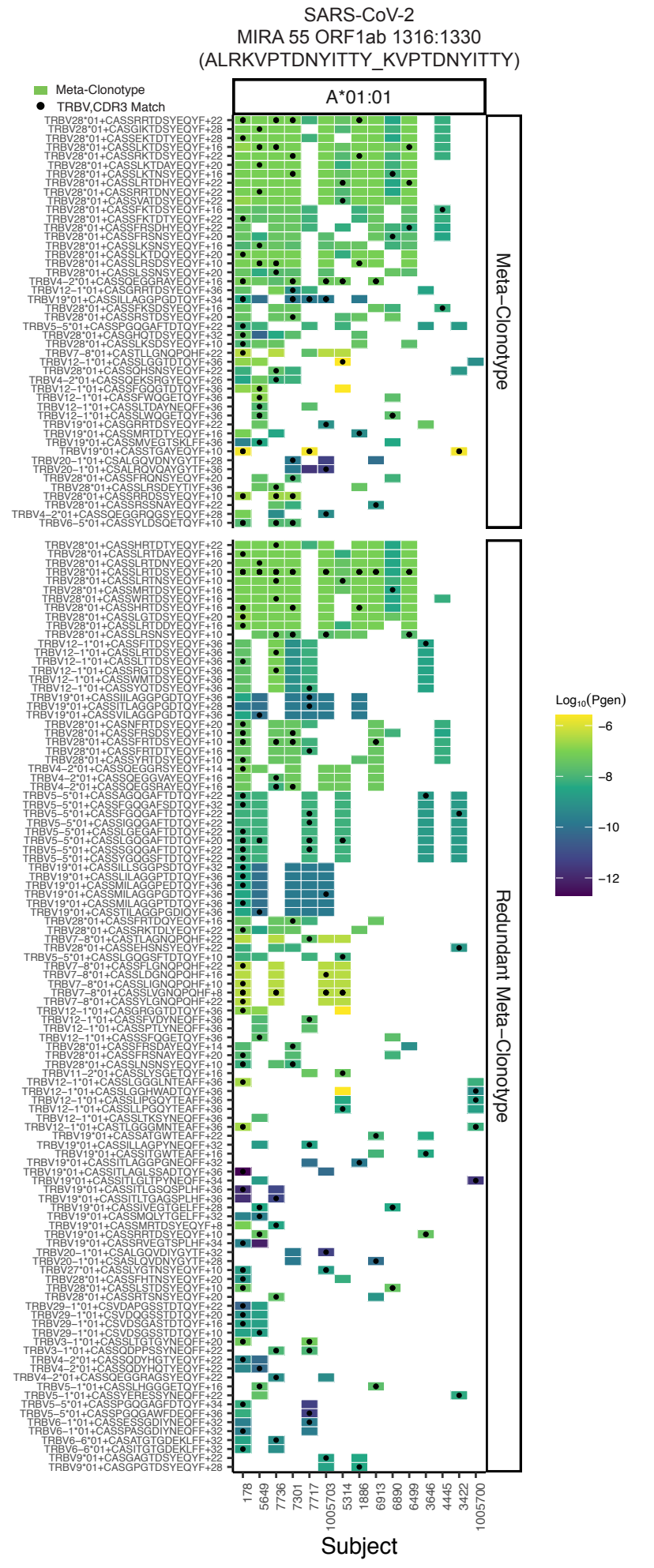

Figure S1: Publicity analysis in MIRA participants of CD8+ TCR β-chain features activated by SARS-CoV-2 peptide ORF1ab (MIRA55) predicted to bind HLA-A*01. The grid shows all features that were present in 2 or more MIRA participants. TCR feature publicity across individuals was assessed using two methods: (i) *tcrdist3* meta-clonotypes (rectangles) – inclusion criteria defined by a centroid TCR and all TCRs within an optimized TCRdist radius selected to span < 10^{-6} TCRs in a bulk unenriched background repertoire, and (ii) exact public clonotypes (circles) are defined by matching TRBV gene usage and identical CDR3 amino acid sequence. Per subject, the color-scale shows the meta-clonotype conformant clone with the highest probability of generation (P_{gen}). All TCRs captured by a "redundant" meta-clonotypes were completely captured by a higher ranked meta-clonotype. Redundant meta-clonotypes were not subsequently evaluated.

