

## Supplement figure I

## ClustalX1.8 alignment of the 120 amino acids from the N-terminal sequences of cohesins from the RAD21/REC8 family

21mou	1	--MFYAHFVLSKRGPLAKIWLAAHW-D
21hum	1	--MFYAHFVLSKRGPLAKIWLAAHW-D
COH2	1	--MFYAQFVLAKKGPLAKWLAHW-E
COH1	1	MCHPIEFCICTISDASAHTSSRTSFCTPSTSIVSPSFPICIAAKCSRGCVAAMFYADRVLSKKGPLSKWVLAHW-E
21Ar3	1	--MFYSQFTLAKKGPLGTIWIAAHL-E
21oryzKaa	1	--MFYSQFTLAKKGPLGTIWIAAHL-E
21oryz3	1	--MFYSQFTLARKSPLGTWVIAAHL-E
21Ar2	1	--MFYSQFTLARKGPLGTWCAAHV-H
21Ar1	1	--MFYSQCLVSRKGPLCAIWVAAFY-F
21oryz4	1	--MFYSQCLLARKAPLGOIWMAATL-H
8Ar	1	--MFYSQCLLARKAPLGOIWMAATL-H
8hum	1	--MFYYPNVIQRHTGCFATIWLAASTR-G
8mou	1	--MFYYPNVIQRHTGCFATIWLAASTR-G
21oryz2	1	--MSCSKVILSKKGVLGTVWAAYSGV
CeIREC8	1	--MVVSABEVIRKDAVFHVAILGTGDS
COH3	1	--MYRSKRRRKRLGIWFGSHKKLG
21mou	25	KKLTKAHVFECNLLESSVESII-----PKVK-MALRTSGHLLLGVVRVYHRKAKYLLADCNEAFIKIKMAFRP
21hum	25	KKLTKAHVFECNLLESSVESII-----PKVK-MALRTSGHLLLGVVRVYHRKAKYLLADCNEAFIKIKMAFRP
COH2	25	KKLTKAQIFETDVVPQAIEEVIR-----PKVK-MALRTVGHLLLGVVRVYIYSKKTRYLLADTNNEAYQKMKINFRN
COH1	80	KKLSKAQIFETDVDEAVNEIMQ-----PSOK-LALRTGHLLLGICR-----
21Ar3	25	RKLRKNQVADTDIGVSVDSILF-----PEAP-IALRLSSHLLLGVVRIYSRKVNLYFDDCSEALLKVKQAFRS
21oryzKaa	25	RKLRKNQVADTDIGVSVDSIIF-----PEPV-IALRLSSHMLGVVRVYIYSRKVNLYFHDCSEALLKIKQAFRS
21oryz3	25	RKIKKPQIDGIDTPSYAEFIMF-----PEPV-IALRLSGHLLLGVVRVYIYSRKVNLYFHDCSEALLKIKQAFRS
21Ar2	25	QELKKKSQYTSINIPDTVDNIMF-----PEPV-LALRTSSHLLGVVRVYIYSRKVNLYNDWNLLNTWAKAFVS
21Ar1	25	KKLKKSQVKATHTPSSVQDILQ-----KEIDALTYRVLAYLLLGVVRIYSKKVDYLYNDWNLLNTWAKAFVS
21oryz4	25	SKENRKRLDKLDIPIKICEEILN-----PSVP-MALRLSGILMGGVAIVYERKVKALYDDVSRFELBINEAWRV
8Ar	25	AKINRKKLDKLDIPIKICEEILN-----PSVP-MALRLSGILMGGVVIVYERKVKLLFDDVNRFLEVINGAWRT
8hum	26	SRLVKREYLRLNVNVKTCEEILNYVLVRVQPPQPGPGLPFRFSLYLSAQIQLGIVIRVYSQQCQYLVVEDIQHILEHLHRAQLQ
8mou	26	SRLVKREYLNVNVKTCEEILNYEQVRVQPPVAGLPRPRFSLYLSAQIQLGIVIRVYFQQCQYLVVEDIQHILEHLHRAQLR
21oryz2	26	AALSRDQVVRTNVACVDKILP-----DDNDKTTYRVLGHLGGIVVRVYIYSKKVEYLCHECNELLGSYSAHCN
CeIREC8	26	KKLSSRREILDQNIPELCHSIEMVERH-----GSATKTGLYLLSLITYCTVLIHOVQVDELKRDVEKLKELMKKKSF
COH3	23	LQSNRRECFRDVLQASKLIQWILSN-----ERKNRRSLSIACNLVYGNТИVLSQVARILQDAIRAREIVAFTSYL
21mou	92	GVVDLPEENREAAYNAITLPEEFHDFDQP---
21hum	92	GVVDLPEENREAAYNAITLPEEFHDFDQP---
COH2	92	-GFSFEVDIPENAEIEEDFSNFIDKYNITV--
COH1	-----	
21Ar3	92	AAVDLPPEESTAP---YHSITTPETFDLDDFE
21oryzKaa	92	TAVDLPPEESTAP---YHSITTPETFDLDDFE
21oryz3	92	VQVDLPLHADHAP---FDTITPDTFHLDDDF
21Ar2	92	TQVNLPEDARQAP---PESVTIPOALNLDEFD
21Ar1	93	ERNREKTGVSLPASIE-CFSIAPPERFEL---
21oryz4	92	KFVADPTVLPKGKTQAKYEAVTLPENIMD---
8Ar	92	KSPVDPTEPLLPEKTHARKEAVTLPENEEA---
8hum	106	IRIDMET-ELPSLLLP-----
8mou	106	IRIDMEEADLPSLLL-----
21oryz2	94	ELS IPTGGATNRVSKQAKKPVRARRLV-----
CeIREC8	101	LLMAERFDRNQELQRKEDKF-----
COH3	95	AEEDERKRKTREQMEGDNNSKTPKKR-----

