

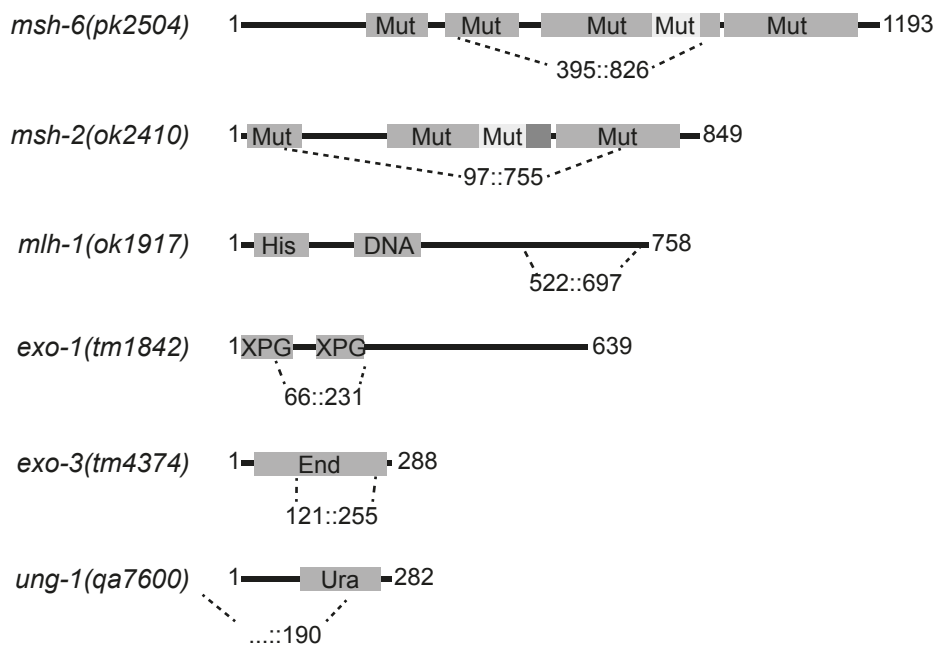
# **Base Excision Repair AP-endonucleases and Mismatch Repair act together to Induce Checkpoint Mediated Autophagy**

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## **SUPPLEMENTARY INFORMATION LISTING**

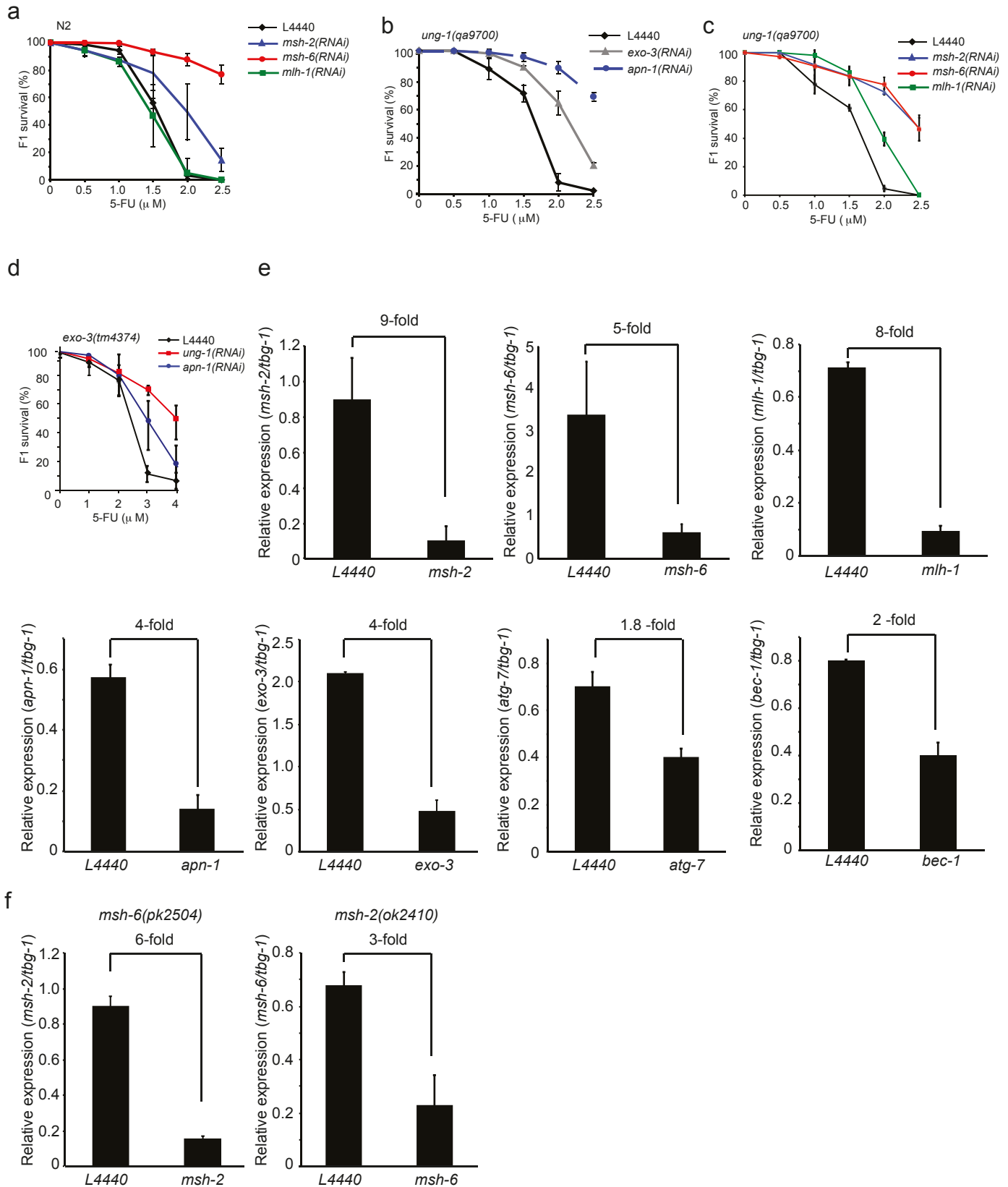
- **Supplementary Figure S1** Mutants
- **Supplementary Figure S2** BER and MMR mediated toxicity of 5-FU
- **Supplementary Figure S3** DNA damage checkpoint activation in the *C. elegans* germline and embryos in response to 5-FU.
- **Supplementary Figure S4** Global chromatin decondensation in 5-FU treated embryos.
- **Supplementary Figure S5** 5-FU induced autophagy in *C. elegans* embryos.
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- **Supplementary Figure S7** Depletion of DNA repair pathways other than BER and MMR does not lead to 5-FU resistance
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## Supplementary Fig S1



