Supplementary Material

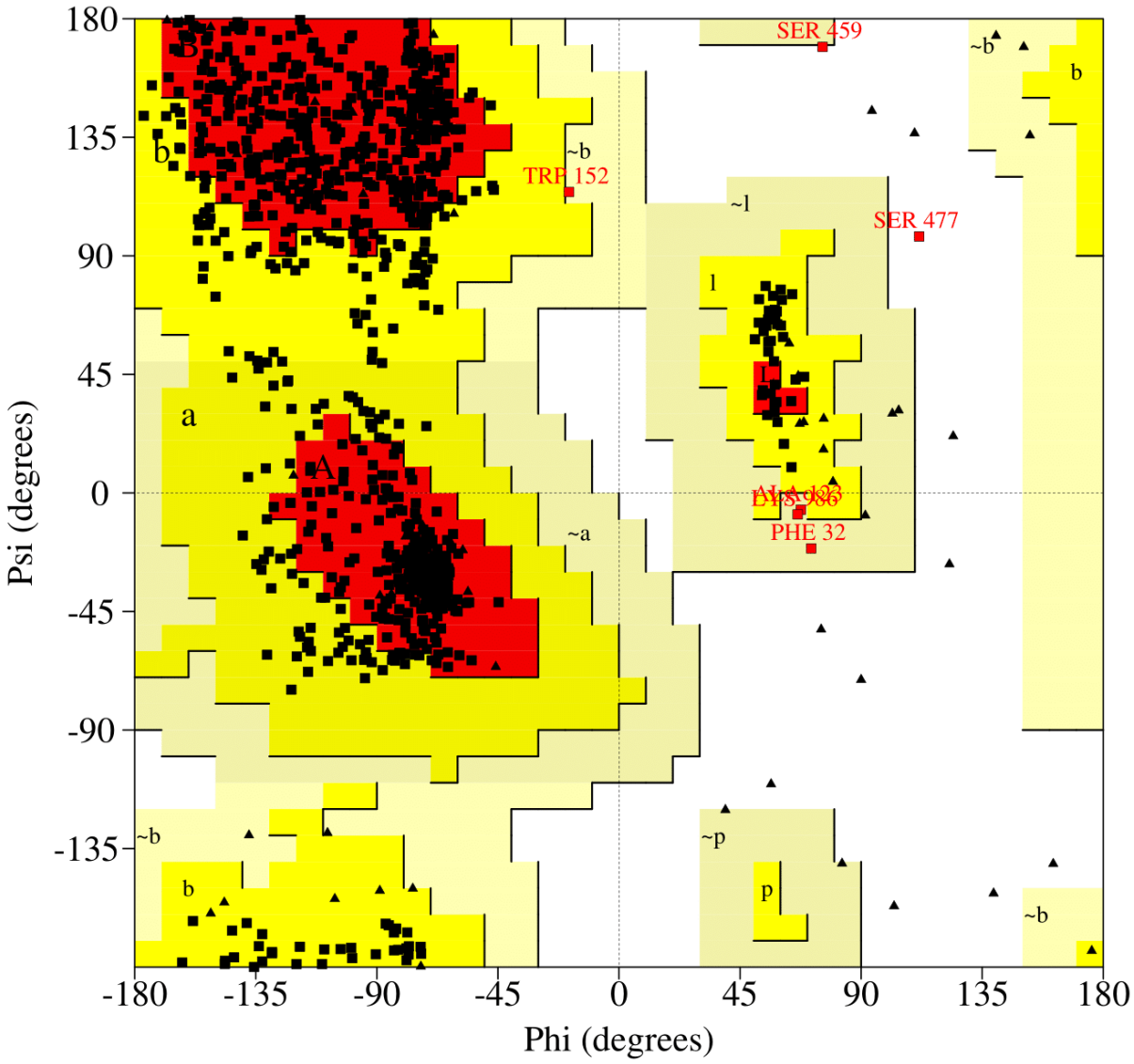
1 Supplementary Data

Multiple sequence alignment uploaded as pdf file.

