# **SUPPLEMENTARY FIGURES AND TABLES**

**Dissecting adaptive traits with nested association mapping: Genetic architecture of inflorescence morphology in sorghum**

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**Table S1: The sorghum NAM founders, their origin, and number of RILs used for each family.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Founder** | **Origin** | **Founder Type** | **RILs** |
| RTx430 | Texas A & M University | Common Parent | - |
| P898012 | Purdue University | Diverse Founder | 213 |
| Ajabsido | Sudan | Diverse Founder | 214 |
| Macia | ICRISAT | Diverse Founder | 231 |
| SC1103 | Nigeria | Diverse Founder | 231 |
| SC1345 | Mali | Diverse Founder | 231 |
| SC265 | Burkina Faso | Diverse Founder | 232 |
| SC283 | Tanzania | Diverse Founder | 223 |
| SC35 | Ethiopia | Diverse Founder | 208 |
| SC971 | Puerto Rico, United States | Diverse Founder | 233 |
| Segaolane | Botswana | Diverse Founder | 204 |

**Table S2:** Within-family and across population additive effect size (AES) for QTL identified using joint linkage mapping with marker nested within family (NJL) and joint linkage with no nesting (JL).

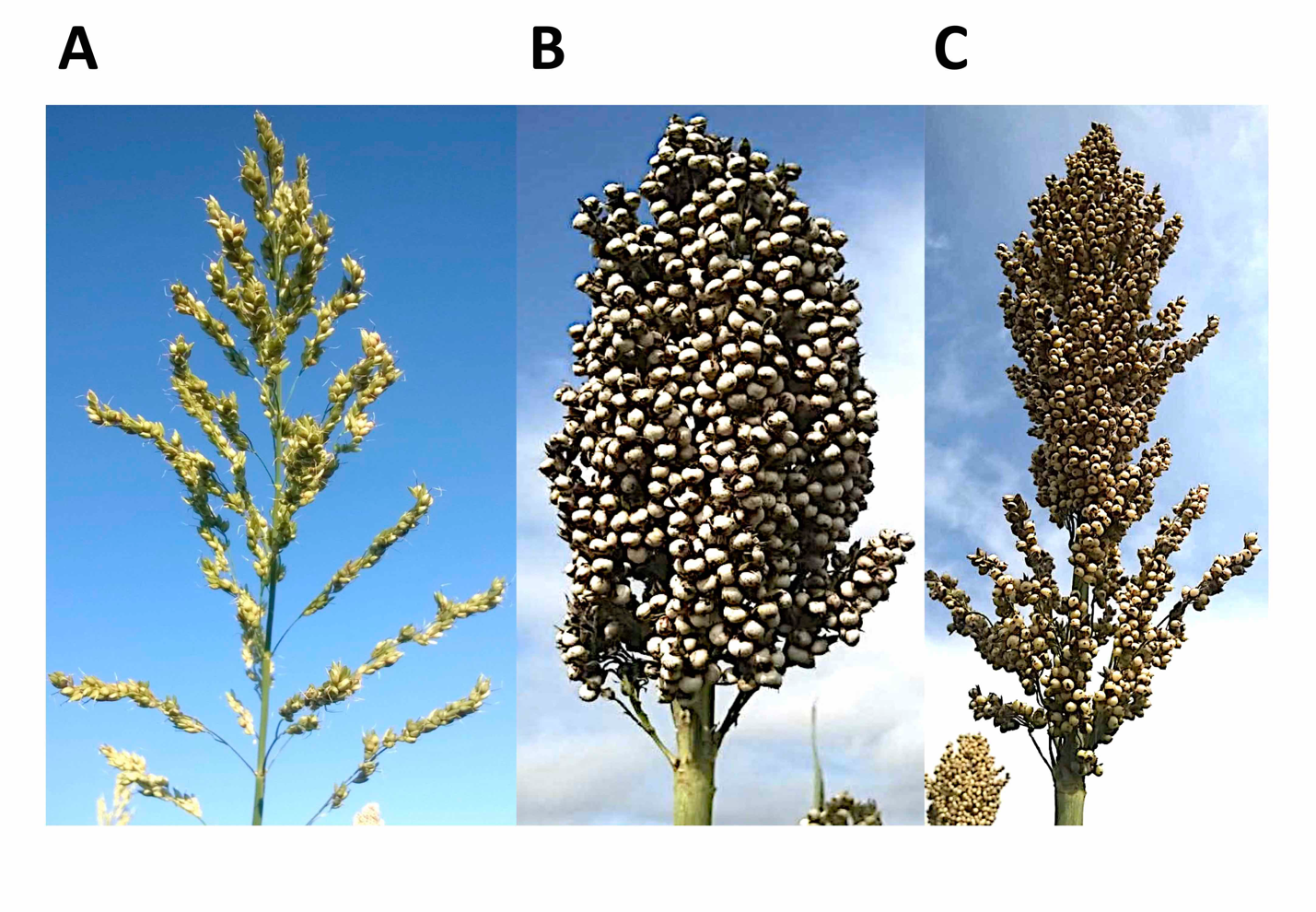
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **Model** | **Number of QTL** | **Trait Mean (mm)** | **Range of WF-AES (mm)** | **Range of AP-AES (mm)** | **Range of PVE (%)** |
| LBL | NJL | 14 | 85 | -30–16 | -4–2 | 0.1–2.0 |
| LBL | JL | 21 | - | -26–19 | -12–8 | 0.6–5.0 |
| UBL | NJL | 1 | 49 | - 29.0–0 | -4 | 3.0 |
| UBL | JL | 17 | - | -33–5 | -11–2 | 0.6–4.0 |
| RL | NJL | 16 | 276 | -44–52 | -10–12 | 0.1–3.0 |
| RL | JL | 22 | - | -49.5–52 | -20–20 | 0.6–3.0 |
| RD | NJL | 9 | 8 | -2.0–1 | -0.4–0.2 | 0.1–1.0 |
| RD | JL | 21 | - | -2.4–1 | -0.9–1.5 | 0.2–1.0 |

