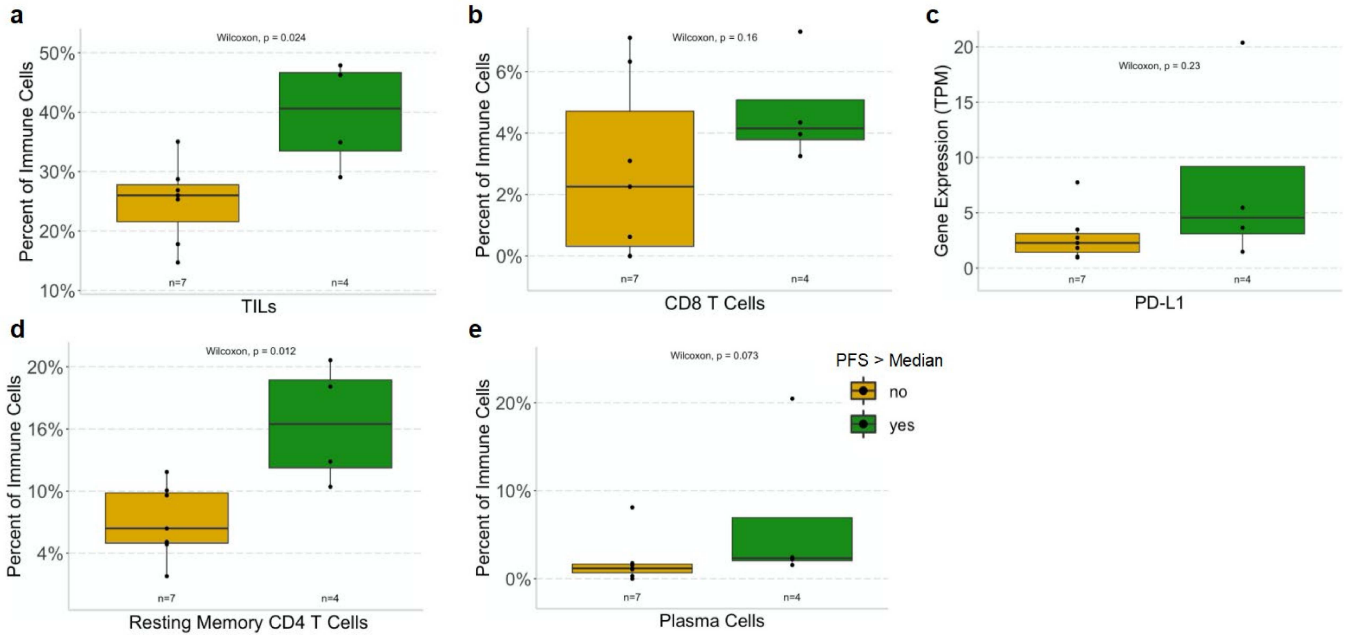
SUPPLEMENTARY FIGURES

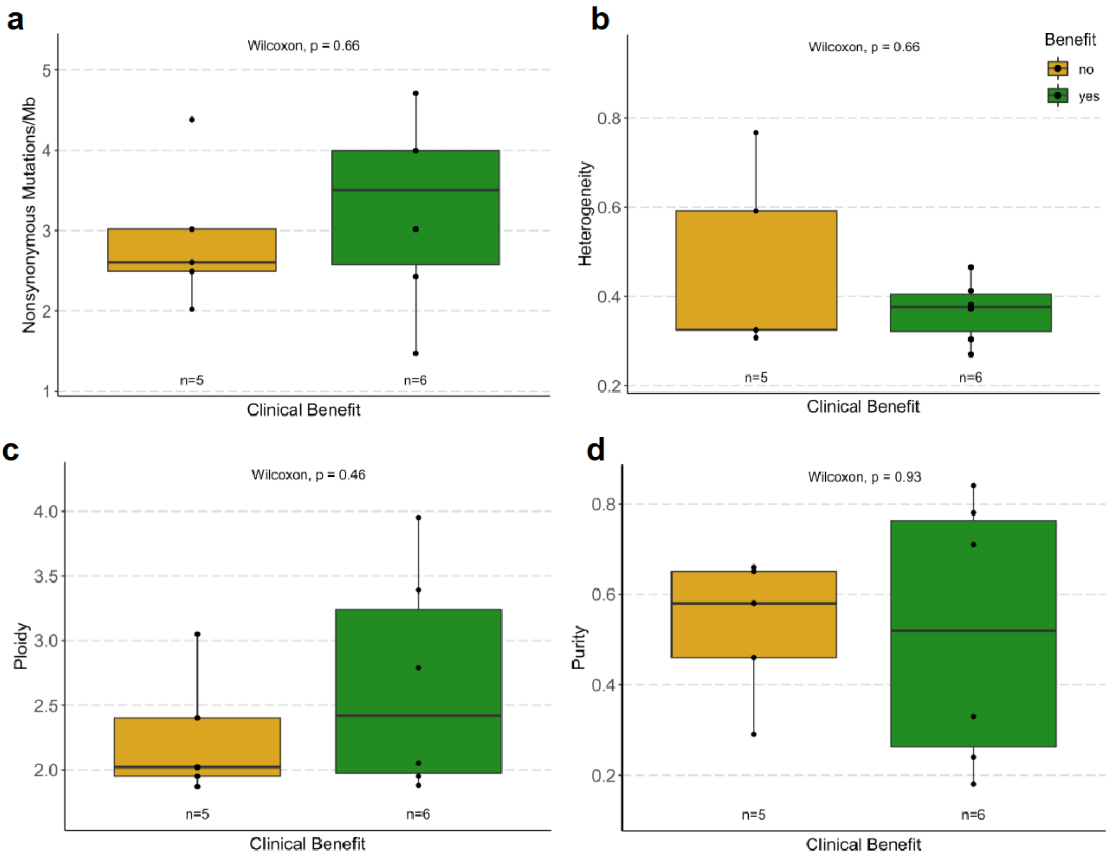
Supplemental Figure S1. Tumor Immune Infiltration Inferred by RNA Sequencing

a-c) Tumor infiltrating lymphocytes (TILs, **a**) measured by RNA sequencing were higher in patients with above median progression-free survival (PFS; green) versus those with below median PFS (yellow), although CD8 T cells (**b**) and PD-L1 gene expression (**c**) were not different. **d-e**) Resting memory CD4 T cells (**d**) measured by RNA sequencing were higher in patients with above median progression-free survival (PFS; green) versus those with below median PFS (yellow), and plasma cells (**e**) trended towards being higher. Unadjusted Mann-Whitney-Wilcoxon p values are shown. Boxplot limits indicate the interquartile range (IQR; 25th to 75th percentile), with a center line indicating the median. Whiskers show the value ranges up to 1.5 × IQR above the 75th or below the 25th percentile with outliers beyond those ranges shown as individual points.



