Supplemental Table 4: Complete GSEA results of PDLS vs 2D cultures analysis

HALLMARKS (H)				
Biological process	**GeneSet**	**SIZE**	**NES**	**FDR q-val**
Cell cycle regulation	HALLMARK_E2F_TARGETS	200	3,27	0
	HALLMARK_G2M_CHECKPOINT	198	3,09	0
	HALLMARK_MITOTIC_SPINDLE	196	2,17	0
Cytokines	HALLMARK_IL2_STAT5_SIGNALING	188	-1,51	0,009
	HALLMARK_IL6_JAK_STAT3_SIGNALING	78	-1,66	0,002
	HALLMARK_INTERFERON_ALPHA_RESPONSE	97	-1,76	0,001
	HALLMARK_INTERFERON_GAMMA_RESPONSE	193	-1,96	0
DNA Repair	HALLMARK_DNA_REPAIR	147	1,93	0
Inflammation	HALLMARK_INFLAMMATORY_RESPONSE	175	-2,44	0
mTOR Signaling	HALLMARK_MTORC1_SIGNALING	199	2,21	0
MYC regulated genes	HALLMARK_MYC_TARGETS_V1	200	1,72	0,001
Oxidative phosphorylation (OXPHOS)	HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	2,49	0
Regulation of cell death	HALLMARK_APOPTOSIS	149	-1,45	0,015
TGF-Beta signaling	HALLMARK_TGF_BETA_SIGNALING	53	-1,79	0
TNF Signaling	HALLMARK_TNFA_SIGNALING_VIA_NFKB	195	-3,14	0

CANONICAL PATHWAYS (C2CP)				
Biological process	**GeneSet**	**SIZE**	**NES**	**FDR q-val**
Allograft reaction	WP_ALLOGRAFT_REJECTION	74	-1,63	0,012
Amino acid metabolism	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	324	1,72	0,003
	REACTOME_SELENOAMINO_ACID_METABOLISM	112	1,71	0,004
	WP_AMINO_ACID_METABOLISM	74	1,63	0,01
Angiogenesis	REACTOME_SIGNALING_BY_PDGF	53	-1,62	0,024
Cell adhesion	KEGG_CELL_ADHESION_MOLECULES_CAMS	108	-1,68	0,01
Cell cycle regulation	KEGG_CELL_CYCLE	124	2,46	0
	KEGG_OXIDATIVE_PHOSPHORYLATION	116	2,39	0
	KEGG_P53_SIGNALING_PATHWAY	66	1,61	0,011
	PID_E2F_PATHWAY	70	2,37	0
	PID_P73PATHWAY	72	1,73	0,015
	PID_RB_1PATHWAY	57	1,65	0,023
	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS	87	2,16	0
	REACTOME_AURKA_ACTIVATION_BY_TPX2	71	2,07	0
	REACTOME_CELL_CYCLE	652	2,76	0
	REACTOME_CELL_CYCLE_CHECKPOINTS	277	2,86	0
	REACTOME_CELL_CYCLE_MITOTIC	525	2,75	0
	REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	50	2,22	0
	REACTOME_G2_M_CHECKPOINTS	154	2,64	0
	REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT	82	2,4	0
	REACTOME_M_PHASE	383	2,51	0
	REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION	148	2,46	0
	REACTOME_MITOTIC_G2_G2_M_PHASES	189	2,15	0
	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	226	2,48	0

