

Table S1. Genes subjected to targeted deep sequencing

(QIAseq Targeted DNA Custom panel-QIAGEN (CDHS-31667Z-1041))

Gene	Target (exon)	Gene	Target (exon)	Gene	Target (exon)	Gene	Target (exon)
ANKRD26	5'utr	ETV6/TEL	1-8	KRAS	2, 3	SF3B1	13-16
ASXL1	12	EZH2	All exons	MBD4	1-8	SMC1A	2, 11, 16, 17
BCOR	All exons	FLT3	14,15,20	MPL	10	SRSF2	1
BCORL1	All exons	GATA1	2	NPM1	12	STAG2	All exons
BRAF	15	GATA2	4-6	NRAS	2, 3	TET2	3-11
CALR	9	HRAS	2, 3	PHF6	All exons	TP53	2-11
CBL	8-9	IDH1	4	PPM1D	5-6	U2AF1	2, 6
CEBPA	All exons	IDH2	4	PTPN11	3, 13	WT1	7,9
CSF3R	10,14-18	JAK2	12, 14	RAD21	All exons	ZRSR2	All exons
DDX41	5,17	JAK3	13	RUNX1	1-6		
DNMT3A	All exons	KIT	2, 8-11, 13, 17	SETBP1	4 (partial)		

Table S2. List of somatic mutations by barcoded-targeted NGS of myeloid recurrent genes in peripheral blood of AML patient Rm.

Gene	Chr	Coordinate	HGVS coding sequence name	HGVS protein sequence name	Variant type	Variant allele frequency (%)	Unique Variant coverage depth
<i>SRSF2</i>	17	74732959	NM_003016.4:c.284C>G	NP_003007.2:p.Pro95Arg	missense	50.2	510
<i>TET2</i>	4	106157477	NM_001127208.2:c.2379_2385delATCAAGC	NP_001120680.1:p.Glu796ArgfsTer15	frameshift	47.2	688
<i>NPM1</i>	5	170837562	NM_002520.6:c.879_*1delTCTTTAAG	NP_002511.1:p.Leu294Lys	frameshift	20.5	108
<i>NPM1</i>	5	170837543	NM_002520.6:c.859_860insTCTG	NP_002511.1:p.Trp288CysfsTer12	frameshift	16.1	80
<i>ASXL1</i>	20	31024010	NM_015338.5:c.3497_3510delGCCCCAGTTCTTTA	NP_056153.2:p.Ser1166LysfsTer11	frameshift	8.7	104