Description of additional supplementary file

File name: Supplementary Data 1
Contents:
Supplementary Table 1. Low-complexity regions excluded from analysis
Supplementary Table 2. Homopolymeric regions (≥9 base pairs) excluded from analysis
Supplementary Table 3. Polymorphic genes excluded from analysis
Supplementary Table 4. Somatic variant calling references for five well characterized cell lines (COLO829, HCC1143, HCC1937, HCC1395, and NCI-H1770)
Supplementary Table 5. Wild-type (WT) genes for each cell line in the reference exome
Supplementary Table 6. Clinically actionable genes used in the study
Supplementary Table 7. FF and FFPE expression correlations for differentially expressed genes
Supplementary Table 8. Correlation of gene expression with qPCR
Supplementary Table 9. Reference fusions and performance characteristics
Supplementary Table 10. Comparison of RNA-seq fusion detection with qPCR
Supplementary Table 11. Fusion databases
Supplementary Table 12. Major BCR clonotypes for FF and FFPE samples
Supplementary Table 13. Performance metrics of somatic mutation calling (detection of SNVs and INDELs) using the reference cell lines at varying tumor purities
Supplementary Table 14. Sequencing results of 53 clinical tumor samples
Supplementary Table 15. Overall performance characteristics
Supplementary Table 16. MSI status of clinical samples
Supplementary Table 17. CNV mixes calling results
Supplementary Table 18. Performance characteristics of CNV calling on the reference cell lines at varying tumor purities
Supplementary Table 19. Distribution of diagnosis for cohort of patients
Supplementary Table 20. Comparison of the assay results to large-scale genomic profiling studies
Supplementary Table 21. Distribution of variant types in RNA-seq data
Supplementary Table 22. Genes with allele-specific expression based on observed somatic mutations

File name: Supplementary Data 2
Contents: Source data for the main figures are available in the Supplementary Data 2 file.