Figure S1. Transfection efficiency determination by reverse transcription-quantitative PCR. (A) sh-MALAT1-1 and sh-MALAT1-2 were designed to inhibit the expression of lncRNA *MALAT1* in primary cells isolated from cervical carcinoma tissue, and sh-Control was used as the negative control. (B) sh-MALAT1-1 and sh-Control were subsequently transfected into U14 cells. n=5; ***P<0.001. (C) MALAT1 overexpression vector plasmid was used to increase the expression of lncRNA *MALAT1* in primary cells isolated from cervical carcinoma tissue; empty vector was used as the negative control. n=5; ***P<0.001. (D and E) sh-MALAT1-1 and the *MALAT1* overexpression vector were successfully transfected into HeLa cells; sh-Control and empty vector were used as the respective negative controls. n=5; *P<0.05, ***P<0.001. lncRNA, long non-coding RNA; *MALAT1*, metastasis-associated lung adenocarcinoma transcript 1; sh, short hairpin RNA.

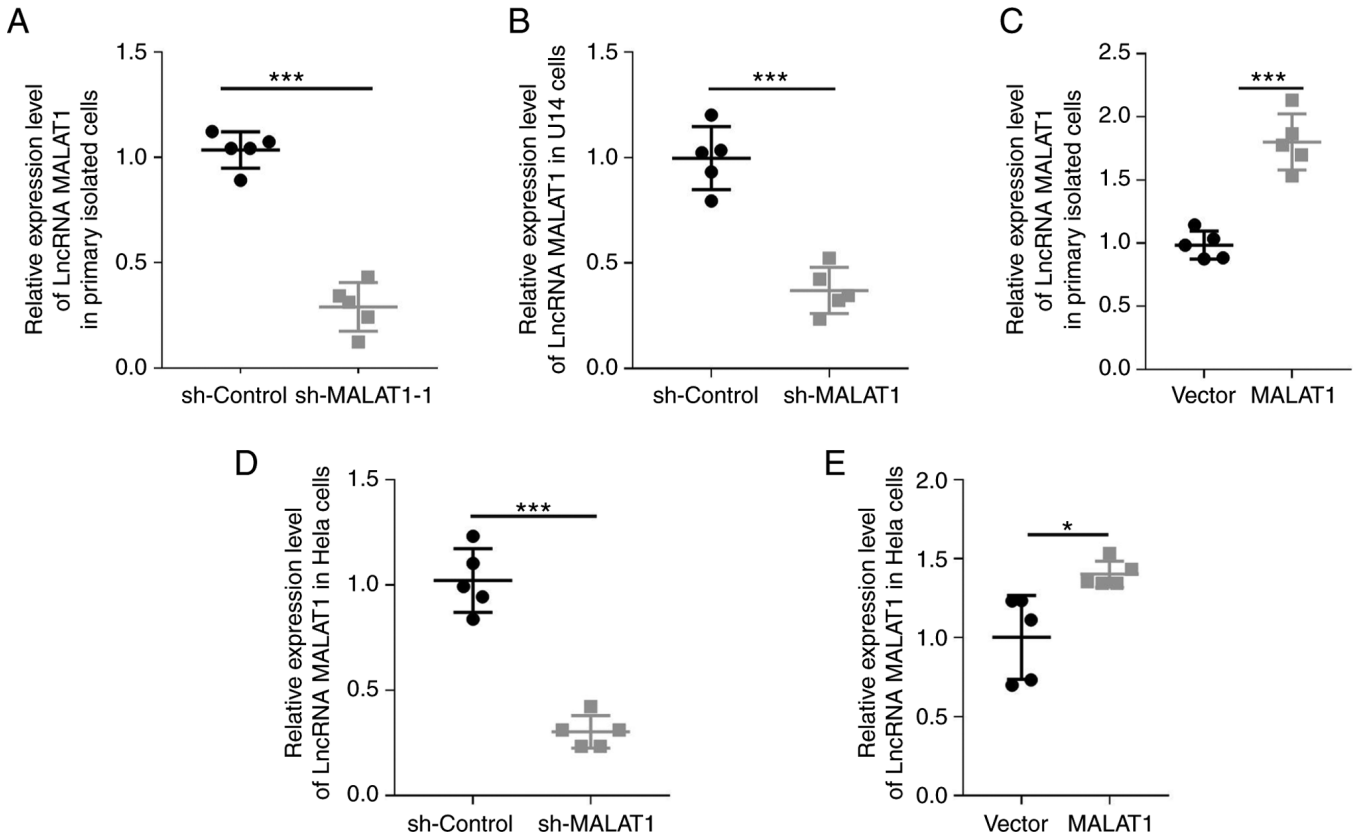


Figure S2. Detection of the number of viable and dead cells in primary cervical carcinoma cells overexpressing lncRNA MALAT1 by using Trypan blue staining. The number of viable and dead cells were determined after overexpression of lncRNA *MALAT1*. n=5; ***P<0.001. lncRNA, long non-coding RNA; *MALAT1*, metastasis-associated lung adenocarcinoma transcript 1.