	REACTOME_MITOTIC_PROMETAPHASE	194	2,77	0
	REACTOME_MITOTIC_PROPHASE	119	1,95	0
	REACTOME_MITOTIC_SPINDLE_CHECKPOINT	110	2,75	0
	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	51	1,78	0,002
	REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	80	1,92	0
	REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES	87	1,85	0,001
	REACTOME_REGULATION_OF_PLK1_ACTIVITY_AT_G2_M_TRANSITION	86	1,94	0
	REACTOME_REGULATION_OF_TP53_ACTIVITY	157	1,94	0
	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLATION	91	2,35	0
	REACTOME_RHO_GTPASE_EFFECTORS	287	2,37	0
	REACTOME_RHOD_GTPASE_CYCLE	50	1,48	0,04
	REACTOME_RHOJ_GTPASE_CYCLE	51	1,43	0,061
	REACTOME_S_PHASE	161	2,57	0
	REACTOME_TELOMERE_MAINTENANCE	95	2,24	0
	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	172	2,43	0
	WP_CELL_CYCLE	119	2,38	0
	WP_G1_TO_S_CELL_CYCLE_CONTROL	62	2,43	0
	WP_RETINOBLASTOMA_GENE_IN_CANCER	86	2,91	0
Chemokines	KEGG_CHEMOKINE_SIGNALING_PATHWAY	153	-1,52	0,023
	WP_CHEMOKINE_SIGNALING_PATHWAY	139	-1,48	0,033
Cyclins	REACTOME_CYCLIN_A_CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY	84	1,54	0,022
Cytokines	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	185	-1,61	0,014
	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	634	-1,47	0,068
	REACTOME_DDX58_IFIH1_MEDIATED_INDUCTION_OF_INTERFERON_ALPHA_BETA	67	-1,57	0,031
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	58	-1,58	0,033
	REACTOME_INTERLEUKIN_1_SIGNALING	111	-1,47	0,069
	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	98	-1,82	0,011
	REACTOME_SIGNALING_BY_INTERLEUKINS	412	-1,48	0,065
	WP_IL1_SIGNALING_PATHWAY	52	-1,72	0,005
	WP_IL18_SIGNALING_PATHWAY	240	-1,48	0,033
	WP_IL4_SIGNALING_PATHWAY	53	-1,44	0,042
DNA Repair	REACTOME_BASE_EXCISION_REPAIR	75	2,29	0
	REACTOME_CHROMOSOME_MAINTENANCE	122	2,66	0
	REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR	153	2,6	0
	REACTOME_DNA_REPAIR	312	2,44	0
	REACTOME_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NER	83	1,72	0,003
	REACTOME_HOMOLOGY_DIRECTED_REPAIR	123	2,73	0
	REACTOME_NUCLEOTIDE_EXCISION_REPAIR	109	1,68	0,005
	REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS	85	2,48	0
	WP_DNA_DAMAGE_RESPONSE	68	2,01	0
	WP_DNA_REPAIR_PATHWAYS_FULL_NETWORK	119	2,57	0
DNA replication	REACTOME_DNA_REPLICATION	164	2,57	0
	REACTOME_DNA_REPLICATION_PRE_INITIATION	137	2,3	0
	REACTOME_SEPARATION_OF_SISTER_CHROMATIDS	181	2,62	0
	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE	91	2,16	0
	REACTOME_SYNTHESIS_OF_DNA	120	2,64	0
DNA structure	REACTOME_COMPLEX_I_BIOGENESIS	57	1,9	0

Epigenetic regulation	REACTOME_PRC2_METHYLATES_HISTONES_AND_DNA	50	1,69	0,004
	REACTOME_RMTS_METHYLATE_HISTONE_ARGININES	59	1,44	0,055
Glucose metabolism	REACTOME_GLUCOSE_METABOLISM	79	1,61	0,011
Immune response	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	50	-1,97	0
	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	55	-1,74	0,009
	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	103	-1,5	0,024
	PID_CD8_TCR_DOWNSTREAM_PATHWAY	54	-1,61	0,032
	WP_TCELL_ACTIVATION_SARSCOV2	83	-1,77	0,003
	WP_TH17_CELL_DIFFERENTIATION_PATHWAY	63	-2,01	0
MAPK signaling	KEGG_MAPK_SIGNALING_PATHWAY	214	-1,8	0,007
	WP_MAPK_SIGNALING_PATHWAY	202	-1,69	0,005
Metabolite transport	REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	119	1,78	0,002
Notch signaling	REACTOME_SIGNALING_BY_NOTCH1	69	-1,78	0,005
	REACTOME_SIGNALING_BY_NOTCH1_PEST_DOMAIN_MUTANTS_IN_CANCER	55	-1,79	0,007
	WP_NOTCH_SIGNALING_PATHWAY	57	-1,83	0,002
Nucleotide metabolism	KEGG_PURINE_METABOLISM	139	1,58	0,015
	KEGG_PYRIMIDINE_METABOLISM	92	1,97	0
	REACTOME_METABOLISM_OF_NUCLEOTIDES	90	1,63	0,009
	WP_PYRIMIDINE_METABOLISM	81	1,89	0
Organelle organization	REACTOME_MITOCHONDRIAL_TRANSLATION	96	1,92	0
	REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE	277	1,5	0,031
Oxidative phosphorylation (OXPHOS)	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	102	2,37	0
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS	125	2,53	0
	WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTEM_IN_MITOCHONDRIA	100	2,6	0
	WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODEL_OXPHOS_SYSTEM	56	1,95	0
	WP_OXIDATIVE_PHOSPHORYLATION	59	2,15	0
Regulation of cell death	KEGG_APOPTOSIS	81	-1,62	0,016
	REACTOME_DEATH_RECEPTOR_SIGNALLING	130	-1,42	0,094
	WP_APOPTOSIS	81	-1,56	0,021
	WP_APOPTOSIS_MODULATION_AND_SIGNALING	84	-1,59	0,016
T cell receptor signaling	WP_TCELL_RECEPTOR_SIGNALING_PATHWAY	88	-1,44	0,043
TGF-Beta signaling	KEGG_TGF_BETA_SIGNALING_PATHWAY	74	-1,55	0,018
	REACTOME_SIGNALING_BY_TGFB_FAMILY_MEMBERS	113	-1,57	0,031
TNF Signaling	WP_TNFALPHA_SIGNALING_PATHWAY	87	-2,02	0
Toll-like Receptor Signaling	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	85	-1,99	0
	REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE	105	-1,68	0,013
	REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	102	-1,46	0,066
	REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	154	-1,46	0,067
	REACTOME_TOLL_LIKE_RECEPTOR_TLR1_TLR2_CASCADE	108	-1,54	0,04
	WP_TOLLLIKE_RECEPTOR_SIGNALING_PATHWAY	86	-2,03	0
Transcription Factors	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION	87	1,44	0,056
	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DNA_REPAIR_GENES	60	1,55	0,02
	REACTOME_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR_TC_NER	77	1,9	0
	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_SMALL_RNAS	84	1,6	0,012
	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53	355	1,93	0
Wnt signaling	PID_BETA_CATENIN_NUC_PATHWAY	66	-1,65	0,024

