	.***	*:*: *:* : *:	****	***** *****	** *:.*:* :::::** :	 * ***;* ;;*;;;*** * ****
ZmMRE11 AtMRE11		HLGYMEKDEIRRFDS HLGYMEKDEIRRHDS	FQAFEEICALADKNKVDFI FKAFEEICSIAEEKQVDFL	LLGGDLFHENKPSRSTLVKTIE LLGGDLFHENKPSRTTLVKAIE	ILRRYCLNDQPVKFQVVSDQTVN ILRRHCLNDKPVQFQVVSDQTVN	F <mark>PN - RFG</mark> KV NYEDPNFNVGLPVFTIHGNHD FQN - AFGQV NYEDP HFNVGLPVFSIHGNHD
PpMRE11 HsMRE11	MHVDSSMKRSRLSRNLLLSFSNFFWRAADINILRILVAID MSTADALDDENTFKILVAID	HVGYLENDEIRRFDS HLGFMEKDAVRGNDT	FNAFEEICSIASOROVDFV FVTLDEILRLACENEVDFI	LLGGDLFHENKPSRSTLVRTIE LLGGDLFHENKPSRKTLHTCLE	LLRKYCMNDKPIQFQVVSDQTIN LLRKYCMGDRPVOFEILSDOSVN	PPN-KFGVVNYEDPNFNVGLPVFTIHGNHD FGFSKFPWVNYODGNLNISIPVFSIHGNHD
ScMRE11	MDYPDPDTIRILITTD	HVGYNENDPI 1GDDS	KT FHEVMMLA KNNNVDMV	VQS <mark>GDLFHVNKPSKKSLYQ</mark> VLK	TLRLCCMGDKPCELELLSDPSQV	FHYDEFTNVNYEDPNFNISIPVFGISGNHD
ruler	. 1				100110120	130140150
ZmMRE11	*.:* *. :*** .::*:*: :* :* :* :* :* :* :* :* :* :* :*	*.:** *.:*****	TRDERLNRMFOT PHSVOW	* :	NRIKTNPESAINEHFLPRFLDFT	VWGHRHECLIEPORVPGMGFHITOPGSSVA
AtMRE11	DPAGVDNLSAIDILSACNLVNYFGKMVLGGSGVGQITLYPI	LMKKG <mark>ST</mark> TVALYGLG	IRDERLNRMFOTPHAVOW	MRPEVQECCDVSDWFNILVLHC	NRVKSNPKNAISEHFLPRFLDFI	VW <mark>GHEHECLIDPQEVSGMGFHITQPGSS</mark> VA
PpMRE11 HsMRE11	DPAGVDNLSAIDILAACNLVNYFGKVALGGNGVGNIALHPI DPTGADALCALDILSCAGFVNHFGRSMSVEKIDISPV	LLRKGSTNVALYGLG	IRDERLNRMFOTPHAVOW	IRPESTDDCPFSDWFNIFVLHC LRPKEDENSWFNLFVIHC	NRVKAN PKNAINEHMLAKFLDFV NRSKHGSTNFIPEOFLDDFIDLV	VWGHEHECLVDPQEVLGMDFHITQPGSSVA IWGHEHECKIAPTKNEOOLFYISOPGSSVV
ScMRE11	DASGDSLLCPMDILHATGLINHFGKVIESDKIKVVPI	LFQKGSTKLALYGLA	WRDERLFRTFKD-GGVTF	EVPTMRE GEWFNLMCVHC	NH <mark>TGH</mark> TNTAFLPEQFLPDFLDMV	IWGHEHECIPNLVHNPIKNFDVLQPGSSVA
ruler			.210		250	
ZmMRE11	TSLIDGEAKPKHVLLLEIK - GNQYRPTKIPLRSVRPFEYAE	VVLKDEADVNSNDQD	VLEHLDKIVRNLIEKSSO	PTASRSEPKLPL	VRIKVDYSGFSTIN	PORFGORYVGKVANPODILIFSKSAKKROT
