

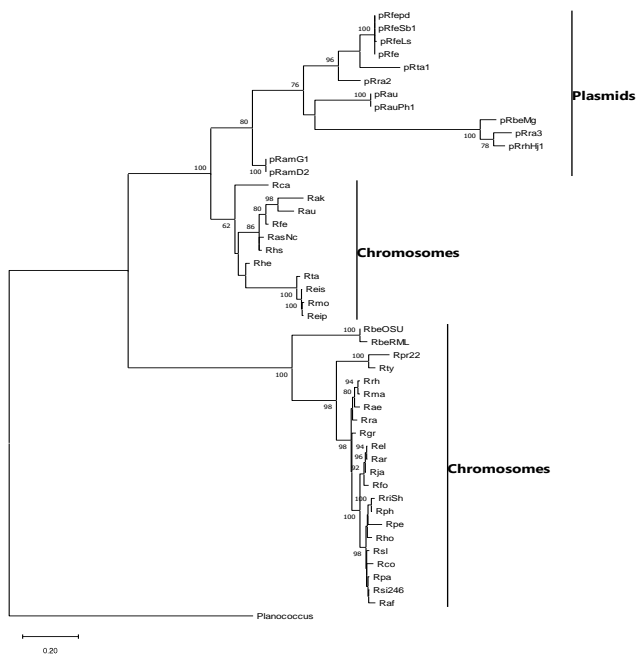


**Supplementary Figure S2.** Phylogenetic trees of *Rickettsia* plasmids and chromosomes inferred from five genes including DnaA-like replication initiator protein (A, 39 plasmids/26 strains and 17 chromosomes), patatin-like phospholipase (B, 13 plasmids/12 strains and 35 chromosomes), helix-turn-helix DNA-binding domain (C, 18 plasmids/13 strains), cell surface antigen Sca12 (D, 10 plasmids/10 strains and 30 chromosomes) and small heat shock protein (E, 21 plasmids/18 strains and 30 chromosomes). *Orientia tsutsugamushi* Ikeda (NC\_010793.1), *Planococcus antarcticus* (ZP\_10207867.1) and *Halobellus rufus* (WP\_049986146.1) were used as best homologues to rickettsial genes. Bootstrap values that were lower than 60% were removed from the trees.

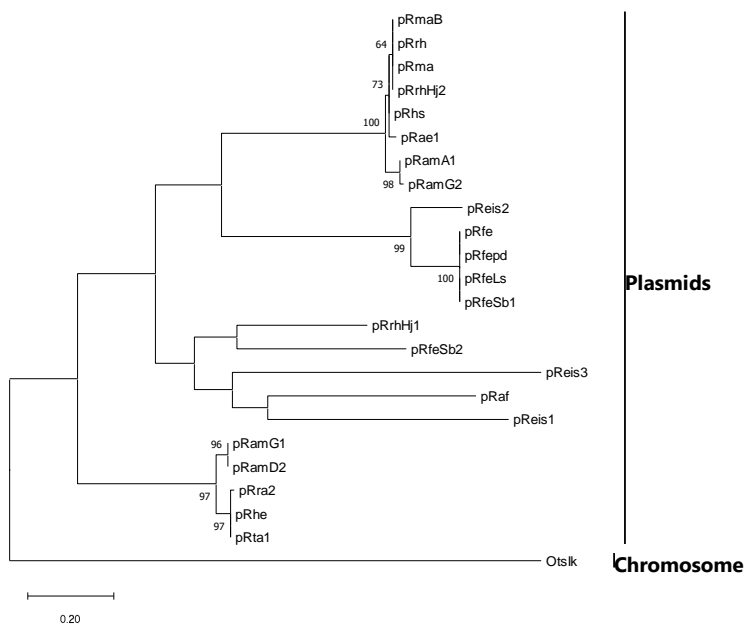
**A**



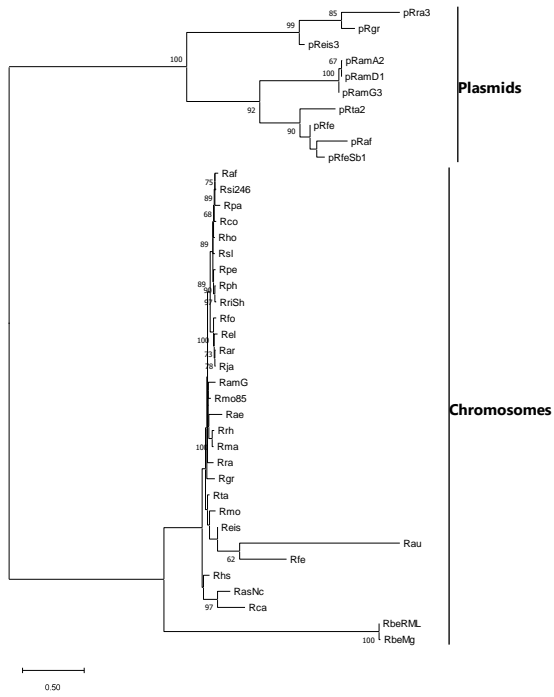
B



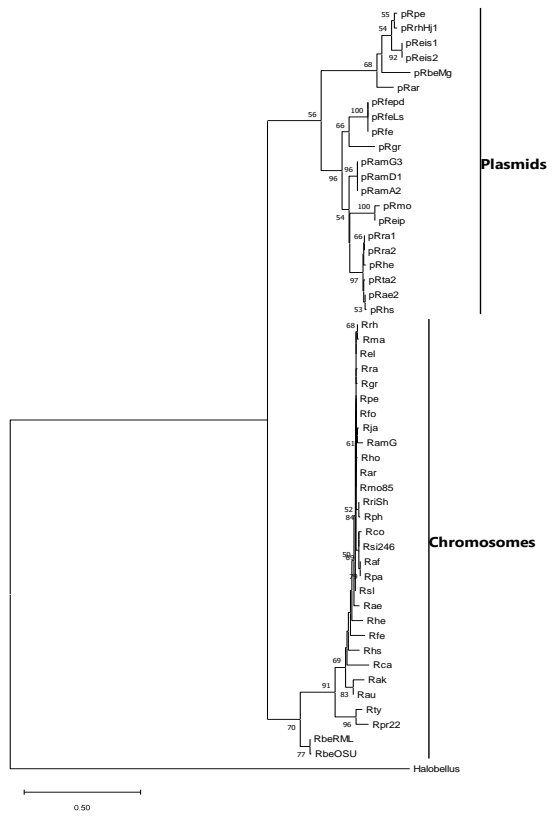
C



D



E



**Supplementary Figure S3.** Example of the pan-chromosome pattern obtained from complete chromosomes of 10 *Rickettsia* species belonging to the five major *Rickettsia* phylogenomic groups (SFGI, SFGII, TG, CG and BG). All species share 755 core genes and display a patchy distribution of flexible genes across them. Each blue column represents the total number of cRiGs common to at most 10 species.

