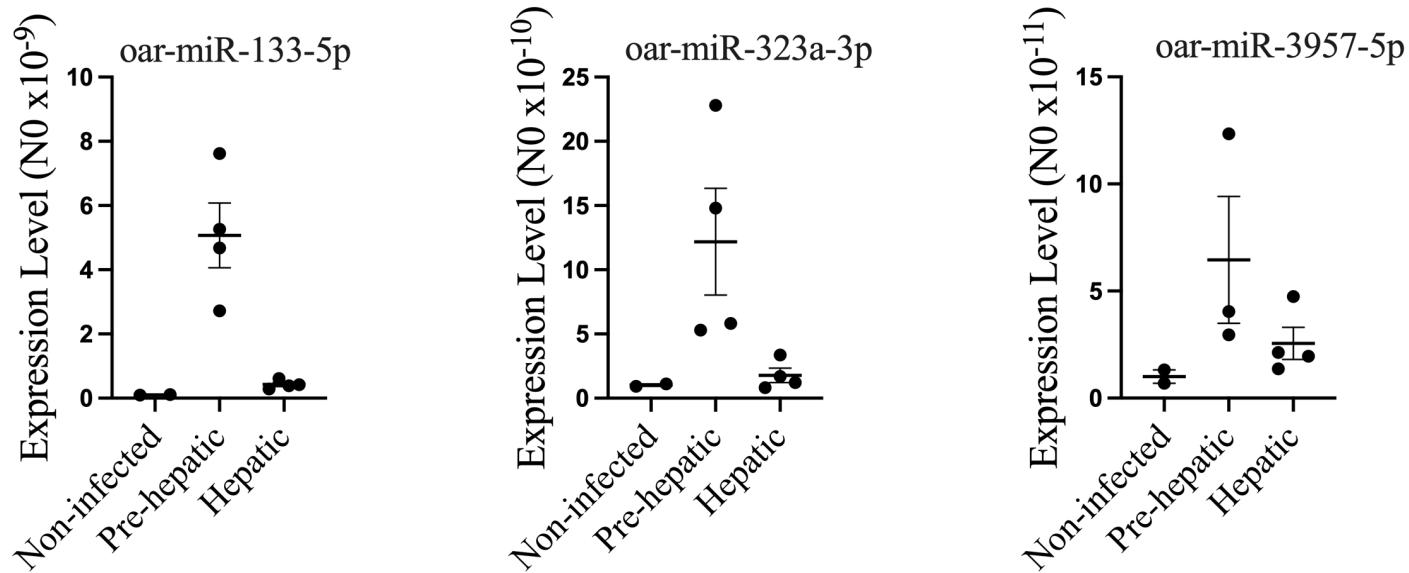
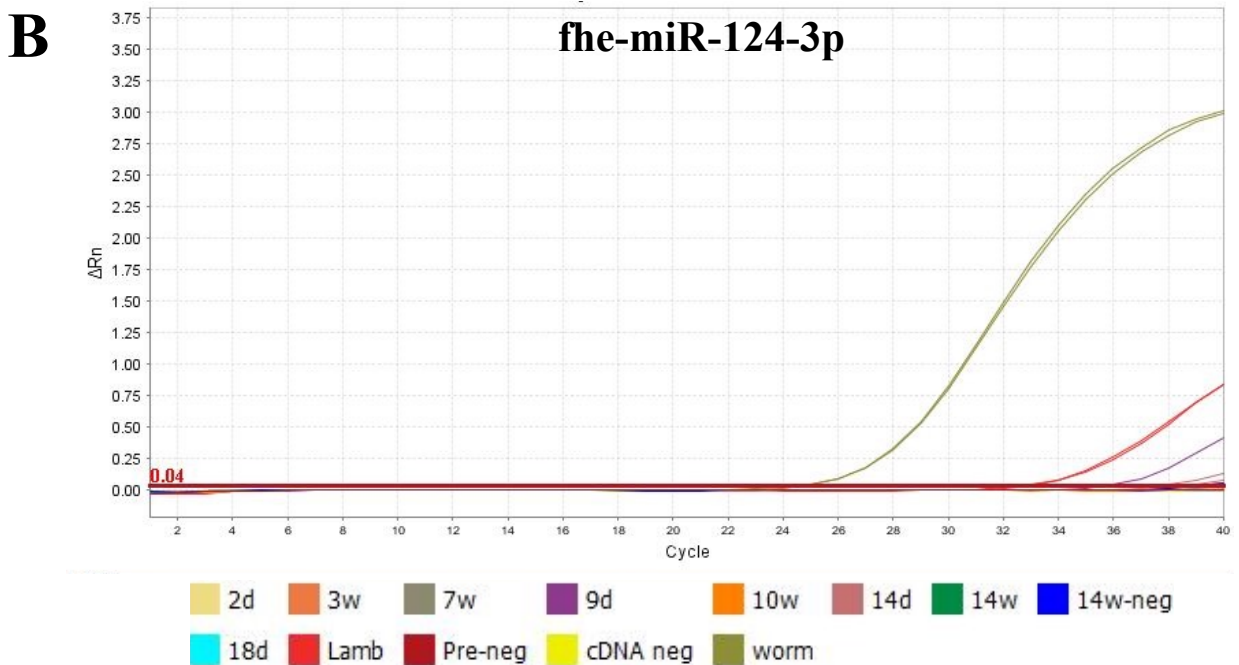
