**Supplementary Table 1 TruSight Myeloid (Illumina) NGS Gene Panel.** (A) Genes in the TruSight Myeloid (Illumina) NGS Gene Panel (B) Exon coverage for hotspot genes

**(A)**

|  |  |
| --- | --- |
| **Complete coding region coverage (15/54)**  | **Hotspot coverage** **(39/54)** |
| *BCOR* | *ABL1* |
| *BCORL1* | *ASXL1* |
| *CDKN2A* | *ATRX* |
| *CEBPA* | *BRAF* |
| *CUX1* | *CALR* |
| *DNMT3A* | *CBL* |
| *ETV6/TEL* | *CBLB* |
| *EZH2* | *CBLC* |
| *IKZF1* | *CSF3R* |
| *KDM6A* | *FBXW7* |
| *PHF6* | *FLT3* |
| *RAD21* | *GATA1* |
| *RUNX1* | *GATA2* |
| *STAG2* | *GNAS* |
| *ZRSR2* | *HRAS* |
|  | *IDH1* |
|  | *IDH2* |
|  | *JAK2* |
|  | *JAK3* |
|  | *KIT* |
|  | *KMT2A* |
|  | *KRAS* |
|  | *MPL* |
|  | *MYD88* |
|  | *NOTCH1* |
|  | *NPM1* |
|  | *NRAS* |
|  | *PDGFRA* |
|  | *PTEN* |
|  | *PTPN11* |
|  | *SETBP1* |
|  | *SF3B1* |
|  | *SMC1A* |
|  | *SMC3* |
|  | *SRSF2* |
|  | *TET2* |
|  | *TP53* |
|  | *U2AF1* |
|  | *WT1* |

**(B)**

|  |  |
| --- | --- |
| **Hotspot coverage** **(39/54)** | **Exon Coverage** |
| *ABL1* | 4-6 |
| *ASXL1* | 12 |
| *ATRX* | 8-10 and 17-31 |
| *BRAF* | 15 |
| *CALR* | 9 |
| *CBL* | 8, 9 |
| *CBLB* | 9, 10 |
| *CBLC* | 9, 10 |
| *CSF3R* | 14-17 |
| *FBXW7* | 9-11 |
| *FLT3* | 14, 15, 20 |
| *GATA1* | 2 |
| *GATA2* | 2-6 |
| *GNAS* | 8, 9 |
| *HRAS* | 2, 3 |
| *IDH1* | 4 |
| *IDH2* | 4 |
| *JAK2* | 12, 14 |
| *JAK3* | 13 |
| *KIT* | 2, 8-11, 13, 17 |
| *KMT2A* | 2, 3 |
| *KRAS* | 5–8 |
| *MPL* | 10 |
| *MYD88* | 3-5 |
| *NOTCH1* | 26-28, 34 |
| *NPM1* | 12 |
| *NRAS* | 2, 3 |
| *PDGFRA* | 12, 14, 18 |
| *PTEN* | 5, 7 |
| *PTPN11* | 3, 13 |
| *SETBP1* | 4 (partial) |
| *SF3B1* | 13-16 |
| *SMC1A* | 2, 11, 16, 17 |
| *SMC3* | 10, 13, 19, 23, 25, 28 |
| *SRSF2* | 1 |
| *TET2* | 3-11 |
| *TP53* | 2-11 |
| *U2AF1* | 2, 6 |
| *WT1* | 7, 9 |

