yRad52	1	MNEIMDMDEKKPVFGNHSEDIQTKLDKKLGPE	32
hRad52	1	MSGTEEAILGGRDSHPAAGGGSVLCFGQCQYTAEEYQAIQKALRQRLGPE	50
yRad52	33	YISKRVGFGTSRIAYIEGWRVINLANQIFGYNGWSTEVKSVVIDFLDERQ	82
hRad52	51	YISSRMAGGGQKVCYIEGHRVINLANEMFGYNGWAHSITQQNVDFVDLNN	100
yRad52	83	GKFSIGCTAIVRVTLTSGTYREDIGYGTVENERRKPAAFERAKKSAVTDA	132
hRad52	101	GKFYVGVCAFVRVQLKDGSYHEDVGYGVSEGLKSKALSLEKARKEAVTDG	150
yRad52	133	LKRSLRGFGNALGNCLYDKDFLAKIDKVKFD-PPDFDENNLFRPTDEIS-	180
hRad52	151	LKRALRSFGNALGNCILDKDYLRSLNKLPRQLPLEVDLTKAKRQDLEPSV	200
yRad52	<b>18</b> 1	ESSRTNTLHENQEQQQYPNKRRQLTKVTNTNPDSTKNLVKIENTVSRGTP	230
hRad52	<b>20</b> 1	EEARYNSCRPNM-ALGHPQLQQVTSPSRPSHAVIPADQDCSSRSLS	245
yRad52	231	MMAAPAEANSKNSSNKDTDLKSLDASKQDQDDLLDDSLMFSDDFQDDDLI . .:  :.	280
hRad52	246	SSAVESEATHQRKLRQKQLQQQFRERMEKQQVRVSTP	282
yRad52	281	NMGNTNSNVLTTEKDPVVAKQSPTASSNPEAEQITFVTAK	320
hRad52	283	SAEK SEAAPPAPPVTHSTPVTVSEPLLEKDFLAGVTQELI	322
yRad52	321	AATSVQNERYIGEESIFDPKYQAQSIRHTVDQTTSKHIPA	360
hRad52	323	KTLEDNSEKWAVTPDAGDGVVKPSSRADPAQTSDTLALNNQMVTQNRTPH	372
yRad52	361	SVLKDKTMTTARDSVYEKFAPKGKQL	386
hRad52	373	SVCHQKPQAKSGSWDLQTYSADQRTTGNWESHRKSQDMKKRKYDPS	418
yRad52	387	SMKNNDKELGPHMLEGAGNQVPRETTPIKTNATAFPPAAAPRFAPPSKVV	436
hRad52	419		418
yRad52	437	HPNGNGAVPAVPQQRSTRREVGRPKINPLHARKPT 471	

S1 Fig. Homologous alignment of yeast and human Rad52.