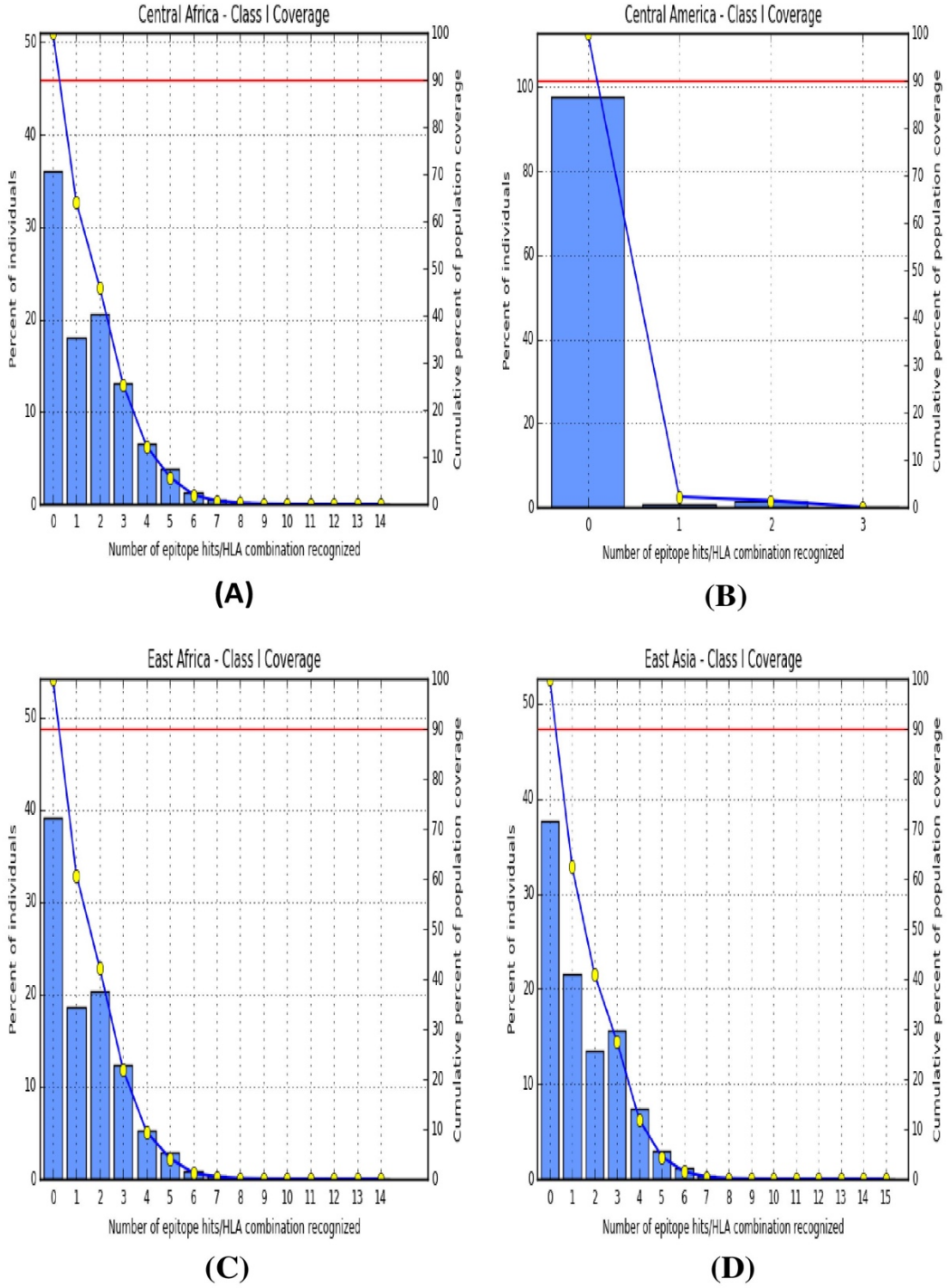
2 Supplementary Figures and Tables

2.1 Supplementary Figures

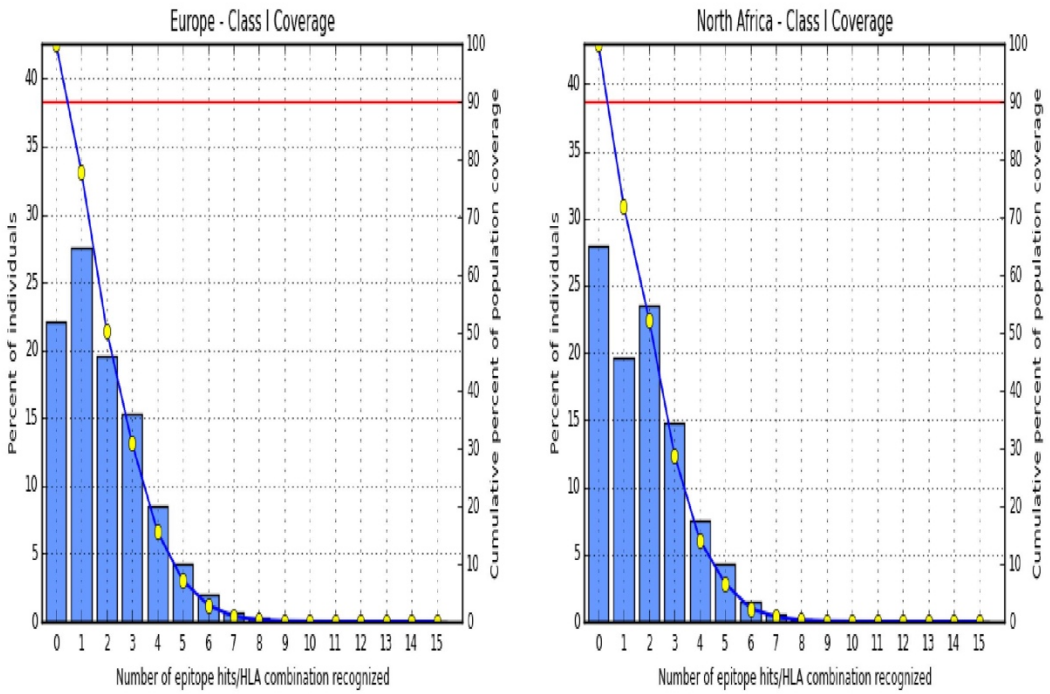
Supplementary Figure 1. Evolutionary divergence analysis of available spike glycoproteins of different strains of SARS-CoV-2; results are represented in a phylogenetic tree.



Supplementary Figure 2. Ramachandran plot analysis for the tertiary structure of the SARS-CoV-2 SGP.

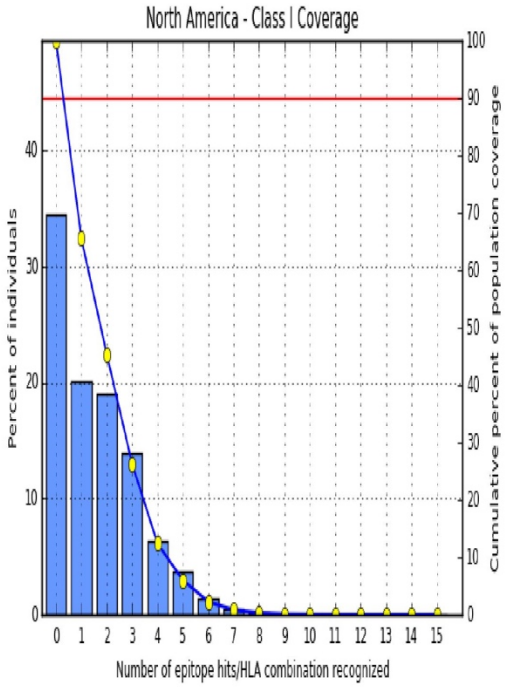


Supplementary Figure 3. Population coverage based on MHC restriction data for **(A)** Central Africa, **(B)** Central America, **(C)** East Africa, **(D)** East Asia - using the Immune Epitope Database analysis resource.

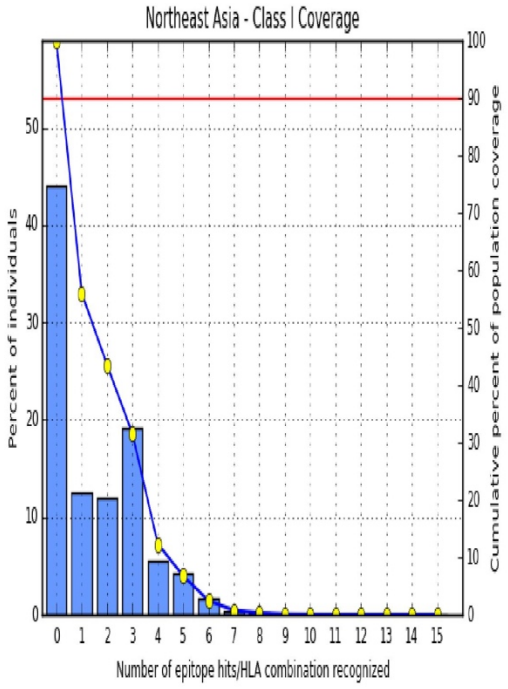


(E)

(F)

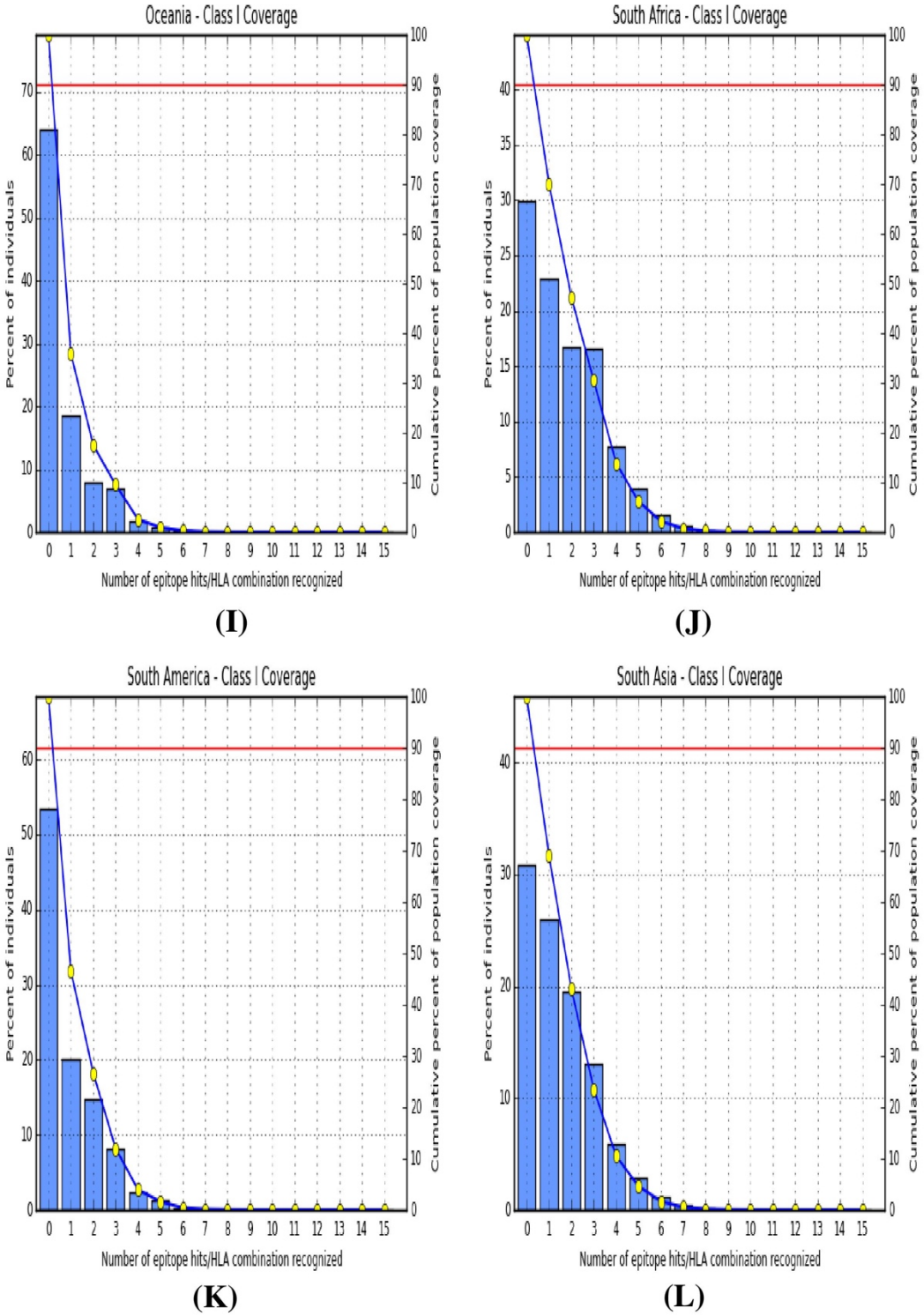


(G)

