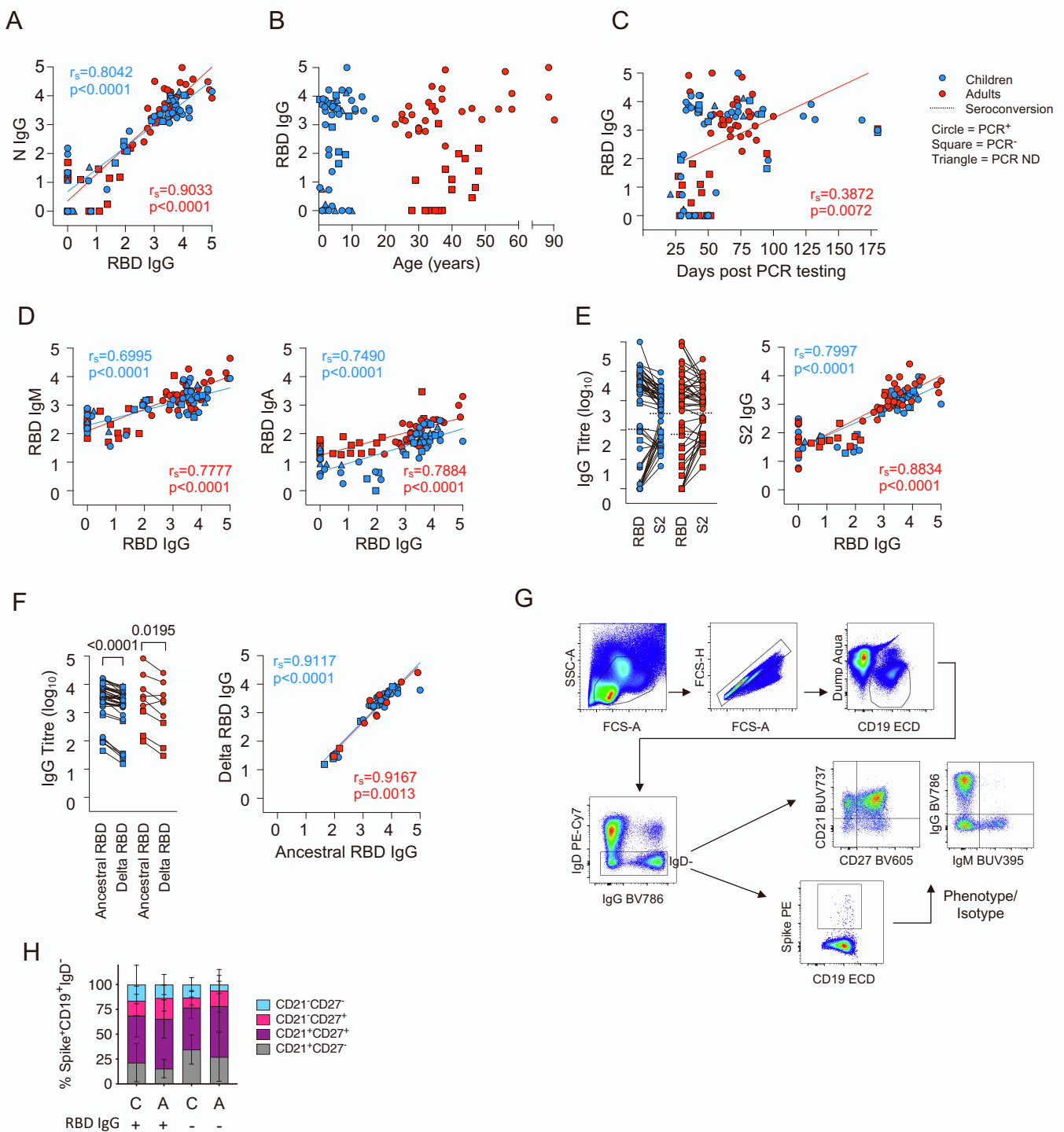


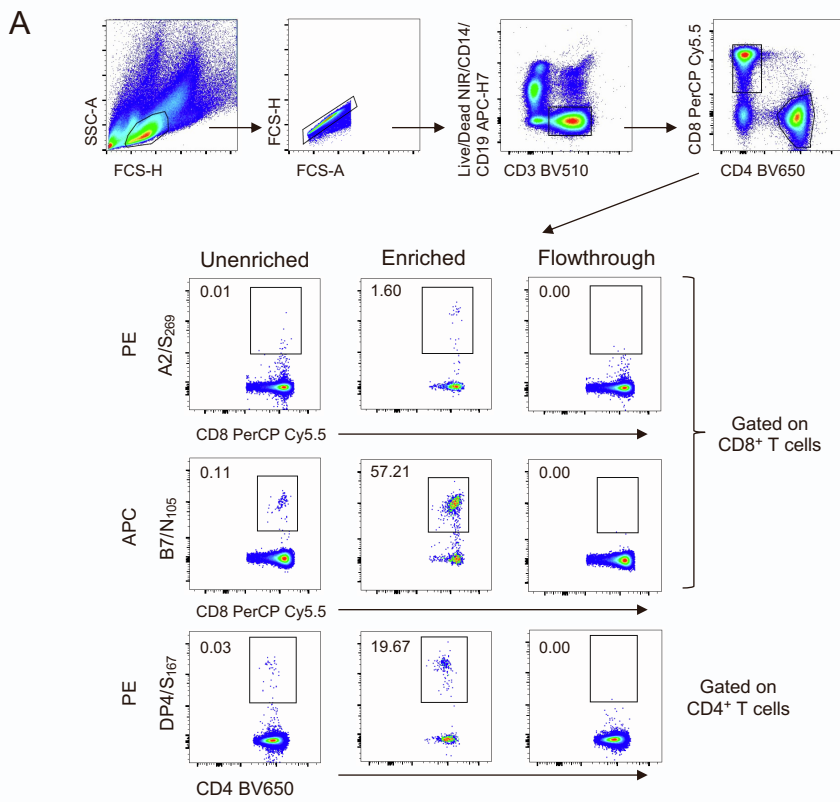
**Supplemental information**

**SARS-CoV-2-specific T cell memory with common  
TCR $\alpha\beta$  motifs is established in unvaccinated  
children who seroconvert after infection**

**Louise C. Rowntree, Thi H.O. Nguyen, Lukasz Kedzierski, Melanie R. Neeland, Jan Petersen, Jeremy Chase Crawford, Lilith F. Allen, E. Bridie Clemens, Brendon Chua, Hayley A. McQuilten, Anastasia A. Minervina, Mikhail V. Pogorelyy, Priyanka Chaurasia, Hyon-Xhi Tan, Adam K. Wheatley, Xiaoxiao Jia, Fatima Amanat, Florian Krammer, E. Kaitlynn Allen, Sabrina Sonda, Katie L. Flanagan, Jaycee Jumarang, Pia S. Pannaraj, Paul V. Licciardi, Stephen J. Kent, Katherine A. Bond, Deborah A. Williamson, Jamie Rossjohn, Paul G. Thomas, Shidan Tosif, Nigel W. Crawford, Carolien E. van de Sandt, and Katherine Kedzierska**

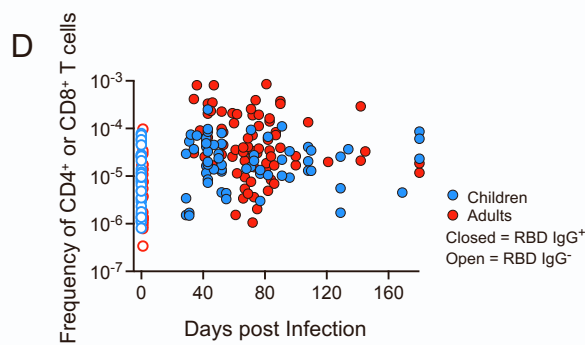
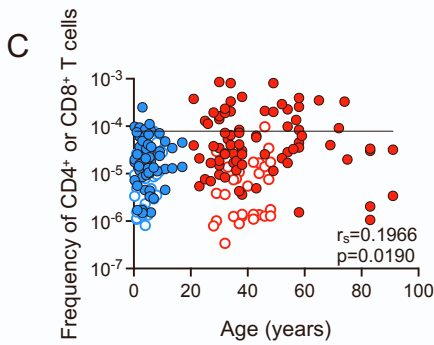


**Figure S1. SARS-CoV-2-specific antibody and B cell response, refer to Figure 1.