Supplemental Figures

Chemotherapy weakly contributes to predicted neoantigen expression in ovarian cancer

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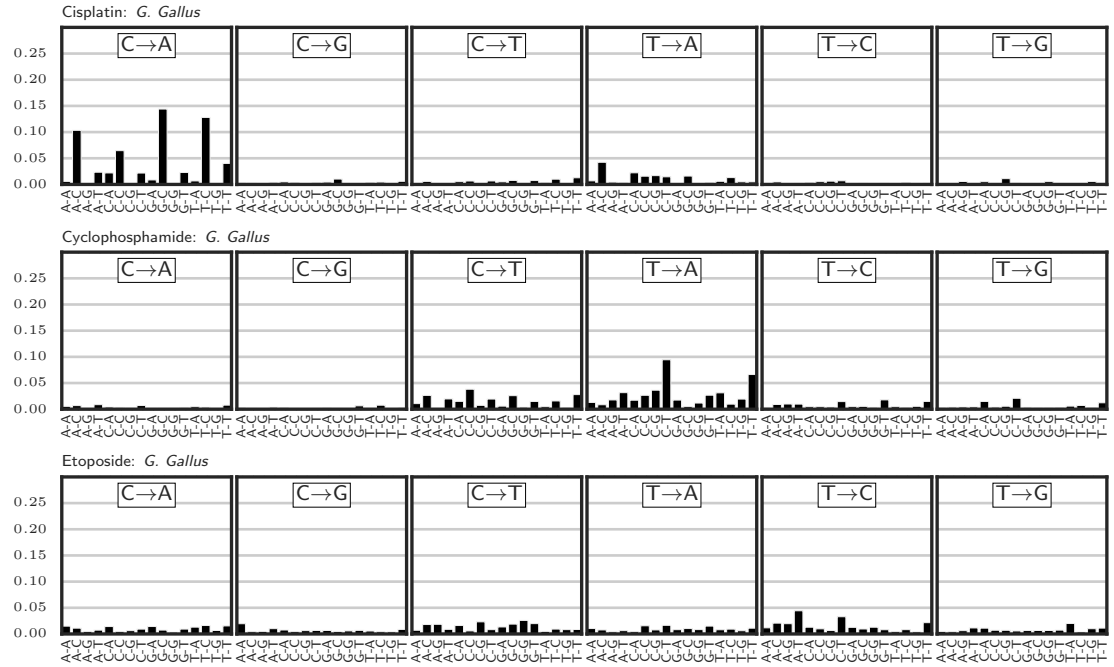

Figure S1: Mutational signatures extracted from Szikriszt et al. [1]

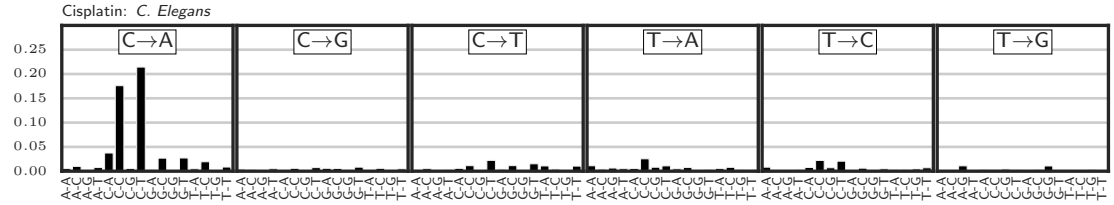

Figure S2: Mutational signature extracted from Meier et al. [2]

