Supplementary Table 6. Significantly enriched pathways in the GSEA of glandular epithelial cells

Pathway name	S6 vs C3					S6 vs M3+C3					S6 vs M3				
	SIZE	ES	NES	NOM p-value	FDR q-value	SIZE	ES	NES	NOM p-value	FDR q-value	SIZE	ES	NES	NOM p-value	FDR q-value
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	197	0.532	2.195	0.000	0.000	197	0.447	1.798	0.000	0.000	197	0.263	1.058	0.305	0.372
HALLMARK_APICAL_JUNCTION	194	0.507	2.090	0.000	0.000	194	0.458	1.846	0.000	0.000	194	0.331	1.347	0.010	0.077
REACTOME_SMOOTH_MUSCLE_CONTRACTION	35	0.725	2.263	0.000	0.000	35	0.679	2.088	0.000	0.003	35	0.470	1.448	0.044	0.195
HALLMARK_KRAS_SIGNALING_UP	193	0.448	1.838	0.000	0.001	193	0.493	1.983	0.000	0.001	193	0.470	1.889	0.000	0.001
GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	44	0.676	2.205	0.000	0.001	44	0.652	2.068	0.000	0.004	44	0.609	1.921	0.000	0.075
HALLMARK_TGF_BETA_SIGNALING	54	0.539	1.848	0.000	0.001	54	0.533	1.741	0.000	0.003	54	0.467	1.555	0.016	0.043
HALLMARK_INTERFERON_ALPHA_RESPONSE	95	0.465	1.736	0.000	0.002	95	0.518	1.881	0.000	0.000	95	0.412	1.482	0.013	0.034

HALLMARK_ALLOGRAFT_REJECTION	194	0.419	1.718	0.000	0.002	194	0.338	1.357	0.010	0.056	194	0.265	1.084	0.246	0.350
HALLMARK_COMPLEMENT	198	0.425	1.743	0.000	0.002	198	0.404	1.620	0.000	0.006	198	0.307	1.254	0.051	0.149
GO_PLASMINOGEN_ACTIVATION	24	0.764	2.158	0.000	0.003	24	0.757	2.151	0.000	0.001	24	0.635	1.776	0.006	0.147
HALLMARK_IL2_STAT5_SIGNALING	195	0.401	1.668	0.000	0.004	195	0.354	1.405	0.004	0.040	195	0.269	1.091	0.224	0.357
REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	27	0.677	2.003	0.000	0.005	27	0.596	1.702	0.006	0.050	27	0.295	0.853	0.700	0.866
REACTOME_SIGNALING_BY_VEGF	103	0.531	2.007	0.000	0.005	103	0.506	1.877	0.000	0.015	103	0.390	1.433	0.019	0.206
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	32	0.649	1.995	0.000	0.005	32	0.656	1.931	0.000	0.014	32	0.549	1.607	0.018	0.099
REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS	18	0.768	2.014	0.000	0.005	18	0.843	2.178	0.000	0.001	18	0.681	1.785	0.002	0.025
REACTOME_VEGFR2_MEDIATED_CELL_PROLIFERATION	19	0.737	1.984	0.000	0.006	19	0.662	1.760	0.004	0.043	19	0.557	1.485	0.039	0.171

REACTOME_CELL_JUNCTION_ORGANIZATION	85	0.545	2.018	0.000	0.007	85	0.470	1.678	0.004	0.055	85	0.361	1.310	0.056	0.330
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_TRANSPORT_AND_UPTAKE_BY_INSULIN_LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS	120	0.512	1.965	0.000	0.007	120	0.439	1.641	0.002	0.069	120	0.272	1.040	0.353	0.648
REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS	38	0.639	2.021	0.000	0.008	38	0.599	1.861	0.000	0.017	38	0.462	1.444	0.042	0.199
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	153	0.519	2.084	0.000	0.008	153	0.512	1.986	0.000	0.014	153	0.442	1.749	0.000	0.154
GO_POSITIVE_REGULATION_OF_AXONOGENESIS	87	0.561	2.071	0.000	0.008	87	0.505	1.802	0.002	0.057	87	0.424	1.525	0.010	0.273
GO_PLATELET_AGGREGATION	59	0.602	2.086	0.000	0.009	59	0.577	1.925	0.000	0.023	59	0.500	1.715	0.002	0.181
REACTOME_EPHB_MEDIATED_FORWARD_SIGNALING	41	0.638	2.036	0.000	0.011	41	0.614	1.894	0.000	0.017	41	0.482	1.505	0.019	0.160
HALLMARK_INFLAMMATORY_RESPONSE	198	0.379	1.551	0.000	0.011	198	0.362	1.445	0.002	0.029	198	0.338	1.380	0.008	0.064
GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	52	0.597	2.043	0.000	0.011	52	0.643	2.098	0.000	0.003	52	0.542	1.798	0.000	0.128

GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	35	0.674	2.088	0.000	0.011	35	0.734	2.212	0.000	0.000	35	0.616	1.914	0.000	0.062
GO_REGULATION_OF_CELLULAR_EXTRAVASATION	27	0.690	2.015	0.000	0.012	27	0.576	1.647	0.017	0.112	27	0.445	1.279	0.156	0.426
GO_REGULATION_OF_RECEPTOR_BINDING	24	0.706	2.007	0.000	0.012	24	0.742	2.064	0.000	0.004	24	0.488	1.375	0.083	0.373
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	43	0.612	1.997	0.000	0.012	43	0.615	1.972	0.000	0.017	43	0.480	1.511	0.017	0.281
GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	37	0.634	2.016	0.000	0.013	37	0.619	1.876	0.002	0.036	37	0.460	1.414	0.052	0.348
HALLMARK_MITOTIC_SPINDLE	198	0.374	1.532	0.000	0.013	198	0.413	1.652	0.000	0.006	198	0.349	1.410	0.006	0.054
GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	22	0.705	1.989	0.000	0.013	22	0.535	1.452	0.057	0.201	22	-0.365	-1.000	0.437	0.759
GO_DETOXIFICATION_OF_INORGANIC_COMPOUND	17	0.761	1.991	0.000	0.013	17	0.753	1.943	0.000	0.020	17	0.708	1.866	0.004	0.091
GO_RESPONSE_TO_COPPER_ION	39	0.631	1.998	0.000	0.013	39	0.630	1.947	0.000	0.020	39	0.501	1.534	0.018	0.265

GO_NEUROMUSCULAR_SYNAPTIC_TRANSMISSION	31	0.681	2.024	0.000	0.014	31	0.634	1.839	0.004	0.048	31	0.504	1.501	0.037	0.287
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	17	0.780	2.017	0.000	0.014	17	0.644	1.635	0.010	0.119	17	0.567	1.451	0.060	0.326
GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	96	0.534	1.974	0.000	0.015	96	0.539	1.938	0.000	0.020	96	0.451	1.654	0.002	0.202
HALLMARK_INTERFERON_GAMMA_RESPONSE	197	0.355	1.474	0.000	0.016	197	0.384	1.537	0.002	0.012	197	0.290	1.169	0.114	0.250
GO_POSITIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	48	0.585	1.966	0.000	0.016	48	0.524	1.670	0.004	0.104	48	0.350	1.139	0.219	0.536
HALLMARK_COAGULATION	136	0.376	1.477	0.004	0.016	136	0.391	1.500	0.000	0.017	136	-0.277	-1.061	0.328	0.387
REACTOME_RHO_GTPASES_ACTIVATE_IQGAPS	30	0.625	1.860	0.000	0.017	30	0.589	1.716	0.004	0.047	30	0.406	1.193	0.197	0.490
REACTOME_KINESINS	59	0.538	1.855	0.000	0.017	59	0.553	1.847	0.000	0.018	59	0.430	1.455	0.033	0.191
GO_DORSAL_SPINAL_CORD_DEVELOPMENT	22	0.696	1.958	0.004	0.017	22	0.556	1.526	0.037	0.164	22	0.478	1.336	0.098	0.402

REACTOME_MET_ACTIVATES_PTK2_SIGNALING	30	0.628	1.861	0.002	0.017	30	0.662	1.957	0.000	0.012	30	0.527	1.558	0.031	0.126
GO_REGULATION_OF_EXTENT_OF_CELL_GROWTH	107	0.518	1.951	0.000	0.017	107	0.495	1.826	0.000	0.052	107	0.413	1.547	0.004	0.264
GO_NEGATIVE_REGULATION_OF_COAGULATION	54	0.567	1.944	0.000	0.017	54	0.535	1.760	0.000	0.071	54	0.386	1.293	0.095	0.415
GO_HOMOTYPIC_CELL_CELL_ADHESION	79	0.538	1.941	0.000	0.018	79	0.464	1.617	0.004	0.126	79	0.390	1.409	0.038	0.354
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	58	0.570	1.952	0.000	0.018	58	0.545	1.845	0.000	0.045	58	0.416	1.387	0.045	0.367
REACTOME_RHO_GTPASE_CYCLE	135	0.469	1.863	0.000	0.018	135	0.464	1.758	0.000	0.042	135	0.406	1.585	0.004	0.109
GO_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	93	0.521	1.944	0.000	0.018	93	0.555	2.006	0.000	0.010	93	0.446	1.622	0.000	0.210
GO_ACTIN_FILAMENT_ORGANIZATION	368	0.445	1.945	0.000	0.018	368	0.449	1.916	0.000	0.025	368	0.374	1.629	0.000	0.211
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3	94	0.504	1.874	0.000	0.018	94	0.520	1.879	0.000	0.016	94	0.477	1.753	0.000	0.031

REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	15	0.724	1.864	0.004	0.018	15	0.759	1.912	0.000	0.014	15	0.704	1.763	0.000	0.029
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	23	0.670	1.867	0.000	0.019	23	0.558	1.528	0.031	0.113	23	0.310	0.865	0.680	0.865
REACTOME_CELL_CELL_COMMUNICATION	121	0.488	1.876	0.000	0.019	121	0.462	1.737	0.000	0.043	121	0.374	1.422	0.014	0.216
GO_SMOOTH_MUSCLE_CELL_MIGRATION	66	0.547	1.934	0.000	0.019	66	0.630	2.128	0.000	0.001	66	0.549	1.897	0.000	0.076
GO_REGULATION_OF_AXONOGENESIS	181	0.469	1.915	0.000	0.019	181	0.431	1.703	0.000	0.095	181	0.327	1.311	0.039	0.413
GO_AXON_EXTENSION	120	0.498	1.928	0.000	0.019	120	0.479	1.784	0.000	0.060	120	0.406	1.549	0.002	0.262
GO_CELLULAR_RESPONSE_TO_COPPER_ION	27	0.660	1.917	0.000	0.019	27	0.625	1.825	0.000	0.051	27	0.507	1.447	0.054	0.331
GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	109	0.506	1.918	0.000	0.020	109	0.466	1.737	0.002	0.081	109	0.424	1.583	0.002	0.233
GO_FIBRINOLYSIS	28	0.645	1.929	0.000	0.020	28	0.614	1.784	0.004	0.061	28	0.501	1.454	0.050	0.324

