Figure S1. Original western blot gel of the Keratin 8.

Notes: IPEC-J2 cells were treated with 0.0 or 2.0 mg/mL SBA for 24 h. The representative images of KRT8 was detected by the western blot technique. This original gel was used to make Figure 3.

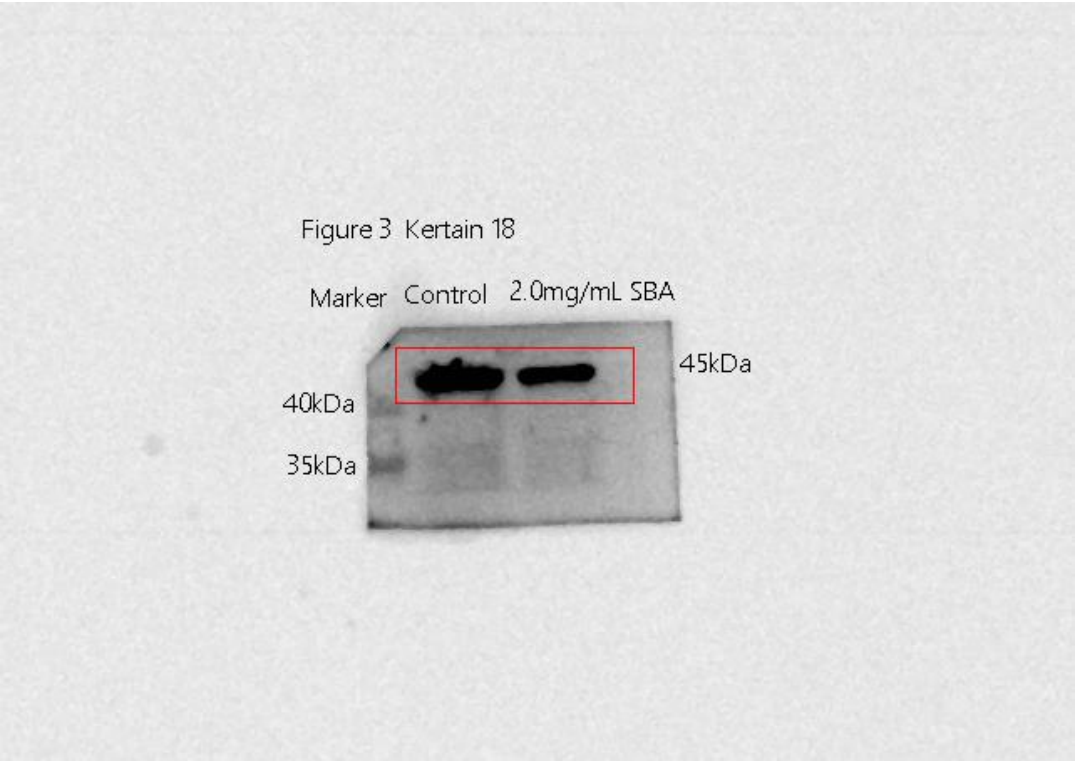

Figure S2. Original western blot gel of the Keratin 18.

Notes: IPEC-J2 cells were treated with 0.0 or 2.0 mg/mL SBA for 24 h. The representative images of KRT18 was detected by the western blot technique. This original gel was used to make Figure 3.

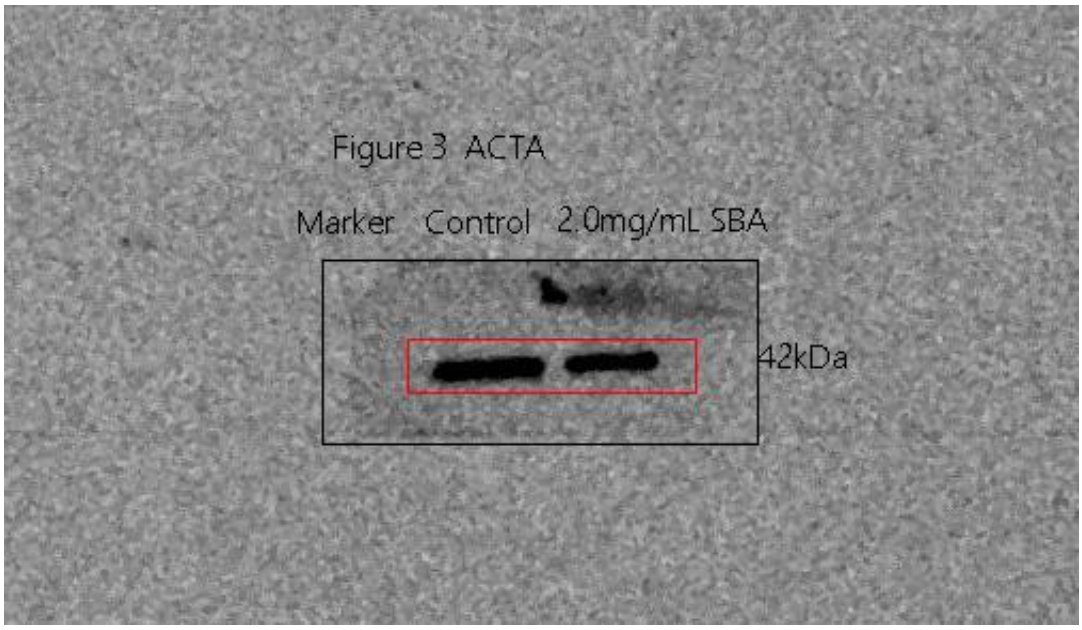

Figure S3. Original western blot gel of the ACTA.

Notes: IPEC-J2 cells were treated with 0.0 or 2.0 mg/mL SBA for 24 h. The representative images of ACTA was detected by the western blot technique. This original gel was used to make Figure 3.

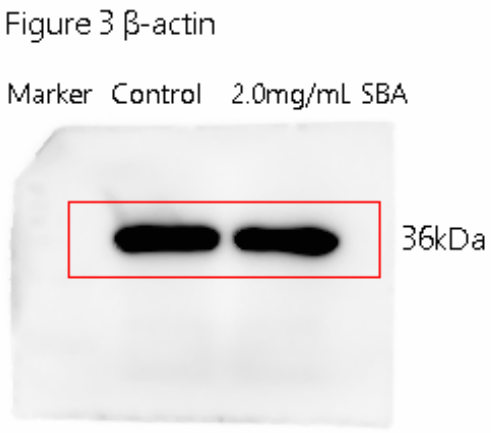

Figure S4. Original western blot gel of the β-actin.

Notes: IPEC-J2 cells were treated with 0.0 or 2.0 mg/mL SBA for 24 h. This original gel of the β-actin was used as house-keeping protein to make Figure 3.

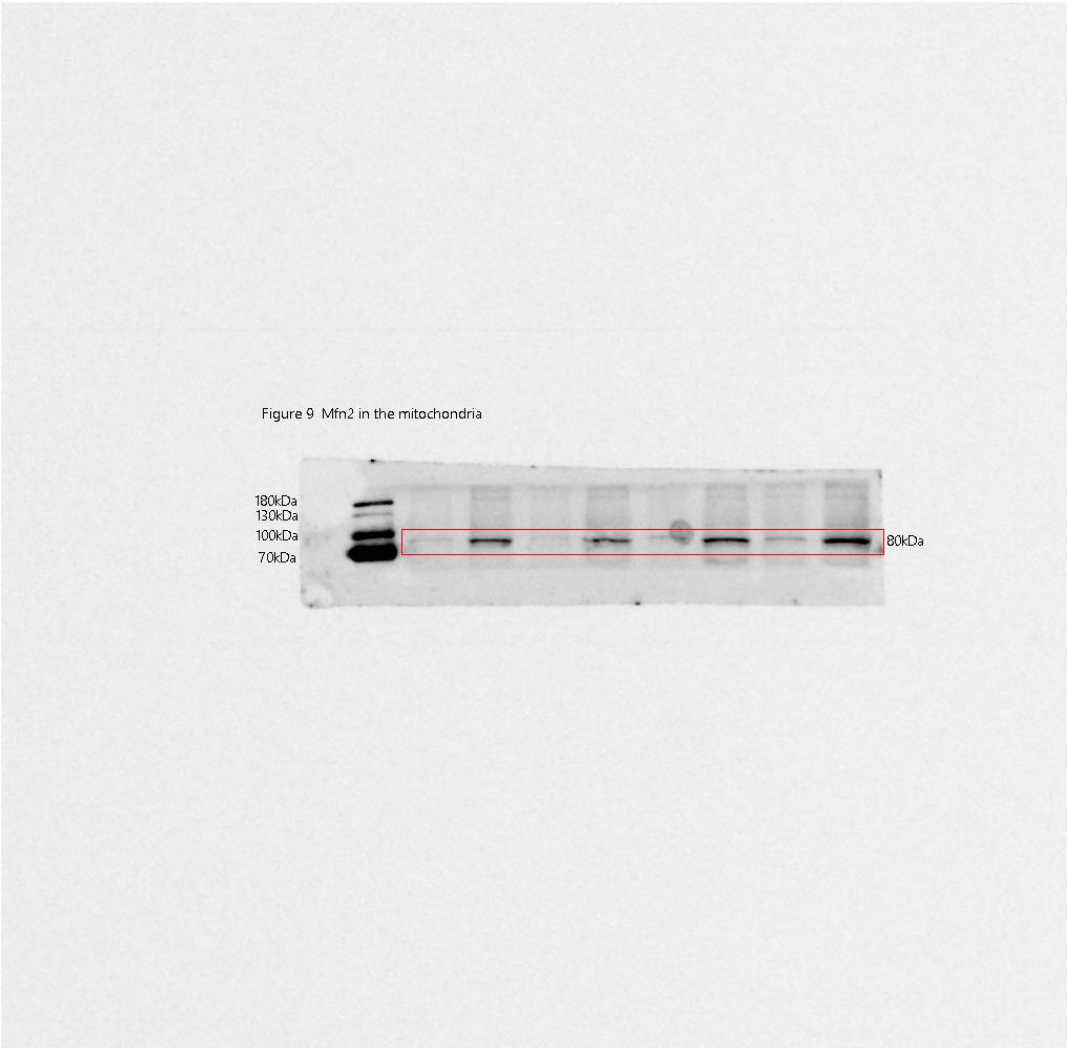

Figure S5. Original western blot gel of the Mnf2 in the mitochondria

Notes: After being treated for 24 h, the expression of Mnf2 in the mitochondria was determined using the western blot. This original gel of the Mnf2 in the mitochondria was used to make Figure 9.