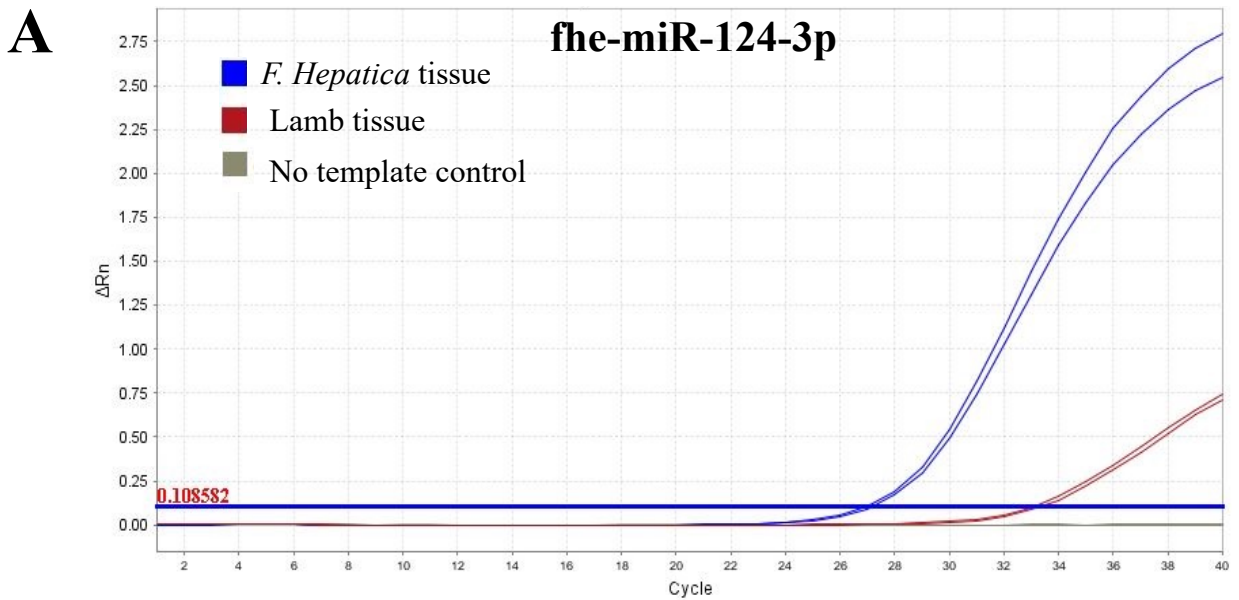
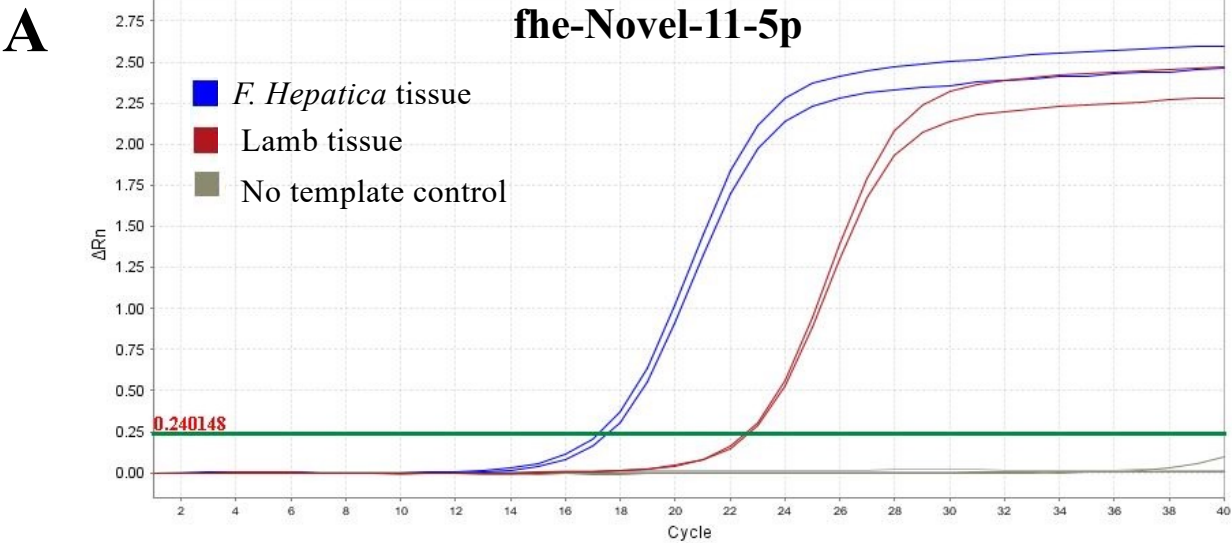




