

**SUPPLEMENTARY 4.** Genomic and *in silico* Predictive Scores of the Novel *KMT2A* Variants Identified in this Cohort .

Patient	Genomic (hg38)	Ref > Alt	Consequence	Exon number	CADD raw	CADD PHRED	PhastCons (vertebrate)	PhyloP (vertebrate)	SpliceAI (max)	Predicted effect
P3	chr11-118505028	AACCAG > A	Frameshift deletion	27	6.5	35	1	5.4	0.01	Likely NMD, LoF
P4	chr11-118504271	AAC > A	Frameshift deletion	27	5.4	32	0.3	4.8	0	Likely NMD, LoF
P8	chr11-118473693	C > CT	Stop gained	3	4.8	26.9	0.9	3.3	0.06	Likely NMD, LoF
P9	chr11-118509947	G > T	Canonical splice acceptor	Intron 29	7	35	1	8.2	1	Splice site disruption, LoF
P10	chr11-118522082	CACTT > C	Frameshift deletion	36	7.7	36	1	8.8	0.01	Terminal truncation, LoF
P11	chr11-118506637	C > G	Stop gained	27	8.8	39	0.9	2.4	0.03	Likely NMD, LoF
P12	chr11-118484257	TAG > T	Frameshift deletion	9	5.1	29	1	3.9	0.01	Likely NMD, LoF
P14	chr11-118471936	A > AC	Frameshift insertion	3	5.4	31	1	5.9	0.03	Likely NMD, LoF
P16	chr11-118473728	G > T	Stop gained	3	7.7	36	1	7.9	0.14	Likely NMD, LoF

CADD (PHRED  $\geq 20$  = high deleteriousness); PhastCons (vertebrate) (0-1 = conservation probability); PhyloP (vertebrate) ( $> 0$  = conservation strength); SpliceAI (max) ( $\geq 0.5$  = high splice impact). Higher CADD, PhastCons, and PhyloP values indicate functionally constrained, evolutionarily conserved regions.

CADD, Combined Annotation Dependent Depletion; Max, maximum.