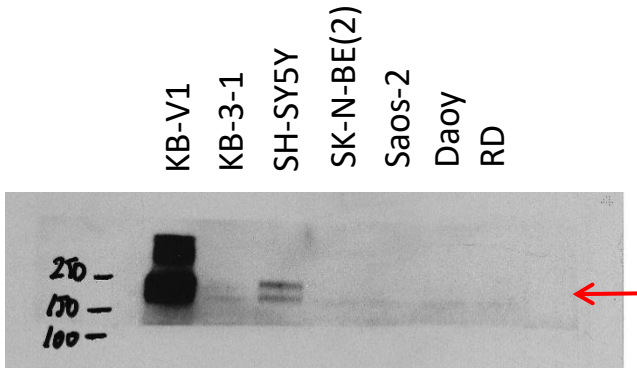


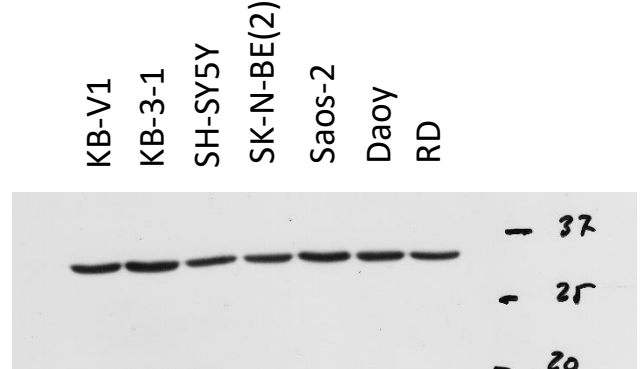
SUPPLEMENTARY FIGURE S1

Experiment 1:

Pgp

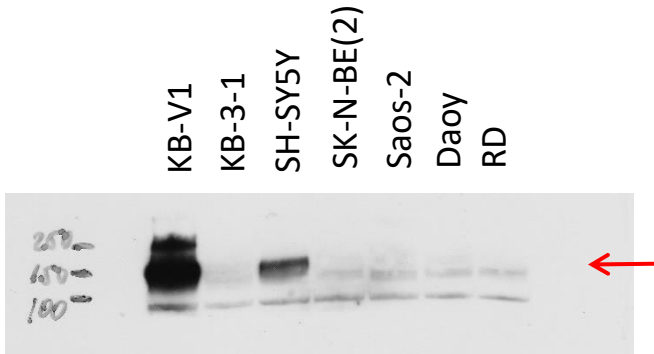


GAPDH

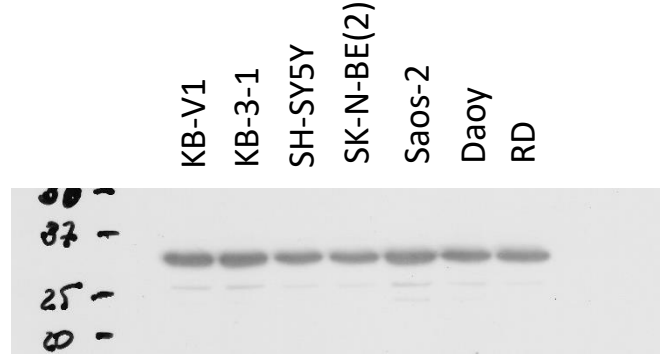


Experiment 2:

Pgp

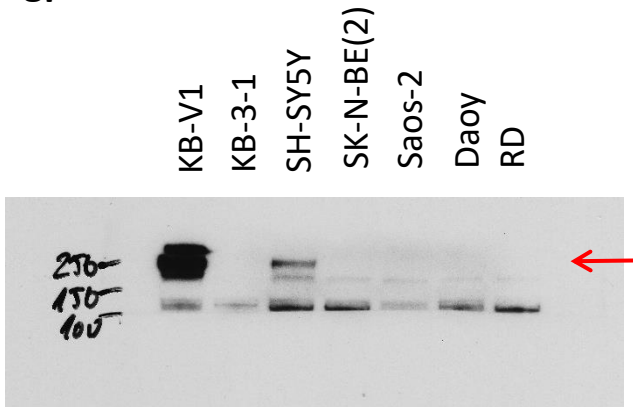


GAPDH



Experiment 3:

Pgp



GAPDH

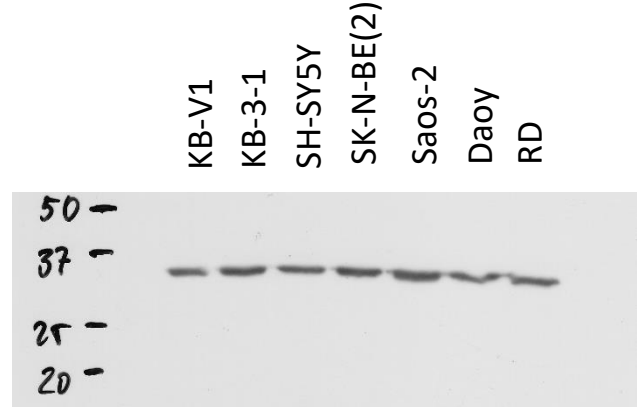
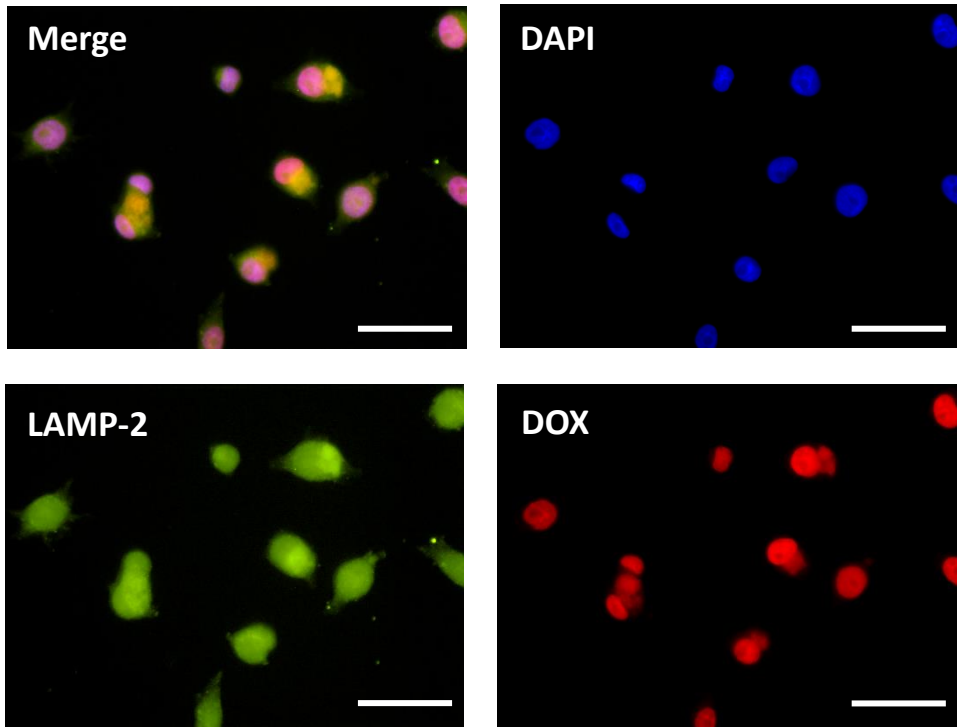


Figure S1: Immunoblotting to determine endogenous Pgp levels in untreated cell lines. GAPDH served as the loading control. The experiments were performed in biological triplicates.

SUPPLEMENTARY FIGURE S2

(A) KB-V1 cell line (positive control)



(B) KB-3-1 cell line (negative control)

