Supplemental Figures

Chemotherapy weakly contributes to predicted neoantigen expression in ovarian cancer

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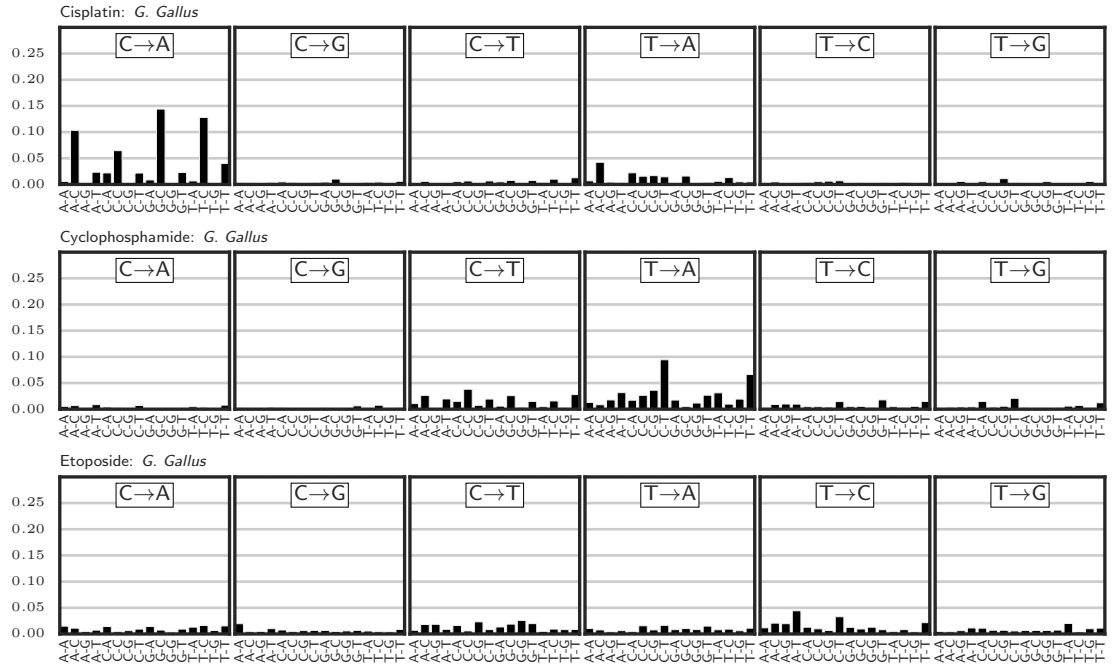

Figure S1: **Mutational signatures extracted from Szikriszt et al.** [?]

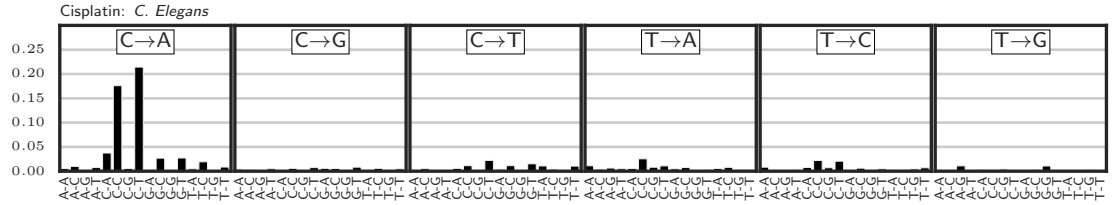

Figure S2: **Mutational signature extracted from Meier et al.** [?]

