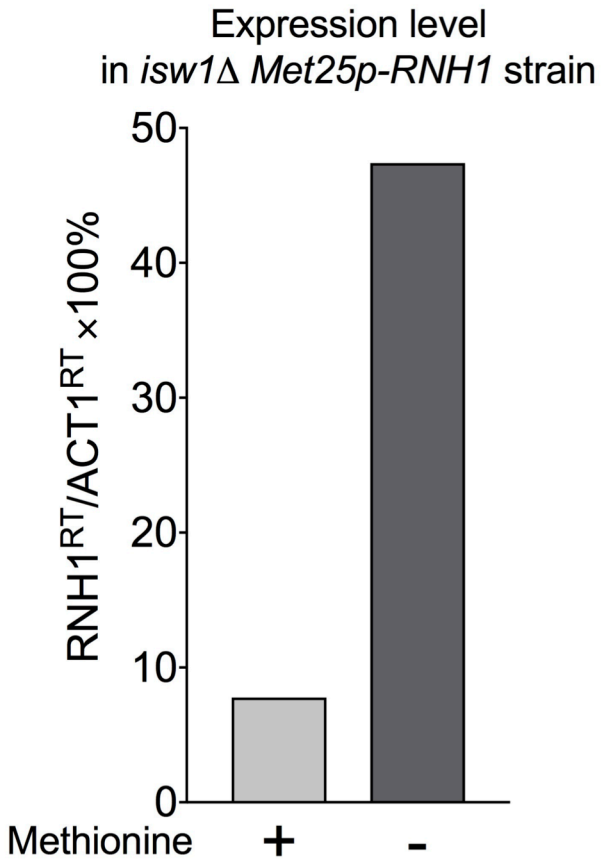

Figure S1. Confirmation of increased *RNH1* expression upon induction of the *MET25* promoter. qRT-PCR of *RNH1* transcript levels in *isw1*Δ strains with p*MET25-RNH1* in non-inducing (+ Methionine) and inducing (- Methionine) conditions. *RNH1* transcript level is normalized to the level of *ACT1* transcript and is presented as percent of *ACT1* transcript level. qRT-PCR confirmation of increased *RNH1* expression is from one experiment.

