

List of Supplementary Figures and Tables

Table S1. List of fungal species from different taxonomic class containing MoeIF4E3 orthologous

Group	Class	Organism
Oomycetes	<i>Not found</i>	
Fungi	<i>Agaricomycetes</i>	<i>Not found</i>
	<i>Blastocladiomycetes</i>	<i>Not found</i>
	<i>Pneumocystidomycetes</i>	<i>Not found</i>
	<i>Pucciniomycetes</i>	<i>Not found</i>
	<i>Saccharomycetes</i>	<i>Not found</i>
	<i>Schizosaccharomycetes</i>	<i>Not found</i>
	<i>Tremellomycetes</i>	<i>Not found</i>
	<i>Ustilaginomycetes</i>	<i>Not found</i>
	<i>Zygomycetes</i>	<i>Not found</i>
	<i>Glomeromycetes</i>	<i>Not found</i>
	<i>Chytridiomycetes</i>	<i>Cenococcum geophilum</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus fumigatus</i>
	<i>Eurotiomycetes</i>	<i>Penicillioptosis zonata</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus brasiliensis</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus clavatus</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus luchuensis</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus novofumigatus</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus ochraceoroseus</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus tubingensis</i>
	<i>Eurotiomycetes</i>	<i>Aspergillus zonatus</i>
	<i>Eurotiomycetes</i>	<i>Cladophialophora carrionii</i>
	<i>Eurotiomycetes</i>	<i>Cladophialophora immunda</i>
	<i>Eurotiomycetes</i>	<i>Histoplasma capsulatum</i>
	<i>Eurotiomycetes</i>	<i>Paracoccidioides brasiliensis</i>
	<i>Eurotiomycetes</i>	<i>Paracoccidioides lutzii</i>
	<i>Eurotiomycetes</i>	<i>Talaromyces marneffeii</i>
	<i>Eurotiomycetes</i>	<i>Talaromyces stipitatus</i>
	<i>Eurotiomycetes</i>	<i>Uncinocarpus reesii</i>
	<i>Leotiomycetes</i>	<i>Botrytis cinerea</i>
	<i>Leotiomycetes</i>	<i>Sclerotinia sclerotiorum</i>
	<i>Sordariomycetes</i>	<i>Fusarium fujikuroi</i>
	<i>Sordariomycetes</i>	<i>Fusarium graminearum</i>
	<i>Sordariomycetes</i>	<i>Fusarium oxysporum</i>
	<i>Sordariomycetes</i>	<i>Fusarium proliferatum</i>
	<i>Sordariomycetes</i>	<i>Fusarium verticillioides</i>
	<i>Sordariomycetes</i>	<i>Lomentospora prolificans</i>

	<i>Sordariomycetes</i>	<i>Magnaporthe oryzae</i>
	<i>Sordariomycetes</i>	<i>Neurospora crassa</i>
	<i>Sordariomycetes</i>	<i>Neurospora tetrasperma</i>
	<i>Sordariomycetes</i>	<i>Scedosporium apiospermum</i>
	<i>Sordariomycetes</i>	<i>Sordaria macrospora</i>
	<i>Sordariomycetes</i>	<i>Sporothrix brasiliensis</i>
	<i>Sordariomycetes</i>	<i>Sporothrix schenckii</i>
	<i>Sordariomycetes</i>	<i>Trichoderma reesei</i>

List of MoeIF4E3 orthologous in *M. oryzae*

CLASS	ORGANISM	GENE ID	Given name	%protein-query covered	domain %-query covered	protein length	domain ranged
<i>Sordariomycetes</i>	<i>M. oryzae</i>	MGG_08170	MoeIF4E3	100%-100	100%-100	368 aa	152-309
<i>Sordariomycetes</i>	<i>M. oryzae</i>	MGG_12301	MoeIF4E	28.93%-95.1	96%-31.65	271aa	48-209
<i>Sordariomycetes</i>	<i>M. oryzae</i>	MGG_04647	MoeIF4E1	36.11%-50	86%-35.92	244aa	42-224

