

001 TAACACTCGC CTATTGTAA AGTGTGTCCT TTG<sup>▼▼</sup>TCGATAC T<sup>▼▼</sup>GGTACTAAT  
 ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA

051 GCGG<sup>▼</sup>TTCGAA<sup>▼</sup> CGTAC<sup>▼</sup>GGACG<sup>▼</sup> TCCAGCTGAG<sup>▼</sup> ATCTCCTAGG<sup>▼</sup> GGCCTCTTAC<sup>▼</sup>  
 CGCCAAGCTT GCATGCCTGC AGGTCTGACTC TAGAGGATCC CCGGAGAATG

101 CCCCT<sup>▼</sup>ATCCA CATACT<sup>▼</sup>TGTA CTCCCACAAA AG<sup>▼</sup>AGCACACT<sup>▼</sup> TACTCCCAA<sup>▼</sup>A  
 GGGGATAGGT GTATGAACAT GAGGGTGTTT TCTCGTGTGA ATGAGGGTTT

151 ATACAACAAT<sup>▼</sup> T<sup>▼</sup>ACACCACCC ACTCACTCGG<sup>▼</sup> G<sup>▼▼</sup>GTAACACAA CACCATTTAT  
 TATGTTGTTA ATGTGGTGGG TGAGTGAGCC CCATTGTGTT GTGGTAAATA

201 ACATCTCCCT CATATCCC<sup>▼</sup>GA C<sup>▼</sup>ACTGATCAT ACAACTCAGG<sup>▼▼</sup> ACATTCATCC  
 TGTAGAGGGA GTATAGGGCT GTGACTAGTA TGTTGAGTCC TGTAAGTAGG

251 TCTCACTATA AACTAG<sup>▼</sup>TCCT CTTGCACCAA<sup>▼</sup> TGATC<sup>▼</sup>GTGTC TCTCAAGAGG<sup>▼▼</sup>  
 AGAGTGATAT TTGATCAGGA GAACGTGGTT ACTAGCACAG AGAGTTCTCC

301<sup>▼</sup> GTCATCCAAT TATCACCCCC CATTCC<sup>▼</sup>GCTC CAATCG<sup>▼</sup>CTCC CATGG<sup>▼</sup>CTCGA  
 CAGTAGGTTA ATAGTGGGGG GTAAGGCGAG GTTAGCGAGG GTACCGAGCT

351 GCTTAAGTGA CCGG<sup>▼▼</sup>CAGCAA<sup>▼</sup> AATGTTGCAG CACTGACCCT TTTGGGACCG  
 CGAATTCCT GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC

401 CAAT<sup>▼▼</sup>G<sup>▼</sup>GTTG AATTAGCGGA ACGTCGTGTA GGGGGAAAGC GGTC  
 GTTACCCAAC TTAATCGCCT TGCAGCACAT CCCCTTTTCG CCAG

**Supplementary Figure 1. The highest intensity IR-induced DNA damage sites with the Mito 15 plasmid as analysed by the LA/PS assay.**

A mitochondrial region, corresponding to bp 11,851 – 12,097 in the hg19 human mitochondrial sequence, was inserted into pUC19. The underlined region indicates the location of the REV2 primer. The locations of the 44 highest intensity radiation-induced damage sites are indicated with black arrows on the corresponding strand. The 5 most intense sites on each strand are shown with a double arrow. The top strand is written 3' to 5', while the bottom strand is 5' to 3'.

001 TAACACTCGC CTATTGTTAA AGTGTGTCCT TTGTCGATAC TGGTACTAAT  
 ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA

051 GCGGTTTCGAG GATTGGGAT TGGGATTGGG ATTGGGATTG GATTGGGAT  
 CGCCAAGCTC CCTAACCCCTA ACCCTAACCC TAACCCTAAC CCTAACCCCTA

101 TCTAGGGGCC CATGGCTCGA TTTTTCGCTG CGTGCCTGCG TTTTTCGCTG  
 AGATCCCCGG GTACCGAGCT AAAAACGCAC GCACGCACGC AAAAACGCAC

151 CGTTTTTCGCG TTTATGCGTT TTCGAGCTTA ATGGGGGGGG GGTAAAGTGA  
 GCAAAAACGC AAATACGCAA AAGCTCGAAT TACCCCCCCC CCAATTCACT

201 CCGGCAGCAA AATGTTGCAG CACTGACCCT TTTGGGACCG CAATGGGTTG  
 GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC

251 AATTAGCGGA ACGTCGTGTA GGGGGAAAGC GGTC  
 TTAATCGCCT TGCAGCACAT CCCCTTTTCG CCAG

**Supplementary Figure 2. The highest intensity IR-induced DNA damage sites with the T7.GCGT.G10 plasmid as analysed by the LA/PS technique.**

A region containing seven telomeric repeats (T7), a GCGT repeating sequence, and a run of ten consecutive guanines (G10) was inserted into pUC19. The underlined region indicates the location of the REV2 primer. The locations of the 28 highest intensity radiation-induced damage sites are indicated with black arrows on the corresponding strand. The 5 most intense sites on each strand are shown with a double arrow. The top strand is written 3' to 5', while the bottom strand is 5' to 3'.

001 TAACACTCGC CTATTGTTAA AGTGTGTCCT TTGTCGATAC TGGTACTAAT  
 ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA

051 GCGGTTTCGAA TGAAGAGTAA TGATGTAGTT TGTATTATGTT TGTATTGTTT  
 CGCCAAGCTT ACTTCTCATT ACTACATCAA ACAAATACAA ACATAACAAA

101 AATTATTTAT TTTGTTATTG TTTTATTTAT TTGGGGGGT TATTTATGTA  
 TTAATAAATA AAACAATAAC AAAATAAATA AACCCCCCAA ATAAATACAT

151 TTTGGGTTTT ATGGTATTTT GGGGGGGGGG TTTATTTATG GTATTTGGGT  
 AAACCCAAAA TACCATAAAA CCCCCCCCCC AAATAAATAC CATAAACCCA

201 TTATTTTATG TATTTGGGGG GTTTTGTTAT TAATTGTTTA TGTTTGTATT  
 AATAAAATAC ATAAACCCCC CAAAACAATA ATTAACAAAT ACAAACATAA

251 GTTTAATTAT TTATTTTGTT ATTGTGTAAG TGTATTGTTT GACTTAAGTG  
 CAAATTAATA AATAAAACAA TAACACATTC ACATAACAAA CTGAATTCAC

301 ACCGGCAGCA AAATGTTGCA GCACTGACCC TTTTGGGACC GCAATGGGTT  
 TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG CGTTACCCAA

351 GAATTAGCGG AACGTCGTGT AGGGGGAAAG CGGTC  
 CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAG

**Supplementary Figure 3. The highest intensity IR-induced DNA damage sites with the J clone as analysed by the LA/PS process.**

A region containing runs of guanines of varying lengths (from a GG dinucleotide to a run of ten consecutive guanines) was inserted into pUC19. The underlined region indicates the location of the REV2 primer. The locations of the 37 highest intensity radiation-induced damage sites are indicated with black arrows on the corresponding strand. The 5 most intense sites on each strand are shown with a double arrow. The top strand is written 3' to 5', while the bottom strand is 5' to 3'.