



S10 Figure. Variation in nucleotide diversity (π) between subgenomes of *C. bursa-pastoris* in HomeoRoq phased data. The distributions of π were estimated from 797,806 SNPs using 100 Kb sliding windows and scaled to whole genome scale. *Co* and *Cg* indicate *C. orientalis* and *C. grandiflora/rubella* descendant subgenomes, respectively. ASI, EUR, and ME correspond to Asian, European and Middle Eastern populations of *C. bursa-pastoris*, respectively.