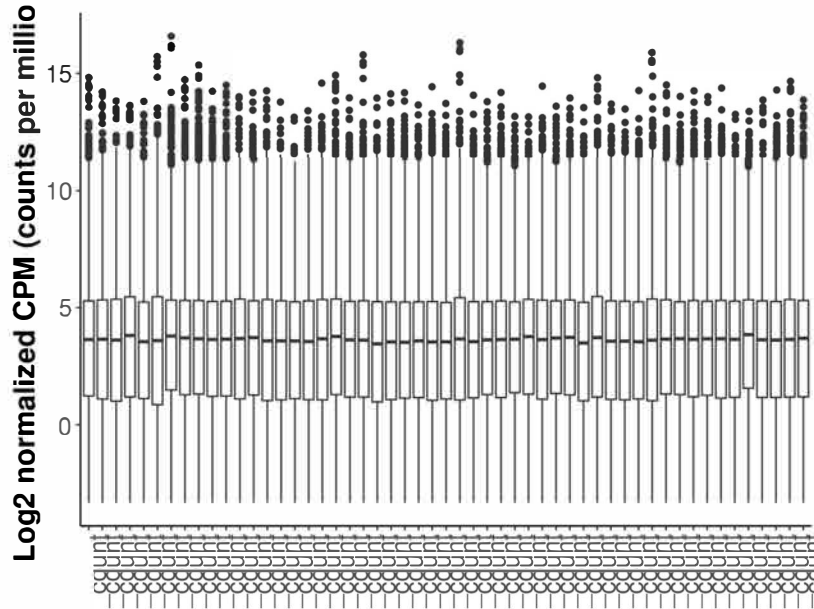
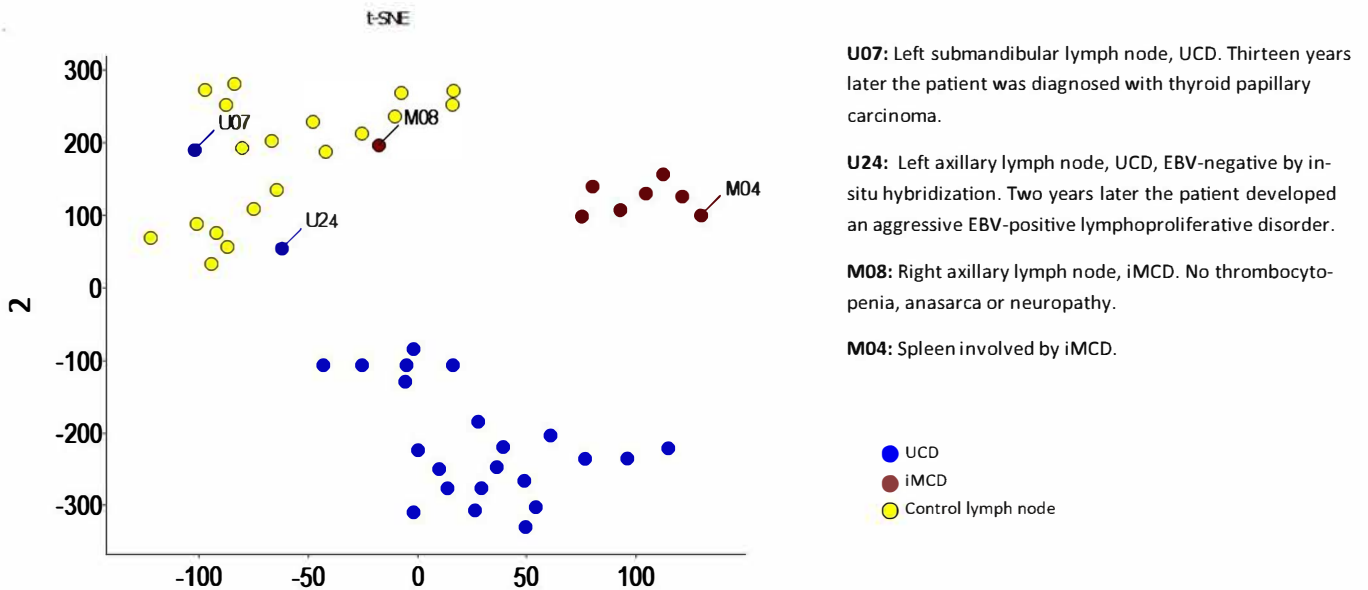


**Figure S1**



**Figure S1A.** Normalized transcript counts for all samples studied.



**Figure S1B.** t-SNE plot of differentially expressed genes (3-group ANOVA), showing clinical information of sample outliers (U07, M08 and U24); in addition to a non-outlier spleen sample included in this study (M04). The described outliers are the same as those identified by hierarchical clustering on Figure 1C. UCD: Unicentric Castleman disease. iMCD: Idiopathic multicentric Castleman disease.

**Table S1****Sample and Patient Characteristics.**

Sample ID	Diagnosis group	Specimen	Site	Age	Sex	Histology	Clinical features	Relevant prior therapy
M01	Multicentric Castleman, patient 1	Lymph node	Cervical	41	M	Mixed	Cervical and anterior mediastinal lymphadenopathy, recurrent after excisions.	Chemotherapy (unknown), steroids and surgical resection 8 years ago. Multiple subsequent resections. No therapy for at least the last 2 years.
M02	Multicentric Castleman, patient 2	Lymph node	Axillary	58	M	plasma cell	Inguinal and peripancreatic lymphadenopathy, splenomegaly.	None
M04	Multicentric Castleman, patient 3	Spleen	Spleen	59	F	plasma cell	Splenomegaly, hilar lymphadenopathy, anemia.	None
M05	Multicentric Castleman, patient 4	Lymph node	Cervical	46	M	Mixed	Generalized lymphadenopathy, splenomegaly, polyradiculoneuropathy, anasarca, no plasma cell neoplasm, no thrombocytopenia.	Plasmapheresis, cytoxan, rituxan.
M06	Multicentric Castleman, patient 5	Lymph node	Axillary	45	M	Mixed	Generalized lymphadenopathy, anasarca, renal failure, no organomegaly, normal platelet counts.	None
M07	Multicentric Castleman, patient 6	Lymph node	Axillary	41	F	plasma cell	Generalized lymphadenopathy.	None
M08	Multicentric Castleman, patient 7	Lymph node	Axillary	47	M	plasma cell	Generalized lymphadenopathy.	None
M10	Multicentric Castleman, patient 8	Lymph node	Axillary	68	M	plasma cell	Mediastinal and axillary lymphadenopathy, severe coronary artery disease, anasarca, thrombocytopenia, mild visceromegaly.	None
U01	Unicentric Castleman, patient 1	Lymph node	Retroperitoneal	72	M	Hyaline-vascular	Retroperitoneal mass	None

U02	Unicentric Castleman, patient 2	Lymph node	Retroperitoneal	55	F	Mixed	Retroperitoneal mass	None
U03	Unicentric Castleman, patient 3	Lymph node	Retroperitoneal	46	F	Mixed	Retroperitoneal mass	None
U04	Unicentric Castleman, patient 4	Lymph node	Mediastinal	18	F	Hyaline-vascular	Mediastinal mass	None
U05	Unicentric Castleman, patient 5	Lymph node	Pelvic	41	F	Hyaline-vascular	Left pelvic lymphadenopathy	None
U06	Unicentric Castleman, patient 6	Lymph node	Mediastinal	74	M	Hyaline-vascular	Mediastinal mass	None
U07	Unicentric Castleman, patient 7	Lymph node	Cervical	86	F	Hyaline-vascular	Left submandibular mass, EBV-negative by in-situ hybridization. Two years later developed aggressive EBV-positive lymphoproliferative disorder.	None
U08	Unicentric Castleman, patient 8	Lymph node	Retroperitoneal	60	F	Hyaline-vascular	Retroperitoneal lymphadenopathy	None
U09	Unicentric Castleman, patient 9	Lymph node	Cervical	27	M	Hyaline-vascular	Left submandibular mass	None
U10	Unicentric Castleman, patient 10	Lymph node	Axillary	49	F	Hyaline-vascular	Right axillary lymphadenopathy	None
U11	Unicentric Castleman, patient 11	Lymph node	Axillary	44	F	Hyaline-vascular	Right axillary lymphadenopathy	None
U12	Unicentric Castleman, patient 12	Lymph node	Retroperitoneal	28	M	Hyaline-vascular	Right iliac lymphadenopathy. History of Hodgkin lymphoma 15 years ago.	Chemotherapy and radiation for Hodgkin lymphoma 15 years ago.
U13	Unicentric Castleman, patient 13	Lymph node	Pelvic	75	F	Hyaline-vascular	Right pelvic mass	None
U14	Unicentric Castleman, patient 14	Lymph node	Mediastinal	65	M	Hyaline-vascular	Mediastinal mass.	None
U15	Unicentric Castleman, patient 15	Lymph node	Retroperitoneal	30	F	Hyaline-vascular	Retroperitoneal mass, mouth and anal ulcers.	Prednisone for mucosal ulcers until 6 months ago. Prior resection of same site 8 months ago.

U16	Unicentric Castleman, patient 16	Lymph node	Mediastinal	34	M	Hyaline-vascular	Mediastinal mass	Prior incisional biopsy 3 months ago.
U17	Unicentric Castleman, patient 17	Lymph node	Retroperitoneal	38	F	Hyaline-vascular	Retroperitoneal mass involving left adrenal gland	None
U18	Unicentric Castleman, patient 18	Lymph node	Parotid	43	M	Hyaline-vascular	Parotid/parapharyngeal mass	None
U19	Unicentric Castleman, patient 19, sample 2	Lymph node	Abdominal	38	F	Hyaline-vascular	Peripancreatic lymphadenopathy. 4 years ago left axillary lymphadenopathy with same process, excised and resolved.	None
U20	Unicentric Castleman, patient 20, sample 1	Lymph node	Retroperitoneal	27	F	Hyaline-vascular	Peripancreatic/retroduodenal mass.	None
U21	Unicentric Castleman, patient 20, sample 2	Lymph node	Abdominal	27	F	Hyaline-vascular	Peripancreatic/retroduodenal mass.	Recent laparoscopic diagnostic biopsy.
U22	Unicentric Castleman, patient 21	Lymph node	Cervical	53	M	Hyaline-vascular	Right supraclavicular lymphadenopathy	None
U23	Unicentric Castleman, patient 22	Lymph node	Abdominal	50	M	Mixed	Mesenteric mass.	None
U24	Unicentric Castleman, patient 19, sample 1	Lymph node	Axillary	33	F	Mixed	Left axillary lymphadenopathy.	None
N01	Control, patient 1	Lymph node	Cervical	44	M	Unremarkable lymph node	Enlarged cervical and inguinal lymph nodes. History of Hodgkin lymphoma, on maintenance therapy	N/A
N02	Control, patient 2	Lymph node	Axillary	49	F	Unremarkable lymph node	Enlarged axillary lymph nodes, uncertain etiology.	N/A
N03	Control, patient 3	Lymph node	Cervical	41	F	Unremarkable lymph node	Enlarged cervical lymph nodes, uncertain etiology.	N/A
N04	Control, patient 4	Lymph node	Cervical	3	M	Unremarkable lymph node	Enlarged cervical lymph nodes, uncertain etiology.	N/A
N05	Control, patient 5	Lymph node	Cervical	63	M	Unremarkable lymph node	Enlarged cervical lymph nodes. History of diffuse large B-cell lymphoma.	N/A

