Molecular heterogeneity in breast carcinoma cells with increased invasive capacities

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SUPPLEMENTARY TABLE 1.

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
125-dihydroxyvitamin_Dsub3sub_biosynthesis	-0,108	0,324	0,002	3	-0,053
1D-imyoi-inositol_hexakisphosphate_biosynthesis_II_mammalian	-0,015	0,080	-0,025	15	-0,020
1D-imyoi-inositol_hexakisphosphate_biosynthesis_V_from_Ins134P3	-0,035	-0,034	-0,016	3	-0,026
2-amino-3-carboxymuconate_semialdehyde_degradation_to_glutaryl-CoA	-0,053	-0,262	0,005	2	-0,024
2-deoxy-alpha-D-ribose_1-phosphate_degradation	-0,064	0,163	0,012	6	-0,026
2-oxobutanoate_degradation	-0,095	0,026	-0,076	8	-0,085
2-oxoglutarate_decarboxylation_to_succinyl-CoA	-0,181	-0,112	-0,014	3	-0,097
2-oxoisovalerate_decarboxylation_to_isobutanoyl-CoA	-0,103	-0,026	-0,097	4	-0,100
3-phosphoinositide_biosynthesis	0,013	-0,022	0,015	28	0,014
3-phosphoinositide_degradation	0,002	0,033	-0,034	19	-0,016
4-aminobutyrate_degradation	-0,749	0,684	0,289	2	-0,230
4-hydroxy-2-nonenal_detoxification	0,021	0,089	-0,009	5	0,006
4-hydroxybenzoate_biosynthesis	0	0	0	1	0
4-hydroxyproline_degradation	-0,029	-0,032	0,025	4	-0,002
5-aminoimidazole_ribonucleotide_biosynthesis	0,026	0,087	-0,045	3	-0,009
7-3-amino-3-carboxypropyl-wyosine_biosynthesis	-0,265	2,571	-0,216	2	-0,241
acetate_conversion_to_acetyl-CoA	0	0	0	3	0
acetone_degradation_I_to_methylglyoxal	-0,104	0,071	-0,074	8	-0,089
acetyl-CoA_biosynthesis_from_citrate	0,086	-0,208	0,093	1	0,090
acyl_carrier_protein_metabolism	0,272	0,150	0,016	1	0,144
acyl-CoA_hydrolysis	-0,070	-0,139	0,034	3	-0,018
adenine_and_adenosine_salvage_I	0,130	0,302	-0,107	1	0,011
adenine_and_adenosine_salvage_II	-0,050	0,418	-0,161	1	-0,106
adenine_and_adenosine_salvage_III	-0,007	0,077	0,061	3	0,027
adenosine_deoxyribonucleotides_ide_novoi_biosynthesis	-0,015	-0,016	-0,043	11	-0,029
adenosine_nucleotides_degradation	-0,019	0,100	0,015	8	-0,002
adenosine_ribonucleotides_ide_novoi_biosynthesis	-0,020	0,141	-0,025	24	-0,023
AHR_Pathway	-0,186	0,219	-0,186	27	-0,186
AHR_Pathway_Cath_D_expression_via_SP1	-0,314	0,352	-0,314	15	-0,314
AHR_Pathway_C-myc_expression_via_RELA	-0,316	0,331	-0,304	15	-0,310
AHR_Pathway_CYP1A1_CYP1B1_CYP1A2_AHRR_gene_expression_via_POLR2B	-0,013	0,022	-0,024	5	-0,018
AHR_Pathway_PS2_Gene_expression_via_ESR1	-0,342	0,351	-0,326	15	-0,334
Akt_Pathway_Regulation_by_GH	-0,106	0,022	0,024	41	-0,041
Akt_Signaling_Pathway	-0,014	-0,015	0,006	651	-0,004
Akt_Signaling_Pathway_Acetylation_of_proteins	0,036	-0,121	0,034	18	0,035
Akt_Signaling_Pathway_Aggregation_and_Neurodegeneration	0,018	-0,054	0,011	22	0,014
Akt_Signaling_Pathway_Apoptosis	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_AR_mediated_apoptosis	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Blocks_Apoptosis	0,029	-0,105	0,029	18	0,029
Akt_Signaling_Pathway_Blood_cell_differentiation	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Cell_Cycle	0,011	-0,041	0,015	4	0,013
Akt_Signaling_Pathway_Cell_Cycle_Progression	0,030	-0,110	0,024	19	0,027
Akt_Signaling_Pathway_Cell_Survival	0,024	-0,024	0,003	29	0,013
Akt_Signaling_Pathway_Elevation_of_Glucose_Import	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Enhancement_of_Breast_Epithelial	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_ERK_mediated_apoptosis	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Genetic_Stability	0,033	-0,100	0,023	18	0,028
Akt_Signaling_Pathway_Glucose_Uptake	-0,061	0,464	-0,057	3	-0,059
Akt_Signaling_Pathway_Glycogen_Synthesis_and_Apoptosis	0,028	-0,104	0,022	19	0,025

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
Akt_Signaling_Pathway_Increased_GLUT4_translocation	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Induction_of_Chromatin_Condensation	0,030	-0,106	0,021	18	0,026
Akt_Signaling_Pathway_JNK_mediated_apoptosis	0,030	-0,110	0,024	19	0,027
Akt_Signaling_Pathway_Neuroprotection	0,028	-0,080	0,017	20	0,023
Akt_Signaling_Pathway_NFAT_degradation	0,013	-0,043	0,015	34	0,014
Akt_Signaling_Pathway_NF-kB_dependent_transciption	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_NF-kB_pathway	0,027	-0,126	0,035	20	0,031
Akt_Signaling_Pathway_NO_production	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_p73_mediated_apoptosis	0,036	-0,123	0,026	18	0,031
Akt_Signaling_Pathway_Promotes_Adipogenesis	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Protein_Synthesis	0,012	-0,056	0,021	25	0,017
Akt_Signaling_Pathway_Proto-Oncogenic_and_RTK-signaling	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Regulation_of_Cyclic_Nucleotide	0,031	-0,117	0,025	18	0,028
Akt_Signaling_Pathway_Regulation_of_Na+_Transport	0,026	-0,078	0,020	3	0,023
Akt_Signaling_Pathway_Splicing_Regulation	0,016	-0,033	0,005	5	0,010
Akt_Signaling_Pathway_Survival_Genes	0,020	-0,085	0,020	21	0,020
Akt_Signaling_Pathway_Synaptic_Transmission	0,018	-0,066	0,014	32	0,016
Akt_Signaling_Pathway_Translation	-0,676	0,006	0,078	7	-0,299
Akt_Signaling_Pathway_Tumor_Supression	0,031	-0,117	0,025	18	0,028
alanine_biosynthesisdegradation	0	0	0	2	0
allopregnanolone_biosynthesis	0	0	0	6	0
alpha-tocopherol_degradation	0	0	0	1	0
anandamide_degradation	0	0	0	2	0
androgen_biosynthesis	-0,039	0,066	-0,033	7	-0,036
Angiotensin-PTK2B_Pathway	-0,018	0,063	0,034	13	0,008
arsenate_detoxification_I_glutaredoxin	0,012	-0,005	0,018	3	0,015
ascorbate_recycling_cytosolic	-0,131	0,216	-0,028	2	-0,079
asparagine_biosynthesis	0,011	0,077	-0,117	2	-0,053
asparagine_degradation	0,043	0,009	-0,036	4	0,003
aspartate_biosynthesis	0	0	0	2	0
aspirin_triggered_resolvin_D_biosynthesis	0	0	0	2	0
aspirin_triggered_resolvin_E_biosynthesis	0	0	0	2	0
aspirin-triggered_lipoxin_biosynthesis	0	0	0	2	0
ATM_Pathway	0,015	-0,031	0,022	47	0,018
ATM_Pathway_Apoptosis	-0,013	0,141	-0,048	3	-0,030
ATM_Pathway_Apoptosis_and_Senescence	0,053	0,016	0,020	6	0,037
ATM_Pathway_Cell_Cycle_Checkpoint_Control	0,072	0,142	-0,007	4	0,032
ATM_Pathway_Cell_Survival	0,013	0,079	-0,004	14	0,004
ATM_Pathway_Checkpoint_Activation	0,069	0,095	-0,032	4	0,019
ATM_Pathway_DNA_repair	0,007	0,075	0,004	9	0,005
ATM_Pathway_G2_M_Checkpoint_Arrest	-0,024	0,018	0,011	12	-0,007
ATM_Pathway_G2-Mitosis_progression	-0,024	0,018	0,011	12	-0,007
ATM_Pathway_NF-kB_Pathway	0,069	0,095	-0,032	4	0,019
ATM_Pathway_Repair_and_Recombination	0,101	0,110	-0,115	3	-0,007
ATM_Pathway_S-phase_arrest	0,069	0,050	-0,047	4	0,011
ATM_Pathway_S-phase_progression	0,008	-0,018	-0,004	6	0,002
ATM_Pathway_Synaptic_Vesicle_Transport	0,234	-0,389	0,151	4	0,192
Base_Excision_Repair_Pathway	-0,018	-0,002	0,015	20	-0,001
beta-alanine_degradation	-0,113	0,081	-0,112	2	-0,113
bile_acid_biosynthesis_neutral_pathway	-0,063	0,094	-0,032	15	-0,047
biocarta__U_00DF_arrestins_in_gpcr_desensitization_Main_Pathway	-0,047	-0,027	0,008	26	-0,020
biocarta_acetylation_and_deacetylation_of_rela_in_nucleus_Main_Pathway	-0,023	0,059	0,030	5	0,004
biocarta_actions_of_nitric_oxide_in_the_heart_Main_Pathway	-0,028	-0,050	0,023	39	-0,002
biocarta_activation_of_camp_dependent_protein_kinase_pka_Main_Pathway	-0,026	0,010	-0,007	27	-0,016
biocarta_activation_of_csk_by_camp_dependent_protein_kinase_inhibits_signaling_through_the_t_cell_receptor_Main_Pathway	-0,010	-0,003	0,004	41	-0,003
biocarta_activation_of_pkc_through_g_protein_coupled_receptors_Main_Pathway	-0,014	-0,015	0,008	11	-0,003

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biocarta_activation_of_pkc_through_g_protein_coupled_receptors_Pathway_(secretion)	-0,009	0,015	0,010	4	0,001
biocarta_adp_ribosylation_factor_Main_Pathway	0,024	-0,015	0,016	28	0,020
biocarta_agrin_in_postsynaptic_differentiation_Main_Pathway	-0,003	-0,124	0,041	43	0,019
biocarta_ahr_signal_transduction_Main_Pathway	-0,057	-0,012	0,058	4	0,001
biocarta_akap95_role_in_mitosis_and_chromosome_dynamics_Main_Pathway	-0,035	0,046	-0,031	13	-0,033
biocarta_akap95_role_in_mitosis_and_chromosome_dynamics_Pathway_(mitotic_chromosome_condensation)	-0,035	0,046	-0,031	13	-0,033
biocarta_akap95_role_in_mitosis_and_chromosome_dynamics_Pathway_(mitotic_chromosome_decondensation)	-0,035	0,046	-0,031	13	-0,033
biocarta_akt_signaling_Main_Pathway	0,009	-0,067	0,035	16	0,022
biocarta_akt_signaling_Pathway_(apoptosis)	0,008	-0,168	0,063	5	0,035
biocarta_akt_signaling_Pathway_(cell_survival)	0,008	-0,168	0,063	5	0,035
biocarta_akt_signaling_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	0,026	-0,072	0,042	4	0,034
biocarta_alk_in_cardiac_myocytes_Main_Pathway	-0,028	0,084	0,020	22	-0,004
biocarta_alternative_complement_Main_Pathway	0,064	-0,072	0,147	9	0,105
biocarta_angiotensin_ii_mediated_activation_of_jnk_pathway_via_pyk2_dependent_signaling_Main_Pathway	-0,016	-0,081	0,050	23	0,017
biocarta_apoptotic_signaling_in_response_to_dna_damage_Main_Pathway	0,013	-0,000	-0,036	12	-0,011
biocarta_apoptotic_signaling_in_response_to_dna_damage_Pathway_(apoptosis)	0,013	-0,022	-0,051	11	-0,019
biocarta_aspirin_blocks_signaling_pathway_involved_in_platelet_activation_Main_Pathway	-0,012	-0,028	-0,001	16	-0,006
biocarta_aspirin_blocks_signaling_pathway_involved_in_platelet_activation_Pathway_(vasoconstriction)	-0,005	-0,040	-0,008	12	-0,007
biocarta_atm_signaling_Main_Pathway	0,020	-0,104	0,054	15	0,037
biocarta_atm_signaling_Pathway_(apoptosis)	0,029	-0,104	0,056	6	0,043
biocarta_atm_signaling_Pathway_(DNA_repair)	-0,030	-0,066	0,074	7	0,022
biocarta_atm_signaling_Pathway_(Pathway_protein_ubiquitination_of_ATM)	0,049	-0,174	0,093	3	0,071
biocarta_attenuation_of_gpcr_signaling_Main_Pathway	-0,094	-0,052	0,002	13	-0,046
biocarta_b_cell_survival_Main_Pathway	0,031	-0,158	0,083	11	0,057
biocarta_b_cell_survival_Pathway_(apoptosis)	0,072	-0,298	0,060	4	0,066
biocarta_b_cell_survival_Pathway_(cell_proliferation)	0,026	-0,076	0,041	3	0,033
biocarta_basic_mechanism_of_action_of_ppara_pparb_d_and_pparg_and_effects_on_gene_expression_Main_Pathway	0	0	0	5	0
biocarta_basic_mechanisms_of_sumoylation_Main_Pathway	-0,100	0,252	-0,028	6	-0,064
biocarta_basic_mechanisms_of_sumoylation_Pathway_(protein_modification_process)	-0,100	0,252	-0,028	6	-0,064
biocarta_bcr_signaling_Main_Pathway	-0,045	0,233	-0,003	31	-0,024
biocarta_bcr_signaling_Pathway_(re_entry_into_mitotic_cell_cycle)	-0,036	0,076	0,002	9	-0,017
biocarta_bioactive_peptide_induced_signaling_Main_Pathway	-0,013	0,032	0,011	20	-0,001
biocarta_bone_remodeling_Main_Pathway	-0,009	-0,014	0,053	14	0,022
biocarta_bone_remodeling_Pathway_(osteoclast_differentiation)	-0,074	0,033	0,083	6	0,004
biocarta_bone_remodeling_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	0,023	-0,053	0,042	6	0,032
biocarta_brca1_dependent_ub_ligase_activity_Main_Pathway	0	-0,031	-0,010	6	-0,005
biocarta_ca_calmodulin_dependent_protein_kinase_activation_Main_Pathway	0,023	-0,031	0,021	8	0,022
biocarta_calcium_signaling_by_hbx_of_hepatitis_b_virus_Main_Pathway	-0,019	0,025	0,018	15	-0,001
biocarta_calcium_signaling_by_hbx_of_hepatitis_b_virus_Pathway_(viral_genome_replication)	0,053	-0,197	0,020	4	0,036
biocarta_caspase_cascade_in_apoptosis_Main_Pathway	-0,008	0,027	-0,067	18	-0,037
biocarta_caspase_cascade_in_apoptosis_Pathway_(Pathway_degradation_of_CASP1_CASP3_CASP4_CASP10_GZMB)	0,064	0,003	-0,051	9	0,006
biocarta_cd40l_signaling_Main_Pathway	0,042	-0,150	0,090	7	0,066
biocarta_cd40l_signaling_Pathway_(Pathway_protein_ubiquitination_of_TNFAIP3_MAP3K1_MAP4K4)	0,042	-0,150	0,090	7	0,066
biocarta_cdc25_and_chk1_regulatory_pathway_in_response_to_dna_damage_Main_Pathway	0,004	0,031	-0,012	7	-0,004
biocarta_cdk_regulation_of_dna_replication_Main_Pathway	-0,059	0,059	-0,003	17	-0,031
biocarta_cell_cycle_g1_s_check_point_Main_Pathway	-0,012	0,012	-0,000	21	-0,006
biocarta_cell_cycle_g2_m_checkpoint_Main_Pathway	-0,022	0,008	0,012	19	-0,005
biocarta_cell_cycle_g2_m_checkpoint_Pathway_(DNA_repair)	-0,027	0,181	-0,048	3	-0,037
biocarta_cell_to_cell_adhesion_signaling_Main_Pathway	0,011	-0,023	0,033	8	0,022

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biocarta_cell_to_cell_adhesion_signaling_Pathway_(cell_cell_adhesion)	0,011	-0,023	0,033	8	0,022
biocarta_cell_to_cell_adhesion_signaling_Pathway_(cell_migration)	0,011	-0,023	0,033	8	0,022
biocarta_ceramide_signaling_Main_Pathway	0,015	-0,045	0,024	32	0,020
biocarta_ceramide_signaling_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	-0,040	0,017	0,033	12	-0,003
biocarta_chaperones_modulate_interferon_signaling_Main_Pathway	-0,043	0,031	0,007	9	-0,018
biocarta_chaperones_modulate_interferon_signaling_Pathway_(apoptosis)	-0,026	-0,058	-0,013	2	-0,019
biocarta_chaperones_modulate_interferon_signaling_Pathway_(Pathway_protein_ubiquitination_of_DNAJA3)	-0,009	-0,019	-0,004	6	-0,006
biocarta_chrebp_regulation_by_carbohydrates_and_camp_Main_Pathway	-0,026	0,021	-0,014	38	-0,020
biocarta_chromatin_remodeling_by_hswi_snf_atp_dependent_complexes_Main_Pathway	-0,066	0,066	0,025	16	-0,021
biocarta_chromatin_remodeling_by_hswi_snf_atp_dependent_complexes_Pathway_(chromatin_remodeling)	-0,066	0,066	0,025	10	-0,021
biocarta_control_of_skeletal_myogenesis_by_hdac_and_calcium_calmodulin_dependent_kinase_camk__Main_Pathway	0,014	-0,036	0,010	10	0,012
biocarta_ctcf_first_multivalent_nuclear_factor_Main_Pathway	-0,249	-0,007	0,041	22	-0,104
biocarta_cxcr4_signaling_Main_Pathway	-0,062	0,026	-0,001	11	-0,031
biocarta_cycling_of_ran_in_nucleocytoplasmic_transport_Main_Pathway	-0,015	-0,005	0,036	9	0,010
biocarta_cyclins_and_cell_cycle_regulation_Main_Pathway	0,001	0,004	-0,006	23	-0,002
biocarta_cystic_fibrosis_transmembrane_conductance_regulator_cftr_and_beta_2_adrenergic_receptor_b2ar_Main_Pathway	-0,042	0,040	-0,009	20	-0,025
biocarta_d4gdi_signaling_Main_Pathway	-0,025	0,110	-0,033	6	-0,029
biocarta_d4gdi_signaling_Pathway_(apoptosis)	-0,025	0,110	-0,033	6	-0,029
biocarta_deregulation_of_cdk5_in_alzheimers_disease_Main_Pathway	-0,014	0,075	-0,004	5	-0,009
biocarta_deregulation_of_cdk5_in_alzheimers_disease_Pathway_(apoptosis)	-0,014	0,075	-0,004	5	-0,009
biocarta_double_stranded_rna_induced_gene_expression_Main_Pathway	0,016	-0,075	0,039	10	0,028
biocarta_double_stranded_rna_induced_gene_expression_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	0,015	-0,124	0,083	5	0,049
biocarta_double_stranded_rna_induced_gene_expression_Pathway_(translational_initiation)	0,097	-0,116	0,009	5	0,053
biocarta_downregulated_of_mta_3_in_er_negative_breast_tumors_Main_Pathway	0	0	0	13	0
biocarta_e2f1_destruction_Main_Pathway	-0,025	0,072	0,024	6	-0,000
biocarta_egf_signaling_Main_Pathway	-0,037	-0,124	0,015	20	-0,011
biocarta_endocytotic_role_of_ndk_phosphins_and_dynamin_Main_Pathway	-0,061	0,051	0,014	16	-0,024
biocarta_endocytotic_role_of_ndk_phosphins_and_dynamin_Pathway_(endocytosis)	-0,073	0,022	0,024	10	-0,024
biocarta_epo_signaling_Main_Pathway	-0,049	0,056	-0,000	11	-0,025
biocarta_erk_and_pi_3_kinase_are_necessary_for_collagen_binding_in_corneal_epithelia_Main_Pathway	-0,063	0,141	-0,057	29	-0,060
biocarta_erk_and_pi_3_kinase_are_necessary_for_collagen_binding_in_corneal_epithelia_Pathway_(actin_filament_stabilization)	0,050	0,051	-0,047	5	0,002
biocarta_erk_and_pi_3_kinase_are_necessary_for_collagen_binding_in_corneal_epithelia_Pathway_(cell_matrix_adhesion)	-0,079	0,129	-0,059	22	-0,069
biocarta_erk1_erk2_mapk_signaling_Main_Pathway	0,003	-0,058	0,014	22	0,008
biocarta_eukaryotic_protein_translation_Main_Pathway	-0,009	0,062	-0,007	14	-0,008
biocarta_extrinsic_prothrombin_activation_Main_Pathway	0	0	0	13	0
biocarta_fas_signaling_pathway_cd95__Main_Pathway	0,052	-0,095	0,064	12	0,058
biocarta_fc_epsilon_receptor_i_signaling_in_mast_cells_Main_Pathway	-0,017	0,185	0,015	27	-0,001
biocarta_fc_epsilon_receptor_i_signaling_in_mast_cells_Pathway_(acid_secretion)	0,040	0,053	-0,028	5	0,006
biocarta_fmlp_induced_chemokine_gene_expression_in_hmc_1_cells_Main_Pathway	-0,017	0,031	-0,008	28	-0,013
biocarta_fmlp_induced_chemokine_gene_expression_in_hmc_1_cells_Pathway_(Pathway_degradation_of_PRKCA)	-0,036	0,027	-0,007	7	-0,022
biocarta_g_protein_signaling_through_tubby_proteins_Main_Pathway	-0,033	-0,009	-0,003	10	-0,018
biocarta_g_secretase_mediated_erbb4_signaling_Main_Pathway	0,019	-0,146	0,063	8	0,041
biocarta_gamma_aminobutyric_acid_receptor_life_cycle_Main_Pathway	0,012	-0,090	0,030	12	0,021
biocarta_granzyme_a_mediated_apoptosis_Main_Pathway	-0,038	0,192	-0,058	8	-0,048
biocarta_granzyme_a_mediated_apoptosis_Pathway_(DNA_fragmentation_during_apoptosis)	-0,051	0,256	-0,078	6	-0,064
biocarta_granzyme_a_mediated_apoptosis_Pathway_(DNA_repair)	-0,051	0,256	-0,078	6	-0,064

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
biocarta_granzyme_a_mediated_apoptosis_Pathway_(Pathway_degradation_of_GZMB)	0	0	0	3	0
biocarta_granzyme_a_mediated_apoptosis_Pathway_(Pathway_regulation_of_transcription_via_SET_ANP32A_APEX1)	-0,051	0,256	-0,078	6	-0,064
biocarta_growth_hormone_signaling_Main_Pathway	-0,029	0,035	-0,008	19	-0,018
biocarta_hiv_1_nef_negative_effector_of_fas_and_tnf_Main_Pathway	0,004	0,006	0,028	28	0,016
biocarta_hiv_1_nef_negative_effector_of_fas_and_tnf_Pathway_(Pathway_degradation_of_CASP8_BIRC2_APAF1)	0,018	-0,017	0,035	13	0,026
biocarta_hiv_1_nef_negative_effector_of_fas_and_tnf_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	-0,034	0,092	0,011	13	-0,012
biocarta_hop_pathway_in_cardiac_development_Main_Pathway	-0,040	0,192	0,053	4	0,006
biocarta_hop_pathway_in_cardiac_development_Pathway_(cell_differentiation)	-0,040	0,192	0,053	4	0,006
biocarta_hop_pathway_in_cardiac_development_Pathway_(cell_proliferation)	-0,040	0,192	0,053	4	0,006
biocarta_how_does_salmonella_hijack_a_cell_Main_Pathway	0,038	-0,101	0,004	11	0,021
biocarta_how_does_salmonella_hijack_a_cell_Pathway_(lamellipodium_assembly)	0,038	-0,101	0,004	11	0,021
biocarta_how_progesterone_initiates_the_oocyte_maturation_Main_Pathway	0,011	-0,007	-0,021	23	-0,005
biocarta_how_progesterone_initiates_the_oocyte_maturation_Pathway_(oocyte_maturation)	0,050	0,029	-0,025	13	0,012
biocarta_human_cytomegalovirus_and_map_kinase_pathways_Main_Pathway	-0,004	0,008	0,014	16	0,005
biocarta_hypoxia_and_p53_in_the_cardiovascular_system_Main_Pathway	-0,007	0,040	-0,002	15	-0,004
biocarta_hypoxia_inducible_factor_in_the_cardivascular_system_Main_Pathway	-0,015	-0,036	-0,000	16	-0,008
biocarta_ifn_alpha_signaling_Main_Pathway	0,077	-0,271	0,001	8	0,039
biocarta_ifn_gamma_signaling_Main_Pathway	0,125	-0,338	0,004	6	0,064
biocarta_igf_1_signaling_Main_Pathway	0,010	-0,006	-0,002	20	0,004
biocarta_il_2_receptor_beta_chain_in_t_cell_activation_Main_Pathway	-0,135	-0,053	0,033	45	-0,051
biocarta_il_2_receptor_beta_chain_in_t_cell_activation_Pathway_(apoptosis)	0,011	0,039	0,005	10	0,008
biocarta_il_2_receptor_beta_chain_in_t_cell_activation_Pathway_(cell_proliferation)	-0,660	0,022	0,075	16	-0,292
biocarta_il_2_signaling_Main_Pathway	-0,078	0,050	-0,014	14	-0,046
biocarta_il_3_signaling_Main_Pathway	-0,046	0,065	0,026	11	-0,010
biocarta_il_4_signaling_Main_Pathway	0,055	-0,271	0,032	13	0,043
biocarta_il_4_signaling_Pathway_(cell_proliferation)	0,012	-0,147	-0,031	6	-0,010
biocarta_il_4_signaling_Pathway_(cell_survival)	0,022	-0,166	-0,013	7	0,004
biocarta_il_4_signaling_Pathway_(G1_phase_of_mitotic_cell_cycle)	0,008	-0,120	-0,034	7	-0,013
biocarta_il_6_signaling_Main_Pathway	-0,028	-0,106	0,004	12	-0,012
biocarta_il_7_signal_transduction_Main_Pathway	-0,005	-0,101	0,051	15	0,023
biocarta_il_7_signal_transduction_Pathway_(cell_proliferation)	-0,019	-0,035	0,003	8	-0,008
biocarta_il_7_signal_transduction_Pathway_(cell_survival)	0,037	-0,205	-0,003	6	0,017
biocarta_il12_and_stat4_dependent_signaling_pathway_in_th1_development_Main_Pathway	-0,023	-0,024	0,046	9	0,011
biocarta_il22_soluble_receptor_signaling_Main_Pathway	0,037	-0,205	-0,003	6	0,017
biocarta_inactivation_of_gsk3_by_akt_causes_accumulation_of_b_catenin_in_alveolar_macrophages_Main_Pathway	0,036	-0,089	0,042	22	0,039
biocarta_inactivation_of_gsk3_by_akt_causes_accumulation_of_b_catenin_in_alveolar_macrophages_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	0,007	-0,118	0,062	6	0,034
biocarta_induction_of_apoptosis_through_dr3_and_dr4_5_death_receptors_Main_Pathway	-0,217	0,238	0,020	19	-0,099
biocarta_induction_of_apoptosis_through_dr3_and_dr4_5_death_receptors_Pathway_(apoptosis)	-0,243	0,255	0,017	17	-0,113
biocarta_induction_of_apoptosis_through_dr3_and_dr4_5_death_receptors_Pathway_(Pathway_degradation_of_CASP3_CASP10_CASP10)	-0,367	0,404	0,004	12	-0,182
biocarta_influence_of_ras_and_rho_proteins_on_g1_to_s_transition_Main_Pathway	-0,019	0,029	0,012	15	-0,004
biocarta_influence_of_ras_and_rho_proteins_on_g1_to_s_transition_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	0,013	-0,142	0,070	5	0,042
biocarta_inhibition_of_cellular_proliferation_by_gleevec_Main_Pathway	0,037	-0,089	0,053	22	0,045
biocarta_inhibition_of_matrix_metalloproteinases_Main_Pathway	-0,049	-0,091	0,010	6	-0,020
biocarta_inhibition_of_matrix_metalloproteinases_Pathway_(Pathway_degradation_of_RECK_TIMP4_MMP14_TIMP2_TIMP1_TIMP3)	-0,049	-0,091	0,010	6	-0,020
biocarta_insulin_signaling_Main_Pathway	-0,040	0,052	-0,025	11	-0,032
biocarta_integrin_signaling_Main_Pathway	0,093	-0,164	0,051	24	0,072
biocarta_internal_ribosome_entry_Main_Pathway	0,050	0,037	-0,008	18	0,021

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
biocarta_internal_ribosome_entry_Pathway_(translational_initiation)	0,050	0,037	-0,008	18	0,021
biocarta_keratinocyte_differentiation_Main_Pathway	-0,018	-0,065	0,045	48	0,014
biocarta_keratinocyte_differentiation_Pathway_(apoptosis)	0,042	-0,186	0,068	12	0,055
biocarta_keratinocyte_differentiation_Pathway_(keratinocyte_differentiation)	-0,040	0,056	0,048	10	0,004
biocarta_keratinocyte_differentiation_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	-0,013	-0,023	0,048	9	0,018
biocarta_lck_and_fyn_tyrosine_kinases_in_initiation_of_tcr_activation_Main_Pathway	-0,029	0,079	-0,008	12	-0,018
biocarta_lissencephaly_gene_lis1_in_neuronal_migration_and_development_Main_Pathway	0,009	-0,033	-0,017	18	-0,004
biocarta_lissencephaly_gene_lis1_in_neuronal_migration_and_development_Pathway_(negative_regulation_of_microtubule_depolymerization)	0,004	-0,035	0,028	9	0,016
biocarta_lissencephaly_gene_lis1_in_neuronal_migration_and_development_Pathway_(retrograde_axon_cargo_transport)	0,020	-0,069	-0,041	11	-0,010
biocarta_map_kinase_inactivation_of_smrt_corepressor_Main_Pathway	-0,028	-0,131	0,044	12	0,008
biocarta_mapkinase_signaling_Main_Pathway	0,008	-0,004	0,022	55	0,015
biocarta_mcalpain_and_friends_in_cell_motility_Main_Pathway	0,012	-0,050	0,012	30	0,012
biocarta_mcalpain_and_friends_in_cell_motility_Pathway_(cell_migration)	0,077	-0,144	0,026	9	0,051
biocarta_mechanism_of_acetaminophen_activity_and_toxicity_Main_Pathway	0	0	0	4	0
biocarta_mechanism_of_acetaminophen_activity_and_toxicity_Pathway_(fever)	0	0	0	1	0
biocarta_mechanism_of_acetaminophen_activity_and_toxicity_Pathway_(inflammatory_response)	0	0	0	1	0
biocarta_mechanism_of_acetaminophen_activity_and_toxicity_Pathway_(platelet_activation)	0	0	0	1	0
biocarta_mechanism_of_acetaminophen_activity_and_toxicity_Pathway_(prostaglandin_biosynthetic_process)	0	0	0	1	0
biocarta_mechanism_of_protein_import_into_the_nucleus_Main_Pathway	-0,004	0,004	0,023	12	0,010
biocarta_mechanisms_of_transcriptional_repression_by_dna_methylation_Main_Pathway	-0,067	0,160	-0,013	14	-0,040
biocarta_mechanisms_of_transcriptional_repression_by_dna_methylation_Pathway_(histone_deacetylation)	-0,067	0,160	-0,013	14	-0,040
biocarta_melanocyte_development_and_pigmentation_Main_Pathway	-0,003	0,050	-0,000	12	-0,002
biocarta_mets_affect_on_macrophage_differentiation_Main_Pathway	-0,053	0,047	0,002	10	-0,025
biocarta_mets_affect_on_macrophage_differentiation_Pathway_(RNA_processing)	-0,095	0,050	0,003	1	-0,046
biocarta_multi_step_regulation_of_transcription_by_pitx2_Main_Pathway	-0,042	0,060	-0,011	23	-0,027
biocarta_multiple_antiapoptotic_pathways_from_igf_1r_signaling_lead_to_bad_phosphorylation_Main_Pathway	-0,024	-0,053	0,029	10	0,003
biocarta_multiple_antiapoptotic_pathways_from_igf_1r_signaling_lead_to_bad_phosphorylation_Pathway_(apoptosis)	0,025	-0,160	0,061	6	0,043
biocarta_multiple_antiapoptotic_pathways_from_igf_1r_signaling_lead_to_bad_phosphorylation_Pathway_(cell_growth_and_or_maintenance)	0,025	-0,160	0,061	6	0,043
biocarta_nerve_growth_factor_pathway_ngf__Main_Pathway	-0,015	0,056	0,020	17	0,003
biocarta_nf_kb_signaling_Main_Pathway	-0,008	0,049	0,028	21	0,010
biocarta_nf_kb_signaling_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	-0,016	0,072	0,024	18	0,004
biocarta_nfat_and_hypertrophy_of_the_heart__Main_Pathway	-0,157	0,002	0,036	37	-0,061
biocarta_nfkb_activation_by_nontypeable_hemophilus_influenzae_Main_Pathway	-0,014	0,002	0,025	16	0,005
biocarta_nfkb_activation_by_nontypeable_hemophilus_influenzae_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	-0,004	-0,045	0,083	5	0,039
biocarta_nitric_oxide_signaling_Main_Pathway	0,009	0,009	0,001	19	0,005
biocarta_no2_dependent_il_12_pathway_in_nk_cells_Main_Pathway	-0,019	-0,024	0,048	9	0,014
biocarta_no2_dependent_il_12_pathway_in_nk_cells_Pathway_(interleukin_12_biosynthetic_process)	0	0	0	1	0
biocarta_nuclear_receptors_coordinate_the_activities_of_chromatin_remodeling_complexes_and_coactivators_to_facilitate_initiation_of_transcription_in_carcinoma_cells_Main_Pathway	-0,065	-0,005	0,007	8	-0,029
biocarta_opposing_roles_of_aif_in_apoptosis_and_cell_survival_Main_Pathway	0,089	-0,091	0,056	3	0,073
biocarta_opposing_roles_of_aif_in_apoptosis_and_cell_survival_Pathway_(DNA_fragmentation_during_apoptosis)	0,089	-0,091	0,056	3	0,073
biocarta_opposing_roles_of_aif_in_apoptosis_and_cell_survival_Pathway_(removal_of_superoxide_radicals)	0,089	-0,091	0,056	3	0,073
biocarta_overview_of_telomerase_rna_component_gene_hterc_transcriptional_regulation_Main_Pathway	-0,044	-0,081	0,071	7	0,014
biocarta_oxidative_stress_induced_gene_expression_via_nrf2_Main_Pathway	-0,048	0,150	0,047	12	-0,001

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
biocarta_p38_mapk_signaling_Main_Pathway	0,011	-0,070	0,022	30	0,016
biocarta_p53_signaling_Main_Pathway	-0,018	0,054	-0,011	11	-0,014
biocarta_pdgf_signaling_Main_Pathway	0,030	-0,110	0,043	26	0,036
biocarta_pelp1_modulation_of_estrogen_receptor_activity_Main_Pathway	0,039	-0,009	0,084	4	0,062
biocarta_phospholipids_as_signalling_intermediaries_Main_Pathway	-0,017	-0,027	0,014	33	-0,002
biocarta_phospholipids_as_signalling_intermediaries_Pathway_(actin_filament_organization)	-0,089	0,020	-0,004	10	-0,047
biocarta_phospholipids_as_signalling_intermediaries_Pathway_(cell_proliferation)	0,040	0,014	-0,016	5	0,012
biocarta_phospholipids_as_signalling_intermediaries_Pathway_(cell_survival)	0,040	0,014	-0,016	5	0,012
biocarta_phospholipids_as_signalling_intermediaries_Pathway_(chemotaxis)	-0,089	0,020	-0,004	10	-0,047
biocarta_phospholipids_as_signalling_intermediaries_Pathway_(lamellipodium_assembly)	-0,063	-0,016	0,027	11	-0,018
biocarta_phosphorylation_of_mek1_by_cdk5_p35_down_regulates_the_map_kinase_Main_Pathway	-0,017	0,081	0,000	14	-0,008
biocarta_pkc_catalyzed_phosphorylation_of_inhibitory_phosphoprotein_of_myosin_phosphatase_Main_Pathway	-0,009	-0,038	0,014	21	0,002
biocarta_pkc_catalyzed_phosphorylation_of_inhibitory_phosphoprotein_of_myosin_phosphatase_Pathway_(secretion)	0,009	0,013	0,006	7	0,007
biocarta_polyadenylation_of_mrna_Main_Pathway	0,004	0,078	0,024	8	0,014
biocarta_prion_Main_Pathway	0,014	-0,143	0,039	18	0,027
biocarta_proteasome_complex_Main_Pathway	-0,042	0,133	-0,036	21	-0,039
biocarta_proteasome_complex_Pathway_(Pathway_degradation_of_PSMA1)	-0,042	0,133	-0,036	21	-0,039
biocarta_protein_kinase_a_at_the_centrosome_Main_Pathway	-0,015	-0,018	-0,019	12	-0,017
biocarta_pten_dependent_cell_cycle_arrest_and_apoptosis_Main_Pathway	-0,004	-0,053	0,014	15	0,005
biocarta_pten_dependent_cell_cycle_arrest_and_apoptosis_Pathway_(cell_migration)	-0,021	-0,060	-0,014	7	-0,017
biocarta_pten_dependent_cell_cycle_arrest_and_apoptosis_Pathway_(cell_survival)	0,020	-0,070	0,023	4	0,022
biocarta_rac1_cell_motility_signaling_Main_Pathway	-0,151	-0,018	0,011	33	-0,070
biocarta_rac1_cell_motility_signaling_Pathway_(actin_filament_depolymerization)	-0,065	0,176	-0,007	3	-0,036
biocarta_rac1_cell_motility_signaling_Pathway_(actin_filament_organization)	-0,002	-0,054	-0,005	22	-0,003
biocarta_rac1_cell_motility_signaling_Pathway_(phosphatidic_acid_metabolic_process)	-0,018	-0,063	-0,002	21	-0,010
biocarta_ras_independent_pathway_in_nk_cell_mediated_cytotoxicity_Main_Pathway	-0,006	0,057	-0,020	22	-0,013
biocarta_ras_independent_pathway_in_nk_cell_mediated_cytotoxicity_Pathway_(positive_regulation_of_natural_killer_cell_mediated_cytotoxicity)	-0,035	0,260	-0,034	3	-0,034
biocarta_rb_tumor_suppressor_checkpoint_signaling_in_response_to_dna_damage_Main_Pathway	-0,027	0,054	-0,010	9	-0,019
biocarta_regulation_of_bad_phosphorylation_Main_Pathway	-0,012	-0,020	0,003	23	-0,004
biocarta_regulation_of_bad_phosphorylation_Pathway_(apoptosis)	-0,122	-0,057	-0,018	3	-0,070
biocarta_regulation_of_ck1_cdk5_by_type_1_glutamate_receptors_Main_Pathway	-0,018	0,008	-0,013	24	-0,016
biocarta_regulation_of_eif_4e_and_p70s6_kinase_Main_Pathway	-0,224	-0,062	0,035	22	-0,094
biocarta_regulation_of_eif2_Main_Pathway	0,034	-0,011	-0,005	11	0,014
biocarta_regulation_of_map_kinase_pathways_through_dual_specificity_phosphatases_Main_Pathway	0,021	-0,017	0,003	9	0,012
biocarta_regulation_of_pgc_1a_Main_Pathway	0,015	-0,018	0,017	19	0,016
biocarta_regulation_of_spermatogenesis_by_crem_Main_Pathway	-0,034	0,007	-0,021	10	-0,027
biocarta_regulation_of_spermatogenesis_by_crem_Pathway_(spermatogenesis)	-0,020	-0,009	-0,019	6	-0,020
biocarta_regulation_of_splicing_through_sam68_Main_Pathway	-0,022	0,049	-0,005	10	-0,014
biocarta_regulation_of_splicing_through_sam68_Pathway_(negative_regulation_of_cell_growth)	-0,015	0,065	-0,013	8	-0,014
biocarta_regulation_of_splicing_through_sam68_Pathway_(positive_regulation_of_nuclear_mRNA_splicing_via_spliceosome)	-0,015	0,065	-0,013	8	-0,014
biocarta_regulation_of_transcriptional_activity_by_pml_Main_Pathway	-0,065	0,034	0,041	8	-0,012
biocarta_regulation_of_transcriptional_activity_by_pml_Pathway_(negative_regulation_of_cell_proliferation)	-0,065	0,034	0,041	8	-0,012
biocarta_regulators_of_bone_mineralization_Main_Pathway	0,071	-0,250	0,071	11	0,071
biocarta_repression_of_pain_sensation_by_the_transcriptional_regulator_dream_Main_Pathway	-0,046	0,091	0,009	13	-0,018
biocarta_reversal_of_insulin_resistance_by_leptin_Main_Pathway	-0,066	0,128	-0,057	10	-0,061

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
biocarta_reversal_of_insulin_resistance_by_leptin_Pathway_(fatty_acid_oxidation)	-0,066	0,128	-0,057	10	-0,061
biocarta_rho_cell_motility_signaling_Main_Pathway	0,023	-0,050	0,007	32	0,015
biocarta_rho_cell_motility_signaling_Pathway_(actin_filament_polymerization)	0,004	-0,041	0,003	24	0,004
biocarta_rho_cell_motility_signaling_Pathway_(actin_filament_stabilization)	-0,008	0,038	-0,015	7	-0,012
biocarta_rho_cell_motility_signaling_Pathway_(focal_adhesion_formation)	0,161	-0,182	0,052	5	0,106
biocarta_rho_selective_guanine_exchange_factor_akap13_mediates_stress_fiber_formation_Main_Pathway	-0,003	-0,018	-0,026	10	-0,014
biocarta_rna_polymerase_iii_transcription_Main_Pathway	0,003	-0,157	0,067	7	0,035
biocarta_rna_polymerase_iii_transcription_Pathway_(Pathway_transcription_initiation_via_BDP1)	0,003	-0,157	0,067	7	0,035
biocarta_role_of_brca1_brca2_and_atr_in_cancer_susceptibility_Main_Pathway	0,012	-0,069	0,008	16	0,010
biocarta_role_of_brca1_brca2_and_atr_in_cancer_susceptibility_Pathway_(DNA_replication_termination)	-0,003	-0,085	0,033	11	0,015
biocarta_role_of_brca1_brca2_and_atr_in_cancer_susceptibility_Pathway_(Pathway_protein_ubiquitination_of_ATM_BRCA1)	-0,006	-0,044	0,010	8	0,002
biocarta_role_of_brca1_brca2_and_atr_in_cancer_susceptibility_Pathway_(regulation_of_DNA_replication)	0,005	-0,100	0,041	6	0,023
biocarta_role_of_egf_receptor_transactivation_by_gpcrs_in_cardiac_hypertrophy_Main_Pathway	-0,038	-0,045	0,040	19	0,001
biocarta_role_of_egf_receptor_transactivation_by_gpcrs_in_cardiac_hypertrophy_Pathway_(cell_growth)	-0,033	-0,065	0,047	10	0,007
biocarta_role_of_egf_receptor_transactivation_by_gpcrs_in_cardiac_hypertrophy_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	0,018	-0,078	0,044	6	0,031
biocarta_role_of_erbb2_in_signal_transduction_and_oncology_Main_Pathway	-0,022	-0,057	0,032	21	0,005
biocarta_role_of_erk5_in_neuronal_survival_Main_Pathway	-0,009	-0,026	0,018	26	0,005
biocarta_role_of_erk5_in_neuronal_survival_Pathway_(cell_survival)	-0,005	0,001	0,022	12	0,008
biocarta_role_of_erk5_in_neuronal_survival_Pathway_(positive_regulation_of_axon_extension)	0,029	-0,025	0,018	9	0,024
biocarta_role_of_mal_in_rho_mediated_activation_of_srf_Main_Pathway	0,011	0,050	-0,021	19	-0,005
biocarta_role_of_mef2d_in_t_cell_apoptosis_Main_Pathway	-0,008	-0,007	-0,009	27	-0,009
biocarta_role_of_mef2d_in_t_cell_apoptosis_Pathway_(Pathway_degradation_of_CAPN2)	-0,042	-0,072	-0,038	4	-0,040
biocarta_role_of_mitochondria_in_apoptotic_signaling_Main_Pathway	-0,058	0,069	-0,070	12	-0,064
biocarta_role_of_nicotinic_acetylcholine_receptors_in_the_regulation_of_apoptosis_Main_Pathway	0,030	-0,040	0,012	17	0,021
biocarta_role_of_parkin_in_ubiquitin_proteasomal_Main_Pathway	0,039	-0,039	-0,004	8	0,018
biocarta_role_of_pi3k_subunit_p85_in_regulation_of_actin_organization_and_cell_migration_Main_Pathway	0,004	-0,044	0,018	16	0,011
biocarta_role_of_pi3k_subunit_p85_in_regulation_of_actin_organization_and_cell_migration_Pathway_(filopodium_formation)	0,046	-0,157	0,029	9	0,038
biocarta_role_of_pi3k_subunit_p85_in_regulation_of_actin_organization_and_cell_migration_Pathway_(negative_regulation_of_actin_polymerization_and_or_depolymerization)	-0,042	0,180	0,021	3	-0,010
biocarta_role_of_ppar_gamma_coactivators_in_obesity_and_thermogenesis_Main_Pathway	-0,018	0,009	-0,009	5	-0,013
biocarta_role_of_ppar_gamma_coactivators_in_obesity_and_thermogenesis_Pathway_(fat_cell_differentiation)	-0,018	0,009	-0,009	4	-0,013
biocarta_role_of_ran_in_mitotic_spindle_regulation_Main_Pathway	0,038	-0,150	0,032	10	0,035
biocarta_role_of_U_00DF_arrestins_in_the_activation_and_targeting_of_map_kinases_Main_Pathway	-0,027	-0,026	-0,000	28	-0,013
biocarta_segmentation_clock_Main_Pathway	-0,029	0,035	0,010	17	-0,009
biocarta_signal_dependent_regulation_of_myogenesis_by_corepressor_mitr_Main_Pathway	0,019	-0,021	0,010	8	0,015
biocarta_signal_transduction_through_il1r_Main_Pathway	-0,015	0,021	0,013	34	-0,001
biocarta_signal_transduction_through_il1r_Pathway_(Pathway_protein_ubiquitination_of_CHUK_PEBP1)	-0,006	-0,021	0,038	10	0,016
biocarta_signaling_pathway_from_g_protein_families_Main_Pathway	-0,056	0,059	-0,012	26	-0,034
biocarta_skeletal_muscle_hypertrophy_is_regulated_via_akt_mtor_Main_Pathway	-0,242	-0,010	0,034	20	-0,104
biocarta_skeletal_muscle_hypertrophy_is_regulated_via_akt_mtor_Pathway_(muscle_development)	-0,574	0,068	0,026	8	-0,274
biocarta_sodd_tnfr1_signaling_Main_Pathway	-0,051	0,071	0,015	9	-0,018
biocarta_sonic_hedgehog_receptor_ptc1_regulates_cell_cycle_Main_Pathway	0,009	-0,023	-0,027	9	-0,009
biocarta_sonic_hedgehog_receptor_ptc1_regulates_cell_cycle_Pathway_(cell_cycle_arrest)	0,029	0,094	-0,035	3	-0,003

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
biocarta_sonic_hedgehog_receptor_ptc1_regulates_cell_cycle_Pathway_(re_entry_into_mitotic_cell_cycle)	0,009	-0,023	-0,027	9	-0,009
biocarta_spliceosomal_assembly_Main_Pathway	-0,030	0,234	-0,031	8	-0,031
biocarta_sprouty_regulation_of_tyrosine_kinase_signals_Main_Pathway	0,010	-0,123	0,030	19	0,020
biocarta_sprouty_regulation_of_tyrosine_kinase_signals_Pathway_(cell_migration)	0	0	0	5	0
biocarta_sprouty_regulation_of_tyrosine_kinase_signals_Pathway_(Pathway_protein_ubiquitination_of_CBL)	-0,008	-0,284	0,081	8	0,036
biocarta_srebp_control_of_lipid_synthesis_Main_Pathway	0,036	-0,069	-0,009	7	0,014
biocarta_srebp_control_of_lipid_synthesis_Pathway_(cholesterol_biosynthetic_process)	0,036	-0,069	-0,009	5	0,014
biocarta_stat3_signaling_Main_Pathway	0,048	-0,231	0,016	8	0,032
biocarta_stathmin_and_breast_cancer_resistance_to_antimicrotubule_agents_Main_Pathway	-0,016	0,064	0,004	24	-0,006
biocarta_stress_induction_of_hsp_regulation_Main_Pathway	0,054	-0,058	0,033	13	0,044
biocarta_stress_induction_of_hsp_regulation_Pathway_(cell_survival)	0,093	-0,185	0,064	5	0,079
biocarta_stress_induction_of_hsp_regulation_Pathway_(Pathway_degradation_of_HSPB1)	0,093	-0,185	0,064	5	0,079
biocarta_sumoylation_as_a_mechanism_to_modulate_ctbp_dependent_gene_responses_Main_Pathway	-0,022	0,033	-0,045	7	-0,033
biocarta_sumoylation_by_ranbp2_regulates_transcriptional_repression_Main_Pathway	-0,026	0,046	0,021	14	-0,002
biocarta_t_cell_receptor_signaling_Main_Pathway	-0,021	0,012	0,010	53	-0,005
biocarta_t_cell_receptor_signaling_Pathway_(Pathway_protein_ubiquitination_of_PRKCA)	-0,020	0,059	0,006	4	-0,007
biocarta_tgf_beta_signaling_Main_Pathway	0,001	-0,044	0,007	15	0,004
biocarta_the_41bb_dependent_immune_response_Main_Pathway	-0,007	0,017	-0,007	13	-0,007
biocarta_the_co_stimulatory_signal_during_t_cell_activation_Main_Pathway	-0,030	0,063	-0,012	18	-0,021
biocarta_the_co_stimulatory_signal_during_t_cell_activation_Pathway_(T_cell_activation)	-0,030	0,063	-0,012	18	-0,021
biocarta_the_igf_1_receptor_and_longevity_Main_Pathway	-0,004	-0,050	0,024	15	0,010
biocarta_the_igf_1_receptor_and_longevity_Pathway_(cell_survival)	0,061	-0,196	0,050	6	0,056
biocarta_the_igf_1_receptor_and_longevity_Pathway_(Pathway_degradation_of_CAT)	0,061	-0,196	0,050	6	0,056
biocarta_the_igf_1_receptor_and_longevity_Pathway_(superoxide_release)	-0,048	0,043	-0,010	6	-0,029
biocarta_the_prc2_complex_sets_long_term_gene_silencing_through_modification_of_histone_tails_Main_Pathway	-0,092	0,114	0,001	8	-0,046
biocarta_the_prc2_complex_sets_long_term_gene_silencing_through_modification_of_histone_tails_Pathway_(histone_deacetylation)	-0,092	0,114	0,001	8	-0,046
biocarta_the_prc2_complex_sets_long_term_gene_silencing_through_modification_of_histone_tails_Pathway_(histone_methylation)	-0,092	0,114	0,001	8	-0,046
biocarta_thrombin_signaling_and_protease_activated_receptors_Main_Pathway	-0,020	-0,006	0,008	26	-0,006
biocarta_tnf_stress_related_signaling_Main_Pathway	-0,000	-0,058	0,045	23	0,022
biocarta_tnfr1_signaling_Main_Pathway	-0,036	-0,044	0,036	16	-0,000
biocarta_tnfr2_signaling_Main_Pathway	-0,006	-0,009	0,021	10	0,007
biocarta_tnfr2_signaling_Pathway_(Pathway_protein_ubiquitination_of_MAP3K1_TNFAIP3_MAP3K14)	-0,006	-0,009	0,021	10	0,007
biocarta_toll_like_receptor_Main_Pathway	0,001	-0,003	0,025	31	0,013
biocarta_toll_like_receptor_Pathway_(Pathway_protein_ubiquitination_of_CHUK_MAP3K1)	0,010	0,001	0,031	10	0,020
biocarta_tpo_signaling_Main_Pathway	0,023	-0,044	0,031	24	0,027
biocarta_transcription_factor_creb_and_its_extracellular_signals_Main_Pathway	-0,032	0,009	0,011	21	-0,010
biocarta_transcription_regulation_by_methyltransferase_of_carm1_Main_Pathway	-0,033	0,047	0,014	13	-0,009
biocarta_transcription_regulation_by_methyltransferase_of_carm1_Pathway_(histone_acetylation)	0,016	0,012	0,048	6	0,032
biocarta_transcription_regulation_by_methyltransferase_of_carm1_Pathway_(histone_methylation)	0,016	0,012	0,048	6	0,032
biocarta_transcriptional_activation_of_dbpb_from_mrna_Main_Pathway	-0,014	-0,004	0,097	3	0,041
biocarta_trefoil_factors_initiate_mucosal_healing_Main_Pathway	-0,041	-0,025	0,018	20	-0,011
biocarta_trefoil_factors_initiate_mucosal_healing_Pathway_(Pathway_protein_ubiquitination_of_CHUK)	0,018	-0,078	0,044	6	0,031
biocarta_trka_receptor_signaling_Main_Pathway	-0,026	-0,077	0,044	13	0,009
biocarta_trka_receptor_signaling_Pathway_(cell_growth_and_or_maintenance)	0,015	-0,074	0,061	4	0,038