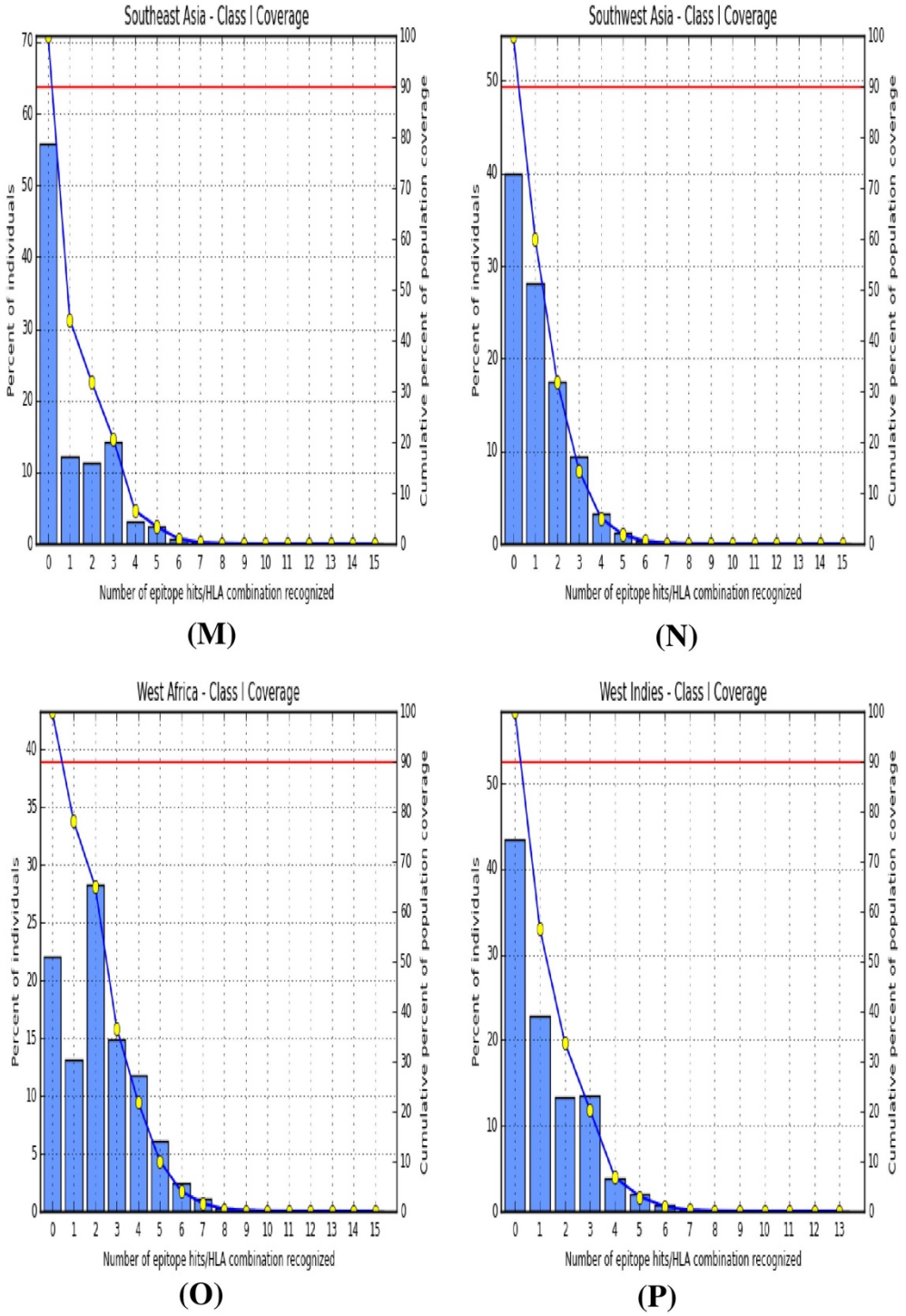


(H)

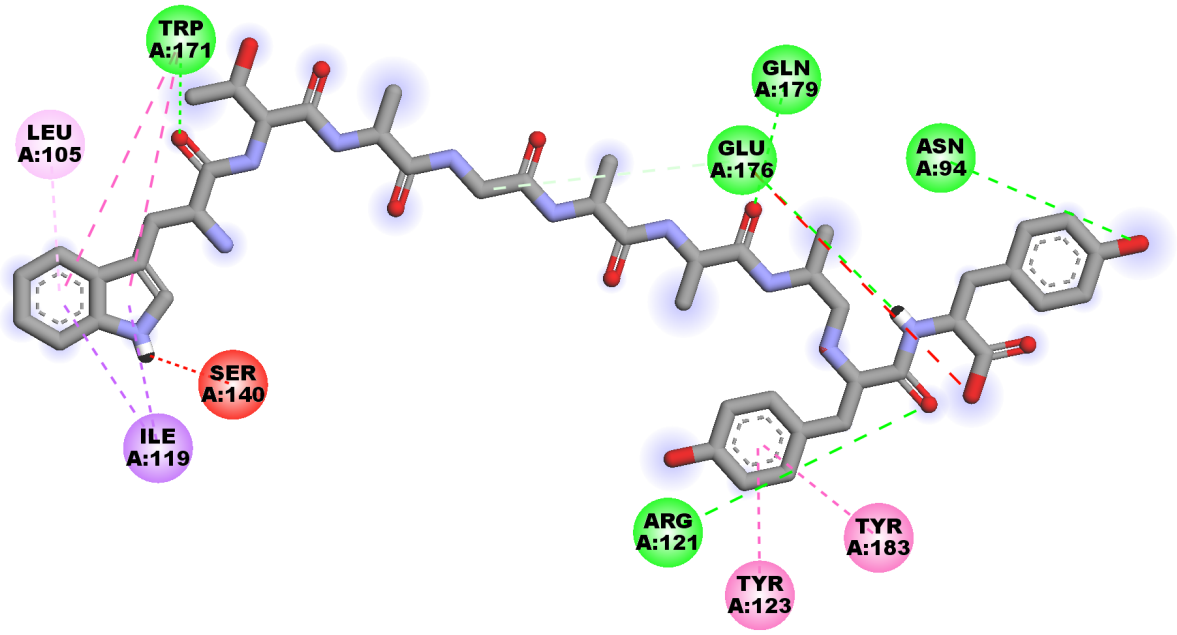
Supplementary Figure 4. Population coverage based on MHC restriction data for **(E)** Europe, **(F)** North Africa, **(G)** North America, **(H)** Northeast Asia - using the Immune Epitope Database analysis resource.