N06	Control, patient 6	Lymph node	Axillary	42	M	Unremarkable lymph node	Generalized lymphadenopathy. History of diffuse large B-cell lymphoma.	N/A
N07	Control, patient 7	Lymph node	Abdominal	80	F	Unremarkable lymph node	Enlarged mesenteric and retroperitoneal lymph nodes, uncertain etiology.	N/A
N08	Control, patient 8	Lymph node	Cervical	47	F	Unremarkable lymph node	Enlarged cervical lymph nodes, uncertain etiology.	N/A
N09	Control, patient 9	Lymph node	Axillary	56	F	Unremarkable lymph node	Generalized lymphadenopathy. Rheumatoid arthritis, Crohn's disease, scleroderma, psoriasis.	N/A
N10	Control, patient 10	Lymph node	Cervical	80	F	Unremarkable lymph node	Enlarged cervical lymph nodes. Lung mass, eventually diagnosed as adenocarcinoma.	N/A
N11	Control, patient 11	Lymph node	Axillary	38	M	Unremarkable lymph node	Enlarged axillary lymph nodes, uncertain etiology.	N/A
N12	Control, patient 12	Lymph node	Axillary	59	F	Unremarkable lymph node	Enlarged axillary lymph nodes, uncertain etiology.	N/A
N13	Control, patient 13	Lymph node	Inguinal	79	F	Unremarkable lymph node	Generalized lymphadenopathy, uncertain etiology.	N/A
N14	Control, patient 14	Lymph node	Cervical	15	F	Unremarkable lymph node	Enlarged cervical lymph nodes. Crohn's disease.	N/A
N15	Control, patient 15	Lymph node	Retroperitoneal	65	F	Unremarkable lymph node	Enlarged paraspinal lymph node. Incidental finding during spinal orthopedic surgery.	N/A
N16	Control, patient 16	Lymph node	Cervical	17	M	Unremarkable lymph node	Enlarged cervical lymph nodes, uncertain etiology.	N/A
N17	Control, patient 17	Lymph node	Retroperitoneal	59	F	Unremarkable lymph node	Sampled lymph node during surgery for renal cell carcinoma.	N/A
N18	Control, patient 18	Lymph node	Pelvic	46	M	Unremarkable lymph node	Generalized lymphadenopathy, uncertain etiology.	N/A
N19	Control, patient 19	Lymph node	Cervical	45	F	Unremarkable lymph node	Enlarged cervical lymph nodes. History of thyroid carcinoma.	N/A

# Data S1

## Gene Set Enrichment Analysis (GSEA)

### Gene sets investigated, mSigDB, accessed 08/18/2021

Hallmark gene sets  
Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways  
Pathway Interaction Database (PID)  
Gene Ontology-Biological Process (GO-BP)  
Gene Ontology-Molecular Function (GO-MF)

### FDR cutoff

$q < 0.05$

### P significant

$p < 0.05$

### Tab Contents

UCD: Gene sets significantly differential between UCD and control samples.  
iMCD: Gene sets significantly differential between iUCD and control samples.

### Permutation method

Variables

Gen sets are listed ordered by normalized enrichment score (NES)

Gene set list	Trend	Name	Size	Matches	ES	abs(ES)	NES	p	q
KEGG	Up	KEGG_RIBOSOME	88	85	0.797735	0.797735	3.36371	0	0
GOBP	Up	GOBP_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	107	103	0.764446	0.764446	3.33775	0	0
GOBP	Up	GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	121	116	0.722762	0.722762	3.18711	0	0
GOBP	Up	GOBP_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	149	142	0.681931	0.681931	3.10411	0	0
GOBP	Up	GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	120	119	0.666398	0.666398	2.95301	0	0
GOMF	Up	GOMF_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	167	158	0.634766	0.634766	2.92722	0	0
GOBP	Up	GOBP_TRANSLATIONAL_INITIATION	193	185	0.606766	0.606766	2.88821	0	0
GOBP	Up	GOBP_PROTEIN_TARGETING_TO_MEMBRANE	208	187	0.5793	0.5793	2.71691	0	0
HALLMARK	Up	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	200	191	0.538055	0.538055	2.54424	0	0
GOBP	Up	GOBP_VIRAL_GENE_EXPRESSION	198	191	0.520439	0.520439	2.46511	0	0
GOBP	Up	GOBP_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	72	67	0.586666	0.586666	2.38867	0	9.34E-05
GOBP	Up	GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	208	196	0.503055	0.503055	2.37069	0	8.57E-05
GOBP	Up	GOBP_CYTOPLASMIC_TRANSLATION	102	98	0.546624	0.546624	2.34024	0	7.91E-05
GOBP	Up	GOBP_RIBOSOME_ASSEMBLY	64	56	0.58835	0.58835	2.32749	0	0.000147
GOBP	Up	GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	351	314	0.460859	0.460859	2.30411	0	0.000206
HALLMARK	Up	HALLMARK_ANGIOGENESIS	36	34	0.654733	0.654733	2.29143	0	0.000257
GOBP	Up	GOBP_PROTEIN_TARGETING	438	400	0.444686	0.444686	2.26986	0	0.000423
GOMF	Up	GOMF_CELL_ADHESION_MEDIATOR_ACTIVITY	58	50	0.593717	0.593717	2.25699	0	0.000571
GOBP	Up	GOBP_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	62	50	0.585539	0.585539	2.24472	0	0.000649
GOBP	Up	GOBP_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	167	130	0.490576	0.490576	2.22358	0	0.000874
HALLMARK	Up	HALLMARK_COAGULATION	138	106	0.495673	0.495673	2.13064	0	0.004454
GOBP	Up	GOBP_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	28	25	0.648874	0.648874	2.1266	0	0.004485
GOBP	Up	GOBP_ADHERENS_JUNCTION_ORGANIZATION	66	50	0.560376	0.560376	2.12295	0	0.004693
GOMF	Up	GOMF_CELL_CELL_ADHESION_MEDIATOR_ACTIVITY	49	41	0.577144	0.577144	2.11936	0	0.005182
KEGG	Up	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	69	50	0.553214	0.553214	2.11237	0	0.005468
GOMF	Up	GOMF_RRNA_BINDING	64	59	0.536435	0.536435	2.10812	0	0.005653
GOBP	Up	GOBP_COLLAGEN_FIBRIL_ORGANIZATION	54	49	0.546507	0.546507	2.09074	0	0.00731
GOBP	Up	GOBP_RETROGRADE_AXONAL_TRANSPORT	21	16	0.728187	0.728187	2.09049	0	0.007085
GOMF	Up	GOMF_ALPHA_CATENIN_BINDING	10	9	0.8346	0.8346	2.0884	0	0.007124
GOMF	Up	GOMF_EXTRACELLULAR_MATRIX_BINDING	55	49	0.544303	0.544303	2.07722	0	0.00836
GOMF	Up	GOMF_STRUCTURAL_MOLECULE_ACTIVITY	686	518	0.396669	0.396669	2.07237	0	0.008853
GOBP	Up	GOBP_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	33	23	0.647289	0.647289	2.06768	0.001667	0.009251
HALLMARK	Up	HALLMARK_UV_RESPONSE_DN	144	137	0.45492	0.45492	2.05954	0	0.009812
PID	Up	PID_S1P_S1P3_PATHWAY	29	29	0.61238	0.61238	2.05938	0.001639	0.009553
GOMF	Up	GOMF_COLLAGEN_BINDING	68	58	0.531226	0.531226	2.05916	0	0.00931
GOBP	Up	GOBP_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	96	85	0.490579	0.490579	2.05778	0	0.009194
GOMF	Up	GOMF_GAMMA_CATENIN_BINDING	12	10	0.803042	0.803042	2.04794	0	0.010918
PID	Up	PID_AVB3_INTEGRIN_PATHWAY	74	70	0.503997	0.503997	2.04189	0	0.011659
GOMF	Up	GOMF_LAMININ_BINDING	29	26	0.613467	0.613467	2.03785	0	0.011992
GOBP	Up	GOBP_MEMBRANE_BIOGENESIS	41	37	0.56552	0.56552	2.03146	0	0.013286
GOBP	Up	GOBP_EXTERNAL_ENCAPSULATING_STRUCTURE_ORGANIZATION	396	324	0.407526	0.407526	2.0295	0	0.013338
PID	Up	PID_INTEGRIN1_PATHWAY	66	61	0.515552	0.515552	2.02569	0	0.01395
GOBP	Up	GOBP_PROTEIN_LOCALIZATION_TO_MEMBRANE	658	577	0.384535	0.384535	2.01948	0	0.01451
GOBP	Up	GOBP_EOSINOPHIL_MIGRATION	22	17	0.676984	0.676984	1.9882	0	0.022217
GOBP	Up	GOBP_RIBOSOMAL_SMALL_SUBUNIT_ASSEMBLY	21	18	0.662823	0.662823	1.98769	0	0.021883
GOBP	Up	GOBP_REGULATION_OF_WOUND_HEALING	131	97	0.460969	0.460969	1.98391	0	0.022502
GOBP	Up	GOBP_HEPARAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	25	22	0.622345	0.622345	1.98058	0	0.023095
GOBP	Up	GOBP_REGULATION_OF_AMYLOID_FIBRIL_FORMATION	15	13	0.725627	0.725627	1.97849	0	0.023513