Table S2. List of MoeIF4E3 orthologous used for sequence homology

	CLASS	ORGANISM	GENE ID	Given name	%protein-query covered	domain %-query covered	protein length
1	Eurotiomycetes	<i>Aspergillus fumigatus</i>	AFUB_051690	AfeIF4E3	52.89%-89	66.24%-99	347aa
2	<i>Eurotiomycetes</i>	<i>Penicillioptis zonata</i>	ASPZODRAFT_129280	PzeIF4E	54.34%-94	67.09%-100	373aa
3	<i>Eurotiomycetes</i>	<i>Aspergillus brasiliensis</i>	ASPBRDRAFT_76906	AbeIF4E	51.96%-89	64.56%-100	350aa
4	<i>Leotiomycetes</i>	<i>Botrytis cinerea</i>	Bcin15g02340	BceIF4E	57.44%-89	70.06%-99	339aa
5	<i>Leotiomycetes</i>	<i>Sclerotinia sclerotiorum</i>	SS1G_07827	SseIF4E	55.24%-94	70.06%-99	342aa
6	<i>Sordariomycetes</i>	<i>Fusarium fujikuroi</i>	FFUJ_03080	FfeIF4E	59.17%-91	71.34%-99	341 aa
7	<i>Sordariomycetes</i>	<i>Fusarium graminearum</i>	FGRAMPH1_01T23195	FgeIF4E	57.14%-98	70.25%-100	338 aa
8	<i>Sordariomycetes</i>	<i>Fusarium oxysporum</i>	FOYG_02867	FoeIF4E	58.88%-91	70.70%-99	341 aa
9	<i>Sordariomycetes</i>	<i>Fusarium proliferatum</i>	FPRO_04851	FpeIF4E	59.17%-91	70.70%-99	341 aa
10	<i>Sordariomycetes</i>	<i>Fusarium verticillioides</i>	FVEG_05198	FveIF4E	58.88%-91	71.34%-99	341aa
11	<i>Sordariomycetes</i>	<i>Lomentospora prolificans</i>	jhhlp_006576	LpeIF4E	52.99%-98	68.35%-100	386aa
12	<i>Sordariomycetes</i>	<i>Magnaporthe oryzae</i>	MGG_08170	MoeIF4E3	100%-100	100%-100	368 aa
13	<i>Sordariomycetes</i>	<i>Neurospora crassa</i>	NCU09546	NceIF4E3	63.54%-92	75.80%-99	355aa
14	<i>Sordariomycetes</i>	<i>Neurospora tetrasperma</i>	NEUTE1DRAFT_75712	NteIF4E	63.54%-92	75.16%-99	355aa
15	<i>Sordariomycetes</i>	<i>Scedosporium apiospermum</i>	SAPIO_CDS8916	SaeIF4E4	51.34%-97	67.72%-100	354 aa
16	<i>Sordariomycetes</i>	<i>Sordaria macrospora</i>	SMAC_07065	SmeIF4E3	64.07%-92	75.16%-99	357aa
17	<i>Sordariomycetes</i>	<i>Sporothrix brasiliensis</i>	SPBR_07228	SbeIF4E3	62.29%-90	80.89%-99	422aa
18	<i>Sordariomycetes</i>	<i>Sporothrix schenckii</i>	SPSK_05268	SsceIF4E3	62.57%-90	80.89%-99	422aa
19	<i>Sordariomycete s</i>	<i>Trichoderma reesei</i>	TRIREDRAFT_103322	TreIF4E3	56.82%-93	71.34%-99	337aa
20	<i>Sordariomycetes</i>	<i>Trichoderma virens</i>	TRIVIDRAFT_33839	TveIF4E3	57.26%-93	71.34%-99	337aa
21	<i>Saccharomyces</i>	<i>Saccharomyces cerevisiae</i>	NP_014502	SceIF4E	34%-44	33%-99	213 aa
22	Planta	<i>Arabidopsis thaliana</i>	NP_193538	AteIF4E3	35%-43	34%-88	235 aa
23	Animalia	<i>Drosophila melanogaster</i>	NP_648194	DmeIF4E3	35%-45	38%-93	244aa
24	Humans	<i>Homo Sapiens</i>	NP_001124150	HseIF4E	37%-44	36%-96	237 aa

