

Identification of Metabolism-Associated Molecular Subtypes of Chronic Obstructive Pulmonary Disease

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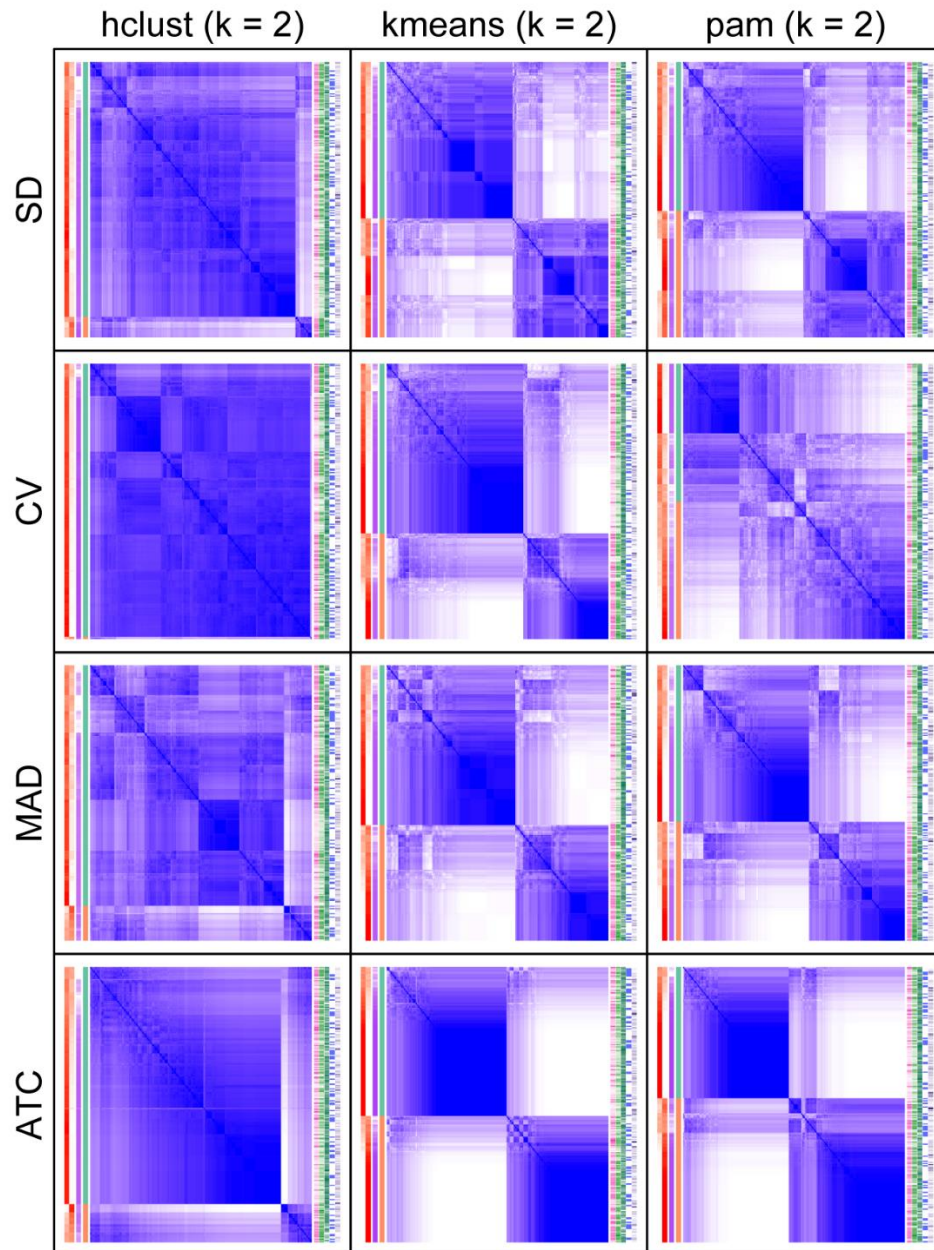
Supplementary Table 1. Genes selected using Boruta and linear regression with various thresholds.

Approach	Parameter	value	Associated with FEV1/FVC	Associated with FEV1	Number of genes in union
Boruta	pValue	0.01	ADCY4, ATP6AP1, CA8, B3GALT2, ENPP1, GPX7, HDC, HSD3B7, PFKFB4, PIK3C2B, SCLY, ST6GAL1, ST8SIA1	ACAA1, ADCY4, HDC, AHCYL2, ENPP1, ETFA, GLA, HSD3B7, PIK3C2B, SCLY, ST6GAL1, UPB1, UPP1	19
Boruta	pValue	0.05	ACAA1, ADCY4, ATP6AP1, CA8, CEPT1, GPX7, GSTO1, HDC, HSD3B7, MGAT5, PFKFB4, PIK3C2B, SCLY, ST6GAL1, ST8SIA1	ADCY4, ATP6AP1, CA8, B3GALT2, ENPP1, HDC, HSD3B7, PFKFB4, PIK3C2B, SCLY, GPX7, ST6GAL1, ST8SIA1	27
Boruta	pValue	0.1	ACAA1, ADCY4, ATP6AP1, B3GALT2, CA8, CBR1, ENPP1, GPX7, HDC, SCLY, PFKFB4, PIK3C2B, UPB1, ST6GAL1, ST8SIA1	ACAA1, ADCY4, GLA, AHCYL2, ATP6AP1, ENPP1, ETFA, HDC, HSD3B7, MGST1, UPB1, NDUFB6, NT5E, SCLY, PFKFB4, PIK3C2B, UPP1, SGMS2, ST6GAL1	24
Linear regression	effect size	Top 5%	PTDSS1, NADK, SIRT7, GAPDH, CS, FDFT1, ATP6AP1, UXS1, MAT2A, HAO1, RNMT, ADH7, CHST11, ITPKB, ACAA1, MCCC2, CRABP2, ITPK1, CEPT1, MAN1A2, TKT, ST6GAL1, SDHC, CERK, PLD2, GMPR2, RPN1	CS, GAPDH, PTDSS1, FDFT1, SIRT7, ND2, ITPKB, UXS1, ADH7, ACAA1, NADK, HAO1, ATP6AP1, ST6GAL1, MAT2A, CALM3, TKT, MCCC2, DDOST, DPYS, RNMT, CRABP2	31
Linear regression	effect size	Top 10%	PTDSS1, NADK, SIRT7, GAPDH, CS, FDFT1, ATP6AP1, UXS1, MAT2A, HAO1, RNMT, ADH7, CHST11, ITPKB, ACAA1, MCCC2, CRABP2, ITPK1, CEPT1, MAN1A2, TKT,	CS, GAPDH, PTDSS1, FDFT1, SIRT7, ND2, ITPKB, UXS1, ADH7, ACAA1, NADK, ATP6AP1, ST6GAL1, MAT2A, CALM3, HAO1, MCCC2, DDOST, TKT,	61

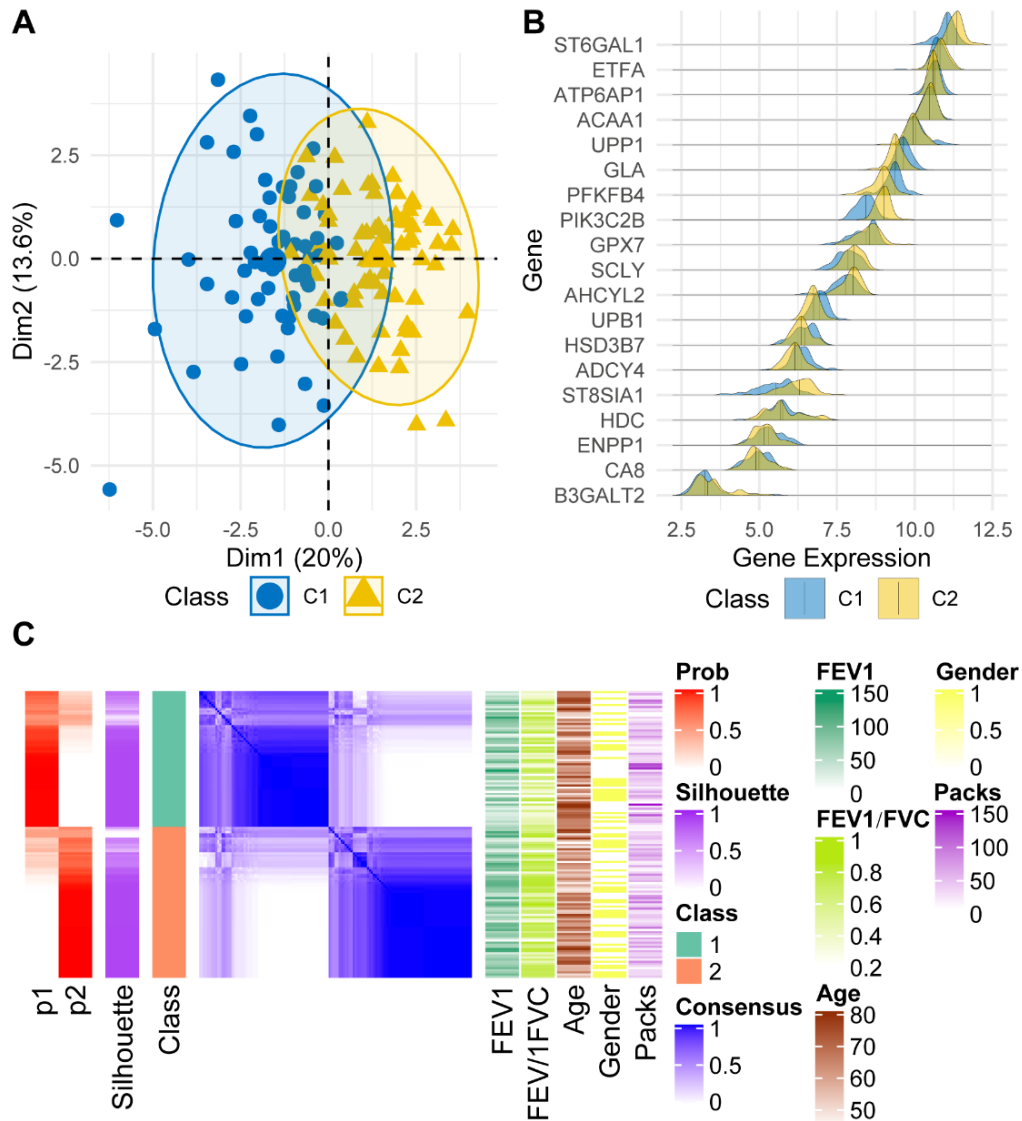
ST6GAL1, SDHC, CERK, DPYS, RNMT, CRABP2,
 PLD2, GMPR2, RPN1, INPPL1, CEPT1, SDHB,
 GALNS, TALDO1, DPYS, CERK, GMPR2, ITPK1,
 ALDOA, GOT1, POLR2H, ALDH9A1, PLD2,
 POLR1B, PFKFB4, KDSR, GALNT1, PDE1C, RPN1,
 POGLUT1, PDE1C, DDOST, HS6ST2, ALDH4A1,
 HS6ST2, CHFR, ATP6V0B, CHFR, ATP6V1E1,
 SOAT1, KMT2D, SEPHS2, POLR1B, GOT1, GLA,
 GPX7, ALDH4A1, PI4KB, PI4KB, PPP1R3C,
 CHKA, OPLAH, NADSYN1, CHST11, MAN1A2
 PPP1R3C, AGPAT2

Supplementary Table 2. Best consistent clustering models evaluated in ever parameter combination using mean silhouette score, PAC score and concordance.

Parameter combination	Best k	1-PAC score	Mean silhouette	concordance	Jaccard
ATC:kmeans	2	0.58354668	0.8065742	0.9161572	0.501264
ATC:pam	2	0.54173067	0.7756717	0.9037904	0.498966
MAD:kmeans	2	0.30888377	0.6732604	0.8498341	0.510917
CV:kmeans	2	0.29625363	0.6595365	0.8497118	0.524707
MAD:pam	2	0.24722649	0.5907090	0.8252227	0.50701
SD:kmeans	2	0.24278887	0.7169657	0.8495197	0.50701
SD:pam	2	0.20383171	0.6693103	0.8354934	0.501264
CV:hclust	3	0.18276751	0.7336567	0.8337817	0.92284
CV:pam	2	0.16734938	0.5797081	0.8052576	0.497817
ATC:hclust	3	0.16619730	0.5262195	0.7283144	0.458657
MAD:hclust	2	0.12698413	0.5422373	0.7888559	0.777829
SD:hclust	3	0.07579909	0.4944082	0.7170655	0.912934



Supplementary Figure 1. Consensus matrix visualizing the stability with the two subtypes and various parameter combinations.



Supplementary Figure 2. Identification of two metabolim related-subtypes in the COPDGene dataset. (A) Principal component analysis displaying the distribution of the two subtypes in the COPDGene dataset. (B) Multiple density plot showing the distribution of 19 selected genes on the two subtypes in the COPDGene dataset. (C) Consensus matrix visualizing the stability of the two subtypes in the COPDGene dataset. The labels “p1” and “p2” refer to the probability of the sample staying in C1 and C2, respectively. The label “Prob” refers to the probability of the sample staying in the corresponding subgroup. The label “Packs” refers to the pack-years of cigarette smoking.

Supplementary Table 3. Difference in clinical characteristic between C1 and C2 in the ECLIPSE dataset.

Characteristic	N	C1 (N = 124) ¹	C2 (N = 105) ¹	p-value ²
FEV1 (% predicted)	229	55 (38, 72)	92 (56, 108)	<0.001***
FEV1/FVC	229	0.46 (0.35, 0.66)	0.72 (0.47, 0.81)	<0.001***
Age (years)	229	66 (62, 70)	62 (57, 67)	<0.001***
Gender	229			0.6
Female		80 (65%)	72 (69%)	
Male		44 (35%)	33 (31%)	
Pack-years	229	38 (24, 54)	31 (20, 48)	0.060
GOLD Grade	229			<0.001***
GOLD 0 ³		28 (23%)	58 (55%)	
GOLD 1		1 (0.8%)	2 (1.9%)	
GOLD 2		42 (34%)	27 (26%)	
GOLD 3		43 (35%)	14 (13%)	
GOLD 4		10 (8.1%)	4 (3.8%)	

Note: 1 Statistics presented: median (IQR); n (%).

2 Statistical tests performed: Wilcoxon rank-sum test; chi-square test of independence; Fisher's exact test. ***, <0.001.

3 GOLD 0 was defined as FEV1 (% predicted) ≥ 80% and FEV1/FVC ≥ 0.7.

Supplementary Table 4. Difference in clinical characteristics between C1 and C2 in the COPDGene dataset.

Characteristic	N	C1 (N = 64) ¹	C2 (N = 71) ¹	p-value ²
FEV1 (% predicted)	135	59 (36, 82)	75 (58, 92)	0.009**
FEV1/FVC	135	0.57 (0.39, 0.67)	0.71 (0.58, 0.76)	<0.001***
Age (years)	135	65 (59, 72)	61 (56, 68)	0.083
Pack-years	135	41 (29, 63)	44 (28, 61)	>0.9
BMI (kg/m²)	135	26.6 (23.8, 31.0)	27.3 (24.6, 31.2)	0.4
Gender	135			0.3
Female		26 (41%)	36 (51%)	
Male		38 (59%)	35 (49%)	
Six-minute-walk distance (ft)	135	1316 (996, 1600)	1515 (1238, 1705)	0.017*
Emphysema (%)³	116	5 (2, 17)	1 (0, 5)	<0.001***
Gas Trapping (%)³	114	22 (11, 52)	10 (5, 30)	0.002**
Current Smoking Status	134			0.024*
No		53 (83%)	46 (65%)	
Yes		11 (17%)	24 (34%)	
GOLD Grade	135			0.001**
GOLD 0 ⁴		13 (20%)	29 (41%)	
PRISm ⁴		1 (1.6%)	9 (13%)	
GOLD 1		6 (9.4%)	1 (1.4%)	
GOLD 2		18 (28%)	17 (24%)	

GOLD 3	15 (23%)	10 (14%)	
GOLD 4	11 (17%)	5 (7.0%)	
Airflow Obstruction⁴	135		<0.001***
No	14 (21.9%)	38 (53.5%)	
Yes	50 (78.1%)	33 (46.5%)	

Note: 1 Statistics presented: median (IQR); n (%).

2 Statistical tests performed: Wilcoxon rank-sum test; chi-square test of independence; Fisher's exact test. P-value: *, <0.05; **, <0.01; ***, <0.001.

3 Emphysema(%) was defined as percent of lung attenuation voxels below -950 Hounsfield units (HU); Gas trapping(%) was defined as the percent of lung voxels less than -856 HU on the expiratory images of the CT scan.

4 PRISm was defined as FEV1 (% predicted) <80% and FEV1/FVC \geq 0.7. GOLD 0 was defined as FEV1 (% predicted) \geq 80% and FEV1/FVC \geq 0.7. Airflow obstruction was defined as FEV1/FVC < 0.7.

Supplementary Table 5. Difference in clinical characteristics between COPD and Healthy Smokers in the two datasets.

Characteristic	ECLIPSE			COPDGene		
	COPD, N = 143	Healthy Smoker, N = 86	P-value ¹	COPD, N = 83	Healthy Smoker, N = 52	P-value ¹
Subtypes			<0.001***			<0.001***
C1	96 (67%)	28 (33%)		50 (60%)	14 (27%)	
C2	47 (33%)	58 (67%)		33 (40%)	38 (73%)	
FEV1 (% predicted)	50 (36, 62)	108 (101, 118)	<0.001***	50 (35, 66)	90 (81, 104)	<0.001***
FEV1/FVC (%)	41 (35, 52)	80 (76, 82)	<0.001***	46 (38, 62)	77 (74, 79)	<0.001***
Age (years)	65 (61, 69)	62 (57, 69)	0.002**	66 (59, 71)	60 (54, 66)	0.006**
Gender			>0.9			0.2
Female	95 (66%)	57 (66%)		49 (59%)	24 (46%)	
Male	48 (34%)	29 (34%)		34 (41%)	28 (54%)	
Pack-years	42 (26, 58)	26 (16, 38)	<0.001***	44 (34, 66)	38 (22, 52)	0.062
BMI (kg/m²)	--	--	--	27.3 (23.9, 31.2)	26.8 (24.4, 31.1)	0.8
Six-minute-walk distance (ft)	--	--	--	1,230 (970, 1,565)	1,628 (1,460, 1,800)	<0.001***
Emphysema (%)³	--	--	--	11 (3, 20)	1 (0, 1)	<0.001***
Gas Trapping (%)³	--	--	--	34 (17, 58)	8 (4, 10)	<0.001***
Current Smoking Status			--			0.053
No	--	--		66 (80%)	33 (63%)	
Yes	--	--		17 (20%)	18 (35%)	

Note: 1 P-value: **, <0.01; ***, <0.001.

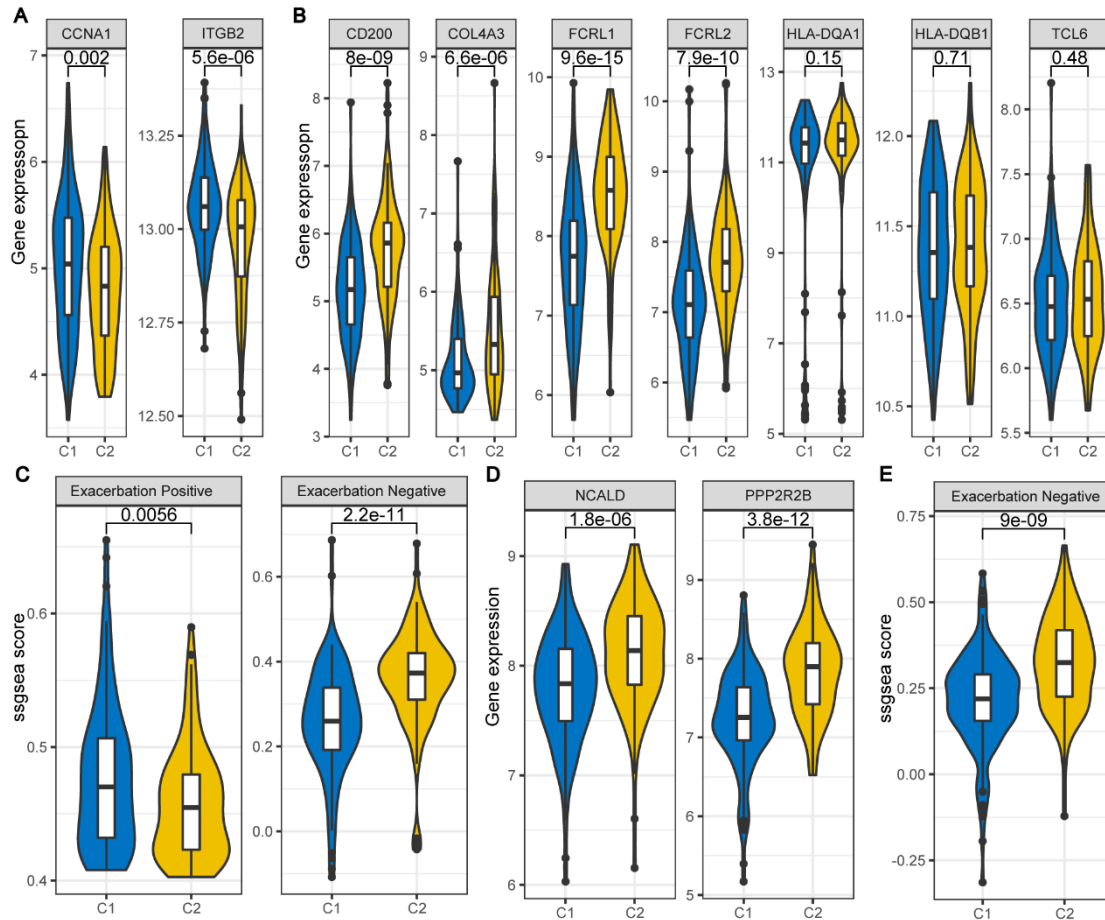
Supplementary Table 6. Association of subtypes with FEV1/FVC and FEV1 correcting for confounding factors.

Correction for confounding factors	FEV1/FVC (% predicted)		FEV1 (%)	
	β (95%CI)	P value ¹	β (95%CI)	P value ¹
ECLIPSE				
Age	11.55(6.41, 16.69)	1.49e-05***	17.86(9.28, 26.45)	5.74e-05***
Gender	13.73(8.75, 18.72)	1.46e-07***	20.79(12.54, 29.04)	1.34e-06***
Gender+Age	11.49(6.30, 16.67)	1.95e-05***	18.20(9.55, 26.86)	4.84e-05***
COPDGene				
Age	9.93(4.35, 15.51)	5.91e-04***	11.28(1.90, 20.66)	0.0189*
Gender	10.92(5.19, 16.64)	2.44e-04***	12.43(3.00, 21.87)	0.0100*
Gender+Age	9.87(4.25, 15.48)	6.88e-04***	11.40(1.96, 20.84)	0.0183*
BMI	10.67(5.08, 16.27)	2.43e-04***	12.26 (2.86, 21.66)	0.0110*
Age+BMI	9.58(4.08,15.08)	7.73e-04***	11.19(1.76, 20.62)	0.0204*
Gender+BMI	10.33(4.71,15.95)	3.97e-04***	12.24(2.75, 21.73)	0.0119*
Age +Gender+BMI	9.47(3.93, 15.00)	9.50e-04***	11.31(1.82, 20.79)	0.0199*
Current Smoking	9.70(3.96,15.43)	1.08e-03**	11.154(1.60, 20.71)	0.0225*

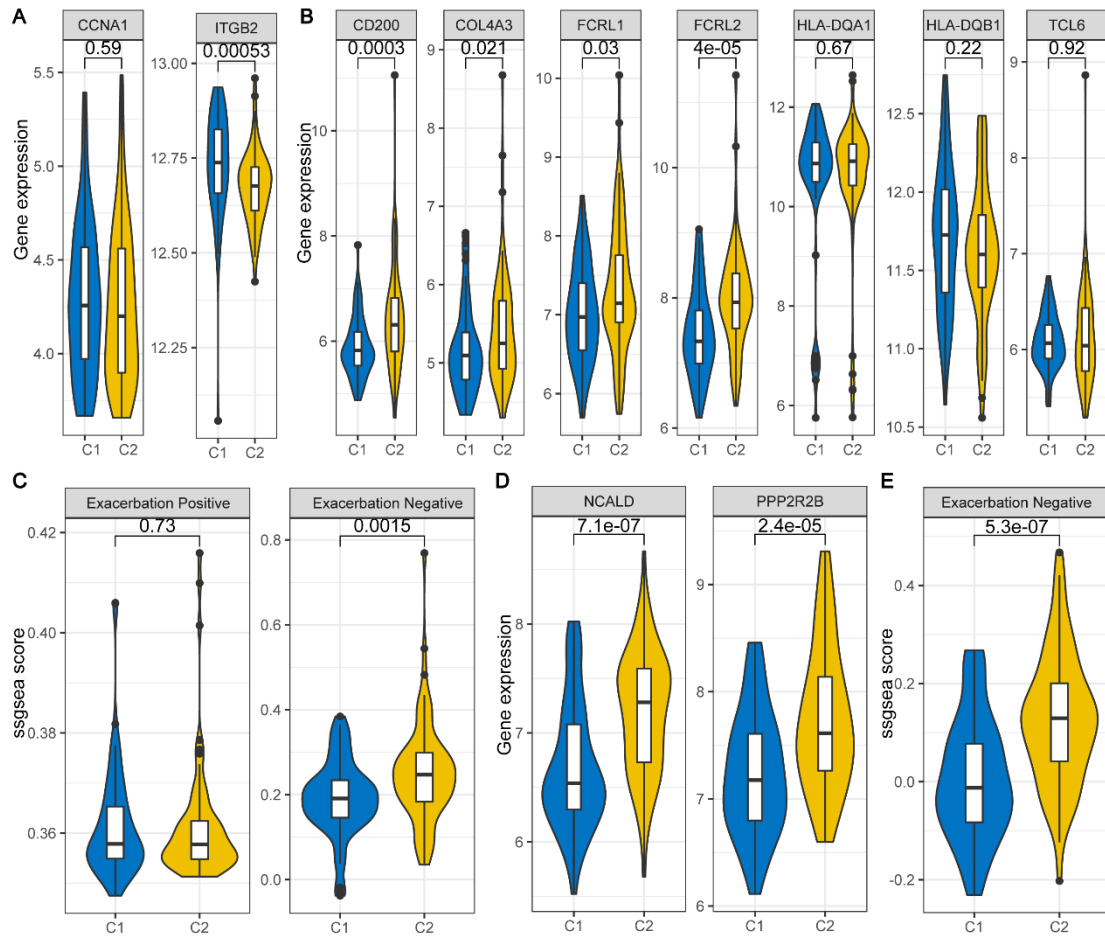
Note: 1 P-value: *, <0.05; **, <0.01; ***, <0.001.

Supplementary Table 7. Gene signatures associated with exacerbation risk obtained from previous study.

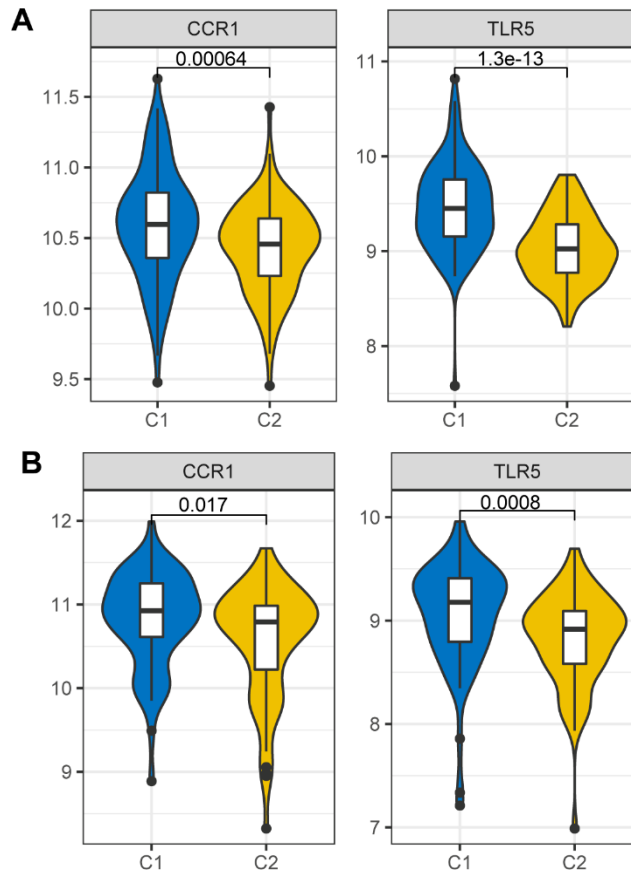
Study	Gene signatures	Association with exacerbation risk	Reference
Singh D et.al.	ITGB2, CCNA1, RHCE	Positive	PMID: 25265030
Singh D et.al.	HLA-DQA1, HLA-DQB1, TCL6, CD200, FCRL1, FCRL2, COL4A3	Negative	PMID: 25265030
Morrow JD et.al.	NCALD, PPP2R2B	Negative	PMID: 25582225



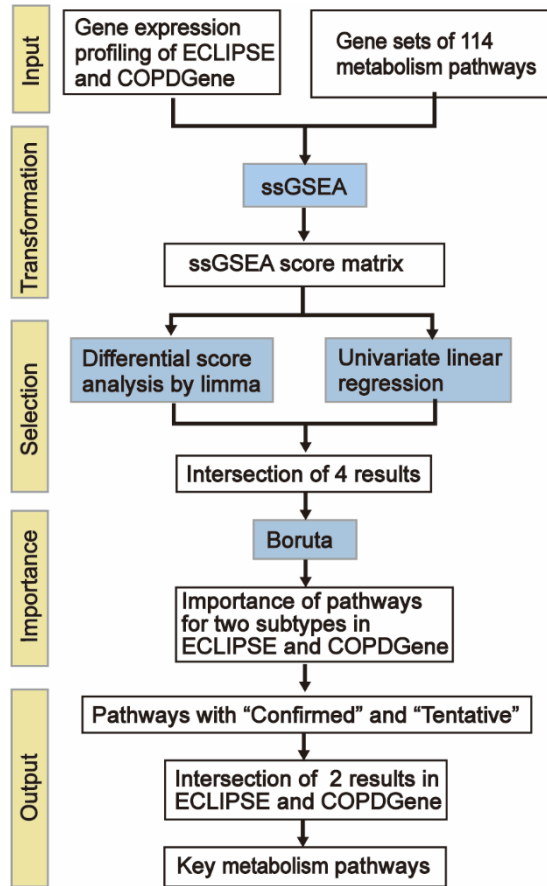
Supplementary Figure 3. Infer the difference in exacerbation risk between C1 and C2 in the ECLIPSE dataset from the point of view of gene signatures. (A) Difference in gene expression of gene signature from *Singh D et.al.*, which was positively associated with exacerbation risk. (B) Difference in gene expression of gene signature from *Singh D et.al.*, which was negatively associated with exacerbation risk. (C) Difference in ssGSEA scores calculated by gene signature from *Singh D et.al.* (D) Difference in gene expression of gene signature from *Morrow JD et.al.*, which was negatively associated with exacerbation risk. (E) Difference in ssGSEA score calculated by gene signature from *Morrow JD et.al.*



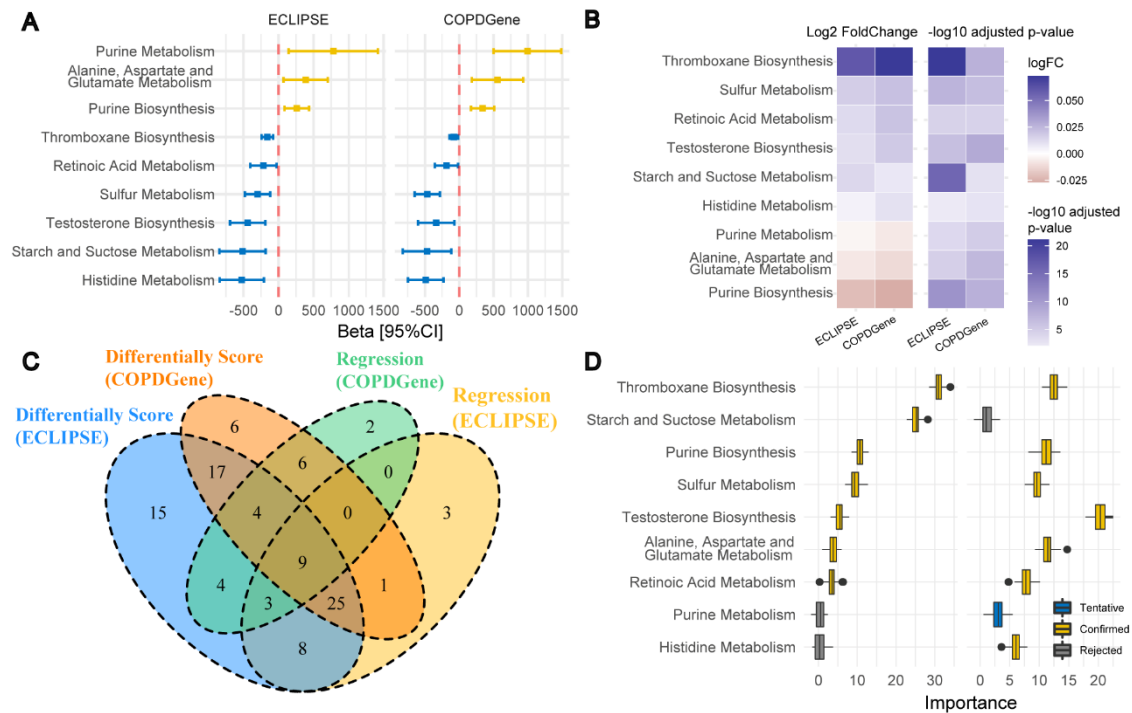
Supplementary Figure 4. Infer the difference in exacerbation risk between C1 and C2 in the COPDGenes dataset from the point of view of gene signatures. (A) Difference in gene expression of gene signature from *Singh D et.al.*, which was positively associated with exacerbation risk. (B) Difference in gene expression of gene signature from *Singh D et.al.*, which was negatively associated with exacerbation risk. (C) Difference in ssGSEA scores calculated by gene signature from *Singh D et.al.* (D) Difference in gene expression of gene signature from *Morrow JD et.al.*, which was negatively associated with exacerbation risk. (E) Difference in ssGSEA score calculated by gene signature from *Morrow JD et.al.*



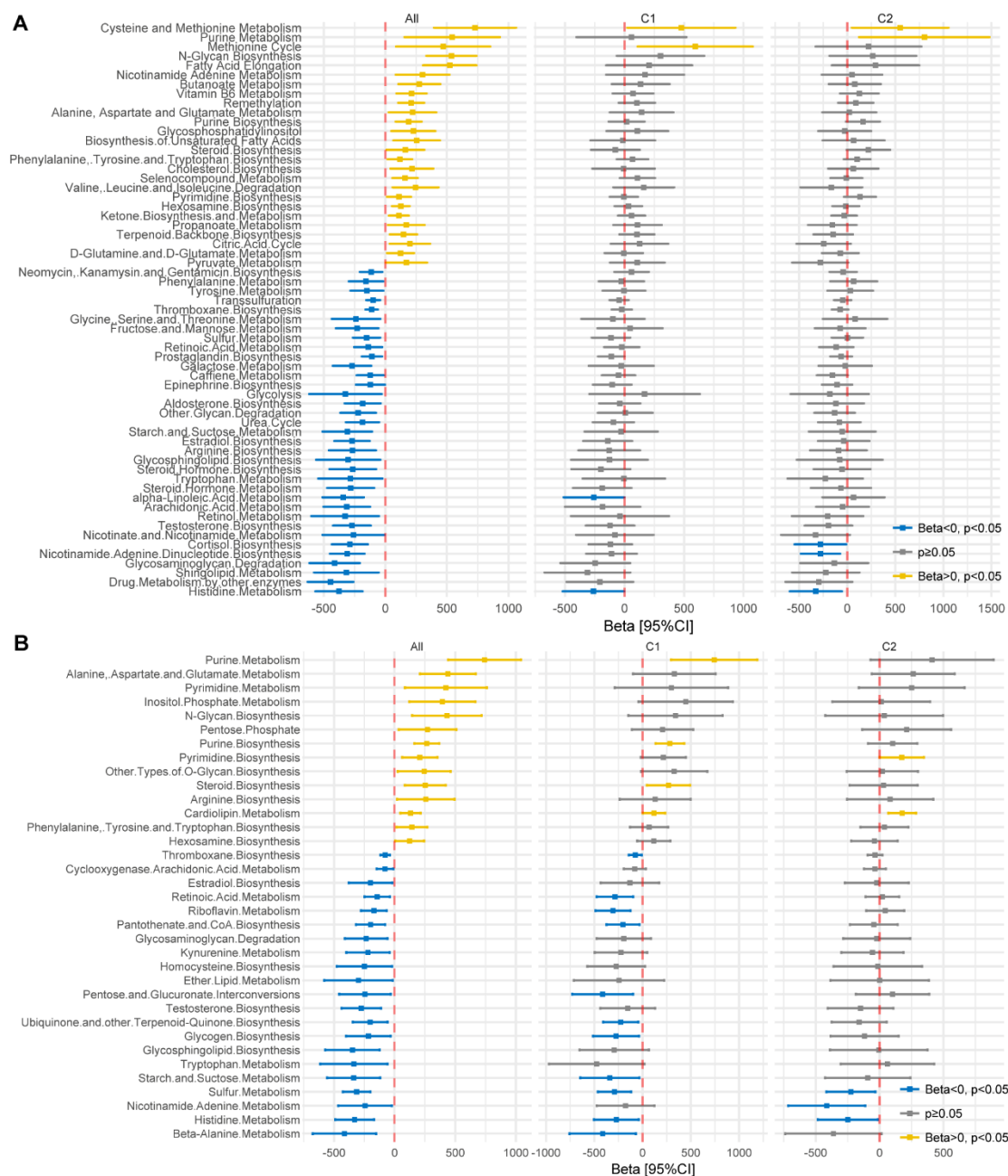
Supplementary Figure 5. Differences in gene expression related to FEV1 decline between C1 and C2 in the (A) ECLIPSE and (B) COPDGene datasets.



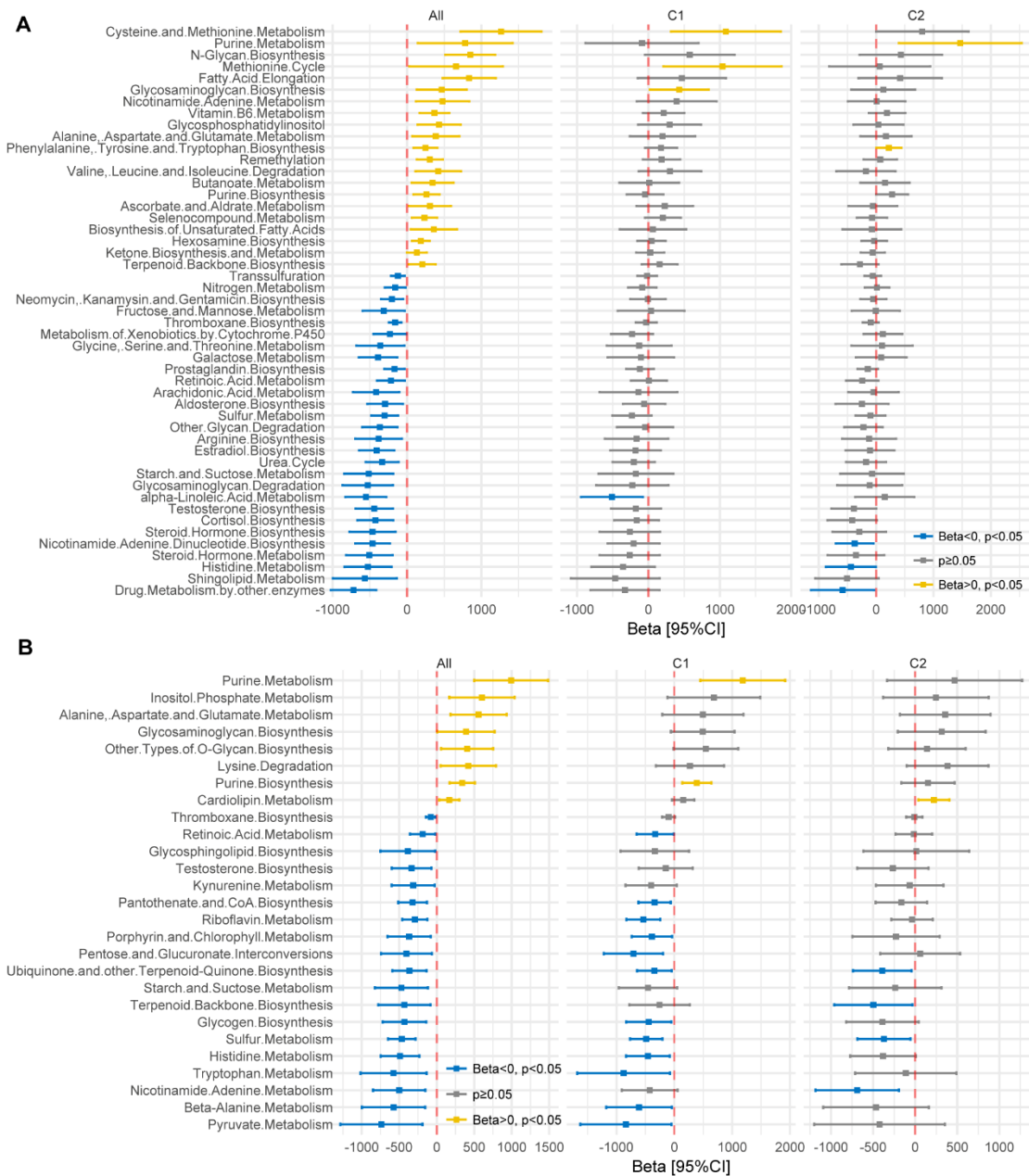
Supplementary Figure 6. Flow diagram depicting the processes of identifying the key pathways for the two subtypes and airway limitation.