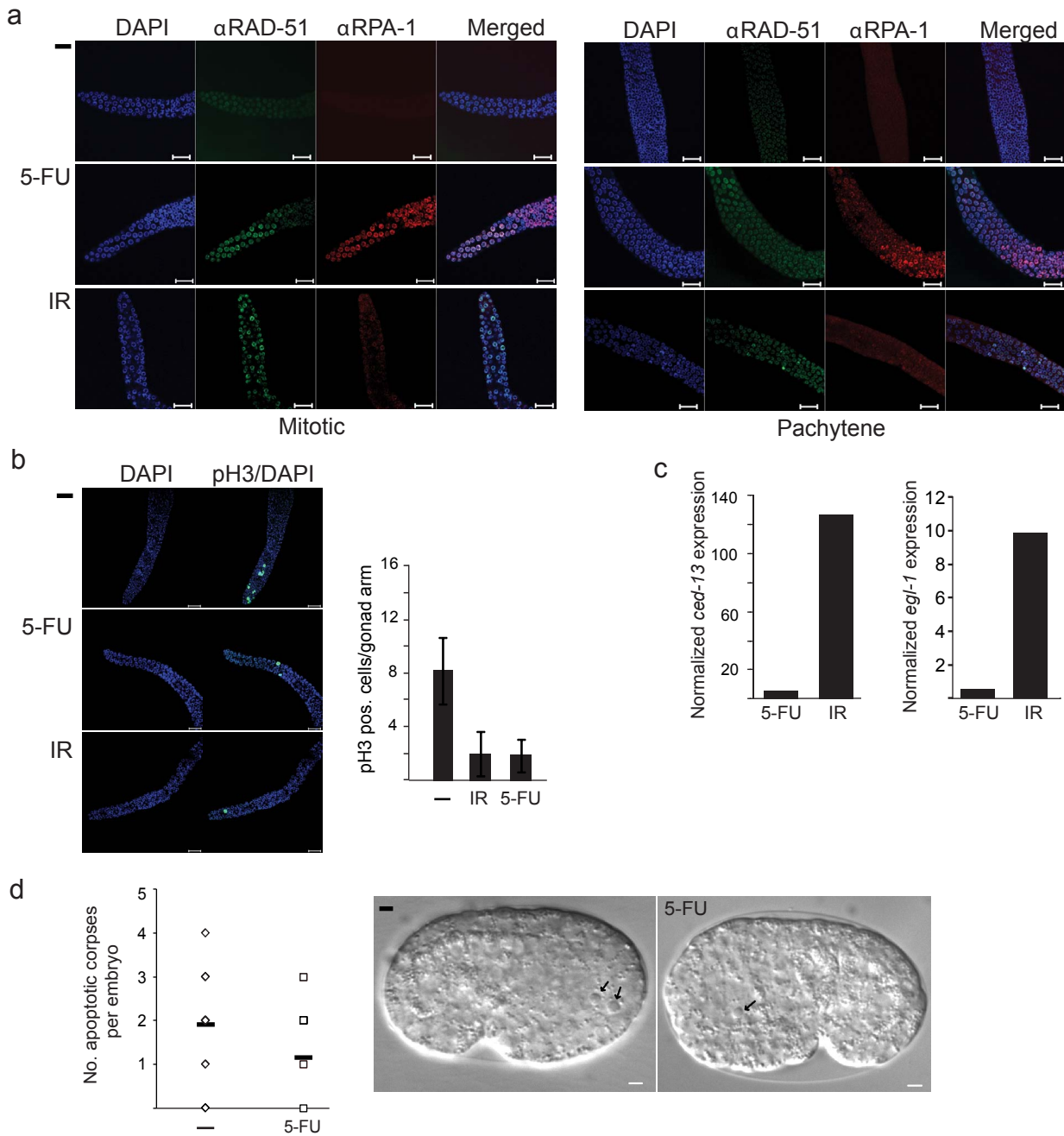
**Supplementary Figure S1** Mutants. Cartoons showing the architecture of the indicated DNA repair proteins with conserved pfam domains important for DNA binding or activity as given in Wormbase ([www.wormbase.org](http://www.wormbase.org)). The deletions expected from the mutant alleles used in this study are indicated with amino acid numbers. All deletion mutations are expected to be loss-of-function alleles, with the possible exception of the *mlh-1(ok1917)* allele that might lead to the production of a truncated protein.

Supplementary Fig S2



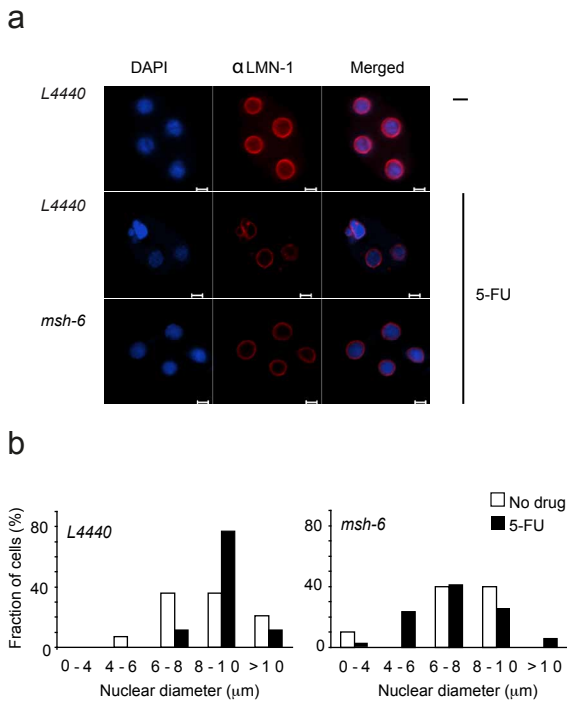
**Supplementary Figure S2** BER and MMR mediated toxicity of 5-FU. **(a)** F1 survival following depletion of MSH-6 (red circles), and MSH-2 (blue triangles) and MLH-1 (green squares) in N2. **(b)** F1 survival following depletion of the AP-endonucleases EXO-3 (grey triangles) and APN-1 (blue circles) in the *ung-1(qa7600)* mutant. **(c)** F1 survival following the depletion of MSH-6 (red circles), and MSH-2 (blue triangles) and MLH-1 (green squares) in *ung-1(qa7600)*. **(d)** F1 survival after depletion on APN-1 (blue circles) and UNG-1 (red squares) in *exo-3(tm4374)* mutant animals. **(a-d)** The survival curves show the mean  $\pm$  s.d. for each data point from three independent experiments. **(e)** qRT-PCR determination of mRNA expression levels of the indicated genes after RNAi depletion in N2. **(f)** qRT-PCR determination of mRNA expression levels after RNAi depletion in the mutants indicated. **(e, f)** Bar graphs present mean  $\pm$  s.d. from three independent experiments.

