

Table S14. Functional categories of down-regulated genes associated with *NPM1* mutations

GO category	Corrected p-value	No. of genes	Other tags with downregulated genes	Other tags with upregulated genes
Biological Processes				
cell cycle process	2.63E-13	36	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i> <i>poor prognosis</i>
cell cycle phase	4.63E-13	32	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i> <i>poor prognosis</i>
mitotic cell cycle	1.49E-12	30	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i> <i>poor prognosis</i>
M phase	3.09E-10	26	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>poor prognosis</i>
M phase of mitotic cell cycle	4.17E-09	22	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>poor prognosis</i>
regulation of protein kinase activity	1.03E-08	22	<i>euploid</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>high centrosome aberrations</i>
regulation of kinase activity	1.53E-08	22	<i>euploid</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>high centrosome aberrations</i>
mitosis	1.89E-08	21	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>FLT3-ITD</i> <i>good prognosis</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>poor prognosis</i>
regulation of transferase activity	2.26E-08	22	<i>euploid</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>high centrosome aberrations</i>
hemopoiesis	1.30E-06	16	<i>poor prognosis</i>	<i>good prognosis</i> <i>inv(16)</i>
hemopoietic or lymphoid organ development	3.74E-06	16	<i>poor prognosis</i>	<i>good prognosis</i> <i>inv(16)</i>
regulation of molecular function	1.11E-05	32	<i>euploid</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>good prognosis</i> <i>high centrosome aberrations</i>
regulation of catalytic activity	1.51E-05	30	<i>euploid</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>good prognosis</i> <i>high centrosome aberrations</i>
regulation of cyclin-dependent protein kinase activity	3.60E-05	9	<i>euploid</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>high centrosome aberrations</i>
interphase of mitotic cell cycle	3.71E-05	11	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i> <i>poor prognosis</i>
interphase	7.56E-05	11	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i> <i>poor prognosis</i>
cell division	1.00E-04	17	<i>CD34+CD38- fraction</i> <i>euploid</i> <i>good prognosis</i> <i>low centrosome aberrations</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>high centrosome aberrations</i> <i>poor prognosis</i>
nervous system development	1.90E-04	30	<i>CD34+CD38+ fraction</i> <i>inv(16)</i> <i>poor prognosis</i>	<i>CD34+CD38- fraction</i> <i>good prognosis</i>
leukocyte differentiation	5.20E-04	10		
leukocyte activation	1.92E-03	13	<i>FLT3 mutation</i> <i>t(8;21)</i>	<i>inv(16)</i>

membrane organization and biogenesis	3.37E-03	16	<i>CD34+CD38- fraction poor prognosis t(8;21)</i>	<i>CD34+CD38+ fraction inv(16) MLL fusion gene</i>
catabolic process	5.10E-03	34		<i>MLL fusion gene</i>
barbed-end actin filament capping	8.47E-03	5		
actin filament capping	8.47E-03	5		

Molecular Functions

identical protein binding	3.81E-05	21	<i>CD34+CD38+ fraction FLT3 mutation normal cytogenetics t(8;21)</i>	<i>abnormal cytogenetics CD34+CD38- fraction MLL fusion gene</i>
GTPase activity	2.34E-03	16		
cytoskeletal protein binding	4.28E-03	24		<i>MLL fusion gene</i>
cytokine binding	6.78E-03	9		

Cellular Components

soluble fraction	9.72E-06	17		
cytoplasmic part	4.28E-05	109	<i>FLT3-ITD normal cytogenetics t(8;21)</i>	<i>abnormal cytogenetics FAB-M7 inv(16) MLL fusion gene</i>
actin cytoskeleton	2.00E-04	18		
cytoskeleton	2.10E-04	46	<i>euploid good prognosis</i>	<i>aneuploid</i>
cell surface	3.50E-04	12		
spindle	4.60E-04	9	<i>CD34+CD38- fraction euploid good prognosis</i>	<i>aneuploid CD34+CD38+ fraction poor prognosis</i>
coated pit	4.60E-04	7		

Significantly over-represented functional gene ontology (GO) categories of down-regulated genes associated with *NPM1* mutations are presented here. GO categories that are also over-represented in up-regulated genes associated with *NPM1* mutations 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.