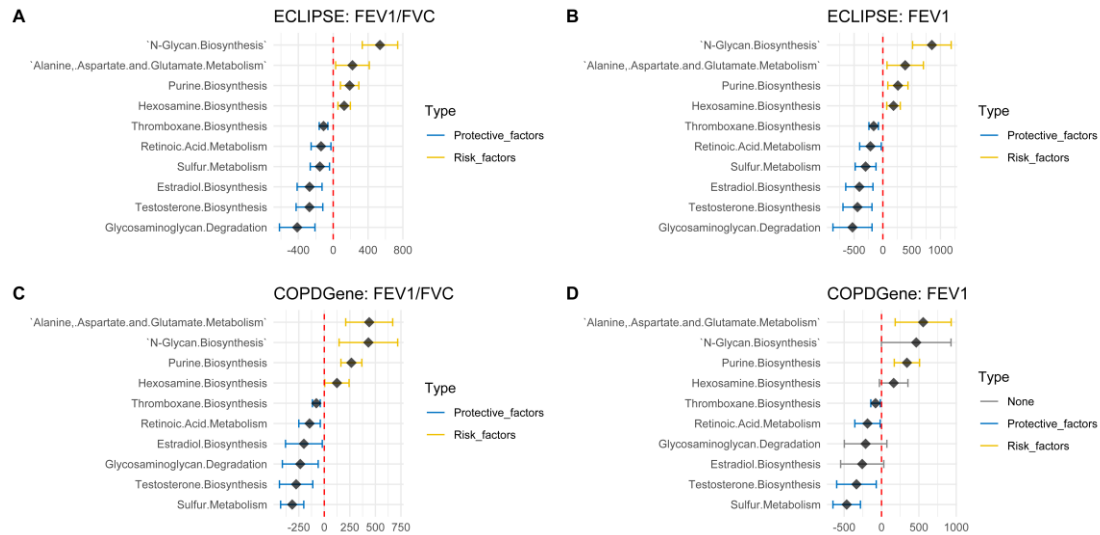
Supplementary Figure 7. Correlations of the COPD subtypes with FEV1-related metabolic pathways. | (A) Forest plot of association between ssGSEA scores of 9 metabolic pathways and FEV1. (B) Heatmap displaying the differences in ssGSEA scores of 9 metabolic pathways in COPD subtypes (C1 vs C2). (C) Venn diagram showing the overlapping result of univariate linear regression (ssGSEA score to FEV1) and difference analysis (C1 vs C2) in Evaluation of COPD to ECLIPSE and COPDGene datasets. (D) Boxplot showing the attribute importance of 9 metabolism pathway ssGSEA score for two COPD subtypes in ECLIPSE and COPDGene datasets based on Boruta method.



Supplementary Figure 8. Forest plot displaying the association between metabolic pathway ssGSEA scores of and FEV1/FVC in the (A) ECLIPSE and (B) COPDGene datasets. From left to right, the association with ssGSEA scores in whole dataset, C1 and C2 are shown.



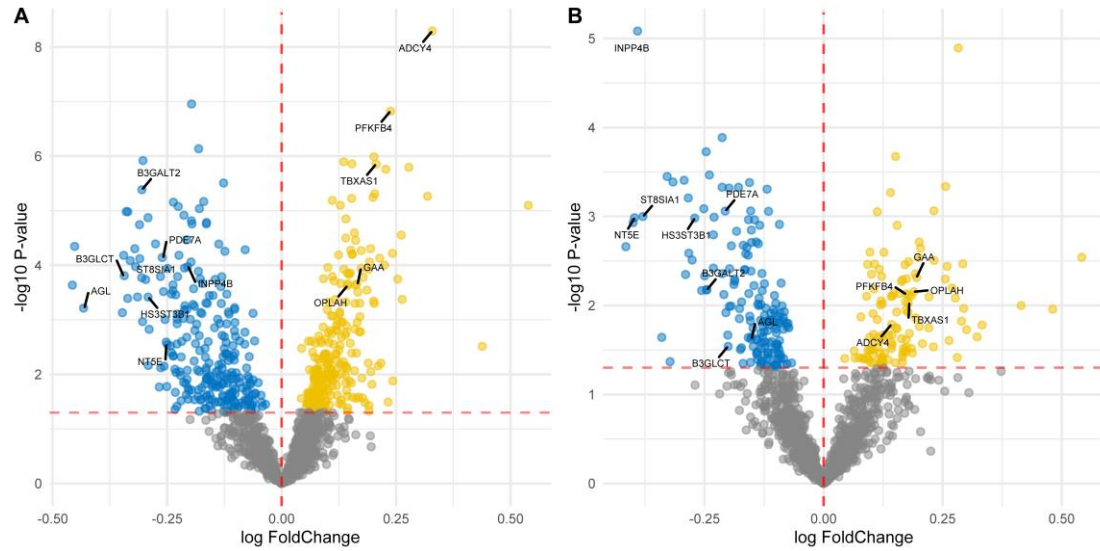
Supplementary Figure 9. Forest plot displaying the association between metabolic pathway ssGSEA scores and FEV1 in the (A) ECLIPSE and (B) COPDGene datasets. From left to right, the association with ssGSEA scores in whole dataset, C1 and C2 are shown.



Supplementary Figure 10. Association of ten key pathways with FEV1 or FEV1/FVC in two datasets.

Supplementary Table 8. Top-10 up-regulated and down-regulated genes (C1 vs C2) sorted by RRA score.

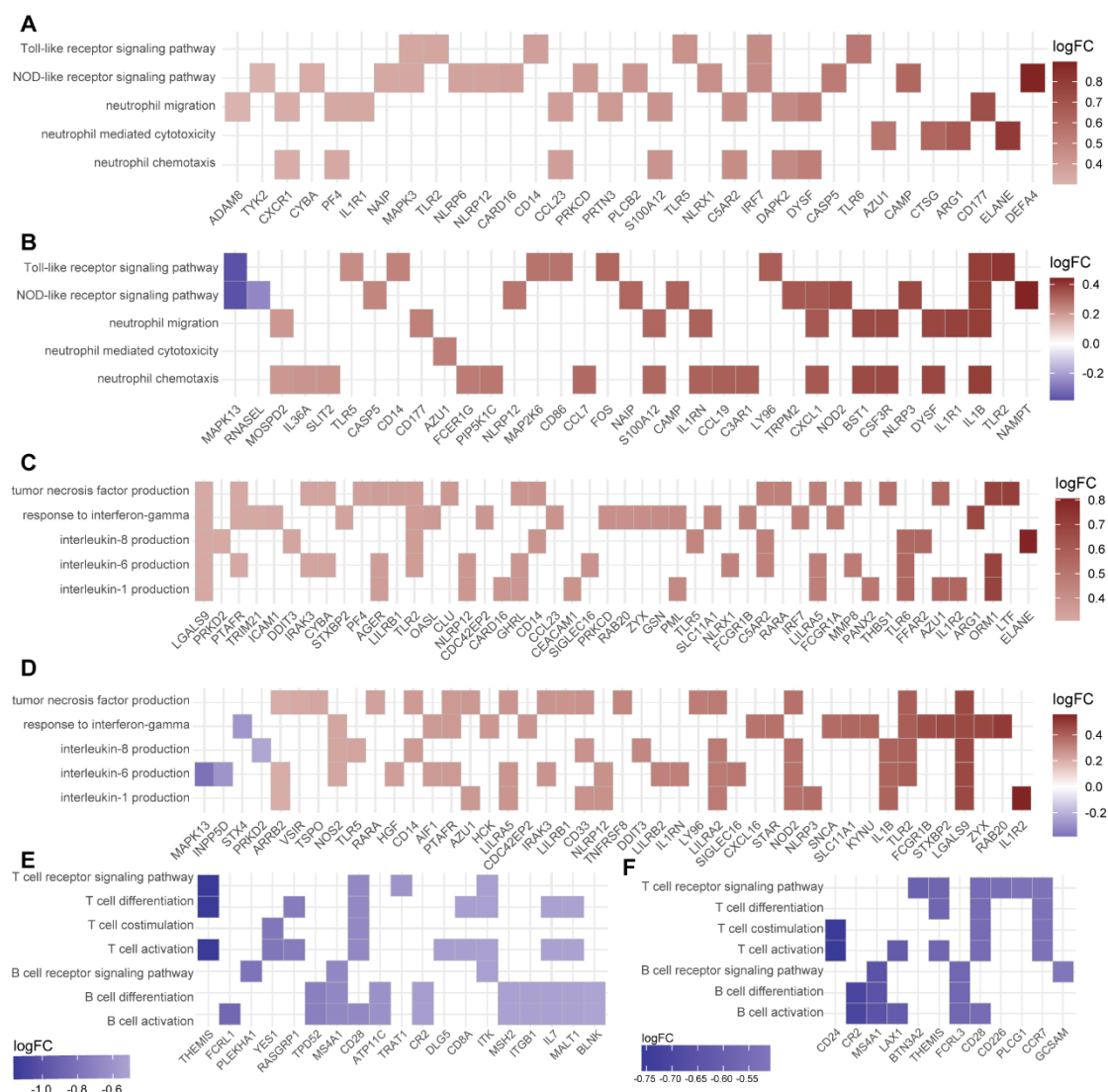
Gene symbol	ECLIPSE			COPDGene			RRA Score
	logFC	P-Value	Adjusted P	logFC	P-Value	Adjusted P	
ENPP5	-0.82101	4.61E-12	4.68E-11	-0.74673	7.06E-07	1.57E-05	1.74E-05
CENPK	-0.80845	4.45E-11	3.84E-10	-0.87919	2.55E-08	1.17E-06	2.34E-05
SLAIN1	-0.78351	4.90E-30	3.19E-27	-0.6023	2.92E-10	3.62E-08	3.79E-05
THEMIS	-1.16241	2.01E-29	1.13E-26	-0.57466	5.39E-08	2.10E-06	6.26E-05
PLEKHG1	-0.76366	2.11E-12	2.27E-11	-0.60829	2.13E-06	3.78E-05	8.12E-05
KLRC4	-0.69721	6.26E-12	6.19E-11	-0.52337	0.001512	0.006888	0.000333
NAP1L2	-0.72422	3.98E-14	5.84E-13	-0.51134	1.40E-08	7.20E-07	0.0004
FAM169A	-0.69481	3.29E-16	7.22E-15	-0.50525	5.27E-09	3.43E-07	0.000445
OSBPL10	-0.67977	5.03E-13	6.03E-12	-0.58567	8.98E-06	0.000118	0.000464
TMEM64	-0.67856	1.13E-18	4.00E-17	-0.51234	1.15E-11	3.11E-09	0.000474
LRG1	0.564423	1.32E-21	8.49E-20	0.539592	3.39E-05	0.000338	4.81E-05
IL1R2	0.562114	1.11E-24	1.56E-22	0.554873	4.39E-05	0.000414	5.01E-05
CA1	0.541289	0.000331	0.000754	0.463952	0.011934	0.034972	8.99E-05
ADAMTSL4	0.538026	1.32E-25	2.46E-23	0.582234	5.14E-08	2.03E-06	9.81E-05
AHSP	0.531073	0.000181	0.000438	0.552153	0.004042	0.014918	0.000119
MCEMP1	0.524359	8.1E-14	1.13E-12	0.446085	2.86E-06	4.75E-05	0.000155
HP	0.498903	1.4E-06	5.37E-06	0.751921	4.16E-05	0.000396	0.000204
S100P	0.497304	1.42E-05	4.41E-05	0.573979	0.000146	0.001084	0.000212
MRVII	0.537425	7.07E-25	1.06E-22	0.430851	1.4E-07	4.47E-06	0.000221
RARA-AS1	0.496019	1.4E-23	1.51E-21	0.490217	2.04E-12	9.35E-10	0.000221



Supplementary Figure 11. Volcano plot showing differentially expressed genes (DEGs) related to between COPD patients and healthy smokers in the (A) ECLIPSE and (B) COPDGene datasets. The upregulated and downregulated genes with RRA score<0.05 are labelled in the figure.

Supplementary Table 9. Up-regulated and down-regulated genes (COPD patients vs Healthy smokers) sorted by RRA score.

Genes	RRA score	FEV1/FVC (ECLIPSE)		FEV1/FVC (COPDGene)		FEV1 (ECLIPSE)		FEV1 (COPDGene)	
		Beta	P-value	Beta	P-value	Beta	P-value	Beta	P-value
B3GALT2	0.006	11.66	9.47E-06	5.90	0.042	14.93	6.17E-04	7.89	0.088
ST8SIA1	0.006	10.17	4.20E-06	6.33	0.005	15.56	1.93E-05	10.32	0.004
HS3ST3B1	0.007	6.58	0.002	8.60	0.006	10.39	0.004	11.24	0.026
PDE7A	0.013	9.21	6.28E-04	15.74	1.44E-04	14.51	0.001	20.46	0.002
B3GLCT	0.016	7.53	1.05E-04	4.66	0.106	10.53	0.001	5.58	0.226
NT5E	0.018	7.61	3.52E-04	6.50	0.002	12.18	5.00E-04	9.34	0.006
AGL	0.032	3.55	0.012	5.15	0.190	4.15	0.075	3.72	0.553
INPP4B	0.043	16.57	4.95E-07	12.58	9.75E-06	21.28	1.01E-04	19.82	1.29E-05
ADCY4	0.012	-17.41	7.32E-09	-5.25	0.241	25.64	2.63E-07	-9.64	0.177
PFKFB4	0.024	-21.17	2.24E-08	-13.32	9.20E-04	-30.52	1.11E-06	-17.65	0.006
TBXAS1	0.025	-17.18	2.62E-05	-14.25	1.68E-04	-26.33	9.08E-05	-15.68	0.011
GAA	0.036	-15.35	1.19E-04	-11.48	0.002	-23.55	3.32E-04	-14.60	0.015
OPLAH	0.039	-19.36	1.76E-05	-9.74	0.009	-25.99	4.89E-04	-15.23	0.011



Supplementary Figure 12. Gene expression (C1 vs C2) of genes in the immune process-related pathways. Pathogen recognition and neutrophil-related pathways in the (A) ECLIPSE and (B) COPDGen datasets. Cytokine-related pathways in the (C) ECLIPSE and (D) COPDGen datasets. T and B cell-related pathways in the (E) ECLIPSE and (F) COPDGen datasets.

Supplementary Table 10. Detailed results of GSEA for GO-BP, KEGG and Reactome in the ECLIPSE dataset.

Source	ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues
KEGG	hsa05168	Herpes simplex virus 1 infection	445	-0.52805	-2.24632	0.000102	0.00863	0.006691
KEGG	hsa03010	Ribosome	113	-0.55032	-2.1037	0.000118	0.00863	0.006691
KEGG	hsa03013	RNA transport	148	-0.49553	-1.95052	0.000113	0.00863	0.006691
KEGG	hsa03008	Ribosome biogenesis in eukaryotes	71	-0.53893	-1.9229	0.000127	0.00863	0.006691
KEGG	hsa03060	Protein export	23	-0.64305	-1.85801	0.001045	0.016627	0.012891
KEGG	hsa04612	Antigen processing and presentation	65	-0.52764	-1.85629	0.000129	0.00863	0.006691
KEGG	hsa04710	Circadian rhythm	28	-0.61364	-1.85163	0.000871	0.016627	0.012891

KEGG	hsa03018	RNA degradation	76	-0.50544	-1.82309	0.000251	0.011975	0.009284
KEGG	hsa00062	Fatty acid elongation	23	-0.61538	-1.77805	0.002838	0.030572	0.023702
KEGG	hsa00900	Terpenoid backbone biosynthesis	22	-0.61553	-1.76049	0.003318	0.03358	0.026034
KEGG	hsa04660	T cell receptor signaling pathway	102	-0.46374	-1.74774	0.000239	0.011975	0.009284
KEGG	hsa03460	Fanconi anemia pathway	48	-0.51566	-1.72494	0.002148	0.027384	0.021231
KEGG	hsa00280	Valine, leucine and isoleucine degradation	48	-0.51487	-1.72227	0.002282	0.027384	0.021231
KEGG	hsa00513	Various types of N-glycan biosynthesis	38	-0.53187	-1.69945	0.005679	0.047884	0.037124
KEGG	hsa03022	Basal transcription factors	40	-0.52279	-1.69176	0.004675	0.041095	0.031861
KEGG	hsa05340	Primary immunodeficiency	36	-0.5357	-1.69104	0.006021	0.047884	0.037124
KEGG	hsa04110	Cell cycle	122	-0.43727	-1.68567	0.000349	0.014571	0.011296
KEGG	hsa00510	N-Glycan biosynthesis	48	-0.4984	-1.6672	0.004564	0.041095	0.031861
KEGG	hsa03040	Spliceosome	119	-0.42381	-1.62936	0.00117	0.017763	0.013771
KEGG	hsa03420	Nucleotide excision repair	43	-0.49184	-1.61329	0.011958	0.073963	0.057343
KEGG	hsa04120	Ubiquitin mediated proteolysis	135	-0.40936	-1.59645	0.002296	0.027384	0.021231
KEGG	hsa03015	mRNA surveillance pathway	84	-0.41333	-1.51536	0.011092	0.071244	0.055235
KEGG	hsa04390	Hippo signaling pathway	148	-0.37352	-1.47026	0.009711	0.066193	0.051319
KEGG	hsa04218	Cellular senescence	154	-0.37128	-1.46525	0.010034	0.067026	0.051965
KEGG	hsa04141	Protein processing in endoplasmic reticulum	164	-0.35757	-1.42205	0.014588	0.088589	0.068682
KEGG	hsa04015	Rap1 signaling pathway	203	0.265467	1.357058	0.010817	0.070843	0.054924
KEGG	hsa05132	Salmonella infection	242	0.263382	1.375444	0.007692	0.055853	0.043302
KEGG	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	70	0.329899	1.445286	0.016211	0.096688	0.074962
KEGG	hsa04270	Vascular smooth muscle contraction	126	0.299597	1.44747	0.007931	0.056359	0.043695
KEGG	hsa05418	Fluid shear stress and atherosclerosis	132	0.300528	1.460297	0.006011	0.047884	0.037124
KEGG	hsa04611	Platelet activation	119	0.315469	1.510299	0.004124	0.039352	0.030509
KEGG	hsa00590	Arachidonic acid metabolism	55	0.363314	1.516467	0.016577	0.097135	0.075308
KEGG	hsa04620	Toll-like receptor signaling pathway	95	0.331231	1.532619	0.006395	0.048547	0.037638
KEGG	hsa00983	Drug metabolism - other enzymes	61	0.359303	1.534851	0.011658	0.073468	0.056959
KEGG	hsa05323	Rheumatoid arthritis	85	0.344743	1.555603	0.004336	0.040229	0.031189
KEGG	hsa04640	Hematopoietic cell lineage	92	0.337899	1.557226	0.006201	0.048163	0.037341
KEGG	hsa05140	Leishmaniasis	70	0.357586	1.566582	0.006021	0.047884	0.037124
KEGG	hsa05152	Tuberculosis	170	0.317274	1.589979	0.001012	0.016627	0.012891
KEGG	hsa05133	Pertussis	70	0.367275	1.60903	0.003705	0.0364	0.028221
KEGG	hsa04666	Fc gamma R-mediated phagocytosis	91	0.356134	1.638095	0.002793	0.030572	0.023702
KEGG	hsa05202	Transcriptional misregulation in cancer	174	0.327786	1.648079	0.001037	0.016627	0.012891
KEGG	hsa00350	Tyrosine metabolism	36	0.438645	1.655077	0.009091	0.063258	0.049043
KEGG	hsa05034	Alcoholism	149	0.34118	1.68226	0.000871	0.016627	0.012891
KEGG	hsa04142	Lysosome	123	0.350697	1.687109	0.001413	0.020525	0.015913
KEGG	hsa05221	Acute myeloid leukemia	66	0.389693	1.688856	0.003138	0.032749	0.02539
KEGG	hsa04080	Neuroactive ligand-receptor interaction	327	0.315751	1.719838	0.002653	0.03055	0.023685
KEGG	hsa00592	alpha-Linolenic acid metabolism	20	0.542671	1.733851	0.007278	0.054019	0.041881
KEGG	hsa04621	NOD-like receptor signaling pathway	167	0.348463	1.74282	0.00098	0.016627	0.012891

KEGG	hsa04610	Complement and coagulation cascades	81	0.394437	1.77713	0.001026	0.016627	0.012891
KEGG	hsa05033	Nicotine addiction	38	0.478661	1.822385	0.001797	0.024796	0.019224
KEGG	hsa05219	Bladder cancer	41	0.48495	1.881077	0.001856	0.024796	0.019224
KEGG	hsa04721	Synaptic vesicle cycle	77	0.431822	1.921829	0.000503	0.015258	0.011829
KEGG	hsa04145	Phagosome	138	0.403478	1.976493	0.000782	0.016627	0.012891
KEGG	hsa05150	Staphylococcus aureus infection	75	0.446743	1.983105	0.000484	0.015258	0.011829
KEGG	hsa04380	Osteoclast differentiation	125	0.438514	2.115038	0.000713	0.016627	0.012891
KEGG	hsa05144	Malaria	46	0.540767	2.156147	0.000393	0.014571	0.011296
KEGG	hsa05322	Systemic lupus erythematosus	93	0.496957	2.292681	0.000567	0.015787	0.01224
GO-BP	GO:0006399	tRNA metabolic process	182	-0.56416	-2.2704	0.000111	0.015459	0.013196
GO-BP	GO:0006400	tRNA modification	82	-0.61455	-2.25193	0.000124	0.015459	0.013196
GO-BP	GO:0008033	tRNA processing	123	-0.58208	-2.25186	0.000117	0.015459	0.013196
GO-BP	GO:0042254	ribosome biogenesis	274	-0.53627	-2.22673	0.000106	0.015459	0.013196
GO-BP	GO:0022613	ribonucleoprotein complex biogenesis	433	-0.51866	-2.20878	0.000102	0.015459	0.013196
GO-BP	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	80	-0.60372	-2.20248	0.000125	0.015459	0.013196
GO-BP	GO:0006613	cotranslational protein targeting to membrane	84	-0.59824	-2.19553	0.000124	0.015459	0.013196
GO-BP	GO:0034470	ncRNA processing	348	-0.51784	-2.18148	0.000104	0.015459	0.013196
GO-BP	GO:0001510	RNA methylation	77	-0.59917	-2.1711	0.000126	0.015459	0.013196
GO-BP	GO:0006413	translational initiation	167	-0.5357	-2.13583	0.000112	0.015459	0.013196
GO-BP	GO:0006364	rRNA processing	197	-0.52225	-2.11506	0.00011	0.015459	0.013196
GO-BP	GO:0072599	establishment of protein localization to endoplasmic reticulum	96	-0.56303	-2.10993	0.000122	0.015459	0.013196
GO-BP	GO:0045047	protein targeting to ER	92	-0.56352	-2.09901	0.000122	0.015459	0.013196
GO-BP	GO:0030488	tRNA methylation	38	-0.64771	-2.09603	0.000139	0.016525	0.014105
GO-BP	GO:0006405	RNA export from nucleus	123	-0.54089	-2.09251	0.000117	0.015459	0.013196
GO-BP	GO:0009451	RNA modification	153	-0.52768	-2.08963	0.000113	0.015459	0.013196
GO-BP	GO:0000959	mitochondrial RNA metabolic process	42	-0.62997	-2.07036	0.000139	0.016525	0.014105
GO-BP	GO:0097064	ncRNA export from nucleus	37	-0.64117	-2.06188	0.00014	0.016525	0.014105
GO-BP	GO:0016072	rRNA metabolic process	234	-0.49718	-2.04417	0.000107	0.015459	0.013196
GO-BP	GO:0045292	mRNA cis splicing, via spliceosome	28	-0.67203	-2.04072	0.000147	0.017027	0.014533
GO-BP	GO:0071426	ribonucleoprotein complex export from nucleus	115	-0.53134	-2.03721	0.000119	0.015459	0.013196
GO-BP	GO:0071166	ribonucleoprotein complex localization	116	-0.53036	-2.0362	0.000118	0.015459	0.013196
GO-BP	GO:0051236	establishment of RNA localization	179	-0.5047	-2.02616	0.000111	0.015459	0.013196
GO-BP	GO:0140053	mitochondrial gene expression	159	-0.5098	-2.0243	0.000112	0.015459	0.013196
GO-BP	GO:0090070	positive regulation of ribosome biogenesis	9	-0.88335	-2.02297	0.000173	0.019516	0.016659
GO-BP	GO:2000234	positive regulation of rRNA processing	9	-0.88335	-2.02297	0.000173	0.019516	0.016659
GO-BP	GO:0042273	ribosomal large subunit biogenesis	63	-0.57168	-2.01833	0.000259	0.02337	0.019948
GO-BP	GO:0022618	ribonucleoprotein complex assembly	220	-0.49242	-2.01534	0.000108	0.015459	0.013196
GO-BP	GO:0006403	RNA localization	211	-0.49154	-2.00422	0.000109	0.015459	0.013196
GO-BP	GO:0090069	regulation of ribosome biogenesis	14	-0.7734	-1.99722	0.000815	0.029038	0.024786

GO-BP	GO:0050657	nucleic acid transport	176	-0.49576	-1.98783	0.000111	0.015459	0.013196
GO-BP	GO:0050658	RNA transport	176	-0.49576	-1.98783	0.000111	0.015459	0.013196
GO-BP	GO:0000381	regulation of alternative mRNA splicing, via spliceosome	58	-0.57061	-1.98748	0.000263	0.02337	0.019948
GO-BP	GO:0002181	cytoplasmic translation	89	-0.53351	-1.97987	0.000123	0.015459	0.013196
GO-BP	GO:0051031	tRNA transport	34	-0.62601	-1.97914	0.000286	0.024493	0.020906
GO-BP	GO:0000380	alternative mRNA splicing, via spliceosome	67	-0.55596	-1.97674	0.000258	0.02337	0.019948
GO-BP	GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	13	-0.77646	-1.96459	0.000821	0.029038	0.024786
GO-BP	GO:2000232	regulation of rRNA processing	12	-0.79149	-1.959	0.000498	0.025683	0.021922
GO-BP	GO:0071826	ribonucleoprotein complex subunit organization	234	-0.47585	-1.95646	0.000107	0.015459	0.013196
GO-BP	GO:0006409	tRNA export from nucleus	33	-0.62139	-1.95448	0.000287	0.024493	0.020906
GO-BP	GO:0071431	tRNA-containing ribonucleoprotein complex export from nucleus	33	-0.62139	-1.95448	0.000287	0.024493	0.020906
GO-BP	GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	14	-0.7559	-1.95204	0.000815	0.029038	0.024786
GO-BP	GO:0015931	nucleobase-containing compound transport	221	-0.47585	-1.94788	0.000108	0.015459	0.013196
GO-BP	GO:0006607	NLS-bearing protein import into nucleus	12	-0.78454	-1.9418	0.000831	0.029038	0.024786
GO-BP	GO:0000054	ribosomal subunit export from nucleus	13	-0.75816	-1.91827	0.001313	0.037238	0.031785
GO-BP	GO:0033750	ribosome localization	13	-0.75816	-1.91827	0.001313	0.037238	0.031785
GO-BP	GO:0007062	sister chromatid cohesion	57	-0.55072	-1.91339	0.000264	0.02337	0.019948
GO-BP	GO:0034502	protein localization to chromosome	78	-0.52676	-1.91215	0.000252	0.02337	0.019948
GO-BP	GO:0006448	regulation of translational elongation	17	-0.70537	-1.90637	0.000787	0.029036	0.024784
GO-BP	GO:0071578	zinc ion import across plasma membrane	8	-0.85296	-1.89846	0.000868	0.029977	0.025588
GO-BP	GO:0000460	maturation of 5.8S rRNA	26	-0.63204	-1.88935	0.000888	0.030429	0.025973
GO-BP	GO:0051028	mRNA transport	136	-0.4822	-1.88536	0.000115	0.015459	0.013196
GO-BP	GO:0000956	nuclear-transcribed mRNA catabolic process	183	-0.46746	-1.88259	0.000111	0.015459	0.013196
GO-BP	GO:0000469	cleavage involved in rRNA processing	21	-0.66237	-1.8811	0.000919	0.031017	0.026475
GO-BP	GO:0000470	maturation of LSU-rRNA	19	-0.67424	-1.88065	0.001696	0.041246	0.035207
GO-BP	GO:0046112	nucleobase biosynthetic process	19	-0.66956	-1.8676	0.001696	0.041246	0.035207
GO-BP	GO:0016556	mRNA modification	20	-0.66138	-1.86413	0.001535	0.040114	0.03424
GO-BP	GO:0070911	global genome nucleotide-excision repair	25	-0.62852	-1.86327	0.001186	0.034882	0.029774
GO-BP	GO:0045005	DNA-dependent DNA replication maintenance of fidelity	39	-0.57192	-1.85892	0.001114	0.03376	0.028817
GO-BP	GO:0032543	mitochondrial translation	132	-0.47702	-1.85859	0.000116	0.015459	0.013196
GO-BP	GO:0043414	macromolecule methylation	294	-0.44515	-1.85711	0.000105	0.015459	0.013196

GO-BP	GO:1900034	regulation of cellular response to heat	75	-0.5137	-1.8563	0.000633	0.027137	0.023164
GO-BP	GO:0006406	mRNA export from nucleus	99	-0.49188	-1.84877	0.000121	0.015459	0.013196
GO-BP	GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	99	-0.49188	-1.84877	0.000121	0.015459	0.013196
GO-BP	GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	21	-0.65096	-1.84868	0.001379	0.038228	0.032631
GO-BP	GO:0035459	cargo loading into vesicle	20	-0.65547	-1.84748	0.001535	0.040114	0.03424
GO-BP	GO:0000725	recombinational repair	128	-0.47509	-1.84498	0.000117	0.015459	0.013196
GO-BP	GO:0015693	magnesium ion transport	16	-0.69047	-1.84301	0.001431	0.038842	0.033154
GO-BP	GO:1901844	regulation of cell communication by electrical coupling involved in cardiac conduction	8	-0.82717	-1.84105	0.001389	0.038371	0.032752
GO-BP	GO:0071459	protein localization to chromosome, centromeric region	21	-0.64777	-1.83964	0.001686	0.041246	0.035207
GO-BP	GO:0070972	protein localization to endoplasmic reticulum	120	-0.47715	-1.83798	0.000236	0.02337	0.019948
GO-BP	GO:0048291	isotype switching to IgG isotypes	13	-0.72521	-1.83491	0.002134	0.047073	0.04018
GO-BP	GO:0019080	viral gene expression	170	-0.45947	-1.83425	0.000112	0.015459	0.013196
GO-BP	GO:1901796	regulation of signal transduction by p53 class mediator	173	-0.45821	-1.83285	0.000112	0.015459	0.013196
GO-BP	GO:1903830	magnesium ion transmembrane transport	15	-0.69596	-1.83088	0.002083	0.046571	0.039751
GO-BP	GO:0031123	RNA 3'-end processing	128	-0.47087	-1.82858	0.000117	0.015459	0.013196
GO-BP	GO:0042255	ribosome assembly	52	-0.53451	-1.82658	0.001072	0.033277	0.028404
GO-BP	GO:0000724	double-strand break repair via homologous recombination	127	-0.46988	-1.82296	0.000117	0.015459	0.013196
GO-BP	GO:0000963	mitochondrial RNA processing	17	-0.67446	-1.82282	0.002362	0.048898	0.041738
GO-BP	GO:0019083	viral transcription	156	-0.45895	-1.82031	0.000113	0.015459	0.013196
GO-BP	GO:0032259	methylation	346	-0.43051	-1.81343	0.000104	0.015459	0.013196
GO-BP	GO:0042274	ribosomal small subunit biogenesis	63	-0.51304	-1.81127	0.000777	0.028779	0.024565
GO-BP	GO:0035871	protein K11-linked deubiquitination	9	-0.79035	-1.81	0.002417	0.049218	0.042011
GO-BP	GO:0007063	regulation of sister chromatid cohesion	22	-0.62969	-1.80904	0.002288	0.04809	0.041048
GO-BP	GO:0031365	N-terminal protein amino acid modification	27	-0.60059	-1.80859	0.002365	0.048898	0.041738
GO-BP	GO:0000729	DNA double-strand break processing	23	-0.62311	-1.80803	0.00242	0.049218	0.042011
GO-BP	GO:0006417	regulation of translation	318	-0.43072	-1.80613	0.000105	0.015459	0.013196
GO-BP	GO:0036297	interstrand cross-link repair	49	-0.53417	-1.80314	0.000948	0.031207	0.026637
GO-BP	GO:0061157	mRNA destabilization	28	-0.59264	-1.79966	0.002201	0.047407	0.040465
GO-BP	GO:0033683	nucleotide-excision repair, DNA incision	38	-0.55605	-1.79942	0.001953	0.044849	0.038281
GO-BP	GO:0090503	RNA phosphodiester bond hydrolysis, exonucleolytic	41	-0.54827	-1.79615	0.001803	0.042887	0.036607
GO-BP	GO:0031023	microtubule organizing center	128	-0.46226	-1.79517	0.000233	0.02337	0.019948

		organization						
GO-BP	GO:0007064	mitotic sister chromatid cohesion	23	-0.61863	-1.79502	0.00242	0.049218	0.042011
GO-BP	GO:0006289	nucleotide-excision repair	105	-0.47127	-1.78928	0.00012	0.015459	0.013196
GO-BP	GO:0031297	replication fork processing	30	-0.58136	-1.78785	0.002331	0.04843	0.041338
GO-BP	GO:0043484	regulation of RNA splicing	120	-0.46361	-1.78582	0.000236	0.02337	0.019948
GO-BP	GO:0017148	negative regulation of translation	123	-0.46149	-1.78534	0.000351	0.02533	0.021621
GO-BP	GO:0061014	positive regulation of mRNA catabolic process	46	-0.53476	-1.78521	0.001367	0.03801	0.032444
GO-BP	GO:0061087	positive regulation of histone H3-K27 methylation	6	-0.87013	-1.78251	0.001086	0.033277	0.028404
GO-BP	GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	61	-0.50525	-1.77458	0.001433	0.038842	0.033154
GO-BP	GO:0016444	somatic cell DNA recombination	61	-0.50525	-1.77458	0.001433	0.038842	0.033154
GO-BP	GO:0006446	regulation of translational initiation	73	-0.4929	-1.77455	0.000763	0.028621	0.02443
GO-BP	GO:0032392	DNA geometric change	115	-0.45941	-1.76143	0.000356	0.02533	0.021621
GO-BP	GO:1905515	non-motile cilium assembly	54	-0.51152	-1.76056	0.001864	0.043724	0.037321
GO-BP	GO:0051168	nuclear export	181	-0.43788	-1.76053	0.000111	0.015459	0.013196
GO-BP	GO:0008380	RNA splicing	396	-0.41481	-1.75986	0.000103	0.015459	0.013196
GO-BP	GO:0000375	RNA splicing, via transesterification reactions	317	-0.41971	-1.75905	0.000105	0.015459	0.013196
GO-BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	314	-0.41927	-1.75643	0.000105	0.015459	0.013196
GO-BP	GO:0000398	mRNA splicing, via spliceosome	314	-0.41927	-1.75643	0.000105	0.015459	0.013196
GO-BP	GO:0048024	regulation of mRNA splicing, via spliceosome	88	-0.47396	-1.75636	0.000614	0.026873	0.022938
GO-BP	GO:0006415	translational termination	101	-0.46521	-1.75433	0.000241	0.02337	0.019948
GO-BP	GO:0051298	centrosome duplication	64	-0.49466	-1.75082	0.001552	0.040225	0.034335
GO-BP	GO:0006397	mRNA processing	463	-0.40937	-1.74861	0.000102	0.015459	0.013196
GO-BP	GO:0016925	protein sumoylation	77	-0.4823	-1.74762	0.000757	0.028509	0.024335
GO-BP	GO:0007098	centrosome cycle	120	-0.45341	-1.74651	0.000354	0.02533	0.021621
GO-BP	GO:0032508	DNA duplex unwinding	106	-0.45925	-1.74555	0.000358	0.02533	0.021621
GO-BP	GO:0031503	protein-containing complex localization	264	-0.41839	-1.7333	0.000106	0.015459	0.013196
GO-BP	GO:0006402	mRNA catabolic process	328	-0.41142	-1.72782	0.000104	0.015459	0.013196
GO-BP	GO:0006261	DNA-dependent DNA replication	149	-0.43788	-1.72778	0.000228	0.02337	0.019948
GO-BP	GO:2001020	regulation of response to DNA damage stimulus	203	-0.42369	-1.72184	0.000109	0.015459	0.013196
GO-BP	GO:0006414	translational elongation	124	-0.44369	-1.71869	0.000583	0.026355	0.022496
GO-BP	GO:0000819	sister chromatid segregation	180	-0.42558	-1.71052	0.000111	0.015459	0.013196
GO-BP	GO:0050684	regulation of mRNA processing	124	-0.44115	-1.70882	0.0007	0.027687	0.023633
GO-BP	GO:0006611	protein export from nucleus	166	-0.42665	-1.70133	0.000112	0.015459	0.013196
GO-BP	GO:0006310	DNA recombination	276	-0.4095	-1.7003	0.000106	0.015459	0.013196

GO-BP	GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	74	-0.47051	-1.69594	0.001651	0.04119	0.035159
GO-BP	GO:0006892	post-Golgi vesicle-mediated transport	102	-0.44846	-1.69479	0.001442	0.038842	0.033154
GO-BP	GO:0031124	mRNA 3'-end processing	88	-0.45633	-1.69102	0.00172	0.041594	0.035503
GO-BP	GO:0002200	somatic diversification of immune receptors	71	-0.47162	-1.68997	0.001915	0.04433	0.037839
GO-BP	GO:0034248	regulation of cellular amide metabolic process	374	-0.39928	-1.68873	0.000103	0.015459	0.013196
GO-BP	GO:0007030	Golgi organization	117	-0.43771	-1.68241	0.000944	0.031207	0.026637
GO-BP	GO:0006479	protein methylation	173	-0.41991	-1.67966	0.000112	0.015459	0.013196
GO-BP	GO:0008213	protein alkylation	173	-0.41991	-1.67966	0.000112	0.015459	0.013196
GO-BP	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	100	-0.44461	-1.67469	0.001689	0.041246	0.035207
GO-BP	GO:0051225	spindle assembly	99	-0.44534	-1.67384	0.001936	0.044576	0.038049
GO-BP	GO:0098781	ncRNA transcription	104	-0.44126	-1.67202	0.00192	0.04433	0.037839
GO-BP	GO:0034605	cellular response to heat	124	-0.42941	-1.66338	0.000933	0.031135	0.026576
GO-BP	GO:0070126	mitochondrial translational termination	87	-0.44897	-1.66209	0.002211	0.047407	0.040465
GO-BP	GO:0070125	mitochondrial translational elongation	86	-0.45013	-1.66183	0.002223	0.047539	0.040578
GO-BP	GO:0006401	RNA catabolic process	360	-0.39208	-1.65582	0.000104	0.015459	0.013196
GO-BP	GO:0045727	positive regulation of translation	112	-0.43291	-1.65472	0.00167	0.041246	0.035207
GO-BP	GO:0006302	double-strand break repair	229	-0.40271	-1.65293	0.000108	0.015459	0.013196
GO-BP	GO:0098813	nuclear chromosome segregation	250	-0.3994	-1.6503	0.000106	0.015459	0.013196
GO-BP	GO:0034249	negative regulation of cellular amide metabolic process	142	-0.41943	-1.64746	0.00103	0.032569	0.0278
GO-BP	GO:0006260	DNA replication	266	-0.39649	-1.64378	0.000106	0.015459	0.013196
GO-BP	GO:0051169	nuclear transport	321	-0.38934	-1.63246	0.000105	0.015459	0.013196
GO-BP	GO:0072331	signal transduction by p53 class mediator	255	-0.39207	-1.62137	0.000106	0.015459	0.013196
GO-BP	GO:0006913	nucleocytoplasmic transport	318	-0.38541	-1.61613	0.000105	0.015459	0.013196
GO-BP	GO:1903311	regulation of mRNA metabolic process	301	-0.38578	-1.61157	0.000105	0.015459	0.013196
GO-BP	GO:0090305	nucleic acid phosphodiester bond hydrolysis	276	-0.38697	-1.60673	0.000106	0.015459	0.013196
GO-BP	GO:0009411	response to UV	136	-0.40999	-1.60303	0.002077	0.046571	0.039751
GO-BP	GO:0000070	mitotic sister chromatid segregation	148	-0.40467	-1.59542	0.001821	0.043072	0.036765
GO-BP	GO:0070646	protein modification by small protein removal	266	-0.38444	-1.59382	0.000106	0.015459	0.013196
GO-BP	GO:0043543	protein acylation	234	-0.38739	-1.59277	0.000215	0.02337	0.019948
GO-BP	GO:0050851	antigen receptor-mediated signaling pathway	237	-0.38534	-1.58477	0.000322	0.02533	0.021621
GO-BP	GO:0016573	histone acetylation	149	-0.40091	-1.58187	0.002048	0.046291	0.039512
GO-BP	GO:0007051	spindle organization	159	-0.39291	-1.56016	0.001912	0.04433	0.037839
GO-BP	GO:0018205	peptidyl-lysine modification	379	-0.3674	-1.5554	0.000103	0.015459	0.013196
GO-BP	GO:0007059	chromosome segregation	307	-0.37127	-1.55179	0.000105	0.015459	0.013196