Supplementary Fig S3



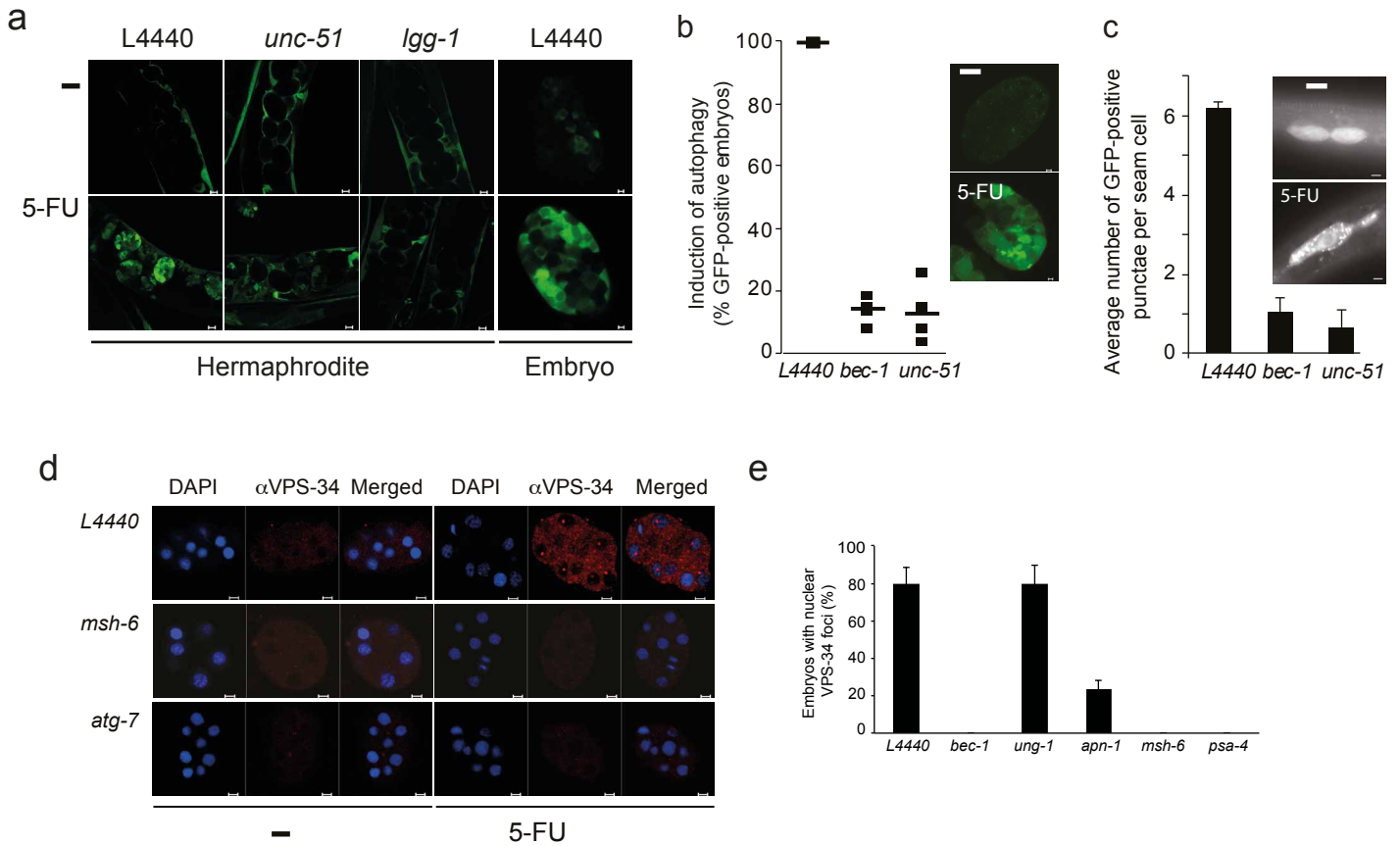
**Supplementary Figure S3** DNA damage checkpoint activation in the *C. elegans* germline and embryos in response to 5-FU. **(a)** All cytological markers for the activation of DNA damage response signaling (DDR) were similar in germlines treated with 5-FU and ionizing radiation (IR). Immunostaining showing the accumulation of anti-RPA-1 and anti-RAD-51 positive foci in the mitotic (left panel) and pachytene (right panel) regions of the germline, following 5-FU treatment. Immunostaining in untreated germlines (upper panel) and after ionizing radiation (125 Gy, IR; lower panel) are shown as negative and positive controls, respectively. DNA was stained with 4',6-diamidino-2-phenylindole (DAPI) (20  $\mu$ m scale bars). **(b)** Activation of cell-cycle arrest in response to 5-FU and IR illustrated by staining with antibodies recognizing phosphorylated H3 (pH3) in the germline mitotic region (10  $\mu$ m scale bars). The number of pH3-positive nuclei per gonad arm was counted in 10 animals per treatment group in three independent experiments and is given as an average  $\pm$  s.d. **(c)** Transcriptional induction of the CEP-1 responsive genes *ced-13* and *egl-1* in 5-FU treated and irradiated worms. mRNA levels were measured by qRT-PCR in triplicate and normalized to an internal tubulin (*tbg-1*) control. **(d)** The number of apoptotic corpses in embryos induced by 5-FU was scored in a minimum of 10 embryos under DIC microscopy (scale bar = 5  $\mu$ m). The average number of corpses is indicated by the black horizontal bar.