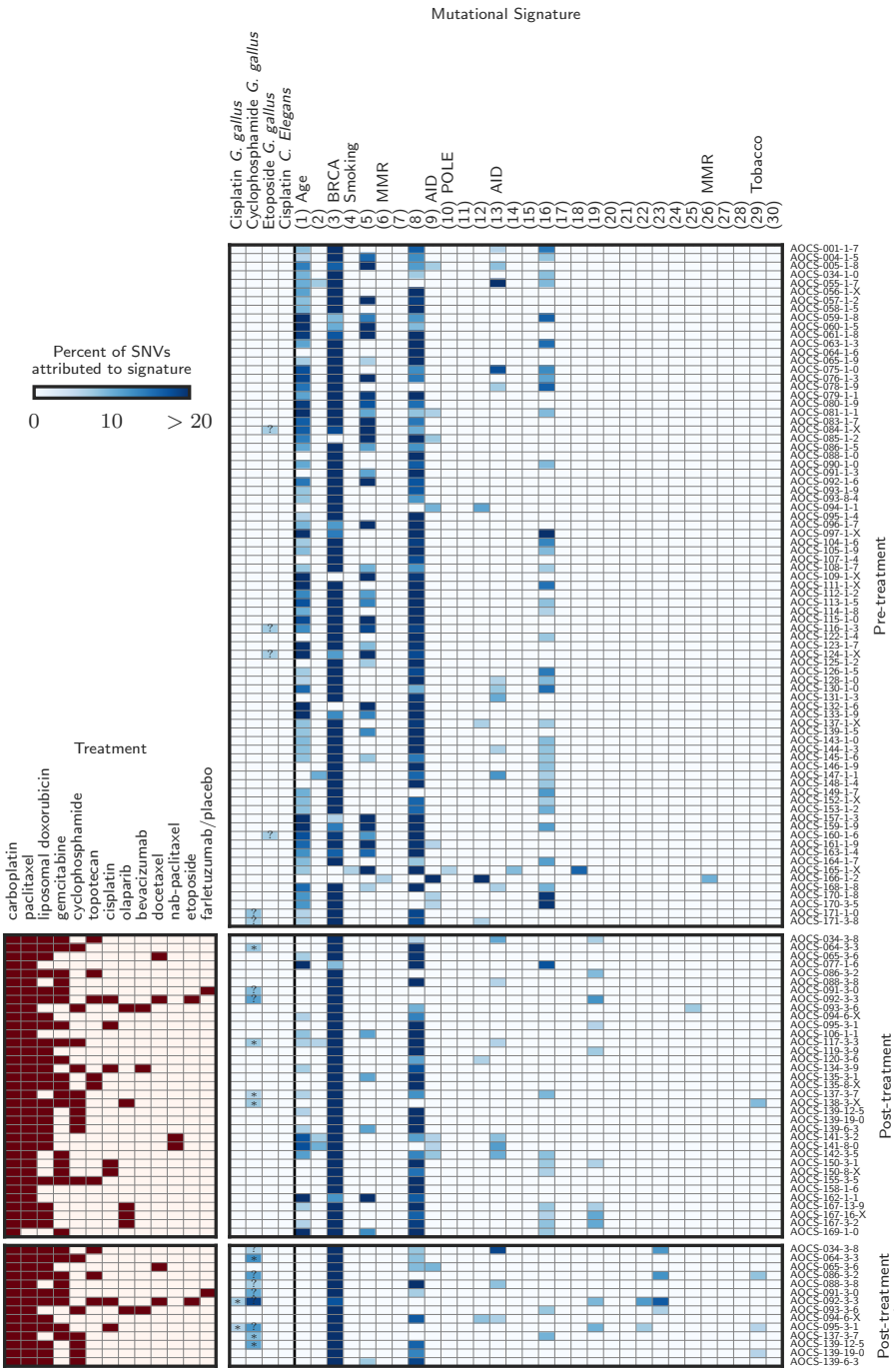

Figure S3: **Detected mutational signatures across all samples.** The symbols are as in main text Figure 1. The top and middle panels show the signature deconvolutions for all pre- and post-treatment samples, respectively. The bottom panel shows deconvolutions for the mutations unique to the paired post-treatment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

