**Table S2. Primers used in this study.**

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| Name  | Sequence | Purpose |
| cas9\_cdc13-1\_F | TTTATACTGGCGAATTGAGGGTTTT | gRNA for *cdc13-1*  |
| cas9\_cdc13-1\_R | CCTCAATTCGCCAGTATAAAGATCA | gRNA for *cdc13-1*  |
| 80mer\_cas9\_cdc13-1 | AGGTTAGAGGGCAAAATTGTTGGCATGAATTCACCTCAATTCGCCAGTATAAATGAGTTCAAATATTGCACATTGAAATT | Template for *cdc13-1* via CRISPR |
| KSG163F | CATGGGAGAGGAAATGCATG | Amplify *cdc13-1* mutation for sequencing |
| KSG159R | CCCACAGGATCCTTTCAACTTC | Amplify *cdc13-1* mutation for sequencing |
| KSG175\_cdc13-2\_gRNA\_R | GCTGCGAGTTGAATTCGTTTGTTTT | gRNA for *cdc13-2* |
| KSG176\_cdc13-2\_gRNA\_F | AAACGAATTCAACTCGCAGCGATCA | gRNA for *cdc13-2* |
| KSG181\_80mer\_cdc13-2\_CRISPR | CAAATAGACTAGGGATACCTTACATTGAATCCCTAAACAAATTCAACTCGCAGCTTATGACGCTTAATGTAGATGAACCG | Template for *cdc13-2* via CRISPR |
| KSG185\_F | ATGAGGATCCTGCAGATATCCATCACACTGGC | BamHI site. To amplify GAA repeats from pYES3 to clone into pYES6 |
| KSG186\_R | ACGATCTAGATAGTAGGTTGAGGCCGTTGAGC | XbaI site. To amplify GAA repeats from pYES3 to clone into pYES6 |
| pYES-Hybr\_regionCHF | GGATCGGACTACTAGCAGCTG | Oligo hybridizing to Gal promoter used to probe 2D gels |
| Tcyc1\_CHF | GGAGGGCGTGAATGTAAGCGTG | 2D gels |
| KSG193\_F | TATTACCCGGGTATCTGCAGATATCCATCACACTGGC | XmaI site. For cloning GAA repeats into DDRA construct |
| KSG194\_R | TATCACTAGTTACTAGTAGGTTGAGGCCGTTGAGC | SpeI site. For cloning GAA repeats into DDRA construct |
| RM282\_ URA3\_ChrVnoness\_int\_F | AAACAAACAAGGCCGCAACAATAACATCATCTAAAGACTTCCTTTGTGACCCGGAGATCTAGCTTTTCAATTCAATTC | Amplifies UR-GAA100-A3 along with TRP1 with flanking homology to Chr.V |
| RM283\_ URA3\_ChrVnoness\_int\_R | TCTGTATCTATACTCAACGTTACTTTCTGGCCATACCATAAGTTCTACACCCGGCGATAAGCTAGCAGGCAA | Amplifies UR-GAA100-A3 along with TRP1 with flanking homology to Chr.V |
| RM144\_RAD51\_Hyg\_Int\_F

|  |  |
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|  | ATGTTGGAAATGCACCACTACCGTTCTTCAACCAATCTAGTTTAGCTATTTAGAACGCGGCTACAATTA |
|  | AAAGAGGAGAATTGAAAGTAAACCTGTGTAAATAAATAGAGACAAGAGACCAAATACCTACCCTGATTCTGTGGATAACC |