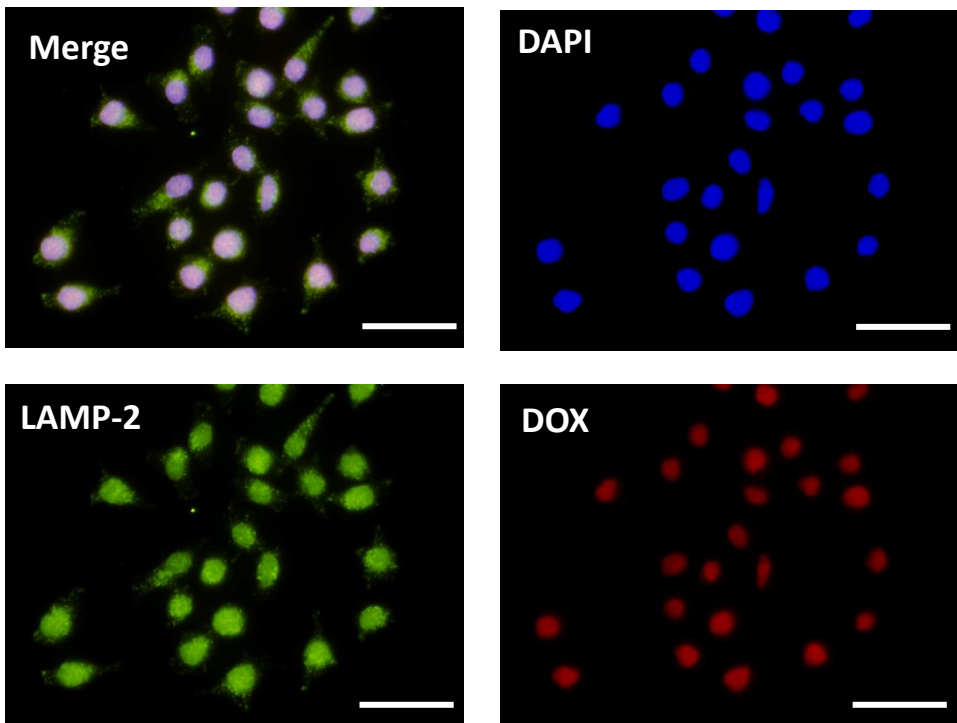
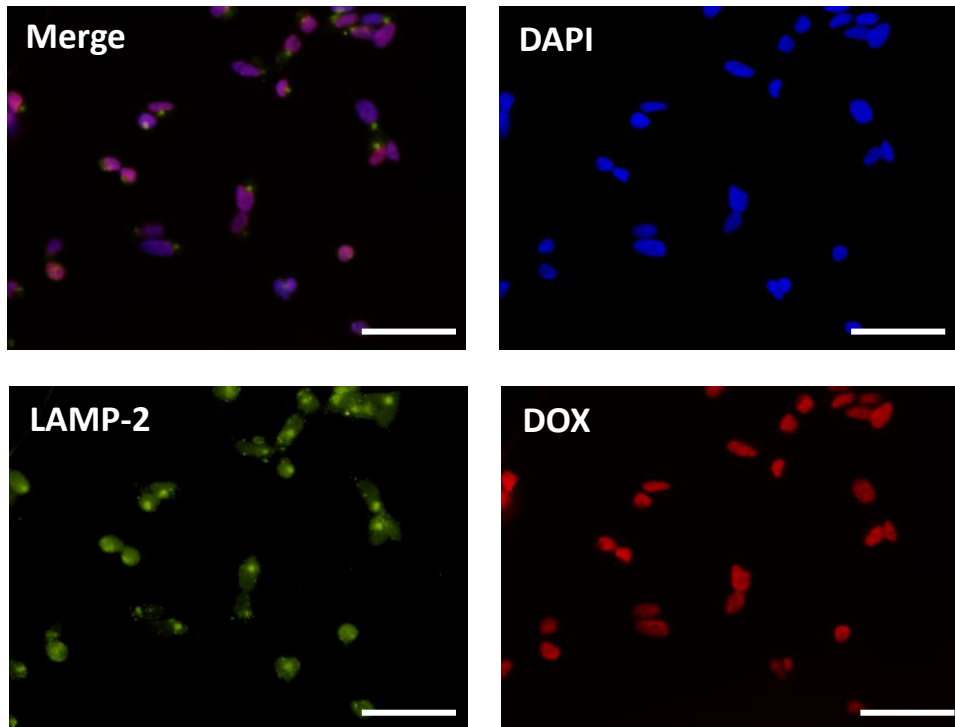


Figure S2: Intracellular localization of doxorubicin. The localization of doxorubicin (DOX) within the cells after 2 h of treatment with 10 μ M DOX (red) was observed using immunofluorescence microscopy. The target organelles, lysosomes and nuclei, were also stained. The lysosomes were visualized by indirect immunofluorescence using LAMP-2 primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled with DAPI (blue). **(A)** KB-V1 cell line served as a positive control for the lysosomal sequestration of DOX; **(B)** KB-3-1 cell line served as a negative control. Scale bars, 50 μ m.

SUPPLEMENTARY FIGURE S2

(C) SH-SY5Y cell line



(D) SK-N-BE(2) cell line

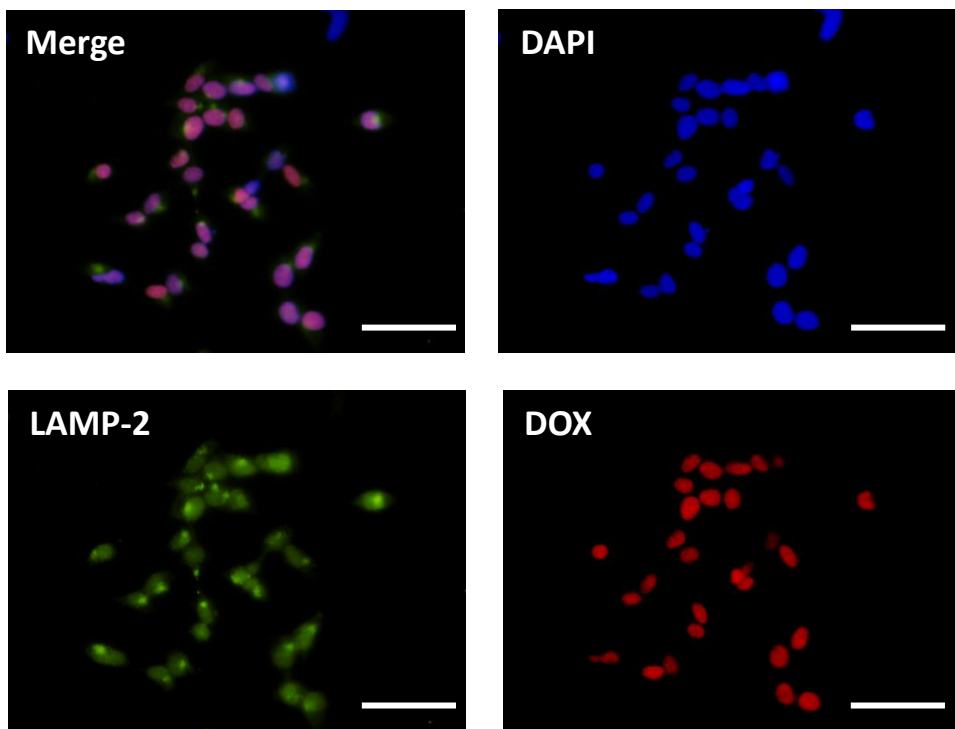
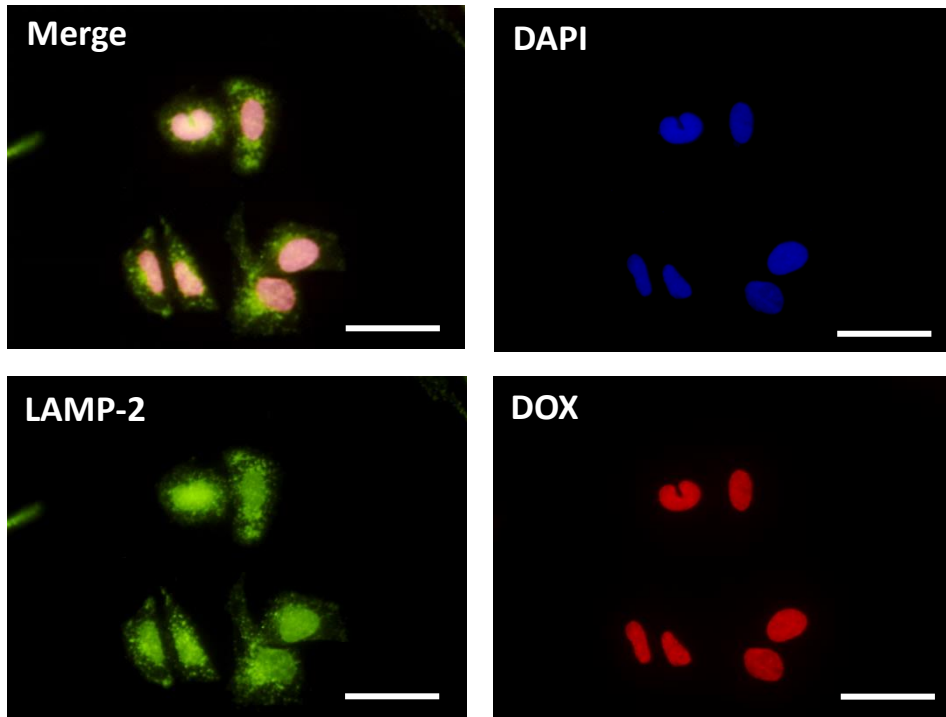


Figure S2: Intracellular localization of doxorubicin. The localization of doxorubicin (DOX) within the cells after 2 h of treatment with 10 μ M DOX (red) was observed using immunofluorescence microscopy. The target organelles, lysosomes and nuclei, were also stained. The lysosomes were visualized by indirect immunofluorescence using LAMP-2 primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled with DAPI (blue). Scale bars, 50 μ m.

SUPPLEMENTARY FIGURE S2

(E) Saos-2 cell line



(F) Daoy cell line

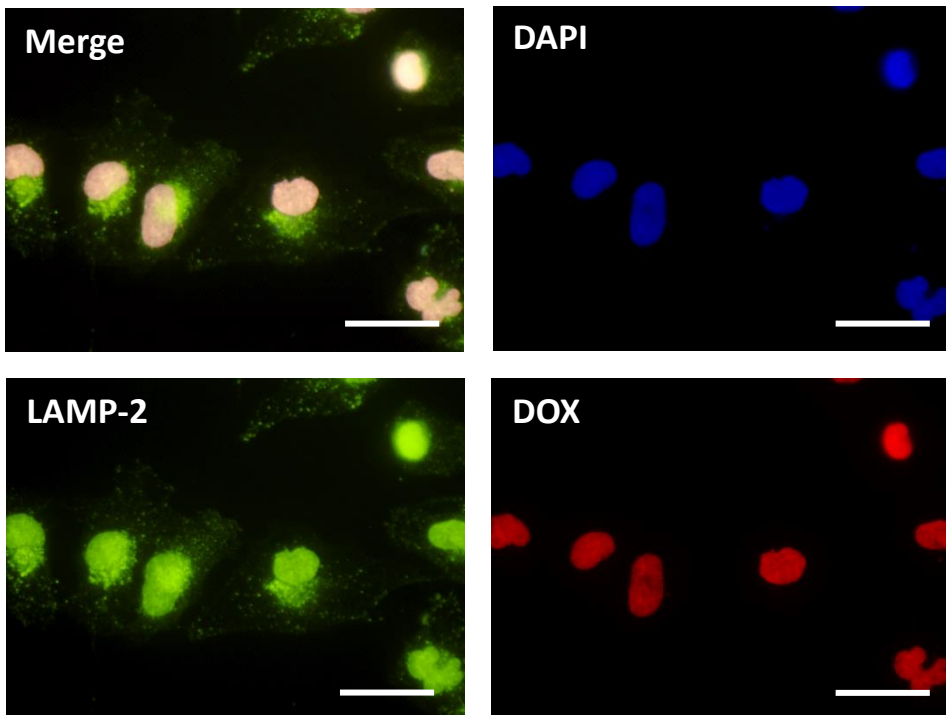


Figure S2: Intracellular localization of doxorubicin. The localization of doxorubicin (DOX) within the cells after 2 h of treatment with 10 μ M DOX (red) was observed using immunofluorescence microscopy. The target organelles, lysosomes and nuclei, were also stained. The lysosomes were visualized by indirect immunofluorescence using LAMP-2 primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled with DAPI (blue). Scale bars, 50 μ m.

