Figure S1

Figure S1: Publicity analysis in MIRA participants of CD8+ TCR β-chain features activated by SARS-CoV-2 peptide ORF1ab 4211:4252 (MIRA55) predicted to bind HLA-A*01. TCR features publicity across individual was determined using two methods for clustering similar TCR sequences: **(A)** tcrdist3 meta-clonotoypes defined by a centroid TCR and all TCRs within an optimized radius chosen to span 1e-6 TCRs in a bulk unenriched TRBV-TRBJ matched background data, and **(B)** public clonotypes defined by identical TRBV gene usage and identical CDR3, at the amino acid level.
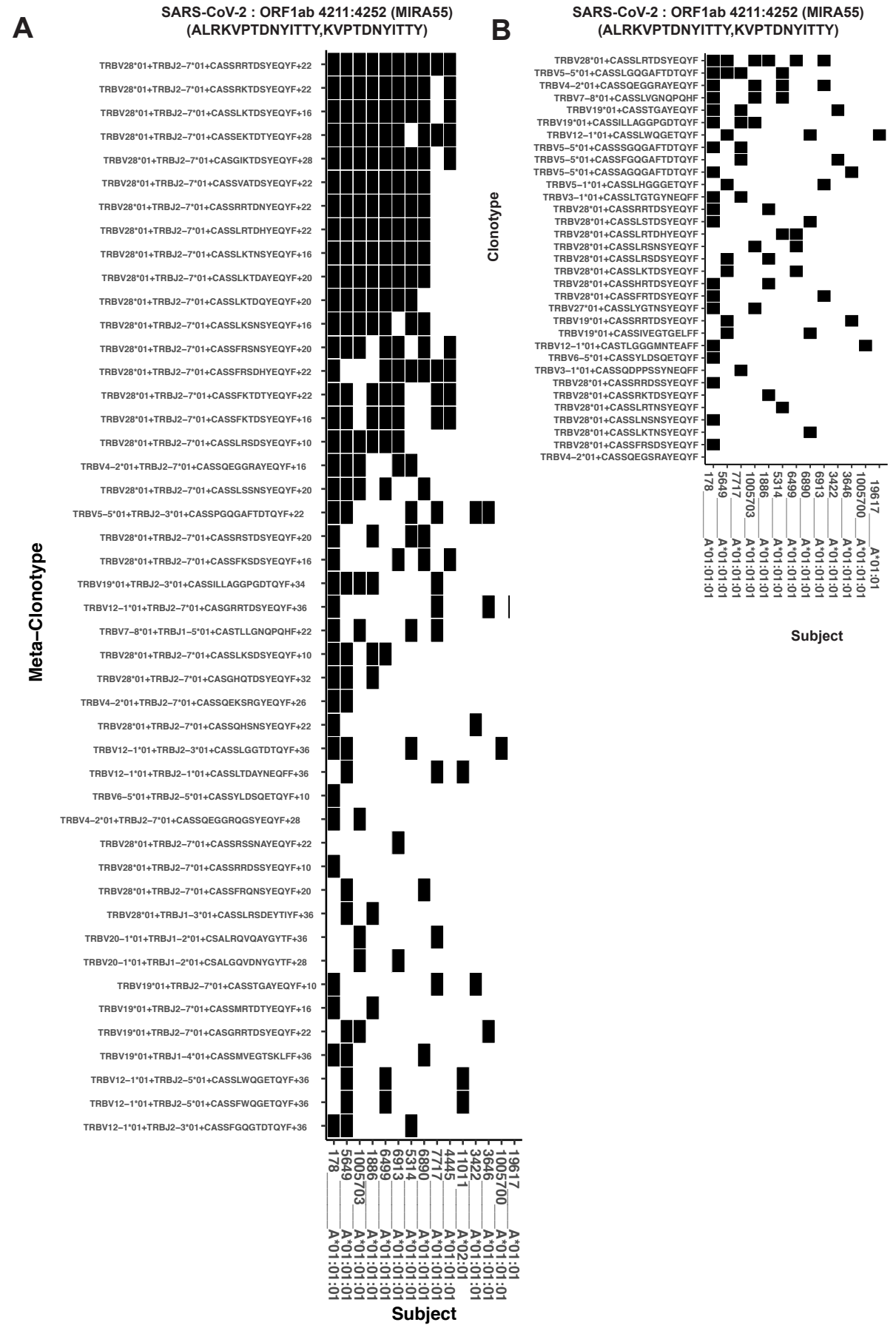

t3/SI_F2.R

Figure S2

Figure S2: Publicity and breadth analysis of CD8+ TCR β-chain features activated by SARS-CoV-2 peptide ORF1ab 4211:4252 (MIRA55) using tcrdist3 and GLIPH2. TCR feature publicity was determined using two methods for clustering similar TCR sequences: (A) tcrdist3 meta-clonotypes (with radii based on θ =1Ee-6) and (B) GLIPH2-groups, sets of TCRs with a shared CDR3 k-mer pattern uncommon in the default background CD8+ receptor data (using default Fisher's p-value < 0.001). Grid fill color shows the breadth of clones clustered. See Methods for details.