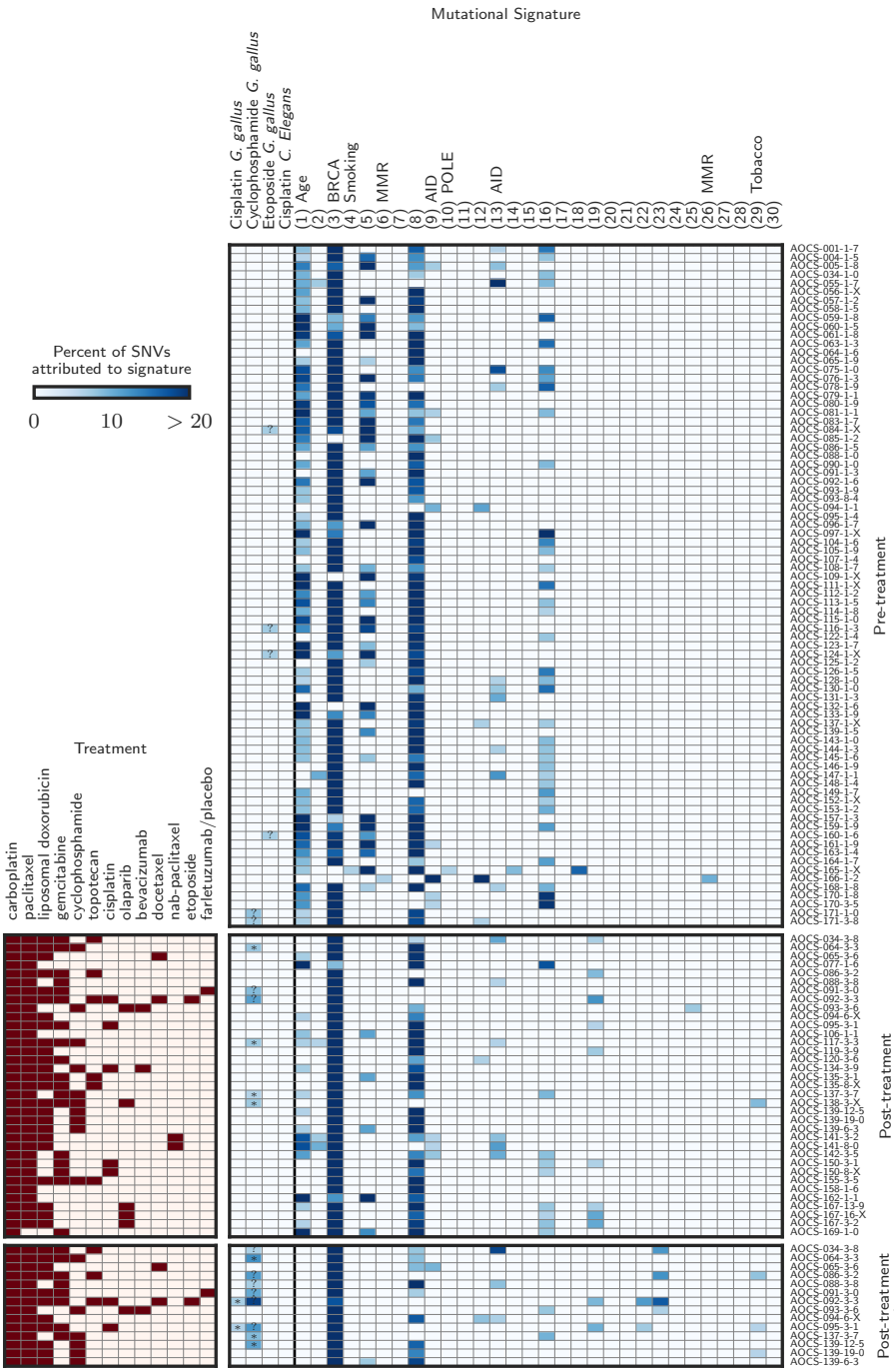

Figure S3: **Detected mutational signatures across all samples.** The symbols are as in main text Figure 1. The top and middle panels show the signature deconvolutions for all pre- and post-treatment samples, respectively. The bottom panel shows deconvolutions for the mutations unique to the paired post-treatment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

