

Significant pathways with gene

path_id	path_name	enrichment	pvalue	FDR	gene_id	gene_name
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	14811	Grin2a
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	14829	Grpr
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	15558	Htr2a
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	16438	Itpr1
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	18216	Ntsr1
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	19056	Ppp3cb
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	19218	Ptger3
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	20190	Ryr1
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	20541	Slc8a1
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	67972	Atp2b1
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	269999	Orai3
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	12323	Camk2b
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	12326	Camk4
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	13867	Erbp3
04020	Calcium signaling pathway	7.800565291	5.25396E-09	1.30298E-06	11515	Adcy9
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	14924	Magi1
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	16334	Ins2
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	18441	P2ry1
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	19353	Rac1
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	16001	Igflr
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	74206	Sipa1l3
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	11515	Adcy9
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	12387	Ctnnb1
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	70549	Tln2
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	14168	Fgf13
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	14180	Fgf9
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	14811	Grin2a
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	192786	Rapgef6
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	13638	Efna3
04015	Rap1 signaling pathway	6.701894123	4.17511E-08	5.17714E-06	109880	Braf
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	19218	Ptger3
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	15245	Hhip
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	19013	Ppara
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	11515	Adcy9

04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	19353	Rac1
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	26414	Mapk10
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	54393	Gabbr1
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	12326	Camk4
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	14802	Gria4
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	14811	Grin2a
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	11517	Adcyap1r1
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	12323	Camk2b
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	67972	Atp2b1
04024	cAMP signaling pathway	6.763129704	1.14762E-07	9.48701E-06	109880	Braf
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	22348	Slc32a1
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	26414	Mapk10
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	66377	Ndufc1
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	140919	Slc17a6
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	269060	Dagla
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	17719	ND4
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	14802	Gria4
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	16438	Itpr1
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	16524	Kcnj9
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	14397	Gabra4
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	14402	Gabrb3
04723	Retrograde endocannabinoid signaling	7.613351724	3.05362E-07	1.89324E-05	11515	Adcy9
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	16438	Itpr1
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	19052	Ppp2ca
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	16001	Igf1r
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	16334	Ins2
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	64930	Tsc1
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	18761	Prkcq
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	67526	Atg12
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	26414	Mapk10
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	76559	Atg2b
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	74244	Atg7
04140	Autophagy - animal	8.052583554	6.0018E-07	2.97689E-05	68441	Rraga
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	26932	Ppp2r5e
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	12323	Camk2b
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	14811	Grin2a
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	73699	Ppp2r1b
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	214084	Slc18a2

04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	14802	Gria4
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	19056	Ppp3cb
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	26414	Mapk10
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	16438	Itpr1
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	16524	Kcnj9
04728	Dopaminergic synapse	7.812207926	8.17354E-07	3.3784E-05	19052	Ppp2ca
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	12869	Cox8b
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	11950	Atp5f1
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	11820	App
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	56175	Bace2
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	14811	Grin2a
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	68585	Rtn4
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	16438	Itpr1
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	17705	ATP6
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	19056	Ppp3cb
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	68318	Aph1c
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	20168	Rtn3
05010	Alzheimer's disease	6.525730049	1.63508E-06	5.79285E-05	66377	Ndufc1
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	18386	Oprd1
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	18387	Oprk1
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	18216	Ntsr1
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	14829	Grpr
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	14811	Grin2a
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	19218	Ptger3
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	15558	Htr2a
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	14608	Gpr83
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	14802	Gria4
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	18441	P2ry1
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	14402	Gabrb3
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	14397	Gabra4
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	19116	Prlr
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	11517	Adcyap1r1
04080	Neuroactive ligand-receptor interaction	5.008784029	1.87463E-06	5.81136E-05	54393	Gabbr1
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	14168	Fgf13
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	12387	Ctnnb1
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	13542	Dvl1
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	13389	Dll3
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	14180	Fgf9

05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	109880	Braf
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	56198	Heyl
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	14371	Fzd9
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	14296	Frat1
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	16001	Igflr
05224	Breast cancer	6.932687828	2.71827E-06	6.98504E-05	18131	Notch3
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	13542	Dvl1
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	14371	Fzd9
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	319481	Wdr59
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	268706	Slc38a9
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	16001	Igflr
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	109880	Braf
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	17168	Nprl3
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	64930	Tsc1
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	16334	Ins2
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	68441	Rraga
04150	mTOR signaling pathway	6.842064458	3.0982E-06	6.98504E-05	56692	Lamtor3
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	11515	Adcy9
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	319734	Cacna2d4
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	12326	Camk4
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	16438	Itpr1
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	12300	Cacng2
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	60596	Gucyl1a3
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	12323	Camk2b
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	20190	Ryr1
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	54720	Rcan1
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	19056	Ppp3cb
04921	Oxytocin signaling pathway	6.842064458	3.0982E-06	6.98504E-05	16524	Kcnj9
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	16334	Ins2
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	14104	Fasn
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	19052	Ppp2ca
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	26932	Ppp2r5e
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	19017	Ppargc1a
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	56421	Pfklp
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	16001	Igflr
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	73699	Ppp2r1b
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	64930	Tsc1
04152	AMPK signaling pathway	7.552928298	3.983E-06	7.7112E-05	15568	Elavl1

04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	60596	Gucyla3
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	16438	Itpr1
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	16524	Kcnj9
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	11517	Adcyap1r1
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	14811	Grin2a
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	11515	Adcy9
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	14802	Gria4
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	12323	Camk2b
04713	Circadian entrainment	8.73981703	4.07208E-06	7.7112E-05	20190	Ryr1
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	64930	Tsc1
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	12840	Col9a2
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	14180	Fgf9
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	12986	Csf3r
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	26932	Ppp2r5e
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	73699	Ppp2r1b
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	19353	Rac1
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	19052	Ppp2ca
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	21828	Thbs4
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	19116	Prlr
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	14168	Fgf13
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	319480	Itga11
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	13638	Efna3
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	16001	Igflr
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	16775	Lama4
04151	PI3K-Akt signaling pathway	4.400781343	4.3531E-06	7.7112E-05	16334	Ins2
04730	Long-term depression	10.92079141	1.46612E-05	0.000217791	19052	Ppp2ca
04730	Long-term depression	10.92079141	1.46612E-05	0.000217791	109880	Braf
04730	Long-term depression	10.92079141	1.46612E-05	0.000217791	16438	Itpr1
04730	Long-term depression	10.92079141	1.46612E-05	0.000217791	16001	Igflr
04730	Long-term depression	10.92079141	1.46612E-05	0.000217791	60596	Gucyla3
04730	Long-term depression	10.92079141	1.46612E-05	0.000217791	73699	Ppp2r1b
04730	Long-term depression	10.92079141	1.46612E-05	0.000217791	20190	Ryr1
05033	Nicotine addiction	14.27503448	1.49374E-05	0.000217791	14402	Gabrb3
05033	Nicotine addiction	14.27503448	1.49374E-05	0.000217791	14802	Gria4
05033	Nicotine addiction	14.27503448	1.49374E-05	0.000217791	140919	Slc17a6
05033	Nicotine addiction	14.27503448	1.49374E-05	0.000217791	22348	Slc32a1
05033	Nicotine addiction	14.27503448	1.49374E-05	0.000217791	14811	Grin2a
05033	Nicotine addiction	14.27503448	1.49374E-05	0.000217791	14397	Gabra4

04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	14371	Fzd9
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	26414	Mapk10
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	76441	Daam2
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	13542	Dvl1
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	14296	Frat1
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	19353	Rac1
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	12323	Camk2b
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	19056	Ppp3cb
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	12387	Ctnnb1
04310	Wnt signaling pathway	6.518280586	1.51657E-05	0.000217791	319478	Cxxc4
04721	Synaptic vesicle cycle	10.74464961	1.63778E-05	0.000217791	22348	Slc32a1
04721	Synaptic vesicle cycle	10.74464961	1.63778E-05	0.000217791	140919	Slc17a6
04721	Synaptic vesicle cycle	10.74464961	1.63778E-05	0.000217791	67300	Cltc
04721	Synaptic vesicle cycle	10.74464961	1.63778E-05	0.000217791	214084	Slc18a2
04721	Synaptic vesicle cycle	10.74464961	1.63778E-05	0.000217791	22249	Unc13b
04721	Synaptic vesicle cycle	10.74464961	1.63778E-05	0.000217791	103967	Dnm3
04721	Synaptic vesicle cycle	10.74464961	1.63778E-05	0.000217791	21871	Atp6v0a2
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	73699	Ppp2r1b
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	16438	Itpri
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	19056	Ppp3cb
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	19052	Ppp2ca
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	12323	Camk2b
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	26932	Ppp2r5e
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	16334	Ins2
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	11515	Adcy9
04114	Oocyte meiosis	7.383638526	1.66856E-05	0.000217791	16001	Igflr
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	19353	Rac1
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	16775	Lama4
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	14180	Fgf9
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	19218	Ptger3
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	14371	Fzd9
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	13542	Dvl1
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	14168	Fgfl3
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	16001	Igflr
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	11863	Arnt
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	11515	Adcy9
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	12387	Ctnnb1
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	15245	Hhip

05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	109880	Braf
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	26414	Mapk10
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	12986	Csf3r
05200	Pathways in cancer	3.864645545	2.2895E-05	0.000277383	76551	Ccdc6
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	13542	Dvl1
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	14924	Magi1
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	56198	Heyl
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	12387	Ctnnb1
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	14371	Fzd9
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	12840	Col9a2
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	26932	Ppp2r5e
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	19052	Ppp2ca
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	319480	Itgal1
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	21828	Thbs4
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	18131	Notch3
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	21871	Atp6v0a2
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	64930	Tsc1
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	73699	Ppp2r1b
05165	Human papillomavirus infection	4.078581281	2.34881E-05	0.000277383	16775	Lama4
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	16524	Kcnj9
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	16438	Itpr1
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	11820	App
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	214084	Slc18a2
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	15558	Htr2a
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	14402	Gabrb3
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	230459	Cyp2j13
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	56448	Cyp2d22
04726	Serotonergic synapse	6.488652038	4.78608E-05	0.000539521	109880	Braf
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	13867	ErbB3
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	17022	Lum
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	109880	Braf
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	19353	Rac1
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	12323	Camk2b
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	12387	Ctnnb1
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	11733	Ank1
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	14371	Fzd9
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	16001	Igflr
05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	14734	Gpc3