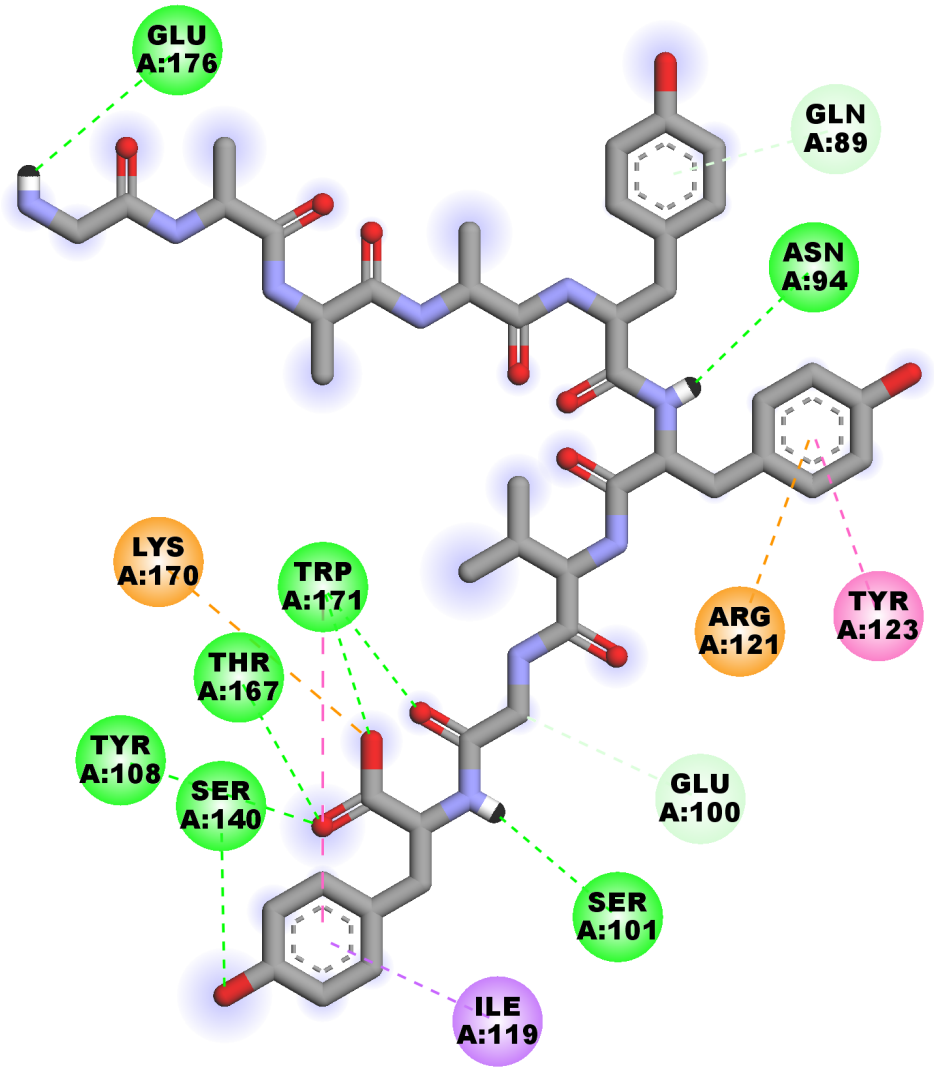
Supplementary Figure 5. Population coverage based on MHC restriction data for **(I)** Oceania, **(J)** South Africa, **(K)** South America, **(L)** South Asia - using the Immune Epitope Database analysis resource.



Supplementary Figure 6. Population coverage based on MHC restriction data for **(M)** Southeast Asia, **(N)** Southwest Asia, **(O)** West Africa, **(P)** West Indies - using the Immune Epitope Database analysis resource.



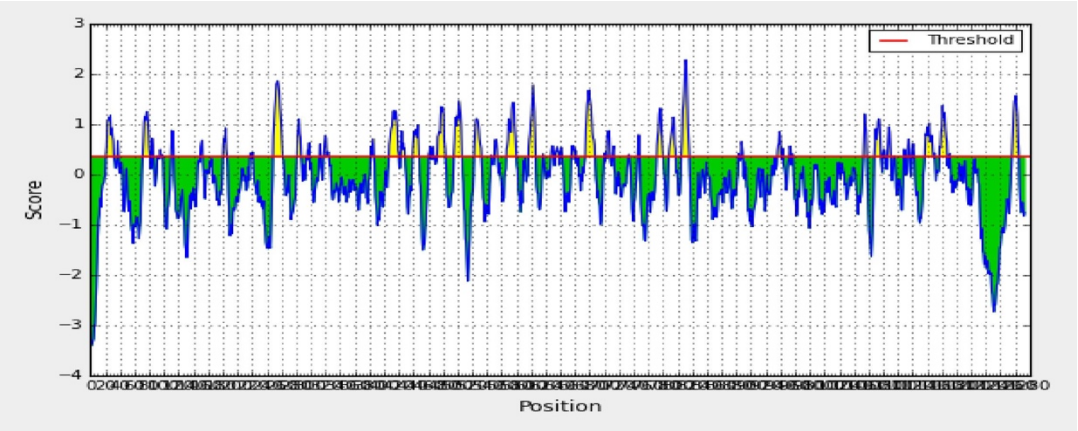
Supplementary Figure 7. 2D representation of the interaction between epitope WTAGAAAYY and HLA-B*15:25 allele.



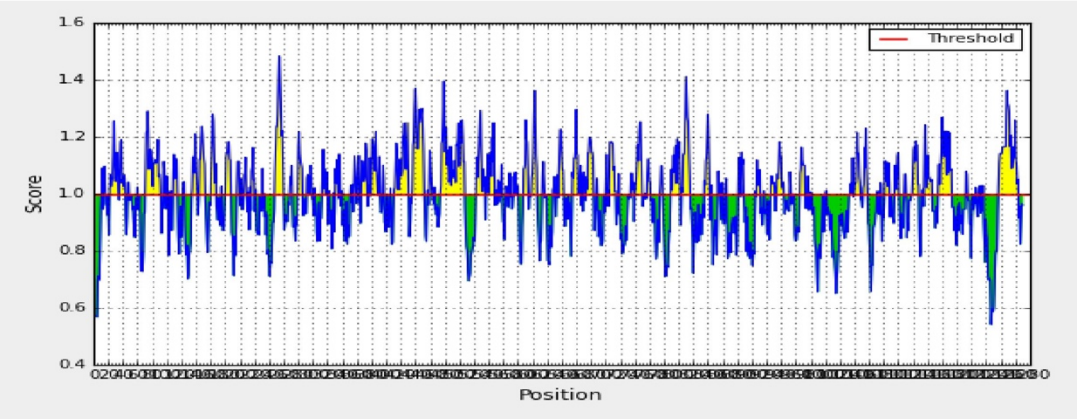
41

42 **Supplementary Figure 8.** 2D representation of the interaction between epitope GAAAYYVGY and
43 HLA-B*15:25 allele.

