ADSCs						BMSCs						DPSCs						WJSCs					
GO-ID	*p* -value	Corrected *p* -value# selected	# total	Description	Genes in test set	GO-ID	*p* -value	Corrected *p* -value# selected	# total	Description	Genes in test set	GO-ID	*p* -value	Corrected *p* -value# selected	# total	Description	Genes in test set	GO-ID	*p* -value	Corrected *p* -value# selected	# total	Description	Genes in test set
5488	2.92E-10	1.03E-06	1386	10241	binding	7155	1.92E-06	6.11E-03	84	645	cell adhesion	9987	1.01E-06	1.40E-03	869	11834	cellular process	278	6.98E-11	2.29E-07	54	204	mitotic cell cycle
43231	2.69E-09	3.54E-06	766	5271	intracellular membrane-bound organelle	5575	5.94E-06	7.30E-03	1042	12600	cellular_component	5515	1.04E-06	1.40E-03	381	4580	protein binding	5515	2.14E-10	3.52E-07	590	4580	protein binding
43227	3.02E-09	3.54E-06	766	5274	membrane-bound organelle	43231	1.02E-05	7.30E-03	480	5271	intracellular membrane-bound organelle	8150	9.92E-06	7.05E-03	944	13151	biological_process	7049	9.82E-10	1.08E-06	126	708	cell cycle
8151	8.32E-09	7.31E-06	1328	9844	cellular physiological process	43227	1.09E-05	7.30E-03	480	5274	membrane-bound organelle	8151	1.14E-05	7.05E-03	734	9844	cellular physiological process	51726	7.65E-09	6.28E-06	88	456	regulation of cell cycle
50794	2.74E-08	1.92E-05	514	3398	regulation of cellular process	5488	1.15E-05	7.30E-03	867	10241	binding	45012	1.69E-05	7.05E-03	8	19	MHC class II receptor activity	30554	2.11E-08	1.23E-05	206	1371	adenyl nucleotide binding
50789	4.04E-08	2.37E-05	544	3634	regulation of biological process	50789	2.16E-05	1.14E-02	343	3634	regulation of biological process	19884	1.69E-05	7.05E-03	8	19	antigen presentation, exogenous antigen	74	2.25E-08	1.23E-05	86	452	regulation of progression through cell cycle
44238	7.82E-08	3.93E-05	956	6868	primary metabolism	50794	4.21E-05	1.91E-02	321	3398	regulation of cellular process	5886	1.92E-05	7.05E-03	157	1687	plasma membrane	5524	6.01E-08	2.82E-05	195	1300	ATP binding
5515	1.50E-07	5.49E-05	663	4580	protein binding	51726	7.80E-05	2.58E-02	59	456	regulation of cell cycle	5887	2.10E-05	7.05E-03	117	1186	integral to plasma membrane	279	7.11E-08	2.92E-05	46	194	M phase
43283	1.50E-07	5.49E-05	401	2594	biopolymer metabolism	43118	9.32E-05	2.58E-02	81	684	negative regulation of physiological process	19886	2.66E-05	7.94E-03	8	20	antigen processing, exogenous antigen via MHC class II	4674	9.15E-08	3.34E-05	79	416	protein serine/threonine kinase activity
8152	1.64E-07	5.49E-05	1040	7567	metabolism	48523	9.35E-05	2.58E-02	85	726	negative regulation of cellular process	31226	3.04E-05	8.18E-03	117	1196	intrinsic to plasma membrane	87	2.27E-07	7.46E-05	38	152	M phase of mitotic cell cycle
16740	1.72E-07	5.49E-05	260	1573	transferase activity	48519	1.08E-04	2.58E-02	90	782	negative regulation of biological process	43412	4.18E-05	1.02E-02	138	1469	biopolymer modification	17076	3.35E-07	1.00E-04	242	1720	purine nucleotide binding
43412	1.95E-07	5.70E-05	245	1469	biopolymer modification	3824	1.12E-04	2.58E-02	435	4829	catalytic activity	6464	4.73E-05	1.06E-02	134	1422	protein modification	7067	4.68E-07	1.28E-04	37	150	mitosis
6464	2.23E-07	6.03E-05	238	1422	protein modification	74	1.12E-04	2.58E-02	58	452	regulation of progression through cell cycle	5488	6.23E-05	1.29E-02	754	10241	binding	50794	1.05E-06	2.46E-04	432	3398	regulation of cellular process
51244	4.22E-07	1.06E-04	474	3164	regulation of cellular physiological process	51243	1.21E-04	2.58E-02	78	658	negative regulation of cellular physiological process	44459	7.21E-05	1.39E-02	134	1435	plasma membrane part	51301	1.13E-06	2.46E-04	36	149	cell division
