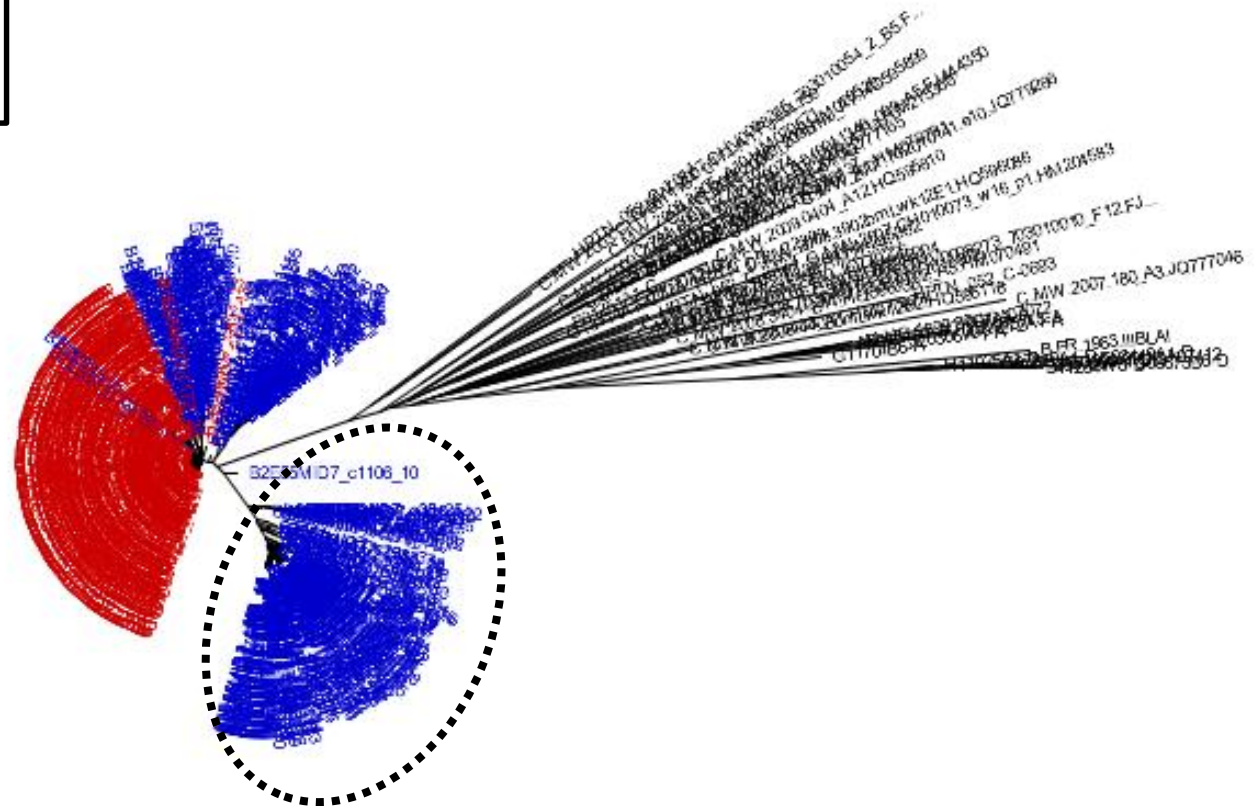


- **Supplemental Figure 1:** Phylogenetic trees of consensus *p24* and/or *gp41* viral sequences (≥ 10 reads) derived from 454 pyrosequencing of a subject's baseline (red) and follow-up sample (blue) with the superinfecting strain indicated (dashed circle) are shown for the 10 cases identified. Number of repeated sequences represented by each consensus sequence is shown at the end of the consensus identifier. Distance is indicated for the tree by the scale at bottom, and samples are grouped with a selection of subtype reference sequences and a collection of sequences from Malawi (black). Total genetic distance and a rate of genetic distance by year between the original and superinfecting strain are indicated. Full 454 sequence reads and consensus sequences are shown in a text box for each tree.

