Ulrich and Takahashi – Supplementary Figure 1

a

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        Rad18:                                         RING
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Sc      -MD---------HQITTASDFTTTSIPSLYQLDTLLRCHICKDFLKVPVLTP-CGHTFCSLCIRTHLNNQPN-CPLCLFEFRESLLRSEF          78
Nc      -MN---------QLALNTKDFKTTKIPKLQEIDTLLRCHICKDFLKVPVLTP-CSHTFCSLCIREYLKDNSK-CPLCLNELRESMLRSEF          78
Cg      -MD----------VLTSAADFKKSKVPQLQELDDLLRCHICKDFLKNPVLTP-CGHTFCSLCIRGYLSNEPK-CPLCLHELRESMLRSEY          77
Tp      -MN---------NSVSDPTDYAKSSIPKLSQLDSLLRCHICKNFLKNPVLTP-CSHTFCSICMRLYLSKEAK-CPLCLKEVRESMLRSEY          78
Zr      -MN---------YNVSDATDFSHTSIPQLSQLDTLVRCHICKDLLKIPVLTP-CSHTFCSLCIREYLTREPK-CPLCLSELRESNLRSEF          78
Lt      -MSRLPKLSEQIQDVSDPRDFLRTKLPELVDLDTLLRCHICKGFIKTPVLTP-CGHTFCSLCIREYLNRELK-CPLCLAELRESMLRSEF          87
Kl      -MKLSVP-----ETISNPRDFLHTSVPQLTDLDSLLRCHICKDFLKASVLTP-CGHSFCSICIRKYLQKESK-CPLCLSDLTESMLQKEF          82
Ag      -MSIQPG-----QVVTDPSDFAGTTIPELADLDSLLRCHICKDMLQTPVLTQ-CGHTFCSLCIREYLNKESR-CPLCLAELRQNMLQKEF          82
Ec      MTTAKLD-----AEVSNPSDFQGTLIPEIADIDSLLRCHICKEFLQTPVLGH-CGHTFCSLCIRTYLNKEAR-CPLCLVELRQNMLQKEF          83
Dh      -MNSNPF-TKNLQNVTDPSDWEPTKLPNLKELDSLQRCYICKEFLKAPVITS-CNHTFCSHCIREYLIVNSH-CPLCKAEQFESNLKRVI          86
Mg      -MD-NPF-ANNLQNVTDPSDFKSTKMPKLTELDALQRCFICKEFMKAPMTTS-CNHTFCSHCIREYLVVNSS-CPLCKTEQFESNLKKVI          85
Ca      -MN--------LKDITDPSDFKTTKLPALAELDILKRCYICKDLLNAPVRTQ-CDHTYCSQCIREFLLRDNR-CPLCKTEVFESGLKRDP          79
Yl      -MN---------SDIPDPSDWIDSKLSGLKDVDETLRCHICKEFFTAPMITG-CGHTFCSLCIQRYLTNTSQRCPTCMQEQQISQLRKNV          79
Sp      -MN--------ELDATDPSDWNQTKIPSLKGLDSSLRCLICHEYFRAPLITS-CSHTFCSFCIRDYLREHPM-CPACRAPEQESRLRKNT          79
Xt      ------------MATTPEPGSKAKGKQPVQDLDDLLRCAICFDYYNIAVIIPQCSHNYCSLCIRKFLSYKTQ-CPTCCVAVAEPDLRNNR          77
Gg      -----------MALALPEP-PWPASLTPLKAVDDLLRCGICFDYFSIAVIIPQCSHNYCSLCIRKFLSYKTQ-CPTCCVAVSESDLKNNR          77
Hs      ------------MDSLAES-RWPPGLAVMKTIDDLLRCGICFEYFNIAMIIPQCSHNYCSLCIRKFLSYKTQ-CPTCCVTVTEPDLKNNR          76


