Supplemental material to Luise Hartmann, Judith S. Hecker, et al.:

*Compartment-specific mutational landscape of clonal hematopoiesis*
Supplemental Methods

Flow-sorting and genetic analyses of mature and precursor cell populations from BM samples

Antibodies used for cell sorting are listed in Supplemental Table 1.

After thawing BM samples, one fourth of the sample was stained with 100μl of an antibody mix for sorting mature cell populations (granulocytes, T lymphocytes, and B lymphocytes) along with CD34+ cells (Supplemental Figure 1A). Dead cell exclusion was performed using DAPI 1μg/ml (BioLegend, #422801). The rest of the sample was sorted into fractions containing hematopoietic stem cells (HSC: lin-CD34+CD38-CD45RA-CD90+), common-myeloid progenitors (CMP: lin-CD34+CD38+CD45RA-CD123+), granulocyte-monocyte progenitors (GMP: lin-CD34+CD38+CD45RA-CD123+), and megakaryocyte-erythroid progenitors (MEP: lin-CD34+CD38+CD45RA-CD123+) (Supplemental Figure 1B). For this panel, dead cells were excluded using propidium iodide 0.4μg/ml (Sigma, #P4170). Sorting was performed using a BD FACS Aria III cell sorter and a 100μm nozzle.

DNA from flow-sorted cells (9,000-200,000 cells per population) was isolated using the QIAamp DNA Micro kit (Qiagen, Hilden, Germany). A custom unique molecular identifier-based QIAseq gene panel (Qiagen) targeting ASXL1 exon 13 was used for library preparation, and sequencing was performed on a MiSeq instrument (Illumina, San Diego, USA). Variants were detected using the QIAGEN CLC Genomics Workbench. VAFs within flow-sorted cell populations were compared using the Friedman test followed by Dunn's multiple comparison test. ASXL1 mutation VAFs in each flow-sorted population were compared to the same individual’s bulk BM cells using Fisher's test, with multiple testing correction using the Benjamini-Hochberg procedure.
**Supplemental Tables**

**Supplemental Table 1: List of antibodies used for FACS sorting of mature and progenitor BM cell populations.**

| Panel     | Antibody | Conjugate | Dilution | Company         | Catalogue Number |
|-----------|----------|-----------|----------|-----------------|------------------|
| Mature    | Anti-CD3 | APC-Cy7   | 1:30     | BioLegend       | 344818           |
| Mature    | Anti-CD15| FITC      | 1:10     | Beckman Coulter | B36298           |
| Mature    | Anti-CD19| PE        | 1:30     | BioLegend       | 302208           |
| Mature    | Anti-CD34| PE-Cy7    | 1:30     | BioLegend       | 343616           |
| Mature    | Anti-CD45| APC       | 1:100    | eBioscience     | 17-0459-42       |
| Progenitor| Anti-CD4 | biotin    | 1:100    | BioLegend       | 300504           |
| Progenitor| Anti-CD8a| biotin    | 1:100    | BioLegend       | 301004           |
| Progenitor| Anti-CD15| biotin    | 1:100    | BioLegend       | 301914           |
| Progenitor| Anti-CD19| biotin    | 1:100    | BioLegend       | 302204           |
| Progenitor| Anti-CD34| FITC      | 1:15     | BD Pharmingen   | 555821           |
| Progenitor| Anti-CD38| APC       | 1:25     | BD Biosciences  | 345807           |
| Progenitor| Anti-CD45| PerCP-Cy5.5| 1:100   | BioLegend       | 304028           |
| Progenitor| Anti-CD45RA| PE-Cy7    | 1:20     | BD Biosciences  | 560675           |
| Progenitor| Anti-CD90 | PE        | 1:25     | BD Biosciences  | 555596           |
| Progenitor| Anti-CD123| BV421     | 1:25     | BioLegend       | 306018           |
| Progenitor| Anti-CD235a| biotin    | 1:100    | Invitrogen      | 13-9987-80       |
| Progenitor| Straptavidin| APC-Cy7   | 1:100    | BioLegend       | 405208           |
### Supplemental Table 2: Variants identified in individuals with clonal hematopoiesis.

| Subject | Gene   | Variant                          | Mutation type | VAF [%] | Specimen |
|---------|--------|----------------------------------|---------------|---------|----------|
| UPN_1   | ASXL1  | NM_015338.6:c.2036dup;p.(Gly680Argfs*38) | InDel         | 3.71    | BM       |
| UPN_1   | ASXL1  | NM_015338.6:c.2385del;p.(Trp796Glyfs*22) | InDel         | 5.93    | BM       |
| UPN_1   | STAT3  | NM_139276.2:c.1940A>T;p.(Asn647Ile) | Missense      | 1.79    | BM       |
| UPN_1   | TET2   | NM_001127208.2:c.5760A>T;p.(Lys1920Asn) | Missense      | 4.75    | BM       |
| UPN_1   | U2AF1  | NM_01025203.1:c.470A>C;p.(Gln157Pro) | Missense      | 9.73    | BM       |
| UPN_10  | BCO RL | NM_021946.4:c.4013G>A;p.(Arg1338Gln) | Missense      | 6.39    | BM       |
| UPN_10  | TET2   | NM_001127208.2:c.5582G>A;p.(Gly1861Glu) | Missense      | 4.49    | BM       |
| UPN_100 | ZBTB7A | NM_015898.4:c.149C>T;p.(Ser50Leu)  | Missense      | 3.18    | BM       |
| UPN_11  | BCO RL | NM_021946.4:c.4853+1G>C;p.?         | Splice site   | 10.86   | BM       |
| UPN_12  | DNMT3A | NM_175629.2:c.2567_2568delAG;p.(Glu856Glyfs*7) | InDel         | 1.56    | PB       |
| UPN_12  | TET2   | NM_001127208.2:c.2339T>C;p.(Leu780Pro) | Missense      | 1.13    | PB       |
| UPN_13  | DNMT3A | NM_175629.2:c.2393T>C;p.(Leu780Pro)  | Missense      | 1.00    | BM       |
| UPN_13  | TET2   | NM_001127208.2:c.5686A>G;p.(Arg1896Gly) | Missense      | 5.34    | BM       |
| UPN_14  | DNMT3A | NM_175629.2:c.2339T>C;p.(Leu780Pro)  | Missense      | 1.14    | BM       |
| UPN_14  | TET2   | NM_001127208.2:c.4079T>G;p.(Leu1360Arg) | Missense      | 1.19    | BM       |
| UPN_15  | DNMT3A | NM_175629.2:c.1940T>G;p.(Leu647Arg)  | Missense      | 4.47    | BM       |
| UPN_15  | TET2   | NM_001127208.2:c.1842dup;p.(Leu615Alafs*23) | InDel         | 23.6    | BM       |
| UPN_16  | DNMT3A | NM_175629.2:c.2106T>G;p.(Asp702Glu)  | Missense      | 1.11    | BM       |
| UPN_16  | IDH2   | NM_002168.3:c.678+1G>T;p.?          | Splice site   | 1.07    | BM       |
| UPN_16  | TET2   | NM_001127208.2:c.2567_2568delAG;p.(Glu856Glyfs*7) | InDel         | 1.18    | BM       |
| UPN_17  | DNMT3A | NM_175629.2:c.1904T>G;p.(Leu647Arg)  | Missense      | 4.47    | BM       |
| UPN_17  | TET2   | NM_001127208.2:c.4163C>A;p.(Ala1379Asp) | Missense      | 2.42    | BM       |
| UPN_17  | TET2   | NM_001127208.2:c.3116C>A;p.(Ser1039*) | Nonsense      | 2.81    | BM       |
| UPN_18  | DNMT3A | NM_175629.2:c.2092T>G;p.(Trp698Gly)  | Missense      | 5.77    | PB       |
| UPN_19  | DNMT3A | NM_175629.2:c.2195T>C;p.(Ser714Cys)  | Missense      | 1.08    | BM       |
| UPN_19  | NFE2   | NM_001136023.3:c.814C>T;p.(Arg272*) | Nonsense      | 5.39    | BM       |
| UPN_20  | DNMT3A | NM_175629.2:c.2591T>A;p.(Met864Lys)  | Missense      | 21.29   | PB       |
| UPN_20  | DNMT3A | NM_175629.2:c.2591T>A;p.(Met864Lys)  | Missense      | 21.29   | PB       |
| UPN_201 | DNMT3A | NM_175629.2:c.1506del p.(Thr503Profs*148) | InDel         | 4.28    | BM       |
| UPN_205 | DNMT3A | NM_175629.2:c.942G>A;p.(Trp314*)     | Nonsense      | 5.39    | BM       |
| UPN_206 | DNMT3A | NM_175629.2:c.2408+6T>G;p.?          | Splice site   | 1.41    | BM       |
| UPN_208 | DNMT3A | NM_175629.2:c.2204A>G;p.(Tyr735Cys)  | Missense      | 1.24    | BM       |
| UPN_21  | DNMT3A | NM_175629.2:c.2047_2056del; p.(Tyr683Thrfs*19) | InDel         | 3.41    | PB       |
| UPN_213 | TET2   | NM_001127208.2:c.4791_4792del;p.(Phe1597Leufs*16) | Missense      | 1.39    | BM       |
| UPN_213 | TET2   | NM_001127208.2:c.444_447del;p.(Lys148Asnsfs*3) | InDel         | 2.12    | BM       |
| UPN_214 | PPM1D  | NM_003620.4:c.1654C>T;p.(Arg552*)   | Nonsense      | 10.63   | BM       |
| Subject | Gene | Variant | Mutation type | VAF [%] | Specimen |
|---------|------|---------|---------------|---------|----------|
| UPN_216 | PPM1D | NM_003620.4:c.1654C>T;p.(Arg552*) | Nonsense | 2.00 | BM |
| UPN_218 | DNMT3A | NM_175629.2:c.2086del;p.(Gln696Argfs*9) | InDel | 1.16 | BM |
| UPN_22  | DNMT3A | NM_175629.2:c.2711C>T;p.(Pro904Leu) | Missense | 6.64 | BM |
| UPN_220 | DNMT3A | NM_175629.2:c.2711C>T;p.(Pro904Leu) | Missense | 1.16 | BM |
| UPN_222 | TET2  | NM_001127208.2:c.2340_2343del;p.(Val781Lysfs*31) | InDel | 1.77 | BM |
| UPN_223 | DNMT3A | NM_175629.2:c.2645G>A;p.(Arg882His) | Missense | 3.04 | BM |
| UPN_225 | DNMT3A | NM_175629.2:c.1674T>G;p.(Phe558Leu) | Missense | 1.28 | BM |
| UPN_225 | TET2  | NM_001127208.2:c.1441C>T;p.(Gln481*) | Nonsense | 1.30 | BM |
| UPN_226 | ASXL1 | NM_015338.6:c.2179G>T;p.(Glu727*) | Nonsense | 2.67 | BM |
| UPN_227 | PPM1D | NM_003620.4:c.1709C>G;p.(Ser570*) | Nonsense | 1.18 | BM |
| UPN_23  | DNMT3A | NM_175629.2:c.1506delT;p.(Thr503Profs*148) | InDel | 4.73 | PB |
| UPN_231 | DNMT3A | NM_175629.2:c.2339T>C;p.(Ile780Thr) | Missense | 1.64 | BM |
| UPN_231 | DNMT3A | NM_175629.2:c.2408G>A;p.(Arg803Lys) | Missense | 1.79 | BM |
| UPN_231 | TET2  | NM_001127208.2:c.2919C>A;p.(Cys973*) | Nonsense | 1.89 | BM |
| UPN_232 | ASXL1 | NM_015338.6:c.2885_2886del;p.(Val962Alafs*7) | InDel | 1.87 | BM |
| UPN_235 | U2AF1 | NM_001025203.1:c.470A>G;p.(Gln157Arg) | Missense | 2.07 | BM |
| UPN_238 | DNMT3A | NM_175629.2:c.1123-1G>C;p.? | Splice site | 8.24 | BM |
| UPN_24  | DNMT3A | NM_175629.2:c.1258A>T;p.(Lys420*) | Nonsense | 3.99 | BM |
| UPN_242 | ASXL1 | NM_015338.6:c.2885_2886del;p.(Val962Alafs*7) | InDel | 1.87 | BM |
| UPN_243 | TET2  | NM_001127208.2:c.2919C>A;p.(Cys973*) | Missense | 1.89 | BM |
| UPN_245 | TP53  | NM_000546.5:c.623A>G;p.(Asp208Gly) | Missense | 1.35 | BM |
| UPN_248 | ASXL1 | NM_015338.6:c.2258_2259dup;p.(Ser535Pro) | InDel | 4.87 | BM |
| UPN_248 | SH2B3 | NM_005475.2:c.1522dup;p.(Arg508Profs*38) | InDel | 40.42 | BM |
| UPN_248 | TET2  | NM_001127208.2:c.5165del;p.(Pro1722Leufs*23) | InDel | 30.10 | BM |
| UPN_248 | TET2  | NM_001127208.2:c.5481_5482del;p.(Gln1828Alafs*17) | InDel | 32.3 | BM |
| UPN_25  | DNMT3A | NM_175629.2:c.1258A>T;p.(Lys420*) | Nonsense | 3.99 | BM |
| UPN_250 | TET2  | NM_001127208.2:c.2375C>A;p.(Ser792*) | Nonsense | 1.10 | BM |
| UPN_251 | TET2  | NM_001127208.2:c.5618T>C;p.(Thr1884Ala) | Missense | 1.15 | BM |
| UPN_251 | DNMT3A | NM_175629.2:c.2530A>G;p.(Lys844Glu) | Missense | 1.45 | BM |
| UPN_252 | SF3B1 | NM_012433.3c.1986C>G;p.(His662Gln) | Missense | 1.42 | BM |
| UPN_252 | TET2  | NM_001127208.2:c.5686A>T;p.(Arg1896Trp) | Missense | 2.10 | BM |
| UPN_254 | SRSF2 | NM_003016.4:c.242A>T;p.(Asp81Val) | Missense | 2.30 | BM |
| UPN_254 | TET2  | NM_001127208.2:c.2375C>A;p.(Ser792*) | Nonsense | 1.10 | BM |
| UPN_255 | PIGA  | NM_002641.3:c.217G>A;p.(Ala73Thr) | Missense | 4.95 | BM |
| UPN_26  | DNMT3A | NM_175629.2:c.2332G>A;p.(Val778Met) | Missense | 5.07 | BM |
| UPN_266 | DNMT3A | NM_175629.2:c.2207G>A;p.(Arg736His) | Missense | 7.17 | BM |
| UPN_267 | DNMT3A | NM_175629.2:c.1238del;p.(Gly413Alafs*238) | InDel | 1.00 | BM |
| UPN_27  | DNMT3A | NM_175629.2:c.1271del;p.(Pro424Hisfs*227) | InDel | 1.49 | BM |
| UPN_272 | SRP72 | NM_006947.3:c.869A>G;p.(Asn290Ser) | Missense | 3.16 | PB |
| UPN_275 | DNMT3A | NM_175629.2:c.2657del;p.(Gln886Argfs*20) | InDel | 1.94 | PB |
| Subject  | Gene    | Variant                                                                 | Mutation type | VAF [%] | Specimen |
|---------|---------|--------------------------------------------------------------------------|---------------|---------|----------|
| UPN_276 | DNMT3A  | NM_175629.2:c.1238dup;p.(Phe414Leufs*7)                                  | InDel         | 1.42    | PB       |
| UPN_28  | DNMT3A  | NM_175629.2:c.2711C>T;p.(Pro904Leu)                                      | Missense      | 5.33    | BM       |
| UPN_280 | PPM1D   | NM_003620.4:c.1332_1335del;p.(Phe445Glufs*5)                             | InDel         | 1.24    | PB       |
| UPN_282 | DNMT3A  | NM_175629.2:c.2190_2215del;p.(Phe731*)                                   | InDel         | 10.81   | PB       |
| UPN_283 | DNMT3A  | NM_175629.2:c.2207G>A;p.(Arg736His)                                      | Missense      | 5.68    | PB       |
| UPN_288 | DNMT3A  | NM_175629.2:c.1903C>T;p.(Gln696*)                                       | Nonsense      | 2.69    | PB       |
| UPN_288 | SF3B1   | NM_012433.3:c.1997A>G; p.(Lys666Arg)                                     | Missense      | 1.45    | PB       |
| UPN_29  | DNMT3A  | NM_175629.2:c.2322+2T>C;p.?                                             | Splice site   | 1.64    | PB       |
| UPN_291 | DNMT3A  | NM_175629.2:c.2245C>T;p.(Arg749Cys)                                      | Missense      | 2.03    | PB       |
| UPN_3   | ASXL1   | NM_015338.6:c.2954_2957del;p.(Ile985Thrfs*7)                             | InDel         | 4.73    | BM       |
| UPN_30  | DNMT3A  | NM_175629.2:c.1948C>G;p.(Leu650Val)                                     | Missense      | 1.06    | PB       |
| UPN_31  | DNMT3A  | NM_175629.2:c.1904G>A;p.(Arg635Gln)                                      | Missense      | 6.54    | BM       |
| UPN_32  | DNMT3A  | NM_175629.2:c.2204A>G;p.(Tyr735Cys)                                      | Missense      | 2.65    | PB       |
| UPN_33  | DNMT3A  | NM_175629.2:c.2330C>G;p.(Pro777Arg)                                      | Missense      | 1.32    | BM       |
| UPN_34  | DNMT3A  | NM_175629.2:c.2393T>A, p.(Leu798His)                                     | Missense      | 4.37    | BM       |
| UPN_35  | DNMT3A  | NM_175629.2:c.2401A>G; p.(Met801Val)                                     | Missense      | 8.48    | BM       |
| UPN_36  | DNMT3A  | NM_175629.2:c.1015-2A>G;p.?                                             | Splice site   | 4.76    | BM       |
| UPN_37  | DNMT3A  | NM_175629.2:c.1532G>A;p.(Gly511Glu)                                      | Missense      | 1.49    | BM       |
| UPN_38  | DNMT3A  | NM_175629.2:c.2141C>G;p.(Ser714Cys)                                      | Missense      | 2.14    | BM       |
| UPN_39  | DNMT3A  | NM_175629.2:c.2644C>T;p.(Arg882Cys)                                      | Missense      | 8.48    | BM       |
| UPN_4   | ASXL1   | NM_015338.5:c.2512_2537dup; p.(Ser846Argfs*5)                            | InDel         | 11.42   | PB       |
| UPN_4   | ASXL1   | NM_015338.6:c.2512_2537dup; p.(Ser846Argfs*5)                            | InDel         | 6.07    | BM       |
| UPN_40  | DNMT3A  | NM_175629.2:c.1900A>T; p.(Ile634Phe)                                      | Missense      | 1.07    | BM       |
| UPN_41  | DNMT3A  | NM_175629.2:c.1430-3C>G;p.?                                             | Splice site   | 3.08    | BM       |
| UPN_42  | DNMT3A  | NM_175629.2:c.2377T>C;p.(Tyr793His)                                      | Missense      | 1.74    | BM       |
| UPN_43  | DNMT3A  | NM_175629.2:c.2141C>G;p.(Ser714Cys)                                      | Missense      | 2.14    | BM       |
| UPN_44  | DNMT3A  | NM_175629.2:c.1924G>A;p.(Gly642Arg)                                      | Missense      | 1.17    | BM       |
| UPN_45  | DNMT3A  | NM_175629.2:c.2322+3A>G;p.?                                             | Splice site   | 1.44    | BM       |
| UPN_49  | DNMT3A  | NM_175629.2:c.2727T>A; p.(Phe909Leu)                                      | Missense      | 1.85    | PB       |
| UPN_49  | SF3B1   | NM_012433.3:c.1997A>C; p.(Lys666Thr)                                      | Missense      | 9.01    | PB       |
| UPN_5   | ASXL1   | NM_015338.6:c.1934dup;p.(Gly646Trfps*12)                                  | InDel         | 6.07    | BM       |
| UPN_51  | DNMT3A  | NM_175629.2:c.2494A>G;p.(Thr832Ala)                                      | Missense      | 6.42    | BM       |
| UPN_51  | ZRSR2   | NM_005089.3:c.370C>T;p.(Gln124*)                                          | Nonsense      | 2.93    | BM       |
| UPN_52  | DNMT3A  | NM_175629.2:c.1949T>G, p.(Leu650Arg)                                     | Missense      | 1.28    | BM       |
| UPN_52  | TP53    | NM_000546.5:c.536A>G, p.(His179Arg)                                      | Missense      | 4.48    | BM       |
| UPN_53  | DNMT3A  | NM_175629.2:c.2644C>T, p.(Arg882Cys)                                     | Missense      | 27.42   | BM       |
| UPN_53  | NFE2    | NM_001136023.3:c.578_581del, p.(Asn193Ilefs*12)                           | InDel         | 24.62   | BM       |
| UPN_54  | DNMT3A  | NM_175629.2:c.2332G>A;p.(Val778Met)                                      | Missense      | 1.03    | BM       |
| UPN_54  | U2AF2   | NM_007279.2:c.977G>C;p.(Gly326Ala)                                        | Missense      | 7.93    | BM       |
| UPN_55  | DNMT3A  | NM_175629.2:c.1668-2A>G;p.?                                             | Splice site   | 2.32    | BM       |
| Subject | Gene        | Variant                                                                 | Mutation type | VAF [%] | Specimen |
|---------|-------------|-------------------------------------------------------------------------|---------------|---------|----------|
| UPN_55  | MYD88       | NM_001172567.1:c.818T>C;p.(Leu273Pro)                                    | Missense      | 27.86   | BM       |
| UPN_57  | DNMT3A      | M_175629.2:c.2096G>T; p.(Gly699Val)                                       | Missense      | 1.44    | BM       |
| UPN_57  | DNMT3A      | NM_175629.2:c.1911_1914delGTCT;p.(Phe640Metfs*10)                        | InDel         | 3.33    | BM       |
| UPN_58  | DNMT3A      | NM_175629.2:c.2656C>T;p.(Gln886)*                                        | Nonsense      | 1.20    | BM       |
| UPN_58  | DNMT3A      | NM_175629.2:c.1936+1G>T;p.?                                              | Splice site   | 6.30    | BM       |
| UPN_59  | DNMT3A      | NM_175629.2:c.1093_1096delCT;p.(Thr358Profs*27)                          | InDel         | 5.38    | BM       |
| UPN_59  | DNMT3A      | NM_175629.2:c.2206C>T;p.(Arg736Cys)                                       | Missense      | 31.70   | BM       |
| UPN_60  | DNMT3A      | NM_175629.2:c.2106_2107insA;p.(Leu703Thrfs*10)                           | InDel         | 4.19    | BM       |
| UPN_61  | DNMT3A      | NM_175629.2:c.2045T>G;p.(Met682Arg)                                       | Missense      | 2.39    | BM       |
| UPN_61  | DNMT3A      | NM_175629.2:c.2245C>T;p.(Arg749Cys)                                       | Missense      | 3.29    | BM       |
| UPN_62  | DNMT3A      | NM_175629.2:c.2339T>C;p.(Ile780Thr)                                      | Missense      | 1.22    | PB       |
| UPN_62  | DNMT3A      | NM_175629.2:c.1040T>C;p.(Leu347Pro)                                       | Missense      | 32.70   | BM       |
| UPN_64  | TP53        | NM_000546.5:c.524G>A;p.(Arg175His)                                        | Missense      | 1.99    | BM       |
| UPN_64  | U2AF2       | NM_007279.2:c.866A>G;p.(Asn289Ser)                                        | Missense      | 1.58    | BM       |
| UPN_65  | DNMT3A      | NM_175629.2:c.1154del;p.(Pro385Argfs*22)                                  | InDel         | 4.88    | BM       |
| UPN_65  | DNMT3A      | NM_175629.2:c.1851+1G>T;p.?                                              | Splice site   | 2.57    | PB       |
| UPN_65  | DNMT3A      | NM_175629.2:c.2458G>T;p.(Glu820*)                                        | Nonsense      | 2.20    | PB       |
| UPN_65  | DNMT3A      | NM_175629.2:c.2644C>T;p.(Arg882Cys)                                       | Missense      | 1.96    | PB       |
| UPN_66  | DNMT3A      | NM_175629.2:c.1240_1245delTTCACG; p.(Phe414_Gln415del)                     | InDel         | 1.18    | PB       |
| UPN_66  | IDH2        | NM_002168.3:c.419G>A;p.(Arg140Gln)                                        | Missense      | 7.43    | PB       |
| UPN_69  | JAK2        | NM_004972.3:c.1849G>T p.(Val617Phe)                                       | Missense      | 9.92    | BM       |
| UPN_69  | TET2        | NM_001127208.2:c.4045-2A>G;p.?                                           | Splice site   | 3.56    | BM       |
| UPN_7   | ASXL1       | NM_015338.6:c.2644C>T; p.(Gln882*)                                       | Nonsense      | 1.05    | PB       |
| UPN_7   | PHF6        | NM_032458.3:c.998A>T;p.(Asp333Val)                                        | Missense      | 1.43    | BM       |
| UPN_7   | NOTCH1      | ENST00000277541:c.7541_7542delCT;p.Pro2514fs                            | Nonsense      | 2.69    | BM       |
| UPN_7   | MYD88       | NM_001172567.1:c.818T>C;p.(Leu273Pro)                                    | Missense      | 2.38    | BM       |
| UPN_7   | TET2        | NM_001127208.2:c.2156del;p.(Leu719Cysfs*32)                               | InDel         | 1.21    | BM       |
| UPN_7   | TET2        | NM_001127208.2:c.5629A>G;p.(Lys1877Glu)                                  | Missense      | 1.78    | BM       |
| UPN_7   | TET2        | NM_001127208.2:c.3647G>A;p.(Arg1216Gln)                                  | Missense      | 2.42    | BM       |
| UPN_7   | KRAS        | NM_033360.3:c.35G>A;p.(Gly12Asp)                                          | Missense      | 22.19   | PB       |
| UPN_7   | TET2        | NM_001127208.2:c.4393C>T;p.(Arg1465*)                                    | Nonsense      | 3.02    | PB       |
| UPN_7   | ZBTB7A      | NM_015898.4:c.1228T>A;p.(Tyrr10Asn)                                       | Missense      | 2.89    | PB       |
| UPN_7   | JAK2        | NM_004972.3:c.1849G>T p.(Val617Phe)                                       | Missense      | 3.54    | BM       |
| UPN_7   | TET2        | NM_001127208.2:c.3789T>A;p.(Cys1263*)                                    | Nonsense      | 2.60    | BM       |
| UPN_7   | TET2        | NM_001127208.2:c.1081C>T; p.(Gln361*)                                    | Nonsense      | 1.37    | PB       |
| Subject | Gene | Variant | Mutation type | VAF [%] | Specimen |
|---------|------|---------|---------------|---------|----------|
| UPN_79  | RUNX1| NM_001754.4:c.833C>A;p.(Pro278Gln) | Missense | 1.76 | BM |
| UPN_79  | TERT | NM_198253.3:c.1573+6G>T;p.? | Splice site | 4.96 | BM |
| UPN_8   | BCOR | NM_001123385.2:c.4163C>T; p.(Ala1388Val) | Missense | 1.23 | PB |
| UPN_8   | DNMT3A| NM_175629.2:c.886G>A; p.(Val296Met) | Missense | 3.21 | PB |
| UPN_8   | TET2 | NM_001127208.2:c.4525A>T;p.(Lys1509*) | Nonsense | 2.46 | PB |
| UPN_8   | ZRSR2| NM_005089.3:c.1338_1343dup;p.(Ser447_Arg448dup) | InDel | 31.32 | PB |
| UPN_80  | SF3B1| NM_012433.3:c.2230G>C;p.(Ala744Pro) | Missense | 2.61 | PB |
| UPN_81  | SF3B1| NM_012433.3:c.1873C>T, p.(Arg625Cys) | Missense | 14.97 | BM |
| UPN_82  | SRSF2| NM_003016.4:c.283C>G;p.(Pro95Ala) | Missense | 26.53 | BM |
| UPN_85  | TET2 | NM_001127208.2:c.3885delC; p.(Tyr1295*) | InDel | 2.81 | PB |
| UPN_86  | TET2 | NM_001127208.2:c.5127dup;p.(Thr1710Tyrfs*3) | InDel | 1.66 | PB |
| UPN_87  | TET2 | NM_001127208.2:c.670G>T;p.(Glu224*) | Nonsense | 2.16 | PB |
| UPN_88  | TET2 | NM_001127208.2:c.456_457dup;p.(Ser153Phefs*3) | InDel | 2.24 | PB |
| UPN_89  | TET2 | NM_001127208.2:c.3954+5G>A;p.? | Splice site | 2.10 | BM |
| UPN_9   | BCOR | NM_001123385.2:c.838G>A;p.(Val280Ile) | Missense | 13.32 | BM |
| UPN_9   | CXCR4| NM_001008540.2:c.1045dup;p.(Glu349Glyfs*13) | InDel | 1.92 | BM |
| UPN_90  | TET2 | NM_001127208.2:c.4353del;p.(Arg1452Glufs*6) | InDel | 5.17 | BM |
| UPN_91  | TET2 | NM_001127208.2:c.5079_5082del;p.(Tyr1693*) | InDel | 7.13 | BM |
| UPN_92  | TET2 | NM_001127208.2:c.1486del;p.(Met496*) | InDel | 1.30 | BM |
| UPN_96  | TET2 | NM_001127208.2:c.3662G>A;p.(Cys1221Tyr) | Missense | 3.24 | PB |
| UPN_96  | TET2 | NM_001127208.2:c.3482G>C;p.(Arg1161Thr) | Missense | 5.00 | PB |
| UPN_97  | TET2 | NM_001127208.2:c.5650A>G;p.(Thr1884Ala) | Missense | 1.11 | BM |
| UPN_97  | TET2 | NM_001127208.2:c.4161C>A;p.(Asn1387Lys) | Missense | 15.24 | BM |
| UPN_98  | TET2 | NM_001127208.2:c.663_666delACAT;p.(His222Valfs*27) | InDel | 2.14 | PB |
| UPN_98  | TET2 | NM_001127208.2:c.1038_1039delAG;p.(Ala347Valfs*3) | InDel | 3.27 | PB |
| UPN_99  | U2AF2| NM_007279.2:c.259_261delAG;p.(Lys87del) | InDel | 1.08 | BM |

