



Article

Paraburkholderia tropica primes a multilayered transcriptional defense response to the nematode *Meloidogyne* spp. in tomato

Carolina González-Cardona ¹, Walter Ricardo López ², Juan Jovel ^{1,3}, Mauricio Soto-Suárez ^{1,4} and Nelson Ceballos-Aguirre ^{1*}

¹ Universidad de Caldas. Doctorado en Ciencias Agrarias, Facultad de Ciencias Agropecuarias. Calle 65 No. 26-10, 170003. Manizales, Caldas, Colombia carolina.gonzalez@ucaldas.edu.co, nelson.ceballos@ucaldas.edu.co

² Universidad Nacional de Colombia sede Manizales. Departamento de Física y Química. Facultad de Ciencias Naturales. Km 9 vía aeropuerto La Nubia 170003, Manizales, Caldas, Colombia. wrlopez@unal.edu.co

³ University of Calgary. Faculty of Veterinary Medicine. Cal Wenzel Precision Health Building, CWPH 1E08, Calgary, AB T2N 4Z6. Canadá. juan.jovel@ucalgary.ca

⁴ Corporación Colombiana de Investigación Agropecuaria-AGROSAVIA. Km 14 Vía, Mosquera, Bogotá, 250047, Mosquera, Cundinamarca, Colombia. msoto@agrosavia.co

* Correspondence: author: nelson.ceballos@ucaldas.edu.co

Supplementary Materials

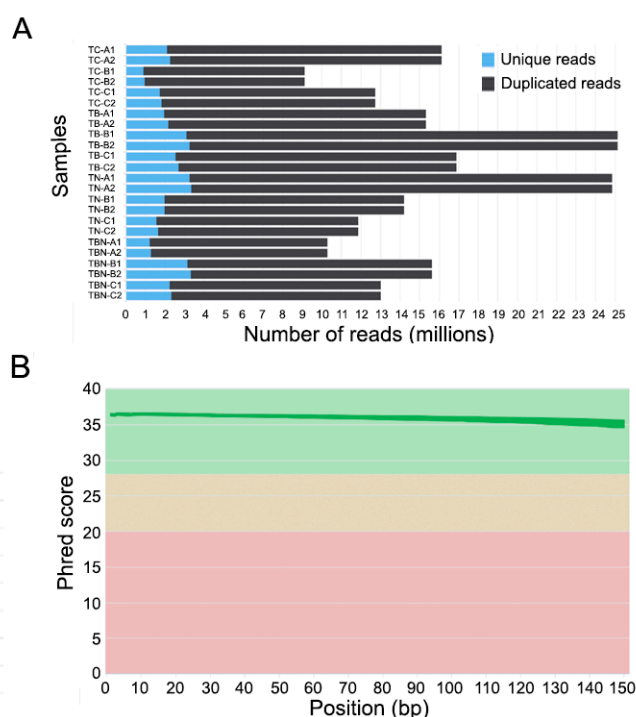


Figure S1. Size and quality of NGS libraries. (A) Number of total reads and unique library and end. (B) Average quality of reads before trimming.