PID	Up	PID_INTEGRIN3_PATHWAY	43	38	0.555144	0.555144	1.97573	0	0.023873
GOBP	Up	GOBP_NEGATIVE_REGULATION_OF_PROTEIN_MATURATION	27	22	0.605995	0.605995	1.97111	0	0.024855
GOBP	Up	GOBP_POSITIVE_REGULATION_OF_CHEMOTAXIS	139	118	0.445191	0.445191	1.96568	0	0.026443
GOBP	Up	GOBP_SECONDARY_METABOLIC_PROCESS	56	35	0.552173	0.552173	1.96124	0	0.027635
GOBP	Up	GOBP_REGULATION_OF_TUBE_SIZE	128	93	0.461123	0.461123	1.95363	0	0.030411
GOBP	Up	GOBP_NEURON_RECOGNITION	46	39	0.532298	0.532298	1.95295	0	0.030019
GOBP	Up	GOBP_CHONDROITIN_SULFATE_BIOSYNTHETIC_PROCESS	25	20	0.637195	0.637195	1.95283	0.001639	0.029529
GOBP	Up	GOBP_REGULATION_OF_COMPLEMENT_ACTIVATION	114	102	0.445552	0.445552	1.94873	0	0.030452
PID	Up	PID_ALK1_PATHWAY	26	24	0.606205	0.606205	1.94837	0.001637	0.03008
GOBP	Up	GOBP_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	346	265	0.395352	0.395352	1.94644	0	0.030394
GOBP	Up	GOBP_ARTERY_DEVELOPMENT	95	77	0.470405	0.470405	1.94581	0	0.030106
GOBP	Up	GOBP_DORSAL_AORTA_DEVELOPMENT	10	10	0.76149	0.76149	1.94387	0	0.030375
GOBP	Up	GOBP_DENDRITIC_CELL_ANTIGEN_PROCESSING_AND_PRESENTATION	15	14	0.701518	0.701518	1.94	0	0.030669
GOBP	Up	GOBP_AMINOGLYCAN_BIOSYNTHETIC_PROCESS	114	94	0.457541	0.457541	1.94155	0	0.030406
GOBP	Up	GOBP_AMYLOID_FIBRIL_FORMATION	25	22	0.615681	0.615681	1.94103	0	0.030234
GOBP	Up	GOBP_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	273	205	0.402178	0.402178	1.93978	0	0.030484
GOBP	Up	GOBP_MESODERMAL_CELL_DIFFERENTIATION	32	23	0.599162	0.599162	1.93717	0	0.031043
GOMF	Up	GOMF_GAP_JUNCTION_CHANNEL_ACTIVITY	21	8	0.815371	0.815371	1.93511	0	0.031305
GOBP	Up	GOBP_MESENCHYME_DEVELOPMENT	287	225	0.397283	0.397283	1.93338	0	0.031497
GOBP	Up	GOBP_REGULATION_OF_POSITIVE_CHEMOTAXIS	26	21	0.610009	0.610009	1.93071	0	0.032258
GOBP	Up	GOBP_BRANCHING_INVOLVED_IN_BLOOD_VESSEL_MORPHOGENESIS	34	26	0.59295	0.59295	1.9307	0	0.031806
GOBP	Up	GOBP_VENTRICULAR TRABECULA_MYOCARDIUM_MORPHOGENESIS	13	12	0.723957	0.723957	1.92943	0.001745	0.031953
GOBP	Up	GOBP_REGULATION_OF_ACTIN_FILAMENT_BASED_MOVEMENT	37	32	0.552305	0.552305	1.92722	0	0.032343
HALLMARK	Up	HALLMARK_PROTEIN_SECRETION	96	93	0.455127	0.455127	1.92173	0	0.034478
GOBP	Up	GOBP_DORSAL_VENTRAL_PATTERN_FORMATION	77	49	0.50713	0.50713	1.92076	0	0.03447
GOBP	Up	GOBP_RENAL_FILTRATION	25	22	0.600125	0.600125	1.91906	0	0.034907
GOBP	Up	GOBP_POSITIVE_REGULATION_OF_WOUND_HEALING	59	43	0.526645	0.526645	1.91721	0.001572	0.035223
GOBP	Up	GOBP_MATURATION_OF_LSU_RRNA	28	27	0.580923	0.580923	1.9145	0	0.036301
GOBP	Up	GOBP_MESODERM_MORPHOGENESIS	70	52	0.491131	0.491131	1.90832	0	0.039194
GOBP	Up	GOBP_PROTEOGLYCAN_METABOLIC_PROCESS	87	69	0.471666	0.471666	1.90725	0	0.039219
GOMF	Up	GOMF_CELL_ADHESION_MOLECULE_BINDING	540	463	0.367648	0.367648	1.90468	0	0.040062
GOMF	Up	GOMF_TYPE_I_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	9	9	0.767001	0.767001	1.90124	0.005405	0.041515
GOBP	Up	GOBP_MUSCLE_CELL_MIGRATION	101	76	0.462512	0.462512	1.89922	0	0.042233
GOBP	Up	GOBP_REGULATION_OF_COLLAGEN_METABOLIC_PROCESS	47	33	0.545592	0.545592	1.89909	0.001626	0.041793
GOBP	Up	GOBP_NEURON_CELL_CELL_ADHESION	17	16	0.650397	0.650397	1.89792	0.003521	0.041971
KEGG	Up	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	62	0.475723	0.475723	1.89593	0	0.042548
GOBP	Up	GOBP_BONE_MORPHOGENESIS	90	72	0.468751	0.468751	1.89458	0	0.042894
GOBP	Up	GOBP_IRON_ION_HOMEOSTASIS	86	74	0.46365	0.46365	1.8932	0	0.04322
GOBP	Up	GOBP_VASOCONSTRICTION	79	56	0.487497	0.487497	1.89237	0	0.043196
GOMF	Up	GOMF_BETA_CATENIN_BINDING	85	77	0.458012	0.458012	1.88911	0	0.044691
GOBP	Up	GOBP_HEART TRABECULA_MORPHOGENESIS	30	26	0.579294	0.579294	1.8854	0	0.046545
GOMF	Up	GOMF_ACTININ_BINDING	36	29	0.555779	0.555779	1.88142	0.003289	0.048586
GOBP	Up	GOBP_CHONDROITIN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	30	24	0.578829	0.578829	1.87946	0	0.049227
GOBP	Up	GOBP_DORSAL_AORTA_MORPHOGENESIS	8	8	0.78234	0.78234	1.87924	0.005263	0.048814
GOMF	Up	GOMF_MRNA_5_UTR_BINDING	26	25	0.571927	0.571927	1.87655	0.001706	0.049959
GOMF	Up	GOMF_CORECEPTOR_ACTIVITY_INVOLVED_IN_WNT_SIGNALING_PATHWAY	9	9	0.748924	0.748924	1.87623	0.001718	0.049613
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_DNA_RECOMBINATION	45	34	-0.48185	0.481847	-1.81369	0	0.04977
GOBP	Down	GOBP_MIRNA_METABOLIC_PROCESS	29	22	-0.54646	0.546458	-1.8168	0.00241	0.048496
GOBP	Down	GOBP_MEIOTIC_CELL_CYCLE_CHECKPOINT	8	7	-0.76629	0.766287	-1.81731	0.002217	0.048478



GOBP	Down	GOBP_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	35	32	-0.48078	0.480776	-1.8182	0	0.048214
GOMF	Down	GOMF_5_3_DNA_HELICASE_ACTIVITY	8	7	-0.77113	0.771132	-1.82053	0.008547	0.047271
GOBP	Down	GOBP_REGULATION_OF_HISTONE_METHYLATION	61	53	-0.43794	0.437937	-1.82619	0	0.044653
GOBP	Down	GOBP_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_SOMATIC_MUTATION	16	15	-0.60951	0.609513	-1.83126	0.004435	0.04243
GOMF	Down	GOMF_UNMETHYLATED_CPG_BINDING	8	8	-0.74491	0.744914	-1.83151	0.008658	0.042478
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE	395	326	-0.3284	0.328404	-1.8321	0	0.042441
GOBP	Down	GOBP_G2_DNA_DAMAGE_CHECKPOINT	36	28	-0.50988	0.509879	-1.83216	0.002532	0.042596
GOBP	Down	GOBP_MRNA_3_END_PROCESSING	99	94	-0.39527	0.395267	-1.83347	0	0.042148
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCHORE	6	6	-0.8084	0.808402	-1.83401	0.002217	0.042165
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	44	35	-0.47313	0.473129	-1.83796	0.004988	0.040624
KEGG	Down	KEGG_PRIMARY_IMMUNODEFICIENCY	35	35	-0.47969	0.479685	-1.83852	0.002538	0.040612
GOBP	Down	GOBP_HISTONE_H3_K4_METHYLATION	53	46	-0.46018	0.460176	-1.83859	0.002577	0.040759
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	24	21	-0.55761	0.557607	-1.83956	0.004926	0.040559
GOBP	Down	GOBP_CD4_POSITIVE_OR_CD8_POSITIVE_ALPHA_BETA_T_CELL_LINEAGE_COMMITMENT	22	20	-0.5665	0.566497	-1.84067	0	0.040221
GOMF	Down	GOMF_HISTONE_BINDING	241	214	-0.3497	0.349697	-1.84728	0	0.037682
GOMF	Down	GOMF_3_5_DNA_HELICASE_ACTIVITY	17	16	-0.60728	0.607281	-1.84801	0	0.037577
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE_CHECKPOINT	10	9	-0.72045	0.720446	-1.8492	0.004566	0.037261
GOBP	Down	GOBP_3_UTR_MEDIATED_MRNA_DESTABILIZATION	17	15	-0.61329	0.613289	-1.85101	0.004751	0.036739
GOBP	Down	GOBP_REGULATION_OF_HISTONE_H3_K27_METHYLATION	9	7	-0.79895	0.798947	-1.8525	0	0.036402
GOMF	Down	GOMF_HISTONE_KINASE_ACTIVITY	16	14	-0.6329	0.632898	-1.85492	0.002331	0.035604
GOBP	Down	GOBP_CENTRIOLE_ASSEMBLY	45	40	-0.47566	0.475663	-1.85657	0	0.035227
GOBP	Down	GOBP_BASE_EXCISION_REPAIR_GAP_FILLING	6	6	-0.84074	0.84074	-1.85853	0.004237	0.034745
GOBP	Down	GOBP_REGULATION_OF_SISTER_CHROMATID_COHESION	22	18	-0.59373	0.593728	-1.86216	0.004566	0.033564
GOBP	Down	GOBP_MITOTIC_G1_S_TRANSITION_CHECKPOINT	63	59	-0.43219	0.432185	-1.86221	0	0.033675
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	359	307	-0.32957	0.329568	-1.8645	0	0.032974
GOMF	Down	GOMF_PRIMARY_MIRNA_BINDING	8	8	-0.7433	0.743302	-1.86454	0.004255	0.033116
GOMF	Down	GOMF_KINETOCHORE_BINDING	6	6	-0.83838	0.838376	-1.87048	0.004158	0.031186
PID	Down	PID_IL27_PATHWAY	26	24	-0.55029	0.550288	-1.87127	0	0.031071
GOBP	Down	GOBP_TELOMERIC_LOOP_DISASSEMBLY	11	10	-0.71289	0.712893	-1.87247	0	0.030789
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	31	28	-0.52997	0.529972	-1.87547	0.002681	0.029961
GOMF	Down	GOMF_ATPASE_ACTIVITY	479	417	-0.33046	0.330458	-1.8759	0	0.029939
GOBP	Down	GOBP_CELLULAR_RESPONSE_TO_DNA_DAMAGE_STIMULUS	869	759	-0.31211	0.312113	-1.87615	0	0.030003
GOBP	Down	GOBP_DNA_METHYLATION_DEPENDENT_HETEROCHROMATIN_ASSEMBLY	20	17	-0.61152	0.611518	-1.87648	0	0.030053
GOBP	Down	GOBP_REGULATION_OF_CHROMATIN_ASSEMBLY	20	17	-0.60565	0.60565	-1.87956	0.002242	0.029156
GOMF	Down	GOMF_DNA_CLAMP_LOADER_ACTIVITY	9	9	-0.72776	0.727759	-1.87988	0.002315	0.029192
GOBP	Down	GOBP_REGULATION_OF_MEIOTIC_CELL_CYCLE	47	31	-0.50982	0.509823	-1.88315	0	0.028242
GOBP	Down	GOBP_CELLULAR_ANION_HOMEOSTASIS	14	9	-0.71921	0.719208	-1.8851	0.002252	0.02785
GOBP	Down	GOBP_T_HELPER_17_CELL_LINEAGE_COMMITMENT	14	13	-0.65951	0.659513	-1.88912	0.002257	0.026844
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	19	17	-0.60222	0.602217	-1.88966	0	0.026824
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLOGOUS_RECOMBINATION	19	13	-0.65265	0.65265	-1.88978	0	0.026935
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	268	228	-0.34423	0.344231	-1.89079	0	0.026815
GOBP	Down	GOBP_HISTONE_METHYLATION	130	110	-0.39249	0.392488	-1.89088	0	0.026926
GOBP	Down	GOBP_REGULATION_OF_CD40_SIGNALING_PATHWAY	6	6	-0.85267	0.852667	-1.90081	0	0.023923
GOBP	Down	GOBP_BASE_EXCISION_REPAIR	39	38	-0.47619	0.476186	-1.9011	0	0.023954
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_CYTOKINESIS	40	27	-0.52805	0.528052	-1.90597	0.002463	0.022673
GOBP	Down	GOBP_REGULATION_OF_MITOTIC_CELL_CYCLE	605	536	-0.321	0.320997	-1.90738	0	0.022392
KEGG	Down	KEGG_BASE_EXCISION_REPAIR	35	34	-0.49851	0.49851	-1.91014	0	0.021879
GOBP	Down	GOBP_MEIOTIC_SPINDLE_ORGANIZATION	12	9	-0.74515	0.745154	-1.91319	0.006329	0.021303
GOBP	Down	GOBP_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	32	8	-0.77173	0.771727	-1.91385	0.004577	0.021299

