Supplemental Table 1: GSA results for all analyzed pathways.

				Gene-set association p-value			
KEGG pathway ID	KEGG pathway name	N genes	N SNPs	$GM_{0.1}$	$PC\text{-}GM_{0.1}$	GM_1	$PC\text{-}GM_1$
72	Synthesis and degradation of ketone bodies	9	128	0.051	**0.003**	0.086	**0.0009**
3320	PPAR signaling pathway	69	1377	**0.042**	**0.004**	0.1	**0.034**
4260	Cardiac muscle contraction	80	2667	0.186	**0.011**	0.174	**0.025**
4520	Adherens junction	77	4063	0.154	**0.012**	0.132	**0.014**
3410	Base excision repair	35	487	0.06	**0.015**	**0.015**	**0.007**
5414	Dilated cardiomyopathy	92	5405	0.71	**0.019**	0.764	0.199
910	Nitrogen metabolism	23	359	**0.016**	**0.02**	**0.031**	**0.011**
5410	Hypertrophic cardiomyopathy (HCM)	89	5006	0.591	**0.02**	0.641	0.265
511	Other glycan degradation	16	193	0.077	**0.023**	0.225	0.091
4320	Dorso-ventral axis formation	25	987	**0.016**	**0.025**	**0.022**	0.055
650	Butanoate metabolism	34	560	0.438	**0.035**	0.659	0.167
4080	Neuroactive ligand-receptor interaction	302	8682	**0.008**	0.073	**0.008**	**0.022**
4740	Olfactory transduction	389	3513	0.344	0.073	0.332	0.188
3060	Protein export	9	114	0.288	0.081	0.214	0.264
4340	Hedgehog signaling pathway	56	1302	0.261	0.085	0.23	**0.05**
3420	Nucleotide excision repair	44	727	0.101	0.088	0.107	0.055
100	Steroid biosynthesis	17	253	**0.023**	0.09	**0.02**	**0.034**
3440	Homologous recombination	28	653	0.203	0.092	0.194	0.117
4514	Cell adhesion molecules (CAMs)	134	6142	0.068	0.096	0.097	0.054
620	Pyruvate metabolism	40	833	0.402	0.102	0.545	0.199
5110	Vibrio cholerae infection	56	1428	0.75	0.103	0.794	0.2
680	Methane metabolism	6	139	0.334	0.108	0.695	0.134
4110	Cell cycle	128	2154	**0.01**	0.11	**0.035**	0.072
310	Lysine degradation	44	835	0.231	0.116	0.227	0.345
4810	Regulation of actin cytoskeleton	216	6849	0.265	0.129	0.058	**0.021**
920	Sulfur metabolism	13	621	0.775	0.129	0.805	0.142
601	Glycosphingolipid biosynthesis - lacto and neolacto series	26	527	**0.017**	0.133	**0.006**	**0.04**
4130	SNARE interactions in vesicular transport	38	762	0.379	0.134	0.446	0.244
520	Amino sugar and nucleotide sugar metabolism	44	942	**0.045**	0.137	0.089	0.446
240	Pyrimidine metabolism	98	2047	0.253	0.141	0.21	**0.028**
5020	Prion diseases	35	939	0.182	0.148	0.457	0.127
603	Glycosphingolipid biosynthesis - globo series	14	334	**0.037**	0.159	**0.03**	0.112
3430	Mismatch repair	23	459	0.107	0.16	0.281	0.284
4530	Tight junction	134	6157	0.512	0.165	0.398	0.308
3010	Ribosome	88	546	0.347	0.178	0.47	0.22
5220	Chronic myeloid leukemia	75	1949	0.312	0.179	0.171	0.073
5212	Pancreatic cancer	72	1857	0.534	0.203	0.288	0.105
4660	T cell receptor signaling pathway	108	2989	0.291	0.208	0.181	0.146
4020	Calcium signaling pathway	178	8062	0.254	0.211	0.118	0.138

4512	ECM-receptor interaction	84	3716	0.656	0.213	0.677	0.285
514	O-Mannosyl glycan biosynthesis	3	62	0.221	0.214	0.108	0.15
5120	Epithelial cell signaling in Helicobacter pylori infection	68	1538	0.524	0.216	0.463	0.207
533	Keratan sulfate biosynthesis	16	377	0.169	0.217	0.137	0.137
3018	RNA degradation	59	907	0.474	0.228	0.517	0.366
4940	Type I diabetes mellitus	44	1175	0.068	0.229	0.094	0.347
3020	RNA polymerase	29	390	0.274	0.232	0.208	0.116