Sc      LVSEIIQSYTSLRSSLLDALRIPKPTPVPENEEVPGP--ENSSWIELISESESDSVN---------AA---DDDLQIVATS---ERKL-A         150
Nc      LVNEIVQSYQSLRSDLLECLKI----------EPRS---TETSIIELESEPDDLEIKGSSKALFNIST---DDDLQIVGTN---ERP--R         147
Cg      LVNEITETYKAARQRLLDELNSLETNQDNSVIEVVSD--KEPSLLQIDDDVNENSN--------HITV---NDTSDIIDEDNEIQITG-T         153
Tp      LVNEIVGSYTNIRDELLANLKK---------QEARQDG-QDISIVEVESDSESLQVLD--------IE---EDTKQYISKQ---LSNQ-R         143
Zr      LVNEIIESYRSVRDELLESLKE----------DQRNN--AEKSLIELTD--D--------------DN---DDDLQIVGTN---QKEE-V         133
Lt      LVNEIIASYVGLRSKLLEIARSG--P-----DGTVPH--SDTSLIEIAPGDEGAH------EL---SG---DDDLQIIETR---RNRP-A         152
Kl      LVQEICSSYVKLRGSLQKHLT------------------------IS-SQ----EE----------EK---DNEIIISDEAD--TSVG-T         127
Ag      LVGELAACYMELRARLLETVR------------IPPK--KVAEVVQNNSP---IEL----------DS---DGEVEIIESCT--GAVPGS         140
Ec      LLGEIVASYSRIRGRMLENLDN-----------RHAK--RPAQQVAKSSASK-IEI----------IS---DDDIQILDSGQ--SSFD-M         143
Dh      LLEEIVLCFSKFRPILLELLKKE---------ESNEAYDKNRSPFSEIPSKDEDSRKR---------S---SPDQEVIEISS--DESNSL         153
Mg      LLEEIINCYVALRHDLLSVIGNE---------IS--------------P---ENEQK-----------------QEIIEVSD--EEP---         127
Ca      LLEEIVVSYASLRPHLLRLLEIEK-------VESKQEVDREKSANESASNGNRNVNND---------V---DETARVKDQSN--ADELGE         148
Yl      TVETLVEHFSAQRATILRVVK------------------------EAA-------------------K---QPIPEVVEPPSSPDLDDGR         123
Sp      ILEEILESFKVIRPTLFEFLK-------------VEN--VPKPVLQAP------------------------ETVIAQDSAS--GDEEWE         128
Xt      ILDDLVKTFISARQHLSKVVLDSPPMS-PQSNPSTSKIAKMQG--CTGKQVKQENIIMNRFLVKGNCSTPRTHSNTLQDETFLSQDSSYT         164
Gg      TLDELVKSFSSARQQLVQLVLDTPLISSPLACSRRSIGKNHSKTPASLPVVKEEVPVIDSFLKKENVCTL-TKTDGLAGTDWKVCKTEEH         166
Hs      ILDELVKSLNFARNHLLQFALESPAKS-PASSSSKNLAVKVYTPVASRQSLKQGSRLMDNFLIREMSG---STSELLIKENKSKFSPQKE         162

