

A

All common genes (655)

GO Term	Gene count	P-value
Protein amino acid phosphorylation	49	6.2E-8
Intracellular signaling cascade	62	6.7E-8
Phosphorylation	49	1.8E-6
Phosphate metabolic process	54	6.9E-6
Phosphorus metabolic process	54	6.9E-6
Regulation of cell proliferation	23	1.8E-6
Positive regulation of cell proliferation	34	3.8E-4
Hemopoiesis	20	6.0E-4
Activation of protein kinase activity	8	0.0012
Regulation of blood cell differentiation	8	0.0013
Regulation of small GTPase mediated signal transduction	18	0.0013
Protein kinase cascade	18	0.0019
Hemopoiesis or lymphoid organ development	20	0.0022
Positive regulation of molecular function	21	0.0026
Programmed cell death	26	0.0035
Immune system development	20	0.0038
Induction of apoptosis by intracellular signals	6	0.0053
Positive regulation of catalytic activity	18	0.0055
DNA damage response, signal transduction resulting in induction of apoptosis	5	0.0061
Death	29	0.0066
Positive regulation of protein kinase activity	11	0.0074

FIK1⁺ MES specific genes (2300)

GO Term	Gene count	P-value
Cell adhesion	105	3.0E-8
Biological adhesion	105	3.3E-8
Positive reg. of nitrogen compound metabolic process	99	5.9E-8
Positive reg. of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	66	9.6E-8
Reg. of transcription, RNA polymerase II promoter	109	3.1E-7
Positive reg. of RNA metabolic process	81	3.5E-7
Positive reg. of transcription, DNA-dependent	80	5.2E-7
Positive reg. of macromolecule biosynthetic process	88	7.0E-7
Positive reg. of macromolecule expression	95	1.1E-7
Positive reg. of macromolecule metabolic process	99	1.2E-7
Tube development	109	1.2E-6
Tube development	56	1.6E-6
Positive reg. of biosynthetic process	98	1.7E-6
Positive reg. of cellular biosynthetic process	97	2.1E-6

HPC7 specific genes (3158)

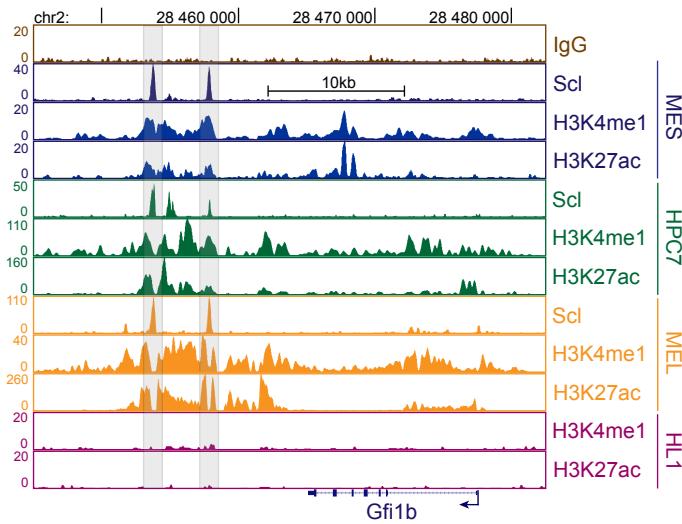
GO Term	Gene count	P-value
Translation	103	2.5E-15
RNA processing	115	2.1E-10
Apoptosis	115	1.0E-8
Programmed cell death	115	2.8E-8
Cell death	120	6.1E-8
Protein catabolic process	128	1.2E-7
Death	121	1.4E-7
Cellular macromolecule catabolic process	136	3.1E-7
DNA repair	136	3.2E-7
Nucleosome organization	144	3.3E-7
RNA splicing	58	3.6E-7
Cellular protein catabolic process	121	3.8E-7
ncRNA metabolic process	57	1.1E-6
Proteolytic involved in cellular protein catabolic process	120	1.2E-6
mRNA metabolic process	76	2.0E-6
mRNA processing	68	2.4E-6
Modification-dependent macromolecule catabolic process	112	7.1E-6
Modification-dependent protein catabolic process	112	7.1E-6
Protein localization	154	1.1E-5
Cell cycle	128	2.1E-5
Negative reg. of cyclin-dependent protein kinase activity	6	4.6E-5
Ribonucleoprotein complex biogenesis	39	5.5E-5
Regulation of apoptosis	115	7.9E-5

FL erythroblast specific genes (976)

GO Term	Gene count	P-value
Nucleosome assembly	15	5.4E-6
Chromatin assembly	15	7.5E-6
Protein-DNA complex assembly	15	8.8E-6
Protein-DNA complex assembly	17	1.5E-6
DNA repair	25	7.6E-5
Cellular macromolecular complex assembly	33	1.0E-4
Porphyrin metabolic process	8	1.3E-4
Tetrapyrrole metabolic process	8	1.3E-4
Chromatin assembly	16	1.5E-4
Cellular macromolecular complex subunit organization	26	1.9E-4
Macromolecular complex subunit organization	33	4.6E-4
Protein catabolic process	43	0.001
Heme metabolic process	6	0.001
Macromolecular catabolic process	48	0.002
Chromatine organization	33	0.002
Response to metal ion	9	0.0029
Modification-dependent macromolecule catabolic process	112	0.0065
Cellular protein catabolic process	39	0.0065
Cellular macromolecule catabolic process	43	0.0067
Splintered metabolic process	9	0.0076
Modification-dependent macromolecule catabolic process	37	0.0077

B

Hematopoietic genes



Cardiac genes

