

Fig. S10. Proportion of deleterious mutations in the two subgenomes of *C. bursa-pastoris* and the genomes of its parental species. CO, CG, ASI, EUR, ME, CASI correspond to *C. orientalis*, *C. grandiflora*, and four populations of *C. bursa-pastoris*, respectively. The two subgenomes are indicated with Co and Cg. Functional effects were annotated with the *A. thaliana* SIFT database.