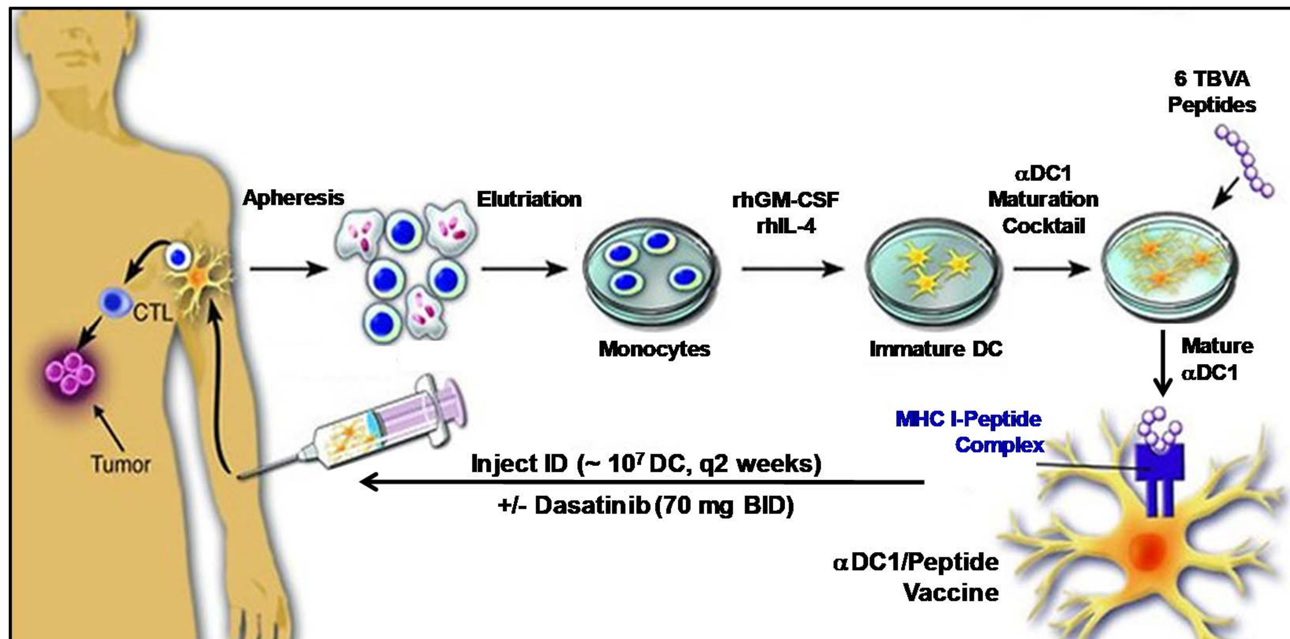

Fig. S1. Generation of autologous αDC1/TBVA peptide-based vaccines and use in NCT01876212. Patient monocytes elutriated from apheresis products were cultured in the presence of rhGM-CSF + rhIL-4 for 5 days to generate immature DC, which were then matured into αDC1 and loaded with a mixture of 6 HLA-A2-binding peptides derived from TBVA as outlined in Materials and Methods. Approximately 107 TBVA peptide-loaded αDC1 were injected i.d. every 2 weeks in the vicinity of the nodal drainage groups of the four extremities. Dasatinib was administered (70 mg p.o. BID) beginning in either week 1 (Arm B) or week 5 (Arm A). Based on our therapeutic paradigm, injected peptide-loaded αDC1 initiate the cross-priming of antigen-specific CD8^{+} T (CTL) cell responses that are competent to target the tumor-associated vasculature, infiltrate the TME and mediate anti-tumor therapeutic activity in effectively vaccinated patients.

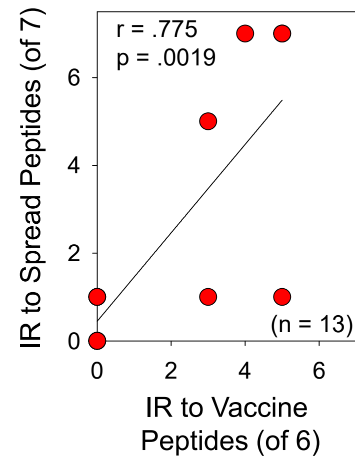

Figure S2. Patient immune response (IR) to vaccine peptides correlates with IR to spread (non-vaccine) peptides. The number of vaccine or non-vaccine peptides to which individual patients developed a positive response on-treatment (per **Fig. 2A**) was determined using IFN-γ ELISPOT assays as outlined in Materials and Methods.

