

Supplementary Table 1. The list of calculated GSVA scores for KEGG curated pathways

Term	Average GSVA score (-1 to 1)				Case 1		Case 2	
	SK-ME L-28	A37 5	A37 5_G 1	A37 5_G 2	p-value	FDR	p-value	FDR
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTONATION_NEOLACTONATION_SERIES	0.18	0.18	0.12	0.20	6.44E-05	5.99E-04	-	-
KEGG_RENIN_ANGIOTENSIN_SYSTEM	0.27	0.27	0.21	0.30	8.93E-07	5.04E-05	-	-
KEGG_SPHINGOLIPID_METABOLISM	0.24	0.24	0.19	0.27	1.18E-04	9.17E-04	-	-
KEGG_OTHER_GLYCAN_DEGRADATION	0.43	0.43	0.60	0.34	1.08E-07	2.02E-05	-	-
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBOSERIES	0.25	0.25	0.25	0.25	3.28E-05	4.01E-04	-	-
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	0.22	0.22	0.25	0.21	2.66E-04	1.76E-03	-	-
KEGG_GLUTATHIONE_METABOLISM	0.11	0.11	0.12	0.10	6.39E-04	3.60E-03	-	-
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	0.27	0.27	0.50	0.15	3.42E-05	4.01E-04	-	-
KEGG_LYSOSOME	0.21	0.21	0.34	0.14	2.93E-06	6.31E-05	-	-

KEGG_ALZHEIMER S_DISEASE	0.19	0.19	0.32	0.12	4.62E- 05	4.77E- 04	-	-
KEGG_RIBOSOME	0.32	0.32	0.39	0.28	3.05E- 05	4.01E- 04	-	-
KEGG_OXIDATIVE _PHOSPHORYLATI ON	0.30	0.30	0.37	0.27	3.06E- 06	6.31E- 05	-	-
KEGG_PARKINSON S_DISEASE	0.25	0.25	0.30	0.22	5.91E- 04	3.55E- 03	-	-
KEGG_BIOSYNTH ESIS_OF_UNSATUR ATED_FATTY_ACI DS	0.15	0.15	0.04	0.21	1.57E- 03	7.13E- 03	-	-
KEGG_ALPHA_LIN OLENIC_ACID_M ETABOLISM	0.19	0.19	0.26	0.16	1.55E- 03	7.13E- 03	-	-
KEGG_FATTY_ACI D_METABOLISM	0.16	0.16	0.36	0.06	7.43E- 05	6.58E- 04	-	-
KEGG_ARACHIDO NIC_ACID_METAB OLISM	0.12	0.12	0.24	0.06	6.79E- 04	3.72E- 03	-	-
KEGG_VALINE_LE UCINE_AND_ISOL EUCINE_DEGRAD ATION	0.27	0.27	0.40	0.21	5.05E- 06	8.54E- 05	-	-
KEGG_PROPANOAT E_METABOLISM	0.25	0.25	0.38	0.19	2.07E- 06	6.31E- 05	-	-
KEGG_BUTANOAT E_METABOLISM	0.24	0.24	0.26	0.23	1.84E- 06	6.31E- 05	-	-
KEGG_LIMONENE_ AND_PINENE_DE GRADATION	0.26	0.26	0.23	0.27	4.39E- 06	8.17E- 05	-	-
KEGG_GALACTOS E_METABOLISM	0.20	0.20	0.30	0.15	1.72E- 03	7.62E- 03	-	-
KEGG_TRYPTOPHA N_METABOLISM	0.18	0.18	0.23	0.16	2.39E- 04	1.65E- 03	-	-
KEGG_CITRATE_C YCLE_TCA_CYCL	0.21	0.21	0.34	0.14	2.76E- 06	6.31E- 05	-	-

E									
KEGG_CARDIAC_MUSCLE_CONTRACTION	0.22	0.22	0.33	0.16	1.08E-06	5.04E-05	-	-	
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	0.03	0.03	0.31	0.11	8.66E-05	1.34E-03	-	-	
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	0.07	0.07	0.19	0.01	9.91E-04	8.02E-03	-	-	
KEGG_JAK_STAT_SIGNALING_PATHWAY	0.03	0.03	0.17	0.04	1.02E-04	1.45E-03	-	-	
KEGG_LINOLEIC_ACID_METABOLISM	0.06	0.06	0.32	0.06	1.87E-05	4.97E-04	-	-	
KEGG_RETINOL_METABOLISM	0.07	0.07	0.31	0.05	3.25E-04	3.56E-03	-	-	
KEGG_ABC_TRANSPORTERS	0.09	0.09	0.29	0.01	4.31E-05	8.49E-04	-	-	
KEGG_INOSITOL_PHOSPHATE_METABOLISM	0.05	0.05	0.34	0.10	1.08E-06	6.70E-05	-	-	
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	0.08	0.08	0.29	0.02	8.90E-04	7.52E-03	-	-	
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	0.12	0.12	0.35	0.01	1.17E-03	8.73E-03	2.47E-03	9.97E-03	
KEGG_PEROXISOME	0.10	0.10	0.29	0.01	4.58E-04	4.48E-03	-	-	
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	0.22	0.22	0.37	0.15	1.99E-03	8.61E-03	-	-	

