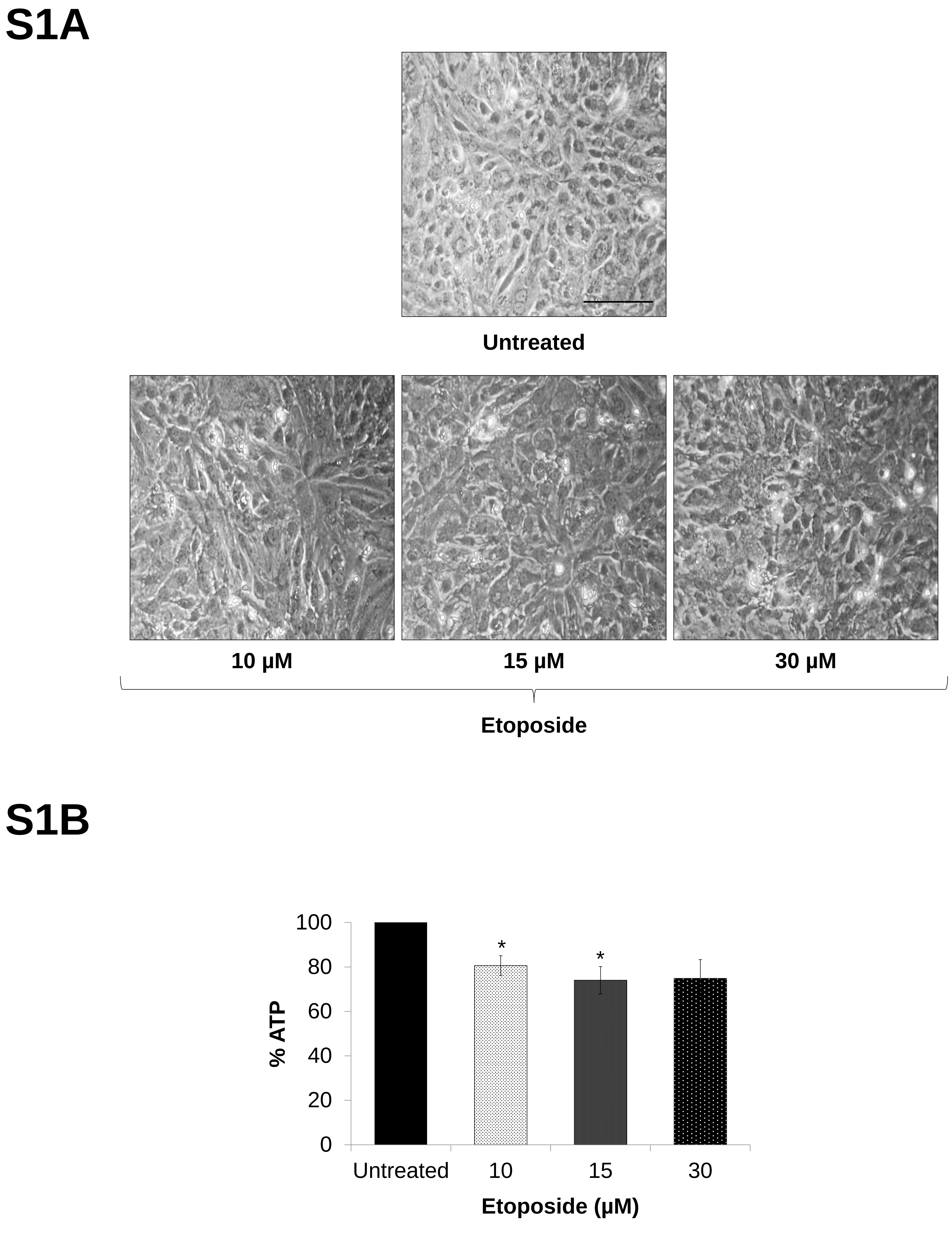
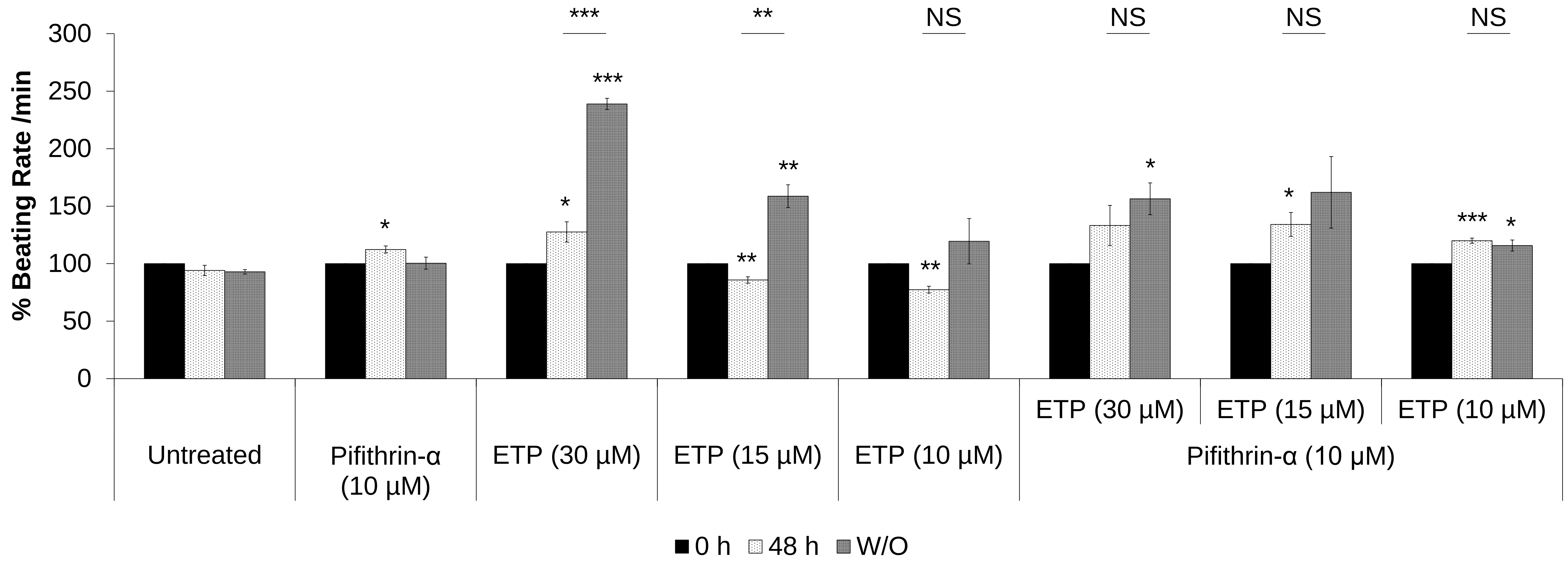
Figure S1



