of protein phosphorylation (GO:0001932)	913	13	1.24	+	10.47	5.56E-11	2.73E-08
negative regulation of cell development (GO:0010721)	281	4	.38	+	10.47	5.63E-04	1.77E-02
protein phosphorylation (GO:0006468)	492	7	.67	+	10.46	3.55E-06	2.64E-04
regulation of cell growth (GO:0001558)	423	6	.58	+	10.43	2.00E-05	1.15E-03
regulation of phosphorylation (GO:0042325)	989	14	1.34	+	10.41	8.04E-12	7.21E-09

muscle cell differentiation (GO:0042692)	283	4	.38	+	10.39	5.78E-04	1.79E-02
immune response-regulating signaling pathway (GO:0002764)	356	5	.48	+	10.33	1.13E-04	4.69E-03
skin development (GO:0043588)	285	4	.39	+	10.32	5.93E-04	1.82E-02
blood vessel morphogenesis (GO:0048514)	431	6	.59	+	10.24	2.22E-05	1.26E-03
leukocyte differentiation (GO:0002521)	432	6	.59	+	10.21	2.25E-05	1.27E-03
growth (GO:0040007)	432	6	.59	+	10.21	2.25E-05	1.26E-03
developmental growth (GO:0048589)	432	6	.59	+	10.21	2.25E-05	1.26E-03
negative regulation of cell migration (GO:0030336)	288	4	.39	+	10.21	6.17E-04	1.87E-02
positive regulation of organelle organization (GO:0010638)	504	7	.69	+	10.21	4.15E-06	3.04E-04
regulation of cell cycle process (GO:0010564)	726	10	.99	+	10.13	2.31E-08	3.56E-06
negative regulation of phosphate metabolic process (GO:0045936)	365	5	.50	+	10.07	1.27E-04	5.16E-03
cell population proliferation (GO:0008283)	732	10	1.00	+	10.05	2.50E-08	3.81E-06
negative regulation of phosphorus metabolic process (GO:0010563)	366	5	.50	+	10.05	1.28E-04	5.16E-03
negative regulation of cell motility (GO:2000146)	303	4	.41	+	9.71	7.44E-04	2.18E-02
regulation of neuron projection development (GO:0010975)	459	6	.62	+	9.61	3.15E-05	1.67E-03
regulation of actin filament-based	383	5	.52	+	9.60	1.58E-04	6.21E-03

process (GO:0032970)							
embryonic organ development (GO:0048568)	460	6	.63	+	9.59	3.19E-05	1.68E-03
response to peptide (GO:1901652)	462	6	.63	+	9.55	3.26E-05	1.71E-03
cellular response to peptide (GO:1901653)	308	4	.42	+	9.55	7.90E-04	2.26E-02
regulation of small GTPase mediated signal transduction (GO:0051056)	308	4	.42	+	9.55	7.90E-04	2.26E-02
activation of immune response (GO:0002253)	387	5	.53	+	9.50	1.66E-04	6.45E-03
positive regulation of cell migration (GO:0030335)	543	7	.74	+	9.48	6.73E-06	4.68E-04
positive regulation of MAPK cascade (GO:0043410)	467	6	.64	+	9.45	3.46E-05	1.77E-03
cellular response to organonitrogen compound (GO:0071417)	547	7	.74	+	9.41	7.05E-06	4.86E-04
regulation of supramolecular fiber organization (GO:1902903)	391	5	.53	+	9.40	1.74E-04	6.73E-03
regulation of cell adhesion (GO:0030155)	789	10	1.07	+	9.32	5.02E-08	6.77E-06
regulation of organelle organization (GO:0033043)	1185	15	1.61	+	9.31	4.99E-12	5.43E-09
cellular response to growth factor stimulus (GO:0071363)	475	6	.65	+	9.29	3.80E-05	1.92E-03
apoptotic signaling pathway (GO:0097190)	317	4	.43	+	9.28	8.79E-04	2.46E-02
epithelial tube morphogenesis (GO:0060562)	317	4	.43	+	9.28	8.79E-04	2.45E-02
transcription by RNA polymerase II (GO:0006366)	400	5	.54	+	9.19	1.93E-04	7.36E-03