GOBP	Down	GOBP_MITOTIC_G2_M_TRANSITION_CHECKPOINT	37	31	-0.51521	0.51521	-1.91441	0	0.021258
GOBP	Down	GOBP_NON_RECOMBINATIONAL_REPAIR	106	75	-0.42457	0.424569	-1.91532	0	0.021099
GOMF	Down	GOMF_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_BINDING	12	7	-0.81622	0.816218	-1.91624	0	0.020928
GOBP	Down	GOBP_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	205	126	-0.38546	0.385456	-1.91779	0	0.020627
GOBP	Down	GOBP_CHROMATIN_ORGANIZATION	807	629	-0.32918	0.329181	-1.91857	0	0.020597
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	125	55	-0.45055	0.450554	-1.91934	0	0.020475
GOBP	Down	GOBP_INOSITOL_METABOLIC_PROCESS	11	9	-0.75668	0.756684	-1.91991	0	0.020477
GOMF	Down	GOMF_HISTONE_LYSINE_N_METHYLTRANSFERASE_ACTIVITY	43	35	-0.51177	0.511767	-1.91998	0	0.020573
GOBP	Down	GOBP_REGULATION_OF_DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	9	9	-0.74489	0.744893	-1.92028	0	0.020609
GOBP	Down	GOBP_NUCLEAR_EXPORT	201	189	-0.36462	0.364624	-1.92058	0	0.020662
GOMF	Down	GOMF_MINOR_GROOVE_OF_ADENINE_THYMINE_RICH_DNA_BINDING	9	6	-0.85562	0.85562	-1.92097	0	0.02071
GOMF	Down	GOMF_LYSINE_ACETYLATED_HISTONE_BINDING	21	20	-0.57947	0.579465	-1.92727	0	0.019328
GOBP	Down	GOBP_ATP_DEPENDENT_CHROMATIN_REMODELING	89	65	-0.45022	0.450216	-1.92736	0	0.019431
GOBP	Down	GOBP_MISMATCH_REPAIR	38	34	-0.51175	0.511746	-1.92894	0	0.01912
GOBP	Down	GOBP_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS	75	66	-0.43761	0.437614	-1.93101	0	0.018673
GOBP	Down	GOBP_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	81	76	-0.42471	0.424714	-1.93681	0	0.017545
GOBP	Down	GOBP_ALPHA_BETA_T_CELL_DIFFERENTIATION	107	99	-0.40331	0.403309	-1.93837	0	0.01728
GOBP	Down	GOBP_CELL_CYCLE_G2_M_PHASE_TRANSITION	276	257	-0.35359	0.35359	-1.94004	0	0.017088
GOBP	Down	GOBP_MITOTIC_DNA_REPLICATION_CHECKPOINT	10	9	-0.74452	0.74452	-1.9405	0	0.017105
GOBP	Down	GOBP_PEPTIDYL_LYSINE_METHYLATION	123	95	-0.41481	0.414808	-1.94105	0	0.017098
GOBP	Down	GOBP_REGULATION_OF_CYTOKINESIS	90	73	-0.44109	0.441087	-1.94364	0	0.016699
GOBP	Down	GOBP_T_HELPER_CELL_LINEAGE_COMMITMENT	17	16	-0.63926	0.639261	-1.94564	0	0.016427
GOMF	Down	GOMF_RNA_BINDING_INVOLVED_IN_POSTTRANSCRIPTIONAL_GENE_SILENCING	245	18	-0.61102	0.61102	-1.94623	0.004728	0.016404
GOMF	Down	GOMF_CHROMATIN_BINDING	558	460	-0.33716	0.337155	-1.94678	0	0.016417
GOBP	Down	GOBP_REGULATION_OF_DNA_METABOLIC_PROCESS	353	297	-0.35014	0.350139	-1.94723	0	0.016436
GOBP	Down	GOBP_REGULATION_OF_CELL_CYCLE_PROCESS	789	672	-0.32697	0.326968	-1.95079	0	0.015664
GOBP	Down	GOBP_MEIOTIC_CHROMOSOME_CONDENSATION	6	6	-0.89067	0.890674	-1.95146	0	0.015598
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE_PROCESS	303	248	-0.36326	0.363261	-1.95489	0	0.015059
GOBP	Down	GOBP_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	478	415	-0.33694	0.336943	-1.95568	0	0.014964
GOMF	Down	GOMF_LYSINE_N_METHYLTRANSFERASE_ACTIVITY	61	42	-0.49649	0.496489	-1.9627	0	0.013778
GOBP	Down	GOBP_RESPONSE_TO_PROTOZOAN	25	20	-0.60091	0.600907	-1.96922	0	0.012874
KEGG	Down	KEGG_MISMATCH_REPAIR	23	22	-0.58561	0.585608	-1.97213	0	0.012423
GOBP	Down	GOBP_OOCYTE_MATURATION	24	18	-0.62469	0.624689	-1.97601	0.00232	0.011942
GOBP	Down	GOBP_POSITIVE_T_CELL_SELECTION	36	33	-0.52625	0.526254	-1.9772	0	0.011815
GOBP	Down	GOBP_CHROMATIN_ORGANIZATION_INVOLVED_IN_REGULATION_OF_TRANSCRIPTION	154	81	-0.43235	0.432352	-1.97929	0	0.011616
GOBP	Down	GOBP_CELL_CYCLE_G1_S_PHASE_TRANSITION	298	253	-0.36454	0.364539	-1.98348	0	0.011033
GOBP	Down	GOBP_SPINDLE_ELONGATION	9	8	-0.77554	0.775541	-1.98664	0	0.010654
GOBP	Down	GOBP_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	67	57	-0.46603	0.466033	-1.98978	0	0.010395
GOBP	Down	GOBP_CELL_CYCLE	1872	1584	-0.3162	0.316195	-1.99415	0	0.009939
PID	Down	PID_NFAT_TFPATHWAY	45	40	-0.50445	0.504452	-2.00124	0	0.009093
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_DNA_REPLICATION	37	34	-0.53271	0.532711	-2.01001	0	0.008098
GOMF	Down	GOMF_FOLIC_ACID_BINDING	12	9	-0.79907	0.799066	-2.01154	0	0.008019
GOBP	Down	GOBP_REGULATION_OF_DNA_REPAIR	130	106	-0.41386	0.413856	-2.01168	0	0.008056
GOBP	Down	GOBP_SPINDLE_ASSEMBLY	114	103	-0.4219	0.421903	-2.01239	0	0.008052
GOBP	Down	GOBP_SIGNAL_TRANSDUCTION_INVOLVED_IN_CELL_CYCLE_CHECKPOINT	76	70	-0.45533	0.455326	-2.01331	0	0.008027
GOBP	Down	GOBP_RNA_EXPORT_FROM_NUCLEUS	142	132	-0.4064	0.406402	-2.01487	0	0.007868
GOBP	Down	GOBP_MITOTIC_DNA_INTEGRITY_CHECKPOINT	106	96	-0.42881	0.428807	-2.01618	0	0.007806
GOBP	Down	GOBP_ATTACHMENT_OF_MITOTIC_SPINDLE_MICROTUBULES_TO_KINETOCHORE	15	15	-0.67252	0.672515	-2.02036	0	0.007493
GOBP	Down	GOBP_MRNA_TRANSPORT	151	142	-0.40634	0.406341	-2.02695	0	0.006844

GOBP	Down	GOBP_DNA_GEOMETRIC_CHANGE	114	107	-0.42623	0.426225	-2.03246	0	0.006403
GOBP	Down	GOBP_MAINTENANCE_OF_DNA_METHYLATION	7	7	-0.87414	0.874144	-2.0332	0	0.0064
GOBP	Down	GOBP_CHROMATIN_REMODELING	209	160	-0.40224	0.402236	-2.03446	0	0.006332
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_DNA_RECOMBINATION	44	27	-0.58129	0.581286	-2.03484	0	0.006366
GOMF	Down	GOMF_MRNA_3_UTR_AU_RICH_REGION_BINDING	24	23	-0.60897	0.608971	-2.0372	0	0.006191
GOBP	Down	GOBP_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	86	68	-0.4663	0.466295	-2.05214	0	0.004951
GOBP	Down	GOBP_CELL_CYCLE_PROCESS	1415	1190	-0.32956	0.329557	-2.05332	0	0.004922
GOBP	Down	GOBP_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	281	187	-0.39392	0.393922	-2.0553	0	0.004809
GOBP	Down	GOBP_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	219	203	-0.39014	0.390141	-2.05819	0	0.00446
GOMF	Down	GOMF_HELICASE_ACTIVITY	157	147	-0.40819	0.408192	-2.05847	0	0.004614
GOBP	Down	GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS	143	130	-0.41501	0.415011	-2.06962	0	0.003993
GOBP	Down	GOBP_CELL_CYCLE_PHASE_TRANSITION	641	568	-0.3502	0.3502	-2.07225	0	0.003908
GOBP	Down	GOBP_FEMALE_MEIOTIC_NUCLEAR_DIVISION	27	19	-0.65581	0.655814	-2.07465	0	0.003797
GOBP	Down	GOBP_RESOLUTION_OF_MEIOTIC_RECOMBINATION_INTERMEDIATES	18	11	-0.77227	0.772271	-2.07892	0	0.003547
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	26	24	-0.61005	0.610054	-2.08022	0	0.003536
PID	Down	PID_HDAC_CLASSII_PATHWAY	34	32	-0.56205	0.56205	-2.08147	0	0.003485
GOBP	Down	GOBP_HOMOLOGOUS_CHROMOSOME_PAIRING_AT_MEIOSIS	49	23	-0.61558	0.615577	-2.08251	0	0.003457
GOBP	Down	GOBP_MEIOTIC_CELL_CYCLE_PHASE_TRANSITION	10	6	-0.96287	0.962871	-2.086	0	0.003329
GOBP	Down	GOBP_PRE_REPLICATIVE_COMPLEX_ASSEMBLY_INVOLVED_IN_CELL_CYCLE_DNA_REPLICATION	8	7	-0.88612	0.886123	-2.08982	0	0.003199
GOBP	Down	GOBP_REGULATION_OF_DNA_METHYLATION_DEPENDENT_HETEROCHROMATIN_ASSEMBLY	14	11	-0.77869	0.778687	-2.09543	0.002141	0.003024
GOBP	Down	GOBP_REGULATION_OF_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCHORE	13	13	-0.72049	0.720492	-2.09653	0	0.003008
GOBP	Down	GOBP_HISTONE_H3_K27_METHYLATION	17	14	-0.72097	0.720969	-2.10444	0	0.002699
GOBP	Down	GOBP_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLOGOUS_RECOMBINATION	47	38	-0.5459	0.545901	-2.10678	0	0.002636
GOBP	Down	GOBP_MITOTIC_METAPHASE_PLATE_CONGRESSION	50	49	-0.5111	0.511095	-2.12137	0	0.00209
GOBP	Down	GOBP_MITOTIC_SPINDLE_ORGANIZATION	118	107	-0.44158	0.44158	-2.12523	0	0.001967
GOMF	Down	GOMF_DNA_POLYMERASE_BINDING	20	18	-0.65103	0.651031	-2.12615	0	0.001959
GOMF	Down	GOMF_SINGLE_STRANDED_DNA_BINDING	116	104	-0.45097	0.450972	-2.12857	0	0.001932
PID	Down	PID_AURORA_A_PATHWAY	31	31	-0.57586	0.575863	-2.13212	0	0.00186
HALLMARK	Down	HALLMARK_MITOTIC_SPINDLE	199	198	-0.40266	0.402655	-2.13555	0	0.001804
GOBP	Down	GOBP_REGULATION_OF_DNA_RECOMBINATION	104	77	-0.47769	0.47769	-2.1366	0	0.001793
GOBP	Down	GOBP_DNA_INTEGRITY_CHECKPOINT	156	141	-0.42426	0.42426	-2.1373	0	0.001802
GOMF	Down	GOMF_FLAP_ENDONUCLEASE_ACTIVITY	10	9	-0.84584	0.845842	-2.13956	0	0.001753
GOBP	Down	GOBP_MITOTIC_RECOMBINATION	24	22	-0.63953	0.639526	-2.15171	0.002268	0.001522
GOBP	Down	GOBP_KINETOCHORE_ASSEMBLY	17	15	-0.72423	0.724227	-2.1528	0	0.001499
GOBP	Down	GOBP_REGULATORY_T_CELL_DIFFERENTIATION	36	33	-0.57487	0.574867	-2.15572	0	0.001475
PID	Down	PID_CD8_TCR_PATHWAY	53	52	-0.52283	0.522826	-2.16138	0	0.001372
GOBP	Down	GOBP_INTERSTRAND_CROSS_LINK_REPAIR	57	49	-0.52458	0.52458	-2.1653	0	0.001286
GOBP	Down	GOBP_SISTER_CHROMATID_COHESION	62	48	-0.53285	0.53285	-2.17206	0	0.001149
GOBP	Down	GOBP_CHROMOSOME_LOCALIZATION	81	71	-0.49363	0.493627	-2.17435	0	0.00113
GOBP	Down	GOBP_CELL_DIVISION	600	509	-0.37783	0.377831	-2.18517	0	0.001009
GOBP	Down	GOBP_METAPHASE_PLATE_CONGRESSION	64	61	-0.50645	0.506448	-2.18543	0	0.00102
GOMF	Down	GOMF_FOUR_WAY_JUNCTION_DNA_BINDING	17	17	-0.69989	0.699894	-2.18869	0	0.000989
GOBP	Down	GOBP_MITOTIC_CELL_CYCLE	1032	914	-0.35877	0.358768	-2.19873	0	0.00084
GOBP	Down	GOBP_MRNA_EXPORT_FROM_NUCLEUS	113	106	-0.46104	0.461041	-2.20049	0	0.000807
GOBP	Down	GOBP_DNA_UNWINDING_INVOLVED_IN_DNA_REPLICATION	16	14	-0.76107	0.76107	-2.21402	0	0.000598
GOBP	Down	GOBP_PROTEIN_LOCALIZATION_TO_CHROMOSOME	91	79	-0.48953	0.489534	-2.21409	0	0.000605
GOMF	Down	GOMF_DNA_DEPENDENT_ATPASE_ACTIVITY	51	48	-0.53042	0.530419	-2.2173	0	0.000556
GOBP	Down	GOBP_MITOTIC_DNA_REPLICATION	16	14	-0.77517	0.775166	-2.21735	0	0.000563
GOBP	Down	GOBP_SPINDLE_MIDZONE_ASSEMBLY	12	11	-0.80242	0.802417	-2.23117	0	0.000444