GO-BP	GO:0042113	B cell activation	241	-0.37283	-1.53603	0.00075	0.028393	0.024235
GO-BP	GO:0006457	protein folding	201	-0.37787	-1.53422	0.001643	0.04119	0.035159
GO-BP	GO:0006473	protein acetylation	193	-0.37906	-1.53396	0.002087	0.046571	0.039751
GO-BP	GO:0048193	Golgi vesicle transport	346	-0.36414	-1.53388	0.000312	0.02533	0.021621
GO-BP	GO:0090150	establishment of protein localization to membrane	297	-0.36689	-1.53149	0.000105	0.015459	0.013196
GO-BP	GO:0044843	cell cycle G1/S phase transition	253	-0.36811	-1.52124	0.000533	0.02597	0.022167
GO-BP	GO:0000082	G1/S transition of mitotic cell cycle	237	-0.36944	-1.51939	0.000966	0.031557	0.026936
GO-BP	GO:0060271	cilium assembly	353	-0.3583	-1.51079	0.000415	0.025369	0.021654
GO-BP	GO:0030217	T cell differentiation	232	-0.36579	-1.50263	0.001613	0.041075	0.035061
GO-BP	GO:0006605	protein targeting	392	-0.35319	-1.49774	0.000206	0.02297	0.019607
GO-BP	GO:0072594	establishment of protein localization to organelle	500	-0.34956	-1.49653	0.000101	0.015459	0.013196
GO-BP	GO:0044782	cilium organization	369	-0.35352	-1.49447	0.00031	0.02533	0.021621
GO-BP	GO:0016579	protein deubiquitination	250	-0.35908	-1.48368	0.001917	0.04433	0.037839
GO-BP	GO:0000209	protein polyubiquitination	296	-0.35466	-1.48044	0.000526	0.02597	0.022167
GO-BP	GO:0000086	G2/M transition of mitotic cell cycle	237	-0.35768	-1.47102	0.002147	0.047073	0.04018
GO-BP	GO:0051052	regulation of DNA metabolic process	408	-0.34458	-1.4635	0.000308	0.02533	0.021621
GO-BP	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	401	-0.34248	-1.45365	0.000308	0.02533	0.021621
GO-BP	GO:0040029	regulation of gene expression, epigenetic	322	-0.34402	-1.44314	0.001568	0.040413	0.034496
GO-BP	GO:0030098	lymphocyte differentiation	343	-0.33994	-1.43142	0.001247	0.036071	0.030789
GO-BP	GO:0016569	covalent chromatin modification	452	-0.33544	-1.43132	0.00051	0.025683	0.021922
GO-BP	GO:0033044	regulation of chromosome organization	327	-0.33957	-1.42529	0.002195	0.047407	0.040465
GO-BP	GO:0016570	histone modification	436	-0.33333	-1.41954	0.000716	0.027687	0.023633
GO-BP	GO:0048285	organelle fission	430	-0.33241	-1.4152	0.000716	0.027687	0.023633
GO-BP	GO:0016311	dephosphorylation	460	-0.32829	-1.40154	0.001018	0.032398	0.027654
GO-BP	GO:0010498	proteasomal protein catabolic process	453	-0.32584	-1.39002	0.00153	0.040114	0.03424
GO-BP	GO:1903522	regulation of blood circulation	278	0.262742	1.40914	0.001808	0.042887	0.036607
GO-BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	203	0.282852	1.455909	0.002309	0.04809	0.041048
GO-BP	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	207	0.283458	1.456616	0.002398	0.049218	0.042011
GO-BP	GO:0051701	interaction with host	194	0.287034	1.471945	0.002255	0.047635	0.04066
GO-BP	GO:0010951	negative regulation of endopeptidase activity	220	0.285455	1.483236	0.001335	0.037366	0.031895
GO-BP	GO:0051147	regulation of muscle cell differentiation	146	0.301132	1.484773	0.002431	0.049316	0.042094
GO-BP	GO:0045765	regulation of angiogenesis	278	0.276976	1.48548	0.001808	0.042887	0.036607
GO-BP	GO:0098742	cell-cell adhesion via	243	0.282447	1.485911	0.00152	0.040114	0.03424

		plasma-membrane adhesion molecules							
GO-BP	GO:0002221	pattern recognition receptor signaling pathway	187	0.292381	1.490392	0.002144	0.047073	0.04018	
GO-BP	GO:0051092	positive regulation of NF-kappaB transcription factor activity	143	0.304199	1.492319	0.001599	0.041048	0.035037	
GO-BP	GO:0071466	cellular response to xenobiotic stimulus	163	0.299086	1.494475	0.001838	0.043243	0.036911	
GO-BP	GO:0051924	regulation of calcium ion transport	241	0.284038	1.494583	0.001488	0.039489	0.033707	
GO-BP	GO:0048167	regulation of synaptic plasticity	181	0.294907	1.499279	0.002035	0.046238	0.039467	
GO-BP	GO:0006941	striated muscle contraction	163	0.300514	1.501608	0.001838	0.043243	0.036911	
GO-BP	GO:0031348	negative regulation of defense response	196	0.292454	1.50263	0.002193	0.047407	0.040465	
GO-BP	GO:0043901	negative regulation of multi-organism process	154	0.303825	1.503406	0.00175	0.042183	0.036006	
GO-BP	GO:0032635	interleukin-6 production	141	0.309408	1.514616	0.001553	0.040225	0.034335	
GO-BP	GO:0002793	positive regulation of peptide secretion	274	0.283736	1.516515	0.001799	0.042887	0.036607	
GO-BP	GO:0050920	regulation of chemotaxis	204	0.295138	1.519312	0.002307	0.04809	0.041048	
GO-BP	GO:0050777	negative regulation of immune response	144	0.309499	1.52051	0.001612	0.041075	0.035061	
GO-BP	GO:0034341	response to interferon-gamma	178	0.29972	1.521393	0.001992	0.04548	0.03882	
GO-BP	GO:0032675	regulation of interleukin-6 production	132	0.31619	1.530601	0.00145	0.038842	0.033154	
GO-BP	GO:0050729	positive regulation of inflammatory response	132	0.316584	1.532511	0.00145	0.038842	0.033154	
GO-BP	GO:0015893	drug transport	200	0.298577	1.537895	0.001124	0.033836	0.028881	
GO-BP	GO:0055001	muscle cell development	168	0.305553	1.538977	0.000934	0.031135	0.026576	
GO-BP	GO:0042737	drug catabolic process	127	0.320083	1.539669	0.002092	0.046571	0.039751	
GO-BP	GO:0045766	positive regulation of angiogenesis	159	0.309483	1.541673	0.000899	0.030576	0.026098	
GO-BP	GO:0060078	regulation of postsynaptic membrane potential	134	0.318423	1.544297	0.001486	0.039489	0.033707	
GO-BP	GO:0008217	regulation of blood pressure	175	0.305447	1.54445	0.000983	0.031602	0.026974	
GO-BP	GO:0043271	negative regulation of ion transport	139	0.316124	1.546297	0.001541	0.040154	0.034274	
GO-BP	GO:1903034	regulation of response to wounding	165	0.309587	1.554454	0.000917	0.031017	0.026475	
GO-BP	GO:0050714	positive regulation of protein secretion	254	0.294511	1.557692	0.001623	0.041075	0.035061	
GO-BP	GO:1904018	positive regulation of vasculature development	179	0.307	1.561234	0.001996	0.04548	0.03882	
GO-BP	GO:0055007	cardiac muscle cell differentiation	110	0.334764	1.576936	0.002459	0.049534	0.042281	
GO-BP	GO:0051146	striated muscle cell differentiation	262	0.296822	1.578102	0.001715	0.041587	0.035497	
GO-BP	GO:0032102	negative regulation of response to external stimulus	317	0.290701	1.578403	0.002208	0.047407	0.040465	
GO-BP	GO:0050766	positive regulation of phagocytosis	63	0.37337	1.586044	0.001754	0.042183	0.036006	
GO-BP	GO:0060191	regulation of lipase activity	93	0.347593	1.592091	0.002203	0.047407	0.040465	
GO-BP	GO:0045637	regulation of myeloid cell differentiation	222	0.306583	1.594598	0.001359	0.037904	0.032354	
GO-BP	GO:0045807	positive regulation of endocytosis	143	0.326991	1.604132	0.000799	0.029038	0.024786	
GO-BP	GO:1903035	negative regulation of response to	88	0.354332	1.609864	0.002146	0.047073	0.04018	

		wounding							
GO-BP	GO:1903426	regulation of reactive oxygen species biosynthetic process	82	0.361185	1.616126	0.00102	0.032398	0.027654	
GO-BP	GO:0002673	regulation of acute inflammatory response	94	0.352497	1.616557	0.002228	0.047539	0.040578	
GO-BP	GO:1990748	cellular detoxification	103	0.347858	1.621243	0.002374	0.048946	0.041779	
GO-BP	GO:0001818	negative regulation of cytokine production	259	0.305264	1.621558	0.001689	0.041246	0.035207	
GO-BP	GO:0002685	regulation of leukocyte migration	186	0.320435	1.631005	0.001079	0.033277	0.028404	
GO-BP	GO:0021782	glial cell development	108	0.348168	1.636144	0.001217	0.035318	0.030146	
GO-BP	GO:0022617	extracellular matrix disassembly	75	0.371254	1.639795	0.002379	0.048946	0.041779	
GO-BP	GO:0072347	response to anesthetic	73	0.37386	1.640975	0.001872	0.043796	0.037383	
GO-BP	GO:1903036	positive regulation of response to wounding	63	0.388307	1.649496	0.000877	0.030178	0.025759	
GO-BP	GO:0015696	ammonium transport	100	0.356018	1.653177	0.001168	0.034566	0.029504	
GO-BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	56	0.398689	1.656023	0.002454	0.049534	0.042281	
GO-BP	GO:0007586	digestion	125	0.346256	1.660911	0.000694	0.027687	0.023633	
GO-BP	GO:0098869	cellular oxidant detoxification	93	0.362876	1.662093	0.002203	0.047407	0.040465	
GO-BP	GO:0051153	regulation of striated muscle cell differentiation	96	0.361933	1.666782	0.001691	0.041246	0.035207	
GO-BP	GO:0006937	regulation of muscle contraction	157	0.336345	1.672233	0.000896	0.030576	0.026098	
GO-BP	GO:0006936	muscle contraction	340	0.304399	1.67694	0.002469	0.049634	0.042366	
GO-BP	GO:0032755	positive regulation of interleukin-6 production	89	0.369472	1.681682	0.001621	0.041075	0.035061	
GO-BP	GO:0032103	positive regulation of response to external stimulus	296	0.311386	1.682108	0.002045	0.046291	0.039512	
GO-BP	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	57	0.403134	1.682566	0.001656	0.04119	0.035159	
GO-BP	GO:0097529	myeloid leukocyte migration	194	0.328597	1.685086	0.001127	0.033836	0.028881	
GO-BP	GO:0060326	cell chemotaxis	275	0.31505	1.686536	0.001789	0.042887	0.036607	
GO-BP	GO:0003073	regulation of systemic arterial blood pressure	91	0.369629	1.688578	0.001636	0.04119	0.035159	
GO-BP	GO:0034121	regulation of toll-like receptor signaling pathway	66	0.393298	1.690948	0.000442	0.025664	0.021906	
GO-BP	GO:0072376	protein activation cascade	96	0.367638	1.693056	0.000564	0.026201	0.022365	
GO-BP	GO:0030595	leukocyte chemotaxis	205	0.331127	1.701531	0.001183	0.034882	0.029774	
GO-BP	GO:0042310	vasoconstriction	75	0.385776	1.703936	0.000476	0.025683	0.021922	
GO-BP	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	79	0.38261	1.709168	0.000491	0.025683	0.021922	
GO-BP	GO:0070527	platelet aggregation	57	0.410214	1.712116	0.000414	0.025369	0.021654	
GO-BP	GO:0001836	release of cytochrome c from mitochondria	58	0.408816	1.713748	0.000834	0.029038	0.024786	

GO-BP	GO:2000377	regulation of reactive oxygen species metabolic process	174	0.340323	1.721875	0.00097	0.031557	0.026936
GO-BP	GO:0071216	cellular response to biotic stimulus	216	0.332033	1.721901	0.00129	0.037189	0.031743
GO-BP	GO:0006949	syncytium formation	56	0.414604	1.722131	0.000818	0.029038	0.024786
GO-BP	GO:0097006	regulation of plasma lipoprotein particle levels	82	0.385477	1.724822	0.00051	0.025683	0.021922
GO-BP	GO:0015695	organic cation transport	34	0.469793	1.724896	0.001995	0.04548	0.03882
GO-BP	GO:0033273	response to vitamin	88	0.379813	1.725634	0.000536	0.02597	0.022167
GO-BP	GO:2000117	negative regulation of cysteine-type endopeptidase activity	87	0.383379	1.731113	0.000537	0.02597	0.022167
GO-BP	GO:0007596	blood coagulation	318	0.320142	1.734968	0.002268	0.047789	0.040791
GO-BP	GO:0098754	detoxification	119	0.363404	1.73571	0.000657	0.027609	0.023566
GO-BP	GO:0019233	sensory perception of pain	101	0.373149	1.736415	0.000585	0.026355	0.022496
GO-BP	GO:0032496	response to lipopolysaccharide	308	0.321144	1.737281	0.002083	0.046571	0.039751
GO-BP	GO:0007599	hemostasis	323	0.318909	1.740481	0.002309	0.04809	0.041048
GO-BP	GO:0050764	regulation of phagocytosis	88	0.383288	1.741419	0.000536	0.02597	0.022167
GO-BP	GO:0072593	reactive oxygen species metabolic process	256	0.328402	1.743262	0.001645	0.04119	0.035159
GO-BP	GO:0030168	platelet activation	149	0.353635	1.745788	0.000826	0.029038	0.024786
GO-BP	GO:0002573	myeloid leukocyte differentiation	195	0.341209	1.747319	0.001131	0.033836	0.028881
GO-BP	GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	48	0.433825	1.748656	0.002255	0.047635	0.04066
GO-BP	GO:0035821	modification of morphology or physiology of other organism	148	0.354831	1.750575	0.000822	0.029038	0.024786
GO-BP	GO:2000249	regulation of actin cytoskeleton reorganization	37	0.467012	1.75097	0.00208	0.046571	0.039751
GO-BP	GO:0046470	phosphatidylcholine metabolic process	80	0.391698	1.751734	0.000496	0.025683	0.021922
GO-BP	GO:0070268	cornification	95	0.381528	1.751747	0.000562	0.026201	0.022365
GO-BP	GO:0032963	collagen metabolic process	103	0.375989	1.75235	0.000593	0.026355	0.022496
GO-BP	GO:0032651	regulation of interleukin-1 beta production	73	0.399739	1.754564	0.000468	0.025683	0.021922
GO-BP	GO:0050817	coagulation	322	0.321592	1.754619	0.002294	0.04809	0.041048
GO-BP	GO:0046645	positive regulation of gamma-delta T cell activation	5	0.867023	1.756828	0.002436	0.049316	0.042094
GO-BP	GO:0030593	neutrophil chemotaxis	94	0.38325	1.757589	0.000557	0.026201	0.022365
GO-BP	GO:0071526	semaphorin-plexin signaling pathway	40	0.459679	1.761576	0.001421	0.038842	0.033154
GO-BP	GO:0051930	regulation of sensory perception of pain	38	0.467718	1.764658	0.001412	0.038842	0.033154
GO-BP	GO:0051931	regulation of sensory perception	39	0.464232	1.765562	0.00248	0.04973	0.042448
GO-BP	GO:0002237	response to molecule of bacterial origin	319	0.325053	1.767148	0.002247	0.047635	0.04066
GO-BP	GO:0071222	cellular response to lipopolysaccharide	185	0.348104	1.770747	0.001082	0.033277	0.028404
GO-BP	GO:0030100	regulation of endocytosis	260	0.334298	1.778519	0.001686	0.041246	0.035207
GO-BP	GO:0072656	maintenance of protein location in	5	0.879493	1.782096	0.001329	0.037317	0.031853

		mitochondrion							
GO-BP	GO:2001199	negative regulation of dendritic cell differentiation	6	0.82613	1.782153	0.002234	0.047545	0.040583	
GO-BP	GO:0030851	granulocyte differentiation	32	0.49471	1.78584	0.001312	0.037238	0.031785	
GO-BP	GO:0045806	negative regulation of endocytosis	59	0.426084	1.788885	0.000421	0.025369	0.021654	
GO-BP	GO:0002526	acute inflammatory response	150	0.362045	1.789414	0.000831	0.029038	0.024786	
GO-BP	GO:0000768	syncytium formation by plasma membrane fusion	54	0.433992	1.790073	0.001205	0.035073	0.029937	
GO-BP	GO:0140253	cell-cell fusion	54	0.433992	1.790073	0.001205	0.035073	0.029937	
GO-BP	GO:1902622	regulation of neutrophil migration	35	0.483725	1.790574	0.00101	0.032323	0.02759	
GO-BP	GO:0031424	keratinization	135	0.368883	1.791637	0.00075	0.028393	0.024235	
GO-BP	GO:0050715	positive regulation of cytokine secretion	129	0.371865	1.79306	0.000704	0.027687	0.023633	
GO-BP	GO:2001137	positive regulation of endocytic recycling	5	0.885484	1.794235	0.001329	0.037317	0.031853	
GO-BP	GO:0150076	neuroinflammatory response	60	0.425634	1.794778	0.000426	0.025369	0.021654	
GO-BP	GO:0015682	ferric iron transport	37	0.479223	1.79675	0.00104	0.032569	0.0278	
GO-BP	GO:0072512	trivalent inorganic cation transport	37	0.479223	1.79675	0.00104	0.032569	0.0278	
GO-BP	GO:0032732	positive regulation of interleukin-1 production	53	0.437225	1.797057	0.000795	0.029038	0.024786	
GO-BP	GO:0006898	receptor-mediated endocytosis	247	0.33982	1.797175	0.001527	0.040114	0.03424	
GO-BP	GO:0050818	regulation of coagulation	81	0.402423	1.79985	0.000507	0.025683	0.021922	
GO-BP	GO:0071622	regulation of granulocyte chemotaxis	43	0.463166	1.81374	0.002164	0.047319	0.04039	
GO-BP	GO:0006801	superoxide metabolic process	67	0.420672	1.815185	0.000447	0.025683	0.021922	
GO-BP	GO:0036155	acylglycerol acyl-chain remodeling	5	0.899404	1.822441	0.001107	0.033703	0.028768	
GO-BP	GO:1900046	regulation of hemostasis	79	0.408446	1.824581	0.000491	0.025683	0.021922	
GO-BP	GO:0006909	phagocytosis	254	0.345171	1.825637	0.001623	0.041075	0.035061	
GO-BP	GO:0006959	humoral immune response	238	0.347576	1.825949	0.00146	0.038977	0.03327	
GO-BP	GO:0032534	regulation of microvillus assembly	6	0.846715	1.82656	0.001117	0.03376	0.028817	
GO-BP	GO:0032640	tumor necrosis factor production	139	0.373939	1.829097	0.00077	0.028657	0.024461	
GO-BP	GO:0002687	positive regulation of leukocyte migration	124	0.383698	1.83457	0.000701	0.027687	0.023633	
GO-BP	GO:0032680	regulation of tumor necrosis factor production	136	0.377544	1.839345	0.000749	0.028393	0.024235	
GO-BP	GO:0032570	response to progesterone	43	0.470399	1.842064	0.001442	0.038842	0.033154	
GO-BP	GO:0030193	regulation of blood coagulation	78	0.413365	1.843641	0.000483	0.025683	0.021922	
GO-BP	GO:0033572	transferrin transport	35	0.498303	1.844536	0.000337	0.02533	0.021621	
GO-BP	GO:1903901	negative regulation of viral life cycle	76	0.417251	1.845026	0.000484	0.025683	0.021922	
GO-BP	GO:2001181	positive regulation of interleukin-10 secretion	5	0.912551	1.849079	0.000664	0.027687	0.023633	
GO-BP	GO:0071219	cellular response to molecule of bacterial origin	192	0.360515	1.850244	0.001101	0.033635	0.02871	
GO-BP	GO:0071706	tumor necrosis factor superfamily cytokine production	144	0.376683	1.850568	0.000806	0.029038	0.024786	

GO-BP	GO:0001906	cell killing	151	0.375187	1.852249	0.00084	0.029116	0.024853
GO-BP	GO:0033006	regulation of mast cell activation involved in immune response	32	0.51429	1.85652	0.000984	0.031602	0.026974
GO-BP	GO:0048680	positive regulation of axon regeneration	8	0.785579	1.856574	0.002122	0.047	0.040118
GO-BP	GO:0032611	interleukin-1 beta production	84	0.412509	1.859598	0.00051	0.025683	0.021922
GO-BP	GO:1901186	positive regulation of ERBB signaling pathway	31	0.519123	1.860294	0.000975	0.031557	0.026936
GO-BP	GO:0051187	cofactor catabolic process	54	0.452078	1.86467	0.000402	0.02533	0.021621
GO-BP	GO:0050707	regulation of cytokine secretion	189	0.364897	1.865329	0.001083	0.033277	0.028404
GO-BP	GO:0030212	hyaluronan metabolic process	37	0.49828	1.868201	0.00104	0.032569	0.0278
GO-BP	GO:0001774	microglial cell activation	41	0.48445	1.869387	0.000717	0.027687	0.023633
GO-BP	GO:0002269	leukocyte activation involved in inflammatory response	41	0.48445	1.869387	0.000717	0.027687	0.023633
GO-BP	GO:0018149	peptide cross-linking	42	0.480849	1.871826	0.000719	0.027687	0.023633
GO-BP	GO:0043304	regulation of mast cell degranulation	31	0.522412	1.872081	0.000975	0.031557	0.026936
GO-BP	GO:0006953	acute-phase response	42	0.482311	1.877516	0.000719	0.027687	0.023633
GO-BP	GO:0014902	myotube differentiation	103	0.403057	1.878504	0.000593	0.026355	0.022496
GO-BP	GO:0006027	glycosaminoglycan catabolic process	60	0.445947	1.880433	0.000426	0.025369	0.021654
GO-BP	GO:0006833	water transport	18	0.608355	1.887199	0.002205	0.047407	0.040465
GO-BP	GO:0032490	detection of molecule of bacterial origin	10	0.736507	1.889378	0.002411	0.049218	0.042011
GO-BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	139	0.386576	1.890909	0.00077	0.028657	0.024461
GO-BP	GO:0032652	regulation of interleukin-1 production	85	0.419221	1.891831	0.000518	0.025784	0.022008
GO-BP	GO:1990266	neutrophil migration	108	0.403582	1.89655	0.000609	0.026805	0.02288
GO-BP	GO:0007588	excretion	59	0.451898	1.897261	0.000421	0.025369	0.021654
GO-BP	GO:0072606	interleukin-8 secretion	28	0.543276	1.898838	0.001883	0.043946	0.037511
GO-BP	GO:0050433	regulation of catecholamine secretion	54	0.460373	1.898883	0.000402	0.02533	0.021621
GO-BP	GO:2001179	regulation of interleukin-10 secretion	7	0.833584	1.901744	0.00114	0.033981	0.029005
GO-BP	GO:2000482	regulation of interleukin-8 secretion	24	0.568386	1.910758	0.002099	0.046605	0.039781
GO-BP	GO:0030049	muscle filament sliding	39	0.504099	1.917186	0.000708	0.027687	0.023633
GO-BP	GO:0033275	actin-myosin filament sliding	39	0.504099	1.917186	0.000708	0.027687	0.023633
GO-BP	GO:0007218	neuropeptide signaling pathway	93	0.419613	1.92197	0.000551	0.026077	0.022259
GO-BP	GO:0032148	activation of protein kinase B activity	31	0.537612	1.926552	0.00065	0.027472	0.02345
GO-BP	GO:0002251	organ or tissue specific immune response	31	0.537738	1.927002	0.00065	0.027472	0.02345
GO-BP	GO:1903011	negative regulation of bone development	9	0.778454	1.927026	0.00095	0.031207	0.026637
GO-BP	GO:0042744	hydrogen peroxide catabolic process	28	0.551408	1.92726	0.001569	0.040413	0.034496
GO-BP	GO:0061515	myeloid cell development	69	0.445669	1.927916	0.000458	0.025683	0.021922
GO-BP	GO:0032760	positive regulation of tumor necrosis factor production	79	0.432512	1.932085	0.000491	0.025683	0.021922
GO-BP	GO:0030574	collagen catabolic process	46	0.485853	1.934051	0.000745	0.028393	0.024235

GO-BP	GO:0045630	positive regulation of T-helper 2 cell differentiation	7	0.848545	1.935876	0.000684	0.027687	0.023633
GO-BP	GO:0002385	mucosal immune response	29	0.547078	1.93771	0.000937	0.031135	0.026576
GO-BP	GO:0006026	aminoglycan catabolic process	64	0.45533	1.939805	0.000441	0.025664	0.021906
GO-BP	GO:0050432	catecholamine secretion	56	0.467094	1.940158	0.000409	0.025369	0.021654
GO-BP	GO:0002741	positive regulation of cytokine secretion involved in immune response	8	0.822665	1.94422	0.000472	0.025683	0.021922
GO-BP	GO:0042116	macrophage activation	83	0.434177	1.949077	0.00051	0.025683	0.021922
GO-BP	GO:0071621	granulocyte chemotaxis	113	0.411713	1.950258	0.000622	0.026947	0.023001
GO-BP	GO:0045410	positive regulation of interleukin-6 biosynthetic process	15	0.668836	1.9513	0.001329	0.037317	0.031853
GO-BP	GO:0051937	catecholamine transport	69	0.451149	1.951622	0.000458	0.025683	0.021922
GO-BP	GO:0045071	negative regulation of viral genome replication	53	0.475103	1.95274	0.000398	0.02533	0.021621
GO-BP	GO:0002888	positive regulation of myeloid leukocyte mediated immunity	31	0.546247	1.957495	0.00065	0.027472	0.02345
GO-BP	GO:0070572	positive regulation of neuron projection regeneration	9	0.791512	1.95935	0.000713	0.027687	0.023633
GO-BP	GO:0070944	neutrophil mediated killing of bacterium	7	0.859268	1.960341	0.000684	0.027687	0.023633
GO-BP	GO:0050663	cytokine secretion	217	0.37869	1.962945	0.001311	0.037238	0.031785
GO-BP	GO:1902563	regulation of neutrophil activation	11	0.741667	1.963006	0.000246	0.02337	0.019948
GO-BP	GO:0097530	granulocyte migration	131	0.405866	1.964964	0.000719	0.027687	0.023633
GO-BP	GO:0002576	platelet degranulation	122	0.413188	1.972221	0.000683	0.027687	0.023633
GO-BP	GO:0032612	interleukin-1 production	97	0.426682	1.973668	0.000566	0.026201	0.022365
GO-BP	GO:0050706	regulation of interleukin-1 beta secretion	39	0.518992	1.973824	0.000354	0.02533	0.021621
GO-BP	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	81	0.441493	1.974594	0.000507	0.025683	0.021922
GO-BP	GO:0033003	regulation of mast cell activation	42	0.507985	1.97746	0.000719	0.027687	0.023633
GO-BP	GO:1903307	positive regulation of regulated secretory pathway	51	0.48584	1.979463	0.000392	0.02533	0.021621
GO-BP	GO:0032930	positive regulation of superoxide anion generation	19	0.63209	1.983727	0.001421	0.038842	0.033154
GO-BP	GO:0042226	interleukin-6 biosynthetic process	23	0.595302	1.984568	0.00059	0.026355	0.022496
GO-BP	GO:0043302	positive regulation of leukocyte degranulation	24	0.591937	1.98993	0.001199	0.035073	0.029937
GO-BP	GO:0042743	hydrogen peroxide metabolic process	52	0.488642	2.001672	0.000394	0.02533	0.021621
GO-BP	GO:0043277	apoptotic cell clearance	41	0.519769	2.005674	0.000358	0.02533	0.021621
GO-BP	GO:2001198	regulation of dendritic cell differentiation	11	0.758062	2.0064	0.000246	0.02337	0.019948
GO-BP	GO:1903010	regulation of bone development	21	0.617537	2.006526	0.001151	0.034185	0.029179
GO-BP	GO:0050718	positive regulation of interleukin-1 beta secretion	29	0.566887	2.007873	0.000937	0.031135	0.026576

GO-BP	GO:0017001	antibiotic catabolic process	52	0.490428	2.008987	0.000394	0.02533	0.021621
GO-BP	GO:0032757	positive regulation of interleukin-8 production	47	0.504657	2.019685	0.000375	0.02533	0.021621
GO-BP	GO:0045730	respiratory burst	32	0.561263	2.026086	0.000328	0.02533	0.021621
GO-BP	GO:0036035	osteoclast development	18	0.653545	2.027383	0.001654	0.04119	0.035159
GO-BP	GO:0042554	superoxide anion generation	35	0.548688	2.031043	0.000337	0.02533	0.021621
GO-BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	92	0.44414	2.031076	0.000547	0.026077	0.022259
GO-BP	GO:0090197	positive regulation of chemokine secretion	15	0.696695	2.032579	0.001063	0.033171	0.028314
GO-BP	GO:0090196	regulation of chemokine secretion	16	0.683269	2.035864	0.000808	0.029038	0.024786
GO-BP	GO:0070943	neutrophil mediated killing of symbiont cell	8	0.865182	2.044702	0.000236	0.02337	0.019948
GO-BP	GO:0061900	glial cell activation	48	0.509252	2.052686	0.000376	0.02533	0.021621
GO-BP	GO:0015844	monoamine transport	82	0.459649	2.056707	0.00051	0.025683	0.021922
GO-BP	GO:0032928	regulation of superoxide anion generation	22	0.625887	2.062056	0.00058	0.026355	0.022496
GO-BP	GO:0016045	detection of bacterium	12	0.755906	2.06218	0.000251	0.02337	0.019948
GO-BP	GO:0050716	positive regulation of interleukin-1 secretion	33	0.569364	2.072997	0.00033	0.02533	0.021621
GO-BP	GO:0072608	interleukin-10 secretion	9	0.842452	2.085449	0.000238	0.02337	0.019948
GO-BP	GO:0032677	regulation of interleukin-8 production	65	0.488966	2.090991	0.000441	0.025664	0.021906
GO-BP	GO:0098543	detection of other organism	14	0.730806	2.096081	0.000517	0.025784	0.022008
GO-BP	GO:0006691	leukotriene metabolic process	27	0.604635	2.097141	0.000618	0.026889	0.022952
GO-BP	GO:0050702	interleukin-1 beta secretion	46	0.529857	2.109217	0.000372	0.02533	0.021621
GO-BP	GO:0045408	regulation of interleukin-6 biosynthetic process	22	0.643187	2.119054	0.00058	0.026355	0.022496
GO-BP	GO:0050704	regulation of interleukin-1 secretion	45	0.535918	2.122697	0.000366	0.02533	0.021621
GO-BP	GO:0002374	cytokine secretion involved in immune response	20	0.666661	2.128898	0.000574	0.026355	0.022496
GO-BP	GO:0032637	interleukin-8 production	73	0.485369	2.130419	0.000468	0.025683	0.021922
GO-BP	GO:0050819	negative regulation of coagulation	54	0.517543	2.134691	0.000402	0.02533	0.021621
GO-BP	GO:0009620	response to fungus	43	0.545541	2.136314	0.000361	0.02533	0.021621
GO-BP	GO:0042730	fibrinolysis	28	0.617623	2.158694	0.000628	0.027049	0.023088
GO-BP	GO:0070942	neutrophil mediated cytotoxicity	10	0.841901	2.159746	0.000241	0.02337	0.019948
GO-BP	GO:0035994	response to muscle stretch	18	0.698162	2.165791	0.000827	0.029038	0.024786
GO-BP	GO:1900047	negative regulation of hemostasis	53	0.527006	2.166068	0.000398	0.02533	0.021621
GO-BP	GO:0097028	dendritic cell differentiation	40	0.567521	2.174845	0.000355	0.02533	0.021621
GO-BP	GO:0030195	negative regulation of blood coagulation	52	0.536008	2.195702	0.000394	0.02533	0.021621
GO-BP	GO:0098581	detection of external biotic stimulus	18	0.711807	2.208118	0.000551	0.026077	0.022259
GO-BP	GO:0002886	regulation of myeloid leukocyte mediated immunity	55	0.534575	2.209917	0.000408	0.025369	0.021654
GO-BP	GO:0050701	interleukin-1 secretion	53	0.538761	2.214381	0.000398	0.02533	0.021621

GO-BP	GO:0002227	innate immune response in mucosa	18	0.7326	2.272623	0.000551	0.026077	0.022259
GO-BP	GO:0050830	defense response to Gram-positive bacterium	76	0.514043	2.273027	0.000484	0.025683	0.021922
GO-BP	GO:0043300	regulation of leukocyte degranulation	46	0.575475	2.290814	0.000372	0.02533	0.021621
GO-BP	GO:0051852	disruption by host of symbiont cells	12	0.853612	2.328731	0.000251	0.02337	0.019948
GO-BP	GO:0051873	killing by host of symbiont cells	12	0.853612	2.328731	0.000251	0.02337	0.019948
GO-BP	GO:0050832	defense response to fungus	32	0.672516	2.427695	0.000328	0.02533	0.021621
GO-BP	GO:0051818	disruption of cells of other organism involved in symbiotic interaction	15	0.83298	2.430183	0.000266	0.02337	0.019948
GO-BP	GO:0051883	killing of cells in other organism involved in symbiotic interaction	15	0.83298	2.430183	0.000266	0.02337	0.019948
GO-BP	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	65	0.575235	2.459907	0.000441	0.025664	0.021906
GO-BP	GO:0050829	defense response to Gram-negative bacterium	69	0.574604	2.485675	0.000458	0.025683	0.021922
GO-BP	GO:0019731	antibacterial humoral response	36	0.670753	2.495245	0.000345	0.02533	0.021621
GO-BP	GO:0031640	killing of cells of other organism	52	0.617041	2.527643	0.000394	0.02533	0.021621
GO-BP	GO:0044364	disruption of cells of other organism	52	0.617041	2.527643	0.000394	0.02533	0.021621
GO-BP	GO:0019730	antimicrobial humoral response	105	0.543883	2.537179	0.00061	0.026805	0.02288
GO-BP	GO:0042742	defense response to bacterium	217	0.492189	2.551271	0.001311	0.037238	0.031785
Reactome	R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	92	-0.62146	-2.32682	0.000122	0.00417	0.003278
Reactome	R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	93	-0.61947	-2.32089	0.000122	0.00417	0.003278
Reactome	R-HSA-1799339	SRP-dependent cotranslational protein targeting to membrane	94	-0.6166	-2.31258	0.000122	0.00417	0.003278
Reactome	R-HSA-72689	Formation of a pool of free 40S subunits	83	-0.62588	-2.31024	0.000124	0.00417	0.003278
Reactome	R-HSA-192823	Viral mRNA Translation	71	-0.6254	-2.25075	0.000128	0.00417	0.003278
Reactome	R-HSA-72613	Eukaryotic Translation Initiation	100	-0.59118	-2.23429	0.000121	0.00417	0.003278
Reactome	R-HSA-72737	Cap-dependent Translation Initiation	100	-0.59118	-2.23429	0.000121	0.00417	0.003278
Reactome	R-HSA-156902	Peptide chain elongation	71	-0.61942	-2.22922	0.000128	0.00417	0.003278
Reactome	R-HSA-72306	tRNA processing	104	-0.58497	-2.21976	0.000121	0.00417	0.003278
Reactome	R-HSA-2408557	Selenocysteine synthesis	75	-0.60657	-2.20475	0.000126	0.00417	0.003278
Reactome	R-HSA-156842	Eukaryotic Translation Elongation	73	-0.60955	-2.2036	0.000127	0.00417	0.003278
Reactome	R-HSA-72764	Eukaryotic Translation Termination	75	-0.60535	-2.20031	0.000126	0.00417	0.003278
Reactome	R-HSA-72649	Translation initiation complex formation	51	-0.63838	-2.17879	0.000134	0.00417	0.003278
Reactome	R-HSA-72695	Formation of the ternary complex, and subsequently, the 43S complex	45	-0.65231	-2.17567	0.000137	0.00417	0.003278
Reactome	R-HSA-72702	Ribosomal scanning and start codon recognition	51	-0.63453	-2.16565	0.000134	0.00417	0.003278
Reactome	R-HSA-6791226	Major pathway of rRNA processing in	159	-0.54242	-2.1655	0.000113	0.00417	0.003278

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Reactome	R-HSA-975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	77	-0.59319	-2.16453	0.000126	0.00417	0.003278	
Reactome	R-HSA-159236	Transport of Mature mRNA derived from an Intron-Containing Transcript	65	-0.61092	-2.1645	0.00013	0.00417	0.003278	
Reactome	R-HSA-72202	Transport of Mature Transcript to Cytoplasm	73	-0.59758	-2.16034	0.000127	0.00417	0.003278	
Reactome	R-HSA-72312	rRNA processing	178	-0.53388	-2.15514	0.000111	0.00417	0.003278	
Reactome	R-HSA-8868773	rRNA processing in the nucleus and cytosol	168	-0.53462	-2.14487	0.000112	0.00417	0.003278	
Reactome	R-HSA-72766	Translation	265	-0.51039	-2.12423	0.000106	0.00417	0.003278	
Reactome	R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	52	-0.60662	-2.07677	0.000134	0.00417	0.003278	
Reactome	R-HSA-159230	Transport of the SLBP Dependant Mature mRNA	35	-0.65147	-2.06864	0.000142	0.00417	0.003278	
Reactome	R-HSA-191859	snRNP Assembly	51	-0.60452	-2.06323	0.000134	0.00417	0.003278	
Reactome	R-HSA-194441	Metabolism of non-coding RNA	51	-0.60452	-2.06323	0.000134	0.00417	0.003278	
Reactome	R-HSA-168255	Influenza Life Cycle	124	-0.52899	-2.05346	0.000117	0.00417	0.003278	
Reactome	R-HSA-168273	Influenza Viral RNA Transcription and Replication	116	-0.53337	-2.05247	0.000119	0.00417	0.003278	
Reactome	R-HSA-159227	Transport of the SLBP independent Mature mRNA	34	-0.64559	-2.04442	0.000141	0.00417	0.003278	
Reactome	R-HSA-6784531	tRNA processing in the nucleus	56	-0.58866	-2.03814	0.000132	0.00417	0.003278	
Reactome	R-HSA-927802	Nonsense-Mediated Decay (NMD)	94	-0.53913	-2.02205	0.000122	0.00417	0.003278	
Reactome	R-HSA-975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	94	-0.53913	-2.02205	0.000122	0.00417	0.003278	
Reactome	R-HSA-159234	Transport of Mature mRNAs Derived from Intronless Transcripts	41	-0.60888	-1.99796	0.000139	0.00417	0.003278	
Reactome	R-HSA-180910	Vpr-mediated nuclear import of PICs	33	-0.63371	-1.99336	0.000142	0.00417	0.003278	
Reactome	R-HSA-6782315	tRNA modification in the nucleus and cytosol	41	-0.60332	-1.97974	0.000139	0.00417	0.003278	
Reactome	R-HSA-168274	Export of Viral Ribonucleoproteins from Nucleus	31	-0.6361	-1.97402	0.000288	0.007323	0.005757	
Reactome	R-HSA-168333	NEP/NS2 Interacts with the Cellular Export Machinery	31	-0.6361	-1.97402	0.000288	0.007323	0.005757	
Reactome	R-HSA-159231	Transport of Mature mRNA Derived from an Intronless Transcript	40	-0.60203	-1.96527	0.000139	0.00417	0.003278	
Reactome	R-HSA-168254	Influenza Infection	134	-0.49733	-1.94666	0.000116	0.00417	0.003278	
Reactome	R-HSA-165054	Rev-mediated nuclear export of HIV RNA	34	-0.61365	-1.94327	0.000424	0.007947	0.006247	
Reactome	R-HSA-2408522	Selenoamino acid metabolism	97	-0.51617	-1.94228	0.000122	0.00417	0.003278	

Reactome	R-HSA-68877	Mitotic Prometaphase	189	-0.47846	-1.93997	0.00011	0.00417	0.003278
Reactome	R-HSA-5685938	HDR through Single Strand Annealing (SSA)	36	-0.60498	-1.93318	0.000706	0.010148	0.007978
Reactome	R-HSA-3371453	Regulation of HSF1-mediated heat shock response	66	-0.54329	-1.9304	0.00013	0.00417	0.003278
Reactome	R-HSA-177243	Interactions of Rev with host cellular proteins	36	-0.60407	-1.93024	0.000706	0.010148	0.007978
Reactome	R-HSA-176033	Interactions of Vpr with host cellular proteins	36	-0.60274	-1.926	0.000706	0.010148	0.007978
Reactome	R-HSA-3108214	SUMOylation of DNA damage response and repair proteins	74	-0.52606	-1.90722	0.000127	0.00417	0.003278
Reactome	R-HSA-141424	Amplification of signal from the kinetochores	92	-0.50865	-1.90445	0.000122	0.00417	0.003278
Reactome	R-HSA-141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	92	-0.50865	-1.90445	0.000122	0.00417	0.003278
Reactome	R-HSA-180746	Nuclear import of Rev protein	33	-0.60521	-1.90372	0.000569	0.008987	0.007065
Reactome	R-HSA-4570464	SUMOylation of RNA binding proteins	44	-0.56868	-1.89066	0.000275	0.007221	0.005677
Reactome	R-HSA-69618	Mitotic Spindle Checkpoint	107	-0.4962	-1.88991	0.00012	0.00417	0.003278
Reactome	R-HSA-72203	Processing of Capped Intron-Containing Pre-mRNA	228	-0.45885	-1.88972	0.000108	0.00417	0.003278
Reactome	R-HSA-170822	Regulation of Glucokinase by Glucokinase Regulatory Protein	31	-0.60625	-1.88138	0.000432	0.007947	0.006247
Reactome	R-HSA-5619107	Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC)	31	-0.60625	-1.88138	0.000432	0.007947	0.006247
Reactome	R-HSA-6804756	Regulation of TP53 Activity through Phosphorylation	90	-0.50387	-1.87938	0.000123	0.00417	0.003278
Reactome	R-HSA-4085377	SUMOylation of SUMOylation proteins	33	-0.5936	-1.86719	0.000711	0.010148	0.007978
Reactome	R-HSA-2025928	Calcineurin activates NFAT	10	-0.78552	-1.86222	0.001019	0.013355	0.010499
Reactome	R-HSA-168271	Transport of Ribonucleoproteins into the Host Nucleus	31	-0.59864	-1.85777	0.00072	0.010148	0.007978
Reactome	R-HSA-5693616	Presynaptic phase of homologous DNA pairing and strand exchange	38	-0.57448	-1.85593	0.001121	0.014587	0.011467
Reactome	R-HSA-5693579	Homologous DNA Pairing and Strand Exchange	41	-0.56234	-1.84527	0.000972	0.01283	0.010086
Reactome	R-HSA-5696395	Formation of Incision Complex in GG-NER	41	-0.56212	-1.84455	0.000972	0.01283	0.010086
Reactome	R-HSA-5620922	BBSome-mediated cargo-targeting to cilium	22	-0.63761	-1.84055	0.001212	0.014874	0.011693
Reactome	R-HSA-2173796	SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	32	-0.58751	-1.83647	0.001144	0.014642	0.011511
Reactome	R-HSA-2980766	Nuclear Envelope Breakdown	52	-0.53591	-1.8347	0.000535	0.008728	0.006861

Reactome	R-HSA-3301854	Nuclear Pore Complex (NPC) Disassembly	35	-0.57657	-1.83083	0.001276	0.01554	0.012216
Reactome	R-HSA-168276	NS1 Mediated Effects on Host Pathways	39	-0.56286	-1.82721	0.001541	0.018134	0.014255
Reactome	R-HSA-5620920	Cargo trafficking to the periciliary membrane	48	-0.53403	-1.80667	0.000811	0.011142	0.008759
Reactome	R-HSA-6790901	rRNA modification in the nucleus and cytosol	57	-0.51776	-1.79951	0.000264	0.007025	0.005523
Reactome	R-HSA-73856	RNA Polymerase II Transcription Termination	58	-0.51555	-1.79701	0.000396	0.007795	0.006128
Reactome	R-HSA-3371556	Cellular response to heat stress	86	-0.48312	-1.79144	0.000124	0.00417	0.003278
Reactome	R-HSA-2500257	Resolution of Sister Chromatid Cohesion	118	-0.46316	-1.78657	0.000118	0.00417	0.003278
Reactome	R-HSA-8953750	Transcriptional Regulation by E2F6	33	-0.56537	-1.7784	0.00256	0.026207	0.020602
Reactome	R-HSA-176187	Activation of ATR in response to replication stress	36	-0.55306	-1.76725	0.002964	0.029003	0.0228
Reactome	R-HSA-72187	mRNA 3'-end processing	49	-0.51911	-1.76277	0.001618	0.018665	0.014673
Reactome	R-HSA-5607763	CLEC7A (Dectin-1) induces NFAT activation	12	-0.70843	-1.76246	0.004491	0.039843	0.031322
Reactome	R-HSA-168253	Host Interactions with Influenza Factors	41	-0.53608	-1.75909	0.002915	0.028813	0.022651
Reactome	R-HSA-5696400	Dual Incision in GG-NER	40	-0.53844	-1.75769	0.002786	0.027747	0.021812
Reactome	R-HSA-5685942	HDR through Homologous Recombination (HRR)	64	-0.49618	-1.75352	0.000523	0.008617	0.006774
Reactome	R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	82	-0.47542	-1.75221	0.000249	0.006725	0.005287
Reactome	R-HSA-2470946	Cohesin Loading onto Chromatin	10	-0.73814	-1.74989	0.005435	0.046545	0.036591
Reactome	R-HSA-2173793	Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	44	-0.52334	-1.73991	0.002479	0.025684	0.020191
Reactome	R-HSA-2468052	Establishment of Sister Chromatid Cohesion	11	-0.71174	-1.73026	0.005729	0.048582	0.038192
Reactome	R-HSA-5617833	Cilium Assembly	191	-0.42347	-1.71822	0.00011	0.00417	0.003278
Reactome	R-HSA-72163	mRNA Splicing - Major Pathway	172	-0.42634	-1.7136	0.000112	0.00417	0.003278
Reactome	R-HSA-5633007	Regulation of TP53 Activity	158	-0.42828	-1.70881	0.000113	0.00417	0.003278
Reactome	R-HSA-1169092	Activation of RAS in B cells	5	-0.87075	-1.70533	0.003673	0.033981	0.026713
Reactome	R-HSA-72172	mRNA Splicing	180	-0.42059	-1.69928	0.000223	0.006112	0.004805
Reactome	R-HSA-68882	Mitotic Anaphase	189	-0.41888	-1.69839	0.00011	0.00417	0.003278
Reactome	R-HSA-429914	Deadenylation-dependent mRNA decay	55	-0.49051	-1.69263	0.002791	0.027747	0.021812
Reactome	R-HSA-69242	S Phase	157	-0.42456	-1.69248	0.000113	0.00417	0.003278
Reactome	R-HSA-8951664	Neddylation	225	-0.41146	-1.69233	0.000108	0.00417	0.003278
Reactome	R-HSA-5368287	Mitochondrial translation	91	-0.45296	-1.69194	0.000858	0.011511	0.009049
Reactome	R-HSA-5663220	RHO GTPases Activate Formins	131	-0.43323	-1.69173	0.000348	0.007423	0.005835

