SUPPLEMENTARY INFORMATION

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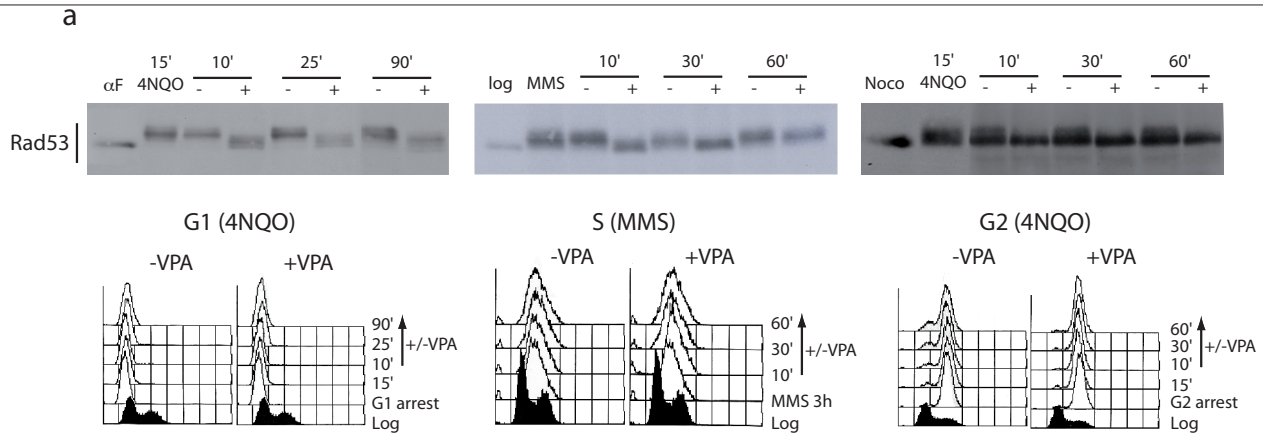
