

Table 30. Significant categories enriched among the downregulated genes. If more that 25 categories were enriched, the top 25 are shown

AML vs. normal cells (NBM and purified hematopoietic cells)						
System	Gene category	List hits	List total	Population hits	Population total	EASE score
Cellular component	Extracellular	39	299	423	5450	1.36E-03
Biological process	Morphogenesis	33	302	382	5586	7.60E-03
Biological process	Blood coagulation	7	302	37	5586	1.32E-02
Biological process	Hemostasis	7	302	41	5586	2.13E-02
Biological process	Organogenesis	28	302	337	5586	2.34E-02
Biological process	Development	50	302	693	5586	2.54E-02
Biological process	Hearing	6	302	32	5586	2.67E-02
Molecular function	Cytoskeletal protein binding	16	314	160	5709	2.85E-02
Biological process	Perception of sound	6	302	33	5586	3.01E-02
Biological process	Cell adhesion	20	302	224	5586	3.20E-02
Biological process	Amino acid derivative metabolism	6	302	35	5586	3.78E-02
Molecular function	Receptor binding	16	314	167	5709	3.96E-02
Cellular component	Extracellular space	14	299	139	5450	3.97E-02
Molecular function	Structural constituent of muscle	5	314	25	5709	4.51E-02
Molecular function	Sulfotransferase activity	4	314	15	5709	4.55E-02
B lineage ALL vs. normal cells (NBM and purified hematopoietic cells)						
System	Gene category	List hits	List total	Population hits	Population total	EASE score
Cellular component	Extracellular	141	1224	444	5871	2.38E-08
Biological process	Cell adhesion	83	1256	245	6009	1.96E-06
Cellular component	Extracellular space	56	1224	147	5871	2.18E-06
Biological process	Response to external stimulus	166	1256	579	6009	2.85E-06
Cellular component	Vacuole	33	1224	73	5871	7.07E-06
Cellular component	Lysosome	30	1224	69	5871	4.94E-05
Cellular component	Lytic vacuole	30	1224	69	5871	4.94E-05
Molecular function	Carbohydrate binding	24	1306	50	6141	7.62E-05
Molecular function	Sugar binding	24	1306	50	6141	7.62E-05
Molecular function	Calcium ion binding	78	1306	244	6141	8.12E-05
Molecular function	Cytoskeletal protein binding	58	1306	169	6141	9.50E-05
Molecular function	Oxidoreductase activity,acting on the CH-CH group of Donors,NAD or NADP as acceptor	13	1306	20	6141	1.83E-04
Biological process	Coenzyme and prosthetic group metabolism	32	1256	81	6009	2.35E-04
Biological process	Cell motility	49	1256	143	6009	2.45E-04
Biological process	Response to abiotic stimulus	64	1256	204	6009	4.15E-04
Molecular function	Structural molecule activity	99	1306	340	6141	4.24E-04
Cellular component	Integral to membrane	320	1224	1319	5871	4.36E-04
Biological process	Cell communication	322	1256	1324	6009	4.37E-04
Molecular function	Extracellular matrix structural constituent	17	1306	33	6141	4.53E-04
Biological process	Heterophilic cell adhesion	18	1256	37	6009	5.37E-04
Biological process	Response to pest/pathogen/parasite	64	1256	206	6009	5.54E-04
Biological process	Coenzyme and prosthetic group biosynthesis	24	1256	58	6009	8.23E-04
Biological process	Coenzyme biosynthesis	17	1256	35	6009	8.36E-04
Cellular component	Extracellular matrix	40	1224	117	5871	1.00E-03
Molecular function	Actin binding	42	1306	123	6141	1.14E-03
T cell ALL vs. normal cells (NBM and purified hematopoietic cells)						

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Biological process	Response to external stimulus	124	726	544	5750	5.99E-12
Biological process	Immune response	81	726	314	5750	1.24E-10
Biological process	Defense response	85	726	339	5750	1.89E-10
Biological process	Response to biotic stimulus	90	726	376	5750	6.73E-10
Biological process	Antigen processing	14	726	18	5750	8.61E-09
Biological process	Antigen presentation	13	726	17	5750	5.02E-08
Molecular function	MHC class II receptor activity	10	745	11	5880	3.45E-07
Cellular component	Integral to membrane	208	702	1250	5620	8.88E-07
Molecular function	Signal transducer activity	147	745	814	5880	1.77E-06
Biological process	Response to pest/pathogen/parasite	48	726	189	5750	2.13E-06
Biological process	Antigen processing\,exogenous antigen via MHC class II	9	726	10	5750	2.20E-06
Biological process	Antigen presentation\ exogenous antigen	9	726	10	5750	2.20E-06
Biological process	Cell communication	205	726	1238	5750	4.03E-06
Cellular component	Membrane	303	702	2001	5620	7.45E-06
Cellular component	Extracellular	83	702	419	5620	1.11E-05
Molecular function	Endopeptidase inhibitor activity	17	745	49	5880	2.13E-04
Molecular function	Protease inhibitor activity	17	745	49	5880	2.13E-04
Biological process	Response to wounding	28	726	108	5750	2.90E-04
Molecular function	Receptor activity	89	745	492	5880	3.01E-04
Molecular function	Transmembrane receptor activity	53	745	267	5880	7.81E-04
Molecular function	Calcium ion binding	47	745	232	5880	1.05E-03
Biological process	humOral defense mechanism (sensu Vertebrata)	17	726	56	5750	1.08E-03
Biological process	Antimicrobial humoral response (sensu Vertebrata)	14	726	41	5750	1.09E-03
Molecular function	Serine-type endopeptidase inhibitor activity	12	745	32	5880	1.28E-03
Biological process	Antimicrobial humoral response	14	726	43	5750	1.78E-03

