Figure S1:

A)

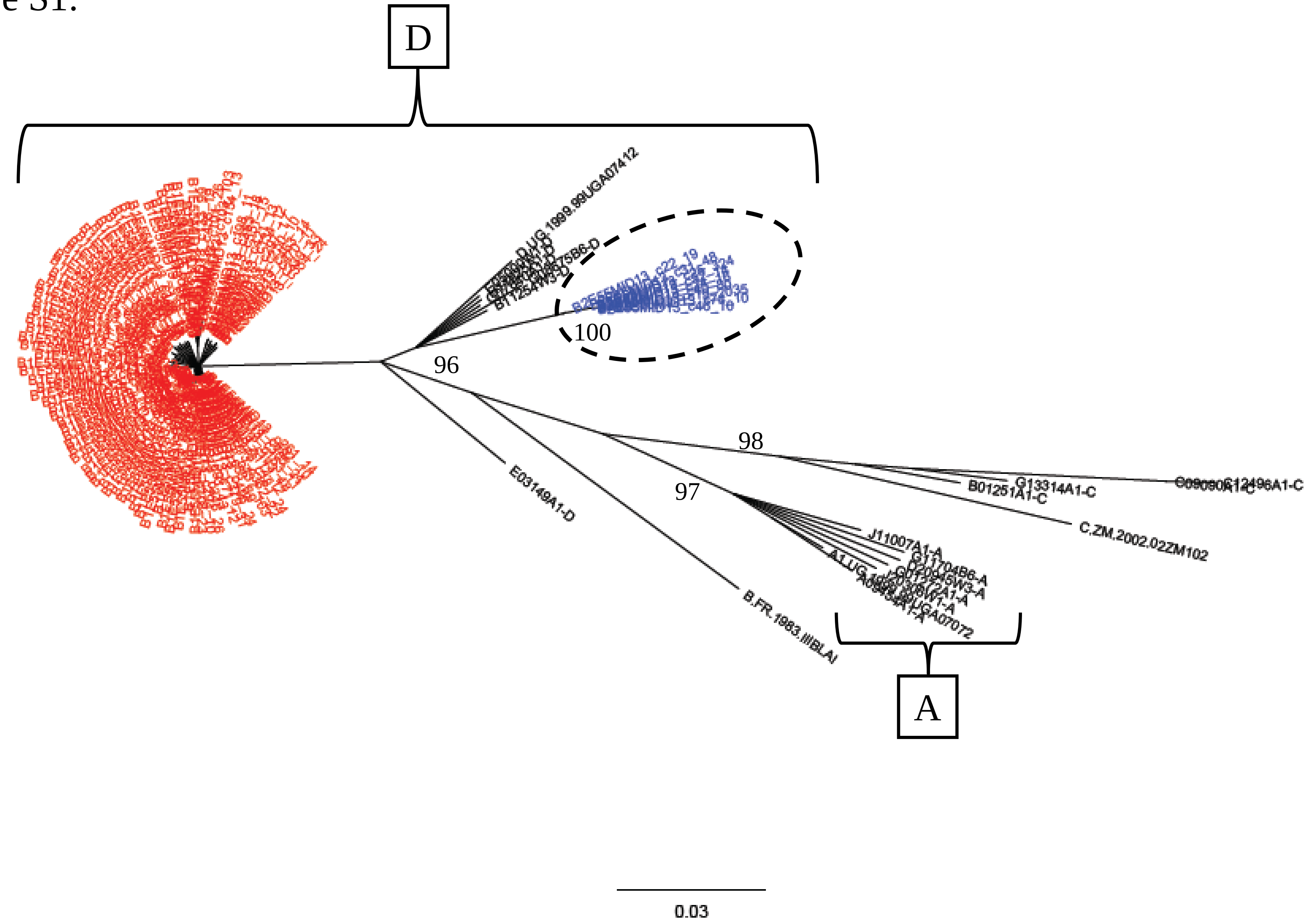
