

The following Supporting Information is available for this article:

Fig. S1 Replication information for the three biological replicates of rhizome meristem (RHI)

tissue, showing A) the sum of fragments for each replicate, B) 1:1 scatterplots of transcript

abundance for all pairwise comparisons of the replicates, C) MA plots (Bland Altman plot) for all

pairwise comparisons of the replicates, and D) the correlation coefficients between all

replicates.

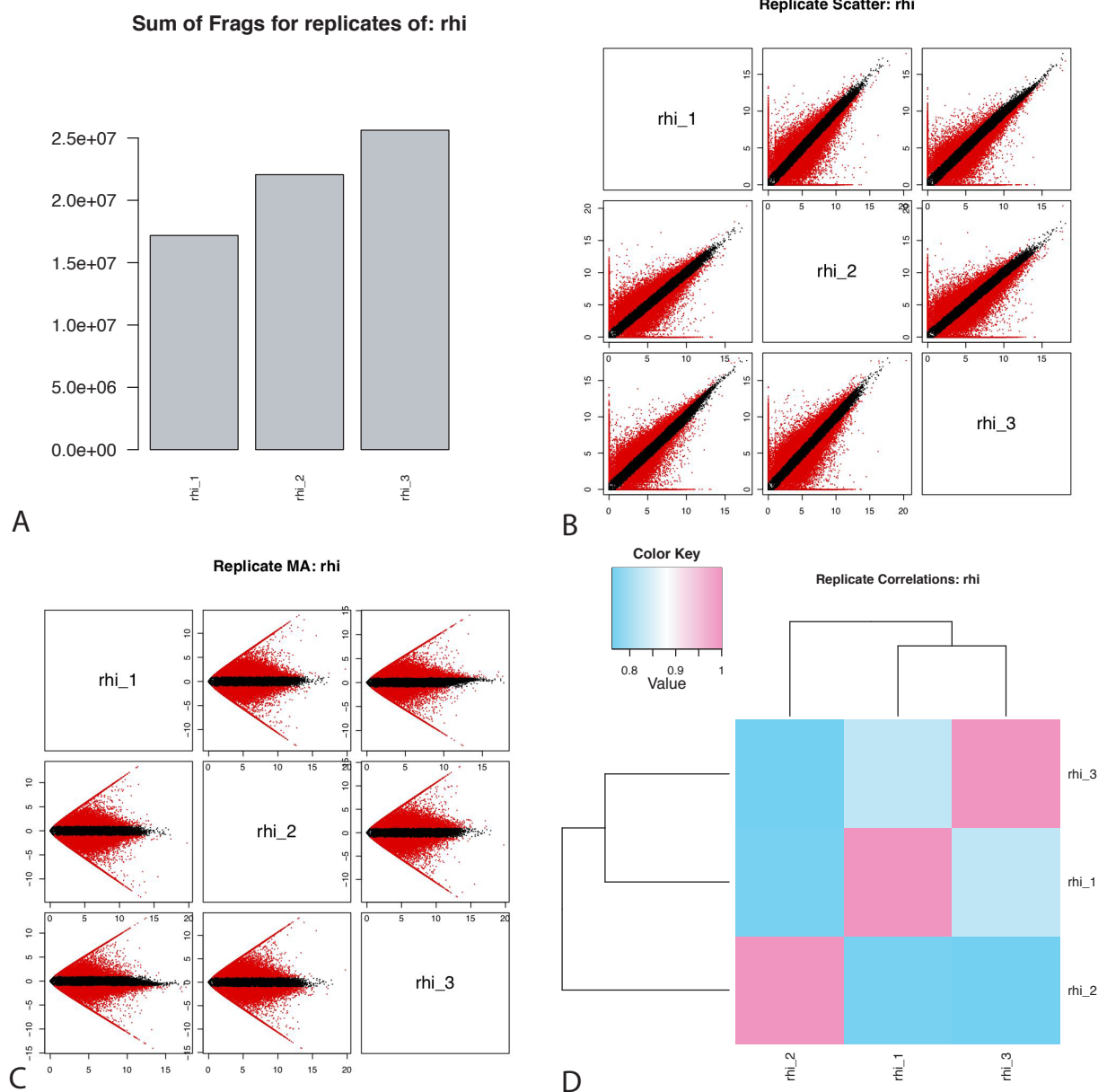


Fig. S2 Replication information for the three biological replicates of root apical meristem (ROO) tissue, showing A) the sum of fragments for each replicate, B) 1:1 scatterplots of transcript abundance for all pairwise comparisons of the replicates, C) MA plots (Bland Altman plot) for all pairwise comparisons of the replicates, and D) the correlation coefficients between all replicates.

