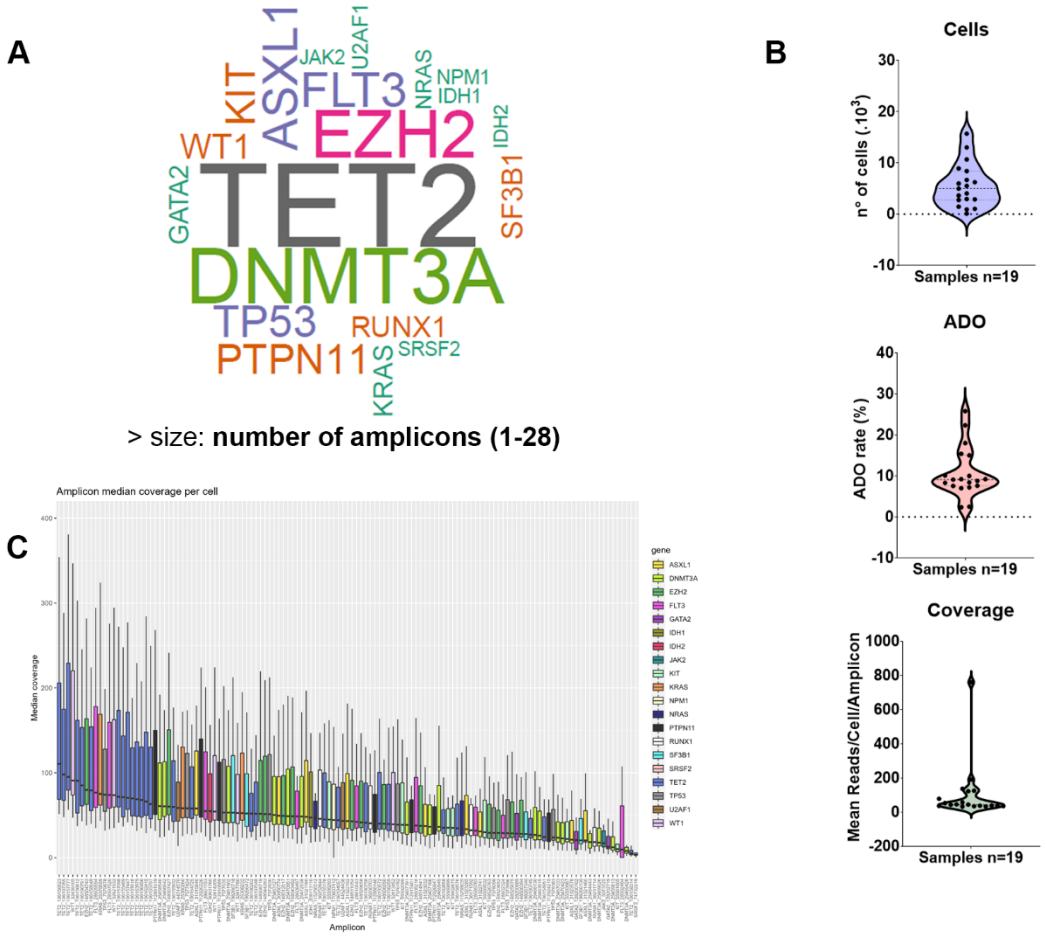
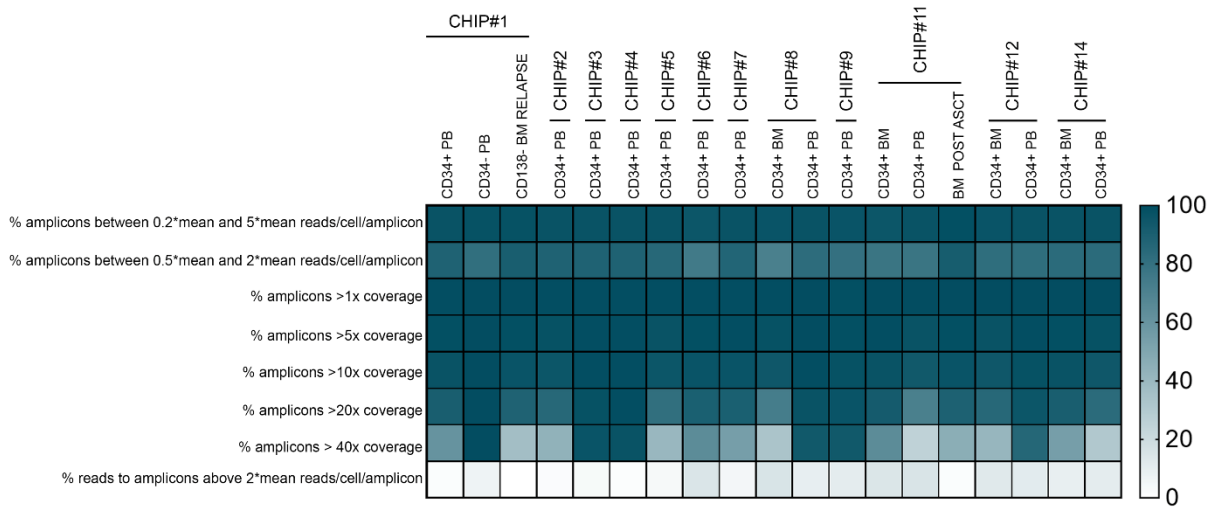
## Supplementary Figures



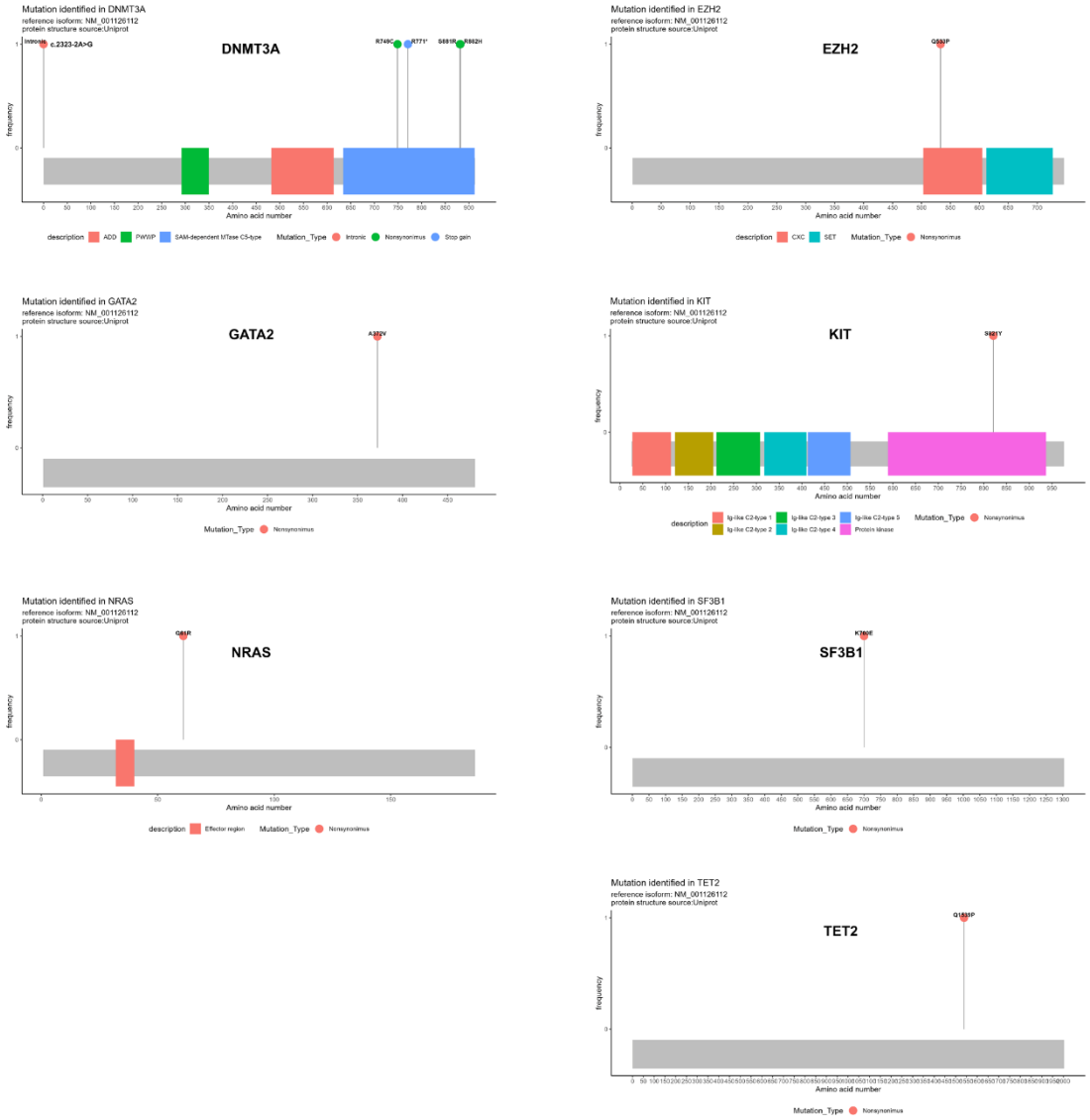

**Supplementary Figure 1**

**Supplementary Figure S1. Single-cell DNA panel coverage and metrics of patient samples processed with the Tapestri platform for single-cell DNA sequencing.** (**A**) The 20 genes included in the 127-amplicon panel, which covers reported mutational hotspots (SNVs and small indels) in acute myeloid leukemia. The text size is proportional to the number of amplicons per gene. Details of the genomic regions covered by the panel are in supplemental Table 1. (**B**) Total number of sequenced cells (top violin plot colored in violet), average allele dropout rate (ADO) per sample (middle violin plot colored in red), and average reads per amplicon per cell (bottom violin plot colored in green). Each point represents a sample (n=19) from 1 of the 12 MM patients. Median value is shown by a horizontal line. (**C**) Bar plot with the distribution of sequencing reads across the 127 amplicons. Each bar represents an amplicon, and the height of the bar shows the median number of raw sequenced reads per cell (n=19 samples). Amplicon name is shown for all the amplicons.




