

Table S6. Functional categories of down-regulated genes associated with poor prognosis

GO category	Corrected p-value	No. of genes	Other tags with downregulated genes	Other tags with upregulated genes
Biological Processes				
protein kinase cascade	7.86E-15	44		<i>good prognosis</i> <i>MLL fusion gene</i> <i>NPM1 mutation</i>
intracellular signaling cascade	1.96E-14	114	<i>t(8;21)</i>	<i>good prognosis</i> <i>inv(16)</i> <i>MLL fusion gene</i> <i>NPM1 mutation</i>
transcription from RNA polymerase II promoter	1.88E-12	54	<i>del(7q)</i> <i>MLL fusion gene</i> <i>t(8;21)</i>	<i>abnormal cytogenetics</i> <i>good prognosis</i> <i>inv(16)</i> <i>NPM1 mutation</i>
signal transduction	3.97E-12	211	<i>CD34+CD38- fraction</i> <i>CEBPA mutation</i> <i>FLT3 mutation</i> <i>t(8;21)</i>	<i>CD34+CD38+ fraction</i> <i>good prognosis</i> <i>inv(16)</i> <i>normal cytogenetics</i>
negative regulation of developmental process	7.73E-12	37	<i>FLT3 mutation</i>	<i>good prognosis</i> <i>NPM1 mutation</i>
cell communication	9.13E-12	222	<i>CD34+CD38- fraction</i> <i>CEBPA mutation</i> <i>t(8;21)</i>	<i>CD34+CD38+ fraction</i> <i>CEBPA silenced</i> <i>good prognosis</i> <i>inv(16)</i> <i>normal cytogenetics</i>
negative regulation of apoptosis	3.74E-10	29		<i>good prognosis</i> <i>NPM1 mutation</i>
negative regulation of programmed cell death	5.23E-10	29		<i>good prognosis</i> <i>NPM1 mutation</i>
positive regulation of metabolic process	2.46E-09	38	<i>low centrosome aberrations</i>	<i>good prognosis</i> <i>high centrosome aberrations</i> <i>inv(16)</i>
RNA metabolic process	3.74E-09	171		<i>abnormal cytogenetics</i> <i>good prognosis</i> <i>NPM1 mutation</i>
macromolecule localization	3.61E-08	64		<i>good prognosis</i> <i>MLL fusion gene</i>
protein localization	9.25E-08	61		<i>good prognosis</i> <i>MLL fusion gene</i>
regulation of cell proliferation	1.06E-07	38	<i>CD34+CD38+ fraction</i> <i>euploid</i> <i>t(8;21)</i>	<i>aneuploid</i> <i>CD34+CD38- fraction</i> <i>good prognosis</i> <i>MLL fusion gene</i> <i>NPM1 mutation</i>
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.43E-07	208		<i>abnormal cytogenetics</i> <i>good prognosis</i> <i>NPM1 mutation</i>
regulation of metabolic process	1.95E-07	165	<i>CEBPA mutation</i> <i>low centrosome aberrations</i> <i>t(15;17)</i>	<i>good prognosis</i> <i>high centrosome aberrations</i> <i>NPM1 mutation</i>
regulation of cellular metabolic process	2.25E-07	161	<i>CEBPA mutation</i> <i>low centrosome aberrations</i> <i>t(15;17)</i>	<i>good prognosis</i> <i>high centrosome aberrations</i> <i>NPM1 mutation</i>
multi-organism process	1.25E-06	29	<i>CD34+CD38- fraction</i>	<i>CD34+CD38+ fraction</i> <i>FAB-M4</i> <i>FAB-M5</i> <i>good prognosis</i> <i>NPM1 mutation</i>
positive regulation of transcription, DNA-dependent	1.32E-06	24		<i>good prognosis</i>
positive regulation of RNA metabolic process	1.58E-06	24		<i>good prognosis</i>