SUPPLEMENTARY FIGURE S2

(G) RD cell line

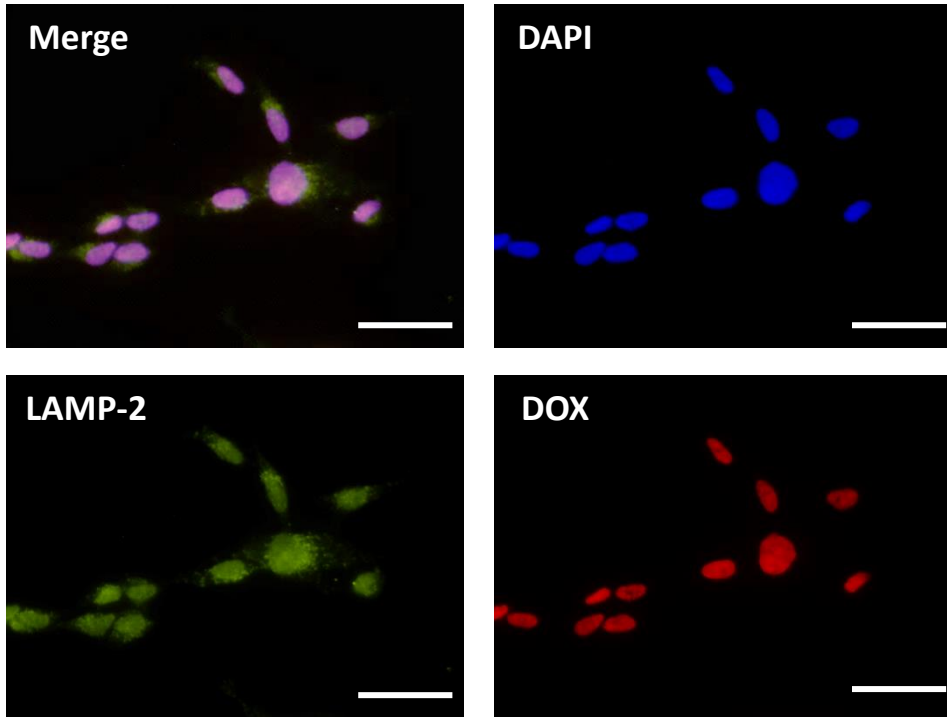
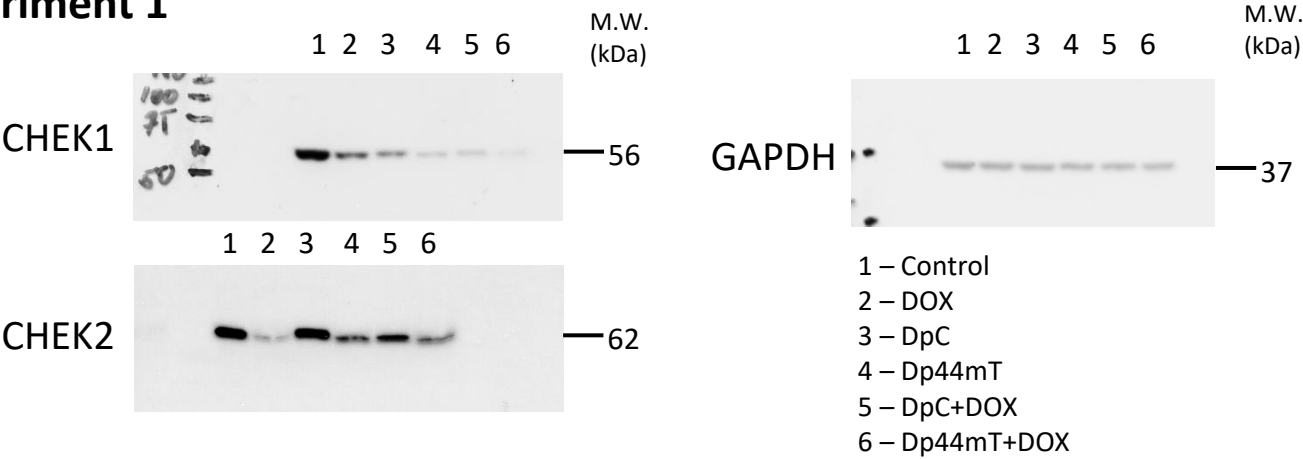


Figure S2: Intracellular localization of doxorubicin. The localization of doxorubicin (DOX) within the cells after 2 h of treatment with 10 μ M DOX (red) was observed using immunofluorescence microscopy. The target organelles, lysosomes and nuclei, were also stained. The lysosomes were visualized by indirect immunofluorescence using LAMP-2 primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled with DAPI (blue). Scale bars, 50 μ m.

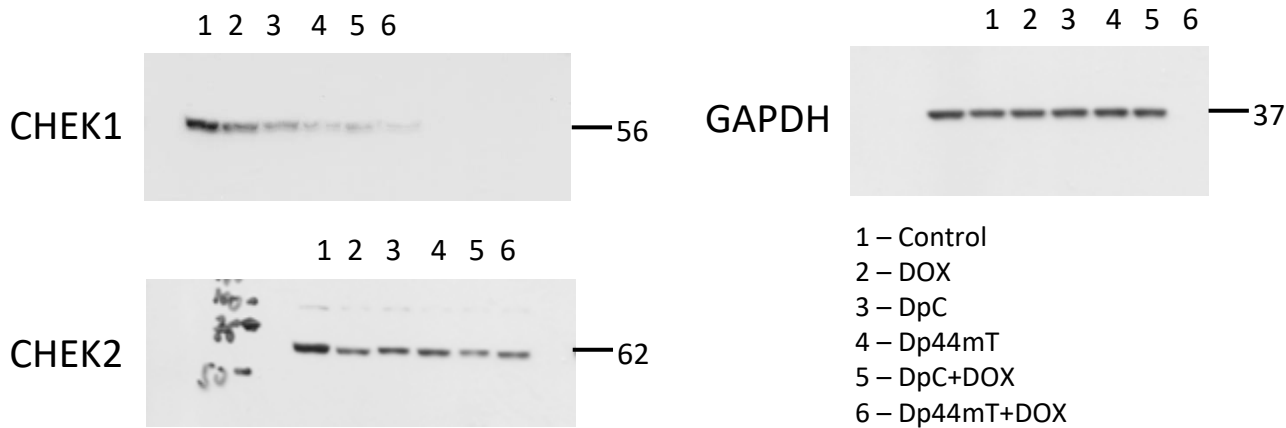
SUPPLEMENTARY FIGURE S3

(A) SH-SY5Y cell line

Experiment 1



Experiment 2



Experiment 3

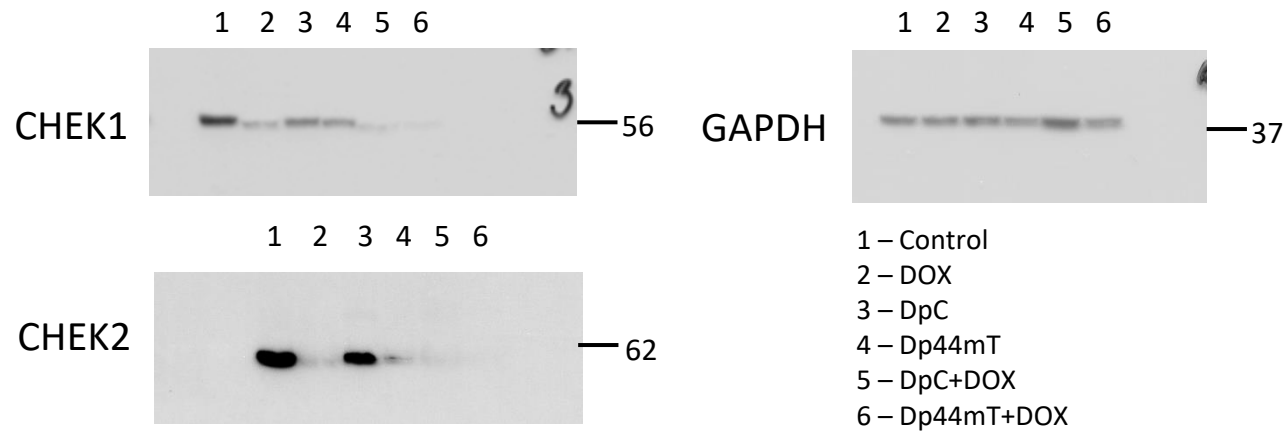
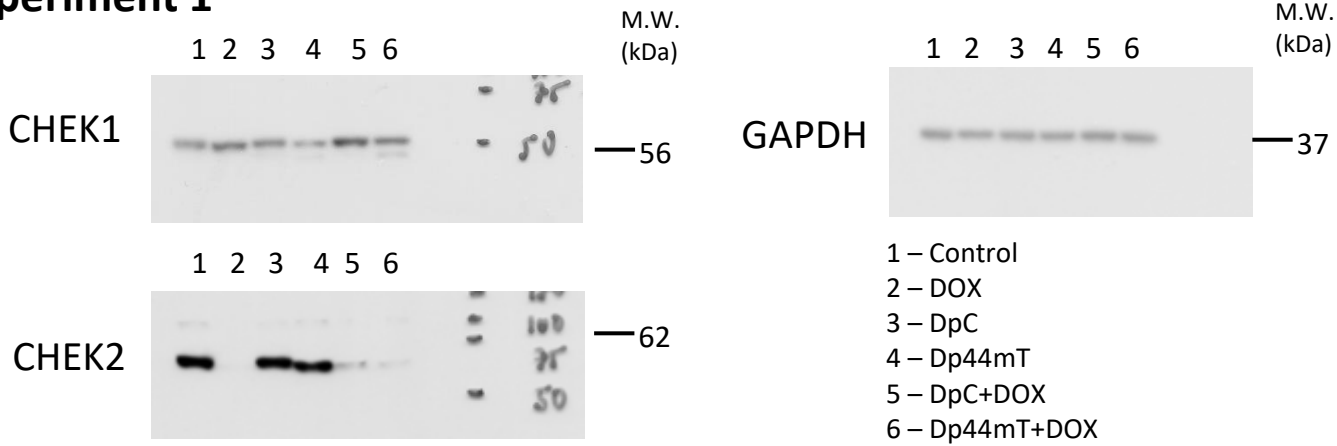