TCF3/PBX1 vs. the remaining B lineage ALLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Cellular component	Plasma membrane	44	169	732	5522	9.53E-06
Biological process	Cell communication	61	169	1246	5663	2.64E-05
Molecular function	Transmembrane receptor activity	22	173	267	5792	3.56E-05
Molecular function	Receptor activity	32	173	492	5792	3.91E-05
Biological process	Inflammatory response	11	169	76	5663	7.10E-05
Biological process	Innate immune response	11	169	78	5663	8.90E-05
Cellular component	Membrane	84	169	1979	5522	1.73E-04
Biological process	Response to pest/pathogen/parasite	17	169	194	5663	1.82E-04
Biological process	Defense response	24	169	349	5663	2.23E-04
Biological process	Signal transduction	50	169	1029	5663	2.75E-04
Biological process	Response to biotic stimulus	25	169	382	5663	3.32E-04
Molecular function	Signal transducer activity	42	173	820	5792	3.93E-04
Biological process	Response to wounding	12	169	115	5663	5.55E-04
Cellular component	Integral to plasma membrane	28	169	468	5522	7.96E-04
Cellular component	Integral to membrane	56	169	1227	5522	9.33E-04
Biological process	Immune response	21	169	323	5663	1.29E-03
Biological process	Response to external stimulus	29	169	540	5663	2.22E-03
Molecular function	Cytokine binding	5	173	25	5792	5.83E-03
Biological process	Cell surface receptor linked signal transduction hematopoietin/interferon-class (D200-domain) cytokine	21	169	377	5663	7.64E-03
Molecular function	Receptor activity	5	173	27	5792	7.73E-03

Molecular function	G protein coupled receptor activity	8	173	80	5792	9.26E-03
Biological process	Response to stress	21	169	399	5663	1.38E-02
Cellular component	Lytic vacuole	7	169	66	5522	1.46E-02
Cellular component	Lysosome	7	169	66	5522	1.46E-02
Biological process	Cell adhesion	14	169	228	5663	1.74E-02

IGH@MYC vs. the remaining B lineage ALLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Biological process	Cellular process	108	173	2860	5663	1.13E-03
Cellular component	Nucleosome	7	167	41	5522	1.27E-03
Biological process	Cell communication	56	173	1246	5663	1.36E-03
Biological process	Signal transduction	48	173	1029	5663	1.72E-03
Biological process	Nucleosome assembly	6	173	35	5663	3.78E-03
Biological process	Establishment and/or maintenance of chromatin architecture	9	173	90	5663	5.73E-03
Molecular function	Signal transducer activity	37	171	820	5792	7.35E-03
Biological process	Chromatin assembly/disassembly	7	173	58	5663	7.87E-03
Biological process	Actin cytoskeleton organization and biogenesis	6	173	42	5663	8.35E-03
Biological process	DNA packaging	9	173	98	5663	9.48E-03
Biological process	Actin filament based process	6	173	44	5663	1.02E-02
Biological process	Chromosome organization and biogenesis (sensu Eukarya)	9	173	111	5663	1.91E-02
Biological process	Nuclear organization and biogenesis	9	173	113	5663	2.10E-02
Biological process	Actin polymerization and/or depolymerization	3	173	9	5663	2.87E-02
Cellular component	Chromatin	8	167	100	5522	3.02E-02
Biological process	Immune response	17	173	323	5663	3.54E-02