**Supplementary Table 2 - Annotation of variants**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| ABL1 | 156 | MF | NM\_005157.4 | c.740A>G | p.Lys247Arg | Missense | 31.8 | 3271 | VUS |
| ASXL1 | 92 | ET | NM\_015338.5 | c.3965C>G | p.Pro1322Arg | Missense | 50.56 | 4966 | VUS |
| ASXL1 | 94 | PV | NM\_015338.5 | c.1926dupA | p.Gly643fs\*15 | Frameshift | 40.7 | 5007 | HMR |
| ASXL1 | 117 | ET | NM\_015338.5 | c.3889G>A | p.Val1297Ile | Missense | 49.33 | 10251 | VUS |
| ASXL1 | 27 | POST-MPN AML | NM\_015338.5 | c.2975\_2979delinsGGA | p.Leu992fs\*5 | Frameshift | 44.24 | 7151 | HMR |
| ASXL1 | 108 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 30 | 3054 | HMR |
| ASXL1 | 74 | MF | NM\_015338.5 | c.2957A>G | p.Asn986Ser | Missense | 48.82 | 9392 | VUS |
| ASXL1 | 43 | MF | NM\_015338.5 | c.1771\_1772insA | p.Tyr591\* | Nonsense | 26.2 | 5802 | HMR |
| ASXL1 | 44 | POST-MPN AML | NM\_015338.5 | c.2562\_2565delTGAT | p.Asp855fs\*11 | Frameshift | 48.71 | 8888 | HMR |
| ASXL1 | 96 | MF | NM\_015338.5 | c.3000\_3001insG | p.Thr1001fs\*4 | Frameshift | 43.25 | 6125 | HMR |
| ASXL1 | 71 | MF | NM\_015338.5 | c.2176A>T | p.Lys726\* | Nonsense | 50.45 | 5243 | HMR |
| ASXL1 | 128 | MF | NM\_015338.5 | c.2422delC | p.Pro808fs\*10 | Frameshift | 43.32 | 11357 | HMR |
| ASXL1 | 52 | MF | NM\_015338.5 | c.2110G>A | p.Gly704Arg | Missense | 45.62 | 5522 | VUS |
| ASXL1 | 37 | MF | NM\_015338.5 | c.2957A>G | p.Asn986Ser | Missense | 49.21 | 6968 | VUS |
| ASXL1 | 186 | Non-classical MPN | NM\_015338.5 | c.2077C>T | p.Arg693\* | Nonsense | 41.58 | 3434 | HMR |
| ASXL1 | 113 | MF | NM\_015338.5 | c.1900\_1922del | p.Glu635fs\*15 | Frameshift | 25.67 | 1075 | HMR |
| ASXL1 | 97 | MF | NM\_015338.5 | c.2167\_2192dup | p.Gln733\* | Nonsense | 14 | 5662 | HMR |
| ASXL1 | 125 | MF | NM\_015338.5 | c.1989dupC | p.Ser664fs\*4 | Frameshift | 34.8 | 4233 | HMR |
| ASXL1 | 49 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 34.8 | 4553 | HMR |
| ASXL1 | 101 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 31 | 3914 | HMR |
| ASXL1 | 100 | MF | NM\_015338.5 | c.2077C>T | p.Arg693\* | Nonsense | 34.94 | 3148 | HMR |
| ASXL1 | 85 | MF | NM\_015338.5 | c.1900\_1922delAGAGAGGCGGCCACCACTGCCAT | p.Glu635fs\*15 | Frameshift | 37.90 | 1166 | HMR |
| ASXL1 | 82 | POST-MPN AML | NM\_015338.5 | c.2582delC | p.Ala861fs\*6 | Frameshift | 26.90 | 12626 | HMR |
| ASXL1 | 20 | MF | NM\_015338.5 | c.1934dupG  | p.Gly646fs\*12 | Frameshift | 32.5 | 6039 | HMR |
| ASXL1 | 78 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 24.7 | 7325 | HMR |
| ASXL1 | 123 | MF | NM\_015338.5 | c.2477delG | p.Gly826fs\*12 | Frameshift | 40.8 | 11201 | HMR |
| ASXL1 | 116 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 13.2 | 7292 | HMR |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| ASXL1 | 116 | MF | NM\_015338.5 | c.2129delG | p.Gly710fs\*15 | Frameshift | 17.3 | 5388 | HMR |
| ASXL1 | 38 | MF | NM\_015338.5 | c.3503G>C | p.Ser1168Thr | Missense | 50 | 5193 | VUS |
| ASXL1 | 88 | PV | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 27.5 | 3961 | HMR |
| ASXL1 | 130 | MF | NM\_015338.5 | c.1900\_1922delAGAGAGGCGGCCACCACTGCCAT | p.Glu635fs\*15 | Frameshift | 8.4 | 1273 | HMR |
| ASXL1 | 81 | MF | NM\_015338.5 | c.2142delC | p.Arg715fs\*10 | Frameshift | 41.3 | 3828 | HMR |
| ASXL1 | 33 | MF | NM\_015338.5 | c.2597T>A | p.Leu866\* | Nonsense | 44.8 | 6135 | HMR |
| ASXL1 | 18 | Non-classical MPN | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 34.7 | 4703 | HMR |
| ASXL1 | 51 | MF | NM\_015338.5 | c.1900\_1922delAGAGAGGCGGCCACCACTGCCAT | p.Glu635fs\*15 | Frameshift | 34.4 | 1332 | HMR |
| ASXL1 | 46 | Non-classical MPN | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 36.9 | 4838 | HMR |
| ASXL1 | 106 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 33.5 | 5359 | HMR |
| ASXL1 | 65 | MF | NM\_015338.5 | c.2385delC | p.Trp796fs\*22 | Frameshift | 45.6 | 5165 | HMR |
| ASXL1 | 9 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 36.6 | 4217 | HMR |
| ASXL1 | 8 | MF | NM\_015338.5 | c.1774C>T | p.Gln592\* | Nonsense | 43.2 | 5078 | HMR |
| ASXL1 | 14 | MF | NM\_015338.5 | c.2423delC | p.Pro808fs\*10 | Frameshift | 39.3 | 7215 | HMR |
| ASXL1 | 143 | MF | NM\_015338.5 | c.2172delG | p.Arg725fs\*19 | Frameshift | 43.2 | 3781 | HMR |
| ASXL1 | 12 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 34.3 | 6066 | HMR |
| ASXL1 | 17 | POST-MPN AML | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 37.2 | 6762 | HMR |
| ASXL1 | 22 | ET | NM\_015338.5 | c.2197C>T | p.Gln733\* | Nonsense | 13.3 | 2085 | HMR |
| ASXL1 | 21 | MF | NM\_015338.5 | c.2332C>T | p.Gln778\* | Nonsense | 6.3 | 3329 | HMR |
| ASXL1 | 150 | POST-MPN AML | NM\_015338.5 | c.2494G>A | p.Asp832Asn | Missense | 49 | 10407 | VUS |
| ASXL1 | 147 | PV | NM\_015338.5 | c.4189G>A | p.Gly1397Ser | Missense | 51.3 | 5062 | VUS |
| ASXL1 | 159 | Non-classical MPN | NM\_015338.5 | c.2921dupA | p.Tyr974\* | Nonsense | 26.5 | 6247 | HMR |
| ASXL1 | 160 | MF | NM\_015338.5 | c.2541delC | p.Thr848fs\*19 | Frameshift | 14.9 | 8641 | HMR |
| ASXL1 | 160 | MF | NM\_015338.5 | c.1773C>G | p.Tyr591\* | Nonsense | 15.2 | 6579 | HMR |
| ASXL1 | 163 | PV | NM\_015338.5 | c.3910C>G | p.Leu1304Val | Missense | 46.5 | 7153 | VUS |
| ASXL1 | 153 | POST-MPN AML | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 40.2 | 5026 | HMR |
| ASXL1 | 154 | MF | NM\_015338.5 | c.3935C>T | p.Ala1312Val | Missense | 42.6 | 8000 | VUS |
| ASXL1 | 154 | MF | NM\_015338.5 | c.2077C>T | p.Arg693\* | Nonsense | 14.5 | 4015 | HMR |
| ASXL1 | 158 | Non-classical MPN | NM\_015338.5 | c.3202C>T | p.Arg1068\* | Nonsense | 33.7 | 10051 | HMR |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| ASXL1 | 166 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 35.6 | 6671 | HMR |
| ASXL1 | 187 | MF | NM\_015338.5 | c.2277\_2280dupCCAG | p.Ala761fs\*14 | Frameshift | 8.6 | 4625 | HMR |
| ASXL1 | 171 | MF | NM\_015338.5 | c.1900\_1922delAGAGAGGCGGCCACCACTGCCAT | p.Glu635fs\*15 | Frameshift | 31.3 | 1288 | HMR |
| ASXL1 | 171 | MF | NM\_015338.5 | c.2191delC | p.Leu731fs\*13 | Frameshift | 6.2 | 4482 | HMR |
| ASXL1 | 162 | MF | NM\_015338.5 | c.1934dupG | p.Gly646fs\*12 | Frameshift | 31.3 | 6355 | HMR |
| ASXL1 | 174 | MF | NM\_015338.5 | c.1772dupA | p.Tyr591\* | Nonsense | 39.7 | 6781 | HMR |
| ASXL1 | 179 | MF | NM\_015338.5 | c.2077C>T | p.Arg693\* | Nonsense | 23.8 | 3343 | HMR |
| ATRX | 128 | MF | NM\_000489.3 | c.3913A>C | p.Lys1305Gln | Missense | 99.38 | 4178 | VUS |
| ATRX | 140 | PV | NM\_000489.3 | c.5579A>G | p.Asn1860Ser | Missense | 99.64 | 2223 | VUS |
| ATRX | 20 | MF | NM\_000489.3 | c.5579A>G | p.Asn1860Ser | Missense | 99.7 | 3477 | VUS |
| ATRX | 135 | MF | NM\_000489.3 | c.5579A>G | p.Asn1860Ser | Missense | 49.1 | 3437 | VUS |
| BCOR | 120 | MF | NM\_001123385.1 | c.4582C>T | p.Gln1528\* | Nonsense | 25.23 | 646 | Oncogenic |
| BCOR | 45 | PV | NM\_001123385.1 | c.3502G>A | p.Asp1168Asn | Missense | 50.09 | 5796 | VUS |
| BCOR | 89 | MF | NM\_001123385.1 | c.4936dupC | p.Leu1646fs\*6 | Frameshift | 19.3 | 3871 | Oncogenic |
| BCOR | 103 | PV | NM\_001123385.1 | c.626C>T | p.Ser209Leu | Missense | 50.5 | 7486 | VUS |
| BCOR | 16 | MF | NM\_001123385.1 | c.5182G>T | p.Glu1728\* | Nonsense | 25.5 | 4120 | VUS |
