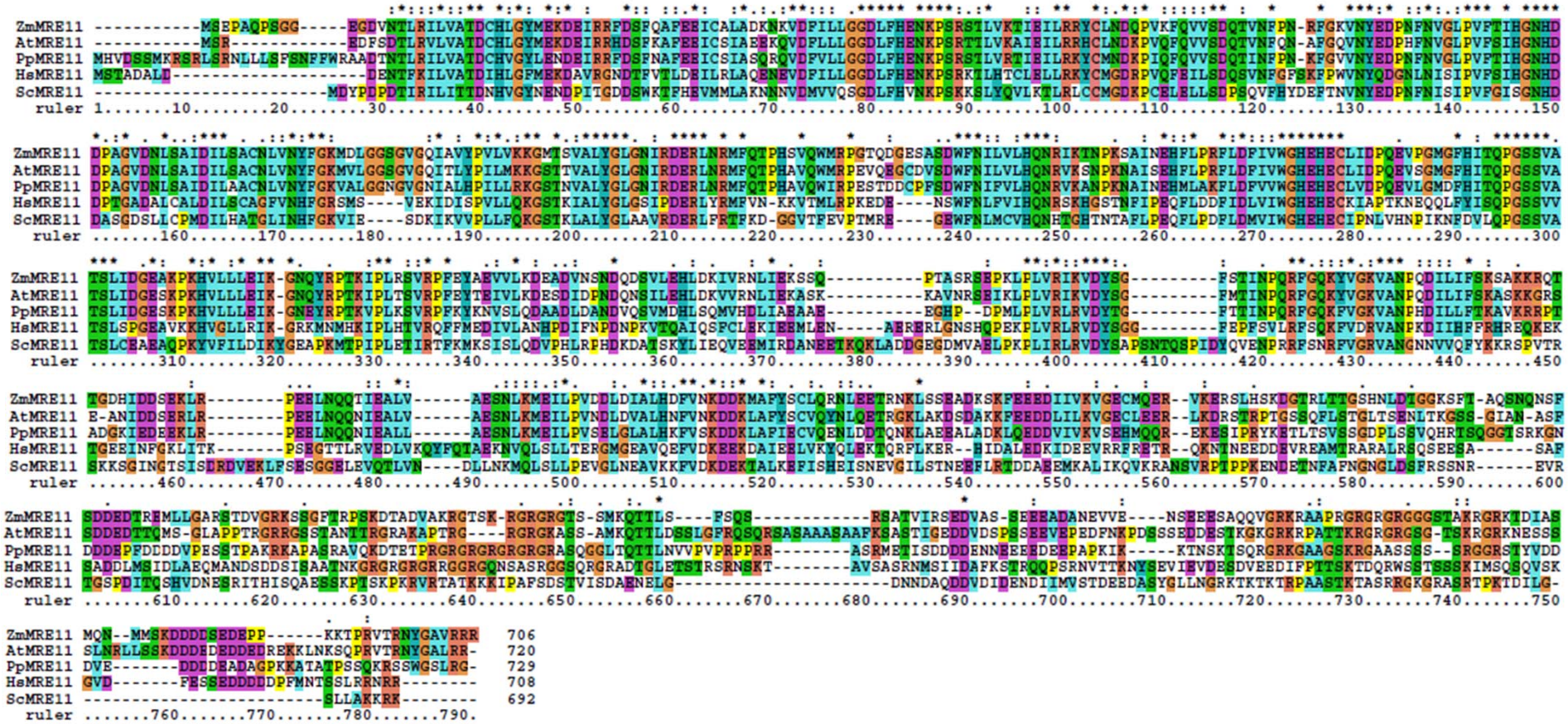