response to lipopolysaccharide (GO:0032496)	321	4	.44	+	9.16	9.20E-04	2.55E-02
cellular response to abiotic stimulus (GO:0071214)	322	4	.44	+	9.14	9.31E-04	2.57E-02
cellular response to environmental stimulus (GO:0104004)	322	4	.44	+	9.14	9.31E-04	2.56E-02
lymphocyte activation (GO:0046649)	487	6	.66	+	9.06	4.36E-05	2.14E-03
cognition (GO:0050890)	325	4	.44	+	9.05	9.63E-04	2.64E-02
regulation of MAPK cascade (GO:0043408)	651	8	.89	+	9.04	1.84E-06	1.52E-04
positive regulation of cell motility (GO:2000147)	570	7	.78	+	9.03	9.20E-06	6.09E-04
regulation of phosphate metabolic process (GO:0019220)	1150	14	1.56	+	8.95	5.88E-11	2.80E-08
regulation of phosphorus metabolic process (GO:0051174)	1151	14	1.57	+	8.95	5.95E-11	2.67E-08
tube development (GO:0035295)	905	11	1.23	+	8.94	1.34E-08	2.27E-06
regulation of cell differentiation (GO:0045595)	1566	19	2.13	+	8.92	2.15E-15	3.27E-11
phosphorylation (GO:0016310)	745	9	1.01	+	8.88	4.12E-07	4.16E-05
positive regulation of locomotion (GO:0040017)	585	7	.80	+	8.80	1.09E-05	6.99E-04
negative regulation of cell differentiation (GO:0045596)	670	8	.91	+	8.78	2.27E-06	1.83E-04
regulation of protein stability (GO:0031647)	335	4	.46	+	8.78	1.08E-03	2.88E-02
regulation of cell cycle (GO:0051726)	1090	13	1.48	+	8.77	4.83E-10	1.29E-07
circulatory system development (GO:0072359)	928	11	1.26	+	8.72	1.73E-08	2.81E-06

negative regulation of locomotion (GO:0040013)	338	4	.46	+	8.70	1.11E-03	2.95E-02
response to molecule of bacterial origin (GO:0002237)	339	4	.46	+	8.68	1.12E-03	2.97E-02
positive regulation of protein modification process (GO:0031401)	763	9	1.04	+	8.67	5.02E-07	4.91E-05
angiogenesis (GO:0001525)	340	4	.46	+	8.65	1.14E-03	2.99E-02
regulation of cell migration (GO:0030334)	940	11	1.28	+	8.61	1.98E-08	3.14E-06
regulation of actin cytoskeleton organization (GO:0032956)	342	4	.47	+	8.60	1.16E-03	3.02E-02
tube morphogenesis (GO:0035239)	684	8	.93	+	8.60	2.65E-06	2.09E-04
response to radiation (GO:0009314)	428	5	.58	+	8.59	2.63E-04	9.60E-03
chemotaxis (GO:0006935)	345	4	.47	+	8.53	1.20E-03	3.09E-02
negative regulation of organelle organization (GO:0010639)	345	4	.47	+	8.53	1.20E-03	3.09E-02
epidermis development (GO:0008544)	346	4	.47	+	8.50	1.21E-03	3.11E-02
taxis (GO:0042330)	347	4	.47	+	8.48	1.22E-03	3.10E-02
regulation of protein modification process (GO:0031399)	1230	14	1.67	+	8.37	1.42E-10	4.93E-08
response to inorganic substance (GO:0010035)	528	6	.72	+	8.36	6.80E-05	3.08E-03
positive regulation of catalytic activity (GO:0043085)	884	10	1.20	+	8.32	1.44E-07	1.66E-05
chromatin remodeling (GO:0006338)	621	7	.84	+	8.29	1.59E-05	9.64E-04
regulation of growth (GO:0040008)	621	7	.84	+	8.29	1.59E-05	9.60E-04
negative regulation of cell population	710	8	.97	+	8.29	3.48E-06	2.60E-04

