We aim to identify recombinants in multiple-source alignment, what we did is to employ the divison method in algorithm. The following plot is the example of three-source alignment, where two recombinants are involved in these four sequences. In fact, the identified recombinants from every two adjacent partitions are the same with true recombinants in each possible phylogenetic network.
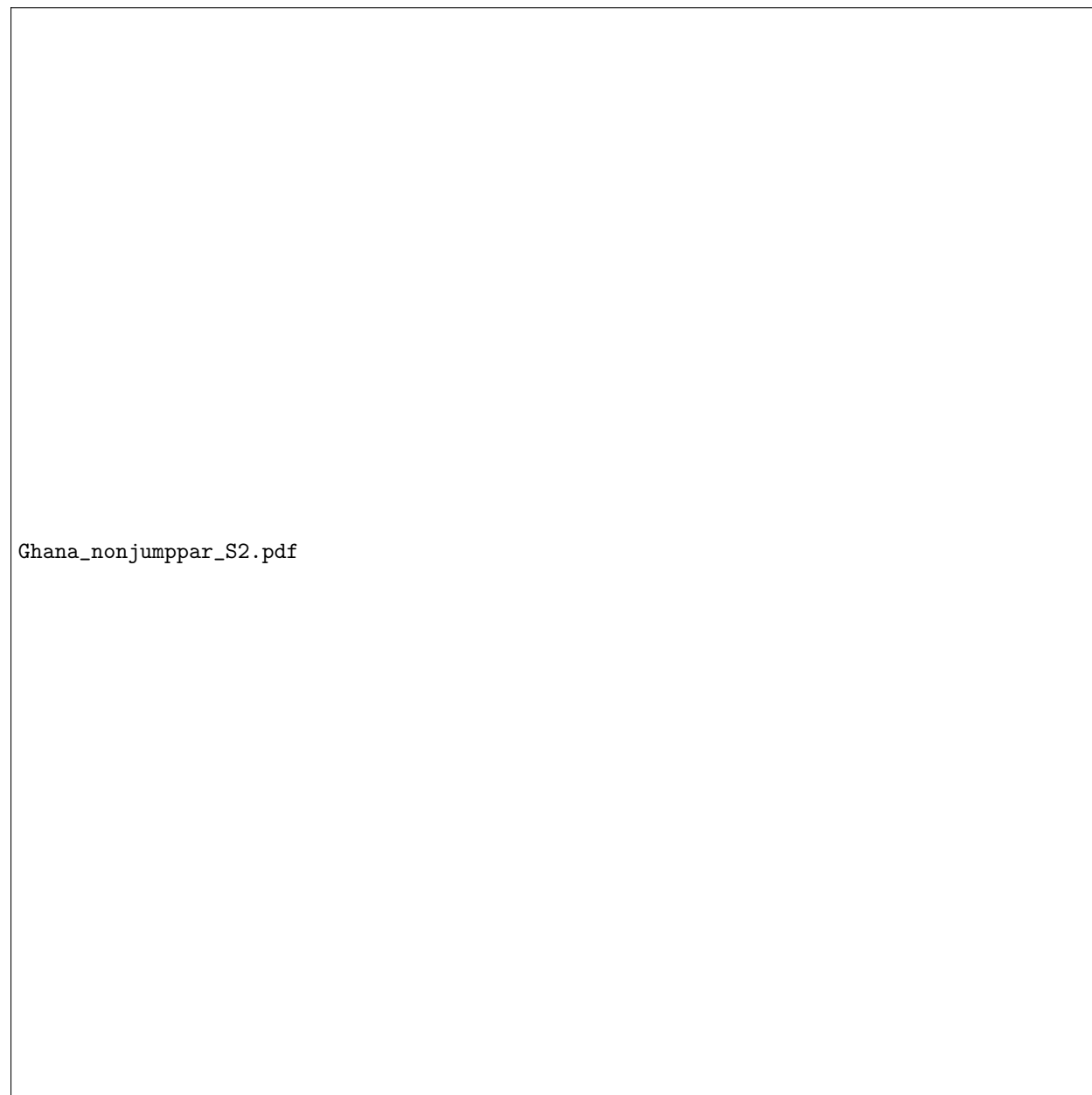
Ghana_nonjumppar_S2.pdf

Figure 1: Survey 2

partition 1 and partition 2	
triple	identified recombinant
ABC	A
ACD	A
ABD	A
BCD	B, C or D

partition 2 and partition 3	
triple	identified recombinant
ABC	B
BCD	B
ABD	B
ACD	A, C or D