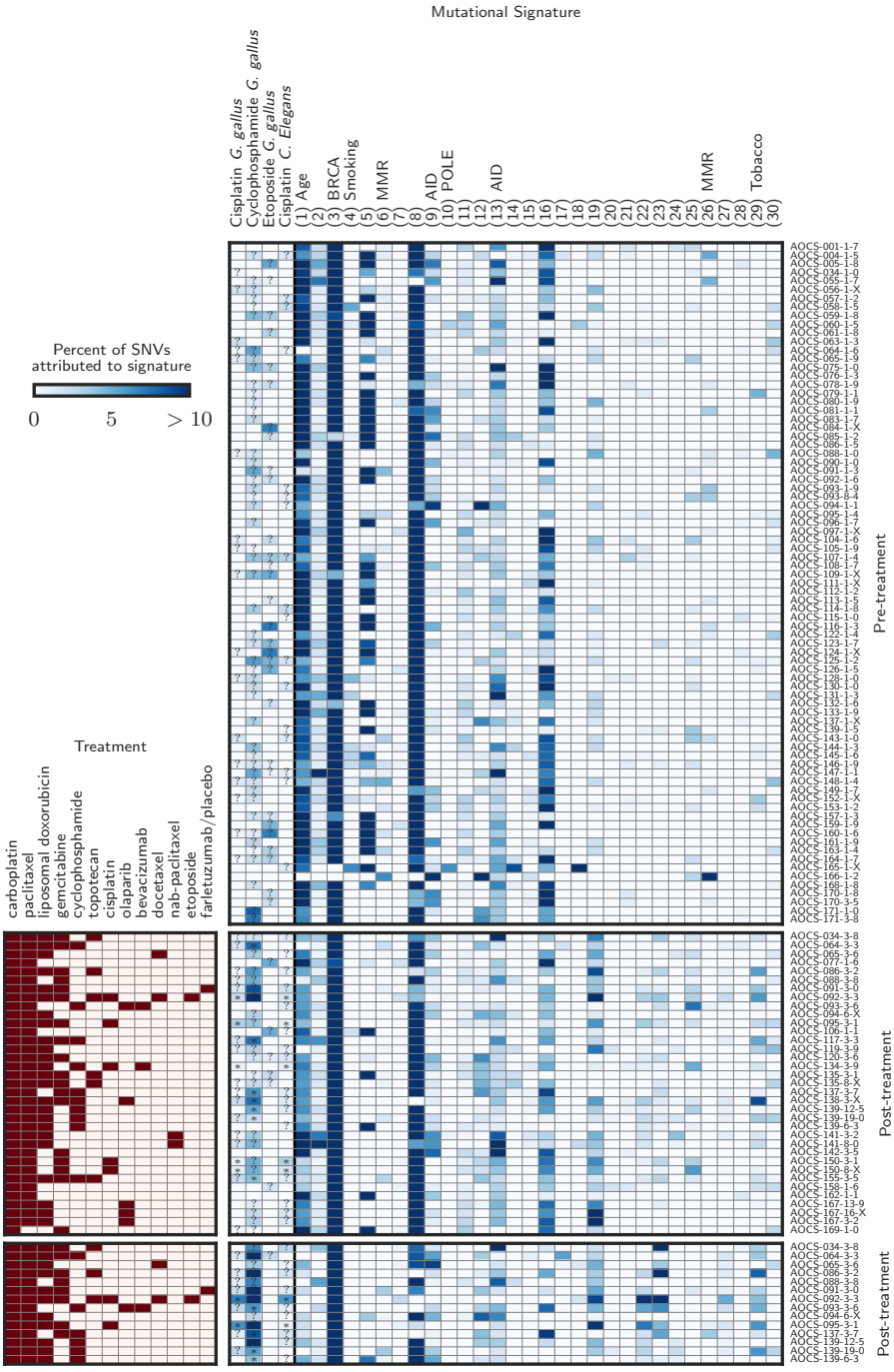

Figure S4: **Mutational signature deconvolutions without any threshold of detection.** Here, signatures accounting for less than the 6% recommended detection threshold are included.