proliferation (GO:0008285)							
positive regulation of developmental process (GO:0051094)	1337	15	1.82	+	8.25	2.74E-11	1.67E-08
cellular response to nitrogen compound (GO:1901699)	624	7	.85	+	8.25	1.64E-05	9.82E-04
germ cell development (GO:0007281)	362	4	.49	+	8.13	1.43E-03	3.49E-02
response to metal ion (GO:0010038)	363	4	.49	+	8.10	1.44E-03	3.52E-02
regulation of cell motility (GO:2000145)	1000	11	1.36	+	8.09	3.71E-08	5.19E-06
positive regulation of immune system process (GO:0002684)	1000	11	1.36	+	8.09	3.71E-08	5.14E-06
negative regulation of intracellular signal transduction (GO:1902532)	547	6	.74	+	8.07	8.25E-05	3.58E-03
programmed cell death (GO:0012501)	1094	12	1.49	+	8.07	7.31E-09	1.34E-06
regulation of DNA-binding transcription factor activity (GO:0051090)	366	4	.50	+	8.04	1.49E-03	3.62E-02
cell death (GO:0008219)	1098	12	1.49	+	8.04	7.61E-09	1.35E-06
RNA biosynthetic process (GO:0032774)	551	6	.75	+	8.01	8.58E-05	3.71E-03
cell activation (GO:0001775)	736	8	1.00	+	7.99	4.53E-06	3.27E-04
locomotion (GO:0040011)	368	4	.50	+	7.99	1.52E-03	3.68E-02
negative regulation of programmed cell death (GO:0043069)	921	10	1.25	+	7.99	2.10E-07	2.25E-05
intracellular signaling cassette (GO:0141124)	831	9	1.13	+	7.96	1.02E-06	8.91E-05
cellular response to organic cyclic compound (GO:0071407)	466	5	.63	+	7.89	3.87E-04	1.31E-02

synaptic signaling (GO:0099536)	467	5	.64	+	7.87	3.91E-04	1.32E-02
regulation of multicellular organismal development (GO:2000026)	1404	15	1.91	+	7.86	5.45E-11	2.77E-08
chromosome organization (GO:0051276)	468	5	.64	+	7.86	3.95E-04	1.33E-02
regulation of transmembrane transport (GO:0034762)	468	5	.64	+	7.86	3.95E-04	1.32E-02
regulation of plasma membrane bounded cell projection organization (GO:0120035)	656	7	.89	+	7.85	2.26E-05	1.26E-03
positive regulation of molecular function (GO:0044093)	1219	13	1.66	+	7.84	1.87E-09	4.39E-07
cellular process involved in reproduction in multicellular organism (GO:0022412)	469	5	.64	+	7.84	3.99E-04	1.33E-02
heart development (GO:0007507)	566	6	.77	+	7.80	9.94E-05	4.17E-03
regulation of locomotion (GO:0040012)	1042	11	1.42	+	7.76	5.63E-08	7.53E-06
apoptotic process (GO:0006915)	1045	11	1.42	+	7.74	5.79E-08	7.68E-06
positive regulation of cell population proliferation (GO:0008284)	950	10	1.29	+	7.74	2.78E-07	2.91E-05
regulation of cell projection organization (GO:0031344)	672	7	.91	+	7.66	2.63E-05	1.44E-03
positive regulation of transcription by RNA polymerase II (GO:0045944)	1265	13	1.72	+	7.56	2.92E-09	6.37E-07
response to hormone (GO:0009725)	785	8	1.07	+	7.49	7.24E-06	4.97E-04

regulation of cellular catabolic process (GO:0031329)	688	7	.94	+	7.48	3.06E-05	1.64E-03
regulation of cell population proliferation (GO:0042127)	1676	17	2.28	+	7.46	2.90E-12	3.69E-09
positive regulation of protein localization (GO:1903829)	495	5	.67	+	7.43	5.09E-04	1.62E-02
negative regulation of apoptotic process (GO:0043066)	894	9	1.22	+	7.40	1.85E-06	1.52E-04
hemopoiesis (GO:0030097)	699	7	.95	+	7.36	3.38E-05	1.74E-03
response to abiotic stimulus (GO:0009628)	1112	11	1.51	+	7.27	1.08E-07	1.33E-05
cellular response to hormone stimulus (GO:0032870)	506	5	.69	+	7.27	5.62E-04	1.77E-02
in utero embryonic development (GO:0001701)	405	4	.55	+	7.26	2.14E-03	4.91E-02
positive regulation of cellular component organization (GO:0051130)	1118	11	1.52	+	7.24	1.14E-07	1.37E-05
leukocyte activation (GO:0045321)	611	6	.83	+	7.22	1.50E-04	5.95E-03
negative regulation of developmental process (GO:0051093)	919	9	1.25	+	7.20	2.32E-06	1.86E-04
muscle structure development (GO:0061061)	517	5	.70	+	7.11	6.19E-04	1.87E-02
neurogenesis (GO:0022008)	1346	13	1.83	+	7.10	6.16E-09	1.17E-06
regulation of cytoskeleton organization (GO:0051493)	522	5	.71	+	7.04	6.46E-04	1.95E-02
positive regulation of signal transduction (GO:0009967)	1568	15	2.13	+	7.04	2.55E-10	7.79E-08
response to organonitrogen	945	9	1.28	+	7.00	2.91E-06	2.27E-04