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
biocarta_tsp_1_induced_apoptosis_in_microvascular_endothelial_cell_Main_Pathway	-0,029	0,136	0,041	7	0,006
biocarta_tumor_suppressor_arf_inhibits_ribosomal_biogenesis_Main_Pathway	-0,065	0,101	-0,004	15	-0,034
biocarta_tumor_suppressor_arf_inhibits_ribosomal_biogenesis_Pathway_(Pathway_degradation_of_CDKN2A)	0	0	0	1	0
biocarta_tumor_suppressor_arf_inhibits_ribosomal_biogenesis_Pathway_(ribosome_biogenesis)	-0,025	0,052	0,030	7	0,003
biocarta_ucalpain_and_friends_in_cell_spread_Main_Pathway	0,097	-0,199	0,047	17	0,072
biocarta_vegf_hypoxia_and_angiogenesis_Main_Pathway	-0,018	-0,055	0,038	27	0,010
biocarta_vegf_hypoxia_and_angiogenesis_Pathway_(cell_migration)	0,009	-0,027	0,026	10	0,018
biocarta_visceral_fat_deposits_and_the_metabolic_syndrome_Main_Pathway	0,029	-0,480	0,271	8	0,150
biocarta_west_nile_virus_Main_Pathway	-0,030	0,100	-0,095	6	-0,063
biocarta_west_nile_virus_Pathway_(apoptosis)	-0,030	0,100	-0,095	6	-0,063
biocarta_wnt_lrp6_signalling_Main_Pathway	0	0	0	5	0
biocarta_wnt_signaling_Main_Pathway	-0,022	-0,010	-0,008	25	-0,015
biocarta_y_branching_of_actin_filaments_Main_Pathway	0,030	-0,142	0,029	16	0,029
biocarta_yaci_and_bcma_stimulation_of_b_cell_immune_responses_Main_Pathway	-0,013	0,097	0,026	8	0,007
biotin-carboxyl_carrier_protein_assembly	-0,183	0,480	-0,047	3	-0,115
BRCA1_Pathway	-0,015	0,043	-0,011	86	-0,013
BRCA1_Pathway_Base_Excission_Repair	-0,096	-0,006	0,048	4	-0,024
BRCA1_Pathway_Cell_Cycle_Arrest_DNA_Repair_Genes_p21_WAF_CIP1_14-3-3_GADD45	-0,000	-0,041	0,062	4	0,031
BRCA1_Pathway_Chromatin_Remodeling	-0,022	0,073	-0,021	33	-0,021
BRCA1_Pathway_E2_Responsive_Genes	0,003	-0,019	0,008	7	0,006
BRCA1_Pathway_G1_S_arrest	0,066	-0,101	0,062	4	0,064
BRCA1_Pathway_Growth_Promoting_Genes_hTert_S100A7	0,066	-0,101	0,062	4	0,064
BRCA1_Pathway_Homologous_Recombination_Repair	0,037	-0,012	-0,011	12	0,013
BRCA1_Pathway_Mismatch_Repair	-0,052	0,151	0,007	12	-0,022
BRCA1_Pathway_NHEJ_DSB_Repair	0,015	-0,008	0,011	7	0,013
BRCA1_Pathway_Nucleotide_Excission_Repair	-0,113	0,120	-0,008	4	-0,060
BRCA1_Pathway_Transciption_Coupled_Repair	0,037	-0,090	0,040	4	0,038
bupropion_degradation	-0,053	0,066	-0,020	5	-0,036
C20_prostanoid_biosynthesis	-0,090	-0,158	0,171	9	0,041
Calcium2+_Signaling	0,050	-0,151	0,047	17	0,048
cAMP_Pathway	-0,006	-0,018	0,005	559	-0,000
cAMP_Pathway_Axonal_Growth	0,008	0,052	-0,007	22	0,001
cAMP_Pathway_Cell_Growth	-0,019	-0,007	0,006	58	-0,006
cAMP_Pathway_Cell_Proliferation	-0,059	0,053	-0,008	12	-0,034
cAMP_Pathway_Cell_Survival	-0,079	0,018	0,003	84	-0,038
cAMP_Pathway_Chemotaxis	-0,113	-0,009	0,013	58	-0,050
cAMP_Pathway_Cytokine_Production	-0,021	0,001	0,008	61	-0,006
cAMP_Pathway_Degradation_of_Cell_Cycle_Regulators	0,004	-0,076	0,001	22	0,002
cAMP_Pathway_Endothelial_Cell_Regulation	-0,018	0,021	-0,022	40	-0,020
cAMP_Pathway_eNOS_Signaling_Cardiovascular_Homeostasis	-0,047	0,037	-0,009	12	-0,028
cAMP_Pathway_Fatty_Acid_Metabolism	-0,012	-0,020	0,008	74	-0,002
cAMP_Pathway_Gene_Expression_via_NFKB2_CREBBP_ELK1	0,030	-0,072	0,040	31	0,035
cAMP_Pathway_Glycogen_Synthesis	-0,057	0,077	-0,018	13	-0,038
cAMP_Pathway_Glycolisis	-0,000	-0,026	-0,044	11	-0,022
cAMP_Pathway_Lipolysis	-0,047	0,037	-0,009	12	-0,028
cAMP_Pathway_Metabolic_Energy	-0,001	-0,013	0,014	27	0,006
cAMP_Pathway_Myocardial_Contraction	-0,005	0,042	-0,013	112	-0,009
cAMP_Pathway_Oncogenesis	-0,046	0,043	-0,011	13	-0,029
cAMP_Pathway_Protein_Retention	-0,026	0,008	0,003	14	-0,011
cAMP_Pathway_Regulation_of_Cytoskeleton	-0,025	0,014	-0,011	14	-0,018
cardiolipin_biosynthesis	0,084	0,038	0,076	3	0,080
carnosine_biosynthesis	0	0	0	1	0
Caspase_Cascade_Pathway	0,025	0,026	-0,013	364	0,006
Caspase_Cascade_Pathway_Activated_Tissue_Trans-glutaminase	-0,013	0,047	-0,022	67	-0,017
Caspase_Cascade_Pathway_DNA_Fragmentation	-0,017	0,218	-0,085	5	-0,051

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
catecholamine_biosynthesis	0	0	0	4	0
CCR3_Pathway_in_Eosinophils	0,008	-0,079	0,025	66	0,017
CD16_Pathway_in_Natural_Killer_cells	0,016	-0,026	0,012	24	0,014
CD40_Pathway	0,041	-0,120	0,069	42	0,055
CD40_Pathway_Cell_Survival	0,114	-0,349	0,174	3	0,144
CD40_Pathway_Gene_Expression_Cell_Adhesion_Molecule_via_NFKB2	0,058	-0,260	0,115	13	0,086
CD40_Pathway_Gene_Expression_Cell_Survival_via_NFKB2	0,058	-0,260	0,115	13	0,086
CD40_Pathway_Gene_Expression_Co-Stimulatory_Molecules_via_NFKB2	0,058	-0,260	0,115	13	0,086
CD40_Pathway_Gene_Expression_COX2_and_Prostaglandins_via_NFKB2	0,058	-0,260	0,115	13	0,086
CD40_Pathway_Gene_Expression_Immunoglobulin_Class_Switch_via_NFKB2	0,058	-0,260	0,115	13	0,086
CD40_Pathway_Gene_Expression_Procoagulant_Activity_via_NFKB2	0,058	-0,260	0,115	13	0,086
CD40_Pathway_Gene_Expression_Pro-Inflamatory_Cytokines_via_NFKB2	0,058	-0,260	0,115	13	0,086
CDC42_Pathway	0,027	-0,075	0,021	34	0,024
CDK5_Pathway_in_Central_Nervous_System	-0,028	0,027	0,014	30	-0,007
CDK5_Signaling_in_Neurons	0,009	0,047	-0,016	31	-0,003
CDP-diacylglycerol_biosynthesis	-0,058	0,022	0,029	22	-0,015
Cell_Adhesion_Regulated_by_CDHs	0,029	-0,154	0,026	38	0,027
Cell_Migration_Adhesion_and_Angiogenesis_driven_by_MMIF	0,016	-0,033	0,005	4	0,010
Cellular_Apoptosis_Pathway	0,023	0,023	-0,002	251	0,011
Cellular_Apoptosis_Pathway_Depolarization	0,010	-0,071	0,062	4	0,036
Cellular_Apoptosis_Pathway_DNA_Fragmentation	0,016	0,073	-0,047	9	-0,016
Cellular_Apoptosis_Pathway_Gene_Expression_BAX_BID_BAK_Ras_Noxa_PUMA_APAF1_Survivin_BCL2_via_TP53	0,000	0,028	0,021	5	0,011
ceramide_ide_novoi_biosynthesis	-0,070	-0,158	0,045	7	-0,013
Chemokine_Ligand_2_Signaling	0,013	-0,102	0,044	23	0,028
Chemokine_Pathway	0,003	-0,027	0,014	203	0,009
Chemokine_Pathway_Cell_Activation	0,016	-0,015	0,005	29	0,010
Chemokine_Pathway_Gene_Expression_and_Apoptosis_via_ELK1	0,025	0,017	0,004	16	0,014
Chemokine_Pathway_Internalization_Degradation_Recycling	-0,026	-0,135	0,032	16	0,003
Chemotaxis_Driven_by_C5a	-0,006	-0,051	0,021	38	0,008
Chemotaxis_Driven_by_CCL2	-0,013	0,060	0,004	46	-0,004
Chemotaxis_Driven_by_CCR4	0,012	-0,123	0,037	45	0,024
Chemotaxis_Driven_by_IL-8_and_LTB4	0,020	-0,110	0,031	52	0,025
Chemotaxis_of_Immune_Cells_During_Allergic_Asthma_and_Eczema_Driven_by_CCR4	0,012	-0,123	0,037	45	0,024
cholesterol_biosynthesis_I	-0,026	-0,235	0,045	13	0,009
cholesterol_biosynthesis_II_via_2425-dihydrolanosterol	-0,026	-0,235	0,045	13	0,009
cholesterol_biosynthesis_III_via_desmosterol	-0,026	-0,235	0,045	13	0,009
choline_degradation	-0,133	0,197	0,009	2	-0,062
chondroitin_and_dermatan_biosynthesis	0	0	0	5	0
chondroitin_sulfate_biosynthesis	-0,015	0,007	0,011	20	-0,002
chondroitin_sulfate_biosynthesis_late_stages	-0,026	-0,005	0,040	13	0,007
chondroitin_sulfate_degradation_metazoa	-0,037	0,193	-0,050	7	-0,044
Chromatin_Pathway	-0,051	0,057	-0,026	15	-0,039
Circadian_Pathway	0,011	0,023	0,006	12	0,008
citrulline-nitric_oxide_cycle	0,009	0,028	-0,094	5	-0,042
CMP_phosphorylation	-0,000	-0,041	-0,029	10	-0,015
CMP-iNi-acetylneuraminate_biosynthesis_I_eukaryotes	0,106	-0,305	0,040	4	0,073
coenzyme_A_biosynthesis	-0,035	0,203	-0,055	6	-0,045
creatine_biosynthesis	0	0	0	2	0
creatine-phosphate_biosynthesis	-0,020	0,087	-0,032	5	-0,026
CREB_Pathway	-0,003	-0,033	0,009	301	0,003
CXC_Chemokine_Receptor_Pathway	-0,017	-0,017	0,013	55	-0,002
cysteine_biosynthesis	-0,025	0,085	-0,003	6	-0,014
cysteine_biosynthesishomocysteine_degradation_trans-sulfuration	0	0	0	2	0
Cytokine_Network_Pathway	-0,000	-0,005	0,003	35	0,001
Cytoskeleton_Reorganization	0,038	-0,092	0,028	100	0,033
dermatan_sulfate_biosynthesis	0,004	0,001	-0,025	16	-0,011
dermatan_sulfate_biosynthesis_late_stages	-0,007	-0,046	0,001	4	-0,003

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
dermatan_sulfate_degradation_metazoa	-0,064	0,174	-0,058	6	-0,061
Development_of_Immune_Synapse	0,013	0,000	-0,032	109	-0,010
D-galactose_degradation_V_Leloir_pathway	0,197	-0,155	0,151	6	0,174
D-glucuronate_degradation	0	0	0	2	0
D-imyoi-inositol_134-trisphosphate_biosynthesis	-0,001	0,096	-0,016	15	-0,009
D-imyoi-inositol_1456-tetrakisphosphate_biosynthesis	-0,098	-0,120	-0,067	3	-0,083
D-imyoi-inositol_145-trisphosphate_biosynthesis	-0,150	0,158	0,009	26	-0,070
D-imyoi-inositol_145-trisphosphate_degradation	-0,012	0,021	-0,023	13	-0,017
D-imyoi-inositol_3456-tetrakisphosphate_biosynthesis	-0,053	-0,052	-0,024	2	-0,039
D-imyoi-inositol-5-phosphate_metabolism	-0,182	0,296	-0,033	19	-0,107
diphthamide_biosynthesis	0,202	0,000	0,137	2	0,169
D-mannose_degradation	-0,016	0,360	-0,111	1	-0,063
dolichol_and_dolichyl_phosphate_biosynthesis	0	0	0	3	0
dolichyl-diphosphooligosaccharide_biosynthesis	-0,518	0,410	-0,036	10	-0,277
dopamine_degradation	-0,020	-0,154	0,004	5	-0,008
dTMP_ide_novoi_biosynthesis_mitochondrial	0,222	-0,547	0,084	3	0,153
EGF_Pathway	0,005	-0,090	0,039	107	0,022
EGF_Pathway_Actin_Cytoskeletal_Rearrangement	-0,033	-0,062	0,023	13	-0,005
EGF_Pathway_Cell_Motility	-0,070	-0,391	0,106	4	0,018
EGF_Pathway_Cell_Survival	-0,015	-0,119	0,044	21	0,015
EGF_Pathway_Cytoskeleton_Regulation	-0,063	-0,412	0,170	9	0,053
EGF_Pathway_EGFR_Endocytosis	-0,068	-0,381	0,132	4	0,032
EGF_Pathway_Gene_Expression_via_FOS_NFKB2_MYC_STAT1_ELK1_STAT3_JUN	0,055	-0,246	0,074	42	0,065
EGF_Pathway_IP3_Signaling	-0,097	-0,342	0,108	4	0,006
EGF_Pathway_Rab5_Regulation_Pathway	-0,135	0,256	-0,045	3	-0,090
eicosapentaenoate_biosynthesis	-0,018	-0,083	0,030	12	0,006
Ephrin-B_Pathway	0,009	-0,058	0,021	85	0,015
Ephrin-mediated_Signaling_Events_During_Cell_Adhesion	-0,017	0,025	-0,006	45	-0,011
epoxysqualene_biosynthesis	0,126	-0,351	-0,026	2	0,050
ErbB_Family_Pathway	-0,055	-0,024	0,024	87	-0,015
ErbB_Family_Pathway_Anti-Apoptosis	0,031	-0,082	0,036	4	0,034
ErbB_Family_Pathway_Gene_Expression_via_JUN_FOS_ELK1	0,009	0,025	-0,002	31	0,003
ErbB_Family_Pathway_Translation	-1,510	-0,080	0,144	3	-0,683
ERK_Signaling_Pathway	0,003	-0,029	0,010	620	0,007
ERK_Signaling_Pathway_Cell_Survival	-0,011	0,057	-0,012	9	-0,012
ERK_Signaling_Pathway_EGFR_signaling	0,008	0,034	-0,009	12	-0,000
ERK_Signaling_Pathway_Gene_Expression_via_CAPN6_TP53_FOS_ATF1_MYC_ELK3_MYLK_ETS1_SRF_HIST1H3B_CREB3_STAT3_NFKB2_HMGN1_ESR2_ELK1_PAX6_JUN	0,015	-0,042	0,030	70	0,022
ERK_Signaling_Pathway_Translation	-0,006	0,014	0,006	15	-0,000
Erythropoietin_Pathway	0,003	-0,031	0,021	159	0,012
Erythropoietin_Pathway_Anti-Apoptosis	0,025	-0,019	0,007	15	0,016
Erythropoietin_Pathway_BCLXL_Gene_Expression_via_STAT5B	0,015	-0,057	0,011	7	0,013
Erythropoietin_Pathway_Cell_Cycle_Progression	0,054	-0,116	0,031	9	0,043
Erythropoietin_Pathway_Cell_Survival	-0,006	0,007	0,017	67	0,005
Erythropoietin_Pathway_GPI_Hidrolysis_and_Ca2+_influx	0,003	0,020	0,007	4	0,005
estradiol_biosynthesis_I	-0,072	0,111	-0,013	5	-0,042
estradiol_biosynthesis_II	0	0	0	2	0
Estrogen_Pathway	-0,006	-0,035	0,009	342	0,001
Estrogen_Pathway_Anti-Apoptosis	-0,023	-0,008	0,004	38	-0,009
Estrogen_Pathway_Gene_Expression_via_FOS_JUN_ELK1_SP1_POLR2B_CREB3_NFKB2	-0,014	-0,004	0,002	119	-0,006
Estrogen_Pathway_Vasodilatation	0	0	0	1	0
ethanol_degradation_II	-0,154	0,062	-0,038	6	-0,096
ethanol_degradation_IV	-0,139	0,056	-0,036	6	-0,088
eumelanin_biosynthesis	0	0	0	4	0
Extracellular_Matrix_Remodeling_during_Adhesion	0,031	-0,199	0,059	48	0,045
FAK_Pathway	0,014	-0,012	0,015	68	0,014
fatty_acid_activation	-0,082	0,019	0,025	8	-0,028

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
fatty_acid_alpha-oxidation	-0,083	-0,182	-0,033	5	-0,058
fatty_acid_alpha-oxidation_III	-0,054	-0,142	-0,030	3	-0,042
fatty_acid_beta-oxidation	-0,097	0,025	-0,026	16	-0,061
fatty_acid_beta-oxidation_peroxisome	-0,092	0,050	0,008	15	-0,042
fatty_acid_beta-oxidation_unsaturated_odd_number	-0,103	0,032	-0,093	3	-0,098
fatty_acid_biosynthesis_initiation	-0,046	0,167	0,014	4	-0,016
fatty_acid_elongation_--_saturated	-0,000	0,224	0,007	2	0,003
FCGR3A-mediated_phagocytosis	0,004	0,130	-0,011	32	-0,003
FGF2_Signaling_in_Epithelial-mesenchymal_transition	0,014	0,005	0,010	7	0,012
FGFR_Signaling	-0,014	0,032	0,001	51	-0,006
flavin_biosynthesis	0,141	-0,277	0,112	2	0,126
FLT3_Signaling_Pathway	-0,060	-0,033	0,034	73	-0,013
FLT3_Signaling_Pathway_Transcription_via_ELK3_MAPK12_CREB3_STAT2	-0,092	-0,084	0,059	45	-0,017
FLT3_Signaling_Pathway_Translation	-0,032	-0,031	0,039	8	0,003
FN1_Influence_on_Cell_Motility_via_Integrins	0,052	-0,161	0,057	34	0,054
folate_polyglutamylation	-0,013	-0,013	0,017	5	0,002
folate_transformations	0,015	-0,003	0,017	11	0,016
formaldehyde_oxidation	0,095	0,268	-0,046	2	0,025
fructose_26-bisphosphate_synthesisdephosphorylation	0	0	0	5	0
GABA_shunt	-0,268	0,149	0,088	7	-0,090
Gamma-Aminobutyric_Acid_A_Receptor_Pathway	-0,064	-0,039	-0,006	15	-0,035
gamma-glutamyl_cycle	-0,016	0,119	-0,023	8	-0,020
gamma-linolenate_biosynthesis	-0,037	-0,028	0,021	14	-0,008
GDP-glucose_biosynthesis_II	0,005	-0,101	0,003	6	0,004
GDP-L-fucose_biosynthesis_I_from_GDP-D-mannose	-0,227	0,593	-0,010	2	-0,118
GDP-L-fucose_biosynthesis_II_from_L-fucose	0	0	0	2	0
GDP-mannose_biosynthesis	0,031	0,111	-0,008	6	0,011
geranylgeranyldiphosphate_biosynthesis	0,115	-0,197	-0,009	1	0,053
glucocorticoid_biosynthesis	0	0	0	3	0
Glucocorticoid_Receptor_Signaling_Pathway	0,014	0,003	-0,006	211	0,004
Glucocorticoid_Receptor_Signaling_Pathway_Cell_Cycle_Arrest	0,029	-0,480	0,271	3	0,150
Glucocorticoid_Receptor_Signaling_Pathway_Cell_Cycle_Progression	-0,048	0,038	0,017	29	-0,016
Glucocorticoid_Receptor_Signaling_Pathway_Gene_Expression_via_CREB3_ STAT5B_SLC22A2_POU2F1	-0,046	0,043	0,013	36	-0,016
Glucocorticoid_Receptor_Signaling_Pathway_Histone_Deacetylation	-0,004	0,029	0,034	17	0,015
Glucocorticoid_Receptor_Signaling_Pathway_Inflammatory_Cytokines	0,035	-0,012	-0,014	72	0,011
gluconeogenesis	-0,021	0,027	0,009	24	-0,006
glutamate_biosynthesisdegradation	0	0	0	2	0
glutamate_dependent_acid_resistance	0,052	-0,208	-0,045	3	0,003
glutamate_removal_from_folates	-0,408	0,629	-0,373	1	-0,390
glutamine_biosynthesis	0,156	-0,625	-0,135	1	0,010
glutamine_degradationglutamate_biosynthesis	-0,184	-0,521	0,168	2	-0,008
glutaryl-CoA_degradation	-0,081	-0,062	-0,046	4	-0,064
glutathione_biosynthesis	-0,010	0,234	-0,050	3	-0,030
glutathione_redox_reactions_I	-0,133	0,207	-0,006	6	-0,069
glutathione_redox_reactions_II	0,068	0,089	-0,047	1	0,010
glutathione-mediated_detoxification	-0,064	0,137	-0,026	21	-0,045
glycerol_degradation	-0,069	0,168	0,033	5	-0,018
glycerol-3-phosphate_shuttle	0	0	0	2	0
glycine_betaine_degradation	0	0	0	5	0
glycine_biosynthesisdegradation	0	0	0	2	0
glycine_cleavage	0	0	0	3	0
glycineserine_biosynthesis	0	0	0	2	0
glycoaminoglycan-protein_linkage_region_biosynthesis	0,011	0,028	-0,048	7	-0,019
glycogen_biosynthesis	0,047	-0,017	0,023	8	0,035
glycogenolysis	0,067	-0,036	-0,017	9	0,025
glycolysis	0,060	0,017	-0,002	24	0,029
GNAQ_Signaling_Events	0,012	-0,106	0,050	8	0,031
GPCR_Pathway	-0,006	-0,046	0,019	265	0,006

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
GPCR_Pathway_Gene_Expression_via_JUN_NFKB2_ELK1_SRF_FOS_CREB3	0,000	-0,052	0,038	90	0,019
Growth_Hormone_Signaling_Pathway	0,019	-0,020	0,005	66	0,012
Growth_Hormone_Signaling_Pathway_Cell_Survival	0,009	0,019	0,002	19	0,005
Growth_Hormone_Signaling_Pathway_Gene_Expression_via_SRF_ELK1_STAT5B_CEBPD_STAT1_STAT3	0,021	-0,022	0,005	59	0,013
Growth_Hormone_Signaling_Pathway_Glucose_Uptake	0,010	0,024	0,001	16	0,005
Growth_Hormone_Signaling_Pathway_Protein_Synthesis	0	0	0	4	0
GSK3_Signaling_Pathway	-0,002	0,034	-0,010	295	-0,006
GSK3_Signaling_Pathway_b-CTNN_Degradation	-0,017	0,028	0,000	30	-0,008
GSK3_Signaling_Pathway_Gene_Expression_via_CTNNB1	-0,006	0,005	-0,006	90	-0,006
GSK3_Signaling_Pathway_Glycogen_Synthesis	-0,010	-0,011	-0,007	34	-0,008
GSK3_Signaling_Pathway_Protein_Synthesis	-0,005	-0,050	0,004	37	-0,000
guanine_and_guanosine_salvage	-0,018	0,072	-0,033	2	-0,025
guanosine_deoxyribonucleotides_ide_novoi_biosynthesis	-0,022	0,044	-0,027	11	-0,024
guanosine_nucleotides_degradation	-0,004	0,066	0,006	4	0,001
guanosine_nucleotides_ide_novoi_biosynthesis	-0,029	0,052	-0,029	15	-0,029
guanosine_ribonucleotides_ide_novoi_biosynthesis	-0,027	0,013	-0,040	12	-0,033
HA_syntesis_pathway	0,020	-0,082	0,033	24	0,027
Hedgehog_Signaling_in_Mammals_no_Tubulin_Pathway	-0,008	-0,042	0,015	102	0,004
Hedgehog_Signaling_in_Mammals_Pathway	-0,027	-0,019	0,009	102	-0,009
heme_biosynthesis	-0,010	0,001	-0,014	9	-0,012
heme_biosynthesis_from_uroporphyrinogen-III_I	-0,056	-0,039	0,015	4	-0,021
heme_degradation	0,051	-0,187	0,069	4	0,060
heparan_sulfate_biosynthesis	-0,006	0,028	-0,018	28	-0,012
heparan_sulfate_biosynthesis_late_stages	-0,012	0,027	-0,008	21	-0,010
HGF_Pathway	-0,002	-0,037	0,022	95	0,010
HGF_Pathway_Anoikis	0,013	0,018	0,011	29	0,012
HGF_Pathway_Cell_Adhesion_and_Cell_Migration	-0,017	-0,065	0,022	31	0,002
HGF_Pathway_Cell_Cycle_Progression	0,029	-0,022	0,026	15	0,027
HGF_Pathway_Cell_Scattering	0,016	-0,056	-0,002	16	0,007
HGF_Pathway_Cell_Survival	0,016	-0,056	-0,002	16	0,007
HGF_Pathway_Gene_Expression_via_JUN_STAT3_FOS_ELK1_ETS2	0,055	-0,158	0,047	17	0,051
HGF_Pathway_IP3_Pathway	0,010	-0,265	-0,010	4	0,000
HGF_Pathway_PKC_Pathway	0,001	-0,167	-0,000	6	0,000
HGF_Pathway_Regulation_of_Cytoskeleton_Cell_Polarity_and_Cell_Motility	-0,040	0,026	0,039	13	-0,000
HIF1Alpha_Pathway	-0,000	-0,018	0,003	54	0,001
HIF1Alpha_Pathway_Gene_Expression_via_JUN_CREB3	0,016	-0,038	0,013	25	0,014
HIF1Alpha_Pathway_HIF1a_Degradation	0,043	-0,129	-0,007	1	0,018
HIF1Alpha_Pathway_NOS_Pathway	0,027	-0,064	0,018	21	0,023
HIF1Alpha_Pathway_p53_Hypoxia_Pathway	0,004	-0,031	0,005	31	0,005
HIF1Alpha_Pathway_VEGF_Pathway	0,027	-0,064	0,018	24	0,023
histamine_biosynthesis	0	0	0	1	0
histamine_degradation	0	0	0	2	0
histidine_degradation	0,014	-0,014	0,006	5	0,010
HMGB1_signaling_through_RAGE	0,028	-0,018	0,016	45	0,022
homocarnosine_biosynthesis	0	0	0	1	0
hydrogen_sulfide_biosynthesis_trans-sulfuration	0	0	0	2	0
Hypoxia_induced_EMT_in_cancer_and_fibrosis_3_copy	-0,027	-0,161	0,032	9	0,003
hypusine_biosynthesis	0,005	0,109	-0,043	2	-0,019
ICOS_signaling_in_T-helper_cells	0,002	-0,032	0,014	16	0,008
IGF1R_Signaling_Pathway	-0,021	-0,031	0,025	173	0,002
IGF1R_Signaling_Pathway_Apoptosis	0,035	-0,026	-0,006	12	0,014
IGF1R_Signaling_Pathway_Cell_Migration	-0,015	-0,050	0,016	36	0,000
IGF1R_Signaling_Pathway_Cell_Proliferation_Diferentiation_and_Apoptosis	0,017	-0,049	0,054	21	0,035
IGF1R_Signaling_Pathway_Cell_Survival	0,044	0,029	0,000	12	0,022
IGF1R_Signaling_Pathway_Gene_Expression_Proliferation_Growth_Survival_via_NFAT5_CREB3	-0,031	0,021	0,009	24	-0,011
IGF1R_Signaling_Pathway_Glucose_Uptake	0,037	0,022	-0,033	4	0,002
IGF1R_Signaling_Pathway_Glycogen_Synthesis	0,005	-0,005	0,001	6	0,003

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
IGF1R_Signaling_Pathway_Protein_Synthesis	-0,220	0,049	0,009	20	-0,106
IL-10_Pathway	0,029	-0,109	0,046	40	0,038
IL-10_Pathway_IL-10_Responsive_Genes_Transcription_of_BCLXL_Cyclin-D1_D2_D3_Pim1_c-Myc_and_P19(INK4D)_via_STAT3	0,014	-0,044	0,012	23	0,013
IL-10_Pathway_Inflammatory_Cytokine_Genes_Expression_via_STAT3	0,014	-0,044	0,012	23	0,013
IL-10_Pathway_Stability_Determination	0	0	0	3	0
IL-10_Pathway_Translational_Modulation	-0,020	0,045	0,019	10	-0,001
IL-2_Pathway	-0,055	0,077	-0,012	148	-0,034
IL-2_Pathway_Actin_Reorganization	-0,024	0,115	0,001	9	-0,011
IL-2_Pathway_Apoptosis	-0,136	0,191	-0,058	3	-0,097
IL-2_Pathway_Apoptosis_Inhibition	0,011	0,025	0,001	15	0,006
IL-2_Pathway_Gene_Expression_via_FYN_LYN_RPS6KB1_PTK2B	-0,321	0,251	0,017	14	-0,152
IL-2_Pathway_IL2_Gene_Expression_via_POLR1E_EGR1_HMGA1_ELF1_POU2F1_MYC	-0,005	-0,033	0,052	45	0,023
IL-2_Pathway_Protein_Synthesis	0,031	-0,166	-0,000	7	0,015
IL-6_Pathway	0,014	-0,051	0,024	209	0,019
ILK_Signaling_Pathway	0,007	-0,041	0,014	507	0,011
ILK_Signaling_Pathway_Actin_Polymerization_Cytoskeletal_Reorganization	0,104	-0,095	0,080	59	0,092
ILK_Signaling_Pathway_Apoptosis	0,016	0,006	-0,010	8	0,003
ILK_Signaling_Pathway_Cell_Adhesion	0	0	0	3	0
ILK_Signaling_Pathway_Cell_Cycle_Proliferation	-0,009	-0,031	0,014	41	0,002
ILK_Signaling_Pathway_Cell_Migration_Retraction	-0,009	-0,029	0,015	41	0,003
ILK_Signaling_Pathway_Cell_Motility	0,086	-0,079	0,066	62	0,076
ILK_Signaling_Pathway_Cytoskeletal_Adhesion_Complexes	0,003	-0,048	0,015	118	0,009
ILK_Signaling_Pathway_Epithelial_Mesenchymal_Transition	-0,015	0,072	-0,033	31	-0,024
ILK_Signaling_Pathway_Epithelial_Mesenchymal_Transition_Tubulo-Interstitial_Fibrosis	0,008	-0,044	0,013	137	0,010
ILK_Signaling_Pathway_G2_Phase_Arrest	-0,009	-0,031	0,014	41	0,002
ILK_Signaling_Pathway_Induced_Cell_Proliferation	-0,025	-0,054	-0,003	10	-0,014
ILK_Signaling_Pathway_Loss_of_Occludin_Barrier_Dysfunction	0,008	-0,058	0,028	37	0,018
ILK_Signaling_Pathway_Migration_Vasculogenesis	0,008	-0,044	0,013	137	0,010
ILK_Signaling_Pathway_MMP2_MMP9_Gene_Expression_Tissue_Invasion_via_FOS	-0,007	-0,015	0,045	24	0,019
ILK_Signaling_Pathway_Opsonization	0	0	0	3	0
ILK_Signaling_Pathway_Regulation_of_Intermediate_Filaments	0	0	0	1	0
ILK_Signaling_Pathway_Regulation_of_Junction_Assembly_at_Desmosomes	0	0	0	3	0
ILK_Signaling_Pathway_Tissue_Morphogenesis	-0,007	-0,015	0,045	24	0,019
ILK_Signaling_Pathway_Tumor_Angiogenesis	0	0	0	6	0
ILK_Signaling_Pathway_Wound_Healing	0	0	0	3	0
imyoi-inositol_ide_novoi_biosynthesis	0,183	-0,379	0,067	3	0,125
iNi-acetylglucosamine_degradation_I	0,013	0,190	-0,021	3	-0,004
iNi-acetylglucosamine_degradation_II	0,057	0,036	0,001	4	0,029
inosine-5-phosphate_biosynthesis	0,058	0,145	-0,004	3	0,027
inositol_pyrophosphates_biosynthesis	-0,006	0,018	-0,001	7	-0,003
Inside-out_Signaling_through_Integrins	-0,009	-0,057	0,023	67	0,007
Integrin-based_Cell_Migration_and_Adhesion	0,064	-0,144	0,035	73	0,049
Integrins_Function_in_Carcinoma_Progression	0,002	-0,107	0,014	49	0,008
Integrins_Signaling_in_Natural_Killer_Cells	-0,019	0,109	0,007	44	-0,006
Interferon_Pathway	-0,049	-0,014	-0,001	99	-0,025
Interferon_Pathway_Gene_Expression_via_HIST1H3B_CREB3	-0,022	0,023	0,009	24	-0,006
Interferon_Pathway_Transciption	0,036	-0,091	0,002	23	0,019
Interferon_Pathway_Translation	-0,907	0,160	0,031	5	-0,438
Interleukin-8-induced_Cell_Adhesion_and_Migration	-0,008	0,025	-0,005	18	-0,007
Intermediate_Filaments_in_Epithelial_Cells	-0,018	0,085	-0,018	15	-0,018
IP3_Pathway	-0,009	-0,022	0,014	175	0,002
IP3_Pathway_Gene_Expression_via_CREB3_NFATC2_MEF2D	0,004	0,019	0,013	27	0,008
iron-sulfur_cluster_biosynthesis	-0,240	-0,175	0,219	1	-0,010
iSi-methyl-5-thioadenosine_degradation	-0,076	0,376	-0,119	1	-0,097
iSi-methyl-5-thio-alpha-D-ribose_1-phosphate_degradation	-0,082	0,371	0,005	4	-0,039
isoleucine_degradation	-0,116	0,020	-0,074	12	-0,095

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
ITGA4-mediated_Cell_Adhesion_and_Migration	0,047	-0,095	0,007	24	0,027
itrans_transi-farnesyl_diphosphate_biosynthesis	0,108	-0,139	0,016	4	0,062
JAK-STAT_Pathway	-0,008	-0,031	0,014	324	0,003
JAK-STAT_Pathway_Akt_Pathway	0,025	-0,055	0,001	18	0,013
JAK-STAT_Pathway_Gene_Expression_via_MYC	0,040	-0,249	0,001	5	0,021
JAK-STAT_Pathway_IFN-Inducible_Gene_Expression_via_STAT2_STAT1	0,020	-0,072	0,000	30	0,010
JAK-STAT_Pathway_JAK_Degradation	0,017	-0,028	-0,000	30	0,008
JAK-STAT_Pathway_Nml_SOCS_BCL-XL_p21_Myc_Nos2_Gene_Expression_via_STAT2	-0,012	-0,030	0,008	241	-0,002
JNK_Pathway	-0,019	-0,004	0,010	306	-0,005
JNK_Pathway_Gene_Expression_Apoptosis_Inflammation_Tumorigenesis_Cell_Migration_via_SMAD4_STAT4_HSF1_TP53_MAP2_DCX_ATF2_NFATC3_SPIRE1_MAP1B_TCF15_ELK1_BCL2_JUN_PXN_NFATC2	-0,000	-0,036	0,024	56	0,012
JNK_Pathway_Insulin_Signaling	0,041	-0,089	0,032	18	0,036
Junctional_Cell_Adhesion_in_Endothelium	0,020	-0,050	0,016	31	0,018
KEGG_ABC_transporters_Main_Pathway	-0,026	0,028	0,012	44	-0,007
KEGG_Acute_myeloid_leukemia_Main_Pathway	-0,112	0,031	0,020	49	-0,046
KEGG_Adherens_junction_Main_Pathway	-0,018	0,091	-0,036	60	-0,027
KEGG_Adipocytokine_signaling_Main_Pathway	-0,004	0,008	0,011	33	0,004
KEGG_Adrenergic_signaling_in_cardiomyocytes_Main_Pathway	0,001	-0,020	0,009	148	0,005
KEGG_African_trypanosomiasis_Main_Pathway	0,007	-0,077	0,029	9	0,018
KEGG_Alanine_aspartate_and_glutamate_metabolism_Main_Pathway	-0,062	0,030	-0,012	31	-0,037
KEGG_Alcoholism_Main_Pathway	-0,007	-0,008	0,012	76	0,002
KEGG_Aldosterone_regulated_sodium_reabsorption_Main_Pathway	-0,030	0,307	-0,067	22	-0,049
KEGG_Allograft_rejection_Main_Pathway	0	0	0	2	0
KEGG_alpha_Linolenic_acid_metabolism_Main_Pathway	0,013	-0,063	0,012	22	0,013
KEGG_Alzheimer_s_disease_Main_Pathway	0,000	0,082	0,018	6	0,009
KEGG_Amino_sugar_and_nucleotide_sugar_metabolism_Main_Pathway	0,026	0,062	0,013	43	0,020
KEGG_Aminoacyl_tRNA_biosynthesis_Main_Pathway	-0,115	0,158	-0,005	5	-0,060
KEGG_Amoebiasis_Main_Pathway	-0,043	0,049	-0,014	9	-0,029
KEGG_Amphetamine_addiction_Main_Pathway	0,005	0,035	0,004	34	0,005
KEGG_AMPK_signaling_Main_Pathway	0,046	0,008	-0,015	88	0,015
KEGG_Amyotrophic_lateral_sclerosis_ALS__Main_Pathway	0,025	-0,062	-0,013	27	0,006
KEGG_Antigen_processing_and_presentation_Main_Pathway	-0,007	-0,091	0,051	29	0,022
KEGG_Apoptosis_Main_Pathway	-0,119	0,141	-0,024	43	-0,072
KEGG_Arachidonic_acid_metabolism_Main_Pathway	-0,026	-0,024	0,029	62	0,002
KEGG_Arginine_and_proline_metabolism_Main_Pathway	-0,038	-0,000	-0,026	56	-0,032
KEGG_Arrhythmogenic_right_ventricular_cardiomyopathy_ARVC__Main_Pathway	-0,075	0,141	0,023	6	-0,026
KEGG_Ascorbate_and_aldarate_metabolism_Main_Pathway	-0,002	0,029	-0,006	21	-0,004
KEGG_Asthma_Main_Pathway	-0,011	0,128	-0,143	32	-0,077
KEGG_Autoimmune_thyroid_disease_Main_Pathway	0	0	0	3	0
KEGG_Axon_guidance_Main_Pathway	0,015	-0,040	0,012	95	0,013
KEGG_B_cell_receptor_signaling_Main_Pathway	-0,006	0,106	0,005	58	-0,000
KEGG_Bacterial_invasion_of_epithelial_cells_Main_Pathway	0,017	-0,098	0,019	53	0,018
KEGG_Basal_cell_carcinoma_Main_Pathway	0	0	0	27	0
KEGG_Basal_transcription_factors_Main_Pathway	-0,038	0,000	-0,038	45	-0,038
KEGG_Base_excision_repair_Main_Pathway	-0,022	0,063	0,008	33	-0,007
KEGG_beta_Alanine_metabolism_Main_Pathway	-0,280	0,209	0,015	26	-0,132
KEGG_Bile_secretion_Main_Pathway	0	0	0	8	0
KEGG_Biosynthesis_of_unsaturated_fatty_acids_Main_Pathway	-0,039	-0,069	-0,013	23	-0,026
KEGG_Biotin_metabolism_Main_Pathway	-0,101	0,272	-0,031	2	-0,066
KEGG_Bladder_cancer_Main_Pathway	-0,015	0,138	-0,012	16	-0,013
KEGG_Butanoate_metabolism_Main_Pathway	-0,013	0,038	-0,013	22	-0,013
KEGG_Butirosin_and_neomycin_biosynthesis_Main_Pathway	-0,058	0,004	0,054	5	-0,002
KEGG_Caffeine_metabolism_Main_Pathway	0	0	0	5	0
KEGG_Calcium_signaling_Main_Pathway	-0,001	-0,041	0,018	65	0,009
KEGG_cAMP_signaling_Main_Pathway	0,003	-0,012	0,002	196	0,002
KEGG_Carbohydrate_digestion_and_absorption_Main_Pathway	0	0	0	6	0
KEGG_Cardiac_muscle_contraction_Main_Pathway	0,140	-0,272	0,111	8	0,125

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
KEGG_Cell_adhesion_molecules_CAMs__Main_Pathway	-0,009	-0,072	0,017	28	0,004
KEGG_Cell_cycle_Main_Pathway	0,003	-0,014	0,008	118	0,006
KEGG_Central_carbon_metabolism_in_cancer_Main_Pathway	-0,033	-0,029	0,023	67	-0,005
KEGG_cGMP_PKG_signaling_Main_Pathway	0,003	-0,026	-0,001	143	0,001
KEGG_Chagas_disease_American_trypanosomiasis__Main_Pathway	0,021	-0,023	0,020	52	0,020
KEGG_Chemical_carcinogenesis_Main_Pathway	0,001	-0,017	0,014	35	0,007
KEGG_Chemokine_signaling_Main_Pathway	-0,001	-0,010	0,015	189	0,007
KEGG_Choline_metabolism_in_cancer_Main_Pathway	-0,015	0,010	0,013	55	-0,001
KEGG_Cholinergic_synapse_Main_Pathway	-0,016	0,027	0,004	81	-0,006
KEGG_Chronic_myeloid_leukemia_Main_Pathway	0,002	0,039	-0,001	53	0,001
KEGG_Circadian_entrainment_Main_Pathway	-0,008	0,013	-0,006	97	-0,007
KEGG_Circadian_rhythm_Main_Pathway	0,003	0,047	0,004	17	0,004
KEGG_Citrate_cycle_TCA_cycle__Main_Pathway	-0,092	0,052	-0,027	30	-0,059
KEGG_Cocaine_addiction_Main_Pathway	-0,008	0,033	-0,017	40	-0,013
KEGG_Collecting_duct_acid_secretion_Main_Pathway	-0,034	0,035	-0,007	27	-0,020
KEGG_Colorectal_cancer_Main_Pathway	0,013	0,042	0,001	36	0,007
KEGG_Complement_and_coagulation_cascades_Main_Pathway	0,032	-0,033	0,044	35	0,038
KEGG_Cyanoamino_acid_metabolism_Main_Pathway	-0,017	0,034	0,009	7	-0,004
KEGG_Cysteine_and_methionine_metabolism_Main_Pathway	-0,019	0,095	0,005	24	-0,007
KEGG_Cytokine_cytokine_receptor_interaction_Main_Pathway	0	0	0	25	0
KEGG_Cytosolic_DNA_sensing_Main_Pathway	0,046	-0,116	0,059	18	0,052
KEGG_D_Arginine_and_D_ornithine_metabolism_Main_Pathway	0	0	0	1	0
KEGG_D_Glutamine_and_D_glutamate_metabolism_Main_Pathway	-0,144	-0,220	0,055	4	-0,045
KEGG_Dilated_cardiomyopathy_Main_Pathway	0,066	-0,115	0,052	13	0,059
KEGG_DNA_replication_Main_Pathway	-0,082	0,144	-0,014	36	-0,048
KEGG_Dopaminergic_synapse_Main_Pathway	0,002	-0,026	0,011	125	0,007
KEGG_Dorso_ventral_axis_formation_Main_Pathway	0,027	0,029	-0,017	7	0,005
KEGG_Drug_metabolism_cytochrome_P450_Main_Pathway	0	0	0	36	0
KEGG_Drug_metabolism_other_enzymes_Main_Pathway	-0,019	0,030	-0,007	37	-0,013
KEGG_ECM_receptor_interaction_Main_Pathway	-0,006	-0,101	0,028	88	0,011
KEGG_Endocrine_and_other_factor_regulated_calcium_reabsorption_Main_Pathway	-0,016	-0,047	0,013	34	-0,001
KEGG_Endocytosis_Main_Pathway	-0,011	-0,072	0,029	19	0,009
KEGG_Endometrial_cancer_Main_Pathway	-0,016	0,034	0,002	32	-0,007
KEGG_Epithelial_cell_signaling_in_Helicobacter_pylori_infection_Main_Pathway	-0,013	-0,020	0,049	12	0,018
KEGG_Epstein_Barr_virus_infection_Main_Pathway	0,007	0,056	0,040	55	0,024
KEGG_ErbB_signaling_Main_Pathway	-0,042	-0,050	0,027	87	-0,008
KEGG_Estrogen_signaling_Main_Pathway	-0,007	-0,004	0,005	89	-0,001
KEGG_Ether_lipid_metabolism_Main_Pathway	-0,113	-0,008	0,009	44	-0,052
KEGG_Fanconi_anemia_Main_Pathway	0,019	-0,073	-0,005	38	0,007
KEGG_Fat_digestion_and_absorption_Main_Pathway	-0,043	0,036	-0,032	9	-0,037
KEGG_Fatty_acid_biosynthesis_Main_Pathway	-0,044	0,112	0,011	6	-0,016
KEGG_Fatty_acid_degradation_Main_Pathway	-0,102	0,050	-0,017	28	-0,059
KEGG_Fatty_acid_elongation_Main_Pathway	-0,154	-0,084	-0,059	5	-0,107
KEGG_Fc_epsilon_RI_signaling_Main_Pathway	0,000	0,092	0,007	62	0,004
KEGG_Fc_gamma_R_mediated_phagocytosis_Main_Pathway	-0,043	0,028	0,007	85	-0,018
KEGG_Focal_adhesion_Main_Pathway	0,021	-0,069	0,024	213	0,023
KEGG_Folate_biosynthesis_Main_Pathway	-0,003	0,069	-0,002	10	-0,002
KEGG_FoxO_signaling_Main_Pathway	0,000	-0,002	-0,007	118	-0,004
KEGG_Fructose_and_mannose_metabolism_Main_Pathway	0,002	0,060	0,003	31	0,002
KEGG_GABAergic_synapse_Main_Pathway	-0,014	-0,035	0,017	44	0,002
KEGG_Galactose_metabolism_Main_Pathway	0,021	0,023	0,030	27	0,025
KEGG_Gap_junction_Main_Pathway	0,015	0,012	-0,010	53	0,003
KEGG_Gastric_acid_secretion_Main_Pathway	-0,004	0,024	-0,017	32	-0,010
KEGG_Glioma_Main_Pathway	-0,012	0,021	0,006	54	-0,003
KEGG_Glucagon_signaling_Main_Pathway	-0,012	-0,010	-0,011	76	-0,012
KEGG_Glutamatergic_synapse_Main_Pathway	0,005	0,010	-0,002	91	0,001
KEGG_Glutathione_metabolism_Main_Pathway	-0,045	0,088	0,008	41	-0,018
KEGG_Glycerolipid_metabolism_Main_Pathway	-0,027	0,003	0,018	58	-0,005

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
KEGG_Glycerophospholipid_metabolism_Main_Pathway	-0,036	-0,020	0,016	92	-0,010
KEGG_Glycine_serine_and_threonine_metabolism_Main_Pathway	-0,002	0,001	-0,011	35	-0,007
KEGG_Glycolysis_Gluconeogenesis_Main_Pathway	0,002	-0,014	0,011	67	0,006
KEGG_Glycosaminoglycan_biosynthesis_chondroitin_sulfate_dermatan_sulfate_Main_Pathway	0,007	0,018	-0,031	11	-0,012
KEGG_Glycosaminoglycan_biosynthesis_heparan_sulfate_heparin_Main_Pathway	-0,006	0,028	-0,018	28	-0,012
KEGG_Glycosaminoglycan_biosynthesis_keratan_sulfate_Main_Pathway	-0,006	0,003	0,008	15	0,001
KEGG_Glycosaminoglycan_degradation_Main_Pathway	-0,042	0,143	-0,056	19	-0,049
KEGG_Glycosphingolipid_biosynthesis_ganglio_series_Main_Pathway	-0,027	0,028	-0,007	15	-0,017
KEGG_Glycosphingolipid_biosynthesis_globo_series_Main_Pathway	-0,060	0,097	-0,051	13	-0,055
KEGG_Glycosphingolipid_biosynthesis_lacto_and_neolacto_series_Main_Pathway	0,005	-0,009	0,002	26	0,003
KEGG_Glycosylphosphatidylinositol_GPI_anchor_biosynthesis_Main_Pathway	-0,021	0,003	-0,006	23	-0,014
KEGG_Glyoxylate_and_dicarboxylate_metabolism_Main_Pathway	-0,028	-0,026	-0,010	16	-0,019
KEGG_GnRH_signaling_Main_Pathway	-0,016	-0,018	0,008	72	-0,004
KEGG_Graft_versus_host_disease_Main_Pathway	0	0	0	3	0
KEGG_Hedgehog_signaling_Main_Pathway	0,009	0,014	0,017	42	0,013
KEGG_Hematopoietic_cell_lineage_Main_Pathway	-0,000	-0,032	0,016	89	0,008
KEGG_Hepatitis_B_Main_Pathway	0,007	-0,055	0,026	61	0,017
KEGG_Hepatitis_C_Main_Pathway	0,015	-0,039	0,032	47	0,023
KEGG_Herpes_simplex_infection_Main_Pathway	-0,019	0,031	-0,025	44	-0,022
KEGG_HIF_1_signaling_Main_Pathway	-0,101	-0,014	0,025	85	-0,038
KEGG_Hippo_signaling_Main_Pathway	-0,006	0,006	-0,015	110	-0,010
KEGG_Histidine_metabolism_Main_Pathway	-0,034	-0,046	0,023	22	-0,006
KEGG_Homologous_recombination_Main_Pathway	-0,020	0,031	-0,038	28	-0,029
KEGG_HTLV_I_infection_Main_Pathway	0,008	-0,011	-0,003	97	0,003
KEGG_Huntington_s_disease_Main_Pathway	0,015	-0,095	0,033	21	0,024
KEGG_Hypertrophic_cardiomyopathy_HCM__Main_Pathway	0,066	-0,115	0,052	13	0,059
KEGG_Inflammatory_bowel_disease_IBD__Main_Pathway	0,012	-0,031	0,019	14	0,016
KEGG_Inflammatory_mediator_regulation_of_TRP_channels_Main_Pathway	-0,004	-0,016	0,003	89	-0,001
KEGG_Influenza_A_Main_Pathway	-0,034	0,069	-0,027	66	-0,031
KEGG_Inositol_phosphate_metabolism_Main_Pathway	-0,067	0,078	-0,004	61	-0,036
KEGG_Insulin_secretion_Main_Pathway	-0,007	-0,013	0,003	55	-0,002
KEGG_Insulin_signaling_Main_Pathway	-0,062	0,030	0,006	72	-0,028
KEGG_Intestinal_immune_network_for_IgA_production_Main_Pathway	0	0	0	5	0
KEGG_Jak_STAT_signaling_Main_Pathway	0,006	-0,034	0,009	156	0,008
KEGG_Legionellosis_Main_Pathway	-0,016	0,050	-0,007	14	-0,012
KEGG_Leishmaniasis_Main_Pathway	0,022	-0,028	0,022	49	0,022
KEGG_Leukocyte_transendothelial_migration_Main_Pathway	0,005	-0,021	0,008	78	0,006
KEGG_Linoleic_acid_metabolism_Main_Pathway	0,005	-0,029	0,006	29	0,006
KEGG_Lipoic_acid_metabolism_Main_Pathway	0,043	0,123	-0,017	3	0,013
KEGG_Long_term_depression_Main_Pathway	-0,012	0,076	0,007	59	-0,003
KEGG_Long_term_potentiation_Main_Pathway	-0,014	0,035	0,001	67	-0,006
KEGG_Lysine_biosynthesis_Main_Pathway	-0,027	0,077	-0,045	2	-0,036
KEGG_Lysine_degradation_Main_Pathway	-0,062	-0,048	-0,016	16	-0,039
KEGG_Lysosome_Main_Pathway	-0,052	0,080	-0,031	122	-0,042
KEGG_Malaria_Main_Pathway	-0,020	0,062	-0,009	4	-0,015
KEGG_MAPK_signaling_Main_Pathway	0,003	-0,030	0,013	244	0,008
KEGG_Maturity_onset_diabetes_of_the_young_Main_Pathway	0	0	0	4	0
KEGG_Measles_Main_Pathway	0,019	-0,029	-0,003	23	0,008
KEGG_Melanogenesis_Main_Pathway	-0,008	0,153	-0,025	14	-0,016
KEGG_Melanoma_Main_Pathway	-0,004	-0,005	-0,000	58	-0,002
KEGG_Metabolism_of_xenobiotics_by_cytochrome_P450_Main_Pathway	-0,014	0,021	0,005	72	-0,005
KEGG_MicroRNAs_in_cancer_Main_Pathway	0,012	-0,005	0,002	153	0,007
KEGG_Mineral_absorption_Main_Pathway	-0,089	0,100	0,077	5	-0,006
KEGG_Mismatch_repair_Main_Pathway	-0,086	0,187	-0,026	23	-0,056
KEGG_Morphine_addiction_Main_Pathway	-0,001	-0,020	-0,001	52	-0,001
KEGG_mRNA_surveillance_Main_Pathway	0,001	0,031	-0,002	40	-0,000

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
KEGG_mTOR_signaling_Main_Pathway	0,108	-0,008	-0,023	49	0,043
KEGG_Mucin_type_O_Glycan_biosynthesis_Main_Pathway	-0,003	0,053	-0,007	31	-0,005
KEGG_N_Glycan_biosynthesis_Main_Pathway	-0,153	0,057	0,007	48	-0,073
KEGG_Natural_killer_cell_mediated_cytotoxicity_Main_Pathway	-0,010	0,063	-0,011	105	-0,011
KEGG_Neuroactive_ligand_receptor_interaction_Main_Pathway	0,001	-0,008	0,001	275	0,001
KEGG_Neurotrophin_signaling_Main_Pathway	-0,006	0,015	0,002	116	-0,002
KEGG_NF_kappa_B_signaling_Main_Pathway	-0,008	-0,005	0,026	72	0,009
KEGG_Nicotinate_and_nicotinamide_metabolism_Main_Pathway	-0,017	0,027	0,035	28	0,009
KEGG_Nicotine_addiction_Main_Pathway	0	0	0	40	0
KEGG_Nitrogen_metabolism_Main_Pathway	-0,013	-0,116	-0,063	4	-0,038
KEGG_NOD_like_receptor_signaling_Main_Pathway	0,025	-0,034	0,026	42	0,026
KEGG_Non_alcoholic_fatty_liver_disease_NAFLD__Main_Pathway	0,013	0,002	-0,021	28	-0,004
KEGG_Non_homologous_end_joining_Main_Pathway	-0,000	0,006	-0,016	13	-0,008
KEGG_Non_small_cell_lung_cancer_Main_Pathway	-0,023	0,042	0,004	43	-0,010
KEGG_Notch_signaling_Main_Pathway	0,011	-0,027	0,034	48	0,023
KEGG_Nucleotide_excision_repair_Main_Pathway	-0,030	0,047	0,009	47	-0,010
KEGG_Olfactory_transduction_Main_Pathway	-0,000	0,000	-0,000	408	-0,000
KEGG_One_carbon_pool_by_folate_Main_Pathway	0,024	-0,028	0,025	20	0,024
KEGG_Oocyte_meiosis_Main_Pathway	0,018	-0,010	-0,005	90	0,006
KEGG_Osteoclast_differentiation_Main_Pathway	-0,010	0,019	0,015	109	0,002
KEGG_Other_glycan_degradation_Main_Pathway	-0,056	0,138	-0,060	18	-0,058
KEGG_Other_types_of_O_glycan_biosynthesis_Main_Pathway	-0,048	-0,011	0,009	31	-0,020
KEGG_Ovarian_steroidogenesis_Main_Pathway	-0,005	-0,026	-0,003	36	-0,004
KEGG_Oxidative_phosphorylation_Main_Pathway	-0,113	0,062	-0,014	133	-0,064
KEGG_Oxytocin_signaling_Main_Pathway	-0,003	-0,017	0,010	151	0,004
KEGG_p53_signaling_Main_Pathway	-0,008	-0,005	0,019	48	0,005
KEGG_Pancreatic_cancer_Main_Pathway	-0,001	0,035	-0,009	40	-0,005
KEGG_Pancreatic_secretion_Main_Pathway	0,002	-0,059	0,021	17	0,012
KEGG_Pantothenate_and_CoA_biosynthesis_Main_Pathway	0,011	0,109	-0,023	12	-0,006
KEGG_Parkinson_s_disease_Main_Pathway	-0,027	0,031	-0,034	12	-0,030
KEGG_Pathogenic_Escherichia_coli_infection_Main_Pathway	0,027	-0,033	0,005	22	0,016
KEGG_Pathways_in_cancer_Main_Pathway	0,011	-0,074	0,027	234	0,019
KEGG_Pentose_and_glucuronate_interconversions_Main_Pathway	-0,002	0,079	-0,001	30	-0,002
KEGG_Pentose_phosphate_Main_Pathway	0,031	0,002	0,035	29	0,033
KEGG_Peroxisome_Main_Pathway	-0,115	0,022	0,008	82	-0,054
KEGG_Pertussis_Main_Pathway	-0,006	0,041	0,006	25	-0,000
KEGG_Phagosome_Main_Pathway	0,008	-0,048	0,006	27	0,007
KEGG_Phenylalanine_metabolism_Main_Pathway	-0,023	-0,006	-0,000	17	-0,011
KEGG_Phenylalanine_tyrosine_and_tryptophan_biosynthesis_Main_Pathway	-0,067	0,127	-0,079	5	-0,073
KEGG_Phosphatidylinositol_signaling_system_Main_Pathway	0,004	-0,005	0,010	77	0,007
KEGG_Phototransduction_Main_Pathway	0,003	0,099	-0,027	18	-0,012
KEGG_PI3K_Akt_signaling_Main_Pathway	-0,017	-0,003	0,009	225	-0,004
KEGG_Platelet_activation_Main_Pathway	0,005	0,033	0,006	124	0,006
KEGG_Porphyrin_and_chlorophyll_metabolism_Main_Pathway	-0,021	-0,025	0,008	15	-0,007
KEGG_PPAR_signaling_Main_Pathway	-0,030	0,012	-0,028	59	-0,029
KEGG_Primary_bile_acid_biosynthesis_Main_Pathway	-0,051	-0,015	-0,021	17	-0,036
KEGG_Primary_immunodeficiency_Main_Pathway	-0,005	-0,025	0,025	36	0,010
KEGG_Prion_diseases_Main_Pathway	-0,028	0,050	-0,016	20	-0,022
KEGG_Progesterone_mediated_oocyte_maturation_Main_Pathway	0,021	0,034	-0,039	23	-0,009
KEGG_Prolactin_signaling_Main_Pathway	0,013	0,010	0,009	64	0,011
KEGG_Propanoate_metabolism_Main_Pathway	-0,140	0,116	-0,010	23	-0,075
KEGG_Prostate_cancer_Main_Pathway	-0,012	0,025	0,009	78	-0,001
KEGG_Proteasome_Main_Pathway	-0,022	0,048	-0,014	44	-0,018
KEGG_Protein_digestion_and_absorption_Main_Pathway	-0,005	-0,041	0,011	89	0,003
KEGG_Protein_export_Main_Pathway	-0,070	-0,019	-0,009	23	-0,039
KEGG_Protein_processing_in_endoplasmic_reticulum_Main_Pathway	0,052	-0,026	0,007	26	0,029
KEGG_Proteoglycans_in_cancer_Main_Pathway	-0,029	-0,038	0,020	166	-0,005
KEGG_Proximal_tubule_bicarbonate_reclamation_Main_Pathway	-0,144	-0,220	0,055	4	-0,045

