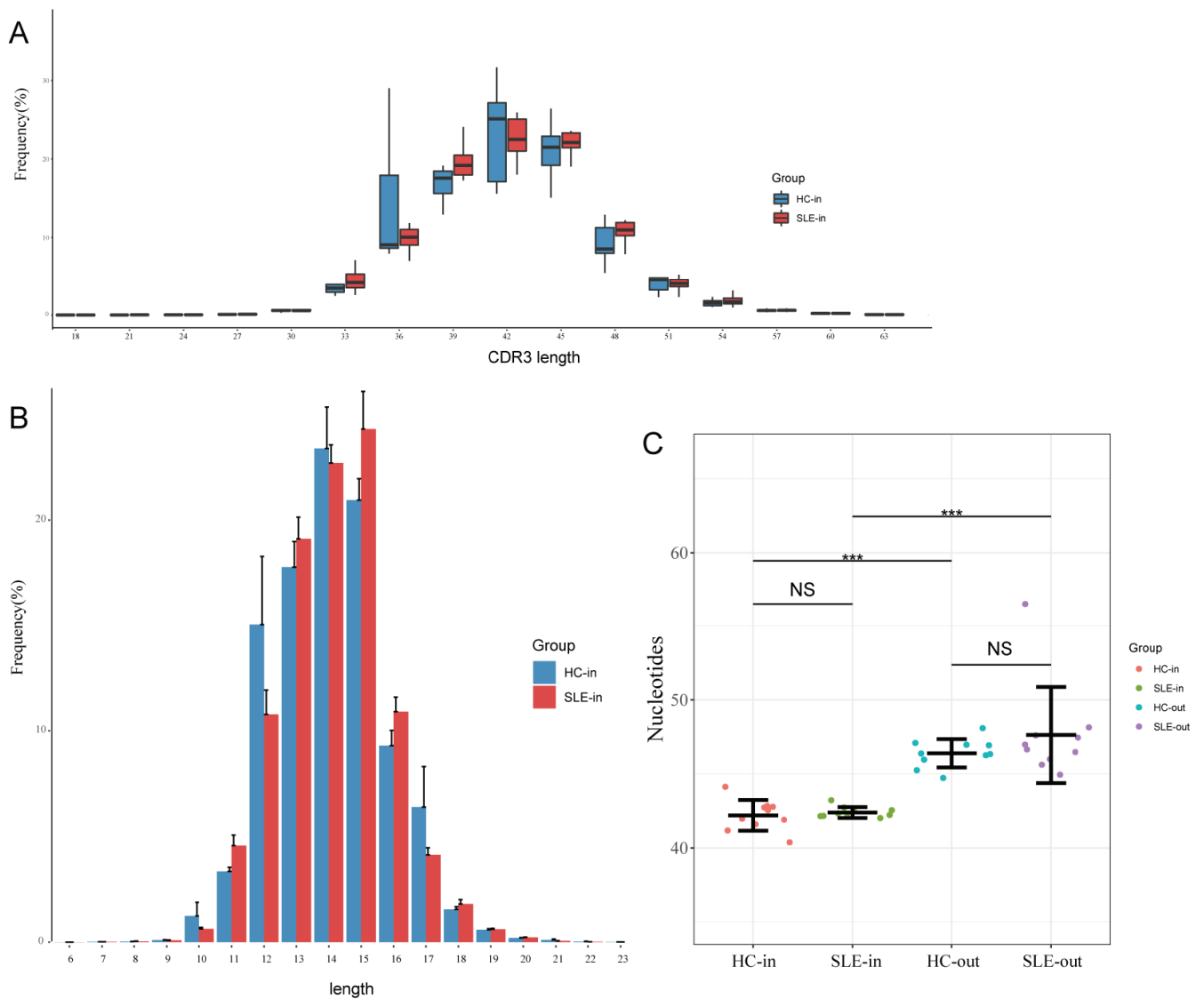
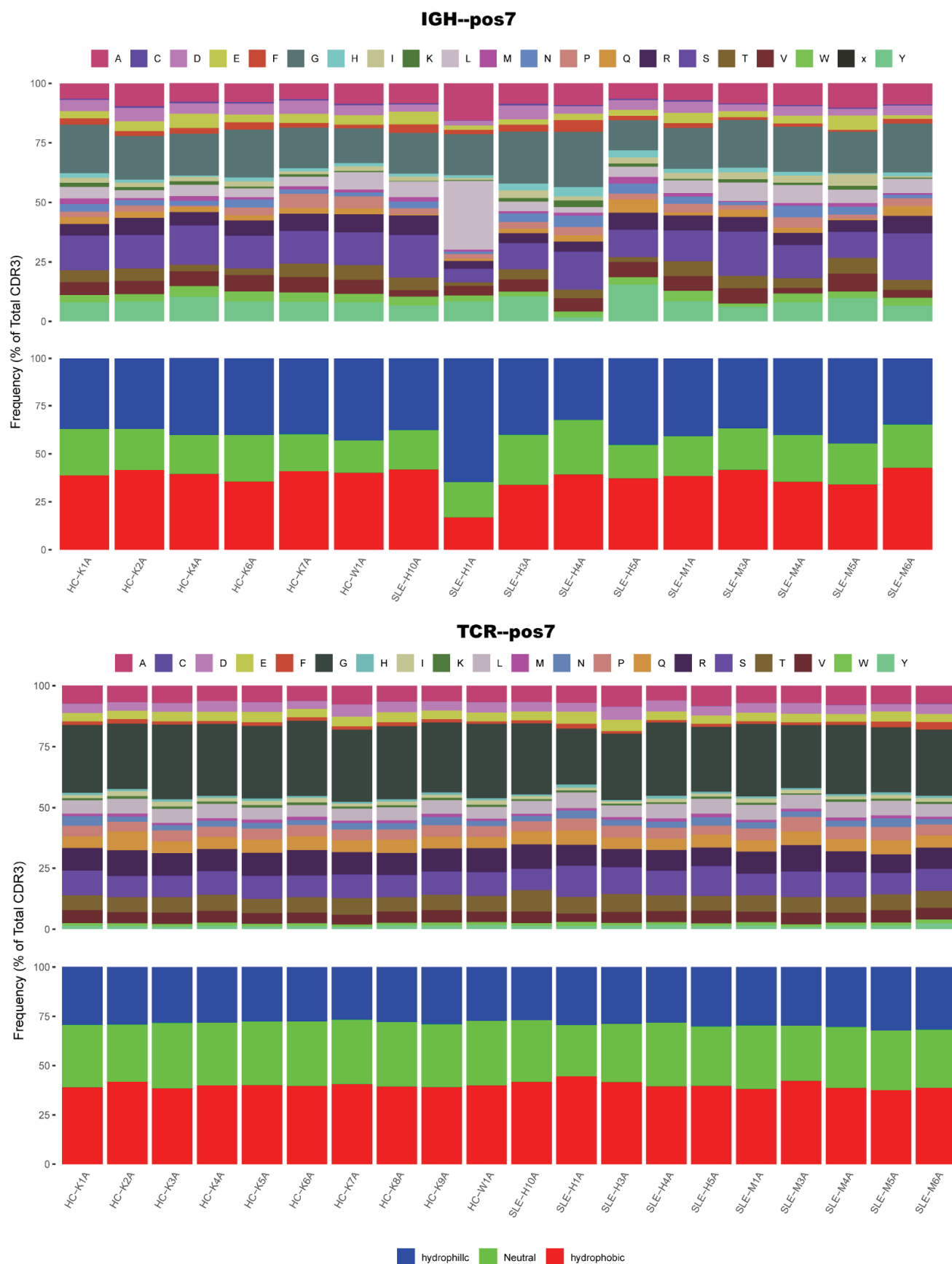