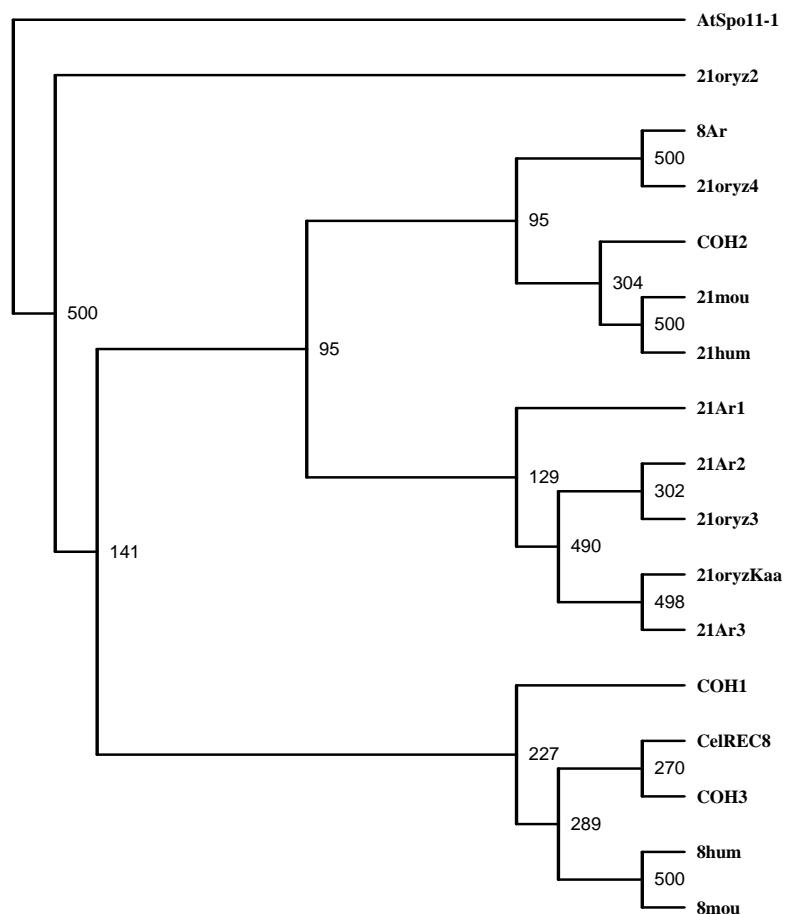
## Supplement figure II

ClustalX1.8 alignment of the 120 amino acids from the C-terminal sequences of cohesins from the RAD21/REC8 family