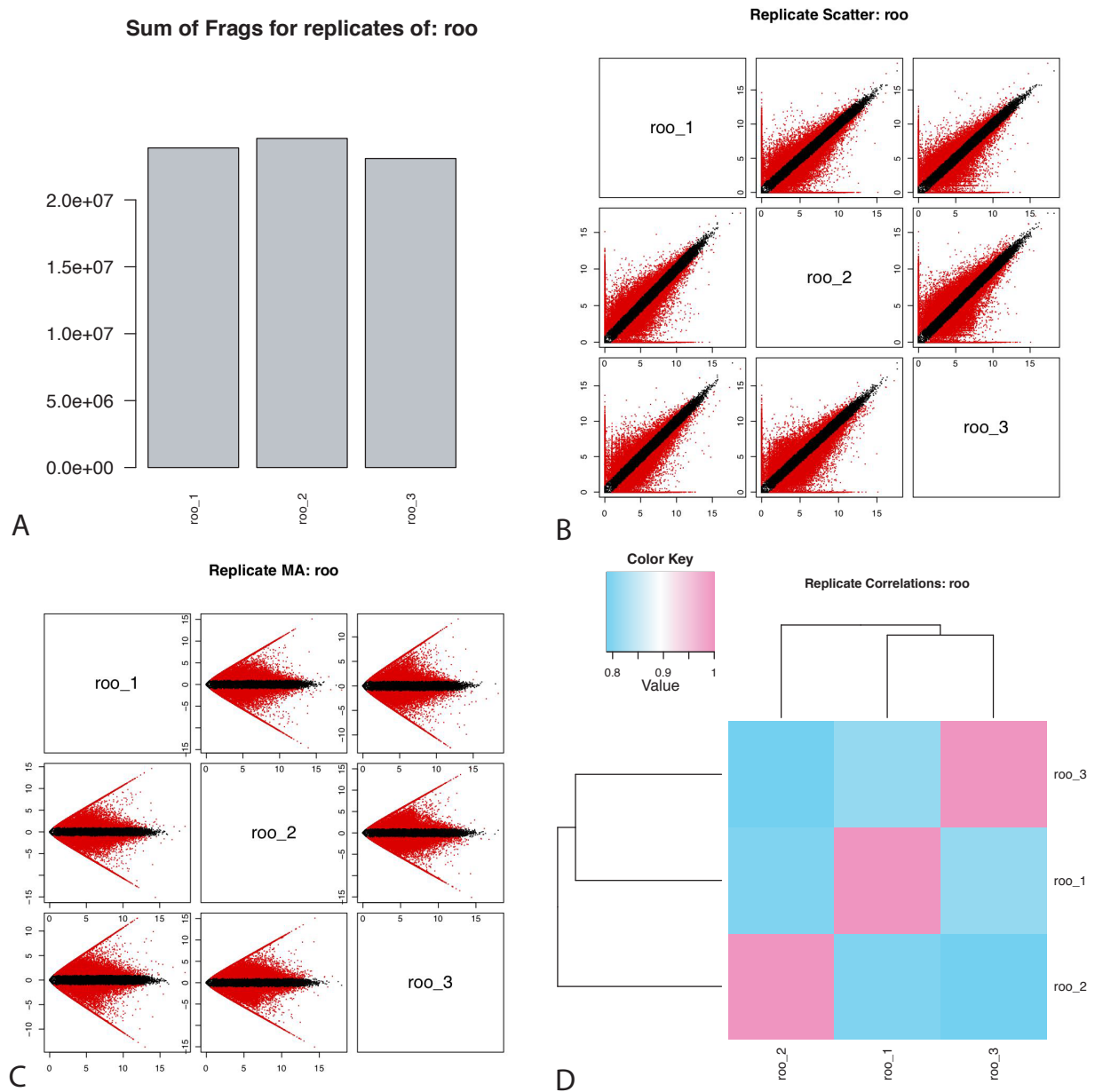


Fig. S3 Replication information for the three biological replicates of shoot apical meristem

(SAM) showing A) the sum of fragments for each replicate, B) 1:1 scatterplots of transcript abundance for all pairwise comparisons of the replicates, C) MA plots (Bland Altman plot) for all pairwise comparisons of the replicates, and D) the correlation coefficients between all replicates.