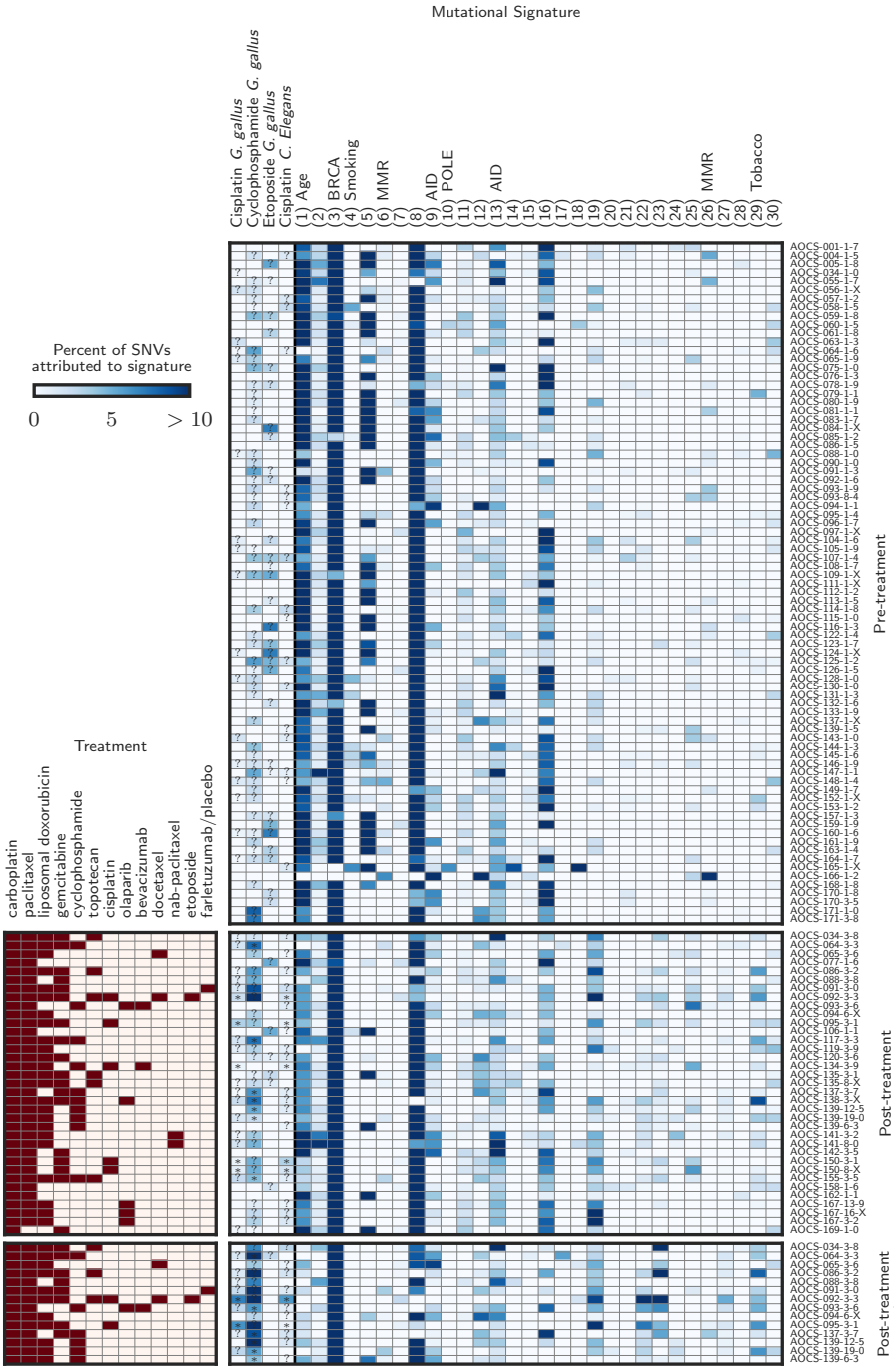

Figure S4: **Mutational signature deconvolutions without any threshold of detection.** Signatures accounting for less than the 6% recommended detection threshold are included.