## Supplementary Fig S4



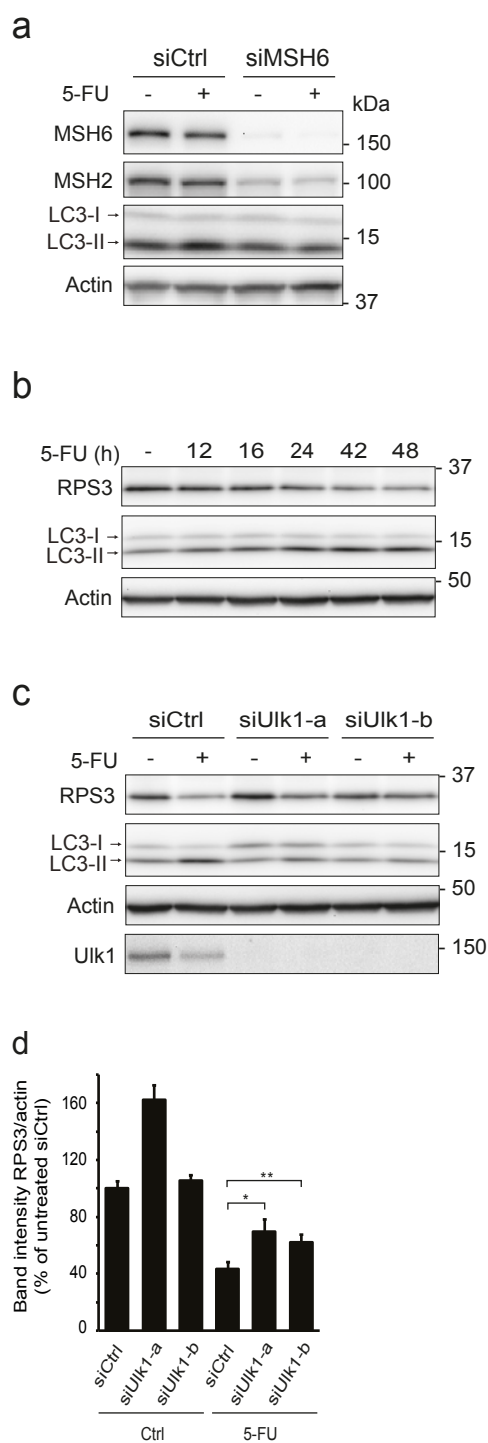
**Supplementary Figure S4** Global chromatin decompaction in 5-FU treated embryos. **(a)** Visualization of the nuclear envelope by confocal microscopy after immunostaining with anti-LMN-1 antibodies in wild-type embryos grown on bacteria expressing empty vector control (L4440) or *msh-6* RNAi. DNA was counterstained with DAPI (scale bars in IF images = 5 μm). **(b)** The maximum nuclear diameter of a minimum of 15 nuclei were identified from z-stacks and measured using the LSM-software. The size distribution was plotted as the fraction (%) of nuclei of the indicated size intervals in the absence (white bars) or presence (black bars) of 5-FU. The maximum nuclear diameter increased from 8.2 μm to 9.0 μm (Student t-test,  $p < 0.05$ ) by 5-FU treatment. The maximum nuclear diameter was unaffected by 5-FU in MSH-6 depleted embryos (maximum nuclear diameter of 7.6 and 7.3 μm in untreated and treated embryos, respectively (Student's t-test  $p = 0.3$ )).

Supplementary Fig S5



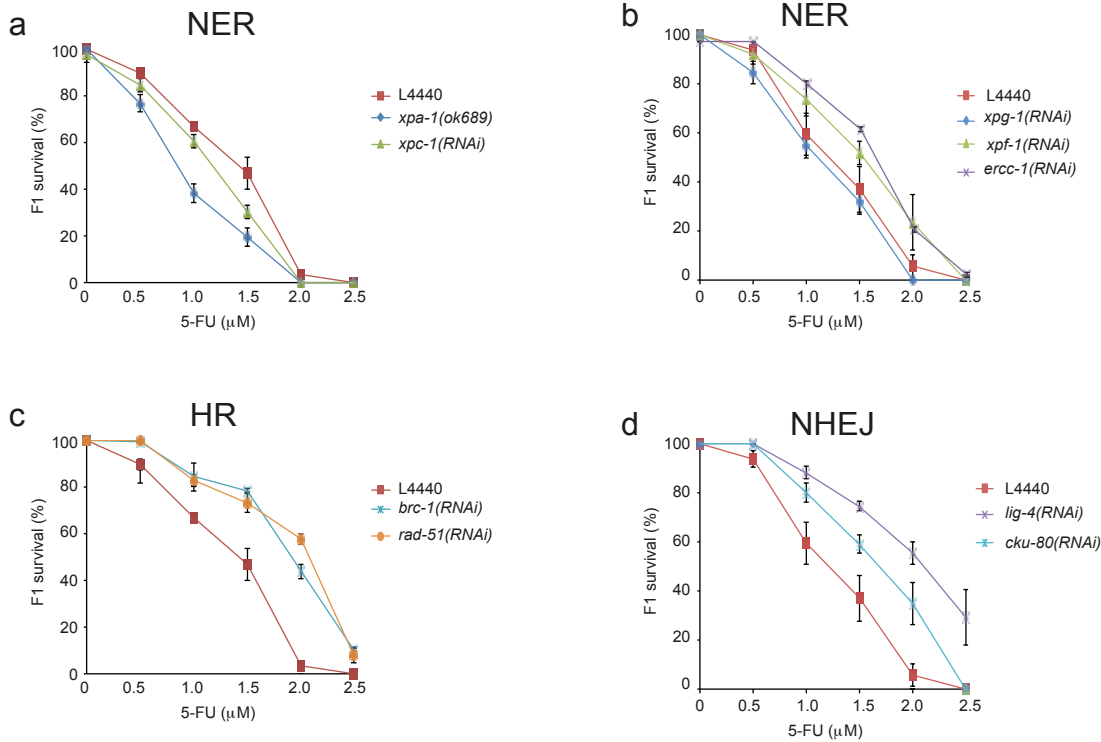
**Supplementary Figure S5** 5-FU induced autophagy in *C. elegans* embryos. **(a)** 5-FU-induced autophagy monitored in the BEC-1::GFP translational reporter strain grown for three generations on bacteria expressing empty vector control (L4440) or RNAi targeting the indicated autophagy genes (scale bar = 10  $\mu$ m). Embryos show increased GFP expression levels and distinct GFP-positive puncta (scale bar = 2  $\mu$ m). **(b)** Confocal images showing excessive GFP expression and GFP positive puncta in dissected embryos (2  $\mu$ m scale bar) in response to 5-FU in an GFP::LGG-1 translational fusion reporter strain fed control or RNAi targeting the indicated core autophagy genes. The fraction (as % of the untreated control) of hermaphrodites having embryos with excessive GFP expression following 5-FU treatment was quantified in each experiment (filled square) and the mean value indicated (line) are presented. **(c)** Induction of autophagy in between four to eight L3 stage seam cells per animal was scored and presented as the average number of GFP-positive puncta per seam cell (5  $\mu$ m scale bar). **(b, c)** 10 to 40 animals were scored for each condition in four independent experiments. **(d)** Confocal images showing induction of autophagy by immunostaining with anti-VPS-34 antibodies in embryos dissected out from N2 wild-type worms grown on bacteria expressing the indicated RNAi (scale bar = 5  $\mu$ m). VPS-34 accumulation depended on ATG-7, confirming that the accumulation is part of the autophagic programme. **(e)** Quantification of the fraction (as % of total) of embryos with nucleolar VPS-34 foci. **(c, e)** Bar graphs present mean  $\pm$  s.d. from three independent experiments.