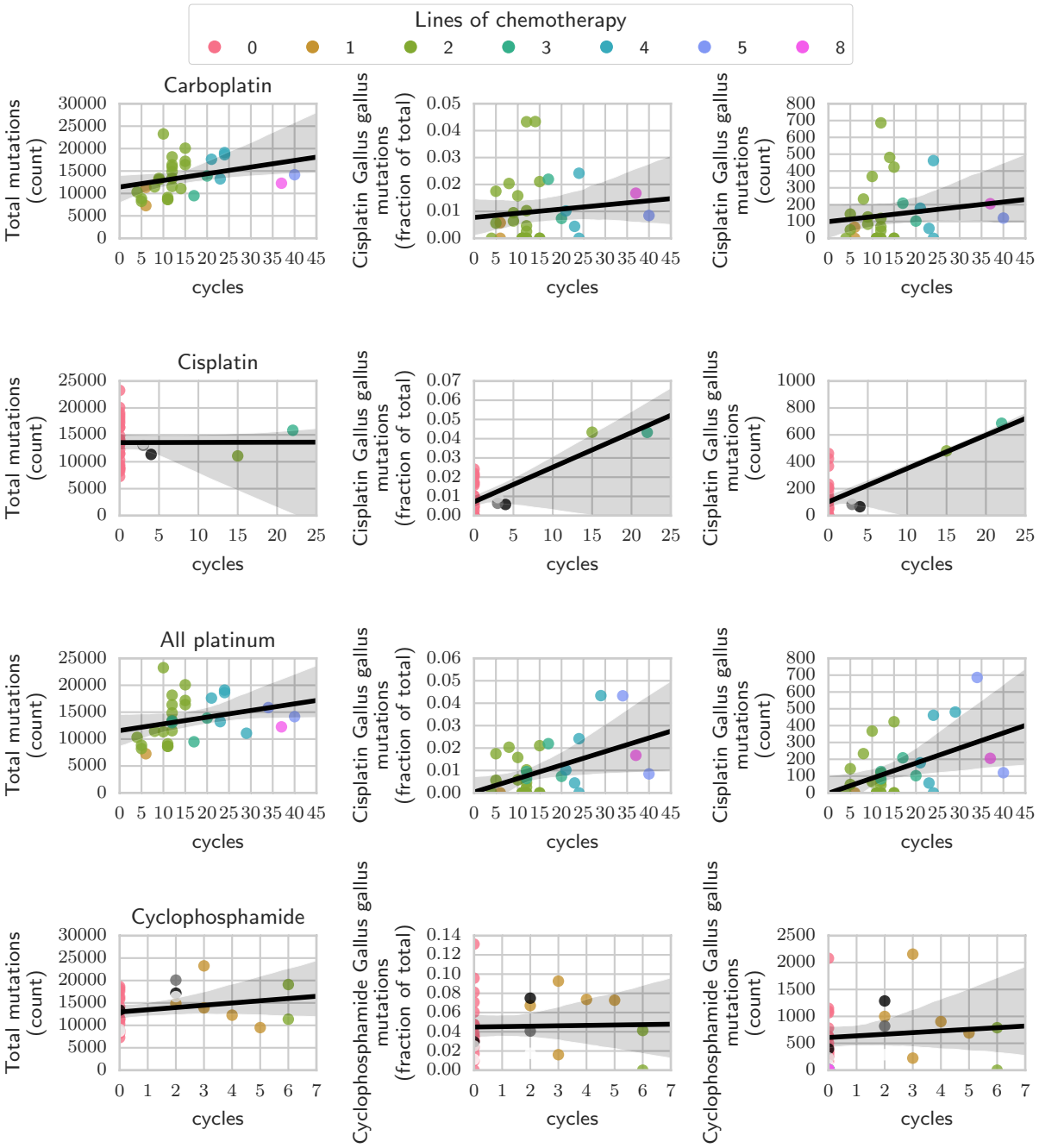

Figure S5: **Association of chemotherapy cycles on total genome-wide mutation burden (left) and mutations attributed to the *G. Gallus* cisplatin and cyclophosphamide signatures as a fraction of total (middle) and as a count (right)**. The total mutation burden includes both SNVs and indels. Cycles indicated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

