

## **Supplemental Figures**

Chemotherapy weakly contributes to predicted neoantigen expression in  
ovarian cancer

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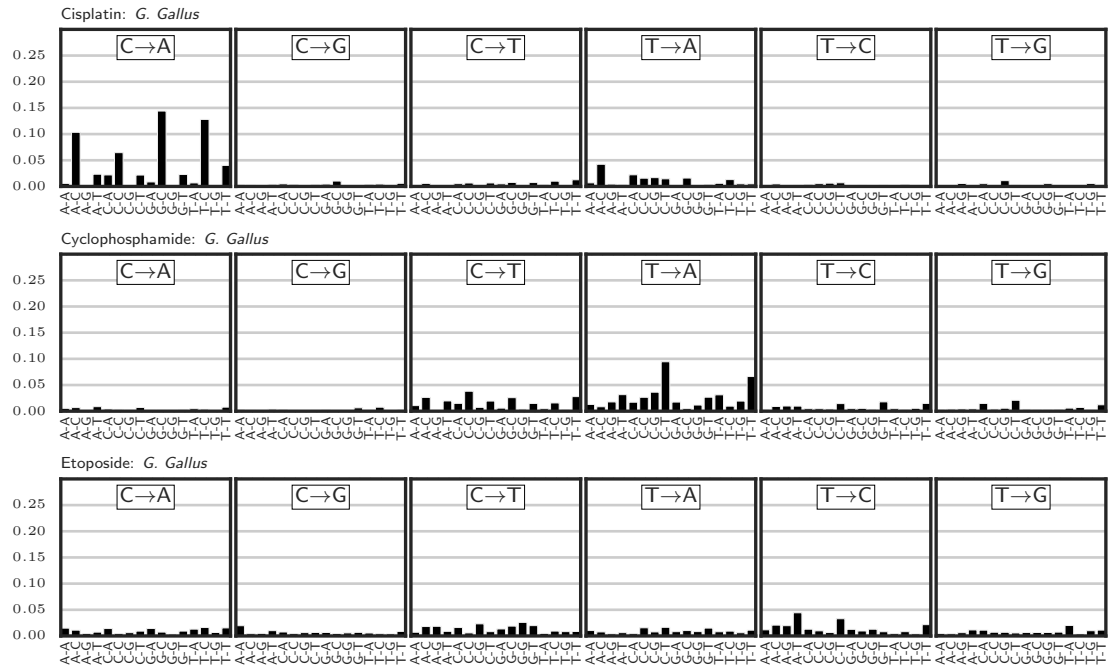


Figure S1: Mutational signatures extracted from Szikriszt et al. [?]

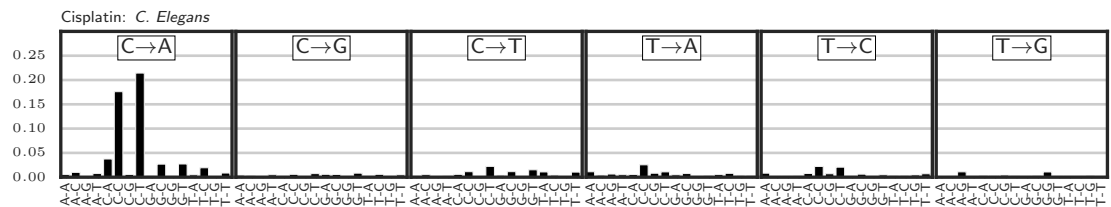


Figure S2: Mutational signature extracted from Meier et al. [?]