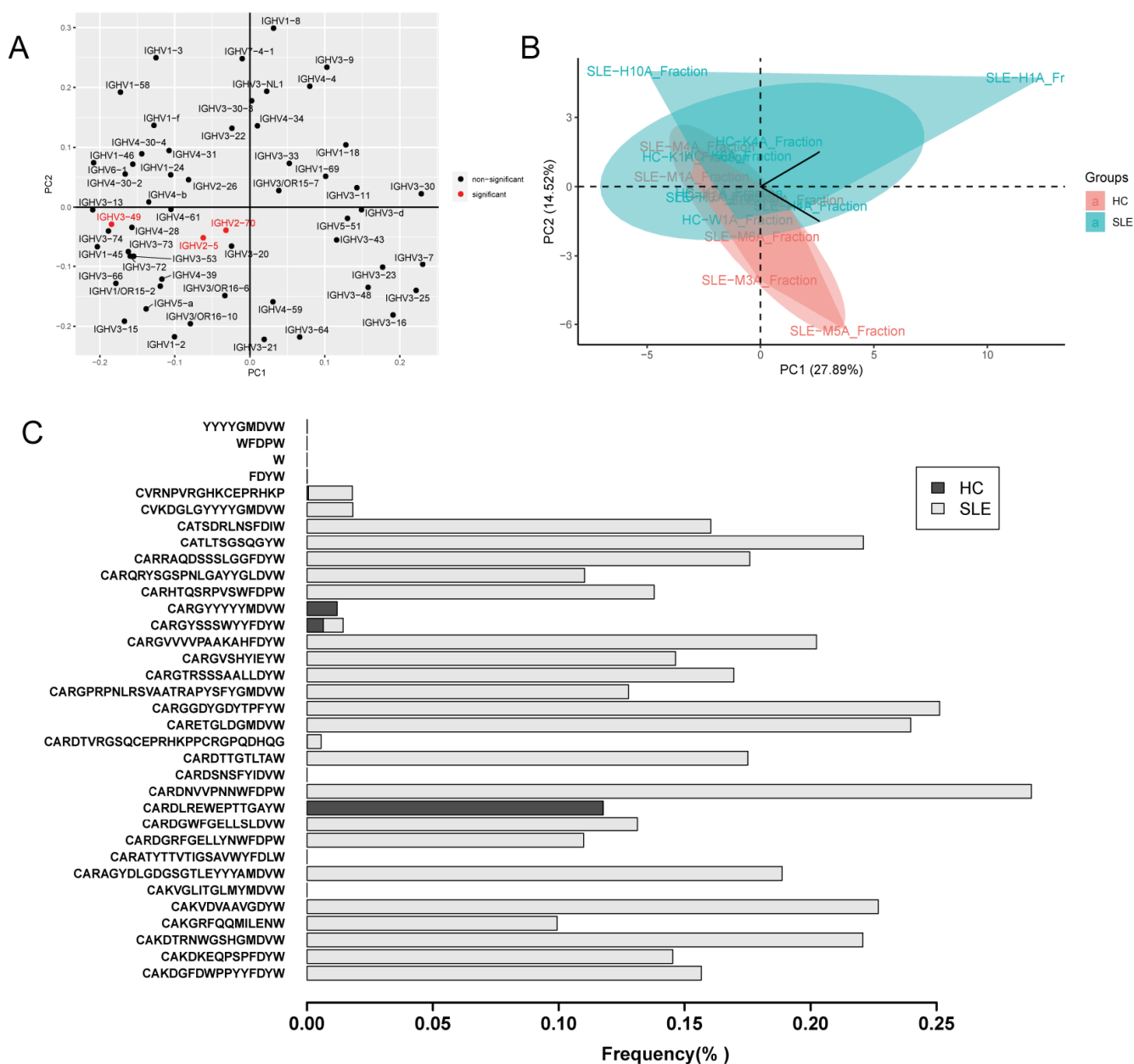




