



Supplementary Figure 1 Quality of sequencing in this study.

A and B, Average read depth (**A**) and fraction of bases covered by at least 100× sequencing reads (**B**) stratified by tissue and specimen type in targeted DNA-seq. **C**, Proportion of specimens evaluable by copy number analysis stratified by tissue and specimen type in 179 specimens excluding 9 collected after allogeneic HSCT. **D**, Proportion of specimens evaluable by targeted RNA-seq stratified by tissue and specimen type in 188 specimens. **E**, Number of uniquely mapped reads stratified by tissue and specimen type in targeted RNA-seq. **F**, Effect of storage duration from specimen collection on DNA integrity number for FFPE specimens ($n = 108$). Two-sided Welch's t-test. **A-F**, n denotes number of available specimens. **A, B, E and F**, Box plots show medians (lines), IQRs (boxes), and $\pm 1.5 \times$ IQR (whiskers). **A, B and E**, Fresh and FFPE specimens were compared with two-sided Welch's t-test.