** (A) Correlation between RBD IgG and N IgG titres for SARS-CoV-2 exposed children and adults. (B-C) Correlation between RBD IgG titres and (B) age or (C) days post PCR testing. (D) Correlation of RBD IgG titres against RBD IgM (left) and IgA (right). (E) Paired analysis (left) and correlation (right) of RBD- and S2-specific IgG antibody titres in SARS-CoV-2 exposed children and adults. Dashed lines indicate seroconversion cut-off based on healthy children and adult titres (mean plus two standard deviations). (F) Paired analysis (left) and correlation (right) of ancestral and delta RBD-specific IgG antibody titres. Statistical significance was determined using Wilcoxon matched-pairs signed rank test (E-F) and Spearman's rank correlation (A-F). (G) Gating strategy for Spike-specific B cells; gated on FSC/SSC, singlets, live cells excluding T cell/NK cell/monocyte lineage markers, expression of CD19, then gated as IgD<sup>-</sup>, IgM<sup>+/-</sup>, IgG<sup>+/-</sup> and binding to Spike probe, with expression of CD21/CD27. (H) Memory phenotypes of Spike<sup>+</sup> B cells from RBD IgG positive and negative individuals; data are shown as mean with SD. Statistical significance was determined with Sidak's multiple comparisons test.