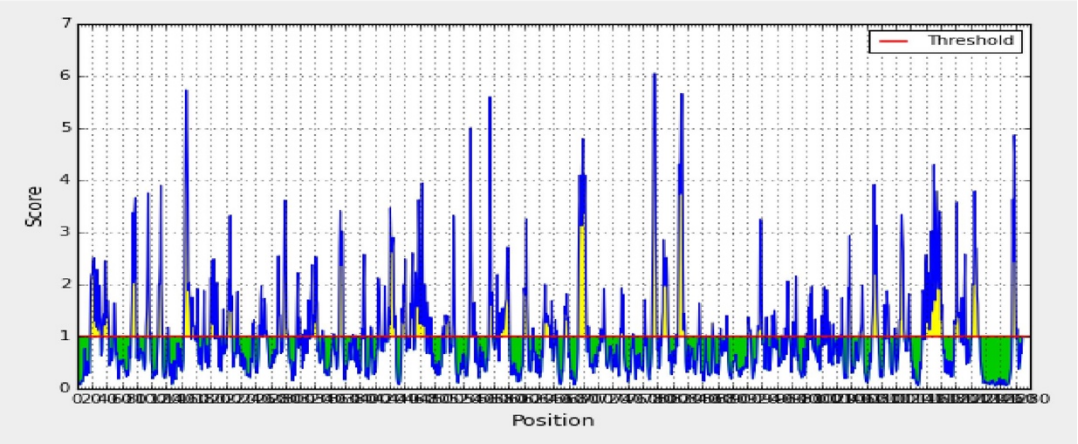
44



(A)

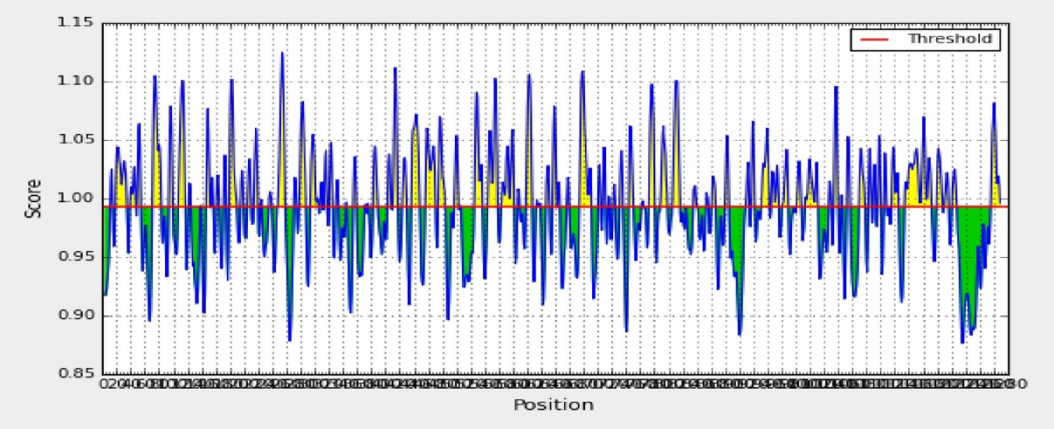


(B)

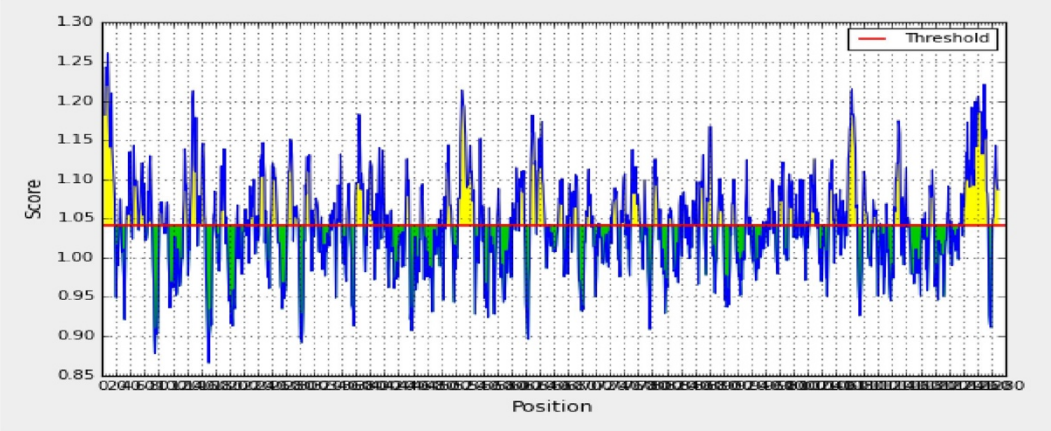


(C)

Supplementary Figure 9. Combined B-cell linear epitope prediction using **(A)** Bepipred linear epitope prediction, **(B)** Chou & Fasman beta-turn prediction, **(C)** Emini surface accessibility prediction methods.



(D)



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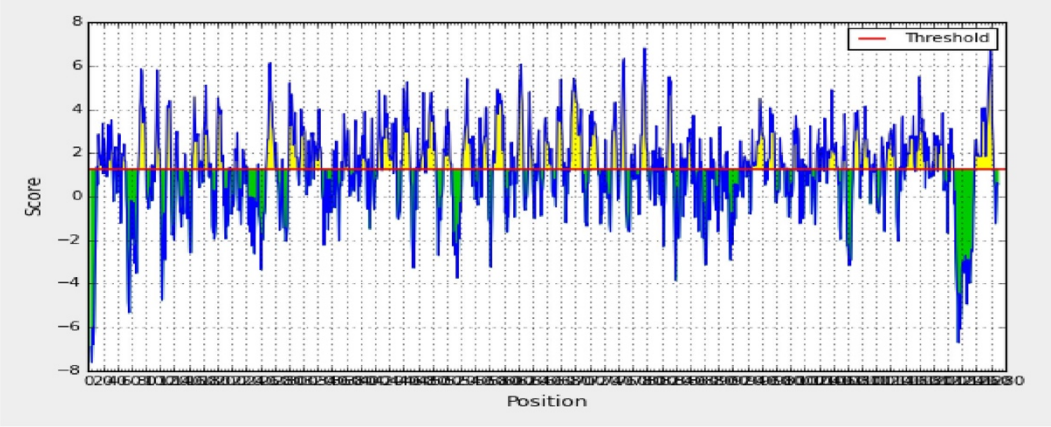


(F)

Supplementary Figure 10. Combined B-cell linear epitope prediction using **(D)** Karplus & Schulz flexibility prediction, **(E)** Kolaskar & Tongaonkar antigenicity, **(F)** Parker hydrophilicity prediction methods.

2.2 Supplementary Tables

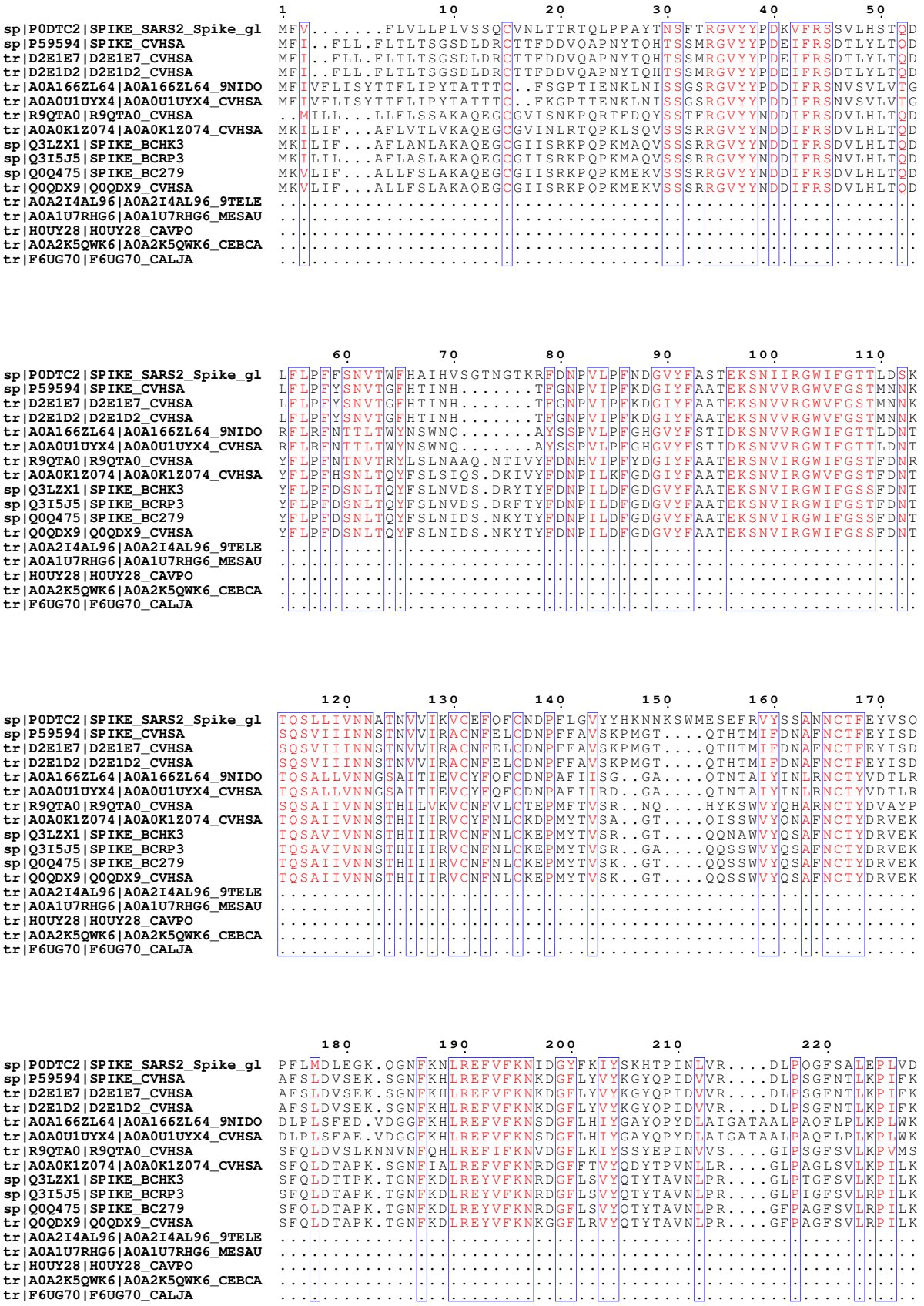
TABLE S1 Antigenicity prediction of selected epitopes using VaxiJen 2.0 server

