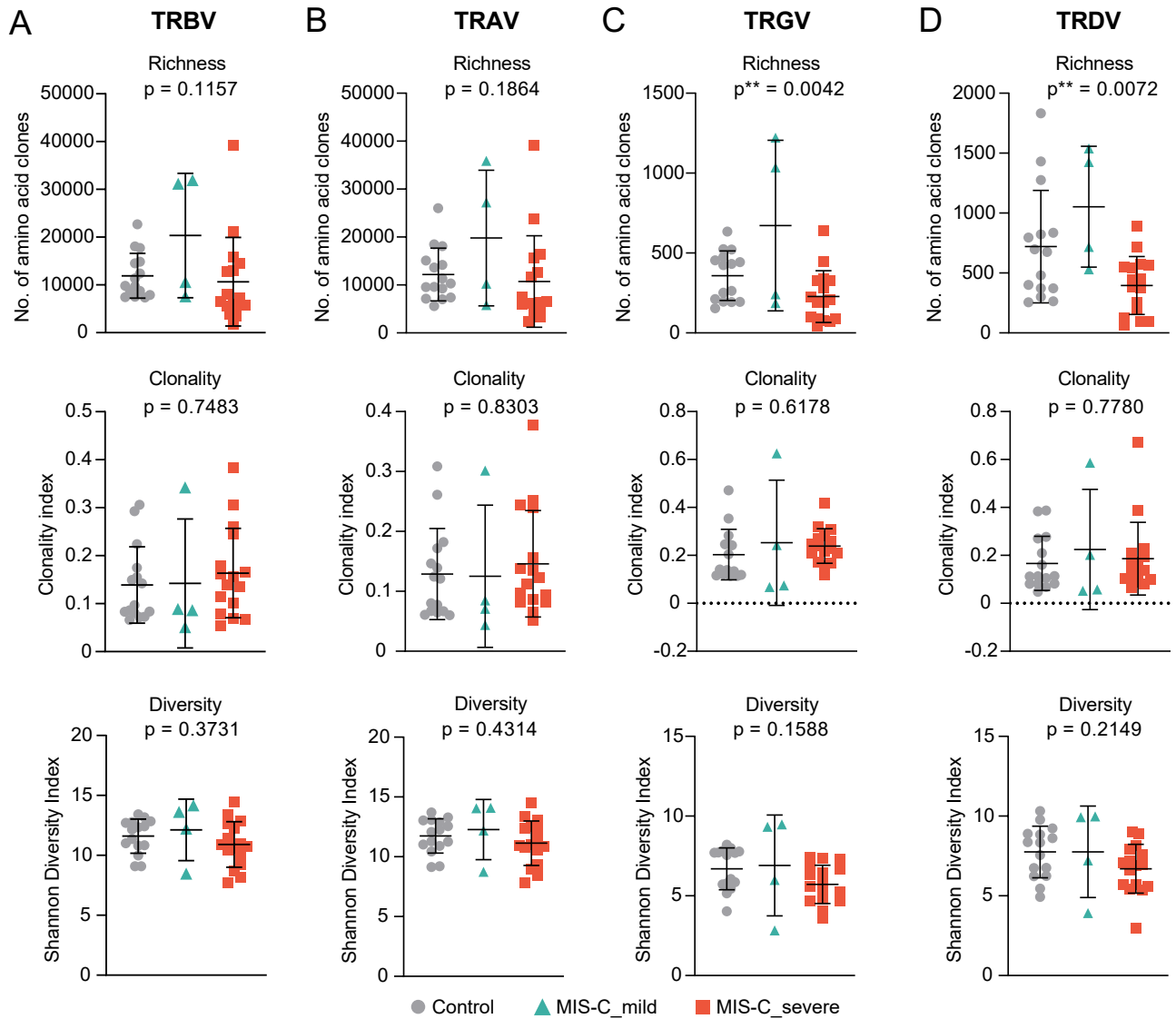Supplemental Figure 1

Figure S1. T Cell Repertoire Metrics of MIS-C patients, Related to Figure 1. Richness, clonality and Shannon diversity of the productive TRBV, TRAV, TRGV and TRDV repertoires derived from the peripheral blood of mild (n=4) and severe MIS-C (n=16) patients were compared to the respective T cell repertoires derived from the blood of age-matched febrile control patients (n=15). Bars