

'Sle.Female patients vs Healthy.Female donors' :

NAME	SIZE	ES	NES
RSRFC4_01	187	-0.59416026	-1.2942672
GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_I	21	-0.7568987	-1.2943696
GO_GLIOGENESIS	139	-0.6077455	-1.2957691
GO_DEVELOPMENTAL_CELL_GROWTH	64	-0.6566167	-1.2946366
GO_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_	173	-0.60245657	-1.295714
GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOP	210	-0.5970224	-1.2956916
GO_NEGATIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMEN	26	-0.7402888	-1.2956074
CEBP_01	208	-0.59075737	-1.295557
GO_ZYMOGEN_ACTIVATION	97	-0.62551033	-1.2949806
GO_REGULATION_OF_CGMP_METABOLIC_PROCESS	18	-0.7768401	-1.2951607
GO_AMINO_SUGAR_METABOLIC_PROCESS	37	-0.7021244	-1.2949332
GO_LIPOPOLYSACCHARIDE_BINDING	17	-0.762747	-1.2954592
GO_EMBRYONIC_ORGAN_MORPHOGENESIS	205	-0.5942936	-1.2955569
GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_A	101	-0.6237242	-1.2953839
GO_CELLULAR_RESPONSE_TO_PEPTIDE	233	-0.58692175	-1.2951308
GO_NEGATIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR	60	-0.6533085	-1.296137
GO_RESPONSE_TO_PROSTAGLANDIN_E	24	-0.7445781	-1.2953407
NKX61_01	176	-0.60081786	-1.2963411
GO_INTERMEDIATE_FILAMENT_BASED_PROCESS	28	-0.7225801	-1.2962646
GO_INSULIN_RECEPTOR_BINDING	29	-0.72714084	-1.2970047
GO_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_K	261	-0.59138453	-1.2964982
GO_CELLULAR_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	95	-0.6301414	-1.2972761
GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	28	-0.7208249	-1.2966317
GO_REGULATION_OF_VASCULAR_PERMEABILITY	28	-0.73491424	-1.2975725
NKX22_01	141	-0.6102952	-1.29698
GO_REGULATION_OF_ORGAN_MORPHOGENESIS	207	-0.5937481	-1.297499
GO_REGULATION_OF_PROTEIN_HOMOOLOGOMERIZATION	15	-0.7942096	-1.2972454
GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	137	-0.6186217	-1.2974359
GO_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	54	-0.6723608	-1.2971853
GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	130	-0.6154753	-1.2969743
GO_REGULATION_OF_PROTEIN_SECRETION	316	-0.5867887	-1.2969592
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFEREN	41	-0.6810087	-1.2968988
PAX3_B	76	-0.64706725	-1.2986878
GO_MUSCLE_TISSUE_DEVELOPMENT	206	-0.5937419	-1.2992024
GO_ENDOSOMAL_PART	395	-0.58548266	-1.2987905
GO_VACUOLE_ORGANIZATION	156	-0.6078749	-1.2978815
GO_POSITIVE_REGULATION_OF_HEART_RATE	17	-0.7786275	-1.2979652
GO_MANNOSE_BINDING	15	-0.7850971	-1.2986478
GO_REGULATION_OF_THYMOCYTE_AGGREGATION	22	-0.7382465	-1.2991602
GO_REGULATION_OF_MUSCLE_ADAPTATION	56	-0.6628221	-1.2990979
GO_PODOSOME	23	-0.759422	-1.2990155
GO_SARCOPLASM	58	-0.6622105	-1.2986197
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	127	-0.6164601	-1.2989792
GO_METANEPHROS_DEVELOPMENT	58	-0.67464036	-1.2986053
GO_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_RECEPTO	17	-0.7698597	-1.298578
GO_REGULATION_OF_MEMBRANE_POTENTIAL	275	-0.588706	-1.2985487
KEGG_REGULATION_OF_AUTOPHAGY	20	-0.75830144	-1.2984056
GO_INOSITOL_PHOSPHATE_METABOLIC_PROCESS	54	-0.6681675	-1.2983232
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_I	25	-0.7340136	-1.2985008

GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	20	-0.7571097	-1.3001221
SOX9_B1	204	-0.5984356	-1.3013008
GO_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	328	-0.5910473	-1.3012345
GO_LYSOSOMAL_TRANSPORT	64	-0.65510094	-1.3012192
CEBPA_O1	192	-0.6021553	-1.3015286
NFY_Q6_O1	233	-0.5975652	-1.3012065
GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PF	26	-0.7366199	-1.300849
GO_PROTEIN_SERINE_THREONINE_TYROSINE_KINASE_ACTIVITY	38	-0.699253	-1.3010375
GO_ENDOMEMBRANE_SYSTEM_ORGANIZATION	441	-0.5821628	-1.3007948
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUN	42	-0.69632876	-1.3009801
HSF2_O1	194	-0.5948222	-1.3017132
E47_O1	207	-0.59535486	-1.3011986
GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	112	-0.62042296	-1.3018724
GO_CILIARY_TRANSITION_ZONE	24	0.6948719	1.4034233
GO_NCRNA_3_END_PROCESSING	20	0.72476363	1.4033467
GO_STRUCTURE_SPECIFIC_DNA_BINDING	102	0.54860014	1.4046215
GO_RIBOSOME_ASSEMBLY	49	0.6186102	1.3998489
GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROC	17	0.74055964	1.4031426
PBX1_O1	192	-0.6064535	-1.3028641
GO_HETEROTYPIC_CELL_CELL_ADHESION	26	-0.7356483	-1.3027855
GO ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	51	0.6216245	1.4030577
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP	20	0.71964014	1.4009767
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	126	0.5416697	1.4028472
VDR_Q3	182	-0.6092242	-1.30382
RYTGCNWTGGR_UNKNOWN	96	-0.63610584	-1.3037592
GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	287	0.4784813	1.4024338
GO_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	476	-0.5808401	-1.303712
GO_REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	143	-0.6104134	-1.303561
GO_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	46	-0.6883835	-1.3037069
GO_ANAPHASE_PROMOTING_COMPLEX	20	0.7293212	1.4019854
GO_REGULATION_OF_CARDIAC_CONDUCTION	60	-0.6577678	-1.3043317
GO_ORGAN_GROWTH	51	-0.6802743	-1.3045156
GO_HINDBRAIN_DEVELOPMENT	106	-0.63238555	-1.3043077
GO_PROTEIN_POLYMERIZATION	61	-0.6635409	-1.3044742
GCCNNNWTAAAR_UNKNOWN	125	-0.6161395	-1.3042655
GO_EPITHELIAL_CELL_PROLIFERATION	76	-0.6456792	-1.3048925
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICIT	15	-0.79567546	-1.305502
GO_REGULATION_OF_CELL_MATRIX_ADHESION	82	-0.64200133	-1.3054594
OCT1_O6	201	-0.59907734	-1.3057901
GO_GASTRULATION	129	-0.61538446	-1.3060076
GO_GLIAL_CELL_DIFFERENTIATION	106	-0.6248816	-1.3060036
GO_PROTEIN_LOCALIZATION_TO_LYSOSOME	17	0.755067	1.4078159
GO_BILE_ACID_BIOSYNTHETIC_PROCESS	16	0.76816136	1.4087687
GO_CORE_PROMOTER_BINDING	126	-0.6200629	-1.3066386
GO_B_CELL_PROLIFERATION	20	-0.7692192	-1.3068739
GO_DNA_POLYMERASE_ACTIVITY	33	0.6694595	1.4191256
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	54	0.6089449	1.4209181
GO_PSEUDOURIDINE_SYNTHESIS	17	0.7488571	1.4129018
GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	19	0.7453284	1.4140031
GO_FIBRINOLYSIS	16	-0.77589405	-1.307491
GO_FATTY_ACID_TRANSPORT	45	0.6354341	1.4190799

GO_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	187	0.52011687	1.4121197
GO_WALKING_BEHAVIOR	22	0.71913594	1.4149035
GO_MEIOTIC_CELL_CYCLE_PROCESS	119	0.5399615	1.412769
GO_SMALL_RIBOSOMAL_SUBUNIT	67	0.5943106	1.4165791
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	18	0.7423555	1.4209117
GO_STRAND_DISPLACEMENT	26	0.7020253	1.4171253
KEGG_ONE_CARBON_POOL_BY_FOLATE	16	0.76626897	1.4107062
GO_MITOCHONDRIAL_MEMBRANE_PART	154	0.5194038	1.4139501
GO_SNRNA_PROCESSING	21	0.71133375	1.4161733
GO_NCRNA_TRANSCRIPTION	81	0.5661461	1.411327
GO_MONOCARBOXYLIC_ACID_TRANSPORT	91	0.5650222	1.4189937
GO_S_ACYLTRANSFERASE_ACTIVITY	27	0.6875671	1.4206662
GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PRC	21	-0.74197066	-1.3080167
GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	19	0.72427446	1.415723
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_B	18	0.7599709	1.4184695
GO_CONDENSED_CHROMOSOME	177	0.50492054	1.4120572
GO_POSITIVE_REGULATION_OF_LYASE_ACTIVITY	39	-0.70505595	-1.3084403
TTNNANAGCYR_UNKNOWN	105	0.5568532	1.4181173
GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATI	155	-0.6187709	-1.3084385
GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	106	-0.63675165	-1.3082838
GO_POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHOF	133	-0.61454487	-1.308404
GO_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	48	-0.68400246	-1.30885
GO_BONE_REMODELING	31	-0.71140605	-1.3093764
GO_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	219	-0.60201734	-1.3092965
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFEREN	33	-0.71823496	-1.3092252
GO_REGULATION_OF_ION_TRANSPORT	472	-0.5837492	-1.3095729
GO_CELLULAR_RESPONSE_TO_FATTY_ACID	47	-0.69242084	-1.3096559
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	100	-0.6373998	-1.3103355
GO_EMBRYONIC_HINDLIMB_MORPHOGENESIS	21	-0.77314585	-1.3095592
GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	301	-0.5923091	-1.309925
GO_INORGANIC_ION_TRANSMEMBRANE_TRANSPORT	431	-0.5860228	-1.3102927
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SU	21	-0.75153834	-1.3104697
GO_ACTIN_NUCLEATION	23	-0.758393	-1.3101426
GO_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME	16	-0.8019536	-1.3102661
GO_LAMELLIPODIUM_ORGANIZATION	35	-0.71554613	-1.3099189
GO_RENAL_SYSTEM_VASCULATURE_DEVELOPMENT	16	-0.7880115	-1.310741
GO_NEGATIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_A	18	-0.77122146	-1.310107
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRAN	382	-0.58673257	-1.3107195
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	18	-0.7690094	-1.3110725
GO_DNA_RECOMBINATION	188	0.51569396	1.4239317
GO_REGULATION_OF_CIRCADIAN_RHYTHM	85	-0.65141976	-1.3113992
GO_GLYOXYLATE_METABOLIC_PROCESS	23	0.71081644	1.424756
GO_MESENCHYME_DEVELOPMENT	135	-0.6182217	-1.3124111
GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSPORT	34	-0.7160441	-1.313119
GO_EMBRYONIC_ORGAN_DEVELOPMENT	314	-0.5904471	-1.3132162
GO_STEM_CELL_DIFFERENTIATION	141	-0.62095284	-1.3125169
TITF1_Q3	186	-0.60393345	-1.3119673
GO_NEGATIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOL	100	-0.63234955	-1.3127911
GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_AC	169	-0.6093554	-1.3123602
GO_MUSCLE_CELL_CELLULAR_HOMEOSTASIS	17	-0.7707899	-1.313086
GO_POSITIVE_REGULATION_OF_DNA_RECOMBINATION	16	-0.79745406	-1.3126514

GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	37	0.6484562	1.4257164
GO_NEURON_MIGRATION	79	-0.65059024	-1.3129297
GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_TRANSPOSI	19	-0.7734634	-1.3127851
GO_ECTODERM_DEVELOPMENT	16	-0.7793969	-1.3123584
GO_NEGATIVE_REGULATION_OF_AXON_EXTENSION	34	-0.7309166	-1.3130713
GO_PROTEIN_LOCALIZATION_TO_CYTOSKELETON	28	-0.7337372	-1.3122216
GO_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	26	-0.73817426	-1.3123561
GO_SMN_SM_PROTEIN_COMPLEX	15	0.7861969	1.4265454
GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_	16	0.77351	1.4271195
PAX3_01	15	-0.783312	-1.3136204
GO_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	32	-0.71824044	-1.313744
GO_DORSAL_VENTRAL_AXIS_SPECIFICATION	19	-0.7766898	-1.3138783
NFAT_Q6	197	-0.60703593	-1.3141603
GO_MORPHOGENESIS_OF_EMBRYONIC_EPITHELIUM	110	-0.6253141	-1.3141414
GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	42	-0.7062611	-1.3152944
GO_REGULATION_OF_METAL_ION_TRANSPORT	269	-0.60029143	-1.3152086
GO_KIDNEY_MORPHOGENESIS	62	-0.667909	-1.3151653
GO_CALCIIUM_ION_IMPORT_INTO_CYTOSOL	35	-0.7109548	-1.3151293
COREBINDINGFACTOR_Q6	232	-0.60322326	-1.315053
HFH1_01	195	-0.60925496	-1.3155313
GO_INNATE_IMMUNE_RESPONSE	468	-0.5827891	-1.3157856
GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	61	0.60547924	1.4293683
GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CE	33	-0.7350777	-1.3160381
GO_REGULATION_OF_INTERLEUKIN_13_PRODUCTION	15	-0.797706	-1.3166158
GO_REGULATION_OF_LIPASE_ACTIVITY	70	-0.6626005	-1.3165898
KEGG_PROSTATE_CANCER	85	-0.654844	-1.3165382
PAX6_01	84	-0.6539228	-1.3171126
GO_SENSORY_ORGAN_DEVELOPMENT	373	-0.5936654	-1.3176513
GO_FAT_CELL_DIFFERENTIATION	92	-0.63768333	-1.3178629
GO_SYNAPTIC_MEMBRANE	185	-0.611893	-1.3181504
GO_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	28	-0.74127537	-1.318312
GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	24	-0.7596997	-1.318414
GO_REGULATION_OF_CYTOSKELETON_ORGANIZATION	456	-0.59093165	-1.3188614
GO_CHROMOSOME_CONDENSATION	23	0.7260271	1.4320718
NFKB_Q6_01	204	-0.604814	-1.3189893
NKX25_01	93	-0.6435712	-1.3188405
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	197	-0.60820067	-1.3192047
GO_CELL_LEADING_EDGE	320	-0.6004688	-1.3187857
GO_MESODERM_DEVELOPMENT	94	-0.6460737	-1.31916
GO_GLUCURONOSYLTRANSFERASE_ACTIVITY	16	-0.79270905	-1.3187399
GO_ENDORIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOM	26	0.6973591	1.4328482
GO_AXONAL_GROWTH_CONE	18	-0.7788977	-1.3193735
GO_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	15	-0.8006837	-1.3205191
SMAD3_Q6	183	-0.6158548	-1.3204554
GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	24	-0.7588699	-1.3208266
GO_NEPHRON_DEVELOPMENT	91	-0.6506246	-1.3209432
GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	56	-0.6669676	-1.3207878
GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION	135	-0.6241957	-1.3204468
GO_NEGATIVE_REGULATION_OF_CALCIIUM_ION_TRANSPORT_IN	16	-0.77681726	-1.3207636
GO_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	33	-0.72042066	-1.3204253
GO_EMBRYONIC_PLACENTA_MORPHOGENESIS	18	-0.7793662	-1.321176

GO_ENDOCYTOSIS	439	-0.59364504	-1.3203748
GO_REGULATION_OF_STEROID_METABOLIC_PROCESS	61	-0.6726418	-1.3200731
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPO	46	-0.69620216	-1.3203601
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGR	16	-0.79979545	-1.3213995
GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	20	-0.7791701	-1.3200376
AP4_01	214	-0.61243886	-1.3198401
GO_POSITIVE_REGULATION_OF_COAGULATION	20	-0.77725005	-1.3202343
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_MOVEMENT	29	-0.7298364	-1.3199672
GO_Glutamate_Receptor_Binding	34	-0.70854497	-1.3203483
GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNAL	15	-0.80048835	-1.3217691
GO_FC_RECEPTOR_SIGNALING_PATHWAY	182	-0.6128139	-1.3225745
STAT6_01	205	-0.608839	-1.3224949
AAAYRNCTG_UNKNOWN	314	-0.5981748	-1.3224463
GO_ERBB_SIGNALING_PATHWAY	73	-0.6550092	-1.3217589
GO_SOLUTE_CATION_SYMPORTER_ACTIVITY	69	-0.6628434	-1.322434
AREB6_04	210	-0.6031552	-1.3223907
GO_REGULATION_OF_PHOSPHATASE_ACTIVITY	111	-0.6383598	-1.3230505
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	16	-0.79629904	-1.3229556
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING	86	-0.6485964	-1.3231475
MYAATNNNNNNNGGC_UNKNOWN	85	-0.64909285	-1.3233562
STAT3_01	20	-0.7709356	-1.3232687
GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPME	349	-0.59684247	-1.3229148
GO_LYMPHOCYTE_HOMEOSTASIS	49	-0.68462145	-1.3223802
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUC	57	-0.6766651	-1.3235078
GO_BASAL_PLASMA_MEMBRANE	31	-0.72129387	-1.3223656
GO_BETA_CATENIN_BINDING	76	-0.65344095	-1.3222642
GO_POSITIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	81	-0.65621424	-1.3223584
GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS	24	0.71660566	1.4353622
GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	153	-0.6292736	-1.3242861
GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	26	-0.7465553	-1.3245562
GO_ANATOMICAL_STRUCTURE_MATURATION	35	-0.72368485	-1.3245444
GO_SUBPALLIUM_DEVELOPMENT	16	-0.81269556	-1.3247217
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	92	-0.64146256	-1.324852
GO_NEGATIVE_REGULATION_OF_PROTEIN_BINDING	74	-0.6690527	-1.3249817
GO_EXONUCLEASE_ACTIVITY	73	0.59192425	1.4375082
GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	20	0.762025	1.4381719
GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_I	432	-0.5906589	-1.3252492
GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	18	-0.7899714	-1.3254225
MMEF2_Q6	207	-0.6129265	-1.3255628
GO_RETINA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	100	-0.64572126	-1.3257505
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	43	0.65149814	1.4373988
GO_MYOSIN_II_COMPLEX	16	-0.8102252	-1.3262788
GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSI	33	-0.7273572	-1.3262181
GO_FATTY_ACID_BINDING	25	-0.7519149	-1.3264037
GO_FRIZZLED_BINDING	29	-0.7352102	-1.3265249
KEGG_PYRUVATE_METABOLISM	37	0.6747914	1.43737
GO_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	42	-0.7065616	-1.3266649
GO_BONE_RESORPTION	19	-0.78249484	-1.3270655
GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	171	-0.6185017	-1.3270322
GO_ADHERENS_JUNCTION_ORGANIZATION	65	-0.66883916	-1.3270077
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMER	31	-0.7373582	-1.3269175

RAAGNYNNCTTY_UNKNOWN	116	-0.6301191	-1.3274347
ELK1_01	244	-0.5972966	-1.3274109
GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIUM_I	15	-0.7897286	-1.3278035
GO_REGULATION_OF_GLUCOSE_IMPORT	50	-0.68529886	-1.3277706
KEGG_MTOR_SIGNALING_PATHWAY	50	-0.70366186	-1.3284508
GO_RESPONSE_TO_KETONE	161	-0.6200885	-1.3282591
GO_REGULATION_OF_BLOOD_PRESSURE	128	-0.6300141	-1.32836
FAC1_01	174	-0.6142235	-1.3286378
HFH3_01	156	-0.62607926	-1.3285719
FOXO4_02	216	-0.60983187	-1.3282019
GO_EXCITATORY_SYNAPSE	170	-0.6170629	-1.3288116
GO_REGULATION_OF_HEART_CONTRACTION	168	-0.6169509	-1.3281537
GO_TRNA_BINDING	42	0.6685752	1.4411465
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	24	0.72139835	1.4447585
GO_DEOXYRIBONUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROC	16	0.79214543	1.442503
DBP_Q6	194	-0.6198846	-1.3291215
GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PI	59	-0.67165154	-1.3292897
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_KINASE_ACTIVITY	15	-0.8102464	-1.3294204
GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	21	0.7311669	1.4409796
GO_NUCLEOTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	19	0.7581227	1.4446536
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	65	-0.67862046	-1.3297211
GO_SYNAPTONEMAL_COMPLEX	27	0.6941499	1.4423988
GO_CELL_CELL_CONTACT_ZONE	60	-0.68035084	-1.3300667
GO_RRNA_TRANSCRIPTION	17	0.7670958	1.4470199
GO_EMBRYONIC_DIGESTIVE_TRACT_DEVELOPMENT	22	-0.7826244	-1.3299099
GO_ANION_CHANNEL_ACTIVITY	60	-0.6828161	-1.3300277
GO_90S_PRERIBOSOME	23	0.7239139	1.4445126
GO_RAN_GTPASE_BINDING	29	0.6870931	1.4490488
AP4_Q5	228	-0.6085664	-1.3304454
GO_NUCLEASE_ACTIVITY	182	0.5242991	1.4479516
GO_AMINOGLYCAN_BIOSYNTHETIC_PROCESS	94	-0.6525368	-1.330542
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRAI	17	0.75894266	1.4462548
GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	122	0.56486607	1.4441402
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	106	0.55613315	1.4486165
GO_HORMONE_ACTIVITY	55	0.6105771	1.4498456
GO_EXCRETION	28	0.6895362	1.4469396
GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	47	-0.6985248	-1.331063
GO_PANCREAS_DEVELOPMENT	49	-0.6905542	-1.33158
GO_DENDRITIC_SPINE_ORGANIZATION	16	-0.7994201	-1.3310314
GO_REGULATION_OF_ARP2_3_COMPLEX_MEDIATED_ACTIN_NU	15	-0.812952	-1.3317186
GO_POSITIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	32	-0.7293148	-1.3315524
GO_CELL_KILLING	41	-0.7085302	-1.3309926
GO_AUDITORY_RECEPTOR_CELL_DIFFERENTIATION	23	-0.7602979	-1.3314701
GO_HAIR_CELL_DIFFERENTIATION	27	-0.74212366	-1.3309301
GO_REGULATION_OF_LYASE_ACTIVITY	57	-0.68419564	-1.3314092
AP1_Q4_01	220	-0.609861	-1.3314008
GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	19	0.7580917	1.4523592
GO_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	175	-0.62012064	-1.3324761
GO_RESPONSE_TO_STEROL	21	-0.77028185	-1.3323814
GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	226	0.5109038	1.4538305
GO_NEGATIVE_REGULATION_OF_COAGULATION	38	-0.7178386	-1.3328593

GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	16	0.76737607	1.4522686
KEGG_RNA_POLYMERASE	29	0.68470186	1.4535663
GO_MITOTIC_NUCLEAR_DIVISION	343	0.5050144	1.4518601
NFKB_Q6	223	-0.60718375	-1.333865
GO_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS	225	-0.6162655	-1.3338012
GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	34	-0.72494125	-1.3340739
GO_TRNA_TRANSPORT	33	0.6912113	1.455693
GO_COCHLEA_MORPHOGENESIS	19	-0.7795353	-1.3342679
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_SIGNALING_PATHWAY	24	-0.7655183	-1.3343995
GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	106	-0.64891887	-1.3348202
GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	31	-0.7326681	-1.3350196
GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	361	-0.6002869	-1.3352063
GO_DOPAMINE_RECEPTOR_SIGNALING_PATHWAY	22	-0.77771515	-1.3353573
GO_DNA_SECONDARY_STRUCTURE_BINDING	23	0.74253184	1.4626743
GO_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CHROMOSOMES	15	0.8010566	1.4622258
GO_PHOSPHATIDYLINOSITOL_METABOLIC_PROCESS	167	-0.61732745	-1.3364366
GO_REGULATION_OF_CALCINEURIN_NFAT_SIGNALING_CASCADE	15	-0.8068583	-1.3359758
GO_POSITIVE_REGULATION_OF_G1_S_TRANSITION_OF_MITOTIC_CYCLE	22	0.74015033	1.46057
GO_REGULATION_OF_SYNAPTIC_PLASTICITY	113	-0.6434248	-1.3368161
GO_MUSCLE_ORGAN_DEVELOPMENT	211	-0.61373097	-1.3360838
GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	138	-0.6268724	-1.335919
KEGG_BASAL_CELL_CARCINOMA	48	-0.69835013	-1.3364247
GO_INNERVATION	17	-0.79912084	-1.3369964
GO_RESPONSE_TO_PROTOZOAN	18	-0.7895542	-1.3368102
GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	56	-0.68967944	-1.3359095
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA	19	0.75218713	1.4601035
GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PROTEIN_IMPORT	18	-0.7858416	-1.3367556
GO_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	22	-0.770456	-1.3364195
GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	89	-0.64727795	-1.3371686
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	123	0.56038684	1.4613689
GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	34	-0.72638595	-1.3367472
GO_REGULATION_OF_CARBOHYDRATE_CATABOLIC_PROCESS	37	-0.71255034	-1.3363856
GO_LONG_CHAIN_FATTY_ACID_TRANSPORT	33	0.6855745	1.4620808
GO_MATURATION_OF_5_8S_RRNA	28	0.712777	1.4596822
GO_MODULATION_OF_SYNAPTIC_TRANSMISSION	239	-0.6088062	-1.3375194
GO_ORGANELLE_INNER_MEMBRANE	467	0.4778594	1.457827
GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	387	-0.5968535	-1.3374627
ACTWSNACTNY_UNKNOWN	89	0.5706713	1.4592023
GO_REGULATION_OF_CYTOKINE_PRODUCTION	498	-0.5977606	-1.3380756
GO_CHEMOKINE_BINDING	17	-0.7939631	-1.3379911
GO_COATED_PIT	64	-0.67828226	-1.337802
GO_REGULATION_OF_CHOLESTEROL_EFFLUX	18	-0.7913341	-1.3379885
GO_RESPONSE_TO_NERVE_GROWTH_FACTOR	32	-0.7266944	-1.3382953
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP	22	0.7396685	1.4587725
GO_INTERACTION_WITH_HOST	125	-0.6377846	-1.3379525
GATA6_01	201	-0.6168491	-1.3384477
TGASTMAGC_NFE2_01	173	-0.62627274	-1.3388216
PU1_Q6	202	-0.62226766	-1.3387738
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	34	-0.7374901	-1.3387625
GO_SYMPORTER_ACTIVITY	103	-0.6458261	-1.338737
GAANNYNYGACNY_UNKNOWN	62	-0.6714383	-1.3391232

GO_MUSCLE_STRUCTURE_DEVELOPMENT	337	-0.60696536	-1.3402503
GO_CORE_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	83	-0.65761817	-1.3401684
P53_02	211	-0.61375785	-1.3401259
PAX2_02	205	-0.61684495	-1.3407928
GO_POSITIVE_REGULATION_OF_PROTEIN_SECRETION	173	-0.62439364	-1.340708
GO_CELLULAR_RESPONSE_TO_HYDROGEN_PEROXIDE	58	-0.6837796	-1.3400966
GO_EYE_DEVELOPMENT	249	-0.6120426	-1.3409699
GO_CELLULAR_RESPONSE_TO_ALCOHOL	96	-0.65642506	-1.3406959
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	31	-0.75630075	-1.3406191
GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	234	-0.61008143	-1.3400773
GO_EMBRYONIC_MORPHOGENESIS	424	-0.60233444	-1.3411385
P53_DECAMER_Q2	218	-0.6066043	-1.3400478
GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	194	-0.61315405	-1.3406159
GO_RESPONSE_TO_INORGANIC_SUBSTANCE	402	-0.60092044	-1.3396972
KEGG_TASTE_TRANSDUCTION	29	-0.7389714	-1.3412837
GO_SECRETORY GRANULE MEMBRANE	62	-0.68202275	-1.339811
GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	282	-0.60842556	-1.3400102
FOXJ2_01	145	-0.6398832	-1.3400087
GO_MESODERMAL_CELL_DIFFERENTIATION	22	-0.76438916	-1.341701
HNF3B_01	162	-0.6336169	-1.3416742
GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	182	-0.6258045	-1.3418722
GO_GROWTH_FACTOR_ACTIVITY	111	-0.64414203	-1.3415892
GO_SYNAPTONEMAL_COMPLEX_ORGANIZATION	15	0.79643685	1.46584
GO_MYOFIBRIL_ASSEMBLY	33	-0.73224205	-1.3424329
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNA	117	-0.6402032	-1.3427446
GO_AMIDE_BIOSYNTHETIC_PROCESS	466	0.50826246	1.4670215
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	22	0.74773216	1.4678506
GO_NEUTROPHIL_MEDIATED_IMMUNITY	21	-0.77355295	-1.3432363
GO_NUCLEAR_EXPORT	139	0.53976333	1.4686947
GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEV	20	-0.7847266	-1.3436009
GO_ANION_TRANSMEMBRANE_TRANSPORT	181	-0.62791723	-1.3437811
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	143	-0.6374464	-1.3435922
GO_REGULATION_OF_EXOSOMAL_SECRETION	17	-0.80047095	-1.3440789
GO_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	44	-0.7085245	-1.3435221
GO_SIGNAL_RELEASE	125	-0.63748366	-1.3440578
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	60	-0.69486636	-1.3440232
GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_	32	0.6976133	1.469773
GO_NEGATIVE_REGULATION_OF_NEURON_DIFFERENTIATION	159	-0.62944144	-1.3444848
GO_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATI	274	-0.610607	-1.3448887
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	106	-0.6546887	-1.3451955
GO_EPHRIN_RECEPTOR_BINDING	21	-0.77839243	-1.3452986
GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BINDING	28	-0.7338805	-1.3454516
GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATH	42	-0.7196155	-1.3450799
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACT	187	-0.63057935	-1.3448877
GO_CELLULAR_RESPONSE_TO_KETONE	66	-0.67392653	-1.3451955
GO_NUCLEAR_CHROMOSOME	456	0.5027679	1.4710939
GO_GROWTH	327	-0.6107628	-1.3458592
AR_03	47	-0.7046948	-1.3461403
GO_POSITIVE_REGULATION_OF_CELL_GROWTH	131	-0.63386375	-1.3460858
GO_CARBOHYDRATE_DERIVATIVE_CATABOLIC_PROCESS	154	-0.62563074	-1.3460033
GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVIT	101	-0.64648384	-1.3467256

GO_TRNA_MODIFICATION	55	0.6409405	1.4739019
GO_LEUKOCYTE_MEDIATED_IMMUNITY	136	-0.63503116	-1.3464645
GO_STRIATED_MUSCLE_CONTRACTION	79	-0.66869307	-1.3470438
GO_MONOSACCHARIDE_TRANSPORT	44	-0.7084914	-1.3468603
GO_COCHLEA_DEVELOPMENT	30	-0.7362137	-1.3471496
GO_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA	23	-0.76122904	-1.346719
ELF1_Q6	217	-0.61623615	-1.3466338
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZA	40	-0.720649	-1.3481693
GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	81	-0.6689524	-1.3470122
GO_REGULATION_OF_DEPHOSPHORYLATION	138	-0.6352074	-1.347307
KEGG_NUCLEOTIDE_EXCISION_REPAIR	43	0.6686523	1.4745843
EVI1_Q6	16	-0.8020931	-1.3481339
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	53	0.6386156	1.4722459
GO_REGULATION_OF_BONE_REMODELING	31	-0.7410521	-1.3480636
GO_FORMATION_OF_PRIMARY_GERM_LAYER	95	-0.6595958	-1.3479701
GO_HEART_DEVELOPMENT	387	-0.60957044	-1.3479247
GO_PHOTORECEPTOR_INNER_SEGMENT	23	-0.7781918	-1.3478802
GO_ORGANIC_CATION_TRANSPORT	15	-0.818876	-1.3476449
GO_REGULATION_OF_CYTOKINE_SECRETION	122	-0.64128536	-1.3478752
GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	17	-0.8060925	-1.34781
GO_CAJAL_BODY	45	0.6511325	1.4738729
GO_MEIOSIS_I	67	0.6158946	1.4732713
GO_NEGATIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTI	32	-0.74586856	-1.3488728
GO_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_FROM_RNA_	17	-0.8006342	-1.3492807
GO_RESPONSE_TO_BACTERIUM	389	-0.60520893	-1.3495458
GO_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	108	-0.65264994	-1.3494833
GO_NEGATIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALIN	17	-0.81269294	-1.3497053
GO_REGULATION_OF_CAMP_METABOLIC_PROCESS	90	-0.65738785	-1.3498706
GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	37	-0.73450303	-1.3500904
HNF4ALPHA_Q6	218	-0.6215952	-1.3500276
GO_OLIGODENDROCYTE_DIFFERENTIATION	45	-0.71360886	-1.3507317
MYOD_Q6	206	-0.6194202	-1.350889
GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	65	-0.6843795	-1.3506056
GO_ENDOCYTIC_RECYCLING	23	-0.77576756	-1.3507156
GO_REGULATION_OF_STEM_CELL_PROLIFERATION	73	-0.67666686	-1.3511488
CCTNTMAGA_UNKNOWN	106	-0.64427775	-1.3513317
GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEI	98	-0.6561713	-1.3516484
GO_CYTOKINE_BINDING	76	-0.6690138	-1.3516387
GO_PERIKARYON	74	-0.67344767	-1.3515723
GO_REGULATION_OF_HEMOPOIESIS	272	-0.61126727	-1.3519706
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTIC	21	-0.7875299	-1.3519397
GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_I	17	-0.79714715	-1.3524513
GO_NEGATIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGAN	15	-0.83228683	-1.3531756
GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	27	-0.76838964	-1.3535436
KEGG_GNRH_SIGNALING_PATHWAY	82	-0.66894275	-1.3533773
GO_MUSCLE_CELL_DEVELOPMENT	93	-0.65316796	-1.3534651
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_IOI	23	-0.77832204	-1.3537234
GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATI	51	-0.7110911	-1.3538988
GO_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGR	46	-0.7168783	-1.3542284
T3R_Q6	194	-0.6238477	-1.354445
GO_RELAXATION_OF_MUSCLE	19	-0.80411315	-1.3546168

GO_ENZYME_ACTIVATOR_ACTIVITY	426	-0.59906995	-1.3547305
GO_CARBOHYDRATE_TRANSPORT	78	-0.6730564	-1.3552259
GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	69	-0.67515045	-1.3554809
GO_EPIBOLY	19	-0.8058141	-1.3553953
GO_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	18	0.7611147	1.48039
GO_INNER_EAR_MORPHOGENESIS	69	-0.6854391	-1.3559159
SOX5_01	218	-0.62147474	-1.3563372
GO_CELL_RECOGNITION	103	-0.6564567	-1.3560389
GO_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	27	-0.74845815	-1.3562454
TFIII_Q6	167	-0.63899755	-1.3561795
GO_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	244	-0.6197821	-1.3567885
GO_NEGATIVE_REGULATION_OF_LIPID_STORAGE	15	-0.83243793	-1.3569182
GO_T_CELL_PROLIFERATION	33	-0.74506557	-1.3570852
GO_NEGATIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	110	-0.6454946	-1.3573117
YNTTTNNNANGCARM_UNKNOWN	45	-0.70994776	-1.357307
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	31	-0.76128334	-1.3576111
GO_DEMETHYLASE_ACTIVITY	30	-0.7484414	-1.3577286
GO_AMMONIUM_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	21	-0.78104556	-1.3575186
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ONE_CARBON_GROUP	185	0.5405215	1.4823483
GO_REGULATION_OF_PH	74	-0.6792793	-1.3582311
TAL1BETA47_01	198	-0.63235897	-1.3584483
GO_METHYLATION	238	0.523022	1.4852604
GO_FATTY_ACYL_COA_BINDING	29	0.7197796	1.4834265
GO_POSITIVE_REGULATION_OF_GROWTH	199	-0.6233645	-1.3587857
GO_CELLULAR_PROTEIN_COMPLEX_LOCALIZATION	22	-0.7913381	-1.358947
GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	21	0.7665661	1.4849685
GO_PRERIBOSOME_LARGE_SUBUNIT_PRECURSOR	20	0.7740039	1.4847237
GO_RRNA_MODIFICATION	26	0.75271356	1.486606
GO_CELLULAR_RESPONSE_TO_OSMOTIC_STRESS	20	-0.7964307	-1.3598646
GO_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	42	-0.73138154	-1.3598351
GO_METAL_ION_TRANSPORT	438	-0.6125661	-1.3606362
KCCGNSWTTT_UNKNOWN	94	-0.6641795	-1.3604403
GO_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	31	-0.7512569	-1.3603734
GO_ESTABLISHMENT_OF_ENDOTHELIAL_BARRIER	29	-0.7608505	-1.3605922
GO_ANCHORING_JUNCTION	463	-0.60987157	-1.3603499
GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	27	-0.75428516	-1.3602103
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATION_OF_CALCIUM	18	-0.79462487	-1.3603354
AP3_Q6	183	-0.6312073	-1.361003
GO_NEGATIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	47	-0.71408767	-1.3611808
GO_ENDOCYTIC_VESICLE	227	-0.6261104	-1.3613756
GO_RECYCLING_ENDOSOME	111	-0.6544797	-1.3615965
CREL_01	219	-0.62638426	-1.3617188
CART1_01	167	-0.629779	-1.3624465
GO_LIMBIC_SYSTEM_DEVELOPMENT	68	-0.6820145	-1.3624023
GO_Glutamate_SECRETION	25	-0.77294576	-1.3623081
IK1_01	223	-0.62416077	-1.3622403
GO_COFACTOR_CATABOLIC_PROCESS	16	0.7835286	1.490652
GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX	18	0.7947278	1.4900542
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY_INHIBITION	20	-0.7916265	-1.3622106
GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	29	-0.7561634	-1.36204
VDR_Q6	207	-0.63075376	-1.3635001