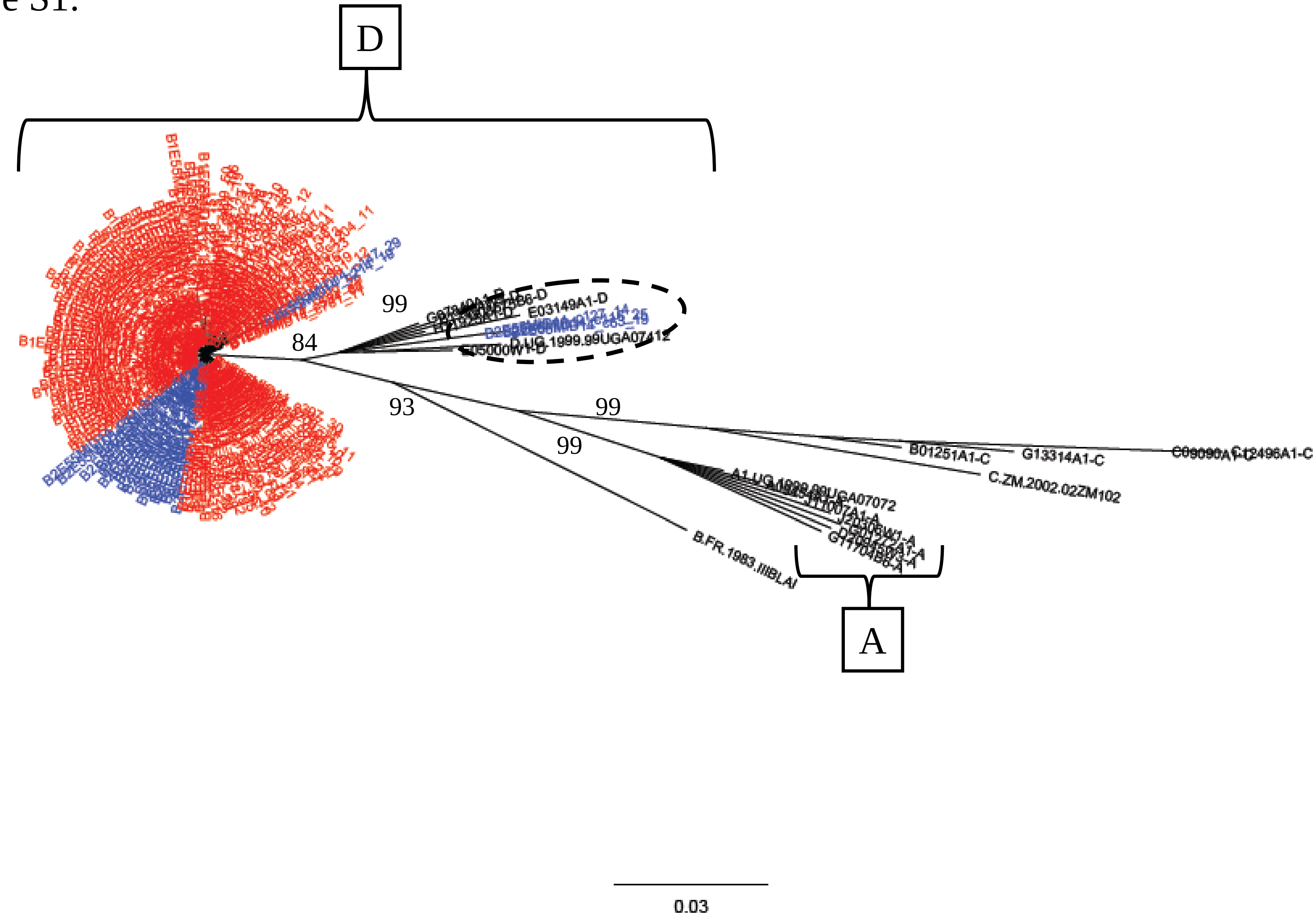