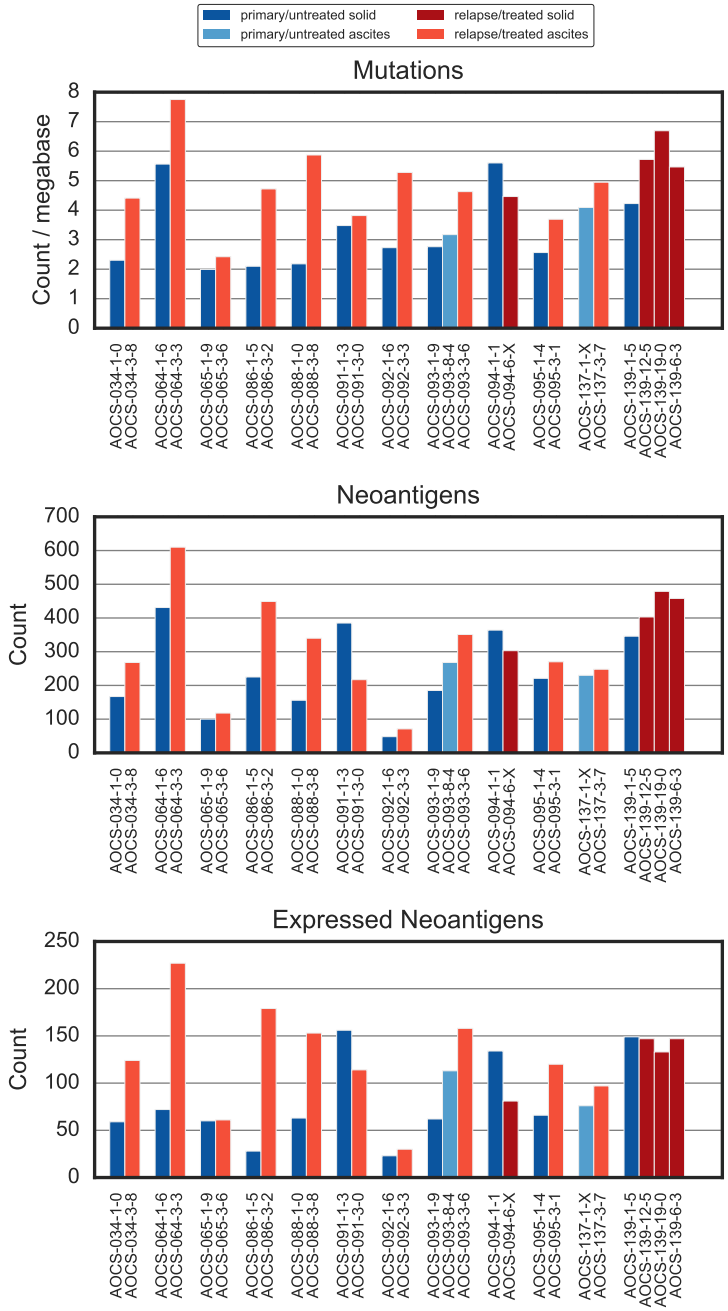

Figure S6: Mutations, neoantigens, and expressed neoantigens for donor-matched primary/untreated and relapse/treated samples.

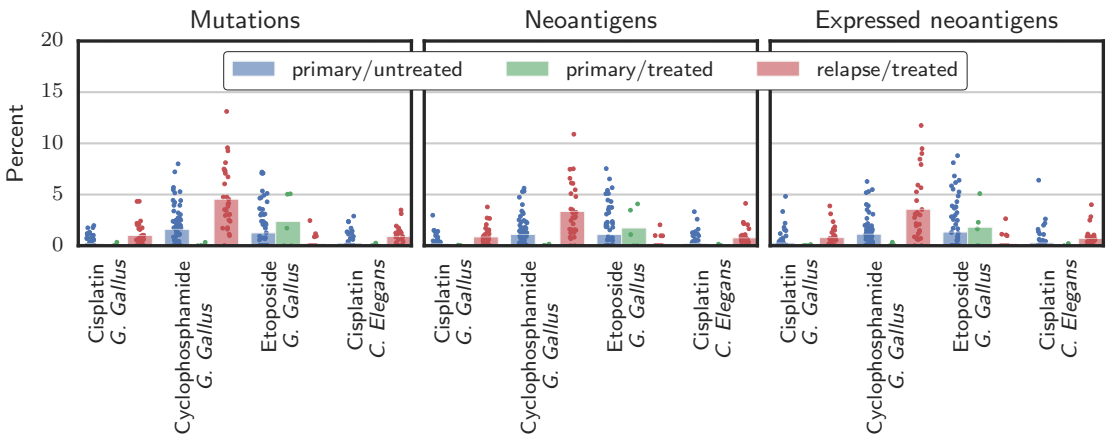

Figure S7: **Contribution of chemotherapy SNV signatures.** The fraction of each sample's mutations, neoantigens, and expressed neoantigens attributed to putative chemotherapy signatures is shown. Bars give the mean, and points indicate individual samples.