AtMRE11	TSLIDGESKPKHVLLLEIK-GNQYRPTKIPLTSVRPFEYTE	IVLKDESDIDPNDQNS	ILEHLDKVVRNLIEKASK	KAVNRSEIKLFL	VRIKVDYSGFMTIN	PORFGOKYVGKVANPQDILIFSKASKKGRS
HsMRE11	TSLSPGEAVKKHVGLLRIK - GRKMNMHKIPLHTVRQFFMEL	IVLANHPD IFNPDNP	(VTQAIQSFCLEKIEEMLE	NAERERLGNSHOPEKPL	VRLRVDYSGGFEPFS	VLRFSQKFVDRVANPKDIIHFFRHREQKEK
ScMRE11	TSLCEAEAOPKYVFILDIKYGEAPKMTPIPLETIRTFKMKS	ISLODVPHLRPHDKDA	TSKYLIEQVERMIRDANE	ETKQKLADDGEGDMVABLPKPL	IRLEVDYSAPSNTQSPIDYQVEN	PREFSNEFVGRVANGNNVVQFYKKRSPVTR
Turer			***.*******	* *		
ZmMRE11	TGDHIDDSEKLRPEELNQQTIEALVAE	SNLKMEILPVDDLDIA	ALHDFVNKDDKMAFYSCLQ	RNLEETRNKLSSEADKSKFEEE	DIIVKVGECMQER VKERSLHS	KDGTRLTTGSHNLDIGGKSFT-AQSNQNSF
PpMRE11	ADCKIEDEEKLRPEELNQQNIEALLAE	SNLKMEILPVNDLDVA	ALHKFVSKDDKLAFIECVO	ENLODTONKLAEEALADKLOEL	DVIVKVSEHMOOR EKESIPRY	KETLTSVSSCOPLSTVOHRTSOCCISKCN
HsMRE11	TGEEINFGKLITKPSEGTTLRVEDLVKQYFQTAE	KNVQLSLLTERGMGE	VQEFVDKEEKDAIEELVK	YQLEKTORFLKER HIDALEI	KIDEEVRRFRETR QKNTNEED	DEVREAMTRARALRSQSEESASAF
ruler			510		550	
ZmMPP11		POPOPOTE SMIT	* Pene	PEATUTPOPPUAG PP		
AtMRE11	SDDEDTTOMS-GLAPPTRGRRGSSTANTTRGRAKAPTRG	- RGRGKASS - AMKQT	TLDSSLGFROSORSASAA	SAAFKSASTIGEDDVDSPSSE	EVEPEDENKPDESSEDDESTKCK	GRKRPATTKRGRGRGSG-TSKRGRKNESSS
PpMRE11 HeMRR11	DDDEPFDDDDVPESETPAKRKAPASRAVQKDTETPRGRGRG SADDLMSTDLARCMANDSDDSTSAATNKGRGRGRGRGRGRGRG	RGRGRGRASOGGL TOT	LNVVPVPRPPRR	ASRMETISDDDDENNBEEB	DEEPAPKIK KTNSKISQR	GRKGAAGSKRGAASSSS SRGGRSTYVDD RDIFPTTSKTDORWSSTSSSKIMSOSOVSK
ScMRE11	TGSPDITCSHVDNESRITHISQAESSKPTSKPKRVRTATKK	IPAFSDSTVISDAEN	ELG	DNNDAQDDVDIDEND	IIMV STDEEDAS YGLLNGRKTKT	KTRPAASTKTASRRCKGRASRTPKTDILG-
ruler		650	660670	.680	700710720	730740750
ZmMRE11	MONMMSKDDDDSEDEPPKKTPRVTRNYGAVRRR	706				
PpMRE11	DVEDDDDEDEDEDREKKLNKSQPRVTRNIGALRK-	720				
HsMRE11	GVDFESSEDDDDDDPFMNTSSLRRNRR	708				
ruler		072				

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).

