SUPPLEMENTAL MATERIAL

Hatlen et al., http://www.jem.org/cgi/content/full/jem.20150524/DC1

Table S1. **The *TET2* mutations in AML patients from studies by the Cancer Genome Atlas Research Network (2013) and Patel et al. (2012)**

Patient database	Frequency of patients with a *TET2* mutation	*TET2* mutations	Effect	t(8;21) status
TCGA	2.00%	Q481	Nonsense	Negative
		R550	Nonsense	Negative
		315	Frameshift	Negative
ECOG	9.55%	270	Frameshift	Negative
		S327X	Missense	Negative
		P426L	Missense	Negative
		K433X	Missense	Negative
		E452A	Missense	Negative
		R544X	Missense	Negative
		R550X	Missense	Negative
		586	Frameshift	Negative
		Q622X	Missense	Negative
		F868L	Missense	Negative
		Q891X	Missense	Negative
		912	Frameshift	Negative
		Q916X	Missense	Negative
		921	Frameshift	Negative
		958	Frameshift	Negative
		966	Frameshift	Negative
		W1003X	Missense	Negative
		Q1021R	Missense	Negative
		1034	Frameshift	Negative
		Q1084P	Missense	Negative
		1114	Frameshift	Negative
		1118	Frameshift	Negative
		E1141K	Missense	Negative
		H1219Y	Missense	Negative
		N1260K	Missense	Negative
		R1261C	Missense	Negative
		G1283D	Missense	Negative
		W1292R	Missense	Negative
		1299	Frameshift	Negative
		1322	Frameshift	Negative
		R1365H	Missense	**Positive**
		G1369V	Frameshift	Negative
		1395	Frameshift	Negative
		E1405X	Missense	Negative
		1439	Frameshift	**Positive**
		1448	Frameshift	Negative
		S1486X	Missense	Negative
		Q1524X	Missense	Negative
		R1572W	Missense	Negative
		H1817N	Missense	Negative
		E1851K	Missense	**Positive**
		I1873T	Missense	Negative
		1893	Frameshift	Negative
		R1896M	Missense	Negative
		S1898F	Missense	Negative
		Y1902X	Missense	Negative
		1960	Frameshift	Negative
		P1962L	Missense	Negative

Table S2. **Statistics of *TET2* mutations in AML patients from the ECOG E1900 trial from the Patel et al. (2012) study**

Given gene	% Patients mutant for given gene	% Patients mutant for given gene and *TET2*	% Patients mutant for *TET2* that are mutant for given gene	% Patients mutant for given gene that are mutant for *TET2*	Tendency for mutations to co-occur	
					P-value	Adj. p-value
FLT3	36.93%	3.27%	34.21%	8.84%	0.17	1.00
NPM1	29.65%	3.02%	31.58%	10.17%	0.15	1.00
DNMT3A	25.63%	2.01%	21.05%	7.84%	0.18	1.00
NRAS	10.30%	1.76%	18.42%	17.07%	0.09	1.00
RUNX1	8.79%	1.51%	15.79%	17.14%	0.09	1.00
CBF	18.09%	1.26%	13.16%	6.94%	0.20	1.00
ASXL1	3.02%	1.01%	10.53%	33.33%	0.03	0.71
CEBPa	9.55%	1.01%	10.53%	10.53%	0.15	1.00
WT1	9.05%	0.75%	7.89%	8.33%	0.18	1.00
AML1-ETO	7.29%	0.75%	7.89%	10.34%	0.15	1.00
PHF6	3.27%	0.50%	5.26%	15.38%	0.10	1.00
Monosomy 7	1.01%	0.50%	5.26%	50.00%	0.01	0.27
IDH2	8.54%	0.25%	2.63%	2.94%	0.29	1.00
KIT	5.78%	0.25%	2.63%	4.35%	0.25	1.00
TP53	4.02%	0.25%	2.63%	6.25%	0.21	1.00
PTEN	1.76%	0.25%	2.63%	14.29%	0.11	1.00
EVI1^{+}	1.26%	0.25%	2.63%	20.00%	0.07	1.00
split *MLL*	5.53%	0.25%	2.63%	4.55%	0.25	1.00
Trisomy 8	3.77%	0.25%	2.63%	6.67%	0.20	1.00
IDH1	6.28%	0.00%	0.00%	0.00%	0.50	1.00
KRAS	2.76%	0.00%	0.00%	0.00%	0.50	1.00
5q deletion	1.51%	0.00%	0.00%	0.00%	0.50	1.00
MLL-PTD	4.52%	0.00%	0.00%	0.00%	0.50	1.00
t69	0.50%	0.00%	0.00%	0.00%	0.50	1.00

Table S3. **The *PTPN11* mutations in AML patients from the Cancer Genome Atlas Research Network (2013) study**

Patient database	Frequency of patients with a *PTPN11* mutation	*PTPN11* mutations	Effect	t(8;21) status
TCGA	13.33%	G60V	Missense	Negative
		D61Y	Missense	Negative
		D61V	Missense	Negative
		F71L	Missense	Negative
		T73I	Missense	Negative
		S189A	Missense	Negative
		Y197*	Nonsense	Negative
		L206L	Missense	Negative
		N308D	Missense	Negative
		S502P	Missense	Negative
		Q510L	Missense	Negative

REFERENCES

Cancer Genome Atlas Research Network. 2013. Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *N. Engl. J. Med.* 368:2059–2074. http://dx.doi.org/10.1056/NEJMoa1301689

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