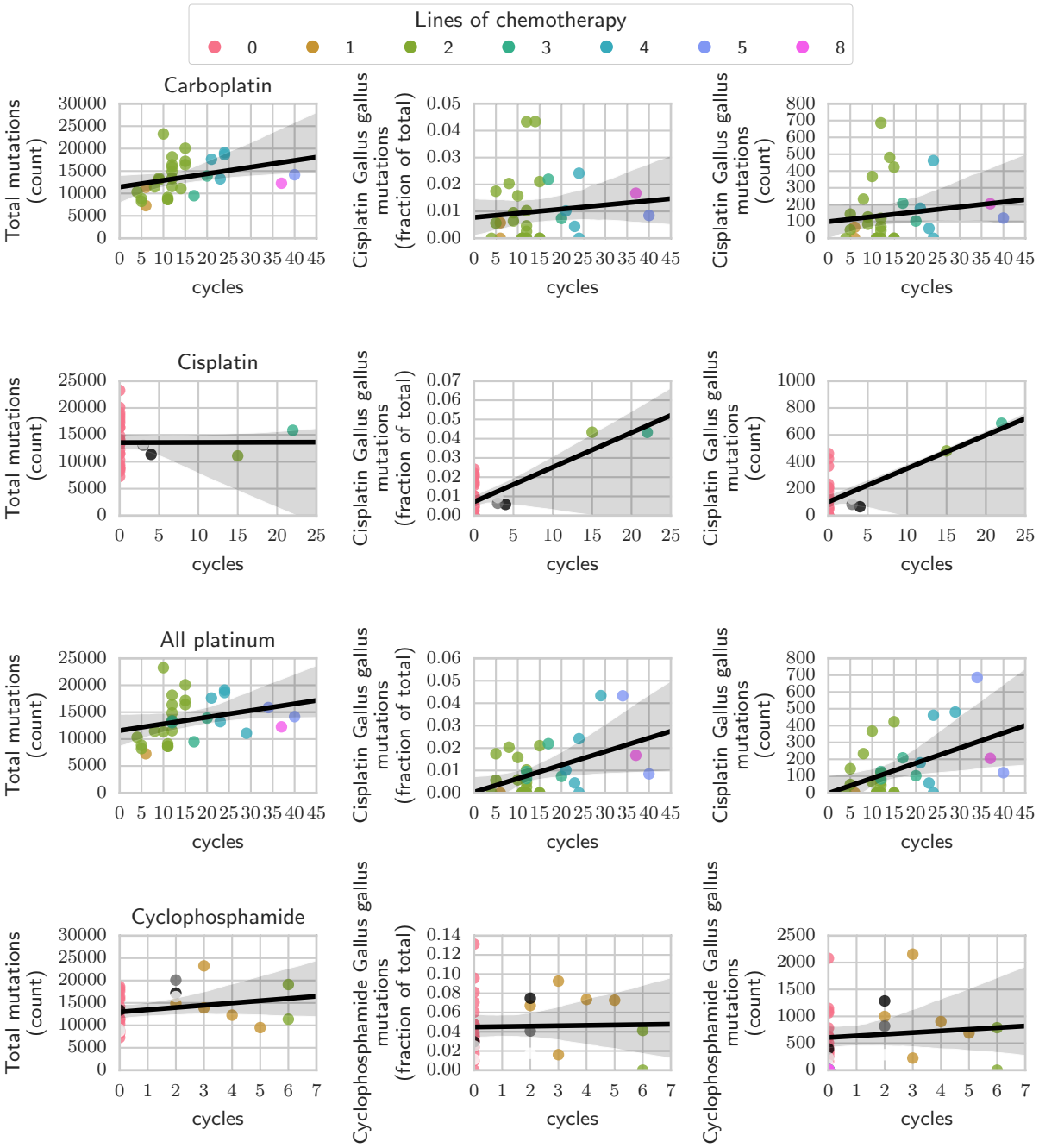

Figure S5: **Association of chemotherapy cycles on total genome-wide mutation burden (left) and mutations attributed to the *G. Gallus* cisplatin and cyclophosphamide signatures as a fraction of total (middle) and as a count (right)**. The total mutation burden includes both SNVs and indels. Cycles indicated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