05205	Proteoglycans in cancer	5.081727486	5.45443E-05	0.00058813	16438	Itpr1
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	16598	Klf2
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	16438	Itpr1
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	17258	Mef2a
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	20541	Slc8a1
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	19017	Ppargc1a
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	18131	Notch3
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	11515	Adcy9
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	20190	Ryr1
04371	Apelin signaling pathway	6.161885388	7.24393E-05	0.000748539	12326	Camk4
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	73699	Ppp2r1b
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	67972	Atp2b1
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	20541	Slc8a1
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	319734	Cacna2d4
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	26932	Ppp2r5e
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	19052	Ppp2ca
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	12323	Camk2b
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	12300	Cacng2
04261	Adrenergic signaling in cardiomyocytes	5.826544687	0.000112945	0.001120419	11515	Adcy9
05032	Morphine addiction	7.24095952	0.000222326	0.002026397	29863	Pde7b
05032	Morphine addiction	7.24095952	0.000222326	0.002026397	14402	Gabrb3
05032	Morphine addiction	7.24095952	0.000222326	0.002026397	54393	Gabbr1
05032	Morphine addiction	7.24095952	0.000222326	0.002026397	11515	Adcy9
05032	Morphine addiction	7.24095952	0.000222326	0.002026397	14397	Gabra4
05032	Morphine addiction	7.24095952	0.000222326	0.002026397	22348	Slc32a1
05032	Morphine addiction	7.24095952	0.000222326	0.002026397	16524	Kcnj9
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	16775	Lama4
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	26414	Mapk10
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	19353	Rac1
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	70549	Tln2
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	21828	Thbs4
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	319480	Itga11
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	16001	Igflr
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	12840	Col9a2
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	12387	Ctnnb1
04510	Focal adhesion	4.782256108	0.000222689	0.002026397	109880	Braf
04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	16438	Itpr1
04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	26414	Mapk10

04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	230459	Cyp2j13
04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	11515	Adcy9
04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	18761	Prkcq
04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	15558	Htr2a
04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	12323	Camk2b
04750	Inflammatory mediator regulation of TRP channels	6.090681379	0.000228787	0.002026397	11419	Asic1
04720	Long-term potentiation	8.522408646	0.000305442	0.002612055	109880	Braf
04720	Long-term potentiation	8.522408646	0.000305442	0.002612055	16438	Itpr1
04720	Long-term potentiation	8.522408646	0.000305442	0.002612055	19056	Ppp3cb
04720	Long-term potentiation	8.522408646	0.000305442	0.002612055	12323	Camk2b
04720	Long-term potentiation	8.522408646	0.000305442	0.002612055	14811	Grin2a
04720	Long-term potentiation	8.522408646	0.000305442	0.002612055	12326	Camk4
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	11515	Adcy9
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	67972	Atp2b1
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	16334	Ins2
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	19056	Ppp3cb
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	60596	Gucyl1a3
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	20541	Slc8a1
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	18386	Oprd1
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	17258	Mef2a
04022	cGMP-PKG signaling pathway	5.098226601	0.000319292	0.002639477	16438	Itpr1
05031	Amphetamine addiction	8.397079108	0.000332042	0.002656337	214084	Slc18a2
05031	Amphetamine addiction	8.397079108	0.000332042	0.002656337	12323	Camk2b
05031	Amphetamine addiction	8.397079108	0.000332042	0.002656337	14802	Gria4
05031	Amphetamine addiction	8.397079108	0.000332042	0.002656337	19056	Ppp3cb
05031	Amphetamine addiction	8.397079108	0.000332042	0.002656337	14811	Grin2a
05031	Amphetamine addiction	8.397079108	0.000332042	0.002656337	12326	Camk4
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	27425	Atp5l
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	21871	Atp6v0a2
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	17719	ND4
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	74776	Ppa2
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	66377	Ndufc1
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	11950	Atp5f1
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	17705	ATP6
00190	Oxidative phosphorylation	5.681605764	0.000373265	0.002892806	12869	Cox8b
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	12496	Entpd2
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	11515	Adcy9
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	229363	Gmps

00230	Purine metabolism	4.811809376	0.000495981	0.003727373	14198	Fhit
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	107569	Nt5c3
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	20017	Polr1b
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	29863	Pde7b
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	68870	Ak8
00230	Purine metabolism	4.811809376	0.000495981	0.003727373	60596	Gucyl1a3
04144	Endocytosis	3.87716986	0.00062589	0.004530361	19157	Cyth1
04144	Endocytosis	3.87716986	0.00062589	0.004530361	13854	Epn1
04144	Endocytosis	3.87716986	0.00062589	0.004530361	11840	Arf1
04144	Endocytosis	3.87716986	0.00062589	0.004530361	227733	Pip5kl1
04144	Endocytosis	3.87716986	0.00062589	0.004530361	268451	Rab11fip4
04144	Endocytosis	3.87716986	0.00062589	0.004530361	20404	Sh3gl2
04144	Endocytosis	3.87716986	0.00062589	0.004530361	16001	Igflr
04144	Endocytosis	3.87716986	0.00062589	0.004530361	67300	Cltc
04144	Endocytosis	3.87716986	0.00062589	0.004530361	103967	Dnm3
04144	Endocytosis	3.87716986	0.00062589	0.004530361	65114	Vps35
04144	Endocytosis	3.87716986	0.00062589	0.004530361	54189	Rabep1
04931	Insulin resistance	6.111635558	0.000648633	0.004530361	26414	Mapk10
04931	Insulin resistance	6.111635558	0.000648633	0.004530361	19013	Ppara
04931	Insulin resistance	6.111635558	0.000648633	0.004530361	105651	Ppp1r3e
04931	Insulin resistance	6.111635558	0.000648633	0.004530361	170826	Ppargc1b
04931	Insulin resistance	6.111635558	0.000648633	0.004530361	19017	Ppargc1a
04931	Insulin resistance	6.111635558	0.000648633	0.004530361	16334	Ins2
04931	Insulin resistance	6.111635558	0.000648633	0.004530361	18761	Prkcq
04330	Notch signaling pathway	9.710907811	0.000657633	0.004530361	68318	Aph1c
04330	Notch signaling pathway	9.710907811	0.000657633	0.004530361	66935	Cir1
04330	Notch signaling pathway	9.710907811	0.000657633	0.004530361	13389	Dil3
04330	Notch signaling pathway	9.710907811	0.000657633	0.004530361	18131	Notch3
04330	Notch signaling pathway	9.710907811	0.000657633	0.004530361	13542	Dvl1
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	26414	Mapk10
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	19415	Rasa1
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	16706	Ksr1
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	16334	Ins2
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	13638	Efna3
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	14180	Fgf9
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	14168	Fgf13
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	16001	Igflr
04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	14811	Grin2a

04014	Ras signaling pathway	4.173986691	0.000682446	0.004574231	19353	Rac1
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	17705	ATP6
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	11950	Atp5f1
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	12869	Cox8b
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	19017	Ppargc1a
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	16438	Itpr1
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	67300	Cltc
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	215114	Hip1
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	66377	Ndufc1
05016	Huntington's disease	4.414959118	0.000944642	0.006165029	237806	Dnah9
04961	Endocrine and other factor-regulated calcium reabsorption	8.811749681	0.00104458	0.006642459	67300	Cltc
04961	Endocrine and other factor-regulated calcium reabsorption	8.811749681	0.00104458	0.006642459	11515	Adcy9
04961	Endocrine and other factor-regulated calcium reabsorption	8.811749681	0.00104458	0.006642459	103967	Dnm3
04961	Endocrine and other factor-regulated calcium reabsorption	8.811749681	0.00104458	0.006642459	20541	Slc8a1
04961	Endocrine and other factor-regulated calcium reabsorption	8.811749681	0.00104458	0.006642459	67972	Atp2b1
04136	Autophagy - other	11.89586207	0.001376447	0.008533972	76559	Atg2b
04136	Autophagy - other	11.89586207	0.001376447	0.008533972	67526	Atg12
04136	Autophagy - other	11.89586207	0.001376447	0.008533972	74244	Atg7
04136	Autophagy - other	11.89586207	0.001376447	0.008533972	19052	Ppp2ca
04142	Lysosome	5.372324805	0.001431673	0.008659875	21871	Atp6v0a2
04142	Lysosome	5.372324805	0.001431673	0.008659875	27029	Sgsh
04142	Lysosome	5.372324805	0.001431673	0.008659875	108011	Ap4e1
04142	Lysosome	5.372324805	0.001431673	0.008659875	55946	Ap3m1
04142	Lysosome	5.372324805	0.001431673	0.008659875	83429	Ctns
04142	Lysosome	5.372324805	0.001431673	0.008659875	67300	Cltc
04142	Lysosome	5.372324805	0.001431673	0.008659875	94178	Mcoln1
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	12300	Cacng2
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	14180	Fgf9
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	14168	Fgf13
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	19353	Rac1
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	19056	Ppp3cb
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	109880	Braf
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	71751	Map3k13
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	26414	Mapk10
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	319734	Cacna2d4
04010	MAPK signaling pathway	3.776464149	0.001514478	0.008942633	56692	Lamtor3
04211	Longevity regulating pathway	6.34445977	0.001554603	0.008966081	64930	Tsc1
04211	Longevity regulating pathway	6.34445977	0.001554603	0.008966081	12326	Camk4