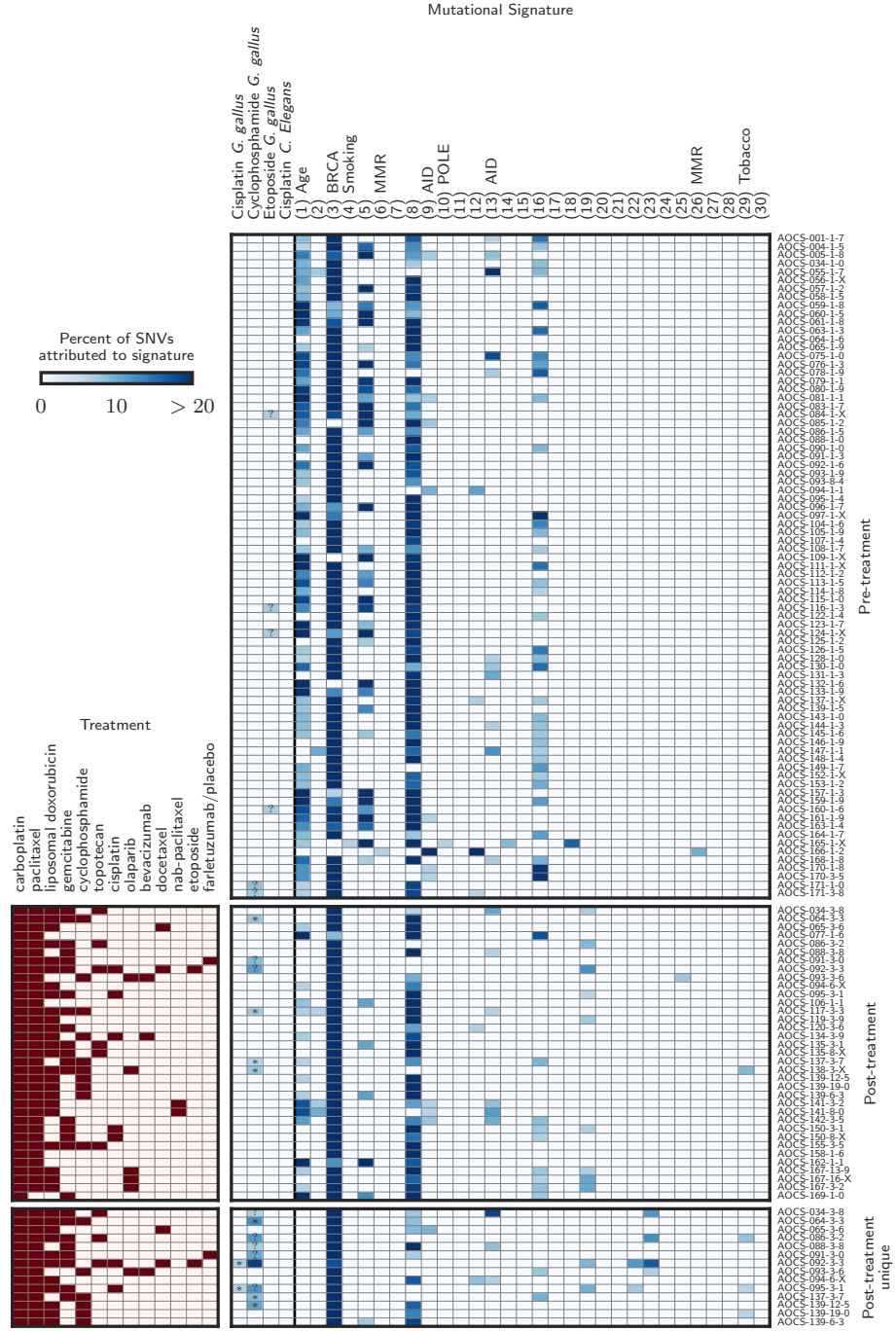


Figure S3: **Detected mutational signatures across all samples.** The symbols are as in main text Figure 1. The top and middle panels show the signature deconvolutions for all pre- and post-treatment samples, respectively. The bottom panel shows deconvolutions for the mutations unique to the paired post-treatment samples, requiring high coverage and no variant reads in the donor-matched pre-treatment sample.

