

**Table S1. Frequencies of Lys<sup>+</sup> revertants and of survivors that lost the ZFN cleavage site**

Spacer Sequence	Relevant Genotype	Lys <sup>+</sup> revertants		Survivors	
		Frequency x 10 <sup>-4</sup> (CI)	# of cultures	Frequency x 10 <sup>-4</sup> (CI)	# of cultures
ACGAAT	WT	2.03 (1.78-2.28)	47	9.53 (7.89-11.2)	113
	<i>ku70Δ</i>	ND	6	5.54 (3.98-7.18)	6
	<i>dnl4Δ</i>	ND	4	4.28 (3.08-5.56)	8
	<i>mre11Δ</i>	ND	12	1.65 (1.07-2.22)	12
	<i>mre11-D56N</i>	16.3 (14.2-18.4)	12	11.3 (8.72-14.1)	9
	<i>pol4Δ</i>	0.197 (0.167-0.226)	8	6.33 (4.28-8.45)	8
	<i>pol4-D367E</i>	0.417 (0.374-0.460)	16	5.53 (3.87-7.31)	16
	<i>pol4Δ mre11-D56N</i>	2.36 (2.12-2.59)	12	12.7 (10.0-15.2)	12
	<i>pol4Δ rad1Δ</i>	0.339 (0.301-0.377)	8	9.98 (4.26-16.5)	12
	<i>pol4Δ rev3Δ</i>	0.73 (0.519-0.942)	10	3.39 (2.09-4.74)	10
	<i>pol4Δ rad30Δ</i>	0.397 (0.349-0.445)	11		
	<i>pol4Δ rev3Δ rad30Δ</i>	0.174 (0.151-0.197)	10	6.89 (5.19-8.63)	10
	<i>rev3Δ</i>	2.58 (2.07-3.09)	11	11.5 (7.39-15.6)	11
	<i>rev3-D975A</i>	2.56 (2.17-2.95)	12	11.5 (7.71-15.2)	12
	<i>rev7Δ</i>	1.33 (1.12-1.55)	8	26.2 (14.6-37.4)	8
	<i>rad30Δ</i>	2.02 (1.41-2.64)	11	10.8 (7.72-13.8)	11
	<i>rev3Δ rad30Δ</i>	1.02 (0.897-1.14)	10	8.15 (5.10-11.2)	10
	<i>sgs1Δ exo1Δ</i>	1.93 (1.28-2.59)	10	0.579 (0.404-0.762)	14
	<i>rad52Δ</i>	2.24 (1.77-2.71)	10	1.43 (1.06-1.80)	20
	<i>tdp1Δ</i>	1.97 (1.53-2.40)	7	10.8 (8.22-13.5)	7
	<i>rad1Δ</i>	2.32 (1.66-2.99)	14	15.2 (9.19-21.0)	10
	<i>rad10Δ</i>	2.04 (1.65-2.42)	8	5.22 (4.00-6.35)	12
	<i>mus81Δ</i>	3.68 (2.50-4.86)	9	6.61 (4.93-8.40)	8
	<i>rad1Δ mus81Δ</i>	3.06 (1.97-4.15)	10	3.97 (3.05-4.83)	10
	<i>slx4Δ</i>	2.40	14	4.24	14

		(1.76-3.04)		(2.90-5.53)	
ACGTAT	<i>WT</i>	3.63 (3.12-4.13)	15		
	<i>mre11-D56N</i>	49.6 (32.9-66.2)	12		
	<i>pol4Δ</i>	0.252 (0.200-0.304)	12		
	<i>pol4Δ mre11-D56N</i>	2.21 (1.88-2.54)	12		
	<i>pol4Δ mre11Δ</i>	ND	12	1.10 (0.70-1.49)	12
	<i>pol4Δ pol3-D520V</i>	0.145 (0.119-0.172)	13	1.66 (0.98-2.60)	13