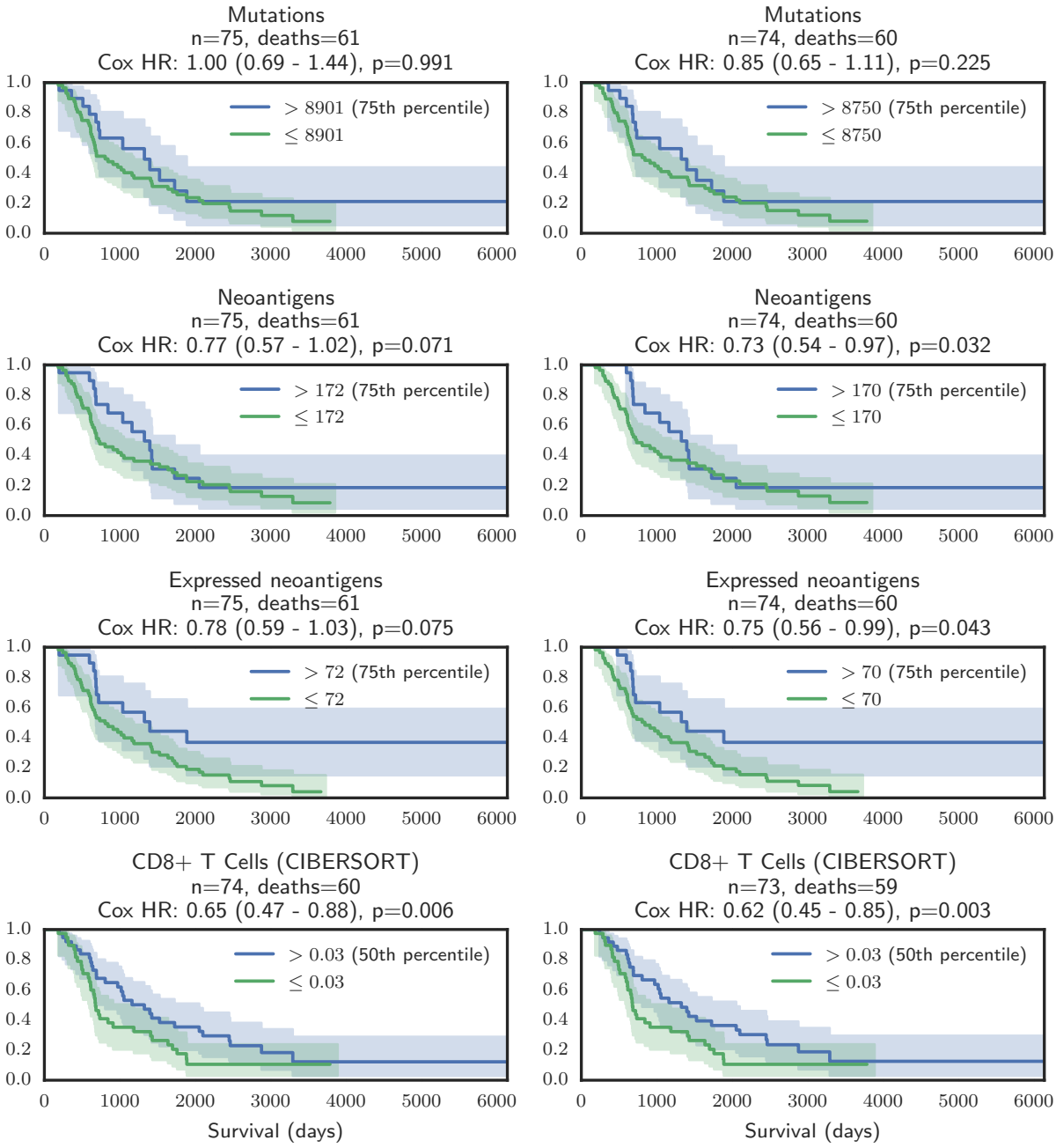

Figure S8: **TODO TODO.** TODO TODO.

Figure S9: **RNA-seq based immune deconvolution (CIBERSORT) on solid-tissue samples.** TODO TODO.