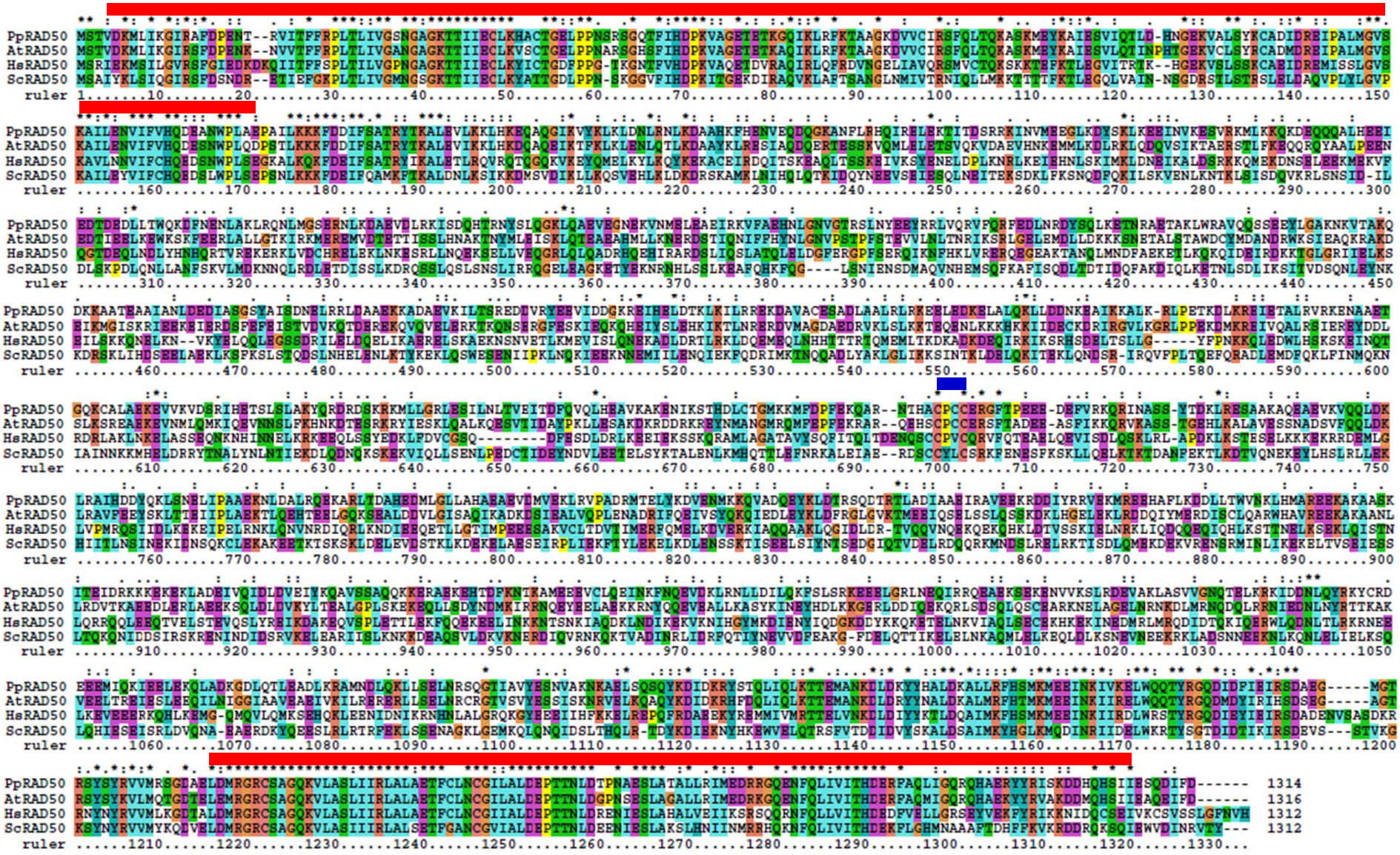
Supplemental Figure 1