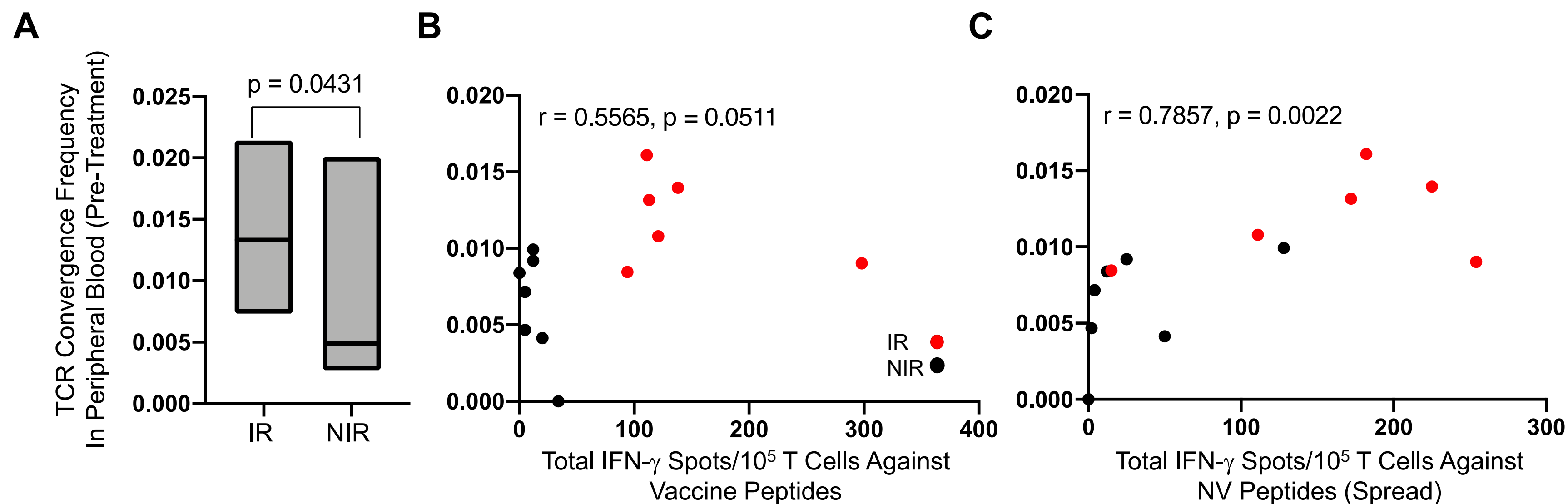

Figure S3. Peripheral blood TCR convergence at baseline is associated with patient response to vaccine peptides and epitope spreading (ES). In **A**, patient baseline peripheral blood TCR convergence is reported based on patient immune response (IR) to vaccine peptides vs. no immune response (NIR) to vaccine peptides. TCR convergence is plotted vs. cumulative T cell response to vaccine (**B**) or non-vaccine (NV) peptides (**C**) as determined in IFN-γ ELISPOT assays, with the latter serving as an index of epitope spreading in the patient T cell repertoire on-treatment.