Figure S3: Immunoblotting to determine CHEK1 and CHEK2 levels in cell lines after the experimental treatment. CHEK1 and CHEK2 levels were examined after 3 days of incubation with IC₅₀ doses of DOX, DpC, Dp44mT or their combinations. GAPDH served as the loading control. The experiments were performed in biological triplicates.

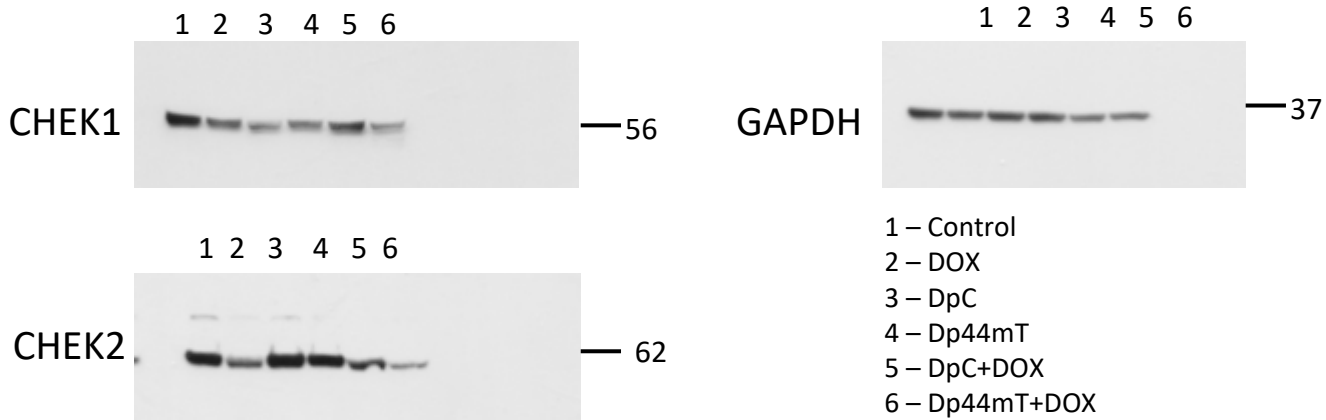
SUPPLEMENTARY FIGURE S3

(B) SK-N-BE(2) cell line

Experiment 1



Experiment 2



Experiment 3

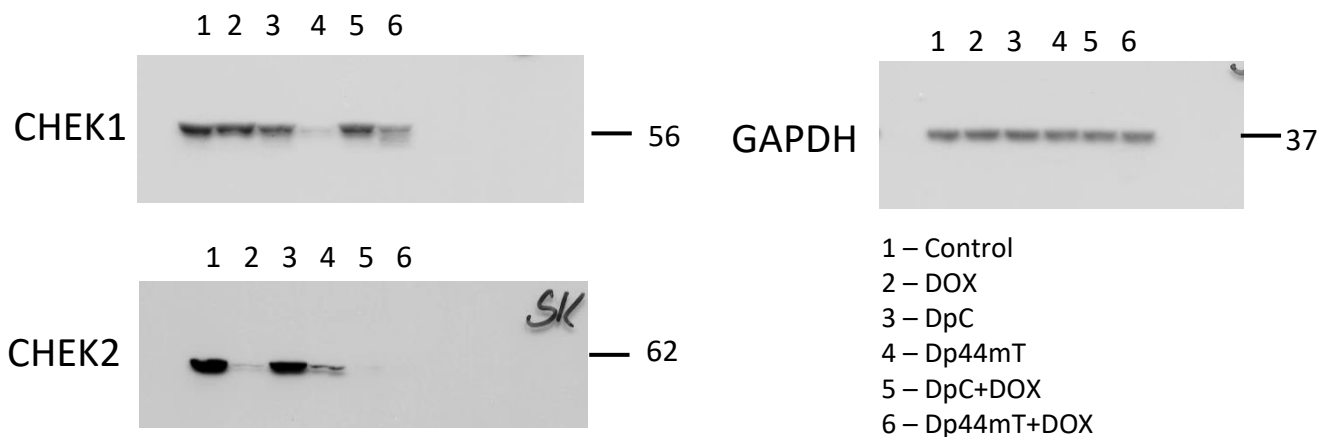
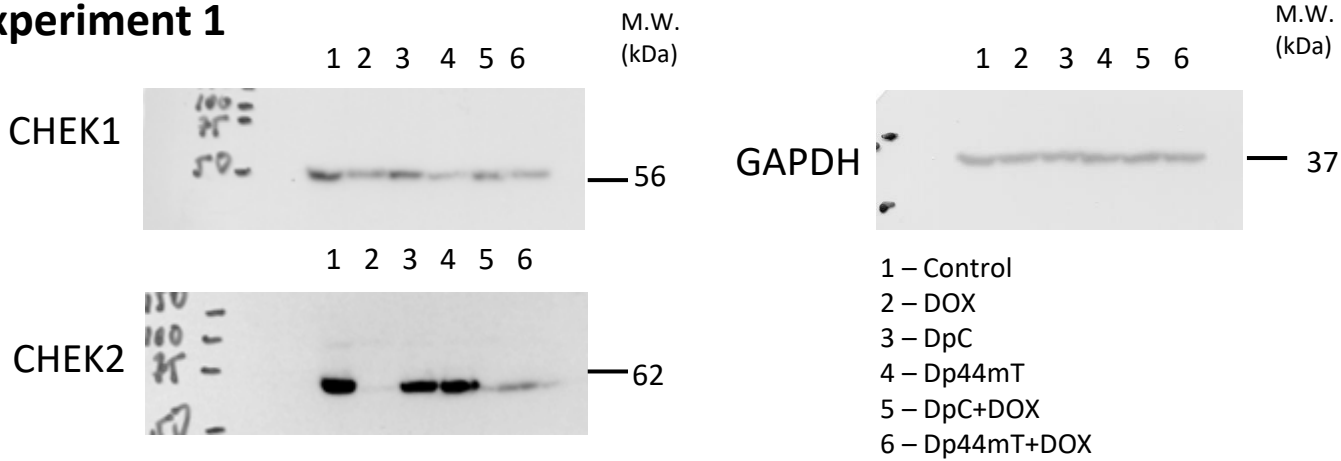


Figure S3: Immunoblotting to determine CHEK1 and CHEK2 levels in cell lines after the experimental treatment. CHEK1 and CHEK2 levels were examined after 3 days of incubation with IC₅₀ doses of DOX, DpC, Dp44mT or their combinations. GAPDH served as the loading control. The experiments were performed in biological triplicates.

