Supplementary Figures

Immune phenotype in high- versus low-NRF2 high grade serous ovarian cancer and the impact on prognosis

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 # Equally contributed to this work

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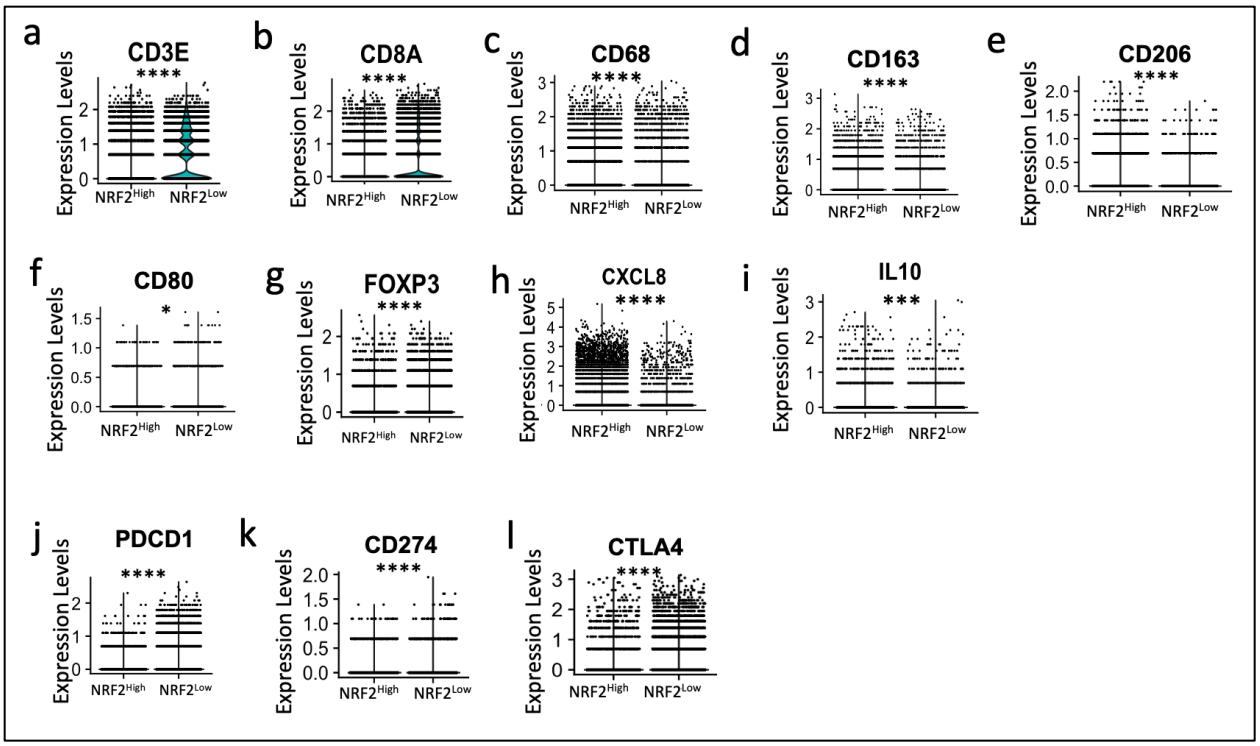
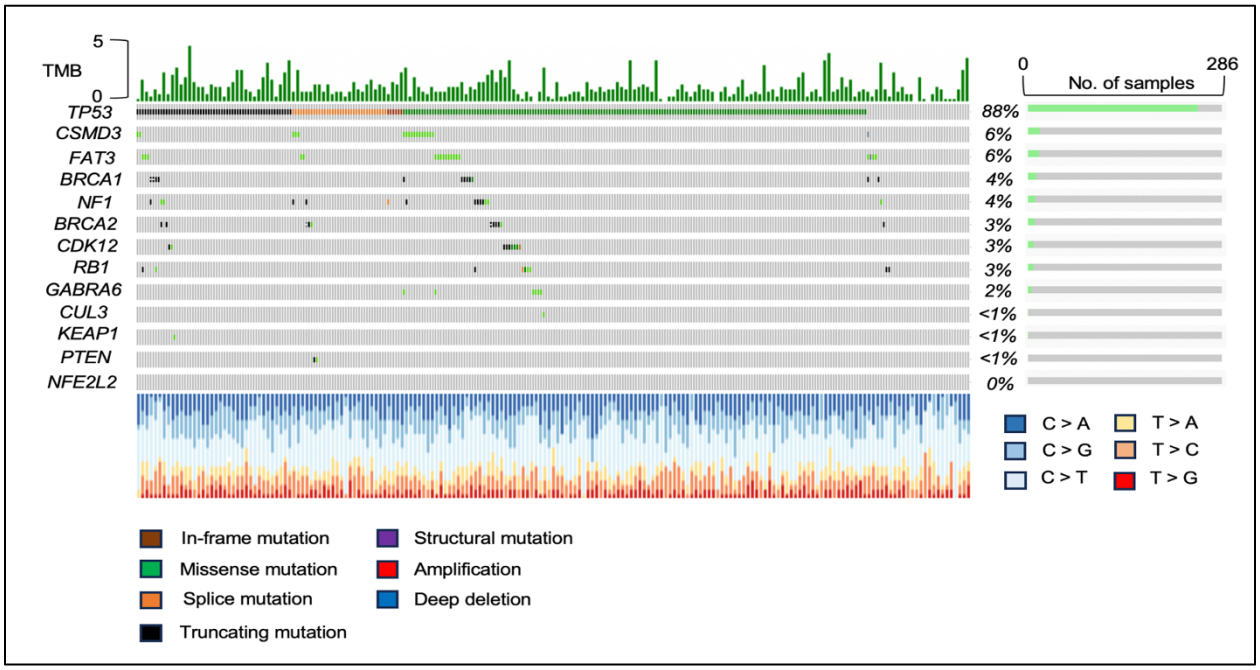
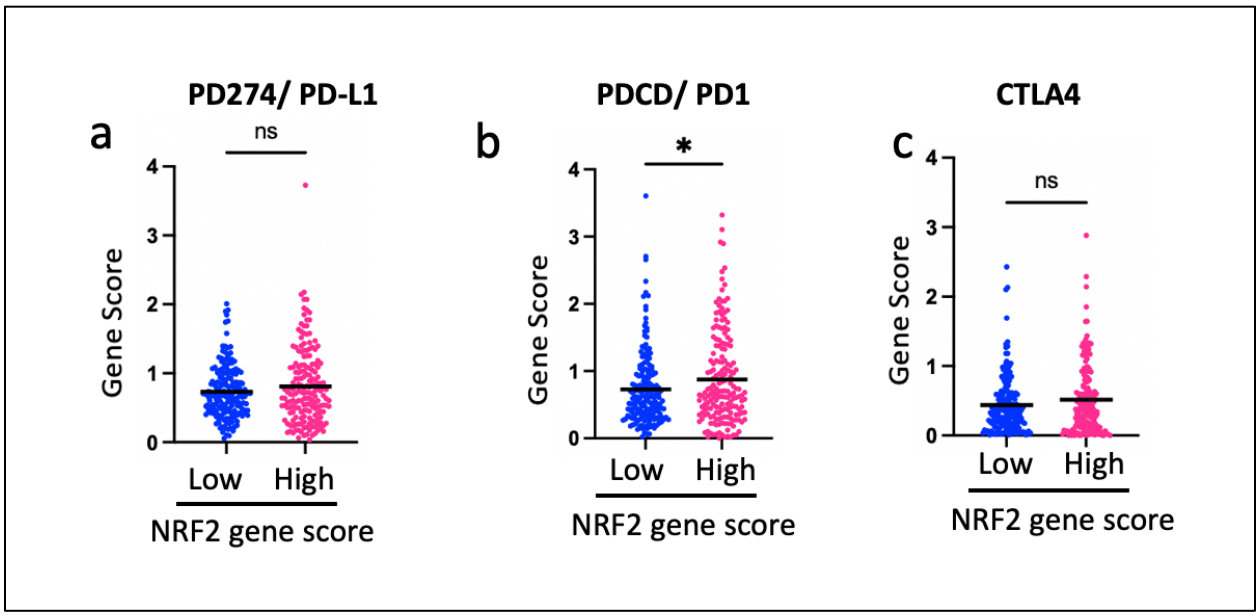