indicate mean ± SD. Statistical analysis: Ordinary one-way ANOVA.
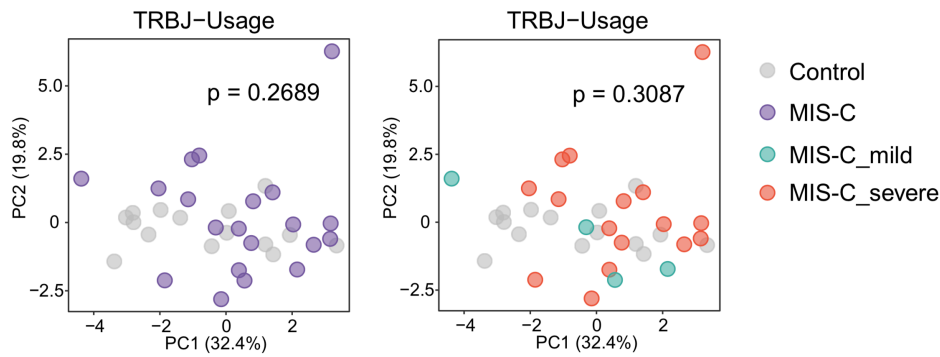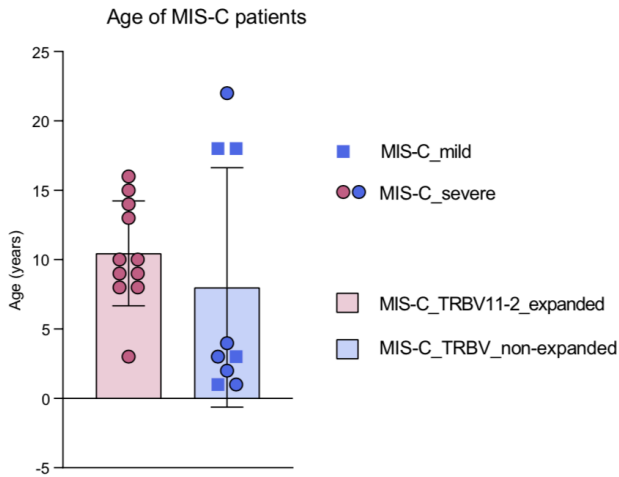
Figure S2. Principal Component Analysis of TRBJ Usage, Related to Figure 1. TRBJ usage in MIS-C patients (n=20) versus febrile controls (n=15) and between mild MIS-C (n=4) and severe MIS-C (n=16) patients. Statistical analysis: Pillai–Bartlett test of MANOVA of all principal components.

