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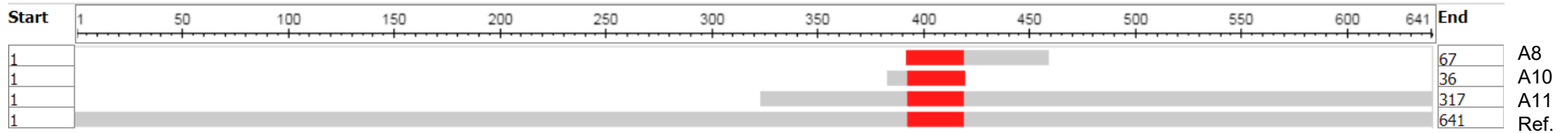
1 -----ASAGTGALASSAPSTAVAQSATPSVSSISSLRAATSGAT-----AAAAVDTGSGG 51

81 SVAGAGAHAHLGGSSATPVQQAQAAASAGTGALASSAPSTAVAQSATPSVSSISSLRAATSGATAAASAAAAVDTGSGG 160

52 GGQPHDTAPRGARKKQ 67

161 GGQPQDTAPRGARKKQ 176

Supplementary Figure 1. Amino acid sequence alignment of the VCA-p18 (for assays A1 and A4, GenBank accession number: NC_007605.1). The sequence alignment was done using Protein BLAST (blast.ncbi.nlm.nih.gov). Red depicts the identical amino acid residues in all the sequences. Targeted antigen in assay A4 is the full length VCA-p18.



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1      -----PPRRPP 6
1      -----SSQSSSSGSPPRRPP 15
1      GGGGRGRGGSGGRGRGGSGGRGRGGSGRRRGRGRERARGGSRERARGRGRGRGEKRPRSPSSQSSSSGSPPRRPP 75
1      [ 324 ]GGGGRGRGGSGGRGRGGSGGRGRGGSGRRRGRGRERARGGSRERARGRGRGRGEKRPRSPSSQSSSSGSPPRRPP 399

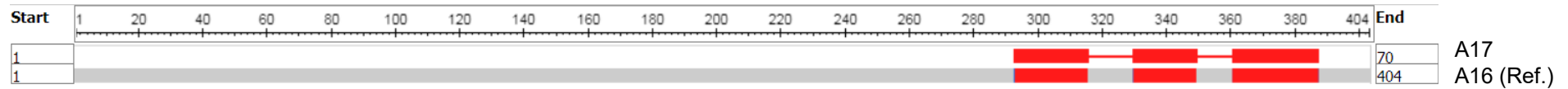
7      PGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGPRGQGDGGRRK----- 67
16     PGRRPF FHPVGEADYFEYHQE----- 36
76     PGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKGGWFGKHRGQGGSNPKFE 155
400    PGRRPF FHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKGGWFGKHRGQGGSNPKFE 479

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156    NIAEGLRALLARSHVERTTDEGTWAGVFVYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQGPLRESIV 235
480    NIAEGLRALLARSHVERTTDEGTWAGVFVYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQGPLRESIV 559

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Supplementary Figure 2. Amino acid sequence alignment of the EBNA1 (for assays A8, A10, and A11, GenBank accession number: NC_007605.1). The sequence alignment was done using Protein BLAST (blast.ncbi.nlm.nih.gov). Red depicts the identical amino acid residues in all the sequences.



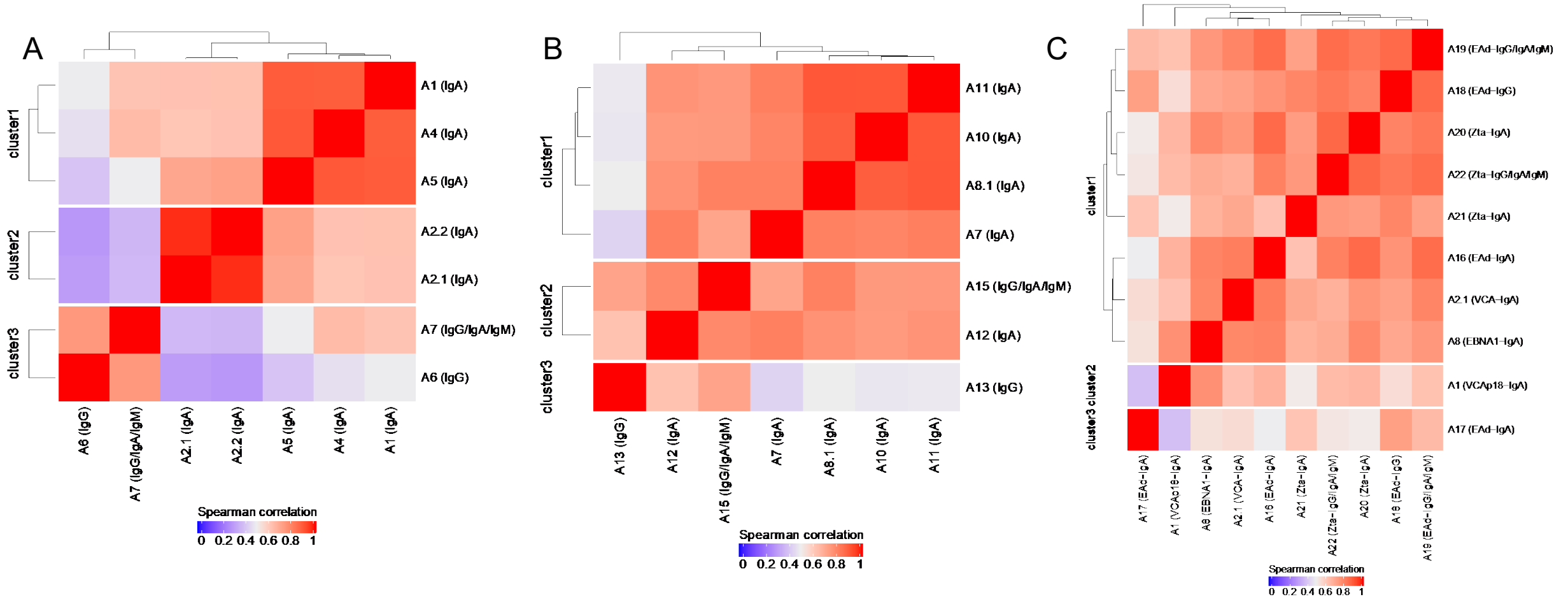
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1  -----LFNHASEEAAASTASEPEDKSPR----- 23
241 CSVAADSLAAALSLCRIPAVSVPILRFYRSGIIAVVAGLLTSAGDLPLDLSVILFNHASEEAAASTASEPEDKSPRVQPL 320

24  -----TVSPSPSPPPPRTPTWESP-----SHSSNTALERPLAVQLARKRTSSEARQ----- 70
321 GTGLQQRPRHTVSPSPSPPPPRTPTWESPARPETPSPAIPSHSSNTALERPLAVQLARKRTSSEARQKQKHPKKVKQAF 400

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Supplementary Figure 3. Amino acid sequence alignment of the EAd (for assays A16 and A17, GenBank accession number: NC_007605.1). The sequence alignment was done using Protein BLAST (blast.ncbi.nlm.nih.gov). Red depicts the identical amino acid residues in all the sequences.



Supplementary Figure 4. Unsupervised hierarchical clustering based on Spearman correlation coefficient between assays measuring anti-EBV antibodies in plasma. **A) Antibodies against VCA; B) Antibodies against EBNA1; C) Antibodies against Zta (ZEBRA), EAd, VCA, and EBNA1.** Red depicts a strong positive correlation, and blue indicates a weak correlation.