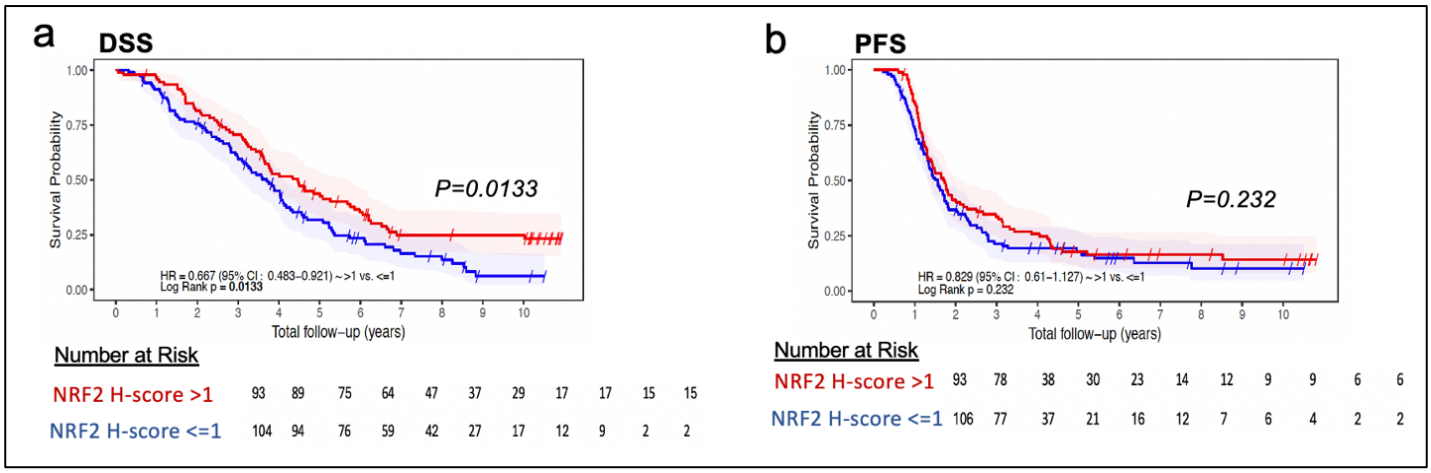
Supplementary Figure 1. Single cell RNA-seq data analysis of 7 human HGSOC tumor samples show different immune markers and checkpoints in high (n=4) versus low (n=3) NRF2 HGSOC. a-b Expression levels of T-cell markers (CD3E and CD8A), **c-f** Expression levels of macrophages markers (CD68, CD163, CD206, and CD80), **h-i** Expression levels of cytokines and chemokines, and **j-l** Expression levels of immune checkpoints in high versus low NRF2 samples, *P<0.05, ***P<0.001, ****P<0.0001.



Supplementary Figure 2. RNA-seq data analysis of HGSOC tumor samples from TCGA. Major mutations in n=365 HGSOC tumor samples among which mutations in the queried genes were observed in n=286 samples. KEAP1-NRF2 pathways shows no mutations in this set of samples.



Supplementary Figure 3. Higher expression of PD1 in high NRF2 HGSOC compared to NRF2 low tumors. a No changes in expression levels of PD-L1 in high versus low NRF2 HGSOC, **b** significantly higher expression levels in PD1 in high compared to low NRF2 HGSOC, with **c** no significant changes in expression levels of CTLA4 in high versus low NRF2 HGSOC.



Supplementary Figure 4. Survival of HGSOC patient samples with $NRF2^{High}$ (H-score >1) and $NRF2^{Low}$ (H-score <=1) HGSOC. **a** Significantly higher disease-specific survival (DSS) of patients with $NRF2^{High}$ HGSOC compared to patients with $NRF2^{Low}$ HGSOC, but **b** no significant change in progression-free survival (PFS) between patients with $NRF2^{high}$ and those with $NRF2^{Low}$ tumors.