5

GO GENESETS (C5)				
Biological process	**GeneSet**	**SIZE**	**NES**	**FDR q-val**
Amino acid metabolism	GOBP_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	135	1,72	0,005
	GOBP_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	68	1,69	0,006
	GOBP_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	84	1,69	0,006
	GOBP_ORGANIC_ACID_METABOLIC_PROCESS	764	1,62	0,013
	GOBP_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	250	1,61	0,014
	GOBP_ALPHA_AMINO_ACID_METABOLIC_PROCESS	167	1,6	0,016
	GOBP_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	247	1,57	0,022
	GOBP_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	468	1,56	0,023
	GOBP_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	68	1,53	0,029
Angiogenesis	GOBP_VASCULATURE_DEVELOPMENT	595	-1,53	0,049
	GOBP_REGULATION_OF_VASCULATURE_DEVELOPMENT	230	-1,54	0,045
	GOBP_VASCULOGENESIS	58	-1,79	0,01
B cell receptor signaling	GOBP_B_CELL_RECEPTOR_SIGNALING_PATHWAY	72	1,59	0,018
Catalytic activity	GOMF_CATALYTIC_ACTIVITY_ACTING_ON_DNA	226	2,3	0
	GOMF_DEOXYRIBONUCLEASE_ACTIVITY	55	2,22	0
	GOMF_EXONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	57	1,88	0,001
	GOMF_EXONUCLEASE_ACTIVITY	81	1,8	0,002
	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	82	1,73	0,004
	GOMF_NUCLEASE_ACTIVITY	191	1,73	0,004
	GOMF_OXIDOREDUCTASE_ACTIVITY	602	1,69	0,007
	GOMF_KINASE_REGULATOR_ACTIVITY	216	1,68	0,007
	GOBP_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY	53	1,65	0,01
	GOMF_ENDONUCLEASE_ACTIVITY	109	1,62	0,013
	GOMF_HELICASE_ACTIVITY	152	1,62	0,014
	GOMF_LIGASE_ACTIVITY	160	1,6	0,016
	GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	57	1,58	0,019
	GOMF_ATP_DEPENDENT_ACTIVITY	501	1,57	0,021
	GOMF_HYDRO_LYASE_ACTIVITY	55	1,54	0,028
	GOMF_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS	111	1,52	0,032
	GOMF_KINASE_ACTIVATOR_ACTIVITY	101	1,52	0,032
	GOMF_ATP_HYDROLYSIS_ACTIVITY	323	1,52	0,034
	GOMF_CATALYTIC_ACTIVITY_ACTING_ON_A_NUCLEIC_ACID	568	1,48	0,046
Cell adhesion	GOBP_CELL_CELL_ADHESION	732	-1,48	0,06
	GOBP_REGULATION_OF_CELL_ADHESION	658	-1,57	0,039
	GOBP_NEGATIVE_REGULATION_OF_CELL_ADHESION	234	-1,57	0,039
	GOBP_POSITIVE_REGULATION_OF_CELL_ADHESION	409	-1,58	0,036
	GOBP_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	110	-1,59	0,034
	GOBP_LEUKOCYTE_CELL_CELL_ADHESION	350	-1,6	0,032
	GOBP_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	153	-1,62	0,028
	GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	279	-1,62	0,029
	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	244	-1,63	0,027
	GOBP_REGULATION_OF_CELL_CELL_ADHESION	405	-1,7	0,019
Cell cycle regulation	GOBP_MITOTIC_CELL_CYCLE_CHECKPOINT_SIGNALING	139	2,84	0

