

Supplementary Table 1. The twenty highest intensity damage sites in Mito 15

Base number	Sequence			Damage percentage
161	ATACAACAAT	T*	ACACCACCCA	1.46
67	CGAACGTACG	G*	ACGTCCAGCT	1.41
239	ATACAACCTCA	G*	GACATTTCATC	1.26
71	CGTACGGACG	T*	CCAGCTGAGA	1.22
59	ATGCGGTTCG	A*	ACGTACGGAC	1.22
63	GGTTCGAACG	T*	ACGGACGTCC	1.01
75	CGGACGTCCA	G*	CTGAGATCTC	1.00
43	GTCGATACTG	G*	TACTAATGCG	0.98
286	ACCAATGATC	G*	TGTCTCTCAA	0.94
91	ATCTCCTAGG	G*	GCCTCTTACC	0.94
219	CTCATATCCC	G*	ACACTGATCA	0.94
299	TCTCTCAAGA	G*	GGTCATCCAA	0.86
117	TCCACATACT	T*	GTAATCCAC	0.86
90	GATCTCCTAG	G*	GGCCTCTTAC	0.83
240	TACAACCTCAG	G*	ACATTCATCC	0.80
301	TCTCAAGAGG	G*	TCATCCAATT	0.77
180	CACTCACTCG	G*	GGTAACACAA	0.76
345	CGCTCCCATG	G*	CTCGAGCTTA	0.73
300	CTCTCAAGAG	G*	GTCATCCAAT	0.72
81	TCCAGCTGAG	A*	TCTCCTAGGG	0.72

Data from three independent ionising radiation damage experiments were averaged to determine the 20 most intense damage sites which are listed in descending order with the surrounding sequence context (written 5' to 3') and damage percentage. * indicates the damaged nucleotide.

Supplementary Table 2. The twenty highest intensity damage sites in T7.GCGT.G10

Base number	Sequence			Damage percentage
59	ATGCGGTTTCG	A*	GGGATTGGGA	1.68
50	CTGGTACTAA	T*	GCGGTTTCGAG	1.38
273	GTCGTGTAGG	G*	GGAAAGCGGT	0.96
73	ATTGGGATTG	G*	GATTGGGATT	0.92
257	GTTGAATTAG	C*	GGAACGTCGT	0.92
246	GACCGCAATG	G*	GTTGAATTAG	0.84
67	CGAGGGATTG	G*	GATTGGGATT	0.83
52	GGTACTAATG	C*	GGTTCGAGGG	0.82
61	GCGGTTTCGAG	G*	GATTGGGATT	0.82
256	GGTTGAATTA	G*	CGGAACGTCG	0.82
259	TGAATTAGCG	G*	AACGTCGTGT	0.80
229	AGCACTGACC	C*	TTTTGGGACC	0.80
86	TTGGGATTGG	G*	ATTGGGATTG	0.80
91	ATTGGGATTG	G*	GATTGGGATT	0.79
80	TTGGGATTGG	G*	ATTGGGATTG	0.77
115	GGGGCCCATG	G*	CTCGATTTTT	0.77
33	TGTGTCCTTT	G*	TCGATACTGG	0.76
247	ACCGCAATGG	G*	TTGAATTAGC	0.76
97	ATTGGGATTG	G*	GATTCTAGGG	0.75
74	TTGGGATTGG	G*	ATTGGGATTG	0.74

Data from three independent ionising radiation damage experiments were averaged to determine the 20 most intense damage sites which are listed in descending order with the surrounding sequence context (written 5' to 3') and damage percentage. * indicates the damaged nucleotide.

Supplementary Table 3. The twenty highest intensity damage sites in the J clone.

Base number	Sequence			Damage percentage
59	ATGCGGTTTCG	A*	ATGAAGAGTA	1.71
174	GTATTTTGGG	G*	GGGGGGTTTA	1.57
364	TTAGCGGAAC	G*	TCGTGTAGGG	1.16
97	TGTTTGTATT	G*	TTTAATTATT	1.15
67	CGAATGAAGA	G*	TAATGATGTA	1.08
155	TATGTATTTG	G*	GTTTTATGGT	1.08
173	GGTATTTTGG	G*	GGGGGGGTTT	1.06
43	GTCGATACTG	G*	TACTAATGCG	0.93
92	GTTTATGTTT	G*	TATTGTTTAA	0.93
148	GTTTATTTAT	G*	TATTTGGGTT	0.93
134	TATTTATTTG	G*	GGGGTTTATT	0.91
114	TATTTATTTT	G*	TTATTGTTTT	0.86
342	TTTGGGACCG	C*	AATGGGTTGA	0.86
44	TCGATACTGG	T*	ACTAATGCGG	0.86
164	GGGTTTTATG	G*	TATTTTGGGG	0.85
198	ATGGTATTTG	G*	GTTTATTTTA	0.85
54	TACTAATGCG	G*	TTCGAATGAA	0.83
72	GAAGAGTAAT	G*	ATGTAGTTTG	0.82
120	TTTTGTTATT	G*	TTTTATTTAT	0.80
348	ACCGCAATGG	G*	TTGAATTAGC	0.80

Data from three independent ionising radiation damage experiments were averaged to determine the 20 most intense damage sites which are listed in descending order with the surrounding sequence context (written 5' to 3') and damage percentage. * indicates the damaged nucleotide.