Supplementary Figure 1. Validation of sequencing data using PCR and primers designed to detect the expression of sheep miRNAs. RT-qPCR quantification of oar-miR-133-5p, oar-miR-323a-3p and oar-miR-2957-5p expression in the RNA isolated from the Set A and Set B sheep sera samples that had previously been sequenced. The data is presented as the starting quantity of genetic material prior to amplification (N0) as determined by LinRegPCR (v.11) This is calculated in the unit of the Y-axis of the PCR amplification plot, which are arbitrary fluorescence units. The average N0 value of two technical replicates are shown for each time point.



Supplementary Figure 2. Detection of fhe-miR-124-3p. RT-qPCR amplification plot showing (A) detection of canonical fhe-miR-124-3p in *F. hepatica* tissue and lamb tissue, (B) canonical fhe-miR-124-3p was hardly amplified or in Set A and B sheep sera samples (n = 6 sheep sera samples pooled at each time point). d: days; w: weeks; Pre-neg: Pre-infection timepoint at day 0; 14w-neg: non-infected age-matched control at 14 weeks. Results of two technical replicates for each sample are shown in the amplification plots.



B

Ovis aries 18S ribosomal RNA gene, complete sequence

Sequence ID: [KY129860.1](#) Length: 1869 Number of Matches: 1

Range 1: 671 to 688 [GenBank](#) [Graphics](#) [▼ Next Match ▲](#)

Score	Expect	Identities	Gaps	Strand
36.2 bits(18)	0.024	18/18(100%)	0/18(0%)	Plus/Plus

Query	1	AAGCTCGTAGTTGGATCT	18
Sbjct	671	AAGCTCGTAGTTGGATCT	688

Supplementary Figure 3. Detection of fhe-Novel-11-5p (A) RT-qPCR amplification plot showing amplification of canonical fhe-Novel-11-5p in *F. hepatica* tissue and lamb tissue. Results of two technical replicates for each sample are shown. (B) BLASTN output showing that the shorter Novel-11-5p isomiR sequence found in sheep sera matched 100% with the ribosomal RNA in sheep transcriptome.