Reactome	R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	295	-0.40358	-1.69091	0.000105	0.00417	0.003278
Reactome	R-HSA-2555396	Mitotic Metaphase and Anaphase	190	-0.41623	-1.68869	0.000331	0.007423	0.005835
Reactome	R-HSA-2467813	Separation of Sister Chromatids	178	-0.41705	-1.68352	0.000334	0.007423	0.005835
Reactome	R-HSA-1852241	Organelle biogenesis and maintenance	282	-0.40177	-1.67926	0.000106	0.00417	0.003278
Reactome	R-HSA-162587	HIV Life Cycle	142	-0.42541	-1.67805	0.000344	0.007423	0.005835
Reactome	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	148	-0.41805	-1.65621	0.000342	0.007423	0.005835
Reactome	R-HSA-5696398	Nucleotide Excision Repair	108	-0.43423	-1.65611	0.000839	0.011386	0.008951
Reactome	R-HSA-5389840	Mitochondrial translation elongation	85	-0.44624	-1.65152	0.001734	0.01974	0.015518
Reactome	R-HSA-5368286	Mitochondrial translation initiation	85	-0.44619	-1.6513	0.001734	0.01974	0.015518
Reactome	R-HSA-162599	Late Phase of HIV Life Cycle	129	-0.42128	-1.64178	0.000699	0.010148	0.007978
Reactome	R-HSA-5419276	Mitochondrial translation termination	85	-0.44169	-1.63466	0.00223	0.023667	0.018606
Reactome	R-HSA-6807505	RNA polymerase II transcribes snRNA genes	73	-0.44752	-1.61783	0.003695	0.033999	0.026728
Reactome	R-HSA-69620	Cell Cycle Checkpoints	271	-0.38585	-1.60782	0.000106	0.00417	0.003278
Reactome	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	108	-0.42155	-1.60773	0.001798	0.020215	0.015892
Reactome	R-HSA-380270	Recruitment of mitotic centrosome proteins and complexes	77	-0.44027	-1.60651	0.003657	0.033981	0.026713
Reactome	R-HSA-380287	Centrosome maturation	77	-0.44027	-1.60651	0.003657	0.033981	0.026713
Reactome	R-HSA-69278	Cell Cycle, Mitotic	496	-0.37425	-1.60587	0.000102	0.00417	0.003278
Reactome	R-HSA-6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	77	-0.43407	-1.5839	0.005422	0.046545	0.036591
Reactome	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	79	-0.43038	-1.57552	0.005639	0.048057	0.037779
Reactome	R-HSA-9609507	Protein localization	158	-0.39399	-1.57201	0.001923	0.021056	0.016553
Reactome	R-HSA-68886	M Phase	356	-0.36894	-1.56222	0.000104	0.00417	0.003278
Reactome	R-HSA-69206	G1/S Transition	128	-0.40113	-1.56116	0.002688	0.027347	0.021498
Reactome	R-HSA-3700989	Transcriptional Regulation by TP53	353	-0.36656	-1.55168	0.000208	0.005798	0.004558
Reactome	R-HSA-5663205	Infectious disease	346	-0.36313	-1.5365	0.000208	0.005798	0.004558
Reactome	R-HSA-983169	Class I MHC mediated antigen processing & presentation	356	-0.35832	-1.51726	0.000208	0.005798	0.004558
Reactome	R-HSA-162906	HIV Infection	220	-0.36609	-1.50261	0.002719	0.027347	0.021498
Reactome	R-HSA-376176	Signaling by ROBO receptors	194	-0.36839	-1.49678	0.003525	0.033146	0.026057
Reactome	R-HSA-2990846	SUMOylation	176	-0.37052	-1.49365	0.004239	0.037803	0.029718
Reactome	R-HSA-73894	DNA Repair	305	-0.3416	-1.43376	0.002418	0.0252	0.01981
Reactome	R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	311	0.239437	1.29625	0.002169	0.023454	0.018438
Reactome	R-HSA-500792	GPCR ligand binding	432	0.253664	1.403389	0.004098	0.037317	0.029336
Reactome	R-HSA-375276	Peptide ligand-binding receptors	186	0.280166	1.439712	0.004086	0.037317	0.029336
Reactome	R-HSA-112316	Neuronal System	396	0.262586	1.448082	0.003378	0.032113	0.025245
Reactome	R-HSA-202733	Cell surface interactions at the vascular wall	135	0.305286	1.497273	0.002967	0.029003	0.0228
Reactome	R-HSA-373760	L1CAM interactions	112	0.318414	1.512479	0.004881	0.042647	0.033526

Reactome	R-HSA-1474290	Collagen formation	90	0.341079	1.553927	0.005952	0.049988	0.039297
Reactome	R-HSA-2559583	Cellular Senescence	167	0.313193	1.581437	0.001808	0.020215	0.015892
Reactome	R-HSA-5617472	Activation of anterior HOX genes in hindbrain development during early embryogenesis	97	0.341351	1.581508	0.003331	0.031842	0.025032
Reactome	R-HSA-5619507	Activation of HOX genes during differentiation	97	0.341351	1.581508	0.003331	0.031842	0.025032
Reactome	R-HSA-1296071	Potassium Channels	96	0.347295	1.604572	0.002211	0.023613	0.018563
Reactome	R-HSA-1442490	Collagen degradation	64	0.37862	1.617088	0.005098	0.044317	0.034839
Reactome	R-HSA-373080	Class B/2 (Secretin family receptors)	90	0.355642	1.620274	0.002706	0.027347	0.021498
Reactome	R-HSA-211945	Phase I - Functionalization of compounds	101	0.349201	1.626361	0.001146	0.014642	0.011511
Reactome	R-HSA-157118	Signaling by NOTCH	208	0.324148	1.686697	0.00116	0.014642	0.011511
Reactome	R-HSA-6806667	Metabolism of fat-soluble vitamins	47	0.425701	1.70347	0.002255	0.023785	0.018698
Reactome	R-HSA-201722	Formation of the beta-catenin:TCF transactivating complex	67	0.398555	1.717745	0.002195	0.023585	0.018541
Reactome	R-HSA-174577	Activation of C3 and C5	5	0.842474	1.717887	0.003072	0.029859	0.023473
Reactome	R-HSA-3928665	EPH-ephrin mediated repulsion of cells	50	0.425719	1.723046	0.001949	0.021201	0.016667
Reactome	R-HSA-2142700	Synthesis of Lipoxins (LX)	6	0.800594	1.735757	0.005886	0.049675	0.039051
Reactome	R-HSA-977606	Regulation of Complement cascade	42	0.445901	1.738537	0.002504	0.025781	0.020267
Reactome	R-HSA-166658	Complement cascade	53	0.424109	1.74012	0.001603	0.018614	0.014633
Reactome	R-HSA-6805567	Keratinization	127	0.360123	1.750328	0.000683	0.010148	0.007978
Reactome	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	102	0.37592	1.752093	0.000577	0.008993	0.00707
Reactome	R-HSA-397014	Muscle contraction	205	0.338715	1.756636	0.001157	0.014642	0.011511
Reactome	R-HSA-6809371	Formation of the cornified envelope	98	0.379108	1.756718	0.000561	0.008987	0.007065
Reactome	R-HSA-1474228	Degradation of the extracellular matrix	138	0.3584	1.762977	0.000762	0.010541	0.008286
Reactome	R-HSA-76002	Platelet activation, signaling and aggregation	253	0.333146	1.769541	0.001565	0.018293	0.014381
Reactome	R-HSA-437239	Recycling pathway of L1	41	0.461716	1.789244	0.00143	0.016946	0.013322
Reactome	R-HSA-5602498	MyD88 deficiency (TLR2/4)	10	0.699189	1.808487	0.004618	0.040656	0.031961
Reactome	R-HSA-1614517	Sulfide oxidation to sulfate	6	0.835447	1.811322	0.001811	0.020215	0.015892
Reactome	R-HSA-909733	Interferon alpha/beta signaling	67	0.42099	1.814439	0.001317	0.015932	0.012525
Reactome	R-HSA-5686938	Regulation of TLR by endogenous ligand	17	0.595598	1.817772	0.005171	0.044733	0.035166
Reactome	R-HSA-76005	Response to elevated platelet cytosolic Ca ²⁺	127	0.374437	1.819902	0.000683	0.010148	0.007978
Reactome	R-HSA-917977	Transferrin endocytosis and recycling	31	0.508591	1.830975	0.002292	0.024032	0.018892
Reactome	R-HSA-2559580	Oxidative Stress Induced Senescence	98	0.395316	1.831825	0.000561	0.008987	0.007065
Reactome	R-HSA-1482883	Acyl chain remodeling of DAG and TAG	5	0.899404	1.833974	0.000658	0.010079	0.007923
Reactome	R-HSA-549127	Organic cation transport	8	0.765757	1.834955	0.001882	0.020875	0.01641
Reactome	R-HSA-177504	Retrograde neurotrophin signalling	14	0.638772	1.839773	0.004176	0.037528	0.029501

Reactome	R-HSA-5603041	IRAK4 deficiency (TLR2/4)	11	0.691331	1.845744	0.003196	0.030893	0.024286
Reactome	R-HSA-445355	Smooth Muscle Contraction	39	0.483353	1.848904	0.001397	0.016669	0.013104
Reactome	R-HSA-2559586	DNA Damage/Telomere Stress Induced Senescence	63	0.435169	1.852989	0.000842	0.011386	0.008951
Reactome	R-HSA-8866427	VLDLR internalisation and degradation	12	0.678979	1.860435	0.003509	0.033146	0.026057
Reactome	R-HSA-5260271	Diseases of Immune System	24	0.552448	1.867965	0.004187	0.037528	0.029501
Reactome	R-HSA-5602358	Diseases associated with the TLR signaling cascade	24	0.552448	1.867965	0.004187	0.037528	0.029501
Reactome	R-HSA-448706	Interleukin-1 processing	8	0.779758	1.868507	0.001176	0.014642	0.011511
Reactome	R-HSA-2299718	Condensation of Prophase Chromosomes	50	0.461768	1.86895	0.001169	0.014642	0.011511
Reactome	R-HSA-114608	Platelet degranulation	122	0.38979	1.879788	0.000665	0.010097	0.007937
Reactome	R-HSA-975634	Retinoid metabolism and transport	43	0.482918	1.891096	0.000722	0.010148	0.007978
Reactome	R-HSA-1247673	Erythrocytes take up oxygen and release carbon dioxide	7	0.829099	1.896907	0.000463	0.008085	0.006355
Reactome	R-HSA-140877	Formation of Fibrin Clot (Clotting Cascade)	38	0.502744	1.907565	0.001395	0.016669	0.013104
Reactome	R-HSA-212300	PRC2 methylates histones and DNA	49	0.476559	1.920087	0.000387	0.007776	0.006113
Reactome	R-HSA-1474244	Extracellular matrix organization	295	0.358397	1.936725	0.001923	0.021056	0.016553
Reactome	R-HSA-5668599	RHO GTPases Activate NADPH Oxidases	23	0.590572	1.971645	0.001194	0.014755	0.011599
Reactome	R-HSA-73929	Base-Excision Repair, AP Site Formation	45	0.501456	1.988196	0.000734	0.010247	0.008056
Reactome	R-HSA-110328	Recognition and association of DNA glycosylase with site containing an affected pyrimidine	43	0.511674	2.003705	0.000361	0.007423	0.005835
Reactome	R-HSA-110329	Cleavage of the damaged pyrimidine	43	0.511674	2.003705	0.000361	0.007423	0.005835
Reactome	R-HSA-73928	Depyrimidination	43	0.511674	2.003705	0.000361	0.007423	0.005835
Reactome	R-HSA-1222556	ROS and RNS production in phagocytes	35	0.542756	2.01064	0.000339	0.007423	0.005835
Reactome	R-HSA-427359	SIRT1 negatively regulates rRNA expression	44	0.515122	2.029391	0.000365	0.007423	0.005835
Reactome	R-HSA-912446	Meiotic recombination	61	0.483516	2.043471	0.000418	0.007947	0.006247
Reactome	R-HSA-166663	Initial triggering of complement	20	0.637494	2.04391	0.000571	0.008987	0.007065
Reactome	R-HSA-1912408	Pre-NOTCH Transcription and Translation	68	0.473559	2.045609	0.000443	0.007977	0.006271
Reactome	R-HSA-1237044	Erythrocytes take up carbon dioxide and release oxygen	11	0.768152	2.050843	0.000492	0.008423	0.006622
Reactome	R-HSA-1480926	O2/CO2 exchange in erythrocytes	11	0.768152	2.050843	0.000492	0.008423	0.006622
Reactome	R-HSA-1912422	Pre-NOTCH Expression and Processing	84	0.457689	2.052862	0.000516	0.008617	0.006774
Reactome	R-HSA-3214815	HDACs deacetylate histones	67	0.480177	2.069528	0.000439	0.007977	0.006271
Reactome	R-HSA-2559582	Senescence-Associated Secretory	85	0.462151	2.076639	0.000518	0.008617	0.006774

Phenotype (SASP)									
Reactome	R-HSA-1592389	Activation of Matrix Metalloproteinases	31	0.585769	2.108821	0.000655	0.010079	0.007923	
Reactome	R-HSA-427389	ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	52	0.525225	2.148394	0.000397	0.007795	0.006128	
Reactome	R-HSA-9616222	Transcriptional regulation of granulopoiesis	65	0.503675	2.15937	0.000428	0.007947	0.006247	
Reactome	R-HSA-110330	Recognition and association of DNA glycosylase with site containing an affected purine	39	0.57192	2.187689	0.000349	0.007423	0.005835	
Reactome	R-HSA-110331	Cleavage of the damaged purine	39	0.57192	2.187689	0.000349	0.007423	0.005835	
Reactome	R-HSA-73927	Depurination	39	0.57192	2.187689	0.000349	0.007423	0.005835	
Reactome	R-HSA-171306	Packaging Of Telomere Ends	35	0.592036	2.193197	0.000339	0.007423	0.005835	
Reactome	R-HSA-8936459	RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	72	0.514486	2.25718	0.000457	0.008064	0.00634	
Reactome	R-HSA-6803157	Antimicrobial peptides	65	0.541303	2.320691	0.000428	0.007947	0.006247	
Reactome	R-HSA-5625740	RHO GTPases activate PKNs	71	0.532258	2.32466	0.000454	0.008064	0.00634	
Reactome	R-HSA-5625886	Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	43	0.610762	2.391732	0.000361	0.007423	0.005835	
Reactome	R-HSA-5334118	DNA methylation	41	0.63855	2.474514	0.000358	0.007423	0.005835	
Reactome	R-HSA-73728	RNA Polymerase I Promoter Opening	39	0.652007	2.494037	0.000349	0.007423	0.005835	
Reactome	R-HSA-977225	Amyloid fiber formation	83	0.560545	2.511793	0.000514	0.008617	0.006774	
Reactome	R-HSA-6798695	Neutrophil degranulation	456	0.498737	2.777591	0.00463	0.040656	0.031961	

Supplementary Table 11. Detailed results of GSEA for GO-BP, KEGG and Reactome in the COPDGene dataset.

Source	ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues
KEGG	hsa04979	Cholesterol metabolism	50	0.529643	2.026492	0.000187	0.003278	0.002454
KEGG	hsa05134	Legionellosis	53	0.510459	1.977749	0.000187	0.003278	0.002454
KEGG	hsa05144	Malaria	46	0.60307	2.264855	0.000187	0.003278	0.002454

KEGG	hsa04142	Lysosome	123	0.414809	1.870826	0.000188	0.003278	0.002454
KEGG	hsa05150	Staphylococcus aureus infection	75	0.462193	1.917484	0.000188	0.003278	0.002454
KEGG	hsa04145	Phagosome	138	0.449557	2.062009	0.000188	0.003278	0.002454
KEGG	hsa05323	Rheumatoid arthritis	85	0.473541	2.011097	0.000189	0.003278	0.002454
KEGG	hsa05171	Coronavirus disease - COVID-19	206	0.345188	1.674933	0.000189	0.003278	0.002454
KEGG	hsa04610	Complement and coagulation cascades	81	0.478347	2.012954	0.000189	0.003278	0.002454
KEGG	hsa04080	Neuroactive ligand-receptor interaction	327	0.397639	2.031411	0.00019	0.003278	0.002454
KEGG	hsa05146	Amoebiasis	101	0.504002	2.20394	0.00019	0.003278	0.002454
KEGG	hsa04974	Protein digestion and absorption	95	0.416681	1.804389	0.000191	0.003278	0.002454
KEGG	hsa00970	Aminoacyl-tRNA biosynthesis	41	-0.57567	-2.11918	0.00021	0.003278	0.002454
KEGG	hsa04070	Phosphatidylinositol signaling system	94	-0.43113	-1.87725	0.000211	0.003278	0.002454
KEGG	hsa04660	T cell receptor signaling pathway	102	-0.4343	-1.9178	0.000211	0.003278	0.002454
KEGG	hsa03015	mRNA surveillance pathway	84	-0.48565	-2.07718	0.000211	0.003278	0.002454
KEGG	hsa03030	DNA replication	36	-0.6473	-2.30785	0.000212	0.003278	0.002454
KEGG	hsa05340	Primary immunodeficiency	36	-0.57475	-2.04917	0.000212	0.003278	0.002454
KEGG	hsa04110	Cell cycle	122	-0.40671	-1.84412	0.000212	0.003278	0.002454
KEGG	hsa03008	Ribosome biogenesis in eukaryotes	71	-0.45374	-1.87536	0.000214	0.003278	0.002454
KEGG	hsa03040	Spliceosome	119	-0.45344	-2.04591	0.000214	0.003278	0.002454
KEGG	hsa05168	Herpes simplex virus 1 infection	445	-0.52024	-2.76103	0.000215	0.003278	0.002454
KEGG	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	70	0.454157	1.858905	0.000375	0.004912	0.003678
KEGG	hsa05152	Tuberculosis	170	0.362043	1.716635	0.000376	0.004912	0.003678
KEGG	hsa04020	Calcium signaling pathway	235	0.326213	1.610495	0.000378	0.004912	0.003678
KEGG	hsa04657	IL-17 signaling pathway	92	0.404932	1.744774	0.00038	0.004912	0.003678
KEGG	hsa03430	Mismatch repair	22	-0.64466	-2.03745	0.000425	0.00496	0.003714
KEGG	hsa03018	RNA degradation	76	-0.42534	-1.78483	0.000427	0.00496	0.003714
KEGG	hsa03460	Fanconi anemia pathway	48	-0.51289	-1.94851	0.000428	0.00496	0.003714
KEGG	hsa04742	Taste transduction	75	0.43619	1.809606	0.000564	0.005954	0.004458
KEGG	hsa04740	Olfactory transduction	120	0.403091	1.811668	0.000565	0.005954	0.004458
KEGG	hsa04380	Osteoclast differentiation	125	0.382713	1.729638	0.000567	0.005954	0.004458
KEGG	hsa04950	Maturity onset diabetes of the young	24	0.594662	1.908822	0.000757	0.007705	0.005769
KEGG	hsa05133	Pertussis	70	0.431926	1.767909	0.000937	0.008864	0.006637
KEGG	hsa04060	Cytokine-cytokine receptor interaction	276	0.294759	1.480697	0.000949	0.008864	0.006637
KEGG	hsa04966	Collecting duct acid secretion	27	0.579564	1.910425	0.00095	0.008864	0.006637
KEGG	hsa03420	Nucleotide excision repair	43	-0.5119	-1.90667	0.001478	0.013419	0.010048
KEGG	hsa04658	Th1 and Th2 cell differentiation	88	-0.38879	-1.67587	0.001687	0.014685	0.010996
KEGG	hsa04721	Synaptic vesicle cycle	77	0.408972	1.70431	0.001705	0.014685	0.010996
KEGG	hsa05140	Leishmaniasis	70	0.412353	1.687795	0.001873	0.015224	0.011399
KEGG	hsa04659	Th17 cell differentiation	102	-0.36937	-1.63105	0.001901	0.015224	0.011399
KEGG	hsa05033	Nicotine addiction	38	0.495557	1.774744	0.001903	0.015224	0.011399
KEGG	hsa05204	Chemical carcinogenesis	63	0.437164	1.751844	0.002054	0.016051	0.012018

KEGG	hsa05202	Transcriptional misregulation in cancer	174	0.316016	1.50255	0.002445	0.018674	0.013982
KEGG	hsa00770	Pantothenate and CoA biosynthesis	21	0.588236	1.822898	0.00321	0.023968	0.017946
KEGG	hsa03022	Basal transcription factors	40	-0.48485	-1.77264	0.003386	0.024729	0.018516
KEGG	hsa04976	Bile secretion	76	0.391751	1.630293	0.003573	0.025546	0.019128
KEGG	hsa04928	Parathyroid hormone synthesis, secretion and action	104	0.350657	1.543444	0.003797	0.026576	0.019898
KEGG	hsa04911	Insulin secretion	85	0.372151	1.580499	0.00416	0.028528	0.02136
KEGG	hsa03013	RNA transport	148	-0.32153	-1.50276	0.00463	0.030641	0.022942
KEGG	hsa04621	NOD-like receptor signaling pathway	167	0.310406	1.467508	0.004711	0.030641	0.022942
KEGG	hsa04613	Neutrophil extracellular trap formation	151	0.320453	1.48953	0.004742	0.030641	0.022942
KEGG	hsa04640	Hematopoietic cell lineage	92	-0.36015	-1.56238	0.005485	0.033957	0.025425
KEGG	hsa03320	PPAR signaling pathway	72	0.384333	1.582608	0.005602	0.033957	0.025425
KEGG	hsa05143	African trypanosomiasis	34	0.488583	1.711288	0.005641	0.033957	0.025425
KEGG	hsa04120	Ubiquitin mediated proteolysis	135	-0.32799	-1.51051	0.005742	0.033957	0.025425
KEGG	hsa03410	Base excision repair	32	-0.49618	-1.71907	0.005761	0.033957	0.025425
KEGG	hsa04978	Mineral absorption	57	0.414663	1.626735	0.006017	0.034859	0.0261
KEGG	hsa04921	Oxytocin signaling pathway	146	0.315899	1.457534	0.006496	0.036994	0.027699
KEGG	hsa05219	Bladder cancer	41	0.451515	1.647708	0.008197	0.045324	0.033936
KEGG	hsa04141	Protein processing in endoplasmic reticulum	164	-0.30687	-1.45255	0.008301	0.045324	0.033936
KEGG	hsa05032	Morphine addiction	88	0.354453	1.514341	0.008363	0.045324	0.033936
GO-BP	GO:0043312	neutrophil degranulation	464	0.448378	2.378848	0.000187	0.004738	0.003574
GO-BP	GO:0031667	response to nutrient levels	475	0.282893	1.504065	0.000187	0.004738	0.003574
GO-BP	GO:0002446	neutrophil mediated immunity	478	0.442863	2.356628	0.000187	0.004738	0.003574
GO-BP	GO:0042119	neutrophil activation	477	0.451692	2.403062	0.000187	0.004738	0.003574
GO-BP	GO:0002283	neutrophil activation involved in immune response	467	0.448289	2.379314	0.000187	0.004738	0.003574
GO-BP	GO:0036230	granulocyte activation	482	0.446529	2.377123	0.000187	0.004738	0.003574
GO-BP	GO:0030335	positive regulation of cell migration	484	0.292198	1.556713	0.000187	0.004738	0.003574
GO-BP	GO:1901652	response to peptide	493	0.328524	1.753573	0.000187	0.004738	0.003574
GO-BP	GO:0009636	response to toxic substance	494	0.298921	1.595794	0.000187	0.004738	0.003574
GO-BP	GO:0007389	pattern specification process	426	0.302549	1.592018	0.000187	0.004738	0.003574
GO-BP	GO:0043434	response to peptide hormone	419	0.322991	1.696465	0.000187	0.004738	0.003574
GO-BP	GO:0048871	multicellular organismal homeostasis	465	0.284328	1.508152	0.000187	0.004738	0.003574
GO-BP	GO:0048732	gland development	417	0.312803	1.642127	0.000187	0.004738	0.003574
GO-BP	GO:0050804	modulation of chemical synaptic transmission	424	0.336815	1.770951	0.000187	0.004738	0.003574
GO-BP	GO:0099177	regulation of trans-synaptic signaling	425	0.336185	1.768409	0.000188	0.004738	0.003574
GO-BP	GO:0002791	regulation of peptide secretion	468	0.29569	1.569218	0.000188	0.004738	0.003574
GO-BP	GO:0048568	embryonic organ development	416	0.301318	1.581413	0.000188	0.004738	0.003574
GO-BP	GO:0003012	muscle system process	423	0.324704	1.706806	0.000188	0.004738	0.003574
GO-BP	GO:0001525	angiogenesis	479	0.319981	1.701666	0.000188	0.004738	0.003574

GO-BP	GO:0043410	positive regulation of MAPK cascade	500	0.314962	1.68198	0.000188	0.004738	0.003574
GO-BP	GO:0051051	negative regulation of transport	457	0.319949	1.694754	0.000188	0.004738	0.003574
GO-BP	GO:0019932	second-messenger-mediated signaling	420	0.317936	1.669832	0.000188	0.004738	0.003574
GO-BP	GO:0061458	reproductive system development	414	0.308639	1.618983	0.000188	0.004738	0.003574
GO-BP	GO:0001819	positive regulation of cytokine production	432	0.305638	1.609288	0.000188	0.004738	0.003574
GO-BP	GO:0015711	organic anion transport	455	0.28489	1.507913	0.000188	0.004738	0.003574
GO-BP	GO:0034765	regulation of ion transmembrane transport	455	0.337727	1.787579	0.000188	0.004738	0.003574
GO-BP	GO:0042391	regulation of membrane potential	407	0.378777	1.982963	0.000188	0.004738	0.003574
GO-BP	GO:0052547	regulation of peptidase activity	407	0.310978	1.628021	0.000188	0.004738	0.003574
GO-BP	GO:0015672	monovalent inorganic cation transport	489	0.342078	1.823127	0.000188	0.004738	0.003574
GO-BP	GO:0042445	hormone metabolic process	217	0.417672	2.039681	0.000188	0.004738	0.003574
GO-BP	GO:0042742	defense response to bacterium	217	0.382901	1.869875	0.000188	0.004738	0.003574
GO-BP	GO:0051047	positive regulation of secretion	410	0.356205	1.866655	0.000188	0.004738	0.003574
GO-BP	GO:0010951	negative regulation of endopeptidase activity	220	0.380743	1.863406	0.000188	0.004738	0.003574
GO-BP	GO:0048608	reproductive structure development	411	0.30922	1.620668	0.000188	0.004738	0.003574
GO-BP	GO:0050708	regulation of protein secretion	441	0.294921	1.556267	0.000188	0.004738	0.003574
GO-BP	GO:0032494	response to peptidoglycan	10	0.884747	2.1969	0.000188	0.004738	0.003574
GO-BP	GO:0051924	regulation of calcium ion transport	241	0.327734	1.619593	0.000188	0.004738	0.003574
GO-BP	GO:0006813	potassium ion transport	221	0.364933	1.787572	0.000188	0.004738	0.003574
GO-BP	GO:0009743	response to carbohydrate	221	0.337632	1.65384	0.000188	0.004738	0.003574
GO-BP	GO:0090324	negative regulation of oxidative phosphorylation	7	0.84294	1.867844	0.000188	0.004738	0.003574
GO-BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	243	0.345973	1.711782	0.000188	0.004738	0.003574
GO-BP	GO:0071216	cellular response to biotic stimulus	216	0.373539	1.822945	0.000188	0.004738	0.003574
GO-BP	GO:0043062	extracellular structure organization	403	0.38052	1.989552	0.000188	0.004738	0.003574
GO-BP	GO:0044706	multi-multicellular organism process	214	0.37035	1.805221	0.000188	0.004738	0.003574
GO-BP	GO:0023061	signal release	451	0.36601	1.934872	0.000189	0.004738	0.003574
GO-BP	GO:0010466	negative regulation of peptidase activity	230	0.378877	1.861112	0.000189	0.004738	0.003574
GO-BP	GO:0050706	regulation of interleukin-1 beta secretion	39	0.571257	2.06222	0.000189	0.004738	0.003574
GO-BP	GO:0071224	cellular response to peptidoglycan	5	0.965476	1.912723	0.000189	0.004738	0.003574
GO-BP	GO:0001763	morphogenesis of a branching structure	191	0.403133	1.933796	0.000189	0.004738	0.003574
GO-BP	GO:0002573	myeloid leukocyte differentiation	195	0.366592	1.763096	0.000189	0.004738	0.003574
GO-BP	GO:0007584	response to nutrient	211	0.337736	1.641984	0.000189	0.004738	0.003574
GO-BP	GO:0010575	positive regulation of vascular endothelial growth factor production	28	0.643147	2.133323	0.000189	0.004738	0.003574
GO-BP	GO:0017157	regulation of exocytosis	211	0.339245	1.64932	0.000189	0.004738	0.003574

GO-BP	GO:0042730	fibrinolysis	28	0.618759	2.052428	0.000189	0.004738	0.003574
GO-BP	GO:0042744	hydrogen peroxide catabolic process	28	0.68641	2.276826	0.000189	0.004738	0.003574
GO-BP	GO:0045980	negative regulation of nucleotide metabolic process	28	0.672434	2.230467	0.000189	0.004738	0.003574
GO-BP	GO:1903532	positive regulation of secretion by cell	383	0.360915	1.877888	0.000189	0.004738	0.003574
GO-BP	GO:0007187	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	233	0.414012	2.035828	0.000189	0.004738	0.003574
GO-BP	GO:0008016	regulation of heart contraction	233	0.344703	1.695013	0.000189	0.004738	0.003574
GO-BP	GO:0019935	cyclic-nucleotide-mediated signaling	203	0.367124	1.77672	0.000189	0.004738	0.003574
GO-BP	GO:0030099	myeloid cell differentiation	386	0.310015	1.614234	0.000189	0.004738	0.003574
GO-BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	190	0.366086	1.754773	0.000189	0.004738	0.003574
GO-BP	GO:0015850	organic hydroxy compound transport	231	0.35866	1.761702	0.000189	0.004738	0.003574
GO-BP	GO:0050953	sensory perception of light stimulus	212	0.334905	1.629029	0.000189	0.004738	0.003574
GO-BP	GO:0050716	positive regulation of interleukin-1 secretion	33	0.602029	2.090574	0.000189	0.004738	0.003574
GO-BP	GO:0015893	drug transport	200	0.385756	1.862301	0.000189	0.004738	0.003574
GO-BP	GO:0050718	positive regulation of interleukin-1 beta secretion	29	0.656142	2.196483	0.000189	0.004738	0.003574
GO-BP	GO:0060541	respiratory system development	194	0.358975	1.724149	0.000189	0.004738	0.003574
GO-BP	GO:0097529	myeloid leukocyte migration	194	0.366126	1.758495	0.000189	0.004738	0.003574
GO-BP	GO:0030595	leukocyte chemotaxis	205	0.346553	1.678763	0.000189	0.004738	0.003574
GO-BP	GO:0045745	positive regulation of G protein-coupled receptor signaling pathway	32	0.619384	2.132343	0.000189	0.004738	0.003574
GO-BP	GO:0046879	hormone secretion	306	0.35316	1.792689	0.000189	0.004738	0.003574
GO-BP	GO:0050890	cognition	286	0.323067	1.629003	0.000189	0.004738	0.003574
GO-BP	GO:2001057	reactive nitrogen species metabolic process	72	0.514188	2.114019	0.000189	0.004738	0.003574
GO-BP	GO:0022617	extracellular matrix disassembly	75	0.484704	2.007145	0.000189	0.004738	0.003574
GO-BP	GO:0031016	pancreas development	75	0.453634	1.878484	0.000189	0.004738	0.003574
GO-BP	GO:0042310	vasoconstriction	75	0.515704	2.135514	0.000189	0.004738	0.003574
GO-BP	GO:0046889	positive regulation of lipid biosynthetic process	75	0.462051	1.91334	0.000189	0.004738	0.003574
GO-BP	GO:0055013	cardiac muscle cell development	75	0.477266	1.976343	0.000189	0.004738	0.003574
GO-BP	GO:0071219	cellular response to molecule of bacterial origin	192	0.391376	1.877614	0.000189	0.004738	0.003574
GO-BP	GO:1904407	positive regulation of nitric oxide metabolic process	38	0.575288	2.063973	0.000189	0.004738	0.003574
GO-BP	GO:0006959	humoral immune response	238	0.32463	1.600404	0.000189	0.004738	0.003574
GO-BP	GO:0003207	cardiac chamber formation	12	0.77626	2.03637	0.000189	0.004738	0.003574
GO-BP	GO:0060670	branching involved in labyrinthine layer morphogenesis	12	0.850678	2.231593	0.000189	0.004738	0.003574

GO-BP	GO:0071404	cellular response to low-density lipoprotein particle stimulus	18	0.688558	2.035441	0.000189	0.004738	0.003574
GO-BP	GO:0098581	detection of external biotic stimulus	18	0.715598	2.115374	0.000189	0.004738	0.003574
GO-BP	GO:0001667	ameboidal-type cell migration	380	0.306933	1.595743	0.000189	0.004738	0.003574
GO-BP	GO:0032651	regulation of interleukin-1 beta production	73	0.499604	2.058729	0.000189	0.004738	0.003574
GO-BP	GO:0052548	regulation of endopeptidase activity	380	0.313027	1.627426	0.000189	0.004738	0.003574
GO-BP	GO:0060841	venous blood vessel development	15	0.708247	1.990788	0.000189	0.004738	0.003574
GO-BP	GO:0007601	visual perception	208	0.338233	1.640169	0.000189	0.004738	0.003574
GO-BP	GO:0099643	signal release from synapse	164	0.385124	1.810066	0.000189	0.004738	0.003574
GO-BP	GO:1900543	negative regulation of purine nucleotide metabolic process	27	0.640368	2.103931	0.00019	0.004738	0.003574
GO-BP	GO:0007606	sensory perception of chemical stimulus	167	0.45299	2.13241	0.00019	0.004738	0.003574
GO-BP	GO:0090276	regulation of peptide hormone secretion	206	0.344887	1.671165	0.00019	0.004738	0.003574
GO-BP	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	207	0.412948	2.001205	0.00019	0.004738	0.003574
GO-BP	GO:0030324	lung development	168	0.380511	1.79278	0.00019	0.004738	0.003574
GO-BP	GO:0042116	macrophage activation	83	0.471278	1.986217	0.00019	0.004738	0.003574
GO-BP	GO:0055001	muscle cell development	168	0.44409	2.092334	0.00019	0.004738	0.003574
GO-BP	GO:0003018	vascular process in circulatory system	166	0.431875	2.031741	0.00019	0.004738	0.003574
GO-BP	GO:0030072	peptide hormone secretion	246	0.343515	1.699581	0.00019	0.004738	0.003574
GO-BP	GO:0032642	regulation of chemokine production	77	0.472356	1.96446	0.00019	0.004738	0.003574
GO-BP	GO:0048469	cell maturation	166	0.389605	1.832883	0.00019	0.004738	0.003574
GO-BP	GO:0060537	muscle tissue development	376	0.31374	1.629182	0.00019	0.004738	0.003574
GO-BP	GO:0035249	synaptic transmission, glutamatergic	91	0.46252	1.981245	0.00019	0.004738	0.003574
GO-BP	GO:0042136	neurotransmitter biosynthetic process	91	0.466253	1.997234	0.00019	0.004738	0.003574
GO-BP	GO:0007611	learning or memory	249	0.361216	1.790993	0.00019	0.004738	0.003574
GO-BP	GO:0070371	ERK1 and ERK2 cascade	282	0.363734	1.830627	0.00019	0.004738	0.003574
GO-BP	GO:0090130	tissue migration	282	0.325526	1.63833	0.00019	0.004738	0.003574
GO-BP	GO:0003015	heart process	270	0.357446	1.789559	0.00019	0.004738	0.003574
GO-BP	GO:0021700	developmental maturation	270	0.316835	1.58624	0.00019	0.004738	0.003574
GO-BP	GO:1901342	regulation of vasculature development	309	0.31844	1.617966	0.00019	0.004738	0.003574
GO-BP	GO:0006836	neurotransmitter transport	261	0.384414	1.916931	0.00019	0.004738	0.003574
GO-BP	GO:0060047	heart contraction	261	0.354684	1.768682	0.00019	0.004738	0.003574
GO-BP	GO:0070372	regulation of ERK1 and ERK2 cascade	266	0.369232	1.844357	0.00019	0.004738	0.003574
GO-BP	GO:1903579	negative regulation of ATP metabolic process	25	0.648771	2.086365	0.00019	0.004738	0.003574
GO-BP	GO:0006898	receptor-mediated endocytosis	247	0.383667	1.899366	0.00019	0.004738	0.003574
GO-BP	GO:0016079	synaptic vesicle exocytosis	114	0.405281	1.809237	0.00019	0.004738	0.003574
GO-BP	GO:0032496	response to lipopolysaccharide	308	0.373297	1.895875	0.00019	0.004738	0.003574

GO-BP	GO:0048167	regulation of synaptic plasticity	181	0.381185	1.814345	0.00019	0.004738	0.003574
GO-BP	GO:0071804	cellular potassium ion transport	198	0.380344	1.83158	0.00019	0.004738	0.003574
GO-BP	GO:0071805	potassium ion transmembrane transport	198	0.380344	1.83158	0.00019	0.004738	0.003574
GO-BP	GO:0008217	regulation of blood pressure	175	0.399877	1.894388	0.00019	0.004738	0.003574
GO-BP	GO:0019933	cAMP-mediated signaling	175	0.380291	1.801601	0.00019	0.004738	0.003574
GO-BP	GO:0046883	regulation of hormone secretion	262	0.349821	1.745313	0.00019	0.004738	0.003574
GO-BP	GO:0050906	detection of stimulus involved in sensory perception	176	0.391085	1.854259	0.00019	0.004738	0.003574
GO-BP	GO:0051146	striated muscle cell differentiation	262	0.339844	1.695538	0.00019	0.004738	0.003574
GO-BP	GO:0006941	striated muscle contraction	163	0.368334	1.729508	0.00019	0.004738	0.003574
GO-BP	GO:0007269	neurotransmitter secretion	163	0.38548	1.810017	0.00019	0.004738	0.003574
GO-BP	GO:0050673	epithelial cell proliferation	375	0.315827	1.638735	0.00019	0.004738	0.003574
GO-BP	GO:0050806	positive regulation of synaptic transmission	163	0.381271	1.790256	0.00019	0.004738	0.003574
GO-BP	GO:0055006	cardiac cell development	80	0.461412	1.933236	0.00019	0.004738	0.003574
GO-BP	GO:0071466	cellular response to xenobiotic stimulus	163	0.386251	1.813636	0.00019	0.004738	0.003574
GO-BP	GO:0006909	phagocytosis	254	0.349066	1.734668	0.00019	0.004738	0.003574
GO-BP	GO:0009410	response to xenobiotic stimulus	268	0.34487	1.723897	0.00019	0.004738	0.003574
GO-BP	GO:0032963	collagen metabolic process	103	0.456931	2.001356	0.00019	0.004738	0.003574
GO-BP	GO:0045165	cell fate commitment	254	0.338758	1.683443	0.00019	0.004738	0.003574
GO-BP	GO:0050714	positive regulation of protein secretion	254	0.346923	1.724019	0.00019	0.004738	0.003574
GO-BP	GO:0099565	chemical synaptic transmission, postsynaptic	103	0.464484	2.034438	0.00019	0.004738	0.003574
GO-BP	GO:1903409	reactive oxygen species biosynthetic process	103	0.427446	1.872213	0.00019	0.004738	0.003574
GO-BP	GO:0030323	respiratory tube development	172	0.371956	1.756417	0.00019	0.004738	0.003574
GO-BP	GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	79	0.459132	1.919176	0.00019	0.004738	0.003574
GO-BP	GO:0050907	detection of chemical stimulus involved in sensory perception	122	0.482989	2.175126	0.00019	0.004738	0.003574
GO-BP	GO:0014706	striated muscle tissue development	360	0.310348	1.603009	0.00019	0.004738	0.003574
GO-BP	GO:0051591	response to cAMP	93	0.464872	1.997886	0.00019	0.004738	0.003574
GO-BP	GO:0032612	interleukin-1 production	97	0.49613	2.150145	0.00019	0.004738	0.003574
GO-BP	GO:0045765	regulation of angiogenesis	278	0.334447	1.680681	0.00019	0.004738	0.003574
GO-BP	GO:1903522	regulation of blood circulation	278	0.377417	1.896615	0.00019	0.004738	0.003574
GO-BP	GO:0007215	glutamate receptor signaling pathway	98	0.445624	1.935221	0.00019	0.004738	0.003574
GO-BP	GO:0030100	regulation of endocytosis	260	0.374568	1.86583	0.00019	0.004738	0.003574
GO-BP	GO:0032602	chemokine production	84	0.450079	1.898786	0.00019	0.004738	0.003574
GO-BP	GO:0032611	interleukin-1 beta production	84	0.499123	2.105693	0.00019	0.004738	0.003574
GO-BP	GO:0046427	positive regulation of JAK-STAT	84	0.455315	1.920876	0.00019	0.004738	0.003574

		cascade						
GO-BP	GO:0048663	neuron fate commitment	63	0.536977	2.145886	0.00019	0.004738	0.003574
GO-BP	GO:0050766	positive regulation of phagocytosis	63	0.496651	1.984734	0.00019	0.004738	0.003574
GO-BP	GO:0050911	detection of chemical stimulus involved in sensory perception of smell	84	0.465293	1.962968	0.00019	0.004738	0.003574
GO-BP	GO:0060079	excitatory postsynaptic potential	95	0.45444	1.962216	0.000191	0.004738	0.003574
GO-BP	GO:0098739	import across plasma membrane	104	0.417313	1.831449	0.000191	0.004738	0.003574
GO-BP	GO:1904018	positive regulation of vasculature development	179	0.375335	1.782196	0.000191	0.004738	0.003574
GO-BP	GO:0032755	positive regulation of interleukin-6 production	89	0.469838	2.003983	0.000191	0.004738	0.003574
GO-BP	GO:0061138	morphogenesis of a branching epithelium	178	0.40257	1.910332	0.000191	0.004738	0.003574
GO-BP	GO:0007608	sensory perception of smell	107	0.449966	1.984998	0.000191	0.004738	0.003574
GO-BP	GO:1904062	regulation of cation transmembrane transport	322	0.330481	1.68558	0.000191	0.004738	0.003574
GO-BP	GO:2000377	regulation of reactive oxygen species metabolic process	174	0.417356	1.973646	0.000191	0.004738	0.003574
GO-BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	92	0.534274	2.289955	0.000191	0.004738	0.003574
GO-BP	GO:0032732	positive regulation of interleukin-1 production	53	0.527938	2.034246	0.000191	0.004738	0.003574
GO-BP	GO:0046209	nitric oxide metabolic process	69	0.501199	2.038426	0.000191	0.004738	0.003574
GO-BP	GO:0050701	interleukin-1 secretion	53	0.552301	2.128122	0.000191	0.004738	0.003574
GO-BP	GO:0050727	regulation of inflammatory response	362	0.346634	1.79093	0.000191	0.004738	0.003574
GO-BP	GO:0015849	organic acid transport	314	0.328172	1.668613	0.000191	0.004738	0.003574
GO-BP	GO:0017001	antibiotic catabolic process	52	0.584314	2.242452	0.000191	0.004738	0.003574
GO-BP	GO:0042743	hydrogen peroxide metabolic process	52	0.600643	2.305118	0.000191	0.004738	0.003574
GO-BP	GO:0046942	carboxylic acid transport	314	0.328172	1.668613	0.000191	0.004738	0.003574
GO-BP	GO:0006026	aminoglycan catabolic process	64	0.489238	1.962155	0.000191	0.004738	0.003574
GO-BP	GO:0006809	nitric oxide biosynthetic process	64	0.480711	1.927956	0.000191	0.004738	0.003574
GO-BP	GO:0032652	regulation of interleukin-1 production	85	0.498503	2.10732	0.000191	0.004738	0.003574
GO-BP	GO:0032731	positive regulation of interleukin-1 beta production	47	0.554932	2.084977	0.000191	0.004738	0.003574
GO-BP	GO:1901653	cellular response to peptide	365	0.315842	1.632685	0.000191	0.004738	0.003574
GO-BP	GO:0002237	response to molecule of bacterial origin	319	0.360663	1.836909	0.000191	0.004738	0.003574
GO-BP	GO:0006953	acute-phase response	42	0.571029	2.09333	0.000191	0.004738	0.003574
GO-BP	GO:0032103	positive regulation of response to external stimulus	296	0.393572	1.987989	0.000191	0.004738	0.003574
GO-BP	GO:0034754	cellular hormone metabolic process	116	0.409663	1.830781	0.000191	0.004738	0.003574
GO-BP	GO:0050678	regulation of epithelial cell proliferation	319	0.308515	1.571315	0.000191	0.004738	0.003574

