**S1**

**Immagine che contiene diagramma, Piano, Disegno tecnico, Rettangolo

Descrizione generata automaticamente**

**S1 Legend:** Age distribution in CHIP mutated HCC patients. While DNMT3A cases show a trend for a higher median age in the subset of hepatocellular carcinoma patients this is not observed in TET2 variants. Differences were assessed by Wilcoxon test.

Attached below is the patient level data for Clonal Hematopoiesis of Indeterminate Potential (CHIP) attribution.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Tumor\_Sample\_Barcode | Hugo\_Symbol | Chromosome | Genome\_Change | VAF | Variant\_Classification | Protein\_Change | coverage |
| 581052 | TP53 | 17 | g.chr17:7577547C>T | 0.02734375 | Missense\_Mutation | p.G245D | 262 |
| C18 | DNMT3A | 2 | g.chr2:25469939G>A | 0.0277777777777778 | Missense\_Mutation | p.A368V | 113 |
| C19 | DNMT3A | 2 | g.chr2:25469945C>T | 0.0222222222222222 | Missense\_Mutation | p.R366H | 135 |
| C24 | SRSF2 | 17 | g.chr17:74732959G>T | 0.0393700787401575 | Missense\_Mutation | p.P95H | 133 |
| C27 | DNMT3A | 2 | g.chr2:25457243G>A | 0.1 | Missense\_Mutation | p.R882C | 43 |
| C30 | ASXL1 | 20 | g.chr20:31023395G>A | 0.0273972602739726 | Nonsense\_Mutation | p.W960\* | 191 |
| C31 | ASXL1 | 20 | g.chr20:31022727G>T | 0.0245901639344262 | Nonsense\_Mutation | p.G738\* | 128 |
| C31 | DNMT3A | 2 | g.chr2:25463509C>A | 0.0975609756097561 | Splice\_Site | p.E725\* | 49 |
| C31 | DNMT3A | 2 | g.chr2:25467029C>A | 0.0408163265306122 | Nonsense\_Mutation | p.E616\* | 98 |
| C34 | TP53 | 17 | g.chr17:7577121G>A | 25 | Missense\_Mutation | p.R273C | 120 |
| C38 | TET2 | 4 | g.chr4:106197519G>A | 0.0677966101694915 | Missense\_Mutation | p.R1951Q | 81 |
| C39 | TP53 | 17 | g.chr17:7578212G>A | 0.0854700854700855 | Nonsense\_Mutation | p.R213\* | 137 |
| C44 | DNMT3A | 2 | g.chr2:25457243G>A | 0.386363636363636 | Missense\_Mutation | p.R882C | 65 |
| C45 | ASXL1 | 20 | g.chr20:31022441\_31022442insG | 0.133720930232558 | Frame\_Shift\_Ins | p.G646fs | 172 |
| C45 | ASXL1 | 20 | g.chr20:31022441\_31022442insG | 0.123711340206186 | Frame\_Shift\_Ins | p.G646fs | 209 |
| C7 | DNMT3A | 2 | g.chr2:25469570C>A | 0.0634920634920635 | Nonsense\_Mutation | p.E400\* | 118 |
| CIR01 | TET2 | 4 | g.chr4:106180823C>T | 0.020979020979021 | Missense\_Mutation | p.S1305F | 145 |
| CIR01 | TP53 | 17 | g.chr17:7577547C>T | 0.0228571428571429 | Missense\_Mutation | p.G245D | 175 |
| CIR015 | DNMT3A | 2 | g.chr2:25468133G>A | 0.0408163265306122 | Nonsense\_Mutation | p.Q292\* | 151 |
| D1 | DNMT3A | 2 | g.chr2:25467428C>T | 0.0476190476190476 | Missense\_Mutation | p.G550R | 142 |