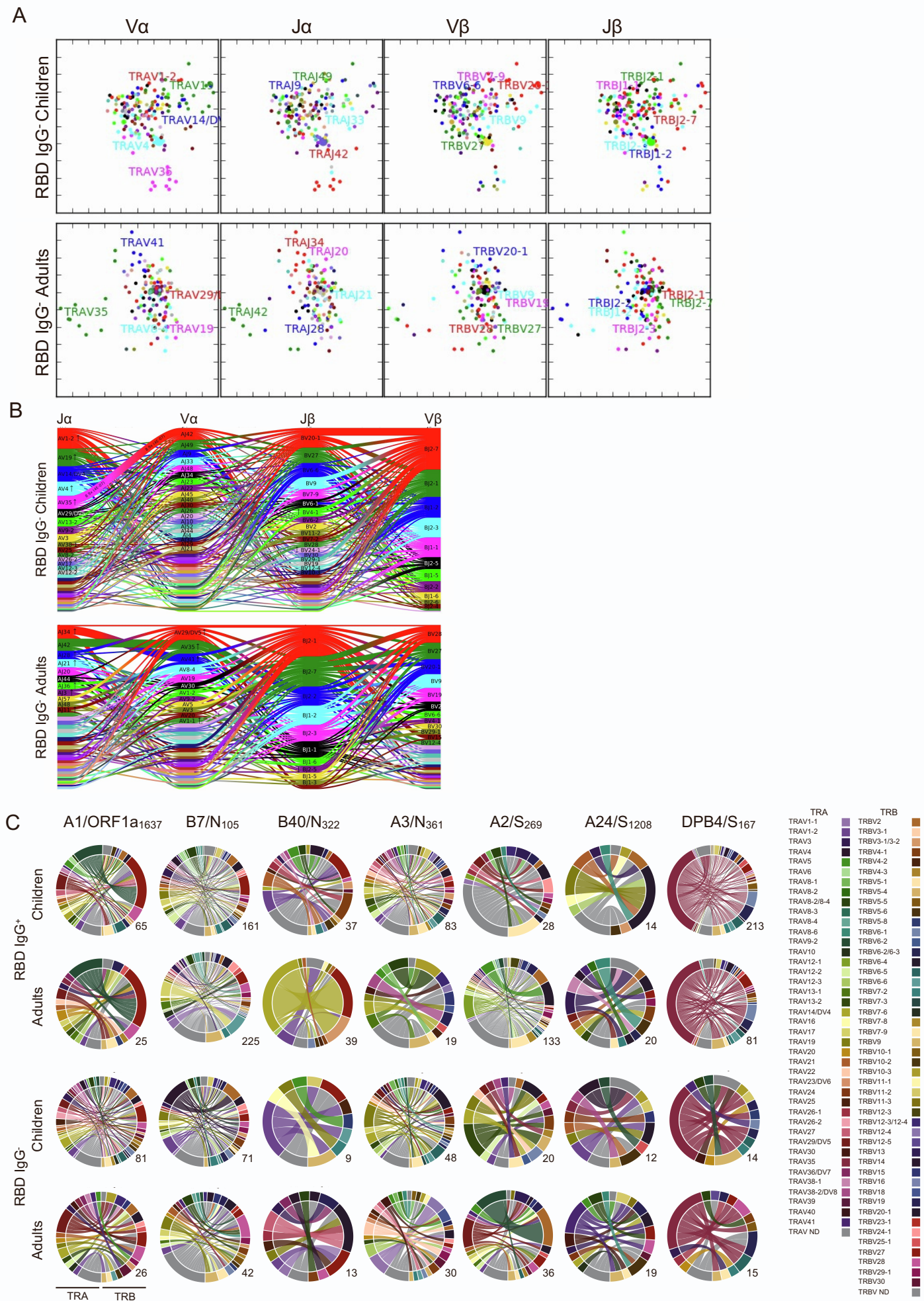


**B**

HLA	Region	Sequence tetramer	B.1.1.7 (Alpha)		B.1.351 (Beta)		P.1 (Gamma)		B.1.617.2 (Delta)		B.1.1.529 (Omicron)	
			Sequence	%	Sequence	%	Sequence	%	Sequence	%	Sequence	%
HLA-A*01:01	ORF1a <sub>1637-1646</sub>	TTDPSFLGRY	-----	99.9	-----	99.9	-----	>99.9	-----	90.9	-----	>99.9
			---L-----	0.1	---L-----	0.1	---L-----	<0.1	---L-----	9.1	---L-----	<0.1
HLA-A*02:01	S <sub>289-277</sub>	YLQPRTFLL	-----	100	-----	100	-----	100	-----	100	-----	100
HLA-A*03:01	N <sub>361-369</sub>	KTFPPTEPK	-----	99.9	-----	92	-----	99.9	-----	99.6	-----	99.9
			-I-----	0.1	-I-----	8	-I-----	0.1	-I-----	0.4	-I-----	0.1
HLA-A*24:02	S <sub>1208-1216</sub>	QYIKWPWYI	-----	100	-----	100	-----	100	-----	100	-----	100
HLA-B*07:02	N <sub>105-113</sub>	SPRWYFYLL	-----	100	-----	100	-----	100	-----	100	-----	100
HLA-B*40:01	N <sub>322-331</sub>	MEVTPSGTWL	-----	99.9	-----	99.9	-----	99.8	-----	98.2	-----	100
			---L---	0.1	---L---	0.1	---L---	0.2	---L---	1.8	---L---	0.1
HLA-DPB1*04:01	S <sub>167-180</sub>	TFEYVSQPFLMDLE	-----	99.5	-----	>99.9	-----	>99.9	-----	>99.9	-----	100
			-----H--	0.5	-----H--	<0.1	-----H--	<0.1	-----H--	<0.1	-----H--	<0.1



