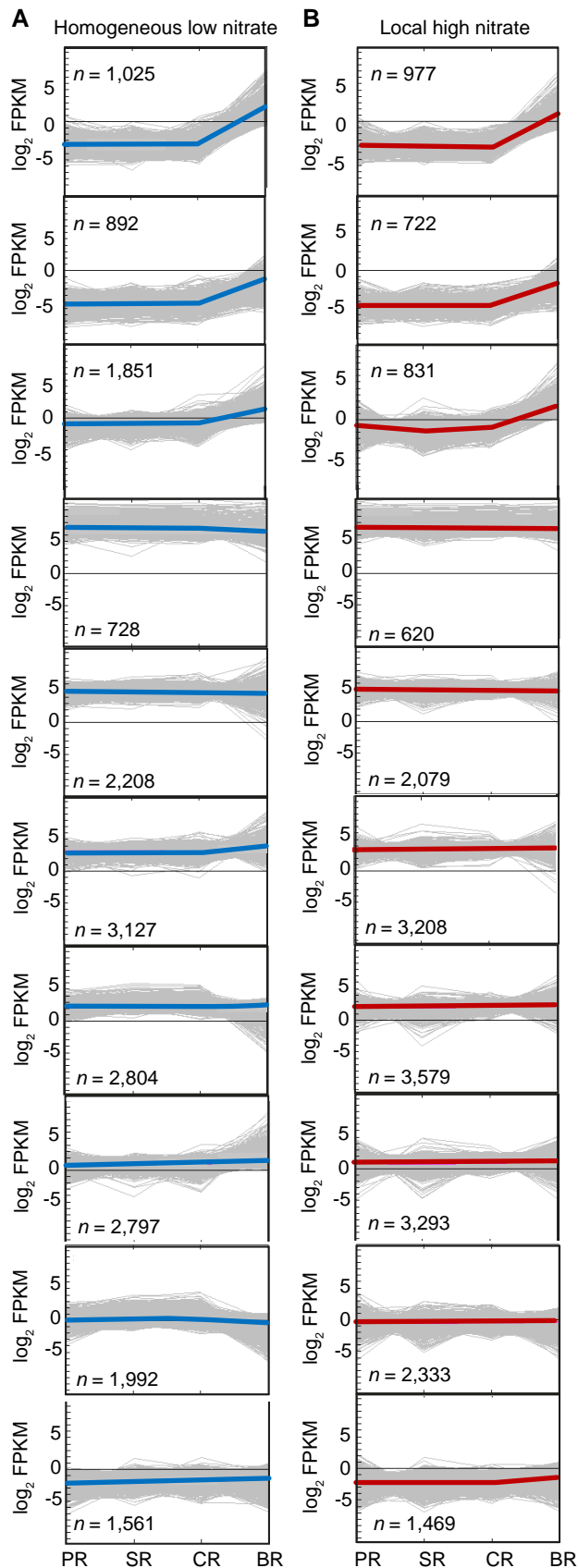
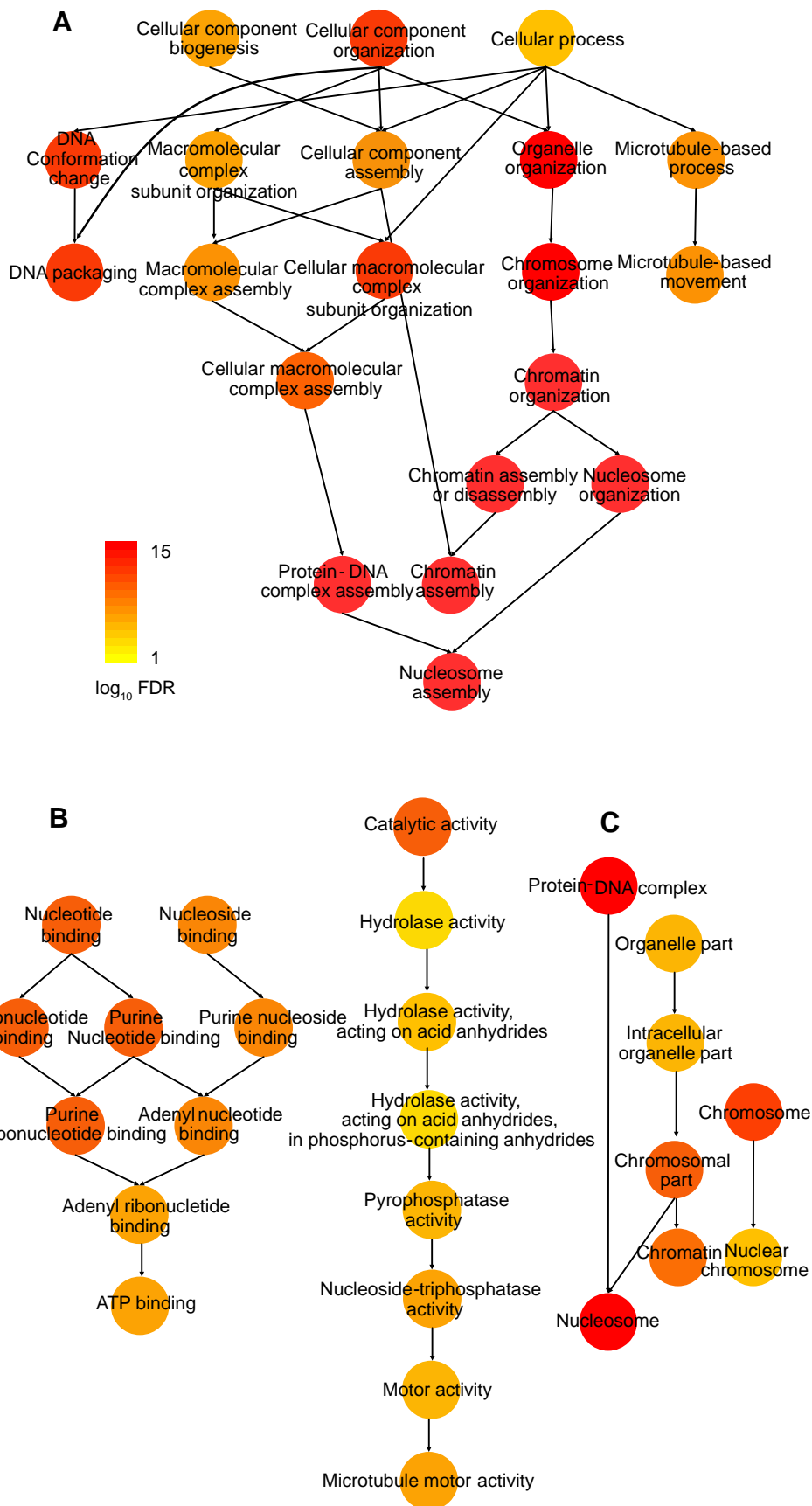


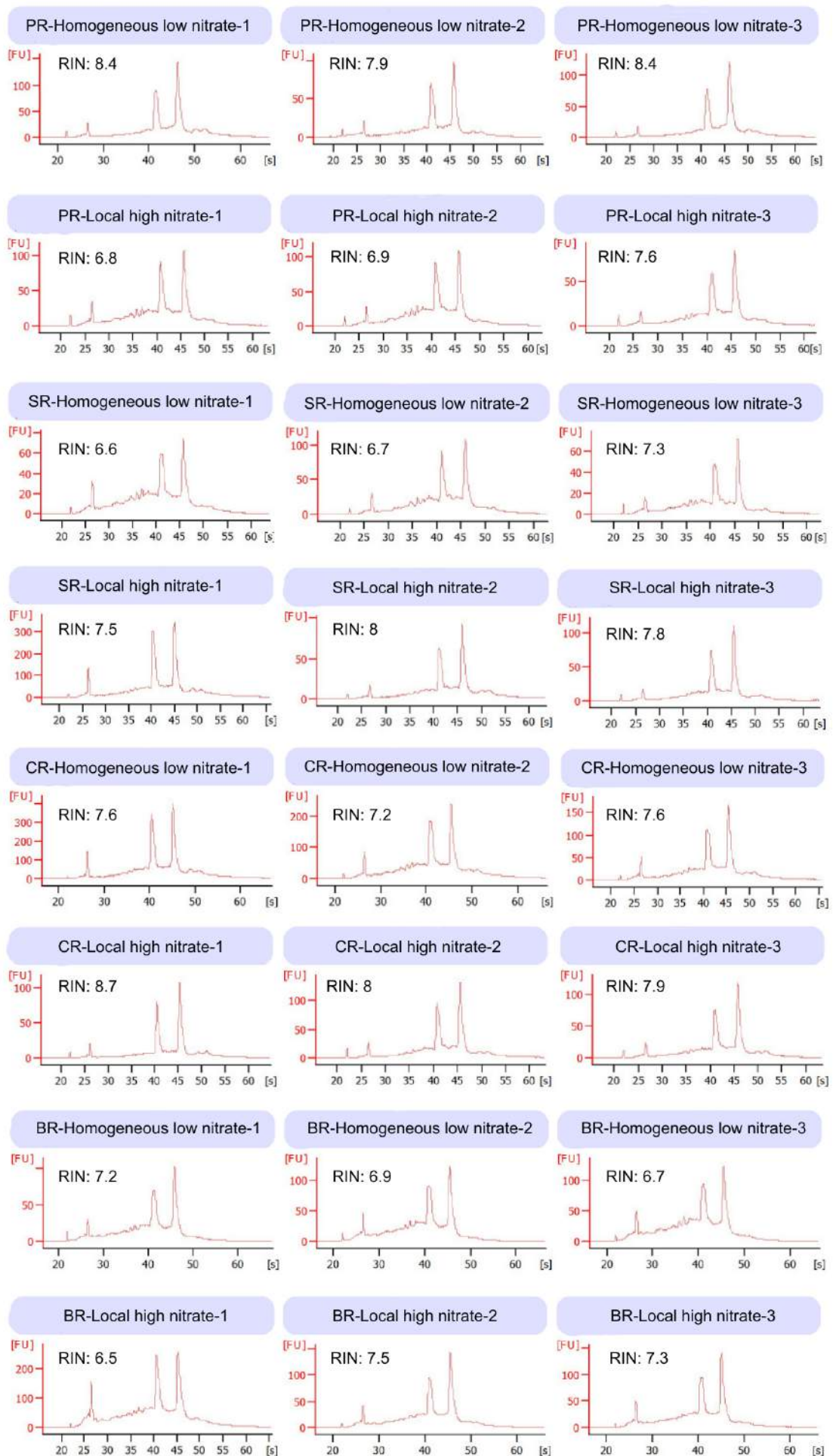
Supplemental Figure S1. Transverse sections at a distance of 3 mm from the tip of the four root types (A, primary root; B, seminal root; C, crown root; D, brace root). Pe, pericycle; En, endodermis; Co, cortex; X, xylem vessel.



Supplemental Figure S2. Expression patterns of the pericycle transcriptomes of the four maize root types using K-means clustering based on the expression (\log_2 FPKM transformed) of 18,985 expressed genes under (A) homogeneous low nitrate and (B) 19,111 expressed genes under local high nitrate conditions. Blue or red lines showing overall expression trends across the four maize roots types (PR, primary root; SR, seminal root; CR, crown root; BR, brace root). The numbers of all expressed genes that follow similar absolute values of Euclidean distance were indicated and clustered as an expression pattern. The K-means Support module (KMS) embedded in the MEV program (<http://www.tm4.org/mev>) was used to generate clusters.



Supplemental Figure S3. Simplified hierarchical tree graphs of overrepresented GO terms obtained by singular enrichment analyses (SEA) on 2,740 genes which displayed differential expression upon local high nitrate stimulation compared to homogeneous low nitrate exclusively in brace roots. (A) biological process, (B) molecular function and (C) cellular component. SEA was performed with agriGO and GO terms were declared enriched when $FDR < 0.001$. Circles in the graphs represent GO terms labelled by term definition and were colored according to significance levels normalized by the $\log_{10} FDR$ algorithm. The degree of color saturation of a circle is positively correlated to its enrichment level.



Supplemental Figure S4. Quality assessment of the 24 LCM-dissected cell samples used for RNA-sequencing. RIN represents the RNA integrity number as a measure of RNA quality (Agilent Technologies). PR, primary root; SR, seminal root; CR, crown root; BR, brace root.