ND – None detected

Gray shading indicates that the strain was not analyzed

**Table S2. Spectra in Lys+ revertants**

**SJR4848 (-1,ACGAAT) Lys+ revertants**

Mutation	#	T	A	C	A						C	G	A	A				T				G	G	C	
+CGAA	69	T	A	C	A						C	G	A	A	C	G	A	A	T				G	G	C
2A>3A	59	T	A	C	A						C	G	A	A	A			T					G	G	C
1T>2T	61	T	A	C	A						C	G	A	A			T	T					G	G	C
1A>2A	14	T	A	C	A	A					C	G	A	A			T						G	G	C
1G>2G	5	T	A	C	A						C	G	G	A	A		T						G	G	C
1C>2C	4	T	A	C	A					C	C	G	A	A			T						G	G	C
2G>3G	1	T	A	C	A						C	G	A	A			T					G	G	C	
+CGAACCC	1	T	A	C	A	C	G	A	A	C	C	C	C	C	C	G	A	A					G	G	C
+CGAATGG	1	T	A	C	A	C	G	A	A	T	G	G	G	G	C	G	A	A					G	G	C
+GAAT	1	T	A	C	A						C	G	A	A			T	G	A	A	T		G	G	C
-AC	1	T	A	C	-						-	G	A	A			T						G	G	C
-GAATG	2	T	A	C	A						C	-	-	-			-					-	G	C	
-TGGCG	1	T	A	C	A						C	G	A	A			-					-	-	-	
-23 bp	1	-	-	-	-						-	-	-	-			-					-	-	-	
-29 bp	4	-	-	-	-						-	-	-	-			-					-	-	-	
-56 bp	1	-	-	-	-						-	-	A	A			T					G	G	C	
TOTAL	226																								

None  
GCC  
AAT

**SJR4883 (-1,ACGAAT) ku70Δ Lys+ revertants**

**SJR4880 (-1,ACGAAT) dni4Δ Lys+ revertants**

**SJR5247 (-1,ACGAAT) mre11Δ Lys+ revertants**

**SJR5223 (-1,ACGAAT) mre11-D56N Lys+ Revertants**

Mutation	#	T	A	C	A						C	G	A	A				T	G	G	C				
+CGAA	18	T	A	C	A						C	G	A	A	C	G	A	A	T	G	G	C			
2A>3A	51	T	A	C	A						C	G	A	A	A			T	G	G	C				
1T>2T	10	T	A	C	A						C	G	A	A			T	T	G	G	C				
1A>2A	5	T	A	C	A	A					C	G	A	A			T	G	G	C					
1G>2G	3	T	A	C	A						C	G	G	A	A		T	G	G	C					
1C>2C	2	T	A	C	A					C	C	G	A	A			T	G	G	C					
+CGAATGG	1	T	A	C	A	C	G	A	A	T	G	G	G	G	C	G	A	A				T	G	G	C
-AC	1	T	A	C	-						-	G	A	A			T	G	G	C					
-GAATG	1	T	A	C	A						C	-	-	-			-	-	G	C					
Complex Del	1	T	A	C	A						C	G	G	-	-		-	-	G	C					
TOTAL	93																								

**SJR4876 (-1,ACGAAT) pol4Δ Lys+ Revertants**

Mutation	#	T	A	C	A		C	G	A	A	T	G	G	C
2A>3A	121	T	A	C	A	C	G	A	A	A	T	G	G	C
1G>2G	3	T	A	C	A	C	G	G	A	A	T	G	G	C
2G>3G	1	T	A	C	A	C	G	A	A	T	G	G	C	
1C>2C	1	T	A	C	A	C	C	G	A	A	T	G	G	C
-TGGCG	1	T	A	C	A	C	G	A	A	-	-	-	-	
-20 bp	1	-	-	-	-	-	-	A	A	T	G	G	C	
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-		
-29 bp	48	-	-	-	-	-	-	-	-	-	-	-		
-50 bp	6	-	-	-	-	-	-	-	-	-	-	-		
TOTAL	183													

None  
None  
GCC  
CCAAG

**SJR5097 (-1,ACGAAT) pol4-D367E Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A				T	G	G	C
+CGAA	3	T	A	C	A	C	G	A	A	C	G	A	A	T	G	C
2A>3A	66	T	A	C	A	C	G	A	A	A			T	G	C	
1G>2G	1	T	A	C	A	C	G	G	A	A			T	G	C	
2G>3G	2	T	A	C	A	C	G	A	A				T	G	C	
-TGGCG	1	T	A	C	A	C	G	A	A	-	-	-	-			
-14 bp	1	T	A	C	-	-	-	-	-	-	-	-				
-23 bp	1	-	-	-	-	-	-	-	-	-	-					
-29 bp	1	-	-	-	-	-	-	-	-	-	-					
-29 bp	1	-	-	-	-	-	-	-	-	-	-					
-29 bp	16	-	-	-	-	-	-	-	-	-	-					
-50 bp	2	-	-	-	-	-	-	-	-	-	-					

ACG  
None  
None  
None  
GCC  
CCAAG

**SJR5169 (-1,ACGAAT) pol4Δ mre11-D56N Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C	
2A>3A	91	T	A	C	A	C	G	A	A	A	T	G	G	C
1G>2G	3	T	A	C	A	C	G	G	A	A	T	G	G	C
2G>3G	1	T	A	C	A	C	G	A	A	T	G	G	G	C
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL	96													