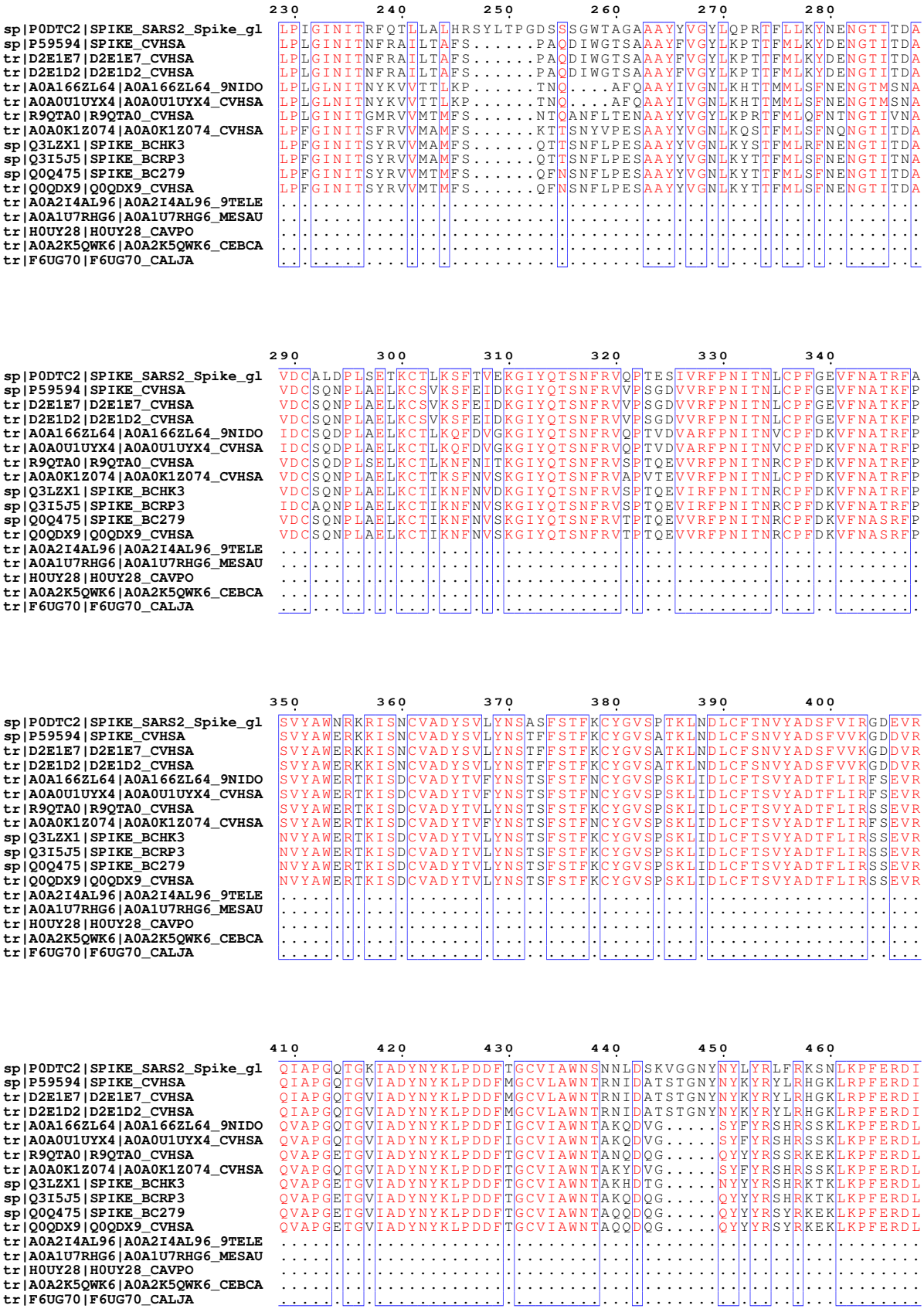
Epitopes	Antigen Prediction
LTDEMIAQY	Probable NON-ANTIGEN
WTAGAAAYY	Probable ANTIGEN
TSNQVAVLY	Probable ANTIGEN
CVADYSVLY	Probable NON-ANTIGEN
KTSVDCTMY	Probable ANTIGEN
STECSNLLL	Probable ANTIGEN
GAEHVNNSY	Probable ANTIGEN
NIDGYFKIY	Probable NON-ANTIGEN
YSSANNCTF	Probable NON-ANTIGEN
WMESEFRVY	Probable NON-ANTIGEN
SANNCTFEY	Probable NON-ANTIGEN
VASQSIIAY	Probable NON-ANTIGEN
NSFTRGVYY	Probable NON-ANTIGEN
CNDPFLGVY	Probable ANTIGEN
FTNVYADSF	Probable NON-ANTIGEN
GAAAYYVGY	Probable ANTIGEN
RISNCVADY	Probable NON-ANTIGEN
ERDISTEIY	Probable NON-ANTIGEN
ITDAVDCAL	Probable ANTIGEN
RVDFCGKGY	Probable NON-ANTIGEN
NATRFASVY	Probable NON-ANTIGEN
MTSCCSCLK	Probable ANTIGEN
STQDLFLPF	Probable ANTIGEN

TABLE S2 MHC-NP probability score for the selected epitopes

Epitopes	Alleles	Length	Probability score
GAAAYYVGY	HLA-B*44:03	9	0.7289
	HLA-B*53:01	9	0.2176
	HLA-B*35:01	9	0.0634
	HLA-B*57:01	9	0.0549
	HLA-A*02:01	9	0.0005
	HLA-B*07:02	9	0.0003
STQDLFLPF	HLA-B*44:03	9	0.8754
	HLA-B*53:01	9	0.2737
	HLA-B*57:01	9	0.0423
	HLA-B*35:01	9	0.0395
	HLA-B*07:02	9	0.0122
	HLA-A*02:01	9	0.0019
WTAGAAAYY	HLA-B*44:03	9	0.8185
	HLA-B*53:01	9	0.5287
	HLA-B*57:01	9	0.0527
	HLA-B*35:01	9	0.0374
	HLA-B*07:02	9	0.0001
	HLA-A*02:01	9	0

