

Supplementary Table 1. 20 GSEA enriched gene sets significantly

GS follow link to MSigDB	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
KEGG_PENTOSE_PHOSPHATE_PATHWAY	27	0.72	1.94	0	0.115	0.037	10881	tags=70%, list=20%, signal=88%
KEGG_ETHER_LIPID_METABOLISM	33	0.57	1.68	0.002	0.094	0.295	8725	tags=52%, list=16%, signal=61%
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	16	0.77	1.89	0.004	0.075	0.071	6709	tags=63%, list=12%, signal=71%
KEGG_GLYCOLYSIS_GLUONEOGENESIS	62	0.64	1.87	0.004	0.078	0.092	9099	tags=53%, list=16%, signal=64%
KEGG_GLYCEROLIPID_METABOLISM	49	0.59	1.87	0.004	0.07	0.099	10950	tags=55%, list=20%, signal=69%
KEGG_ARGININE_AND_PROLINE_METABOLISM	54	0.61	1.84	0.004	0.076	0.123	10289	tags=59%, list=19%, signal=73%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	114	0.58	1.83	0.004	0.078	0.132	8725	tags=46%, list=16%, signal=54%
KEGG_BLADDER_CANCER	42	0.6	1.78	0.004	0.11	0.173	13421	tags=62%, list=24%, signal=82%
KEGG_PPAR_SIGNALING_PATHWAY	69	0.58	1.74	0.004	0.096	0.21	12181	tags=61%, list=22%, signal=78%
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	23	0.72	1.91	0.006	0.086	0.06	10922	tags=74%, list=20%, signal=92%
KEGG_CALCIIUM_SIGNALING_PATHWAY	177	0.49	1.69	0.006	0.109	0.28	9019	tags=43%, list=16%, signal=51%
KEGG_RETINOL_METABOLISM	64	0.54	1.76	0.008	0.108	0.197	10882	tags=52%, list=20%, signal=64%
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	51	0.51	1.7	0.008	0.103	0.265	10646	tags=45%, list=19%, signal=56%
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	271	0.47	1.69	0.008	0.101	0.286	13242	tags=52%, list=24%, signal=68%
KEGG_P53_SIGNALING_PATHWAY	68	0.57	1.69	0.01	0.105	0.281	12731	tags=56%, list=23%, signal=73%

Note: Gene Set Enrichment Analysis: GSEA; Kyoto Encyclopedia of Genes and Genomes: KEGG