GCC

**SJR5196 (-1,ACGAAT) pol4Δrad1Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C	
2A>3A	80	T	A	C	A	C	G	A	A	A	T	G	G	C
1G>2G	2	T	A	C	A	C	G	G	A	A	T	G	G	C
2G>3G	1	T	A	C	A	C	G	A	A	T	G	G	G	C
+GAAT	1	T	A	C	A	C	G	A	A	T	G	A	A	T
-AC	1	T	A	C	-	-	G	A	A	T	-	-	-	-
-14 bp	1	T	A	C	-	-	-	-	-	-	-	-	-	-
-29 bp	7	-	-	-	-	-	-	-	-	-	-	-	-	-
-59 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	-
-86 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL	95													

ACG

GCC

None

None

**SJR52422 (-1,ACGAAT) pol4Δrev3Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C	
2A>3A	72	T	A	C	A	C	G	A	A	A	T	G	G	C
1G>2G	2	T	A	C	A	C	G	G	A	A	T	G	G	C
-CGTGG	1	T	A	C	A	C	G	A	A	T	G	G	-	
-29 bp	9	-	-	-	-	-	-	-	-	-	-	-	-	
-50 bp	4	-	-	-	-	-	-	-	-	-	-	-	-	
-74 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	
-86 bp	2	-	-	-	-	-	-	-	-	-	-	-	-	
-95 bp	3	-	-	-	-	-	-	-	-	-	-	-	-	
TOTAL	94													

GCC

CCAAG

None

None

GACGAG

**SJR4882 (-1,ACGAAT) pol4Δrad30Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	1	T	A	C	A	C	G	A	A	C	G	A	A
2A>3A	61	T	A	C	A	-	-	C	G	A	A	A	T
1G>2G	5	T	A	C	A	-	-	C	G	G	A	A	T
-GA	1	T	A	C	A	-	-	C	-	-	A	T	G
-29 bp	21	-	-	-	-	-	-	-	-	-	-	-	-
-50 bp	5	-	-	-	-	-	-	-	-	-	-	-	-
-56 bp	1	-	-	-	-	-	-	-	-	A	A	T	G
TOTAL	95												

GCC

CCAAG

AAT

**SJR4006 (-1,ACGAAT) pol4Δrev3Δrad30Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C	G	T
2A>3A	87	T	A	C	A	C	G	A	A	A	T	G	G	C	G
1G>2G	2	T	A	C	A	C	G	G	A	A	T	G	G	C	G
-TGGCG	1	T	A	C	A	C	G	A	A	-	-	-	-	-	T
-GT	1	T	A	C	A	C	G	A	A	T	G	G	C	-	-
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-29 bp	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-50 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL	96														

None

GCC

CCAAG

**SJR4884 (-1,ACGAAT) rev3Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	58	T	A	C	A	C	G	A	A	C	G	A	A
2A>3A	14	T	A	C	A	C	G	A	A	A	T	G	G
1T>2T	12	T	A	C	A	C	G	A	A	-	T	T	G
1A>2A	3	T	A	C	A	A	C	G	A	A	-	T	G
1G>2G	2	T	A	C	A	C	G	G	A	A	T	G	G
-29 bp	5	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL	94												

GCC

**SJR5098 (-1,ACGAAT) rev3-D975A Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
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Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	24	T	A	C	A								
2A>3A	26	T	A	C	A	C	G	A	A	A		T	G
1T>2T	34	T	A	C	A	C	G	A	A		T	T	G
1A>2A	4	T	A	C	A	A	C	G	A	A		T	G
1G>2G	1	T	A	C	A	C	G	G	A	A		T	G
+TTTT	1	T	A	C	A	C	G	A	A	T	T	T	T
-CA	2	T	A	-	-	C	G	A	A			T	G
-29 bp	3	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL	95												

GCC

**SIR5193 (-1,ACGAAT) rev7Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	18	T	A	C	A								
2A>3A	29	T	A	C	A	C	G	A	A	A		T	G
1T>2T	33	T	A	C	A	C	G	A	A		T	T	G
1C>2C	4	T	A	C	A	C						T	G
1A>2A	6	T	A	C	A	A	C	G	A	A		T	G
2G>3G	2	T	A	C	A	C	G	A	A		T	G	G
1G>2G	2	T	A	C	A	C	G	G	A	A		T	G
+CGAACCC	1	T	A	C	A	C	G	A	A	C	C	C	C
-AT	1	T	A	C	A	C	G	A	-			-	G
TOTAL	96												