44237	5.13E-07	1.20E-04	974	7072	cellular metabolism	45786	1.48E-04	2.58E-02	27	163	negative regulation of progression through cell cycle	16337	7.83E-05	1.40E-02	32	229	cell-cell adhesion	5488	1.19E-06	2.46E-04	1157	10241	binding
50791	6.19E-07	1.36E-04	487	3272	regulation of physiological process	9987	1.48E-04	2.58E-02	976	11834	cellular process	7156	9.34E-05	1.57E-02	23	143	homophilic cell adhesion	16772	1.20E-06	2.46E-04	142	925	transferase activity, transferring phosphorus-containing groups
3824	7.51E-07	1.55E-04	689	4829	catalytic activity	30695	1.55E-04	2.58E-02	41	291	GTPase regulator activity	30225	1.00E-04	1.58E-02	4	5	macrophage differentiation	166	1.88E-06	3.63E-04	268	1979	nucleotide binding
5634	1.77E-06	3.46E-04	543	3727	nucleus	50755	1.72E-04	2.58E-02	4	5	chemokine metabolism	7155	1.09E-04	1.63E-02	69	645	cell adhesion	43283	2.65E-06	4.74E-04	338	2594	biopolymer metabolism
6796	2.36E-06	4.14E-04	146	822	phosphate metabolism	42033	1.72E-04	2.58E-02	4	5	chemokine biosynthesis	8277	1.21E-04	1.72E-02	8	24	regulation of G-protein coupled receptor protein signaling pathway	50789	2.79E-06	4.74E-04	455	3634	regulation of biological process
6793	2.36E-06	4.14E-04	146	822	phosphorus metabolism	5515	1.73E-04	2.58E-02	413	4580	protein binding	8092	1.29E-04	1.74E-02	42	341	cytoskeletal protein binding	6260	2.89E-06	4.74E-04	40	180	DNA replication
4674	2.78E-06	4.64E-04	84	416	protein serine/threonine kinase activity	5083	1.76E-04	2.58E-02	26	156	small GTPase regulator activity	43283	2.15E-04	2.75E-02	219	2594	biopolymer metabolism	43412	3.60E-06	5.63E-04	206	1469	biopolymer modification
48519	3.97E-06	6.35E-04	139	782	negative regulation of biological process	5634	1.79E-04	2.58E-02	343	3727	nucleus	42113	2.59E-04	3.16E-02	9	33	B cell activation	50222	3.82E-06	5.71E-04	94	568	protein kinase activity
6139	6.49E-06	9.37E-04	484	3314	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	43167	2.03E-04	2.80E-02	343	3733	ion binding	43169	2.83E-04	3.31E-02	279	3426	cation binding	16773	5.08E-06	7.26E-04	107	672	phosphotransferase activity, alcohol group as acceptor
31267	6.60E-06	9.37E-04	19	52	small GTPase binding													16740	6.06E-06	8.29E-04	217	1573	transferase activity
50222	6.67E-06	9.37E-04	106	568	protein kinase activity													5634	9.13E-06	1.20E-03	461	3727	nucleus
30036	7.94E-06	1.07E-03	38	149	actin cytoskeleton organization and biogenesis													16301	9.57E-06	1.21E-03	121	792	kinase activity
48523	9.04E-06	1.14E-03	129	726	negative regulation of cellular process													6464	1.31E-05	1.55E-03	197	1422	protein modification
50790	9.05E-06	1.14E-03	55	248	regulation of enzyme activity													6796	1.37E-05	1.55E-03	124	822	phosphate metabolism
8270	1.20E-05	1.45E-03	316	2068	zinc ion binding													6793	1.37E-05	1.55E-03	124	822	phosphorus metabolism
51243	1.42E-05	1.66E-03	118	658	negative regulation of cellular physiological process													51329	1.50E-05	1.64E-03	18	58	interphase of mitotic cell cycle
46914	1.85E-05	2.08E-03	369	2474	transition metal ion binding													4114	1.73E-05	1.84E-03	11	25	3',5'-cyclic-nucleotide phosphodiesterase activity
8150	1.90E-05	2.08E-03	1687	13151	biological_process													75	2.19E-05	2.25E-03	15	44	cell cycle checkpoint
43118	2.11E-05	2.20E-03	121	684	negative regulation of physiological process													5792	2.35E-05	2.34E-03	29	124	microsome
9892	2.13E-05	2.20E-03	54	249	negative regulation of metabolism													8150	2.47E-05	2.38E-03	1433	13151	biological_process