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
KEGG_Purine_metabolism_Main_Pathway	-0,006	0,032	0,003	168	-0,002
KEGG_Pyrimidine_metabolism_Main_Pathway	-0,025	0,064	0,001	102	-0,012
KEGG_Pyruvate_metabolism_Main_Pathway	-0,016	0,004	-0,017	40	-0,017
KEGG_Rap1_signaling_Main_Pathway	0,001	-0,028	0,005	199	0,003
KEGG_Ras_signaling_Main_Pathway	-0,008	-0,019	0,006	223	-0,001
KEGG_Regulation_of_actin_cytoskeleton_Main_Pathway	0,012	0,006	-0,011	165	0,000
KEGG_Regulation_of_autophagy_Main_Pathway	0,015	0,057	-0,004	10	0,005
KEGG_Regulation_of_lipolysis_in_adipocytes_Main_Pathway	-0,002	0,021	-0,014	32	-0,008
KEGG_Renal_cell_carcinoma_Main_Pathway	-0,004	-0,054	0,008	25	0,002
KEGG_Renin_angiotensin_system_Main_Pathway	-0,025	0,002	-0,005	17	-0,015
KEGG_Retinol_metabolism_Main_Pathway	-0,009	0,001	-0,003	65	-0,006
KEGG_Retrograde_endocannabinoid_signaling_Main_Pathway	-0,007	-0,022	0,015	51	0,004
KEGG_Rheumatoid_arthritis_Main_Pathway	0	0	0	4	0
KEGG_Riboflavin_metabolism_Main_Pathway	0,087	-0,124	0,075	3	0,081
KEGG_Ribosome_biogenesis_in_eukaryotes_Main_Pathway	-0,020	-0,002	-0,033	87	-0,026
KEGG_Ribosome_Main_Pathway	-0,045	0,087	0,007	137	-0,019
KEGG_RIG_I_like_receptor_signaling_Main_Pathway	0,029	-0,021	0,017	45	0,023
KEGG_RNA_degradation_Main_Pathway	-0,032	0,122	-0,023	77	-0,028
KEGG_RNA_polymerase_Main_Pathway	-0,018	0,015	0,007	32	-0,006
KEGG_RNA_transport_Main_Pathway	-0,032	0,020	-0,028	51	-0,030
KEGG_Salivary_secretion_Main_Pathway	0	0	0	15	0
KEGG_Salmonella_infection_Main_Pathway	0,030	-0,045	0,011	44	0,021
KEGG_Selenocompound_metabolism_Main_Pathway	0,000	0,032	-0,035	14	-0,018
KEGG_Serotonergic_synapse_Main_Pathway	-0,008	-0,050	0,017	63	0,005
KEGG_Shigellosis_Main_Pathway	0,026	-0,077	0,013	25	0,020
KEGG_Signaling_pathways_regulating_pluripotency_of_stem_cells_Main_Pathway	-0,196	0,805	-0,020	5	-0,108
KEGG_Small_cell_lung_cancer_Main_Pathway	0,035	-0,181	0,068	57	0,052
KEGG_SNARE_interactions_in_vesicular_transport_Main_Pathway	-0,014	-0,166	0,009	8	-0,003
KEGG_Sphingolipid_metabolism_Main_Pathway	-0,036	-0,026	0,005	47	-0,016
KEGG_Sphingolipid_signaling_Main_Pathway	-0,017	0,013	0,009	98	-0,004
KEGG_Spliceosome_Main_Pathway	-0,039	0,116	-0,035	132	-0,037
KEGG_Staphylococcus_aureus_infection_Main_Pathway	0,029	-0,033	0,066	20	0,047
KEGG_Starch_and_sucrose_metabolism_Main_Pathway	0,018	0,012	-0,004	55	0,007
KEGG_Steroid_biosynthesis_Main_Pathway	-0,007	-0,236	0,062	17	0,027
KEGG_Steroid_hormone_biosynthesis_Main_Pathway	-0,006	-0,004	-0,009	51	-0,008
KEGG_Sulfur_metabolism_Main_Pathway	-0,056	-0,135	-0,083	9	-0,069
KEGG_Sulfur_relay_system_Main_Pathway	-0,070	0,060	-0,014	6	-0,042
KEGG_Synaptic_vesicle_cycle_Main_Pathway	-0,004	-0,006	0,045	7	0,020
KEGG_Synthesis_and_degradation_of_ketone_bodies_Main_Pathway	0,021	0,060	-0,023	10	-0,001
KEGG_Systemic_lupus_erythematosus_Main_Pathway	0,064	-0,072	0,147	9	0,105
KEGG_T_cell_receptor_signaling_Main_Pathway	-0,010	0,038	0,013	92	0,001
KEGG_Taste_transduction_Main_Pathway	-0,031	0,027	-0,025	14	-0,028
KEGG_Taurine_and_hypotaurine_metabolism_Main_Pathway	0,009	0,010	0,020	11	0,015
KEGG_Terpenoid_backbone_biosynthesis_Main_Pathway	0,033	-0,023	0,003	21	0,018
KEGG_TGF_beta_signaling_Main_Pathway	-0,083	-0,006	0,010	65	-0,037
KEGG_Thiamine_metabolism_Main_Pathway	0,065	-0,063	0,025	3	0,045
KEGG_Thyroid_cancer_Main_Pathway	-0,011	0,234	-0,042	15	-0,026
KEGG_Thyroid_hormone_signaling_Main_Pathway	0,016	-0,005	0,018	69	0,017
KEGG_Thyroid_hormone_synthesis_Main_Pathway	0	0	0	17	0
KEGG_Tight_junction_Main_Pathway	0,010	-0,044	0,022	124	0,016
KEGG_TNF_signaling_Main_Pathway	0,018	-0,025	0,036	54	0,027
KEGG_Toll_like_receptor_signaling_Main_Pathway	0,017	-0,027	0,022	97	0,019
KEGG_Toxoplasmosis_Main_Pathway	0,002	0,030	-0,016	34	-0,007
KEGG_Transcriptional_misregulation_in_cancer_Main_Pathway	-0,009	-0,014	0,008	179	-0,000
KEGG_Tryptophan_metabolism_Main_Pathway	-0,027	0,008	-0,005	31	-0,016
KEGG_Tuberculosis_Main_Pathway	-0,012	0,023	-0,003	48	-0,007
KEGG_Type_I_diabetes_mellitus_Main_Pathway	-0,017	0,076	-0,101	45	-0,059
KEGG_Type_II_diabetes_mellitus_Main_Pathway	0	0	0	10	0

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
KEGG_Tyrosine_metabolism_Main_Pathway	-0,006	-0,004	-0,013	25	-0,010
KEGG_Ubiquinone_and_other_terpenoid_quinone_biosynthesis_Main_Pathway	-0,061	0,106	-0,016	4	-0,039
KEGG_Ubiquitin_mediated_proteolysis_Main_Pathway	0,011	0,010	0,010	137	0,010
KEGG_Valine_leucine_and_isoleucine_biosynthesis_Main_Pathway	0,058	-0,176	0,061	4	0,060
KEGG_Valine_leucine_and_isoleucine_degradation_Main_Pathway	-0,120	0,081	-0,025	47	-0,072
KEGG_Vascular_smooth_muscle_contraction_Main_Pathway	0,161	-0,144	0,053	6	0,107
KEGG_Vasopressin_regulated_water_reabsorption_Main_Pathway	-0,025	0,040	-0,017	21	-0,021
KEGG_VEGF_signaling_Main_Pathway	0,011	0,024	0,002	61	0,006
KEGG_Vibrio_cholerae_infection_Main_Pathway	-0,055	0,085	-0,030	10	-0,043
KEGG_Viral_carcinogenesis_Main_Pathway	0,003	0,009	0,017	206	0,010
KEGG_Viral_myocarditis_Main_Pathway	0,015	0,048	-0,033	5	-0,009
KEGG_Vitamin_B6_metabolism_Main_Pathway	-0,024	0,111	-0,000	5	-0,012
KEGG_Vitamin_digestion_and_absorption_Main_Pathway	-0,014	0,013	0,007	24	-0,003
KEGG_Wnt_signaling_Main_Pathway	-0,005	0,004	0,015	112	0,005
ketogenesis	0,014	0,100	-0,057	5	-0,021
ketolysis	-0,004	0,192	-0,066	4	-0,035
lactate_fermentation_reoxidation_of_cytosolic_NADH	0	0	0	3	0
lactose_degradation_III	-0,171	0,267	-0,152	1	-0,161
lanosterol_biosynthesis	-0,063	0,152	-0,057	1	-0,060
L-carnitine_biosynthesis	-0,031	-0,004	-0,017	3	-0,024
L-cysteine_degradation_I	0	0	0	2	0
L-cysteine_degradation_II	-0,006	0,064	-0,122	2	-0,064
L-dopa_degradation	0,093	-0,431	-0,024	1	0,034
L-dopachrome_biosynthesis	0	0	0	1	0
leucine_degradation	-0,120	0,026	-0,060	12	-0,090
leukotriene_biosynthesis	0,007	0,008	-0,005	7	0,001
L-glutamine_tRNA_biosynthesis	-0,154	0,213	-0,069	2	-0,111
lipoate_biosynthesis_and_incorporation	0,064	0,184	-0,026	2	0,019
lipoate_salvage	0	0	0	1	0
lipoxin_biosynthesis	0	0	0	3	0
Lipoxins_Influence_on_Cell_Growth_and_Proliferation	-0,031	-0,049	0,014	41	-0,009
Lipoxins_Influence_on_Neutrophil_Chemotaxis	0,054	-0,124	0,049	8	0,052
L-kynurenine_degradation	-0,014	-0,047	-0,004	12	-0,009
L-serine_degradation	0,232	-0,703	0,244	1	0,238
lysine_degradation_I_saccharopine_pathway	-0,051	-0,270	0,013	4	-0,019
lysine_degradation_II_pipecolate_pathway	-0,021	-0,110	-0,000	6	-0,010
malate-aspartate_shuttle	-0,094	0,074	-0,105	4	-0,099
MAPK_Family_Pathway	-0,003	-0,025	0,012	294	0,005
MAPK_Family_Pathway_Chromatin_Remodelling	0,006	0,007	-0,001	22	0,003
MAPK_Family_Pathway_Cytoskeleton	0,042	-0,055	0,055	8	0,049
MAPK_Family_Pathway_Gene_Expression_via_ATF2_JUN_ELK1_NFKB2_CREB3	0,039	-0,160	0,069	31	0,054
MAPK_Family_Pathway_Translation	0,025	0,024	-0,008	8	0,009
MAPK_Signaling_Pathway	-0,001	-0,038	0,014	533	0,007
MAPK_Signaling_Pathway_Cell_Motility_Inflammation_Apoptosis_Osmoregulation	-0,032	0,072	-0,001	18	-0,017
MAPK_Signaling_Pathway_Cell_Survival	0	0	0	4	0
MAPK_Signaling_Pathway_Gene_Expression_Apoptosis_Inflammation_Tumorigenesis_via_MYC_HSF1_STAT2	0,045	-0,189	0,059	28	0,052
MAPK_Signaling_Pathway_Gene_Expression_Cell_Proliferation_Cell_Survival_Tumorigenesis_Differentiation_Development_via_PXN_CREB3_RPS6KA5_RPS6KA6	-0,012	-0,021	0,021	53	0,004
melatonin_degradation_I	-0,095	0,208	-0,037	11	-0,066
melatonin_degradation_II	0	0	0	1	0
methionine_degradation	-0,037	0,127	-0,004	4	-0,021
methionine_salvage	0,018	0,006	0,012	3	0,015
methylglyoxal_degradation_I	0,086	-0,088	-0,053	3	0,016
methylglyoxal_degradation_III	0,189	-0,081	0,165	3	0,177
methylglyoxal_degradation_VI	0	0	0	1	0
methylthiopropionate_biosynthesis	-0,242	0,437	0,084	1	-0,079
mevalonate_pathway	0,085	-0,068	0,017	10	0,051

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
mineralocorticoid_biosynthesis	0	0	0	3	0
Mismatch_Repair_in_Eukaryotes_Pathway	-0,103	0,226	-0,017	19	-0,060
Mitochondrial_Apoptosis_Pathway	0,052	0,022	-0,012	98	0,020
Mitochondrial_Apoptosis_Pathway_Apoptosis	0,017	0,000	-0,017	19	-0,000
Mitochondrial_Apoptosis_Pathway_Depolarization	-0,077	0,169	-0,034	7	-0,055
Mitochondrial_Apoptosis_Pathway_DNA_Fragmentation	0,020	-0,039	-0,029	5	-0,005
Mitochondrial_Apoptosis_Pathway_Gene_Expression_via_TP53	-0,090	0,197	-0,039	6	-0,064
mitochondrial_L-carnitine_shuttle	-0,175	0,242	-0,056	5	-0,116
Mitosis_Initiation	-0,025	0,092	-0,022	22	-0,023
molybdenum_cofactor_biosynthesis	-0,048	-0,079	0,062	4	0,007
mRNA_capping	-0,023	0,026	-0,026	4	-0,024
mTOR_Pathway	-0,015	-0,031	0,017	351	0,001
mTOR_Pathway_Actin_Organization	-0,023	-0,066	0,005	50	-0,009
mTOR_Pathway_Autophagy	0,005	0,050	-0,024	4	-0,009
mTOR_Pathway_Cap-dependent_Translation	-0,600	0,151	0,078	8	-0,261
mTOR_Pathway_Inflammation_Stress_Resistance	0,078	-0,344	0,146	9	0,112
mTOR_Pathway_Lipid_Synthesis	-0,021	-0,072	0,011	48	-0,005
mTOR_Pathway_Metabolism_Stress_Response_and_Apoptosis	0,013	-0,038	0,021	6	0,017
mTOR_Pathway_Microtubule_Organization	-0,021	-0,085	0,014	45	-0,004
mTOR_Pathway_Mitochondria_Proliferation_and_Function	-0,047	0,036	0,015	4	-0,016
mTOR_Pathway_mRNA_Biogenesis	-1,563	0,006	0,102	3	-0,730
mTOR_Pathway_Ribosome_Biogenesis	-1,554	0,091	0,126	3	-0,714
mTOR_Pathway_Translation_Elongation	-0,312	0,116	-0,015	17	-0,163
mTOR_Pathway_VEGF_Pathway	-0,002	0,022	0,004	3	0,001
mucin_core_1_and_core_2_iOi-glycosylation	0,013	0,034	-0,002	28	0,005
NAD_biosynthesis_from_2-amino-3-carboxymuconate_semialdehyde	-0,086	-0,157	0,001	5	-0,043
NAD_ide_novoi_biosynthesis	-0,036	-0,065	0,000	12	-0,018
NAD_phosphorylation_and_dephosphorylation	-0,041	0,206	-0,030	2	-0,036
NAD_salvage	0,004	-0,117	-0,056	4	-0,026
NADH_repair	-0,023	0,055	-0,008	3	-0,015
NCI_a4b7_Integrin_signaling_Main_Pathway	-0,090	0,134	-0,045	6	-0,067
NCI_a6b1_and_a6b4_Integrin_signaling_Main_Pathway	-0,128	-0,158	0,036	43	-0,046
NCI_a6b1_and_a6b4_Integrin_signaling_Pathway_(apoptosis)	-0,125	-0,272	0,015	8	-0,055
NCI_a6b1_and_a6b4_Integrin_signaling_Pathway_(cell_migration)	-0,125	-0,272	0,015	8	-0,055
NCI_a6b1_and_a6b4_Integrin_signaling_Pathway_(hemidesmosome_assembly)	-0,432	0,024	-0,160	1	-0,296
NCI_a6b1_and_a6b4_Integrin_signaling_Pathway_(Pathway_degradation_of_ ITGA6)	-0,125	-0,272	0,015	8	-0,055
NCI_a6b1_and_a6b4_Integrin_signaling_Pathway_(proteasomal_ubiquitin_ dependent_protein_catabolic_process)	-0,166	-0,162	0,001	4	-0,082
NCI_a6b1_and_a6b4_Integrin_signaling_Pathway_(Tumor_Cell_Invasion)	-0,163	0,045	-0,025	5	-0,094
NCI_ALK1_signaling_events_Main_Pathway	0,036	-0,109	0,059	24	0,047
NCI_ALK1_signaling_events_Pathway_(endothelial_cell_migration)	0,110	-0,079	0,062	7	0,086
NCI_ALK1_signaling_events_Pathway_(endothelial_cell_proliferation)	0,088	-0,064	0,050	10	0,069
NCI_ALK1_signaling_events_Pathway_(sprouting_angiogenesis)	0,189	-0,136	0,106	6	0,147
NCI_ALK2_signaling_events_Main_Pathway	0,063	0,013	0,022	10	0,042
NCI_Alpha_synuclein_signaling_Main_Pathway	0,023	0,170	-0,002	30	0,011
NCI_Alpha_synuclein_signaling_Pathway_(cell_death)	0,024	0,293	-0,009	21	0,007
NCI_Alpha_synuclein_signaling_Pathway_(neuron_apoptosis)	0,025	0,234	0,003	22	0,014
NCI_Alpha_synuclein_signaling_Pathway_(Pathway_degradation_of_SNCA)	-0,019	-0,082	0,009	4	-0,005
NCI_Alpha_synuclein_signaling_Pathway_(Pathway_negative_regulation_of_ transcription_via_SNCA)	-0,027	-0,009	-0,042	3	-0,035
NCI_Alpha_synuclein_signaling_Pathway_(Pathway_negative_regulation_of_ transcription_via_TOR1A_SNCA_STUB1_FKBP1A)	0,024	0,293	-0,009	21	0,007
NCI_Alpha_synuclein_signaling_Pathway_(Pathway_positive_regulation_of_ gene_specific_transcription_via_SNCA)	-0,027	-0,009	-0,042	3	-0,035
NCI_Alpha_synuclein_signaling_Pathway_(Pathway_positive_regulation_of_ gene_specific_transcription_via_TOR1A_SNCA_FKBP1A_STUB1)	0,024	0,293	-0,009	21	0,007
NCI_Alpha_synuclein_signaling_Pathway_(proteasomal_ubiquitin_dependent_ protein_catabolic_process)	0,024	0,293	-0,009	21	0,007
NCI_Alpha_synuclein_signaling_Pathway_(protein_targeting_to_lysosome)	0,024	0,293	-0,009	21	0,007
NCI_Alpha4_beta1_integrin_signaling_events_Main_Pathway	-0,006	-0,040	0,031	20	0,013

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Alpha4_beta1_integrin_signaling_events_Pathway_(cell_adhesion)	0,044	-0,102	0,025	12	0,035
NCI_Alpha4_beta1_integrin_signaling_events_Pathway_(cell_migration)	-0,022	-0,042	0,022	10	-0,000
NCI_Alpha4_beta1_integrin_signaling_events_Pathway_(lamellipodium_assembly)	-0,000	0,036	0,031	8	0,015
NCI_Alpha6_beta4_integrin_ligand_interactions_Main_Pathway	-0,050	-0,211	0,050	11	-0,000
NCI_Alpha9_beta1_integrin_signaling_events_Main_Pathway	0,060	-0,144	0,024	21	0,042
NCI_Alpha9_beta1_integrin_signaling_events_Pathway_(cell_migration)	0,018	-0,168	0,006	8	0,012
NCI_AlphaE_beta7_integrin_cell_surface_interactions_Main_Pathway	-0,170	0,209	-0,045	3	-0,108
NCI_Alternative_NF_kappaB_Main_Pathway	0,120	-0,435	0,208	5	0,164
NCI_Alternative_NF_kappaB_Pathway_(regulation_of_B_cell_activation)	0,120	-0,435	0,208	5	0,164
NCI_amb2_Integrin_signaling_Main_Pathway	0,031	-0,086	0,027	30	0,029
NCI_amb2_Integrin_signaling_Pathway_(actin_filament_polymerization)	-0,011	0,054	-0,021	5	-0,016
NCI_amb2_Integrin_signaling_Pathway_(dendritic_cell_antigen_processing_and_presentation)	0,103	-0,207	0,094	7	0,098
NCI_amb2_Integrin_signaling_Pathway_(leukocyte_adhesion)	0,063	-0,116	0,049	9	0,056
NCI_amb2_Integrin_signaling_Pathway_(phagocytosis_triggered_by_activation_of_immune_response_cell_surface_activating_receptor)	0,103	-0,207	0,094	7	0,098
NCI_amb2_Integrin_signaling_Pathway_(positive_regulation_of_phagocytosis)	0,069	-0,196	0,086	9	0,078
NCI_Angiopoietin_receptor_Tie2_mediated_signaling_Main_Pathway	-0,133	-0,007	0,015	39	-0,059
NCI_Angiopoietin_receptor_Tie2_mediated_signaling_Pathway_(chemokinesis)	-0,034	0,052	-0,015	8	-0,024
NCI_Angiopoietin_receptor_Tie2_mediated_signaling_Pathway_(MAPKKK_cascade)	-0,031	0,038	-0,005	6	-0,018
NCI_Angiopoietin_receptor_Tie2_mediated_signaling_Pathway_(negative_regulation_of_caspase_activity)	0,006	-0,030	0,021	8	0,013
NCI_Angiopoietin_receptor_Tie2_mediated_signaling_Pathway_(tube_development)	-0,001	0,049	0,028	3	0,014
NCI_Angiopoietin_receptor_Tie2_mediated_signaling_Pathway_(vasculogenesis)	0,014	-0,070	0,056	4	0,035
NCI_AP_1_transcription_factor_network_Main_Pathway	-0,068	0,012	0,081	22	0,007
NCI_Arf1_Main_Pathway	0,006	-0,075	0,034	20	0,020
NCI_Arf1_Pathway_(actin_filament_polymerization)	-0,009	0,036	-0,041	6	-0,025
NCI_Arf6_downstream_Main_Pathway	0,005	0,006	0,018	15	0,012
NCI_Arf6_downstream_Pathway_(actin_filament_bundle_formation)	0,037	-0,107	0,026	2	0,031
NCI_Arf6_downstream_Pathway_(cortical_actin_cytoskeleton_organization)	-0,126	0,170	-0,042	5	-0,084
NCI_Arf6_downstream_Pathway_(lamellipodium_assembly)	-0,126	0,170	-0,042	5	-0,084
NCI_Arf6_downstream_Pathway_(liver_development)	-0,077	0,071	-0,132	1	-0,105
NCI_Arf6_downstream_Pathway_(myoblast_fusion)	-0,077	0,071	-0,132	1	-0,105
NCI_Arf6_downstream_Pathway_(regulation_of_axonogenesis)	0,063	-0,145	0,079	4	0,071
NCI_Arf6_downstream_Pathway_(regulation_of_epithelial_cell_migration)	-0,077	0,071	-0,132	1	-0,105
NCI_Arf6_downstream_Pathway_(ruffle_organization)	0,063	-0,145	0,079	4	0,071
NCI_Arf6_downstream_Pathway_(substrate_adhesion_dependent_cell_spreading)	-0,077	0,071	-0,132	1	-0,105
NCI_Arf6_downstream_Pathway_(Tumor_Cell_Invasion)	0,025	-0,004	-0,042	3	-0,008
NCI_Arf6_signaling_events_Main_Pathway	-0,011	-0,169	0,037	35	0,013
NCI_Arf6_trafficking_events_Main_Pathway	-0,021	-0,019	0,027	44	0,003
NCI_Arf6_trafficking_events_Pathway_(calcium_ion_dependent_exocytosis)	-0,068	0,119	-0,013	12	-0,040
NCI_Arf6_trafficking_events_Pathway_(cell_adhesion_mediated_by_integrin)	0,025	-0,205	0,079	14	0,052
NCI_Arf6_trafficking_events_Pathway_(clathrin_coat_assembly)	-0,058	0,087	-0,010	13	-0,034
NCI_Arf6_trafficking_events_Pathway_(clathrin_independent_pinocytosis)	-0,077	0,071	-0,132	1	-0,105
NCI_Arf6_trafficking_events_Pathway_(endocytosis)	-0,078	0,254	-0,024	3	-0,051
NCI_Arf6_trafficking_events_Pathway_(membrane_fusion)	-0,083	0,083	-0,029	5	-0,056
NCI_Arf6_trafficking_events_Pathway_(positive_regulation_of_endocytosis)	-0,077	0,071	-0,132	1	-0,105
NCI_Arf6_trafficking_events_Pathway_(positive_regulation_of_phagocytosis)	-0,038	0,036	-0,066	2	-0,052
NCI_Arf6_trafficking_events_Pathway_(receptor_recycling)	-0,077	0,071	-0,132	1	-0,105
NCI_Arf6_trafficking_events_Pathway_(regulation_of_calcium_dependent_cell_cell_adhesion)	-0,066	0,168	-0,001	6	-0,034
NCI_Arf6_trafficking_events_Pathway_(substrate_adhesion_dependent_cell_spreading)	-0,042	-0,006	-0,016	8	-0,029
NCI_ATF_2_transcription_factor_network_Main_Pathway	-0,001	0,011	0,022	41	0,010
NCI_ATM_Main_Pathway	-0,013	0,043	0,002	32	-0,005
NCI_ATM_Pathway_(apoptosis)	-0,061	0,260	-0,074	3	-0,068
NCI_ATM_Pathway_(chromatin_remodeling)	0,007	0,057	0,022	9	0,014

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_ATM_Pathway_(double_strand_break_repair_via_nonhomologous_end_joining)	0,018	0,023	0,017	9	0,017
NCI_ATM_Pathway_(G1_S_transition_checkpoint)	0,006	0,012	0,010	21	0,008
NCI_ATM_Pathway_(G2_M_transition_checkpoint)	-0,112	0,210	-0,013	6	-0,062
NCI_ATM_Pathway_(Pathway_rRNA_transcription_via_ATM)	-0,026	0,041	0,023	6	-0,002
NCI_ATR_signaling_Main_Pathway	-0,023	0,056	-0,021	27	-0,022
NCI_ATR_signaling_Pathway_(Pathway_negative_regulation_of_transcription_during_mitosis_via_CHEK1)	-0,048	0,064	-0,004	22	-0,026
NCI_ATR_signaling_Pathway_(regulation_of_double_strand_break_repair_via_homologous_recombination)	-0,030	0,055	-0,012	24	-0,021
NCI_ATR_signaling_Pathway_(response_to_G2_M_transition_DNA_damage_checkpoint_signal)	-0,046	0,062	-0,004	23	-0,025
NCI_Atypical_NF_kappaB_Main_Pathway	-0,035	0,029	0,033	13	-0,001
NCI_Atypical_NF_kappaB_Pathway_(Pathway_degradation_of_NFKB1_NFKBIA)	-0,040	0,035	0,024	11	-0,008
NCI_Atypical_NF_kappaB_Pathway_(Pathway_degradation_of_NFKBIA)	0,085	-0,152	0,080	4	0,083
NCI_Atypical_NF_kappaB_Pathway_(positive_regulation_of_anti_apoptosis)	-0,047	0,028	0,044	10	-0,001
NCI_Aurora_A_signaling_Main_Pathway	0,015	-0,055	-0,002	30	0,007
NCI_Aurora_A_signaling_Pathway_(centrosome_duplication)	-0,002	0,006	-0,014	10	-0,008
NCI_Aurora_A_signaling_Pathway_(negative_regulation_of_DNA_binding)	0,051	-0,121	-0,007	9	0,022
NCI_Aurora_A_signaling_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	0,023	-0,105	-0,007	8	0,008
NCI_Aurora_A_signaling_Pathway_(protein_catabolic_process)	0,073	-0,171	0,001	10	0,037
NCI_Aurora_A_signaling_Pathway_(regulation_of_centrosome_cycle)	0,034	-0,128	0,006	9	0,020
NCI_Aurora_A_signaling_Pathway_(spindle_assembly)	0,039	-0,100	-0,003	10	0,018
NCI_Aurora_B_signaling_Main_Pathway	-0,022	0,023	0,003	39	-0,009
NCI_Aurora_B_signaling_Pathway_(cytokinesis)	0,028	-0,111	0,014	12	0,021
NCI_Aurora_C_signaling_Main_Pathway	-0,003	-0,130	-0,034	4	-0,018
NCI_BARD1_signaling_events_Main_Pathway	-0,013	0,036	-0,023	23	-0,018
NCI_BARD1_signaling_events_Pathway_(DNA_damage_checkpoint)	-0,024	0,059	-0,053	3	-0,038
NCI_BARD1_signaling_events_Pathway_(DNA_repair)	-0,006	0,037	-0,014	20	-0,010
NCI_BARD1_signaling_events_Pathway_(protein_ubiquitination)	-0,036	0,062	-0,001	11	-0,019
NCI_BCR_signaling_Main_Pathway	0,004	0,050	0,016	60	0,010
NCI_BCR_signaling_Pathway_(actin_cytoskeleton_organization)	-0,127	0,682	-0,042	8	-0,084
NCI_BCR_signaling_Pathway_(cell_survival)	-0,116	0,626	-0,013	8	-0,065
NCI_BCR_signaling_Pathway_(cytokine_secretion)	-0,064	0,332	0,008	15	-0,028
NCI_BCR_signaling_Pathway_(re_entry_into_mitotic_cell_cycle)	-0,040	0,319	0,000	13	-0,020
NCI_BCR_signaling_Pathway_(ubiquitin_dependent_protein_catabolic_process)	0,046	-0,100	0,052	13	0,049
NCI_Beta1_integrin_cell_surface_interactions_Main_Pathway	0,045	-0,149	0,048	66	0,046
NCI_Beta2_integrin_cell_surface_interactions_Main_Pathway	0,061	-0,131	0,077	29	0,069
NCI_Beta3_integrin_cell_surface_interactions_Main_Pathway	0,027	-0,110	0,024	39	0,025
NCI_Beta5_beta6_beta7_and_beta8_integrin_cell_surface_interactions_Main_Pathway	0,008	-0,044	0,029	14	0,018
NCI_BMP_receptor_signaling_Main_Pathway	0,004	0,003	-0,001	38	0,001
NCI_C_MYB_transcription_factor_network_Main_Pathway	-0,005	0,072	0,008	75	0,001
NCI_C_MYC_Main_Pathway	-0,057	0,058	-0,049	25	-0,053
NCI_Calcineurin_regulated_NFAT_dependent_transcription_in_lymphocytes_Main_Pathway	-0,070	0,069	0,084	31	0,007
NCI_Calcineurin_regulated_NFAT_dependent_transcription_in_lymphocytes_Pathway_(T_cell_anergy)	-0,053	0,155	0,092	8	0,020
NCI_Calcium_signaling_in_the_CD4_TCR_Main_Pathway	-0,091	-0,028	0,107	20	0,008
NCI_Canonical_NF_kappaB_Main_Pathway	0,027	-0,074	0,031	23	0,029
NCI_Canonical_NF_kappaB_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	0,012	-0,078	0,039	11	0,025
NCI_Canonical_Wnt_signaling_Main_Pathway	-0,011	-0,034	0,035	20	0,012
NCI_Caspase_Cascade_in_Apoptosis_Main_Pathway	-0,138	0,142	-0,001	47	-0,069
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(actin_filament_polymerization)	-0,165	0,508	-0,183	3	-0,174
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(apoptosis)	0,057	-0,109	0,040	10	0,048
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(apoptotic_nuclear_changes)	0,089	-0,162	0,069	9	0,079
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(DNA_fragmentation_during_apoptosis)	0,027	0,010	0,015	12	0,021
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(DNA_repair)	0,031	-0,029	0,066	10	0,049
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(JNK_cascade)	0,035	-0,043	0,014	9	0,024

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(neuron_apoptosis)	-0,335	0,370	-0,020	14	-0,178
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(nuclear_fragmentation_during_apoptosis)	0,031	-0,044	0,027	10	0,029
NCI_Caspase_Cascade_in_Apoptosis_Pathway_(positive_regulation_of_apoptosis)	-0,111	0,111	-0,065	6	-0,088
NCI_CD40_CD40L_signaling_Main_Pathway	0,040	-0,055	0,023	25	0,031
NCI_CD40_CD40L_signaling_Pathway_(B_cell_affinity_maturation)	0,019	0,223	-0,082	4	-0,031
NCI_CD40_CD40L_signaling_Pathway_(B_cell_proliferation)	-0,052	0,262	-0,105	4	-0,078
NCI_CD40_CD40L_signaling_Pathway_(plasma_cell_differentiation)	0,019	0,223	-0,082	4	-0,031
NCI_CD40_CD40L_signaling_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	-0,052	0,262	-0,105	4	-0,078
NCI_CD40_CD40L_signaling_Pathway_(regulation_of_germinal_center_formation)	0,005	0,167	-0,056	8	-0,025
NCI_CD40_CD40L_signaling_Pathway_(regulation_of_isotype_switching_to_IgE_isotypes)	0,005	0,167	-0,056	8	-0,025
NCI_CD40_CD40L_signaling_Pathway_(regulation_of_isotype_switching_to_IgG_isotypes)	-0,052	0,262	-0,105	4	-0,078
NCI_CDC42_signaling_events_Main_Pathway	-0,068	-0,031	0,024	58	-0,022
NCI_CDC42_signaling_events_Pathway_(actin_cytoskeleton_organization)	0,039	-0,135	0,039	15	0,039
NCI_CDC42_signaling_events_Pathway_(actin_filament_depolymerization)	-0,027	0,092	-0,005	5	-0,016
NCI_CDC42_signaling_events_Pathway_(cell_motility)	-0,013	0,042	0,005	8	-0,004
NCI_CDC42_signaling_events_Pathway_(cell_proliferation)	-0,025	0,209	-0,022	1	-0,024
NCI_CDC42_signaling_events_Pathway_(cytokinesis)	-0,025	0,209	-0,022	1	-0,024
NCI_CDC42_signaling_events_Pathway_(establishment_of_cell_polarity)	-0,007	0,112	-0,087	3	-0,047
NCI_CDC42_signaling_events_Pathway_(neuron_projection_development)	0,002	0,002	-0,015	7	-0,007
NCI_CDC42_signaling_events_Pathway_(Pathway_positive_regulation_of_NF_kappaB_transcription_factor_activity_via_CDC42)	-0,013	0,057	-0,018	6	-0,016
NCI_CDC42_signaling_events_Pathway_(regulation_of_filopodium_assembly)	0,019	0,064	-0,028	7	-0,004
NCI_CDC42_signaling_events_Pathway_(retrograde_vesicle_mediated_transport_Golgi_to_ER)	0,040	-0,183	0,049	10	0,044
NCI_CDC42_signaling_events_Pathway_(RNA_splicing)	-0,625	0,047	0,032	8	-0,296
NCI_Cellular_roles_of_Anthrax_toxin_Main_Pathway	-0,029	0,077	-0,038	16	-0,034
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(apoptosis)	0	0	0	2	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(inflammatory_response)	0	0	0	2	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(macrophage_activation)	0,025	-0,012	-0,010	4	0,008
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(MAPKKK_cascade)	-0,081	0,183	-0,081	7	-0,081
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(monocyte_activation)	0	0	0	4	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(necrosis)	0	0	0	2	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(negative_regulation_of_macrophage_activation)	0	0	0	2	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(negative_regulation_of_myeloid_dendritic_cell_antigen_processing_and_presentation)	0	0	0	2	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(negative_regulation_of_phagocytosis)	0	0	0	2	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(platelet_activation)	0	0	0	2	0
NCI_Cellular_roles_of_Anthrax_toxin_Pathway_(regulation_of_endothelial_cell_proliferation)	0	0	0	2	0
NCI_Ceramide_signaling_Main_Pathway	0,002	-0,003	0,013	48	0,007
NCI_Ceramide_signaling_Pathway_(cell_survival)	-0,026	0,047	-0,003	18	-0,015
NCI_Ceramide_signaling_Pathway_(ganglioside_biosynthetic_process)	-0,027	0,045	0,002	17	-0,012
NCI_Ceramide_signaling_Pathway_(negative_regulation_of_cell_cycle)	-0,029	0,054	0,002	17	-0,014
NCI_Ceramide_signaling_Pathway_(regulation_of_nitric_oxide_biosynthetic_process)	0,015	-0,069	0,070	6	0,043
NCI_Circadian_rhythm_Main_Pathway	-0,016	0,051	-0,014	5	-0,015
NCI_Circadian_rhythm_Pathway_(chromatin_modification)	-0,016	0,051	-0,014	5	-0,015
NCI_Circadian_rhythm_Pathway_(S_phase_of_mitotic_cell_cycle)	-0,016	0,051	-0,014	5	-0,015
NCI_Class_I_PI3K_signaling_events_Main_Pathway	-0,036	0,235	-0,013	41	-0,024
NCI_Class_I_PI3K_signaling_events_mediated_by_Akt_Main_Pathway	-0,026	-0,026	0,001	34	-0,012
NCI_Class_I_PI3K_signaling_events_mediated_by_Akt_Pathway_(cell_survival)	0,006	-0,102	0,025	12	0,016
NCI_Class_I_PI3K_signaling_events_mediated_by_Akt_Pathway_(G1_S_transition_of_mitotic_cell_cycle)	0,002	-0,085	0,021	13	0,012
NCI_Class_I_PI3K_signaling_events_mediated_by_Akt_Pathway_(glucose_import)	-0,006	0,050	-0,024	3	-0,015

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Class_I_PI3K_signaling_events_mediated_by_Akt_Pathway_(negative_regulation_of_cell_cycle)	-0,021	-0,032	0,002	25	-0,010
NCI_Class_I_PI3K_signaling_events_Pathway_(actin_cytoskeleton_reorganization)	-0,032	0,161	-0,008	13	-0,020
NCI_Class_I_PI3K_signaling_events_Pathway_(cell_survival)	-0,008	0,065	0,002	14	-0,003
NCI_Class_IB_PI3K_non_lipid_kinase_events_Main_Pathway	0,038	0,041	-0,024	5	0,007
NCI_Class_IB_PI3K_non_lipid_kinase_events_Pathway_(cAMP_biosynthetic_process)	0	0	0	3	0
NCI_Coregulation_of_Androgen_receptor_activity_Main_Pathway	0,005	0,004	-0,002	14	0,001
NCI_Coregulation_of_Androgen_receptor_activity_Pathway_(cell_proliferation)	0,016	0,004	0,004	6	0,010
NCI_CXCR3_mediated_signaling_events_Main_Pathway	-0,027	-0,007	0,010	38	-0,008
NCI_CXCR3_mediated_signaling_events_Pathway_(actin_polymerization_or_depolymerization)	-0,032	-0,028	0,007	14	-0,013
NCI_CXCR3_mediated_signaling_events_Pathway_(cAMP_biosynthetic_process)	0	0	0	5	0
NCI_CXCR3_mediated_signaling_events_Pathway_(cell_adhesion)	-0,067	-0,079	0,018	16	-0,024
NCI_CXCR3_mediated_signaling_events_Pathway_(cell_proliferation)	-0,014	-0,014	-0,003	23	-0,008
NCI_CXCR3_mediated_signaling_events_Pathway_(chemotaxis)	-0,029	-0,022	0,001	18	-0,014
NCI_CXCR3_mediated_signaling_events_Pathway_(regulation_of_stress_fiber_assembly)	0	0	0	5	0
NCI_CXCR4_mediated_signaling_events_Main_Pathway	-0,004	0,066	-0,003	76	-0,004
NCI_CXCR4_mediated_signaling_events_Pathway_(actin_filament_depolymerization)	0	0	0	1	0
NCI_CXCR4_mediated_signaling_events_Pathway_(cell_adhesion)	-0,025	0,236	-0,024	28	-0,024
NCI_CXCR4_mediated_signaling_events_Pathway_(cell_proliferation)	-0,001	0,004	-0,000	11	-0,000
NCI_CXCR4_mediated_signaling_events_Pathway_(chemotaxis)	-0,014	0,031	-0,005	60	-0,010
NCI_CXCR4_mediated_signaling_events_Pathway_(establishment_of_cell_polarity)	-0,034	0,055	-0,016	17	-0,025
NCI_CXCR4_mediated_signaling_events_Pathway_(positive_regulation_of_lamellipodium_assembly)	-0,112	0,278	-0,060	4	-0,086
NCI_CXCR4_mediated_signaling_events_Pathway_(regulation_of_heterotypic_cell_cell_adhesion)	-0,001	0,004	-0,000	12	-0,000
NCI_Degradation_of_beta_catenin_Main_Pathway	0,005	-0,012	0,002	18	0,004
NCI_Direct_p53_effectors_Main_Pathway	-0,076	0,083	-0,042	7	-0,059
NCI_DNA_PK_pathway_in_nonhomologous_end_joining_Main_Pathway	0,005	-0,003	-0,017	13	-0,006
NCI_DNA_PK_pathway_in_nonhomologous_end_joining_Pathway_(double_strand_break_repair_via_homologous_recombination)	-0,040	0,022	-0,053	4	-0,047
NCI_DNA_PK_pathway_in_nonhomologous_end_joining_Pathway_(double_strand_break_repair_via_nonhomologous_end_joining)	0,005	-0,003	-0,017	13	-0,006
NCI_DNA_PK_pathway_in_nonhomologous_end_joining_Pathway_(immunoglobulin_heavy_chain_V_D_J_recombination)	-0,016	0,028	-0,026	7	-0,021
NCI_DNA_PK_pathway_in_nonhomologous_end_joining_Pathway_(immunoglobulin_light_chain_V_J_recombination)	-0,016	0,028	-0,026	7	-0,021
NCI_DNA_PK_pathway_in_nonhomologous_end_joining_Pathway_(V_D_J_recombination)	0,006	0,001	-0,016	10	-0,005
NCI_Downstream_signaling_in_naive_CD8_T_cells_Main_Pathway	-0,047	0,088	0,035	41	-0,006
NCI_Downstream_signaling_in_naive_CD8_T_cells_Pathway_(alpha_beta_T_cell_proliferation)	0	0	0	1	0
NCI_Downstream_signaling_in_naive_CD8_T_cells_Pathway_(Pathway_regulation_of_survival_gene_product_expression_via_IL2RG)	-0,060	0,045	0,023	11	-0,019
NCI_E_cadherin_signaling_in_keratinocytes_Main_Pathway	-0,004	-0,070	0,032	21	0,014
NCI_E_cadherin_signaling_in_keratinocytes_Pathway_(actin_cable_formation)	-0,034	0,022	-0,002	9	-0,018
NCI_E_cadherin_signaling_in_keratinocytes_Pathway_(adherens_junction_organization)	-0,014	0,036	-0,009	10	-0,011
NCI_E_cadherin_signaling_in_keratinocytes_Pathway_(apoptosis)	0,019	-0,035	0,027	10	0,023
NCI_E_cadherin_signaling_in_keratinocytes_Pathway_(establishment_of_polarity_of_embryonic_epithelium)	-0,038	0,025	-0,002	8	-0,020
NCI_E_cadherin_signaling_in_keratinocytes_Pathway_(keratinocyte_differentiation)	0,027	-0,060	0,035	13	0,031
NCI_E_cadherin_signaling_in_the_nascent_adherens_junction_Main_Pathway	-0,005	-0,032	0,024	33	0,009
NCI_E_cadherin_signaling_in_the_nascent_adherens_junction_Pathway_(actin_cytoskeleton_organization)	0,004	0,048	0,004	6	0,004
NCI_E_cadherin_signaling_in_the_nascent_adherens_junction_Pathway_(adherens_junction_assembly)	-0,054	0,162	-0,002	6	-0,028
NCI_E_cadherin_signaling_in_the_nascent_adherens_junction_Pathway_(regulation_of_actin_nucleation)	-0,021	-0,006	0,013	12	-0,004

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_E_cadherin_signaling_in_the_nascent_adherens_junction_Pathway_(regulation_of_calcium_dependent_cell_cell_adhesion)	-0,063	0,157	-0,015	5	-0,039
NCI_E_cadherin_signaling_in_the_nascent_adherens_junction_Pathway_(regulation_of_cell_cell_adhesion)	-0,030	-0,028	0,022	4	-0,004
NCI_E2F_transcription_factor_network_Main_Pathway	-0,022	0,073	-0,028	40	-0,025
NCI_Effects_of_Botulinum_toxin_Main_Pathway	0,009	-0,047	0,044	4	0,027
NCI_EGFR_dependent_Endothelin_signaling_events_Main_Pathway	-0,086	-0,387	0,112	4	0,013
NCI_Endogenous_TLR_signaling_Main_Pathway	-0,024	0,055	-0,031	17	-0,027
NCI_Endogenous_TLR_signaling_Pathway_(cell_migration)	-0,062	0,150	-0,080	4	-0,071
NCI_Endogenous_TLR_signaling_Pathway_(cytokine_production_involved_in_inflammatory_response)	0	0	0	6	0
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_apoptosis)	-0,029	0,067	-0,038	11	-0,033
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_cell_adhesion)	-0,011	0,012	-0,023	7	-0,017
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_cell_matrix_adhesion)	-0,062	0,150	-0,080	4	-0,071
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_cell_proliferation)	-0,029	0,067	-0,038	11	-0,033
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_granulocyte_colony_stimulating_factor_production)	0	0	0	4	0
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_interleukin_1_beta_production)	-0,029	0,067	-0,038	11	-0,033
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_interleukin_10_production)	0	0	0	4	0
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_interleukin_6_production)	0	0	0	5	0
NCI_Endogenous_TLR_signaling_Pathway_(regulation_of_tumor_necrosis_factor_production)	0	0	0	5	0
NCI_Endogenous_TLR_signaling_Pathway_(respiratory_burst_involved_in_inflammatory_response)	-0,022	0,058	-0,031	7	-0,026
NCI_Endothelins_Main_Pathway	0,003	-0,051	0,015	62	0,009
NCI_Endothelins_Pathway_(arachidonic_acid_secretion)	0,050	-0,146	0,029	5	0,039
NCI_Endothelins_Pathway_(cAMP_biosynthetic_process)	-0,017	-0,031	0,008	19	-0,005
NCI_Endothelins_Pathway_(positive_regulation_of_muscle_contraction)	-0,037	0,024	-0,027	4	-0,032
NCI_Endothelins_Pathway_(regulation_of_vascular_smooth_muscle_contraction)	0,040	0,014	-0,016	5	0,012
NCI_EPHA_forward_signaling_Main_Pathway	-0,009	0,209	-0,004	26	-0,007
NCI_EPHA_forward_signaling_Pathway_(actin_filament_depolymerization)	0	0	0	6	0
NCI_EPHA_forward_signaling_Pathway_(axon_guidance)	-0,003	0,029	0,000	16	-0,001
NCI_EPHA_forward_signaling_Pathway_(cell_cell_adhesion)	-0,008	0,013	-0,003	14	-0,005
NCI_EPHA_forward_signaling_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	-0,011	0,248	-0,002	20	-0,006
NCI_EPHA_forward_signaling_Pathway_(regulation_of_stress_fiber_assembly)	-0,008	0,013	-0,003	14	-0,005
NCI_EPHA2_forward_signaling_Main_Pathway	0,018	-0,041	0,010	10	0,014
NCI_EPHB_forward_signaling_Main_Pathway	0,012	0,005	-0,032	8	-0,010
NCI_Ephrin_A_reverse_signaling_Main_Pathway	-0,001	0,049	0,028	3	0,014
NCI_Ephrin_A_reverse_signaling_Pathway_(beta_integrin_mediated_adhesion)	-0,001	0,049	0,028	3	0,014
NCI_Ephrin_A_reverse_signaling_Pathway_(MAPKKK_cascade)	0	0	0	2	0
NCI_Ephrin_A_reverse_signaling_Pathway_(neuron_projection_morphogenesis)	0	0	0	2	0
NCI_Ephrin_B_reverse_signaling_Main_Pathway	0,002	0,206	0,021	20	0,011
NCI_Ephrin_B_reverse_signaling_Pathway_(angiogenesis)	-0,030	0,355	-0,020	15	-0,025
NCI_Ephrin_B_reverse_signaling_Pathway_(cell_adhesion)	-0,028	0,314	-0,010	17	-0,019
NCI_Ephrin_B_reverse_signaling_Pathway_(endothelial_cell_migration)	-0,030	0,355	-0,020	15	-0,025
NCI_Ephrin_B_reverse_signaling_Pathway_(endothelial_cell_proliferation)	0,119	-0,160	-0,062	2	0,029
NCI_EPO_signaling_Main_Pathway	0,015	0,157	0,003	33	0,009
NCI_EPO_signaling_Pathway_(beta_integrin_mediated_adhesion)	-0,012	0,025	0,000	7	-0,006
NCI_EPO_signaling_Pathway_(cell_proliferation)	-0,012	1,167	-0,045	5	-0,028
NCI_EPO_signaling_Pathway_(elevation_of_cytosolic_calcium_ion_concentration)	-0,054	1,237	-0,054	5	-0,054
NCI_ErbB_receptor_signaling_network_Main_Pathway	0,000	-0,253	0,057	15	0,029
NCI_ErbB1_downstream_signaling_Main_Pathway	0,029	-0,098	0,026	82	0,028
NCI_ErbB1_downstream_signaling_Pathway_(cell_migration)	0,042	0,050	-0,006	9	0,018
NCI_ErbB1_downstream_signaling_Pathway_(cell_proliferation)	0,022	-0,208	0,066	22	0,044
NCI_ErbB1_downstream_signaling_Pathway_(cytoskeleton_organization)	0,051	0,104	0,038	5	0,044
NCI_ErbB1_downstream_signaling_Pathway_(lamellipodium_assembly)	0,077	-0,204	0,030	7	0,054

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_ErbB1_downstream_signaling_Pathway_(ruffle_organization)	0,035	-0,167	0,049	18	0,042
NCI_ErbB1_downstream_signaling_Pathway_(tight_junction_assembly)	0,045	0,213	0,003	3	0,024
NCI_ErbB2_ErbB3_signaling_events_Main_Pathway	0,026	0,016	-0,011	33	0,008
NCI_ErbB2_ErbB3_signaling_events_Pathway_(activation_of_caspase_activity)	0,035	-0,064	0,065	7	0,050
NCI_ErbB2_ErbB3_signaling_events_Pathway_(apoptosis)	0,029	0,067	0,008	8	0,018
NCI_ErbB2_ErbB3_signaling_events_Pathway_(cell_migration)	0,015	0,065	-0,039	6	-0,012
NCI_ErbB2_ErbB3_signaling_events_Pathway_(cell_proliferation)	-0,098	0,430	-0,142	7	-0,120
NCI_ErbB2_ErbB3_signaling_events_Pathway_(heart_morphogenesis)	-0,043	0,158	-0,058	7	-0,051
NCI_ErbB2_ErbB3_signaling_events_Pathway_(mammary_gland_morphogenesis)	-0,043	0,158	-0,058	7	-0,051
NCI_ErbB2_ErbB3_signaling_events_Pathway_(myelination)	0,012	-0,058	0,053	10	0,032
NCI_ErbB2_ErbB3_signaling_events_Pathway_(nervous_system_development)	-0,043	0,158	-0,058	7	-0,051
NCI_ErbB4_signaling_events_Main_Pathway	-0,011	-0,005	0,014	27	0,002
NCI_ErbB4_signaling_events_Pathway_(apoptosis)	0,018	-0,023	0,024	10	0,021
NCI_ErbB4_signaling_events_Pathway_(axon_guidance)	0,027	-0,062	0,011	5	0,019
NCI_ErbB4_signaling_events_Pathway_(cell_proliferation)	0,021	-0,048	0,008	6	0,015
NCI_ErbB4_signaling_events_Pathway_(chemotaxis)	0,018	-0,023	0,024	10	0,021
NCI_ErbB4_signaling_events_Pathway_(dendrite_morphogenesis)	0,018	-0,023	0,024	10	0,021
NCI_ErbB4_signaling_events_Pathway_(epithelial_cell_differentiation)	-0,007	-0,047	0,010	14	0,002
NCI_ErbB4_signaling_events_Pathway_(glial_cell_differentiation)	-0,008	-0,086	0,032	10	0,012
NCI_ErbB4_signaling_events_Pathway_(heart_development)	0,027	-0,062	0,011	5	0,019
NCI_ErbB4_signaling_events_Pathway_(neural_crest_cell_migration)	0	0	0	3	0
NCI_Fanconi_anemia_Main_Pathway	-0,036	0,013	-0,009	45	-0,022
NCI_Fanconi_anemia_Pathway_(DNA_repair)	-0,007	-0,096	-0,043	3	-0,025
NCI_Fanconi_anemia_Pathway_(G1_S_transition_checkpoint)	-0,031	0,032	-0,047	5	-0,039
NCI_Fanconi_anemia_Pathway_(regulation_of_double_strand_break_repair_via_homologous_recombination)	-0,034	0,012	-0,014	37	-0,024
NCI_Fanconi_anemia_Pathway_(Sister_Chromatid_Exchange_Process)	-0,050	0,070	-0,018	30	-0,034
NCI_FAS_CD95_signaling_Main_Pathway	0,017	-0,006	0,014	31	0,015
NCI_FAS_CD95_signaling_Pathway_(cell_cycle)	0,081	0,085	0,028	4	0,054
NCI_FAS_CD95_signaling_Pathway_(cell_migration)	-0,026	-0,022	0,049	9	0,012
NCI_FAS_CD95_signaling_Pathway_(necroptosis)	0,066	-0,005	0,055	6	0,060
NCI_FAS_CD95_signaling_Pathway_(neuron_projection_development)	0,067	-0,087	0,017	8	0,042
NCI_FAS_CD95_signaling_Pathway_(release_of_cytochrome_c_from_mitochondria)	0,081	-0,069	0,038	7	0,059
NCI_Fc_epsilon_receptor_I_signaling_in_mast_cells_Main_Pathway	-0,035	0,090	-0,024	56	-0,030
NCI_Fc_epsilon_receptor_I_signaling_in_mast_cells_Pathway_(regulation_of_mast_cell_degranulation)	-0,023	0,052	-0,050	10	-0,037
NCI_FGF_signaling_Main_Pathway	-0,019	0,059	-0,027	18	-0,023
NCI_FGF_signaling_Pathway_(cell_migration)	-0,061	0,253	-0,051	4	-0,056
NCI_FGF_signaling_Pathway_(MAPKKK_cascade)	0,001	-0,049	0,002	8	0,001
NCI_FGF_signaling_Pathway_(negative_regulation_of_apoptosis)	0,011	-0,016	-0,021	5	-0,005
NCI_FOXA1_transcription_factor_network_Main_Pathway	0	0	0	12	0
NCI_FOXA2_and_FOXA3_transcription_factor_networks_Main_Pathway	0,041	-0,140	0,045	24	0,043
NCI_FOXM1_transcription_factor_network_Main_Pathway	0,030	-0,022	0,038	39	0,034
NCI_FoxO_family_signaling_Main_Pathway	0,022	-0,030	-0,002	40	0,010
NCI_Glucocorticoid_receptor_regulatory_network_Main_Pathway	-0,031	0,026	0,006	64	-0,013
NCI_Glucocorticoid_receptor_regulatory_network_Pathway_(apoptosis)	-0,060	0,038	0,029	19	-0,016
NCI_Glucocorticoid_receptor_regulatory_network_Pathway_(histone_acetylation)	-0,060	0,038	0,029	19	-0,016
NCI_Glucocorticoid_receptor_regulatory_network_Pathway_(MAPKKK_cascade)	-0,060	0,038	0,029	19	-0,016
NCI_Glypican_1_network_Main_Pathway	-0,003	-0,011	-0,016	18	-0,010
NCI_Glypican_1_network_Pathway_(BMP_signaling_pathway)	-0,017	-0,020	-0,036	9	-0,027
NCI_Glypican_1_network_Pathway_(cell_growth)	-0,014	-0,017	-0,030	11	-0,022
NCI_Glypican_1_network_Pathway_(fibroblast_growth_factor_receptor_signaling_pathway)	-0,014	-0,017	-0,030	11	-0,022
NCI_Glypican_2_network_Main_Pathway	0	0	0	2	0
NCI_Glypican_3_network_Main_Pathway	0,045	-0,003	-0,016	6	0,014
NCI_Glypican_3_network_Pathway_(apoptosis)	0,067	-0,004	-0,024	4	0,021
NCI_Glypican_3_network_Pathway_(embryonic_digit_morphogenesis)	0	0	0	2	0