**SIR4963 (-1,ACGAAT) rad30Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	45	T	A	C	A								
2A>3A	14	T	A	C	A	C	G	A	A	A		T	G
1T>2T	21	T	A	C	A	C	G	A	A		T	T	G
1A>2A	5	T	A	C	A	A	C	G	A	A		T	G
1G>2G	4	T	A	C	A	C	G	G	A	A		T	G
1C>2C	1	T	A	C	A	C	C	G	A	A		T	G
+CGAAAAA	1	T	A	C	A	C	G	A	A	A	A	A	A
Complex Del.	1	T	-	C	-							T	G
-29 bp	2	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL	94												

GCC

**SIR4964 (-1,ACGAAT) rev3Δrad30Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	12	T	A	C	A	C	G	A	A	A		T	G
2A>3A	33	T	A	C	A	C	G	A	A	A		T	G
1T>2T	38	T	A	C	A	C	G	A	A		T	T	G
1A>2A	9	T	A	C	A	A	C	G	A	A		T	G
1G>2G	1	T	A	C	A	C	G	G	A	A		T	G
2G>3G	1	T	A	C	A	C	G	A	A		T	G	G
+TTTT	1	T	A	C	A	C	G	A	A	T	T	T	T
-TGGCG	1	T	A	C	A	C	G	A	A		-	-	-
TOTAL	96												

**SIR5013 (-1,ACGAAT) sgs1Δexo1Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	31	T	A	C	A								
2A>3A	8	T	A	C	A	C	G	A	A	A		T	G
1T>2T	3	T	A	C	A	C	G	A	A		T	T	G
1A>2A	1	T	A	C	A	A	C	G	A	A		T	G
2G>3G	1	T	A	C	A	C	G	A	A		T	G	G
+GAAT	1	T	A	C	A	C	G	A	A		T	G	A
+CGAAGGG	2	T	A	C	A	C	G	A	A	G	G	G	G
+CGAAAAA	2	T	A	C	A	C	G	A	A	A	A	A	A
-29 bp	36	-	-	-	-	-	-	-	-	-	-	-	-
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-50 bp	2	-	-	-	-	-	-	-	-	-	-	-	-
-71 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-71 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-95 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-119 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL	94												

GCC  
None  
None  
None  
None  
CCAAG  
None  
None  
GACGAG  
GAC



**SJR5201 (-1,ACGAAT) mus81Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	28	T	A	C	A	C	G	A	A	C	G	A	A
2A>3A	10	T	A	C	A	C	G	A	A	A	T	G	G
1T>2T	39	T	A	C	A	C	G	A	A	T	T	G	G
1A>2A	7	T	A	C	A	A	C	G	A	A	T	G	G
2G>3G	1	T	A	C	A	C	G	A	A	T	G	G	G
1G>2G	1	T	A	C	A	C	G	G	A	A	T	G	G
1C>2C	1	T	A	C	A	C	G	A	A	T	G	G	C
+CAAA	1	T	A	C	A	C	G	A	A	C	A	A	A
-CA	2	T	A	-	-	C	G	A	A	T	G	G	C
Complex Del	1	T	A	C	A	C	G	A	A	C	-	-	C
<b>TOTAL</b>	<b>91</b>												

**SJR5202 (-1,ACGAAT) mus81Δrad1Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	39	T	A	C	A	C	G	A	A	C	G	A	A
2A>3A	13	T	A	C	A	C	G	A	A	A	T	G	G
1T>2T	31	T	A	C	A	C	G	A	A	T	T	G	G
1A>2A	3	T	A	C	A	A	C	G	A	A	T	G	G
2G>3G	1	T	A	C	A	C	G	A	A	T	G	G	G
1G>2G	2	T	A	C	A	C	G	G	A	A	T	G	G
1C>2C	1	T	A	C	A	C	G	A	A	T	G	G	C
-GC	1	T	A	C	A	C	G	A	A	T	G	-	-
-CA	1	T	A	-	-	C	G	A	A	T	G	G	C
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-50 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
<b>TOTAL</b>	<b>94</b>												

GCC  
CCAAG

**SJR5240 (-1,ACGAAT) slx4Δ Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	37	T	A	C	A	C	G	A	A	C	G	A	A
2A>3A	32	T	A	C	A	C	G	A	A	A	T	G	G
1T>2T	18	T	A	C	A	C	G	A	A	T	T	G	G
1A>2A	3	T	A	C	A	A	C	G	A	A	T	G	G
1G>2G	2	T	A	C	A	C	G	G	A	A	T	G	G
1C>2C	1	T	A	C	A	C	G	A	A	T	G	G	C
+TTTT	1	T	A	C	A	C	G	A	A	T	T	T	T
-GA	1	T	A	C	A	C	-	-	A	T	G	G	C
-29 bp	7	-	-	-	-	-	-	-	-	-	-	-	-
-35 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-50 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-53 bp (Complex)	1	-	-	-	-	-	-	-	-	-	-	-	-
-74 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
-95 bp	2	-	-	-	-	-	-	-	-	-	-	-	-
<b>TOTAL</b>	<b>108</b>												