D
D.UG.1999.99UGA07412
B11254W3-D
100
96
98
97
E03149A1-D
B.FR.1983.IIIBLAI
G13314A1-C
B01251A1-C
C12496A1-C
C.ZM.2002.02ZM102
J11007A1-A
A
0.03

Figure S1:
B)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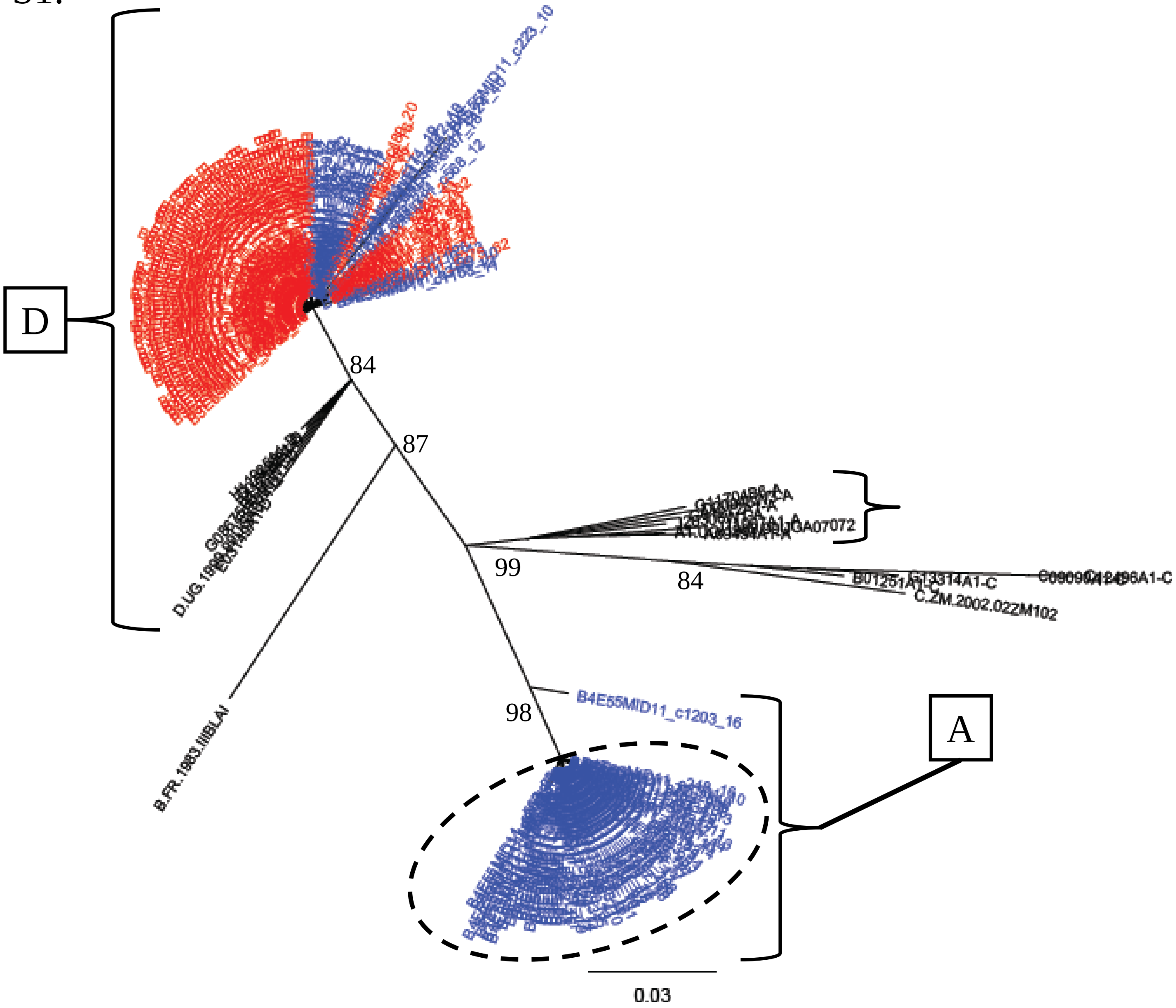
99
84
E03149A1-D
D.UG.1999.99UGA07412
E05000W1-D
93
99
99
B01251A1-C
G13314A1-C
C12496A1-C
C.ZM.2002.02ZM102
A1.UG.1999.99UGA07072
B.FR.1983.IIIBLAI
A
0.03

Figure S1:

C)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84
98
A
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B.FR.1983.IIIBLAI
C.ZM.2002.02ZM102
B01251A1-C
C13314A1-C
0.03

Supplemental Figure Legends

Figure S1: Phylogenetic trees of consensus gp41 viral sequences (≥10 reads) derived from 454 pyrosequenced serum baseline (red) and follow-up (blue) samples are shown for intra- (A & B) and inter-subtype (C) superinfection events. All consensus sequences were combined in a joint tree for identification of superinfecting strains as indicated (dashed circle). HIV subtypes A and D are indicated by brackets. Number of repeated sequences represented by each consensus sequence is shown at the end of the consensus identifier. Distance is indicated for each individual tree and samples are grouped with a selection of subtype reference sequences and random sequences from individuals in Rakai (black)(*1*).