KEGG	Down	KEGG_HOMOLOGOUS_RECOMBINATION	28	25	-0.64475	0.644754	-2.24283	0	0.000415
GOBP	Down	GOBP_DNA_METABOLIC_PROCESS	949	803	-0.36567	0.365667	-2.24317	0	0.00042
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	13	13	-0.76135	0.761352	-2.24637	0	0.000402
GOBP	Down	GOBP_MITOTIC_CHROMOSOME_CONDENSATION	15	14	-0.7864	0.786396	-2.28188	0	0.000203
GOBP	Down	GOBP_TELOMERE_MAINTENANCE_VIA_SEMI_CONSERVATIVE_REPLICATION	27	27	-0.65265	0.652653	-2.28597	0	0.00017
GOBP	Down	GOBP_TELOMERE_ORGANIZATION	174	138	-0.45414	0.45414	-2.28919	0	0.000172
GOBP	Down	GOBP_DOUBLE_STRAND_BREAK_REPAIR_VIA_BREAK_INDUCED_REPLICATION	12	11	-0.84139	0.841394	-2.29127	0	0.000162
PID	Down	PID_BARD1_PATHWAY	29	28	-0.64321	0.64321	-2.2923	0	0.000164
GOBP	Down	GOBP_REGULATION_OF_DNA_REPLICATION	107	96	-0.48476	0.484764	-2.29374	0	0.000153
GOBP	Down	GOBP_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	47	46	-0.57255	0.572554	-2.29457	0	0.000155
GOBP	Down	GOBP_DNA_REPAIR	569	483	-0.39599	0.395992	-2.29633	0	0.000157
GOMF	Down	GOMF_CATALYTIC_ACTIVITY_ACTING_ON_DNA	199	185	-0.442	0.442003	-2.30574	0	0.000146
GOBP	Down	GOBP_SPINDLE_ORGANIZATION	182	166	-0.44536	0.445362	-2.31364	0	0.000108
GOBP	Down	GOBP_CHROMOSOME_ORGANIZATION	1244	1009	-0.38166	0.381661	-2.31658	0	0.000109
GOBP	Down	GOBP_REPLICATION_FORK_PROCESSING	40	33	-0.63531	0.635313	-2.3199	0	0.000111
GOBP	Down	GOBP_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	35	34	-0.6195	0.619501	-2.3263	0	9.85E-05
GOBP	Down	GOBP_DNA_REPLICATION_CHECKPOINT	17	16	-0.73688	0.736879	-2.32645	0	1E-04
GOBP	Down	GOBP_PROTEIN_LOCALIZATION_TO_KINETOCHORE	19	17	-0.75002	0.750017	-2.33364	0	0.000102
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_NUCLEAR_DIVISION	54	52	-0.55616	0.556162	-2.33662	0	0.000103
GOBP	Down	GOBP_PROTEIN_LOCALIZATION_TO_CHROMOSOME_CENTROMERIC_REGION	25	23	-0.68554	0.685536	-2.34767	0	5.98E-05
PID	Down	PID_ATM_PATHWAY	34	30	-0.64773	0.647728	-2.36075	0	6.08E-05
GOBP	Down	GOBP_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCHORE	35	31	-0.64213	0.642132	-2.36496	0	6.17E-05
GOBP	Down	GOBP_REGULATION_OF_CHROMOSOME_ORGANIZATION	273	248	-0.44076	0.440763	-2.38611	0	6.28E-05
GOBP	Down	GOBP_HOMOLOGOUS_CHROMOSOME_SEGREGATION	60	28	-0.6597	0.659696	-2.38841	0	6.38E-05
GOBP	Down	GOBP_CELL_CYCLE_CHECKPOINT	209	191	-0.45594	0.455943	-2.39123	0	6.49E-05
GOBP	Down	GOBP_REGULATION_OF_NUCLEAR_DIVISION	135	118	-0.49332	0.49332	-2.40538	0	4.95E-05
GOBP	Down	GOBP_NUCLEOSOME_ORGANIZATION	183	94	-0.5168	0.516801	-2.4059	0	5.04E-05
GOBP	Down	GOBP_HISTONE_EXCHANGE	58	35	-0.63781	0.637806	-2.41196	0	1.71E-05
KEGG	Down	KEGG_CELL_CYCLE	125	120	-0.49323	0.493228	-2.42726	0	1.74E-05
GOBP	Down	GOBP_CHROMATIN_REMODELING_AT_CENTROMERE	47	28	-0.6854	0.685401	-2.43061	0	1.77E-05
GOMF	Down	GOMF_DNA_REPLICATION_ORIGIN_BINDING	23	22	-0.71909	0.719093	-2.43512	0	1.81E-05
GOBP	Down	GOBP_MEIOTIC_CHROMOSOME_SEPARATION	25	16	-0.79486	0.794862	-2.44386	0	1.84E-05
PID	Down	PID_FANCONI_PATHWAY	47	41	-0.63843	0.638434	-2.45317	0	1.88E-05
GOBP	Down	GOBP_MITOTIC_CELL_CYCLE_CHECKPOINT	159	146	-0.48039	0.480394	-2.46363	0	0
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE	41	40	-0.63084	0.630842	-2.466	0	0
GOBP	Down	GOBP_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	49	42	-0.63115	0.63115	-2.47218	0	0
GOBP	Down	GOBP_KINETOCHORE_ORGANIZATION	22	20	-0.76381	0.763806	-2.47627	0	0
GOBP	Down	GOBP_CHROMOSOME_CONDENSATION	46	25	-0.72289	0.722889	-2.4863	0	0
PID	Down	PID_FOXM1_PATHWAY	40	38	-0.65618	0.65618	-2.48741	0	0
GOBP	Down	GOBP_NUCLEOSOME_ASSEMBLY	145	64	-0.57004	0.570043	-2.49554	0	0
GOBP	Down	GOBP_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	109	102	-0.52838	0.528382	-2.49728	0	0
PID	Down	PID_PLK1_PATHWAY	46	44	-0.6239	0.623897	-2.49735	0	0
GOMF	Down	GOMF_DNA_HELICASE_ACTIVITY	74	68	-0.56633	0.566331	-2.50057	0	0
GOBP	Down	GOBP_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEGREGATION	45	43	-0.61988	0.61988	-2.51692	0	0
PID	Down	PID_E2F_PATHWAY	73	70	-0.57222	0.572224	-2.51816	0	0
GOMF	Down	GOMF_SINGLE_STRANDED_DNA_HELICASE_ACTIVITY	19	19	-0.78553	0.785527	-2.53223	0	0
GOBP	Down	GOBP_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	221	133	-0.51688	0.516877	-2.53503	0	0
GOBP	Down	GOBP_HOMOLOGOUS_RECOMBINATION	60	40	-0.6471	0.647095	-2.53811	0	0
GOBP	Down	GOBP_ORGANELLE_FISSION	486	395	-0.44338	0.443378	-2.54172	0	0

GOBP	Down	GOBP_CENTROMERE_COMPLEX_ASSEMBLY	56	37	-0.66031	0.660306	-2.54771	0	0
GOBP	Down	GOBP_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	19	18	-0.80393	0.803927	-2.54853	0	0
PID	Down	PID_ATR_PATHWAY	39	38	-0.66578	0.66578	-2.55858	0	0
GOBP	Down	GOBP_REGULATION_OF_CHROMOSOME_SEPARATION	71	66	-0.57771	0.577706	-2.55921	0	0
GOBP	Down	GOBP_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CELL_CYCLE	66	36	-0.66724	0.667241	-2.57445	0	0
PID	Down	PID_AURORA_B_PATHWAY	39	37	-0.65931	0.65931	-2.58068	0	0
GOBP	Down	GOBP_DOUBLE_STRAND_BREAK_REPAIR	268	211	-0.49	0.490003	-2.5898	0	0
KEGG	Down	KEGG_DNA_REPLICATION	36	35	-0.68223	0.682234	-2.5918	0	0
GOBP	Down	GOBP_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	54	35	-0.6719	0.671896	-2.59493	0	0
GOBP	Down	GOBP_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE	64	61	-0.60319	0.603191	-2.59955	0	0
GOBP	Down	GOBP_DNA_STRAND_ELONGATION	26	24	-0.76298	0.762982	-2.60819	0	0
GOBP	Down	GOBP_DNA_REPLICATION_INITIATION	40	37	-0.68205	0.682053	-2.61387	0	0
GOBP	Down	GOBP_MITOTIC_NUCLEAR_DIVISION	296	266	-0.47524	0.47524	-2.61599	0	0
GOBP	Down	GOBP_RECOMBINATIONAL_REPAIR	140	120	-0.54353	0.543532	-2.64356	0	0
GOBP	Down	GOBP_DNA_CONFORMATION_CHANGE	352	246	-0.49384	0.493842	-2.66065	0	0
GOBP	Down	GOBP_DNA_RECOMBINATION	294	236	-0.49917	0.499171	-2.68448	0	0
GOBP	Down	GOBP_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	91	82	-0.58059	0.580587	-2.68601	0	0
GOBP	Down	GOBP_MEIOTIC_CELL_CYCLE	250	167	-0.52137	0.521366	-2.70035	0	0
GOBP	Down	GOBP_REGULATION_OF_CHROMOSOME_SEGREGATION	89	79	-0.59046	0.590462	-2.71375	0	0
GOMF	Down	GOMF_DNA_SECONDARY_STRUCTURE_BINDING	36	32	-0.72694	0.726939	-2.72001	0	0
GOBP	Down	GOBP_CHROMOSOME_SEPARATION	95	83	-0.60245	0.602453	-2.77958	0	0
GOBP	Down	GOBP_MITOTIC_SISTER_CHROMATID_SEGREGATION	164	150	-0.55958	0.559581	-2.81736	0	0
GOBP	Down	GOBP_MEIOSIS_I_CELL_CYCLE_PROCESS	126	78	-0.62108	0.621084	-2.82248	0	0
GOBP	Down	GOBP_CELL_CYCLE_DNA_REPLICATION	64	62	-0.66401	0.664008	-2.83809	0	0
GOBP	Down	GOBP_SISTER_CHROMATID_SEGREGATION	199	178	-0.55187	0.551871	-2.83983	0	0
GOBP	Down	GOBP_DNA_PACKAGING	240	140	-0.57387	0.573869	-2.85984	0	0
GOBP	Down	GOBP_MEIOTIC_CELL_CYCLE_PROCESS	190	124	-0.58305	0.583049	-2.86755	0	0
GOBP	Down	GOBP_CHROMOSOME_SEGREGATION	337	278	-0.52285	0.522849	-2.87536	0	0
GOBP	Down	GOBP_MEIOTIC_CHROMOSOME_SEGREGATION	89	50	-0.69411	0.694112	-2.88457	0	0
GOBP	Down	GOBP_NUCLEAR_CHROMOSOME_SEGREGATION	273	219	-0.5441	0.544095	-2.88554	0	0
GOBP	Down	GOBP_DNA_REPLICATION	280	257	-0.54881	0.548812	-3.00633	0	0
GOBP	Down	GOBP_DNA_DEPENDENT_DNA_REPLICATION	157	145	-0.60267	0.602667	-3.03601	0	0
HALLMARK	Down	HALLMARK_E2F_TARGETS	200	195	-0.6876	0.687597	-3.59496	0	0
HALLMARK	Down	HALLMARK_G2M_CHECKPOINT	200	189	-0.69623	0.696227	-3.64175	0	0

