LETTER TO THE EDITOR

A novel *SART3::RARG* fusion gene in acute myeloid leukemia with acute promyelocytic leukemia phenotype and differentiation escape to retinoic acid

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Supplementary data

Figure S1: Single-nucleotide polymorphism (SNP) array analysis of the bone marrow sample of the patient. (A) A mosaic loss of chromosome Y is indicated by a light red bar. (B) A 2.26 Mb microdeletion in 12q21.2 and a 1.99 Mb microdeletion in 12q23.3q24.11 encompassing *SART3* are represented by dark red boxes. (C) A uniparental disomy of a 5.42 Mb segment at 17q21.2q21.32 is shown as a purple box.

Figure S2: Reverse transcription polymerase chain reaction and Sanger sequencing verified the *WT1* c.1114-2A>G mutation, and the *KDM6A* c.3318_3319insGCCTCCC (p.Pro1107AlafsTer46) as acquired heterozygous somatic mutations. A. Heterozygous *WT1* c.1114-2A>G mutation was detected from the patient's bone marrow sample but not his oral mucosa swab. B. Heterozygous *KDM6A* c.3318_3319insGCCTCCC (p.Pro1107AlafsTer46) was detected from the patient's bone marrow sample but not his oral mucosa swab sample.

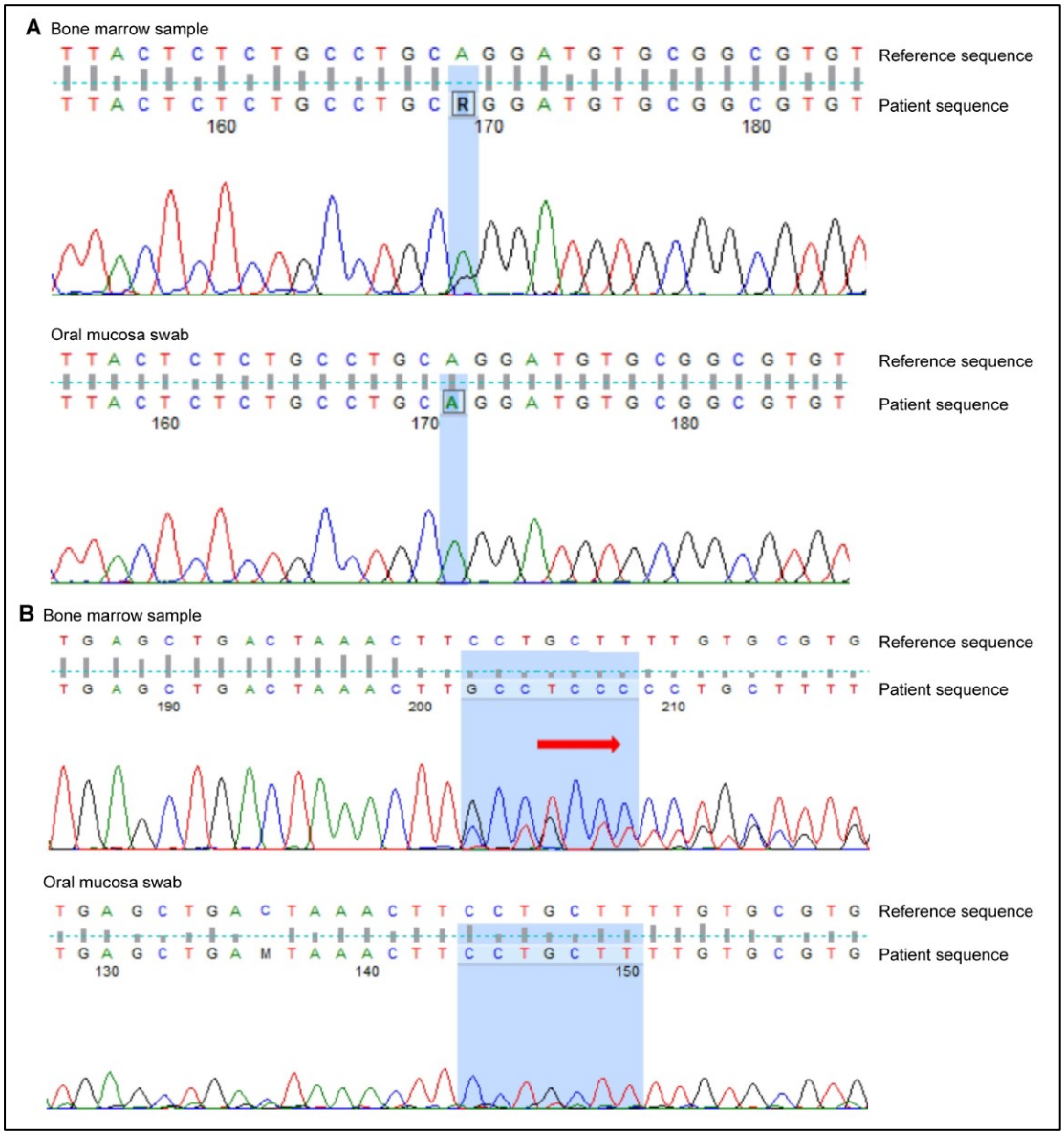

Table S1: MPO mutations identified by whole exome sequencing.

Gene	Chr	Coordinate	GenoType	Alt Variant Freq	Read Depth	refAD	altAD	HGVSc	HGVSp
MPO	***chr17***	***56355507***	het	50	124	78	46	NM_000250.2:c.886-1G>A	
MPO	***chr17***	***56357271***	het	50	429	249	175	NM_000250.2:c.352dup	NP_000241.1:p.Tyr118LeufsTer25
MPO	***chr17***	***56357818***	het	50	167	93	74	NM_000250.2:c.157G>T	NP_000241.1:p.Val53Phe

Gene	Chr	Coordinate	dbSNP ID	Type	Exon	Intron	Filters	Consequence
MPO	***chr17***	***56355507***		SNV		6 of 11	PASS	splice_acceptor_variant
MPO	***chr17***	***56357271***		insertion	3 of 12		PASS	frameshift_variant
MPO	***chr17***	***56357818***	rs7208693	SNV	2 of 12		PASS	missense_variant&splice_region_variant