

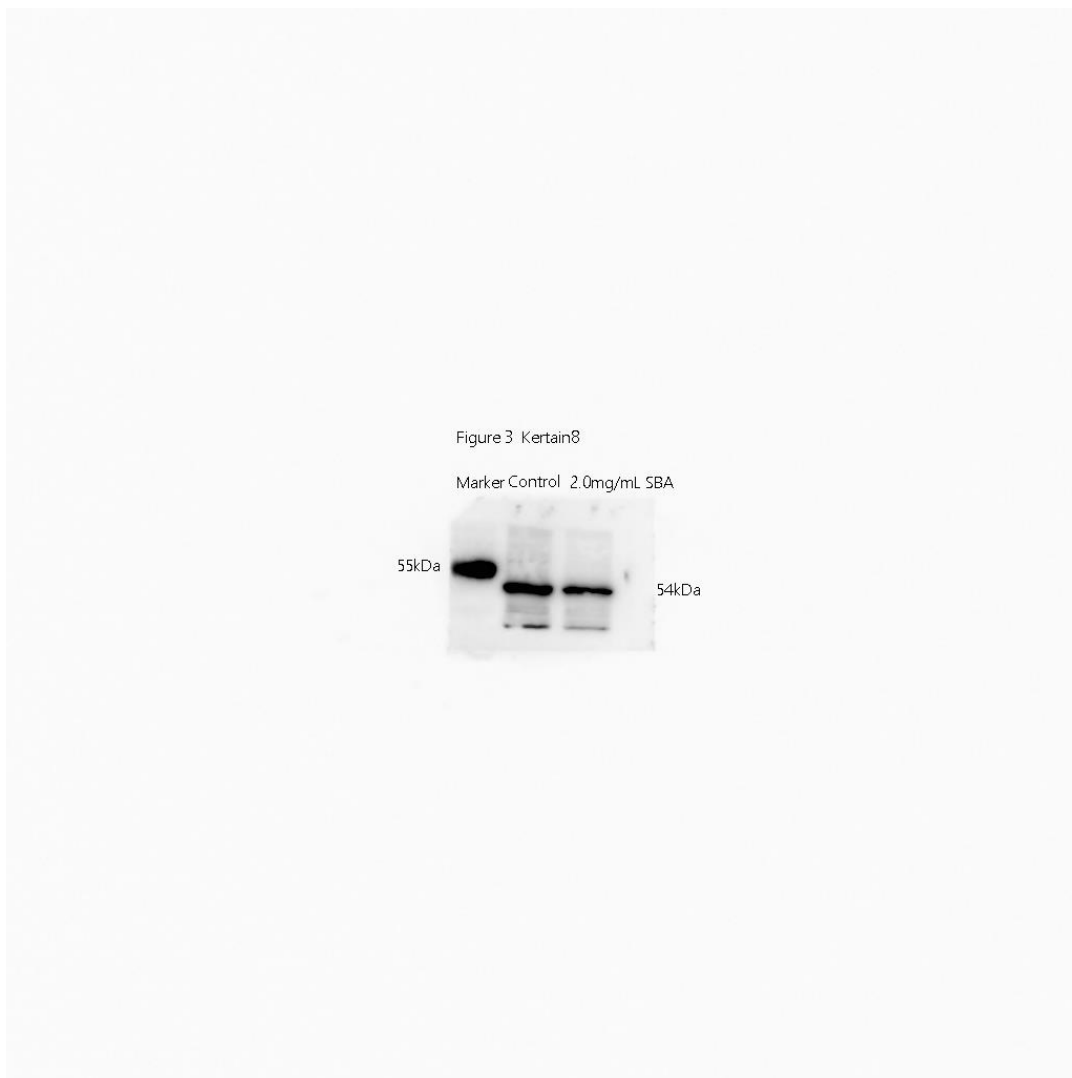


Figure S1.