Supplemental Figure 3

A

Age of MIS-C patients

MIS-C_mild
MIS-C_severe

MIS-C_TRBV11-2_expanded
MIS-C_TRBV_non-expanded

B

TRBV11−2 Usage

p = 0.502 ns

TRBV24−1 Usage

p = 0.102 ns

TRBV11−3 Usage

p = 0.702 ns
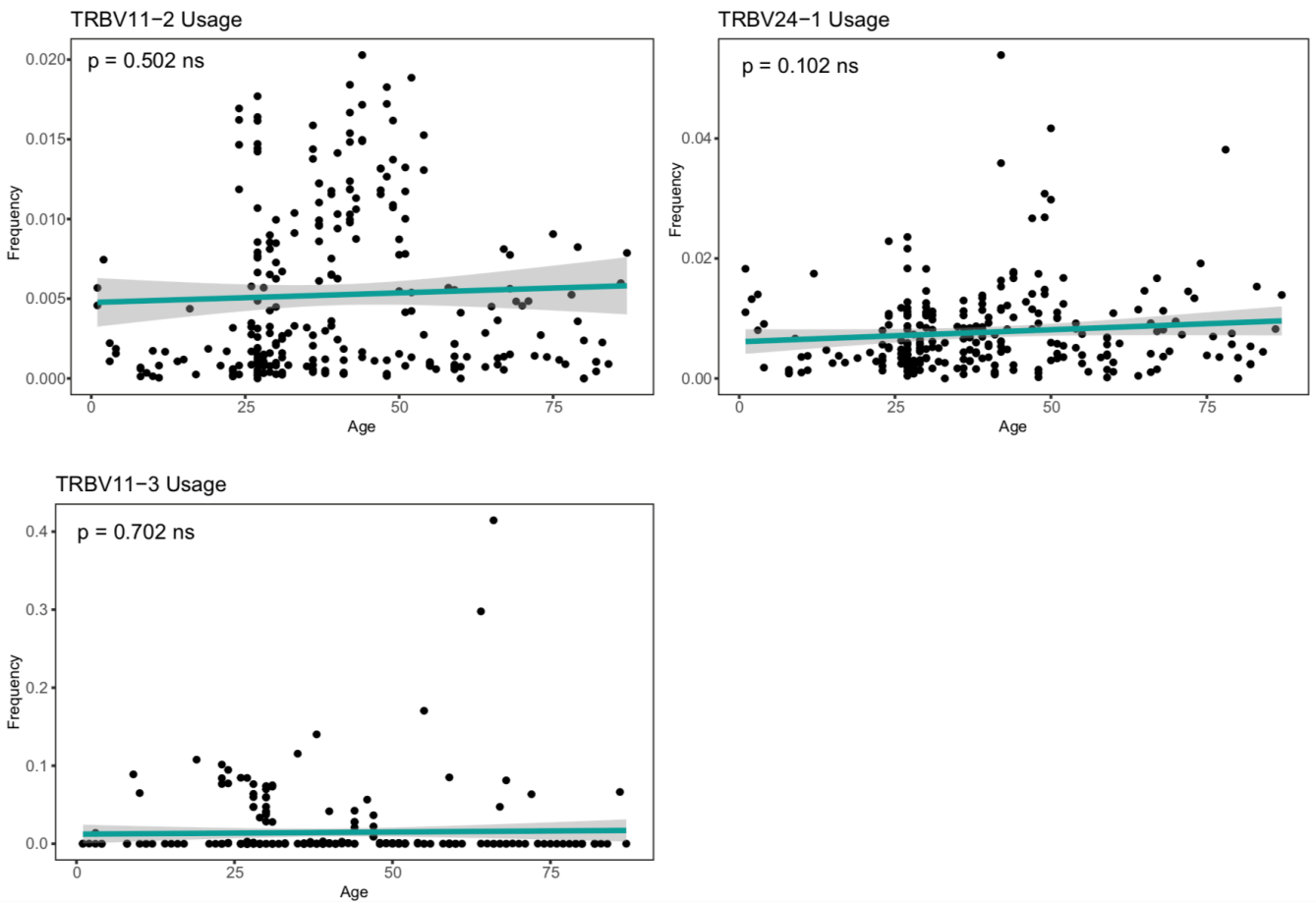
Figure S3. Association of TRBV Expansion and usage with Age, Related to Figure 2. A.
Association of Patient Age with MIS-C Severity and TRBV11-2 Expansions **B.** Frequencies of
rearranged TRBV11-2, TRBV24-1 and TRBV11-3 genes in 254 repertoires of healthy individuals of
all age groups plotted against age. Statistical analysis: Pearson correlation.

Figure S4: TRBV11-2 Usage in pediatric and adult patient repertoires, Related to Figure 2. Annotated TRB repertoires of COVID-19 patients were downloaded from public databases (Corrie et al., 2018; Nolan et al., 2020). Bars correspond to mean ± SD.