21Ar3	1	-----MENAHTGFLNVDDDEVDEDHEEDDIQYDDDETRLLENSGWSSRTRAVAKYLQTLFDK--ETENG-K
21Ar1	1	-----TSFEEHPSVYYVENDLDTILNDEQVNADERQDLQQETWSSRTRNVAKFLEKTFLE--QREREEE
21Ar2	1	-----LGLSPVSERTDEELYLEVGGNSPVGTPASQDSAALTGRARALAQYLKQRSSSSPTSSHPS
21oryzKaa	1	-----SAIQGVDTDFLMD-EVDCDEANDEPNPEFQSLDNSGWSSRTRGVARYLKTLFDE--ESGLG-R
21oryz4	1	-----PVVEEFPFEQELRDFKMRRLSDVGPTPD--ILEEIEPTQTPYEKKSNPIDQVTQSIIHSYLLKFDT--PGA---S
COH1	1	-----VPQRNPLSPFAPMVEDEEMSPSEKRKKRDEKEEPEPETDEDNRWSKRTTHALLQNIATK--LENQN-G
21oryz2	1	-----KNPQLDHALDADIDSMEEDTHMDEQHARDEGLLRSTRTRTVARYFHQLLVQ--QKCQQRN
21oryz3	1	DMSYMPGQDSDPQVSPFPFNDELGDLP-----IPSLMSTPGVISTAGTGTGLGMSARTRAVAYQFKDQMAS--ATSDDQP
COH2	1	-----LEAYGFGNSTYKEDGKWAKRAKHILKKVSADIETSGQADFSSVTATAKRNKOAAEQFYSSLTLAKSQ
COH3	1	-----NVNPISPKFQMEEPADFEDNWNSKPTWSNTSENIA达尔TRGNTIRQLDD---KSPFE
21mou	1	-----ICQLIPELELLPEKEKEKEKEEEEEEDEDASGGDQDQEERRWNKRTQQMLHGLQRA--LAKTG-A
21hum	1	-----ICQLIPELELLPEKEKEKEKEEDDEEEEEEDEDASGGDQDQEERRWNKRTQQMLHGLQRA--LAKTG-A
8Ar	1	-----AERPWEHREYEFESMLPKRFTADKELFETASTQTQKPVCNQSEDEMTDSIKSHLKTHFET--PGA---P
8hum	1	-----KSRSISSLIPPERWAWPEVDAPEAPALPVVEELPEVPMEMPLVLPPPELELLSLEAVHRAVALEL--QAN---R
8mou	1	--EAAEDEKSRTSLIPP-EWWAWSEEGQPEPPALPMLPELPEVPMEMPPRPE---LSSEAVALRAVALKL--QAN---K
CelREC8	1	-----SSLGVQFMRTDDLEEDTRRNRI-----FEDDEERTRDAREDELFFYSSGSLLPNNRNIHIKELLNEAEARYP
21Ar3	64	NVLVADKLLACKTRKEASRMFFETLVLKTRDYIQLVEQGKPYYESIIIIKPRPKLTKSIF-----
21Ar1	65	EKVSLQLCRGRTOKEASRLFYETLVLKTKGYVEVKONHPYSDVFLMRVSRPKAC-----
21Ar2	63	GDLISLSEIILACKTRKLAARMFEETLVLKSRGLIDMQODRPYGDIALKLMPALFSKVQT-----
21oryzKaa	64	KSVIAIDHLLSCKTRKEASRMFFETLVLITIKDFISVDPNSFDFVSKKGKLLKSDF-----
21oryz4	69	QSESLSQLAHGMMTTAKAARLFYQACVIALTHDFIKVNOLEPYGDILISRGPKM-----
COH1	64	QVELDEMILKKGTSRKVAAAKFYSLLCLKKNQCIDIIEKEPYGDIMIKAGENININTI-----
21oryz2	59	NSVCLGQALEGTTKRTKSARFFYETLILKSGSLIEVNOEQTYGDIVSATPRLEAALRSSEKQ--
21oryz3	79	GKFILNRILEGRHRKQAARMFFETLVLKSYDYIDVECEAYG-----
COH2	70	AISVDQSEPYGEIVIRPGANFKEACFLSSPKPMGLGNTMENSTMRTPMRFV-----
COH3	57	VIIIDSMIPVAAITSRREAARTFYTVIELLKERKIKATQRAPYENIDILLLSTDSEDIDDLAMADF
21mou	66	ESISLLELCRNTNMRKQAAAKFYSLVLLKKQQAIETIQLQEEPYSDIIATPGPRFHII-----
21hum	66	ESISLLELCRNTNMRKQAAAKFYSLVLLKKQQAIETIQLQEEPYSDIIATPGPRFHII-----
8Ar	69	QVESLNKLAVGMDRNAAAAKLFFQSCVLAATRGVIKVNAEPPYGDILIARGPNM-----
8hum	68	EPDFSSLVSPPLSPRMAARVFYLLLVLSAQQILHVKEKPYGRLLIQPGPRFH-----
8mou	68	ELDFSSLVPPPLSPRKLASRVFYLLLVLSHQKILLVBPQKPYGPLLIRPGPKFP-----
CelREC8	67	EWVNNEFTADHDRKKAATAFEGLLISLKNMKVEAKQEDPYFPIILVRHISHEEM-----