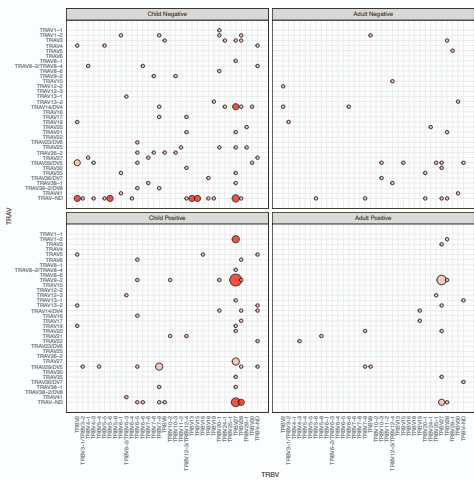
**Figure S2. SARS-CoV-2-specific T cell frequencies and peptide conservation analysis, refer to Figure 2.** (A) Gating strategy of enriched tetramer<sup>+</sup> CD4<sup>+</sup> and CD8<sup>+</sup> T cells and phenotype populations. (B) Amino acid sequence identity of the viral peptides of the SARS-CoV-2 tetramers across the different variants of concern (VOC). (C-D) Correlation of SARS-CoV-2 exposed individuals' frequency of tetramer<sup>+</sup> T cells against (C) age and (D) days post infection. Statistical significance was determined using Spearman's rank correlation.



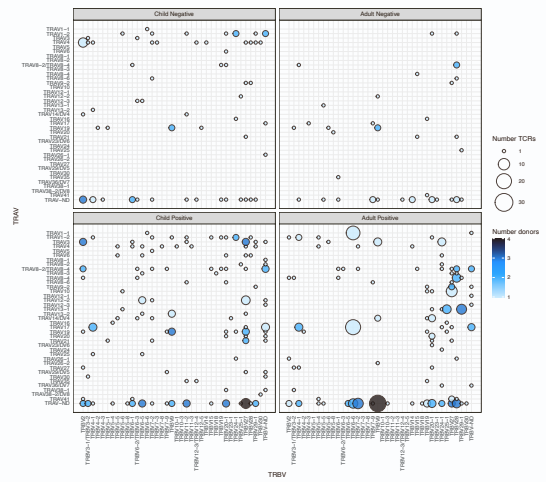
**Figure S3. Diverse SARS-CoV-2-specific TCRab repertoires in RBD IgG<sup>-</sup> children and adults, refer to Figure 5.** (A) Kernel PCA projections of pooled SARS-CoV-2-specific TCRs depicting Va, Ja, Vb, and Jb usage for RBD IgG<sup>-</sup> children and adults. Encoding clone size indicated by symbol size. (B) V and J gene segment usage and covariation in SARS-CoV-2-specific responses in RBD IgG<sup>-</sup> children and adults. (C) CIRCOS plots of TRAV and TRBV clonotype pairings in children and adults; left arch and segment color indicate TRAV usage, and right outer arch color depicts TRBV usage. Segments shown by the same color represent TCRab clonotypes with the same V segment usage but different CDR3 sequences. The number of sequences considered for each CIRCOS plot is shown at the bottom right.



