

Additional file 15: *Fusarium circinatum* DE genes related to hormone production with hits in the Pathogen Host Interaction (PHI) database.

Query ID	Gene description	Gene name	PHI accession	Species	% identity	E-value	PHI phenotype
<b>FCIRG_03 234T1</b>	Isochorismatase family hydrolase (ICSH)	EntB	6565	<i>Klebsiella pneumoniae</i>	26.000	2,85E-05	unaffected pathogenicity, reduced virulence
<b>FCIRG_14 291T1</b>	Catalyzes the formation of formate and 2-keto-4- methylthiobutyrate (KMTB) from 1,2-dihydroxy-3-keto-5- methylthiopentene (DHK-MTPene)	FTF1	5483	<i>Fusarium oxysporum</i>	90.909	6,31E-55	reduced virulence
<b>FCIRG_05 399T1</b>	Gibberellin cluster-C13-oxidase	Akt7	4194	<i>Alternaria alternata</i>	22.794	5,95E-06	increased virulence (hypervirulence), reduced virulence
		Cyp51a	2907	<i>Fusarium graminearum</i>	25.248	4,55E-05	unaffected pathogenicity, reduced virulence
		Cyp51a	1155	<i>Zymoseptoria tritici</i>	22.330	6,82E-04	chemistry target: resistance to chemical
		Hic-15	7173	<i>Verticillium dahliae</i>	25.366	8,41E-04	reduced virulence
<b>FCIRG_05 404T1</b>	Gibberellin cluster-GA14-synthase	o- methylsteri gmatocysti n_ oxidored uctase	2393	<i>Fusarium graminearum</i>	27.485	4,39E-10	increased virulence (hypervirulence)
		Mocyp51a	2190	<i>Magnaporthe oryzae</i>	23.767	4,16E-07	reduced virulence
		Mocyp51b	2191	<i>Magnaporthe oryzae</i>	24.878	5,87E-07	unaffected pathogenicity
		Fgerg5a	3037	<i>Fusarium graminearum</i>	27.950	3,90E-06	reduced virulence
		Akt7	4194	<i>Alternaria alternata</i>	27.273	1,90E-05	increased virulence

						(hypervirulence), reduced virulence	
		Cyp51b	2908	<i>Fusarium graminearum</i>	24.752	3,26E-05	unaffected pathogenicity, reduced virulence
		Fgerg5b	3038	<i>Fusarium graminearum</i>	29.747	1,09E-04	reduced virulence
		Hic-15	7173	<i>Verticillium dahliae</i>	23.529	1,11E-04	reduced virulence
		Bxcyp33c9	4607	<i>Bursaphelenchus xylophilus</i>	24.675	1,57E-04	reduced virulence
		C14dm	3258	<i>Leishmania major</i>	26.490	2,99E-04	reduced virulence
		Erg11	8030	<i>Candida albicans</i>	21.285	5,69E-04	loss of pathogenicity