### Supplement figure III

Cladogram of the alignment of the 120 amino acids from the N- terminal sequences of cohesins from the RAD21/REC8 family



## Supplement IV

Number of emerging and fully expanded true leaves in seedlings (Col-0 and *atrad21.1*) 14 (or 15 days) after 100Gy or mock seed irradiation.

4 independent replicates were done. The numbers of true leaves (TL) represented by 3 or more seedlings are highlighted in grey cells.

a) Tables - number of true leaves formed 14 days after seed irradiation.

Replica 1

0 Gy		100 Gy	
w.t. Columbia	<i>atrad21.1</i>	w.t. Columbia	<i>atrad21.1</i>
0 TL - 0 plants	0 TL - 0 plants	0 TL - 4 plants	0 TL - 8 plants
1 TL - 0 plants	1 TL - 0 plants	1 TL - 7 plants	1 TL - 10 plants
2 TL - 1 plant	2 TL - 0 plants	2 TL - 6 plants	2 TL - 11 plants
3 TL - 0 plants	3 TL - 1 plant	3 TL - 5 plants	3 TL - 6 plants
4 TL - 6 plants	4 TL - 1 plant	4 TL - 7 plants	4 TL - 1 plant
5 TL - 7 plants	5 TL - 21 plants	5 TL - 6 plants	5 TL - 0 plants
6 TL - 12 plants	6 TL - 13 plants	6 TL - 1 plant	6 TL - 0 plants
7 TL - 0 plants	7 TL - 5 plants	7 TL - 0 plants	7 TL - 0 plants
8 TL - 0 plants	8 TL - 2 plants	8 TL - 0 plants	8 TL - 0 plants
26/34 seeds germinated	43/44 seeds germinated	36/44 seeds germinated	36/36 seeds germinated
Average number of true leaves: <b>5,115385</b>	Average number of true leaves: <b>5,604651</b>	Average number of true leaves: <b>2,722222</b>	Average number of true leaves: <b>1,5</b>
Stdev: <b>1,032547</b>	Stdev: <b>0,979298</b>	Stdev: <b>1,750283</b>	Stdev: <b>1,108409</b>