Table S3. List of primers used in this study

Primer Name	Primer sequence(5'-3')
eIF AF	GGCTCTCGGGATGATGG
eIF AR	TTGGTAGGGCGGCTGGT
eIF OF	CACCAACCACCACCCTTCA
eIF OR	TCAGCACCGCACACAGACC
eIF BF	TGTTTTGTGGTGGGATGG
eIF BR	AAAGGGAAGGCTGCGTAG
eIF UAH F	GGGAACATCCATCCTCAA
eIF UAH R	GCTCCATACAAGCCAACC
eIF Comp F	TCGTCGGGAATGGCGTA
eIF Comp R	TTGAGTCGCGCCGCTG
eIF4E3 qPCR F	GGAATGGTGAGGATATTTTG
eIF4E3 qPCR R	ATTTTGTTCACGCTTCTCC
eIF4E qPCR F:	GAAGTTGGTGCAGCTTGTTG
eIF4E qPCR R:	AGTTGTCGGGCTTGGGTC
eIF4E1 qPCR F:	ATTCCCATCTCTCCCGAT
Eif4E1 qPCR R:	TCCTCTACTGAGTTAAATGTGATA
ChitinD qPCR F	CCGTGCTAAAGGTCTCTC
ChitinD qPCR R	TTAGTTGCAAGTGCCAAAG
ChitinS1 qPCR F	TTATTCTACTCGCCTTGA
ChitinS1 qPCR R	CTTCATTACTGTCGGATC
ChitinS2 qPCR F	TACACTCTGATCCTACTC
ChitinS2 qPCR R	AACTGCCTTATGACAATG
T peroxidase qPCR F	GAGTGTTTCGTTATTGACAAGA
T peroxidase qPCR R	CTCCTCTACCACCTCCTTA
C peroxidase qPCR F	CTCCTTCCAAGCTTATCCA
C peroxidase qPCR R	CCTTCTTGCCACTCTTCT
S dismutase 1 qPCR F	CTGGAAAAGACCGAAAAGG
S dismutase 1 qPCR R	CCACCACCTGCTAACATA
S dismutase 2 qPCR F	CGTATTTGGCGTTGACAT
S dismutase 2 qPCR R	ACAGGGAAGCATGTAGTG
eIF1A qPCR F	GTCACTGAGAGGCATCTTC
eIF1A qPCR R	CTTGTGTCGCTCGTTAGG
eIF1 qPCR F	CGAGGACACTGGTGATAA
eIF1 qPCR R	CTTCTTTGGGATGCCTTG
eIF2S1 qPCR F	TATATCAGCAAGCGGTTGA
eIF2S1 qPCR R	TACTGGTAAGAACGTAGAGC
eIF2S2 qPCR F	AGTATCTGTTTGCTGAGTTG
eIF2S2 qPCR R	CAGTCTTGATGGCAGTAAC

eIF2S3 qPCR F	TCAGCAGAATAGTGCCTT
eIF2S3 qPCR R	GGAGCAGGTAGAAGTTGA
eIF2A qPCR F	AACCGTCTGGCTAACATT
eIF2A qPCR R	CTTCTTCATCTGAGTATCTTCG
eIF2B1 qPCR F	TCTACTTTGCTGCCGAAA
eIF2B1 qPCR R	ATCATCTTTGGCGGAGTAT
eIF2B2 qPCR F	CGACGGTTGAGAAGTTTC
eIF2B2 qPCR R	ATCTTGTGGCTTGCTAGT
eIF2B3 qPCR F	CCATCAAGGAGTCTGTCA
eIF2B3 qPCR R	ACTTCGCATTCCATCAAC
eIF2B4 qPCR F	AGGCGTCAAGGTTTCATA
eIF2B4 qPCR R	CGTTGTAGGTCAGAGGTT
eIF2B5 qPCR F	AATGAAGACAGCAGTAGGAA
eIF2B5-qPCR R	TTAATTGTACGCCGAATGAG
eIF5-qPCR F	AGGAGTTTGGCATTGAGA
eIF5-qPCR R	GGTGGTAGTACAGTTGAAGA
eIF5A-qPCR F	AGAGATGAGGGAGGACATTA
eIF5A-qPCR R	GGAACCTCCTCACCCATA
eIF5B-qPCR F	CATCAAGACCAACATCAGAG
eIF5B-qPCR R	TCCAAGTCAGATTTCGTCAT
eIF6-qPCR F	CTCAGTTCGAAAACTCCAA
eIF6-qPCR R	TGTAAGACGACCCACTATC
eIF4A-qPCR F	CTTATTGCCACCGACTTG
eIF4A-qPCR R	TGCTGTAGAACTGCTCAA
eIF4A3-qPCR F	ACAGCCGAGTGTTGATAT
eIF4A3-qPCR R	TCGATGTCTCTGAGGATTC
eIF4B-qPCR F	GAGTGGTAACTGGAGGTC
eIF4B-qPCR R	CTAGGATGCAATAGGACGA
eIF4E1-qPCR F	ATTCCCATCTCTCCCGAT
eIF4E1-qPCR R	TCCTCTACTGAGTTAAATGTGATA
eIF4E3-qPCR F	CAAGATTGAGTGGAAGAGC
eIF4E3-qPCR R	CTGCTGTTTCTGGTCATC
eIF4G-qPCR F	CATCAGCATCAAGGACAAG
eIF4G-qPCR R	TGTATAACTACCAATGAACTG
eIF3K-qPCR F	CGCTTCTGGGCCACTATC
eIF3K-qPCR R	TTCATCACGGAGGCTTGC
eIF3A-qPCR F	ACAGGGTCCCATTCTCAA
eIF3A-qPCR R	CAGCACGAGCAAGGTAA
eIF3B-qPCR F	GAAGTCTCAGGCAACAAC
eIF3B-qPCR R	TCGTAGGTGCTTGAAGTT
eIF3C-qPCR F	TACCACGAGAGGCCAAATC