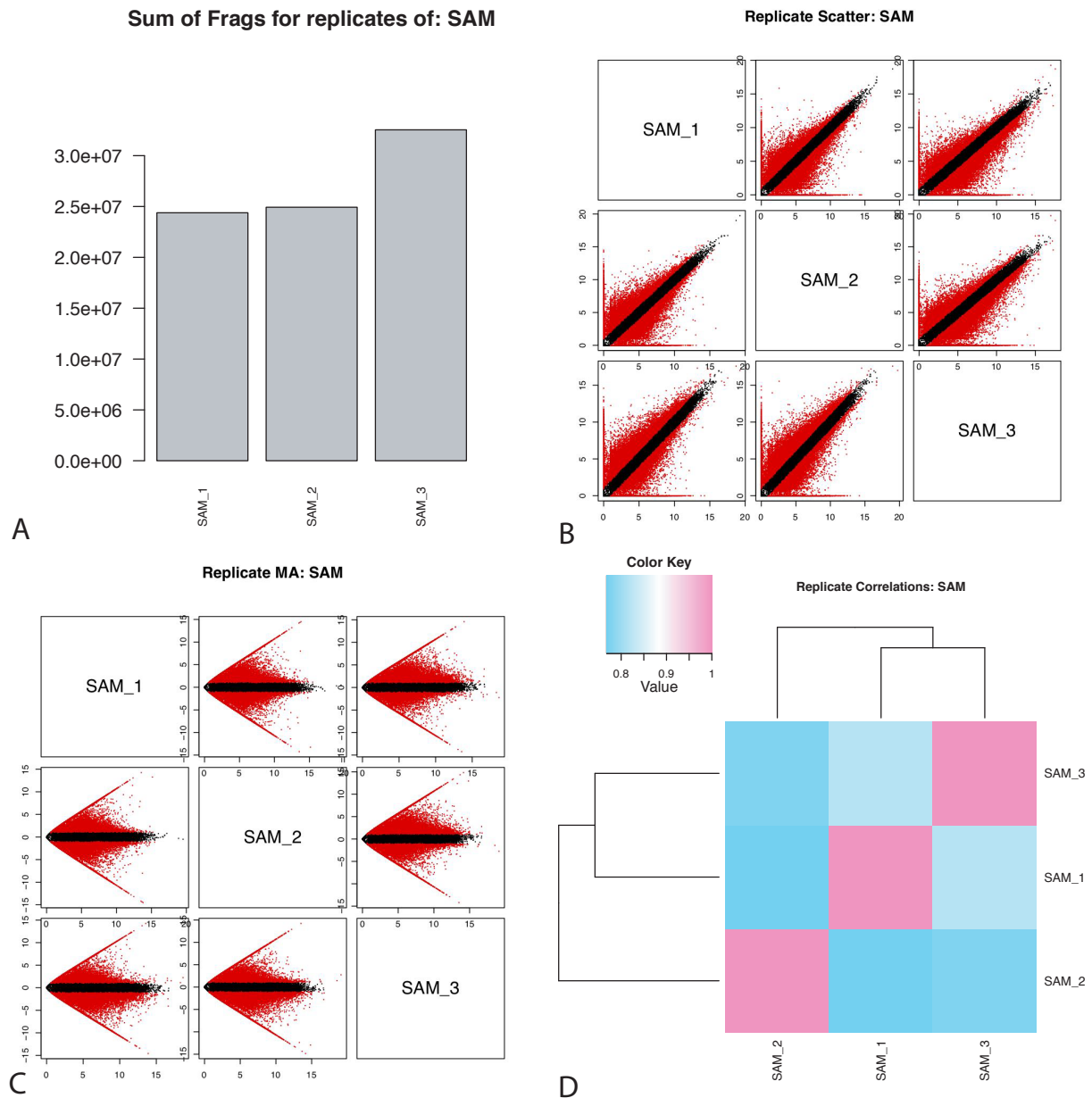


Fig. S4 Replication information for the three biological replicates of tuber tissue (TUB) showing A) the sum of fragments for each replicate, B) 1:1 scatterplots of transcript abundance for all

pairwise comparisons of the replicates, C) MA plots (Bland Altman plot) for all pairwise comparisons of the replicates, and D) the correlation coefficients between all replicates.