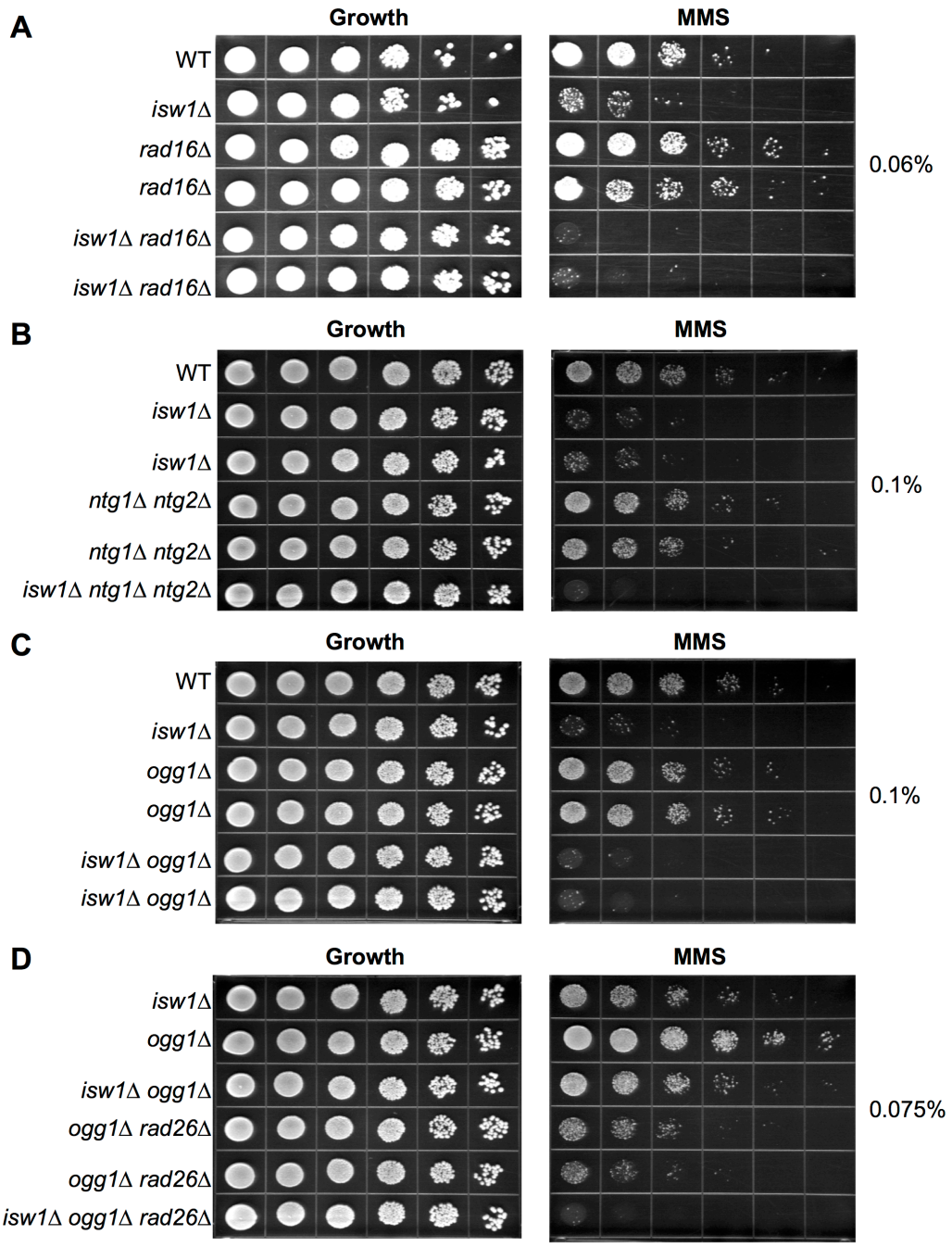

Figure S2. NER and BER gene mutations exhibit a synergistic increase in MMS sensitivity when combined with *isw1*Δ. The indicated strains were plated on growth control plates (YC-Leu-Ura) or MMS plates to test MMS sensitivity of WT and *isw1*Δ strains combined with (A) deletion of the NER gene *RAD16* on plates containing 0.06% MMS, (B) deletion of the BER genes *NTG1* and *NTG2* on plates containing 0.1% MMS, (C) deletion of the BER gene *OGG1* on plates containing 0.1% MMS, and (D) combined deletion of the BER gene *OGG1* and the TCR gene *RAD26* on plates containing 0.075% MMS. Plates were incubated at 30˚C for 3 days prior to capturing images.