GO_U12_TYPE_SPLICEOSOMAL_COMPLEX	25	0.7322358	1.4895126
GO_CARDIAC_CELL_DEVELOPMENT	34	-0.7335188	-1.3636171
GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	235	-0.62452817	-1.3621969
GO_REGULATION_OF_BONE_RESORPTION	26	-0.7732803	-1.3637536
GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	140	-0.64467365	-1.3634945
KEGG_ERBB_SIGNALING_PATHWAY	81	-0.67694247	-1.3630742
GO_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	18	-0.8155182	-1.3630018
GO_REGULATION_OF_SYNAPSE_ORGANIZATION	86	-0.6696028	-1.3634847
GO_NEURON_PROJECTION_REGENERATION	27	-0.7742631	-1.3634146
KEGG_PROPANOATE_METABOLISM	32	0.70018995	1.4891145
GO_SH2_DOMAIN_BINDING	29	-0.75430614	-1.3632331
GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVI	18	-0.8327073	-1.3629763
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_REGULATOR_ACTIVITY_IN	38	-0.7331947	-1.3633748
YATTNATC_UNKNOWN	270	-0.6237965	-1.3642944
GO_CHROMOSOME_CENTROMERIC_REGION	163	0.54998034	1.4924756
CATTGTYT_SOX9_B1	307	-0.6205182	-1.3652081
GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	73	-0.675702	-1.3651654
GO_RNA_METHYLTRANSFERASE_ACTIVITY	42	0.6695152	1.4935621
GO_NUCLEOBASE_METABOLIC_PROCESS	35	0.7034731	1.4942714
AP1_Q6	221	-0.62811625	-1.3661547
KEGG_NON_SMALL_CELL_LUNG_CANCER	53	-0.7045929	-1.3662997
GO_SEMAPHORIN_RECEPTOR_BINDING	21	-0.80316544	-1.3665661
GO_CONDENSED_NUCLEAR_CHROMOSOME	73	0.614351	1.4963616
GO_RESPONSE_TO_ORGANOPHOSPHORUS	122	-0.65019447	-1.3671942
GATA1_01	195	-0.63165694	-1.3673356
GO_NEUROMUSCULAR_JUNCTION	48	-0.71102935	-1.3671894
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	331	-0.6215457	-1.3675497
GO_PROTEIN_DEPHOSPHORYLATION	175	-0.6382055	-1.3676884
GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	16	-0.8144624	-1.3685796
GO_HEPARAN_SULFATE_PROTEOGLYCAN_BINDING	15	-0.8522419	-1.3684785
GO_CELL_CORTEX_PART	109	-0.6598354	-1.3684074
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATIC	41	-0.73161906	-1.368106
HNF1_01	164	-0.6326153	-1.3680422
GO_OLIGODENDROCYTE_DEVELOPMENT	25	-0.7770577	-1.3683727
ZIC2_01	205	-0.6267859	-1.3682975
GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	257	-0.62299174	-1.3680097
GO_NERVE_DEVELOPMENT	48	-0.71054965	-1.369103
GO_CORTICAL_ACTIN_CYTOSKELETON	56	-0.6982258	-1.3690106
GO_BONE_GROWTH	15	-0.8077577	-1.3689946
GO_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	38	-0.7381737	-1.3696015
GO_REGULATION_OF_BLOOD_CIRCULATION	224	-0.6286623	-1.3695316
GO_REGULATION_OF_HOMEOSTATIC_PROCESS	381	-0.6170481	-1.3694066
GO_NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPM	219	-0.63253886	-1.3695304
GO_SULFUR_COMPOUND_BINDING	190	-0.6311719	-1.3698735
GO_NEGATIVE_REGULATION_OF_WOUND_HEALING	47	-0.71420383	-1.3700577
AP1_Q2_01	221	-0.6202784	-1.3701966
GCM_Q2	195	-0.63385475	-1.3705769
GO_ACIDIC_AMINO_ACID_TRANSPORT	16	-0.81750315	-1.3705412
GO_ENDOCARDIAL_CUSHION_DEVELOPMENT	24	-0.7888039	-1.3707559
GO_TISSUE_MORPHOGENESIS	423	-0.6148643	-1.3712676
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_AC	15	-0.8309825	-1.3712338

GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_BINDING	30	-0.7651513	-1.37182
GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	16	-0.82250696	-1.3712025
GO_LEARNING	103	-0.66596824	-1.371538
GO_ACTIN_FILAMENT_POLYMERIZATION	21	-0.7844248	-1.3711389
GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	196	-0.62716013	-1.371809
GO_KINESIN_BINDING	30	-0.76408446	-1.3717109
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GRO	52	0.64687276	1.4991163
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	369	-0.6129616	-1.3721548
GO_MULTICELLULAR_ORGANISMAL_MOVEMENT	34	-0.75948167	-1.372376
GO_CHEMOREPELLANT_ACTIVITY	24	-0.7881547	-1.3722996
GO_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	128	-0.64820546	-1.3727123
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACT	29	-0.7597976	-1.3732027
GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	55	-0.7077018	-1.372913
GO_PROTEIN_COMPLEX_SCAFFOLD	63	-0.69186664	-1.3733544
GO_NUCLEOSIDE_TRIPHOSPHATASE_REGULATOR_ACTIVITY	307	-0.6266711	-1.3730406
GO_PROTEIN_KINASE_A_CATALYTIC_SUBUNIT_BINDING	15	-0.8346706	-1.373142
GO_HOMOLOGOUS_CHROMOSOME_SEGREGATION	32	0.7173439	1.5007362
GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRAN	262	-0.62854564	-1.3743607
GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	144	-0.64887524	-1.3751515
GO_SYNAPSE_PART	471	-0.61251014	-1.3747642
SMTTTTGT_UNKNOWN	326	-0.6188004	-1.3750732
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_CAI	22	-0.79496443	-1.3748701
ETS_Q4	237	-0.62823606	-1.3750012
TCF11_01	208	-0.63689816	-1.3747256
GO_LIPID_PHOSPHORYLATION	85	-0.6757625	-1.374659
GO_REGULATION_OF_CHROMATIN_BINDING	15	-0.846291	-1.3745762
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	128	-0.65426373	-1.375436
GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	15	-0.83495027	-1.3755629
GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	72	-0.6838964	-1.3757684
GO_MEMBRANE_DEPOLARIZATION	47	-0.7049366	-1.3760357
GO_IMMUNE_EFFECTOR_PROCESS	394	-0.6178746	-1.3765023
GO_POSITIVE_REGULATION_OF_STEROL_TRANSPORT	15	-0.8431965	-1.3763349
GO_RESPONSE_TO_EXTRACELLULAR_STIMULUS	353	-0.6147551	-1.3766258
GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	49	-0.7211285	-1.3767589
RORA1_01	202	-0.6312041	-1.3764981
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIM	223	-0.6322229	-1.3771013
CTCNANGTGN_UNKNOWN	67	-0.696864	-1.3770558
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMM	32	-0.7497635	-1.377397
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BIND	44	-0.7192963	-1.3780422
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE_MEMBRANE	42	-0.7281632	-1.3778517
GO_DENDRITE	379	-0.6208006	-1.3778031
RTTTNNNYTGGM_UNKNOWN	128	-0.65587044	-1.3780183
GO_ACTION_POTENTIAL	70	-0.6920717	-1.37892
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	97	-0.66773784	-1.3788203
GO_REGULATION_OF_ACTION_POTENTIAL	32	-0.7536674	-1.3787397
GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOI	90	-0.6793436	-1.379849
GO_LYMPHOCYTE_MIGRATION	38	-0.75154144	-1.3787264
TST1_01	194	-0.6334343	-1.3799673
GO_POSITIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	15	-0.8275267	-1.3797884
GO_REGULATION_OF_CELL_SHAPE	130	-0.6575348	-1.3786386
GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	116	-0.6596845	-1.3797134

GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	37	-0.7448659	-1.3795325
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRAN	22	-0.7901508	-1.3796723
GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	230	-0.6415482	-1.3794748
GO_CYTOSOLIC_CALCIUM_ION_TRANSPORT	44	-0.72812665	-1.3792737
GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	200	-0.6413221	-1.3802541
GO_HEART TRABECULA MORPHOGENESIS	19	-0.81947565	-1.3794653
TAL1BETAIF2_01	205	-0.640281	-1.3811138
GO_CELL_MATRIX_ADHESION	106	-0.6692529	-1.3810272
GO_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	172	-0.64242136	-1.3809787
GO_POSITIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KI	125	-0.65439	-1.3809768
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	30	-0.76822424	-1.3808659
GO_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	21	-0.80920595	-1.3815926
GO_MESODERM MORPHOGENESIS	55	-0.715755	-1.3815414
GO_KINASE_REGULATOR_ACTIVITY	165	-0.64167863	-1.3814523
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	322	-0.6201283	-1.3831269
POU6F1_01	177	-0.64577425	-1.3830296
SRF_Q4	186	-0.6415587	-1.3833449
GO_BASE_EXCISION_REPAIR	38	0.69180554	1.506566
GO_LABYRINTHINE_LAYER_DEVELOPMENT	35	-0.7521084	-1.3836265
GO_ANTIGEN_BINDING	72	-0.67754495	-1.383582
GO_REGULATION_OF_MACROPHAGE_ACTIVATION	23	-0.8013607	-1.3838509
GO_RESPONSE_TO_CAMP	88	-0.67608994	-1.384183
GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCI	17	-0.8232045	-1.3844843
GO_ACID_SECRETION	50	-0.714911	-1.3849083
GO_CELL_CELL_ADHERENS_JUNCTION	51	-0.7216669	-1.3844488
GO_PROTEIN_DEALKYLATION	27	-0.7779923	-1.3848794
ETS2_B	253	-0.6387553	-1.3848376
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECC	110	-0.66635925	-1.38473
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	35	-0.74951583	-1.3853116
ISRE_01	216	-0.6345282	-1.3856786
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_BIPOLAR_CELL_PO	31	-0.7589009	-1.3862692
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZA1	62	-0.70507574	-1.3856456
GO_CALCIUM_ION_IMPORT	53	-0.7150206	-1.3855528
YTAAYNGCT_UNKNOWN	120	-0.66610825	-1.3858668
GO_ENDOTHELIAL_CELL_DEVELOPMENT	43	-0.7350716	-1.3859835
GO_EPIDERMIS_DEVELOPMENT	166	-0.64294034	-1.3861315
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	65	-0.70092374	-1.3864607
GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORT	21	-0.80977577	-1.3865883
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFER	18	-0.8319019	-1.3862658
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	52	-0.7131916	-1.3871489
GO_RESPONSE_TO_DRUG	363	-0.6212634	-1.3870964
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	22	-0.80034125	-1.3873559
GO_LONG_TERM_MEMORY	21	-0.7972645	-1.3870478
GO_NEGATIVE_REGULATION_OF_PROTEIN_MATURATION	30	-0.756557	-1.3870127
GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	94	-0.6739774	-1.3877156
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_	441	-0.6254778	-1.3881227
GO_HISTONE_METHYLTRANSFERASE_ACTIVITY	46	0.66274256	1.5143005
GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	49	-0.7296166	-1.3883057
GO_NEGATIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	19	-0.8110656	-1.3881105
WWTAAGGC_UNKNOWN	107	-0.6715797	-1.3880447
GO_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVI	56	-0.7038739	-1.388602

GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	338	-0.6260116	-1.3888203
GO_NEURON_RECOGNITION	26	-0.77817756	-1.3887408
GO_IONOTROPIC_Glutamate_Receptor_Complex	31	-0.7635362	-1.3891429
GO_HYDROLASE_ACTIVITY_HYDROLYZING_N_GLYCOSYL_COMPO	20	0.7891965	1.5142823
KEGG_MISMATCH_REPAIR	23	0.7820351	1.5138925
GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	17	0.8048025	1.5100319
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	181	0.5519113	1.5135098
GO_REGULATION_OF_NEURON_DIFFERENTIATION	465	-0.6207947	-1.3900081
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSI	44	-0.7295741	-1.3901653
GO_PROTEIN_OLIGOMERIZATION	370	-0.6196711	-1.3902736
GO_DNA_METHYLATION_OR_DEMETHYLATION	50	0.65864587	1.5119696
GO_REGULATION_OF_IMMUNOGLOBULIN_SECRETION	15	-0.8362679	-1.3904423
GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	22	-0.80035937	-1.3908265
BRN2_01	187	-0.6476215	-1.3907907
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXOI	30	0.71877265	1.513428
GO_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	30	-0.76062506	-1.3907112
GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	25	-0.7868904	-1.3915186
GO_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	46	-0.74410856	-1.3914611
GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	34	-0.74683803	-1.3914045
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	25	0.75899553	1.5130191
GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	39	-0.7486097	-1.391366
GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	32	-0.76295763	-1.3912745
GO_U1_SNRNP	16	0.81771827	1.5118635
GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	16	0.81815016	1.5173197
SPZ1_01	190	-0.64516574	-1.392489
GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	184	-0.6541919	-1.3923099
GO_MYELOID_LEUKOCYTE_ACTIVATION	85	-0.6818211	-1.3926657
PAX_Q6	207	-0.64241594	-1.3924665
GO_DIENCEPHALON_DEVELOPMENT	48	-0.7317192	-1.3929458
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	23	-0.7931933	-1.3928349
GO_SISTER_CHROMATID_SEGREGATION	165	0.56404984	1.5184802
GO_KINASE_ACTIVATOR_ACTIVITY	57	-0.7175289	-1.3936179
GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	157	-0.6501039	-1.3935248
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	20	-0.8207233	-1.3940153
GO_CLATHRIN_COATED_VESICLE	138	-0.66210365	-1.39393
GO_NEURON_MATURATION	25	-0.7883261	-1.3943332
GO_POSTSYNAPSE	293	-0.6358472	-1.3942658
GO_CALMODULIN_BINDING	154	-0.648553	-1.394979
GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	230	-0.6447113	-1.3978399
GO_HEART_VALVE_DEVELOPMENT	27	-0.79480857	-1.3980306
GO_EAR_MORPHOGENESIS	85	-0.69285387	-1.3978039
GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	265	-0.63855743	-1.3983783
GO_PHOSPHATASE_INHIBITOR_ACTIVITY	29	-0.7619575	-1.3983228
GO_REGULATION_OF_STAT_CASCADE	97	-0.68051445	-1.3953488
GO_ACTIN_BASED_CELL_PROJECTION	151	-0.6573404	-1.3977972
GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	69	-0.6958833	-1.3982496
GO_RESPONSE_TO_NITRIC_OXIDE	16	-0.845333	-1.3954965
HNF3ALPHA_Q6	171	-0.6448925	-1.3977344
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	47	-0.73376757	-1.3975288
GO_DEVELOPMENTAL_INDUCTION	18	-0.83326495	-1.3976604
GO_POLYPEPTIDE_N_ACETYL GALACTOSAMINYLTRANSFERASE_AC	15	-0.8651913	-1.3973746

GO_POSITIVE_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	17	-0.85429746	-1.3975235
GO_CARDIAC_SEPTUM_MORPHOGENESIS	35	-0.77214897	-1.3973243
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	252	0.5372398	1.5224915
GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	25	-0.7932908	-1.3971527
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PRO	18	0.82587063	1.523892
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	133	-0.6579587	-1.3959053
KEGG_HEDGEHOG_SIGNALING_PATHWAY	45	-0.7296412	-1.3970613
GO_LEUKOCYTE_DIFFERENTIATION	255	-0.6376888	-1.396972
GO_REGULATION_OF_ISOTYPE_SWITCHING	23	-0.7921034	-1.3968817
GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACT	85	-0.6856356	-1.3973143
GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCES	106	-0.67520183	-1.3964972
GO_RNA_METHYLATION	50	0.6575788	1.5232604
GO_TELENCEPHALON_DEVELOPMENT	183	-0.6456035	-1.3958867
GO_EPHRIN_RECEPTOR_SIGNALING_PATHWAY	76	-0.6894853	-1.3968362
CTGRYYNATT_UNKNOWN	48	-0.7245365	-1.3991427
GO_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	34	-0.7635035	-1.3963357
GO_AMMONIUM_TRANSMEMBRANE_TRANSPORT	21	-0.8086252	-1.3964463
GO_DRUG_TRANSMEMBRANE_TRANSPORT	16	-0.8352186	-1.3967562
GO_SALIVARY_GLAND_DEVELOPMENT	28	-0.7860141	-1.3990691
GO_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	47	-0.7260466	-1.3966656
GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	65	-0.6975947	-1.3962727
GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	15	-0.8530865	-1.398968
STAT5A_01	204	-0.65175855	-1.3962636
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_M	19	-0.81193596	-1.3994182
GO_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CE	36	0.7126046	1.5224886
GO_NEUROTROPHIN_SIGNALING_PATHWAY	21	-0.8100533	-1.3997862
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	87	0.5954971	1.52521
NFKAPPAB_01	217	-0.64165014	-1.400147
E2F_01	60	0.6527752	1.5222466
GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_	56	-0.7237855	-1.4011081
KEGG_WNT_SIGNALING_PATHWAY	136	-0.6634596	-1.4010319
GO_NEGATIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIC	38	-0.74988866	-1.4004098
GO_CONTRACTILE_FIBER	167	-0.65037376	-1.4010288
GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	124	-0.665195	-1.400634
GO_REACTIVE_NITROGEN_SPECIES_METABOLIC_PROCESS	16	-0.8484091	-1.4007629
TBP_01	181	-0.6480441	-1.400992
GO_RESPONSE_TO_VITAMIN_D	26	-0.7798597	-1.4009824
GO_RESPONSE_TO_AUDITORY_STIMULUS	20	-0.8143791	-1.4020269
GO_POSITIVE_REGULATION_OF_HEART_CONTRACTION	28	-0.7890792	-1.4022255
GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	19	-0.8198581	-1.4030715
GO_CELL_BODY	409	-0.62884134	-1.4032917
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	37	-0.7567665	-1.4029868
GO_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	20	-0.82675296	-1.4027609
GO_INORGANIC_ANION_TRANSPORT	91	-0.6877918	-1.4028881
GO_REGULATION_OF_FATTY_ACID_OXIDATION	25	-0.7860805	-1.403254
GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZAT	44	-0.7420725	-1.4035234
GO_CELL_FATE_SPECIFICATION	39	-0.7424893	-1.4036629
YKACATTT_UNKNOWN	233	-0.63819915	-1.4040083
GO_SECRETORY_VESICLE	362	-0.63283247	-1.4050065
GO_PHOSPHATASE_REGULATOR_ACTIVITY	78	-0.6958817	-1.4051448
GO_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	64	-0.71420443	-1.404669

GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATIC	47	-0.74536115	-1.4049256
GO_CANONICAL_WNT_SIGNALING_PATHWAY	80	-0.6926068	-1.4045722
GO_LAMELLIPODIUM_MEMBRANE	17	-0.8447276	-1.4048339
GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	149	-0.65340436	-1.404486
GO_DOUBLE_STRAND_BREAK_REPAIR	147	0.5687815	1.5286552
GO_CALCIIUM_CHANNEL_REGULATOR_ACTIVITY	32	-0.76829743	-1.4054428
KEGG_CELL_ADHESION_MOLECULES_CAMS	121	-0.65883696	-1.4057989
GO_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	22	-0.8123636	-1.4053705
GO_STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	78	-0.6941973	-1.4057697
GO_EAR_DEVELOPMENT	148	-0.66067433	-1.4056623
GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PRC	37	0.7240905	1.5297339
KEGG_CITRATE_CYCLE_TCA_CYCLE	29	0.75168645	1.5308685
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIF	59	-0.72297853	-1.4068215
SREBP1_02	73	-0.69535583	-1.4066432
GO_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY	91	-0.69321245	-1.4071261
GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	29	-0.7820796	-1.4067961
GO_POSITIVE_REGULATION_OF_CAMP_METABOLIC_PROCESS	61	-0.7115108	-1.4070382
STAT3_02	121	-0.66590756	-1.4078349
GO_L_ALPHA_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	21	-0.82179135	-1.4079862
GO_REGULATION_OF_ERK1_AND_ERK2_CASCADE	182	-0.64763117	-1.4078183
GO_MIDDLE_EAR_MORPHOGENESIS	17	-0.84009117	-1.4077653
GO_PROTEIN_KINASE_C_ACTIVITY	15	-0.8567206	-1.4076761
GO_NUCLEOID	40	0.71783346	1.5320404
RYAAAKNNNNNNNTTGW_UNKNOWN	65	-0.7065558	-1.4084446
GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	20	-0.8131147	-1.4089587
GO_POSITIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLI	73	-0.70786005	-1.4083704
GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	410	-0.6286424	-1.4086376
GO_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATC	453	-0.6333546	-1.4076577
GO_NEURONAL_POSTSYNAPTIC_DENSITY	46	-0.7403108	-1.4089456
HOXA4_Q2	202	-0.6571985	-1.4088365
GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	390	-0.62953115	-1.4096048
GO_REGULATION_OF_ANOIKIS	22	-0.8223492	-1.4101826
HEB_Q6	210	-0.64719486	-1.4114884
GO_T_TUBULE	37	-0.7525444	-1.4112978
GO_CIRCULATORY_SYSTEM_PROCESS	289	-0.63712835	-1.4114673
GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIA	31	-0.7744635	-1.4112728
MEF2_01	101	-0.6832645	-1.4109368
GO_REGULATION_OF_CELL_SIZE	155	-0.6601351	-1.4110502
GO_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	62	-0.7167054	-1.4112236
GO_NEGATIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PRO	16	-0.8396585	-1.4120883
GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	16	-0.8574655	-1.4119852
GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_PO	20	-0.82856923	-1.413031
GO_MYOSIN_V_BINDING	15	-0.85431844	-1.4122175
KEGG_NOTCH_SIGNALING_PATHWAY	46	-0.73709756	-1.413236
CEBPB_01	217	-0.65838224	-1.4119668
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	41	-0.7587601	-1.4130238
GO_NEGATIVE_REGULATION_OF_AXON_GUIDANCE	25	-0.80241793	-1.4130102
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	54	-0.7275305	-1.4139086
AAANWWTGC_UNKNOWN	160	-0.6503982	-1.4130045
GO_VOLTAGE_GATED_CALCIIUM_CHANNEL_COMPLEX	28	-0.79846543	-1.4126685
MAZR_01	191	-0.65448564	-1.4136102

PPARA_01	33	-0.78006494	-1.4138676
GO_CYTOPLASMIC_REGION	253	-0.6454639	-1.41297
FOXD3_01	149	-0.66312826	-1.4138527
MEF2_03	189	-0.6570106	-1.4142121
GO_G_PROTEIN_COUPLED_PURINERGIC_RECEPTOR_SIGNALING_	19	-0.8323578	-1.412931
GO_REGULATION_OF_CELL_CYCLE_CHECKPOINT	27	-0.79861385	-1.4149672
GO_MICROFILAMENT_MOTOR_ACTIVITY	15	-0.8716339	-1.4150786
GO_CLATHRIN_COATED_VESICLE_MEMBRANE	70	-0.70665026	-1.4148681
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	65	-0.7143152	-1.4155967
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGI	34	-0.76968735	-1.4152193
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULL	30	-0.7922944	-1.415479
GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	35	-0.76593184	-1.4157286
GO_AMINO_ACID_TRANSPORT	94	-0.6822383	-1.4154168
ATF1_Q6	187	-0.6538004	-1.4160242
GO_FOLIC_ACID_CONTAINING_COMPOUND_METABOLIC_PROCE	26	0.7595124	1.5359689
GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	380	-0.63525057	-1.4160172
GO_IONOTROPIC GLUTAMATE RECEPTOR BINDING	21	-0.813896	-1.4164143
NFY_01	214	-0.6466903	-1.4172045
GO_RESPONSE_TO_STEROID_HORMONE	415	-0.6346547	-1.4170802
SMAD4_Q6	196	-0.6547197	-1.4169922
GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	69	-0.7144854	-1.416797
GO_NEURAL_CREST_CELL_MIGRATION	37	-0.76149434	-1.4166889
GO_SECRETION	468	-0.6361774	-1.4174429
GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	34	-0.76680523	-1.4169798
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	22	-0.8248606	-1.4178069
GO_L_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVIT	36	-0.781162	-1.4183713
GO_DOPAMINE_METABOLIC_PROCESS	16	-0.8489425	-1.4181992
TCF1P_Q6	212	-0.6522098	-1.4183593
GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	26	0.75254124	1.5375867
GO_METENCEPHALON_DEVELOPMENT	78	-0.7058862	-1.4181988
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	43	-0.75887626	-1.4188285
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_IMPORT	20	-0.8184057	-1.4187516
GO_RESPONSE_TO_FATTY_ACID	75	-0.70948225	-1.4191086
PITX2_Q2	195	-0.6566854	-1.4197955
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	402	-0.6369094	-1.4197729
GO_POSITIVE_CHEMOTAXIS	26	-0.7848468	-1.4200087
GO_REGULATION_OF_MUSCLE_CONTRACTION	114	-0.6778833	-1.4209206
GGCNCCATNK_UNKNOWN	108	-0.68700916	-1.4203676
GO_CAMERA_TYPE_EYE_MORPHOGENESIS	76	-0.7137868	-1.4211015
GO_SKELETAL_MUSCLE_CONTRACTION	26	-0.79686004	-1.4207869
GO_REGULATION_OF_OSSIFICATION	148	-0.6701127	-1.4209012
RNCTGNYNRNCTGNY_UNKNOWN	59	-0.71877426	-1.420698
GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_C	24	-0.818264	-1.4206679
GO_U4_U6_X_U5_TRI_SNRNP_COMPLEX	20	0.78548217	1.5411233
GO_POSITIVE_REGULATION_OF_ORGANELLE_ASSEMBLY	41	-0.7499275	-1.4215634
GO_NON_RECOMBINATIONAL_REPAIR	60	0.66178524	1.5401144
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_P	16	0.8245006	1.5408908
STAT5B_01	203	-0.66028523	-1.4221312
GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	88	-0.7024943	-1.4222685
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_IMPORT	41	-0.75614536	-1.4224501
GO_PROTEIN_TYROSINE_SERINE_THREONINE_PHOSPHATASE_AC	40	-0.76112264	-1.4226444

GO_CELL_SUBSTRATE_ADHESION	150	-0.66968375	-1.4229373
GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX	25	0.7739727	1.5428957
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	282	-0.642052	-1.4238352
GO_HOMOTYPIC_CELL_CELL_ADHESION	45	-0.73786294	-1.4232737
IK3_01	180	-0.6600219	-1.4237626
GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	30	-0.78858864	-1.4237478
GO_VIRUS_RECEPTOR_ACTIVITY	64	-0.72217894	-1.4236201
LFA1_Q6	193	-0.6581733	-1.4237429
GO_INACTIVATION_OF_MAPK_ACTIVITY	23	-0.8235186	-1.424316
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	121	-0.68340474	-1.4246879
GO_AMINOGLYCAN_CATABOLIC_PROCESS	58	-0.72995406	-1.4248947
KEGG_MAPK_SIGNALING_PATHWAY	226	-0.6549134	-1.4251947
AREB6_03	225	-0.6476952	-1.4256313
GO_REGULATION_OF_PLASMA_MEMBRANE_ORGANIZATION	68	-0.71290714	-1.4255949
GO_CORTICAL_CYTOSKELETON	75	-0.7140383	-1.4259511
GO_ALPHA_BETA_T_CELL_ACTIVATION	50	-0.74683446	-1.4263033
GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	28	-0.79621077	-1.4267485
GO_REGULATION_OF_ORGANELLE_ASSEMBLY	136	-0.6711977	-1.4280019
GO_REGULATION_OF_RESPONSE_TO_WOUNDING	335	-0.6382514	-1.4277469
GO_STRUCTURAL_CONSTITUENT_OF_MUSCLE	35	-0.77874714	-1.427626
GO_ACTIN_FILAMENT	66	-0.7257596	-1.4281626
GO_MESENCHYMAL_CELL_DIFFERENTIATION	101	-0.6926097	-1.4275422
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFAT	21	-0.8302695	-1.4279493
GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	71	0.63828135	1.5467371
GNCF_01	55	-0.73853683	-1.4274678
GTGGGTGK_UNKNOWN	231	-0.6587102	-1.4274609
TGCTGAY_UNKNOWN	431	-0.6414998	-1.4273474
GO_NEGATIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	62	-0.7288962	-1.4299282
GO_PDZ_DOMAIN_BINDING	80	-0.70823026	-1.4295989
GO_REGULATION_OF_GLUCOSE_IMPORT_IN_RESPONSE_TO_INS	16	-0.8563553	-1.428532
GO_NEGATIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	37	-0.7742597	-1.4304919
AP2ALPHA_01	206	-0.6573073	-1.4303811
GO_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	54	-0.7474432	-1.4298975
CTAWWWATA_RSRFC4_Q2	281	-0.6451806	-1.4291397
GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	50	-0.74253905	-1.4295707
GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	33	-0.78986955	-1.4303368
GO_CALCIIUM_CHANNEL_COMPLEX	46	-0.75060314	-1.4298404
RP58_01	164	-0.66671026	-1.429497
KEGG_TGF_BETA_SIGNALING_PATHWAY	80	-0.70750636	-1.4293649
GO_EXOCYTOSIS	258	-0.65069944	-1.4291099
GO_CELL_CYCLE_G1_S_PHASE_TRANSITION	105	0.599545	1.5479332
GO_CELL_FATE_COMMITMENT_INVOLVED_IN_FORMATION_OF_	21	-0.8311168	-1.430276
GO_ORGANELLE_FISSION	444	0.5255639	1.546557
GO_SH3_DOMAIN_BINDING	110	-0.67527384	-1.4288994
CDC5_01	188	-0.6659814	-1.4290714
GO_RESPONSE_TO_OXIDATIVE_STRESS	317	-0.64741033	-1.4310426
GO_REGULATION_OF_THE_FORCE_OF_HEART_CONTRACTION	20	-0.82791406	-1.4311645
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALIN	38	-0.7693058	-1.43133
PR_02	112	-0.69089806	-1.4317713
RSRFC4_Q2	166	-0.667711	-1.4316387
GO_DNA_MODIFICATION	70	0.6376958	1.5498747

GO_REGULATED_EXOCYTOSIS	181	-0.6603628	-1.4316261
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINC	49	0.6766568	1.549347
GO_HEART_PROCESS	68	-0.7145997	-1.4321581
GO_REGULATION_OF_CATENIN_IMPORT_INTO_NUCLEUS	24	-0.8215462	-1.4329888
GO_CATALYTIC_STEP_2_SPLICEOSOME	84	0.6287046	1.5535365
GO_REGULATION_OF_PLATELET_AGGREGATION	15	-0.87412727	-1.4329569
GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	41	0.70683205	1.551688
PBX1_O2	94	-0.69717103	-1.4328346
NFY_C	205	-0.6594428	-1.4325697
GO_HINDLIMB_MORPHOGENESIS	24	-0.8122067	-1.4332743
GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	79	-0.7142921	-1.4328234
TAL1ALPHA47_01	201	-0.65920967	-1.4325597
GO_WNT_SIGNALING_PATHWAY	315	-0.65109944	-1.4342233
GO_CELL_SUBSTRATE_ADHERENS_JUNCTION_ASSEMBLY	23	-0.8263679	-1.4340945
GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	303	-0.6475964	-1.4340246
NFKAPPAB65_01	199	-0.6625195	-1.4340107
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	31	0.7260166	1.553447
GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	38	-0.76482123	-1.4338897
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	20	0.81194097	1.5516015
GO_DNA_ALKYLATION	38	0.7116596	1.5652224
GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMB	23	-0.8183138	-1.4338522
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRA	25	0.76953506	1.5668776
KEGG_PRION_DISEASES	30	-0.78951603	-1.4347984
GO_REGULATION_OF_ACTIN_NUCLEATION	26	-0.802645	-1.4349744
GO_KINASE_INHIBITOR_ACTIVITY	76	-0.71120083	-1.4351376
GO_REPLISOME	29	0.7428656	1.5630591
GO_SYNAPSIS	24	0.80867624	1.5677912
GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	44	-0.7526054	-1.4353782
PEA3_Q6	239	-0.65235615	-1.435504
GO_QUINONE_METABOLIC_PROCESS	26	0.7481393	1.5648415
GO_CYTOSKELETAL_ADAPTOR_ACTIVITY	16	-0.8617367	-1.4356992
GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCES	32	0.75245947	1.5533775
GO_DNA_BIOSYNTHETIC_PROCESS	110	0.6047489	1.5666741
GO_NUCLEOTIDE_EXCISION_REPAIR	109	0.6097553	1.5628102
GO_RNA_3_END_PROCESSING	93	0.61581224	1.5643988
GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	44	-0.75453454	-1.4363002
GO_CHEMOKINE_ACTIVITY	35	-0.7808876	-1.4361724
GO_GLOMERULAR_EPITHELIUM_DEVELOPMENT	16	0.8320905	1.5579634
GO_HISTONE_METHYLATION	69	0.6400815	1.5693502
GO_SMALL_SUBUNIT_PROCESSOME	33	0.73259586	1.5558875
GO_PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	18	0.8249126	1.5572788
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTI	35	-0.78368026	-1.4365681
GO_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	33	0.72768056	1.5568144
GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS	88	0.6220824	1.5591286
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_	33	0.72806853	1.5627847
GO_CARBOXY_LYASE_ACTIVITY	28	0.756612	1.570938
GO_TELOMERE_CAPPING	21	0.79805756	1.5625592
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGEI	51	0.68294793	1.5614746
GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	39	0.70996094	1.5724671
GO_LENS_FIBER_CELL_DIFFERENTIATION	21	-0.8370615	-1.4381158
GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGEI	346	-0.6439952	-1.4379907

GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCES	47	0.6880374	1.5625186
GO_EXOCRINE_SYSTEM_DEVELOPMENT	37	-0.78552884	-1.43863
KEGG_HOMOLOGOUS_RECOMBINATION	28	0.7603816	1.5611954
GO_NEURONAL_ACTION_POTENTIAL	18	-0.8520837	-1.438425
GO_RECEPTOR_INTERNALIZATION	40	-0.7724165	-1.4385542
GO_MUSCLE_CONTRACTION	187	-0.6668449	-1.4391948
GO_MUSCLE_SYSTEM_PROCESS	226	-0.6589675	-1.4393759
GO_REGULATION_OF_ION_HOMEOSTASIS	162	-0.67926633	-1.439548
GO_CHLORIDE_TRANSPORT	68	-0.7254019	-1.4398059
KEGG_PRIMARY_IMMUNODEFICIENCY	34	-0.76607555	-1.4400005
GO_L_AMINO_ACID_TRANSPORT	42	-0.770143	-1.4405432
GO_DICARBOXYLIC_ACID_TRANSPORT	58	-0.7453551	-1.4404293
NKX25_02	198	-0.6674299	-1.4406974
GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	269	-0.65401864	-1.4403085
GO_CEREBELLAR_CORTEX_MORPHOGENESIS	23	-0.8254092	-1.4409252
GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	45	-0.7506478	-1.4415445
IRF1_01	208	-0.6619747	-1.4417859
GO_ANTIPORTER_ACTIVITY	56	-0.73471403	-1.4430919
GO_NEUTRAL_LIPID_BIOSYNTHETIC_PROCESS	24	0.7801684	1.5771736
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	86	-0.70679	-1.4441031
GO_POSITIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	26	-0.82586354	-1.4444805
GO_SENSORY_ORGAN_MORPHOGENESIS	180	-0.6653424	-1.4444772
GO_CGMP_METABOLIC_PROCESS	18	-0.85072905	-1.4451835
CIZ_01	189	-0.66701883	-1.4451312
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	30	-0.8068029	-1.4456028
GO_CARDIAC_SEPTUM_DEVELOPMENT	68	-0.7312696	-1.4451089
KEGG_DILATED_CARDIOMYOPATHY	71	-0.7271184	-1.4455236
GO_ACTIN_FILAMENT_ORGANIZATION	157	-0.6848411	-1.4460467
GO_PLATELET_AGGREGATION	34	-0.79093903	-1.4459414
GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_IN	81	-0.7127192	-1.4463748
YAATNANRNNNCAG_UNKNOWN	51	-0.7562636	-1.4463414
GO_ENDOSOME_LUMEN	20	-0.84024	-1.4468014
GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	17	-0.8613235	-1.4467514
GO_PHOSPHATIDYLINOSITOL_BINDING	179	-0.6702059	-1.4481301
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BIND	41	-0.77525926	-1.4482777
GO_NEGATIVE_REGULATION_OF_STEROID_METABOLIC_PROCES	19	-0.8616432	-1.4480543
TEF_Q6	203	-0.6661135	-1.4493299
GO_GRANULOCYTE_ACTIVATION	18	-0.8573741	-1.4472382
GO_AXONAL_FASCICULATION	16	-0.8803483	-1.447471
EVI1_02	101	-0.7037306	-1.4480482
GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACT	21	-0.8359038	-1.4493201
GO_NITRIC_OXIDE_SYNTHASE_BINDING	18	-0.8529524	-1.447971
GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANS	96	-0.7017764	-1.4486377
KEGG_O_GLYCAN_BIOSYNTHESIS	23	-0.8277561	-1.4478623
GO_COGNITION	199	-0.6687201	-1.4489377
GO_GROWTH_FACTOR_RECEPTOR_BINDING	93	-0.70802575	-1.4477322
GO_MONOSACCHARIDE_TRANSMEMBRANE_TRANSPORTER_ACT	18	-0.85061145	-1.4492569
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSC	76	-0.7263553	-1.4488282
RACCACAR_AML_Q6	220	-0.66460377	-1.4492488
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	103	-0.7035574	-1.4499559
GO_REGULATION_OF_FIBROBLAST_MIGRATION	27	-0.8138801	-1.4501667

GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	42	-0.7720753	-1.4503853
AP2REP_01	145	-0.685018	-1.4522797
GO_NEURAL_CREST_CELL_DIFFERENTIATION	55	-0.74372894	-1.4534044
GO_NEGATIVE_REGULATION_OF_CHEMOTAXIS	44	-0.75842816	-1.4522003
GO_CELL_GROWTH	115	-0.69985723	-1.4532523
GR_01	163	-0.6778022	-1.453573
GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	153	-0.68773735	-1.4531263
GO_POSITIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PRC	30	-0.7965962	-1.4515772
GO_POSITIVE_REGULATION_OF_CELL_DIVISION	97	-0.70474374	-1.4530474
GO_PLATELET_ALPHA_GRANULE_LUMEN	47	-0.76146704	-1.4521464
GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	17	-0.8637292	-1.4515035
GO_LYMPH_VESSEL_DEVELOPMENT	18	-0.85706574	-1.4521
GO_MYELIN_ASSEMBLY	15	-0.8842099	-1.4530292
GO_ACTIN_MEDIATED_CELL_CONTRACTION	59	-0.73706913	-1.4514813
GO_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	101	-0.7104544	-1.4519063
GO_REGULATION_OF_AXON_GUIDANCE	35	-0.79229295	-1.4529252
GO_LEUKOCYTE_CHEMOTAXIS	99	-0.7057083	-1.4527861
GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	39	-0.77811056	-1.4544516
GO_MESENCHYME_MORPHOGENESIS	26	-0.8240084	-1.4520963
GO_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	324	-0.6545296	-1.4543858
KEGG_VEGF_SIGNALING_PATHWAY	64	-0.7382701	-1.4543706
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_C	36	0.7243437	1.5826858
GO_AEROBIC_RESPIRATION	49	0.6875426	1.5819782
TCF4_Q5	165	-0.6685098	-1.4543339
GO_CELL_CORTEX	213	-0.6658082	-1.4551141
GO_ACTOMYOSIN	56	-0.76034683	-1.4550649
GO_MYOSIN_BINDING	50	-0.7641064	-1.4570237
GO_CELL_FATE_DETERMINATION	29	-0.8115263	-1.4574195
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASI	83	-0.7238066	-1.4569821
GO_RECEPTOR_SIGNALING_COMPLEX_SCAFFOLD_ACTIVITY	21	-0.84014714	-1.4572747
GO_SENSORY_PERCEPTION	353	-0.655255	-1.4568413
GO_GLYCOSAMINOGLYCAN_BINDING	155	-0.67751163	-1.4576608
GO_REGULATION_OF_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	17	-0.87096983	-1.4567323
GO_RESPONSE_TO_ISOQUINOLINE_ALKALOID	20	-0.8565505	-1.4560914
GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	50	-0.7587886	-1.4567184
NERF_Q2	228	-0.66663057	-1.4562876
GO_MULTICELLULAR_ORGANISMAL_SIGNALING	93	-0.7104567	-1.4581639
GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_I	39	-0.7725716	-1.4566255
GO_HEPARIN_BINDING	119	-0.6998639	-1.4560689
GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	89	-0.7054131	-1.4565225
GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	62	-0.7388194	-1.4592223
GO_VENTRICULAR_SEPTUM_DEVELOPMENT	45	-0.7645408	-1.4581522
GO_ACTIN_MYOSIN_FILAMENT_SLIDING	27	-0.8100706	-1.4587874
GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	74	-0.7250423	-1.4560509
GO_NEGATIVE_REGULATION_OF_LOCOMOTION	229	-0.669591	-1.4584912
GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	29	-0.8198975	-1.4594638
GO_CEREBELLAR_CORTEX_DEVELOPMENT	36	-0.78925484	-1.4592017
GO_HISTONE_DEMETHYLASE_ACTIVITY	24	-0.82558036	-1.4596534
PR_01	117	-0.69931483	-1.4587636
GO_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	26	-0.81645936	-1.4560397
GO_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	87	-0.7211882	-1.4591404

GO_POSTREPLICATION_REPAIR	50	0.695768	1.5854023
GO_ACTIN_FILAMENT_BASED_MOVEMENT	78	-0.7316102	-1.4632235
GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROC	55	-0.75206536	-1.4612678
GO_RAB_GTPASE_BINDING	107	-0.6989641	-1.4631819
GO_CELL_CHEMOTAXIS	141	-0.7009579	-1.4624863
IK2_01	223	-0.67091805	-1.4636232
GO_RESPONSE_TO_ALCOHOL	307	-0.6625418	-1.4631546
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	43	-0.7730211	-1.4629966
KEGG_CALCIIUM_SIGNALING_PATHWAY	137	-0.695693	-1.4638776
GO_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	44	-0.7697305	-1.4624432
HMGIIY_Q6	200	-0.67382133	-1.462894
GO_CELL_CELL_JUNCTION_ASSEMBLY	65	-0.7437226	-1.4618595
GO_ACTIN_FILAMENT_BASED_PROCESS	403	-0.66013575	-1.4620186
ALPHACP1_01	215	-0.66890275	-1.4622145
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	28	-0.808958	-1.4628451
GO_LAMELLIPODIUM	160	-0.6875639	-1.4624361
GO_ENDOSOME_ORGANIZATION	61	-0.7396014	-1.4618049
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_	45	-0.7644857	-1.4649326
KEGG_SPLICEOSOME	123	0.6111739	1.5948201
GO_GENE_SILENCING_BY_RNA	112	0.60122323	1.5932051
GO_CHROMATIN_SILENCING_AT_RDNA	24	0.8047189	1.5956775
GO_CARDIAC_VENTRICLE_MORPHOGENESIS	38	-0.7971555	-1.4655731
GO_MEIOTIC_CHROMOSOME_SEGREGATION	47	0.70177203	1.5944399
GO_MHC_CLASS_II_PROTEIN_COMPLEX_BINDING	15	-0.8849132	-1.4655044
GO_CYTOPLASMIC_TRANSLATION	40	0.7304651	1.592826
FOXO1_02	203	-0.6709529	-1.465979
KEGG_BASE_EXCISION_REPAIR	33	0.7449477	1.5897667
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE	15	-0.8862331	-1.4663087
GO_RNA_POLYMERASE_ACTIVITY	43	0.70059454	1.5926481
GO_RESPONSE_TO_GLUCAGON	41	-0.78688174	-1.4669496
GO_LONG_TERM_SYNAPTIC_POTENTIATION	33	-0.813098	-1.4669137
GO_DAMAGED_DNA_BINDING	63	0.6696538	1.5897622
GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	15	-0.8912996	-1.4674313
GO_RNA_MODIFICATION	110	0.61393285	1.5915403
KEGG_HEMATOPOIETIC_CELL_LINEAGE	79	-0.7186698	-1.4676757
GO_PYRIMIDINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	27	0.77187514	1.5989709
GO_UNFOLDED_PROTEIN_BINDING	88	0.63862664	1.5924292
FREAC2_01	206	-0.67186826	-1.4681375
SRF_01	41	-0.7702642	-1.4685154
GO_MISMATCH_REPAIR	31	0.76270986	1.600056
GO_PROTEIN_KINASE_B_SIGNALING	31	-0.8075381	-1.4683625
MEIS1BHOXA9_01	100	-0.7108979	-1.4681305
LBP1_Q6	181	-0.68098056	-1.4690485
GO_NEGATIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_F	37	-0.7922158	-1.4689093
GO_DNA_REPAIR	435	0.52629167	1.5986832
GO_REGULATION_OF_AXONOGENESIS	152	-0.6892865	-1.4714689
GO_MYOFILAMENT	20	-0.8573668	-1.4711531
GO_RESPONSE_TO_PEPTIDE	340	-0.66335887	-1.4713619
LYF1_01	210	-0.6763314	-1.4694934
KEGG_VIBRIO_CHOLERAЕ_INFECTION	47	-0.77854216	-1.4720937
GO_DICARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_AC	25	-0.8328273	-1.4710575

GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	114	-0.70074487	-1.4702448
GO_NEGATIVE_REGULATION_OF_CALCIIUM_ION_TRANSMEMBRAN	24	-0.8448066	-1.4706225
GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	23	-0.83033574	-1.4723909
GO_LYSOSOMAL_LUMEN	80	-0.7264515	-1.4710118
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE	53	-0.7571283	-1.472076
GO_CHEMOKINE_RECEPTOR_BINDING	43	-0.7685057	-1.4701947
HMEF2_Q6	95	-0.71655744	-1.4705498
GO_DIVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSP	131	-0.70604426	-1.4719743
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIC	72	-0.7298624	-1.470133
GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBR	36	-0.7889602	-1.4709724
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROC	93	-0.71435773	-1.4700626
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	0.7330643	1.6022042
GO_RESPONSE_TO_NUTRIENT	153	-0.690351	-1.4737531
GO_SECRETORY_GRANULE_LUMEN	67	-0.75451887	-1.473631
CEBPDELTA_Q6	196	-0.680563	-1.4739767
GO_SECRETORY_GRANULE	276	-0.6729783	-1.4741666
GO_EYE_MORPHOGENESIS	103	-0.72147524	-1.47446
GO_CHROMOSOME_SEGREGATION	245	0.5696905	1.6040375
GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_BINDING	43	-0.7707381	-1.4753026
KEGG_MELANOGENESIS	88	-0.7263085	-1.4756832
GO_PROTEIN_HETEROTETRAMERIZATION	28	0.7912684	1.6062281
GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	431	-0.6648959	-1.4770426
GO_INFLAMMATORY_RESPONSE	375	-0.65516156	-1.4772079
TATA_01	172	-0.6841744	-1.4770234
GO_RHO_PROTEIN_SIGNAL_TRANSDUCTION	44	-0.78141314	-1.4768686
GO_REGULATION_OF_COAGULATION	72	-0.7385813	-1.4781772
GO_NEGATIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHE!	89	-0.7264109	-1.4788201
GO_NEGATIVE_REGULATION_OF_CALCIIUM_ION_TRANSPORT	40	-0.80059755	-1.4786887
KEGG_TIGHT_JUNCTION	111	-0.71466404	-1.4785241
GO_MEMORY	77	-0.7417483	-1.4781728
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_I	27	-0.8353941	-1.4798266
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	392	-0.6581308	-1.4803457
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIIUM_IO!	62	-0.75387913	-1.4798262
GO_REGULATION_OF_PLATELET_ACTIVATION	28	-0.83707756	-1.480261
GO_PLATELET_ALPHA_GRANULE	66	-0.7452586	-1.482068
KEGG_ENDOCYTOSIS	172	-0.6928987	-1.4797696
GO_REGULATION_OF_B_CELL_DIFFERENTIATION	22	-0.8524656	-1.4815655
GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	63	-0.75688463	-1.4796138
GO_FOREBRAIN_DEVELOPMENT	276	-0.6674537	-1.4814072
GO_REGULATION_OF_CELL_MORPHOGENESIS	489	-0.6630643	-1.4817922
E2A_Q2	197	-0.68149143	-1.4813104
GO_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	123	-0.6982977	-1.4820389
GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	126	-0.70615727	-1.4808831
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATI!	100	-0.7180645	-1.4810798
GO_ACTIN_BINDING	343	-0.66618836	-1.4830567
GO_MORPHOGENESIS_OF_AN_ENDOTHELIUM	15	-0.8971872	-1.481285
GO_ACTIN_FILAMENT_BUNDLE	51	-0.7748928	-1.4827611
GO_T_CELL_RECEPTOR_COMPLEX	19	-0.86763865	-1.4833158
GO_REGULATION_OF_RECEPTOR_RECYCLING	19	-0.87239516	-1.4835615
GO_RESPONSE_TO_OXYGEN_LEVELS	271	-0.67212564	-1.4829904
GO_BLOOD_VESSEL_MORPHOGENESIS	314	-0.66993284	-1.4839932

GO_MACROPHAGE_ACTIVATION	29	-0.8246722	-1.4826999
GO_NEGATIVE_REGULATION_OF_ANOIKIS	16	-0.88970745	-1.4845299
GO_POSITIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	40	-0.79354984	-1.4839842
MEF2_Q4	19	-0.8801152	-1.484379
GO_CELL_SUBSTRATE_JUNCTION_ASSEMBLY	39	-0.7932753	-1.4856097
GO_T_CELL_MEDIATED_IMMUNITY	27	-0.83619815	-1.4855152
GO_POSITIVE_REGULATION_OF_VASOCONSTRICTION	28	-0.82456636	-1.4851482
GO_SECOND_MESSENGER_MEDIATED_SIGNALING	128	-0.7024533	-1.4864101
GO_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	74	-0.7396895	-1.4867936
GO_SECRETION_BY_CELL	395	-0.6650727	-1.4851012
GO_GLYCOPROTEIN_BINDING	88	-0.71625495	-1.486253
AP4_Q6	184	-0.6913023	-1.4854822
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	201	-0.6835816	-1.4866476
GO_ANGIOGENESIS	256	-0.67825073	-1.4862425
GO_ENDOTHELIUM_DEVELOPMENT	84	-0.7369258	-1.4872911
TAXCREB_Q2	23	0.81650543	1.6116525
GO_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	88	-0.73005855	-1.4885557
GO_CARDIAC_CHAMBER_DEVELOPMENT	106	-0.7237223	-1.4884119
GO_REGULATION_OF_WNT_SIGNALING_PATHWAY	274	-0.67178893	-1.4880207
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	97	-0.7276713	-1.4883792
GO_MACROPHAGE_DIFFERENTIATION	19	0.8504326	1.6111702
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	204	-0.68625396	-1.4892036
GO_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_F	49	-0.7831314	-1.4898177
GGGNNTTCC_NFKB_Q6_Q1	120	-0.70215183	-1.4896296
FREAC4_Q1	120	-0.7020949	-1.4902014
GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORT	77	-0.74495184	-1.4906564
EVI1_Q4	180	-0.69525486	-1.4910891
GO_ENDOTHELIAL_CELL_DIFFERENTIATION	68	-0.7573254	-1.4956577
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	128	-0.71596915	-1.492943
GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	32	-0.8189316	-1.4909675
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	72	-0.742554	-1.4927657
CEBP_Q3	201	-0.6899958	-1.4955537
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATIO	132	-0.7183369	-1.4926245
GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	18	-0.87249994	-1.4925232
GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	35	-0.8232543	-1.4955117
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	71	-0.75327784	-1.4947258
GO_ACTIVATION_OF_IMMUNE_RESPONSE	364	-0.6724823	-1.4922627
GO_ADHERENS_JUNCTION_ASSEMBLY	33	-0.8079027	-1.4916701
GO_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	23	-0.8453859	-1.495386
GO_CARDIAC_VENTRICLE_DEVELOPMENT	76	-0.7483854	-1.4924992
GO_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	52	-0.77256024	-1.4919196
GO_DEFENSE_RESPONSE_TO_GRAM_NEGATIVE_BACTERIUM	33	-0.8186839	-1.4944147
GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	61	-0.76476276	-1.4952661
GO_CALCIUM_ACTIVATED_CATION_CHANNEL_ACTIVITY	19	-0.86548454	-1.4938128
GGARNTKYCCA_UNKNOWN	59	-0.75933015	-1.4936357
GO_REGULATION_OF_ACTIN_FILAMENT_LENGTH	141	-0.7094619	-1.4946898
GO_PROTEOGLYCAN_BINDING	26	-0.8447858	-1.4922515
CACCCBINDINGFACTOR_Q6	231	-0.6891108	-1.496415
GO_NEURONAL_STEM_CELL_POPULATION_MAINTENANCE	17	-0.8841806	-1.4951514
GO_FC_GAMMA_RECEPTOR_SIGNALING_PATHWAY	73	-0.73710215	-1.4943073
GO_CELL_CELL_JUNCTION	326	-0.6700804	-1.4941484

GO_RESPONSE_TO_BMP	73	-0.74663794	-1.4969349
GO_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	43	-0.78872204	-1.4968934
GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	38	-0.8146476	-1.4985511
GO_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	72	-0.7418461	-1.4992951
GO_PLASMA_MEMBRANE_RAFT	78	-0.7294437	-1.4990731
GO_THYMOCYTE_AGGREGATION	44	-0.7919081	-1.4984635
TTCYNRGAA_STAT5B_01	276	-0.6848123	-1.4978206
NFY_Q6	214	-0.6847023	-1.4989109
GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	34	-0.8013302	-1.4983002
AML_Q6	218	-0.6865968	-1.4976814
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSUL	19	-0.8580298	-1.5003053
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	41	-0.79680514	-1.4983001
TAAWWATAG_RSRFC4_Q2	138	-0.71143574	-1.5006626
GO_REGULATION_OF_B_CELL_PROLIFERATION	50	-0.7841024	-1.5002447
GO_RESPONSE_TO_CORTICOSTEROID	147	-0.7052503	-1.5021024
GO_CELL_FATE_COMMITMENT	157	-0.6996193	-1.502578
GO_LYMPHOCYTE_DIFFERENTIATION	180	-0.69651747	-1.500177
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	29	-0.8434587	-1.4999189
RGAANN TTC_HSF1_01	368	-0.67563367	-1.5020252
MAF_Q6	217	-0.68226814	-1.5018274
YNGTTNNNATT_UNKNOWN	293	-0.6780527	-1.5025362
GO_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	35	-0.81500673	-1.5039312
GO_REGULATION_OF_EXTENT_OF_CELL_GROWTH	92	-0.7319911	-1.5017056
GO_SPECTRIN_BINDING	23	-0.8581326	-1.5043641
KEGG_GLIOMA	62	-0.7574513	-1.5016564
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	140	-0.71011025	-1.5039277
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTI	22	-0.8632779	-1.5014342
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	185	-0.69822115	-1.5033568
KEGG_ADHERENS_JUNCTION	72	-0.7531991	-1.5039138
GO_NUCLEAR_CHROMOSOME_SEGREGATION	202	0.58748704	1.6161835
GO_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	45	-0.7966515	-1.5037868
GO_POSITIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	160	-0.7057937	-1.5054477
GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_S	170	-0.69919723	-1.5053471
GO_NEURON_PROJECTION_DEVELOPMENT	456	-0.67681944	-1.506517
GO_POSITIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATI	20	-0.8856108	-1.5062746
GO_GOLGI_LUMEN	60	-0.76546293	-1.5085653
GO_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	49	-0.79546195	-1.5109234
GO_CELL_JUNCTION_ORGANIZATION	167	-0.70270735	-1.5106819
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPON	28	-0.8539326	-1.5071877
GO_NEGATIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	24	-0.8649236	-1.5084796
GO_CELL_ADHESION_MOLECULE_BINDING	165	-0.70497745	-1.5090114
YWATTWNNRGCT_UNKNOWN	55	-0.76592654	-1.5075567
GO_BONE_MINERALIZATION	35	-0.8240656	-1.51057
GO_RECEPTOR_METABOLIC_PROCESS	71	-0.7501268	-1.5083402
GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	136	-0.70990497	-1.507991
GO_CEREBELLAR_CORTEX_FORMATION	16	-0.90405875	-1.5104355
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASI	126	-0.7119552	-1.5082037
GO_HINDBRAIN_MORPHOGENESIS	31	-0.8333594	-1.5098269
GO_AMINO_ACID_ACTIVATION	50	0.7243655	1.6230099
GO_RAS_PROTEIN_SIGNAL_TRANSDUCTION	137	-0.71390325	-1.5103462
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	170	-0.7074237	-1.5123296

GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTC	282	-0.6889466	-1.5102501
GO_MYOSIN_COMPLEX	54	-0.783378	-1.5127044
SREBP1_Q6	199	-0.69565856	-1.5131826
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIAT	18	-0.8974029	-1.5097944
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	69	-0.75714445	-1.5122774
CCAWWNAAGG_SRF_Q4	68	-0.75064117	-1.5121341
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	71	-0.7488005	-1.5131712
GO_RESPONSE_TO_MECHANICAL_STIMULUS	183	-0.6998042	-1.51202
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBL	63	0.687131	1.6226153
GO_SPROUTING_ANGIOGENESIS	39	-0.81290066	-1.5140516
GO_MITOCHONDRIAL_MATRIX	377	0.5533776	1.6222357
GO_RNA_SPLICING	337	0.5511616	1.6215086
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION	38	0.73585564	1.6205924
NCX_01	127	-0.7209779	-1.5184927
GO_CELL_CELL_ADHESION	484	-0.6792329	-1.5179425
GO_OUTFLOW_TRACT_MORPHOGENESIS	39	-0.80504036	-1.5176744
GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASM	93	-0.7459295	-1.5172117
GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	30	-0.8425465	-1.5174868
TGTYNNNNNRGCARM_UNKNOWN	73	-0.75824326	-1.5169632
GO_ENSHEATHMENT_OF_NEURONS	77	-0.75318944	-1.5184611
TEF1_Q6	185	-0.70300925	-1.520356
GO_SISTER_CHROMATID_COHESION	103	0.64582366	1.6308887
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMU	30	-0.84906036	-1.5198739
GO_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	121	-0.7375648	-1.5193768
GO_MATURATION_OF_SSU_RRNA	41	0.7317701	1.6301208
GO_PROTEIN_HETEROOLIGOMERIZATION	95	-0.7423367	-1.5203505
GO_NEURON_PROJECTION_GUIDANCE	164	-0.711991	-1.5210077
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLA	104	0.64454734	1.6293273
GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ORGANIZATIO	22	-0.86467355	-1.5198615
GO_CARDIAC_CHAMBER_MORPHOGENESIS	71	-0.7590908	-1.5216902
GO_PROTEIN_DNA_COMPLEX	131	0.62213063	1.6291654
GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILI'	91	-0.74673	-1.5228205
TATA_C	205	-0.6984643	-1.5232002
GO_EMBRYONIC_CAMERA_TYPE_EYE_DEVELOPMENT	25	-0.86827993	-1.5227965
GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	423	-0.6856111	-1.523727
GO_COLLAGEN_BINDING	55	-0.78289825	-1.5247197
GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_BINDING	62	-0.77529794	-1.5247138
GO_NEGATIVE_CHEMOTAXIS	36	-0.8237779	-1.5257962
GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIF	293	-0.68973583	-1.5255724
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	48	-0.79675454	-1.524708
GO_SINGLE_ORGANISM_CELL_ADHESION	403	-0.681897	-1.5263238
GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	180	-0.7138585	-1.5270693
GO_CARTILAGE_DEVELOPMENT_INVOLVED_IN_ENDOCHONDRAL	17	-0.912099	-1.5269216
GO_THYMIC_T_CELL_SELECTION	18	-0.8975369	-1.527798
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	115	-0.7270855	-1.52887
GO_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	88	-0.7508162	-1.5288669
KEGG_VIRAL_MYOCARDITIS	59	-0.7827082	-1.5307283
STAT_Q6	212	-0.70617175	-1.5320433
LEF1_Q2	179	-0.7084355	-1.5315213
GO_NEURON_PROJECTION_MORPHOGENESIS	328	-0.69219285	-1.532001
MEF2_Q6_01	191	-0.7036357	-1.5336294

GO_ION_GATED_CHANNEL_ACTIVITY	27	-0.8586906	-1.5333886
GO_VACUOLAR_LUMEN	100	-0.74577993	-1.5420514
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	94	-0.7462198	-1.5390592
GO_INTEGRIN_BINDING	95	-0.7482506	-1.5386802
GO_FILOPODIUM	85	-0.75568795	-1.5418338
GO_ACTIN_CYTOSKELETON	399	-0.68641037	-1.5397775
GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS	16	-0.9364515	-1.5425123
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	140	-0.72352386	-1.5395554
GO_VESICLE_LUMEN	86	-0.74687815	-1.5385689
CRX_Q4	188	-0.71054167	-1.5417666
GO_CYTOKINE_ACTIVITY	143	-0.7228564	-1.5377862
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUI	53	-0.80455464	-1.5404878
GO_AORTA_MORPHOGENESIS	17	-0.9125207	-1.5356883
GO_CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENT	300	-0.6911061	-1.5348836
GO_REGULATION_OF_WOUND_HEALING	104	-0.74399745	-1.535472
GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	480	-0.686484	-1.5363607
MEF2_02	172	-0.7157611	-1.5416427
GO_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	32	-0.84564024	-1.5376493
GO_REGULATION_OF_CELL_SUBSTRATE_ADHESION	150	-0.71916115	-1.5352336
GO_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	210	-0.7040198	-1.5385466
GO_CYTOLYSIS	19	-0.89860445	-1.541031
GO_T_CELL_DIFFERENTIATION	117	-0.7353579	-1.5432467
GO_NEGATIVE_REGULATION_OF_STAT_CASCADE	33	-0.84176666	-1.5413924
GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	159	-0.71174914	-1.5383632
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	35	0.74888504	1.638888
GO_SKELETAL_SYSTEM_MORPHOGENESIS	155	-0.7194818	-1.5363054
GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_BINDING	104	-0.7487552	-1.5375992
GO_POSITIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_1	31	-0.8421528	-1.537443
GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALIN	34	-0.84221536	-1.5371221
GO_GENE_SILENCING	167	0.61061937	1.6422265
GO_MUSCLE_ORGAN_MORPHOGENESIS	46	-0.8150119	-1.5469824
GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	171	-0.7217779	-1.5475656
GO_HELICASE_ACTIVITY	147	0.6058525	1.6444975
GO_REGULATION_OF_T_CELL_PROLIFERATION	131	-0.7343091	-1.5480572
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	95	0.6407226	1.6458436
GO_POSITIVE_REGULATION_OF_CELL_KILLING	36	-0.8353267	-1.5492246
GO_PROTEIN_LOCALIZATION_TO_NUCLEUS	143	-0.72525823	-1.5504794
GO_TRANSMISSION_OF_NERVE_IMPULSE	35	-0.8423182	-1.5535568
GO_EMBRYONIC_SKELETAL_SYSTEM_DEVELOPMENT	92	-0.7564691	-1.5532093
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	119	-0.7353366	-1.5530156
GO_CELLULAR_RESPONSE_TO_LIPID	389	-0.69576067	-1.5526552
KEGG_AXON_GUIDANCE	115	-0.73145324	-1.5524242
GO_MHC_PROTEIN_COMPLEX_BINDING	18	-0.9234474	-1.5520906
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	146	-0.73528636	-1.5543998
GO_POSITIVE_REGULATION_OF_AXONOGENESIS	65	-0.7941866	-1.5577133
KEGG_LONG_TERM_POTENTIATION	57	-0.8014336	-1.5550382
GO_NATURAL_KILLER_CELL_ACTIVATION	32	-0.8570852	-1.55544
GO_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	206	-0.71815616	-1.5576401
GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	16	-0.93709373	-1.5570766
GO_REGULATION_OF_CALCIIUM_ION_IMPORT	82	-0.7642836	-1.5574541
GO_LEUKOCYTE_CELL_CELL_ADHESION	223	-0.7107512	-1.5566667

GO_RESPONSE_TO_ESTROGEN	184	-0.72180045	-1.5565172
GO_PALATE_DEVELOPMENT	66	-0.7809065	-1.5599815
CEBP_C	161	-0.73180026	-1.5614952
GO_RECEPTOR_COMPLEX	261	-0.711563	-1.5608484
KEGG_AUTOIMMUNE_THYROID_DISEASE	33	-0.856086	-1.5598898
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIM	251	-0.7140585	-1.5652671
GO TRABECULA FORMATION	17	-0.9425308	-1.5614762
GO_CORECEPTOR_ACTIVITY	33	-0.8479186	-1.5651746
GO_PLATELET_DEGRANULATION	92	-0.7586458	-1.5626509
KEGG_LONG_TERM_DEPRESSION	53	-0.80274415	-1.5631216
GO_SMALL_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX	58	0.7061679	1.6535218
GO_LEUKOCYTE_ACTIVATION	362	-0.7068158	-1.5646149
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMML	65	-0.7890051	-1.5651387
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	180	-0.72573864	-1.5645915
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	79	-0.7793855	-1.5641158
GO_DEOXYRIBONUCLEASE_ACTIVITY	63	0.6922957	1.6532522
GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	57	-0.7940227	-1.5674535
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	43	-0.84457284	-1.5764419
GO_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	22	-0.8985519	-1.576436
GO_HEART_MORPHOGENESIS	167	-0.74152786	-1.5763948
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	86	-0.77524835	-1.5694643
GO_TAXIS	382	-0.7081954	-1.570941
GO_SENSORY_PERCEPTION_OF_LIGHT_STIMULUS	130	-0.7435666	-1.5762429
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	67	-0.7955864	-1.5782182
GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	35	-0.8499284	-1.5756404
DR4_Q2	217	-0.72039163	-1.5709184
GO_BONE_MORPHOGENESIS	64	-0.7867818	-1.570426
GO_BONE_DEVELOPMENT	135	-0.7488353	-1.5761873
GO_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	244	-0.71137506	-1.5749031
GO_CELL_JUNCTION_ASSEMBLY	118	-0.75583136	-1.5754465
GO_REGULATION_OF_B_CELL_ACTIVATION	97	-0.7669315	-1.5799601
MYOGENIN_Q6	215	-0.73099583	-1.5794439
GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	160	-0.72852737	-1.5748469
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUN	81	-0.77887726	-1.5834712
GO_NEGATIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	46	-0.8363297	-1.5748179
GO_NEURON_SPINE	101	-0.76067764	-1.5740057
GO_SIDE_OF_MEMBRANE	359	-0.7140771	-1.5833864
GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	33	-0.8433816	-1.573591
GO_RESPONSE_TO_VITAMIN	76	-0.7965026	-1.5830402
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_F	85	-0.77999884	-1.5825983
GO_ADAPTIVE_IMMUNE_RESPONSE	213	-0.7251594	-1.5747793
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	279	-0.72447515	-1.5875049
GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	54	-0.79760814	-1.5735637
GO_POSITIVE_T_CELL_SELECTION	20	-0.9148267	-1.5816853
GO_VASCULATURE_DEVELOPMENT	405	-0.710553	-1.587114
GO_NUCLEAR_REPLICATION_FORK	39	0.7609983	1.6584287
GO_LYMPHOCYTE_ACTIVATION	303	-0.71240103	-1.582313
GO_AORTA_DEVELOPMENT	36	-0.8682218	-1.5915189
GO_SMAD_BINDING	64	-0.7981877	-1.585203
KEGG_TYPE_I_DIABETES_MELLITUS	37	-0.84975296	-1.5870883
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERA1	63	-0.7973041	-1.59233

HTF_01	58	-0.82159615	-1.5861562
GO_CHROMOSOMAL_REGION	296	0.57238114	1.6601267
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	254	-0.72644764	-1.5915189
GO_COMPLEX_OF_COLLAGEN_TRIMERS	22	-0.923813	-1.5869625
KEGG_ALLOGRAFT_REJECTION	32	-0.86340463	-1.5905294
GO_SKELETAL_SYSTEM_DEVELOPMENT	365	-0.7136755	-1.5912919
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLISM	75	0.6774476	1.6618493
TFIIA_Q6	206	-0.733207	-1.5942515
GO_DNA_STRAND_ELONGATION	30	0.8251552	1.6630569
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	105	-0.76295954	-1.59375
GO_CALCIIUM_MEDIATED_SIGNALING	76	-0.79555774	-1.590462
GO_NUCLEOLAR_PART	60	0.70427215	1.6640109
GO_SECRETORY_GRANULE_ORGANIZATION	23	-0.91604584	-1.5952317
GO_CELLULAR_RESPONSE_TO_VITAMIN	20	-0.9162693	-1.5903432
GO_TRNA_PROCESSING	108	0.652903	1.6746658
GO_DNA_DEPENDENT_ATPASE_ACTIVITY	77	0.6734991	1.6738005
GO_CENTROMERE_COMPLEX_ASSEMBLY	39	0.75394213	1.6736214
GO_ODONTOGENESIS	84	-0.7843305	-1.5978866
GO_RECOMBINATIONAL_REPAIR	69	0.69542867	1.6709774
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	43	0.7244599	1.6721226
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	32	0.78683853	1.6682969
GO_CYTOSOLIC_RIBOSOME	107	0.650292	1.6734632
GO_DNA_PACKAGING_COMPLEX	68	0.69831735	1.6677091
GO_TRANSLESION_SYNTHESIS	38	0.755714	1.6696051
GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	23	0.82750666	1.6707661
GO_CYTOKINE_RECEPTOR_BINDING	198	-0.738068	-1.6041033
GO_IMMUNOLOGICAL_SYNAPSE	32	-0.8772821	-1.60405
GO_CHROMOSOME_TELOMERIC_REGION	140	0.6156161	1.6799244
GO_DIVALENT_INORGANIC_CATION_TRANSPORT	208	-0.7379766	-1.6037663
GO_LIGAND_DEPENDENT_NUCLEAR_RECEPTOR_BINDING	21	-0.9277253	-1.6056647
GO_EXTRACELLULAR_MATRIX_COMPONENT	111	-0.769626	-1.6029153
GO_CALCIIUM_ION_TRANSPORT	170	-0.7490567	-1.6035807
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	93	-0.7824973	-1.6027025
GO_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	93	-0.78490865	-1.6017351
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	69	0.7033367	1.6830789
GO_RRNA_METABOLIC_PROCESS	248	0.6004545	1.682112
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	112	0.64218277	1.6843641
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	327	-0.7241011	-1.6025647
GO_DNA_REPLICATION	196	0.6110762	1.6798596
GO_REGULATION_OF_CELL_KILLING	58	-0.8129729	-1.6073372
KEGG_OXIDATIVE_PHOSPHORYLATION	106	0.6476476	1.6889858
GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	101	-0.7825921	-1.6087441
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	56	0.734413	1.6936263
GO_HISTONE_EXCHANGE	42	0.75901735	1.6888219
GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	43	0.76637197	1.6930481
GO_EXTRACELLULAR_MATRIX	335	-0.7295163	-1.6120695
GO_T_CELL_SELECTION	35	-0.87761176	-1.6109728
KEGG_GAP_JUNCTION	77	-0.78984874	-1.6119536
GO_ATP_DEPENDENT_CHROMATIN_REMODELING	63	0.70359355	1.6923281
GO_REGULATION_OF_CHEMOTAXIS	153	-0.7628017	-1.6173117
GO_MITOTIC_RECOMBINATION	41	0.7540665	1.6887815