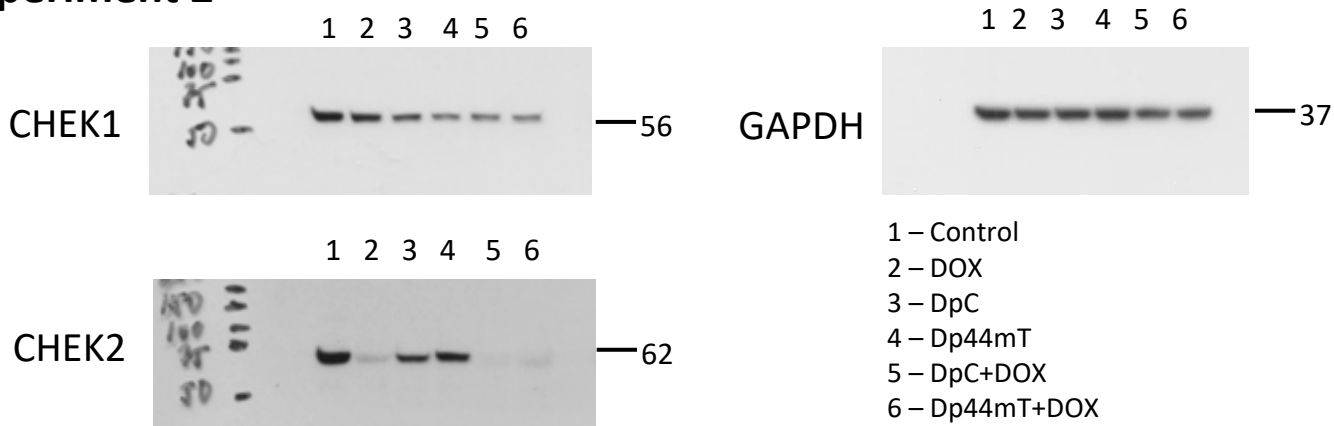
SUPPLEMENTARY FIGURE S3

(C) Saos-2 cell line

Experiment 1



Experiment 2



Experiment 3

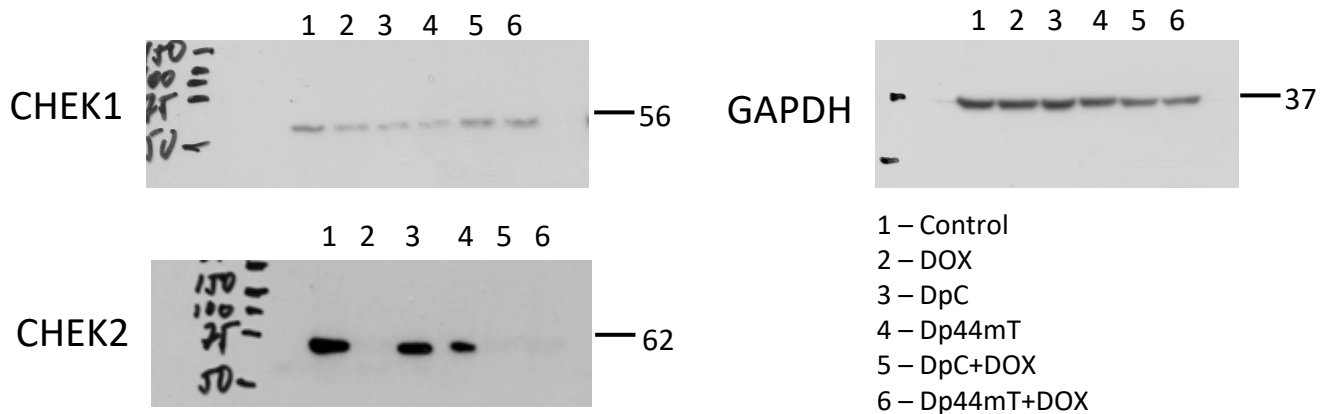
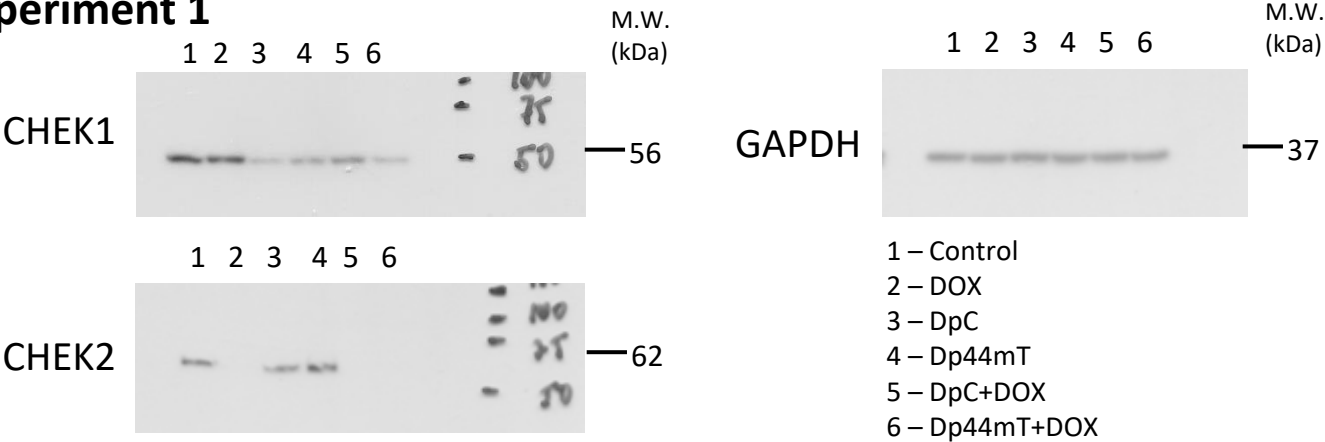


Figure S3: Immunoblotting to determine CHEK1 and CHEK2 levels in cell lines after the experimental treatment. CHEK1 and CHEK2 levels were examined after 3 days of incubation with IC_{50} doses of DOX, DpC, Dp44mT or their combinations. GAPDH served as the loading control. The experiments were performed in biological triplicates.

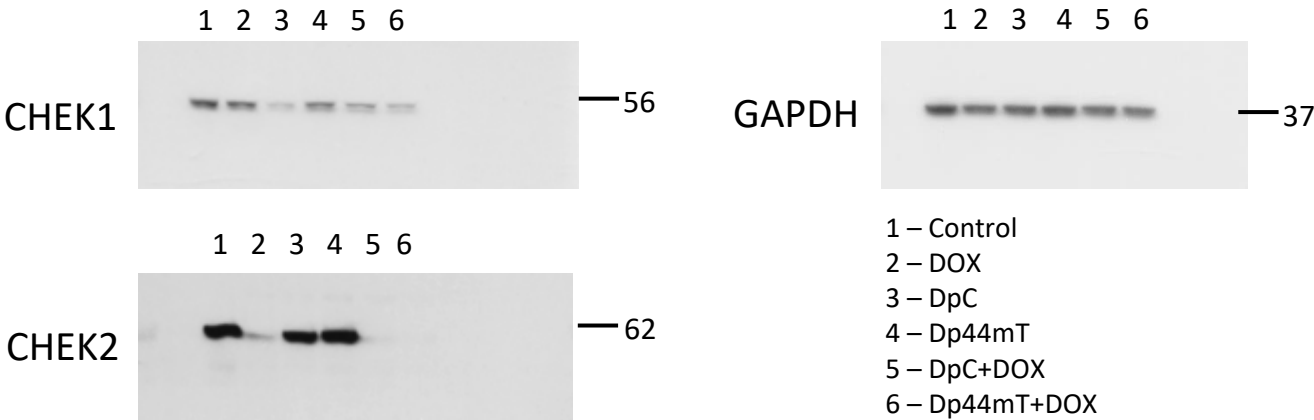
SUPPLEMENTARY FIGURE S3

(D) Daoy cell line

Experiment 1



Experiment 2



Experiment 3

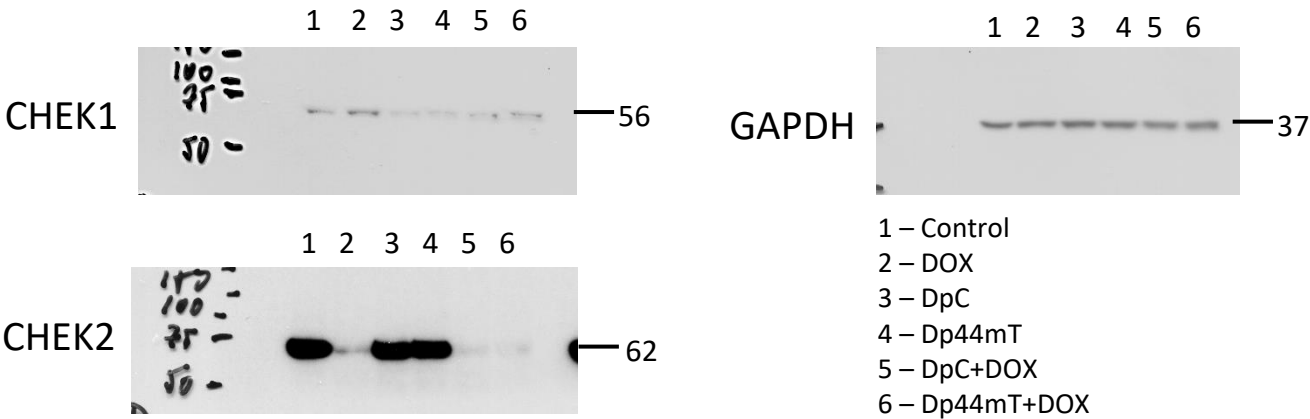
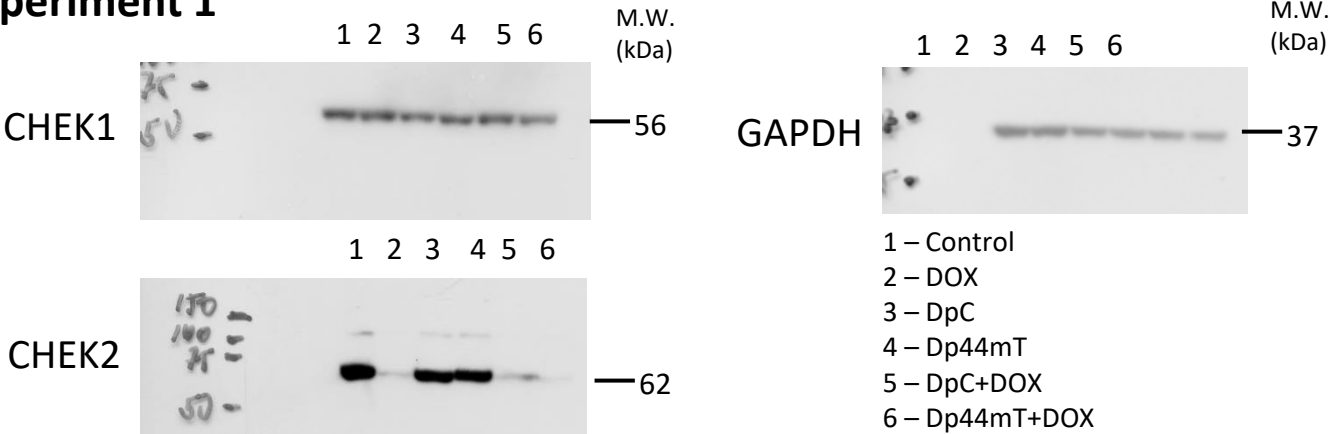


Figure S3: Immunoblotting to determine CHEK1 and CHEK2 levels in cell lines after the experimental treatment. CHEK1 and CHEK2 levels were examined after 3 days of incubation with IC₅₀ doses of DOX, DpC, Dp44mT or their combinations. GAPDH served as the loading control. The experiments were performed in biological triplicates.