| BCOR | 24 | MF | NM\_001123385.1 | c.626C>T | p.Ser209Leu | Missense | 99.2 | 3236 | VUS |
| BCOR | 144 | MF | NM\_001123385.1 | c.2035G>A | p.Val679Ile | Missense | 0.502 | 13750 | VUS |
| BCORL1 | 113 | MF | NM\_021946.4 | c.388G>A | p.Ala130Thr | Missense | 48.84 | 6276 | VUS |
| BCORL1 | 49 | MF | NM\_021946.4 | c.3332C>T | p.Thr1111Met | Missense | 46.25 | 3812 | VUS |
| BCORL1 | 63 | MF | NM\_021946.4 | c.3356T>G | p.Met1119Arg | Missense | 51.3 | 5323 | VUS |
| BCORL1 | 174 | MF | NM\_021946.4 | c.3332C>T | p.Thr1111Met | Missense | 98.6 | 1386 | VUS |
| CALR | 92 | ET | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 17 | 1144 | Driver |
| CALR | 117 | ET | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 7.96 (NG), 20% (Script) | 1248 | Driver |
| CALR | 107 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 20.90 | 1248 | Driver |
| CALR | 120 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 39 | 1798 | Driver |
| CALR | 40 | ET | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 66 | 2029 | Driver |
| CALR | 66 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 57 | 1886 | Driver |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| CALR | 109 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 51 | 5760 | Driver |
| CALR | 30 | ET | NM\_004343.3 | c.1154\_1155insTTGTC | p.Lys385fs\*47 | Frameshift | 39.24 | 1496 | Driver |
| CALR | 119 | MF | NM\_004343.3 | c.1103\_1136delAGGAGGAGGAAGAAGACAAGAAACGCAAAGAGGA | p.Lys368fs\*51 | Frameshift | 41 | 2565 | Driver |
| CALR | 58 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 44 | 3700 | Driver |
| CALR | 47 | ET | NM\_004343.3 | c.1103\_1136del | p.Lys368fs\*51 | Frameshift | 42 | 1761 | Driver |
| CALR | 100 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 59.2 | 776 | Driver |
| CALR | 68 | MF | NM\_004343.3 | c.1154\_1155insTTGTC | p.Lys385fs\*47 | Frameshift | 34.70 | 1545 | Driver |
| CALR | 77 | MF | NM\_004343.3 | c.1120\_1139delinsG | p.Lys374fs\*50 | Frameshift | 35 | 1277 | Driver |
| CALR | 104 | ET | NM\_004343.3 | c.1154\_1155insTTGTC | p.Lys385fs\*47 | Frameshift | 29.5 | 1618 | Driver |
| CALR | 123 | MF | NM\_004343.3 | c.1154\_1155insTTGTC | p.Lys385fs\*47 | Frameshift | 60.7 | 2243 | Driver |
| CALR | 50 | MF | NM\_004343.3 | c.1154\_1155insTTGTC | p.Lys385fs\*47 | Frameshift | 78.6 | 1250 | Driver |
| CALR | 81 | MF | NM\_004343.3 | c.1154\_1155insTTGTC | p.Lys385fs\*47 | Frameshift | 39.6 | 1855 | Driver |
| CALR | 62 | MF | NM\_004343.3 | c.1125\_1146delACGCAAAGAGGAGGAGGAGGCA | p.Lys377fs\*46 | Frameshift | 40.6 | 1184 | Driver |
| CALR | 5 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 58.8 | 1088 | Driver |
| CALR | 14 | MF | NM\_004343.3 | c.1102\_1154delinsG | p.Lys368fs\*51 | Frameshift | 55.5 | 1754 | Driver |
| CALR | 22 | ET | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 29.9 | 1194 | Driver |
| CALR | 146 | POST-MPN AML | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 56.6 | 3007 | Driver |
| CALR | 151 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 57 | 1685 | Driver |
| CALR | 165 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 57.2 | 1931 | Driver |
| CALR | 167 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 56.9 | 2772 | Driver |
| CALR | 169 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 53.5 | 1824 | Driver |
| CALR | 187 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 50.2 | 2644 | Driver |
| CALR | 162 | MF | NM\_004343.3 | c.1154\_1155insTTGTC | p.Lys385fs\*47 | Frameshift | 41.1 | 1868 | Driver |
| CALR | 174 | MF | NM\_004343.3 | c.1113\_1143delAGAAGACAAGAAACGCAAAGAGGAGGAGGAG | p.Glu372fs\*48 | Frameshift | 46.3 | 2173 | Driver |
| CALR | 179 | MF | NM\_004343.3 | c.1099\_1150del | p.Leu367fs\*46 | Frameshift | 52.7 | 1409 | Driver |
| CALR | 180 | MF | NM\_004343.3 | c.1154delinsTTTGTC | p.Lys385fs\*47 | Frameshift | 37.4 | 1673 | Driver |
| CBL | 27 | POST-MPN AML | NM\_005188.3 | c.1111T>C | p.Tyr371His | Missense | 90.58 | 5498 | Oncogenic |
| CBL | 96 | MF | NM\_005188.3 | c.1380\_1382dupTGA | p.Asp460dup | Duplication | 39.1 | 3509 | VUS |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| CBL | 110 | MF | NM\_005188.3 | c.1139T>C | p.Leu380Pro | Missense | 24.13 | 5690 | Oncogenic |
| CBL | 110 | MF | NM\_005188.3 | c.1127C>T | p.Ser376Phe | Missense | 9.42 | 5678 | Oncogenic |
| CBL | 83 | MF | NM\_005188.3 | c.1228-2A>G | p.? | Splice Site | 7.8 | 2799 | Oncogenic |
| CBL | 130 | MF | NM\_005188.3 | c.1380\_1382dupTGA | p.Asp460dup | Duplication | 6.9 | 3875 | VUS |
| CBL | 81 | MF | NM\_005188.3 | c.1169A>T | p.Asp390Val | Missense | 90.8 | 4667 | Oncogenic |
| CBL | 9 | MF | NM\_005188.3 | c.1199T>G | p.Met400Arg | Missense | 38.1 | 3372 | Oncogenic |
| CBL | 162 | MF | NM\_005188.3 | c.1255T>C | p.Cys419Arg | Missense | 43.2 | 4095 | Oncogenic |
| CDKN2A | 55 | MF | NM\_001195132.1 | c.496C>T | p.His166Tyr | Missense | 51.35 | 6713 | VUS |
| CEPBA | 93 | MF | NM\_004364.3 | c.564\_566dupGCC | p.Pro188dup | Duplication | 34.36 | 195 | VUS |
| CSF3R | 29 | Non-classical MPN | NM\_156039.3 | c.2326C>T | p.Gln776\* | Nonsense | 60.3 | 234 | Oncogenic |
| CSF3R | 29 | Non-classical MPN | NM\_156039.3 | c.1853C>T | p.Thr618Ile | Missense | 41.8 | 1339 | Oncogenic |
| CSF3R | 114 | MF | NM\_156039.3 | c.2503G>A | p.Glu835Lys | Missense | 50.20 | 3499 | VUS |
| CSF3R | 84 | MF | NM\_156039.3 | c.2323G>A | p.Asp775Asn | Missense | 50 | 444 | VUS |
| CSF3R | 169 | MF | NM\_156039.3 | c.2503G>A | p.Glu835Lys | Missense | 49.4 | 2846 | VUS |
| CUX1 | 93 | MF | NM\_001202543.1 | c.3161C>T | p.Ser1054Leu | Missense | 50.75 | 1269 | VUS |
| CUX1 | 117 | ET | NM\_001202543.1 | c.295G>A | p.Val99Ile | Missense | 55.18 | 859 | VUS |
| CUX1 | 28 | Non-classical MPN | NM\_001202543.1 | c.3641G>A | p.Arg1214Gln | Missense | 50.84 | 3566 | VUS |
| CUX1 | 97 | MF | NM\_001202543.1 | c.870delC | p.Ile291\* | Nonsense | 83.66 | 3096 | Oncogenic |
| CUX1 | 125 | MF | NM\_001202543.1 | c.295G>A | p.Val99Ile | Missense | 45.51 | 3562 | VUS |
| CUX1 | 101 | MF | NM\_001202543.1 | c.1438A>G | p.Ser480Gly | Missense | 51.6 | 1062 | VUS |
| CUX1 | 77 | MF | NM\_001202543.1 | c.726G>T | p.Met242Ile | Missense | 51.8 | 10852 | VUS |
| CUX1 | 130 | MF | NM\_001202543.1 | c.295G>A | p.Val99Ile | Missense | 48.5 | 163 | VUS |
| CUX1 | 84 | MF | NM\_001202543.1 | c.3814C>T | p.Arg1272\* | Nonsense | 12.7 | 3178 | Oncogenic |
| CUX1 | 84 | MF | NM\_001202543.1 | c.3047G>A | p.Trp1016\* | Nonsense | 15.1 | 1534 | Oncogenic |
| CUX1 | 9 | MF | NM\_001202543.1 | c.634delC | p.Gln212fs\*14 | Frameshift | 74.4 | 4205 | Oncogenic |
| CUX1 | 12 | MF | NM\_001202543.1 | c.3330\_3337dup | p.Thr1114fs\*20 | Frameshift | 19 | 4441 | Oncogenic |
| CUX1 | 11 | PV | NM\_001202543.1 | c.262G>A | p.Val88Ile | Nonsense | 52.1 | 1231 | VUS |
| CUX1 | 23 | MF | NM\_001202543.1 |  c.4103G>A | p.Arg1368Gln | Nonsense | 64.4 | 873 | VUS |
| CUX1 | 21 | MF | NM\_001202543.1 | c.4136G>A | p.Arg1379Gln | Nonsense | 49.3 | 920 | VUS |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| DNMT3A | 91 | MF | NM\_022552.4 | c.1405G>T | p.Glu469\* | Nonsense | 34.73 | 4475 | Oncogenic |
| DNMT3A | 36 | MF | NM\_022552.4 | c.1547delA | p.Asn516fs\*135 | Frameshift | 20.03 | 2127 | Oncogenic |
| DNMT3A | 96 | MF | NM\_022552.4 | c.2606G>A | p.Gly869Asp | Missense | 43.92 | 2639 | Oncogenic |