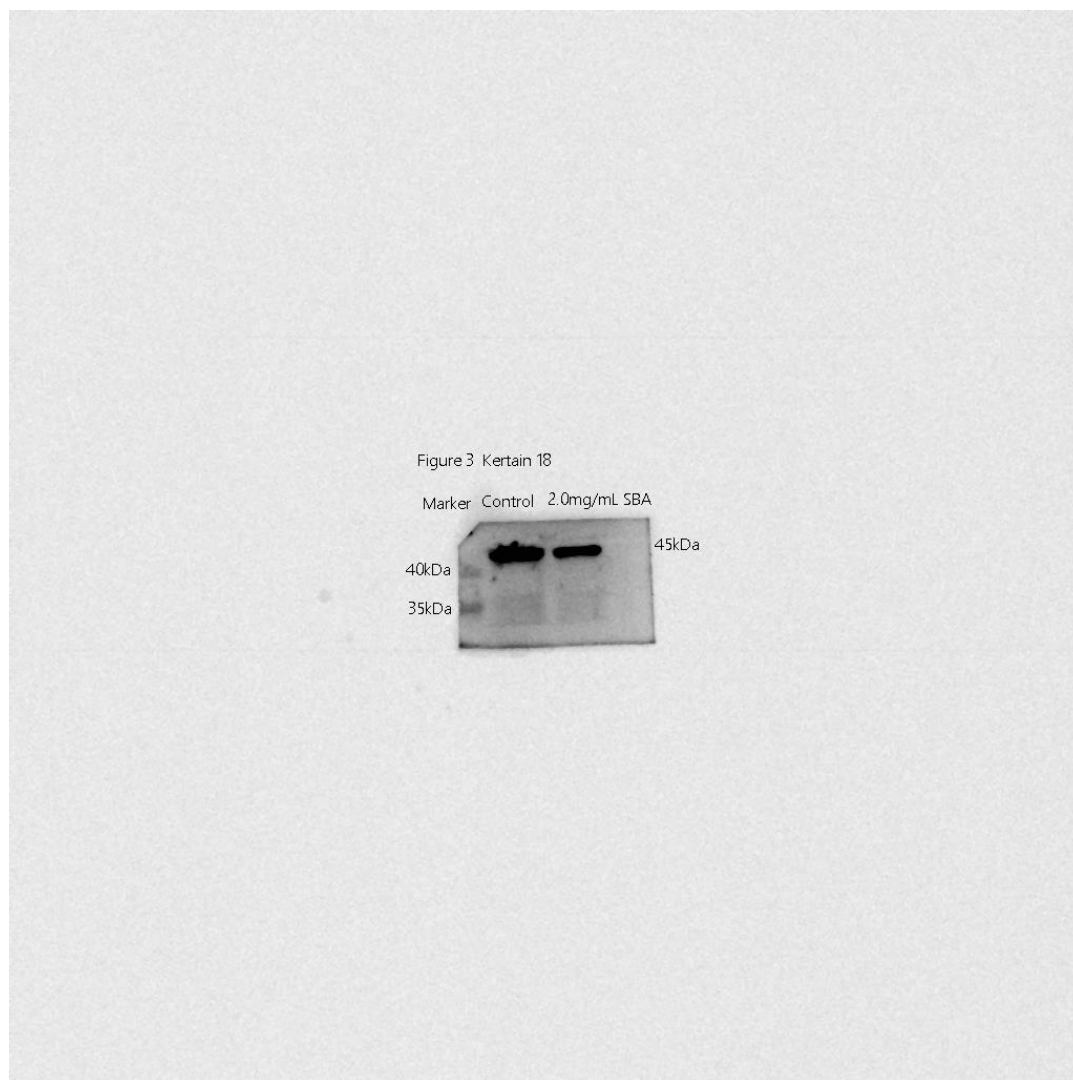


Figure S2.

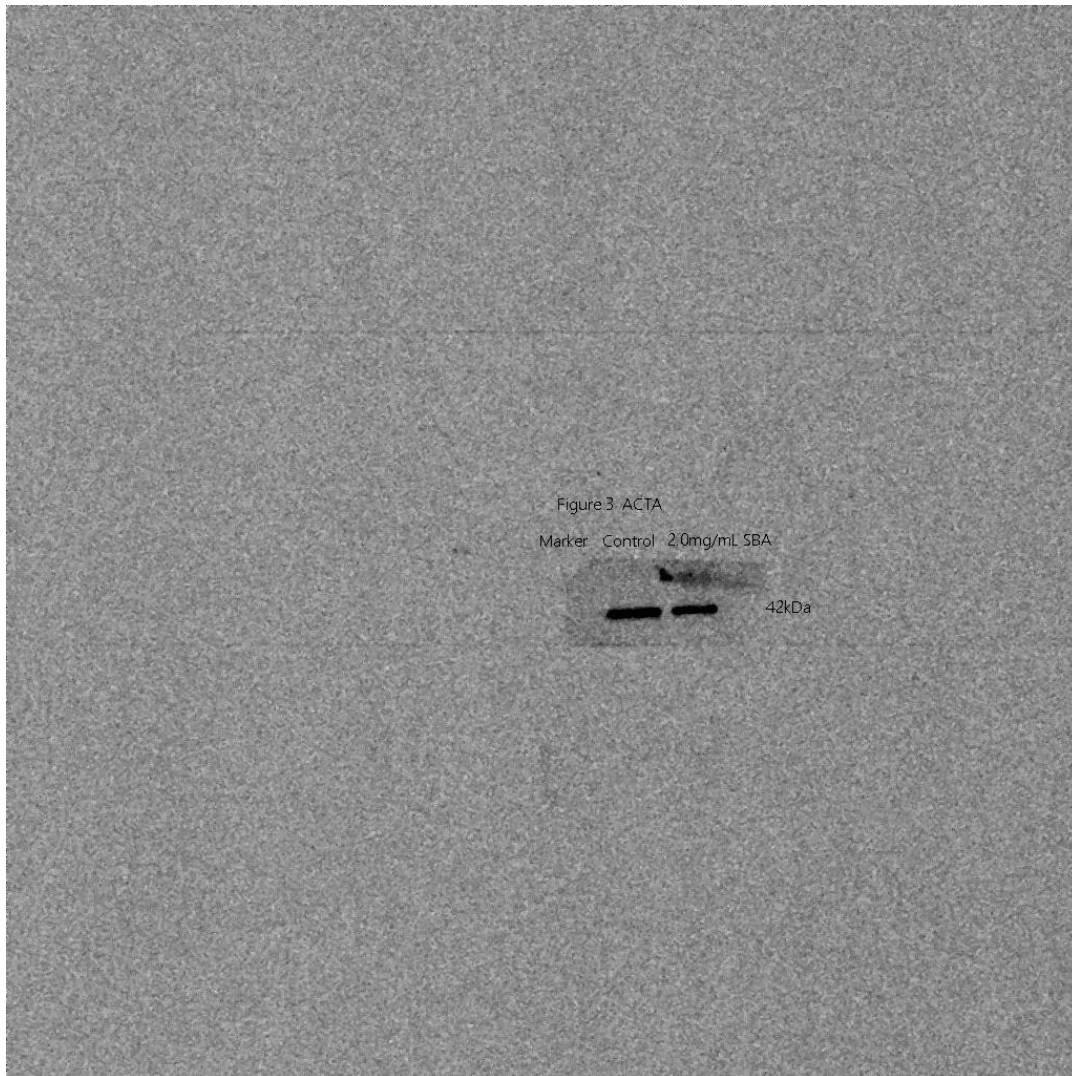


Figure S3.

Figure 3 β -actin

Marker Control 2.0mg/mL SBA



Figure S4.

