

Supplementary information, Figure S3

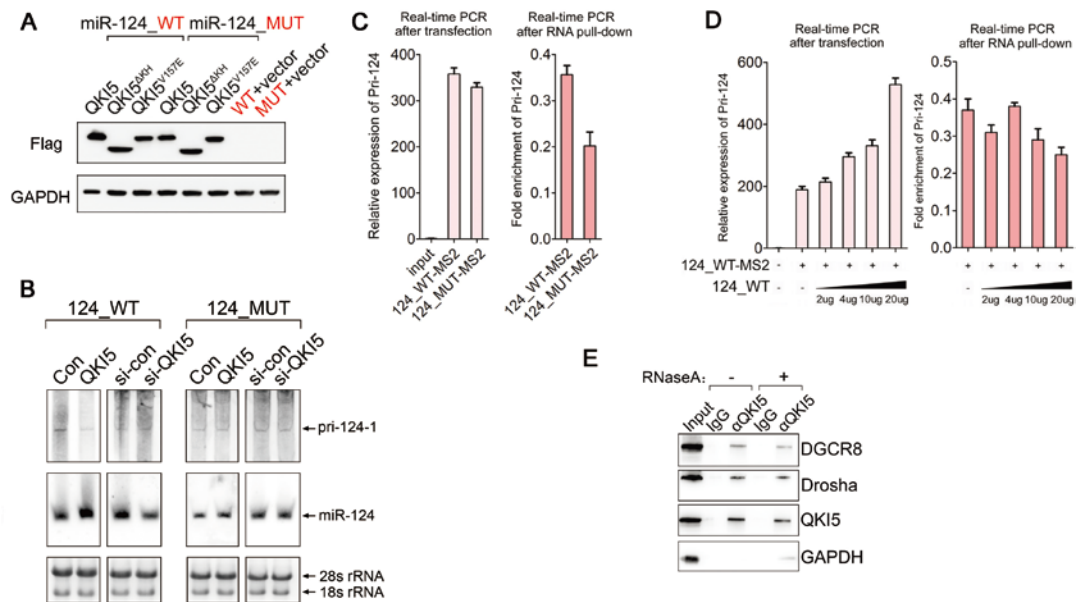


Figure S3 QKI5 binds to pri-124-1 transcript. **(A)** Immunoblot of QKI5 variants level in 293T cells co-transfected with either wild-type (124_WT) or mutant (124_MUT) pri-124-1, and either wild-type (QKI5) or mutant (QKI5^{AKH} and QKI5^{V157E}) QKI5 corresponding to **Figure 3B**. **(B)** The northern blot analysis of pri-124-1 and miR-124 levels upon QKI5 overexpression or knockdown. The 28s and 18s rRNA are used as loading control. **(C)** The left panel: q-PCR analysis of pri-124-1 transcripts in 293T cells transfected with either MS2-tagged wild-type pri-124-1 (124_WT-MS2) or MS2-tagged QRE mutant pri-124-1 (124_MUT-MS2). The right panel: q-PCR analysis of precipitated pri-124-1 transcripts in RNA pull-down assays. **(D)** The left panel: q-PCR analysis of pri-124-1 transcripts in 293T cells co-transfected with 124_WT-MS2 and increased dosages of 124_WT. The right panel: q-PCR analysis of precipitated pri-124-1 transcripts in competitive RNA pull-down assays. **(E)** Identification of the interaction of QKI5 with Drosha and DGCR8 by co-IP analysis in K562 cells. GAPDH was used as a negative control.