## Supplementary Fig S6



**Supplementary Figure S6** RPS3 is degraded by autophagy in 5-FU treated U2OS cells. **(a)** Western blot showing effective knockdown of MSH6 using specific siRNA, accompanied by loss of MSH2 stability in U2OS cells. **(b)** Western blot showing progressive reduction in RPS3 level and increased LC3 II levels after 5-FU treatment. **(c)** The 5-FU induced reduction in RPS3 protein level is partially rescued upon knockdown of Ulk1. Western blot of lysates from control or 5-FU treated U2OS cell transfected with siRNA oligos against Ulk1 or non-targeting control. **(d)** Normalized RPS3 protein levels upon 5-FU-treatment of control- or siUlk1-transfected U2OS cells presented as the mean  $\pm$  SEM, from at least 3 independent experiments (Student's t-test \*  $p < 0.03$ , \*\*  $p < 0.001$ ).

Supplementary Fig S7

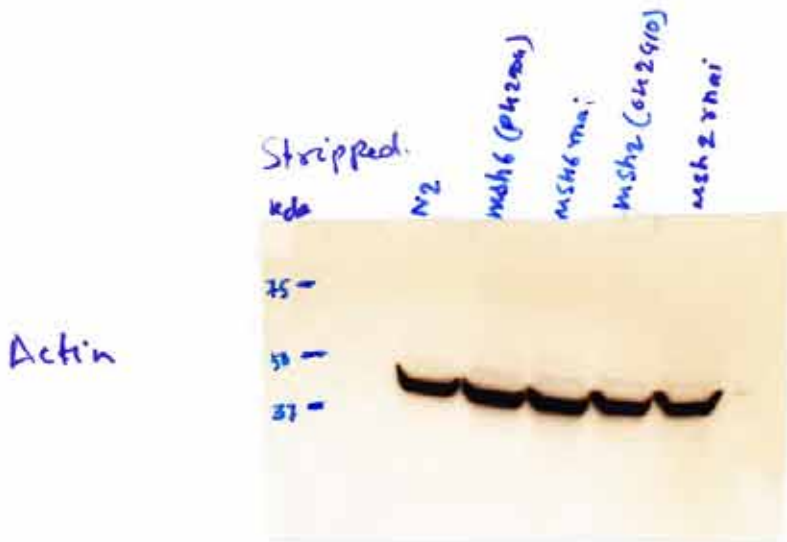


**Supplementary Figure S7** Depletion of DNA repair pathways other than BER and MMR does not lead to 5-FU resistance. **(a)** F1 survival experiments in the Nucleotide Excision Repair (NER) mutant *xpa-1(ok689)*, or survival of N2 animals grown for three generations on food expressing control RNAi (L4440) or RNAi directed against the NER DNA damage recognition protein XPC-1. **(b)** F1 survival of N2 animals after depletion of the NER structure-specific endonucleases XPG-1, XPF-1, or ERCC-1. **(c)** F1 survival of N2 animals after depletion of Homologous Recombination (HR) repair proteins BRC-1 or RAD-51. **(d)** F1 survival following depletion of Non-Homologous End-Joining (NHEJ) proteins LIG-4 or CKU-80. **(a-d)** The survival curves show the mean  $\pm$  s.d. for each data point from three independent experiments.

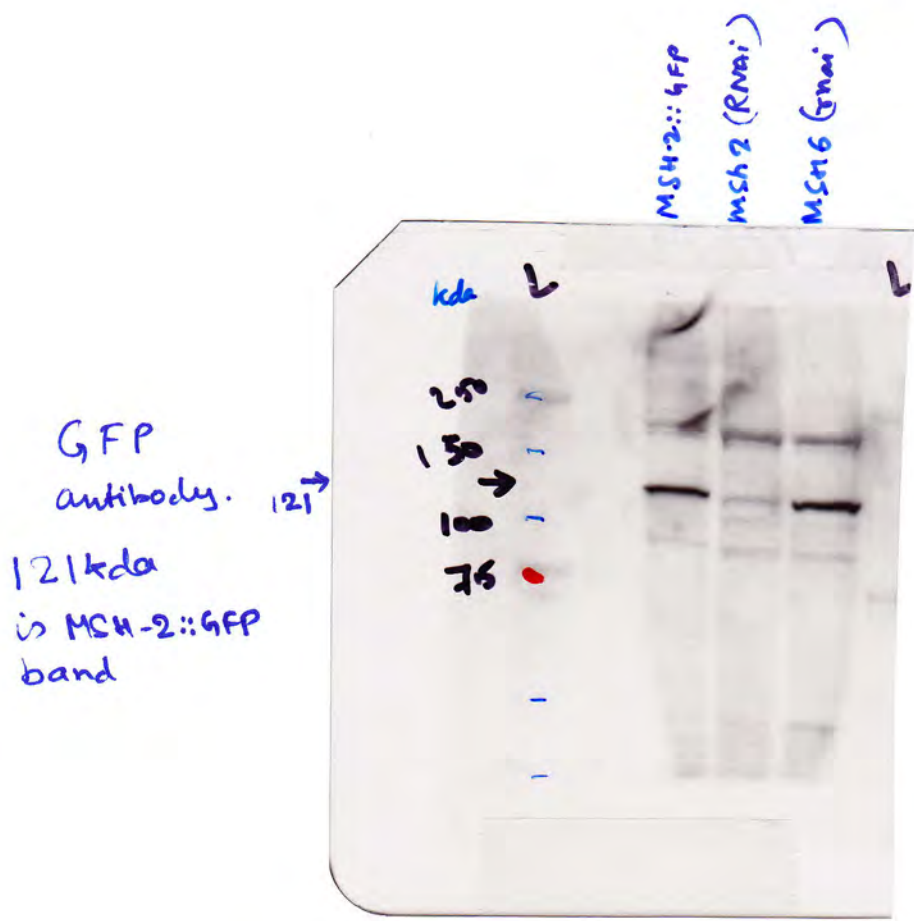


Supplementary Fig S8

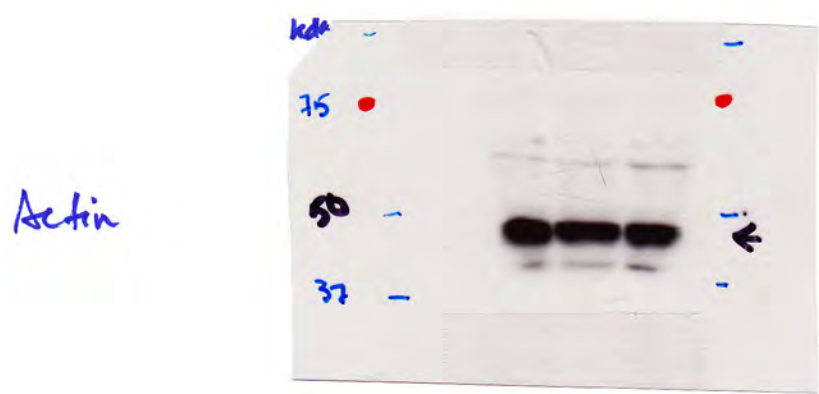
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Top panel