Figure 9 Mfn2 in the mitochondria

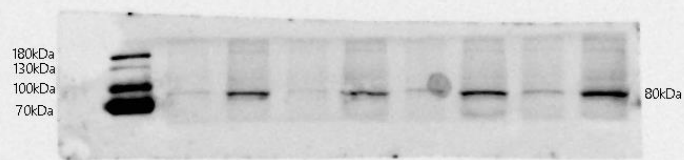


Figure S5.

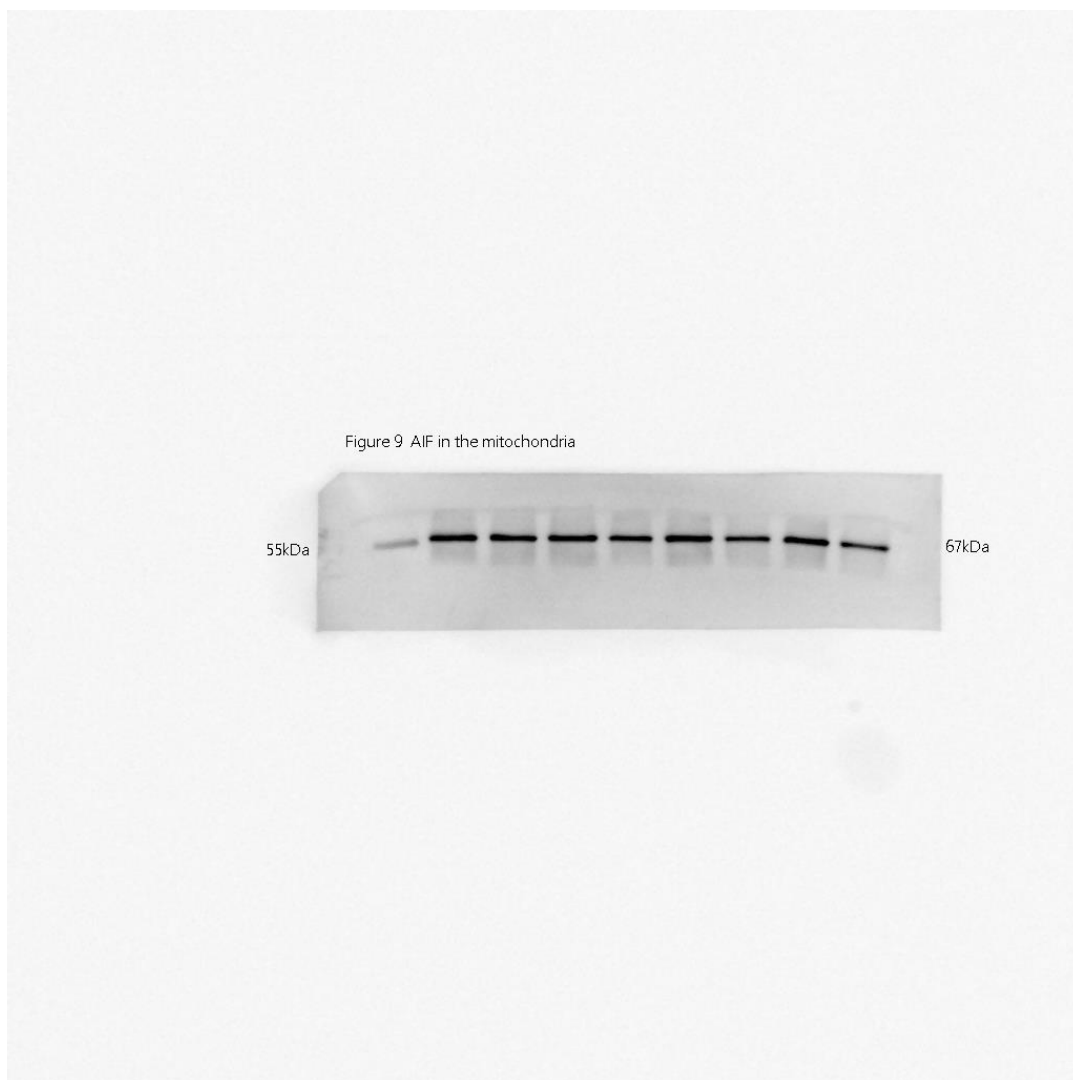


Figure S6.