**Supplementary Figure 2**

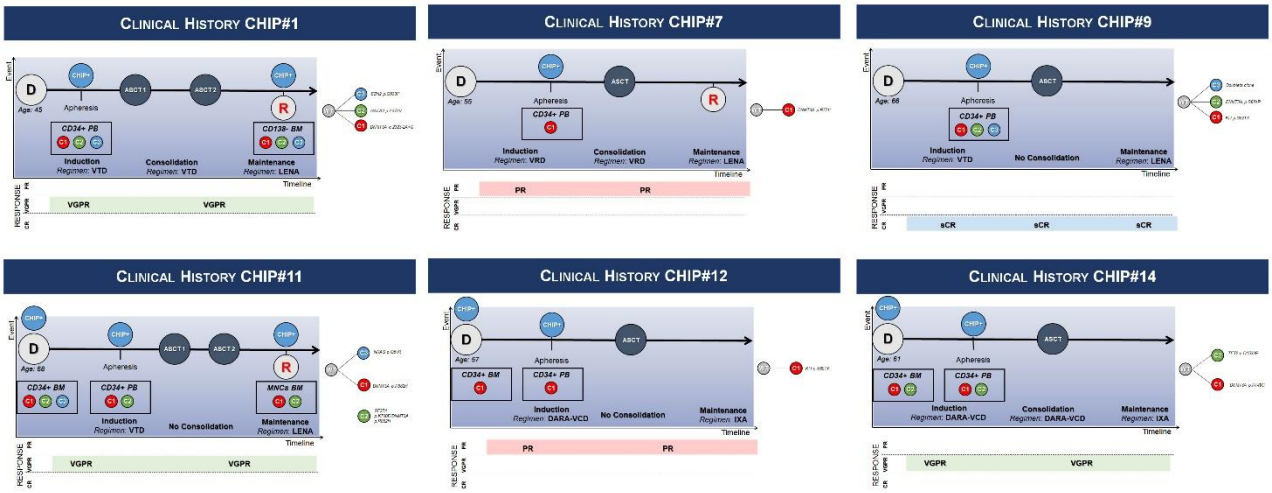
**Supplementary Figure S2.** Panel performance for all patient's samples processed with the Tapestri platform for single-cell DNA sequencing. The AML panel used includes 127 amplicons and the heatmap shows the total coverage for all samples analysed (n=19). Each column represents a sample, and each row represents the relative percentage of reads/cell/amplicon for any given samples.




**Supplementary Figure 3**

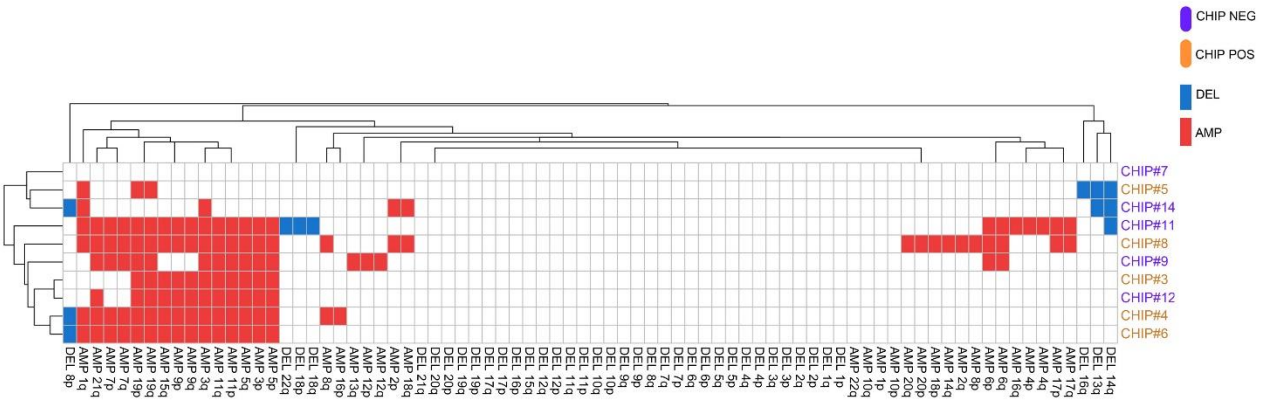
**Supplementary Figure S3.** CHIP pathogenic mutations identified in MM patients in stem cells compartment at the time of transplant. Lolli plot showing the somatic mutation spectra throughout the protein sequence of DNMT3A, EZH2, GATA2, NRAS, KIT, SF3B1 and TET2. The scale bar represents the length (amino acids) of the protein sequence, and the corresponding domains are

indicated with coloured boxes. The corresponding variant name is shown on the top of the lolli plot specifying the coding impact.




Supplementary Figure 4

**Supplementary Figure S4. Clinical history and CHIP mutated clones for CHIP+ patients.** D=Diagnosis, R=Relapse, ASCT=Autologous stem cell transplantation, CD34+BM=bone marrow stem cells, CD34+ PB=stem cells from apheresis product, CD138- BM=bone marrow CD138- cells fraction, MNCs BM=bone marrow mononuclear cells, VTD=bortezomib-thalidomide-dexamethasone, VCD=bortezomib-cyclophosphamide-dexamethasone, VRD=bortezomib-lenalidomi-dexamethasone, DARA=daratumumab, LENA=lenalidomide, IXA=ixazomib.




**Supplementary Figure 5**

**Supplementary Figure S5. Copy Number Alterations (CNAs) of myeloma patients.** On the CD138+ enriched fractions a genomic characterization by Ultra Low Pass-Whole Genome Sequencing (ULP-WGS) to evaluate whole genome's Copy Number Alterations (CNAs) profile were performed. ULP-WGS (0.1X coverage) was performed on genomic DNA samples from BM-PCs CD138+ cell fractions extracted by Maxwell® (Promega Italia Srl, Milan, Italy) using Maxwell® 16 LEV Blood DNA Kit. Library preparation was completed with SMARTer® ThruPLEX® DNA-Seq kit (Takara Bio, Mountain View, CA, USA). Sequencing was conducted on NextSeq 500 (Illumina Inc, San Diego, CA, USA), and IchorCNA was employed to assess CNAs profile. For CHIP#1 and CHIP#2, we were unable to assess the CNAs status due to insufficient material available for analysis.

**Supplementary Table S1. Panel Targets**

| Gene | Exon | Protein-level Variants | cDNA Variants |
|---|---|---|---|
| **ASXL1** | 3 | G67 | |
| | 4 | K85 | |
| | 11 | R417; Q428; QA491; P511; A530 | |
| | 12 | W583; Q588; R606; A611; K618; A772; L775; Q778; R786; T787; E797; A809; W898; G927; W960; K982; V1060 | |
| **DNMT3A** | 7 | D268 | |
| | 8 | P307; S312; W313; R320; W327 | |
| | 9 | L344; L347; R366 | |
| | 10 | W409; L422 | |
| | 11 | K429; Y436; E444; A447 | |
| | 13 | C494; C497; G511; M513 | |
| | 14 | Q527; C540; G543; L547; G550; C554; C555 | |
| | 15 | E561; W581; L595; R598; Q606; D614 | |
| | 16 | R635; L637 | |
| | 17 | L653; Y660; A662; S669; I681; D686; R688; V690 | |
| | 18 | G699; D702; I705; G707; N711; L713; S714; V716; P718 | |
| | 19 | F732; R736; R749; F751; F752; A760; S770; R771; L773; E774 | |
| | 20 | P777; R792; W795; G796; N797; M801; R803 | |
| | 21 | E817; H821 | |
| | 22 | K829; T835; N838; Q842; P849; M852; E863 | |
| | 23 | F868; D876; N879; M880; S881; R882; Q886; W893; I898; R899; P904 | |
| | Intron | | c.640-1437G>A; c.1429+2T>C; c.1667+1G>A; c.2408+5G>A; c.2479-1G>T |
| **EZH2** | 2 | M1; V13; Q28 | |
| | 3 | N57 | |
| | 4 | M121 | |
| | 5 | H129; I131; Y133; Y153; G155 | |
| | 6 | R207 | |
| | 8 | E249; G266 | |
| | 10 | T374 | |
| | 14 | C548 | |
| | 15 | K568; T573 | |
| | 16 | G628; E645; Y646; C647; G648 | |
| | 17 | A656; D664; N675 | |
| | 18 | R684; R690; N693; H694; S695 | |
| | 19 | Y731 | |
| | 20 | D737; I744; E745 | |
| **FLT3** | 11 | E444; S451 | |
| | 12 | V491; Q494; A506; I507; S519; S531 | |
| | 13 | I548 | |
| | 14 | Y572; L576; V592; F594 | |
| | 16 | M659; K663; M664; N676; A680 | |
| | 17 | Q730 | |
| | 19 | N781; T784 | |

