

Table S1. **Values ± SDs for Fig. 2 apoptosis assays**

	Normal conditions				Serum starved			
	Ann V ⁻ /PI ⁻	Ann V ⁺ /PI ⁻	Ann V ⁺ /PI ⁺	Ann V ⁻ /PI ⁺	Ann V ⁻ /PI ⁻	Ann V ⁺ /PI ⁻	Ann V ⁺ /PI ⁺	Ann V ⁻ /PI ⁺
	%	%	%	%	%	%	%	%
Akt wild type								
vector	89.4 ± 3.1	4.4 ± 1.7	4.3 ± 1.9	1.8 ± 0.2	40.8 ± 3.9	40.5 ± 5.8	17.2 ± 1.9	1.5 ± 0.5
4E wild type	86.2 ± 3.1	5.8 ± 1.6	5.6 ± 1.3	2.4 ± 1.0	77.6 ± 2.8	11.7 ± 3.6	8.3 ± 0.5	2.3 ± 1.3
W73A	87.6 ± 0.8	5.1 ± 1.0	4.8 ± 1.0	2.4 ± 0.9	78.2 ± 2.3	11.6 ± 4.1	7.7 ± 1.8	2.5 ± 1.6
W56A	85.6 ± 3.5	6.2 ± 1.7	5.5 ± 1.6	2.7 ± 1.1	43.0 ± 5.9	38.3 ± 6.0	17.2 ± 1.8	1.5 ± 0.3
Bcl2	95.3 ± 0.6	1.4 ± 0.4	1.9 ± 0.7	1.3 ± 0.2	84.8 ± 1.9	5.8 ± 2.9	4.0 ± 2.9	5.4 ± 2.3
Akt1^{-/-}								
vector	90.8 ± 2.1	3.9 ± 1.5	3.6 ± 0.9	1.8 ± 0.2	19.7 ± 4.5	63.8 ± 2.3	15.8 ± 6.6	0.6 ± 0.1
4E wild type	89.3 ± 4.6	4.3 ± 1.4	5.5 ± 4.6	0.9 ± 0.7	21.4 ± 1.7	64.5 ± 4.2	13.4 ± 5.3	0.6 ± 0.5
W73A	89.8 ± 4.2	6.2 ± 4.1	3.5 ± 1.6	0.6 ± 0.3	19.8 ± 7.4	67.0 ± 9.5	12.6 ± 3.1	0.6 ± 0.5
W56A	89.5 ± 3.6	5.1 ± 1.5	4.1 ± 1.7	1.3 ± 1.3	17.7 ± 4.5	70.1 ± 5.8	11.7 ± 4.0	0.5 ± 0.4
Bcl2	93.8 ± 1.5	1.6 ± 1.4	1.8 ± 0.6	2.9 ± 2.4	83.4 ± 0.3	6.4 ± 2.2	4.1 ± 1.3	6.1 ± 1.2
Akt1^{-/-}								
vector	83.2 ± 2.4	5.5 ± 0.8	6.1 ± 1.5	5.1 ± 1.7	27.6 ± 0.4	54.5 ± 0.5	11.4 ± 0.8	6.5 ± 0.1
4E	85.3 ± 0.6	5.5 ± 0.6	4.6 ± 0.2	4.5 ± 0.4	23.2 ± 0.1	58.2 ± 0.6	12.5 ± 0.6	6.0 ± 0.2
Akt1	85.2 ± 0.7	5.6 ± 1.0	4.9 ± 1.4	4.3 ± 0.4	37.8 ± 3.1	49.1 ± 0.6	6.7 ± 2.0	6.4 ± 1.4
4E + Akt1	82.0 ± 4.9	10.3 ± 7.5	4.0 ± 0.8	3.7 ± 1.8	71.9 ± 0.6	9.9 ± 0.4	10.6 ± 0.2	7.6 ± 0.3

Ann V, annexin V. Measured percentages (shown in Fig. 2) with SD of annexin V/PI staining of Akt wild type– and Akt1^{-/-}-derived cells (vector, eIF4E wild type and mutants, Akt1 add back, and Bcl2 control). All experiments were repeated at least three times.

Table S2. **Values ± SDs for Fig. 6 apoptosis assays**

	Normal conditions				Serum starved			
	Ann V ⁻ /PI ⁻	Ann V ⁺ /PI ⁻	Ann V ⁺ /PI ⁺	Ann V ⁻ /PI ⁺	Ann V ⁻ /PI ⁻	Ann V ⁺ /PI ⁻	Ann V ⁺ /PI ⁺	Ann V ⁻ /PI ⁺
	%	%	%	%	%	%	%	%
Vector								
Vector	91.6 ± 2.5	3.5 ± 1.5	3.3 ± 1.4	1.7 ± 1.3	37.0 ± 3.7	47.7 ± 7.9	14.4 ± 4.5	0.9 ± 0.4
PML	91.2 ± 3.1	3.2 ± 2.6	3.9 ± 2.0	1.7 ± 1.1	25.7 ± 3.8	53.9 ± 6.1	19.4 ± 8.3	1.0 ± 0.4
4E wild type	91.7 ± 2.7	4.1 ± 3.7	3.1 ± 0.6	1.1 ± 0.8	82.2 ± 2.2	8.4 ± 2.9	7.1 ± 2.7	2.3 ± 2.0
4E + PML	90.5 ± 0.9	4.2 ± 1.3	3.9 ± 0.7	1.4 ± 0.9	40.7 ± 5.7	47.9 ± 4.8	10.5 ± 1.3	0.9 ± 0.5
W73A	90.9 ± 1.4	4.0 ± 1.3	3.7 ± 0.8	1.4 ± 0.7	80.0 ± 1.1	13.3 ± 1.5	6.0 ± 0.8	0.9 ± 0.4
W73A + PML	92.4 ± 2.2	3.5 ± 1.7	3.3 ± 0.6	0.9 ± 0.4	82.5 ± 2.5	11.0 ± 2.4	5.3 ± 1.3	1.2 ± 0.5
RING	89.7 ± .6	4.8 ± 3.1	4.0 ± 1.4	1.6 ± 1.1	41.2 ± 3.2	44.9 ± 2.1	12.8 ± 1.7	1.1 ± 0.8
4E + RING	92.5 ± 0.9	3.4 ± 2.2	2.6 ± 0.3	1.4 ± 1.1	82.3 ± 3.9	11.7 ± 3.4	4.9 ± 0.9	1.0 ± 0.4

Ann V, annexin V. Measured percentages (shown in Fig. 6) with SDs of annexin V/PI staining of PML + eIF4E wild-type and mutant overexpressing cells. All experiments were repeated at least three times.