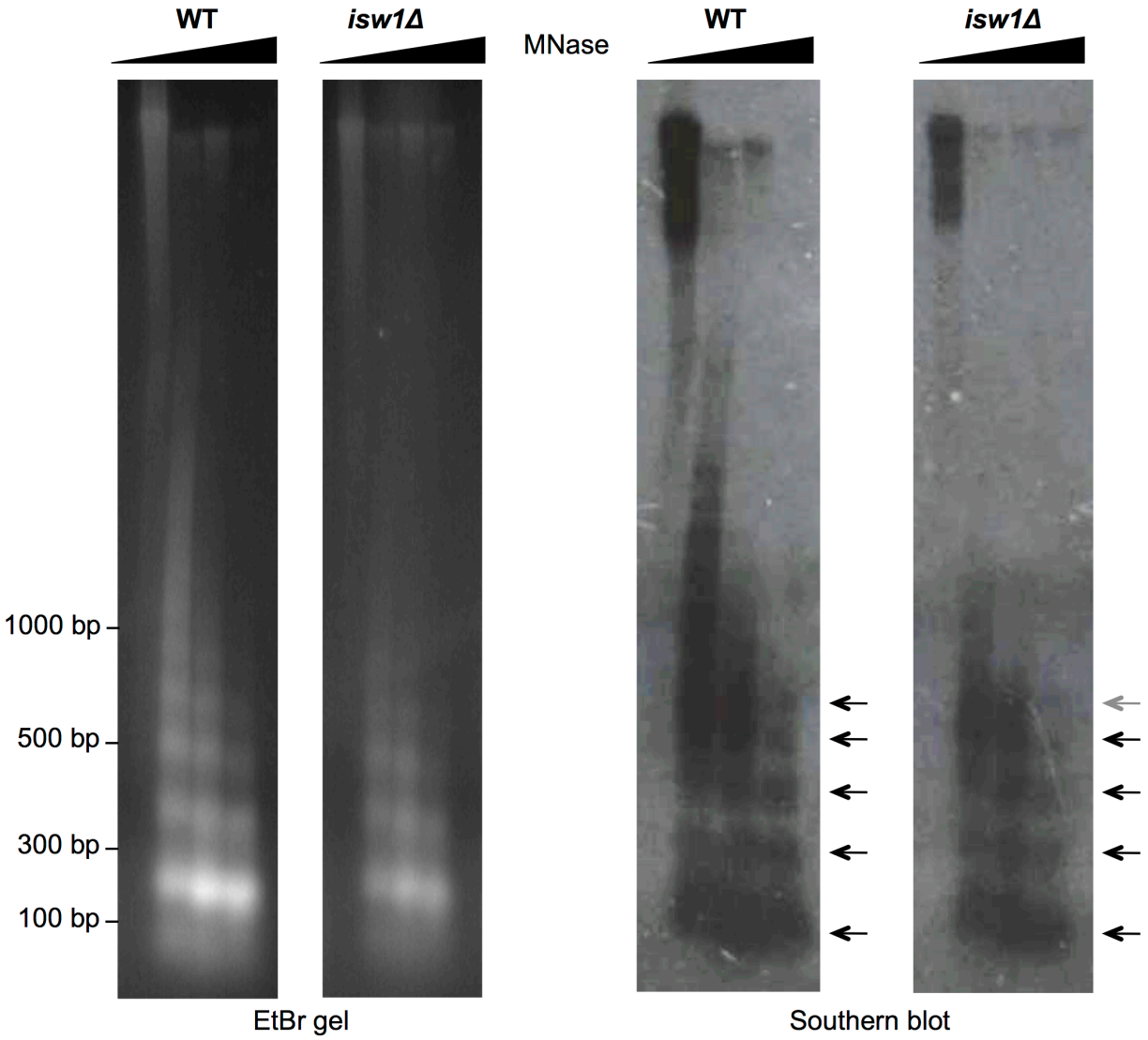

Figure S3. Absence of Isw1 alters the nucleosome array at the CAG-85 repeat on the *URA3*-YAC. MNase assay of WT and *isw1*Δ strains containing the CAG-85 *URA3*-YAC. The wedge indicates increasing MNase level (0-7.5 U). MNase digested DNA (20-30 µg) was run on 1.5% agarose with EtBr (left panels) and Southern blotted using a probe ~100bp upstream of the CAG repeat (right panels).

Table S1. Yeast strains used in this study[a]

Strain	Genotype	YAC	Reference
VPS105	*MATα ade2 ade3 can1 leu2-3,112 ura3Δ0 trp1Δ lys2-801*	none	Schultz and Zakian 1994
BY4705	*MATα ade2Δ::hisG his3Δ200 leu2Δ0 lys2Δ0 met15Δ0 trp1Δ63 ura3Δ0*	none	Brachmann et al. 1998
BY4742	*MATα his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0*	none	Brachmann et al. 1998
CFY809, 810	BY4705	CAG-85 *LEU2 URA3*	Yang and Freudenreich 2007
CFY967, 968	BY4742, *isw1Δ::kanMX4*	CAG-85 *LEU2 URA3*	
CFY1359, 1360	BY4742, *cbf1Δ::kanMX6*	CAG-85 *LEU2 URA3*	
CFY1683	BY4705, *isw1Δ::kanMX4*	CAG-85 *LEU2 URA3*	
CFY2001, 2002	BY4742, *isw1Δ::kanMX4 rad52Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2050	BY4705, *esa1-1851-kanMX6*	CAG-85 *LEU2 URA3*	House et al. 2014
CFY2097, 2098	BY4705, *isw2Δ::kanMX4*	CAG-85 *LEU2 URA3*	
CFY2101, 2102	BY4705, *apn1Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2103, 2104	BY4742, *apn1Δ::HIS3MX6 isw1Δ::kanMX4*	CAG-85 *LEU2 URA3*	
CFY2105, 2106	BY4705, *rad14Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2107, 2108	BY4742*, isw1Δ::kanMX4 rad14Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2181, 2182	BY4705, *ioc4Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2190, 2191	BY4705, *ioc3Δ::TRP1 ioc4Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2205, 2206	BY4705, *ioc2Δ::kanMX4*	CAG-85 *LEU2 URA3*	
CFY2207, 2208	BY4705, *ioc3Δ::TRP1*	CAG-85 *LEU2 URA3*	
CFY2209, 2210	BY4705, *ioc2Δ::kanMX4 ioc4Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	

