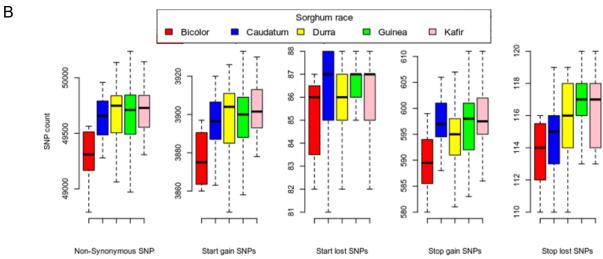
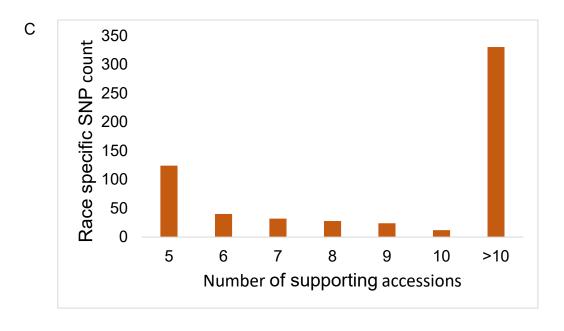
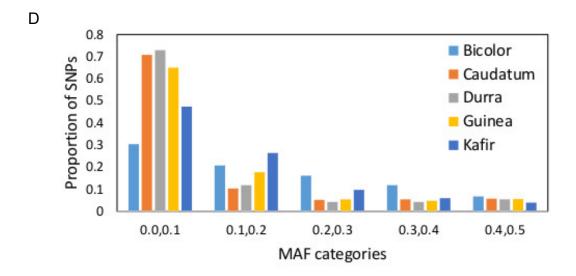


Supplementary Figure 1: Sorghum WGRS mapped stats showing the **A)** reference genome covered in both horizontal and vertical coverage, **B)** inset size of complete datasets **C)** GC content in all sorghum accessions.

