Description of Additional Supplementary Files

Supplementary Data 1: Overview of all primary PBL samples with corresponding clinical and experimental data (IHC/FISH, WES, and SNP).

Supplementary Data 2: Overview of the optimized multistage filter hierarchy showing all variant filter steps in the applied order for calling somatic mutations.

Supplementary Data 3: Cancer gene prediction according to MutSig2CV.

Supplementary Data 4: List of all called somatic variants in 85 primary PBL samples.

Supplementary Data 5: Subcohort comparisons for selected gene sets.

Supplementary Data 6: Mutations revealed by targeted resequencing of the selected cancer candidate genes TP53, NRAS, KRAS, BRAF, STAT3, and TET2.

Supplementary Data 7: List of recurrent somatic copy number alterations in 82 primary PBL samples.

Supplementary Data 8: Gene level view of copy number alterations in 82 primary PBL samples and the PBL-1 cell line.

Supplementary Data 9: Survival analysis for preselected variables using log-rank tests and unbiased univariate screening of all available biological covariates using Cox proportional hazard models.

Supplementary Data 10: Depletion ratios of all used shRNAs in the performed shRNA screen.