PprADS0 METVDRVLIGTBATDENT - NUTPERPILITUG - MAGRETTITECLEMACTOR: DELAGASTUTUG - MAGRETTIRECUSCIC PARSES DE SCOPTEDDE VAGETER COLTENEE VAGETER COLT
Scrabs MEATERIZICIAL COLLEMENTS NEODESILEE Scrabs NEODESILEE NEODESILEE Scrabs NEODESILEE NEODESILEE Scrabs
PpRAD50 KALLENVIEVHODEANNELAEDAILAKKKPDDIFAARYYKALEVIKKLENGAGUK VYKLEDAKKLENGIGAGUKANFLEHIKKITDERKKIVVMEEGLKVSKIKKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENVKENKENKENVKENKENKENVKENKENKENVKENKENKENVKENKENKENKENVKENKENKENVKENKENKENVKENKENVKENKENKENVKENKENKENKENVKENKENKENKENKENKENKENKENKENKENKENKENKENK
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PpRAD50 EDTIDEDLINGKEPNENLAKLRONLMGSEENLKDAEVDIETTISSENNKISDETRINSIGKLAAEVEGNEKVNMELEAEITAKUPATENLGNVGTRSINYEEYREVULAIKTAKUPATENLGNUSSEETLGAKNKVTAK ATRAD50 EDTISELKEWKSKFEERLALLGTXIRKMEREVUTETTISSENAATNNNLEISKLTEAEAAHMLKKEPGTEINIPPHYLICHVPSTFFITVVILITIKKSEGELEMDLLDKKKEN ETALSTAWDCYMANDRKKSIEAQKRAKL HERAD50 OCTDERGLNDLYNHENGTVERKEERLVUCHRELEKKNESSELEVEGGELGLGADREDETIKARDELIGSLAGUGELGERGFSERDINPHKLVREVGEGEATANDIMNDFAKKEILKOKGIGEITEKK SCRAD50 DLEKPDLQNLLAFSKVLMEKNNQLRDIETDISSLKDGGELGGESUSSLSUEGGELGADREDETIKARDELIGSLGERTEKE SCRAD50 DLEKPDLQNLLAFSKVLMEKNNQLRDIETDISSLKDGGELGGESUSSLSUEGGELGADREDETIKARDELIGSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHLSSLKRAGGESKIEVEKNNEHSFERFIGUESKIEVEKENTINSTENDEN TUIET
Atradso EDI IBELKEWKSKFEERLALLGTKIRKMEREMVDTETTISELHNAKTNYMLEISKLOTEAAEAEMLLKMERD TIONIPPHYNLGNVPBTPFTYVULLTNRIKSLGELEMDLLDKKKEN ETALSTAWDCYMDANDRWKSIEAQKRAKI Heradso OGTEDGIANLYNNHERTYRKERKLUDCHELEKLINKSRLINGEN ELLVEQGEL LDADRHGEH IRARDS LIOSLATDIELDGPERGPFSERDIN PHKUVRE GEGEAKTANDLMNDFAKETLKOKOLDEINDKKWIGLERILKKKUCHELEKLINKSRLOGEN SLUKKEN SCHUCHELEKLINKSRLOGEN SLUKKEN SCHUCHELEKLINKSRLOGEN SLUKKEN SCHUCHEN
PpRAD50 KKAATEAAIANLEEIASSAAISDNELRRLDAAEKKADAEVKILTSREDDVRYEEVIDGKREIHELDTKLKILTRREKDAVACESADLAALRERELELDKELALQKLLDUNKEAIKKALK-RLPETKULKREIETALRYKENAAEV AtRAD50 BILMMGISKRIEEKEIERDSFEFISTUVKGTDEREKQVOVELERKTKONSERGFESKIECHEIYSLEHKIKTNRERDVAAGDAEDRVLSLKKTEQENLKKEKKIIDECKDRINGVLKGRLPPEKUKREIETALRYKENAAEVID HISKKONSLKN-VKYELQDEGSSDRILELDGELIKAEREISKAEKNSNVETLKMEVISLONKLALDDTLRKLDCEMEQINHITTROMEMITKDKADKDEGIRKIKSRHSDELTSLGYFPNKKGLEDWLHSKSKIINGT SCRAD50 KDRSKLIHDSEIAEKLKSFKSLSTQDSLNHELENLATYKEKLGSWESENIIPKLNEWISLONKLALDDTLRKLDCEMEQINKTNQAADLYAKLGLIKKSINTKLDELGKITEKLQNDSR-IRQVFPLTGEFQRADLEMDFQKLFINNQKN ruler460470480490500510