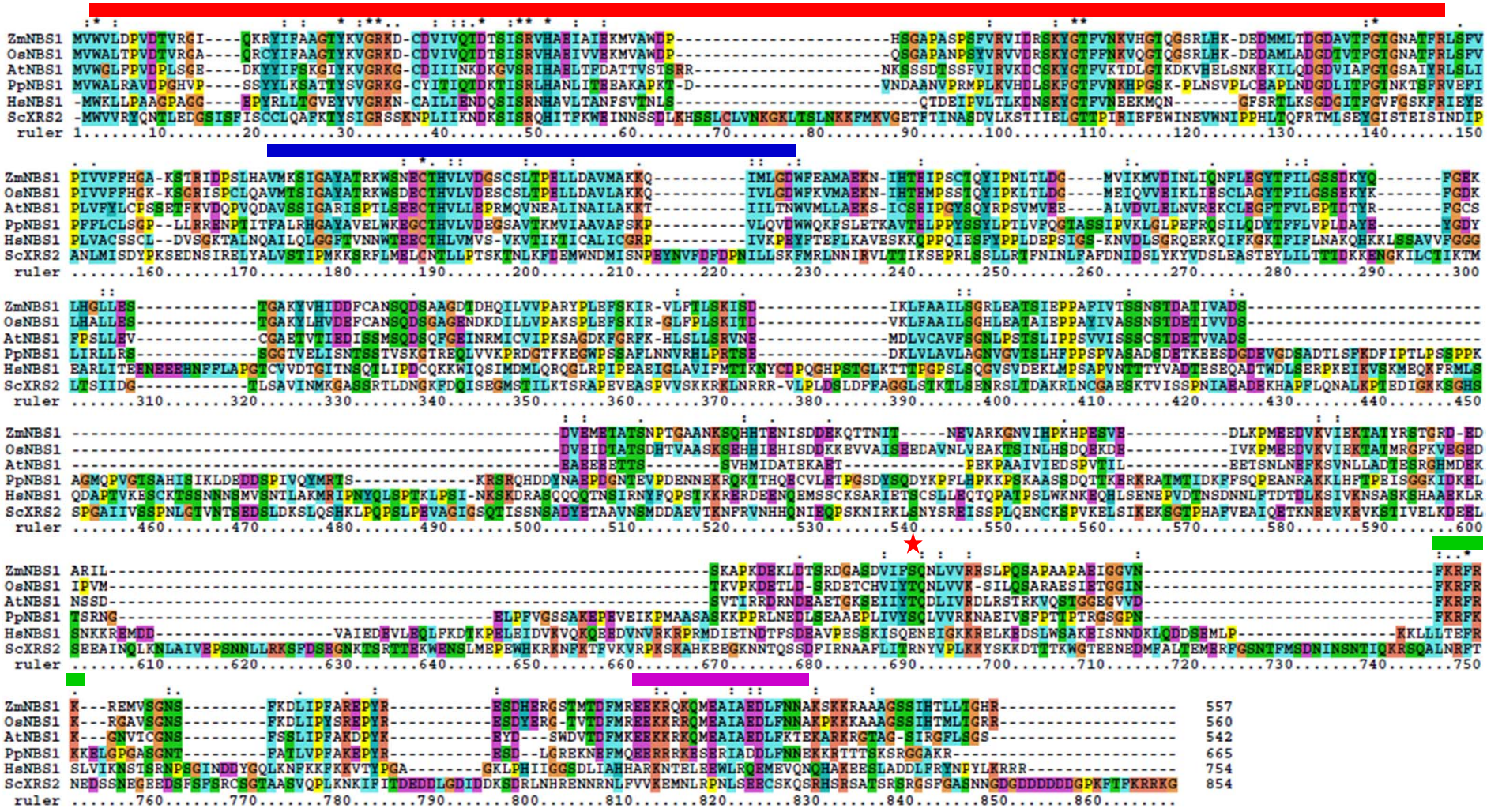


Supplemental figure 1: Sequence alignments of MRN polypeptides.
1a: The deduced polypeptide sequence of PpMRE11 was aligned with the orthologous sequences from maize (ZmMRE11), *Arabidopsis* (AtMRE11), human (HsMRE11) and yeast (ScMRE11).



Supplemental figure 1: Sequence alignments of MRN polypeptides.

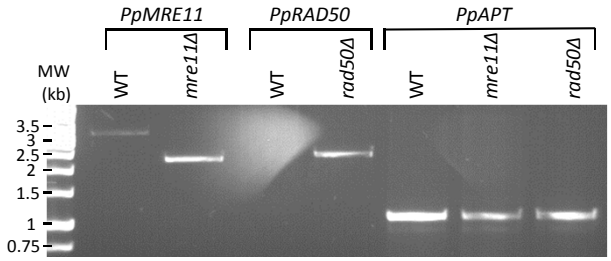
1b: The deduced polypeptide sequence of PpRad50 was aligned with those of *Arabidopsis* (AtRad50), human (HsRad50) and yeast (ScRad50) polypeptides. The N- and C-terminal Walker A and Walker B domains are overlined in red, and the central CXXC zinc hook motif is overlined in blue.



Supplemental figure 1: Sequence alignments of MRN polypeptides.