| D12 | TP53 | 17 | g.chr17:7577547C>T | 0.0540540540540541 | Missense\_Mutation | p.G245D | 75 |
| D21 | SRSF2 | 17 | g.chr17:74732960G>T | 0.0454545454545455 | Missense\_Mutation | p.P95T | 68 |
| D30 | SF3B1 | 2 | g.chr2:198266834T>C | 0.0461538461538462 | Missense\_Mutation | p.K700E | 66 |
| D30 | TET2 | 4 | g.chr4:106197599G>A | 0.0317460317460317 | Missense\_Mutation | p.V1978M | 126 |
| D33 | PPM1D | 17 | g.chr17:58740439delT | 0.0465116279069767 | Frame\_Shift\_Del | p.L450fs | 136 |
| D33 | PPM1D | 17 | g.chr17:58740439delT | 0.049645390070922 | Frame\_Shift\_Del | p.L450fs | 146 |
| D45 | TET2 | 4 | g.chr4:106183004A>G | 0.0681818181818182 | Splice\_Site | p.Q1348R | 44 |
| D45 | TET2 | 4 | g.chr4:106183004A>G | 0.0769230769230769 | Splice\_Site | p.Q1369R | 39 |
| FE1 | TET2 | 4 | g.chr4:106164880G>A | 0.0483870967741935 | Missense\_Mutation | p.E1271K | 68 |
| H104 | DNMT3A | 2 | g.chr2:25464520C>A | 0.0317460317460317 | Missense\_Mutation | p.V665L | 126 |
| H104 | TET2 | 4 | g.chr4:106156072C>T | 0.0298507462686567 | Nonsense\_Mutation | p.Q325\* | 137 |
| H106 | SF3B1 | 2 | g.chr2:198267360T>C | 0.0508474576271186 | Missense\_Mutation | p.K666R | 59 |
| H106 | SF3B1 | 2 | g.chr2:198267360T>C | 0.0625 | Missense\_Mutation | p.K666R | 49 |
| H108 | TET2 | 4 | g.chr4:106193771G>T | 0.210526315789474 | Missense\_Mutation | p.E1411D | 32 |
| H110 | BCORL1 | X | g.chrX:129149404G>T | 0.0666666666666667 | Nonsense\_Mutation | p.E886\* | 120 |
| H110 | TET2 | 4 | g.chr4:106157626G>T | 0.0754716981132075 | Nonsense\_Mutation | p.E843\* | 112 |
| H111 | DNMT3A | 2 | g.chr2:25467083G>A | 0.0769230769230769 | Nonsense\_Mutation | p.R598\* | 135 |
| H111 | DNMT3A | 2 | g.chr2:25467083G>A | 0.0789473684210526 | Nonsense\_Mutation | p.R375\* | 114 |
| H111 | DNMT3A | 2 | g.chr2:25469996G>T | 0.0266666666666667 | Nonsense\_Mutation | p.S126\* | 154 |
| H111 | DNMT3A | 2 | g.chr2:25469996G>T | 0.0263157894736842 | Nonsense\_Mutation | p.S349\* | 178 |
| H116 | DNMT3A | 2 | g.chr2:25466779C>A | 0.0297029702970297 | Nonsense\_Mutation | p.G642\* | 101 |
| H118 | ASXL1 | 20 | g.chr20:31022441\_31022442insG | 0.109243697478992 | Frame\_Shift\_Ins | p.G646fs | 119 |
| H118 | SRSF2 | 17 | g.chr17:74732959G>C | 0.0465116279069767 | Missense\_Mutation | p.P95R | 145 |
| H118 | SRSF2 | 17 | g.chr17:74732959G>C | 0.0476190476190476 | Missense\_Mutation | p.P95R | 174 |
| H118 | U2AF1 | 21 | g.chr21:44514777T>G | 0.171779141104294 | Missense\_Mutation | p.Q157P | 171 |
| H118 | U2AF1 | 21 | g.chr21:44514777T>G | 0.172413793103448 | Missense\_Mutation | p.Q157P | 217 |
| H120 | TET2 | 4 | g.chr4:106162586G>T | 0.155555555555556 | Splice\_Site | p.R1188M | 45 |