compound (GO:0010243)							
regulation of anatomical structure morphogenesis (GO:0022603)	845	8	1.15	+	6.96	1.23E-05	7.87E-04
peptidyl-amino acid modification (GO:0018193)	529	5	.72	+	6.95	6.86E-04	2.03E-02
response to organic cyclic compound (GO:0014070)	848	8	1.15	+	6.94	1.27E-05	7.97E-04
response to lipid (GO:0033993)	852	8	1.16	+	6.91	1.31E-05	8.11E-04
positive regulation of DNA-templated transcription (GO:0045893)	1711	16	2.33	+	6.88	6.31E-11	2.75E-08
positive regulation of RNA biosynthetic process (GO:1902680)	1714	16	2.33	+	6.87	6.48E-11	2.74E-08
epithelial cell differentiation (GO:0030855)	643	6	.87	+	6.86	1.98E-04	7.53E-03
DNA-templated transcription (GO:0006351)	539	5	.73	+	6.82	7.46E-04	2.18E-02
negative regulation of signal transduction (GO:0009968)	1301	12	1.77	+	6.78	4.95E-08	6.73E-06
response to endogenous stimulus (GO:0009719)	1411	13	1.92	+	6.78	1.08E-08	1.87E-06
actin cytoskeleton organization (GO:0030036)	547	5	.74	+	6.72	7.97E-04	2.27E-02
positive regulation of cell communication (GO:0010647)	1754	16	2.39	+	6.71	9.13E-11	3.66E-08
chromatin organization (GO:0006325)	768	7	1.04	+	6.70	6.11E-05	2.82E-03
positive regulation of signaling (GO:0023056)	1756	16	2.39	+	6.70	9.29E-11	3.54E-08
regulation of immune system	1540	14	2.09	+	6.69	2.64E-09	5.83E-07

process (GO:0002682)							
positive regulation of multicellular organismal process (GO:0051240)	1652	15	2.25	+	6.68	5.28E-10	1.36E-07
regulation of response to stress (GO:0080134)	1356	12	1.84	+	6.51	7.78E-08	1.01E-05
head development (GO:0060322)	792	7	1.08	+	6.50	7.41E-05	3.28E-03
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	2059	18	2.80	+	6.43	5.18E-12	5.26E-09
cellular response to endogenous stimulus (GO:0071495)	1148	10	1.56	+	6.41	1.55E-06	1.31E-04
gamete generation (GO:0007276)	807	7	1.10	+	6.38	8.33E-05	3.61E-03
positive regulation of RNA metabolic process (GO:0051254)	1852	16	2.52	+	6.35	2.05E-10	6.64E-08
positive regulation of intracellular signal transduction (GO:1902533)	1043	9	1.42	+	6.35	6.48E-06	4.53E-04
cell morphogenesis (GO:0000902)	696	6	.95	+	6.34	3.02E-04	1.08E-02
negative regulation of cell communication (GO:0010648)	1397	12	1.90	+	6.32	1.08E-07	1.33E-05
negative regulation of signaling (GO:0023057)	1398	12	1.90	+	6.31	1.08E-07	1.32E-05
response to nitrogen compound (GO:1901698)	1053	9	1.43	+	6.29	7.00E-06	4.85E-04
regulation of programmed cell death (GO:0043067)	1521	13	2.07	+	6.29	2.64E-08	3.98E-06
positive regulation of response to stimulus (GO:0048584)	2242	19	3.05	+	6.23	1.39E-12	1.93E-09