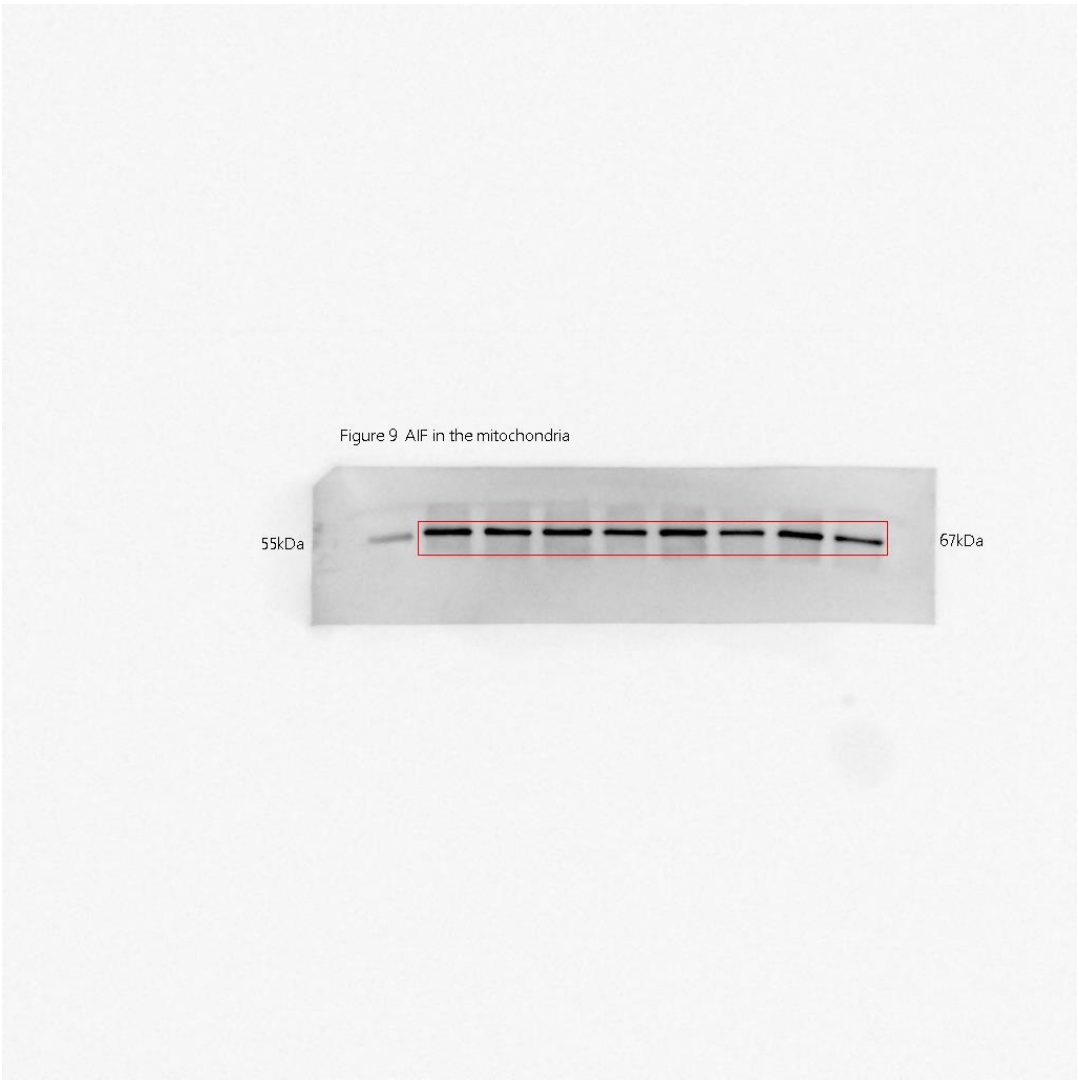

Figure S6. Original western blot gel of the AIF in the mitochondria

Notes: After being treated for 24 h, the expression of AIF in the mitochondria was determined using the western blot. This original gel of the AIF in the mitochondria was used to make Figure 9.

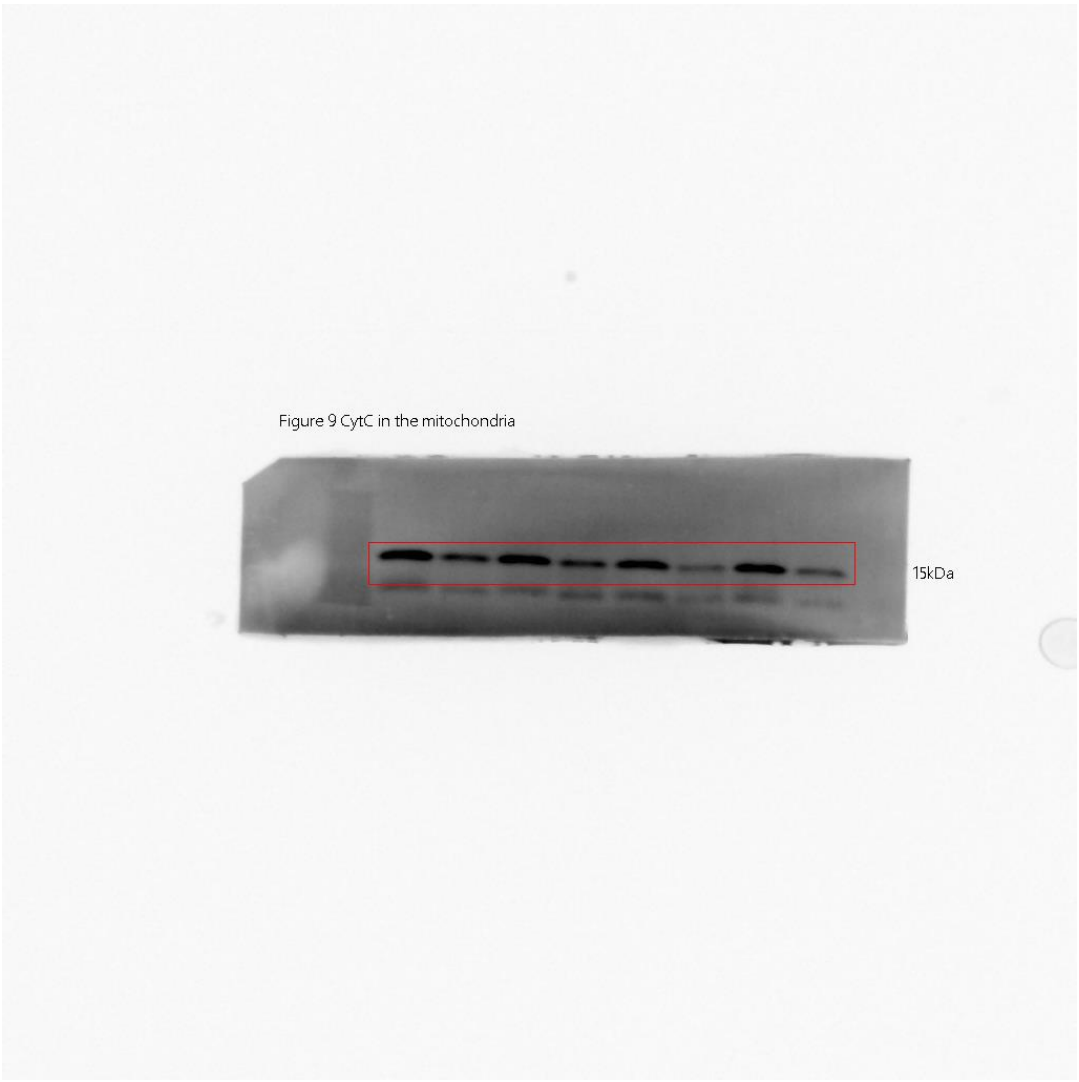

Figure S7. Original western blot gel of the CytC in the mitochondria

Notes: After being treated for 24 h, the expression of CytC in the mitochondria was determined using the western blot. This original gel of the CytC in the mitochondria was used to make Figure 9.