REACTOME_EPH_EPHRIN_SIGNALING	91	0.495	1.840	0.000	0.020	91	0.453	1.636	0.002	0.068	91	0.322	1.182	0.152	0.498
GO_T_CELL_MIGRATION	63	0.554	1.919	0.000	0.020	63	0.387	1.311	0.069	0.275	63	-0.261	-0.888	0.676	0.866
REACTOME_G_ALPHA_12_13_SIGNALLING_EVENTS	78	0.517	1.876	0.000	0.020	78	0.484	1.690	0.002	0.051	78	0.373	1.336	0.044	0.302
GO_EMBRYO_IMPLANTATION	46	0.585	1.908	0.000	0.021	46	0.534	1.713	0.000	0.088	46	0.449	1.453	0.040	0.324
GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	29	0.638	1.919	0.002	0.021	29	0.618	1.782	0.002	0.060	29	0.515	1.503	0.022	0.285
GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	19	0.708	1.921	0.004	0.021	19	0.654	1.744	0.004	0.079	19	0.521	1.378	0.082	0.374
GO_CELL_JUNCTION_ORGANIZATION	281	0.444	1.896	0.000	0.021	281	0.390	1.627	0.000	0.123	281	-0.287	-1.212	0.041	0.594
GO_MEMBRANE_RAFT_ORGANIZATION	23	0.676	1.904	0.000	0.021	23	0.585	1.617	0.012	0.126	23	0.446	1.235	0.195	0.455
GO_REGULATION_OF_ACTIN_FILAMENT_ORGANIZATION	238	0.449	1.896	0.000	0.022	238	0.462	1.893	0.000	0.033	238	0.406	1.690	0.000	0.184

REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	129	0.468	1.832	0.000	0.022	129	0.408	1.561	0.008	0.095	129	0.296	1.133	0.198	0.533
REACTOME_LDL_CLEARANCE	19	0.705	1.877	0.000	0.022	19	0.747	1.915	0.000	0.015	19	0.678	1.806	0.002	0.021
GO_EPIBOLY	29	0.653	1.897	0.000	0.022	29	0.434	1.235	0.165	0.333	29	-0.415	-1.192	0.232	0.609
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	30	0.624	1.899	0.000	0.022	30	0.646	1.910	0.000	0.026	30	0.568	1.716	0.004	0.189
REACTOME_GAP_JUNCTION_TRAFFICKING_AND_REGULATION	50	0.555	1.826	0.000	0.022	50	0.432	1.411	0.047	0.174	50	-0.377	-1.220	0.145	0.484
REACTOME_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY	54	0.554	1.881	0.000	0.022	54	0.588	1.944	0.000	0.012	54	0.629	2.126	0.000	0.000
GO_PODOSOME_ASSEMBLY	19	0.701	1.900	0.000	0.022	19	0.628	1.610	0.014	0.127	19	0.416	1.101	0.339	0.564
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	21	0.657	1.817	0.000	0.023	21	0.537	1.419	0.073	0.167	21	0.253	0.688	0.925	0.981
REACTOME_SIGNALLING_TO_RAS	20	0.680	1.819	0.002	0.023	20	0.556	1.484	0.040	0.135	20	0.409	1.092	0.331	0.570

REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	15	0.721	1.808	0.006	0.025	15	0.632	1.567	0.018	0.095	15	0.487	1.221	0.214	0.453
GO_NEURON_PROJECTION_EXTENSION	163	0.474	1.881	0.000	0.025	163	0.464	1.804	0.000	0.058	163	0.379	1.494	0.004	0.292
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	37	0.599	1.883	0.002	0.025	37	0.657	2.024	0.000	0.008	37	0.539	1.651	0.006	0.203
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_SIGNALING_PATHWAY	33	0.610	1.877	0.000	0.026	33	0.541	1.616	0.008	0.125	33	0.451	1.358	0.080	0.385
GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	28	0.632	1.874	0.002	0.026	28	0.585	1.659	0.006	0.109	28	0.461	1.308	0.108	0.412
REACTOME_REGULATION_OF_RAS_BY_GAPS	67	0.499	1.793	0.000	0.027	67	0.534	1.853	0.000	0.017	67	0.598	2.043	0.000	0.001
REACTOME_COPI_DEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC	95	0.486	1.796	0.000	0.027	95	0.456	1.635	0.000	0.067	95	0.329	1.187	0.162	0.499
REACTOME_PCP_CE_PATHWAY	90	0.490	1.789	0.000	0.027	90	0.528	1.867	0.000	0.016	90	0.544	1.967	0.000	0.006
GO_MUSCLE_CELL_MIGRATION	79	0.521	1.861	0.000	0.028	79	0.630	2.187	0.000	0.001	79	0.555	1.971	0.000	0.091

GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	348	0.428	1.861	0.000	0.028	348	0.426	1.803	0.000	0.057	348	0.373	1.621	0.000	0.206
GO_CELL_JUNCTION_ASSEMBLY	239	0.442	1.861	0.000	0.029	239	0.402	1.650	0.000	0.111	239	0.300	1.236	0.056	0.454
GO_ESTABLISHMENT_OF_ENDOTHELIAL_BARRIER	40	0.596	1.863	0.000	0.029	40	0.516	1.578	0.007	0.142	40	0.355	1.112	0.285	0.559
GO_PINOCYTOSIS	20	0.692	1.857	0.002	0.029	20	0.546	1.442	0.067	0.204	20	0.362	0.970	0.488	0.705
REACTOME_O_LINKED_GLYCOSYLATION	103	0.471	1.770	0.000	0.029	103	0.451	1.649	0.000	0.067	103	0.324	1.200	0.154	0.483
GO_TRACHEA_DEVELOPMENT	20	0.672	1.853	0.002	0.029	20	0.671	1.785	0.004	0.063	20	0.526	1.428	0.082	0.343
GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	26	0.630	1.852	0.000	0.029	26	0.559	1.565	0.012	0.147	26	0.333	0.955	0.491	0.727
GO_LONG_TERM_SYNAPTIC_POTENTIATION	85	0.505	1.866	0.000	0.029	85	0.414	1.474	0.012	0.188	85	0.278	0.999	0.428	0.671
REACTOME_CRMPS_IN_SEMA3A_SIGNALING	16	0.681	1.767	0.000	0.029	16	0.802	1.998	0.000	0.010	16	0.563	1.454	0.072	0.190

GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	293	0.436	1.863	0.000	0.029	293	0.444	1.851	0.000	0.042	293	0.372	1.579	0.000	0.235
GO_CELL_SUBSTRATE_JUNCTION_ORGANIZATION	97	0.500	1.854	0.000	0.029	97	0.440	1.590	0.002	0.134	97	0.333	1.235	0.105	0.454
REACTOME_SYNDECAN_INTERACTIONS	27	0.593	1.772	0.006	0.029	27	0.468	1.335	0.113	0.241	27	0.409	1.172	0.216	0.507
GO_REGULATION_OF_SYNAPTIC_PLASTICITY	182	0.453	1.864	0.000	0.029	182	0.380	1.507	0.000	0.171	182	0.296	1.189	0.104	0.493
REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	141	0.457	1.778	0.000	0.030	141	0.492	1.883	0.000	0.016	141	0.478	1.867	0.000	0.011
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	26	0.620	1.773	0.002	0.030	26	0.665	1.878	0.000	0.015	26	0.587	1.669	0.008	0.064
GO_REGULATION_OF_CELL_MORPHOGENESIS	473	0.411	1.849	0.000	0.030	473	0.432	1.883	0.000	0.036	473	0.360	1.601	0.000	0.230
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	96	0.474	1.775	0.000	0.030	96	0.449	1.658	0.000	0.062	96	0.415	1.499	0.006	0.161
GO_CHONDROCYTE_DIFFERENTIATION	116	0.482	1.846	0.000	0.030	116	0.418	1.566	0.006	0.147	116	0.291	1.088	0.267	0.576

GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	36	0.597	1.842	0.000	0.031	36	0.575	1.748	0.002	0.079	36	0.433	1.338	0.072	0.402
REACTOME_RECYCLING_PATHWAY_OF_L1	47	0.541	1.759	0.000	0.031	47	0.613	1.964	0.000	0.013	47	0.498	1.630	0.012	0.085
REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	33	0.581	1.761	0.002	0.031	33	0.466	1.389	0.081	0.189	33	-0.357	-1.046	0.375	0.685
GO_REGULATION_OF_PODOSOME_ASSEMBLY	15	0.721	1.842	0.008	0.031	15	0.714	1.808	0.006	0.058	15	0.546	1.340	0.116	0.400
GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	190	0.450	1.843	0.000	0.031	190	0.470	1.877	0.000	0.038	190	0.406	1.650	0.000	0.201
GO_REGULATION_OF_PLATELET_AGGREGATION	18	0.687	1.838	0.000	0.032	18	0.669	1.733	0.006	0.080	18	0.457	1.193	0.230	0.488
GO_REGULATION_OF_RENAL_SYSTEM_PROCESS	35	0.582	1.827	0.000	0.033	35	0.411	1.221	0.182	0.344	35	-0.330	-0.994	0.465	0.766
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	356	0.418	1.828	0.000	0.034	356	0.362	1.537	0.000	0.160	356	-0.246	-1.039	0.336	0.726
REACTOME_DISEASES_ASSOCIATED_WITH_O_GLYCOSYLATION_OF_PROTEINS	64	0.498	1.748	0.000	0.034	64	0.469	1.600	0.004	0.082	64	0.343	1.191	0.148	0.490

GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_SECRETION	31	0.606	1.828	0.000	0.034	31	0.496	1.446	0.039	0.202	31	0.301	0.902	0.635	0.794
GO_POSITIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	51	0.544	1.831	0.000	0.034	51	0.568	1.867	0.000	0.037	51	0.446	1.478	0.016	0.312
GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	19	0.677	1.828	0.000	0.034	19	0.580	1.494	0.051	0.175	19	0.327	0.859	0.683	0.853
REACTOME_REGULATION_OF_ACTIN_DYNAMICS_FOR_PHAGOCYTIC_CUP_FORMATION	60	0.496	1.743	0.002	0.035	60	0.520	1.742	0.004	0.043	60	0.532	1.789	0.000	0.024
GO_ENDODERM_FORMATION	50	0.546	1.824	0.000	0.035	50	0.580	1.856	0.000	0.042	50	0.494	1.621	0.002	0.209
REACTOME_SIGNALING_BY_RAS_MUTANTS	58	0.517	1.739	0.000	0.035	58	0.498	1.660	0.002	0.062	58	0.464	1.562	0.006	0.123
GO_POSITIVE_REGULATION_OF_CELLULAR_EXTRAVASATION	16	0.703	1.821	0.006	0.036	16	0.642	1.606	0.012	0.128	16	0.498	1.261	0.165	0.433
REACTOME_NON_INTEGRIN_MEMBRANE_ECM_INTERACTIONS	59	0.510	1.734	0.002	0.037	59	0.418	1.422	0.043	0.166	59	0.312	1.052	0.346	0.626
GO_CELLULAR_RESPONSE_TO_ZINC_ION	23	0.649	1.818	0.002	0.037	23	0.683	1.869	0.006	0.038	23	0.689	1.962	0.000	0.052

GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	21	0.663	1.814	0.002	0.038	21	0.587	1.553	0.033	0.152	21	0.276	0.755	0.822	0.939
GO_INACTIVATION_OF_MAPK_ACTIVITY	27	0.619	1.812	0.002	0.039	27	0.616	1.760	0.000	0.072	27	0.581	1.680	0.008	0.190
GO_ENDOTHELIAL_CELL_DEVELOPMENT	55	0.542	1.811	0.000	0.039	55	0.517	1.699	0.002	0.093	55	0.431	1.442	0.022	0.336
GO_POSITIVE_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	16	0.694	1.798	0.004	0.040	16	0.793	1.971	0.000	0.016	16	0.756	1.875	0.000	0.086
GO_LENS_FIBER_CELL_DIFFERENTIATION	29	0.611	1.799	0.000	0.040	29	0.588	1.736	0.006	0.079	29	0.480	1.418	0.061	0.346
GO_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	147	0.458	1.807	0.000	0.040	147	0.433	1.680	0.000	0.100	147	0.362	1.421	0.014	0.346
REACTOME_CELLULAR_HEXOSE_TRANSPORT	20	0.637	1.724	0.010	0.040	20	0.516	1.400	0.084	0.185	20	0.434	1.183	0.243	0.499
GO_REGULATION_OF_CELL_SIZE	172	0.446	1.799	0.000	0.040	172	0.424	1.668	0.000	0.105	172	0.363	1.453	0.006	0.324
GO_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	362	0.412	1.799	0.000	0.041	362	0.389	1.673	0.000	0.105	362	0.293	1.264	0.022	0.435

GO_REGULATION_OF_T_CELL_MIGRATION	42	0.564	1.800	0.002	0.041	42	0.369	1.134	0.279	0.430	42	-0.338	-1.066	0.344	0.713
GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	226	0.431	1.803	0.000	0.041	226	0.425	1.712	0.000	0.087	226	0.337	1.377	0.010	0.373
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	358	0.412	1.801	0.000	0.041	358	0.420	1.788	0.000	0.062	358	0.339	1.473	0.000	0.316
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2PLUS	130	0.441	1.716	0.000	0.041	130	0.431	1.637	0.000	0.068	130	0.297	1.147	0.185	0.522
GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	25	0.636	1.803	0.000	0.041	25	0.583	1.632	0.016	0.120	25	0.309	0.865	0.650	0.847
GO_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	43	0.561	1.801	0.000	0.041	43	0.437	1.397	0.065	0.228	43	0.288	0.899	0.641	0.797
REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	20	0.634	1.717	0.000	0.042	20	0.572	1.527	0.033	0.113	20	0.401	1.084	0.337	0.581
REACTOME_THE_ROLE_OF_NEF_IN_HIV_1_REPLICATION_AND_DISEASE_PATHOGENESIS	27	0.597	1.718	0.004	0.042	27	0.511	1.466	0.049	0.142	27	-0.227	-0.662	0.929	1.000
GO_POSTSYNAPTIC_CYTOSKELETON_ORGANIZATION	18	0.671	1.789	0.000	0.043	18	0.655	1.741	0.002	0.080	18	0.550	1.434	0.081	0.339

GO_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	178	0.440	1.790	0.000	0.043	178	0.397	1.577	0.000	0.142	178	0.270	1.103	0.220	0.564
GO_RETINAL_GANGLION_CELL_AXON_GUIDANCE	21	0.656	1.787	0.004	0.043	21	0.467	1.273	0.157	0.301	21	-0.298	-0.807	0.747	0.925
GO_ZINC_ION_HOMEOSTASIS	37	0.570	1.785	0.000	0.044	37	0.502	1.551	0.024	0.153	37	0.410	1.283	0.122	0.423
GO_PLATELET_ACTIVATION	152	0.444	1.770	0.000	0.044	152	0.414	1.601	0.000	0.131	152	0.388	1.527	0.002	0.271
GO_HIPPO_SIGNALING	38	0.564	1.768	0.007	0.044	38	0.498	1.504	0.022	0.171	38	0.293	0.918	0.587	0.778
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	87	0.480	1.767	0.000	0.044	87	0.448	1.598	0.002	0.132	87	0.316	1.136	0.239	0.541
GO_EXTRACELLULAR_MATRIX_ASSEMBLY	40	0.554	1.768	0.006	0.044	40	0.481	1.502	0.018	0.172	40	0.382	1.197	0.191	0.486
GO_KERATAN_SULFATE_METABOLIC_PROCESS	33	0.580	1.770	0.004	0.044	33	0.478	1.440	0.050	0.204	33	-0.360	-1.087	0.331	0.697
REACTOME_INTERLEUKIN_10_SIGNALING	45	0.521	1.707	0.004	0.045	45	0.492	1.572	0.016	0.095	45	0.365	1.175	0.195	0.509

