

**Table 29. Significant categories enriched among the upregulated 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	Lytic vacuole	14	258	67	5450	1.09E-05
Cellular component	Lysosome	14	258	67	5450	1.09E-05
Cellular component	Vacuole	14	258	71	5450	2.10E-05
Molecular function	Transporter activity	55	273	779	5709	2.28E-03
Biological process	Catabolism	34	270	415	5586	2.61E-03
Biological process	Carbohydrate catabolism	8	270	40	5586	2.64E-03
Molecular function	Catalytic activity	134	273	2340	5709	4.16E-03
Cellular component	Mitochondrion	32	258	404	5450	4.34E-03
Biological process	Transport	57	270	835	5586	4.90E-03
Molecular function	Hydrolase activity\, hydrolyzing O-glycosyl compounds	8	273	47	5709	6.31E-03
Biological process	Carbohydrate metabolism	19	270	203	5586	8.56E-03
Molecular function	Electron transporter activity	18	273	191	5709	9.16E-03
Biological process	Hexose catabolism	6	270	29	5586	1.14E-02
Biological process	Alcohol catabolism	6	270	30	5586	1.32E-02
Biological process	Monosaccharide catabolism	6	270	30	5586	1.32E-02
Molecular function	Hydrolase activity\,acting on glycosyl bonds	8	273	56	5709	1.62E-02
Biological process	Glycolysis	5	270	23	5586	2.26E-02
Biological process	Nucleocytoplasmic transport	8	270	60	5586	2.42E-02
Molecular function	Metal ion transporter activity	7	273	48	5709	2.53E-02
Cellular component	Cytoplasm	132	258	2446	5450	2.60E-02
Molecular function	Oxidoreductase activity\,acting on paired donors\, with incorporation or reduction of molecular oxygen\,2-oxoglutarate as one donor\, and incorporation of one atom each of oxygen into both donors	4	273	14	5709	2.63E-02
Biological process	Energy derivation by oxidation of organic compounds	9	270	76	5586	2.88E-02
Biological process	Main pathways of carbohydrate metabolism	7	270	50	5586	3.16E-02
Biological process	Alcohol metabolism	11	270	107	5586	3.25E-02
Molecular function	Di-\,tri-valent inorganic cation transporter activity	4	273	16	5709	3.78E-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
Biological process	Nucleobase\,nucleoside\,nucleotide and nucleic acid metabolism	359	1037	1556	6009	5.42E-12
Molecular function	Nucleic acid binding	351	1052	1532	6141	1.27E-11
Cellular component	Nucleus	368	1010	1640	5871	7.93E-11
Biological process	Transcription	238	1037	1018	6009	3.61E-08
Molecular function	DNA binding	254	1052	1108	6141	3.67E-08
Biological process	Transcription\ DNA-dependent	227	1037	977	6009	1.49E-07
Biological process	Regulation of transcription	219	1037	958	6009	1.04E-06
Molecular function	Binding	677	1052	3558	6141	2.13E-06
Biological process	Regulation of transcription\,DNA-dependent	211	1037	935	6009	4.73E-06
Cellular component	Chromosome	52	1010	172	5871	2.94E-05
Biological process	Chromosome organization and biogenesis (sensu Eukarya)	37	1037	115	6009	1.40E-04
Cellular component	Nuclear pore	17	1010	37	5871	1.79E-04
Cellular component	Pore complex	17	1010	37	5871	1.79E-04
Biological process	Nuclear organization and biogenesis	37	1037	117	6009	2.06E-04

Biological process	mRNA-nucleus export	10	1037	15	6009	2.41E-04
Biological process	DNA packaging	33	1037	101	6009	2.54E-04
Biological process	Establishment and/or maintenance of chromatin architecture	31	1037	93	6009	2.76E-04
Cellular component	Chromatin	33	1010	105	5871	5.19E-04
Biological process	Chromatin assembly/disassembly	22	1037	60	6009	6.73E-04
Molecular function	ATP dependent helicase activity	25	1052	73	6141	7.28E-04
Cellular component	Transcription factor complex	67	1010	270	5871	1.22E-03
Cellular component	Nuclear membrane	23	1010	67	5871	1.29E-03
Molecular function	RNA binding	71	1052	292	6141	1.38E-03
Cellular component	Intracellular	735	1010	4043	5871	1.79E-03
Biological process	RNA-nucleus export	10	1037	19	6009	2.30E-03

T cell ALL vs. normal cells (NBM and purified hematopoietic cells)

