Supplemental Data Table S2. Mutations identified as drivers of CHIP in the study cohort

Chr	Position	Consequence	Gene	Reference sequence:DNA	Protein	COSMIC ID	OncoKB
chr17	7578212	stop_gained	*TP53*	NM_000546.5:c.637C>T	p.Arg213Ter	COSV52665560	Likely oncogenic
chr17	7578260	missense_variant	*TP53*	NM_000546.6:c.589G>A	p.Val197Met	COSV52711079	ND
chrX	15840874	frameshift_variant	*ZRSR2*	NM_005089.4:c.959del	p.Cys320PhefsTer?	ND	Likely oncogenic
chr2	25457242	missense_variant	*DNMT3A*	NM_022552.5:c.2645G>A	p.Arg882His	COSV53036153	Likely oncogenic
chr2	25457243	missense_variant	*DNMT3A*	NM_022552.5:c.2644C>T	p.Arg882Cys	COSV53036332	Likely oncogenic
chr2	25458595	missense_variant	*DNMT3A*	NM_022552.4:c.2578T>C	p.Trp860Arg	COSV53043807	ND
chr2	25458643	frameshift_variant	*DNMT3A*	NM_022552.5:c.2523_2529del	p.Gln842LysfsTer9	ND	Likely oncogenic
chr2	25459805	missense_variant	*DNMT3A*	NM_022552.5:c.2478G>C	p.Lys826Asn	ND	ND
chr2	25462020	missense_variant	*DNMT3A*	NM_022552.4:c.2387G>A	p.Gly796Asp	COSV53074031	ND
chr2	25463182	stop_gained	*DNMT3A*	NM_022552.4:c.2311C>T	p.Arg771Ter	COSV53041751	Likely oncogenic
chr2	25463182	stop_gained	*DNMT3A*	NM_022552.5:c.2311C>T	p.Arg771Ter	COSV53041751	Likely oncogenic
chr2	25463287	missense_variant	*DNMT3A*	NM_022552.4:c.2206C>T	p.Arg736Cys	COSV53038112	ND
chr2	25463289	missense_variant	*DNMT3A*	NM_022552.5:c.2204A>G	p.Tyr735Cys	COSV53036596	ND
chr2	25463295	frameshift_variant	*DNMT3A*	NM_022552.4:c.2186_2196delinsA	p.Arg729GlnfsTer47	ND	Likely oncogenic
chr2	25463301	missense_variant	*DNMT3A*	NM_022552.4:c.2192T>G	p.Phe731Cys	COSV53060451	ND
chr2	25463600	splice_variant	*DNMT3A*	NM_022552.4:c.2083-1G>A	NA	ND	Likely oncogenic
chr2	25464439	stop_gained	*DNMT3A*	NM_022552.4:c.2074C>T	p.Gln692Ter	ND	Likely oncogenic
chr2	25464544	missense_variant	*DNMT3A*	NM_022552.4:c.1969G>T	p.Val657Leu	ND	ND
chr2	25464568	missense_variant	*DNMT3A*	NM_022552.5:c.1945G>T	p.Val649Leu	COSV53047274	ND
chr2	25467023	splice_variant	*DNMT3A*	NM_022552.5:c.1851+1G>A	NA	COSV53067586	Likely oncogenic
chr2	25467187	frameshift_variant	*DNMT3A*	NM_022552.4:c.1687del	p.Val563TrpfsTer88	ND	Likely oncogenic
chr2	25467436	missense_variant	*DNMT3A*	NM_022552.4:c.1640T>A	p.Leu547His	COSV53040940	ND
chr2	25467497	stop_gained	*DNMT3A*	NM_022552.5:c.1579C>T	p.Gln527Ter	COSV53063669	Likely oncogenic
chr2	25469055	missense_variant	*DNMT3A*	NM_022552.4:c.1403A>G	p.Lys468Arg	COSV53081990	ND
chr2	25469176	frameshift_variant	*DNMT3A*	NM_022552.4:c.1281del	p.Glu428ArgfsTer223	ND	ND
chr2	25469529	frameshift_variant	*DNMT3A*	NM_022552.5:c.1238dup	p.Phe414LeufsTer7	ND	Likely oncogenic
chr2	25469612	frameshift_variant	*DNMT3A*	NM_022552.4:c.1137_1155del	p.Ala380CysfsTer21	ND	Likely oncogenic
chr2	25469613	frameshift_variant	*DNMT3A*	NM_022552.5:c.1154del	p.Pro385ArgfsTer22	ND	Likely oncogenic
chr2	25469917	splice_variant	*DNMT3A*	NM_022552.5:c.1122+2del	NA	ND	Likely oncogenic
chr2	25469919	splice_variant	*DNMT3A*	NM_022552.5:c.1122+1G>A	NA	COSV53048881	Likely oncogenic
chr2	25470011	missense_variant	*DNMT3A*	NM_022552.5:c.1031T>G	p.Leu344Arg	ND	ND
chr2	25470473	missense_variant	*DNMT3A*	NM_022552.4:c.1001G>A	p.Gly334Asp	ND	ND
chr2	25470485	stop_gained	*DNMT3A*	NM_022552.5:c.989G>A	p.Trp330Ter	ND	Likely oncogenic
chr2	25470532	stop_gained	*DNMT3A*	NM_022552.5:c.942G>A	p.Trp314Ter	ND	Likely oncogenic
chr2	25505308	splice_variant	*DNMT3A*	NM_022552.5:c.448+2T>C	NA	ND	Likely oncogenic
chrX	44938399	frameshift_variant	*KDM6A*	NM_001291415.2:c.3107del	p.Phe1036SerfsTer15	ND	Likely oncogenic
chrX	44942740	missense_variant	*KDM6A*	NM_001291415.2:c.3476C>T	p.Pro1159Leu	ND	ND
chr17	58740726	frameshift_variant	*PPM1D*	NM_003620.4:c.1636del	p.Leu546Ter	ND	ND
chr17	74732959	missense_variant	*SRSF2*	NM_003016.4:c.284C>A	p.Pro95His	COSV57969816	Oncogenic
chr4	106156747	stop_gained	*TET2*	NM_001127208.2:c.1648C>T	p.Arg550Ter	COSV54395664	Likely oncogenic