REACTOME_SIGNAL_TRANSDUCTION_BY_L1	19	0.631	1.705	0.012	0.045	19	0.505	1.339	0.126	0.237	19	0.239	0.644	0.943	0.983
GO_CELL_SUBSTRATE_ADHESION	333	0.411	1.773	0.000	0.045	333	0.399	1.687	0.000	0.096	333	0.323	1.391	0.004	0.365
GO_POSITIVE_REGULATION_OF_NEUTROPHIL_MIGRATION	27	0.604	1.774	0.002	0.045	27	0.528	1.502	0.047	0.172	27	0.346	0.999	0.436	0.672
GO_NEPHRON_TUBULE_EPITHELIAL_CELL_DIFFERENTIATION	15	0.702	1.772	0.002	0.045	15	0.639	1.590	0.026	0.134	15	0.461	1.157	0.288	0.514
GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	477	0.394	1.771	0.000	0.045	477	0.385	1.679	0.000	0.101	477	0.302	1.333	0.002	0.408
GO_CELLULAR_EXTRAVASATION	60	0.511	1.770	0.000	0.045	60	0.429	1.432	0.027	0.207	60	0.276	0.936	0.596	0.753
GO_NEGATIVE_REGULATION_OF_WOUND_HEALING	72	0.499	1.777	0.000	0.045	72	0.492	1.717	0.000	0.086	72	0.400	1.401	0.030	0.361
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	476	0.394	1.775	0.000	0.045	476	0.395	1.722	0.000	0.084	476	0.352	1.563	0.000	0.250
GO_MAST_CELL_MEDIATED_IMMUNITY	45	0.548	1.781	0.002	0.045	45	0.561	1.769	0.000	0.067	45	0.494	1.598	0.009	0.226

GO_REGULATION_OF_AMPA_RECEPTOR_ACTIVITY	24	0.633	1.774	0.002	0.045	24	0.479	1.331	0.109	0.263	24	0.301	0.834	0.705	0.876
GO_DENDRITIC_SPINE_MORPHOGENESIS	59	0.511	1.776	0.000	0.045	59	0.485	1.616	0.004	0.125	59	0.327	1.108	0.269	0.562
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	122	0.431	1.688	0.002	0.045	122	0.380	1.441	0.015	0.157	122	-0.281	-1.062	0.320	0.662
GO_REGULATION_OF_COAGULATION	81	0.494	1.778	0.000	0.045	81	0.442	1.549	0.002	0.154	81	-0.302	-1.066	0.315	0.715
GO_CHONDROCYTE_DEVELOPMENT	44	0.539	1.764	0.004	0.045	44	0.522	1.624	0.002	0.121	44	0.299	0.949	0.538	0.730
GO_REGULATION_OF_PLATELET_ACTIVATION	31	0.587	1.779	0.000	0.045	31	0.589	1.702	0.006	0.094	31	0.336	0.997	0.446	0.674
GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_PROCESS	62	0.510	1.780	0.000	0.045	62	0.479	1.629	0.014	0.123	62	0.408	1.396	0.038	0.365
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	39	0.560	1.763	0.004	0.046	39	0.584	1.793	0.000	0.062	39	0.320	1.010	0.448	0.660
REACTOME_METABOLISM_OF_POLYAMINES	58	0.497	1.689	0.004	0.046	58	0.544	1.837	0.000	0.019	58	0.567	1.927	0.000	0.006

REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	293	0.395	1.692	0.000	0.046	293	0.359	1.500	0.000	0.126	293	0.247	1.040	0.325	0.648
GO_POSITIVE_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELL_MIGRATION	16	0.666	1.758	0.006	0.046	16	0.748	1.877	0.000	0.037	16	0.651	1.678	0.006	0.187
REACTOME_NEUREXINS_AND_NEUROLIGINS	56	0.489	1.682	0.000	0.046	56	0.403	1.323	0.078	0.252	56	0.401	1.348	0.065	0.290
REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHESIS	60	0.492	1.693	0.000	0.046	60	0.510	1.734	0.002	0.041	60	0.437	1.480	0.020	0.176
GO_NUCLEOSIDE_SALVAGE	15	0.700	1.759	0.010	0.046	15	0.689	1.702	0.012	0.095	15	0.432	1.087	0.352	0.577
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	58	0.512	1.758	0.000	0.046	58	0.393	1.324	0.071	0.266	58	-0.309	-1.045	0.371	0.724
REACTOME_SEMAPHORIN_INTERACTIONS	62	0.485	1.689	0.000	0.047	62	0.511	1.735	0.000	0.042	62	0.370	1.253	0.110	0.410
REACTOME_RHO_GTPASES_ACTIVATE_PAKS	20	0.621	1.683	0.006	0.047	20	0.431	1.167	0.267	0.412	20	-0.336	-0.916	0.572	0.867
GO_NON_CANONICAL_WNT_SIGNALING_PATHWAY	149	0.442	1.759	0.000	0.047	149	0.451	1.729	0.000	0.081	149	0.398	1.553	0.000	0.258

