SUPPLEMENTARY MATERIAL

Figure S1. Banding patterns of double-stranded RNA isolated from *A. bisporus* fruitbodies and used for SSH. The ds-RNAs were fractionated by agarose gel electrophoresis and visualized.

Lane A: Non-infected sample from Warwick HRI mushroom unit. Lane B: white-infected without brown symptom. Lane C: brown-infected with brown symptom. (Lanes D and E are DNA molecular weight markers).

[Selected lane D marker sizes are indicated in Kbp, far right].

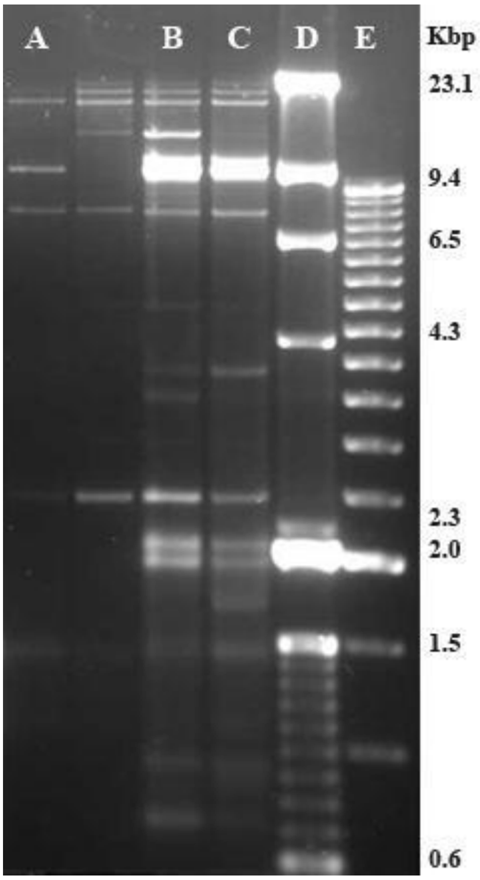
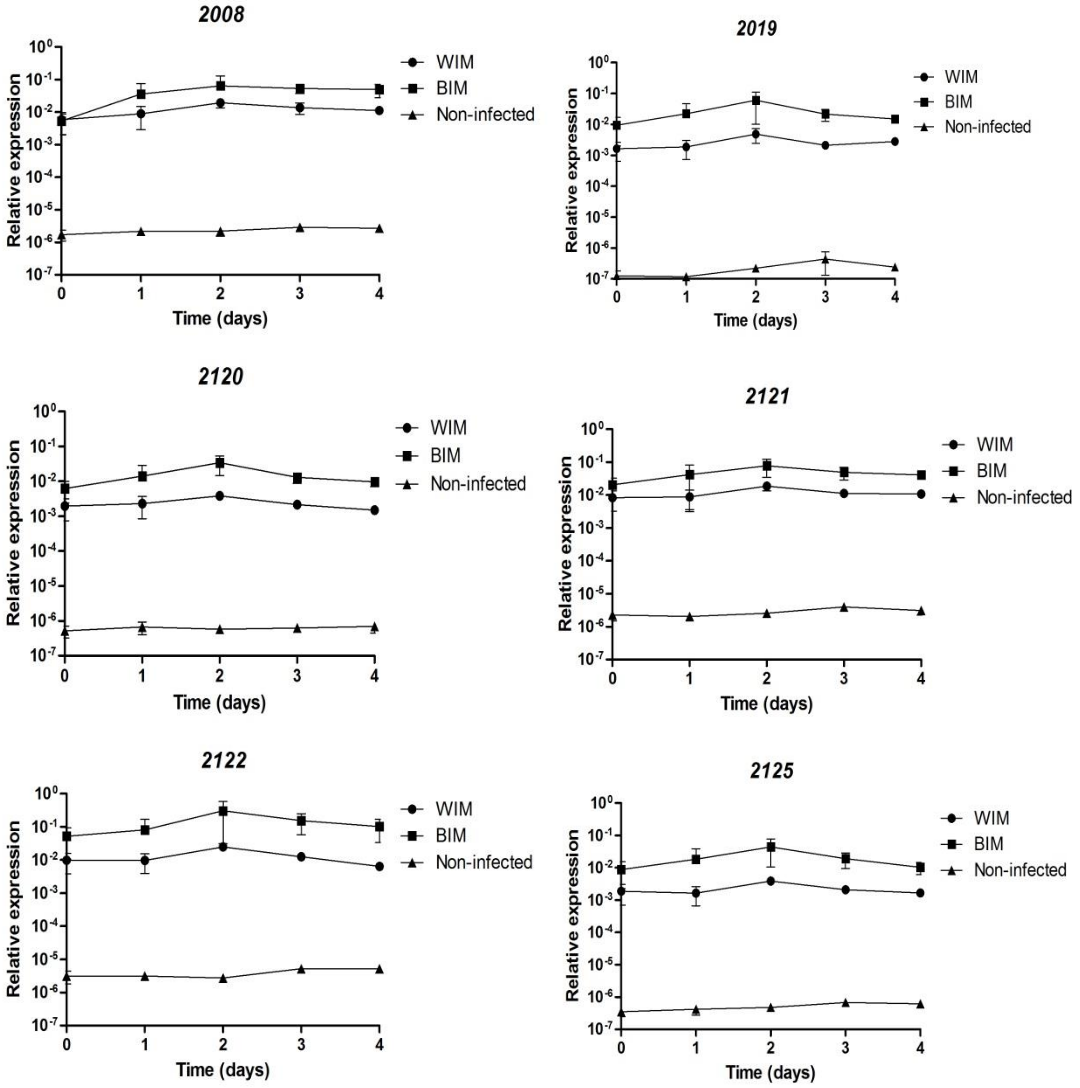
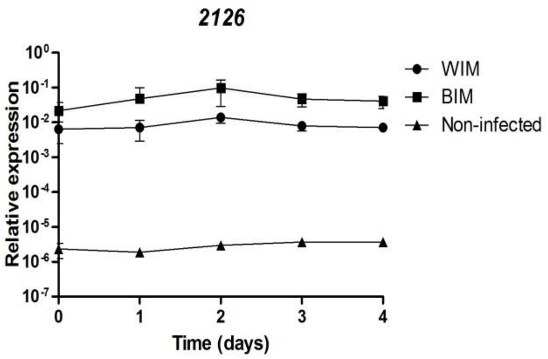
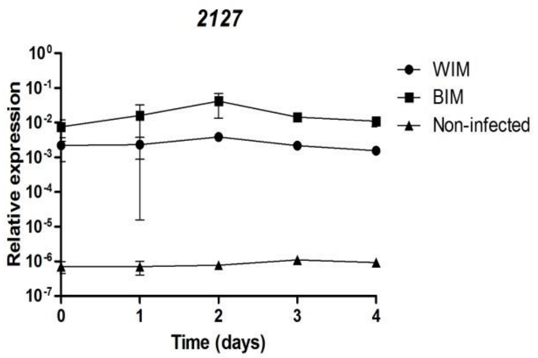