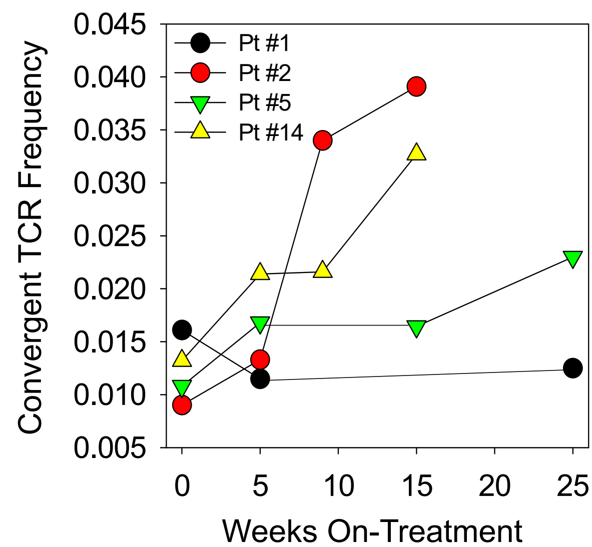

Figure S4. TCR convergence in the peripheral blood T cell repertoire remains stable or increases over time on-treatment in PR patients. Peripheral blood specimens isolated from patients at baseline vs. the indicated time points on-treatment were analyzed using Oncomine TCRB-LR assays for TCR convergence as described in Materials and Methods.

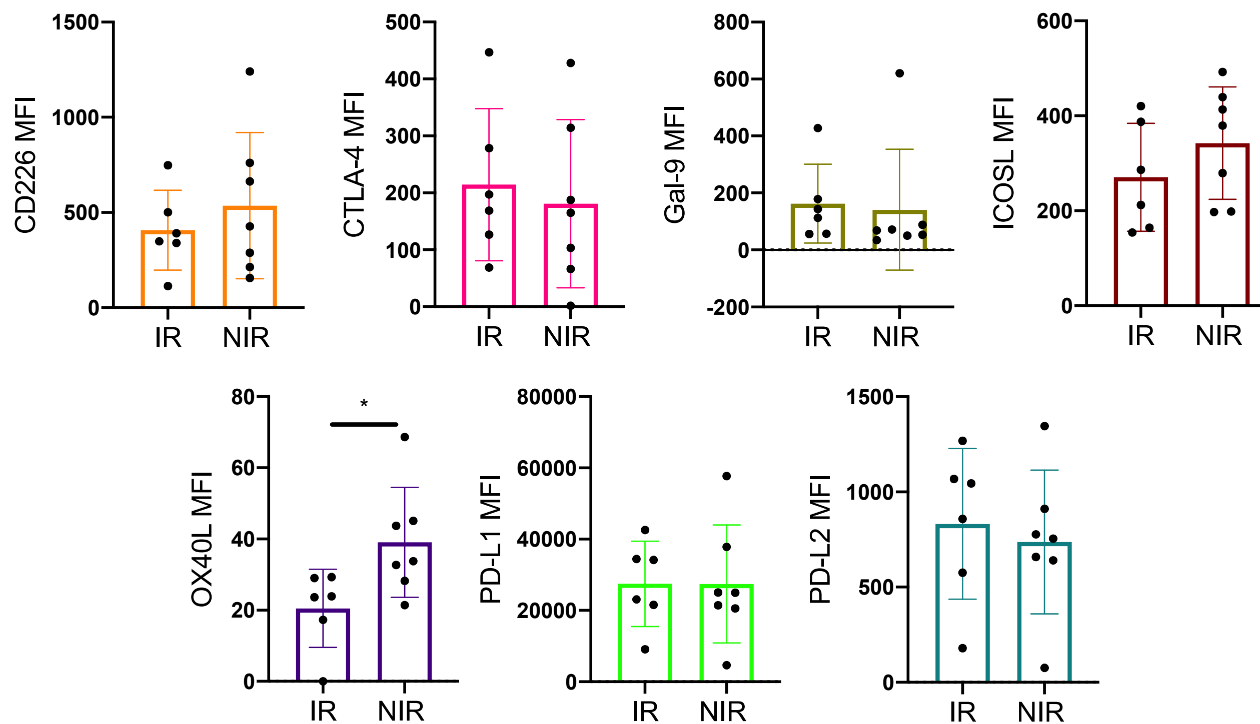

Figure S5. Flow cytometry analysis of cell surface costimulatory and checkpoint molecules on vaccine αDC1 segregated based on patient immunologic/clinical response to treatment. Aliquots of cryopreserved vaccine αDC1 were stained for the indicated cell surface proteins and analyzed by flow cytometry as outlined in Materials and Methods. Abbreviations: IR, immune response to vaccination; MFI, mean fluorescence intensity; NIR, no immunologic response to vaccination.