04211	Longevity regulating pathway	6.34445977	0.001554603	0.008966081	16001	Igflr
04211	Longevity regulating pathway	6.34445977	0.001554603	0.008966081	16334	Ins2
04211	Longevity regulating pathway	6.34445977	0.001554603	0.008966081	11515	Adcy9
04211	Longevity regulating pathway	6.34445977	0.001554603	0.008966081	19017	Ppargc1a
04530	Tight junction	4.558893248	0.001677573	0.009455409	71960	Myh14
04530	Tight junction	4.558893248	0.001677573	0.009455409	26414	Mapk10
04530	Tight junction	4.558893248	0.001677573	0.009455409	19052	Ppp2ca
04530	Tight junction	4.558893248	0.001677573	0.009455409	192786	Rapgef6
04530	Tight junction	4.558893248	0.001677573	0.009455409	73699	Ppp2r1b
04530	Tight junction	4.558893248	0.001677573	0.009455409	19353	Rac1
04530	Tight junction	4.558893248	0.001677573	0.009455409	17884	Myh4
04530	Tight junction	4.558893248	0.001677573	0.009455409	14924	Magil
01522	Endocrine resistance	6.139799778	0.001853502	0.010214857	26414	Mapk10
01522	Endocrine resistance	6.139799778	0.001853502	0.010214857	13389	Dil3
01522	Endocrine resistance	6.139799778	0.001853502	0.010214857	11515	Adcy9
01522	Endocrine resistance	6.139799778	0.001853502	0.010214857	18131	Notch3
01522	Endocrine resistance	6.139799778	0.001853502	0.010214857	16001	Igflr
01522	Endocrine resistance	6.139799778	0.001853502	0.010214857	109880	Braf
04068	FoxO signaling pathway	5.046729363	0.002085982	0.011246162	109880	Braf
04068	FoxO signaling pathway	5.046729363	0.002085982	0.011246162	67526	Atg12
04068	FoxO signaling pathway	5.046729363	0.002085982	0.011246162	16334	Ins2
04068	FoxO signaling pathway	5.046729363	0.002085982	0.011246162	329934	Foxo6
04068	FoxO signaling pathway	5.046729363	0.002085982	0.011246162	16598	Klf2
04068	FoxO signaling pathway	5.046729363	0.002085982	0.011246162	16001	Igflr
04068	FoxO signaling pathway	5.046729363	0.002085982	0.011246162	26414	Mapk10
04360	Axon guidance	4.3504867	0.002285947	0.012062018	19056	Ppp3cb
04360	Axon guidance	4.3504867	0.002285947	0.012062018	218877	Sema3g
04360	Axon guidance	4.3504867	0.002285947	0.012062018	13839	Epha5
04360	Axon guidance	4.3504867	0.002285947	0.012062018	19353	Rac1
04360	Axon guidance	4.3504867	0.002285947	0.012062018	13638	Efna3
04360	Axon guidance	4.3504867	0.002285947	0.012062018	12323	Camk2b
04360	Axon guidance	4.3504867	0.002285947	0.012062018	117600	Srgap1
04360	Axon guidance	4.3504867	0.002285947	0.012062018	12162	Bmp7
05231	Choline metabolism in cancer	5.7676907	0.00258428	0.013173812	64930	Tsc1
05231	Choline metabolism in cancer	5.7676907	0.00258428	0.013173812	19012	Plpp1
05231	Choline metabolism in cancer	5.7676907	0.00258428	0.013173812	30805	Slc22a4
05231	Choline metabolism in cancer	5.7676907	0.00258428	0.013173812	26414	Mapk10
05231	Choline metabolism in cancer	5.7676907	0.00258428	0.013173812	19353	Rac1

05231	Choline metabolism in cancer	5.7676907	0.00258428	0.013173812	236899	Pcytlb
04550	Signaling pathways regulating pluripotency of stem cells	4.86254216	0.00260289	0.013173812	69587	Pcgf3
04550	Signaling pathways regulating pluripotency of stem cells	4.86254216	0.00260289	0.013173812	14371	Fzd9
04550	Signaling pathways regulating pluripotency of stem cells	4.86254216	0.00260289	0.013173812	16001	Igflr
04550	Signaling pathways regulating pluripotency of stem cells	4.86254216	0.00260289	0.013173812	11480	Acvr2a
04550	Signaling pathways regulating pluripotency of stem cells	4.86254216	0.00260289	0.013173812	12387	Ctnnb1
04550	Signaling pathways regulating pluripotency of stem cells	4.86254216	0.00260289	0.013173812	26380	Esrrb
04550	Signaling pathways regulating pluripotency of stem cells	4.86254216	0.00260289	0.013173812	13542	Dvl1
04910	Insulin signaling pathway	4.724597701	0.003085444	0.0153038	109880	Braf
04910	Insulin signaling pathway	4.724597701	0.003085444	0.0153038	105651	Ppp1r3e
04910	Insulin signaling pathway	4.724597701	0.003085444	0.0153038	16334	Ins2
04910	Insulin signaling pathway	4.724597701	0.003085444	0.0153038	64930	Tsc1
04910	Insulin signaling pathway	4.724597701	0.003085444	0.0153038	19017	Ppargcla
04910	Insulin signaling pathway	4.724597701	0.003085444	0.0153038	14104	Fasn
04910	Insulin signaling pathway	4.724597701	0.003085444	0.0153038	26414	Mapk10
04072	Phospholipase D signaling pathway	4.531756979	0.003938958	0.01817786	103967	Dnm3
04072	Phospholipase D signaling pathway	4.531756979	0.003938958	0.01817786	19157	Cyth1
04072	Phospholipase D signaling pathway	4.531756979	0.003938958	0.01817786	11515	Adcy9
04072	Phospholipase D signaling pathway	4.531756979	0.003938958	0.01817786	11840	Arfl
04072	Phospholipase D signaling pathway	4.531756979	0.003938958	0.01817786	64930	Tsc1
04072	Phospholipase D signaling pathway	4.531756979	0.003938958	0.01817786	19012	Plpp1
04072	Phospholipase D signaling pathway	4.531756979	0.003938958	0.01817786	16334	Ins2
04520	Adherens junction	6.608812261	0.003958082	0.01817786	12387	Ctnnb1
04520	Adherens junction	6.608812261	0.003958082	0.01817786	19271	Ptprj
04520	Adherens junction	6.608812261	0.003958082	0.01817786	11431	Acp1
04520	Adherens junction	6.608812261	0.003958082	0.01817786	16001	Igflr
04520	Adherens junction	6.608812261	0.003958082	0.01817786	19353	Rac1
04924	Renin secretion	6.608812261	0.003958082	0.01817786	11516	Adcyap1
04924	Renin secretion	6.608812261	0.003958082	0.01817786	19056	Ppp3cb
04924	Renin secretion	6.608812261	0.003958082	0.01817786	16438	Itpr1
04924	Renin secretion	6.608812261	0.003958082	0.01817786	60596	Gucyl a3
04924	Renin secretion	6.608812261	0.003958082	0.01817786	11517	Adcyap1r1
05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6.608812261	0.003958082	0.01817786	20541	Slc8a1
05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6.608812261	0.003958082	0.01817786	12300	Cacng2
05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6.608812261	0.003958082	0.01817786	12387	Ctnnb1
05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6.608812261	0.003958082	0.01817786	319480	Itga11
05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6.608812261	0.003958082	0.01817786	319734	Cacna2d4
04962	Vasopressin-regulated water reabsorption	8.852734563	0.004311692	0.019441813	11515	Adcy9

04962	Vasopressin-regulated water reabsorption	8.852734563	0.004311692	0.019441813	56455	Dynll1
04962	Vasopressin-regulated water reabsorption	8.852734563	0.004311692	0.019441813	13427	Dync1i2
04962	Vasopressin-regulated water reabsorption	8.852734563	0.004311692	0.019441813	68097	Dynll2
00532	Glycosaminoglycan biosynthesis - chondroitin sulfate	14.27503448	0.004610999	0.02042014	338362	Ust
00532	Glycosaminoglycan biosynthesis - chondroitin sulfate	14.27503448	0.004610999	0.02042014	59031	Chst12
00532	Glycosaminoglycan biosynthesis - chondroitin sulfate	14.27503448	0.004610999	0.02042014	58250	Chst11
05100	Bacterial invasion of epithelial cells	6.260980036	0.005049998	0.021971922	19353	Rac1
05100	Bacterial invasion of epithelial cells	6.260980036	0.005049998	0.021971922	140579	Elmo2
05100	Bacterial invasion of epithelial cells	6.260980036	0.005049998	0.021971922	12387	Ctnnb1
05100	Bacterial invasion of epithelial cells	6.260980036	0.005049998	0.021971922	103967	Dnm3
05100	Bacterial invasion of epithelial cells	6.260980036	0.005049998	0.021971922	67300	Cltc
04390	Hippo signaling pathway	4.325768025	0.005158255	0.022055986	12387	Ctnnb1
04390	Hippo signaling pathway	4.325768025	0.005158255	0.022055986	73699	Ppp2r1b
04390	Hippo signaling pathway	4.325768025	0.005158255	0.022055986	241324	Crb2
04390	Hippo signaling pathway	4.325768025	0.005158255	0.022055986	14371	Fzd9
04390	Hippo signaling pathway	4.325768025	0.005158255	0.022055986	19052	Ppp2ca
04390	Hippo signaling pathway	4.325768025	0.005158255	0.022055986	13542	Dvl1
04390	Hippo signaling pathway	4.325768025	0.005158255	0.022055986	12162	Bmp7
04724	Glutamatergic synapse	5.008784029	0.00539015	0.022656901	16438	Itpr1
04724	Glutamatergic synapse	5.008784029	0.00539015	0.022656901	14811	Grin2a
04724	Glutamatergic synapse	5.008784029	0.00539015	0.022656901	140919	Slc17a6
04724	Glutamatergic synapse	5.008784029	0.00539015	0.022656901	14802	Gria4
04724	Glutamatergic synapse	5.008784029	0.00539015	0.022656901	11515	Adcy9
04724	Glutamatergic synapse	5.008784029	0.00539015	0.022656901	19056	Ppp3cb
04722	Neurotrophin signaling pathway	4.719019664	0.007304801	0.030193175	109880	Braf
04722	Neurotrophin signaling pathway	4.719019664	0.007304801	0.030193175	12323	Camk2b
04722	Neurotrophin signaling pathway	4.719019664	0.007304801	0.030193175	108960	Irak2
04722	Neurotrophin signaling pathway	4.719019664	0.007304801	0.030193175	26414	Mapk10
04722	Neurotrophin signaling pathway	4.719019664	0.007304801	0.030193175	12326	Camk4
04722	Neurotrophin signaling pathway	4.719019664	0.007304801	0.030193175	19353	Rac1
04071	Sphingolipid signaling pathway	4.680339175	0.007615544	0.030961556	18386	Oprd1
04071	Sphingolipid signaling pathway	4.680339175	0.007615544	0.030961556	26414	Mapk10
04071	Sphingolipid signaling pathway	4.680339175	0.007615544	0.030961556	19052	Ppp2ca
04071	Sphingolipid signaling pathway	4.680339175	0.007615544	0.030961556	73699	Ppp2r1b
04071	Sphingolipid signaling pathway	4.680339175	0.007615544	0.030961556	19353	Rac1
04071	Sphingolipid signaling pathway	4.680339175	0.007615544	0.030961556	26932	Ppp2r5e
04611	Platelet activation	4.604849833	0.008266923	0.031670802	16438	Itpr1
04611	Platelet activation	4.604849833	0.008266923	0.031670802	60596	Gucyl1a3