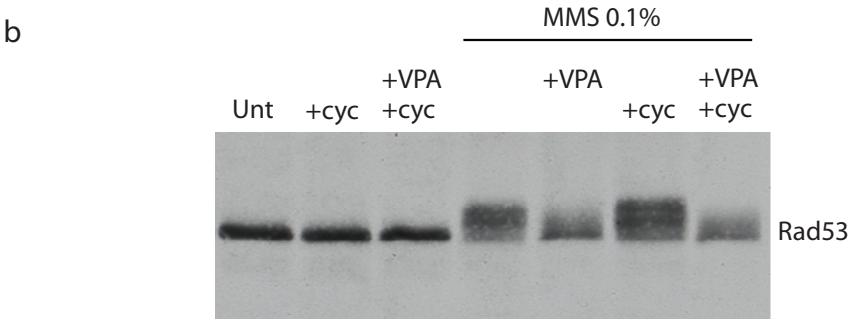
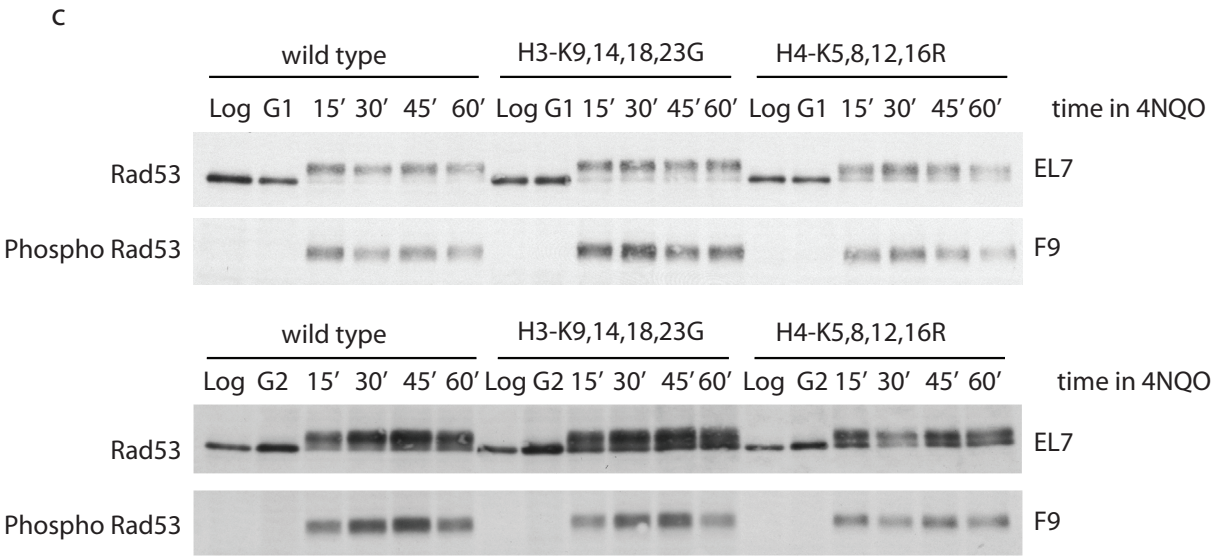
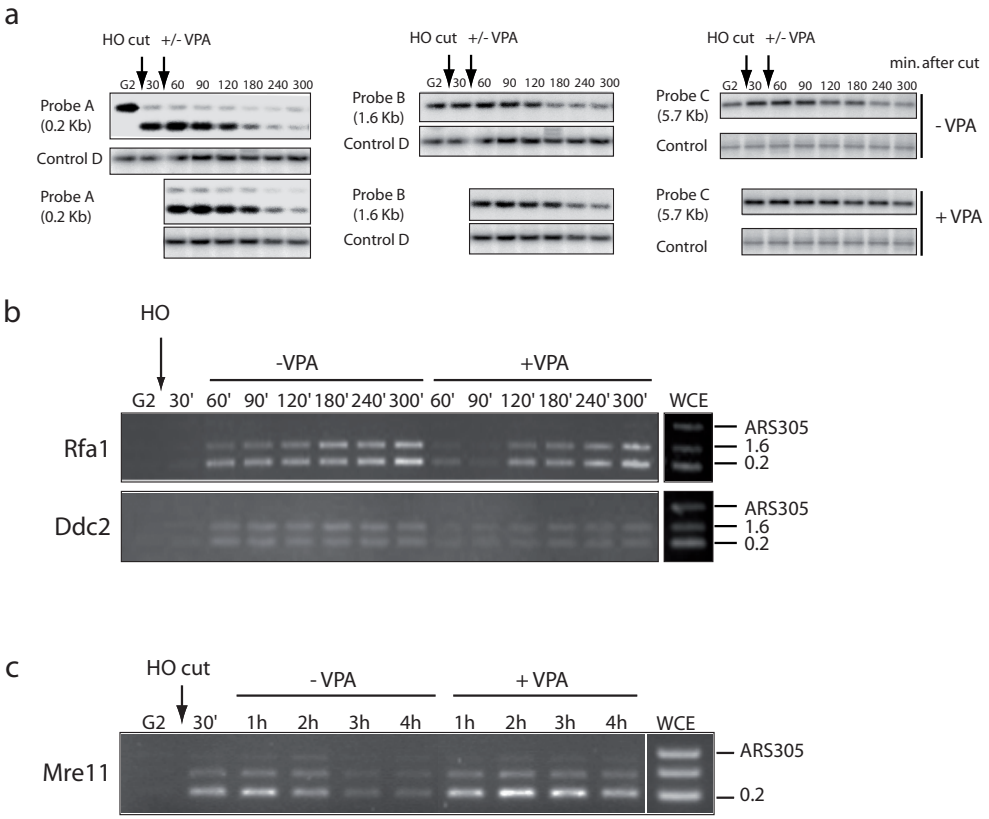