Gene set list	Trend	Name	Size	Matches	ES	abs(ES)	NES	p	q
GOBP	Up	GOBP_COMPLEMENT_ACTIVATION	171	148	0.688038	0.688038	3.25443	0	0
GOBP	Up	GOBP_REGULATION_OF_COMPLEMENT_ACTIVATION	114	102	0.717756	0.717756	3.22451	0	0
GOBP	Up	GOBP_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	149	136	0.674185	0.674185	3.12818	0	0
GOBP	Up	GOBP_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	137	117	0.680733	0.680733	3.09431	0	0
GOMF	Up	GOMF_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	167	158	0.636895	0.636895	3.05268	0	0
GOBP	Up	GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	121	116	0.67306	0.67306	3.04215	0	0
GOBP	Up	GOBP_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	149	142	0.6478	0.6478	3.02612	0	0
GOBP	Up	GOBP_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	107	103	0.673614	0.673614	3.00324	0	0
KEGG	Up	KEGG_RIBOSOME	88	85	0.689157	0.689157	2.98701	0	0
GOBP	Up	GOBP_TRANSLATIONAL_INITIATION	193	185	0.58441	0.58441	2.83998	0	0
GOBP	Up	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	100	96	0.625498	0.625498	2.7648	0	0
GOMF	Up	GOMF_ANTIGEN_BINDING	158	147	0.587634	0.587634	2.76359	0	0
GOBP	Up	GOBP_OXIDATIVE_PHOSPHORYLATION	148	119	0.601064	0.601064	2.75516	0	0
GOBP	Up	GOBP_HUMORAL_IMMUNE_RESPONSE	373	255	0.543085	0.543085	2.72929	0	0
GOMF	Up	GOMF_ELECTRON_TRANSFER_ACTIVITY	138	124	0.586026	0.586026	2.70602	0	0
GOBP	Up	GOBP_ELECTRON_TRANSPORT_CHAIN	178	160	0.560963	0.560963	2.69012	0	0
GOBP	Up	GOBP_PHAGOCYTOSIS_RECOGNITION	91	80	0.634929	0.634929	2.68416	0	0
GOMF	Up	GOMF_IMMUNOGLOBULIN_RECEPTOR_BINDING	72	65	0.659289	0.659289	2.66863	0	0
GOBP	Up	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	117	112	0.583073	0.583073	2.65332	0	0
GOBP	Up	GOBP_PROTEIN_N_LINKED_GLYCOSYLATION	74	69	0.640812	0.640812	2.64169	0	0
GOBP	Up	GOBP_IMMUNOGLOBULIN_PRODUCTION	197	177	0.543211	0.543211	2.6406	0	0
GOBP	Up	GOBP_B_CELL_MEDIATED_IMMUNITY	219	197	0.536599	0.536599	2.63907	0	0
HALLMARK	Up	HALLMARK_PROTEIN_SECRETION	96	93	0.603982	0.603982	2.63904	0	0
GOBP	Up	GOBP_PEPTIDYL_ASPARAGINE_MODIFICATION	31	30	0.773128	0.773128	2.63687	0	0
GOBP	Up	GOBP_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	168	167	0.549505	0.549505	2.63353	0	0
KEGG	Up	KEGG_PROTEIN_EXPORT	24	23	0.799311	0.799311	2.59945	0	0
KEGG	Up	KEGG_OXIDATIVE_PHOSPHORYLATION	132	105	0.581036	0.581036	2.59304	0	0
KEGG	Up	KEGG_PARKINSONS_DISEASE	130	105	0.574008	0.574008	2.55619	0	0
HALLMARK	Up	HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	184	0.523118	0.523118	2.54242	0	0
GOBP	Up	GOBP_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	144	142	0.536872	0.536872	2.52396	0	0
GOBP	Up	GOBP_CELLULAR_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	168	151	0.529	0.529	2.5131	0	0
GOBP	Up	GOBP_PROTEIN_TARGETING_TO_MEMBRANE	208	187	0.516599	0.516599	2.51015	0	0
GOBP	Up	GOBP_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	62	56	0.626297	0.626297	2.5098	0	0
GOBP	Up	GOBP_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE	55	54	0.633396	0.633396	2.49996	0	0
GOBP	Up	GOBP_CELLULAR_RESPIRATION	187	173	0.516662	0.516662	2.48822	0	0
GOBP	Up	GOBP_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_RESPONSE	127	114	0.547511	0.547511	2.48007	0	0
GOBP	Up	GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	101	95	0.561479	0.561479	2.4773	0	0
GOMF	Up	GOMF_HEME_COPPER_TERMINAL_OXIDASE_ACTIVITY	28	23	0.759964	0.759964	2.47726	0	0
GOBP	Up	GOBP_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION	89	88	0.564419	0.564419	2.47054	0	0
GOBP	Up	GOBP_ENDOPLASMIC_RETICULUM_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	206	184	0.510341	0.510341	2.45748	0	0
KEGG	Up	KEGG_PROTEASOME	46	42	0.643616	0.643616	2.45512	0	0
GOBP	Up	GOBP_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	205	187	0.499445	0.499445	2.44827	0	0
GOBP	Up	GOBP_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	295	262	0.476796	0.476796	2.44093	0	0
GOMF	Up	GOMF_NAD_P_H_DEHYDROGENASE_QUINONE_ACTIVITY	48	48	0.629644	0.629644	2.43816	0	0
GOBP	Up	GOBP_CYTOPLASMIC_TRANSLATION	102	98	0.543348	0.543348	2.39436	0	0
GOMF	Up	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_A	60	59	0.595227	0.595227	2.38729	0	0

GOBP	Up	GOBP_MITOCHONDRIAL_TRANSLATION	134	130	0.512384	0.512384	2.36832	0	2.04E-05
GOBP	Up	GOBP_AEROBIC_RESPIRATION	86	77	0.561422	0.561422	2.36705	0	2E-05
GOMF	Up	GOMF_TRANSLATION_INITIATION_FACTOR_ACTIVITY	51	49	0.60894	0.60894	2.3448	0	3.91E-05
GOBP	Up	GOBP_VESICLE_TARGETING	95	87	0.542081	0.542081	2.33919	0	3.83E-05
GOBP	Up	GOBP_MEMBRANE_INVAGINATION	136	127	0.510417	0.510417	2.33066	0	5.64E-05
GOBP	Up	GOBP_FC_RECEPTOR_SIGNALING_PATHWAY	238	235	0.462706	0.462706	2.32784	0	5.53E-05
GOBP	Up	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	99	98	0.518634	0.518634	2.32044	0	5.43E-05
GOBP	Up	GOBP_ENDOPLASMIC_RETICULUM_TO_CYTOSOL_TRANSPORT	28	25	0.691304	0.691304	2.31641	0	5.32E-05
GOBP	Up	GOBP_TRANSLATIONAL_TERMINATION	105	103	0.516502	0.516502	2.31492	0	5.23E-05
GOBP	Up	GOBP_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	77	65	0.562737	0.562737	2.31469	0	5.13E-05
GOBP	Up	GOBP_PROTEIN_TARGETING	438	400	0.436586	0.436586	2.30182	0	6.73E-05
GOBP	Up	GOBP_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	47	41	0.619549	0.619549	2.3011	0	6.61E-05
GOBP	Up	GOBP_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY	65	62	0.558423	0.558423	2.30042	0	6.5E-05
GOBP	Up	GOBP_VESICLE_TARGETING_TO_FROM_OR_WITHIN_GOLGI	74	69	0.555313	0.555313	2.28464	0	7.99E-05
GOBP	Up	GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	120	119	0.494493	0.494493	2.28141	0	7.86E-05
KEGG	Up	KEGG_ALZHEIMERS_DISEASE	166	137	0.491543	0.491543	2.27844	0	0.000108
GOMF	Up	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	102	92	0.517007	0.517007	2.27794	0	0.000106
HALLMARK	Up	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	113	106	0.504376	0.504376	2.27475	0	0.000105
GOBP	Up	GOBP_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	285	250	0.448972	0.448972	2.26383	0	0.000133
KEGG	Up	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	69	50	0.576493	0.576493	2.25133	0	0.000218
GOBP	Up	GOBP_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_INTRINSIC_APOPTO	18	14	0.789827	0.789827	2.25088	0	0.000215
KEGG	Up	KEGG_HUNTINGTONS_DISEASE	182	151	0.470651	0.470651	2.23882	0	0.000268
GOBP	Up	GOBP_SIGNAL_PEPTIDE_PROCESSING	12	11	0.857202	0.857202	2.23231	0	0.000292
GOMF	Up	GOMF_ANTIOXIDANT_ACTIVITY	86	61	0.551277	0.551277	2.2313	0	0.000288
GOMF	Up	GOMF_PEPTIDE_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	13	12	0.820859	0.820859	2.21949	0	0.000337
GOBP	Up	GOBP_RETROGRADE_VESICLE_MEDIATED_TRANSPORT_GOLGI_TO_ENDOPLASMIC_RETICULUM	87	81	0.515396	0.515396	2.21911	0	0.000333
GOBP	Up	GOBP_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN	21	18	0.734982	0.734982	2.21801	0	0.000341
GOBP	Up	GOBP_GLYCOSYLATION	262	208	0.45027	0.45027	2.20751	0	0.000363
GOBP	Up	GOBP_VESICLE_CARGO_LOADING	27	19	0.702909	0.702909	2.19241	0	0.000486
GOBP	Up	GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	351	314	0.425485	0.425485	2.19148	0	0.000479
GOBP	Up	GOBP_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNAL	30	25	0.660107	0.660107	2.19109	0	0.000473
GOBP	Up	GOBP_CELL_RECOGNITION	225	174	0.454349	0.454349	2.18737	0	0.000504
GOBP	Up	GOBP_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_	77	72	0.517848	0.517848	2.17278	0	0.000631
GOBP	Up	GOBP_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	81	73	0.510255	0.510255	2.17029	0	0.000647
GOBP	Up	GOBP_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	278	244	0.433224	0.433224	2.16916	0	0.000651
KEGG	Up	KEGG_N_GLYCAN_BIOSYNTHESIS	46	45	0.569727	0.569727	2.1598	0	0.000771
GOBP	Up	GOBP_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	67	61	0.53128	0.53128	2.15515	0	0.000797
GOBP	Up	GOBP_TRANSLATIONAL_ELONGATION	134	126	0.465441	0.465441	2.15337	0	0.000799
HALLMARK	Up	HALLMARK_MYC_TARGETS_V1	200	194	0.435456	0.435456	2.14413	0	0.000857
GOBP	Up	GOBP_CYTOPLASMIC_TRANSLATIONAL_INITIATION	34	33	0.610106	0.610106	2.14337	0	0.000858
GOBP	Up	GOBP_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	83	79	0.498522	0.498522	2.13898	0	0.000892
GOMF	Up	GOMF_2_IRON_2_SULFUR_CLUSTER_BINDING	22	20	0.680299	0.680299	2.13744	0	0.000904
GOBP	Up	GOBP_COPII_COATED_VESICLE_BUDDING	73	68	0.519491	0.519491	2.1354	0	0.000926
GOBP	Up	GOBP_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	143	127	0.463901	0.463901	2.12455	0	0.001086
GOBP	Up	GOBP_VESICLE_BUDDING_FROM_MEMBRANE	109	102	0.484136	0.484136	2.12338	0	0.001116
GOMF	Up	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	58	51	0.539556	0.539556	2.12121	0	0.001156
GOBP	Up	GOBP_EXOCYTTIC_PROCESS	78	70	0.502453	0.502453	2.11918	0	0.001185

