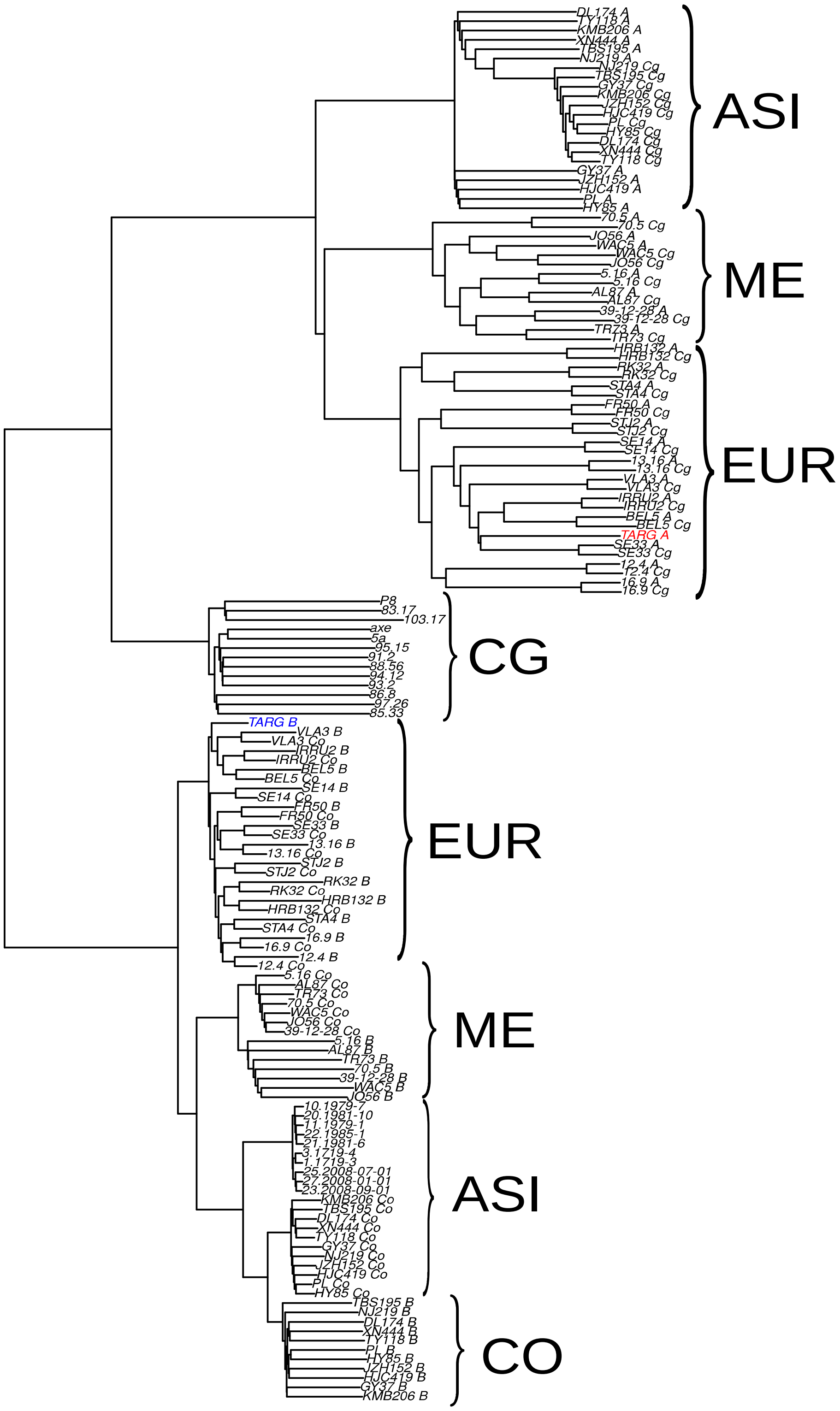

S9 Figure. Phylogenetic relationship of the alternatively phased datasets with parental species. The tree was reconstructed with the neighbor-joining algorithm and absolute genetic distance for 800K SNPs. HomeoRoq phased samples have _A and _B in their names to indicate *Cbp*$_{Cg}$ and *Cbp*$_{Co}$ subgenomes, respectively, whereas samples phased with HapCUT are marked with _Cg and _Co for the corresponding subgenomes. The reference sequences of the assembled *C.bursa-pastoris* are named with *TARG.* CO, CG, ASI, EUR, ME indicate *C. orientalis*, and *C. grandiflora*, and Asian, European and Middle Eastern populations of *C. bursa-pastoris*, respectively.