Supplementary Fig. S1. Comparison of TCR- β CDR3 nucleotide length (A) and amino acid sequence length (B) between SLE patients and healthy controls. BCR-H CDR3s were shorter in SLE patients. C, Comparison of the mean length of the nucleotide sequences between SLE patients and healthy controls, analysis performed on the pre-selection TCR- β repertoire (out, out of frame) and post-selection TCR- β repertoires (in, in frame). Data were presented as the mean $\pm$ SD values and compared using an unpaired t -test. *** p <0.001 (two-tailed).



Supplementary Fig. S2. Analysis of amino acid composition in SLE patients. Amino acid composition of CDR3 in SLE patients and healthy controls for amino acid positions 7 of the 13-amino acid-long BCR-H CDR3s (**top**) and TCR- β CDR3s (**bottom**).



Supplementary Fig. S3. Differential usage of IGHV gene and abnormal abundance of BCR-H CDR3 amino acid sequences in SLE patients.

Supplementary Fig. S6. Differential usage of IGHV gene and abnormal abundance of BCR-H CDR3 amino acid sequences in SLE patients. **A-B:** Differential usage of IGHV genes, segregating control and SLE patient samples and the various genes according to PC1 and PC2, is shown as variable plots (**A**) and sample plots (**B**). **C:** Comparing of the abundance of BCR-H CDR3 sequences between SLE patients and healthy controls.

Supplementary Table S1. Multiplex-PCR amplification primers of the BCR-H CDR3 region.