| H120 | TET2 | 4 | g.chr4:106162586G>T | 0.296296296296296 | Splice\_Site | p.R1167M | 51 |
| H128 | DNMT3A | 2 | g.chr2:25459834C>A | 0.0689655172413793 | Nonsense\_Mutation | p.E817\* | 87 |
| H130 | TP53 | 17 | g.chr17:7577547C>T | 0.0566037735849057 | Missense\_Mutation | p.G245D | 53 |
| H133 | TP53 | 17 | g.chr17:7577547C>T | 0.15 | Missense\_Mutation | p.G245D | 38 |
| H136 | TET2 | 4 | g.chr4:106162586G>T | 0.0892857142857143 | Splice\_Site | p.R1167M | 115 |
| H16 | PPM1D | 17 | g.chr17:58740749C>T | 0.0337078651685393 | Nonsense\_Mutation | p.R552\* | 180 |
| H16 | PPM1D | 17 | g.chr17:58740749C>T | 0.0350877192982456 | Nonsense\_Mutation | p.R552\* | 228 |
| H16 | TET2 | 4 | g.chr4:106193748C>T | 0.0952380952380952 | Nonsense\_Mutation | p.R1404\* | 45 |
| H19 | DNMT3A | 2 | g.chr2:25470498G>T | 0.0466666666666667 | Missense\_Mutation | p.R326S | 150 |
| H23 | U2AF1 | 21 | g.chr21:44514777T>C | 0.453488372093023 | Missense\_Mutation | p.Q157R | 162 |
| H26 | TP53 | 17 | g.chr17:7577139G>A | 0.0930232558139535 | Missense\_Mutation | p.R267W | 43 |
| H35 | CBL | 11 | g.chr11:119149250C>T | 0.179487179487179 | Nonsense\_Mutation | p.R420\* | 40 |
| H35 | CBL | 11 | g.chr11:119149250C>T | 0.235294117647059 | Nonsense\_Mutation | p.R420\* | 43 |
| H35 | DNMT3A | 2 | g.chr2:25463271G>A | 0.105263157894737 | Missense\_Mutation | p.A741V | 39 |
| H35 | SF3B1 | 2 | g.chr2:198267360T>G | 0.191489361702128 | Missense\_Mutation | p.K666T | 49 |
| H35 | SF3B1 | 2 | g.chr2:198267360T>G | 0.272727272727273 | Missense\_Mutation | p.K666T | 59 |
| H42 | TP53 | 17 | g.chr17:7577094G>A | 0.0405405405405405 | Missense\_Mutation | p.R282W | 74 |
| H44 | TET2 | 4 | g.chr4:106157684\_106157685insG | 0.0598290598290598 | Frame\_Shift\_Ins | p.H863fs | 239 |
| H56 | GNB1 | 1 | g.chr1:1747229T>C | 0.0789473684210526 | Missense\_Mutation | p.K57E | 76 |
| H56 | GNB1 | 1 | g.chr1:1747229T>C | 0.0769230769230769 | Missense\_Mutation | p.K57E | 65 |
| H60 | ASXL1 | 20 | g.chr20:31024748G>A | 0.0870786516853933 | Nonsense\_Mutation | p.W1411\* | 357 |
| H60 | ASXL1 | 20 | g.chr20:31024748G>A | 0.0899280575539568 | Nonsense\_Mutation | p.W1411\* | 284 |
| H61 | DNMT3A | 2 | g.chr2:25464487G>A | 0.0307692307692308 | Missense\_Mutation | p.R676W | 132 |
| H62 | TET2 | 4 | g.chr4:106157431C>T | 0.0285714285714286 | Nonsense\_Mutation | p.Q778\* | 164 |
| H66 | TET2 | 4 | g.chr4:106197333C>T | 0.0508474576271186 | Missense\_Mutation | p.P1889L | 139 |
| H67 | DNMT3A | 2 | g.chr2:25463562C>T | 0.0517241379310345 | Missense\_Mutation | p.G707D | 59 |
| H68 | DNMT3A | 2 | g.chr2:25466779C>A | 0.0576923076923077 | Nonsense\_Mutation | p.G642\* | 116 |
