Figure S1. The RNA expression of HOTTIP in overexpression or knockdown OS cells. HOTTIP (A) overexpression or (B) knockdown OS cell lines were constructed and the RNA expression of HOTTIP in overexpression or knockdown OS cells were validated by reverse transcription-quantitative PCR. The overexpression or knockdown efficiency were about triple that of the respective control. ***P<0.001; HOTTIP, HOXA transcript at the distal tip; OS, osteosarcoma; sh, short hairpin; NC, negative control.

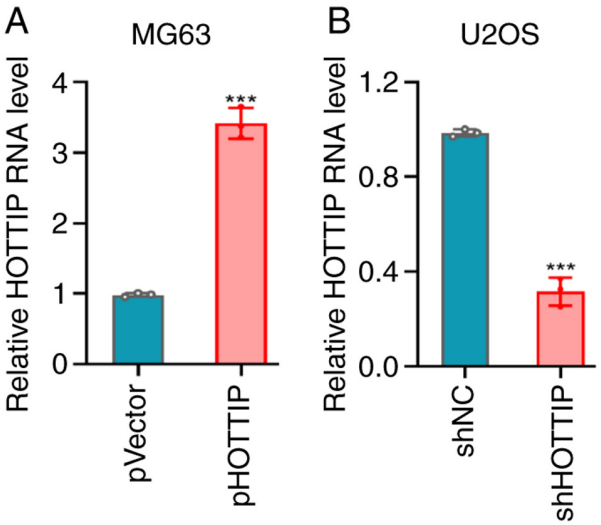

Figure S2. The RNA expression of DGCR8 in HOTTIP overexpression or knockdown OS cells. The expression level of DGCR8 mRNA was verified by reverse transcription-quantitative PCR in HOTTIP overexpression or knockdown cell lines. ns, not significant vs. control. DGCR8, DiGeorge Critical Region 8; HOTTIP, HOXA transcript at the distal tip.

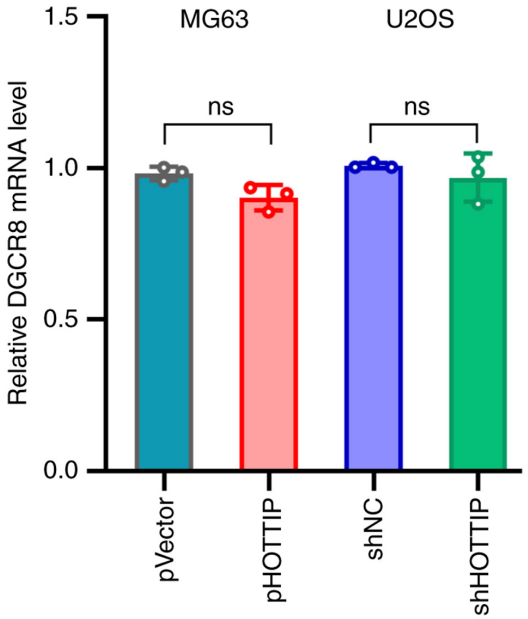

Figure S3. The RNA expression of miR-214-3p and HOTTIP in MG63 cells. (A) The RNA expression of miR-214-3p in mimics transfected MG63 cells were validated by reverse transcription-quantitative PCR. (B) These mimics were transfected in HOTTIP overexpression MG63 cell and the relative RNA expressions were validated. $^{*}$P<0.05, $^{***}$P<0.001, ns, not significant; miRNA, micro RNA; HOTTIP, HOXA transcript at the distal tip.

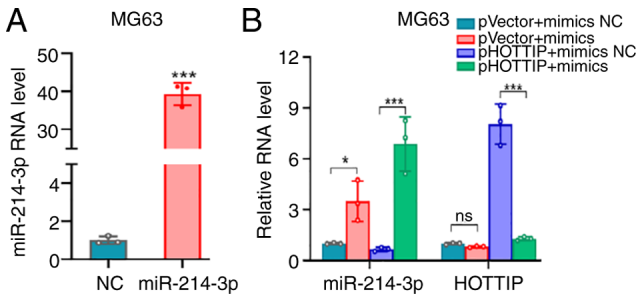

Figure S4. GPX4 is a potential target gene of miR-214-3p. (A) Venn diagrams showing the intersection between target genes identified in microRNA databases (TargetScan. https://www.targetscan.org/) and Ferroptosis Marker (FerrDb V2 database. http://www.zhounan.org/). (B) The online bioinformatics programs, miRBase (https://www.mirbase.org/), TargetScan and RNAhybrid (https://bibiserv) were applied to predict miR-214-3p's binding site with GPX4. GPX4, glutathione peroxidase 4; miRNA, micro RNA.