Supporting information
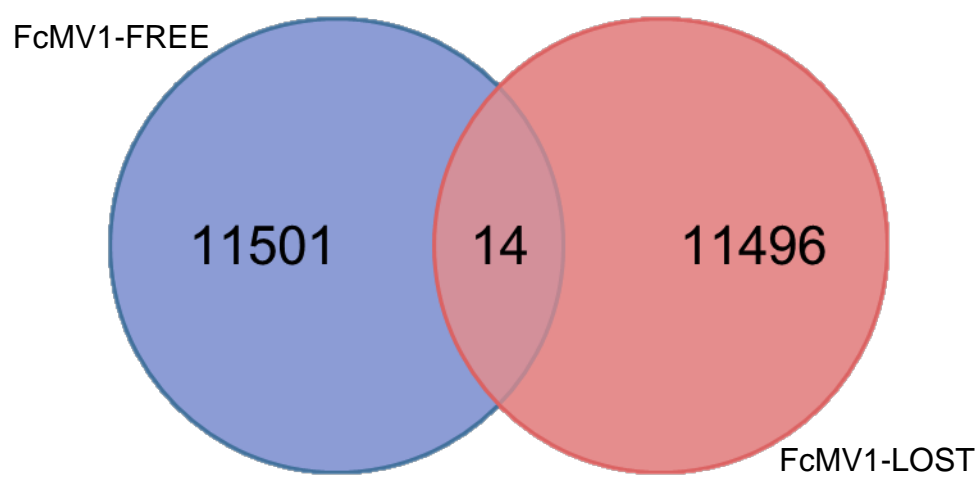
S1 Figure. Venn diagram of the differentially expressed genes by the post-infection of the virus FcMV1.

FcMV1-FREE

11501   14   11496

FcMV1-LOST

S2 Figure. Sequences of the differentially expressed genes by the post-infection of the virus FcMV1 without a known function.
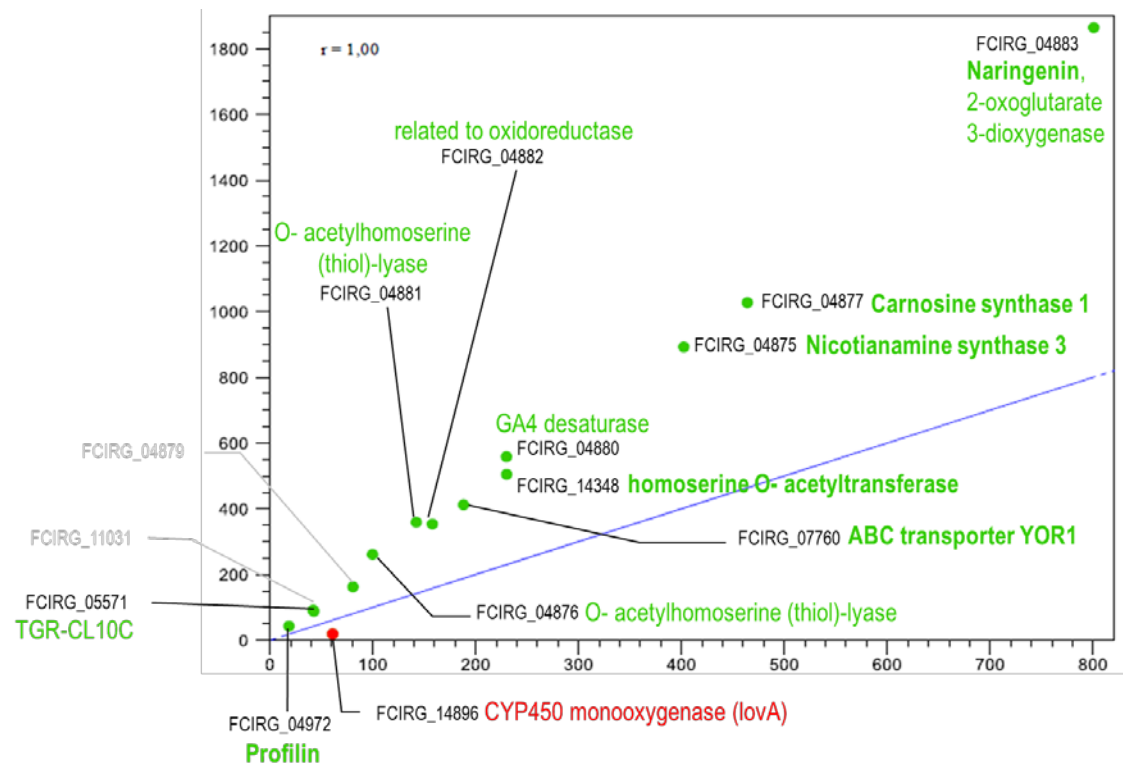
>FCIRG_04879