04611	Platelet activation	4.604849833	0.008266923	0.031670802	12825	Col3a1
04611	Platelet activation	4.604849833	0.008266923	0.031670802	70549	Tln2
04611	Platelet activation	4.604849833	0.008266923	0.031670802	11515	Adcy9
04611	Platelet activation	4.604849833	0.008266923	0.031670802	18441	P2ry1
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	14168	Fgf13
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	16334	Ins2
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	71960	Myh14
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	14180	Fgf9
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	319480	Itga11
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	73341	Arhgef6
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	19353	Rac1
04810	Regulation of actin cytoskeleton	3.557640993	0.00826917	0.031670802	109880	Braf
04350	TGF-beta signaling pathway	5.598052738	0.008300815	0.031670802	19052	Ppp2ca
04350	TGF-beta signaling pathway	5.598052738	0.008300815	0.031670802	12162	Bmp7
04350	TGF-beta signaling pathway	5.598052738	0.008300815	0.031670802	110542	Amhr2
04350	TGF-beta signaling pathway	5.598052738	0.008300815	0.031670802	73699	Ppp2r1b
04350	TGF-beta signaling pathway	5.598052738	0.008300815	0.031670802	11480	Acvr2a
04911	Insulin secretion	5.598052738	0.008300815	0.031670802	11517	Adcyap1r1
04911	Insulin secretion	5.598052738	0.008300815	0.031670802	11515	Adcy9
04911	Insulin secretion	5.598052738	0.008300815	0.031670802	11516	Adcyap1
04911	Insulin secretion	5.598052738	0.008300815	0.031670802	12323	Camk2b
04911	Insulin secretion	5.598052738	0.008300815	0.031670802	16334	Ins2
04925	Aldosterone synthesis and secretion	5.532959102	0.00873814	0.032834222	16438	Itpr1
04925	Aldosterone synthesis and secretion	5.532959102	0.00873814	0.032834222	11515	Adcy9
04925	Aldosterone synthesis and secretion	5.532959102	0.00873814	0.032834222	12326	Camk4
04925	Aldosterone synthesis and secretion	5.532959102	0.00873814	0.032834222	269060	Dagla
04925	Aldosterone synthesis and secretion	5.532959102	0.00873814	0.032834222	12323	Camk2b
04658	Th1 and Th2 cell differentiation	5.469361871	0.009192005	0.034024139	13389	Dil3
04658	Th1 and Th2 cell differentiation	5.469361871	0.009192005	0.034024139	19056	Ppp3cb
04658	Th1 and Th2 cell differentiation	5.469361871	0.009192005	0.034024139	26414	Mapk10
04658	Th1 and Th2 cell differentiation	5.469361871	0.009192005	0.034024139	18131	Notch3
04658	Th1 and Th2 cell differentiation	5.469361871	0.009192005	0.034024139	18761	Prkcq
04727	GABAergic synapse	5.407210031	0.009662773	0.035240702	11515	Adcy9
04727	GABAergic synapse	5.407210031	0.009662773	0.035240702	22348	Slc32a1
04727	GABAergic synapse	5.407210031	0.009662773	0.035240702	14397	Gabra4
04727	GABAergic synapse	5.407210031	0.009662773	0.035240702	54393	Gabbr1
04727	GABAergic synapse	5.407210031	0.009662773	0.035240702	14402	Gabbr3
05414	Dilated cardiomyopathy (DCM)	5.346454862	0.010150805	0.036484053	319480	Itga11

05414	Dilated cardiomyopathy (DCM)	5.346454862	0.010150805	0.036484053	20541	Slc8a1
05414	Dilated cardiomyopathy (DCM)	5.346454862	0.010150805	0.036484053	12300	Cacng2
05414	Dilated cardiomyopathy (DCM)	5.346454862	0.010150805	0.036484053	319734	Cacna2d4
05414	Dilated cardiomyopathy (DCM)	5.346454862	0.010150805	0.036484053	11515	Adcy9
04914	Progesterone-mediated oocyte maturation	5.287049808	0.010656464	0.037222579	26414	Mapk10
04914	Progesterone-mediated oocyte maturation	5.287049808	0.010656464	0.037222579	16334	Ins2
04914	Progesterone-mediated oocyte maturation	5.287049808	0.010656464	0.037222579	109880	Braf
04914	Progesterone-mediated oocyte maturation	5.287049808	0.010656464	0.037222579	11515	Adcy9
04914	Progesterone-mediated oocyte maturation	5.287049808	0.010656464	0.037222579	16001	Igflr
04974	Protein digestion and absorption	5.287049808	0.010656464	0.037222579	12825	Col3a1
04974	Protein digestion and absorption	5.287049808	0.010656464	0.037222579	20541	Slc8a1
04974	Protein digestion and absorption	5.287049808	0.010656464	0.037222579	12840	Col9a2
04974	Protein digestion and absorption	5.287049808	0.010656464	0.037222579	70008	Ace2
04974	Protein digestion and absorption	5.287049808	0.010656464	0.037222579	71355	Col24a1
04913	Ovarian steroidogenesis	6.563234245	0.013096127	0.045108882	16001	Igflr
04913	Ovarian steroidogenesis	6.563234245	0.013096127	0.045108882	16334	Ins2
04913	Ovarian steroidogenesis	6.563234245	0.013096127	0.045108882	230459	Cyp2j13
04913	Ovarian steroidogenesis	6.563234245	0.013096127	0.045108882	11515	Adcy9
05418	Fluid shear stress and atherosclerosis	4.021136474	0.016180948	0.05497089	16598	Klf2
05418	Fluid shear stress and atherosclerosis	4.021136474	0.016180948	0.05497089	12387	Ctnnb1
05418	Fluid shear stress and atherosclerosis	4.021136474	0.016180948	0.05497089	19353	Rac1
05418	Fluid shear stress and atherosclerosis	4.021136474	0.016180948	0.05497089	17258	Mef2a
05418	Fluid shear stress and atherosclerosis	4.021136474	0.016180948	0.05497089	11480	Acvr2a
05418	Fluid shear stress and atherosclerosis	4.021136474	0.016180948	0.05497089	26414	Mapk10
04916	Melanogenesis	4.758344828	0.016762305	0.056176373	12323	Camk2b
04916	Melanogenesis	4.758344828	0.016762305	0.056176373	12387	Ctnnb1
04916	Melanogenesis	4.758344828	0.016762305	0.056176373	11515	Adcy9
04916	Melanogenesis	4.758344828	0.016762305	0.056176373	14371	Fzd9
04916	Melanogenesis	4.758344828	0.016762305	0.056176373	13542	Dvl1
05012	Parkinson's disease	3.965287356	0.017318941	0.057267966	17705	ATP6
05012	Parkinson's disease	3.965287356	0.017318941	0.057267966	214084	Slc18a2
05012	Parkinson's disease	3.965287356	0.017318941	0.057267966	66377	Ndufc1
05012	Parkinson's disease	3.965287356	0.017318941	0.057267966	12869	Cox8b
05012	Parkinson's disease	3.965287356	0.017318941	0.057267966	11950	Atp5f1
05012	Parkinson's disease	3.965287356	0.017318941	0.057267966	17719	ND4
05217	Basal cell carcinoma	6.042342638	0.017645686	0.05758066	14371	Fzd9
05217	Basal cell carcinoma	6.042342638	0.017645686	0.05758066	12387	Ctnnb1
05217	Basal cell carcinoma	6.042342638	0.017645686	0.05758066	13542	Dvl1