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Glypican_3_network_Pathway_(kidney_development)	0	0	0	2	0
NCI_Glypican_3_network_Pathway_(skeletal_system_development)	0	0	0	2	0
NCI_GMCSF_mediated_signaling_events_Main_Pathway	-0,009	-0,072	0,041	8	0,016
NCI_Hedgehog_signaling_events_mediated_by_Gli_proteins_Main_Pathway	0,062	-0,164	0,023	13	0,042
NCI_Hedgehog_signaling_events_mediated_by_Gli_proteins_Pathway_(embryonic_limb_morphogenesis)	0,102	-0,226	0,025	7	0,063
NCI_Hedgehog_signaling_events_mediated_by_Gli_proteins_Pathway_(forebrain_development)	0,102	-0,226	0,025	7	0,063
NCI_HIF_1_alpha_transcription_factor_network_Main_Pathway	0,020	-0,181	0,079	59	0,050
NCI_HIF_2_alpha_transcription_factor_network_Main_Pathway	0,057	-0,087	0,039	29	0,048
NCI_HIF_2_alpha_transcription_factor_network_Pathway_(neuron_apoptosis)	0,010	-0,119	0,072	3	0,041
NCI_HIV_1_Nef_Negative_effector_of_Fas_and_TNF_alpha_Main_Pathway	0,004	0,031	0,005	30	0,004
NCI_HIV_1_Nef_Negative_effector_of_Fas_and_TNF_alpha_Pathway_(Pathway_degradation_of_CASP3_CASP7_CASP6)	0,016	0,026	-0,019	14	-0,001
NCI_HIV_1_Nef_Negative_effector_of_Fas_and_TNF_alpha_Pathway_(protein_ubiquitination)	-0,036	0,096	0,011	13	-0,012
NCI_Hypoxic_and_oxygen_homeostasis_regulation_of_HIF_1_alpha_Main_Pathway	0,019	-0,084	0,018	19	0,018
NCI_IFN_gamma_Main_Pathway	0,031	-0,074	0,017	35	0,024
NCI_IFN_gamma_Pathway_(Antibacterial_Response)	0,047	-0,135	0,012	15	0,029
NCI_IFN_gamma_Pathway_(antigen_processing_and_presentation_of_peptide_antigen_via_MHC_class_I)	0,047	-0,135	0,012	15	0,029
NCI_IFN_gamma_Pathway_(antigen_processing_and_presentation_of_peptide_antigen_via_MHC_class_II)	0,047	-0,135	0,012	15	0,029
NCI_IFN_gamma_Pathway_(Antiviral_Response)	0,047	-0,135	0,012	15	0,029
NCI_IFN_gamma_Pathway_(apoptosis)	0,047	-0,135	0,012	15	0,029
NCI_IFN_gamma_Pathway_(Immunoregulation)	0,047	-0,135	0,012	15	0,029
NCI_IFN_gamma_Pathway_(negative_regulation_of_cell_growth)	0,047	-0,135	0,012	15	0,029
NCI_IGF1_Main_Pathway	-0,182	-0,016	0,010	28	-0,086
NCI_IGF1_Pathway_(positive_regulation_of_MAPKKK_cascade)	0,040	-0,055	0,007	10	0,024
NCI_IL1_mediated_signaling_events_Main_Pathway	-0,001	0,030	-0,009	26	-0,005
NCI_IL12_mediated_signaling_events_Main_Pathway	0,038	-0,129	0,039	41	0,038
NCI_IL12_signaling_mediated_by_STAT4_Main_Pathway	-0,020	-0,067	0,135	10	0,058
NCI_IL12_signaling_mediated_by_STAT4_Pathway_(natural_killer_cell_mediated_cytotoxicity)	-0,155	-0,192	0,384	1	0,114
NCI_IL12_signaling_mediated_by_STAT4_Pathway_(T_helper_1_cell_differentiation)	-0,155	-0,192	0,384	1	0,114
NCI_IL12_signaling_mediated_by_STAT4_Pathway_(T_helper_2_cell_differentiation)	-0,155	-0,192	0,384	1	0,114
NCI_IL2_mediated_signaling_events_Main_Pathway	-0,009	0,024	-0,006	48	-0,007
NCI_IL2_mediated_signaling_events_Pathway_(G1_S_transition_of_mitotic_cell_cycle)	0,041	0,071	-0,036	5	0,003
NCI_IL2_mediated_signaling_events_Pathway_(natural_killer_cell_mediated_cytotoxicity)	-0,013	-0,000	-0,010	19	-0,012
NCI_IL2_mediated_signaling_events_Pathway_(positive_regulation_of_cell_cell_adhesion)	-0,055	0,037	-0,020	13	-0,038
NCI_IL2_mediated_signaling_events_Pathway_(T_cell_proliferation)	-0,048	0,032	-0,018	15	-0,033
NCI_IL2_signaling_events_mediated_by_PI3K_Main_Pathway	-0,156	0,025	0,000	32	-0,078
NCI_IL2_signaling_events_mediated_by_PI3K_Pathway_(actin_cytoskeleton_organization)	-0,019	-0,012	-0,013	15	-0,016
NCI_IL2_signaling_events_mediated_by_PI3K_Pathway_(cell_proliferation)	-0,008	0,038	-0,019	17	-0,013
NCI_IL2_signaling_events_mediated_by_PI3K_Pathway_(cell_survival)	-0,035	0,001	-0,013	18	-0,024
NCI_IL2_signaling_events_mediated_by_PI3K_Pathway_(T_cell_proliferation)	-0,019	-0,012	-0,013	15	-0,016
NCI_IL2_signaling_events_mediated_by_STAT5_Main_Pathway	-0,009	-0,072	0,041	8	0,016
NCI_IL2_signaling_events_mediated_by_STAT5_Pathway_(activation_induced_cell_death_of_T_cells)	-0,009	-0,072	0,041	2	0,016
NCI_IL2_signaling_events_mediated_by_STAT5_Pathway_(CD4_positive_CD25_positive_alpha_beta_regulatory_T_cell_lineage_commitment)	-0,009	-0,072	0,041	2	0,016
NCI_IL23_mediated_signaling_events_Main_Pathway	0,033	-0,119	0,056	33	0,045
NCI_IL23_mediated_signaling_events_Pathway_(keratinocyte_proliferation)	0	0	0	6	0
NCI_IL23_mediated_signaling_events_Pathway_(positive_regulation_of_chronic_inflammatory_response)	0	0	0	6	0
NCI_IL23_mediated_signaling_events_Pathway_(positive_regulation_of_dendritic_cell_antigen_processing_and_presentation)	0	0	0	2	0

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_IL23_mediated_signaling_events_Pathway_(positive_regulation_of_humoral_immune_response)	0	0	0	6	0
NCI_IL23_mediated_signaling_events_Pathway_(positive_regulation_of_T_cell_mediated_cytotoxicity)	0	0	0	6	0
NCI_IL23_mediated_signaling_events_Pathway_(T_cell_proliferation)	0	0	0	6	0
NCI_IL27_mediated_signaling_events_Main_Pathway	0,044	-0,250	0,047	20	0,045
NCI_IL27_mediated_signaling_events_Pathway_(cytokine_production_during_immune_response)	0	0	0	6	0
NCI_IL27_mediated_signaling_events_Pathway_(MAPKKK_cascade)	0	0	0	6	0
NCI_IL27_mediated_signaling_events_Pathway_(mast_cell_activation)	0	0	0	6	0
NCI_IL27_mediated_signaling_events_Pathway_(positive_regulation_of_mast_cell_cytokine_production)	0,010	-0,091	0,024	7	0,017
NCI_IL27_mediated_signaling_events_Pathway_(positive_regulation_of_T_cell_mediated_cytotoxicity)	0	0	0	6	0
NCI_IL27_mediated_signaling_events_Pathway_(T_cell_proliferation)	0	0	0	6	0
NCI_IL27_mediated_signaling_events_Pathway_(T_cell_proliferation_during_immune_response)	0	0	0	6	0
NCI_IL27_mediated_signaling_events_Pathway_(T_helper_2_cell_differentiation)	0	0	0	6	0
NCI_IL3_mediated_signaling_events_Main_Pathway	0,004	-0,008	0,009	18	0,007
NCI_IL4_mediated_signaling_events_Main_Pathway	0,001	-0,094	0,005	37	0,003
NCI_IL4_mediated_signaling_events_Pathway_(T_cell_proliferation)	0,355	-1,319	0,434	1	0,395
NCI_IL4_mediated_signaling_events_Pathway_(T_helper_1_cell_differentiation)	0,355	-1,319	0,434	1	0,395
NCI_IL4_mediated_signaling_events_Pathway_(T_helper_2_cell_differentiation)	0,355	-1,319	0,434	1	0,395
NCI_IL5_mediated_signaling_events_Main_Pathway	-0,005	-0,006	0,024	11	0,009
NCI_IL5_mediated_signaling_events_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	0	0	0	4	0
NCI_IL5_mediated_signaling_events_Pathway_(regulation_of_isotype_switching_to_IgG_isotypes)	-0,003	-0,024	0,014	6	0,005
NCI_IL6_mediated_signaling_events_Main_Pathway	0,015	-0,121	0,032	38	0,024
NCI_IL6_mediated_signaling_events_Pathway_(cell_cycle_arrest)	0,176	-0,819	0,275	9	0,225
NCI_IL6_mediated_signaling_events_Pathway_(cell_survival)	0,176	-0,819	0,275	9	0,225
NCI_IL6_mediated_signaling_events_Pathway_(macrophage_differentiation)	0,176	-0,819	0,275	9	0,225
NCI_IL6_mediated_signaling_events_Pathway_(MAPKKK_cascade)	-0,043	0,044	0,019	7	-0,012
NCI_IL8_and_CXCR1_mediated_signaling_events_Main_Pathway	-0,024	0,115	0,016	25	-0,004
NCI_IL8_and_CXCR1_mediated_signaling_events_Pathway_(basophil_degranulation)	-0,001	-0,080	0,016	5	0,008
NCI_IL8_and_CXCR1_mediated_signaling_events_Pathway_(cAMP_biosynthetic_process)	-0,057	-0,128	0,032	10	-0,012
NCI_IL8_and_CXCR1_mediated_signaling_events_Pathway_(chemotaxis)	0,030	-0,078	0,035	6	0,032
NCI_IL8_and_CXCR2_mediated_signaling_events_Main_Pathway	-0,040	0,127	0,012	28	-0,014
NCI_IL8_and_CXCR2_mediated_signaling_events_Pathway_(cAMP_biosynthetic_process)	-0,075	-0,034	0,009	14	-0,033
NCI_IL8_and_CXCR2_mediated_signaling_events_Pathway_(Pathway_degradation_of_CXCL8)	-0,069	-0,039	0,012	16	-0,028
NCI_IL8_and_CXCR2_mediated_signaling_events_Pathway_(regulation_of_cell_migration)	0,025	-0,098	0,057	6	0,041
NCI_Insulin_mediated_glucose_transport_Main_Pathway	0,042	-0,135	0,028	19	0,035
NCI_Insulin_Pathway_Main_Pathway	-0,158	-0,008	0,045	44	-0,056
NCI_Insulin_Pathway_Pathway_(negative_regulation_of_MAPKKK_cascade)	-0,118	0,111	-0,021	9	-0,069
NCI_Integrin_linked_kinase_signaling_Main_Pathway	0,031	-0,016	0,008	43	0,019
NCI_Integrin_linked_kinase_signaling_Pathway_(anoikis)	0,087	-0,038	0,050	10	0,069
NCI_Integrin_linked_kinase_signaling_Pathway_(apoptosis)	0,087	-0,038	0,050	10	0,069
NCI_Integrin_linked_kinase_signaling_Pathway_(centrosome_localization)	0,051	-0,062	0,004	16	0,027
NCI_Integrin_linked_kinase_signaling_Pathway_(DNA_biosynthetic_process)	0,031	-0,019	0,001	13	0,016
NCI_Integrin_linked_kinase_signaling_Pathway_(microtubule_cytoskeleton_organization)	0,060	-0,038	0,005	3	0,033
NCI_Integrin_linked_kinase_signaling_Pathway_(substrate_adhesion_dependent_cell_spreading)	-0,046	0,107	-0,029	8	-0,037
NCI_Integrins_in_angiogenesis_Main_Pathway	-0,055	-0,043	0,021	63	-0,017
NCI_Integrins_in_angiogenesis_Pathway_(angiogenesis)	-0,003	-0,011	0,006	19	0,001
NCI_Internalization_of_ErbB1_Main_Pathway	-0,005	-0,027	0,016	38	0,005
NCI_JNK_signaling_in_the_CD4_TCR_Main_Pathway	0,023	-0,086	0,054	14	0,039
NCI_Lissencephaly_gene_LIS1_in_neuronal_migration_and_development_Main_Pathway	0,016	-0,046	-0,010	19	0,003

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Lissencephaly_gene_LIS1_in_neuronal_migration_and_development_Pathway_(anaphase)	0,046	-0,242	0,054	2	0,050
NCI_Lissencephaly_gene_LIS1_in_neuronal_migration_and_development_Pathway_(microtubule_based_movement)	-0,073	0,079	-0,035	3	-0,054
NCI_LKB1_signaling_events_Main_Pathway	0,013	-0,010	-0,005	40	0,004
NCI_LKB1_signaling_events_Pathway_(anoikis)	-0,027	0,016	-0,007	6	-0,017
NCI_LKB1_signaling_events_Pathway_(ATP_biosynthetic_process)	-0,017	0,017	-0,018	5	-0,018
NCI_LKB1_signaling_events_Pathway_(ATP_metabolic_process)	-0,017	0,017	-0,018	5	-0,018
NCI_LKB1_signaling_events_Pathway_(chromatin_remodeling)	0	0	0	2	0
NCI_LKB1_signaling_events_Pathway_(establishment_of_cell_polarity)	0,004	-0,021	-0,012	10	-0,004
NCI_LKB1_signaling_events_Pathway_(Pathway_degradation_of_CDC37)	0,008	-0,040	-0,018	3	-0,005
NCI_LKB1_signaling_events_Pathway_(Pathway_positive_regulation_of_CREB_transcription_factor_activity_via_CRTC2)	0,043	-0,044	0,013	15	0,028
NCI_LKB1_signaling_events_Pathway_(tubulin_complex_assembly)	0,022	-0,037	0,006	9	0,014
NCI_LKB1_signaling_events_Pathway_(Wnt_receptor_signaling_pathway)	-0,017	0,017	-0,018	5	-0,018
NCI_LPA_receptor_mediated_events_Main_Pathway	-0,014	0,011	0,031	60	0,009
NCI_LPA_receptor_mediated_events_Pathway_(arachidonic_acid_secretion)	-0,061	-0,025	0,009	9	-0,026
NCI_LPA_receptor_mediated_events_Pathway_(cAMP_biosynthetic_process)	-0,026	-0,023	0,006	17	-0,010
NCI_LPA_receptor_mediated_events_Pathway_(contractile_ring_contraction_involved_in_cytokinesis)	-0,016	0,028	-0,001	8	-0,009
NCI_LPA_receptor_mediated_events_Pathway_(MAPKKK_cascade)	-0,061	-0,025	0,009	9	-0,026
NCI_LPA_receptor_mediated_events_Pathway_(positive_regulation_of_dendritic_cell_cytokine_production)	0	0	0	3	0
NCI_LPA_receptor_mediated_events_Pathway_(positive_regulation_of_microtubule_depolymerization)	-0,014	0,012	-0,011	3	-0,013
NCI_LPA_receptor_mediated_events_Pathway_(positive_regulation_of_mitosis)	-0,061	-0,025	0,009	9	-0,026
NCI_LPA_receptor_mediated_events_Pathway_(stress_fiber_assembly)	0,029	-0,046	0,016	8	0,023
NCI_LPA4_mediated_signaling_events_Main_Pathway	0	0	0	9	0
NCI_LPA4_mediated_signaling_events_Pathway_(cAMP_biosynthetic_process)	0	0	0	9	0
NCI_mTOR_signaling_Main_Pathway	-0,083	0,026	0,016	60	-0,034
NCI_mTOR_signaling_Pathway_(lipid_biosynthetic_process)	0,009	0,020	0,029	12	0,019
NCI_mTOR_signaling_Pathway_(Pathway_rRNA_transcription_via_RRN3)	0,005	0,018	0,025	14	0,015
NCI_mTOR_signaling_Pathway_(regulation_of_actin_cytoskeleton_organization)	-0,004	-0,008	0,074	9	0,035
NCI_mTOR_signaling_Pathway_(regulation_of_protein_stability)	-0,004	-0,008	0,074	9	0,035
NCI_mTOR_signaling_Pathway_(translational_initiation)	0,018	0,059	0,009	13	0,014
NCI_N_cadherin_signaling_events_Main_Pathway	-0,014	-0,009	0,001	34	-0,007
NCI_N_cadherin_signaling_events_Pathway_(actin_filament_polymerization)	0,018	-0,013	-0,010	11	0,004
NCI_N_cadherin_signaling_events_Pathway_(adherens_junction_organization)	-0,018	0,089	-0,036	3	-0,027
NCI_N_cadherin_signaling_events_Pathway_(apoptosis)	0,037	-0,134	-0,006	7	0,015
NCI_N_cadherin_signaling_events_Pathway_(axon_guidance)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(axonogenesis)	0	0	0	4	0
NCI_N_cadherin_signaling_events_Pathway_(cardiac_muscle_tissue_morphogenesis)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(cortical_microtubule_organization)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(endothelial_cell_proliferation)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(gap_junction_assembly)	0,030	-0,121	-0,003	9	0,013
NCI_N_cadherin_signaling_events_Pathway_(lamellipodium_assembly)	0,029	-0,117	0,012	9	0,020
NCI_N_cadherin_signaling_events_Pathway_(long_term_synaptic_potentiation)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(myoblast_differentiation)	0,001	-0,097	-0,012	10	-0,006
NCI_N_cadherin_signaling_events_Pathway_(osteoblast_differentiation)	0,003	-0,097	0,029	6	0,016
NCI_N_cadherin_signaling_events_Pathway_(protein_transport_into_membrane_raft)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(regulation_of_cell_cell_adhesion)	0,018	-0,033	-0,002	13	0,008
NCI_N_cadherin_signaling_events_Pathway_(regulation_of_short_term_neuronal_synaptic_plasticity)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(regulation_of_synapse_organization)	0,037	-0,134	-0,006	7	0,015
NCI_N_cadherin_signaling_events_Pathway_(regulation_of_synaptic_plasticity)	0,043	-0,156	-0,007	6	0,018
NCI_N_cadherin_signaling_events_Pathway_(synaptic_vesicle_fusion_to_presynaptic_membrane)	0,043	-0,156	-0,007	6	0,018
NCI_Nectin_adhesion_Main_Pathway	0,008	-0,031	0,022	30	0,015
NCI_Nectin_adhesion_Pathway_(positive_regulation_of_JNK_cascade)	0,017	-0,172	0,042	5	0,030

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Nectin_adhesion_Pathway_(positive_regulation_of_lamellipodium_assembly)	0,031	-0,006	-0,007	4	0,012
NCI_Nephrin_Neph1_signaling_in_the_kidney_podocyte_Main_Pathway	0,011	-0,010	0,010	27	0,010
NCI_Nephrin_Neph1_signaling_in_the_kidney_podocyte_Pathway_(apoptosis)	0,029	0,067	0,008	5	0,018
NCI_Nephrin_Neph1_signaling_in_the_kidney_podocyte_Pathway_(lamellipodium_assembly)	0,016	-0,038	0,019	8	0,017
NCI_Netrin_mediated_signaling_events_Main_Pathway	0,039	-0,069	0,009	23	0,024
NCI_Netrin_mediated_signaling_events_Pathway_(apoptosis)	0	0	0	4	0
NCI_Netrin_mediated_signaling_events_Pathway_(axon_guidance)	0,124	-0,250	-0,006	5	0,059
NCI_Netrin_mediated_signaling_events_Pathway_(negative_chemotaxis)	0,029	-0,070	0,020	9	0,025
NCI_Neurotrophic_factor_mediated_Trk_receptor_signaling_Main_Pathway	-0,011	0,002	0,010	54	-0,001
NCI_Neurotrophic_factor_mediated_Trk_receptor_signaling_Pathway_(axon_guidance)	0,023	0,004	-0,003	9	0,010
NCI_Neurotrophic_factor_mediated_Trk_receptor_signaling_Pathway_(MAPKKK_cascade)	-0,025	-0,133	0,058	10	0,017
NCI_Neurotrophic_factor_mediated_Trk_receptor_signaling_Pathway_(neuron_projection_morphogenesis)	-0,026	0,005	0,010	23	-0,008
NCI_Neurotrophic_factor_mediated_Trk_receptor_signaling_Pathway_(Schwann_cell_development)	-0,015	0,035	0,000	20	-0,007
NCI_Noncanonical_Wnt_signaling_Main_Pathway	0,139	0,027	0,075	4	0,107
NCI_Nongenotropic_Androgen_signaling_Main_Pathway	-0,010	-0,018	0,012	27	0,001
NCI_Nongenotropic_Androgen_signaling_Pathway_(actin_cytoskeleton_reorganization)	-0,070	0,146	-0,021	4	-0,046
NCI_Nongenotropic_Androgen_signaling_Pathway_(apoptosis)	0,004	-0,026	0,013	15	0,008
NCI_Nongenotropic_Androgen_signaling_Pathway_(cAMP_biosynthetic_process)	-0,056	-0,049	0,012	8	-0,022
NCI_Nongenotropic_Androgen_signaling_Pathway_(cell_proliferation)	-0,001	-0,043	0,012	18	0,005
NCI_Notch_mediated_HES_HEY_network_Main_Pathway	-0,032	0,012	0,014	28	-0,009
NCI_Notch_mediated_HES_HEY_network_Pathway_(Pathway_degradation_of_HEY1)	0	0	0	5	0
NCI_Notch_signaling_Main_Pathway	-0,026	-0,033	0,007	47	-0,009
NCI_Notch_signaling_Pathway_(Bergmann_glial_cell_differentiation)	-0,031	-0,059	-0,000	26	-0,016
NCI_Notch_signaling_Pathway_(oligodendrocyte_development)	-0,029	-0,055	-0,000	28	-0,015
NCI_Notch_signaling_Pathway_(skeletal_muscle_tissue_development)	-0,188	0,062	-0,142	5	-0,165
NCI_Osteopontin_mediated_events_Main_Pathway	-0,015	0,000	0,048	30	0,017
NCI_Osteopontin_mediated_events_Pathway_(bone_resorption)	-0,076	-0,057	0,072	11	-0,002
NCI_Osteopontin_mediated_events_Pathway_(ruffle_organization)	-0,023	0,232	-0,063	5	-0,043
NCI_p38_MAPK_signaling_Main_Pathway	-0,006	0,049	-0,002	27	-0,004
NCI_p38_signaling_mediated_by_MAPKAP_kinases_Main_Pathway	0,063	-0,063	0,029	21	0,046
NCI_p38_signaling_mediated_by_MAPKAP_kinases_Pathway_(actin_cytoskeleton_reorganization)	0,083	-0,190	0,070	5	0,077
NCI_p38_signaling_mediated_by_MAPKAP_kinases_Pathway_(chemotaxis)	-0,013	-0,007	0,007	4	-0,003
NCI_p38_signaling_mediated_by_MAPKAP_kinases_Pathway_(regulation_of_mRNA_stability)	-0,017	-0,009	0,010	3	-0,004
NCI_p53_Main_Pathway	-0,104	0,095	-0,110	44	-0,107
NCI_p53_Pathway_(apoptosis)	0,014	-0,029	0,014	40	0,014
NCI_p53_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	-0,044	0,013	0,038	4	-0,003
NCI_p73_transcription_factor_network_Main_Pathway	-0,013	-0,002	0,014	76	0,001
NCI_p73_transcription_factor_network_Pathway_(apoptosis)	-0,004	-0,043	0,007	22	0,001
NCI_p75_NTR_mediated_signaling_Main_Pathway	-0,021	-0,021	0,012	60	-0,004
NCI_p75_NTR_mediated_signaling_Pathway_(activation_of_caspase_activity)	-0,050	0,147	0,025	7	-0,013
NCI_p75_NTR_mediated_signaling_Pathway_(cell_cycle_arrest)	-0,028	0,081	0,022	9	-0,003
NCI_p75_NTR_mediated_signaling_Pathway_(neuron_apoptosis)	-0,006	-0,037	0,040	24	0,017
NCI_p75_NTR_mediated_signaling_Pathway_(neuron_projection_morphogenesis)	-0,025	0,055	0,009	17	-0,008
NCI_PAR1_mediated_thrombin_signaling_events_Main_Pathway	-0,031	-0,035	0,020	43	-0,005
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(cAMP_biosynthetic_process)	-0,046	-0,096	0,034	21	-0,006
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(chemotaxis)	-0,062	0,140	-0,036	4	-0,049
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(focal_adhesion_assembly)	-0,012	0,048	0,001	7	-0,005
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(MAPKKK_cascade)	-0,011	-0,057	0,022	13	0,005

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(platelet_aggregation)	-0,023	-0,011	0,008	17	-0,008
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(positive_regulation_of_stress_fiber_assembly)	-0,020	0,073	-0,001	12	-0,011
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(Regulation_of_Cell_Shape)	-0,062	0,140	-0,036	4	-0,049
NCI_PAR1_mediated_thrombin_signaling_events_Pathway_(regulation_of_vascular_permeability)	0,017	0,019	0,021	12	0,019
NCI_PAR4_mediated_thrombin_signaling_events_Main_Pathway	-0,044	0,019	-0,009	15	-0,027
NCI_PAR4_mediated_thrombin_signaling_events_Pathway_(platelet_aggregation)	-0,062	0,140	-0,036	4	-0,049
NCI_PAR4_mediated_thrombin_signaling_events_Pathway_(Regulation_of_Cell_Shape)	-0,062	0,140	-0,036	4	-0,049
NCI_PDGF_receptor_signaling_network_Main_Pathway	0	0	0	6	0
NCI_PDGF_receptor_signaling_network_Pathway_(platelet_derived_growth_factor_receptor_signaling_pathway)	0	0	0	6	0
NCI_PDGFR_alpha_signaling_Main_Pathway	0,019	-0,177	0,072	20	0,046
NCI_PDGFR_alpha_signaling_Pathway_(JAK_STAT_cascade)	0,047	-0,947	0,212	3	0,130
NCI_PDGFR_alpha_signaling_Pathway_(positive_regulation_of_JUN_kinase_activity)	-0,073	-0,271	0,119	5	0,023
NCI_PDGFR_alpha_signaling_Pathway_(Ras_protein_signal_transduction)	-0,073	-0,271	0,119	5	0,023
NCI_PDGFR_beta_signaling_Main_Pathway	0,013	-0,032	0,028	122	0,021
NCI_PDGFR_beta_signaling_Pathway_(actin_cytoskeleton_organization)	0,048	-0,151	0,016	5	0,032
NCI_PDGFR_beta_signaling_Pathway_(cell_migration)	-0,088	0,422	-0,019	15	-0,054
NCI_PDGFR_beta_signaling_Pathway_(chemotaxis)	-0,034	0,290	0,007	19	-0,014
NCI_PDGFR_beta_signaling_Pathway_(focal_adhesion_assembly)	0,007	-0,134	0,053	6	0,030
NCI_PDGFR_beta_signaling_Pathway_(receptor_recycling)	-0,008	0,054	0,030	13	0,011
NCI_PDGFR_beta_signaling_Pathway_(ruffle_organization)	0,018	-0,088	0,035	29	0,027
NCI_Plasma_membrane_estrogen_receptor_signaling_Main_Pathway	-0,013	-0,021	0,015	36	0,001
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(apoptosis)	0,047	-0,141	0,067	7	0,057
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(cAMP_biosynthetic_process)	-0,053	0,011	-0,021	6	-0,037
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(cell_adhesion)	-0,007	-0,086	0,035	16	0,014
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(JNK_cascade)	0	0	0	1	0
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(MAPKKK_cascade)	-0,012	0,033	0,007	2	-0,002
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(pseudopodium_formation)	0,010	0,008	-0,024	3	-0,007
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(regulation_of_stress_fiber_assembly)	0,010	0,008	-0,024	3	-0,007
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(ruffle_organization)	0,010	0,008	-0,024	3	-0,007
NCI_Plasma_membrane_estrogen_receptor_signaling_Pathway_(vasodilation)	-0,007	-0,086	0,035	16	0,014
NCI_Plexin_D1_Signaling_Main_Pathway	0,020	-0,128	0,065	19	0,042
NCI_Plexin_D1_Signaling_Pathway_(cell_adhesion_mediated_by_integrin)	0,025	-0,162	0,082	15	0,054
NCI_Plexin_D1_Signaling_Pathway_(endothelial_cell_migration)	-0,015	0,171	-0,003	3	-0,009
NCI_Plexin_D1_Signaling_Pathway_(focal_adhesion_assembly)	0	0	0	3	0
NCI_Plexin_D1_Signaling_Pathway_(receptor_recycling)	0,008	0,111	0,031	4	0,020
NCI_Plexin_D1_Signaling_Pathway_(regulation_of_synapse_organization)	0	0	0	3	0
NCI_PLK1_signaling_events_Main_Pathway	0,016	-0,034	-0,016	42	0,000
NCI_PLK1_signaling_events_Pathway_(chromosome_segregation)	0,077	-0,192	0,004	2	0,041
NCI_PLK1_signaling_events_Pathway_(cytokinesis)	0,006	0,042	-0,017	13	-0,005
NCI_PLK1_signaling_events_Pathway_(G2_M_transition_of_mitotic_cell_cycle)	0,054	-0,023	-0,021	5	0,016
NCI_PLK1_signaling_events_Pathway_(Golgi_organization)	0,032	0,024	-0,013	14	0,010
NCI_PLK1_signaling_events_Pathway_(metaphase_plate_congression)	0,033	0,005	-0,007	11	0,013
NCI_PLK1_signaling_events_Pathway_(microtubule_cytoskeleton_organization)	0,028	0,030	-0,013	12	0,007
NCI_PLK1_signaling_events_Pathway_(positive_regulation_of_microtubule_depolymerization)	0,019	0,011	-0,008	12	0,005
NCI_PLK1_signaling_events_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	0,054	-0,085	0,006	12	0,030
NCI_PLK1_signaling_events_Pathway_(regulation_of_attachment_of_spindle_microtubules_to_kinetochore)	0,040	0,003	-0,007	16	0,017
NCI_PLK1_signaling_events_Pathway_(regulation_of_centriole_centriole_cohesion)	0,032	0,002	-0,005	14	0,013

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_PLK1_signaling_events_Pathway_(regulation_of_mitotic_centrosome_separation)	0,032	0,024	-0,013	14	0,010
NCI_PLK1_signaling_events_Pathway_(spindle_assembly)	0,028	0,021	-0,011	16	0,008
NCI_PLK1_signaling_events_Pathway_(spindle_elongation)	0,032	0,024	-0,013	14	0,010
NCI_PLK1_signaling_events_Pathway_(spindle_stabilization)	0,012	0,020	-0,014	12	-0,001
NCI_PLK2_and_PLK4_events_Main_Pathway	0	0	0	2	0
NCI_PLK2_and_PLK4_events_Pathway_(regulation_of_centriole_replication)	0	0	0	2	0
NCI_PLK3_signaling_events_Main_Pathway	0,031	-0,003	-0,001	5	0,015
NCI_Posttranslational_regulation_of_adherens_junction_stability_and_dissassembly_Main_Pathway	-0,018	-0,056	0,005	48	-0,007
NCI_Posttranslational_regulation_of_adherens_junction_stability_and_dissassembly_Pathway_(axonogenesis)	-0,015	-0,132	0,017	26	0,001
NCI_Presenilin_action_in_Notch_and_Wnt_signaling_Main_Pathway	0,006	-0,014	0,014	41	0,010
NCI_Presenilin_action_in_Notch_and_Wnt_signaling_Pathway_(apoptosis)	0,013	-0,013	-0,005	15	0,004
NCI_Presenilin_action_in_Notch_and_Wnt_signaling_Pathway_(Pathway_degradation_of_CTNNB1)	0,003	-0,020	0,021	33	0,012
NCI_Proteoglycan_syndecan_mediated_signaling_events_Main_Pathway	-0,105	0,112	-0,035	4	-0,070
NCI_RAC1_signaling_Main_Pathway	0,030	-0,080	0,035	54	0,033
NCI_RAC1_signaling_Pathway_(actin_filament_depolymerization)	-0,065	0,176	-0,007	3	-0,036
NCI_RAC1_signaling_Pathway_(actin_filament_polymerization)	0,008	0,148	0,051	4	0,030
NCI_RAC1_signaling_Pathway_(lamellipodium_assembly)	0,030	-0,085	0,033	18	0,031
NCI_RAC1_signaling_Pathway_(neuron_projection_development)	-0,060	0,191	-0,018	4	-0,039
NCI_RAC1_signaling_Pathway_(Pathway_positive_regulation_of_NF_kappaB_transcription_factor_activity_via_RAC1)	-0,133	0,435	-0,026	3	-0,079
NCI_RAC1_signaling_Pathway_(positive_regulation_of_Wnt_receptor_signaling_pathway)	0,017	0,133	0,048	4	0,033
NCI_RAC1_signaling_Pathway_(regulation_of_cell_cycle)	-0,066	0,132	-0,024	4	-0,045
NCI_Rapid_glucocorticoid_signaling_Main_Pathway	-0,080	0,016	-0,031	4	-0,055
NCI_Rapid_glucocorticoid_signaling_Pathway_(glutamate_secretion)	-0,080	0,016	-0,031	4	-0,055
NCI_Ras_signaling_in_the_CD4_TCR_Main_Pathway	-0,016	0,151	0,004	14	-0,006
NCI_Reelin_signaling_Main_Pathway	0,065	-0,158	0,048	22	0,057
NCI_Reelin_signaling_Pathway_(long_term_memory)	-0,000	0,021	0,012	7	0,006
NCI_Reelin_signaling_Pathway_(neuron_migration)	0,005	0,017	0,010	8	0,008
NCI_Regulation_of_Androgen_receptor_activity_Main_Pathway	0,014	-0,005	0,005	30	0,009
NCI_Regulation_of_Androgen_receptor_activity_Pathway_(cell_proliferation)	0,016	-0,005	0,006	26	0,011
NCI_Regulation_of_Androgen_receptor_activity_Pathway_(Pathway_positive_regulation_of_transcription_via_GATA2)	0	0	0	1	0
NCI_Regulation_of_CDC42_activity_Main_Pathway	0,003	0,019	-0,005	30	-0,001
NCI_Regulation_of_cytoplasmic_and_nuclear_SMAD2_3_signaling_Main_Pathway	0,007	-0,059	0,015	18	0,011
NCI_Regulation_of_nuclear_beta_catenin_signaling_and_target_gene_transcription_Main_Pathway	0,020	-0,043	0,034	78	0,027
NCI_Regulation_of_nuclear_SMAD2_3_signaling_Main_Pathway	-0,002	-0,056	0,029	63	0,013
NCI_Regulation_of_nuclear_SMAD2_3_signaling_Pathway_(muscle_cell_differentiation)	-0,003	-0,081	0,045	42	0,021
NCI_Regulation_of_nuclear_SMAD2_3_signaling_Pathway_(negative_regulation_of_cell_growth)	0	0	0	1	0
NCI_Regulation_of_nuclear_SMAD2_3_signaling_Pathway_(Pathway_degradation_of_SMAD3)	-0,002	-0,091	0,052	38	0,025
NCI_Regulation_of_p38_alpha_and_p38_beta_Main_Pathway	-0,043	0,237	-0,016	26	-0,029
NCI_Regulation_of_p38_alpha_and_p38_beta_Pathway_(positive_regulation_of_innate_immune_response)	-0,043	0,237	-0,016	26	-0,029
NCI_Regulation_of_RAC1_activity_Main_Pathway	-0,012	0,027	-0,007	38	-0,009
NCI_Regulation_of_Ras_family_activation_Main_Pathway	0,024	-0,017	-0,005	32	0,010
NCI_Regulation_of_retinoblastoma_protein_Main_Pathway	-0,014	0,037	0,012	52	-0,001
NCI_Regulation_of_retinoblastoma_protein_Pathway_(erythrocyte_differentiation)	-0,029	0,044	0,019	9	-0,005
NCI_Regulation_of_retinoblastoma_protein_Pathway_(histone_methylation)	-0,023	0,049	0,026	6	0,002
NCI_Regulation_of_retinoblastoma_protein_Pathway_(Pathway_rRNA_transcription_via_RB1)	0,009	0,013	0,032	25	0,021
NCI_Regulation_of_retinoblastoma_protein_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	0,015	0,011	0,034	19	0,024
NCI_Regulation_of_RhoA_activity_Main_Pathway	0,007	-0,044	0,005	46	0,006
NCI_Regulation_of_Telomerase_Main_Pathway	-0,152	0,059	-0,021	40	-0,087

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Regulation_of_Telomerase_Pathway_(cell_cycle)	0,034	-0,016	-0,013	3	0,010
NCI_Retinoic_acid_receptors_mediated_signaling_Main_Pathway	-0,028	-0,004	0,006	29	-0,011
NCI_Retinoic_acid_receptors_mediated_signaling_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	-0,004	-0,023	0,007	19	0,002
NCI_RhoA_signaling_Main_Pathway	0,027	-0,085	0,037	27	0,032
NCI_RhoA_signaling_Pathway_(actin_cytoskeleton_organization)	-0,004	-0,130	0,009	2	0,002
NCI_RhoA_signaling_Pathway_(actin_filament_depolymerization)	-0,019	0,046	-0,005	5	-0,012
NCI_RhoA_signaling_Pathway_(Golgi_organization)	-0,098	0,177	-0,053	2	-0,075
NCI_RhoA_signaling_Pathway_(Pathway_positive_regulation_of_NF_kappaB_transcription_factor_activity_via_RHOA)	-0,094	0,196	-0,105	1	-0,099
NCI_Role_of_Calcineurin_dependent_NFAT_signaling_in_lymphocytes_Main_Pathway	0,017	-0,022	0,006	49	0,011
NCI_Role_of_Calcineurin_dependent_NFAT_signaling_in_lymphocytes_Pathway_(apoptosis)	0,040	-0,023	-0,028	4	0,006
NCI_Role_of_Calcineurin_dependent_NFAT_signaling_in_lymphocytes_Pathway_(positive_T_cell_selection)	-0,023	0,057	0,026	4	0,001
NCI_RXR_and_RAR_heterodimerization_with_other_nuclear_receptor_Main_Pathway	-0,015	0,011	-0,001	12	-0,008
NCI_S1P1_Main_Pathway	-0,035	0,011	-0,005	19	-0,020
NCI_S1P1_Pathway_(negative_regulation_of_cAMP_metabolic_process)	-0,038	-0,087	0,030	6	-0,004
NCI_S1P1_Pathway_(negative_regulation_of_T_cell_proliferation)	-0,038	-0,087	0,030	6	-0,004
NCI_S1P1_Pathway_(receptor_internalization)	-0,030	-0,032	0,023	11	-0,003
NCI_S1P2_Main_Pathway	0,003	-0,052	0,019	26	0,011
NCI_S1P2_Pathway_(chemotaxis)	0,010	-0,023	-0,014	8	-0,002
NCI_S1P2_Pathway_(regulation_of_vascular_permeability)	-0,036	0,038	-0,035	5	-0,036
NCI_S1P3_Main_Pathway	-0,016	-0,065	0,007	23	-0,005
NCI_S1P3_Pathway_(Sinus_Bradycardia)	-0,038	-0,087	0,030	6	-0,004
NCI_S1P4_Main_Pathway	-0,027	0,000	-0,005	14	-0,016
NCI_S1P4_Pathway_(cell_migration)	-0,036	-0,045	0,023	7	-0,006
NCI_S1P5_Main_Pathway	-0,040	-0,041	0,010	8	-0,015
NCI_S1P5_Pathway_(negative_regulation_of_cAMP_metabolic_process)	-0,038	-0,087	0,030	6	-0,004
NCI_S1P5_Pathway_(telencephalon_oligodendrocyte_cell_migration)	-0,046	-0,047	0,011	7	-0,017
NCI_SHP2_signaling_Main_Pathway	-0,034	-0,059	0,017	48	-0,009
NCI_Signaling_events_mediated_by_focal_adhesion_kinase_Main_Pathway	0,026	-0,063	0,033	47	0,030
NCI_Signaling_events_mediated_by_focal_adhesion_kinase_Pathway_(apoptosis)	0,095	-0,206	0,104	4	0,099
NCI_Signaling_events_mediated_by_focal_adhesion_kinase_Pathway_(cell_migration)	0,016	-0,031	0,019	12	0,017
NCI_Signaling_events_mediated_by_focal_adhesion_kinase_Pathway_(negative_regulation_of_cell_adhesion_involved_in_substrate_bound_cell_migration)	0,040	-0,004	0,032	12	0,036
NCI_Signaling_events_mediated_by_focal_adhesion_kinase_Pathway_(regulation_of_cell_cycle)	0,143	-0,338	0,109	4	0,126
NCI_Signaling_events_mediated_by_HDAC_Class_I_Main_Pathway	-0,037	0,023	0,017	52	-0,010
NCI_Signaling_events_mediated_by_HDAC_Class_I_Pathway_(histone_deacetylation)	-0,055	0,129	-0,006	18	-0,031
NCI_Signaling_events_mediated_by_HDAC_Class_I_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	-0,030	-0,007	0,024	4	-0,003
NCI_Signaling_events_mediated_by_HDAC_Class_II_Main_Pathway	-0,024	0,022	0,010	29	-0,007
NCI_Signaling_events_mediated_by_HDAC_Class_III_Main_Pathway	-0,004	-0,057	0,069	17	0,032
NCI_Signaling_events_mediated_by_HDAC_Class_III_Pathway_(muscle_cell_differentiation)	-0,075	-0,193	0,075	8	0,000
NCI_Signaling_events_mediated_by_HDAC_Class_III_Pathway_(regulation_of_S_phase_of_mitotic_cell_cycle)	-0,090	-0,232	0,090	7	0,000
NCI_Signaling_events_mediated_by_Hepatocyte_Growth_Factor_Receptor_c_Met__Main_Pathway	0,009	0,001	0,010	72	0,010
NCI_Signaling_events_mediated_by_Hepatocyte_Growth_Factor_Receptor_c_Met__Pathway_(apoptosis)	0,018	0,112	-0,045	4	-0,014
NCI_Signaling_events_mediated_by_Hepatocyte_Growth_Factor_Receptor_c_Met__Pathway_(Pathway_positive_regulation_of_NF_kappaB_transcription_factor_activity_via_RAF1)	-0,040	-0,000	-0,001	9	-0,020
NCI_Signaling_events_mediated_by_Hepatocyte_Growth_Factor_Receptor_c_Met__Pathway_(positive_regulation_of_tyrosine_phosphorylation_of_STAT_protein)	0,033	-0,056	0,030	17	0,031
NCI_Signaling_events_mediated_by_Hepatocyte_Growth_Factor_Receptor_c_Met__Pathway_(translational_initiation)	0,013	0,122	-0,015	9	-0,001

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Signaling_events_mediated_by_PRL_Main_Pathway	0,032	-0,056	0,018	21	0,025
NCI_Signaling_events_mediated_by_PRL_Pathway_(cell_motility)	-0,002	0,057	-0,020	5	-0,011
NCI_Signaling_events_mediated_by_PRL_Pathway_(mitosis)	0,081	-0,283	0,083	2	0,082
NCI_Signaling_events_mediated_by_PTP1B_Main_Pathway	0,025	-0,100	-0,004	13	0,011
NCI_Signaling_events_mediated_by_PTP1B_Pathway_(cell_migration)	-0,100	0,127	-0,075	3	-0,087
NCI_Signaling_events_mediated_by_PTP1B_Pathway_(Ras_protein_signal_transduction)	-0,100	0,127	-0,075	3	-0,087
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Main_Pathway	-0,083	0,053	0,015	50	-0,034
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(actin_filament_polymerization)	0	0	0	3	0
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(cell_migration)	0	0	0	3	0
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(cell_motility)	0,066	-0,160	0,023	9	0,045
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(cell_proliferation)	0,059	-0,025	-0,004	3	0,028
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(megakaryocyte_differentiation)	0	0	0	3	0
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(Pathway_positive_regulation_of_transcription_via_MAPK3)	0,025	0,029	-0,010	4	0,007
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(positive_regulation_of_cell_proliferation)	0,066	-0,160	0,023	9	0,045
NCI_Signaling_events_mediated_by_Stem_cell_factor_receptor_c_Kit__Pathway_(response_to_radiation)	0	0	0	3	0
NCI_Signaling_events_mediated_by_TCPTP_Main_Pathway	-0,007	0,104	-0,027	32	-0,017
NCI_Signaling_events_mediated_by_TCPTP_Pathway_(G1_S_transition_of_mitotic_cell_cycle)	0,031	-0,161	0,032	12	0,032
NCI_Signaling_events_mediated_by_TCPTP_Pathway_(macrophage_differentiation)	0,048	-0,217	0,041	13	0,044
NCI_Signaling_events_mediated_by_TCPTP_Pathway_(MAPKKK_cascade)	0,031	-0,161	0,032	12	0,032
NCI_Signaling_events_mediated_by_TCPTP_Pathway_(positive_regulation_of_S_phase_of_mitotic_cell_cycle)	0,001	0,029	0,013	14	0,007
NCI_Signaling_events_mediated_by_TCPTP_Pathway_(regulation_of_gluconeogenesis)	0,059	-0,269	0,050	11	0,055
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Main_Pathway	0,011	-0,048	0,016	21	0,013
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Pathway_(catabolic_process)	0	0	0	3	0
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Pathway_(determination_of_left_right_symmetry)	0,042	-0,060	0,027	6	0,035
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Pathway_(heart_development)	0,042	-0,060	0,027	6	0,035
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Pathway_(heart_looping)	0,042	-0,060	0,027	6	0,035
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Pathway_(pancreas_development)	0	0	0	2	0
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Pathway_(receptor_mediated_endocytosis)	0,012	-0,052	0,007	13	0,009
NCI_Signaling_events_mediated_by_the_Hedgehog_family_Pathway_(somite_specification)	0,042	-0,060	0,027	6	0,035
NCI_Signaling_events_mediated_by_VEGFR1_and_VEGFR2_Main_Pathway	-0,008	-0,024	0,019	63	0,006
NCI_Signaling_events_mediated_by_VEGFR1_and_VEGFR2_Pathway_(angiogenesis)	-0,019	-0,094	0,057	31	0,019
NCI_Signaling_events_mediated_by_VEGFR1_and_VEGFR2_Pathway_(cell_proliferation)	0,043	-0,049	0,007	13	0,025
NCI_Signaling_events_mediated_by_VEGFR1_and_VEGFR2_Pathway_(focal_adhesion_assembly)	0,068	-0,157	0,040	13	0,054
NCI_Signaling_events_mediated_by_VEGFR1_and_VEGFR2_Pathway_(Pathway_degradation_of_AKAP1)	-0,334	0,262	0,110	1	-0,112
NCI_Signaling_events_mediated_by_VEGFR1_and_VEGFR2_Pathway_(regulation_of_vascular_permeability)	-0,018	-0,090	0,055	32	0,018
NCI_Signaling_events_mediated_by_VEGFR1_and_VEGFR2_Pathway_(stress_fiber_assembly)	-0,006	0,009	-0,035	3	-0,021
NCI_Signaling_events_regulated_by_Ret_tyrosine_kinase_Main_Pathway	0,002	0,002	-0,001	31	0,001
NCI_Signaling_events_regulated_by_Ret_tyrosine_kinase_Pathway_(activation_of_MAPKK_activity)	-0,022	0,063	-0,024	7	-0,023
NCI_Signaling_events_regulated_by_Ret_tyrosine_kinase_Pathway_(lamellipodium_assembly)	-0,003	0,031	-0,035	12	-0,019

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_Signaling_events_regulated_by_Ret_tyrosine_kinase_Pathway_(MAPKKK_cascade)	-0,030	0,069	-0,034	5	-0,032
NCI_Signaling_events_regulated_by_Ret_tyrosine_kinase_Pathway_(tube_development)	-0,030	0,069	-0,034	5	-0,032
NCI_Signaling_mediated_by_p38_alpha_and_p38_beta_Main_Pathway	-0,018	-0,003	0,011	33	-0,003
NCI_Signaling_mediated_by_p38_gamma_and_p38_delta_Main_Pathway	-0,010	0,071	0,006	11	-0,002
NCI_Signaling_mediated_by_p38_gamma_and_p38_delta_Pathway_(G2_M_transition_checkpoint)	0,025	-0,007	0,014	4	0,020
NCI_Sphingosine_1_phosphate_S1P_Main_Pathway	-0,025	-0,065	0,028	20	0,001
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Main_Pathway	0,014	0,026	0,013	41	0,013
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(actin_cable_formation)	0,023	0,019	0,019	15	0,021
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(actin_cytoskeleton_organization)	-0,012	0,008	0,023	6	0,005
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(adherens_junction_assembly)	-0,019	0,050	0,005	13	-0,007
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(adherens_junction_organization)	-0,018	0,089	-0,036	3	-0,027
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(cortical_microtubule_organization)	-0,056	0,148	0,008	4	-0,024
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(epithelial_cell_differentiation)	-0,056	0,148	0,008	4	-0,024
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(establishment_of_epithelial_cell_apical_basal_polarity)	-0,040	-0,011	0,009	9	-0,015
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(regulation_of_calcium_dependent_cell_cell_adhesion)	-0,045	0,118	0,006	5	-0,019
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(regulation_of_cell_cell_adhesion)	-0,014	0,035	0,003	9	-0,005
NCI_Stabilization_and_expansion_of_the_E_cadherin_adherens_junction_Pathway_(Wnt_receptor_signaling_pathway)	-0,056	0,148	0,008	4	-0,024
NCI_Sumoylation_by_RanBP2_regulates_transcriptional_repression_Main_Pathway	-0,040	0,052	0,014	15	-0,013
NCI_Syndecan_1_mediated_signaling_events_Main_Pathway	0,008	-0,045	0,012	32	0,010
NCI_Syndecan_1_mediated_signaling_events_Pathway_(homophilic_cell_adhesion)	-0,020	0,022	0,001	27	-0,009
NCI_Syndecan_1_mediated_signaling_events_Pathway_(positive_regulation_of_cell_migration)	-0,020	0,022	0,001	27	-0,009
NCI_Syndecan_1_mediated_signaling_events_Pathway_(Tumor_Cell_Invasion)	-0,020	0,022	0,001	27	-0,009
NCI_Syndecan_2_mediated_signaling_events_Main_Pathway	0,023	-0,097	0,018	27	0,021
NCI_Syndecan_2_mediated_signaling_events_Pathway_(dendrite_morphogenesis)	-0,004	-0,043	-0,012	6	-0,008
NCI_Syndecan_2_mediated_signaling_events_Pathway_(determination_of_left_right_symmetry)	-0,004	-0,043	-0,012	6	-0,008
NCI_Syndecan_2_mediated_signaling_events_Pathway_(positive_regulation_of_cell_cell_adhesion)	0,042	-0,042	-0,014	7	0,014
NCI_Syndecan_3_mediated_signaling_events_Main_Pathway	0,017	-0,278	0,100	15	0,058
NCI_Syndecan_3_mediated_signaling_events_Pathway_(limb_bud_formation)	0,032	-0,155	0,078	12	0,055
NCI_Syndecan_4_mediated_signaling_events_Main_Pathway	0,026	-0,010	-0,009	21	0,008
NCI_Syndecan_4_mediated_signaling_events_Pathway_(cell_migration)	0,018	0,007	0,001	11	0,009
NCI_TCR_signaling_in_naive_CD4_T_cells_Main_Pathway	-0,002	0,012	0,007	60	0,003
NCI_TCR_signaling_in_naive_CD4_T_cells_Pathway_(proteasomal_ubiquitin_dependent_protein_catabolic_process)	-0,025	0,045	-0,017	19	-0,021
NCI_TCR_signaling_in_naive_CD8_T_cells_Main_Pathway	-0,005	0,001	-0,004	53	-0,004
NCI_TCR_signaling_in_naive_CD8_T_cells_Pathway_(Pathway_regulation_of_survival_gene_product_expression_via_AKT1)	-0,065	0,105	-0,008	17	-0,037
NCI_TGF_beta_receptor_signaling_Main_Pathway	0,012	0,155	-0,042	34	-0,015
NCI_TGF_beta_receptor_signaling_Pathway_(JNK_cascade)	-0,017	0,141	0,020	8	0,001
NCI_Thromboxane_A2_receptor_signaling_Main_Pathway	-0,015	0,074	0,006	48	-0,004
NCI_Thromboxane_A2_receptor_signaling_Pathway_(cAMP_biosynthetic_process)	0,021	-0,082	0,037	21	0,029
NCI_Thromboxane_A2_receptor_signaling_Pathway_(JNK_cascade)	0,120	-0,242	0,057	13	0,088
NCI_Thromboxane_A2_receptor_signaling_Pathway_(MAPKKK_cascade)	0,017	-0,055	0,021	25	0,019
NCI_Thromboxane_A2_receptor_signaling_Pathway_(platelet_activation)	0,018	-0,070	0,032	24	0,025
NCI_TNF_receptor_signaling_pathway__Main_Pathway	0,015	-0,073	0,045	36	0,030
NCI_TNF_receptor_signaling_pathway__Pathway_(JNK_cascade)	-0,001	0,025	0,022	14	0,010