MEELEACVLFPSPKQQETQRLRERNRIAKRASSMLPRLYCNCLPFSVLTCLRSAPTAT*AAQRQYCGRCS
TANANCRSNFAGLGSAIAPATISWLWLWLWL*L*LRLCTGRGVGRPWRLGTRRPPRRPYRPALALFSR*G
LAWF*WFTSGHA*PSSALSLSPSLSPEDIQPRAESTTSIFHDFTHLRLQRSQQ*TI*ATPHRRSQWNDRY
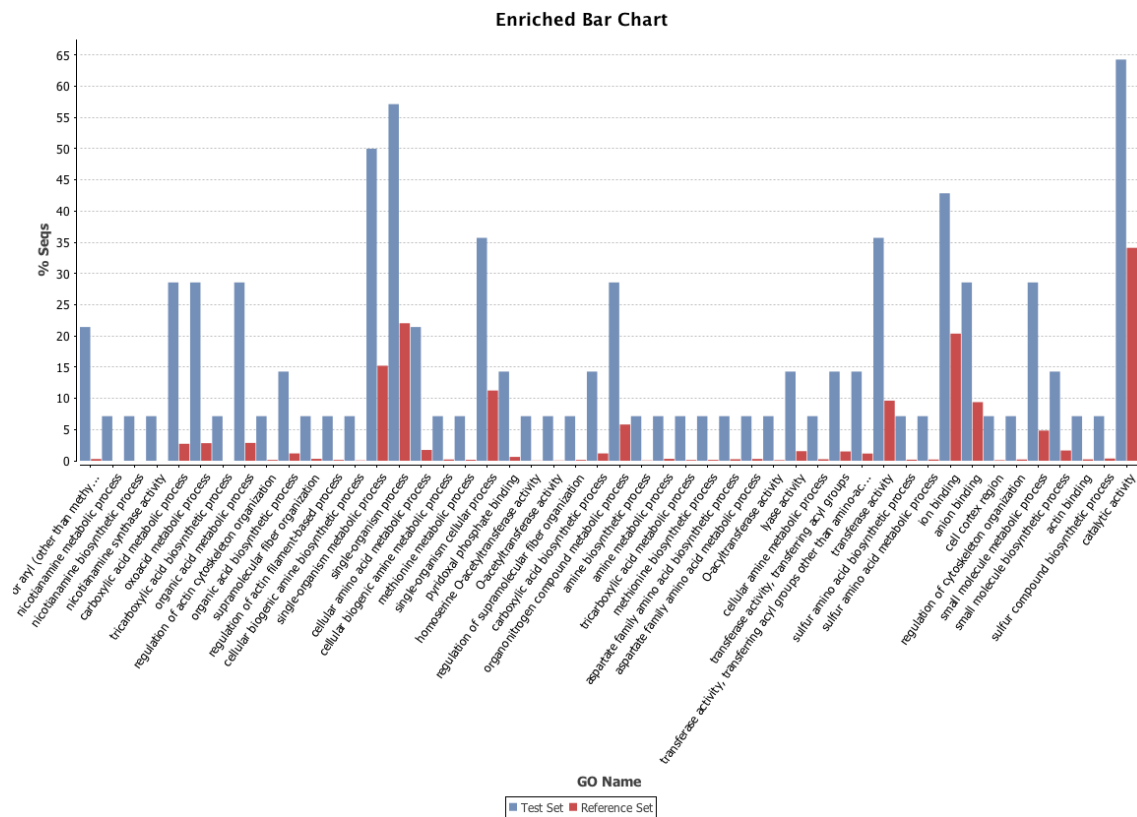SPLVDQGRRRRELARLLRHNSPPYRCTLSTCKCSRAAGESRSKYQCPGLGQHDGP*SSSEGSGRRARQYS
PLWWS*ASL