homeostatic process (GO:0042592)	1430	12	1.94	+	6.17	1.39E-07	1.61E-05
embryonic morphogenesis (GO:0048598)	596	5	.81	+	6.17	1.17E-03	3.03E-02
anatomical structure formation involved in morphogenesis (GO:0048646)	971	8	1.32	+	6.06	3.33E-05	1.72E-03
neuron differentiation (GO:0030182)	1095	9	1.49	+	6.04	9.58E-06	6.32E-04
protein-DNA complex organization (GO:0071824)	856	7	1.16	+	6.01	1.20E-04	4.95E-03
regulation of developmental process (GO:0050793)	2448	20	3.33	+	6.01	4.05E-13	8.81E-10
regulation of apoptotic process (GO:0042981)	1476	12	2.01	+	5.98	1.96E-07	2.13E-05
actin filament-based process (GO:0030029)	617	5	.84	+	5.96	1.36E-03	3.36E-02
positive regulation of protein metabolic process (GO:0051247)	1243	10	1.69	+	5.92	3.17E-06	2.44E-04
regulation of cellular localization (GO:0060341)	999	8	1.36	+	5.89	4.08E-05	2.02E-03
cell cycle process (GO:0022402)	880	7	1.20	+	5.85	1.43E-04	5.66E-03
behavior (GO:0007610)	632	5	.86	+	5.82	1.51E-03	3.67E-02
regulation of catalytic activity (GO:0050790)	1408	11	1.91	+	5.75	1.14E-06	9.78E-05
cell migration (GO:0016477)	901	7	1.23	+	5.71	1.65E-04	6.42E-03
cell surface receptor signaling pathway (GO:0007166)	2079	16	2.83	+	5.66	1.13E-09	2.82E-07
generation of neurons (GO:0048699)	1171	9	1.59	+	5.65	1.64E-05	9.83E-04
multicellular organismal	913	7	1.24	+	5.64	1.79E-04	6.90E-03

reproductive process (GO:0048609)							
positive regulation of immune response (GO:0050778)	653	5	.89	+	5.63	1.74E-03	4.17E-02
regulation of immune response (GO:0050776)	917	7	1.25	+	5.61	1.84E-04	7.07E-03
positive regulation of gene expression (GO:0010628)	1181	9	1.61	+	5.60	1.75E-05	1.03E-03
chordate embryonic development (GO:0043009)	664	5	.90	+	5.54	1.87E-03	4.43E-02
nucleobase-containing compound biosynthetic process (GO:0034654)	938	7	1.28	+	5.49	2.11E-04	7.98E-03
negative regulation of protein metabolic process (GO:0051248)	810	6	1.10	+	5.45	6.73E-04	2.00E-02
cell motility (GO:0048870)	1081	8	1.47	+	5.44	7.10E-05	3.19E-03
regulation of cellular component organization (GO:0051128)	2442	18	3.32	+	5.42	9.06E-11	3.73E-08
positive regulation of nitrogen compound metabolic process (GO:0051173)	2998	22	4.08	+	5.40	6.35E-14	3.23E-10
regulation of intracellular signal transduction (GO:1902531)	1781	13	2.42	+	5.37	1.69E-07	1.88E-05
multicellular organism reproduction (GO:0032504)	959	7	1.30	+	5.37	2.41E-04	9.00E-03
embryo development ending in birth or egg hatching (GO:0009792)	685	5	.93	+	5.37	2.14E-03	4.91E-02
regulation of response to external stimulus (GO:0032101)	1098	8	1.49	+	5.36	7.92E-05	3.48E-03

