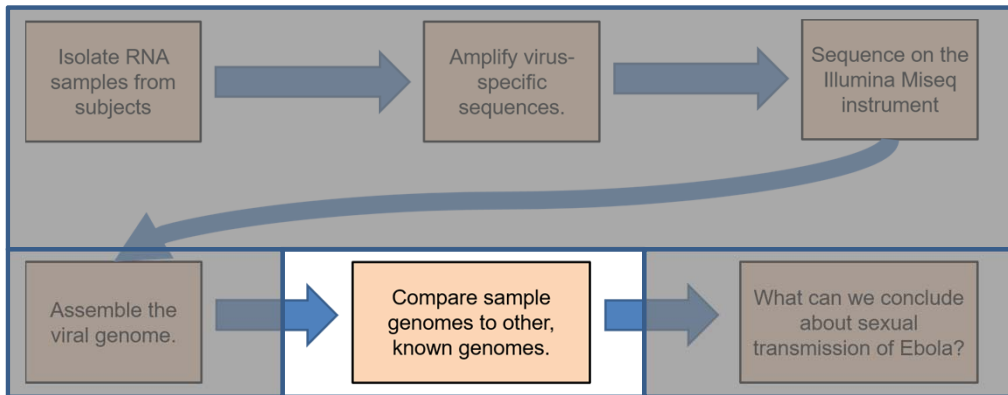
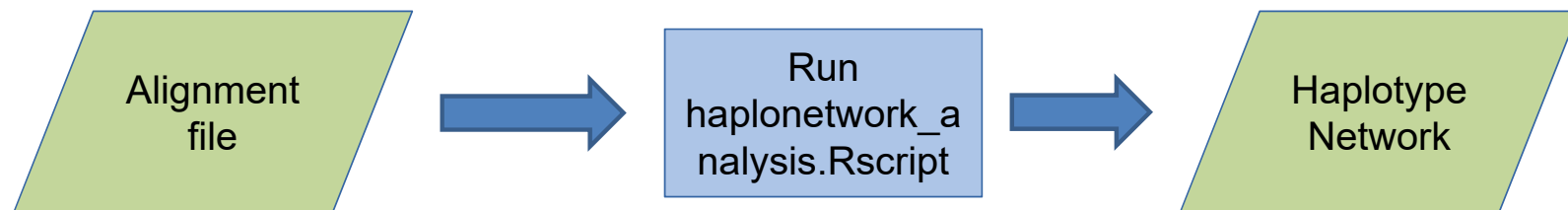


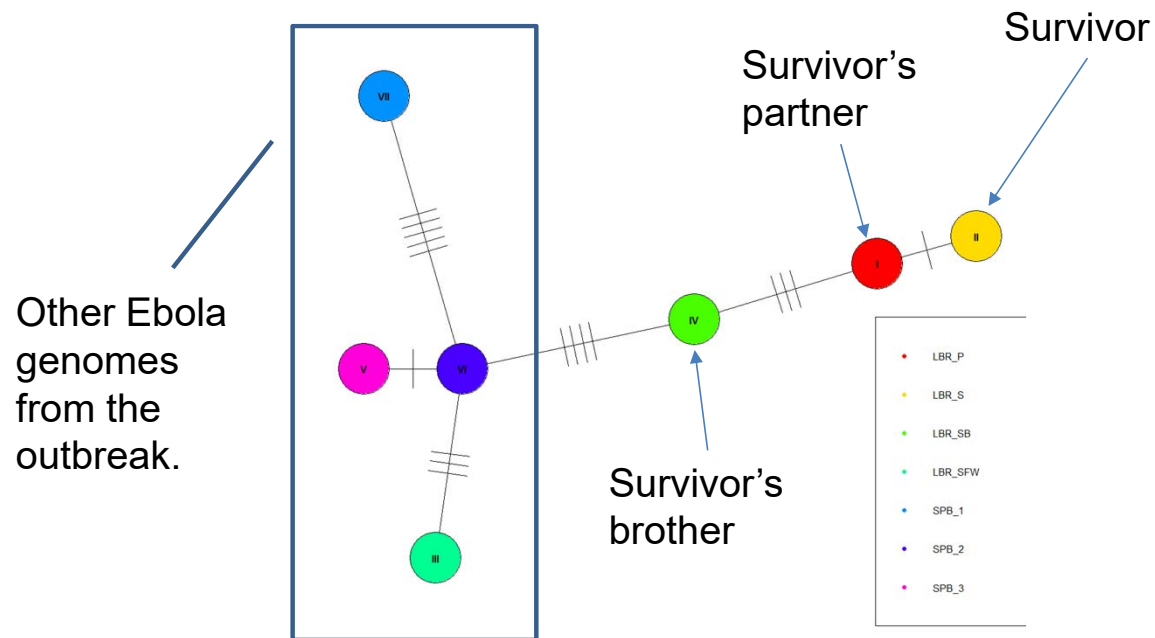
Haplotype Network Analysis



- **Start with the alignment file made in the previous step.**
- **Arrange the genomes in a haplotype network: where each genome is connected by a line to the genomes it is most similar to.**
- **This allows us to visually depict the differences between several genomes.**

