ADDITIONAL FILE 1: Supplementary Figures

Genomic analysis of 63,220 tumors reveals insights into tumor uniqueness and targeted cancer immunotherapy strategies

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SUPPLEMENTAL FIGURES

Figure S1

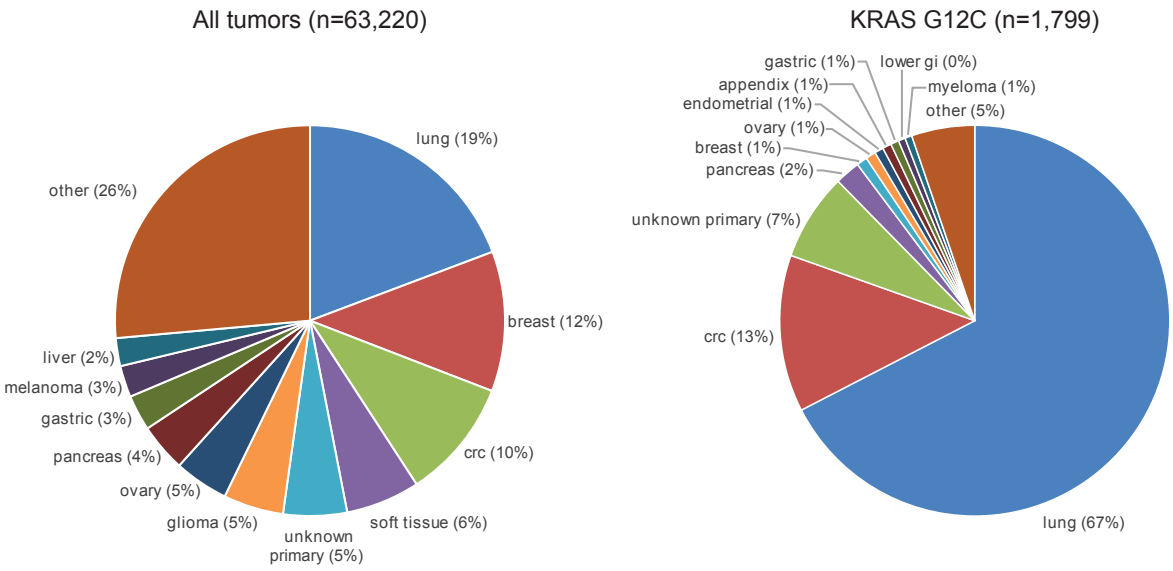

Figure S1: Tumor type breakdown.

Pie charts show the breakdown of tumor types across all tumors (n=63,220) and within the *KRAS* G12C containing tumors (n=1,799). The top 11 tumor types are shown with all others being categorized as 'other.'

Figure S2

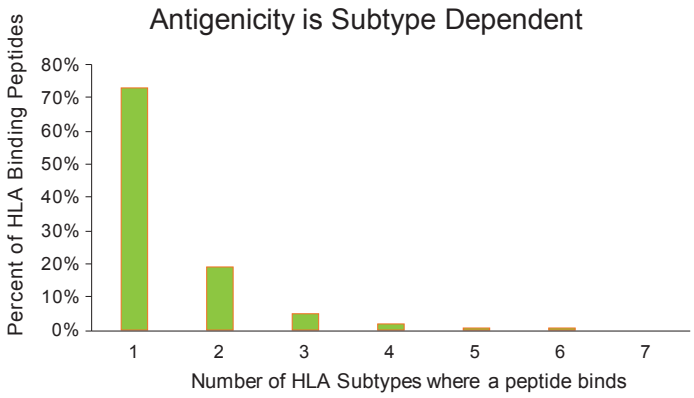

Figure S2: Antigenicity is HLA-subtype dependent

MHC-I binders were determined across 12 common HLA-subtypes. The total number of HLA-subtypes predicted to bind a given peptide were counted. Most peptides bind to a single HLA-subtype.

Figure S3

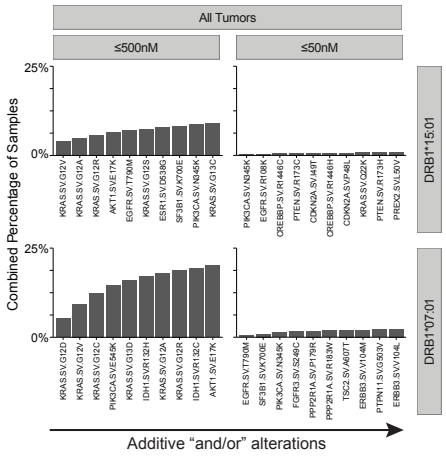

Figure S3: Applicability of poly-neoantigen, non-individualized targeted cancer immunotherapies MHC-II binding predictions

Top additive "and/or" alterations predicted to produce an MHC-II neoantigen are shown for all tumors using 'low' and 'high' affinity thresholds (500nM and 50nM). This was done for two common HLA-DRB1 subtypes (DRB1*15:01 and DRB1*07:01).