regulation of signal transduction (GO:0009966)	3021	22	4.11	+	5.36	7.46E-14	2.27E-10
negative regulation of gene expression (GO:0010629)	968	7	1.32	+	5.32	2.56E-04	9.36E-03
negative regulation of response to stimulus (GO:0048585)	1664	12	2.26	+	5.30	7.09E-07	6.63E-05
regulation of cellular component biogenesis (GO:0044087)	974	7	1.32	+	5.29	2.65E-04	9.65E-03
cell development (GO:0048468)	2240	16	3.05	+	5.25	3.36E-09	7.21E-07
cell cycle (GO:0007049)	1265	9	1.72	+	5.23	3.02E-05	1.63E-03
positive regulation of cellular biosynthetic process (GO:0031328)	2686	19	3.65	+	5.20	3.46E-11	1.88E-08
positive regulation of biosynthetic process (GO:0009891)	2707	19	3.68	+	5.16	3.97E-11	2.09E-08
positive regulation of transport (GO:0051050)	855	6	1.16	+	5.16	8.91E-04	2.48E-02
developmental process involved in reproduction (GO:0003006)	1000	7	1.36	+	5.15	3.11E-04	1.11E-02
central nervous system development (GO:0007417)	1008	7	1.37	+	5.11	3.27E-04	1.15E-02
positive regulation of macromolecule biosynthetic process (GO:0010557)	2604	18	3.54	+	5.08	2.64E-10	7.73E-08
heterocycle biosynthetic process (GO:0018130)	1014	7	1.38	+	5.08	3.39E-04	1.18E-02
positive regulation of cellular metabolic process (GO:0031325)	3341	23	4.54	+	5.06	3.07E-14	2.34E-10
regulation of catabolic process (GO:0009894)	1022	7	1.39	+	5.04	3.55E-04	1.22E-02

aromatic compound biosynthetic process (GO:0019438)	1024	7	1.39	+	5.03	3.59E-04	1.23E-02
regulation of transport (GO:0051049)	1617	11	2.20	+	5.00	4.37E-06	3.19E-04
nervous system development (GO:0007399)	2207	15	3.00	+	5.00	2.79E-08	4.17E-06
regulation of multicellular organismal process (GO:0051239)	2966	20	4.03	+	4.96	1.49E-11	1.19E-08
regulation of protein localization (GO:0032880)	891	6	1.21	+	4.95	1.10E-03	2.93E-02
anatomical structure morphogenesis (GO:0009653)	2239	15	3.04	+	4.93	3.39E-08	4.79E-06
sexual reproduction (GO:0019953)	1052	7	1.43	+	4.89	4.23E-04	1.39E-02
cellular response to oxygen-containing compound (GO:1901701)	1055	7	1.43	+	4.88	4.30E-04	1.40E-02
embryo development (GO:0009790)	1059	7	1.44	+	4.86	4.40E-04	1.43E-02
intracellular signal transduction (GO:0035556)	1514	10	2.06	+	4.86	1.80E-05	1.06E-03
regulation of protein metabolic process (GO:0051246)	2145	14	2.92	+	4.80	1.77E-07	1.94E-05
regulation of molecular function (GO:0065009)	2008	13	2.73	+	4.76	6.75E-07	6.35E-05
positive regulation of macromolecule metabolic process (GO:0010604)	3413	22	4.64	+	4.74	9.52E-13	1.81E-09
cell-cell signaling (GO:0007267)	1086	7	1.48	+	4.74	5.11E-04	1.63E-02
response to oxygen-containing compound (GO:1901700)	1554	10	2.11	+	4.73	2.26E-05	1.26E-03
regulation of localization (GO:0032879)	2028	13	2.76	+	4.71	7.56E-07	6.94E-05

regulation of signaling (GO:0023051)	3434	22	4.67	+	4.71	1.08E-12	1.83E-09
regulation of cell communication (GO:0010646)	3440	22	4.68	+	4.70	1.12E-12	1.71E-09
epithelium development (GO:0060429)	1111	7	1.51	+	4.63	5.86E-04	1.80E-02
cellular response to stress (GO:0033554)	1588	10	2.16	+	4.63	2.72E-05	1.48E-03
positive regulation of metabolic process (GO:0009893)	3719	23	5.06	+	4.55	3.23E-13	8.20E-10
regulation of transcription by RNA polymerase II (GO:0006357)	2603	16	3.54	+	4.52	2.95E-08	4.36E-06
organic cyclic compound biosynthetic process (GO:1901362)	1150	7	1.56	+	4.48	7.19E-04	2.12E-02
response to organic substance (GO:0010033)	2467	15	3.35	+	4.47	1.24E-07	1.47E-05
regulation of response to stimulus (GO:0048583)	3982	24	5.41	+	4.43	7.12E-14	2.71E-10
animal organ morphogenesis (GO:0009887)	996	6	1.35	+	4.43	1.95E-03	4.54E-02
phosphate-containing compound metabolic process (GO:0006796)	1711	10	2.33	+	4.30	5.16E-05	2.47E-03
negative regulation of cellular metabolic process (GO:0031324)	2572	15	3.50	+	4.29	2.16E-07	2.31E-05
regulation of DNA-templated transcription (GO:0006355)	3440	20	4.68	+	4.28	2.33E-10	7.25E-08
cellular response to organic substance (GO:0071310)	1725	10	2.35	+	4.26	5.53E-05	2.61E-03
regulation of RNA biosynthetic process (GO:2001141)	3459	20	4.70	+	4.25	2.58E-10	7.71E-08