GO_ZYMOGEN_ACTIVATION	51	0.526	1.756	0.000	0.047	51	0.432	1.405	0.044	0.224	51	0.384	1.251	0.140	0.441
GO_INTERLEUKIN_6_SECRETION	45	0.543	1.760	0.002	0.047	45	0.397	1.263	0.141	0.311	45	-0.303	-0.960	0.533	0.796
REACTOME_L1CAM_INTERACTIONS	116	0.442	1.693	0.000	0.047	116	0.463	1.699	0.000	0.049	116	0.419	1.572	0.002	0.118
REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	94	0.454	1.697	0.000	0.047	94	0.436	1.566	0.004	0.095	94	0.371	1.346	0.043	0.291
REACTOME_PURINE_CATABOLISM	18	0.631	1.695	0.010	0.048	18	0.557	1.442	0.070	0.157	18	0.590	1.551	0.044	0.127
GO_ACTIN_FILAMENT_POLYMERIZATION	163	0.432	1.752	0.000	0.048	163	0.464	1.815	0.000	0.056	163	0.431	1.700	0.000	0.188
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHARIDE_ANTIGEN_VIA_MHC_CLASS_II	100	0.466	1.751	0.000	0.048	100	0.337	1.232	0.108	0.335	100	0.260	0.963	0.540	0.715
GO_PYRIMIDINE_RIBONUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	15	0.702	1.753	0.000	0.048	15	0.694	1.748	0.008	0.080	15	0.596	1.475	0.059	0.314
GO_DEVELOPMENTAL_CELL_GROWTH	216	0.421	1.747	0.000	0.049	216	0.431	1.750	0.000	0.079	216	0.343	1.419	0.004	0.346

GO_COLLAGEN_FIBRIL_ORGANIZATION	52	0.527	1.746	0.000	0.049	52	0.460	1.499	0.016	0.173	52	0.351	1.160	0.214	0.514
GO_RHO_PROTEIN_SIGNAL_TRANSDUCTION	192	0.426	1.747	0.000	0.049	192	0.400	1.592	0.000	0.135	192	0.273	1.107	0.183	0.562
REACTOME_NUCLEOBASE_CATABOLISM	36	0.539	1.675	0.006	0.049	36	0.527	1.617	0.004	0.074	36	0.499	1.521	0.014	0.150
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	385	0.394	1.740	0.000	0.049	385	0.381	1.625	0.000	0.122	385	0.311	1.347	0.004	0.396
GO_SPINAL_CORD_DEVELOPMENT	103	0.457	1.743	0.000	0.049	103	0.321	1.177	0.162	0.387	103	-0.234	-0.872	0.743	0.880
GO_POSITIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	30	0.587	1.747	0.000	0.049	30	0.587	1.743	0.002	0.079	30	0.459	1.370	0.075	0.380
GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	27	0.608	1.744	0.006	0.049	27	0.577	1.638	0.012	0.117	27	0.502	1.494	0.042	0.296
GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	48	0.525	1.738	0.000	0.050	48	0.414	1.328	0.086	0.264	48	0.365	1.171	0.188	0.507
GO_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	132	0.444	1.740	0.000	0.050	132	0.422	1.610	0.000	0.128	132	0.302	1.158	0.170	0.514

GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	31	0.582	1.741	0.002	0.050	31	0.572	1.693	0.002	0.094	31	0.380	1.128	0.274	0.542
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	86	0.472	1.741	0.000	0.050	86	0.463	1.651	0.000	0.111	86	0.418	1.534	0.009	0.265
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	131	0.451	1.747	0.000	0.050	131	0.423	1.615	0.000	0.125	131	0.345	1.311	0.033	0.415
REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS	63	0.474	1.658	0.004	0.050	63	0.521	1.753	0.002	0.040	63	0.572	1.959	0.000	0.006
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	51	0.502	1.662	0.004	0.051	51	0.574	1.885	0.000	0.017	51	0.635	2.115	0.000	0.001
HALLMARK_ANDROGEN_RESPONSE	95	0.360	1.336	0.046	0.055	95	0.448	1.623	0.000	0.006	95	0.406	1.494	0.012	0.036
REACTOME_DEGRADATION_OF_AXIN	54	0.479	1.625	0.006	0.062	54	0.566	1.861	0.000	0.016	54	0.612	2.026	0.000	0.001
GO_CORTICAL_CYTOSKELETON_ORGANIZATION	47	0.515	1.698	0.002	0.062	47	0.602	1.957	0.000	0.018	47	0.591	1.937	0.000	0.066
REACTOME_REGULATION_OF_RUNX1_EXPRESSION_AND_ACTIVITY	17	0.625	1.621	0.024	0.062	17	0.687	1.737	0.002	0.042	17	0.616	1.593	0.023	0.107