**Abbreviations:** VAF, variant allele frequency; InDel, insertion/deletion variant; BM, bone marrow; PB, peripheral blood; UPN, unique patient number.
Supplemental Table 3: Comparison of variant allele frequencies in paired BM and PB samples from 21 individuals with clonal hematopoiesis.

| Subject | Gene | Variant | VAF [%] | Coverage | VAF [%] | Coverage |
|---------|------|---------|---------|----------|---------|----------|
| UPN_6   | ASXL1| c.2512_2537dup; p.(Ser846Argfs*5) | 16.92   | 1876     | 11.42   | 1655     |
|         | ETV6 | c.844dup;p.(Arg282Profs*18) | 0.37    | 2685     | 0.58    | 1719     |
| UPN_7   | ASXL1| c.2644C>T; p.(Gln882*) | 6.95    | 820      | 1.05    | 1045     |
|          | ZBTB7A| c.1228T>A; p.(Tyr410Asn) | 2.50    | 1482     | 2.89    | 1383     |
| UPN_8   | BCOR*| c.4163C>T; p.(Ala1388Val) | ND      | 700      | 1.22    | 734      |
|          | TET2 | c.4525A>T; p.(Lys1509*) | 7.06    | 1126     | 2.46    | 1342     |
|          | DNMT3A| c.886G>A;p.(Val296Met) | 1.62    | 618      | 3.21    | 654      |
|          | DNMT3A| c.2339T>G;p.(Ile780Ser) | 1.51    | 1323     | 0.06    | 3451     |
|          | ZRSR2| c.1338_1343dup;p.(Ser447_Arg448dup) | 43.06  | 353      | 31.32   | 514      |
| UPN_18  | DNMT3A| c.2092T>G;p.(Trp698Gly) | 6.97    | 717      | 5.77    | 762      |
| UPN_19  | DNMT3A| c.2195T>G;p.(Phe732Ser) | 1.32    | 683      | 1.15    | 786      |
| UPN_21  | DNMT3A| c.2047_2056del;p.(Tyr683Thrfs*19) | 4.55   | 857      | 3.41    | 586      |
| UPN_29  | DNMT3A| c.2322+2T>C;p.?(Val296Met) | 0.64    | 1634     | 2.20    | 1407     |
| UPN_49  | SF3B1| c.1997A>C; p.(Lys666Thr) | 9.88    | 921      | 9.01    | 677      |
| UPN_65  | DNMT3A| c.2580G>A;p.(Trp880*) | 3.18    | 1634     | 2.20    | 1407     |
| UPN_66  | DNMT3A| c.1240_1245delTTCCAG;p.(Phe414_Gln415del) | 1.91   | 489      | 3.02    | 1055     |
|          | DNMT3A| c.2644C>T;p.(Arg882Cys) | 3.91    | 818      | 1.96    | 1124     |
|          | IDH2 | c.419G>A;p.(Arg140Gln) | 2.67    | 1422     | 7.43    | 1790     |
|          | DNMT3A| c.1429+1G>A;p.? | 1.96    | 1018     | 0.66    | 1958     |
| UPN_71  | TET2 | c.4393C>T;p.(Arg1465*) | 3.07    | 489      | 3.02    | 364      |
|          | KRAS | c.35G>A;p.(Gly12Asp) | 16.50   | 721      | 22.19   | 1005     |
| UPN_75  | TET2 | c.3883T>G;p.(Tyr1295Asp) | 1.28    | 1249     | 0.75    | 2259     |
|          | PPM1D| c.1545_1546delGT;p.(Met515Ilefs*12) | 3.75   | 773      | 1.82    | 881      |
| UPN_76  | PPM1D| c.1636delC;p.(Leu546*) | 3.11    | 644      | 2.66    | 826      |
| UPN_80  | SF3B1| c.2230G>C;p.(Ala744Pro) | 6.35    | 929      | 2.61    | 881      |
| UPN_86  | TET2 | c.5127dup;p.(Phe244Leufs*72) | 1.21   | 828      | ND      | 874      |
| UPN_88  | TET2 | c.456_457del;p.(Ser153Phefs*3) | 4.19   | 1337     | 2.24    | 848      |
| UPN_96  | TET2 | c.3662G>A;p.(Cys1221Tyr) | 3.29    | 3682     | 3.24    | 2408     |
|          | TET2 | c.3482G>C;p.(Arg1161Thr) | 9.84    | 2257     | 5.00    | 1341     |
|          | DNMT3A| c.1945G>T;p.(Val649Met) | 1.42    | 1615     | 0.73    | 2042     |
|          | TET2 | c.822del;p.(Asn275Valfs*3) | 2.63    | 3226     | 0.67    | 4480     |
| UPN_98  | DNMT3A*| c.731del;p.(Pro244Leufs*2) | 1.21   | 828      | ND      | 874      |
|          | TET2 | c.663_666delACAT;p.(His222Valfs*27) | 1.40   | 714      | 2.14    | 1167     |
|          | TET2 | c.1038_1039delAG;p.(Ala347Valfs*3) | 2.23   | 1165     | 3.27    | 1588     |
| UPN_27  | SRP72| c.869A>G;p.(Asn290Ser) | 4.07    | 589      | 3.16    | 792      |
|          | TET2 | c.3883T>G;p.(Tyr1295Asp) | 1.28    | 1249     | 0.75    | 2259     |
| UPN_27  | DNMT3A| c.1238dup;p.(Phe414Leufs*7) | 1.86    | 1557     | 1.42    | 1973     |
|          | STAG2| p.(Leu203Phe) | 1.47    | 955      | 0.34    | 2336     |

* Highlighted variants were validated by digital droplet PCR, results are shown in Supplemental Table 4

**Abbreviations:** VAF, variant allele frequency; InDel, insertion/deletion variant; BM, bone marrow; PB, peripheral blood; ND, not detectable; UPN, unique patient number.
**Supplemental Table 4: Orthogonal validation by mutation-specific digital droplet PCR of variants identified in paired BM and PB samples (UPN_98 and UPN_8) and in paired bone marrow samples from individuals undergoing simultaneous bilateral hip replacement (UPN_2 and UPN_248).**

| Subject   | Gene   | Variant                      | Sample | VAF [%] |
|-----------|--------|-------------------------------|--------|---------|
| UPN_98    | DNMT3A | c.731del; p.(Pro244Leufs*72)  | BM     | 0.831   |
|           |        |                               | PB     | 0.084   |
| UPN_8     | DNMT3A | c.2339T>G; p.(Ile780Ser)      | BM     | 1.584   |
|           |        |                               | PB     | 0.267   |
| UPN_2     | ASXL1  | c.2083C>T; p.(Gln695*)        | Hip 1  | 1.087   |
|           |        |                               | Hip 2  | 0.050   |
| UPN_248   | ASXL1  | c.2258_2259dup; p.(Thr754Profs*19) | Hip 1 | 0.274   |
|           |        |                               | Hip 2  | 4.154   |

**Abbreviations:** VAF, variant allele frequency; BM, bone marrow; PB, peripheral blood; UPN, unique patient number.
**Supplemental Table 5: Overview of variants found in patients with ‘large-clone’ CHIP.**

Large-clone CHIP was defined as at least one variant with a VAF >20% (highlighted in red in the table). Subjects are grouped according to their clonal profile (single variants, multiple variants with one “dominant” variant, or several variants with VAF >20%).

| Mutational profile | UPN          | Gene          | Variant                          | Mutation type | VAF [%] |
|-------------------|--------------|---------------|----------------------------------|---------------|---------|
| Single variant    | UPN_82       | SRSF2         | NM_003016.4:c.283C>G;p.(Pro95Ala) | Missense      | 26.5    |
|                   | UPN_20       | DNMT3A        | NM_175629.2:c.2591T>A;p.(Met864Lys) | Missense      | 21.3    |
|                   | UPN_254      | TET2          | NM_001127208.2:c.5650A>G;p.(Thr1884Ala) | Missense      | 43.9    |
|                   |              | SRSF2         | NM_003016.4:c.242A>T;p.(Asp81Val) | Missense      | 3.2     |
|                   |              | DNMT3A        | NM_175629.2:c.1040T>C;p.(Leu347Pro) | Missense      | 32.7    |
|                   |              | DNMT3A        | NM_175629.2:c.2339T>C;p.(Ile780Thr) | Missense      | 1.2     |
|                   | UPN_59       | DNMT3A        | NM_175629.2:c.2206C>T;p.(Arg736Cys) | Missense      | 31.7    |
|                   |              | ZRSR2         | NM_005089.3:c.1338_1343dup;p.(Ser447_Arg448dup) | InDel         | 31.2    |
|                   |              | DNMT3A        | NM_175629.2:c.886G>A;p.(Val296Met) | Missense      | 3.2     |
|                   |              | TET2          | NM_001127208.2:c.4525A>T;p.(Lys1509*) | Nonsense      | 2.5     |
|                   |              | BCOR          | NM_001123385.2:c.4163C>T;p.(Ala1388Val) | Missense      | 1.2     |
|                   | UPN_85       | MYD88         | NM_001172567.1:c.818T>C;p.(Leu273Pro) | Missense      | 27.9    |
|                   |              | DNMT3A        | NM_175629.2:c.1668-2A>G;p.?        | Splice site   | 2.3     |
|                   | UPN_15       | DNMT3A        | NM_175629.2:c.1123-2A>G;p.?        | Splice site   | 23.6    |
|                   |              | TET2          | NM_001127208.2:c.4079T>G;p.(Arg1465*) | Nonsense      | 3.0     |
|                   | UPN_71       | KRAS          | NM_003360.3:c.35G>A;p.(Gly12Asp)   | Missense      | 22.3    |
|                   |              | TET2          | NM_001127208.2:c.4393C>T;p.(Arg1465*) | Nonsense      | 3.0     |
|                   | UPN_248      | SH2B3         | NM_0005475.2:c.1522dup;p.(Arg508Profs*38) | InDel         | 40.4    |
|                   |              | TET2          | NM_001127208.2:c.5481_5482del;p.(Gln1828Alafs*17) | InDel         | 32.3    |
|                   |              | TET2          | NM_001127208.2:c.5165del;p.(Pro1722Leufs*23) | InDel         | 30.1    |
|                   |              | ASXL1         | NM_015338.6:c.2258_2259dup;p.(Thr754Profs*19) | InDel         | 4.9     |
|                   | UPN_53       | DNMT3A        | NM_175629.2:c.2644C>T;p.(Arg882Cys) | Missense      | 27.4    |
|                   |              | NFE2          | NM_001136023.3:c.578_581del;p.(Asn193Ilefs*12) | InDel         | 24.6    |