phosphorus metabolic process (GO:0006793)	1737	10	2.36	+	4.23	5.87E-05	2.74E-03
negative regulation of metabolic process (GO:0009892)	2828	16	3.85	+	4.16	9.61E-08	1.21E-05
tissue development (GO:0009888)	1769	10	2.41	+	4.16	6.85E-05	3.10E-03
immune system process (GO:0002376)	2316	13	3.15	+	4.13	3.41E-06	2.57E-04
cytoskeleton organization (GO:0007010)	1255	7	1.71	+	4.10	1.20E-03	3.09E-02
animal organ development (GO:0048513)	2869	16	3.90	+	4.10	1.18E-07	1.40E-05
reproductive process (GO:0022414)	1470	8	2.00	+	4.00	5.81E-04	1.79E-02
reproduction (GO:0000003)	1482	8	2.02	+	3.97	6.13E-04	1.86E-02
negative regulation of macromolecule metabolic process (GO:0010605)	2609	14	3.55	+	3.95	1.96E-06	1.60E-04
system development (GO:0048731)	3546	19	4.82	+	3.94	4.40E-09	8.94E-07
negative regulation of macromolecule biosynthetic process (GO:0010558)	2061	11	2.80	+	3.93	4.36E-05	2.14E-03
regulation of RNA metabolic process (GO:0051252)	3758	20	5.11	+	3.91	1.18E-09	2.90E-07
negative regulation of cellular biosynthetic process (GO:0031327)	2113	11	2.87	+	3.83	5.48E-05	2.60E-03
cell differentiation (GO:0030154)	3654	19	4.97	+	3.82	7.36E-09	1.34E-06
cellular nitrogen compound biosynthetic process (GO:0044271)	1539	8	2.09	+	3.82	7.86E-04	2.26E-02
cellular developmental process (GO:0048869)	3657	19	4.97	+	3.82	7.46E-09	1.34E-06
negative regulation of biosynthetic	2127	11	2.89	+	3.80	5.83E-05	2.73E-03

process (GO:0009890)							
cellular response to chemical stimulus (GO:0070887)	2389	12	3.25	+	3.69	3.05E-05	1.64E-03
regulation of nucleobase-containing compound metabolic process (GO:0019219)	4061	20	5.52	+	3.62	4.84E-09	9.70E-07
protein modification process (GO:0036211)	2069	10	2.81	+	3.55	2.53E-04	9.29E-03
response to external stimulus (GO:0009605)	2290	11	3.11	+	3.53	1.15E-04	4.74E-03
multicellular organism development (GO:0007275)	3964	19	5.39	+	3.53	2.95E-08	4.32E-06
response to chemical (GO:0042221)	3780	18	5.14	+	3.50	1.13E-07	1.36E-05
regulation of gene expression (GO:0010468)	4898	23	6.66	+	3.45	1.27E-10	4.49E-08
regulation of cellular biosynthetic process (GO:0031326)	5159	24	7.01	+	3.42	2.65E-11	1.68E-08
protein localization (GO:0008104)	1944	9	2.64	+	3.40	7.84E-04	2.26E-02
regulation of biosynthetic process (GO:0009889)	5190	24	7.06	+	3.40	3.04E-11	1.78E-08
cellular macromolecule localization (GO:0070727)	1951	9	2.65	+	3.39	8.05E-04	2.29E-02
nucleic acid metabolic process (GO:0090304)	2180	10	2.96	+	3.37	3.87E-04	1.31E-02
regulation of macromolecule biosynthetic process (GO:0010556)	5026	23	6.83	+	3.37	2.20E-10	7.00E-08
negative regulation of nitrogen compound metabolic process (GO:0051172)	2188	10	2.98	+	3.36	3.99E-04	1.33E-02

