Table 1. Ku overexpression did not change the breakpoint junction spectra

DNA damage	Control	yKu70-yKu80 overexpression
HO break	V34108-34026 AAGAAAAAAAACAAAAAAAAGAAATAAAATAACGGCAAACAGCAAA:GGCCACAGAACCGTATTCATGTTACTTCTGCAATAT CGGGCGGTTGTACATTTCTGCGTAAATCTCGATGTTATGCACACCT:GGATCTATCAATTCAATGTAAGAAGGTGCTGGAGAA V27857-27776 V34090-34008 AAAGAAATAAAATAACGGCAAACAGCAAAGGCCACAGAACCG:TATTCATGTTACTTCTGCAATATCAATCACTTACTGGCAAG GTACATTTCTGCGTAAATCTCGATGTTATGCACACCTGGATC:TATCAATTCAATGTAAGAAGGTGCTGGAGAAGATGTGGTTA V27848-27766 V32594-32510 TAACGCTGCCTTCACATTTCAAGGTACTGAACTAGTTGGTATCAC:TGCTGGTGAAGCTGCAAACCCCAGAAAATCCGTTCCAAGA AATATCCTTTGGGGGTTCCTGCCTGGTTGGGATAGTGGTATCAC:AGCAGGTTTCATTAACATGGACAACTTTAAAATGAACTTC V23043-22959 V33296-33220 GAGAGTAAATGGCGAGGATACGTTCTCTATGGAGGATGGCA:TAGGTGATGAAGATGAAGGAGAAGTACAGAACGCTG AGAAGATTACCAAGAACCACGTTATTTGAGAGAGGATGGCA:AGGTGACGACAATCACACCAAGACCACATTTTGGGT I219758-219834 V32271-32195 GTATTTTATTTGGTCTATCAAAGAACAAGTTGGCTCCTA:AATTCCTGTCAAGGACCACCAAAGGTGGTGTTCCATAC ATGTGGTTAGCGTTGGCTTGACATCGACCTTGGCTCCTA:CTTCCTTTTCCAGCATCTCGGGAACGACAACCTCTTCA V27774-27698 V33783-33699 TGTCTCTATCAATGAAAATTTCGAGGAA:GACGATAAGGTTAAGATAAGTAGATAAGAGAATGATACGAGATAAAGCACAAATTAG ACCGAAATCAAAAAAAGAATAAAAAAAAAGATGAATTGAAAGCTT GTACATTTCTGCGTAAATCTCGATGTTATGCACACCTGGATC:TATCAATT CAATGTAAGAAGGTGCTGGAGAAGATGTGGTT V27848-27767 AGGATTTGGCGTGGATGAAGGACCTGCAGTGGAGGGTGTTGTTGTGGAgtgtgtgtgggtggtg [34833] TGAGTTGGTGTGGTGTTACTACTAGGATTTGGCGTGGgtgtggtgtgggtg [34867] CTTACATGGAGACATCTACTGGTGGTGACAAAGTTTTCGAATGGgtgtgtgggttgtgggtgtgtg [32114] CTAGGATTTGGCGTGGATGAAGGACCTGCAGTGGAGGGTGtgtgggttgtgggtgg [34843] TAGCCATTATCGGGTTTCTAATATACTGTTTTTGTATGGgtgtgtgggtgtggg [32720]	V32575-32499 CAAGGTACTGAACTAGTTGGTATCACTGCTGGTGAAGC:TGCAAACCCCAGAAAATCCGTTCCAAGAGCCATCAAAAA CAAGGTACTGAACTGGTTGGGATAACCGCTGGTGAAGC:GGCTAACCCAAGAAAAGCTCTCCCGAGGGCAATAAAGAA XIV136820-136744 V34785-34702 TGGATAGCAATTGATTTTGTTCTTCAAGAACTTTGAAC:ATTTTGCCCAGCCTAGTAATAGCTGGTTCGTAGGGAGACGTCTCAC ATACCTTTACTTGGTGCTGTTCTTTGAGAACTTTGAAC:CTTTGCACCTCTACAAAGCCAAGCTTCTTTTCATAGTAACCCAATA V14338-14255 V33090-33006 ATTTATTTATGGGTTCTTTGGCATATTCTGTCACGCAGTCC:TTGGGTGAAATGGCTACATTCATCCCTGTTACATCCTCTTTCAC TATGCGCAAATGAACATAGTGTTTGTCGAAATTTATCGTTC:AAGGGTGTGAGGTCGTATCTTCCAGCAAGTAATTGCAACTAAAA V23439-23355 V33800-33713 ATTTCTTTTTTTGCAGTTGTCTCTATCAATGAAAATTTC:GAGGAAGACGATAAGGTTAAGATAAGTAGATAAGAGAATGATACGAGAT AAGGAAACCGAAATCAAAAAAAAGAATAAAAAAAAAGATGAATTGAAAGT CTAAGGAAACCGAAATCAAAAAAAAAGAATAAAAAAAAAAGATGAATTGAAAGCTT ATTTCTGCGTAAATCTCGATGTTATGCACACCTGGATC:TATCAATTCAATGTAAGAAGGTGCTGGAGAAGAT