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
NCI_TRAIL_signaling_Main_Pathway	0,004	0,020	-0,017	21	-0,006
NCI_Trk_receptor_signaling_mediated_by_PI3K_and_PLC_gamma_Main_Pathway	-0,032	0,047	-0,005	33	-0,019
NCI_Trk_receptor_signaling_mediated_by_PI3K_and_PLC_gamma_Pathway_(axonogenesis)	-0,047	0,143	-0,001	11	-0,024
NCI_Trk_receptor_signaling_mediated_by_PI3K_and_PLC_gamma_Pathway_(neuron_apoptosis)	-0,047	0,143	-0,001	11	-0,024
NCI_Trk_receptor_signaling_mediated_by_PI3K_and_PLC_gamma_Pathway_(regulation_of_long_term_neuronal_synaptic_plasticity)	-0,044	0,177	-0,016	1	-0,030
NCI_Trk_receptor_signaling_mediated_by_the_MAPK_Main_Pathway	-0,014	0,042	-0,000	30	-0,007
NCI_Trk_receptor_signaling_mediated_by_the_MAPK_Pathway_(neuron_apoptosis)	-0,016	-0,001	0,009	10	-0,004
NCI_Trk_receptor_signaling_mediated_by_the_MAPK_Pathway_(neuron_projection_morphogenesis)	0,042	-0,038	0,008	7	0,025
NCI_Urokinase_type_plasminogen_activator_uPA_and_uPAR_mediated_signaling_Main_Pathway	0,037	-0,171	0,063	37	0,050
NCI_Urokinase_type_plasminogen_activator_uPA_and_uPAR_mediated_signaling_Pathway_(cell_adhesion)	0,240	-0,482	0,220	3	0,230
NCI_Urokinase_type_plasminogen_activator_uPA_and_uPAR_mediated_signaling_Pathway_(cell_migration)	0,206	-0,460	0,204	5	0,205
NCI_Urokinase_type_plasminogen_activator_uPA_and_uPAR_mediated_signaling_Pathway_(cell_proliferation)	0,165	-0,352	0,164	6	0,165
NCI_Validated_nuclear_estrogen_receptor_alpha_network_Main_Pathway	-0,176	0,173	-0,136	47	-0,156
NCI_Validated_nuclear_estrogen_receptor_beta_network_Main_Pathway	-0,324	0,337	-0,345	15	-0,335
NCI_Validated_targets_of_C_MYC_transcriptional_activation_Main_Pathway	-0,016	0,038	0,025	56	0,005
NCI_Validated_targets_of_C_MYC_transcriptional_activation_Pathway_(Pathway_rRNA_transcription_via_MAX)	-0,026	0,040	0,035	5	0,005
NCI_Validated_targets_of_C_MYC_transcriptional_repression_Main_Pathway	-0,026	-0,056	0,027	53	0,000
NCI_Validated_targets_of_C_MYC_transcriptional_repression_Pathway_(cell_cycle_arrest)	-0,010	-0,074	0,031	12	0,010
NCI_Validated_transcriptional_targets_of_AP1_family_members_Fra1_and_Fra2_Main_Pathway	-0,241	0,050	0,023	17	-0,109
NCI_Validated_transcriptional_targets_of_deltaNp63_isoforms_Main_Pathway	-0,005	-0,005	-0,001	47	-0,003
NCI_Validated_transcriptional_targets_of_deltaNp63_isoforms_Pathway_(Pathway_degradation_of_TP63)	-0,001	-0,004	-0,001	9	-0,001
NCI_Validated_transcriptional_targets_of_TAp63_isoforms_Main_Pathway	-0,017	0,099	0,037	53	0,010
NCI_Validated_transcriptional_targets_of_TAp63_isoforms_Pathway_(Metastasis)	-0,030	0,111	0,031	14	0,001
NCI_Validated_transcriptional_targets_of_TAp63_isoforms_Pathway_(Pathway_degradation_of_TP63)	-0,030	0,111	0,031	13	0,001
NCI_VEGF_and_VEGFR_signaling_network_Main_Pathway	0,014	0,003	-0,065	10	-0,026
NCI_VEGFR1_specific_signals_Main_Pathway	0,023	0,005	-0,109	6	-0,043
NCI_VEGFR3_signaling_in_lymphatic_endothelium_Main_Pathway	-0,013	0,006	0,017	16	0,002
NCI_VEGFR3_signaling_in_lymphatic_endothelium_Pathway_(cell_migration)	0,024	-0,130	0,043	10	0,033
NCI_VEGFR3_signaling_in_lymphatic_endothelium_Pathway_(cell_proliferation)	-0,023	0,027	-0,012	8	-0,018
NCI_VEGFR3_signaling_in_lymphatic_endothelium_Pathway_(DNA_mediated_transformation)	-0,048	0,043	-0,010	6	-0,029
NCI_VEGFR3_signaling_in_lymphatic_endothelium_Pathway_(lymphangiogenesis)	0	0	0	3	0
NCI_VEGFR3_signaling_in_lymphatic_endothelium_Pathway_(vasculogenesis)	0	0	0	3	0
NCI_Visual_signal_transduction_Cones_Main_Pathway	0	0	0	5	0
NCI_Visual_signal_transduction_Rods_Main_Pathway	-0,027	0,016	-0,011	8	-0,019
NCI_Wnt_signaling_network_Main_Pathway	0,003	-0,059	0,028	28	0,016
NCI_Wnt_signaling_network_Pathway_(Wnt_receptor_signaling_pathway_through_beta_catenin)	-0,003	-0,011	0,006	24	0,001
Neuronal_Development_Induced_by_CDK5	0,017	-0,025	0,001	81	0,009
Neuronal_Intermediate_Filaments	-0,011	0,001	0,000	10	-0,006
NGF_Pathway	0,018	-0,063	0,036	87	0,027
NGF_Pathway_Actin_Polymerization_Neurite_Outgrowth_and_Differentiation	-0,012	-0,134	0,020	11	0,004
NGF_Pathway_Apoptosis	0,004	0,016	0,010	12	0,007
NGF_Pathway_Gene_Expression_via_MYC_ELK1_CREB3_NFKB2	0,062	-0,160	0,076	22	0,069
NGF_Pathway_Neurite_Outgrowth_and_Differentiation	0,025	-0,073	0,022	21	0,024
NGF_Pathway_Neuronal_Survival	0,016	0,010	0,009	16	0,013
nicotine_degradation_III	-0,033	0,041	-0,012	8	-0,023
nicotine_degradation_IV	-0,019	0,023	-0,007	14	-0,013

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
Nicotine_Influence_on_Glutamatergic_Neurons	-0,035	0,010	0,006	56	-0,015
Nitric_Oxide_Pathway_in_Skeletal_Muscle	-0,010	0,005	0,000	36	-0,005
Non-Junctional_Cell_Adhesion_in_Endothelium	0,042	-0,163	0,046	35	0,044
noradrenaline_and_adrenaline_degradation	-0,061	-0,011	-0,019	11	-0,040
Notch_Signaling_Pathway	0,021	-0,068	0,027	33	0,024
Notch_Signaling_Pathway_gamma_Secretase	0,009	-0,263	0,084	6	0,047
Notch_Signaling_Pathway_Gene_Expression_Chromatin_Remodeling_via_RBPJ	0,023	-0,025	0,014	27	0,019
Notch_Signaling_Pathway_Transcription_of_Target_Genes_Hairy_E-Spl_via_RBPJ	0,023	-0,025	0,014	27	0,019
oleate_biosynthesis	0,024	-0,090	0,014	6	0,019
ornithine_ide_novo_i_biosynthesis	-0,122	-0,008	0,045	4	-0,039
Outside-in_Signaling_through_Integrins	0,045	-0,059	0,019	50	0,032
oxidative_ethanol_degradation_III	-0,110	0,044	-0,027	7	-0,068
oxidized_GTP_and_dGTP_detoxification	-0,023	0,225	0,147	1	0,062
p38_Signaling_Pathway	-0,012	-0,023	0,011	487	-0,001
p38_Signaling_Pathway_Actin_Cytoskeleton_Reorganiztion	0,083	-0,190	0,070	5	0,077
p38_Signaling_Pathway_Apoptosis	0	0	0	2	0
p38_Signaling_Pathway_Gene_Expression_Cell_Motility_Inflammation_Apoptosis_Osmoregulation_via_MEF2D_TP53_CREB1_ATF2_JUND_ETV1_NFKB2_AP2A1_MAX_FOSL1_CEBPG_ELK1_CDC25C_JUNB_STAT1_SP1_DDIT3_ELK4_CEBPA	-0,001	-0,119	0,065	36	0,032
p38_Signaling_Pathway_Translation	-0,018	0,000	-0,019	4	-0,018
p53_Signaling_Pathway	0,024	-0,051	0,016	130	0,020
p53_Signaling_Pathway_Apoptosis	0,038	-0,073	0,022	49	0,030
p53_Signaling_Pathway_Breast_Cancer	0,031	-0,049	0,010	35	0,020
p53_Signaling_Pathway_Cancer	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Cell_Cycle_Arrest	0,031	-0,049	0,010	49	0,020
p53_Signaling_Pathway_Cell_Growth_Accumulation	0,031	-0,049	0,010	35	0,020
p53_Signaling_Pathway_DNA_Repair	0,031	-0,049	0,010	36	0,020
p53_Signaling_Pathway_Exosome_Mediated_Secretion	0,031	-0,049	0,010	35	0,020
p53_Signaling_Pathway_Gene_Expression_Anti-Apoptosis_via_TP53	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Gene_Expression_Cell_Cycle_and_Cell_Growth_via_TP53	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Gene_Expression_Cell_Fate_and_Development_via_TP53	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Gene_Expression_Cell_Signaling_via_TP53	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Gene_Expression_DNA_Replication_and_Repair_via_TP53	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Gene_Expression_ECM_and_Adhesion_via_TP53	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Gene_Expression_Infection_and_Immune_Response_via_TP53	0,038	-0,073	0,022	39	0,030
p53_Signaling_Pathway_Inhibition_of_Angiogenesis_and_Metastasis	0,031	-0,049	0,010	38	0,020
p53_Signaling_Pathway_Inhibition_of_IGF1R_mTOR_Pathways	-0,264	0,237	0	4	-0,132
p53_Signaling_Pathway_Normal_Cell_Cycle_Progression	0,038	-0,073	0,022	39	0,030
PAK_Pathway	0,011	-0,039	0,010	343	0,010
PAK_Pathway_Actin_Organization	0,007	-0,016	0,005	250	0,006
PAK_Pathway_Cell_Survival	0,007	-0,016	0,005	250	0,006
PAK_Pathway_Contractility_Stress_Fibres_and_Focal_Adhesion	0,032	-0,087	0,036	53	0,034
PAK_Pathway_Lamelliopodia_and_Filopodia_Outgrowth	0,008	-0,019	0,007	260	0,007
PAK_Pathway_Paxillin_Disassembly	0	0	0	1	0
PAK_Pathway_Transciptional_Activation_and_Filopodia_Formation	0,124	-0,268	0,095	6	0,109
palmitate_biosynthesis	-0,038	0,040	0,032	7	-0,003
pentose_phosphate_pathway	-0,013	0,124	0,027	7	0,007
pentose_phosphate_pathway_non-oxidative_branch	-0,042	0,131	-0,009	4	-0,025
pentose_phosphate_pathway_oxidative_branch	0,024	0,115	0,075	3	0,049
phenylalanine_degradationtyrosine_biosynthesis	0	0	0	4	0
phenylethylamine_degradation_I	-0,192	0,078	-0,047	4	-0,120
phosphatidylcholine_biosynthesis	-0,122	0,068	-0,041	6	-0,082
phosphatidylethanolamine_biosynthesis_II	-0,167	0,144	-0,053	6	-0,110
phosphatidylserine_biosynthesis_I	-0,042	-0,159	0,104	1	0,031
phospholipases	-0,102	0,083	0,003	39	-0,050
phytol_degradation	-0,140	-0,236	-0,041	2	-0,090

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
PLAU-mediated_Signaling_Events_During_Cell_Adhesion	-0,001	-0,092	0,001	30	-0,000
PPAR_Pathway	-0,009	-0,010	0,005	229	-0,002
PPAR_Pathway_Adipocyte_Differentiation_Glucose_Homeostasis_and_Macrophage_Function	0,014	-0,003	0,045	5	0,029
PPAR_Pathway_Fatty_Acid_Metabolism_Lipid_Homeostasis_and_Skin_Proliferation	0,014	-0,003	0,045	5	0,029
PPAR_Pathway_Peroxisome_Proliferation_Hepatocarcinogenesis_Fatty_Acid_Metbolism_and_Lipid_Homeostasis	0,014	-0,003	0,045	5	0,029
pregnenolone_biosynthesis	0	0	0	1	0
PRL_Pathway	0,007	-0,054	0,023	61	0,015
progesterone_biosynthesis	0	0	0	2	0
proline_biosynthesis	-0,073	0,100	-0,067	3	-0,070
proline_degradation	-0,043	-0,047	0,038	2	-0,003
propionyl-CoA_degradation	-0,086	0,078	-0,055	4	-0,070
protein_citrullination	-0,111	0,087	-0,006	5	-0,058
protein_iOi-iNi-acetyl-glucosylation	0,022	-0,132	-0,037	2	-0,007
Protein_kinase_A_Pathway	-0,019	-0,149	-0,002	6	-0,010
PRPP_biosynthesis	0,000	0,112	-0,006	3	-0,003
PTEN_Pathway	0,013	0,018	-0,006	491	0,003
PTEN_Pathway_Adhesion_or_Migration	0,004	0,016	-0,002	343	0,001
PTEN_Pathway_Angiogenesis_and_Tumorigenesis	0,007	-0,014	0,003	175	0,005
PTEN_Pathway_Apoptosis	-0,077	0,236	-0,086	19	-0,082
PTEN_Pathway_Ca2+_Signaling	0,007	-0,014	0,003	175	0,005
PTEN_Pathway_Cell_Cycle	0,003	0,014	-0,008	95	-0,003
PTEN_Pathway_Cell_Survival	-0,011	-0,067	0,022	16	0,005
PTEN_Pathway_Differentiation	0,002	0,013	-0,007	102	-0,003
PTEN_Pathway_DNA_Repair	0,009	0,018	-0,021	86	-0,006
PTEN_Pathway_Genomic_Stability	0,003	0,021	-0,008	83	-0,003
PTEN_Pathway_Growth	0,003	0,014	-0,008	95	-0,003
PTEN_Pathway_Migration	0,009	0,022	-0,008	115	0,000
PTEN_Pathway_Neuronal_Survival	0,021	-0,046	0,006	7	0,013
PTEN_Pathway_Proliferation	0,008	0,025	-0,010	114	-0,001
PTEN_Pathway_Proliferation_CyclinA2_Geminin_AuroraA_PLK1	-0,000	-0,018	0,020	37	0,010
PTEN_Pathway_Protein_Synthesis	2,306	-0,021	-0,171	2	1,068
PTEN_Pathway_Senescence_Ets2_p16	-0,000	-0,018	0,020	37	0,010
PTEN_Pathway_Synaptic_Transmission	0,003	0,021	-0,008	85	-0,003
purine_deoxyribonucleosides_degradation	0,015	0,088	0,250	2	0,132
purine_deoxyribonucleosides_salvage	-0,041	0,028	-0,043	12	-0,042
purine_nucleotides_degradation	-0,003	0,053	0,009	11	0,003
purine_nucleotides_ide_novoi_biosynthesis	-0,014	0,087	-0,029	44	-0,022
purine_ribonucleosides_degradation_to_ribose-1-phosphate	0,012	0,183	0,080	3	0,046
putrescine_biosynthesis_I	0	0	0	1	0
putrescine_biosynthesis_II	-0,100	0,338	-0,082	2	-0,091
putrescine_degradation_III	-0,145	0,116	-0,037	10	-0,091
pyridoxal_5-phosphate_salvage	-0,006	0,026	0,005	5	-0,001
pyrimidine_deoxyribonucleosides_degradation	-0,022	0,069	-0,015	4	-0,019
pyrimidine_deoxyribonucleosides_salvage	0,037	-0,135	0,033	5	0,035
pyrimidine_deoxyribonucleotide_phosphorylation	-0,008	0,001	-0,032	11	-0,020
pyrimidine_deoxyribonucleotides_biosynthesis_from_CTP	0,004	0,033	-0,009	15	-0,003
pyrimidine_deoxyribonucleotides_ide_novoi_biosynthesis	0,013	0,017	-0,005	15	0,004
pyrimidine_ribonucleosides_degradation	-0,015	0,046	-0,010	6	-0,012
pyrimidine_ribonucleosides_salvage_I	-0,032	0,005	-0,036	4	-0,034
pyruvate_decarboxylation_to_acetyl_CoA	-0,072	-0,095	-0,002	5	-0,037
Rac1_Signaling	0,033	-0,064	0,010	15	0,021
RALA_Signaling	-0,095	-0,031	-0,010	8	-0,052
RALB_Signaling	-0,018	0,015	0,008	5	-0,005
RANK_Signaling_in_Osteoclasts_Pathway	0,011	-0,014	0,038	73	0,024
RANK_Signaling_in_Osteoclasts_Pathway_Expression_of_Osteoclastic_Genes_via_JUN_NFAT5_NFKB2_MITF_FOS	0,014	-0,076	0,062	33	0,038
RANK_Signaling_in_Osteoclasts_Pathway_Inhibition_of_Death	0,051	-0,095	0,057	29	0,054

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
RANK_Signaling_in_Osteoclasts_Pathway_Resorption	0,029	-0,065	0,042	32	0,036
Rapoport-Luebering_glycolytic_shunt	-0,046	-0,069	-0,043	2	-0,044
Ras_Pathway	-0,001	-0,042	0,016	441	0,007
Ras_Pathway_Apoptosis	0,024	-0,091	0,068	33	0,046
Ras_Pathway_CDC42_Pathway	-0,119	-0,006	-0,037	4	-0,078
Ras_Pathway_Cell-Cell_Junctions	0,007	-0,039	0,034	25	0,021
Ras_Pathway_Gene_Expression_Cell_Proliferation_Cell_Survival_Differentiation_Development_Cell_Cycle_Control_Cell_Motility_Tumorigenesis_via_ELK4_ATF2_MEF2D_STAT2_CREB3_CCNA1_MYC_ELK1_JUN_CDK4	0,025	-0,058	0,018	64	0,022
Ras_Pathway_Golgi_Trafficking_and_Vesicle_Formation	-0,089	0,010	-0,028	10	-0,058
Ras_Pathway_Increased_T-cell_Adhesion	-0,021	-0,072	0,026	28	0,002
Ras_Pathway_Receptor_Endocytosis	-0,007	-0,056	0,094	8	0,044
Ras_Pathway_RhoA_Pathway	-0,023	0,105	-0,026	9	-0,024
Ras_Signaling	-0,020	0,012	-0,008	36	-0,014
reactome_2_LTR_circle_formation_Main_Pathway	-0,064	0,211	-0,120	7	-0,092
reactome_A_tetrasaccharide_linker_sequence_is_required_for_GAG_synthesis_Main_Pathway	-0,025	0,020	0,002	23	-0,011
reactome_A_third_proteolytic_cleavage_releases_NICD_Main_Pathway	-0,037	-0,064	0,007	9	-0,015
reactome_Abacavir_metabolism_Main_Pathway	-0,066	0,121	-0,025	5	-0,045
reactome_Abacavir_transmembrane_transport_Main_Pathway	0	0	0	5	0
reactome_ABC_family_proteins_mediated_transport_Main_Pathway	-0,018	0,023	0,014	15	-0,002
reactome_ABCA_transporters_in_lipid_homeostasis_Main_Pathway	-0,014	0,002	0,002	14	-0,006
reactome_Abnormal_metabolism_in_phenylketonuria_Main_Pathway	0,020	0,119	-0,013	4	0,003
reactome_Abortive_elongation_of_HIV_1_transcript_in_the_absence_of_Tat_Main_Pathway	-0,021	-0,037	-0,015	23	-0,018
reactome_Acetylcholine_Neurotransmitter_Release_Cycle_Main_Pathway	-0,001	0,026	-0,017	16	-0,009
reactome_Acetylcholine_regulates_insulin_secretion_Main_Pathway	-0,041	0,054	0,030	10	-0,006
reactome_Activated_NOTCH1_Transmits_Signal_to_the_Nucleus_Main_Pathway	-0,027	-0,088	0,017	30	-0,005
reactome_Activated_point_mutants_of_FGFR2_Main_Pathway	0	0	0	14	0
reactome_activated_TAK1_mediates_p38_MAPK_activation_Main_Pathway	-0,017	-0,034	-0,008	6	-0,013
reactome_Activation_of_ATR_in_response_to_replication_stress_Main_Pathway	-0,064	0,081	-0,021	37	-0,043
reactome_Activation_of_BAD_and_translocation_to_mitochondria_Main_Pathway	0,014	0,005	0,031	8	0,023
reactome_Activation_of_BID_and_translocation_to_mitochondria_Main_Pathway	0,102	-0,066	0,061	4	0,081
reactome_Activation_of_BIM_and_translocation_to_mitochondria_Main_Pathway	0,043	-0,064	0,046	3	0,044
reactome_Activation_of_BMF_and_translocation_to_mitochondria_Main_Pathway	0,040	0,166	-0,032	3	0,004
reactome_Activation_of_C3_and_C5_Main_Pathway	0,192	-0,217	0,440	3	0,316
reactome_Activation_of_caspases_through_apoptosome_mediated_cleavage_Main_Pathway	-0,051	0,065	-0,123	5	-0,087
reactome_Activation_of_DNA_fragmentation_factor_Main_Pathway	-0,040	-0,014	-0,010	11	-0,025
reactome_Activation_of_G_protein_gated_Potassium_channels_Main_Pathway	-0,038	-0,052	0,023	15	-0,008
reactome_Activation_of_gene_expression_by_SREBF_SREBP__Main_Pathway	0,021	-0,104	0,053	38	0,037
reactome_Activation_of_IRF3_IRF7_mediated_by_TBK1_IKK_epsilon_Main_Pathway	0,081	-0,086	0,010	11	0,046
reactome_Activation_of_Matrix_Metalloproteinases_Main_Pathway	-0,014	-0,042	0,015	21	0,000
reactome_Activation_of_NF_kappaB_in_B_cells_Main_Pathway	-0,003	0,006	0,004	56	0,001
reactome_Activation_of_NIMA_Kinases_NEK9_NEK6_NEK7_Main_Pathway	0,052	-0,106	0,035	4	0,043
reactome_Activation_of_NOXA_and_translocation_to_mitochondria_Main_Pathway	-0,116	0,142	0,031	3	-0,043
reactome_Activation_of_PKB_Main_Pathway	-0,056	0,175	-0,063	4	-0,059
reactome_Activation_of_PPARGC1A_PGC_1alpha_by_phosphorylation_Main_Pathway	-0,012	0,026	-0,016	10	-0,014
reactome_Activation_of_PUMA_and_translocation_to_mitochondria_Main_Pathway	-0,116	0,142	0,031	3	-0,043
reactome_Activation_of_Rac_Main_Pathway	-0,054	0,089	-0,006	14	-0,030
reactome_Activation_of_RAS_in_B_cells_Main_Pathway	-0,057	0,322	-0,039	5	-0,048
reactome_Activation_of_the_AP_1_family_of_transcription_factors_Main_Pathway	0,022	0,034	0,017	10	0,020
reactome_Activation_of_the_mRNA_upon_binding_of_the_cap_binding_complex_and_eIFs_and_subsequent_binding_to_43S_Main_Pathway	-0,029	0,128	-0,008	7	-0,019

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Activation_of_the_phototransduction_cascade_Main_Pathway	-0,022	0,013	-0,009	10	-0,015
reactome_Activation_of_the_pre_replicative_complex_Main_Pathway	-0,061	0,073	-0,003	30	-0,032
reactome_Acyl_chain_remodeling_of_CL_Main_Pathway	-0,051	-0,146	-0,004	6	-0,027
reactome_Acyl_chain_remodeling_of_DAG_and_TAG_Main_Pathway	-0,035	-0,002	0,076	5	0,021
reactome_Acyl_chain_remodelling_of_PC_Main_Pathway	-0,039	-0,022	0,037	17	-0,001
reactome_Acyl_chain_remodelling_of_PE_Main_Pathway	-0,046	-0,026	0,032	15	-0,007
reactome_Acyl_chain_remodelling_of_PG_Main_Pathway	-0,006	-0,001	0,030	10	0,012
reactome_Acyl_chain_remodelling_of_PI_Main_Pathway	0,023	-0,141	0,037	9	0,030
reactome_Acyl_chain_remodelling_of_PS_Main_Pathway	-0,032	0,015	0,028	10	-0,002
reactome_Adenosine_P1_receptors_Main_Pathway	0	0	0	4	0
reactome_Adenylate_cyclase_activating_Main_Pathway	0	0	0	10	0
reactome_Adenylate_cyclase_inhibitory_Main_Pathway	-0,016	-0,037	0,013	14	-0,002
reactome_Adherens_junctions_interactions_Main_Pathway	0,029	-0,131	0,029	24	0,029
reactome_ADP_signalling_through_P2Y_purinoceptor_1_Main_Pathway	-0,024	-0,086	0,030	24	0,003
reactome_ADP_signalling_through_P2Y_purinoceptor_12_Main_Pathway	-0,036	-0,059	0,024	22	-0,006
reactome_Adrenaline_noradrenaline_inhibits_insulin_secretion_Main_Pathway	-0,036	-0,035	0,015	23	-0,010
reactome_Adrenaline_signalling_through_Alpha_2_adrenergic_receptor_Main_Pathway	0	0	0	3	0
reactome_Adrenoceptors_Main_Pathway	0	0	0	9	0
reactome_Advanced_glycosylation_endproduct_receptor_signaling_Main_Pathway	-0,018	-0,038	-0,052	8	-0,035
reactome_Aflatoxin_activation_and_detoxification_Main_Pathway	0	0	0	4	0
reactome_AKT_mediated_inactivation_of_FOXO1A_Main_Pathway	0,016	-0,033	0,005	4	0,010
reactome_AKT_phosphorylates_targets_in_the_cytosol_Main_Pathway	0,024	-0,059	0,022	13	0,023
reactome_AKT_phosphorylates_targets_in_the_nucleus_Main_Pathway	-0,011	0,024	-0,002	8	-0,007
reactome_Alpha_defensins_Main_Pathway	0	0	0	6	0
reactome_alpha_linolenic_acid_ALA_metabolism_Main_Pathway	-0,099	-0,028	0,002	10	-0,048
reactome_Alpha_oxidation_of_phytanate_Main_Pathway	-1,248	0,860	-0,080	4	-0,664
reactome_Alternative_complement_activation_Main_Pathway	0,144	-0,163	0,330	4	0,237
reactome_Amine_compound_SLC_transporters_Main_Pathway	-0,053	0,618	-0,035	8	-0,044
reactome_Amine_ligand_binding_receptors_Main_Pathway	0	0	0	7	0
reactome_Amino_acid_and_oligopeptide_SLC_transporters_Main_Pathway	0	0	0	6	0
reactome_Amino_acid_synthesis_and_interconversion_transamination__Main_Pathway	-0,065	0,082	-0,097	9	-0,081
reactome_Amino_acid_transport_across_the_plasma_membrane_Main_Pathway	-0,038	0,012	0,002	30	-0,018
reactome_AMPK_inhibits_chREBP_transcriptional_activation_activity_Main_Pathway	0	0	0	5	0
reactome_Amyloids_Main_Pathway	-0,022	0,028	-0,004	50	-0,013
reactome_Anchoring_fibril_formation_Main_Pathway	0,047	-0,336	0,068	7	0,057
reactome_Androgen_biosynthesis_Main_Pathway	-0,008	-0,022	-0,006	9	-0,007
reactome_Antigen_activates_B_Cell_Receptor_BCR_leading_to_generation_of_second_messengers_Main_Pathway	-0,011	0,156	0,016	29	0,002
reactome_Antigen_Presentation_Folding_assembly_and_peptide_loading_of_class_I_MHC_Main_Pathway	-0,007	-0,169	0,092	27	0,042
reactome_Antigen_processing_Ubiquitination_Proteasome_degradation_Main_Pathway	0,013	-0,009	0,004	211	0,009
reactome_APC_C_Cdc20_mediated_degradation_of_Cyclin_B_Main_Pathway	-0,001	0,049	-0,013	21	-0,007
reactome_APC_C_Cdc20_mediated_degradation_of_mitotic_proteins_Main_Pathway	-0,011	0,018	-0,002	18	-0,007
reactome_APC_C_Cdc20_mediated_degradation_of_Securin_Main_Pathway	-0,012	0,033	-0,006	64	-0,009
reactome_APC_C_Cdh1_mediated_degradation_of_Cdc20_and_other_APC_C_Cdh1_targeted_proteins_in_late_mitosis_early_G1_Main_Pathway	-0,008	0,012	-0,008	69	-0,008
reactome_APC_Cdc20_mediated_degradation_of_Nek2A_Main_Pathway	0,003	0,027	-0,005	23	-0,001
reactome_APOBEC3G_mediated_resistance_to_HIV_1_infection_Main_Pathway	-0,120	0,321	-0,168	4	-0,144
reactome_Apoptotic_cleavage_of_cell_adhesion_proteins_Main_Pathway	-0,023	0,038	0,014	10	-0,005
reactome_Apoptotic_cleavage_of_cellular_proteins_Main_Pathway	0,031	-0,052	0,024	10	0,028
reactome_Arachidonate_production_from_DAG_Main_Pathway	-0,057	0,056	0,010	3	-0,023
reactome_ARMS_mediated_activation_Main_Pathway	0,035	-0,298	0,096	5	0,065
reactome_Asparagine_N_linked_glycosylation_Main_Pathway	-0,064	-0,223	0,070	7	0,003
reactome_Assembly_Of_The_HIV_Virion_Main_Pathway	0,023	0,135	-0,028	5	-0,002

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Assembly_of_the_ORC_complex_at_the_origin_of_replication_Main_Pathway	-0,091	0,076	0,010	6	-0,041
reactome_Assembly_of_the_RAD50_MRE11_NBS1_complex_at_DNA_double_strand_breaks_Main_Pathway	-0,030	-0,044	0,070	4	0,020
reactome_Assembly_of_the_RAD51_ssDNA_nucleoprotein_complex_Main_Pathway	0,025	0,047	-0,050	5	-0,012
reactome_Association_of_TriC_CCT_with_target_proteins_during_biosynthesis_Main_Pathway	-0,048	0,153	-0,042	28	-0,045
reactome_Astrocytic_Glutamate_Glutamine_Uptake_And_Metabolism_Main_Pathway	0,055	-0,116	-0,040	4	0,007
reactome_Asymmetric_localization_of_PCP_proteins_Main_Pathway	0,012	0,005	0,008	17	0,010
reactome_ATF6_alpha_activates_chaperone_genes_Main_Pathway	0	0	0	5	0
reactome_ATF6_alpha_activates_chaperones_Main_Pathway	0,019	-0,076	0,016	4	0,017
reactome_ATM_mediated_phosphorylation_of_repair_proteins_Main_Pathway	-0,024	0,088	0,025	5	0,001
reactome_ATP_sensitive_Potassium_channels_Main_Pathway	0	0	0	4	0
reactome_Attachment_of_GPI_anchor_to_uPAR_Main_Pathway	-0,050	-0,020	0,046	7	-0,002
reactome_Attenuation_phase_Main_Pathway	0,003	0,072	-0,032	11	-0,015
reactome_AUF1_hnRNP_D0_destabilizes_mRNA_Main_Pathway	0,071	-0,002	0,024	9	0,048
reactome_Autodegradation_of_Cdh1_by_Cdh1_APC_C_Main_Pathway	-0,018	0,052	-0,007	60	-0,013
reactome_Autodegradation_of_the_E3_ubiquitin_ligase_COP1_Main_Pathway	-0,014	0,045	-0,008	51	-0,011
reactome_Autointegration_results_in_viral_DNA_circles_Main_Pathway	-0,109	0,300	-0,206	3	-0,157
reactome_Axonal_growth_inhibition_RHOA_activation__Main_Pathway	-0,002	-0,066	0,017	5	0,007
reactome_Axonal_growth_stimulation_Main_Pathway	-0,042	0,135	-0,034	4	-0,038
reactome_Basigin_interactions_Main_Pathway	-0,044	-0,071	0,059	14	0,008
reactome_Beta_catenin_phosphorylation_cascade_Main_Pathway	0,034	-0,051	-0,007	16	0,013
reactome_Beta_oxidation_of_butanoyl_CoA_to_acetyl_CoA_Main_Pathway	-0,090	-0,013	-0,032	3	-0,061
reactome_Beta_oxidation_of_decanoyl_CoA_to_octanoyl_CoA_CoA_Main_Pathway	-0,146	-0,077	-0,034	5	-0,090
reactome_Beta_oxidation_of_hexanoyl_CoA_to_butanoyl_CoA_Main_Pathway	-0,110	-0,070	-0,035	5	-0,072
reactome_Beta_oxidation_of_lauroyl_CoA_to_decanoyl_CoA_CoA_Main_Pathway	-0,110	-0,070	-0,035	5	-0,072
reactome_Beta_oxidation_of_myristoyl_CoA_to_lauroyl_CoA_Main_Pathway	-0,094	-0,104	-0,026	3	-0,060
reactome_Beta_oxidation_of_octanoyl_CoA_to_hexanoyl_CoA_Main_Pathway	-0,146	-0,077	-0,034	5	-0,090
reactome_Beta_oxidation_of_palmitoyl_CoA_to_myristoyl_CoA_Main_Pathway	-0,162	0,004	-0,037	3	-0,099
reactome_Beta_oxidation_of_pristanoyl_CoA_Main_Pathway	-0,133	-0,067	-0,064	7	-0,098
reactome_Beta_oxidation_of_very_long_chain_fatty_acids_Main_Pathway	-0,254	0,157	-0,027	5	-0,141
reactome_betaKlotho_mediated_ligand_binding_Main_Pathway	0	0	0	3	0
reactome_BH3_only_proteins_associate_with_and_inactivate_anti_apoptotic_BCL_2_members_Main_Pathway	0,000	-0,058	0,045	7	0,023
reactome_Bicarbonate_transporters_Main_Pathway	-0,081	-0,142	0,077	9	-0,002
reactome_Bile_salt_and_organic_anion_SLC_transporters_Main_Pathway	0	0	0	3	0
reactome_Binding_and_entry_of_HIV_virion_Main_Pathway	-0,039	0,096	-0,014	4	-0,026
reactome_binding_of_TCF_LEF_CTNNB1_to_target_gene_promoters_Main_Pathway	-0,106	0,245	0,052	7	-0,027
reactome_Biosynthesis_of_the_N_glycan_precursor_dolichol_lipid_linked_oligosaccharide_LLO_and_transfer_to_a_nascent_protein_Main_Pathway	-0,366	0,311	-0,040	15	-0,203
reactome_Biotin_transport_and_metabolism_Main_Pathway	-0,094	0,159	-0,031	11	-0,062
reactome_Branched_chain_amino_acid_catabolism_Main_Pathway	-0,101	0,053	-0,038	17	-0,070
reactome_Budding_and_maturation_of_HIV_virion_Main_Pathway	0,007	0,092	-0,021	25	-0,007
reactome_Butyrate_Response_Factor_1_BRF1_destabilizes_mRNA_Main_Pathway	0,025	0,085	-0,040	17	-0,007
reactome_Ca_activated_K_channels_Main_Pathway	0	0	0	9	0
reactome_Ca2_Main_Pathway	-0,007	-0,091	0,040	30	0,016
reactome_Calmodulin_induced_events_Main_Pathway	0,002	-0,049	0,012	5	0,007
reactome_Calnexin_calreticulin_cycle_Main_Pathway	-0,047	-0,096	-0,028	5	-0,037
reactome_CaMK_IV_mediated_phosphorylation_of_CREB_Main_Pathway	-0,049	0,107	-0,013	3	-0,031
reactome_Carnitine_synthesis_Main_Pathway	0,005	-0,056	0,018	4	0,011
reactome_Caspase_mediated_cleavage_of_cytoskeletal_proteins_Main_Pathway	-0,025	0,097	0,025	6	-0,000
reactome_Catecholamine_biosynthesis_Main_Pathway	0	0	0	4	0
reactome_Cation_coupled_Chloride_cotransporters_Main_Pathway	-0,040	0,117	-0,027	7	-0,034
reactome_CD28_co_stimulation_Main_Pathway	-0,065	0,715	-0,037	8	-0,051

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_CD28_dependent_PI3K_Akt_signaling_Main_Pathway	-0,014	0,050	0,009	21	-0,003
reactome_CD28_dependent_Vav1_Main_Pathway	-0,085	0,221	-0,033	11	-0,059
reactome_Cdc20_Phospho_APC_C_mediated_degradation_of_Cyclin_A_Main_Pathway	-0,007	0,031	-0,003	69	-0,005
reactome_CDC6_association_with_the_ORC_origin_complex_Main_Pathway	-0,068	0,057	0,007	11	-0,031
reactome_CDK_mediated_phosphorylation_and_removal_of_Cdc6_Main_Pathway	-0,008	0,035	-0,006	50	-0,007
reactome_CDO_in_myogenesis_Main_Pathway	-0,001	0,006	-0,000	28	-0,001
reactome_CDT1_association_with_the_CDC6_ORC_origin_complex_Main_Pathway	-0,016	0,033	-0,005	58	-0,011
reactome_cell_division_Main_Pathway	0,073	-0,158	0,025	4	0,049
reactome_Ceramide_signalling_Main_Pathway	-0,051	-0,046	0,120	3	0,034
reactome_cGMP_effects_Main_Pathway	0	0	0	17	0
reactome_Chk1_Chk2_Cds1_mediated_inactivation_of_Cyclin_B_Cdk1_complex_Main_Pathway	0,030	0,052	-0,065	5	-0,017
reactome_CHL1_interactions_Main_Pathway	-0,007	0,012	-0,003	5	-0,005
reactome_Cholesterol_biosynthesis_Main_Pathway	0,038	-0,227	0,074	19	0,056
reactome_Chondroitin_sulfate_biosynthesis_Main_Pathway	-0,022	0,013	0,035	19	0,006
reactome_ChREBP_activates_metabolic_gene_expression_Main_Pathway	0	0	0	7	0
reactome_Chylomicron_mediated_lipid_transport_Main_Pathway	-0,033	0,049	-0,022	17	-0,028
reactome_Circadian_Clock_Main_Pathway	0,016	-0,009	-0,004	24	0,006
reactome_Citric_acid_cycle_TCA_cycle__Main_Pathway	-0,156	0,080	-0,029	19	-0,093
reactome_Class_A_1_Rhodopsin_like_receptors__Main_Pathway	0	0	0	16	0
reactome_Class_C_3_Metabotropic_glutamate_pheromone_receptors__Main_Pathway	0	0	0	38	0
reactome_Class_II_GLUTs_Main_Pathway	0	0	0	4	0
reactome_Classical_antibody_mediated_complement_activation_Main_Pathway	0,005	-0,011	0,002	11	0,004
reactome_Classical_Kir_channels_Main_Pathway	0	0	0	4	0
reactome_Clathrin_derived_vesicle_budding_Main_Pathway	-0,014	-0,094	0,037	5	0,012
reactome_Clearance_of_Nuclear_Envelope_Membranes_from_Chromatin_Main_Pathway	0,136	0,154	0,014	5	0,075
reactome_Cleavage_of_Growing_Transcript_in_the_Termination_Region_Main_Pathway	-0,061	0,137	-0,021	33	-0,041
reactome_Cleavage_of_the_damaged_purine_Main_Pathway	0,029	0,161	-0,015	3	0,007
reactome_Cleavage_of_the_damaged_pyrimidine_Main_Pathway	0,050	0,089	0,019	5	0,034
reactome_Cobalamin_Cbl_vitamin_B12_transport_and_metabolism_Main_Pathway	-0,042	0,028	0,014	19	-0,014
reactome_Coenzyme_A_biosynthesis_Main_Pathway	-0,017	0,145	-0,037	8	-0,027
reactome_Cohesin_Loading_onto_Chromatin_Main_Pathway	-0,090	0,148	-0,066	10	-0,078
reactome_Collagen_biosynthesis_and_modifying_enzymes_Main_Pathway	0,004	-0,091	0,034	54	0,019
reactome_Collagen_degradation_Main_Pathway	0,013	-0,031	0,013	25	0,013
reactome_Common_Pathway_Main_Pathway	0	0	0	14	0
reactome_Condensation_of_Prometaphase_Chromosomes_Main_Pathway	-0,077	0,266	-0,019	6	-0,048
reactome_Condensation_of_Prophase_Chromosomes_Main_Pathway	-0,004	0,022	0,010	40	0,003
reactome_Conjugation_of_benzoate_with_glycine_Main_Pathway	0	0	0	5	0
reactome_Conjugation_of_salicylate_with_glycine_Main_Pathway	0	0	0	7	0
reactome_Constitutive_PI3K_AKT_Signaling_in_Cancer_Main_Pathway	0,001	-0,005	0,014	23	0,007
reactome_Constitutive_Signaling_by_NOTCH1_HD_Domain_Mutants_Main_Pathway	-0,025	0,002	-0,030	15	-0,027
reactome_Constitutive_Signaling_by_NOTCH1_HD_PEST_Domain_Mutants_Main_Pathway	-0,008	-0,012	0,013	53	0,002
reactome_Constitutive_Signaling_by_NOTCH1_PEST_Domain_Mutants_Main_Pathway	-0,008	-0,012	0,013	53	0,002
reactome_Constitutive_Signaling_by_NOTCH1_t_7_9_NOTCH1_M1580_K2555_Translocation_Mutant_Main_Pathway	-0,080	-0,104	0,015	3	-0,033
reactome_Conversion_from_APC_C_Cdc20_to_APC_C_Cdh1_in_late_anaphase_Main_Pathway	-0,022	0,027	-0,006	17	-0,014
reactome_COPI_Mediated_Transport_Main_Pathway	0,019	-0,003	-0,025	10	-0,003
reactome_COPII_Coat_Protein_2_Mediated_Vesicle_Transport_Main_Pathway	0,042	-0,006	0,016	9	0,029
reactome_Costimulation_by_the_CD28_family_Main_Pathway	-0,010	0,057	-0,001	9	-0,006
reactome_Creatine_metabolism_Main_Pathway	0	0	0	6	0
reactome_CREB_phosphorylation_Main_Pathway	-0,028	0,040	0,007	7	-0,011

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_CREB_phosphorylation_through_the_activation_of_Adenylate_Cyclase_Main_Pathway	-0,048	0,077	-0,039	7	-0,044
reactome_CREB_phosphorylation_through_the_activation_of_CaMKII_Main_Pathway	0,003	-0,018	0,016	15	0,010
reactome_CREB_phosphorylation_through_the_activation_of_CaMKK_Main_Pathway	0,097	-0,133	0,040	4	0,068
reactome_CREB_phosphorylation_through_the_activation_of_Ras_Main_Pathway	0,004	-0,034	0,035	13	0,020
reactome_CRMPs_in_Sema3A_signaling_Main_Pathway	0,018	-0,011	-0,009	16	0,005
reactome_Cross_presentation_of_particulate_exogenous_antigens_phagosomes__Main_Pathway	0,042	-0,081	-0,004	8	0,019
reactome_Cross_presentation_of_soluble_exogenous_antigens_endosomes__Main_Pathway	-0,014	0,028	-0,004	49	-0,009
reactome_Crosslinking_of_collagen_fibrils_Main_Pathway	0,007	-0,186	0,048	9	0,027
reactome_CS_DS_degradation_Main_Pathway	0,005	0,068	-0,028	12	-0,012
reactome_CTLA4_inhibitory_signaling_Main_Pathway	-0,001	0,242	-0,014	21	-0,007
reactome_Cyclin_A_B1_associated_events_during_G2_M_transition_Main_Pathway	0,050	-0,054	-0,020	21	0,015
reactome_Cyclin_A_Cdk2_associated_events_at_S_phase_entry_Main_Pathway	0,008	-0,028	0,011	13	0,009
reactome_Cyclin_B2_mediated_events_Main_Pathway	0,063	0,089	-0,097	5	-0,017
reactome_Cyclin_D_associated_events_in_G1_Main_Pathway	0,015	-0,019	-0,004	38	0,006
reactome_Cyclin_E_associated_events_during_G1_S_transition_Main_Pathway	-0,005	-0,018	0,021	14	0,008
reactome_CYP2E1_reactions_Main_Pathway	-0,024	0,030	-0,009	11	-0,016
reactome_Cytosolic_iron_sulfur_cluster_assembly_Main_Pathway	-0,037	0,058	-0,006	13	-0,022
reactome_Cytosolic_sensors_of_pathogen_associated_DNA_Main_Pathway	-0,023	0,033	-0,024	22	-0,023
reactome_Cytosolic_sulfonation_of_small_molecules_Main_Pathway	-0,109	0,274	-0,095	4	-0,102
reactome_Cytosolic_tRNA_aminoacylation_Main_Pathway	-0,037	0,078	-0,037	24	-0,037
reactome_DAG_and_IP3_signaling_Main_Pathway	-0,004	-0,074	0,016	6	0,006
reactome_DAP12_interactions_Main_Pathway	-0,017	-0,027	0,021	21	0,002
reactome_DAP12_signaling_Main_Pathway	-0,061	0,134	0,008	26	-0,026
reactome_DARPP_32_events_Main_Pathway	-0,024	0,031	-0,012	22	-0,018
reactome_DCC_mediated_attractive_signaling_Main_Pathway	0,007	-0,053	0,009	13	0,008
reactome_Deadenylation_of_mRNA_Main_Pathway	-0,031	0,099	-0,003	23	-0,017
reactome_degradation_of_AXIN_Main_Pathway	-0,022	0,032	0,016	54	-0,003
reactome_Degradation_of_beta_catenin_by_the_destruction_complex_Main_Pathway	0,006	0,006	-0,002	66	0,002
reactome_Degradation_of_cysteine_and_homocysteine_Main_Pathway	0,094	-0,111	-0,037	3	0,029
reactome_degradation_of_DVL_Main_Pathway	-0,003	0,026	0,001	55	-0,001
reactome_Degradation_of_the_extracellular_matrix_Main_Pathway	0,003	-0,121	0,033	32	0,018
reactome_Depolymerisation_of_the_Nuclear_Lamina_Main_Pathway	0,035	0,049	0,024	12	0,030
reactome_Deposition_of_new_CENPA_containing_nucleosomes_at_the_centromere_Main_Pathway	-0,005	0,026	0,001	45	-0,002
reactome_Dermatan_sulfate_biosynthesis_Main_Pathway	-0,010	0,012	0,014	11	0,002
reactome_Detoxification_of_Reactive_Oxygen_Species_Main_Pathway	-0,039	0,018	-0,020	25	-0,029
reactome_Digestion_of_dietary_carbohydrate_Main_Pathway	0	0	0	8	0
reactome_Digestion_of_dietary_lipid_Main_Pathway	0	0	0	5	0
reactome_Dimerization_of_procaspase_8_Main_Pathway	-0,473	0,545	0,008	9	-0,233
reactome_disassembly_of_the_destruction_complex_and_recruitment_of_AXIN_to_the_membrane_Main_Pathway	0,007	-0,012	0,005	27	0,006
reactome_Displacement_of_DNA_glycosylase_by_APE1_Main_Pathway	0,041	0,112	-0,002	9	0,019
reactome_Dissolution_of_Fibrin_Clot_Main_Pathway	0,064	-0,229	0,092	13	0,078
reactome_DNA_Damage_Telomere_Stress_Induced_Senescence_Main_Pathway	-0,017	0,054	0,002	38	-0,008
reactome_DNA_replication_initiation_Main_Pathway	-0,088	0,092	-0,000	6	-0,044
reactome_Dopamine_Neurotransmitter_Release_Cycle_Main_Pathway	-0,001	0,025	-0,016	17	-0,008
reactome_Dopamine_receptors_Main_Pathway	0	0	0	5	0
reactome_Downregulation_of_ERBB2_ERBB3_signaling_Main_Pathway	0,044	0,045	-0,021	9	0,011
reactome_Downregulation_of_ERBB4_signaling_Main_Pathway	0,105	-0,038	0,010	7	0,058
reactome_Downregulation_of_SMAD2_3_SMAD4_transcriptional_activity_Main_Pathway	0,025	-0,072	0,031	23	0,028
reactome_Downregulation_of_TGF_beta_receptor_signaling_Main_Pathway	0,002	-0,027	0,009	25	0,006
reactome_Downstream_signal_transduction_Main_Pathway	0,031	-0,048	0,037	22	0,034

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Downstream_TCR_signaling_Main_Pathway	-0,015	0,140	-0,114	41	-0,065
reactome_DSCAM_interactions_Main_Pathway	-0,038	0,131	-0,011	10	-0,024
reactome_Dual_incision_reaction_in_GG_NER_Main_Pathway	-0,020	-0,029	0,005	20	-0,007
reactome_Dual_incision_reaction_in_TC_NER_Main_Pathway	-0,010	-0,032	0,004	28	-0,003
reactome_E2F_enabled_inhibition_of_pre_replication_complex_formation_Main_Pathway	-0,046	0,074	-0,005	10	-0,025
reactome_E2F_mediated_regulation_of_DNA_replication_Main_Pathway	-0,042	0,094	0,046	17	0,002
reactome_Early_Phase_of_HIV_Life_Cycle_Main_Pathway	-0,084	0,292	-0,004	3	-0,044
reactome_ECM_proteoglycans_Main_Pathway	0,001	-0,013	0,001	21	0,001
reactome_Effects_of_PIP2_hydrolysis_Main_Pathway	0,016	-0,085	0,023	22	0,019
reactome_EGFR_downregulation_Main_Pathway	-0,007	-0,103	0,031	25	0,012
reactome_EGFR_interacts_with_phospholipase_C_gamma_Main_Pathway	-0,129	-0,457	0,144	3	0,008
reactome_EGFR_Transactivation_by_Gastrin_Main_Pathway	-0,098	-0,001	0,057	8	-0,020
reactome_Eicosanoids_Main_Pathway	0	0	0	12	0
reactome_Elastic_fibre_formation_Main_Pathway	0,005	-0,128	0,033	13	0,019
reactome_Electric_Transmission_Across_Gap_Junctions_Main_Pathway	0,001	-0,006	0,011	5	0,006
reactome_Elevation_of_cytosolic_Ca2_levels_Main_Pathway	0,005	-0,030	0,011	9	0,008
reactome_Elongation_arrest_and_recovery_Main_Pathway	-0,006	-0,043	0,004	31	-0,001
reactome_Endogenous_sterols_Main_Pathway	-0,005	-0,097	0,034	18	0,014
reactome_Endosomal_Sorting_Complex_Required_For_Transport_ESCRT__Main_Pathway	0,015	0,046	-0,009	28	0,003
reactome_Endosomal_Vacuolar_Main_Pathway	-0,038	-0,123	0,079	14	0,021
reactome_eNOS_activation_Main_Pathway	-0,012	-0,265	0,095	7	0,041
reactome_EPH_ephrin_mediated_repulsion_of_cells_Main_Pathway	-0,017	0,088	-0,005	46	-0,011
reactome_EPHA_mediated_growth_cone_collapse_Main_Pathway	0,038	0,076	0,007	32	0,023
reactome_EPHB_mediated_forward_signaling_Main_Pathway	-0,024	0,138	-0,011	40	-0,018
reactome_Ephrin_signaling_Main_Pathway	0,004	0,071	-0,025	18	-0,011
reactome_ER_Phagosome_Main_Pathway	-0,021	-0,016	0,022	67	0,000
reactome_ER_Quality_Control_Compartment_ERQC__Main_Pathway	-0,046	-0,013	-0,041	6	-0,043
reactome_ERK_MAPK_targets_Main_Pathway	0,018	-0,049	0,000	17	0,009
reactome_ERK1_activation_Main_Pathway	-0,007	0,153	-0,039	3	-0,023
reactome_ERKs_are_inactivated_Main_Pathway	0,044	-0,082	-0,002	12	0,021
reactome_Erythrocytes_take_up_carbon_dioxide_and_release_oxygen_Main_Pathway	0	0	0	6	0
reactome_Erythrocytes_take_up_oxygen_and_release_carbon_dioxide_Main_Pathway	0	0	0	6	0
reactome_Establishment_of_Sister_Chromatid_Cohesion_Main_Pathway	-0,082	0,135	-0,060	11	-0,071
reactome_Ethanol_oxidation_Main_Pathway	-0,143	0,162	-0,058	4	-0,100
reactome_Eukaryotic_Translation_Elongation_Main_Pathway	-0,047	0,036	0,024	6	-0,011
reactome_Eukaryotic_Translation_Termination_Main_Pathway	-0,004	0,067	0,029	84	0,012
reactome_Extrinsic_Pathway_Main_Pathway	0	0	0	5	0
reactome_Facilitative_Na_independent_glucose_transporters_Main_Pathway	0	0	0	7	0
reactome_Fanconi_Anemia_Main_Pathway	0,028	0,007	-0,030	17	-0,001
reactome_FasL_CD95L_signaling_Main_Pathway	0,076	-0,015	0,047	5	0,061
reactome_Fatty_Acids_bound_to_GPR40_FFAR1_regulate_insulin_secretion_Main_Pathway	0,013	-0,117	0,042	8	0,027
reactome_Fatty_acids_Main_Pathway	0	0	0	15	0
reactome_Fatty_Acyl_CoA_Biosynthesis_Main_Pathway	-0,021	0,057	0,073	4	0,026
reactome_Fc_epsilon_receptor_FCERI_signaling_Main_Pathway	-0,104	0,802	-0,029	7	-0,066
reactome_FCERI_mediated_Ca_2_mobilization_Main_Pathway	-0,042	0,226	0,015	26	-0,013
reactome_FCERI_mediated_MAPK_activation_Main_Pathway	-0,032	0,274	0,017	27	-0,007
reactome_FCERI_mediated_NF_kB_activation_Main_Pathway	0,015	0,159	0,024	23	0,019
reactome_FCGR_activation_Main_Pathway	-0,044	0,376	-0,007	15	-0,025
reactome_FGFR1b_ligand_binding_and_activation_Main_Pathway	0	0	0	5	0
reactome_FGFR1c_ligand_binding_and_activation_Main_Pathway	0	0	0	7	0
reactome_FGFR2b_ligand_binding_and_activation_Main_Pathway	0	0	0	5	0
reactome_FGFR2c_ligand_binding_and_activation_Main_Pathway	0	0	0	9	0
reactome_FGFR3b_ligand_binding_and_activation_Main_Pathway	0	0	0	4	0
reactome_FGFR3c_ligand_binding_and_activation_Main_Pathway	0	0	0	8	0
reactome_FGFR4_ligand_binding_and_activation_Main_Pathway	0	0	0	11	0

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Fibronectin_matrix_formation_Main_Pathway	0,076	-0,470	0,106	3	0,091
reactome_Ficolins_bind_to_repetitive_carbohydrate_structures_on_the_target_cell_surface_Main_Pathway	0	0	0	4	0
reactome_FMO_oxidizes_nucleophiles_Main_Pathway	0	0	0	3	0
reactome_Folding_of_actin_by_CCT_TriC_Main_Pathway	-0,114	0,300	-0,061	9	-0,087
reactome_Formation_of_a_pool_of_free_40S_subunits_Main_Pathway	-0,010	0,073	0,025	94	0,008
reactome_Formation_of_annular_gap_junctions_Main_Pathway	-0,058	-0,017	0,019	8	-0,019
reactome_Formation_of_apoptosome_Main_Pathway	-0,084	0,003	-0,066	3	-0,075
reactome_Formation_of_ATP_by_chemiosmotic_coupling_Main_Pathway	-0,133	0,016	-0,008	18	-0,070
reactome_Formation_of_HIV_1_elongation_complex_containing_HIV_1_Tat_Main_Pathway	-0,008	-0,058	-0,005	41	-0,007
reactome_Formation_of_HIV_elongation_complex_in_the_absence_of_HIV_Tat_Main_Pathway	-0,007	-0,064	-0,002	42	-0,004
reactome_Formation_of_incision_complex_in_GG_NER_Main_Pathway	-0,020	-0,029	0,005	20	-0,007
reactome_Formation_of_RNA_Pol_II_elongation_complex_Main_Pathway	-0,007	-0,064	-0,002	42	-0,004
reactome_Formation_of_Senescence_Associated_Heterochromatin_Foci_SAHF__Main_Pathway	-0,051	-0,022	0,005	16	-0,023
reactome_Formation_of_the_active_cofactor_UDP_glucuronate_Main_Pathway	-0,375	0,299	-0,150	3	-0,262
reactome_formation_of_the_beta_catenin_TCF_transactivating_complex_Main_Pathway	-0,010	0,050	0,008	51	-0,001
reactome_Formation_of_the_Early_Elongation_Complex_Main_Pathway	-0,014	-0,071	-0,015	32	-0,015
reactome_Formation_of_the_HIV_1_Early_Elongation_Complex_Main_Pathway	-0,014	-0,071	-0,015	32	-0,015
reactome_Formation_of_the_ternary_complex_and_subsequently_the_43S_complex_Main_Pathway	-0,020	0,104	0,004	48	-0,008
reactome_Formation_of_transcription_coupled_NER_TC_NER_repair_complex_Main_Pathway	-0,010	-0,032	0,004	28	-0,003
reactome_Formation_of_tubulin_folding_intermediates_by_CCT_TriC_Main_Pathway	-0,007	0,036	-0,003	20	-0,005
reactome_Formyl_peptide_receptors_bind_formyl_peptides_and_many_other_ligands_Main_Pathway	0,065	-0,266	0,010	5	0,037
reactome_Free_fatty_acid_receptors_Main_Pathway	0	0	0	5	0
reactome_Frs2_mediated_activation_Main_Pathway	0,008	-0,124	0,041	9	0,025
reactome_FRS2_mediated_cascade_Main_Pathway	-0,029	0,112	-0,002	22	-0,016
reactome_G_alpha_12_13_signalling_events_Main_Pathway	-0,013	0,021	-0,005	74	-0,009
reactome_G_alpha_i_signalling_events_Main_Pathway	0,001	-0,018	0,011	218	0,006
reactome_G_alpha_q_signalling_events_Main_Pathway	-0,001	-0,023	0,006	161	0,003
reactome_G_alpha_s_signalling_events_Main_Pathway	-0,005	-0,001	0,001	121	-0,002
reactome_G_alpha_z_signalling_events_Main_Pathway	-0,011	-0,017	0,004	43	-0,003
reactome_G_beta_gamma_signalling_through_PI3Kgamma_Main_Pathway	-0,024	-0,029	0,011	25	-0,007
reactome_G_beta_gamma_signalling_through_PLC_beta_Main_Pathway	-0,018	-0,065	0,026	20	0,004
reactome_G_protein_activation_Main_Pathway	-0,029	-0,047	0,019	28	-0,005
reactome_G0_and_Early_G1_Main_Pathway	-0,024	0,049	-0,002	20	-0,013
reactome_G1_S_Specific_Transcription_Main_Pathway	-0,042	0,094	0,046	17	0,002
reactome_G2_M_DNA_damage_checkpoint_Main_Pathway	-0,103	0,024	-0,039	4	-0,071
reactome_G2_M_DNA_replication_checkpoint_Main_Pathway	0,074	0,048	-0,004	5	0,035
reactome_G2_Phase_Main_Pathway	0,032	-0,005	0,022	5	0,027
reactome_GAB1_signalosome_Main_Pathway	-0,056	-0,110	0,065	9	0,005
reactome_GABA_A_rho_receptor_activation_Main_Pathway	0	0	0	3	0
reactome_GABA_synthesis_release_reuptake_and_degradation_Main_Pathway	-0,035	0,103	-0,038	10	-0,036
reactome_Galactose_catabolism_Main_Pathway	0,115	-0,221	0,175	3	0,145
reactome_Gamma_carboxylation_of_protein_precursors_Main_Pathway	-0,019	-0,027	0,009	9	-0,005
reactome_Gap_junction_assembly_Main_Pathway	-0,008	-0,008	-0,018	19	-0,013
reactome_Gap_junction_degradation_Main_Pathway	-0,056	-0,044	0,021	9	-0,017
reactome_Gastrin_CREB_signalling_pathway_via_PKC_and_MAPK_Main_Pathway	-0,001	0,069	-0,010	7	-0,005
reactome_Generation_of_second_messenger_molecules_Main_Pathway	-0,052	0,239	-0,172	32	-0,112
reactome_Glucagon_like_Peptide_1_GLP1_regulates_insulin_secretion_Main_Pathway	-0,028	-0,013	0,005	39	-0,011
reactome_Glucagon_signaling_in_metabolic_regulation_Main_Pathway	-0,026	-0,032	0,012	26	-0,007
reactome_Glucagon_type_ligand_receptors_Main_Pathway	-0,031	-0,038	0,014	22	-0,008
reactome_Glucocorticoid_biosynthesis_Main_Pathway	0	0	0	6	0
reactome_Gluconeogenesis_Main_Pathway	-0,062	0,121	-0,044	19	-0,053

