

Supplementary information, Figure S9

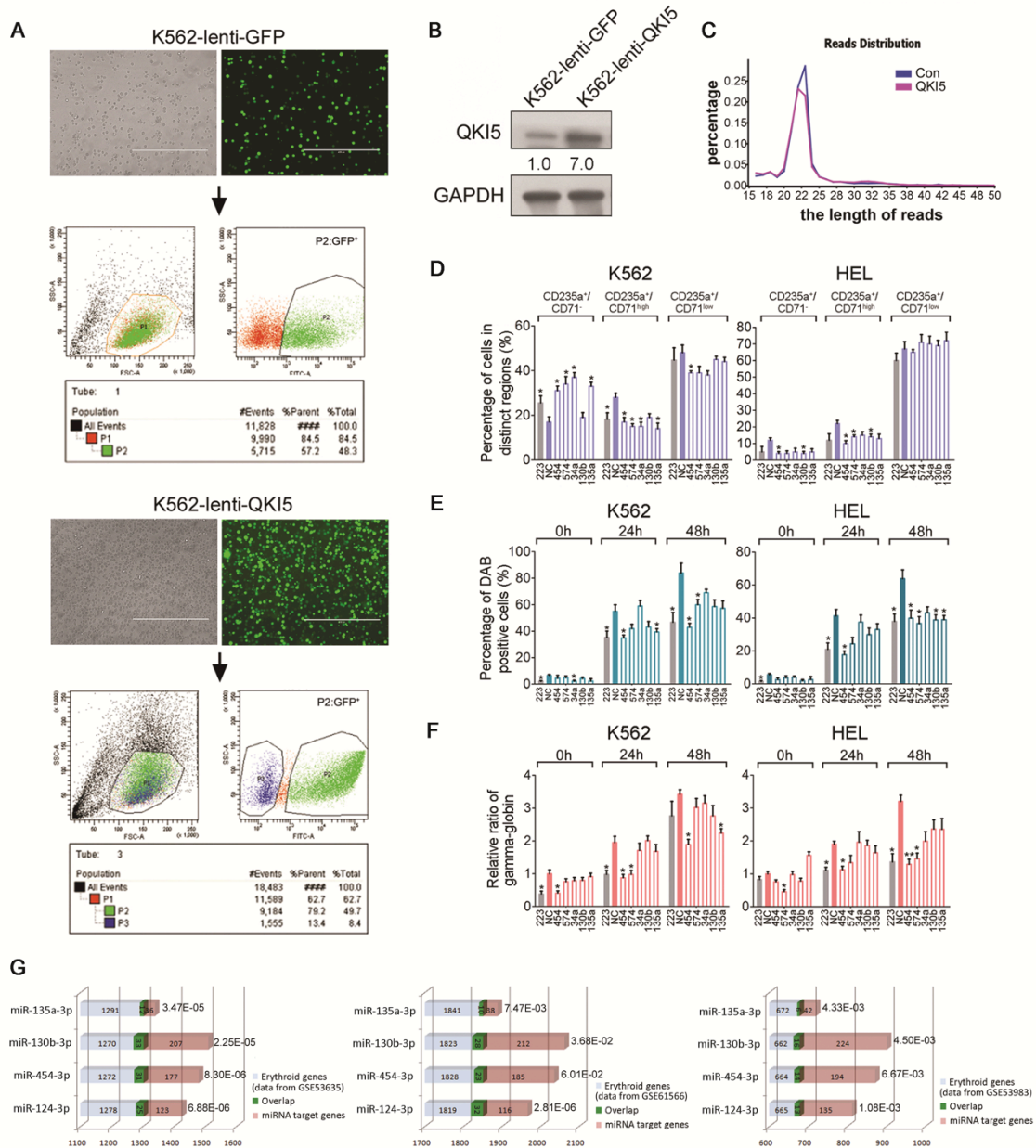


Figure S9 The regulation of multiple miRNAs by QKI5 in erythroid cells. **(A)** The microscopy images of K562 cells transduced with either lenti-GFP or lenti-QKI5. These cells are subsequently sorted by FACS (right panel). **(B)** Immunoblot of QKI5 in K562 cells transduced with lenti-QKI5 or lenti-GFP. **(C)** Length distribution of small RNA-seq reads in two samples (Con: K562 cells transduced with lenti-GFP

control; QKI5: K562 cells transduced with lenti-QKI5). **(D-F)** Quantitative data of functional analysis of selected miRNAs in K562 and HEL cells transfected with miRNA mimics or negative control (NC). **(D)** Quantitative data of the percentage of cells gated within CD235a⁻/CD71⁻ (R1), CD235a⁺/CD71^{high} (R2), and CD235a⁺/CD71^{low} (R3) regions in 24 h of E culture. **(E)** Quantitative data of the percentage of DAB-positive cells. **(F)** Quantitative data of relative γ -globin mRNA expression. **(G)** Hypergeometric test suggested a significant overlap between miRNA target genes and “Erythroid genes” in datasets GSE53635, GSE61566 and GSE53983. Error bars reflect SEM from three biological replicates if not stated otherwise. Significance was determined by *t*-test with **P* < 0.05; ***P* < 0.01.