	GOBP_CELL_CYCLE_CHECKPOINT_SIGNALING	184	2,77	0
	GOCC_CONDENSED_CHROMOSOME_CENTROMERIC_REGION	169	2,73	0
	GOBP_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE	93	2,71	0
	GOBP_MITOTIC_NUCLEAR_DIVISION	309	2,71	0
	GOBP_NEGATIVE_REGULATION_OF_NUCLEAR_DIVISION	61	2,68	0
	GOBP_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	108	2,67	0
	GOCC_CHROMOSOME_CENTROMERIC_REGION	240	2,66	0
	GOCC_CHROMOSOMAL_REGION	366	2,65	0
	GOBP_MITOTIC_SPINDLE_ORGANIZATION	128	2,65	0
	GOBP_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	91	2,6	0
	GOBP_MITOTIC_CELL_CYCLE_PROCESS	718	2,56	0
	GOBP_SPINDLE_ORGANIZATION	188	2,56	0
	GOBP_REGULATION_OF_NUCLEAR_DIVISION	128	2,56	0
	GOBP_CHROMOSOME_ORGANIZATION	562	2,55	0
	GOCC_NUCLEAR_CHROMOSOME	229	2,52	0
	GOBP_CELL_DIVISION	579	2,5	0
	GOBP_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	286	2,48	0
	GOBP_MITOTIC_CELL_CYCLE	855	2,46	0
	GOBP_MEIOSIS_I_CELL_CYCLE_PROCESS	110	2,46	0
	GOBP_SPINDLE_ASSEMBLY	126	2,46	0
	GOBP_HOMOLOGOUS_RECOMBINATION	55	2,44	0
	GOBP_MEIOTIC_CELL_CYCLE	240	2,43	0
	GOBP_NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	218	2,43	0
	GOBP_METAPHASE_PLATE_CONGRESSION	70	2,42	0
	GOBP_MITOTIC_DNA_INTEGRITY_CHECKPOINT_SIGNALING	83	2,42	0
	GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE_PROCESS	219	2,41	0
	GOBP_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	403	2,4	0
	GOBP_NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE_PHASE_TRANSITION	171	2,4	0
	GOBP_DNA_RECOMBINATION	298	2,38	0
	GOCC_CONDENSED_NUCLEAR_CHROMOSOME	70	2,38	0
	GOBP_DNA_INTEGRITY_CHECKPOINT_SIGNALING	127	2,38	0
	GOBP_REGULATION_OF_CHROMOSOME_ORGANIZATION	242	2,38	0
	GOBP_REGULATION_OF_CELL_CYCLE_PROCESS	646	2,37	0
	GOBP_CELL_CYCLE_G2_M_PHASE_TRANSITION	148	2,37	0
	GOBP_CELL_CYCLE_PHASE_TRANSITION	515	2,37	0
	GOBP_REGULATION_OF_MITOTIC_CELL_CYCLE_PHASE_TRANSITION	314	2,37	0
	GOBP_MITOTIC_METAPHASE_PLATE_CONGRESSION	57	2,35	0
	GOBP_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	106	2,35	0
	GOBP_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CELL_CYCLE	63	2,35	0
	GOBP_MITOTIC_CELL_CYCLE_PHASE_TRANSITION	422	2,34	0
	GOBP_NEGATIVE_REGULATION_OF_CELL_CYCLE	358	2,3	0
	GOMF_DNA_HELICASE_ACTIVITY	70	2,3	0
	GOBP_REGULATION_OF_MITOTIC_CELL_CYCLE	459	2,29	0
	GOBP_MITOTIC_G2_M_TRANSITION_CHECKPOINT	50	2,26	0
	GOCC_SPINDLE_MICROTUBULE	83	2,26	0
	GOBP_MITOTIC_SPINDLE_ASSEMBLY	73	2,25	0
	GOCC_SPINDLE	399	2,24	0