Original Scan for fig: 1 e  
Lower panel

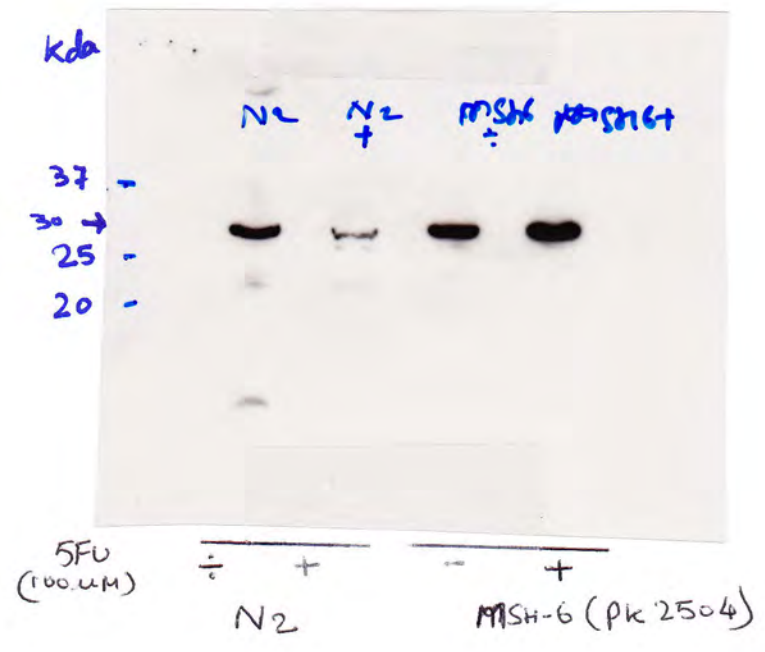


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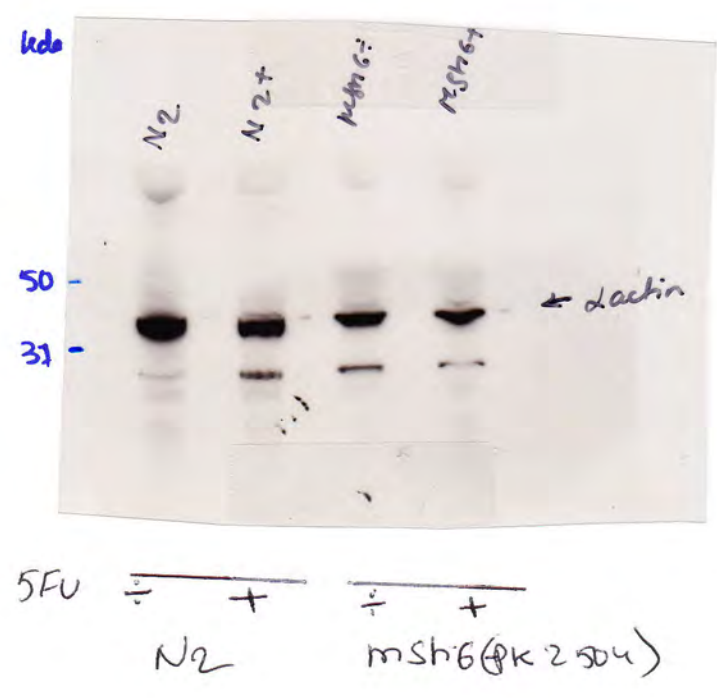