1c: The deduced polypeptide sequence of PpNBS1 was aligned with the corresponding sequences from *Arabidopsis* (AtNBS1), human (HsNBS1) and yeast (ScXRS2). The N-terminal fork-head associated domain is overlined in red, and the BRCT domain overlined in blue. The FKRFKK motif overlined in green corresponds to the *Arabidopsis* MRE11-binding motif, whilst the C-terminal domain overlined in purple contains the ATM-interaction domain. An SQ dipeptide conserved in all the plant proteins and is a putative site for phosphorylation by ATM is indicated by a red star.

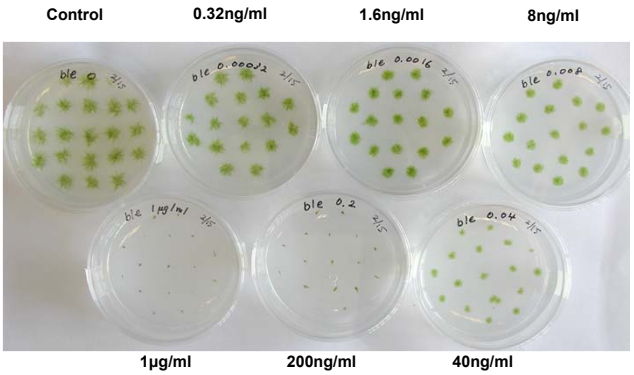
Supplemental Figure 2



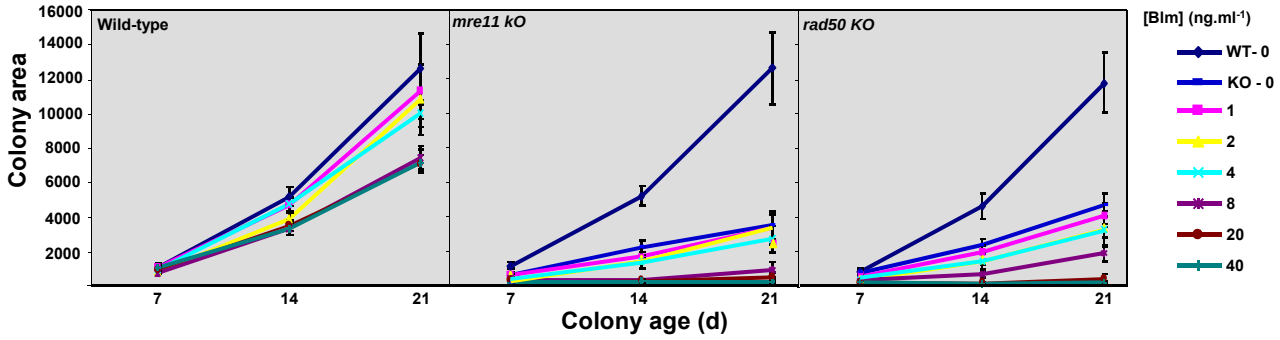
Supplemental figure 2. Molecular analysis of *mre11*Δ and *rad50*Δ mutants.

PCR on genomic DNA with primers flanking the deleted region after Cre recombination, PpMRE11#3+PpMRE#4 for *MRE11* and PpRAD50#3+PpRAD50#4 for *RAD50*. Detection of the 10kb WT fragment for PpRAD50 is not possible with these PCR conditions. The *PpAPT* gene has been used as control (primers: APT#16 + APT#19).