CFY2211, 2212	BY4705, *ioc2Δ::kanMX4 ioc3Δ::TRP1 ioc4Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2213, 2214	BY4705, *rad26Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2216	BY4742, *isw1Δ::kanMX4 rad26Δ::HISMX6*	CAG-85 *LEU2 URA3*	
CFY2319, 2320	BY4705, *rad16Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2321, 2322	BY4742, *isw1Δ::kanMX4 rad16Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2323, 2324	BY4705, *ogg1Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2325, 2326	BY4742, *isw1Δ::kanMX4 ogg1Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2335, 2336	BY4705, *set1Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2339, 2340	BY4705, *sas3Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2341, 2342	BY4742, *isw1Δ::kanMX4 sas3Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2345, 2346	BY4705, *esa1-1851-kanMX6 isw1Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2423, 2424	BY4705, *apn1Δ::HIS3MX6 rad26Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY2425, 2426	BY4742, *apn1Δ::HIS3MX6 isw1Δ::kanMX4 rad26Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY2427, 2428	BY4705, *ogg1Δ::HIS3MX6 rad26Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY2429	BY4742, *isw1Δ::kanMX4 ogg1Δ::HIS3MX6 rad26Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY2441	BY4705, *rad52Δ::kanMX4*	CAG-85 *LEU2 URA3*	House et al 2014
CFY2447, 2448	BY4705, *ntg1Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2449, 2450	BY4742, *isw1Δ::kanMX4 ntg1Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY2451, 2452	BY4705, *ntg2Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY2453, 2454	BY4742, *isw1Δ::kanMX4 ntg2Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY2455, 2456	BY4705, *ntg1Δ::HIS3MX6 ntg2Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY2457	BY4742, *isw1Δ::kanMX4 ntg1Δ::HIS3MX6 ntg2Δ::HPH*	CAG-85 *LEU2 URA3*	

CFY3012	BY4705	p*GAL1* CAG-100 *LEU2 URA3*	
CFY3013	BY4705, *isw1Δ::kanNMX4*	p*GAL1* CAG-100 *LEU2 URA3*	
CFY3273, 3274	VPS105	*CAG-85 LEU2 ADE2-URA3*	
CFY3331, 3332	VPS105, *isw1Δ::kanMX4*	CAG-85 *LEU2 ADE2-URA3*	
CFY3399, 3411	BY4742, *isw1Δ::kanMX4 MET17 pMET25-RNH1-natMX*	CAG-85 *LEU2 URA3*	
CFY3580	BY4705	CAG-70 *LEU2 URA3* 2T	Su and Freudenreich 2017
CFY3694, 3695	BY4705, *set2Δ::HIS3MX6*	CAG-85 *LEU2 URA3*	
CFY3817, 3818	BY4705, *isw1Δ::kanMX4*	CAG-70 *LEU2 URA3* 2T	
CFY4035, 4036	BY4705, *chd1Δ::HPH*	CAG-85 *LEU2 URA3*	
CFY4037, 4038	BY4742, *chd1Δ::HPH isw1Δ::kanMX4*	CAG-85 *LEU2 URA3*	

[a]Unless otherwise noted, strains were constructed during the course of this study or are part of the standard lab collection.

Table S2. CAG repeat stability assay data

		Contractions				Expansions				
WT, CAG-85 *URA3*-YAC	Total Rxns	#	%	Fold/ WT	p-value[b] to WT	#	%	Fold/ WT	p-value[b] to WT	p-value[b] to *isw1Δ*
Wild-type	299	33	11.0	--	--	4	1.3	--	--	--
Chromatin remodeling										
isw1Δ	307	42	13.7	1.2	0.33	25	8.1	6.1	**7.0 x10^{-5}**	--
isw2Δ	158	24	15.2	1.4	0.23	3	1.9	1.4	0.07	--
chd1Δ	104	11	10.6	0.96	1	7	6.7	5.0	**8.0 x10^{-3}**	--
isw1Δ chd1Δ	104	14	13.5	1.2	0.48	5	4.8	3.6	**0.053**	0.38
Isw1 complexes										
ioc3Δ	156	15	9.6	0.87	0.75	6	3.9	2.9	0.099	--
ioc2Δ	156	23	14.7	1.3	0.29	6	3.9	2.9	0.099	--
ioc4Δ	156	19	12.2	1.1	0.76	8	5.1	3.8	**0.027**	--
ioc2Δ ioc4Δ	156	18	11.5	1.1	0.88	8	5.1	3.8	**0.027**	--
ioc3Δ ioc4Δ	156	16	10.3	0.93	0.87	7	4.5	3.4	**0.052**	--
ioc2Δ ioc3Δ ioc4Δ	156	13	8.3	0.76	0.42	5	3.2	2.4	0.29	--
***CBF1* and histone methyltransferases (HMTs)**										
set1Δ	149	19	12.8	1.2	0.16	1	0.67	0.50	1	--
set2Δ	180	30	16.7	1.5	0.094	5	2.8	2.1	0.31	--
cbf1Δ	104	5	4.8	0.44	0.08	4	3.8	2.9	0.2	--
Histone acetyltransferases (HATs)										
sas3Δ	154	23	14.9	1.4	0.23	4	2.6	1.9	0.45	--
esa1-1851	125	25	20.0	1.8	**0.054**	10	8.0	6.0	**5.0 x10^{-3}**	--
isw1Δ sas3Δ	156	19	12.2	1.1	0.76	12	7.7	5.8	**8.7 x10^{-4}**	1
isw1Δ esa1-1851	104	28	26.9	2.4	**2.2 x 10^{-4}**	13	12.5	9.3	**1.1 x10^{-5}**	0.24
CAG-85 *ADE2-URA3*-YAC										
WT	148	27	18.2	--	--	3	2.0	--	--	--
isw1Δ	200	34	17.0	0.93	0.78	3	1.5	0.74	0.70	--