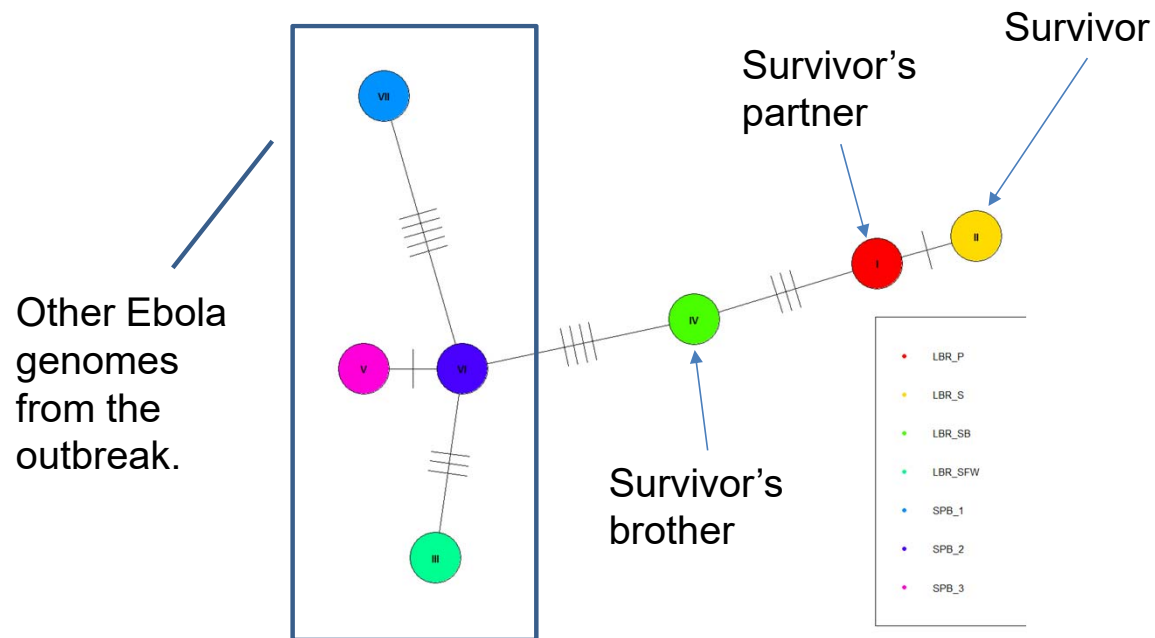


Compare the genomes in the study and other Ebola genomes using a haplotype network



- A haplotype is a region of DNA inherited from the parent.
- NOTE: for viruses, the haplotype is the full genome.
- Each circle (node) represents a genome sequence.
- Hash marks on the lines show the number of differences between the genomes connected by the lines.
- Remember our original question: Is the partner sample more similar to the survivor sequence? Or to the other samples from this outbreak?

Compare the genomes in the study and other Ebola genomes using a haplotype network



- The Survivor and Survivor's Partner have one difference between them.
- There are at least three differences between the Survivor's Partner and the next most similar genome.

What can we conclude about sexual transmission of Ebola?

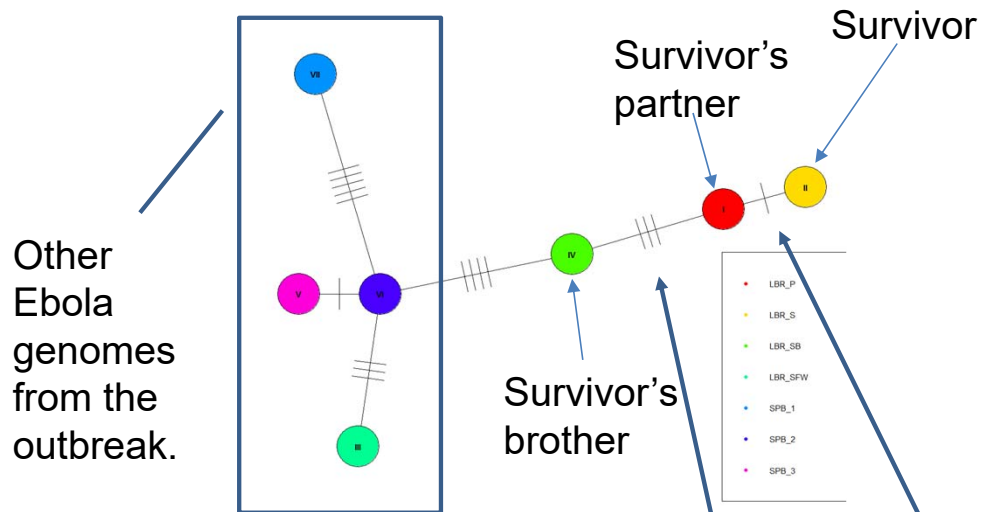


Table 1. Distinct Ebola Virus Genome Substitutions in the Patient, the Survivor, and the Survivor's Older Brother.^a

Position [†]	Reference	Alternative	Samples with Alternative	Survivor-Corrected Depth [‡]	Nature of Substitution [§]
4,107	G	A	P, S	1	VP35, V327I
8,592	A	T	P, S	1	VP30, synonymous
16,636	G	A	P, S	5	L, G1686S
4,384	A	C	P, S, SB	3	Noncoding
12,996	C	A	P, S, SB	1	L, synonymous
18,399	AAAAAA	AAAAAA	P, S, SB	2	Noncoding
11,263	C	T	S	1	Noncoding

- We see a similar pattern from the chart we previously produced.
- There is one position unique to the Survivor.
- There are three positions shared by the Survivor and Survivor's partner, but different in the Survivor's brother.
- **This data is consistent with sexual transmission from the Survivor to the Survivor's Partner.**