a Lower branch length (LBL), upper branch length (UBL), rachis length (RL), and rachis diameter (RD).

b Quantitative trait loci (QTL).

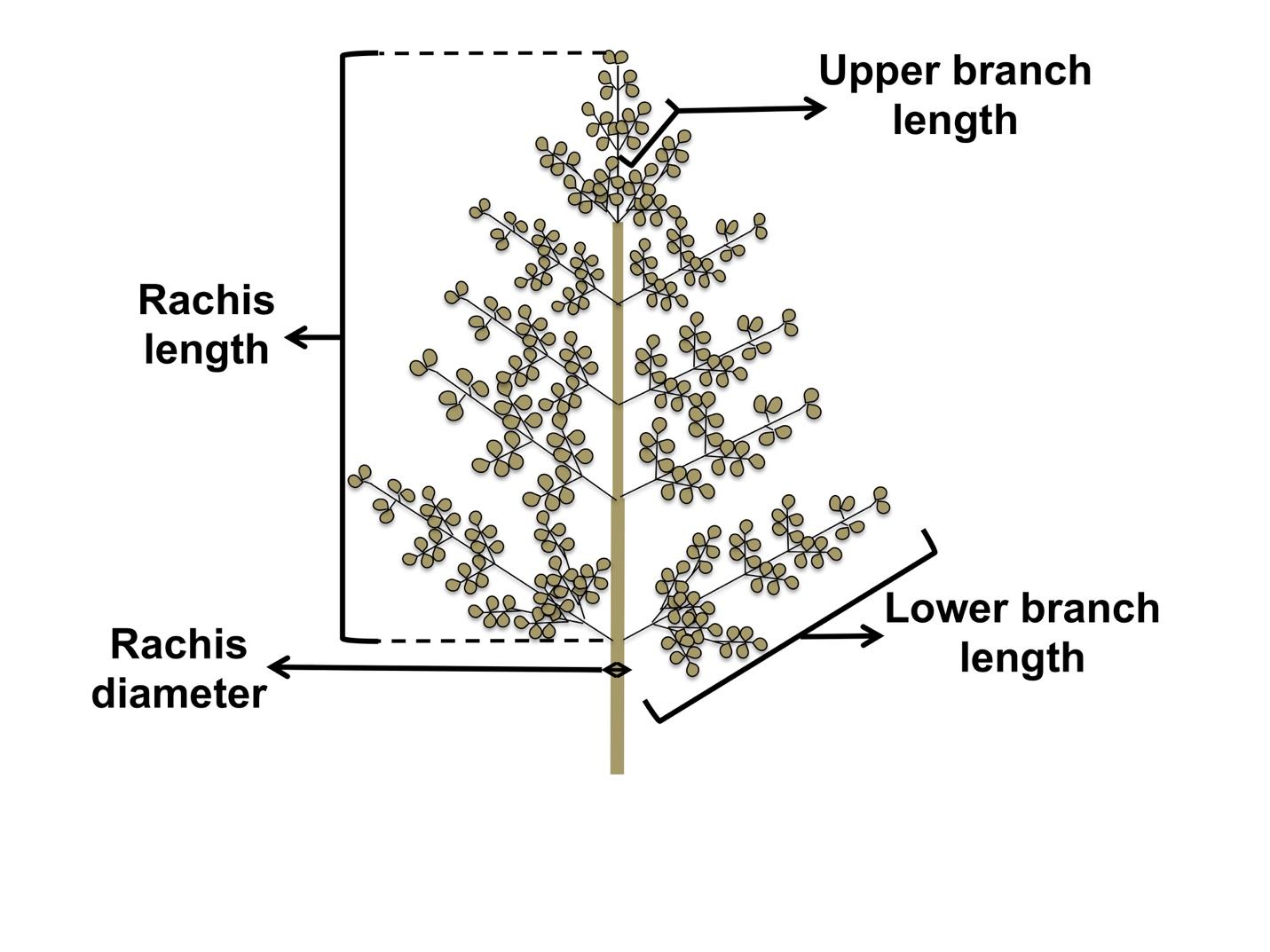
c Within Family Additive Effect Size (WF-AES), and Across Population Additive Effect Size (AP-AES).

d Phenotypic Variation Explained (PVE).