360	Phenylalanine metabolism	22	337	**0.004**	0.235	0.069	0.34
140	Steroid hormone biosynthesis	55	1925	0.878	0.239	0.73	0.614
4914	Progesterone-mediated oocyte maturation	86	2679	0.493	0.244	0.39	0.133
62	Fatty acid elongation in mitochondria	8	122	0.301	0.25	0.321	0.387
250	Alanine aspartate and glutamate metabolism	31	629	0.5	0.256	0.873	0.605
330	Arginine and proline metabolism	54	709	0.356	0.257	0.244	0.384
565	Ether lipid metabolism	36	709	0.373	0.262	0.213	0.135
790	Folate biosynthesis	11	154	0.608	0.268	0.42	0.282
564	Glycerophospholipid metabolism	69	1645	0.406	0.27	0.53	0.245
561	Glycerolipid metabolism	45	1387	0.385	0.273	0.54	0.485
3050	Proteasome	48	592	0.178	0.278	0.134	0.318
4350	TGF-beta signaling pathway	87	1754	0.576	0.291	0.683	0.373
4610	Complement and coagulation cascades	69	1390	0.704	0.291	0.721	0.55
270	Cysteine and methionine metabolism	34	595	0.536	0.295	0.193	0.143
4666	Fc gamma R-mediated phagocytosis	97	3294	0.061	0.32	0.054	0.108
4930	Type II diabetes mellitus	47	1935	0.294	0.321	0.463	0.517
4144	Endocytosis	187	5235	0.26	0.327	**0.041**	0.109
590	Arachidonic acid metabolism	58	1153	0.33	0.329	0.168	0.444
532	Chondroitin sulfate biosynthesis	22	1208	0.863	0.341	0.86	0.258
640	Propanoate metabolism	33	902	0.819	0.341	0.767	0.441
1040	Biosynthesis of unsaturated fatty acids	22	476	0.643	0.352	0.65	0.24
4620	Toll-like receptor signaling pathway	101	1524	0.275	0.353	0.312	0.263
280	Valine leucine and isoleucine degradation	44	994	0.504	0.362	0.391	0.313
860	Porphyrin and chlorophyll metabolism	41	1476	0.57	0.363	0.681	0.605
4210	Apoptosis	88	1820	**0.033**	0.372	0.056	0.243
300	Lysine biosynthesis	4	75	0.443	0.372	0.291	0.308
380	Tryptophan metabolism	40	837	**0.024**	0.378	0.091	0.487
980	Metabolism of xenobiotics by cytochrome P450	70	2005	0.876	0.384	0.753	0.687
5210	Colorectal cancer	85	2645	0.594	0.389	0.325	0.421
5322	Systemic lupus erythematosus	140	1860	0.158	0.394	0.164	0.226
4060	Cytokine-cytokine receptor interaction	278	4254	0.166	0.395	0.093	0.346
3022	Basal transcription factors	38	583	0.694	0.395	0.836	0.916

5014	Amyotrophic lateral sclerosis (ALS)	53	1671	0.109	0.398	**0.039**	0.142
4670	Leukocyte transendothelial migration	118	3811	0.452	0.405	0.398	0.075
4270	Vascular smooth muscle contraction	125	5555	0.965	0.405	0.895	0.513
562	Inositol phosphate metabolism	54	2147	0.99	0.405	0.968	0.795
5213	Endometrial cancer	52	2505	0.476	0.41	0.395	0.348
4070	Phosphatidylinositol signaling system	76	3675	0.987	0.415	0.985	0.868
52	Galactose metabolism	26	603	0.058	0.421	0.07	0.465
534	Heparan sulfate biosynthesis	26	1103	0.818	0.424	0.636	0.269
770	Pantothenate and CoA biosynthesis	15	816	0.401	0.426	0.491	0.24
10	Glycolysis / Gluconeogenesis	62	1030	0.622	0.446	0.334	0.378
51	Fructose and mannose metabolism	34	866	0.103	0.46	0.063	0.367
340	Histidine metabolism	29	541	**0.012**	0.461	0.077	0.425
2010	ABC transporters	44	2362	0.504	0.472	0.506	0.612
4950	Maturity onset diabetes of the young	25	359	0.959	0.473	0.927	0.858
5219	Bladder cancer	42	894	0.809	0.49	0.386	0.319
5416	Viral myocarditis	73	2768	0.725	0.49	0.773	0.783
5412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	76	6053	0.776	0.492	0.777	0.796
5221	Acute myeloid leukemia	60	1509	0.225	0.493	0.178	0.39
