

Table S2 Gene ontology analysis (processes) of RAD52-like genes from the solid screen in this study

GO-Slim term	Genes annotated to the term
Transport	<i>AGP1, APQ12, ATG9, AVL9, AVT5, CCZ1, CIK1, CLA4, DRS2, FKS1, GCS1, GET2, GOS1, GTR1, KAR3, LST4, MMM1, NUM1, PEX12, PEX14, PEX19, PEX5, PMR1, RIM8, RPS18B, SEC28, SEC66, SGF73, SKY1, SLG1, SNX4, SPC2, SPF1, SSO2, STE20, THR4, TIM18, TLG2, UBP3, UBX2, VAM3, VAM6, VAM7, VPS1, VPS4, VPS41, VPS5, VPS51, VTH1, YDL183C, YPT7, ZRC1</i>
Response to stress	<i>ASF1, ATG9, BRE1, CAC2, CCZ1, CKB1, CTF18, CTF4, CTF8, DCC1, ELM1, GSH1, HDA1, MGA2, MMS1, MMS22, MRC1, MRE11, NHP10, NPL4, OPI1, PHO5, PHO80, POL32, RAD50, RAD52, RAD54, RAD55, RAD57, RMI1, RPN4, RTT109, SIC1, SIN3, SLG1, SLX5, SLX8, SNF6, SOH1, STB5, STE20, TAX4, TIM18, TMA19, TPS2, UBI4, URM1, VAM3, VPS75, XRS2, YKU80</i>
RNA metabolic process	<i>ASF1, BRE1, CAC2, CKB1, DEG1, ELP2, ELP3, ELP4, ELP6, GRS1, GTR1, HAP4, HDA1, HTZ1, INO2, IPK1, MED1, MGA2, MMS1, MRC1, MRE11, NCS6, NOP12, OPI1, PHO80, POL32, RPL35B, RPN4, RPS11B, RPS16A, RPS18B, RTF1, RTT109, SDS3, SGF11, SGF73, SIN3, SKY1, SNF4, SNF6, SOH1, STB5, SWD1, SWD3, URM1, YGR122W, YKU80, YPL205C, ZDS2</i>
Chromosome organization	<i>ARP6, ASF1, BRE1, CAC2, CIK1, CTF18, CTF4, CTF8, DCC1, HDA1, KAR3, LGE1, MMS22, MRC1, NHP10, RAD50, RAD51, RAD52, RAD54, RAD57, RMI1, RTF1, RTS1, RTT109, SDS3, SGF11, SGF29, SGF73, SIN3, SLX5, SLX8, SNF6, SOH1, SWD1, SWD3, VPS75, XRS2, YKU80</i>
Transcription, DNA-dependent	<i>ASF1, BRE1, CAC2, CKB1, ELP2, ELP3, ELP4, ELP6, GRS1, GTR1, HAP4, HDA1, HTZ1, INO2, MED1, MGA2, MRC1, MRE11, OPI1, PHO80, RPN4, RTF1, RTT109, SDS3, SGF11, SGF73, SIN3, SNF4, SNF6, SOH1, STB5, SWD1, SWD3, YGR122W, YKU80, YPL205C, ZDS2</i>
Protein modification process	<i>ASF1, BRE1, CKB1, CLA4, DIA2, ELM1, ELP2, ELP6, HDA1, HPM1, LGE1, MUB1, NCS6, OST4, PHO80, RTF1, RTS1, RTT109, SDS3, SGF11, SGF29, SGF73, SIC1, SIN3, SKY1, SLX5, SLX8, SNF4, STE20, SWD1, SWD3, UBI4, UBP3, UBP6, URM1, VPS75</i>
DNA metabolic process	<i>BRE1, CAC2, CTF18, CTF4, CTF8, DCC1, DIA2, HUR1, LGE1, MMS1, MMS22, MRC1, MRE11, NHP10, POL32, RAD50, RAD51, RAD52, RAD54, RAD55, RAD57, RIM1, RPN4, RTT109, SIN3, SLX5, SLX8, SNF6, SOH1, SWD1, SWD3, VPS75, XRS2, YKU80</i>
Cell cycle	<i>BRE1, CIK1, CLA4, CTF18, CTF4, CTF8, DCC1, ELM1, FAR1, GCS1, KAR3, MMS22, MRC1, MRE11, PHO80, RAD50, RAD51, RAD52, RAD55, RAD57, RIM8, RMI1, RPN4, RTS1, SAP155, SHE1, SIC1, SIN3, SMI1, SOH1, STE20, XRS2, ZDS2</i>
Vesicle-mediated transport	<i>AVL9, CCZ1, DRS2, FKS1, GCS1, GET2, GOS1, LST4, PMR1, RIM8, SEC28, SLG1, SNX4, SSO2, THR4, TLG2, UBP3, VAM3, VAM6, VAM7, VPS1, VPS4, VPS41, VPS5, VPS51, VTH1, YPT7</i>
Cellular membrane organization	<i>APQ12, ATG9, CCZ1, DRS2, FKS1, GET2, GOS1, MEH1, MMM1, RIM8, SEC28, SLG1, SNX4, SSO2, THR4, TIM18, TLG2, VAM10, VAM3, VAM6, VAM7, VPS1, VPS4, VPS41, YPT7</i>
Biological process unknown	<i>AIM4, AIM44, IES2, IES5, MTC1, MTC5, PAR32, RTC2, YBR174C, YDR149C, YGL024W, YGL081W, YGR125W, YGR182C, YIL054W, YLR065C, YLR108C, YLR287C, YML012C-A, YNL170W, YPL102C</i>
Meiosis	<i>BRE1, CIK1, KAR3, MMS22, MRE11, RAD50, RAD51, RAD52, RAD55, RAD57, RIM8, RTS1, SOH1, XRS2</i>