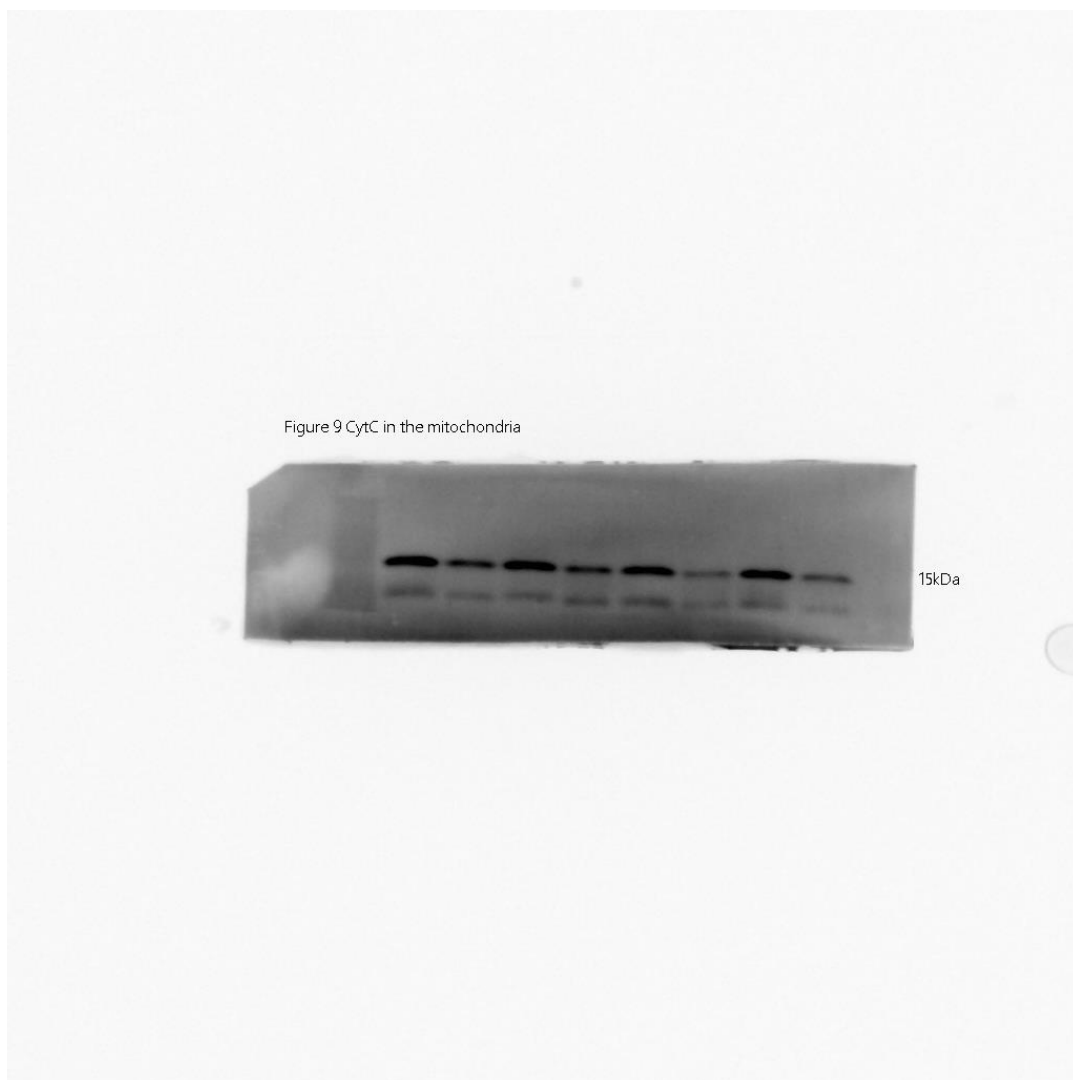


Figure S7.

Figure 9 FIS1 in the mitochondria

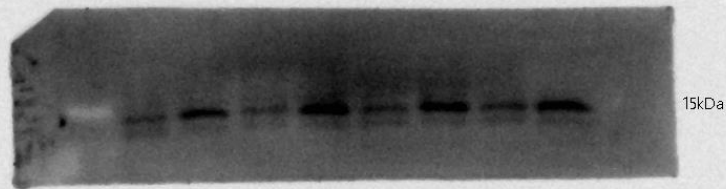


Figure S8.

Figure 9 β -actin in the mitochondria

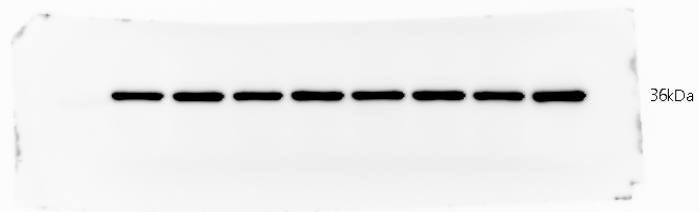


Figure S9.