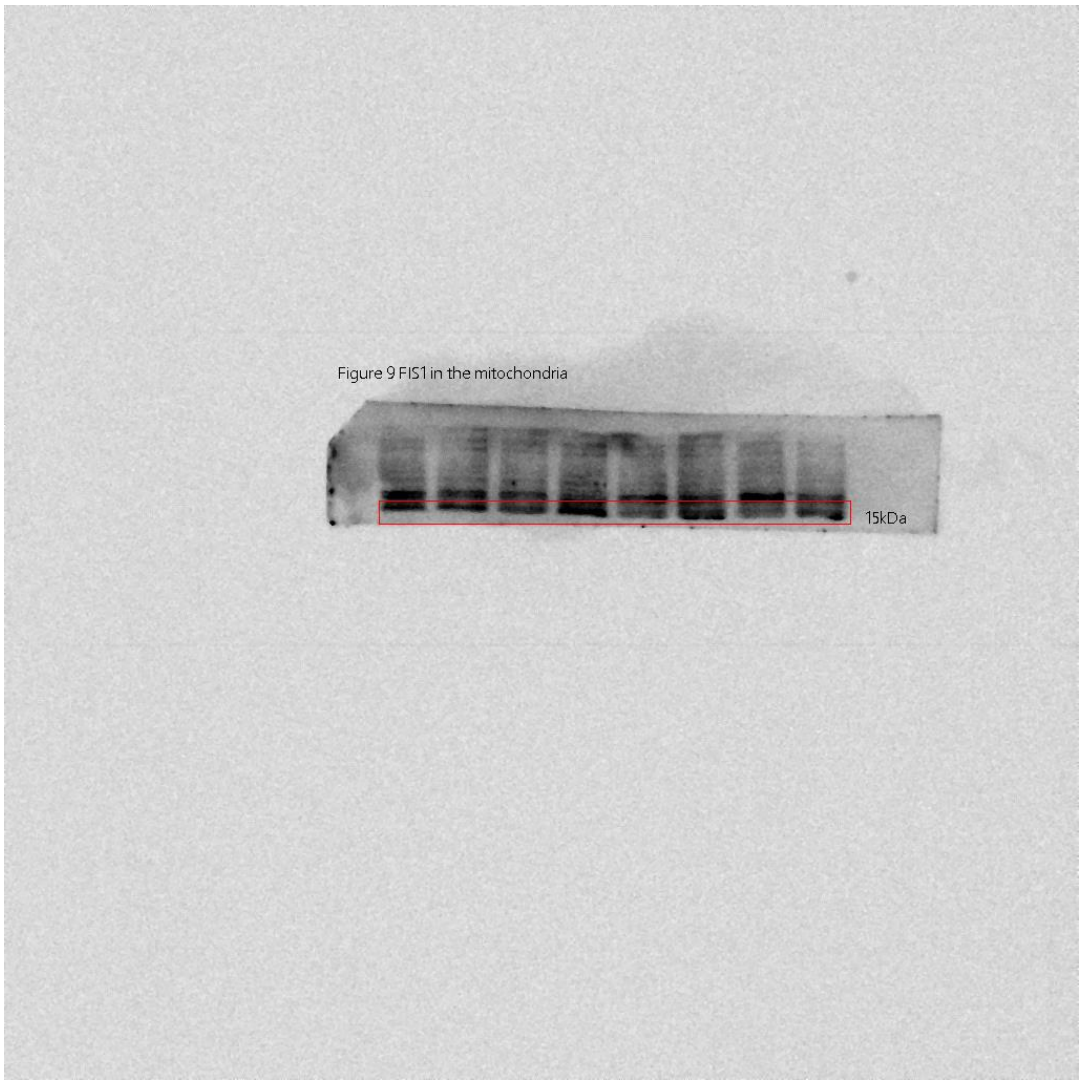

Figure S8. Original western blot gel of the FIS1 in the mitochondria

Notes: After being treated for 24 h, the expression of FIS1 in the mitochondria was determined using the western blot. This original gel of the FIS1 in the mitochondria was used to make Figure 9.

Figure S9. Original western blot gel of the β-actin in the mitochondria

Notes: After being treated for 24 h, the expression of β-actin in the mitochondria was determined using the western blot. This original gel of the β-actin in the mitochondria as an internal marker was used to make Figure 9.

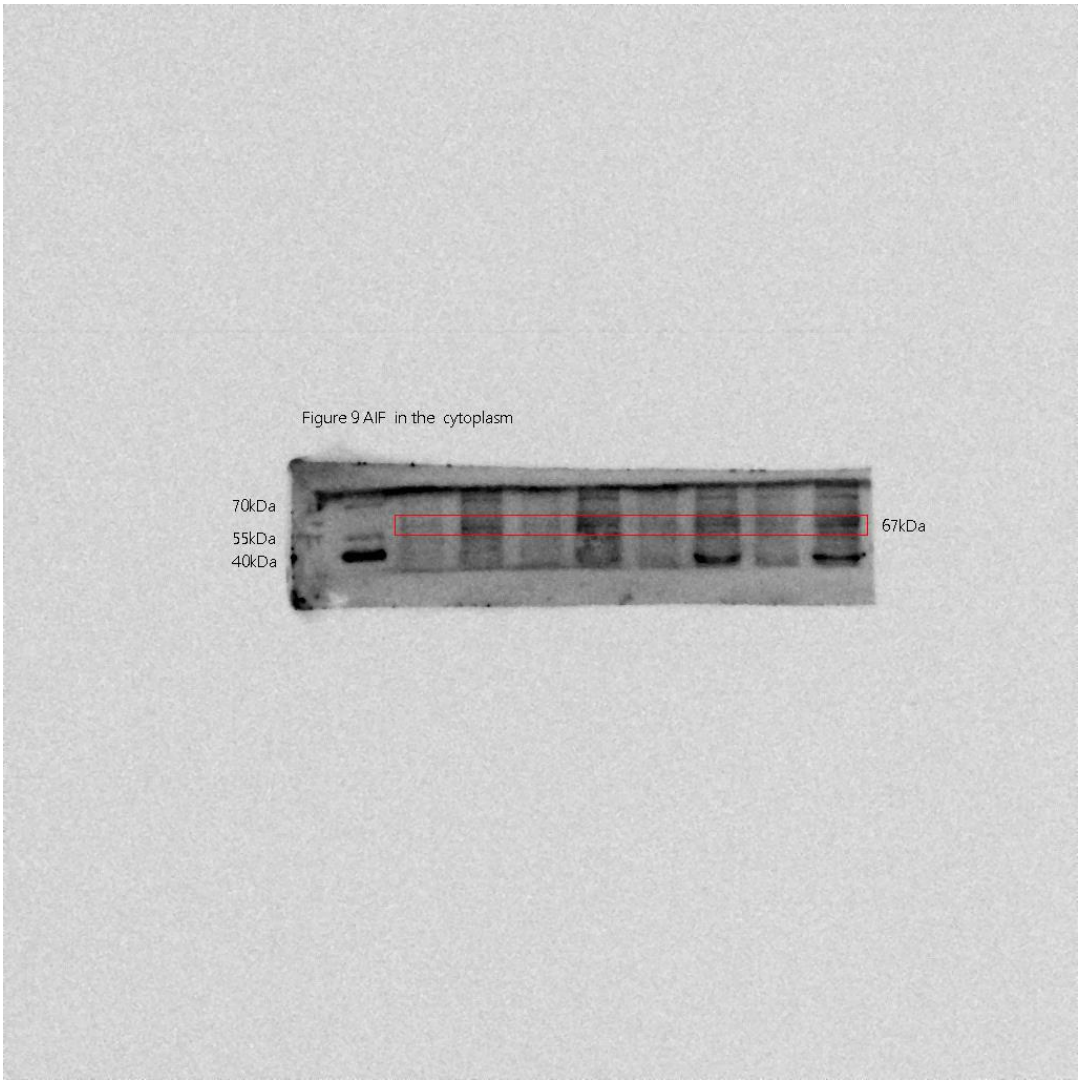

Figure S10. Original western blot gel of the AIF in the cytoplasm

Notes: After being treated for 24 h, the expression of AIF in the cytoplasm was determined using the western blot. This original gel of the AIF in the cytoplasm was used to make Figure 9.

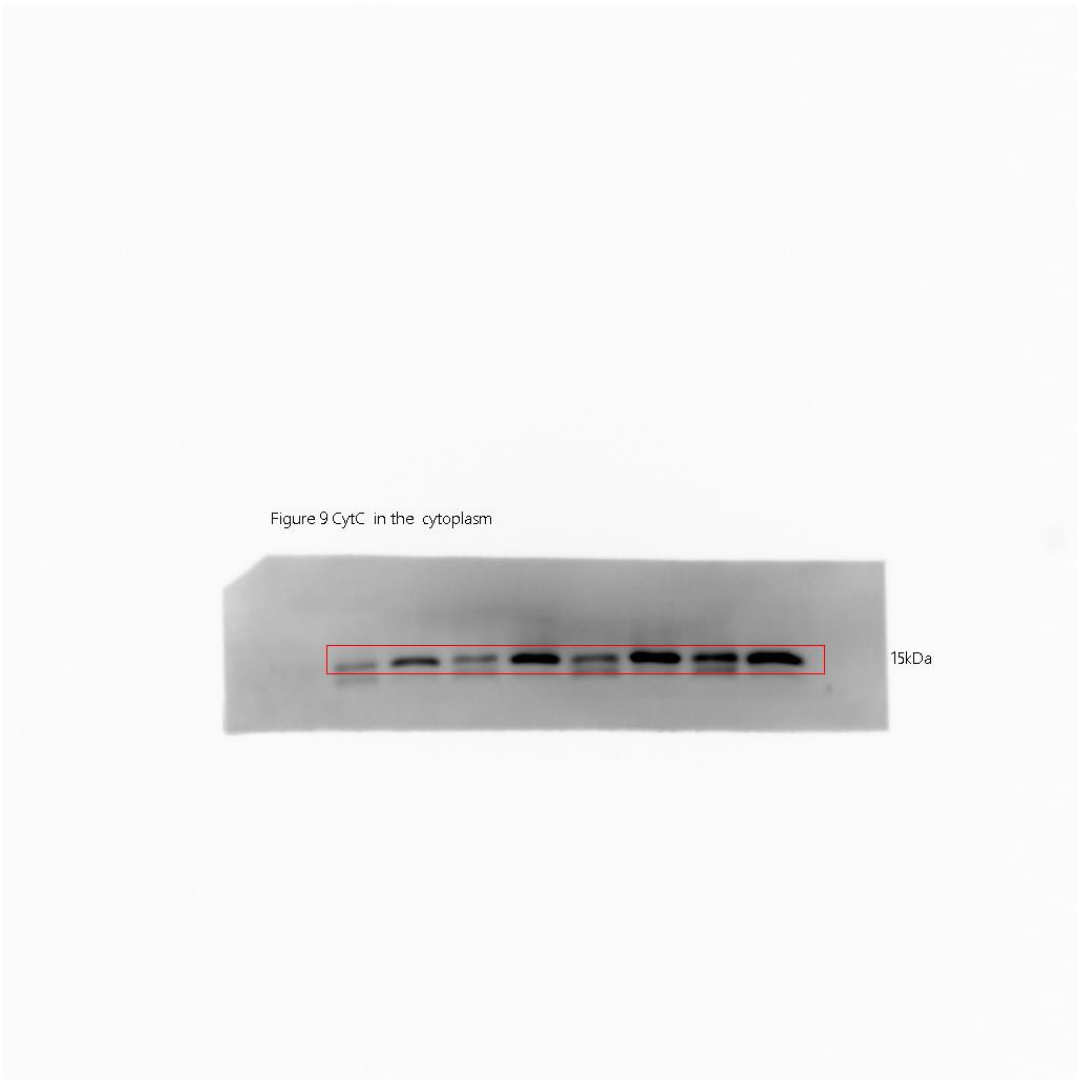

Figure S11. Original western blot gel of the CytC in the cytoplasm

Notes: After being treated for 24 h, the expression of CytC in the cytoplasm was determined using the western blot. This original gel of the CytC in the cytoplasm was used to make Figure 9.