5340	Primary immunodeficiency	35	502	0.096	0.507	0.087	0.444
4662	B cell receptor signaling pathway	75	2192	0.293	0.509	0.174	0.286
3040	Spliceosome	128	1396	0.842	0.514	0.782	0.556
4330	Notch signaling pathway	47	1160	0.743	0.514	0.856	0.623
970	Aminoacyl-tRNA biosynthesis	41	944	0.519	0.515	0.696	0.473
4360	Axon guidance	129	6537	0.544	0.517	0.382	0.261
785	Lipoic acid metabolism	3	24	0.641	0.52	0.73	0.489
450	Selenoamino acid metabolism	26	393	0.863	0.528	0.888	0.852
4720	Long-term potentiation	70	4033	0.166	0.533	0.08	0.315
4142	Lysosome	117	1973	0.608	0.534	0.584	0.336
4622	RIG-I-like receptor signaling pathway	71	842	0.935	0.535	0.845	0.458
5217	Basal cell carcinoma	55	1104	0.679	0.541	0.621	0.515
900	Terpenoid backbone biosynthesis	15	223	0.603	0.549	0.506	0.57
4650	Natural killer cell mediated cytotoxicity	141	2804	0.345	0.561	0.232	0.308
4114	Oocyte meiosis	114	3244	0.555	0.564	0.332	0.238
4621	NOD-like receptor signaling pathway	62	907	0.986	0.568	0.942	0.804
5222	Small cell lung cancer	84	3549	0.56	0.571	0.393	0.553
4920	Adipocytokine signaling pathway	67	1642	0.244	0.579	0.145	0.401
230	Purine metabolism	157	5506	0.427	0.59	0.387	0.235
760	Nicotinate and nicotinamide metabolism	24	528	0.387	0.594	0.427	0.448
4012	ErbB signaling pathway	87	3884	0.265	0.596	**0.048**	0.367

604	Glycosphingolipid biosynthesis - ganglio series	20	725	0.759	0.597	0.753	0.789
4510	Focal adhesion	201	7682	0.66	0.598	0.469	0.565
4115	p53 signaling pathway	69	1129	0.072	0.605	0.232	0.385
5330	Allograft rejection	38	665	0.279	0.609	0.21	0.528
5332	Graft-versus-host disease	42	643	0.305	0.61	0.259	0.605
5016	Huntington's disease	185	3669	0.396	0.613	0.617	0.69
4010	MAPK signaling pathway	273	8509	0.302	0.616	**0.029**	0.188
4120	Ubiquitin mediated proteolysis	138	3396	0.821	0.621	0.553	0.383
5310	Asthma	30	500	0.205	0.621	0.131	0.48
4640	Hematopoietic cell lineage	88	1588	0.684	0.621	0.44	0.545
5012	Parkinson's disease	133	1804	0.767	0.648	0.562	0.732
290	Valine leucine and isoleucine biosynthesis	11	269	0.419	0.654	0.438	0.536
903	Limonene and pinene degradation	14	157	0.596	0.659	0.439	0.64
4623	Cytosolic DNA-sensing pathway	56	533	0.759	0.662	0.634	0.413
3030	DNA replication	36	567	0.363	0.665	0.448	0.634
630	Glyoxylate and dicarboxylate metabolism	16	398	0.261	0.666	0.355	0.564
4960	Aldosterone-regulated sodium reabsorption	42	1147	0.711	0.673	0.687	0.567
5216	Thyroid cancer	29	841	0.895	0.679	0.833	0.535
592	alpha-Linolenic acid metabolism	19	284	0.686	0.682	0.264	0.463
4612	Antigen processing and presentation	89	1010	0.187	0.688	0.063	0.478
30	Pentose phosphate pathway	27	447	0.667	0.692	0.683	0.739
5218	Melanoma	71	2219	0.308	0.696	0.137	0.452
3450	Non-homologous end-joining	14	262	0.857	0.699	0.907	0.664
4630	Jak-STAT signaling pathway	155	2570	0.144	0.704	0.059	0.243
5215	Prostate cancer	89	2496	0.659	0.712	0.387	0.533
480	Glutathione metabolism	50	569	0.798	0.712	0.713	0.601
40	Pentose and glucuronate interconversions	28	1337	0.82	0.715	0.777	0.688
982	Drug metabolism - cytochrome P450	72	2239	0.712	0.716	0.739	0.802
4310	Wnt signaling pathway	151	4179	0.776	0.732	0.46	0.305
53	Ascorbate and aldarate metabolism	25	1263	0.892	0.735	0.843	0.774
4912	GnRH signaling pathway	101	3859	0.868	0.745	0.611	0.585
