Fig S3. Method used for identifying candidate effector genes in a whole genome shotgun assembly.
(a) Putative effectors were identified by looking for uninterrupted ORFs in a region of i) 2500 bp or ii) 5000 bp downstream of a miniature Impala (mimp) terminal inverted repeat (TIR). Maximum distance between the mimp terminal inverted repeat (TIR) and the start codon (ATG) of the putative ORF was set in both cases to 2000 bp. (b) Workflow diagram of mimp-associated putative effector discory pipeline from *de novo* genome assembly to identification of effector candidates, clustering them and identifying presence/absence patterns in each genome. In blue, the number of records found for the assessed Fo genomes is represented.