GO-BP	GO:0072593	reactive oxygen species metabolic process	256	0.441992	2.197903	0.000191	0.004738	0.003574
GO-BP	GO:0007565	female pregnancy	185	0.361331	1.723652	0.000191	0.004738	0.003574
GO-BP	GO:0007586	digestion	125	0.383272	1.729649	0.000191	0.004738	0.003574
GO-BP	GO:0071222	cellular response to lipopolysaccharide	185	0.400963	1.912708	0.000191	0.004738	0.003574
GO-BP	GO:0003206	cardiac chamber morphogenesis	127	0.380317	1.720461	0.000191	0.004738	0.003574
GO-BP	GO:0042737	drug catabolic process	127	0.403907	1.827175	0.000191	0.004738	0.003574
GO-BP	GO:0046683	response to organophosphorus	127	0.444038	2.008717	0.000191	0.004738	0.003574
GO-BP	GO:0050704	regulation of interleukin-1 secretion	45	0.561179	2.087294	0.000191	0.004738	0.003574
GO-BP	GO:0007588	excretion	59	0.579623	2.286106	0.000191	0.004738	0.003574
GO-BP	GO:0045861	negative regulation of proteolysis	321	0.334608	1.705735	0.000191	0.004738	0.003574
GO-BP	GO:0071706	tumor necrosis factor superfamily cytokine production	144	0.389749	1.798018	0.000191	0.004738	0.003574
GO-BP	GO:0010631	epithelial cell migration	273	0.327657	1.642389	0.000191	0.004738	0.003574
GO-BP	GO:0032675	regulation of interleukin-6 production	132	0.384387	1.750207	0.000191	0.004738	0.003574
GO-BP	GO:0048660	regulation of smooth muscle cell proliferation	132	0.399066	1.817045	0.000191	0.004738	0.003574
GO-BP	GO:0050729	positive regulation of inflammatory response	132	0.407678	1.856258	0.000191	0.004738	0.003574
GO-BP	GO:0051606	detection of stimulus	325	0.310815	1.585968	0.000191	0.004738	0.003574
GO-BP	GO:0060326	cell chemotaxis	275	0.331459	1.663174	0.000191	0.004738	0.003574
GO-BP	GO:0006720	isoprenoid metabolic process	126	0.399063	1.802203	0.000191	0.004738	0.003574
GO-BP	GO:0030574	collagen catabolic process	46	0.558597	2.088542	0.000191	0.004738	0.003574
GO-BP	GO:0046425	regulation of JAK-STAT cascade	126	0.389142	1.757397	0.000191	0.004738	0.003574
GO-BP	GO:0048662	negative regulation of smooth muscle cell proliferation	46	0.53376	1.995678	0.000191	0.004738	0.003574
GO-BP	GO:0050702	interleukin-1 beta secretion	46	0.564362	2.110097	0.000191	0.004738	0.003574
GO-BP	GO:0001659	temperature homeostasis	170	0.37276	1.757174	0.000191	0.004738	0.003574
GO-BP	GO:0090132	epithelium migration	276	0.325111	1.631507	0.000191	0.004738	0.003574
GO-BP	GO:0019730	antimicrobial humoral response	105	0.435227	1.912094	0.000191	0.004738	0.003574
GO-BP	GO:0009914	hormone transport	316	0.354447	1.802539	0.000191	0.004738	0.003574
GO-BP	GO:0002793	positive regulation of peptide secretion	274	0.350809	1.758992	0.000191	0.004738	0.003574
GO-BP	GO:0035150	regulation of tube size	138	0.438533	2.009745	0.000191	0.004738	0.003574
GO-BP	GO:0042133	neurotransmitter metabolic process	138	0.421585	1.932075	0.000191	0.004738	0.003574
GO-BP	GO:0046887	positive regulation of hormone secretion	129	0.412189	1.868801	0.000191	0.004738	0.003574
GO-BP	GO:0050715	positive regulation of cytokine secretion	129	0.383461	1.738553	0.000191	0.004738	0.003574
GO-BP	GO:0055123	digestive system development	138	0.374089	1.714409	0.000191	0.004738	0.003574
GO-BP	GO:0019229	regulation of vasoconstriction	57	0.531464	2.08119	0.000191	0.004738	0.003574
GO-BP	GO:0055002	striated muscle cell development	155	0.431023	2.008555	0.000191	0.004738	0.003574
GO-BP	GO:1903305	regulation of regulated secretory	155	0.392334	1.828267	0.000191	0.004738	0.003574

		pathway						
GO-BP	GO:0006027	glycosaminoglycan catabolic process	60	0.501577	1.984965	0.000191	0.004738	0.003574
GO-BP	GO:0032640	tumor necrosis factor production	139	0.402453	1.845722	0.000191	0.004738	0.003574
GO-BP	GO:0055007	cardiac muscle cell differentiation	110	0.440804	1.953323	0.000191	0.004738	0.003574
GO-BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	139	0.40287	1.847634	0.000191	0.004738	0.003574
GO-BP	GO:0050764	regulation of phagocytosis	88	0.494939	2.105579	0.000191	0.004738	0.003574
GO-BP	GO:0001890	placenta development	147	0.400362	1.851774	0.000191	0.004738	0.003574
GO-BP	GO:0008277	regulation of G protein-coupled receptor signaling pathway	143	0.368937	1.698971	0.000191	0.004738	0.003574
GO-BP	GO:0019359	nicotinamide nucleotide biosynthetic process	143	0.371316	1.709929	0.000191	0.004738	0.003574
GO-BP	GO:0019363	pyridine nucleotide biosynthetic process	143	0.371316	1.709929	0.000191	0.004738	0.003574
GO-BP	GO:0045807	positive regulation of endocytosis	143	0.374655	1.725303	0.000191	0.004738	0.003574
GO-BP	GO:0055067	monovalent inorganic cation homeostasis	147	0.404943	1.872963	0.000191	0.004738	0.003574
GO-BP	GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	128	0.388115	1.757136	0.000191	0.004738	0.003574
GO-BP	GO:0045766	positive regulation of angiogenesis	159	0.387257	1.810293	0.000191	0.004738	0.003574
GO-BP	GO:0048659	smooth muscle cell proliferation	134	0.397494	1.811997	0.000192	0.004738	0.003574
GO-BP	GO:0060078	regulation of postsynaptic membrane potential	134	0.477559	2.17698	0.000192	0.004738	0.003574
GO-BP	GO:0006638	neutral lipid metabolic process	119	0.380357	1.702141	0.000192	0.004738	0.003574
GO-BP	GO:0010959	regulation of metal ion transport	370	0.304255	1.575105	0.000192	0.004738	0.003574
GO-BP	GO:0015844	monoamine transport	82	0.451598	1.896075	0.000192	0.004738	0.003574
GO-BP	GO:0097756	negative regulation of blood vessel diameter	81	0.503304	2.109622	0.000192	0.004738	0.003574
GO-BP	GO:0098754	detoxification	119	0.404712	1.81113	0.000192	0.004738	0.003574
GO-BP	GO:1903426	regulation of reactive oxygen species biosynthetic process	82	0.447054	1.876994	0.000192	0.004738	0.003574
GO-BP	GO:0009593	detection of chemical stimulus	153	0.445114	2.069386	0.000192	0.004738	0.003574
GO-BP	GO:0010038	response to metal ion	349	0.295992	1.521306	0.000192	0.004738	0.003574
GO-BP	GO:0001505	regulation of neurotransmitter levels	333	0.39174	2.00294	0.000192	0.004738	0.003574
GO-BP	GO:0097530	granulocyte migration	131	0.384287	1.746563	0.000192	0.004738	0.003574
GO-BP	GO:1903428	positive regulation of reactive oxygen species biosynthetic process	48	0.572375	2.157213	0.000192	0.004738	0.003574
GO-BP	GO:0002526	acute inflammatory response	150	0.437695	2.029057	0.000192	0.004738	0.003574
GO-BP	GO:0003002	regionalization	334	0.312541	1.598222	0.000192	0.004738	0.003574
GO-BP	GO:0006936	muscle contraction	340	0.321028	1.644797	0.000192	0.004738	0.003574
GO-BP	GO:0006140	regulation of nucleotide metabolic process	140	0.39448	1.810158	0.000192	0.004738	0.003574
GO-BP	GO:0035051	cardiocyte differentiation	140	0.425707	1.953448	0.000192	0.004738	0.003574

GO-BP	GO:0031960	response to corticosteroid	158	0.407804	1.905192	0.000192	0.004738	0.003574
GO-BP	GO:0016999	antibiotic metabolic process	142	0.416717	1.915605	0.000192	0.004738	0.003574
GO-BP	GO:0051384	response to glucocorticoid	142	0.410885	1.888799	0.000192	0.004738	0.003574
GO-BP	GO:0035296	regulation of tube diameter	137	0.440299	2.014549	0.000192	0.004738	0.003574
GO-BP	GO:0045834	positive regulation of lipid metabolic process	137	0.42045	1.923729	0.000192	0.004738	0.003574
GO-BP	GO:0050880	regulation of blood vessel size	137	0.440299	2.014549	0.000192	0.004738	0.003574
GO-BP	GO:0097746	regulation of blood vessel diameter	137	0.440299	2.014549	0.000192	0.004738	0.003574
GO-BP	GO:0051588	regulation of neurotransmitter transport	135	0.402843	1.837402	0.000192	0.004738	0.003574
GO-BP	GO:1905952	regulation of lipid localization	135	0.384694	1.75462	0.000192	0.004738	0.003574
GO-BP	GO:0032680	regulation of tumor necrosis factor production	136	0.407343	1.860182	0.000192	0.004738	0.003574
GO-BP	GO:0014074	response to purine-containing compound	141	0.439838	2.019436	0.000192	0.004738	0.003574
GO-BP	GO:0032635	interleukin-6 production	141	0.380198	1.745608	0.000192	0.004738	0.003574
GO-BP	GO:0035690	cellular response to drug	343	0.298091	1.527618	0.000192	0.004738	0.003574
GO-BP	GO:0062013	positive regulation of small molecule metabolic process	141	0.41782	1.918345	0.000192	0.004738	0.003574
GO-BP	GO:0042692	muscle cell differentiation	339	0.328752	1.682892	0.000192	0.004738	0.003574
GO-BP	GO:0030198	extracellular matrix organization	351	0.371936	1.911864	0.000193	0.004738	0.003574
GO-BP	GO:0030098	lymphocyte differentiation	343	-0.31353	-1.62351	0.000208	0.004738	0.003574
GO-BP	GO:0016571	histone methylation	136	-0.4468	-2.05016	0.000208	0.004738	0.003574
GO-BP	GO:0006261	DNA-dependent DNA replication	149	-0.49743	-2.31206	0.000208	0.004738	0.003574
GO-BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	352	-0.34024	-1.76526	0.000209	0.004738	0.003574
GO-BP	GO:0034470	ncRNA processing	348	-0.45474	-2.35756	0.000209	0.004738	0.003574
GO-BP	GO:0060271	cilium assembly	353	-0.39223	-2.03475	0.000209	0.004738	0.003574
GO-BP	GO:0034728	nucleosome organization	150	-0.40641	-1.89086	0.000209	0.004738	0.003574
GO-BP	GO:0031497	chromatin assembly	131	-0.4348	-1.98337	0.000209	0.004738	0.003574
GO-BP	GO:0061647	histone H3-K9 modification	48	-0.56009	-2.12813	0.000209	0.004738	0.003574
GO-BP	GO:0006333	chromatin assembly or disassembly	157	-0.40339	-1.89146	0.000209	0.004738	0.003574
GO-BP	GO:0033046	negative regulation of sister chromatid segregation	44	-0.56847	-2.1275	0.000209	0.004738	0.003574
GO-BP	GO:0034724	DNA replication-independent nucleosome organization	44	-0.56616	-2.11887	0.000209	0.004738	0.003574
GO-BP	GO:0000070	mitotic sister chromatid segregation	148	-0.45215	-2.09745	0.000209	0.004738	0.003574
GO-BP	GO:0009451	RNA modification	153	-0.47632	-2.22379	0.000209	0.004738	0.003574
GO-BP	GO:0006400	tRNA modification	82	-0.53046	-2.24484	0.000209	0.004738	0.003574
GO-BP	GO:0007051	spindle organization	159	-0.40116	-1.88578	0.000209	0.004738	0.003574
GO-BP	GO:0036297	interstrand cross-link repair	49	-0.59893	-2.28387	0.000209	0.004738	0.003574
GO-BP	GO:0000725	recombinational repair	128	-0.45498	-2.06825	0.000209	0.004738	0.003574
GO-BP	GO:0031023	microtubule organizing center organization	128	-0.42635	-1.93813	0.000209	0.004738	0.003574

GO-BP	GO:0031123	RNA 3'-end processing	128	-0.42663	-1.93936	0.000209	0.004738	0.003574
GO-BP	GO:0032259	methylation	346	-0.37594	-1.94713	0.000209	0.004738	0.003574
GO-BP	GO:0000375	RNA splicing, via transesterification reactions	317	-0.40788	-2.09138	0.000209	0.004738	0.003574
GO-BP	GO:0000723	telomere maintenance	147	-0.44813	-2.0756	0.000209	0.004738	0.003574
GO-BP	GO:0031124	mRNA 3'-end processing	88	-0.45439	-1.94424	0.000209	0.004738	0.003574
GO-BP	GO:0007098	centrosome cycle	120	-0.41399	-1.86437	0.000209	0.004738	0.003574
GO-BP	GO:2001251	negative regulation of chromosome organization	139	-0.45673	-2.10027	0.000209	0.004738	0.003574
GO-BP	GO:0006334	nucleosome assembly	111	-0.44862	-1.99677	0.000209	0.004738	0.003574
GO-BP	GO:0010970	transport along microtubule	155	-0.38681	-1.80931	0.000209	0.004738	0.003574
GO-BP	GO:0099111	microtubule-based transport	155	-0.38681	-1.80931	0.000209	0.004738	0.003574
GO-BP	GO:0042254	ribosome biogenesis	274	-0.4207	-2.12577	0.00021	0.004738	0.003574
GO-BP	GO:0006310	DNA recombination	276	-0.38885	-1.96525	0.00021	0.004738	0.003574
GO-BP	GO:0044782	cilium organization	369	-0.38519	-2.00743	0.00021	0.004738	0.003574
GO-BP	GO:0090305	nucleic acid phosphodiester bond hydrolysis	276	-0.36158	-1.82745	0.00021	0.004738	0.003574
GO-BP	GO:0032200	telomere organization	156	-0.42481	-1.98792	0.00021	0.004738	0.003574
GO-BP	GO:0033047	regulation of mitotic sister chromatid segregation	67	-0.47215	-1.92329	0.00021	0.004738	0.003574
GO-BP	GO:0042073	intraciliary transport	51	-0.53583	-2.06331	0.00021	0.004738	0.003574
GO-BP	GO:0033260	nuclear DNA replication	59	-0.51126	-2.03075	0.00021	0.004738	0.003574
GO-BP	GO:0034968	histone lysine methylation	112	-0.46859	-2.08814	0.00021	0.004738	0.003574
GO-BP	GO:0000724	double-strand break repair via homologous recombination	127	-0.458	-2.07829	0.00021	0.004738	0.003574
GO-BP	GO:0034508	centromere complex assembly	45	-0.56327	-2.11431	0.00021	0.004738	0.003574
GO-BP	GO:0018022	peptidyl-lysine methylation	125	-0.47028	-2.12758	0.00021	0.004738	0.003574
GO-BP	GO:0033048	negative regulation of mitotic sister chromatid segregation	42	-0.57064	-2.11012	0.00021	0.004738	0.003574
GO-BP	GO:0044839	cell cycle G2/M phase transition	256	-0.3429	-1.71612	0.00021	0.004738	0.003574
GO-BP	GO:0140014	mitotic nuclear division	256	-0.35254	-1.76433	0.00021	0.004738	0.003574
GO-BP	GO:0045058	T cell selection	47	-0.52616	-1.99015	0.00021	0.004738	0.003574
GO-BP	GO:0050853	B cell receptor signaling pathway	64	-0.54436	-2.1959	0.00021	0.004738	0.003574
GO-BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	314	-0.40846	-2.09314	0.00021	0.004738	0.003574
GO-BP	GO:0000398	mRNA splicing, via spliceosome	314	-0.40846	-2.09314	0.00021	0.004738	0.003574
GO-BP	GO:0072331	signal transduction by p53 class mediator	255	-0.343	-1.71511	0.00021	0.004738	0.003574
GO-BP	GO:0033077	T cell differentiation in thymus	69	-0.45816	-1.87624	0.00021	0.004738	0.003574
GO-BP	GO:0050854	regulation of antigen receptor-mediated signaling pathway	62	-0.60851	-2.43887	0.00021	0.004738	0.003574
GO-BP	GO:0097711	ciliary basal body-plasma membrane docking	94	-0.47361	-2.05264	0.00021	0.004738	0.003574

GO-BP	GO:0030705	cytoskeleton-dependent intracellular transport	174	-0.36019	-1.7145	0.00021	0.004738	0.003574
GO-BP	GO:0033044	regulation of chromosome organization	327	-0.36302	-1.86668	0.00021	0.004738	0.003574
GO-BP	GO:0051983	regulation of chromosome segregation	100	-0.45912	-2.01209	0.00021	0.004738	0.003574
GO-BP	GO:0008033	tRNA processing	123	-0.49836	-2.25115	0.00021	0.004738	0.003574
GO-BP	GO:0051236	establishment of RNA localization	179	-0.37209	-1.77696	0.00021	0.004738	0.003574
GO-BP	GO:0006336	DNA replication-independent nucleosome assembly	43	-0.55717	-2.0714	0.00021	0.004738	0.003574
GO-BP	GO:0018023	peptidyl-lysine trimethylation	43	-0.53349	-1.98336	0.00021	0.004738	0.003574
GO-BP	GO:0031060	regulation of histone methylation	63	-0.51955	-2.09005	0.00021	0.004738	0.003574
GO-BP	GO:0032508	DNA duplex unwinding	106	-0.53901	-2.38134	0.000211	0.004738	0.003574
GO-BP	GO:0006301	postreplication repair	50	-0.5145	-1.96871	0.000211	0.004738	0.003574
GO-BP	GO:0032392	DNA geometric change	115	-0.51743	-2.31424	0.000211	0.004738	0.003574
GO-BP	GO:0072698	protein localization to microtubule cytoskeleton	50	-0.5999	-2.29546	0.000211	0.004738	0.003574
GO-BP	GO:0043414	macromolecule methylation	294	-0.39597	-2.01593	0.000211	0.004738	0.003574
GO-BP	GO:1905515	non-motile cilium assembly	54	-0.53882	-2.0972	0.000211	0.004738	0.003574
GO-BP	GO:0044380	protein localization to cytoskeleton	55	-0.56363	-2.20328	0.000211	0.004738	0.003574
GO-BP	GO:0033045	regulation of sister chromatid segregation	79	-0.46216	-1.94023	0.000211	0.004738	0.003574
GO-BP	GO:0007059	chromosome segregation	307	-0.3683	-1.88293	0.000211	0.004738	0.003574
GO-BP	GO:0031503	protein-containing complex localization	264	-0.32293	-1.62117	0.000211	0.004738	0.003574
GO-BP	GO:0006323	DNA packaging	176	-0.40856	-1.947	0.000211	0.004738	0.003574
GO-BP	GO:0006399	tRNA metabolic process	182	-0.501	-2.3938	0.000211	0.004738	0.003574
GO-BP	GO:0050657	nucleic acid transport	176	-0.36982	-1.7624	0.000211	0.004738	0.003574
GO-BP	GO:0050658	RNA transport	176	-0.36982	-1.7624	0.000211	0.004738	0.003574
GO-BP	GO:0006479	protein methylation	173	-0.43147	-2.05039	0.000211	0.004738	0.003574
GO-BP	GO:0008213	protein alkylation	173	-0.43147	-2.05039	0.000211	0.004738	0.003574
GO-BP	GO:1901796	regulation of signal transduction by p53 class mediator	173	-0.37357	-1.77526	0.000211	0.004738	0.003574
GO-BP	GO:0044786	cell cycle DNA replication	70	-0.49602	-2.03363	0.000211	0.004738	0.003574
GO-BP	GO:0006260	DNA replication	266	-0.44071	-2.2152	0.000211	0.004738	0.003574
GO-BP	GO:0070646	protein modification by small protein removal	266	-0.31685	-1.59263	0.000211	0.004738	0.003574
GO-BP	GO:0000819	sister chromatid segregation	180	-0.44227	-2.11078	0.000211	0.004738	0.003574
GO-BP	GO:0006353	DNA-templated transcription, termination	71	-0.45513	-1.8706	0.000211	0.004738	0.003574
GO-BP	GO:0016579	protein deubiquitination	250	-0.32202	-1.60597	0.000211	0.004738	0.003574
GO-BP	GO:0034502	protein localization to chromosome	78	-0.46326	-1.93681	0.000211	0.004738	0.003574
GO-BP	GO:0043044	ATP-dependent chromatin remodeling	78	-0.49076	-2.0518	0.000211	0.004738	0.003574
GO-BP	GO:0071824	protein-DNA complex subunit	249	-0.40627	-2.02584	0.000211	0.004738	0.003574

		organization						
GO-BP	GO:0098813	nuclear chromosome segregation	250	-0.38309	-1.91053	0.000211	0.004738	0.003574
GO-BP	GO:0010389	regulation of G2/M transition of mitotic cell cycle	188	-0.36144	-1.73519	0.000211	0.004738	0.003574
GO-BP	GO:0050852	T cell receptor signaling pathway	188	-0.4434	-2.12871	0.000211	0.004738	0.003574
GO-BP	GO:0001510	RNA methylation	77	-0.52069	-2.17233	0.000212	0.004738	0.003574
GO-BP	GO:0010639	negative regulation of organelle organization	376	-0.32079	-1.67389	0.000212	0.004738	0.003574
GO-BP	GO:0071103	DNA conformation change	289	-0.43067	-2.18657	0.000212	0.004738	0.003574
GO-BP	GO:0032886	regulation of microtubule-based process	207	-0.33609	-1.63596	0.000212	0.004738	0.003574
GO-BP	GO:0000086	G2/M transition of mitotic cell cycle	237	-0.34479	-1.70768	0.000212	0.004738	0.003574
GO-BP	GO:0050851	antigen receptor-mediated signaling pathway	237	-0.4812	-2.38331	0.000212	0.004738	0.003574
GO-BP	GO:0000075	cell cycle checkpoint	208	-0.36233	-1.76399	0.000212	0.004738	0.003574
GO-BP	GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	22	-0.67973	-2.15153	0.000212	0.004738	0.003574
GO-BP	GO:0016072	rRNA metabolic process	234	-0.44575	-2.20273	0.000212	0.004738	0.003574
GO-BP	GO:0071826	ribonucleoprotein complex subunit organization	234	-0.37526	-1.85439	0.000212	0.004738	0.003574
GO-BP	GO:0033683	nucleotide-excision repair, DNA incision	38	-0.57253	-2.0659	0.000212	0.004738	0.003574
GO-BP	GO:1902749	regulation of cell cycle G2/M phase transition	205	-0.35451	-1.72287	0.000212	0.004738	0.003574
GO-BP	GO:1905508	protein localization to microtubule organizing center	32	-0.60327	-2.09247	0.000212	0.004738	0.003574
GO-BP	GO:0006364	rRNA processing	197	-0.45246	-2.18728	0.000212	0.004738	0.003574
GO-BP	GO:0043368	positive T cell selection	34	-0.60702	-2.13606	0.000212	0.004738	0.003574
GO-BP	GO:0018205	peptidyl-lysine modification	379	-0.33365	-1.74188	0.000212	0.004738	0.003574
GO-BP	GO:0065004	protein-DNA complex assembly	210	-0.43142	-2.10301	0.000212	0.004738	0.003574
GO-BP	GO:0045930	negative regulation of mitotic cell cycle	304	-0.32401	-1.65285	0.000212	0.004738	0.003574
GO-BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	385	-0.32921	-1.72192	0.000212	0.004738	0.003574
GO-BP	GO:0006403	RNA localization	211	-0.36237	-1.76653	0.000213	0.004738	0.003574
GO-BP	GO:0035735	intraciliary transport involved in cilium assembly	39	-0.61901	-2.24363	0.000213	0.004738	0.003574
GO-BP	GO:0045005	DNA-dependent DNA replication maintenance of fidelity	39	-0.56745	-2.05674	0.000213	0.004738	0.003574
GO-BP	GO:0050856	regulation of T cell receptor signaling pathway	39	-0.61364	-2.22415	0.000213	0.004738	0.003574
GO-BP	GO:2000816	negative regulation of mitotic sister chromatid separation	39	-0.552	-2.00075	0.000213	0.004738	0.003574
GO-BP	GO:0031055	chromatin remodeling at centromere	37	-0.57519	-2.06224	0.000213	0.004738	0.003574

GO-BP	GO:0031062	positive regulation of histone methylation	37	-0.55283	-1.98205	0.000213	0.004738	0.003574
GO-BP	GO:0051567	histone H3-K9 methylation	37	-0.5532	-1.98339	0.000213	0.004738	0.003574
GO-BP	GO:0002250	adaptive immune response	405	-0.30217	-1.5906	0.000213	0.004738	0.003574
GO-BP	GO:0016569	covalent chromatin modification	452	-0.32544	-1.73286	0.000213	0.004738	0.003574
GO-BP	GO:0051052	regulation of DNA metabolic process	408	-0.30151	-1.5886	0.000213	0.004738	0.003574
GO-BP	GO:0000280	nuclear division	391	-0.30282	-1.58698	0.000213	0.004738	0.003574
GO-BP	GO:0042113	B cell activation	241	-0.33976	-1.68453	0.000213	0.004738	0.003574
GO-BP	GO:0006302	double-strand break repair	229	-0.41048	-2.01954	0.000213	0.004738	0.003574
GO-BP	GO:0022618	ribonucleoprotein complex assembly	220	-0.39043	-1.91088	0.000214	0.004738	0.003574
GO-BP	GO:0016570	histone modification	436	-0.32129	-1.70472	0.000214	0.004738	0.003574
GO-BP	GO:0048285	organelle fission	430	-0.29862	-1.58115	0.000214	0.004738	0.003574
GO-BP	GO:0022613	ribonucleoprotein complex biogenesis	433	-0.41703	-2.21104	0.000214	0.004738	0.003574
GO-BP	GO:0008380	RNA splicing	396	-0.39357	-2.0643	0.000215	0.004738	0.003574
GO-BP	GO:1901987	regulation of cell cycle phase transition	428	-0.28289	-1.49689	0.000215	0.004738	0.003574
GO-BP	GO:1901990	regulation of mitotic cell cycle phase transition	396	-0.29981	-1.57254	0.000215	0.004738	0.003574
GO-BP	GO:0006397	mRNA processing	463	-0.38964	-2.07638	0.000215	0.004738	0.003574
GO-BP	GO:0031349	positive regulation of defense response	478	0.273499	1.455386	0.000374	0.007355	0.005548
GO-BP	GO:0006979	response to oxidative stress	418	0.28184	1.480313	0.000375	0.007355	0.005548
GO-BP	GO:0051048	negative regulation of secretion	218	0.327102	1.598674	0.000375	0.007355	0.005548
GO-BP	GO:0097237	cellular response to toxic substance	226	0.319766	1.569434	0.000375	0.007355	0.005548
GO-BP	GO:0001501	skeletal system development	500	0.281351	1.502491	0.000375	0.007355	0.005548
GO-BP	GO:0032490	detection of molecule of bacterial origin	10	0.796288	1.97725	0.000376	0.007355	0.005548
GO-BP	GO:0010632	regulation of epithelial cell migration	214	0.327022	1.594025	0.000377	0.007355	0.005548
GO-BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	37	0.575952	2.053809	0.000377	0.007355	0.005548
GO-BP	GO:0043304	regulation of mast cell degranulation	31	0.572176	1.953735	0.000377	0.007355	0.005548
GO-BP	GO:0043435	response to corticotropin-releasing hormone	5	0.922839	1.828254	0.000377	0.007355	0.005548
GO-BP	GO:0051194	positive regulation of cofactor metabolic process	31	0.566472	1.934258	0.000377	0.007355	0.005548
GO-BP	GO:0071376	cellular response to corticotropin-releasing hormone stimulus	5	0.922839	1.828254	0.000377	0.007355	0.005548
GO-BP	GO:0009746	response to hexose	193	0.346612	1.66458	0.000378	0.007355	0.005548
GO-BP	GO:0030073	insulin secretion	204	0.340143	1.6472	0.000378	0.007355	0.005548
GO-BP	GO:0010574	regulation of vascular endothelial growth factor production	33	0.576898	2.003306	0.000378	0.007355	0.005548
GO-BP	GO:0048665	neuron fate specification	33	0.575424	1.998188	0.000378	0.007355	0.005548
GO-BP	GO:0045444	fat cell differentiation	205	0.32815	1.589613	0.000379	0.007355	0.005548

GO-BP	GO:0007626	locomotory behavior	192	0.342447	1.642879	0.000379	0.007355	0.005548
GO-BP	GO:0070482	response to oxygen levels	376	0.286888	1.489743	0.000379	0.007355	0.005548
GO-BP	GO:0006690	icosanoid metabolic process	102	0.414679	1.813303	0.00038	0.007355	0.005548
GO-BP	GO:0030004	cellular monovalent inorganic cation homeostasis	102	0.406237	1.776389	0.00038	0.007355	0.005548
GO-BP	GO:1903524	positive regulation of blood circulation	70	0.481341	1.965323	0.00038	0.007355	0.005548
GO-BP	GO:0034284	response to monosaccharide	198	0.336849	1.622127	0.00038	0.007355	0.005548
GO-BP	GO:0071375	cellular response to peptide hormone stimulus	308	0.308227	1.565401	0.00038	0.007355	0.005548
GO-BP	GO:0050679	positive regulation of epithelial cell proliferation	182	0.357077	1.701069	0.00038	0.007355	0.005548
GO-BP	GO:0050905	neuromuscular process	103	0.410243	1.796865	0.00038	0.007355	0.005548
GO-BP	GO:0051917	regulation of fibrinolysis	14	0.701875	1.927063	0.00038	0.007355	0.005548
GO-BP	GO:0097485	neuron projection guidance	268	0.304631	1.522757	0.00038	0.007355	0.005548
GO-BP	GO:0097755	positive regulation of blood vessel diameter	56	0.49335	1.926326	0.00038	0.007355	0.005548
GO-BP	GO:0098543	detection of other organism	14	0.706652	1.940178	0.00038	0.007355	0.005548
GO-BP	GO:0032760	positive regulation of tumor necrosis factor production	79	0.443386	1.853359	0.00038	0.007355	0.005548
GO-BP	GO:0045981	positive regulation of nucleotide metabolic process	54	0.510041	1.975241	0.000381	0.007355	0.005548
GO-BP	GO:0051187	cofactor catabolic process	54	0.4945	1.915056	0.000381	0.007355	0.005548
GO-BP	GO:1900544	positive regulation of purine nucleotide metabolic process	54	0.510041	1.975241	0.000381	0.007355	0.005548
GO-BP	GO:0007218	neuropeptide signaling pathway	93	0.427439	1.837009	0.000381	0.007355	0.005548
GO-BP	GO:0060191	regulation of lipase activity	93	0.431885	1.856117	0.000381	0.007355	0.005548
GO-BP	GO:0099504	synaptic vesicle cycle	187	0.359198	1.716633	0.000381	0.007355	0.005548
GO-BP	GO:0050711	negative regulation of interleukin-1 secretion	13	0.724989	1.944801	0.000381	0.007355	0.005548
GO-BP	GO:0015696	ammonium transport	100	0.442728	1.927145	0.000381	0.007355	0.005548
GO-BP	GO:0018958	phenol-containing compound metabolic process	96	0.411331	1.78068	0.000381	0.007355	0.005548
GO-BP	GO:0062014	negative regulation of small molecule metabolic process	96	0.409162	1.771288	0.000381	0.007355	0.005548
GO-BP	GO:0090277	positive regulation of peptide hormone secretion	96	0.434714	1.881908	0.000381	0.007355	0.005548
GO-BP	GO:0015837	amine transport	94	0.414969	1.786757	0.000381	0.007355	0.005548
GO-BP	GO:0016485	protein processing	255	0.314528	1.563254	0.000382	0.007355	0.005548
GO-BP	GO:0045598	regulation of fat cell differentiation	116	0.383093	1.712038	0.000382	0.007355	0.005548
GO-BP	GO:0060359	response to ammonium ion	125	0.3768	1.700445	0.000382	0.007355	0.005548
GO-BP	GO:1990266	neutrophil migration	108	0.404579	1.787353	0.000382	0.007355	0.005548
GO-BP	GO:0060562	epithelial tube morphogenesis	313	0.312578	1.588457	0.000382	0.007355	0.005548
GO-BP	GO:2000179	positive regulation of neural precursor	51	0.500423	1.913902	0.000382	0.007355	0.005548

		cell proliferation						
GO-BP	GO:0097479	synaptic vesicle localization	156	0.359495	1.677871	0.000382	0.007355	0.005548
GO-BP	GO:0035270	endocrine system development	126	0.37737	1.704233	0.000382	0.007355	0.005548
GO-BP	GO:0001508	action potential	124	0.376922	1.699449	0.000382	0.007355	0.005548
GO-BP	GO:0015718	monocarboxylic acid transport	151	0.36357	1.688152	0.000383	0.007355	0.005548
GO-BP	GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	143	0.36384	1.675498	0.000383	0.007355	0.005548
GO-BP	GO:0017156	calcium ion regulated exocytosis	147	0.358055	1.656095	0.000383	0.007355	0.005548
GO-BP	GO:0048565	digestive tract development	128	0.371394	1.681437	0.000383	0.007355	0.005548
GO-BP	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	81	0.450112	1.886666	0.000383	0.007355	0.005548
GO-BP	GO:0061900	glial cell activation	48	0.519248	1.956984	0.000383	0.007355	0.005548
GO-BP	GO:0007259	JAK-STAT cascade	142	0.368398	1.693488	0.000384	0.007355	0.005548
GO-BP	GO:0031424	keratinization	135	0.372998	1.701275	0.000384	0.007355	0.005548
GO-BP	GO:0043039	tRNA aminoacylation	44	-0.52072	-1.94882	0.000418	0.007865	0.005934
GO-BP	GO:0007093	mitotic cell cycle checkpoint	160	-0.36405	-1.71339	0.000419	0.007865	0.005934
GO-BP	GO:0010948	negative regulation of cell cycle process	323	-0.30961	-1.59078	0.000419	0.007865	0.005934
GO-BP	GO:0043038	amino acid activation	45	-0.51867	-1.94692	0.00042	0.007865	0.005934
GO-BP	GO:0051985	negative regulation of chromosome segregation	45	-0.54123	-2.03158	0.00042	0.007865	0.005934
GO-BP	GO:0006402	mRNA catabolic process	328	-0.29928	-1.53975	0.00042	0.007865	0.005934
GO-BP	GO:0042274	ribosomal small subunit biogenesis	63	-0.4692	-1.8875	0.000421	0.007865	0.005934
GO-BP	GO:0006268	DNA unwinding involved in DNA replication	14	-0.74929	-2.09469	0.000422	0.007865	0.005934
GO-BP	GO:0002363	alpha-beta T cell lineage commitment	19	-0.67112	-2.04272	0.000422	0.007865	0.005934
GO-BP	GO:0007052	mitotic spindle organization	101	-0.42953	-1.88344	0.000422	0.007865	0.005934
GO-BP	GO:0002200	somatic diversification of immune receptors	71	-0.44879	-1.84456	0.000423	0.007865	0.005934
GO-BP	GO:0070987	error-free translesion synthesis	20	-0.70154	-2.16783	0.000423	0.007865	0.005934
GO-BP	GO:0006270	DNA replication initiation	36	-0.56523	-2.01636	0.000424	0.007865	0.005934
GO-BP	GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	36	-0.55613	-1.98392	0.000424	0.007865	0.005934
GO-BP	GO:0071539	protein localization to centrosome	31	-0.59245	-2.04092	0.000425	0.007875	0.005941
GO-BP	GO:0060560	developmental growth involved in morphogenesis	226	0.314425	1.543218	0.000563	0.009485	0.007155
GO-BP	GO:0051346	negative regulation of hydrolase activity	422	0.282188	1.482433	0.000563	0.009485	0.007155
GO-BP	GO:0051222	positive regulation of protein transport	398	0.283305	1.480176	0.000563	0.009485	0.007155
GO-BP	GO:0050663	cytokine secretion	217	0.327114	1.597442	0.000564	0.009485	0.007155
GO-BP	GO:0006816	calcium ion transport	412	0.283696	1.486547	0.000565	0.009485	0.007155
GO-BP	GO:0098542	defense response to other organism	443	0.273871	1.445423	0.000565	0.009485	0.007155

