

Table S15. Functional categories of up-regulated genes associated with t(15;17)

GO category	Corrected p-value	No. of genes	Other tags with upregulated genes	Other tags with downregulated genes
Biological Processes				
system development	1.62E-05	21	<i>CD34+CD38- fraction</i>	<i>CD34+CD38+ fraction t(8;21)</i>
Molecular Functions				
calcium ion binding	2.04E-03	16	<i>inv(16)</i>	
Cellular Components				
cytoplasm	3.30E-03	44	<i>abnormal cytogenetics aneuploid FAB-M7 FLT3-ITD FLT3 mutation</i>	<i>euploid normal cytogenetics</i>
endoplasmic reticulum lumen	5.59E-03	4		
proteinaceous extracellular matrix	6.49E-03	8		
extracellular region	7.95E-03	20	<i>11q23 CD34+CD38+ fraction inv(16) NPM1 mutation</i>	<i>CD34+CD38- fraction t(8;21)</i>
extracellular matrix	8.13E-03	8		

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