                                                      UBZ                      Srs2:
                                             ______________________
Sc      KR-S-MTDILPLSSKPSKR-----NFAMFRSERIKKKSKPNEQMAQCPICQQFYPLKALEKTHLDEC     210      ...KLNNGEIIVID      1174
Nc      KRLA-STTFIGKANKSNTYK-RPSSFQSVLKGSTDR--KNKQPQAQCPICQEAFPIQVLERSHLDEC     210      ...KTNKGEIIIID      1147
Cg      KR---TARTILNGSRPTKA----AKISDMFTTRKAK--T--EEKAPCPICSQLFPIRYLERTHLDEC     209      ...KLNDSDIIVID      1088
Tp      NRIN-NSHMTKKVTKKSND------IHSFLKSKSNDIMLKNSQLIECPVCSKMVPKQTLESLHLDKC     203      ...KGNNSEIIIID      1086
Zr      KRDK-NEKSVGKVTKPSTS----TGLNSLLNSQRDKS-KTKEKLAQCPICSNFYPIQALERTHLDEC     194      ...KMNDGEIIVID      1161
Lt      KR---NAEIVLMPSKKSRRDSEKPGISSMISKSKSP--ALPEDSAECPICQKHFPLEYLQRTHLDEC     214      ...DSDKDTVIVID      1190
Kl      KRGTPDSPSLSSVSTKKR---KHDGITTLLMKKKTDHPQRQEKKAQCPICSKHLPLSELEGSHIDEC     191      ...EEWDGEIIDLRSSQ   1064
Ag      KRGSPQVEEVEAAAKRQRT--KQNGIQYMLQKK----PKAVGEKVPCPICNRLYNKEFLERVHLDEC     201      ...PSINDEVIVLD      1131
Ec      KRSAPVTTEFEVISKRPRA--KKNGIQSLLSRK----SKIRDNTVECPICNKSFSKDFLERTHLDEC     204      ...PTISDEVIVLD      1185
Dh      EL---SEASNDVPKKKIKA-----EINSNSRN----AIPTRNEMVECPICAEVMSADLLQTQHIDYC     208      ...-----------       934
Mg      ------------PLKKHKN-----AA----------AIPTRDELVDCPICSRKMTAQVLQSRHIDEC     167      ...-----------       830
Ca      EK---GQAQHGEQVNEQTT-----EVISLLSDD---EENGSDSLVKCPICFERMELDVLQGKHIDDC     204      ...-----------       859
Yl      RR------SGRKRTRTNYT-------ETLVSSD-----D---IQVECPVCQAMLPGAAINRHLDNNC     169      ...-----------       820
Sp      DDLASNSSPASIAKKTSRD-----------SKK-----RKREDLVHCPACSNLVPHNQIN-QHLDSC     178      ...-----------       887
Xt      SANTSNIDLAGEAGSVMTETF--GTFSPSTSALAAPSSASKV-RVDCPVCGVSIPEQYIN-KHLDSC     227      /
Gg      HSSSSSSPEAGSKDNKAGSRE--CSEGTNSGEKPSTSVVKVVNKVDCPVCGVAIPEEYIN-KHLDSC     230      /
Hs      ASPAAKTKETRSVEEIAPDP----SEAKRP-EPPSTSTLKQVTKVDCPVCGVNIPESHIN-KHLDSC     223      /
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b

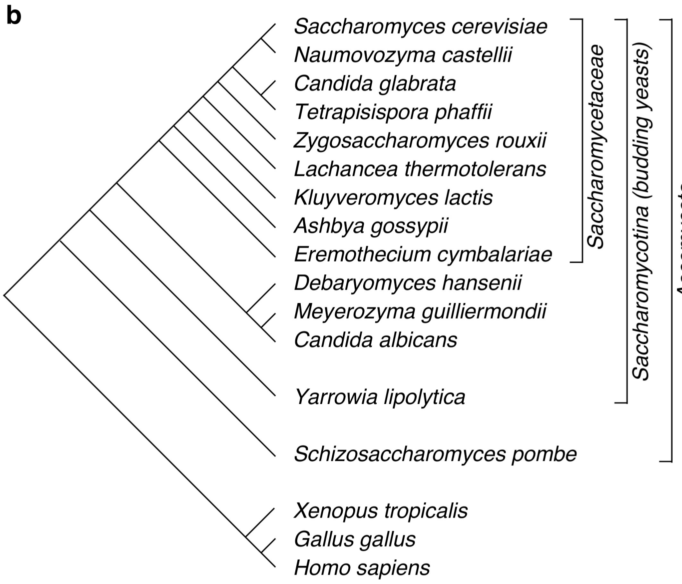

Fig. S1. Conservation of SIMs in Rad18 and Srs2. **a** Sequence alignment of the N-terminal regions of Rad18 (spanning the RING and UBZ domains) and the C-termini of Srs2 in selected yeast and vertebrate species. Red: High-probability SIM, based on homology with the S. cerevisiae genes. Green: high-probability SIM in reverse orientation. Orange: possible SIM. Alignments were performed with Clustal-W. **b** Phylogenetic tree of the relevant species and their classifications. Note that the tree branches are not to scale (adapted from Dujon 2010 and Kurtzman and Robnett 2003).