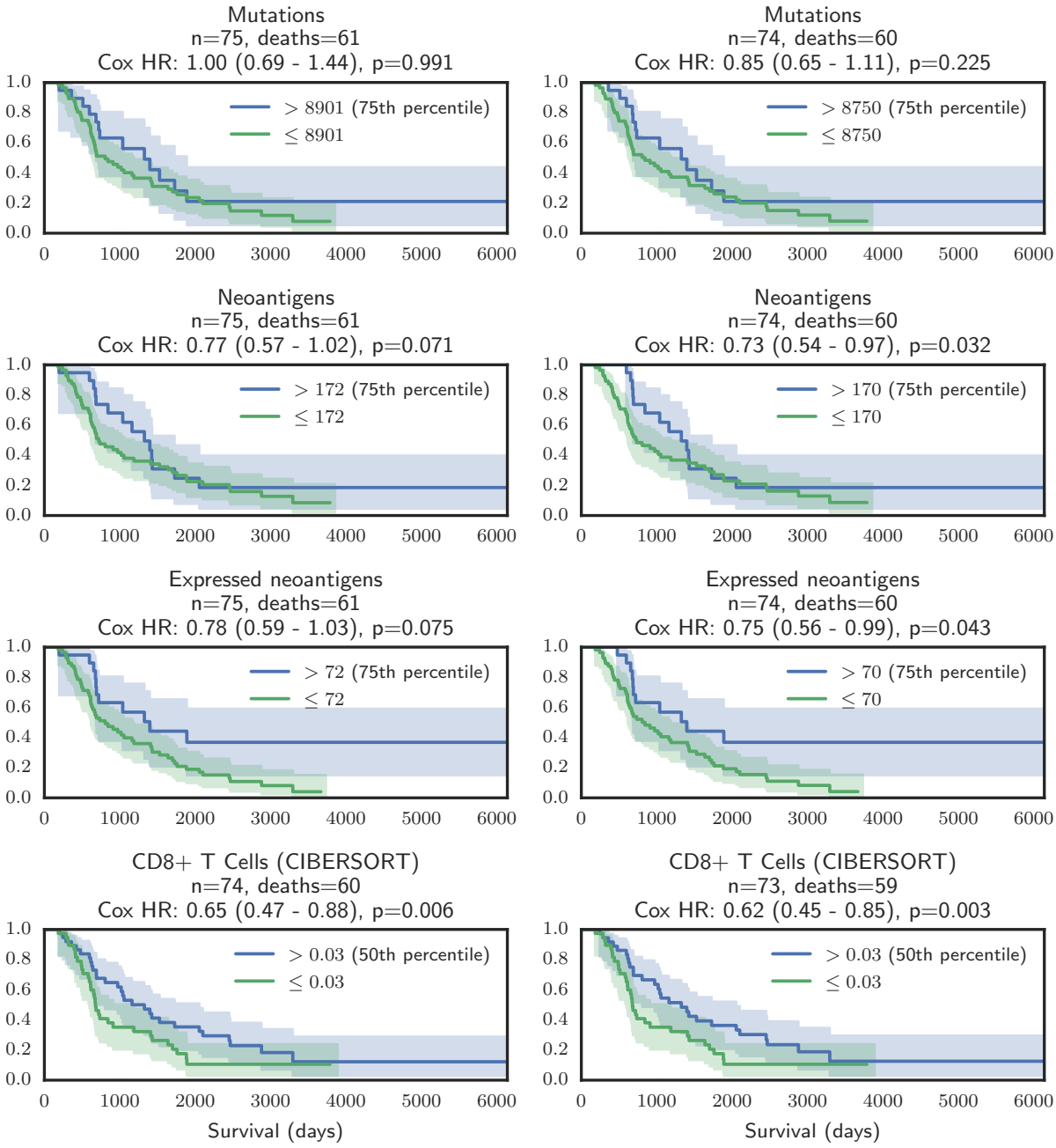

Figure S6: **Kaplan-Meier curves for patients split by the number of mutations, neoantigens, expressed neoantigens, or estimate of CD8+ T cell infiltrate.** Only primary/untreated solid-tissue samples are considered. The survival curves split the samples into high and low groups using a percentile threshold, 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.**

