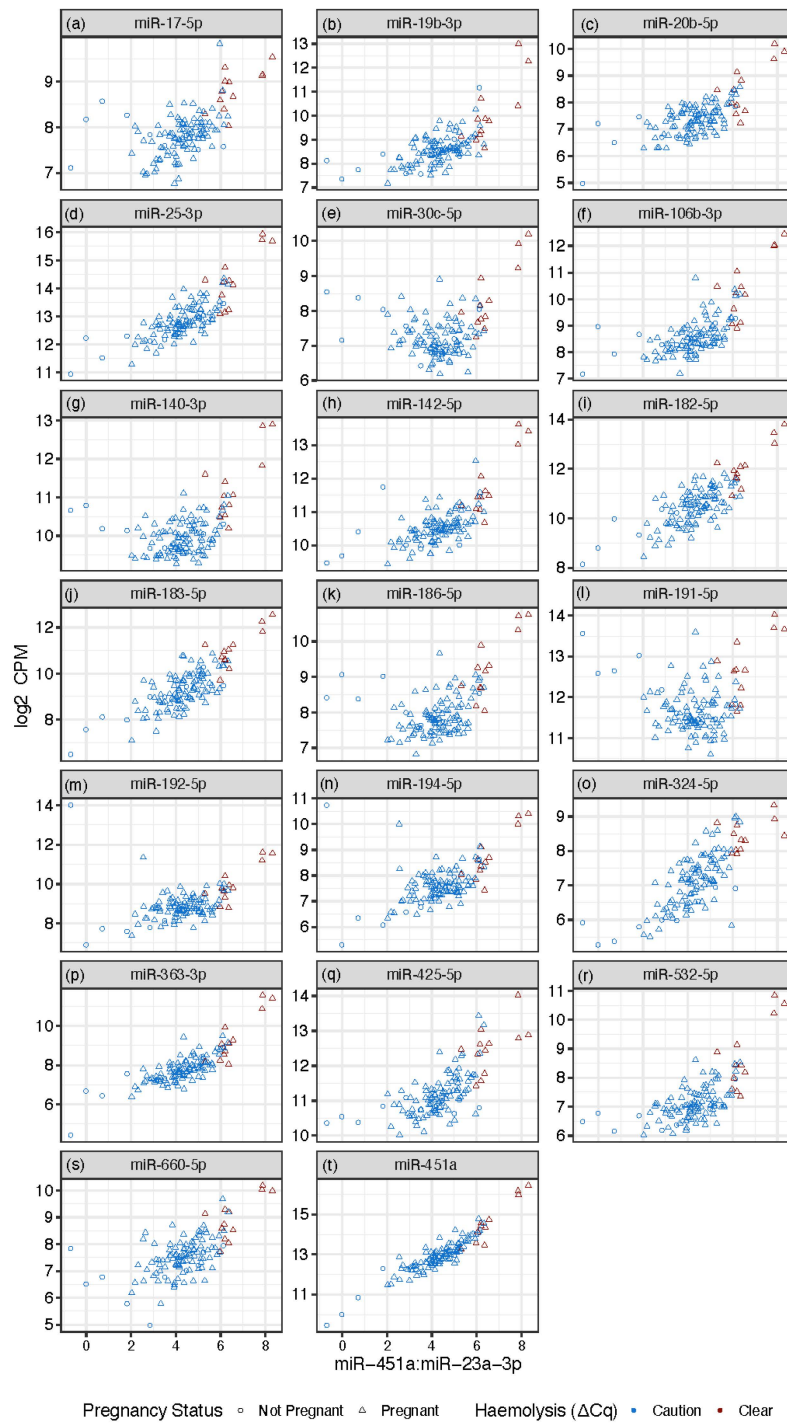
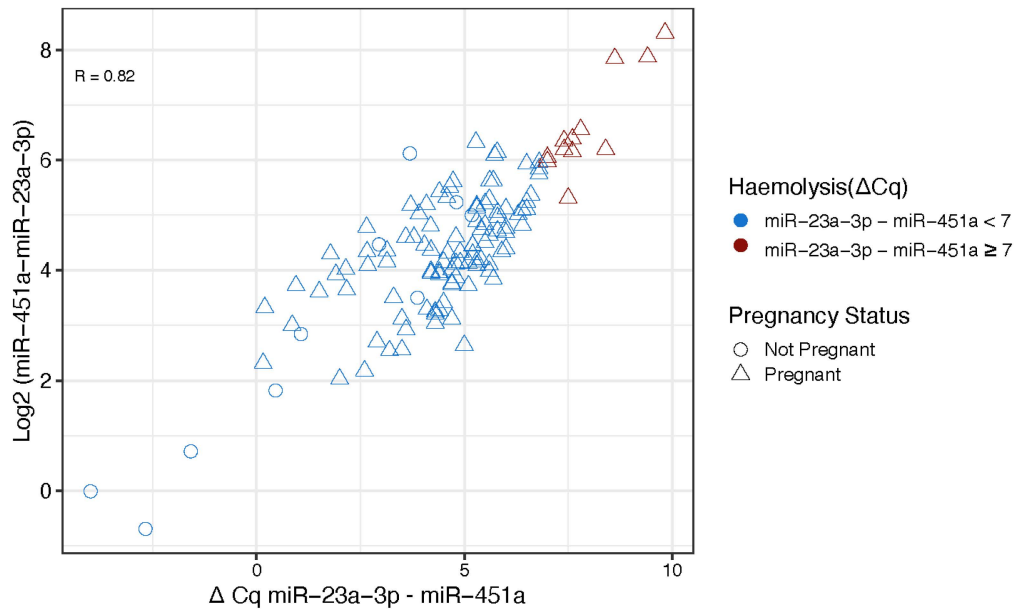


Supplementary Figure S4.1: Scatter plots of \log_2 expression for all miRNAs in our 20 miRNA haemolysis signature set as a function of the ΔCq (miR-451a-miR-23a-3p) gold standard method of haemolysis detection. Signature miRNAs are presented in ascending numeric order from miR-17-5p (a) to miR-451a (t). For each miRNA there is a strong positive correlation between expression and the sample measure of ΔCq (miR-451a-miR-23a-3p).



Supplementary Figure S4.2: Scatter plots of log₂ signature microRNA (miRNA) counts per million (CPM) as a function of a simple, proxy, measure of haemolysis calculated by subtracting the log₂ CPM expression of the invariant miRNA miR-23a-3p from the red blood cell associated miR-451a. Samples are coloured according to the measure of a haemolysis assayed using the ΔCq (miR-451a-miR-23a-3p) gold standard method. For all signature miRNAs there is a strong correlation between the expression of the signature miRNAs and the gold standard haemolysis metric.



Supplementary Figure S4.3: Scatter plot of the simple, proxy, measure of haemolysis calculated by subtracting the \log_2 CPM expression of the invariant miRNA miR-23a-3p from the red blood cell associated miR-451a as a function of the ΔCq (miR-451a-miR-23a-3p) gold standard method of haemolysis detection. We identified a strong, statistically significant ($P\text{-Value} < 2.2 \times 10^{-16}$) correlation between these two measures of haemolysis.