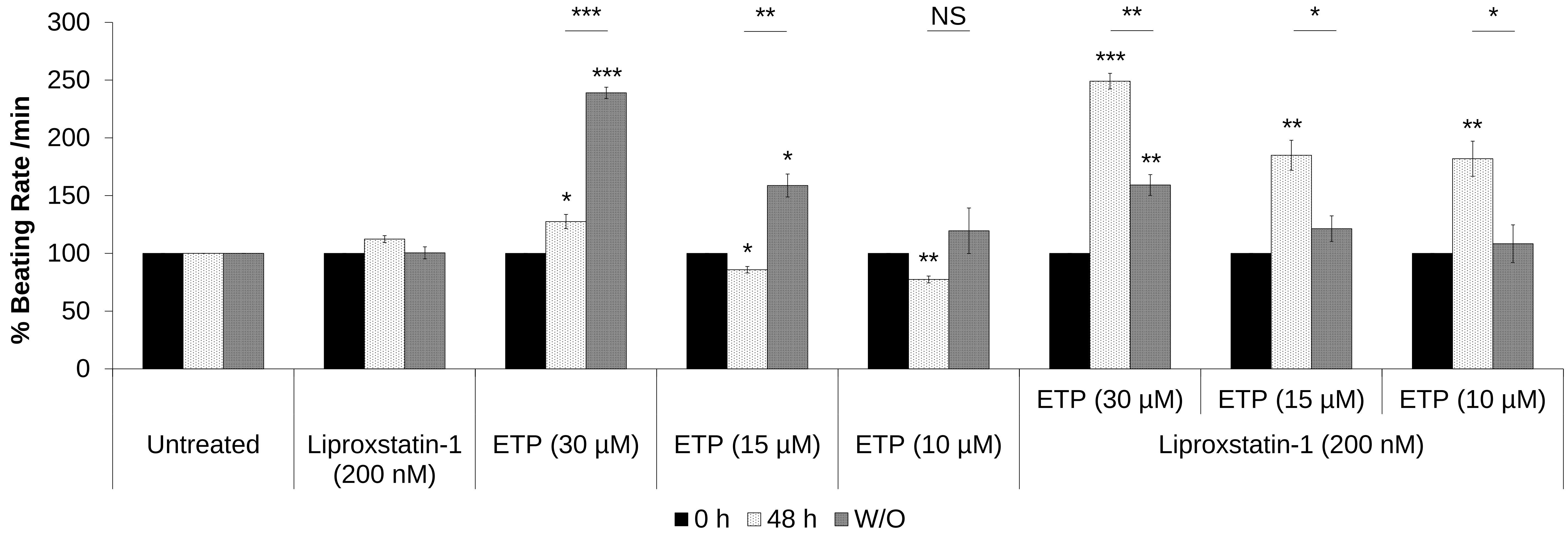
Supplementary figure 1. A) Influence of single high-dose of ETP (10 µM, 15 µM and 30 µM) on cell density and cell morphology. The scale bar represents 50 µm. B) Influence of single high-dose of ETP (10 µM, 15 µM and 30 µM) on intracellular ATP levels in hiPSC-CMs. (n = 3, error bars represent ± SEM) (t test, $*p \leq 0.05$).