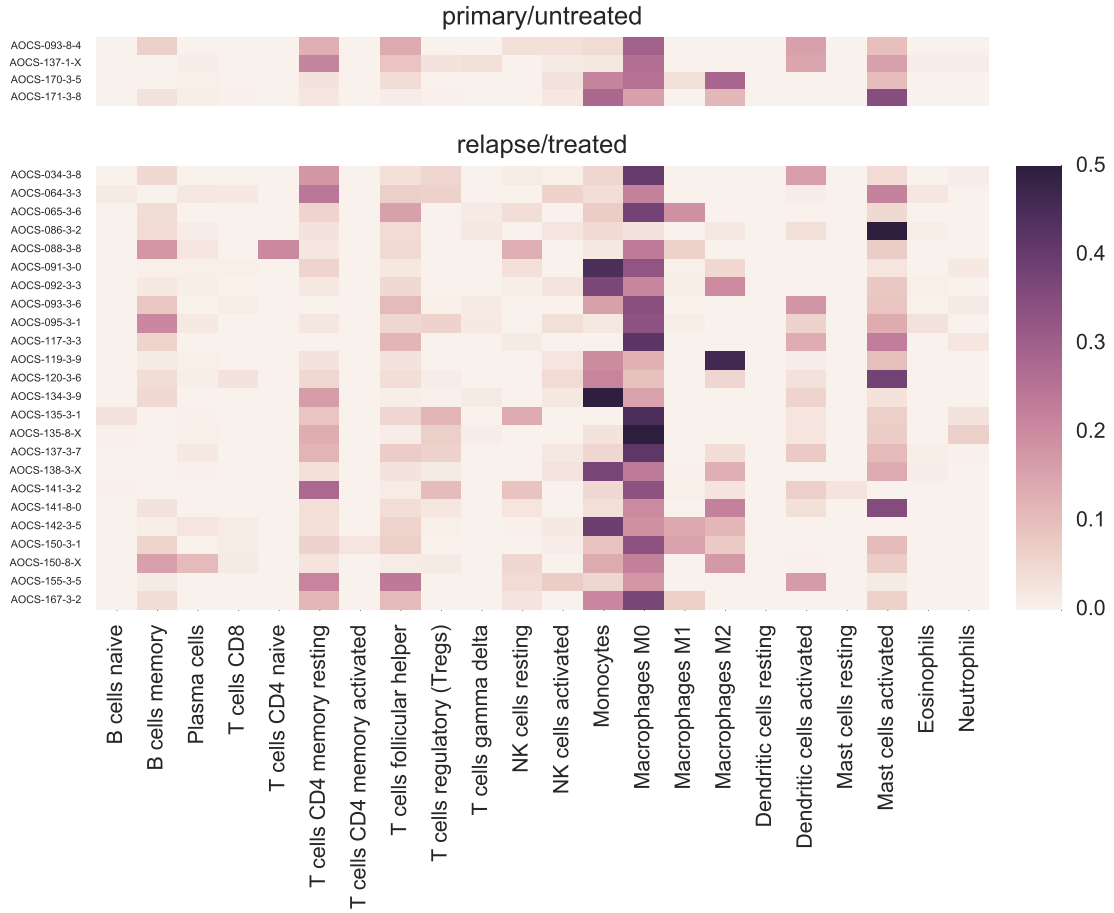

Figure S8: **RNA-seq based immune deconvolution (CIBERSORT) of ascites samples.**