eIF3C-qPCR R	GCGTCTCAATGCTCAATG
eIF3D-qPCR F	TAAGGCAGATGTCCTCAAG
eIF3D-qPCR R	CGCTTCAGACACATATCG
eIF3E-qPCR F	TCGCATCTGAGATTCTGT
eIF3E-qPCR R	GAGGTCTGGATAGTGTTGA
eIF3F-qPCR F	TGTCAATACTAGACCACGC
eIF3F-qPCR R	TCATGGCTGGTGGTGTAC
eIF3H-qPCR F	AACCACCATTCTACATCTC
eIF3H-qPCR R	TTGCCACGCTGTAATCTT
eIF3I-qPCR F	GAGGCTAGGTTCTACCATAA
eIF3I-qPCR R	CTGCTCCATCTTGTTCTTC
eIF3L-qPCR F	GCACTTCACAACCTACTACTA
eIF3L-qPCR R	CACCGAACTTCTCACGAA
eIF3M-qPCR F	AGGAGAACCTTGACAATGA
eIF3M-qPCR R	CCGAGTGAATCAGGAAGA

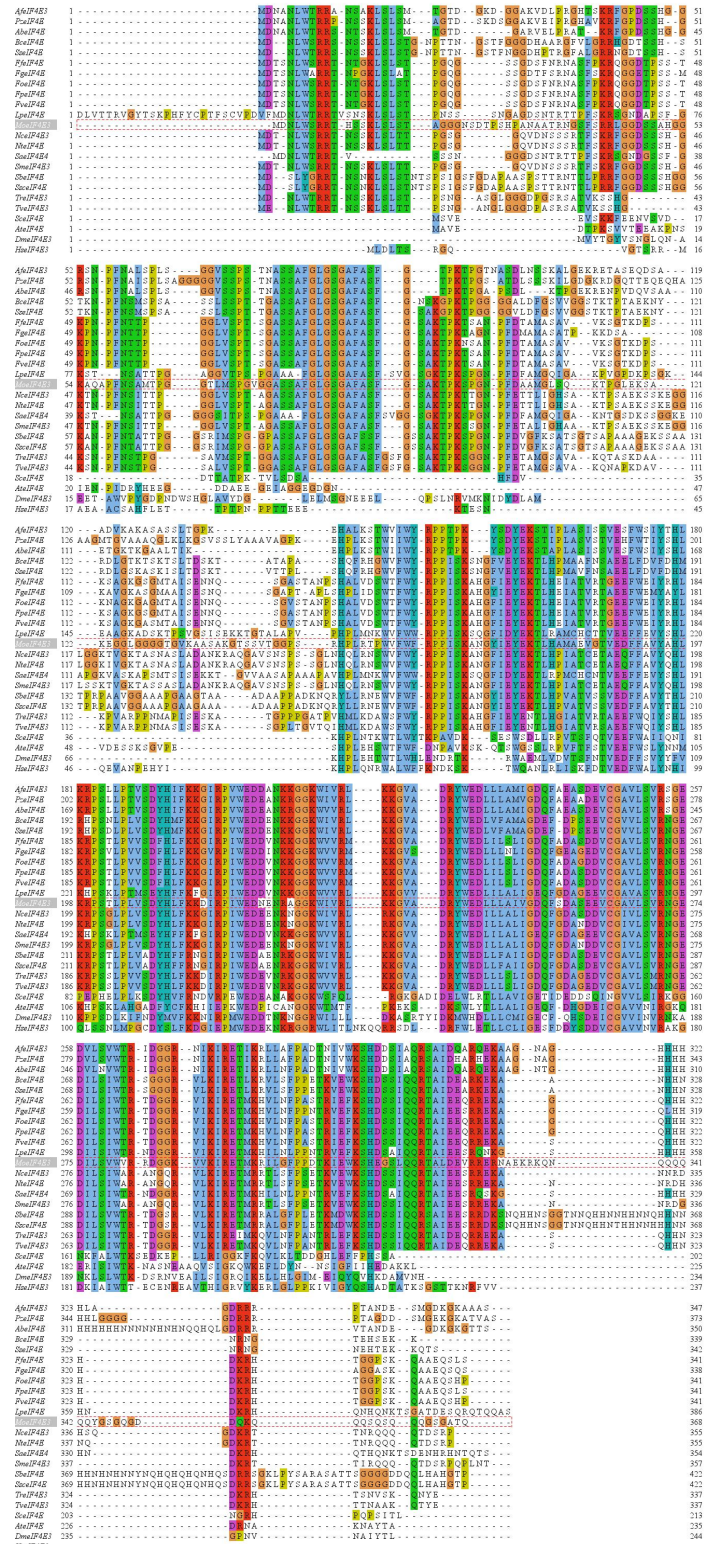


Fig. S1. Multiple sequence alignment of MoelF4E3 orthologous in fungal specie, Arabidopsis, Drosophila and Humans.

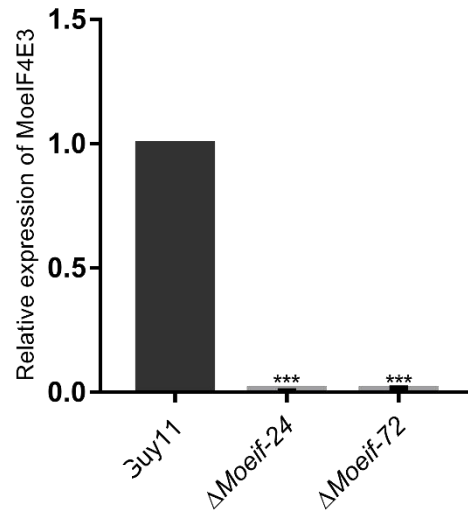