**Abbreviations:** VAF, variant allele frequency; InDel, insertion/deletion variant; UPN, unique patient number.
**Supplemental Table 6: Paired-sample sequencing results for 11 patients undergoing bilateral hip replacements.**

| Hip pair  | Variant                        | Hip 1 |       |       |       |       |       |       |       |
|-----------|--------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|
|           |                                | Variant reads | VAF [%] |       | Variant reads | VAF [%] |       |       |       |
| UPN_2     | *ASXL1*: c.2083C>T; p.(Gln695*) | 29/2307 | 1.29   | 2/4015 | NA     | <.0001 |
|           | *JAK2*: c.1849G>T, p.(Val617Phe) | 94/1577 | 5.96   | 141/2589 | 5.45  | .49   |
|           | *DNMT3A*: c.2141C>G; p.(Ser714Cys) | 20/2358 | 0.85   | 67/5779 | 1.15   | .24   |
| UPN_248   | *ASXL1*: c.2258_2259dup; p.(Thr754Profs*19) | 9/2779 | 0.32   | 144/2950 | 4.88  | <.0001 |
|           | *TET2*: c.5165del; p.(Pro1722Leufs*23) | 432/1485 | 29.09 | 450/1495 | 30.1  | .55   |
|           | *TET2*: c.5481_5482del; p.(Gln1828Alafs*17) | 549/1644 | 33.39 | 575/1780 | 32.3  | .51   |
|           | *SH2B3*: c.1522dup; p.(Arg508Profs*38) | 565/1535 | 36.81 | 679/1680 | 40.42 | .04   |
| UPN_242   | *ASXL1*: c.2885_2886del; p.(Val962Alafs*7) | 18/1402 | 1.28   | 40/2143 | 1.87   | .22   |
| UPN_243   | *TET2*: c.2919C>A; p.(Cys973*) | 26/1544 | 1.68   | 9/477  | 1.89   | .84   |
| UPN_73    | *NOTCH1*: c.7541_7542delCT; p.Pro2514fs | 11/552  | 1.99   | 7/503  | 1.39   | .49   |
| UPN_26    | *DNMT3A*: c.2332G>A; p.(Val778Met) | 76/1498 | 5.07   | 80/1688 | 4.74   | .68   |
| UPN_251   | *TET2*: c.5618T>C; p.(Ile1873Thr) | 25/2851 | 0.88   | 28/2252 | 1.15   | .21   |
|           | *DNMT3A*: c.2530A>G; p.(Lys844Glu) | 13/1447 | 0.90   | 20/1285 | 1.45   | .16   |
| UPN_250   | *TET2*: c.2375C>A; p.(Ser792*) | 23/1988 | 1.1    | 17/1785 | 0.95   | .63   |
| UPN_249   | No variants identified          | NA     | NA     | NA     | NA     | NA     |
| UPN_240   | No variants identified          | NA     | NA     | NA     | NA     | NA     |
| UPN_241   | No variants identified          | NA     | NA     | NA     | NA     | NA     |

**Footnotes:** Variants that were detected by manual inspection of sequencing reads are highlighted in red.

**Abbreviations:** VAF, variant allele frequency; NA, not applicable; UPN, unique patient number.
Supplemental material to Hartmann, Hecker et al.

**Supplemental Table 7: Allelic burden of eight flow-sorted subpopulations and bulk of five ASXL1 mutated individuals.**

| Subject | ASXL1 (NM_015338.6) variant | VAF in flowsorted cell fractions |
|---------|-----------------------------|----------------------------------|
|         | bulk | CD34⁺ | HSC | CMP | MEP | GMP | CD15⁺ | CD3⁺ | CD19⁺ |
| UPN_226 | c.2179G>T;p.(Glu727*) | 1.70 | 2.94 | 2.33 | 3.97 | 6.00 | 2.29 | 1.42 | 0.00 | 0.53 |
| UPN_1   | c.2036dup;p.(Gly680Argfs*38) | 3.31 | 3.81 | 2.64 | 5.56 | 9.86 | 3.79 | 7.91 | 0.23 | 0.54 |
|         | c.2385del;p.(Trp796Glyfs*22) | 4.72 | 8.93 | 8.79 | 11.42 | 9.68 | 5.48 | 7.57 | 0.00 | 0.00 |
| UPN_4   | c.1934dup;p.(Gly646Trpfs*12) | 7.38 | 11.60 | 12.23 | 12.70 | 19.67 | 10.60 | 7.58 | 5.12 | 11.11 |
| UPN_5   | c.1934dup;p.(Gly646Trpfs*12) | 9.24 | 12.18 | 13.37 | 12.93 | 5.13 | 10.64 | 4.83 | 1.23 | 8.82 |
| UPN_3   | c.2954_2957del;p.(Ile985Thrfs*7) | 4.90 | 6.15 | 18.11 | 13.58 | 6.48 | 2.56 | 1.17 | 0.00 | 0.34 |

**Abbreviations:** HSC, hematopoietic stem cells; CMP, common-myeloid progenitors; MEP, megakaryocyte-erythroid progenitors; GMP, granulocyte-monocyte progenitors; VAF, variant allele frequency; UPN, unique patient number.
### Supplemental Table 8: Statistical analyses of differential clonal involvement of flow-sorted subpopulations and bulk marrow in ASXL1-mutated individuals.

Corrected $p$-values are indicated for the analysis of each pair of subpopulations using Fisher’s test followed by correction for multiple hypothesis testing using the Benjamini-Hochberg procedure. Significant differences are indicated in red.

| UPN  | HSC | CO34+ | CMP | GMP | MEP | CO33+ | CD13+ | CD15+ | bulk |
|------|-----|-------|-----|-----|-----|-------|-------|-------|------|
| NM_015336.6:c.2169G>T | 1.00 | 1.00 | 0.81 | 0.78 | 0.60 | 0.59 | 0.52 | 0.42 | 0.36 |
| NM_015336.6:c.2584dup6 | 0.64 | 0.74 | 0.76 | 0.71 | 0.65 | 0.60 | 0.60 | 0.60 | 0.60 |
| NM_015336.6:c.2584dup6 | 0.35 | 0.33 | 0.33 | 0.34 | 0.33 | 0.33 | 0.33 | 0.33 | 0.33 |
| NM_015336.6:c.2584dup6 | 0.74 | 0.77 | 0.77 | 0.77 | 0.77 | 0.77 | 0.77 | 0.77 | 0.77 |

**Abbreviations:** HSC, hematopoietic stem cells; CMP, common-myeloid progenitors; MEP, megakaryocyte-erythroid progenitors; GMP, granulocyte-monocyte progenitors; VAF, variant allele frequency; UPN, unique patient number.
Supplemental Table 9: Longitudinal analysis in the baseline non-CH cohort over a time of up to 24 months.

Variants highlighted in red were not called during primary data analysis, but detected upon manual inspection of sequencing reads.

| Subject | Gene   | Variant                                                                 | Screening | 6 mo | 12 mo | 18 mo | 24 mo |
|---------|--------|--------------------------------------------------------------------------|-----------|------|-------|-------|-------|
| UPN_281 | none   | none                                                                     | none      | none | none  | NA    | NA    |
| UPN_284 | none   | none                                                                     | none      | none | none  | NA    | NA    |
| UPN_285 | none   | none                                                                     | none      | none | none  | NA    | NA    |
| UPN_102 | DNMT3A | NM_175629.2:c.[1257delT]; p.(Lys420Argfs*231)                            | 0.70      | NA   | 1.32  | NA    | 2.00  |
| UPN_103 | none   | none                                                                     | none      | NA   | none  | none  | NA    |
| UPN_104 | none   | none                                                                     | none      | NA   | none  | NA    | NA    |
| UPN_105 | none   | none                                                                     | none      | NA   | none  | NA    | NA    |
| UPN_106 | PRPF8  | NM_006445.4:c.3361A>G; p.(Asn1121Asp)                                     | 0.91      | 0.82 | 1.02  | 1.20  | NA    |
| UPN_107 | none   | none                                                                     | none      | NA   | none  | NA    | NA    |
| UPN_108 | none   | none                                                                     | none      | NA   | none  | NA    | NA    |
| UPN_109 | none   | none                                                                     | none      | NA   | none  | NA    | NA    |
| UPN_110 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_111 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_112 | none   | none                                                                     | none      | NA   | none  | NA    | NA    |
| UPN_113 | none   | none                                                                     | none      | none | none  | NA    | NA    |
| UPN_114 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_115 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_116 | none   | none                                                                     | none      | none | none  | NA    | NA    |
| UPN_117 | none   | none                                                                     | none      | none | none  | NA    | NA    |
| UPN_118 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_119 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_120 | ASXL1  | NM_015338.6:c.2036dup; p.(Gly680Argfs*38)                                | 1.16      | 1.78 | NA    | NA    | NA    |
| UPN_121 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_122 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_124 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_126 | none   | none                                                                     | none      | none | NA    | NA    | NA    |
| UPN_127 | none   | none                                                                     | none      | NA   | none  | NA    | NA    |

Abbreviations: VAF, variant allele frequency; mo, months; NA, not analyzed; UPN, unique patient number.
Supplemental Table 10: Longitudinal analysis of CH temporal evolution over a time of up to 18 months.

Bold font indicates variants that emerged or dropped below the limit of detection during follow-up. Variants in red were not called during primary data analysis, but detected upon manual inspection of sequencing reads.

| Subject | Gene | Variant | Screening | VAF [%] |
|---------|------|---------|-----------|---------|
| UPN_49  | DNMT3A | c.2727T>A; p.(Phe909Leu) | 1.85 | 1.19 | 2.20 | NA |
|         | SF3B1  | c.1997A>C; p.(Lys666Thr) | 9.01 | 6.97 | 9.25 | NA |
| UPN_85  | TET2   | c.3858delC; p.(Trp1295*) | 2.81 | 3.71 | 5.05 | 4.53 |
| UPN_18  | DNMT3A | c.2092T>G; p.(Trp698Gly) | 5.77 | 7.57 | 4.75 | 4.54 |
| UPN_75  | TET2   | c.980C>G; p.(Ser327*) | 1.50 | 2.42 | 1.41 | 1.85 |
|         | TET2   | c.3817T>C; p.(Cys1273Arg) | 3.44 | 3.05 | 4.33 | 3.95 |
|         | PPM1D  | c.1545_1546delGT; p.(Met515Leufs*12) | 1.82 | 2.93 | 3.56 | 2.9 |
| UPN_65  | DNMT3A | c.2458G>T; p.(Glu820*) | 2.20 | 1.70 | 2.99 | NA |
|         | DNMT3A | c.1851+1G>A; p.? | 2.57 | 3.70 | 3.99 | NA |
|         | DNMT3A | c.2580G>A; p.(Trp860*) | 1.21 | 1.00 | 0.39 | NA |
| UPN_6   | ASXL1  | c.2512_2537dup; p.(Ser846Argfs*5) | 11.42 | 11.320 | 9.19 | NA |
|         | ETV6   | c.844dup;p.(Arg282Profs*18) | 0.58 | 1.40 | 0.30 | NA |
| UPN_19  | DNMT3A | c.2195T>C; p.(Phe732Ser) | 1.15 | 0.89 | 0.95 | NA |
| UPN_20  | DNMT3A | c.2591T>A; p.(Met864Lys) | 21.29 | 15.28 | 9.38 | NA |
| UPN_21  | DNMT3A | c.2047_2056del; p.(Tyr683Thrfs*19) | 3.41 | 5.23 | 3.68 | NA |
| UPN_76  | PPM1D  | c.1638delC; p.(Leu546*) | 2.66 | 1.31 | 2.04 | NA |
| UPN_23  | DNMT3A | c.1506delT; p.(Thr503Profs*148) | 4.73 | 4.07 | NA | NA |
| UPN_80  | SF3B1  | c.2230G>C; p.(Ala744Pro) | 2.61 | 8.73 | 3.80 | NA |
| UPN_78  | TET2   | c.1081C>T; p.(Gln361*) | 1.37 | NA | 1.20 | NA |
| UPN_32  | DNMT3A | c.2204A>G; p.(Tyr735Cys) | 2.60 | 1.04 | 2.64 | NA |
| UPN_12  | DNMT3A | c.2567_2568delAG; p.(Glu856Glyfs*7) | 1.56 | 0.56 | NA | NA |
| UPN_87  | TET2   | c.670G>T; p.(Glu224*) | 2.16 | 1.92 | NA | NA |
| UPN_86  | TET2   | c.5127dup;p.(Thr1710Tyrfs*3) | 1.66 | 1.89 | NA | NA |
| UPN_29  | DNMT3A | c.2322+2T>C; p.? | 1.35 | NA | NA | 1.13 |
| UPN_282 | DNMT3A | c.2190_2215del; p.(Phe731*) | 10.81 | 20.92 | NA | NA |
| UPN_283 | DNMT3A | c.890G>C; p.(Trp297Ser) | 1.65 | 2.31 | NA | NA |
|         | DNMT3A | c.2207G>A; p.(Arg736His) | 5.68 | 6.87 | NA | NA |
|         | SF3B1  | c.1997A>G; p.(Lys666Arg) | 2.69 | 3.70 | NA | NA |
| ASXL1   | c.1934dup;p.(Gly646Trpfs*12) | 0.68 | 1.16 | NA | NA |
| UPN_7   | ASXL1  | c.2644C>T; p.(Gln882*) | 1.05 | NA | ND | NA |
|         | ZBTB7A | c.1228T>A; p.(Tyr410Asn) | 2.89 | NA | 1.88 | NA |

Abbreviations: VAF, variant allele frequency; ND, not detected; mo, months; NA, not analyzed; UPN, unique patient number
**Supplemental Table 11: Variants identified in patients with MDS or sAML.**

| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| MDS_1   | CBL  | NM_005188.3:c.1244G>A: p.(Gly415Asp) | Missense | 38.0    |
| MDS_1   | TET2 | NM_001127208.2:c.3404G>A: p.(Cys1135Tyr) | Missense | 36.8    |
| MDS_1   | TP53 | NM_000546.5:c.827C>G: p.(Ala276Gly) | Missense | 25.1    |
| MDS_2   | DDX41| NM_016222.c.1574G>A: p.R525H | Missense | 4.3     |
| MDS_2   | DNMT3A | NM_175629.2:c.2645G>A: p.(Arg982His) | Missense | 4.7     |
| MDS_3   | BCOR | NM_001123385.2:c.3649del: p.(Arg1217Aspfs*21) | InDel | 32.3    |
| MDS_3   | BCORL1 | NM_021946.4:c.4230dup: p.(Glu1411*) | InDel | 4.9     |
| MDS_3   | DNMT3A | NM_175629.2:c.2644C>A: p.(Arg882Ser) | Missense | 19.3    |
| MDS_3   | NRAS | NM_002524.5:c.38G>T: p.(Gly13Val) | Missense | 14.3    |
| MDS_3   | U2AF1 | NM_001025203.1:c.101C>T: p.(Ser34Phe) | Missense | 20.3    |
| MDS_4   | RAD21 | NM_006265.3:c.742C>G: p.(Leu248Val) | Missense | 37.1    |
| MDS_4   | SF3B1 | NM_012433.3:c.2098A>G: p.(Lys700Glu) | Missense | 42.6    |
| MDS_4   | TET2 | NM_001127208.2:c.3854_3856del: p.(Phe1285del) | InDel | 30.5    |
| MDS_4   | TET2 | NM_001127208.2:c.3197_3198dup: p.(Arg1067Leufs*16) | InDel | 34.0    |
| MDS_5   | BCOR | NM_001123385.2:c.2340dup: p.(Thr781Hisfs*36) | InDel | 9.5     |
| MDS_5   | ETNK1 | NM_018638.4:c.731A>G: p.(Asn244Ser) | Missense | 5.5     |
| MDS_5   | RUNX1 | NM_001754.4:c.431T>C: p.(Leu144Pro) | Missense | 18.8    |
| MDS_5   | SRSF2 | NM_003016.4:c.284C>G: p.(Pro95Arg) | Missense | 25.8    |
| MDS_5   | TET2 | NM_001127208.2:c.3908G>A: p.(Ser1303Asn) | Missense | 16.1    |
| MDS_5   | TET2 | NM_001127208.2:c.1630C>T: p.(Arg544*) | Nonsense | 27.0    |
| MDS_6   | IDH1 | NM_005896.3: c.394C>T: p.(Thr132Asp) | Missense | 4.3     |
| MDS_7   | SRSF2 | NM_003016.4:c.284C>G: p.(Pro95Arg) | Missense | 11.6    |
| MDS_7   | TET2 | NM_001127208.2:c.2147G>T: p.(Ser716*) | Nonsense | 10.3    |
| MDS_7   | RUNX1 | NM_001754.4:602G>A: p.(Glu138Lys) | Missense | 11.9    |
| MDS_7   | STAG2 | NM_001042750.2:c.1644dup: p.(Thr548Leufs*11) | InDel | 20.6    |
| MDS_7   | BCOR | NM_001123385.2:c.2972_2976del: p.(Leu991Profs*25) | InDel | 21.9    |
| MDS_8   | BCORL1 | NM_021946.4:c.1202C>T: p.(Thr401Met) | Missense | 19.5    |
| MDS_8   | GATA2 | NM_001145661.2:c.952G>A: p.(Ala318Thr) | Missense | 17.3    |
| MDS_8   | RUNX1 | NM_001754.4:c.749delinsCC: p.(Arg250Profs*11) | InDel | 15.7    |
| MDS_8   | SF3B1 | NM_012433.3:c.2098A>G: p.(Lys700Glu) | Missense | 18.0    |
| MDS_9   | SF3B1 | NM_012433.3:c.2098A>G: p.(Lys700Glu) | Missense | 52.5    |
| MDS_9   | TET2 | NM_001127208.2:c.4636C>T: p.(Gln1546*) | Nonsense | 43.7    |
| MDS_10  | TET2 | NM_001127208.2:c.4210C>T: p.(Arg1404*) | Nonsense | 2.9     |
| MDS_10  | TET2 | NM_001127208.2:c.3781C>T: p.(R1261C) | Missense | 20.3    |
| MDS_10  | ZRSR2 | NM_005089.3:c.900_901del: p.(Glu300Asps*16) | InDel | 39.0    |
| MDS_11  | ASXL1 | NM_015338.8:c.2904dup: p.(Asp969*) | InDel | 20.6    |
| MDS_11  | TET2 | NM_001127208.2:c.1813-2A>G: p.? | Splice site | 2.4     |
| MDS_11  | TET2 | NM_001127208.2:c.4352del: p.(Arg1516*) | Nonsense | 17.6    |
| MDS_11  | TET2 | NM_001127208.2:c.4546C>T: p.(Arg1516*) | Nonsense | 22.4    |
| MDS_11  | TP53 | NM_000546.5:c.665C>T: p.(Phe222Leu) | Missense | 40.2    |
| MDS_11  | U2AF1 | NM_001025203.1:c.470A>C: p.(Gln157Pro) | Missense | 20.2    |
| Subject | Gene   | Variant                                                                 | Mutation type | VAF [%] |
|---------|--------|-------------------------------------------------------------------------|---------------|---------|
| MDS_12  | ASXL1  | NM_015338.6:c.1900_1922del;p.(Glu635Argfs*15)                           | InDel         | 2.1     |
| MDS_12  | ASXL1  | NM_015338.6:c.2082_2092del;p.(Gln695Alafs*19)                           | InDel         | 15.3    |
| MDS_12  | ETNK1  | NM_018638.4:c.731A>G;p.(Asn244Ser)                                      | Missense      | 5.3     |
| MDS_12  | U2AF1  | NM_001025203.1:c.470A>C;p.(Gln157Pro)                                   | Missense      | 20.2    |
| MDS_13  | SETBP1 | NM_015559.3:c.2082_2092del;p.(Gln695Alafs*19)                           | InDel         | 21.9    |
| MDS_13  | SETBP1 | NM_015559.3:c.2602G>A;p.(Asp868Asn)                                     | Missense      | 4.7     |
| MDS_13  | SF3B1  | NM_012433.3:c.2098A>G;p.(Lys700Glu)                                     | Missense      | 26.4    |
| MDS_13  | TET2   | NM_001127208.2:c.4956del;p.(Gln1652Hisfs*43)                             | InDel         | 1.1     |
| MDS_13  | TET2   | NM_001127208.2:c.4097G>A;p.(Gly1370Arg)                                 | Missense      | 3.8     |
| MDS_13  | TET2   | NM_001127208.2:c.5071del;p.(Ser1691Leufs*4)                              | Missense      | 7.7     |
| MDS_15  | U2AF1  | NM_018638.4:c.284C>T;p.(Pro95Leu)                                       | Missense      | 13.8    |
| MDS_15  | DNMT3A | NM_0175629.2:c.1531del;p.(Ser777Argfs*30)                                | Missense      | 6.0     |
| MDS_15  | TP53   | NM_000546.4:c.377A>G;p.(Tyr592*)                                       | Nonsense      | 22.6    |
| MDS_15  | KRAS   | NM_001754.4:c.1274C>T;p.(Pro425Leu)                                     | Missense      | 14.2    |
| MDS_15  | RUNX1  | NM_001754.4:c.422C>T;p.(Ser141Leu)                                      | Missense      | 1.9     |
| MDS_15  | DNMT3A | NM_001754.4:c.412G>T;p.(Gly138*)                                       | Nonsense      | 23.6    |
| MDS_15  | MPL    | NM_001754.4:c.1771T>G;p.(Tyr591Asp)                                     | Missense      | 41.0    |
| MDS_15  | TET2   | NM_001127208.2:c.2553del;p.(Glu852Asnfs*21)                              | InDel         | 30.0    |
| MDS_15  | TET2   | NM_001127208.2:c.2243del;p.(Leu748Tyrfs*3)                               | InDel         | 20.0    |
| MDS_15  | TET2   | NM_001127208.2:c.3784C>T;p.(Arg1262Trp)                                 | Missense      | 7.6     |
| MDS_15  | SRSF2  | NM_003016.4:c.284C>T;p.(Pro95Leu)                                       | Missense      | 1.5     |
| MDS_15  | ASXL1  | NM_015338.5:c.1900_1922del;p.(Glu635Argfs*15)                           | InDel         | 35.0    |
| MDS_15  | EZH2   | NM_014466.4:c.190A>T;p.(Lys661*)                                       | Nonsense      | 45.0    |
| MDS_15  | RUNX1  | NM_001754.4:c.492_493insGG;p.(Arg166Valfs*11)                           | InDel         | 13.0    |
| MDS_15  | STAG2  | NM_001042749.2:c.1117G>G;p.(Asn366Asn)                                  | Splice site   | 9.0     |
| MDS_15  | TET2   | NM_001127208.2:c.4075C>T;p.(Arg1359Cys)                                 | Missense      | 12.0    |
| MDS_15  | TET2   | NM_001127208.2:c.1326delC;p.(Glu138*)                                   | Nonsense      | 2.0     |
| MDS_16  | ASXL1  | NM_015338.5:c.1934dup;p.(Pro95Leu)                                      | Missense      | 22.0    |
| MDS_16  | ASXL1  | NM_015338.5:c.1900_1922del;p.(Glu635Argfs*15)                           | InDel         | 52.0    |
| MDS_16  | ASXL1  | NM_015338.5:c.1934dup;p.(Pro95Leu)                                      | InDel         | 37.0    |
| MDS_16  | ASXL1  | NM_015338.5:c.1900_1922del;p.(Glu635Argfs*15)                           | InDel         | 22.0    |
| MDS_16  | JAK2   | NM_001025203.1:c.470A>C;p.(Gln157Pro)                                   | Missense      | 21.9    |
| MDS_16  | RUNX1  | NM_001754.4:c.1167dup;p.(Gln390Alafs*210)                                | InDel         | 34.0    |
| MDS_16  | ASXL1  | NM_015338.5:c.1900_1922del;p.(Glu635Argfs*15)                           | InDel         | 22.0    |
| MDS_16  | CBL    | NM_001518.3:c.1249C>A;p.(Pro417Thr)                                     | Missense      | 21.0    |
| MDS_16  | ETNK1  | NM_0018638.4:c.728A>G;p.(Asn442Lysfs*5)                                  | Missense      | 18.0    |
| MDS_16  | EZH2   | NM_004546.4:c.540delA;p.(Glu180Hisfs*61)                                 | InDel         | 36.0    |
| MDS_16  | TET2   | NM_001127208.2:c.3594+3A>G;p.(Ser1196fs*5)                              | Missite       | 20.0    |
| MDS_18  | SRSF2  | NM_003016.4:c.284C>T;p.(Pro95Leu)                                       | Missense      | 27.0    |
| MDS_18  | TET2   | NM_001127208.2:c.4956del;p.(Gln1652Hisfs*43)                             | InDel         | 41.0    |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| MDS_22  | TET2 | NM_001127208.2:c.4138C>T; p.(His1380Tyr) | Missense | 35.0 |
| MDS_22  | ZRSR2| NM_005089.3:c.491del; p.(Val164Glufs*74) | InDel | 72.0 |
| MDS_23  | SF3B1| NM_012433.3:c.2098A>G; p.(Lys700Glu) | Missense | 82.0 |
| MDS_24  | DNMT3A| NM_175629.2:c.2645G>C; p.(Arg882Pro) | Missense | 32.0 |
| MDS_24  | SF3B1| NM_012433.3:c.1866G>T; p.(Glu622Asp) | Missense | 36.0 |
| MDS_24  | TET2 | NM_001127208.2:c.5618T>C; p.(Ile1873Thr) | Missense | 16.0 |
| MDS_25  | DNMT3A| NM_175629.2:c.2206C>T; p.(Arg736Cys) | Missense | 12.0 |
| MDS_25  | RUNX1| NM_001754.4:c.611G>A; p.(Arg204Gln) | Missense | 38.0 |
| MDS_26  | MPL  | NM_005373.2:c.1544G>T; p.(Trp515Leu) | Missense | 56.0 |
| MDS_26  | TET2 | NM_001127208.2:c.2713del; p.(Asp905Ilefs*16) | Missense | 35.0 |
| MDS_27  | RUNX1| NM_001754.4:c.356_358dup; p.(Val119dup) | InDel | 3.0 |
| MDS_27  | TP53 | NM_000546.5:c.814G>A; p.(Val272Met) | Missense | 13.0 |
| MDS_27  | TP53 | NM_000546.5:c.273G>A; p.(Trp91*) | Nonsense | 10.0 |
| MDS_28  | ASXL1| NM_015338.5:c.1934dup (p.Gly646Trpfs*12) | InDel | 23.0 |
| MDS_28  | KIT  | NM_000222.2:c.2447A>T; p.(Asp816Val) | Missense | 12.0 |
| MDS_28  | SETBP1| NM_015559.3:c.2608G>A; p.(Gly870Ser) | Missense | 6.0 |
| MDS_28  | STAT3| NM_139276.2:c.1846G>A; p.(Glu616Lys) | Missense | 2.6 |
| MDS_28  | STAT3| NM_139276.2:c.743G>A; p.(Arg248Gln) | Missense | 7.0 |
| MDS_29  | DNMT3A| NM_175629.2:c.1093T>A; p.(Tyr365Asn) | Missense | 4.0 |
| MDS_29  | SRSF2| NM_003016.4:c.284C>T; p.(Pro95Leu) | Missense | 1.4 |
| MDS_29  | TET2 | NM_001127208.2:c.4211_4217del; p.(Arg1404Leufs*42) | InDel | 23.0 |
| MDS_30  | SRSF2| NM_003016.4:c.284C>A; p.(Pro95His) | Missense | 25.0 |
| MDS_31  | STAG2| NM_01042749.2:c.3034G>T; p.(Arg1012*) | Nonsense | 31.0 |
| MDS_31  | BCOR | NM_01123385.1:c.2375del; p.(Asn792Ilefs*15) | InDel | 4.7 |
| MDS_31  | DNMT3A| NM_175629.2:c.2098C>G; p.(Pro700Ala) | Missense | 1.1 |
| MDS_32  | SF3B1| NM_012433.3:c.2098A>G; p.(Lys700Glu) | Missense | 27.0 |
| MDS_32  | TET2 | NM_001127208.2:c.4109G>A; p.(Gly1370Glu) | Missense | 30.0 |
| MDS_33  | SF3B1| NM_012433.3:c.2098A>G; p.(Lys700Glu) | Missense | 27.0 |
| MDS_33  | ASXL2| NM_018263.5:442C>T; p.(Gln148*) | Nonsense | 35.0 |
| MDS_34  | FLT3 | FLT3-ITD (66nt) | InDel | 27.0 |
| MDS_34  | SF3B1| NM_012433.3:c.2098A>G; p.(Lys700Glu) | Missense | 37.0 |
| MDS_35  | MPL  | NM_005373.2:c.1654-1T>A | Splice site | 15.3 |
| MDS_35  | DNMT3A| NM_175629.2:c.788_789dup; p.(Asn263Serfs*53) | InDel | 33.0 |
| MDS_35  | SF3B1| NM_012433.3:c.2098A>G; p.(Lys700Glu) | Missense | 37.0 |
| MDS_35  | TET2 | NM_001127208.2:c.1389_1411del; p.(Ile464Tyrfs*23) | InDel | 42.0 |
| MDS_35  | TET2 | NM_001127208.2:c.2872_2873delCA; p.(Gln958Glu*13) | InDel | 36.0 |
| MDS_35  | TET2 | NM_001127208.2:c.4075G>T; p.(Gln1359Ser) | Missense | 6.3 |
| MDS_36  | DNMT3A| NM_175629.2:c.1851+5G>A; p.(Arg617Gln) | Splice site | 3.8 |
| Subject   | Gene        | Variant                                                                 | Mutation type | VAF [%] |
|-----------|-------------|--------------------------------------------------------------------------|---------------|---------|
| MDS_36    | TP53        | NM_000546.5:c.466_477dup; p.(Arg156_AlA159dup)                           | InDel         | 3.0     |
| MDS_37    | DNMT3A      | NM_175629.2:c.1475-1G>C; p.?                                             | Splice site   | 44.0    |
| MDS_37    | SF3B1       | NM_012433.3:c.1972T>G; p.(Trp658Gly)                                      | Missense      | 21.0    |
| MDS_37    | SF3B1       | NM_012433.3:c.1973G>T; p.(Trp658Leu)                                     | Missense      | 6.0     |
| MDS_37    | SF3B1       | NM_012433.3:c.1866G>C; p.(Glu622Asp)                                     | Missense      | 2.1     |
| MDS_38    | RUNX1       | NM_001754.4:c.611G>A; p.(Arg204Gln)                                      | Missense      | 6.0     |
| MDS_38    | RUNX1       | NM_001754.4:c.602G>A; p.(Arg201Gln)                                      | Missense      | 2.3     |
| MDS_38    | RUNX1       | NM_001754.4:c.860G>A; p.(Arg201Gln)                                      | Missense      | 6.0     |
| MDS_38    | RUNX1       | NM_001754.4:c.1454_1455delTG; p.(Val485Glufs*4)                         | InDel         | 15.0    |
| MDS_38    | TP53        | NM_000546.5:c.646G>A; p.(Val216Met)                                      | Missense      | 7.0     |
| MDS_38    | TP53        | NM_000546.5:c.743G>A; p.(Arg248Gln)                                      | Missense      | 2.2     |
| MDS_39    | TET2        | NM_001127208.2:c.3646C>T; p.(Arg1216*)                                  | Nonsense      | 23.0    |
| MDS_39    | TET2        | NM_001127208.2:c.1454_1455delTG; p.(Val485Glufs*4)                      | InDel         | 15.0    |
| MDS_40    | U2AF1       | NM_001025203.1:c.101C>T; p.(Ser34Phe)                                    | Missense      | 24.0    |
| MDS_41    | DDX41       | NM_016222.4:c.209dup; p.(Arg71Profs*4)                                   | InDel         | 39.0    |
| MDS_41    | TERT        | ENST00000310581:c.3037C>T; p.[His1013Tyr]                               | Missense      | 1.3     |
| MDS_42    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 46.4    |
| MDS_42    | SF3B1       | NM_012433.3:c.1997A>G; p.(Lys666Arg)                                     | Missense      | 32.0    |
| MDS_42    | SH2B3       | NM_005475.2:c.1090T>C;p.(Trp364Arg)                                      | Missense      | 2.8     |
| MDS_42    | ASXL1       | NM_015338.5:c.1934dup; (p.Gly646Trps*12)                                 | InDel         | 19.0    |
| MDS_43    | IDH1        | NM_005896.3:c.395G>A; p.(Arg132His)                                      | Missense      | 1.4     |
| MDS_43    | IDH2        | NM_002168.3:c.419G>A; p.(Arg140Gln)                                      | Missense      | 27.0    |
| MDS_43    | SRSF2       | NM_003016.4:c.284C>G; p.(Pro95Arg)                                       | Missense      | 29.0    |
| MDS_44    | STAG2       | NM_001042749.2:c.3097C>T; p.(Arg1033*)                                  | Nonsense      | 36.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 24.0    |
| MDS_44    | SH2B3       | NM_005475.2:c.1090T>C;p.(Trp364Arg)                                      | Missense      | 2.8     |
| MDS_44    | ASXL1       | NM_015338.5:c.1934dup; (p.Gly646Trps*12)                                 | InDel         | 19.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 46.4    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 32.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 32.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 32.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 32.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 32.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 32.0    |
| MDS_44    | SF3B1       | NM_012433.3:c.2098A>G; p.(Lys700Glu)                                     | Missense      | 32.0    |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| MDS_50 | DNMT3A | NM_175629.2:c.2309C>T; p.(Ser770Leu) | Missense | 29.0 |
| MDS_50 | SF3B1 | NM_012433.3:c.1984C>T; p.(His662Tyr) | Missense | 33.0 |
| MDS_51 | DNMT3A | NM_175629.2:c.2645G>A; p.(Arg882His) | Missense | 19.0 |
| MDS_51 | DNMT3A | NM_175629.2:c.1667+1G>A; p.? | Splice site | 2.3 |
| MDS_51 | SF3B1 | NM_012433.3:c.2098A>G; p.(Lys700Glu) | Missense | 19.0 |
| MDS_51 | TET2 | NM_001127208.2:c.4263C>G; p.(Tyr1421*) | Nonsense | 1.4 |
| MDS_52 | ASXL1 | NM_015338.5:c.2290dup;p.(Leu764Profs*10) | InDel | 1.3 |
| MDS_52 | CBL | NM_005188.3:c.1202G>C; p.(Cys401Ser) | Missense | 1.3 |
| MDS_52 | TET2 | NM_001127208.2:c.3764dup;p.(Tyr1255*) | InDel | 87.0 |
| MDS_53 | ASXL1 | NM_015338.5:c.1934dup;p.(Gly646Trpfs*12) | InDel | 12.0 |
| MDS_53 | MPL | NM_005373.2:c.1775G>A;p.(Arg592Gln) | Missense | 15.0 |
| MDS_53 | TET2 | NM_001127208.2:c.3894dup;p.(Lys1299*) | InDel | 16.0 |
| MDS_54 | ASXL1 | NM_015338.5:c.1819_1820delGG;p.(Gly607Leufs*11) | InDel | 14.0 |
| MDS_54 | SF3B1 | NM_012433.3:c.1874G>T;p.(Arg625Leu) | Missense | 30.0 |
| MDS_54 | TET2 | NM_001127208.2:c.3658delA;p.(Thr1220Profs*6) | InDel | 7.7 |
| MDS_55 | DNMT3A | NM_175629.2:c.1429+1G>A; p.? | Splice site | 1.5 |
| MDS_56 | DNMT3A | NM_175629.2:c.2612delC;p.(Pro871Glnfs*10) | InDel | 23.4 |
| MDS_56 | SRSF2 | NM_003016.4:c.284_307delCCCCGGACTCACACCAGCCGCC;p.(Pro95Arg82His) | Missense | 3.7 |
| MDS_56 | TET2 | NM_001127208.2:c.3894dup;p.(Lys1299*) | Splice site | 10.0 |
| MDS_57 | ASXL1 | NM_015338.5:c.1819_1820delGG;p.(Gly607Leufs*11) | InDel | 1.1 |
| MDS_57 | SF3B1 | NM_012433.3:c.1874G>T;p.(Arg625Leu) | Missense | 6.4 |
| MDS_57 | TET2 | NM_001127208.2:c.3658delA;p.(Thr1220Profs*6) | InDel | 2.2 |
| MDS_58 | RAD21 | NM_006265.3:c.1064C>T;p.(Pro355Leu) | Missense | 21.4 |
| MDS_58 | SRSF2 | NM_003016.4:c.284_307delCCCCGGACTCACACCAGCCGCC;p.(Pro95Arg82His) | Missense | 21.4 |
| MDS_58 | TET2 | NM_001127208.2:c.4044+1G>C;p.? | Splice site | 3.0 |
| MDS_59 | ASXL1 | NM_015338.5:c.1934dup;p.(Gly646Trpfs*12) | InDel | 26.0 |
| MDS_59 | SRSF2 | NM_003016.4:c.284_307delCCCCGGACTCACACCAGCCGCC;p.(Pro95Arg82His) | Missense | 4.2 |
| MDS_59 | TET2 | NM_001127208.2:c.4044+1G>C;p.? | Splice site | 4.0 |
| MDS_60 | RUNX1 | NM_001754.4:c.292delC;p.(Leu98Serfs*24) | InDel | 1.7 |
| MDS_60 | SRSF2 | NM_003016.4:c.284_307delCCCCGGACTCACACCAGCCGCC;p.(Pro95Arg82His) | Missense | 3.8 |
| MDS_60 | TET2 | NM_001127208.2:c.3862dup>G;p.(Gly1288Arg) | Missense | 4.0 |
| MDS_60 | TET2 | NM_001127208.2:c.327delC;p.(Lys110Argfs*3) | InDel | 3.0 |
| MDS_61 | ASXL1 | NM_015338.5:c.1934dup;p.(Gly646Trpfs*12) | InDel | 2.2 |