Primers	Sequences
IGHV1-18	CAGACGTGTGCTCTTCCGATCTAGAGAGTCACCATGACCACAGAC
IGHV1-2/1-46	CAGACGTGTGCTCTTCCGATCTAGAGAGTCACCAKKACCAGGGAC
IGHV1-24	CAGACGTGTGCTCTTCCGATCTAGAGAGTCACCATGACCGAGGAC
IGHV1-3/1-45	CAGACGTGTGCTCTTCCGATCTAGAGAGTCACCATTACYAGGGAC
IGHV1-69/1-f	CAGACGTGTGCTCTTCCGATCTAGAGAGTCACGATWACCRCCGAC
IGHV1-8	CAGACGTGTGCTCTTCCGATCTAGAGAGTCACCATGACCAGGAAC
IGH2-70/26/5	CAGACGTGTGCTCTTCCGATCTAGACCAGGCTCACCATYWCCAAGG
IGHV3	CAGACGTGTGCTCTTCCGATCTAGGGCCGATTACCATCTCMAG
IGH4	CAGACGTGTGCTCTTCCGATCTAGCGAGTCACCATRTCMGTAGAC
IGHV5-51	CAGACGTGTGCTCTTCCGATCTAGCAGCCGACAAGTCCATCAGC
IGHV6-1	CAGACGTGTGCTCTTCCGATCTAGAGTCAATAACCATCAACCCAG
IGHV7-NEW	CAGACGTGTGCTCTTCCGATCTAGGACGGTTTGTCTTCTCCTTG
HIGHJ-Rev1	CTACACGACGCTCTTCCGATCTCTGAGGAGACRGTGACCAGGGTG
HIGHJ-Rev2	CTACACGACGCTCTTCCGATCTCTGAAGAGACGGTGACCATTGTC
HIGHJ-Rev3	CTACACGACGCTCTTCCGATCTCTGAGGAGACGGTGACCAGGGT
HIGHJ-Rev4	CTACACGACGCTCTTCCGATCTTGAAGGAGACGGTGACCGTGGTC

Supplementary Table S2. Multiplex-PCR amplification primers of the TCR- β CDR3 region.

TRB V Primers	TRB J Primers
TRBV2	ATTTCACTCTGAAGATCCGGTCCAC
TRBV3-1	AAACAGTTCCAAATCGMTTCTCAC
TRBV4-1/2/3	CAAGTCGCTTCTCACCTGAATG
TRBV5-1	GCCAGTTCTCTAACTCTCGCTCT
TRBV5-4/5/6/8	TCAGGTCGCCAGTTCCCTAAYTAT
TRBV6-4.1	CACGTTGGCGTCTGCTGTACCCT
TRBV6-8/5/1.2	CAGGCTGGTGTGCGCTGCTCCCT
TRBV6-9/7/1.1/6	CAGGCTGGAGTCAGCTGCTCCCT
TRBV6-4.2	AGTCGCTTGTCTGTACCCTCTCAG
TRBV6-2/3	GGGGTTGGAGTCGGCTGCTCCCT
TRBV7-2/4/6/7/8	GGGATCCGTCTCCACTCTGAMGAT
TRBV7-3	GGGATCCGTCTCTACTCTGAAGAT
TRBV7-9	GGGATCTTCTCCACCTTGGAGAT
TRBV9	CCTGACTTGCACTCTGAACCTAAACCT
TRBV10-1	CCTCACTCTGGAGTCTGCTGCC
TRBV10-2/3	CCTCACTCTGGAGTCMGCTACC
TRBV11-1/2/3	GCAGAGAGGCTCAAAGGAGTAGACT
TRBV12-3.2/5.2	GAAGGTGCAGCCTGCAGAACCCAG
TRBV12-3.1/4/5.1	GAAGATCCAGCCCTCAGAACCCAG
TRBV13	TCGATTCTCAGCTCAACAGTTC
TRBV14	GGAGGGACGTATTCTACTCTGAAGG
TRBV15	TTCTTGACATCCGCTCACCAGG
TRBV16	CTGTAGCCTTGAGATCCAGGCTACGA
TRBV18	TAGATGAGTCAGGAATGCCAAAG
TRBV19	TCCTTTCCTCTCACTGTGACATCGG
TRBV20-1	AACCATGCAAGCCTGACCTT
TRBV24-1	CTCCCTGTCCCTAGAGTCTGCCAT
TRBV25-1	GCCCTCACATACCTCTCAGTACCTC
TRBV27-1	GATCCTGGAGTCGCCCAGC
TRBV28	ATTCTGGAGTCCGCCAGC
TRBV29-1	AACCTGACTGTGAGCAACATGAG
TRBV30-F5	CAGATCAGCTCTGAGGTGCCCCA
TRBJ1.1	CTTACCTACAACCTGTGAGTCTGGTG
TRBJ1.2	CTTACCTACAACGGTTAACCTGGTC
TRBJ1.3	CTTACCTACAACAGTGAGCCAACTT
TRBJ1.4	AAGACAGAGAGCTGGGTTCCTACT
TRBJ1.5	CTTACCTAGGATGGAGAGTCGAGTC
TRBJ1.6	CATACCTGTACAGTGAGCCTG
TRBJ2.1	CCTTCTTACCTAGCACGGTGA
TRBJ2.2	CTTACCCAGTACGGTCAGCCT
TRBJ2.3	CCGCTTACCGAGCACTGTGAG
TRBJ2.4	AGCACTGAGAGCCGGGTCC
TRBJ2.5	CGAGACCAAGGAGCCGCGT
TRBJ2.6	CTCGCCAGCACGGTCAGCCT
TRBJ2.7	CTTACCTGTGACCGTGAGCCTG