Fig. S2. Relative expression of MoeIF4E3 in wild type and MoeIF4E KO mutants. MoeIF4E3 Knockout mutants were confirmed through expression profiling of MoeIF4E3 in each strain as compared to wild type with qPCR. Results were generated from three independent biological with five technical replicates.

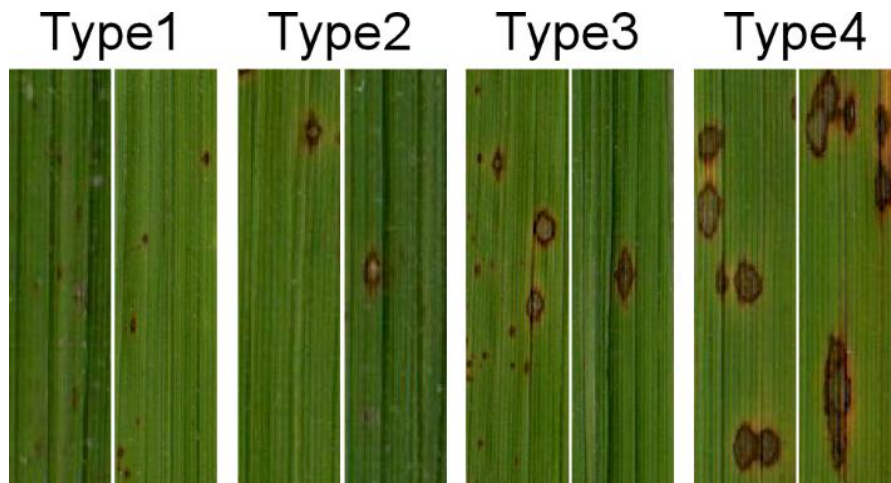


Fig. S3. Different types of lesion on leaf segments of rice cultivar C039. Type 1: uniform dark brown spot (0.5mm in diameter), Type 2: small lesions with distinct centers (1 mm in diameter), Type 3: small eyespot lesions (2 mm in length) with tan centers surrounded by dark brown margins, Type 4: large size eyespot lesions (3-4 mm in length).