| MDS_61 | BRAF | NM_001354609.2:c.602A>G;p.(Gln201Arg) | Missense | 44.0 |
| MDS_61 | EZH2 | NM_004456.5:c.324delC;p.(Ile109*) | InDel | 51.0 |
| MDS_61 | FLT3 | NM_004119.3:c.2523C>A;p.(Asn841Lys) | Missense | 40.0 |
| MDS_61 | GATA2 | NM_001145661.2:c.229+1G>T;p.? | Splice site | 40.0 |
| MDS_61 | RUNX1 | NM_001754.4:c.[1207_1210del];p.(His404Leufs*197) | InDel | 4.2 |
| MDS_61 | RUNX1 | NM_001754.4:c.[951_952delT];p.(Ser318Glnfs*281) | InDel | 34.0 |
| MDS_62 | ASXL1 | NM_015338.5:c.1934dup;p.(Gly646Trpfs*12) | InDel | 12.3 |
| MDS_62 | CEBPA | NM_004364.c.514C>T;p.(Gln172*) | Nonsense | 19.0 |
| Subject | Gene  | Variant                                                                 | Mutation type | VAF [%] |
|---------|-------|--------------------------------------------------------------------------|---------------|---------|
| MDS_62  | SF3B1 | NM_012433.3:c.1873C>T;p.(Arg625Cys)                                      | Missense      | 15.0    |
| MDS_62  | STAG2 | NM_001042750.2STAG2:c.1907dup;p.(Tyr636*)                                | InDel         | 30.0    |
| MDS_62  | TET2  | NM_001127208.2:c.1813_1814delTA;p.(Tyr605Hisfs*32)                      | InDel         | 8.4     |
| MDS_62  | TET2  | NM_001127208.2:c.5456delT;p.(Leu1819*)                                  | InDel         | 18.0    |
| MDS_63  | MPL   | NM_005373.3:c.545C>A; p.(Pro182His)                                      | Missense      | 16.3    |
| MDS_63  | NOTCH1| ENST00000277541:c.7541_7542delCT:p.Pro2514fs                            | InDel         | 1.6     |
| MDS_63  | TET2  | NM_001127208.2:c.4029_4030insC; p.(Ala1344Argfs*3)                      | InDel         | 34.6    |
| MDS_64  | CBL   | NM_005188.3:c.1222T>G:p.(Trp408Gly)                                      | Missense      | 16.3    |
| MDS_64  | MPL   | NM_005373.3:c.545C>A; p.(Pro182His)                                      | Missense      | 16.3    |
| MDS_64  | TET2  | NM_001127208.2:c.822del;p.(Asn275Ilefs*18)                               | InDel         | 3.1     |
| MDS_65  | CSF3R | NM_156039.3:c.2302C>T;p.(Gln768*)                                       | Nonsense      | 2.5     |
| MDS_65  | TP53  | NM_000546.5:c.394C>T p.(Arg132Cys)                                       | Missense      | 3.5     |
| MDS_65  | TN1   | NM_0015559.3:c.2608G>A; (p.Gly870Ser)                                   | Missense      | 40.7    |
| MDS_65  | U2AF1 | NM_001025203.1:c.470A>C p.(Gln157Pro)                                   | Missense      | 6.9     |
| MDS_65  | ASXL1 | NM_015338.6:c.1804G>T;p.(Glu602*)                                       | Nonsense      | 39.8    |
| MDS_66  | CBL   | NM_005188.3:c.1151G>T;p.(Cys383Phe)                                      | Missense      | 13.4    |
| MDS_66  | TP53  | NM_000546.5:c.427G>A; p.(Val143Met)                                      | Missense      | 27.4    |
| MDS_66  | IDH1  | NM_005896.3:c.394C>T p.(Arg132Cys)                                       | Missense      | 3.5     |
| MDS_66  | RUNX1 | NM_001754.4:c.293T>C; p.(Leu98Pro)                                      | Missense      | 30.3    |
| MDS_66  | U2AF1 | NM_001025203.1:c.470A>C p.(Gln157Pro)                                   | Missense      | 36.1    |
| MDS_67  | ASXL1 | NM_015338.6:c.1804G>T;p.(Glu602*)                                       | Nonsense      | 39.8    |
| MDS_67  | CALR  | NM_004343.3.c.1099_1150del;p.(Leu367Thrfs*46)                           | Indel         | 1.8     |
| MDS_67  | EZH2  | NM_001754.4:c.731A>G;p.(Asn244Ser)                                      | Missense      | 7.8     |
| MDS_67  | SETBP1| NM_003016.4:c.284C>T p.(Pro95Leu)                                       | Missense      | 27.9    |
| MDS_67  | ZRSR2 | NM_005089.3:c.1318_1319insCGGCC;p.(Arg440Profs*?)                       | InDel         | 36.0    |
| MDS_68  | CALR  | NM_004343.3.c.1099_1150del;p.(Leu367Thrfs*46)                           | Indel         | 1.8     |
| MDS_68  | SF3B1 | NM_012433.3:c.1986C>G;p.(His662Gln)                                     | Missense      | 42.7    |
| Subject | Gene     | Variant            | Mutation type | VAF [%] |
|---------|----------|--------------------|---------------|---------|
| MDS_75  | DDX41    | NM_016222.2:c.1127C>T;p.(Ala376Val) | Missense      | 6.0     |
| MDS_75  | DNMT3A   | NM_175629.2:c.2723A>C;p.(Tyr908Ser)  | Missense      | 11.9    |
| MDS_75  | TET2     | NM_001127208.2:c.3865T>G;p.(Cys1289Gly) | Missense      | 2.0     |
| MDS_76  | DNMT3A   | NM_175629.2:c.2645G>A;p.(Arg882His)  | Missense      | 14.3    |
| MDS_76  | TET2     | NM_001127208.2:c.1397del;p.(Ser466Leufs*20) | InDel      | 4.6     |
| MDS_76  | DNMT3A   | NM_175629.2:c.2327A>G;p.(Asn776Ser)  | Missense      | 17.9    |
| MDS_77  | SF3B1    | NM_012433.3:c.2098A>G;p.(Lys700Glu)  | Missense      | 5.0     |
| MDS_77  | RAD21    | NM_006265.3:c.415_419del;p.(Arg139Glyfs*19) | InDel | 4.6     |
| MDS_77  | TET2     | NM_001127208.2:c.1397del;p.(Ser466Leufs*20) | InDel      | 2.2     |
| MDS_77  | DDX41    | NM_016222.2:c.4546C>T;p.(Arg1516*)  | Nonsense      | 20.3    |
| MDS_77  | DNMT3A   | NM_175629.2:c.3014-3A>G;p.(Tyr1005fs) | Splice site   | 43.8    |
| MDS_78  | TET2     | NM_001127208.2:c.3410-4A>G;p.?      | Splice site   | 36.5    |
| MDS_78  | DDX41    | NM_016222.2:c.3410-4A>G;p.?      | Splice site   | 36.5    |
| MDS_78  | DNMT3A   | NM_175629.2:c.1302del;p.(Val435Cysfs*216) | InDel      | 44.9    |
| MDS_78  | TET2     | NM_001127208.2:c.1397del;p.(Ser466Leufs*20) | InDel      | 2.2     |
| MDS_78  | JAK2     | NM_004972.3:c.1849G>T;p.(Val617Phe)  | Missense      | 2.5     |
| MDS_78  | RAD21    | NM_006265.3:c.559+1G>T,p.?        | Splice site   | 11.0    |
| MDS_78  | TET2     | NM_001127208.2:c.3410-4A>G;p.?      | Splice site   | 36.5    |
| MDS_80  | SRSF2    | NM_003016.4:c.284C>A;p.(Pro95His)   | Missense      | 35.2    |
| MDS_80  | ASXL1    | NM_015338.6:c.1904_1905del;p.(Glu635Glyfs*22) | InDel | 37.6    |
| MDS_80  | RUNX1    | NM_001754.4:c.998dup;p.(Arg334Alafs*266) | InDel | 33.8    |
| MDS_80  | KRAS     | NM_004333.4:c.437C>T;p.(Ala146Val)  | Missense      | 20.3    |
| MDS_80  | ZBTB7A   | NM_015338.6:c.2182G>T;p.(Glu728*)   | Nonsense      | 41.0    |
| MDS_81  | SRSF2    | NM_003016.4:c.284C>A;p.(Pro95His)   | Missense      | 46.6    |
| MDS_81  | ASXL1    | NM_015338.6:c.2182G>T;p.(Glu728*)   | Nonsense      | 41.0    |
| MDS_81  | U2AF1    | NM_001025203.1:c.470A>G;p.(Gln157Arg) | Splice site   | 11.0    |
| MDS_82  | TET2     | NM_001127208.2:c.3671del;p.(Ala1224Glufs*2) | InDel      | 1.8     |
| MDS_82  | TP53     | NM_000546.5:c.559+1G>T;p.?        | Splice site   | 36.5    |
| MDS_82  | SRSF2    | NM_003016.4:c.284C>A;p.(Pro95His)   | Missense      | 35.2    |
| MDS_82  | ASXL1    | NM_015338.6:c.2182G>T;p.(Glu728*)   | Nonsense      | 86.0    |
| AML_1   | ASXL1    | NM_015338:exon12:c.1927dupG;p.G642fs | InDel | 11.6    |
| AML_1   | BCR      | NM_001123385:exon7:c.3446_3447del;p.A1149fs | InDel | 63.9    |
| AML_1   | BCR      | NM_001123385:exon7:c.3444_3446G  | InDel | 35.2    |
| AML_1   | CSF3R    | NM_156039:exon17:c.2436_2437insGCAG;p.S813fs | InDel | 1.2     |
| AML_1   | IDH2     | NM_002168:exon4:c.419G>A;p.R140Q  | Missense      | 32.7    |
| AML_1   | NRAS     | NM_002524:exon4:c.35G>T;p.G12V   | Missense      | 18.9    |
| AML_1   | PHF6     | NM_032458:exon9:c.954dupA;p.S318fs | InDel | 5.9     |
| AML_1   | RUNX1    | NM_001754:exon9:c.1141_1142insCGCC;p.L381fs | InDel | 31.8    |
| AML_1   | SRSF2    | NM_003016:exon1:c.284C>A;p.P95H   | Missense      | 2.5     |
| AML_1   | STAG2    | NM_001042750:exon15:c.1409delA;p.E470fs | InDel | 61.0    |
| AML_1   | TET2     | NM_001127208:exon3:c.2692G>T;p.G898X | Nonsense      | 4.0     |
| AML_2   | ASXL1    | NM_015338:exon12:c.1927dupG;p.G642fs | InDel | 18.4    |
| AML_2   | CEBPA    | NM_004364:exon1:c.898C>T;p.R300C  | Missense      | 25.1    |
| AML_2   | RUNX1    | NM_001754:exon4:c.317G>T;p.W106L | Missense      | 33.8    |
| AML_2   | STAG2    | NM_001042750:exon24:c.2308C>T;p.Q770X | Nonsense | 27.6    |
| AML_2   | U2AF1    | NM_001025203:exon6:c.470A>G;p.Q157P  | Missense      | 28.8    |
| AML_3   | ASXL1    | NM_015338:exon12:c.1927dupG;p.G642fs | InDel | 15.2    |
| AML_3   | BRAF     | NM_004333:c.1790T>A;p.L597Q   | Missense      | 90.5    |
| Subject | Gene  | Variant                  | Mutation type | VAF [%] |
|---------|-------|--------------------------|---------------|---------|
| AML_3   | EZH2  | NM_004456:exon19:c.2186T>C:p.F729S | Missense      | 92.3    |
| AML_3   | IDH2  | NM_002168:exon4:c.419G>A:p.R140Q | Missense      | 46.4    |
| AML_3   | RUNX1 | NM_001754:exon4:c.329A>C:p.K110T | Missense      | 3.1     |
| AML_3   | STAG2 | NM_001042750:exon20:c.1840C>T:p.R614X | Nonsense     | 5.5     |
| AML_3   | STAG2 | NM_001042750:exon21:c.2086_2096del:p.A696fs | InDel       | 7.9     |
| AML_3   | STAG2 | NM_001042750:exon31:c.3394_3395insTA:p.L1132fs | InDel       | 27.9    |
| AML_4   | ASXL1 | NM_015338:exon12:c.2160delC:p.D720fs | InDel       | 42.9    |
| AML_4   | RUNX1 | NM_001754:exon6:c.610C>T:p.R204X | Nonsense      | 38.6    |
| AML_4   | SRSF2 | NM_001042750:exon2:c.101C>A:p.S34Y | Missense     | 52.4    |
| AML_5   | FLT3  | NM_004119:exon20:c.2508_2510del:p.836_837del | InDel       | 7.2     |
| AML_5   | U2AF1 | NM_001025203:exon2:c.101C>T:p.S34F | Missense     | 50.9    |
| AML_6   | ASXL1 | NM_001754:exon5:c.369dupT:p.V124fs | InDel       | 47.2    |
| AML_6   | RUNX1 | NM_001754:exon9:c.1007_1008insAGGGCCC:p.F336fs | InDel       | 41.0    |
| AML_6   | SRSF2 | NM_001042750:exon28:c.2857C>T:p.R953X | Nonsense     | 26.2    |
| AML_6   | TET2  | NM_001127208:exon3:c.757_770del:p.N253fs | InDel       | 40.0    |
| AML_7   | IDH1  | NM_005896:exon4:c.394C>T:p.R132C | Missense      | 44.6    |
| AML_7   | RUNX1 | NM_001754:exon5:c.369dupT:p.V124fs | Missense      | 47.2    |
| AML_7   | SRSF2 | NM_001042750:exon2:c.101C>A:p.S34Y | Missense     | 52.4    |
| AML_8   | BCOR  | NM_001123385:exon11:c.1422C>T:p.G1422A | Splice site  | 50.8    |
| AML_8   | BCORL1| NM_001123385:exon11:c.1422C>T:p.G1422A | Splice site  | 50.8    |
| AML_8   | DNMT3A| NM_00175629:exon23:c.2644C>T:p.R882C | Missense     | 56.4    |
| AML_8   | KIT   | NM_000222:exon8:c.1256_1261del:p.419_421del | InDel       | 41.3    |
| AML_8   | RUNX1 | NM_001754:exon9:c.1007_1008insAGGGCCC:p.F336fs | InDel       | 41.0    |
| AML_8   | SF3B1 | NM_0012433:exon15:c.2409C>T:p.K700E | Missense     | 49.0    |
| AML_9   | DNMT3A| NM_00175629:exon23:c.2645G>A:p.R882H | Missense     | 34.5    |
| AML_9   | IDH2  | NM_0012433:exon15:c.2409C>T:p.K700E | Missense     | 49.0    |
| AML_9   | RUNX1 | NM_001754:exon9:c.1015_1016insAGGGCCC:p.S333fs | InDel       | 50.2    |
| AML_9   | RUNX1 | NM_001754:exon9:c.1015_1016insAGGGCCC:p.S333fs | InDel       | 50.2    |
| AML_10  | ET6V  | NM_001987:exon3:c.313_314insT:p.R105fs | Missense     | 37.7    |
| AML_10  | FLT3  | NM_004119:exon14:c.1769_1770insTCAGCCCATCCTGACATCTCAAGATAATGACATT:p.F590delinsFQPIGGSDNEYF | InDel       | 25.3    |
| AML_10  | NPM1  | NM_002520:exon10:c.805_806insGGGCCG:p.I269delinsRAL | InDel       | 37.9    |
| AML_11  | DNMT3A| NM_00175629:exon23:c.1474+1G>A,p.? | Splice site  | 46.5    |
| AML_11  | FLT3  | NM_004119:exon14:c.1799_1800insTCAGCCCATCCTGACATCTCAAGATAATGACATT:p.F590delinsFQPIGGSDNEYF | InDel       | 1.2     |
| AML_11  | RUNX1 | NM_001754:exon5:c.356dupT:p.V119fs | InDel       | 29.0    |
| AML_11  | RUNX1 | NM_001754:exon4:c.299_300insATCGCAGAGGAGCA:p.S100delinsSSORSN | InDel       | 9.5     |
| AML_11  | STAG2 | NM_001042750:exon28:c.2857C>T:p.R953X | Nonsense     | 26.2    |
| AML_11  | U2AF1 | NM_001025203:exon2:c.101C>T:p.S34Y | Missense     | 52.4    |
| AML_11  | SRSF2 | NM_001042750:exon2:c.101C>T:p.S34Y | Missense     | 52.4    |
| AML_12  | ASXL1 | NM_0015338:exon12:c.1888_1910del:p.H630fs | InDel       | 33.9    |
| AML_12  | IDH2  | NM_002168:exon4:c.419G>A:p.R140Q | Missense     | 47.0    |
| AML_12  | STAG2 | NM_001042750:exon20:c.1840C>T:p.R614X | Nonsense     | 46.4    |
| AML_12  | STAG2 | NM_001042750:exon29:c.3034C>T:p.R1012X | Nonsense     | 65.2    |
| AML_12  | NRAS  | NM_002524:exon2:c.38G>A:p.G13D | Missense     | 39.8    |
| Subject | Gene     | Variant                                                                 | Mutation type | VAF [%] |
|---------|----------|--------------------------------------------------------------------------|---------------|---------|
| AML_13  | SF3B1    | NM_012433:exon15:c.2098A>G:p.K700E                                       | Missense      | 32.0    |
| AML_14  | ASXL1    | NM_015338:exon12:c.1888_1910del:p.630_637del                            | InDel         | 43.7    |
| AML_14  | BCOR     | NM_001123385:exon7:c.3490C>T:p.R1164X                                    | Nonsense      | 94.2    |
| AML_14  | DNMT3A   | NM_175629:exon18:c.2163G>C:p.K721N                                       | Missense      | 89.3    |
| AML_14  | ETV6     | NM_001987:exon3:c.164-2A>G:p.74_A1                                    | Splice site   | 44.5    |
| AML_14  | N-RAS    | NM_002524:exon2:c.35G>A:p.G12D                                          | Missense      | 53.1    |
| AML_14  | PTPN11   | NM_002834:exon3:c.181G>T:p.D61Y                                         | Missense      | 12.9    |
| AML_14  | RUNX1    | NM_001754:exon7:c.664delT:p.S222fs                                      | InDel         | 39.5    |
| AML_15  | KIT      | NM_000222:exon17:c.2447A>T:p.D816V                                       | Missense      | 38.3    |
| AML_15  | N-RAS    | NM_002524:exon3:c.183A>G:p.Q61H                                         | Missense      | 5.7     |
| AML_15  | N-RAS    | NM_002524:exon3:c.182A>G:p.Q61R                                         | Missense      | 21.0    |
| AML_15  | PTPN11   | NM_002834:exon3:c.226G>A:p.E76K                                         | Missense      | 14.7    |
| AML_16  | SF3B1    | NM_012433:exon15:c.2098A>G:p.K700E                                       | Missense      | 44.7    |
| AML_16  | CEBP-A   | NM_004364:exon1:c.175G>T:p.E59X                                         | Nonsense      | 76.7    |
| AML_16  | CSF3R    | NM_156039:exon15:c.1919C>A:p.T640N                                       | Missense      | 18.4    |
| AML_16  | RUNX1    | NM_001754:exon9:c.1354G>A:p.V452M                                        | Missense      | 57.5    |
| AML_16  | SRSF2    | NM_003016:exon1:c.284C>A:p.P95H                                         | Missense      | 41.6    |
| AML_16  | STAG2    | NM_001042750:exon11:c.1015delA:p.K339fs                                  | InDel         | 28.5    |
| AML_16  | TET2     | NM_001127208:exon3:c.3315_3316del:p.I1105fs                              | InDel         | 44.1    |
| AML_16  | TET2     | NM_001127208:exon6:c.3796A>G:p.N1266D                                     | Missense      | 49.1    |
| AML_16  | WT1      | NM_024426:exon7:c.1099-1G>A:p.7                                         | Splice site   | 12.5    |
| AML_17  | ASXL1    | NM_015338:exon12:c.2058_2059del:p.K686fs                                 | InDel         | 45.3    |
| AML_17  | B-COR    | NM_001123385:exon11:c.4540C>T:p.R1514X                                   | Nonsense      | 38.9    |
| AML_17  | N-RAS    | NM_002524:exon2:c.35G>A:p.G12D                                          | Missense      | 48.0    |
| AML_17  | RUNX1    | NM_001754:exon4:c.245_246insAGCA:p.L82fs                                 | InDel         | 56.0    |
| AML_17  | SRSF2    | NM_003016:exon1:c.284C>A:p.P95H                                         | Missense      | 44.4    |
| AML_17  | STAG2    | NM_001042750:exon9:c.775C>T:p.R259X                                      | Nonsense      | 45.1    |
| AML_17  | TET2     | NM_001127208:exon5:c.3589A>G:p.K1197E                                     | Missense      | 47.6    |
| AML_18  | ASXL1    | NM_015338:exon12:c.1888_1910del:p.630_637del                            | InDel         | 25.8    |
| AML_18  | IDH2     | NM_002168:exon4:c.515G>A:p.R172K                                         | Missense      | 21.7    |
| AML_18  | PTPN11   | NM_002834:exon13:c.1517A>C:p.Q506P                                       | Missense      | 14.4    |
| AML_18  | RUNX1    | NM_001754:exon6:c.610C>T:p.R204X                                         | Nonsense      | 36.9    |
| AML_18  | RUNX1    | NM_001754:exon6:c.592G>A:p.D198N                                         | Missense      | 4.1     |
| AML_18  | SRSF2    | NM_003016:exon1:c.284C>A:p.P95H                                         | Missense      | 37.4    |
| AML_18  | TET2     | NM_001127208:exon11:c.4834_4835del:p.1612_1612del                        | InDel         | 40.8    |
| AML_19  | ASXL1    | NM_015338:exon12:c.2084delA:p.Q695fs                                     | InDel         | 2.0     |
| AML_19  | SRSF2    | NM_003016:exon1:c.284C>A:p.P95H                                         | Missense      | 44.9    |
| AML_19  | TET2     | NM_001127208:exon3:c.2218C>T:p.Q740X                                     | Nonsense      | 48.3    |
| AML_19  | TET2     | NM_001127208:exon7:c.3863G>A:p.G1288D                                     | Missense      | 44.5    |
| AML_20  | IDH2     | NM_002168:exon4:c.419G>A:p.R140Q                                         | Missense      | 44.0    |
| AML_21  | DNMT3A   | NM_175629:exon23:c.2645G>A:p.R882H                                       | Missense      | 48.6    |
| AML_22  | DNMT3A   | NM_175629:exon23:c.2644C>T:p.R882C                                       | Missense      | 45.8    |
| AML_22  | FLT3     | NM_004119:exon20:c.2503G>T:p.D835Y                                       | Missense      | 7.6     |
| AML_22  | RUNX1    | NM_001754:exon9:c.978_979insG:p.L327fs                                   | InDel         | 46.1    |
| AML_22  | SF3B1    | NM_012433:exon15:c.2098A>G:p.K700E                                       | Missense      | 49.8    |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| AML_23  | GATA2| NM_001145661:exon7:c.1160_1171del:p.387_391del | InDel | 33.7 |