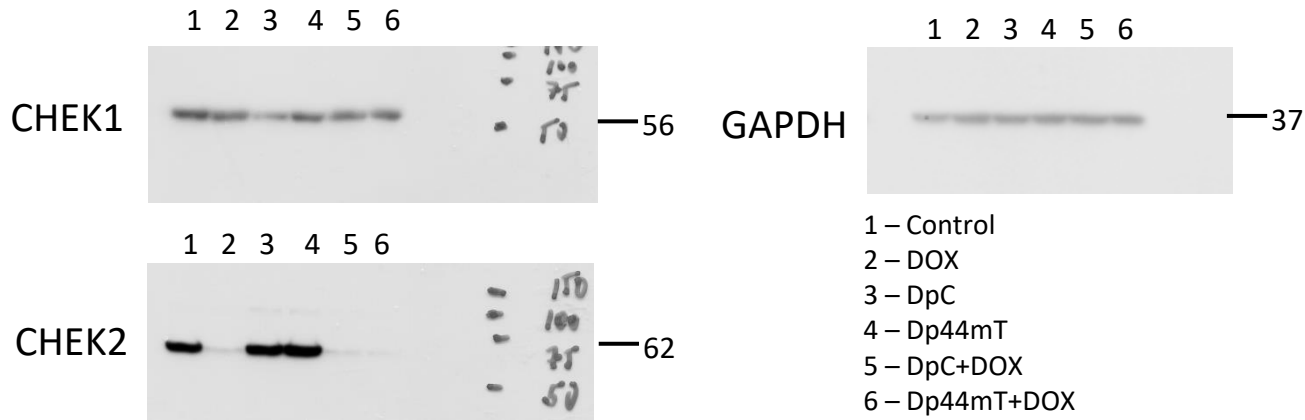
SUPPLEMENTARY FIGURE S3

(E) RD cell line

Experiment 1



Experiment 2



Experiment 3

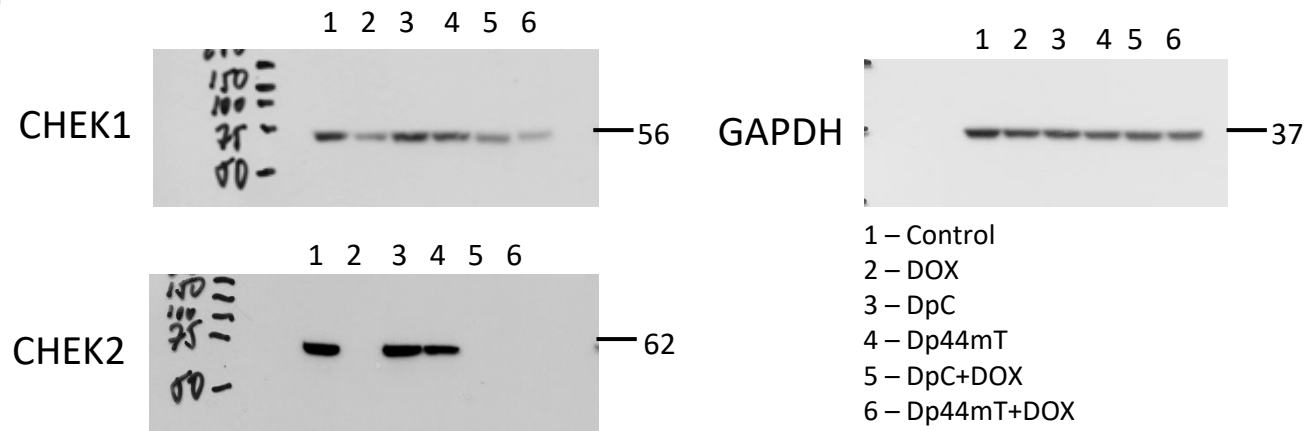


Figure S3: Immunoblotting to determine CHEK1 and CHEK2 levels in cell lines after the experimental treatment. CHEK1 and CHEK2 levels were examined after 3 days of incubation with IC₅₀ doses of DOX, DpC, Dp44mT or their combinations. GAPDH served as the loading control. The experiments were performed in biological triplicates.

SUPPLEMENTARY FIGURE S4

(A) SH-SY5Y cell line

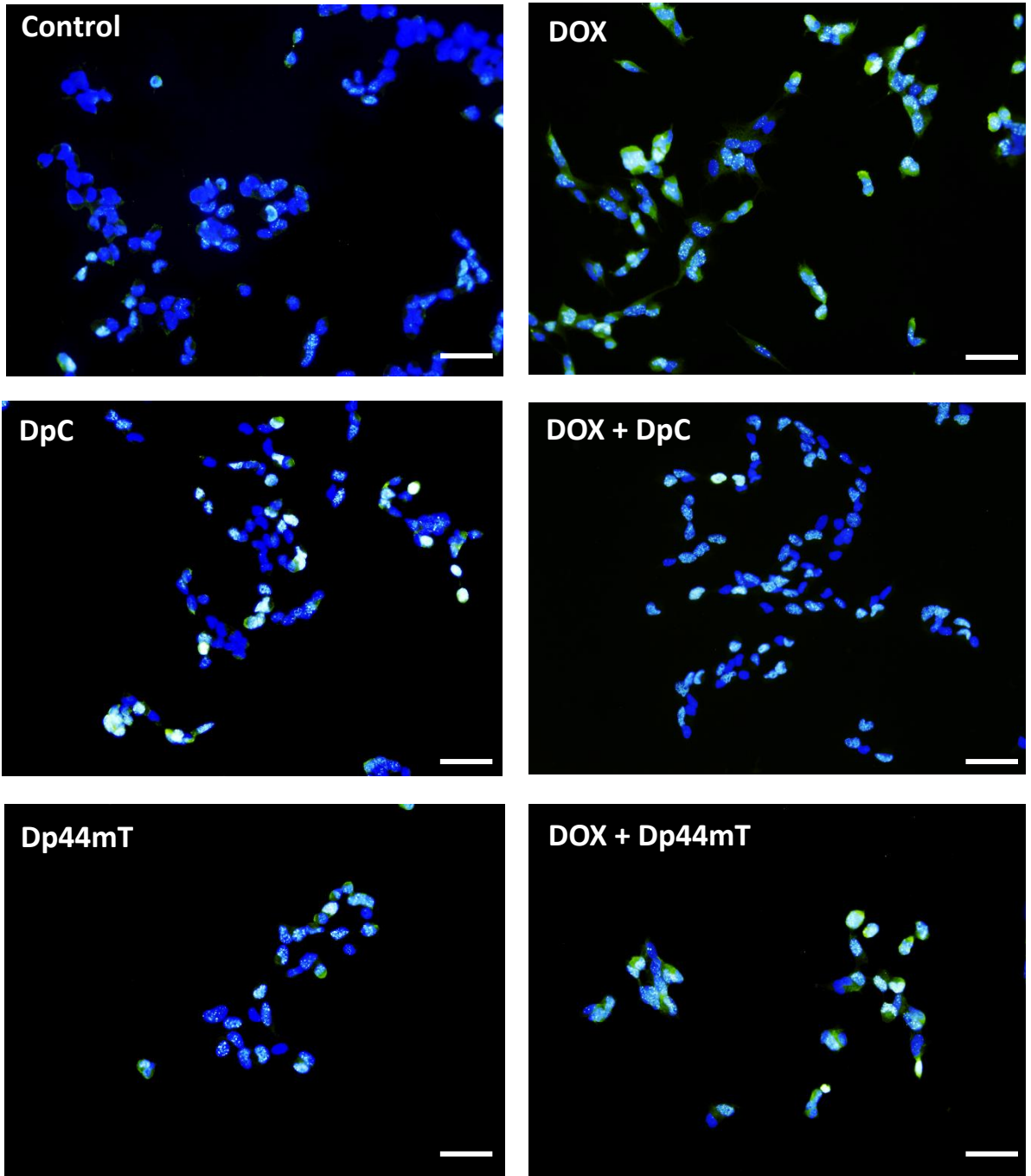


Figure S4: Detection of phosphorylated γ -H2AX as double-strand break marker in cell lines after the experimental treatment. Immunofluorescence was performed after 48 h treatment with IC_{50} doses of DpC, Dp44mT, DOX or their combinations. Phosphorylated γ -H2AX was visualized using the γ -H2AX primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled by DAPI (blue). Scale bars, 50 μ m.