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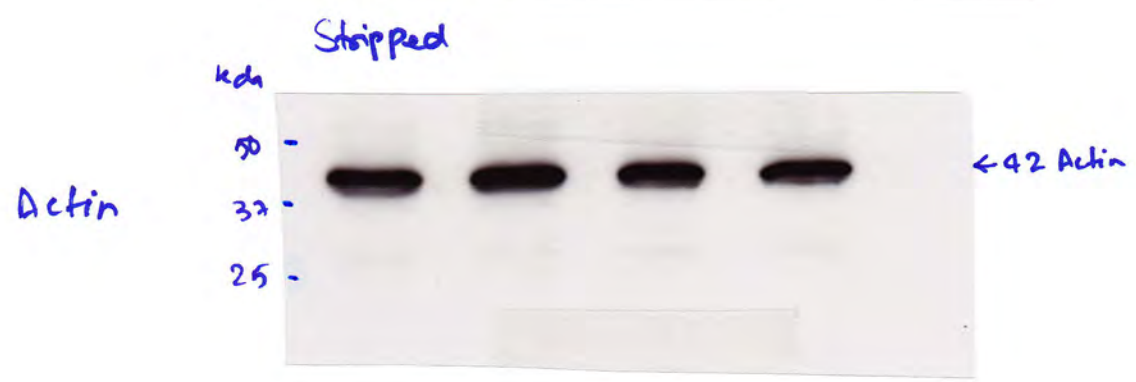
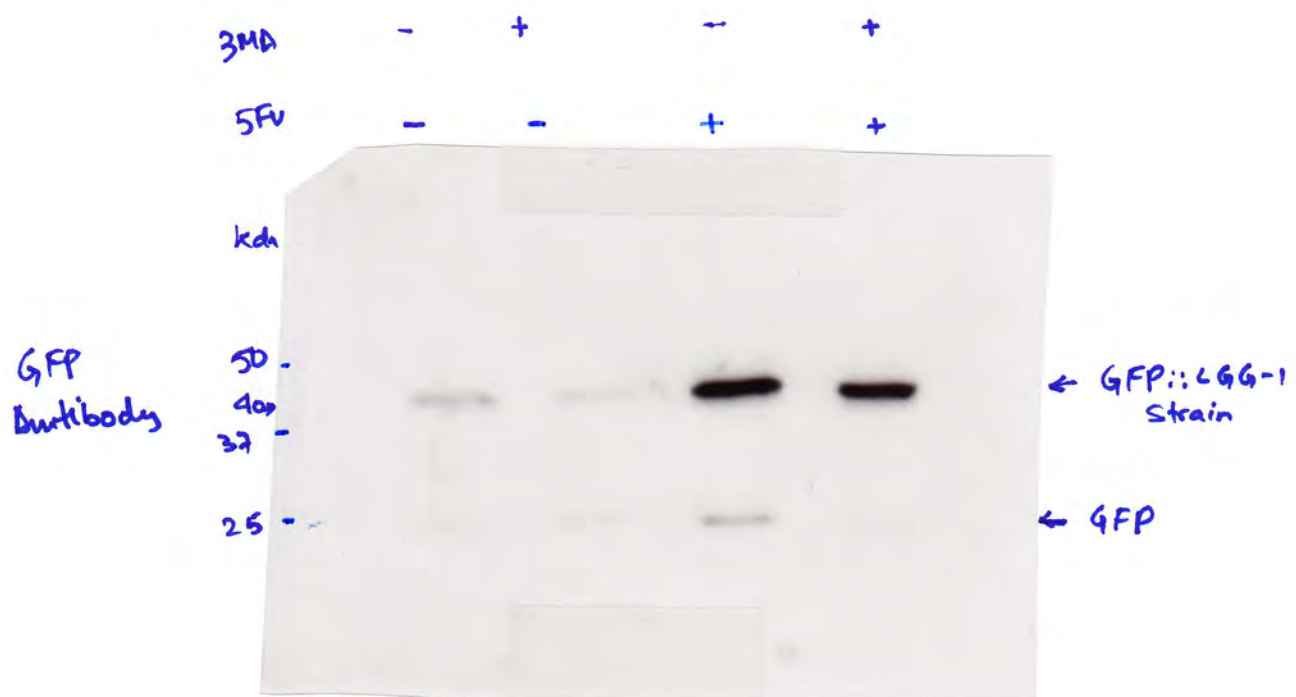
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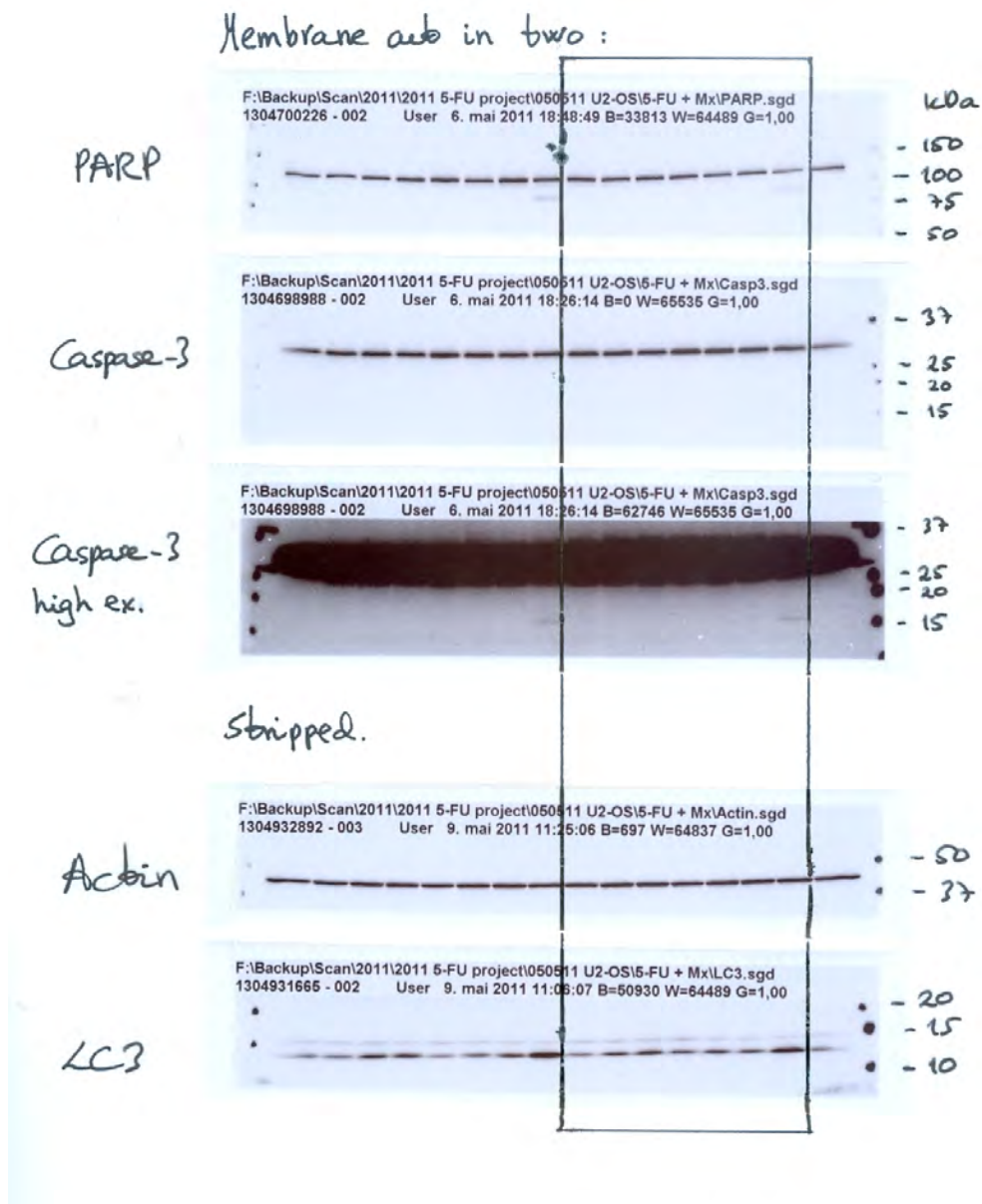
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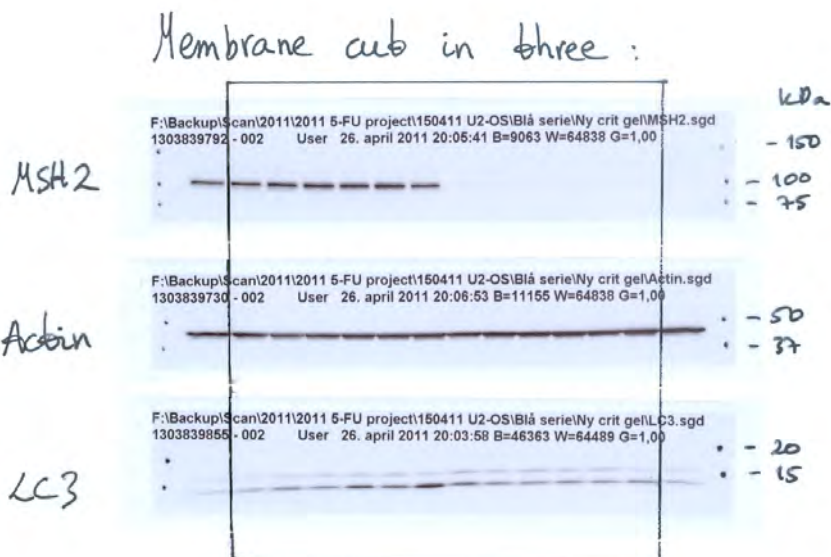
Original Scan for fig 3c