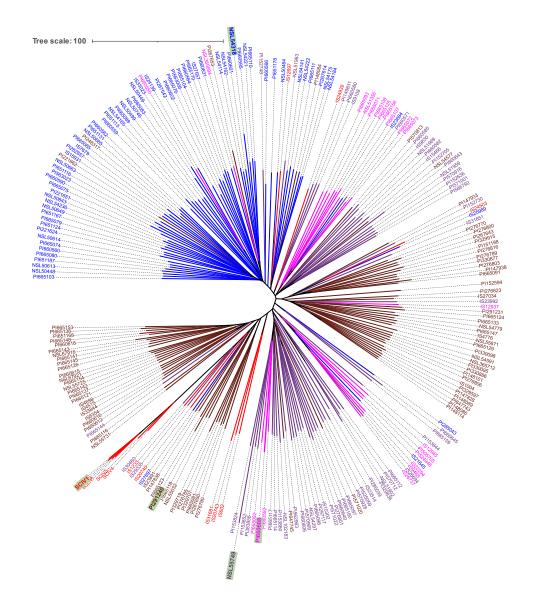




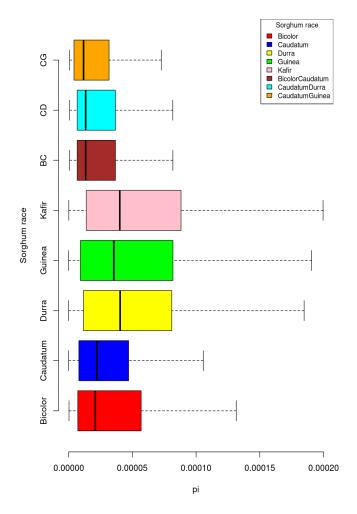




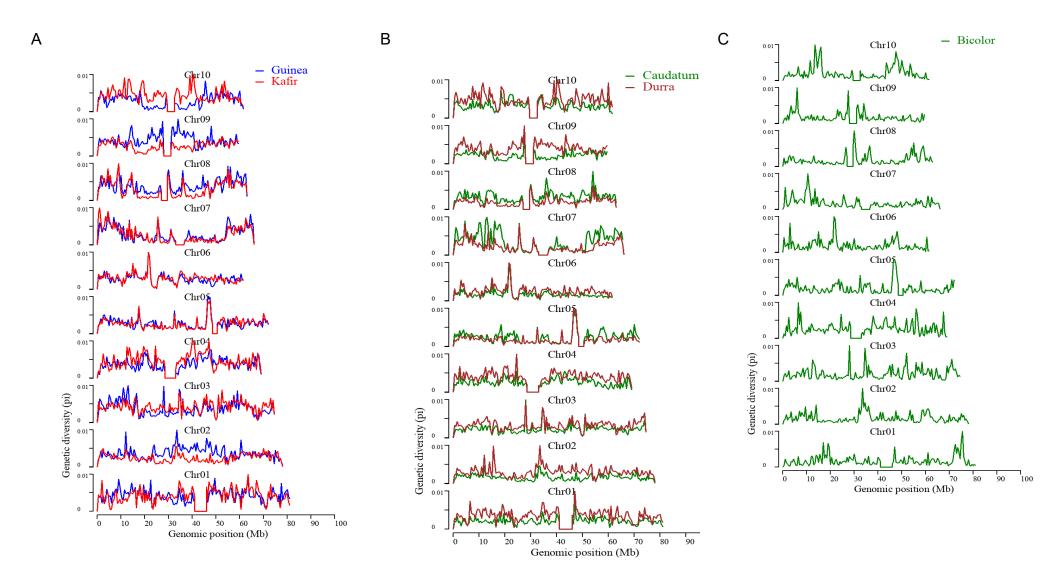
Supplementary Figure 2: Genomic landscape of sorghum. A) Indel length distribution B) SNP annotations C) race-specific SNP calls with a number of supporting sorghum accessions D) The distribution of minor allele frequencies for all sorghum races. SNPs were binned into five categories on the MAF.



Supplementary Figure 3. Sorghum race accession NJ tree with nodes in blue color are *Guinea*, pink colour accessions are *Kafir*, red color for *bicolor*, brown color in *Durra*, purple color for *Caudatum*. Highlighted node labels are the most distinct accessions in respective sorghum race accessions. The phylogenetic tree contained a distinct cluster of 63 *Guinea* race accessions (nodes in blue colour) mixed with a few other race individuals, like PI221662, PI248317, PI267653 and PI148084 from *Durra* race (nodes in brown colour), PI660555 and NSL365694 from *Kafir* race (nodes in pink colour), IS12697 from *bicolor* race (nodes in red colour). The other sorghum race clusters were split with non-corresponding sorghum race accessions. For example, *Durra* race has 91 accessions split into two clusters with *Caudatum* and *Kafir* race accessions. The sorghum *bicolor* race which was assumed to be more distinct to other race were placed mostly in *Durra* and *Guinea* race cluster. Among the *bicolor* race, the China origin accessions were grouped distinctly in *Durra* cluster compared to other *bicolor* race accessions.

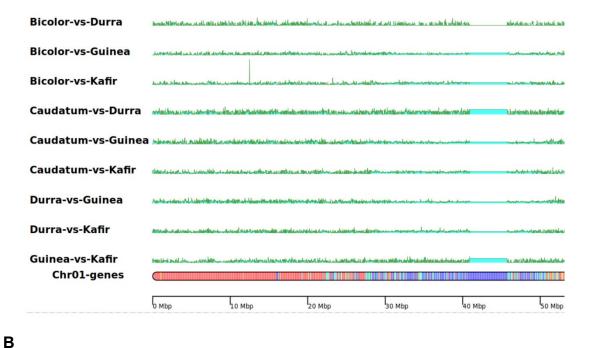


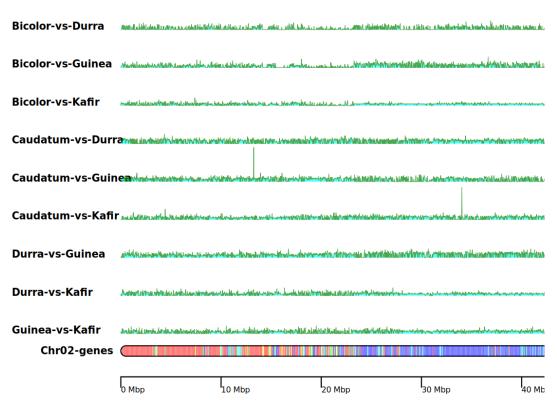
Supplementary Figure 4. The nucleotide diversity comparison between the five sorghum races and three intermediate races.

