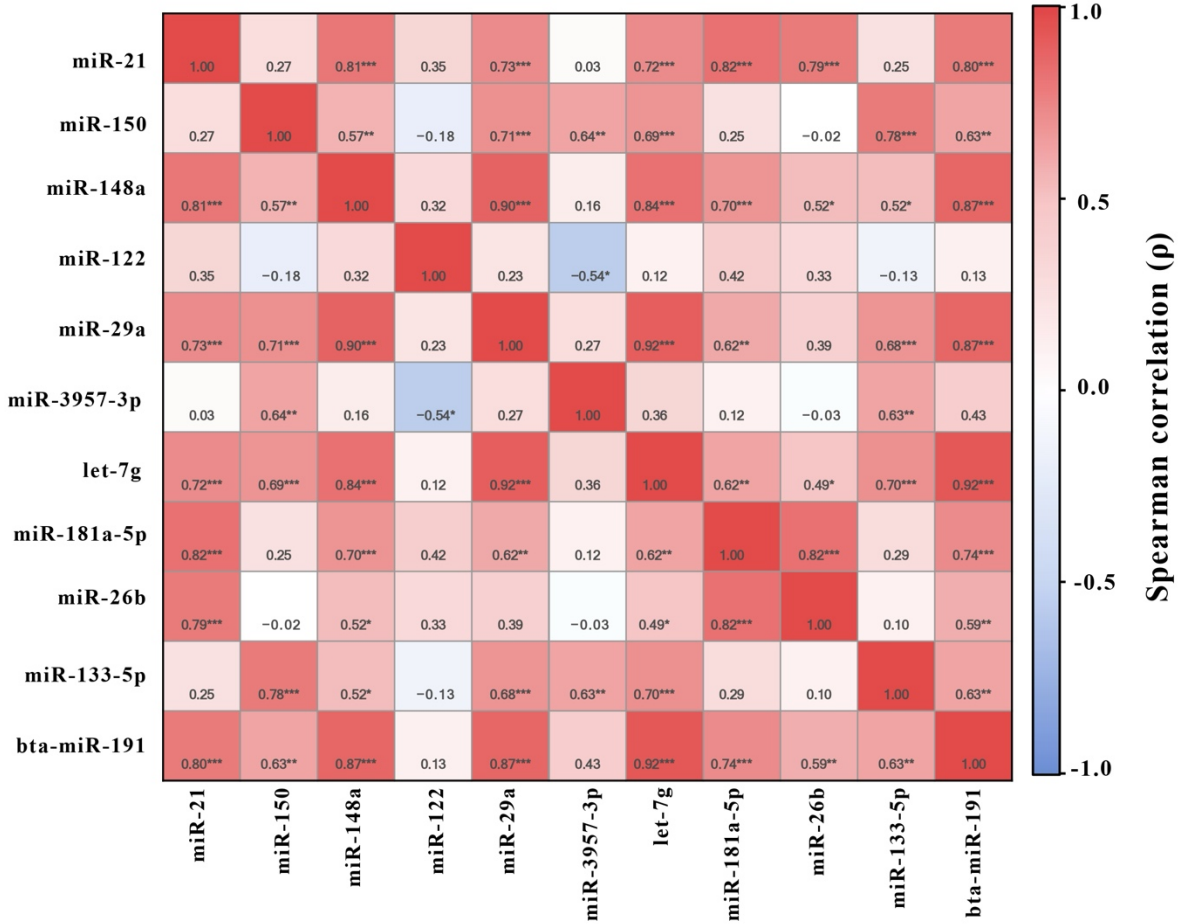
Supplementary Figure S1. Complete Spearman correlation matrix of infection-associated circulating microRNAs during early experimental fasciolosis. Pairwise Spearman's rank correlation analysis performed using absolute circulating microRNA abundance values obtained from experimentally infected sheep throughout the study period (n = 24 infected animals). Correlation coefficients (ρ) are represented by both color intensity and numerical values within each cell. Positive correlations are shown in red, whereas negative correlations are shown in blue. Statistical significance after Benjamini-Hochberg correction is indicated as follows: P < 0.05 (*), P < 0.01 (**), and P < 0.001 (**).



Top significant positive and negative correlations

Circulating miRNAs	ρ	Adjusted p
Positive correlations		
let-7g vs bta-miR-191	0.92	<0.001
miR-29a vs let-7g	0.92	<0.001
miR-148a vs miR-29a	0.90	<0.001
miR-29a vs bta-miR-191	0.87	<0.001
miR-148a vs bta-miR-191	0.87	<0.001
Negative correlations		
miR-122 vs miR-3957-3p	-0.54	<0.005

Supplementary Figure S2. Selected temporal trajectories of relative expression following infection. Changes in $\log_2$ fold-change relative to controls are shown for miR-150, TGF-β, miR-122, and TNF-α across the post-infection time points. Lines connect the available measurements for each marker, and symbols denote the respective variables. The horizontal dashed line indicates no change relative to the control ($\log_2$ fold-change = 0).