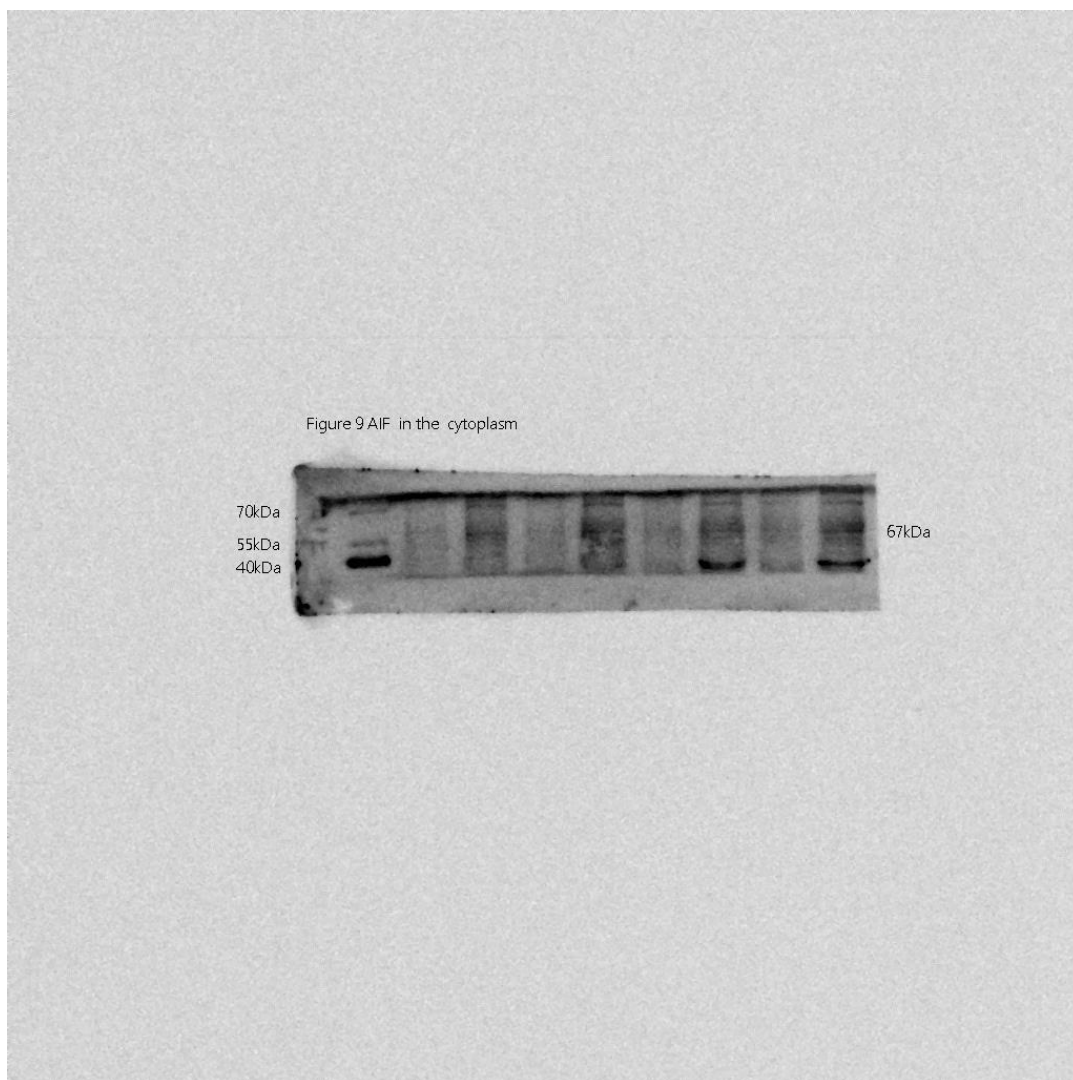


Figure S10.

Figure 9 CytC in the cytoplasm

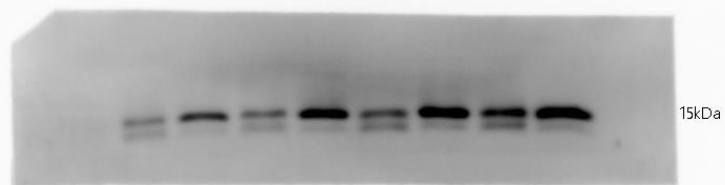


Figure S11.

Figure 9 β -actin in the cytoplasm



Figure S12.

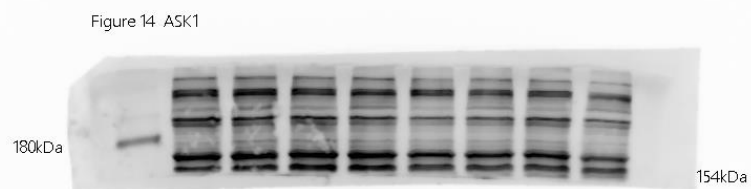


Figure S13.

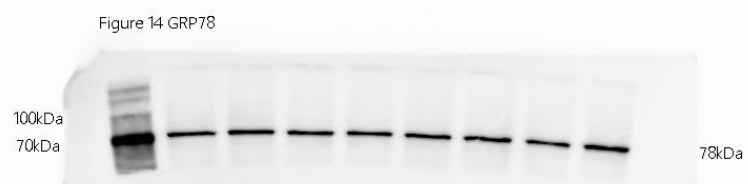


Figure S14.

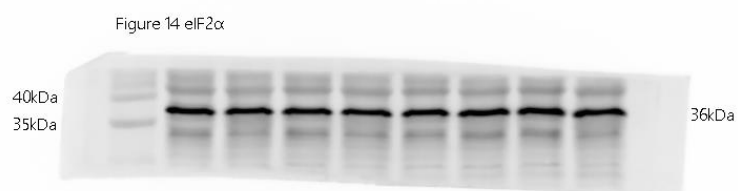


Figure S15.

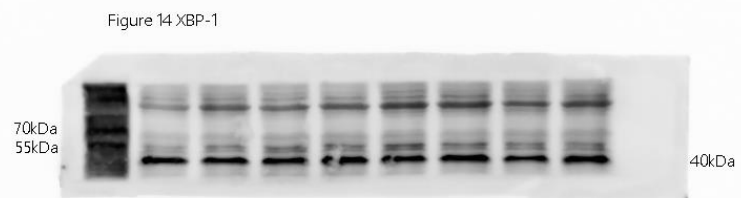


Figure S16.

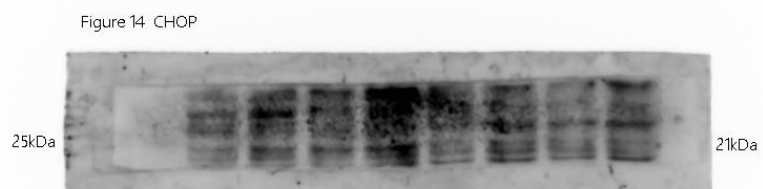


Figure S17.

Figure 14 β -actin

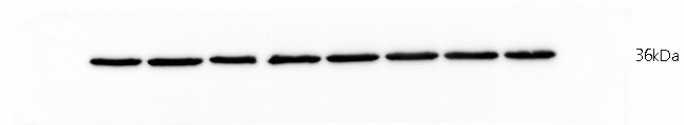


Figure S18.