regulation of nitrogen compound metabolic process (GO:0051171)	5474	25	7.44	+	3.36	5.80E-12	5.53E-09
regulation of biological quality (GO:0065008)	2849	13	3.87	+	3.36	3.34E-05	1.72E-03
negative regulation of cellular process (GO:0048523)	4848	22	6.59	+	3.34	1.28E-09	3.10E-07
regulation of primary metabolic process (GO:0080090)	5622	25	7.64	+	3.27	1.10E-11	9.29E-09
protein-containing complex organization (GO:0043933)	2027	9	2.76	+	3.27	1.06E-03	2.86E-02
anatomical structure development (GO:0048856)	5231	23	7.11	+	3.23	5.18E-10	1.36E-07
response to stress (GO:0006950)	3419	15	4.65	+	3.23	8.61E-06	5.78E-04
positive regulation of cellular process (GO:0048522)	5707	25	7.76	+	3.22	1.57E-11	1.14E-08
macromolecule modification (GO:0043412)	2291	10	3.12	+	3.21	5.77E-04	1.79E-02
regulation of cellular metabolic process (GO:0031323)	6054	26	8.23	+	3.16	3.03E-12	3.56E-09
negative regulation of biological process (GO:0048519)	5208	22	7.08	+	3.11	5.42E-09	1.07E-06
organelle organization (GO:0006996)	3099	13	4.21	+	3.09	8.21E-05	3.58E-03
regulation of macromolecule metabolic process (GO:0060255)	6033	25	8.20	+	3.05	5.89E-11	2.72E-08
positive regulation of biological process (GO:0048518)	6210	25	8.44	+	2.96	1.17E-10	4.25E-08
nucleobase-containing compound metabolic process (GO:0006139)	2743	11	3.73	+	2.95	5.68E-04	1.76E-02

developmental process (GO:0032502)	5739	23	7.80	+	2.95	3.71E-09	7.75E-07
regulation of metabolic process (GO:0019222)	6559	26	8.92	+	2.92	2.27E-11	1.50E-08
heterocycle metabolic process (GO:0046483)	2931	11	3.99	+	2.76	1.00E-03	2.74E-02
cellular aromatic compound metabolic process (GO:0006725)	2971	11	4.04	+	2.72	1.13E-03	2.97E-02
cellular nitrogen compound metabolic process (GO:0034641)	3288	12	4.47	+	2.68	6.75E-04	2.01E-02
multicellular organismal process (GO:0032501)	6745	24	9.17	+	2.62	1.08E-08	1.85E-06
signal transduction (GO:0007165)	4789	17	6.51	+	2.61	2.47E-05	1.36E-03
cellular component organization (GO:0016043)	5636	20	7.66	+	2.61	1.59E-06	1.33E-04
cellular component organization or biogenesis (GO:0071840)	5852	20	7.96	+	2.51	3.02E-06	2.34E-04
signaling (GO:0023052)	5109	17	6.95	+	2.45	6.01E-05	2.79E-03
cell communication (GO:0007154)	5262	17	7.16	+	2.38	8.98E-05	3.84E-03
cellular response to stimulus (GO:0051716)	6448	20	8.77	+	2.28	1.54E-05	9.38E-04
response to stimulus (GO:0050896)	8182	25	11.13	+	2.25	7.53E-08	9.90E-06
macromolecule metabolic process (GO:0043170)	5648	16	7.68	+	2.08	1.03E-03	2.79E-02
cellular metabolic process (GO:0044237)	6416	18	8.72	+	2.06	3.43E-04	1.19E-02
metabolic process (GO:0008152)	7979	21	10.85	+	1.94	1.28E-04	5.17E-03
regulation of cellular process (GO:0050794)	11167	27	15.18	+	1.78	1.07E-06	9.35E-05

regulation of biological process (GO:0050789)	11722	27	15.94	+	1.69	3.62E-06	2.68E-04
biological regulation (GO:0065007)	12141	27	16.51	+	1.64	9.19E-06	6.11E-04