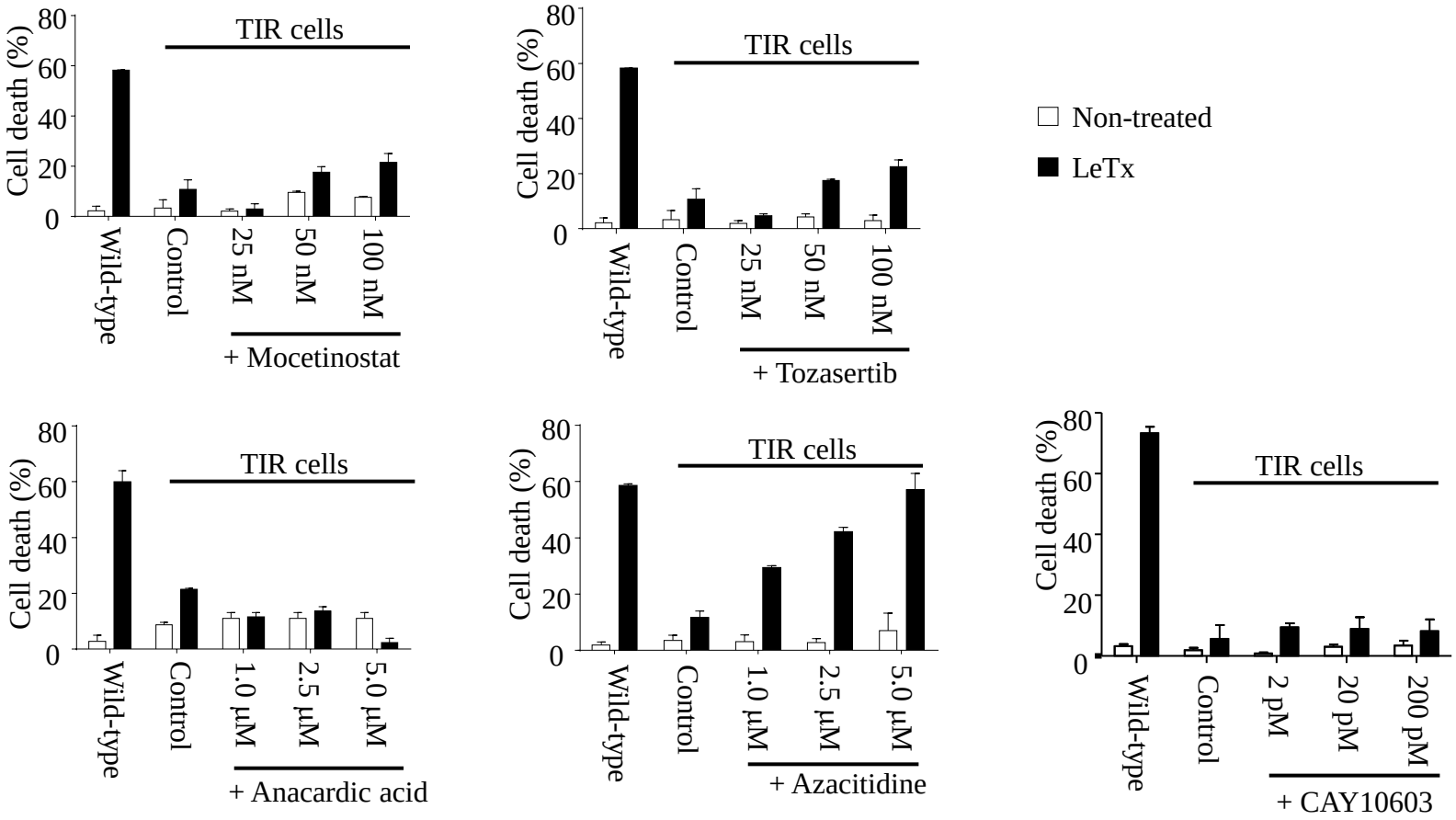
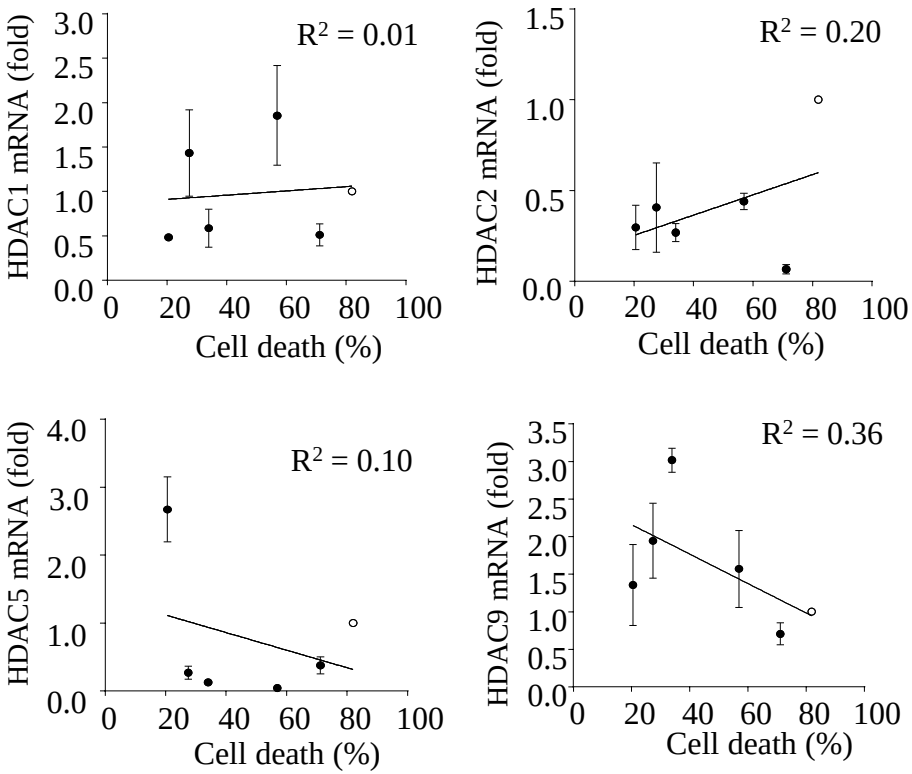
Supplemental Table S1. Primer sequences used for qPCR and ChIP assays.