SUPPLEMENTARY FIGURE S4

(B) SK-N-BE(2) cell line

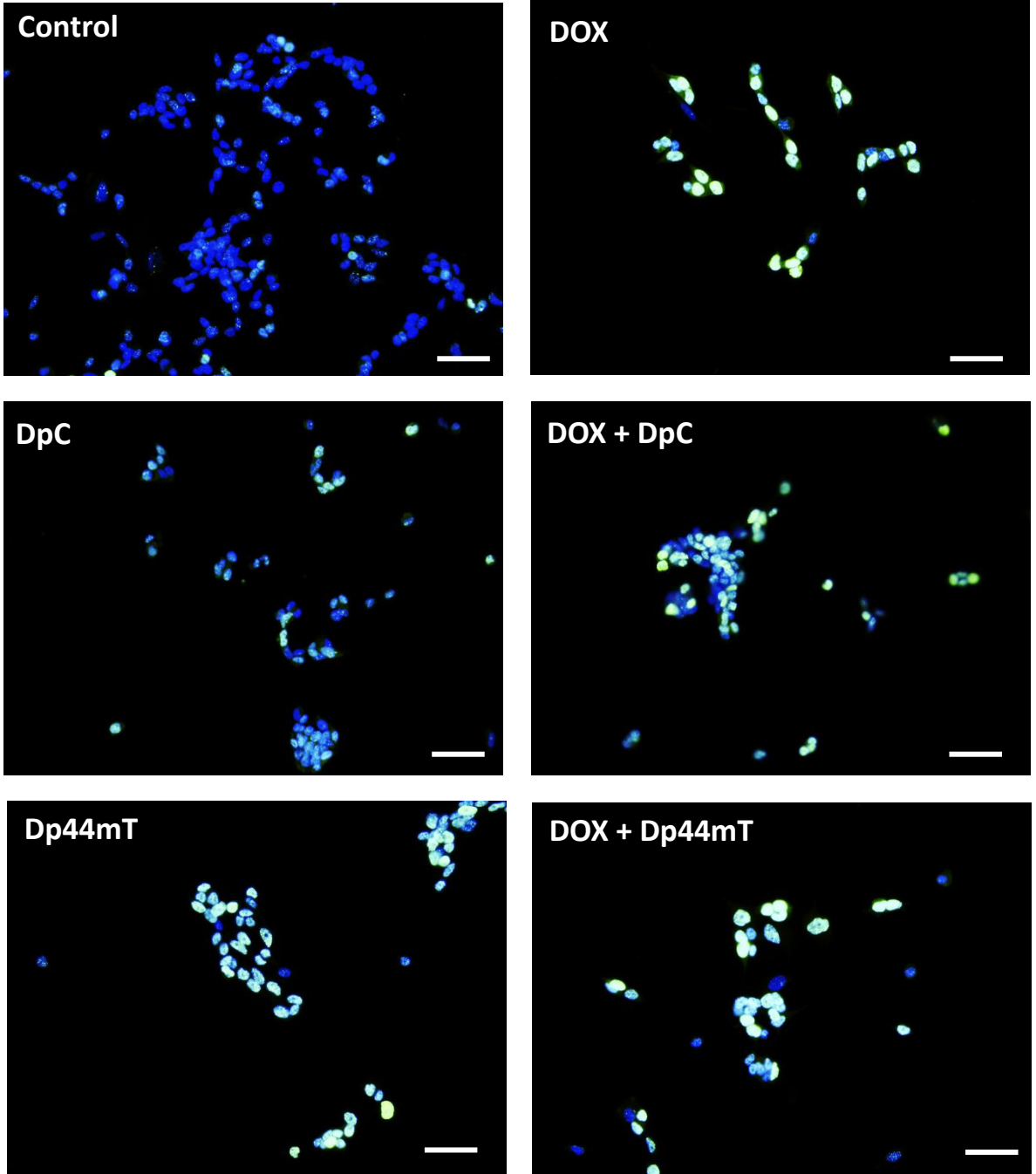


Figure S4: Detection of phosphorylated γ -H2AX as double-strand break marker in cell lines after the experimental treatment. Immunofluorescence was performed after 48 h treatment with IC_{50} doses of DpC, Dp44mT, DOX or their combinations. Phosphorylated γ -H2AX was visualized using the γ -H2AX primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled by DAPI (blue). Scale bars, 50 μ m.

SUPPLEMENTARY FIGURE S4

(C) Saos-2 cell line

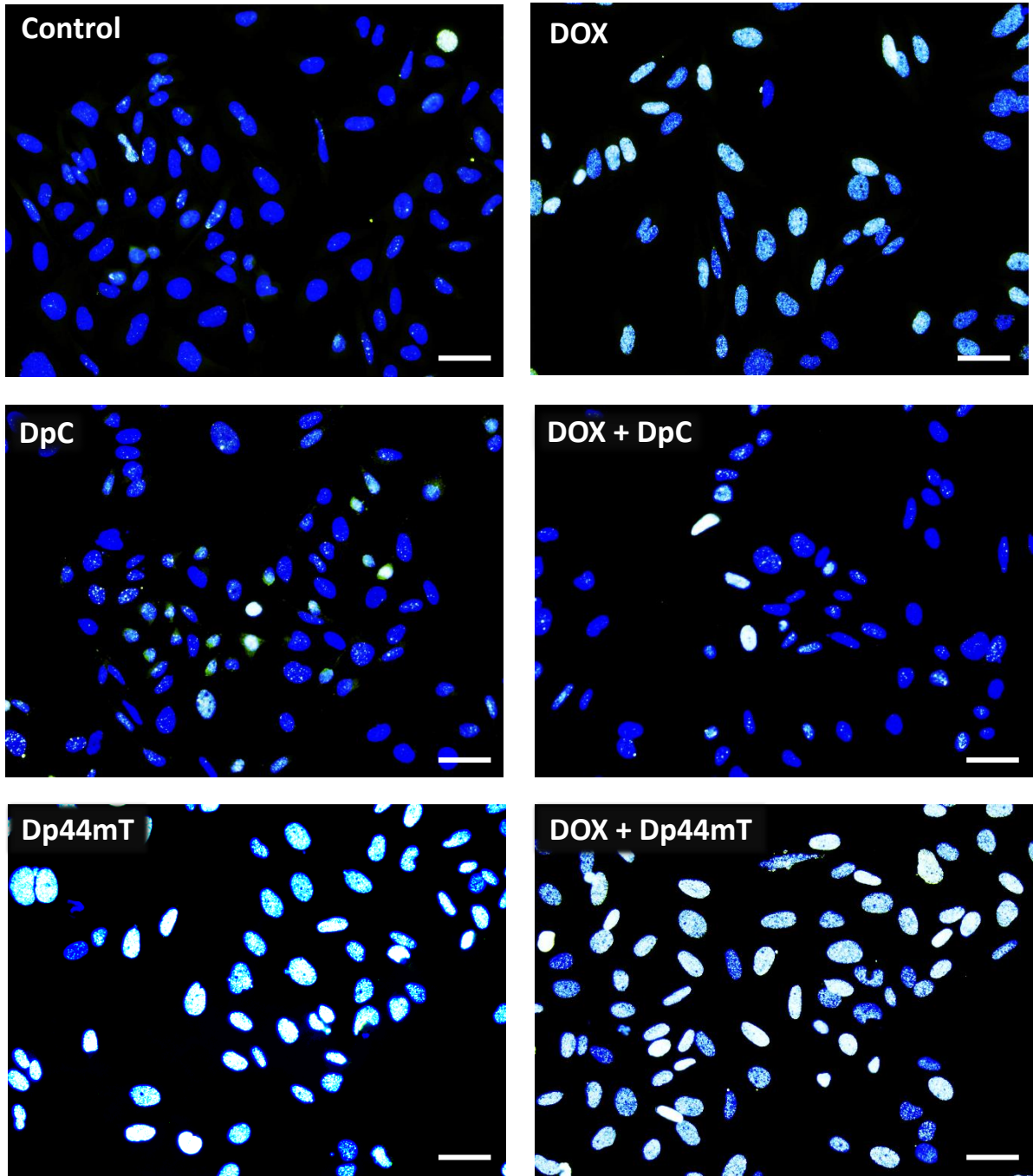


Figure S4: Detection of phosphorylated γ -H2AX as double-strand break marker in cell lines after the experimental treatment. Immunofluorescence was performed after 48 h treatment with IC_{50} doses of DpC, Dp44mT, DOX or their combinations. Phosphorylated γ -H2AX was visualized using the γ -H2AX primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled by DAPI (blue). Scale bars, 50 μ m.