positive regulation of transcription	1.63E-06	27	<i>low centrosome aberrations</i>	<i>good prognosis high centrosome aberrations</i>
protein transport	2.15E-06	54		<i>good prognosis MLL fusion gene</i>
cellular localization	2.75E-06	64		<i>good prognosis MLL fusion gene</i>
response to external stimulus	3.41E-06	43	<i>CD34+CD38- fraction control del(7q) t(8;21)</i>	<i>CD34+CD38+ fraction good prognosis inv(16) MLL fusion gene monocytic normal cytogenetics NPM1 mutation</i>
positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4.04E-06	27	<i>low centrosome aberrations</i>	<i>good prognosis high centrosome aberrations inv(16)</i>
establishment of protein localization	5.13E-06	55		<i>good prognosis MLL fusion gene</i>
anti-apoptosis	7.03E-06	20		<i>good prognosis NPM1 mutation</i>
regulation of gene expression	8.13E-06	149	<i>abnormal cytogenetics CEBPA mutation t(15;17)</i>	<i>good prognosis NPM1 mutation</i>
ubiquitin cycle	1.09E-05	38		<i>good prognosis</i>
localization	1.17E-05	172	<i>t(8;21)</i>	<i>FAB-M7 good prognosis inv(16) MLL fusion gene</i>
anatomical structure morphogenesis	2.44E-05	50	<i>t(15;17) t(8;21)</i>	<i>FLT3-ITD FLT3 mutation good prognosis MLL fusion gene normal cytogenetics</i>
regulation of transcription, DNA-dependent	2.75E-05	132	<i>abnormal cytogenetics CEBPA mutation</i>	<i>good prognosis</i>
enzyme linked receptor protein signaling pathway	3.16E-05	26		<i>good prognosis</i>
regulation of RNA metabolic process	3.61E-05	132	<i>abnormal cytogenetics CEBPA mutation</i>	<i>good prognosis</i>
transcription, DNA-dependent	3.71E-05	134	<i>abnormal cytogenetics CEBPA mutation</i>	<i>good prognosis NPM1 mutation</i>
transcription	3.95E-05	145	<i>abnormal cytogenetics CEBPA mutation</i>	<i>good prognosis NPM1 mutation</i>
response to molecule of bacterial origin	4.09E-05	6		<i>good prognosis NPM1 mutation</i>
RNA biosynthetic process	4.18E-05	134	<i>abnormal cytogenetics CEBPA mutation</i>	<i>good prognosis NPM1 mutation</i>
hemopoietic or lymphoid organ development	4.27E-05	19	<i>NPM1 mutation</i>	<i>good prognosis inv(16)</i>
gene expression	4.54E-05	191		<i>abnormal cytogenetics good prognosis</i>
hemopoiesis	7.32E-05	18	<i>NPM1 mutation</i>	<i>good prognosis inv(16)</i>
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7.96E-05	141	<i>abnormal cytogenetics CEBPA mutation</i>	<i>good prognosis NPM1 mutation</i>
establishment of cellular localization	8.87E-05	59		<i>good prognosis MLL fusion gene</i>
immune system development	9.70E-05	19		<i>good prognosis inv(16)</i>
response to other organism	1.20E-04	20	<i>CD34+CD38- fraction</i>	<i>CD34+CD38+ fraction FAB-M4 FAB-M5 good prognosis NPM1 mutation</i>

response to wounding	1.30E-04	31	<i>CD34+CD38- fraction control t(8;21)</i>	<i>CD34+CD38+ fraction good prognosis inv(16) MLL fusion gene monocytic normal cytogenetics NPM1 mutation</i>
mRNA metabolic process	1.40E-04	27		<i>good prognosis</i>
regulation of transcription	1.40E-04	138	<i>abnormal cytogenetics CEBPA mutation</i>	<i>good prognosis NPM1 mutation</i>
positive regulation of developmental process	1.50E-04	27	<i>t(8;21)</i>	<i>good prognosis inv(16) MLL fusion gene</i>
regulation of signal transduction	1.50E-04	46		<i>good prognosis</i>
vesicle-mediated transport	1.80E-04	38	<i>t(8;21)</i>	<i>inv(16) MLL fusion gene</i>
protein complex assembly	2.00E-04	27		
intracellular transport	2.30E-04	51		<i>good prognosis</i>
positive regulation of cell proliferation	2.80E-04	21	<i>t(8;21)</i>	<i>inv(16) MLL fusion gene NPM1 mutation</i>
mRNA processing	3.50E-04	23		<i>good prognosis</i>
localization of cell	3.70E-04	28	<i>CD34+CD38- fraction normal cytogenetics t(8;21)</i>	<i>CD34+CD38+ fraction good prognosis inv(16) MLL fusion gene NPM1 mutation</i>
cell motility	3.70E-04	28	<i>CD34+CD38- fraction normal cytogenetics t(8;21)</i>	<i>CD34+CD38+ fraction good prognosis inv(16) MLL fusion gene NPM1 mutation</i>
lipid metabolic process	4.10E-04	50		<i>MLL fusion gene</i>
positive regulation of signal transduction	4.60E-04	17		<i>good prognosis MLL fusion gene NPM1 mutation</i>
response to biotic stimulus	6.60E-04	23	<i>CD34+CD38- fraction</i>	<i>CD34+CD38+ fraction good prognosis NPM1 mutation</i>
response to hormone stimulus	7.60E-04	12		
regulation of biological quality	8.30E-04	55	<i>t(8;21)</i>	<i>FAB-M7 good prognosis MLL fusion gene t(8;14)</i>
organ morphogenesis	9.60E-04	26	<i>t(8;21)</i>	<i>good prognosis inv(16) normal cytogenetics NPM1 mutation</i>
nervous system development	1.07E-03	40	<i>CD34+CD38+ fraction inv(16) NPM1 mutation</i>	<i>CD34+CD38- fraction good prognosis</i>
protein targeting	1.97E-03	19		<i>good prognosis</i>
response to hypoxia	2.06E-03	9		<i>good prognosis</i>
response to endogenous stimulus	2.22E-03	33	<i>euploid low centrosome aberrations</i>	<i>abnormal cytogenetics aneuploid good prognosis high centrosome aberrations</i>
RNA splicing	3.14E-03	19		<i>good prognosis</i>
response to chemical stimulus	4.65E-03	34	<i>11q23 CD34+CD38- fraction t(8;21)</i>	<i>CD34+CD38+ fraction good prognosis inv(16) normal cytogenetics NPM1 mutation</i>