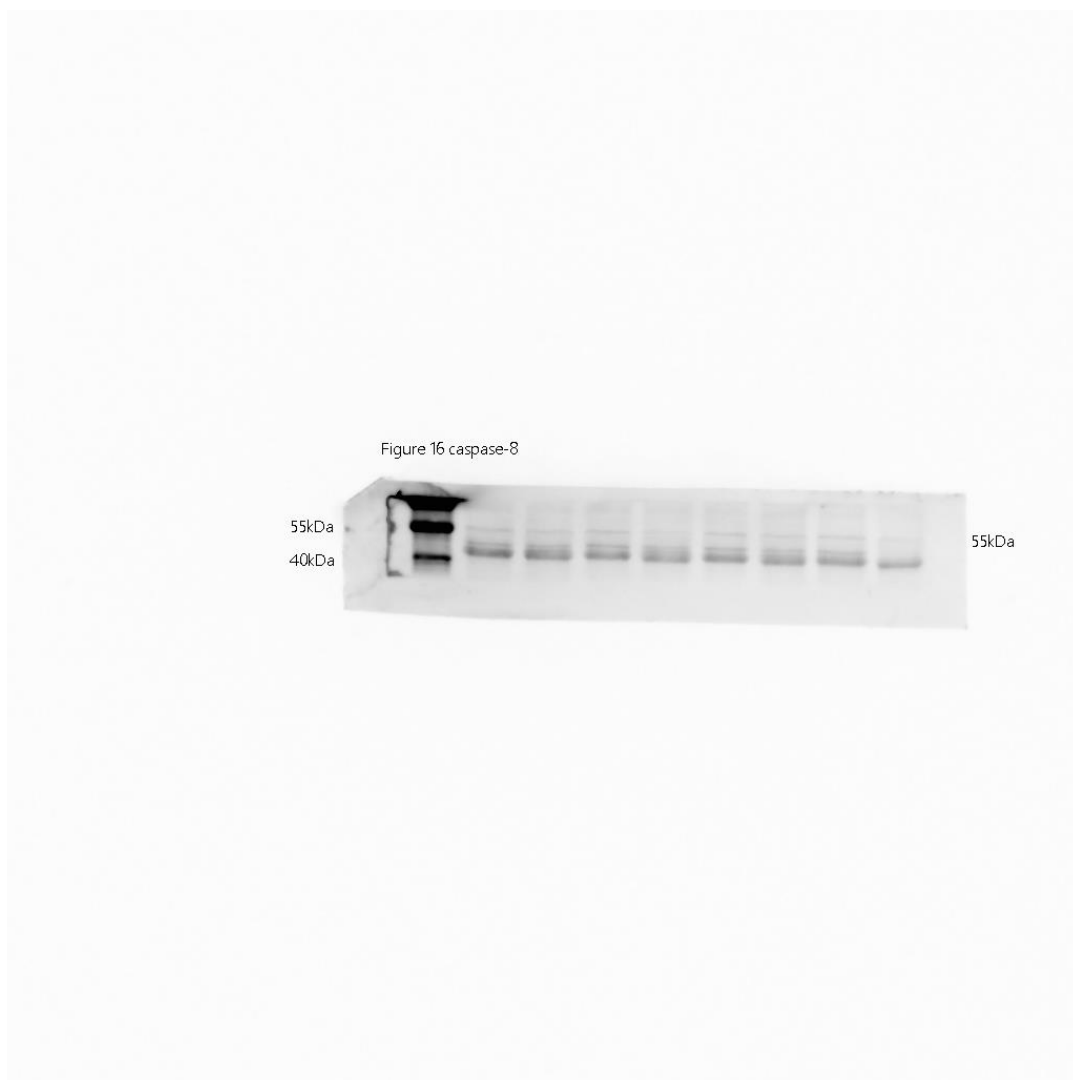


Figure S19.

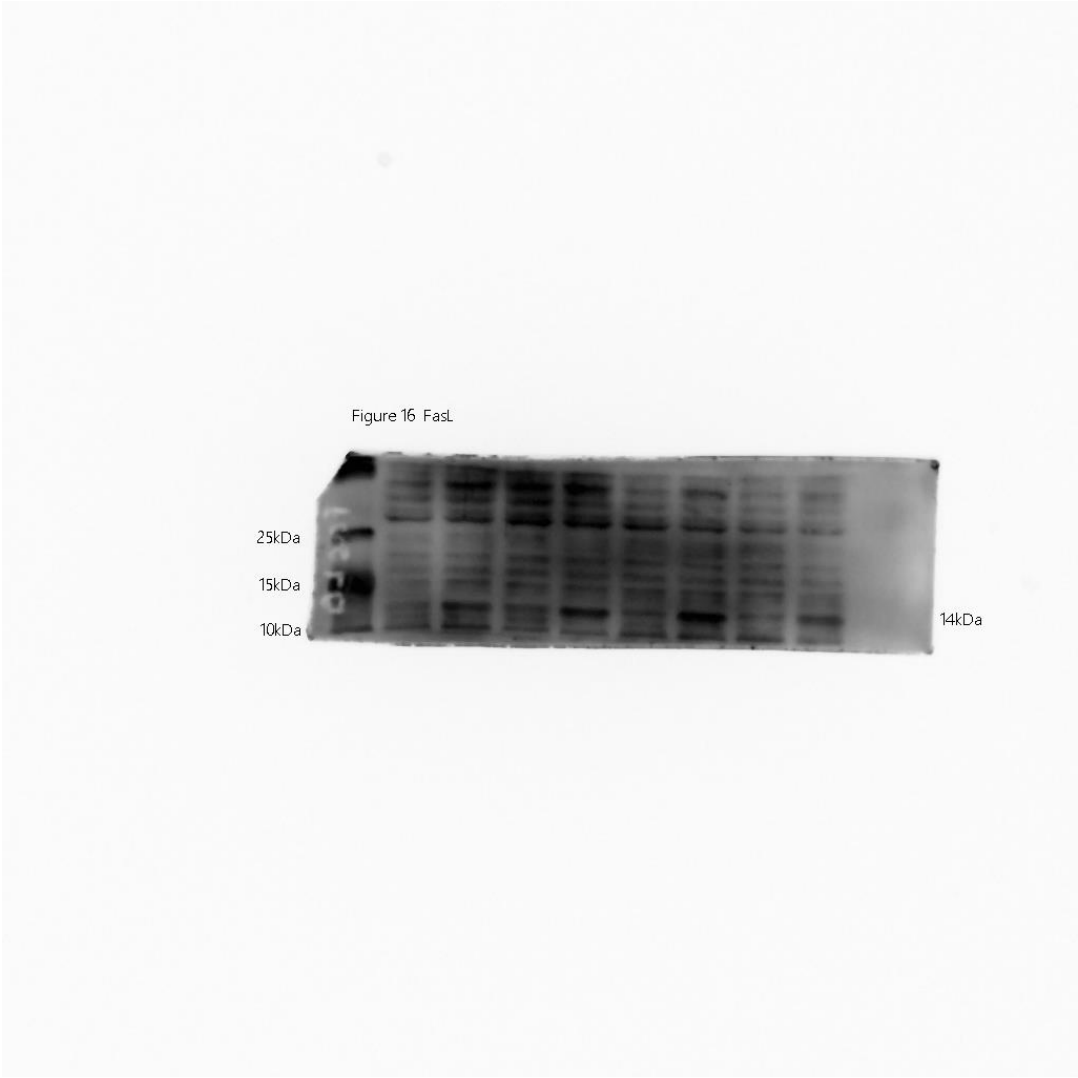


Figure S20.

