

The lymph node transcriptome of unicentric and idiopathic multicentric Castleman disease

Pedro Horna,¹ Rebecca L. King,¹ Dragan Jevremovic,¹ David C. Fajgenbaum² and Angela Dispenzieri³

¹Division of Hematopathology, Mayo Clinic, Rochester, MN; ²Center for Cytokine Storm Treatment & Laboratory, University of Pennsylvania, Philadelphia, PA and ³Division of Hematology, Mayo Clinic, Rochester, MN, USA

Correspondence: P. Horna
horna.pedro@mayo.edu

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Figure S1

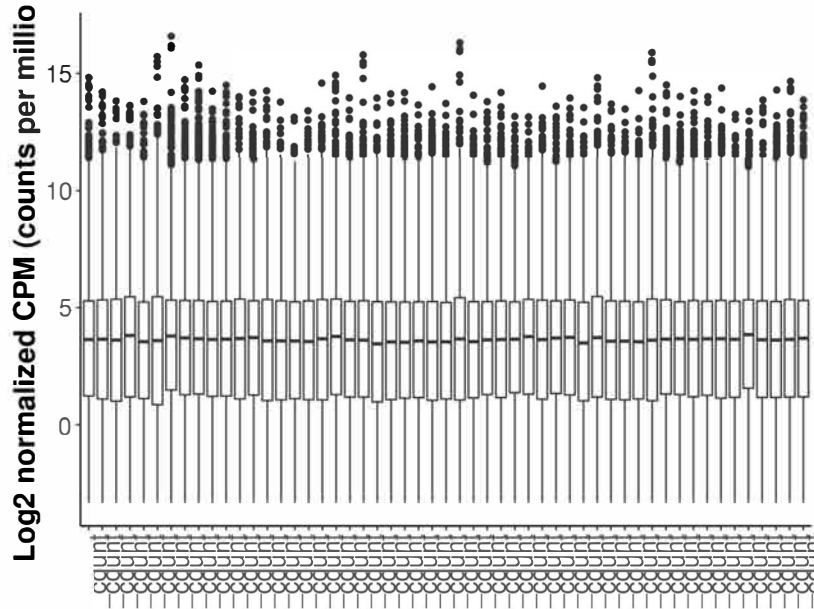


Figure S1A. Normalized transcript counts for all samples studied.

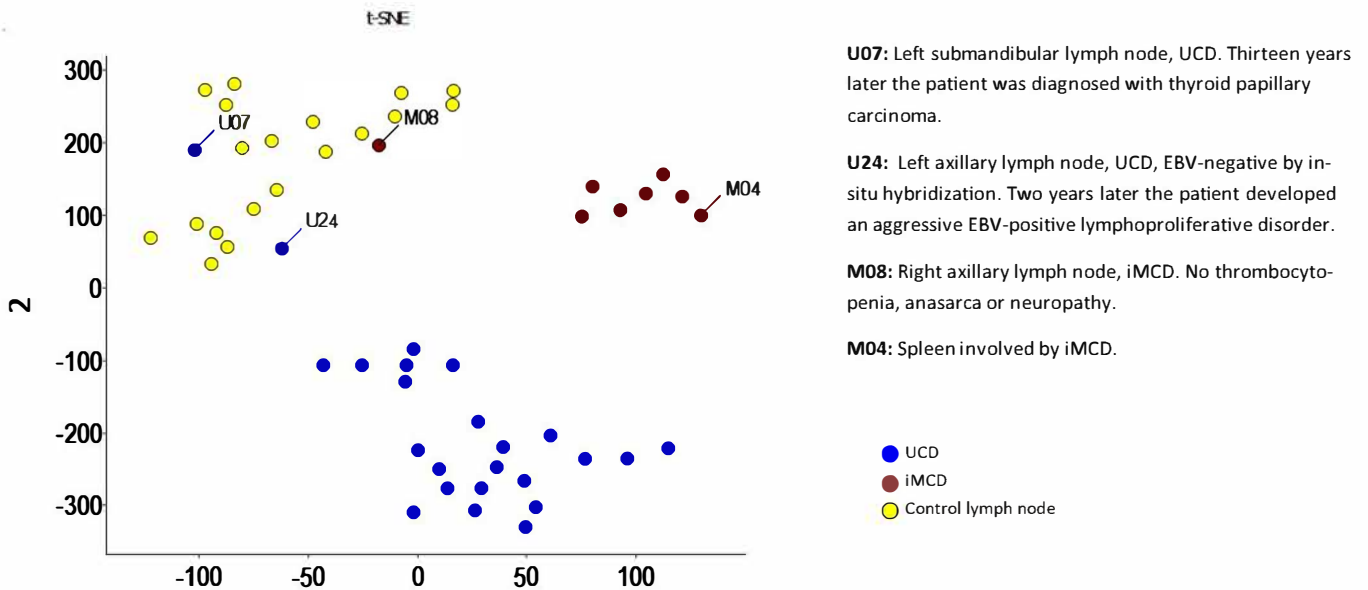


Figure S1B. t-SNE plot of differentially expressed genes (3-group ANOVA), showing clinical information of sample outliers (U07, M08 and U24); in addition to a non-outlier spleen sample included in this study (M04). The described outliers are the same as those identified by hierarchical clustering on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