

Supplementary Table 1B

C5-Gene Ontology

Liver Cirrhosis (LC) vs Healthy Donor (HD)

NAME	SIZE	NES	NOM p-val	FDR q-val
GO_MITOCHONDRIAL_MEMBRANE_PART	137	2.077	0.000	0.001
GO_RESPIRATORY_CHAIN	67	2.077	0.000	0.001
GO_OXIDOREDUCTASE_COMPLEX	79	2.084	0.000	0.001
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	46	2.081	0.000	0.001
GO_QUINONE_METABOLIC_PROCESS	19	2.105	0.000	0.001
GO_MITOCHONDRIAL_TRANSLATION	100	2.085	0.000	0.001
GO_LYASE_ACTIVITY	115	2.093	0.000	0.001
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	62	2.090	0.000	0.001
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	15	2.106	0.000	0.001
GO_CELLULAR_RESPIRATION	123	2.060	0.000	0.001
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	48	2.097	0.000	0.001
GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	121	2.061	0.000	0.001
GO_OXIDATIVE_PHOSPHORYLATION	71	2.061	0.000	0.001
GO_CARBON_OXYGEN_LYASE_ACTIVITY	48	2.056	0.000	0.001
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	89	2.062	0.000	0.001
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	72	2.114	0.000	0.001
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	106	2.069	0.000	0.001
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	47	2.063	0.000	0.001
GO_NADH_DEHYDROGENASE_COMPLEX	42	2.046	0.000	0.001
GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	181	2.044	0.000	0.001
GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	63	2.193	0.000	0.001
GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS	57	2.131	0.000	0.001
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	90	2.134	0.000	0.001
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	115	2.146	0.000	0.001
GO_TRANSLATIONAL_TERMINATION	90	2.144	0.000	0.001
GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	47	2.048	0.000	0.001
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	39	2.047	0.000	0.001
GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	261	2.032	0.000	0.001
GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	18	2.153	0.000	0.001
GO_ELECTRON_TRANSPORT_CHAIN	79	2.025	0.000	0.001
GO_ORGANELLAR_RIBOSOME	69	2.017	0.000	0.001
GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	32	2.015	0.000	0.002
GO_TRANSLATIONAL_ELONGATION	104	2.010	0.000	0.002
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	70	2.007	0.000	0.002
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	361	2.006	0.000	0.002
GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	169	2.011	0.000	0.002
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	63	2.196	0.000	0.002
GO_ORGANELLE_INNER_MEMBRANE	398	2.002	0.000	0.002
GO_HYDRO_LYASE_ACTIVITY	34	1.996	0.000	0.002
GO_MITOCHONDRIAL_MATRIX	331	1.985	0.000	0.002
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	25	1.978	0.000	0.002
GO_NUCLEOBASE_METABOLIC_PROCESS	29	1.984	0.000	0.002
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	91	1.982	0.000	0.002
GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	32	1.979	0.000	0.002
GO_COFACTOR_METABOLIC_PROCESS	233	1.966	0.000	0.003
GO_SMALL_MOLECULE_CATABOLIC_PROCESS	197	1.964	0.000	0.003
GO_ELECTRON_CARRIER_ACTIVITY	80	1.953	0.000	0.004
GO_NAD_BINDING	40	1.957	0.000	0.004
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	67	1.954	0.000	0.004
GO_PIGMENT_BIOSYNTHETIC_PROCESS	33	1.954	0.001	0.004
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	23	1.946	0.000	0.004
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	41	1.936	0.000	0.005
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	40	1.937	0.000	0.005
GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY	152	1.934	0.000	0.005
GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	257	1.934	0.000	0.005
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	17	1.922	0.000	0.005
GO_ORGANIC_ACID_CATABOLIC_PROCESS	120	1.919	0.000	0.006
GO_REGULATION_OF_ACTIN_NUCLEATION	19	1.919	0.000	0.006
GO_FATTY_ACID_BETA_OXIDATION	37	1.915	0.000	0.006
GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	27	1.915	0.000	0.006
GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	26	1.909	0.000	0.006
GO_KETONE_BIOSYNTHETIC_PROCESS	18	1.903	0.000	0.007
GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	40	1.903	0.000	0.007
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	168	1.900	0.000	0.007
GO_PYRIMIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	59	1.904	0.000	0.007
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	44	1.896	0.000	0.007
GO_OXIDOREDUCTASE_ACTIVITY	400	1.892	0.000	0.007
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	17	1.889	0.001	0.007
GO_RESPONSE_TO_INTERFERON_BETA	18	1.883	0.001	0.008
GO_COENZYME_METABOLIC_PROCESS	181	1.879	0.000	0.008
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	216	1.880	0.000	0.008
GO_PIGMENT_METABOLIC_PROCESS	38	1.874	0.000	0.009

GO_PYRIMIDINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	25	1.874	0.000	0.009
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	19	1.872	0.000	0.009
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	80	1.865	0.000	0.010
GO_LIPOSACCHARIDE_METABOLIC_PROCESS	68	1.865	0.000	0.010
GO_AMINO_ACID_ACTIVATION	41	1.861	0.000	0.010
GO_COFACTOR_BINDING	167	1.859	0.000	0.010
GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	28	1.850	0.000	0.012
GO_FATTY_ACID_CATABOLIC_PROCESS	51	1.847	0.000	0.012
GO_CELLULAR_KETONE_METABOLIC_PROCESS	43	1.846	0.000	0.012
GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	260	1.842	0.000	0.012
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_CYCLIC_AMIDINES	26	1.837	0.002	0.013
GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT	19	1.837	0.001	0.013
GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	288	1.824	0.000	0.016
GO_ATP_BIOSYNTHETIC_PROCESS	26	1.821	0.002	0.016
GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	61	1.821	0.000	0.016
GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	53	1.818	0.000	0.017
GO_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	29	1.815	0.000	0.017
GO_COENZYME_BINDING	121	1.814	0.000	0.017
GO_LYSINE_ACETYLATED_HISTONE_BINDING	16	-2.248	0.000	0.017
GO_CYTOCHROME_COMPLEX_ASSEMBLY	16	1.815	0.003	0.017
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX	20	1.812	0.000	0.017
GO_TRNA_METABOLIC_PROCESS	138	1.806	0.000	0.018
GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS	15	1.807	0.004	0.018
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	38	1.801	0.002	0.020
GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	198	1.800	0.000	0.020
GO_MONOSACCHARIDE_METABOLIC_PROCESS	118	1.793	0.000	0.022
GO_PYRIMIDINE_NUCLEOSIDE_METABOLIC_PROCESS	37	1.788	0.000	0.023
GO_COFACTOR_BIOSYNTHETIC_PROCESS	123	1.785	0.000	0.023
GO_METAL_CLUSTER_BINDING	53	1.780	0.000	0.025
GO_4_IRON_4_SULFUR_CLUSTER_BINDING	36	1.778	0.000	0.025
GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	28	1.779	0.000	0.025
GO_TRNA_PROCESSING	88	1.774	0.000	0.026
GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	53	1.771	0.000	0.027
GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	38	1.770	0.000	0.027
GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	15	-2.199	0.000	0.027
GO_FATTY_ACYL_COA_BINDING	24	1.768	0.000	0.027
GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCESS	33	1.765	0.002	0.028
GO_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	63	1.763	0.001	0.029
GO_MONOSACCHARIDE_BINDING	43	1.760	0.001	0.030
GO_AMIDE_BIOSYNTHETIC_PROCESS	407	1.755	0.000	0.031
GO_NUCLEOTIDE_SUGAR_BIOSYNTHETIC_PROCESS	18	1.750	0.004	0.033
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	49	1.751	0.000	0.033
GO_PYRIMIDINE_RIBONUCLEOSIDE_METABOLIC_PROCESS	26	1.749	0.003	0.033
GO_NON_CANONICAL_WNT_SIGNALING_PATHWAY	100	1.743	0.000	0.035
GO_RIBOSOME	202	1.741	0.000	0.036
GO_MEMBRANE_LIPID_METABOLIC_PROCESS	106	1.740	0.000	0.036
GO_PEPTIDE_METABOLIC_PROCESS	435	1.739	0.000	0.036
GO_GLYCOSPHINGOLIPID_METABOLIC_PROCESS	39	1.735	0.001	0.038
GO_LIPID_OXIDATION	48	1.734	0.000	0.038
GO_AEROBIC_RESPIRATION	48	1.735	0.003	0.038
GO_CARBON_CARBON_LYASE_ACTIVITY	35	1.734	0.000	0.038
GO_EXTRACELLULAR_MATRIX_BINDING	18	-2.139	0.000	0.038
GO_CERAMIDE_BIOSYNTHETIC_PROCESS	21	1.728	0.004	0.040
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	61	1.728	0.001	0.040
GO_COENZYME_BIOSYNTHETIC_PROCESS	89	1.729	0.000	0.040
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN	17	1.724	0.003	0.041
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	188	1.722	0.000	0.042
GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	140	1.721	0.000	0.042
GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	49	1.713	0.001	0.046
GO_CARBOHYDRATE_CATABOLIC_PROCESS	75	1.710	0.000	0.048
GO_GLYCOLIPID_BIOSYNTHETIC_PROCESS	36	1.709	0.002	0.048
GO_OLFACTORY_RECEPTOR_ACTIVITY	15	-2.094	0.000	0.048
GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT	68	1.706	0.001	0.049
GO_SULFUR_COMPOUND_METABOLIC_PROCESS	211	1.701	0.000	0.049
GO ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	16	1.703	0.004	0.049
GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	20	1.701	0.009	0.049
GO_HEXOSE_METABOLIC_PROCESS	103	1.705	0.000	0.049
GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS	78	1.703	0.001	0.049
GO ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	33	1.702	0.001	0.049
GO_PHAGOCYTIC_CUP	15	1.705	0.011	0.049
GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	78	1.704	0.001	0.049
GO_NUCLEOTIDE_PHOSPHORYLATION	43	1.697	0.001	0.050
GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	15	1.699	0.007	0.050
GO_PEROXISOME_ORGANIZATION	25	1.699	0.004	0.050
GO PEPTIDYL ASPARAGINE MODIFICATION	29	1.698	0.005	0.050
GO_MICROBODY_PART	61	1.696	0.001	0.050
GO_THIOLESTER_HYDROLASE_ACTIVITY	21	1.693	0.003	0.052