GO-BP	GO:0043542	endothelial cell migration	196	0.329752	1.587087	0.000566	0.009485	0.007155
GO-BP	GO:0016052	carbohydrate catabolic process	191	0.328975	1.57807	0.000566	0.009485	0.007155
GO-BP	GO:1903531	negative regulation of secretion by cell	193	0.327678	1.573652	0.000567	0.009485	0.007155
GO-BP	GO:0097242	amyloid-beta clearance	34	0.570134	1.993143	0.000567	0.009485	0.007155
GO-BP	GO:0035637	multicellular organismal signaling	194	0.338912	1.627788	0.000568	0.009485	0.007155
GO-BP	GO:0033006	regulation of mast cell activation involved in immune response	32	0.560744	1.930463	0.000568	0.009485	0.007155
GO-BP	GO:0045056	transcytosis	18	0.653524	1.931877	0.000568	0.009485	0.007155
GO-BP	GO:0006733	oxidoreduction coenzyme metabolic process	201	0.323548	1.56263	0.000568	0.009485	0.007155
GO-BP	GO:0006814	sodium ion transport	206	0.324241	1.571122	0.000569	0.009485	0.007155
GO-BP	GO:0033002	muscle cell proliferation	189	0.343061	1.643432	0.000569	0.009485	0.007155
GO-BP	GO:0050707	regulation of cytokine secretion	189	0.32911	1.5766	0.000569	0.009485	0.007155
GO-BP	GO:0043406	positive regulation of MAP kinase activity	246	0.306093	1.514429	0.000569	0.009485	0.007155
GO-BP	GO:0072524	pyridine-containing compound metabolic process	188	0.332033	1.588933	0.000569	0.009485	0.007155
GO-BP	GO:0003007	heart morphogenesis	247	0.305035	1.510095	0.000569	0.009485	0.007155
GO-BP	GO:0030808	regulation of nucleotide biosynthetic process	114	0.382967	1.709624	0.00057	0.009485	0.007155
GO-BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	56	0.491521	1.919186	0.00057	0.009485	0.007155
GO-BP	GO:0045591	positive regulation of regulatory T cell differentiation	14	0.690136	1.894833	0.00057	0.009485	0.007155
GO-BP	GO:0050918	positive chemotaxis	56	0.482805	1.885152	0.00057	0.009485	0.007155
GO-BP	GO:0060688	regulation of morphogenesis of a branching structure	56	0.481519	1.880131	0.00057	0.009485	0.007155
GO-BP	GO:1990748	cellular detoxification	103	0.38827	1.70062	0.00057	0.009485	0.007155
GO-BP	GO:2001044	regulation of integrin-mediated signaling pathway	14	0.692756	1.902026	0.00057	0.009485	0.007155
GO-BP	GO:0002886	regulation of myeloid leukocyte mediated immunity	55	0.483302	1.880662	0.000571	0.009485	0.007155
GO-BP	GO:0032722	positive regulation of chemokine production	55	0.494735	1.925148	0.000571	0.009485	0.007155
GO-BP	GO:0071621	granulocyte chemotaxis	113	0.378309	1.684992	0.000571	0.009485	0.007155
GO-BP	GO:1900371	regulation of purine nucleotide biosynthetic process	113	0.383095	1.706311	0.000571	0.009485	0.007155
GO-BP	GO:0006641	triglyceride metabolic process	97	0.402196	1.743048	0.000571	0.009485	0.007155
GO-BP	GO:0045820	negative regulation of glycolytic process	13	0.716552	1.92217	0.000571	0.009485	0.007155
GO-BP	GO:0019915	lipid storage	63	0.470905	1.881844	0.000571	0.009485	0.007155
GO-BP	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial	65	0.465022	1.87123	0.000572	0.009485	0.007155

		peptide						
GO-BP	GO:0019362	pyridine nucleotide metabolic process	183	0.338499	1.61242	0.000572	0.009485	0.007155
GO-BP	GO:0031099	regeneration	183	0.337714	1.608683	0.000572	0.009485	0.007155
GO-BP	GO:0046496	nicotinamide nucleotide metabolic process	183	0.338499	1.61242	0.000572	0.009485	0.007155
GO-BP	GO:0045428	regulation of nitric oxide biosynthetic process	53	0.493529	1.901661	0.000572	0.009485	0.007155
GO-BP	GO:0009595	detection of biotic stimulus	21	0.654985	2.013295	0.000572	0.009485	0.007155
GO-BP	GO:0031638	zymogen activation	52	0.4927	1.890862	0.000572	0.009485	0.007155
GO-BP	GO:0060713	labyrinthine layer morphogenesis	21	0.644016	1.979577	0.000572	0.009485	0.007155
GO-BP	GO:1905207	regulation of cardiocyte differentiation	47	0.508411	1.910191	0.000572	0.009485	0.007155
GO-BP	GO:0048545	response to steroid hormone	371	0.285637	1.479699	0.000573	0.009485	0.007155
GO-BP	GO:0006721	terpenoid metabolic process	108	0.384717	1.699606	0.000573	0.009485	0.007155
GO-BP	GO:0021782	glial cell development	108	0.381742	1.686465	0.000573	0.009485	0.007155
GO-BP	GO:0035272	exocrine system development	45	0.528358	1.965218	0.000573	0.009485	0.007155
GO-BP	GO:0045600	positive regulation of fat cell differentiation	59	0.469679	1.852472	0.000573	0.009485	0.007155
GO-BP	GO:0045806	negative regulation of endocytosis	59	0.456149	1.799111	0.000573	0.009485	0.007155
GO-BP	GO:0046503	glycerolipid catabolic process	59	0.474775	1.872574	0.000573	0.009485	0.007155
GO-BP	GO:0060711	labyrinthine layer development	46	0.52326	1.956418	0.000573	0.009485	0.007155
GO-BP	GO:0006805	xenobiotic metabolic process	109	0.386638	1.709961	0.000574	0.009485	0.007155
GO-BP	GO:0071385	cellular response to glucocorticoid stimulus	57	0.469303	1.837769	0.000574	0.009485	0.007155
GO-BP	GO:0031214	biomineral tissue development	151	0.354718	1.647051	0.000574	0.009485	0.007155
GO-BP	GO:0150076	neuroinflammatory response	60	0.483719	1.914296	0.000574	0.009485	0.007155
GO-BP	GO:0072525	pyridine-containing compound biosynthetic process	146	0.359351	1.660468	0.000574	0.009485	0.007155
GO-BP	GO:0071674	mononuclear cell migration	81	0.432742	1.81386	0.000575	0.009485	0.007155
GO-BP	GO:1904892	regulation of STAT cascade	130	0.368134	1.671746	0.000575	0.009485	0.007155
GO-BP	GO:1900542	regulation of purine nucleotide metabolic process	136	0.36956	1.687644	0.000577	0.009493	0.007161
GO-BP	GO:0051028	mRNA transport	136	-0.39522	-1.81346	0.000625	0.010086	0.007609
GO-BP	GO:0002377	immunoglobulin production	110	-0.39911	-1.77397	0.000628	0.010086	0.007609
GO-BP	GO:0006289	nucleotide-excision repair	105	-0.40763	-1.80129	0.000629	0.010086	0.007609
GO-BP	GO:0045839	negative regulation of mitotic nuclear division	52	-0.49984	-1.93273	0.00063	0.010086	0.007609
GO-BP	GO:0006354	DNA-templated transcription, elongation	107	-0.39655	-1.75434	0.000631	0.010086	0.007609
GO-BP	GO:1903311	regulation of mRNA metabolic process	301	-0.29552	-1.50808	0.000631	0.010086	0.007609
GO-BP	GO:0000731	DNA synthesis involved in DNA repair	50	-0.50403	-1.92864	0.000632	0.010086	0.007609
GO-BP	GO:0006401	RNA catabolic process	360	-0.28425	-1.47618	0.000632	0.010086	0.007609

GO-BP	GO:0019985	translesion synthesis	41	-0.51749	-1.90318	0.000632	0.010086	0.007609
GO-BP	GO:0050862	positive regulation of T cell receptor signaling pathway	14	-0.73382	-2.05144	0.000633	0.010086	0.007609
GO-BP	GO:0042276	error-prone translesion synthesis	20	-0.68046	-2.10268	0.000634	0.010086	0.007609
GO-BP	GO:0070734	histone H3-K27 methylation	20	-0.68455	-2.11531	0.000634	0.010086	0.007609
GO-BP	GO:0022616	DNA strand elongation	27	-0.62047	-2.06795	0.000635	0.010086	0.007609
GO-BP	GO:1905819	negative regulation of chromosome separation	40	-0.51765	-1.89046	0.000635	0.010086	0.007609
GO-BP	GO:0043543	protein acylation	234	-0.31935	-1.57812	0.000635	0.010086	0.007609
GO-BP	GO:0008608	attachment of spindle microtubules to kinetochore	32	-0.58058	-2.0138	0.000636	0.010086	0.007609
GO-BP	GO:0050855	regulation of B cell receptor signaling pathway	26	-0.63311	-2.08909	0.000636	0.010086	0.007609
GO-BP	GO:2001020	regulation of response to DNA damage stimulus	203	-0.3252	-1.57833	0.000637	0.010086	0.007609
GO-BP	GO:0046602	regulation of mitotic centrosome separation	9	-0.82101	-2.00428	0.000638	0.010086	0.007609
GO-BP	GO:1905064	negative regulation of vascular smooth muscle cell differentiation	8	-0.82814	-1.95538	0.000638	0.010086	0.007609
GO-BP	GO:0031297	replication fork processing	30	-0.59264	-2.0208	0.000639	0.010086	0.007609
GO-BP	GO:1904837	beta-catenin-TCF complex assembly	30	-0.59187	-2.01817	0.000639	0.010086	0.007609
GO-BP	GO:0015931	nucleobase-containing compound transport	221	-0.31902	-1.56233	0.00064	0.010086	0.007609
GO-BP	GO:0003401	axis elongation	30	0.564247	1.90881	0.000754	0.011367	0.008575
GO-BP	GO:0051968	positive regulation of synaptic transmission, glutamatergic	30	0.569497	1.926569	0.000754	0.011367	0.008575
GO-BP	GO:0043416	regulation of skeletal muscle tissue regeneration	8	0.81005	1.867731	0.000755	0.011367	0.008575
GO-BP	GO:0060947	cardiac vascular smooth muscle cell differentiation	8	0.813201	1.874997	0.000755	0.011367	0.008575
GO-BP	GO:0097084	vascular smooth muscle cell development	9	0.788588	1.887891	0.000755	0.011367	0.008575
GO-BP	GO:0030809	negative regulation of nucleotide biosynthetic process	18	0.64716	1.913065	0.000758	0.011367	0.008575
GO-BP	GO:1900372	negative regulation of purine nucleotide biosynthetic process	18	0.64716	1.913065	0.000758	0.011367	0.008575
GO-BP	GO:0003073	regulation of systemic arterial blood pressure	91	0.406832	1.7427	0.000759	0.011367	0.008575
GO-BP	GO:0009749	response to glucose	188	0.324335	1.552092	0.000759	0.011367	0.008575
GO-BP	GO:0060602	branch elongation of an epithelium	20	0.650494	1.974989	0.000759	0.011367	0.008575
GO-BP	GO:0032868	response to insulin	261	0.306593	1.528868	0.000759	0.011367	0.008575
GO-BP	GO:0099003	vesicle-mediated transport in synapse	198	0.319651	1.53931	0.00076	0.011367	0.008575
GO-BP	GO:0051966	regulation of synaptic transmission, glutamatergic	68	0.459611	1.866822	0.00076	0.011367	0.008575

GO-BP	GO:1903670	regulation of sprouting angiogenesis	68	0.4718	1.916331	0.00076	0.011367	0.008575
GO-BP	GO:0045986	negative regulation of smooth muscle contraction	14	0.687859	1.88858	0.00076	0.011367	0.008575
GO-BP	GO:0022612	gland morphogenesis	115	0.37477	1.673722	0.000761	0.011367	0.008575
GO-BP	GO:0098869	cellular oxidant detoxification	93	0.40936	1.75931	0.000761	0.011367	0.008575
GO-BP	GO:0032570	response to progesterone	43	0.526989	1.941727	0.000762	0.011367	0.008575
GO-BP	GO:0071827	plasma lipoprotein particle organization	43	0.518817	1.911615	0.000762	0.011367	0.008575
GO-BP	GO:0046928	regulation of neurotransmitter secretion	100	0.400193	1.741996	0.000762	0.011367	0.008575
GO-BP	GO:0002673	regulation of acute inflammatory response	94	0.410757	1.768621	0.000763	0.011367	0.008575
GO-BP	GO:0030593	neutrophil chemotaxis	94	0.404823	1.743067	0.000763	0.011367	0.008575
GO-BP	GO:0051937	catecholamine transport	69	0.447309	1.819249	0.000763	0.011367	0.008575
GO-BP	GO:0021879	forebrain neuron differentiation	52	0.469981	1.803671	0.000763	0.011367	0.008575
GO-BP	GO:1904894	positive regulation of STAT cascade	87	0.416526	1.769693	0.000763	0.011367	0.008575
GO-BP	GO:2001023	regulation of response to drug	85	0.422917	1.787794	0.000763	0.011367	0.008575
GO-BP	GO:0008544	epidermis development	371	0.282676	1.464363	0.000763	0.011367	0.008575
GO-BP	GO:0046660	female sex differentiation	112	0.374953	1.666524	0.000764	0.011367	0.008575
GO-BP	GO:0001655	urogenital system development	325	0.292608	1.493066	0.000764	0.011367	0.008575
GO-BP	GO:0048747	muscle fiber development	67	0.462564	1.871635	0.000764	0.011367	0.008575
GO-BP	GO:0032147	activation of protein kinase activity	318	0.294516	1.499019	0.000765	0.011367	0.008575
GO-BP	GO:0098693	regulation of synaptic vesicle cycle	109	0.380214	1.68155	0.000765	0.011367	0.008575
GO-BP	GO:0032102	negative regulation of response to external stimulus	317	0.298018	1.516164	0.000766	0.011367	0.008575
GO-BP	GO:0030810	positive regulation of nucleotide biosynthetic process	44	0.520602	1.925331	0.000767	0.011367	0.008575
GO-BP	GO:1900373	positive regulation of purine nucleotide biosynthetic process	44	0.520602	1.925331	0.000767	0.011367	0.008575
GO-BP	GO:0007612	learning	142	0.362558	1.666643	0.000768	0.011374	0.00858
GO-BP	GO:0006338	chromatin remodeling	170	-0.34406	-1.63215	0.000839	0.012277	0.009262
GO-BP	GO:1902850	microtubule cytoskeleton organization involved in mitosis	126	-0.3812	-1.72735	0.000839	0.012277	0.009262
GO-BP	GO:0051304	chromosome separation	87	-0.42668	-1.8217	0.00084	0.012277	0.009262
GO-BP	GO:0070507	regulation of microtubule cytoskeleton organization	178	-0.33943	-1.61996	0.000841	0.012277	0.009262
GO-BP	GO:0043967	histone H4 acetylation	65	-0.44439	-1.79719	0.000841	0.012277	0.009262
GO-BP	GO:0010569	regulation of double-strand break repair via homologous recombination	43	-0.49588	-1.84353	0.000842	0.012277	0.009262
GO-BP	GO:0006418	tRNA aminoacylation for protein translation	41	-0.50594	-1.8607	0.000843	0.012277	0.009262
GO-BP	GO:0000018	regulation of DNA recombination	99	-0.40403	-1.76573	0.000844	0.012277	0.009262
GO-BP	GO:0006271	DNA strand elongation involved in DNA replication	20	-0.66095	-2.04239	0.000846	0.012277	0.009262

GO-BP	GO:0006303	double-strand break repair via nonhomologous end joining	76	-0.41938	-1.74483	0.000848	0.012277	0.009262
GO-BP	GO:0019240	citulline biosynthetic process	5	-0.90037	-1.84684	0.000851	0.012277	0.009262
GO-BP	GO:0110011	regulation of basement membrane organization	5	-0.90442	-1.85514	0.000851	0.012277	0.009262
GO-BP	GO:1904259	regulation of basement membrane assembly involved in embryonic body morphogenesis	5	-0.90442	-1.85514	0.000851	0.012277	0.009262
GO-BP	GO:1904261	positive regulation of basement membrane assembly involved in embryonic body morphogenesis	5	-0.90442	-1.85514	0.000851	0.012277	0.009262
GO-BP	GO:2001197	basement membrane assembly involved in embryonic body morphogenesis	5	-0.90442	-1.85514	0.000851	0.012277	0.009262
GO-BP	GO:0015677	copper ion import	6	0.8557	1.804053	0.000942	0.013272	0.010013
GO-BP	GO:0038156	interleukin-3-mediated signaling pathway	5	0.904512	1.791947	0.000944	0.013272	0.010013
GO-BP	GO:0008202	steroid metabolic process	305	0.294134	1.49368	0.000944	0.013272	0.010013
GO-BP	GO:0001964	startle response	26	0.584637	1.900396	0.000946	0.013272	0.010013
GO-BP	GO:0055003	cardiac myofibril assembly	26	0.584721	1.900667	0.000946	0.013272	0.010013
GO-BP	GO:0045410	positive regulation of interleukin-6 biosynthetic process	15	0.679102	1.908866	0.000947	0.013272	0.010013
GO-BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	180	0.327777	1.559259	0.000948	0.013272	0.010013
GO-BP	GO:0051235	maintenance of location	309	0.298557	1.516938	0.000949	0.013272	0.010013
GO-BP	GO:0001963	synaptic transmission, dopaminergic	25	0.609109	1.958817	0.000949	0.013272	0.010013
GO-BP	GO:0090025	regulation of monocyte chemotaxis	25	0.595523	1.915126	0.000949	0.013272	0.010013
GO-BP	GO:0050796	regulation of insulin secretion	175	0.331068	1.568411	0.00095	0.013272	0.010013
GO-BP	GO:0006957	complement activation, alternative pathway	14	0.683051	1.87538	0.000951	0.013272	0.010013
GO-BP	GO:0034370	triglyceride-rich lipoprotein particle remodeling	14	0.684845	1.880304	0.000951	0.013272	0.010013
GO-BP	GO:0045824	negative regulation of innate immune response	54	0.450527	1.744761	0.000952	0.013272	0.010013
GO-BP	GO:0034219	carbohydrate transmembrane transport	106	0.381521	1.681206	0.000952	0.013272	0.010013
GO-BP	GO:0016101	diterpenoid metabolic process	98	0.393822	1.710259	0.000952	0.013272	0.010013
GO-BP	GO:0046545	development of primary female sexual characteristics	98	0.39253	1.704649	0.000952	0.013272	0.010013
GO-BP	GO:0048771	tissue remodeling	162	0.347141	1.627526	0.000954	0.013272	0.010013
GO-BP	GO:0055078	sodium ion homeostasis	51	0.473705	1.811717	0.000955	0.013272	0.010013
GO-BP	GO:0006801	superoxide metabolic process	67	0.451377	1.826368	0.000955	0.013272	0.010013
GO-BP	GO:0015872	dopamine transport	46	0.50216	1.87753	0.000955	0.013272	0.010013
GO-BP	GO:0001503	ossification	369	0.284111	1.470548	0.000956	0.013272	0.010013

GO-BP	GO:0048638	regulation of developmental growth	316	0.287725	1.463223	0.000956	0.013272	0.010013
GO-BP	GO:0048489	synaptic vesicle transport	145	0.35638	1.644551	0.000959	0.013272	0.010013
GO-BP	GO:0097480	establishment of synaptic vesicle localization	145	0.35638	1.644551	0.000959	0.013272	0.010013
GO-BP	GO:0033619	membrane protein proteolysis	58	0.45214	1.77595	0.000959	0.013272	0.010013
GO-BP	GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	61	-0.44479	-1.77933	0.001046	0.014426	0.010883
GO-BP	GO:0016444	somatic cell DNA recombination	61	-0.44479	-1.77933	0.001046	0.014426	0.010883
GO-BP	GO:0006417	regulation of translation	318	-0.28433	-1.45861	0.001048	0.01443	0.010886
GO-BP	GO:0030490	maturation of SSU-rRNA	45	-0.50378	-1.89101	0.00105	0.014432	0.010887
GO-BP	GO:0040029	regulation of gene expression, epigenetic	322	-0.28299	-1.45269	0.001051	0.014432	0.010887
GO-BP	GO:0043486	histone exchange	50	-0.49566	-1.8966	0.001053	0.014432	0.010887
GO-BP	GO:0031573	intra-S DNA damage checkpoint	15	-0.70895	-2.01895	0.001059	0.014484	0.010927
GO-BP	GO:0030217	T cell differentiation	232	-0.31587	-1.55883	0.00106	0.014484	0.010927
GO-BP	GO:0060896	neural plate pattern specification	8	-0.80613	-1.9034	0.001063	0.014504	0.010942
GO-BP	GO:0042110	T cell activation	444	-0.26511	-1.40903	0.001069	0.014556	0.010981
GO-BP	GO:0090066	regulation of anatomical structure size	484	0.264616	1.409766	0.001122	0.015045	0.01135
GO-BP	GO:0033500	carbohydrate homeostasis	228	0.306918	1.506621	0.001128	0.015045	0.01135
GO-BP	GO:0090257	regulation of muscle system process	227	0.307397	1.508605	0.001129	0.015045	0.01135
GO-BP	GO:0032692	negative regulation of interleukin-1 production	28	0.587622	1.949147	0.001133	0.015045	0.01135
GO-BP	GO:0001709	cell fate determination	38	0.544049	1.951896	0.001136	0.015045	0.01135
GO-BP	GO:0090026	positive regulation of monocyte chemotaxis	18	0.631525	1.866846	0.001136	0.015045	0.01135
GO-BP	GO:0006825	copper ion transport	16	0.661286	1.889702	0.001137	0.015045	0.01135
GO-BP	GO:2001170	negative regulation of ATP biosynthetic process	16	0.654842	1.871285	0.001137	0.015045	0.01135
GO-BP	GO:0035235	ionotropic glutamate receptor signaling pathway	24	0.617277	1.968161	0.001138	0.015045	0.01135
GO-BP	GO:1904861	excitatory synapse assembly	24	0.614868	1.96048	0.001138	0.015045	0.01135
GO-BP	GO:0042246	tissue regeneration	70	0.425506	1.737345	0.001139	0.015045	0.01135
GO-BP	GO:0007411	axon guidance	267	0.302499	1.511522	0.001139	0.015045	0.01135
GO-BP	GO:2001257	regulation of cation channel activity	163	0.344841	1.619198	0.00114	0.015045	0.01135
GO-BP	GO:0002548	monocyte chemotaxis	56	0.450478	1.758932	0.001141	0.015045	0.01135
GO-BP	GO:0043277	apoptotic cell clearance	41	0.521711	1.900477	0.001142	0.015045	0.01135
GO-BP	GO:0050433	regulation of catecholamine secretion	54	0.450201	1.743498	0.001142	0.015045	0.01135
GO-BP	GO:0051193	regulation of cofactor metabolic process	115	0.366728	1.637806	0.001142	0.015045	0.01135
GO-BP	GO:0032488	Cdc42 protein signal transduction	13	0.703348	1.88675	0.001143	0.015045	0.01135
GO-BP	GO:0001892	embryonic placenta development	85	0.41695	1.762569	0.001145	0.015045	0.01135
GO-BP	GO:0031279	regulation of cyclase activity	42	0.515885	1.891178	0.001145	0.015045	0.01135
GO-BP	GO:0045773	positive regulation of axon extension	42	0.516273	1.8926	0.001145	0.015045	0.01135

GO-BP	GO:0071675	regulation of mononuclear cell migration	46	0.492308	1.840694	0.001147	0.015045	0.01135
GO-BP	GO:0001822	kidney development	274	0.297553	1.491964	0.001147	0.015045	0.01135
GO-BP	GO:0002065	columnar/cuboidal epithelial cell differentiation	110	0.371003	1.644018	0.001148	0.015045	0.01135
GO-BP	GO:0048754	branching morphogenesis of an epithelial tube	146	0.353898	1.635274	0.001148	0.015045	0.01135
GO-BP	GO:0042446	hormone biosynthetic process	82	0.422772	1.775044	0.001149	0.015045	0.01135
GO-BP	GO:0006639	acylglycerol metabolic process	118	0.369249	1.650643	0.001153	0.015062	0.011363
GO-BP	GO:0043966	histone H3 acetylation	57	-0.46663	-1.84205	0.001257	0.016364	0.012345
GO-BP	GO:0006405	RNA export from nucleus	123	-0.36905	-1.66707	0.001262	0.016364	0.012345
GO-BP	GO:0006297	nucleotide-excision repair, DNA gap filling	23	-0.61094	-1.95737	0.001267	0.016364	0.012345
GO-BP	GO:0002836	positive regulation of response to tumor cell	11	-0.76386	-1.98378	0.001268	0.016364	0.012345
GO-BP	GO:0002839	positive regulation of immune response to tumor cell	11	-0.76386	-1.98378	0.001268	0.016364	0.012345
GO-BP	GO:0002295	T-helper cell lineage commitment	16	-0.67297	-1.94798	0.001269	0.016364	0.012345
GO-BP	GO:0036124	histone H3-K9 trimethylation	16	-0.6802	-1.96889	0.001269	0.016364	0.012345
GO-BP	GO:2001252	positive regulation of chromosome organization	167	-0.33322	-1.57612	0.00127	0.016364	0.012345
GO-BP	GO:2000779	regulation of double-strand break repair	72	-0.42301	-1.74319	0.001271	0.016364	0.012345
GO-BP	GO:0034080	CENP-A containing nucleosome assembly	34	-0.54843	-1.92987	0.001273	0.016364	0.012345
GO-BP	GO:0061641	CENP-A containing chromatin organization	34	-0.54843	-1.92987	0.001273	0.016364	0.012345
GO-BP	GO:0072511	divalent inorganic cation transport	465	0.26909	1.427324	0.001311	0.016753	0.012638
GO-BP	GO:0031348	negative regulation of defense response	196	0.31689	1.525181	0.001321	0.016753	0.012638
GO-BP	GO:1901201	regulation of extracellular matrix assembly	9	0.776385	1.858677	0.001321	0.016753	0.012638
GO-BP	GO:0045137	development of primary sexual characteristics	210	0.314614	1.528238	0.001323	0.016753	0.012638
GO-BP	GO:0002064	epithelial cell development	204	0.313952	1.520363	0.001324	0.016753	0.012638
GO-BP	GO:0008406	gonad development	204	0.312959	1.515555	0.001324	0.016753	0.012638
GO-BP	GO:0048738	cardiac muscle tissue development	205	0.316724	1.534263	0.001325	0.016753	0.012638
GO-BP	GO:0051195	negative regulation of cofactor metabolic process	22	0.624004	1.945778	0.001326	0.016753	0.012638
GO-BP	GO:0072001	renal system development	289	0.294971	1.488119	0.001327	0.016753	0.012638
GO-BP	GO:0001774	microglial cell activation	41	0.518234	1.88781	0.001332	0.016753	0.012638
GO-BP	GO:0002269	leukocyte activation involved in inflammatory response	41	0.518234	1.88781	0.001332	0.016753	0.012638
GO-BP	GO:0071825	protein-lipid complex subunit	47	0.483396	1.816204	0.001336	0.016753	0.012638

		organization						
GO-BP	GO:1903317	regulation of protein maturation	116	0.365391	1.632931	0.001336	0.016753	0.012638
GO-BP	GO:0034763	negative regulation of transmembrane	108	0.373887	1.65176	0.001336	0.016753	0.012638
		transport						
GO-BP	GO:0060048	cardiac muscle contraction	127	0.358287	1.620801	0.001336	0.016753	0.012638
GO-BP	GO:0030199	collagen fibril organization	51	0.460408	1.760861	0.001337	0.016753	0.012638
GO-BP	GO:0071384	cellular response to corticosteroid	60	0.438017	1.73343	0.001339	0.016753	0.012638
		stimulus						
GO-BP	GO:0006584	catecholamine metabolic process	49	0.470661	1.783023	0.00134	0.016753	0.012638
GO-BP	GO:0009712	catechol-containing compound	49	0.470661	1.783023	0.00134	0.016753	0.012638
		metabolic process						
GO-BP	GO:0006937	regulation of muscle contraction	157	0.346643	1.618614	0.001342	0.016753	0.012638
GO-BP	GO:0030879	mammary gland development	136	0.355975	1.625606	0.001346	0.016786	0.012664
GO-BP	GO:0090501	RNA phosphodiester bond hydrolysis	136	-0.35033	-1.60749	0.001458	0.017954	0.013545
GO-BP	GO:0009116	nucleoside metabolic process	117	-0.37341	-1.67683	0.001464	0.017954	0.013545
GO-BP	GO:0071166	ribonucleoprotein complex	116	-0.37279	-1.67135	0.00147	0.017954	0.013545
		localization						
GO-BP	GO:0006342	chromatin silencing	98	-0.39388	-1.71922	0.001473	0.017954	0.013545
GO-BP	GO:0000727	double-strand break repair via	11	-0.7592	-1.97169	0.00148	0.017954	0.013545
		break-induced replication						
GO-BP	GO:2000001	regulation of DNA damage	15	-0.6936	-1.97523	0.001482	0.017954	0.013545
		checkpoint						
GO-BP	GO:0045911	positive regulation of DNA	38	-0.52013	-1.87682	0.001483	0.017954	0.013545
		recombination						
GO-BP	GO:0002717	positive regulation of natural killer	29	-0.58352	-1.97707	0.001484	0.017954	0.013545
		cell mediated immunity						
GO-BP	GO:0007018	microtubule-based movement	271	-0.29377	-1.4796	0.001484	0.017954	0.013545
GO-BP	GO:0007094	mitotic spindle assembly checkpoint	34	-0.54603	-1.92142	0.001485	0.017954	0.013545
GO-BP	GO:0031577	spindle checkpoint	34	-0.54603	-1.92142	0.001485	0.017954	0.013545
GO-BP	GO:0071173	spindle assembly checkpoint	34	-0.54603	-1.92142	0.001485	0.017954	0.013545
GO-BP	GO:0071174	mitotic spindle checkpoint	34	-0.54603	-1.92142	0.001485	0.017954	0.013545
GO-BP	GO:1904124	microglial cell migration	6	-0.85191	-1.84991	0.001491	0.017954	0.013545
GO-BP	GO:1904139	regulation of microglial cell migration	6	-0.85191	-1.84991	0.001491	0.017954	0.013545
GO-BP	GO:0045785	positive regulation of cell adhesion	389	0.274132	1.429951	0.001502	0.017954	0.013545
GO-BP	GO:0042593	glucose homeostasis	227	0.304488	1.494326	0.001506	0.017954	0.013545
GO-BP	GO:0090385	phagosome-lysosome fusion	7	0.827488	1.833603	0.001506	0.017954	0.013545
GO-BP	GO:0099068	postsynapse assembly	30	0.544278	1.841255	0.001507	0.017954	0.013545
GO-BP	GO:0015682	ferric iron transport	37	0.542044	1.932894	0.001509	0.017954	0.013545
GO-BP	GO:0072512	trivalent inorganic cation transport	37	0.542044	1.932894	0.001509	0.017954	0.013545
GO-BP	GO:0007263	nitric oxide mediated signal	28	0.554658	1.839806	0.00151	0.017954	0.013545
		transduction						
GO-BP	GO:0010873	positive regulation of cholesterol	9	0.775151	1.855723	0.00151	0.017954	0.013545
		esterification						
GO-BP	GO:0034368	protein-lipid complex remodeling	28	0.555039	1.84107	0.00151	0.017954	0.013545

GO-BP	GO:0034369	plasma lipoprotein particle remodeling	28	0.555039	1.84107	0.00151	0.017954	0.013545
GO-BP	GO:0009612	response to mechanical stimulus	203	0.307874	1.489974	0.001511	0.017954	0.013545
GO-BP	GO:0019216	regulation of lipid metabolic process	379	0.275692	1.433355	0.001513	0.017954	0.013545
GO-BP	GO:0032928	regulation of superoxide anion generation	22	0.609287	1.899887	0.001516	0.017954	0.013545
GO-BP	GO:0015721	bile acid and bile salt transport	25	0.586828	1.887166	0.001518	0.017954	0.013545
GO-BP	GO:0070613	regulation of protein processing	114	0.361023	1.611665	0.001519	0.017954	0.013545
GO-BP	GO:0032930	positive regulation of superoxide anion generation	19	0.627076	1.87893	0.00152	0.017954	0.013545
GO-BP	GO:0043523	regulation of neuron apoptotic process	199	0.310175	1.494803	0.00152	0.017954	0.013545
GO-BP	GO:0050909	sensory perception of taste	56	0.445114	1.737986	0.001521	0.017954	0.013545
GO-BP	GO:0046461	neutral lipid catabolic process	41	0.508961	1.854032	0.001522	0.017954	0.013545
GO-BP	GO:0046464	acylglycerol catabolic process	41	0.508961	1.854032	0.001522	0.017954	0.013545
GO-BP	GO:0051602	response to electrical stimulus	43	0.503476	1.85509	0.001524	0.017954	0.013545
GO-BP	GO:0015749	monosaccharide transmembrane transport	104	0.372884	1.636466	0.001524	0.017954	0.013545
GO-BP	GO:0046890	regulation of lipid biosynthetic process	179	0.326542	1.550514	0.001524	0.017954	0.013545
GO-BP	GO:0071248	cellular response to metal ion	179	0.32619	1.54884	0.001524	0.017954	0.013545
GO-BP	GO:0030239	myofibril assembly	69	0.423626	1.72293	0.001526	0.017954	0.013545
GO-BP	GO:0046888	negative regulation of hormone secretion	66	0.433699	1.749422	0.001526	0.017954	0.013545
GO-BP	GO:2000177	regulation of neural precursor cell proliferation	85	0.402384	1.700994	0.001526	0.017954	0.013545
GO-BP	GO:0033273	response to vitamin	88	0.40403	1.718835	0.001531	0.017978	0.013562
GO-BP	GO:0097006	regulation of plasma lipoprotein particle levels	82	0.408805	1.716403	0.001533	0.017978	0.013562
GO-BP	GO:0016573	histone acetylation	149	-0.35462	-1.64827	0.001667	0.019466	0.014685
GO-BP	GO:0000726	non-recombinational repair	82	-0.40528	-1.71509	0.001673	0.019466	0.014685
GO-BP	GO:0000956	nuclear-transcribed mRNA catabolic process	183	-0.3254	-1.55697	0.001682	0.019466	0.014685
GO-BP	GO:0071426	ribonucleoprotein complex export from nucleus	115	-0.36863	-1.64874	0.001685	0.019466	0.014685
GO-BP	GO:0031295	T cell costimulation	54	-0.46645	-1.81552	0.001685	0.019466	0.014685
GO-BP	GO:0070838	divalent metal ion transport	459	0.266379	1.411258	0.001694	0.019466	0.014685
GO-BP	GO:0042417	dopamine metabolic process	37	0.523837	1.86797	0.001698	0.019466	0.014685
GO-BP	GO:0050912	detection of chemical stimulus involved in sensory perception of taste	37	0.534566	1.906229	0.001698	0.019466	0.014685
GO-BP	GO:0006003	fructose 2,6-bisphosphate metabolic process	5	0.890536	1.76426	0.001698	0.019466	0.014685
GO-BP	GO:0070487	monocyte aggregation	5	0.882695	1.748725	0.001698	0.019466	0.014685
GO-BP	GO:0098532	histone H3-K27 trimethylation	7	-0.82359	-1.87075	0.001705	0.019466	0.014685

GO-BP	GO:1904667	negative regulation of ubiquitin protein ligase activity	7	-0.82481	-1.8735	0.001705	0.019466	0.014685
GO-BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	78	0.404454	1.687104	0.001707	0.019466	0.014685
GO-BP	GO:0016311	dephosphorylation	460	-0.25954	-1.38342	0.001708	0.019466	0.014685
GO-BP	GO:0060669	embryonic placenta morphogenesis	25	0.573303	1.843669	0.001708	0.019466	0.014685
GO-BP	GO:0008645	hexose transmembrane transport	102	0.377287	1.649796	0.001708	0.019466	0.014685
GO-BP	GO:0048562	embryonic organ morphogenesis	280	0.28976	1.457308	0.001709	0.019466	0.014685
GO-BP	GO:0001657	ureteric bud development	97	0.383439	1.661761	0.001714	0.019466	0.014685
GO-BP	GO:0022600	digestive system process	97	0.382579	1.658034	0.001714	0.019466	0.014685
GO-BP	GO:0072163	mesonephric epithelium development	97	0.383439	1.661761	0.001714	0.019466	0.014685
GO-BP	GO:0072164	mesonephric tubule development	97	0.383439	1.661761	0.001714	0.019466	0.014685
GO-BP	GO:0048661	positive regulation of smooth muscle cell proliferation	84	0.406825	1.716306	0.001714	0.019466	0.014685
GO-BP	GO:0071242	cellular response to ammonium ion	63	0.43512	1.738841	0.001714	0.019466	0.014685
GO-BP	GO:0010876	lipid localization	368	0.278115	1.439585	0.001716	0.019466	0.014685
GO-BP	GO:0051952	regulation of amine transport	87	0.40192	1.707637	0.001717	0.019466	0.014685
GO-BP	GO:0002040	sprouting angiogenesis	112	0.364432	1.619763	0.001719	0.019466	0.014685
GO-BP	GO:0002067	glandular epithelial cell differentiation	46	0.487344	1.822134	0.00172	0.019466	0.014685
GO-BP	GO:0097696	STAT cascade	147	0.345913	1.599934	0.001723	0.019468	0.014687
GO-BP	GO:0046717	acid secretion	117	0.359256	1.605686	0.001724	0.019468	0.014687
GO-BP	GO:0006475	internal protein amino acid acetylation	158	-0.34298	-1.61044	0.001877	0.020899	0.015766
GO-BP	GO:0050900	leukocyte migration	422	0.264271	1.388309	0.001878	0.020899	0.015766
GO-BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	241	0.298915	1.477172	0.001882	0.020899	0.015766
GO-BP	GO:0015824	proline transport	7	0.820481	1.818077	0.001883	0.020899	0.015766
GO-BP	GO:0001558	regulation of cell growth	390	0.272576	1.420875	0.001886	0.020899	0.015766
GO-BP	GO:0045907	positive regulation of vasoconstriction	31	0.541489	1.848952	0.001887	0.020899	0.015766
GO-BP	GO:0003156	regulation of animal organ formation	35	0.516142	1.815058	0.00189	0.020899	0.015766
GO-BP	GO:0010573	vascular endothelial growth factor production	35	0.530939	1.867091	0.00189	0.020899	0.015766
GO-BP	GO:0033572	transferrin transport	35	0.527013	1.853285	0.00189	0.020899	0.015766
GO-BP	GO:0042554	superoxide anion generation	35	0.519324	1.826249	0.00189	0.020899	0.015766
GO-BP	GO:0097107	postsynaptic density assembly	17	0.632968	1.840308	0.001891	0.020899	0.015766
GO-BP	GO:0032409	regulation of transporter activity	263	0.296549	1.480864	0.001894	0.020899	0.015766
GO-BP	GO:0045408	regulation of interleukin-6 biosynthetic process	22	0.601667	1.876125	0.001895	0.020899	0.015766
GO-BP	GO:0030813	positive regulation of nucleotide catabolic process	24	0.577828	1.84238	0.001896	0.020899	0.015766
GO-BP	GO:0051197	positive regulation of coenzyme metabolic process	24	0.577828	1.84238	0.001896	0.020899	0.015766
GO-BP	GO:0001823	mesonephros development	101	0.378366	1.650241	0.001898	0.020899	0.015766
GO-BP	GO:0006413	translational initiation	167	-0.32816	-1.55216	0.001904	0.020899	0.015766

GO-BP	GO:0042278	purine nucleoside metabolic process	73	-0.4171	-1.72281	0.001906	0.020899	0.015766
GO-BP	GO:1904659	glucose transmembrane transport	100	0.377072	1.641352	0.001906	0.020899	0.015766
GO-BP	GO:0001708	cell fate specification	96	0.381267	1.65053	0.001906	0.020899	0.015766
GO-BP	GO:0045841	negative regulation of mitotic metaphase/anaphase transition	36	-0.52948	-1.88885	0.001907	0.020899	0.015766
GO-BP	GO:0010833	telomere maintenance via telomere lengthening	76	-0.40906	-1.70191	0.001908	0.020899	0.015766
GO-BP	GO:0000462	maturaton of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	34	-0.53385	-1.87856	0.001909	0.020899	0.015766
GO-BP	GO:0043271	negative regulation of ion transport	139	0.348631	1.598885	0.001914	0.020899	0.015766
GO-BP	GO:1990845	adaptive thermogenesis	151	0.339702	1.577325	0.001914	0.020899	0.015766
GO-BP	GO:1903935	response to sodium arsenite	5	-0.87517	-1.79516	0.001914	0.020899	0.015766
GO-BP	GO:0043382	positive regulation of memory T cell differentiation	6	-0.84644	-1.83804	0.001917	0.020906	0.015771
GO-BP	GO:0106106	cold-induced thermogenesis	141	0.351172	1.612342	0.001924	0.020906	0.015771
GO-BP	GO:0120161	regulation of cold-induced thermogenesis	141	0.351172	1.612342	0.001924	0.020906	0.015771
GO-BP	GO:0051249	regulation of lymphocyte activation	407	-0.26803	-1.41149	0.001924	0.020906	0.015771
GO-BP	GO:0050878	regulation of body fluid levels	477	0.26246	1.396321	0.002055	0.02226	0.016793
GO-BP	GO:1904951	positive regulation of establishment of protein localization	433	0.266205	1.401975	0.002064	0.02226	0.016793
GO-BP	GO:0070391	response to lipoteichoic acid	10	0.768874	1.909177	0.00207	0.02226	0.016793
GO-BP	GO:0071223	cellular response to lipoteichoic acid	10	0.768874	1.909177	0.00207	0.02226	0.016793
GO-BP	GO:0001974	blood vessel remodeling	39	0.508239	1.834726	0.002075	0.02226	0.016793
GO-BP	GO:0007341	penetration of zona pellucida	8	0.791114	1.824071	0.002076	0.02226	0.016793
GO-BP	GO:0034372	very-low-density lipoprotein particle remodeling	12	0.713471	1.871654	0.002083	0.02226	0.016793
GO-BP	GO:0097028	dendritic cell differentiation	40	0.50205	1.822785	0.002084	0.02226	0.016793
GO-BP	GO:0048143	astrocyte activation	22	0.593663	1.85117	0.002084	0.02226	0.016793
GO-BP	GO:0045821	positive regulation of glycolytic process	23	0.585565	1.846672	0.002088	0.02226	0.016793
GO-BP	GO:0007260	tyrosine phosphorylation of STAT protein	80	0.400212	1.676817	0.00209	0.02226	0.016793
GO-BP	GO:0018393	internal peptidyl-lysine acetylation	153	-0.34241	-1.59862	0.002091	0.02226	0.016793
GO-BP	GO:0008585	female gonad development	93	0.390966	1.680262	0.002094	0.02226	0.016793
GO-BP	GO:0021513	spinal cord dorsal/ventral patterning	21	0.603145	1.85395	0.002098	0.02226	0.016793
GO-BP	GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	66	0.426962	1.722246	0.002099	0.02226	0.016793
GO-BP	GO:0071300	cellular response to retinoic acid	66	0.425157	1.714967	0.002099	0.02226	0.016793
GO-BP	GO:0033003	regulation of mast cell activation	42	0.500481	1.834708	0.002099	0.02226	0.016793
GO-BP	GO:0016266	O-glycan processing	59	0.434747	1.714699	0.0021	0.02226	0.016793
GO-BP	GO:0000187	activation of MAPK activity	144	0.346395	1.598014	0.002101	0.02226	0.016793

GO-BP	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	65	-0.42	-1.69855	0.002103	0.02226	0.016793
GO-BP	GO:0045216	cell-cell junction organization	152	0.33827	1.57154	0.002104	0.02226	0.016793
GO-BP	GO:0090308	regulation of methylation-dependent chromatin silencing	13	-0.71521	-1.96123	0.002105	0.02226	0.016793
GO-BP	GO:0043968	histone H2A acetylation	16	-0.65382	-1.89255	0.002116	0.022343	0.016856
GO-BP	GO:0006450	regulation of translational fidelity	18	-0.63198	-1.8916	0.002118	0.022343	0.016856
GO-BP	GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	26	-0.58237	-1.92166	0.002121	0.022349	0.01686
GO-BP	GO:0002370	natural killer cell cytokine production	7	-0.81715	-1.85612	0.002132	0.022355	0.016865
GO-BP	GO:0002449	lymphocyte mediated immunity	243	-0.29904	-1.48484	0.002132	0.022355	0.016865
GO-BP	GO:0002727	regulation of natural killer cell cytokine production	7	-0.81715	-1.85612	0.002132	0.022355	0.016865
GO-BP	GO:0030953	astral microtubule organization	7	-0.81593	-1.85333	0.002132	0.022355	0.016865
GO-BP	GO:1901991	negative regulation of mitotic cell cycle phase transition	217	-0.30314	-1.48234	0.002136	0.022376	0.01688
GO-BP	GO:0003211	cardiac ventricle formation	10	0.765723	1.901353	0.002258	0.023441	0.017684
GO-BP	GO:0035376	sterol import	10	0.768121	1.907308	0.002258	0.023441	0.017684
GO-BP	GO:0060174	limb bud formation	10	0.763315	1.895374	0.002258	0.023441	0.017684
GO-BP	GO:0070508	cholesterol import	10	0.768121	1.907308	0.002258	0.023441	0.017684
GO-BP	GO:0046466	membrane lipid catabolic process	30	0.529811	1.792315	0.002261	0.023441	0.017684
GO-BP	GO:0048845	venous blood vessel morphogenesis	9	0.769213	1.841507	0.002265	0.023441	0.017684
GO-BP	GO:0090049	regulation of cell migration involved in sprouting angiogenesis	40	0.497968	1.807966	0.002273	0.023441	0.017684
GO-BP	GO:0006022	aminoglycan metabolic process	168	0.327884	1.544827	0.002275	0.023441	0.017684
GO-BP	GO:0032225	regulation of synaptic transmission, dopaminergic	16	0.638868	1.825638	0.002275	0.023441	0.017684
GO-BP	GO:0050886	endocrine process	83	0.398521	1.679583	0.002275	0.023441	0.017684
GO-BP	GO:0046677	response to antibiotic	308	0.28271	1.435811	0.002279	0.023441	0.017684
GO-BP	GO:0050432	catecholamine secretion	56	0.433686	1.693364	0.002281	0.023441	0.017684
GO-BP	GO:0060732	positive regulation of inositol phosphate biosynthetic process	14	0.671597	1.843931	0.002281	0.023441	0.017684
GO-BP	GO:0031623	receptor internalization	106	0.366382	1.614494	0.002285	0.023441	0.017684
GO-BP	GO:0034341	response to interferon-gamma	178	0.317684	1.507516	0.002287	0.023441	0.017684
GO-BP	GO:0034599	cellular response to oxidative stress	277	0.289775	1.455515	0.002289	0.023441	0.017684
GO-BP	GO:0001541	ovarian follicle development	52	0.450452	1.728723	0.002289	0.023441	0.017684
GO-BP	GO:0030277	maintenance of gastrointestinal epithelium	21	0.599719	1.843417	0.002289	0.023441	0.017684
GO-BP	GO:0030878	thyroid gland development	21	0.59912	1.841576	0.002289	0.023441	0.017684
GO-BP	GO:0043300	regulation of leukocyte degranulation	46	0.474775	1.775138	0.002293	0.023454	0.017694
GO-BP	GO:0002448	mast cell mediated immunity	48	0.461357	1.738798	0.0023	0.023498	0.017727
GO-BP	GO:0050684	regulation of mRNA processing	124	-0.35476	-1.60402	0.002306	0.023531	0.017752
GO-BP	GO:0034248	regulation of cellular amide metabolic process	374	-0.27333	-1.42614	0.002316	0.023603	0.017806