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Glucose_transport_Main_Pathway	-0,082	0,124	-0,013	10	-0,047
reactome_Glucuronidation_Main_Pathway	0	0	0	16	0
reactome_Glutamate_Neurotransmitter_Release_Cycle_Main_Pathway	-0,023	0,042	-0,027	18	-0,025
reactome_Glutathione_synthesis_and_recycling_Main_Pathway	-0,030	0,135	-0,006	6	-0,018
reactome_Glycogen_breakdown_glycogenolysis__Main_Pathway	0,001	-0,001	-0,018	12	-0,008
reactome_Glycogen_synthesis_Main_Pathway	0,042	0,015	0,004	13	0,023
reactome_Glycolysis_Main_Pathway	0,039	-0,038	-0,028	9	0,005
reactome_Glycoprotein_hormones_Main_Pathway	0	0	0	10	0
reactome_Glycosphingolipid_metabolism_Main_Pathway	-0,044	0,049	-0,035	35	-0,039
reactome_Glyoxylate_metabolism_Main_Pathway	0	0	0	5	0
reactome_Golgi_Associated_Vesicle_Biogenesis_Main_Pathway	-0,013	-0,001	0,018	45	0,002
reactome_Golgi_Cisternae_Pericentriolar_Stack_Reorganization_Main_Pathway	0,020	-0,103	0,034	9	0,027
reactome_GP1b_IX_V_activation_signalling_Main_Pathway	0,049	-0,060	0,025	9	0,037
reactome_GPVI_mediated_activation_cascade_Main_Pathway	-0,030	0,250	-0,018	30	-0,024
reactome_GRB2_events_in_EGFR_signaling_Main_Pathway	-0,125	-0,011	0,070	6	-0,028
reactome_GRB2_events_in_ERBB2_signaling_Main_Pathway	-0,102	0,370	-0,007	4	-0,055
reactome_GRB2_SOS_provides_linkage_to_MAPK_signaling_for_Integrins_Main_Pathway	0,020	-0,066	0,026	13	0,023
reactome_Growth_hormone_receptor_signaling_Main_Pathway	0,002	0,183	-0,008	21	-0,003
reactome_GTP_hydrolysis_and_joining_of_the_60S_ribosomal_subunit_Main_Pathway	-0,012	0,072	0,022	105	0,005
reactome_HATs_acetylate_histones_Main_Pathway	-0,005	0,031	0,007	79	0,001
reactome_HDACs_deacetylate_histones_Main_Pathway	-0,004	-0,012	0,021	36	0,009
reactome_HDL_mediated_lipid_transport_Main_Pathway	-0,013	-0,017	-0,021	12	-0,017
reactome_HDMs_demethylate_histones_Main_Pathway	-0,067	0,047	-0,016	23	-0,042
reactome_Hedgehog_ligand_biogenesis_Main_Pathway	-0,020	0,018	0,000	59	-0,010
reactome_Heme_biosynthesis_Main_Pathway	-0,031	-0,005	0,045	9	0,007
reactome_Heme_degradation_Main_Pathway	0,041	-0,149	0,056	5	0,048
reactome_Hexose_uptake_Main_Pathway	0	0	0	7	0
reactome_Hh_ligand_biogenesis_disease_Main_Pathway	-0,021	0,019	0,002	55	-0,010
reactome_Histamine_receptors_Main_Pathway	0	0	0	4	0
reactome_Histidine_catabolism_Main_Pathway	0	0	0	5	0
reactome_HIV_elongation_arrest_and_recovery_Main_Pathway	-0,006	-0,043	0,004	31	-0,001
reactome_HIV_Transcription_Initiation_Main_Pathway	-0,041	0,016	-0,040	43	-0,040
reactome_Hormone_sensitive_lipase_HSL_mediated_triacylglycerol_hydrolysis_Main_Pathway	-0,066	-0,083	0,015	12	-0,026
reactome_HS_GAG_biosynthesis_Main_Pathway	-0,025	0,039	-0,012	31	-0,019
reactome_HS_GAG_degradation_Main_Pathway	-0,038	0,045	-0,015	14	-0,026
reactome_HSF1_activation_Main_Pathway	-0,057	0,099	0,007	10	-0,025
reactome_HSF1_dependent_transactivation_Main_Pathway	-0,030	0,122	-0,031	16	-0,030
reactome_HuR_stabilizes_mRNA_Main_Pathway	-0,034	0,044	-0,019	8	-0,027
reactome_Hyaluronan_biosynthesis_and_export_Main_Pathway	0	0	0	4	0
reactome_Hyaluronan_uptake_and_degradation_Main_Pathway	-0,022	-0,268	0,072	10	0,025
reactome_Hydrolysis_of_LPC_Main_Pathway	0,046	-0,079	0,043	8	0,045
reactome_Hydroxycarboxylic_acid_binding_receptors_Main_Pathway	0	0	0	3	0
reactome_Hypusinylation_Main_Pathway	0,012	0,073	-0,026	4	-0,007
reactome_IKK_complex_recruitment_mediated_by_RIP1_Main_Pathway	-0,001	-0,074	0,068	5	0,034
reactome_Inactivation_of_APC_C_via_direct_inhibition_of_the_APC_C_complex_Main_Pathway	-0,011	0,018	-0,002	18	-0,007
reactome_Inactivation_of_Cdc42_and_Rac_Main_Pathway	-0,055	-0,051	0,087	9	0,016
reactome_Inflammasomes_Main_Pathway	0,121	-0,458	0,211	3	0,166
reactome_Inhibition_of_replication_initiation_of_damaged_DNA_by_RB1_E2F1_Main_Pathway	-0,030	0,047	0,000	12	-0,015
reactome_Inhibition_of_TSC_complex_formation_by_PKB_Main_Pathway	0,032	-0,002	-0,018	3	0,007
reactome_Inhibition_of_voltage_gated_Ca2_channels_via_Gbeta_gamma_subunits_Main_Pathway	-0,038	-0,052	0,023	15	-0,008
reactome_Initial_triggering_of_complement_Main_Pathway	0,005	-0,010	0,002	12	0,003
reactome_Initiation_of_Nuclear_Envelope_Reformation_Main_Pathway	0,084	0,060	0,010	9	0,047
reactome_Inositol_transporters_Main_Pathway	0	0	0	7	0
reactome_Insulin_like_Growth_Factor_2_mRNA_Binding_Proteins_IGF2BPs_IMPs_VICKZs_bind_RNA_Main_Pathway	-0,045	0,166	-0,080	3	-0,062

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Insulin_processing_Main_Pathway	0,015	-0,035	0,005	18	0,010
reactome_Insulin_receptor_recycling_Main_Pathway	-0,073	0,086	-0,030	26	-0,051
reactome_Integration_of_energy_metabolism_Main_Pathway	0,063	-0,145	-0,014	5	0,024
reactome_Integration_of_provirus_Main_Pathway	-0,120	0,321	-0,168	4	-0,144
reactome_Integration_of_viral_DNA_into_host_genomic_DNA_Main_Pathway	-0,109	0,300	-0,206	3	-0,157
reactome_Integrin_alphaIIb_beta3_signaling_Main_Pathway	-0,025	0,028	0,004	20	-0,011
reactome_Integrin_cell_surface_interactions_Main_Pathway	0,002	-0,092	0,028	45	0,015
reactome_Interaction_With_The_Zona_Pellucida_Main_Pathway	0,007	0,006	-0,006	10	0,000
reactome_Interconversion_of_2_oxoglutarate_and_2_hydroxyglutarate_Main_Pathway	-0,097	0,080	0,003	3	-0,047
reactome_Interconversion_of_polyamines_Main_Pathway	-1,535	1,243	-0,023	3	-0,779
reactome_Interferon_alpha_beta_signaling_Main_Pathway	0,011	-0,088	-0,002	60	0,004
reactome_Interferon_gamma_signaling_Main_Pathway	0,018	-0,079	0,000	66	0,009
reactome_Interleukin_1_processing_Main_Pathway	0,052	-0,196	0,090	7	0,071
reactome_Interleukin_1_signaling_Main_Pathway	0,020	-0,040	0,026	35	0,023
reactome_Interleukin_2_signaling_Main_Pathway	-0,059	0,026	-0,015	12	-0,037
reactome_Interleukin_6_signaling_Main_Pathway	0,040	-0,223	-0,003	6	0,019
reactome_Interleukin_7_signaling_Main_Pathway	0,022	-0,109	0,004	11	0,013
reactome_Interleukin_receptor_SHC_signaling_Main_Pathway	-0,029	-0,004	-0,004	13	-0,017
reactome_Intrinsic_Pathway_Main_Pathway	-0,019	-0,015	-0,020	17	-0,019
reactome_Ion_transport_by_P_type_ATPases_Main_Pathway	-0,023	-0,025	-0,003	42	-0,013
reactome_IRAK1_recruits_IKK_complex_Main_Pathway	-0,029	0,059	0,014	10	-0,008
reactome_IRAK1_recruits_IKK_complex_upon_TLR7_8_or_9_stimulation_Main_Pathway	-0,029	0,059	0,014	10	-0,008
reactome_IRAK2_mediated_activation_of_TAK1_complex_Main_Pathway	0,057	-0,007	0,009	10	0,033
reactome_IRAK2_mediated_activation_of_TAK1_complex_upon_TLR7_8_or_9_stimulation_Main_Pathway	0,057	-0,007	0,009	10	0,033
reactome_IRF3_mediated_activation_of_type_1_IFN_Main_Pathway	0,047	-0,047	0,013	5	0,030
reactome_IRF3_mediated_induction_of_type_I_IFN_Main_Pathway	-0,017	0,131	-0,045	12	-0,031
reactome_Iron_uptake_and_transport_Main_Pathway	0,124	-0,210	0,025	13	0,075
reactome_IRS_activation_Main_Pathway	0,076	-0,079	-0,027	5	0,025
reactome_IRS_related_events_triggered_by_IGF1R_Main_Pathway	0,063	-0,066	-0,022	6	0,021
reactome_ISG15_antiviral_mechanism_Main_Pathway	-0,068	-0,053	0,011	67	-0,028
reactome_JNK_c_Jun_kinases_phosphorylation_and_activation_mediated_by_activated_human_TAK1_Main_Pathway	0,148	-0,322	0,114	5	0,131
reactome_Keratan_sulfate_biosynthesis_Main_Pathway	0,003	-0,006	0,007	22	0,005
reactome_Keratan_sulfate_degradation_Main_Pathway	-0,029	0,036	-0,031	10	-0,030
reactome_Ketone_body_catabolism_Main_Pathway	-0,085	0,192	-0,112	3	-0,099
reactome_Kinesins_Main_Pathway	0,058	-0,128	0,058	22	0,058
reactome_KSRP_destabilizes_mRNA_Main_Pathway	0,005	0,086	-0,027	17	-0,011
reactome_L13a_mediated_translational_silencing_of_Ceruloplasmin_expression_Main_Pathway	-0,011	0,074	0,023	104	0,006
reactome_L1CAM_interactions_Main_Pathway	0,023	0,011	0,028	11	0,026
reactome_Laminin_interactions_Main_Pathway	-0,011	-0,180	0,044	14	0,017
reactome_LDL_endocytosis_Main_Pathway	-0,029	0,038	-0,019	6	-0,024
reactome_Leading_Strand_Synthesis_Main_Pathway	-0,080	0,209	-0,035	9	-0,057
reactome_Leukotriene_receptors_Main_Pathway	0	0	0	5	0
reactome_Ligand_gated_ion_channel_transport_Main_Pathway	0	0	0	13	0
reactome_Linoleic_acid_LA_metabolism_Main_Pathway	-0,006	-0,091	0,020	6	0,007
reactome_Loss_of_Nlp_from_mitotic_centrosomes_Main_Pathway	0,002	-0,040	0,022	60	0,012
reactome_Loss_of_proteins_required_for_interphase_microtubule_organizationA_from_the_centrosome_Main_Pathway	0,002	-0,040	0,022	60	0,012
reactome_LRR_FLII_interacting_protein_1_LRRFIP1_activates_type_I_IFN_production_Main_Pathway	0,028	0,065	0,095	5	0,061
reactome_Lysine_catabolism_Main_Pathway	-0,097	-0,095	-0,009	8	-0,053
reactome_Lysosome_Vesicle_Biogenesis_Main_Pathway	-0,064	0,038	-0,010	22	-0,037
reactome_Lysosphingolipid_and_LPA_receptors_Main_Pathway	0	0	0	9	0
reactome_Meiotic_recombination_Main_Pathway	-0,004	0,027	0,000	54	-0,002
reactome_Meiotic_synapsis_Main_Pathway	-0,012	0,027	-0,008	55	-0,010
reactome_MEK_activation_Main_Pathway	-0,028	0,259	-0,031	7	-0,029

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Membrane_binding_and_targetting_of_GAG_proteins_Main_Pathway	-0,002	0,082	-0,029	11	-0,015
reactome_Metabolism_of_Angiotensinogen_to_Angiotensins_Main_Pathway	-0,006	0,023	0,001	16	-0,002
reactome_Metabolism_of_folate_and_pterines_Main_Pathway	0,023	-0,077	0,042	8	0,033
reactome_Metabolism_of_polyamines_Main_Pathway	0,013	0,072	-0,013	4	-0,000
reactome_Metal_ion_SLC_transporters_Main_Pathway	-0,021	0,644	-0,022	8	-0,022
reactome_Methionine_salvage_Main_Pathway	-0,077	0,374	-0,032	6	-0,054
reactome_Methylation_Main_Pathway	-0,024	0,115	0,159	7	0,068
reactome_MHC_class_II_antigen_presentation_Main_Pathway	-0,023	0,062	-0,053	93	-0,038
reactome_MicroRNA_miRNA_biogenesis_Main_Pathway	-0,001	0,016	-0,008	11	-0,005
reactome_Mineralocorticoid_biosynthesis_Main_Pathway	0	0	0	5	0
reactome_Miscellaneous_substrates_Main_Pathway	-0,022	0,027	-0,008	12	-0,015
reactome_Mismatch_repair_MMR_directed_by_MSH2_MSH3_MutSbeta__Main_Pathway	-0,068	0,180	-0,012	14	-0,040
reactome_Mismatch_repair_MMR_directed_by_MSH2_MSH6_MutSalpha__Main_Pathway	-0,065	0,175	-0,013	14	-0,039
reactome_misspliced_LRP5_mutants_have_enhanced_beta_catenin_dependent_signaling_Main_Pathway	-0,029	-0,107	0,111	8	0,041
reactome_mitochondrial_fatty_acid_beta_oxidation_of_unsaturated_fatty_acids_Main_Pathway	-0,142	-0,050	-0,066	6	-0,104
reactome_Mitochondrial_iron_sulfur_cluster_biogenesis_Main_Pathway	-0,059	-0,046	0,001	4	-0,029
reactome_Mitochondrial_transcription_initiation_Main_Pathway	-0,256	0,211	-0,099	3	-0,178
reactome_Mitochondrial_tRNA_aminoacylation_Main_Pathway	-0,083	0,067	-0,010	21	-0,047
reactome_Mitotic_Prometaphase_Main_Pathway	0,006	-0,004	0,016	85	0,011
reactome_Molecules_associated_with_elastic_fibres_Main_Pathway	0,004	0,012	-0,002	22	0,001
reactome_Molybdenum_cofactor_biosynthesis_Main_Pathway	0,257	0,211	-0,157	4	0,050
reactome_mRNA_3_end_processing_Main_Pathway	-0,061	0,137	-0,021	33	-0,041
reactome_mRNA_Capping_Main_Pathway	-0,026	-0,006	-0,022	28	-0,024
reactome_mRNA_decay_by_3_to_5_exoribonuclease_Main_Pathway	-0,011	0,162	-0,059	11	-0,035
reactome_mRNA_decay_by_5_to_3_exoribonuclease_Main_Pathway	-0,066	0,144	-0,013	15	-0,039
reactome_mTOR_signalling_Main_Pathway	-0,008	0,186	0,018	4	0,005
reactome_Multifunctional_anion_exchangers_Main_Pathway	0	0	0	7	0
reactome_Muscarinic_acetylcholine_receptors_Main_Pathway	0	0	0	5	0
reactome_MyD88_cascade_initiated_on_plasma_membrane_Main_Pathway	-0,052	0,057	-0,059	7	-0,056
reactome_MyD88_dependent_cascade_initiated_on_endosome_Main_Pathway	-0,073	0,079	-0,083	5	-0,078
reactome_MyD88_independent_cascade_Main_Pathway	0	0	0	6	0
reactome_N_Glycan_antennae_elongation_Main_Pathway	-0,022	0,038	0,007	9	-0,008
reactome_N_glycan_trimming_in_the_ER_and_Calnexin_Calreticulin_cycle_Main_Pathway	-0,090	-0,213	0,020	4	-0,035
reactome_Na_Cl_dependent_neurotransmitter_transporters_Main_Pathway	0	0	0	19	0
reactome_Na_dependent_glucose_transporters_Main_Pathway	0	0	0	6	0
reactome_NADE_modulates_death_signalling_Main_Pathway	-0,074	0,142	-0,035	6	-0,055
reactome_NCAM_signaling_for_neurite_out_growth_Main_Pathway	-0,030	0,077	0,041	17	0,006
reactome_NCAM1_interactions_Main_Pathway	-0,015	0,049	-0,002	32	-0,008
reactome_Nectin_Necl_trans_heterodimerization_Main_Pathway	0,011	-0,116	0,024	7	0,017
reactome_Nef_and_signal_transduction_Main_Pathway	-0,102	0,242	-0,046	7	-0,074
reactome_Nef_Mediated_CD4_Down_regulation_Main_Pathway	-0,131	0,177	-0,043	9	-0,087
reactome_Nef_Mediated_CD8_Down_regulation_Main_Pathway	-0,127	0,074	-0,026	7	-0,076
reactome_Nef_mediated_downregulation_of_MHC_class_I_complex_cell_surface_expression_Main_Pathway	-0,024	0,003	0,042	10	0,009
reactome_Negative_regulation_of_FGFR_signaling_Main_Pathway	0,015	0,018	-0,000	22	0,008
reactome_negative_regulation_of_TCF_dependent_signaling_by_DVL_interacting_proteins_Main_Pathway	-0,049	0,024	-0,003	5	-0,026
reactome_negative_regulation_of_TCF_dependent_signaling_by_WNT_ligand_antagonists_Main_Pathway	-0,010	-0,032	0,016	8	0,003
reactome_Negative_regulation_of_the_PI3K_AKT_network_Main_Pathway	-0,018	0,054	-0,022	8	-0,020
reactome_Negative_regulators_of_RIG_I_MDA5_signaling_Main_Pathway	0,025	0,001	-0,002	21	0,012
reactome_NEP_NS2_Interacts_with_the_Cellular_Export_Machinery_Main_Pathway	-0,074	-0,027	0,012	26	-0,031
reactome_Nephrin_interactions_Main_Pathway	0,095	-0,176	0,065	20	0,080
reactome_Netrin_mediated_repulsion_signals_Main_Pathway	0	0	0	6	0

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Neurofascin_interactions_Main_Pathway	0,046	-0,006	-0,004	7	0,021
reactome_Neurotransmitter_Clearance_In_The_Synaptic_Cleft_Main_Pathway	0	0	0	4	0
reactome_NF_kB_activation_through_FADD_RIP_1_pathway_mediated_by_caspase_8_and_10_Main_Pathway	0,033	-0,037	0,081	8	0,057
reactome_NF_kB_is_activated_and_signals_survival_Main_Pathway	0,034	0,031	0,022	13	0,028
reactome_NGF_independant_TRKA_activation_Main_Pathway	0,016	-0,274	0,075	5	0,045
reactome_NGF_processing_Main_Pathway	0	0	0	4	0
reactome_NICD_traffics_to_nucleus_Main_Pathway	0,004	0,018	0,025	13	0,014
reactome_Nicotinamide_salvaging_Main_Pathway	0,071	-0,074	0,024	5	0,047
reactome_Nicotinate_metabolism_Main_Pathway	-0,035	-0,149	0,006	6	-0,014
reactome_Nitric_oxide_stimulates_guanylate_cyclase_Main_Pathway	-0,010	-0,004	-0,004	7	-0,007
reactome_NOD1_2_Signaling_Pathway_Main_Pathway	0,038	-0,021	0,027	29	0,033
reactome_Non_integrin_membrane_ECM_interactions_Main_Pathway	-0,010	-0,031	0,008	8	-0,001
reactome_Nonhomologous_End_joining_NHEJ__Main_Pathway	-0,022	0,039	-0,037	5	-0,029
reactome_Nonsense_Mediated_Decay_NMD_enhanced_by_the_Exon_Junction_Complex_EJC__Main_Pathway	-0,004	0,057	0,021	106	0,009
reactome_Nonsense_Mediated_Decay_NMD_independent_of_the_Exon_Junction_Complex_EJC__Main_Pathway	-0,008	0,070	0,027	89	0,010
reactome_NoRC_negatively_regulates_rRNA_expression_Main_Pathway	-0,015	0,007	0,001	72	-0,007
reactome_Norepinephrine_Neurotransmitter_Release_Cycle_Main_Pathway	-0,001	0,025	-0,016	17	-0,008
reactome_NOSTRIN_mediated_eNOS_trafficking_Main_Pathway	-0,037	-0,401	0,180	5	0,072
reactome_Notch_HLH_transcription_Main_Pathway	0,004	0,018	0,025	13	0,014
reactome_NOTCH1_Intracellular_Domain_Regulates_Transcription_Main_Pathway	0,009	0,006	0,025	42	0,017
reactome_NOTCH2_Activation_and_Transmission_of_Signal_to_the_Nucleus_Main_Pathway	-0,009	-0,026	-0,013	21	-0,011
reactome_NOTCH2_intracellular_domain_regulates_transcription_Main_Pathway	-0,004	0,111	0,019	12	0,008
reactome_NRAGE_signals_death_through_JNK_Main_Pathway	0,010	-0,008	-0,001	45	0,004
reactome_NrCAM_interactions_Main_Pathway	0,026	-0,014	-0,074	7	-0,024
reactome_NRIF_signals_cell_death_from_the_nucleus_Main_Pathway	0,059	-0,047	0,025	15	0,042
reactome_Nuclear_import_of_Rev_protein_Main_Pathway	-0,061	-0,020	0,013	28	-0,024
reactome_Nuclear_Pore_Complex_NPC_Disassembly_Main_Pathway	-0,069	-0,028	0,019	27	-0,025
reactome_Nuclear_Receptor_transcription_Main_Pathway	-0,016	-0,002	-0,002	38	-0,009
reactome_Nuclear_signaling_by_ERBB4_Main_Pathway	-0,012	-0,085	0,035	17	0,011
reactome_O_glycosylation_of_TSR_domain_containing_proteins_Main_Pathway	0,001	-0,004	0,000	38	0,001
reactome_O_linked_glycosylation_of_mucins_Main_Pathway	-0,004	0,031	-0,004	53	-0,004
reactome_Olfactory_Signaling_Pathway_Main_Pathway	-0,001	0,000	-0,000	375	-0,000
reactome_Oncogene_Induced_Senescence_Main_Pathway	0,002	0,059	-0,032	22	-0,015
reactome_Opioid_Signalling_Main_Pathway	0	0	0	3	0
reactome_Opsins_Main_Pathway	0	0	0	9	0
reactome_Orc1_removal_from_chromatin_Main_Pathway	-0,019	0,039	-0,001	70	-0,010
reactome_Organic_anion_transport_Main_Pathway	0	0	0	5	0
reactome_Organic_anion_transporters_Main_Pathway	0	0	0	8	0
reactome_Organic_cation_transport_Main_Pathway	-0,029	0,062	-0,024	8	-0,027
reactome_Oxidative_Stress_Induced_Senescence_Main_Pathway	0,004	-0,023	0,039	80	0,022
reactome_Oxygen_dependent_asparagine_hydroxylation_of_Hypoxia_inducible_Factor_Alpha_Main_Pathway	0,042	-0,014	-0,005	3	0,019
reactome_Oxygen_dependent_proline_hydroxylation_of_Hypoxia_inducible_Factor_Alpha_Main_Pathway	0,038	-0,008	0,005	15	0,021
reactome_p130Cas_linkage_to_MAPK_signaling_for_integrins_Main_Pathway	0,031	-0,058	0,032	14	0,031
reactome_P2Y_receptors_Main_Pathway	0	0	0	12	0
reactome_p38MAPK_events_Main_Pathway	-0,045	0,188	-0,005	10	-0,025
reactome_p53_Dependent_G1_DNA_Damage_Response_Main_Pathway	0,001	0,018	-0,007	5	-0,003
reactome_p75NTR_negatively_regulates_cell_cycle_via_SC1_Main_Pathway	-0,072	0,096	-0,044	6	-0,058
reactome_p75NTR_recruits_signalling_complexes_Main_Pathway	0,014	0,052	-0,004	13	0,005
reactome_Packaging_Of_Telomere_Ends_Main_Pathway	-0,007	0,045	0,008	31	0,001
reactome_Pausing_and_recovery_of_HIV_elongation_Main_Pathway	-0,006	-0,043	0,004	31	-0,001
reactome_Pausing_and_recovery_of_Tat_mediated_HIV_elongation_Main_Pathway	-0,008	-0,034	0,000	30	-0,004
reactome_PCP_CE_Main_Pathway	0,007	-0,045	0,023	21	0,015

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reactome_PD_1_signaling_Main_Pathway	-0,049	0,299	-0,229	23	-0,139
reactome_PECAM1_interactions_Main_Pathway	-0,060	0,552	-0,007	11	-0,033
reactome_Pentose_phosphate_pathway_hexose_monophosphate_shunt__Main_Pathway	-0,003	0,077	0,015	6	0,006
reactome_Peptide_chain_elongation_Main_Pathway	-0,009	0,079	0,027	84	0,009
reactome_PERK_regulates_gene_expression_Main_Pathway	0,032	-0,096	-0,000	4	0,016
reactome_Phagosomal_maturation_early_endosomal_stage__Main_Pathway	-0,056	0,059	-0,022	33	-0,039
reactome_Phenylalanine_and_tyrosine_catabolism_Main_Pathway	0,032	0,048	0,002	9	0,017
reactome_Phosphate_bond_hydrolysis_by_NUDT_proteins_Main_Pathway	0,024	0,126	-0,047	3	-0,011
reactome_Phospholipase_C_mediated_cascade_Main_Pathway	-0,003	0,011	-0,001	16	-0,002
reactome_Phosphorylation_of_CD3_and_TCR_zeta_chains_Main_Pathway	-0,050	0,326	-0,263	20	-0,157
reactome_Phosphorylation_of_Emi1_Main_Pathway	0,087	-0,198	0,009	6	0,048
reactome_Phosphorylation_of_proteins_involved_in_G1_S_transition_by_active_Cyclin_E_Cdk2_complexes_Main_Pathway	-0,017	0,061	0,013	4	-0,002
reactome_Phosphorylation_of_proteins_involved_in_the_G2_M_transition_by_Cyclin_A_Cdc2_complexes_Main_Pathway	0,030	0,047	0,030	3	0,030
reactome_Phosphorylation_of_the_APC_C_Main_Pathway	-0,025	0,084	-0,020	17	-0,022
reactome_PI_3K_cascade_Main_Pathway	-0,001	0,005	0,007	20	0,003
reactome_PI3K_AKT_activation_Main_Pathway	0,054	-0,153	0,017	9	0,035
reactome_PI3K_Cascade_Main_Pathway	0,071	-0,029	-0,017	7	0,027
reactome_PI3K_events_in_ERBB2_signaling_Main_Pathway	-0,008	0	0,045	3	0,018
reactome_PIP3_activates_AKT_signaling_Main_Pathway	0,009	-0,032	0,039	10	0,024
reactome_PKA_activation_in_glucagon_signalling_Main_Pathway	-0,039	0,022	-0,009	17	-0,024
reactome_PKA_mediated_phosphorylation_of_CREB_Main_Pathway	-0,084	0,135	-0,069	4	-0,076
reactome_PKA_mediated_phosphorylation_of_key_metabolic_factors_Main_Pathway	-0,037	0,044	-0,047	5	-0,042
reactome_Plasmalogen_biosynthesis_Main_Pathway	-0,002	-0,019	0,004	4	0,001
reactome_Platelet_Adhesion_to_exposed_collagen_Main_Pathway	-0,019	0,546	-0,013	9	-0,016
reactome_Platelet_Aggregation_Plug_Formation__Main_Pathway	0	0	0	5	0
reactome_Platelet_sensitization_by_LDL_Main_Pathway	0,014	-0,053	0,004	17	0,009
reactome_PLC_beta_mediated_events_Main_Pathway	-0,002	-0,091	0,030	15	0,014
reactome_PLC_gamma1_signalling_Main_Pathway	0,011	-0,398	0,120	3	0,066
reactome_Polo_like_kinase_mediated_events_Main_Pathway	0,029	0,026	-0,036	16	-0,003
reactome_Polymerase_switching_Main_Pathway	-0,097	0,238	-0,039	14	-0,068
reactome_Polymerase_switching_on_the_C_strand_of_the_telomere_Main_Pathway	-0,097	0,238	-0,039	14	-0,068
reactome_Post_chaperonin_tubulin_folding_Main_Pathway	0,067	-0,125	0,044	18	0,056
reactome_Post_transcriptional_silencing_by_small_RNAs_Main_Pathway	-0,013	0,013	0,042	3	0,014
reactome_POU5F1_OCT4_SOX2_NANOG_activate_genes_related_to_proliferation_Main_Pathway	-0,014	0,019	0,017	9	0,001
reactome_POU5F1_OCT4_SOX2_NANOG_repress_genes_related_to_differentiation_Main_Pathway	-0,065	0,268	-0,007	3	-0,036
reactome_PP2A_mediated_dephosphorylation_of_key_metabolic_factors_Main_Pathway	0,045	-0,104	-0,010	7	0,017
reactome_PPARA_activates_gene_expression_Main_Pathway	0,018	-0,059	0,031	61	0,025
reactome_PRC2_methylates_histones_and_DNA_Main_Pathway	-0,012	0,026	0,023	35	0,005
reactome_pre_mRNA_splicing_Main_Pathway	-0,067	0,129	-0,035	113	-0,051
reactome_Pre_NOTCH_Processing_in_Golgi_Main_Pathway	-0,014	0,027	-0,021	18	-0,018
reactome_Pre_NOTCH_Processing_in_the_Endoplasmic_Reticulum_Main_Pathway	-0,101	0,062	-0,028	6	-0,064
reactome_Prefoldin_mediated_transfer_of_substrate_to_CCT_TriC_Main_Pathway	0,013	0,021	0,001	26	0,007
reactome_Pregnenolone_biosynthesis_Main_Pathway	0,095	-0,041	0,082	6	0,089
reactome_Presynaptic_function_of_Kainate_receptors_Main_Pathway	-0,017	-0,062	0,024	21	0,004
reactome_Presynaptic_phase_of_homologous_DNA_pairing_and_strand_exchange_Main_Pathway	-0,054	0,082	-0,013	4	-0,033
reactome_Processing_of_Capped_Intron_Containing_Pre_mRNA_Main_Pathway	-0,082	0,102	-0,031	35	-0,057
reactome_Processing_of_DNA_double_strand_break_ends_Main_Pathway	-0,071	0,110	-0,017	3	-0,044
reactome_Processing_of_DNA_ends_prior_to_end_rejoining_Main_Pathway	-0,019	-0,067	0,012	4	-0,004
reactome_Processing_of_Intronless_Pre_mRNAs_Main_Pathway	-0,025	0,095	0,004	14	-0,011
reactome_Processive_synthesis_on_the_C_strand_of_the_telomere_Main_Pathway	-0,057	0,214	-0,021	6	-0,039

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Processive_synthesis_on_the_lagging_strand_Main_Pathway	-0,080	0,209	-0,035	9	-0,057
reactome_Progressive_trimming_of_alpha_1_2_linked_mannose_residues_from_Man9_8_7GlcNAc2_to_produce_Man5GlcNAc2_Main_Pathway	-0,166	0,046	-0,041	3	-0,104
reactome_Prolactin_receptor_signaling_Main_Pathway	0,019	-0,038	0,027	13	0,023
reactome_Propionyl_CoA_catabolism_Main_Pathway	-0,069	0,062	-0,044	5	-0,056
reactome_Prostacyclin_signalling_through_prostacyclin_receptor_Main_Pathway	-0,035	-0,044	0,016	19	-0,010
reactome_Prostanoid_ligand_receptors_Main_Pathway	0	0	0	9	0
reactome_Proton_coupled_monocarboxylate_transport_Main_Pathway	-0,088	0,262	-0,021	4	-0,054
reactome_Proton_oligopeptide_cotransporters_Main_Pathway	0	0	0	4	0
reactome_Purine_catabolism_Main_Pathway	-0,041	-0,012	0,054	10	0,006
reactome_Purine_ribonucleoside_monophosphate_biosynthesis_Main_Pathway	0,048	0,081	0,017	7	0,033
reactome_Purine_salvage_Main_Pathway	0,005	0,155	-0,011	8	-0,003
reactome_Pyrimidine_biosynthesis_Main_Pathway	-0,038	0,219	0,027	5	-0,006
reactome_Pyrimidine_catabolism_Main_Pathway	-0,025	0,056	-0,012	11	-0,018
reactome_Pyrimidine_salvage_reactions_Main_Pathway	-0,018	0,016	-0,005	9	-0,011
reactome_Pyruvate_metabolism_Main_Pathway	-0,057	-0,064	-0,000	8	-0,028
reactome_RAF_activation_Main_Pathway	-0,058	0,300	-0,023	5	-0,041
reactome_RAF_phosphorylates_MEK_Main_Pathway	-0,028	0,259	-0,031	7	-0,029
reactome_Rap1_signalling_Main_Pathway	-0,004	-0,043	0,006	15	0,001
reactome_Ras_activation_uopn_Ca2_infux_through_NMDA_receptor_Main_Pathway	0,005	-0,025	0,016	17	0,010
reactome_Receptor_ligand_binding_initiates_the_second_proteolytic_cleavage_of_Notch_receptor_Main_Pathway	-0,024	-0,002	-0,036	14	-0,030
reactome_Recognition_and_association_of_DNA_glycosylase_with_site_containing_an_affected_purine_Main_Pathway	0,029	0,161	-0,015	3	0,007
reactome_Recognition_and_association_of_DNA_glycosylase_with_site_containing_an_affected_pyrimidine_Main_Pathway	0,050	0,089	0,019	5	0,034
reactome_Recruitment_of_mitotic_centrosome_proteins_and_complexes_Main_Pathway	-0,001	-0,025	0,016	68	0,007
reactome_Recruitment_of_NuMA_to_mitotic_centrosomes_Main_Pathway	-0,006	0,029	-0,005	11	-0,006
reactome_Recruitment_of_repair_and_signaling_proteins_to_double_strand_breaks_Main_Pathway	0,055	0,056	0,037	5	0,046
reactome_Recycling_of_bile_acids_and_salts_Main_Pathway	-0,011	-0,006	-0,014	16	-0,013
reactome_Recycling_of_eIF2_GDP_Main_Pathway	0,010	0,108	-0,049	8	-0,020
reactome_Recycling_pathway_of_L1_Main_Pathway	0,009	-0,101	0,029	26	0,019
reactome_Reduction_of_cytosolic_Ca_levels_Main_Pathway	-0,030	-0,048	-0,061	10	-0,046
reactome_Regulated_proteolysis_of_p75NTR_Main_Pathway	0,034	-0,142	0,054	10	0,044
reactome_Regulation_by_c_FLIP_Main_Pathway	-0,473	0,545	0,008	9	-0,233
reactome_Regulation_of_actin_dynamics_for_phagocytic_cup_formation_Main_Pathway	0,014	-0,059	0,025	60	0,020
reactome_Regulation_of_activated_PAK_2p34_by_proteasome_mediated_degradation_Main_Pathway	-0,011	0,041	-0,006	49	-0,009
reactome_Regulation_of_AMPK_activity_via_LKB1_Main_Pathway	-0,011	0,032	-0,027	14	-0,019
reactome_Regulation_of_APC_C_activators_between_G1_S_and_early_anaphase_Main_Pathway	-0,006	0,032	-0,004	22	-0,005
reactome_Regulation_of_cholesterol_biosynthesis_by_SREBP_SREBF__Main_Pathway	0,073	-0,084	0,023	14	0,048
reactome_Regulation_of_Commissural_axon_pathfinding_by_Slit_and_Robo_Main_Pathway	-0,020	0,096	-0,046	3	-0,033
reactome_Regulation_of_Complement_cascade_Main_Pathway	0,013	-0,021	0,098	13	0,055
reactome_regulation_of_FZD_by_ubiquitination_Main_Pathway	0,018	-0,059	0,032	21	0,025
reactome_Regulation_of_gene_expression_by_Hypoxia_inducible_Factor_Main_Pathway	0,012	-0,076	0,085	9	0,048
reactome_Regulation_of_gene_expression_in_endocrine_committed_NEUROG3_progenitor_cells_Main_Pathway	0	0	0	5	0
reactome_Regulation_of_gene_expression_in_late_stage_branching_morphogenesis_pancreatic_bud_precursor_cells_Main_Pathway	0	0	0	4	0
reactome_Regulation_of_Glucokinase_by_Glucokinase_Regulatory_Protein_Main_Pathway	-0,073	-0,027	0,015	26	-0,029
reactome_Regulation_of_HSF1_mediated_heat_shock_response_Main_Pathway	-0,018	0,067	-0,019	15	-0,019
reactome_Regulation_of_IFNA_signaling_Main_Pathway	-0,010	-0,047	-0,003	23	-0,006
reactome_Regulation_of_IFNG_signaling_Main_Pathway	0,001	-0,057	-0,003	12	-0,001
reactome_Regulation_of_IGF_Activity_by_IGFBP_Main_Pathway	-0,014	-0,024	0,013	21	-0,000

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Regulation_of_innate_immune_responses_to_cytosolic_DNA_Main_Pathway	0,140	0,017	-0,005	11	0,067
reactome_Regulation_of_KIT_signaling_Main_Pathway	-0,050	0,505	-0,015	12	-0,032
reactome_Regulation_of_lipid_metabolism_by_Peroxisome_proliferator_activated_receptor_alpha_PPARalpha__Main_Pathway	-0,073	-0,029	0,047	19	-0,013
reactome_Regulation_of_ornithine_decarboxylase_ODC__Main_Pathway	-0,013	0,031	0,002	50	-0,006
reactome_Regulation_of_PLK1_Activity_at_G2_M_Transition_Main_Pathway	0,006	-0,037	0,019	71	0,013
reactome_Regulation_of_pyruvate_dehydrogenase_PDH_complex_Main_Pathway	-0,042	-0,055	-0,033	13	-0,038
reactome_Regulation_of_Rheb_GTPase_activity_by_AMPK_Main_Pathway	0,002	0,015	-0,022	10	-0,010
reactome_Regulation_of_signaling_by_CBL_Main_Pathway	-0,047	0,514	0,005	11	-0,021
reactome_Regulation_of_signaling_by_NODAL_Main_Pathway	0	0	0	4	0
reactome_Regulation_of_the_Fanconi_anemia_Main_Pathway	0,022	-0,142	-0,020	8	0,001
reactome_Relaxin_receptors_Main_Pathway	0	0	0	3	0
reactome_Release_of_eIF4E_Main_Pathway	0,016	0,211	-0,025	6	-0,005
reactome_Release_of_Hh_Np_from_the_secreting_cell_Main_Pathway	-0,050	0,023	0,011	8	-0,019
reactome_Removal_of_aminoterminal_propeptides_from_gamma_carboxylated_proteins_Main_Pathway	0	0	0	9	0
reactome_Removal_of_DNA_patch_containing_abasic_residue_Main_Pathway	-0,051	0,152	-0,006	9	-0,029
reactome_Removal_of_the_Flap_Intermediate_from_the_C_strand_Main_Pathway	-0,064	0,186	-0,035	10	-0,050
reactome_Removal_of_the_Flap_Intermediate_Main_Pathway	-0,078	0,191	-0,032	14	-0,055
reactome_Repair_synthesis_for_gap_filling_by_DNA_polymerase_in_TC_NER_Main_Pathway	-0,080	0,171	-0,029	15	-0,054
reactome_Repair_synthesis_of_patch_27_30_bases_long_by_DNA_polymerase_Main_Pathway	-0,080	0,171	-0,029	15	-0,054
reactome_repression_of_WNT_target_genes_Main_Pathway	0,048	-0,139	0,004	10	0,026
reactome_Resolution_of_AP_sites_via_the_multiple_nucleotide_patch_replacement_Main_Pathway	-0,028	0,162	-0,036	6	-0,032
reactome_Resolution_of_AP_sites_via_the_single_nucleotide_replacement_Main_Pathway	-0,084	-0,060	0,039	3	-0,023
reactome_Resolution_of_Sister_Chromatid_Cohesion_Main_Pathway	-0,004	0,012	0,008	94	0,002
reactome_Respiratory_electron_transport_Main_Pathway	-0,140	0,091	-0,028	86	-0,084
reactome_Response_to_elevated_platelet_cytosolic_Ca2__Main_Pathway	-0,012	0,020	0,013	3	0,001
reactome_Retinoid_metabolism_and_transport_Main_Pathway	-0,051	0,061	-0,014	41	-0,032
reactome_Retrograde_neurotrophin_signalling_Main_Pathway	-0,056	-0,103	0,034	13	-0,011
reactome_Reuptake_of_GABA_Main_Pathway	0	0	0	4	0
reactome_Rev_mediated_nuclear_export_of_HIV_RNA_Main_Pathway	-0,061	-0,017	0,012	29	-0,025
reactome_Rhesus_glycoproteins_mediate_ammonium_transport__Main_Pathway	0	0	0	3	0
reactome_Rho_GTPase_cycle_Main_Pathway	-0,005	-0,016	0,006	119	0,001
reactome_Ribosomal_scanning_and_start_codon_recognition_Main_Pathway	-0,024	0,103	0,005	55	-0,009
reactome_RIG_I_MDA5_mediated_induction_of_IFN_alpha_beta_pathways_Main_Pathway	-0,002	-0,057	-0,011	13	-0,007
reactome_RIP_mediated_NFkB_activation_via_ZBP1_Main_Pathway	-0,003	-0,065	0,025	21	0,011
reactome_RMTs_methylate_histone_arginines_Main_Pathway	-0,020	0,048	-0,003	43	-0,012
reactome_RNA_Pol_II_CTD_phosphorylation_and_interaction_with_CE_Main_Pathway	-0,024	-0,009	-0,021	26	-0,022
reactome_RNA_Polymerase_I_Chain_Elongation_Main_Pathway	-0,010	-0,009	0,009	56	-0,000
reactome_RNA_Polymerase_I_Promoter_Escape_Main_Pathway	-0,024	-0,030	0,003	29	-0,010
reactome_RNA_Polymerase_I_Promoter_Opening_Main_Pathway	-0,010	-0,010	-0,009	30	-0,010
reactome_RNA_Polymerase_I_Transcription_Initiation_Main_Pathway	-0,039	0,025	0,002	46	-0,018
reactome_RNA_Polymerase_I_Transcription_Termination_Main_Pathway	-0,022	-0,026	0,002	30	-0,010
reactome_RNA_Polymerase_II_HIV_Promoter_Escape_Main_Pathway	-0,041	0,016	-0,040	43	-0,040
reactome_RNA_Polymerase_II_Pre_transcription_Events_Main_Pathway	-0,022	-0,025	-0,022	60	-0,022
reactome_RNA_Polymerase_II_Promoter_Escape_Main_Pathway	-0,041	0,016	-0,040	43	-0,040
reactome_RNA_Polymerase_II_Transcription_Elongation_Main_Pathway	-0,004	-0,068	-0,000	40	-0,002
reactome_RNA_Polymerase_II_Transcription_Initiation_And_Promoter_Clearance_Main_Pathway	-0,041	0,016	-0,040	43	-0,040
reactome_RNA_Polymerase_II_Transcription_Initiation_Main_Pathway	-0,041	0,016	-0,040	43	-0,040
reactome_RNA_Polymerase_II_Transcription_Pre_Initiation_And_Promoter_Opening_Main_Pathway	-0,041	0,016	-0,040	43	-0,040

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_RNA_Polymerase_III_Abortive_And_Retractive_Initiation_Main_Pathway	-0,005	0,049	0,001	40	-0,002
reactome_RNA_Polymerase_III_Chain_Elongation_Main_Pathway	-0,019	0,035	-0,018	18	-0,018
reactome_RNA_Polymerase_III_Transcription_Initiation_From_Type_1_Promoter_Main_Pathway	-0,019	0,025	-0,004	27	-0,012
reactome_RNA_Polymerase_III_Transcription_Initiation_From_Type_2_Promoter_Main_Pathway	-0,018	0,021	-0,016	26	-0,017
reactome_RNA_Polymerase_III_Transcription_Initiation_From_Type_3_Promoter_Main_Pathway	-0,009	0,056	-0,007	28	-0,008
reactome_RNA_Polymerase_III_Transcription_Termination_Main_Pathway	-0,005	0,043	-0,013	23	-0,009
reactome_RNF_mutants_show_enhanced_WNT_signaling_and_proliferation_Main_Pathway	-0,029	-0,107	0,111	8	0,041
reactome_Role_of_Abl_in_Robo_Slit_signaling_Main_Pathway	0,066	0,013	-0,012	9	0,027
reactome_Role_of_DCC_in_regulating_apoptosis_Main_Pathway	0,035	-0,080	0,004	10	0,019
reactome_Role_of_LAT2_NTAL_LAB_on_calcium_mobilization_Main_Pathway	-0,056	0,447	0,006	13	-0,025
reactome_Role_of_phospholipids_in_phagocytosis_Main_Pathway	-0,016	-0,002	0,013	28	-0,002
reactome_Role_of_second_messengers_in_netrin_1_signaling_Main_Pathway	-0,004	0,018	-0,002	10	-0,003
reactome_RSK_activation_Main_Pathway	0,024	0,024	-0,002	6	0,011
reactome_S6K1_mediated_signalling_Main_Pathway	-1,131	0,101	0,118	5	-0,507
reactome_S6K1_signalling_Main_Pathway	-0,988	0,096	0,104	5	-0,442
reactome_Scavenging_by_Class_A_Receptors_Main_Pathway	-0,031	-0,058	-0,001	8	-0,016
reactome_Scavenging_by_Class_B_Receptors_Main_Pathway	-0,057	0,076	-0,038	3	-0,048
reactome_Scavenging_by_Class_F_Receptors_Main_Pathway	-0,123	0,022	-0,006	6	-0,064
reactome_Scavenging_of_heme_from_plasma_Main_Pathway	-0,006	0,003	-0,024	14	-0,015
reactome_SCF_beta_TrCP_mediated_degradation_of_Emi1_Main_Pathway	0,000	0,006	-0,001	53	-0,001
reactome_SCF_Skp2_mediated_degradation_of_p27_p21_Main_Pathway	-0,001	0,022	-0,001	56	-0,001
reactome_Sema3A_PAK_dependent_Axon_repulsion_Main_Pathway	-0,034	0,084	-0,011	16	-0,023
reactome_SEMA3A_Plexin_repulsion_signaling_by_inhibiting_Integrin_adhesion_Main_Pathway	0,025	-0,079	0,037	14	0,031
reactome_Sema4D_induced_cell_migration_and_growth_cone_collapse_Main_Pathway	0,054	-0,082	0,011	24	0,032
reactome_Sema4D_mediated_inhibition_of_cell_attachment_and_migration_Main_Pathway	-0,011	-0,173	-0,012	8	-0,011
reactome_Senescence_Associated_Secretory_Phenotype_SASP__Main_Pathway	-0,003	0,042	0,008	69	0,003
reactome_Separation_of_Sister_Chromatids_Main_Pathway	-0,009	0,027	0,001	158	-0,004
reactome_Serine_biosynthesis_Main_Pathway	-0,062	0,318	-0,125	3	-0,094
reactome_Serotonin_and_melatonin_biosynthesis_Main_Pathway	0	0	0	5	0
reactome_Serotonin_Neurotransmitter_Release_Cycle_Main_Pathway	-0,001	0,025	-0,016	17	-0,008
reactome_Serotonin_receptors_Main_Pathway	0	0	0	12	0
reactome_SHC_activation_Main_Pathway	-0,004	0,014	-0,018	3	-0,011
reactome_SHC_mediated_cascade_Main_Pathway	-0,021	0,078	-0,002	19	-0,012
reactome_SHC_mediated_signalling_Main_Pathway	-0,060	0,217	-0,012	7	-0,036
reactome_SHC_related_events_triggered_by_IGF1R_Main_Pathway	0	0	0	3	0
reactome_SHC1_events_in_EGFR_signaling_Main_Pathway	-0,109	-0,003	0,052	7	-0,028
reactome_SHC1_events_in_ERBB2_signaling_Main_Pathway	-0,077	-0,002	0,037	10	-0,020
reactome_SHC1_events_in_ERBB4_signaling_Main_Pathway	-0,035	0,127	-0,007	12	-0,021
reactome_Sialic_acid_metabolism_Main_Pathway	-0,008	-0,014	-0,009	33	-0,008
reactome_Signal_attenuation_Main_Pathway	0,044	-0,065	0,004	10	0,024
reactome_Signal_regulatory_protein_SIRP_family_interactions_Main_Pathway	0,017	-0,082	0,031	9	0,024
reactome_Signal_transduction_by_L1_Main_Pathway	-0,001	-0,097	0,037	12	0,018
reactome_Signaling_by_activated_point_mutants_of_FGFR1_Main_Pathway	0	0	0	8	0
reactome_Signaling_by_activated_point_mutants_of_FGFR3_Main_Pathway	0	0	0	9	0
reactome_Signaling_by_Activin_Main_Pathway	0,032	-0,105	0,020	9	0,026
reactome_Signaling_by_BMP_Main_Pathway	-0,001	-0,016	0,012	23	0,006
reactome_Signaling_by_constitutively_active_EGFR_Main_Pathway	-0,057	0,003	0,035	14	-0,011
reactome_Signaling_by_EGFR_Main_Pathway	-0,045	-0,346	0,105	6	0,030
reactome_Signaling_by_ERBB2_Main_Pathway	0,015	-0,122	0,026	18	0,021
reactome_Signaling_by_ERBB4_Main_Pathway	-0,038	-0,172	0,050	9	0,006
reactome_Signaling_by_FGFR_Main_Pathway	-0,048	-0,156	0,052	4	0,002
reactome_Signaling_by_FGFR_mutants_Main_Pathway	-0,021	0,072	0,004	23	-0,008

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Signaling_by_FGFR1_fusion_mutants_Main_Pathway	0,014	-0,061	0,046	17	0,030
reactome_Signaling_by_FGFR3_mutants_Main_Pathway	0	0	0	8	0
reactome_Signaling_by_Hippo_Main_Pathway	0,008	-0,098	0,047	19	0,027
reactome_Signaling_by_Leptin_Main_Pathway	0,057	-0,145	0,016	9	0,036
reactome_Signaling_by_NODAL_Main_Pathway	0,019	-0,062	0,011	15	0,015
reactome_Signaling_by_NOTCH3_Main_Pathway	-0,039	-0,081	-0,022	11	-0,031
reactome_Signaling_by_NOTCH4_Main_Pathway	-0,039	-0,081	-0,022	11	-0,031
reactome_Signaling_by_Robo_receptor_Main_Pathway	-0,045	0,144	-0,051	8	-0,048
reactome_Signaling_by_SCF_KIT_Main_Pathway	-0,015	0,178	-0,011	34	-0,013
reactome_Signaling_by_Type_1_Insulin_like_Growth_Factor_1_Receptor_IGF1R__Main_Pathway	0	0	0	3	0
reactome_Signaling_by_Wnt_Main_Pathway	-0,029	-0,107	0,111	8	0,041
reactome_Signalling_to_p38_via_RIT_and_RIN_Main_Pathway	0,016	-0,274	0,075	5	0,045
reactome_Signalling_to_RAS_Main_Pathway	-0,038	0,017	0,033	9	-0,003
reactome_Signalling_to_STAT3_Main_Pathway	0,049	-0,669	0,182	3	0,115
reactome_SIRT1_negatively_regulates_rRNA_Expression_Main_Pathway	0,004	0,007	0,016	35	0,010
reactome_SLBP_Dependent_Processing_of_Replication_Dependent_Histone_Pre_mRNAs_Main_Pathway	-0,057	0,141	-0,074	11	-0,066
reactome_SLBP_independent_Processing_of_Histone_Pre_mRNAs_Main_Pathway	-0,063	0,155	-0,082	10	-0,072
reactome_SMAC_binds_to_IAPs_Main_Pathway	-0,063	0,124	-0,091	5	-0,077
reactome_SMAC_mediated_dissociation_of_IAP_caspase_complexes_Main_Pathway	-0,063	0,124	-0,091	5	-0,077
reactome_SMAD2_3_MH2_Domain_Mutants_in_Cancer_Main_Pathway	0,055	-0,179	0,033	5	0,044
reactome_SMAD2_3_Phosphorylation_Motif_Mutants_in_Cancer_Main_Pathway	0,055	-0,179	0,033	5	0,044
reactome_SMAD2_SMAD3_SMAD4_heterotrimer_regulates_transcription_Main_Pathway	-0,016	-0,240	0,081	16	0,032
reactome_Small_interfering_RNA_siRNA_biogenesis_Main_Pathway	-0,019	0,002	0,043	7	0,012
reactome_snRNP_Assembly_Main_Pathway	-0,047	0,021	0,008	46	-0,019
reactome_Sodium_Calcium_exchangers_Main_Pathway	0	0	0	9	0
reactome_Sodium_coupled_sulphate_di_and_tri_carboxylate_transporters_Main_Pathway	0	0	0	5	0
reactome_Sodium_Proton_exchangers_Main_Pathway	-0,016	0,001	0,004	9	-0,006
reactome_SOS_mediated_signalling_Main_Pathway	-0,005	0,181	-0,027	6	-0,016
reactome_Sperm_Motility_And_Taxes_Main_Pathway	0	0	0	9	0
reactome_Sperm_Oocyte_Membrane_Binding_Main_Pathway	0	0	0	5	0
reactome_Sphingolipid_de_novo_biosynthesis_Main_Pathway	-0,023	-0,059	0,011	28	-0,006
reactome_Spry_regulation_of_FGF_signaling_Main_Pathway	0,014	-0,025	-0,001	7	0,006
reactome_SRP_dependent_cotranslational_protein_targeting_to_membrane_Main_Pathway	-0,021	0,041	0,022	107	0,000
reactome_Stabilization_of_p53_Main_Pathway	-0,101	0,220	-0,048	3	-0,074
reactome_STAT6_mediated_induction_of_chemokines_Main_Pathway	0,130	-0,458	0,154	3	0,142
reactome_STING_mediated_induction_of_host_immune_responses_Main_Pathway	-0,047	0,193	-0,010	5	-0,028
reactome_Striated_Muscle_Contraction_Main_Pathway	0,048	-0,095	0,043	31	0,045
reactome_Sulfide_oxidation_to_sulfate_Main_Pathway	-0,074	-0,257	-0,056	5	-0,065
reactome_Sulfur_amino_acid_metabolism_Main_Pathway	0,023	0,058	0,055	7	0,039
reactome_SUMO_is_conjugated_to_E1_UBA2_SAE1__Main_Pathway	-0,103	0,247	-0,024	5	-0,064
reactome_SUMO_is_proteolytically_processed_Main_Pathway	-0,037	0,035	0,016	6	-0,011
reactome_SUMO_is_transferred_from_E1_to_E2_UBE2I_UBC9__Main_Pathway	-0,100	0,252	-0,028	6	-0,064
reactome_Switching_of_origins_to_a_post_replicative_state_Main_Pathway	-0,077	0,076	-0,011	6	-0,044
reactome_Synthesis_of_12_eicosatetraenoic_acid_derivatives_Main_Pathway	-0,173	0,230	0,002	5	-0,085
reactome_Synthesis_of_15_eicosatetraenoic_acid_derivatives_Main_Pathway	-0,216	0,288	0,003	4	-0,107
reactome_Synthesis_of_16_20_hydroxyeicosatetraenoic_acids_HETE__Main_Pathway	0	0	0	9	0
reactome_Synthesis_of_5_eicosatetraenoic_acids_Main_Pathway	-0,144	0,192	0,002	6	-0,071
reactome_Synthesis_of_bile_acids_and_bile_salts_Main_Pathway	0	0	0	7	0
reactome_Synthesis_of_bile_acids_and_bile_salts_via_24_hydroxycholesterol_Main_Pathway	-0,058	0,074	-0,053	14	-0,055
reactome_Synthesis_of_bile_acids_and_bile_salts_via_27_hydroxycholesterol_Main_Pathway	-0,018	0,031	-0,015	15	-0,017