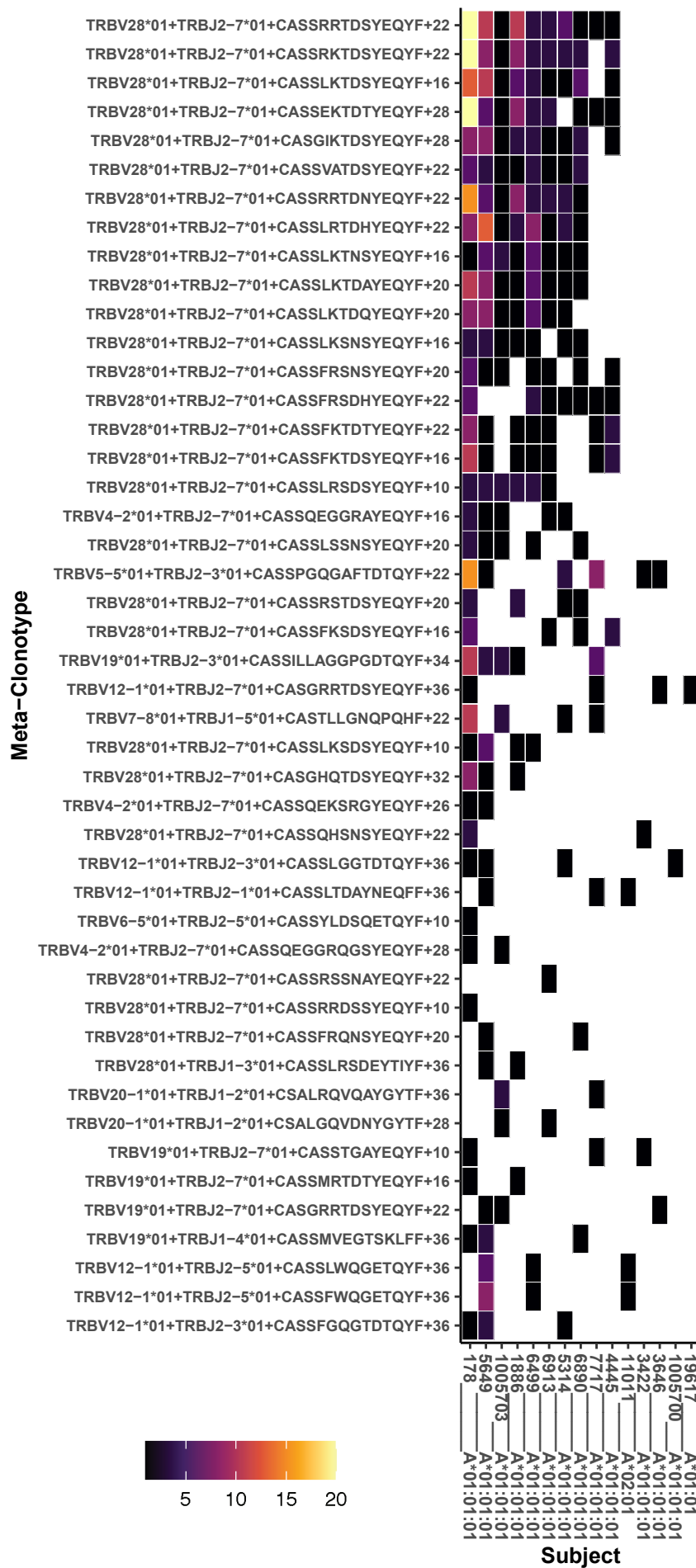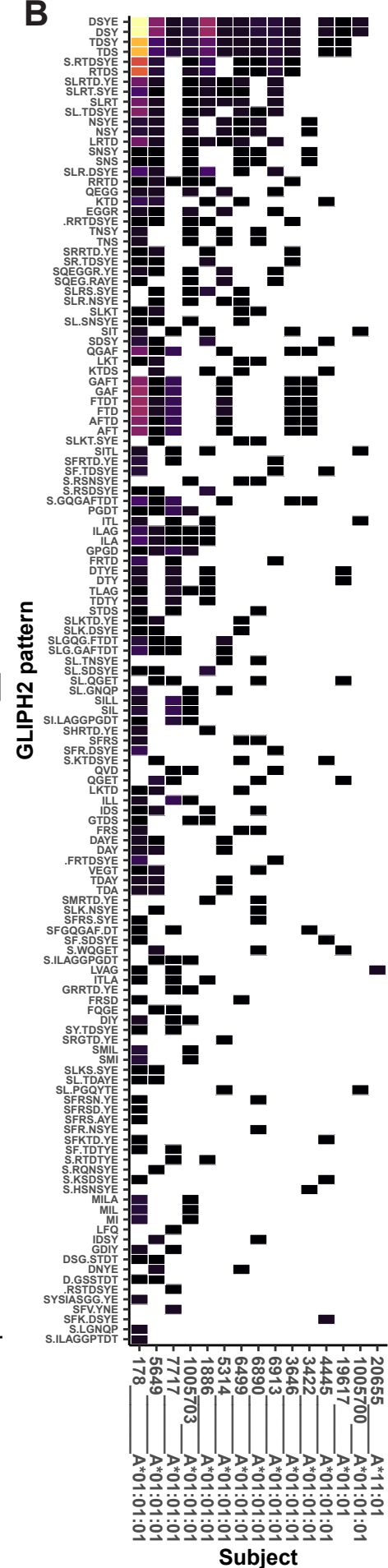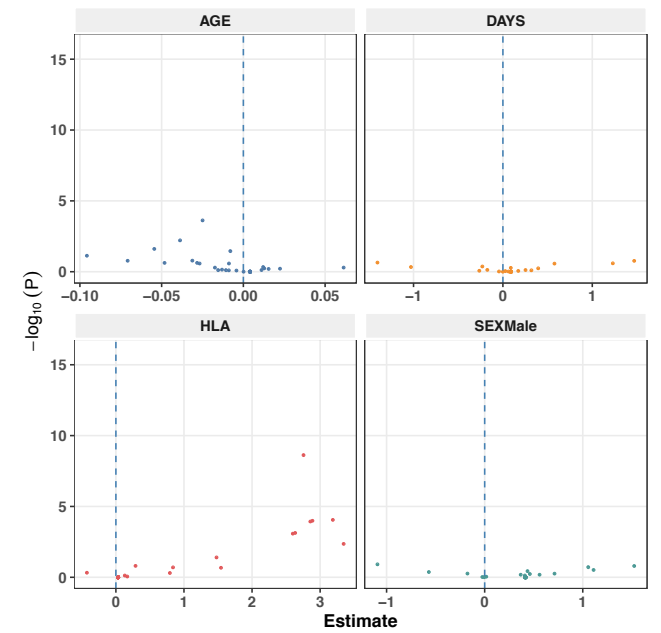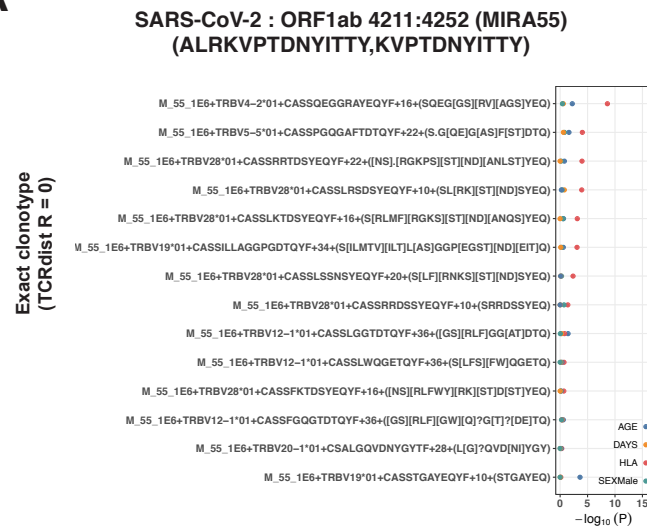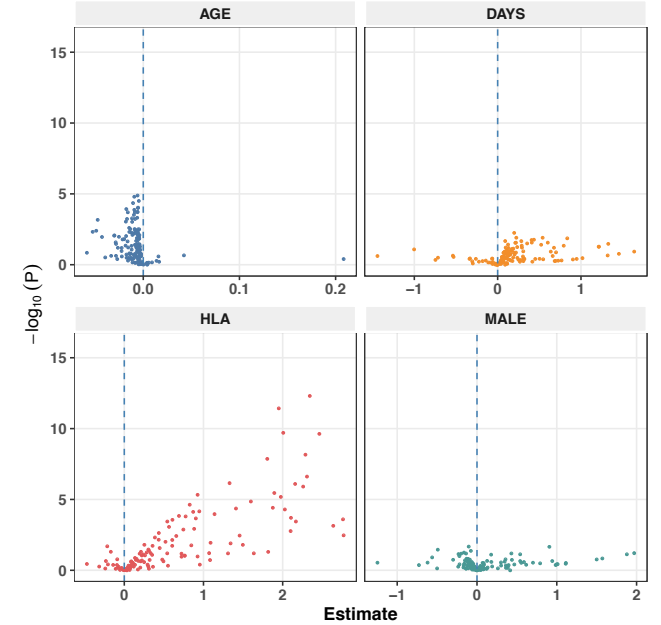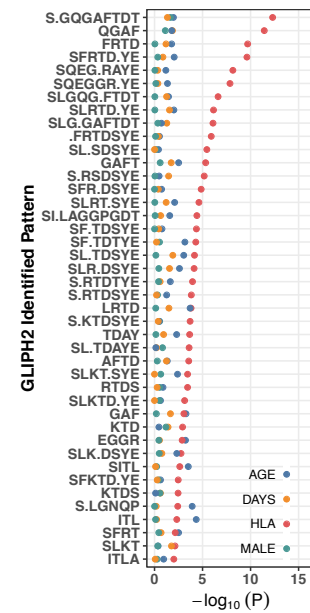
Figure S3

Figure S3 : Associations of TCR features with participant age, days-post diagnosis, HLA-type, and sex in bulk TCR β-chain repertoires of COVID-19 patients (n=694). TCR features shown here were identified from publicity analysis of CD8+ TCRs activated by an illustrative SARS-CoV-2 peptide ORF1ab 4211:4252 (MIRA55), which is predicted to bind HLA-A*01. Using beta-binomial regression models estimated for each feature, volcano plots show associations between participant characteristics and abundance of TCRs matching either: (A) EXACT clonotypes (TRBV+CDR3), (B) GLIPH2 patterns (TRBV+CDR3 k-mer), or (C) tcrdist3 based RADIUS+MOTIF meta-clonotype. See Methods for details.