defense response	4.99E-03	34	<i>CD34+CD38- fraction t(8;21)</i>	11q23 <i>CD34+CD38+ fraction good prognosis inv(16) MLL fusion gene monocytic normal cytogenetics</i>
I-kappaB kinase/NF-kappaB cascade	6.01E-03	14		<i>good prognosis MLL fusion gene NPM1 mutation</i>
membrane organization and biogenesis	6.46E-03	21	<i>CD34+CD38- fraction NPM1 mutation t(8;21)</i>	<i>CD34+CD38+ fraction inv(16) MLL fusion gene</i>
nuclear transport	6.53E-03	15		<i>good prognosis</i>
positive regulation of transcription from RNA polymerase II promoter	6.55E-03	14		<i>good prognosis</i>
mRNA transport	6.78E-03	11		<i>good prognosis</i>
immune response-regulating signal transduction	8.01E-03	7		<i>good prognosis</i>
cellular lipid metabolic process	8.15E-03	40		<i>MLL fusion gene</i>

Molecular Functions

transcription factor binding	2.99E-10	39		<i>good prognosis NPM1 mutation</i>
transcription cofactor activity	5.79E-09	31		<i>good prognosis</i>
transcription activator activity	1.22E-08	31	<i>t(8;21)</i>	<i>good prognosis inv(16) NPM1 mutation</i>
RNA binding	5.25E-08	59		<i>good prognosis</i>
transcription coactivator activity	7.18E-08	23	<i>t(8;21)</i>	<i>good prognosis inv(16)</i>
transcription regulator activity	7.05E-05	91	<i>abnormal cytogenetics control MLL fusion gene t(15;17)</i>	<i>good prognosis NPM1 mutation</i>
receptor signaling protein activity	1.10E-04	18		<i>good prognosis MLL fusion gene</i>
enzyme binding	1.30E-04	24		<i>good prognosis</i>
transcription repressor activity	1.59E-03	18		<i>good prognosis</i>
DNA binding	2.03E-03	127	<i>abnormal cytogenetics</i>	<i>good prognosis NPM1 mutation</i>
RNA helicase activity	2.16E-03	7		
molecular adaptor activity	4.81E-03	9		<i>good prognosis</i>
protein serine/threonine kinase activity	7.93E-03	36	<i>euploid</i>	<i>aneuploid good prognosis</i>

Cellular Components

nuclear body	6.21E-09	19		<i>good prognosis</i>
Golgi apparatus	2.23E-08	49	<i>t(8;21)</i>	<i>good prognosis inv(16) MLL fusion gene</i>
organelle membrane	4.49E-08	80	<i>t(8;21)</i>	<i>MLL fusion gene</i>
nuclear speck	2.67E-07	15		<i>good prognosis</i>
endomembrane system	6.15E-07	59	<i>CEBPA mutation t(8;21)</i>	<i>CEBPA silenced good prognosis inv(16) MLL fusion gene NPM1 mutation</i>
vacuole	2.30E-04	20	<i>CD34+CD38- fraction CEBPA silenced t(8;21)</i>	<i>CD34+CD38+ fraction CEBPA mutation FAB-M4 FAB-M5 good prognosis inv(16) MLL fusion gene monocytic</i>

lysosome	4.40E-04	18	<i>CD34+CD38- fraction</i> <i>CEBPA silenced</i> <i>t(8;21)</i>	<i>CD34+CD38+ fraction</i> <i>CEBPA mutation</i> <i>FAB-M4</i> <i>FAB-M5</i> <i>good prognosis</i> <i>inv(16)</i> <i>MLL fusion gene</i> <i>monocytic</i>
Golgi membrane	4.70E-04	26	<i>t(8;21)</i>	<i>inv(16)</i>
lytic vacuole	5.40E-04	18	<i>CD34+CD38- fraction</i> <i>CEBPA silenced</i> <i>t(8;21)</i>	<i>CD34+CD38+ fraction</i> <i>CEBPA mutation</i> <i>FAB-M4</i> <i>FAB-M5</i> <i>good prognosis</i> <i>inv(16)</i> <i>MLL fusion gene</i> <i>monocytic</i>
endoplasmic reticulum	1.10E-03	45	<i>t(8;21)</i>	<i>CEBPA silenced</i> <i>MLL fusion gene</i>
cellular_component	1.54E-03	40		<i>good prognosis</i>
endosome	1.94E-03	17		<i>good prognosis</i> <i>MLL fusion gene</i>
Golgi apparatus part	2.10E-03	27	<i>t(8;21)</i>	<i>inv(16)</i> <i>MLL fusion gene</i>

Significantly over-represented functional gene ontology (GO) categories of down-regulated genes associated with poor prognosis are presented here. GO categories that are also over-represented in up-regulated genes associated with poor prognosis are not included. Corrected p-value is the Bonferroni multiple hypothesis. Identification tags that are both up-regulated and down-regulated are not included in the 'other tags' columns. Identification tag descriptions can be found in Table S1.