Replica 2

0 Gy		100 Gy	
w.t. Columbia	<i>atrad21.1</i>	w.t. Columbia	<i>atrad21.1</i>
0 TL - 0 plants	0 TL - 0 plants	0 TL - 0 plants	0 TL - 16 plants
1 TL - 0 plants	1 TL - 0 plants	1 TL - 0 plants	1 TL - 10 plants
2 TL - 0 plants	2 TL - 0 plants	2 TL - 6 plants	2 TL - 4 plants
3 TL - 1 plant	3 TL - 0 plants	3 TL - 11 plants	3 TL - 0 plants
4 TL - 7 plants	4 TL - 7 plants	4 TL - 6 plants	4 TL - 0 plants
5 TL - 13 plants	5 TL - 17 plants	5 TL - 4 plants	5 TL - 0 plants
6 TL - 7 plants	6 TL - 4 plants	6 TL - 6 plants	6 TL - 0 plants
7 TL - 4 plants	7 TL - 3 plants	7 TL - 5 plants	7 TL - 0 plants
8 TL - 3 plants	8 TL - 1 plant	8 TL - 0 plants	8 TL - 0 plants
9 TL - 1 plant	9 TL - 0 plants	9 TL - 0 plants	9 TL - 0 plants
36/36 seeds germinated	32/32 seeds germinated	38/38 seeds germinated	30/30 seeds germinated
Average number of true leaves: <b>5,527778</b>	Average number of true leaves: <b>5,1875</b>	Average number of true leaves: <b>4,210526</b>	Average number of true leaves: <b>0,6</b>
Stdev: 1,38329	Stdev: <b>0,997982</b>	Stdev: <b>1,695111</b>	Stdev: <b>0,723974</b>

b) Tables (number of true leaves (TL) 15 days after seed irradiation)

Replica 3

0 Gy		100 Gy	
w.t. Columbia	<i>atrad21.1</i>	w.t. Columbia	<i>atrad21.1</i>
0 TL - 0 plants	0 TL - 0 plants	0 TL - 1 plants	0 TL - 8 plants
1 TL - 0 plants	1 TL - 0 plants	1 TL - 3 plants	1 TL - 10 plants
2 TL - 1 plant	2 TL - 0 plants	2 TL - 9 plants	2 TL - 7 plants
3 TL - 0 plants	3 TL - 0 plant	3 TL - 10 plants	3 TL - 1 plants
4 TL - 0 plants	4 TL - 0 plant	4 TL - 4 plants	4 TL - 0 plant
5 TL - 11 plants	5 TL - 15 plants	5 TL - 4 plants	5 TL - 0 plants
6 TL - 7 plants	6 TL - 7 plants	6 TL - 2 plant	6 TL - 0 plants
7 TL - 5 plants	7 TL - 1 plants	7 TL - 0 plants	7 TL - 0 plants
8 TL - 4 plants	8 TL - 1 plants	8 TL - 0 plants	8 TL - 0 plants
9 TL - 2 plants	9 TL - 1 plants	9 TL - 0 plants	9 TL - 0 plants
30/30 seeds germinated	25/25 seeds germinated	33/34 seeds germinated	26/27 seeds germinated
Average number of true leaves: <b>6,133333</b>	Average number of true leaves: <b>5,64</b>	Average number of true leaves: <b>3</b>	Average number of true leaves: <b>1,038462</b>
Stdev: <b>1,502488</b>	Stdev: <b>1,036018</b>	Stdev: <b>1,457738</b>	Stdev: <b>0,870897</b>

Replica 4

0 Gy		100 Gy	
w.t. Columbia	<i>atrad21.1</i>	w.t. Columbia	<i>atrad21.1</i>
0 TL - 0 plants	0 TL - 0 plants	0 TL - 1 plants	0 TL - 4 plants
1 TL - 0 plants	1 TL - 0 plants	1 TL - 1 plants	1 TL - 12 plants
2 TL - 0 plant	2 TL - 0 plants	2 TL - 4 plants	2 TL - 8 plants
3 TL - 0 plants	3 TL - 1 plant	3 TL - 5 plants	3 TL - 1 plants
4 TL - 1 plants	4 TL - 4 plant	4 TL - 8 plants	4 TL - 1 plant
5 TL - 8 plants	5 TL - 11 plants	5 TL - 5 plants	5 TL - 1 plants
6 TL - 8 plants	6 TL - 5 plants	6 TL - 5 plant	6 TL - 0 plants
7 TL - 3 plants	7 TL - 1 plants	7 TL - 0 plants	7 TL - 1 plants
8 TL - 0 plants	8 TL - 4 plants	8 TL - 2 plants	8 TL - 0 plants
9 TL - 1 plants	9 TL - 0 plants	9 TL - 0 plants	9 TL - 0 plants
21/24 seeds germinated	26/26 seeds germinated	31/33 seeds germinated	28/28 seeds germinated
Average number of true leaves: <b>5,809524</b>	Average number of true leaves: <b>5,5</b>	Average number of true leaves: <b>4,096774</b>	Average number of true leaves: <b>1,678571</b>
Stdev: <b>1,077917</b>	Stdev: <b>1,363818</b>	Stdev: <b>1,850312</b>	Stdev: <b>1,540889</b>