| | | | |
|---|---|---|---|
| | 20 | A814; V819; R834; D835; M837; S838; D839; N841; Y842 | |
| | 21 | A856; T866 | |
| **GATA2** | 4 | P304; N317; A318; G320; L321; R330 | |
| | 5 | T358; L359; R361; R362; A372 | |
| | 6 | R398 | |
| **IDH1** | 4 | R132 | |
| **IDH2** | 4 | R140; R172 | |
| **JAK2** | 14 | V617 | |
| **KIT** | 2 | P34; D52 | |
| | 5 | D265 | |
| | 9 | G487; G498 | |
| | 11 | M552; W557; L576 | |
| | 12 | T594; A617; M618; P627 | |
| | 17 | D816; D829; N822; Y823 | |
| | 18 | A837 | |
| **KRAS** | 2 | G12; G13; H27 | |
| | 3 | T58; Q61 | |
| | 4 | K117; A146 | |
| **NPM1** | 11 | L287; W290 | c.860_861lin-sCTGC; c.861_862lin-sTGCA; c.863_864lin-sCATG; c.867_868lin-sAGGA; |
| **NRAS** | 2 | G12; G13 | |
| | 3 | Q61 | |
| **PTPN11** | 3 | N58; G60; D61; E69; F71; A72; T73; E76; Q79 | |
| | 4 | E139 | |
| | 7 | F285 | |
| | 8 | M311 | |
| | 11 | D437 | |
| | 12 | A461; G464 | |
| | 13 | P491; S502; G503; T507; Q510 | |
| **RUNX1** | 5 | G127; E138; S141; A142; R145; R157; D160; R162; G165; R166; S167; G168R; K171 | |
| | 6 | V197; D198; S200; R201; R204 | |
| | 7 | R207; G217; S226; E229; R250; N260; M267 | |
| | 8 | Y281; P298; E316 | |
| | Intron | | c.805+1G>A |
| **SF3B1** | 14 | G605; S611; R625; H662; K666; A672 | |
| | 15 | K700; V701; I704 | |

| | | | |
|---|---|---|---|
| | 16 | G742; A749; R775; E776; D781 | |
| | 17 | D799 | |
| | Intron | | c.2224-1G>A |
| **SRSF2** | 2 | R167 | |
| **TET2** | 3 | V9; E10; T27; L34; P46; Q80; G92; R96; D143; S145; S152; P174; E283; N312; Q325; Q414; Q147; Q481; R544; Q574; S588; Q591; Q622; Q635; H682; S714; Q734; Q810; S794; R814; S825; G898; Q913; Q916; P491; Q966; P989; W1003; Q1020; Q1053; Q1083; E1106; L1119 | |
| | 4 | E1144; Y1148; N1156; R1167 | |
| | 5 | Q1170; E1178; Q1191; C1193; W1198 | |
| | 6 | S1203; S1204; R1214; R1216; D1242; Y1245; Y1255; R1261; R1262 | |
| | 7 | C1271; F1287; G1288; C1289; Y1294; C1298; E1318 | |
| | 8 | L1322; E1323; L1340 | |
| | 9 | R1359; H1366; C1378; H1380 | |
| | 10 | C1396; E1401; R1404; R1440; R1452; R1465; S1486; L1511; A1512 | |
| | 11 | R1516; Q1532; Q1539; Q1542; Q1548; Q1624; Q1652; V1718; L1721; P1723S; R1739; L1740; H1757; I1762; C1811; L1819; Q1828; G1861; S1898; V1900; H1904; H1912; A1919; R1926; P1941; P1962; R1966; P1988; Y1998; R2000; I2002 | |
| | Intron | | c.3409+70G>A |
| **TP53** | 2 | | c.-87G>C; c.-93A>G |
| | 5 | L91; K93; F95; T101; V104; W107; V108; G115; R119; Y124; K125; Q126; H129; V134; R136; C137 | |
| | 6 | H154; I156; R157; V164; Y166; R174; S176; Y181; P184 | |
| | 7 | Y195; VM198; C199; N200; S202; C203; G206; R209; I215; E219 | |
| | 8 | G223; L226; G227; R228; V233; R234; C236; A237; P239; D242; R244; R251 | |
| | 10 | F302; R303 | |
| | 11 | F346 | |
| | Intron | | c.259-2A>G; c.259-1G>A; c.443-1G>A; c.876+1G>A; c.877-1G>A; |
| **U2AF1** | 2 | R28; S34; R35 | |
| | 6 | R156; Q157 | |
| | 7 | R188 | |

| | | | |
|---|---|---|---|
| **WT1** | 4 | L299; M302; K321 | |
| | 6 | G356 | |
| | 7 | R374; R375; S386 | |
| | 8 | R435; R436; R439; Q442 | |
| | 9 | R463; R467; D469; H470 | |
| | Intron | | c.1115_1264+1del;<br>c.1264+3_1264+4insT |

**Supplementary Table S2. Called somatic Variants.** All somatic coding variants identified in all samples analyzed (n=19). Overall 235 nucleotide variants have been called. SNV=Single Nucleotide Variant.