GO-BP	GO:0010457	centriole-centriole cohesion	14	-0.6919	-1.93426	0.00232	0.023615	0.017815
GO-BP	GO:0030488	tRNA methylation	38	-0.50488	-1.82178	0.002331	0.023697	0.017877
GO-BP	GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	17	-0.63638	-1.87411	0.002334	0.023705	0.017883
GO-BP	GO:0048304	positive regulation of isotype switching to IgG isotypes	10	-0.76076	-1.91652	0.002346	0.023803	0.017957
GO-BP	GO:0001580	detection of chemical stimulus involved in sensory perception of bitter taste	33	0.52814	1.833992	0.002458	0.02491	0.018792
GO-BP	GO:0010001	glial cell differentiation	209	0.301052	1.460588	0.002465	0.024916	0.018797
GO-BP	GO:2000311	regulation of AMPA receptor activity	24	0.568829	1.813688	0.002465	0.024916	0.018797
GO-BP	GO:0090208	positive regulation of triglyceride metabolic process	19	0.608969	1.824676	0.00247	0.024916	0.018797
GO-BP	GO:0030282	bone mineralization	106	0.364468	1.60606	0.002475	0.024916	0.018797
GO-BP	GO:1900449	regulation of glutamate receptor signaling pathway	63	0.428415	1.712045	0.002476	0.024916	0.018797
GO-BP	GO:1903036	positive regulation of response to wounding	63	0.426899	1.705989	0.002476	0.024916	0.018797
GO-BP	GO:0043405	regulation of MAP kinase activity	321	0.280928	1.43209	0.002483	0.024944	0.018818
GO-BP	GO:0006096	glycolytic process	111	0.3581	1.589368	0.002487	0.024944	0.018818
GO-BP	GO:0001935	endothelial cell proliferation	139	0.338703	1.553351	0.002488	0.024944	0.018818
GO-BP	GO:0002279	mast cell activation involved in immune response	48	0.458479	1.727951	0.002492	0.024949	0.018822
GO-BP	GO:0051145	smooth muscle cell differentiation	58	0.429976	1.688894	0.002494	0.024949	0.018822
GO-BP	GO:0030534	adult behavior	136	0.346045	1.58026	0.0025	0.024983	0.018847
GO-BP	GO:0031570	DNA integrity checkpoint	151	-0.33908	-1.57855	0.002513	0.02508	0.01892
GO-BP	GO:0006284	base-excision repair	41	-0.48004	-1.76545	0.002528	0.02518	0.018996
GO-BP	GO:0031294	lymphocyte costimulation	55	-0.45778	-1.78949	0.002528	0.02518	0.018996
GO-BP	GO:0002360	T cell lineage commitment	26	-0.56863	-1.87633	0.002545	0.025317	0.019099
GO-BP	GO:0051054	positive regulation of DNA metabolic process	222	-0.30124	-1.47609	0.002564	0.025477	0.01922
GO-BP	GO:0016049	cell growth	453	0.261193	1.382026	0.002629	0.026093	0.019685
GO-BP	GO:0071447	cellular response to hydroperoxide	8	0.782945	1.805235	0.002642	0.026171	0.019744
GO-BP	GO:2000300	regulation of synaptic vesicle exocytosis	75	0.40299	1.668769	0.002651	0.026171	0.019744
GO-BP	GO:0010884	positive regulation of lipid storage	18	0.610219	1.803864	0.002652	0.026171	0.019744
GO-BP	GO:0035994	response to muscle stretch	18	0.614244	1.815763	0.002652	0.026171	0.019744
GO-BP	GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	15	0.649118	1.824584	0.002652	0.026171	0.019744
GO-BP	GO:0098698	postsynaptic specialization assembly	20	0.609721	1.851197	0.002656	0.026176	0.019748
GO-BP	GO:0006939	smooth muscle contraction	103	0.365259	1.599832	0.002662	0.026177	0.019748
GO-BP	GO:0060134	prepulse inhibition	14	0.669718	1.838771	0.002662	0.026177	0.019748
GO-BP	GO:0017158	regulation of calcium ion-dependent exocytosis	107	0.363137	1.601958	0.002669	0.026217	0.019778

GO-BP	GO:0043534	blood vessel endothelial cell migration	112	0.35492	1.577488	0.002673	0.026233	0.01979
GO-BP	GO:0071322	cellular response to carbohydrate stimulus	137	0.340602	1.558391	0.00269	0.026364	0.019889
GO-BP	GO:0043484	regulation of RNA splicing	120	-0.35897	-1.6166	0.002722	0.02665	0.020105
GO-BP	GO:0031122	cytoplasmic microtubule organization	52	-0.45461	-1.75784	0.002731	0.026709	0.02015
GO-BP	GO:0006406	mRNA export from nucleus	99	-0.37896	-1.65615	0.002744	0.026779	0.020202
GO-BP	GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	99	-0.37896	-1.65615	0.002744	0.026779	0.020202
GO-BP	GO:0035025	positive regulation of Rho protein signal transduction	29	-0.56106	-1.90098	0.002757	0.026868	0.020269
GO-BP	GO:0006294	nucleotide-excision repair, preincision complex assembly	28	-0.56579	-1.8985	0.002764	0.026907	0.020298
GO-BP	GO:1901976	regulation of cell cycle checkpoint	30	-0.56013	-1.90995	0.002769	0.026934	0.020319
GO-BP	GO:0062012	regulation of small molecule metabolic process	429	0.261626	1.376959	0.002815	0.027349	0.020632
GO-BP	GO:0050808	synapse organization	393	0.267678	1.396566	0.002823	0.02739	0.020663
GO-BP	GO:0043152	induction of bacterial agglutination	5	0.864466	1.71261	0.002831	0.027423	0.020688
GO-BP	GO:0014046	dopamine secretion	34	0.514776	1.799614	0.002837	0.027423	0.020688
GO-BP	GO:0014059	regulation of dopamine secretion	34	0.514776	1.799614	0.002837	0.027423	0.020688
GO-BP	GO:0019217	regulation of fatty acid metabolic process	83	0.394286	1.661735	0.002844	0.027423	0.020688
GO-BP	GO:1901616	organic hydroxy compound catabolic process	71	0.410725	1.683694	0.002845	0.027423	0.020688
GO-BP	GO:0014902	myotube differentiation	103	0.363004	1.589959	0.002852	0.027423	0.020688
GO-BP	GO:0020027	hemoglobin metabolic process	14	0.667514	1.832721	0.002852	0.027423	0.020688
GO-BP	GO:0000041	transition metal ion transport	107	0.358682	1.582304	0.002859	0.027423	0.020688
GO-BP	GO:0032368	regulation of lipid transport	107	0.35822	1.580264	0.002859	0.027423	0.020688
GO-BP	GO:0001523	retinoid metabolic process	92	0.382721	1.640382	0.00286	0.027423	0.020688
GO-BP	GO:0090303	positive regulation of wound healing	53	0.438085	1.688023	0.002861	0.027423	0.020688
GO-BP	GO:0072330	monocarboxylic acid biosynthetic process	318	0.277856	1.414222	0.002868	0.027423	0.020688
GO-BP	GO:0042107	cytokine metabolic process	111	0.355427	1.577502	0.00287	0.027423	0.020688
GO-BP	GO:0001704	formation of primary germ layer	110	0.355785	1.576579	0.00287	0.027423	0.020688
GO-BP	GO:0002708	positive regulation of lymphocyte mediated immunity	98	-0.3795	-1.65644	0.002947	0.028123	0.021216
GO-BP	GO:0033632	regulation of cell-cell adhesion mediated by integrin	11	-0.72958	-1.89475	0.002959	0.028203	0.021277
GO-BP	GO:0140056	organelle localization by membrane tethering	168	-0.32556	-1.54024	0.002962	0.028203	0.021277
GO-BP	GO:0048302	regulation of isotype switching to IgG isotypes	12	-0.71334	-1.90487	0.002965	0.028203	0.021277
GO-BP	GO:0003223	ventricular compact myocardium morphogenesis	8	-0.77723	-1.83517	0.002977	0.028286	0.021339

GO-BP	GO:0061842	microtubule organizing center localization	30	-0.54705	-1.86532	0.002983	0.02831	0.021357
GO-BP	GO:0061564	axon development	497	0.252627	1.349326	0.002988	0.028335	0.021376
GO-BP	GO:0007409	axonogenesis	456	0.258002	1.365737	0.003009	0.028486	0.02149
GO-BP	GO:0072070	loop of Henle development	10	0.752236	1.867865	0.003011	0.028486	0.02149
GO-BP	GO:0071549	cellular response to dexamethasone stimulus	30	0.522993	1.769249	0.003014	0.028487	0.021491
GO-BP	GO:0010092	specification of animal organ identity	32	0.52769	1.816671	0.003028	0.028581	0.021562
GO-BP	GO:0030325	adrenal gland development	25	0.552651	1.777255	0.003037	0.028581	0.021562
GO-BP	GO:0033141	positive regulation of peptidyl-serine phosphorylation of STAT protein	19	0.600036	1.79791	0.00304	0.028581	0.021562
GO-BP	GO:0048639	positive regulation of developmental growth	163	0.327528	1.537904	0.00304	0.028581	0.021562
GO-BP	GO:0022898	regulation of transmembrane transporter activity	251	0.291785	1.4474	0.003041	0.028581	0.021562
GO-BP	GO:1903672	positive regulation of sprouting angiogenesis	41	0.49069	1.787474	0.003045	0.028585	0.021564
GO-BP	GO:1902476	chloride transmembrane transport	84	0.387435	1.634503	0.003048	0.028585	0.021564
GO-BP	GO:0035924	cellular response to vascular endothelial growth factor stimulus	52	0.443844	1.703362	0.003052	0.028597	0.021574
GO-BP	GO:0010634	positive regulation of epithelial cell migration	138	0.335539	1.537737	0.00306	0.028623	0.021593
GO-BP	GO:0072073	kidney epithelium development	139	0.335242	1.537477	0.003062	0.028623	0.021593
GO-BP	GO:1902803	regulation of synaptic vesicle transport	81	0.393538	1.649534	0.003065	0.028625	0.021595
GO-BP	GO:0006282	regulation of DNA repair	116	-0.35514	-1.59223	0.00315	0.029386	0.022169
GO-BP	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	100	-0.37281	-1.63383	0.003155	0.029391	0.022173
GO-BP	GO:0048291	isotype switching to IgG isotypes	13	-0.70075	-1.92156	0.003157	0.029391	0.022173
GO-BP	GO:0051168	nuclear export	181	-0.31611	-1.50938	0.003167	0.029446	0.022214
GO-BP	GO:0016458	gene silencing	266	-0.28665	-1.44087	0.00317	0.029446	0.022214
GO-BP	GO:0000154	rRNA modification	32	-0.52317	-1.81466	0.003179	0.029458	0.022223
GO-BP	GO:0051642	centrosome localization	29	-0.55765	-1.88941	0.003181	0.029458	0.022223
GO-BP	GO:0034453	microtubule anchoring	26	-0.55926	-1.84541	0.003181	0.029458	0.022223
GO-BP	GO:0006473	protein acetylation	193	-0.31393	-1.51156	0.003185	0.029458	0.022223
GO-BP	GO:0051918	negative regulation of fibrinolysis	10	0.749661	1.861471	0.003199	0.029559	0.0223
GO-BP	GO:0019433	triglyceride catabolic process	33	0.51367	1.783744	0.003215	0.029669	0.022382
GO-BP	GO:1903034	regulation of response to wounding	165	0.324246	1.525115	0.003223	0.029669	0.022382
GO-BP	GO:0002374	cytokine secretion involved in immune response	20	0.603014	1.830833	0.003225	0.029669	0.022382
GO-BP	GO:0099601	regulation of neurotransmitter receptor activity	71	0.405471	1.662157	0.003225	0.029669	0.022382
GO-BP	GO:0031670	cellular response to nutrient	68	0.410213	1.666182	0.003231	0.029687	0.022396
GO-BP	GO:0035809	regulation of urine volume	21	0.588099	1.807701	0.003243	0.029687	0.022396

GO-BP	GO:0002532	production of molecular mediator involved in inflammatory response	64	0.41457	1.662686	0.003244	0.029687	0.022396
GO-BP	GO:0009948	anterior/posterior axis specification	47	0.465236	1.747976	0.003244	0.029687	0.022396
GO-BP	GO:0043303	mast cell degranulation	47	0.465212	1.747883	0.003244	0.029687	0.022396
GO-BP	GO:0061025	membrane fusion	146	0.331646	1.53245	0.003254	0.029713	0.022416
GO-BP	GO:0003158	endothelium development	121	0.342891	1.539617	0.003257	0.029713	0.022416
GO-BP	GO:0030301	cholesterol transport	82	0.38913	1.633796	0.003257	0.029713	0.022416
GO-BP	GO:0046631	alpha-beta T cell activation	129	-0.34017	-1.54748	0.003351	0.030546	0.023044
GO-BP	GO:0000245	spliceosomal complex assembly	55	-0.44377	-1.73476	0.003371	0.030694	0.023156
GO-BP	GO:0043981	histone H4-K5 acetylation	16	-0.6404	-1.85368	0.003385	0.030753	0.0232
GO-BP	GO:0043982	histone H4-K8 acetylation	16	-0.6404	-1.85368	0.003385	0.030753	0.0232
GO-BP	GO:0002740	negative regulation of cytokine secretion involved in immune response	6	0.822969	1.735047	0.003391	0.030774	0.023216
GO-BP	GO:0006298	mismatch repair	33	-0.52554	-1.83159	0.003394	0.030774	0.023216
GO-BP	GO:0031935	regulation of chromatin silencing	37	-0.50106	-1.79645	0.003404	0.030827	0.023256
GO-BP	GO:0042035	regulation of cytokine biosynthetic process	101	0.363444	1.585157	0.003417	0.030871	0.023289
GO-BP	GO:0042866	pyruvate biosynthetic process	115	0.348886	1.558122	0.003427	0.030871	0.023289
GO-BP	GO:0045778	positive regulation of ossification	84	0.384692	1.622932	0.003429	0.030871	0.023289
GO-BP	GO:0042475	odontogenesis of dentin-containing tooth	89	0.376226	1.6047	0.00343	0.030871	0.023289
GO-BP	GO:0051196	regulation of coenzyme metabolic process	92	0.372839	1.598026	0.003432	0.030871	0.023289
GO-BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	47	0.463462	1.741308	0.003434	0.030871	0.023289
GO-BP	GO:0006757	ATP generation from ADP	112	0.350485	1.557773	0.003437	0.030871	0.023289
GO-BP	GO:0030900	forebrain development	372	0.269047	1.393821	0.003438	0.030871	0.023289
GO-BP	GO:0001936	regulation of endothelial cell proliferation	124	0.345699	1.558672	0.00344	0.030871	0.023289
GO-BP	GO:0030521	androgen receptor signaling pathway	61	-0.42467	-1.69883	0.003556	0.031874	0.024045
GO-BP	GO:0046460	neutral lipid biosynthetic process	37	0.497463	1.77392	0.003584	0.031986	0.024131
GO-BP	GO:0046463	acylglycerol biosynthetic process	37	0.497463	1.77392	0.003584	0.031986	0.024131
GO-BP	GO:0061309	cardiac neural crest cell development involved in outflow tract morphogenesis	9	0.746848	1.787965	0.003586	0.031986	0.024131
GO-BP	GO:0071241	cellular response to inorganic substance	204	0.299926	1.452443	0.003592	0.031986	0.024131
GO-BP	GO:0051383	kinetochore organization	20	-0.60981	-1.88438	0.003594	0.031986	0.024131
GO-BP	GO:1901988	negative regulation of cell cycle phase transition	234	-0.29307	-1.44822	0.0036	0.031986	0.024131
GO-BP	GO:0003151	outflow tract morphogenesis	77	0.397941	1.654978	0.003603	0.031986	0.024131
GO-BP	GO:0060561	apoptotic process involved in morphogenesis	25	0.54866	1.764421	0.003606	0.031986	0.024131

GO-BP	GO:0019233	sensory perception of pain	101	0.361439	1.576412	0.003607	0.031986	0.024131
GO-BP	GO:0006885	regulation of pH	93	0.374987	1.611588	0.003617	0.031986	0.024131
GO-BP	GO:0070555	response to interleukin-1	187	0.310509	1.483942	0.003617	0.031986	0.024131
GO-BP	GO:0007631	feeding behavior	95	0.37364	1.613335	0.00362	0.031986	0.024131
GO-BP	GO:0001759	organ induction	21	0.585879	1.800878	0.003625	0.031986	0.024131
GO-BP	GO:0021545	cranial nerve development	47	0.459965	1.728168	0.003625	0.031986	0.024131
GO-BP	GO:1903708	positive regulation of hemopoiesis	177	0.312411	1.481226	0.003627	0.031986	0.024131
GO-BP	GO:0044262	cellular carbohydrate metabolic process	273	0.284852	1.42783	0.00363	0.031986	0.024131
GO-BP	GO:0120163	negative regulation of cold-induced thermogenesis	46	0.462477	1.729156	0.003631	0.031986	0.024131
GO-BP	GO:0042476	odontogenesis	130	0.336206	1.526758	0.003644	0.03207	0.024194
GO-BP	GO:0001820	serotonin secretion	10	0.729094	1.810401	0.003764	0.033083	0.024958
GO-BP	GO:0030183	B cell differentiation	127	-0.34072	-1.54613	0.003778	0.033083	0.024958
GO-BP	GO:0048741	skeletal muscle fiber development	32	0.514753	1.772131	0.003785	0.033083	0.024958
GO-BP	GO:0060192	negative regulation of lipase activity	15	0.643114	1.807709	0.003789	0.033083	0.024958
GO-BP	GO:0060080	inhibitory postsynaptic potential	16	0.625564	1.787622	0.003791	0.033083	0.024958
GO-BP	GO:0097091	synaptic vesicle clustering	16	0.625249	1.786722	0.003791	0.033083	0.024958
GO-BP	GO:2000027	regulation of animal organ morphogenesis	246	0.292184	1.445612	0.003792	0.033083	0.024958
GO-BP	GO:0031100	animal organ regeneration	71	0.402798	1.651197	0.003794	0.033083	0.024958
GO-BP	GO:0043500	muscle adaptation	99	0.363527	1.581389	0.003799	0.033083	0.024958
GO-BP	GO:0032890	regulation of organic acid transport	56	0.425423	1.661101	0.003802	0.033083	0.024958
GO-BP	GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	20	-0.59711	-1.84513	0.003805	0.033083	0.024958
GO-BP	GO:1904666	regulation of ubiquitin protein ligase activity	20	-0.60099	-1.85713	0.003805	0.033083	0.024958
GO-BP	GO:0016075	rRNA catabolic process	18	-0.6178	-1.84916	0.003812	0.033083	0.024958
GO-BP	GO:0051004	regulation of lipoprotein lipase activity	21	0.58334	1.793073	0.003815	0.033083	0.024958
GO-BP	GO:0030641	regulation of cellular pH	85	0.378441	1.599783	0.003816	0.033083	0.024958
GO-BP	GO:0072144	glomerular mesangial cell development	5	0.85378	1.691441	0.003963	0.034308	0.025882
GO-BP	GO:0007568	aging	303	0.277758	1.408902	0.003967	0.034308	0.025882
GO-BP	GO:0140053	mitochondrial gene expression	159	-0.32324	-1.51946	0.003975	0.034308	0.025882
GO-BP	GO:0032352	positive regulation of hormone metabolic process	15	0.642353	1.80557	0.003978	0.034308	0.025882
GO-BP	GO:0045932	negative regulation of muscle contraction	22	0.57102	1.780563	0.003979	0.034308	0.025882
GO-BP	GO:0042693	muscle cell fate commitment	16	0.623947	1.783001	0.003981	0.034308	0.025882
GO-BP	GO:1901214	regulation of neuron death	294	0.278653	1.407064	0.003997	0.034381	0.025937
GO-BP	GO:1902275	regulation of chromatin organization	179	-0.31592	-1.50871	0.003997	0.034381	0.025937
GO-BP	GO:0002834	regulation of response to tumor cell	14	-0.66846	-1.86874	0.004007	0.034393	0.025946
GO-BP	GO:0002837	regulation of immune response to	14	-0.66846	-1.86874	0.004007	0.034393	0.025946

		tumor cell							
GO-BP	GO:0042542	response to hydrogen peroxide	132	0.330574	1.505185	0.004012	0.034406	0.025956	
GO-BP	GO:0061337	cardiac conduction	138	0.326773	1.497565	0.004017	0.034412	0.02596	
GO-BP	GO:0006346	methylation-dependent chromatin silencing	22	-0.58406	-1.8487	0.004022	0.034422	0.025968	
GO-BP	GO:0061041	regulation of wound healing	137	0.330285	1.511188	0.004035	0.034475	0.026008	
GO-BP	GO:0031589	cell-substrate adhesion	337	0.270587	1.384532	0.004037	0.034475	0.026008	
GO-BP	GO:0001666	response to hypoxia	343	0.271293	1.390286	0.00404	0.034475	0.026008	
GO-BP	GO:0051581	negative regulation of neurotransmitter uptake	6	0.816854	1.722154	0.004145	0.035333	0.026656	
GO-BP	GO:0034367	protein-containing complex remodeling	29	0.529054	1.771047	0.004162	0.035446	0.02674	
GO-BP	GO:0021511	spinal cord patterning	23	0.562062	1.772553	0.004176	0.03549	0.026773	
GO-BP	GO:0060004	reflex	19	0.591253	1.771594	0.004179	0.03549	0.026773	
GO-BP	GO:1904469	positive regulation of tumor necrosis factor secretion	19	0.590548	1.769479	0.004179	0.03549	0.026773	
GO-BP	GO:0030225	macrophage differentiation	43	0.475775	1.753025	0.00419	0.03555	0.026819	
GO-BP	GO:1903580	positive regulation of ATP metabolic process	45	0.46113	1.715164	0.0042	0.035568	0.026832	
GO-BP	GO:0007004	telomere maintenance via telomerase	66	-0.40875	-1.65878	0.004201	0.035568	0.026832	
GO-BP	GO:0042089	cytokine biosynthetic process	110	0.350856	1.55474	0.00421	0.03558	0.026841	
GO-BP	GO:0007100	mitotic centrosome separation	14	-0.66481	-1.85852	0.004218	0.03558	0.026841	
GO-BP	GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	14	-0.66457	-1.85784	0.004218	0.03558	0.026841	
GO-BP	GO:0051225	spindle assembly	99	-0.36763	-1.60666	0.004222	0.03558	0.026841	
GO-BP	GO:0030856	regulation of epithelial cell differentiation	140	0.327469	1.502665	0.004223	0.03558	0.026841	
GO-BP	GO:0032201	telomere maintenance via semi-conservative replication	27	-0.54948	-1.83137	0.004233	0.035631	0.02688	
GO-BP	GO:0070317	negative regulation of G0 to G1 transition	37	-0.49723	-1.78272	0.004254	0.035778	0.026991	
GO-BP	GO:0009313	oligosaccharide catabolic process	13	0.666602	1.788178	0.00438	0.0368	0.027762	
GO-BP	GO:0022406	membrane docking	177	-0.31582	-1.50716	0.004409	0.037007	0.027918	
GO-BP	GO:0046128	purine ribonucleoside metabolic process	70	-0.40431	-1.65761	0.004435	0.03719	0.028056	
GO-BP	GO:0043984	histone H4-K16 acetylation	20	-0.5929	-1.83212	0.00444	0.037193	0.028058	
GO-BP	GO:0046600	negative regulation of centriole replication	8	-0.77287	-1.82489	0.004465	0.037371	0.028192	
GO-BP	GO:0007000	nucleolus organization	7	-0.78573	-1.78475	0.004477	0.03743	0.028237	
GO-BP	GO:0050769	positive regulation of neurogenesis	450	0.253235	1.33837	0.004527	0.037797	0.028514	
GO-BP	GO:0015858	nucleoside transport	8	0.765593	1.765228	0.004529	0.037797	0.028514	
GO-BP	GO:0045923	positive regulation of fatty acid metabolic process	34	0.499313	1.745556	0.004539	0.03781	0.028524	
GO-BP	GO:2000191	regulation of fatty acid transport	26	0.539712	1.754363	0.004539	0.03781	0.028524	

GO-BP	GO:0001990	regulation of systemic arterial blood pressure by hormone	40	0.474708	1.723513	0.004546	0.037831	0.02854
GO-BP	GO:0046697	decidualization	23	0.557372	1.75776	0.004556	0.037874	0.028572
GO-BP	GO:1902893	regulation of pri-miRNA transcription by RNA polymerase II	41	0.475238	1.731186	0.004567	0.037931	0.028615
GO-BP	GO:0051784	negative regulation of nuclear division	60	-0.41925	-1.6712	0.004606	0.038221	0.028834
GO-BP	GO:1902107	positive regulation of leukocyte differentiation	141	0.325593	1.494901	0.004617	0.038274	0.028874
GO-BP	GO:0006278	RNA-dependent DNA biosynthetic process	68	-0.40878	-1.66714	0.004641	0.038438	0.028998
GO-BP	GO:0072393	microtubule anchoring at microtubule organizing center	12	-0.68281	-1.82336	0.004659	0.038548	0.029081
GO-BP	GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	37	-0.49211	-1.76437	0.00468	0.03868	0.029181
GO-BP	GO:0001840	neural plate development	10	-0.73106	-1.84169	0.004693	0.03868	0.029181
GO-BP	GO:0090309	positive regulation of methylation-dependent chromatin silencing	10	-0.7287	-1.83575	0.004693	0.03868	0.029181
GO-BP	GO:1904779	regulation of protein localization to centrosome	10	-0.73179	-1.84353	0.004693	0.03868	0.029181
GO-BP	GO:0032412	regulation of ion transmembrane transporter activity	243	0.289518	1.432458	0.004707	0.038718	0.029209
GO-BP	GO:1901642	nucleoside transmembrane transport	7	0.79408	1.759576	0.004707	0.038718	0.029209
GO-BP	GO:0048588	developmental cell growth	214	0.292183	1.424208	0.004711	0.038718	0.029209
GO-BP	GO:0007190	activation of adenylate cyclase activity	36	0.48855	1.72849	0.004732	0.038813	0.029281
GO-BP	GO:0007618	mating	40	0.472286	1.714721	0.004736	0.038813	0.029281
GO-BP	GO:0033344	cholesterol efflux	40	0.472381	1.715065	0.004736	0.038813	0.029281
GO-BP	GO:0090287	regulation of cellular response to growth factor stimulus	261	0.283052	1.411476	0.004744	0.038843	0.029303
GO-BP	GO:0051453	regulation of intracellular pH	79	0.389563	1.628379	0.004756	0.038903	0.029348
GO-BP	GO:0061351	neural precursor cell proliferation	144	0.324198	1.495614	0.004775	0.039022	0.029438
GO-BP	GO:0030203	glycosaminoglycan metabolic process	159	0.319332	1.49277	0.004787	0.039084	0.029485
GO-BP	GO:0036293	response to decreased oxygen levels	353	0.267956	1.378749	0.004796	0.039084	0.029485
GO-BP	GO:0051926	negative regulation of calcium ion transport	58	0.414829	1.629398	0.004796	0.039084	0.029485
GO-BP	GO:0006661	phosphatidylinositol biosynthetic process	109	-0.35634	-1.58179	0.004817	0.039219	0.029587
GO-BP	GO:0010886	positive regulation of cholesterol storage	7	0.790222	1.751027	0.004895	0.039735	0.029976
GO-BP	GO:0061087	positive regulation of histone H3-K27 methylation	6	-0.82124	-1.7833	0.0049	0.039735	0.029976

GO-BP	GO:0045008	depyrimidination	7	-0.78415	-1.78116	0.004903	0.039735	0.029976
GO-BP	GO:0043415	positive regulation of skeletal muscle tissue regeneration	5	0.844548	1.673152	0.004907	0.039735	0.029976
GO-BP	GO:0034371	chylomicron remodeling	9	0.738322	1.767553	0.004908	0.039735	0.029976
GO-BP	GO:0045761	regulation of adenylate cyclase activity	28	0.525966	1.744634	0.004908	0.039735	0.029976
GO-BP	GO:1905874	regulation of postsynaptic density organization	15	0.636229	1.788356	0.004925	0.039841	0.030056
GO-BP	GO:0042226	interleukin-6 biosynthetic process	23	0.553287	1.744878	0.004935	0.03985	0.030063
GO-BP	GO:0089718	amino acid import across plasma membrane	23	0.553315	1.744967	0.004935	0.03985	0.030063
GO-BP	GO:0042551	neuron maturation	47	0.452275	1.699276	0.004961	0.040018	0.03019
GO-BP	GO:0018394	peptidyl-lysine acetylation	161	-0.3192	-1.50335	0.005026	0.040507	0.030559
GO-BP	GO:0046599	regulation of centriole replication	21	-0.58372	-1.82721	0.005042	0.040597	0.030627
GO-BP	GO:0043970	histone H3-K9 acetylation	13	-0.67016	-1.83768	0.005052	0.040637	0.030656
GO-BP	GO:0006541	glutamine metabolic process	23	-0.56665	-1.81547	0.00507	0.040745	0.030738
GO-BP	GO:0007020	microtubule nucleation	24	-0.56213	-1.81949	0.005076	0.040759	0.030749
GO-BP	GO:0070198	protein localization to chromosome, telomeric region	26	-0.53979	-1.78116	0.00509	0.040834	0.030805
GO-BP	GO:0090383	phagosome acidification	28	0.525409	1.742786	0.005096	0.040845	0.030814
GO-BP	GO:0006449	regulation of translational termination	8	-0.7634	-1.80252	0.005103	0.040863	0.030827
GO-BP	GO:0019722	calcium-mediated signaling	207	0.290693	1.408736	0.005118	0.040866	0.03083
GO-BP	GO:0007416	synapse assembly	166	0.31375	1.476024	0.005119	0.040866	0.03083
GO-BP	GO:0045913	positive regulation of carbohydrate metabolic process	77	0.390643	1.624626	0.005119	0.040866	0.03083
GO-BP	GO:0031282	regulation of guanylate cyclase activity	11	0.702749	1.798529	0.005122	0.040866	0.03083
GO-BP	GO:0043279	response to alkaloid	103	0.350379	1.534658	0.005133	0.040914	0.030866
GO-BP	GO:0007219	Notch signaling pathway	185	0.304592	1.452993	0.005154	0.041041	0.030961
GO-BP	GO:0048193	Golgi vesicle transport	346	-0.2617	-1.35543	0.005231	0.04162	0.031398
GO-BP	GO:1905065	positive regulation of vascular smooth muscle cell differentiation	6	0.806249	1.699796	0.005275	0.041917	0.031623
GO-BP	GO:0045814	negative regulation of gene expression, epigenetic	114	-0.35081	-1.56574	0.00528	0.041917	0.031623
GO-BP	GO:0071548	response to dexamethasone	39	0.47209	1.704229	0.005283	0.041917	0.031623
GO-BP	GO:0072540	T-helper 17 cell lineage commitment	12	-0.67735	-1.80878	0.005294	0.041925	0.031628
GO-BP	GO:0097164	ammonium ion metabolic process	194	0.300517	1.443379	0.005298	0.041925	0.031628
GO-BP	GO:0038066	p38MAPK cascade	40	0.468073	1.699425	0.005304	0.041925	0.031628
GO-BP	GO:0002675	positive regulation of acute inflammatory response	27	0.529499	1.73967	0.005306	0.041925	0.031628
GO-BP	GO:0090196	regulation of chemokine secretion	16	0.616453	1.761586	0.005308	0.041925	0.031628
GO-BP	GO:0019226	transmission of nerve impulse	70	0.399478	1.631075	0.005316	0.041951	0.031648
GO-BP	GO:0051339	regulation of lyase activity	43	0.462476	1.704023	0.005333	0.042017	0.031697
GO-BP	GO:0042698	ovulation cycle	66	0.400426	1.615211	0.005342	0.042017	0.031697

GO-BP	GO:0030857	negative regulation of epithelial cell differentiation	42	0.465686	1.707156	0.005344	0.042017	0.031697
GO-BP	GO:0071496	cellular response to external stimulus	321	0.272538	1.38932	0.005348	0.042017	0.031697
GO-BP	GO:0003205	cardiac chamber development	169	0.313814	1.478496	0.005349	0.042017	0.031697
GO-BP	GO:0001101	response to acid chemical	330	0.267646	1.367397	0.005358	0.042029	0.031707
GO-BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	317	0.271345	1.380466	0.00536	0.042029	0.031707
GO-BP	GO:1903578	regulation of ATP metabolic process	117	0.337566	1.508743	0.005365	0.042032	0.031709
GO-BP	GO:0043524	negative regulation of neuron apoptotic process	140	0.322437	1.479573	0.005374	0.042066	0.031735
GO-BP	GO:0000077	DNA damage checkpoint	139	-0.32909	-1.51332	0.005444	0.042573	0.032117
GO-BP	GO:0032609	interferon-gamma production	104	-0.35725	-1.57486	0.00547	0.042673	0.032192
GO-BP	GO:0032350	regulation of hormone metabolic process	37	0.485647	1.731786	0.005471	0.042673	0.032192
GO-BP	GO:0050863	regulation of T cell activation	300	-0.27139	-1.38443	0.005471	0.042673	0.032192
GO-BP	GO:0070897	transcription preinitiation complex assembly	41	-0.46151	-1.69728	0.005477	0.04268	0.032198
GO-BP	GO:0010669	epithelial structure maintenance	29	0.519386	1.738681	0.005486	0.042703	0.032216
GO-BP	GO:0090197	positive regulation of chemokine secretion	15	0.632458	1.777756	0.005493	0.042703	0.032216
GO-BP	GO:0046886	positive regulation of hormone biosynthetic process	11	0.69875	1.788293	0.005502	0.042703	0.032216
GO-BP	GO:0002714	positive regulation of B cell mediated immunity	36	-0.48708	-1.73757	0.00551	0.042703	0.032216
GO-BP	GO:0002891	positive regulation of immunoglobulin mediated immune response	36	-0.48708	-1.73757	0.00551	0.042703	0.032216
GO-BP	GO:0046839	phospholipid dephosphorylation	36	-0.4881	-1.74121	0.00551	0.042703	0.032216
GO-BP	GO:0001938	positive regulation of endothelial cell proliferation	92	0.3644	1.561857	0.005529	0.042816	0.0323
GO-BP	GO:0030308	negative regulation of cell growth	177	0.307561	1.458229	0.005535	0.042819	0.032303
GO-BP	GO:0070169	positive regulation of biomineral tissue development	46	0.454375	1.698864	0.005542	0.042819	0.032303
GO-BP	GO:0050728	negative regulation of inflammatory response	129	0.331162	1.501439	0.005547	0.042819	0.032303
GO-BP	GO:0007585	respiratory gaseous exchange	60	0.410183	1.623281	0.005549	0.042819	0.032303
GO-BP	GO:0051402	neuron apoptotic process	226	0.287602	1.411572	0.005629	0.043341	0.032697
GO-BP	GO:0022604	regulation of cell morphogenesis	470	0.248993	1.321564	0.005635	0.043341	0.032697
GO-BP	GO:0045906	negative regulation of vasoconstriction	7	0.786112	1.741921	0.005649	0.043341	0.032697
GO-BP	GO:0098910	regulation of atrial cardiac muscle cell action potential	6	0.801547	1.689885	0.005652	0.043341	0.032697
GO-BP	GO:0016445	somatic diversification of immunoglobulins	60	-0.41197	-1.64218	0.005653	0.043341	0.032697

GO-BP	GO:0019080	viral gene expression	170	-0.31062	-1.47348	0.00566	0.043341	0.032697
GO-BP	GO:0045940	positive regulation of steroid metabolic process	26	0.532957	1.732408	0.005674	0.043341	0.032697
GO-BP	GO:0061082	myeloid leukocyte cytokine production	29	0.518684	1.736332	0.005675	0.043341	0.032697
GO-BP	GO:1901215	negative regulation of neuron death	194	0.300047	1.441121	0.005676	0.043341	0.032697
GO-BP	GO:0002920	regulation of humoral immune response	72	0.393336	1.617153	0.005679	0.043341	0.032697
GO-BP	GO:1901032	negative regulation of response to reactive oxygen species	15	0.629387	1.769124	0.005683	0.043341	0.032697
GO-BP	GO:1903206	negative regulation of hydrogen peroxide-induced cell death	15	0.629387	1.769124	0.005683	0.043341	0.032697
GO-BP	GO:2001039	negative regulation of cellular response to drug	15	0.629387	1.769124	0.005683	0.043341	0.032697
GO-BP	GO:0061307	cardiac neural crest cell differentiation involved in heart development	11	0.691433	1.769569	0.005692	0.043341	0.032697
GO-BP	GO:0061308	cardiac neural crest cell development involved in heart development	11	0.691433	1.769569	0.005692	0.043341	0.032697
GO-BP	GO:0007213	G protein-coupled acetylcholine receptor signaling pathway	19	0.58457	1.751569	0.005699	0.043361	0.032712
GO-BP	GO:0071415	cellular response to purine-containing compound	13	0.661173	1.773613	0.005713	0.043392	0.032735
GO-BP	GO:1904889	regulation of excitatory synapse assembly	13	0.66235	1.776772	0.005713	0.043392	0.032735
GO-BP	GO:0030195	negative regulation of blood coagulation	52	0.423335	1.624655	0.005723	0.043429	0.032763
GO-BP	GO:0071326	cellular response to monosaccharide stimulus	129	0.329827	1.495388	0.005738	0.04349	0.032809
GO-BP	GO:0036289	peptidyl-serine autophosphorylation	8	-0.76074	-1.79625	0.005741	0.04349	0.032809
GO-BP	GO:2000241	regulation of reproductive process	136	0.32667	1.491781	0.005769	0.043666	0.032941
GO-BP	GO:0045360	regulation of interleukin-1 biosynthetic process	7	0.781199	1.731033	0.005837	0.043996	0.033191
GO-BP	GO:0045362	positive regulation of interleukin-1 biosynthetic process	7	0.781199	1.731033	0.005837	0.043996	0.033191
GO-BP	GO:0050722	regulation of interleukin-1 beta biosynthetic process	7	0.781199	1.731033	0.005837	0.043996	0.033191
GO-BP	GO:0050725	positive regulation of interleukin-1 beta biosynthetic process	7	0.781199	1.731033	0.005837	0.043996	0.033191
GO-BP	GO:0014807	regulation of somitogenesis	8	0.751701	1.733196	0.00585	0.043996	0.033191
GO-BP	GO:0042533	tumor necrosis factor biosynthetic process	28	0.519001	1.721532	0.005851	0.043996	0.033191
GO-BP	GO:0042534	regulation of tumor necrosis factor biosynthetic process	28	0.519001	1.721532	0.005851	0.043996	0.033191