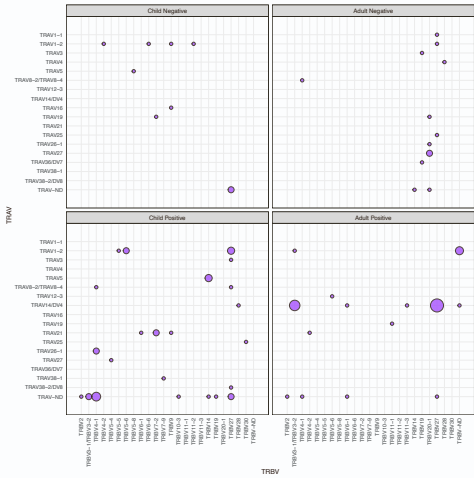
### A1/ORF1<sub>1637</sub>



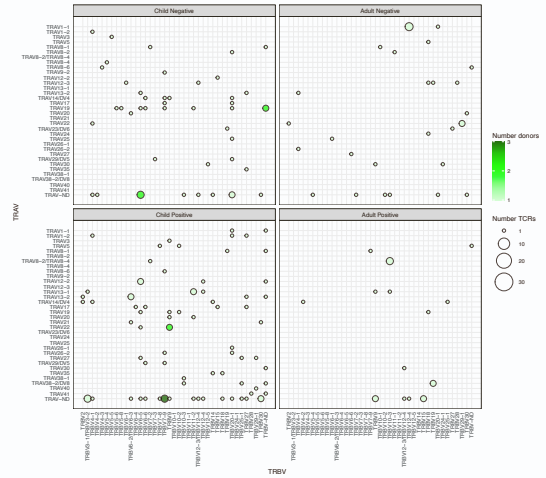
### B7/N<sub>105</sub>



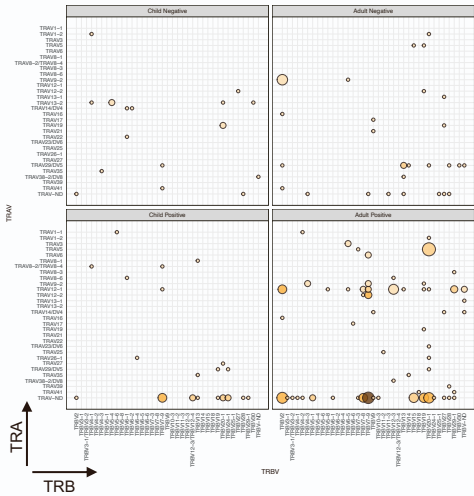
### B40/N<sub>322</sub>



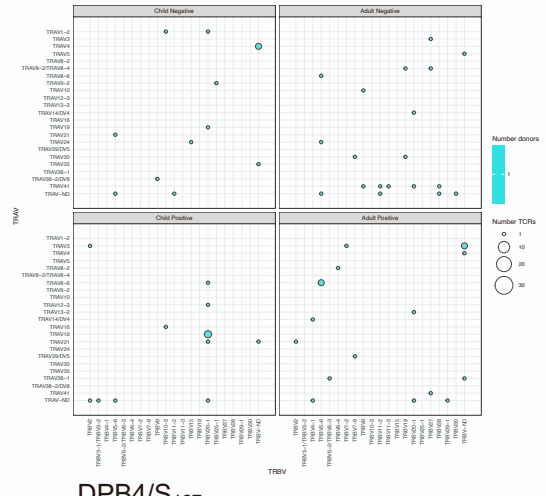
### A3/N<sub>361</sub>



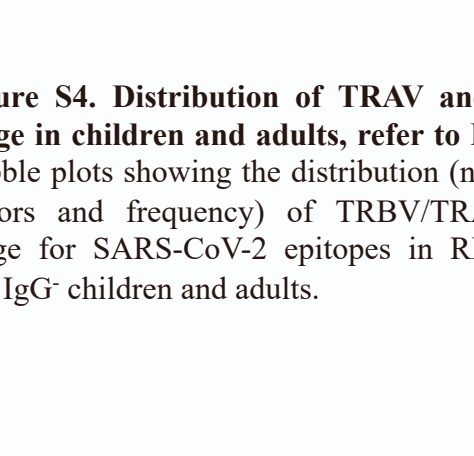
### A2/S<sub>269</sub>



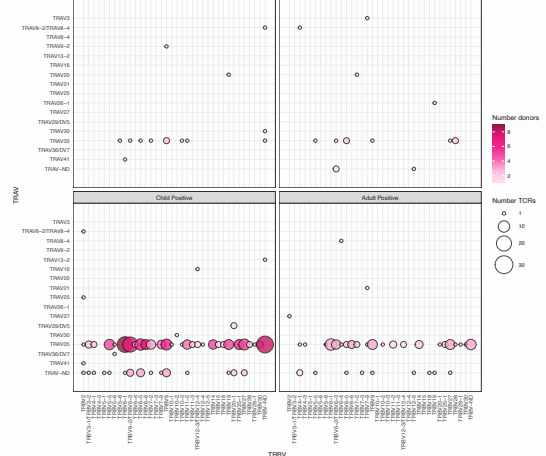
### A24/S<sub>1208</sub>



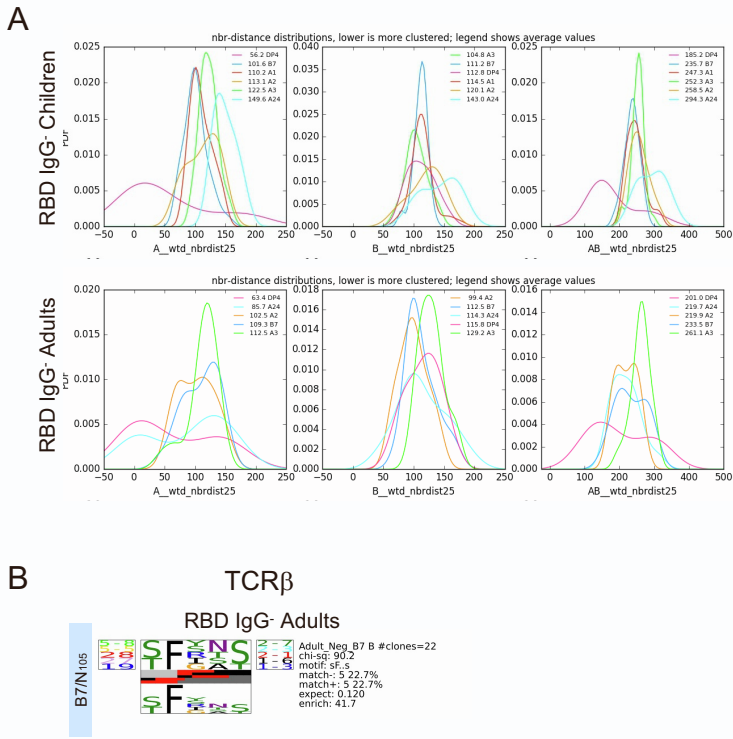
### A2/S<sub>269</sub>



### DPB4/S<sub>167</sub>



**Figure S4. Distribution of TRAV and TRBV usage in children and adults, refer to Figure 5.** Bubble plots showing the distribution (number of donors and frequency) of TRBV/TRAV gene usage for SARS-CoV-2 epitopes in RBD IgG<sup>+</sup> and IgG<sup>-</sup> children and adults.



**Figure S5. Similar distribution and probability of generation for SARS-CoV-2-specific TCR $\alpha\beta$  repertoires between RBD IgG<sup>-</sup> children and adults, refer to Figure 6.** (A) Epitope-specific populations from RBD IgG<sup>-</sup> children and adults were quantified for defining features using a neighbour distance distribution. The lower distribution peak indicates a more clustered epitope-specific TCRab repertoire; average distance values for each epitope are depicted within the plot. Analyses for both single and paired chains are shown, as indicated in the plot labels. PDF, probability density function. (B) TCR logo representations of CDR3a and b sequence motif for RBD IgG<sup>-</sup> adults. The motif scores were determined by chi-squared, with values greater than 90 considered highly significant.

## Supplementary Tables

**Table S1.** Cohort demographics, refer to Figure 1.

Cohort	Participant	Age (years)	Sex	RBD IgG ELISA	Symptomatic	Ct value*	Days post infection	HLA-A	HLA-A	HLA-B	HLA-B	HLA-DPB1	HLA-DPB1
MEL	9.2	40	F	-	-	-	28	02:01	11:02	07:02	27:04	03:01	05:01
MEL	9.3	3	M	-	+	e-Gene 32.44	30	02:05	11:02	27:04	58:01	05:01	104:01
MEL	18.2	44	F	-	-	-	38	02:01/614	68:01/164	40:01	49:01	04:01	104:01