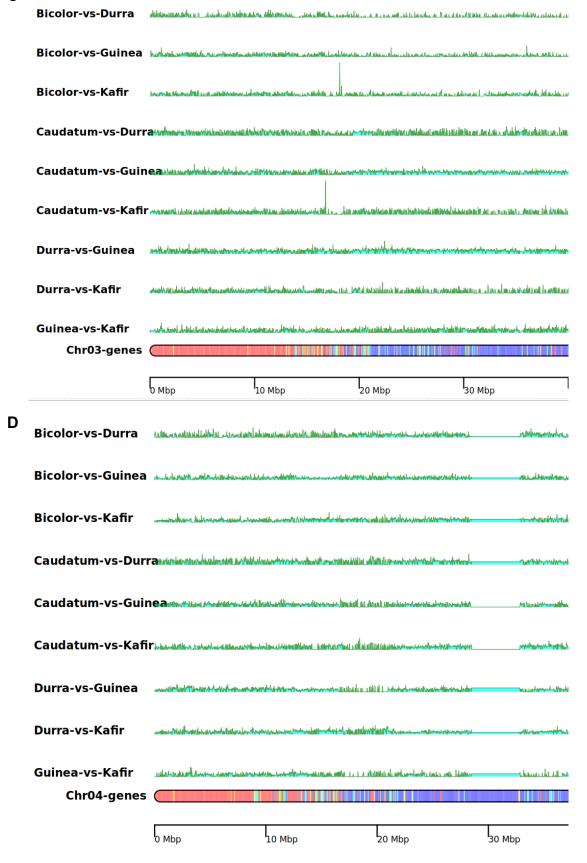


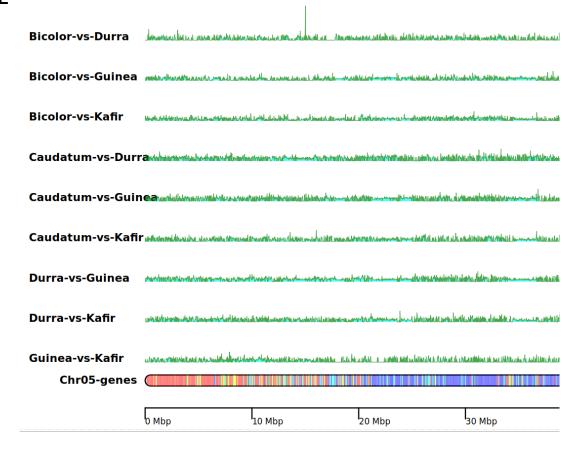
Supplementary Figure 5. Nucleotide diversity (π) in sorghum race populations A) Guinea and kafir B) Caudatum and Durra C) Bicolor

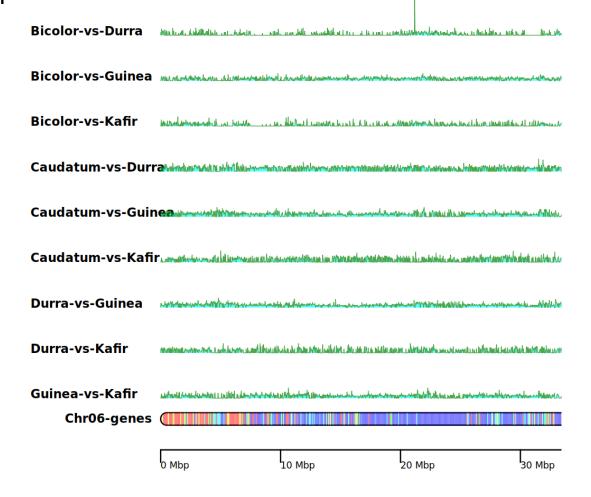
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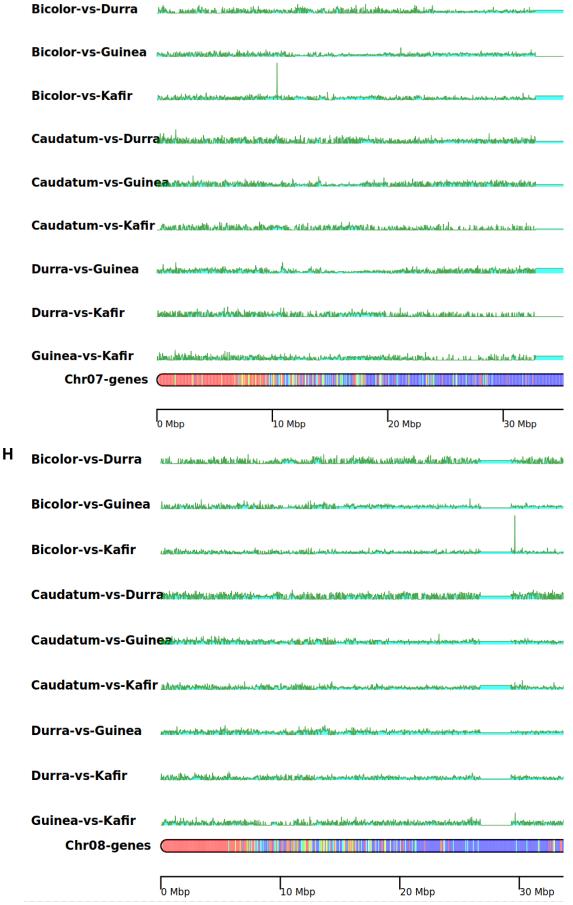