System	Gene Category	List hits	List total	Population hits	Population total + F152	EASE score
Biological process	nucleobase\ nucleoside\ nucleotide and nucleic acid metabolism	234	572	1489	5750	1.53E-16
Cellular component	Nucleus	227	559	1584	5620	2.67E-11
Molecular function	Nucleic acid binding	214	583	1482	5880	8.24E-11
Biological process	mRNA metabolism	30	572	104	5750	1.47E-07
Biological process	DNA metabolism	62	572	318	5750	1.90E-07
Biological process	RNA localization	12	572	19	5750	3.04E-07
Biological process	mRNA processing	28	572	99	5750	6.48E-07
Molecular function	RNA binding	56	583	292	5880	1.33E-06
Biological process	Nucleic acid transport	11	572	18	5750	1.81E-06
Biological process	RNA transport	11	572	18	5750	1.81E-06
Biological process	RNA-nucleus export	11	572	18	5750	1.81E-06
Biological process	RNA metabolism	49	572	245	5750	2.24E-06
Molecular function	DNA binding	149	583	1066	5880	2.28E-06
Cellular component	Pore complex	15	559	37	5620	5.41E-06
Cellular component	Nuclear pore	15	559	37	5620	5.41E-06
Biological process	RNA processing	46	572	232	5750	6.21E-06
Biological process	Transcription	135	572	966	5750	9.91E-06
Cellular component	Nuclear membrane	20	559	66	5620	1.28E-05
Biological process	mRNA-nucleus export	9	572	14	5750	1.57E-05
Biological process	Nucleobase\,nucleoside\ nucleotide and nucleic acid transport	11	572	22	5750	1.85E-05
Biological process	RNA splicing	22	572	80	5750	2.18E-05
Molecular function	Binding	381	583	3384	5880	3.60E-05
Biological process	Metabolism	386	572	3433	5750	3.74E-05
Biological process	Transcription\,DNA-dependent	128	572	929	5750	3.79E-05
Biological process	Nucleocytoplasmic transport	19	572	65	5750	3.87E-05

TCF3/PBX1 vs.. the remaining B lineage ALLs

System	Gene category	List hits	List total	Population hits	Population total	EASE score
Biological process	Cell cycle	33	255	450	5663	5.61E-03
Biological process	Cell proliferation	42	255	617	5663	5.83E-03
Biological process	Mitotic cell cycle	20	255	230	5663	7.00E-03

Biological process	Cellular process	148	255	2860	5663	9.54E-03
Biological process	Sex differentiation	3	255	4	5663	1.13E-02
Biological process	Organic acid metabolism	20	255	244	5663	1.28E-02
Molecular function	Transferase activity	47	256	763	5792	1.46E-02
Molecular function	Catalytic activity	122	256	2363	5792	1.64E-02
Biological process	Main pathways of carbohydrate metabolism	7	255	49	5663	2.13E-02
Biological process	Cell growth and/or maintenance	100	255	1869	5663	2.36E-02
Molecular function	Transferase activity\,transferring nitrogenous groups	4	256	15	5792	2.59E-02
Molecular function	Transaminase activity	4	256	15	5792	2.59E-02
Biological process	DNA replication and chromosome cycle	12	255	128	5663	2.80E-02
Molecular function	Kinase activity	29	256	441	5792	3.01E-02
Molecular function	Phosphotransferase activity\, alcohol group as acceptor	25	256	368	5792	3.28E-02
Biological process	Branched chain family amino acid metabolism	3	255	7	5663	3.62E-02
Biological process	Regulation of cell cycle	18	255	242	5663	4.31E-02
Biological process	Carboxylic acid metabolism	18	255	242	5663	4.31E-02
Molecular function	Protein-tyrosine kinase activity	13	256	159	5792	4.69E-02

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*IGH@MYC* vs. the remaining B lineage ALLs

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System	Gene category	List hits	List total	Population hits	Population total	EASE score
Cellular component	Nucleus	50	122	1579	5522	2.98E-03
Cellular component	Nucleolus	7	122	66	5522	3.04E-03
Cellular component	Intracellular	96	122	3854	5522	1.98E-02
Biological process	Growth	4	129	26	5663	2.01E-02
Molecular function	RNA binding	13	131	283	5792	2.44E-02
Molecular function	Nucleic acid binding	43	131	1466	5792	4.22E-02

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*ETV6/RUNX1* vs. the remaining B lineage ALLs