| H70 | TET2 | 4 | g.chr4:106164880G>A | 0.0297029702970297 | Missense\_Mutation | p.E1271K | 108 |
| H73 | JAK2 | 9 | g.chr9:5073770G>T | 0.864864864864865 | Missense\_Mutation | p.V617F | 37 |
| H74 | TET2 | 4 | g.chr4:106164772C>T | 0.109090909090909 | Missense\_Mutation | p.R1214W | 110 |
| H74 | TET2 | 4 | g.chr4:106164772C>T | 125 | Missense\_Mutation | p.R1235W | 98 |
| H80 | TET2 | 4 | g.chr4:106196246C>T | 0.0740740740740741 | Nonsense\_Mutation | p.Q1527\* | 54 |
| H80 | TP53 | 17 | g.chr17:7577547C>T | 0.0655737704918033 | Missense\_Mutation | p.G245D | 61 |
| H83 | DNMT3A | 2 | g.chr2:25463184G>T | 0.0588235294117647 | Nonsense\_Mutation | p.S770\* | 69 |
| H83 | PPM1D | 17 | g.chr17:58740713G>T | 0.046875 | Nonsense\_Mutation | p.E540\* | 139 |
| H83 | SF3B1 | 2 | g.chr2:198266834T>C | 0.216216216216216 | Missense\_Mutation | p.K700E | 39 |
| H83 | SF3B1 | 2 | g.chr2:198266834T>C | 0.195121951219512 | Missense\_Mutation | p.K700E | 41 |
| H86 | ASXL1 | 20 | g.chr20:31022403\_31022425delCACCACTGCCATAGAGAGGCGGC | 0.0480769230769231 | Frame\_Shift\_Del | p.E635fs | 106 |
| H86 | ASXL1 | 20 | g.chr20:31022403\_31022425delCACCACTGCCATAGAGAGGCGGC | 0.0546875 | Frame\_Shift\_Del | p.E635fs | 128 |
| H89 | DNMT3A | 2 | g.chr2:25469053C>A | 0.0232558139534884 | Nonsense\_Mutation | p.E469\* | 180 |
| H90 | DNMT3A | 2 | g.chr2:25470498G>A | 0.275167785234899 | Missense\_Mutation | p.R326C | 154 |
| H92 | DNMT3A | 2 | g.chr2:25457236G>A | 0.0555555555555556 | Missense\_Mutation | p.A884V | 73 |
| H94 | TP53 | 17 | g.chr17:7577139G>A | 0.0512820512820513 | Missense\_Mutation | p.R267W | 78 |
| H96 | DNMT3A | 2 | g.chr2:25459806T>C | 0.0547945205479452 | Splice\_Site | p.K603R | 73 |
| H96 | DNMT3A | 2 | g.chr2:25464544C>T | 0.0476190476190476 | Missense\_Mutation | p.V657M | 130 |
| HA3 | PPM1D | 17 | g.chr17:58740809C>T | 0.106382978723404 | Nonsense\_Mutation | p.R572\* | 282 |
| HA3 | PPM1D | 17 | g.chr17:58740809C>T | 0.102678571428571 | Nonsense\_Mutation | p.R572\* | 224 |
| HCC07 | SF3B1 | 2 | g.chr2:198267359C>A | 0.0404411764705882 | Missense\_Mutation | p.K666N | 272 |
| HCC07 | SF3B1 | 2 | g.chr2:198267359C>A | 0.0296296296296296 | Missense\_Mutation | p.K666N | 270 |
| HCC08 | TET2 | 4 | g.chr4:106180783\_106180784insG | 0.0421052631578947 | Frame\_Shift\_Ins | p.C1271fs | 192 |
| HV1 | DNMT3A | 2 | g.chr2:25470497C>T | 0.446153846153846 | Missense\_Mutation | p.R326H | 260 |
| HV3 | ASXL1 | 20 | g.chr20:31022441\_31022442insG | 0.0979020979020979 | Frame\_Shift\_Ins | p.G646fs | 154 |
| HV3 | ASXL1 | 20 | g.chr20:31022441\_31022442insG | 0.0928571428571429 | Frame\_Shift\_Ins | p.G646fs | 154 |