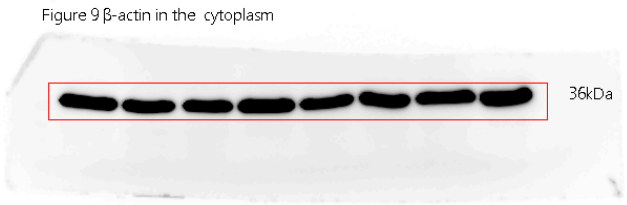

Figure S12. Original western blot gel of the β-actin in the cytoplasm

Notes: After being treated for 24 h, the expression of β-actin in the cytoplasm was determined using the western blot. This original gel of the β-actin in the cytoplasm as an internal marker was used to make Figure 9.

Figure S13. Original western blot gel of the p-Caspase

Notes: After being treated for 24 h, the expression of p-Caspase was determined using the western blot. This original gel of the p-Caspase was used to make Figure 12.

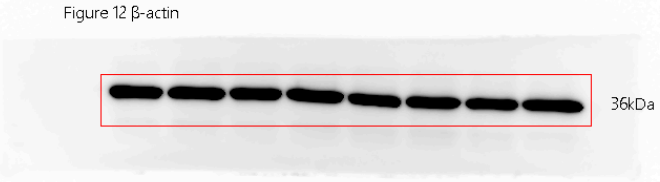

Figure S14. Original western blot gel of the β-actin

Notes: After being treated for 24 h, the expression of β-actin was determined using the western blot. This original gel of the β-actin was used as an internal marker to make Figure 12.

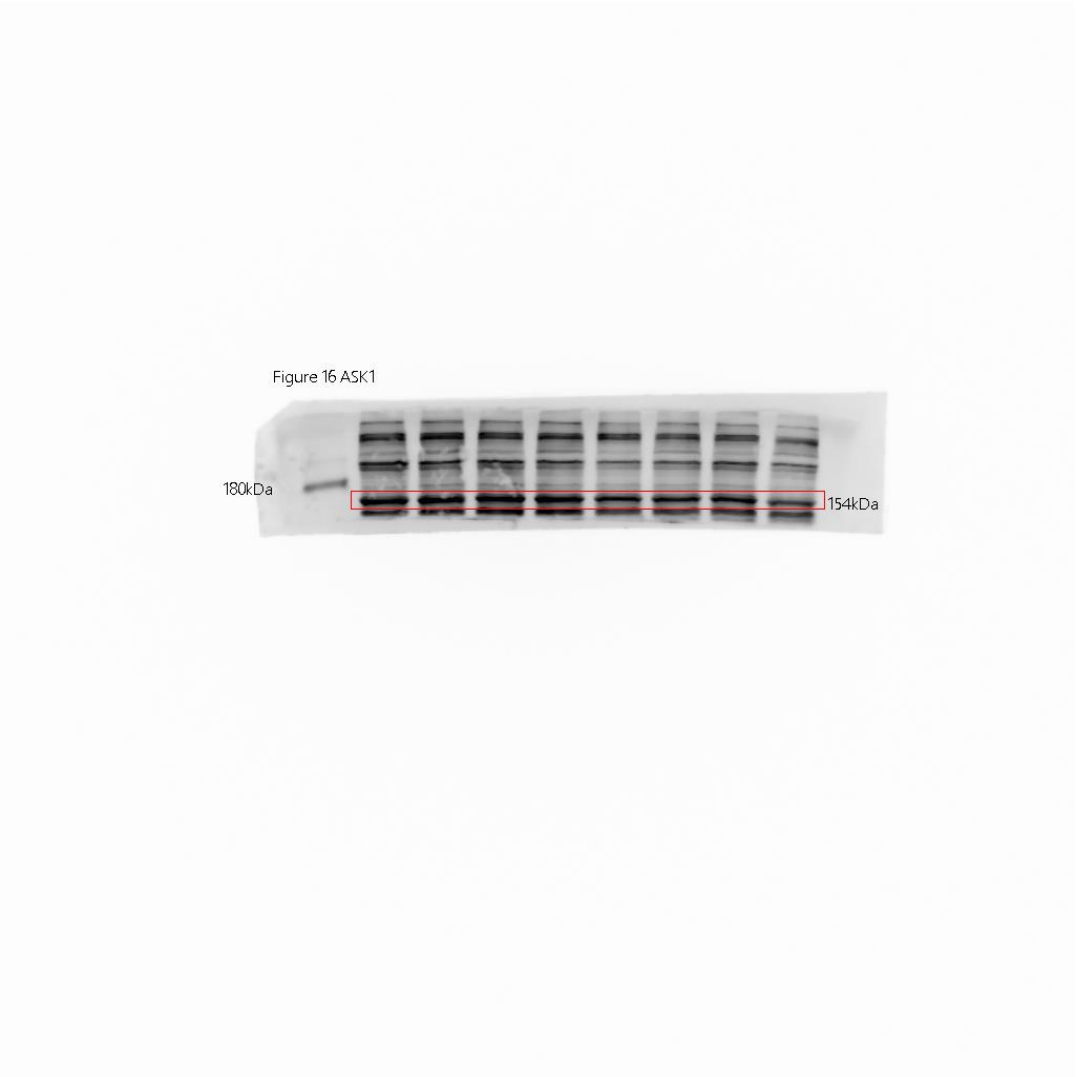

Figure S15. Original western blot gel of the ASK

Notes: After being treated for 24 h, the expression of ASK was determined using the western blot. This original gel of the ASK to make Figure 16.

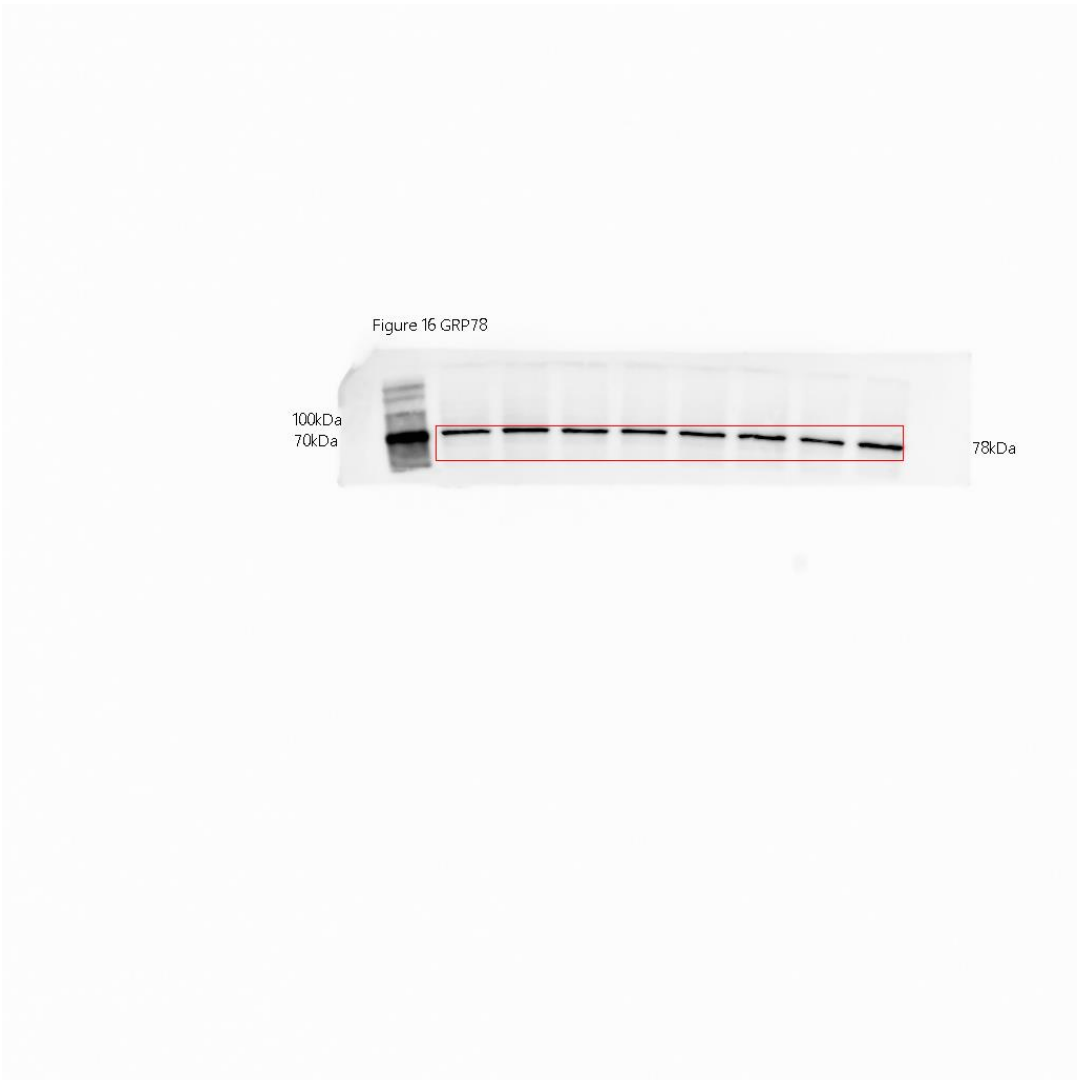

Figure S16. Original western blot gel of the GRP78

Notes: After being treated for 24 h, the expression of GRP78 was determined using the western blot. This original gel of the GRP78 to make Figure 16.