SRF_C	180	-0.7451294	-1.6144927
GO_CELLULAR_RESPONSE_TO_EPIDERMAL_GROWTH_FACTOR_S	21	-0.92296255	-1.6150855
CCAWNWWNNNGGC_UNKNOWN	72	-0.8199788	-1.6140623
GO_RESPONSE_TO_HYDROGEN_PEROXIDE	102	-0.7837479	-1.6160071
GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	116	-0.76754737	-1.6173038
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	92	-0.79228115	-1.6170892
GO_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	139	-0.7656474	-1.620078
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	47	0.7416006	1.6996834
CP2_01	217	-0.7446001	-1.6220438
GO_CARTILAGE_DEVELOPMENT	120	-0.79345864	-1.652404
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	93	-0.7890275	-1.6230634
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	64	-0.81520915	-1.6253966
COMP1_01	86	-0.8117604	-1.6523243
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	104	-0.78757536	-1.6251783
GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	198	-0.76774913	-1.6544427
GO_PROTEINACEOUS_EXTRACELLULAR_MATRIX	278	-0.73876333	-1.6249236
GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATI	25	0.84261835	1.703362
GO_OSTEOBLAST_DIFFERENTIATION	113	-0.80115014	-1.6615678
GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	148	-0.7732647	-1.6519707
GO_ARTERY_DEVELOPMENT	63	-0.82908034	-1.6286708
GO_RESPONSE_TO_WOUNDING	467	-0.74289256	-1.6582987
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NON	118	0.64872694	1.7048502
GO_SENSORY_PERCEPTION_OF_MECHANICAL_STIMULUS	113	-0.7836747	-1.6282166
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	97	-0.79958844	-1.6313232
GO_RESPONSE_TO_EPIDERMAL_GROWTH_FACTOR	25	-0.92185366	-1.6560035
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	65	-0.8119651	-1.6280323
GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	168	-0.7594071	-1.6302104
GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	138	-0.7763398	-1.6600186
GO_EMBRYONIC_EYE_MORPHOGENESIS	23	-0.9058484	-1.6308684
GO_SIGNALING_ADAPTOR_ACTIVITY	73	-0.8234169	-1.6518763
GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	41	-0.8673364	-1.6510894
GO_SKIN_DEVELOPMENT	147	-0.77732867	-1.6468582
GO_OSSIFICATION	219	-0.7613479	-1.6614747
GO_RESPONSE_TO ESTRADIOL	124	-0.7747996	-1.6369662
GO_LEUKOCYTE_MIGRATION	236	-0.7433427	-1.6333764
KEGG_GRAFT_VERSUS_HOST_DISEASE	35	-0.89861137	-1.6582483
GO_LYMPHOCYTE_COSTIMULATION	70	-0.8176808	-1.6403875
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	210	-0.75618416	-1.6364309
GO_ARTERY_MORPHOGENESIS	40	-0.85513455	-1.632845
GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	90	-0.8015436	-1.6463127
KEGG_CHEMOKINE_SIGNALING_PATHWAY	170	-0.7740311	-1.6575931
SRF_Q5_01	185	-0.7578374	-1.6361811
GO_MEMBRANE_MICRODOMAIN	261	-0.74484146	-1.640036
GO_RESPONSE_TO_GROWTH_FACTOR	403	-0.728343	-1.6385409
GO_PROTEIN_TRIMERIZATION	34	-0.89159346	-1.63946
GO_BODY_MORPHOGENESIS	40	-0.88321096	-1.6510345
GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	50	-0.8613927	-1.635045
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	262	-0.7408644	-1.6358638
GO_REGULATION_OF_BODY_FLUID_LEVELS	413	-0.73722816	-1.6454152
GO_CELLULAR_RESPONSE_TO_NUTRIENT	31	-0.9090152	-1.646209
GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	21	-0.94470596	-1.6503627

GO_POSITIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_F	109	-0.8026725	-1.644195
GO_HEAD_MORPHOGENESIS	33	-0.90060043	-1.6450845
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLV	147	-0.778073	-1.6435252
GO_CELLULAR_DEFENSE_RESPONSE	51	-0.8677129	-1.6430225
GO_COLLAGEN_FIBRIL_ORGANIZATION	32	-0.89665365	-1.6503148
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	92	-0.8190736	-1.6658405
GO_SH3_SH2_ADAPTOR_ACTIVITY	51	-0.8498865	-1.6498144
GO_SINGLE_STRANDED_DNA_BINDING	81	0.68353724	1.7117823
GO_REGULATION_OF_CELL_CELL_ADHESION	329	-0.7557962	-1.6859747
GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	136	0.6452735	1.7106577
GO TRABECULA MORPHOGENESIS	31	-0.9149413	-1.6835712
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONIN	163	-0.7874173	-1.6824379
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGN,	90	-0.81315184	-1.6857537
GO_REGULATION_OF_CELL_ACTIVATION	416	-0.74418527	-1.6717278
KEGG_ECM_RECEPTOR_INTERACTION	78	-0.8240574	-1.6741773
GO_BIOMINERAL_TISSUE_DEVELOPMENT	57	-0.8615067	-1.6696334
GO_WOUND_HEALING	390	-0.7555216	-1.6898025
GO_MULTICELLULAR_ORGANISM_METABOLIC_PROCESS	76	-0.84540933	-1.6889126
GO_REPLACEMENT_OSSIFICATION	24	-0.94777447	-1.6756793
GO_FACE_DEVELOPMENT	45	-0.88790345	-1.6736271
GO_CONNECTIVE_TISSUE_DEVELOPMENT	160	-0.78016245	-1.6714461
GO_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL	31	-0.9198619	-1.6822089
GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	272	-0.76129764	-1.6773664
GO_RESPONSE_TO_RETINOIC_ACID	87	-0.8275086	-1.6786549
GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITI	55	-0.8625327	-1.681475
GO_RESPONSE_TO_ACID_CHEMICAL	266	-0.7675359	-1.680345
GO_DNA_REPLICATION_INITIATION	28	0.8351203	1.7228247
KRCTCNNNNMANAGC_UNKNOWN	53	0.75964725	1.7200596
GO_DNA_GEOMETRIC_CHANGE	79	0.7076891	1.7218819
GO_POSITIVE_REGULATION_OF_LOCOMOTION	361	-0.7571602	-1.694613
GO_MULTI_ORGANISM_METABOLIC_PROCESS	137	0.65034944	1.727993
GO_DNA_HELICASE_ACTIVITY	53	0.7415409	1.7345563
GO_TELOMERE_ORGANIZATION	90	0.6843639	1.7305489
KEGG_RIBOSOME	86	0.679321	1.7344868
GO_PRERIBOSOME	59	0.72584856	1.7333641
GO_NUCLEAR_CHROMOSOME_TELOMERIC_REGION	112	0.6699938	1.7621665
GO_ORGANELLE_ENVELOPE_LUMEN	73	0.72552806	1.7389376
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	99	-0.82145184	-1.700856
GO_COLLAGEN_TRIMER	70	-0.8660159	-1.7275788
GO_CHROMATIN_SILENCING	65	0.7426629	1.7607275
GO_ENDODEOXYRIBONUCLEASE_ACTIVITY	47	0.7599587	1.7411227
GO_BINDING_BRIDGING	163	-0.8028865	-1.7135115
SRF_Q6	196	-0.78525794	-1.7171576
GO_HEMOSTASIS	260	-0.774069	-1.7056519
KEGG_LYSINE_DEGRADATION	43	0.7688314	1.7602122
GO_ENDOPLASMIC_RETICULUM_LUMEN	168	-0.8034505	-1.7128093
GO_POSITIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	43	-0.88948005	-1.7053386
GO_RIBOSOME	211	0.6364852	1.7596397
KEGG_DNA_REPLICATION	36	0.8169704	1.7473577
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	416	0.5999903	1.7557473
GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	82	0.7025978	1.7536099

GO_MULTICELLULAR_ORGANISMAL_MACROMOLECULE_METABC	65	-0.8601243	-1.7089912
GO_SPLICEOSOMAL_COMPLEX	161	0.6340668	1.7495778
GO_DNA_PACKAGING	146	0.63704264	1.7577046
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	55	-0.8781452	-1.73347
GO_GROWTH_FACTOR_BINDING	113	-0.83031446	-1.7270162
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	45	-0.9062486	-1.712212
GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	184	0.63510174	1.7533356
GO_CELL_ACTIVATION	495	-0.771212	-1.7229122
KEGG_FOCAL_ADHESION	187	-0.801358	-1.7259561
GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	147	-0.821793	-1.7497631
GO_ORGANELLAR_RIBOSOME	68	0.72768414	1.801024
GO_RIBOSOMAL_SUBUNIT	157	0.67647874	1.8053501
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	196	0.66666615	1.8095806
GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	133	-0.83140624	-1.7655813
GO_MITOCHONDRIAL_TRANSLATION	105	0.7321736	1.8774577
GO_NCRNA_PROCESSING	367	0.6346052	1.8323182
GO_RESPONSE_TO_AMINO_ACID	91	-0.85300165	-1.7649966
GO_RIBOSOME_BIOGENESIS	297	0.6437904	1.8534199
GO_TRANSLATIONAL_ELONGATION	108	0.71348894	1.8252252
GO_NCRNA_METABOLIC_PROCESS	498	0.6122608	1.8431338
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	57	0.77532214	1.8623121
GO_REPLICATION_FORK	62	0.77046466	1.8221438
GO_DNA_CONFORMATION_CHANGE	223	0.6448686	1.8310634
GO_TRANSLATIONAL_TERMINATION	92	0.7330999	1.851195
GO_TRNA_METABOLIC_PROCESS	167	0.6782879	1.8429025
GO_LARGE_RIBOSOMAL_SUBUNIT	90	0.75928545	1.8737193
GO_PLATELET_ACTIVATION	129	-0.8632341	-1.8233081
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	107	-0.8669985	-1.8056678
GO_DNA_DEPENDENT_DNA_REPLICATION	92	0.79502875	2.0361915

NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
0.05420354	0.2598758	1	1904
0.124076806	0.259824	1	1026
0.05698324	0.25943083	1	2103
0.10102302	0.25940868	1	2727
0.046255507	0.25936005	1	2286
0.038751345	0.25921413	1	2144
0.10458453	0.25921112	1	2404
0.0349345	0.25913543	1	2229
0.084337346	0.25905234	1	2324
0.1161103	0.25903714	1	1851
0.10773481	0.2589712	1	2600
0.13914374	0.25896853	1	2174
0.04403867	0.25894058	1	1307
0.071174376	0.25893953	1	1518
0.034820456	0.25889826	1	1885
0.114137486	0.2588375	1	2202
0.11465893	0.2588327	1	1879
0.03634361	0.2587753	1	1849
0.118476726	0.25875825	1	1521
0.1106383	0.25863957	1	1024
0.03846154	0.258606	1	2818
0.083129585	0.25858942	1	1832
0.13564214	0.2585043	1	2845
0.107913665	0.25849903	1	1741
0.062929064	0.2584983	1	2872
0.04525862	0.25847986	1	1761
0.12538226	0.25847137	1	609
0.054298643	0.25842717	1	453
0.08530184	0.2584266	1	1896
0.059859157	0.25831634	1	2698
0.019832985	0.2581581	1	2731
0.13243243	0.25809768	1	1893
0.07865169	0.25806877	1	1322
0.0342246	0.25803125	1	1907
0.021560576	0.25800878	1	2630
0.06989853	0.25797063	1	2956
0.11076923	0.257956	1	2523
0.12893082	0.25795537	1	413
0.14285715	0.25793028	1	1160
0.08432148	0.25787488	1	1516
0.09077599	0.25785202	1	2996
0.10243278	0.2578192	1	2578
0.05469679	0.25774384	1	1566
0.08792651	0.2576524	1	1202
0.14175655	0.2575334	1	2888
0.034446765	0.25740466	1	2032
0.098130845	0.25734267	1	1956
0.09821428	0.25733414	1	579
0.12879884	0.257306	1	1788

0.12293853	0.2561342	1	1576
0.041170098	0.25528485	1	2080
0.01875	0.25524527	1	2202
0.093231164	0.25508213	1	538
0.04977876	0.25495648	1	2327
0.029001074	0.25491008	1	806
0.12463343	0.25489473	1	363
0.10869565	0.25487196	1	1805
0.018499486	0.25481302	1	2324
0.11246613	0.25480565	1	2102
0.04828326	0.2547439	1	2763
0.039173014	0.25472656	1	2249
0.06398104	0.25458387	1	1377
0.05263158	0.25430945	1	4751
0.08108108	0.25348938	1	3410
0.013793103	0.25319245	1	3631
0.05462185	0.2530581	1	4174
0.08516484	0.25288537	1	3051
0.03399123	0.25269276	1	1332
0.119760476	0.25267372	1	2054
0.037383176	0.2520935	1	1441
0.095846646	0.2520927	1	4262
0.014285714	0.25160652	1	4081
0.03618421	0.2514867	1	2035
0.064209275	0.25143582	1	2148
0	0.25138304	1	2758
0.011247444	0.25137547	1	1558
0.052213393	0.25131655	1	1329
0.08807588	0.2511908	1	1326
0.08022922	0.2511554	1	3583
0.080872916	0.25092235	1	2612
0.10626703	0.25088897	1	2364
0.055354994	0.2507924	1	1174
0.09577114	0.25077128	1	2277
0.058152795	0.25069088	1	1485
0.06973848	0.25020948	1	1392
0.12974684	0.24925973	1	1788
0.08230958	0.24914461	1	2662
0.040659342	0.24881926	1	2155
0.06422018	0.24871732	1	2263
0.060606062	0.24852818	1	1734
0.085443035	0.24850951	1	3232
0.06703911	0.24782959	1	1454
0.058207218	0.24748993	1	1853
0.10494753	0.24715905	1	1606
0.056537103	0.24682225	1	2868
0.034632035	0.24648981	1	3573
0.07826087	0.24629544	1	2771
0.09146342	0.24619597	1	3787
0.12996942	0.24597286	1	337
0.05836576	0.24590315	1	492

0.010752688	0.24576661	1	1979
0.08598726	0.24556687	1	818
0.006622517	0.24552043	1	2023
0.024271844	0.24549924	1	3028
0.079178885	0.24546266	1	3344
0.086666666	0.24540782	1	3224
0.070028014	0.2453957	1	3935
0.010309278	0.24529222	1	4434
0.094512194	0.24521372	1	3811
0.027173912	0.24521121	1	3977
0.012422361	0.245038	1	736
0.09030101	0.24503481	1	4112
0.10279001	0.24496932	1	1814
0.077151336	0.24496536	1	3811
0.07647059	0.24496067	1	152
0.010869565	0.2449228	1	3686
0.10548523	0.24483535	1	2010
0.007142857	0.24465917	1	1221
0.050167225	0.2446433	1	2394
0.05232558	0.24459498	1	1556
0.048331417	0.24451357	1	2081
0.09920635	0.24412732	1	2025
0.11640954	0.24348386	1	2140
0.029567054	0.24347642	1	2055
0.10013908	0.24346581	1	1788
0.01525941	0.2434108	1	2133
0.08276798	0.24340712	1	1808
0.068801895	0.24327035	1	1486
0.10678211	0.2432485	1	917
0.02189781	0.24320133	1	2052
0.012182741	0.24317633	1	2177
0.12352941	0.24316257	1	2317
0.11060606	0.24308226	1	166
0.10271903	0.24304062	1	2711
0.093706295	0.24302277	1	2577
0.12634823	0.24298976	1	1186
0.125	0.24295978	1	1612
0.018499486	0.24284089	1	1713
0.109445274	0.24241967	1	2404
0.010752688	0.24201167	1	2098
0.077111386	0.24186714	1	1425
0.071875	0.24140944	1	3757
0.053775743	0.2408338	1	2223
0.11248285	0.24082346	1	938
0.028037382	0.24081577	1	2397
0.043673012	0.24080722	1	2223
0.0449069	0.2408022	1	1872
0.06875754	0.24079144	1	2248
0.046943232	0.24075207	1	1809
0.11332312	0.24070528	1	2428
0.12460568	0.24069865	1	1606

0.055944055	0.24068792	1	492
0.07334963	0.24066484	1	1307
0.111111111	0.24060465	1	434
0.13607594	0.24055956	1	1218
0.07776262	0.2405368	1	1628
0.10694444	0.24045128	1	685
0.12518194	0.24036983	1	1648
0.08405797	0.24026799	1	2278
0.06410257	0.24020539	1	2437
0.12540716	0.24013256	1	610
0.10497238	0.24006617	1	430
0.0949464	0.23995629	1	757
0.033879783	0.2397136	1	1715
0.065804936	0.2395556	1	1307
0.08689655	0.23815577	1	1298
0.025236594	0.23815356	1	2133
0.08701135	0.23805808	1	1202
0.09335219	0.2379407	1	2177
0.032327585	0.2379238	1	1491
0.031728666	0.23780873	1	2681
0.012219959	0.23743653	1	2132
0.038647342	0.23739609	1	4038
0.06901218	0.23709852	1	755
0.13282442	0.23643418	1	2226
0.0721519	0.23628744	1	1636
0.07004831	0.23619802	1	2731
0.069767445	0.23552112	1	1642
0.01948718	0.23449811	1	2597
0.07004831	0.23419751	1	2872
0.03812636	0.23378772	1	2584
0.08802309	0.23360172	1	183
0.09943182	0.23357858	1	2621
0.011201629	0.23342001	1	1973
0.04054054	0.23341261	1	2799
0.040348966	0.23332542	1	2157
0.054958183	0.23326808	1	1230
0.030139936	0.23322234	1	1745
0.019812305	0.23319955	1	2582
0.05804111	0.2331327	1	2597
0.09419152	0.23312041	1	1757
0.062091503	0.23310667	1	3003
0.103343464	0.2330206	1	2103
0.11912226	0.23292318	1	2174
0.035986915	0.23285754	1	2846
0.09269663	0.23280369	1	1092
0.06082725	0.23276335	1	1202
0.09600998	0.23269792	1	1636
0.038548753	0.23267613	1	1828
0.11010558	0.23255603	1	2049
0.09012876	0.23251861	1	2170
0.09119011	0.23245518	1	1578

0.015306123	0.2324382	1	2546
0.086683415	0.23231381	1	1329
0.086842105	0.23227699	1	1538
0.10543131	0.2321944	1	1832
0.1028481	0.23218846	1	1656
0.0342246	0.23218608	1	2899
0.09270517	0.2321659	1	2459
0.09504132	0.2321364	1	1892
0.104417674	0.23211266	1	1839
0.10510046	0.23175837	1	1939
0.028697573	0.23173022	1	2024
0.032258064	0.23172615	1	1923
0.027139874	0.23162216	1	2301
0.06740196	0.23157562	1	1358
0.060568605	0.23145302	1	580
0.03767492	0.23134759	1	2576
0.050947867	0.23131889	1	1995
0.10429448	0.23131801	1	1667
0.06439854	0.23128703	1	2846
0.06545454	0.23125836	1	2860
0.09117647	0.2312378	1	1841
0.016477859	0.2312234	1	2049
0.08171206	0.2311636	1	2073
0.07891332	0.23114787	1	1882
0.097765364	0.23100038	1	1326
0.06435644	0.23084627	1	1230
0.06942753	0.2308178	1	2826
0.044217687	0.22978759	1	4040
0.043381535	0.22964269	1	1805
0.10984308	0.22945096	1	933
0.09861111	0.2292768	1	1648
0.101265825	0.22927581	1	844
0.062126644	0.22920881	1	2050
0.0608365	0.22914782	1	1136
0.032786883	0.2290009	1	2102
0.06287425	0.2288242	1	235
0.01319797	0.22877613	1	2327
0.11329305	0.22857392	1	918
0.037694015	0.22846201	1	2578
0.058333334	0.22826225	1	1425
0.028688524	0.22818376	1	2614
0.094081946	0.22744268	1	1084
0.078125	0.22739808	1	1431
0.101321585	0.22735551	1	1970
0.093969144	0.22728042	1	1234
0.05904059	0.22720526	1	2948
0.07967033	0.2271488	1	1329
0.104321904	0.22705527	1	2140
0.043572985	0.22693868	1	2294
0.085051544	0.22679679	1	1781
0.08285714	0.22678219	1	1609

0.039443154	0.22661737	1	3031
0.024651662	0.22646663	1	2015
0.11254019	0.22618452	1	1892
0.07723036	0.22604093	1	1685
0.072632946	0.22583291	1	312
0.028792912	0.22583121	1	1667
0.04418605	0.22582543	1	2133
0.03003337	0.22582076	1	2847
0.037288137	0.22577406	1	1837
0.019251337	0.22574247	1	1737
0.031354982	0.22567712	1	2802
0.032715376	0.22564395	1	2010
0.051660515	0.22561653	1	4513
0.03206997	0.2253359	1	3787
0.05785124	0.22524188	1	2586
0.030871004	0.22516805	1	2158
0.079738565	0.22500403	1	2224
0.09294872	0.2249269	1	2044
0.07594936	0.22485024	1	2586
0.027355623	0.22448364	1	596
0.06306306	0.22444923	1	2005
0.07023411	0.22437438	1	1867
0.08108108	0.22429307	1	2099
0.055393588	0.22427732	1	858
0.06921944	0.22421032	1	1578
0.06527415	0.22418606	1	1724
0.08832808	0.2237664	1	4702
0.034013607	0.22375898	1	3552
0.027659575	0.22365959	1	2744
0	0.22364071	1	3003
0.06105006	0.2236392	1	2325
0.069565214	0.22352827	1	3513
0.006896552	0.22346152	1	3107
0.007575758	0.22344793	1	3410
0.00921659	0.2233871	1	1362
0.06268657	0.22337663	1	967
0.082474224	0.22331667	1	1576
0.07152318	0.22322969	1	1230
0.09797823	0.22319193	1	368
0.09559939	0.22311217	1	249
0.099857345	0.22308537	1	1190
0.090174966	0.2230798	1	1764
0.08248915	0.22305228	1	2291
0.076258995	0.22299847	1	3327
0.05994898	0.22299491	1	2010
0.032258064	0.22281255	1	3010
0.05846154	0.22201937	1	3051
0.030601094	0.2218177	1	2081
0.09806835	0.22180729	1	1302
0	0.22152838	1	3621
0.07377049	0.22121362	1	1516

0.07453416	0.22112834	1	3706
0.050541516	0.2209357	1	4210
0	0.22074588	1	3583
0.028753994	0.21943033	1	1651
0.025531914	0.2193795	1	1842
0.09861111	0.21915503	1	2787
0.046979867	0.21900772	1	4973
0.10977443	0.2189302	1	379
0.08260869	0.21882449	1	2324
0.05574913	0.21810739	1	2148
0.085872576	0.21786183	1	1788
0.012422361	0.2176268	1	2269
0.10313901	0.21751846	1	1538
0.039634146	0.21746698	1	3551
0.0652819	0.21699499	1	3170
0.039779004	0.21680036	1	2601
0.09034268	0.21678126	1	2731
0.037383176	0.21678089	1	3473
0.042704627	0.21676847	1	1662
0.026086956	0.21675435	1	1832
0.04180791	0.21672584	1	2148
0.07529723	0.21663071	1	1234
0.108024694	0.21658503	1	1631
0.103125	0.21658157	1	1606
0.06940874	0.21654443	1	2327
0.061946902	0.21653263	1	2208
0.088989444	0.2165012	1	2726
0.0952381	0.21644299	1	1379
0.05447942	0.21640198	1	2324
0.008130081	0.21639843	1	3493
0.07972028	0.21632506	1	976
0.09298999	0.21632436	1	1944
0.038596492	0.21614802	1	492
0.036544852	0.21606708	1	3409
0.026595745	0.21602285	1	1895
0	0.21595849	1	3764
0.010277492	0.21594073	1	2286
0.025	0.21585888	1	3672
0.006097561	0.21579972	1	2246
0.08805031	0.21578811	1	1826
0.06928105	0.21560213	1	2750
0.08630952	0.2155924	1	3060
0.1	0.21553178	1	485
0.053412464	0.21547636	1	2920
0.040462427	0.21546115	1	2440
0.025219299	0.21538915	1	1715
0.03264418	0.21535246	1	2918
0.028138528	0.2152681	1	2137
0.07883818	0.21509805	1	2286
0.055757575	0.21494423	1	625
0.060225848	0.21490525	1	2786

0.00935551	0.21445887	1	1892
0.052375153	0.21443892	1	1853
0.028969957	0.21432075	1	3044
0.031659387	0.21424332	1	2561
0.020765027	0.21422434	1	2731
0.062087186	0.2141924	1	2060
0.030752916	0.21406399	1	1724
0.037439615	0.21405265	1	1667
0.070028014	0.21404159	1	918
0.018518519	0.21402839	1	2079
0.012170386	0.21388458	1	2650
0.02771855	0.21388261	1	3037
0.029443838	0.2138457	1	2560
0.012345679	0.21384133	1	2060
0.07528409	0.21379267	1	2823
0.0663199	0.2137892	1	1296
0.007322176	0.21376169	1	2377
0.03514739	0.21356188	1	1635
0.08819133	0.21348856	1	2263
0.03452116	0.2133412	1	1854
0.026373627	0.21332224	1	1662
0.04225352	0.21332017	1	1358
0.047091413	0.21268384	1	2377
0.07670851	0.2122887	1	1878
0.031496063	0.21179362	1	2327
0	0.21165174	1	3944
0.05379747	0.21130522	1	4174
0.077147014	0.21092135	1	1150
0	0.21084927	1	4184
0.079341315	0.21077469	1	680
0.034820456	0.21060924	1	1809
0.028376844	0.21058753	1	1893
0.0640625	0.21057098	1	2685
0.07816712	0.21053275	1	1742
0.03189066	0.21041143	1	2547
0.07079646	0.21027043	1	2857
0.033898305	0.20989142	1	3003
0.04171364	0.20985243	1	2103
0.029787235	0.2094323	1	2144
0.036556605	0.20940842	1	2722
0.08059701	0.20939864	1	1016
0.096045196	0.2092494	1	759
0.072524406	0.20924911	1	1135
0.029411765	0.20923074	1	2583
0.07097592	0.20920433	1	1965
0	0.208716	1	2568
0.015706806	0.20857994	1	2737
0.07171854	0.20857552	1	3031
0.03912543	0.20848058	1	1342
0.024886878	0.20846778	1	2193
0.052757792	0.20815389	1	689

0.033492822	0.20810203	1	4040
0.043181818	0.20808975	1	1486
0.041923553	0.20807226	1	2039
0.068456374	0.20807204	1	2245
0.080168776	0.20806818	1	1036
0.10044313	0.20796567	1	1261
0.024784483	0.20795126	1	2137
0.05945946	0.2079505	1	1077
0.051344745	0.20794365	1	1541
0.03926097	0.2079266	1	1995
0.032388665	0.20787783	1	3986
0.08396947	0.20780964	1	2561
0.025210084	0.20779562	1	4434
0.076712325	0.20774145	1	2722
0.034688994	0.20773715	1	2263
0.011235955	0.20762771	1	2247
0.07278021	0.20751433	1	2426
0.07946027	0.20740332	1	1535
0.034207527	0.2073152	1	2245
0.07305936	0.20724891	1	1298
0.021818181	0.20704754	1	2785
0.013824885	0.20698628	1	2023
0.06039326	0.20669313	1	2110
0.084485404	0.20603602	1	1450
0.010298661	0.20588261	1	1817
0.044879172	0.20580618	1	1329
0.06911765	0.20573258	1	973
0.048076924	0.20561363	1	2051
0.074324325	0.2055375	1	1940
0.01626898	0.20546716	1	1342
0.07114094	0.20478964	1	1360
0.018498369	0.20466907	1	2099
0.0648379	0.20465444	1	1930
0.078034684	0.20461528	1	522
0.06407035	0.20431821	1	1866
0.0493537	0.20410226	1	2202
0.042219542	0.2040264	1	2409
0.051533744	0.20383547	1	2631
0.04568528	0.20376523	1	1667
0.020042194	0.20374078	1	1893
0.067349926	0.2036004	1	1278
0.08049536	0.20291172	1	1961
0.07339449	0.20161335	1	1816
0.08438819	0.20142832	1	2512
0.041966427	0.20139469	1	2614
0.050887574	0.20139363	1	1878
0.08011445	0.2012496	1	2471
0.049808428	0.20105527	1	1298
0.06781915	0.2005697	1	1298
0.019629225	0.20032743	1	2064
0.08532934	0.20017548	1	1656

0.00404449	0.20013212	1	2647
0.04556355	0.19923928	1	1929
0.051378448	0.19910485	1	1546
0.08024691	0.19907449	1	1738
0.056213018	0.19862057	1	1403
0.058301646	0.1984107	1	1307
0.017259978	0.19837096	1	1867
0.049043063	0.1983466	1	1058
0.082969435	0.19834208	1	1381
0.023385301	0.19826682	1	2824
0.01910828	0.19760032	1	2248
0.0570523	0.19750911	1	1150
0.073446326	0.19737749	1	1990
0.03908046	0.19727309	1	2177
0.062834226	0.19707154	1	2706
0.042432815	0.1970352	1	3143
0.086657494	0.19700874	1	564
0.079222724	0.19700222	1	1535
0	0.19629802	1	2864
0.049242426	0.19614749	1	2722
0.021436227	0.19589072	1	2428
0	0.19579317	1	2864
0.045296166	0.19548938	1	2614
0.01910828	0.19537602	1	1342
0.06158358	0.19523528	1	334
0.06422018	0.19518521	1	2023
0.050314464	0.19450004	1	2730
0.03514377	0.1944153	1	2689
0.066079296	0.19371194	1	2049
0.06518724	0.19357517	1	2060
0.005070994	0.19355735	1	2009
0.04211793	0.19353367	1	1217
0.061516453	0.19345765	1	1030
0.061079547	0.19341753	1	2732
0.010183299	0.19330378	1	2327
0.068278804	0.19317997	1	1310
0.082442746	0.19312379	1	2428
0.029867256	0.19291537	1	2001
0.069986545	0.19276738	1	2060
0.010706638	0.19257876	1	2818
0.036655214	0.19228442	1	1660
0.020430107	0.19223322	1	2157
0.023542602	0.19203615	1	1353
0.0622665	0.1919327	1	1578
0.059334297	0.19192782	1	657
0.019438446	0.19186963	1	1753
0.042168673	0.19177549	1	592
0.03880597	0.19176635	1	3194
0.08160237	0.19173053	1	2286
0.06428572	0.1917225	1	1606
0.020585049	0.19159625	1	1989

0.03883495	0.19159424	1	4003
0.08594816	0.1915641	1	1625
0.025559105	0.19155423	1	1329
0.06295754	0.1914516	1	1893
0.026166098	0.19139925	1	2245
0.05049261	0.19129167	1	2601
0.065648854	0.1912339	1	2246
0.03884712	0.19120914	1	1308
0.06944445	0.19117364	1	1450
0.029045643	0.19116159	1	3114
0.08169014	0.19115692	1	1975
0.041990668	0.19109575	1	1578
0.055107526	0.19106072	1	2294
0.010638298	0.1905884	1	1563
0	0.18962264	1	3686
0.016546018	0.18912506	1	2080
0.041062802	0.18900682	1	2604
0.03358209	0.18895335	1	4502
0.033210333	0.18894053	1	3344
0.018299246	0.1872759	1	2580
0.058441557	0.18718609	1	442
0.06442167	0.18684506	1	1628
0.018691588	0.18663093	1	1889
0.016646849	0.18600838	1	1794
0.013274336	0.18593791	1	1337
0.06167979	0.1858132	1	2718
0.007291667	0.18567497	1	1667
0.029213483	0.18560287	1	1907
0.07704655	0.18538933	1	1656
0.035825547	0.18538386	1	8
0.039007094	0.18534525	1	2800
0.06940874	0.18533705	1	1305
0.0234375	0.1852678	1	1901
0.070809245	0.18521187	1	1360
0.017877094	0.18517701	1	2496
0.011802576	0.18513389	1	1557
0.04920213	0.1848752	1	1158
0.040364582	0.18485811	1	2787
0.08071749	0.1846969	1	2364
0.0634278	0.1846527	1	2372
0.010559662	0.18461236	1	2612
0.00409836	0.18446836	1	2722
0.012889367	0.18441056	1	2103
0.021857923	0.18429767	1	1892
0.06658131	0.18414083	1	1516
0.007551241	0.18405522	1	1878
0.016538037	0.18368763	1	2302
0.06807867	0.1835495	1	580
0.052473765	0.18352388	1	2200
0.00204499	0.18328631	1	2637
0.0637037	0.18315333	1	741

0.05865922	0.18303046	1	2056
0.068554394	0.18301278	1	1516
0.034924332	0.18294355	1	1812
0.06859756	0.18293898	1	525
0.009761388	0.18284287	1	1774
0.06017192	0.18281417	1	424
0.014084507	0.1828073	1	4370
0.006185567	0.18259141	1	2228
0.05196629	0.18254055	1	2578
0.046043165	0.18249388	1	1628
0.022118744	0.1820586	1	2637
0.07153076	0.18191287	1	1667
0.044444446	0.18186563	1	2247
0.04336735	0.1818286	1	3147
0.014629049	0.18182507	1	1904
0.06119403	0.18182428	1	2245
0.021671826	0.18101734	1	1617
0.015923567	0.17999825	1	2732
0.018223235	0.179987	1	2435
0.002030457	0.17995349	1	2167
0.003141361	0.17993902	1	1973
0.058479533	0.17993322	1	2428
0.008501594	0.17987718	1	2319
0.018259935	0.17982854	1	3020
0.03325123	0.1797589	1	2081
0.044094488	0.17972428	1	63
0.02433372	0.17960718	1	1578
0.0549273	0.17955738	1	797
0.044665013	0.17936137	1	2637
0.06216216	0.17901452	1	2283
0.007150153	0.17867325	1	2082
0.046801873	0.17863084	1	792
0.004119465	0.17862427	1	2049
0.043421052	0.17852265	1	1788
0.01632209	0.17847593	1	1642
0.014023732	0.1782332	1	2162
0.03404792	0.17811503	1	1397
0.046025105	0.17783009	1	2040
0.0474359	0.17738709	1	2818
0.043927647	0.1773649	1	2598
0.006116208	0.17725453	1	2820
0.02467685	0.17723626	1	1516
0.049056605	0.17666376	1	1894
0.022326674	0.1766589	1	1578
0.04834254	0.17661007	1	1521
0.029020555	0.1764571	1	2228
0.0472879	0.17642295	1	1711
0.020674646	0.17642261	1	2428
0.060371518	0.17637809	1	1432
0.025142858	0.17636998	1	2889
0.027777778	0.17632423	1	1326

0.050824177	0.17628385	1	1679
0.042682927	0.17619182	1	2776
0.012820513	0.17618997	1	1708
0.05327869	0.1761707	1	2177
0.018660812	0.17601034	1	2802
0.05105105	0.17599878	1	2458
0.016008537	0.17537826	1	2447
0.023837902	0.17534563	1	2132
0.016778523	0.17524321	1	2732
0.026436782	0.17503639	1	2551
0.054208275	0.17502257	1	2025
0.062222224	0.17499976	1	2049
0.047557842	0.17491186	1	2263
0.016797312	0.17490037	1	2636
0.011458334	0.17228666	1	2226
0.023255814	0.17226167	1	1634
0.013333334	0.1720627	1	2573
0.01459854	0.17193423	1	2409
0.045643155	0.171892	1	1578
0.03995006	0.1717792	1	1298
0.05087209	0.17162003	1	1261
0.024937656	0.17115793	1	1588
0.043923866	0.17096864	1	1939
0.034528553	0.17096761	1	1821
0.037419356	0.17083451	1	2099
0.0509915	0.17080952	1	1615
0.009564294	0.17067379	1	2754
0.03180212	0.17067234	1	1486
0.053521127	0.17036864	1	1078
0.009857613	0.170278	1	2482
0.057991512	0.17013317	1	2394
0.044585988	0.17013091	1	2158
0.036793694	0.17012537	1	2177
0.028153153	0.17009279	1	2726
0.053908356	0.17005505	1	2732
0.019955654	0.16996363	1	2527
0.048811015	0.16995694	1	822
0.05794948	0.16993631	1	960
0.03975535	0.16992821	1	1236
0.053908356	0.16963239	1	2722
0.006185567	0.16952561	1	1567
0.048529413	0.16945419	1	1298
0.05743741	0.16940649	1	1125
0.047486033	0.16927144	1	2170
0.029761905	0.16895665	1	2226
0.002038736	0.16876775	1	1761
0.020491803	0.1686359	1	1516
0.037371133	0.16861364	1	2111
0.05214724	0.16858314	1	2316
0.023529412	0.16848598	1	2598
0.044871796	0.16818789	1	1137