| HV3 | TP53 | 17 | g.chr17:7577547C>T | 0.0461538461538462 | Missense\_Mutation | p.G245D | 69 |
| HV3 | TP53 | 17 | g.chr17:7577547C>T | 0.0454545454545455 | Missense\_Mutation | p.G245D | 69 |
| HV6 | ASXL1 | 20 | g.chr20:31022403\_31022425delCACCACTGCCATAGAGAGGCGGC | 0.1375 | Frame\_Shift\_Del | p.E635fs | 175 |
| HV6 | ASXL1 | 20 | g.chr20:31022403\_31022425delCACCACTGCCATAGAGAGGCGGC | 0.1375 | Frame\_Shift\_Del | p.E635fs | 175 |
| OC05 | BCORL1 | X | g.chrX:129159032\_129159034delAGA | 0.0461538461538462 | In\_Frame\_Del | p.E1253del | 65 |
| OC22 | TP53 | 17 | g.chr17:7577547C>T | 0.0236686390532544 | Missense\_Mutation | p.G245D | 172 |
| OC32 | ASXL1 | 20 | g.chr20:31024624\_31024626delAGA | 0.436363636363636 | In\_Frame\_Del | p.K1371del | 56 |
| OC54 | SRSF2 | 17 | g.chr17:74732959G>A | 0.0487804878048781 | Missense\_Mutation | p.P95L | 85 |
| OC60 | DNMT3A | 2 | g.chr2:25463598A>T | 0.0704225352112676 | Splice\_Site | p.I472N | 144 |
| OC60 | TP53 | 17 | g.chr17:7578212G>A | 0.0276497695852535 | Nonsense\_Mutation | p.R213\* | 217 |
| OH021 | TP53 | 17 | g.chr17:7577539G>A | 0.0485436893203883 | Missense\_Mutation | p.R248W | 207 |
| OH028 | ASXL1 | 20 | g.chr20:31021250C>T | 0.105960264900662 | Nonsense\_Mutation | p.R417\* | 151 |
| OH03 | SF3B1 | 2 | g.chr2:198267359C>G | 0.150602409638554 | Missense\_Mutation | p.K666N | 166 |
| OH04 | GNB1 | 1 | g.chr1:1747227C>A | 0.047244094488189 | Missense\_Mutation | p.K57N | 130 |
| OH05 | ASXL1 | 20 | g.chr20:31021535C>T | 0.0268456375838926 | Nonsense\_Mutation | p.Q512\* | 150 |
| OH05 | ASXL1 | 20 | g.chr20:31021535C>T | 0.0273972602739726 | Nonsense\_Mutation | p.Q512\* | 147 |
| OH10 | DNMT3A | 2 | g.chr2:25470594C>A | 0.0833333333333333 | Nonsense\_Mutation | p.E71\* | 97 |
| OH10 | DNMT3A | 2 | g.chr2:25470594C>A | 0.0842105263157895 | Nonsense\_Mutation | p.E294\* | 96 |
| OH11 | TET2 | 4 | g.chr4:106156747C>T | 0.037037037037037 | Nonsense\_Mutation | p.R550\* | 135 |
| VAL1-205 | DNMT3A | 2 | g.chr2:25464450C>T | 0.0254237288135593 | Missense\_Mutation | p.R688H | 118 |
| VAL1-224 | PPM1D | 17 | g.chr17:58740836C>T | 0.0238095238095238 | Nonsense\_Mutation | p.R581\* | 128 |
| VAL1-235 | SRSF2 | 17 | g.chr17:74732959G>A | 0.146739130434783 | Missense\_Mutation | p.P95L | 186 |
| VAL | PPM1D | 17 | g.chr17:58740836C>T | 0.0238095238095238 | Nonsense\_Mutation | p.R581\* | 128 |
| VAL | SRSF2 | 17 | g.chr17:74732959G>A | 0.151351351351351 | Missense\_Mutation | p.P95L | 186 |
| VAL1-004 | DNMT3A | 2 | g.chr2:25457176G>A | 0.024390243902439 | Missense\_Mutation | p.P904L | 126 |
| VAL1-005 | DNMT3A | 2 | g.chr2:25463184G>A | 0.0459770114942529 | Missense\_Mutation | p.S770L | 262 |