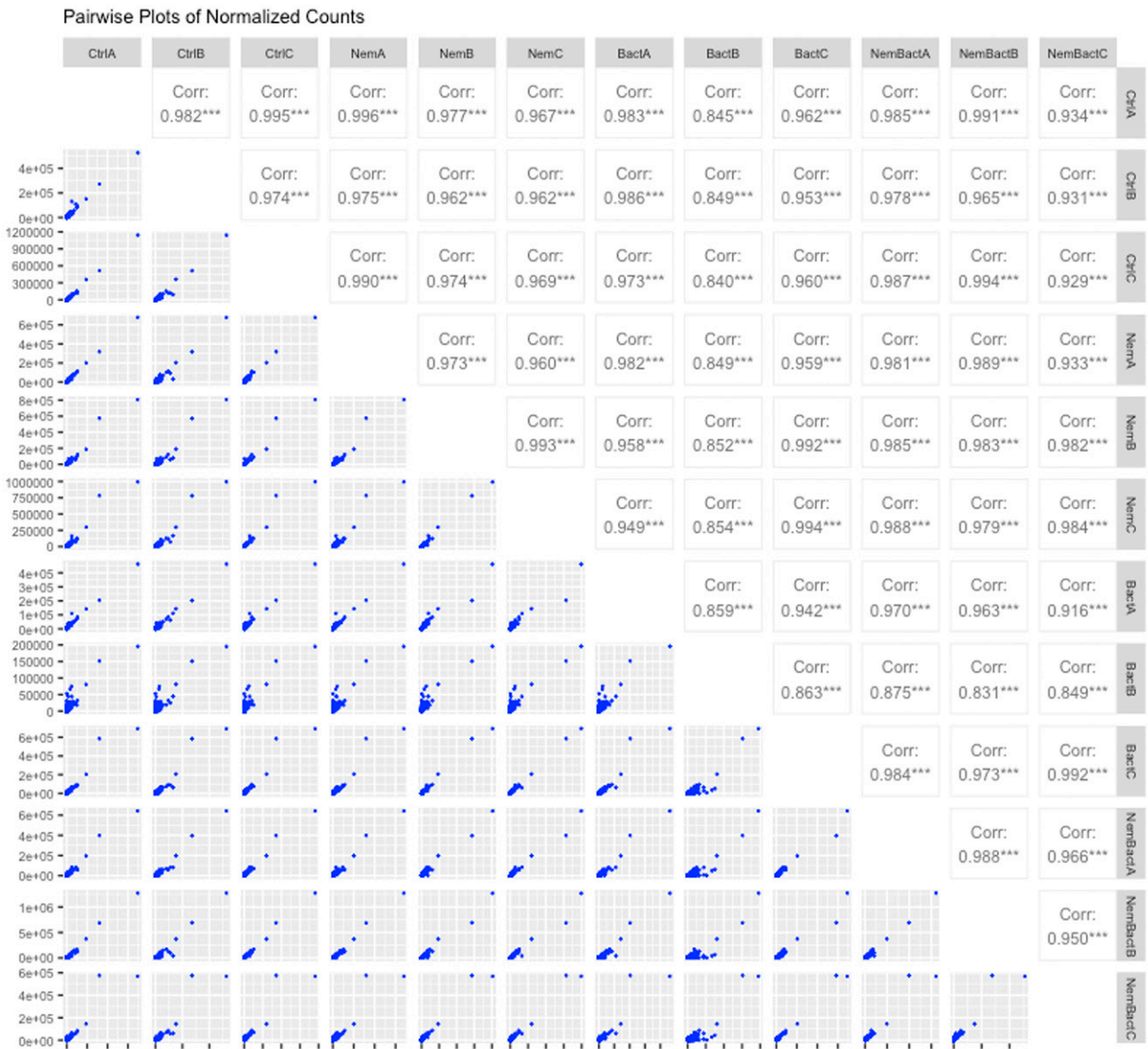


Figure S2. Correlation coefficients of gene counts for all libraries sequenced. Counts for all genes were plotted in a pairwise manner (each sample against all other samples). Correlation coefficients greater than 0.8 and 0.9 are considered good and excellent quality libraries, respectively.

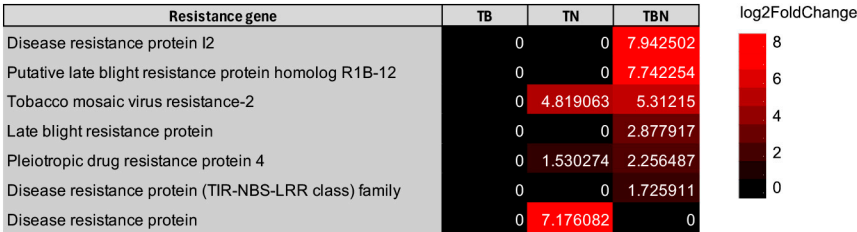


Figure S3. Heatmap with name and fold change of DE transcripts derived from resistance genes.

