**Figure S2.1:** Size distribution and concentration of nanoparticles in cell-free supernatants of exponential and stationary phase *Pectobacterium* *brasiliense* 1692 cultures.

Graphical user interface

Description automatically generated

**Figure S3.1:** Differentially secreted proteins (DSPs) in the *Pectobacterium brasiliense* 1692 type 6 secretion system (T6SS) inactive strain secretome versus the T6SS-active secretome**.** The heatmap shows the 49 DSPs in the T6SS-inactive strain secretome in comparison to the T6SS-active strain secretome. Shades of blue show downregulated proteins and shades of red show upregulated proteins at a scale of -5 (blue) to 5 (red). Nineteen and 30 proteins were upregulated and downregulated respectively.

A firework exploding in the sky

Description automatically generated with low confidence

**Figure S4.2:** Inter-species protein-protein interaction. The fuzzy Cytoscape IntAct network shows the entire InterSPPI PPI network of interactors of AvrL. Each green dot represents each *Arabidopsis thaliana* protein. Other colors represent interactors from other organisms.

A picture containing chart

Description automatically generatedA picture containing chart

Description automatically generatedA picture containing bubble chart

Description automatically generated

**Figure S4.3:** Functional annotation of candidate Avirulence L interacting proteins in *Arabidopsis thaliana*. The image shows the highly enriched GO terms associated with *A. thaliana* proteins predicted to interact with AvrL. The REVIGO scatterplot shows the enriched proteins in (**A**) biological process ontology, (**B**) molecular activity ontology, and (**C**) cellular component ontology. The colors indicate the *p*-value. The log size indicates the log10 (the number of proteins associated with the GO term).



**Figure S4.4:** Differentially expressed predicted Avirulence L target genes in *Solanum tuberosum* cultivars infected with *Pectobacterium brasiliense* 1692. The graph shows the number of expressed genes by tolerant and susceptible potato cultivars *S. tuberosum* cv. BP1 and Valor respectively. A total of 15 proteins are expressed by both cultivars. *S. tuberosum* cv. Valor expresses 19 potential AvrL targets, three of which are intrinsic to the cultivar. *S. tuberosum* cv. BP1 expresses eight potential targets of AvrL. Two BP1 proteins are intrinsic to BP1.