

Supplementary information, Figure S1

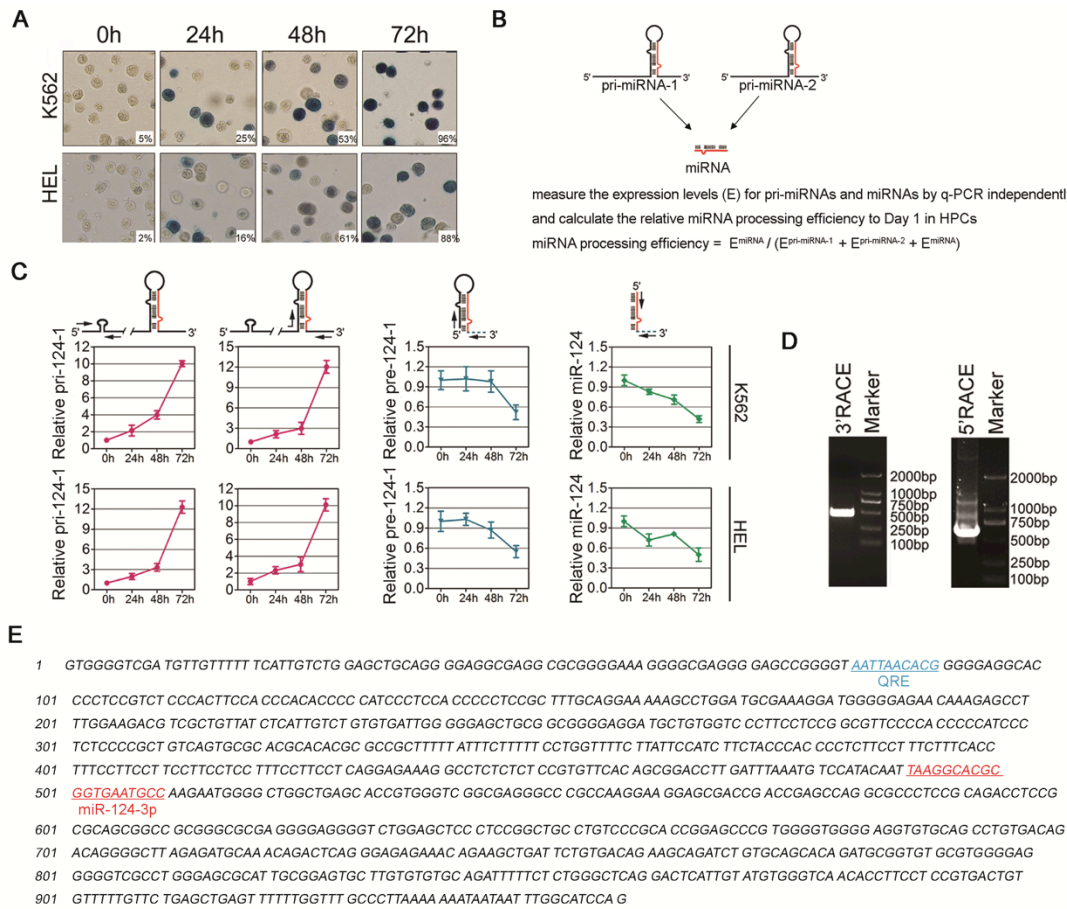


Figure S1 The post-transcriptional regulation of miR-124-1 during erythropoiesis. **(A)** Representative DAB staining of K562 and HEL cells undergoing erythroid differentiation caused by hemin treatment for 0, 24, 48 and 72 h. **(B)** Formula utilized to detect the processing efficiency of each miRNA in HPCs. The relative expression level of pri-miRNAs and miRNAs was determined by q-PCR independently, and the relative miRNA processing efficiency was calculated as the ratio of miRNA to total transcripts (miRNA + pri-miRNA), related to **Figure 1C**. **(C)** Q-PCR results shows the relative expression levels of pri-124-1, pre-124-1 and miR-124 as in K562 and HEL cells undergoing E culture. **(D)** The agarose gel electrophoresis results of 5' RACE and 3' RACE assays. **(E)** The full length of pri-124-1 transcript obtained from RACE assays. Error bars reflect SEM from three biological replicates if not stated otherwise.