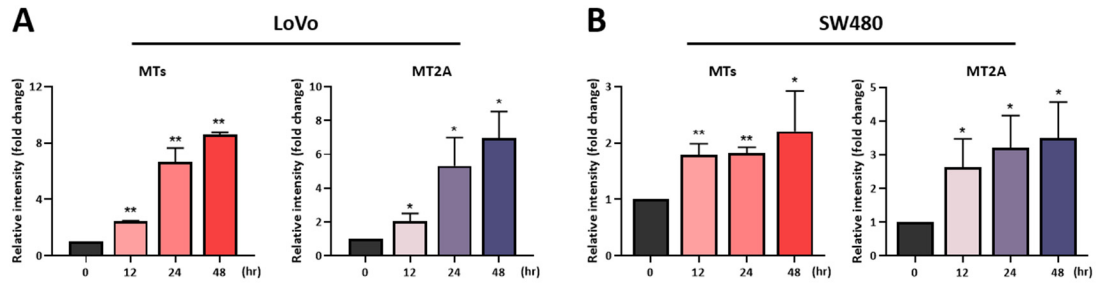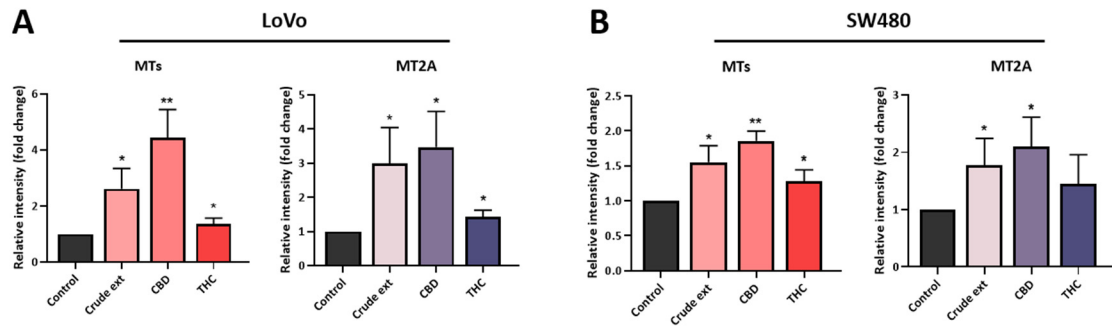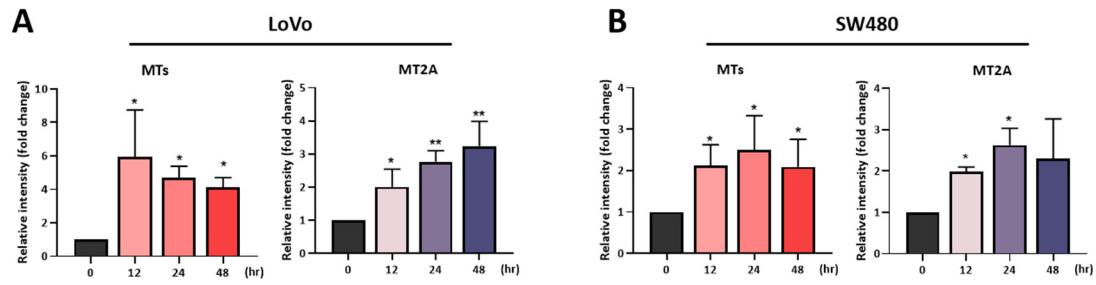Supplementary Figures.

Supplementary Figure S1. Densitometric analysis on Western blot data of MT expression by CBD treatment. Western Blot data were quantified by densitometry using ImageJ v1.54d. The graphs of metallothionein protein levels were shown in (A) LoVo and (B) SW480 cells. Statistical significance was considered with p -value (*, $p \leq 0.05$; **, $p \leq 0.01$).

Supplementary Figure S2. Densitometric analysis on Western blot data of MT expression by cannabinoid treatment. Western Blot data were quantified by densitometry using ImageJ v1.54d. The graphs of metallothionein protein levels were shown in (A) LoVo and (B) SW480 cells. Statistical significance was considered with p - value (*, $p \leq 0.05$; **, $p \leq 0.01$).

Supplementary Figure S3. Densitometric analysis on Western blot data of MT expression by zinc ion treatment. Western Blot data were quantified by densitometry using ImageJ v1.54d. The graphs of metallothionein protein levels were shown in (A) LoVo and (B) SW480 cells. Statistical significance was considered with p-value (*, $p \leq 0.05$; **, $p \leq 0.01$).

Supplementary Table S1. List of primers used for qPCR

Gene	Sequence (5'→3')
MT1F	Forward: CTG GTG TCT CCT GCA CCT G
	Reverse: CAG CAG CTG CAC TTC TCT GA
MT1G	Forward: AAA GGG GCA TCG GAG AAG TG
	Reverse: GCA AAG GGG TCA AGA TTG TAG C
MT1H	Forward: TGG ACC CCA ACT GCT CCT
	Reverse: ACT TCT CTG ACG CCC CTT TG
MT1M	Forward: TCG AAA TGG ACC CCA ACT GCT
	Reverse: TTC CCA CAT CAG GCA CAG CA
MT1X	Forward: CTG CTT CTC CTT GCC TCG AA
	Reverse: TGT CTG ACG TCC CTT TGC AG
MT2A	Forward: GGA TCC CAA CTG CTC CTC CTG C
	Reverse: CTT GTC CGA CGC CCC TTT
Beta-actin	Forward: CCA CCA TGR ACC CTG GCA TT
	Reverse: CGG ACT CGT CAT ACT CCT GC