

Table S3. Expression summaries of HOX and TALE genes

Gene symbol	No. of references	No. of platforms	No. of differentially expressed features	Expression Summary		
				AML Baseline		No Baseline (bold tag is up-regulated)
				up-regulated tags	down-regulated tags	
HOXB2	12	6	32	<i>FLT3-ITD</i> <i>NPM1 mutation</i> <i>normal cytogenetics</i>	<i>CEBPA mutation</i> <i>MLL fusion gene</i> <i>abnormal cytogenetics</i>	<i>inv(16)</i> vs <i>t(15;17)</i> <i>inv(16)</i> vs <i>t(8;21)</i> prognosis*
PBX3	12	5	31	<i>MLL fusion gene</i> <i>NPM1 mutation</i> <i>normal cytogenetics</i>	<i>abnormal cytogenetics</i> <i>inv(16)</i> <i>t(15;17)</i> <i>control</i>	<i>inv(16)</i> vs <i>t(8;21)</i> prognosis*
HOXA9	11	4	35	<i>MLL fusion gene</i> <i>11q23</i> <i>NPM1 mutation</i> <i>normal cytogenetics</i>	<i>CEBPA mutation</i> <i>t(8;21)</i> <i>abnormal cytogenetics</i> <i>inv(16)</i> <i>t(15;17)</i> <i>control</i>	AML vs <i>ALL</i>
HOXB5	9	5	32	<i>NRAS-PM</i> <i>FLT3-ITD</i> <i>FLT3-TKD</i> <i>normal cytogenetics</i> <i>NPM1 mutation</i>	<i>CEBPA mutation</i> <i>11q23</i> <i>t(8;21)</i> <i>inv(16)</i> <i>t(15;17)</i>	poor prognosis vs <i>good prognosis</i> euploid vs <i>aneuploid</i>
HOXA10	9	4	34	<i>MLL fusion gene</i> <i>NPM1 mutation</i> <i>normal cytogenetics</i>	<i>CEBPA mutation</i> <i>abnormal cytogenetics</i> <i>inv(16)</i> <i>t(15;17)</i> <i>control</i>	poor prognosis vs <i>good prognosis</i> <i>inv(16)</i> vs. <i>t(15;17)</i>
MEIS1	9	3	16	<i>MLL fusion gene</i> <i>NPM1 mutation</i> <i>normal cytogenetics</i> <i>good prognosis</i>	<i>CEBPA mutation</i> <i>t(15;17)</i>	<i>inv(16)</i> vs <i>t(8;21)</i>
HOXA4	8	4	18	<i>MLL fusion gene</i> <i>11q23</i> <i>NPM1 mutation</i> <i>normal cytogenetics</i>	<i>t(8;21)</i> <i>t(15;17)</i> <i>inv(16)</i>	poor prognosis vs <i>good prognosis</i>
HOXA5	6	1	15	<i>MLL fusion gene</i> <i>NPM1 mutation</i> <i>FLT3-ITD</i>	<i>inv(16)</i> <i>t(15;17)</i> <i>control</i>	
HOXB6	5	2	7	<i>NPM1 mutation</i> <i>FLT3-ITD</i>		
HOXA7	5	1	12	<i>MLL fusion gene</i> <i>NPM1 mutation</i>	<i>inv(16)</i> <i>t(15;17)</i> <i>control</i>	
PBX1	3	3	3	<i>t(11;19)</i> <i>poor prognosis</i>		
HOXA2	3	2	4	<i>NPM1 mutation</i> <i>normal cytogenetics</i>	<i>t(15;17)</i>	
HOXA6	3	1	6	<i>MLL fusion gene</i> <i>NPM1 mutation</i>		
HOXB3	3	1	3	<i>NPM1 mutation</i>		
PBX2	3	1	3		<i>MLL fusion gene</i> <i>NPM1 mutation</i>	
HOXB4	2	2	4	<i>NPM1 mutation</i> <i>FLT3-ITD</i> <i>normal cytogenetics</i>		
HOXB9	2	1	4	<i>MLL fusion gene</i> <i>NPM1 mutation</i>		
HOXA1	1	1	2	<i>NPM1 mutation</i>		
HOXB7	1	1	2	<i>NPM1 mutation</i>		
HOXA11	1	1	1	<i>NPM1 mutation</i>		
HOXA3	1	1	1	<i>NPM1 mutation</i>		
HOXC4	1	1	1		<i>NPM1 mutation</i>	
HOXC6	1	1	1			
HOXD4	1	1	1	<i>NPM1 mutation</i>		

Listing of all HOX/TALE family genes in our analysis. Gene symbols are approved by HUGO Gene Nomenclature Committee. Identification tag descriptions can be found in Table S1.

*Contradictory prognosis expression directions.