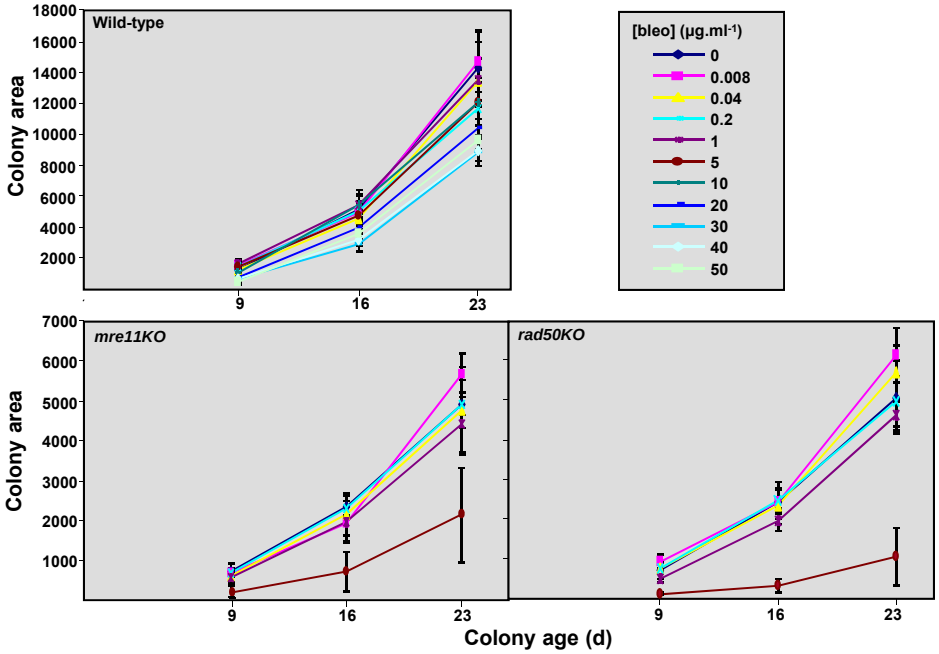
Supplemental Figure 3



Supplemental figure 3A: Hypersensitivity of the *rad50* and *mre11* mutants to bleomycin.
Physcomitrella explants were inoculated as "spot inocula" onto BCD-agar plates supplemented with bleomycin at the indicated concentrations, and photographed 10d following inoculation.

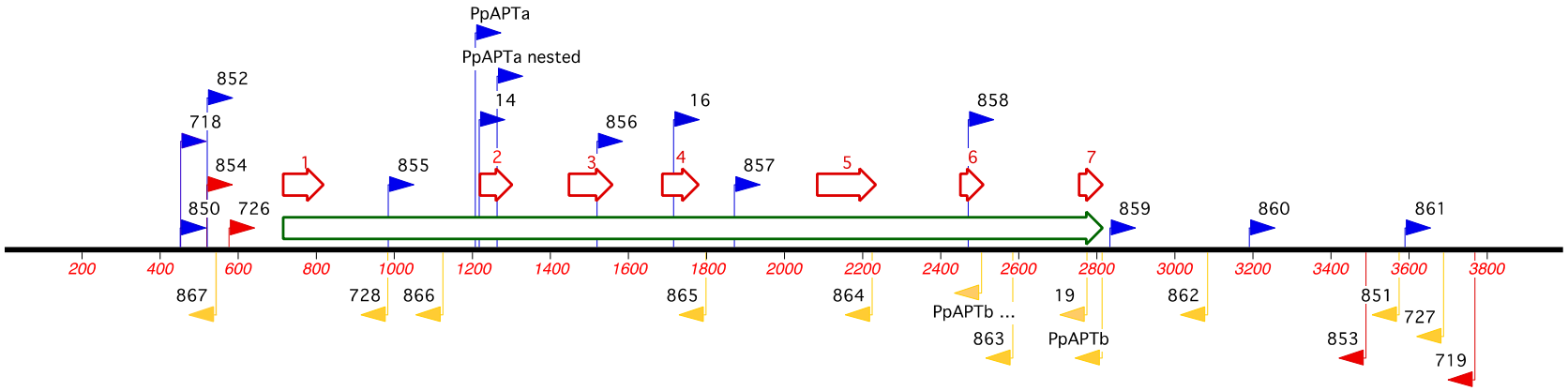


Supplemental figure 3B: Growth rates of WT, *rad50* and *mre11* mutants chronically exposed to bleomycin.
Colony growth was measured over a 3-week period following inoculation. The extent of colony growth was estimated following digital photography of the plates. The image analysis software "ImageJ" was used to determine the colony area based on counting the number of pixels corresponding to each colony. Colony area determinations based on different photographs were normalised for each colony using the estimated area of the plate. Note that the growth curve of the wild-type strain in the absence of bleomycin is included in each panel to facilitate comparison between mutant and wild-type.



Supplemental Figure 3C: Recovery of WT, *mre11* and *rad50* strains following acute treatment with bleomycin.
A protonemal homogenate was incubated in BCDAT liquid medium for 1 hour at the concentrations indicated. After washing, explants were inoculated on drug-free BCDAT-agar and growth rate determined over a 3-week period.