0.005159959	0.16818555	1	2133
0.047328245	0.16815315	1	914
0.03971631	0.16774918	1	3056
0.01754386	0.16759354	1	1607
0.026402641	0.16714525	1	2409
0.027692307	0.16703974	1	1319
0	0.16666648	1	3940
0.001027749	0.16616705	1	1628
0.045572918	0.16610529	1	2698
0.003064351	0.1661009	1	1615
0.02232143	0.1660779	1	1639
0.046898637	0.16598924	1	2228
0.054363377	0.16589512	1	1788
0.021905806	0.16577037	1	1246
0.028753994	0.16570148	1	4436
0.039835166	0.16570078	1	2404
0.06789251	0.16558641	1	1635
0.023968043	0.16546904	1	1534
0.054131053	0.1653854	1	1288
0.03539823	0.16532192	1	2901
0.040469974	0.16525191	1	1329
0.047210302	0.16520733	1	2664
0.029972753	0.16520339	1	2278
0.023255814	0.16471703	1	2469
0.012061403	0.1643851	1	2153
0.016483517	0.16427158	1	2750
0.020408163	0.16421619	1	1450
0.012944984	0.16420525	1	1880
0.035904255	0.16413093	1	1174
0.045454547	0.16412349	1	1882
0	0.16396709	1	3641
0.025608195	0.16321236	1	2546
0.023755657	0.16318546	1	1913
0.039573822	0.1628296	1	762
0.023228804	0.16278729	1	2750
0.047210302	0.16262065	1	1849
0.009503696	0.16254196	1	2802
0.016574586	0.16165666	1	2493
0.010604454	0.16149402	1	2413
0.037463978	0.16134816	1	2466
0.02877698	0.16134053	1	1036
0.012711864	0.16129303	1	2273
0.047210302	0.16117981	1	955
0.026862027	0.16116017	1	1606
0.016835017	0.1611359	1	2741
0.03566879	0.1611285	1	1340
0.03821656	0.1610649	1	1326
0.012074643	0.1610402	1	1030
0.038043477	0.1610388	1	1340
0.056801196	0.16098012	1	663
0.024	0.16091731	1	226

0.034108527	0.16083568	1	887
0.029891305	0.16079292	1	2561
0	0.16075613	1	4265
0.05676856	0.16071434	1	1208
0.017492712	0.16071372	1	2220
0.016	0.16071115	1	2226
0.057534248	0.16069135	1	1234
0.011578947	0.16066834	1	1613
0.046309695	0.16064143	1	1606
0.037220843	0.16059238	1	1724
0.01988304	0.1605744	1	2051
0.029166667	0.16055298	1	4502
0.022246942	0.1605368	1	1558
0.03629537	0.16051851	1	2316
0.043708608	0.16049264	1	2584
0.040221915	0.16049065	1	1273
0.044576522	0.16048807	1	1535
0.0431433	0.16046394	1	1257
0.038356163	0.16043659	1	2327
0.040268455	0.16043086	1	2637
0.041614123	0.16040982	1	2471
0.044444446	0.16038603	1	1713
0.009911894	0.160213	1	2131
0.04855842	0.16015586	1	1432
0.02364865	0.1597046	1	1992
0.047413792	0.15961269	1	639
0.005555556	0.15942816	1	3648
0.015151516	0.15911356	1	2157
0.014423077	0.15902814	1	1429
0.035220128	0.15899333	1	2228
0.018285714	0.15889095	1	1450
0.056149732	0.1588165	1	374
0.012181616	0.15867215	1	2108
0.019721577	0.15858999	1	1578
0.03767661	0.15856509	1	1516
0.019079685	0.1585137	1	1673
0.048882682	0.15830569	1	2637
0.039940827	0.15737608	1	1150
0.039835166	0.1572294	1	2523
0.039039038	0.15650316	1	1961
0	0.15647168	1	1725
0.03305785	0.15646245	1	3147
0.04041916	0.15644851	1	1794
0.02754491	0.15642881	1	1724
0.05007364	0.1563225	1	938
0.024032043	0.15625963	1	1655
0.043600563	0.15617277	1	2147
0.008705114	0.15568778	1	3069
0.004166667	0.15516178	1	1821
0.023514852	0.15513277	1	1199
0.034956306	0.15511928	1	2578

0.03773585	0.15509528	1	1236
0.023199024	0.15506448	1	1134
0.035555556	0.15504469	1	1022
0.01986755	0.15501413	1	1817
0	0.15500085	1	2098
0.04526749	0.1549942	1	2680
0.015222482	0.15498705	1	1930
0.044992745	0.1548975	1	1652
0.01939394	0.15481089	1	2675
0.013348165	0.15476163	1	2348
0.018450184	0.15432505	1	2469
0.039285716	0.15380633	1	80
0.024675325	0.15367974	1	2731
0.033210333	0.15355113	1	3409
0.021403091	0.1535337	1	1460
0.03521127	0.15349896	1	387
0.030456852	0.15347718	1	2051
0.024647888	0.15326065	1	2777
0.029717682	0.15321065	1	689
0.01419214	0.15306099	1	2247
0.029985007	0.15294792	1	917
0.045801528	0.15288198	1	747
0.035842296	0.15282822	1	3940
0.040391676	0.15282339	1	1160
0.031152649	0.15276417	1	2010
0.025188917	0.15271018	1	2051
0.002034588	0.15270019	1	2008
0.001017294	0.15269254	1	1748
0.025675675	0.15255739	1	1497
0.015217391	0.15251462	1	1861
0.001035197	0.15173185	1	1667
0.02690583	0.15083499	1	1840
0.015184382	0.14993566	1	2200
0.049157303	0.14984171	1	2245
0.005268704	0.14975408	1	2133
0.04397163	0.14965361	1	2283
0.01902497	0.14964122	1	2004
0.013513514	0.14963703	1	1648
0.024111675	0.14954633	1	1606
0.029275808	0.14946182	1	2060
0.025487257	0.14945573	1	1310
0.029282577	0.14945099	1	1727
0.03125	0.14943914	1	1337
0.033163264	0.14929223	1	2465
0.008686211	0.14926855	1	1631
0.03038674	0.14923075	1	1882
0.03524229	0.14902939	1	2223
0.024423338	0.14890781	1	2476
0.016722407	0.14881806	1	2786
0.04087591	0.14880425	1	1310
0.010729614	0.14876819	1	2056

0.029372497	0.14876011	1	1107
0.005364807	0.14866501	1	2800
0.014672686	0.14854875	1	1485
0.012035011	0.14854112	1	1909
0.031914894	0.14849257	1	1274
0.026392963	0.14766286	1	6
0.03210273	0.14765844	1	653
0.024937656	0.14759177	1	1381
0.02354399	0.14758563	1	1892
0.036414567	0.14757954	1	1125
0.022955524	0.14757939	1	1939
0.028688524	0.14753449	1	1101
0.014218009	0.14746018	1	689
0.005512679	0.14740814	1	1397
0.024242423	0.14727214	1	2656
0.003089598	0.14718872	1	2132
0.03448276	0.14690652	1	1839
0.011853448	0.14676572	1	1454
0.00304878	0.146742	1	2336
0.009771987	0.1466851	1	1372
0.03817734	0.1466315	1	2601
0.028688524	0.14660646	1	2223
0.00203252	0.14655024	1	1954
0.04055944	0.14648394	1	1278
0.026865672	0.14601332	1	1377
0.025459688	0.14596494	1	689
0.030674847	0.14581291	1	1812
0.007616975	0.14576074	1	2250
0.027522936	0.14572942	1	2791
0.013597033	0.14558268	1	1174
0.021768708	0.14558116	1	1340
0.043348283	0.14549327	1	1298
0.02117061	0.14525932	1	2025
0.010964912	0.14441212	1	2200
0	0.14421515	1	2158
0.04084507	0.1442105	1	828
0.016336055	0.14386348	1	2578
0.014184397	0.14379452	1	1122
0.024783147	0.14377765	1	1288
0.03362573	0.14367147	1	929
0.021590909	0.14365068	1	1715
0.02375	0.14359201	1	1625
0.044207316	0.14342575	1	1298
0.015822785	0.14313042	1	3204
0.028328612	0.14311492	1	2044
0.023923445	0.14259627	1	3621
0.03508772	0.142443	1	2220
0.010905125	0.14230375	1	2157
0.015681544	0.1422803	1	2224
0.02834008	0.14219964	1	2133
0.027063599	0.14206788	1	1371

0.016987542	0.14175695	1	2291
0.015723271	0.14155254	1	3204
0.006329114	0.14142627	1	1817
0.032133676	0.14134663	1	1567
0.008733625	0.1413304	1	1809
0.034532376	0.14111578	1	1817
0.033163264	0.14090158	1	1682
0.012168142	0.1408888	1	2584
0.026548672	0.1407896	1	1954
0.016222479	0.14037044	1	1652
0.017565873	0.14018142	1	2193
0.013844515	0.13986348	1	1578
0.009656653	0.13952598	1	2081
0.025873221	0.13936381	1	1655
0.014833127	0.13912272	1	2671
0.024203822	0.13870797	1	1340
0.03133903	0.13810039	1	1727
0.021814007	0.13761085	1	541
0.001034126	0.13759872	1	2025
0.025139665	0.13758527	1	978
0.017721519	0.13753219	1	1832
0.022891566	0.13750899	1	2223
0.027272727	0.1374675	1	363
0.009950249	0.13745174	1	3787
0.032216493	0.13743633	1	2532
0.005399568	0.13721178	1	1711
0	0.13718694	1	2116
0.019255456	0.13715029	1	1576
0.020481927	0.13712305	1	2394
0.012084592	0.13710542	1	1153
0.02147651	0.1370766	1	1329
0.004338395	0.1370283	1	1866
0.024296675	0.13697846	1	1340
0.005274262	0.13696937	1	1904
0.027741084	0.13692962	1	1417
0.0259366	0.13688047	1	1450
0.03773585	0.13686313	1	2214
0.014573991	0.1368097	1	1839
0.023114355	0.13680929	1	2364
0.008537887	0.13678968	1	1727
0.006666667	0.13676633	1	2114
0.03240059	0.13674697	1	401
0	0.13667282	1	3239
0.018327607	0.13666368	1	2167
0.007734807	0.13661055	1	2157
0.003108808	0.13628337	1	1859
0.029325513	0.13625485	1	2010
0.028688524	0.13616946	1	3028
0.021403091	0.13604982	1	2025
0.016483517	0.1360492	1	1904
0.02293578	0.1358561	1	1639

0.010905125	0.13583937	1	1727
0.007434944	0.13565461	1	3648
0.025706941	0.13550031	1	2039
0.023633678	0.1354562	1	870
0.005524862	0.13529591	1	4657
0.03021148	0.13526075	1	1325
0.022222223	0.13524303	1	2469
0.014492754	0.13523084	1	1866
0.005482456	0.13521759	1	822
0.023977432	0.13513926	1	917
0.021091811	0.1350132	1	2263
0.008695652	0.13501142	1	2447
0.002074689	0.13485551	1	1624
0.028528528	0.13482217	1	1742
0.002074689	0.1346784	1	2079
0.010799136	0.1344534	1	2726
0.02749141	0.1344377	1	3651
0.024827586	0.13439396	1	2153
0.01510574	0.13434155	1	1808
0.02112676	0.13423382	1	957
0.03372434	0.13419205	1	1312
0.029508196	0.13413021	1	1429
0.029453015	0.13400519	1	2246
0.019005848	0.13390906	1	249
0.018610422	0.13387847	1	1612
0.02877698	0.13387024	1	2088
0.006578947	0.13382864	1	1466
0.024128687	0.13365549	1	1599
0.009584664	0.13365185	1	2472
0.025236594	0.13362044	1	2680
0.01993865	0.13356888	1	1625
0.010135135	0.1335145	1	1215
0	0.13325843	1	3224
0	0.13313662	1	3986
0.005952381	0.13299535	1	4038
0.019736841	0.13288805	1	2120
0.022068966	0.1328784	1	1711
0.026865672	0.13286541	1	533
0.005291005	0.1328325	1	3653
0.022364218	0.13282047	1	3844
0.023952097	0.13274913	1	1241
0.024096385	0.13265674	1	1882
0.042704627	0.13231401	1	2586
0.00591716	0.1322565	1	2899
0.021201413	0.1320236	1	4250
0.022364218	0.13173933	1	899
0.018461538	0.13130975	1	614
0.016806724	0.13069099	1	5125
0.019607844	0.1304475	1	2581
0.030172413	0.1303685	1	1338
0.00308642	0.13035378	1	2201

0	0.13028194	1	1317
0.016348774	0.13016112	1	1761
0.024390243	0.13014199	1	3621
0.031296574	0.13005853	1	1517
0.02086231	0.13004999	1	2245
0.008898776	0.12937474	1	2039
0.009503696	0.1292935	1	2039
0.014412417	0.12922527	1	2177
0.013941699	0.12906036	1	1724
0.03021978	0.12899312	1	1606
0.020188425	0.12876342	1	689
0.020356234	0.1287118	1	657
0.0077951	0.12870096	1	2301
0.003108808	0.12868519	1	2732
0.02366864	0.12852386	1	1036
0.026595745	0.12760855	1	1606
0.004343106	0.12737915	1	1490
0.03178808	0.12540582	1	1526
0.013377926	0.12455773	1	423
0.017114915	0.12376533	1	2133
0.028148148	0.123665474	1	1631
0.008928572	0.123436294	1	1323
0.022865854	0.123182446	1	1326
0.005458515	0.12303621	1	2471
0.013947002	0.12288457	1	1534
0.0225	0.12282869	1	2202
0.013924051	0.122794725	1	2010
0.007847534	0.12261158	1	2249
0.02503477	0.12258243	1	1567
0.008536586	0.12249928	1	2440
0.015686275	0.1222979	1	1077
0.020186335	0.122284405	1	1072
0.018838305	0.12211387	1	870
0.010055866	0.12200095	1	2413
0.02387268	0.12194548	1	2202
0.011976048	0.121898256	1	1329
0.006564552	0.12185681	1	2409
0.021052632	0.12181742	1	678
0.015625	0.12172345	1	914
0.009367681	0.12166641	1	1485
0.02265861	0.1216229	1	2039
0.02118003	0.1215688	1	553
0.016847173	0.12154445	1	2560
0.021929825	0.12153533	1	506
0.007462686	0.12148985	1	1662
0.016766466	0.121477805	1	1987
0.020344287	0.12145253	1	183
0.013924051	0.121425584	1	2560
0.009677419	0.12121225	1	1353
0.008187135	0.12102691	1	1828
0.023611112	0.12096216	1	1930

0.022972973	0.12085437	1	1340
0.011185682	0.11980564	1	2073
0.02110818	0.11968562	1	2637
0.023383768	0.11967837	1	2223
0.010465116	0.119664416	1	1625
0.010135135	0.119647324	1	1342
0.013559322	0.119632944	1	2060
0.012711864	0.11956233	1	680
0.013142174	0.11952143	1	1821
0.023591088	0.119509995	1	1567
0.013615734	0.119422756	1	1298
0.017857144	0.11935491	1	803
0.019354839	0.11929716	1	1284
0.020075282	0.119213894	1	1894
0.013253012	0.11921156	1	1325
0.02141901	0.11920573	1	2223
0.01173709	0.11918546	1	1893
0.017567568	0.11916991	1	1635
0.023121387	0.11911147	1	870
0.002068252	0.11901702	1	2547
0.0078125	0.118792474	1	1516
0.018726591	0.118704244	1	1222
0.012765957	0.11863243	1	4470
0.006535948	0.11860729	1	2123
0.004357298	0.118514895	1	2800
0.01509434	0.11832445	1	1832
0.018300654	0.11831862	1	2158
0.021186441	0.118168436	1	981
0.01517067	0.11814104	1	1498
0.020833334	0.11813207	1	1662
0.002066116	0.11810266	1	2318
0.012331839	0.11801002	1	1871
0.008902078	0.11800971	1	1160
0.012158055	0.117867514	1	411
0.006622517	0.1177684	1	1338
0.0087241	0.11776542	1	2298
0.006067961	0.11771482	1	1894
0.024096385	0.11765037	1	2200
0.01146789	0.117646486	1	1871
0.008443909	0.11758935	1	1346
0.016393442	0.11747589	1	2202
0.027586207	0.11746763	1	2561
0.028089888	0.11741008	1	978
0.010309278	0.11740912	1	1708
0.003232759	0.11740875	1	2226
0.011730205	0.117262535	1	2006
0.021947874	0.11724173	1	1036
0.013333334	0.117184475	1	564
0.009467456	0.11718427	1	1178
0.015988372	0.1171771	1	833
0.011990408	0.11707621	1	1449

0.004545454	0.11573464	1	3355
0.012422361	0.114861526	1	2069
0.011673152	0.114675395	1	1261
0.002333722	0.11466926	1	2893
0.010135135	0.11456238	1	1711
0.002159827	0.11446708	1	1624
0	0.11445442	1	1822
0.017105263	0.114436254	1	2818
0.009174312	0.1143724	1	2133
0.016774194	0.11437103	1	2147
0.008752735	0.114308864	1	1283
0.025608195	0.11427985	1	2099
0	0.11425393	1	2279
0.008602151	0.11423652	1	629
0.018651363	0.11415425	1	1377
0.01	0.11411838	1	2582
0.020942409	0.11410963	1	1323
0.018741634	0.112907946	1	1805
0	0.11278059	1	4945
0	0.112671316	1	1959
0.022950819	0.112512454	1	1118
0.016438356	0.11225734	1	2217
0.004329004	0.11222056	1	2023
0.009202454	0.112097114	1	838
0.007434944	0.11195523	1	3742
0.002178649	0.11187358	1	1313
0.013201321	0.111778386	1	3032
0.011164274	0.11157854	1	112
0.011450382	0.111073405	1	4311
0.012228261	0.111046046	1	1531
0.008450705	0.11083468	1	1662
0.004672897	0.11067108	1	4051
0.009259259	0.110503666	1	938
0	0.11048786	1	3866
0.014851485	0.110368565	1	2136
0.012987013	0.11032019	1	2220
0	0.110261716	1	2699
0.006451613	0.110156305	1	1556
0.021621622	0.11009291	1	2108
0.024822695	0.11008317	1	2409
0.018207284	0.11003606	1	1667
0.010613208	0.109904096	1	1490
0.00886918	0.10971138	1	2069
0.016620498	0.10968205	1	2085
0	0.109417886	1	3630
0.004464286	0.10941158	1	2103
0.01369863	0.10939832	1	978
0	0.109334305	1	1566
0.004338395	0.10927994	1	1904
0.012113055	0.10925232	1	317
0.016105417	0.10923601	1	580

0.010380623	0.109172225	1	1893
0.012987013	0.10911729	1	1656
0.012838801	0.10908292	1	671
0.017326733	0.10903481	1	2225
0.011826544	0.109010026	1	1072
0.020435967	0.10900076	1	1711
0.007281554	0.10893015	1	1921
0.005800464	0.10888507	1	2052
0.013647643	0.108815186	1	1719
0.010043042	0.10880446	1	1828
0.00729927	0.108687215	1	2051
0.01632653	0.10816443	1	3927
0.005506608	0.10753344	1	1880
0.016476553	0.10745948	1	1567
0.004366812	0.107458465	1	1608
0.003161222	0.10745301	1	1298
0.007117438	0.107207	1	1323
0	0.106934234	1	2799
0.021650879	0.106113315	1	1608
0.007389163	0.105786964	1	1234
0.013888889	0.105264865	1	1241
0	0.104508966	1	2295
0	0.10450848	1	1882
0.009049774	0.104271814	1	2039
0.020915033	0.10420008	1	1881
0.011612903	0.10356385	1	2152
0.011990408	0.1034985	1	2516
0.014511873	0.10342476	1	1656
0.007100592	0.103378415	1	2125
0.010830325	0.10330113	1	1497
0.01174743	0.103034005	1	1567
0.001021451	0.102773905	1	1557
0.020460358	0.10275703	1	2560
0.014513788	0.10263337	1	1636
0.011306533	0.10259759	1	1567
0.006688963	0.102567144	1	2356
0.012139605	0.10255984	1	908
0.009032258	0.10253284	1	1882
0.001051525	0.10252742	1	1346
0	0.102490455	1	2027
0.004405286	0.102388784	1	2023
0.009237875	0.10236038	1	2147
0.013808976	0.10227781	1	1923
0.011778563	0.10224139	1	1631
0	0.10223272	1	2800
0.004622496	0.1021526	1	6
0.006544503	0.1021406	1	2074
0.010463378	0.10211003	1	1490
0.006015038	0.10206047	1	424
0.001058201	0.10205525	1	2305
0.001049318	0.10201168	1	2379

0.008658009	0.10193653	1	1450
0.01399689	0.10177978	1	1655
0.01650619	0.101736754	1	1578
0.004559271	0.101708345	1	1141
0.013586956	0.1015966	1	1990
0.015736766	0.101429716	1	1486
0.007153076	0.10142866	1	2133
0.007963595	0.10124646	1	2614
0.008805032	0.101229355	1	2404
0	0.10119803	1	1954
0.007220217	0.1011923	1	2477
0.003264418	0.10119201	1	1917
0.002159827	0.10116647	1	1893
0.003151261	0.10091838	1	2379
0.009815951	0.10072174	1	2839
0.009090909	0.100252405	1	644
0.008215962	0.10005003	1	2560
0.005813954	0.09996597	1	2466
0.001055966	0.09993164	1	1679
0.007168459	0.09970765	1	2052
0	0.0996014	1	1680
0.002134472	0.09929374	1	2123
0.01305483	0.09892497	1	2202
0.007001167	0.098918274	1	2264
0.011494253	0.09865776	1	1454
0.008578432	0.0983311	1	689
0.007692308	0.09824996	1	2523
0.016169155	0.098176725	1	2786
0.006864989	0.09815404	1	1667
0.011331445	0.098118104	1	1531
0.007556675	0.09807453	1	3326
0.005382131	0.09804859	1	1160
0.003378379	0.09801109	1	2327
0.007727976	0.09786453	1	1068
0.010899182	0.09780462	1	1628
0.010204081	0.09770055	1	2112
0.001027749	0.09770011	1	2209
0.011396011	0.0976971	1	1781
0.01472754	0.09766558	1	663
0.008663367	0.09761391	1	2217
0.01058201	0.097583644	1	689
0.008438818	0.097538404	1	1788
0.015404365	0.09749542	1	1913
0.012030075	0.09747343	1	2248
0.008962868	0.09744316	1	1302
0.008988764	0.09743608	1	2024
0.014577259	0.09741183	1	1399
0	0.097360805	1	2735
0.005961252	0.09735842	1	1230
0.012610341	0.09734875	1	2024
0.003125	0.09731825	1	2099

0.003685504	0.09717762	1	2202
0.011920529	0.09690716	1	1077
0.010610079	0.09685084	1	1741
0.00877193	0.09666313	1	2698
0.013597033	0.09665324	1	2537
0.008253095	0.09663972	1	1336
0.001062699	0.09659779	1	2413
0.005399568	0.09658279	1	897
0.014880952	0.09653675	1	1331
0.002145923	0.09648619	1	1737
0.020833334	0.096398115	1	1024
0.013850415	0.096214965	1	1340
0.006872852	0.09619688	1	1500
0.010709505	0.09615586	1	1713
0.006651885	0.096055545	1	1965
0.001121076	0.0960365	1	1302
0.003318584	0.09595646	1	1534
0.007132668	0.09593842	1	574
0	0.09587182	1	2101
0.004287245	0.095818646	1	2483
0	0.09576312	1	1306
0.004178273	0.09573475	1	1648
0.013349514	0.09566489	1	2079
0.011994003	0.09543053	1	2234
0.012886598	0.09539774	1	1180
0.003329634	0.09539273	1	1713
0.008608322	0.09534317	1	349
0.002217295	0.09523931	1	2327
0.007575758	0.09506759	1	2787
0	0.09504245	0.999	3594
0.010484928	0.09491954	1	689
0.003325942	0.09453057	1	2698
0.004405286	0.0943345	1	2202
0	0.09363565	1	2427
0.00736377	0.09362833	1	318
0.010075566	0.093149535	1	2287
0.007822686	0.09305321	1	1648
0.005599104	0.093036294	1	2099
0.008746356	0.09302283	1	1340
0.005830904	0.09294479	1	1267
0.002304148	0.09287786	1	1828
0.010178117	0.092867896	1	1269
0.00807537	0.09284924	1	1648
0.005121639	0.0927865	1	2245
0.006833713	0.09263351	1	2085
0.006144393	0.09263223	1	1036
0.012629162	0.092603244	1	1589
0.013062409	0.09242755	1	1036
0.012605042	0.09240829	0.999	3345
0.004592422	0.09240588	1	1881
0.001111111	0.09238672	1	2133

0	0.09217717	1	2024
0.006587615	0.092167	1	1084
0.005524862	0.092162885	1	1456
0.008	0.09211656	1	1486
0.006273526	0.09207944	1	1788
0.005025126	0.09192454	1	1538
0.001259446	0.09180476	1	1788
0.004415011	0.09173119	1	1752
0.004504505	0.09163986	0.999	4007
0.005340454	0.09126082	1	1522
0	0.09102772	0.999	3690
0	0.090686604	0.999	4097
0.006734007	0.090610825	0.999	3986
0.007001167	0.08801431	1	1460
0	0.08792481	1	1828
0.01076716	0.08785807	1	1578
0.003623189	0.087815866	1	1741
0.007112376	0.08781242	1	1713
0.009950249	0.0877789	1	1921
0.007237636	0.08769465	1	2247
0.002207506	0.08739733	1	1849
0	0.087311335	0.997	2309
0.008219178	0.08718081	1	1486
0.004576659	0.08710593	1	2214
0.007462686	0.08707176	0.997	4005
0.001230012	0.08703543	1	726
0.006479482	0.08698273	1	2271
0	0.086864844	0.997	3493
0.00433526	0.08681866	1	859
0.010727056	0.08643121	1	2466
0	0.08593354	0.997	1990
0.004778972	0.08575132	1	2051
0.003303965	0.08565113	1	1338
0.00728863	0.08541187	1	856
0	0.08535941	1	1342
0.006329114	0.08525343	1	1808
0.010088272	0.08489101	1	1608
0.007092198	0.08458586	1	1331
0.001037345	0.08455524	1	2027
0.008086253	0.08452303	1	2040
0	0.0843125	1	2477
0.002234637	0.08408724	1	2025
0.003081664	0.08391536	1	1048
0.007407407	0.0836671	1	948
0.002355713	0.083058655	1	1882
0.005012531	0.082683906	1	2229
0.00390625	0.08119805	1	1828
0.00330033	0.08077186	1	1377
0.001084599	0.08061876	1	1864
0	0.08045171	1	2529
0.003278689	0.079704605	1	2009

0.005805515	0.07961119	1	2248
0.003567182	0.07934511	1	2327
0.007185629	0.07919526	1	1734
0.004784689	0.07918795	1	1542
0.00476758	0.0791726	1	2668
0	0.07911768	1	2726
0.003053435	0.07910189	1	844
0.003355705	0.0789779	1	1788
0.003571429	0.07892401	1	1567
0.001096491	0.07885424	1	2471
0.002229655	0.07884247	1	2147
0.009067358	0.07878924	1	2025
0.003159558	0.07873487	1	806
0	0.07865546	1	2455
0.007211539	0.078611225	1	1648
0	0.07860376	1	2025
0.001109878	0.07859666	1	1482
0.006944445	0.07859025	1	859
0.002272727	0.07858403	1	2025
0.004324324	0.07857755	1	1406
0.004524887	0.07856667	1	432
0.004705882	0.07856422	1	1340
0.008230452	0.07854504	1	344
0.003397509	0.0784786	1	1741
0.014184397	0.07843145	0.996	3855
0.002254791	0.07830107	1	1180
0.002347418	0.0782374	1	1699
0.004255319	0.0780347	1	318
0.005398111	0.078033604	1	1180
0	0.07589169	0.996	2552
0.005277045	0.07467123	1	2006
0.003307608	0.074480586	1	1859
0	0.07429964	0.996	3042
0.004592422	0.0742825	1	2336
0	0.07399629	0.995	4038
0.009695291	0.07339257	1	1788
0.004672897	0.07248723	1	1450
0.001445087	0.07158854	1	1517
0.006075334	0.07154982	1	1195
0.002350176	0.07137515	1	2132
0	0.07133227	1	1853
0.003452244	0.07111646	1	2103
0.001577287	0.071075596	1	838
0.001145475	0.071074665	1	1788
0.003831418	0.0709206	1	2027
0.001278772	0.07090275	1	1497
0.005625879	0.070868984	1	944
0.001077586	0.070547424	1	1711
0.001501502	0.07037239	1	379
0.004895961	0.07035804	1	2560
0	0.0703573	1	1601

0.001098901	0.07010764	1	1566
0.001293661	0.06927815	1	1417
0.003318584	0.06918221	1	1869
0.002096436	0.068961576	1	1839
0.001449275	0.06894653	1	1606
0	0.06882282	1	1970
0.001547988	0.06877091	1	592
0.005706134	0.06844446	1	1483
0.004854369	0.06842539	1	1673
0.00530504	0.068341315	1	834
0	0.06815617	0.987	3855
0	0.06815292	1	1606
0.002617801	0.06803238	1	1788
0.00220022	0.067747846	1	1927
0.00120919	0.06774773	1	1667
0	0.067453004	0.987	2098
0.005154639	0.06725609	1	1715
0.005256242	0.06652993	1	2194
0.002906977	0.06603344	1	2
0	0.06561094	1	2228
0.008474576	0.06551208	1	1813
0	0.06531531	1	1894
0	0.065282755	1	1190
0.005284016	0.06519842	1	1667
0.001377411	0.06490707	1	2006
0	0.06488076	1	1840
0.006150062	0.06486713	1	1115
0.003370787	0.064857095	1	1686
0	0.06469922	1	2327
0.002298851	0.06463353	1	2099
0.00122549	0.06438416	1	1713
0	0.064372554	1	2331
0.003370787	0.06428987	1	1230
0.004968944	0.06418663	1	1788
0.005449591	0.06386521	1	1261
0.003601441	0.06375393	1	2802
0	0.06375311	1	1817
0.004092769	0.063733384	1	1432
0.003717472	0.063571535	1	1667
0.003645201	0.063479185	1	2263
0.001068376	0.063453496	1	1636
0	0.06335311	1	2024
0.00530504	0.06333774	1	2039
0.001472754	0.06333708	1	1160
0	0.06333141	1	1842
0	0.06332816	0.982	2114
0	0.06324798	1	1606
0.001369863	0.06302642	1	1172
0.003856041	0.06290923	1	846
0.002894356	0.062820315	1	1635
0.003802281	0.06267754	1	851

0.005256242	0.06260718	1	634
	0 0.06254779	0.981	3713
	0 0.062468663	1	1861
	0 0.062416453	1	1048
0.00284495	0.062275276	1	1606
	0 0.06220967	1	1648
0.004901961	0.06205333	0.979	4548
	0 0.061971053	1	1642
	0 0.0618496	0.978	2088
0.00120048	0.061842892	1	1635
0.007518797	0.06178976	1	2578
	0 0.0616858	0.975	4053
0.003012048	0.06154726	0.999	169
0.001453488	0.061321143	1	411
	0 0.06115115	0.956	4063
	0 0.06082242	0.956	2973
	0 0.059900843	0.956	2294
0.001191895	0.059894733	0.999	1326
	0 0.059677407	0.965	2601
0.004310345	0.059454445	0.96	3291
0.003412969	0.05935674	0.97	2409
	0 0.058953978	0.956	3493
0.005050505	0.058932457	0.97	1296
0.010948905	0.058907714	0.968	1987
0.003184713	0.05887556	0.965	1216
	0 0.05853177	0.998	2147
0.0013947	0.057996266	0.998	698
	0 0.05764777	0.943	2023
	0 0.057639368	0.999	2214
0.001459854	0.057603583	0.997	6
0.002344666	0.057566367	0.999	1290
0.001088139	0.057259876	0.999	2214
0.006345178	0.05720412	0.999	1667
0.004825091	0.056998808	0.999	1115
	0 0.05686378	0.933	2098
	0 0.05679643	0.936	3901
	0 0.056784578	0.929	5071
	0 0.05673531	0.999	1832
	0 0.056577843	0.943	2114
0.003836317	0.05656492	0.997	2073
	0 0.056016188	0.919	4414
0.003567182	0.055846024	0.996	1298
	0 0.055388603	0.897	4307
	0 0.05488322	0.92	2294
	0 0.054704454	0.899	2294
	0 0.05465605	0.996	1746
0.0027894	0.054544825	0.996	1160
0.003703704	0.054191563	0.996	1333
	0 0.054067615	0.901	2294
0.001119821	0.053747334	0.994	2079
	0 0.053712342	0.92	2088

0.001075269	0.053424347	0.995	2200
0.001510574	0.05341958	0.994	379
0.001264223	0.0532881	0.995	220
0.001177856	0.053133693	0.994	1541
0.003525264	0.05312955	0.994	1567
0.00120048	0.0526842	0.994	1411
	0 0.0516933	0.99	738
	0 0.05103197	0.871	4184
	0 0.050599042	0.988	1302
	0 0.050475966	0.885	1299
	0 0.050127104	0.986	1962
0.001285347	0.04995028	0.984	1298
	0 0.04952905	0.885	882
	0 0.049431846	0.984	1667
	0 0.049070083	0.873	1558
	0 0.049023625	0.984	1306
0.003311258	0.048977107	0.849	2409
0.001166861	0.0489308	0.829	1078
	0 0.0488923	0.885	1588
0.002590674	0.048879597	0.98	1340
	0 0.048823673	0.858	1832
	0 0.048670407	0.838	4009
0.002320186	0.048648585	0.98	1190
	0 0.04832631	0.974	1298
0.00140056	0.048261136	0.867	379
0.001262626	0.048171625	0.98	883
	0 0.048118085	0.977	1636
	0 0.048101533	0.84	1636
0.002936858	0.04808076	0.976	1068
	0 0.04797591	0.886	1490
	0 0.047972143	0.891	1115
0.001138952	0.047924507	0.911	1449
	0 0.047803767	0.829	1940
	0 0.04779158	0.954	1566
	0 0.047783762	0.964	1833
	0 0.04773189	0.858	1323
	0 0.047723703	0.938	1741
	0 0.047676444	0.955	2194
0.001383126	0.04763516	0.968	1340
	0 0.047478564	0.913	1917
	0 0.047457654	0.86	1754
	0 0.04727427	0.956	1542
	0 0.047211196	0.941	2443
	0 0.047094118	0.948	1808
	0 0.047082506	0.945	37
0.004010695	0.047050957	0.891	750
0.002617801	0.04696743	0.96	1090
	0 0.046940297	0.956	1813
	0 0.04692359	0.917	1648
	0 0.04673259	0.913	411
	0 0.046683084	0.893	432

0	0.04660578	0.925	738
0.002853067	0.0464325	0.917	750
0.002280502	0.04626627	0.926	1556
0	0.046017513	0.929	1101
0.001369863	0.045839764	0.893	253
0	0.045703415	0.804	869
0.003880983	0.045471333	0.897	1490
0	0.04487907	0.781	3735
0	0.044559196	0.624	1988
0	0.044506736	0.791	1956
0	0.043503996	0.648	633
0	0.043237966	0.655	2202
0.002444988	0.04296779	0.628	2202
0	0.042611342	0.751	1813
0	0.042503454	0.728	1290
0.00128866	0.042319637	0.769	1715
0	0.042231843	0.565	1832
0	0.042170167	0.586	607
0	0.042006314	0.716	15
0.00131406	0.041911066	0.736	856
0	0.041793197	0.751	1346
0	0.041728575	0.658	440
0	0.041083228	0.698	1893
0.001184834	0.04078216	0.685	886
0	0.04066302	0.661	440
0	0.04056512	0.672	1340
0.003436426	0.039378747	0.696	2114
0.004347826	0.039205965	0.717	1221
0	0.03887827	0.705	3787
0	0.038474876	0.516	1761
0	0.03631928	0.65	3787
0.004166667	0.03588689	0.605	1328
0	0.03537404	0.633	2088
0	0.034754433	0.606	3493
0	0.03440415	0.609	3844
0	0.034057032	0.408	3120
0	0.0336003	0.578	3560
0	0.03357251	0.457	1534
0	0.033339866	0.214	1353
0.004739337	0.032999042	0.416	1732
0.004132231	0.032841302	0.556	2098
0	0.032575417	0.325	1727
0	0.032275118	0.302	1656
0	0.0322214	0.416	1254
0	0.03144827	0.417	1601
0	0.030835066	0.332	1082
0	0.030619716	0.418	491
0	0.0301083	0.421	3681
0	0.029998675	0.512	2915
0	0.029891014	0.452	4326
0	0.029862328	0.469	1732

0	0.029849166	0.369	607
0	0.029819857	0.494	4265
0	0.029818818	0.434	2316
0	0.02958478	0.166	1290
0	0.0295436	0.217	1578
0	0.02906207	0.338	607
0	0.02869435	0.47	2294
0	0.028022183	0.253	1606
0	0.027369447	0.225	1574
0	0.017544203	0.083	1340
0	0.015256234	0.206	4238
0	0.01466891	0.187	3681
0	0.014561567	0.172	3681
0	0.013285575	0.04	1808
0	0.012084848	0.024	3903
0	0.010897203	0.088	4127
0	0.010715875	0.043	607
0	0.010493218	0.049	4308
0	0.010489444	0.103	3651
0	0.010404327	0.067	3901
0	0.010362125	0.04	3493
0	0.01028578	0.111	2114
0	0.010006802	0.089	1992
0	0.009436363	0.052	3651
0	0.009103786	0.067	4063
0	0.009077021	0.027	3681
0	0.001000259	0.001	1606
0	9.95E-04	0.002	1323
0	0	0	2114