	GOMF_ATP_DEPENDENT_ACTIVITY_ACTING_ON_DNA	114	2,24	0
	GOCC_SPINDLE_POLE	162	2,23	0
	GOBP_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE_PHASE_TRANSITION	85	2,22	0
	GOCC_MITOTIC_SPINDLE	172	2,22	0
	GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	103	2,21	0
	GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE	291	2,15	0
	GOBP_MITOTIC_CYTOKINESIS	81	2,13	0
	GOBP_REGULATION_OF_CYTOKINESIS	82	2,12	0
	GOBP_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	63	2,11	0
	GOBP_REGULATION_OF_CELL_CYCLE	990	2	0
	GOBP_HOMOLOGOUS_CHROMOSOME_SEGREGATION	51	1,98	0
	GOBP_CYTOKINESIS	167	1,98	0
	GOBP_REGULATION_OF_CELL_DIVISION	152	1,95	0
	GOBP_CYTOSKELETON_DEPENDENT_CYTOKINESIS	105	1,94	0
	GOBP_CENTROSOME_DUPLICATION	70	1,92	0
	GOBP_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	111	1,9	0
	GOBP_REGULATION_OF_CENTROSOME_CYCLE	51	1,79	0,002
	GOBP_REGULATION_OF_MEIOTIC_CELL_CYCLE	53	1,76	0,003
	GOBP_POSITIVE_REGULATION_OF_CELL_DIVISION	65	1,7	0,006
	GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	52	1,61	0,015
	GOBP_CELL_CYCLE_G1_S_PHASE_TRANSITION	234	1,61	0,015
	GOBP_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	172	1,51	0,036
Cell Migration	GOBP_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	76	-1,56	0,041
	GOBP_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	100	-1,57	0,037
	GOBP_NEUTROPHIL_MIGRATION	101	-1,6	0,032
	GOBP_AMEBOIDAL_TYPE_CELL_MIGRATION	354	-1,62	0,03
	GOBP_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	53	-1,64	0,027
	GOBP_ENDOTHELIAL_CELL_MIGRATION	183	-1,67	0,022
	GOBP_GRANULOCYTE_MIGRATION	120	-1,68	0,022
	GOBP_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	138	-1,73	0,016
	GOBP_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	190	-1,78	0,01
Chemokines	GOBP_GRANULOCYTE_CHEMOTAXIS	99	-1,53	0,048
	GOBP_NEUTROPHIL_CHEMOTAXIS	82	-1,55	0,045
	GOBP_RESPONSE_TO_CHEMOKINE	67	-1,78	0,01
	GOBP_CELLULAR_RESPONSE_TO_INTERLEUKIN_1	85	-1,8	0,009
Cyclins	GOBP_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	92	1,83	0,001
Cytokines	GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	225	-1,5	0,057
	GOBP_INTERLEUKIN_2_PRODUCTION	56	-1,53	0,048
	GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	62	-1,55	0,045
	GOBP_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	136	-1,56	0,039
	GOBP_CYTOKINE_PRODUCTION	616	-1,62	0,029
	GOBP_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	104	-1,65	0,025
	GOBP_RESPONSE_TO_CYTOKINE	743	-1,65	0,025
	GOBP_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	75	-1,65	0,025
	GOBP_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	398	-1,69	0,021
	GOBP_RESPONSE_TO_INTERLEUKIN_1	108	-1,7	0,019
	GOBP_INTERLEUKIN_12_PRODUCTION	58	-1,77	0,011