Transmitter Case #1-gp41

Genetic distance 2.4%; PY=2.0 (Rate=1.2 per year)

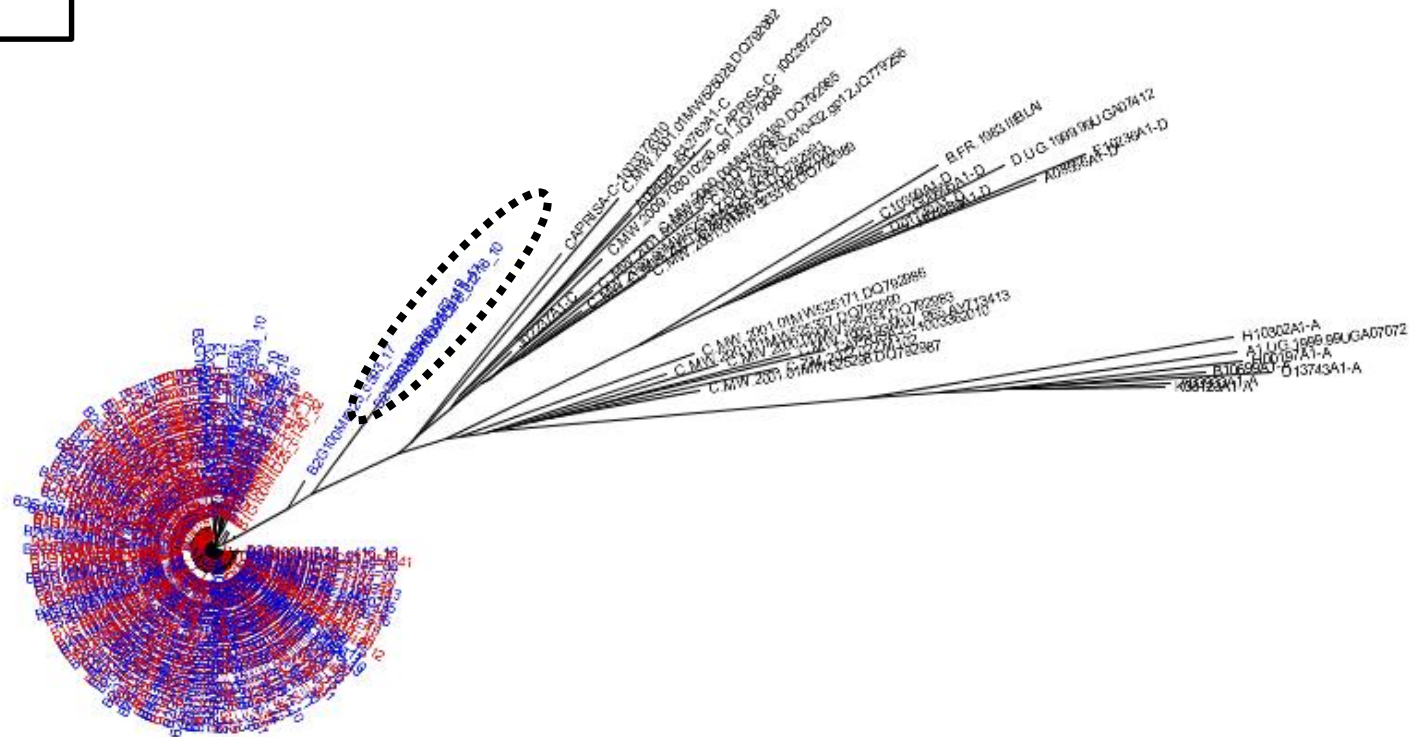
Reads/Consensus sequences
Baseline=15050/216
Follow-up=13961/277



Transmitter Case #2-p24

Genetic distance 1.3%; PY=0.75 (Rate=1.7 per year)