| Sample | Sample Type | Gene | Chromosome | Variant | Function | Coding Impact | Variant Type | cDNA | Protein Change | Genotyped Cells | Mutated Cells | VAF by cell count (%) | VAF by read count (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP14** | CD34+ BM | ASXL1 | 20 | ASXL1:chr20:31015949:T/G | Coding | Missense | SNV | c.271T>G | p.S91A | 4081 (54%) | 101 (2%) | 1.2 | 8.7 |
| **CHIP12** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31015949:T/G | Coding | Missense | SNV | c.271T>G | p.S91A | 3066 (56%) | 55 (2%) | 0.9 | 9.1 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31021202:A/C | Coding | Missense | SNV | c.1201A>C | p.T401P | 2160 (78%) | 37 (2%) | 0.9 | 5.1 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31021207:A/C | Coding | Synonymous | SNV | c.1206A>C | p.R402= | 2032 (74%) | 42 (2%) | 1.0 | 5.2 |
| **CHIP8** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31021461:C/T | Coding | Missense | SNV | c.1460C>T | p.A487V | 1495 (52%) | 703 (47%) | 23.6 | 17.0 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31021479:A/C | Coding | Missense | SNV | c.1478A>C | p.E493A | 1705 (62%) | 31 (2%) | 0.9 | 5.4 |
| **CHIP4** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31021634:C/T | Coding | Missense | SNV | c.1633C>T | p.R545C | 778 (86%) | 11 (1%) | 0.7 | 1.7 |
| **CHIP3** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31021634:C/T | Coding | Missense | SNV | c.1633C>T | p.R545C | 1216 (84%) | 16 (1%) | 0.7 | 1.6 |
| **CHIP5** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31022396:G/A | Coding | Synonymous | SNV | c.1881G>A | p.A627= | 3013 (50%) | 80 (3%) | 1.3 | 2.1 |
| **CHIP8** | CD34+ BM | ASXL1 | 20 | ASXL1:chr20:31022396:G/A | Coding | Synonymous | SNV | c.1881G>A | p.A627= | 6999 (55%) | 160 (2%) | 1.1 | 2.0 |
| **CHIP4** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31022938:C/A | Coding | Missense | SNV | c.2423C>A | p.P808H | 862 (95%) | 818 (95%) | 50.2 | 51.2 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023033:C/G | Coding | Missense | SNV | c.2518C>G | p.P840A | 1909 (69%) | 39 (2%) | 1.0 | 4.2 |
| **CHIP14** | CD34+ BM | ASXL1 | 20 | ASXL1:chr20:31023033:C/G | Coding | Missense | SNV | c.2518C>G | p.P840A | 4963 (66%) | 117 (2%) | 1.2 | 1.8 |
| **CHIP12** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023033:C/G | Coding | Missense | SNV | c.2518C>G | p.P840A | 3920 (72%) | 115 (3%) | 1.5 | 2.2 |
| **CHIP11** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023033:C/G | Coding | Missense | SNV | c.2518C>G | p.P840A | 5744 (61%) | 160 (3%) | 1.4 | 1.9 |
| **CHIP11** | CD34+ BM | ASXL1 | 20 | ASXL1:chr20:31023033:C/G | Coding | Missense | SNV | c.2518C>G | p.P840A | 798 (78%) | 24 (3%) | 1.5 | 2.5 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023045:A/C | Coding | Missense | SNV | c.2530A>C | p.T844P | 1434 (52%) | 55 (4%) | 1.9 | 6.6 |
| **CHIP8** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023122:T/G | Coding | Synonymous | SNV | c.2607T>G | p.G869= | 1505 (52%) | 29 (2%) | 1.0 | 9.0 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023126:T/G | Coding | Missense | SNV | c.2611T>G | p.S871A | 1653 (60%) | 42 (3%) | 1.3 | 5.8 |
| **CHIP1** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023286:C/T | Coding | Missense | SNV | c.2771C>T | p.P924L | 3160 (87%) | 38 (1%) | 0.6 | 1.1 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023362:T/G | Coding | Synonymous | SNV | c.2847T>G | p.G949= | 2031 (74%) | 141 (7%) | 3.5 | 7.5 |
| **CHIP9** | CD34+ PB | ASXL1 | 20 | ASXL1:chr20:31023714:T/G | Coding | Missense | SNV | c.3199T>G | p.S1067A | 1417 (51%) | 35 (2%) | 1.2 | 7.3 |
| **CHIP9** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25457213:A/C | Coding | Missense | SNV | c.2674T>G | p.S892A | 1607 (58%) | 87 (5%) | 2.7 | 6.6 |
| **CHIP9** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25457221:A/C | Coding | Missense | SNV | c.2666T>G | p.L889R | 1897 (69%) | 45 (2%) | 1.2 | 5.9 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP11** | BM post ASCT | DNMT3A | 2 | DNMT3A:chr2:25457242:C/T | Coding | Missense | SNV | c.2645G>A | p.R882H | 5376 (88%) | 3985 (74%) | 39.6 | 38.5 |
| **CHIP11** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25457242:C/T | Coding | Missense | SNV | c.2645G>A | p.R882H | 6843 (72%) | 5312 (78%) | 41.3 | 37.1 |
| **CHIP11** | CD34+ BM | DNMT3A | 2 | DNMT3A:chr2:25457242:C/T | Coding | Missense | SNV | c.2645G>A | p.R882H | 837 (81%) | 521 (62%) | 35.2 | 34.5 |
| **CHIP9** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25457246:T/G | Coding | Missense | SNV | c.2641A>C | p.S881R | 1661 (60%) | 320 (19%) | 9.6 | 13.4 |
| **CHIP1** | CD34- PB | DNMT3A | 2 | DNMT3A:chr2:25457246:T/G | Coding | Missense | SNV | c.2641A>C | p.S881R | 70 (71%) | 20 (29%) | 14.3 | 16.8 |
| **CHIP8** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25457246:T/G | Coding | Missense | SNV | c.2641A>C | p.S881R | 2555 (88%) | 50 (2%) | 1.0 | 4.3 |
| **CHIP1** | CD34- PB | DNMT3A | 2 | DNMT3A:chr2:25457269:TG/T | NMD, coding[(2)] | Frameshift | Deletion | c.2617del | p.H873Tfs*8 | 97 (99%) | 2 (2%) | 1.0 | 3.2 |
| **CHIP12** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25462007:A/C | Coding, splicing | Synonymous | SNV | c.2400T>G | p.G800= | 3241 (60%) | 58 (2%) | 0.9 | 6.6 |
| **CHIP1** | CD34- PB | DNMT3A | 2 | DNMT3A:chr2:25462086:T/G | Intronic, splicing, splicing-ACMG[(1)] | | SNV | c.2323-2A>C | | 61 (62%) | 5 (8%) | 4.1 | 4.6 |
| **CHIP7** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25463182:G/A | NMD, coding[(2)] | Nonsense | SNV | c.2311C>T | p.R771* | 4758 (96%) | 134 (3%) | 1.5 | 1.9 |
| **CHIP14** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25463248:G/A | Coding | Missense | SNV | c.2245C>T | p.R749C | 4973 (80%) | 121 (2%) | 1.2 | 3.3 |
| **CHIP14** | CD34+ BM | DNMT3A | 2 | DNMT3A:chr2:25463248:G/A | Coding | Missense | SNV | c.2245C>T | p.R749C | 6361 (85%) | 100 (2%) | 0.8 | 3.0 |
| **CHIP1** | CD34- PB | DNMT3A | 2 | DNMT3A:chr2:25463595:T/G | Coding, splicing | Missense | SNV | c.2087A>C | p.Q696P | 66 (67%) | 9 (14%) | 6.8 | 8.4 |
| **CHIP1** | CD34- PB | DNMT3A | 2 | DNMT3A:chr2:25464452:G/A | Coding | Synonymous | SNV | c.2061C>T | p.V687= | 93 (95%) | 1 (1%) | 0.5 | 3.5 |
| **CHIP8** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25467131:T/G | Coding | Missense | SNV | c.1744A>C | p.N582H | 1537 (53%) | 41 (3%) | 1.3 | 4.9 |
| **CHIP1** | CD138- BM | DNMT3A | 2 | DNMT3A:chr2:25467453:A/C | Coding | Missense | SNV | c.1623T>G | p.C541W | 4601 (54%) | 131 (3%) | 1.4 | 5.3 |
| **CHIP9** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25467455:A/C | Coding | Missense | SNV | c.1621T>G | p.C541G | 1660 (60%) | 28 (2%) | 0.8 | 3.5 |
| **CHIP8** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25467487:T/G | Coding | Missense | SNV | c.1589A>C | p.D530A | 1452 (50%) | 30 (2%) | 1.0 | 7.5 |
| **CHIP4** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25469502:C/T | Coding | Synonymous | SNV | c.1266G>A | p.L422= | 776 (86%) | 694 (89%) | 52.4 | 52.8 |
| **CHIP3** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25469502:C/T | Coding | Synonymous | SNV | c.1266G>A | p.L422= | 1269 (88%) | 1157 (91%) | 50.9 | 51.3 |
| **CHIP1** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25469502:C/T | Coding | Synonymous | SNV | c.1266G>A | p.L422= | 2103 (58%) | 1985 (94%) | 54.4 | 53.7 |
| **CHIP1** | CD34- PB | DNMT3A | 2 | DNMT3A:chr2:25469502:C/T | Coding | Synonymous | SNV | c.1266G>A | p.L422= | 81 (83%) | 69 (85%) | 46.9 | 43.7 |
| **CHIP8** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25469502:C/T | Coding | Synonymous | SNV | c.1266G>A | p.L422= | 1703 (59%) | 1514 (89%) | 52.2 | 51.2 |
| **CHIP5** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148508780:G/C | Coding | Synonymous | SNV | c.1884C>G | p.G628= | 5776 (97%) | 5705 (99%) | 50.2 | 51.1 |
| **CHIP1** | CD138- BM | EZH2 | 7 | EZH2:chr7:148511139:T/G | Coding | Missense | SNV | c.1763A>C | p.D588A | 4782 (56%) | 131 (3%) | 1.4 | 6.5 |
| **CHIP9** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148511145:T/G | Coding | Missense | SNV | c.1757A>C | p.D586A | 1960 (71%) | 36 (2%) | 0.9 | 7.3 |
| **CHIP6** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148511171:C/T | Coding | Synonymous | SNV | c.1731G>A | p.P577= | 2558 (87%) | 2463 (96%) | 50.1 | 52.1 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP11** | BM post ASCT | EZH2 | 7 | EZH2:chr7:148512080:T/G | Coding | Missense | SNV | c.1598A>C | p.Q533P | 3386 (55%) | 124 (4%) | 1.8 | 5.1 |
| **CHIP1** | CD138- BM | EZH2 | 7 | EZH2:chr7:148512080:T/G | Coding | Missense | SNV | c.1598A>C | p.Q533P | 5084 (60%) | 182 (4%) | 1.8 | 4.8 |
| **CHIP14** | CD34+ BM | EZH2 | 7 | EZH2:chr7:148512080:T/G | Coding | Missense | SNV | c.1598A>C | p.Q533P | 4309 (57%) | 134 (3%) | 1.6 | 4.8 |
| **CHIP8** | CD34+ BM | EZH2 | 7 | EZH2:chr7:148512080:T/G | Coding | Missense | SNV | c.1598A>C | p.Q533P | 6765 (53%) | 130 (2%) | 1.0 | 3.2 |
| **CHIP12** | CD34+ BM | EZH2 | 7 | EZH2:chr7:148512080:T/G | Coding | Missense | SNV | c.1598A>C | p.Q533P | 2175 (54%) | 49 (2%) | 1.1 | 3.5 |
| **CHIP1** | CD34- PB | EZH2 | 7 | EZH2:chr7:148514997:CTCT/C | Coding | In frame | Deletion | c.1209_1211del | p.E404del | 72 (73%) | 1 (1%) | 0.7 | 4.8 |