TT CAG-70 TT *URA3*-YAC (2T-YAC)										
WT	326	17	5.2	--	--	3	0.92	--	--	--
isw1Δ	88	4	4.6	0.87	1	2	2.3	2.5	0.29	--
p*GAL1* CAG-100 *URA3*-YAC										
WT, glucose	200	16	8.0	--	--	2	1.0	--	--	--
isw1Δ, glucose	199	14	7.0	0.88	0.85	4	2.0	2.0	0.45	--
WT, galactose	200	8	4.0	--	--	4	2.0	--	--	--
isw1Δ, galactose	200	14	7.0	1.8	0.27	9	4.5	2.3	0.26	--
RNase H overexpression										
isw1Δ, RNase H not induced	103	8	7.8	0.71	0.45	7	6.8	5.2	**7.9 x10^{-3}**	--
isw1Δ, RNase H induced	104	10	9.6	0.87	0.85	8	7.7	5.9	**3.0 x10^{-3}**	--
HR pathway										
rad52Δ	199	45	22.6	2.1	**6.4 x 10^{-4}**	4	2.0	1.5	1	--
isw1Δ rad52Δ	256	24	9.4	0.85	0.58	20	7.8	5.8	**2.1 x10^{-4}**	1
NER pathway										
rad14Δ	204	25	12.3	1.1	0.67	11	5.4	4.0	**0.014**	--
rad26Δ	143	20	14.0	1.3	0.43	2	1.4	1.1	1	--
rad16Δ	156	23	14.7	1.3	0.29	9	5.8	4.3	**0.014**	--
isw1Δ rad14Δ	208	15	7.2	0.65	0.17	5	2.4	1.8	0.50	**6.6 x10^{-3}**
isw1Δ rad26Δ	123	12	9.8	0.88	0.86	4	3.3	2.4	0.24	0.087
isw1Δ rad16Δ	156	22	14.1	1.3	0.37	11	7.1	5.3	**3.6 x10^{-3}**	0.86
BER pathway										
apn1Δ	208	16	7.7	0.70	0.23	1	0.48	0.36	0.65	--
ogg1Δ	156	23	14.7	1.3	0.29	4	2.6	1.9	0.46	--
ntg1Δ	208	22	10.6	0.96	1	4	1.9	1.4	0.72	--
ntg2Δ	208	20	9.6	0.87	0.66	6	2.9	2.2	0.33	--
ntg1Δ ntg2Δ	207	26	12.7	1.1	0.67	2	0.97	0.72	1	--

isw1Δ apn1Δ	208	15	7.2	0.65	0.17	3	1.4	1.1	1	**6.1×10^{-4}**
isw1Δ ogg1Δ	156	13	8.3	0.76	0.42	3	1.9	1.4	0.70	**6.8×10^{-3}**
isw1Δ ntg1Δ	208	23	11.1	1.0	1	4	1.9	1.4	0.72	**2.8×10^{-3}**
isw1Δ ntg2Δ	208	23	11.1	1.0	1	8	3.9	2.9	0.08	0.066
isw1Δ ntg1Δ ntg2Δ	208	23	11.1	1.0	1	10	4.8	3.6	**0.026**	0.16
NER and BER pathway										
apn1Δ rad26Δ	102	17	16.7	1.5	0.16	2	2.0	1.5	0.65	--
isw1Δ apn1Δ rad26Δ	96	18	18.8	1.7	**0.057**	2	2.1	1.6	0.64	**0.037**

[b] p-values in bold font show significant differences of $p \leq 0.05$.

Supporting Information References

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