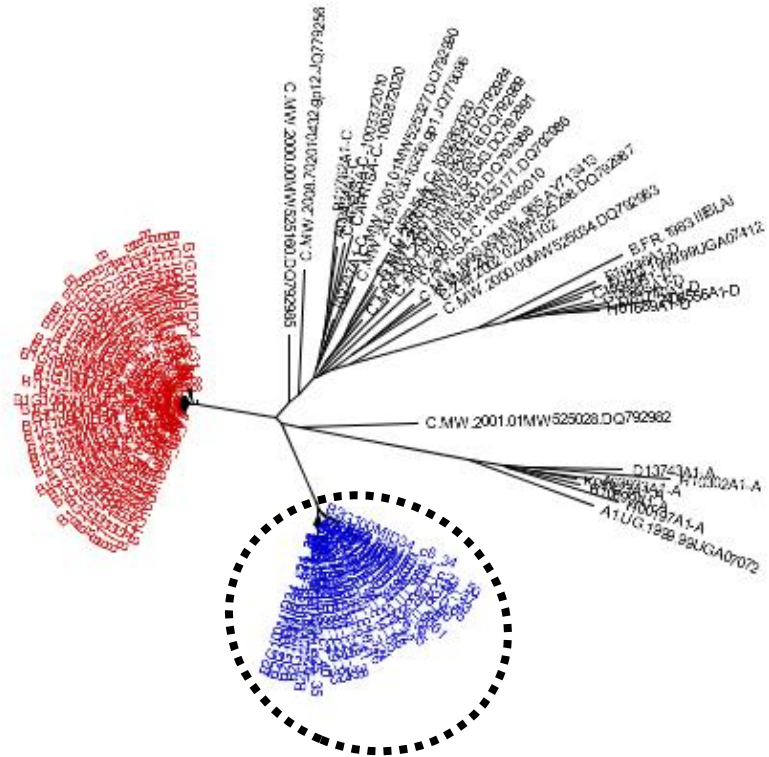
Reads/Consensus sequences
Baseline=16015/111
Follow-up=11364/102



Transmitter Case #4-p24

Genetic distance 2.6%; PY=2.0 (Rate=1.3 per year)

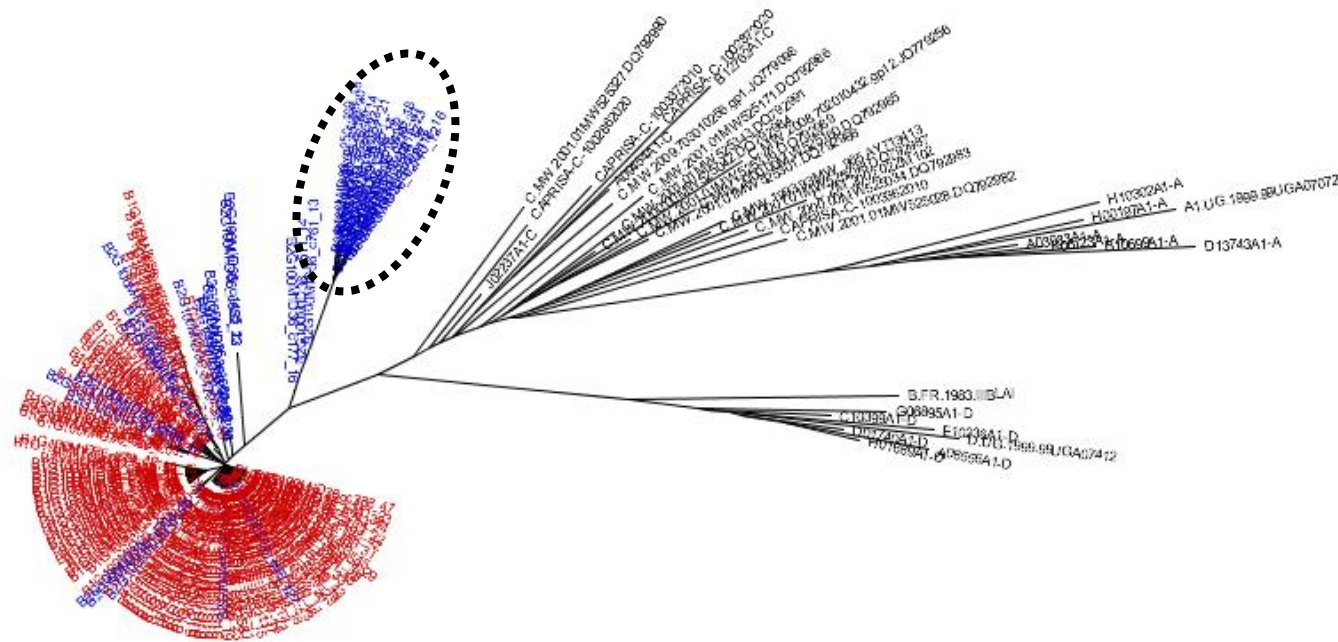
Reads/Consensus sequences
Baseline=17901/51
Follow-up=12873/29