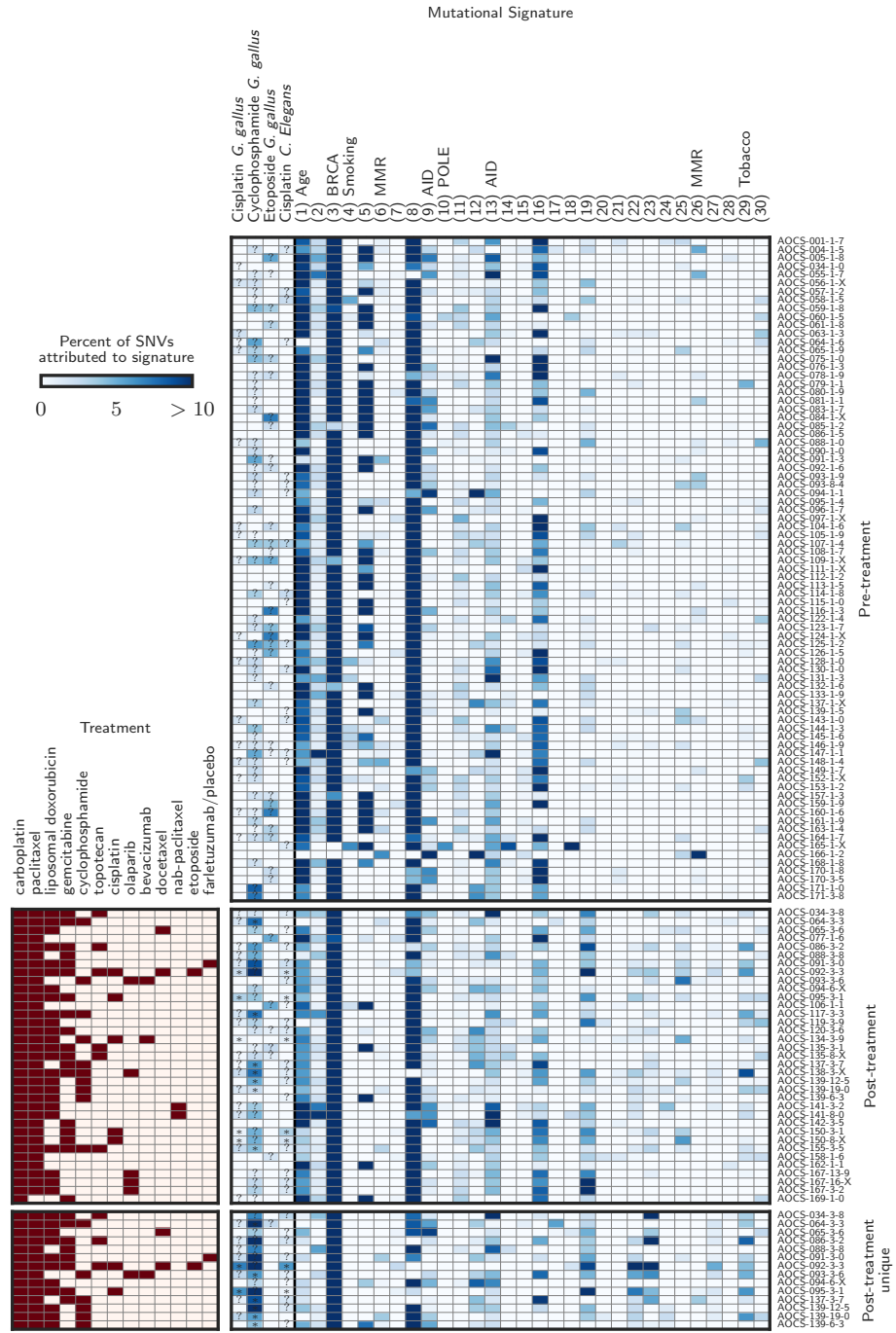


Figure S4: **Mutational signature deconvolutions without any threshold of detection.** Signatures accounting for less than the 6% recommended detection threshold are included.