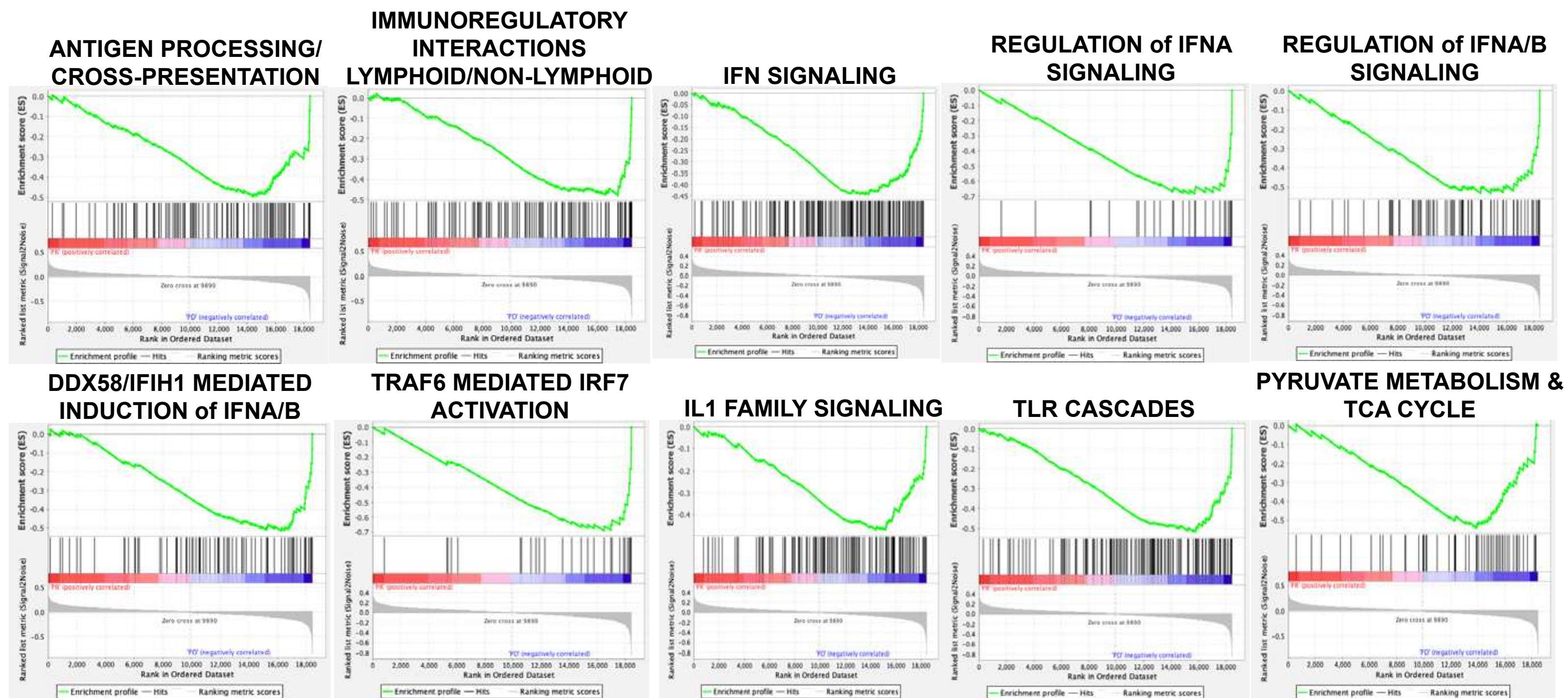

Figure S6. Predominance of gene signatures associated with deficiency in antigen-presenting cell function and IFN/TLR/IL1 family cytokine signaling in αDC1 from NIR/PD vs. IR/PR patients. Gene array **profiling of patient vaccine αDC1 tumor biopsy tissues was performed as outlined in Fig. 4 and Materials and Methods, with gene set enrichment ($p < 0.05$) then assessed using GSEA software (V.4.1.0) as described in Supplemental Materials and Methods.**