GO-BP	GO:2001171	positive regulation of ATP biosynthetic process	35	0.488132	1.71656	0.00586	0.043996	0.033191
GO-BP	GO:0055070	copper ion homeostasis	17	0.598793	1.740947	0.005861	0.043996	0.033191
GO-BP	GO:1905209	positive regulation of cardiocyte differentiation	26	0.532272	1.730179	0.005863	0.043996	0.033191
GO-BP	GO:1905953	negative regulation of lipid localization	41	0.458034	1.668515	0.005899	0.044188	0.033335
GO-BP	GO:1990573	potassium ion import across plasma membrane	41	0.458643	1.670731	0.005899	0.044188	0.033335
GO-BP	GO:0070167	regulation of biomineral tissue development	87	0.368273	1.564683	0.005914	0.04423	0.033367
GO-BP	GO:1904357	negative regulation of telomere maintenance via telomere lengthening	24	-0.55154	-1.78521	0.005922	0.04423	0.033367
GO-BP	GO:0032204	regulation of telomere maintenance	75	-0.38843	-1.61297	0.005932	0.04423	0.033367
GO-BP	GO:0051147	regulation of muscle cell differentiation	146	0.31979	1.477666	0.005933	0.04423	0.033367
GO-BP	GO:0050867	positive regulation of cell activation	317	0.269203	1.369567	0.005934	0.04423	0.033367
GO-BP	GO:0071331	cellular response to hexose stimulus	128	0.331614	1.501335	0.005935	0.04423	0.033367
GO-BP	GO:0006869	lipid transport	335	0.26725	1.367144	0.005947	0.044239	0.033374
GO-BP	GO:0048645	animal organ formation	58	0.408521	1.604621	0.005947	0.044239	0.033374
GO-BP	GO:0031441	negative regulation of mRNA 3'-end processing	8	-0.75843	-1.79079	0.005954	0.044253	0.033385
GO-BP	GO:1902742	apoptotic process involved in development	35	0.486836	1.712002	0.006049	0.044773	0.033777
GO-BP	GO:0015698	inorganic anion transport	164	0.313158	1.471828	0.006063	0.044773	0.033777
GO-BP	GO:0060445	branching involved in salivary gland morphogenesis	22	0.55763	1.73881	0.006063	0.044773	0.033777
GO-BP	GO:0030322	stabilization of membrane potential	16	0.611862	1.748466	0.006066	0.044773	0.033777
GO-BP	GO:0098659	inorganic cation import across plasma membrane	77	0.387195	1.610287	0.006068	0.044773	0.033777
GO-BP	GO:0099587	inorganic ion import across plasma membrane	77	0.387195	1.610287	0.006068	0.044773	0.033777
GO-BP	GO:0034330	cell junction organization	285	0.274949	1.385511	0.006076	0.044773	0.033777
GO-BP	GO:0002544	chronic inflammatory response	19	0.58061	1.739704	0.006079	0.044773	0.033777
GO-BP	GO:0051767	nitric-oxide synthase biosynthetic process	19	0.58171	1.742998	0.006079	0.044773	0.033777
GO-BP	GO:0051769	regulation of nitric-oxide synthase biosynthetic process	19	0.58171	1.742998	0.006079	0.044773	0.033777
GO-BP	GO:0071347	cellular response to interleukin-1	163	0.313782	1.473361	0.00608	0.044773	0.033777
GO-BP	GO:0051152	positive regulation of smooth muscle cell differentiation	13	0.658043	1.765218	0.006094	0.044797	0.033795
GO-BP	GO:0060712	spongiotrophoblast layer development	13	0.657902	1.76484	0.006094	0.044797	0.033795
GO-BP	GO:0072376	protein activation cascade	96	0.355109	1.537292	0.0061	0.044797	0.033795
GO-BP	GO:0051315	attachment of mitotic spindle	13	-0.66227	-1.81605	0.006104	0.044797	0.033795

		microtubules to kinetochore							
GO-BP	GO:0007043	cell-cell junction assembly	120	0.334266	1.499258	0.006123	0.044859	0.033842	
GO-BP	GO:0003231	cardiac ventricle development	128	0.330128	1.494609	0.006127	0.044859	0.033842	
GO-BP	GO:0050885	neuromuscular process controlling balance	49	0.439249	1.664023	0.006128	0.044859	0.033842	
GO-BP	GO:0007063	regulation of sister chromatid cohesion	22	-0.57154	-1.80905	0.006139	0.044901	0.033874	
GO-BP	GO:0002857	positive regulation of natural killer cell mediated immune response to tumor cell	7	-0.7759	-1.76241	0.006182	0.045179	0.034083	
GO-BP	GO:0007265	Ras protein signal transduction	425	-0.24955	-1.31995	0.00621	0.045344	0.034208	
GO-BP	GO:0050803	regulation of synapse structure or activity	215	0.289064	1.409861	0.006219	0.045368	0.034226	
GO-BP	GO:0010727	negative regulation of hydrogen peroxide metabolic process	8	0.74949	1.728099	0.006228	0.045368	0.034226	
GO-BP	GO:0034764	positive regulation of transmembrane transport	195	0.298146	1.433911	0.006229	0.045368	0.034226	
GO-BP	GO:0032024	positive regulation of insulin secretion	72	0.391401	1.609195	0.006246	0.045459	0.034294	
GO-BP	GO:0043501	skeletal muscle adaptation	25	0.533513	1.71571	0.006263	0.045521	0.034341	
GO-BP	GO:0002758	innate immune response-activating signal transduction	280	0.275298	1.384571	0.006265	0.045521	0.034341	
GO-BP	GO:1905818	regulation of chromosome separation	61	-0.40929	-1.63732	0.006275	0.045551	0.034364	
GO-BP	GO:0009620	response to fungus	43	0.455703	1.679067	0.006286	0.045577	0.034384	
GO-BP	GO:0070997	neuron death	327	0.266993	1.363281	0.006292	0.045577	0.034384	
GO-BP	GO:0050829	defense response to Gram-negative bacterium	69	0.392989	1.598324	0.006294	0.045577	0.034384	
GO-BP	GO:0090329	regulation of DNA-dependent DNA replication	53	-0.43068	-1.67115	0.006304	0.04561	0.034408	
GO-BP	GO:0006267	pre-replicative complex assembly involved in nuclear cell cycle DNA replication	7	-0.77185	-1.75322	0.006395	0.046118	0.034791	
GO-BP	GO:0036388	pre-replicative complex assembly	7	-0.77185	-1.75322	0.006395	0.046118	0.034791	
GO-BP	GO:0043983	histone H4-K12 acetylation	7	-0.7722	-1.75401	0.006395	0.046118	0.034791	
GO-BP	GO:1902299	pre-replicative complex assembly involved in cell cycle DNA replication	7	-0.77185	-1.75322	0.006395	0.046118	0.034791	
GO-BP	GO:0060685	regulation of prostatic bud formation	6	0.798452	1.683359	0.006405	0.046153	0.034818	
GO-BP	GO:0060441	epithelial tube branching involved in lung morphogenesis	28	0.513965	1.704827	0.006418	0.046202	0.034855	
GO-BP	GO:1904738	vascular associated smooth muscle cell migration	23	0.543479	1.713948	0.006454	0.046385	0.034993	
GO-BP	GO:1904752	regulation of vascular associated smooth muscle cell migration	23	0.543479	1.713948	0.006454	0.046385	0.034993	
GO-BP	GO:1904706	negative regulation of vascular	19	0.579373	1.735996	0.006459	0.046385	0.034993	

		smooth muscle cell proliferation						
GO-BP	GO:1901657	glycosyl compound metabolic process	140	-0.32707	-1.50676	0.006469	0.046406	0.035009
GO-BP	GO:0060993	kidney morphogenesis	93	0.358832	1.542158	0.006472	0.046406	0.035009
GO-BP	GO:1900047	negative regulation of hemostasis	53	0.41662	1.605316	0.006485	0.046435	0.035031
GO-BP	GO:0043470	regulation of carbohydrate catabolic process	85	0.369116	1.560363	0.006487	0.046435	0.035031
GO-BP	GO:0045061	thymic T cell selection	21	-0.57718	-1.80672	0.006513	0.046578	0.035139
GO-BP	GO:0006368	transcription elongation from RNA polymerase II promoter	80	-0.37422	-1.573	0.006541	0.046746	0.035265
GO-BP	GO:0000082	G1/S transition of mitotic cell cycle	237	-0.28401	-1.40665	0.006559	0.046828	0.035327
GO-BP	GO:0051382	kinetochore assembly	15	-0.62996	-1.794	0.006564	0.046828	0.035327
GO-BP	GO:0045292	mRNA cis splicing, via spliceosome	28	-0.52306	-1.75514	0.00659	0.046978	0.035441
GO-BP	GO:0051590	positive regulation of neurotransmitter transport	37	0.473851	1.689724	0.006603	0.047028	0.035478
GO-BP	GO:0010878	cholesterol storage	17	0.595908	1.73256	0.006618	0.047096	0.03553
GO-BP	GO:0001845	phagolysosome assembly	12	0.676791	1.775432	0.006629	0.047138	0.035561
GO-BP	GO:0002066	columnar/cuboidal epithelial cell development	55	0.41413	1.611494	0.006659	0.047315	0.035694
GO-BP	GO:0071333	cellular response to glucose stimulus	126	0.328426	1.483201	0.006688	0.047484	0.035822
GO-BP	GO:0007498	mesoderm development	120	0.332533	1.491484	0.006697	0.047506	0.035839
GO-BP	GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	49	0.437696	1.658138	0.006702	0.047506	0.035839
GO-BP	GO:0051169	nuclear transport	321	-0.2638	-1.35438	0.006714	0.047551	0.035873
GO-BP	GO:0035725	sodium ion transmembrane transport	135	0.322649	1.471629	0.006728	0.047591	0.035903
GO-BP	GO:0008643	carbohydrate transport	136	0.322248	1.471588	0.006731	0.047591	0.035903
GO-BP	GO:0032489	regulation of Cdc42 protein signal transduction	7	0.771538	1.709625	0.006778	0.04782	0.036076
GO-BP	GO:0048842	positive regulation of axon extension involved in axon guidance	7	0.77236	1.711447	0.006778	0.04782	0.036076
GO-BP	GO:0098534	centriole assembly	38	-0.46668	-1.68393	0.00678	0.04782	0.036076
GO-BP	GO:0008306	associative learning	76	0.385672	1.600931	0.006813	0.047982	0.036198
GO-BP	GO:0051350	negative regulation of lyase activity	22	0.548488	1.710302	0.006821	0.047982	0.036198
GO-BP	GO:0042033	chemokine biosynthetic process	16	0.609262	1.741035	0.006825	0.047982	0.036198
GO-BP	GO:0050755	chemokine metabolic process	16	0.609262	1.741035	0.006825	0.047982	0.036198
GO-BP	GO:0007342	fusion of sperm to egg plasma membrane involved in single fertilization	14	0.632401	1.736316	0.006844	0.048069	0.036263
GO-BP	GO:0110110	positive regulation of animal organ morphogenesis	79	0.381961	1.5966	0.006848	0.048069	0.036263
GO-BP	GO:0090382	phagosome maturation	42	0.454543	1.666305	0.00687	0.048186	0.036351
GO-BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	51	-0.43165	-1.66215	0.006923	0.048478	0.036572
GO-BP	GO:1904064	positive regulation of cation	136	0.321709	1.469125	0.006923	0.048478	0.036572

		transmembrane transport						
GO-BP	GO:0000959	mitochondrial RNA metabolic process	42	-0.44929	-1.66141	0.00693	0.048487	0.036579
GO-BP	GO:0046605	regulation of centrosome cycle	55	-0.42044	-1.64353	0.006953	0.048611	0.036672
GO-BP	GO:0055074	calcium ion homeostasis	451	0.248856	1.315554	0.006975	0.048721	0.036755
GO-BP	GO:0045823	positive regulation of heart contraction	38	0.462597	1.659668	0.007005	0.048894	0.036886
GO-BP	GO:0045214	sarcomere organization	50	0.431145	1.643956	0.007044	0.049123	0.037058
GO-BP	GO:0070268	cornification	95	0.352423	1.521718	0.007049	0.049123	0.037058
GO-BP	GO:0045851	pH reduction	51	0.426576	1.631468	0.007068	0.049215	0.037128
GO-BP	GO:0045669	positive regulation of osteoblast differentiation	58	0.406507	1.596709	0.007098	0.049383	0.037254
GO-BP	GO:0045727	positive regulation of translation	112	-0.33914	-1.51129	0.007135	0.049606	0.037423
GO-BP	GO:0002639	positive regulation of immunoglobulin production	41	-0.45311	-1.66639	0.007162	0.049754	0.037534
GO-BP	GO:0045927	positive regulation of growth	244	0.280637	1.388463	0.007178	0.049807	0.037574
GO-BP	GO:0006892	post-Golgi vesicle-mediated transport	102	-0.35229	-1.54641	0.007182	0.049807	0.037574
GO-BP	GO:0031061	negative regulation of histone methylation	20	-0.57206	-1.76773	0.007188	0.049807	0.037574
GO-BP	GO:0033555	multicellular organismal response to stress	72	0.388817	1.59857	0.007193	0.049807	0.037574
Reactome	R-HSA-1442490	Collagen degradation	64	0.46866	1.882141	0.000188	0.003902	0.002972
Reactome	R-HSA-373076	Class A/I (Rhodopsin-like receptors)	311	0.336925	1.721576	0.000189	0.003902	0.002972
Reactome	R-HSA-500792	GPCR ligand binding	432	0.350929	1.851049	0.00019	0.003902	0.002972
Reactome	R-HSA-1474228	Degradation of the extracellular matrix	138	0.452687	2.07787	0.00019	0.003902	0.002972
Reactome	R-HSA-112316	Neuronal System	396	0.327716	1.716344	0.00019	0.003902	0.002972
Reactome	R-HSA-1474244	Extracellular matrix organization	295	0.377301	1.915415	0.00019	0.003902	0.002972
Reactome	R-HSA-418594	G alpha (i) signalling events	382	0.303709	1.585055	0.00019	0.003902	0.002972
Reactome	R-HSA-6806942	MET Receptor Activation	6	0.917508	1.935467	0.00019	0.003902	0.002972
Reactome	R-HSA-418555	G alpha (s) signalling events	228	0.373224	1.835054	0.00019	0.003902	0.002972
Reactome	R-HSA-6798695	Neutrophil degranulation	456	0.44449	2.356019	0.000191	0.003902	0.002972
Reactome	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	39	0.612848	2.21532	0.000191	0.003902	0.002972
Reactome	R-HSA-1222556	ROS and RNS production in phagocytes	35	0.593112	2.089038	0.000191	0.003902	0.002972
Reactome	R-HSA-6805567	Keratinization	127	0.391273	1.77353	0.000191	0.003902	0.002972
Reactome	R-HSA-381753	Olfactory Signaling Pathway	94	0.461704	1.987109	0.000191	0.003902	0.002972
Reactome	R-HSA-6783783	Interleukin-10 signaling	43	0.611163	2.258893	0.000191	0.003902	0.002972
Reactome	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	121	0.416281	1.872661	0.000191	0.003902	0.002972
Reactome	R-HSA-2168880	Scavenging of heme from plasma	11	0.792756	2.032799	0.000192	0.003902	0.002972
Reactome	R-HSA-8957275	Post-translational protein	105	0.425087	1.862561	0.000192	0.003902	0.002972

		phosphorylation							
Reactome	R-HSA-5693567	HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA)	115	-0.46948	-2.11586	0.000208	0.003902	0.002972	
Reactome	R-HSA-69239	Synthesis of DNA	115	-0.45051	-2.03036	0.000208	0.003902	0.002972	
Reactome	R-HSA-69306	DNA Replication	123	-0.4425	-2.01614	0.000208	0.003902	0.002972	
Reactome	R-HSA-69618	Mitotic Spindle Checkpoint	107	-0.49794	-2.21911	0.000208	0.003902	0.002972	
Reactome	R-HSA-3214847	HATs acetylate histones	113	-0.43707	-1.96364	0.000208	0.003902	0.002972	
Reactome	R-HSA-2500257	Resolution of Sister Chromatid Cohesion	118	-0.4694	-2.12285	0.000208	0.003902	0.002972	
Reactome	R-HSA-72306	tRNA processing	104	-0.45551	-2.02041	0.000208	0.003902	0.002972	
Reactome	R-HSA-5620912	Anchoring of the basal body to the plasma membrane	96	-0.46936	-2.05245	0.000208	0.003902	0.002972	
Reactome	R-HSA-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	159	-0.44037	-2.0786	0.000209	0.003902	0.002972	
Reactome	R-HSA-73933	Resolution of Abasic Sites (AP sites)	38	-0.60485	-2.20152	0.000209	0.003902	0.002972	
Reactome	R-HSA-5693616	Presynaptic phase of homologous DNA pairing and strand exchange	38	-0.56378	-2.05204	0.000209	0.003902	0.002972	
Reactome	R-HSA-2871809	FCERI mediated Ca ²⁺ mobilization	32	-0.57844	-2.0221	0.000209	0.003902	0.002972	
Reactome	R-HSA-69190	DNA strand elongation	32	-0.70255	-2.456	0.000209	0.003902	0.002972	
Reactome	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	108	-0.47326	-2.1105	0.000209	0.003902	0.002972	
Reactome	R-HSA-5656169	Termination of translesion DNA synthesis	31	-0.57417	-1.98909	0.000209	0.003902	0.002972	
Reactome	R-HSA-983695	Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	31	-0.65184	-2.25818	0.000209	0.003902	0.002972	
Reactome	R-HSA-69206	G1/S Transition	128	-0.47942	-2.19486	0.000209	0.003902	0.002972	
Reactome	R-HSA-72163	mRNA Splicing - Major Pathway	172	-0.43291	-2.06644	0.000209	0.003902	0.002972	
Reactome	R-HSA-5693538	Homology Directed Repair	121	-0.47395	-2.15133	0.000209	0.003902	0.002972	
Reactome	R-HSA-5617833	Cilium Assembly	191	-0.46309	-2.24334	0.00021	0.003902	0.002972	
Reactome	R-HSA-68962	Activation of the pre-replicative complex	33	-0.65797	-2.31448	0.00021	0.003902	0.002972	
Reactome	R-HSA-69275	G2/M Transition	183	-0.39346	-1.89206	0.00021	0.003902	0.002972	
Reactome	R-HSA-5633007	Regulation of TP53 Activity	158	-0.47579	-2.2416	0.00021	0.003902	0.002972	
Reactome	R-HSA-69278	Cell Cycle, Mitotic	496	-0.43194	-2.31445	0.00021	0.003902	0.002972	
Reactome	R-HSA-176187	Activation of ATR in response to replication stress	36	-0.66271	-2.3822	0.00021	0.003902	0.002972	
Reactome	R-HSA-72172	mRNA Splicing	180	-0.43386	-2.0812	0.00021	0.003902	0.002972	
Reactome	R-HSA-73886	Chromosome Maintenance	89	-0.49296	-2.12531	0.00021	0.003902	0.002972	
Reactome	R-HSA-3247509	Chromatin modifying enzymes	242	-0.36479	-1.81975	0.00021	0.003902	0.002972	
Reactome	R-HSA-4839726	Chromatin organization	242	-0.36479	-1.81975	0.00021	0.003902	0.002972	
Reactome	R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	82	-0.45086	-1.91611	0.00021	0.003902	0.002972	

Reactome	R-HSA-2555396	Mitotic Metaphase and Anaphase	190	-0.38711	-1.87252	0.00021	0.003902	0.002972
Reactome	R-HSA-5693579	Homologous DNA Pairing and Strand Exchange	41	-0.57647	-2.13588	0.00021	0.003902	0.002972
Reactome	R-HSA-69002	DNA Replication Pre-Initiation	82	-0.45315	-1.92584	0.00021	0.003902	0.002972
Reactome	R-HSA-3700989	Transcriptional Regulation by TP53	353	-0.33347	-1.72829	0.00021	0.003902	0.002972
Reactome	R-HSA-68877	Mitotic Prometaphase	189	-0.51138	-2.4719	0.00021	0.003902	0.002972
Reactome	R-HSA-68882	Mitotic Anaphase	189	-0.3886	-1.87839	0.00021	0.003902	0.002972
Reactome	R-HSA-8868773	rRNA processing in the nucleus and cytosol	168	-0.44546	-2.11841	0.00021	0.003902	0.002972
Reactome	R-HSA-453274	Mitotic G2-G2/M phases	185	-0.39267	-1.89112	0.00021	0.003902	0.002972
Reactome	R-HSA-6783310	Fanconi Anemia Pathway	35	-0.55967	-1.99675	0.00021	0.003902	0.002972
Reactome	R-HSA-5696400	Dual Incision in GG-NER	40	-0.55633	-2.04335	0.00021	0.003902	0.002972
Reactome	R-HSA-6804756	Regulation of TP53 Activity through Phosphorylation	90	-0.51288	-2.21362	0.00021	0.003902	0.002972
Reactome	R-HSA-8852135	Protein ubiquitination	76	-0.46692	-1.96255	0.00021	0.003902	0.002972
Reactome	R-HSA-69242	S Phase	157	-0.46386	-2.18201	0.00021	0.003902	0.002972
Reactome	R-HSA-453279	Mitotic G1-G1/S phases	146	-0.42961	-2.0001	0.00021	0.003902	0.002972
Reactome	R-HSA-72187	mRNA 3'-end processing	49	-0.52392	-2.01682	0.00021	0.003902	0.002972
Reactome	R-HSA-72203	Processing of Capped Intron-Containing Pre-mRNA	228	-0.42049	-2.08105	0.00021	0.003902	0.002972
Reactome	R-HSA-141424	Amplification of signal from the kinetochores	92	-0.53839	-2.33149	0.00021	0.003902	0.002972
Reactome	R-HSA-141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	92	-0.53839	-2.33149	0.00021	0.003902	0.002972
Reactome	R-HSA-69620	Cell Cycle Checkpoints	271	-0.44995	-2.26867	0.000211	0.003902	0.002972
Reactome	R-HSA-69205	G1/S-Specific Transcription	28	-0.62766	-2.11536	0.000211	0.003902	0.002972
Reactome	R-HSA-69473	G2/M DNA damage checkpoint	81	-0.4703	-1.9931	0.000211	0.003902	0.002972
Reactome	R-HSA-110373	Resolution of AP sites via the multiple-nucleotide patch replacement pathway	26	-0.63799	-2.11279	0.000211	0.003902	0.002972
Reactome	R-HSA-5663220	RHO GTPases Activate Formins	131	-0.4184	-1.91891	0.000211	0.003902	0.002972
Reactome	R-HSA-1852241	Organelle biogenesis and maintenance	282	-0.40456	-2.04846	0.000211	0.003902	0.002972
Reactome	R-HSA-110320	Translesion Synthesis by POLH	19	-0.69746	-2.12493	0.000211	0.003902	0.002972
Reactome	R-HSA-195258	RHO GTPase Effectors	290	-0.3184	-1.61787	0.000211	0.003902	0.002972
Reactome	R-HSA-2467813	Separation of Sister Chromatids	178	-0.40545	-1.94051	0.000211	0.003902	0.002972
Reactome	R-HSA-72312	rRNA processing	178	-0.4476	-2.14226	0.000211	0.003902	0.002972
Reactome	R-HSA-73894	DNA Repair	305	-0.4316	-2.20352	0.000211	0.003902	0.002972
Reactome	R-HSA-380270	Recruitment of mitotic centrosome proteins and complexes	77	-0.49979	-2.1026	0.000211	0.003902	0.002972
Reactome	R-HSA-380287	Centrosome maturation	77	-0.49979	-2.1026	0.000211	0.003902	0.002972
Reactome	R-HSA-174417	Telomere C-strand (Lagging Strand) Synthesis	24	-0.64601	-2.09334	0.000211	0.003902	0.002972
Reactome	R-HSA-69481	G2/M Checkpoints	151	-0.44566	-2.08386	0.000211	0.003902	0.002972

Reactome	R-HSA-5693532	DNA Double-Strand Break Repair	148	-0.45739	-2.13297	0.000211	0.003902	0.002972
Reactome	R-HSA-69186	Lagging Strand Synthesis	20	-0.67739	-2.09251	0.000211	0.003902	0.002972
Reactome	R-HSA-5693607	Processing of DNA double-strand break ends	83	-0.52263	-2.22464	0.000211	0.003902	0.002972
Reactome	R-HSA-68886	M Phase	356	-0.40073	-2.07691	0.000211	0.003902	0.002972
Reactome	R-HSA-8866654	E3 ubiquitin ligases ubiquitinate target proteins	56	-0.53715	-2.12644	0.000212	0.003902	0.002972
Reactome	R-HSA-380259	Loss of Nlp from mitotic centrosomes	68	-0.48497	-1.99494	0.000212	0.003902	0.002972
Reactome	R-HSA-380284	Loss of proteins required for interphase microtubule organization from the centrosome	68	-0.48497	-1.99494	0.000212	0.003902	0.002972
Reactome	R-HSA-8854518	AURKA Activation by TPX2	71	-0.49067	-2.03228	0.000212	0.003902	0.002972
Reactome	R-HSA-194315	Signaling by Rho GTPases	413	-0.28663	-1.5087	0.000212	0.003902	0.002972
Reactome	R-HSA-380320	Recruitment of NuMA to mitotic centrosomes	87	-0.43718	-1.8726	0.000212	0.003902	0.002972
Reactome	R-HSA-6790901	rRNA modification in the nucleus and cytosol	57	-0.5245	-2.0817	0.000212	0.003902	0.002972
Reactome	R-HSA-2565942	Regulation of PLK1 Activity at G2/M Transition	86	-0.49939	-2.13596	0.000212	0.003902	0.002972
Reactome	R-HSA-5685942	HDR through Homologous Recombination (HRR)	64	-0.49387	-2.00379	0.000214	0.003902	0.002972
Reactome	R-HSA-73856	RNA Polymerase II Transcription Termination	58	-0.48949	-1.94692	0.000214	0.003902	0.002972
Reactome	R-HSA-913709	O-linked glycosylation of mucins	61	0.466843	1.856544	0.000378	0.00647	0.004929
Reactome	R-HSA-425366	Transport of bile salts and organic acids, metal ions and amine compounds	81	0.427245	1.787344	0.000381	0.00647	0.004929
Reactome	R-HSA-3299685	Detoxification of Reactive Oxygen Species	35	0.540105	1.902341	0.000381	0.00647	0.004929
Reactome	R-HSA-174577	Activation of C3 and C5	5	0.906603	1.802776	0.000381	0.00647	0.004929
Reactome	R-HSA-375276	Peptide ligand-binding receptors	186	0.369604	1.771214	0.000382	0.00647	0.004929
Reactome	R-HSA-8963901	Chylomicron remodeling	9	0.798634	1.922367	0.000383	0.00647	0.004929
Reactome	R-HSA-1296071	Potassium Channels	96	0.435593	1.880366	0.000384	0.00647	0.004929
Reactome	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	106	0.40852	1.792546	0.000385	0.00647	0.004929
Reactome	R-HSA-5607763	CLEC7A (Dectin-1) induces NFAT activation	12	-0.76556	-2.06511	0.000417	0.006484	0.004939
Reactome	R-HSA-110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	38	-0.53977	-1.96465	0.000418	0.006484	0.004939
Reactome	R-HSA-202403	TCR signaling	110	-0.42141	-1.88585	0.000418	0.006484	0.004939
Reactome	R-HSA-73893	DNA Damage Bypass	47	-0.52322	-1.99308	0.00042	0.006484	0.004939
Reactome	R-HSA-73762	RNA Polymerase I Transcription Initiation	46	-0.51688	-1.95963	0.000421	0.006484	0.004939

Reactome	R-HSA-180786	Extension of Telomeres	29	-0.59888	-2.03853	0.000421	0.006484	0.004939
Reactome	R-HSA-202433	Generation of second messenger molecules	29	-0.58735	-1.99929	0.000421	0.006484	0.004939
Reactome	R-HSA-1538133	G0 and Early G1	27	-0.60079	-2.00899	0.000422	0.006484	0.004939
Reactome	R-HSA-72202	Transport of Mature Transcript to Cytoplasm	73	-0.4312	-1.79921	0.000423	0.006484	0.004939
Reactome	R-HSA-73884	Base Excision Repair	74	-0.45601	-1.90592	0.000424	0.006484	0.004939
Reactome	R-HSA-388841	Costimulation by the CD28 family	65	-0.46981	-1.91171	0.000427	0.006484	0.004939
Reactome	R-HSA-112315	Transmission across Chemical Synapses	259	0.307286	1.533962	0.000569	0.008192	0.006241
Reactome	R-HSA-5576891	Cardiac conduction	138	0.351514	1.613477	0.00057	0.008192	0.006241
Reactome	R-HSA-449147	Signaling by Interleukins	438	0.274903	1.451068	0.000572	0.008192	0.006241
Reactome	R-HSA-373080	Class B/2 (Secretin family receptors)	90	0.406975	1.73782	0.000572	0.008192	0.006241
Reactome	R-HSA-1592389	Activation of Matrix Metalloproteinases	31	0.569029	1.944702	0.000575	0.008192	0.006241
Reactome	R-HSA-211859	Biological oxidations	193	0.334082	1.607719	0.000575	0.008192	0.006241
Reactome	R-HSA-112314	Neurotransmitter receptors and postsynaptic signal transmission	194	0.335104	1.614198	0.000575	0.008192	0.006241
Reactome	R-HSA-425407	SLC-mediated transmembrane transport	239	0.322219	1.591369	0.000578	0.008192	0.006241
Reactome	R-HSA-8953750	Transcriptional Regulation by E2F6	33	-0.54787	-1.92721	0.000629	0.008535	0.006502
Reactome	R-HSA-5620920	Cargo trafficking to the periciliary membrane	48	-0.48458	-1.85671	0.000631	0.008535	0.006502
Reactome	R-HSA-72766	Translation	265	-0.30368	-1.52831	0.000633	0.008535	0.006502
Reactome	R-HSA-5688426	Deubiquitination	256	-0.30486	-1.52848	0.000633	0.008535	0.006502
Reactome	R-HSA-5689880	Ub-specific processing proteases	179	-0.3374	-1.61603	0.000633	0.008535	0.006502
Reactome	R-HSA-170834	Signaling by TGF-beta Receptor Complex	72	-0.425	-1.76515	0.000635	0.008535	0.006502
Reactome	R-HSA-3108214	SUMOylation of DNA damage response and repair proteins	74	-0.43383	-1.8132	0.000636	0.008535	0.006502
Reactome	R-HSA-157579	Telomere Maintenance	64	-0.45202	-1.83397	0.000642	0.008542	0.006507
Reactome	R-HSA-163125	Post-translational modification: synthesis of GPI-anchored proteins	84	0.402248	1.694096	0.000761	0.009761	0.007436
Reactome	R-HSA-5621480	Dectin-2 family	25	0.600686	1.944887	0.000762	0.009761	0.007436
Reactome	R-HSA-1474290	Collagen formation	90	0.40094	1.712048	0.000763	0.009761	0.007436
Reactome	R-HSA-977443	GABA receptor activation	54	0.46601	1.809084	0.000763	0.009761	0.007436
Reactome	R-HSA-211945	Phase I - Functionalization of compounds	101	0.387258	1.687324	0.000767	0.009761	0.007436
Reactome	R-HSA-549132	Organic cation/anion/zwitterion transport	13	0.726721	1.95548	0.000767	0.009761	0.007436
Reactome	R-HSA-5620924	Intraflagellar transport	51	-0.47154	-1.83378	0.000836	0.010277	0.007829
Reactome	R-HSA-5685938	HDR through Single Strand Annealing (SSA)	36	-0.52997	-1.90505	0.000839	0.010277	0.007829
Reactome	R-HSA-606279	Deposition of new CENPA-containing	54	-0.47499	-1.8689	0.000841	0.010277	0.007829

		nucleosomes at the centromere						
Reactome	R-HSA-774815	Nucleosome assembly	54	-0.47499	-1.8689	0.000841	0.010277	0.007829
Reactome	R-HSA-5693571	Nonhomologous End-Joining (NHEJ)	55	-0.47944	-1.89268	0.000842	0.010277	0.007829
Reactome	R-HSA-1362277	Transcription of E2F targets under negative control by DREAM complex	19	-0.65976	-2.01007	0.000844	0.010277	0.007829
Reactome	R-HSA-418990	Adherens junctions interactions	31	0.551485	1.884743	0.000958	0.01151	0.008768
Reactome	R-HSA-917977	Transferrin endocytosis and recycling	31	0.553313	1.89099	0.000958	0.01151	0.008768
Reactome	R-HSA-212165	Epigenetic regulation of gene expression	124	-0.38276	-1.74721	0.001039	0.012397	0.009444
Reactome	R-HSA-159236	Transport of Mature mRNA derived from an Intron-Containing Transcript	65	-0.4353	-1.77127	0.001068	0.012657	0.009642
Reactome	R-HSA-975634	Retinoid metabolism and transport	43	0.483375	1.786581	0.001147	0.013326	0.010151
Reactome	R-HSA-977444	GABA B receptor activation	37	0.505485	1.802361	0.001149	0.013326	0.010151
Reactome	R-HSA-991365	Activation of GABAB receptors	37	0.505485	1.802361	0.001149	0.013326	0.010151
Reactome	R-HSA-5173105	O-linked glycosylation	107	0.385812	1.694823	0.001155	0.013326	0.010151
Reactome	R-HSA-110314	Recognition of DNA damage by PCNA-containing replication complex	30	-0.56036	-1.92927	0.001251	0.014154	0.010783
Reactome	R-HSA-5696398	Nucleotide Excision Repair	108	-0.38418	-1.71324	0.001254	0.014154	0.010783
Reactome	R-HSA-5696395	Formation of Incision Complex in GG-NER	41	-0.4968	-1.84068	0.00126	0.014154	0.010783
Reactome	R-HSA-6782315	tRNA modification in the nucleus and cytosol	41	-0.4967	-1.84033	0.00126	0.014154	0.010783
Reactome	R-HSA-201722	Formation of the beta-catenin:TCF transactivating complex	67	-0.4305	-1.76597	0.001273	0.014203	0.01082
Reactome	R-HSA-77387	Insulin receptor recycling	26	0.585548	1.918996	0.001332	0.014772	0.011253
Reactome	R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	92	-0.4001	-1.73262	0.001473	0.015807	0.012041
Reactome	R-HSA-6804760	Regulation of TP53 Activity through Methylation	19	-0.64196	-1.95583	0.001476	0.015807	0.012041
Reactome	R-HSA-69183	Processive synthesis on the lagging strand	15	-0.68778	-1.96359	0.001481	0.015807	0.012041
Reactome	R-HSA-68949	Orc1 removal from chromatin	68	-0.42194	-1.73566	0.001482	0.015807	0.012041
Reactome	R-HSA-5686938	Regulation of TLR by endogenous ligand	17	0.653113	1.907629	0.001512	0.015807	0.012041
Reactome	R-HSA-1296041	Activation of G protein gated Potassium channels	23	0.599694	1.902541	0.001514	0.015807	0.012041
Reactome	R-HSA-1296059	G protein gated Potassium channels	23	0.599694	1.902541	0.001514	0.015807	0.012041
Reactome	R-HSA-997272	Inhibition of voltage gated Ca ²⁺ channels via Gbeta/gamma subunits	23	0.599694	1.902541	0.001514	0.015807	0.012041
Reactome	R-HSA-166663	Initial triggering of complement	20	0.635829	1.938192	0.001519	0.015807	0.012041
Reactome	R-HSA-1296065	Inwardly rectifying K ⁺ channels	29	0.550509	1.852839	0.001523	0.015807	0.012041
Reactome	R-HSA-74713	IRS activation	5	0.876875	1.743661	0.001526	0.015807	0.012041
Reactome	R-HSA-72706	GTP hydrolysis and joining of the	93	-0.39178	-1.70133	0.00168	0.016956	0.012917

60S ribosomal subunit

Reactome	R-HSA-1483255	PI Metabolism	80	-0.40848	-1.72875	0.001681	0.016956	0.012917
Reactome	R-HSA-5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	25	-0.57424	-1.88506	0.001682	0.016956	0.012917
Reactome	R-HSA-5651801	PCNA-Dependent Long Patch Base Excision Repair	21	-0.62077	-1.94343	0.001685	0.016956	0.012917
Reactome	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	79	-0.40854	-1.72356	0.001693	0.016956	0.012917
Reactome	R-HSA-5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	63	-0.43137	-1.74586	0.001696	0.016956	0.012917
Reactome	R-HSA-176974	Unwinding of DNA	12	-0.74234	-2.00247	0.001875	0.018104	0.013792
Reactome	R-HSA-6806003	Regulation of TP53 Expression and Degradation	37	-0.49898	-1.80493	0.001882	0.018104	0.013792
Reactome	R-HSA-8939245	RUNX1 regulates transcription of genes involved in BCR signaling	5	-0.87543	-1.78972	0.001891	0.018104	0.013792
Reactome	R-HSA-429914	Deadenylation-dependent mRNA decay	55	-0.45261	-1.78677	0.001894	0.018104	0.013792
Reactome	R-HSA-113510	E2F mediated regulation of DNA replication	21	-0.61658	-1.93032	0.001895	0.018104	0.013792
Reactome	R-HSA-5638302	Signaling by Overexpressed Wild-Type EGFR in Cancer	7	0.814701	1.809371	0.001907	0.018104	0.013792
Reactome	R-HSA-5638303	Inhibition of Signaling by Overexpressed EGFR	7	0.814701	1.809371	0.001907	0.018104	0.013792
Reactome	R-HSA-5655862	Translesion synthesis by POLK	17	-0.65714	-1.93936	0.00191	0.018104	0.013792
Reactome	R-HSA-5656121	Translesion synthesis by POLI	17	-0.6598	-1.94722	0.00191	0.018104	0.013792
Reactome	R-HSA-2672351	Stimuli-sensing channels	101	0.373185	1.626009	0.001918	0.018104	0.013792
Reactome	R-HSA-5693606	DNA Double Strand Break Response	64	-0.4292	-1.74138	0.001926	0.018104	0.013792
Reactome	R-HSA-211897	Cytochrome P450 - arranged by substrate type	61	0.429441	1.707804	0.002079	0.019438	0.014808
Reactome	R-HSA-2454202	Fc epsilon receptor (FCER1) signaling	128	-0.36075	-1.65156	0.002091	0.01945	0.014817
Reactome	R-HSA-983712	Ion channel transport	178	0.316735	1.507882	0.002281	0.021102	0.016075
Reactome	R-HSA-191859	snRNP Assembly	51	-0.44778	-1.74135	0.002509	0.022605	0.01722
Reactome	R-HSA-194441	Metabolism of non-coding RNA	51	-0.44778	-1.74135	0.002509	0.022605	0.01722
Reactome	R-HSA-174411	Polymerase switching on the C-strand of the telomere	14	-0.67535	-1.89607	0.00252	0.022605	0.01722
Reactome	R-HSA-69091	Polymerase switching	14	-0.67535	-1.89607	0.00252	0.022605	0.01722
Reactome	R-HSA-69109	Leading Strand Synthesis	14	-0.67535	-1.89607	0.00252	0.022605	0.01722
Reactome	R-HSA-162906	HIV Infection	220	-0.29598	-1.45918	0.002524	0.022605	0.01722
Reactome	R-HSA-9603798	Class I peroxisomal membrane protein import	20	-0.61682	-1.90538	0.002535	0.022605	0.01722
Reactome	R-HSA-549127	Organic cation transport	8	0.77976	1.807753	0.002655	0.02355	0.01794
Reactome	R-HSA-72689	Formation of a pool of free 40S	83	-0.39718	-1.69063	0.002748	0.024254	0.018476

		subunits							
Reactome	R-HSA-5576886	Phase 4 - resting membrane potential	17	0.634221	1.852449	0.002836	0.024901	0.018969	
Reactome	R-HSA-2514853	Condensation of Prometaphase Chromosomes	11	-0.74003	-1.9377	0.00292	0.025511	0.019434	
Reactome	R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	295	-0.27612	-1.40537	0.002953	0.025671	0.019556	
Reactome	R-HSA-1187000	Fertilization	22	0.586674	1.836744	0.003035	0.026257	0.020002	
Reactome	R-HSA-110312	Translesion synthesis by REV1	16	-0.65261	-1.89521	0.00318	0.02737	0.02085	
Reactome	R-HSA-69166	Removal of the Flap Intermediate	14	-0.66819	-1.87598	0.00336	0.028776	0.021921	
Reactome	R-HSA-1300645	Acrosome Reaction and Sperm:Oocyte Membrane Binding	5	0.858768	1.707656	0.003433	0.029258	0.022288	
Reactome	R-HSA-6782210	Gap-filling DNA repair synthesis and ligation in TC-NER	63	-0.41522	-1.6805	0.003603	0.030557	0.023278	
Reactome	R-HSA-6809371	Formation of the cornified envelope	98	0.359729	1.55985	0.003635	0.030676	0.023368	
Reactome	R-HSA-2142753	Arachidonic acid metabolism	58	0.42967	1.696427	0.003749	0.031483	0.023983	
Reactome	R-HSA-2990846	SUMOylation	176	-0.31421	-1.50333	0.003789	0.031577	0.024055	
Reactome	R-HSA-4420332	Defective B3GALT6 causes EDSP2 and SEMDJL1	20	0.588557	1.794093	0.003797	0.031577	0.024055	
Reactome	R-HSA-202424	Downstream TCR signaling	89	-0.38557	-1.66233	0.003986	0.032992	0.025133	
Reactome	R-HSA-6782135	Dual incision in TC-NER	64	-0.4059	-1.64687	0.004065	0.033488	0.025511	
Reactome	R-HSA-6784531	tRNA processing in the nucleus	56	-0.42237	-1.67205	0.004231	0.03469	0.026427	
Reactome	R-HSA-68867	Assembly of the pre-replicative complex	65	-0.40124	-1.63268	0.004273	0.034866	0.02656	
Reactome	R-HSA-68884	Mitotic Telophase/Cytokinesis	13	-0.67524	-1.85964	0.004385	0.03549	0.027036	
Reactome	R-HSA-166658	Complement cascade	53	0.433442	1.676817	0.00439	0.03549	0.027036	
Reactome	R-HSA-72764	Eukaryotic Translation Termination	75	-0.3902	-1.63585	0.004429	0.035642	0.027151	
Reactome	R-HSA-375280	Amine ligand-binding receptors	41	0.453569	1.656619	0.00458	0.036434	0.027755	
Reactome	R-HSA-977606	Regulation of Complement cascade	42	0.452763	1.662574	0.00459	0.036434	0.027755	
Reactome	R-HSA-927802	Nonsense-Mediated Decay (NMD)	94	-0.37258	-1.6216	0.004612	0.036434	0.027755	
Reactome	R-HSA-975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	94	-0.37258	-1.6216	0.004612	0.036434	0.027755	
Reactome	R-HSA-3560783	Defective B4GALT7 causes EDS, progeroid type	20	0.582637	1.776048	0.004746	0.037318	0.028428	
Reactome	R-HSA-379724	tRNA Aminoacylation	39	-0.47665	-1.74235	0.004835	0.037848	0.028833	
Reactome	R-HSA-912631	Regulation of signaling by CBL	22	-0.56637	-1.79638	0.004862	0.037885	0.02886	
Reactome	R-HSA-1650814	Collagen biosynthesis and modifying enzymes	67	0.399567	1.616242	0.004918	0.038151	0.029063	
Reactome	R-HSA-6804757	Regulation of TP53 Degradation	36	-0.48447	-1.74151	0.005033	0.038867	0.029609	
Reactome	R-HSA-434316	Fatty Acids bound to GPR40 (FFAR1) regulate insulin secretion	8	0.748117	1.734393	0.005119	0.039233	0.029888	
Reactome	R-HSA-2142691	Synthesis of Leukotrienes (LT) and Eoxins (EX)	20	0.578146	1.762358	0.005125	0.039233	0.029888	
Reactome	R-HSA-379726	Mitochondrial tRNA aminoacylation	19	-0.60188	-1.83373	0.005272	0.040179	0.030608	

Reactome	R-HSA-69052	Switching of origins to a post-replicative state	86	-0.37975	-1.62425	0.005312	0.040283	0.030687
Reactome	R-HSA-8857538	PTK6 promotes HIF1A stabilization	6	0.806405	1.701097	0.005332	0.040283	0.030687
Reactome	R-HSA-400451	Free fatty acids regulate insulin secretion	11	0.684095	1.754171	0.005377	0.040447	0.030812
Reactome	R-HSA-5358508	Mismatch Repair	14	-0.65604	-1.84186	0.00546	0.04089	0.03115
Reactome	R-HSA-73864	RNA Polymerase I Transcription	87	-0.37462	-1.60464	0.005517	0.041137	0.031338
Reactome	R-HSA-1500931	Cell-Cell communication	124	0.335171	1.512174	0.005588	0.041431	0.031562
Reactome	R-HSA-113507	E2F-enabled inhibition of pre-replication complex formation	9	-0.72896	-1.79776	0.005649	0.041431	0.031562
Reactome	R-HSA-421270	Cell-cell junction organization	61	0.407169	1.61923	0.005669	0.041431	0.031562
Reactome	R-HSA-159418	Recycling of bile acids and salts	16	0.611873	1.756427	0.005676	0.041431	0.031562
Reactome	R-HSA-983170	Antigen Presentation: Folding, assembly and peptide loading of class I MHC	25	-0.54215	-1.77972	0.005678	0.041431	0.031562
Reactome	R-HSA-975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	77	-0.3874	-1.62977	0.0057	0.041431	0.031562
Reactome	R-HSA-5602498	MyD88 deficiency (TLR2/4)	10	0.704292	1.758617	0.005747	0.041601	0.031691
Reactome	R-HSA-4641265	Repression of WNT target genes	12	-0.67744	-1.82741	0.005832	0.04204	0.032025
Reactome	R-HSA-168179	Toll Like Receptor TLR1:TLR2 Cascade	92	0.360472	1.546616	0.006094	0.043565	0.033187
Reactome	R-HSA-181438	Toll Like Receptor 2 (TLR2) Cascade	92	0.360472	1.546616	0.006094	0.043565	0.033187
Reactome	R-HSA-73854	RNA Polymerase I Promoter Clearance	85	-0.37327	-1.59509	0.006361	0.045288	0.0345
Reactome	R-HSA-397014	Muscle contraction	205	0.290791	1.411054	0.006489	0.046005	0.035046
Reactome	R-HSA-1660499	Synthesis of PIPs at the plasma membrane	50	-0.42658	-1.6511	0.006934	0.048964	0.0373
