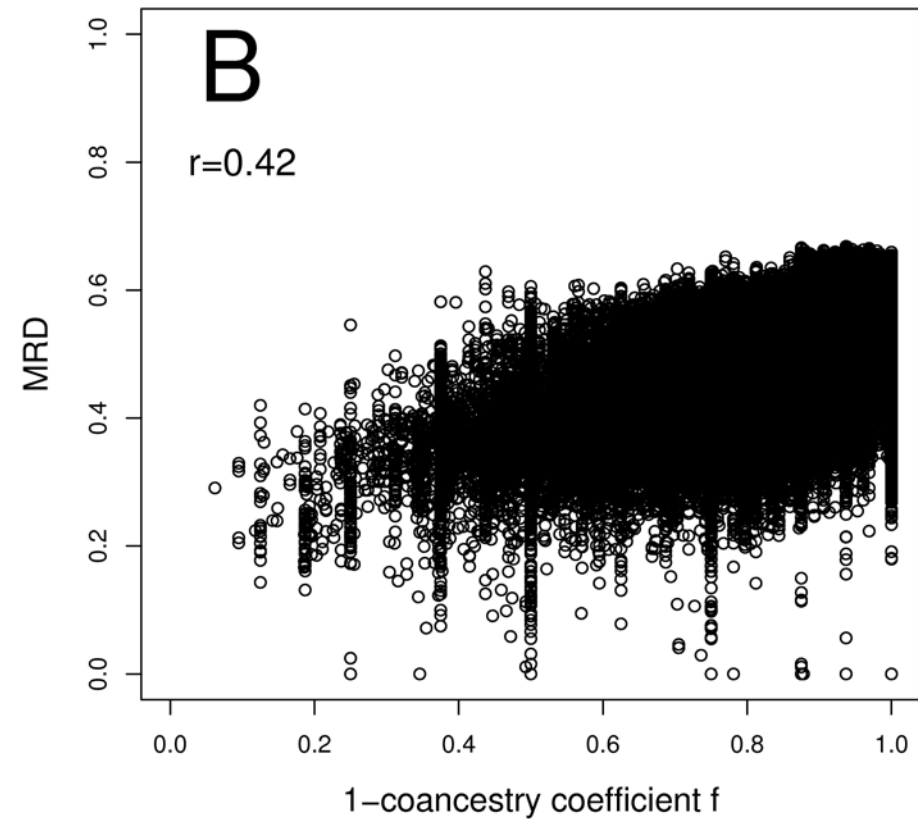
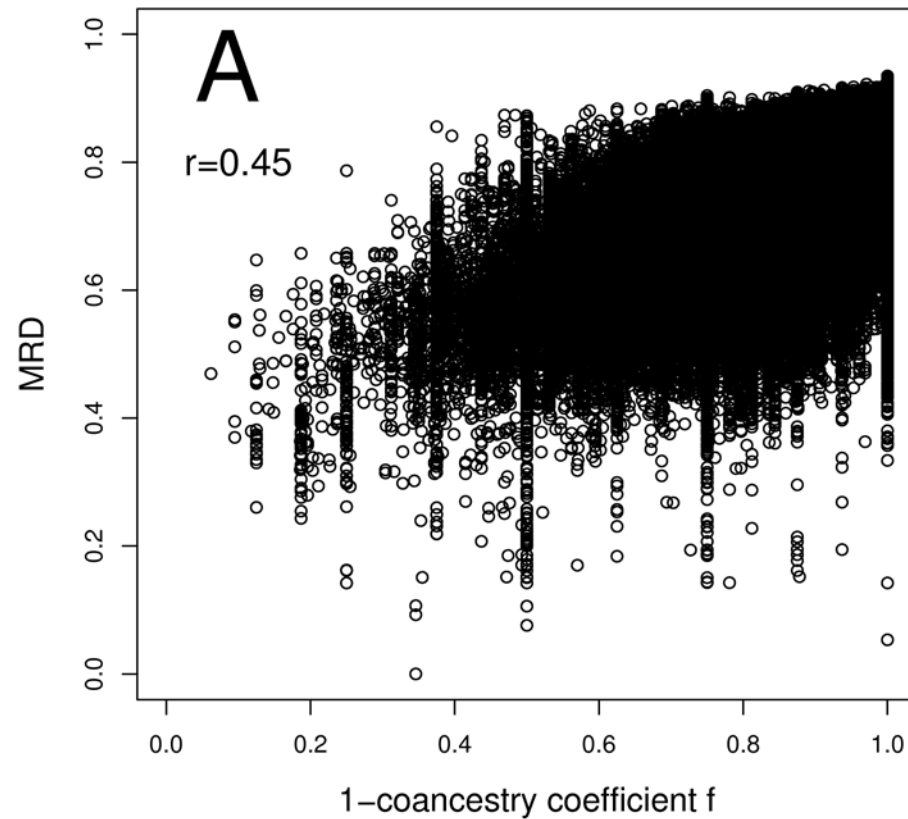
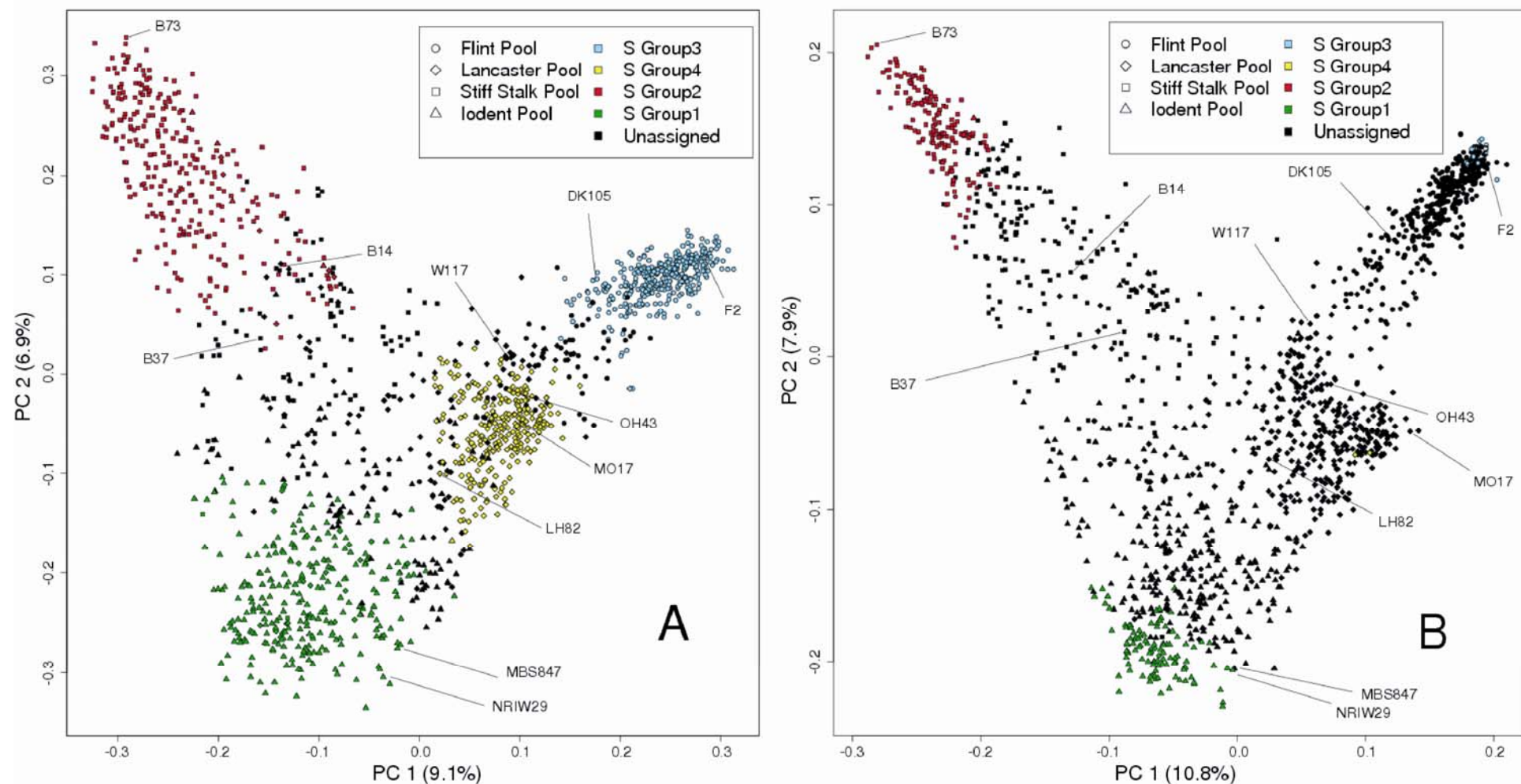
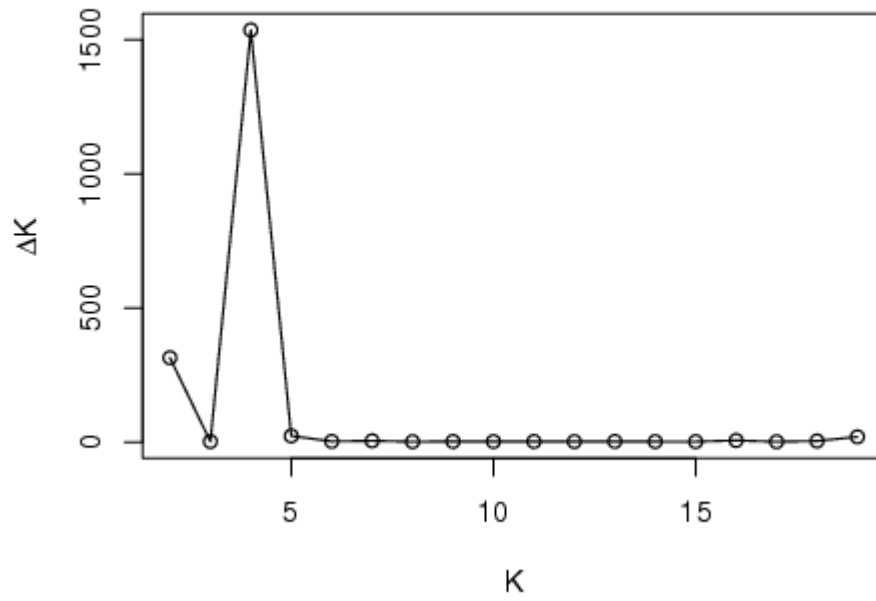




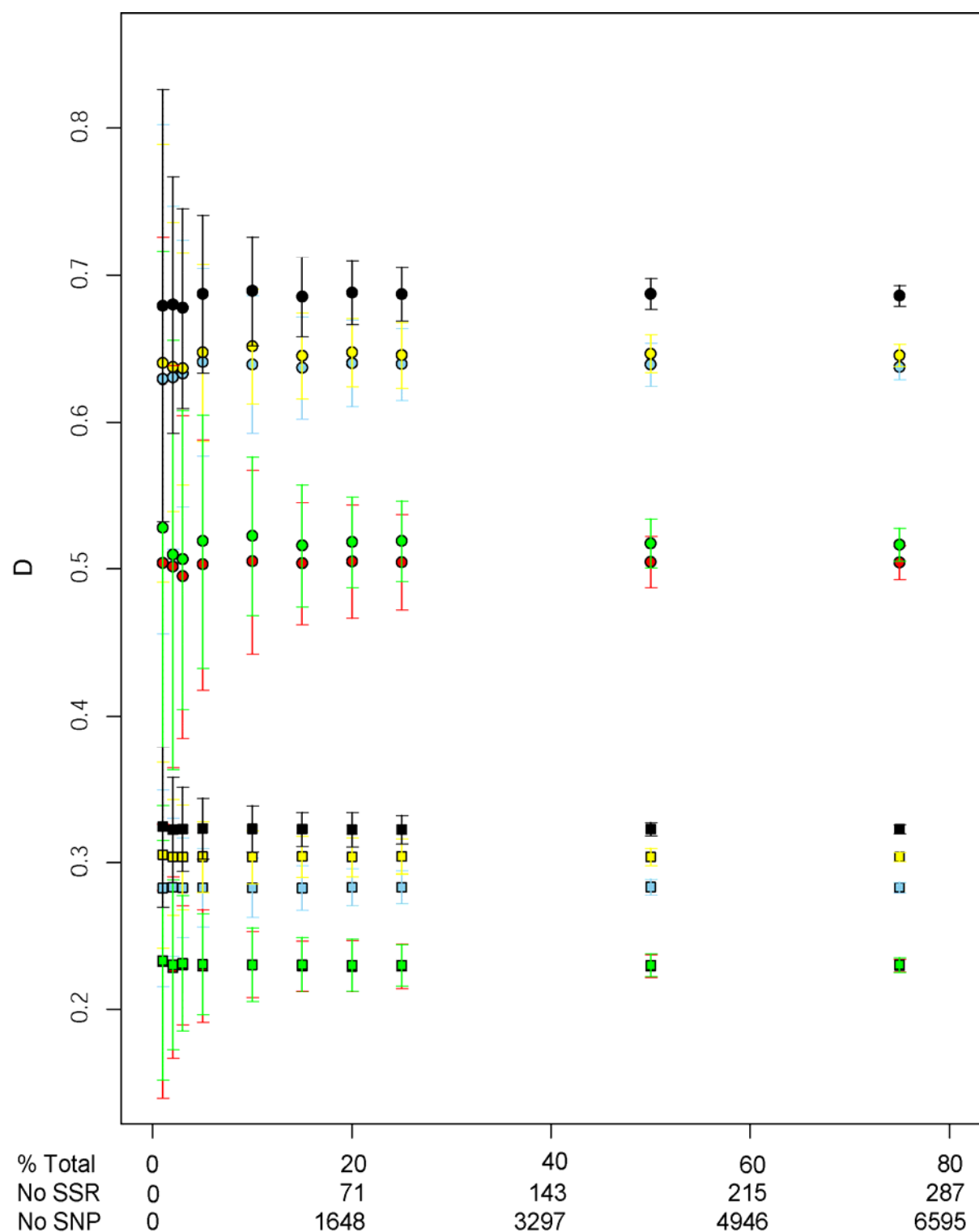
S 1. Modified Roger's distance (MRD) estimates between 1537 maize genotypes assessed with (A) simple sequence repeat (SSR) and (B) single nucleotide polymorphism (SNP) markers as a function of 1-coancestry coefficient f calculated from pedigree records. Spearman correlation coefficient r is mentioned on the graphics.



S 2. Principal coordinate analysis of 1537 maize inbred lines based on modified Roger's distance calculated from 359 SSR (A) or from 8244 SNP (B) marker loci. Genotypes were assigned to a sub-group if a membership probability ≥ 0.7 was observed. PC 1 and PC 2 are the first and second principal coordinate, respectively, and number in parentheses refer to the proportion of variance explained by the principal coordinates. Symbols identify the heterotic pools and colors the STRUCTURE groups.



S3. Determination of the number of sub-groups K based on STRUCTURE software and SSR markers using the ad hoc criterion ΔK . For details see Materials and methods.



S4. Mean gene diversity estimates (D) as well as the corresponding coefficient of variation for the four heterotic pools (Flint: blue; Lancaster: yellow; SSS: red; Iodent: green) and the entire germplasm set (black) assessed by random sampling of different numbers of simple sequence repeat (No SSR) and single nucleotide polymorphism (No SNP) markers in percent of the total number of markers (% Total). Circles and squares represent the SSR and SNP results, respectively. For details see Materials and methods.