Figure S2

S2A

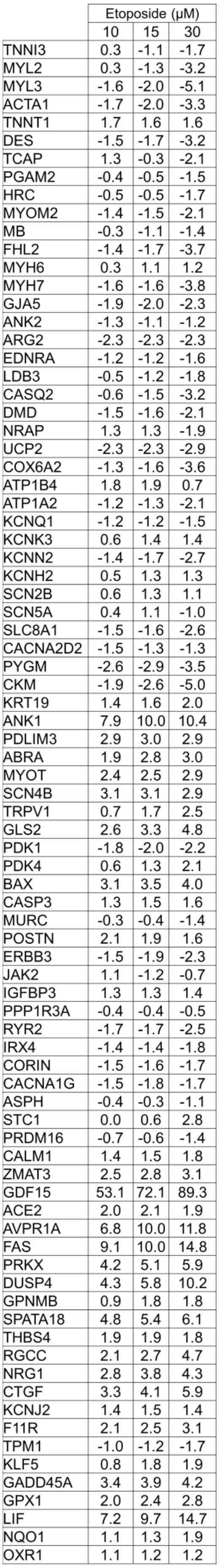


S2B



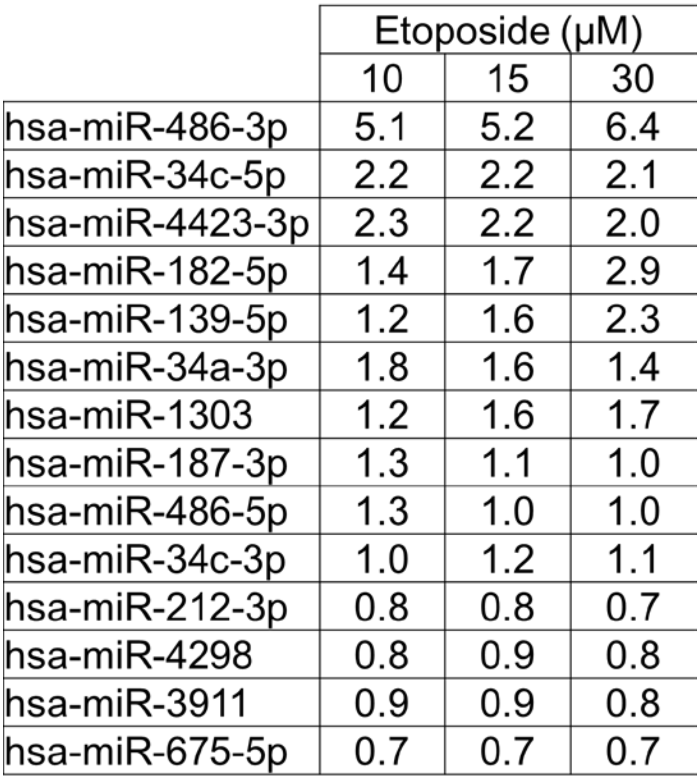
Supplementary figure 2. A) The hiPSC-CMs were co-treated with ETP and 10 µM Pifithrin-α (apoptosis inhibitor) for 48 h. Real time data of CMs beating rate was obtained using xCELLigence RTCA system. Representative graphs display % beating rate values. (n = 3, error bars represent ± SEM) (t test, *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001, NS, non-significant). B) The hiPSC-CMs were co-treated with ETP and 200 nM Liproxstatin-1 (ferroptosis inhibitor) for 48 h. Real time data of CMs beating rate was obtained using xCELLigence RTCA system. Representative graphs display % beating rate values. (n = 3, error bars represent ± SEM) (t test, *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001, NS, non-significant).