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Synthesis_of_bile_acids_and_bile_salts_via_7alpha_hydroxycholesterol_Main_Pathway	-0,052	0,033	-0,024	23	-0,038
reactome_Synthesis_of_Dolichyl_phosphate_Main_Pathway	0,011	-0,097	0,015	5	0,013
reactome_Synthesis_of_dolichyl_phosphate_mannose_Main_Pathway	-0,014	-0,130	0,069	3	0,027
reactome_Synthesis_of_epoxy_EET_and_dihydroxyeicosatrienoic_acids_DHET__Main_Pathway	0	0	0	8	0
reactome_Synthesis_of_GDP_mannose_Main_Pathway	0,032	0,073	0,001	5	0,017
reactome_Synthesis_of_glycosylphosphatidylinositol_GPI__Main_Pathway	-0,004	0,008	-0,026	15	-0,015
reactome_Synthesis_of_IP2_IP_and_Ins_in_the_cytosol_Main_Pathway	0,023	-0,116	0,011	9	0,017
reactome_Synthesis_of_IP3_and_IP4_in_the_cytosol_Main_Pathway	-0,028	0,070	-0,019	9	-0,023
reactome_Synthesis_of_IPs_in_the_nucleus_Main_Pathway	0	0	0	4	0
reactome_Synthesis_of_Ketone_Bodies_Main_Pathway	-0,042	0,078	-0,089	4	-0,066
reactome_Synthesis_of_Leukotrienes_LT_and_Eoxins_EX__Main_Pathway	0,036	-0,079	0,029	15	0,032
reactome_Synthesis_of_Lipoxins_LX__Main_Pathway	0,091	-0,205	0,064	6	0,077
reactome_Synthesis_of_PA_Main_Pathway	-0,041	0,008	0,013	20	-0,014
reactome_Synthesis_of_PC_Main_Pathway	-0,063	0,409	-0,017	12	-0,040
reactome_Synthesis_of_PE_Main_Pathway	-0,112	0,070	-0,071	7	-0,092
reactome_Synthesis_of_PG_Main_Pathway	-0,025	-0,076	0,067	8	0,021
reactome_Synthesis_of_PIPs_at_the_early_endosome_membrane_Main_Pathway	-0,016	0,113	-0,021	11	-0,018
reactome_Synthesis_of_PIPs_at_the_ER_membrane_Main_Pathway	-0,069	-0,127	-0,041	3	-0,055
reactome_Synthesis_of_PIPs_at_the_Golgi_membrane_Main_Pathway	-0,010	0,011	-0,014	14	-0,012
reactome_Synthesis_of_PIPs_at_the_late_endosome_membrane_Main_Pathway	-0,025	0,100	-0,005	7	-0,015
reactome_Synthesis_of_PIPs_at_the_plasma_membrane_Main_Pathway	0,024	0,054	-0,013	33	0,006
reactome_Synthesis_of_Prostaglandins_PG_and_Thromboxanes_TX__Main_Pathway	-0,035	-0,138	0,115	14	0,040
reactome_Synthesis_of_pyrophosphates_in_the_cytosol_Main_Pathway	-0,071	0,078	-0,050	7	-0,061
reactome_Synthesis_of_UDP_N_acetyl_glucosamine_Main_Pathway	0,195	-0,224	0,029	5	0,112
reactome_Synthesis_of_very_long_chain_fatty_acyl_CoAs_Main_Pathway	-0,046	-0,052	0,024	16	-0,011
reactome_Synthesis_secretion_and_deacylation_of_Ghrelin_Main_Pathway	-0,047	-0,025	0,009	15	-0,019
reactome_Synthesis_secretion_and_inactivation_of_Glucagon_like_Peptide_1_GLP_1__Main_Pathway	-0,044	-0,023	0,008	16	-0,018
reactome_Synthesis_secretion_and_inactivation_of_Glucose_dependent_Insulinotropic_Polypeptide_GIP__Main_Pathway	-0,070	-0,037	0,013	10	-0,028
reactome_Tachykinin_receptors_bind_tachykinins_Main_Pathway	0	0	0	3	0
reactome_TAK1_activates_NFkB_by_phosphorylation_and_activation_of_IKKs_complex_Main_Pathway	-0,004	-0,088	0,027	16	0,011
reactome_Tat_mediated_elongation_of_the_HIV_1_transcript_Main_Pathway	-0,005	-0,062	-0,004	39	-0,004
reactome_Tat_mediated_HIV_elongation_arrest_and_recovery_Main_Pathway	-0,008	-0,034	0,000	30	-0,004
reactome_TCF_dependent_signaling_in_response_to_WNT_Main_Pathway	-0,000	0,004	0,004	17	0,002
reactome_Telomere_C_strand_Lagging_Strand_Synthesis_Main_Pathway	-0,053	0,211	-0,045	5	-0,049
reactome_Telomere_C_strand_synthesis_initiation_Main_Pathway	-0,088	0,092	-0,000	6	-0,044
reactome_Telomere_Extension_By_Telomerase_Main_Pathway	-0,100	0,095	-0,022	6	-0,061
reactome_temp_Immunoregulatory_interactions_between_a_Lymphoid_and_a_non-Lymphoid_cell	0,003	-0,023	0,015	221	0,009
reactome_temp_Nuclear_Receptor_transcription_pathway	-0,009	-0,020	0,009	51	-0,000
reactome_temp_Post-translational_modification_synthesis_of_GPI-anchored_proteins	-0,007	0,003	0,002	92	-0,002
reactome_Terminal_pathway_of_complement_Main_Pathway	0	0	0	7	0
reactome_Termination_of_O_glycan_biosynthesis_Main_Pathway	-0,004	-0,000	-0,000	24	-0,002
reactome_TGF_beta_receptor_signaling_activates_SMADs_Main_Pathway	-0,329	0,364	-0,425	11	-0,377
reactome_TGF_beta_receptor_signaling_in_EMT_epithelial_to_mesenchymal_transition__Main_Pathway	0,053	-0,001	0,006	16	0,030
reactome_TGFBR1_KD_Mutants_in_Cancer_Main_Pathway	0,153	0,029	0,013	4	0,083
reactome_TGFBR2_Kinase_Domain_Mutants_in_Cancer_Main_Pathway	0,153	0,029	0,013	4	0,083
reactome_The_activation_of_arylsulfatases_Main_Pathway	0,021	0,043	-0,026	13	-0,003
reactome_The_AIM2_inflammasome_Main_Pathway	0	0	0	3	0
reactome_The_canonical_retinoid_cycle_in_rods_twilight_vision__Main_Pathway	-0,058	0,072	-0,025	21	-0,042
reactome_The_fatty_acid_cycling_model_Main_Pathway	0	0	0	3	0
reactome_The_NLRP1_inflammasome_Main_Pathway	-0,120	0,141	-0,092	3	-0,106
reactome_The_NLRP3_inflammasome_Main_Pathway	0,013	-0,011	-0,064	12	-0,026
reactome_The_proton_buffering_model_Main_Pathway	0	0	0	3	0

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_The_retinoid_cycle_in_cones_daylight_vision__Main_Pathway	-0,013	0,036	0,019	6	0,003
reactome_Thrombin_signalling_through_proteinase_activated_receptors_PARs__Main_Pathway	-0,029	-0,089	0,027	29	-0,001
reactome_Thromboxane_signalling_through_TP_receptor_Main_Pathway	-0,033	-0,052	0,019	23	-0,007
reactome_Thyroxine_biosynthesis_Main_Pathway	0	0	0	5	0
reactome_Tie2_Signaling_Main_Pathway	-0,016	0,110	-0,011	17	-0,014
reactome_Toll_Like_Receptor_4_TLR4_Cascade_Main_Pathway	-0,024	0,032	0,004	10	-0,010
reactome_Toll_Like_Receptor_9_TLR9_Cascade_Main_Pathway	-0,040	0,059	-0,019	5	-0,030
reactome_Toll_Like_Receptor_TLR6_TLR2_Cascade_Main_Pathway	0	0	0	4	0
reactome_Toxicity_of_botulinum_toxin_type_A_BoNT_A__Main_Pathway	0	0	0	4	0
reactome_Toxicity_of_botulinum_toxin_type_B_BoNT_B__Main_Pathway	-0,014	0,192	-0,108	3	-0,061
reactome_Toxicity_of_botulinum_toxin_type_C_BoNT_C__Main_Pathway	0	0	0	3	0
reactome_Toxicity_of_botulinum_toxin_type_D_BoNT_D__Main_Pathway	0	0	0	5	0
reactome_Toxicity_of_botulinum_toxin_type_E_BoNT_E__Main_Pathway	0	0	0	3	0
reactome_Toxicity_of_botulinum_toxin_type_F_BoNT_F__Main_Pathway	0	0	0	5	0
reactome_Toxicity_of_botulinum_toxin_type_G_BoNT_G__Main_Pathway	-0,014	0,192	-0,108	3	-0,061
reactome_TRAF3_dependent_IRF_activation_Main_Pathway	0,064	-0,112	0,055	10	0,060
reactome_TRAF6_Mediated_Induction_of_proinflammatory_cytokines_Main_Pathway	0,085	0,078	-0,014	5	0,035
reactome_TRAF6_mediated_induction_of_TAK1_complex_Main_Pathway	0,062	0,077	-0,000	9	0,031
reactome_TRAF6_mediated_IRF7_activation_in_TLR7_8_or_9_signaling_Main_Pathway	-0,027	0,140	-0,059	8	-0,043
reactome_TRAF6_mediated_NF_kB_activation_Main_Pathway	-0,005	-0,050	0,025	20	0,010
reactome_Trafficking_and_processing_of_endosomal_TLR_Main_Pathway	-0,084	0,055	-0,010	13	-0,047
reactome_Trafficking_of_AMPA_receptors_Main_Pathway	-0,042	0,042	0,016	14	-0,013
reactome_Trafficking_of_GluR2_containing_AMPA_receptors_Main_Pathway	-0,019	0,007	0,032	5	0,006
reactome_TRAIL_signaling_Main_Pathway	-0,704	0,783	-0,004	6	-0,354
reactome_Transcription_coupled_NER_TC_NER__Main_Pathway	-0,036	0,033	-0,011	12	-0,023
reactome_Transcription_of_the_HIV_genome_Main_Pathway	-0,041	0,016	-0,040	43	-0,040
reactome_Transcriptional_activation_of_mitochondrial_biogenesis_Main_Pathway	-0,040	0,027	-0,009	36	-0,025
reactome_Transcriptional_regulation_of_pluripotent_stem_cells_Main_Pathway	-0,009	0,012	0,011	15	0,001
reactome_Transcriptional_regulation_of_white_adipocyte_differentiation_Main_Pathway	-0,059	0,009	-0,019	62	-0,039
reactome_Transferrin_endocytosis_and_recycling_Main_Pathway	-0,062	0,076	-0,021	29	-0,041
reactome_Translation_initiation_complex_formation_Main_Pathway	-0,023	0,105	0,006	55	-0,009
reactome_Translocation_of_GLUT4_to_the_plasma_membrane_Main_Pathway	-0,037	-0,038	0,014	53	-0,012
reactome_Translocation_of_ZAP_70_to_Immunological_synapse_Main_Pathway	-0,049	0,337	-0,292	18	-0,170
reactome_Transport_and_synthesis_of_PAPS_Main_Pathway	-0,034	0,047	-0,001	6	-0,017
reactome_Transport_of_fatty_acids_Main_Pathway	-0,150	-0,013	-0,023	3	-0,086
reactome_Transport_of_glucose_and_other_sugars_bile_salts_and_organic_acids_metal_ions_and_amine_compounds_Main_Pathway	-0,038	0,450	-0,025	11	-0,032
reactome_Transport_of_inorganic_cations_anions_and_amino_acids_oligopeptides_Main_Pathway	0	0	0	6	0
reactome_Transport_of_Mature_mRNA_derived_from_an_Intron_Containing_Transcript_Main_Pathway	-0,077	0,062	-0,013	47	-0,045
reactome_Transport_of_Mature_mRNA_Derived_from_an_Intronless_Transcript_Main_Pathway	-0,065	0,003	0,010	32	-0,027
reactome_Transport_of_nucleosides_and_free_purine_and_pyrimidine_bases_across_the_plasma_membrane_Main_Pathway	0,002	-0,073	0,056	7	0,029
reactome_Transport_of_nucleotide_sugars_Main_Pathway	-0,153	0,030	-0,048	9	-0,101
reactome_Transport_of_organic_anions_Main_Pathway	-0,016	-0,020	-0,026	10	-0,021
reactome_Transport_of_Ribonucleoproteins_into_the_Host_Nucleus_Main_Pathway	-0,070	-0,020	0,014	26	-0,028
reactome_Transport_of_the_SLBP_Dependant_Mature_mRNA_Main_Pathway	-0,077	0,002	0,002	30	-0,037
reactome_Transport_of_the_SLBP_independent_Mature_mRNA_Main_Pathway	-0,079	0,002	0,002	29	-0,039
reactome_Transport_of_vitamins_nucleosides_and_related_molecules_Main_Pathway	0,047	-0,100	0,007	3	0,027
reactome_TRIF_mediated_programmed_cell_death_Main_Pathway	0,098	-0,007	0,083	4	0,090
reactome_Triglyceride_Biosynthesis_Main_Pathway	-0,046	0,091	0,002	20	-0,022
reactome_Tristetraprolin_TTP_destabilizes_mRNA_Main_Pathway	0,003	0,115	-0,041	17	-0,019
reactome_TRP_channels_Main_Pathway	-0,011	-0,021	0,021	25	0,005

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
reactome_Tryptophan_catabolism_Main_Pathway	-0,005	0,014	-0,008	11	-0,007
reactome_TWIK_related_potassium_channel_TREK__Main_Pathway	0	0	0	3	0
reactome_Type_I_hemidesmosome_assembly_Main_Pathway	-0,040	-0,263	0,033	9	-0,003
reactome_Type_II_Na_Pi_cotransporters_Main_Pathway	0	0	0	3	0
reactome_U12_Dependent_Splicing_Main_Pathway	-0,072	0,170	-0,062	42	-0,067
reactome_Ubiquinol_biosynthesis_Main_Pathway	-0,035	0,061	-0,009	7	-0,022
reactome_Ubiquitin_dependent_degradation_of_Cyclin_D1_Main_Pathway	-0,008	0,031	-0,009	50	-0,008
reactome_Ubiquitin_Mediated_Degradation_of_Phosphorylated_Cdc25A_Main_Pathway	-0,009	0,035	-0,007	51	-0,008
reactome_Unblocking_of_NMDA_receptor_glutamate_binding_and_activation_Main_Pathway	0,015	-0,045	0,022	13	0,018
reactome_Unwinding_of_DNA_Main_Pathway	0,002	0,009	0,015	11	0,008
reactome_Uptake_and_function_of_anthrax_toxins_Main_Pathway	0,084	-0,182	0,075	7	0,080
reactome_Urea_cycle_Main_Pathway	-0,040	0,134	-0,070	9	-0,055
reactome_Vasopressin_like_receptors_Main_Pathway	0	0	0	4	0
reactome_Vasopressin_regulates_renal_water_homeostasis_via_Aquaporins_Main_Pathway	-0,029	-0,009	0,005	43	-0,012
reactome_VEGF_binds_to_VEGFR_leading_to_receptor_dimerization_Main_Pathway	0	0	0	3	0
reactome_VEGF_ligand_receptor_interactions_Main_Pathway	0	0	0	5	0
reactome_VEGFA_VEGFR2_Pathway_Main_Pathway	0,008	-0,018	0,016	56	0,012
reactome_VEGFR2_mediated_cell_proliferation_Main_Pathway	-0,039	0,103	-0,012	16	-0,026
reactome_VEGFR2_mediated_vascular_permeability_Main_Pathway	-0,019	-0,035	0,022	25	0,001
reactome_Vif_mediated_degradation_of_APOBEC3G_Main_Pathway	-0,002	0,028	-0,005	52	-0,003
reactome_Viral_Messenger_RNA_Synthesis_Main_Pathway	-0,045	0,063	-0,017	14	-0,031
reactome_Viral_mRNA_Translation_Main_Pathway	-0,014	0,082	0,026	84	0,006
reactome_Vitamin_B1_thiamin_metabolism_Main_Pathway	0	0	0	4	0
reactome_Vitamin_B2_riboflavin_metabolism_Main_Pathway	0,056	-0,111	0,045	5	0,051
reactome_Vitamin_B5_pantothenate_metabolism_Main_Pathway	0,032	0,150	0,017	4	0,025
reactome_Vitamin_C_ascorbate_metabolism_Main_Pathway	-0,110	-0,011	0,008	6	-0,051
reactome_Vitamin_D_calciferol_metabolism_Main_Pathway	-0,052	0,051	-0,056	7	-0,054
reactome_Vitamins_B6_activation_to_pyridoxal_phosphate_Main_Pathway	-0,025	0,114	0,004	3	-0,010
reactome_Vitamins_Main_Pathway	0	0	0	6	0
reactome_Voltage_gated_Potassium_channels_Main_Pathway	-0,001	0,021	-0,004	43	-0,002
reactome_Vpr_mediated_induction_of_apoptosis_by_mitochondrial_outer_membrane_permeabilization_Main_Pathway	-0,185	0,295	0,013	3	-0,086
reactome_Vpr_mediated_nuclear_import_of_PICs_Main_Pathway	-0,080	0,014	-0,009	28	-0,044
reactome_Vpu_mediated_degradation_of_CD4_Main_Pathway	-0,007	0,030	-0,005	51	-0,006
reactome_WNT_ligand_biogenesis_and_trafficking_Main_Pathway	-0,009	0,008	-0,012	26	-0,011
reactome_WNT_mediated_activation_of_DVL_Main_Pathway	-0,000	0,011	0,010	6	0,005
reactome_WNT5A_dependent_internalization_of_FZD2_FZD5_and_ROR2_Main_Pathway	-0,041	-0,057	0,001	13	-0,020
reactome_WNT5A_dependent_internalization_of_FZD4_Main_Pathway	-0,025	-0,084	0,018	12	-0,004
reactome_XAV939_inhibits_tankyrase_stabilizing_AXIN_Main_Pathway	0,017	0,064	-0,078	10	-0,030
reactome_XBP1_S_activates_chaperone_genes_Main_Pathway	0	0	0	44	0
reactome_Xenobiotics_Main_Pathway	-0,014	0,017	-0,005	19	-0,010
reactome_Zinc_efflux_and_compartmentalization_by_the_SLC30_family_Main_Pathway	0,035	-0,063	-0,019	7	0,008
reactome_Zinc_influx_into_cells_by_the_SLC39_gene_family_Main_Pathway	-0,455	0,217	0,099	10	-0,178
Regulation_of_Angiogenesis_by_Interleukin-8	0,012	-0,369	0,132	6	0,072
Regulation_of_Cell_Migration_and_Proliferation_by_Somatostatin_Receptor	-0,008	-0,015	0,017	38	0,004
Regulation_of_Cell_Migration_by_Platelet-derived_Growth_Factors	-0,011	0,034	0,010	22	-0,000
Regulation_of_Cytoskeleton_Remodeling_by_Activin_A	0,059	-0,149	0,046	20	0,052
Regulation_of_Cytoskeleton_Remodeling_by_Protein_Kinase_A	-0,019	-0,029	0,016	75	-0,002
Regulation_of_Cytoskeleton_Remodeling_by_TGF_and_WNT	0,023	-0,049	0,024	118	0,023
Regulation_of_Epithelial-mesenchymal_transition	0,014	0,020	0,002	3	0,008
Regulation_of_Repulsive_Axonal_Pathfinding	0,013	-0,049	0,016	83	0,015
resolvin_D_biosynthesis	0	0	0	2	0
retinoate_biosynthesis_I	0,029	-0,215	0,086	8	0,058
retinoate_biosynthesis_II	-0,004	-0,050	0,031	4	0,013
retinol_biosynthesis	-0,021	-0,039	0,011	17	-0,005

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
RhoA_Signaling	-0,038	-0,016	-0,008	29	-0,023
RhoB_Signaling	0,027	0,098	0,035	5	0,031
Role_of_Cholinergic_Receptors_in_Migration_of_Kertinocytes	0	0	0	7	0
Role_of_KITLG_in_Haematopoiesis	-0,068	0,062	0,010	66	-0,029
Role_of_NTN1_in_Axon_Pathfinding	-0,022	-0,007	0,002	51	-0,010
Role_of_Rho_GTPases_in_of_Actin_Cytoskeleton_Organization	0,051	-0,106	0,013	52	0,032
Role_of_Small_GTPases_in_G1-S_Transition	0,045	-0,061	0,021	51	0,033
S-adenosyl-L-methionine_biosynthesis	-0,065	0,159	-0,018	3	-0,041
selenocysteine_biosynthesis	0,016	0,027	-0,018	5	-0,001
serine_and_glycine_biosynthesis	-0,028	0,164	-0,060	7	-0,044
serine_biosynthesis_phosphorylated_route	-0,035	0,205	-0,075	4	-0,055
serotonin_and_melatonin_biosynthesis	0	0	0	5	0
serotonin_degradation	-0,136	0,145	-0,056	9	-0,096
Slit-Robo_Pathway	0,037	-0,072	0,021	61	0,029
SMAD_Signaling_Network_Pathway	0,004	-0,012	0,006	126	0,005
Smooth_Muscle_Tone_Regulation_by_G-protein_Coupled_Receptors	-0,010	-0,024	0,008	49	-0,001
sorbitol_degradation_I	0,026	0,365	-0,062	1	-0,018
spermidine_biosynthesis	0	0	0	2	0
spermine_and_spermidine_degradation_I	-0,989	0,845	-0,065	5	-0,527
spermine_biosynthesis	0	0	0	2	0
sphingomyelin_metabolismceramide_salvage	0,009	0,000	0,018	8	0,014
sphingosine_and_sphingosine-1-phosphate_metabolism	0,037	-0,078	0,007	10	0,022
SPP1_Pathway_in_Osteoclasts	0,020	-0,094	0,038	34	0,029
S-reticuline_biosynthesis	0	0	0	1	0
STAT3_Pathway	-0,012	-0,005	0,006	233	-0,003
STAT3_Pathway_Anti-Apoptosis	0,023	-0,212	0,056	3	0,040
STAT3_Pathway_G1_to_S_Cell_Cycle_Progression	0,023	-0,212	0,056	3	0,040
STAT3_Pathway_Growth_Arrest_and_Differentiation	-0,038	0,009	0,005	105	-0,017
STATs_Pathway_Regulation_by_GH	0,029	-0,076	0,035	29	0,032
stearate_biosynthesis	-0,048	-0,025	0,040	12	-0,004
sucrose_degradation	-0,004	-0,215	-0,031	8	-0,017
sulfate_activation_for_sulfonation	0,064	0,032	0,006	2	0,035
sulfite_oxidation	-0,006	-1,118	-0,105	1	-0,055
superoxide_radicals_degradation	0,070	-0,220	0,048	4	0,059
superpathway_of_cholesterol_biosynthesis	0,024	-0,166	0,031	25	0,027
superpathway_of_choline_degradation_to_L-serine	-0,064	0,106	-0,004	7	-0,034
superpathway_of_D-imyoi-inositol_145-trisphosphate_metabolism	-0,021	0,101	-0,025	20	-0,023
superpathway_of_geranylgeranyldiphosphate_biosynthesis_I_via_mevalonate	0,088	-0,076	0,013	12	0,051
superpathway_of_inositol_phosphate_compounds	-0,051	0,098	-0,008	69	-0,029
superpathway_of_melatonin_degradation	-0,087	0,191	-0,034	12	-0,060
superpathway_of_methionine_degradation	-0,057	-0,025	-0,046	17	-0,051
superpathway_of_purine_nucleotide_salvage	-0,060	0,081	-0,022	44	-0,041
superpathway_of_pyrimidine_deoxyribonucleoside_salvage	0,006	-0,041	-0,011	16	-0,003
superpathway_of_pyrimidine_deoxyribonucleotides_ide_novoi_biosynthesis	0,011	0,052	-0,007	21	0,002
superpathway_of_pyrimidine_ribonucleotides_ide_novoi_biosynthesis	-0,006	0,049	-0,029	14	-0,018
superpathway_of_steroid_hormone_biosynthesis	-0,039	0,064	-0,018	16	-0,029
superpathway_of_tryptophan_utilization	-0,064	0,041	-0,019	37	-0,042
Target_drugs_pathway	0,004	-0,008	0,007	190	0,005
taurine_biosynthesis	-0,011	0,096	0,023	3	0,006
TCA_cycle	-0,131	0,061	-0,034	18	-0,083
terminal_iOi-glycans_residues_modification	-0,009	0,030	-0,018	13	-0,014
tetrahydrobiopterin_ide_novoi_biosynthesis	0	0	0	3	0
tetrahydrofolate_salvage_from_510-methenyltetrahydrofolate	0,072	-0,059	0,030	2	0,051
tetrapyrrole_biosynthesis	0,027	0,033	-0,037	5	-0,005
TGF-Beta_Pathway	-0,018	0,002	0,010	218	-0,004
TGF-Beta_Pathway_Epithelial_Mesenchymal_Transdifferentiation	0,017	0,007	0,007	14	0,012
TGF-Beta_Pathway_Post_Transciptional_G1_Arrest	0,030	-0,041	-0,007	16	0,012
TGF-Beta_Pathway_Transciption_Arrested_Growth_Apoptosis	0,032	-0,041	0,039	30	0,036

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
TGF-Beta_Pathway_Transciption_Cell_Growth_and_Mobility_and_Angiogenesis	0,032	-0,041	0,039	30	0,036
TGF-beta_Signaling_in_Epithelial-mesenchymal_transition	0,029	-0,021	0,028	52	0,029
the_visual_cycle_I_vertebrates	-0,033	-0,027	0,007	16	-0,013
thiamin_salvage_III	0	0	0	1	0
thio-molybdenum_cofactor_biosynthesis	0,983	0,985	-0,655	1	0,164
thioredoxin_pathway	0,027	-0,047	-0,022	5	0,002
thiosulfate_disproportionation_III_rhodanese	-0,166	0,282	-0,079	1	-0,123
threonine_degradation	-0,019	-0,185	-0,037	6	-0,028
thymine_degradation	0	0	0	3	0
thyroid_hormone_biosynthesis	0	0	0	2	0
thyroid_hormone_metabolism_I_via_deiodination	-0,056	0,016	0,027	3	-0,014
thyroid_hormone_metabolism_II_via_conjugation_andor_degradation	-0,104	0,174	-0,039	6	-0,071
thyronamine_and_iodothyronamine_metabolism	-0,056	0,016	0,027	3	-0,014
Tight_Junctions	-0,015	-0,067	0,026	28	0,006
TNF_Signaling_Pathway	0,013	-0,042	0,037	64	0,025
TNF_Signaling_Pathway_Apoptosis	-0,020	0,091	-0,024	14	-0,022
TNF_Signaling_Pathway_Gene_Expression_and_Cell_Survival_via_FOS_NFKB2_JUN_ELK1_ATF6	0,034	-0,108	0,062	37	0,048
TRAF_Pathway	0,013	-0,040	0,033	100	0,023
TRAF_Pathway_Apoptosis	0,018	0,018	0,023	13	0,021
TRAF_Pathway_Cell_Survival	0,037	-0,020	0,010	14	0,024
TRAF_Pathway_Gene_Expression_via_FOS_JUN	0,037	-0,066	0,086	11	0,061
Transport_between_Cytoplasm_and_Mitochondria	-0,046	-0,032	0,054	5	0,004
trehalose_degradation	-0,046	-0,038	0,045	3	-0,001
TRH_Influence_on_Cytoskeleton	-0,050	0,029	0,006	37	-0,022
TRH_Pathway	-0,023	-0,024	0,021	77	-0,001
triacylglycerol_biosynthesis	-0,060	0,033	0,004	24	-0,028
triacylglycerol_degradation	-0,017	-0,006	0,021	14	0,002
tRNA_charging	-0,043	0,041	-0,013	39	-0,028
tRNA_splicing	-0,119	0,300	0,003	5	-0,058
tryptophan_degradation	-0,012	-0,058	0,001	9	-0,005
tryptophan_degradation_to_2-amino-3-carboxymuconate_semialdehyde	0	0	0	7	0
tryptophan_degradation_X_mammalian_via_tryptamine	-0,055	-0,033	-0,020	4	-0,038
TSPANs_Influence_on_Integrin-based_Cell_Migration_and_Adhesion	0,031	-0,149	0,039	55	0,035
Tumour_Infiltration_Pathway	-0,014	-0,023	0,021	200	0,004
TYROBP_Signaling_in_Natural_Killer_Cells	-0,010	0,012	0,007	63	-0,001
tyrosine_degradation	-0,021	0,027	-0,023	5	-0,022
ubiquinol-10_biosynthesis	-0,035	0,061	-0,009	7	-0,022
Ubiquitin-Proteasome_Dependent_Proteolysis_Pathway	-0,003	-0,005	0,001	131	-0,001
UDP-D-xylose_and_UDP-D-glucuronate_biosynthesis	0,087	0,342	-0,129	2	-0,021
UDP-iNi-acetyl-D-galactosamine_biosynthesis_I	0,046	-0,247	0,085	1	0,065
UDP-iNi-acetyl-D-galactosamine_biosynthesis_II	0,115	-0,212	0,076	8	0,096
UDP-iNi-acetyl-D-glucosamine_biosynthesis_II	0,232	-0,294	0,070	5	0,151
UMP_biosynthesis	-0,062	0,434	-0,076	2	-0,069
uracil_degradation	0	0	0	3	0
urate_biosynthesisinosine_5-phosphate_degradation	0,017	0,008	0,001	6	0,009
urea_cycle	0,009	0,028	-0,094	5	-0,042
UTP_and_CTP_dephosphorylation_I	0,076	0,015	0,035	3	0,056
UTP_and_CTP_dephosphorylation_II	-0,047	0,124	0,001	4	-0,023
UTP_and_CTP_ide_novoi_biosynthesis	0,003	-0,015	-0,022	12	-0,009
valine_degradation	-0,096	-0,013	-0,040	13	-0,068
VEGF_Pathway	0,013	-0,037	0,016	77	0,014
VEGF_Pathway_Actin_Reorganization	0,059	-0,102	0,034	8	0,046
VEGF_Pathway_Cell_Migration	0,059	-0,102	0,034	8	0,046
VEGF_Pathway_Cell_Survival	0,017	0,046	-0,008	15	0,004
VEGF_Pathway_Focal_Adhesion_Turnover	0,053	-0,154	0,019	5	0,036
VEGF_Pathway_Gene_Expression_and_Cell_Proliferation_via_MAPK7	0,049	-0,105	0,033	12	0,041
VEGF_Pathway_Nitric_Oxide_Production	-0,002	-0,080	0,004	3	0,001
VEGF_Pathway_Prostaglandin_Production	0,037	-0,092	0,028	20	0,033

Pathway	Tumour_ MDA. MB.231. Invasive	Tumour_ AU565. Invasive	Tumour_ T47D. Invasive	Number of genes in PW	Mean (MDA. MB.231, T47D)
VEGFR2_Signaling	-0,004	0,000	0,020	94	0,008
WNT_Pathway	-0,004	-0,022	0,014	253	0,005
WNT_Pathway_Cell_Fate_Proliferation_Differentiation_Adhesion_and_Survival	-0,009	0,013	0,003	87	-0,003
WNT_Pathway_Cell_Survival	0,043	-0,080	0,036	19	0,040
WNT_Pathway_Cytoskeletal_Rearrangement	-0,071	0,122	-0,035	4	-0,053
WNT_Pathway_Gene_Expression_via_CREB3	-0,013	-0,028	0,023	51	0,005
WNT_Pathway_NFAT_Pathway	-0,006	0,021	0,039	21	0,016
WNT_Pathway_PKC_Pathway	-0,007	-0,048	0,020	54	0,006
wybutosine_biosynthesis	-0,132	1,761	-0,125	3	-0,129
zymosterol_biosynthesis	-0,032	-0,340	0,106	6	0,037

SUPPLEMENTARY TABLE 2.

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_CONTRACTILE_FIBER	GO_CONTRACTILE_FIBER	Details ...	23	0,611	2,104	0	0,284	0,241	104	tags=57%, list=18%, signal=66%
GO_DEVELOPMENTAL_PROCESS_INVOLVED_IN_REPRODUCTION	GO_DEVELOPMENTAL_PROCESS_INVOLVED_IN_REPRODUCTION	Details ...	19	0,629	2,053	0,004	0,273	0,419	90	tags=42%, list=16%, signal=48%
GO_CELLULAR_CHEMICAL_HOMEOSTASIS	GO_CELLULAR_CHEMICAL_HOMEOSTASIS	Details ...	21	0,553	1,885	0,009	1	0,951	48	tags=33%, list=8%, signal=35%
GO_GAMETE_GENERATION	GO_GAMETE_GENERATION	Details ...	16	0,604	1,859	0,008	0,932	0,976	18	tags=13%, list=3%, signal=13%
GO_SEXUAL_REPRODUCTION	GO_SEXUAL_REPRODUCTION	Details ...	17	0,581	1,844	0,020	0,837	0,987	18	tags=12%, list=3%, signal=12%
GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION	GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION	Details ...	54	0,465	1,820	0,003	0,836	0,996	142	tags=41%, list=25%, signal=49%
GO_REGULATION_OF_GROWTH	GO_REGULATION_OF_GROWTH	Details ...	24	0,527	1,818	0,02	0,725	0,996	59	tags=33%, list=10%, signal=36%
GO_CELL_JUNCTION	GO_CELL_JUNCTION	Details ...	78	0,442	1,811	0,002	0,666	0,997	203	tags=58%, list=36%, signal=77%
GO_CELL_SUBSTRATE_JUNCTION	GO_CELL_SUBSTRATE_JUNCTION	Details ...	55	0,459	1,811	0,005	0,593	0,997	196	tags=60%, list=34%, signal=83%
GO_RIBONUCLEOPROTEIN_COMPLEX	GO_RIBONUCLEOPROTEIN_COMPLEX	Details ...	15	0,584	1,803	0,028	0,567	0,998	0	tags=7%, list=0%, signal=6%
GO_CELLULAR_HOMEOSTASIS	GO_CELLULAR_HOMEOSTASIS	Details ...	28	0,506	1,796	0,022	0,539	0,999	21	tags=25%, list=4%, signal=25%
GO_MULTI_ORGANISM_REPRODUCTIVE_PROCESS	GO_MULTI_ORGANISM_REPRODUCTIVE_PROCESS	Details ...	20	0,540	1,786	0,019	0,531	0,999	36	tags=15%, list=6%, signal=15%
GO_MUSCLE_ORGAN_DEVELOPMENT	GO_MUSCLE_ORGAN_DEVELOPMENT	Details ...	16	0,570	1,770	0,021	0,546	0,999	155	tags=63%, list=27%, signal=83%
GO_MULTICELLULAR_ORGANISM_REPRODUCTION	GO_MULTICELLULAR_ORGANISM_REPRODUCTION	Details ...	20	0,538	1,767	0,024	0,521	1	36	tags=15%, list=6%, signal=15%
GO_CELL_DEVELOPMENT	GO_CELL_DEVELOPMENT	Details ...	64	0,441	1,764	0,002	0,494	1	75	tags=23%, list=13%, signal=24%
GO_ORGAN_MORPHOGENESIS	GO_ORGAN_MORPHOGENESIS	Details ...	32	0,485	1,755	0,008	0,490	1	166	tags=56%, list=29%, signal=75%
GO_ION_HOMEOSTASIS	GO_ION_HOMEOSTASIS	Details ...	20	0,532	1,745	0,021	0,494	1	48	tags=30%, list=8%, signal=32%
GO_ANCHORING_JUNCTION	GO_ANCHORING_JUNCTION	Details ...	58	0,446	1,738	0	0,487	1	196	tags=59%, list=34%, signal=80%
GO_MUSCLE_STRUCTURE_DEVELOPMENT	GO_MUSCLE_STRUCTURE_DEVELOPMENT	Details ...	34	0,480	1,727	0,015	0,497	1	160	tags=53%, list=28%, signal=69%
GO_CELL_PROJECTION_PART	GO_CELL_PROJECTION_PART	Details ...	47	0,433	1,700	0,013	0,553	1	199	tags=57%, list=35%, signal=81%
GO_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	GO_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS		15	0,553	1,689	0,032	0,563	1	0	tags=7%, list=0%, signal=6%
GO_STRUCTURAL_MOLECULE_ACTIVITY	GO_STRUCTURAL_MOLECULE_ACTIVITY		39	0,453	1,689	0,018	0,537	1	94	tags=38%, list=17%, signal=43%
GO_CYTOSKELETAL_PROTEIN_BINDING	GO_CYTOSKELETAL_PROTEIN_BINDING		73	0,418	1,687	0,006	0,518	1	196	tags=55%, list=34%, signal=73%
GO_REPRODUCTION	GO_REPRODUCTION		38	0,450	1,668	0,024	0,554	1	90	tags=26%, list=16%, signal=29%
GO_CHEMICAL_HOMEOSTASIS	GO_CHEMICAL_HOMEOSTASIS		29	0,473	1,663	0,033	0,548	1	48	tags=28%, list=8%, signal=29%
GO_CYTOSKELETON	GO_CYTOSKELETON		128	0,396	1,661	0	0,533	1	203	tags=52%, list=36%, signal=63%
GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION	GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION		17	0,526	1,650	0,055	0,544	1	0	tags=6%, list=0%, signal=6%
GO_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	GO_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING		15	0,527	1,635	0,043	0,569	1	206	tags=73%, list=36%, signal=112%
GO_HOMEOSTATIC_PROCESS	GO_HOMEOSTATIC_PROCESS		50	0,404	1,577	0,038	0,738	1	160	tags=44%, list=28%, signal=56%
GO_ACTIN_BINDING	GO_ACTIN_BINDING		50	0,410	1,577	0,033	0,716	1	196	tags=56%, list=34%, signal=78%
GO_KINASE_BINDING	GO_KINASE_BINDING		32	0,426	1,536	0,060	0,848	1	193	tags=50%, list=34%, signal=71%
GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION		21	0,463	1,534	0,074	0,827	1	59	tags=29%, list=10%, signal=31%
GO_TRANSCRIPTION_FACTOR_ACTIVITY_PROTEIN_BINDING	GO_TRANSCRIPTION_FACTOR_ACTIVITY_PROTEIN_BINDING		22	0,455	1,533	0,065	0,806	1	120	tags=41%, list=21%, signal=50%
GO_SINGLE_ORGANISM_CELL_ADHESION	GO_SINGLE_ORGANISM_CELL_ADHESION		37	0,410	1,533	0,035	0,784	1	266	tags=76%, list=47%, signal=133%
GO_ACTIN_CYTOSKELETON	GO_ACTIN_CYTOSKELETON		55	0,394	1,530	0,034	0,773	1	135	tags=40%, list=24%, signal=47%
GO_TISSUE_DEVELOPMENT	GO_TISSUE_DEVELOPMENT		71	0,379	1,527	0,027	0,762	1	193	tags=49%, list=34%, signal=65%
GO_RESPONSE_TO_GROWTH_FACTOR	GO_RESPONSE_TO_GROWTH_FACTOR		19	0,469	1,513	0,078	0,791	1	70	tags=32%, list=12%, signal=35%
GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY		16	0,486	1,510	0,087	0,782	1	84	tags=38%, list=15%, signal=43%
GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT		19	0,457	1,508	0,079	0,767	1	284	tags=89%, list=50%, signal=173%
GO_CELL_CELL_SIGNALING	GO_CELL_CELL_SIGNALING		17	0,471	1,503	0,071	0,767	1	108	tags=47%, list=19%, signal=56%
GO_MUSCLE_CONTRACTION	GO_MUSCLE_CONTRACTION		16	0,483	1,503	0,085	0,751	1	142	tags=56%, list=25%, signal=73%
GO_EPITHELIUM_DEVELOPMENT	GO_EPITHELIUM_DEVELOPMENT		44	0,387	1,498	0,057	0,749	1	193	tags=50%, list=34%, signal=70%
GO_NEURON_PROJECTION	GO_NEURON_PROJECTION		39	0,409	1,497	0,056	0,733	1	99	tags=31%, list=17%, signal=35%
REACTOME_CELL_CELL_COMMUNICATION	REACTOME_CELL_CELL_COMMUNICATION		16	0,485	1,496	0,082	0,722	1	260	tags=88%, list=46%, signal=157%
GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION		18	0,468	1,495	0,094	0,708	1	112	tags=44%, list=20%, signal=54%
GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS		51	0,386	1,489	0,052	0,712	1	132	tags=37%, list=23%, signal=44%

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_REGULATORY_REGION_NUCLEIC_ACID_BINDING	GO_REGULATORY_REGION_NUCLEIC_ACID_BINDING		18	0,463	1,486	0,092	0,706	1	68	tags=33%, list=12%, signal=37%
GO_NEURON_PART	GO_NEURON_PART		48	0,382	1,486	0,062	0,692	1	108	tags=31%, list=19%, signal=35%
GO_CILIUM	GO_CILIUM		16	0,477	1,485	0,077	0,681	1	170	tags=63%, list=30%, signal=87%
GO_CELL_PROJECTION	GO_CELL_PROJECTION		89	0,361	1,479	0,025	0,687	1	203	tags=49%, list=36%, signal=65%
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION		18	0,450	1,478	0,083	0,676	1	131	tags=44%, list=23%, signal=56%
GO_NEGATIVE_REGULATION_OF_NITROGEN_COMPOUND_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_NITROGEN_COMPOUND_METABOLIC_PROCESS		56	0,380	1,475	0,060	0,671	1	142	tags=39%, list=25%, signal=47%
GO_EPITHELIAL_CELL_DIFFERENTIATION	GO_EPITHELIAL_CELL_DIFFERENTIATION		21	0,445	1,475	0,104	0,658	1	171	tags=52%, list=30%, signal=72%
GO_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_MORPHOGENESIS	GO_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_MORPHOGENESIS		47	0,390	1,473	0,062	0,651	1	89	tags=30%, list=16%, signal=32%
GO_CATION_TRANSPORT	GO_CATION_TRANSPORT		19	0,443	1,473	0,102	0,641	1	48	tags=26%, list=8%, signal=28%
GO_SUPRAMOLECULAR_FIBER	GO_SUPRAMOLECULAR_FIBER		38	0,399	1,472	0,096	0,630	1	152	tags=42%, list=27%, signal=54%
GO_ION_TRANSPORT	GO_ION_TRANSPORT		28	0,414	1,466	0,093	0,639	1	108	tags=36%, list=19%, signal=42%
GO_SIGNAL_TRANSDUCER_ACTIVITY	GO_SIGNAL_TRANSDUCER_ACTIVITY		27	0,413	1,466	0,094	0,628	1	188	tags=56%, list=33%, signal=79%
GO_POSITIVE_REGULATION_OF_CELL_PROLIFERATION	GO_POSITIVE_REGULATION_OF_CELL_PROLIFERATION		20	0,446	1,465	0,111	0,621	1	201	tags=65%, list=35%, signal=97%
GO_HEART_DEVELOPMENT	GO_HEART_DEVELOPMENT		23	0,433	1,461	0,107	0,620	1	215	tags=65%, list=38%, signal=101%
GO_RESPONSE_TO_PEPTIDE	GO_RESPONSE_TO_PEPTIDE		15	0,471	1,460	0,092	0,612	1	114	tags=47%, list=20%, signal=57%
GO_ACTIN_FILAMENT_BASED_PROCESS	GO_ACTIN_FILAMENT_BASED_PROCESS		51	0,374	1,460	0,066	0,603	1	199	tags=51%, list=35%, signal=71%
GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND		22	0,429	1,459	0,101	0,597	1	137	tags=45%, list=24%, signal=58%
GO_CIRCULATORY_SYSTEM_DEVELOPMENT	GO_CIRCULATORY_SYSTEM_DEVELOPMENT		38	0,395	1,458	0,084	0,589	1	215	tags=61%, list=38%, signal=91%
GO_CYTOSKELETAL_PART	GO_CYTOSKELETAL_PART		92	0,358	1,457	0,03	0,583	1	203	tags=50%, list=36%, signal=65%
GO_NEGATIVE_REGULATION_OF_CELL_PROLIFERATION	GO_NEGATIVE_REGULATION_OF_CELL_PROLIFERATION		19	0,445	1,456	0,105	0,577	1	131	tags=42%, list=23%, signal=53%
GO_EXTRACELLULAR_SPACE	GO_EXTRACELLULAR_SPACE		35	0,412	1,454	0,092	0,576	1	196	tags=57%, list=34%, signal=82%
GO_MUSCLE_CELL_DIFFERENTIATION	GO_MUSCLE_CELL_DIFFERENTIATION		20	0,435	1,449	0,087	0,579	1	112	tags=40%, list=20%, signal=48%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	GO_POSITIVE_REGULATION_OF_CELL_ADHESION		15	0,467	1,448	0,108	0,574	1	188	tags=60%, list=33%, signal=87%
GO_CELL_CELL_JUNCTION	GO_CELL_CELL_JUNCTION		24	0,420	1,447	0,104	0,567	1	196	tags=58%, list=34%, signal=85%
GO_CELLULAR_COMPONENT_MORPHOGENESIS	GO_CELLULAR_COMPONENT_MORPHOGENESIS		45	0,377	1,442	0,080	0,574	1	59	tags=22%, list=10%, signal=23%
GO_MUSCLE_SYSTEM_PROCESS	GO_MUSCLE_SYSTEM_PROCESS		19	0,455	1,435	0,098	0,583	1	142	tags=53%, list=25%, signal=68%
GO_CELL_SURFACE	GO_CELL_SURFACE		23	0,417	1,435	0,107	0,576	1	178	tags=57%, list=31%, signal=79%
GO_TISSUE_MORPHOGENESIS	GO_TISSUE_MORPHOGENESIS		23	0,419	1,434	0,120	0,571	1	89	tags=30%, list=16%, signal=35%
GO_ACTIN_FILAMENT	GO_ACTIN_FILAMENT		15	0,464	1,422	0,113	0,596	1	49	tags=27%, list=9%, signal=28%
GO_CELL_PROJECTION_MEMBRANE	GO_CELL_PROJECTION_MEMBRANE		16	0,449	1,416	0,106	0,603	1	193	tags=63%, list=34%, signal=92%
GO_BIOLOGICAL_ADHESION	GO_BIOLOGICAL_ADHESION		60	0,361	1,415	0,076	0,597	1	266	tags=68%, list=47%, signal=115%
GO_REGULATION_OF_ION_TRANSPORT	GO_REGULATION_OF_ION_TRANSPORT		20	0,439	1,413	0,124	0,596	1	312	tags=95%, list=55%, signal=203%
GO_ZINC_ION_BINDING	GO_ZINC_ION_BINDING		49	0,364	1,410	0,108	0,594	1	133	tags=35%, list=23%, signal=41%
GO_ORGANELLE_ASSEMBLY	GO_ORGANELLE_ASSEMBLY		30	0,391	1,409	0,109	0,589	1	75	tags=27%, list=13%, signal=29%
GO_TRANSITION_METAL_ION_BINDING	GO_TRANSITION_METAL_ION_BINDING		64	0,354	1,405	0,066	0,594	1	81	tags=25%, list=14%, signal=26%
GO_ACTIN_BASED_CELL_PROJECTION	GO_ACTIN_BASED_CELL_PROJECTION		16	0,461	1,403	0,117	0,592	1	269	tags=88%, list=47%, signal=161%
GO_LEUKOCYTE_ACTIVATION	GO_LEUKOCYTE_ACTIVATION		18	0,433	1,402	0,122	0,587	1	266	tags=78%, list=47%, signal=141%
GO_CELL_CELL_ADHESION	GO_CELL_CELL_ADHESION		36	0,384	1,402	0,093	0,581	1	266	tags=72%, list=47%, signal=127%
GO_METAL_ION_TRANSPORT	GO_METAL_ION_TRANSPORT		16	0,442	1,395	0,116	0,592	1	108	tags=38%, list=19%, signal=45%
GO_RESPONSE_TO_NITROGEN_COMPOUND	GO_RESPONSE_TO_NITROGEN_COMPOUND		37	0,375	1,393	0,125	0,588	1	148	tags=43%, list=26%, signal=55%
GO_PLASMA_MEMBRANE_REGION	GO_PLASMA_MEMBRANE_REGION		33	0,376	1,386	0,116	0,600	1	215	tags=58%, list=38%, signal=87%
GO_LEUKOCYTE_CELL_CELL_ADHESION	GO_LEUKOCYTE_CELL_CELL_ADHESION		18	0,422	1,384	0,143	0,600	1	266	tags=78%, list=47%, signal=141%
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	GO_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS		55	0,354	1,367	0,112	0,637	1	188	tags=47%, list=33%, signal=64%

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_CELLULAR_COMPONENT_ASSEMBLY_INVOLVED_IN_MORPHOGENESIS	GO_CELLULAR_COMPONENT_ASSEMBLY_INVOLVED_IN_MORPHOGENESIS		17	0,426	1,363	0,140	0,640	1	75	tags=29%, list=13%, signal=33%
GO_CALCIUM_ION_BINDING	GO_CALCIUM_ION_BINDING		25	0,391	1,358	0,155	0,647	1	160	tags=48%, list=28%, signal=64%
GO_REGULATION_OF_CELL_PROLIFERATION	GO_REGULATION_OF_CELL_PROLIFERATION		47	0,355	1,352	0,138	0,656	1	160	tags=43%, list=28%, signal=54%
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION		21	0,402	1,351	0,157	0,652	1	111	tags=33%, list=20%, signal=40%
REACTOME_DEVELOPMENTAL_BIOLOGY	REACTOME_DEVELOPMENTAL_BIOLOGY		28	0,382	1,342	0,141	0,671	1	246	tags=68%, list=43%, signal=114%
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER		24	0,395	1,341	0,149	0,667	1	142	tags=46%, list=25%, signal=58%
REACTOME_AXON_GUIDANCE	REACTOME_AXON_GUIDANCE		24	0,386	1,335	0,153	0,678	1	177	tags=54%, list=31%, signal=75%
GO_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	GO_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT		32	0,360	1,330	0,140	0,684	1	199	tags=53%, list=35%, signal=77%
GO_BLOOD_VESSEL_MORPHOGENESIS	GO_BLOOD_VESSEL_MORPHOGENESIS		19	0,399	1,328	0,165	0,682	1	210	tags=63%, list=37%, signal=97%
GO_MUSCLE_TISSUE_DEVELOPMENT	GO_MUSCLE_TISSUE_DEVELOPMENT		15	0,429	1,323	0,163	0,691	1	81	tags=33%, list=14%, signal=38%
GO_RESPONSE_TO_METAL_ION	GO_RESPONSE_TO_METAL_ION		17	0,409	1,320	0,170	0,692	1	287	tags=82%, list=50%, signal=161%
GO_REGULATION_OF_MULTI_ORGANISM_PROCESS	GO_REGULATION_OF_MULTI_ORGANISM_PROCESS		15	0,439	1,320	0,151	0,686	1	57	tags=27%, list=10%, signal=29%
GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES		17	0,411	1,319	0,161	0,682	1	131	tags=41%, list=23%, signal=52%
GO_MICROTUBULE_CYTOSKELETON	GO_MICROTUBULE_CYTOSKELETON		52	0,333	1,318	0,141	0,677	1	201	tags=52%, list=35%, signal=73%
GO_POLY_A_RNA_BINDING	GO_POLY_A_RNA_BINDING		35	0,366	1,314	0,184	0,681	1	70	tags=14%, list=12%, signal=15%
GO_REGULATION_OF_TRANSPORT	GO_REGULATION_OF_TRANSPORT		62	0,328	1,314	0,143	0,677	1	189	tags=47%, list=33%, signal=62%
GO_REGULATION_OF_RESPONSE_TO_WOUNDING	GO_REGULATION_OF_RESPONSE_TO_WOUNDING		15	0,430	1,313	0,175	0,672	1	144	tags=47%, list=25%, signal=61%
GO_CYTOSKELETON_ORGANIZATION	GO_CYTOSKELETON_ORGANIZATION		68	0,324	1,312	0,124	0,668	1	199	tags=46%, list=35%, signal=62%
GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE		15	0,429	1,312	0,164	0,662	1	98	tags=40%, list=17%, signal=47%
GO_WOUND_HEALING	GO_WOUND_HEALING		28	0,370	1,310	0,164	0,661	1	156	tags=43%, list=27%, signal=56%
GO_LYMPHOCYTE_ACTIVATION	GO_LYMPHOCYTE_ACTIVATION		17	0,415	1,309	0,170	0,657	1	266	tags=76%, list=47%, signal=139%
GO_PROTEIN_DOMAIN_SPECIFIC_BINDING	GO_PROTEIN_DOMAIN_SPECIFIC_BINDING		36	0,354	1,309	0,167	0,653	1	114	tags=33%, list=20%, signal=39%
GO_INNATE_IMMUNE_RESPONSE	GO_INNATE_IMMUNE_RESPONSE		22	0,384	1,306	0,173	0,654	1	144	tags=41%, list=25%, signal=53%
GO_RESPONSE_TO_INORGANIC_SUBSTANCE	GO_RESPONSE_TO_INORGANIC_SUBSTANCE		29	0,367	1,300	0,176	0,664	1	173	tags=48%, list=30%, signal=66%
GO_IMMUNE_RESPONSE	GO_IMMUNE_RESPONSE		32	0,359	1,291	0,188	0,682	1	144	tags=38%, list=25%, signal=47%
GO_SECRETION	GO_SECRETION		16	0,420	1,290	0,195	0,681	1	196	tags=63%, list=34%, signal=93%
GO_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	GO_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY		17	0,404	1,289	0,191	0,676	1	251	tags=71%, list=44%, signal=123%
GO_VASCULATURE_DEVELOPMENT	GO_VASCULATURE_DEVELOPMENT		20	0,380	1,286	0,170	0,678	1	310	tags=85%, list=54%, signal=180%
GO_ANATOMICAL_STRUCTURE_HOMEOSTASIS	GO_ANATOMICAL_STRUCTURE_HOMEOSTASIS		19	0,391	1,286	0,188	0,672	1	182	tags=53%, list=32%, signal=75%
GO_TUBE_DEVELOPMENT	GO_TUBE_DEVELOPMENT		19	0,395	1,284	0,186	0,673	1	89	tags=32%, list=16%, signal=36%
GO_REGULATION_OF_MULTICELLULAR_ORGANISMAL_DEVELOPMENT	GO_REGULATION_OF_MULTICELLULAR_ORGANISMAL_DEVELOPMENT		66	0,315	1,278	0,152	0,683	1	160	tags=36%, list=28%, signal=45%
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION		33	0,350	1,269	0,187	0,703	1	210	tags=52%, list=37%, signal=77%
GO_SYSTEM_PROCESS	GO_SYSTEM_PROCESS		49	0,325	1,266	0,188	0,706	1	156	tags=41%, list=27%, signal=51%
GO_REGULATION_OF_CELL_MORPHOGENESIS	GO_REGULATION_OF_CELL_MORPHOGENESIS		35	0,348	1,266	0,196	0,702	1	188	tags=49%, list=33%, signal=68%
GO_CELL_PROLIFERATION	GO_CELL_PROLIFERATION		21	0,378	1,263	0,202	0,702	1	131	tags=38%, list=23%, signal=48%
GO_DEFENSE_RESPONSE	GO_DEFENSE_RESPONSE		31	0,349	1,259	0,208	0,710	1	144	tags=39%, list=25%, signal=49%
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS		48	0,327	1,258	0,196	0,705	1	206	tags=48%, list=36%, signal=69%
GO_CELL_ACTIVATION	GO_CELL_ACTIVATION		36	0,336	1,252	0,210	0,717	1	266	tags=64%, list=47%, signal=112%
GO_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY		15	0,406	1,250	0,229	0,718	1	90	tags=33%, list=16%, signal=39%
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE		19	0,377	1,249	0,209	0,714	1	166	tags=47%, list=29%, signal=65%