SUPPLEMENTARY FIGURE S4

(D) Daoy cell line

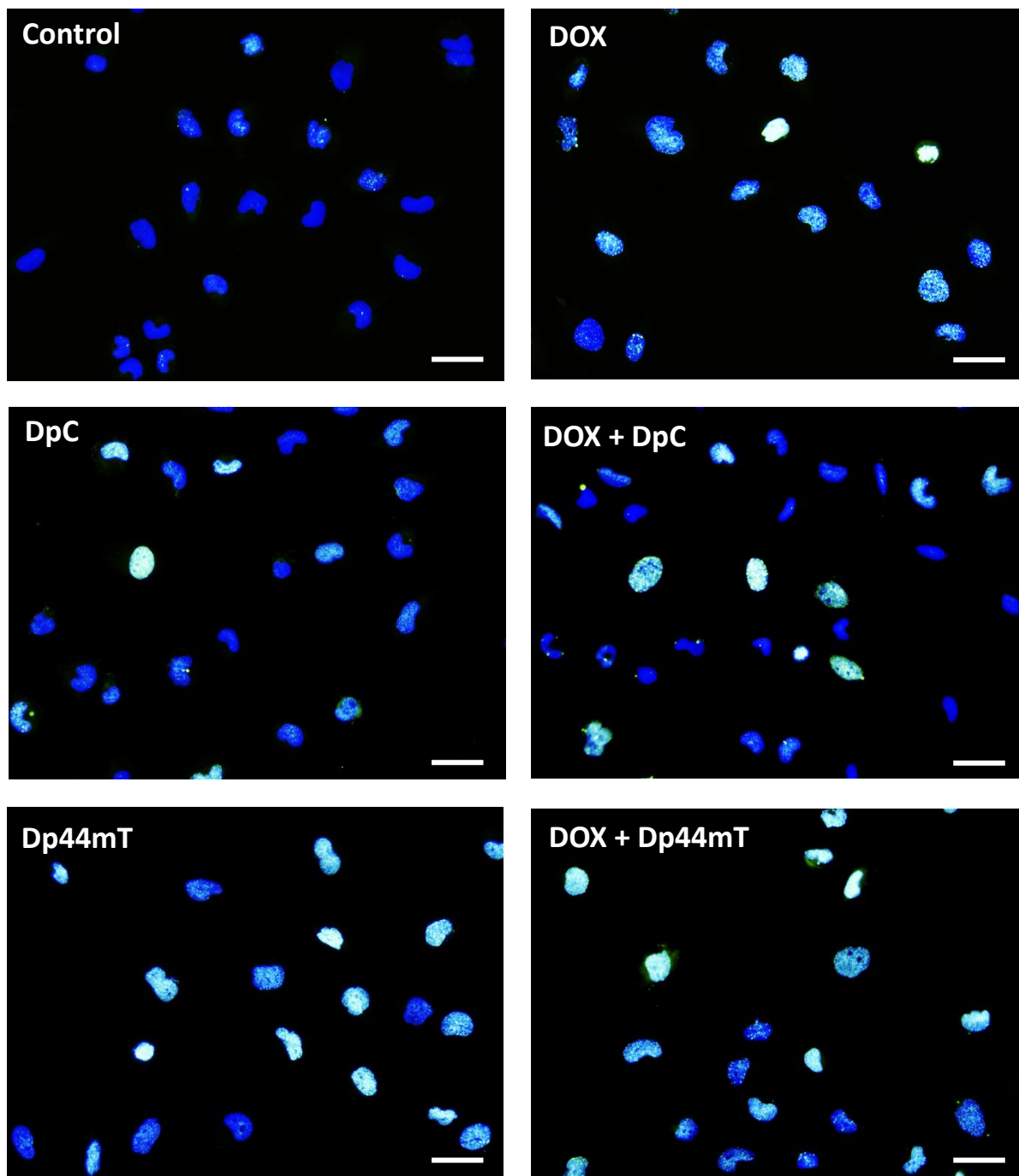


Figure S4: Detection of phosphorylated γ -H2AX as double-strand break marker in cell lines after the experimental treatment. Immunofluorescence was performed after 48 h treatment with IC_{50} doses of DpC, Dp44mT, DOX or their combinations. Phosphorylated γ -H2AX was visualized using the γ -H2AX primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled by DAPI (blue). Scale bars, 50 μ m.

SUPPLEMENTARY FIGURE S4

(E) RD cell line

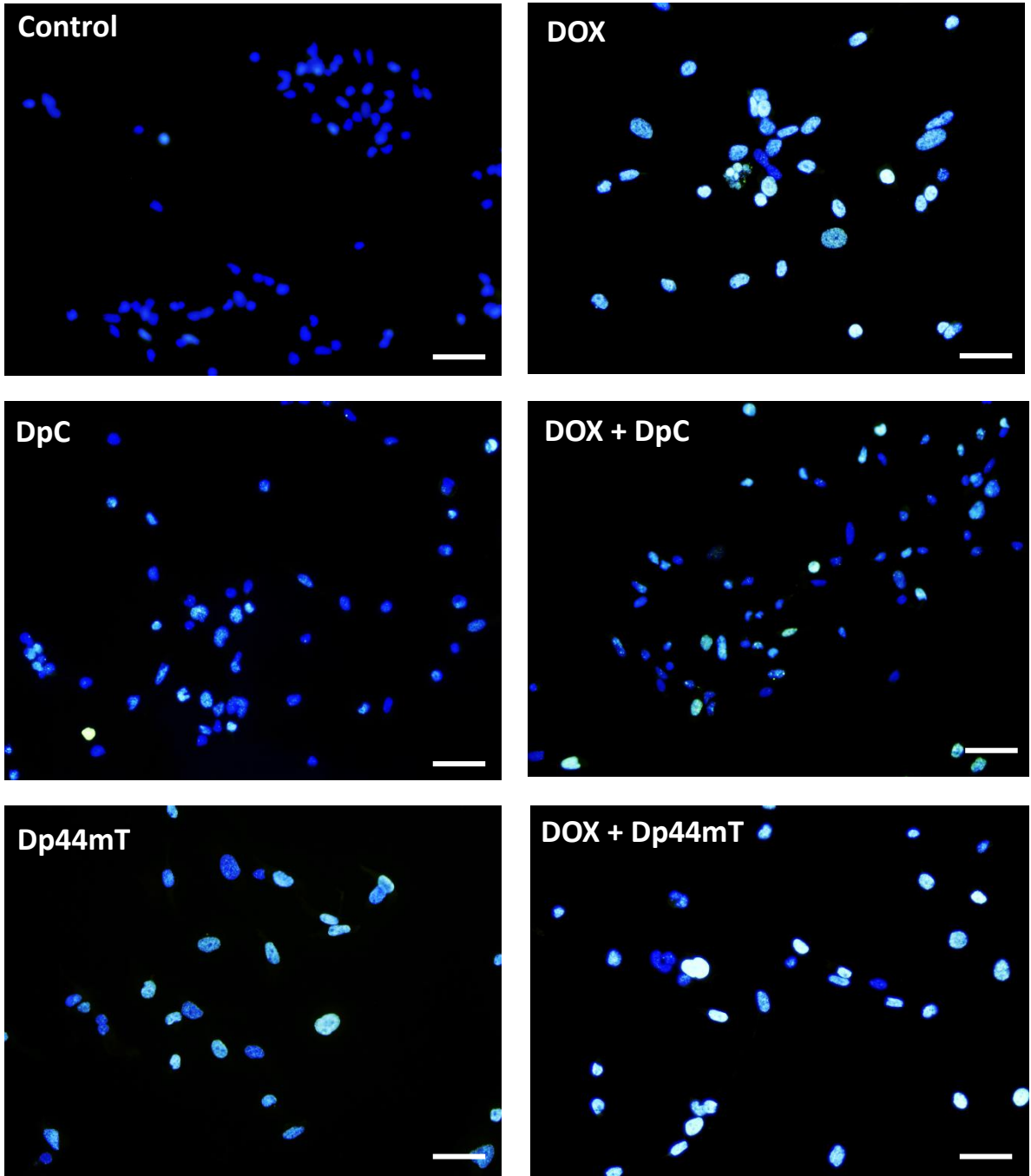


Figure S4: Detection of phosphorylated γ -H2AX as double-strand break marker in cell lines after the experimental treatment. Immunofluorescence was performed after 48 h treatment with IC_{50} doses of DpC, Dp44mT, DOX or their combinations. Phosphorylated γ -H2AX was visualized using the γ -H2AX primary antibody and Alexa 488-conjugated secondary antibody (green). The nuclei were labeled by DAPI (blue). Scale bars, 50 μ m.

SUPPLEMENTARY TABLE S1

		Control [mean ± sd]	DOX [mean ± sd]	DAU [mean ± sd]	MIT [mean ± sd]
SH-SY5Y	sub G ₁	3.2 ± 1.6	19.5 ± 3.4	32.6 ± 4.4	29.2 ± 7.3
	G ₀ /G ₁	59.9 ± 6.0	42.7 ± 9.4	36.3 ± 9.7	41.9 ± 7.3
	S	11.0 ± 4.8	11.6 ± 3.1	12.3 ± 0.8	12.6 ± 2.4
	G ₂ /M	25.9 ± 4.9	26.1 ± 8.2	18.8 ± 5.5	16.3 ± 1.1
SK-N-BE(2)	sub G ₁	2.7 ± 1.4	7.7 ± 2.4	13.6 ± 5.2	15.3 ± 0.9
	G ₀ /G ₁	54.7 ± 0.5	13.7 ± 2.0	15.8 ± 1.8	24.3 ± 6.1
	S	13.8 ± 0.7	23.0 ± 13.2	19.4 ± 4.2	20.4 ± 1.6
	G ₂ /M	28.8 ± 1.0	55.6 ± 14.2	51.1 ± 3.2	40.1 ± 7.3
Saos-2	sub G ₁	1.7 ± 0.7	18.7 ± 12.1	42.7 ± 3.1	23.1 ± 5.4
	G ₀ /G ₁	61.4 ± 2.7	16.5 ± 12.7	7.7 ± 0.3	9.3 ± 2.4
	S	14.0 ± 2.1	11.3 ± 1.5	10.7 ± 2.1	10.6 ± 1.0
	G ₂ /M	22.9 ± 1.0	53.5 ± 12.6	38.8 ± 3.3	57.0 ± 5.1
Daoy	sub G ₁	1.6 ± 0.5	25.5 ± 4.4	26.1 ± 7.3	26.0 ± 4.3
	G ₀ /G ₁	63.7 ± 2.2	14.7 ± 4.6	12.3 ± 3.3	16.0 ± 2.5
	S	16.2 ± 2.4	13.6 ± 0.6	18.0 ± 2.5	13.3 ± 1.9
	G ₂ /M	18.5 ± 1.0	46.2 ± 8.4	43.6 ± 10.5	44.7 ± 2.3
RD	sub G ₁	1.3 ± 0.1	13.4 ± 6.4	25.4 ± 15.7	18.7 ± 13.1
	G ₀ /G ₁	55.5 ± 4.9	20.7 ± 17.5	23.7 ± 5.3	23.1 ± 3.6
	S	12.0 ± 2.8	11.6 ± 5.6	11.2 ± 2.2	11.0 ± 2.4
	G ₂ /M	31.2 ± 2.5	54.4 ± 25.4	39.7 ± 21.6	47.2 ± 18.9

Table S1: Cell cycle analysis in cell lines after the treatment with IC₅₀ doses of anthracyclines. DNA content was measured after propidium iodide staining with subsequent flow cytometry detection. The changes in the cell cycle were obtained after 72 h of treatment with IC₅₀ doses of doxorubicin (DOX), daunorubicin (DAU) or mitoxantrone (MIT). The table provides values representing mean ± sd (%) for each cell proportion in the cell cycle phases (sub G₁, G₀/G₁, S and G₂/M). All experiments were performed in biological triplicates.