

Table S5. Functional categories of up-regulated genes associated with poor prognosis

GO category	Corrected p-value	No. of genes	Other tags with upregulated genes	Other tags with downregulated genes
Biological Processes				
cell cycle	2.49E-15	50	<i>abnormal cytogenetics</i> <i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>low centrosome aberrations</i> <i>MLL fusion gene</i>
cell cycle process	8.04E-12	33	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>low centrosome aberrations</i> <i>NPM1 mutation</i>
mitotic cell cycle	6.61E-10	26	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>low centrosome aberrations</i> <i>NPM1 mutation</i>
cell cycle phase	6.37E-09	26	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>low centrosome aberrations</i> <i>NPM1 mutation</i>
cell division	2.18E-08	21	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i> <i>NPM1 mutation</i>
mitosis	4.00E-08	20	<i>aneuploid</i> <i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>NPM1 mutation</i>
M phase of mitotic cell cycle	6.37E-08	20	<i>aneuploid</i> <i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>NPM1 mutation</i>
regulation of cell cycle	2.91E-07	21	<i>abnormal cytogenetics</i> <i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i>
M phase	8.37E-07	21	<i>aneuploid</i> <i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>NPM1 mutation</i>
negative regulation of transcription	3.84E-06	20	<i>good prognosis</i>	
negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4.31E-06	21	<i>good prognosis</i>	
interphase of mitotic cell cycle	1.90E-04	10	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i> <i>NPM1 mutation</i>
regulation of cellular component organization and biogenesis	3.20E-04	17		
interphase	3.70E-04	10	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i> <i>NPM1 mutation</i>
organelle organization and biogenesis	1.47E-03	45	<i>aneuploid</i>	<i>euploid</i>

G1 phase of mitotic cell cycle	1.85E-03	5	<i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>good prognosis</i>
regulation of organelle organization and biogenesis	1.95E-03	10		
organic acid metabolic process	1.95E-03	28		<i>good prognosis</i>
microtubule-based process	2.00E-03	19		
DNA metabolic process	2.46E-03	30	<i>abnormal cytogenetics</i> <i>aneuploid</i> <i>high centrosome aberrations</i>	<i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i>
G1 phase	4.49E-03	5	<i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>good prognosis</i>
carboxylic acid metabolic process	5.34E-03	27		<i>good prognosis</i>
regulation of cytoskeleton organization and biogenesis	5.74E-03	9		

Cellular Components

microtubule cytoskeleton	3.65E-06	26	<i>aneuploid</i> <i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i>
spindle	2.68E-05	10	<i>aneuploid</i> <i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>NPM1 mutation</i>
protein complex	8.99E-05	73	<i>aneuploid</i> <i>high centrosome aberrations</i>	<i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i>
mitochondrion	3.30E-04	34	<i>MLL fusion gene</i>	<i>good prognosis</i>
non-membrane-bound organelle	2.30E-03	68	<i>aneuploid</i>	<i>euploid</i>
intracellular non-membrane-bound organelle	2.30E-03	68	<i>aneuploid</i>	<i>euploid</i>
plasma membrane part	7.59E-03	54	<i>11q23</i> <i>CBF</i> <i>CEBPA silenced</i> <i>FAB-M4</i> <i>FAB-M5</i> <i>FAB-M7</i> <i>inv(16)</i>	<i>CEBPA mutation</i> <i>t(15;17)</i> <i>good prognosis</i>
microtubule organizing center	7.77E-03	10	<i>aneuploid</i> <i>CD34+CD38+ fraction</i>	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i>
organelle outer membrane	9.09E-03	8		

Significantly over-represented functional gene ontology (GO) categories of up-regulated genes associated with poor prognosis are presented here. GO categories that are also over-represented in down-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.