GO_GLYCOSYL_COMPOUND_CATABOLIC_PROCESS	29	1.689	0.002	0.053
GO_MONOSACCHARIDE_CATABOLIC_PROCESS	41	1.687	0.002	0.054
GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	114	1.684	0.000	0.056
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROCESS	18	1.683	0.008	0.056
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	27	1.680	0.007	0.057
GO_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	357	1.678	0.000	0.058
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	26	1.677	0.003	0.059
GO_ENDONUCLEASE_ACTIVITY	77	1.675	0.002	0.060
GO_GPI_ANCHOR_METABOLIC_PROCESS	24	1.673	0.006	0.061
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	15	1.671	0.011	0.062
GO_PYRIMIDINE_RIBONUCLEOTIDE_METABOLIC_PROCESS	20	1.668	0.011	0.064
GO_CARBOXY_LYASE_ACTIVITY	24	1.666	0.005	0.065
GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	126	1.661	0.000	0.068
GO_PROTEASOME_ACCESSORY_COMPLEX	24	1.660	0.005	0.068
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	38	1.660	0.004	0.069
GO_MICROBODY	93	1.656	0.000	0.071
GO_PROTEIN_HOMOTETRAMERIZATION	42	1.656	0.005	0.071
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	66	1.654	0.002	0.072
GO_SPHINGOLIPID_METABOLIC_PROCESS	77	1.654	0.002	0.072
GO_GLYOXYLATE_METABOLIC_PROCESS	19	1.651	0.009	0.073
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	27	1.651	0.007	0.073
GO_NUCLEASE_ACTIVITY	135	1.649	0.000	0.074
GO_GLUTATHIONE_METABOLIC_PROCESS	33	1.647	0.009	0.074
GO_PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	16	1.648	0.011	0.074
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	23	1.647	0.012	0.074
GO_MANNOSYLATION	22	1.648	0.009	0.074
GO_DEAMINASE_ACTIVITY	25	1.641	0.006	0.078
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	92	1.639	0.000	0.080
GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	31	-2.024	0.000	0.081
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS	18	1.637	0.006	0.081
GO_POSITIVE_REGULATION_OF_RECEPTOR_ACTIVITY	25	1.635	0.007	0.082
GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	16	1.635	0.009	0.082
GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	275	1.634	0.000	0.083
GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	23	1.631	0.010	0.085
GO_NEGATIVE_REGULATION_OF_GENE_SILENCING	15	-1.982	0.009	0.087
GO_EXOPEPTIDASE_ACTIVITY	56	1.628	0.006	0.087
GO_RIBOSOMAL_SUBUNIT	151	1.626	0.001	0.089
GO_CELLULAR_PROTEIN_COMPLEX_ASSEMBLY	228	1.621	0.000	0.093
GO_DIGESTIVE_SYSTEM_PROCESS	28	-1.984	0.006	0.093
GO_CERAMIDE_METABOLIC_PROCESS	40	1.619	0.008	0.094
GO_HEME_METABOLIC_PROCESS	22	1.617	0.006	0.096
GO_ISOMERASE_ACTIVITY	102	1.616	0.000	0.096
GO_DIGESTION	41	-1.958	0.000	0.096
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	27	-1.895	0.005	0.097
GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	46	1.613	0.004	0.097
GO_RESPONSE_TO_AMINE	26	1.614	0.012	0.098
GO_ADP_METABOLIC_PROCESS	34	1.614	0.011	0.098
GO_HYDROGEN_TRANSPORT	91	1.613	0.000	0.098
GO_SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	42	-1.899	0.000	0.098
GO_TRANSCRIPTION_COFACTOR_BINDING	19	-1.991	0.000	0.098
GO GRANULOCYTE MIGRATION	43	-1.885	0.000	0.099
GO_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	28	-1.918	0.000	0.100
GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	20	1.608	0.014	0.101
GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	22	1.608	0.020	0.101
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	50	-1.923	0.000	0.103
GO_REGULATION_OF_VASOCONSTRICTION	21	-1.900	0.004	0.103
GO_MITOCHONDRION_ORGANIZATION	458	1.603	0.000	0.104
GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	15	1.602	0.017	0.104
GO_OLIGODENDROCYTE_DEVELOPMENT	15	1.604	0.019	0.105
GO_MICROBODY_MEMBRANE	42	1.603	0.011	0.105
GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	15	-1.929	0.004	0.105
GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	23	1.600	0.015	0.105
GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	21	1.603	0.009	0.105
GO_HEME_BIOSYNTHETIC_PROCESS	18	1.603	0.012	0.105
GO_CARBOHYDRATE_BINDING	130	1.601	0.001	0.105
GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	19	1.598	0.015	0.106
GO_CARBOXYPEPTIDASE_ACTIVITY	16	1.599	0.016	0.106
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	36	1.598	0.011	0.106
GO_PYRUVATE_METABOLIC_PROCESS	43	1.596	0.014	0.107
GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	67	1.595	0.006	0.107
GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	17	-1.861	0.000	0.108
GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	26	1.595	0.013	0.108
GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	19	-1.865	0.000	0.108
GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	26	-1.901	0.006	0.108
GO_MANNOSYLTRANSFERASE_ACTIVITY	18	1.593	0.021	0.109
GO_OLIGODENDROCYTE_DIFFERENTIATION	24	1.593	0.018	0.109
GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	18	1.591	0.023	0.110

GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	21	1.588	0.022	0.113
GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	29	-1.929	0.005	0.113
GO_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	19	1.586	0.021	0.115
GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	121	1.585	0.001	0.115
GO_GLUCOSE_METABOLIC_PROCESS	78	1.584	0.003	0.116
GO_CARBOHYDRATE_METABOLIC_PROCESS	387	1.582	0.000	0.117
GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	25	-1.841	0.000	0.118
GO_ORGANELLE_ENVELOPE_LUMEN	64	1.581	0.004	0.118
GO_RESPONSE_TO_ANTIOTIBIC	31	1.580	0.011	0.119
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	16	-1.832	0.008	0.120
GO_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	38	1.578	0.012	0.121
GO_NEGATIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	22	1.577	0.020	0.121
GO_INTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	199	1.575	0.000	0.123
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC	44	1.571	0.009	0.128
GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	16	-1.805	0.012	0.130
GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIIUM_RELEASE_CHANNEL_ACTIVITY	16	1.568	0.031	0.131
GO_ENDORIBONUCLEASE_ACTIVITY	38	1.566	0.016	0.131
GO_HEXOSE_CATABOLIC_PROCESS	34	1.566	0.012	0.132
GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	16	1.567	0.019	0.132
GO_PEPTIDE_CROSS_LINKING	15	-1.807	0.012	0.133
GO_MAGNESIUM_ION_BINDING	135	1.563	0.002	0.133
GO_PROTEIN_N_LINKED_GLYCOSYLATION	55	1.563	0.015	0.134
GO_SKELETAL_MUSCLE_CONTRACTION	20	-1.811	0.008	0.134
GO_PROTEIN_TETRAMERIZATION	100	1.560	0.001	0.137
GO_MICROBODY_LUMEN	26	1.559	0.021	0.138
GO_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	56	1.553	0.010	0.145
GO_HYDROLASE_ACTIVITY_HYDROLYZING_N_GLYCOSYL_COMPOUNDS	17	1.550	0.030	0.148
GO_LARGE_RIBOSOMAL_SUBUNIT	87	1.550	0.003	0.148
GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS	21	1.547	0.022	0.152
GO_POSITIVE_REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	15	1.546	0.034	0.153
GO_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	18	1.544	0.021	0.154
GO_ATP_GENERATION_FROM_ADP	28	1.542	0.022	0.157
GO_SKELETAL_MUSCLE_TISSUE_REGENERATION	15	-1.771	0.000	0.157
GO_DICARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	1.541	0.028	0.158
GO_REGULATION_OF_ACTIN_FILAMENT_LENGTH	99	1.540	0.005	0.159
GO_PEPTIDE_ANTIEN_BINDING	25	-1.750	0.000	0.161
GO_REGULATION_OF_LIGASE_ACTIVITY	108	1.537	0.000	0.162
GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	17	-1.772	0.030	0.162
GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	52	-1.761	0.000	0.162
GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	29	-1.745	0.000	0.162
GO_DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	22	1.535	0.024	0.163
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	24	1.536	0.025	0.163
GO_NADP_BINDING	25	1.536	0.026	0.164
GO_NEURAL_CREST_CELL_MIGRATION	18	-1.754	0.012	0.166
GO_LEUKOCYTE_CHEMOTAXIS	60	-1.750	0.000	0.166
GO_REGULATION_OF_PROTEIN_POLYMERIZATION	114	1.533	0.004	0.166
GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY	18	1.532	0.031	0.166
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	30	1.533	0.025	0.167
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	23	1.531	0.028	0.167
GO_PROTEIN_TARGETING_TO_MITOCHONDRION	42	1.530	0.020	0.168
GO_FOLIC_ACID_CONTAINING_COMPOUND_METABOLIC_PROCESS	21	1.529	0.030	0.168
GO_NADP_METABOLIC_PROCESS	19	1.527	0.034	0.172
GO_PYRIMIDINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	24	1.524	0.032	0.174
GO_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	45	1.524	0.028	0.175
GO_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS_VIA_THE_MULTIVESICULAR_BODY_SORTING_PATHWAY	15	1.522	0.038	0.176
GO_NEGATIVE_REGULATION_OF_CALCIIUM_MEDIATED_SIGNALING	15	1.522	0.038	0.176
GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	26	-1.730	0.006	0.176
GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	111	1.523	0.004	0.176
GO_MITOTIC_RECOMBINATION	29	1.520	0.018	0.178
GO_RIBONUCLEOSIDE_CATABOLIC_PROCESS	18	1.519	0.032	0.180
GO_ONE_CARBON_METABOLIC_PROCESS	22	1.518	0.032	0.181
GO_FC_RECEPTOR_SIGNALING_PATHWAY	157	1.516	0.003	0.183
GO_GLOMERULUS_DEVELOPMENT	15	1.516	0.039	0.183
GO_PERIKARYON	43	1.514	0.022	0.185
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	15	1.513	0.038	0.185
GO_CLATHRIN_VESICLE_COAT	19	1.512	0.035	0.186
GO_DENDRITIC_CELL_DIFFERENTIATION	18	-1.716	0.022	0.188
GO_GLUCAN_BIOSYNTHETIC_PROCESS	17	1.509	0.036	0.190
GO_RIBONUCLEASE_ACTIVITY	72	1.508	0.014	0.192
GO_ORGANIC_HYDROXY_COMPOUND_CATABOLIC_PROCESS	34	1.506	0.041	0.194
GO_ALDITOL_PHOSPHATE_METABOLIC_PROCESS	15	1.504	0.037	0.197
GO_CELLULAR_RESPONSE_TO_HEAT	21	-1.703	0.014	0.200
GO_FATTY_ACYL_COA_METABOLIC_PROCESS	33	1.502	0.027	0.201
GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	132	-1.699	0.000	0.201
GO_NIK_NF_KAPPAB_SIGNALING	74	1.500	0.011	0.203

GO_TRANSMISSION_OF_NERVE_IMPULSE	15	-1.685	0.008	0.204
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	18	1.498	0.033	0.205
GO_RUFFLE_ORGANIZATION	15	1.499	0.043	0.205
GO_HYDROLASE_ACTIVITY_ACTING_ON_GLYCOSYL_BONDS	72	1.497	0.013	0.206
GO_PIGMENT_GRANULE	82	1.497	0.011	0.207
GO_REGULATION_OF_AXON_GUIDANCE	17	-1.691	0.012	0.207
GO_HYDROGEN_EXPORTING_ATPASE_ACTIVITY	21	1.496	0.032	0.207
GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	34	-1.686	0.006	0.208
GO_CELL_CELL_CONTACT_ZONE	30	1.494	0.034	0.209
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION	34	1.493	0.035	0.210
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	19	-1.677	0.009	0.211
GO_WNT_SIGNALING_PATHWAY_CALCIIUM_MODULATING_PATHWAY	27	1.493	0.035	0.211
GO_HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS	422	1.492	0.000	0.212
GO_DNA_RECOMBINATION	134	1.491	0.009	0.212
GO_ORGANIC_HYDROXY_COMPOUND_BIOSYNTHETIC_PROCESS	96	1.490	0.007	0.213
GO_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	25	-1.668	0.005	0.214
GO_3_5_EXONUCLEASE_ACTIVITY	39	1.489	0.031	0.215
GO_ACTIN_MYOSIN_FILAMENT_SLIDING	15	-1.663	0.030	0.216
GO_INACTIVATION_OF_MAPK_ACTIVITY	20	-1.655	0.014	0.217
GO_ACTIN_FILAMENT_BASED_MOVEMENT	36	-1.669	0.000	0.218
GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE	15	1.487	0.043	0.218
GO_HISTONE_H4_ACETYLATION	33	1.486	0.033	0.218
GO_VESICLE_COAT	38	1.485	0.028	0.219
GO_BONE_MINERALIZATION	15	-1.657	0.032	0.219
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	32	-1.631	0.025	0.224
GO_OLIGOSACCHARIDE_LIPID_INTERMEDIATE_BIOSYNTHETIC_PROCESS	17	1.481	0.044	0.226
GO_PRESYNAPTIC_MEMBRANE	20	-1.646	0.018	0.226
GO_RESPONSE_TO_INTERFERON_ALPHA	16	1.480	0.049	0.227
GO_CADHERIN_BINDING	17	-1.632	0.030	0.228
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	85	1.478	0.016	0.228
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	56	1.478	0.027	0.229
GO_METALLO_SULFUR_CLUSTER_ASSEMBLY	16	1.479	0.046	0.229
GO_ACTIN_MEDIATED_CELL_CONTRACTION	22	-1.640	0.010	0.229
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	22	1.477	0.047	0.229
GO_PROTEIN_K63_LINKED_UBIQUITINATION	30	1.479	0.035	0.229
GO_POSITIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	16	-1.634	0.036	0.229
GO_MESODERM_DEVELOPMENT	48	1.476	0.027	0.230
GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	194	1.476	0.003	0.230
GO_SMALL_RIBOSOMAL_SUBUNIT	64	1.476	0.026	0.230
GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	25	1.476	0.032	0.231
GO_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	17	-1.636	0.033	0.231
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	24	-1.619	0.016	0.234
GO_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	30	-1.622	0.016	0.235
GO_FATTY_ACID_METABOLIC_PROCESS	176	1.472	0.000	0.235
GO_LIPID_BIOSYNTHETIC_PROCESS	305	1.472	0.000	0.236
GO_PRERIBOSOME	47	1.471	0.028	0.236
GO_NUCLEOTIDE_EXCISION_REPAIR	99	1.469	0.010	0.240
GO_NEGATIVE_REGULATION_OF_CHROMATIN_MODIFICATION	31	-1.591	0.006	0.249
GO_THIOESTER_METABOLIC_PROCESS	54	1.464	0.017	0.249
GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	19	1.464	0.047	0.249
GO_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	149	1.463	0.005	0.249
GO_DNA_DEPENDENT_DNA_REPLICATION	71	1.464	0.022	0.249