05217	Basal cell carcinoma	6.042342638	0.017645686	0.05758066	15245	Hhip
04922	Glucagon signaling pathway	4.665043949	0.018231193	0.058718647	19056	Ppp3cb
04922	Glucagon signaling pathway	4.665043949	0.018231193	0.058718647	19013	Ppara
04922	Glucagon signaling pathway	4.665043949	0.018231193	0.058718647	19017	Ppargc1a
04922	Glucagon signaling pathway	4.665043949	0.018231193	0.058718647	16438	Itpr1
04922	Glucagon signaling pathway	4.665043949	0.018231193	0.058718647	12323	Camk2b
04932	Non-alcoholic fatty liver disease (NAFLD)	3.781466088	0.021769654	0.069216335	19353	Rac1
04932	Non-alcoholic fatty liver disease (NAFLD)	3.781466088	0.021769654	0.069216335	66377	Ndufc1
04932	Non-alcoholic fatty liver disease (NAFLD)	3.781466088	0.021769654	0.069216335	19013	Ppara
04932	Non-alcoholic fatty liver disease (NAFLD)	3.781466088	0.021769654	0.069216335	26414	Mapk10
04932	Non-alcoholic fatty liver disease (NAFLD)	3.781466088	0.021769654	0.069216335	12869	Cox8b
04932	Non-alcoholic fatty liver disease (NAFLD)	3.781466088	0.021769654	0.069216335	16334	Ins2
00760	Nicotinate and nicotinamide metabolism	8.157162562	0.023557051	0.07395125	68646	Nadk2
00760	Nicotinate and nicotinamide metabolism	8.157162562	0.023557051	0.07395125	107569	Nt5c3
00760	Nicotinate and nicotinamide metabolism	8.157162562	0.023557051	0.07395125	226518	Nmnat2
05143	African trypanosomiasis	7.930574713	0.025500328	0.079051016	15129	Hbb-b1
05143	African trypanosomiasis	7.930574713	0.025500328	0.079051016	16775	Lama4
05143	African trypanosomiasis	7.930574713	0.025500328	0.079051016	209176	Ido2
04920	Adipocytokine signaling pathway	5.361515299	0.026954373	0.082526969	19013	Ppara
04920	Adipocytokine signaling pathway	5.361515299	0.026954373	0.082526969	19017	Ppargc1a
04920	Adipocytokine signaling pathway	5.361515299	0.026954373	0.082526969	26414	Mapk10
04920	Adipocytokine signaling pathway	5.361515299	0.026954373	0.082526969	18761	Prkcq
05216	Thyroid cancer	7.716234856	0.027536372	0.083280734	12387	Ctnnb1
05216	Thyroid cancer	7.716234856	0.027536372	0.083280734	76551	Ccdc6
05216	Thyroid cancer	7.716234856	0.027536372	0.083280734	109880	Braf
00562	Inositol phosphate metabolism	5.287049808	0.028307096	0.08357333	83493	Sacm11
00562	Inositol phosphate metabolism	5.287049808	0.028307096	0.08357333	75678	Ippk
00562	Inositol phosphate metabolism	5.287049808	0.028307096	0.08357333	227733	Pip5k11
00562	Inositol phosphate metabolism	5.287049808	0.028307096	0.08357333	54384	Mtmr7
04917	Prolactin signaling pathway	5.287049808	0.028307096	0.08357333	12700	Cish
04917	Prolactin signaling pathway	5.287049808	0.028307096	0.08357333	19116	Prlr
04917	Prolactin signaling pathway	5.287049808	0.028307096	0.08357333	16334	Ins2
04917	Prolactin signaling pathway	5.287049808	0.028307096	0.08357333	26414	Mapk10
04971	Gastric acid secretion	5.14415657	0.031145262	0.089814244	110895	Slc9a4
04971	Gastric acid secretion	5.14415657	0.031145262	0.089814244	16438	Itpr1
04971	Gastric acid secretion	5.14415657	0.031145262	0.089814244	12323	Camk2b
04971	Gastric acid secretion	5.14415657	0.031145262	0.089814244	11515	Adcy9
05210	Colorectal cancer	5.14415657	0.031145262	0.089814244	12387	Ctnnb1

05210	Colorectal cancer	5.14415657	0.031145262	0.089814244	19353	Rac1
05210	Colorectal cancer	5.14415657	0.031145262	0.089814244	26414	Mapk10
05210	Colorectal cancer	5.14415657	0.031145262	0.089814244	109880	Braf
05212	Pancreatic cancer	5.075567816	0.032631845	0.093019513	73341	Arhgef6
05212	Pancreatic cancer	5.075567816	0.032631845	0.093019513	109880	Braf
05212	Pancreatic cancer	5.075567816	0.032631845	0.093019513	19353	Rac1
05212	Pancreatic cancer	5.075567816	0.032631845	0.093019513	26414	Mapk10
05218	Melanoma	5.008784029	0.03416417	0.096280844	14168	Fgf13
05218	Melanoma	5.008784029	0.03416417	0.096280844	14180	Fgf9
05218	Melanoma	5.008784029	0.03416417	0.096280844	109880	Braf
05218	Melanoma	5.008784029	0.03416417	0.096280844	16001	Igflr
04260	Cardiac muscle contraction	4.880353669	0.0373682	0.102970151	20541	Slc8a1
04260	Cardiac muscle contraction	4.880353669	0.0373682	0.102970151	12869	Cox8b
04260	Cardiac muscle contraction	4.880353669	0.0373682	0.102970151	12300	Cacng2
04260	Cardiac muscle contraction	4.880353669	0.0373682	0.102970151	319734	Cacna2d4
04970	Salivary secretion	4.880353669	0.0373682	0.102970151	16438	Itpr1
04970	Salivary secretion	4.880353669	0.0373682	0.102970151	11515	Adcy9
04970	Salivary secretion	4.880353669	0.0373682	0.102970151	60596	Gucyl a3
04970	Salivary secretion	4.880353669	0.0373682	0.102970151	67972	Atp2b1
00604	Glycosphingolipid biosynthesis - ganglio series	12.68891954	0.042297199	0.114018535	20447	St6galnac3
00604	Glycosphingolipid biosynthesis - ganglio series	12.68891954	0.042297199	0.114018535	20449	St8sia1
00730	Thiamine metabolism	12.68891954	0.042297199	0.114018535	68870	Ak8
00730	Thiamine metabolism	12.68891954	0.042297199	0.114018535	11431	Acp1
04512	ECM-receptor interaction	4.58635646	0.046215246	0.123240657	12840	Col9a2
04512	ECM-receptor interaction	4.58635646	0.046215246	0.123240657	16775	Lama4
04512	ECM-receptor interaction	4.58635646	0.046215246	0.123240657	319480	Itga11
04512	ECM-receptor interaction	4.58635646	0.046215246	0.123240657	21828	Thbs4
05152	Tuberculosis	3.207872917	0.046921896	0.123793938	19056	Ppp3cb
05152	Tuberculosis	3.207872917	0.046921896	0.123793938	16706	Ksr1
05152	Tuberculosis	3.207872917	0.046921896	0.123793938	108960	Irak2
05152	Tuberculosis	3.207872917	0.046921896	0.123793938	26414	Mapk10
05152	Tuberculosis	3.207872917	0.046921896	0.123793938	12323	Camk2b
05152	Tuberculosis	3.207872917	0.046921896	0.123793938	21871	Atp6v0a2
04270	Vascular smooth muscle contraction	3.688639401	0.04791651	0.124341065	18761	Prkcq
04270	Vascular smooth muscle contraction	3.688639401	0.04791651	0.124341065	11515	Adcy9
04270	Vascular smooth muscle contraction	3.688639401	0.04791651	0.124341065	109880	Braf
04270	Vascular smooth muscle contraction	3.688639401	0.04791651	0.124341065	16438	Itpr1
04270	Vascular smooth muscle contraction	3.688639401	0.04791651	0.124341065	60596	Gucyl a3

05410	Hypertrophic cardiomyopathy (HCM)	4.531756979	0.048132025	0.124341065	319734	Cacna2d4
05410	Hypertrophic cardiomyopathy (HCM)	4.531756979	0.048132025	0.124341065	12300	Cacng2
05410	Hypertrophic cardiomyopathy (HCM)	4.531756979	0.048132025	0.124341065	20541	Slc8a1
05410	Hypertrophic cardiomyopathy (HCM)	4.531756979	0.048132025	0.124341065	319480	Itga11
04012	ErbB signaling pathway	4.478442191	0.050098998	0.128088161	26414	Mapk10
04012	ErbB signaling pathway	4.478442191	0.050098998	0.128088161	13867	ErbB3
04012	ErbB signaling pathway	4.478442191	0.050098998	0.128088161	12323	Camk2b
04012	ErbB signaling pathway	4.478442191	0.050098998	0.128088161	109880	Braf
04540	Gap junction	4.426367281	0.052116601	0.131886909	15558	Htr2a
04540	Gap junction	4.426367281	0.052116601	0.131886909	16438	Itpr1
04540	Gap junction	4.426367281	0.052116601	0.131886909	60596	Gucyl1a3
04540	Gap junction	4.426367281	0.052116601	0.131886909	11515	Adcy9
00450	Selenocompound metabolism	11.19610548	0.054031143	0.134379436	214580	Pstk
00450	Selenocompound metabolism	11.19610548	0.054031143	0.134379436	211006	Sepsecs
05215	Prostate cancer	4.375489497	0.054185257	0.134379436	109880	Braf
05215	Prostate cancer	4.375489497	0.054185257	0.134379436	16334	Ins2
05215	Prostate cancer	4.375489497	0.054185257	0.134379436	16001	Igflr
05215	Prostate cancer	4.375489497	0.054185257	0.134379436	12387	Ctnnb1
05160	Hepatitis C	3.551003603	0.055721536	0.135578326	19052	Ppp2ca
05160	Hepatitis C	3.551003603	0.055721536	0.135578326	73699	Ppp2r1b
05160	Hepatitis C	3.551003603	0.055721536	0.135578326	109880	Braf
05160	Hepatitis C	3.551003603	0.055721536	0.135578326	19013	Ppara
05160	Hepatitis C	3.551003603	0.055721536	0.135578326	26414	Mapk10
04742	Taste transduction	4.325768025	0.056305375	0.135578326	12496	Entpd2
04742	Taste transduction	4.325768025	0.056305375	0.135578326	14397	Gabra4
04742	Taste transduction	4.325768025	0.056305375	0.135578326	54393	Gabbr1
04742	Taste transduction	4.325768025	0.056305375	0.135578326	18441	P2ry1
00600	Sphingolipid metabolism	5.947931034	0.05630874	0.135578326	77626	Smpd4
00600	Sphingolipid metabolism	5.947931034	0.05630874	0.135578326	58994	Smpd3
00600	Sphingolipid metabolism	5.947931034	0.05630874	0.135578326	19012	Plpp1
04912	GnRH signaling pathway	4.27716389	0.058477355	0.139445999	16438	Itpr1
04912	GnRH signaling pathway	4.27716389	0.058477355	0.139445999	26414	Mapk10
04912	GnRH signaling pathway	4.27716389	0.058477355	0.139445999	11515	Adcy9
04912	GnRH signaling pathway	4.27716389	0.058477355	0.139445999	12323	Camk2b
04657	IL-17 signaling pathway	4.183160288	0.062978431	0.148749056	15568	Elavl1
04657	IL-17 signaling pathway	4.183160288	0.062978431	0.148749056	26414	Mapk10
04657	IL-17 signaling pathway	4.183160288	0.062978431	0.148749056	225724	Mapk4
04657	IL-17 signaling pathway	4.183160288	0.062978431	0.148749056	239114	Il17d