Supplemental Figure 4



Supplemental figure 4. Map and localization of *APT* primers listed in Supplemental Table 1. Black line represents genomic sequence DQ117987 with indicated nucleotide numbers. Arrows indicate position and orientation of particular sequence: Empty green – transcribed CDS region, empty red - *PpAPT* exons, solid blue - forward and solid yellow reverse sequencing primers, solid red – entire *APT* amplification primers.

Supplemental Table 1.

Locus	Primer name	orientation	Sequence 5’-3’
MRE11	PpMRE11#1	Forward	ACTATGAGGATCCGAATTTC
	PpMRE11#2	Reverse	CCGCTGTGGATTGATTGT
	PpMRE11#3	Forward	GCTGGTGTGGTATGTTTGG
	PpMRE11#4	Reverse	CGTAGCTTTTCCTCATCTTC
RAD50	PpRAD50#1	Forward	CAGATGCGGAGGTTAAGAT
	PpRAD50#2	Reverse	ACCCGTAGCTTCTCAACCAT
	PpRAD50#3	Forward	ATCGTGGGGTCAAATGGTG
	PpRAD50#4	Reverse	CTTGGCCCCGATAGGTTTG
NBS1	PpNBS1#1	Forward	GGCGAGGAGGGTAGCGTAGGT
	PpNBS1#2	Reverse	CTGTGCGAGGCTCCATTGAACGAT
APT	PpAPT#14	Forward	AGATGTCGGCCTCCAAGGATG
	PpAPT#16	Forward	CCACCCATTGCTCTTGCCATC
	PpAPT#19	Reverse	CCCGACAACTTCTCACGACCC
	PpAPT#a	Forward	CAGGAAGTGAAGATGTCG
	PpAPT#a nested	Forward	GGACAGCATCCGTACCATTC
	PpAPT#718	Forward	ATAAACAACGCGAGGATGAC
	PpAPT#726	Forward	ATTCCACTCGCCGAAGGGAC
	PpAPT#854	Forward	TTGGGTAACCGTGGAATCAG
	PpAPT#855	Forward	CAGTGCCTGTGATGCGGTTG
	PpAPT#856	Forward	TTGAGCGTTACCGGGACCAG
	PpAPT#857	Forward	CAATGTGACCGAGACTTCATCC
	PpAPT#858	Forward	GTGGAATGCGCGTGCTTGGTTG
	PpAPT#859	Forward	GTCGCCGTGGTCATTGGTTC
	PpAPT#860	Forward	GCCTCCTGATGTTTCTCTTACC
	PpAPT#861	Forward	TCCACAAGGACCCAGTTACC
	PpAPT#b	Reverse	GGTGGAATATGAGGGCGAGTA
	PpAPT#b nested	Reverse	CTTGGTTGAGCTGGTAGACC
	PpAPT#719	Reverse	CAATCCACATCCAGCCAATG
	PpAPT#727	Reverse	CCGTCGAATCTGAACCGCGA
	PpAPT#728	Reverse	GAATTTGCTGTGGGTTATGGGC
	PpAPT#851	Reverse	GAATATCCTCACGTCGGAAAGC
	PpAPT#853	Reverse	GATGAGAAAGGAACTGCGC
	PpAPT#862	Reverse	CTTCTAACCTCGGAAACG
	PpAPT#863	Reverse	GAGTTCAATGCCGTCTGGAG
	PpAPT#864	Reverse	CACTCTTGGAGCTGCCATCA
	PpAPT#865	Reverse	GGTAAGGGTTGACAGGCACT
	PpAPT#866	Reverse	GGTCAATGTGGCAGCAAGTA
	PpAPT#867	Reverse	GTAACCGTGGAATCAGCAAC

Supplemental Table 2. Number of selected Wild-type and *Pprad50KO apt* mutants

genotypes	1st selection	2nd selection	3rd selection
RAD50/apt	77	14	4 (5%)
rad50/apt	113	27	11 (10%)

Supplemental Table 3. Spontaneous mutation rate in mutant lines

Genotype	Population	2-FA resistant	Rate in 10^6
WT	2880000	0	< 0.3
*mre11*Δ	2500000	1 (p= 0.465) [a]	0.4
*rad50*Δ	2200000	0	< 0.5
nbs1KO	2640000	0	< 0.4
*msh2*Δ	2110000	78	37

[a] Differences were compared using Fisher's exact test.