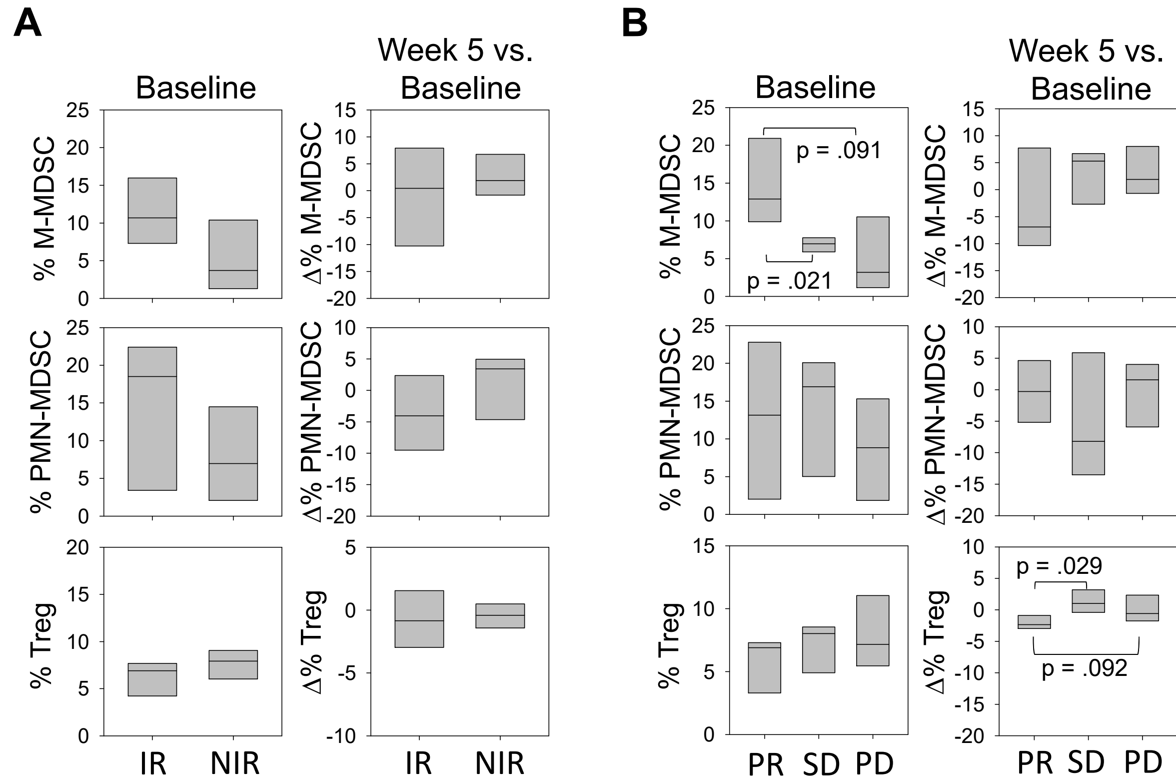

Figure S7. Peripheral blood regulatory cells exhibited modest changes in frequency on-treatment. Frequencies of myeloid-derived suppressor cells (M-MDSC and PMN-MDSC) and FoxP3⁺CD4⁺ Treg cells in patient peripheral blood were determined by flow cytometry at baseline and on-treatment (week 5 vs. baseline). Bar and wisker plots are provided based on the segregation of patients based on IR (panel **A**) or OCR (panel **B**) status. Abbreviations: IR, immune response to vaccination; NIR, no immune response to vaccination; PD, progressive disease; PR, partial response; SD, stable disease.