04740	Olfactory transduction	0.339275924	0.067904737	0.158871461	258329	Olfr135
04740	Olfactory transduction	0.339275924	0.067904737	0.158871461	20541	Slc8a1
04740	Olfactory transduction	0.339275924	0.067904737	0.158871461	257734	Olfr1355
04740	Olfactory transduction	0.339275924	0.067904737	0.158871461	12323	Camk2b
05014	Amyotrophic lateral sclerosis (ALS)	5.490397878	0.069771433	0.161713227	19056	Ppp3cb
05014	Amyotrophic lateral sclerosis (ALS)	5.490397878	0.069771433	0.161713227	19353	Rac1
05014	Amyotrophic lateral sclerosis (ALS)	5.490397878	0.069771433	0.161713227	14811	Grin2a
03015	mRNA surveillance pathway	3.965287356	0.075164235	0.171015874	26932	Ppp2r5e
03015	mRNA surveillance pathway	3.965287356	0.075164235	0.171015874	67897	Rnmt
03015	mRNA surveillance pathway	3.965287356	0.075164235	0.171015874	19052	Ppp2ca
03015	mRNA surveillance pathway	3.965287356	0.075164235	0.171015874	73699	Ppp2r1b
04915	Estrogen signaling pathway	3.965287356	0.075164235	0.171015874	11515	Adcy9
04915	Estrogen signaling pathway	3.965287356	0.075164235	0.171015874	16524	Kcnj9
04915	Estrogen signaling pathway	3.965287356	0.075164235	0.171015874	54393	Gabbr1
04915	Estrogen signaling pathway	3.965287356	0.075164235	0.171015874	16438	Itpr1
04070	Phosphatidylinositol signaling system	3.884363125	0.080418627	0.180845125	83493	Sacm11
04070	Phosphatidylinositol signaling system	3.884363125	0.080418627	0.180845125	75678	Ippk
04070	Phosphatidylinositol signaling system	3.884363125	0.080418627	0.180845125	16438	Itpr1
04070	Phosphatidylinositol signaling system	3.884363125	0.080418627	0.180845125	54384	Mtmr7
04923	Regulation of lipolysis in adipocytes	5.19092163	0.080942778	0.180845125	16334	Ins2
04923	Regulation of lipolysis in adipocytes	5.19092163	0.080942778	0.180845125	19218	Ptger3
04923	Regulation of lipolysis in adipocytes	5.19092163	0.080942778	0.180845125	11515	Adcy9
04659	Th17 cell differentiation	3.732035159	0.091591523	0.202809801	18761	Prkcq
04659	Th17 cell differentiation	3.732035159	0.091591523	0.202809801	239114	Il17d
04659	Th17 cell differentiation	3.732035159	0.091591523	0.202809801	26414	Mapk10
04659	Th17 cell differentiation	3.732035159	0.091591523	0.202809801	19056	Ppp3cb
04972	Pancreatic secretion	3.695801808	0.094524557	0.207452125	16438	Itpr1
04972	Pancreatic secretion	3.695801808	0.094524557	0.207452125	19353	Rac1
04972	Pancreatic secretion	3.695801808	0.094524557	0.207452125	11515	Adcy9
04972	Pancreatic secretion	3.695801808	0.094524557	0.207452125	67972	Atp2b1
04066	HIF-1 signaling pathway	3.625405583	0.100559952	0.218762002	16334	Ins2
04066	HIF-1 signaling pathway	3.625405583	0.100559952	0.218762002	12323	Camk2b
04066	HIF-1 signaling pathway	3.625405583	0.100559952	0.218762002	16001	Igflr
04066	HIF-1 signaling pathway	3.625405583	0.100559952	0.218762002	11863	Arnt
04060	Cytokine-cytokine receptor interaction	2.45818552	0.101715189	0.219351015	19116	Prlr
04060	Cytokine-cytokine receptor interaction	2.45818552	0.101715189	0.219351015	21944	Tnfsf12
04060	Cytokine-cytokine receptor interaction	2.45818552	0.101715189	0.219351015	12162	Bmp7
04060	Cytokine-cytokine receptor interaction	2.45818552	0.101715189	0.219351015	12986	Csf3r

04060	Cytokine-cytokine receptor interaction	2.45818552	0.101715189	0.219351015	239114	Il17d
04060	Cytokine-cytokine receptor interaction	2.45818552	0.101715189	0.219351015	110542	Amhr2
04060	Cytokine-cytokine receptor interaction	2.45818552	0.101715189	0.219351015	11480	Acvr2a
04630	Jak-STAT signaling pathway	2.992669703	0.107524834	0.229880679	239114	Il17d
04630	Jak-STAT signaling pathway	2.992669703	0.107524834	0.229880679	12986	Csf3r
04630	Jak-STAT signaling pathway	2.992669703	0.107524834	0.229880679	12700	Cish
04630	Jak-STAT signaling pathway	2.992669703	0.107524834	0.229880679	19116	Prlr
04630	Jak-STAT signaling pathway	2.992669703	0.107524834	0.229880679	14580	Gfap
04213	Longevity regulating pathway - multiple species	4.604849833	0.110606455	0.23444787	16334	Ins2
04213	Longevity regulating pathway - multiple species	4.604849833	0.110606455	0.23444787	16001	Igflr
04213	Longevity regulating pathway - multiple species	4.604849833	0.110606455	0.23444787	11515	Adcy9
05167	Kaposi's sarcoma-associated herpesvirus infection	2.631342762	0.111800148	0.234969802	19353	Rac1
05167	Kaposi's sarcoma-associated herpesvirus infection	2.631342762	0.111800148	0.234969802	16438	Itpr1
05167	Kaposi's sarcoma-associated herpesvirus infection	2.631342762	0.111800148	0.234969802	54720	Rcan1
05167	Kaposi's sarcoma-associated herpesvirus infection	2.631342762	0.111800148	0.234969802	19056	Ppp3cb
05167	Kaposi's sarcoma-associated herpesvirus infection	2.631342762	0.111800148	0.234969802	26414	Mapk10
05167	Kaposi's sarcoma-associated herpesvirus infection	2.631342762	0.111800148	0.234969802	12387	Ctnnb1
04725	Cholinergic synapse	3.368739701	0.126985361	0.263876669	16438	Itpr1
04725	Cholinergic synapse	3.368739701	0.126985361	0.263876669	12323	Camk2b
04725	Cholinergic synapse	3.368739701	0.126985361	0.263876669	11515	Adcy9
04725	Cholinergic synapse	3.368739701	0.126985361	0.263876669	12326	Camk4
04141	Protein processing in endoplasmic reticulum	2.84930828	0.128949067	0.263876669	26414	Mapk10
04141	Protein processing in endoplasmic reticulum	2.84930828	0.128949067	0.263876669	71853	Pdia6
04141	Protein processing in endoplasmic reticulum	2.84930828	0.128949067	0.263876669	54609	Ubqln2
04141	Protein processing in endoplasmic reticulum	2.84930828	0.128949067	0.263876669	103963	Rpn1
04141	Protein processing in endoplasmic reticulum	2.84930828	0.128949067	0.263876669	20334	Sec23a
00010	Glycolysis / Gluconeogenesis	4.325768025	0.129810297	0.263876669	56421	Pfkip
00010	Glycolysis / Gluconeogenesis	4.325768025	0.129810297	0.263876669	621603	Aldh3b2
00010	Glycolysis / Gluconeogenesis	4.325768025	0.129810297	0.263876669	230163	Aldob
05211	Renal cell carcinoma	4.325768025	0.129810297	0.263876669	109880	Braf
05211	Renal cell carcinoma	4.325768025	0.129810297	0.263876669	19353	Rac1
05211	Renal cell carcinoma	4.325768025	0.129810297	0.263876669	11863	Arnt
04621	NOD-like receptor signaling pathway	2.832348112	0.131800724	0.265744549	101613	Nlrp6
04621	NOD-like receptor signaling pathway	2.832348112	0.131800724	0.265744549	67526	Atg12
04621	NOD-like receptor signaling pathway	2.832348112	0.131800724	0.265744549	16438	Itpr1
04621	NOD-like receptor signaling pathway	2.832348112	0.131800724	0.265744549	26414	Mapk10
04621	NOD-like receptor signaling pathway	2.832348112	0.131800724	0.265744549	59125	Nek7
04919	Thyroid hormone signaling pathway	3.310152924	0.134168295	0.268336589	54720	Rcan1