# Original scans for Fig. 6 A.

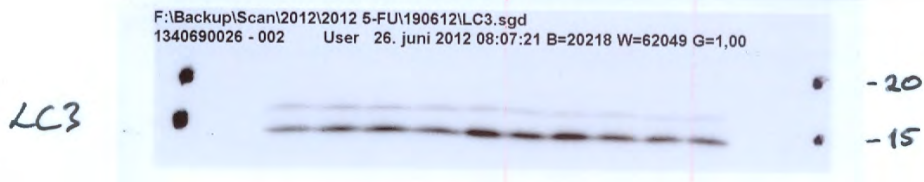
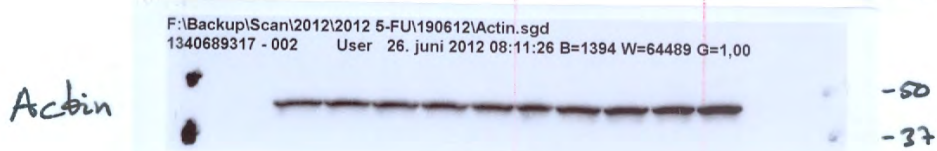
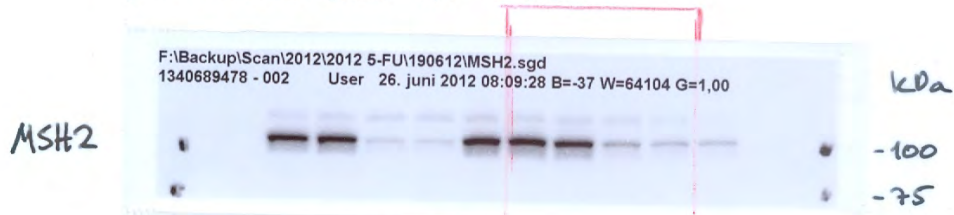


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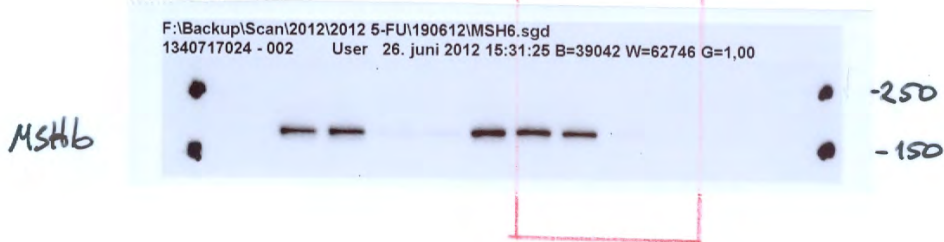


Original scans for supplementary fig. 56A.

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Original scans for supplementary Fig. S6 D.

Membrane cut in three, two pieces used:

RPS3

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LC3

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Actin

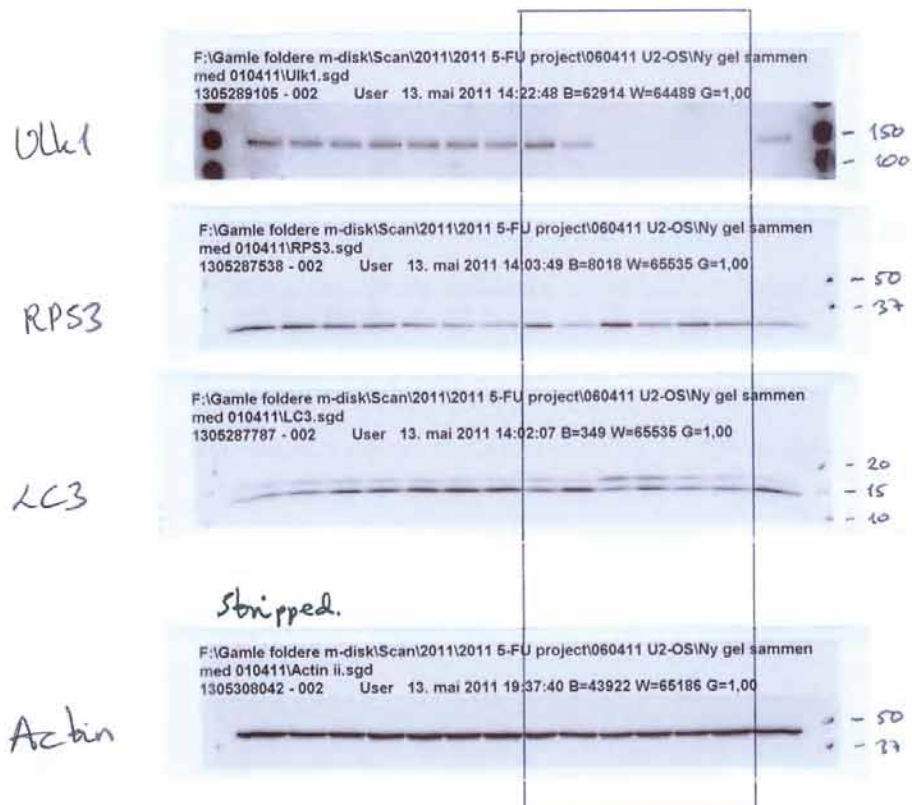
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Original scans for supplementary Fig. S6 c.

Membrane cut in three :



Supplementary Figure S8. Scanned images of all original western blots used in this study. The primary antibodies are written on the left of the panels.



**Supplementary Table S1** *5-FU induced RPA-1 foci in embryos*

RNAi	<i>L4440</i>	<i>bec-1</i>	<i>ung-1</i>	<i>apn-1</i>	<i>exo-3</i>	<i>msh-6</i>	<i>atl-1</i>
No RPA foci	32	11	10	26	3	2	0
No embryos scored	35	13	10	35	14	17	11

**Supplementary Table S2** *5-FU induced RPA-1 foci in embryos in mutants*

RNAi	Control RNAi			<i>apn-1(RNAi)</i>		
	N2	<i>mlh-1(ok1917)</i>	<i>exo-1(tm1842)</i>	N2	<i>mlh-1(ok1917)</i>	<i>exo-1(tm1842)</i>
No RPA-1+	32	0	1	26	0	0
No embryos scored	35	11	14	35	10	11

**Supplementary Table S3** *Fraction of embryos with RAD-51 foci*

RNAi	4-6 cells stage			>100 cells stage		
	Untreated	IR	5-FU	Untreated	5-FU	IR
No RAD-51+	0	8	1	0	5	6
No embryos scored	6	13	7	0	7	6
RAD-51+ embryos (%)	0	63	14	0	71	100

**Supplementary Table S4** *5-FU induced autophagy in embryos*

RNAi	<i>L4440</i>	<i>bec-1</i>	<i>unc-51</i>	<i>msh-2</i>	<i>msh-6</i>	<i>mlh-1</i>	<i>pms-2</i>	<i>ung-1</i>	<i>apn-1</i>	<i>exo-3</i>	<i>atl-1</i>	<i>cep-1</i>
No GFP+	245	19	13	74	13	10	22	141	31	48	75	70
No embryos scored	246	332	125	155	160	168	122	158	142	136	146	81