Supplementary table 1. The fold change values for 84 genomic markers after Etoposide treatment



	Etoposide (µM)		
	10	15	30
TNNI3	0.3	-1.1	-1.7
MYL2	0.3	-1.3	-3.2
MYL3	-1.6	-2.0	-5.1
ACTA1	-1.7	-2.0	-3.3
TNNT1	1.7	1.6	1.6
DES	-1.5	-1.7	-3.2
TCAP	1.3	-0.3	-2.1
PGAM2	-0.4	-0.5	-1.5
HRC	-0.5	-0.5	-1.7
MYOM2	-1.4	-1.5	-2.1
MB	-0.3	-1.1	-1.4
FHL2	-1.4	-1.7	-3.7
MYH6	0.3	1.1	1.2
MYH7	-1.6	-1.6	-3.8
GJA5	-1.9	-2.0	-2.3
ANK2	-1.3	-1.1	-1.2
ARG2	-2.3	-2.3	-2.3
EDNRA	-1.2	-1.2	-1.6
LDB3	-0.5	-1.2	-1.8
CASQ2	-0.6	-1.5	-3.2
DMD	-1.5	-1.6	-2.1
NRAP	1.3	1.3	-1.9
UCP2	-2.3	-2.3	-2.9
COX6A2	-1.3	-1.6	-3.6
ATP1B4	1.8	1.9	0.7
ATP1A2	-1.2	-1.3	-2.1
KCNQ1	-1.2	-1.2	-1.5
KCNK3	0.6	1.4	1.4
KCNN2	-1.4	-1.7	-2.7
KCNH2	0.5	1.3	1.3
SCN2B	0.6	1.3	1.1
SCN5A	0.4	1.1	-1.0
SLC8A1	-1.5	-1.6	-2.6
CACNA2D2	-1.5	-1.3	-1.3
PYGM	-2.6	-2.9	-3.5
CKM	-1.9	-2.6	-5.0
KRT19	1.4	1.6	2.0
ANK1	7.9	10.0	10.4
PDLIM3	2.9	3.0	2.9
ABRA	1.9	2.8	3.0
MYOT	2.4	2.5	2.9
SCN4B	3.1	3.1	2.9
TRPV1	0.7	1.7	2.5
GLS2	2.6	3.3	4.8
PDK1	-1.8	-2.0	-2.2
PDK4	0.6	1.3	2.1
BAX	3.1	3.5	4.0
CASP3	1.3	1.5	1.6
MURC	-0.3	-0.4	-1.4
POSTN	2.1	1.9	1.6
ERBB3	-1.5	-1.9	-2.3
JAK2	1.1	-1.2	-0.7
IGFBP3	1.3	1.3	1.4
PPP1R3A	-0.4	-0.4	-0.5
RYR2	-1.7	-1.7	-2.5
IRX4	-1.4	-1.4	-1.8
CORIN	-1.5	-1.6	-1.7
CACNA1G	-1.5	-1.8	-1.7
ASPH	-0.4	-0.3	-1.1
STC1	0.0	0.6	2.8
PRDM16	-0.7	-0.6	-1.4
CALM1	1.4	1.5	1.8
ZMAT3	2.5	2.8	3.1
GDF15	53.1	72.1	89.3
ACE2	2.0	2.1	1.9
AVPR1A	6.8	10.0	11.8
FAS	9.1	10.0	14.8
PRKX	4.2	5.1	5.9
DUSP4	4.3	5.8	10.2
GPNMB	0.9	1.8	1.8
SPATA18	4.8	5.4	6.1
THBS4	1.9	1.9	1.8
RGCC	2.1	2.7	4.7
NRG1	2.8	3.8	4.3
CTGF	3.3	4.1	5.9
KCNJ2	1.4	1.5	1.4
F11R	2.1	2.5	3.1
TPM1	-1.0	-1.2	-1.7
KLF5	0.8	1.8	1.9
GADD45A	3.4	3.9	4.2
GPX1	2.0	2.4	2.8
LIF	7.2	9.7	14.7
NQO1	1.1	1.3	1.9
OXR1	1.1	1.2	1.2

Supplementary table 2. The fold change values of 14 miRNAs after Etoposide treatment



	Etoposide (µM)		
	10	15	30
hsa-miR-486-3p	5.1	5.2	6.4
hsa-miR-34c-5p	2.2	2.2	2.1
hsa-miR-4423-3p	2.3	2.2	2.0
hsa-miR-182-5p	1.4	1.7	2.9
hsa-miR-139-5p	1.2	1.6	2.3
hsa-miR-34a-3p	1.8	1.6	1.4
hsa-miR-1303	1.2	1.6	1.7
hsa-miR-187-3p	1.3	1.1	1.0
hsa-miR-486-5p	1.3	1.0	1.0
hsa-miR-34c-3p	1.0	1.2	1.1
hsa-miR-212-3p	0.8	0.8	0.7
hsa-miR-4298	0.8	0.9	0.8
hsa-miR-3911	0.9	0.9	0.8
hsa-miR-675-5p	0.7	0.7	0.7