HCC vs HD

NAME	SIZE	NES	NOM p-val	FDR q-val
GO_ORGANELLE_INNER_MEMBRANE	398	2.200	0.000	0.001
GO_MITOCHONDRIAL_MATRIX	331	2.202	0.000	0.002
GO_PYRIMIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	59	2.207	0.000	0.002
GO_ORGANELLAR_RIBOSOME	69	2.177	0.000	0.002
GO_QUINONE_METABOLIC_PROCESS	19	2.149	0.000	0.002
GO_TRNA_PROCESSING	88	2.150	0.000	0.002
GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	28	2.233	0.000	0.002
GO_OXIDOREDUCTASE_COMPLEX	79	2.125	0.000	0.002
GO_HYDRO_LYASE_ACTIVITY	34	2.123	0.000	0.002
GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS	57	2.134	0.000	0.002
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	115	2.120	0.000	0.002
GO_COFACTOR_METABOLIC_PROCESS	233	2.129	0.000	0.002
GO_MITOCHONDRIAL_TRANSLATION	100	2.212	0.000	0.002
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	106	2.155	0.000	0.002
GO_NUCLEOBASE_METABOLIC_PROCESS	29	2.162	0.000	0.002
GO_TRNA_METABOLIC_PROCESS	138	2.113	0.000	0.002
GO_LYASE_ACTIVITY	115	2.105	0.000	0.002
GO_TRANSLATIONAL_TERMINATION	90	2.233	0.000	0.002
GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	40	2.091	0.000	0.003

GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	16	2.079	0.000	0.003
GO_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	29	2.249	0.000	0.003
GO_RECOMBINATIONAL_REPAIR	43	2.067	0.000	0.004
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	361	2.055	0.000	0.004
GO_CARBON_OXYGEN_LYASE_ACTIVITY	48	2.056	0.000	0.004
GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	26	2.058	0.000	0.004
GO_MHC_CLASS_II_PROTEIN_COMPLEX	16	-2.306	0.000	0.004
GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	15	-2.327	0.000	0.004
GO_OLFACTORY_RECEPTOR_ACTIVITY	15	-2.288	0.000	0.004
GO_COENZYME_METABOLIC_PROCESS	181	2.035	0.000	0.005
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	62	2.036	0.000	0.005
GO_DNA_RECOMBINATION	134	2.041	0.000	0.005
GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	33	2.037	0.000	0.005
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	48	2.038	0.000	0.005
GO_LIPOSACCHARIDE_METABOLIC_PROCESS	68	2.007	0.000	0.007
GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	261	2.009	0.000	0.007
GO_TRANSCRIPTION_COFACTOR_BINDING	19	-2.336	0.000	0.007
GO_GLYCOSPHINGOLIPID_METABOLIC_PROCESS	39	2.010	0.000	0.007
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	90	1.995	0.000	0.008
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	17	1.994	0.002	0.008
GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	38	1.979	0.000	0.010
GO_CELLULAR_RESPIRATION	123	1.976	0.000	0.010
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	46	1.961	0.000	0.010
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	15	1.976	0.000	0.010
GO_ORGANOPHOSPHATE_CATABOLIC_PROCESS	66	1.959	0.000	0.010
GO_FATTY_ACID_CATABOLIC_PROCESS	51	1.961	0.000	0.010
GO_NUCLEASE_ACTIVITY	135	1.962	0.000	0.010
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	63	1.964	0.000	0.010
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	23	1.965	0.000	0.010
GO_TRANSLATIONAL_ELONGATION	104	1.967	0.000	0.010
GO_NUCLEOTIDE_SUGAR_BIOSYNTHETIC_PROCESS	18	1.969	0.000	0.010
GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	32	1.953	0.000	0.010
GO_SKELETAL_MUSCLE_TISSUE_REGENERATION	15	-2.205	0.000	0.011
GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	20	1.945	0.000	0.011
GO_FATTY_ACID_BETA_OXIDATION	37	1.939	0.000	0.012
GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	28	1.937	0.000	0.012
GO_PEPTIDE_ANTIGEN_BINDING	25	-2.212	0.000	0.012
GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	16	1.935	0.000	0.012
GO_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	44	1.930	0.002	0.013
GO_ORGANELLE_ENVELOPE_LUMEN	64	1.926	0.000	0.013
GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY	152	1.911	0.000	0.015
GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	178	1.910	0.000	0.015
GO_RESPIRATORY_CHAIN	67	1.908	0.000	0.015
GO_CYTOCHROME_COMPLEX_ASSEMBLY	16	1.911	0.002	0.015
GO_NADH_DEHYDROGENASE_COMPLEX	42	1.912	0.000	0.015
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	27	1.913	0.000	0.015
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	19	1.894	0.003	0.017
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	72	1.892	0.000	0.017
GO_RIBONUCLEASE_ACTIVITY	72	1.886	0.000	0.018
GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	257	1.880	0.000	0.019
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	89	1.882	0.000	0.019
GO_SMALL_MOLECULE_CATABOLIC_PROCESS	197	1.880	0.000	0.019
GO_GLYCOSYL_COMPOUND_CATABOLIC_PROCESS	29	1.875	0.003	0.020
GO_ENDONUCLEASE_ACTIVITY	77	1.869	0.000	0.021
GO_NEGATIVE_CHEMOTAXIS	15	-2.131	0.003	0.022
GO_MITOCHONDRIAL_MEMBRANE_PART	137	1.860	0.000	0.023
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	25	1.857	0.000	0.023
GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	181	1.860	0.000	0.023
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	41	1.857	0.000	0.024
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	70	1.848	0.001	0.025
GO_ISOMERASE_ACTIVITY	102	1.847	0.000	0.025
GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	121	1.849	0.000	0.025
GO_PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	16	1.850	0.008	0.025
GO_COFACTOR_BIOSYNTHETIC_PROCESS	123	1.848	0.000	0.025
GO_OXIDATIVE_PHOSPHORYLATION	71	1.845	0.000	0.025
GO_MITOTIC_RECOMBINATION	29	1.840	0.000	0.025
GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	17	-2.131	0.000	0.026
GO_MEMBRANE_LIPID_METABOLIC_PROCESS	106	1.841	0.000	0.026
GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	198	1.830	0.000	0.028
GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCESS	33	1.823	0.002	0.030
GO_DOUBLE_STRAND_BREAK_REPAIR	110	1.824	0.000	0.030
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	168	1.819	0.000	0.031
GO_MHC_PROTEIN_COMPLEX	25	-2.092	0.000	0.033
GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	23	1.810	0.002	0.033
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	30	1.810	0.000	0.034
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	15	1.806	0.013	0.034
GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	260	1.805	0.000	0.034