GCC  
GTT  
CCAAG  
None  
None  
GACGAG

**SJR5224 (-1,ACGTAT) Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	T	A	T	G	G	C
+CGTA	43	T	A	C	A	C	G	T	A	C	G	T	A
+CGTC	1	T	A	C	A	C	G	T	C	C	G	T	A
+CGTAAAA	1	T	A	C	A	C	G	T	A	A	A	A	A
1C>2C	3	T	A	C	A	C	G	T	A	T	G	G	C
1T>2T	63	T	A	C	A	C	G	T	A	T	T	G	G
-AT	1	T	A	C	A	C	G	T	-	-	G	G	C
-TG	1	T	A	C	A	C	G	T	A	-	-	G	C
-AC	1	T	A	C	-	-	G	T	A	T	G	G	C
-29 bp	2	-	-	-	-	-	-	-	-	-	-	-	-
<b>TOTAL</b>	<b>116</b>												

GCC

**SJR5227 (-1,ACGTAT) mre11-D56N Lys+ Revertants**

Mutation	#	T	A	C	A	C	G	T	A	T	G	G	C
+CGTA	73	T	A	C	A	C	G	T	A	C	G	T	A
1C>2C	1	T	A	C	A	C	G	T	A	T	G	G	C
1T>2T	14	T	A	C	A	C	G	T	A	T	T	G	G
Complex Del	1	T	A	C	A	C	G	T	A	T	A	-	-
-AT	4	T	A	C	A	C	G	T	-	-	G	G	C
-CG	1	T	A	C	A	-	-	T	A	T	G	G	C
-TG	1	T	A	C	A	C	G	T	A	-	-	G	C





**Table S3. Spectra in survivors**

**SJR4848 (-1,ACGAAT) Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+AC	26	T	A	C	A	C	G	A	A	T	G	G	C
+CGAAC	1	T	A	C	A	C	G	A	A	C	G	A	A
+CGA	1	T	A	C	A	C	G	A	A	T	G	G	C
+AA	1	T	A	C	A	A	A	A	A	T	G	G	C
+AA	1	T	A	C	A	A	A	A	A	T	G	G	C
+AAAA	1	T	A	C	A	A	A	A	A	T	G	G	C
-A	1	T	A	C	-	-	-	-	-	T	G	G	C
-A	1	T	A	C	A	-	-	-	-	T	G	G	C
-37 bp	1	T	A	C	A	-	-	-	-	-	-	-	-
-19 bp	1	-	-	-	-	-	-	-	-	T	G	G	C
-15 bp	1	-	-	-	-	-	-	-	-	-	G	C	
-1175 bp	36	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	11	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	72	T	A	C	A	-	-	-	-	T	G	G	C
TOTAL sequenced	155												

None  
None  
None  
CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR4883 (-1,ACGAAT) ku70Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
-1175 bp	35	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	3	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	56	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	94												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR4880 (-1,ACGAAT) dnl4Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
-1175 bp	24	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	14	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	58	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	96												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5247 (-1,ACGAAT) mre11Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
-1175 bp	46	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	47	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	94												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5223 (-1,ACGAAT) mre11-D56N Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+AC	7	T	A	C	A	C	G	A	A	T	G	G	C
+CGAA	1	T	A	C	A	C	G	A	A	C	G	A	A
2A>3A	8	T	A	C	A	C	G	A	A	A	T	G	C
+AA	2	T	A	C	A	C	G	A	A	A	A	T	C
-A	1	T	A	C	A	C	G	A	-	-	T	G	C
-1175 bp	29	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	5	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	34	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	87												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR4876 (-1,ACGAAT) pol4Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
2A>3A	2	T	A	C	A	C	G	A	A	A	T	G	C
-1175 bp	29	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	8	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	54	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	93												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5097 (-1,ACGAAT) pol4-D367E Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
-1175 bp	32	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	2	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	62	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	96												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5169 (-1,ACGAAT) pol4Δ mre11-D56N Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+CACGAA	1	T	A	C	A	C	A	C	G	A	A	C	G
2A>3A	10	T	A	C	A	-	-	-	-	C	G	A	A
+GA	1	T	A	C	A	-	-	-	-	C	G	A	A
-55 bp	1	T	A	C	-	-	-	-	-	-	-	-	-
-1175 bp	42	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	8	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	33	T	A	C	A	-	-	-	-	C	G	A	A
TOTAL sequenced	96												