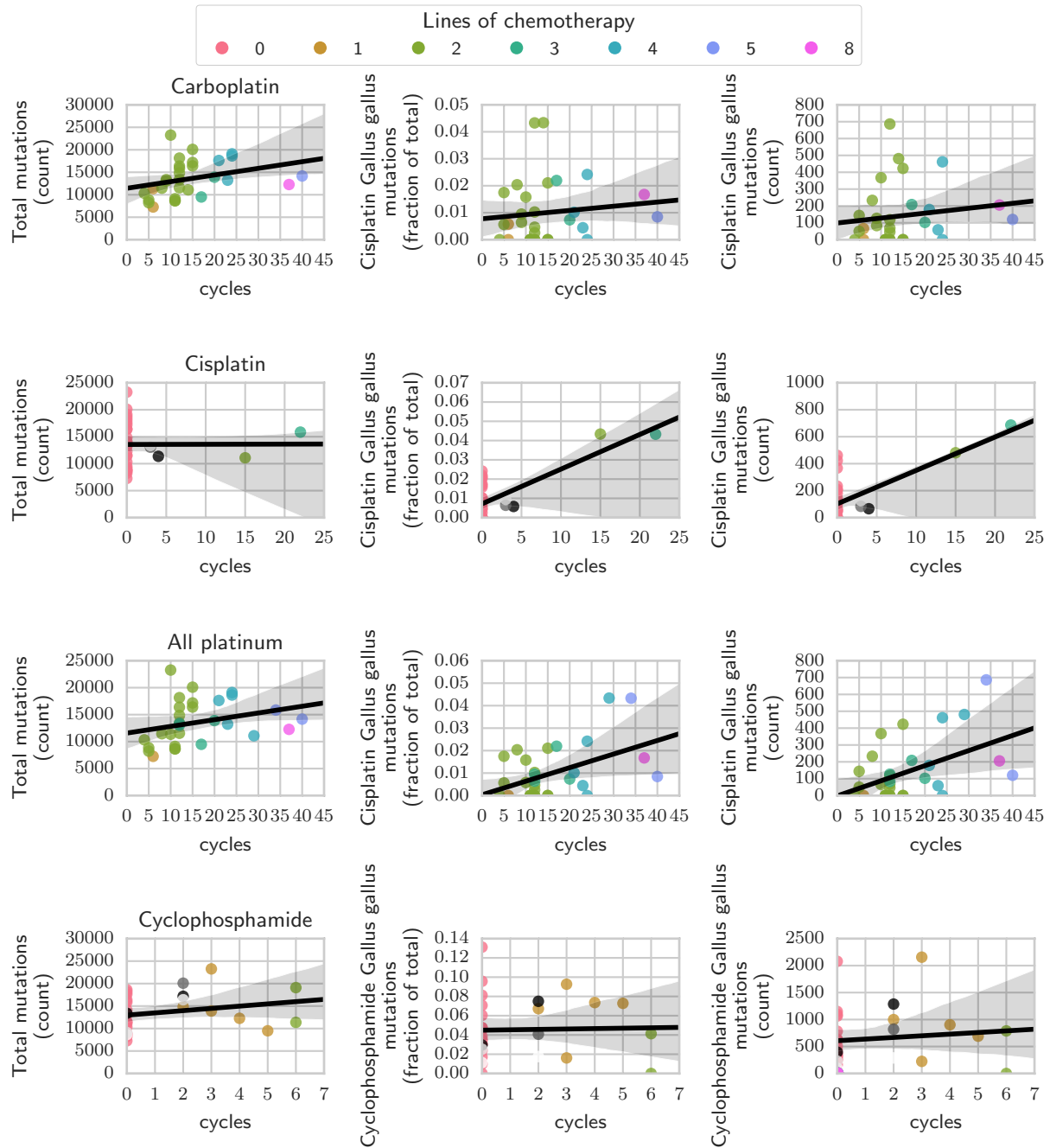


Figure S5: Association of chemotherapy cycles on total genome-wide mutation burden (left) and mutations attributed to the *G. Gallus* cisplatin and cyclophosphamide signatures as a fraction of total (middle) and as a count (right). The total mutation burden includes both SNVs and indels. Cycles indicated are of the labelled chemotherapy. Colors indicate the number of lines of chemotherapy.