MEL	18.3	7	M	-	+	e-Gene 40	40	01:01	02:01	49:01	50:01	04:01	104:01
MEL	21.2	29	F	-	+	-	30	02:01	25:01	07:02	18:01	04:01	
MEL	21.3	2	F	-	+	Inconclusive	31	03:01	25:01	18:01	50:01	04:01	04:02
MEL	25.2	47	F	-	-	-	45	02:01	11:01	07:02	44:02	01:01	15:01
MEL	25.4	10	F	-	+	Inconclusive	48	01:01	11:01	07:02	35:02	02:01	15:01
MEL	28.2	40	F	-	+	-	44	02:06	24:02	51:01	52NEW^	05:01	
MEL	28.3	5	M	-	+	Inconclusive	48	02:06	30:01	07:02	51:01	04:01	05:01
MEL	34.2	46	F	-	-	-	37	01:01	02:01	51:01	57:01	04:01	104:01
MEL	34.3	1	M	-	+	e-Gene 29.43	40	01:01	02:01	14:02	51:01	04:01	13:01
MEL	36.2	33	F	-	-	-	49	03:01	25:01	08:01	38:01	02:01	04:02
MEL	36.5	2	F	-	+	e-Gene 32.94	49	01:01	03:01	08:01	40:01	01:01	04:02
MEL	43.2	28	F	-	+	-	36	11:01	29:01	07:05	51:01	04:01	11:01
MEL	43.3	1	M	-	+	e-Gene 34.98	35	02:01	29:01	07:05	13:02	03:01	04:01
MEL	46.2	33	F	+	+	e-Gene 12.81	42	01:03	02:05	07:02	37:01	02:01	104:01
MEL	46.3	4	M	+	+	e-Gene 13.65	42	02:05	03:01	07:02	37:01	02:01	104:01
MEL	46.4	2	F	+	+	e-Gene 13.23	42	01:03	03:01	07:02		104:01	
MEL	52.1	38	F	-	+	-	51	02:01		44:02	51:01	04:01	
MEL	52.3	4	M	-	-	e-Gene 33.25	29	02:01	32:01	07:02	44:02	04:01	
MEL	52.4	1	F	-	+	Inconclusive	21	02:01	32:01	07:02	44:02	04:01	
MEL	53.1	37	F	-	-	-	43	02:01		15:01	39:01	03:01	04:01
MEL	53.4	0.33	M	-	+	e-Gene 36	56	01:01	02:01	15:01	51:01	03:01	
MEL	55.2	36	F	-	-	-	28	02:01	30:01	13:02	18:01	04:02	05:01
MEL	55.4	4	F	-	-	e-Gene 31.95	31	01:01	30:01	07:02	13:02	04:01	04:02
MEL	57.2	48	F	-	-	-	27	02:01	24:02	18:01	27:05	04:01	04:02
MEL	57.3	9	M	-	+	e-Gene 28.73	29	02:01		27:05	44:02	02:01	04:02
MEL	58.1	32	F	-	+	-	52	03:01	30:04	14:02		04:01	30:01
MEL	58.2	11	M	+	+	e-Gene 24.11	52	03:01	30:04	07:02	14:02	04:01	
MEL	58.3	6	M	+	-	e-Gene 24.25	52	03:01		07:02	14:02	04:01	30:01
MEL	61.3	46	F	+	+	-	59	24:02	24:10	35:30	40:01	01:01	13:01
MEL	61.5	17	M	+	-	e-Gene 25.45	47	24:02	24:33	40:01	51:06	01:01	
MEL	75.2	35	F	-	+	-	49	02:01	29:02	44:02	44:03	04:01	
MEL	75.3	3	F	-	+	e-Gene 27.37	50	01:01	29:02	37:01	44:03	04:01	
MEL	78.1	34	F	+	+	-	43	01:01	02:01	07:02	55:01	04:01	