ACGA  
CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5196 (-1,ACGAAT) pol4Δrad1Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
-55 bp	2	T	A	C	-	-	-	-	-	-	-	-	-
-231 bp	1	T	A	C	-	-	-	-	-	-	-	-	-

ACGA  
None

-1175 bp	38	T A C A C G A A T G G C
-11,731 bp	32	T A C A C G A A T G G C
Maintain Cut Site	17	T A C A C G A A T G G C
TOTAL sequenced	90	

**SJR5242 (-1,ACGAAT) pol4Δrev3Δ Survivors**

Mutation	#	T A C A C G A A T G G C	ACGA GAA None CCAAGCTACTACA TGGAAAAAAAAAAAA
2A>3A	2	T A C A C G A A A T G G C	
-55 bp	1	T A C - - - - -	
-154 bp	1	T A C A C - - - - -	
-231 bp	1	T A C - - - - -	
-1175 bp	20	T A C A - - - - -	
-11,731 bp	10	- - - - -	
Maintain Cut Site	55	T A C A C G A A T G G C	
TOTAL sequenced	90		

**SJR4882 (-1,ACGAAT) pol4Δrad30Δ Survivors**

**SJR4006 (-1,ACGAAT) pol4Δrev3Δrad30Δ Survivors**

Mutation	#	T A C A C G A A T G G C	CCAAGCTACTACA TGGAAAAAAAAAAAA
2A>3A	2	T A C A C G A A A T G G C	
-A	2	T A C A C G A - T G G C	
-1175 bp	29	T A C A - - - - -	
-11,731 bp	10	- - - - -	
Maintain Cut Site	50	T A C A C G A A T G G C	
TOTAL sequenced	93		

**SJR4884 (-1,ACGAAT) rev3Δ Survivors**

Mutation	#	T A C A C G A A T G G C	CCAAGCTACTACA TGGAAAAAAAAAAAA
+AC	14	T A C A C A C G A A T G G C	
+CGAA	1	T A C A C A C G A A C G A A T G G C	
2A>3A	1	T A C A C A C G A A A T G G C	
+AA	1	T A C A A A C G A A T G G C	
-A	1	T A C A C G A - T G G C	
-1175 bp	22	T A C A - - - - -	
-11,731 bp	12	- - - - -	
Maintain Cut Site	39	T A C A C G A A T G G C	
TOTAL sequenced	91		

**SJR5098 (-1,ACGAAT) rev3-D975A Survivors**

Mutation	#	T A C A C G A A T G G C	CCAAGCTACTACA TGGAAAAAAAAAAAA
+AC	13	T A C A C A C G A A T G G C	
2A>3A	5	T A C A C A C G A A A T G G C	
+GAA	1	T A C A C A C G A A G A A T G G C	
+TT	1	T A C A C A C G A A T T T G G C	
-1175 bp	20	T A C A - - - - -	
-11,731 bp	6	- - - - -	
Maintain Cut Site	46	T A C A C G A A T G G C	
TOTAL sequenced	92		

**SJR5193 (-1,ACGAAT) rev7Δ Survivors**

Mutation	#	T A C T A C A C G A A T G G C	CCAAGCTACTACA TGGAAAAAAAAAAAA
+AC	6	T A C T A C A C A C G A A T G G C	
+CGAAAA	1	T A C T A C A C A C G A A A A A C G A A T G G C	
+CGAAAA	1	T A C T A C A C A C G A A A A A C G A A T G G C	
+CGAAT	1	T A C T A C A C A C G A A T C G A A T G G C	
+CGAAA	1	T A C T A C A C A C G A A A C G A A T G G C	
+CGAA	1	T A C T A C A C A C G A A C G A A T G G C	
+CGA	2	T A C T A C A C A C G A C G A A T G G C	
+CGG	1	T A C T A C A C A C G G C G A A T G G C	
+TT	1	T A C T A C A C A C G A A T T T G G C	
+GAA	1	T A C T A C A C A C G A A G A A T G G C	
+AAA	1	T A C T A C A C A C G A A A A A T G G C	
+AAAA	1	T A C T A C A C A C G A A A A A A T G G C	
+CCCGAA	1	T A C T A C A C A C G A A C C C G A A T G G C	
2A>3A	3	T A C T A C A C A C G A A A T G G C	
1C>2C	1	T A C T A C A C A C G A A T G G C	
1G>2G	1	T A C T A C A C A C G G A A T G G C	
1T>2T	1	T A C T A C A C A C G A A T T G G C	
-CG	1	T A C T A C A C A - - A A T G G C	
-AGCT	1	- A C T A C A C A C G A A T G G C	
-1175 bp	25	T A C T A C A C A - - - - -	
-11,731 bp	18	- - - - -	
Maintain Cut Site	21	T A C T A C A C A C G A A T G G C	
TOTAL sequenced	91		