740	Riboflavin metabolism	16	342	0.17	0.745	0.358	0.866
4150	mTOR signaling pathway	52	1409	0.331	0.758	0.227	0.655
500	Starch and sucrose metabolism	52	1940	0.697	0.758	0.579	0.718
780	Biotin metabolism	2	99	0.839	0.766	0.786	0.767
190	Oxidative phosphorylation	135	1358	0.555	0.774	0.327	0.479
4140	Regulation of autophagy	35	368	0.451	0.774	0.673	0.713
1100	Metabolic pathways	1104	24490	0.836	0.774	0.781	0.796
4664	Fc epsilon RI signaling pathway	79	2494	0.495	0.775	0.348	0.528
410	beta-Alanine metabolism	22	919	0.852	0.777	0.896	0.908
5200	Pathways in cancer	330	10613	0.853	0.781	0.596	0.745
20	Citrate cycle (TCA cycle)	32	550	0.215	0.782	0.063	0.408
563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	25	403	0.391	0.782	0.49	0.804

5320	Autoimmune thyroid disease	53	975	0.522	0.785	0.399	0.701
5214	Glioma	65	2015	0.282	0.789	0.132	0.57
5010	Alzheimer's disease	169	4346	0.534	0.789	0.442	0.765
4370	VEGF signaling pathway	76	1800	0.552	0.799	0.214	0.373
4730	Long-term depression	70	3992	0.791	0.802	0.666	0.517
472	D-Arginine and D-ornithine metabolism	1	14	0.8	0.803	0.767	0.803
600	Sphingolipid metabolism	40	718	0.896	0.808	0.77	0.552
5211	Renal cell carcinoma	70	1810	0.346	0.811	0.135	0.646
4672	Intestinal immune network for IgA production	48	824	0.371	0.814	0.317	0.788
510	N-Glycan biosynthesis	46	1135	0.997	0.815	1	0.951
5130	Pathogenic Escherichia coli infection	59	1020	0.562	0.824	0.631	0.555
5223	Non-small cell lung cancer	54	2469	0.555	0.827	0.277	0.731
61	Fatty acid biosynthesis	6	212	0.992	0.841	0.995	0.968
4614	Renin-angiotensin system	17	309	0.849	0.843	0.772	0.736
71	Fatty acid metabolism	42	721	0.89	0.85	0.769	0.99
591	Linoleic acid metabolism	29	494	0.77	0.862	0.408	0.746
983	Drug metabolism - other enzymes	51	2245	0.959	0.87	0.938	0.888
4742	Taste transduction	52	1518	0.512	0.879	0.772	0.945
4146	Peroxisome	78	1266	0.429	0.896	0.618	0.755
260	Glycine serine and threonine metabolism	31	497	0.887	0.896	0.941	0.98
350	Tyrosine metabolism	46	910	0.267	0.913	0.534	0.97
830	Retinol metabolism	64	1893	0.963	0.914	0.83	0.946
120	Primary bile acid biosynthesis	16	438	0.953	0.917	0.821	0.945
531	Glycosaminoglycan degradation	21	595	0.232	0.925	0.312	0.935
4540	Gap junction	90	4042	0.928	0.933	0.839	0.796
4710	Circadian rhythm - mammal	13	273	0.896	0.94	0.835	0.941
750	Vitamin B6 metabolism	6	156	0.802	0.945	0.795	0.901
4062	Chemokine signaling pathway	190	5233	0.627	0.946	0.292	0.667
4722	Neurotrophin signaling pathway	126	3668	0.534	0.947	0.145	0.632
670	One carbon pool by folate	17	521	0.836	0.956	0.677	0.914
471	D-Glutamine and D-glutamate metabolism	4	43	0.979	0.957	0.925	0.923
460	Cyanoamino acid metabolism	7	79	0.872	0.957	0.829	0.953
730	Thiamine metabolism	8	284	0.639	0.958	0.846	0.961
4910	Insulin signaling pathway	137	3427	0.601	0.959	0.434	0.872
130	Ubiquinone and other terpenoid-quinone biosynthesis	7	75	0.986	0.96	0.977	0.979
4916	Melanogenesis	102	2979	0.954	0.97	0.861	0.86
232	Caffeine metabolism	7	175	0.937	0.974	0.948	0.962
430	Taurine and hypotaurine metabolism	10	123	0.971	0.975	0.95	0.97
512	O-Glycan biosynthesis	30	1450	0.852	0.987	0.926	0.973
400	Phenylalanine tyrosine and tryptophan biosynthesis	5	100	0.994	0.991	0.956	0.985