

Stam et al, The *de novo* reference genome and transcriptome assemblies of the wild tomato species *Solanum chilense* confirms birth and death of NLR genes between tomato species.

Legends for Supplementary Figures S1, S2 and S3

Figure S1

The box-plot shows percent of read pairs in the 24 *S. chilense* RNA-Seq libraries aligned to the genome sequences of *Homo sapiens* (Human), *Escherichia coli*, *Fusarium* (Fungi) and chloroplast and mitochondrial genomes of *Nicotiana tabacum* (Plant organelles).

Figure S2

GenomeScope (Vurture *et al.* 2017) output profile with indication of the estimated genome length.

Figure S3

Maximum Likelihood (ML) phylogenetic tree of *S. pennellii* and *S. chilense* NLRs in red and black, respectively. Several previously identified NLR genes from different species are included for comparison and Apaf1.1 and Ced4 are used as an outgroup, similar as in Andolfo *et al.* (2014) and Stam *et al.* (2016). These genes are shown in blue. A list of the genes and their species of origin can be found in Table S8. Several clades are highlighted to illustrate clades with even numbers (NRC), clades with higher numbers for *S. pennellii* (CNL8), for *S. chilense* (CNL6) and newly discovered clades (CNL20, CNL21). The branch length is shown as expected number of substitutions per site.

References for Supplementary Figures S1, S2 and S3

- Andolfo, G., F. Jupe, K. Witek, G. J. Etherington, M. R. Ercolano *et al.*, 2014 Defining the full tomato NB-LRR resistance gene repertoire using genomic and cDNA RenSeq. BMC Plant Biol. 14: 120.
- Stam, R., D. Scheikl, and A. Tellier, 2016 Pooled Enrichment Sequencing Identifies Diversity and Evolutionary Pressures at NLR Resistance Genes within a Wild Tomato Population. Genome Biol. Evol. 8: 1501–1515.
- Vurture, G. W., F. J. Sedlazeck, M. Nattestad, C. J. Underwood, H. Fang *et al.*, 2017 GenomeScope: fast reference-free genome profiling from short reads. Bioinformatics 33: 2202–2204.