| DNMT3A | 128 | MF | NM\_022552.4 | c.2270delA | p.Asn757fs\*22 | Frameshift | 45.44 | 5926 | Oncogenic |
| DNMT3A | 37 | MF | NM\_022552.4 | c.2359G>A | p.Ala787Thr | Missense | 81.95 | 4820 | Oncogenic |
| DNMT3A | 58 | MF | NM\_022552.4 | c.1510delC | p.Leu504fs\*147 | Frameshift | 43.84 | 3700 | Oncogenic |
| DNMT3A | 89 | MF | NM\_022552.4 | c.1792C>T | p.Arg598\* | Nonsense | 42.1 | 3978 | Oncogenic |
| DNMT3A | 3 | PV | NM\_022552.4 | c.1934C>T | p.Thr645Ile | Missense | 42.7 | 3729 | Oncogenic |
| DNMT3A | 104 | ET | NM\_022552.4 | c.977G>A | p.Arg326His | Missense | 10.1 | 2239 | Oncogenic |
| DNMT3A | 13 | ET | NM\_022552.4 | c.2645G>A | p.Arg882His | Missense | 20.6 | 2268 | Oncogenic |
| DNMT3A | 144 | MF | NM\_022552.4 | c.1122+1G>A | p.? | Splice Site | 5.2 | 1690 | Oncogenic |
| DNMT3A | 150 | POST-MPN AML | NM\_022552.4 | c.2645G>A | p.Arg882His | Missense | 61 | 3780 | Oncogenic |
| DNMT3A | 160 | MF | NM\_022552.4 | c.972delC | p.Thr325fs\*20 | Frameshift | 37.8 | 3736 | Oncogenic |
| DNMT3A | 163 | PV | NM\_022552.4 | c.891G>C | p.Trp297Cys | Missense | 46.4 | 4840 | Oncogenic |
| ETV6 | 93 | MF | NM\_001987.4 | c.496G>A | p.Val166Met | Missense | 48.04 | 2344 | VUS |
| ETV6 | 27 | POST-MPN AML | NM\_001987.4 | c.778C>T | p.Gln260\* | Nonsense | 29.19 | 5495 | Oncogenic |
| ETV6 | 108 | MF | NM\_001987.4 | c.580delC | p.Pro194fs\*15 | Frameshift | 42.64 | 2221 | Oncogenic |
| ETV6 | 20 | MF | NM\_001987.4 | c.219\_221dupTGA | p.Ala73\_Glu74insAsp | Insertion | 39.5 | 6599 | VUS |
| ETV6 | 4 | MF | NM\_001987.4 | c.419\_420dupTA | p.His141fs\*69 | Frameshift | 19.6 | 4685 | Oncogenic |
| ETV6 | 84 | MF | NM\_001987.4 | c.1130C>T | p.Ala377Val | Missense | 35.5 | 5817 | Oncogenic |
| ETV6 | 179 | MF | NM\_001987.4 | c.496G>A | p.Val166Met | Missense | 47.6 | 2789 | VUS |
| EZH2 | 124 | MF | NM\_004456.4 | c.2029G>A | p.Asp677Asn | Missense | 46.81 | 2399 | HMR |
| EZH2 | 128 | MF | NM\_004456.4 | c.2007C>G | p.Ser669Arg | Missense | 41.98 | 3852 | HMR |
| EZH2 | 97 | MF | NM\_004456.4 | c.1850delA | p.Lys617fs\*58 | Frameshift | 80.35 | 4508 | HMR |
| EZH2 | 101 | MF | NM\_004456.4 | c.126\_128delinsAA | p.Phe42fs\*15 | Frameshift | 40 | 1120 | HMR |
| EZH2 | 130 | MF | NM\_004456.4 | c.187C>T | p.Arg63\* | Nonsense | 13.7 | 2323 | HMR |
| EZH2 | 130 | MF | NM\_004456.4 | c.1655G>A | p.Cys552Tyr | Missense | 9.1 | 7009 | HMR |
| EZH2 | 81 | MF | NM\_004456.4 | c.1021delG | p.Ala341fs\*8 | Frameshift | 89.9 | 4569 | HMR |
| EZH2 | 46 | Non-classical MPN | NM\_004456.4 | c.2048C>T | p.Thr683Ile | Missense | 21.9 | 7226 | HMR |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| EZH2 | 46 | Non-classical MPN | NM\_004456.4 | c.1988A>G | p.Tyr663Cys | Missense | 14.8 | 2978 | HMR |
| EZH2 | 10 | MF | NM\_004456.4 | c.2198A>C | p.Tyr733Ser | Missense | 22.5 | 1246 | HMR |
| EZH2 | 17 | POST-MPN AML | NM\_004456.4 | c.457T>G | p.Tyr153Asp | Missense | 47.3 | 6182 | VUS |
| EZH2 | 22 | ET | NM\_004456.4 | c.1616G>A | p.Cys539Tyr | Missense | 19.7 | 4609 | HMR |
| EZH2 | 187 | MF | NM\_004456.4 | c.1973G>C | p.Arg658Thr | Missense | 12.4 | 3299 | HMR |
| EZH2 | 171 | MF | NM\_004456.4 | c.1990G>C | p.Asp664His | Missense | 43.2 | 2994 | HMR |
| EZH2 | 162 | MF | NM\_004456.4 | c.2084C>T | p.Ser695Leu | Missense | 18.7 | 5485 | HMR |
| EZH2 | 188 | Non-classical MPN | NM\_004456.4 | c.866G>A | p.Cys289Tyr | Missense | 36 | 6571 | VUS |
| EZH2 | 188 | Non-classical MPN | NM\_004456.4 | c.1851G>T | p.Lys617Asn | Missense | 37.6 | 3580 | HMR |
| FBXW7 | 120 | MF | NM\_033632.3 | c.1394G>T | p.Arg465Leu | Missense | 15.12 | 4100 | VUS |
| FLT3 | 46 | Non-classical MPN | NM\_004119.2 | c.2525A>G | p.Tyr842Cys | Missense | 50.3 | 9196 | Oncogenic |
| GATA2 | 18 | Non-classical MPN | NM\_032638.4 | c.1168\_1170delAAG | p.Lys390del | Deletion | 38.4 | 1283 | VUS |
| GATA2 | 18 | Non-classical MPN | NM\_032638.4 | c.673delA | p.Ser225fs\*9 | Frameshift | 43.6 | 3079 | Oncogenic |
| GATA2 | 13 | ET | NM\_032638.4 | c.121C>G | p.Pro41Ala | Missense | 51.8 | 2828 | VUS |
| GATA2 | 160 | MF | NM\_032638.4 | c.1161\_1172delCATGAAGAAGGA | p.Met388\_Glu391del | Deletion | 14.5 | 1645 | VUS |
| GATA2 | 174 | MF | NM\_032638.4 | c.208G>T | p.Val70Phe | Missense | 46.6 | 2376 | VUS |
| GNAS | 18 | Non-classical MPN | NM\_000516.4 | c.601C>T | p.Arg201Cys | Missense | 42.7 | 3821 | Oncogenic |
| IDH1 | 34 | MF | NM\_005896.2 | c.395G>A | p.Arg132His | Missense | 42.97 | 4296 | HMR |
| IDH1 | 82 | POST-MPN AML | NM\_005896.2 | c.394C>T | p.Arg132Cys | Missense | 12.60 | 5386 | HMR |
| IDH1 | 21 | MF | NM\_005896.2 | c.395G>A | p.Arg132His | Missense | 16.9 | 3000 | HMR |
| IDH2 | 115 | MF | NM\_002168.2 |  c.419G>A | p.Arg140Gln | Missense | 3.5 | 4193 | HMR |
| IDH2 | 111 | POST-MPN AML | NM\_002168.2 | c.514A>T | p.Arg172Trp | Missense | 15.04 | 4017 | HMR |
| IDH2 | 111 | POST-MPN AML | NM\_002168.2 | c.508A>G | p.Ile170Val | Missense | 15.02 | 4108 | VUS |
| IDH2 | 126 | MF | NM\_002168.2 | c.419G>A | p.Arg140Gln | Missense | 47.94 | 4143 | HMR |
| IDH2 | 166 | MF | NM\_002168.2 | c.419G>A | p.Arg140Gln | Missense | 9.8 | 4464 | HMR |
| IKZF1 | 125 | MF | NM\_006060.5 | c.1121T>C | p.Leu374Pro | Missense | 30.81 | 714 | VUS |
| IKZF1 | 150 | POST-MPN AML | NM\_006060.5 | c.660delA | p.Glu221fs\*36 | Frameshift | 42.2 | 1660 | VUS |
| JAK2 | 90 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 57.27 | 3576 | Driver |
| JAK2 | 93 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 82.82 | 4354 | Driver |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| JAK2 | 94 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 94.24 | 4237 | Driver |
| JAK2 | 95 | Non-classical MPN | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 46.44 | 4003 | Driver |
| JAK2 | 35 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 34.33 | 5636 | Driver |
| JAK2 | 124 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 86.26 | 4368 | Driver |
| JAK2 | 36 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 18.37 | 5067 | Driver |
| JAK2 | 39 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 86.97 | 4621 | Driver |
| JAK2 | 115 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 65.23 | 4892 | Driver |
| JAK2 | 67 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 35.63 | 4541 | Driver |
| JAK2 | 73 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 51.12 | 4030 | Driver |
| JAK2 | 41 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 20.7 | 3798 | Driver |
| JAK2 | 74 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 88.4 | 4181 | Driver |
| JAK2 | 131 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 14 | 3285 | Driver |
| JAK2 | 42 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 55.91 | 4718 | Driver |
| JAK2 | 43 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 32.7 | 4015 | Driver |
| JAK2 | 134 | PV | NM\_004972.3 | c.1622\_1627delGAAATG | p.Arg541\_Glu543delinsLys | Deletion | 21.28 | 893 | Driver |
| JAK2 | 96 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 62.01 | 6254 | Driver |
| JAK2 | 71 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 43.3 | 4039 | Driver |
| JAK2 | 45 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 60.19 | 3720 | Driver |
| JAK2 | 128 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 90.95 | 3866 | Driver |