'Sle.Female patients vs Healthy.Female donors' :

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_	149	-0.6036884	-1.291812	0.06758305	0.2578256	1	1096
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTOR_	179	-0.6038466	-1.2952149	0.044857766	0.2566086	1	2133
REACTOME_GAP_JUNCTION_TRAFFICKING	17	-0.7843927	-1.2933998	0.1130031	0.2563405	1	1270
REACTOME_TIE2_SIGNALING	17	-0.7719544	-1.2945262	0.13392857	0.25601843	1	2488
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINAT	20	0.66027856	1.2564553	0.19469027	0.25263503	1	4411
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	23	-0.74205995	-1.2983532	0.11031519	0.2519248	1	1689
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_	167	0.4641348	1.2555524	0.028846154	0.25153655	1	2619
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVEN	54	0.54970115	1.2703738	0.09243698	0.24414268	1	4068
REACTOME_FORMATION_OF_RNA_POL_II_ELONGAT	38	0.57873267	1.2702012	0.11785714	0.24217856	1	4068
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_	42	0.5796106	1.2674358	0.11382114	0.24098854	1	5773
REACTOME_OXYGEN_DEPENDENT_PROLINE_HYDRO	16	0.66834706	1.2694212	0.1859155	0.24086921	1	301
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	0.67535764	1.2776921	0.17318435	0.23966259	1	4593
REACTOME_FORMATION_OF_THE_TERNARY_COMPL	48	0.57387495	1.2776915	0.12295082	0.2373801	1	3472
REACTOME_SIGNALLING_BY_NGF	204	-0.5883379	-1.3086296	0.04202586	0.2337468	1	1766
REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_	22	-0.7545838	-1.3080896	0.11959654	0.23283331	1	2743
REACTOME_MEMBRANE_TRAFFICKING	113	-0.6379694	-1.315426	0.06936416	0.22193953	1	2099
REACTOME_SIGNALING_BY_RHO_GTPASES	107	-0.63745373	-1.3182892	0.045346063	0.21745025	1	2582
REACTOME_NEPHRIN_INTERACTIONS	18	-0.77782816	-1.320107	0.08562691	0.21593642	1	2787
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_	122	-0.6284845	-1.3250251	0.06696935	0.21076779	1	2413
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	27	-0.7457095	-1.3245848	0.08381503	0.20959221	1	2601
REACTOME_NEURONAL_SYSTEM	206	-0.61205935	-1.3311201	0.02771855	0.20086524	1	2125
REACTOME_THROMBOXANE_SIGNALLING_THROUGH	22	-0.76352996	-1.3323246	0.09855072	0.20059775	1	1689
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	21	-0.77875173	-1.3346869	0.07164634	0.19794977	1	437
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	0.6699855	1.3148483	0.14330219	0.19644359	1	249
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_	52	0.5751049	1.3187596	0.10576923	0.19618306	1	5209
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	22	0.66325694	1.3228514	0.13939394	0.1959253	1	3621
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BIN	55	0.5693752	1.3177005	0.071428575	0.19548258	1	4368
REACTOME_G0_AND_EARLY_G1	23	0.6769594	1.3214686	0.12460064	0.19525728	1	4617
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	19	0.6971252	1.3258911	0.13607594	0.19443233	1	5070
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKY	19	-0.78642875	-1.33914	0.09411765	0.19114245	1	1077
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_	23	0.6465612	1.3307346	0.13870968	0.19090346	1	4038

REACTOME_INTERFERON_GAMMA_SIGNALING	58	-0.68549705	-1.3419613	0.06812339	0.18975851	1	1566
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_I	29	-0.74806356	-1.3419138	0.08567416	0.18802138	1	2076
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTI	18	0.7326923	1.3408734	0.13915858	0.1814204	1	3922
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUIT	47	0.5831222	1.3437555	0.09448819	0.18010637	1	4850
REACTOME_G_PROTEIN_ACTIVATION	23	-0.7710167	-1.3491142	0.068214804	0.17981845	1	1689
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_S	15	0.7322275	1.3467015	0.12209302	0.1789994	1	1454
REACTOME_TRANSPORT_OF_MATURING_MRNA_DERIV	32	0.64850295	1.3487693	0.08992806	0.17840719	1	4857
REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	18	-0.79048777	-1.3489598	0.071104385	0.17836753	1	561
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING	62	0.5577484	1.350403	0.039647575	0.17826274	1	4610
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	24	-0.77508026	-1.3525212	0.07471264	0.17523852	1	1689
REACTOME_DIABETES_PATHWAYS	115	-0.64651865	-1.3557283	0.042577676	0.17117727	1	2337
REACTOME_RNA_POL_II_TRANSCRIPTION	96	0.547418	1.3613867	0.03550296	0.16791265	1	4068
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH	19	-0.8119051	-1.3618805	0.051612902	0.16178201	1	1689
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLU	27	0.6882603	1.371932	0.1013986	0.1611697	1	4857
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATIO	19	0.729483	1.371731	0.096273296	0.15952583	1	3922
REACTOME_NETRIN1_SIGNALING	33	-0.75301206	-1.3690449	0.059722222	0.15076394	1	1273
REACTOME_METABOLISM_OF_MRNA	209	0.50124955	1.3853452	0	0.1505436	1	4264
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	0.7242398	1.3850931	0.09552239	0.14905022	1	3922
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAG	48	0.62031674	1.3900969	0.05	0.14749314	1	4548
REACTOME_CGMP_EFFECTS	18	-0.8138636	-1.3724939	0.067381315	0.14686076	1	1132
REACTOME_SCF5P2_MEDIATED_DEGRADATION_OF	53	0.6024161	1.3926177	0.06726457	0.14671466	1	4610
REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATI	22	-0.8053542	-1.3750606	0.04486252	0.1441509	1	1516
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_TH	15	-0.8399943	-1.3767023	0.05287714	0.1430127	1	1497
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATIO	21	0.73857766	1.4032278	0.07826087	0.14277562	1	3922
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	96	0.55964756	1.401866	0.006097561	0.14243954	1	4068
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_C	32	0.6771858	1.3995104	0.048109967	0.14182597	1	4857
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS	27	0.6806369	1.4014702	0.08012821	0.14134723	1	4857
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH	24	-0.78707135	-1.3793811	0.054755043	0.14001772	1	2601
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDI	104	-0.6688739	-1.382111	0.028202115	0.1399972	1	2125
REACTOME_SIGNALING_BY_WNT	62	0.59051895	1.4084127	0.019138755	0.13954993	1	4548
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	95	-0.6784229	-1.3814193	0.029761905	0.13953434	1	2325
REACTOME_ER_PHAGOSOME_PATHWAY	58	0.6092966	1.4129149	0.02283105	0.13896257	1	5788
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	26	-0.7858226	-1.3813277	0.05589124	0.13811034	1	580

REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSIO	22	-0.79843795	-1.385236	0.05050505	0.13778625	1	634
REACTOME_METABOLISM_OF_NUCLEOTIDES	62	0.5839775	1.412897	0.039647575	0.13722354	1	2350
REACTOME_MYOGENESIS	23	-0.79630286	-1.3849196	0.049253732	0.13667968	1	680
REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSI	23	-0.8107345	-1.3974195	0.03742515	0.11951816	1	634
REACTOME_SIGNALING_BY_CONSTITUTIVELY_ACTIVI	17	-0.8346444	-1.4004543	0.04477612	0.11919007	1	442
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF	20	-0.8302283	-1.3989941	0.036390103	0.11866607	1	1400
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_B	43	-0.74374783	-1.4003222	0.045333333	0.11799712	1	1896
REACTOME_HIV_LIFE_CYCLE	109	0.5598702	1.4392762	0.007092198	0.11509536	0.999	4068
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN	20	0.72907346	1.4437087	0.061488673	0.11427094	0.999	3986
REACTOME_BASE_EXCISION_REPAIR	18	0.75888914	1.4419483	0.06363636	0.11419197	0.999	2409
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_	50	0.63417655	1.4488393	0.025423728	0.11097908	0.998	5788
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF	15	-0.8550569	-1.4086643	0.02388535	0.10856659	1	797
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	40	0.6629236	1.4550067	0.03629032	0.107043035	0.997	4224
REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_A	25	-0.8096885	-1.4150811	0.029411765	0.1049757	1	2316
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_E	30	-0.78573835	-1.4133822	0.037089873	0.104674295	1	1497
REACTOME_SMOOTH_MUSCLE_CONTRACTION	21	-0.8384023	-1.412398	0.017167382	0.10453318	1	1185
REACTOME_CREB_PHOSPHORYLATION_THROUGH_TI	25	-0.8091441	-1.4147712	0.027859237	0.10412945	1	2915
REACTOME_GPCR_LIGAND_BINDING	245	-0.64564264	-1.4181602	0.005307856	0.102097854	1	2051
REACTOME_L1CAM_INTERACTIONS	75	-0.70556676	-1.4228752	0.018703243	0.097550176	1	2334
REACTOME_DEGRADATION_OF_THE_EXTRACELLULA	21	0.7703298	1.4839464	0.040880505	0.09151589	0.98	1330
REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	43	-0.74890983	-1.4302968	0.0313779	0.091402374	1	1689
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EX	46	0.6546464	1.4762169	0.025751073	0.09117853	0.989	5788
REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPT	16	-0.86477166	-1.4297405	0.021052632	0.090903856	1	479
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPC	30	-0.78573835	-1.4319677	0.015850144	0.09056088	1	1497
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APO	49	0.65566725	1.4788723	0.025641026	0.09054516	0.988	5045
REACTOME_REGULATION_OF_ORNITHINE_DECARBO	48	0.635107	1.4838103	0.019305019	0.090302445	0.98	4548
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATA	17	0.7899862	1.4826943	0.042735044	0.089915976	0.982	2614
REACTOME_DNA_REPAIR	101	0.5723674	1.4811614	0.012738854	0.08990369	0.987	4051
REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVAT	84	-0.70350415	-1.42968	0.021978023	0.08974719	1	1940
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MI	16	0.7870585	1.4895748	0.03380282	0.08858498	0.976	2409
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	20	-0.83719736	-1.434709	0.03076923	0.08831212	1	1803
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCC	16	0.80532527	1.4919766	0.04375	0.08814168	0.974	1663
REACTOME_CHONDROITIN_SULFATE_DERMATAN_SL	44	-0.74003446	-1.4374793	0.032440055	0.086215176	1	2317

REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	20	-0.85383373	-1.4419292	0.019345239	0.08238009	1	1689
REACTOME_DEADENYLATION_DEPENDENT_MRNA_D	42	0.6758252	1.501113	0.018050542	0.08228282	0.964	4525
REACTOME_SIGNAL_AMPLIFICATION	30	-0.7942394	-1.4445555	0.016973127	0.08196546	1	1689
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENC	23	-0.826533	-1.443741	0.021929825	0.081756376	1	2172
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLAT	21	0.7747439	1.5034034	0.048295453	0.08155621	0.959	3927
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	18	-0.8702967	-1.4478996	0.016641453	0.08036381	1	66
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	495	-0.6472175	-1.447312	0	0.079726316	1	1755
REACTOME_REGULATION_OF_INSULIN_SECRETION_I	35	-0.78190863	-1.4520062	0.01920439	0.07666515	0.998	1689
REACTOME_MITOTIC_PROMETAPHASE	82	0.6239243	1.5133723	0.010309278	0.07566897	0.947	2309
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	48	0.674571	1.5121852	0.021008404	0.07524744	0.95	3986
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SY	143	-0.6851359	-1.4558569	0.013605442	0.07501291	0.998	2125
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADAT	49	0.6550807	1.5158386	0.016129032	0.07483703	0.944	4548
REACTOME_MRNA_PROCESSING	150	0.56875896	1.5185984	0	0.074261665	0.938	5071
REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCAD	40	-0.76481235	-1.4558449	0.019553073	0.073848575	0.998	1940
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NEF	43	0.6755719	1.524427	0.015564202	0.07096885	0.928	3977
REACTOME_PEPTIDE_CHAIN_ELONGATION	86	0.61276656	1.5280113	0.005747126	0.07029366	0.923	3493
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_A	46	0.66949296	1.5274587	0.012605042	0.06947558	0.923	4610
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	30	-0.81330824	-1.4622718	0.019690577	0.069229096	0.996	2316
REACTOME_CIRCADIAN_CLOCK	49	-0.7688015	-1.4663267	0.014473684	0.06870603	0.994	634
REACTOME_GPCR_DOWNSTREAM_SIGNALING	359	-0.6630401	-1.464338	0.00310559	0.068373755	0.995	1883
REACTOME_STRIATED_MUSCLE_CONTRACTION	20	-0.845987	-1.465844	0.02643857	0.068129964	0.994	978
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC	34	-0.7972135	-1.4717295	0.013623978	0.06688953	0.985	689
REACTOME_RECYCLING_PATHWAY_OF_L1	25	-0.8465551	-1.471124	0.022099448	0.06627265	0.986	553
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH	56	0.6630227	1.541036	0.014218009	0.06612937	0.895	4548
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REC	104	0.59795517	1.5397143	0	0.06594679	0.899	3493
REACTOME_INTEGRIN_ALPHAIB_BETA3_SIGNALING	24	-0.85461426	-1.4934075	0.016417911	0.065852426	0.953	1808
REACTOME_CD28_CO_STIMULATION	31	-0.81019294	-1.4760273	0.014084507	0.06529221	0.982	472
REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	109	-0.7019432	-1.4711037	0.010752688	0.06516828	0.986	1230
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	0.7665275	1.5395104	0.040133778	0.0648092	0.899	3345
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	136	-0.69853246	-1.4754685	0.011441648	0.0645591	0.983	1461
REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRC	33	-0.822519	-1.4931176	0.014184397	0.064489625	0.954	634
REACTOME_MRNA_SPLICING	104	0.6035232	1.5382296	0.007092198	0.0644159	0.903	5471
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	80	-0.7343364	-1.4929969	0.007308161	0.0631324	0.955	1340

REACTOME_PLATELET_AGGREGATION_PLUG_FORMA	31	-0.83115894	-1.4981276	0.013100437	0.063124694	0.946	2030
REACTOME_SIGNALING_BY_FGFR	95	-0.71847975	-1.4797497	0.004728132	0.06255655	0.973	1230
REACTOME_G_ALPHA1213_SIGNALLING_EVENTS	69	-0.7480988	-1.492889	0.003787879	0.06173911	0.955	2582
REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_	43	-0.79107827	-1.4924831	0.003994674	0.060731795	0.957	2236
REACTOME_METABOLISM_OF_RNA	252	0.54165447	1.5504444	0	0.060131617	0.868	4307
REACTOME_PD1_SIGNALING	17	-0.89580554	-1.491848	0.013412816	0.05987777	0.957	1175
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_	70	-0.7548967	-1.503195	0.004895961	0.05982855	0.929	1395
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_	18	-0.86963487	-1.4912877	0.015804598	0.0589166	0.957	1689
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	-0.8649431	-1.4902292	0.004559271	0.058706	0.959	437
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTIN	21	-0.86325717	-1.4857864	0.002915452	0.058028758	0.966	469
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY	24	-0.84799916	-1.4900675	0.011816839	0.057586037	0.959	1689
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION	102	0.6072273	1.5575721	0	0.056956872	0.848	3493
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THI	128	-0.7122399	-1.4897349	0.004576659	0.056648917	0.959	1230
REACTOME_REGULATION_OF_WATER_BALANCE_BY_	38	-0.82143545	-1.5082384	0.006877579	0.05651848	0.914	1689
REACTOME_SIGNALING_BY_GPCR	437	-0.6657053	-1.4891768	0	0.056126095	0.959	1883
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANC	107	0.59783787	1.5614628	0	0.05536577	0.832	3681
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PI	109	0.60030365	1.5640533	0.016393442	0.05478016	0.824	3524
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOF	29	-0.83451617	-1.5127814	0.012640449	0.054332096	0.9	1101
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC	29	-0.835042	-1.5184038	0.013024602	0.051315546	0.877	1291
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	49	0.69767195	1.5717355	0.003831418	0.051276706	0.789	4390
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	32	0.7508376	1.5703413	0.014440433	0.0512642	0.802	3986
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGG	15	0.8415543	1.5748807	0.015584416	0.050645035	0.777	2409
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTO	59	-0.77275133	-1.5245054	0.010256411	0.04830703	0.857	1291
REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_	15	-0.9144643	-1.5267928	0.001597444	0.04809223	0.849	948
REACTOME_OPIOID_SIGNALLING	70	-0.7759165	-1.5328673	0.007653061	0.046581775	0.821	1310
REACTOME_SIGNALING_BY_ERBB2	93	-0.74601495	-1.5351804	0.004667445	0.04655769	0.813	2614
REACTOME_MUSCLE_CONTRACTION	37	-0.8416606	-1.532092	0.004054054	0.045616765	0.826	1185
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMO	43	-0.8117004	-1.5442176	0.006527415	0.04299389	0.763	2045
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATIO	65	0.68120855	1.5909737	0.005076142	0.041944772	0.705	4548
REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATI	27	-0.8642531	-1.5438341	0.00433526	0.041711822	0.765	574
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	18	-0.91718435	-1.5500346	0.003169572	0.041096207	0.735	932
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_A	80	0.6512982	1.5944458	0.005405406	0.04106746	0.686	4414
REACTOME_LAGGING_STRAND_SYNTHESIS	19	0.8477074	1.596318	0.003154574	0.040771015	0.673	2409

REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	17	0.86501515	1.6002147	0.005830904	0.039870817	0.657	1429
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	65	0.68006474	1.6104528	0	0.035903215	0.598	4544
REACTOME_TRANSLATION	144	0.59574676	1.608757	0	0.035884257	0.609	3524
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_C	54	0.70102966	1.6138554	0	0.035509907	0.582	4548
REACTOME_PROCESSING_OF_CAPPED_INTRON_CON	133	0.60397613	1.6151379	0	0.035499427	0.572	5625
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_	33	0.76909536	1.6176711	0.008064516	0.03536956	0.562	3331
REACTOME_GENERATION_OF_SECOND_MESSENGER	26	-0.89414436	-1.563109	0.00286533	0.035269015	0.662	948
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOC	95	0.63492036	1.6227103	0	0.034532033	0.542	1296
REACTOME_TRANSCRIPTION	176	0.59059983	1.6207727	0	0.034347292	0.549	2658
REACTOME_INFLUENZA_LIFE_CYCLE	136	0.6099918	1.6265551	0	0.034191355	0.512	3787
REACTOME_AMYLOIDS	50	0.7304805	1.6251439	0.004132231	0.0339761	0.52	1296
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	65	0.6809666	1.6331125	0	0.032054707	0.478	4610
REACTOME_DOWNSTREAM_TCR_SIGNALING	34	-0.8592917	-1.5773888	0.006944445	0.02947132	0.58	948
REACTOME_IMMUNOREGULATORY_INTERACTIONS_I	57	-0.82070065	-1.5820589	0.00129199	0.028878992	0.561	1606
REACTOME_PLATELET_HOMEOSTASIS	70	-0.79889405	-1.592484	0.00125	0.028591348	0.511	1689
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATIO	64	0.6821629	1.643306	0.013953488	0.028283248	0.433	4548
REACTOME_PL_C_BETA_MEDIATED_EVENTS	39	-0.85176015	-1.5987012	0	0.027495006	0.477	797
REACTOME_SEMAPHORIN_INTERACTIONS	63	-0.8052696	-1.591945	0.007614213	0.027366955	0.511	2316
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	41	-0.8446673	-1.5894831	0.003926701	0.027112855	0.524	1689
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_C	63	0.71011966	1.6578758	0.01010101	0.024481267	0.366	4548
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	0.6682694	1.6565058	0	0.024146995	0.373	4610
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CY	72	-0.81242764	-1.6142615	0.001272265	0.022254074	0.387	1298
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	61	-0.82968384	-1.6189656	0.002580645	0.022027936	0.37	1741
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE	30	0.81690323	1.668422	0.006430868	0.020906713	0.313	2114
REACTOME_METABOLISM_OF_NON_CODING_RNA	46	0.7316405	1.6723306	0.008	0.020340053	0.298	3855
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTION	74	-0.82151586	-1.6322665	0	0.019990537	0.308	1273
REACTOME_CA_DEPENDENT_EVENTS	27	-0.90399307	-1.629916	0.001426534	0.019546404	0.317	797
REACTOME_MITOTIC_G1_G1_S_PHASES	130	0.6365381	1.6777456	0	0.019104537	0.271	3355
REACTOME_CELL_CYCLE_MITOTIC	303	0.5873392	1.6851518	0	0.016779847	0.239	3583
REACTOME_EXTENSION_OF_TELOMERES	27	0.8263602	1.6869979	0.003484321	0.016589234	0.229	2689
REACTOME_DAG_AND_IP3_SIGNALING	29	-0.91549236	-1.6539435	0.00141844	0.014053339	0.22	797
REACTOME_TCR_SIGNALING	51	-0.86288655	-1.6636957	0.001324503	0.011804588	0.179	1534
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	89	-0.82698756	-1.6666933	0.002444988	0.011570267	0.163	1230

REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATIO	71	-0.84121096	-1.671361	0	0.010602902	0.141	699
REACTOME_NCAM1_INTERACTIONS	31	-0.92195797	-1.678762	0.001451379	0.009613696	0.117	607
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	102	-0.8037488	-1.685758	0	0.008839736	0.099	797
REACTOME_G2_M_CHECKPOINTS	41	0.76296145	1.7171646	0	0.008424254	0.118	2114
REACTOME_TRNA_AMINOACYLATION	42	0.7653105	1.7204782	0	0.008053645	0.108	3345
REACTOME_HEMOSTASIS	402	-0.760443	-1.6916641	0	0.007607798	0.077	1298
REACTOME_M_G1_TRANSITION	78	0.7121183	1.746042	0	0.005688463	0.065	4255
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO	35	0.8061258	1.7394241	0	0.005640128	0.075	2114
REACTOME_CELL_CYCLE_CHECKPOINTS	111	0.6814811	1.7434739	0	0.005615857	0.067	4189
REACTOME_G1_S_TRANSITION	106	0.6648319	1.7415137	0	0.005553701	0.07	3355
REACTOME_COLLAGEN_FORMATION	50	-0.8886728	-1.70923	0.001305483	0.004911517	0.043	1082
REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDI	26	0.87573165	1.775903	0	0.003241773	0.035	356
REACTOME_RNA_POL_I_TRANSCRIPTION	63	0.748728	1.7857065	0	0.003105022	0.027	1296
REACTOME_MITOTIC_M_M_G1_PHASES	164	0.6614313	1.7853789	0	0.002982903	0.028	4610
REACTOME_MEIOTIC_SYNAPSIS	54	0.74855596	1.7819506	0	0.00287928	0.029	1368
REACTOME_S_PHASE	106	0.6801362	1.792616	0	0.002720195	0.022	3355
REACTOME_RNA_POL_I_PROMOTER_OPENING	39	0.8255264	1.8275903	0	0.002490172	0.01	1296
REACTOME_MEIOSIS	85	0.7180784	1.811096	0	0.002317167	0.014	2098
REACTOME_PACKAGING_OF_TELOMERE_ENDS	33	0.8475357	1.8016297	0	0.002288159	0.017	793
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_	84	-0.8530687	-1.7293388	0	0.002270797	0.018	701
REACTOME_CELL_CYCLE	377	0.62140644	1.8106078	0	0.002230611	0.015	3355
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAIN	47	0.81145257	1.8390151	0	0.002136205	0.007	1889
REACTOME_DNA_REPLICATION	184	0.677016	1.826476	0	0.002134433	0.01	3581
REACTOME_DNA_STRAND_ELONGATION	30	0.8628528	1.8223654	0.003236246	0.001867629	0.01	2088
REACTOME_MEIOTIC_RECOMBINATION	59	0.7838217	1.8776149	0	0.001579069	0.002	2098
REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	31	-0.95785254	-1.7384292	0	0.001536898	0.01	437
REACTOME_SYNTHESIS_OF_DNA	90	0.72569484	1.8625588	0	0.001198625	0.003	3355
REACTOME_TELOMERE_MAINTENANCE	60	0.81668764	1.8764756	0	0.001052712	0.002	2088
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_	56	-0.9030643	-1.7567817	0	0.001050744	0.005	1077
REACTOME_DEVELOPMENTAL_BIOLOGY	333	-0.78897566	-1.7517003	0	8.41E-04	0.005	1331
REACTOME_AXON_GUIDANCE	218	-0.8177026	-1.7801396	0	5.58E-04	0.002	1574
REACTOME_PLATELET_ACTIVATION_SIGNALING_ANC	183	-0.8478189	-1.8292865	0	4.22E-04	0.001	1298
REACTOME_SIGNALING_BY_PDGF	114	-0.8875805	-1.8497458	0	0	0	1261

REACTOME_CHROMOSOME_MAINTENANCE	100	0.7488205	1.9589261	0	0	0	2281
---------------------------------	-----	-----------	-----------	---	---	---	------

'IN Sle.Female: Severe SLE vs Moderate SLE' :

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
GO_REGUL	20	0.8273591	1.3176827	0.08203678	0.25999185	1	1739
TAAWWAT	130	0.7005618	1.3175685	0.04103967	0.25981295	1	1358
GO_PEPTIC	27	0.8081295	1.3176751	0.06775068	0.25972798	1	920
GO_COLLA	53	0.7535926	1.317963	0.07180851	0.25929615	1	1846
GO_NEGA1	23	0.8155723	1.3185217	0.07103064	0.25909758	1	1797
GO_CENTR	20	0.8340457	1.3182772	0.07396871	0.25907457	1	1758
GO_RESPO	46	0.76203465	1.3181204	0.07619048	0.25903454	1	842
GO_REGUL	67	0.7395277	1.3183799	0.05020353	0.2589747	1	1157
GO_ARACH	35	0.78681964	1.3184755	0.081491716	0.25896716	1	816
GO_PROTE	224	0.66306907	1.3182535	0.03178808	0.2588696	1	1738
GO_REGUL	57	0.75878525	1.3191975	0.07622739	0.25791484	1	1956
GO_SULFU	170	0.6873586	1.3194137	0.036939315	0.2577389	1	2068
GO_HEXOS	131	0.7044413	1.3191693	0.05285118	0.25772196	1	765
GO_LIVER_	18	0.84488523	1.3193496	0.06760564	0.25767985	1	1851
GO_AXON_	169	0.6783836	1.3196112	0.030985916	0.25765407	1	2186
GO_CELL_	378	0.63548505	1.3190364	0.020512821	0.25761554	1	1770
GATA_C	187	0.6815024	1.3191173	0.040650405	0.25761116	1	1799
GO_POSITI	29	0.794228	1.3195995	0.08344733	0.25741455	1	1279
GO_POSITI	46	0.77106905	1.3199457	0.06749311	0.25733748	1	1656
GO_ACUTE	27	0.813101	1.319783	0.061898213	0.25730824	1	1540
GO_POSITI	24	0.8144601	1.3199079	0.078541376	0.25717992	1	1274
GO_ISOPRI	18	0.82939434	1.3202285	0.07445256	0.25669736	1	1495
GO_PYRIDI	17	0.8469415	1.3203338	0.08464849	0.25663668	1	965
GO_POSITI	26	0.8162211	1.3205664	0.09568733	0.2561433	1	1656
GO_CYCLIN	18	0.8372445	1.3210125	0.077793494	0.25549677	1	1160
GO_NEGA1	114	0.70940804	1.3210049	0.039051604	0.25522447	1	1138
GO_ACTIV	120	0.7005783	1.3209463	0.04172462	0.25514475	1	1925
AR_02	32	0.7959766	1.3215371	0.05890411	0.25484595	1	798
GO_REGUL	92	0.72723114	1.3216358	0.058124173	0.25480908	1	1852
GO_GLIAL_	59	0.7562858	1.3213842	0.057377048	0.25480577	1	1696
GO_TUBE_	432	0.6245384	1.3214833	0.013977128	0.25472996	1	1657
GO_APICA	264	0.6613941	1.3217676	0.02642559	0.2546619	1	2061
GO_ORGAI	36	0.780463	1.3213452	0.06548431	0.2546435	1	1674
GO_RESPO	54	0.75636744	1.3219206	0.049543675	0.25442666	1	1536
GO_BETA_	34	0.79366285	1.3224945	0.06359946	0.25356573	1	630
GO_POSITI	27	0.8216597	1.3223364	0.07042254	0.253533	1	1362
GO_REGUL	33	0.8003378	1.3224572	0.05196629	0.2534119	1	2709
GO_GLUCC	100	0.73303086	1.3226265	0.043941412	0.2533994	1	765
GO_REGUL	18	0.8323358	1.3223262	0.07814761	0.25328168	1	1426
GO_TRANS	16	0.8560719	1.3227477	0.07	0.25325695	1	1598
GO_NEGA1	15	0.85640335	1.3229576	0.068814054	0.25312483	1	1656
GO_NEUR/	23	0.81963867	1.3234292	0.0781893	0.2530047	1	1160
GO_OSTEC	26	0.809722	1.3229283	0.07244318	0.25293514	1	2622
COUP_01	195	0.67829853	1.3234097	0.02739726	0.25277779	1	1550
GO_RESPO	195	0.6775803	1.3235962	0.027624309	0.2527247	1	1739
PAX8_B	80	0.7391467	1.3233657	0.053867403	0.25262108	1	1160
GO_RHO_(74	0.74908435	1.3232901	0.034246575	0.25259554	1	1460
GO_NEGA1	42	0.7791676	1.3237501	0.060055867	0.2524845	1	1677

E2F1_Q6_C	218	0.6678321	1.3232737	0.01780822	0.25235584	1	1349
GO_B_CELI	57	0.74681765	1.3245698	0.055555556	0.2513287	1	671
GO_STEM_	133	0.6965722	1.324174	0.04426003	0.25127137	1	2374
GO_REGUL	127	0.7079729	1.3244638	0.029166667	0.25114238	1	1696
GO_LAMEL	159	0.70111513	1.3245586	0.030428769	0.25105876	1	2096
AP1_Q4	224	0.6671422	1.3249238	0.032388665	0.2509756	1	1624
GO_POSITI	66	0.74672943	1.3244249	0.054495912	0.25096267	1	1851
GO_POSITI	58	0.7491509	1.324364	0.0585034	0.2508959	1	2121
GO_REGUL	418	0.63470167	1.3248684	0.023778072	0.25085118	1	2171
GO_CARDI	17	0.83921665	1.325037	0.085260116	0.25083774	1	1689
GO_HUMC	29	0.80802256	1.3248279	0.078947365	0.25070208	1	671
GO_REGUL	89	0.7278973	1.3253388	0.048714478	0.2500151	1	1818
GO_POSITI	90	0.734559	1.3263305	0.037333332	0.24862565	1	1780
GO_REGUL	24	0.8203597	1.3262511	0.0678426	0.24859369	1	793
GO_REGUL	32	0.8022399	1.3262477	0.06077348	0.24830507	1	1261
GO_SARCC	28	0.80447346	1.326112	0.06849315	0.24818161	1	2354
GO_CYCLIC	43	0.78178453	1.3262308	0.055702917	0.24805795	1	1570
GO_DETEC	28	0.80951375	1.3260942	0.07272727	0.24794441	1	1505
MEIS1AHO	72	0.7456964	1.3260684	0.061662197	0.24774197	1	592
GO_REGUL	18	0.8451308	1.3268023	0.07234043	0.24755497	1	1578
HNf4_01	207	0.6708047	1.3267589	0.026560426	0.24742633	1	1847
GO_RESPO	21	0.8352153	1.326976	0.058238637	0.24726757	1	1349
RRCCGTTA	76	0.74235195	1.3274935	0.04216074	0.24698903	1	1762
GO_NEGA1	26	0.80868006	1.3273273	0.063858695	0.24695215	1	1094
GO_POSITI	372	0.63636583	1.3272622	0.018276762	0.24691008	1	1691
LHX3_01	143	0.6901852	1.32717	0.031292517	0.24688548	1	1689
GO_POSITI	37	0.7883048	1.327493	0.06162465	0.24668854	1	1639
GO_APICA	104	0.72343755	1.3280318	0.048275862	0.24656463	1	1790
GO_PLASM	19	0.846967	1.3280306	0.07692308	0.24626686	1	853
GO_DETEC	66	0.7448809	1.327918	0.048582997	0.2460422	1	1574
GO_CARBC	20	0.83303964	1.3282741	0.06714286	0.24602692	1	1694
GO_STERO	37	0.79541224	1.3280152	0.066401064	0.24600723	1	1014
E2F_Q3_01	207	0.6866744	1.3278764	0.017639078	0.24588236	1	1346
GO_METHI	17	0.85224926	1.3284444	0.077809796	0.2457002	1	58
GO_REGUL	80	0.72005105	1.3286043	0.0627451	0.24545887	1	1138
AP1_01	207	0.67563045	1.3291194	0.02387268	0.24399863	1	2330
GO_ACTIN	70	0.7472149	1.3296393	0.043941412	0.24250458	1	1622
GO_PDZ_D	77	0.7448739	1.3298111	0.04109589	0.24222721	1	1764
GO_ENDOI	21	0.83733743	1.3303912	0.07560628	0.24169932	1	1494
GO_ADHEF	31	0.8053064	1.3300585	0.0627558	0.24169293	1	1443
GO_DICAR	54	0.7556563	1.3302482	0.05277402	0.24160741	1	2242
GO_PROTE	84	0.7404454	1.330174	0.047156725	0.24157499	1	1925
GO_BLOO	22	0.83744204	1.3303603	0.07254623	0.2415067	1	1215
GO_EMBR'	67	0.7418953	1.3306385	0.046791445	0.24116889	1	1333
POU3F2_0	67	0.75486076	1.3307476	0.054054055	0.2410564	1	1443
GO_CLATH	135	0.7080825	1.330938	0.03108108	0.24100561	1	1246
GO_CARDI	51	0.7599539	1.3308634	0.06325707	0.24095614	1	1598
GO_POSITI	17	0.844506	1.3320631	0.08057554	0.24022903	1	1829
GO_SEMAI	34	0.80409163	1.331991	0.04834254	0.24019094	1	1797
GO_CELL_	160	0.69480556	1.3319705	0.028378379	0.23998602	1	1568