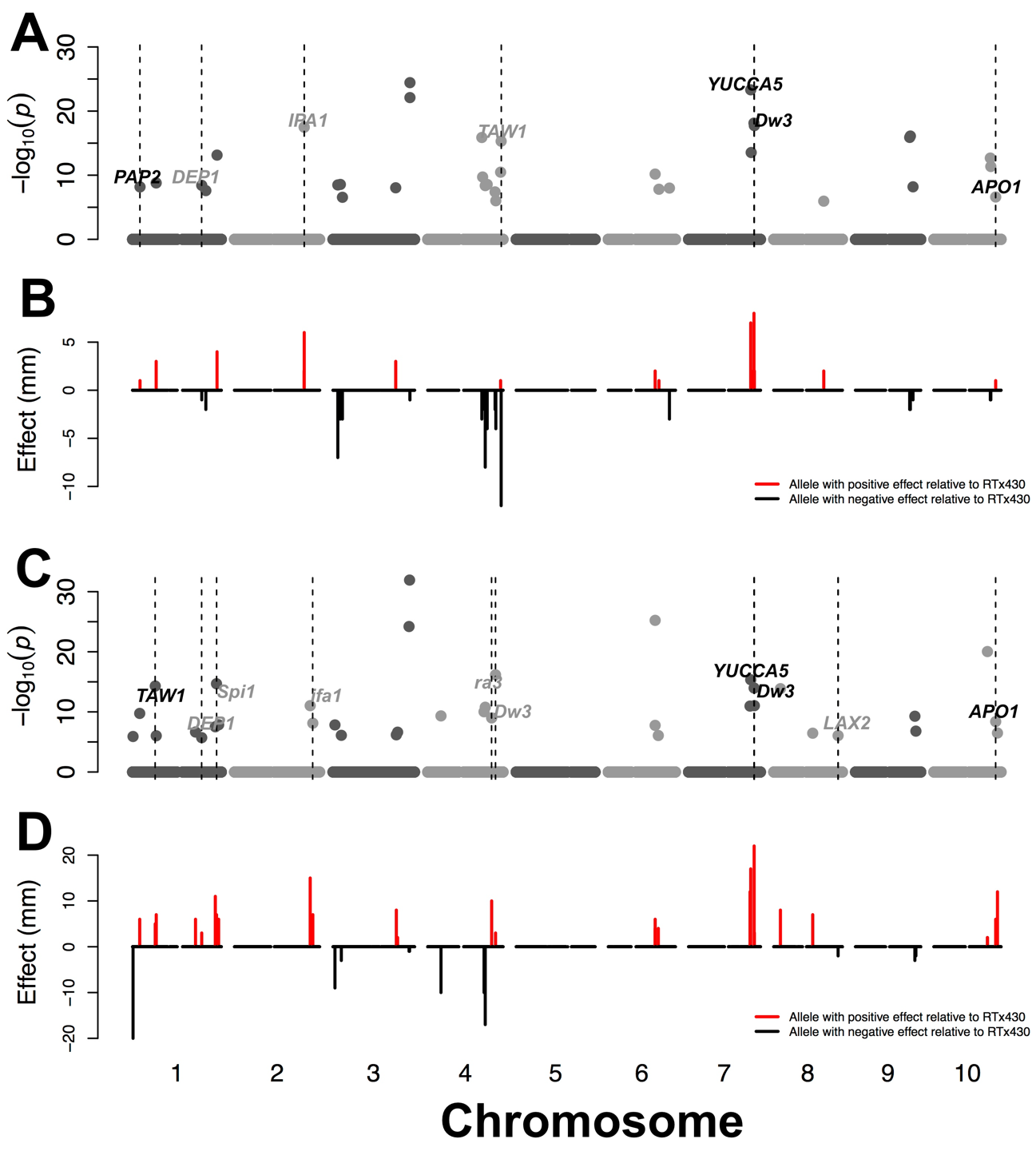


**Figure S1: Examples of variation in sorghum inflorescence morphology.**

(A) Open inflorescence morphology represented by SC1103 parent, (B) compact inflorescence morphology represented by Ajabsido parent, and (C) semi-compact inflorescence morphology as represented by RTx430 the common parent.

