Cell Reports Medicine, Volume *2*

Supplemental information

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Landscape of epitopes targeted by T cells in 852 convalescent COVID-19 patients: Meta-analysis, immunoprevalence and web platform

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SUPPLEMENTAL FIGURES

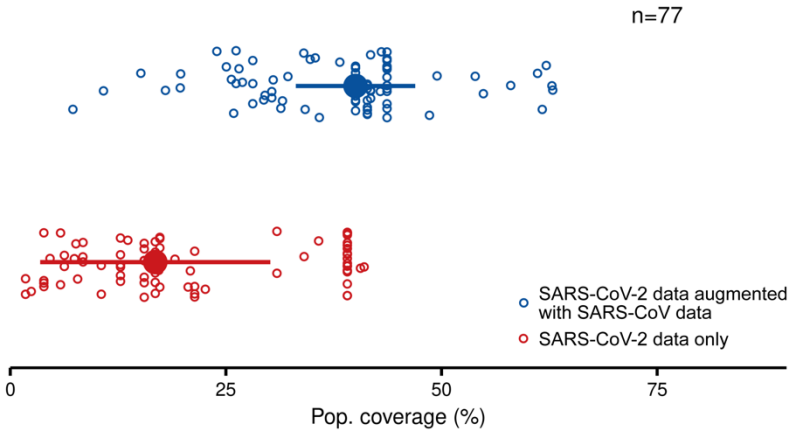

Figure S1. Estimated global population coverage of SARS-CoV-2 epitopes after augmenting HLA alleles associated with genetically-matched SARS-CoV epitopes. Related to Figure 1E. For 90 of the 711 experimentally-determined SARS-CoV-2 T cell epitopes, both epitope sequence and associated HLA alleles matched exactly with those of experimentally-determined SARS-CoV epitopes. This suggests that an epitope-HLA pair associated with a T cell response for one virus is likely to be associated with a response for the other[1,2], and hence any additional HLA associations known for SARS-CoV epitopes[3,4] could augment the limited information available for SARS-CoV-2. Based on this rationale, additional HLA alleles from SARS-CoV data were identified for 77 of the 90 genetically-matched SARS-CoV-2 epitopes. For these 77 epitopes, the median population coverage significantly increased from 16.8% to 40.3% after augmenting HLA alleles from SARS-CoV data. Specific SARS-CoV-2 epitopes, such as $_{66}$FPRGQGVPI$_{74}$ in N and $_{171}$ATSRTLSYY$_{179}$ in M, were estimated to cover a high percentage of global population (~60%) after data augmentation (Supplementary File S1).

