

**A**

All common genes (655)			Flk1 <sup>+</sup> MES specific genes (2300)			HPC7 specific genes (3158)			FL erythroblast specific genes (976)		
GO Term	Gene count	P-value	GO Term	Gene count	P-value	GO Term	Gene count	P-value	GO Term	Gene count	P-value
Protein amino acid phosphorylation	49	6.2E-8	Cell adhesion	105	3.0E-8	Translation	103	2.5E-15	Nucleosome assembly	15	5.4E-6
Intracellular signaling cascade	62	6.7E-8	Biological adhesion	105	3.3E-8	RNA processing	115	2.1E-10	Chromatin assembly	15	7.5E-6
Phosphorylation	49	1.8E-6	Positive reg. of nitrogen compound metabolic process	99	5.9E-8	Apoptosis	115	1.0E-8	Protein-DNA complex assembly	15	8.8E-6
Phosphate metabolic process	54	6.9E-6	Positive reg. of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	96	9.6E-8	Programmed cell death	115	2.8E-8	Nucleosome organization	15	8.8E-6
Phosphorous metabolic process	54	6.9E-6	Reg. of transcription from RNA polymerase II promoter	109	3.1E-7	Cell death	120	6.7E-8	DNA packaging	17	1.5E-5
Positive regulation of cell proliferation	23	1.6E-4	Positive reg. of RNA metabolic process	81	3.5E-7	Protein catabolic process	128	1.2E-7	Cellular macromolecular complex assembly	25	7.0E-5
Regulation of cell proliferation	34	3.8E-4	Positive reg. of transcription, DNA-dependent	80	5.2E-7	Death	121	1.4E-7	Macromolecular complex assembly	33	1.0E-4
Hemopoiesis	20	6.0E-4	Positive reg. of gene expression	89	1.2E-6	Cellular macromolecule catabolic process	136	3.1E-7	Porphyrin metabolic process	8	1.3E-4
Activation of protein kinase activity	8	0.0012	Positive reg. of transcription	88	7.0E-7	Macromolecule catabolic process	144	3.3E-7	Tetraynole metabolic process	9	1.3E-4
Regulation of myeloid cell differentiation	8	0.0012	Positive reg. of macromolecule biosynthetic process	95	1.1E-6	RNA splicing	58	3.9E-7	Chromatin assembly or disassembly	16	1.5E-4
Regulation of small GTPase mediated signal transduction	18	0.0013	Positive reg. of gene expression	89	1.2E-6	Cellular protein catabolic process	121	9.3E-7	Cellular macromolecular complex subunit organization	26	1.9E-4
Protein kinase cascade	18	0.0019	Positive reg. of macromolecule metabolic process	109	1.2E-6	mRNA metabolic process	57	1.1E-6	Macromolecular complex subunit organization	33	4.6E-4
Hemopoietic or lymphoid organ development	20	0.0022	Tube development	56	1.6E-6	Proteolysis involved in cellular protein catabolic process	120	1.2E-6	Protein catabolic process	43	0.001
Positive regulation of molecular function	21	0.0026	Positive reg. of biosynthetic process	98	1.7E-6	mRNA metabolic process	76	2.0E-6	Heme metabolic process	6	0.001
Programmed cell death	28	0.0035	Positive reg. of cellular biosynthetic process	97	2.1E-6	mRNA processing	68	2.4E-6	Macromolecule catabolic process	48	0.002
Immune system development	6	0.0038	Positive reg. of transcription from RNA polymerase II promoter	69	3.2E-6	Modification-dependent macromolecule catabolic process	112	7.1E-6	Chromosome organization	33	0.002
Induction of apoptosis by intracellular signals	6	0.0053	Positive regulation of DNA binding	17	3.9E-6	Protein localization	154	1.1E-5	Response to metal ion	9	0.0029
Positive regulation of catalytic activity	18	0.0055	Metal ion transport	80	5.9E-6	Cell cycle	128	2.1E-5	Chromatin organization	27	0.0033
DNA damage response, signal transduction resulting in induction of apoptosis	5	0.0061	Heart development	48	6.5E-6	Negative reg. of cyclin-dependent protein kinase activity	8	4.0E-5	Cellular protein catabolic process	39	0.0065
Death	29	0.0066	Positive regulation of binding	17	1.1E-5	Ribonucleoprotein complex biogenesis	39	5.5E-5	Cellular macromolecule catabolic process	43	0.0067
Positive regulation of protein kinase activity	11	0.0074	Cell motion	68	1.4E-5	Regulation of apoptosis	115	7.9E-5	Sphingolipid metabolic process	9	0.0076
									Modification-dependent macromolecule catabolic process	37	0.0077