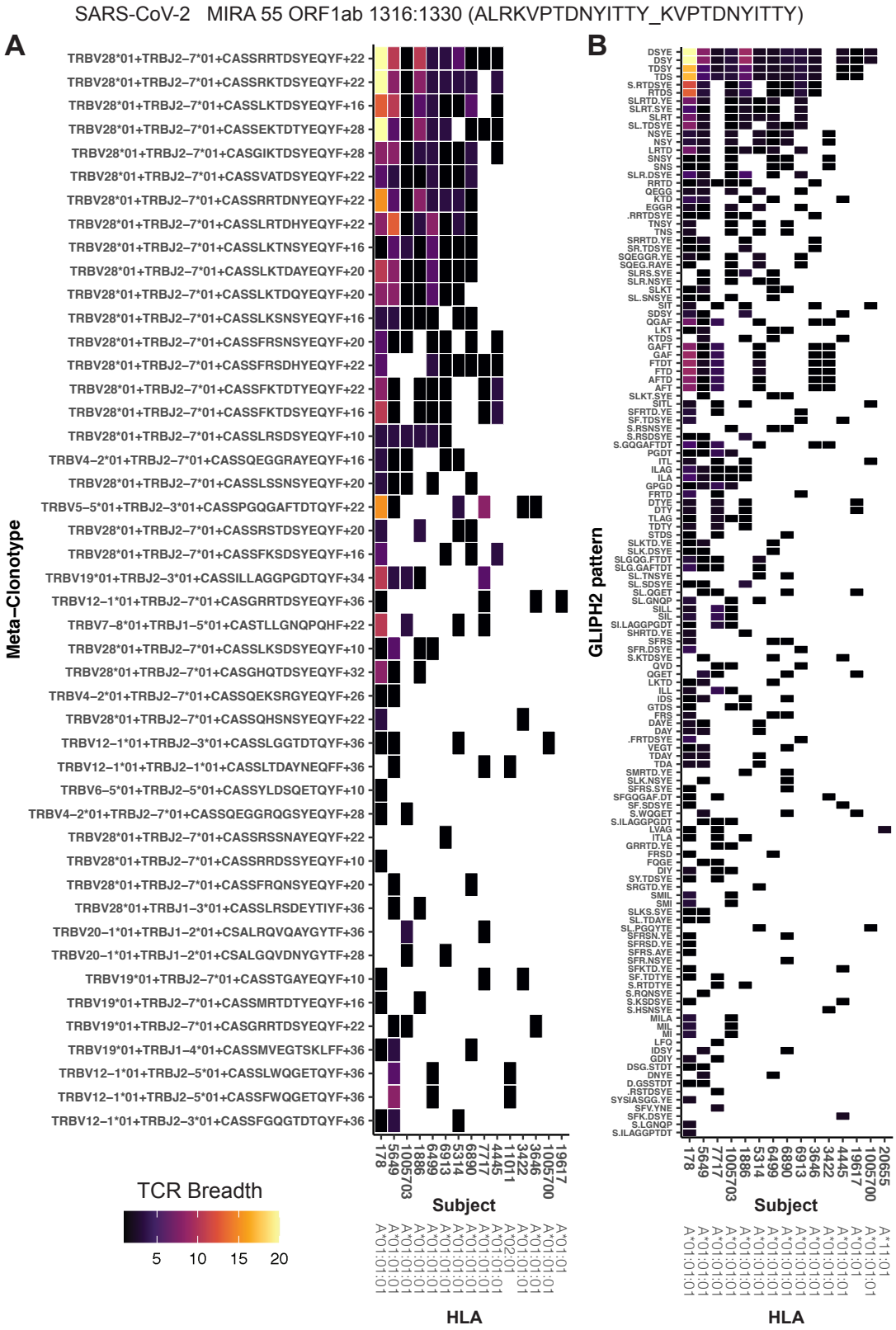

Figure S2: Publicity and breadth analysis of CD8+ TCR β-chain features activated by SARS-CoV-2 peptide ORF1ab (MIRA55) using *tcrdist3* and GLIPH2. TCR feature publicity was determined using two methods for clustering similar TCR sequences: (A) *tcrdist3*-identified meta-clonotypes and (B) GLIPH2 specificity-groups, sets of TCRs with a shared CDR3 k-mer pattern uncommon in the program's default background CD8+ receptor data. Grid fill color shows the breadth – or number of conformant clones – withing each patient's repertoire.

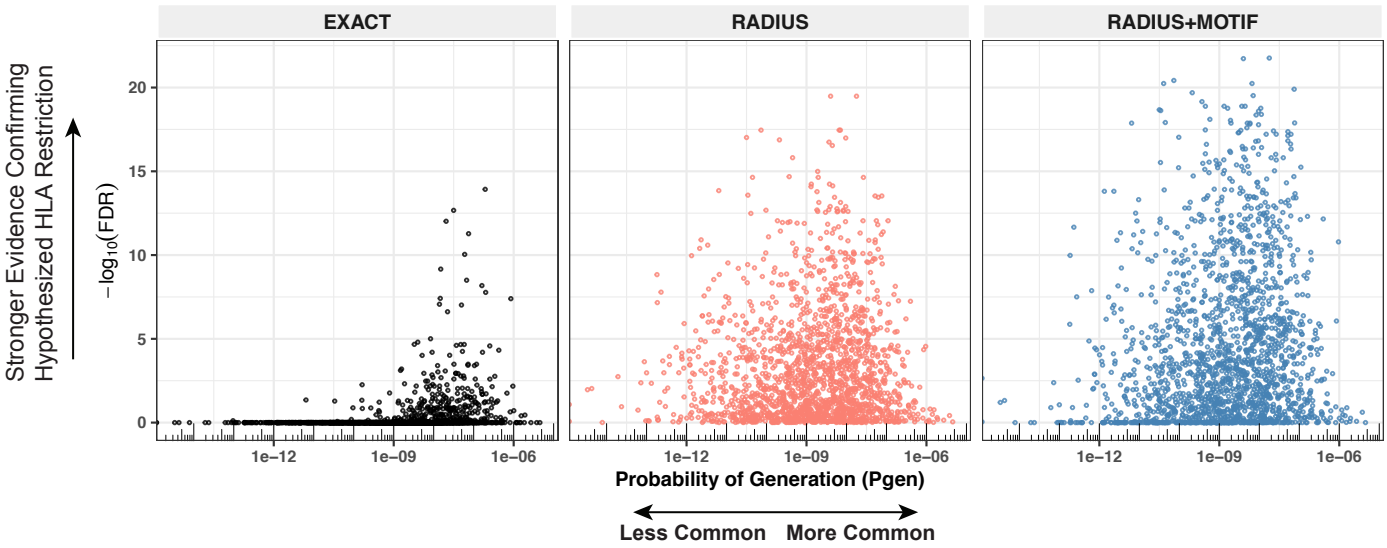

Figure S3. Detectable HLA-association and CDR3 probability of generation. We evaluated meta-clonotypes from 17 MIRA sets in a cohort of 694 COVID-19 patients for their association with predicted HLA-restricting alleles. Statistical evidence of the HLA association for each meta-clonotype (RADIUS or RADIUS+MOTIF) and the centroid alone (EXACT) is indicated by the associated false discovery rate (FDR; y-axis) in beta-binomial regressions (see Methods for model details). The probability of generation (P_{gen}) of each centroid's CDR3-β was estimated using the software OLGA (x-axis). Using exact matching, only associations with high probability of generation (P_{gen}) antigen-specific TCRs are likely to be detected reliably. However, using meta-clonotypes, tcrdist3 revealed strong evidence of HLA-restriction for TCRs with both high and low probability of generation.