(*Continued to the next page*)

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Supplemental Data Table S2. Continued

Chr	Position	Consequence	Gene	Reference sequence:DNA	Protein	COSMIC ID	OncoKB
chr4	106157543	frameshift_variant	*TET2*	NM_001127208.2:c.2447del	p.Asn816IlefsTer8	ND	Likely oncogenic
chr4	106158471	frameshift_variant	*TET2*	NM_001127208.2:c.3373_3374del	p.Lys1125AspfsTer4	ND	Likely oncogenic
chr4	106162566	frameshift_variant	*TET2*	NM_001127208.3:c.3481_3483delinsG	p.Glu1162AsnfsTer11	ND	Likely oncogenic
chr4	106164068	missense_variant	*TET2*	NM_001127208.2:c.3578G>T	p.Cys1193Phe	COSV54399446	ND
chr4	106180770	splice_variant	*TET2*	NM_001127208.2:c.3804-3_3811del	NA	ND	ND
chr4	106196313	frameshift_variant	*TET2*	NM_001127208.2:c.4647del	p.His1550IlefsTer21	ND	Likely oncogenic
chr4	106196396	frameshift_variant	*TET2*	NM_001127208.2:c.4730del	p.Ser1577IlefsTer19	ND	Likely oncogenic
chr10	112359532	frameshift_variant	*SMC3*	NM_005445.4:c.2391_2394dup	p.Ala799ArgfsTer5	ND	ND
chr10	112361580	stop_gained	*SMC3*	NM_005445.4:c.2830C>T	p.Arg944Ter	COSV62420070	ND
chr3	136323216	structural_variant	*STAG1*	NA	NA	ND	ND
chr7	140453193	missense_variant	*BRAF*	NM_004333.4:c.1742A>C	p.Asn581Thr	COSV56110832	ND

Genomic positions are described based on human genome build 19.
Abbreviations: Chr, chromosome; NA, not available; ND, no data; CHIP, clonal hematopoiesis of indeterminate potential; COSMIC, Catalogue of Somatic Mutations in Cancer (https://cancer.sanger.ac.uk/cosmic); OncoKB, Oncology Knowledge Base (https://www.oncokb.org/).