>FCIRG_11031

MHASAAVLAFVAVAAAQTPVAPVATPVATPGAR*F*PFLTILCSRQFN*HQR**PPTVLSPAPAPAPPP
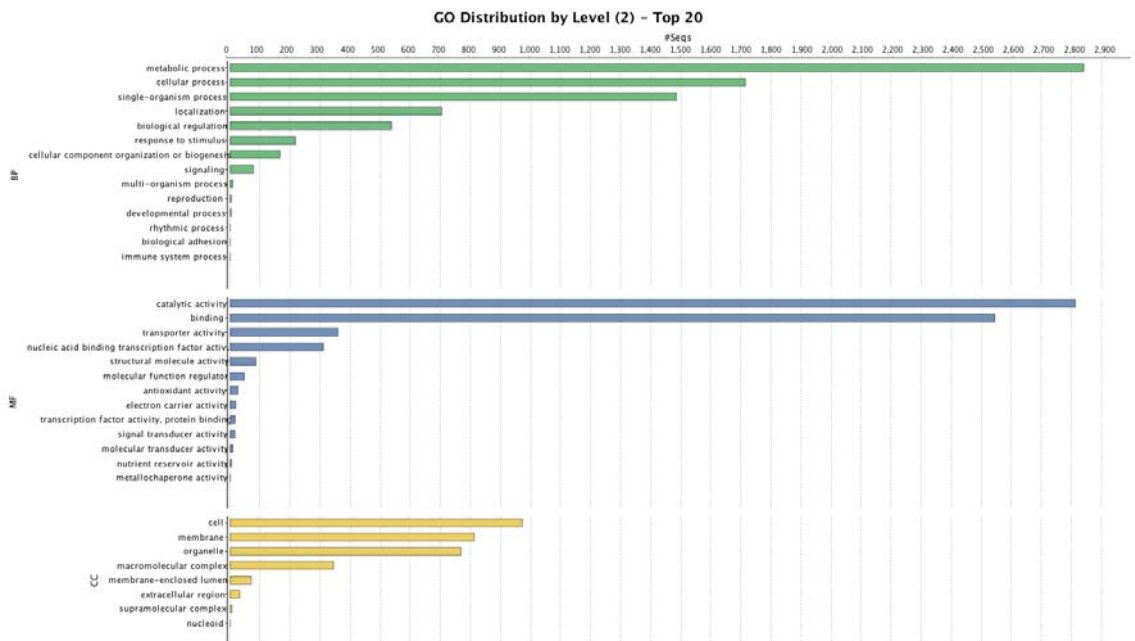PTALVPSASAASLVPSLLPLPC

S3 Figure. Scatter plot representing the differentially expressed genes of this analysis. X-axis: normalized means in condition free of FcMV1 infection. Y-axis: normalized means in condition of FcMV1 post-infection. Red dot: down-regulated genes; green dot: up-regulated genes.
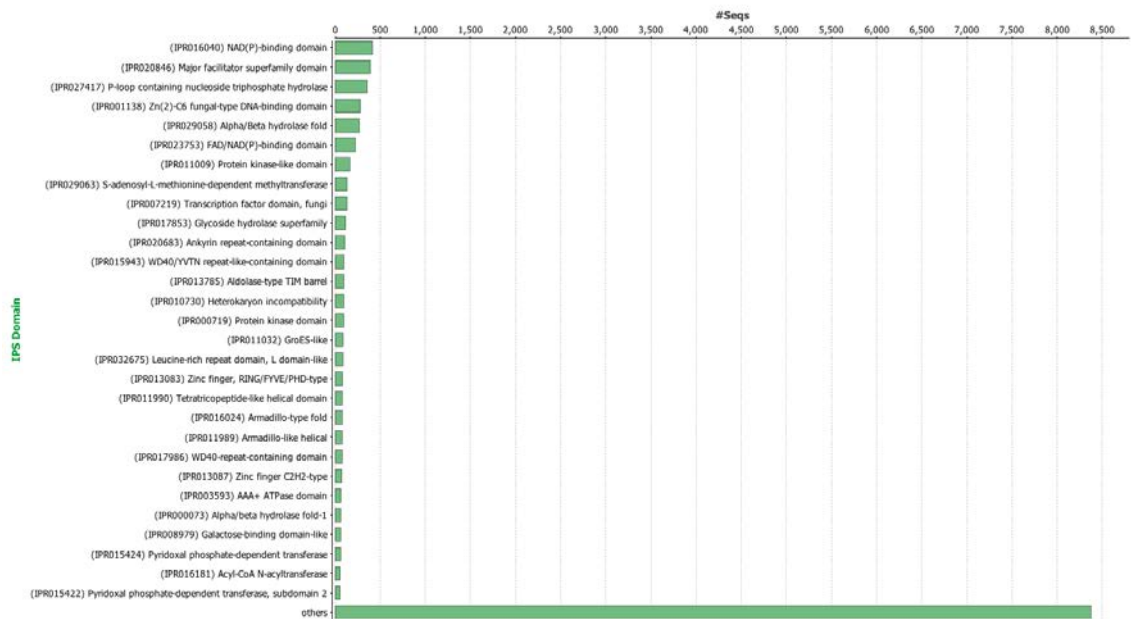
S4 Figure. FET enriched GO terms associated with the differentially expressed genes of
Fusarium circinatum **previously infected by FcMV1.**

S5 Figure. Distribution of GO terms represented in this analysis by biological processes, cellular components and molecular functions.

GO Distribution by Level (2) – Top 20

S6 Figure. Distribution of the sequences of the analysis in the InterProScan domains.

S7 Figure. Blast2GO blast results of the highest similarity species with higher Max ident and lower e-values.