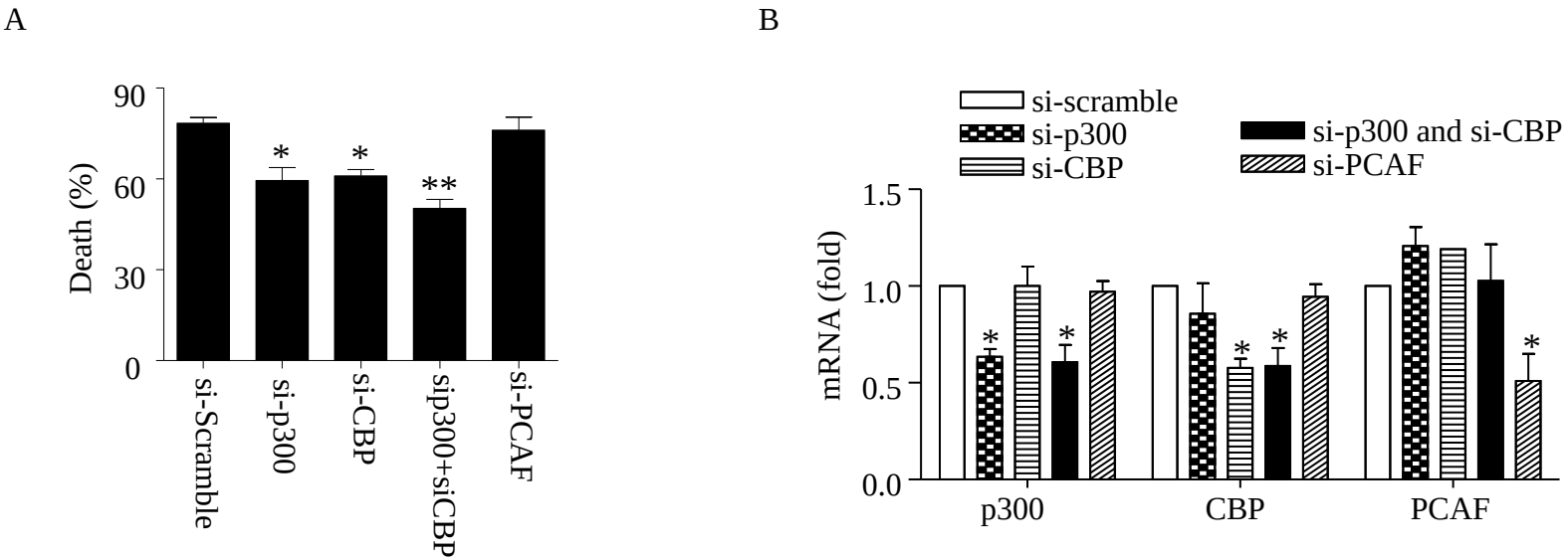
Analysis	**Gene**	**Primer sequence (5'→ 3')**
Quantitative Real Time PCR	BNIP3	F: 5′-GCTCCCAGACACCACAAGAT-3′ R: 5′-TGAGAGTAGCTGTGCGCTTC-3′
	BNIP3L	F: 5′-CCTCGTCTTCCATCCACAAT-3′ R: 5′-GTCCCTGCTGGTATGCATCT-3′
	MLN64	F: 5′-CAGGCAGTCACCGTCTTGTT-3′ R: 5'-TGCGGTGGTGGATCAGATCT-3'
	HDAC1	F: 5'-TGAAGCCTCACCGAATCCG -3' R: 5'-GGGCGAATAGAACGCAGGA-3'
	HDAC2	F: 5'-GGAGGAGGCTACACAATCCG-3' R: 5'-TCTGGAGTGTTCTGGTTTGTCA-3'
	HDAC5	F: 5'-AGCACCGAGGTAAAGCTGAG-3' R: 5'-GAACTCTGGTCCAAAGAAGCG-3'
	HDAC8	F: 5'-ACGGGAAGTGTAAAGTAGCCA-3' R: 5'-TCCACGTAGAGAATACGGTCAAA-3'
	HDAC9	F: 5'-GAGAGGCATCGCAGAGAGC-3' R: 5'-CCCACGGAATGATTCTTTCCA-3'
	CBP	F: 5`-CACAGCTAATGGCAGCTTTCAT-3` R: 5`-CTGGCACTATTTTGTTGTTGCT-3
	P300	F: 5`-GTTCTCCCTTACAGCAGCAACA-3' R: 5`-GCAGAGGATTCATGTTCTGCAAG-3`
	PCAF	5`-GAGAACAAGTCCTGGATGCAGA-3 5`-GGTCCAAGCATCCCTGCAGG-3`
	CASPASE-1	5`-CTTGGAGACATCCTGTCAGGG-3 5`-AGTCACAAGACCAGGCATATTCT-3`
	GAPDH	F: 5′-GCATTGTGGAAGGGCTCATG-3′ R: 5′-TTGCTGTTGAAGTCGCAGGAG-3
ChIP: H3K27Ac, HDAC3, and HDAC8 Analysis	BNIP3	F: 5'-AATCTGTCCCTCAACGGCTG-3' R: 5'-GTTGGTAGATGCACCAGGCT-3'
	BNIP3L	F: 5'-TCTTCCTCCAGTCCTACCCA-3' R: 5'-CCTGGGACAGTGTTAGCCTC-3'
	MLN64	F: 5'- CCTTCCGCTCTGAGGAGTTG -3′ R: 5′- GACCGAACCAAAGACGGACA -3′
	GAPDH	F: 5'-GTTCAGACCCATCCCGTAATC-3' R: 5'-CAAAGGTATGCACCTCACAAC3'
ChIP: RNA polymerase II analysis	BNIP3	F: 5'-CCCTTGTCCCTCAGTCCA-3' R: 5'-GAACCCAACTGCGACAGG-3' Probe: 5'-/56- FAM/TGTCGCCTG/ZEN/GCCTCAGAACT/3IABkFQ/-3'
	BNIP3L	F: 5'-AGCTGCCTGTGTTGTCATC-3' R: 5'-ACACAACAAGTCGAGTTCCC-3' Probe: 5'-/56 FAM/TGACGTCAC/ZEN/GAAGGGAGGGACT/3IABkFQ/-3'
	MLN64	F: 5'-AATTGTCCTGAGACTCCTCTTTC-3' R: 5'-CAAGATCCTGACCCTAAGATAACC-3