Atradso BIKMGISKRIEEKBIERDSFEFFISTUUVKOTDEREKOVOVELERKTKONSERGFESKIEOKOHEIYSLEHKIKTENRERDVMAGDAEDRVKLSLKETEOENLKKKHKIIDECKDRIRGVLKGRLPPEKDMKREIVOALRSIEREYDDL HeRADSO BILEKKONELKNVKYELOOLEGSSDRILELDOELIKAERELSKAEKNSNVETLKMEVISLONEKADLDRTLEKLDOEMEOLNHHTTRE OMEMLIKKABKDED IRKIKSRHSDELTSLLGYFPNKKCLEDWLHSKSKEINOT SCRADSO KDRSKLINDSELAEKLKSFKSLSTODSINHELENLKTYKEKLOSWEEENIIPKLNGVIEEKNEMIILENOIEKFODRIMKINODALLYAKLGLIKKSINTKLDELOKITEKLONDER-IRQVPPLTGEFORADLEMDFOKLFINNOKN ruler
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PpRAD50 GCKCALAKEVVKVDERIHETSLELAKVGRURDSKRKHLGRLESILNLTVEITDGVOLHEAVKAKENIKSTHDLCTGMKKMFDPFEKGARNTACCCCERGFTPEE -DEFVRKGRINASS-TTCHINAGALAVESANAKOCALVKOLDK AtRAD50 SLKSREAEKEVNMLGMKIQEVNNSLFKHNKDTESRKRYIESKLGALKQESVTIDAYPKLESAKDKRDDRKREYNMANGMROMFPFFKRARQHSCPCCERGFTADER-ASFIKKORVKASS-TGEHLKALAVESSNADSVFGOLDK HeRAD50 RDRLAKLNKELASSEONKNHINNELKRKEEQLSSYEDKLFDVCGSQDFESDLDRLKEEIEKSSKGRAMLAGATAVYSQFITGITDENGSCCPVCGRVFQTEAELQEVISDLOSKLRL-APDKLKSTESELKKKEKRRDEMLG ScRAD50 IAINNKKMHELDRRYTNALYNLNTIEKDLODNGKSKEKVIQLLSENLPECTIDEYNDVLEETELSYKTALENLKMHQTTLEFNRKALEIAERDSCCYLCSRKFENSFKSKLLQELKKKEKRDVONEKEYLHSIRLLEK ruler610620630640650
PpRAD50 GOKCALAEKEVVKVDSRIHETSISLAKYGRDRDSKRKMLLGRLESILNLTVEITDFOVOLHEAVKAKENIKSTHDLCTGMKKMFDPFEKOARNIHACPCCERGFTPEEE-DEFVRKGRINASS-YTDKLRESAAKAQEAEVKVOOLDK AtRAD50 SIKSREAEKEVNMLGMKIQEVNNSLFKHNKDTESRKRYIESKLGALKQESVTIDATPKLLESAKDKRDDKKEYNMANGMRMFEPFEKRARQEHSCPCCERSFTADEE-ASFIKKORVKASS-TGEHLKALAVESSNADSVFOOLDK HøRAD50 RDRLAKLNKELASSEONKNHINNELKKKEEQISSYEDKLFDVCGSQDFESDLDRLKEEIEKSSKORAMLAGATAVNSQFITDITDENGSCCPVCORVFQTEAELQEVISDLOSKLRL-APDKLKSTESELKKKEKRRDEMLG SCRAD50 IAINNKKHELDRRYTNALYNLNTIEKDLODNGKSKEKVIQLLSENLPEDCTIDEYNDVLEETELSYKTALENLKMEQTTLEFNRKALEIAERDSCVLCSRKFENESFKSKLLQELKTKTDANPEKTLKDTVONEKEYLHSIRLEK ruler610620630640