| **CHIP1** | CD34- PB | EZH2 | 7 | EZH2:chr7:148515091:G/A | Coding | Missense | SNV | c.1118C>T | p.P373L | 98 (100%) | 1 (1%) | 0.5 | 4.5 |
| **CHIP1** | CD34- PB | EZH2 | 7 | EZH2:chr7:148525854:T/C | Coding | Synonymous | SNV | c.603A>G | p.K201= | 98 (100%) | 2 (2%) | 1.0 | 1.8 |
| **CHIP1** | CD34- PB | EZH2 | 7 | EZH2:chr7:148526901:C/T | Coding | Missense | SNV | c.403G>A | p.G135R | 98 (100%) | 1 (1%) | 0.5 | 5.6 |
| **CHIP6** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 1799 (61%) | 1746 (97%) | 48.5 | 32.3 |
| **CHIP7** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 2887 (58%) | 2726 (94%) | 47.2 | 29.8 |
| **CHIP4** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 588 (65%) | 558 (95%) | 47.4 | 28.9 |
| **CHIP3** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 1101 (76%) | 1075 (98%) | 48.8 | 30.2 |
| **CHIP11** | BM post ASCT | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 3477 (57%) | 3236 (93%) | 46.5 | 28.7 |
| **CHIP1** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 2291 (63%) | 2189 (96%) | 47.8 | 29.2 |
| **CHIP14** | CD34+ BM | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 4515 (60%) | 4150 (92%) | 46.0 | 29.4 |
| **CHIP8** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 2079 (72%) | 1960 (94%) | 47.1 | 31.4 |
| **CHIP12** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 3817 (70%) | 3704 (97%) | 48.5 | 33.1 |
| **CHIP12** | CD34+ BM | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 2148 (53%) | 1994 (93%) | 46.4 | 30.5 |
| **CHIP11** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 5113 (54%) | 4903 (96%) | 47.9 | 31.8 |
| **CHIP11** | CD34+ BM | EZH2 | 7 | EZH2:chr7:148526923:A/G | Coding | Synonymous | SNV | c.381T>C | p.V127= | 691 (67%) | 664 (96%) | 48.0 | 33.8 |
| **CHIP9** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148529751:C/A | Coding | Missense | SNV | c.338G>T | p.W113L | 1650 (60%) | 35 (2%) | 1.1 | 3.6 |
| **CHIP9** | CD34+ PB | EZH2 | 7 | EZH2:chr7:148529754:G/T | Coding | Missense | SNV | c.335C>A | p.S112Y | 1586 (57%) | 29 (2%) | 0.9 | 4.1 |
| **CHIP1** | CD34- PB | FLT3 | 13 | FLT3:chr13:28601250:TG/T | NMD, coding[(2)] | Frameshift | Deletion | c.2181del | p.T728Lfs*53 | 93 (95%) | 2 (2%) | 1.1 | 7.5 |
| **CHIP1** | CD34- PB | FLT3 | 13 | FLT3:chr13:28608288:A/G | Coding | Missense | SNV | c.1768T>C | p.F590L | 98 (100%) | 1 (1%) | 0.5 | 5.6 |
| **CHIP1** | CD34- PB | FLT3 | 13 | FLT3:chr13:28609667:C/T | Coding | Missense | SNV | c.1562G>A | p.G521D | 98 (100%) | 1 (1%) | 0.5 | 6.1 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP6** | CD34+ PB | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 2423 (82%) | 30 (1%) | 0.6 | 1.3 |
| **CHIP7** | CD34+ PB | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 3454 (70%) | 67 (2%) | 1.0 | 1.5 |
| **CHIP4** | CD34+ PB | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 768 (85%) | 10 (1%) | 0.7 | 1.7 |
| **CHIP11** | BM post ASCT | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 4017 (66%) | 105 (3%) | 1.3 | 2.4 |
| **CHIP1** | CD34+ PB | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 2549 (70%) | 51 (2%) | 2.4 | 1.6 |
| **CHIP1** | CD138- BM | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 5010 (59%) | 127 (3%) | 1.3 | 2.6 |
| **CHIP11** | CD34+ BM | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 674 (66%) | 13 (2%) | 1.0 | 1.6 |
| **CHIP9** | CD34+ PB | GATA2 | 3 | GATA2:chr3:128200787:A/T | Coding, splicing, splicing-ACMG[(1)] | Missense | SNV | c.1018T>A | p.S340T | 1967 (71%) | 181 (9%) | 4.6 | 4.7 |
| **CHIP1** | CD34- PB | IDH1 | 2 | IDH1:chr2:209113159:AT/A | NMD, coding[(2)] | Frameshift | Deletion (homopolymer) | c.347del | p.N116Ifs*6 | 98 (100%) | 1 (1%) | 0.5 | 5.9 |
| **CHIP4** | CD34+ PB | IDH1 | 2 | IDH1:chr2:209113192:G/A | Coding | Synonymous | SNV | c.315C>T | p.G105= | 864 (96%) | 831 (96%) | 49.7 | 50.4 |
| **CHIP9** | CD34+ PB | IDH2 | 15 | IDH2:chr15:90631828:A/C | Coding, splicing | Missense | SNV | c.525T>G | p.H175Q | 1485 (54%) | 49 (3%) | 1.6 | 4.3 |
| **CHIP1** | CD34- PB | JAK2 | 9 | JAK2:chr9:5073752:T/A | Coding | Missense | SNV | c.1831T>A | p.L611I | 96 (98%) | 1 (1%) | 0.5 | 6.1 |
| **CHIP1** | CD34- PB | KIT | 4 | KIT:chr4:55561718:ACCAT/A | NMD, coding[(2)] | Frameshift | Deletion | c.120_123del | p.H40Qfs*6 | 93 (95%) | 1 (1%) | 0.5 | 3.4 |
| **CHIP6** | CD34+ PB | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 2300 (78%) | 50 (2%) | 1.1 | 1.9 |
| **CHIP5** | CD34+ PB | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 3316 (56%) | 117 (4%) | 1.8 | 2.1 |
| **CHIP2** | CD34+ PB | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 6544 (54%) | 255 (4%) | 1.9 | 2.1 |
| **CHIP14** | CD34+ BM | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 4988 (66%) | 131 (3%) | 1.3 | 1.8 |
| **CHIP8** | CD34+ PB | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 2472 (86%) | 44 (2%) | 0.9 | 1.9 |
| **CHIP12** | CD34+ PB | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 3880 (71%) | 151 (4%) | 1.9 | 2.1 |
| **CHIP12** | CD34+ BM | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 2370 (59%) | 42 (2%) | 0.9 | 1.3 |
| **CHIP11** | CD34+ PB | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 5025 (53%) | 151 (3%) | 1.5 | 1.5 |
| **CHIP11** | CD34+ BM | KIT | 4 | KIT:chr4:55569900:A/T | Coding | Missense | SNV | c.767A>T | p.Q256L | 709 (69%) | 20 (3%) | 1.4 | 2.1 |
| **CHIP9** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 1463 (53%) | 926 (63%) | 31.6 | 23.8 |
| **CHIP3** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 981 (68%) | 27 (3%) | 1.4 | 7.4 |
| **CHIP2** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 10534 (87%) | 183 (2%) | 0.9 | 3.4 |
| **CHIP11** | BM post ASCT | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 4887 (80%) | 133 (3%) | 1.4 | 4.8 |
| **CHIP1** | CD138- BM | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 6809 (80%) | 142 (2%) | 1.0 | 3.8 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP1** | CD34- PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 54 (55%) | 50 (93%) | 46.3 | 26.7 |
| **CHIP14** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 3937 (63%) | 203 (5%) | 2.6 | 6.1 |
| **CHIP14** | CD34+ BM | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 5479 (73%) | 462 (8%) | 4.2 | 8.8 |
| **CHIP8** | CD34+ BM | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 8445 (66%) | 226 (3%) | 1.3 | 3.9 |
| **CHIP12** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 3424 (63%) | 533 (16%) | 7.8 | 14.4 |
| **CHIP12** | CD34+ BM | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 2500 (62%) | 185 (7%) | 3.7 | 7.4 |
| **CHIP11** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 7001 (74%) | 125 (2%) | 0.9 | 2.9 |
| **CHIP11** | CD34+ BM | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 674 (66%) | 60 (9%) | 4.5 | 9.2 |
| **CHIP6** | CD34+ PB | KIT | 4 | KIT:chr4:55602765:G/C | Coding | Synonymous | SNV | c.2586G>C | p.L862= | 2591 (88%) | 2505 (97%) | 49.9 | 51.3 |
| **CHIP2** | CD34+ PB | KIT | 4 | KIT:chr4:55602765:G/C | Coding | Synonymous | SNV | c.2586G>C | p.L862= | 11162 (92%) | 11061 (99%) | 50.1 | 50.5 |
| **CHIP8** | CD34+ PB | KIT | 4 | KIT:chr4:55602765:G/C | Coding | Synonymous | SNV | c.2586G>C | p.L862= | 2550 (88%) | 2436 (96%) | 49.8 | 51.3 |
| **CHIP8** | CD34+ BM | KIT | 4 | KIT:chr4:55602765:G/C | Coding | Synonymous | SNV | c.2586G>C | p.L862= | 8154 (64%) | 8092 (99%) | 49.9 | 50.2 |
| **CHIP8** | CD34+ PB | KRAS | 12 | KRAS:chr12:25380328:C/A | Coding | Missense | SNV | c.130G>T | p.V44L | 1678 (58%) | 110 (7%) | 3.3 | 8.5 |
| **CHIP12** | CD34+ PB | KRAS | 12 | KRAS:chr12:25380328:C/A | Coding | Missense | SNV | c.130G>T | p.V44L | 4131 (76%) | 122 (3%) | 1.5 | 6.2 |
| **CHIP6** | CD34+ PB | NRAS | 1 | NRAS:chr1:115256513:G/A | Coding | Synonymous | SNV | c.198C>T | p.A66= | 2594 (88%) | 40 (2%) | 0.8 | 2.2 |
| **CHIP7** | CD34+ PB | NRAS | 1 | NRAS:chr1:115256513:G/A | Coding | Synonymous | SNV | c.198C>T | p.A66= | 4241 (86%) | 72 (2%) | 0.8 | 1.9 |
| **CHIP4** | CD34+ PB | NRAS | 1 | NRAS:chr1:115256513:G/A | Coding | Synonymous | SNV | c.198C>T | p.A66= | 765 (85%) | 11 (1%) | 0.7 | 3.1 |
| **CHIP3** | CD34+ PB | NRAS | 1 | NRAS:chr1:115256513:G/A | Coding | Synonymous | SNV | c.198C>T | p.A66= | 1150 (79%) | 23 (2%) | 1.0 | 3.3 |
| **CHIP11** | BM post ASCT | NRAS | 1 | NRAS:chr1:115256513:G/A | Coding | Synonymous | SNV | c.198C>T | p.A66= | 4666 (76%) | 67 (1%) | 0.7 | 2.8 |
| **CHIP1** | CD34+ PB | NRAS | 1 | NRAS:chr1:115256513:G/A | Coding | Synonymous | SNV | c.198C>T | p.A66= | 2981 (82%) | 72 (2%) | 1.2 | 2.3 |
| **CHIP11** | CD34+ BM | NRAS | 1 | NRAS:chr1:115256513:G/A | Coding | Synonymous | SNV | c.198C>T | p.A66= | 860 (84%) | 11 (1%) | 0.6 | 2.4 |
| **CHIP11** | CD34+ BM | NRAS | 1 | NRAS:chr1:115256529:T/C | Coding | Missense | SNV | c.182A>G | p.Q61R | 945 (92%) | 19 (2%) | 1.1 | 2.3 |
| **CHIP11** | BM post ASCT | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 5006 (82%) | 166 (3%) | 1.7 | 6.2 |
| **CHIP1** | CD138- BM | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 7432 (87%) | 91 (1%) | 0.6 | 5.0 |
| **CHIP14** | CD34+ PB | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 5026 (81%) | 250 (5%) | 2.5 | 6.2 |
| **CHIP14** | CD34+ BM | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 5856 (78%) | 186 (3%) | 1.6 | 6.2 |

