



Figure S4. Yeast two-hybrid analysis of the interaction between MRT-2/Rad1 and ZTF-8.

Wild type full-length ZTF-8 as well as point mutants for the SUMOylation sites of ZTF-8 were tested for their interactions with MRT-2. K14R, K494R, K518R and K527R denote single point mutants, whereas 3KR denotes a construct carrying three mutations of K to R at amino acids 494, 518 and 527. Wild type and mutant ZTF-8 were fused to the DNA binding domain and full length MRT-2 was fused to the activation domain of GAL4. One negative (No. 1) and four positive controls (No. 2-5) were used as described in (37). Interactions were scored by growth on -Ade, -His and -His+3AT plates and compared to growth on -Leu-Trp control media.