Multiple Sequence Analysis

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350 360 370 380 390 400
410 420 430 440 450 460
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sp|P59594|SPIKE_CVHSA
tr|D2E1E7|D2E1E7_CVHSA
tr|D2E1D2|D2E1D2_CVHSA
tr|A0A166ZL64|A0A166ZL64_9NIDO
tr|A0A0U1UYX4|A0A0U1UYX4_CVHSA
tr|R9QTA0|R9QTA0_CVHSA
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sp|Q3I5J5|SPIKE_BCRP3
sp|Q0Q475|SPIKE_BC279
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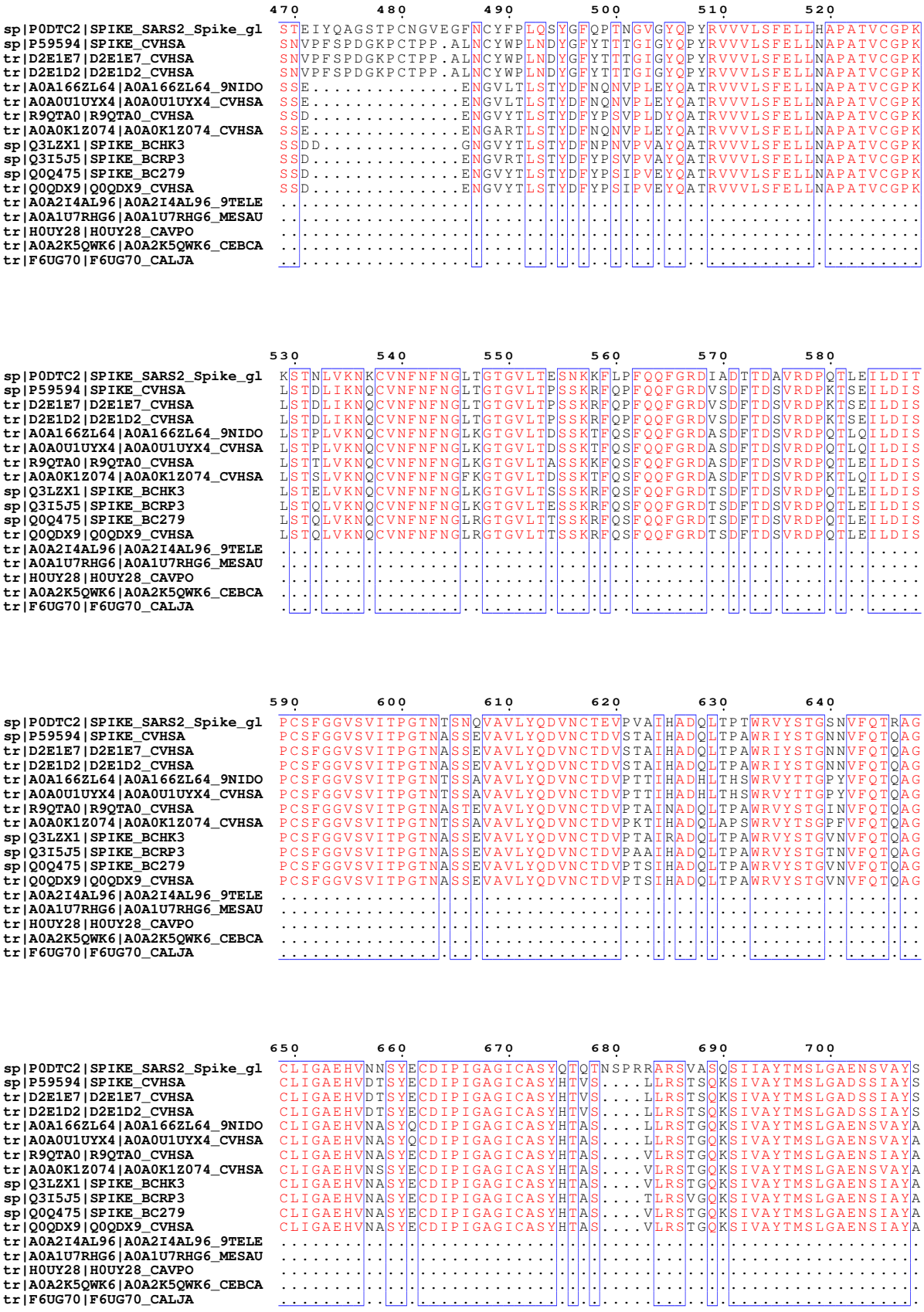