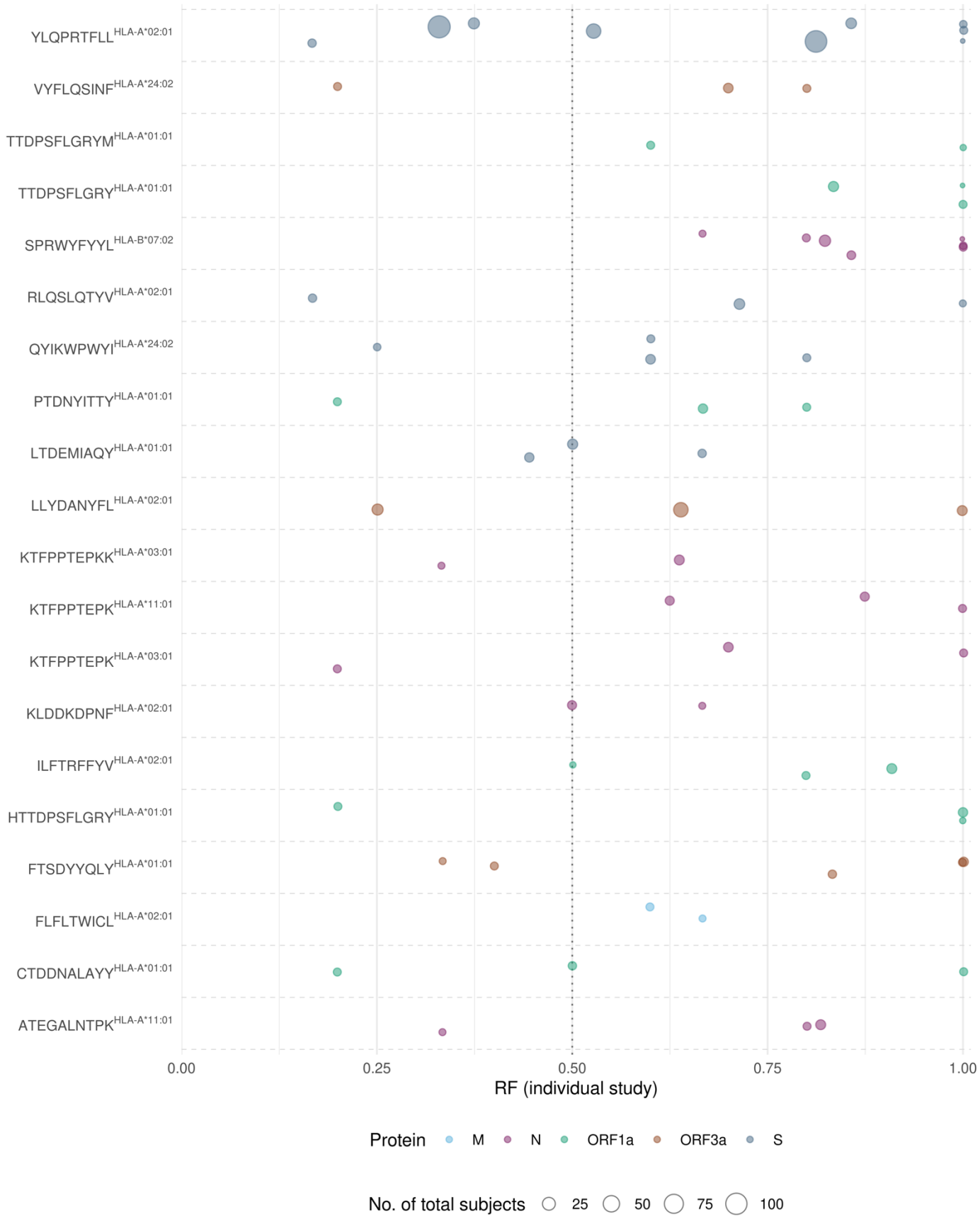

Figure S2. Response frequencies (RF) of immunoprevalent epitope-HLA pairs per individual study. Related to Figure 2. For the 20 immunoprevalent epitope-HLA pairs (having RF > 0.5 and reported in more than one study) (Figure 2B), the RF computed per study is represented by circles. The size of these points indicates the total number of subjects that were tested for the specific epitope-HLA pair in a study. Note that each epitope-HLA pair in this set has RF > 0.5 in most of the immunological studies that reported a response against it.

Table S1. List of S-derived epitopes with conservation less than 0.9 and their association with SARS-CoV-2 variants of concern (VOC). Related to Figure 1B.

No.	Epitope	HLA	Start	Stop	Conservation[#]	Mutation[$]	VOC[$]
1	AYSNNSIAIPTNFTI	HLA-DQB1*03:01	706	720	0.660	T716I	B.1.1.7
2	GVYYHKNNK	HLA-A*03:01	142	150	0.649	Y144-	B.1.1.7, B.1.525
3	HVSGTNGTK	HLA-A*68:01	69	77	0.634	H69-	B.1.1.7, B.1.525
						V70-	
4	IAIPTNFTI	HLA-B*51:01, HLA-B*53:01	712	720	0.661	T716I	B.1.1.7
5	IPTNFTISV	HLA-B*07:02, HLA-B*51:01	714	722	0.661	T716I	B.1.1.7
6	LPQGFSAL	HLA-B*08:01, HLA-B*07:02	216	223	0.851	A222V	B.1.177 (lineage but not currently a VOC)
7	NLVRDLPQGFSALEP	HLA-DRB1*03:01	211	225	0.841	D215G	B.1.351
8	NSIAIPTNF	HLA-B*57:01	710	718	0.661	T716I	B.1.1.7
9	QTNSPRRAR	HLA-A*31:01	677	685	0.621	Q677H	B.1.525
						P681H/ P681R	B.1.1.7 / B.1.617.1, B.1.617.2
10	SPRRARSV	HLA-B*08:01	680	687	0.639	P681H/ P681R	B.1.1.7 / B.1.617.1, B.1.617.2
11	SPRRARSVA	HLA-B*07:02	680	688	0.636	P681H/ P681R	B.1.1.7 / B.1.617.1, B.1.617.2
12	SVLNDILSR	HLA-A*68:01	975	983	0.664	S982A	B.1.1.7
13	VLNDILSRL	HLA-A*02:01	976	984	0.664	S982A	B.1.1.7
14	YGFQPTNGV	HLA-B*51:01	495	503	0.643	N501Y	B.1.1.7, B.1.351, P.1
15	YQDVNCTEV	HLA-A*02:06	612	620	0.023	D614G	B.1.1.7, B.1.351, P.1, P.2, B.1.427, B.1.525, B.1.526
16	YYHKNNKSW	HLA-A*24:02	144	152	0.636	Y144-	B.1.1.7, B.1.525
						W152C	B.1.427

[#] Computed based on 859,233 genomes.
[$] Information of VOC and their associated mutations was obtained from https://covariants.org/shared-mutations (accessed on 11 May 2021).

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