



Supplementary Figure S2: (a) Volcano plot of differential expression. Linear regression identified 138 miRNA which were more highly abundant in haemolysed compared to non-haemolysed samples with $\text{FDR} < 0.05$ (green). (b) MA plot (M (log ratio) and A (mean average)) of Log_2 fold change as a function of Log_2 average expression indicates most miRNA have an average expression $< 10 \text{ Log}_2$ CPM. miR-451a and miR-16-5p, both highly red blood cell associated, are highly expressed and more abundant in the haemolysed group (green).