**SJR4963 (-1,ACGAAT) rad30Δ Survivors**

Mutation	#	T A C A C G A A T G G C	None CCAAGCTACTACA TGGAAAAAAAAAAAA
+AC	14	T A C A C A C G A A T G G C	
+CGAAA	1	T A C A C A C G A A A C G A A T G G C	
-A	1	T A C A C G A - T G G C	
-231 bp	1	T A C A - - - - -	
-1175 bp	25	T A C A - - - - -	
-11,731 bp	11	- - - - -	

Maintain Cut Site	38
TOTAL sequenced	91

**SJR4964 (-1,ACGAAT) rev3Δrad30Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+AC	12	T	A	C	A	C	G	A	A	T	G	G	C
2A>3A	1	T	A	C	A	C	G	A	A	A	T	G	C
-A	1	T	A	C	A	C	G	A	-	T	G	G	C
-751 bp	1	T	A	C	A	-	-	-	-	-	-	-	-
-1175 bp	22	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	11	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	48	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	96												

None  
CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5013 (-1,ACGAAT) sgs1Δexo1Δ Survivors**

Mutation	#	A	G	C	T	A	C	T	A	C	A	A	C	G	A	A	T	G	G	C						
+AC	24	A	G	C	T	A	C	T	A	C	A	A	C	G	A	A	T	G	G	C						
+CGAACCC	1	A	G	C	T	A	C	T	A	C	A	C	G	A	A	C	C	C	C	G	A	A	T	G	G	C
+CGAA	5	A	G	C	T	A	C	T	A	C	A	C	G	A	A	C	G	A	A	T	G	G	C			
+CGA	1	A	G	C	T	A	C	T	A	C	A	C	G	A	A	C	G	A	A	T	G	G	C			
+CG	1	A	G	C	T	A	C	T	A	C	A	C	G	A	A	C	G	A	A	T	G	G	C			
+GAA	1	A	G	C	T	A	C	T	A	C	A	A	C	G	A	A	G	A	A	T	G	G	C			
-29 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
-75 bp	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
-231 bp	1	A	G	C	T	A	C	T	A	C	A	A	C	G	A	A	T	G	G	C						
-1175 bp	2	A	G	C	T	A	C	T	A	C	A	A	C	G	A	A	T	G	G	C						
-1384 bp	1	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Maintain Cut Site	52	A	G	C	T	A	C	T	A	C	A	A	C	G	A	A	T	G	G	C						
TOTAL sequenced	91																									

GCC  
AGTT  
None  
CCAAGCTACTACA  
None

**SJR5194 (-1,ACGAAT) rad52Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+AC	36	T	A	C	A	C	G	A	A	T	G	G	C
2A>3A	2	T	A	C	A	C	G	A	A	A	T	G	C
+AA	1	T	A	C	A	C	G	A	A	A	T	G	C
-1175 bp	18	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	1	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	65	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	123												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR4885 (-1,ACGAAT) tdp1Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+AC	12	T	A	C	A	C	G	A	A	T	G	G	C
2A>3A	2	T	A	C	A	C	G	A	A	A	T	G	C
-A	1	T	A	C	A	C	G	A	-	T	G	G	C
-56 bp	1	-	-	-	-	-	-	-	A	A	T	G	C
-75 bp	1	T	A	C	A	-	-	-	-	-	-	-	-
-1175 bp	28	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	14	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	51	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	110												

ATT  
None  
CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5199 (-1,ACGAAT) rad1Δ Survivors**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+AC	33	T	A	C	A	C	G	A	A	T	G	G	C
1A>2A	1	T	A	C	A	C	G	A	A	T	G	G	C
2A>3A	3	T	A	C	A	C	G	A	A	A	T	G	C
1T>2T	1	T	A	C	A	C	G	A	A	T	T	G	C
1G>2G	1	T	A	C	A	C	G	G	A	A	T	G	C
-A	4	T	A	C	A	C	G	A	-	T	G	G	C
-1175 bp	28	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	9	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	5	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	85												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5200 (-1,ACGAAT) rad10Δ Survivors combined**