TRBV11-2 Usage

HLA types

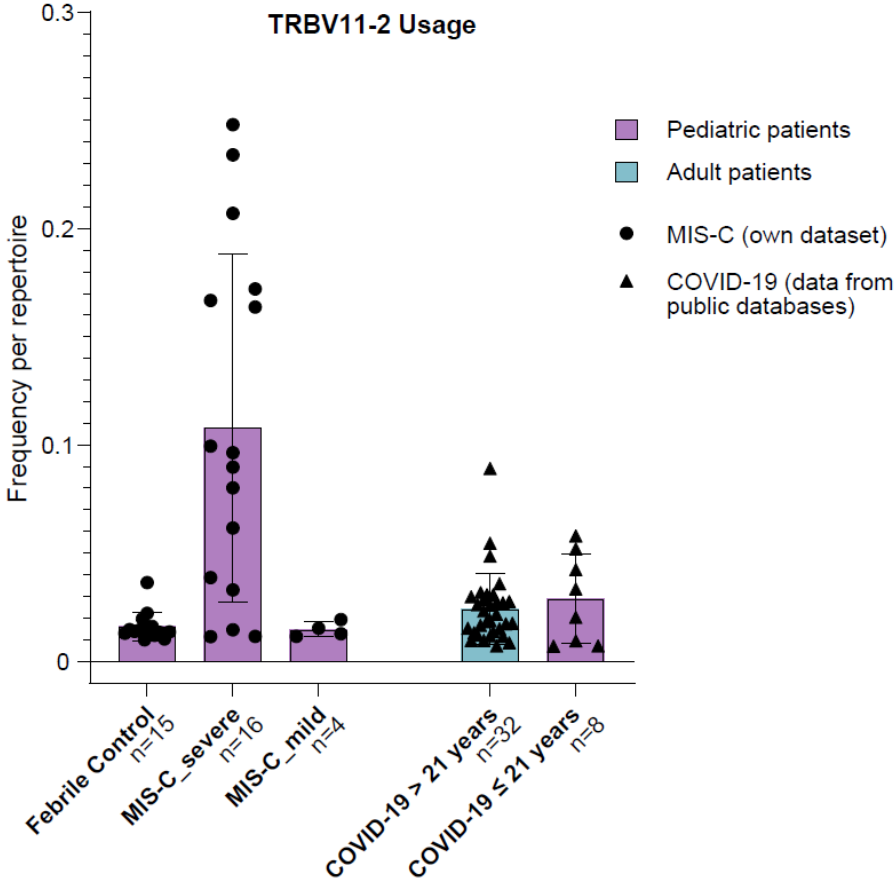| Patient	HLA-I			HLA-II				
	A	B	C	DPA1	DPB1	DQA1	DQB1	DRB1
1	*01; *24	*18; *57	*05; *07	*01; *01	*04; *04	*02; *05	*02; *03	*03; *07
2	*03; *24	*07; *08	*07; *07	*01; *01	*04; *04	*01; *05	*02; *06	*03; *15
3	*01; *31	*08; *40	*03; *07	*01; *02	*01; *06	*03; *05	*02; *03	*03; *04
3	*24; *24	*15; *40	*08; *15	*02; *02	*01; *01	*01; *01	*05; *05	*04; *04
5	*24; *33	*15; *51	*07; *14	*02; *02	*01; *05	*01; *03	*03; *05	*09; *15
6	*01; *02	*08; *13	*06; *07	*01; *02	*04; *05	*01; *05	*02; *06	*03; *15