	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	373	-1,88	0,004
DNA Repair	GOBP_RECOMBINATIONAL_REPAIR	166	2,5	0
	GOBP_DOUBLE_STRAND_BREAK_REPAIR	287	2,37	0
	GOBP_DNA_REPAIR	557	2,31	0
	GOMF_DAMAGED_DNA_BINDING	72	2,25	0
	GOMF_SINGLE_STRANDED_DNA_BINDING	121	2,2	0
	GOBP_CELLULAR_RESPONSE_TO_DNA_DAMAGE_STIMULUS	827	2,01	0
	GOCC_SITE_OF_DNA_DAMAGE	105	1,96	0
	GOBP_SIGNAL_TRANSDUCTION_IN_RESPONSE_TO_DNA_DAMAGE	175	1,91	0
	GOBP_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLOGOUS_RECOMBINATION	70	1,73	0,004
	GOBP_REGULATION_OF_DNA_REPAIR	206	1,71	0,005
	GOBP_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	131	1,66	0,01
	GOBP_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	302	1,63	0,012
	GOBP_DOUBLE_STRAND_BREAK_REPAIR_VIA_NONHOMOLOGOUS_END_JOINING	70	1,54	0,028
	GOBP_RESPONSE_TO_UV	139	1,51	0,037
	GOBP_POSITIVE_REGULATION_OF_DNA_REPAIR	124	1,48	0,046
DNA replication	GOBP_CHROMOSOME_SEPARATION	125	2,87	0
	GOBP_REGULATION_OF_CHROMOSOME_SEPARATION	105	2,86	0
	GOBP_SISTER_CHROMATID_SEGREGATION	226	2,86	0
	GOBP_DNA_TEMPLATED_DNA_REPLICATION	163	2,85	0
	GOBP_REGULATION_OF_CHROMOSOME_SEGREGATION	122	2,85	0
	GOBP_CHROMOSOME_SEGREGATION	352	2,84	0
	GOCC_CONDENSED_CHROMOSOME	259	2,8	0
	GOBP_NUCLEAR_CHROMOSOME_SEGREGATION	293	2,78	0
	GOBP_REGULATION_OF_DNA_TEMPLATED_DNA_REPLICATION	57	2,74	0
	GOBP_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEGREGATION	54	2,74	0
	GOBP_DNA_REPLICATION	277	2,65	0
	GOCC_REPLICATION_FORK	65	2,59	0
	GOBP_DNA_TEMPLATED_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	54	2,59	0
	GOBP_REGULATION_OF_DNA_REPLICATION	131	2,39	0
	GOBP_DNA_CONFORMATION_CHANGE	102	2,38	0
	GOBP_REGULATION_OF_DNA_RECOMBINATION	123	1,56	0,022
DNA structure	GOCC_DNA_PACKAGING_COMPLEX	129	2,19	0
	GOBP_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	222	2,08	0
Epigenetic regulation	GOCC_NUCLEOSOME	87	1,64	0,011
	GOBP_NUCLEOSOME_ASSEMBLY	80	1,62	0,014
	GOBP_NUCLEOSOME_ORGANIZATION	113	1,5	0,038
Glucose metabolism	GOBP_RIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	218	1,84	0,001
	GOBP_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	536	1,56	0,022
	GOBP_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	584	1,56	0,023
	GOBP_ORGANOPHOSPHATE_METABOLIC_PROCESS	877	1,54	0,027
	GOBP_CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	950	1,53	0,031
	GOBP_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	57	1,47	0,051
Immune response	GOBP_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	175	-1,47	0,064
	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	99	-1,47	0,066
	GOBP_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	68	-1,48	0,064
	GOBP_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	52	-1,49	0,057

	GOBP_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	56	-1,49	0,058
	GOBP_POSITIVE_REGULATION_OF_CELL_ACTIVATION	360	-1,49	0,06
	GOBP_T_CELL_PROLIFERATION	186	-1,51	0,052
	GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	269	-1,52	0,049
	GOBP_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	520	-1,52	0,048
	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	146	-1,53	0,049
	GOBP_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	180	-1,53	0,048
	GOBP_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	394	-1,54	0,045
	GOBP_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	118	-1,54	0,046
	GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	357	-1,55	0,042
	GOBP_T_CELL_ACTIVATION	474	-1,55	0,045
	GOBP_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	103	-1,57	0,037
	GOBP_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	53	-1,57	0,039
	GOBP_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	62	-1,6	0,033
	GOBP_REGULATION_OF_T_CELL_ACTIVATION	325	-1,6	0,032
	GOBP_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	58	-1,61	0,03
	GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	153	-1,63	0,027
	GOBP_T_CELL_MEDIATED_IMMUNITY	100	-1,63	0,028
	GOBP_ALPHA_BETA_T_CELL_ACTIVATION	156	-1,65	0,025
	GOBP_T_CELL_DIFFERENTIATION	265	-1,67	0,022
	GOBP_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	67	-1,69	0,02
	GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	98	-1,75	0,013
	GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	182	-1,79	0,01
	GOBP_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	71	-1,84	0,006
	GOBP_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	52	-1,85	0,006
	GOBP_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	93	-1,85	0,006
	GOBP_ALPHA_BETA_T_CELL_DIFFERENTIATION	107	-1,92	0,003
	GOBP_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	104	-1,94	0,003
	GOBP_T_CELL_DIFFERENTIATION_IN_THYMUS	74	-1,94	0,003
	GOBP_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	69	-1,94	0,003
	GOBP_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	81	-2,03	0,001
Inflammation	GOBP_REGULATION_OF_INFLAMMATORY_RESPONSE	286	-1,52	0,051
MAPK signaling	GOBP_MAPK_CASCADE	607	-1,5	0,055
	GOBP_POSITIVE_REGULATION_OF_MAPK_CASCADE	366	-1,57	0,037
	GOBP_P38MAPK_CASCADE	50	-1,71	0,019
Metabolite transport	GOBP_PROTON_TRANSMEMBRANE_TRANSPORT	131	1,85	0,001
	GOMF_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	106	1,77	0,002
	GOMF_PRIMARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	148	1,63	0,012
	GOBP_CARBOHYDRATE_DERIVATIVE_TRANSPORT	66	1,62	0,013
NF-kappaB pathway	GOBP_NIK_NF_KAPPAB_SIGNALING	113	-1,65	0,025
	GOBP_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	175	-1,8	0,009
	GOBP_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	259	-1,9	0,003
Notch signaling	GOBP_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	76	-1,68	0,021
	GOBP_NOTCH_SIGNALING_PATHWAY	137	-1,68	0,022
Nucleotide metabolism	GOBP_ATP_BIOSYNTHETIC_PROCESS	101	2,09	0
	GOBP_DNA_METABOLIC_PROCESS	967	2,03	0
	GOBP_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	266	1,94	0