GO_SULFUR_COMPOUND_METABOLIC_PROCESS	211	1.794	0.000	0.037
GO_DIGESTION	41	-2.070	0.000	0.037
GO_INTERSTRAND_CROSS_LINK_REPAIR	31	1.797	0.000	0.037
GO_RESPONSE_TO_INTERFERON_BETA	18	1.794	0.007	0.038
GO_GLYOXYLATE_METABOLIC_PROCESS	19	1.794	0.003	0.038
GO_PIGMENT_BIOSYNTHETIC_PROCESS	33	1.790	0.002	0.038
GO_DNA_DEPENDENT_DNA_REPLICATION	71	1.788	0.002	0.039
GO_MONOSACCHARIDE_METABOLIC_PROCESS	118	1.785	0.000	0.040
GO_LIPID_OXIDATION	48	1.781	0.005	0.041
GO_OXIDOREDUCTASE_ACTIVITY	400	1.778	0.000	0.042
GO_LAMELLIPODIUM_ASSEMBLY	19	1.778	0.005	0.042
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC	44	1.768	0.003	0.044
GO_CERAMIDE_BIOSYNTHETIC_PROCESS	21	1.772	0.003	0.044
GO_SPHINGOLIPID_METABOLIC_PROCESS	77	1.768	0.004	0.044
GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	126	1.770	0.000	0.044
GO_DEOXYRIBONUCLEASE_ACTIVITY	43	1.769	0.000	0.044
GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	114	1.766	0.000	0.044
GO_ACTIN_FILAMENT_BASED_MOVEMENT	36	-2.044	0.000	0.044
GO_HISTONE_H4_ACETYLATION	33	1.757	0.010	0.045
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	91	1.759	0.000	0.045
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	89	1.758	0.000	0.045
GO_PHOSPHATIDIC_ACID_METABOLIC_PROCESS	18	1.762	0.005	0.045
GO_TRNA_MODIFICATION	47	1.760	0.002	0.045
GO_PURINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	33	1.759	0.003	0.045
GO_PIGMENT_METABOLIC_PROCESS	38	1.762	0.006	0.046
GO_HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS	422	1.760	0.000	0.046
GO_ELECTRON_TRANSPORT_CHAIN	79	1.754	0.000	0.046
GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	63	1.751	0.000	0.047
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	80	1.750	0.000	0.047
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	216	1.744	0.000	0.050
GO_HEXOSE_METABOLIC_PROCESS	103	1.740	0.000	0.051
GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	288	1.741	0.000	0.051
GO_DNA_DIRECTED_RNA_POLYMERASE_III_COMPLEX	15	1.733	0.008	0.053
GO_ENDODEOXYRIBONUCLEASE_ACTIVITY	29	1.735	0.002	0.054
GO_CELLULAR_KETONE_METABOLIC_PROCESS	43	1.734	0.002	0.054
GO_CERAMIDE_METABOLIC_PROCESS	40	1.731	0.001	0.054
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	38	1.731	0.008	0.054
GO_EXONUCLEASE_ACTIVITY	57	1.728	0.000	0.054
GO_3_5_EXONUCLEASE_ACTIVITY	39	1.724	0.003	0.054
GO_COENZYME_BIOSYNTHETIC_PROCESS	89	1.728	0.000	0.054
GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	16	1.729	0.012	0.055
GO_FOLIC_ACID_CONTAINING_COMPOUND_METABOLIC_PROCESS	21	1.725	0.003	0.055
GO_ELECTRON_CARRIER_ACTIVITY	80	1.724	0.000	0.055
GO_ORGANIC_ACID_CATABOLIC_PROCESS	120	1.726	0.001	0.055
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ONE_CARBON_GROUPS	136	1.722	0.000	0.056
GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	169	1.719	0.001	0.056
GO_ENDORIBONUCLEASE_ACTIVITY	38	1.714	0.003	0.058
GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	61	1.715	0.000	0.059
GO_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	357	1.711	0.000	0.059
GO_RNA_MODIFICATION	81	1.709	0.001	0.060
GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	19	1.708	0.013	0.061
GO_LAMELLIPODIUM_ORGANIZATION	24	1.704	0.000	0.062
GO_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	63	1.704	0.000	0.062
GO_AEROBIC_RESPIRATION	48	1.701	0.009	0.063
GO_COFACTOR_BINDING	167	1.700	0.000	0.063
GO_CARBOHYDRATE_METABOLIC_PROCESS	387	1.700	0.000	0.063
GO_SITE_OF_DOUBLE_STRAND_BREAK	23	1.698	0.008	0.064
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	44	1.696	0.006	0.064
GO_GLYCOLIPID_BIOSYNTHETIC_PROCESS	36	1.696	0.009	0.064
GO_HYDROLASE_ACTIVITY_HYDROLYZING_N_GLYCOSYL_COMPOUNDS	17	1.692	0.007	0.067
GO_CARBON_CARBON_LYASE_ACTIVITY	35	1.689	0.005	0.067
GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	21	1.689	0.013	0.067
GO_CULLIN_RING_UBIQUITIN_LIGASE_COMPLEX	98	1.683	0.004	0.068
GO_RNA_POLYMERASE_COMPLEX	98	1.687	0.000	0.068
GO_MITOCHONDRION_ORGANIZATION	458	1.686	0.000	0.068
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	92	1.683	0.004	0.068
GO_CELLULAR_LIPID_CATABOLIC_PROCESS	87	1.686	0.001	0.068
GO_HYDROLASE_ACTIVITY_ACTING_ON_GLYCOSYL_BONDS	72	1.683	0.004	0.068
GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	53	1.685	0.011	0.068
GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	102	1.683	0.000	0.069
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	52	1.681	0.005	0.069
GO_NAD_BINDING	40	1.680	0.006	0.069
GO_PYRIMIDINE_NUCLEOSIDE_METABOLIC_PROCESS	37	1.679	0.006	0.069
GO_RNA_POLYMERASE_ACTIVITY	40	1.676	0.009	0.070
GO_ONE_CARBON_METABOLIC_PROCESS	22	1.676	0.013	0.071
GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	18	1.673	0.018	0.071
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_III_PROMOTER	35	1.672	0.009	0.072

GO_METAL_CLUSTER_BINDING	53	1.665	0.006	0.076
GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	49	1.660	0.005	0.079
GO_NCRNA_METABOLIC_PROCESS	420	1.659	0.000	0.080
GO_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	39	1.658	0.008	0.080
GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	27	1.656	0.011	0.080
GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS	78	1.654	0.001	0.082
GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	140	1.652	0.001	0.082
GO_DNA_REPLICATION	144	1.651	0.001	0.083
GO_DIGESTIVE_SYSTEM_PROCESS	28	-1.976	0.000	0.086
GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS	15	1.640	0.017	0.090
GO_MICROBODY_PART	61	1.640	0.008	0.090
GO_KETONE_BIOSYNTHETIC_PROCESS	18	1.641	0.024	0.091
GO_LIGASE_ACTIVITY	280	1.637	0.000	0.091
GO_THIOESTER_METABOLIC_PROCESS	54	1.637	0.005	0.091
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_EXONUCLEOLYTIC	29	1.638	0.011	0.091
GO_AMINO_ACID_ACTIVATION	41	1.636	0.008	0.091
GO_COENZYME_BINDING	121	1.635	0.000	0.092
GO_POSTREPLICATION_REPAIR	46	1.633	0.006	0.092
GO_HEME_METABOLIC_PROCESS	22	1.632	0.026	0.093
GO_THIOLESTER_HYDROLASE_ACTIVITY	21	1.632	0.011	0.093
GO_MAGNESIUM_ION_BINDING	135	1.630	0.003	0.093
GO_ACETYLGUCOSAMINYLTRANSFERASE_ACTIVITY	29	1.626	0.019	0.096
GO_EXONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	38	1.623	0.009	0.098
GO_CARBOHYDRATE_DERIVATIVE_CATABOLIC_PROCESS	107	1.622	0.001	0.099
GO_DETECTION_OF_BIOTIC_STIMULUS	16	-1.953	0.000	0.099
GO_HEME_BIOSYNTHETIC_PROCESS	18	1.621	0.029	0.099
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	49	1.619	0.019	0.100
GO_AMIDE_BIOSYNTHETIC_PROCESS	407	1.617	0.000	0.101
GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	26	1.612	0.019	0.102
GO_GLUCAN_BIOSYNTHETIC_PROCESS	17	1.613	0.019	0.103
GO_SPECIFICATION_OF_SYMMETRY	45	1.613	0.006	0.103
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	26	1.615	0.018	0.103
GO_EMBRYONIC_HEART_TUBE_DEVELOPMENT	31	1.615	0.012	0.103
GO_POLYSACCHARIDE_BIOSYNTHETIC_PROCESS	27	1.614	0.026	0.103
GO_METHYLATION	173	1.609	0.001	0.105
GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	121	1.607	0.000	0.106
GO_PYRIMIDINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	24	1.603	0.013	0.109
GO_GLUCOSE_METABOLIC_PROCESS	78	1.603	0.004	0.109
GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	29	1.603	0.019	0.109
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	66	1.600	0.009	0.111
GO_ERROR_FREE_TRANSLESION_SYNTHESIS	17	1.599	0.025	0.111
GO_DNA_STRAND_ELONGATION	24	1.598	0.018	0.111
GO_EMBRYONIC_HEART_TUBE_MORPHOGENESIS	25	1.600	0.021	0.111
GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	19	1.597	0.022	0.111
GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	275	1.593	0.001	0.114
GO_PYRIMIDINE_RIBONUCLEOTIDE_METABOLIC_PROCESS	20	1.593	0.012	0.114
GO_ALDITOL_PHOSPHATE_METABOLIC_PROCESS	15	1.589	0.031	0.117
GO_FATTY_ACYL_COA_BINDING	24	1.589	0.028	0.117
GO_PYRIMIDINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	25	1.590	0.023	0.117
GO_4_IRON_4_SULFUR_CLUSTER_BINDING	36	1.587	0.020	0.117
GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS	21	1.581	0.033	0.123
GO_REGULATION_OF_LIGASE_ACTIVITY	108	1.580	0.006	0.124
GO_MICROBODY_MEMBRANE	42	1.579	0.016	0.124
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	29	1.576	0.020	0.125
GO_RIBONUCLEOSIDE_CATABOLIC_PROCESS	18	1.577	0.025	0.126
GO_GPI_ANCHOR_METABOLIC_PROCESS	24	1.575	0.026	0.127
GO_RIBOSOME	202	1.571	0.000	0.130
GO_PYRUVATE_METABOLIC_PROCESS	43	1.569	0.016	0.131
GO_PROTEIN_POLYUBIQUITINATION	209	1.569	0.000	0.131
GO_CARBOXY_LYASE_ACTIVITY	24	1.566	0.028	0.132
GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	15	1.567	0.034	0.133
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	61	1.566	0.012	0.133
GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY	18	1.565	0.028	0.133
GO_PROTEIN_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	18	1.561	0.044	0.136
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	36	1.559	0.009	0.136
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	47	1.560	0.020	0.136
GO_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	33	1.559	0.022	0.136
GO_NCRNA_PROCESSING	315	1.561	0.000	0.136
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	188	1.556	0.001	0.138
GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE	15	1.555	0.028	0.138
GO_PROTEIN_N_LINKED_GLYCOSYLATION	55	1.555	0.011	0.138
GO_PROTEIN_AUTOUBIQUITINATION	36	1.556	0.016	0.139
GO_EXOPEPTIDASE_ACTIVITY	56	1.556	0.015	0.139
GO_CHROMOSOMAL_REGION	233	1.553	0.001	0.139
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	40	1.552	0.015	0.140
GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	42	1.548	0.021	0.143