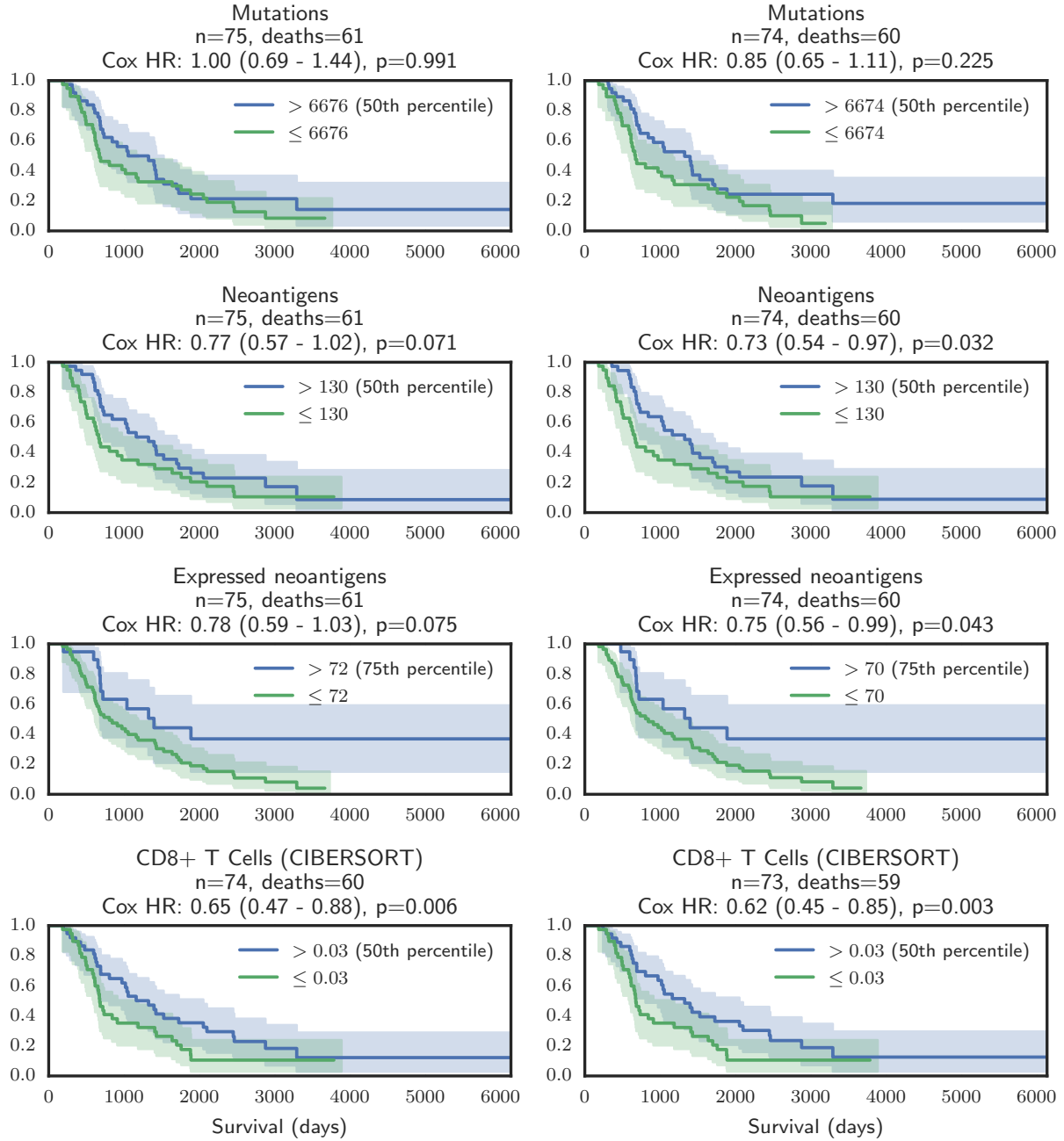


Figure S6: **Kaplan-Meier curves for patients split by the number of mutations, neoantigens, expressed neoantigens, or estimate of CD8+ T cell infiltrate.** Only primary/untreated solid-tissue samples are considered. The survival curves split the samples into high and low groups using a percentile threshold, but the annotated Cox hazard ratio (HR) and p-value correspond to a regression model that treats the value of interest as a continuous covariate. The left plots include all primary/untreated samples; the right plots exclude outlier sample AOCS-166-1-2. The CD8+ T cell analyses exclude sample AOCS-056-1-X, which failed deconvolution.



Figure S7: RNA-seq based immune deconvolution (CIBERSORT) of solid-tissue samples.