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| **CHIP8** | CD34+ BM | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 10982 (86%) | 187 (2%) | 0.9 | 4.3 |
| **CHIP12** | CD34+ PB | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 3593 (66%) | 253 (7%) | 3.5 | 7.7 |
| **CHIP12** | CD34+ BM | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 3451 (86%) | 43 (1%) | 0.6 | 5.1 |
| **CHIP11** | CD34+ BM | PTPN11 | 12 | PTPN11:chr12:112891084:A/C | Coding | Missense | SNV | c.418A>C | p.S140R | 775 (75%) | 24 (3%) | 1.5 | 6.4 |
| **CHIP9** | CD34+ PB | PTPN11 | 12 | PTPN11:chr12:112891098:T/G | Coding | Synonymous | SNV | c.432T>G | p.P144= | 2054 (74%) | 125 (6%) | 3.0 | 6.5 |
| **CHIP1** | CD34- PB | PTPN11 | 12 | PTPN11:chr12:112926935:C/T | NMD, coding[2] | Nonsense | SNV | c.1555C>T | p.Q519* | 94 (96%) | 2 (2%) | 1.1 | 3.5 |
| **CHIP1** | CD34- PB | RUNX1 | 21 | RUNX1:chr21:36171713:G/A | Coding | Synonymous | SNV | c.852C>T | p.S284= | 90 (92%) | 1 (1%) | 0.6 | 2.4 |
| **CHIP4** | CD34+ PB | RUNX1 | 21 | RUNX1:chr21:36206776:T/G | Coding | Missense | SNV | c.736A>C | p.T246P | 558 (62%) | 10 (2%) | 0.9 | 8.5 |
| **CHIP3** | CD34+ PB | RUNX1 | 21 | RUNX1:chr21:36206776:T/G | Coding | Missense | SNV | c.736A>C | p.T246P | 816 (56%) | 23 (3%) | 1.4 | 8.0 |
| **CHIP3** | CD34+ PB | RUNX1 | 21 | RUNX1:chr21:36206787:T/G | Coding | Missense | SNV | c.725A>C | p.H242P | 956 (66%) | 23 (2%) | 1.2 | 6.3 |
| **CHIP4** | CD34+ PB | RUNX1 | 21 | RUNX1:chr21:36206790:T/G | Coding | Missense | SNV | c.722A>C | p.H242P | 484 (54%) | 110 (23%) | 11.4 | 12.8 |
| **CHIP3** | CD34+ PB | RUNX1 | 21 | RUNX1:chr21:36206792:T/G | Coding | Synonymous | SNV | c.720A>C | p.P240= | 788 (54%) | 647 (82%) | 41.1 | 27.8 |
| **CHIP11** | CD34+ PB | SF3B1 | 2 | SF3B1:chr2:198266834:T/C | Coding | Missense | SNV | c.2098A>G | p.K700E | 9040 (95%) | 175 (2%) | 1.0 | 1.6 |
| **CHIP11** | CD34+ BM | SF3B1 | 2 | SF3B1:chr2:198266834:T/C | Coding | Missense | SNV | c.2098A>G | p.K700E | 986 (96%) | 24 (2%) | 1.3 | 2.1 |
| **CHIP1** | CD34- PB | SF3B1 | 2 | SF3B1:chr2:198267531:A/G | Coding | Missense | SNV | c.1826T>C | p.M609T | 96 (98%) | 1 (1%) | 0.5 | 3.1 |
| **CHIP1** | CD34- PB | SF3B1 | 2 | SF3B1:chr2:198267543:C/A | Coding, splicing | Missense | SNV | c.1814G>T | p.G605V | 59 (60%) | 4 (7%) | 3.4 | 6.9 |
| **CHIP1** | CD34+ PB | TET2 | 4 | TET2:chr4:106155185:C/G | Coding | Missense | SNV | c.86C>G | p.P29R | 2904 (80%) | 2706 (93%) | 47.9 | 41.2 |
| **CHIP1** | CD138- BM | TET2 | 4 | TET2:chr4:106155185:C/G | Coding | Missense | SNV | c.86C>G | p.P29R | 6498 (76%) | 6415 (99%) | 49.4 | 38.4 |
| **CHIP7** | CD34+ PB | TET2 | 4 | TET2:chr4:106155199:C/T | Coding | Missense | SNV | c.100C>T | p.L34F | 4471 (90%) | 4312 (96%) | 50.0 | 50.7 |
| **CHIP8** | CD34+ BM | TET2 | 4 | TET2:chr4:106155490:A/G | Coding | Missense | SNV | c.391A>G | p.R131G | 8071 (63%) | 137 (2%) | 0.8 | 2.1 |
| **CHIP1** | CD34- PB | TET2 | 4 | TET2:chr4:106156138:G/A | Coding | Missense | SNV | c.1039G>A | p.A347T | 98 (100%) | 1 (1%) | 0.5 | 4.6 |
| **CHIP1** | CD34+ PB | TET2 | 4 | TET2:chr4:106157870:A/G | Coding | Missense | SNV | c.2771A>G | p.H924R | 3229 (89%) | 3063 (95%) | 49.2 | 50.1 |
| **CHIP1** | CD138- BM | TET2 | 4 | TET2:chr4:106157870:A/G | Coding | Missense | SNV | c.2771A>G | p.H924R | 7072 (83%) | 6900 (98%) | 48.9 | 49.4 |
| **CHIP1** | CD34- PB | TET2 | 4 | TET2:chr4:106158346:C/T | NMD, coding[2] | Nonsense | SNV | c.3247C>T | p.Q1083* | 61 (62%) | 1 (2%) | 1.6 | 3.7 |
| **CHIP1** | CD34- PB | TET2 | 4 | TET2:chr4:106158427:A/G | Coding | Missense | SNV | c.3328A>G | p.K1110E | 74 (76%) | 1 (1%) | 1.4 | 3.0 |
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106162497:G/T | Coding, splicing, splicing-ACMG[1] | Missense | SNV | c.3411G>T | p.E1137D | 1780 (65%) | 50 (3%) | 1.4 | 5.0 |
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106164829:T/G | Coding | Missense | SNV | c.3697T>G | p.W1233G | 1428 (52%) | 56 (4%) | 2.0 | 3.4 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106180822:T/G | Coding | Missense | SNV | c.3850T>G | p.S1284A | 2124 (77%) | 221 (10%) | 5.2 | 9.0 |
| **CHIP3** | CD34+ PB | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 860 (59%) | 15 (2%) | 0.9 | 5.3 |
| **CHIP11** | BM post ASCT | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 3948 (65%) | 436 (11%) | 5.5 | 9.7 |
| **CHIP1** | CD138- BM | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 5421 (63%) | 323 (6%) | 3.0 | 5.8 |
| **CHIP14** | CD34+ PB | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 3425 (55%) | 216 (6%) | 3.2 | 7.0 |
| **CHIP14** | CD34+ BM | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 4372 (58%) | 369 (8%) | 4.2 | 8.6 |
| **CHIP12** | CD34+ BM | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 2788 (69%) | 154 (6%) | 2.8 | 5.7 |
| **CHIP11** | CD34+ PB | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 6362 (67%) | 105 (2%) | 0.8 | 2.7 |
| **CHIP11** | CD34+ BM | TET2 | 4 | TET2:chr4:106190805:T/G | Coding | Synonymous | SNV | c.4083T>G | p.G1361= | 689 (67%) | 73 (11%) | 5.3 | 8.8 |
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106190821:C/T | Coding | Missense | SNV | c.4099C>T | p.P1367S | 2652 (96%) | 57 (2%) | 1.1 | 1.8 |
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106190834:T/G | Coding | Missense | SNV | c.4112T>G | p.V1371G | 2151 (78%) | 138 (6%) | 3.2 | 8.0 |
| **CHIP1** | CD34- PB | TET2 | 4 | TET2:chr4:106190834:T/G | Coding | Missense | SNV | c.4112T>G | p.V1371G | 58 (59%) | 6 (10%) | 5.2 | 10.8 |
| **CHIP8** | CD34+ PB | TET2 | 4 | TET2:chr4:106196253:A/C | Coding | Missense | SNV | c.4586A>C | p.Q1529P | 2164 (75%) | 29 (1%) | 0.7 | 6.8 |
| **CHIP12** | CD34+ PB | TET2 | 4 | TET2:chr4:106196253:A/C | Coding | Missense | SNV | c.4586A>C | p.Q1529P | 3715 (68%) | 67 (2%) | 0.9 | 6.7 |
| **CHIP4** | CD34+ PB | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 594 (66%) | 10 (2%) | 0.8 | 5.1 |
| **CHIP14** | CD34+ BM | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 4033 (54%) | 199 (5%) | 2.5 | 8.2 |
| **CHIP8** | CD34+ PB | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 1742 (60%) | 116 (7%) | 3.3 | 9.0 |
| **CHIP12** | CD34+ PB | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 3306 (61%) | 205 (6%) | 3.1 | 8.7 |
| **CHIP12** | CD34+ BM | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 2019 (50%) | 62 (3%) | 1.5 | 6.1 |
| **CHIP11** | CD34+ PB | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 5092 (54%) | 163 (3%) | 1.6 | 6.6 |
| **CHIP11** | CD34+ PB | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 627 (61%) | 35 (6%) | 2.8 | 8.1 |
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 1810 (66%) | 52 (3%) | 1.4 | 5.1 |
| **CHIP6** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 2437 (83%) | 67 (3%) | 1.4 | 2.6 |
| **CHIP7** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 3838 (77%) | 136 (4%) | 1.8 | 3.0 |
| **CHIP4** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 759 (84%) | 16 (2%) | 1.1 | 2.7 |
| **CHIP2** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 7423 (61%) | 158 (2%) | 1.1 | 2.7 |
| **CHIP11** | BM post ASCT | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 4934 (81%) | 94 (2%) | 1.0 | 2.8 |