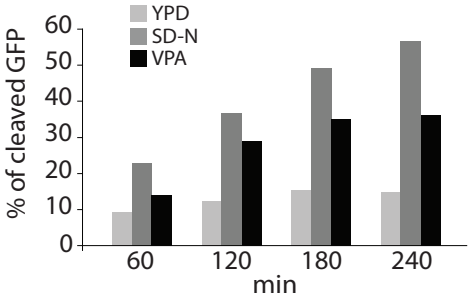




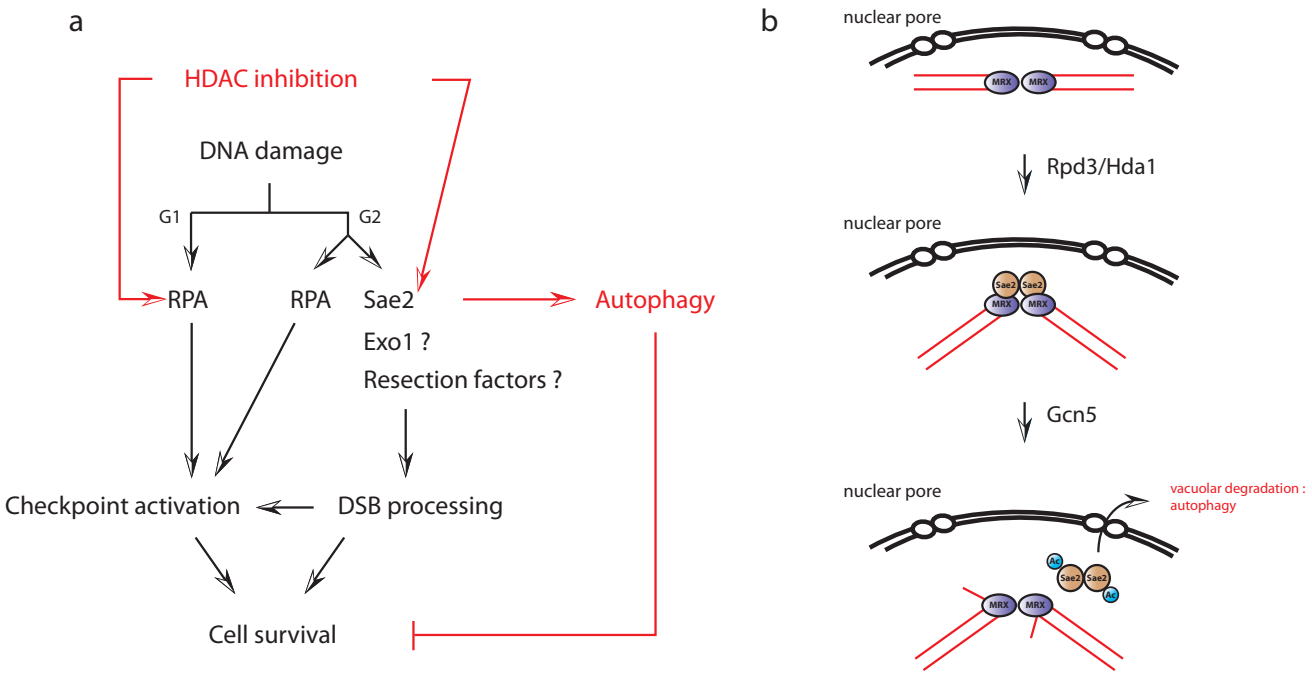
Supp. Fig. 1 (**a**) W303 cells were arrested in G1 with α-factor or G2 with Nocodazole and treated with 2 μg/ml 4NQO. After 15′, VPA was added (+) or not added (-). Log cells were treated with 0.02% MMS. After 3h, VPA was added (+) or not added (-). At the indicated times cell samples were processed for Western blot and FACS analysis. (**b**) Log-phase WT W303 cells were treated with 0.1% MMS for 1h to activate Rad53. 10 mM VPA was added for 10 min before collecting the sample (+VPA). 5μg/ml of cycloheximide was added 10 min before VPA treatment (+cyc). Subsequently, samples were anaylsed by Western blot. (**c**) WT (RMY200), H3-K9, 14, 18, 23G (RMY250), H4-K5, 8, 12, 16R (FLY722) cells were arrested with α–factor or with Nocodazole and treated with 4NQO (0.8 μg/ml). At the indicated time points, samples were collected for Western blot analysis using antibodies that recognize the Rad53 protein backbone (EL7) and the phosphorylated Rad53 (F9).



Supp. Fig. 2 VPA treatment counteracts the DSB processing. (**a-b-c**) *DDC2::MYC RFA1::FLAG* (CY8122) and *MRE11::MYC* (CY6213) cells grown in YP-raffinose were arrested in G2 with Nocodazole and subsequently released in YP-galactose to induce HO endonuclease expression. After 30' from HO induction, 10 mM VPA was added (+VPA) or not added (-VPA) to half of the culture. At the indicated time points cell samples were taken and processed for: southern blot analasys using probe A (0.2 Kb), B (1.6 Kb) and C (5.7 Kb) (**a**) and ChIP analysis of Rfa1-Flag, Ddc2-Myc or Mre11-Myc (**b-c**).



Supp. Fig. 3 Quantification of GFP-Atg8 cleavage. % of cleaved band is calculated as the ratio of the GFP cleaved product over GFP + GFP-Atg8 total amount of protein.



Supp. Fig4: HDACs influence DNA damage response and cell survival (a) Following DNA damages, HDAC activity regulates checkpoint activation throughout the cell cycle. In G1 and G2, Rfa1-acetylation might influence RPA nucleofilament formation and checkpoint control. Moreover, in G2, acetylation influences the stability of resection factors by inducing vacuolar degradation (autophagy). Acetylation and autophagy influence cell survival after exposure to DNA damaging agents (b) A model linking HDAC activities, DSB processing and autophagy. Sae2 acetylation level might facilitate the degradation of Sae2 oligomers through an autophagic pathway (see text for details).

