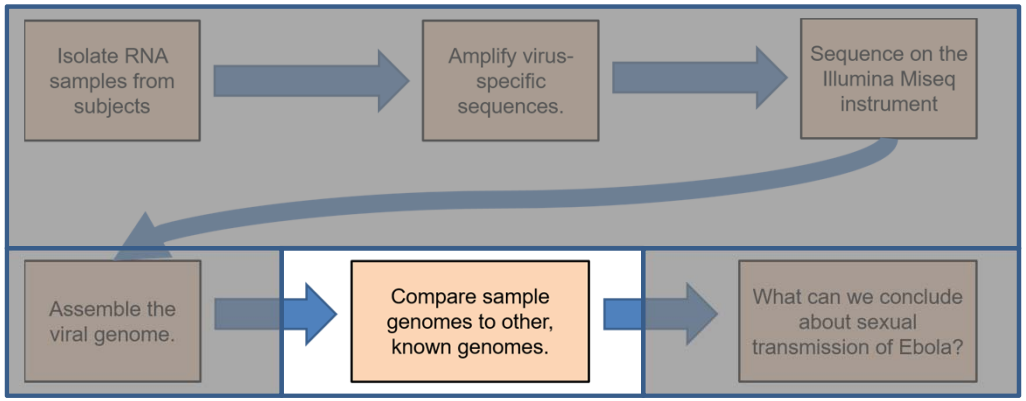
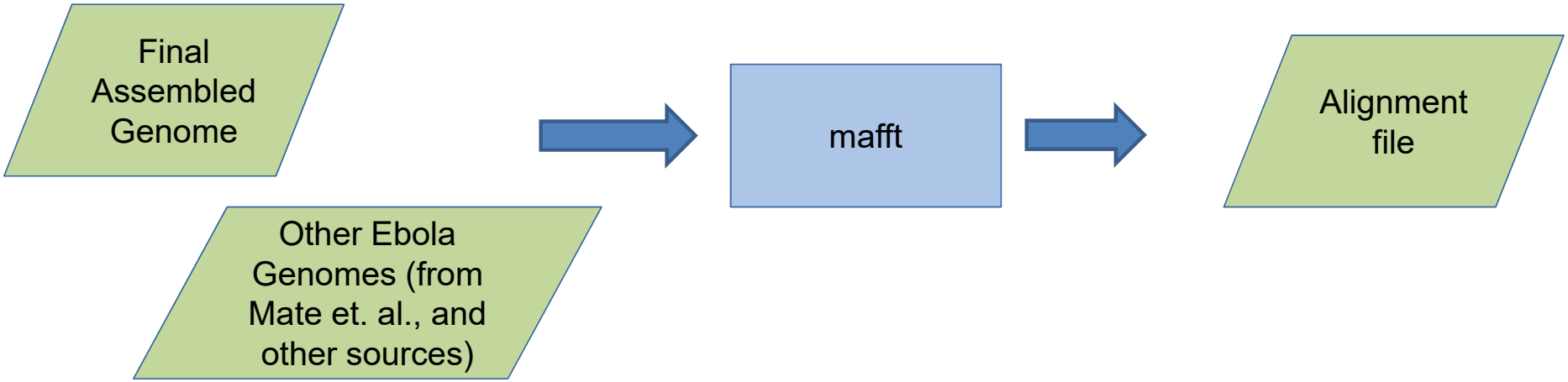
Multiple Genome Alignment



- **Take the final assembled genome, along with a diversity of other Ebola genomes.**
- **Align the genomes to each other, allowing us to quantify how different the genomes from each patient are from each other, and from other Ebola sequences.**



Summary of the alignment.

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

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	AAAAAAA	P, S, SB	2	Noncoding
11,263	C	T	S	1	Noncoding

* The GenBank accession numbers for the tested genomes are as follows: for the patient (P), the number is KT587343, for the survivor (S), the number is KT587344, and for the survivor's older brother (SB), the number is KT587346. L denotes RNA-dependent RNA polymerase, and VP viral protein.
† Positions were relative to the reference genome Ebola virus/H.sapiens-wt/GIN/2014/Makona-C15 (GenBank accession number, KJ660346.2).
‡ The number indicates the depth at each position from the survivor after correction for duplicates resulting from polymerase-chain-reaction amplification.
§ The gene abbreviation is provided for substitutions within coding regions, followed by a description of the amino acid change for substitutions that are nonsynonymous.

- **List the differences between the Mate et al. samples and a reference genome in a chart.**
- **There are three positions where the Survivor and Survivor's Partner differ from the reference, but not from each other (lines 1-3).**
- **There are three positions where the Survivor, Survivor's partner and Survivor's brother differ from the reference (lines 4-6).**
- **There is one position where only the Survivor differs from the reference (line 7).**