ETV6/RUNX1 vs. the remaining B lineage ALLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Molecular function	Magnesium ion binding	12	234	70	5792	9.34E-05
Molecular function	Transferase activity\ transferring alkyl or aryl (other than methyl) groups	7	234	30	5792	1.05E-03
Molecular function	Metal ion binding	37	234	536	5792	1.32E-03
Biological process	Biosynthesis	36	224	577	5663	5.79E-03
Molecular function	Structural constituent of ribosome	12	234	117	5792	7.11E-03
Cellular component	Mitochondrion	28	224	414	5522	8.34E-03
Molecular function	Molecular_function unknown	21	234	282	5792	9.19E-03
Molecular function	Manganese ion binding	5	234	22	5792	1.05E-02
Cellular component	Cytoplasm	117	224	2494	5522	2.14E-02
Molecular function	Ion transporter activity	12	234	140	5792	2.49E-02
Cellular component	Ribosome	13	224	163	5522	3.14E-02
Biological process	Macromolecule biosynthesis	28	224	477	5663	3.36E-02
Biological process	TCA intermediate metabolism	3	224	9	5663	4.63E-02
Cellular component	Eukaryotic 43S preinitiation complex	5	224	34	5522	4.65E-02

Hyperdiploidy vs. the remaining B lineage ALLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Molecular function	Electron transporter activity	14	209	194	5790	2.18E-02

MLL vs. the remaining B lineage ALLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
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Biological process	Cell proliferation	12	35	617	5663	6.40E-04
Biological process	Regulation of transcription from Pol II promoter	6	35	137	5663	1.22E-03
Biological process	Cell growth and/or maintenance	20	35	1869	5663	4.88E-03
Biological process	Cellular process	25	35	2860	5663	1.39E-02
Molecular function	Serine-type endopeptidase inhibitor activity	3	35	32	5792	1.49E-02
Biological process	Transcription from Pol II promoter	6	35	248	5663	1.52E-02
Cellular component	Transcription factor complex	6	34	259	5522	1.76E-02
Biological process	Negative regulation of transcription from Pol II promoter	3	35	40	5663	2.37E-02
Molecular function	Protease inhibitor activity	3	35	45	5792	2.83E-02
Molecular function	Endopeptidase inhibitor activity	3	35	45	5792	2.83E-02
Biological process	Negative regulation of transcription\, DNA-dependent	3	35	47	5663	3.20E-02
Cellular component	Golgi apparatus	5	34	224	5522	4.29E-02

MLL vs. the remaining AMLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Cellular component	Extracellular	20	81	360	4554	9.30E-06
Biological process	Cell growth and/or maintenance	43	83	1530	4666	3.78E-04
Biological process	Metal ion homeostasis	5	83	29	4666	1.51E-03
Biological process	Cation homeostasis	5	83	37	4666	3.77E-03
Biological process	Cell ion homeostasis	5	83	38	4666	4.15E-03
Biological process	Ion homeostasis	5	83	38	4666	4.15E-03
Cellular component	Extracellular space	8	81	119	4554	4.57E-03
Biological process	Cell homeostasis	5	83	42	4666	5.97E-03
Biological process	Homeostasis	5	83	42	4666	5.97E-03
Biological process	Regulation of cellular process	8	83	134	4666	8.73E-03
Biological process	Regulation of biological process	8	83	135	4666	9.08E-03
Biological process	Di-\,tri-valent inorganic cation transport	4	83	26	4666	1.02E-02
Biological process	Di-\ tri-valent inorganic cation homeostasis	4	83	27	4666	1.13E-02
Biological process	Cellular process	53	83	2384	4666	1.57E-02
Cellular component	Integral to membrane	28	81	1053	4554	1.90E-02
Biological process	Cell proliferation	16	83	483	4666	1.95E-02
Molecular function	Transmembrane receptor activity	10	82	241	4760	2.03E-02
Biological process	Transition metal ion transport	3	83	13	4666	2.10E-02
Biological process	Regulation of cell growth	4	83	37	4666	2.65E-02
Biological process	Transition metal ion homeostasis	3	83	16	4666	3.12E-02
Biological process	Metal ion transport	5	83	74	4666	4.03E-02
Molecular function	Receptor binding	7	82	152	4760	4.38E-02
Molecular function	Signal transducer activity	19	82	706	4760	4.71E-02

MLL vs. the remaining AMLs and B lineage ALLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Cellular component	Cell fraction	13	59	354	5556	2.29E-04
Cellular component	Membrane fraction	10	59	250	5556	1.01E-03
Cellular component	Extracellular	12	59	407	5556	2.80E-03
Cellular component	Integral to plasma membrane	13	59	488	5556	3.87E-03
Molecular function	Signal transducer activity	16	56	849	5826	1.01E-02
Cellular component	Extracellular space	6	59	130	5556	1.10E-02
Cellular component	Integral to membrane	22	59	1255	5556	1.26E-02
Molecular function	Hormone activity	3	56	19	5826	1.35E-02

Molecular function	Molecular_function unknown	8	56	282	5826	1.60E-02
Molecular function	Cytoskeletal protein binding	6	56	160	5826	1.69E-02
Cellular component	Plasma membrane	15	59	756	5556	2.09E-02
Molecular function	Protein binding	15	56	868	5826	2.76E-02
Biological process	Protein complex assembly	4	59	65	5697	2.80E-02