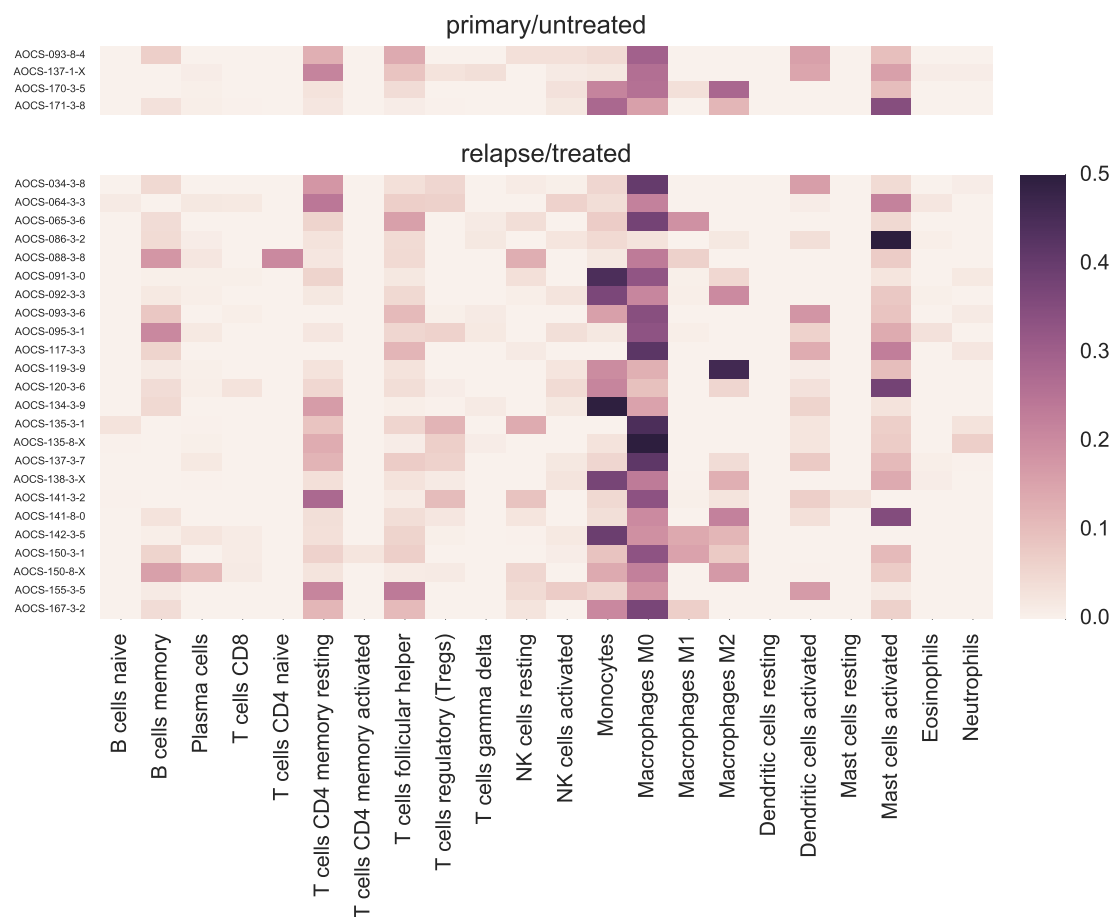


Figure S8: RNA-seq based immune deconvolution (CIBERSORT) of ascites samples.