Mutation	#	T	A	C	A	C	G	A	A	T	G	G	C
+AC	58	T	A	C	A	C	G	A	A	T	G	G	C
+AA	1	T	A	C	A	A	A	C	G	A	A	T	G
1G>2G	1	T	A	C	A	C	G	G	A	A	T	G	C
1T>2T	1	T	A	C	A	C	G	A	A	T	T	G	C
2A>3A	5	T	A	C	A	C	G	A	A	A	T	G	C
+CGAAC	1	T	A	C	A	C	G	A	A	C	G	A	T
+CGAA	2	T	A	C	A	C	G	A	A	C	G	A	T
+GAAT	1	T	A	C	A	C	G	A	A	T	G	A	T
+GGAAT	1	T	A	C	A	C	G	A	A	T	G	G	A
-A	4	T	A	C	A	C	G	A	-	T	G	G	C
-43 bp	1	-	-	-	-	-	-	-	G	A	A	T	G
-56 bp	1	-	-	-	-	-	-	-	A	A	T	G	C
-1175 bp	55	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	17	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	31	T	A	C	A	C	G	A	A	T	G	G	C
TOTAL sequenced	180												

None  
AAT  
CCAAGCTACTACA  
TGGAAAAAAAAAAAA

Mutation	#	T	A	C		A	C	G	A	A	T	G	G	C
+AC	16	T	A	C		A	C	G	A	A	T	G	G	C
-1175 bp	18	T	A	C		A	-	-	-	-	-	-	-	-
-11,731 bp	6	-	-	-		-	-	-	-	-	-	-	-	-
Maintain Cut Site	55	T	A	C		A	C	G	A	A	T	G	G	C
TOTAL sequenced	95													

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5202 (-1,ACGAAT) mus81Δrad1Δ Survivors**

Mutation	#	T	A	C		A				C	G	A	A	T	G	G	C	
+AC	24	T	A	C		A				C	G	A	A	T	G	G	C	
+CGAA	4	T	A	C		A	C	G	A	A	C	G	A	A	T	G	G	C
2A>3A	1	T	A	C		A				C	G	A	A	A	T	G	G	C
-A	2	T	A	C		A				C	G	A	-	T	G	G	C	
-1175 bp	26	T	A	C		A				-	-	-	-	-	-	-	-	
-11,731 bp	7	-	-	-		-				-	-	-	-	-	-	-	-	
Maintain Cut Site	22	T	A	C		A				C	G	A	A	T	G	G	C	
TOTAL sequenced	86																	

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5240 (-1,ACGAAT) slx4Δ Survivors**

Mutation	#	T	A	C				A	C				G	A	A			T	G	G	C		
+AC	32	T	A	C				A	C				G	A	A			T	G	G	C		
+CGAA	1	T	A	C				A	C				G	A	A	C	G	A	A	T	G	G	C
2A>3A	2	T	A	C				A	C				G	A	A	A		T	G	G	C		
+GAATG	1	T	A	C				A	C	G	A	A	T	G	G	A	A	T	G	G	C		
+CGAAA	1	T	A	C				C	G	A	A	A	A	C		G	A	A	T	G	G	C	
-A	1	T	A	C				A	C				G	A	-			T	G	G	C		
-CTA	1	-	-	C				A	C				G	A	A			T	G	G	C		
-1175 bp	32	T	A	C				A	-				-	-	-			-	-	-	-		
-11,731 bp	0	-	-	-				-	-				-	-	-			-	-	-	-		
Maintain Cut Site	18	T	A	C				A	C				G	A	A			T	G	G	C		
TOTAL sequenced	89																						

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5224 (-1,ACGTAT) Survivors**

**SJR5227 (-1,ACGTAT) mre11-D56N Survivors**

**SJR5225 (-1,ACGTAT) pol4Δ Survivors**

**SJR5226 (-1,ACGTAT) pol4Δ mre11-D56N Survivors**

**SJR5248 (-1,ACGTAT) pol4Δmre11Δ Survivors**

Mutation	#	T	A	C	A	C	G	T	A	T	G	G	C
-1175 bp	45	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	0	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	43	T	A	C	A	C	G	T	A	T	G	G	C
TOTAL sequenced	88												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA

**SJR5241 (-1,ACGTAT) pol4Δ pol3-DV Survivors**

Mutation	#	T	A	C	A	C	G	T	A	T	G	G	C
Complex Insertion	1	T	A	C	A	C	G	T	A	T	G	G	C
-1175 bp	11	T	A	C	A	-	-	-	-	-	-	-	-
-11,731 bp	3	-	-	-	-	-	-	-	-	-	-	-	-
Maintain Cut Site	81	T	A	C	A	C	G	T	A	T	G	G	C
TOTAL sequenced	96												

CCAAGCTACTACA  
TGGAAAAAAAAAAAA