| JAK2 | 110 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 20.31 | 7520 | Driver |
| JAK2 | 111 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 5.91 | 5042 | Driver |
| JAK2 | 112 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 67.10 | 4866 | Driver |
| JAK2 | 113 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 1.50 | NA\* | Driver |
| JAK2 | 102 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 93.66 | 4965 | Driver |
| JAK2 | 31 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 14.06 | 5504 | Driver |
| JAK2 | 97 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 22 | 6618 | Driver |
| JAK2 | 125 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 84.89 | 5275 | Driver |
| JAK2 | 126 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 67.48 | 5280 | Driver |
| JAK2 | 60 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 92.45 | 5229 | Driver |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| JAK2 | 55 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 48.94 | 2037 | Driver |
| JAK2 | 133 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 48.44 | 4362 | Driver |
| JAK2 | 49 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 39.98 | 5017 | Driver |
| JAK2 | 56 | PV | NM\_004972.3 | c.1620\_1629delinsGAG | p.Ile540fs\*4 | Frameshift | 24.51 | 620 | Driver |
| JAK2 | 140 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 47.57 | 5884 | Driver |
| JAK2 | 114 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 48.10 | 6948 | Driver |
| JAK2 | 85 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 61.80 | 6474 | Driver |
| JAK2 | 69 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 32.70 | 5133 | Driver |
| JAK2 | 82 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 16.60 | 6728 | Driver |
| JAK2 | 87 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 87.00 | 7297 | Driver |
| JAK2 | 86 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 89.00 | 5872 | Driver |
| JAK2 | 20 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 42.5 | 6400 | Driver |
| JAK2 | 78 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 6.7 | 8332 | Driver |
| JAK2 | 79 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 91.5 | 6606 | Driver |
| JAK2 | 141 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 44 | 7624 | Driver |
| JAK2 | 72 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 2.9 | NA\* | Driver |
| JAK2 | 2 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 16.3 | 4731 | Driver |
| JAK2 | 64 | PV | NM\_004972.3 | c.1622\_1627delGAAATG | p.Arg541\_Glu543delinsLys | Deletion | 25.3 | 1768 | Driver |
| JAK2 | 80 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 63 | 10935 | Driver |
| JAK2 | 89 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 37.4 | 6511 | Driver |
| JAK2 | 4 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 54.1 | 1529 | Driver |
| JAK2 | 3 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 44.3 | 5533 | Driver |
| JAK2 | 105 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 28.3 | 4338 | Driver |
| JAK2 | 127 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 92 | 5573 | Driver |
| JAK2 | 75 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 60 | 3871 | Driver |
| JAK2 | 116 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 76.6 | 5945 | Driver |
| JAK2 | 76 | MF | NM\_004972.3 |  c.1849G>T | p.Val617Phe | Missense | 35 | 3640 | Driver |
| JAK2 | 38 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 18.8 | 4100 | Driver |
| JAK2 | 83 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 86.8 | 2825 | Driver |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| JAK2 | 88 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 64.3 | 4781 | Driver |
| JAK2 | 84 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 55.3 | 1603 | Driver |
| JAK2 | 121 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 76.6 | 6752 | Driver |
| JAK2 | 122 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 24 | 5659 | Driver |
| JAK2 | 48 | Non-classical MPN | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 87 | 5957 | Driver |
| JAK2 | 118 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 92.3 | 3867 | Driver |
| JAK2 | 51 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 35.2 | 6879 | Driver |
| JAK2 | 46 | Non-classical MPN | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 47.8 | 5006 | Driver |
| JAK2 | 106 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 41.1 | 5043 | Driver |
| JAK2 | 59 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 44.8 | 4995 | Driver |
| JAK2 | 54 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 67 | 4250 | Driver |
| JAK2 | 65 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 41.6 | 4314 | Driver |
| JAK2 | 103 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 74.4 | 2003 | Driver |
| JAK2 | 63 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 46 | 2765 | Driver |
| JAK2 | 70 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 10.4 | 3318 | Driver |
| JAK2 | 6 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 46.8 | 3058 | Driver |
| JAK2 | 10 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 92.2 | 2863 | Driver |
| JAK2 | 9 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 21.9 | 4037 | Driver |
| JAK2 | 7 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 71.9 | 3192 | Driver |
| JAK2 | 8 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 91.4 | 4047 | Driver |
| JAK2 | 15 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 64.4 | 5665 | Driver |
| JAK2 | 143 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 27.8 | 5038 | Driver |
| JAK2 | 12 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 9.2 | 3717 | Driver |
| JAK2 | 11 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 3 | 4588 | Driver |
| JAK2 | 13 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 6.1 | 4125 | Driver |
| JAK2 | 16 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 13.4 | 4783 | Driver |
| JAK2 | 17 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 50.9 | 5971 | Driver |
| JAK2 | 24 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 46.5 | 5850 | Driver |
| JAK2 | 23 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 2.6 | 4403 | Driver |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| JAK2 | 21 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 89.8 | 4184 | Driver |
| JAK2 | 144 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 1.9 | 5310 | Driver |
| JAK2 | 145 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 76.2 | 7681 | Driver |
| JAK2 | 149 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 92 | 6502 | Driver |
| JAK2 | 150 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 90.7 | 5336 | Driver |
| JAK2 | 147 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 31.1 | 2201 | Driver |
| JAK2 | 148 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 7 | 3080 | Driver |
| JAK2 | 161 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 94.5 | 5033 | Driver |
| JAK2 | 163 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 46.1 | 6179 | Driver |
| JAK2 | 164 | ET | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 2.9 | 6249 | Driver |
| JAK2 | 152 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 19.3 | 4218 | Driver |
