

Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population

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Supplemental Figures

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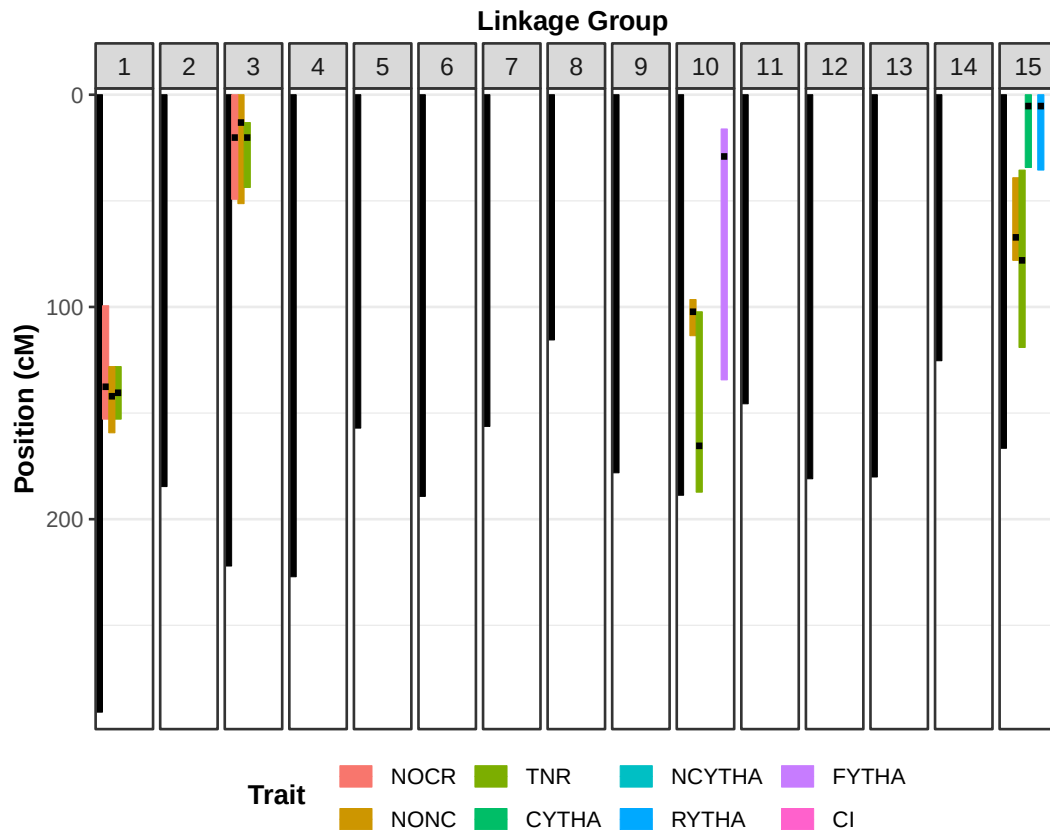


Figure S1 QTL support intervals from random-effect multiple interval mapping (REMIM) of yield-related traits from ‘Beauregard’ × ‘Tanzania’ (BT) full-sib family. Black dots represent the QTL peaks, and colored bars represent the ~95% support interval computed as $LOP - 1.5$. Trait abbreviations: number of commercial (NOCR), noncommercial (NONC) and total (TNR) roots per plant, commercial (CYTHA), noncommercial (NCYTHA) and total (RYTHA) root yield in $t \cdot ha^{-1}$, foliage yield (FYTHA) in $t \cdot ha^{-1}$, and commercial index (CI).