Transmitter Case #5-p24

Genetic distance 3.2%; PY=2.0 (Rate=1.6 per year)

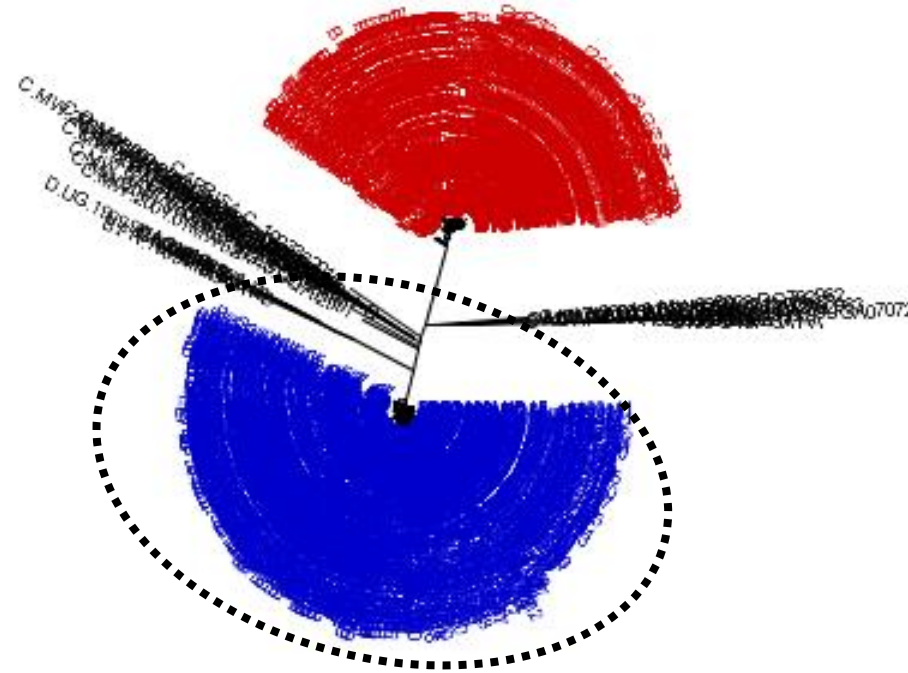
Reads/Consensus sequences
Baseline=11821/118
Follow-up=9616/38



Non-transmitter Case #6-p24

Genetic distance 3.8%; PY=0.6 (Rate=6.3 per year)