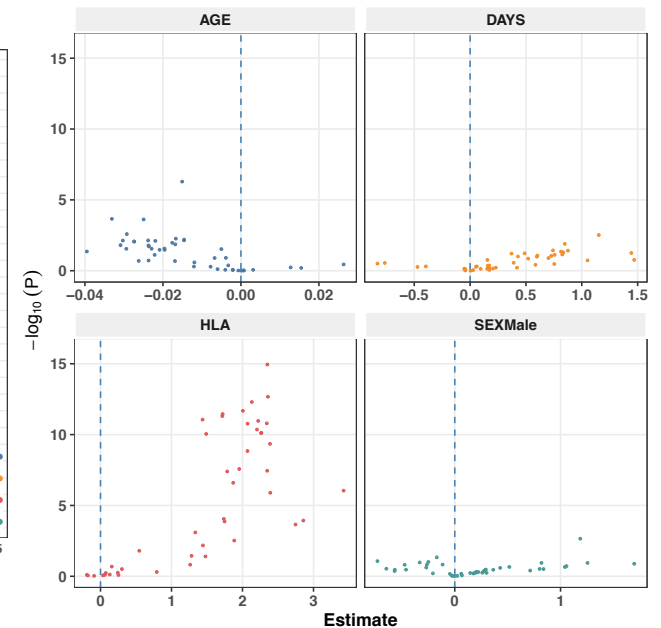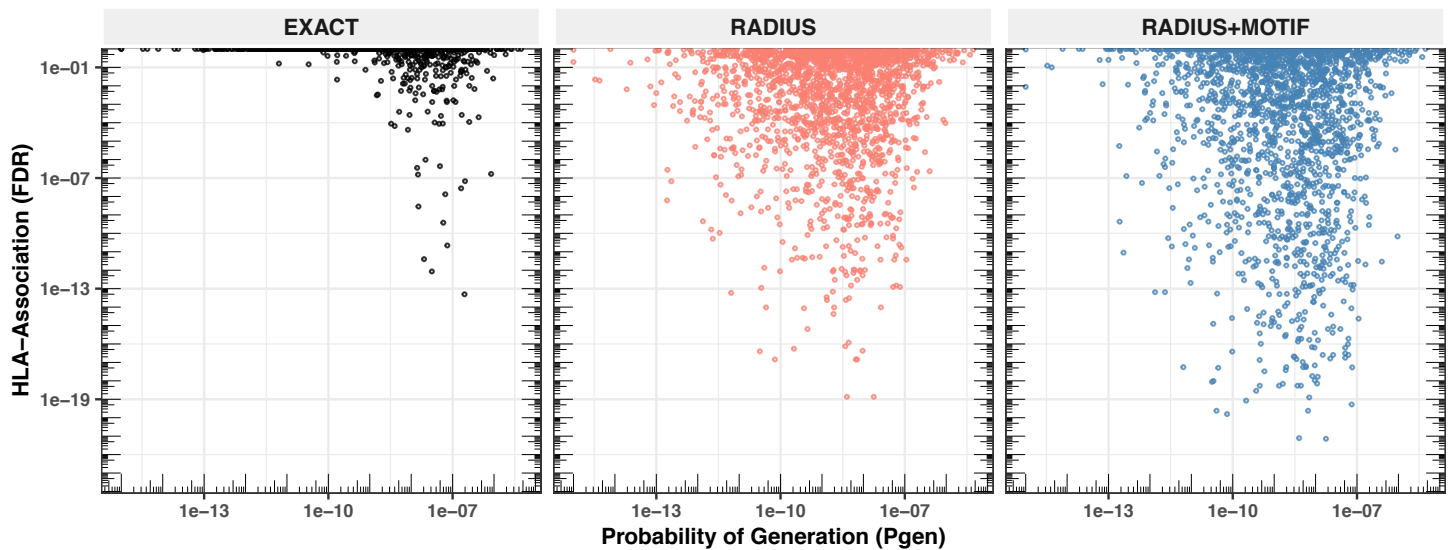
Figure S4

Figure S4. Detectable HLA-association and CDR3 probability of generation. We evaluated meta-clonotypes from 18 MIRA sets in a cohort of 694 COVID-19 patients for their association with predicted HLA-restricting alleles. 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 adjusted p-value (FDR; y-axis) in beta-binomial regressions (see Methods for model details). The probability of generation (Pgen) of each centroid's CDR3-β was estimated using the software OLGA (x-axis). Given the extent of TCR diversity across individuals, population-scale analysis of exact antigen-specific clonotype abundance is likely limited to public (i.e., higher Pgen) TCR features. Using meta-clonotypes, *tcrdist3* revealed strong evidence of HLA-restriction for TCRs with both high and low Pgen.