MEL	78.3	3	M	+	+	-	43	01:01	02:01	07:02	08:01	04:01	
MEL	78.4	0.33	F	+	+	-	43	01:01	02:01	07:02	08:01	04:01	
MEL	80.1	42	F	-	-	-	29	02:01	24:02	07:02		04:01	06:01
MEL	80.3	6	F	+	-	-	29	24:02		07:02	27:04	04:01	06:01
MEL	80.4	8	F	-	-	-	29	24:02		07:02	27:04	04:01	06:01
MEL	80.5	3	M	+	+	e-Gene 33.77	31	02:01	30:02	07:02	18:01	02:02	04:01
MEL	84.1	48	F	+	-	-	95	02:03	11:01	38:02	39:05	02:02	296:01
MEL	84.3	3	M	-	-	e-Gene 31.22	96	11:01	32:01	28:02	44:02	04:01	296:01
MEL	84.4	6	M	-	-	-	95	02:03	24:02	07:02	39:05	02:01	02:02
MEL	88.1	35	F	+	+	-	100	02:01	26:01	35:08	38:01	04:01	
MEL	88.2	2	M	+	+	e-Gene 32.84	71	01:01	26:01	35:01	38:01	02:01	04:01
MEL	94.1	36	F	+	+	-	180	02:01	32:01	15:01	51:01	04:01	11:01
MEL	94.3	4	M	+	+	-	180	01:01	02:01	08:01	15:01	02:01	11:01
MEL	94.4	2	M	+	+	-	180	01:01	32:01	08:01	15:01	02:01	11:01
MEL	97.1	38	F	+	ND	-	35	02:01	03:01	07:02	57:01	02:01	26:01
MEL	97.3	2	F	+	+	-	35	03:01	11:01	52:01	57:01	02:01	
MEL	102.2	34	F	+	ND	-	36	01:01	26:01	08:01	38:01	02:01	09:01
MEL	102.3	13	M	+	+	E: 37.82, RDRP/S: N/A, N: 38.97	33	02:06	29:02	40:06	58:01	02:01	3:01
MEL	102.4	1	M	+	+	E: 14.36, RDRP/S: 15.67, N: 16.98	33	01:01		08:01	15:01	02:01	09:01
MEL	104.4	9	F	+	+	E: 20.08, RDRP/S: 21.50, N: 22.16	37	03:01	32:01	35:02	41:01	04:02	104:01:00
MEL	104.5	7	F	+	+	-	44	29:01		07:05		04:02	
MEL	104.6	5	M	+	+	E: 26.96, RDRP/S: 29.21, N: 29.85	37	29:01		07:05		04:02	
MEL	104.7	3	F	+	ND	-	43	03:01	29:01	07:05	35:02	04:02	
LA	HT1M6	4.36	F	+	+	N1 18.3, N2 20.8	92	02:01	11:01	35:01	38:01	04:01	
LA	HT34M5	3.93	M	+	-	N1 16.868, N2 17.882	168	30:01	32:01	15:01	52:01	04:01	04:02
LA	HT36M4	10.89	F	+	-	N1 32.8, N2 35.7	65	30:02	68:01	14:02	51:01	02:01	14:01
LA	HT47M1	5.02	M	+	+	N1 36, N2 36.4	88	02:01	03:01	07:02	18:01	04:01	105:01
LA	HT50M1	5.52	M	+	-	-	91	01:01	02:01	18:01	51:01	04:01	
LA	HT51M1	8.24	M	+	-	Inconclusive	77	24:02	68:01	35:12	39:11	04:02	14:01
LA	HT56M3	9.88	F	+	-	N1 31.3, N2 32.3	73						
LA	HT56M4	8.47	M	+	-	N1 31.7, N2 32.9	73	02:05	23:01	15:03	50:01	04:01	11:01
LA	HT59M1	1.27	F	+	+	N1 33.4, N2 35.4	129	02:01	68:03	07:02	39:05	04:01	04:02
LA	HT60M1	9.07	M	+	-	Undetected	50	01:01	02:06	07:02	15:30	02:01	04:02
LA	HT62M1	13.5	M	+	-	N1 34.1, N2 36.3	123	02:01	02:06	35:12	35:17	04:01	04:02
LA	HT64M1	5.59	F	+	+	Inconclusive	55	02:01	24:02	35:17	35:43	04:02	05:01
LA	HT66M5	4.21	M	+	-	N1 32.4, N2 35.9	73	03:01	11:01	39:01	44:02	03:01	04:02
LA	HT66M6	5.2	F	+	-	Undetected	82	02:01	68:03	35:01	39:01	04:01	04:02
LA	HT75M1	1.82	M	+	+	N1 24.6, N2 25	68	02:11	11:01	38:02	40:01	01:01	05:01
LA	HT83M1	6.98	F	+	-	Not tested	77	11:01	24:02	40:02	55:01	04:01	04:02