PpRAD50 LRATHDDNQKLSNELIPAAEKNLDALRQEKARLTDAHEDMLGLLAHAEAEVDMVEKLRVPADRMTELYKDVENMKKQVADQEYKLDTRSQDTRTLADIAAEIRAVEEKRDDIYRRVEKMREEHAFLKDDLLTWVMKLHMAREEKAKAAB Atrad50 Lravferyskliteiiplaektigekterddiylgisagikadkusiealvoplenadrifoeivsyckoiedleykloprologyktmeeioselssloskuklhgeleklrddiymerdiscloarwhavreekakaan
H#RAD50 LVPMROSIIDLKEKEIPELRNKLONVNRDIORLKNDIE OETLLGTIMPEEESAKVCLTDVIIMERPOMELKDVERKIAOOAAKLOGIDLDR. TVOOVNOEKOEKUHKLDTVSSKIELNEKLIOOOAAKLOOOAAKLOGIDLDR. TVOOVNOEKOEKUHKLDTVSSKIELNEKLIOOOAAKLOOOAAKLOGIDLDR. TVOOVNOEKOEKUHKLDTVSSKIELNEKLIOOOAAKLOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLDTVSSKIELNEKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLDTVSSKIELNEKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLDTVSSKIELNEKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLDTVSSKIELNEKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIONOKUHKUNOEKOEKUHKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIOOOAAKLOOIDLDR. TVOOVNOEKOEKUHKLIONOKUHKUHKUNOIDLIKEKELTVSEILISTINELKEELINEKLIOIDUN KUUHKUHKUHKUHKUHKUHKUHKUHKUHKUHKUHKUHKUH
ATRAD50 LRDVTKAEEDLERLAEEKSOLDLDVKYLTEALGPLSKEKEOLLEDYNDMKIRRNQEYEELAEKKRNYQOEVEALLKASYKINEYHDLKKGERLDDIQEKQRLSDSOLQSCEARKNELAGELNRNKDLMRNODOLRRNIEDNLNYRTTKAK
HeRADSO LORROQLERGTVELSTEVQSLYREIKDARROVSPLETTLERFOORKEELINKKNTSNKIAODKLNDIKEKVKNIHGYMKDIENVIQDGKDJYKKQKETELNKVIAOLSECEKHKEKINEDMRLMRODIDTGKIGERWLQDNLTLEKKNEE ScRADSO LTGKONIDDSIRSKRENINDIDSRVKELEARIISLKNKKDEAGSVLDKVKNERDIGVRNKKKTVADINRLIGRPOTIVNEVVDFEAKG-FDELQTTIKELELNKAGMLELKEQLDLKSNEVNEEKRKLADSNNEEKNLKONLELINKKNTADINRLIGRPOTIVNEVVDFEAKG-FDELQTTIKELELNKAGMLELKEQLDLKSNEVNEEKRKLADSNNEEKNLKONLELINKKNTADINRLIGRPOTIVNEVVDFEAKG-FDELQTTIKELENKIAGMLELKEQLDLKSNEVNEEKRKLADSNNEEKNLKONLELINKKNTADINRLIGRPOTIVNEVVDFEAKG-FDELQTTIKELENKAGMLELKEQLDLKSNEVNEEKRKLADSNNEEKNLKONLELINKKNTADINRLIGRPOTIVNEVVDFEAKG-FDELQTTIKELENKAGMLELKEQLDLKSNEVNEEKRKLADSNNEEKNLKONLELINKKNTADINRLIGRPOTIVNEVVDFEAKG-FDELQTTIKELENKAGMLELKEQLDLKSNEVNEEKRKLADSNNEEKNLKONLELINKKNTADINRLIGRPOTIVNEVVDFEAKG-FDELQTTIKELENKAGMLELKEQLDLKSNEVNEEKRKLADSNNEEKNLKONLELINKNTONLIGT
