Table S1. Primers used in this study.

Primer name	Nucleotide sequence (5' to 3')
OGG-F1	
	AAACTACTATTTCCAGCGGAAGAAGGCATTTGAAGCGTCCTGATTCCAGCTGAA GCTTCGTACGC
OGG-R1	
	CGATTTCTTTAGAGAATAGGACACCTTGGGCCCAACCAGCGTATGGCATAGGCC ACTAGTGGATCTG
MSH2-F1	
	GGGTCGACAACCAAGTTACTGGGCGATG
MSH2-R1	
	GGGAGCTCACAACCAATTTGGGCCATTA

Table S2. DNA sequence context of mutations among carbon ion beam irradiation mutations in *ura3* of *rad52*-type. Box indicates that the sequence "3'-ACA-5" or "3'-TGT-5" changed. Underline indicates the position of mutation.

Position	Change	Sequence context	(Amino acid)	[numbers]
69	TTAAT insert	AAT △ATC ATG		[1]
79	G > T	CCA ACA AAC	Thr > Ile	[5]
89	C > T	CCA ACA AAC	Thr > Ile	[5]
218	C > A	GGC ACA GTT	Thr > Lys	[2]
252	C > G	AAG TAC AAT	Tyr > Stop	[1]
286	G > T	GCT GAC ATT	Asp > Tyr	[2]
340	G > T	GCA GAA TGG	Glu > Stop	[2]
344	G > T	GAA TGG GCA	Trp > His	[14]
345	G > C	GAA TGG GCA	Trp > Cys	[1]
427	G > T	AAG GAA CCT	Gle > Stop	[1]
550	G > C	ATT GCT CAA	Ala > Pro	[1]
593	T > A	TGG TTG ATT	Leu > Stop	[1]
608	G > T	CCC GGT GTG	Gly > Asp	[2]
642	T del.	TTG GGT CAA		[1]
655	A del.	AGA ACC GTG		[1]
666	T insert	GAT △GTG GTC		[1]
689	T > G	GAC ATT ATT	Ile > Ser	[1]
Total				[42]

Table S3.   DNA sequence context of mutations among carbon ion beam irradiation mutations in *ura3* of *ogg1*-type. Open box indicates that the sequence "3'-ACA-5" or "3'-TGT-5" changed. Underline indicates the position of mutation.

Position	Change	Sequence context	Amino acid	Numbers
49	G > T	CCT GTT GCT	Val > Phe	[2]
59	G > T	TCC TGT TGC	Cys > Phe	[1]
89	C > A	CCA ACA AAC	Thr > Lys	[2]
89	C > T	CCA ACA AAC	Thr > Lys	[1]
93	C > A	ACA AAC TTG	Asn > Lys	[2]
145	G > T	GTT GAA AAG	Glu > Stop	[1]
167	G > T	ATT TGT TTA	Cys > Phe	[1]
173	T > A	TTA CTA AAA	Leu > Gln	[1]
179	C > A	AAA ACA CAT	Thr > Lys	[1]
181	C > A	ACA CAT GTG	His > Asn	[1]
200	A > T	ACT GAT TTT	Asp > Val	[2]
204	T > G	GAT TTT TCC	Phe > Leu	[2]
233	A > T	CTA AAG GCA	Lys > Met	[1]
252	C > A	AAG TAC AAT	Tyr > Stop	[1]
330	C > A	GTA TAC AGA	Tyr > Stop	[3]
347	C > A	TGG GCA GAC	Val > Glu	[1]
356	C > A	ATT ACG GAA	Thr > Lys	[1]
464	G > T	TCA TGC AAG	Cys > Phe	[1]
487	G > T	GGA GAA TAT	Glu > Stop	[1]
515	C > A	ATT GCG AAG	Ala > Glu	[6]
541	G > A	ATC GGC TTT	Gly > Ser	[1]
566	G > T	GGG TGG AAG	Trp > Leu	[1]
586	G > T	TAC GAT TGG	Asp > Tyr	[1]
602	A > C	TGA CAC CCG	His > Pro	[3]
608	G > T	CCC GGT GTG	Gly > Val	[1]
617	T > G	GGT TTA GAT	Leu > Stop	[1]
637	T > G	GCA TTG GGT	Leu > Val	[1]
643	C > A	GGT CAA CAG	Gln > Lys	[2]
687	C > A	TCT GAC ATT	Asp > Glu	[1]
700	G > T	TTG TTG GAA	Leu > Phe	[1]
745	G > T	GGT GAA CGT	Glu > Stop	[4]
767	G > A	GGC TGG GAA	Trp > Stop	[1]
Total				[50]

Table S4.   DNA sequence context of mutations among carbon ion beam irradiation mutations in *ura3* of *msh2-* type. Open box indicates that the sequence "3'-ACA-5" or "3'-TGT-5" changed.   Underline indicates the position of mutation.

Position	Change	Sequence context	Amino acid	Numbers
3	G > A	ATG TCG	Met > Ile	[2]
83	A del.	GAA AAG CAA		[6]
91	A > G	ACA AAC TTG	Asn > Asp	[1]
93	C > G	ACA AAC TTG	Asn > Lys	[1]
178	A del.	AAA ACA CAT		[6]
181	C del.	ACA CAT GTG		[1]
181	C > G	ACA CAT GTG	His > Asp	[1]
205	T del.	TTT TCC ATG		[2]
206	C > T	TTT TCC ATG	Ser > Phe	[1]
260	T del.	TTT TTA CTC		[5]
261	T insert	TTT TT△A CTC		[1]
271	G > T	CGA AGA CAG	Arg > Ile	[1]
331	A > T	TAC AGA ATA	Arg > Stop	[1]
345	G > A	GAA TGG GCA	Trp > Stop	[4]
405	G > T	AAG CAG GCG	Gln > His	[1]
437	G > T	AGA GGC CTT	Gly > Val	[1]
542	G > A	ATC GGC TTT	Gly > Asp	[1]
605	C > T	ACA CCC GGT	Pro > Ser	[1]
606	C del.	ACA CCC GGT		[3]
679	G > T	ACA GGA TCT	Gly > Stop	[10]
Total				[50]