GO_CARBOHYDRATE_CATABOLIC_PROCESS	75	1.549	0.011	0.143
GO_DNA_CATABOLIC_PROCESS	19	1.547	0.028	0.143
GO_PHOSPHATIDYLOSITOL_3_KINASE_BINDING	20	1.547	0.049	0.144
GO_REPLISOME	27	1.546	0.031	0.144
GO_DICARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	1.543	0.045	0.147
GO_ACETYLTTRANSFERASE_COMPLEX	65	1.541	0.018	0.147
GO_RNA_METHYLTRANSFERASE_ACTIVITY	27	1.541	0.030	0.147
GO_FATTY_ACID_METABOLIC_PROCESS	176	1.542	0.001	0.148
GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	17	1.538	0.036	0.150
GO_NEURAL_CRESCENT_CELL_MIGRATION	18	-1.867	0.003	0.150
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	67	1.537	0.013	0.150
GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	90	1.536	0.017	0.152
GO_ACID_SECRETION	25	-1.884	0.000	0.152
GO_HISTONE_MRNA_METABOLIC_PROCESS	23	1.533	0.033	0.154
GO_PROTEINACEOUS_EXTRACELLULAR_MATRIX	103	-1.869	0.000	0.155
GO_SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	42	-1.855	0.003	0.156
GO_UBIQUITIN_LIGASE_COMPLEX	193	1.528	0.000	0.159
GO_MICROBODY	93	1.528	0.011	0.159
GO_REGULATION_OF_VASOCONSTRICTION	21	-1.886	0.000	0.159
GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	22	1.527	0.031	0.160
GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	38	1.527	0.029	0.160
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	17	1.525	0.030	0.160
GO_POSITIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	25	-1.870	0.000	0.163
GO_ACTIN_MEDIATED_CELL_CONTRACTION	22	-1.844	0.008	0.164
GO_POSITIVE_REGULATION_OF_OSSIFICATION	35	-1.888	0.003	0.167
GO_TRANSCRIPTIONALLY_ACTIVE_CHROMATIN	15	1.519	0.059	0.167
GO_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX	37	1.518	0.029	0.168
GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	25	1.516	0.040	0.169
GO_VACUOLE_FUSION	17	1.516	0.058	0.170
GO_NADP_BINDING	25	1.516	0.030	0.170
GO_PEPTIDE_METABOLIC_PROCESS	435	1.513	0.000	0.172
GO_DNA_BIOSYNTHETIC_PROCESS	82	1.512	0.012	0.173
GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	21	1.511	0.031	0.173
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	85	1.511	0.019	0.173
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION	34	1.510	0.027	0.174
GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	32	1.506	0.035	0.178
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_GLYCOSYL_GROUPS	152	1.504	0.005	0.180
GO_PROTEIN_TRIMERIZATION	25	1.503	0.054	0.181
GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	15	1.502	0.054	0.181
GO_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	19	1.501	0.044	0.181
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	15	1.503	0.047	0.181
GO_REGULATION_OF_MUSCLE_CONTRACTION	59	-1.785	0.000	0.185
GO_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	149	1.498	0.005	0.186
GO_TRANSFERASE_COMPLEX_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	181	1.496	0.001	0.187
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	50	-1.823	0.000	0.189
GO_REGULATION_OF_VIRAL_GENOME_REPLICATION	60	1.494	0.015	0.190
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER	19	-1.786	0.000	0.190
GO_NUCLEOTIDE_PHOSPHORYLATION	43	1.490	0.038	0.193
GO_CARBOXYLIC_ESTER_HYDROLASE_ACTIVITY	62	1.490	0.025	0.193
GO_PROTEIN_UBIQUITINATION	449	1.491	0.000	0.193
GO_TISSUE_REGENERATION	27	-1.788	0.008	0.194
GO_PEPTIDYL_ASPARAGINE_MODIFICATION	29	1.489	0.047	0.194
GO_REPLICATION_FORK	51	1.486	0.026	0.197
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	22	1.486	0.060	0.197
GO_ACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY	16	1.484	0.050	0.198
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	38	1.481	0.040	0.198
GO_BASE_EXCISION_REPAIR	35	1.484	0.053	0.199
GO_CHROMOSOME_TELOMERIC_REGION	124	1.483	0.010	0.199
GO_LIPID_BIOSYNTHETIC_PROCESS	305	1.482	0.000	0.199
GO_PRERIBOSOME	47	1.481	0.029	0.199
GO_TRNA_BINDING	32	1.482	0.039	0.199
GO_DNA_HELICASE_ACTIVITY	42	1.483	0.043	0.199
GO_LYSINE_ACETYLATED_HISTONE_BINDING	16	-1.788	0.013	0.200
GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	17	1.479	0.046	0.200
GO_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	17	-1.730	0.012	0.202
GO_REGULATION_OF_INSULIN_RECEPTOR_SIGNALING_PATHWAY	24	-1.721	0.018	0.202
GO_INOSITOL_LIPID_MEDIATED_SIGNALING	63	-1.709	0.000	0.202
GO_MYOSIN_COMPLEX	26	-1.724	0.013	0.202
GO_PEPTIDE_CROSS_LINKING	15	-1.710	0.008	0.203
GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	25	-1.717	0.006	0.204
GO_REGULATION_OF_ERK1_AND_ERK2_CASCADE	111	-1.712	0.000	0.204
GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	31	-1.736	0.006	0.205
GO_RIBOSOME_BINDING	33	-1.693	0.006	0.205
GO_STEROL_BINDING	21	-1.691	0.011	0.205
GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	15	-1.730	0.013	0.205
GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	52	-1.704	0.003	0.205