Atradso VEELTREIESLEEQILNIGGIAAVEAEIVKILRERERILSELNRCRGTVSVYESSISKNRVELKQAQYKDIDKRHFDQLIQLKTEMANKULDRYYNALDKALMRFHTMKMEEINKIIRELWQQTYRGQDMDYIRIHSDSEGAG
H&RAD50 LKEVEEERKOHLKENG-OMOVLOMKSEHOKLEENIDNIKRNHNLALGROKGYEEEIIHFKKELREPOFRDAEEKYREMMIVMRTTELVNKDLDIYYKTLDOAIMKFHSMKMEEINKIIRDLWRSTYRGODIEYIEIRSDADENVSASDKI SCRAD50 LAHTESEISPLDVONA BAERDYVGERSLELETEERKIGENKOLONOTDSLTHOLE, TOYKDIEKNYHKEWVELOTESPUTDIIVYSKALDSATMKYHCLEMODINEITDELWKETYSGTDTDTIKTESDEVSSTUK
ruler106010701080109011001110112011301140115011601170118011801190120
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H&RAD50 ENYNYRVWLKGDTALDMRGRCSAGOKVLASLIIRLALAETFCLNCGIIALDEPTTNLDRENIESLAHALVEIIKSRSQORNFOLLVITHDEDFVELLGRSEYVEKFYRIKKNIDOCSEIVKCSVSSLGFNVH 1312
ScRAD50 KSYNYRVWYKQEVELDMRGRCSAGOKVLASIIIRLALSETFGANCGVIALDEPTTNLDEENIESLAKSLHNIINMRRHOKNFOLIVITHDEKFLGHMNAAAFTDHFFKVKRDDRGKSQIEWVDINRVTY 1312 ruler1210122012301240125012601270128012901300131013201320

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.

ZmNBS1	MVWVLDPVDTVRG1OKKYIFAAGTYKVGRKD-CDVIVQTDTSISRV	HABIAIEKMVAWDP	HSGAPASPSFVRVIDRSKYGTFVNKVHGI	QGSRLHK-DEDMMLTDGDAVTFGTGNATFRLSFV
OSNBS1	MVWALTPVDTVRGAQRCYIFAAGTYKVGRKD-CDVIVQTDTSISKV	HABI VVEKMVAWUP	QBGAPANPSYVRVVDRSKYGTFFNKVQGI	QGSRLHK-DEDAMLADGDIVIFGIGNATFRLSFV
AtNBS1	MVWGLFPVDPLSGEDKYYIFSKGIYKVGRKG-CDIIINKDKGVSRJ	HAELTFDATTVSTSRR	NKSSSDTSSFVIRVKUCSKYGTFVKTDLG	KDKVHELSNKEKILQDGDVIAFGIGSAIYRLELI
PpNBS1	MVWALRAVDPGHVPSSYYLKSATTYSVGRKG-CYITIQTDKTISRI	HANLITE BAKAPKT - D	VNDAANVPRMPLKVHDLSKFGTFVNKHPG	K-PLNSVPLCEAPLNDGDLITFGINKTSFRVEFI
HsNBS1	-MWKLLPAAGPAGGBPYRLLTGVEYVVGRKN-CAILIENDQSISRN	HAVLTANFSVINLS	QTDEIPVLTLKDNSKYGTFVNEEKMQ	NGFSRTLKSGDGITFGVFGSKFRIEYE
ScXRS2	-MWVVRYQNTLEDGSISFISCCLQAFKTYSIGRSSKNPLIIKNDKSISRQ	HITFKWEINNSSDLKHSSLCLVNKGKLTS	LNKKFMKVGETFTINASDVLKSTIIELGTTPIRIEFE	WINEVWNIPPHLIQFRTMLSEYGISTEISINDIP
ruler	110	0	0	.120130140150
			2	10 . 27
ZmNBS1	PIVVFFHGA-KETRIDPSLHAVMKEIGAYATKKWENECTHVLVDGSCSLT	PELLDAVMAKKQIMLGDWF	EAMAEKN-IHTEIPSCIQYIPNLTLDGMVIKMV	DINLIONFLEGYTFILGSSDKYQFGEK