Response to chemical stimulus	<i>CLA4, ELM1, FAR1, GSH1, NPL4, OPI1, RPN4, SKY1, STB5, STE20, TIM18, TMA19, URM1</i>
Protein complex biogenesis	<i>ATG9, ATP11, COX12, COX23, FMC1, GIM4, PEX14, PEX5, PKR1, SGF73, VAM6, VPS4, VPS41</i>
Cellular amino acid metabolic process	<i>ARO1, ARO2, GRS1, GSH1, GSH2, HOM6, PDC5, SPE1, SPE2, SPE3, THR4, ZRC1</i>
Cellular lipid metabolic process	<i>APQ12, CHO2, ETR1, INO2, INP52, MGA2, OAR1, OPI1, OPI3, PSD1, SCT1, TLG2</i>
Peroxisome organization	<i>ATG9, CCZ1, PEX12, PEX14, PEX19, PEX5, SLG1, SNF4, SNX4, TLG2, VPS1, VPS51</i>
Chromosome segregation	<i>CIK1, CTF18, CTF4, CTF8, DCC1, KAR3, MMS22, MRC1, RMI1, RTS1, SOH1</i>
Mitochondrion organization	<i>ATP11, COX12, COX23, FMC1, GEM1, GRS1, MMM1, MRPL36, NUM1, RIM1, TIM18</i>
Translation	<i>EAP1, GRS1, MRPL36, RPL21B, RPL35B, RPS11B, RPS16A, RPS18B, RPS4A, TEF4, TMA19</i>
Vesicle organization	<i>GOS1, SEC28, SSO2, TLG2, VAM3, VAM6, VAM7, VPS4, VPS41, VPS51</i>
Vacuole organization	<i>ATG9, CLA4, STE20, VAM10, VAM3, VAM6, VAM7, VPS41, YPT7</i>
Cellular carbohydrate metabolic process	<i>ELM1, FKS1, MAL12, OST4, PDC5, PFK2, SNF4, SOL4, TPS2</i>
Signaling	<i>CLA4, FAR1, MRC1, OPI1, PHO80, SLG1, STE20, TAX4</i>
Sporulation resulting in formation of a cellular spore	<i>MRE11, RIM21, RIM9, SSO2, UBI4, XRS2, YPL205C</i>
Cytoskeleton organization	<i>CIK1, GCS1, NUM1, SHE1, SLG1, VPS1</i>
Ribosome biogenesis	<i>DRS2, NOP12, RPL35B, RPS11B, RPS16A, RPS18B</i>
Cytokinesis	<i>CLA4, CTS1, CYK3, ELM1, STE20</i>
Generation of precursor metabolites and energy	<i>CYT1, ETR1, OAR1, PDC5, PFK2</i>
Cofactor metabolic process	<i>CAT5, SOL4, SPE1, SPE2, SPE3</i>
Cell budding	<i>CLA4, ELM1, MUB1, URM1, VPS51</i>
Cellular homeostasis	<i>MEH1, PHO80, SKY1, SPF1, ZRC1</i>
Conjugation	<i>CIK1, FAR1, KAR3, STE20</i>
Pseudohyphal growth	<i>DFG16, ELM1, SOK2, STE20</i>
Fungal-type cell wall organization	<i>ECM8, KRE1, SLG1, TAX4</i>
Heterocycle metabolic process	<i>AAH1, IMD3, PDC5, SOL4</i>
Cellular aromatic compound metabolic process	<i>AAH1, ARO1, ARO2, PDC5</i>
Cellular protein catabolic process	<i>DIA2, NPL4, UBX2, VMS1</i>
Cellular respiration	<i>CYT1, ETR1, OAR1</i>
Nucleus organization	<i>APQ12, CIK1, KAR3</i>
Vitamin metabolic process	<i>SPE1, SPE2, SPE3</i>
Cellular component morphogenesis	<i>ELM1, SSO2</i>
Transposition	<i>MMS1, RTT109</i>
Protein folding	<i>EGD2</i>

Table legend: *RAD52*-like genes in this study were analysed using SGD gene ontology slim mapper

(<http://www.yeastgenome.org/cgi-bin/GO/goSlimMapper.pl>). “Yeast GO-Slim: Process” GO set was used to determine the list of genes that involved in different biological processes.