| **CHIP1** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 2503 (69%) | 126 (5%) | 2.5 | 3.9 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP1** | CD138-BM | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 5562 (65%) | 195 (4%) | 1.8 | 3.3 |
| **CHIP14** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 4542 (73%) | 174 (4%) | 1.9 | 2.8 |
| **CHIP14** | CD34+ BM | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 5117 (68%) | 256 (5%) | 2.5 | 3.4 |
| **CHIP8** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 2431 (84%) | 76 (3%) | 1.6 | 3.0 |
| **CHIP8** | CD34+ BM | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 7166 (56%) | 169 (2%) | 1.2 | 3.5 |
| **CHIP12** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 4032 (74%) | 148 (4%) | 1.8 | 3.2 |
| **CHIP12** | CD34+ BM | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 3276 (81%) | 95 (3%) | 1.4 | 2.8 |
| **CHIP11** | CD34+ PB | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 5944 (63%) | 483 (8%) | 4.1 | 4.4 |
| **CHIP11** | CD34+ BM | TET2 | 4 | TET2:chr4:106196792:T/C | Coding | Missense | SNV | c.5125T>C | p.C1709R | 699 (68%) | 79 (11%) | 5.7 | 5.2 |
| **CHIP6** | CD34+ PB | TET2 | 4 | TET2:chr4:106196829:T/G | Coding | Missense | SNV | c.5162T>G | p.L1721W | 2936 (100%) | 2936 (100%) | 99.9 | 99.7 |
| **CHIP7** | CD34+ PB | TET2 | 4 | TET2:chr4:106196829:T/G | Coding | Missense | SNV | c.5162T>G | p.L1721W | 4667 (94%) | 4479 (96%) | 50.1 | 49.6 |
| **CHIP4** | CD34+ PB | TET2 | 4 | TET2:chr4:106196829:T/G | Coding | Missense | SNV | c.5162T>G | p.L1721W | 875 (97%) | 832 (95%) | 49.7 | 50.8 |
| **CHIP3** | CD34+ PB | TET2 | 4 | TET2:chr4:106196829:T/G | Coding | Missense | SNV | c.5162T>G | p.L1721W | 1406 (97%) | 1345 (96%) | 50.6 | 51.1 |
| **CHIP2** | CD34+ PB | TET2 | 4 | TET2:chr4:106196829:T/G | Coding | Missense | SNV | c.5162T>G | p.L1721W | 11925 (98%) | 11747 (99%) | 50.0 | 49.9 |
| **CHIP14** | CD34+ PB | TET2 | 4 | TET2:chr4:106196829:T/G | Coding | Missense | SNV | c.5162T>G | p.L1721W | 6091 (98%) | 6091 (100%) | 99.9 | 99.5 |
| **CHIP14** | CD34+ BM | TET2 | 4 | TET2:chr4:106196829:T/G | Coding | Missense | SNV | c.5162T>G | p.L1721W | 7448 (99%) | 7448 (100%) | 100.0 | 99.5 |
| **CHIP7** | CD34+ PB | TET2 | 4 | TET2:chr4:106197000:A/G | Coding | Missense | SNV | c.5333A>G | p.H1778R | 4688 (95%) | 4495 (96%) | 49.9 | 52.7 |
| **CHIP1** | CD34+ PB | TET2 | 4 | TET2:chr4:106197000:A/G | Coding | Missense | SNV | c.5333A>G | p.H1778R | 3435 (95%) | 3305 (96%) | 50.0 | 52.9 |
| **CHIP1** | CD138-BM | TET2 | 4 | TET2:chr4:106197000:A/G | Coding | Missense | SNV | c.5333A>G | p.H1778R | 8280 (97%) | 8253 (100%) | 50.1 | 51.1 |
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106197002:G/A | Coding | Missense | SNV | c.5335G>A | p.A1779T | 1418 (51%) | 50 (4%) | 1.8 | 6.1 |
| **CHIP1** | CD34+ PB | TET2 | 4 | TET2:chr4:106197139:T/G | Coding | Synonymous | SNV | c.5472T>G | p.G1824= | 53 (54%) | 11 (21%) | 10.4 | 7.9 |
| **CHIP14** | CD34+ BM | TET2 | 4 | TET2:chr4:106197139:T/G | Coding | Synonymous | SNV | c.5472T>G | p.G1824= | 4093 (54%) | 77 (2%) | 0.9 | 7.9 |
| **CHIP1** | CD34- PB | TET2 | 4 | TET2:chr4:106197172:T/G | Coding | Synonymous | SNV | c.5505T>G | p.G1835= | 49 (50%) | 19 (39%) | 19.4 | 12.3 |
| **CHIP8** | CD34+ PB | TET2 | 4 | TET2:chr4:106197172:T/G | Coding | Synonymous | SNV | c.5505T>G | p.G1835= | 1561 (54%) | 30 (2%) | 1.0 | 9.1 |
| **CHIP9** | CD34+ PB | TET2 | 4 | TET2:chr4:106197204:T/G | Coding | Missense | SNV | c.5537T>G | p.V1846G | 1388 (50%) | 42 (3%) | 1.5 | 3.8 |
| **CHIP9** | CD34+ PB | TP53 | 17 | TP53:chr17:7574022:A/C | Coding | Synonymous | SNV | c.888T>G | p.R296= | 1619 (59%) | 75 (5%) | 2.3 | 6.7 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP9** | CD34+ PB | TP53 | 17 | TP53:chr17:7574028:A/C | Coding, splicing | Synonymous | SNV | c.882T>G | p.R294= | 2064 (75%) | 73 (4%) | 1.8 | 7.5 |
| **CHIP9** | CD34+ PB | TP53 | 17 | TP53:chr17:7576896:T/G | Coding | Missense | SNV | c.833A>C | p.Q278P | 1403 (51%) | 69 (5%) | 2.5 | 5.4 |
| **CHIP1** | CD138-BM | TP53 | 17 | TP53:chr17:7577099:C/G | Coding | Missense | SNV | c.722G>C | p.R241T | 7576 (89%) | 243 (3%) | 1.6 | 2.2 |
| **CHIP1** | CD138-BM | TP53 | 17 | TP53:chr17:7577127:C/T | Coding | Missense | SNV | c.694G>A | p.E232K | 7819 (92%) | 109 (1%) | 0.7 | 2.0 |
| **CHIP9** | CD34+ PB | TP53 | 17 | TP53:chr17:7577500:T/G | Coding, splicing, splicing-ACMG[(1)] | Missense | SNV | c.664A>C | p.S222R | 2151 (78%) | 39 (2%) | 0.9 | 5.4 |
| **CHIP8** | CD34+ PB | TP53 | 17 | TP53:chr17:7578210:T/C | Coding | Synonymous | SNV | c.522A>G | p.R174= | 2442 (85%) | 2293 (94%) | 50.2 | 51.6 |
| **CHIP9** | CD34+ PB | TP53 | 17 | TP53:chr17:7578434:A/C | Coding | Missense | SNV | c.379T>G | p.S127A | 1441 (52%) | 33 (2%) | 1.1 | 4.3 |
| **CHIP1** | CD34- PB | TP53 | 17 | TP53:chr17:7578460:A/G | Coding | Missense | SNV | c.353T>C | p.V118A | 54 (55%) | 1 (2%) | 0.9 | 1.6 |
| **CHIP8** | CD34+ PB | TP53 | 17 | TP53:chr17:7578480:T/G | Coding | Synonymous | SNV | c.333A>C | p.T111= | 1639 (57%) | 38 (2%) | 1.2 | 7.5 |
| **CHIP1** | CD138-BM | TP53 | 17 | TP53:chr17:7578508:C/T | Coding | Missense | SNV | c.305G>A | p.C102Y | 6029 (71%) | 91 (2%) | 0.8 | 2.3 |
| **CHIP1** | CD34+ PB | U2AF1 | 21 | U2AF1:chr21:44514601:C/T | Coding | Synonymous | SNV | c.555G>A | p.L185= | 3246 (90%) | 3045 (94%) | 49.6 | 50.5 |
| **CHIP1** | CD138-BM | U2AF1 | 21 | U2AF1:chr21:44514601:C/T | Coding | Synonymous | SNV | c.555G>A | p.L185= | 7550 (88%) | 7480 (99%) | 49.9 | 50.3 |
| **CHIP1** | CD34- PB | U2AF1 | 21 | U2AF1:chr21:44514601:C/T | Coding | Synonymous | SNV | c.555G>A | p.L185= | 86 (88%) | 78 (91%) | 45.9 | 45.2 |
| **CHIP1** | CD34- PB | WT1 | 11 | WT1:chr11:32413520:G/A | Coding, splicing | Missense | SNV | c.1445C>T | p.T482I | 97 (99%) | 1 (1%) | 0.5 | 4.0 |
| **CHIP1** | CD34- PB | WT1 | 11 | WT1:chr11:32413605:TCA/T | NMD, coding, splicing[(2)] | Frameshift | Deletion | c.1358_1359del | p.V453Efs*6 | 97 (99%) | 2 (2%) | 1.0 | 2.0 |
| **CHIP9** | CD34+ PB | WT1 | 11 | WT1:chr11:32417899:T/G | Coding | Missense | SNV | c.1168A>C | p.T390P | 1506 (55%) | 85 (6%) | 2.8 | 5.9 |
| **CHIP7** | CD34+ PB | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 4583 (92%) | 4496 (98%) | 50.1 | 50.6 |
| **CHIP1** | CD34+ PB | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 3365 (93%) | 3300 (98%) | 50.1 | 50.4 |
| **CHIP1** | CD138-BM | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 8074 (94%) | 8062 (100%) | 50.0 | 49.7 |
| **CHIP1** | CD34- PB | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 79 (81%) | 76 (96%) | 48.7 | 40.8 |
| **CHIP14** | CD34+ PB | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 5225 (84%) | 5225 (100%) | 100.0 | 99.9 |
| **CHIP14** | CD34+ BM | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 7198 (96%) | 7198 (100%) | 99.9 | 99.9 |
| **CHIP8** | CD34+ PB | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 2630 (91%) | 2534 (96%) | 49.9 | 50.7 |
| **CHIP8** | CD34+ BM | WT1 | 11 | WT1:chr11:32417945:T/C | Coding, splicing | Synonymous | SNV | c.1122A>G | p.R374= | 9382 (74%) | 9329 (99%) | 50.0 | 49.2 |