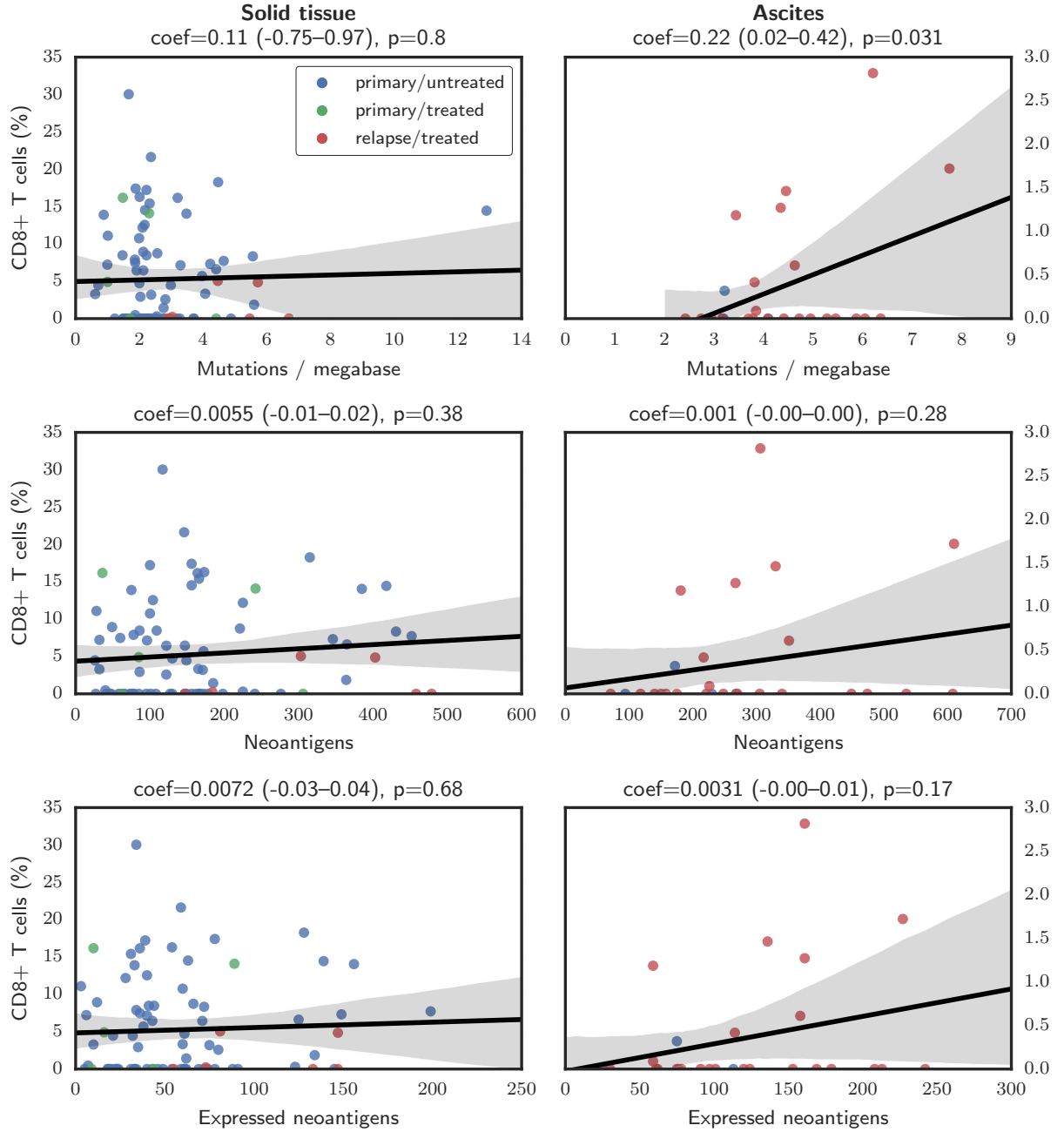


Figure S9: Relationship between CD8+ T cell infiltrate estimated by CIBERSORT and mutations, neoantigens, or expressed neoantigens for solid tissue (left) and ascites (right) samples. Colors indicate sample time point.