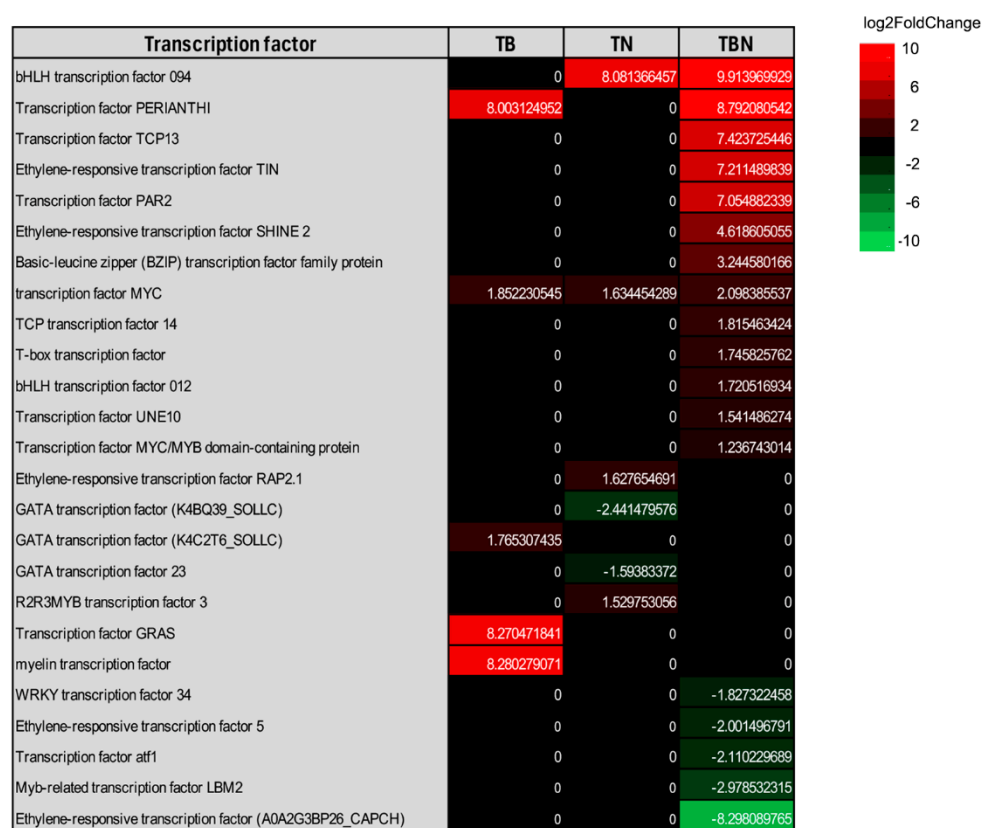


Figure S4. Heatmap with name and fold change of DE transcripts encoding transcription factors.