| JAK2 | 153 | POST-MPN AML | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 96.3 | 5882 | Driver |
| JAK2 | 154 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 38.6 | 6377 | Driver |
| JAK2 | 156 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 26.7 | 5928 | Driver |
| JAK2 | 158 | Non-classical MPN | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 29.8 | 6938 | Driver |
| JAK2 | 166 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 89.9 | 5306 | Driver |
| JAK2 | 168 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 93.9 | 6492 | Driver |
| JAK2 | 170 | PV | NM\_004972.3 | c.1614\_1616delinsATT | p.His538\_Lys539delinsGlnLeu | Deletion-Insertion | 13.1 | 1978 | Driver |
| JAK2 | 171 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 84.1 | 5243 | Driver |
| JAK2 | 172 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 89.7 | 4681 | Driver |
| JAK2 | 173 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 92 | 5297 | Driver |
| JAK2 | 176 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 71.9 | 6782 | Driver |
| JAK2 | 177 | Non-classical MPN | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 91.1 | 6360 | Driver |
| JAK2 | 184 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 54.9 | 2968 | Driver |
| JAK2 | 181 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 79.7 | 4169 | Driver |
| JAK2 | 183 | PV | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 51 | 3690 | Driver |
| JAK2 | 185 | MF | NM\_004972.3 | c.1849G>T | p.Val617Phe | Missense | 88.1 | 3607 | Driver |
| KDM6A | 171 | MF | NM\_021140.3 | c.1586C>A | p.Ala529Asp | Missense | 48.2 | 2909 | VUS |
| KIT | 164 | ET | NM\_000222.2 | c.200C>G | p.Thr67Ser | Missense | 48.9 | 7220 | VUS |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| KIT | 167 | MF | NM\_000222.2 | c.200C>G | p.Thr67Ser | Missense | 49.8 | 7214 | VUS |
| KMT2A | 66 | MF | NM\_001197104.1 | c.227G>C | p.Gly76Ala | Missense | 49.91 | 1150 | VUS |
| KMT2A | 110 | MF | NM\_001197104.1 | c.200\_202delCGG | p.Ala67del | Deletion | 78.52 | 391 | VUS |
| KRAS | 60 | MF | NM\_033360.2 | c.35G>T | p.Gly12Val | Missense | 20.16 | 4647 | Oncogenic |
| KRAS | 153 | POST-MPN AML | NM\_033360.2 | c.34G>C | p.Gly12Arg | Missense | 29.4 | 5542 | Oncogenic |
| MPL | 34 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 62.18 | 3638 | Driver |
| MPL | 52 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 15.83 | 3601 | Driver |
| MPL | 98 | MF | NM\_005373.2 | c.1543\_1544delinsGC | p.Trp515Ala | Missense | 90.75 | 1536 | Driver |
| MPL | 101 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 74.15 | 2561 | Driver |
| MPL | 61 | ET | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 30.70 | 3673 | Driver |
| MPL | 33 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 84 | 3683 | Driver |
| MPL | 9 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 8.8 | 2626 | Driver |
| MPL | 25 | ET | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 22.3 | 2948 | Driver |
| MPL | 135 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 75.2 | 3287 | Driver |
| MPL | 160 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 37.1 | 3621 | Driver |
| MPL | 155 | MF | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 50.1 | 3844 | Driver |
| MPL | 182 | ET | NM\_005373.2 | c.1544G>T | p.Trp515Leu | Missense | 18.2 | 3473 | Driver |
| NOTCH1 | 120 | MF | NM\_017617.3 | c.7541\_7542delCT | p.Pro2514fs\*4 | Frameshift | 5.22 | 977 | Oncogenic |
| NOTCH1 | 37 | MF | NM\_017617.3 | c.7606G>A | p.Val2536Ile | Missense | 53.87 | 865 | VUS |
| NOTCH1 | 113 | MF | NM\_017617.3 | c.6397C>T | p.Pro2133Ser | Missense | 51.02 | 3544 | VUS |
| NOTCH1 | 77 | MF | NM\_017617.3 | c.7157A>G | p.Gln2386Arg | Missense | 49.2 | 2312 | VUS |
| NOTCH1 | 104 | ET | NM\_017617.3 | c.7369C>G | p.Leu2457Val | Missense | 50.7 | 1791 | VUS |
| NOTCH1 | 23 | MF | NM\_017617.3 | c.7541\_7542delCT | p.Pro2514fs\*4 | Frameshift | 45.8 | 1166 | Oncogenic |
| NRAS | 111 | POST-MPN AML | NM\_002524.4 | c.35G>A | p.Gly12Asp | Missense | 18.52 | 8668 | Oncogenic |
| NRAS | 82 | POST-MPN AML | NM\_002524.4 | c.208C>T | p.Gln70\* | Nonsense | 10.90 | 613 | VUS |
| NRAS | 150 | POST-MPN AML | NM\_002524.4 | c.35G>A | p.Gly12Asp | Missense | 43 | 10575 | Oncogenic |
| NRAS | 153 | POST-MPN AML | NM\_002524.4 | c.38G>T | p.Gly13Val | Missense | 4.6 | 9114 | Oncogenic |
| PDGFRA | 71 | MF | NM\_006206.4 | c.2540C>T | p.Ser847Leu | Missense | 51.52 | 5736 | VUS |
| PHF6 | 94 | PV | NM\_032458.2 | c.55delT | p.Cys20fs\*13 | Frameshift | 44.62 | 2100 | Oncogenic |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| PHF6 | 82 | POST-MPN AML | NM\_032458.2 | c.821G>A | p.Arg274Gln | Missense | 29.20 | 2995 | Oncogenic |
| PHF6 | 20 | MF | NM\_032458.2 | c.133\_134dupTG | p.Met46fs\*36 | Frameshift | 79.5 | 1581 | Oncogenic |
| PHF6 | 121 | POST-MPN AML | NM\_032458.2 | c.862\_864dupGCT | p.Ala288dup | Duplication | 44.7 | 1074 | VUS |
| PHF6 | 118 | MF | NM\_032458.2 | c.271A>G | p.Thr91Ala | Missense | 25.3 | 2278 | Oncogenic |
| PHF6 | 51 | MF | NM\_032458.2 | c.643T>G | p.Cys215Gly | Missense | 68 | 2615 | VUS |
| PHF6 | 154 | MF | NM\_032458.2 | c.418+1G>T | p.? | Splice Site | 26.8 | 2154 | Oncogenic |
| PHF6 | 184 | MF | NM\_032458.2 | c.461C>G | p.Ser154\* | Nonsense | 84.3 | 2448 | Oncogenic |
| PTPN11 | 37 | MF | NM\_002834.3 | c.1508G>T | p.Gly503Val | Missense | 31.4 | 8517 | Oncogenic |
| PTPN11 | 100 | MF | NM\_002834.3 | c.1471C>T | p.Pro491Ser | Missense | 41.84 | 6807 | Oncogenic |
| PTPN11 | 82 | POST-MPN AML | NM\_002834.3 | c.1508G>A | p.Gly503Glu | Missense | 14.80 | 10012 | Oncogenic |
| RAD21 | 26 | POST-MPN AML | NM\_006265.2 | c.1576G>C | p.Glu526Gln | Missense | 23.4 | 7563 | VUS |
| RAD21 | 169 | MF | NM\_006265.2 | c.879A>C | p.Gln293His | Missense | 39.4 | 411 | VUS |
| RUNX1 | 29 | Non-classical MPN | NM\_001754.4 | c.331A>C | p.Thr111Pro | Missense | 41.53 | 2295 | VUS |
| RUNX1 | 34 | MF | NM\_001754.4 | c.664delT | p.Ser222fs\*15 | Frameshift | 14.88 | 1405 | Oncogenic |
| RUNX1 | 111 | POST-MPN AML | NM\_001754.4 | c.339dupC | p.Ile114fs\*24 | Frameshift | 18.9 | 2487 | Oncogenic |
| RUNX1 | 98 | MF | NM\_001754.4 | c.638A>G | p.Gln213Arg | Missense | 53.05 | 573 | VUS |
| RUNX1 | 82 | POST-MPN AML | NM\_001754.4 | c.1426\_1436del | p.Val476fs\*120 | Frameshift | 16.40 | 3115 | Oncogenic |
| RUNX1 | 78 | MF | NM\_001754.4 | c.540delC | p.Phe180fs\*31 | Frameshift | 20.8 | 8349 | Oncogenic |
| RUNX1 | 26 | POST-MPN AML | NM\_001754.4 | c.1005G>T | p.Gln335His | Missense | 50.7 | 6156 | VUS |
| RUNX1 | 84 | MF | NM\_001754.4 | c.511A>T | p.Lys171\* | Nonsense | 34 | 8046 | Oncogenic |
| RUNX1 | 143 | MF | NM\_001754.4 | c.611G>A | p.Arg204Gln | Missense | 43.4 | 5056 | Oncogenic |
| RUNX1 | 150 | POST-MPN AML | NM\_001754.4 | c.592G>T | p.Asp198Tyr | Missense | 42.7 | 4103 | Oncogenic |
| RUNX1 | 150 | POST-MPN AML | NM\_001754.4 | c.422C>A | p.Ser141\* | Nonsense | 36.5 | 7007 | Oncogenic |
| RUNX1 | 154 | MF | NM\_001754.4 | c.610C>T | p.Arg204\* | Nonsense | 10.2 | 5809 | Oncogenic |
| SETBP1 | 27 | POST-MPN AML | NM\_015559.2 | c.2602G>A | p.Asp868Asn | Missense | 45.71 | 4181 | Oncogenic |
| SETBP1 | 44 | POST-MPN AML | NM\_015559.2 | c.2605A>G | p.Ser869Gly | Missense | 47.44 | 4085 | Oncogenic |