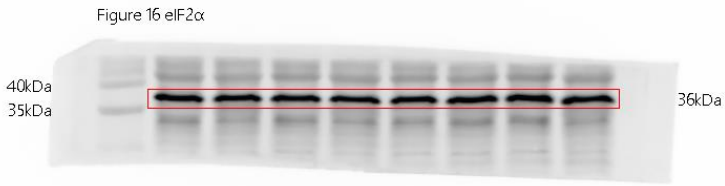

Figure S17. Original western blot gel of the eIF2α

Notes: After being treated for 24 h, the expression of eIF2α was determined using the western blot. This original gel of the eIF2α to make Figure 16.

Figure S18. Original western blot gel of the p-eIF2α

Notes: After being treated for 24 h, the expression of p-eIF2α was determined using the western blot. This original gel of the p-eIF2α to make Figure 16.

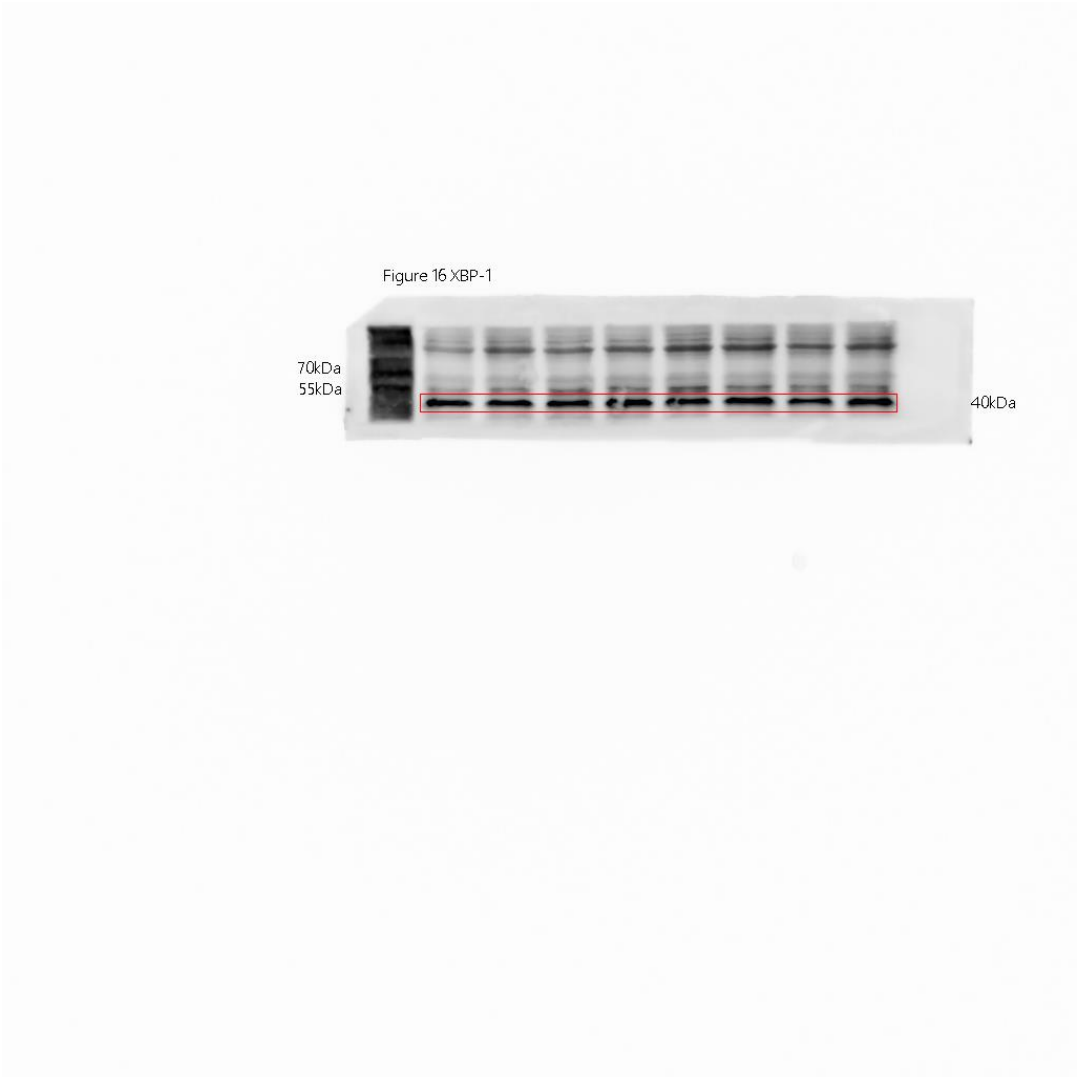

Figure S19. Original western blot gel of the XBP-1

Notes: After being treated for 24 h, the expression of XBP-1 was determined using the western blot. This original gel of the XBP-1 to make Figure 16.

Figure S20. Original western blot gel of the CHOP

Notes: After being treated for 24 h, the expression of CHOP was determined using the western blot. This original gel of the CHOP to make Figure 16.

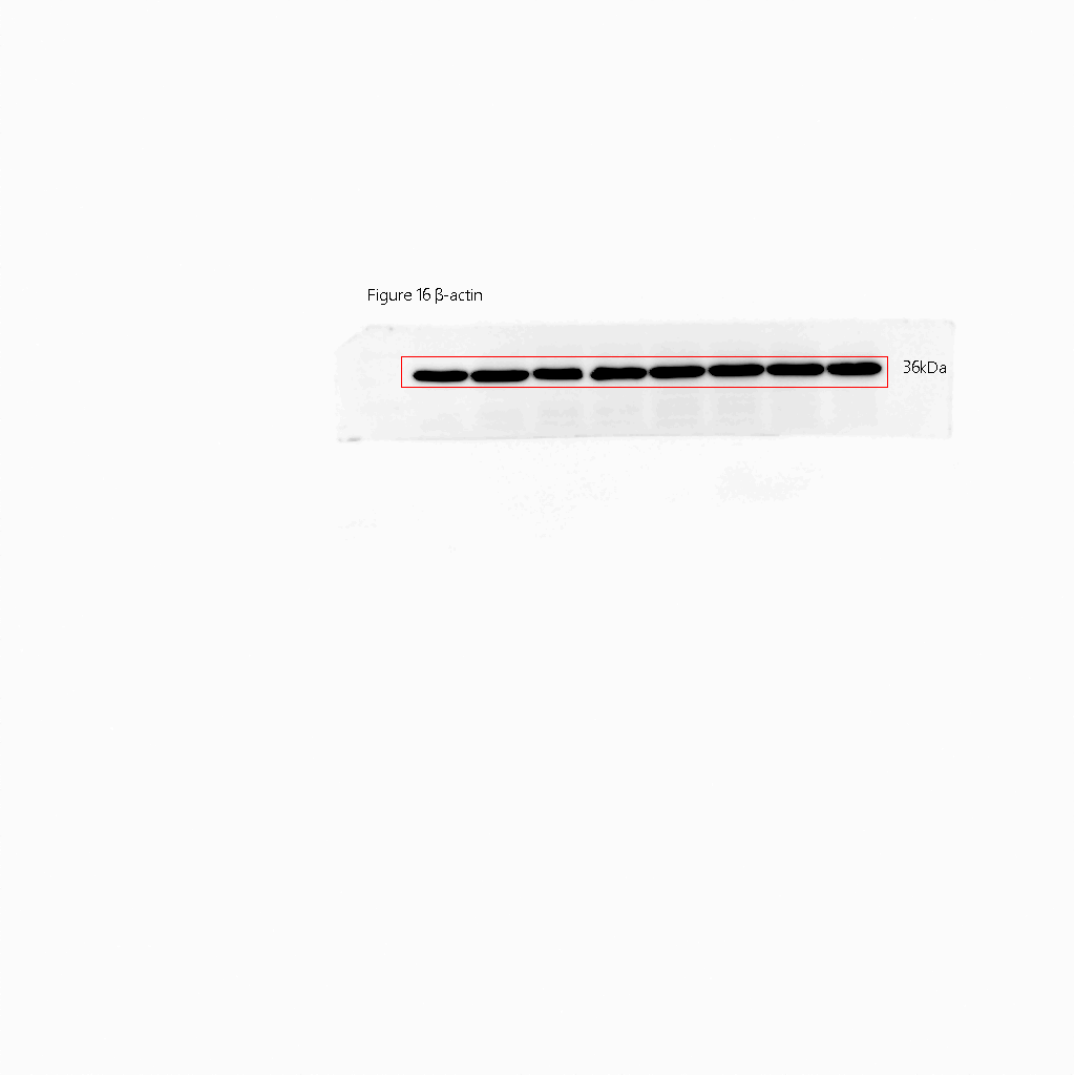

Figure S21. Original western blot gel of the β-actin

Notes: After being treated for 24 h, the expression of β-actin was determined using the western blot. This original gel of the β-actin was used as an internal marker to make Figure 16.