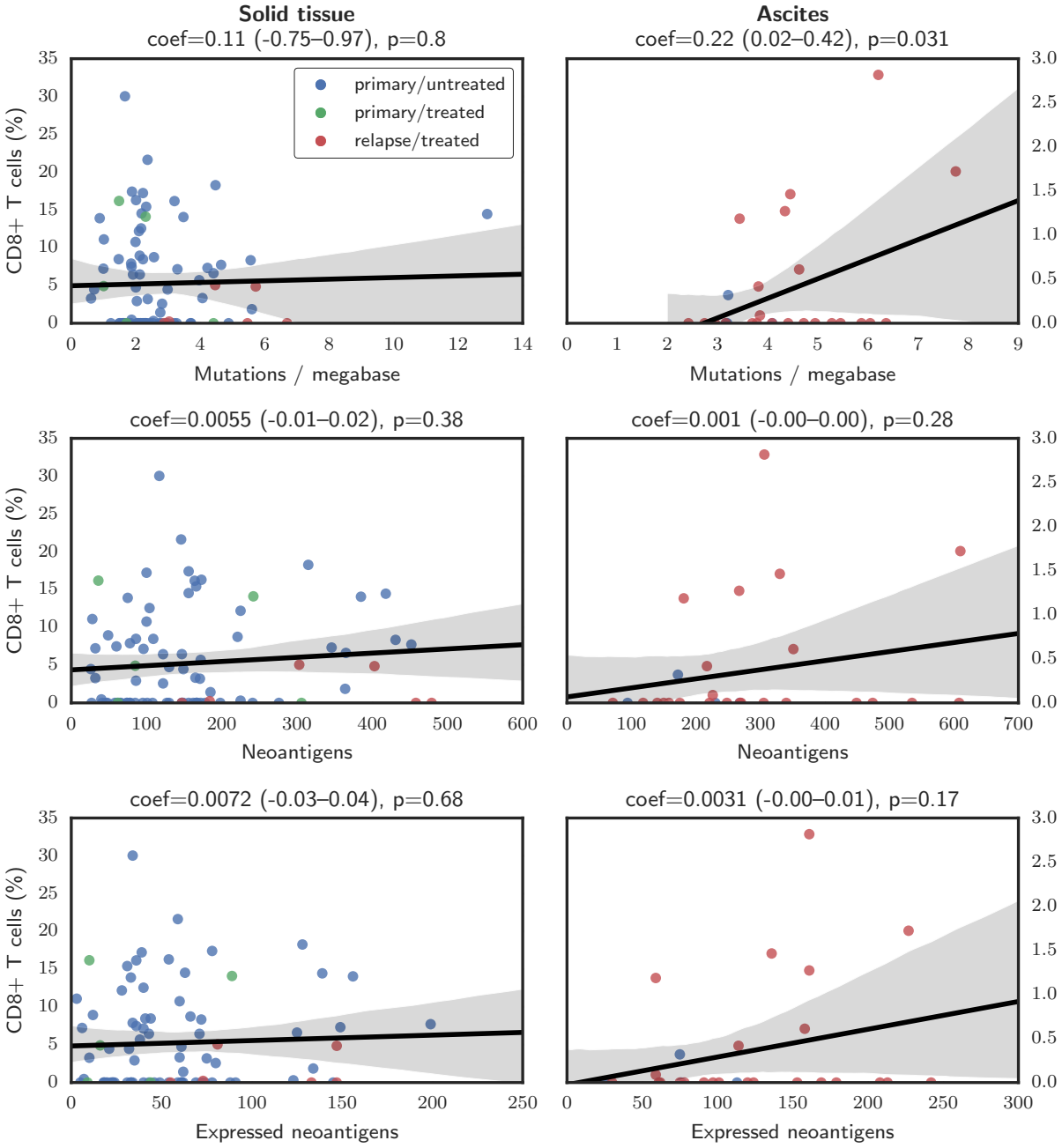

Figure S9: **Relationship between CD8+ T cell infiltrate estimated by CIBERSORT and mutations, neoantigens, or expressed neoantigens for solid tissue (left) and ascites (right) samples.** Colors indicate sample time point.