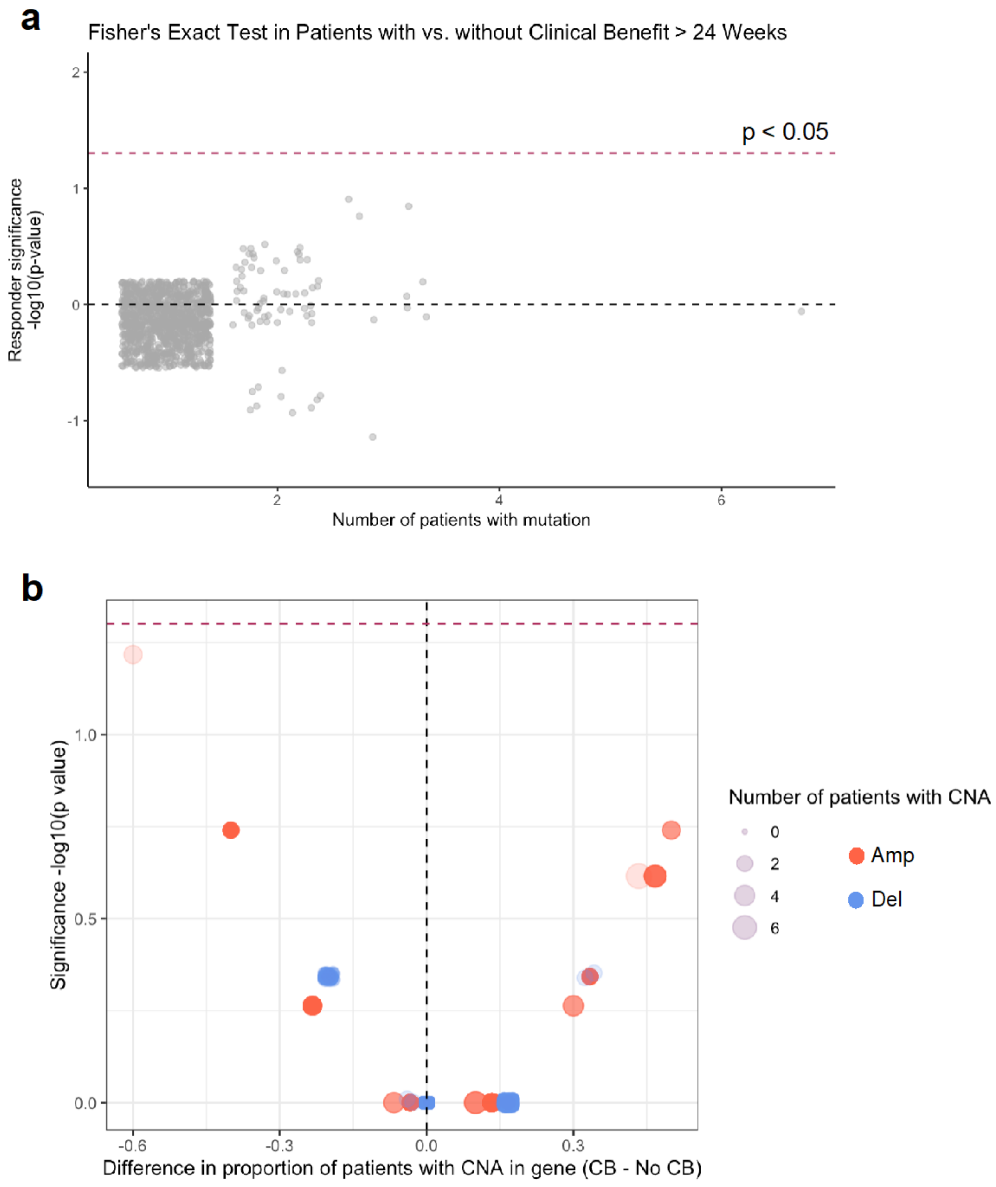
Supplemental Figure S2. Aggregate Genomic Features

a-d) Aggregate genomic features, including nonsynonymous mutational burden (**a**), tumor heterogeneity (**b**), tumor ploidy (**c**), and tumor purity (**d**) were not different in patients with clinical benefit (green) vs. those without clinical benefit (yellow). Tumor heterogeneity was defined as the proportion of subclonal mutations in each tumor, tumor ploidy as the overall genomic copy number (a normal diploid cell has a copy number of 2), and tumor purity as the proportion of DNA from tumor versus other cells in the sample. Unadjusted Mann-Whitney-Wilcoxon p values are shown. Boxplot limits indicate the interquartile range (IQR; 25th to 75th percentile), with a center line indicating the median. Whiskers show the value ranges up to 1.5 × IQR above the 75th or below the 25th percentile with outliers beyond those ranges shown as individual points.



