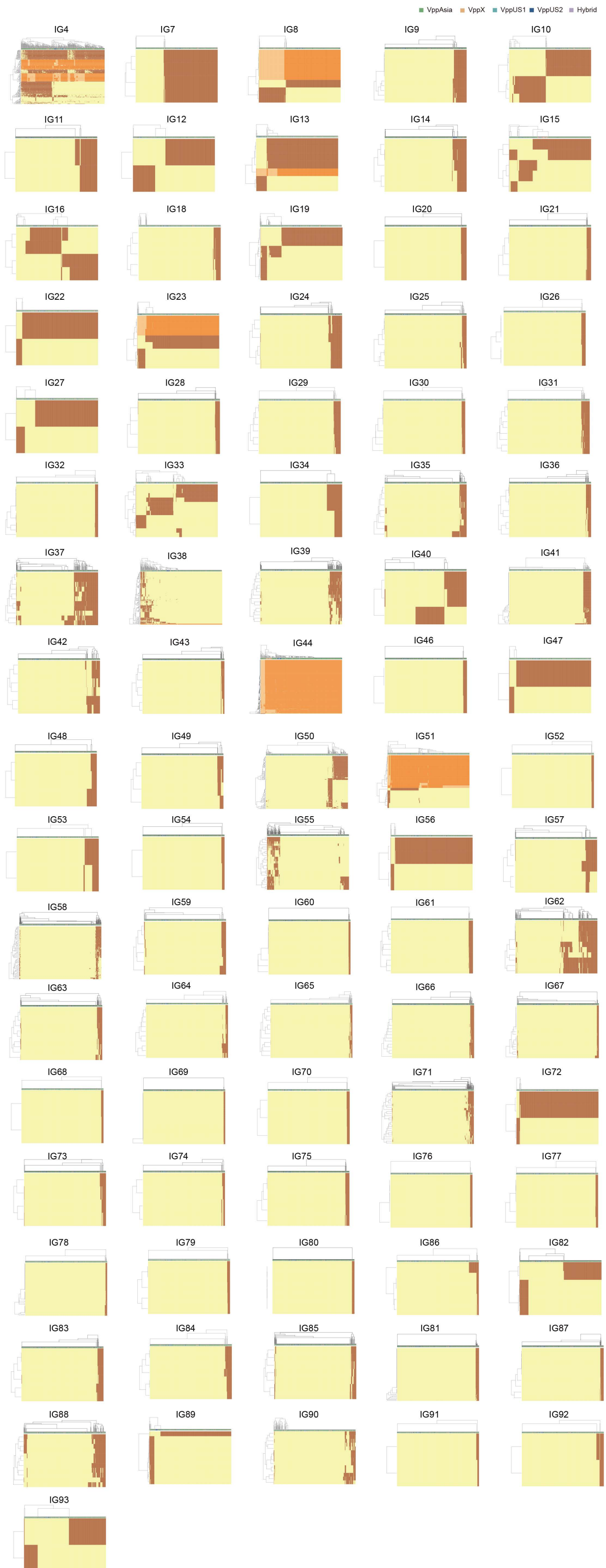
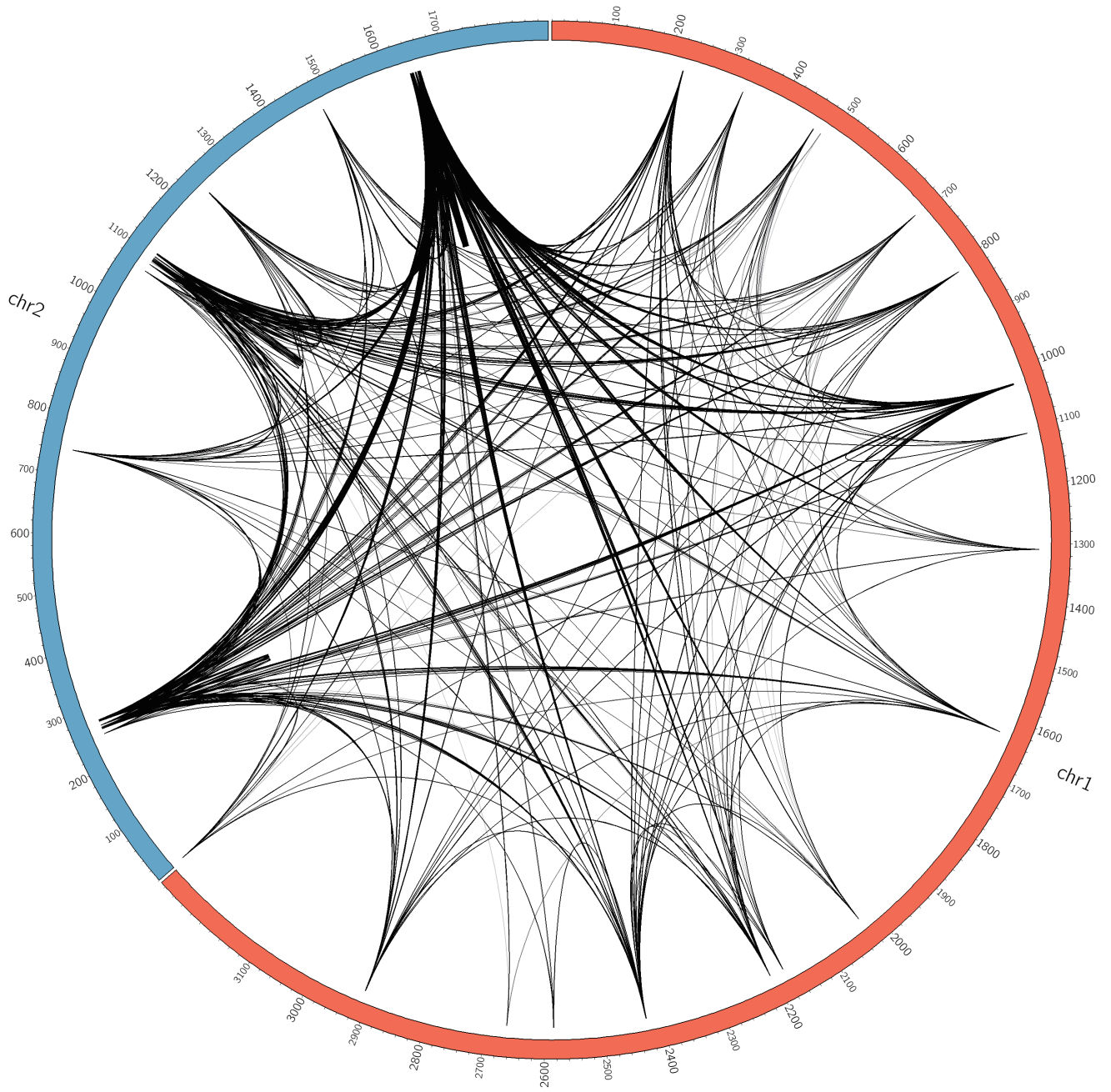




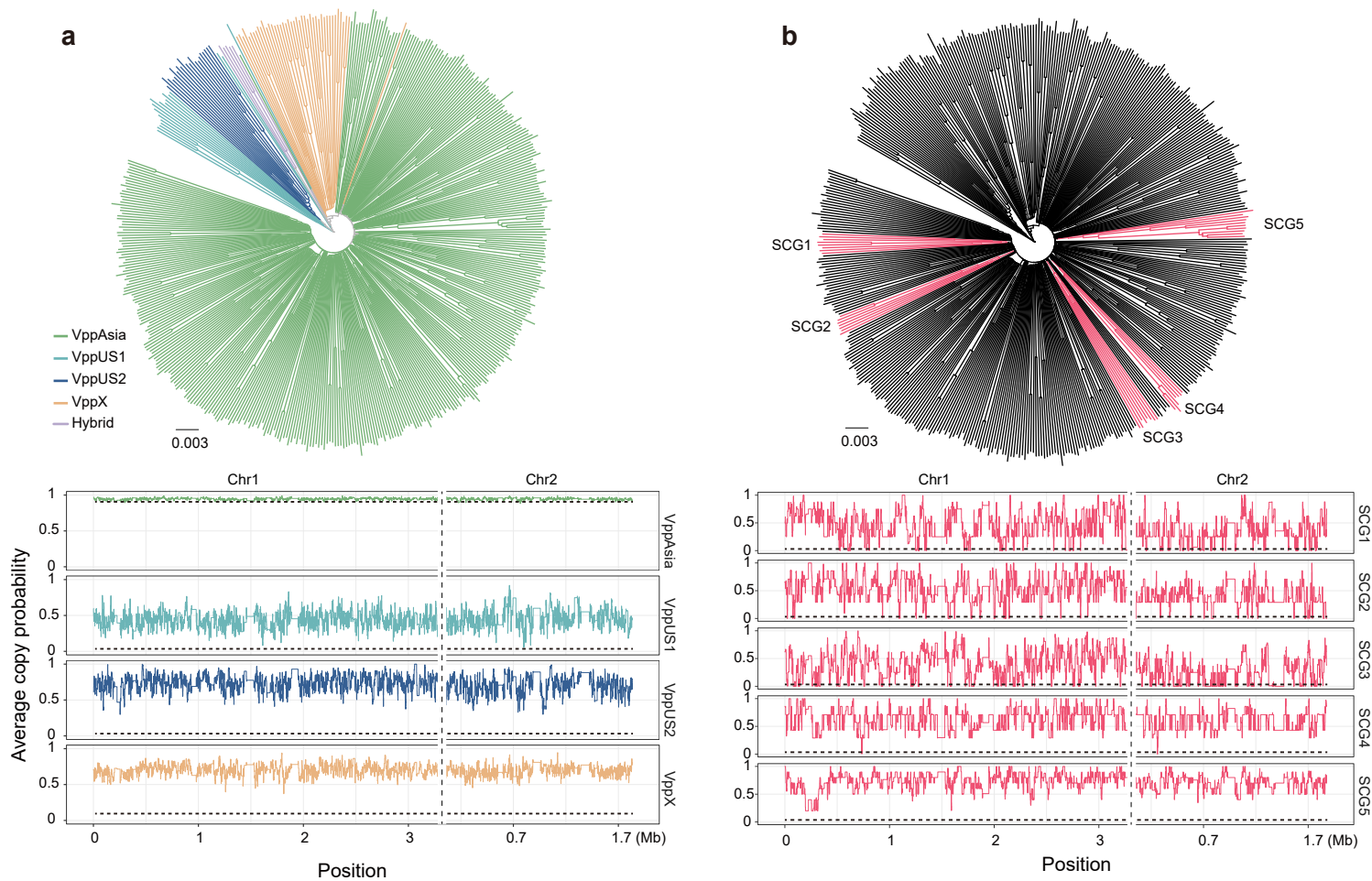
**Figure S1. fineSTRUCTURE showing no clonal frame in 198 VppAsia isolates.** Coancestry matrix of 201 strains, including 198 VppAsia isolates and three isolates respectively from VppX, VppUS1 and VppUS2. The color of each cell indicates the expected chunks numbers imported from a donor (column) to a recipient (row).

**FigureS2. Clustering of 469 strains based on variations of IG4-93.** Hierarchical clustering of strains (column) based on coadaptation loci (row) of all IGs, except for IG1-3, 5, 6, 17, and 45 that had been showed in figures of the main text. Color scheme is the same as in Figure 3.