| SETBP1 | 186 | Non-classical MPN | NM\_015559.2 | c.2608G>A | p.Gly870Ser | Missense | 45.38 | 4819 | Oncogenic |
| SETBP1 | 159 | Non-classical MPN | NM\_015559.2 | c.2606G>C | p.Ser869Thr | Missense | 34.1 | 3149 | Oncogenic |
| SF3B1 | 73 | MF | NM\_012433.2 | c.1998G>T | p.Lys666Asn | Missense | 26.23 | 4895 | Oncogenic |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| SF3B1 | 31 | ET | NM\_012433.2 | c.1997A>G | p.Lys666Arg | Missense | 22.71 | 4759 | Oncogenic |
| SF3B1 | 98 | MF | NM\_012433.2 | c.1996A>C | p.Lys666Gln | Missense | 41.98 | 2001 | Oncogenic |
| SF3B1 | 68 | MF | NM\_012433.2 | c.1998G>T | p.Lys666Asn | Missense | 31.40 | 3846 | Oncogenic |
| SF3B1 | 89 | MF | NM\_012433.2 | c.2098A>G | p.Lys700Glu | Missense | 42.3 | 9409 | Oncogenic |
| SF3B1 | 3 | PV | NM\_012433.2 | c.1998G>C | p.Lys666Asn | Missense | 41.3 | 4242 | Oncogenic |
| SF3B1 | 62 | MF | NM\_012433.2 | c.2098A>G | p.Lys700Glu | Missense | 30.8 | 6418 | Oncogenic |
| SF3B1 | 63 | MF | NM\_012433.2 | c.2098A>G | p.Lys700Glu | Missense | 41.1 | 6795 | Oncogenic |
| SF3B1 | 135 | MF | NM\_012433.2 | c.1837A>G | p.Met613Val | Missense | 47.5 | 3477 | Oncogenic |
| SF3B1 | 160 | MF | NM\_012433.2 | c.2107A>C | p.Thr703Pro | Missense | 36.6 | 8185 | Oncogenic |
| SF3B1 | 156 | MF | NM\_012433.2 | c.2098A>G | p.Lys700Glu | Missense | 26.1 | 8319 | Oncogenic |
| SF3B1 | 158 | Non-classical MPN | NM\_012433.2 | c.1997A>G | p.Lys666Arg | Missense | 3.3 | 5723 | Oncogenic |
| SF3B1 | 165 | MF | NM\_012433.2 | c.1998G>T | p.Lys666Asn | Missense | 36.4 | 2603 | Oncogenic |
| SF3B1 | 168 | MF | NM\_012433.2 | c.1998G>T | p.Lys666Asn | Missense | 45.5 | 4506 | Oncogenic |
| SMC3 | 68 | MF | NM\_005445.3 | c.2062G>C | p.Glu688Gln | Missense | 50.90 | 1113 | VUS |
| SRSF2 | 34 | MF | NM\_001195427.1 | c.284\_307delCCCCGGACTCACACCACAGCCGCC | p.Pro95\_Arg103del | Deletion | 46.61 | 1961 | HMR |
| SRSF2 | 27 | POST-MPN AML | NM\_001195427.1 | c.281\_282insAGCGCG | p.Arg94\_Pro95insAlaArg | Insertion | 51.87 | 2198 | HMR |
| SRSF2 | 115 | MF | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 39.98 | 1721 | HMR |
| SRSF2 | 52 | MF | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 8.82 | 1474 | HMR |
| SRSF2 | 111 | POST-MPN AML | NM\_001195427.1 | c.281\_283dupGCC | p.Arg94dup | Missense | 21.34 | 1059 | HMR |
| SRSF2 | 111 | POST-MPN AML | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 39.19 | 1059 | HMR |
| SRSF2 | 186 | Non-classical MPN | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 42.37 | 1258 | HMR |
| SRSF2 | 126 | MF | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 55.17 | 1189 | HMR |
| SRSF2 | 133 | POST-MPN AML | NM\_001195427.1 | c.283C>A | p.Pro95Thr | Missense | 48.03 | 914 | HMR |
| SRSF2 | 82 | POST-MPN AML | NM\_001195427.1 | c.284C>T | p.Pro95Leu | Missense | 28.00 | 1608 | HMR |
| SRSF2 | 20 | MF | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 40.9 | 2076 | HMR |
| SRSF2 | 4 | MF | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 50.9 | 1188 | HMR |
| SRSF2 | 83 | MF | NM\_001195427.1 | c.284C>A | p.Pro95His | Missense | 9.2 | 993 | HMR |
| SRSF2 | 18 | Non-classical MPN | NM\_001195427.1 | c.284C>T | p.Pro95Leu | Missense | 38.7 | 1312 | HMR |
| SRSF2 | 59 | MF | NM\_001195427.1 | c.284C>G | p.Pro95Arg | Missense | 48.9 | 1688 | HMR |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| SRSF2 | 24 | MF | NM\_001195427.1 | c.284C>G | p.Pro95Arg | Missense | 50.7 | 3236 | HMR |
| SRSF2 | 159 | Non-classical MPN | NM\_001195427.1 | c.284C>T | p.Pro95Leu | Missense | 31.7 | 1595 | HMR |
| SRSF2 | 155 | MF | NM\_001195427.1 | c.284C>G | p.Pro95Arg | Missense | 42 | 1636 | HMR |
| SRSF2 | 166 | MF | NM\_001195427.1 | c.284\_307delCCCCGGACTCACACCACAGCCGCC | p.Pro95\_Arg102del | Deletion | 52.9 | 1999 | HMR |
| STAG2 | 94 | PV | NM\_001042749.1 | c.1535-3\_1535-2insA | p.? | Splice Site | 18.6 | 3857 | Oncogenic |
| STAG2 | 111 | POST-MPN AML | NM\_001042749.1 | c.2438T>A | p.Leu813\* | Nonsense | 12.73 | 8977 | Oncogenic  |
| STAG2 | 101 | MF | NM\_001042749.1 | c.541G>A | p.Val181Met | Missense | 97.81 | 3287 | VUS |
| STAG2 | 20 | MF | NM\_001042749.1 | c.541G>A | p.Val181Met | Missense | 99.4 | 5510 | VUS |
| STAG2 | 121 | POST-MPN AML | NM\_001042749.1 | c.1535-3\_1535-2insA | p.? | Splice Site | 40.7 | 1735 | Oncogenic |
| STAG2 | 122 | POST-MPN AML | NM\_001042749.1 | c.484dupA | p.Thr162fs\*16 | Frameshift | 30.7 | 3248 | Oncogenic |
| TET2 | 95 | Non-classical MPN | NM\_001127208.2 | c.822delC | p.Asn275fs\*18 | Frameshift | 6.24 | 7342 | Oncogenic |
| TET2 | 95 | Non-classical MPN | NM\_001127208.2 | c.3413delA | p.Ile1139fs\*13 | Frameshift | 33.58 | 5387 | Oncogenic |
| TET2 | 39 | ET | NM\_001127208.2 | c.3116C>T | p.Ser1039Leu | Missense | 43.26 | 7656 | VUS |
| TET2 | 115 | MF | NM\_001127208.2 | c.5152G>T | p.Val1718Leu | Missense | 49.7 | 9018 | VUS |
| TET2 | 45 | PV | NM\_001127208.2 | c.3309delT | p.Phe1104fs\*2 | Frameshift | 24.23 | 4111 | Oncogenic |
| TET2 | 128 | MF | NM\_001127208.2 | c.1143delC | p.Phe381fs\*46 | Frameshift | 42.86 | 4951 | Oncogenic |
| TET2 | 52 | MF | NM\_001127208.2 | c.3656A>G | p.His1219Arg | Missense | 10.27 | 4020 | Oncogenic |
| TET2 | 52 | MF | NM\_001127208.2 | c.1333\_1334insT | p.Leu446fs\*8 | Frameshift | 7.46 | 7027 | Oncogenic |
| TET2 | 111 | POST-MPN AML | NM\_001127208.2 | c.1648C>T | p.Arg550\* | Nonsense | 84.88 | 2493 | Oncogenic |
| TET2 | 112 | MF | NM\_001127208.2 | c.5618T>C | p.Ile1873Thr | Missense | 12.93 | 2011 | Oncogenic  |
| TET2 | 97 | MF | NM\_001127208.2 | c.2231delA | p.Gln744fs\*7 | Frameshift | 43.67 | 14046 | Oncogenic |
| TET2 | 58 | MF | NM\_001127208.2 | c.5152G>T | p.Val1718Leu | Missense | 50.24 | 7393 | VUS |
| TET2 | 133 | POST-MPN AML | NM\_001127208.2 | c.5650A>G | p.Thr1884Ala | Missense | 68.96 | 5473 | Oncogenic |
| TET2 | 85 | MF | NM\_001127208.2 | c.218G>A | p.Arg73His | Missense | 49.40 | 1830 | VUS |
| TET2 | 82 | POST-MPN AML | NM\_001127208.2 | c.3604A>G | p.Arg1202Gly | Missense | 44.90 | 3027 | Oncogenic |
| TET2 | 82 | POST-MPN AML | NM\_001127208.2 | c.5606G>A | p.Gly1869Glu | Missense | 30.20 | 2565 | Oncogenic |
| TET2 | 79 | MF | NM\_001127208.2 | c.5890T>C | p.Tyr1964His | Missense | 47.8 | 4764 | VUS |
| TET2 | 80 | MF | NM\_001127208.2 | c.5104C>T | p.Gln1702\* | Nonsense | 43.4 | 7188 | Oncogenic |
| TET2 | 3 | PV | NM\_001127208.2 | c.3850T>G | p.Ser1284Ala | Missense | 46.4 | 6090 | Oncogenic |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| TET2 | 83 | MF | NM\_001127208.2 | c.4317dupA | p.Arg1440fs\*38 | Frameshift | 44.8 | 3363 | Oncogenic |
| TET2 | 83 | MF | NM\_001127208.2 | c.1292delT | p.Leu431\* | Nonsense | 47.2 | 4478 | Oncogenic |
| TET2 | 118 | MF | NM\_001127208.2 | c.4272dupT | p.Asp1425\* | Nonsense | 21.4 | 2982 | Oncogenic |
| TET2 | 51 | MF | NM\_001127208.2 | c.3409+1\_3409+2insT | p.? | Splice Site | 31.6 | 5307 | Oncogenic |
| TET2 | 46 | Non-classical MPN | NM\_001127208.2 | c.3229\_3230insT | p.His1077fs\*27 | Frameshift | 48.4 | 5420 | Oncogenic |
| TET2 | 46 | Non-classical MPN | NM\_001127208.2 | c.3895A>G | p.Lys1299Glu | Missense | 49.4 | 4708 | Oncogenic |
| TET2 | 59 | MF | NM\_001127208.2 | c.5890T>C | p.Tyr1964His | Missense | 49 | 4959 | VUS |
| TET2 | 54 | MF | NM\_001127208.2 | c.521delC | p.Pro174fs\*9 | Frameshift | 16.5 | 8013 | Oncogenic |
