

Figure S1. Population structure analysis of the sorghum diversity panel. (A) Principal component analysis (PCA) plot colored by sorghum lines with botanical race classifications (bicolor, caudatum, durra, guinea, kafir, and intermediates) as reported in the germplasm resources information network (GRIN, <https://www.ars-grin.gov/>). Lines with unknown race classifications are colored grey. (B) Distruct plot of fastSTRUCTURE subpopulation membership with K = 4. (C) PCA colored according to the fastSTRUCTURE subpopulation membership with K=4. Individuals with assignment values (Q) lower than 80% were designated as admixed (black dots). Population 1 predominantly contains individuals belonging to race guinea; population 3 mostly includes races kafir and caudatum; and populations 4 and 2 primarily have race durra (East Africa and India origins, respectively).

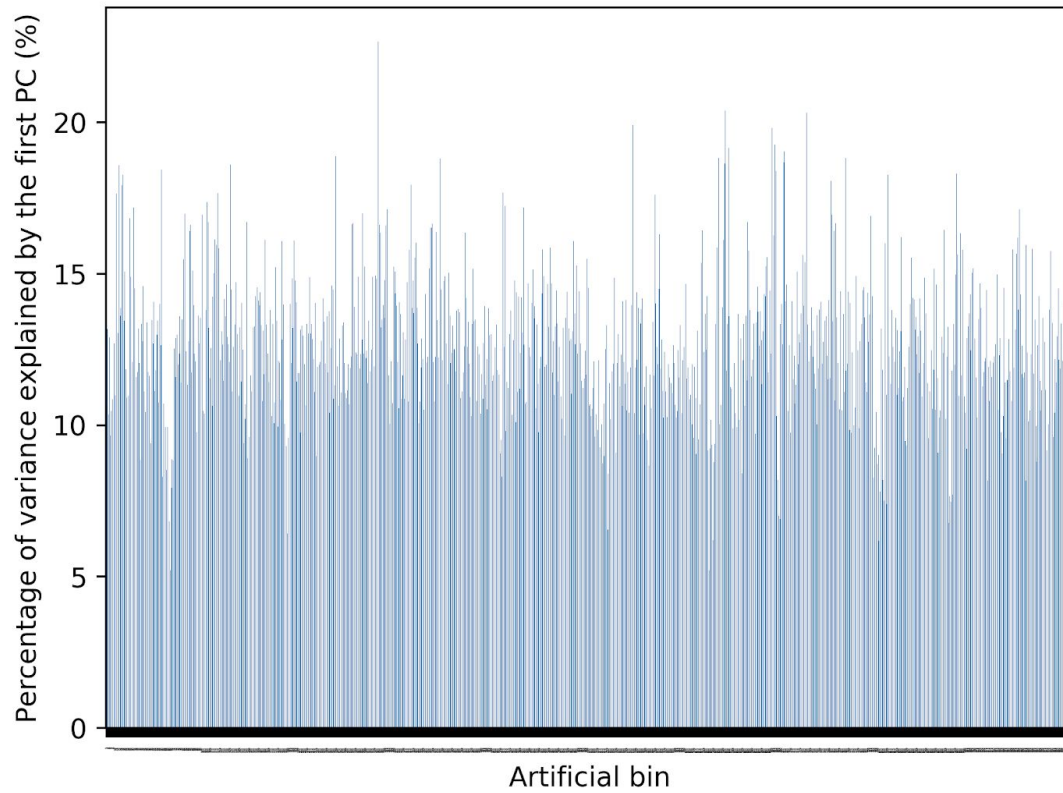


Figure S2. Distribution of the percentage (%) of the variance explained by the first principal component (PC) from each of 1,000 artificial bins. The artificial bins are ordered sequentially from the start of chromosome 1 to the end of chromosome 10.