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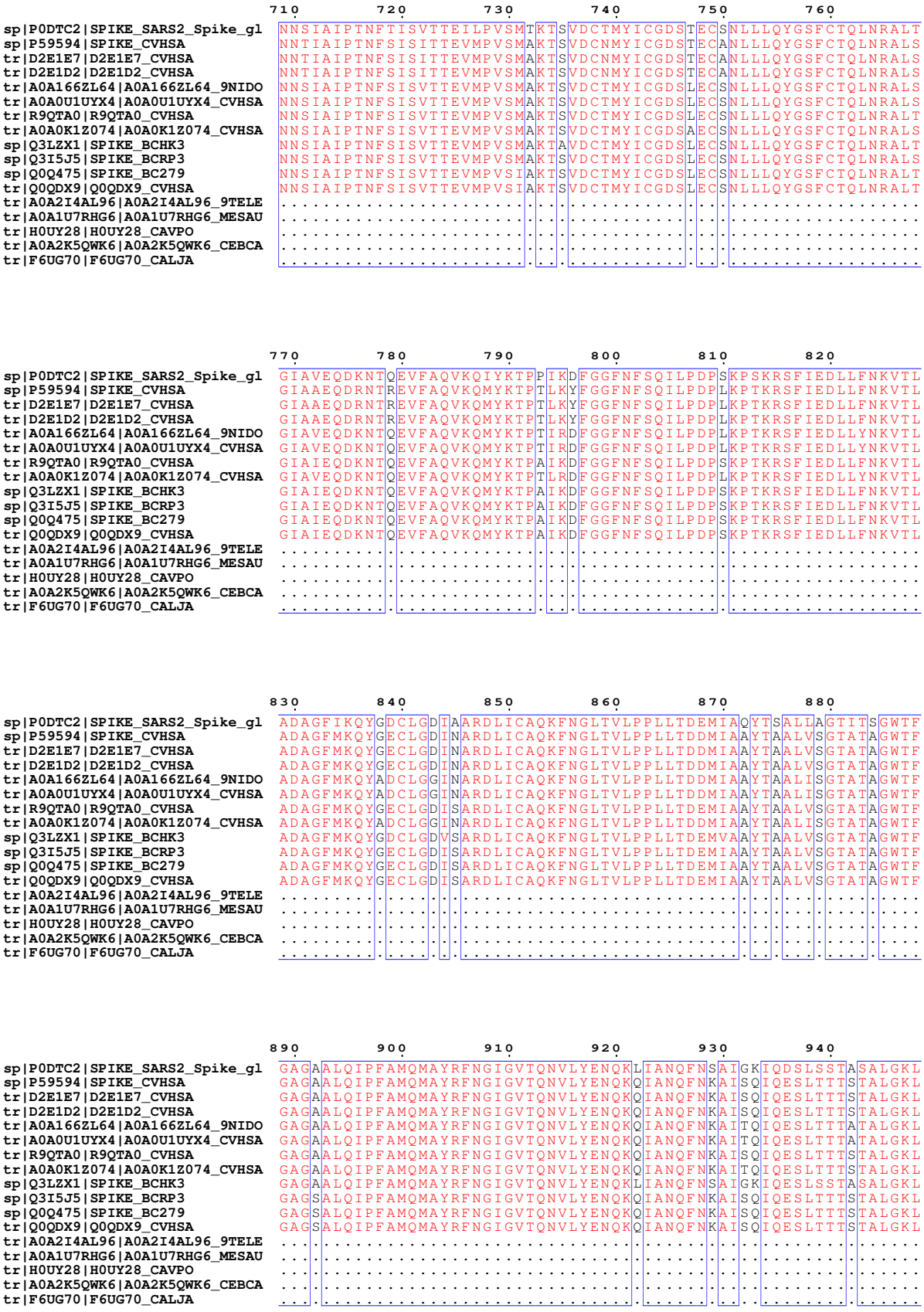
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sp|Q0Q475|SPIKE_BC279 NNSIAIPTNFSISVTTEVMPVSIAKTSVDCTMYICGDSLECSNLLLQYGSFCTQLNRALT
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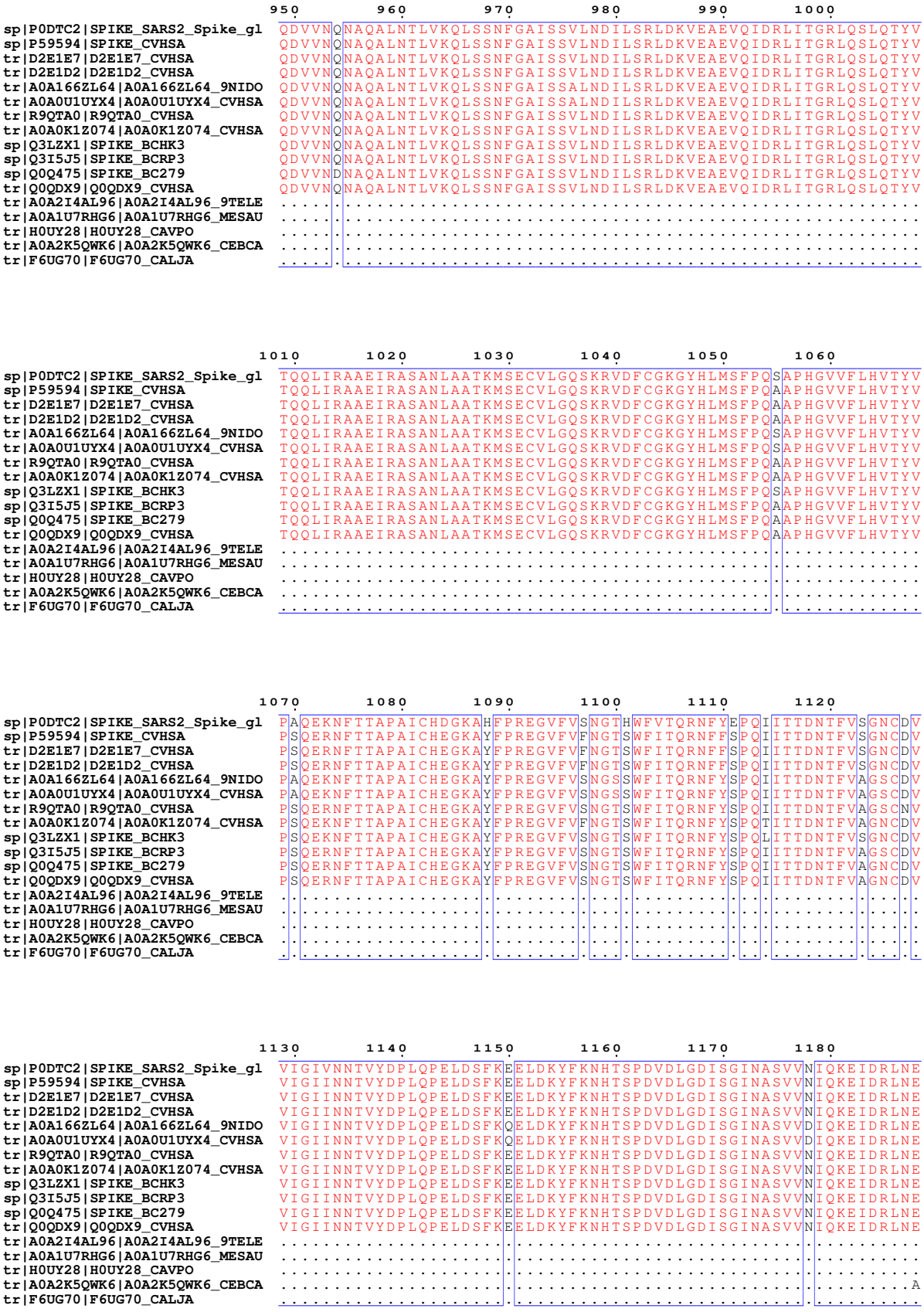
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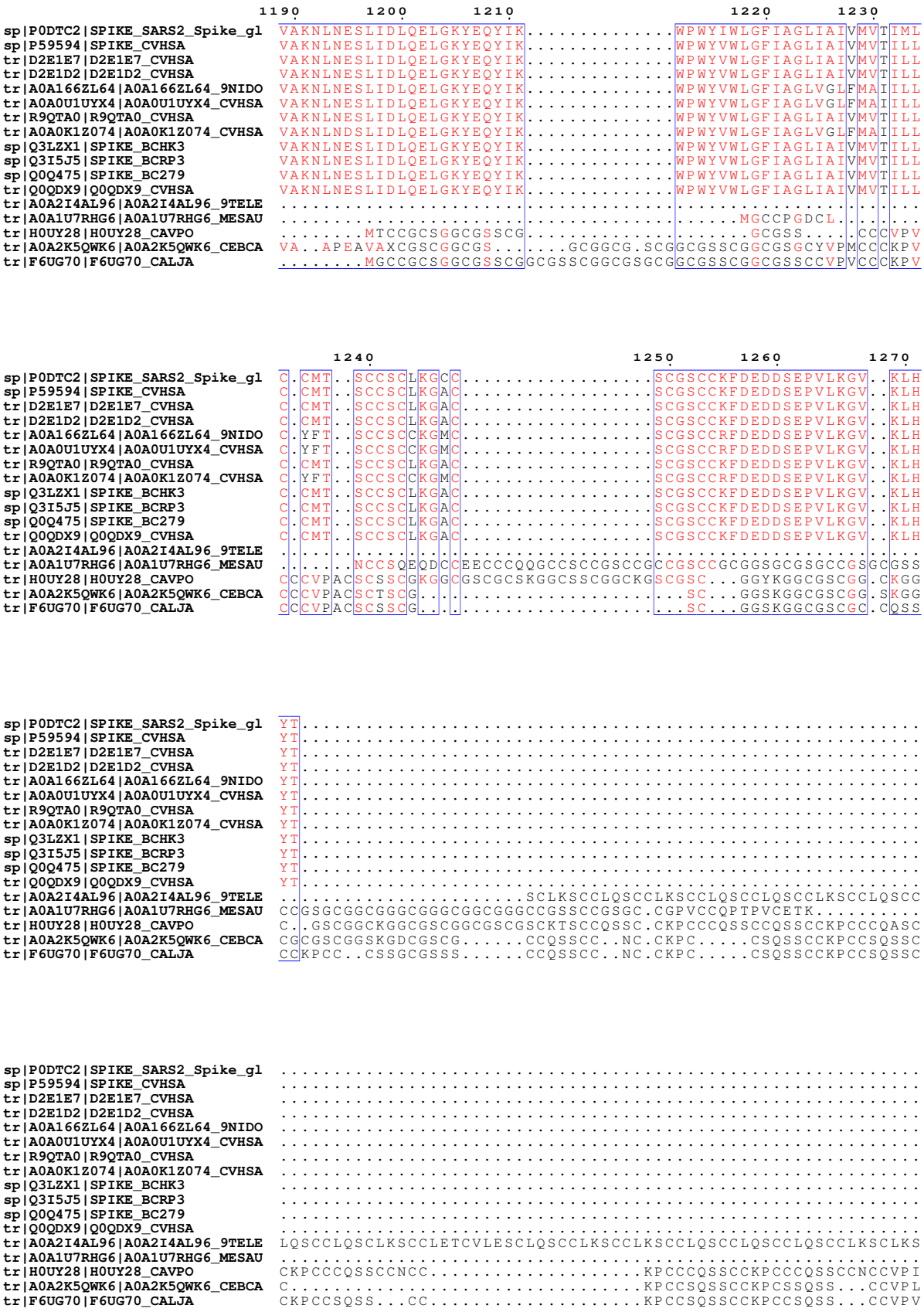
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