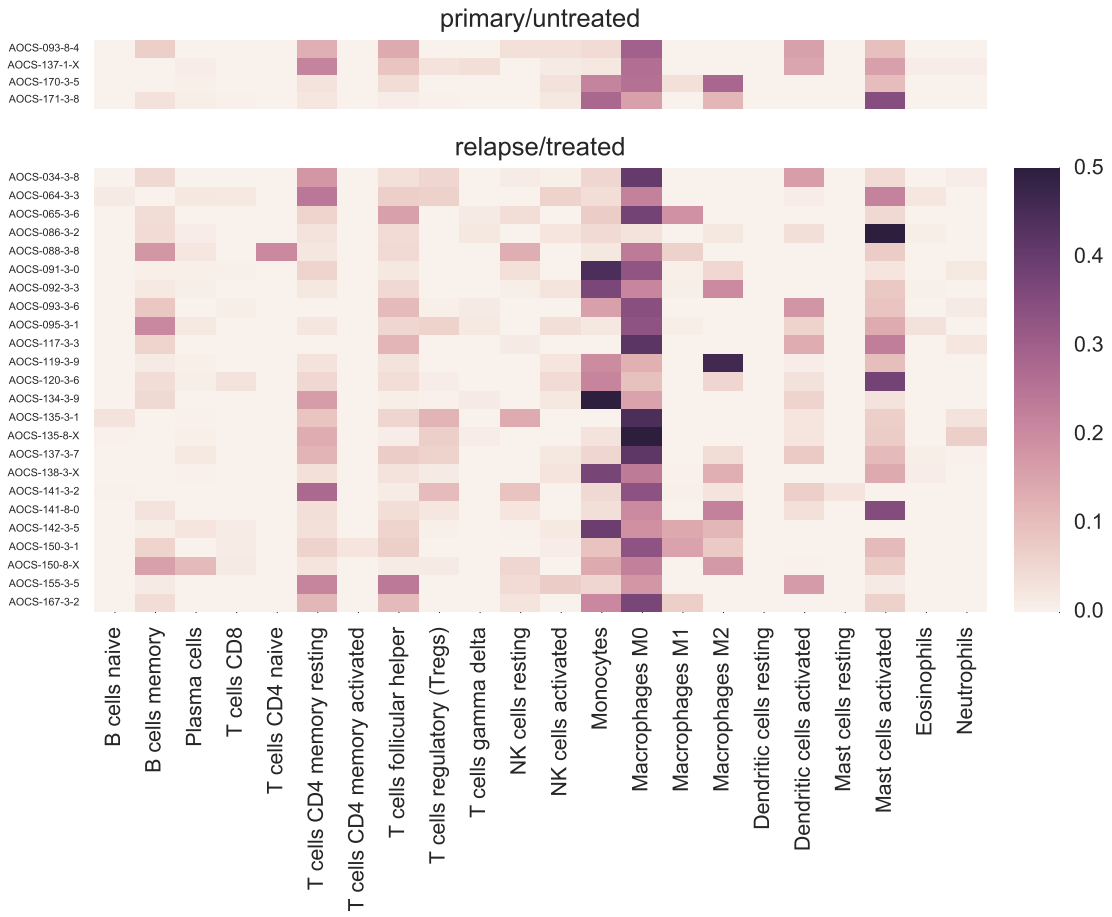

Figure S10: **RNA-seq based immune deconvolution (CIBERSORT) on ascites samples.** TODO TODO.

References

[1] B. Szikriszt, Á. Póti, O. Pipek, M. Krzystanek, N. Kanu, J. Molnár, D. Ribli, Z. Szeltner, G. E. Tusnády, I. Csabai, Z. Szallasi, C. Swanton, and D. Szts, "A comprehensive survey of the mutagenic impact of common cancer cytotoxics," *Genome Biol*, vol. 17, may 2016.

[2] B. Meier, S. L. Cooke, J. Weiss, A. P. Bailly, L. B. Alexandrov, J. Marshall, K. Raine, M. Maddison, E. Anderson, M. R. Stratton, A. Gartner, and P. J. Campbell, "C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency," *Genome Research*, vol. 24, pp. 1624–1636, jul 2014.