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_STIMULUS		52	0,324	1,244	0,194	0,724	1	213	tags=50%, list=37%, signal=73%
GO_RESPONSE_TO_STEROID_HORMONE	GO_RESPONSE_TO_STEROID_HORMONE		19	0,380	1,243	0,215	0,720	1	99	tags=37%, list=17%, signal=43%
GO_MOVEMENT_OF_CELL_OR_SUBCELLULAR_COMPONENT	GO_MOVEMENT_OF_CELL_OR_SUBCELLULAR_COMPONENT		70	0,309	1,240	0,194	0,722	1	85	tags=24%, list=15%, signal=25%
GO_CELL_MOTILITY	GO_CELL_MOTILITY		40	0,327	1,238	0,226	0,724	1	199	tags=48%, list=35%, signal=68%
GO_APOPTOTIC_SIGNALING_PATHWAY	GO_APOPTOTIC_SIGNALING_PATHWAY		16	0,399	1,236	0,230	0,722	1	185	tags=50%, list=33%, signal=72%
GO_SYNAPSE	GO_SYNAPSE		29	0,349	1,226	0,223	0,744	1	334	tags=86%, list=59%, signal=198%
GO_RESPONSE_TO_OXIDATIVE_STRESS	GO_RESPONSE_TO_OXIDATIVE_STRESS		22	0,361	1,223	0,229	0,747	1	148	tags=41%, list=26%, signal=53%
GO_CELL_DEATH	GO_CELL_DEATH		41	0,321	1,220	0,243	0,751	1	198	tags=46%, list=35%, signal=66%
GO_NEGATIVE_REGULATION_OF_TRANSPORT	GO_NEGATIVE_REGULATION_OF_TRANSPORT		17	0,382	1,217	0,240	0,753	1	210	tags=59%, list=37%, signal=90%
GO_IN_UTERO_EMBRYONIC_DEVELOPMENT	GO_IN_UTERO_EMBRYONIC_DEVELOPMENT		15	0,391	1,217	0,243	0,749	1	207	tags=60%, list=36%, signal=92%
GO_REGULATION_OF_SYSTEM_PROCESS	GO_REGULATION_OF_SYSTEM_PROCESS		15	0,396	1,213	0,247	0,755	1	215	tags=60%, list=38%, signal=94%
GO_RESPONSE_TO_WOUNDING	GO_RESPONSE_TO_WOUNDING		34	0,326	1,212	0,237	0,751	1	196	tags=47%, list=34%, signal=67%
GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND		22	0,361	1,204	0,245	0,768	1	185	tags=50%, list=33%, signal=71%
GO_CELLULAR_RESPONSE_TO_ORGANIC_SUBSTANCE	GO_CELLULAR_RESPONSE_TO_ORGANIC_SUBSTANCE		75	0,297	1,201	0,227	0,772	1	137	tags=32%, list=24%, signal=37%
GO_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	GO_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION		66	0,297	1,191	0,232	0,794	1	213	tags=47%, list=37%, signal=66%
GO_RECEPTOR_BINDING	GO_RECEPTOR_BINDING		46	0,313	1,184	0,266	0,810	1	215	tags=50%, list=38%, signal=74%
GO_HEAD_DEVELOPMENT	GO_HEAD_DEVELOPMENT		22	0,355	1,181	0,269	0,811	1	114	tags=32%, list=20%, signal=38%
GO_RESPONSE_TO_CYTOKINE	GO_RESPONSE_TO_CYTOKINE		27	0,333	1,178	0,278	0,815	1	130	tags=33%, list=23%, signal=41%
GO_RNA_BINDING	GO_RNA_BINDING		55	0,303	1,175	0,277	0,819	1	15	tags=5%, list=3%, signal=5%
GO_CELLULAR_RESPONSE_TO_ENDOGENOUS_STIMULUS	GO_CELLULAR_RESPONSE_TO_ENDOGENOUS_STIMULUS		43	0,307	1,172	0,274	0,822	1	121	tags=30%, list=21%, signal=35%
GO_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	GO_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND		36	0,316	1,169	0,284	0,825	1	210	tags=50%, list=37%, signal=74%
GO_SECRETION_BY_CELL	GO_SECRETION_BY_CELL		15	0,383	1,165	0,291	0,830	1	196	tags=60%, list=34%, signal=89%
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION		15	0,372	1,159	0,315	0,842	1	343	tags=93%, list=60%, signal=229%
GO_REGULATION_OF_CELL_ADHESION	GO_REGULATION_OF_CELL_ADHESION		27	0,330	1,157	0,301	0,845	1	133	tags=33%, list=23%, signal=41%
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS		20	0,353	1,155	0,284	0,845	1	297	tags=75%, list=52%, signal=151%
GO_POSITIVE_REGULATION_OF_TRANSPORT	GO_POSITIVE_REGULATION_OF_TRANSPORT		40	0,309	1,151	0,309	0,850	1	189	tags=48%, list=33%, signal=66%
GO_CELLULAR_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	GO_CELLULAR_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND		36	0,311	1,150	0,296	0,848	1	137	tags=33%, list=24%, signal=41%
GO_PERINUCLEAR_REGION_OF_CYTOPLASM	GO_PERINUCLEAR_REGION_OF_CYTOPLASM		38	0,302	1,146	0,328	0,856	1	269	tags=63%, list=47%, signal=112%
GO_IMMUNE_SYSTEM_PROCESS	GO_IMMUNE_SYSTEM_PROCESS		76	0,282	1,144	0,285	0,854	1	256	tags=54%, list=45%, signal=85%
GO_POSITIVE_REGULATION_OF_PROTEOLYSIS	GO_POSITIVE_REGULATION_OF_PROTEOLYSIS		15	0,366	1,143	0,313	0,852	1	112	tags=33%, list=20%, signal=40%
GO_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	GO_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT		24	0,329	1,142	0,312	0,851	1	114	tags=29%, list=20%, signal=35%
GO_RUFFLE	GO_RUFFLE		19	0,344	1,142	0,313	0,845	1	196	tags=47%, list=34%, signal=70%
GO_NUCLEOPLASM_PART	GO_NUCLEOPLASM_PART		23	0,343	1,140	0,313	0,845	1	228	tags=57%, list=40%, signal=91%
GO_PROTEIN_OLIGOMERIZATION	GO_PROTEIN_OLIGOMERIZATION		18	0,357	1,139	0,3	0,841	1	267	tags=72%, list=47%, signal=132%
GO_CELLULAR_RESPONSE_TO_HORMONE_STIMULUS	GO_CELLULAR_RESPONSE_TO_HORMONE_STIMULUS		20	0,346	1,137	0,309	0,842	1	246	tags=65%, list=43%, signal=110%
GO_MICROTUBULE	GO_MICROTUBULE		18	0,357	1,137	0,317	0,837	1	152	tags=44%, list=27%, signal=59%
GO_COFACTOR_METABOLIC_PROCESS	GO_COFACTOR_METABOLIC_PROCESS		25	0,323	1,131	0,309	0,849	1	339	tags=84%, list=60%, signal=199%
GO_NEUROLOGICAL_SYSTEM_PROCESS	GO_NEUROLOGICAL_SYSTEM_PROCESS		24	0,329	1,131	0,321	0,845	1	156	tags=42%, list=27%, signal=55%
GO_POSITIVE_REGULATION_OF_CELL_COMMUNICATION	GO_POSITIVE_REGULATION_OF_CELL_COMMUNICATION		54	0,289	1,129	0,319	0,845	1	169	tags=37%, list=30%, signal=48%
GO_REGULATION_OF_CELL_DIFFERENTIATION	GO_REGULATION_OF_CELL_DIFFERENTIATION		52	0,287	1,123	0,320	0,857	1	210	tags=46%, list=37%, signal=66%
GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION		16	0,355	1,123	0,312	0,853	1	210	tags=56%, list=37%, signal=87%

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION	GO_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION		26	0,316	1,121	0,325	0,853	1	188	tags=46%, list=33%, signal=66%
GO_NEURON_DIFFERENTIATION	GO_NEURON_DIFFERENTIATION		27	0,317	1,120	0,329	0,851	1	100	tags=26%, list=18%, signal=30%
GO_POSITIVE_REGULATION_OF_LOCOMOTION	GO_POSITIVE_REGULATION_OF_LOCOMOTION		18	0,352	1,119	0,349	0,847	1	177	tags=44%, list=31%, signal=62%
GO_RESPONSE_TO_ENDOGENOUS_STIMULUS	GO_RESPONSE_TO_ENDOGENOUS_STIMULUS		60	0,282	1,119	0,314	0,843	1	137	tags=32%, list=24%, signal=37%
GO_LOCOMOTION	GO_LOCOMOTION		48	0,290	1,119	0,347	0,839	1	112	tags=27%, list=20%, signal=31%
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER		55	0,285	1,116	0,344	0,842	1	172	tags=40%, list=30%, signal=52%
GO_NEURON_PROJECTION_DEVELOPMENT	GO_NEURON_PROJECTION_DEVELOPMENT		23	0,330	1,112	0,337	0,848	1	72	tags=22%, list=13%, signal=24%
GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS		21	0,332	1,112	0,342	0,844	1	250	tags=62%, list=44%, signal=106%
GO_MEMBRANE_REGION	GO_MEMBRANE_REGION		46	0,290	1,110	0,347	0,845	1	215	tags=48%, list=38%, signal=71%
GO_CELLULAR_PROTEIN_COMPLEX_ASSEMBLY	GO_CELLULAR_PROTEIN_COMPLEX_ASSEMBLY		15	0,358	1,107	0,335	0,848	1	52	tags=20%, list=9%, signal=21%
GO_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	GO_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY		20	0,335	1,105	0,333	0,849	1	213	tags=55%, list=37%, signal=85%
GO_CHROMOSOME_ORGANIZATION	GO_CHROMOSOME_ORGANIZATION		33	0,304	1,104	0,353	0,845	1	151	tags=36%, list=27%, signal=47%
GO_INTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	GO_INTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE		23	0,331	1,104	0,359	0,842	1	70	tags=22%, list=12%, signal=24%
GO_RESPONSE_TO_HORMONE	GO_RESPONSE_TO_HORMONE		36	0,299	1,100	0,36	0,847	1	248	tags=58%, list=44%, signal=97%
GO_RESPONSE_TO_BIOTIC_STIMULUS	GO_RESPONSE_TO_BIOTIC_STIMULUS		24	0,316	1,098	0,349	0,848	1	119	tags=33%, list=21%, signal=40%
GO_MITOCHONDRIAL_ENVELOPE	GO_MITOCHONDRIAL_ENVELOPE		16	0,349	1,095	0,363	0,851	1	118	tags=38%, list=21%, signal=46%
GO_VESICLE_MEMBRANE	GO_VESICLE_MEMBRANE		22	0,327	1,095	0,346	0,847	1	84	tags=27%, list=15%, signal=31%
GO_DOUBLE_STRANDED_DNA_BINDING	GO_DOUBLE_STRANDED_DNA_BINDING		18	0,341	1,089	0,370	0,858	1	137	tags=39%, list=24%, signal=50%
GO_NEUROGENESIS	GO_NEUROGENESIS		50	0,280	1,089	0,364	0,855	1	100	tags=24%, list=18%, signal=27%
GO_PROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	GO_PROTEIN_COMPLEX_SUBUNIT_ORGANIZATION		73	0,269	1,087	0,369	0,854	1	269	tags=58%, list=47%, signal=95%
GO_SEQUENCE_SPECIFIC_DNA_BINDING	GO_SEQUENCE_SPECIFIC_DNA_BINDING		16	0,346	1,084	0,376	0,859	1	130	tags=38%, list=23%, signal=47%
GO_ENZYME_BINDING	GO_ENZYME_BINDING		88	0,260	1,083	0,380	0,857	1	201	tags=38%, list=35%, signal=49%
GO_CELLULAR_RESPONSE_TO_CYTOKINE_STIMULUS	GO_CELLULAR_RESPONSE_TO_CYTOKINE_STIMULUS		17	0,342	1,082	0,385	0,854	1	130	tags=35%, list=23%, signal=44%
GO_SYNAPSE_PART	GO_SYNAPSE_PART		22	0,322	1,081	0,373	0,852	1	312	tags=77%, list=55%, signal=164%
GO_OXIDATION_REDUCTION_PROCESS	GO_OXIDATION_REDUCTION_PROCESS		43	0,283	1,079	0,387	0,852	1	315	tags=72%, list=55%, signal=149%
GO_HEMOSTASIS	GO_HEMOSTASIS		23	0,321	1,077	0,386	0,853	1	112	tags=30%, list=20%, signal=36%
GO_PROTEIN_C_TERMINUS_BINDING	GO_PROTEIN_C_TERMINUS_BINDING		16	0,348	1,077	0,381	0,850	1	210	tags=56%, list=37%, signal=87%
GO_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	GO_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION		19	0,327	1,077	0,376	0,846	1	188	tags=47%, list=33%, signal=68%
GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION	GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION		54	0,276	1,075	0,381	0,846	1	185	tags=43%, list=33%, signal=57%
GO_LIPID_BIOSYNTHETIC_PROCESS	GO_LIPID_BIOSYNTHETIC_PROCESS		22	0,321	1,072	0,388	0,849	1	193	tags=50%, list=34%, signal=73%
GO_CELL_JUNCTION_ASSEMBLY	GO_CELL_JUNCTION_ASSEMBLY		18	0,332	1,071	0,383	0,848	1	282	tags=72%, list=50%, signal=139%
GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS		16	0,339	1,070	0,392	0,845	1	294	tags=75%, list=52%, signal=151%
GO_PROTEIN_COMPLEX_BIOGENESIS	GO_PROTEIN_COMPLEX_BIOGENESIS		48	0,275	1,066	0,388	0,853	1	267	tags=58%, list=47%, signal=101%
GO_MORPHOGENESIS_OF_AN_EPITHELIUM	GO_MORPHOGENESIS_OF_AN_EPITHELIUM		18	0,333	1,063	0,375	0,856	1	188	tags=44%, list=33%, signal=64%
GO_COENZYME_METABOLIC_PROCESS	GO_COENZYME_METABOLIC_PROCESS		20	0,324	1,062	0,409	0,853	1	339	tags=85%, list=60%, signal=203%
GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS		37	0,282	1,062	0,391	0,851	1	201	tags=46%, list=35%, signal=66%
GO_PROTEIN_PHOSPHORYLATION	GO_PROTEIN_PHOSPHORYLATION		37	0,283	1,056	0,413	0,860	1	238	tags=54%, list=42%, signal=87%
GO_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	GO_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND		59	0,268	1,056	0,409	0,856	1	137	tags=31%, list=24%, signal=36%
GO_IMMUNE_SYSTEM_DEVELOPMENT	GO_IMMUNE_SYSTEM_DEVELOPMENT		26	0,306	1,053	0,412	0,859	1	266	tags=62%, list=47%, signal=110%
GO_TRANSCRIPTION_FACTOR_BINDING	GO_TRANSCRIPTION_FACTOR_BINDING		21	0,314	1,051	0,414	0,860	1	163	tags=38%, list=29%, signal=51%
GO_POSITIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS		38	0,276	1,051	0,393	0,856	1	198	tags=45%, list=35%, signal=64%

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GO_ION_TRANSMEMBRANE_TRANSPORT	GO_ION_TRANSMEMBRANE_TRANSPORT		15	0,345	1,049	0,416	0,857	1	13	tags=13%, list=2%, signal=13%
GO_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS	GO_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS		15	0,348	1,048	0,417	0,855	1	276	tags=73%, list=49%, signal=139%
GO_POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	GO_POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS		27	0,301	1,048	0,410	0,852	1	144	tags=37%, list=25%, signal=47%
GO_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION		30	0,295	1,048	0,419	0,849	1	206	tags=47%, list=36%, signal=69%
GO_KINASE_ACTIVITY	GO_KINASE_ACTIVITY		38	0,281	1,047	0,420	0,845	1	259	tags=61%, list=46%, signal=104%
GO_NEGATIVE_REGULATION_OF_CELL_COMMUNICATION	GO_NEGATIVE_REGULATION_OF_CELL_COMMUNICATION		44	0,277	1,045	0,417	0,848	1	284	tags=61%, list=50%, signal=113%
GO_POSITIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS		56	0,262	1,041	0,423	0,852	1	256	tags=54%, list=45%, signal=88%
GO_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING	GO_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING		19	0,319	1,041	0,425	0,849	1	112	tags=32%, list=20%, signal=38%
GO_MITOCHONDRION	GO_MITOCHONDRION		59	0,261	1,040	0,427	0,848	1	137	tags=27%, list=24%, signal=32%
GO_CARBOHYDRATE_BINDING	GO_CARBOHYDRATE_BINDING		15	0,334	1,039	0,424	0,847	1	214	tags=60%, list=38%, signal=94%
GO_REGULATION_OF_HYDROLASE_ACTIVITY	GO_REGULATION_OF_HYDROLASE_ACTIVITY		56	0,267	1,038	0,443	0,844	1	161	tags=34%, list=28%, signal=43%
GO_EMBRYO_DEVELOPMENT	GO_EMBRYO_DEVELOPMENT		31	0,291	1,038	0,415	0,841	1	90	tags=23%, list=16%, signal=25%
GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS		16	0,328	1,038	0,429	0,839	1	156	tags=38%, list=27%, signal=50%
GO_SMALL_MOLECULE_METABOLIC_PROCESS	GO_SMALL_MOLECULE_METABOLIC_PROCESS		64	0,259	1,031	0,445	0,851	1	361	tags=80%, list=63%, signal=193%
GO_NEURON_DEVELOPMENT	GO_NEURON_DEVELOPMENT		25	0,297	1,029	0,432	0,851	1	100	tags=24%, list=18%, signal=28%
GO_CELL_LEADING_EDGE	GO_CELL_LEADING_EDGE		30	0,287	1,027	0,429	0,852	1	199	tags=43%, list=35%, signal=63%
GO_PHOSPHORYLATION	GO_PHOSPHORYLATION		51	0,263	1,026	0,445	0,852	1	256	tags=57%, list=45%, signal=94%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_STIMULUS		63	0,259	1,025	0,461	0,850	1	210	tags=43%, list=37%, signal=60%
GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	GO_PROTEIN_LOCALIZATION_TO_MEMBRANE		15	0,326	1,025	0,413	0,847	1	248	tags=67%, list=44%, signal=115%
GO_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	GO_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT		28	0,288	1,024	0,429	0,845	1	59	tags=18%, list=10%, signal=19%
GO_REGULATION_OF_CYTOSKELETON_ORGANIZATION	GO_REGULATION_OF_CYTOSKELETON_ORGANIZATION		33	0,285	1,024	0,447	0,842	1	260	tags=58%, list=46%, signal=100%
GO_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	GO_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS		62	0,258	1,023	0,466	0,840	1	185	tags=40%, list=33%, signal=53%
GO_PROTEIN_UBIQUITINATION	GO_PROTEIN_UBIQUITINATION		24	0,299	1,020	0,45	0,843	1	28	tags=13%, list=5%, signal=13%
GO_REGULATION_OF_CELL_DEATH	GO_REGULATION_OF_CELL_DEATH		60	0,259	1,020	0,479	0,840	1	206	tags=42%, list=36%, signal=58%
GO_BEHAVIOR	GO_BEHAVIOR		15	0,325	1,015	0,429	0,847	1	336	tags=87%, list=59%, signal=206%
GO_MEMBRANE_PROTEIN_COMPLEX	GO_MEMBRANE_PROTEIN_COMPLEX		25	0,294	1,012	0,465	0,850	1	212	tags=52%, list=37%, signal=79%
GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS		19	0,304	1,011	0,437	0,850	1	305	tags=74%, list=54%, signal=154%
GO_ORGANOPHOSPHATE_METABOLIC_PROCESS	GO_ORGANOPHOSPHATE_METABOLIC_PROCESS		39	0,267	1,010	0,466	0,847	1	361	tags=82%, list=63%, signal=209%
GO_ACTIN_FILAMENT_ORGANIZATION	GO_ACTIN_FILAMENT_ORGANIZATION		17	0,316	1,010	0,449	0,845	1	196	tags=53%, list=34%, signal=78%
GO_OXIDOREDUCTASE_ACTIVITY	GO_OXIDOREDUCTASE_ACTIVITY		32	0,278	1,008	0,469	0,845	1	305	tags=69%, list=54%, signal=140%
GO_CELL_CYCLE	GO_CELL_CYCLE		54	0,259	1,005	0,474	0,848	1	0	tags=2%, list=0%, signal=2%
GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY		15	0,324	1,004	0,452	0,847	1	130	tags=33%, list=23%, signal=42%
GO_PROTEIN_KINASE_ACTIVITY	GO_PROTEIN_KINASE_ACTIVITY		25	0,289	1,002	0,456	0,847	1	259	tags=60%, list=46%, signal=105%
GO_MITOCHONDRIAL_PART	GO_MITOCHONDRIAL_PART		23	0,290	1,002	0,469	0,844	1	137	tags=35%, list=24%, signal=44%
GO_POSTSYNAPSE	GO_POSTSYNAPSE		15	0,322	1,001	0,469	0,843	1	312	tags=80%, list=55%, signal=172%
GO_ORGANIC_ACID_METABOLIC_PROCESS	GO_ORGANIC_ACID_METABOLIC_PROCESS		33	0,277	0,100	0,483	0,843	1	339	tags=79%, list=60%, signal=184%
GO_NEGATIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS		19	0,301	0,995	0,469	0,850	1	181	tags=42%, list=32%, signal=60%
GO_NEGATIVE_REGULATION_OF_CATALYTIC_ACTIVITY	GO_NEGATIVE_REGULATION_OF_CATALYTIC_ACTIVITY		28	0,283	0,995	0,487	0,846	1	302	tags=68%, list=53%, signal=137%
GO_CELLULAR_RESPONSE_TO_STRESS	GO_CELLULAR_RESPONSE_TO_STRESS		69	0,248	0,994	0,488	0,844	1	214	tags=43%, list=38%, signal=61%
GO_MACROMOLECULAR_COMPLEX_ASSEMBLY	GO_MACROMOLECULAR_COMPLEX_ASSEMBLY		56	0,253	0,994	0,508	0,841	1	238	tags=50%, list=42%, signal=77%

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_ORGANONITROGEN_COMPOUND_METABOLIC_PROCESS	GO_ORGANONITROGEN_COMPOUND_METABOLIC_PROCESS		44	0,262	0,992	0,468	0,842	1	339	tags=75%, list=60%, signal=171%
GO_REGULATION_OF_ORGANELLE_ORGANIZATION	GO_REGULATION_OF_ORGANELLE_ORGANIZATION		66	0,248	0,991	0,501	0,842	1	251	tags=52%, list=44%, signal=81%
GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION		18	0,309	0,990	0,486	0,840	1	248	tags=61%, list=44%, signal=105%
GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	GO_POSITIVE_REGULATION_OF_MAPK_CASCADE		17	0,307	0,986	0,491	0,847	1	160	tags=41%, list=28%, signal=56%
GO_CELL_JUNCTION_ORGANIZATION	GO_CELL_JUNCTION_ORGANIZATION		24	0,287	0,983	0,487	0,849	1	282	tags=67%, list=50%, signal=127%
GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS		22	0,285	0,981	0,489	0,850	1	346	tags=82%, list=61%, signal=201%
GO_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	GO_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS		61	0,245	0,981	0,510	0,847	1	185	tags=39%, list=33%, signal=52%
GO_REGULATION_OF_RESPONSE_TO_STRESS	GO_REGULATION_OF_RESPONSE_TO_STRESS		57	0,244	0,979	0,509	0,848	1	185	tags=37%, list=33%, signal=49%
GO_REGULATION_OF_DEFENSE_RESPONSE	GO_REGULATION_OF_DEFENSE_RESPONSE		28	0,274	0,977	0,487	0,850	1	113	tags=29%, list=20%, signal=34%
GO_INTRACELLULAR_SIGNAL_TRANSDUCTION	GO_INTRACELLULAR_SIGNAL_TRANSDUCTION		64	0,247	0,976	0,537	0,847	1	252	tags=52%, list=44%, signal=82%
GO_REGULATION_OF_BODY_FLUID_LEVELS	GO_REGULATION_OF_BODY_FLUID_LEVELS		26	0,281	0,975	0,497	0,846	1	153	tags=35%, list=27%, signal=45%
GO_MACROMOLECULAR_COMPLEX_BINDING	GO_MACROMOLECULAR_COMPLEX_BINDING		75	0,237	0,974	0,517	0,846	1	269	tags=53%, list=47%, signal=88%
GO_SPINDLE	GO_SPINDLE		21	0,292	0,972	0,489	0,848	1	251	tags=57%, list=44%, signal=98%
GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS		15	0,310	0,969	0,478	0,849	1	350	tags=87%, list=62%, signal=219%
GO_CELL_SUBSTRATE_ADHESION	GO_CELL_SUBSTRATE_ADHESION		15	0,312	0,966	0,511	0,852	1	266	tags=67%, list=47%, signal=122%
GO_TRANSMEMBRANE_TRANSPORT	GO_TRANSMEMBRANE_TRANSPORT		19	0,290	0,966	0,512	0,849	1	13	tags=11%, list=2%, signal=10%
GO_REGULATION_OF_MAPK_CASCADE	GO_REGULATION_OF_MAPK_CASCADE		22	0,286	0,964	0,517	0,850	1	213	tags=50%, list=37%, signal=77%
GO_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	GO_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY		32	0,264	0,958	0,524	0,859	1	82	tags=22%, list=14%, signal=24%
GO_REGULATION_OF_INTRACELLULAR_TRANSPORT	GO_REGULATION_OF_INTRACELLULAR_TRANSPORT		29	0,269	0,956	0,523	0,860	1	248	tags=52%, list=44%, signal=87%
GO_PROTEIN_HOMODIMERIZATION_ACTIVITY	GO_PROTEIN_HOMODIMERIZATION_ACTIVITY		42	0,253	0,954	0,546	0,860	1	346	tags=76%, list=61%, signal=180%
GO_LIPID_METABOLIC_PROCESS	GO_LIPID_METABOLIC_PROCESS		38	0,256	0,952	0,537	0,863	1	193	tags=42%, list=34%, signal=59%
GO_REGULATION_OF_CYTOKINE_PRODUCTION	GO_REGULATION_OF_CYTOKINE_PRODUCTION		28	0,264	0,949	0,522	0,865	1	131	tags=29%, list=23%, signal=35%
GO_TRANSPORTER_ACTIVITY	GO_TRANSPORTER_ACTIVITY		22	0,281	0,949	0,503	0,862	1	26	tags=14%, list=5%, signal=14%
GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL		27	0,268	0,946	0,529	0,865	1	28	tags=11%, list=5%, signal=11%
GO_REGULATION_OF_CELL_DEVELOPMENT	GO_REGULATION_OF_CELL_DEVELOPMENT		35	0,258	0,944	0,533	0,866	1	59	tags=17%, list=10%, signal=18%
GO_RESPONSE_TO_RADIATION	GO_RESPONSE_TO_RADIATION		21	0,284	0,944	0,528	0,863	1	256	tags=57%, list=45%, signal=100%
GO_RESPONSE_TO_LIPID	GO_RESPONSE_TO_LIPID		33	0,263	0,943	0,555	0,861	1	99	tags=24%, list=17%, signal=28%
GO_LIGASE_ACTIVITY	GO_LIGASE_ACTIVITY		20	0,287	0,943	0,532	0,858	1	16	tags=10%, list=3%, signal=10%
GO_REGULATION_OF_CATABOLIC_PROCESS	GO_REGULATION_OF_CATABOLIC_PROCESS		41	0,251	0,941	0,549	0,859	1	267	tags=56%, list=47%, signal=98%
GO_PEPTIDYL_AMINO_ACID_MODIFICATION	GO_PEPTIDYL_AMINO_ACID_MODIFICATION		29	0,265	0,938	0,554	0,861	1	280	tags=62%, list=49%, signal=116%
GO_NEGATIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO_NEGATIVE_REGULATION_OF_MOLECULAR_FUNCTION		44	0,242	0,937	0,572	0,861	1	319	tags=68%, list=56%, signal=143%
GO_REGULATION_OF_CELLULAR_LOCALIZATION	GO_REGULATION_OF_CELLULAR_LOCALIZATION		49	0,241	0,935	0,550	0,861	1	189	tags=39%, list=33%, signal=53%
GO_NUCLEAR_OUTER_MEMBRANE_ENDOPLASMIC_RETICULUM_MEMBRANE_NETWORK	GO_NUCLEAR_OUTER_MEMBRANE_ENDOPLASMIC_RETICULUM_MEMBRANE_NETWORK		28	0,267	0,935	0,567	0,859	1	179	tags=39%, list=31%, signal=54%
GO_PROTEIN_DIMERIZATION_ACTIVITY	GO_PROTEIN_DIMERIZATION_ACTIVITY		48	0,240	0,933	0,574	0,859	1	346	tags=75%, list=61%, signal=175%
GO_CYTOPLASMIC_VESICLE_PART	GO_CYTOPLASMIC_VESICLE_PART		25	0,270	0,932	0,547	0,857	1	84	tags=24%, list=15%, signal=27%
GO_NEGATIVE_REGULATION_OF_CELL_DEATH	GO_NEGATIVE_REGULATION_OF_CELL_DEATH		39	0,250	0,931	0,576	0,857	1	206	tags=44%, list=36%, signal=64%
GO_RESPONSE_TO_ABIOTIC_STIMULUS	GO_RESPONSE_TO_ABIOTIC_STIMULUS		48	0,241	0,929	0,579	0,857	1	310	tags=65%, list=54%, signal=130%

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_CELLULAR_COMPONENT_DISASSEMBLY	GO_CELLULAR_COMPONENT_DISASSEMBLY		26	0,266	0,926	0,555	0,861	1	203	tags=46%, list=36%, signal=68%
GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION	GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION		17	0,290	0,925	0,532	0,860	1	199	tags=47%, list=35%, signal=70%
GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION	GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION		50	0,235	0,922	0,589	0,862	1	189	tags=38%, list=33%, signal=52%
GO_CHROMOSOME	GO_CHROMOSOME		29	0,262	0,921	0,559	0,861	1	236	tags=52%, list=41%, signal=84%
GO_RESPONSE_TO_DRUG	GO_RESPONSE_TO_DRUG		16	0,294	0,921	0,569	0,858	1	185	tags=44%, list=33%, signal=63%
GO_POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY		38	0,248	0,919	0,575	0,858	1	121	tags=26%, list=21%, signal=31%
GO_PROTEIN_COMPLEX_BINDING	GO_PROTEIN_COMPLEX_BINDING		63	0,230	0,919	0,599	0,856	1	260	tags=51%, list=46%, signal=83%
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT		19	0,286	0,918	0,538	0,855	1	248	tags=58%, list=44%, signal=99%
GO_ENDOPLASMIC_RETICULUM	GO_ENDOPLASMIC_RETICULUM		49	0,237	0,918	0,574	0,853	1	179	tags=35%, list=31%, signal=46%
GO_POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	GO_POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION		72	0,227	0,918	0,615	0,850	1	206	tags=39%, list=36%, signal=53%
GO_ENDOPLASMIC_RETICULUM_PART	GO_ENDOPLASMIC_RETICULUM_PART		37	0,249	0,916	0,593	0,850	1	179	tags=38%, list=31%, signal=52%
GO_MEMBRANE_MICRODOMAIN	GO_MEMBRANE_MICRODOMAIN		16	0,293	0,912	0,548	0,855	1	215	tags=50%, list=38%, signal=78%
GO_ORGANELLE_LOCALIZATION	GO_ORGANELLE_LOCALIZATION		21	0,276	0,903	0,563	0,868	1	30	tags=14%, list=5%, signal=15%
GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS		25	0,261	0,901	0,586	0,869	1	339	tags=76%, list=60%, signal=180%
GO_SINGLE_ORGANISM_CATABOLIC_PROCESS	GO_SINGLE_ORGANISM_CATABOLIC_PROCESS		40	0,238	0,897	0,606	0,873	1	360	tags=78%, list=63%, signal=196%
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS		47	0,233	0,897	0,604	0,871	1	259	tags=55%, list=46%, signal=93%
GO_ORGANELLE_SUBCOMPARTMENT	GO_ORGANELLE_SUBCOMPARTMENT		15	0,286	0,895	0,586	0,871	1	33	tags=13%, list=6%, signal=14%
GO_CYTOPLASMIC_REGION	GO_CYTOPLASMIC_REGION		26	0,257	0,889	0,606	0,880	1	60	tags=19%, list=11%, signal=21%
GO_IDENTICAL_PROTEIN_BINDING	GO_IDENTICAL_PROTEIN_BINDING		71	0,218	0,888	0,67	0,878	1	325	tags=66%, list=57%, signal=135%
GO_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	GO_REGULATION_OF_IMMUNE_SYSTEM_PROCESS		48	0,230	0,884	0,639	0,882	1	144	tags=29%, list=25%, signal=36%
GO_DEVELOPMENTAL_GROWTH	GO_DEVELOPMENTAL_GROWTH		18	0,272	0,884	0,591	0,880	1	84	tags=22%, list=15%, signal=25%
GO_PROTEOLYSIS	GO_PROTEOLYSIS		35	0,239	0,881	0,630	0,883	1	231	tags=46%, list=41%, signal=72%
GO_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	GO_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS		38	0,236	0,881	0,638	0,880	1	167	tags=34%, list=29%, signal=45%
KEGG_MAPK_SIGNALING_PATHWAY	KEGG_MAPK_SIGNALING_PATHWAY		15	0,286	0,878	0,604	0,882	1	306	tags=73%, list=54%, signal=154%
GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS		28	0,247	0,873	0,634	0,887	1	302	tags=64%, list=53%, signal=130%
GO_ENDOSOMAL_PART	GO_ENDOSOMAL_PART		17	0,269	0,865	0,615	0,899	1	113	tags=24%, list=20%, signal=28%
GO_PHOSPHATE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_PHOSPHATE_CONTAINING_COMPOUND_METABOLIC_PROCESS		90	0,210	0,863	0,701	0,899	1	361	tags=73%, list=63%, signal=169%
GO_CELL_PROJECTION_ORGANIZATION	GO_CELL_PROJECTION_ORGANIZATION		46	0,228	0,859	0,668	0,903	1	31	tags=11%, list=5%, signal=11%
GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS		15	0,282	0,859	0,626	0,900	1	181	tags=40%, list=32%, signal=57%
GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY		15	0,277	0,856	0,630	0,902	1	31	tags=13%, list=5%, signal=14%
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER		27	0,239	0,855	0,638	0,902	1	200	tags=44%, list=35%, signal=65%
GO_VACUOLAR_PART	GO_VACUOLAR_PART		20	0,257	0,850	0,651	0,906	1	124	tags=25%, list=22%, signal=31%
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_STRESS	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_STRESS		28	0,238	0,846	0,652	0,910	1	267	tags=54%, list=47%, signal=96%
GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT		19	0,257	0,843	0,645	0,914	1	325	tags=74%, list=57%, signal=166%
GO_ENVELOPE	GO_ENVELOPE		26	0,240	0,841	0,672	0,914	1	90	tags=23%, list=16%, signal=26%
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS		20	0,255	0,836	0,664	0,919	1	377	tags=85%, list=66%, signal=243%
GO_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS		22	0,245	0,835	0,661	0,918	1	256	tags=55%, list=45%, signal=95%
GO_IMMUNE_EFFECTOR_PROCESS	GO_IMMUNE_EFFECTOR_PROCESS		20	0,246	0,834	0,658	0,916	1	256	tags=55%, list=45%, signal=96%
GO_PHOSPHOLIPID_BINDING	GO_PHOSPHOLIPID_BINDING		18	0,257	0,833	0,668	0,914	1	84	tags=22%, list=15%, signal=25%
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT		20	0,243	0,833	0,687	0,912	1	59	tags=15%, list=10%, signal=16%

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GO_MICROTUBULE_BASED_PROCESS	GO_MICROTUBULE_BASED_PROCESS		29	0,233	0,832	0,672	0,911	1	327	tags=69%, list=57%, signal=154%
GO_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	GO_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS		35	0,224	0,831	0,679	0,909	1	84	tags=20%, list=15%, signal=22%
GO_SINGLE_ORGANISM_CELLULAR_LOCALIZATION	GO_SINGLE_ORGANISM_CELLULAR_LOCALIZATION		37	0,225	0,830	0,696	0,908	1	251	tags=51%, list=44%, signal=86%
GO_CELLULAR_LIPID_METABOLIC_PROCESS	GO_CELLULAR_LIPID_METABOLIC_PROCESS		30	0,230	0,829	0,693	0,908	1	317	tags=67%, list=56%, signal=143%
GO_MICROTUBULE_ORGANIZING_CENTER	GO_MICROTUBULE_ORGANIZING_CENTER		27	0,236	0,828	0,683	0,906	1	201	tags=44%, list=35%, signal=65%
GO_REGULATION_OF_PROTEOLYSIS	GO_REGULATION_OF_PROTEOLYSIS		30	0,230	0,827	0,681	0,906	1	259	tags=50%, list=46%, signal=87%
GO_CARBOHYDRATE_METABOLIC_PROCESS	GO_CARBOHYDRATE_METABOLIC_PROCESS		25	0,240	0,820	0,686	0,913	1	309	tags=68%, list=54%, signal=142%
GO_GROWTH	GO_GROWTH		20	0,249	0,820	0,687	0,911	1	191	tags=40%, list=34%, signal=58%
GO_POSITIVE_REGULATION_OF_CELL_DEATH	GO_POSITIVE_REGULATION_OF_CELL_DEATH		27	0,235	0,817	0,691	0,912	1	120	tags=22%, list=21%, signal=27%
GO_CATABOLIC_PROCESS	GO_CATABOLIC_PROCESS		68	0,201	0,816	0,738	0,911	1	360	tags=72%, list=63%, signal=173%
GO_MEMBRANE_ORGANIZATION	GO_MEMBRANE_ORGANIZATION		36	0,221	0,816	0,696	0,910	1	250	tags=53%, list=44%, signal=88%
GO_SINGLE_ORGANISM_BIOSYNTHETIC_PROCESS	GO_SINGLE_ORGANISM_BIOSYNTHETIC_PROCESS		51	0,203	0,801	0,737	0,929	1	241	tags=47%, list=42%, signal=74%
GO_POSITIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	GO_POSITIVE_REGULATION_OF_ORGANELLE_ORGANIZATION		29	0,227	0,799	0,681	0,929	1	90	tags=21%, list=16%, signal=23%
GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS		25	0,232	0,797	0,714	0,930	1	337	tags=72%, list=59%, signal=169%
GO_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS		41	0,208	0,796	0,722	0,928	1	259	tags=49%, list=46%, signal=83%
GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	GO_EXTRINSIC_COMPONENT_OF_MEMBRANE		17	0,250	0,795	0,694	0,927	1	430	tags=100%, list=76%, signal=397%
GO_NUCLEOLUS	GO_NUCLEOLUS		26	0,226	0,793	0,710	0,927	1	340	tags=73%, list=60%, signal=173%
GO_GOLGI_VESICLE_TRANSPORT	GO_GOLGI_VESICLE_TRANSPORT		22	0,234	0,791	0,697	0,928	1	72	tags=18%, list=13%, signal=20%
GO_CELLULAR_MACROMOLECULAR_COMPLEX_ASSEMBLY	GO_CELLULAR_MACROMOLECULAR_COMPLEX_ASSEMBLY		24	0,227	0,783	0,719	0,937	1	52	tags=13%, list=9%, signal=13%
GO_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	GO_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS		60	0,197	0,782	0,780	0,934	1	263	tags=50%, list=46%, signal=83%
GO_RESPONSE_TO_EXTERNAL_STIMULUS	GO_RESPONSE_TO_EXTERNAL_STIMULUS		53	0,202	0,780	0,772	0,935	1	276	tags=53%, list=49%, signal=93%
GO_PROTEIN_LOCALIZATION_TO_ORGANELLE	GO_PROTEIN_LOCALIZATION_TO_ORGANELLE		16	0,256	0,780	0,730	0,933	1	76	tags=19%, list=13%, signal=21%
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS		21	0,234	0,774	0,733	0,938	1	390	tags=86%, list=69%, signal=262%
GO_PLATELET_ACTIVATION	GO_PLATELET_ACTIVATION		20	0,235	0,773	0,721	0,936	1	196	tags=40%, list=34%, signal=59%
REACTOME_HEMOSTASIS	REACTOME_HEMOSTASIS		29	0,213	0,772	0,748	0,935	1	196	tags=38%, list=34%, signal=55%
GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS		16	0,248	0,770	0,749	0,936	1	166	tags=38%, list=29%, signal=51%
GO_CELLULAR_RESPONSE_TO_LIPID	GO_CELLULAR_RESPONSE_TO_LIPID		18	0,235	0,759	0,737	0,948	1	99	tags=22%, list=17%, signal=26%
REACTOME_IMMUNE_SYSTEM	REACTOME_IMMUNE_SYSTEM		43	0,198	0,757	0,786	0,947	1	215	tags=40%, list=38%, signal=59%
GO_POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	GO_POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY		63	0,189	0,757	0,814	0,945	1	201	tags=37%, list=35%, signal=50%
GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION		18	0,229	0,755	0,752	0,945	1	189	tags=39%, list=33%, signal=56%
GO_REGULATION_OF_NEURON_DIFFERENTIATION	GO_REGULATION_OF_NEURON_DIFFERENTIATION		22	0,222	0,754	0,752	0,943	1	59	tags=14%, list=10%, signal=15%
GO_REGULATION_OF_MITOTIC_CELL_CYCLE	GO_REGULATION_OF_MITOTIC_CELL_CYCLE		24	0,218	0,754	0,757	0,941	1	248	tags=50%, list=44%, signal=85%
GO_REGULATION_OF_IMMUNE_RESPONSE	GO_REGULATION_OF_IMMUNE_RESPONSE		37	0,199	0,750	0,780	0,944	1	144	tags=27%, list=25%, signal=34%
GO_MITOCHONDRION_ORGANIZATION	GO_MITOCHONDRION_ORGANIZATION		18	0,233	0,750	0,747	0,941	1	275	tags=56%, list=48%, signal=104%
GO_INTRACELLULAR_VESICLE	GO_INTRACELLULAR_VESICLE		56	0,191	0,749	0,792	0,939	1	324	tags=63%, list=57%, signal=131%
GO_MOLECULAR_FUNCTION_REGULATOR	GO_MOLECULAR_FUNCTION_REGULATOR		50	0,195	0,749	0,786	0,937	1	35	tags=10%, list=6%, signal=10%
GO_CELL_CORTEX	GO_CELL_CORTEX		22	0,223	0,741	0,763	0,945	1	246	tags=50%, list=43%, signal=85%
GO_TUBULIN_BINDING	GO_TUBULIN_BINDING		16	0,229	0,727	0,765	0,959	1	182	tags=38%, list=32%, signal=54%
GO_MACROMOLECULE_CATABOLIC_PROCESS	GO_MACROMOLECULE_CATABOLIC_PROCESS		32	0,202	0,726	0,788	0,958	1	356	tags=72%, list=63%, signal=181%

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GO_REGULATION_OF_CYTOPLASMIC_TRANSPORT	GO_REGULATION_OF_CYTOPLASMIC_TRANSPORT		19	0,221	0,719	0,789	0,963	1	284	tags=58%, list=50%, signal=112%
GO_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	GO_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY		21	0,218	0,714	0,794	0,967	1	275	tags=52%, list=48%, signal=98%
GO_HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDES	GO_HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDES		40	0,189	0,711	0,803	0,967	1	152	tags=30%, list=27%, signal=38%
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER		15	0,230	0,711	0,790	0,965	1	416	tags=93%, list=73%, signal=338%
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION		16	0,227	0,709	0,802	0,965	1	250	tags=50%, list=44%, signal=87%
GO_COFACTOR_BINDING	GO_COFACTOR_BINDING		20	0,211	0,704	0,794	0,968	1	35	tags=10%, list=6%, signal=10%
GO_VESICLE_MEDIATED_TRANSPORT	GO_VESICLE_MEDIATED_TRANSPORT		63	0,174	0,687	0,878	0,984	1	210	tags=37%, list=37%, signal=51%
GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION		16	0,216	0,680	0,827	0,989	1	248	tags=50%, list=44%, signal=86%
GO_CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	GO_CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS		33	0,189	0,679	0,847	0,987	1	435	tags=91%, list=76%, signal=364%
GO_POSITIVE_REGULATION_OF_CELL_CYCLE	GO_POSITIVE_REGULATION_OF_CELL_CYCLE		17	0,213	0,673	0,828	0,991	1	6	tags=6%, list=1%, signal=6%
GO_REGULATION_OF_CELL_CYCLE	GO_REGULATION_OF_CELL_CYCLE		37	0,181	0,671	0,841	0,991	1	256	tags=46%, list=45%, signal=78%
GO_DENDRITE	GO_DENDRITE		17	0,210	0,670	0,837	0,988	1	74	tags=18%, list=13%, signal=20%
GO_REGULATION_OF_CELL_CYCLE_PROCESS	GO_REGULATION_OF_CELL_CYCLE_PROCESS		23	0,198	0,670	0,827	0,986	1	248	tags=48%, list=44%, signal=81%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY		22	0,197	0,665	0,834	0,989	1	184	tags=36%, list=32%, signal=52%
GO_CELLULAR_CATABOLIC_PROCESS	GO_CELLULAR_CATABOLIC_PROCESS		49	0,169	0,660	0,886	0,991	1	360	tags=69%, list=63%, signal=173%
GO_VACUOLAR_MEMBRANE	GO_VACUOLAR_MEMBRANE		18	0,206	0,657	0,859	0,991	1	124	tags=22%, list=22%, signal=28%
GO_CELL_PART_MORPHOGENESIS	GO_CELL_PART_MORPHOGENESIS		21	0,197	0,653	0,844	0,992	1	59	tags=14%, list=10%, signal=15%
GO_REGULATION_OF_PROTEIN_LOCALIZATION	GO_REGULATION_OF_PROTEIN_LOCALIZATION		37	0,175	0,651	0,866	0,992	1	189	tags=32%, list=33%, signal=45%
GO_REGULATION_OF_GTPASE_ACTIVITY	GO_REGULATION_OF_GTPASE_ACTIVITY		33	0,176	0,650	0,862	0,991	1	121	tags=21%, list=21%, signal=25%
GO_GOLGI_APPARATUS_PART	GO_GOLGI_APPARATUS_PART		34	0,179	0,646	0,886	0,992	1	127	tags=24%, list=22%, signal=28%
GO_LYTIC_VACUOLE	GO_LYTIC_VACUOLE		19	0,198	0,645	0,858	0,990	1	36	tags=11%, list=6%, signal=11%
GO_CENTROSOME	GO_CENTROSOME		20	0,195	0,645	0,856	0,987	1	341	tags=70%, list=60%, signal=169%
GO_ENDOCYTOSIS	GO_ENDOCYTOSIS		23	0,189	0,643	0,863	0,987	1	407	tags=83%, list=72%, signal=278%
GO_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	GO_REGULATION_OF_CELL_PROJECTION_ORGANIZATION		24	0,186	0,639	0,856	0,987	1	266	tags=50%, list=47%, signal=90%
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM		16	0,203	0,637	0,861	0,987	1	410	tags=88%, list=72%, signal=304%
GO_PROTEIN_LOCALIZATION	GO_PROTEIN_LOCALIZATION		73	0,157	0,636	0,922	0,985	1	127	tags=22%, list=22%, signal=25%
GO_AUTOPHAGY	GO_AUTOPHAGY		17	0,198	0,636	0,845	0,983	1	52	tags=12%, list=9%, signal=13%
GO_NUCLEIC_ACID_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	GO_NUCLEIC_ACID_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY		19	0,195	0,635	0,867	0,981	1	289	tags=58%, list=51%, signal=114%
GO_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION		19	0,193	0,631	0,862	0,982	1	190	tags=37%, list=33%, signal=53%
GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE		21	0,186	0,629	0,868	0,981	1	144	tags=29%, list=25%, signal=37%
GO_GUANYL_NUCLEOTIDE_BINDING	GO_GUANYL_NUCLEOTIDE_BINDING		22	0,185	0,628	0,875	0,980	1	103	tags=18%, list=18%, signal=21%
GO_EMBRYONIC_MORPHOGENESIS	GO_EMBRYONIC_MORPHOGENESIS		18	0,192	0,626	0,864	0,979	1	334	tags=67%, list=59%, signal=156%
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	REACTOME_ADAPTIVE_IMMUNE_SYSTEM		27	0,179	0,625	0,861	0,977	1	250	tags=44%, list=44%, signal=76%
GO_SOMATODENDRITIC_COMPARTMENT	GO_SOMATODENDRITIC_COMPARTMENT		20	0,188	0,625	0,885	0,975	1	99	tags=20%, list=17%, signal=23%
KEGG_FOCAL_ADHESION	KEGG_FOCAL_ADHESION		23	0,176	0,613	0,885	0,982	1	423	tags=87%, list=74%, signal=325%
GO_LIPID_BINDING	GO_LIPID_BINDING		31	0,171	0,613	0,892	0,980	1	84	tags=16%, list=15%, signal=18%
GO_REGULATION_OF_KINASE_ACTIVITY	GO_REGULATION_OF_KINASE_ACTIVITY		24	0,176	0,609	0,879	0,981	1	248	tags=46%, list=44%, signal=78%
GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION		15	0,198	0,602	0,871	0,984	1	238	tags=47%, list=42%, signal=78%
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION		53	0,152	0,593	0,921	0,989	1	250	tags=43%, list=44%, signal=70%
GO_REGULATION_OF_SEQUENCE_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	GO_REGULATION_OF_SEQUENCE_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY		20	0,180	0,591	0,909	0,988	1	6	tags=5%, list=1%, signal=5%

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_MITOTIC_CELL_CYCLE	GO_MITOTIC_CELL_CYCLE		31	0,162	0,586	0,902	0,989	1	260	tags=48%, list=46%, signal=84%
GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS		24	0,172	0,583	0,916	0,989	1	302	tags=54%, list=53%, signal=111%
KEGG_PATHWAYS_IN_CANCER	KEGG_PATHWAYS_IN_CANCER		20	0,175	0,582	0,905	0,987	1	356	tags=70%, list=63%, signal=180%
GO_INTERSPECIES_INTERACTION_BETWEEN_ORGANISMS	GO_INTERSPECIES_INTERACTION_BETWEEN_ORGANISMS		30	0,163	0,580	0,906	0,986	1	402	tags=80%, list=71%, signal=258%
GO_CELL_CYCLE_PROCESS	GO_CELL_CYCLE_PROCESS		47	0,149	0,576	0,932	0,986	1	260	tags=47%, list=46%, signal=79%
GO_PROTEIN_CATABOLIC_PROCESS	GO_PROTEIN_CATABOLIC_PROCESS		25	0,164	0,576	0,906	0,984	1	231	tags=40%, list=41%, signal=64%
GO_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	GO_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY		16	0,183	0,575	0,926	0,982	1	230	tags=44%, list=40%, signal=71%
GO_REGULATION_OF_SECRETION	GO_REGULATION_OF_SECRETION		20	0,174	0,574	0,930	0,980	1	187	tags=35%, list=33%, signal=50%
GO_ENDOSOME	GO_ENDOSOME		24	0,165	0,571	0,898	0,980	1	33	tags=8%, list=6%, signal=8%
GO_ADENYL_NUCLEOTIDE_BINDING	GO_ADENYL_NUCLEOTIDE_BINDING		63	0,141	0,569	0,931	0,979	1	342	tags=62%, list=60%, signal=138%
GO_VACUOLE	GO_VACUOLE		36	0,149	0,555	0,922	0,985	1	36	tags=8%, list=6%, signal=8%
GO_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	GO_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION		24	0,159	0,549	0,920	0,987	1	278	tags=50%, list=49%, signal=94%
GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT		19	0,167	0,545	0,929	0,986	1	334	tags=63%, list=59%, signal=148%
GO_INTRACELLULAR_PROTEIN_TRANSPORT	GO_INTRACELLULAR_PROTEIN_TRANSPORT		28	0,152	0,542	0,935	0,986	1	212	tags=36%, list=37%, signal=54%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON		22	0,157	0,541	0,956	0,984	1	246	tags=45%, list=43%, signal=77%
GO_GTPASE_ACTIVITY	GO_GTPASE_ACTIVITY		16	0,169	0,538	0,917	0,984	1	273	tags=50%, list=48%, signal=93%
GO_CELLULAR_MACROMOLECULE_LOCALIZATION	GO_CELLULAR_MACROMOLECULE_LOCALIZATION		50	0,138	0,536	0,945	0,982	1	282	tags=48%, list=50%, signal=87%
GO_REGULATION_OF_AUTOPHAGY	GO_REGULATION_OF_AUTOPHAGY		18	0,164	0,526	0,946	0,985	1	267	tags=50%, list=47%, signal=91%
GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION		18	0,162	0,525	0,937	0,984	1	199	tags=33%, list=35%, signal=50%
GO_MITOTIC_NUCLEAR_DIVISION	GO_MITOTIC_NUCLEAR_DIVISION		23	0,150	0,505	0,948	0,991	1	201	tags=35%, list=35%, signal=52%
GO_RIBONUCLEOTIDE_BINDING	GO_RIBONUCLEOTIDE_BINDING		83	0,124	0,505	0,979	0,989	1	52	tags=10%, list=9%, signal=9%
GO_REGULATION_OF_TRANSFERASE_ACTIVITY	GO_REGULATION_OF_TRANSFERASE_ACTIVITY		30	0,139	0,498	0,947	0,990	1	300	tags=53%, list=53%, signal=107%
GO_DNA_METABOLIC_PROCESS	GO_DNA_METABOLIC_PROCESS		25	0,142	0,493	0,967	0,989	1	185	tags=32%, list=33%, signal=45%
GO_RNA_PROCESSING	GO_RNA_PROCESSING		18	0,152	0,493	0,955	0,987	1	229	tags=39%, list=40%, signal=63%
GO_PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	GO_PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY		19	0,150	0,487	0,965	0,987	1	447	tags=89%, list=79%, signal=403%
GO_HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS	GO_HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS		29	0,130	0,469	0,968	0,992	1	460	tags=90%, list=81%, signal=444%
GO_ENZYME_REGULATOR_ACTIVITY	GO_ENZYME_REGULATOR_ACTIVITY		33	0,127	0,458	0,966	0,994	1	93	tags=15%, list=16%, signal=17%
GO_ORGANELLE_FISSION	GO_ORGANELLE_FISSION		31	0,127	0,453	0,976	0,993	1	267	tags=45%, list=47%, signal=80%
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION		15	0,151	0,452	0,986	0,991	1	196	tags=33%, list=34%, signal=50%
GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION		24	0,127	0,437	0,979	0,993	1	189	tags=29%, list=33%, signal=42%
GO_ESTABLISHMENT_OF_LOCALIZATION_IN_CELL	GO_ESTABLISHMENT_OF_LOCALIZATION_IN_CELL		71	0,110	0,436	0,991	0,991	1	33	tags=7%, list=6%, signal=7%
GO_ACTIVATION_OF_IMMUNE_RESPONSE	GO_ACTIVATION_OF_IMMUNE_RESPONSE		17	0,133	0,426	0,981	0,991	1	248	tags=41%, list=44%, signal=71%
GO_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	GO_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY		18	0,127	0,412	0,988	0,992	1	60	tags=11%, list=11%, signal=12%
GO_ENDOMEMBRANE_SYSTEM_ORGANIZATION	GO_ENDOMEMBRANE_SYSTEM_ORGANIZATION		22	0,119	0,400	0,987	0,992	1	375	tags=68%, list=66%, signal=192%
GO_ENZYME_ACTIVATOR_ACTIVITY	GO_ENZYME_ACTIVATOR_ACTIVITY		16	0,127	0,394	0,990	0,991	1	199	tags=31%, list=35%, signal=47%