04919	Thyroid hormone signaling pathway	3.310152924	0.134168295	0.268336589	56421	Pfklp
04919	Thyroid hormone signaling pathway	3.310152924	0.134168295	0.268336589	18131	Notch3
04919	Thyroid hormone signaling pathway	3.310152924	0.134168295	0.268336589	12387	Ctnnb1
04622	RIG-I-like receptor signaling pathway	4.198539554	0.14002109	0.277801842	67526	Atg12
04622	RIG-I-like receptor signaling pathway	4.198539554	0.14002109	0.277801842	26414	Mapk10
04622	RIG-I-like receptor signaling pathway	4.198539554	0.14002109	0.277801842	217069	Trim25
05214	Glioma	4.021136474	0.156090703	0.307226145	16001	Igflr
05214	Glioma	4.021136474	0.156090703	0.307226145	12323	Camk2b
05214	Glioma	4.021136474	0.156090703	0.307226145	109880	Braf
00030	Pentose phosphate pathway	5.947931034	0.177748598	0.344387908	230163	Aldob
00030	Pentose phosphate pathway	5.947931034	0.177748598	0.344387908	56421	Pfklp
00052	Galactose metabolism	5.947931034	0.177748598	0.344387908	56421	Pfklp
00052	Galactose metabolism	5.947931034	0.177748598	0.344387908	226413	Lct
04380	Osteoclast differentiation	2.973965517	0.18653224	0.358604617	19353	Rac1
04380	Osteoclast differentiation	2.973965517	0.18653224	0.358604617	19056	Ppp3cb
04380	Osteoclast differentiation	2.973965517	0.18653224	0.358604617	12326	Camk4
04380	Osteoclast differentiation	2.973965517	0.18653224	0.358604617	26414	Mapk10
05132	Salmonella infection	3.660265252	0.197039699	0.375891117	13427	Dync1i2
05132	Salmonella infection	3.660265252	0.197039699	0.375891117	19353	Rac1
05132	Salmonella infection	3.660265252	0.197039699	0.375891117	26414	Mapk10
00051	Fructose and mannose metabolism	5.438108374	0.20891013	0.390848452	230163	Aldob
00051	Fructose and mannose metabolism	5.438108374	0.20891013	0.390848452	56421	Pfklp
03410	Base excision repair	5.438108374	0.20891013	0.390848452	18294	Ogg1
03410	Base excision repair	5.438108374	0.20891013	0.390848452	71726	Smug1
01521	EGFR tyrosine kinase inhibitor resistance	3.568758621	0.209608242	0.390848452	109880	Braf
01521	EGFR tyrosine kinase inhibitor resistance	3.568758621	0.209608242	0.390848452	13867	ErbB3
01521	EGFR tyrosine kinase inhibitor resistance	3.568758621	0.209608242	0.390848452	16001	Igflr
03018	RNA degradation	3.481715728	0.222554036	0.411891051	56421	Pfklp
03018	RNA degradation	3.481715728	0.222554036	0.411891051	78651	Lsm6
03018	RNA degradation	3.481715728	0.222554036	0.411891051	56057	Btg4
00250	Alanine, aspartate and glutamate metabolism	5.14415657	0.230679661	0.42376708	70503	Ddo
00250	Alanine, aspartate and glutamate metabolism	5.14415657	0.230679661	0.42376708	108682	Gpt2
04146	Peroxisome	3.398817734	0.23587173	0.430119037	103737	Pex12
04146	Peroxisome	3.398817734	0.23587173	0.430119037	72129	Pex13
04146	Peroxisome	3.398817734	0.23587173	0.430119037	70503	Ddo
00440	Phosphonate and phosphinate metabolism	15.86114943	0.245664389	0.444706339	236899	Pcytlb
04975	Fat digestion and absorption	4.758344828	0.264721576	0.475731529	19012	Plpp1
04975	Fat digestion and absorption	4.758344828	0.264721576	0.475731529	11303	Abca1

04340	Hedgehog signaling pathway	4.325768025	0.312491226	0.557538303	15245	Hhip
04340	Hedgehog signaling pathway	4.325768025	0.312491226	0.557538303	70425	Csnk1g3
05166	HTLV-I infection	2.024827586	0.315143763	0.558254665	11515	Adcy9
05166	HTLV-I infection	2.024827586	0.315143763	0.558254665	19056	Ppp3cb
05166	HTLV-I infection	2.024827586	0.315143763	0.558254665	70549	Tln2
05166	HTLV-I infection	2.024827586	0.315143763	0.558254665	14371	Fzd9
05166	HTLV-I infection	2.024827586	0.315143763	0.558254665	12387	Ctnnb1
05166	HTLV-I infection	2.024827586	0.315143763	0.558254665	13542	Dvl1
00740	Riboflavin metabolism	11.89586207	0.324157242	0.567303171	11431	Acp1
04978	Mineral absorption	4.229639847	0.324826815	0.567303171	67972	Atp2b1
04978	Mineral absorption	4.229639847	0.324826815	0.567303171	20541	Slc8a1
00564	Glycerophospholipid metabolism	2.943306079	0.331091365	0.574200409	236899	Pcyt1b
00564	Glycerophospholipid metabolism	2.943306079	0.331091365	0.574200409	19012	Plpp1
00564	Glycerophospholipid metabolism	2.943306079	0.331091365	0.574200409	19210	Ptdss1
00380	Tryptophan metabolism	4.137691154	0.337310472	0.580923591	56720	Tdo2
00380	Tryptophan metabolism	4.137691154	0.337310472	0.580923591	209176	Ido2
04933	AGE-RAGE signaling pathway in diabetic complica	2.855006897	0.355079124	0.604575962	26414	Mapk10
04933	AGE-RAGE signaling pathway in diabetic complica	2.855006897	0.355079124	0.604575962	19353	Rac1
04933	AGE-RAGE signaling pathway in diabetic complica	2.855006897	0.355079124	0.604575962	12825	Col3a1
04930	Type II diabetes mellitus	3.965287356	0.36270421	0.604575962	16334	Ins2
04930	Type II diabetes mellitus	3.965287356	0.36270421	0.604575962	26414	Mapk10
05030	Cocaine addiction	3.965287356	0.36270421	0.604575962	214084	Slc18a2
05030	Cocaine addiction	3.965287356	0.36270421	0.604575962	14811	Grin2a
00750	Vitamin B6 metabolism	10.57409962	0.362786945	0.604575962	73373	Phospho2
05142	Chagas disease (American trypanosomiasis)	2.826739502	0.363233139	0.604575962	73699	Ppp2r1b
05142	Chagas disease (American trypanosomiasis)	2.826739502	0.363233139	0.604575962	26414	Mapk10
05142	Chagas disease (American trypanosomiasis)	2.826739502	0.363233139	0.604575962	19052	Ppp2ca
05144	Malaria	3.884363125	0.375605596	0.621001251	15129	Hbb-b1
05144	Malaria	3.884363125	0.375605596	0.621001251	21828	Thbs4
04370	VEGF signaling pathway	3.281617122	0.497113995	0.811080729	19353	Rac1
04370	VEGF signaling pathway	3.281617122	0.497113995	0.811080729	19056	Ppp3cb
05213	Endometrial cancer	3.281617122	0.497113995	0.811080729	109880	Braf
05213	Endometrial cancer	3.281617122	0.497113995	0.811080729	12387	Ctnnb1
04145	Phagosome	2.091580144	0.504751016	0.818158509	21871	Atp6v0a2
04145	Phagosome	2.091580144	0.504751016	0.818158509	13427	Dync1i2
04145	Phagosome	2.091580144	0.504751016	0.818158509	21828	Thbs4
04145	Phagosome	2.091580144	0.504751016	0.818158509	19353	Rac1
04650	Natural killer cell mediated cytotoxicity	2.41949737	0.512958208	0.826062568	109880	Braf

04650	Natural killer cell mediated cytotoxicity	2.41949737	0.512958208	0.826062568	19353	Rac1
04650	Natural killer cell mediated cytotoxicity	2.41949737	0.512958208	0.826062568	19056	Ppp3cb
04218	Cellular senescence	2.046599926	0.53410173	0.854562768	16438	Itpr1
04218	Cellular senescence	2.046599926	0.53410173	0.854562768	67738	Ppid
04218	Cellular senescence	2.046599926	0.53410173	0.854562768	19056	Ppp3cb
04218	Cellular senescence	2.046599926	0.53410173	0.854562768	64930	Tsc1
00061	Fatty acid biosynthesis	6.797635468	0.549938651	0.874261446	14104	Fasn
05223	Non-small cell lung cancer	2.88384535	0.611740347	0.966315963	109880	Braf
05223	Non-small cell lung cancer	2.88384535	0.611740347	0.966315963	14198	Fhit
00603	Glycosphingolipid biosynthesis - globo and isoglobo	5.947931034	0.622078286	0.976426676	20449	St8sia1
05034	Alcoholism	1.912902443	0.634049981	0.987613928	109880	Braf
05034	Alcoholism	1.912902443	0.634049981	0.987613928	12326	Camk4
05034	Alcoholism	1.912902443	0.634049981	0.987613928	214084	Slc18a2
05034	Alcoholism	1.912902443	0.634049981	0.987613928	14811	Grin2a
04926	Relaxin signaling pathway	2.179394578	0.639688085	0.987613928	26414	Mapk10
04926	Relaxin signaling pathway	2.179394578	0.639688085	0.987613928	11515	Adcy9
04926	Relaxin signaling pathway	2.179394578	0.639688085	0.987613928	12825	Col3a1
04664	Fc epsilon RI signaling pathway	2.799026369	0.64115259	0.987613928	19353	Rac1
04664	Fc epsilon RI signaling pathway	2.799026369	0.64115259	0.987613928	26414	Mapk10
04210	Apoptosis	2.099269777	0.690746957	1	19249	Ptpn13
04210	Apoptosis	2.099269777	0.690746957	1	26414	Mapk10
04210	Apoptosis	2.099269777	0.690746957	1	16438	Itpr1
04662	B cell receptor signaling pathway	2.643524904	0.700710817	1	19353	Rac1
04662	B cell receptor signaling pathway	2.643524904	0.700710817	1	19056	Ppp3cb
04918	Thyroid hormone synthesis	2.607312234	0.71573644	1	11515	Adcy9
04918	Thyroid hormone synthesis	2.607312234	0.71573644	1	16438	Itpr1
00220	Arginine biosynthesis	5.008784029	0.727473119	1	108682	Gpt2
05133	Pertussis	2.537783908	0.745931651	1	26414	Mapk10
05133	Pertussis	2.537783908	0.745931651	1	12258	Serping1
00531	Glycosaminoglycan degradation	4.531756979	0.795905501	1	27029	Sgsh
00360	Phenylalanine metabolism	4.137691154	0.862908814	1	621603	Aldh3b2
00515	Mannose type O-glycan biosynthesis	4.137691154	0.862908814	1	246179	Fktn
00900	Terpenoid backbone biosynthesis	4.137691154	0.862908814	1	67422	Dhdds
00534	Glycosaminoglycan biosynthesis - heparan sulfate / h	3.965287356	0.895883907	1	15476	Hs3st1
00340	Histidine metabolism	3.806675862	0.928512861	1	621603	Aldh3b2
04666	Fc gamma R-mediated phagocytosis	2.187744748	0.930074862	1	19353	Rac1
04666	Fc gamma R-mediated phagocytosis	2.187744748	0.930074862	1	19012	Plpp1
04392	Hippo signaling pathway - multiple species	3.660265252	0.960799302	1	215653	Rassf2