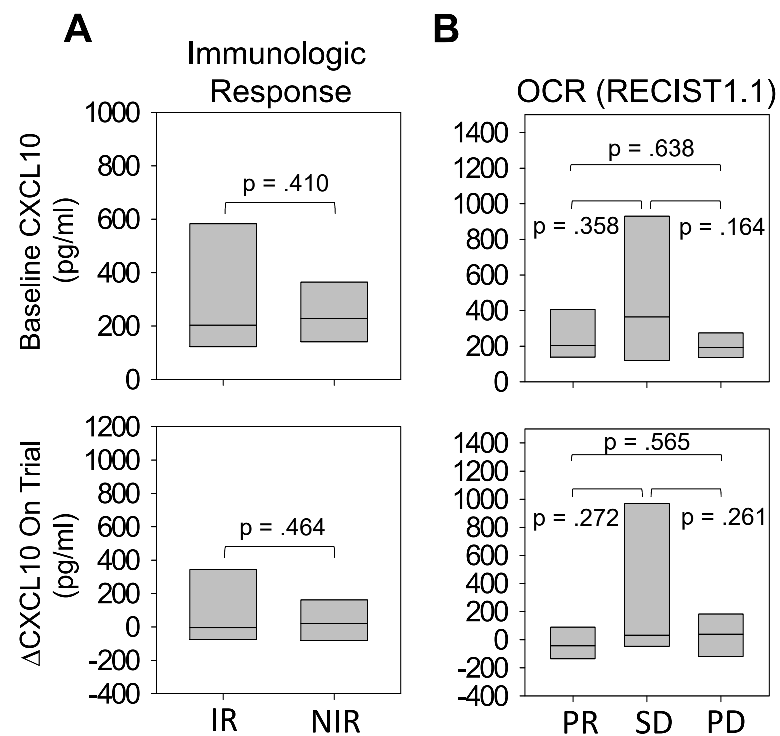

Figure S8. Serum CXCL10 fails to identify patients based on immune and clinical response to vaccination. Patient sera were isolated at baseline and 5 week on-treatment and analyzed for CXCL10 content by specific ELISA as outlined in Materials and Methods. Bar and whisker plots are depicted for patient results segregated based on (**A**) immune response (IR) vs non-immune response (NIR) to vaccine peptides as determined in IFN-γ ELISPOT assays or (**B**) OCR status on trial. Abbreviations: IR, immune response to vaccination; NIR, no immune response to vaccination; OCR, objective clinical response; PD, progressive disease; PR, partial response; SD, stable disease.