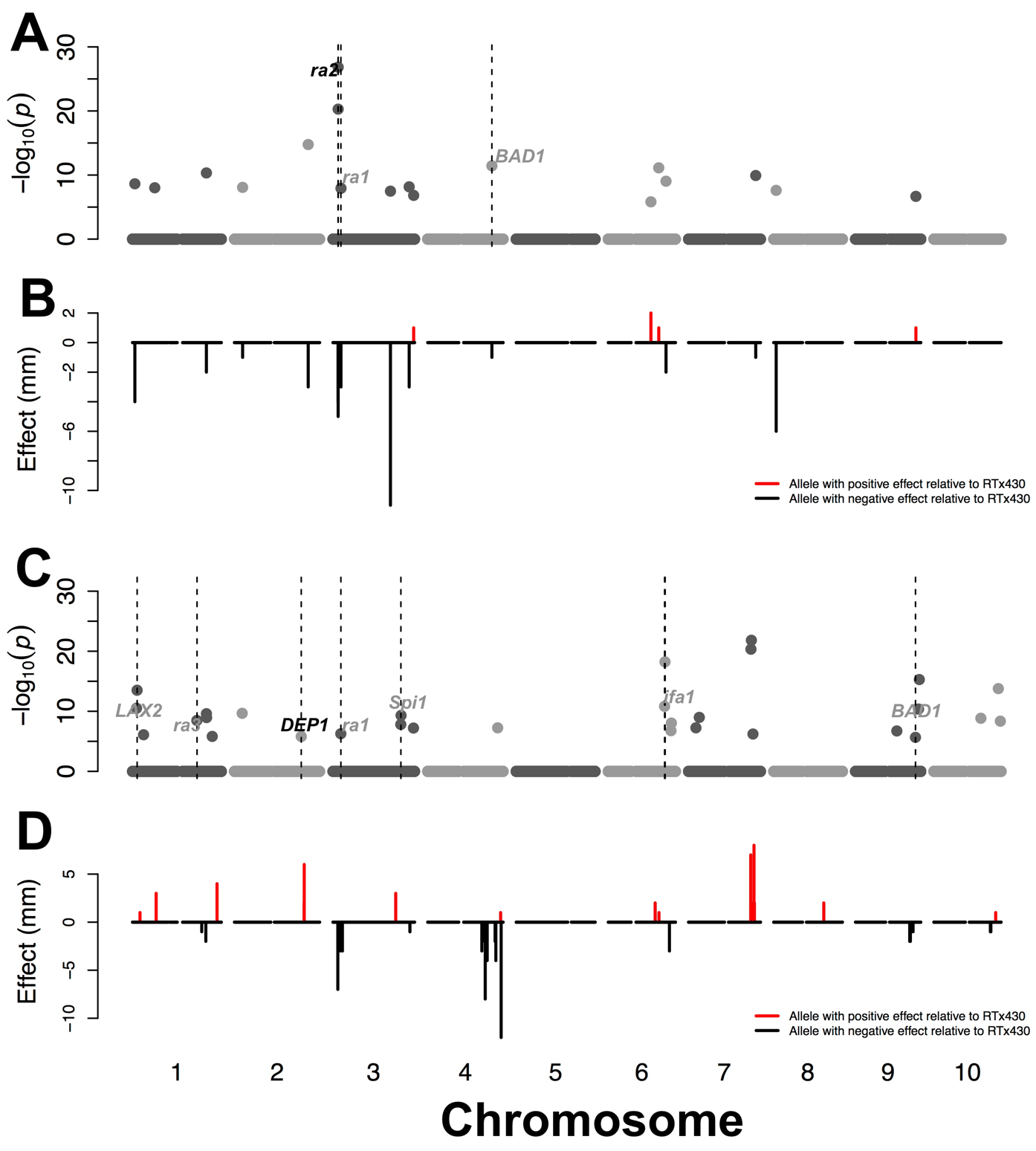


**Figure S2: Sorghum inflorescence morphology traits.**



**Figure S3: Details of joint linkage QTL mapping for lower branch length and rachis length.**

Genome positions of loci and loci additive effect associated with lower branch length (A and B) and rachis length (C and D). *A priori* candidate genes that colocalize with QTL within 150 kb are noted. Black text indicates putative sorghum orthologs of *a priori* candidate genes while gray text indicates paralogs.



**Figure S4: Details of joint linkage QTL mapping for upper branch length and rachis diameter.**

Genome positions of loci and loci additive effect for upper branch length (A and B) and rachis diameter (C and D). *A priori* candidate genes that colocalize with QTL within 150 kb are noted. Black text indicates putative sorghum orthologs of *a priori* candidate genes while gray text indicates paralogs.