[(1)] According to *the American College of Medical Genetics and Genomics-Association for Molecular Pathology* (ACMG-AMP) interpretation guidelines

[(2)] Nonsense-mediated decay (NMD)

**Supplementary Table S3. Called pathogenic somatic Variants.** All pathogenic somatic coding variants identified in all samples analyzed (n=19). SNV=Single Nucleotide Variant.

| Sample | Sample Type | Gene | Chromosome | Variant | Function | Coding Impact | Variant Type | cDNA | Protein Change | Genotyped Cells | Mutated Cells | VAF by cell count (%) | VAF by read count (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHIP11** | BM post ASCT | DNMT3A | 2 | DNMT3A:chr2:25457242:C/T | Coding | Missense | SNV | c.2645G>A | p.R882H | 5376 (88%) | 3985 (74%) | 39.6 | 38.5 |
| **CHIP11** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25457242:C/T | Coding | Missense | SNV | c.2645G>A | p.R882H | 6843 (72%) | 5312 (78%) | 41.3 | 37.1 |
| **CHIP11** | CD34+ BM | DNMT3A | 2 | DNMT3A:chr2:25457242:C/T | Coding | Missense | SNV | c.2645G>A | p.R882H | 837 (81%) | 521 (62%) | 35.2 | 34.5 |
| **CHIP9** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25457246:T/G | Coding | Missense | SNV | c.2641A>C | p.S881R | 1661 (60%) | 320 (19%) | 9.6 | 13.4 |
| **CHIP1** | CD34- PB | DNMT3A | 2 | DNMT3A:chr2:25462086:T/G | Intronic, splicing, splicing-ACMG[1] | | SNV | c.2323-2A>C | | 61 (62%) | 5 (8%) | 4.1 | 4.6 |
| **CHIP7** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25463182:G/A | NMD, coding[2] | Nonsense | SNV | c.2311C>T | p.R771* | 4758 (96%) | 134 (3%) | 1.5 | 1.9 |
| **CHIP14** | CD34+ PB | DNMT3A | 2 | DNMT3A:chr2:25463248:G/A | Coding | Missense | SNV | c.2245C>T | p.R749C | 4973 (80%) | 121 (2%) | 1.2 | 3.3 |
| **CHIP14** | CD34+ BM | DNMT3A | 2 | DNMT3A:chr2:25463248:G/A | Coding | Missense | SNV | c.2245C>T | p.R749C | 6361 (85%) | 100 (2%) | 0.8 | 3.0 |
| **CHIP1** | CD138- BM | EZH2 | 7 | EZH2:chr7:148512080:T/G | Coding | Missense | SNV | c.1598A>C | p.Q533P | 5084 (60%) | 182 (4%) | 1.8 | 4.8 |
| **CHIP1** | CD34+ PB | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 2549 (70%) | 51 (2%) | 2.4 | 1.6 |
| **CHIP1** | CD138- BM | GATA2 | 3 | GATA2:chr3:128200690:G/A | Coding | Missense | SNV | c.1115C>T | p.A372V | 5010 (59%) | 127 (3%) | 1.3 | 2.6 |
| **CHIP9** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 1463 (53%) | 926 (63%) | 31.6 | 23.8 |
| **CHIP12** | CD34+ PB | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 3424 (63%) | 533 (16%) | 7.8 | 14.4 |
| **CHIP12** | CD34+ BM | KIT | 4 | KIT:chr4:55599336:C/A | Coding | Missense | SNV | c.2462C>A | p.S821Y | 2500 (62%) | 185 (7%) | 3.7 | 7.4 |
| **CHIP11** | CD34+ BM | NRAS | 1 | NRAS:chr1:115256529:T/C | Coding | Missense | SNV | c.182A>G | p.Q61R | 945 (92%) | 19 (2%) | 1.1 | 2.3 |
| **CHIP11** | CD34+ PB | SF3B1 | 2 | SF3B1:chr2:198266834:T/C | Coding | Missense | SNV | c.2098A>G | p.K700E | 9040 (95%) | 175 (2%) | 1.0 | 1.6 |
| **CHIP11** | CD34+ BM | SF3B1 | 2 | SF3B1:chr2:198266834:T/C | Coding | Missense | SNV | c.2098A>G | p.K700E | 986 (96%) | 24 (2%) | 1.3 | 2.1 |
| **CHIP14** | CD34+ BM | TET2 | 4 | TET2:chr4:106196283:A/C | Coding | Missense | SNV | c.4616A>C | p.Q1529P | 4033 (54%) | 199 (5%) | 2.5 | 8.2 |

[1] According to *the American College of Medical Genetics and Genomics-Association for Molecular Pathology* (ACMG-AMP) interpretation guidelines

[2] Nonsense-mediated decay (NMD)

**Supplementary Table S4. Patients cytogenic characteristics.**

| | Total (n=12) | Presence of CHIP mutation (n=6) | Absence of CHIP mutation (n=6) |
|---|---|---|---|
| ***t(4;14)*** | | | |
| *Yes* | 2 (17%) | 1 (17%) | 1 (17%) |
| *No* | 8 (66%) | 4 (66%) | 4 (66%) |
| *Not available* | 2 (17%) | 1 (17%) | 1 (17%) |
| | | | |
| ***t(11;14)*** | | | |
| *Yes* | 3 (25%) | 3 (50%) | 0 |
| *No* | 4 (33%) | 2 (33%) | 2 (33%) |
| *Not available* | 5 (42%) | 1 (17%) | 4 (67%) |
| | | | |
| ***t(14;16)*** | | | |
| *Yes* | 0 | 0 | 0 |
| *No* | 10 (83%) | 5 (83%) | 5 (83%) |
| *Not available* | 2 (17%) | 1 (17%) | 1 (17%) |
| | | | |
| ***t(14;20)*** | | | |
| *Yes* | 0 | 0 | 0 |
| *No* | 7 (58%) | 5 (83%) | 2 (33%) |
| *Not available* | 5 (42%) | 1 (17%) | 4 (67%) |
| | | | |
| ***Del17p*** | | | |
| *Yes* | 0 | 0 | 0 |
| *No* | 10 (83%) | 5 (83%) | 5 (83%) |
| *Not available* | 2 (17%) | 1 (17%) | 1 (17%) |
| | | | |
| ***Amp1q*** | | | |
| *Yes* | 7 (58%) | 3 (50%) | 4 (66%) |
| *No* | 3 (25%) | 2 (33%) | 1 (17%) |
| *Not available* | 2 (17%) | 1 (17%) | 1 (17%) |
| | | | |
| ***De1p*** | | | |
| *Yes* | 0 | 0 | 0 |
| *No* | 9 (75%) | 5 (83%) | 4 (67%) |
| *Not available* | 3 (25%) | 1 (17%) | 2 (33%) |
| | | | |

Patients' cytogenetic characteristics were assessed using the standard technique of Fluorescence in situ Hybridization (FISH).