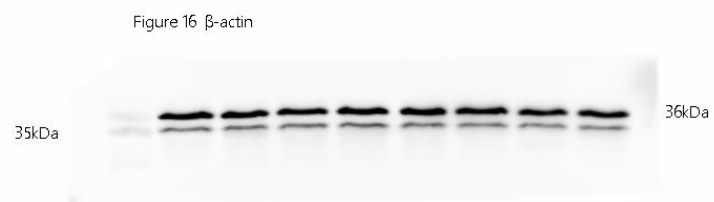


Figure S21.

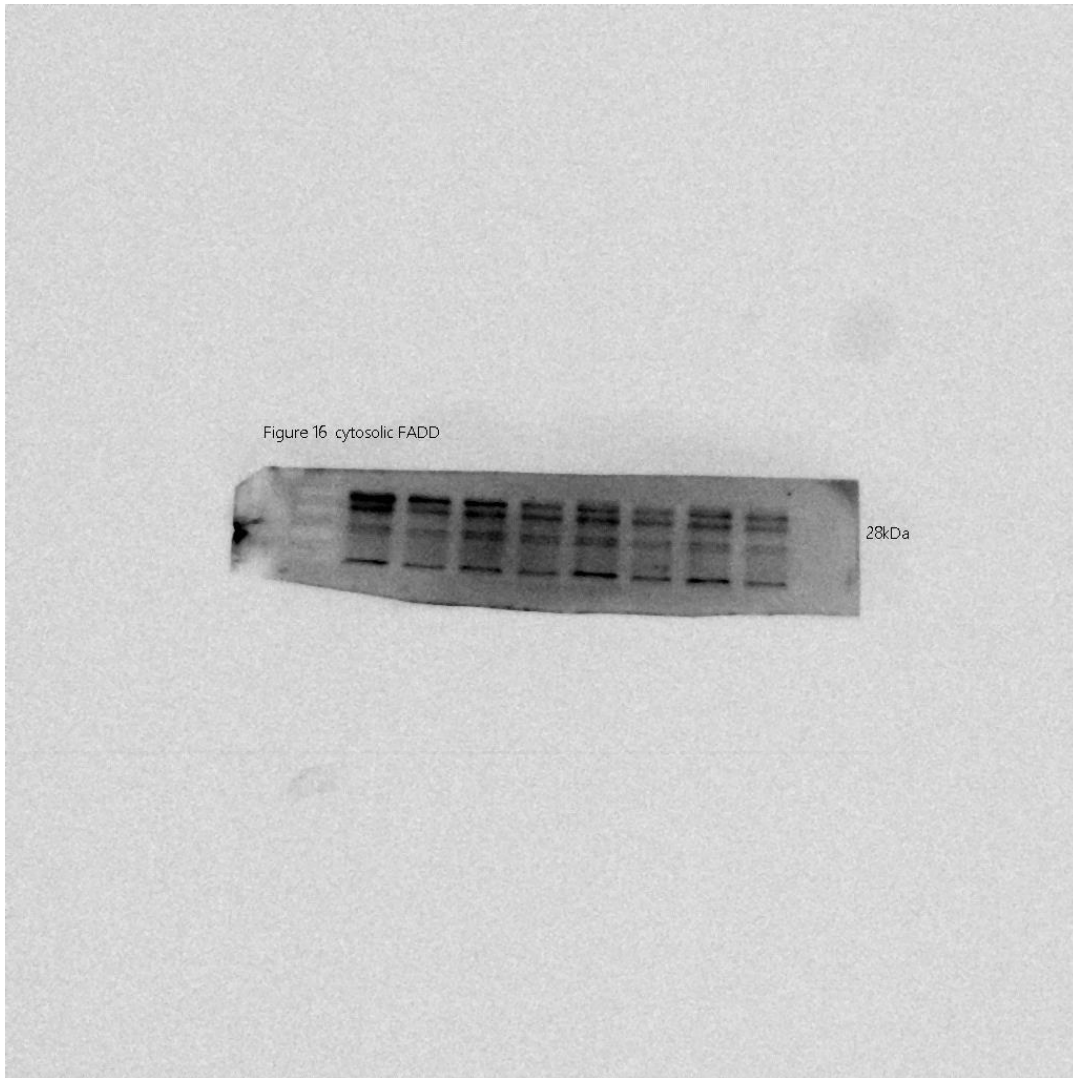


Figure S22.

Figure 16 cytosolic β -actin

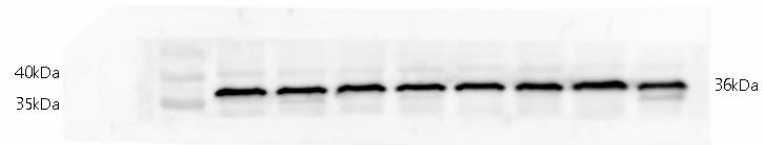


Figure S23.