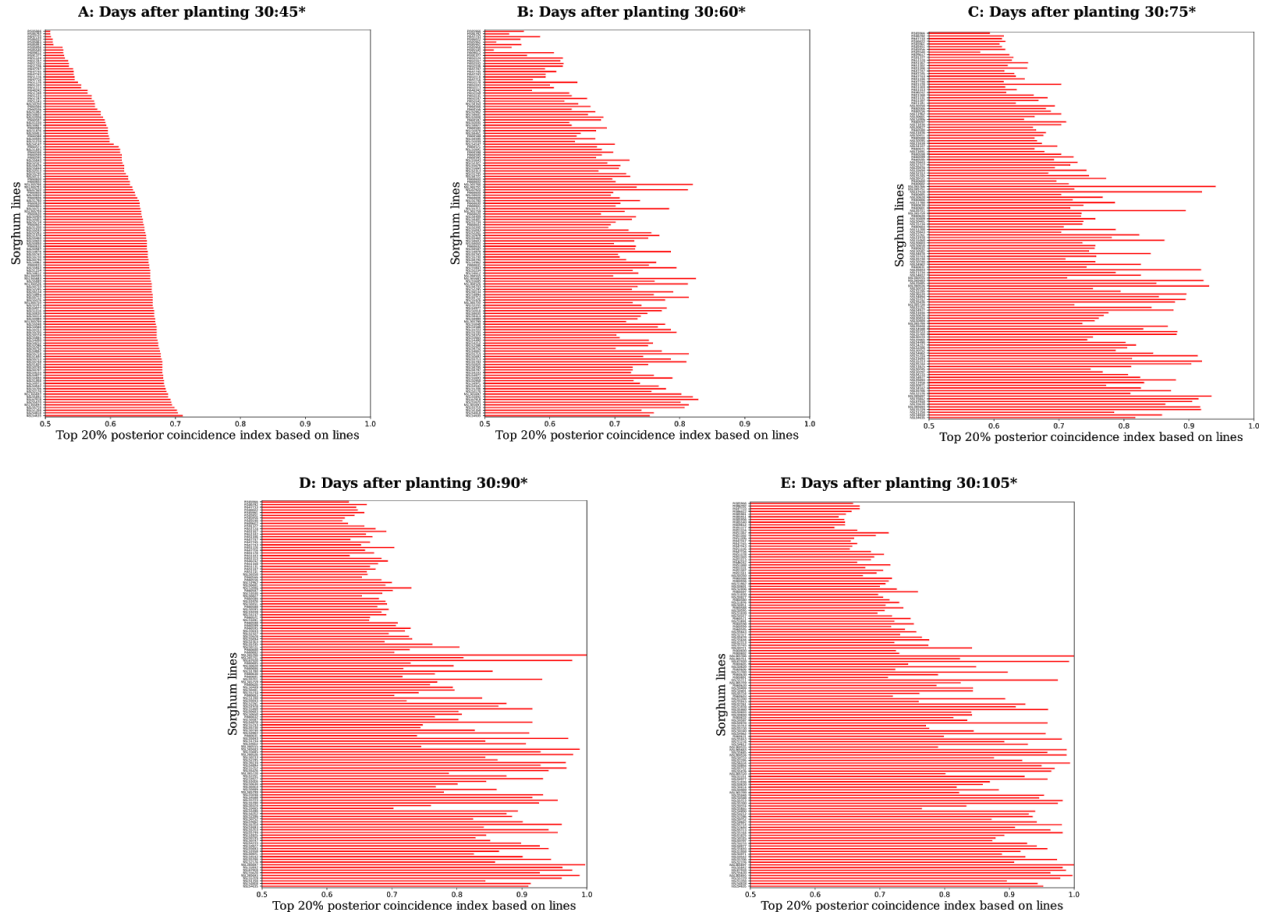


Figure S3. The calculated coincidence index based on lines (CIL) at multiple developmental stages. The top 20% posterior CILs from the results of the dynamic Bayesian network (DBN) are shown. The rank order of the lines in subplot A was fixed for subplots B, C, D, and E to understand phenotypic plasticity over time. Only lines with a CIL > 0.5 were plotted. The '*' symbol denotes the days after planting (DAP) time point that was used to obtain the adjusted means.