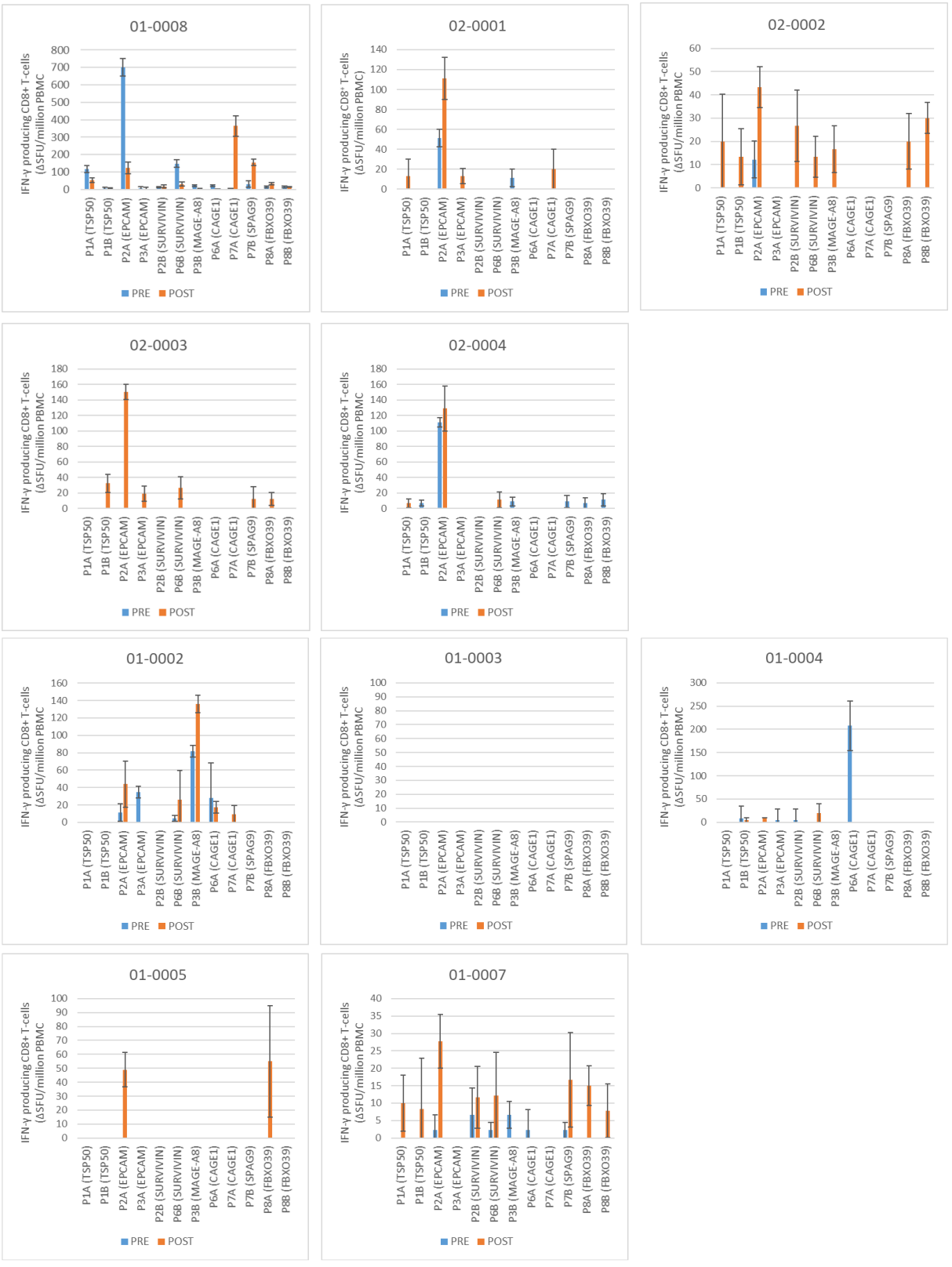
A


01-0008
01-0001
02-0002
02-0003
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01-0007
IFN-γ producing CD8+ T-cells (ΔSFU/million PBMC)
P1A (TSP50)
P1B (TSP50)
P2A (EPCAM)
P3A (EPCAM)
P2B (SURVIVIN)
P6B (SURVIVIN)
P3B (MAGE-A8)
P6A (CAGE1)
P7A (CAGE1)
P7B (SPAG9)
P8A (FBXO39)
P8B (FBXO39)
PRE
POST