NRF2_Q4	219	0.6751448	1.3322088	0.018567638	0.23997904	1	1949
GO_RESPO	29	0.8243855	1.3325318	0.05764075	0.23974368	1	487
GO_REGUL	21	0.8320965	1.332453	0.057182707	0.23974074	1	637
GO_REGUL	45	0.78467983	1.3319619	0.040650405	0.2397169	1	1852
GO_REGUL	137	0.7021462	1.3323764	0.04054054	0.2397088	1	1701
GO_PLACE	24	0.8159189	1.3317144	0.081575245	0.2396629	1	863
GO_SPIND	25	0.821135	1.3327973	0.05826558	0.2394877	1	421
GO_RESPO	29	0.81580055	1.3319516	0.058091287	0.23944838	1	1100
GO_EPITHE	342	0.64939964	1.331711	0.017379679	0.23938046	1	1693
GO_ENDOI	57	0.76731217	1.3327765	0.046767537	0.23925687	1	1621
KEGG_POR	25	0.8114488	1.3315815	0.07162921	0.23920454	1	1415
GO_EXOCY	251	0.6681914	1.3319477	0.021333333	0.23916537	1	1714
GO_POSITI	212	0.6784345	1.331694	0.015341702	0.23915456	1	2512
GO_REGUL	25	0.8203972	1.3330787	0.07017544	0.239131	1	1488
GO_CELL_F	24	0.826898	1.3332088	0.05647383	0.23898755	1	1689
GO_ACTIV	26	0.8210059	1.3330511	0.06733524	0.23893058	1	358
GO_SENSO	314	0.649423	1.333354	0.014965987	0.23877658	1	1601
GO_MEGA	19	0.84244835	1.3336579	0.06703911	0.23806958	1	1978
GO_PROST	33	0.82097346	1.3340085	0.05401662	0.23716873	1	1142
GO_CELLU	41	0.7841602	1.3343344	0.054347824	0.23638366	1	1370
GO_CELLU	20	0.8342432	1.3357496	0.08522727	0.23636119	1	931
GO_PROD	56	-0.8981727	-1.6482965	0	0.2363484	0.994	437
GO_BONE	22	0.8346676	1.3354121	0.063025214	0.23621505	1	1978
GO_CARGO	55	0.7728028	1.3350663	0.042119566	0.23619695	1	1625
GO_INTRA	149	0.70148754	1.3353319	0.028767124	0.23615824	1	1885
LMO2COM	183	0.6845843	1.3352426	0.032388665	0.23614407	1	1833
TGACGTCA	196	0.67672104	1.3349957	0.025920874	0.23612608	1	1483
GO_NEGA1	32	0.80218834	1.3355412	0.06097561	0.23611608	1	513
GO_ION_H	440	0.63073415	1.335628	0.01923077	0.23611453	1	2310
GO_GLIAL	31	0.8002004	1.3349186	0.07082153	0.23608096	1	1704
GO_REGUL	16	0.85240453	1.335747	0.08286517	0.23605427	1	1739
GO_REGUL	53	0.76609606	1.3360394	0.042134833	0.23594265	1	1846
GO_LAMEL	17	0.85625315	1.3348744	0.064935066	0.23593098	1	1763
GO_OSSIFI	204	0.67637753	1.3352154	0.037837837	0.2359251	1	1873
E12_Q6	210	0.6761493	1.3347887	0.030872483	0.23592308	1	1839
GO_POSITI	31	0.802637	1.3359848	0.05585831	0.23581804	1	1142
GO_RESPO	117	0.716486	1.3361614	0.031900138	0.23580548	1	1477
GO_CELLU	178	0.690963	1.33459	0.017496636	0.23572324	1	1164
GO_GLOM	43	0.7822036	1.3347851	0.05156038	0.2356328	1	1780
STAT3_Q1	20	0.83593905	1.3347826	0.07724719	0.2353362	1	817
GO_CATIO	191	0.68737185	1.336729	0.023611112	0.23507547	1	1554
GO_REGUL	45	0.77611274	1.3366505	0.06937173	0.23505583	1	1956
GO_CELL_C	63	0.7663277	1.3364694	0.02834008	0.23504019	1	1750
GO_SMOO	31	0.8032327	1.3365678	0.062322944	0.23499683	1	1916
GO_MACR	18	0.8519278	1.3369479	0.064896755	0.23460017	1	1149
GO_REGUL	146	0.7059733	1.3377179	0.028610354	0.23411478	1	1691
GO_CYCLIC	25	0.8193422	1.3372769	0.052348994	0.23404251	1	1865
GO_REGUL	18	0.8510783	1.3376877	0.0705036	0.23389688	1	153
GO_POSITI	316	0.660374	1.337514	0.014705882	0.23386993	1	1715
GO_POSITI	33	0.79000324	1.3372741	0.06456044	0.23374473	1	1126

GO_MICRC	306	0.66020566	1.3376588	0.010498688	0.23368688	1	1494
GO_REGUL	45	0.7889098	1.3374921	0.04918033	0.2336402	1	1477
GO_NEGA1	96	0.7293856	1.3388819	0.040312093	0.23315036	1	1748
GO_RESPO	16	0.8618769	1.3381782	0.057142857	0.23314247	1	1318
GO_ADEN1	79	0.75233066	1.3388404	0.024691358	0.23300615	1	1717
GO_NEGA1	47	0.7817989	1.3381706	0.044836957	0.23286216	1	1247
GO_RESPO	89	0.73853743	1.3388287	0.02925532	0.23274127	1	1957
GO_EMBR1	43	0.79285985	1.3387499	0.04477612	0.23272072	1	1598
GO_REGUL	175	0.6951897	1.3386651	0.02	0.23270644	1	1714
GO_REGUL	37	0.8032356	1.3385901	0.05602241	0.23264779	1	1509
GO_CELL_I	317	0.65453184	1.3385319	0.020942409	0.232548	1	2330
GO_PLATE1	34	0.81740606	1.3385283	0.04644809	0.23224713	1	1325
KEGG_TIG1	103	0.7279069	1.3397048	0.029649595	0.23083189	1	1082
GO_NEGA1	20	0.8426176	1.3396351	0.06657224	0.2307771	1	1002
GO_PARTL	15	0.88065565	1.3399334	0.06074074	0.23031282	1	312
GO_NEGA1	15	0.8614856	1.3402525	0.077885956	0.22985019	1	726
GO_VENTR	22	0.84677	1.3401551	0.050215207	0.22984362	1	1142
GO_CELLU	60	0.76339775	1.3413024	0.036697246	0.22810519	1	1218
GO_NEGA1	178	0.6907929	1.34097	0.027925532	0.22795825	1	1656
GO_CELLU	194	0.6891639	1.3408953	0.020661157	0.22791885	1	2076
GO_ENTRA	18	0.85821646	1.3410932	0.062937066	0.22786145	1	910
GO_NEGA1	16	0.8752231	1.341301	0.05179856	0.22779442	1	1251
GO_TRANS	89	0.736202	1.3412358	0.044077136	0.22770561	1	1620
GO_REGUL	36	0.80608153	1.3415958	0.0608931	0.22769952	1	1770
GO_CELLU	428	0.632148	1.341535	0.022756005	0.22758752	1	1697
GO_EXOCY	18	0.8592739	1.3417497	0.062228654	0.22748204	1	1577
GO_CELLU	183	0.69022435	1.3420566	0.029769959	0.22735675	1	1598
GO_EPITHE	70	0.75369567	1.341975	0.02892562	0.22733584	1	1160
FOX_Q2	165	0.69500506	1.3419268	0.017735334	0.2272072	1	1664
GO_POSITI	33	0.7952064	1.3423755	0.07017544	0.22720073	1	2121
GO_CALCII	17	0.8556269	1.3425207	0.05730659	0.2269726	1	1276
GO_REGUL	49	0.77190375	1.3422537	0.056430448	0.22693823	1	1362
GO_HYALU	25	0.82587	1.3423715	0.04070556	0.226901	1	866
SRF_Q4	183	0.69222546	1.3426688	0.021857923	0.2267701	1	1885
GO_T_CELI	35	-0.9311241	-1.6644496	0.0078125	0.22645117	0.958	275
GO_REGUL	55	0.76787853	1.3428922	0.036890645	0.22630298	1	1506
GO_G_PRC	18	0.8408961	1.3430829	0.07714286	0.22602876	1	1865
GO_REGUL	15	0.8686235	1.3435476	0.06782107	0.22502893	1	952
GO_UNSA1	44	0.7919182	1.3434812	0.04723347	0.224943	1	723
GO_REGUL	38	0.79930294	1.3436655	0.04295302	0.22492221	1	1656
GO_RESPO	32	0.80062264	1.3440194	0.059556786	0.22464217	1	1142
E2F1_Q4_C	203	0.6856911	1.3441387	0.02872777	0.22450434	1	1346
GO_POTAS	72	0.74663806	1.343892	0.035278156	0.224414	1	1554
GO_BONE_	54	0.7759098	1.3439981	0.044198897	0.22438967	1	1544
GO_SARCC	102	0.7236143	1.3445896	0.040629096	0.22391136	1	1969
GO_BROW	23	0.8339668	1.3444145	0.060606062	0.22390288	1	1851
GO_CELLU	67	0.76769656	1.3446976	0.04260985	0.22383472	1	1495
GO_REGUL	29	0.79606485	1.3445412	0.07040417	0.22376436	1	989
GO_GAME	411	0.6457336	1.3448365	0.010322581	0.22372337	1	1638
CEBP_Q2	177	0.70007825	1.345093	0.008474576	0.22310673	1	1326

GO_RESPO	28	0.8212351	1.34525	0.050964188	0.22288115	1	1745
GO_NEGA1	143	0.7095212	1.3455421	0.026098901	0.22220688	1	1677
GO_POSITI	58	0.7746613	1.3459265	0.029490616	0.2212277	1	1696
GO_REGUL	105	0.7271048	1.3461066	0.038978495	0.22091797	1	1942
GO_INTRA	18	0.85520977	1.3462477	0.054411765	0.22069319	1	1303
GO_REGUL	15	0.8604557	1.3477559	0.05805515	0.22032371	1	480
GO_RESPO	16	0.85944843	1.3464692	0.0632353	0.22028144	1	1737
GO_AXON_	19	0.8515653	1.3480115	0.050946143	0.22011684	1	1240
GO_BILE_A	18	0.85022867	1.3479227	0.054054055	0.22009245	1	1439
GO_POSITI	37	0.8040254	1.3477417	0.04275862	0.22003707	1	266
GO_NEGA1	36	0.813834	1.3476756	0.04874652	0.21993735	1	1445
GO_TRABE	31	0.82486653	1.3466773	0.03918919	0.21986109	1	1852
GO_NEGA1	15	0.8681207	1.3482274	0.05007364	0.2197257	1	535
GO_14_3_	19	0.86544824	1.34766	0.04874652	0.21967451	1	1370
GO_REGUL	31	0.8158885	1.3475039	0.05138889	0.21957584	1	1590
GO_AMIDE	69	0.759103	1.3468608	0.031578947	0.21955773	1	1714
GO_NEGA1	25	0.84098446	1.3473206	0.04378531	0.21955587	1	1002
GO_POSITI	106	0.72866285	1.3476439	0.023192361	0.21940926	1	1780
TGAYRTCA	404	0.6470768	1.3474637	0.010526316	0.219393	1	1658
COUP_DR1	200	0.69565046	1.3473185	0.013386881	0.21924314	1	1929
GO_LYMPT	17	0.8624373	1.3470647	0.060781475	0.21920286	1	1503
GO_MYOFI	30	0.81503934	1.3472549	0.05420054	0.21915676	1	1841
GO_POSITI	417	0.6443204	1.3485078	0.002638523	0.21904585	1	2171
GO_COCHI	17	0.87677646	1.3472164	0.05169867	0.21899267	1	1142
GO_NEGA1	87	0.74822944	1.3496064	0.03387534	0.21793245	1	1701
GO_UBIQL	187	-0.7831086	-1.6553	0	0.21791734	0.987	67
GO_POSITI	62	0.74918437	1.3495094	0.04611331	0.21762642	1	1671
PPARA_01	32	0.81572956	1.3496017	0.044594593	0.2176231	1	1082
GO_REGUL	252	0.66855806	1.3498877	0.019125683	0.21757185	1	1650
GO_REGUL	21	0.839158	1.3494662	0.055934515	0.21742944	1	1639
GO_PLASV	74	0.75251013	1.3498409	0.035665296	0.21741463	1	1195
HNF3ALPH	164	0.7042754	1.3492454	0.023841059	0.21726805	1	1706
GO_REGUL	50	0.78831667	1.3491614	0.03434066	0.21722959	1	1094
GO_PEPTIC	50	0.78056234	1.3500892	0.03963012	0.21722272	1	1714
GO_NEGA1	34	0.81093186	1.34946	0.059620596	0.217132	1	1797
GO_B_CELI	107	-0.8403536	-1.6531795	0	0.21694534	0.99	395
GO_RESPO	390	0.64926124	1.3494334	0.007633588	0.21690516	1	1745
GO_REGUL	103	0.73105884	1.3503118	0.022757698	0.21681137	1	1362
GO_POSITI	30	0.8250024	1.3505223	0.045643155	0.21640304	1	931
KEGG_STEI	23	0.846959	1.3509783	0.03883495	0.21612193	1	1415
GO_AMEBI	123	0.7327729	1.3510901	0.018469658	0.21608454	1	2146
GO_PROTE	22	0.83295286	1.3507243	0.06488011	0.2160365	1	1247
GO_EAR_N	78	0.7561012	1.351238	0.027359782	0.21588457	1	1562
GO_CELLU	30	0.8210937	1.3509581	0.03508772	0.21587898	1	806
GO_ION_G	24	0.83907276	1.3518887	0.033755273	0.2158374	1	1276
GO_ION_C	89	0.7444872	1.351795	0.02422611	0.21582352	1	2235
GO_SERINI	47	0.7873287	1.3517323	0.04306864	0.21574095	1	1202
GO_CENTR	24	0.8339237	1.3521247	0.057771664	0.2156509	1	1758
GO_POSITI	17	0.86807865	1.3509269	0.045454547	0.21564999	1	841
GO_CONTF	156	0.71089494	1.3520323	0.012711864	0.21563227	1	1523

GO_POSITI	53	0.7814788	1.3515924	0.032	0.21560004	1	1865
GO_NEGA1	55	0.7830088	1.3522336	0.028795812	0.21557975	1	1797
NFAT_Q6	189	0.69256335	1.3514464	0.016260162	0.21544641	1	1846
GO_TRABE	17	0.87097144	1.3517302	0.042857144	0.21542232	1	1852
GO_FATTY	34	0.80507493	1.3524618	0.043126684	0.21540377	1	723
GO_RUFFL	73	0.7539231	1.3528411	0.033068784	0.21535677	1	1654
GO_OOCY1	17	0.87397236	1.3527559	0.036931816	0.21533681	1	222
GO_FAT_S1	18	0.85548484	1.3515856	0.054172765	0.21529762	1	1495
GO_REGUL	20	0.86648023	1.3529708	0.05077574	0.21528627	1	1035
GO_POSITI	43	0.7935564	1.352403	0.038821954	0.21528353	1	1671
E2F_03	219	0.68886095	1.3526152	0.020689655	0.21515852	1	1346
GO_REGUL	21	0.8405907	1.3527368	0.058739256	0.21506992	1	1739
GO_REGUL	20	0.85493726	1.3536444	0.04466859	0.21471804	1	976
GO_NEGA1	26	0.83707774	1.3534197	0.0473613	0.21443382	1	865
GO_ACTIV	45	0.79898924	1.3536334	0.045454547	0.214413	1	1565
KEGG_GLIC	60	0.765531	1.3535373	0.03809524	0.2143926	1	1245
GO_CELLU	24	0.8332353	1.3544487	0.047756873	0.21428272	1	1164
GO_REGUL	23	0.8416179	1.3533758	0.05374823	0.21424049	1	1094
GO_NEGA1	24	0.83583367	1.35389	0.050139274	0.21422347	1	1639
GO_REGUL	18	0.8698624	1.3544099	0.038189534	0.21408312	1	424
GO_RESPO	37	0.80071086	1.3546495	0.04774536	0.21391827	1	1357
ZIC3_01	193	0.69218457	1.3543998	0.024096385	0.21377276	1	1817
GO_NEGA1	15	0.870719	1.3550309	0.05783866	0.21358377	1	323
GO_POSITI	15	0.8652067	1.3543881	0.055636898	0.21348758	1	229
CTAWWW	264	0.6712429	1.3549826	0.01650619	0.21343644	1	1554
GO_MEMB	20	0.85261595	1.35436	0.051209103	0.21323125	1	816
GO_SALIV	28	0.8222042	1.3542811	0.030726258	0.2131812	1	2119
GO_NEURC	25	0.84776706	1.3549823	0.03230337	0.21309721	1	1240
GO_CELLU	24	0.83738106	1.3555433	0.046413504	0.21204667	1	1656
GO_CHONI	26	0.83503103	1.3560294	0.03729282	0.2113214	1	1240
GO_REGUL	207	0.69606596	1.3559902	0.010738255	0.2111131	1	2022
MEF2_Q6	182	0.69370204	1.3559657	0.014765101	0.21085478	1	1674
GO_ALCOH	73	0.7545787	1.3562686	0.04134367	0.21083944	1	1163
GO_REGUL	17	0.85636556	1.3567715	0.050215207	0.21073264	1	637
SRF_Q5_0	180	0.70424294	1.3568766	0.017783858	0.21070181	1	1885
GO_REGUL	90	0.75126445	1.3564357	0.023622047	0.21054544	1	1739
GO_FORM	91	0.751775	1.3567343	0.026954178	0.21051426	1	1621
GO_CHEM	51	0.7883855	1.3565787	0.034574468	0.21038486	1	445
GO_NEGA1	179	0.69945985	1.3567272	0.02173913	0.21019927	1	1744
GO_DNA_F	33	-0.913694	-1.6639944	0.008097166	0.20879376	0.959	166
GO_REGUL	32	0.8197687	1.357563	0.040268455	0.20862818	1	1218
GO_MUSC	171	0.7004732	1.3579849	0.017449664	0.20747203	1	1370
GO_REGUL	43	0.7855427	1.3581946	0.038303692	0.20703223	1	1656
KEGG_CYT	40	0.8082091	1.3589243	0.030985916	0.20682527	1	1431
GO_NEGA1	38	0.8083121	1.3588663	0.048010975	0.2066837	1	1034
GO_IN_UT	261	0.67649555	1.3587816	0.022397893	0.20666243	1	1743
GO_RESPO	35	0.8181928	1.3587657	0.03978052	0.20637366	1	1731
GO_REGUL	314	0.66237444	1.3586283	0.023715414	0.20621651	1	1796
GO_REGUL	16	0.85910064	1.3587602	0.04341534	0.2060535	1	1428
GO_POSITI	102	0.73708713	1.3586195	0.020463847	0.20591925	1	1239

GO_POSITI	42	0.7868614	1.359341	0.053645115	0.2057601	1	1477
GO_AXON	325	0.66068316	1.3601115	0.007915568	0.20533696	1	2146
GO_REGUL	68	0.76753676	1.3603194	0.02834008	0.20531934	1	1770
GO_REGUL	65	0.77844924	1.3596635	0.036	0.20522258	1	1334
GO_CELLU	65	0.7618744	1.3598864	0.03429355	0.20509146	1	1057
BACH2_01	219	0.6996504	1.3601015	0.006747638	0.20501998	1	1741
GO_RESPO	154	0.7098611	1.3603073	0.019021738	0.20500503	1	1515
GO_COCHI	27	0.83153963	1.3596406	0.05191257	0.20498654	1	1546
TTCNRGNN	123	0.72083014	1.3598485	0.028037382	0.20488063	1	1482
GO_DEFINI	15	0.8705826	1.3600583	0.058651026	0.20480666	1	1181
GO_METH'	46	-0.9270705	-1.6594901	0.004255319	0.20474452	0.974	6
GO_RHO_F	43	0.80391264	1.3614818	0.032432433	0.20468614	1	2663
YNTTTNNN	41	0.79423904	1.3613095	0.037190083	0.20461152	1	1754
GO_CELLU	451	0.644409	1.3606343	0.002631579	0.20452239	1	1515
GO_NEGA1	94	0.7439086	1.3608526	0.025367156	0.20446922	1	1852
GO_BIOMI	51	0.7977092	1.3614801	0.025069637	0.20434311	1	1465
GO_REGUL	53	0.78589535	1.3612882	0.03230337	0.2043128	1	266
GO_NUCLE	185	0.692536	1.3611932	0.011984021	0.20430794	1	539
FREAC7_01	136	0.7177403	1.3609982	0.015068493	0.20430736	1	1664
GO_GROW	314	0.65958905	1.3608189	0.018324608	0.20424157	1	1878
GO_RELAX	18	0.87558895	1.3617362	0.038291607	0.20419443	1	1671
GO_ERBB2	35	0.8157202	1.3620827	0.04200542	0.20413958	1	1245
GO_POSITI	24	0.8469494	1.3611677	0.029045643	0.2040591	1	825
GO_POSITI	24	0.83851326	1.3619037	0.044198897	0.2039794	1	1035
GO_ESTRO	17	0.8782555	1.3620746	0.037845705	0.2038103	1	948
GO_NEGA1	20	0.8586037	1.3625578	0.040697675	0.20269439	1	1593
GO_OOCY1	30	0.82199854	1.3627195	0.03457815	0.20251895	1	222
GO_ACTIN	146	0.70862824	1.363207	0.021709634	0.20224266	1	2518
GO_ACTIN	390	0.6581593	1.3630356	0.010403121	0.20213655	1	1460
YYCATTCA'	158	0.70771205	1.3629652	0.016666668	0.2020347	1	2485
GO_CELLU	115	0.7273704	1.3631792	0.029294275	0.20199707	1	1332
GO_SUBST	37	0.81304216	1.3634692	0.043296088	0.20166332	1	1220
GO_ACTIV	17	0.85319674	1.3635806	0.056865465	0.20164315	1	1142
GO_ENDO'	50	0.7937715	1.3637875	0.027559055	0.20127366	1	1593
GO_REGUL	266	0.68162733	1.3654746	0.007905139	0.19966237	1	1758
GO_NEGA1	45	0.8056167	1.3654456	0.012362638	0.19939725	1	2104
GO_POSITI	25	0.83290416	1.3652767	0.04526749	0.19932999	1	1829
GO_ENDO'	61	0.7772943	1.3651865	0.042666666	0.1992769	1	1693
GO_RESPO	51	0.7817094	1.3654203	0.024657534	0.19912733	1	1829
GO_MONC	52	0.79356354	1.3651831	0.03434066	0.19893841	1	1538
GO_RIBON	83	0.75360715	1.3649896	0.014986376	0.198925	1	31
KEGG_AXC	110	0.73969793	1.3647133	0.01861702	0.19879933	1	1841
GO_TRANS	54	0.7760251	1.3646308	0.03380282	0.19876158	1	1450
GO_POSITI	72	0.771539	1.3651435	0.02422611	0.19873084	1	1005
GO_REGUL	51	0.79082066	1.364962	0.035809018	0.19865479	1	2022
GO_HISTO	23	-0.9595886	-1.6630036	0.003703704	0.19862951	0.964	9
GO_BLOOE	80	0.75356805	1.3659649	0.025885558	0.19837888	1	1543
GO_REGUL	176	0.7057815	1.3649606	0.016064256	0.1983121	1	1656
GO_REGUL	27	0.8326526	1.3663725	0.036775105	0.19745268	1	793
GO_REGUL	87	0.75117344	1.3668144	0.025198938	0.196896	1	1656

GO_REGUL	16	0.8751283	1.3666542	0.03773585	0.1967654	1	1962
GO_MUSC	88	0.7525947	1.3667578	0.02890933	0.19674577	1	1303
GO_RENAL	15	0.88137156	1.3670106	0.041847043	0.19657692	1	637
GO_POSITI	19	0.8619169	1.367272	0.04857143	0.19597526	1	1738
GO_CARDI	31	0.8305539	1.3676732	0.042016808	0.19569717	1	1281
GO_AXIS_E	20	0.85884106	1.3678975	0.030942334	0.19559397	1	1142
NKX22_01	135	0.7238345	1.3676022	0.028150134	0.19559357	1	1674
GO_ALCOH	286	0.68079394	1.3678445	0.005134788	0.19542049	1	1575
GO_REGUL	22	0.8374554	1.3675823	0.071428575	0.1952896	1	822
GO_REGUL	147	0.7161708	1.3684644	0.011034483	0.19395536	1	1138
GO_PROTE	28	0.8279944	1.368782	0.05284553	0.19391961	1	1701
GO_RESPO	263	0.68996704	1.3686496	0.010652463	0.19369072	1	1745
GO_TISSUE	34	0.82527184	1.368757	0.04155496	0.19364506	1	1706
GO_HOMC	45	0.8012431	1.3714911	0.027624309	0.19328988	1	2076
GO_MUSC	171	0.7111826	1.3714094	0.005464481	0.19321644	1	1916
HFH8_01	150	0.7186868	1.3694128	0.022576362	0.19320154	1	1708
GO_RESPO	40	0.81887126	1.3691181	0.024556616	0.19315739	1	1476
GO_HISTO	22	0.8468235	1.3693657	0.033994336	0.19300173	1	117
GO_REGUL	68	0.7796717	1.3696778	0.027741084	0.19300002	1	1852
GO_REGUL	38	0.81203014	1.3714072	0.030955585	0.19285329	1	1310
TST1_01	188	0.702847	1.3696154	0.017735334	0.19284624	1	1841
GO_VASCL	45	0.80751956	1.3713096	0.02937063	0.19284205	1	1434
GO_POSITI	24	0.85006994	1.3712226	0.03429355	0.19273274	1	1142
GO_POSITI	39	0.81538486	1.3693278	0.025675675	0.19272305	1	1729
GO_REGUL	93	0.7477326	1.3710485	0.019151846	0.19258349	1	1657
GO_ENDO	92	0.755683	1.3711748	0.015027323	0.19254206	1	1540
GO_POSITI	17	0.8691425	1.371018	0.050632913	0.19231659	1	1829
GO_REGUL	17	0.8758214	1.370969	0.035410766	0.1921005	1	48
GO_DENDR	69	0.7663989	1.3705009	0.026760563	0.19191281	1	2325
GO_REGUL	151	0.7218388	1.3709275	0.007926024	0.19188122	1	1428
GO_CELLU	155	0.7196932	1.3708804	0.016260162	0.19166903	1	1413
GO_ACTIN	50	0.78416073	1.3704809	0.035904255	0.19162413	1	1220
GO_REGUL	343	0.6593432	1.370812	0.007989348	0.19150107	1	1691
GO_ENTRA	23	0.8426108	1.3704631	0.042613637	0.19133818	1	910
CEBPD	189	0.7091994	1.3702734	0.008230452	0.19126287	1	1677
GO_RESPO	27	0.83161753	1.3707798	0.036363635	0.19125527	1	322
GO_REGUL	198	0.6979622	1.3704174	0.008163265	0.19113548	1	1656
GO_INTEG	90	0.74343896	1.3724487	0.022049287	0.19071017	1	1568
GO_REGUL	442	0.6465484	1.3723708	0.007653061	0.19061856	1	1509
GO_REGUL	260	0.6761794	1.3726709	0.012032085	0.19030324	1	1736
GO_NEURC	153	0.7165084	1.3729348	0.01899593	0.18974139	1	1758
GO_POSITI	28	0.83793986	1.3734007	0.040983606	0.1885187	1	1943
GO_INNER	63	0.7781012	1.3737792	0.029609691	0.18827432	1	1142
GO_KINAS	53	0.7831152	1.373617	0.022666667	0.18812	1	2115
KEGG_FC	92	0.75937283	1.3737475	0.017615177	0.18799798	1	2481
E2F_Q6_0	208	0.69776607	1.3741918	0.014454665	0.18730493	1	330
GO_REGUL	84	0.7541599	1.374427	0.012195122	0.18685074	1	857
GO_RENAL	27	0.84773517	1.3746282	0.052781742	0.18683632	1	400
GO_REGUL	36	0.8310834	1.375068	0.019178081	0.18677785	1	841
GO_PROTE	27	0.8451242	1.3745526	0.024930747	0.18675523	1	911

GO_POSITI	31	0.8285375	1.3752198	0.038043477	0.18660507	1	1621
GO_REGEN	125	0.7264289	1.375049	0.021276595	0.18648684	1	1851
WGGAATG	295	0.674837	1.3748413	0.006596306	0.18645008	1	1878
GO_REGUL	334	0.6706738	1.3753935	0.005298013	0.18636298	1	1852
GO_REGUL	77	0.768516	1.3749892	0.022222223	0.1863319	1	1175
GO_REGUL	36	0.8303211	1.3757055	0.023611112	0.186099	1	1515
GO_POSITI	22	0.8609747	1.3756155	0.036775105	0.18603927	1	186
GO_SUBST	24	0.8674996	1.3759649	0.020260492	0.18552943	1	1677
GO_REGUL	47	0.78749824	1.376107	0.041265473	0.18543576	1	1656
GO_STERO	86	0.76305395	1.3762988	0.016	0.18511456	1	1516
GO_BILE_A	22	0.868051	1.3765942	0.014025246	0.18497089	1	1355
GO_DETEC	15	0.8938316	1.3765774	0.024460431	0.18464983	1	1357
GO_TRANS	70	0.78150296	1.3770089	0.010899182	0.18464963	1	1604
CEBPA_01	184	0.6989025	1.3770003	0.016348774	0.18430464	1	1290
GO_RESPO	33	0.8338014	1.377345	0.028455285	0.18419598	1	941
GO_NEGA1	18	0.87535036	1.376939	0.03314121	0.18415673	1	1719
GO_FIBROI	21	0.8634402	1.3773167	0.041547276	0.1838999	1	1536
GO_DEVEL	82	0.7685356	1.3780379	0.016645327	0.18296783	1	1878
GO_REGUL	48	0.79494107	1.3782542	0.037037037	0.18295726	1	1488
GO_POSITI	72	0.76835424	1.3792938	0.017496636	0.18292487	1	1729
GO_POSITI	28	0.8457253	1.379198	0.03861518	0.18285276	1	1671
GO_POSITI	15	0.8986857	1.3790938	0.026988637	0.18281777	1	388
GO_REGUL	28	0.8564845	1.3779839	0.01759134	0.1827919	1	952
GO_COATE	209	0.6974927	1.379006	0.010723861	0.18270507	1	1540
GO_REGUL	67	0.7713072	1.3782237	0.0260631	0.18269451	1	1463
GO_POSITI	29	0.83960515	1.3787309	0.026954178	0.18258496	1	1715
TGASTMAC	172	0.7140067	1.3779376	0.014492754	0.18256713	1	2132
SGCGSSAA	154	0.7311988	1.3789696	0.009681881	0.18246037	1	804
GO_CORTI	73	0.76182187	1.3785305	0.02631579	0.18244512	1	1880
GO_REGUL	256	0.7000495	1.37891	0.006756757	0.18232638	1	1554
GO_CELLU	94	0.74862957	1.3787072	0.020491803	0.1822943	1	2058
GO_ENDOF	53	0.7921927	1.379706	0.02387268	0.18189387	1	1540
GO_PROTE	38	0.82527363	1.3798556	0.019310344	0.18177359	1	1097
KEGG_TYR	30	0.8242834	1.37998	0.040787622	0.18170434	1	1085
GATA1_03	180	0.7113965	1.3801376	0.011173184	0.18154883	1	1798
GO_COMP	31	0.8380841	1.3803312	0.035135135	0.18127607	1	843
GO_CHON	23	0.849421	1.3814963	0.027816411	0.18117054	1	1240
GCGNNAN	115	0.75123644	1.3804936	0.008264462	0.18110447	1	1049
GO_REGUL	27	0.85740316	1.381442	0.022788204	0.18098152	1	637
GO_RENAL	20	0.8650527	1.3809204	0.04057971	0.18084303	1	637
GO_CORTI	55	0.7940388	1.3812948	0.018691588	0.18072851	1	1880
GO_REGUL	32	0.8248577	1.3814105	0.03526093	0.1807101	1	1157
GO_REGUL	15	0.8838451	1.3812203	0.041193184	0.18062638	1	859
GO_NEGA1	68	0.77422106	1.3811468	0.02710027	0.18051992	1	1852
GO_EMBR	52	0.7942502	1.3808944	0.024193548	0.18051125	1	1228
GO_REGUL	486	0.6470049	1.3808478	0.003836317	0.18027203	1	1715
ACAWNRN	57	0.7971716	1.3822199	0.018445322	0.17934766	1	1215
GO_CAMP	27	0.84633994	1.3822128	0.028328612	0.17896558	1	1175
GO_NEGA1	81	0.7655035	1.3828546	0.01897019	0.17739485	1	658
TCF1P_Q6	202	0.7028372	1.3830142	0.012162162	0.17722431	1	1677

GO_REGUL	32	0.83650315	1.3831515	0.028129395	0.17706512	1	1145
GO_HYDR	22	0.8628866	1.3833059	0.037142858	0.17689809	1	456
GO_POSIT	423	0.6555678	1.3837298	0.002635046	0.17615637	1	1866
NKX62_Q2	172	0.7131032	1.3836476	0.016393442	0.17604274	1	1838
GO_NEUR	45	0.8079681	1.3842276	0.026845638	0.17512092	1	1741
GO_FLUID	17	0.8997193	1.3841891	0.01161103	0.17488971	1	264
GO_ACUTE	54	0.795438	1.3847036	0.024423338	0.17388022	1	1851
GO_RESPO	15	0.89768386	1.385085	0.03591954	0.1737154	1	1005
GO_REGUL	89	0.7636882	1.385049	0.021917809	0.17345846	1	1852
GO_SECRE	62	0.79113054	1.3850179	0.012311902	0.17320003	1	1202
GATAAGR	205	0.710655	1.3853662	0.007863696	0.17311136	1	1901
GO_HEART	19	0.87511754	1.3861775	0.023426061	0.17302357	1	1344
KEGG_ARA	39	0.82138366	1.386348	0.020775624	0.17278059	1	723
GATA6_01	188	0.7146847	1.3865901	0.013495277	0.17274472	1	1852
GO_NEGA1	451	0.65507275	1.386146	0.00388601	0.1727333	1	1691
GO_AORTA	34	0.8281467	1.3865329	0.035952065	0.1725335	1	1344
GO_PLATE	34	0.8259891	1.3857574	0.025885558	0.17249587	1	2076
GO_APOPT	26	0.8486097	1.3859909	0.030470913	0.17246248	1	1070
GO_REGUL	18	0.8805306	1.3856665	0.024216523	0.17241769	1	500
GO_NEGA1	37	0.82117265	1.3861446	0.023319615	0.1723423	1	815
GO_POSIT	15	0.9023747	1.3859719	0.015669515	0.17213343	1	1357
GO_RAS_G	193	0.7106178	1.3869098	0.006811989	0.17205694	1	2097
GO_REGUL	40	0.8178603	1.3874512	0.03009576	0.17049943	1	1096
GO_CELLU	45	0.8110091	1.3883874	0.022222223	0.16923906	1	1957
GO_LEUKC	230	0.6937028	1.3883287	0.008321775	0.16905089	1	950
GO_SCHW	22	0.8842003	1.3885816	0.020408163	0.16903782	1	371
GO_ORGAI	109	0.7517716	1.3887401	0.021978023	0.16889249	1	1860
GO_REGUL	141	0.7254752	1.3880632	0.008241759	0.16881843	1	1677
GO_REGUL	17	0.8973743	1.3882942	0.021306818	0.16880439	1	752
GO_CELL_F	231	0.69979805	1.388901	0.016	0.1687051	1	1729
GO_NEUR	25	0.8607794	1.3882302	0.025815217	0.16865113	1	999
GO_EXOCR	36	0.8235098	1.3892674	0.025920874	0.16785988	1	2119
GO_NEGA1	30	0.84600264	1.3897859	0.013586956	0.1669407	1	1593
GO_GROW	90	0.7619082	1.3896947	0.019471489	0.16685903	1	1193
GO_CELLU	17	0.89183974	1.3902385	0.021489972	0.16575369	1	956
GO_RETIN	15	0.9011297	1.3910834	0.022988506	0.16574211	1	1132
GO_NEGA1	28	0.8553025	1.3907249	0.01650619	0.16572809	1	857
GO_REGUL	17	0.88938636	1.3904924	0.02601156	0.16568865	1	972
YWATTWN	52	0.808826	1.390431	0.018716577	0.16550758	1	1317
GO_CYTOK	370	0.6703342	1.391763	0.006747638	0.16548823	1	1260
GO_RESPO	131	0.7455841	1.3910406	0.012430939	0.16547656	1	1536
GO_CAMP	27	0.854947	1.3906972	0.024423338	0.16541187	1	1229
AR_01	126	0.74701303	1.3915524	0.006666667	0.16538784	1	1638
GO_POSIT	139	0.7183683	1.3909706	0.017735334	0.16532294	1	1657
GO_AMINC	15	0.8997918	1.3917259	0.021216407	0.16522534	1	58
GO_REGUL	73	0.7809535	1.3913634	0.020380436	0.16520935	1	1315
GO_NEGA1	197	0.71094686	1.3914912	0.001358696	0.16516139	1	1677
GO_ANCH	454	0.65101314	1.3924564	0.002610966	0.16427276	1	1790
GO_REGUL	42	0.8161825	1.3922383	0.019788919	0.16416152	1	952
YNGTTNN	280	0.6919441	1.3924356	0.003984064	0.16392726	1	1790