OSNB51	PIVVFFHGK-KSGRISPCLQAVMISIGATATRKWSDECTHVLVDESCSLT	PELLDAVLAKKQIVLGUWF	KVMAEKN-IHTEMPSSTQTIPKLTLDGMEIQVV	EIKLIESCLAGITFILGSSEKIKFGDK
AtNBS1	PLVFILCPSBETFKVDQPVQDAVBBIGARIBPILBEECTHVLLEPRMQVN	EALINAILAKKIIILTNWV	MLLAERS-ICSEIPGISQIRPSVMVEEALVDVL	BENVREKCLEGFTFVLEPIDTIRFGCS
PpNBS1	PFFLCLSGP LLERENPT ITFALRHGAYAVELWKEGCTHVLVDEGSAVT	KMVIAAVAFSKPVLQVDWW	QKFSLETKAVTELPPYSSYLPTLVPQGTASSIPVKLG	LPEFROSILODYTFFLVPLDAYEYGDY
HsNBS1	PLVACSSCL DVSGKTALNQAILQLGGFTVNNWTEECTHLVMVS-VKVT	IKTICALICGRPIVKPEYF	TEPLKAVESKKCPPQIESFYPPLDEPSICS-KNVDLS	GRQERKQIFKGKTFIFLNAKQHKKLSSAVVFGGG
SCARS2	ANLMISDYPKSEDNSIRELYALVSTIPMKKSRFLMELCNTLLPTSKTNLK	FUEMWNDMISNPEYNVFUFUPNILLSKFM	RENNIRVETTIKSEPRESSEERTFNINEFAFDNIDSE	YKYVDSLEASTEYLILTTIDKKENGKILCTIKTM
ruler	160170180190200		0	.270
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ZmNBS1	LHGLLESTGAKYVHIDDFCANSQDSAAGDTDHQILVV	PARYPLEFSKIR-VLFILSKISD	IKLFAAILSGRLEATSIEPPAFIVTSSNS	TDATIVADS
OsNBS1	LHALLESTGAKYLHVDEFCANSQDSGAGENDKDILLV	PAKSPLEFSKIR-GLFPLSKITD	VKLFAAILSCHLEATAIEPPAYIVASSNS	TDETIVVDS
AtNBS1	FPSLLEVCGAETVTIEDISSMSQDSOFGEINRMICVI	PKSAGDKFGRFK-HLSLLSRVNE	MDLVCAVFSGNLPSTSLIPPSVVISSSCS	TDETVVADS
PpNBS1	LIRLERSSGGTVELISNTSSTVSKGTREQLVVKPRDG	TFKEGWPSSAFLNNVRHLPRTSE	DKLVLAVLAGNVGVTSLHFPPSPVASADS	DETKEESDGDEVGDSADTLSFKDFIPTLPSSPPK
HsNBS1	EARLITEENEEEHNFFLAPGTCVVDTGITNSOTLIPDCQKKWIQSIMDML	QRQGLRPIPEAEIGLAVIFMTTKNYCDPQ	GHPSTGLKTTTPGPSLSQGVSVDEKLMPSAPVNTTTY	VADTESEQADTWOLSERPKEIKVSKMEQKFRMLS
ScXRS2	LTSIIDGTLSAVINMKGASSRTLDNGKFDOISEGMSTI	LKTSRAPEVEASPVVSKKRKLNRRR-VLP	LDSLDFFAGGLSTKTLSENRSLTDAKRLNCGAESKTV	ISSPNIABADEKHAPFLONALKPT EDIGKKSCHS
ruler			0	.420
ZmNBS1		DVEMETATSNPTGAANKSOHHTENISD	DEKOTTNIT NEVARKGNVIHPKHPESVE	DLKPMEEDVKVIEKTATYRSTGRD-ED
OsNBS1		DVEIDTATSDHTVAASKSEHHIEHISD	DKKEVVAISEEDAVNLVEAKTSINLHSDOEKDE	IVKPMEEDVKVIEKTATMRGFKVEGED
AtNBS1			AETPEKPAAIVIEDSPVTIL	EETSNLNEFKSVNLLADTESRGHMDEK
PpNBS1	AGMOPVGISAHIS IKLDEDDSPIVOYMRTSKRSROHD	DYNAEPDGNTEVPDENNEKROKTTHOECV	LETPGSDYSODYKPFLHPKKPSKAASSDOTTKERKRA	TMTIDKFFSOPEANRAKKLHFTPEISGGKIDKEL
HsNBS1	ODAPTVKESCKTSSNNNSMVSNTLAKMRIPNYOLSPTKLPSI-NKSKDRA	SCOODTNSIRNYFOPSIKKRERDEENOEM	SSCKSARIETSCSLLECTOPATPSLWKNKEOHLSENE	PVDTNSDNNLFTDTDLKSIVKNSASKSHAAEKLR
