**Supplementary Figures**

**Supplementary Figure S1**: Schematic diagram of the DNA structure of a *KMT2A* wild-type (WT) and partial tandem duplication of the *KMT2A* gene. A) The boxes represent an exon, and the number above each box represents exon number. The *KMT2A* gene is composed of 36 exons, but for illustration, only the first 13 exons are displayed in the above diagram. The black small arrows indicate the location of the primers used for the analysis (adapted from Caligiuri et al., 1996). The grey boxes illustrate the exons that are duplicated in an e3-e9 *KMT2A*-PTD in the *KMT2A* gene. The PTD can also involve other exons of the *KMT2A* gene. B) Representative RT-PCR analyses KMT2A-PTD. The EOL1 cell line carries *KMT2A-PTD* and served as positive control (1H). The assay limit of detection was determined by diluting the EOL1 cell line (1:10 dilutions (1H-1D (100% - 0.01%)) in HL-60, a cell line without *KMT2A*-PTD.



**Supplementary Figure S2**: *KMT2A*-PTD AML mutation frequency in study (*KMT2A*-PTD AML), validation cohort (*KMT2A*-PTD AML), AML reference cohort and t(11q23) AML. The frequencies of concurrent mutations in *KMT2A*-PTD AML study cohort (blue), *KMT2A*-PTD AML validation cohort (green), reference cohort (red) and t(11q23) (purple).



**Supplementary Figure S3**: Survival analysis *KMT2A*-PTD AML vs. *KMT2A*-WT AMLs. A) Kaplan-Meier graph OS of *KMT2A*-PTD AMLs (red) vs. *KMT2A* wild-type AML (black).



**Supplementary Figure S4**: Survival analysis of *KMT2A* wild-type cohort and concurrent mutations. *KMT2A* wild-type with and without *DNMT3A* mutations (p=0.99).



**Supplementary Figure S5**: Survival analysis of *KMT2A* wild-type cohort and concurrent mutations. *KMT2A* wild-type with and without *NRAS* mutations (p=0.044).



**Supplementary Figure S6**: Survival analysis of *KMT2A*-PTD validation cohort and concurrent mutations. *KMT2A*-PTD with and without *DNMT3A* mutations (p=0.0017).