19222	2.22E-05	2.22E-03	355	2374	regulation of metabolism													4112	2.72E-05	2.55E-03	11	26	cyclic-nucleotide phosphodiesterase activity
44424	2.29E-05	2.23E-03	966	7143	intracellular part													51244	2.95E-05	2.69E-03	394	3164	regulation of cellular physiological process
16773	2.35E-05	2.24E-03	119	672	phosphotransferase activity, alcohol group as acceptor													6468	3.17E-05	2.72E-03	89	559	protein amino acid phosphorylation
30029	2.57E-05	2.38E-03	39	162	actin filament-based process													51325	3.22E-05	2.72E-03	18	61	interphase
16301	2.98E-05	2.68E-03	136	792	kinase activity													42598	3.23E-05	2.72E-03	29	126	vesicular fraction
30554	3.93E-05	3.45E-03	217	1371	adenyl nucleotide binding													3824	3.68E-05	3.02E-03	576	4829	catalytic activity
9987	4.32E-05	3.70E-03	1531	11834	cellular process													50791	3.87E-05	3.10E-03	405	3272	regulation of physiological process
16772	4.68E-05	3.91E-03	154	925	transferase activity, transferring phosphorus-containing groups													45012	5.04E-05	3.85E-03	9	19	MHC class II receptor activity
43229	5.08E-05	4.15E-03	854	6277	intracellular organelle													19884	5.04E-05	3.85E-03	9	19	antigen presentation, exogenous antigen
43226	5.20E-05	4.16E-03	854	6278	organelle													43231	5.43E-05	4.06E-03	622	5271	intracellular membrane-bound organelle
6468	6.98E-05	5.45E-03	100	559	protein amino acid phosphorylation													43227	5.84E-05	4.26E-03	622	5274	membrane-bound organelle
6355	7.63E-05	5.83E-03	301	2004	regulation of transcription, DNA-dependent													19886	8.32E-05	5.94E-03	9	20	antigen processing, exogenous antigen via MHC class II
8219	1.01E-04	7.43E-03	101	571	cell death													19899	9.93E-05	6.94E-03	39	201	enzyme binding
31323	1.02E-04	7.43E-03	340	2304	regulation of cellular metabolism													30333	1.34E-04	9.14E-03	16	56	antigen processing
43167	1.04E-04	7.43E-03	527	3733	ion binding													5575	1.90E-04	1.27E-02	1372	12600	cellular_component
43119	1.15E-04	8.10E-03	89	492	positive regulation of physiological process													7093	2.37E-04	1.54E-02	7	14	mitotic checkpoint
16265	1.32E-04	9.09E-03	101	575	death													3981	2.38E-04	1.54E-02	10	27	glucuronosyltransferase activity
16310	1.40E-04	9.43E-03	114	665	phosphorylation													8151	2.44E-04	1.54E-02	1094	9844	cellular physiological process
6350	1.61E-04	1.07E-02	326	2212	transcription													16310	2.60E-04	1.61E-02	98	665	phosphorylation
31324	1.68E-04	1.10E-02	45	212	negative regulation of cellular metabolism													51020	2.72E-04	1.65E-02	17	65	GTPase binding
6351	1.96E-04	1.25E-02	305	2060	transcription, DNA-dependent													44424	2.83E-04	1.69E-02	813	7143	intracellular part
166	2.05E-04	1.29E-02	294	1979	nucleotide binding													9987	3.12E-04	1.83E-02	1294	11834	cellular process
6915	2.09E-04	1.29E-02	95	541	apoptosis													6263	4.27E-04	2.46E-02	21	92	DNA-dependent DNA replication
51020	2.19E-04	1.33E-02	19	65	GTPase binding													15630	4.51E-04	2.55E-02	46	267	microtubule cytoskeleton
19219	2.23E-04	1.33E-02	319	2169	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism													48523	4.86E-04	2.70E-02	104	726	negative regulation of cellular process
45449	2.28E-04	1.33E-02	314	2132	regulation of transcription													776	5.53E-04	3.03E-02	8	20	kinetochore
48518	2.37E-04	1.35E-02	110	646	positive regulation of biological process													30130	6.53E-04	3.52E-02	7	16	clathrin coat of trans-Golgi network vesicle
12501	2.39E-04	1.35E-02	95	543	programmed cell death													31267	6.73E-04	3.56E-02	14	52	small GTPase binding