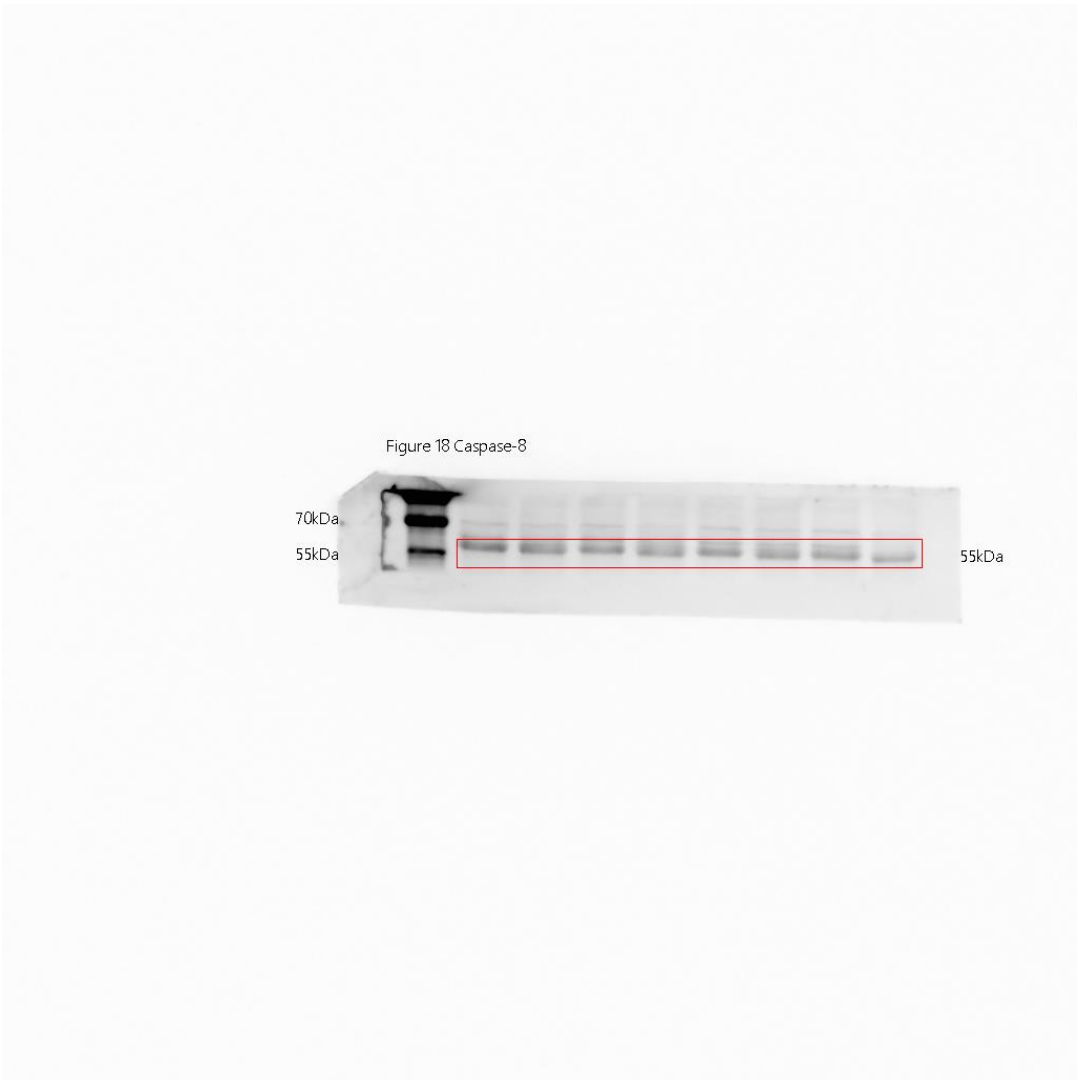

Figure S22. Original western blot gel of the caspase-8

Notes: After being treated for 24 h, the expression of caspase-8 was determined using the western blot. This original gel of the caspase-8 to make Figure 18.

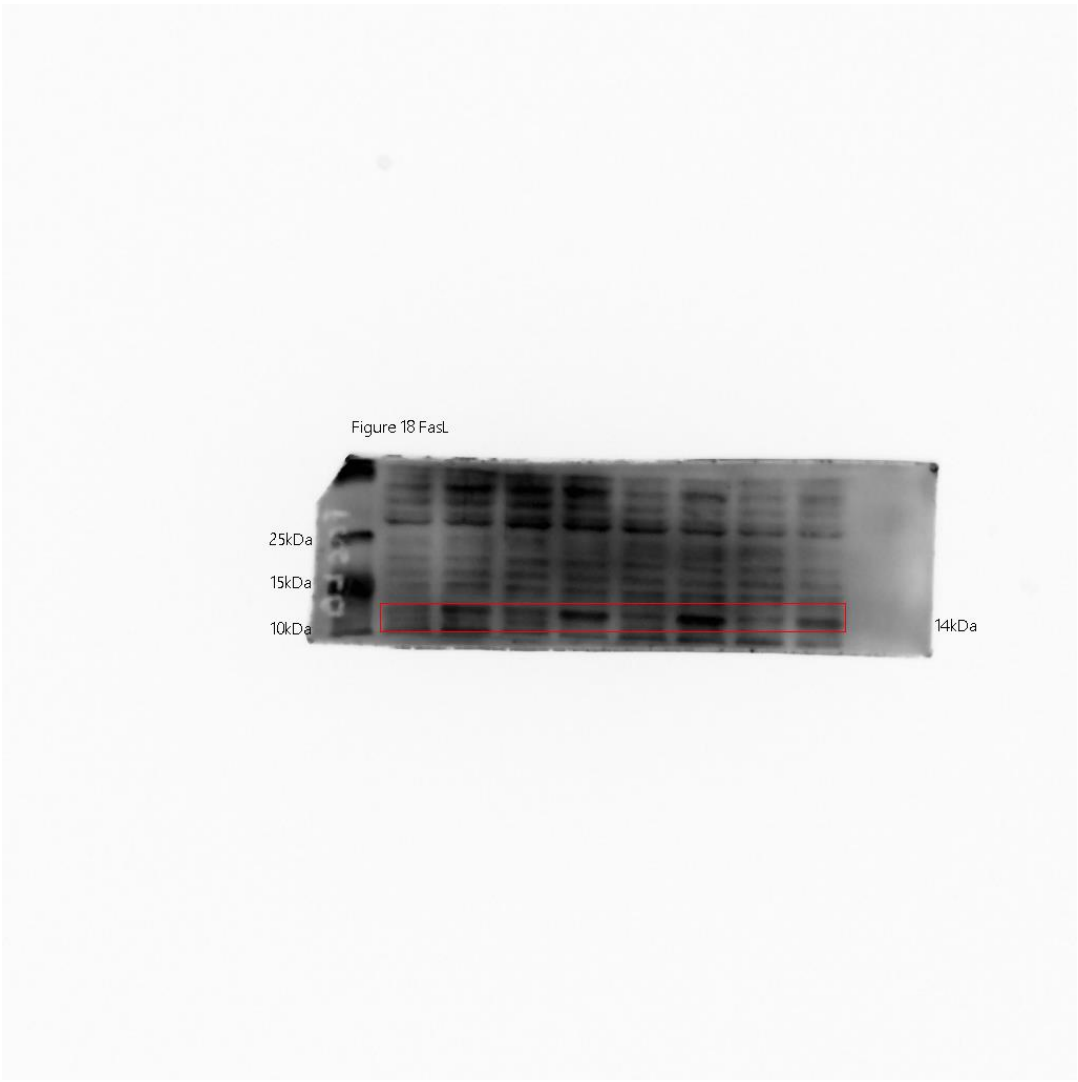

Figure S23. Original western blot gel of the FasL

Notes: After being treated for 24 h, the expression of FasL was determined using the western blot. This original gel of the FasL to make Figure 18.

Figure S24. Original western blot gel of the β-actin

Notes: After being treated for 24 h, the expression of β-actin was determined using the western blot. This original gel of the β-actin was used as an internal marker to make Figure 18.