Supplemental Fig. S1. The DNMT inhibitors sensitize TIR cells to LeTx-induced pyroptosis. TIR cells were cultured in the presence or absence of different concentrations of inhibitors for 24 h as indicated in the figure. Equal number of cells were then re-plated on a 96-well plate dishes with fresh media and then treated with LeTx (500 ng/ml LF and 1µg/ml PA) for 5 h. Cell death was measured using MTT assay as described in Experimental Procedures. Data are expressed as means and ± SD (n=3).



Supplemental Fig. S2. The expression levels of HDAC 1. 2. 5 and 9 are not correlated with the extent of TIR. Total RNAs were purified from wild-type cells (open dots) and five TR clones (closed dots) with different degrees of LeTx sensitivities. Expression of each HDAC were analyzed by quantitative real time PCR. Expression levels of each HDAC relative to those of wild-type cells were plotted against the extent of LeTx sensitivities (500 ng/ml LF and 1 μg/ml PA for 5 h). Correlation of coefficiency (R2) was calculated using GraphPad Prism® program. Results are expressed as means and ± SD (n=3).



Supplemental Fig. S3. Knocking down of p300 and CBP by si-RNAs partially protects RAW264.7 cells from LeTx-induced cell death. RAW264.7 cells were transfected with scrambled (si-scramble), p300 targeting (si-p300), CBP targeting (si-CBP), both si-p300 and si-CBP, or PCAF targeting (si-PCAF) siRNAs for 40 h and then treated with LeTx (500 ng/ml LF and 1 µg/ml PA) for 5 h. (A) Cell death was measured by MTT assay. (B) Toral RNAs were obtained from these cells before treating LeTx and levels of p300, CBP and PCAF mRNAs were measured by RT-qPCR. Data are expressed as means ± SD (n=3). * $p < 0.05$; ** $p < 0.01$.