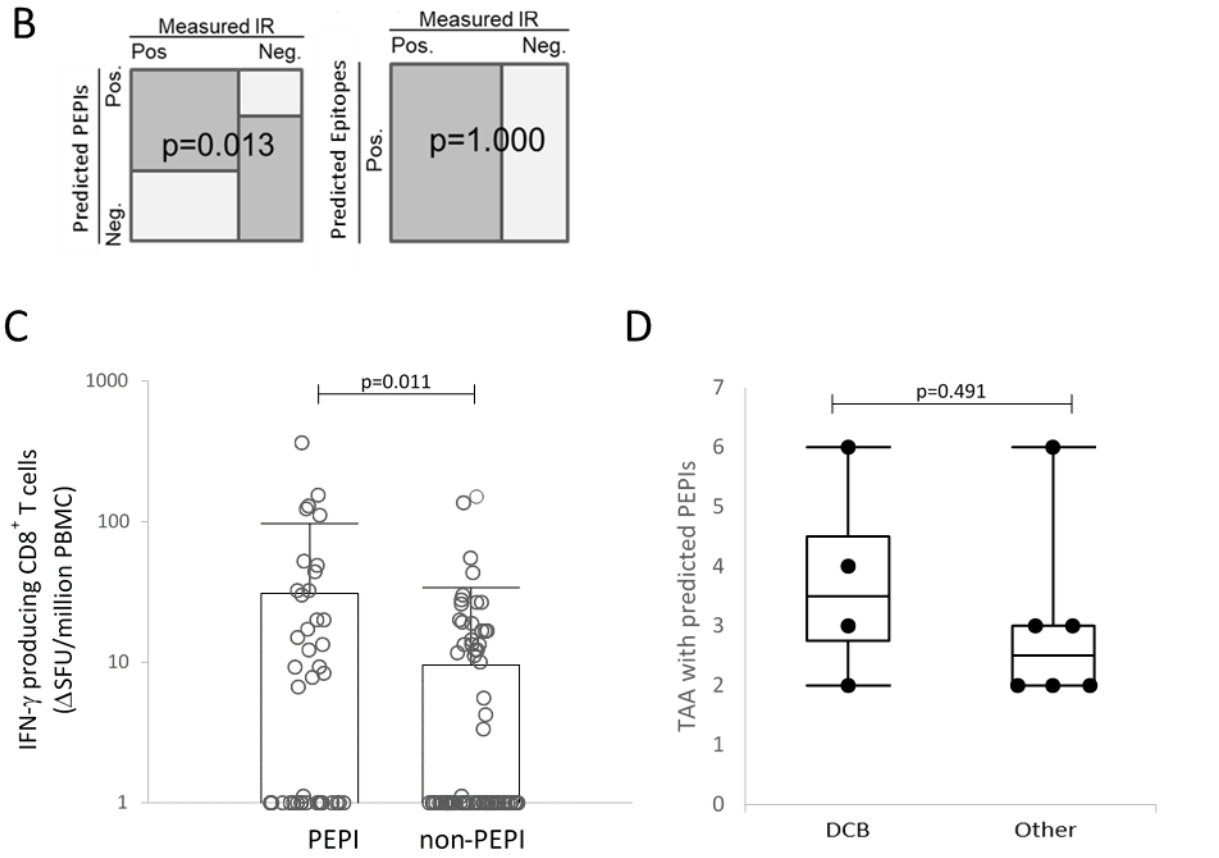

Figure S7: Host HLA genotype through PEPIs predict TAA-specific immune responses and indicate treatment benefit. (A) The number and magnitude of vaccine-specific IFN-γ producing $CD8^+$ T cell responses depicted by patients detected for each of the twelve 9-mer test peptide (core epitopes in Supplementary Table S1). Data presented were measured by IVS ELISpot assay within 12 week after the first dose, n=10. (B) Variable dependency analysis using 2 x 2 contingency table (positive and negative data analysis) and Fisher Exact test between IVS ELISpot measured $CD8^+$ T cell responses (IR) and predicted PEPIs (epitopes binding ≥3 autologous HLA class I alleles) (left panel) and Epitopes (binding ≥1 autologous HLA class I alleles) (right panel) (related to Supplementary Table S3) (C) Magnitude of $CD8^+$ T cell responses detected by IVS ELISpot assay for the 12 peptides (9-mers) predicted as PEPIs (epitopes binding ≥3 autologous HLA class I alleles) and for non-PEPIs (epitopes binding <3 autologous HLA class I alleles, or non-binding) for each patient (12 peptides x 10 patients = 120 datapoints, Supplementary Table S3). Average and individual data for each subject are presented, n=10 (D) Impact of TAA-specific $CD8^+$ T cell responses as predicted by PEPIs on treatment benefit. Predicted multi-antigenic responses were calculated by counting the vaccine TAAs which contain at least one PEPI based on HLA-genotype of each patient. DCB: Patients with objective tumor response (PR) and/or stabilized disease (SD) for at least 50 weeks on maintenance treatment; Others: patients with no DCB. ΔSFU, background corrected spot-forming units.