30695	2.45E-04	1.37E-02	57	291	GTPase regulator activity													5819	7.12E-04	3.66E-02	12	41	spindle
46872	2.75E-04	1.51E-02	513	3660	metal ion binding													8092	7.14E-04	3.66E-02	55	341	cytoskeletal protein binding
7582	3.20E-04	1.73E-02	1452	11246	physiological process													6974	7.70E-04	3.89E-02	45	266	response to DNA damage stimulus
5622	3.48E-04	1.86E-02	1019	7686	intracellular													43229	7.94E-04	3.90E-02	716	6277	intracellular organelle
8656	3.74E-04	1.96E-02	7	13	caspase activator activity													3777	7.95E-04	3.90E-02	18	77	microtubule motor activity
5524	3.96E-04	2.04E-02	200	1300	ATP binding													43226	8.09E-04	3.91E-02	716	6278	organelle
51242	4.27E-04	2.18E-02	83	470	positive regulation of cellular physiological process													30695	9.26E-04	4.41E-02	48	291	GTPase regulator activity
16604	4.57E-04	2.26E-02	8	17	nuclear body													31981	9.76E-04	4.55E-02	57	361	nuclear lumen
45637	4.57E-04	2.26E-02	8	17	regulation of myeloid cell differentiation													5622	1.01E-03	4.55E-02	863	7686	intracellular
16481	4.68E-04	2.29E-02	37	172	negative regulation of transcription													80	1.01E-03	4.55E-02	7	17	G1 phase of mitotic cell cycle
43088	4.81E-04	2.31E-02	5	7	regulation of Cdc42 GTPase activity													12510	1.01E-03	4.55E-02	7	17	trans-Golgi network transport vesicle membrane
43065	5.32E-04	2.50E-02	36	167	positive regulation of apoptosis													51383	1.14E-03	4.98E-02	3	3	kinetochore organization and biogenesis
7266	5.33E-04	2.50E-02	23	91	Rho protein signal transduction													4062	1.14E-03	4.98E-02	3	3	aryl sulfotransferase activity
43169	5.96E-04	2.73E-02	479	3426	cation binding													6268	1.15E-03	4.98E-02	6	13	DNA unwinding during replication
43068	5.98E-04	2.73E-02	36	168	positive regulation of programmed cell death																		
8092	6.21E-04	2.80E-02	63	341	cytoskeletal protein binding																		
12505	6.72E-04	2.99E-02	63	342	endomembrane system																		
7264	7.18E-04	3.15E-02	60	323	small GTPase mediated signal transduction																		
31300	7.27E-04	3.15E-02	26	110	intrinsic to organelle membrane																		
48522	7.39E-04	3.17E-02	94	554	positive regulation of cellular process																		
19899	7.51E-04	3.18E-02	41	201	enzyme binding																		
16311	7.83E-04	3.28E-02	32	146	dephosphorylation																		
7242	8.93E-04	3.67E-02	172	1115	intracellular signaling cascade																		
45934	9.02E-04	3.67E-02	38	184	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism																		
4725	9.08E-04	3.67E-02	24	100	protein tyrosine phosphatase activity																		
51336	9.86E-04	3.93E-02	20	78	regulation of hydrolase activity																		
43549	1.01E-03	3.93E-02	29	130	regulation of kinase activity																		
45859	1.01E-03	3.93E-02	29	130	regulation of protein kinase activity																		
17049	1.04E-03	4.02E-02	4	5	GTP-Rho binding																		
16505	1.12E-03	4.27E-02	7	15	apoptotic protease activator activity																		
43028	1.13E-03	4.27E-02	8	19	caspase regulator activity																		
42981	1.17E-03	4.36E-02	64	356	regulation of apoptosis																		
51338	1.30E-03	4.79E-02	29	132	regulation of transferase activity																		
43067	1.35E-03	4.94E-02	64	358	regulation of programmed cell death																		
17076	1.36E-03	4.94E-02	252	1720	purine nucleotide binding																		
43170	1.38E-03	4.94E-02	580	4249	macromolecule metabolism																		