LA	HT93M1	6.09	F	+	+	N1 27.053, N2 28.464	132	29:02	32:01	18:01	44:03	04:01	131:01
MEL	CA01	25	M	+	+	NA	60	01:01	02:03	37:01	52:01	02:01	15:01
MEL	CA09	30	F	+	+	NA	67	02:01	23:01	49:01	49:01	702:01	14:01
MEL	CA12	23	M	+	+	NA	67	02:01	29:02	57:03	58:01	04:01	
MEL	CA16C1	30	F	+	+	NA	83	01:01	24:02	07:02	08:01	04:01	
MEL	CA17	49	F	+	+	NA	62	01:01	11:01	07:02	40:01	02:01	03:01
MEL	CA19	58	F	+	+	NA	53	02:01		07:02	15:01	04:02	04:02
MEL	CA21	32	F	+	+	NA	72	01:01	24:02	44:02	44:02	04:01	20:01
MEL	CA22	83	F	+	+	NA	75	24:02	33:01	14:02	55:01	04:01	05:01
MEL	CA23	83	F	+	+	NA	72	11:01	24:02	18:01	51:01	04:01	
MEL	CA27	58	F	+	+	NA	61	02:01	24:07	15:35	40:01	05:01	13:FNVU
MEL	CA29	25	F	+	+	NA	71	11:01	33:03	40:01	48:01	03:01	05:01
MEL	CA30	91	F	+	-	NA	66	24:02	26:01	15:01	38:01	02:01	04:01
MEL	CA33	28	F	+	+	NA	76	02:01		40:02	44:03	02:01	04:01
MEL	CA34C1	38	M	+	+	NA	73	03:01	24:02	07:02	52:01	03:01	04:01
MEL	CA35	26	F	+	+	NA	76	01:01	31:01	08:01	27:05	03:01	04:02
MEL	CA37C1	56	M	+	+	NA	54	02:01	26:01	44:02	47:01	02:01	05:01
MEL	CA38	54	F	+	+	NA	52	02:01	03:01	15:01	40:01	02:01	04:01
MEL	CA39	30	F	+	+	NA	81	01:01	02:01	08:01	27:05	04:01	04:02
MEL	CA46	27	M	+	+	NA	81	24:02		18:01	44:03	04:02	11:01
MEL	CA48	32	F	+	+	NA	84	02:01	29:02	14:01	37:01	04:01	11:01
MEL	CA52	27	F	+	-	NA	86	02:01	26:01	27:05	35:03	04:01	
MEL	CA52C1	37	M	+	+	NA	87	02:06	33:03	07:02	44:03	02:01	04:01
MEL	CA56	37	M	+	+	NA	69	01:01	02:01	35:03	40:01	02:01	04:02
MEL	CA61	43	F	+	+	NA	82	01:01	24:02	07:02	57:01	02:01	04:01

\*Ct values were not available for some PCR-positive adults (NA) and were not obtained for PCR-negative adults or children (-).

^The new allele differs from 52:01:01:01 at codon 81 in exon 2 (GCG->GCT) resulting in no amino acid change.

ND, Not determined; NA, Not available.