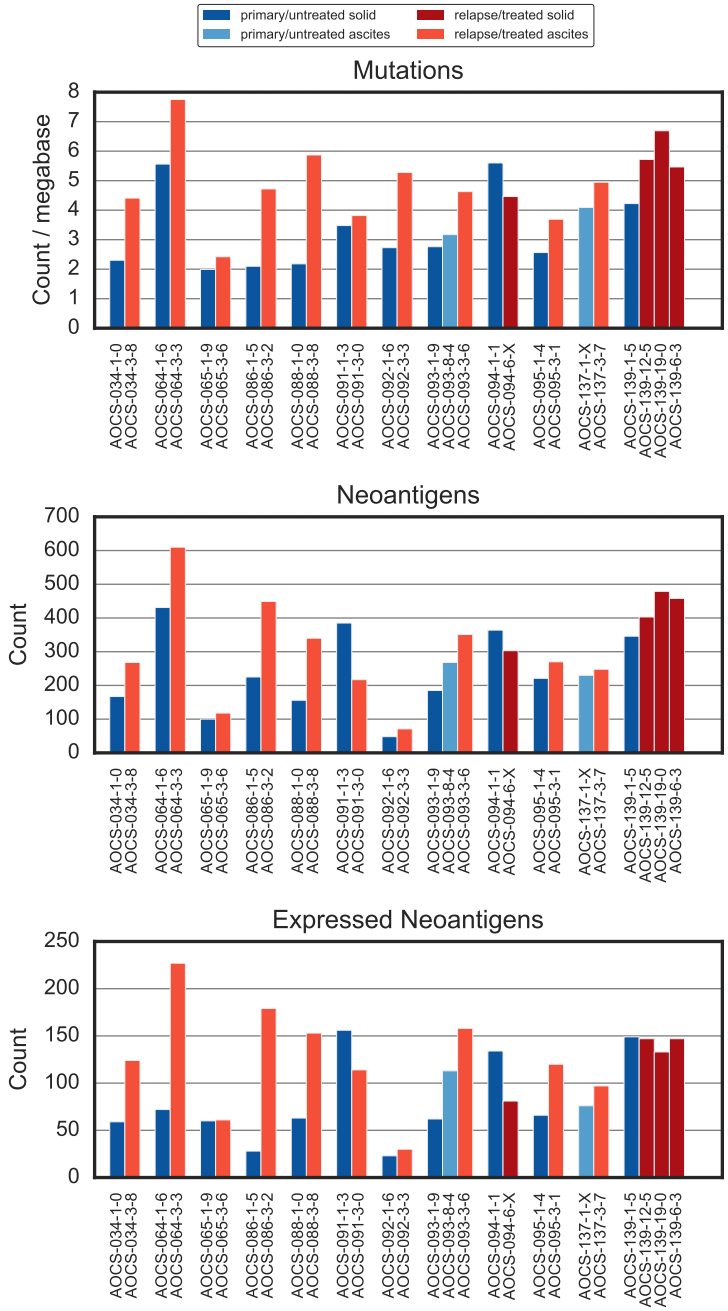

Figure S10: **Mutations, neoantigens, and expressed neoantigens for donor-matched primary/untreated and relapse/treated samples.**

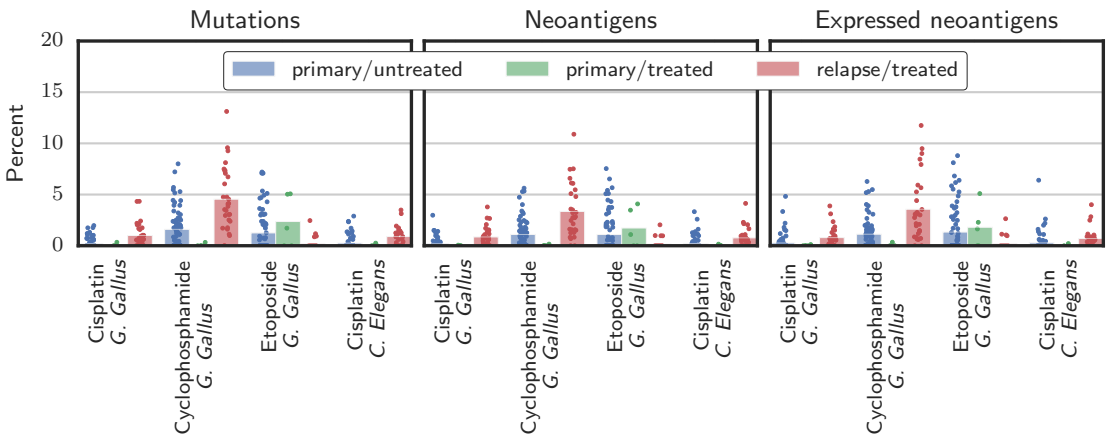

Figure S11: **Contribution of chemotherapy SNV signatures.** The fraction of each sample's mutations, neoantigens, and expressed neoantigens attributed to putative chemotherapy signatures is shown. Bars give the mean, and points indicate individual samples.