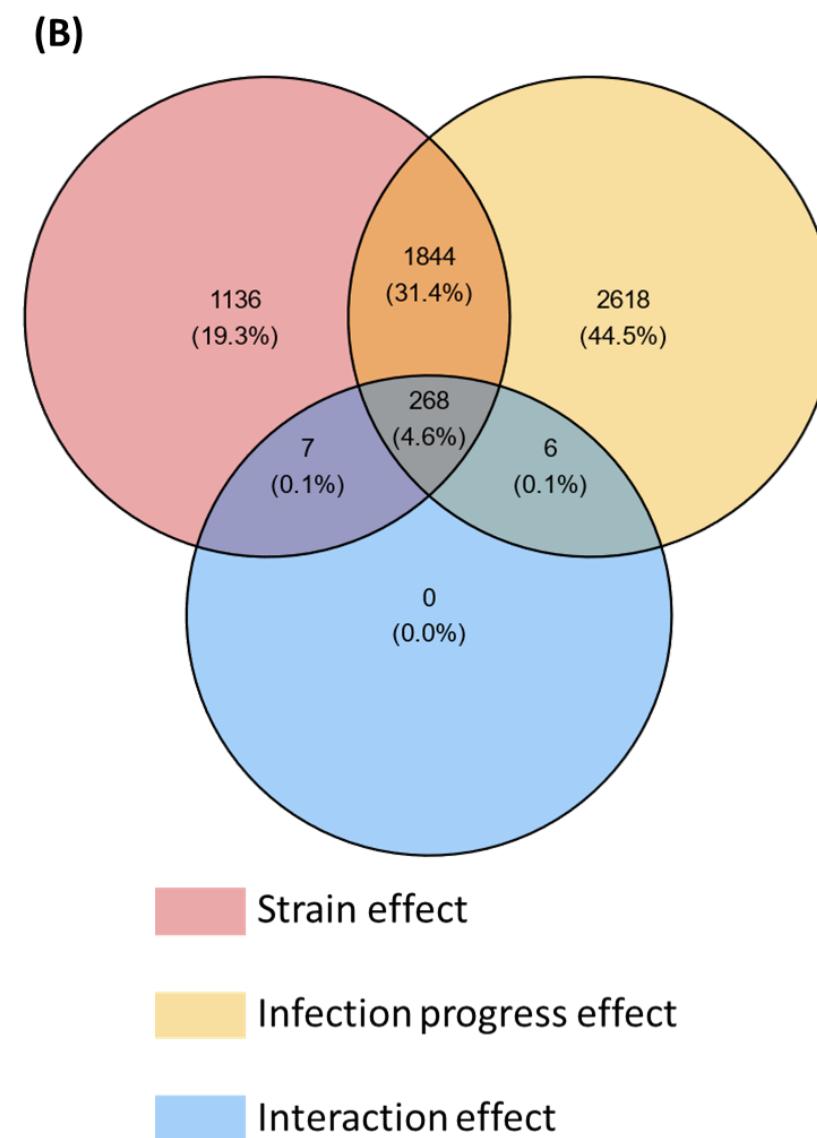
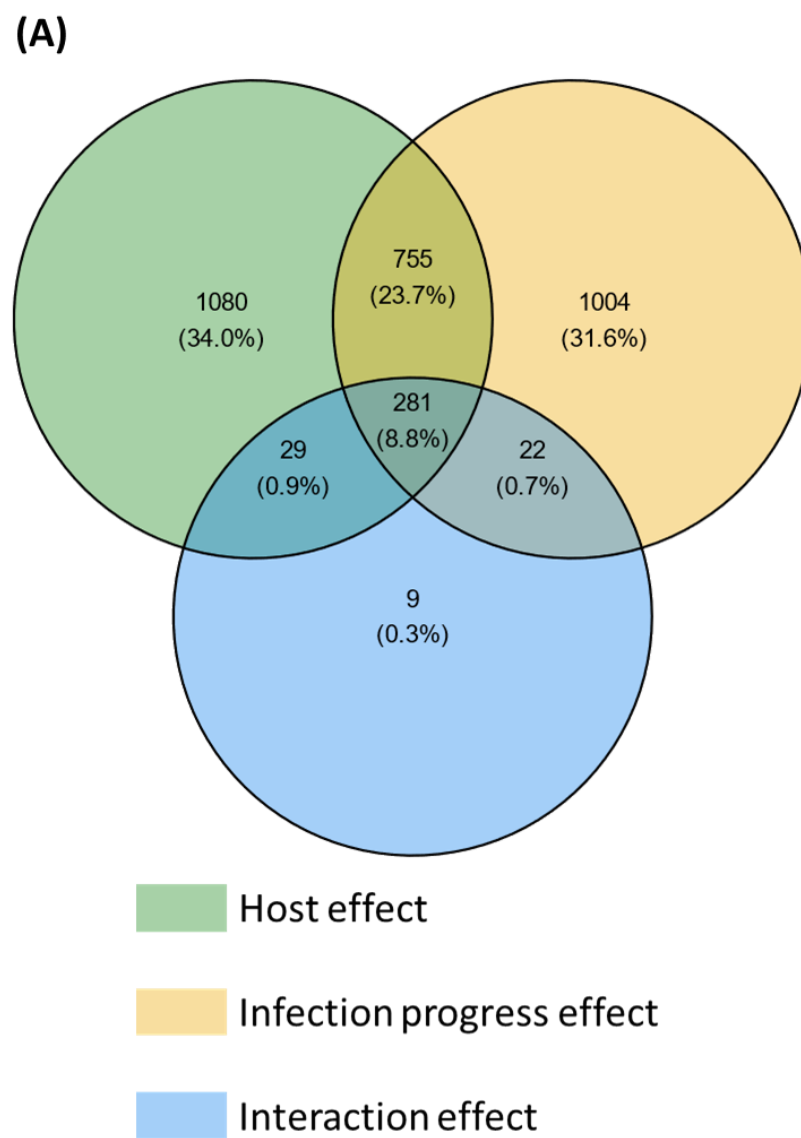
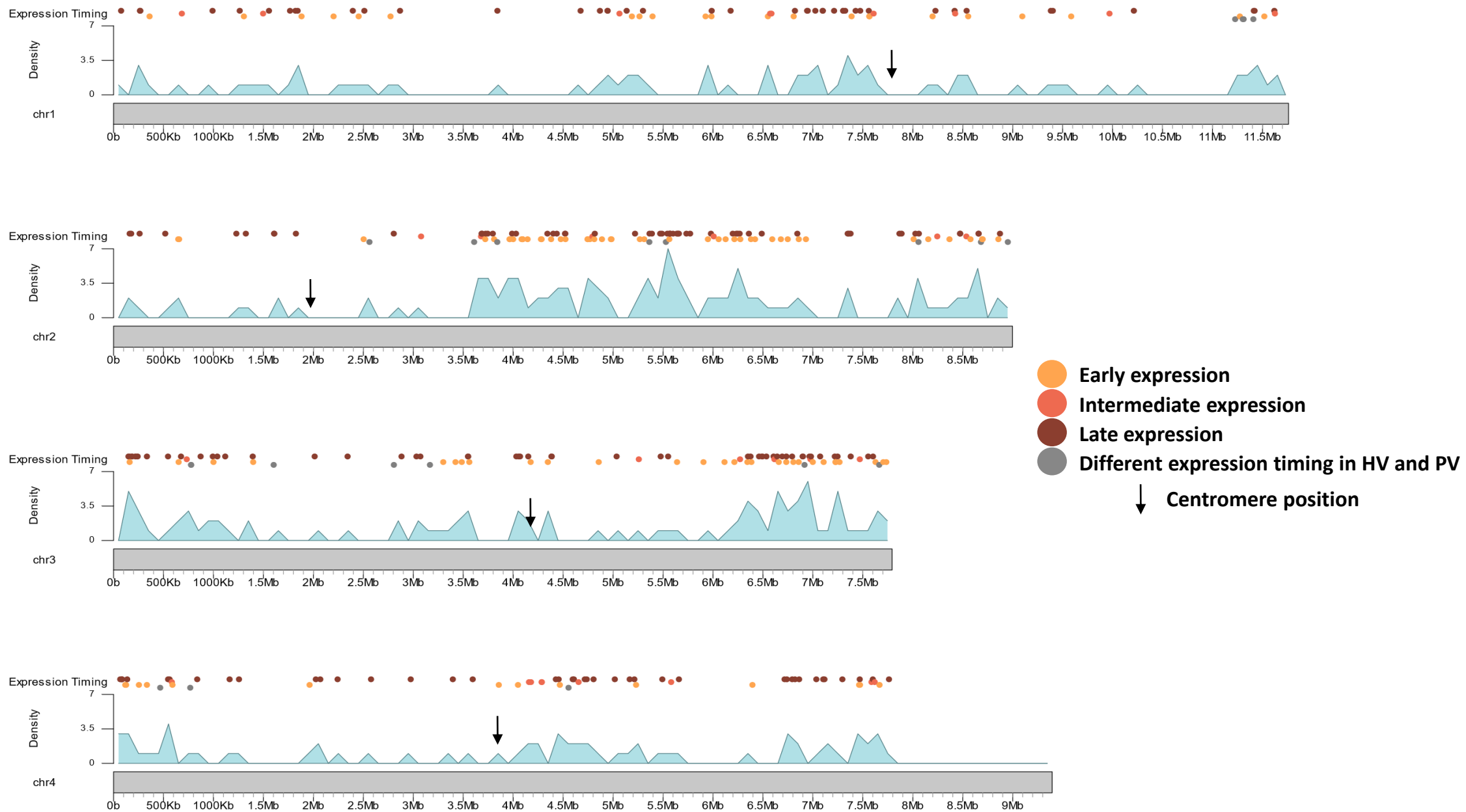


**Figure S1: Number of detected transcripts in the HostV and PathoV experiments at the whole gene set (A) and at the secretome gene set (B) levels.** Venn diagrams represent the number of genes expressed in the HostV (blue) and the PathoV (red) experiments. Genes were filtered per host and per strain with a 4CPM threshold in at least 3 samples.



**Figure S2: Number of genes from HostV (A) and PathoV (B) whole data sets significantly impacted by the different effects tested in the differential expression (DE) analysis.** For each factor of the DE analysis, the Venn diagrams indicate the number of genes displaying significant expression variations. Significance threshold : p-value corrected by Benjamini-Hochberg method  $< 1e-3$ .



**Figure S3: Genomic distribution of the core effectome genes according to their expression timing.** Karyoplot represents the distribution density (light blue) of the genes on *Fusarium graminearum* chromosomes along with information about the expression timing. The window size for density representation is 100kb. Black vertical arrows indicate the centromere position.