GO_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	48	0.508	1.699	0.008	0.063	48	0.590	1.886	0.000	0.035	48	0.500	1.626	0.004	0.210
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	158	0.405	1.609	0.000	0.066	158	0.447	1.752	0.000	0.039	158	0.371	1.476	0.004	0.179
REACTOME_FBXL7_DOWN_REGULATES_AURKA_DURING_MITOTIC_ENTRY_AND_IN_EARLY_MITOSIS	54	0.473	1.605	0.004	0.066	54	0.534	1.762	0.000	0.043	54	0.590	1.933	0.000	0.006
GO_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	28	0.572	1.681	0.006	0.067	28	0.644	1.894	0.000	0.034	28	0.620	1.790	0.000	0.135
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	136	0.426	1.670	0.000	0.071	136	0.498	1.919	0.000	0.025	136	0.459	1.789	0.000	0.130
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	23	0.586	1.659	0.013	0.074	23	0.674	1.853	0.002	0.042	23	0.607	1.667	0.014	0.200
REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT	77	0.440	1.584	0.004	0.074	77	0.521	1.807	0.000	0.027	77	0.494	1.738	0.002	0.037
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	109	0.414	1.580	0.000	0.076	109	0.422	1.559	0.009	0.095	109	0.473	1.796	0.000	0.023
REACTOME_DEGRADATION_OF_DVL	56	0.463	1.572	0.011	0.079	56	0.511	1.707	0.004	0.049	56	0.573	1.946	0.000	0.006

REACTOME_SURFACTANT_METABOLISM	25	0.533	1.567	0.015	0.081	25	0.586	1.633	0.014	0.066	25	0.628	1.729	0.002	0.040
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	48	0.469	1.551	0.011	0.088	48	0.549	1.740	0.004	0.043	48	0.630	2.055	0.000	0.001
REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY	96	0.413	1.548	0.004	0.088	96	0.475	1.711	0.000	0.049	96	0.514	1.881	0.000	0.011
REACTOME_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME	59	0.451	1.545	0.017	0.088	59	0.514	1.733	0.002	0.040	59	0.546	1.870	0.000	0.012
REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	28	0.528	1.540	0.021	0.090	28	0.592	1.697	0.002	0.049	28	0.575	1.700	0.006	0.053
REACTOME_INTERFERON_SIGNALING	192	0.376	1.530	0.000	0.096	192	0.425	1.695	0.000	0.049	192	0.379	1.528	0.000	0.144
REACTOME_UCH_PROTEINASES	99	0.410	1.522	0.004	0.099	99	0.484	1.792	0.000	0.031	99	0.504	1.884	0.000	0.012
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	66	0.426	1.498	0.018	0.109	66	0.491	1.707	0.000	0.050	66	0.394	1.378	0.046	0.251
REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21	59	0.434	1.473	0.022	0.124	59	0.507	1.700	0.004	0.050	59	0.553	1.869	0.000	0.011

REACTOME_NEGATIVE_REGULATION_OF_NOTCH4_SIGNALING	53	0.423	1.436	0.023	0.144	53	0.479	1.578	0.012	0.092	53	0.557	1.846	0.002	0.013
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	67	0.402	1.425	0.024	0.152	67	0.511	1.758	0.000	0.041	67	0.592	2.058	0.000	0.001
REACTOME_NUCLEOTIDE_SALVAGE	22	0.497	1.397	0.076	0.165	22	0.650	1.755	0.002	0.040	22	0.369	1.018	0.438	0.675
REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING	61	0.406	1.398	0.046	0.165	61	0.436	1.466	0.021	0.144	61	0.528	1.769	0.000	0.029
REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS	66	0.393	1.383	0.049	0.174	66	0.494	1.675	0.004	0.056	66	0.532	1.851	0.000	0.013
REACTOME_REGULATION_OF_APOPTOSIS	52	0.401	1.361	0.067	0.190	52	0.501	1.629	0.002	0.068	52	0.550	1.845	0.002	0.013
REACTOME_DEFECTIVE_CFTR_CAUSES_CYSTIC_FIBROSIS	60	0.388	1.329	0.072	0.213	60	0.477	1.589	0.006	0.086	60	0.576	1.945	0.000	0.006
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	70	0.370	1.315	0.052	0.224	70	0.484	1.661	0.000	0.064	70	0.603	2.111	0.000	0.000
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	71	0.366	1.315	0.072	0.225	71	0.466	1.572	0.006	0.094	71	0.533	1.847	0.000	0.013

REACTOME_STABILIZATION_OF_P53	55	0.378	1.271	0.101	0.261	55	0.498	1.633	0.002	0.067	55	0.579	1.954	0.000	0.006
HALLMARK_IL6_JAK_STAT3_SIGNALING	87	0.295	1.084	0.276	0.267	87	-0.319	-1.134	0.204	0.311	87	-0.471	-1.686	0.000	0.015
REACTOME_HEDGEHOG_LIGAND_BIOGENESIS	64	0.348	1.217	0.138	0.311	64	0.464	1.560	0.006	0.095	64	0.540	1.860	0.000	0.012
REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA	54	0.356	1.218	0.131	0.312	54	0.456	1.493	0.019	0.130	54	0.557	1.855	0.000	0.013
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	66	0.344	1.206	0.142	0.329	66	0.407	1.406	0.032	0.179	66	0.514	1.784	0.000	0.025
REACTOME_REGULATION_OF_PTEN_STABILITY_AND_ACTIVITY	67	0.343	1.197	0.156	0.336	67	0.443	1.521	0.019	0.116	67	0.504	1.760	0.000	0.029
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	0.397	1.128	0.302	0.428	24	0.536	1.468	0.062	0.142	24	0.626	1.767	0.006	0.029
REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE	89	0.296	1.105	0.257	0.450	89	0.419	1.473	0.010	0.140	89	0.523	1.883	0.000	0.011
REACTOME_DNA_REPLICATION_PRE_INITIATION	84	0.296	1.078	0.291	0.484	84	0.435	1.546	0.006	0.103	84	0.528	1.913	0.000	0.008

ES, enrichment score; NES, normalized enrichment score.