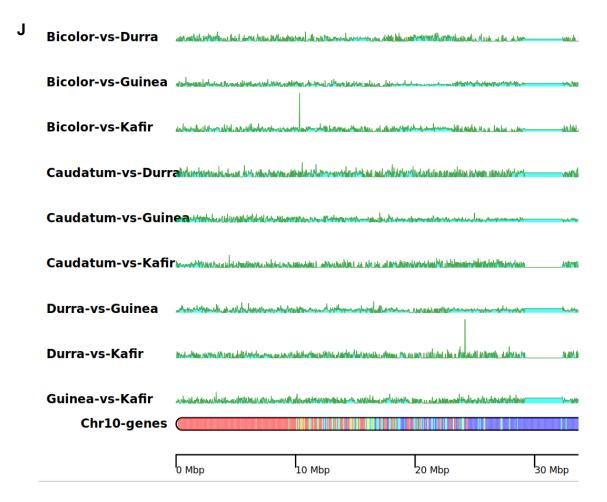






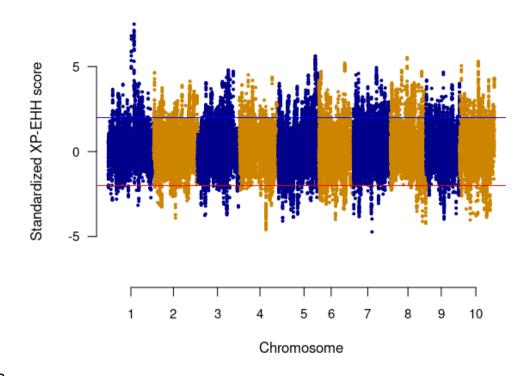


I



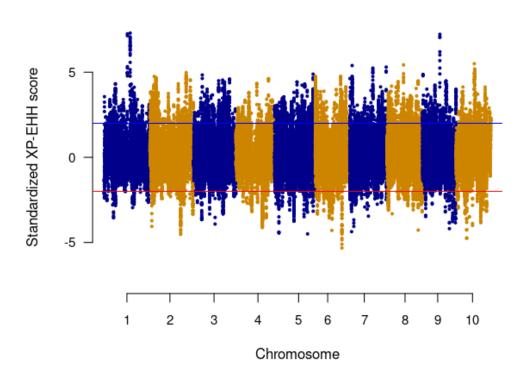
Supplementary Figure 6. Pairwise F_{ST} across the chromosomes of sorghum race populations and gene density heatmap on respective chromosomes.

