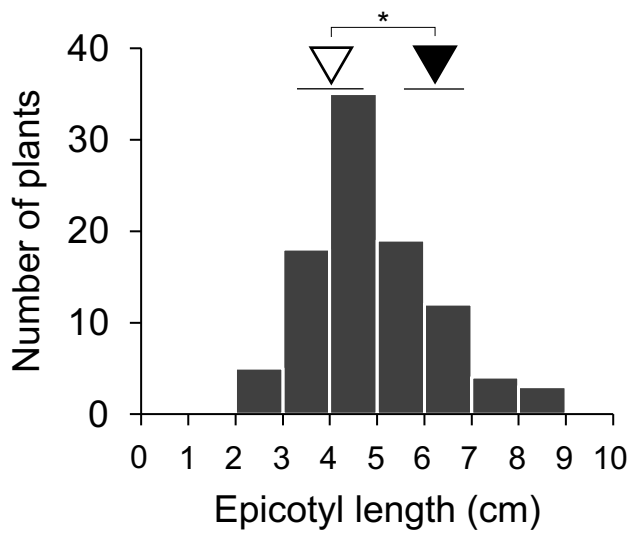


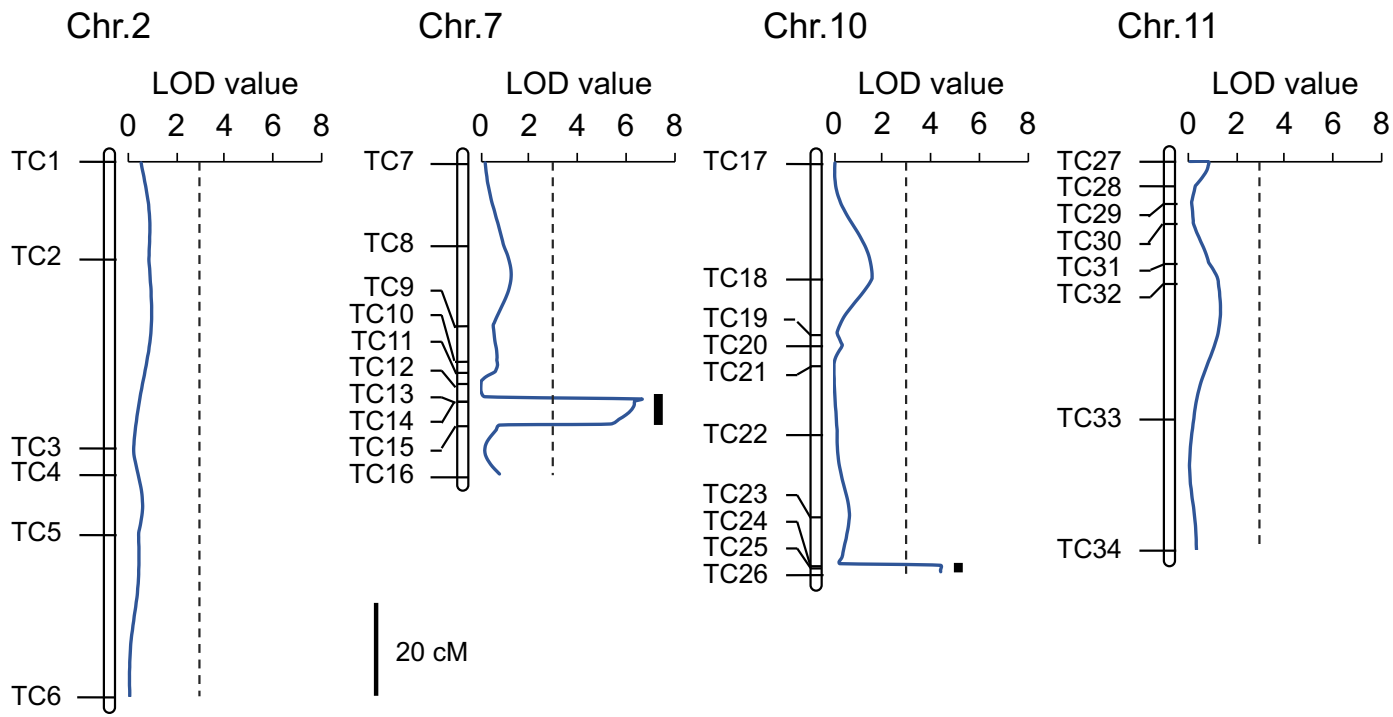
**Figure S1:** Manhattan plot for QTL-seq analysis of epicotyl length on adzuki bean chromosomes 1 to 11. Figure shows plots of the short and long epicotyl bulks on chromosome 1 to 11 and  $\Delta(\text{SNP-index})$  plot with confidence intervals under the null hypothesis of no QTLs (green,  $p < 0.05$ ; orange,  $p < 0.01$ )



F<sub>2</sub> population  
 range: 2.5-8.2  
 mean:  $4.7 \pm 1.3$

Chihayahime:  $4.0 \pm 0.7$   
 Toiku161:  $6.2 \pm 0.6$

**Figure S2:** Frequency distribution of ECL in the 96 F<sub>2</sub> population. *Arrowheads* represents parental means (T161 (*black*) and Chihayahime (*white*)), *vertical lines* represent standard deviation. \* indicate statistical confidence at  $p < 0.01$ .



**Figure S3:** Multiple QTL mapping for ECL QTLs. Linkage map constructed from 96 F<sub>2</sub> RILs. LOD curves are shown on the left (*blue*). The number above each linkage map indicate chromosome number. Marker names are indicated to the right side of each linkage map. Horizontal axis represent marker positions and vertical axis represent LOD score. *Black rectangles* represents the two LOD support factor for candidate region.