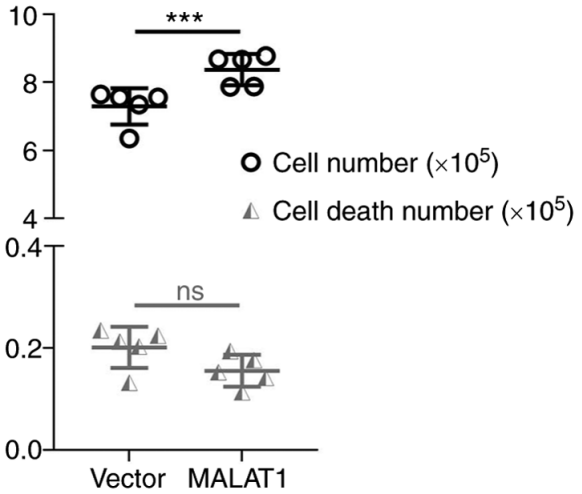
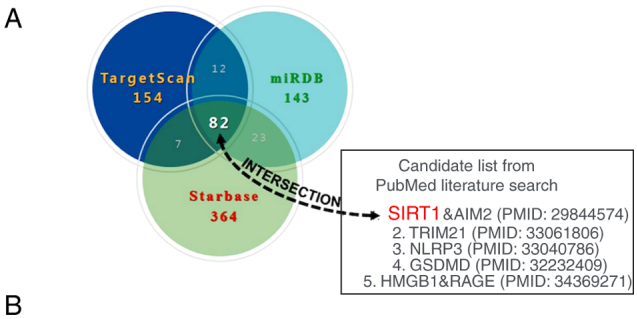


Figure S3. Downstream target prediction of miR-124. (A) Downstream prediction of miR-124 by bioinformatic databases, Venn diagram, and literature search. Three bioinformatic databases (starBase, TargetScan, and miRDB) and Venn diagram, combined with PubMed database searching was adopted to predict the potential targets of miR-124 during cervical cell pyroptosis. (B) Potential putative binding sites between SIRT1 and miR-124 among human, mouse and rat were applied from Targetscan database. AIM2, absent in melanoma 2-like receptor; HMGB, high mobility group box 1; miR, microRNA; NLRP3, NOD-like receptor protein 3; RAGE, advanced glycation end product receptor; SIRT1, sirtuin 1; TRIM21, tripartite motif containing-21.



B

Position 1211-1218 of SIRT1 3′ UTR 5′ ...UUUAAAAGCUUAGCCUGCCUUAA...
hsa-miR-124 3′ CGUAAGUGGCGCACGGAAUU

Position 1068-1975 of SIRT1 3′ UTR 5′ ...UUUAAAAGCUUAGCUUGCCUUAA...
mmu-miR-124 3′ ACCGUAAGUGGCGCACGGAAUU

Position 1040-1046 of SIRT1 3′ UTR 5′ ...UUUAAAAGCUUAGCUUGCCUUAA...
rno-miR-124 3′ CCGUAAGUGGCGCACGGAAU

Figure S4. Transfection efficiency of miR-124 mimics in HeLa cells. The level of miR-124 was determined after transfection of miR-124 mimics and compared with NC group. n=5; ***P<0.001. miR, microRNA; NC, negative control.

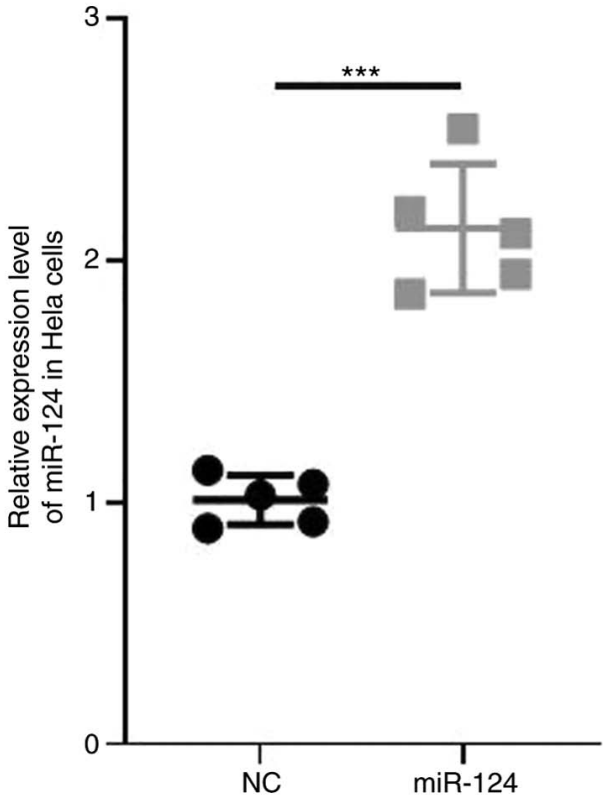


Figure S5. Transfection efficiency of SIRT1 in HeLa cells. (A) Western blot (B) reverse transcription-quantitative PCR were performed to detect the protein and mRNA expression levels, respectively, of SIRT1; sh-NC was used as the control. n=5; ***P<0.001. NC, negative control; 0020sh, shRNA; SIRT1, sirtuin 1.