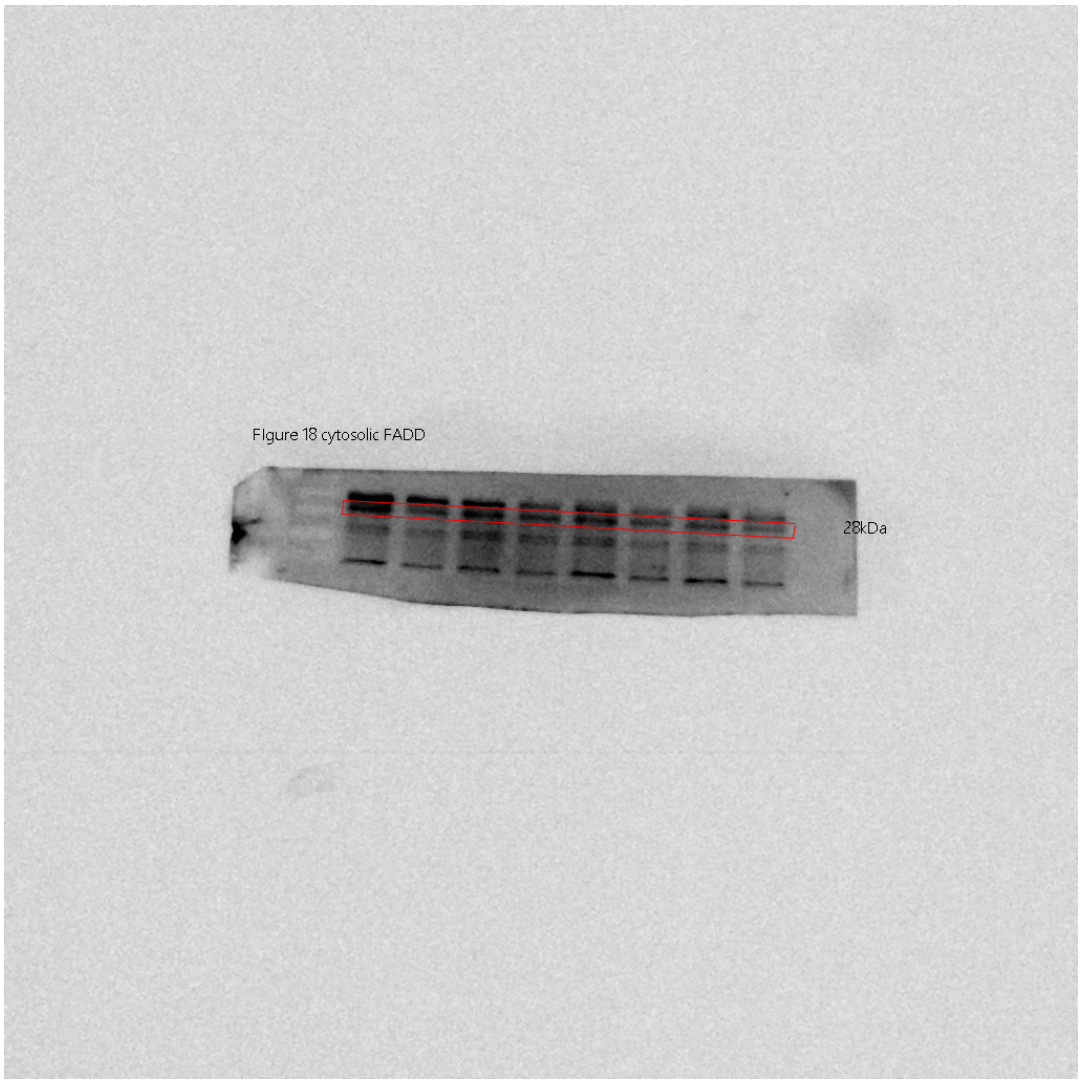

Figure S25. Original western blot gel of the cytosolic FADD

Notes: After being treated for 24 h, the expression of cytosolic FADD was determined using the western blot. This original gel of the cytosolic FADD to make Figure 18.

Figure S26. Original western blot gel of the cytosolic β-actin

Notes: After being treated for 24 h, the expression of cytosolic β-actin was determined using the western blot. This original gel of the cytosolic β-actin was used as an internal marker to make Figure 18.

Figure S27. Original western blot gel of the membrane FADD

Notes: After being treated for 24 h, the expression of membrane FADD was determined using the western blot. This original gel of the membrane FADD to make Figure 18.

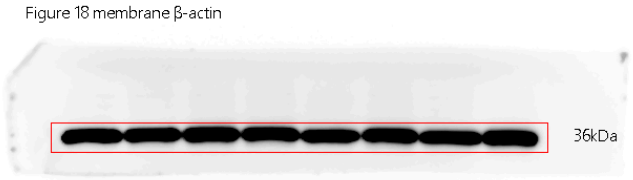

Figure S28. Original western blot gel of the β-actin in the membrane

Notes: After being treated for 24 h, the expression of β-actin in the membrane was determined using the western blot. This original gel of the β-actin in the membrane was used as an internal marker to make Figure 18.

Figure S29. Original western blot gel of the Bcl-2

Notes: After being treated for 24 h, the expression of Bcl-2 was determined using the western blot. This original gel of the Bcl-2 to make Figure 21.

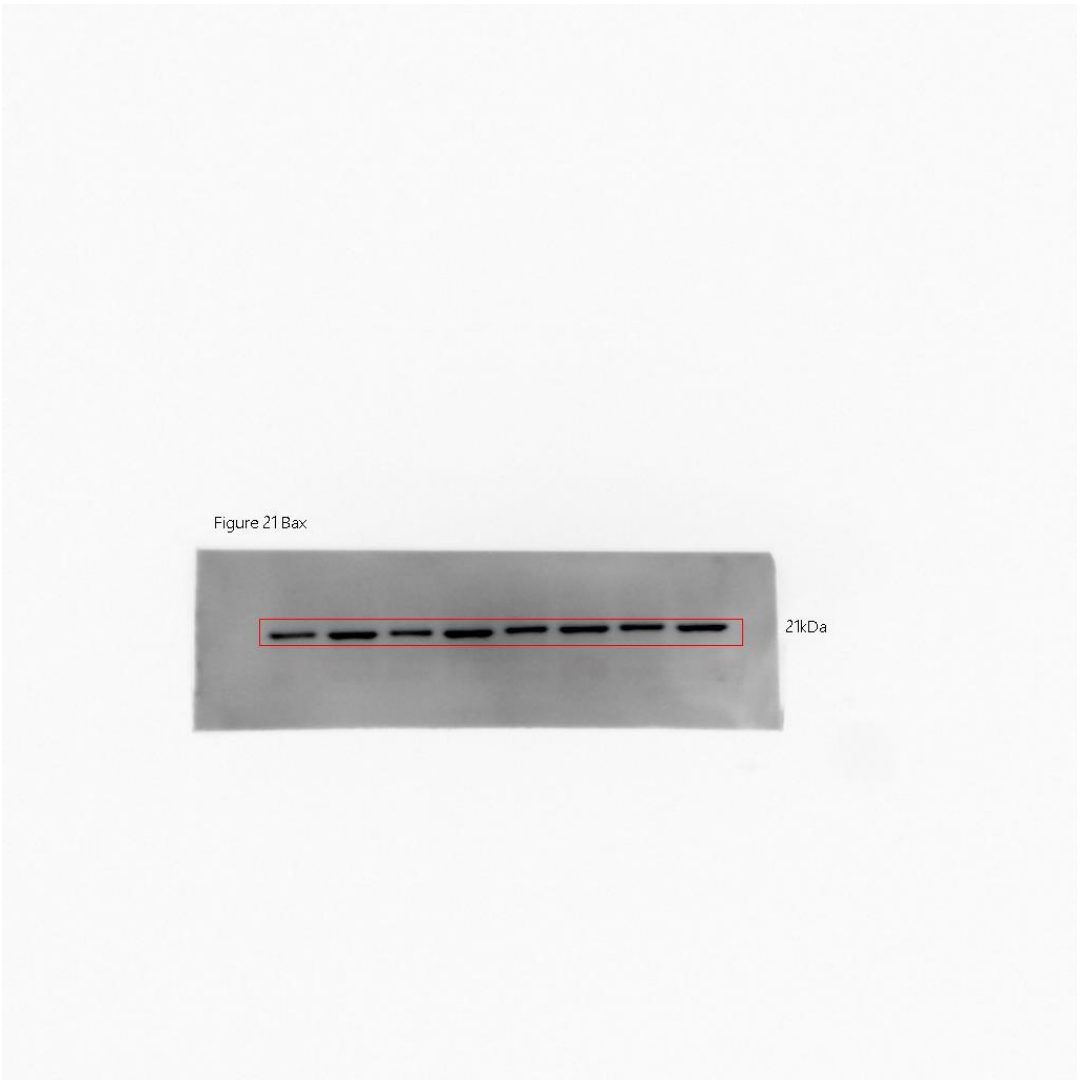

Figure S30. Original western blot gel of the Bax

Notes: After being treated for 24 h, the expression of Bax was determined using the western blot. This original gel of the Bax to make Figure 21.

Figure S31. Original western blot gel of the β-actin

Notes: After being treated for 24 h, the expression of β-actin was determined using the western blot. This original gel of the β-actin was used as an internal marker to make Figure 21.

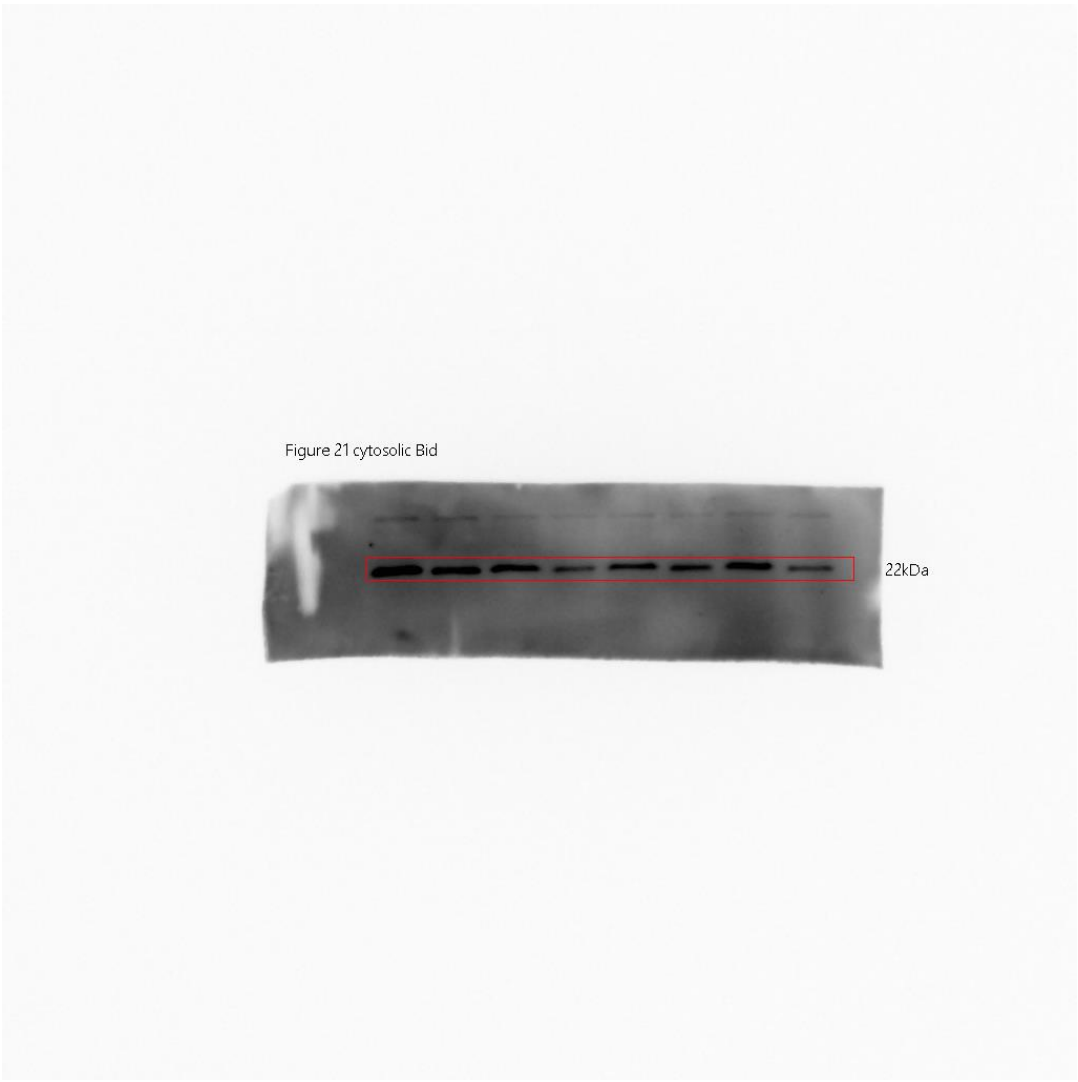

Figure S32. Original western blot gel of the cytosolic Bid

Notes: After being treated for 24 h, the expression of cytosolic Bid was determined using the western blot. This original gel of the cytosolic Bid to make Figure 21.