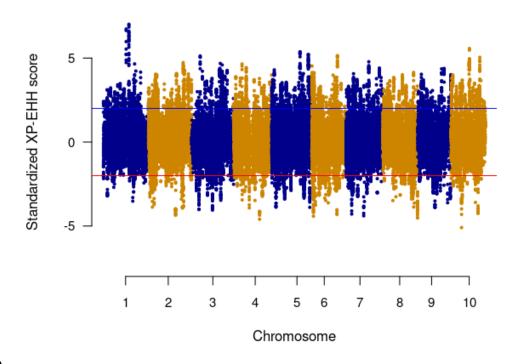
XP-EHH for bicolor-caudatum population



В

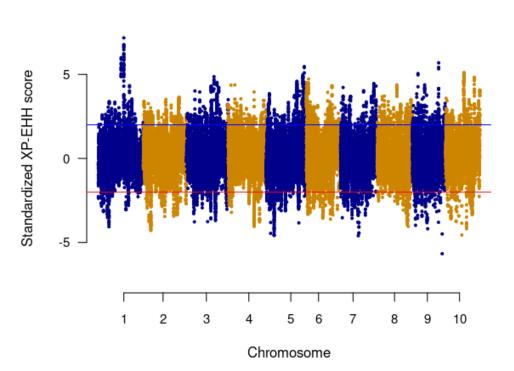
XP-EHH for bicolor-durra population



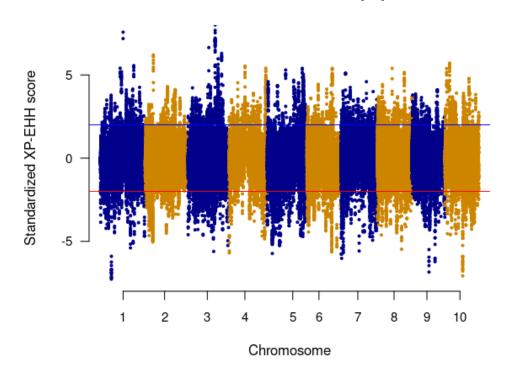


D

XP-EHH for bicolor-kafir population

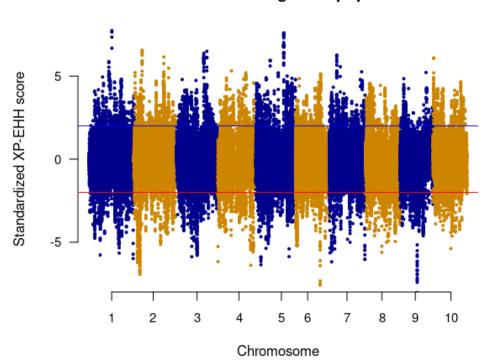


XP-EHH for durra-caudatum population

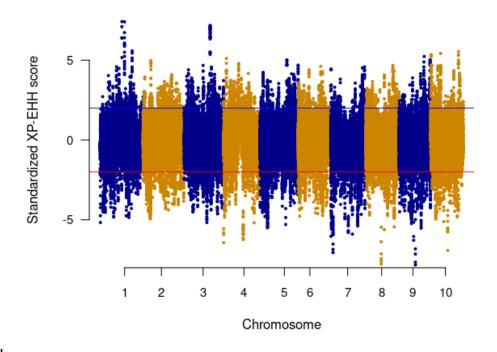


F

XP-EHH for durra-guinea population

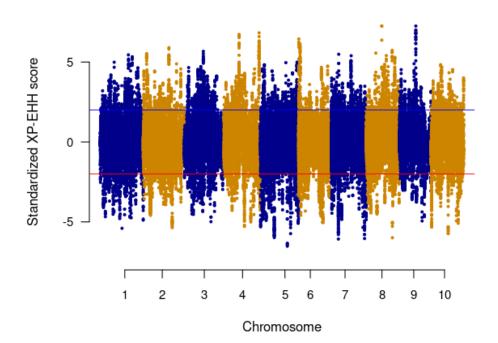


XP-EHH for durra-kafir population



Н

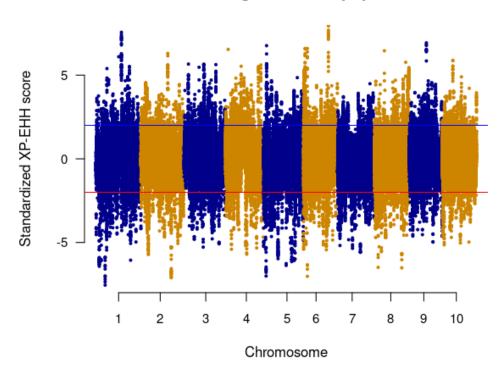
XP-EHH for guinea-caudatum population



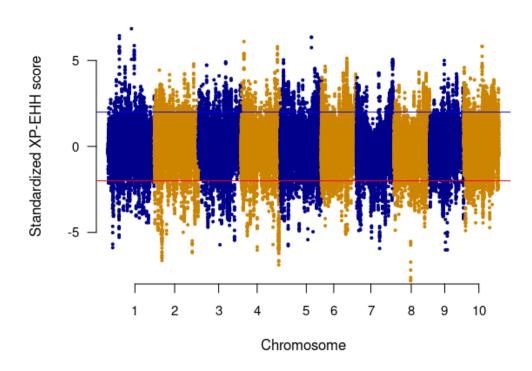
XP-EHH for guinea-kafir population

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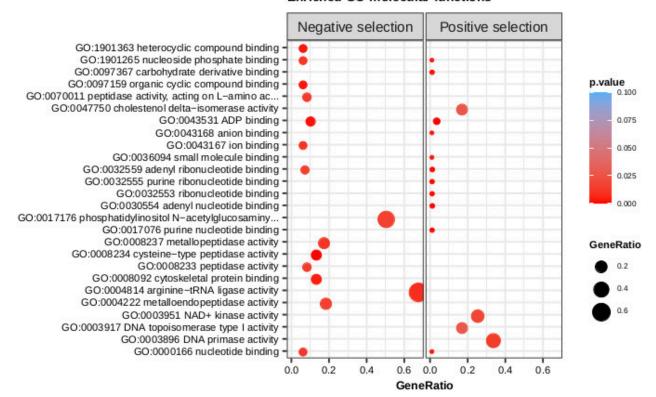


XP-EHH for kafir-caudatum population

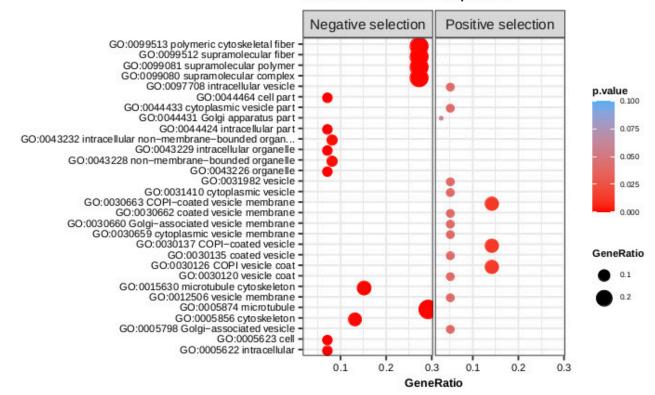