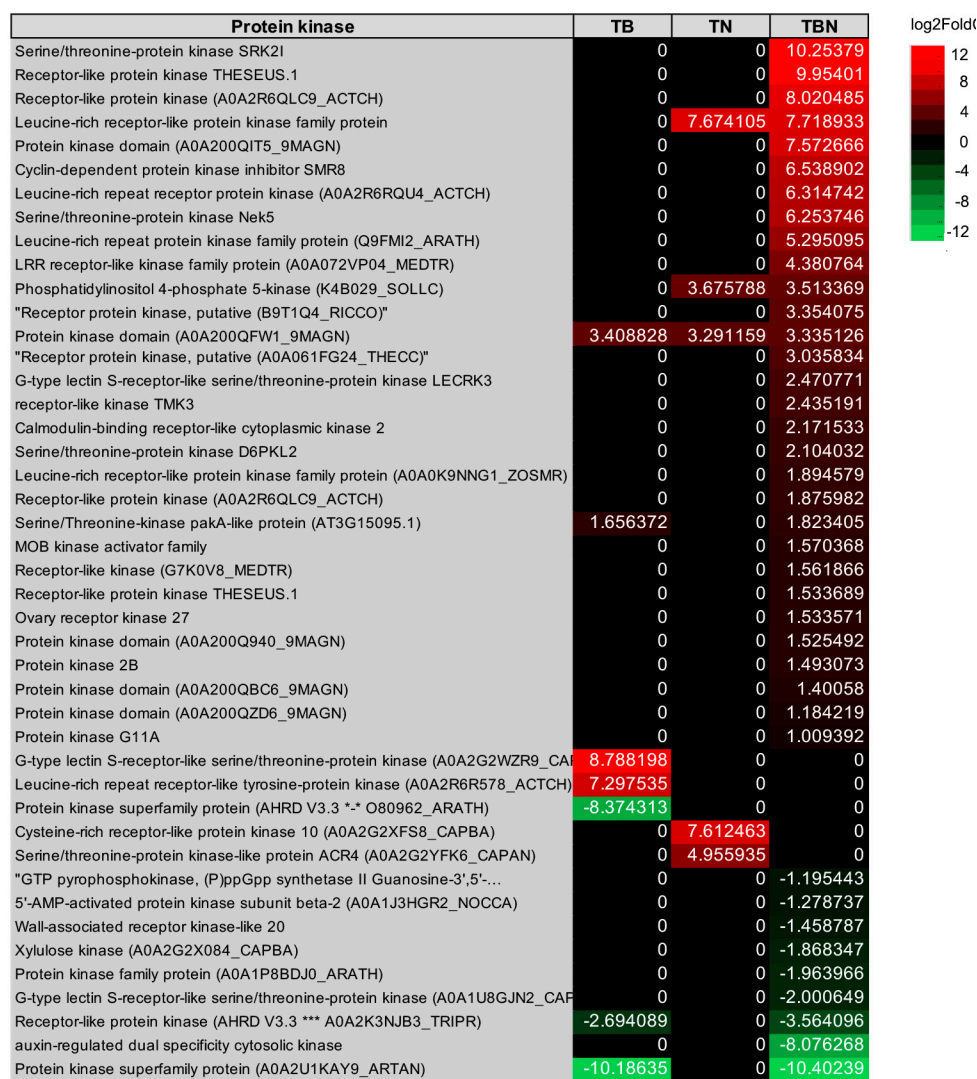


Figure S5. Heatmap with name and fold change of DE transcripts encoding protein kinases.