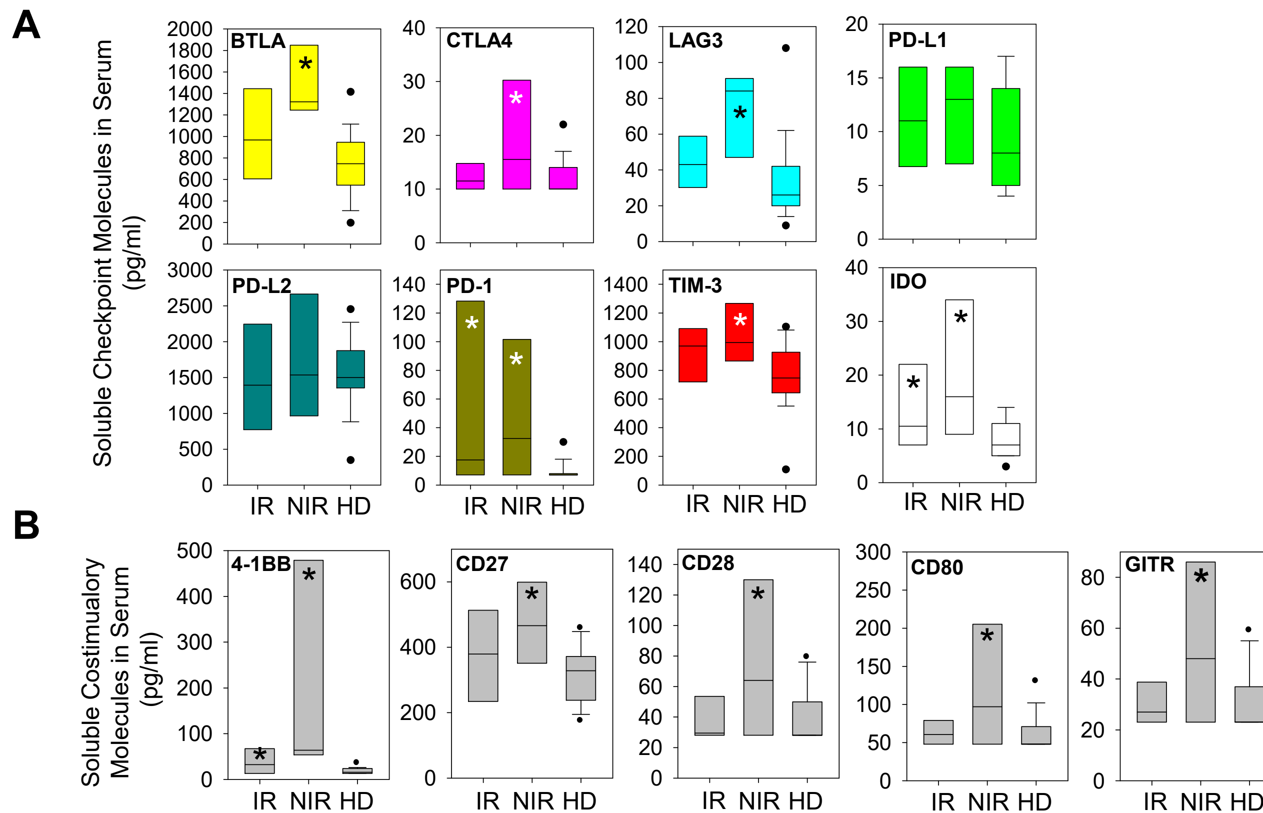

Figure S9. Serum levels of soluble checkpoint or costimulatory molecules fail to identify patients based on immune response to vaccination. Patient sera were isolated at baseline and 5 week on-treatment and analyzed for the indicated soluble checkpoint (**A**) or costimulatory (**B**) molecules using the multiplex Luminex Immuno-Oncology Checkpoint Marker Panel as described in Materials and Methods. Bar and whisker plots are depicted for patient results segregated based on immune response (IR) vs non-immune response (NIR) to vaccine peptides as determined in IFN-γ ELISPOT assays. Not significant (NS) for IR vs. NIR. *$p < 0.05$ vs. HD. Abbreviations: HD, healthy donors; IR, immune response to vaccination; NIR, no immune response to vaccination.

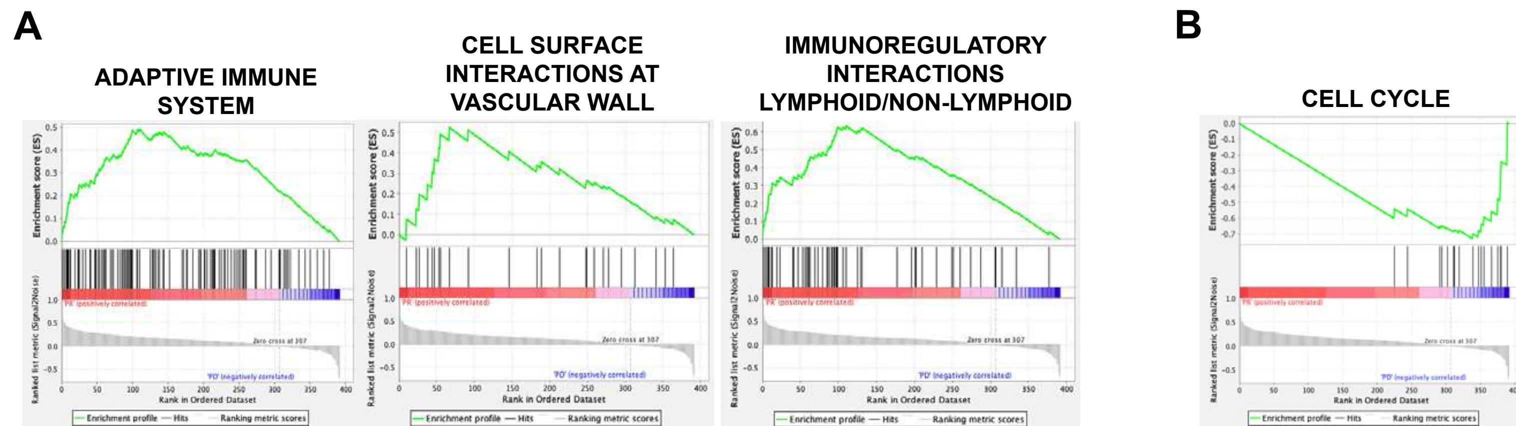

Figure S10. Baseline tumor pathways associated with patient outcomes on trial. **OIRRA profiling of tumor biopsy tissues was performed as outlined in Fig. 5 and Materials and Methods, with gene set enrichment then performed using GSEA software (V.4.1.0) as described in Supplemental Materials and Methods. Baseline tumor pathways positively (A) or negatively (B) associated with PR/IR ($p < 0.05$).**