Reads/Consensus sequences
Baseline=17479/368
Follow-up=26190/533

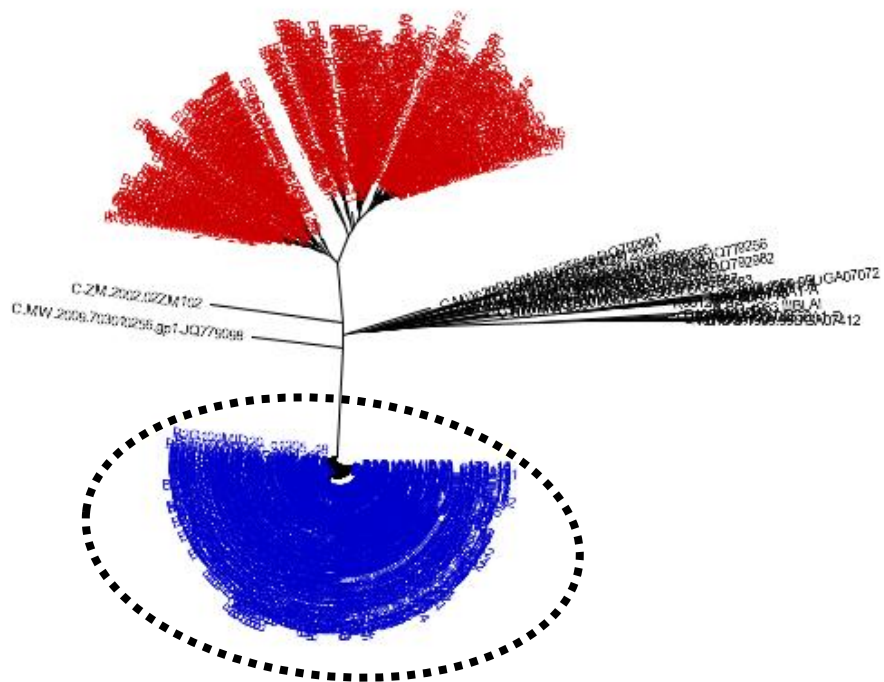


0.0070

Non-transmitter Case #7-p24 & gp41

Gag genetic distance 6.5%; PY= \sim 1.5 (Rate=4.3 per year)

gp41 genetic distance 8.0%; PY= \sim 1.5 (Rate=5.3 per year)