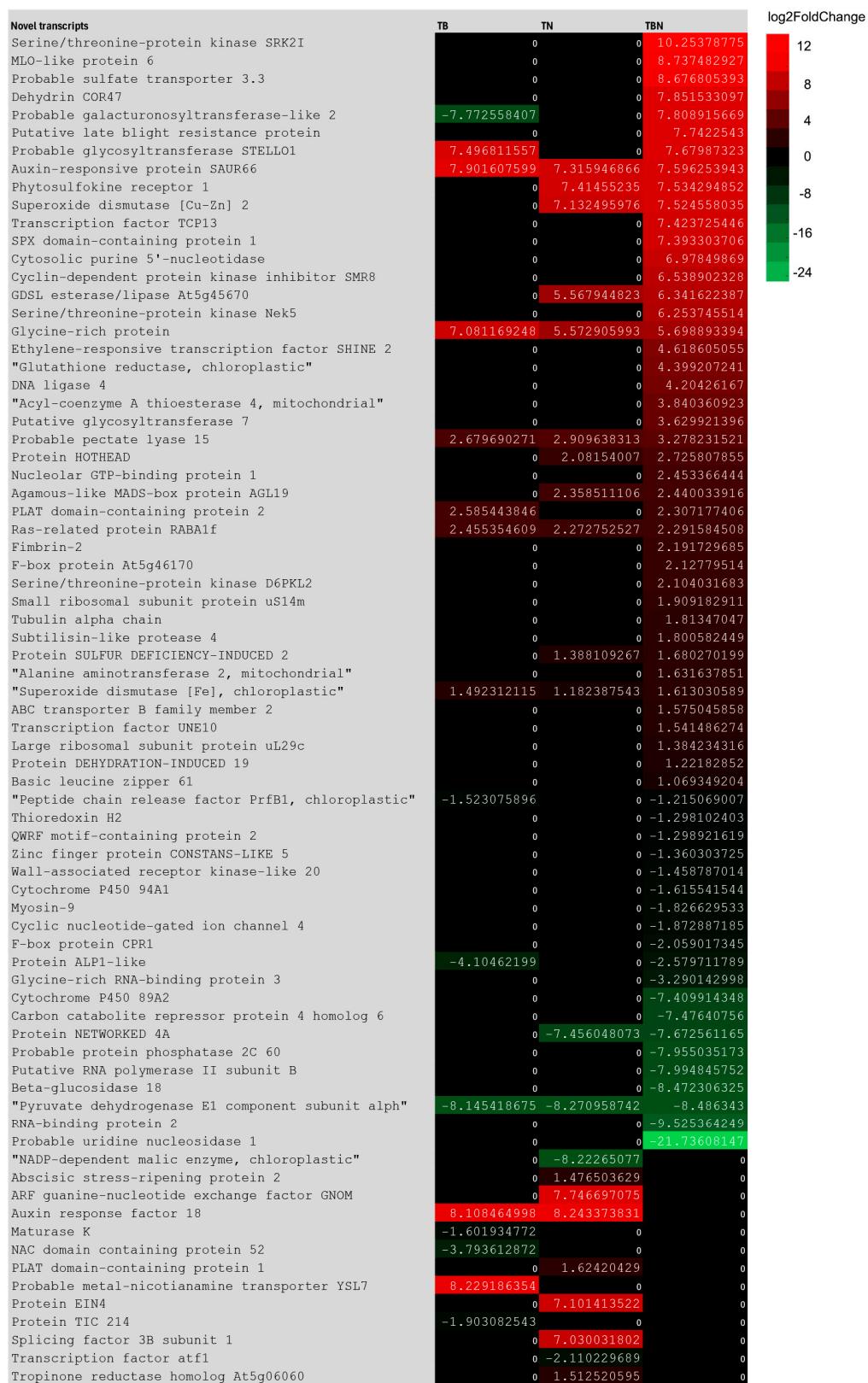


Figure S6. Heatmap with name and fold change of DE putative novel transcripts.