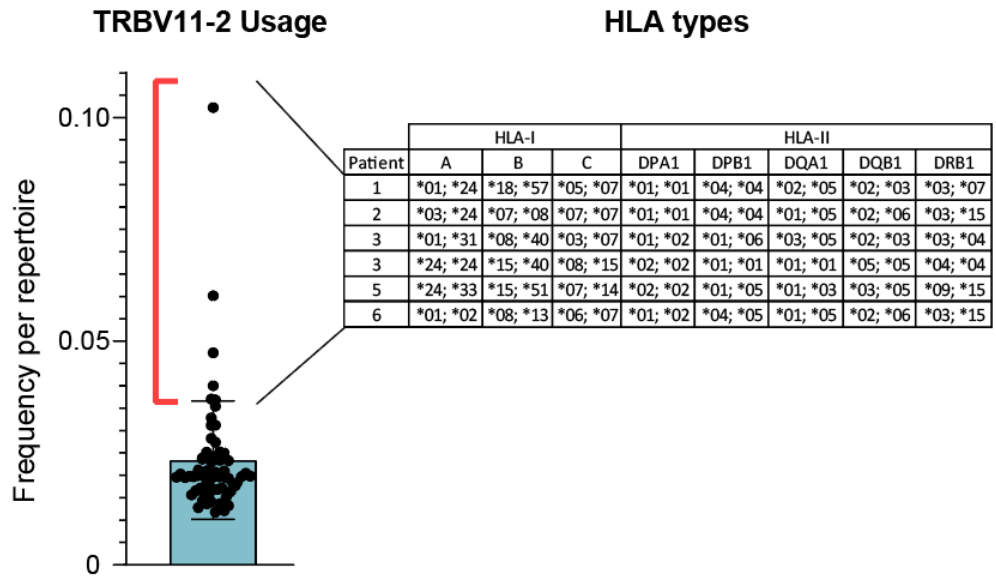**Figure S5. HLA status of adult COVID-19 patients with expansion of TRBV11-2, Related to Figure 5.** TRB repertoires of COVID-19 patients with matching patient information including HLA data were downloaded from public databases (n=63) (Nolan et al., 2020). Bars correspond to mean ± SD. HLA data of patients with TRBV11-2 usage above mean + SD (n=6, red bar) of the cohort are shown on the right.

```
                              CDR1                          CDR2
TRBV11_2|A0A584      EAGVAQSPRYKIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQL   71
TRBV11_3|A0A5A6      EAGVVQSPRYKIIEKKQPVAFWCNPISGHNTLYWYLQNLGQGPELLIRYENEEAVDDSQL   71
TRBV11_1|A0A0K0K1C0  EAEVAQSPRYKITEKSQAVAFWCDPISGHATLYWYRQILGQGPELLVQFQDESVVDDSQL   71
TRBV14|A0A5B0        EAGVTQFPSHSVIEKGQTVTLRCDPISGHDNLYWYRRVMGKEIKFLLHFVKESKQDESGM   71
TRBV7_3|A0A1B0GXH9   GAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGL   71
TRBV12_3|P01733      DAGVIQSPRHEVTEMGQEVTLRCKPISGHNSLFWYRQTMMRGLELLIYFNNNVPIDDSGM   71
TRBV12_4|A0A0B4J2E0  DAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGM   71
TRBV12_5|A0A1B0GX78  DARVTQTPRHKVTEMGQEVTMRCQPILGHNTVFWYRQTMMQGLELLAYFRNRAPLDDSGM   71
TRBV16|A0A087WV62    GEEVAQTPKHLVRGEGQKAKLYCAPIKGHSYVFWYQQVLKNEFKFLISFQNENVFDETGM   71
TRBV18|A0A087X0M5    NAGVMQNPRHLVRRRGQEARLRCSPMKGHSHVYWYRQLPEEGLKFMVYLQKENIIDESGM   71