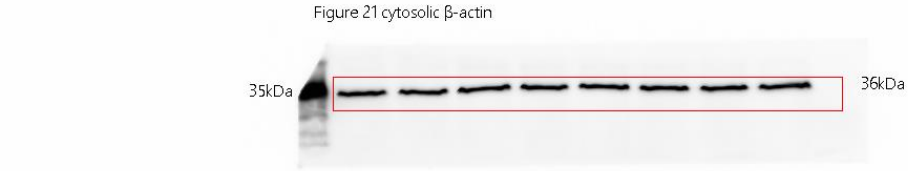

Figure S33. Original western blot gel of the cytosolic β-actin

Notes: After being treated for 24 h, the expression of cytosolic β-actin was determined using the western blot. This original gel of the cytosolic β-actin was used as an internal marker to make Figure 21.

Table S1. The correlations of different cytoskeleton proteins between gene expression and cell apoptosis in different treatments

Different protein expression	Heading	Cell Apoptosis
KRT8 Expression	Pearson correlation	-0.766**
KRT18 Expression	Pearson correlation	-0.747**
ACTA Expression	Pearson correlation	-0.748**

** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The value for the correlation between KRT8 expression and cell apoptosis was from the treatments of the Control treatment (T1); SBA treatment (T9); KRT8-siRNA treatment (T2); KRT8-siRNA+SBA treatment (T10). The value for the correlation between KRT18 expression and cell apoptosis was from the treatments of the Control treatment (T1); SBA treatment (T9); KRT18-siRNA treatment (T3); KRT18-siRNA+SBA treatment (T11). The value for the correlation between ACTA expression and cell apoptosis was from the treatments of the Control treatment (T1); SBA treatment (T9); ACTA-siRNA treatment (T4); ACTA-siRNA+SBA treatment (T12).

Table S2. The Pearson correlations of the indicators in the mitochondrial apoptosis signaling pathway in different treatments (KRT8)

	Heading	KRT8 Expression	Caspase-3 Activity	Caspase-9 Activity	ATP Content	Mitochondrial AIF Expression	Mitochondrial CytC Expression	FIS1 Expression	Mfn2 Expression
KRT8 Expression	Pearson correlation	1	-0.887**	-0.836**	0.801**	0.815**	0.763**	-0.665*	-0.546

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT8-siRNA treatment (T2); KRT8-siRNA+SBA treatment (T10).

Table S3. The Pearson correlations of the indicators in the mitochondrial apoptosis signaling pathway in different treatments (KRT18)

	Heading	KRT18 Expression	Caspase-3 Activity	Caspase-9 Activity	ATP Content	Mitochondrial AIF Expression	Mitochondrial CytC Expression	FIS1 Expression	Mfn2 Expression
KRT18 Expression	Pearson correlation	1	-0.846**	-0.802**	0.808**	0.882**	0.916**	-0.794**	-0.847**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT18-siRNA treatment (T3); KRT18-siRNA+SBA treatment (T11).

Table S4. The Pearson correlations of the indicators in the mitochondrial apoptosis signaling pathway in different treatments (ACTA)

	Heading	ACTA Expression	Caspase-3 Activity	Caspase-9 Activity	ATP Content	Mitochondrial AIF Expression	Mitochondrial CytC Expression	FIS1 Expression	Mfn2 Expression
ACTA Expression	Pearson correlation	1	-0.687*	-0.755**	0.881**	0.799**	0.696*	-0.842**	-0.668*

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); ACTA-siRNA treatment (T4); ACTA-siRNA+SBA treatment (T12).

Table S5. The Pearson correlations of the indicators in the endoplasmic reticulum stress mediated apoptosis pathways in different treatments (KRT8)

	Heading	**KRT8 Expression**	**ASK1 Expression**	**GRP78 Expression**	**eIFα Expression**	**XBP1 Expression**	**CHOP Expression**
KRT8 Expression	Pearson correlation	1	0.855**	-0.818**	-0.881**	-0.833**	-0.882**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT8-siRNA treatment (T2); KRT8-siRNA+SBA treatment (T10).

Table S6. The Pearson correlations of the indicators in the endoplasmic reticulum stress mediated apoptosis pathways in different treatments (KRT18)

	Heading	KRT8 Expression	ASK1 Expression	GRP78 Expression	eIFα Expression	XBP1 Expression	CHOP Expression
KRT18 Expression	Pearson correlation	1	0.917**	-0.812**	-0.855**	-0.822**	-0.725**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT18-siRNA treatment (T3); KRT18-siRNA+SBA treatment (T11).

Table S7. The Pearson correlations of the indicators in the endoplasmic reticulum stress mediated apoptosis pathways in different treatments (ACTA)

	Heading	ACTA Expression	ASK1 Expression	GRP78 Expression	eIFα Expression	XBP1 Expression	CHOP Expression
ACTA Expression	Pearson correlation	1	0.782**	-0.742**	-0.730**	-0.714**	-0.763**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); ACTA-siRNA treatment (T4); ACTA-siRNA+SBA treatment (T12).

Table S8. The Pearson correlations of the indicators in the cytoskeleton-external apoptosis signal pathway in different treatments (KRT8)

	Heading	KRT8 Expression	Caspase-8 Expression	FasLG Expression	Cytoplasmic FADD Expression	Membrane FADD Expression	Caspase-8 Activity
KRT8 Expression	Pearson correlation	1	0.829**	-0.881**	0.781**	-0.850**	-0.780**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT8-siRNA treatment (T2); KRT8-siRNA+SBA treatment (T10).

Table S9. The Pearson correlations of the indicators in the cytoskeleton-external apoptosis signal pathway in different treatments (KRT18)

	Heading	KRT18 Expression	Caspase-8 Expression	FasLG Expression	Cytoplasmic FADD Expression	Membrane FADD8 Expression	Caspase-8 Activity
KRT18 Expression	Pearson correlation	1	0.862**	-0.855**	0.831**	-0.874**	-0.896**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT18-siRNA treatment (T3); KRT18-siRNA+SBA treatment (T11).

Table S10. The Pearson correlations of the indicators in the cytoskeleton-external apoptosis signal pathway in different treatments (ACTA)

	Heading	ACTA Expression	Caspase-8 Expression	FasLG Expression	Cytoplasmic FADD Expression	Membrane FADD8 Expression	Caspase-8 Activity
ACTA Expression	Pearson correlation	1	0.774**	-0.730**	0.722**	-0.797**	-0.746**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); ACTA-siRNA treatment (T4); ACTA-siRNA+SBA treatment (T12).

Table S11. The Pearson correlations of the indicators in the cross-talk pathway in different treatments (KRT8)

	Heading	KRT8 Expression	Bcl-2 Expression	Bax Expression	Bid Expression
KRT8 Expression	Pearson correlation	1	0.839**	-0.803**	0.879**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT8-siRNA treatment (T2); KRT8-siRNA+SBA treatment (T10).

Table S12. The Pearson correlations of the indicators in the cross-talk pathway in different treatments (KRT18)

	Heading	KRT18 Expression	Bcl-2 Expression	Bax Expression	Bid Expression
KRT18 Expression	Pearson correlation	1	0.838**	-0.804**	0.802**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); KRT18-siRNA treatment (T3); KRT18-siRNA+SBA treatment (T11).

Table S13. The Pearson correlations of the indicators in the cross-talk pathway in different treatments (ACTA)

	Heading	ACTA Expression	Bcl-2 Expression	Bax Expression	Bid Expression
ACTA Expression	Pearson correlation	1	0.698*	-0.854**	0.761**

*indicated significant correlation at 0.05 level (bilateral detection, N=12). ** indicated Significant correlation at 0.01 level (bilateral detection, N=12). The different treatments were: Control treatment (T1); SBA treatment (T9); ACTA-siRNA treatment (T4); ACTA-siRNA+SBA treatment (T12).

Table S14. The item numbers of the used primary antibodies.

ABclonal:
β-actin Rabbit mAb（AC038）
Bip/GRP78 Rabbit mAb（A4908）
AIF Rabbit mAb（A19536）
eIF2α Rabbit pAb（A0764）
Phospho-eIF2α-S51 Rabbit mAb（AP0692）
FADD Rabbit mAb（A19049）
DDIT3/CHOP Rabbit pAb（A0221）
FasLG Rabbit pAb（A0234）
ASK1 Rabbit pAb（A3271）
Cytochrome C Rabbit mAb（A4912）
TTC11/FIS1 Rabbit mAb（A19666）
active+pro Caspase-3 Rabbit mAb（A19654）
XBP1 Rabbit pAb（A1731）
Caspase-8 Rabbit mAb（A19549）
Mitofusin 2 Rabbit mAb（A19678）
Bid Rabbit pAb（A0210）
Bcl-2 Rabbit mAb（A19693）
Bax Rabbit mAb（A19684）