Supplementary Table 1:

W303-1A	*MAT***a**, *ade2-1, ura3-1, trp1-1, leu2-3,112, his3-11,15, can1-100, GAL, rad5-535*	R.Rothstein
W303-1B	*MATalpha, ade2-1, ura3-1, trp1-1, leu2-3,112, his3-11,15, can1-100, GAL, rad5-535*	R.Rothstein
SY653	*MAT***a**, *hoΔ, hml1Δ::ADE1, hmrΔ::ADE1, ade1-100, leu2-3,112, lys5, trp1Δ::hisG, ura3-52, ade3::GAL::HO*	J.E. Haber
CY8093	SY653 *rpd3Δ::NAT*	This study
CY8126	SY653 *hda1Δ::NAT*	This study
CY8255	SY653 *hda1Δ::NAT rpd3Δ::NAT*	This study
CY8122	SY653 *ddc2::DDC2::MYC9::TRP1, rfa1::RFA1::3FLAG::KanMX*	This study
CY6213	SY653 *mre11::MRE11::MYC13::KanMX*	Lab. Stock
CY9236	SY653 *sae2::SAE2::6PK::TRP1*	This study
CY9324	SY653 *rpd3Δ::NAT, hda1Δ::NAT, sae2::SAE2::6PK::TRP1*	This study
CY9545	SY653 *mre11::MRE11::MYC13::KanMX, sae2::SAE2::6PK::TRP1, exo1::EXO1::FLAG::KanMX*	This study
CY9541	SY653 *SAE2::6PK::TRP1, erg6Δ::KanMX4*	This Study
CY10298	SY653 *sae2::SAE2::6PK::TRP1, gcn5Δ::KanMX*	This Study
CY10325	SY653 *MATalpha SAE2::6PK::TRP1, atg19Δ::KanMX4*	This Study

SY2451	*MAT***a** *ade2-1, leu2-3,112, his3-15, trp1-1, CAN1, arg4ΔBglII, URA3::arg4Δ EcoRV::ura3-1*	S Gangloff
CY9549	*MATalpha, ade2-1, trp1-1, his3-11,15, leu2-3,112, CAN1, arg4ΔBglII, URA3::arg4Δ EcoRV::ura3-1, hda1Δ::NAT, rpd3Δ::TRP1*	This study
CY9663	*MATalpha, hoΔ, hml1Δ::ADE1, hmrΔ::ADE1, ade1-100, leu2-3,112, lys5, trp1Δ::hisG, ura3-52, ade3::GAL::HO atg1Δ::KanMX*	This study
CY9666	*MATalpha, hoΔ, hml1Δ::ADE1, hmrΔ::ADE1, ade1-100, leu2-3,112, lys5, trp1Δ::hisG, ura3-52, ade3::GAL::HO atg1Δ::KanMX sae2::SAE2::6PK::TRP1*	This study
CY6944	*Mat***a**, *hmlΔ::ADE1, hmrΔ::ADE1 ade1-100, trp1Δ::hisG, leu2-3,112, lys5, ura3-52, ade3::GAL::HO , KanMX6::GAL1::SAE2::4HA::sae2*	Lab. Stock
CY3213	W303-1A , *rfa1::RFA1::9MYC::TRP1*	Lab. Stock
SY2080	*MAT***a**, *ade2-1, ura3-1, trp1-1, leu2-3,112, his3-11,15, can1-100, GAL, RAD5*	H.Klein
CY8270	SY2080 *rpd3Δ::TRP1*	This study
CY8219	SY2080 *hda1Δ::NAT*	This study
CY8335	SY2080 *hda1Δ::NAT, rpd3Δ::TRP1*	This study
YZX288	*MATalpha his3-D200 leu2-3,112 lys2-801 ura3-52 trp1-D901 suc2-D9 Cherry-APE1::TRP1 GFP-ATG8::URA3*	D.Klionsky
YZX298	*MATalpha his3-D200 leu2-3,112 lys2-801 ura3-52 trp1-D901 suc2-D9 Cherry-APE1::TRP1 GFP-ATG8::URA3 atg1Δ::LEU2*	D.Klionsky
TN124	*MAT***a** *leu2-3,112 ura3-52 pho8::pho8Δ60*	D.Klionsky
HAY572	*MAT***a** *leu2-3,112 ura3-52 pho8::pho8Δ60 atg1Δ::URA3*	D.Klionsky

ySP2656	W303 *MAT***a** *MAD3-HA3::URA3, PDS1-MYC18::LEU2*	S. Piatti
RMY200	*MAT***a** *ade2-101, his3,200, lys2-801, trp1-901, ura3-52 hht1, hhf1::LEU2 hht2 hhf2::HIS3* [*CEN4 ARS1 TRP1 HHT2 HHF2*]	M. Grunstein
RMY250	*MAT***a** *ade2-101 his3 200 lys2-801 trp1-901 ura3-52 hht1 hhf1::LEU2 hht2 hhf2::HIS3* [*CEN4 ARS1 TRP1* hht2-K9,14,18,23G HHF2]	M. Grunstein
FLY722	*MAT***a** *ade2-101 leu2-3,112 lys2-801 trp1- 901 ura3-52 hhf1::HIS3 hhf2::TRP1-hhf2-K5,8,12,16R HHT2*	J.K. Tyler