

Gene sets enriched in phenotype high risk score group (185 samples)								
NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	83	0.74	2.48	0	0	0	4552	tags=47%, list=8%, signal=51%
KEGG_DILATED_CARDIOMYOPATHY	90	0.73	2.45	0	0	0	4548	tags=48%, list=8%, signal=52%
KEGG_FOCAL_ADHESION	199	0.71	2.37	0	0	0	5015	tags=47%, list=9%, signal=51%
KEGG_ECM_RECEPTOR_INTERACTION	84	0.81	2.37	0	0	0	4975	tags=60%, list=9%, signal=65%
KEGG_CALCIIUM_SIGNALING_PATHWAY	177	0.63	2.36	0	0	0	7114	tags=46%, list=13%, signal=53%
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	264	0.64	2.31	0	0	0	7060	tags=48%, list=12%, signal=55%
KEGG_HEMATOPOIETIC_CELL_LINEAGE	85	0.76	2.27	0	0	0.001	7247	tags=58%, list=13%, signal=66%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	271	0.57	2.25	0	0	0.001	5667	tags=35%, list=10%, signal=38%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	213	0.58	2.23	0	0	0.003	6383	tags=41%, list=11%, signal=46%
KEGG_CELL_ADHESION_MOLECULES_CAMS	131	0.72	2.2	0	0	0.003	5736	tags=51%, list=10%, signal=57%
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	0.67	2.2	0	0	0.003	4548	tags=43%, list=8%, signal=47%
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	69	0.74	2.18	0	0	0.003	7958	tags=64%, list=14%, signal=74%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	114	0.64	2.17	0	0	0.003	7183	tags=50%, list=13%, signal=57%
KEGG_JAK_STAT_SIGNALING_PATHWAY	155	0.58	2.11	0	0.001	0.017	9340	tags=45%, list=17%, signal=53%
KEGG_MAPK_SIGNALING_PATHWAY	267	0.54	2.06	0	0.004	0.038	6892	tags=38%, list=12%, signal=43%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	188	0.61	2.05	0	0.004	0.04	8272	tags=55%, list=15%, signal=64%
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	116	0.61	2.05	0.002	0.004	0.04	6296	tags=43%, list=11%, signal=48%
KEGG_GAP_JUNCTION	90	0.57	2.04	0	0.004	0.041	3746	tags=32%, list=7%, signal=34%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.77	1.99	0.004	0.007	0.079	6200	tags=73%, list=11%, signal=82%
KEGG_MELANOGENESIS	101	0.55	1.98	0	0.007	0.086	7049	tags=40%, list=12%, signal=45%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	21	0.7	1.97	0	0.009	0.097	6046	tags=57%, list=11%, signal=64%
KEGG_AXON_GUIDANCE	129	0.55	1.97	0	0.009	0.099	4184	tags=34%, list=7%, signal=37%
KEGG_RENAL_CELL_CARCIOMA	70	0.6	1.96	0.002	0.008	0.102	5378	tags=43%, list=10%, signal=47%
KEGG_TOLL LIKE RECEPTOR SIGNALING PATHWAY	102	0.58	1.96	0.002	0.008	0.104	6827	tags=42%, list=12%, signal=48%
KEGG_PATHWAYS_IN_CANCER	325	0.51	1.94	0	0.01	0.121	6338	tags=36%, list=11%, signal=40%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	0.6	1.93	0.002	0.011	0.136	7599	tags=46%, list=13%, signal=54%
KEGG_LONG_TERM_DEPRESSION	70	0.53	1.89	0	0.015	0.169	11402	tags=51%, list=20%, signal=64%
KEGG_TGF_BETA_SIGNALING_PATHWAY	85	0.56	1.89	0.004	0.015	0.176	7251	tags=46%, list=13%, signal=53%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	22	0.72	1.88	0.004	0.015	0.179	6203	tags=50%, list=11%, signal=56%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	26	0.64	1.87	0.006	0.018	0.199	8480	tags=50%, list=15%, signal=59%