GOBP	Up	GOBP_INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	34	30	0.616116	0.616116	2.11911	0	0.001173
GOBP	Up	GOBP_RECEPTOR_MEDIATED_ENDOCYTOSIS	327	284	0.411361	0.411361	2.11309	0	0.001261
GOBP	Up	GOBP_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	122	87	0.491723	0.491723	2.11197	0	0.001288
GOBP	Up	GOBP_MITOCHONDRIAL_GENE_EXPRESSION	165	158	0.444025	0.444025	2.10968	0	0.001324
GOBP	Up	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASSES_II	80	79	0.489656	0.489656	2.10796	0	0.00135
GOBP	Up	GOBP_PHAGOCYTOSIS	374	338	0.404022	0.404022	2.10728	0	0.001355
GOBP	Up	GOBP_DETOXIFICATION	138	97	0.478257	0.478257	2.10711	0	0.001351
GOBP	Up	GOBP_DEFENSE_RESPONSE_TO_BACTERIUM	337	214	0.42552	0.42552	2.10199	0	0.001518
GOMF	Up	GOMF_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	108	97	0.473436	0.473436	2.09142	0	0.001795
GOBP	Up	GOBP_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PROCESS	22	21	0.654236	0.654236	2.0805	0	0.002103
GOBP	Up	GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY	351	314	0.399567	0.399567	2.07518	0	0.00223
GOBP	Up	GOBP_GOLGI_VESICLE_TRANSPORT	372	337	0.398934	0.398934	2.07477	0	0.002209
GOMF	Up	GOMF_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	84	78	0.487957	0.487957	2.07433	0	0.002197
GOMF	Up	GOMF_GDP_BINDING	75	67	0.49971	0.49971	2.07237	0	0.002213
GOBP	Up	GOBP_VESICLE_DOCKING_INVOLVED_IN_EXOCYTOSIS	44	42	0.55118	0.55118	2.06547	0	0.00252
GOBP	Up	GOBP_PEPTIDE_METABOLIC_PROCESS	903	724	0.370109	0.370109	2.06251	0	0.002647
GOBP	Up	GOBP_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS	115	105	0.45906	0.45906	2.05414	0	0.002954
GOBP	Up	GOBP_NEGATIVE_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	9	9	0.810002	0.810002	2.05199	0	0.003039
GOBP	Up	GOBP_INTEGRATED_STRESS_RESPONSE_SIGNALING	27	25	0.612674	0.612674	2.04769	0	0.003278
GOBP	Up	GOBP_VIRAL_GENE_EXPRESSION	198	191	0.413613	0.413613	2.04706	0	0.003283
GOBP	Up	GOBP_ENDOPLASMIC_RETICULUM_ORGANIZATION	86	73	0.487864	0.487864	2.04321	0	0.003447
GOBP	Up	GOBP_PROTEIN_FOLDING_IN_ENDOPLASMIC_RETICULUM	11	8	0.855199	0.855199	2.0385	0	0.00375
GOMF	Up	GOMF_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	40	34	0.575476	0.575476	2.02829	0	0.004379
GOBP	Up	GOBP_HYDROGEN_PEROXIDE_CATABOLIC_PROCESS	31	21	0.641223	0.641223	2.02703	0	0.004465
GOBP	Up	GOBP_PEPTIDE_BIOSYNTHETIC_PROCESS	740	597	0.369098	0.369098	2.02337	0	0.004662
GOBP	Up	GOBP_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	1786	1432	0.348741	0.348741	2.01925	0	0.004978
GOMF	Up	GOMF_UNFOLDED_PROTEIN_BINDING	120	105	0.452392	0.452392	2.01767	0	0.005064
GOBP	Up	GOBP_AMINE_METABOLIC_PROCESS	163	131	0.432997	0.432997	2.01455	0	0.005291
GOMF	Up	GOMF_MISFOLDED_PROTEIN_BINDING	29	28	0.599378	0.599378	2.01409	0	0.005295
GOBP	Up	GOBP_ER_NUCLEUS_SIGNALING_PATHWAY	53	49	0.526038	0.526038	2.01275	0	0.005369
GOMF	Up	GOMF_MEMBRANE_INSERTASE_ACTIVITY	12	12	0.736961	0.736961	2.00927	0	0.00555
GOBP	Up	GOBP_CELLULAR_RESPONSE_TO_ALDEHYDE	12	9	0.803378	0.803378	2.00882	0	0.005574
GOBP	Up	GOBP_CELLULAR_OXIDANT_DETOXIFICATION	102	75	0.477084	0.477084	2.00497	0	0.005842
GOBP	Up	GOBP_PROTEIN_FOLDING	233	201	0.41005	0.41005	2.00042	0	0.006173
GOMF	Up	GOMF_PROTEIN_DISULFIDE_ISOMERASE_ACTIVITY	19	15	0.695459	0.695459	2.00007	0	0.006148
GOBP	Up	GOBP_CYTOCHROME_COMPLEX_ASSEMBLY	36	35	0.550829	0.550829	1.99148	0	0.006969
GOMF	Up	GOMF_ACETYL_COA_C_ACYLTRANSFERASE_ACTIVITY	7	7	0.857212	0.857212	1.98945	0.001931	0.007107
GOMF	Up	GOMF_PROTEIN_TAG	13	11	0.767397	0.767397	1.9889	0	0.007097
GOBP	Up	GOBP_REGULATION_OF_TRANSLATIONAL_INITIATION	80	75	0.470505	0.470505	1.98304	0	0.007726
HALLMARK	Up	HALLMARK_ANDROGEN_RESPONSE	100	89	0.459384	0.459384	1.98156	0	0.00779
GOBP	Up	GOBP_COPPER_ION_TRANSPORT	16	15	0.681414	0.681414	1.97779	0	0.008297
GOBP	Up	GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	44	38	0.543499	0.543499	1.97636	0	0.008463
GOBP	Up	GOBP_REGULATION_OF_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	14	13	0.721317	0.721317	1.97536	0	0.00852
GOBP	Up	GOBP_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	346	265	0.389036	0.389036	1.97288	0	0.008836
GOBP	Up	GOBP_CELLULAR_AMIDE_METABOLIC_PROCESS	1185	946	0.347206	0.347206	1.96537	0	0.009842
GOBP	Up	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN	194	184	0.402006	0.402006	1.9645	0	0.009895
GOMF	Up	GOMF_OLIGOSACCHARYL_TRANSFERASE_ACTIVITY	6	6	0.927288	0.927288	1.96449	0	0.009824



GOBP	Up	GOBP_COPII_COATED_VESICLE_CARGO_LOADING	15	15	0.688812	0.688812	1.96326	0.001815	0.009945
GOBP	Up	GOBP_PROTEIN_INSERTION_INTO_ER_MEMBRANE_BY_STOP_TRANSFER_MEMBRANE_ANCHOR_SEQUENCE	10	10	0.767164	0.767164	1.96309	0	0.009888
GOMF	Up	GOMF_TRANSLATION_REGULATOR_ACTIVITY	138	125	0.429124	0.429124	1.96256	0	0.009846
GOMF	Up	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	57	42	0.524332	0.524332	1.96014	0	0.010204
GOBP	Up	GOBP_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	27	23	0.608553	0.608553	1.95959	0	0.010219
GOBP	Up	GOBP_ERAD_PATHWAY	101	92	0.445085	0.445085	1.95955	0	0.010156
GOBP	Up	GOBP_REGULATION_OF_RETROGRADE_PROTEIN_TRANSPORT_ER_TO_CYTOSOL	13	12	0.736357	0.736357	1.95841	0	0.010224
GOMF	Up	GOMF_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	124	82	0.453496	0.453496	1.95813	0	0.0102
GOBP	Up	GOBP_GLYCOPROTEIN_METABOLIC_PROCESS	419	326	0.378625	0.378625	1.9571	0	0.010337
GOBP	Up	GOBP_B_CELL_RECEPTOR_SIGNALING_PATHWAY	127	119	0.430725	0.430725	1.95617	0	0.010434
GOBP	Up	GOBP_CATECHOLAMINE_UPTAKE_INVOLVED_IN_SYNAPTIC_TRANSMISSION	12	5	0.961895	0.961895	1.95318	0	0.010746
HALLMARK	Up	HALLMARK_ANGIOGENESIS	36	34	0.547608	0.547608	1.95289	0.001715	0.010701
GOMF	Up	GOMF_OXIDOREDUCTASE_ACTIVITY	750	604	0.354624	0.354624	1.94954	0	0.011088
GOBP	Up	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION	234	224	0.387277	0.387277	1.94522	0	0.011682
GOBP	Up	GOBP_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_RESPONSE	29	27	0.580823	0.580823	1.9402	0	0.012336
GOBP	Up	GOBP_REGULATION_OF_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION	74	71	0.460305	0.460305	1.93774	0	0.012687
GOBP	Up	GOBP_TRANSITION_METAL_ION_HOMEOSTASIS	139	114	0.423041	0.423041	1.93584	0	0.012912
GOBP	Up	GOBP_PROTEIN_DEMANNOSYLATION	20	19	0.63033	0.63033	1.93423	0	0.013152
GOMF	Up	GOMF_TRANSFERASE_ACTIVITY_TRANSFERRING_HEXOSYL_GROUPS	200	147	0.413324	0.413324	1.9278	0	0.01422
GOBP	Up	GOBP_FORMATION_OF_CYTOPLASMIC_TRANSLATION_INITIATION_COMPLEX	16	16	0.655073	0.655073	1.92407	0	0.01488
GOBP	Up	GOBP_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	72	67	0.47469	0.47469	1.92376	0	0.014829
GOBP	Up	GOBP_AMIDE_BIOSYNTHETIC_PROCESS	877	711	0.346485	0.346485	1.92319	0	0.01488
GOBP	Up	GOBP_TRANSITION_METAL_ION_TRANSPORT	127	101	0.431674	0.431674	1.91842	0	0.01577
GOBP	Up	GOBP_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTOR	358	326	0.370555	0.370555	1.9161	0	0.016095
GOBP	Up	GOBP_CELLULAR_RESPONSE_TO_NITROGEN_STARVATION	13	11	0.722068	0.722068	1.91144	0	0.017136
GOMF	Up	GOMF_IGG_BINDING	11	9	0.771046	0.771046	1.9106	0	0.017264
GOBP	Up	GOBP_REGULATION_OF_COAGULATION	71	54	0.477997	0.477997	1.90767	0	0.017815
HALLMARK	Up	HALLMARK_MTORC1_SIGNALING	200	195	0.387122	0.387122	1.90294	0	0.019118
GOMF	Up	GOMF_C_ACYLTRANSFERASE_ACTIVITY	20	16	0.645314	0.645314	1.90261	0.001869	0.019118
GOBP	Up	GOBP_PROTEIN_DEGLYCOSYLATION	28	26	0.560176	0.560176	1.90095	0	0.019355
GOBP	Up	GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	576	521	0.351671	0.351671	1.89751	0	0.020122
KEGG	Up	KEGG_CARDIAC_MUSCLE_CONTRACTION	79	60	0.469086	0.469086	1.89704	0	0.02015
GOBP	Up	GOBP_MITOCHONDRIAL_CYTOCHROME_C_OXIDASE_ASSEMBLY	22	21	0.594873	0.594873	1.89687	0.001805	0.0201
GOMF	Up	GOMF_RRNA_BINDING	64	59	0.470456	0.470456	1.89561	0	0.020331
GOMF	Up	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_METAL_IONS	19	15	0.655042	0.655042	1.89531	0.005272	0.020259
GOBP	Up	GOBP_ENDOPLASMIC_RETICULUM_MANNOSE_TRIMMING	16	15	0.654638	0.654638	1.89477	0	0.020362
GOBP	Up	GOBP_ZINC_ION_TRANSPORT	27	20	0.609685	0.609685	1.89259	0	0.020859
GOBP	Up	GOBP_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	23	23	0.587454	0.587454	1.89151	0	0.020968
GOBP	Up	GOBP_UBIQUITIN_DEPENDENT_ERAD_PATHWAY	79	73	0.4538	0.4538	1.88843	0	0.021734
KEGG	Up	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	41	22	0.597534	0.597534	1.8884	0	0.021624
GOBP	Up	GOBP_ATF6_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	10	10	0.739114	0.739114	1.88758	0	0.021727
GOBP	Up	GOBP_GLYCOSIDE_METABOLIC_PROCESS	21	16	0.638576	0.638576	1.88376	0.001845	0.022645
GOBP	Up	GOBP_IRON_ION_HOMEOSTASIS	86	74	0.44418	0.44418	1.88291	0	0.022809
GOBP	Up	GOBP_CATECHOLAMINE_UPTAKE	18	9	0.754728	0.754728	1.87955	0	0.023717
GOBP	Up	GOBP_LEUKOCYTE_MEDIATED_IMMUNITY	873	780	0.334311	0.334311	1.8758	0	0.02463
GOBP	Up	GOBP_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY	103	98	0.42271	0.42271	1.8716	0	0.025976
GOMF	Up	GOMF_PROTEIN_TRANSPORTER_ACTIVITY	29	25	0.574511	0.574511	1.8713	0	0.025935