00601	Glycosphingolipid biosynthesis - lacto and neolacto	3.524699872	0.992746823	1	20449	St8sia1
04950	Maturity onset diabetes of the young	3.524699872	0.992746823	1	16334	Ins2
04966	Collecting duct acid secretion	3.524699872	0.992746823	1	21871	Atp6v0a2
05222	Small cell lung cancer	2.068845577	1	1	16775	Lama4
05222	Small cell lung cancer	2.068845577	1	1	14198	Fhit
05204	Chemical carcinogenesis	2.046599926	1	1	11863	Arnt
05204	Chemical carcinogenesis	2.046599926	1	1	621603	Aldh3b2
05164	Influenza A	1.699408867	1	1	26414	Mapk10
05164	Influenza A	1.699408867	1	1	217069	Trim25
05164	Influenza A	1.699408867	1	1	232989	Hnrnpul1
04514	Cell adhesion molecules (CAMs)	1.689353193	1	1	320840	Negr1
04514	Cell adhesion molecules (CAMs)	1.689353193	1	1	319504	Nrcam
04514	Cell adhesion molecules (CAMs)	1.689353193	1	1	269116	Nfasc
03020	RNA polymerase	3.172229885	1	1	20017	Polr1b
04620	Toll-like receptor signaling pathway	1.922563567	1	1	19353	Rac1
04620	Toll-like receptor signaling pathway	1.922563567	1	1	26414	Mapk10
00640	Propanoate metabolism	3.069899889	1	1	20916	Sucla2
00020	Citrate cycle (TCA cycle)	2.973965517	1	1	20916	Sucla2
04215	Apoptosis - multiple species	2.973965517	1	1	26414	Mapk10
00240	Pyrimidine metabolism	1.884493001	1	1	20017	Polr1b
00240	Pyrimidine metabolism	1.884493001	1	1	107569	Nt5c3
00410	beta-Alanine metabolism	2.88384535	1	1	621603	Aldh3b2
00500	Starch and sucrose metabolism	2.88384535	1	1	70974	Pgm2l1
04660	T cell receptor signaling pathway	1.847900904	1	1	19056	Ppp3cb
04660	T cell receptor signaling pathway	1.847900904	1	1	18761	Prkcq
04064	NF-kappa B signaling pathway	1.830132626	1	1	217069	Trim25
04064	NF-kappa B signaling pathway	1.830132626	1	1	18761	Prkcq
00040	Pentose and glucuronate interconversions	2.799026369	1	1	102448	Xylb
05146	Amoebiasis	1.795601822	1	1	16775	Lama4
05146	Amoebiasis	1.795601822	1	1	12825	Col3a1
04614	Renin-angiotensin system	2.719054187	1	1	70008	Ace2
05145	Toxoplasmosis	1.762349936	1	1	26414	Mapk10
05145	Toxoplasmosis	1.762349936	1	1	16775	Lama4
04960	Aldosterone-regulated sodium reabsorption	2.504392015	1	1	16334	Ins2
00350	Tyrosine metabolism	2.440176835	1	1	621603	Aldh3b2
04670	Leukocyte transendothelial migration	1.655076462	1	1	19353	Rac1
04670	Leukocyte transendothelial migration	1.655076462	1	1	12387	Ctnnb1
00260	Glycine, serine and threonine metabolism	2.379172414	1	1	11655	Alas1

00860	Porphyrin and chlorophyll metabolism	2.321143818	1	1	11655	Alas1
04216	Ferroptosis	2.321143818	1	1	74244	Atg7
05219	Bladder cancer	2.321143818	1	1	109880	Braf
04973	Carbohydrate digestion and absorption	2.213183641	1	1	226413	Lct
03022	Basal transcription factors	2.162884013	1	1	66671	Ccnh
03420	Nucleotide excision repair	2.162884013	1	1	66671	Ccnh
00565	Ether lipid metabolism	2.114819923	1	1	19012	Plpp1
03050	Proteasome	2.068845577	1	1	17463	Psmd7
02010	ABC transporters	2.024827586	1	1	11303	Abca1
00510	N-Glycan biosynthesis	1.942181562	1	1	103963	Rpn1
00520	Amino sugar and nucleotide sugar metabolism	1.942181562	1	1	109785	Pgm3
03040	Spliceosome	1.431081151	1	1	27967	Cherp
03040	Spliceosome	1.431081151	1	1	78651	Lsm6
00071	Fatty acid degradation	1.903337931	1	1	66885	Acadsb
00330	Arginine and proline metabolism	1.903337931	1	1	11702	Amd1
00591	Linoleic acid metabolism	1.903337931	1	1	230459	Cyp2j13
00983	Drug metabolism - other enzymes	1.866017579	1	1	229363	Gmps
04217	Necroptosis	1.612998247	1	1	67738	Ppid
04217	Necroptosis	1.612998247	1	1	26414	Mapk10
04217	Necroptosis	1.612998247	1	1	12323	Camk2b
05134	Legionellosis	1.640808561	1	1	11840	Arf1
04062	Chemokine signaling pathway	1.464106101	1	1	109880	Braf
04062	Chemokine signaling pathway	1.464106101	1	1	19353	Rac1
04062	Chemokine signaling pathway	1.464106101	1	1	11515	Adcy9
00561	Glycerolipid metabolism	1.560113058	1	1	19012	Plpp1
04137	Mitophagy - animal	1.51058566	1	1	26414	Mapk10
05230	Central carbon metabolism in cancer	1.486982759	1	1	56421	Pfkb
00980	Metabolism of xenobiotics by cytochrome P450	1.464106101	1	1	621603	Aldh3b2
00982	Drug metabolism - cytochrome P450	1.420401441	1	1	621603	Aldh3b2
05221	Acute myeloid leukemia	1.379230385	1	1	109880	Braf
04940	Type I diabetes mellitus	1.359527094	1	1	16334	Ins2
04976	Bile secretion	1.340378825	1	1	11515	Adcy9
05220	Chronic myeloid leukemia	1.220088417	1	1	109880	Braf
05323	Rheumatoid arthritis	1.146589115	1	1	21871	Atp6v0a2
03320	PPAR signaling pathway	1.119610548	1	1	19013	Ppara
00140	Steroid hormone biosynthesis	1.093872374	1	1	56448	Cyp2d22
04610	Complement and coagulation cascades	1.093872374	1	1	12258	Serpinc1
05416	Viral myocarditis	1.081442006	1	1	19353	Rac1

00590	Arachidonic acid metabolism	1.069290972	1	1	230459	Cyp2j13
04120	Ubiquitin mediated proteolysis	1.359527094	1	1	67615	Ube2r2
04120	Ubiquitin mediated proteolysis	1.359527094	1	1	75717	Cul5
03013	RNA transport	1.139723312	1	1	54563	Nup210
03013	RNA transport	1.139723312	1	1	66603	Gemin2
03010	Ribosome	1.075332164	1	1	66292	Mrps21
03010	Ribosome	1.075332164	1	1	68052	Rps13
05202	Transcriptional misregulation in cancer	1.040075372	1	1	16001	Igflr
05202	Transcriptional misregulation in cancer	1.040075372	1	1	14048	Eya1
05203	Viral carcinogenesis	0.411977907	1	1	19353	Rac1
04640	Hematopoietic cell lineage	1.001756806	1	1	12986	Csf3r
04668	TNF signaling pathway	0.881174968	1	1	26414	Mapk10
05206	MicroRNAs in cancer	0.677344459	1	1	18131	Notch3
05206	MicroRNAs in cancer	0.677344459	1	1	13867	ErbB3
03008	Ribosome biogenesis in eukaryotes	0.820404281	1	1	110816	Pwp2
04110	Cell cycle	0.767474972	1	1	66671	Ccnh
05161	Hepatitis B	0.665502773	1	1	26414	Mapk10
05162	Measles	0.699756592	1	1	18761	Prkcq
05168	Herpes simplex infection	0.885273456	1	1	67615	Ube2r2
05168	Herpes simplex infection	0.885273456	1	1	26414	Mapk10
05169	Epstein-Barr virus infection	0.865153605	1	1	26414	Mapk10
05169	Epstein-Barr virus infection	0.865153605	1	1	17463	PsmD7
05322	Systemic lupus erythematosus	0.670189412	1	1	14811	Grin2a