Supplemental Figures

Chemotherapy weakly contributes to predicted neoantigen expression in ovarian cancer

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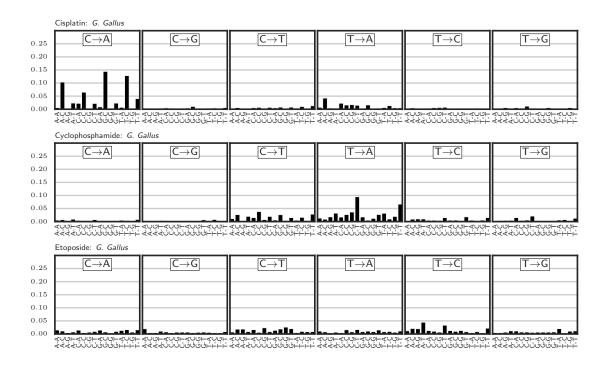


Figure S1: Mutational signatures extracted from Szikriszt et al. [1]



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

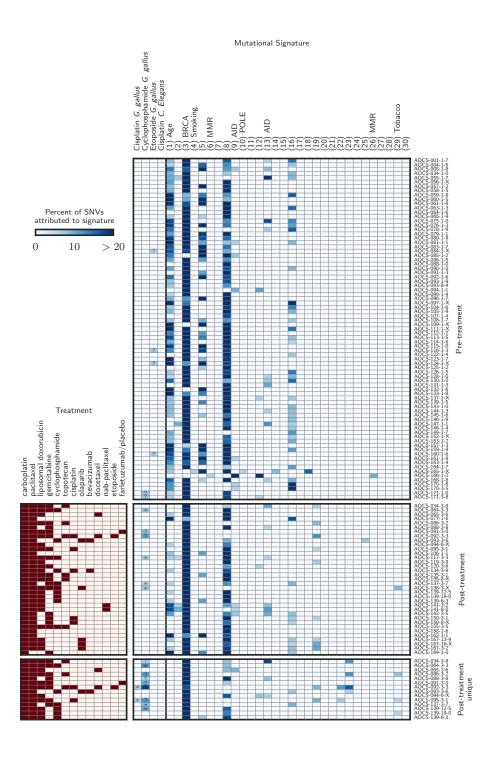


Figure S3: **Detected mutational signatures across all samples.** The symbols are as in main text Figure 1. The top and middle panels show the signature deconvolutions for all pre- and post-treatment samples, respectively. The bottom panel shows deconvolutions for the mutations unique to the paired post-treatment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

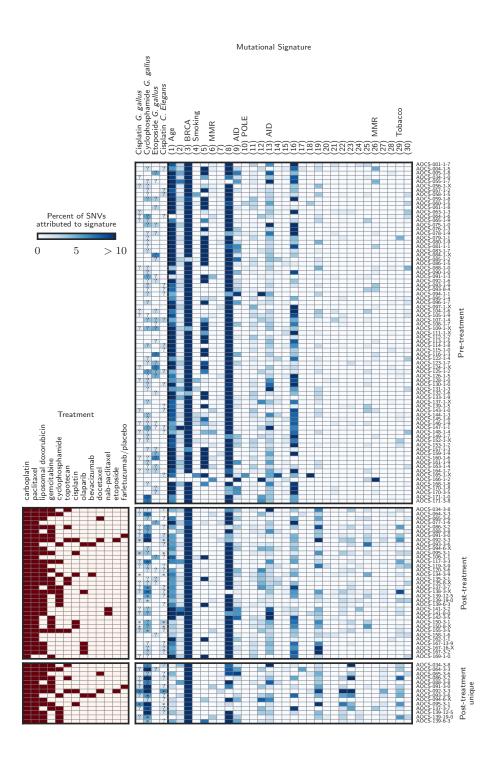


Figure S4: Mutational signature deconvolutions without any threshold of detection. Here, signatures accounting for less than the 6% recommended detection threshold are included.

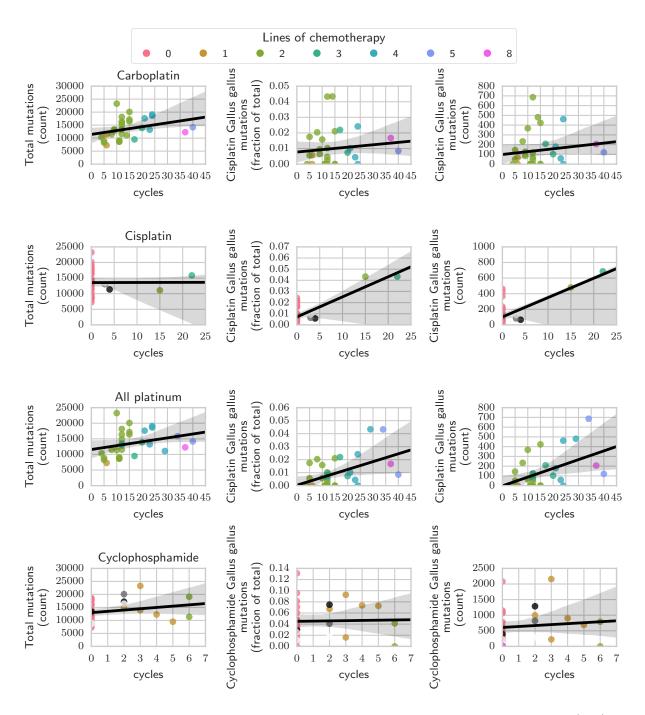


Figure S5: Association of chemotherapy cycles on total genome-wide mutation burden (left) and mutations attributed to the *G. Gallus* cisplatin and cyclophosphamide signatures as a fraction of total (middle) and as a count (right). The total mutation burden includes both SNVs and indels. Cycles indicated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

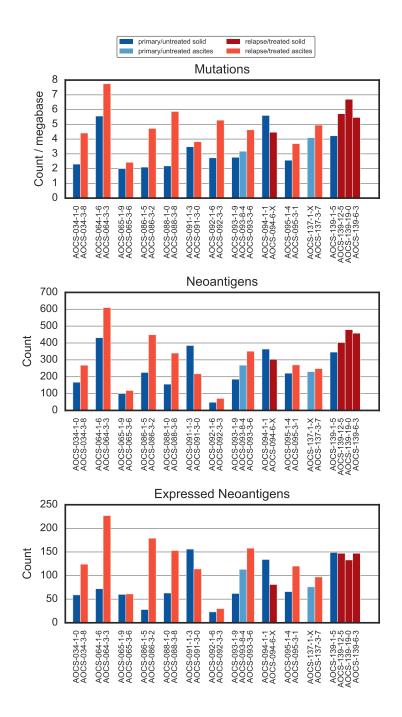


Figure S6: Mutations, neoantigens, and expressed neoantigens for donor-matched primary/untreated and relapse/treated samples.

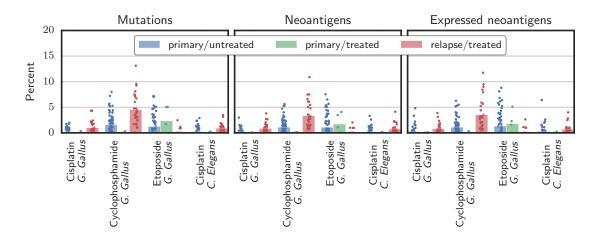


Figure S7: Contribution of chemotherapy SNV signatures. The fraction of each sample's mutations, neoantigens, and expressed neoantigens attributed to putative chemotherapy signatures is shown. Bars give the mean, and points indicate individual samples.

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.