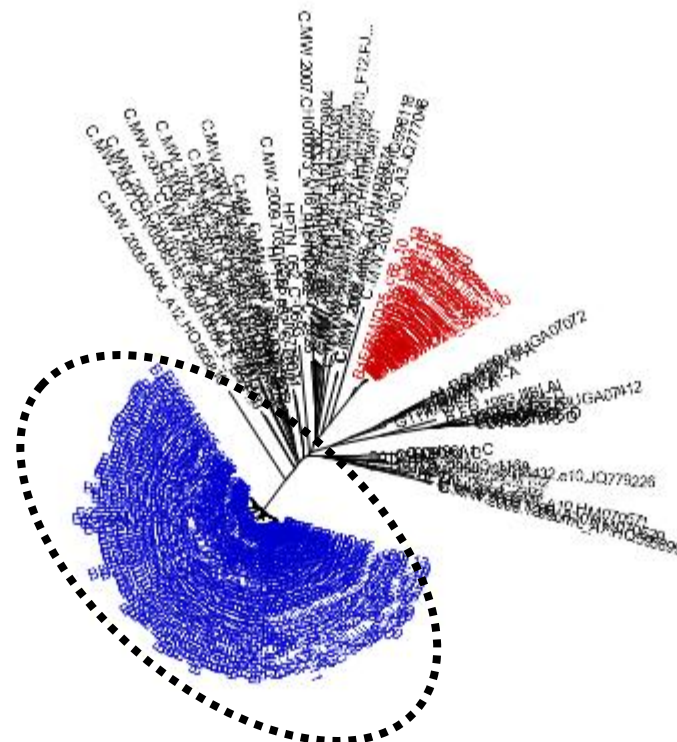


p24 Reads/Consensus sequences

Baseline=13954/302

Follow-up=16944/363

0.0090



gp41 Reads/Consensus sequences

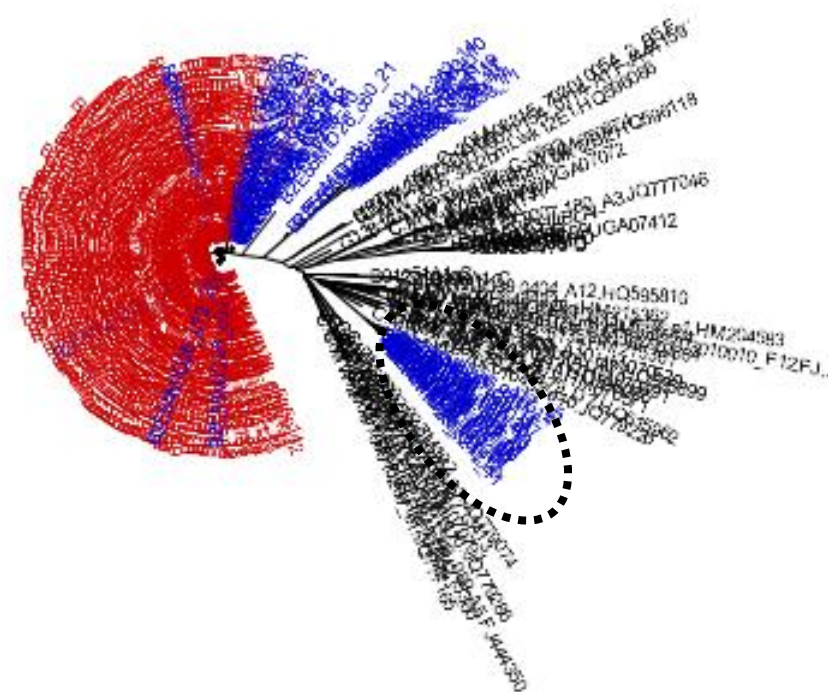
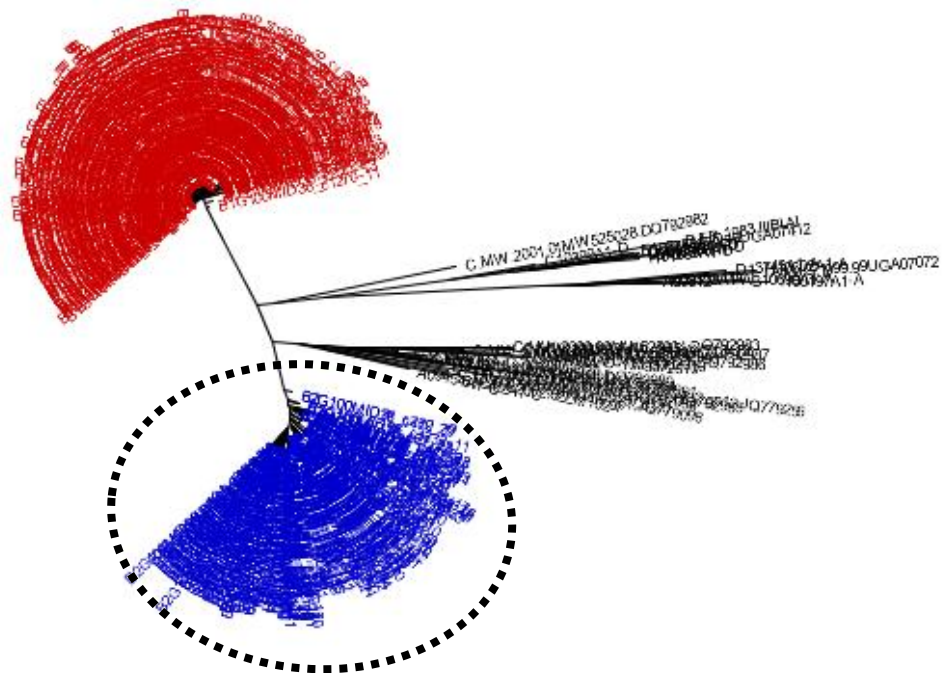
Baseline=1561/33