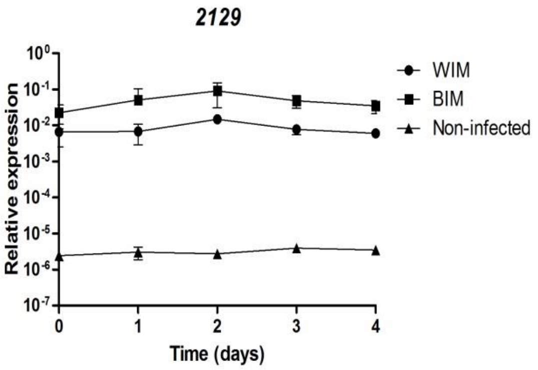
Figure S2. Mean RT-q-PCR analyses of transcripts of putative ds-RNAs 2008, 2019, 2120, 2121, 2122, 2125, 2126, 2127, 2129 and 2135 in white infected mushrooms (WIM), brown infected brown mushrooms (BIM) and non-infected control.

[Relative expression *i.e.* values were normalised against 18S rRNA. Vertical line shows LSD (5 %, 24 d.f.) for comparing means for a given day, as calculated from the residual mean square obtained from the ANOVA.].




2126
Relative expression
10^0
10^-1
10^-2
10^-3
10^-4
10^-5
10^-6
10^-7
0
1
2
3
4
Time (days)
WIM
BIM
Non-infected


2127
Relative expression
10^0
10^-1
10^-2
10^-3
10^-4
10^-5
10^-6
10^-7
0
1
2
3
4
Time (days)
WIM
BIM
Non-infected


2129
Relative expression
10^0
10^-1
10^-2
10^-3
10^-4
10^-5
10^-6
10^-7
0
1
2
3
4
Time (days)
WIM
BIM
Non-infected

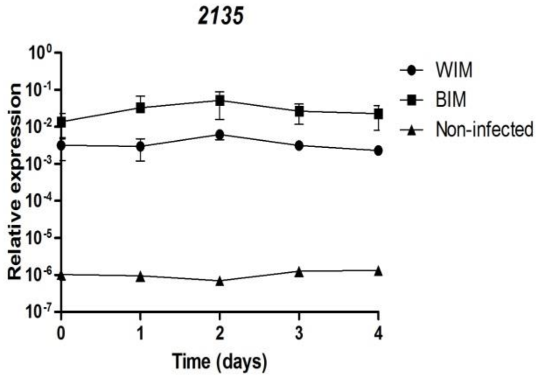

2135
Relative expression
10^0
10^-1
10^-2
10^-3
10^-4
10^-5
10^-6
10^-7
0
1
2
3
4
Time (days)
WIM
BIM
Non-infected

Table S1. Primers designed for RT-q-PCR analysis of the ten most up-regulated genes

Gene ID	Forward	Reverse
2127	TCCACGCATCCAGGCCAACA	CTTGTCTCCCACCTGTATGACAG
2135	CACCCTCGAAGGAGACTACTCA	CGGCGTCGATAATGTAAGCA
2121	GGGTTGACCTGGGACATTAACA	CACGAGGTCGGAATGTCTTCA
2120	AAGGTGTCGAGAATGGTCTCA	AAGCCTGGAATCTTTCCAATG
2125	CACTATTGAACCGGAATTGCACACGA	CGGAAGTGCGTGCCTTTGAATCTA
2008	TCAGCCAAGGCACAGGTCTT	CCCGAACTTCATTATGACCAGTCTC
2126	ACGAGGAAAGGATTAGGAGAAGCA	ACAGGCAAAACCTTGCGAACTG
2019	CACTTTCAGGTGCCCTATGA	TGGGCGGCAGGTGACTT
2122	GCCGACGCCAAACTAACAAT	GAACGCTGAAGTATCCCTTTCG
2129	CGGCGTCCGATGTCTTG	ACTCCGGAAAGCTGCTGAAG

Table S2. Sequences for non-Agaricus (presumed viral) transcripts less than 100bp in length

Transcript ID	**Sequence**
2125	ACACTATTGAACCGGAATTGCACACGACGTATACTTTAATGCGCCGTCGCCTAGATTCAA
2126	ACGAGGAAAGGATTAGGAGAAGCAACTCCGGGAAAACCAGTTCGCAAGGTTTTGCCTGTT