KEGG_COMPLEME NT_AND_COAGU LATION_CASCAD ES	0.14	0.14	0.32	0.04	3.10E- 04	3.56E- 03	-	-
KEGG_MTOR_SIGN ALING_PATHWAY	-	-	0.25	-	6.68E- 05	6.03E- 03	4.97E- 05	8.49E-04
KEGG_ENDOMETR IAL_CANCER	-	-	0.19	-	7.32E- 04	6.49E- 03	-	-
KEGG_MAPK_SIGN ALING_PATHWAY	-	-	-	-	6.12E- 04	3.56E- 03	-	-
KEGG_WNT_SIGN ALING_PATHWAY	-	-	-	-	1.02E- 03	4.99E- 03	-	-
KEGG_BASAL_CEL L_CARCINOMA	-	-	-	-	4.44E- 07	4.13E- 05	-	-
KEGG_HEDGEHOG _SIGNALING_PAT HWAY	-	-	0.02	-	5.45E- 05	5.33E- 04	1.43E- 04	6.03E-03
KEGG_TYPE_II_DI ABETES_MELLIT US	-	-	0.00	-	4.99E- 04	3.09E- 03	-	-
KEGG_ECM_RECEP TOR_INTERACTIO N	-	-	0.04	-	2.37E- 03	9.80E- 03	-	-
KEGG_ADIPOCYTO KINE_SIGNALING _PATHWAY	-	-	0.08	-	1.55E- 04	6.03E- 03	-	-
KEGG_NEUROTRO PHIN_SIGNALING _PATHWAY	-	-	-	-	2.10E- 05	3.25E- 04	-	-
KEGG_RENAL_CEL L_CARCINOMA	-	-	0.02	-	2.48E- 04	6.60E- 03	4.59E- 04	2.95E-03
KEGG_VASOPRESS IN_REGULATED_ WATER_REABSOR PTION	-	-	0.12	-	1.64E- 04	6.03E- 03	-	-
KEGG_CHRONIC_ MYELOID_LEUKE MIA	-	-	0.07	-	7.48E- 04	3.98E- 03	1.32E- 06	2.45E-04

KEGG_AXON_GUI	-	-	0.04	-	1.94E-	6.03E-	-	-
DANCE	0.06	0.06		0.11	04	03		
KEGG_PROTEASO	-	-	-	0.24	5.00E-	1.86E-	-	-
ME	0.01	0.01	0.49		06	04		
KEGG_PYRIMIDIN	-	-	-	0.16	5.02E-	8.49E-	-	-
E_METABOLISM	0.02	0.02	0.39		05	04		
KEGG_RNA_POLY	-	-	-	0.21	1.14E-	8.73E-	-	-
MERASE	0.01	0.01	0.45		03	03		
KEGG_BASE_EXCI	-	-	-	0.09	3.41E-	1.59E-	-	-
SION_REPAIR	0.06	0.06	0.36		06	04		
KEGG_DNA_REPLI	-	-	-	0.17	5.45E-	5.07E-	-	-
CATION	0.13	0.13	0.73		07	05		
KEGG_MISMATCH_	-	-	-	0.11	2.19E-	4.07E-	-	-
REPAIR	0.16	0.16	0.69		07	05		
KEGG_BASAL_TRA	-	-	-	-	1.66E-	2.21E-	1.03E-	8.68E-04
NSCRIPTION_FAC	0.20	0.20	0.38	0.10	04	03	04	
TORS								
KEGG_RNA_DEGR	-	-	-	-	2.13E-	2.64E-	1.45E-	1.08E-03
ADATION	0.19	0.19	0.48	0.05	04	03	04	
KEGG_SPLICEOSO	-	-	-	-	9.51E-	2.95E-	1.08E-	8.73E-04
ME	0.25	0.25	0.62	0.07	06	04	04	
KEGG_CELL_CYCL	-	-	-	-	2.26E-	1.61E-	-	-
E	0.19	0.19	0.48	0.05	04	03		
KEGG_OOCYTE_M	-	-	-	-	3.67E-	4.01E-	4.22E-	4.36E-03
EIOSIS	0.16	0.16	0.35	0.06	05	04	04	
KEGG_NUCLEOTID	-	-	-	-	1.24E-	5.93E-	-	-
E_EXCISION_REP	0.16	0.16	0.44	0.02	03	03		
AIR								
KEGG_ONE_CARB	-	-	-	-	6.23E-	5.79E-	9.95E-	4.99E-03
ON_POOL_BY_FO	0.18	0.18	0.42	0.06	04	03	04	
LATE								
KEGG_HOMOLOG	-	-	-	0.08	2.37E-	5.51E-	-	-
OUS_RECOMBINA	0.15	0.15	0.59		05	04		
TION								
KEGG_DORSO_VE	-	-	-	-	2.20E-	9.31E-	-	-
NTRAL_AXIS_FO	0.15	0.15	0.27	0.10	03	03		
RMATION								
KEGG_GAP_JUNCT	-	-	-	-	3.57E-	4.01E-	-	-