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System	Gene category	List hits	List total	Population hits	Population total	EASE score
Molecular function	Receptor activity	51	333	492	5792	3.36E-05
Molecular function	Signal transducer activity	71	333	820	5792	2.56E-04
Molecular function	Transmembrane receptor activity	31	333	267	5792	2.60E-04
Molecular function	Binding	224	333	3378	5792	4.09E-04
Cellular component	Chromatin	16	314	100	5522	4.47E-04
Biological process	Cell surface receptor linked signal transduction	38	319	377	5663	5.08E-04
Molecular function	Metal ion binding	49	333	536	5792	1.00E-03
Biological process	G protein coupled receptor protein signaling pathway	20	319	162	5663	1.68E-03
Cellular component	Membrane	138	314	1979	5522	1.75E-03
Molecular function	Transmembrane receptor protein kinase activity	9	333	44	5792	3.09E-03
Molecular function	Calcium ion binding	25	333	231	5792	3.12E-03
Biological process	Chromatin assembly/disassembly	10	319	58	5663	4.60E-03
Molecular function	Cytoskeletal protein binding	19	333	161	5792	4.67E-03
Cellular component	Integral to membrane	90	314	1227	5522	4.77E-03
Cellular component	Chromosome	19	314	167	5522	6.07E-03
Biological process	Cyclic-nucleotide-mediated signaling	6	319	23	5663	7.87E-03
Biological process	Enzyme linked receptor protein signaling pathway	13	319	98	5663	8.31E-03
Biological process	DNA packaging	13	319	98	5663	8.31E-03
Cellular component	Plasma membrane	57	314	732	5522	9.97E-03

Biological process	cAMP-mediated signaling	5	319	16	5663	1.04E-02
Biological process	Second-messenger-mediated signaling	7	319	34	5663	1.06E-02
Molecular function	Kinase activity	38	333	441	5792	1.11E-02
Biological process	Establishment and/or maintenance of chromatin architecture	12	319	90	5663	1.14E-02
Biological process	Protein amino acid phosphorylation	28	319	305	5663	1.16E-02
Biological process	Phosphorus metabolism	34	319	398	5663	1.42E-02

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*Hyperdiploidy vs. the remaining B lineage ALLs*

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System	Gene category	List hits	List total	Population hits	Population total	EASE score
Molecular function	Alcohol dehydrogenase activity	5	364	10	5792	2.35E-03
Cellular component	Membrane	152	363	1979	5522	9.75E-03
Molecular function	Alcohol dehydrogenase activity\,zinc-dependent	4	364	8	5792	1.08E-02
Molecular function	Calmodulin regulated protein kinase activity	5	364	15	5792	1.19E-02
Cellular component	Integral to membrane	99	363	1227	5522	1.41E-02
Molecular function	SH3/SH2 adaptor protein activity	7	364	35	5792	2.01E-02
Molecular function	Transmembrane receptor protein tyrosine kinase docking protein activity	7	364	35	5792	2.01E-02
Molecular function	Transporter activity	63	364	783	5792	2.70E-02
Molecular function	Transferase activity\,transferring hexosyl groups	8	364	48	5792	2.85E-02
Molecular function	Transmembrane receptor protein tyrosine kinase signaling protein activity	7	364	40	5792	3.66E-02
Cellular component	Microsome	7	363	39	5522	3.95E-02
Molecular function	Oxidoreductase activity\ acting on the CH-OH group of donors\,NAD or NADP as acceptor	8	364	52	5792	4.19E-02
Cellular component	Vesicular fraction	7	363	40	5522	4.41E-02
Molecular function	Acetylgalactosaminyltransferase activity	3	364	6	5792	4.97E-02

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*MLL vs. the remaining B lineage ALLs*

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System	Gene category	List hits	List total	Population hits	Population total	EASE score
Cellular component	Microvillus	2	38	4	5522	2.65E-02
Molecular function	Structural molecule activity	6	38	315	5792	4.81E-02

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*MLL vs. the remaining AMLs*

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System	Gene category	List hits	List total	Population hits	Population total	EASE score
Biological process	Cell adhesion	7	41	204	4666	7.17E-03
Biological process	Cell communication	17	41	1053	4666	9.77E-03
Molecular function	Lyase activity	4	41	60	4760	1.35E-02

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*MLL vs. the remaining AMLs and B lineage ALLs*

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System	Gene category	List hits	List total	Population hits	Population total	EASE score
Biological process	Cell adhesion	6	31	238	5697	7.38E-03
Molecular function	Carbohydrate binding	3	30	46	5826	2.16E-02
Molecular function	Sugar binding	3	30	46	5826	2.16E-02

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