| AML_23  | NRAS | NM_002524:exon3:c.181T>A:p.Q61K | Missense | 39.8 |
| AML_24  | NPM1 | NM_002520:exon11:c.861_862insTGCA:p.L287fs | InDel | 27.5 |
| AML_24  | PTPN11| NM_002834:exon3:c.179G>T:p.G60V | Missense | 2.3 |
| AML_24  | RAD21| NM_006265:exon6:c.640C>T:p.Q214X | Nonsense | 2.6 |
| AML_25  | ASXL2| NM_018263:exon11:c.1771_1772insCCCCACTGAGAATC:p.R591fs | InDel | 47.2 |
| AML_25  | FLT3 | NM_004119:exon14:c.1802_1803insCTCACCTAATGAGAATATGATCT:p.L601delinsLDFREYEYDL | InDel | 4.1 |
| AML_26  | FL3 | NM_004119:exon13:c.1800_1801insTTCAGAGAATATGAT:p.L601delinsFREYEYDL | InDel | 23.9 |
| AML_26  | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 38.4 |
| AML_27  | KRAS | NM_033360:exon2:c.38G>A:p.G13D | Missense | 20.7 |
| AML_27  | NPM1 | NM_002520:exon11:c.861_862insTGCA:p.L287fs | InDel | 46.2 |
| AML_28  | MPL | NM_005373:exon10:c.1544G>T:p.W515L | Missense | 2.2 |
| AML_28  | U2AF1| NM_001025203:exon6:c.470A>C:p.Q157P | Missense | 20.4 |
| AML_28  | DDX41| NM_016222:exon15:c.1574G>A:p.R525H | Missense | 7.8 |
| AML_29  | TET2 | NM_002834:exon3:c.182A>G:p.D61G | Missense | 0.7 |
| AML_30  | BCORl1| NM_00123385:exon4:c.1000dupC:p.S336fs | InDel | 44.3 |
| AML_30  | BCOR | NM_00123385:exon4:c.1000dupC:p.S336fs | InDel | 44.3 |
| AML_30  | KRAS | NM_00123385:exon4:c.1000dupC:p.S336fs | InDel | 44.3 |
| AML_30  | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 54.2 |
| AML_30  | PTPN11| NM_002834:exon3:c.182A>G:p.D61G | Missense | 4.5 |
| AML_30  | RAD21| NM_006265:exon2:c.59C>T:p.A20V | Missense | 3.7 |
| AML_31  | BCOR | NM_00123385:exon4:c.1000dupC:p.S336fs | InDel | 44.3 |
| AML_31  | KRAS | NM_00123385:exon4:c.1000dupC:p.S336fs | InDel | 44.3 |
| AML_31  | CEBPA | NM_004364:exon1:c.1000G>A:p.E334K | Missense | 34.1 |
| AML_32  | DNMT3A| NM_175629:exon23:c.2644C>T:p.R882C | Missense | 42.9 |
| Subject  | Gene   | Variant                                                                 | Mutation type | VAF [%] |
|---------|--------|--------------------------------------------------------------------------|---------------|---------|
| AML_34  | DNMT3A | NM_175629:exon18:c.2173G>A:p.E725K                                       | Missense      | 42.4    |
| AML_34  | JAK2   | NM_004972:exon14:c.1849G>T:p.V617F                                       | Missense      | 14.9    |
| AML_34  | SRSF2  | NM_003016:exon1:c.284C>A:p.P95H                                         | Missense      | 38.1    |
| AML_34  | TET2   | NM_001127208:exon7:c.3894dupT:p.C1298fs                                 | InDel         | 81.9    |
| AML_35  | NPM1   | NM_002520:exon11:c.859_860insTCTG:p.L878fs                               | InDel         | 36.8    |
| AML_35  | STAG2  | NM_001042750:p.?                                                         | Splice site   | 70.8    |
| AML_36  | TP53   | NM_000546:exon7:c.742C>T:p.R248W                                         | Missense      | 96.3    |
| AML_37  | BCOR   | NM_001123385:exon4:c.2962_2963insGT:p.S988fs                             | InDel         | 67.9    |
| AML_37  | IDH2   | NM_004119:exon14:c.1809_1810insAGAGAATATGAATATGATCTCAGATCGTGGATTTCAAGA:p.E596delinsREYEYDFRE | InDel         | 46.0    |
| AML_38  | NPM1   | NM_002520:exon11:c.859_860insTCTG:p.L878fs                               | InDel         | 37.6    |
| AML_38  | SF3B1  | NM_00123385:exon15:c.2098A>G:p.K700E                                     | Missense      | 42.8    |
| AML_38  | TET2   | NM_001127208:exon3:c.2101C>T:p.Q701X                                      | Nonsense      | 50.7    |
| AML_38  | TET2   | NM_001127208:exon3:c.3249_3250A                                         | InDel         | 2.7     |
| AML_38  | TET2   | NM_001127208:exon10:c.4468G>T:p.E1490X                                   | Nonsense      | 42.2    |
| AML_39  | NRAS   | NM_002524:exon13:c.181C>A:p.P61K                                         | Missense      | 43.0    |
| AML_39  | SF3B1  | NM_00123385:exon15:c.2098A>G:p.K700E                                     | Missense      | 49.5    |
| AML_39  | WT1    | NM_0024426:exon7:c.1144_1145insTCCGG:p.A382fs                            | InDel         | 42.6    |
| AML_40  | FLT3   | NM_004119:exon14:c.1809_1810insAGAGAATATGAATATGATCTCAGATCGTGGATTTCAAGA:p.E596delinsREYEYDFRE | InDel         | 8.9     |
| AML_40  | FLT3   | NM_004119:exon14:c.1787_1788insCTTACTACGTTGAGTTTCAAGA:p.E596delinsDFVYDFRE | InDel         | 14.4    |
| AML_40  | FLT3   | NM_004119:exon14:c.1787_1788insGATGGTACAGGTGACCAGCTCCTCAGATAATGAGTACTTCTAGTGTATTTCAAGA:p.E596delinsEMVQVTGSDDNEYFYDFRE | InDel         | 24.4    |
| AML_41  | SF3B1  | NM_00123385:exon15:c.2098A>G:p.K700E                                     | Missense      | 44.6    |
| AML_41  | TP53   | NM_000546:exon10:c.325T>G:p.F109V                                        | Missense      | 82.5    |
| AML_41  | WT1    | NM_0024426:exon10:c.332dupC:p.P111fs                                     | InDel         | 46.0    |
| AML_42  | BCOR   | NM_001123385:exon4:c.1882G>A:p.A628T                                     | Missense      | 2.3     |
| AML_42  | BCOR   | NM_001123385:exon4:c.1240G>A:p.A414T                                      | Missense      | 3.2     |
| AML_42  | FLT3   | NM_004119:exon15:c.1837+3>GATTTCAGAGAATATGAATATGATCTCAGATCGTGGATTTCAAGA:p.E596delinsEMVQVTGSDDNEYFYDFRE | Splice site   | 37.3    |
| AML_42  | STAG2  | NM_001042750:p.?                                                         | Splice site   | 2.1     |
| AML_42  | TP53   | NM_000546:exon10:c.1004G>A:p.R335H                                       | Missense      | 2.4     |
| AML_42  | WT1    | NM_0024426:exon7:c.1144_1145insTCCGG:p.A382fs                            | InDel         | 43.5    |
| AML_43  | PTPN11 | NM_002834:exon3:c.227A>G:p.E76G                                          | Missense      | 21.7    |
| AML_43  | RUNX1  | NM_001754:exon5:c.496C>T:p.R166X                                        | Nonsense      | 37.1    |
| AML_44  | CSF3R  | NM_156039:exon14:c.1853C>T:p.T618I                                       | Missense      | 41.8    |
| AML_44  | GATA2  | NM_001145661:exon7:c.1187G>T:p.R396L                                     | Missense      | 39.4    |
| AML_44  | NRAS   | NM_002524:exon3:c.182A>G:p.Q61K                                         | Missense      | 16.2    |
| AML_44  | SETBP1 | NM_0015559:exon4:c.2608G>A:p.G870S                                       | Missense      | 46.5    |
| AML_44  | U2AF1  | NM_001025203:exon6:c.470A>C:p.Q157P                                       | Missense      | 46.7    |
| Subject  | Gene    | Variant                      | Mutation type | VAF [%] |
|----------|---------|------------------------------|---------------|---------|
| AML_44   | WT1     | NM_024426:exon2:c.749dupT:p.M250fs | InDel         | 78.7    |
| AML_45   | ASXL1   | NM_015338:exon12:c.1926dupA:p.G642fs | InDel         | 31.1    |
| AML_45   | ETV6    | NM_001987:exon4:c.329-2A>G,p.? | Splice site   | 49.0    |
| AML_45   | RUNX1   | NM_001754:exon7:c.676_677del:p.S226fs | InDel         | 46.7    |
| AML_45   | SRSF2   | NM_003016:exon1:c.284C>G:p.P95R | Missense      | 49.0    |
| AML_45   | TET2    | NM_001127208:exon3:c.2490dupA:p.I830fs | InDel         | 37.9    |
| AML_46   | ASXL1   | NM_015338:exon12:c.1888_1910del:p.H630fs | InDel         | 36.1    |
| AML_46   | ETV6    | NM_001987:exon4:c.749dupT:p.M250fs | InDel         | 78.7    |
| AML_46   | FLT3    | NM_004119:exon14:1769_1770insGCCTAGAATAACGCTACAGATGGTACAGGTGACCGCTCTCAGATAATGAGTACTTCTACGTGATTTCAGAGA:p.F590delinsLPQITGSSDNEYFYVDFRE | InDel         | 69.4    |
| AML_46   | GATA2   | NM_001145661:exon4:c.416_417del:p.S139fs | InDel         | 41.2    |
| AML_46   | PTPN11  | NM_002834:exon3:c.215C>A:p.A72D | Missense      | 4.8     |
| AML_46   | RUNX1   | NM_001754:exon7:c.623dupA:p.Q208fs | InDel         | 34.6    |
| AML_46   | SRSF2   | NM_003016:exon1:c.284C>A:p.P95H | Missense      | 41.0    |
| AML_46   | TET2    | NM_001127208:exon3:c.2490dupA:p.I830fs | InDel         | 37.9    |
| AML_47   | ASXL1   | NM_015338:exon12:c.1888_1910del:p.H630fs | InDel         | 36.1    |
| AML_47   | DDX41   | NM_016222:exon2:c.121C>T:p.Q41X | Nonsense      | 48.8    |
| AML_47   | IDH1    | NM_005896:exon4:c.394C>T:p.R132C | Missense      | 8.3     |
| AML_48   | RUNX1   | NM_001754:exon7:c.623dupA:p.Q208fs | InDel         | 34.6    |
| AML_48   | SRSF2   | NM_003016:exon1:c.284C>A:p.P95H | Missense      | 41.0    |
| AML_48   | STAG2   | NM_001042750:exon13:c.1117-1->GATA,p.? | Splice site   | 12.5    |
| AML_49   | DNMT3A  | NM_175629:exon8:c.958C>T:p.Q1430X | Nonsense      | 32.9    |
| AML_49   | IDH1    | NM_005896:exon4:c.394C>T:p.R132C | Missense      | 48.4    |
| AML_49   | NPM1    | NM_002520:exon11:c.861_862insTGCA:p.L287fs | InDel         | 50.2    |
| AML_50   | DNMT3A  | NM_175629:exon17:c.1936+3G>A,p.? | Splice site   | 66.2    |
| AML_50   | TET2    | NM_001127208:exon11:c.5633G>A:p.R1878H | Missense      | 40.1    |
| AML_50   | TP53    | NM_000546:exon6:c.596_598del:p.199_200del | InDel         | 4.3     |
| AML_50   | TP53    | NM_000546:exon5:c.470T>A:p.V157D | Missense      | 83.3    |
| AML_51   | BCOR    | NM_001123385:exon12:c.4647_4649del:p.1549_1550del | InDel         | 17.9    |
| AML_51   | BCORL1  | NM_021946:c.3268C>T:p.R1090X | Missense      | 28.3    |
| AML_51   | BCORL1  | NM_021946:c.3994C>T:p.R132X | Missense      | 10.3    |
| AML_51   | DNMT3A  | NM_175629:exon23:c.2645G>A:p.R882H | Missense      | 50.2    |
| AML_51   | NRAS    | NM_002524:exon4:c.436G>A:p.A146T | Missense      | 3.4     |
| AML_51   | RUNX1   | NM_001754:exon4:c.325A>T:p.N109Y | Missense      | 48.0    |
| AML_51   | STAG2   | NM_001042750:exon28:c.2857C>T:p.R953X | Nonsense      | 48.3    |
| AML_52   | TET2    | NM_001127208:exon3:c.1294G>T:p.E432X | Nonsense      | 53.0    |
| AML_52   | TET2    | NM_001127208:exon6:c.3987delG:p.L1329fs | InDel         | 52.1    |
| AML_53   | FLT3    | NM_004119:exon14:c.1787_1788insTCCCCACCAGCTACAGATGGTACAGGTGACCGCTCTCAGATAATGAGTACTTCTACGTGATTTCAGAGA:p.E596delinsPHQLQMVQVTGSSDNEYFYVDFRE | Nonsense      | 23.8    |
| AML_54   | CBL     | NM_005188:exon8:c.1199T>G:p.M400R | Missense      | 79.0    |
| AML_54   | IDH1    | NM_005896:exon4:c.395G>A:p.R132H | Missense      | 42.3    |
| AML_54   | RUNX1   | NM_001754:exon6:c.611G>A:p.R204Q | Missense      | 8.7     |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| AML_54 | RUNX1 | NM_001754:exon5:c.370_371insGATG:p.V124fs | InDel | 35.0 |
| AML_54 | SRSF2 | NM_003016:exon1:c.284C>G:p.p.P95R | Missense | 46.2 |
| AML_55 | DNMT3A | NM_175629:exon21:c.2409_2410insTAGG:p.Q804delX | Nonsense | 53.9 |
| AML_55 | RUNX1 | NM_001754:exon6:c.602G>A:p.R201Q | Missense | 13.6 |
| AML_55 | SRSF2 | NM_003016:exon1:c.284C>G:p.P95H | Missense | 46.2 |
| AML_55 | ASXL1 | NM_015338:exon12:c.1927dupG:p.G642fs | InDel | 23.0 |
| AML_55 | BCOR | NM_01123385:exon4:c.466_467insCCCCCCAAAACACCCTGGAATAC:p.R156fs | InDel | 59.0 |
| AML_55 | RUNX1 | NM_001754:exon6:c.610C>T:p.R204X | Nonsense | 20.5 |
| AML_55 | SRSF2 | NM_003016:exon1:c.284C>G:p.P95H | Missense | 42.5 |
| AML_55 | ASXL1 | NM_015338:exon12:c.2243delA:p.Q748fs | InDel | 40.8 |
| AML_55 | BCOR | NM_01123385:exon4:c.466_467insCCCCCCAAAACACCCTGGAAT:p.Q156fs | InDel | 47.3 |
| AML_55 | RUNX1 | NM_001754:exon6:c.610C>T:p.R204X | Nonsense | 42.4 |
| AML_55 | CBL | NM_005188:exon8:c.1186T>C:p.C396R | Missense | 29.0 |
| AML_55 | CBL | NM_005188:exon9:c.1250G>A:p.Q417R | Missense | 4.5 |
| AML_55 | FLT3 | NM_004119:exon14:c.1781_1782insGGTT:p.R594delinsLV | InDel | 2.2 |
| AML_55 | SRSF2 | NM_003016:exon1:c.284C>G:p.P95H | Missense | 48.5 |
| AML_55 | TET2 | NM_00127208:exon3:c.1143delC:p.F381fs | InDel | 46.2 |
| AML_55 | TET2 | NM_00127208:exon3:c.1172delC:p.S391fs | InDel | 45.7 |
| AML_60 | BCORL1 | NM_021946:c.3304A>T:p.K1102X | Nonsense | 89.1 |
| AML_60 | ETV6 | NM_021946:c.3304A>T:p.K1102X | Nonsense | 23.1 |
| AML_60 | FLT3 | NM_004119:exon14:c.1781_1782insGGTT:p.R594delinsLV | InDel | 26.7 |
| AML_60 | NRAS | NM_002524:exon3:c.183A>T:p.Q61H | Missense | 2.5 |
| AML_60 | NRAS | NM_002524:exon2:c.37G>C:p.G12R | Missense | 9.7 |
| AML_61 | ASXL1 | NM_015338:exon12:c.2160delC:p.D720fs | InDel | 48.4 |
| AML_61 | IDH2 | NM_002168:exon4:c.418C>G:p.R140G | Missense | 43.3 |
| AML_61 | KRAS | NM_033360:exon2:c.34G>C:p.G12R | Missense | 3.3 |
| AML_61 | NRAS | NM_002524:exon2:c.35G>T:p.G12V | Missense | 36.7 |
| AML_61 | RUNX1 | NM_001754:exon7:c.694C>T:p.R232W | Missense | 29.3 |
| AML_61 | SRSF2 | NM_003016:exon1:c.284C>G:p.Q95H | Missense | 50.4 |
| AML_61 | STAG2 | NM_001042750:exon17:c.637_639insCTGGAATAC:p.Q156fs | InDel | 94.7 |
| AML_62 | FLT3 | NM_004119:exon14:c.2508_2510del:p.836_837del | InDel | 2.2 |
| AML_62 | IDH1 | NM_008986:exon4:c.395G>C:p.R132H | Missense | 38.4 |
| AML_63 | TP53 | NM_000546:exon8:c.818G>A:p.R273H | Missense | 25.6 |
| AML_63 | TP53 | NM_000546:exon6:c.657delC:p.P219fs | InDel | 23.7 |
| AML_64 | DNMT3A | NM_175629:exon23:c.2645G>A:p.R882H | Missense | 49.0 |
| AML_64 | JAK2 | NM_004972:exon14:c.1849G>T:p.V617F | Missense | 48.0 |
| AML_64 | NRAS | NM_002524:exon2:c.38G>T:p.G13V | Missense | 48.0 |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| AML_64  | STAG2| NM_001042750:exon6:c.328C>T:p.R110X | Nonsense | 48.0 |
| AML_64  | TET2 | NM_001127208:exon3:c.547dupA:p.L182fs | InDel | 50.0 |
| AML_65  | ASXL1| NM_015338:exon12:c.4116_4117del:p.1372_1373del | InDel | 44.7 |
| AML_65  | NRAS | NM_002524:exon2:c.38G>T:p.G13V | Missense | 7.7 |
| AML_65  | RUNX1| NM_001754:exon5:c.492_493insTA:p.G165_R166delinsX | Nonsense | 8.6 |
| AML_65  | SRSF2| NM_003016:exon1:c.284insGCC:p.P95delinsRP | InDel | 47.0 |
| AML_65  | STAG2| NM_001042750:exon21:c.2096+1>T,p.? | Splice site | 71.7 |
| AML_66  | ASXL1| NM_015338:exon12:c.1888_1910del:p.H630fs | InDel | 40.4 |
| AML_66  | NRAS | NM_002524:exon2:c.38G>T:p.G13V | Missense | 7.7 |
| AML_66  | JAK2 | NM_004972:exon14:c.1849G>T:p.V617F | Missense | 3.4 |
| AML_66  | RUNX1| NM_001754:exon4:c.319C>T:p.R107C | Missense | 44.3 |
| AML_66  | SRSF2| NM_003016:exon1:c.284C>A:p.P95H | Missense | 50.8 |
| AML_67  | ASXL1| NM_015338:exon12:c.1888_1910del:p.H630fs | InDel | 40.4 |
| AML_67  | IDH1 | NM_005896:exon4:c.394C>G:p.R132G | Missense | 45.2 |
| AML_67  | JAK2 | NM_004972:exon14:c.1849G>T:p.V617F | Missense | 48.9 |
| AML_67  | RUNX1| NM_001754:exon4:c.319C>T:p.R107C | Missense | 44.3 |
| AML_67  | SRSF2| NM_003016:exon1:c.284C>A:p.P95H | Missense | 50.8 |
| AML_68  | TP53 | NM_000546:exon7:c.743G>A:p.R248Q | Missense | 50.4 |
| AML_68  | FLT3 | NM_004119:exon14:c.1834_1835insATGAATATGATCTCAAA TGGGAGTTTCCAAGAGAAAATTTAGAGTTTGG | InDel | 12.0 |
| AML_68  | FLT3 | NM_004119:exon14:c.1797_1798insCTTAACGTTGATTTCAG AGAATATGAATAT:p.D600delinsLNVDFREYE | InDel | 4.9 |
| AML_68  | FLT3 | NM_004119:exon14:c.1788_1789insGATAATGAGTACTTCTA CGTTGATTTCAGAGAA:p.Y597delinsDYVDFREY | InDel | 3.6 |
| AML_69  | FLT3 | NM_004119:exon15:c.1837+2- >AAAGCGGGTGACCGAGATGAAATGATCTCAATTACAGGAGTTTCCAAGAGAAATTTAGAGTTTGG | Splice site | 2.1 |
| AML_69  | FLT3 | NM_004119:exon14:c.1815_1816insGGAGTTGATTTCAGAGAATATGAATATGATCTCAATTACAGGAGTTT:p.P606delinsGKR VTGSDDNFYVDFREYEDLKWEP | InDel | 11.8 |
| AML_69  | FLT3 | NM_004119:exon14:c.1788_1789insCTACGTTGATTTCAGAGAA:p.Y597delinsDYVDFREY | InDel | 3.6 |
| AML_69  | IDH2 | NM_002168:exon4:c.419G>A:p.R140Q | Missense | 41.1 |
| AML_69  | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 36.8 |
| AML_69  | SRSF2| NM_003016:exon1:c.284C>A:p.P95H | Missense | 29.3 |
| AML_69  | WT1  | NM_024426:exon7:c.1195A>C:p.N399H | Missense | 47.4 |
| AML_70  | BCOR | NM_001123385:exon4:c.524_527del:p.175_176del | InDel | 65.3 |
| AML_70  | NRAS | NM_002524:exon3:c.180_181insGCTCC:p.Q61delinsASQ | InDel | 15.3 |
| AML_70  | RUNX1| NM_001754:exon5:c.495_496insTT:p.R166fs | InDel | 43.3 |
| AML_70  | U2AF1| NM_001025203:exon2:c.101C>T:p.S34F | Missense | 44.6 |
| AML_71  | IDH2 | NM_002168:exon4:c.515G>A:p.R172K | Missense | 35.0 |
| AML_72  | BCOR | NM_001123385:exon11:c.4428+1G>A,p.? | Splice site | 36.2 |
| AML_72  | DNMT3A| NM_175629:exon23:c.2728G>C:p.A910P | Missense | 38.2 |
| AML_72  | DNMT3A| NM_175629:exon8:c.942G>A:p.W314X | Nonsense | 45.8 |
| AML_72  | IDH2 | NM_002168:exon4:c.419G>A:p.R140Q | Missense | 40.2 |
| AML_73  | FLT3 | NM_004119:exon20:c.2503G>T:p.D835Y | Missense | 3.8 |
| AML_73  | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 37.0 |
| AML_73  | NRAS | NM_002524:exon2:c.38G>A:p.G13D | Missense | 14.4 |
| Subject | Gene   | Variant                                                                 | Mutation type | VAF [%] |
|---------|--------|--------------------------------------------------------------------------|---------------|---------|
| AML_73  | PTPN11 | NM_002834:exon3:c.179G>T:p.G60V                                        | Missense      | 3.3     |
| AML_73  | RAD21  | NM_006265:exon8:c.933_934insT:p.T312_V313delinsX                         | Nonsense      | 33.0    |
| AML_74  | FLT3   | NM_004119:exon15:c.1837+1>ATTTCAGAGAATGAAATGATCTCAAAATGGGAGTTTCC         | Splice site   | 7.5     |
| AML_74  | FLT3   | NM_004119:exon14:c.1798_1799insTA:p.T312_V313delinsX                    | InDel         | 33.2    |
| AML_74  | IDH2   | NM_002168:exon4:c.188A>G:p.Y63C                                         | Missense      | 29.2    |
| AML_74  | ASXL1  | NM_015338:exon12:c.1773C>A:p.Y591X                                      | Nonsense      | 23.6    |
| AML_74  | RUNX1  | NM_001754:exon9:c.1003_1013del:p.Q335fs                                 | InDel         | 52.3    |
| AML_74  | IDH1   | NM_005896:exon4:c.395G>A:p.R132H                                        | Missense      | 41.5    |
| AML_75  | FLT3   | NM_004119:exon14:c.1798_1799insTA:p.T312_V313delinsX                    | InDel         | 33.2    |
| AML_75  | IDH1   | NM_005896:exon4:c.395G>A:p.R132H                                        | Missense      | 34.5    |
| AML_75  | ASXL1  | NM_015338:exon12:c.1773C>A:p.Y591X                                      | Nonsense      | 23.6    |
