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ERRATUM

Acute promyelocytic leukemias share cooperative mutations with other myeloid-leukemia subgroups

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Correction to: *Blood Cancer Journal* (2013) **3,** e147; doi: 10.1038/bcj.2013.46; published online 13 September 2013

Since the publication of this article, the authors have identified an error within Table 2, namely that the AML subgroups listed at the bottom of the table were incorrect.

The correct table is shown here.

The article has also been rectified, and now carries the correct information.

The Publishers apologize for any inconvenience this has caused.

Table 2. Genes with a significantly higher mutation rate in APLs and AMLs

Mutated Gene	PML-RARA	NPM1$^+$	NK-NPM1$^-$	Complex karyotype	CBFB/ MYH11	MLL-X	Trisomy 8	RUNX1/ RUNX1T1	Other	Total[a]	TCGA[b]
FLT3	9	32	9	1	3	2	1	1	5	63	x
CSMD1	3	1	0	1	0	0	0	0	1	6	
WT1	3	5	5	0	1	1	0	0	2	17	x
DDR2	2	0	1	0	0	0	0	0	0	3	
KRAS	2	3	2	2	0	0	1	0	1	11	x
CALR	2	0	0	0	0	0	0	0	0	2	
REV3L	2	0	0	0	0	0	0	0	0	2	
TCERG1L	2	0	0	0	0	0	0	0	0	2	
FAM5C	1	2	0	1	0	0	0	0	1	5	x
PHF6	1	1	2	1	0	0	1	0	1	7	x
PTPN11	1	7	0	2	1	0	0	0	0	11	x
ASXL1	0	0	3	0	0	0	2	0	1	6	
CEBPA	0	2	12	1	0	0	1	0	3	19	x
DNMT3A	0	29	15	3	0	0	5	0	4	56	x
EZH2	0	0	1	0	0	0	0	0	3	4	x
GATA2	0	1	6	0	0	0	0	0	0	7	
GRIK2	0	2	0	0	0	1	0	0	0	3	
IDH1	0	12	2	1	0	0	5	0	3	23	x
IDH2	0	5	8	1	0	0	3	0	4	21	x
KIT	0	1	0	1	3	0	0	2	1	8	x
NRAS	0	5	4	2	2	1	0	0	2	16	x
PHACTR1	0	0	0	1	0	0	0	0	2	0	
PLCE1	0	0	1	0	0	0	0	1	2	4	
RAD21	0	3	1	0	0	0	0	1	0	5	x
RUNX1	0	0	12	1	0	0	2	0	7	22	x
SMC1A	0	4	0	0	0	1	1	1	0	7	x
SMC3	0	3	2	1	0	0	1	1	0	8	x
STAG2	0	3	3	0	0	0	0	0	1	7	x
SUZ12	0	0	1	2	0	0	0	0	0	3	
TET2	0	2	9	1	0	0	1	1	4	18	x
TP53	0	0	1	12	0	0	0	0	2	15	x
U2AF1	0	1	2	0	0	0	2	0	3	8	x
BCOR	0	0	3	0	0	0	0	0	0	3	
CHD4	0	0	0	2	0	0	0	0	0	2	
CTCF	0	0	2	0	0	0	0	0	0	2	
DDX41	0	0	2	0	0	0	0	0	0	2	
FAM57B	0	2	0	0	0	0	0	0	0	2	
GIGYF2	0	0	0	0	0	0	0	2	0	2	
GJB3	0	0	0	2	0	0	0	0	0	2	
KDM3B	0	0	0	2	0	0	0	0	0	2	
KRT13	0	2	0	0	0	0	0	0	0	2	
PCDHA13	0	0	2	0	0	0	0	0	0	2	
SCN1A	0	0	0	2	0	0	0	0	0	2	
TBX15	0	2	0	0	0	0	0	0	0	2	
TCEB3B	0	0	2	0	0	0	0	0	0	2	

found in $\geqslant$2 AML subgroups
found in only one AML subgroup
associated to a specific AML subgroup with q$\leqslant$0.01
associated to a specific AML subgroup with q$\leqslant$0.05

[a]Total number of mutations identified for each mutated gene. [b]Significantly mutated genes identified by The Cancer Genome Atlas Research network (TCGA).