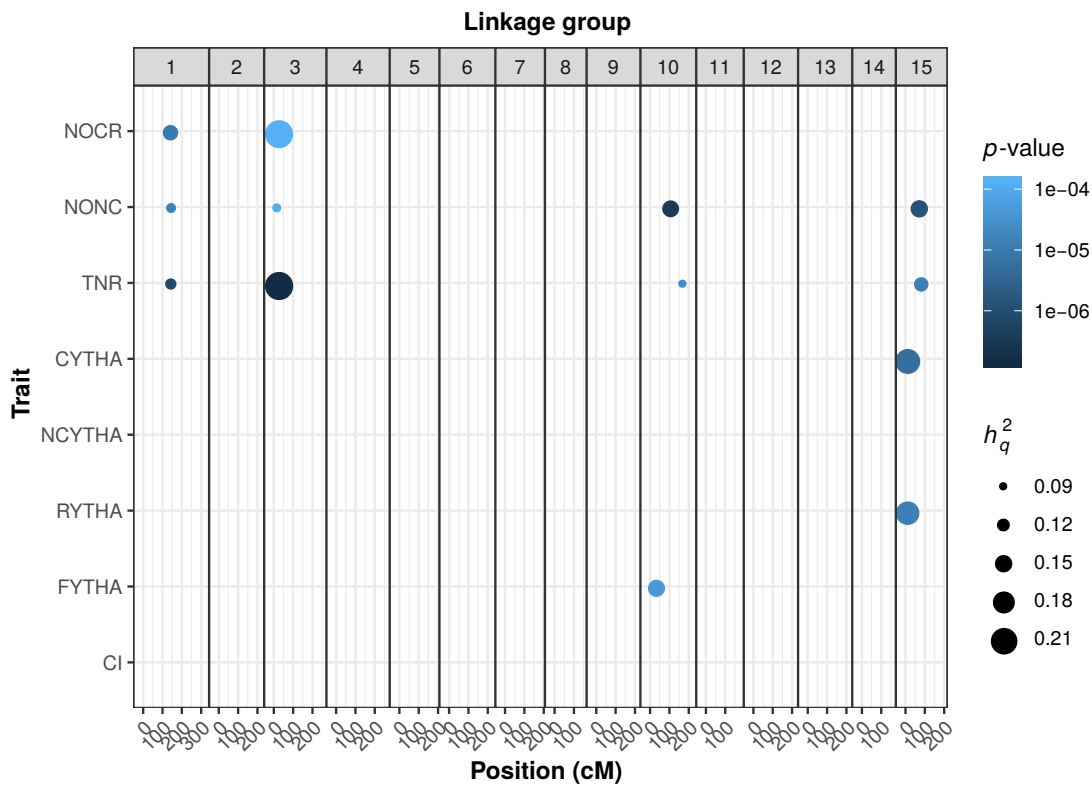


Figure S2 Score-based p -values and QTL heritabilities (h_q^2) from random-effect multiple interval mapping (REMIM) of eight yield-related traits from ‘Beauregard’ \times ‘Tanzania’ (BT) full-sib family. Dots are positioned relative to the QTL peaks: color gradient represents the p -values, while sizes are proportional to heritabilities of mapped QTL. Trait abbreviations: number of commercial (NOCR), noncommercial (NONC) and total (TNR) roots per plant, commercial (CYTHA), noncommercial (NCYTHA) and total (RYTHA) root yield in $\text{t} \cdot \text{ha}^{-1}$, foliage yield (FYTHA) in $\text{t} \cdot \text{ha}^{-1}$, and commercial index (CI).