## **Supplementary figures I, II and III**

### **Alignment of the sequences of proteins of the RAD21/REC8 protein family.**

The conserved domains in the N-terminal and the C-terminal end of RAD21/REC8 proteins are shown in supplementary figures I and II respectively.

Alignments were generated using the following sequences - **21ORYZKAA-** (*Oryza sativa* RAD21 homologue (Rh)), accession number (a.n.) AAP79440; **21ORYZ2-** (*Oryza sativa* Rh), a.n. AAQ75093; **21ORYZ3-** (*Oryza sativa* Rh), a.n. AAQ75094; **21AR3-** *AtRAD21.3* (*Arabidopsis thaliana* Rh), a.n. AAL62060; **21AR2-** *AtRAD21.2* (*Arabidopsis thaliana* Rh), a.n. AAL62059; **21AR1-** *AtRAD21.1* (*Arabidopsis thaliana* Rh), a.n. AAL62057; **21HUM-hRAD21** (*Homo sapiens sapiens* Rh), a.n. CAA66940; **COH2-** celRAD21 (second *Caenorhabditis elegans* Rh), a.n. NP\_494836; **COH1-** celRAD21 (*Caenorhabditis elegans* Rh), a.n. NP\_509262; **8AR-** *DIF1/SYN-1* (*Arabidopsis thaliana* REC8 homologue (Rech)), a.n. CAB64643; **21ORYZ4-** (*Oryza sativa* Rech), a.n. AAQ75095; **8HUM-** *hREC8* (*Homo sapiens sapiens* Rech), a.n. AAD01193; **CELREC8-** celREC8 (*Caenorhabditis elegans* Rech), a.n. NP\_502565; **COH3-** celRAD21 (third *Caenorhabditis elegans* Rh), a.n. NP\_506583; **8MOU-** *mREC8* (*Mus musculus* Rech), a.n. NP\_064386; **21MOU-mHRD21** (*Mus musculus* Rh), a.n. CAA66939; **ATSP011-1** *AtSPO11.1* (*Arabidopsis thaliana* SPO11 homolog), a.n. AAK21002. ClustalX1.8 alignment parameters for both the first (N-terminal) and last (C-terminal) 120 protein a.a : Pairwise alignment parameters: gap opening penalty: 35.00, gap extension penalty: 0.75, Protein weight matrix:gonnet 250; Multiple alignment parameters:

gap opening penalty: 20.00, gap extension penalty: 0.30, Protein weight matrix:gonnet series, delay divergent sequences: 30%. Boxshade display.

The corresponding phylogenetic tree generated from the N-terminal sequence alignments is shown in supplementary figure III. Phylip tree construction: using only the N terminal 120 a.a. alignment mentioned above, protein-parsimony rooted tree (Atspo11-1), and seqboot (500), standard settings, Phylip. Numbers represent the number of tree out of 500 where the group of proteins on the right was grouped together.

#### **Supplementary figure IV**

#### **Tables of number of true leaves (TL) on seedlings of irradiated and non-irradiated seeds.**

Number of emerging and fully expanded true leaves (TL) were counted on seedlings grown from irradiated (100 Gy) and non-irradiated (0 Gy) seeds of wild type Columbia-0 and *atrad21.1* mutant plants. Data shown are representative samples from the four independent replicate treatments. A developmental delay is obvious in the *atrad21.1* mutants two weeks after seeds irradiation at 100 Gy; while few *atrad21.1* plants have a high number of true leaves (expanded or emerging), a much higher number of *atrad21.1* plants have little or no true leaves, compared to wild type Columbia-0 plants.