ScXRS2	SPGAIIVSSPNLGTVNTSEDSLDKSLOSHKLPOPSLPEVAGIGSOTISSN	SADYETAAVNSMDDAEVTKNFRVNHHONI	EOPSKNIRKLSNYSREISSPLOENCKSPVKELSIKEK	SGTPHAFVEAIOETKNREVKRVKSTIVELKDEEL
ruler			0	
				···*
ZmNBS1	ARIL	<mark>S</mark> KAPKDEKLDT	SRDGASDVIFSQNLVVRRSLPQSAPAAPAEIGGVN	FKRFR
OsNBS1	IPVM	TKVPKDETLD-	SRDETCHVIYTCNLVVK-SILQSARAESIETGGIN	FKRFR
AtNBS1	NSSD	SVTIRRDRNDE	AETGKSEIIYTCDLIVRDLRSTRKVQSTGGEGVVD	FKRFR
PpNBS1	TSRNGBLPFV	GSSAKEPEVEIKPMAASASKKPPRLNEDL	SEAAEPLIVYSCLVVRKNAEIVSFPTTPTRGSGPN	FKRFK
HsNBS1	SNKKREMDDVAIEDEVLEQLFKDIKPELEID	VKVQKQEEDVNVRKRPRMDIETNDTFSDE	AVPESSKISQENEIGKKRELKEDSLWSAKEISNNDKL	QDDSEMLPKKLLLTEFR
ScXRS2	SEEAINQLKNLAIVEPSNNLLRKSPDSEGNKTSRTTEKWENSLMEPEWHK	(RKNFKTFVKVRPKSKAHKEEGKNNTQSSD	FIRNAAF LIT RNY <mark>VPLKK</mark> YSKKDT <mark>T</mark> TK WG TEENE D MF	ALTEMERFGSNTFMSDNINSNTIQKRSQALNEFT
ruler			0	.720730740750
Z - NID C 1		DO COMO DAD DE COMO A TA DET DUE	CHERNAN CONTENT TROUP	557
2mmBS1		NGOT MID PAREBARY PROMENTA POT PARA	SARAAAGSSIA ILLIGAR	557
A+MDC1		CUDUTO DAV DEVE DE ALASULFINA		50V
DeMBCI		TODDYND PHOPPODD PROPERTADDLE ATE	ANA AUTO PILOT DO	- 514
PPNBSI		TOODI TAUUADENTOI DENT DE PUDUON		754
Sovper	NDRCCNDA DDRA DA	NUDPHNENI PUUPPMNI PDNI CEBOCYOCI		054
SCARS2	NEWSORDA PENAL BLAKCACINA ANAL ANAL ANAL ANAL ANAL ANAL ANAL A	ADALDARADE VVALMALAPALSECSKOS	AND A DRANG DE GAR ANGUGUDUDUD GPKFT FKKK	10 DT
ruier	/00//0/80/90		0	

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. Molecular analysis of $\textit{mre11} \Delta$ and $\textit{rad50} \Delta$ 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 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. 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	orientatio n	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	1 st selection	2 nd selection	3 rd selection
RAD50/apt	77	14	4 (5%)
rad50/apt	113	27	11 (10%)

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∆	2200000	0	< 0.5
nbs1KO	2640000	0	< 0.4
msh2 Δ	2110000	78	37

Supplemental Table 3. Spontaneous mutation rate in mutant lines

^a Differences were compared using Fisher's exact test.