KEGG_LEISHMANIA_INFECTION	70	0.68	1.86	0.017	0.018	0.202	6320	tags=54%, list=11%, signal=61%
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	0.54	1.86	0.004	0.018	0.21	7980	tags=47%, list=14%, signal=54%
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	42	0.56	1.83	0.002	0.023	0.252	6930	tags=45%, list=12%, signal=52%
KEGG_LYSOSOME	121	0.59	1.8	0.02	0.028	0.295	8571	tags=52%, list=15%, signal=61%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	44	0.53	1.78	0.004	0.032	0.325	6769	tags=41%, list=12%, signal=46%
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	67	0.52	1.76	0.008	0.039	0.364	5778	tags=33%, list=10%, signal=37%
KEGG_BASAL_CELL_CARCIOMA	55	0.57	1.76	0.004	0.039	0.365	7599	tags=44%, list=13%, signal=50%
KEGG_VIRAL_MYOCARDITIS	68	0.58	1.75	0.024	0.038	0.368	5736	tags=43%, list=10%, signal=47%
KEGG_MELANOMA	71	0.49	1.74	0.01	0.042	0.393	5015	tags=32%, list=9%, signal=36%
KEGG_ABC_TRANSPORTERS	44	0.51	1.74	0.01	0.041	0.393	7703	tags=34%, list=14%, signal=39%
KEGG_LONG_TERM_POTENTIATION	70	0.48	1.73	0.01	0.041	0.399	7049	tags=40%, list=12%, signal=46%
KEGG_GNRH_SIGNALING_PATHWAY	101	0.47	1.73	0.012	0.042	0.408	8293	tags=41%, list=15%, signal=47%
KEGG_DORSO_VENTRAL_AXIS_FORMATION	24	0.56	1.72	0.014	0.043	0.416	4319	tags=38%, list=8%, signal=41%
KEGG_ASTHMA	28	0.69	1.72	0.031	0.042	0.417	11853	tags=68%, list=21%, signal=86%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	132	0.5	1.71	0.025	0.045	0.435	10436	tags=45%, list=18%, signal=56%
KEGG_PRION_DISEASES	35	0.56	1.7	0.02	0.046	0.445	6769	tags=46%, list=12%, signal=52%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	96	0.52	1.7	0.018	0.046	0.449	8272	tags=44%, list=15%, signal=51%
KEGG_NOD LIKE RECEPTOR SIGNALING PATHWAY	62	0.54	1.69	0.03	0.047	0.461	6321	tags=42%, list=11%, signal=47%
KEGG_INSULIN_SIGNALING_PATHWAY	137	0.46	1.69	0.014	0.048	0.473	9210	tags=41%, list=16%, signal=49%
KEGG_ACUTE_MYELOID_LEUKEMIA	57	0.55	1.69	0.025	0.047	0.477	6738	tags=46%, list=12%, signal=52%
Gene sets enriched in phenotype low risk score group (186 samples)								
KEGG_SPLICEOSOME	127	-0.7	-2.02	0.008	0.042	0.054	9130	tags=66%, list=16%, signal=79%
KEGG_HOMOLOGOUS_RECOMBINATION	28	-0.75	-1.96	0.008	0.046	0.095	8258	tags=68%, list=15%, signal=79%
KEGG_OXIDATIVE_PHOSPHORYLATION	131	-0.66	-1.95	0.017	0.037	0.108	9250	tags=64%, list=16%, signal=76%
KEGG_HUNTINGTONS_DISEASE	180	-0.55	-1.95	0.012	0.028	0.108	8488	tags=47%, list=15%, signal=55%
KEGG_RNA_POLYMERASE	28	-0.7	-1.94	0.006	0.025	0.117	9322	tags=61%, list=16%, signal=73%

KEGG_PYRIMIDINE_METABOLISM	97	-0.59	-1.92	0.012	0.026	0.133	9322	tags=53%, list=16%, signal=63%
KEGG_PARKINSONS_DISEASE	128	-0.64	-1.89	0.018	0.027	0.16	9688	tags=62%, list=17%, signal=74%
KEGG_BASE_EXCISION_REPAIR	35	-0.7	-1.89	0.004	0.024	0.16	13992	tags=77%, list=25%, signal=102%
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	-0.66	-1.86	0.018	0.03	0.199	9422	tags=59%, list=17%, signal=71%
KEGG_DNA_REPLICATION	36	-0.76	-1.81	0.014	0.041	0.262	7485	tags=75%, list=13%, signal=86%