	GOBP_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	219	1,93	0
	GOBP_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	128	1,92	0
	GOBP_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	590	1,9	0
	GOBP_NUCLEOSIDE_METABOLIC_PROCESS	53	1,85	0,001
	GOBP_PYRIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	71	1,81	0,001
	GOBP_DNA_BIOSYNTHETIC_PROCESS	180	1,8	0,002
	GOBP_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	78	1,79	0,002
	GOBP_REGULATION_OF_DNA_METABOLIC_PROCESS	502	1,75	0,003
	GOBP_DICARBOXYLIC_ACID_METABOLIC_PROCESS	79	1,75	0,003
	GOBP_PYRIMIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	81	1,71	0,005
	GOBP_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	107	1,68	0,008
	GOBP_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	72	1,67	0,008
	GOBP_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	429	1,67	0,008
	GOBP_ATP_METABOLIC_PROCESS	193	1,61	0,014
	GOBP_POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	282	1,6	0,015
	GOBP_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	240	1,6	0,016
	GOBP_NUCLEOSIDE_BISPHOSPHATE_BIOSYNTHETIC_PROCESS	55	1,57	0,021
	GOBP_NEGATIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	127	1,54	0,028
Organelle organization	GOBP_ORGANELLE_FISSION	474	2,59	0
	GOCC_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	150	2,22	0
	GOCC_MITOCHONDRIAL_PROTEIN_CONTAINING_COMPLEX	284	2,19	0
	GOBP_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	324	2,03	0
	GOCC_ORGANELLE_INNER_MEMBRANE	510	1,97	0
	GOCC_MITOCHONDRIAL_MATRIX	459	1,96	0
	HP_ABNORMALITY_OF_THE_MITOCHONDRION	181	1,93	0
	GOBP_NON_MEMBRANE_BOUNDED_ORGANELLE_ASSEMBLY	356	1,92	0
	GOBP_MITOCHONDRIAL_TRANSLATION	131	1,86	0,001
	HP_DECREASED_ACTIVITY_OF_MITOCHONDRIAL_COMPLEX_I	53	1,77	0,002
	GOCC_MITOCHONDRIAL_ENVELOPE	731	1,75	0,003
	GOCC_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	58	1,74	0,003
	GOCC_MITOCHONDRIAL_LARGE_RIBOSOMAL_SUBUNIT	56	1,71	0,005
	GOBP_MITOCHONDRIAL_GENE_EXPRESSION	163	1,66	0,009
	GOCC_ORGANELLE_ENVELOPE_LUMEN	87	1,66	0,01
	GOBP_ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	395	1,6	0,016
	GOCC_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	89	1,56	0,023
	GOBP_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	83	1,54	0,027
Oxidative phosphorylation (OXPHOS)	GOBP_OXIDATIVE_PHOSPHORYLATION	138	2,39	0
	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	94	2,37	0
	GOBP_AEROBIC_RESPIRATION	182	2,36	0
	GOCC_RESPIRASOME	93	2,29	0
	GOMF_ELECTRON_TRANSFER_ACTIVITY	111	2,26	0
	GOMF_OXIDOREDUCTION_DRIVEN_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	66	2,18	0
	GOCC_OXIDOREDUCTASE_COMPLEX	119	2,15	0
	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	113	2,13	0
	GOBP_CELLULAR_RESPIRATION	222	2,09	0
	HP_ABNORMAL_ACTIVITY_OF_MITOCHONDRIAL_RESPIRATORY_CHAIN	96	2,05	0
	GOBP_ELECTRON_TRANSPORT_CHAIN	160	2,04	0

	GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	98	1,95	0
	GOBP_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	288	1,93	0
Regulation of cell death	GOBP_LYMPHOCYTE_APOPTOTIC_PROCESS	71	-1,48	0,063
	GOBP_EPITHELIAL_CELL_APOPTOTIC_PROCESS	102	-1,52	0,048
	GOBP_NEGATIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	579	-1,54	0,047
	GOBP_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	73	-1,55	0,045
	GOBP_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	195	-1,56	0,039
	GOBP_REGULATION_OF_EXTENT_OF_CELL_GROWTH	92	-1,58	0,036
	GOBP_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	77	-1,66	0,023
	GOBP_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	130	-1,7	0,019
	GOBP_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	54	-1,7	0,02
	GOBP_LEUKOCYTE_APOPTOTIC_PROCESS	104	-1,74	0,015
	GOBP_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	85	-1,78	0,01
	GOBP_NECROTIC_CELL_DEATH	59	-1,78	0,011
	GOBP_JNK_CASCADE	152	-1,83	0,007
	GOBP_POSITIVE_REGULATION_OF_JNK_CASCADE	82	-1,87	0,004
	GOBP_REGULATION_OF_JNK_CASCADE	122	-1,95	0,002
	GOBP_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	81	-1,95	0,003
Regulation of cytoskeleton	GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS	154	2,61	0
	GOMF_MICROTUBULE_MOTOR_ACTIVITY	61	2,08	0
	GOBP_MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION	144	2,01	0
	GOBP_MICROTUBULE_CYTOSKELETON_ORGANIZATION	569	1,96	0
	GOMF_MICROTUBULE_BINDING	248	1,92	0
	GOCC_MICROTUBULE	408	1,91	0
	GOCC_MICROTUBULE_ORGANIZING_CENTER	754	1,89	0
	GOMF_CYTOSKELETAL_MOTOR_ACTIVITY	93	1,84	0,001
	GOCC_POLYMERIC_CYTOSKELETAL_FIBER	557	1,77	0,002
	GOBP_MICROTUBULE_BASED_PROCESS	801	1,72	0,005
	GOCC_MICROTUBULE_ASSOCIATED_COMPLEX	141	1,71	0,005
	GOMF_TUBULIN_BINDING	338	1,68	0,007
	GOBP_REGULATION_OF_MICROTUBULE_BASED_PROCESS	215	1,56	0,022
	GOCC_CYTOPLASMIC_MICROTUBULE	83	1,55	0,025
	GOBP_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	113	1,55	0,026
	GOBP_REGULATION_OF_MICROTUBULE_CYTOSKELETON_ORGANIZATION	142	1,51	0,035
	GOMF_MYOSIN_BINDING	60	1,51	0,036
Response to stress	GOBP_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	55	-1,52	0,049
	GOBP_REGULATION_OF_RESPONSE_TO_WOUNDING	126	-1,6	0,032
	GOBP_REGULATION_OF_WOUND_HEALING	98	-1,61	0,031
	GOBP_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	218	-1,7	0,019
	GOBP_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	174	-1,85	0,006
	GOBP_POSITIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	114	-1,93	0,003
Ribosome structure	GOMF_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	162	2,13	0
	GOCC_RIBOSOMAL_SUBUNIT	183	2,09	0
	GOCC_CYTOSOLIC_RIBOSOME	100	2,04	0
	GOCC_RIBOSOME	214	1,96	0
	GOCC_SMALL_RIBOSOMAL_SUBUNIT	75	1,93	0

	GOCC_LARGE_RIBOSOMAL_SUBUNIT	112	1,9	0
	GOCC_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	56	1,84	0,001
	GOCC_ORGANELLAR_RIBOSOME	89	1,82	0,001
T cell receptor signaling	GOBP_T_CELL_RECEPTOR_SIGNALING_PATHWAY	130	-1,63	0,028
TNF Signaling	GOBP_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	93	-1,93	0,003
	GOBP_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	203	-1,97	0,002
Toll-like Receptor Signaling	GOBP_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	62	-1,97	0,002
	GOBP_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	105	-2,05	0,001
Wnt signaling	GOBP_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	112	-1,52	0,049
	GOBP_NON_CANONICAL_WNT_SIGNALING_PATHWAY	56	-1,52	0,049

ONCOGENIC GENE SETS (C6)

Biological process	GeneSet	SIZE	NES	FDR q-val
Cell cycle regulation	RB_P107_DN.V1_UP	120	2,84	0
	RB_DN.V1_UP	107	2,06	0
	E2F1_UP.V1_UP	171	2,06	0
	E2F3_UP.V1_UP	164	1,83	0
	RB_P130_DN.V1_UP	99	1,65	0,003
Cytokines	IL21_UP.V1_DN	109	-1,57	0,013
Epigenetic regulation	PRC2_EZH2_UP.V1_DN	155	2,33	0
	PRC2_EED_DN.V1_DN	174	2,13	0
KRAS pathway	KRAS.DF.V1_DN	150	-1,6	0,013
	KRAS.BREAST_UP.V1_UP	85	-1,61	0,015
mTOR Signaling	MTOR_UP.V1_UP	138	2,06	0
TGF-Beta signaling	TGFB_UP.V1_UP	158	-1,99	0
Wnt signaling	WNT_UP.V1_DN	132	-1,5	0,021