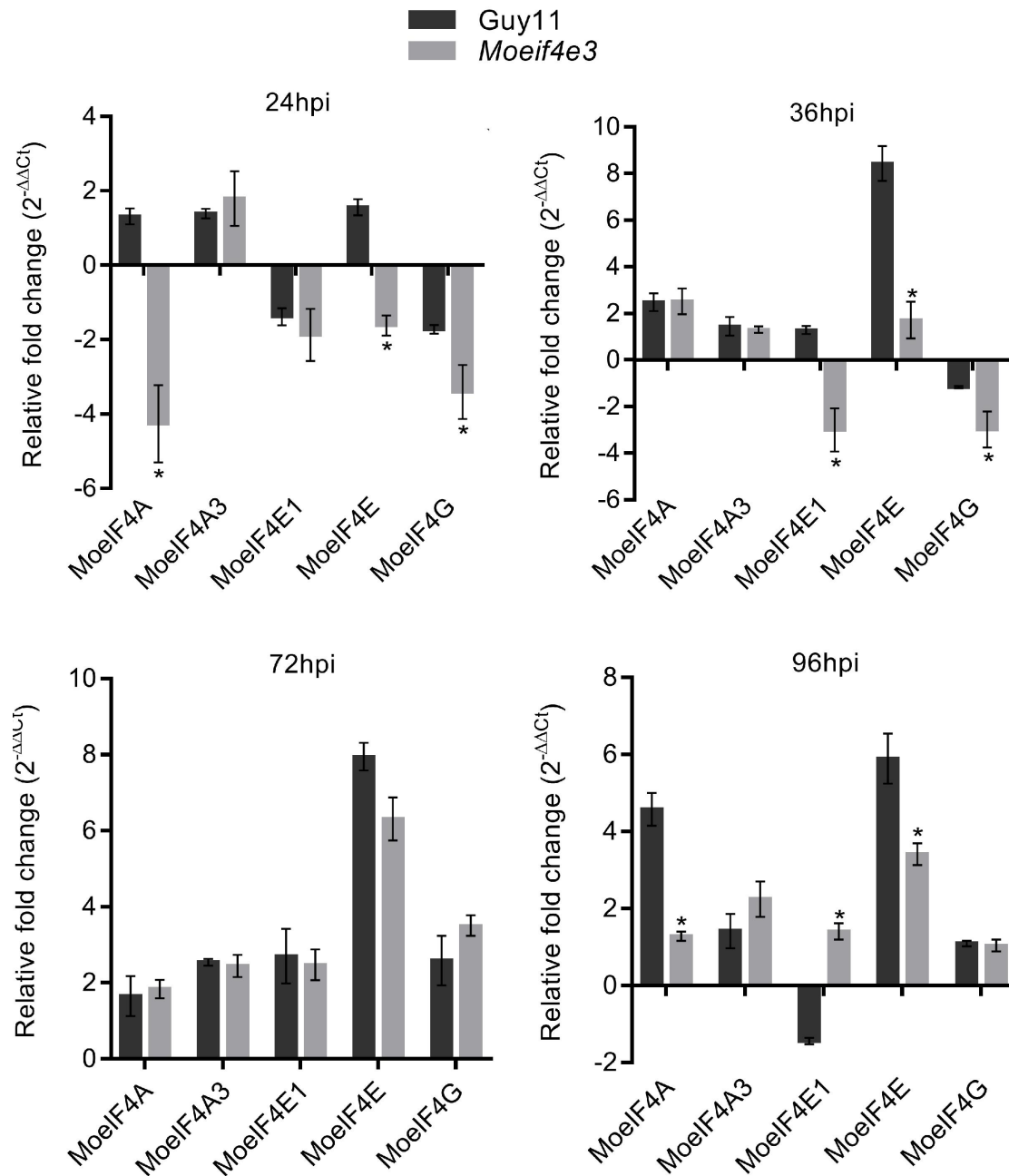


Fig. S4. Transcription expression pattern of MoeIF4F complex, during host pathogen interaction. The relative expression level of MoeIF4F complex proteins i.e. MoeIF4A, MoeIF4A3, MoeIF4E1, MoeIF4E and MoeIF4G in Wild type Guy11 and *Moeif4e3* deletion strains at different time intervals i.e. 12 hpi, 24hpi, 36hpi, 72hpi and 96hpi was assessed using qPCR. Expression at 12hpi was used as a control stage and was assumed as unity (the expression level of MoeIF4A, MoeIF4A3, MoeIF4E1, MoeIF4E and MoeIF4G at 12 hpi =1). Error bars represent standard deviation (SD). SD was calculated from three independent biological replications along with three technical replicates. (*, $P < 0.05$ by t-test).