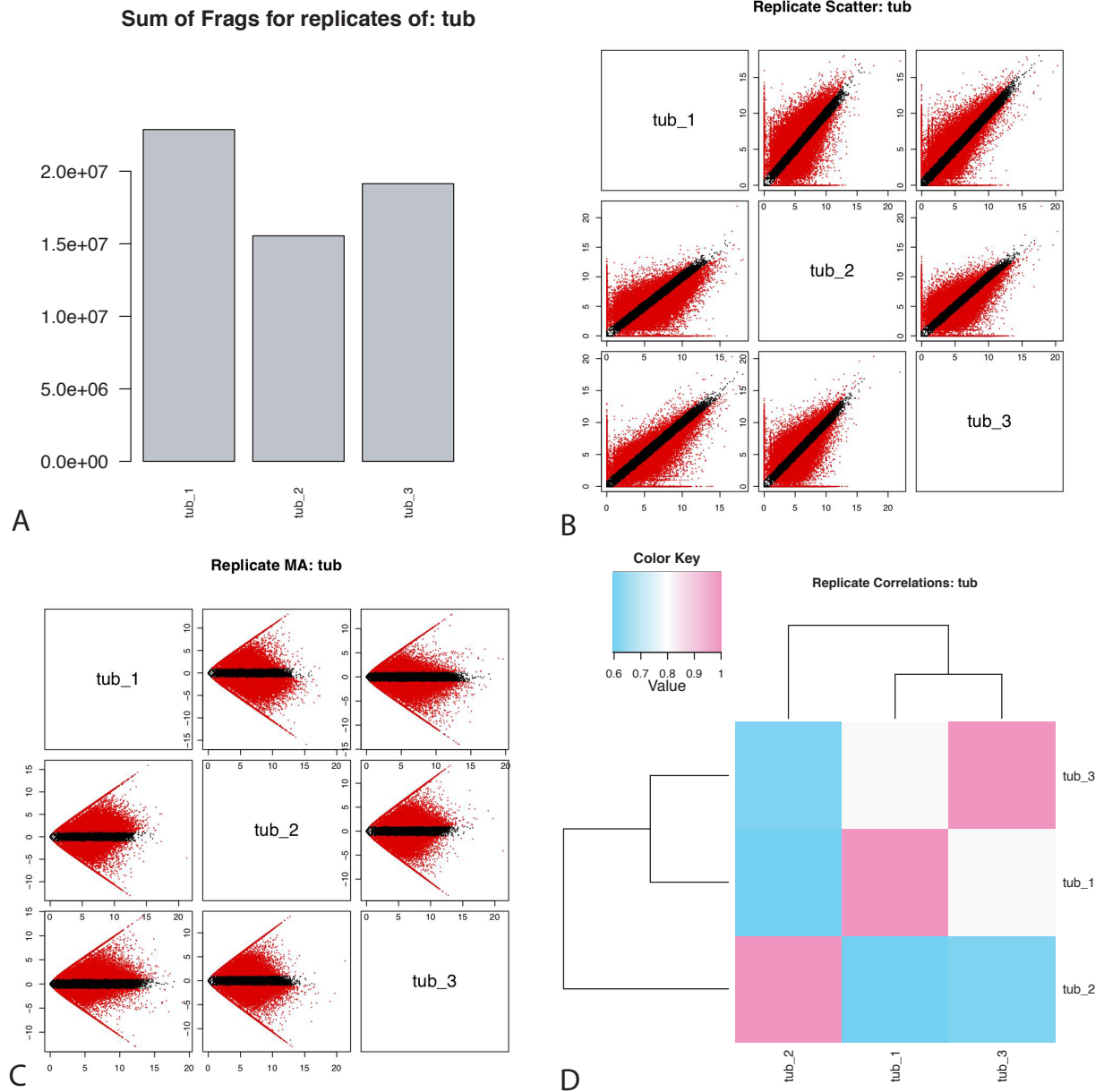


Table S1 Search terms used to identify isoforms in candidate gene groups. We queried the annotated transcriptome using R's `grep()` function to identify the isoforms and then checked their expression levels in the RSEM data using `deseq2`.

Gene Group	Search Term	Search Column	No. Isoforms
Starch	GO:0019252	gene_ontology_blast	168
Cytokinin	GO:0009735	gene_ontology_blast	356
Abscisic Acid	GO:0009737	gene_ontology_blast	1357
Auxin	GO:0009733	gene_ontology_blast	716
MADS-Box	MADS-box	sprot_Top_BLASTX_hit	116
KNOX	KNOX	Pfam	18
Gibberellin	GO:0009739	gene_ontology_blast	295
Expansins	Expansin	sprot_Top_BLASTX_hit	117
Lignin	GO:0009809	gene_ontology_blast	325
14-3-3 genes	14-3-3-like protein	sprot_Top_BLASTX_hit	62
CDPK	Calcium-dependent protein kinase	sprot_Top_BLASTX_hit	180

Table S2 To identify the expression levels of isoforms corresponding to specific candidate genes, we blasted amino acid sequences of the specific candidate gene to a blast-database of the assembled transcriptome.

Candidate Gene	Source	Accession Number	Taxon
FT-like	GenBank	AGZ20207.1	<i>Allium cepa</i>
FT-like	GenBank	AGZ20210.1	<i>Allium cepa</i>
FT-like	SPROT	tr M1C558 M1C558_SOLTU	<i>Solanum tuberosum</i>
Sulfite reductase	GenBank	AAC24584.1	<i>Prunus armeniaca</i>
WOX4	SPROT	sp Q6X7J9 WOX4_ARATH	<i>Arabidopsis thaliana</i>
OsbHLH120	SPROT	tr Q67TR8 Q67TR8_ORYSJ	<i>Oryza sativa</i>
IDD5	SPROT	sp Q9ZUL3 IDD5_ARATH	<i>Arabidopsis thaliana</i>

Table S3 All 271 differentially expressed isoforms, including their full annotation information and differential expression data (see attached excel spreadsheet).