Follow-up=11466/132

0.0090

Non-transmitter Case #8-p24 & gp41

Gag genetic distance 2.3%; PY=2.0 (Rate=1.2 per year)
gp41 genetic distance 6.6%; PY=2.0 (Rate=3.3 per year)



p24 Reads/Consensus sequences
Baseline=16695/311
Follow-up=12989/184

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0.0050

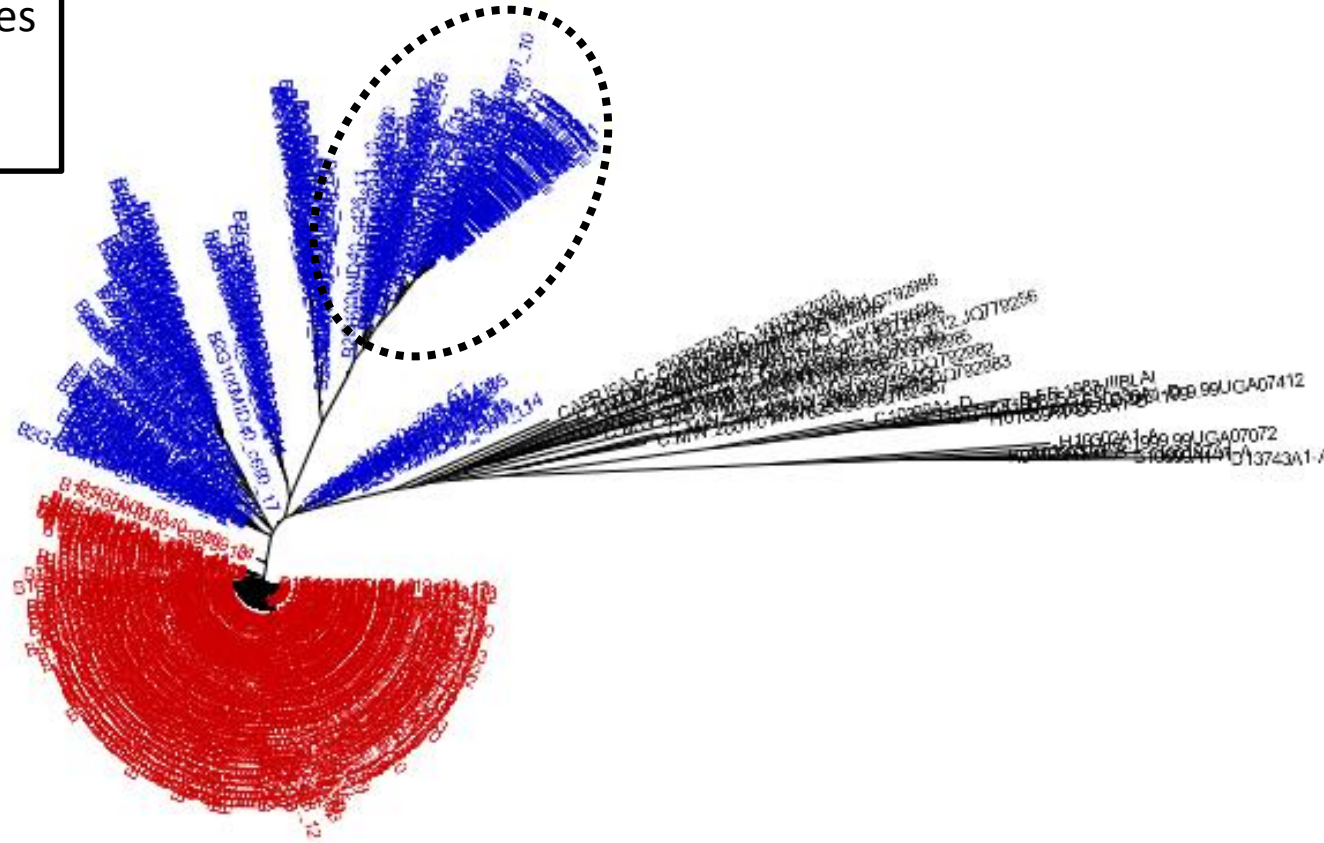
gp41 Reads/Consensus sequences
Baseline=11533/156
Follow-up=3347/60

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0.0070

Non-transmitter Case #10-p24

Genetic distance 3.6%; PY=2.0 (Rate=1.8 per year)

Reads/Consensus sequences
Baseline=16638/290
Follow-up=14661/189



0.0090