| AML_75  | IDH1   | NM_005896:exon4:c.395G>A:p.R132H                                        | Missense      | 23.6    |
| AML_75  | PTPN11 | NM_002834:exon3:c.188A>G:p.Y63C                                         | Missense      | 29.2    |
| AML_75  | RUNX1  | NM_001754:exon9:c.1003_1013del:p.Q335fs                                 | InDel         | 12.7    |
| AML_75  | RUNX1  | NM_001754:exon6:c.508+1G>T:p.?                                         | Splice site   | 15.7    |
| AML_76  | DNMT3A | NM_175629:exon23:c.2645G>A:p.R882H                                      | Missense      | 35.5    |
| AML_76  | KRAS   | NM_004456:exon11:c.1262_1271del:p.T421fs                                 | InDel         | 52.3    |
| AML_76  | IDH1   | NM_005896:exon4:c.395G>A:p.R132H                                        | Missense      | 33.6    |
| AML_76  | NPM1   | NM_002520:exon11:c.859_860insTCTG:p.L287fs                               | InDel         | 38.3    |
| AML_76  | BCOR   | NM_0123385:exon8:c.3649C>T:p.R1217X                                      | Nonsense      | 16.3    |
| AML_76  | DNMT3A | NM_175629:exon8:c.912delC:p.S304fs                                      | InDel         | 28.3    |
| AML_76  | DNMT3A | NM_175629:exon8:c.912delC:p.S304fs                                      | InDel         | 28.3    |
| AML_76  | NRAS   | NM_004456:exon17:c.1973_1974del:p.R658fs                                 | Missense      | 42.9    |
| AML_76  | RUNX1  | NM_001754:exon9:c.1290dupG:p.P431fs                                     | InDel         | 43.2    |
| AML_76  | U2AF1  | NM_001025203:exon2:c.101C>T:p.S34F                                      | Missense      | 47.8    |
| AML_76  | DDX41  | NM_016222:exon15:c.1586_1587del:p.T529fs                                 | InDel         | 46.8    |
| AML_76  | DNMT3A | NM_175629:exon13:c.1502A>G:p.N501S                                       | Missense      | 54.1    |
| AML_76  | NRAS   | NM_004456:exon17:c.1973_1974del:p.R658fs                                 | Missense      | 60.5    |
| AML_80  | ASXL1  | NM_015338:exon12:c.2084dupA:p.Q698X                                      | Missense      | 39.1    |
| AML_80  | RUNX1  | NM_001754:exon4:c.230dupG:p.S77fs                                       | InDel         | 45.6    |
| AML_80  | SRSF2  | NM_003016:exon1:c.284C>A:p.P959H                                        | Missense      | 40.6    |
| AML_80  | SRSF2  | NM_003016:exon1:c.284C>A:p.P959H                                        | Missense      | 40.6    |
| AML_80  | U2AF1  | NM_001025203:exon2:c.101C>T:p.S34F                                      | Missense      | 47.8    |
| AML_80  | STAG2  | NM_001042750:exon27:c.2694_2695insTGGTAGAGTTGA:p.D898delinsDWX            | Nonsense      | 29.4    |
| AML_81  | ASXL1  | NM_015338:exon12:c.1927dupG:p.G642fs                                     | InDel         | 41.4    |
| AML_81  | EZH2   | NM_004456:exon18:c.2050C>T:p.R684C                                       | Missense      | 9.9     |
| AML_81  | NRAS   | NM_002524:exon2:c.38G>A:p.G13D                                          | Missense      | 42.1    |
| AML_81  | RUNX1  | NM_001754:exon6:c.553C>A:p.Q185K                                        | Missense      | 42.3    |
| AML_81  | SRSF2  | NM_003016:exon1:c.284C>A:p.P959H                                        | Missense      | 50.0    |
| AML_81  | STAG2  | NM_001042750:exon30:c.3097C>T:p.R1033X                                   | Nonsense      | 73.5    |
| AML_82  | ASXL1  | NM_015338:exon12:c.1927dupG:p.G642fs                                     | InDel         | 15.4    |
| AML_82  | PHF6   | NM_032458:exon6:c.442G>T:p.E148X                                         | Missense      | 32.9    |
| AML_82  | U2AF1  | NM_001025203:exon2:c.101C>T:p.S34F                                       | Missense      | 30.1    |
| AML_83  | EZH2   | NM_004456:exon19:c.2161A>G:p.I721V                                       | Missense      | 54.0    |
| AML_83  | FLT3   | NM_004119:exon20:c.2503G>T:p.D835Y                                        | Missense      | 13.4    |
| AML_83  | FLT3   | NM_004119:exon14:c.1796_1796delinsSCCTAGATAATGGATCTTCTACGTTGATTTCAGAATATGAAT | InDel         | 0.5     |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| AML_83  | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 36.3 |
| AML_83  | PTPN11 | NM_002834:exon3:c.179G>C:p.G60A | Missense | 6.8 |
| AML_83  | WT1  | NM_024426:exon7:c.1142C>A:p.S381X | Nonsense | 17.2 |
| AML_83  | ASXL1 | NM_015338:exon12:c.1927dupG:p.G642fs | InDel | 33.3 |
| AML_84  | BCOR | NM_001123385:exon11:c.4455_4456insGG:p.K1486fs | InDel | 80.9 |
| AML_84  | WT1  | NM_024426:exon12:c.252_256del:p.84_86del | InDel | 27.0 |
| AML_84  | EZH2 | NM_004456:exon18:c.2051G>A:p.R684H | Missense | 5.2 |
| AML_84  | HNRNPK | NM_002140:exon16:c.1192-2A>G,? | Splice site | 40.6 |
| AML_84  | STAG2 | NM_001042750:exon19:c.1810C>T;p.R604X | Nonsense | 88.2 |
| AML_84  | ASXL1 | NM_015338:exon12:c.1927dupG:p.G642fs | InDel | 92.5 |
| AML_84  | PTPN11 | NM_002834:exon3:c.179G>T:p.G60V | Missense | 46.2 |
| AML_84  | WT1  | NM_024426:exon12:c.1927dupG:p.G642fs | InDel | 92.5 |
| AML_84  | SRSF2 | NM_003016:exon1:c.284C>A:p.R95H | Missense | 48.8 |
| AML_85  | ASXL1 | NM_015338:exon12:c.1927dupG:p.G642fs | InDel | 27.0 |
| AML_85  | GATA1 | NM_002049:exon3:c.325G>C:p.V109L | Missense | 91.9 |
| AML_85  | IDH2 | NM_002168:exon4:c.1487_1490delinsTGG | InDel | 33.3 |
| AML_85  | SRSF2 | NM_003016:exon1:c.284C>A:p.R95H | Missense | 46.2 |
| AML_85  | STAG2 | NM_001042750:exon19:c.1810C>T;p.R604X | Nonsense | 88.2 |
| AML_85  | NRAS | NM_002524:exon2:c.38G>T:p.G13V | Missense | 39.1 |
| AML_85  | TET2 | NM_001127208:exon6:c.3707T>A:p.I1236N | Missense | 46.2 |
| AML_86  | DNMT3A | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 91.9 |
| AML_86  | NRAS | NM_002524:exon2:c.38G>T:p.G13V | Missense | 39.1 |
| AML_86  | TET2 | NM_001127208:exon11:c.4883_4884insTCCATCATATCAATGCAATGGAAACC:p.Y1628fs | InDel | 13.9 |
| AML_87  | KRAS | NM_003360:exon2:c.35G>T:p.G12V | Missense | 5.1 |
| AML_87  | NRAS | NM_002524:exon2:c.35G>A:p.G12S | Missense | 4.1 |
| AML_87  | TET2 | NM_001127208:exon11:c.4883_4884insTCCATCATATCAATGCAATGGAAACC:p.Y1628fs | InDel | 13.9 |
| AML_88  | DNMT3A | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 12.1 |
| AML_88  | FLT3 | NM_004119:exon15:c.1837+10>AGAATAATGAGTACTTCTACGTTGATTTCAGAGAATATGAATATGATCTCAAATGGGAGTTTCCAAGAGA_AAAATTTAGAGTTTG | InDel | 1.6 |
| AML_89  | ASXL1 | NM_015338:exon12:c.2077C>T:p.R693X | Nonsense | 8.3 |
| AML_89  | SRSF2 | NM_003016:exon1:c.284C>A:p.P95H | Missense | 44.6 |
| AML_89  | STAG2 | NM_001042750:exon19:c.1810C>T;p.R604X | Nonsense | 94.9 |
| AML_89  | NRAS | NM_002524:exon3:c.182A>C:p.Q61P | Missense | 4.1 |
| AML_89  | TET2 | NM_001127208:exon11:c.4883_4884insTCCATCATATCAATGCAATGGAAACC:p.Y1628fs | InDel | 13.9 |
| AML_90  | ASXL1 | NM_015338:exon12:c.2077C>T:p.R693X | Nonsense | 8.3 |
| AML_90  | RUNX1 | NM_001754:exon5:c.374delC:p.P125fs | InDel | 46.0 |
| AML_90  | SRSF2 | NM_003016:exon1:c.284C>A:p.P95H | Missense | 46.0 |
| AML_90  | STAG2 | NM_001042750:exon19:c.1810C>T;p.R604X | Nonsense | 94.9 |
| AML_90  | NRAS | NM_002524:exon3:c.182A>C:p.Q61P | Missense | 4.1 |
| AML_90  | TET2 | NM_001127208:exon11:c.4883_4884insTCCATCATATCAATGCAATGGAAACC:p.Y1628fs | InDel | 13.9 |
| AML_91  | IDH2 | NM_002168:exon4:c.419G>A:p.R140Q | Missense | 6.4 |
| AML_91  | NRAS | NM_002524:exon2:c.38G>T:p.G13V | Missense | 4.3 |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| AML_92  | NRAS | NM_002524:exon2:c.35G>A:p.G12D | Missense | 37.1    |
| AML_92  | RAD21 | NM_006265:exon13:c.1621-1G>T.p.? | Splice site | 39.9    |
| AML_93  | DNMT3A | NM_175629:exon19:c.2311C>T:p.R771X | Nonsense | 51.0    |
| AML_93  | DNMT3A | NM_175629:exon15:c.1687G>A:p.V563M | Missense | 52.1    |
| AML_93  | IDH2  | NM_002168:exon4:c.419G>A:p.R140Q | Missense | 48.2    |
| AML_93  | JAK2  | NM_004972:exon14:c.1849G>T:p.V617F | Missense | 47.6    |
| AML_93  | SRSF2 | NM_003016:exon1:c.284C>A:p.P95H | Missense | 40.1    |
| AML_94  | ASXL1 | NM_015338:exon12:c.1888_1910del:p.630_637del | InDel | 21.5    |
| AML_94  | DNMT3A | NM_175629:exon19:c.2118_2119insAC:p.H706fs | InDel | 8.9     |
| AML_94  | DNMT3A | NM_175629:exon19:c.2255_2257del:p.752_753del | InDel | 47.5    |
| AML_94  | DNMT3A | NM_175629:exon19:c.2206C>T:p.R736C | Missense | 47.6    |
| AML_94  | IDH2  | NM_002168:exon4:c.515G>A:p.R172K | Missense | 45.4    |
| AML_94  | TP53  | NM_000546:exon8:c.844C>T:p.R282W | Missense | 63.0    |
| AML_94  | TP53  | NM_000546:exon4:c.97-2A>G,p.? | Splice site | 20.0    |
| AML_95  | DNMT3A | NM_175629:exon23:c.2645G>A:p.R882H | Missense | 38.5    |
| AML_95  | NRAS  | NM_002524:exon3:c.182A>G:p.Q61R | Missense | 11.2    |
| AML_95  | TP53  | NM_000546:exon8:c.844C>T:p.R282W | Missense | 63.0    |
| AML_95  | TP53  | NM_000546:exon4:c.97-2A>G,p.? | Splice site | 20.0    |
| AML_96  | DNMT3A | NM_175629:exon23:c.2645G>A:p.R882H | Missense | 38.5    |
| AML_96  | NPM1  | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 36.5    |
| AML_96  | NRAS  | NM_002524:exon3:c.182A>G:p.Q61R | Missense | 11.2    |
| AML_96  | U2AF1 | NM_001025203:exon2:c.101C>T:p.S34F | Missense | 41.6    |
| AML_97  | DNMT3A | NM_175629:exon23:c.2711C>T:p.P904L | Missense | 18.7    |
| AML_97  | IDH2  | NM_002168:exon4:c.419G>A:p.R140Q | Missense | 19.6    |
| AML_97  | KRAS  | NM_033360:exon2:c.35G>A:p.G12D | Missense | 2.9     |
| AML_97  | NPM1  | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 31.0    |
| AML_97  | TET2  | NM_001127208:exon3:c.1441C>T:p.Q481X | Nonsense | 34.1    |
| AML_97  | TET2  | NM_001127208:exon3:c.2491C>T:p.Q831X | Nonsense | 56.3    |
| AML_99  | DNMT3A | NM_175629:exon16:c.1906G>T:p.V636L | Missense | 96.3    |
| AML_99  | FLT3  | NM_004119:exon14:c.1810_1811insTAGTTGATTTTGAGAACATGAATATGCTCAATGGG:p.E604delinsVVDFREYEDLKWE | InDel | 29.4    |
| AML_99  | FLT3  | NM_004119:exon14:c.1792_1793insTATGATTTCAGAGAAATATGCTCAATGGG:p.E604delinsVVDFREYEDLKWE | InDel | 12.7    |
| AML_99  | RUNX1 | NM_001754:exon4:c.330_331insT:p.T111fs | InDel | 22.8    |
| AML_100 | ETV6  | NM_001987:exon6:c.1138T>G:p.W380Q | Missense | 25.0    |
| AML_100 | KRAS  | NM_033360:exon3:c.183A>C:p.Q61H | Missense | 14.9    |
| AML_100 | WT1   | NM_024426:exon9:c.1395C>A:p.H465Q | Missense | 5.4     |
| AML_100 | WT1   | NM_024426:exon7:c.1199dupA:p.K400fs | InDel | 3.1     |
| AML_101 | ASXL1 | NM_015338:exon12:c.1927dupG:p.K642fs | InDel | 23.2    |
| AML_101 | KDM6A | NM_021140:exon13:c.1310C>T:p.A437V | Missense | 2.5     |
| AML_101 | RUNX1 | NM_001754:exon9:c.989dupT:p.F330fs | InDel | 39.0    |
| AML_101 | TET2  | NM_001127208:exon7:c.3866G>T:p.C1289F | Missense | 36.4    |
| AML_101 | U2AF1 | NM_001025203:exon6:c.467G>A:p.R156H | Missense | 25.5    |
| AML_102 | BCOR  | NM_001123385:exon13:c.4742_1G>T,p.? | Splice site | 25.0    |
| AML_102 | NRAS  | NM_002524:exon2:c.34G>T:p.G12C | Missense | 13.5    |
| AML_102 | RUNX1 | NM_001754:exon6:c.509-3C>G,p.? | Splice site | 58.8    |
| AML_102 | SF3B1 | NM_012433:exon15:c.2098A>G:p.K700E | Missense | 52.4    |
| AML_102 | TET2  | NM_001127208:exon6:c.3641G>A:p.R1214Q | Missense | 20.0    |
| Subject  | Gene   | Variant                                                                 | Mutation type | VAF [%] |
|----------|--------|--------------------------------------------------------------------------|---------------|---------|
| AML_103  | ASXL1  | NM_015338:exon12:c.1931_1932insGGGT:p.G644fs                            | InDel         | 23.9    |
| AML_103  | RUNX1  | NM_001754:exon5:c.496C>T:p.R166X                                         | Nonsense      | 42.1    |
| AML_103  | SRSF2  | NM_003016:exon1:c.284C>A:p.P95H                                          | Missense      | 39.5    |
| AML_103  | TET2   | NM_001127208:exon3:c.1937_1938insAGTG:p.T646fs                           | InDel         | 28.0    |
| AML_103  | TET2   | NM_001127208:exon6:c.3782G>A:p.R1261H                                    | Missense      | 23.7    |
| AML_104  | RUNX1  | NM_001754:exon5:c.508G>C:p.G170R                                         | Missense      | 42.1    |
| AML_104  | RUNX1  | NM_001754:exon5:c.508G>C:p.G170R                                         | Missense      | 26.8    |
| AML_104  | RUNX1  | NM_001754:exon5:c.422C>A:p.S141X                                         | Missense      | 4.3     |
| AML_104  | SF3B1  | NM_012433:exon15:c.2098A>G:p.K700E                                        | Missense      | 40.8    |
| AML_105  | DNMT3A | NM_175629:exon23:c.2645G>A:p.P691Q                                       | Missense      | 43.6    |
| AML_105  | KRAS   | NM_033360:exon3:c.176C>G:p.A59G                                          | Missense      | 4.7     |
| AML_105  | NPM1   | NM_002520:exon11:c.859_860insTCTG:p.L287fs                               | InDel         | 10.2    |
| AML_106  | TP53   | NM_000546:exon6:c.646G>A:p.V216M                                         | Missense      | 82.6    |
| AML_107  | RUNX1  | NM_001754:exon11:c.859_860insTCTG:p.L287fs                               | InDel         | 25.6    |
| AML_107  | SRSF2  | NM_003016:exon1:c.284C>T:p.P95L                                          | Missense      | 37.7    |
| AML_107  | TET2   | NM_001127208:exon7:c.3852_3854del:p.1284_1285del                         | InDel         | 39.4    |
| AML_107  | TET2   | NM_001127208:exon10:c.4393C>T:p.R1465X                                   | Nonsense      | 46.3    |
| AML_108  | DNMT3A | NM_175629:exon23:c.2678G>A:p.W893S                                       | Missense      | 44.0    |
| AML_108  | FLT3   | NM_004119:exon14:c.1831_1832insTTGATTTCAGAGAATATGATATCTCTCAATGGGAGTTCTGCAAGAATATGATCTCTCAATGGGAGTTCTGC:p.E611delinsVDFREYEDLKWEPRENL | InDel         | 22.8    |
| AML_108  | NPM1   | NM_002520:exon11:c.859_860insTCTG:p.L287fs                               | InDel         | 46.3    |
| AML_109  | DNMT3A | NM_175629:exon23:c.2678G>A:p.W893S                                       | Missense      | 39.4    |
| AML_109  | FLT3   | NM_004119:exon14:c.1816_1817insAAATAGGAATCTCTACGTGATTTCAGAGAATATGATATCTCTCAATGGGAGTTCTGC:p.P606delinsQNEFYVDREYEDLKWEP | InDel         | 5.6     |
| AML_109  | NPM1   | NM_002520:exon11:c.859_860insTCTG:p.L287fs                               | InDel         | 3.0     |
| AML_109  | FLT3   | NM_004119:exon14:c.1793_1794insCTACGTTGATTCAGAATATGATATCTCTCAATGGGAGTTCTGC:p.E598delinsDYVDFREY | InDel         | 2.9     |
| AML_109  | FLT3   | NM_004119:exon14:c.1784_1785insCCCTTATTTCAG:p.R595delinsSPYFR              | InDel         | 1.5     |
| AML_109  | KRAS   | NM_033360:exon2:c.35G>A:p.G12D                                          | Missense      | 7.5     |
| AML_109  | NPM1   | NM_002520:exon11:c.859_860insTCTG:p.L287fs                               | InDel         | 39.3    |
| AML_109  | NPM1   | NM_002524:exon2:c.38G>A:p.G12D                                          | Missense      | 6.1     |
| AML_109  | PTTP11 | NM_002834:exon3:c.205G>A:p.E69K                                         | Missense      | 3.9     |
| AML_109  | WT1    | NM_024426:exon7:c.1140_1141insCCGG:p.S381fs                               | InDel         | 6.4     |
| AML_110  | ASXL1  | NM_015338:exon12:c.1927dupG:p.G644fs                                     | InDel         | 21.0    |
| AML_110  | RUNX1  | NM_001754:exon7:c.720_733del:p.240_245del                               | InDel         | 23.2    |
| AML_110  | SRSF2  | NM_003016:exon1:c.284C>T:p.P95L                                          | Missense      | 17.4    |
| AML_110  | STAG2  | NM_001042750:exon5:c.265dupG:p.V88fs                                     | InDel         | 37.8    |
| AML_110  | STAG2  | NM_001042750:exon5:c.269delinsAG                                         | InDel         | 28.3    |
| AML_110  | STAG2  | NM_001042750:exon5:c.269T>G:p.M90R                                       | Missense      | 38.5    |
| Subject | Gene | Variant | Mutation type | VAF [%] |
|---------|------|---------|---------------|---------|
| AML_111 | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 37.8 |
| AML_111 | PTPN11 | NM_002834:exon3:c.179G>T:p.G60V | Missense | 44.2 |
| AML_111 | STAG2 | NM_001042750:exon17:c.1535-3T>A,p.? | Splice site | 47.8 |
| AML_112 | BCOR | NM_001123385:exon4:c.1555_1559del:p.E519fs | InDel | 80.7 |
| AML_112 | FLT3 | NM_004119:exon14:c.1794_1795insAAGGTGACCGGCTCCTCATGTTGATTTCAGAGAATATGA:p.Y599delinsKVTGSSDNEYFYVDFREYEY | InDel | 16.5 |
| AML_112 | NRAS | NM_002524:exon3:c.176C>A:p.A59D | Missense | 14.1 |
| AML_112 | STAG2 | NM_001042750:exon9:c.705_706insT:p.L235fs | InDel | 79.1 |
| AML_112 | U2AF1 | NM_001025203:exon2:c.101C>T:p.S34F | Missense | 42.8 |
| AML_112 | ASXL1 | NM_0015338:exon12:c.1888_1910del:p.H630fs | InDel | 39.5 |
| AML_112 | KRAS | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 43.0 |
| AML_112 | SRSF2 | NM_002524:exon3:c.176C>A:p.A59D | Missense | 10.9 |
| AML_112 | TET2 | NM_001123385:exon3:c.1110T>A:p.Y370X | Nonsense | 68.4 |
| AML_113 | DNMT3A | NM_00175629:exon23:c.2645G>T:p.R882H | Missense | 48.0 |
| AML_113 | FLT3 | NM_004119:exon14:c.1794_1795insAAGGTGACCGGCTCCTCATGTTGATTTCAGAGAATATGA:p.Y599delinsKVTGSSDNEYFYVDFREYEY | InDel | 9.0 |
| AML_113 | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 43.0 |
| AML_113 | WT1 | NM_0024426:exon7:c.1142_1143insAACAAGAGTC:p.S381fs | InDel | 25.0 |
| AML_114 | ASXL1 | NM_0015338:exon12:c.2077C>T:p.R693X | Nonsense | 16.0 |
| AML_114 | CEBPA | NM_0024426:exon7:c.1142_1143insAACAAGAGTC:p.S381fs | InDel | 65.0 |
| AML_115 | CEBPA | NM_0024426:exon7:c.1142_1143insAACAAGAGTC:p.S381fs | InDel | 34.0 |
| AML_116 | DNMT3A | NM_00175629:exon12:c.2196T>G:p.F732L | Nonsense | 43.6 |
| AML_116 | FLT3 | NM_004119:exon14:c.1808_1809insTCCAGATAATGAGTACTTCTACAGTTGATTTCAGAGAATATGAATATGATCTCAATG:p .W603delinsDFESQLQMVQVTGSSDNEYFYVDFREYEY | InDel | 27.7 |
| AML_116 | NPM1 | NM_002520:exon11:c.859_860insTCTG:p.L287fs | InDel | 33.6 |
| AML_116 | WT1 | NM_0024426:exon7:c.1142_1143insAACAAGAGTC:p.S381fs | InDel | 46.1 |
| AML_117 | IDH1 | NM_002520:exon4:c.394C>T:p.R132C | Missense | 18.6 |