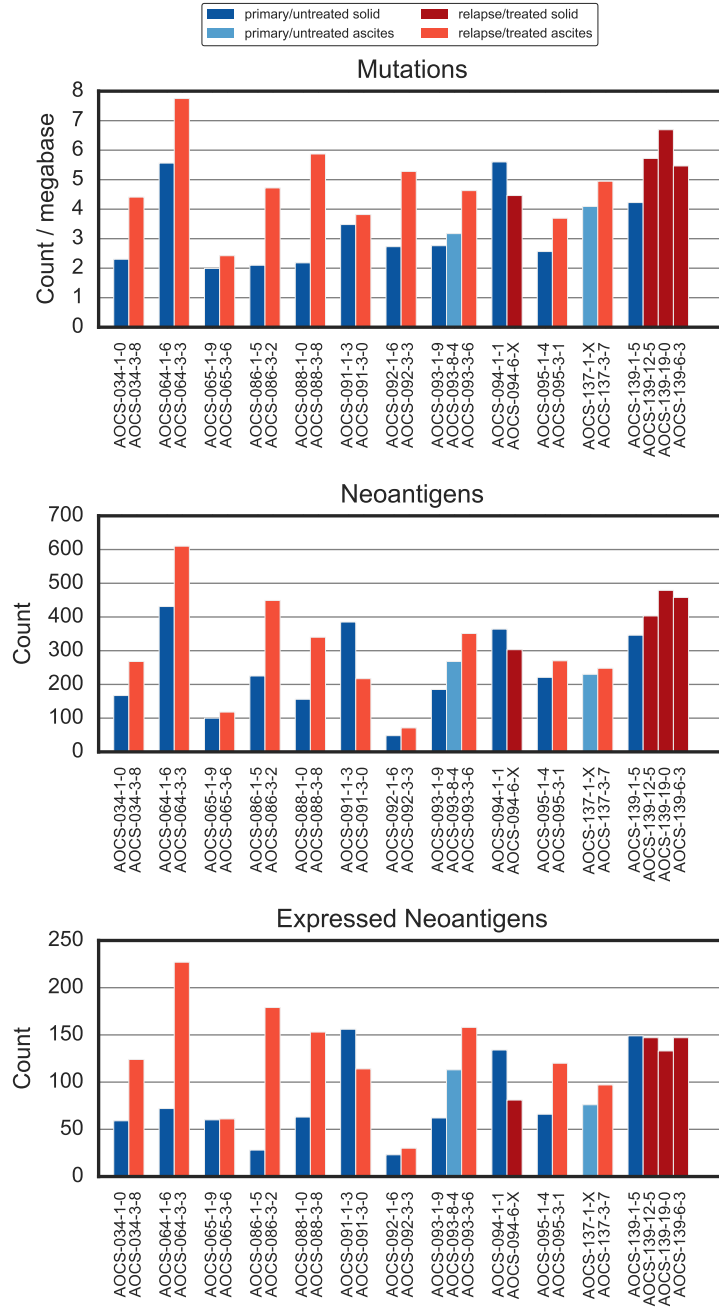


Figure S10: Mutations, neoantigens, and expressed neoantigens for donor-matched primary/untreated and relapse/treated samples.

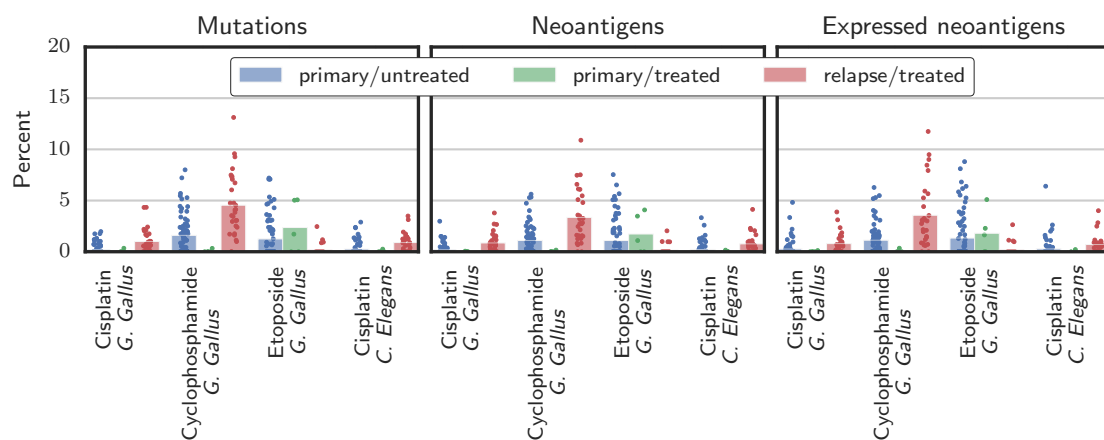


Figure S11: **Contribution of chemotherapy SNV signatures.** The fraction of each sample's mutations, neoantigens, and expressed neoantigens attributed to putative chemotherapy signatures is shown. Bars give the mean, and points indicate individual samples.