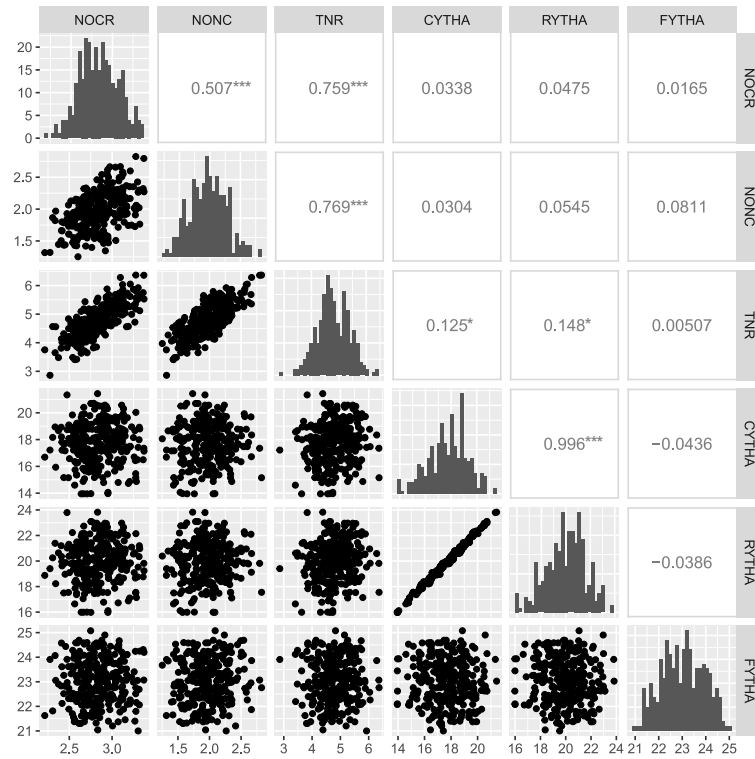
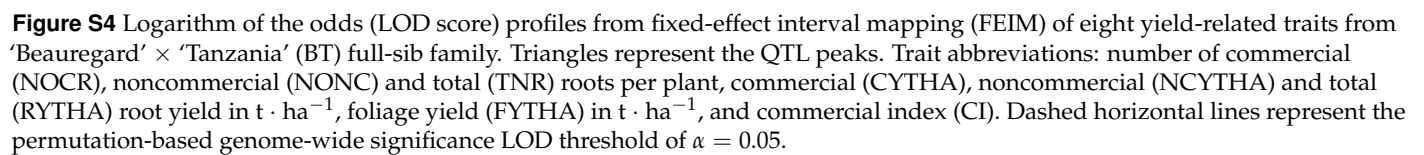


Figure S3 Pearson's correlations ($*p < 0.05$, $***p < 0.001$) among QTL-based breeding values for eight yield-related traits from 'Beauregard' \times 'Tanzania' (BT) full-sib family. Trait abbreviations: number of commercial (NOCR), noncommercial (NONC) and total (TNR) roots per plant, commercial (CYTHA), noncommercial (NCYTHA) and total (RYTHA) root yield in $\text{t} \cdot \text{ha}^{-1}$, foliage yield (FYTHA) in $\text{t} \cdot \text{ha}^{-1}$, and commercial index (CI).



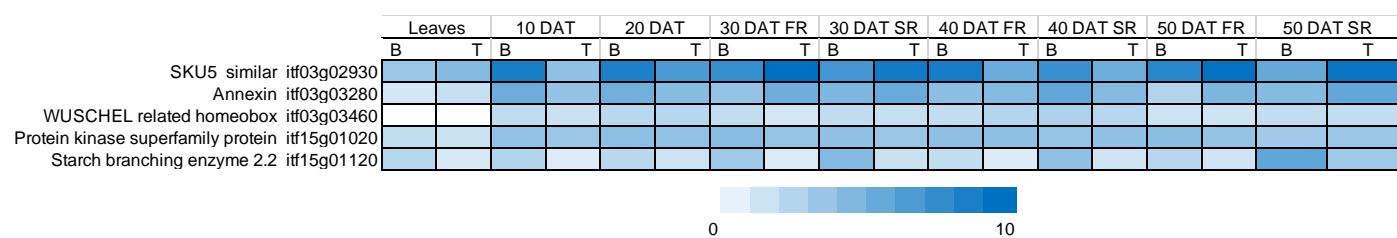


Figure S5 Heatmap with expression abundances in fragments per kilobase exon model per million mapped reads (FPKM, \log_2 -transformed) for five genes in leaves and roots of 'Beauregard' (B) and 'Tanzania' (T). DAT: days after transplanting. SR: storage roots. FR: fibrous roots.