**Abbreviations:** VAF, variant allele frequency; InDel, insertion/deletion variant; MDS, myelodysplastic neoplasm; AML, acute myeloid leukemia.
Supplemental Table 12: Summary statistics of mutations identified in individuals undergoing total hip arthroplasty and patients with MDS or sAML.

|                      | THA (n=261)       | MDS (n=91)       | sAML (n=123)      |
|----------------------|-------------------|------------------|-------------------|
| Individuals with ≥1 somatic variant | 127/261 (49%)     | 84/91 (92%)      | 117/123 (95%)     |
| Variants per individual (range) | 0 - 5             | 0 - 9            | 0 - 11            |
| Among individuals with ≥1 variant: |                   |                  |                   |
| - Median number of variants | 1                 | 3                | 4                 |
| - VAF [%] (median, range) | 2.7 (1 - 44)      | 19 (1 - 87)      | 37 (0.3 - 99)     |

**Abbreviations:** VAF, variant allele frequency; THA, total hip arthroplasty; MDS, myelodysplastic neoplasm; AML, acute myeloid leukemia.
Supplemental Table 13: Comparison of *DNMT3A*, *TET2* and *ASXL1* variant properties between CH, MDS and sAML.

|                   | CH (n=127) | MDS (n=91) | sAML (n=123) |
|-------------------|------------|------------|--------------|
| *DNMT3A* p.R882 vs. others | 4/87 (5%) | 9/28 (32%) | 14/37 (38%) |
| *TET2* InDel or nonsense vs. others | 27/47 (57%) | 43/62 (69%) | 27/37 (73%) |
| *ASXL1* c.1934dup vs. others | 3/12 (25%) | 9/22 (41%) | 12/34 (35%) |

**Abbreviations**: InDel, insertion/deletion variant; MDS, myelodysplastic neoplasm; AML, acute myeloid leukemia.
Supplemental Figures

Supplemental Figure 1: Gating strategy for sorting BM subpopulations from individuals with CH carrying ASXL1 mutations.

A: After dead cell exclusion, CD15$^+$ (granulocytes) cells were sorted, the negative fraction was then used to sort CD34$^+$ cells and the subsequent CD15$^-$CD34$^-$ fraction was used to sort CD3$^+$ (T-cells) and CD19$^+$ (B-cells). B: After dead cell exclusion, lineage negative cells (CD4$^-$/CD8a$^-$/CD15$^-$/CD19$^-$/CD235a$^-$) were selected and subsequently the CD45dim population. The CD34$^+$CD38$^+$ subpopulation was used to sort for CD45RA$^-$CD123$^+$ (CMPs), CD45RA$^+$CD123$^+$ (GMPs) and CD45$^-$CD123$^-$ (MEPs), while the CD34$^+$CD38$^-$ subpopulation was used to sort for CD45RA$^-$CD90$^+$ (HSCs).
Supplemental material to Hartmann, Hecker et al.

Supplemental Figure 2: Frequency of mutations in individuals with CH, MDS or sAML, grouped according to functional category

Classification of genetic variants into functional categories was performed according to Döhner et al., N Engl J Med 2015; 373:1136–1152.

| Epigenetic modifier | Signaling | Other |
|---------------------|-----------|-------|
| **Gene** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** |
| DNMT3A | 27.5 | 26.3 | 25.2 | 0.0 | 22.8 | 22.8 | 0.0 | 11.0 | 11.0 |
| TET2 | 29.1 | 24.2 | 21.1 | 0.0 | 2.2 | 21.1 | 5.5 | 0.0 | 0.0 |
| ASXL1 | 8.7 | 22.6 | 26.8 | 0.8 | 3.3 | 10.6 | 0.0 | 4.3 | 0.8 |
| IDH2 | 1.6 | 1.1 | 13.8 | 0.0 | 0.0 | 13.0 | 0.0 | 1.1 | 0.8 |
| EZH2 | 0.0 | 5.4 | 4.9 | 2.4 | 4.3 | 4.1 | 0.8 | 0.8 | 0.0 |
| IDH1 | 0.0 | 3.3 | 6.5 | 0.0 | 6.5 | 1.6 | 0.0 | 0.0 | 0.0 |
| ASXL2 | 0.0 | 1.1 | 0.8 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| KDM6A | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |

**Splicing factor**

| **Gene** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| SRSF2 | 1.6 | 18.5 | 24.4 | 0.0 | 0.0 | 0.0 | 1.6 | 19.6 | 31.7 |
| SF3B1 | 3.0 | 28.3 | 8.9 | 0.0 | 0.0 | 0.0 | 1.6 | 5.4 | 15.4 |
| U2AF1 | 1.6 | 9.8 | 10.6 | 0.0 | 0.0 | 0.0 | 1.6 | 3.3 | 4.1 |
| DDX41 | 0.0 | 4.3 | 2.4 | 0.0 | 0.0 | 0.0 | 0.0 | 1.1 | 0.0 |
| ZRSPR2 | 1.8 | 4.3 | 0.0 | 0.0 | 0.0 | 0.0 | 2.4 | 0.0 | 0.0 |
| U2AF2 | 2.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |

**Cohesin Complex**

| **Gene** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| STAG2 | 0.0 | 6.5 | 21.1 | 2.4 | 14.1 | 7.3 | 0.0 | 0.0 | 4.9 |
| RAD21 | 0.8 | 3.3 | 3.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.6 |

**Transcription factor**

| **Gene** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| RUNX1 | 1.6 | 19.6 | 31.7 | 0.0 | 1.1 | 3.3 | 0.0 | 0.0 | 0.0 |
| BCL2 | 1.6 | 5.4 | 15.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| BCOR | 1.6 | 3.3 | 4.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| BCORL1 | 1.6 | 3.3 | 4.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| CEBPA | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| NFE2 | 2.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| ZBTB7A | 1.6 | 1.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| GATA2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| GATA1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |

**Tumor Suppressor**

| **Gene** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** | **CH, %** | **MDS, %** | **sAML, %** |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| TP53 | 2.4 | 14.1 | 7.3 | 0.0 | 0.0 | 4.9 | 0.0 | 0.0 | 1.6 |
Supplemental Figure 3: Intra-genic localization of variants in CH, MDS and sAML.

(A) TET2 variants; (B) ASXL1 variants. Green dots indicate missense mutations, black dots indicate InDels, brown dots indicate nonsense mutations. Plots were generated using the MutationMapper tool (Gao et al., Sci. Signal. 2013 and Cerami et al., Cancer Discov. 2012).