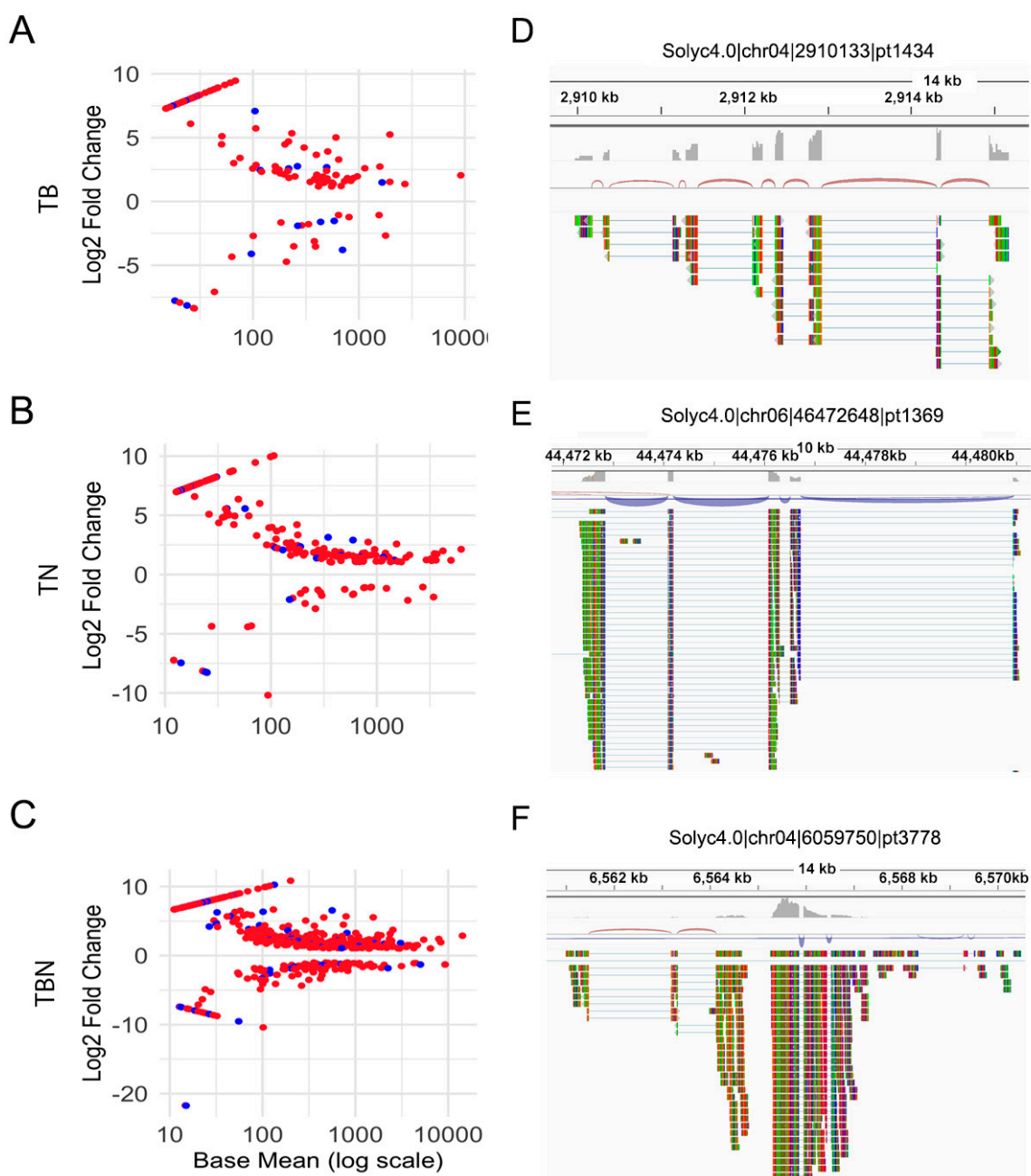


Figure S7. Supporting evidence for putative novel transcripts. MA plot depicting base mean and log₂fold change for TB (A), TN (B) and TBN (C). Red dots represent transcripts in the reference transcriptome, blue dots represent putative novel transcripts. Examples of spliced alignment of putative novel transcripts for TB (D), TN (E) and TBN (F).

