



S5 Figure. Phylogenetic relationship reconstructed for 10K windows for the alternatively phased datasets. The trees were reconstructed with the neighbor-joining algorithm and absolute genetic distance for non-overlapping 10K windows with minimum 1K complete sites (88 trees). HomeoRoq phased samples have _A and _B in their names to indicate *Cbp_{Cg}* and *Cbp_{Co}* subgenomes, respectively, whereas samples phased with HapCUT are marked with _Cg and _Co for the corresponding subgenomes. ASI, EUR ME indicate Asian, European and Middle Eastern populations of *C. bursa-pastoris*, respectively.