GO_PERIPH	19	0.88706195	1.3927529	0.026548672	0.16367224	1	371
GO_OUTEF	168	0.7193582	1.3928908	0.008230452	0.1636194	1	2409
GO_REGUL	54	0.7948491	1.3931665	0.017426273	0.16310129	1	1096
GO_NEGA1	28	0.8479078	1.3937304	0.017711172	0.16154644	1	729
KEGG_OLF	31	0.850461	1.394198	0.017567568	0.16084278	1	341
GO_SENSC	121	0.75252736	1.3941174	0.008108108	0.16069502	1	1574
GO_AXON	31	0.8559797	1.3944303	0.02027027	0.16047178	1	1741
GO_POSITI	41	0.81504107	1.3947628	0.022397893	0.16015747	1	1956
GO_NEGA1	371	0.66764426	1.3946419	0.004016064	0.1601399	1	1748
GO_HYALL	15	0.9065261	1.395333	0.010526316	0.15993935	1	477
GO_RESPO	96	0.7593872	1.3949628	0.009735744	0.15993752	1	1370
CHX10_01	155	0.724263	1.3952286	0.00672043	0.1598885	1	1698
GO_S_ADE	113	0.73961234	1.3951774	0.013315579	0.15962169	1	359
GO_POSITI	237	0.70058155	1.3959025	0.004	0.15915063	1	1780
GO_POSITI	38	0.8364997	1.395797	0.014884979	0.15910436	1	1738
GO_POSITI	32	0.8530635	1.395731	0.014184397	0.1589045	1	1096
GO_REGUL	228	0.6978938	1.39672	0.010973937	0.15802446	1	1310
GO_MUCC	91	0.7612225	1.3973924	0.01780822	0.15797119	1	2058
GO_RENAL	16	0.8988584	1.3971647	0.015341702	0.1579315	1	971
GO_REGUL	131	0.74853873	1.3965001	0.006675568	0.15791434	1	1770
GO_RESPO	175	0.71923333	1.3964502	0.00795756	0.15771048	1	1477
GO_RECEP	71	0.7851208	1.3973582	0.018592298	0.15767123	1	1946
GO_MYELC	76	0.7720695	1.3967056	0.015768725	0.15766045	1	703
GO_NEGA1	23	0.8639913	1.3971403	0.021582734	0.15761305	1	1096
GO_POSITI	27	0.84619117	1.3970635	0.03586207	0.1574362	1	1639
GO_ROUGI	56	0.8001396	1.3977927	0.025032938	0.15739498	1	1554
GO_NEGA1	46	0.83499575	1.3976815	0.01212938	0.1573578	1	1315
GO_REGUL	86	0.76275504	1.3984749	0.019151846	0.1554938	1	2395
GO_BASAL	18	0.8942392	1.4025364	0.013888889	0.15447521	1	1047
GO_VENTR	43	0.82243925	1.4024141	0.021563342	0.15446438	1	1142
GO_MACR	21	0.8862456	1.4017434	0.015006822	0.1541442	1	711
GO_FOREB	45	0.8255062	1.402383	0.013717421	0.15411715	1	1326
GO_PIGME	22	0.8523381	1.3992988	0.038514443	0.15398262	1	1018
GO_CELLU	413	0.6673721	1.4019269	0.00131406	0.15391238	1	2304
GO_COLLA	67	0.7934914	1.4021823	0.007802341	0.15390326	1	1199
GO_TISSUE	67	0.789206	1.3994764	0.008196721	0.15384914	1	1657
GR_01	157	0.727793	1.4023329	0.008462624	0.15383066	1	1770
GO_RESPO	17	0.8971799	1.3991089	0.009957326	0.1538215	1	1303
GO_REGUL	70	0.78003806	1.4028449	0.01608579	0.15382013	1	1739
GO_RESPO	128	0.74489015	1.4017116	0.005594406	0.15380959	1	2082
NKX3A_01	153	0.7264565	1.4020872	0.009708738	0.15379302	1	1735
GTGGGTGF	222	0.70280045	1.3992496	0.00269179	0.15377362	1	1800
GO_CELL_	20	0.9049836	1.4008198	0.011396011	0.15373613	1	524
GO_ENZYM	415	0.657135	1.400565	0.003880983	0.1537305	1	2115
GO_NEGA1	123	0.7586568	1.4016223	0.004076087	0.15369232	1	1591
GO_POSITI	40	0.8294558	1.4007052	0.009749304	0.15368675	1	1037
FOXJ2_01	138	0.7395108	1.4004512	0.00795756	0.153678	1	1674
GO_REGUL	22	0.87811625	1.400322	0.020604396	0.15367648	1	1780
GO_REGUL	20	0.86624825	1.4015528	0.025174825	0.15352938	1	726
GO_POSITI	99	0.7712844	1.400269	0.010840109	0.15340738	1	1729

GO_REPLA	21	0.87631184	1.3997461	0.01810585	0.153407	1	1287
GO_COROI	31	0.83874786	1.4001527	0.012448133	0.15336499	1	1082
KEGG_BLA	40	0.83321273	1.4010842	0.01632653	0.15327881	1	743
CREBP1_0	151	0.7280835	1.4015237	0.011019284	0.15320817	1	2399
KEGG_CHE	163	0.72320586	1.4000764	0.002758621	0.1531367	1	1245
GO_DECID	16	0.89478177	1.3999606	0.023154847	0.15305999	1	1372
GO_PROTE	91	0.77612925	1.4047939	0.002713704	0.15289849	1	1738
GO_ORGAI	373	0.6743024	1.4015188	0.00397351	0.15280397	1	1575
GO_CYTOP	19	0.89383847	1.4014294	0.015235457	0.15266228	1	597
PAX2_02	199	0.71464825	1.4046282	0.004237288	0.15265246	1	1841
GO_EPIDEF	48	0.81568366	1.4042153	0.01994302	0.15261815	1	1530
GO_CORTI	35	0.8344613	1.4038292	0.020718232	0.15254949	1	1750
GO_KINASI	160	0.7288879	1.404775	0.004021448	0.152517	1	2115
GO_POSITI	128	0.739174	1.4050819	0.00665779	0.15249081	1	1738
GO_NEGA1	103	0.7686024	1.4039983	0.010723861	0.15243244	1	1739
CEBPB_02	203	0.7162415	1.4045664	0.005486968	0.15238766	1	1657
GO_PROTE	22	0.87501085	1.4041641	0.02616279	0.15236576	1	841
GO_CYTOK	134	0.7484014	1.403776	0.009333333	0.15231201	1	1243
GO_SPROL	38	0.82645756	1.4044731	0.030303031	0.15225026	1	1220
GO_MAIN_	47	0.808694	1.405299	0.027285129	0.15223894	1	2041
HFH4_01	141	0.7356999	1.4035527	0.004172462	0.15215586	1	1674
PR_01	112	0.7538865	1.4037056	0.010928961	0.1520508	1	1817
GO_ENDOC	221	0.71387035	1.4055434	0.004120879	0.1518758	1	2104
HOX13_01	32	0.83546877	1.4056971	0.023004059	0.15180877	1	1247
GO_LEADIF	113	0.75431275	1.4061168	0.012465374	0.15180239	1	1763
SRF_Q6	188	0.7244946	1.4035443	0.002724796	0.15175085	1	1885
GO_CELLU	216	0.7160882	1.4059931	0	0.1517469	1	1645
GO_REGUL	29	0.8577415	1.4059751	0.02035278	0.15136208	1	1852
GO_PLASM	18	0.9037318	1.4073846	0.013024602	0.15111698	1	834
GO_REGUL	148	0.72927845	1.407591	0	0.15092207	1	1251
GO_REGUL	140	0.7461764	1.4077715	0.004070556	0.15083267	1	1852
GO_NEGA1	20	0.89302844	1.407375	0.005442177	0.15068574	1	1035
GO_DETEC	167	0.72717947	1.4080393	0.00656168	0.15043136	1	1591
GO_CYCLIN	29	0.86402863	1.4073223	0.015130675	0.15039024	1	294
GO_METAI	75	0.7940324	1.4070916	0.008108108	0.15026543	1	1225
GO_POSITI	38	0.83936536	1.4072359	0.01076716	0.15022917	1	1639
GO_NEGA1	86	0.7829438	1.408265	0.00665779	0.1501758	1	1591
GO_POSITI	23	0.86935973	1.4070735	0.013793103	0.1498729	1	1138
GO_POSITI	67	0.7937583	1.4068999	0.01076716	0.14958353	1	1515
GO_RESPO	81	0.78163916	1.4070657	0.010568032	0.14943531	1	1708
GO_RESPO	202	0.71649843	1.408684	0.002785515	0.14919955	1	1656
GO_SMOO	21	0.8715051	1.4089901	0.024045262	0.14905563	1	971
GO_BASEM	79	0.7830178	1.4088677	0.012178619	0.14901936	1	1704
GO_STERO	101	0.7770213	1.4093215	0.008097166	0.14846101	1	1094
GO_AMINC	90	0.7783428	1.409695	0.00397878	0.14782447	1	1645
GO_INTER	120	0.75498074	1.411447	0.009615385	0.14406924	1	2000
KEGG_PAT	50	0.82950044	1.411087	0.006849315	0.14382364	1	1905
GO_ANDRC	21	0.88152915	1.4114304	0.023909986	0.14362842	1	968
GO_CELLU	45	0.83488405	1.4127464	0.009549796	0.14350796	1	1005
GO_REGUL	100	0.7637403	1.4126384	0.008130081	0.14334244	1	2173

GO_MOVE	77	0.79287636	1.411404	0.012244898	0.14325103	1	1348
GO_POSITI	118	0.74773693	1.412296	0.010695187	0.14317623	1	1021
GO_POSITI	76	0.78064096	1.4121716	0.012	0.143159	1	1671
GO_VASO	20	0.9001209	1.412054	0.016528925	0.14307	1	1038
GO_NEGA	27	0.856313	1.4124848	0.013386881	0.14295691	1	1344
GO_WATE	49	0.81068856	1.4119359	0.010973937	0.14295225	1	658
COMP1_01	82	0.7773023	1.4126325	0.005434783	0.14289017	1	1746
GO_NEGA	218	0.7136346	1.4138229	0.006811989	0.14039542	1	1677
KEGG_RET	25	0.8725673	1.4141444	0.013850415	0.1398084	1	1495
GO_POSITI	19	0.8914854	1.4143864	0.016973127	0.13949218	1	1142
GO_ACTIN	50	0.81993943	1.4145793	0.014844804	0.13928914	1	1253
GO_THYMI	18	-0.97385734	-1.6797212	0.003378379	0.13849723	0.804	233
RYTAAWNI	41	0.827092	1.417575	0.020325202	0.1381451	1	1121
GO_NEGA	181	0.72900975	1.4173219	0.005571031	0.13792679	1	1715
GO_REGUL	19	0.88601536	1.4175478	0.012784091	0.13772526	1	1035
GO_LIPID	445	0.66132176	1.4172347	0	0.13764809	1	2034
GO_RESPO	32	0.8435835	1.4152417	0.012311902	0.13753124	1	880
KEGG_MET	34	0.84950566	1.4154278	0.025401069	0.13744047	1	1415
NFE2_01	229	0.7109377	1.4179512	0.006711409	0.13740285	1	2126
GO_NEGA	15	0.91426075	1.4156141	0.009049774	0.1373457	1	409
GO_REGUL	25	0.8597219	1.4159441	0.020775624	0.13730054	1	1753
GO_POSITI	374	0.6836211	1.4172261	0	0.13718383	1	1715
GO_REGUL	40	0.82795894	1.417097	0.018284107	0.13710019	1	726
CCAWWN/	66	0.79575515	1.4163039	0.00795756	0.13697927	1	1842
GO_PEPTIC	449	0.6678534	1.4159192	0.001283697	0.13691765	1	1342
GO_INTRA	19	0.90089136	1.4167421	0.009735744	0.13685437	1	443
GO_NEGA	123	0.75496167	1.4164882	0.005398111	0.13680004	1	1591
GO_RENAL	81	0.7952701	1.4162488	0.006666667	0.13677777	1	1428
PR_02	107	0.76788604	1.4170599	0.009497965	0.136723	1	1807
GO_VIRUS	60	0.8110318	1.418402	0.005405406	0.13651557	1	2000
GO_RESPO	330	0.6946355	1.4167178	0.005134788	0.1364893	1	1515
GO_ORGAI	73	0.7934297	1.4170164	0.016348774	0.13640654	1	2
GO_CELL_	21	0.89651525	1.4186727	0.008379889	0.13614246	1	395
GO_REGUL	104	0.7675352	1.419735	0.00802139	0.1333149	1	1865
GO_CELL_	107	0.762387	1.4202509	0.008064516	0.13312608	1	1758
GO_MULT	62	0.8125463	1.4201787	0.006738544	0.13284369	1	1183
GO_REGUL	33	0.8501173	1.4201717	0.008344923	0.13237785	1	752
GO_GUAN	261	0.7027834	1.4207889	0.001338688	0.13231681	1	2097
GO_GASTR	124	0.74874526	1.4207432	0.006849315	0.13197838	1	1621
GO_RETIN	40	0.8391579	1.4222231	0.008287293	0.13183625	1	658
GO_SERINI	136	0.7533833	1.4220877	0.005298013	0.13179208	1	990
HNF4_DR1	206	0.72103405	1.4217708	0.004166667	0.13172492	1	1871
EN1_01	82	0.79193634	1.4220278	0.005509642	0.13142957	1	1565
GO_CYTOK	186	0.73245037	1.4215549	0.005641749	0.13139325	1	1243
GO_CELL_	35	0.8381305	1.4217486	0.013333334	0.13129479	1	1770
GO_REGUL	246	0.7130731	1.4214267	0.001345895	0.1312482	1	2049
KEGG_PRIC	30	0.8597815	1.4213648	0.014905149	0.130985	1	1161
GO_REGUL	23	0.8873435	1.4229736	0.011267605	0.12993035	1	843
GO_NEGA	15	0.9295409	1.4234402	0.005873715	0.1294241	1	857
GO_FEMAI	73	0.8044374	1.423342	0.00541272	0.12930773	1	858

GO_ADHEF	61	0.81288993	1.4239622	0.006729475	0.1282806	1	1187
GO_REGUL	439	0.6745063	1.4245853	0.001328021	0.12680568	1	1789
GO_NEGA1	59	0.80765986	1.427492	0.01510989	0.12561823	1	1715
GO_POSITI	55	0.80166876	1.4253271	0.010738255	0.12533714	1	2210
GO_CYTOP	38	0.8335345	1.4252028	0.01650619	0.12522241	1	1494
GO_ENDOC	129	0.7569747	1.4274725	0.006811989	0.12515214	1	1160
GO_REGUL	31	0.86038256	1.4263285	0.00947226	0.12504788	1	314
GO_PRIMA	34	0.8621101	1.4259175	0.015006822	0.124856226	1	1310
GO_RESPO	262	0.71183985	1.4267124	0.002649007	0.12481705	1	1485
GO_NEGA1	200	0.7344143	1.4261365	0.006839945	0.12468783	1	1509
PAX4_02	167	0.73903537	1.4274625	0.001367989	0.12467175	1	1679
GO_MODU	222	0.7200379	1.4263033	0.005524862	0.12463004	1	1526
GO_VESICL	80	0.7788903	1.4257	0.012295082	0.124602884	1	1202
GO_INTEG	78	0.7971342	1.4258459	0.009446694	0.12457567	1	1536
GO_REGUL	56	0.81778497	1.426659	0.012178619	0.12450408	1	1142
GO_REGUL	94	0.7793828	1.4272252	0.006684492	0.124365225	1	2041
GO_POSITI	78	0.7978828	1.4270849	0.004043127	0.1242771	1	1019
GO_CYTOP	40	0.8358465	1.4274586	0.016597511	0.12416806	1	597
GO_REGUL	125	0.7747008	1.4287146	0	0.122775726	1	1750
GO_CELLU	70	0.80383986	1.429981	0.007884363	0.1227636	1	1639
GO_ENDOC	77	0.78773975	1.429792	0.012311902	0.122743174	1	1697
GO_RECEP	181	0.7314412	1.4285965	0.005347594	0.12261766	1	1625
GO_POSITI	20	0.8918969	1.4289848	0.014124294	0.12244591	1	1138
E2F_Q3	195	0.7344252	1.4297721	0.002793296	0.12226863	1	1247
GO_CIRCAI	107	0.7775727	1.429765	0.006675568	0.12175581	1	1594
EVI1_05	117	0.7679771	1.429593	0.002781641	0.12168887	1	1735
GO_PROTE	16	0.9092164	1.4295079	0.01746725	0.121435836	1	209
GO_HEART	368	0.69435847	1.4307092	0	0.12102717	1	1635
GO_REGUL	38	0.8590038	1.4312525	0.005594406	0.119849905	1	1357
TGGNNNN	328	0.6981694	1.4321777	0	0.11759586	1	1846
GO_NEGA1	15	0.9339881	1.4331789	0.002976191	0.11613761	1	815
GO_MUSC	21	0.90132886	1.4329177	0.009915014	0.11601859	1	720
GO_LEUKC	94	0.7796492	1.4331032	0.008264462	0.11587324	1	950
GO_GOLGI	54	0.8159741	1.4335344	0.008086253	0.11555807	1	1238
GO_NEGA1	29	0.87398475	1.4341209	0.006896552	0.11472319	1	1218
GO_STERO	169	0.7513209	1.4339776	0.002724796	0.11463482	1	1653
GO_SECRE	350	0.69430107	1.4345763	0.001317523	0.113763094	1	1202
GO_POSITI	37	0.854732	1.4348675	0.012379643	0.11342579	1	1709
GO_REGUL	383	0.68478835	1.4352525	0	0.11339194	1	1637
RGAANNNT	346	0.6872181	1.4354368	0	0.11332808	1	1677
KEGG_P53	62	0.82143617	1.4350944	0.004109589	0.11332317	1	870
GO_CELLU	18	0.90964574	1.4362895	0.013927577	0.11302515	1	941
GO_CYCLIC	35	0.87053216	1.4367483	0.004219409	0.11277151	1	841
KEGG_DRL	34	0.87212235	1.4362665	0.002743484	0.11257973	1	1085
GO_SECRE	62	0.81452584	1.4366447	0.0067659	0.112552375	1	1168
GO_REGUL	58	0.8177061	1.4360937	0.00672043	0.11254942	1	1739
GO_CYCLIC	27	0.87776536	1.4370219	0.013642564	0.11232839	1	1370
GO_CELLU	455	0.6860003	1.4360296	0	0.11220773	1	1263
GO_NEGA1	15	0.92623276	1.4374692	0.004373178	0.11167769	1	1035
GO_SCHW.	26	0.89281994	1.4379667	0.005617978	0.110651694	1	371

GO_ACTOM	56	0.8200394	1.4387763	0.008391609	0.10937019	1	1253
GO_CALCII	73	0.7982832	1.4386045	0.005354752	0.10934862	1	1865
GO_CELLU	23	0.8978258	1.4393584	0.006821282	0.10809391	1	956
GO_REGUL	46	0.8432334	1.4401941	0.005610098	0.10726002	1	857
GO_REGUL	46	0.83603656	1.4399817	0.004054054	0.1071836	1	1251
GO_SULFU	33	0.85826933	1.4398619	0.004026846	0.1070377	1	1329
GO_REGUL	145	0.7564947	1.4415724	0.005277045	0.10641721	1	1019
GO_FATTY	89	0.7876714	1.4418261	0.004160888	0.10611784	1	1538
GO_REGUL	86	0.7843385	1.4409653	0.006648936	0.10611365	1	1847
GO_NEGA1	119	0.7647318	1.4415073	0.005673759	0.10605136	1	658
GO_REGUL	16	0.92238426	1.4408191	0.007122507	0.106003515	1	884
GO_REGUL	147	0.76178586	1.4412396	0.002793296	0.10569694	1	1358
GO_PROTE	43	0.8460997	1.4414543	0.006821282	0.10565525	1	843
GO_ACTIV	244	0.7182835	1.4428694	0.001345895	0.10418442	1	2377
GO_ENDOI	16	0.93069595	1.4433618	0.00295858	0.10394976	1	25
GO_NEGA1	19	0.90984255	1.4427887	0.008559201	0.10388052	1	993
TCCATTKW	196	0.7390228	1.4432931	0	0.10358126	1	1841
GO_REGUL	20	0.89830905	1.4440246	0.010057472	0.102435425	1	1229
GO_POSITI	111	0.77694076	1.4445586	0.001331558	0.10193642	1	1357
GO_MYOSI	15	0.9225898	1.4447685	0.008645534	0.1018836	1	495
GO_LIPID	206	0.7373491	1.4444588	0.002673797	0.101695806	1	1860
GO_RESPO	22	0.9057462	1.4459765	0.004201681	0.10072751	1	1318
GO_MULT	73	0.8035896	1.4462322	0.004115226	0.10052089	1	1183
GO_RESPO	254	0.7176938	1.4455353	0	0.10032771	1	1575
GO_REGUL	280	0.71232903	1.4459431	0	0.10024631	1	1677
GO_STRIA1	17	0.9275068	1.4458873	0.008547009	0.0998475	1	720
GO_MATEI	26	0.8914887	1.4470186	0.006784261	0.099047	1	1372
GO_REGUL	470	0.67971677	1.4483393	0	0.09649295	1	1852
GO_REGUL	48	0.8361136	1.448103	0.006640106	0.09639935	1	769
GO_EXTRA	105	0.78651375	1.4492419	0.001340483	0.09441262	1	1704
GO_CELLU	45	0.8381441	1.4498454	0.003952569	0.093988895	1	1878
GO_AS PAR	21	0.88925725	1.4497032	0.007163324	0.09383974	1	58
GO_NEGA1	65	0.8232305	1.4503143	0.001373626	0.09331754	1	1591
GO_POSITI	61	0.8205618	1.4510075	0.004010695	0.092061505	1	1142
GO_NEGA1	20	0.91142106	1.4517556	0.006944445	0.09109149	1	853
GO_RESPO	175	0.7518517	1.4515241	0	0.09109011	1	2299
GO_ACTOM	57	0.8314455	1.4526483	0.006622517	0.08924002	1	1841
GO_RESPO	24	0.8931485	1.4532924	0.009296149	0.08867146	1	212
GO_POSITI	24	0.90058714	1.4530766	0.006756757	0.088625476	1	829
GO_REGUL	52	0.83619803	1.453954	0.004092769	0.08716404	1	1005
GO_REGUL	486	0.6771604	1.4543281	0.001285347	0.08676301	1	1780
GO_NEGA1	63	0.8177401	1.4552573	0.002721089	0.08543126	1	1593
GO_ACTIN	388	0.6886473	1.4550248	0	0.085430875	1	1770
GO_PLACE	109	0.7865634	1.4557672	0.005405406	0.08525599	1	1372
GO_DEVEL	252	0.7316026	1.4555331	0.001333333	0.08521585	1	1917
GO_MULT	158	0.7615585	1.4565185	0.001347709	0.08378009	1	1748
GO_ORGAI	281	0.7190185	1.4568626	0	0.08346647	1	1329
GO_NEGA1	33	0.86686206	1.458557	0.005563282	0.08083923	1	783
HSF1_01	199	0.7543575	1.4585184	0.002688172	0.08042885	1	1544
GO_AMINC	139	0.766985	1.4584745	0.001373626	0.079975136	1	1240

KEGG_DILA	67	0.8181988	1.4606296	0.006784261	0.07830646	1	1701
GO_RESPO	147	0.7604601	1.459801	0.002617801	0.078262426	1	1623
GO_SMALL	368	0.7018001	1.4611274	0	0.078204006	1	1815
RYAAAKNN	63	0.8349145	1.4609038	0.002785515	0.07815002	1	763
GO_ORGAI	218	0.74374104	1.4614769	0	0.0780602	1	1745
KEGG_REG	179	0.75414735	1.4605553	0.002624672	0.07792027	1	1841
GO_REGUL	25	0.8994664	1.4602209	0.002805049	0.07774744	1	911
GO_TERPE	67	0.8298365	1.4604828	0.001303781	0.07758967	1	1898
KEGG_HYP	62	0.8210594	1.4634202	0.003968254	0.07405232	1	1701
KEGG_ECM	75	0.8142243	1.464204	0.005479452	0.073043935	1	1159
GATA1_04	157	0.7671991	1.4640299	0.001383126	0.07297071	1	1584
GO_MUSC	23	0.90671885	1.466961	0.002836879	0.07260174	1	720
GO_ERBB_	69	0.8269702	1.4675821	0.002670227	0.07223194	1	1545
KEGG_VAS	91	0.80628204	1.4647852	0.001336898	0.07216824	1	1481
GO_POSITI	91	0.79914445	1.4669316	0.001298701	0.07211708	1	950
GO_SEX_D	187	0.753119	1.4681792	0	0.072096325	1	1584
GO_REGUL	106	0.7858899	1.465047	0.002754821	0.07203688	1	1126
GO_NEURC	73	0.8214475	1.4679519	0	0.07203031	1	1741
GO_REGUL	27	0.8971417	1.4668016	0.008298756	0.0718981	1	141
GO_REGUL	33	0.8831378	1.4675754	0.004189944	0.071709804	1	989
GO_ARTER	36	0.87469727	1.4667468	0.002656043	0.07153122	1	1344
GO_POSITI	177	0.7552373	1.4656433	0.002766252	0.07127277	1	2022
GO_VESICL	417	0.6938436	1.4667466	0.001272265	0.07100909	1	1673
E4F1_Q6	243	0.73527825	1.466158	0	0.07100276	1	1340
GO_RESPO	346	0.7150761	1.4693633	0	0.0708875	1	1635
KEGG_TOL	82	0.8115899	1.4691775	0	0.07076083	1	1885
GO_NEGA1	24	0.90851074	1.4660946	0.001388889	0.07072354	1	703
GO_POSITI	174	0.75636905	1.4666438	0.00400534	0.070715696	1	1753
GO_ENSHE	74	0.8073199	1.4690243	0.005486968	0.07066061	1	2456
GO_HEPAF	110	0.7848216	1.4665657	0.003968254	0.07045852	1	1326
GO_ISOPRI	85	0.8138625	1.4701492	0.001329787	0.07025742	1	1085
GO_VASCL	72	0.8226404	1.4699879	0.001426534	0.07014128	1	1619
GO_RESPO	89	0.813619	1.4718047	0.006821282	0.06896257	1	931
GO_SULFU	180	0.764639	1.4717518	0.001347709	0.068510205	1	1326
GO_REGUL	75	0.8230039	1.4715544	0.002617801	0.06844092	1	1739
GO_REGUL	20	0.91679066	1.4725537	0.007122507	0.06822898	1	141
GO_CELL_I	100	0.7962699	1.4715251	0.002673797	0.06796465	1	1536
GO_V_D_J	16	-0.9730612	-1.6989875	0	0.06696311	0.51	174
GO_OVARI	49	0.8464928	1.4734495	0.002747253	0.06683224	1	971
GO_CELL_J	112	0.7946997	1.4742944	0.001373626	0.06539325	1	1770
GO_NEGA1	48	0.8606366	1.4752945	0.004109589	0.064409375	1	1382
AFP1_Q6	192	0.74680847	1.4751678	0	0.064165354	1	1780
GO_PLATEI	44	0.85237736	1.4763775	0.001367989	0.06327563	0.999	1696
GO_NEGA1	17	0.95871216	1.4761338	0	0.063189745	0.999	200
KEGG_GAP	75	0.83200085	1.4775183	0.001303781	0.06135895	0.999	1268
GO_NEGA1	214	0.75804764	1.4792871	0	0.060372386	0.999	1715
KEGG_NOI	57	0.84944785	1.4790037	0.001329787	0.060299244	0.999	703
GO_CELLU	221	0.7430647	1.4788268	0	0.060137164	0.999	1639
GO_VACUC	98	0.8094682	1.4787403	0	0.059868593	0.999	1645
PAX5_01	127	0.7908527	1.479757	0	0.059817165	0.998	1565

GO_REGUL	41	0.8645299	1.4786342	0	0.05959518	0.999	1126
GO_GLYCC	143	0.78447604	1.4812049	0	0.057114296	0.997	1326
GO_REGUL	358	0.7108021	1.4817218	0	0.056560133	0.997	1554
GO_ENDOC	433	0.69991815	1.4835042	0	0.054459687	0.992	1884
GO_RESPO	134	0.7806683	1.4839226	0	0.054271653	0.991	1477
GO_ENDOC	292	0.7244517	1.4833863	0	0.05410788	0.993	1264
GO_CELLU	30	0.8932382	1.4832116	0.00397878	0.054018833	0.994	991
GO_REGUL	155	0.7736527	1.48444	0	0.053880382	0.991	1739
GO_NEGAT	124	0.78906643	1.4859031	0	0.051850937	0.99	1691
GO_MONOC	134	0.7958489	1.4866433	0.004143647	0.051666066	0.989	1815
GO_MATEI	51	0.8514254	1.4865408	0.002762431	0.05132568	0.989	1536
GO_OVULF	68	0.8398631	1.4909761	0.001349528	0.050485972	0.977	1548
GO_RESPO	82	0.8259739	1.488523	0	0.050356098	0.983	1745
GO_NEGAT	26	0.9239134	1.487994	0.001356852	0.0503438	0.984	857
GO_REGUL	86	0.81398475	1.4877709	0.001364257	0.050285194	0.986	1344
GO_NEGAT	61	0.85099816	1.4889125	0.004087193	0.05028365	0.982	1719
GO_RESPO	30	0.8896693	1.488301	0.001396648	0.050249808	0.984	1477
KEGG_CON	44	0.86175984	1.48927	0.00135318	0.05009959	0.982	1334
GO_REGUL	161	0.7795528	1.4908843	0.001312336	0.050098345	0.977	1656
GO_MUSC	209	0.760149	1.4907932	0	0.04964285	0.977	1916
GO_VASCL	127	0.8030785	1.4906852	0.002751032	0.04926146	0.977	1527
GO_CCR_C	21	0.9328772	1.4901626	0.00281294	0.049063317	0.977	445
GO_REGUL	259	0.7398029	1.4904718	0.001358696	0.049011845	0.977	1780
GO_POSIT	59	0.8463488	1.4946321	0.001324503	0.04720138	0.967	1239
GO_POSIT	61	0.8384804	1.4950209	0.002713704	0.04709058	0.966	1325
GO_POSIT	91	0.81567556	1.494545	0.002747253	0.04678416	0.968	1645
GO_FAT_C	91	0.81328994	1.4942479	0.001364257	0.046568792	0.969	1492
GO_REGUL	125	0.7957828	1.4933869	0	0.04655927	0.97	950
GO_CARBC	152	0.77830493	1.4936928	0.001340483	0.046445914	0.969	1413
GO_RESPO	293	0.73164797	1.494205	0	0.046047542	0.969	1536
GO_LYMPH	24	0.9347092	1.4983637	0	0.045423977	0.947	445
GO_RESPO	140	0.7950943	1.4970107	0	0.045275174	0.956	1737
GO_REGUL	195	0.7599353	1.4982325	0	0.04504511	0.947	1656
KEGG_ERB	77	0.8354551	1.4989036	0.001322751	0.04498756	0.944	1245
GO_DEVEL	157	0.7829325	1.4978974	0	0.044966757	0.949	1584
GO_SECRE	267	0.73669034	1.4965237	0.001381216	0.04483302	0.962	1202
GO_ARTER	59	0.85762876	1.496896	0.001408451	0.044802677	0.957	1344
GO_SECON	122	0.80723	1.4978933	0	0.044350773	0.949	1362
GO_INFLAI	367	0.72421145	1.5004921	0	0.044047527	0.936	1738
GO_REGUL	230	0.7511326	1.4999	0	0.04371739	0.937	1664
GO_REGUL	365	0.7258196	1.5002781	0	0.04371608	0.937	1506
GO_RESPO	389	0.7192131	1.502461	0	0.04205668	0.927	2029
GO_RESPO	73	0.8464243	1.5021033	0	0.042017486	0.93	703
GO_GRANI	56	0.86573845	1.5034994	0.002751032	0.041666355	0.913	1476
GO_PLATEI	89	0.8279078	1.5034314	0	0.04109143	0.913	1202
GO_CELLU	145	0.7908208	1.5048931	0	0.04016091	0.904	1851
GO_NEGAT	124	0.81121886	1.5082071	0	0.038912565	0.869	815
GO_REGUL	197	0.7724584	1.5077349	0	0.03890233	0.872	1656
GO_CELLU	97	0.829961	1.5066113	0.001355014	0.038741123	0.886	1239
GO_AMINC	57	0.853873	1.5074362	0	0.038738135	0.877	1238

GO_CELL_C	133	0.80114967	1.5071487	0	0.038541924	0.879	950
GO_REGUL	97	0.8212423	1.5065068	0.001344086	0.03824114	0.887	1640
GO_RESPO	175	0.7827266	1.5107311	0	0.037376925	0.836	1578
GO_REGUL	326	0.72960144	1.5095956	0	0.03720249	0.849	1780
GO_CELL_S	143	0.7918817	1.5106095	0	0.036847122	0.837	1536
GO_FEMAI	88	0.82711464	1.5104265	0	0.03643926	0.838	1584
HSF2_01	179	0.7861907	1.5147585	0	0.034230452	0.775	1494
GO_EXTRA	243	0.7651219	1.513498	0	0.033729378	0.795	1214
GO_REGUL	141	0.79533184	1.5139163	0	0.033727646	0.784	1677
GO_REGUL	191	0.77533793	1.51451	0	0.033722654	0.777	1852
GO_MONC	26	0.91776305	1.5171007	0.001358696	0.03313781	0.742	626
GO_NEGA1	98	0.82496715	1.516968	0	0.032692477	0.746	1474
GO_POSITI	124	0.8067409	1.5169202	0	0.03200554	0.746	1544
GO_CELLU	384	0.73677003	1.522304	0	0.030021047	0.652	1598
GO_LYSOSI	79	0.82771903	1.522207	0	0.02941958	0.653	1645
GO_PLATEI	126	0.80362207	1.5206548	0.001364257	0.029404692	0.679	1568
GO_CELLU	65	0.8540143	1.5203508	0	0.029075988	0.683	931
GO_CELL_I	102	0.8235762	1.5219742	0	0.028930398	0.657	1181
GO_EXTRA	58	0.8678582	1.5219337	0.001347709	0.028278839	0.657	1000
GO_RESPO	115	0.8289103	1.5247326	0	0.027846813	0.611	1745
GO_CHEMI	31	0.9280948	1.5266613	0	0.027792625	0.579	445
GO_REGUL	325	0.7449616	1.5279782	0.001340483	0.027375463	0.561	1264
GO_PLATEI	63	0.86138487	1.5265131	0	0.027124226	0.58	1202
GO_NEGA1	45	0.8883139	1.5317997	0.001345895	0.026873488	0.502	857
GO_REGUL	64	0.851943	1.5262413	0	0.026735377	0.585	1138
GO_CELL_J	159	0.8003012	1.5307078	0	0.026432699	0.525	1790
GO_TAXIS	362	0.7468016	1.5317243	0	0.025984457	0.503	1476
GO_MYOSI	49	0.886231	1.5298837	0	0.025838459	0.534	1280
GO_REGUL	399	0.73481363	1.5305572	0	0.025792686	0.528	1594
GO_RESPO	117	0.82587534	1.537826	0	0.022967817	0.414	1261
GO_RESPO	276	0.7629658	1.5397166	0	0.022677187	0.387	1738
GO_RESPO	396	0.73492455	1.5363979	0	0.022239646	0.428	1515
GO_OVULI	86	0.8435981	1.5376806	0	0.022126403	0.415	1548
GO_REGUL	46	0.8969212	1.5391884	0.001340483	0.022053609	0.39	1138
CEBP_Q2_I	218	0.7926331	1.5421633	0	0.021665417	0.352	1406
GO_REGUL	417	0.7295554	1.543319	0	0.02110999	0.331	1739
KEGG_FOC	179	0.78622794	1.5420284	0	0.020878414	0.355	1409
GO_CYTOP	480	0.72903895	1.547979	0	0.017217284	0.266	1696
GO_REGUL	94	0.8471547	1.550664	0	0.016048094	0.236	1239
GO_PROTE	257	0.77695084	1.555163	0	0.013580743	0.196	1225
GO_WOUN	374	0.7552997	1.5576181	0	0.012923566	0.177	1738
GO_CELLU	374	0.75138324	1.5599947	0	0.011885525	0.156	1878
GO_HISTO	33	-0.9456035	-1.7390821	0	0.009965867	0.079	9
GO_SOMA	40	-0.9520584	-1.7446253	0	0.008831312	0.058	174
GO_SOMA	32	-0.959776	-1.7377832	0	0.008649858	0.08	174
GO_REPRC	307	0.7699589	1.5682501	0	0.008506651	0.099	1372
GO_REGUL	234	0.79729176	1.5675282	0	0.008365969	0.104	1544
GO_CELLU	140	0.82111883	1.5728766	0	0.008099741	0.073	1878
GO_CHEMI	39	0.9273442	1.5721724	0	0.007762189	0.077	445
GO_RESPO	447	0.7486043	1.5709914	0	0.007664839	0.082	1738

GO_DEVEL	440	0.74186754	1.5740587	0	0.007661407	0.062	1598
GO_HEMO	251	0.78620714	1.5759529	0	0.006844134	0.05	1568
KEGG_PRIM	34	-0.96413016	-1.7532626	0	0.00638729	0.034	270
GO_POSITI	350	0.7609499	1.5803412	0	0.005314359	0.034	1691
GO_EXTRA	312	0.7698374	1.5853081	0	0.004748879	0.026	1225
GO_RHYTH	232	0.79781526	1.589682	0	0.004376154	0.016	1594
GO_RESPO	133	0.83193076	1.588552	0	0.003941041	0.018	1745
GO_IMMUN	41	-0.9513771	-1.7708399	0	0.002265235	0.009	41
GO_ANGIC	251	0.8016426	1.6115758	0	7.36E-04	0.002	1647
GO_DNA_F	188	-0.8493431	-1.7956309	0	3.75E-04	0.001	395
GO_HISTO	145	-0.9025069	-1.8257502	0	0	0	127
GO_BLOOD	306	0.8061557	1.6551801	0	0	0	1479
GO_VASCL	396	0.7861527	1.6490165	0	0	0	1647