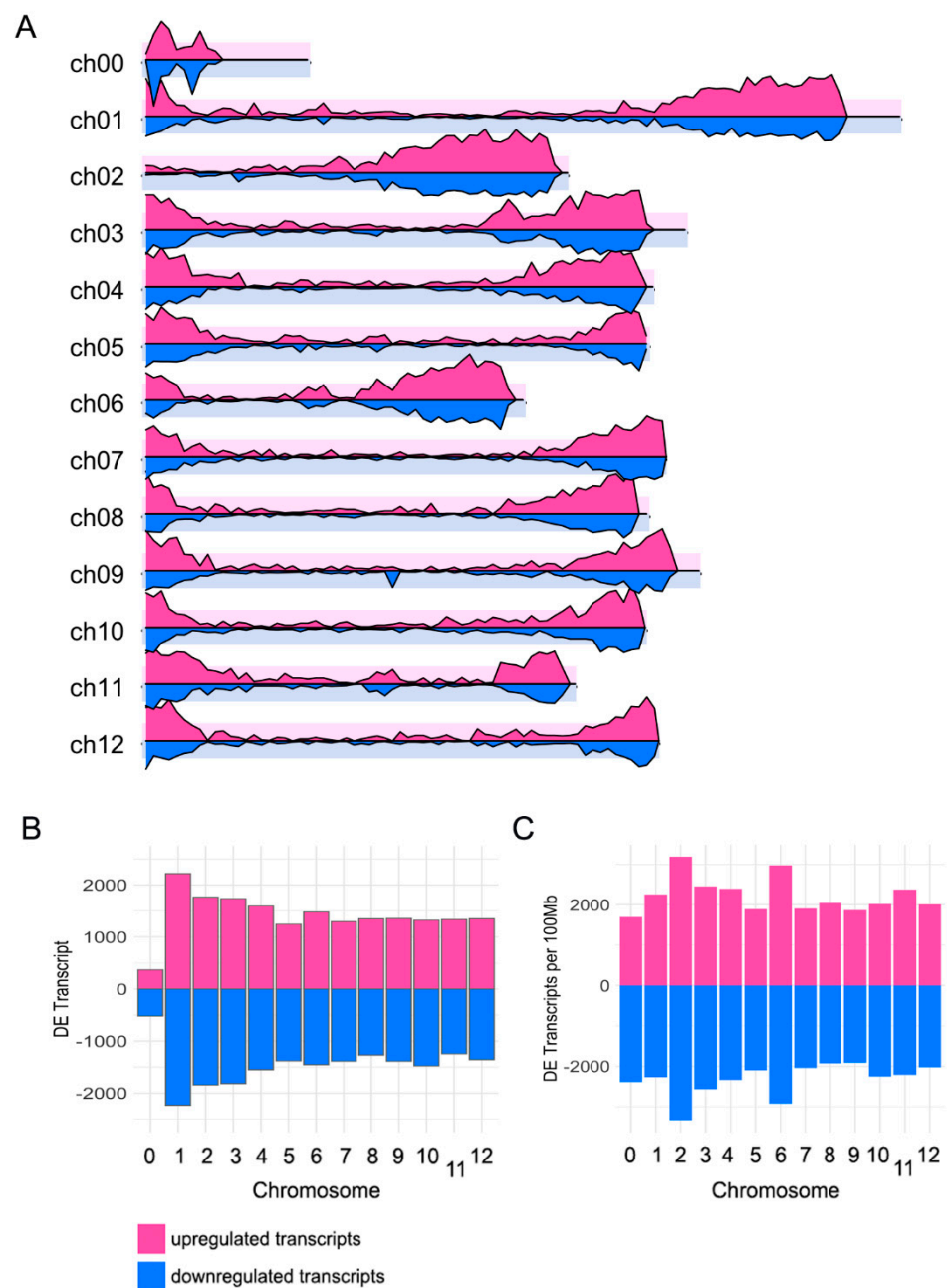


Figure S8. Distribution of transcripts along the tomato genome. (A) Density plot of all transcripts of tomato along the genome. (B) Counts of transcripts per chromosome. (C) Normalized (per 100 mB) number of transcripts per chromosome.