GO_REGULATION_OF_AXON_GUIDANCE	17	-1.702	0.023	0.205
GO_MUSCLE_CELL_DEVELOPMENT	49	-1.695	0.006	0.205
GO_MESONEPHROS_DEVELOPMENT	34	-1.789	0.011	0.206
GO_ACTIN_MYOSIN_FILAMENT_SLIDING	15	-1.725	0.016	0.206
GO_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	28	-1.742	0.008	0.206
GO_POTASSIUM_CHANNEL_ACTIVITY	28	-1.714	0.006	0.206
GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	89	-1.739	0.000	0.207
GO_NEGATIVE_REGULATION_OF_GENE_SILENCING	15	-1.687	0.016	0.207
GO_BONE_MINERALIZATION	15	-1.696	0.020	0.207
GO_NUCLEAR_REPLICATION_FORK	33	1.474	0.035	0.208
GO_SIGNALING_RECEPTOR_ACTIVITY	363	-1.731	0.000	0.208
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	22	-1.750	0.005	0.208
GO_WW_DOMAIN_BINDING	16	1.473	0.070	0.208
GO_STRIATED_MUSCLE_CONTRACTION	44	-1.697	0.003	0.209
GO_EXTRACELLULAR_MATRIX	129	-1.764	0.000	0.209
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	19	-1.747	0.010	0.210
GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	39	-1.760	0.006	0.210
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX	20	1.471	0.030	0.210
GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	132	-1.743	0.000	0.211
GO_LUMENAL_SIDE_OF_MEMBRANE	30	-1.806	0.008	0.211
GO_RESPONSE_TO_CAMP	57	-1.800	0.000	0.211
GO_ANTIGEN_BINDING	59	-1.766	0.003	0.212
GO_NON_RECOMBINATIONAL_REPAIR	55	1.469	0.023	0.213
GO_REGULATION_OF_RESPONSE_TO_INTERFERON_GAMMA	19	1.469	0.062	0.213
GO_STEROID_BINDING	34	-1.789	0.006	0.213
GO_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	30	-1.751	0.011	0.213
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	21	-1.754	0.013	0.213
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	93	-1.675	0.000	0.214
GO_NEGATIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	53	-1.676	0.009	0.216
GO_VITAMIN_METABOLIC_PROCESS	69	1.466	0.019	0.216
GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	47	1.466	0.027	0.216
GO_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	32	-1.677	0.013	0.217
GO_DNA_REPAIR	356	1.464	0.001	0.218
GO_SMALL_RIBOSOMAL_SUBUNIT	64	1.463	0.036	0.218
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	79	1.462	0.017	0.219
GO_CHAPERONE_MEDIATED_PROTEIN_FOLDING	35	1.461	0.049	0.220
GO_POSITIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	22	1.461	0.073	0.220
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	23	1.460	0.056	0.221
GO_REGULATION_OF_LIPID_STORAGE	24	-1.789	0.000	0.222
GO_HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	53	1.459	0.037	0.222
GO_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	38	1.458	0.040	0.222
GO_PYRIMIDINE_RIBONUCLEOSIDE_METABOLIC_PROCESS	26	1.457	0.058	0.223
GO_POTASSIUM_CHANNEL_COMPLEX	25	-1.667	0.011	0.225
GO_RNA_POLYMERASE_BINDING	30	1.452	0.058	0.229
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	17	-1.662	0.024	0.230
GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	18	-1.649	0.031	0.234
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	39	1.449	0.045	0.235
GO_LYMPHOCYTE_COSTIMULATION	53	-1.651	0.000	0.235
GO_THIOESTER_BIOSYNTHETIC_PROCESS	37	1.448	0.046	0.236
GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	194	1.447	0.008	0.236
GO_TRANSLESION_SYNTHESIS	34	1.446	0.059	0.236
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_HEXOSYL_GROUPS	104	1.447	0.024	0.236
GO_SAGA_TYPE_COMPLEX	23	1.444	0.065	0.237
GO_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX	33	1.444	0.072	0.238
GO_AMEBOIDAL_TYPE_CELL_MIGRATION	74	-1.651	0.000	0.238
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	23	1.445	0.064	0.238
GO_CELLULAR_PROTEIN_COMPLEX_ASSEMBLY	228	1.443	0.015	0.239
GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	20	-1.643	0.019	0.239
GO_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	18	-1.652	0.010	0.241
GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	33	-1.643	0.005	0.242
GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	20	1.440	0.070	0.243
GO_NEGATIVE_REGULATION_OF_CHEMOTAXIS	20	-1.652	0.018	0.243
GO_CARDIAC_CELL_DEVELOPMENT	17	-1.637	0.023	0.246
GO TRABECULA MORPHOGENESIS	22	-1.633	0.013	0.247
GO PEPTIDE TRANSPORT	34	-1.634	0.014	0.247
GO MONOSACCHARIDE BINDING	43	1.437	0.043	0.248
GO_UBIQUITIN LIKE PROTEIN TRANSFERASE ACTIVITY	307	1.434	0.002	0.249
GO_CELLULAR CARBOHYDRATE CATABOLIC PROCESS	22	1.434	0.076	0.249
GO_LIPID CATABOLIC PROCESS	122	1.434	0.023	0.249
GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	25	1.435	0.059	0.249
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	39	1.435	0.056	0.250

HCC vs LC

NAME	SIZE	NES	NOM p-val	FDR q-val
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	90	-2.187	0.000	0.000

GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	47	-2.118	0.000	0.001
GO_CYTOSOLIC_RIBOSOME	98	-2.089	0.000	0.002
GO_MITOCHONDRIAL_MEMBRANE_PART	137	-2.014	0.000	0.005
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	115	-2.039	0.000	0.005
GO_TRANSLATIONAL_INITIATION	136	-2.007	0.000	0.005
GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	63	-2.021	0.000	0.005
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	113	-1.974	0.000	0.007
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	23	-1.960	0.000	0.008
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	39	-1.988	0.000	0.008
GO_OLIGODENDROCYTE_DIFFERENTIATION	24	-1.963	0.000	0.008
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	99	-1.970	0.000	0.008
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	47	-1.976	0.000	0.008
GO_NADH_DEHYDROGENASE_COMPLEX	42	-1.966	0.000	0.008
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	55	-1.977	0.000	0.009
GO_ATP_BIOSYNTHETIC_PROCESS	26	-1.948	0.000	0.009
GO_ELECTRON_TRANSPORT_CHAIN	79	-1.941	0.000	0.009
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN	17	-1.939	0.000	0.009
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	62	-1.928	0.000	0.011
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	48	-1.905	0.000	0.015
GO_PROTEIN_TARGETING_TO_MEMBRANE	132	-1.908	0.000	0.015
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	17	-1.890	0.000	0.017
GO_OXIDATIVE_PHOSPHORYLATION	71	-1.892	0.000	0.017
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	46	-1.892	0.000	0.018
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	188	-1.880	0.000	0.018
GO_CORTICAL_ACTIN_CYTOSKELETON	32	-1.880	0.000	0.019
GO_RESPIRATORY_CHAIN	67	-1.859	0.000	0.024
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	112	-1.853	0.000	0.025
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	67	-1.854	0.000	0.026
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	89	-1.835	0.000	0.031
GO_RIBOSOME	202	-1.831	0.000	0.032
GO_RIBOSOMAL_SUBUNIT	151	-1.829	0.000	0.032
GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	169	-1.815	0.000	0.036
GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	181	-1.808	0.000	0.039
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	40	-1.805	0.000	0.040
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	49	-1.786	0.000	0.048
GO_CELLULAR_RESPONSE_TO_CALCIIUM_ION	30	-1.787	0.000	0.049
GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT	68	-1.777	0.000	0.050
GO_Glutathione_TRANSFERase_Activity	18	-1.779	0.000	0.050
GO_LUMENAL_SIDE_OF_MEMBRANE	30	-1.770	0.000	0.054
GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	121	-1.764	0.000	0.056
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	44	-1.762	0.000	0.056
GO_HEXOSE_CATABOLIC_PROCESS	34	-1.750	0.000	0.062
GO_CELL_CELL_CONTACT_ZONE	30	-1.742	0.000	0.067
GO_PEPTIDE_METABOLIC_PROCESS	435	-1.742	0.000	0.068
GO_CELLULAR_RESPIRATION	123	-1.733	0.000	0.069
GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	261	-1.719	0.000	0.081
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	91	-1.713	0.000	0.084
GO_CYTOSOLIC_PART	180	-1.693	0.000	0.099
GO_OXIDOREDUCTASE_ACTIVITY	400	-1.695	0.000	0.100
GO_AMIDE_BIOSYNTHETIC_PROCESS	407	-1.672	0.000	0.120
GO_CELL_SUBSTRATE_JUNCTION	282	-1.660	0.000	0.135
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	361	-1.620	0.000	0.173
GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	257	-1.610	0.000	0.188
GO_MULTI_ORGANISM_METABOLIC_PROCESS	131	-1.596	0.000	0.200
GO_SMALL_MOLECULE_CATABOLIC_PROCESS	197	-1.594	0.000	0.202
GO_MICROBODY	93	-1.589	0.000	0.208
GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	198	-1.548	0.000	0.241
GO_ORGANELLE_INNER_MEMBRANE	398	-1.555	0.000	0.241
GO_PROTEIN_REFOLDING	20	2.586	0.000	0.000
GO_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	24	2.146	0.000	0.062
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	64	2.014	0.000	0.077
GO_NECROPTOTIC_PROCESS	18	2.021	0.000	0.084
GO_NUCLEOCYTOPLASMIC_TRANSPORTER_ACTIVITY	22	1.986	0.000	0.086
GO_AMMONIUM_ION_BINDING	19	2.029	0.000	0.094
GO_ENDODERMAL_CELL_DIFFERENTIATION	20	2.043	0.000	0.103
GO_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	39	1.783	0.000	0.191
GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	19	1.783	0.000	0.201
GO_UNFOLDED_PROTEIN_BINDING	74	1.758	0.000	0.204
GO_SULFUR_COMPOUND_METABOLIC_PROCESS	211	-1.541	0.001	0.245
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	216	-1.551	0.001	0.242
GO_REGULATION_OF_PROTEIN_BINDING	110	-1.534	0.001	0.248
GO_HYDROGEN_TRANSPORT	91	-1.603	0.001	0.196
GO_OXIDOREDUCTASE_COMPLEX	79	-1.719	0.001	0.079
GO_REGENERATION	83	-1.648	0.001	0.138
GO_LARGE_RIBOSOMAL_SUBUNIT	87	-1.735	0.001	0.070
GO_ELECTRON_CARRIER_ACTIVITY	80	-1.659	0.001	0.135
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	72	-1.636	0.001	0.153

GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	63	-1.685	0.001	0.108
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	70	-1.658	0.001	0.134
GO_SMALL_RIBOSOMAL_SUBUNIT	64	-1.668	0.001	0.125
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	38	-1.734	0.001	0.070
GO_MONOSACCHARIDE_CATABOLIC_PROCESS	41	-1.719	0.001	0.080
GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	40	-1.785	0.001	0.048
GO_NAD_BINDING	40	-1.799	0.001	0.043
GO_GUANOSINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	33	-1.681	0.001	0.110
GO_SUBSTANTIA_NIGRA_DEVELOPMENT	33	-1.779	0.001	0.051
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	23	-1.698	0.001	0.098
GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT	19	-1.850	0.001	0.026
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX	20	-1.757	0.001	0.058
GO_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	18	-1.741	0.001	0.066
GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	114	-1.541	0.002	0.248
GO_CLUSTER_OF_ACTIN_BASED_CELL_PROJECTIONS	60	-1.627	0.002	0.164
GO_PODOSOME	16	-1.816	0.003	0.037
GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	15	-1.682	0.003	0.111
GO_OLIGODENDROCYTE_DEVELOPMENT	15	-1.760	0.003	0.057
GO_ORGANIC_ACID_CATABOLIC_PROCESS	120	-1.541	0.003	0.246
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	40	-1.699	0.004	0.099
GO_GLUTATHIONE_METABOLIC_PROCESS	33	-1.629	0.004	0.162
GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	16	-1.649	0.004	0.139
GO_NEUTRAL_AMINO_ACID_TRANSPORT	17	1.734	0.004	0.214
GO_CAMP_METABOLIC_PROCESS	15	2.247	0.005	0.035
GO_EXTRACELLULAR_MATRIX_BINDING	18	1.776	0.005	0.190
GO_MRNA_CLEAVAGE	19	1.847	0.005	0.216
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_CYCLIC_AMIDINES	26	-1.767	0.005	0.055
GO_CELLULAR_RESPONSE_TO_HEAT	21	1.819	0.005	0.192
GO_ENDODERM_FORMATION	25	1.755	0.005	0.199
GO_STEREOCILUM_BUNDLE	15	-1.694	0.005	0.100
GO_PRIMARY_CILIUM	79	-1.596	0.005	0.202
GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	27	1.726	0.005	0.217
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	27	1.789	0.005	0.218
GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	46	-1.654	0.006	0.135
GO_NEURAL_NUCLEUS_DEVELOPMENT	40	-1.637	0.006	0.153
GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	114	-1.548	0.006	0.241
GO_INTERCALATED_DISC	21	-1.644	0.006	0.143
GO_GTP_METABOLIC_PROCESS	16	-1.730	0.006	0.071
GO_NEGATIVE_REGULATION_OF_PROTEIN_BINDING	48	-1.562	0.007	0.235
GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	53	-1.552	0.007	0.244
GO_NUCLEOTIDE_PHOSPHORYLATION	43	-1.568	0.007	0.233
GO_MYOSIN_COMPLEX	26	-1.578	0.007	0.225
GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY	33	-1.674	0.007	0.119
GO_NEGATIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	22	-1.648	0.008	0.139
GO_CARBOHYDRATE_CATABOLIC_PROCESS	75	-1.550	0.008	0.241
GO_REGULATION_OF_ACTIN_NUCLEATION	19	-1.652	0.008	0.136
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	61	-1.575	0.008	0.229
GO_PIGMENT_METABOLIC_PROCESS	38	-1.630	0.008	0.163
GO_CALCIIUM_MEDIATED_SIGNALING	48	-1.574	0.008	0.229
GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	40	-1.603	0.008	0.197
GO_CAMP_MEDIATED_SIGNALING	15	1.839	0.008	0.193
GO_LYSINE_ACETYLATED_HISTONE_BINDING	16	1.787	0.008	0.207
GO_CELL_GROWTH	71	-1.558	0.009	0.238
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	18	-1.571	0.010	0.232
GO_PYRIMIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	59	-1.557	0.010	0.240
GO_MHC_CLASS_II_PROTEIN_COMPLEX	16	-1.597	0.010	0.201
GO_RIBOSOME_ASSEMBLY	43	-1.575	0.010	0.230
GO_PIGMENT_BIOSYNTHETIC_PROCESS	33	-1.603	0.011	0.195
GO_LYMPHOCYTE_COSTIMULATION	53	-1.566	0.011	0.232
GO_ORGAN_REGENERATION	45	-1.568	0.011	0.235
GO_STEROL_HOMEOSTASIS	25	-1.610	0.012	0.187
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS	18	-1.618	0.013	0.176
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	21	-1.625	0.013	0.166
GO_COPI_COATED_VESICLE	19	-1.657	0.013	0.132
GO_MEMBRANE_BIOGENESIS	15	-1.658	0.013	0.133
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	15	-1.616	0.013	0.177
GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	53	-1.553	0.013	0.244
GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	17	1.840	0.014	0.208
GO_RESPONSE_TO_VITAMIN	48	-1.565	0.014	0.231
GO_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	29	-1.552	0.015	0.242
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	19	-1.543	0.015	0.246
GO_DE_NOVO_PROTEIN_FOLDING	15	1.857	0.015	0.223
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE_MEMBRANE	31	-1.593	0.016	0.201
GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	20	-1.600	0.016	0.196
GO_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	20	-1.564	0.017	0.233
GO_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	18	-1.561	0.017	0.234
GO GRANULOCYTE_ACTIVATION	16	-1.579	0.017	0.224

GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	16	1.750	0.017	0.197
GO_PROTEIN_DESTABILIZATION	27	-1.587	0.017	0.209
GO_VIRAL_GENOME_REPLICATION	17	-1.566	0.018	0.234
GO_REGULATION_OF_VESICLE_FUSION	35	-1.559	0.018	0.237
GO_ESTROGEN_RECEPTOR_BINDING	28	-1.550	0.018	0.243
GO_NEURON_PROJECTION_EXTENSION	25	-1.541	0.018	0.249
GO_PHOTORECEPTOR_OUTER_SEGMENT	18	-1.602	0.020	0.194
GO_CHANNEL_INHIBITOR_ACTIVITY	21	-1.547	0.020	0.239
GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	19	1.829	0.020	0.192
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_III_PROMOTER	15	-1.571	0.021	0.231
GO_DEVELOPMENTAL_CELL_GROWTH	38	-1.567	0.021	0.233
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	18	-1.537	0.021	0.248
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	25	-1.590	0.021	0.205
GO_HOMOTYPIC_CELL_CELL_ADHESION	26	-1.549	0.022	0.242
GO_RESPONSE_TO_FLUID_SHEAR_STRESS	23	-1.534	0.022	0.250
GO_NADH_METABOLIC_PROCESS	28	-1.537	0.023	0.247
GO_POLYSACCHARIDE_CATABOLIC_PROCESS	16	-1.547	0.023	0.240
GO_RESPONSE_TO_INTERFERON_BETA	18	-1.571	0.025	0.234
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	15	-1.550	0.025	0.239
GO_PLATELET_AGGREGATION	24	-1.538	0.025	0.248
GO_T_CELL_RECEPTOR_COMPLEX	16	-1.534	0.030	0.249
GO_RESPONSE_TO_MINERALOCORTICOID	18	-1.566	0.030	0.233
GO_PHOTORECEPTOR_CONNECTING_CILIUM	15	-1.537	0.030	0.249
GO_REGULATION_OF_CELLULAR_RESPIRATION	15	-1.555	0.043	0.242