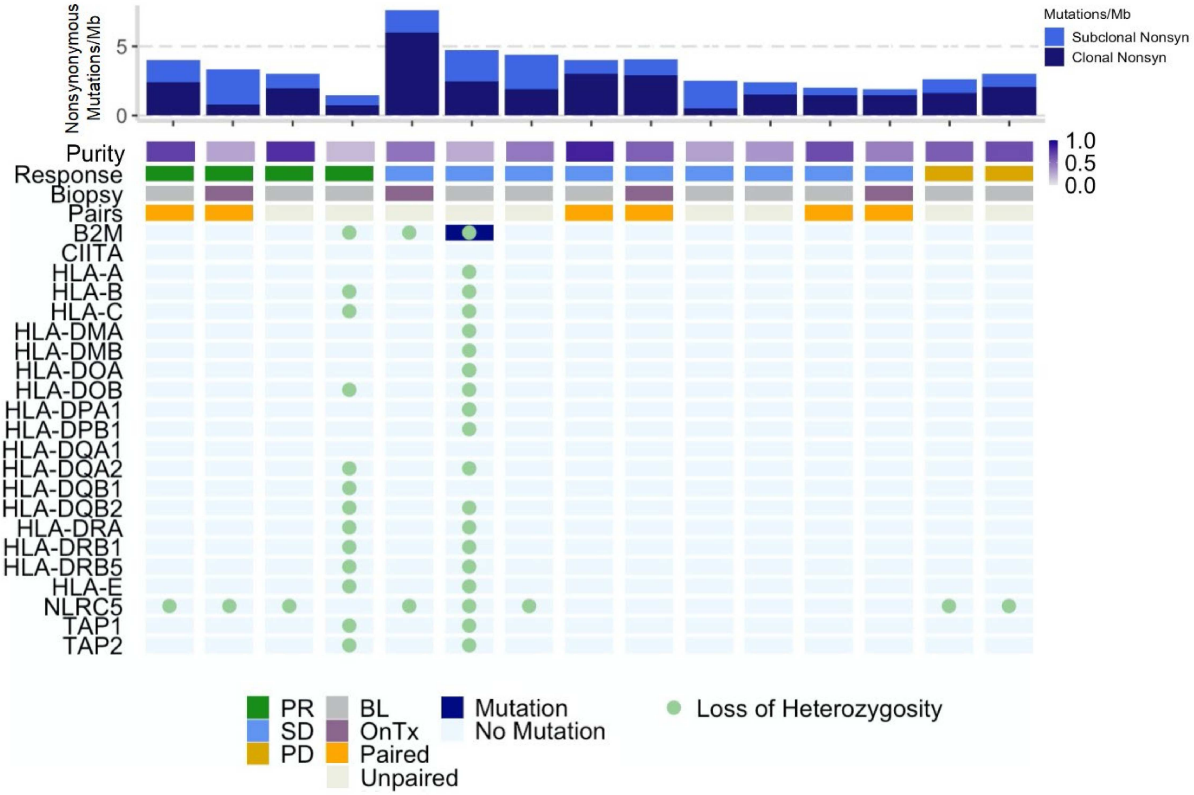
Supplemental Figure S3. Single Gene Mutations and Copy Number Alterations

a) Single-gene alterations: Single-gene nonsynonymous mutations were not associated with clinical benefit at unadjusted Fisher's exact $p < 0.05$ prior to multiple hypothesis testing correction in baseline biopsies (n = 11). Each dot is a gene or group of genes. **b**) Amplifications (amp) and homozygous deletions (del) were not associated with clinical benefit at unadjusted Fisher's exact $p < 0.05$ prior to multiple hypothesis testing correction in baseline biopsies (n = 11). Each dot is a gene or group of genes with the size of the dot corresponding to the number of patients. CB, clinical benefit; CNA, copy number alteration.



Supplemental Figure S4. Antigen Presentation Mutations and Copy Number Alterations

Each column of this comutation plot represents a tumor biopsy. Tumor biopsies are ordered by RECIST response, and within each response subgroup by decreasing nonsynonymous (Nonsyn) mutational load (top row). Nonsynonymous mutational burden is further subdivided into clonal (dark blue) and subclonal (light blue) mutational load. Tumor purity is the inferred proportion of the tumor sample that is from cancer cells compared to other cell types with dark purple corresponding to a purity of 1. The biopsy timing (baseline in gray vs. on-treatment in purple) is indicated, and paired biopsies from the same patient are shown in orange. Mutations and copy number alterations in antigen presentation genes are shown for each tumor.



Supplemental Figure S5. Antigen Presentation Gene Expression

a) Volcano plot shows the log fold change in expression of antigen presentation genes (Supplemental Table 5) in on-treatment vs. baseline biopsies. The x axis displays the log2 fold change in expression of the genes between on-treatment vs. baseline biopsies, and the y axis displays the -log10 of the unadjusted Mann-Whitney Wilcoxon p value for this gene expression difference. **b**) In baseline tumor biopsies, antigen presentation ssGSEA scores were not different by clinical benefit. (**c-d**) ssGSEA of the antigen presentation (**c**) and HLA-II (**d**) gene sets showed a trend towards greater on-treatment log fold changes in ssGSEA scores in patients with clinical benefit (green) vs. no clinical benefit (yellow). Pre, pre-treatment baseline samples; On, on-treatment samples.