| VAL1-014 | DNMT3A | 2 | g.chr2:25463229A>G | 0.0397350993377483 | Missense\_Mutation | p.F755S | 157 |
| VAL1-016 | DNMT3A | 2 | g.chr2:25464537C>T | 0.036036036036036 | Missense\_Mutation | p.R659H | 111 |
| VAL1-017 | DNMT3A | 2 | g.chr2:25467032G>A | 0.12 | Nonsense\_Mutation | p.Q615\* | 53 |
| VAL1-017 | DNMT3A | 2 | g.chr2:25467032G>A | 0.113207547169811 | Nonsense\_Mutation | p.Q392\* | 53 |
| VAL1-020 | DNMT3A | 2 | g.chr2:25467416delA | 0.131818181818182 | Frame\_Shift\_Del | p.C331fs | 220 |
| VAL1-020 | DNMT3A | 2 | g.chr2:25467416delA | 0.13302752293578 | Frame\_Shift\_Del | p.C554fs | 218 |
| VAL1-030 | TET2 | 4 | g.chr4:106180840T>C | 0.114285714285714 | Missense\_Mutation | p.S1290P | 107 |
| VAL1-030 | TET2 | 4 | g.chr4:106180840T>C | 0.114285714285714 | Missense\_Mutation | p.S1311P | 107 |
| VAL1-038 | DNMT3A | 2 | g.chr2:25463229A>G | 0.0437158469945355 | Missense\_Mutation | p.F755S | 191 |
| VAL1-044 | DNMT3A | 2 | g.chr2:25461998C>T | 0.0441176470588235 | Splice\_Site |  | 204 |
| VAL1-051 | DNMT3A | 2 | g.chr2:25470560C>T | 0.147826086956522 | Nonsense\_Mutation | p.W305\* | 115 |
| VAL1-051 | DNMT3A | 2 | g.chr2:25470560C>T | 0.130434782608696 | Nonsense\_Mutation | p.W82\* | 115 |
| VAL1-054 | SF3B1 | 2 | g.chr2:198266834T>C | 0.153225806451613 | Missense\_Mutation | p.K700E | 130 |
| VAL1-054 | SF3B1 | 2 | g.chr2:198266834T>C | 152 | Missense\_Mutation | p.K700E | 130 |
| VAL1-058 | DNMT3A | 2 | g.chr2:25459804C>T | 0.036697247706422 | Splice\_Site |  | 113 |
| VAL1-058 | DNMT3A | 2 | g.chr2:25463589C>T | 0.0414507772020725 | Nonsense\_Mutation | p.W475\* | 199 |
| VAL1-058 | DNMT3A | 2 | g.chr2:25463589C>T | 0.0421052631578947 | Nonsense\_Mutation | p.W698\* | 196 |
| VAL1-059 | GNB1 | 1 | g.chr1:1737942A>T | 0.0333333333333333 | Missense\_Mutation | p.I80N | 151 |
| VAL1-059 | GNB1 | 1 | g.chr1:1737942A>T | 0.0333333333333333 | Missense\_Mutation | p.I80N | 151 |
| VAL1-067 | DNMT3A | 2 | g.chr2:25463236\_25463238delAGA | 0.286343612334802 | In\_Frame\_Del | p.F752del | 238 |
| VAL1-074 | TET2 | 4 | g.chr4:106157329C>T | 0.133928571428571 | Nonsense\_Mutation | p.Q744\* | 113 |
| VAL1-074 | TET2 | 4 | g.chr4:106193748C>T | 0.072289156626506 | Nonsense\_Mutation | p.R1404\* | 166 |
| VAL1-075 | DNMT3A | 2 | g.chr2:25458594C>T | 0.0423728813559322 | Nonsense\_Mutation | p.W637\* | 121 |
| VAL1-075 | DNMT3A | 2 | g.chr2:25458594C>T | 0.0423728813559322 | Nonsense\_Mutation | p.W860\* | 120 |
| VAL1-085 | DNMT3A | 2 | g.chr2:25463308G>A | 0.0247933884297521 | Missense\_Mutation | p.R729W | 122 |
| VAL1-086 | DNMT3A | 2 | g.chr2:25463182G>A | 0.0324074074074074 | Nonsense\_Mutation | p.R548\* | 222 |
