

Table S16. Functional categories of down-regulated genes associated with t(15;17)

GO category	Corrected p-value	No. of genes	Other tags with downregulated genes	Other tags with upregulated genes
Biological Processes				
biological regulation	1.40E-07	34	<i>CD34+CD38- fraction</i> <i>CEBPA mutation</i> <i>control</i> <i>del(7q)</i> <i>euploid</i> <i>low centrosome aberrations</i> <i>t(8;21)</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>CEBPA silenced</i> <i>high centrosome aberrations</i> <i>normal cytogenetics</i>
regulation of biological process	2.33E-07	32	<i>CD34+CD38- fraction</i> <i>CEBPA mutation</i> <i>del(7q)</i> <i>euploid</i> <i>FLT3 mutation</i> <i>low centrosome aberrations</i> <i>t(8;21)</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>CEBPA silenced</i> <i>high centrosome aberrations</i> <i>inv(16)</i> <i>MLL fusion gene</i>
regulation of cellular process	3.21E-07	31	<i>CD34+CD38- fraction</i> <i>CEBPA mutation</i> <i>euploid</i> <i>FLT3 mutation</i> <i>low centrosome aberrations</i> <i>t(8;21)</i>	<i>aneuploid</i> <i>CD34+CD38+ fraction</i> <i>CEBPA silenced</i> <i>high centrosome aberrations</i> <i>inv(16)</i> <i>MLL fusion gene</i>
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	1.07E-05	6	<i>normal cytogenetics</i>	
anatomical structure morphogenesis	8.23E-05	11	<i>poor prognosis</i> <i>t(8;21)</i>	<i>FLT3-ITD</i> <i>FLT3 mutation</i> <i>good prognosis</i> <i>MLL fusion gene</i> <i>normal cytogenetics</i>
regulation of metabolic process	3.50E-04	22	<i>CEBPA mutation</i> <i>low centrosome aberrations</i> <i>poor prognosis</i>	<i>good prognosis</i> <i>high centrosome aberrations</i> <i>NPM1 mutation</i>
regulation of cellular metabolic process	8.90E-04	21	<i>CEBPA mutation</i> <i>low centrosome aberrations</i> <i>poor prognosis</i>	<i>good prognosis</i> <i>high centrosome aberrations</i> <i>NPM1 mutation</i>
immune system process	1.02E-03	12	<i>CD34+CD38- fraction</i> <i>FLT3 mutation</i> <i>normal cytogenetics</i> <i>t(8;21)</i>	<i>CD34+CD38+ fraction</i> <i>FAB-M4</i> <i>FAB-M5</i> <i>inv(16)</i> <i>MLL fusion gene</i> <i>monocytic</i>
antigen processing and presentation	1.26E-03	7	<i>normal cytogenetics</i>	
regulation of gene expression	1.64E-03	20	<i>abnormal cytogenetics</i> <i>CEBPA mutation</i> <i>poor prognosis</i>	<i>good prognosis</i> <i>NPM1 mutation</i>
response to stimulus	3.94E-03	18	<i>CD34+CD38- fraction</i> <i>FLT3 mutation</i> <i>t(8;21)</i>	<i>11q23</i> <i>CD34+CD38+ fraction</i> <i>inv(16)</i> <i>MLL fusion gene</i> <i>monocytic</i>
negative regulation of cellular process	5.51E-03	10	<i>CD34+CD38- fraction</i> <i>t(8;21)</i>	<i>CD34+CD38+ fraction</i> <i>control</i> <i>inv(16)</i> <i>MLL fusion gene</i>
ovulation	7.13E-03	2		
negative regulation of biological process	8.35E-03	10	<i>CD34+CD38- fraction</i> <i>t(8;21)</i>	<i>CD34+CD38+ fraction</i> <i>control</i> <i>MLL fusion gene</i> <i>inv(16)</i> <i>MLL fusion gene</i>

Molecular Functions

sequence-specific DNA binding	2.59E-07	13	<i>abnormal cytogenetics control</i>	<i>FLT3-ITD NPM1 mutation</i>
transcription factor activity	3.02E-06	15	<i>abnormal cytogenetics control MLL fusion gene</i>	<i>good prognosis NPM1 mutation</i>
transcription regulator activity	4.86E-05	16	<i>abnormal cytogenetics control MLL fusion gene poor prognosis</i>	<i>good prognosis NPM1 mutation</i>

Cellular Components

plasma membrane part	6.53E-08	20	<i>CEBPA mutation good prognosis</i>	<i>11q23 CBF CEBPA silenced FAB-M4 FAB-M5 FAB-M7 inv(16) poor prognosis</i>
plasma membrane	3.73E-06	23	<i>CD34+CD38- fraction CEBPA mutation</i>	<i>11q23 CBF CD34+CD38+ fraction CEBPA silenced control FAB-M4 FAB-M5 FAB-M7 good prognosis inv(16) monocytic</i>
MHC class II protein complex	7.87E-06	6	<i>normal cytogenetics</i>	
intrinsic to plasma membrane	1.34E-03	11	<i>CD34+CD38- fraction</i>	<i>CBF CD34+CD38+ fraction FAB-M4 FAB-M5 FAB-M7 good prognosis inv(16) monocytic</i>
MHC protein complex	2.04E-03	6		
intracellular part	3.44E-03	39	<i>low centrosome aberrations</i>	<i>abnormal cytogenetics FAB-M7 FLT3 mutation high centrosome aberrations</i>
cell part	4.93E-03	53	<i>euploid</i>	<i>abnormal cytogenetics aneuploid FAB-M7 FLT3-ITD FLT3 mutation</i>
cell	4.94E-03	53	<i>euploid</i>	<i>abnormal cytogenetics aneuploid FAB-M7 FLT3-ITD FLT3 mutation</i>

Significantly over-represented functional gene ontology (GO) categories of down-regulated genes associated with t(15;17) are presented here. GO categories that are also over-represented in up-regulated genes associated with t(15;17) 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.