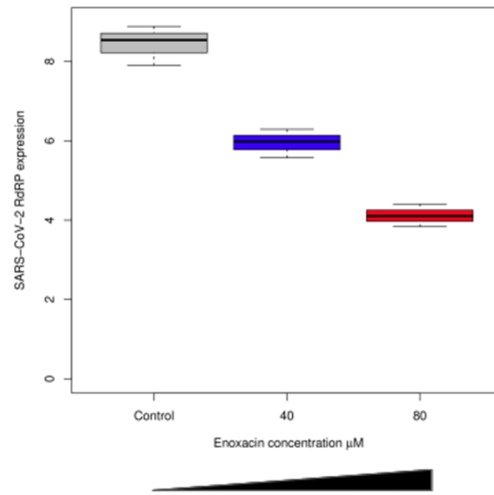


**Supplementary Figure S1:** (A): Negative control locus on the UCSC genome browser. Blue track: miRNA-seq coverage (negative strand) normalized by SARS-CoV-2 mapping reads (RPM) at 24 hrs after infection of Calu-3 cells (GEO GSE148729 data). Green tracks: phastCons score across 44 bat coronaviruses (Bat Phastcons) and 119 vertebrate coronaviruses (Phastcons). (B): putative structure of pre-miR-AS1 computed using RNAfold. Color scale: base-pair probabilities. ©: qPCR amplification plots for miR-AS1 (red line) and negative control (blue line) in Vero E6 and Calu3 SARS-CoV-2 infected cells.



**Supplementary Figure S2:** Enoxacin negatively affects SARS-CoV-2 replication in Calu3 cells. SARS-CoV-2 was assessed by qPCR amplification of RdRP viral gene, normalized against GAPDH (Arbitrary Units)