| VAL1-086 | DNMT3A | 2 | g.chr2:25463182G>A | 0.0324074074074074 | Nonsense\_Mutation | p.R771\* | 221 |
| VAL1-097 | SF3B1 | 2 | g.chr2:198267359C>G | 0.03125 | Missense\_Mutation | p.K666N | 244 |
| VAL1-097 | SF3B1 | 2 | g.chr2:198267359C>G | 0.0300429184549356 | Missense\_Mutation | p.K666N | 243 |
| VAL1-101 | U2AF1 | 21 | g.chr21:44524456G>A | 0.160714285714286 | Missense\_Mutation | p.S34F | 66 |
| VAL1-101 | U2AF1 | 21 | g.chr21:44524456G>A | 0.160714285714286 | Missense\_Mutation | p.S34F | 64 |
| VAL1-108 | DNMT3A | 2 | g.chr2:25469029C>T | 0.111111111111111 | Splice\_Site | p.E254K | 135 |
| VAL1-118 | DNMT3A | 2 | g.chr2:25469525G>A | 0.0810810810810811 | Nonsense\_Mutation | p.Q415\* | 75 |
| VAL1-118 | DNMT3A | 2 | g.chr2:25469525G>A | 0.0810810810810811 | Nonsense\_Mutation | p.Q192\* | 75 |
| VAL1-121 | JAK2 | 9 | g.chr9:5073770G>T | 0.333333333333333 | Missense\_Mutation | p.V617F | 176 |
| VAL1-127 | JAK2 | 9 | g.chr9:5073770G>T | 0.0753424657534247 | Missense\_Mutation | p.V617F | 146 |
| VAL1-135 | DNMT3A | 2 | g.chr2:25462068A>G | 0.100244498777506 | Missense\_Mutation | p.I780T | 413 |
| VAL1-148 | BCOR | X | g.chrX:39922000T>G | 0.1 | Splice\_Site | p.K1357T | 51 |
| VAL1-152 | DNMT3A | 2 | g.chr2:25457242C>T | 0.24 | Missense\_Mutation | p.R882H | 50 |
| VAL1-152 | DNMT3A | 2 | g.chr2:25457242C>T | 0.24 | Missense\_Mutation | p.R659H | 50 |
| VAL1-160 | SRSF2 | 17 | g.chr17:74732959G>A | 0.0596026490066225 | Missense\_Mutation | p.P95L | 155 |
| VAL1-160 | SRSF2 | 17 | g.chr17:74732959G>A | 0.0588235294117647 | Missense\_Mutation | p.P95L | 155 |
| VAL1-161 | DNMT3A | 2 | g.chr2:25463308G>A | 0.0416666666666667 | Missense\_Mutation | p.R729W | 170 |
| VAL1-163 | DNMT3A | 2 | g.chr2:25463182G>A | 0.0378787878787879 | Nonsense\_Mutation | p.R548\* | 265 |
| VAL1-163 | DNMT3A | 2 | g.chr2:25463182G>A | 0.0380228136882129 | Nonsense\_Mutation | p.R771\* | 264 |
| VAL1-172 | DNMT3A | 2 | g.chr2:25470498G>A | 0.266666666666667 | Missense\_Mutation | p.R326C | 90 |
| VAL1-173 | DNMT3A | 2 | g.chr2:25458696T>C | 0.0205479452054795 | Splice\_Site |  | 147 |
| VAL1-179 | CBL | 11 | g.chr11:119170203A>G | 0.45679012345679 | Splice\_Site |  | 162 |
| VAL1-187 | DNMT3A | 2 | g.chr2:25457243G>A | 0.2 | Missense\_Mutation | p.R882C | 55 |
| VAL1\_275 | DNMT3A | 2 | g.chr2:25469028C>T | 0.314285714285714 | Splice\_Site |  | 140 |
| VAL1\_280 | PPM1D | 17 | g.chr17:58740529C>A | 0.0434782608695652 | Nonsense\_Mutation | p.C478\* | 141 |
| VAL1-342 | SF3B1 | 2 | g.chr2:198266834T>C | 0.0535714285714286 | Missense\_Mutation | p.K700E | 113 |
| VAL1-372 | DNMT3A | 2 | g.chr2:25471019G>A | 0.064327485380117 | Nonsense\_Mutation | p.Q25\* | 174 |