

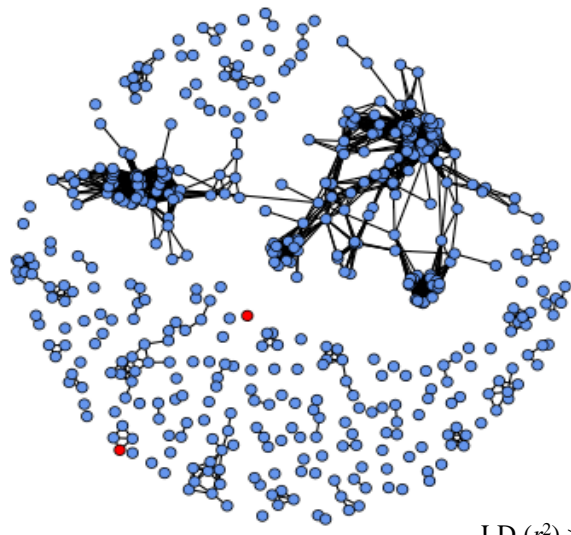
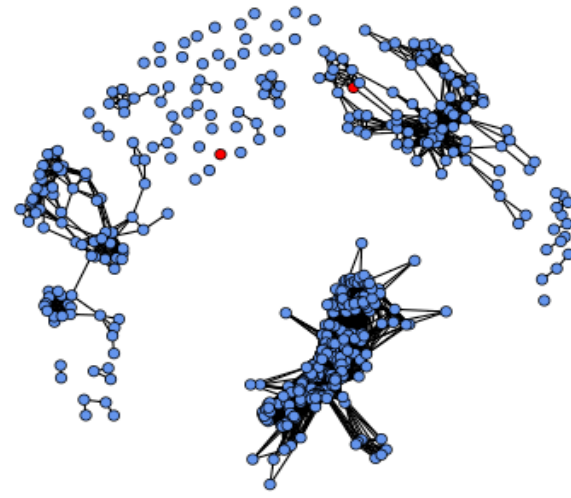
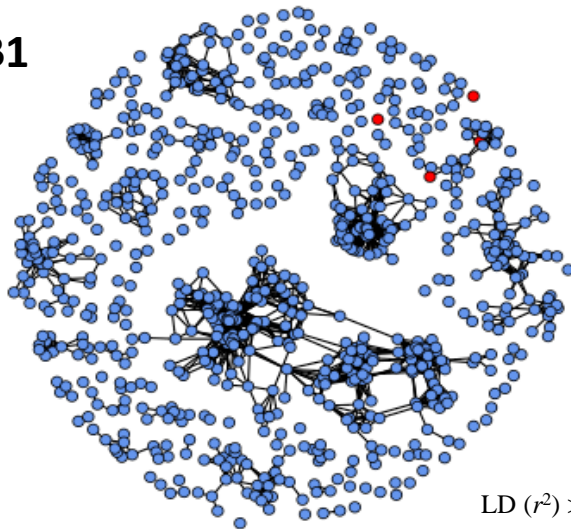
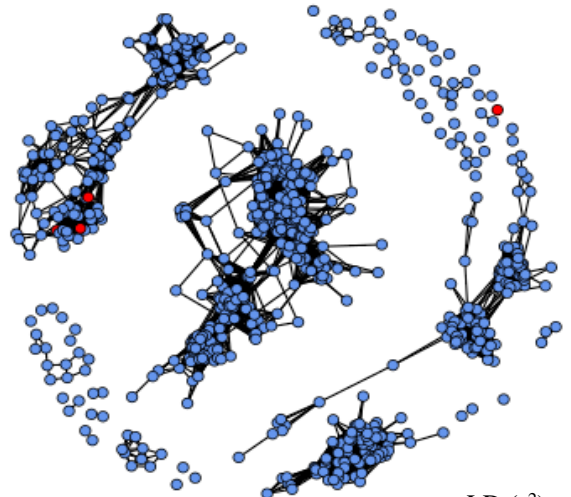
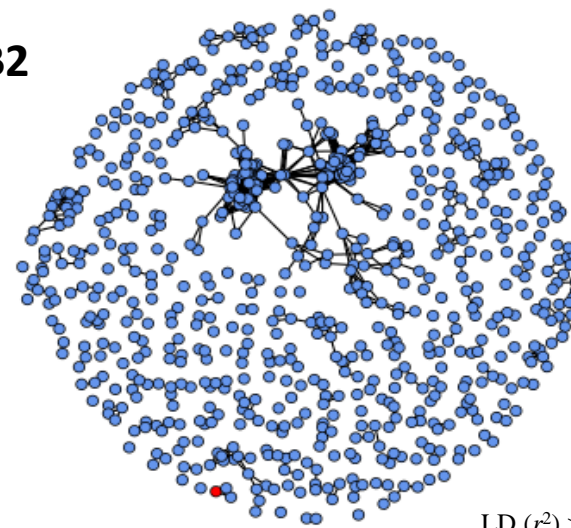
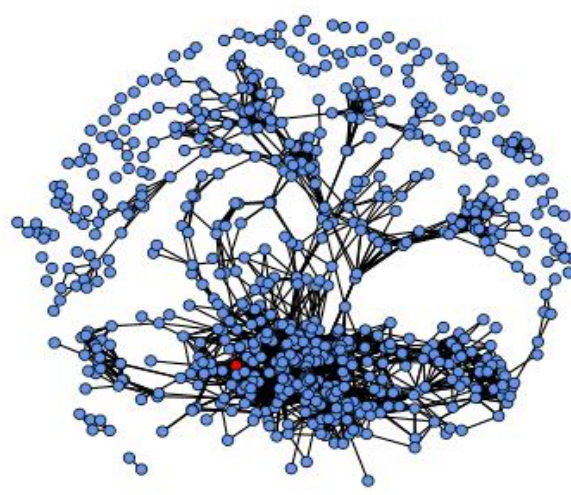
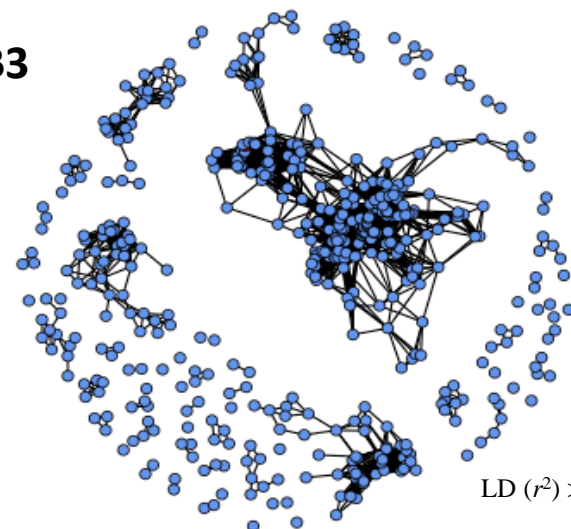
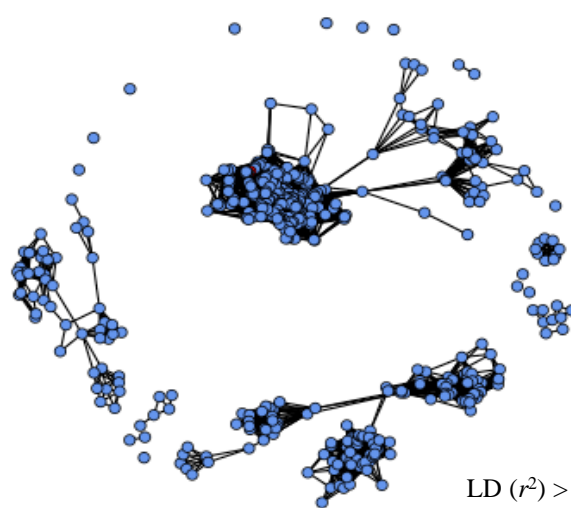
ALD (r^2) > 0.7LD (r^2) > 0.5**B****B1**LD (r^2) > 0.7LD (r^2) > 0.5**B2**LD (r^2) > 0.7LD (r^2) > 0.5**B3**LD (r^2) > 0.7LD (r^2) > 0.5

Figure S6. A. Network plots showing the LD-interconnections among SNPs at r^2 higher than 0.7 and 0.5 in the surrounding regions of ~1Mb of the two SNPs selected as cofactors located on chromosome 9 for flowering period in the GWA analysis of the whole population. The two SNPs selected as cofactors are indicated by red dots. B. Network plots showing the LD-interconnections among SNPs at r^2 higher than 0.7 and 0.5 in the surrounding regions of ~1Mb of the six SNPs selected as cofactors for flowering ripening period in the GWA analysis of the whole population. The four SNPs selected as cofactors and located on chromosome 3 are indicated by red dots in B1. The SNP selected as cofactor and located on chromosome 10 is indicated by a red dot in B2. The SNP selected as cofactor and located on chromosome 16 is located within the biggest cluster of blue dots in B3.