Supplementary Figure 7. Distribution of standardized XP-EHH scores in the sorghum race population comparison

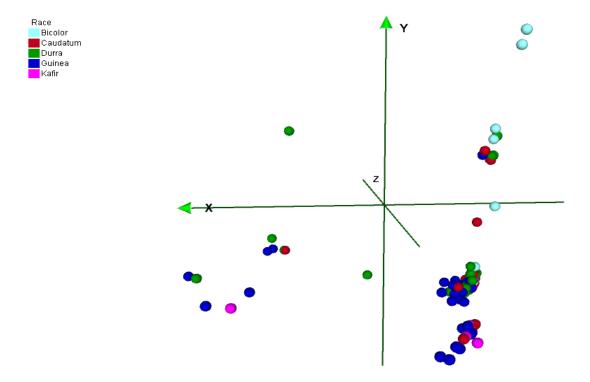
Enriched GO molecular functions



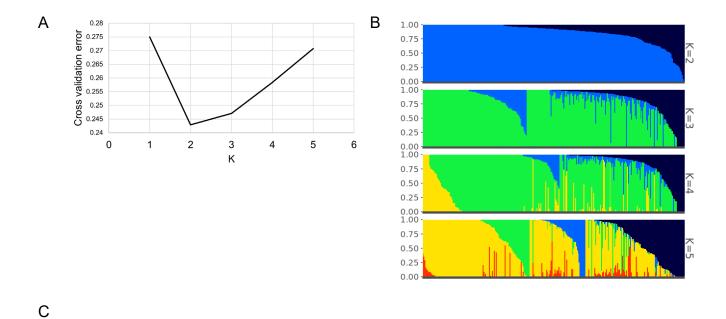
Enriched GO cellular components

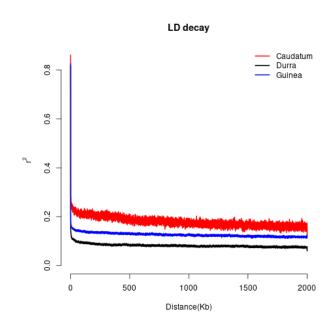


Supplementary Figure 8. Enrichment of genes under selection pressure for **A)** molecular function **B)** Cellular components.



Supplementary Figure 9: PCO analysis of sorghum accessions shows the clusters of accessions with different races.





Supplementary Figure 10: Structure analysis of the sorghum race population shows A) the low cross validation error for K 2,3 B) the population structure with different K values and C) the LD decay in the sorghum race population having more than 50 accessions. Rapid LD decay was observed in Durra followed by Guinea and Caudatum.