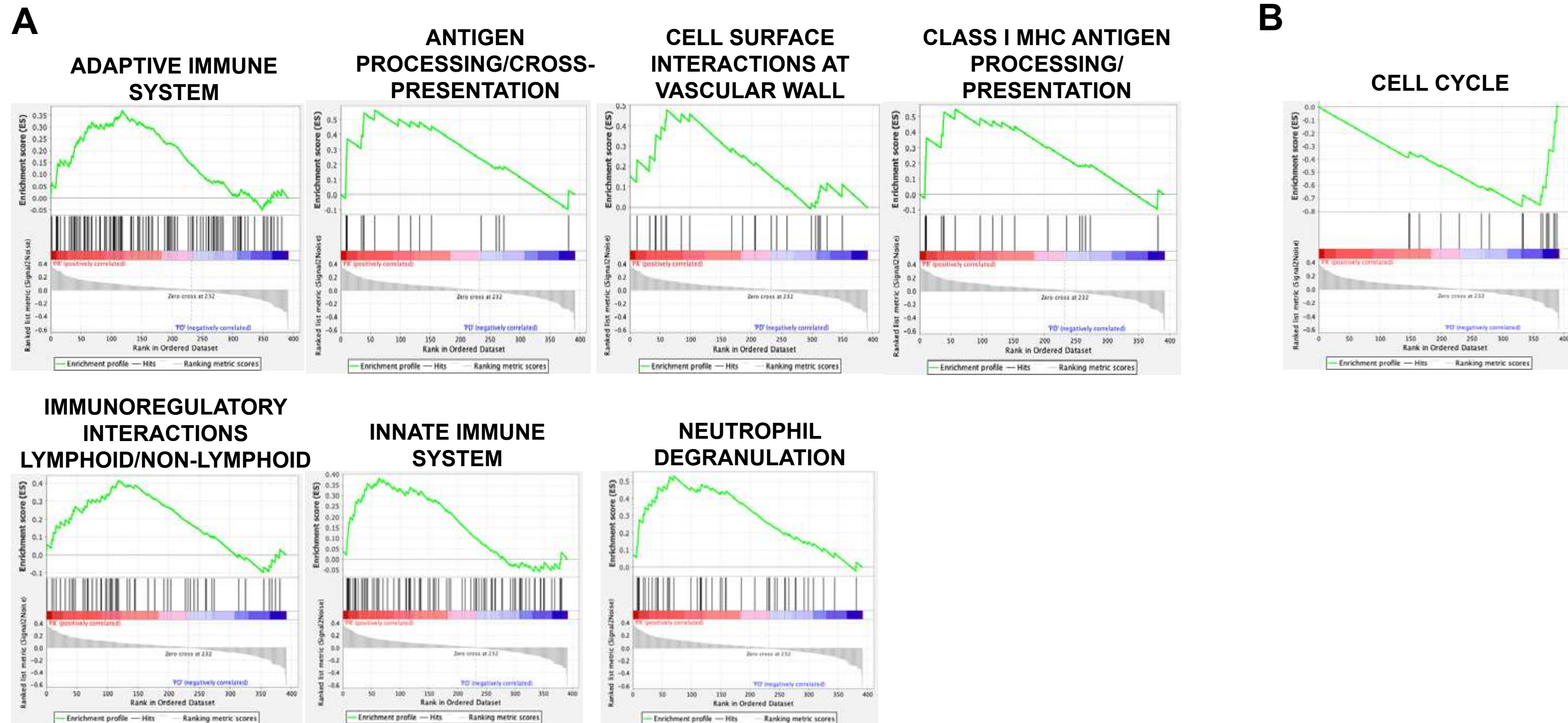

Figure S11. On-treatment tumor pathways associated with patient outcomes on trial. **OIRRA profiling of tumor biopsy tissues was performed as outlined in Fig. 5 and Materials and Methods, with gene set enrichment then performed using GSEA software (V.4.1.0) as described in Supplemental Materials and Methods. On-treatment tumor pathways positively (A) or negatively (B) associated with PR/IR ($p < 0.05$).**