 | AAATGTTGGAAATGCACCACTACCGTTCTTCAACCAATCTAGTTTAGCTATTTAGAACGCGGCTACAATTA | KO of Rad51 |
| RM145\_RAD51\_Hyg\_Int\_R | AAAGAGGAGAATTGAAAGTAAACCTGTGTAAATAAATAGAGACAAGAGACCAAATACCTACCCTGATTCTGTGGATAACC | KO of Rad51 |
| Rad52\_KO\_F | TGTATCATCTGCTTGCCCTGTAATGTCCTTTCGTCTTCTCAATCACACTTACTCATCGCCCAGCTGAAGCTTCGTACGC  | KO of Rad52 |
| Rad52\_KO\_R | ACTCAAACGTAGTTTTCTCTTCTCAAACTTAATGATCTATTGTTTTTCCGAGTTGCCCATAGGCCACTAGTGGATCTG  | KO of Rad52 |
| TOF1/SP | GTAAGTCCTCACATATGATAATACCATCTAGCTTGTGGGGTTTAGTGTATCTTCAGCTGAAGCTTCGTACGC | KO of Tof1 |
| TOF1/ASP | TCTGTAGCTCTTATGCTTTCAATACTTGGTATGGATCCACCAAACAAGCTCGTATCATAGGCCACTAGTGGATCTG | KO of Tof1 |
| RM189\_ MEC1\_pAG\_R | AGAGATGATTAATGAAGACAAAGTGAGGCTGGACAACAAGAACGACATACTTCGGTGATGACGGTGAAA | KO of Mec1 |
| RM190\_MEC1\_pAG\_R | GGTCCATGTTTCTATCGTACATAATTGTTTCGATCACATTCATCAACGCTAAACCGTATTACCGCCTTTG | KO of Mec1 |
| sml1\_nat\_KO\_fwd | TGGGAAGTCATCCGTCCCAAAAAGGAAATAGCCATAACATATCGTTACTGTTTTGGAACATCGCCCCGGGTTAATTAAGGCG | KO of Sml1 |
| sml1\_nat\_KO\_Rev | GCTAGCGATATCTAGCTGTATCAAACGTATTATAGACTATCTTTGATAAAGACACAGAAATACAGCGCCCAATACGCAAACCG | KO of Sml1 |
| Rad53\_pRCC\_F | AACTACTGGGAAAACATTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGG | Introduction of rad53-K227A mutation via CRISPR |
| Rad53\_pRCC\_R | CGAATGTTTTCCCAGTAGTTTCCGATCATTTATCTTTCACTGCGGAG | rad53-K227A mutation |
| Rad53\_repairtemp\_F | TTGCCACAGTAAAGAAAGCCATTGAAAGAACTACTGGGAAAACATTCGCCGTGGCGATTATAAGTAAACGCAAAGTAATAGGCAATATGGATGGTGTGAC | rad53-K227A mutation |
| Rad53\_repairtemp\_R | GTCACACCATCCATATTGCCTATTACTTTGCGTTTACTTATAATCGCCACGGCGAATGTTTTCCCAGTAGTTCTTTCAATGGCTTTCTTTACTGTGGCAA | rad53-K227A mutation |
| KSG164\_Exo1KO\_F | CTTTTTTTTCTTACGCGTCTTTAGCAAAGGCGGGAAGTACAATAACTAGTTTTGTGCACAACCCCGGGTTAATTAAGGCG | KO of Exo1 |
| KSG165\_Exo1KO\_Rev | GTCCTCACATGCGGCGTGCATTGTTCATAGCGGGGCAAACATACTTGTGGCTTAATTTGACGAGCGCCCAATACGCAAAC | KO of Exo1 |
| Hygr\_to\_Rad9\_allF | TTTCTTATTACTGGCACGGCTTTGAATTTTCAGAGTGCAGTTCTGATTAAACACGCGAGGCAGCTGAAGCTTCGTACGC | KO for Rad9 |
| Hygr\_to\_Rad9\_allR | ATCTCACCCATTGGGGTGAATCTCGTTATTGCTCCTTATTTTGGTCCATTTTATATTAAATCCCATAGGCCACTAGTGGATCTG | KO for Rad9 |
| JK219\_POL32\_SP | ATAATATTTCACATTAACTAACAACCAGAAATAGGCTTTAGTTAACTCAATCGGTAATTACAGCTGAAGCTTCGTACGC | KO for Pol32 |
| JK220\_POL32\_ASP | CATTTGTATTATACATTACATCACAATTAGTAATGGAAAGTGTTTGGAAAAAAAAGAAGACATAGGCCACTAGTGGATCTG | KO for Pol32 |
| RM94\_RAD5del-Hyg-F | CCTTACTGCTAAGCGCATTGCTCACTTGAAAGTAAATTATCTACAAAGTTACACATACGATTTAGGTGAC | KO for Rad5 |
| RM95\_RAD5del-Hyg-R | TCTATGCTATCTTGTATGATAAATCTCATAACTTTGACGCTGTTTGTCTGTCTGTGGATAACCGTATTAC | KO for Rad5 |
| A2 | CTCGATGTGCAGAACCTGAAGCTTGATCT | Check for GAA100 tract length |
| B2 | GCTCGAGTGCAGACCTCAAATTCGATGA | Check for GAA100 tract length |