                      *  *  *    :      :  .  :  * * *:  **    ::** :    .   :::    *:: :

TRBV11_2|A0A584      PKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSL   108
TRBV11_3|A0A5A6      PKDRFSAERLKGVDSTLKIQPAELGDSAVYLCASSL   108
TRBV11_1|A0A0K0K1C0  PKDRFSAERLKGVDSTLKIQPAELGDSAMYLCASSL   108
TRBV14|A0A5B0        PNNRFLAERTGGTYSTLKVQPAELEDSGVYFCASSQ   108
TRBV7_3|A0A1B0GXH9   PNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSL   108
TRBV12_3|P01733      PEDRFSAKMPNASFSTLKIQPSEPRDSAVYFCASSL   108
TRBV12_4|A0A0B4J2E0  PEDRFSAKMPNASFSTLKIQPSEPRDSAVYFCASSL   108
TRBV12_5|A0A1B0GX78  PKDRFSAEMPDATLATLKIQPSEPRDSAVYFCASGL   108
TRBV16|A0A087WV62    PKERFSAKCLPNSPCSLEIQATKLEDSAVYFCASSQ   108
TRBV18|A0A087X0M5    PKERFSAEFPKEGPSILRIQQVVRGDSAAYFCASSP   108
                      *:.:** *            . *.:*      **. *.:***.
                                                        CDR3
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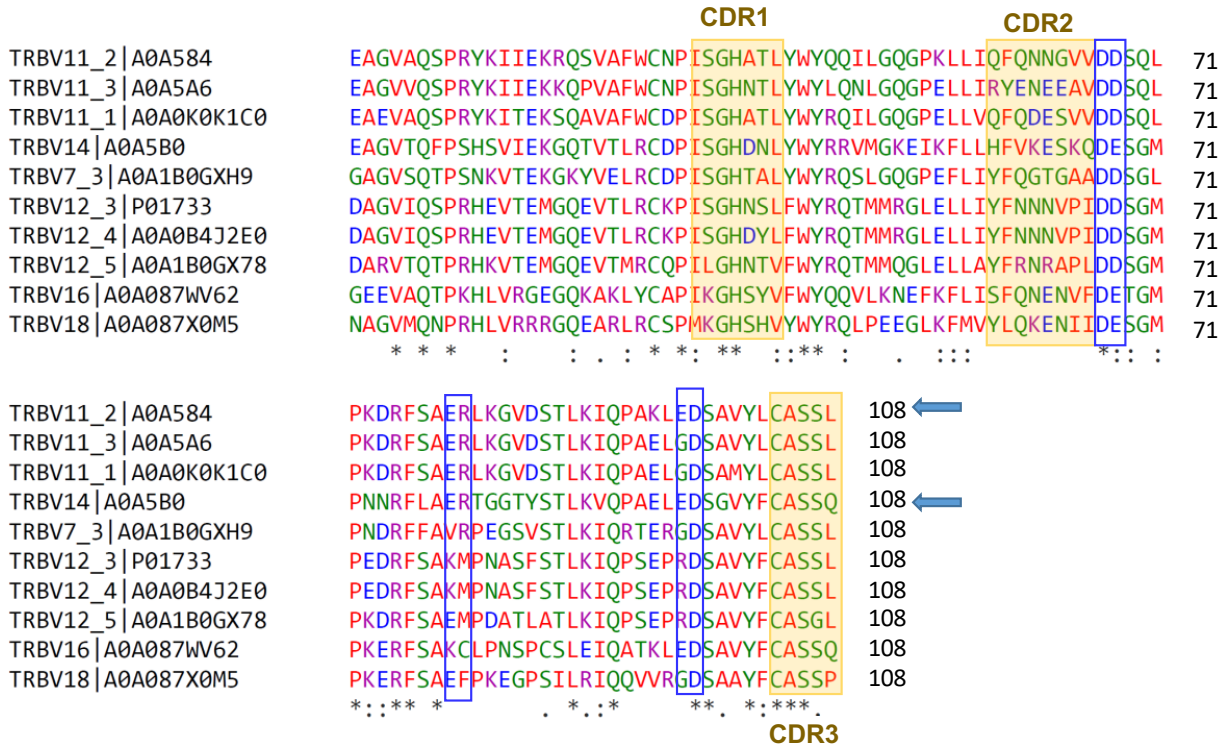
Figure S6: Multiple Sequence Alignment of all TCR Vβ Chains that Contain Polyacidic Residue Pairs D67-D68 or D67-E68 Near their CDR2 Region, Related to Figure 5. TCR Vβ sequences containing polyacidic residues at their CDRs were retrieved from the IMGT Repertoire. The alignment was generated using Clustal Omega (Sievers et al., 2011). CDR1, CDR2 and CDR3 are indicated by *orange shades*.