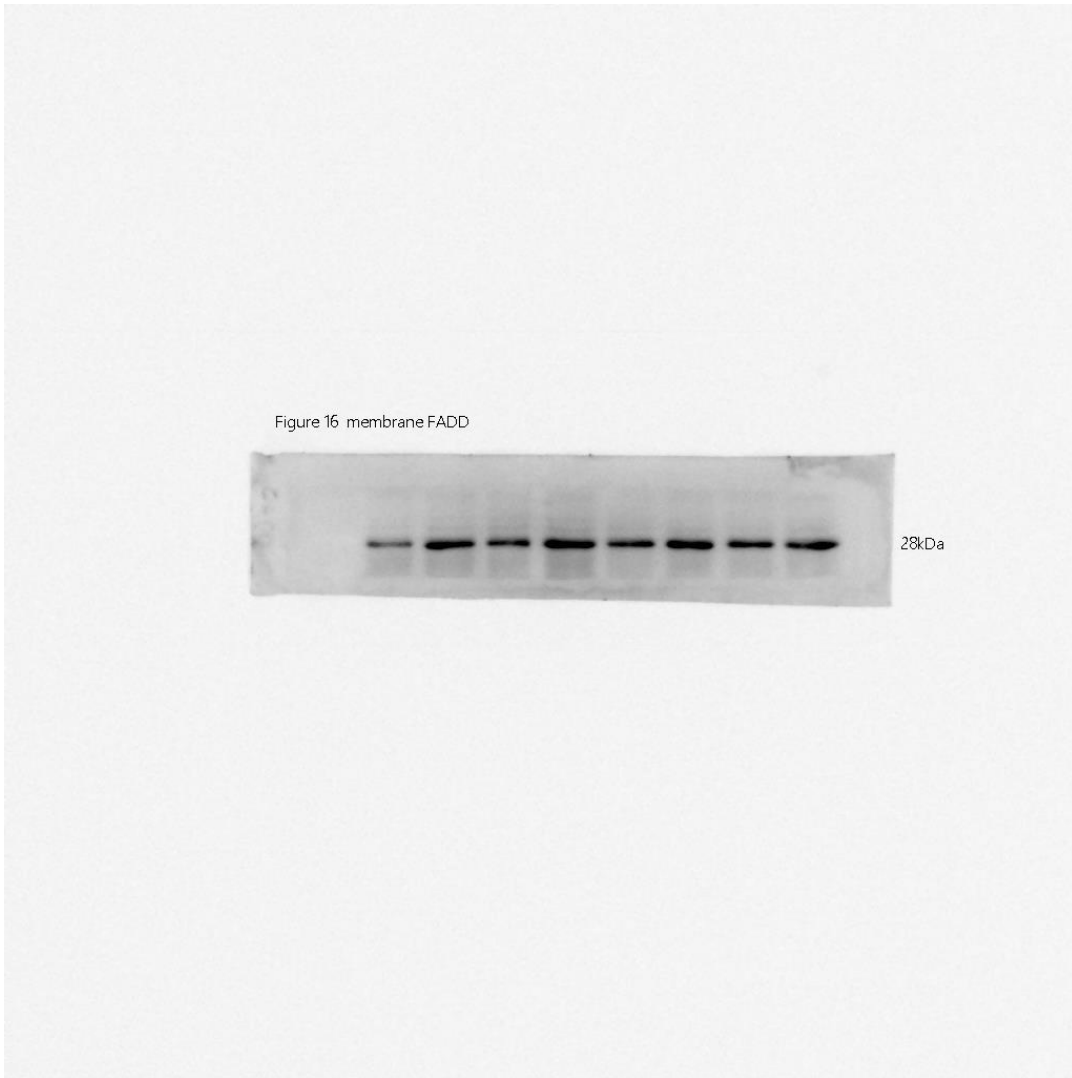


Figure S24.

Figure 16 membrane β -actin

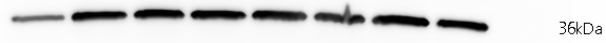


Figure S25.

Figure 19 Bcl-2

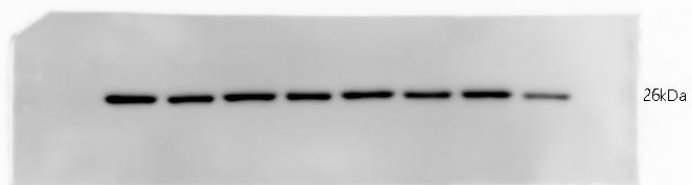


Figure S26.

Figure 19 Bax

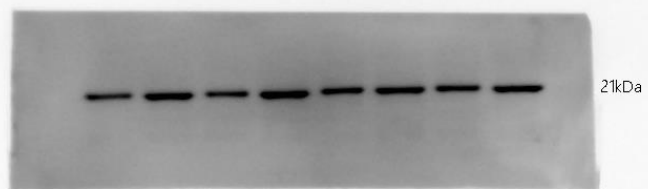


Figure S27.

Figure 19 β -actin

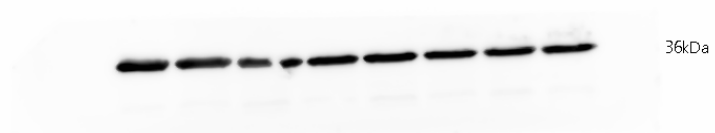


Figure S28.

Figure 19 cytosolic Bid

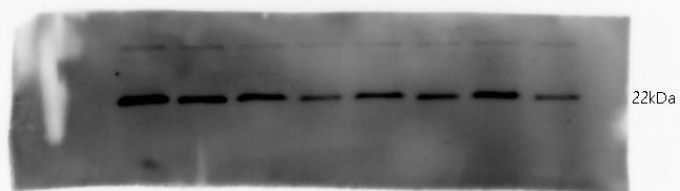


Figure S29.

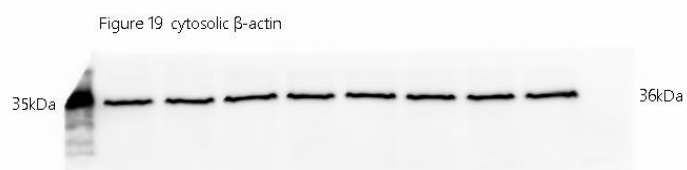


Figure S30.

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 Expressio n	Caspase-3 Activity	Caspase- 9 Activity	ATP Content	Mitochondria I AIF Expression	Mitochondria I 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).