GOBP	Up	GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	208	196	0.378446	0.378446	1.86481	0	0.02804
GOBP	Up	GOBP_VESICLE_FUSION_WITH_GOLGI_APPARATUS	8	8	0.794697	0.794697	1.86239	0	0.028678
GOBP	Up	GOBP_ER_ASSOCIATED_MISFOLDED_PROTEIN_CATABOLIC_PROCESS	12	11	0.693411	0.693411	1.86211	0.001855	0.028648
GOBP	Up	GOBP_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ENDOPLASMIC_RETICULUM	14	13	0.679963	0.679963	1.8617	0	0.028623
GOBP	Up	GOBP_RESPONSE_TO_THYROID_HORMONE	23	18	0.605554	0.605554	1.86025	0.001764	0.028998
GOMF	Up	GOMF_UBIQUITIN_PROTEIN_TRANSFERASE_INHIBITOR_ACTIVITY	6	6	0.856598	0.856598	1.85903	0	0.029365
GOBP	Up	GOBP_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	361	306	0.357731	0.357731	1.85848	0	0.029411
GOMF	Up	GOMF_GLUTATHIONE_PEROXIDASE_ACTIVITY	22	17	0.623995	0.623995	1.85552	0	0.030194
GOMF	Up	GOMF_DOLICHYL_DIPHOSPHOOLIGOSACCHARIDE_PROTEIN_GLYCOTRANSFERASE_ACTIVITY	5	5	0.92724	0.92724	1.8547	0	0.030358
GOBP	Up	GOBP_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	22	18	0.61311	0.61311	1.85442	0.001825	0.030325
GOBP	Up	GOBP_VESICLE_DOCKING	65	62	0.457695	0.457695	1.85362	0	0.03053
GOMF	Up	GOMF_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	57	49	0.478048	0.478048	1.85282	0.001704	0.030738
GOBP	Up	GOBP_PROTEIN_INSERTION_INTO_ER_MEMBRANE	19	17	0.612845	0.612845	1.85003	0.00354	0.031557
GOBP	Up	GOBP_VESICLE_LOCALIZATION	224	201	0.378628	0.378628	1.84868	0	0.031944
GOMF	Up	GOMF_PROTEIN_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	21	19	0.607418	0.607418	1.84823	0	0.031942
GOBP	Up	GOBP_OLIGOSACCHARIDE_LIPID_INTERMEDIATE_BIOSYNTHETIC_PROCESS	21	21	0.595401	0.595401	1.84702	0.001838	0.032229
GOBP	Up	GOBP_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	176	154	0.394431	0.394431	1.84652	0	0.03224
GOBP	Up	GOBP_ACTIVATION_OF_IMMUNE_RESPONSE	563	503	0.34226	0.34226	1.84631	0	0.032181
GOBP	Up	GOBP_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	524	432	0.346155	0.346155	1.8448	0	0.03262
KEGG	Up	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	44	40	0.496984	0.496984	1.84419	0	0.032699
GOBP	Up	GOBP_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY	26	25	0.556911	0.556911	1.84082	0	0.033901
HALLMARK	Up	HALLMARK_COAGULATION	138	106	0.410149	0.410149	1.84053	0	0.033853
GOBP	Up	GOBP_ALDEHYDE_CATABOLIC_PROCESS	12	9	0.73863	0.73863	1.83709	0.00189	0.035157
HALLMARK	Up	HALLMARK_GLYCOLYSIS	200	182	0.378361	0.378361	1.83601	0	0.035467
GOMF	Up	GOMF_UBIQUITIN_LIGASE_INHIBITOR_ACTIVITY	5	5	0.877773	0.877773	1.83576	0	0.035413
GOBP	Up	GOBP_CELLULAR_DETOXIFICATION_OF_ALDEHYDE	8	6	0.849477	0.849477	1.83462	0.003945	0.03567
GOBP	Up	GOBP_ESTABLISHMENT_OF_TISSUE_POLARITY	123	115	0.404775	0.404775	1.83311	0	0.03609
GOBP	Up	GOBP_POSTTRANSLATIONAL_PROTEIN_TARGETING_TO_ENDOPLASMIC_RETICULUM_MEMBRANE	12	11	0.688549	0.688549	1.82679	0.009416	0.038664
GOBP	Up	GOBP_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	331	260	0.361645	0.361645	1.82562	0	0.039022
GOBP	Up	GOBP_REGULATION_OF_TRANSLATIONAL_INITIATION_IN_RESPONSE_TO_STRESS	15	15	0.639904	0.639904	1.82456	0.005597	0.039248
KEGG	Up	KEGG_PROPANOATE_METABOLISM	33	29	0.534944	0.534944	1.82036	0.001887	0.041051
GOBP	Up	GOBP_ATP_METABOLIC_PROCESS	313	255	0.35911	0.35911	1.81994	0	0.041034
GOBP	Up	GOBP_DOLICHOL_METABOLIC_PROCESS	5	5	0.889287	0.889287	1.81922	0.002	0.041153
GOBP	Up	GOBP_NEGATIVE_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	15	15	0.61864	0.61864	1.81663	0.009158	0.04225
GOBP	Up	GOBP_AMINO_SUGAR_METABOLIC_PROCESS	41	35	0.503543	0.503543	1.81546	0.00367	0.042604
GOBP	Up	GOBP_INTRACELLULAR_PROTEIN_TRANSPORT	1161	1052	0.319937	0.319937	1.81484	0	0.042727
GOBP	Up	GOBP_NEGATIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	41	37	0.500995	0.500995	1.81483	0.003527	0.042536
GOBP	Up	GOBP_PROTEIN_LOCALIZATION_TO_MEMBRANE	658	577	0.33211	0.33211	1.81424	0	0.042658
GOBP	Up	GOBP_SECONDARY_METABOLIC_PROCESS	56	35	0.497953	0.497953	1.80773	0.001706	0.045773
GOBP	Up	GOBP_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	89	85	0.416905	0.416905	1.80717	0	0.045871
GOBP	Up	GOBP_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	680	538	0.33201	0.33201	1.8065	0	0.046061
GOMF	Up	GOMF_7S_RNA_BINDING	7	7	0.794927	0.794927	1.80509	0.001894	0.046542
GOMF	Up	GOMF_STRUCTURAL_MOLECULE_ACTIVITY	686	518	0.334245	0.334245	1.8035	0	0.047148
GOMF	Up	GOMF_3_HYDROXYACYL_COA_DEHYDROGENASE_ACTIVITY	8	8	0.758562	0.758562	1.80007	0.003899	0.048778
KEGG	Up	KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	16	11	0.673329	0.673329	1.79865	0.005803	0.049365
GOBP	Up	GOBP_CELLULAR_TRANSITION_METAL_ION_HOMEOSTASIS	118	96	0.404254	0.404254	1.79839	0	0.049338
HALLMARK	Up	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	200	191	0.370083	0.370083	1.79832	0	0.049156

GOBP	Up	GOBP_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION	88	84	0.415082	0.415082	1.79699	0	0.049713
GOBP	Down	GOBP_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	51	47	-0.50305	0.503047	-2.03662	0	0.048979
GOBP	Down	GOBP_3_UTR_MEDIATED_MRNA_DESTABILIZATION	17	15	-0.68443	0.684434	-2.05204	0.002278	0.044902
HALLMARK	Down	HALLMARK_MITOTIC_SPINDLE	199	198	-0.39612	0.396115	-2.07503	0	0.035293
GOBP	Down	GOBP_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	66	62	-0.50094	0.500939	-2.10012	0	0.02672
GOBP	Down	GOBP_DNA_PACKAGING	240	140	-0.42435	0.424346	-2.10138	0	0.028478
GOBP	Down	GOBP_THYMIC_T_CELL_SELECTION	22	20	-0.65167	0.651671	-2.10997	0	0.027951
GOBP	Down	GOBP_POSITIVE_T_CELL_SELECTION	36	33	-0.57642	0.57642	-2.11272	0	0.02965
GOMF	Down	GOMF_UNMETHYLATED_CPG_BINDING	8	8	-0.85672	0.856723	-2.11929	0	0.030719
GOBP	Down	GOBP_MEIOTIC_CHROMOSOME_SEGREGATION	89	50	-0.51424	0.514235	-2.13466	0	0.026971
GOBP	Down	GOBP_T_CELL_SELECTION	48	45	-0.53892	0.538918	-2.16505	0	0.022325
GOBP	Down	GOBP_REGULATION_OF_T_HELPER_17_TYPE_IMMUNE_RESPONSE	22	18	-0.68973	0.689725	-2.21014	0	0.011602
KEGG	Down	KEGG_PRIMARY_IMMUNODEFICIENCY	35	35	-0.61506	0.61506	-2.28443	0	0.00501
KEGG	Down	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	108	101	-0.48986	0.489864	-2.32199	0	0.004219
PID	Down	PID_CD8_TCR_PATHWAY	53	52	-0.64876	0.648763	-2.68711	0	0
PID	Down	PID_TCR_PATHWAY	64	62	-0.65444	0.654439	-2.80779	0	0