| TET2 | 54 | MF | NM\_001127208.2 | c.5683A>C | p.Thr1895Pro | Missense | 15.5 | 10010 | Oncogenic |
| TET2 | 10 | MF | NM\_001127208.2 | c.4513G>A | p.Ala1505Thr | Missense | 49.8 | 5030 | VUS |
| TET2 | 9 | MF | NM\_001127208.2 | c.3821A>G | p.Gln1274Arg | Missense | 44.9 | 3963 | Oncogenic |
| TET2 | 7 | MF | NM\_001127208.2 | c.1763C>A | p.Ser588\* | Nonsense | 50.4 | 4784 | Oncogenic |
| TET2 | 143 | MF | NM\_001127208.2 | c.5103G>A | p.Met1701Ile | Missense | 45.8 | 6071 | VUS |
| TET2 | 13 | ET | NM\_001127208.2 | c.5104C>T | p.Gln1702\* | Nonsense | 9.7 | 4905 | Oncogenic |
| TET2 | 17 | POST-MPN AML | NM\_001127208.2 | c.3991delA | p.Thr1331fs\*32 | Frameshift | 59.5 | 9159 | Oncogenic |
| TET2 | 135 | MF | NM\_001127208.2 | c.2375C>G | p.Ser792\* | Nonsense | 44.5 | 13845 | Oncogenic |
| TET2 | 145 | MF | NM\_001127208.2 | c.928A>G | p.Met310Val | Missense | 51.2 | 8301 | VUS |
| TET2 | 148 | MF | NM\_001127208.2 | c.3035C>T | p.Pro1012Leu | Missense | 45.1 | 4904 | VUS |
| TET2 | 163 | PV | NM\_001127208.2 | c.3149C>A | p.Ser1050\* | Nonsense | 43.1 | 9769 | Oncogenic |
| TET2 | 155 | MF | NM\_001127208.2 | c.4045-1G>T | p.? | Splice Site | 42.9 | 2458 | Oncogenic |
| TET2 | 155 | MF | NM\_001127208.2 | c.487\_488delinsC | p.Phe163fs\*20 | Frameshift | 43.5 | 9791 | Oncogenic |
| TET2 | 167 | MF | NM\_001127208.2 | c.4034\_4038delinsCAGGTGC | p.Tyr1345fs\*19 | Frameshift | 39.3 | 8535 | Oncogenic |
| TET2 | 162 | MF | NM\_001127208.2 | c.3207delC | p.Thr1070fs\*12 | Frameshift | 13.5 | 9225 | Oncogenic |
| TET2 | 172 | MF | NM\_001127208.2 | c.1843C>G | p.Leu615Val | Missense | 48.5 | 9191 | VUS |
| TET2 | 188 | Non-classical MPN | NM\_001127208.2 | c.1936dupA | p.Thr646fs\*35 | Frameshift | 35.2 | 12497 | Oncogenic |
| TET2 | 181 | MF | NM\_001127208.2 | c.2299A>G | p.Asn767Asp | Missense | 49.6 | 7604 | VUS |
| TET2 | 181 | MF | NM\_001127208.2 | c.2771A>G | p.His924Arg | Missense | 50.5 | 4011 | VUS |
| TET2 | 185 | MF | NM\_001127208.2 | c.3116C>T | p.Ser1039Leu | Missense | 50.3 | 12150 | VUS |
| TP53 | 36 | MF | NM\_000546.5 | c.578A>C | p.His193Pro | Missense | 21.13 | 1259 | Oncogenic |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| TP53 | 97 | MF | NM\_000546.5 | c.997C>T | p.Arg333Cys | Missense | 38.8 | 1281 | Oncogenic |
| TP53 | 26 | POST-MPN AML | NM\_000546.5 | c.646G>A | p.Val216Met | Missense | 79.3 | 1142 | Oncogenic |
| TP53 | 8 | MF | NM\_000546.5 | c.743G>A | p.Arg248Gln | Missense | 7.9 | 5050 | Oncogenic |
| TP53 | 8 | MF | NM\_000546.5 | c.742C>T | p.Arg248Trp | Missense | 32.5 | 5051 | Oncogenic |
| TP53 | 17 | POST-MPN AML | NM\_000546.5 | c.856G>A | p.Glu286Lys | Missense | 74.5 | 2826 | Oncogenic |
| TP53 | 150 | POST-MPN AML | NM\_000546.5 | c.524G>A | p.Arg175His | Missense | 4.3 | 3105 | Oncogenic |
| TP53 | 183 | PV | NM\_000546.5 | c.393C>A | p.Asn131Lys | Missense | 48.9 | 3308 | Oncogenic |
| U2AF1 | 95 | Non-classical MPN | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 33.79 | 1107 | Oncogenic |
| U2AF1 | 108 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 47.32 | 1101 | Oncogenic |
| U2AF1 | 43 | MF | NM\_001025203.1 | c.101C>T | p.Ser34Phe | Missense | 31.47 | 7352 | Oncogenic |
| U2AF1 | 96 | MF | NM\_001025203.1 | c.101C>T | p.Ser34Phe | Missense | 44.1 | 7279 | Oncogenic |
| U2AF1 | 71 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 47.2 | 1519 | Oncogenic |
| U2AF1 | 82 | POST-MPN AML | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 15.10 | 1857 | Oncogenic |
| U2AF1 | 78 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 34.7 | 3094 | Oncogenic |
| U2AF1 | 123 | MF | NM\_001025203.1 | c.101C>A | p.Ser34Tyr | Missense | 39.4 | 7696 | Oncogenic |
| U2AF1 | 50 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 41.4 | 1281 | Oncogenic |
| U2AF1 | 38 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 31.9 | 2108 | Oncogenic |
| U2AF1 | 88 | PV | NM\_001025203.1 | c.101C>T | p.Ser34Phe | Missense | 16.3 | 5285 | Oncogenic |
| U2AF1 | 51 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 43.3 | 1544 | Oncogenic |
| U2AF1 | 106 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 41 | 1573 | Oncogenic |
| U2AF1 | 65 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 41.8 | 1253 | Oncogenic |
| U2AF1 | 9 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 43.6 | 1208 | Oncogenic |
| U2AF1 | 8 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 47.6 | 1304 | Oncogenic |
| U2AF1 | 143 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 42.3 | 1733 | Oncogenic |
| U2AF1 | 12 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 44.4 | 2278 | Oncogenic |
| U2AF1 | 16 | MF | NM\_001025203.1 | c.101C>T | p.Ser34Phe | Missense | 27.7 | 9369 | Oncogenic |
| U2AF1 | 144 | MF | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 0.02 | 2072 | Oncogenic |
| U2AF1 | 160 | MF | NM\_001025203.1 | c.470A>G | p.Gln157Arg | Missense | 36.4 | 1928 | Oncogenic |
| U2AF1 | 153 | POST-MPN AML | NM\_001025203.1 | c.101C>T | p.Ser34Phe | Missense | 46 | 8134 | Oncogenic |
| **Gene** | **Patient ID** | **MPN category** | **Transcript ID** | **Variant (cDNA)** | **Variant (AA)** | **Type** | **VAF (%)** | **Read Depth**  | **Classification** |
| U2AF1 | 158 | Non-classical MPN | NM\_001025203.1 | c.470A>C | p.Gln157Pro | Missense | 35.6 | 2384 | Oncogenic |
| WT1 | 154 | MF | NM\_024426.3 | c.1405dupC | p.His469fs\*8 | Frameshift | 11.7 | 5127 | Oncogenic |
| ZRSR2 | 93 | MF | NM\_005089.3 | c.283G>A | p.Ala95Thr | Missense | 52.17 | 1380 | VUS |
| ZRSR2 | 95 | Non-classical MPN | NM\_005089.3 | c.1314\_1315insAGCCGG | p.Gly438\_Ser439insSerArg | Insertion | 35.67 | 1155 | VUS |
| ZRSR2 | 39 | ET | NM\_005089.3 | c.1121A>G | p.Tyr374Cys | Missense | 44.95 | 5678 | VUS |
| ZRSR2 | 66 | MF | NM\_005089.3 | c.283G>A | p.Ala95Thr | Missense | 99.71 | 694 | VUS |
| ZRSR2 | 61 | ET | NM\_005089.3 | c.1291\_1302dupAGGGACCGCAGC | p.Asp432\_Arg435dup | Duplication | 82.40 | 766 | VUS |
| ZRSR2 | 5 | MF | NM\_005089.3 | c.283G>A | p.Ala95Thr | Missense | 47.5 | 736 | VUS |
| ZRSR2 | 162 | MF | NM\_005089.3 | c.505C>T | p.Arg169\* | Nonsense | 84.2 | 3623 | Oncogenic |

\* JAK2 V617F detected by NGS at a frequency that is below the sensitivity of the assay (VAF<5%). The variant was confirmed by ddPCR assay. Read depth is not applicable.

Abbreviations: AA, amino acid; HMR, high molecular risk; NA, not applicable; VAF, variant allele frequency; VUS, variant of unknown significance.

**Supplementary Figure 1**

**High**

**HCT**

Ruxolitinib

OR

Clinical trial

OR

Best supportive care

**Yes**

**No**

Consider early HCT

Delayed HCT

**Int-1/2**

**Low**

**Yes**

**No**

Surveillance

Clinical trial

(if available)

**Low risk of LT /**

**Longer TTF**

**High risk of LT /**

**Short TTF/**

**Ruxolitinib contra-indicated**

Algorithm integrating the role of high molecular risk (HMR) mutation profile as detected by targeted sequencing in the management of myelofibrosis that will be prospectively evaluated at our center. HMR is currently defined as the presence of a mutation in any of *ASXL1*, *EZH2*, *IDH1/2* or *SRSF2*. Abbreviations: DIPSS, dynamic international prognostic scoring system; LT, leukemic transformation; HCT, hematopoietic cell transplantation; Int 1/2, intermediate 1/2 risk; TTF, time to treatment failure.