



Figure 2 Expression pattern analysis of CsTRM5 in cucumber (Adopted from Xie et al., 2023)

Image caption: A Expression levels of CsTRM5 in different organs of 32X line detected by qRT-PCR. B-H In situ hybridization of CsTRM5 in cucumber shoot tip (B), leaf (H), and floral organs (C-G). I, Negative control of CsTRM5 sense probe in fruit cross-section. Le, leaf; SAM, shoot apical meristem; FM, floral meristem; SP, sepal primordium; PP, petal primordium; Se, sepal; Pe, petal; St, stamen; Vb, vascular bundle; Pl, placenta; Ov, ovule; In, integument. Scale bars: 100 μ m (Adopted from Xie et al., 2023)

In studies of fruit size and fruit shape, multi-omics approaches have demonstrated significant advantages. RNA-seq analysis of FS5.2 near-isogenic lines identified hundreds of differentially expressed genes mainly enriched in auxin biosynthesis and signaling, cell cycle regulation, and cell wall formation, thereby establishing the CsCRC-mediated regulatory network controlling fruit size and shape. Comparative transcriptome analyses of early fruits from materials with different fruit lengths identified 3,955 differentially expressed genes, including numerous microtubule-related genes, cell cycle genes, and members of various transcription factor families, providing genome-wide evidence for fruit length regulation. In addition, combined analyses using QTL-seq, bin-map resequencing, and RNA-seq identified multiple major-effect fruit length QTLs and differentially expressed genes related to auxin efflux carriers and hormone signaling, thereby providing important evidence for candidate gene mining (Che et al., 2023; Xing et al., 2023). In studies of parthenocarp and stable fruit set, integrated transcriptomic and metabolomic analyses linked the GA biosynthesis gene CsGA20OX1 and hormone pathways with GA-mediated parthenocarpic fruit development, indicating that multi-omics integration can effectively identify key regulators controlling stable fruit set and yield formation (Meng et al., 2026). Moreover, continuous omics studies in cucumber have identified numerous candidate genes associated with fruit length, locule formation, parthenocarp, and fruit quality traits, thereby providing theoretical support for marker-assisted selection, genomic selection, and molecular design breeding.

The development of molecular breeding technologies is promoting the transition of cucumber yield improvement from empirical selection to precision breeding. Marker-assisted selection (MAS) can rapidly identify superior materials using markers tightly linked to target traits; genomic selection (GS) can predict breeding values of