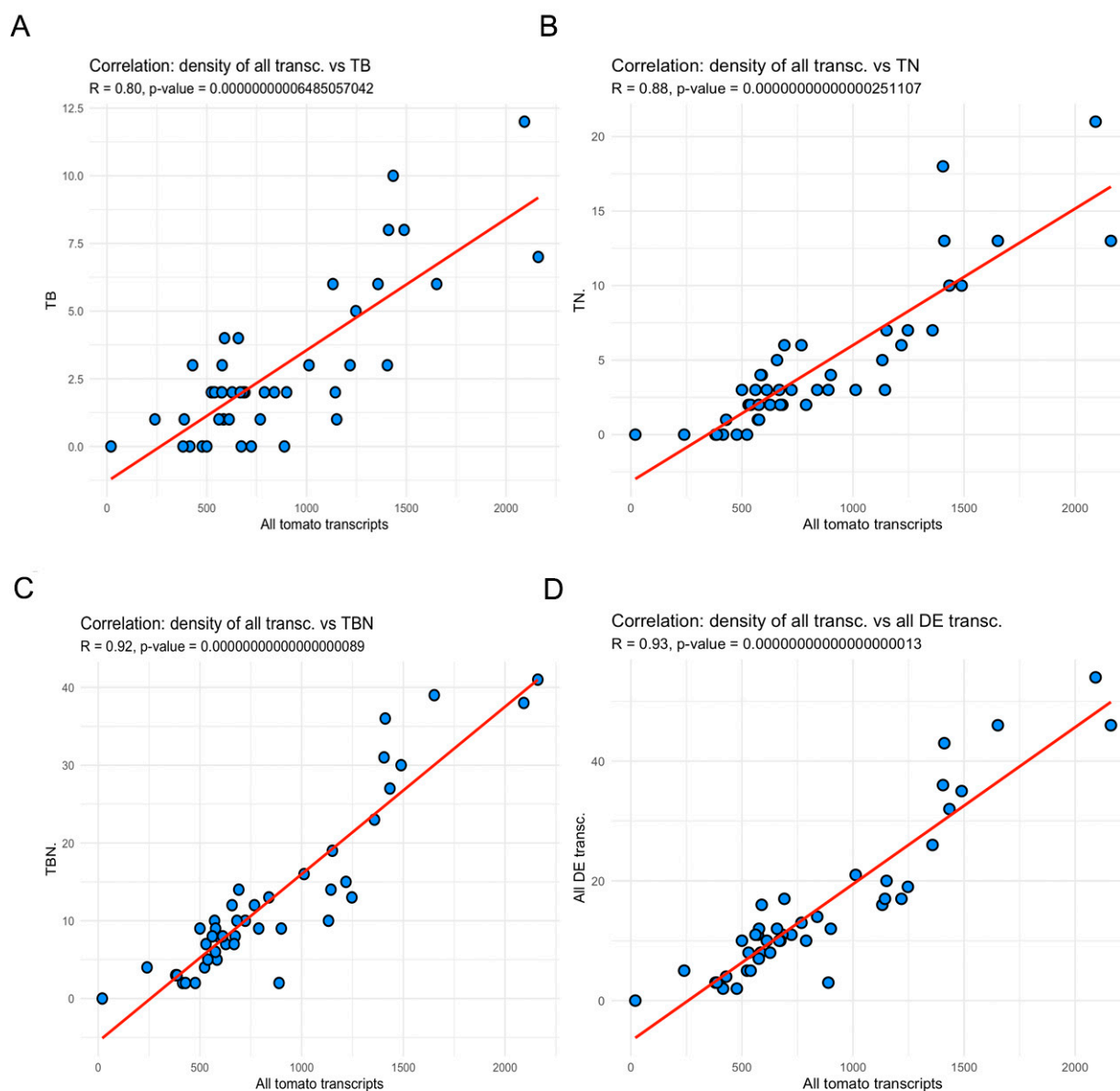


Figure S9. Pearson correlation analysis between the general distribution of genes along the tomato genome and DE transcripts in each of our treatments. All chromosomes were concatenated and each chromosome was divided in four segments. The overall density of genes in the tomato genome or those found DE in each treatment were correlated. r coefficient and p-value are indicated in each case for TB (A), TN (B), TBN (C) or all of them together (D).