

Figure 1: Edges with IBD between 0 and 100% (non inclusive) are white, while those with 100% IBD are coloured by haplotype labels. Edges with IBD < 50% are dashed, while those with IBD > 50% are solid.

Deep-dive into Buenaventura and Tumaco

Assuming travel between cities Tumaco and Buenaventura is symmetrical (try to confirm with expert knowledge / maritime traffic data), the site with higher incidence (Tumaco) is the most likely source.

Vertical lines are compatible with a transmission event (but could also arise due to similar haplotypes being detected at the same time across sites). Diagonal lines are not representative of direct travel.

Assuming Tumaco to be the source, Figure 1 suggests haplotypes 5 and 7 were transmitted from Tumaco to Buenaventura sometime after haplotypes 1 and 12 (circa years 2005 and 2003, respectively). Haplotype 2 was not detected in either site before 2005, we thus speculate that it was transmitted across sites sometime around 2005. Upon inspection of Figure 1 it is important to note however that absence of evidence is not evidence of absence due to non-exhaustive sampling of infections (e.g. all haplotypes could have been present in either site prior to their detection due to unsampled infections) and therefore insight is mostly speculative.

Of the haplotypes shared across Buenaventura and Tumaco, haplotypes 5, 7 and 12 are all highly related to one another, while haplotypes 1 and 2 are not highly related to any of the other repeat haplotypes (Figure 2).

- hap1
- hap2
- hap3
- hap4
- hap5
- hap6
- hap7
- hap8
- hap9
- hap10
- hap11
- hap12
- hap13
- hap14
- hap15
- hap16
- hap17
- hap18
- hap19
- hap20

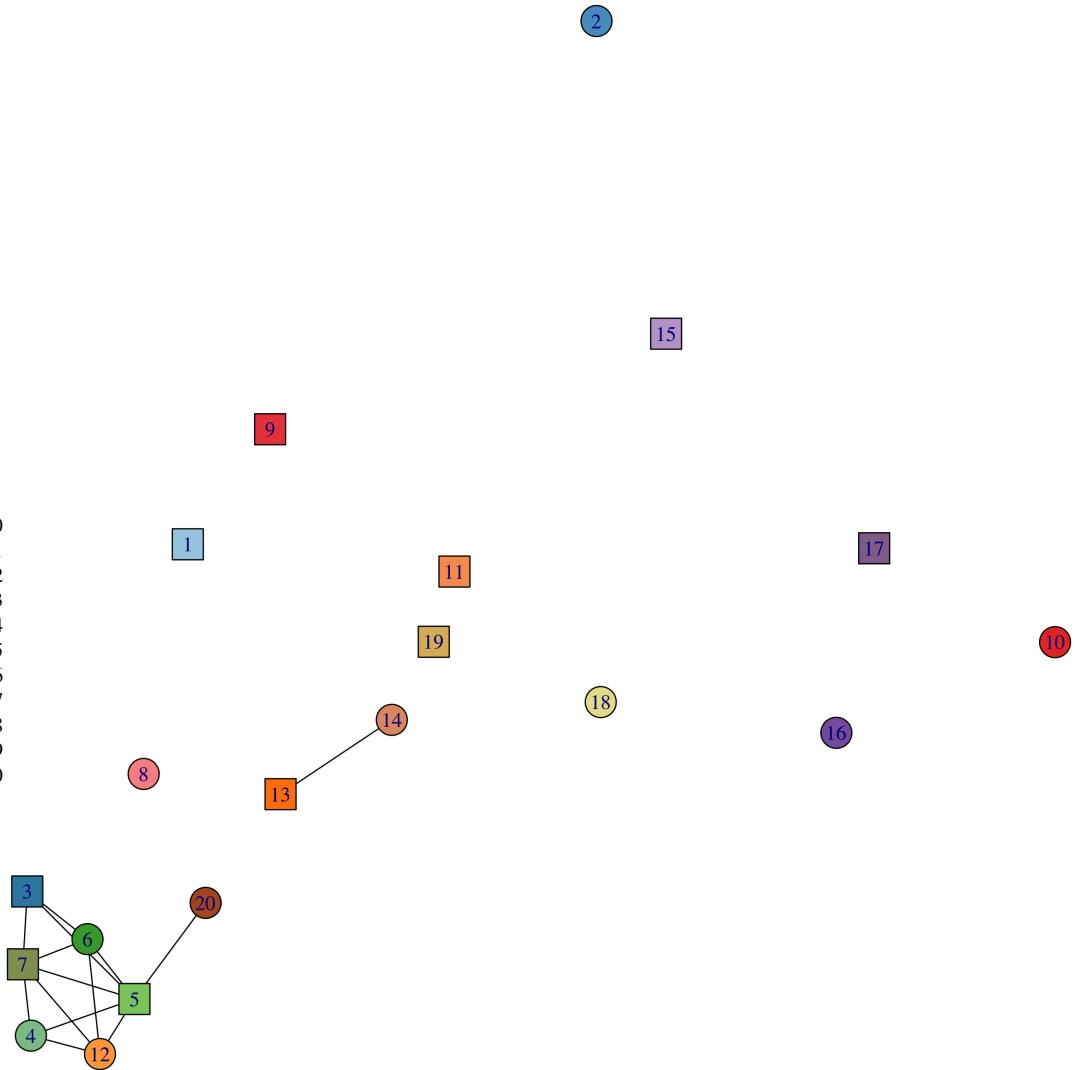


Figure 2: Relatedness across repeat haplotypes.