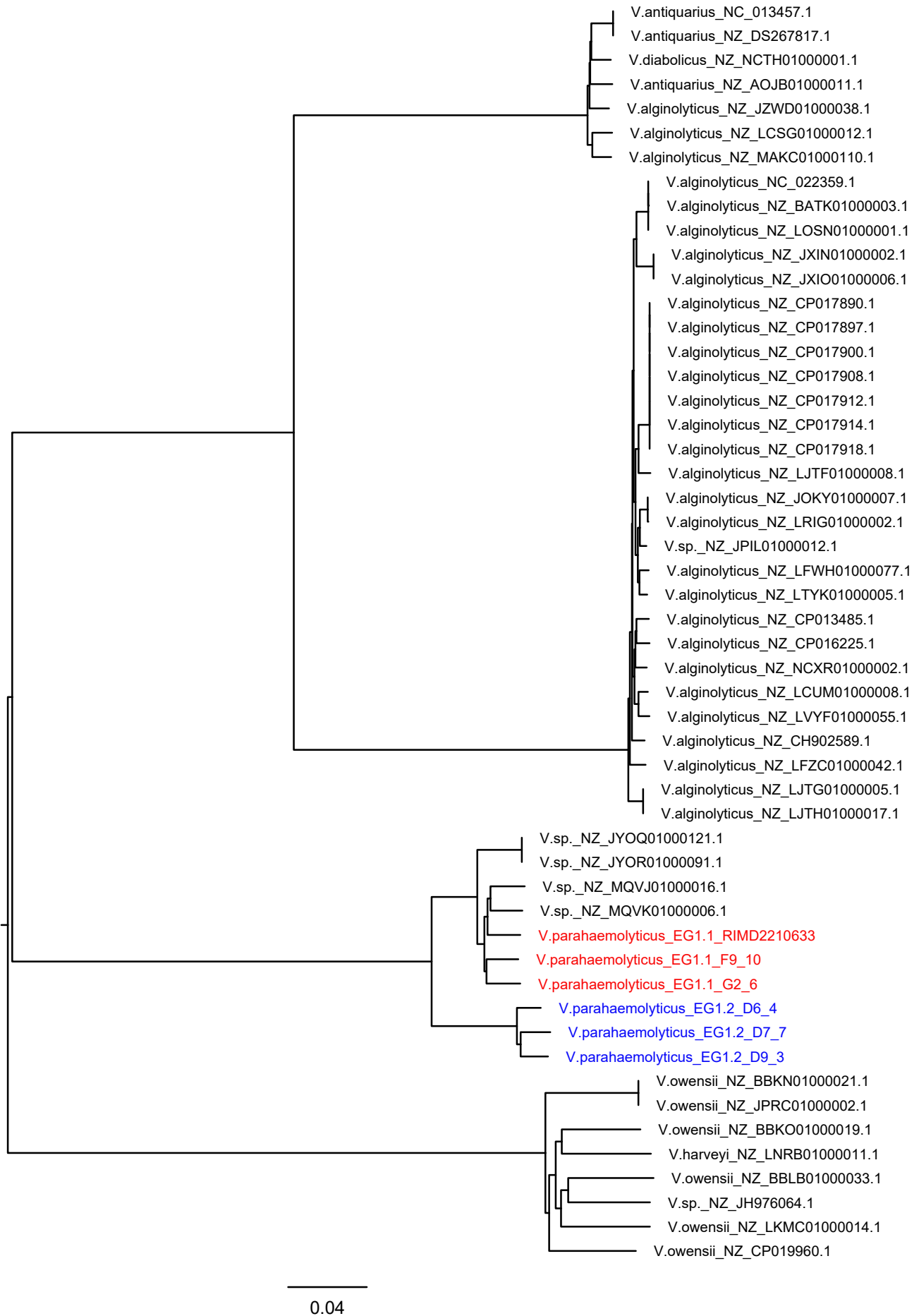




**Figure S3. IG1 interactions that only detected by Fisher exact test.**



**Figure S4. NJ trees (top) and average copy probability value distributions (bottom) of geographical populations (a) and semi-clonal group (SCG) strains (b) of *V. parahaemolyticus*.** Branch colors of the trees indicate populations (a) and SCGs (b), respectively. Horizontal dotted line indicates the expected average copy probability value. Different chromosomes are separated by a vertical dotted line.



**Figure S5. NJ tree of lateral flagellar gene cluster region (VPA1538-1557) in *Vibrio* genus.** Three randomly selected strains of EG1.1 and EG1.2 are used and marked in red and blue, respectively.