Supplementary Materials: Screening of Deoxynivalenol Producing Strains and Elucidation of Possible Toxigenic Molecular Mechanism

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Table S1. Summary of total RNA sequencing quality in Fg1 and Fg2

Sample	Raw reads	Clean reads	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC (%)
Fg1	32447410	26363446	3.95G	0.02	96.09	90.26	52.40
Fg2	33489384	31301746	4.70G	0.03	95.90	88.59	52.74

Table S2. The reads mapped to the reference genome of *F. graminearum* PH-1

Sample_name	Fg1	Fg2
Total reads	26363446	31301746
Total mapped	21449066 (81.36%)	24434800 (78.06%)
Multiple mapped	199832 (0.76%)	37180 (0.12%)
Uniquely mapped	21249234 (80.6%)	24397620 (77.94%)
Reads map to '+'	10619448 (40.28%)	12204521 (38.99%)
Reads map to '-'	10629786 (40.32%)	12193099 (38.95%)
Non-splice reads	17467139 (66.26%)	19627198 (62.7%)
Splice reads	3782095 (14.35%)	4770422 (15.24%)

Table S3. Primers used for verification of differentially expressed genes

Gene ID	Gene description	Forward primer (5'to 3')	Revers primer (5'to 3')
FGSG_08811	EF1A	GGCTTTCACCGACTACCCTCCTC	ACTTCTCGACGGCCTTGATGACAC
FGSG_09266	HMG-CoA Synthase	ACTTCCCCAGCCAGTATGTT	CGGTAAGAGCGAAAGAGTAGAT
FGSG_09197	HMG-CoA reductase	CTCCCACCCAATCCACA	AGACACGGCTTCCTTCAA
FGSG_05912	Mevalonate Kinase	ATGAAACTGAACCGCAAGA	AAAGGGTGGTAACGTGTAGG
FGSG_09764	5′-Phosphomevalonate	CTGAGTGGGATGTTGAGGTT	TTGGAGTCTTCGGGGTTT
FGSG_06784	FPP synthease	TACCGTCAGGAGGGTGTTG	GGAAGGTGGTCTCGTGGAA
FGSG_03537	TRI5	TTTCCCACCGAGTATTTTCT	TAGGGTCTACCTTGAGCATCT
FGSG_03535	TRI4	TGTTGCTGGGATTTTCGC	CGTATTTATCGTGCATCTTGGA
FGSG_07896	TRI101	CTACACCCAAATCAGTCTCCT	TTTCCCTCGCTAATGCC
FGSG_03540	Tri11	TGCTTCCTCGGGGTCTT	CCACGAAATCTGGTCTGTCT
FGSG_03534	TRI3	CGGCAGCCAAGGATAAC	CCCGATAAACTTTCGACAACCGATT
FGSG_03533	TRI7	GAGAACGCCAAAGGAAAA	AAGCAATAACCCCAACGA
FGSG_03532	TRI8	GTCAAGGGCTCTTCGTTTC	CTGGGCGTGTTGGTCAT
FGSG_00469	STPK	CCATCTTCTCCTGACCGACTT	CACCAACTTCTGCTTGACAATG
FGSG_01312	Cek1	GGCTATCTACTACGGCTCTAACA	CCAGGTCTTCCATCCACTTGA
FGSG_10142	Atf1	GAACAACATCCGCCATCCAA	CGCATCGCTCATCGTAGAC