GTGGTTAGCGTTGG V27844-27759 GAGCTAACTATATAAACGTTTGGATTCGTGTGTgggtgtggtgtgtgtgggtgtgggtg [36339] ATTTGGCGTGGATGAAGGACCTGCAGTGGAGGGTGTTGTTGTGGAgggtgttgttgtggtg [34833] TTAGCCATTATCGGGTTTCTAATATACTGTTTTTGTATGGTTTGTGGTGtgggtgtgggtgtggg [32713] ATCCTTTTCGGATGTAGGATGAGTTGGTGTGGTGTTACTACTAGGATTTGGCGTGGgtgtggtgtgtgggtg [34867] GGTTTCTAATATACTGTTTTTGTATGGTTTGTGGTGCTGGGGTgggtgtgttgtgt [32706]
MMS	V35666-35585 TGAACTCGAGCAGGAGGTTTGTGATTGCCTCCAGTCTTTA:TAAATTGATGAAAAAGAGGAATTTAAGGAGGAGTTTTGAGAA TCATTCAGATGTGCATTCTCATCACAGTTCTAGTACTTTA:AAAAGGCCAACTTCAAATTCGATAGAAAAGATGGTTACCCAC VII746037-746118 V42098-42024 CACCCGCGATAAAGAGCGCGATGAATATAAAAGGGGGCCA:ATGTTACGTCCCGTTATATTGGAGTTCTTCCCATA AGGCGCTACCATGAGAAATGGGTGAATAATTAGATAATTG:TTGGGATTCCATTGTTGATAAAGGCTATAATATTA XVI856201-856275 ATCAGGTCTGTGCCTACTATGCACTTATGCCCGGGGTCCCgggtggtgggtgtgtggg [42280] TTATTTCAGAGTTCTTCAGACTTCTTAACTCCTGTAAAAACAAAAAAAAAAAAAGGgttgtgtggggtg [33472] CTTTGCAACCAGGTTCTGATAGTGAATTTTTCGAATTGGGtgtggggtgtggtgtgtgtg [40314] GGGTTTCTAATATACTGTTTTTGTATGGTTTGTGGTGtgtgggtgtgtgggtgt [32713] GTTGGTGTGGTGTTACTACTAGGATTTGGCGTGGgtgtggtgtgtgggtgtgg [34867] TATAGAAATCTAGGGTTTCTGTGTGGTTTCCGGGTGtggtgtgtgtgggtgtgt [33820] CGACATCGATTCCGATAGAAGAGACATTGAGGCAATTGTATGGggtgtggtgtgggtgtggtgtgtg [31748]	V42575-42497 TAGCAACGCTTGACTCACAAACCAACTGCCGGCTGAAAGAGC:TTGTGCAATGGGAGTGCCAATTCAAAGGAGCCGAATA CGTTAGAGTGTGCATCCCATTTGAAAGACTTGGAGATGGAGC:ATGTGCAATGGTCCTCCTCTTGTTCGCTTCGAACTGG II101960-101882 #2 CTAGGATTTGGCGTGGATGAAGGACCTGCAGTGGAGGGTGTgggtgtgtggtgt [34842] CGCAAGGGCCAAGACAAGGAGTCTCCGGAATTCAACGGTAAACgttgtgttgtgttgtg [41694] AGTTGGTGTGGTGTTACTACTAGGATTTGGCGTGGATGAAGGgtgtgggtgtggtgtg [34860] TTGGTGTGGTGTTACTACTAGGATTTGGCGTGGATGAAGGgtgtgggtgtggtgtg [34860] ATTTACGGAAATAAGTTGTAATATTAAAAAAAAAAAAAAACATTTTGggtgtgtggtgtgt [36283] ACTACTAGGATTTGGCGTGGATGAAGGACCTGCAGgtggtgttgtggttgtggtgtgtgtttg [34852]

The structure of rearrangement breakpoints was determined as described under *Materials and Methods*. For translocations, the numbers given above and below the sequences are the standard *Saccharomyces* Genome Database (SGD) nucleotide coordinates for the first and last nucleotide listed with the roman numeral indicating the chromosome number. The underlined nucleotides indicate those present in the translocation chromosome. The nucleotides in bold indicate identities. In the case of telomere additions, the number in bracket indicates the SGD nucleotide coordinate of the last recognizable nucleotide of chromosome V before the added telomere sequences.