

Table S1. Oligonucleotide sequences for the substrate construction. The nucleotides in red are the ones designated for mismatches

Primers		Sequence	Assembled substrates
Template (3'-3')	T1	AACTGTAGGGTAGTCTGGATAGAATTGAAGGAGAGAAGAGGGAGAA G AGCGAGGAGAGGAAGAAAGGAGAAGGGAGAAAA	A1/A2/D1/D 2/D3/D4/E1/ E2
	T2/ T3X6	ACTACCCTAACTTTCCACCTCCTTCTCACTGCTCTATTCCAATAACCT TTA CCACCTCCAATTCAAATCATCACATCTC	A3/A4/B2
	T3X3	ACTACCCTAACTTTCCACCTCCTTCTCGTACTCTATTCCAATAACCT TTA CCACCTCCAATTCAAATCATCACATCTC	B1
	T3X12	ACTACCCTAACTTTCCACCTCCTTCTCACTACTCTAGTCCAATAACCT TTA CCACCTCCAATTCAAATCATCACATCTC	B3
	T3X18	ACTACCCTAACTTTCCACCTCCTTCTCACTACTCTATTCCAATAACCT TTA CCACCTCCAATTCAAATCATCACATCTC	B4
	T4	CGAATTCCTGAGACGGAGTTGAGGTGTCTCGATCTAAAGGTCAATCCT GACGAAGTGTAGGGTTCGCTCTGGATAGAATTG	C
Upstream (5'-3')	U1	TTGACATCCCATCAGACCTATCTTAACTTCCTCTCTTC	A1/A2/D1/E 1/E2
	U2	TGATGGGATTGAAAGGTGGAGG	A3/A4/B
	U3	GCTTAAGGACTCTGCCTCAACTCCACAGAGCTAGATTCCC	C1
	U4	GCTTAAGGACTCTGCCTCAACTCCACAGAGCTAGATTCC	C2/C3/C4
	U5	TTGACATCCCATCAGACCTATCTTAACTTCCTCTCTTCA	D2
	U6	TTGACATCCCATCAGACCTATCTTAACTTCCTCTCTTCTCCC	D3
	U7	TTGACATCCCATCAGACCTATCTTAACTTCCTCTCTTCTCCA	D4
Downstream (5'-3')	F1G	TAAACCATAACTAAATCTTCTCGCTCCTCTCCTTTTCTCTTCCCTC TTTT	A1
	F1T	TAAACCATAACTAAATCTTCTCTCCTCTCCTTTTCTCTTCCCTC TTTT	A2
	F2C	TTTTTTAGTGACGAGATAAGGGTTATTGGAAATGGTGGAGGTTAAGTT TAGTAGGTAGAG	A3
	F2T/ F3X6	TTTTTTAGTGATGAGATAAGGGTTATTGGAAATGGTGGAGGTTAAGTT TAGTAGGTAGAG	A4/B2
	F3X3	TTTTTTAGTGATGAGATAAGGGTTATTGGAAATGGTGGAGGTTAAGTT TAGTAGGTAGAG	B1
	F3X12	TTTTTTAGTGATGAGATTAGGGTTATTGGAAATGGTGGAGGTTAAGTT TAGTAGGTAGAG	B3
	F3X18	TTTTTTAGTGATGAGATAAGGGTTATTGGAAATGGTGGAGGTTAAGTT TAGTAGGTAGAG	B4
	F40	CAGTTGTTGAATGCAAAGAAGAGTGCATTAATACCGGTAGTTAGG ACTGCTTGACATCCAAGCAGACCTATCTTAAC	C1/C2
	F5	CCGGTAGTTAGGACTGCTTGACATCCAAGCAGACCTATCTTAAC	C3
	F0	AGTTAGGA CTGCTTGACATCCAAGCAGACCTATCTTAAC	C4
	F1GRNA	UAAACCAUAAACUAAATCTTCTCGCTCCTCTCCTTTTCTCTTCCCTC TTTT	E1
	F1TRNA	UAAACCAUAAACUAAATCTTCTCTCCTCTCCTTTTCTCTTCCCTC TTTT	E2
	F1TNF	TCTTCTCTCTCCTCTCCTTTTCTCTTCCCTTTTT	D1/D2/D3/ D4

Table S2. *CAN^r* mutation spectra of yeast *rad27* mutant cells

Genotype	Mutation type	Occurrence
wild type	Base substitution	23/32 (72%)
	Frame shift	7/32 (22%)
	Duplication	0/32 (0%)
	Complex	2/32 (6%)
<i>rad27</i> Δ	Base substitution	0/32 (0%)
	Frame shift	0/32 (0%)
	Duplication	23/32 (72%)
	Complex	9/32 (28%)
<i>rad27-E158D</i>	Base substitution	18/23 (79%)
	Frame shift	4/23 (17%)
	Duplication	0/23 (0%)
	Complex	1/23 (4%)
<i>rad27-A157V</i>	Base substitution	5/66 (7%)
	Frame shift	4/66 (6%)
	Duplication	56/66 (85%)
	Complex	1/66 (2%)

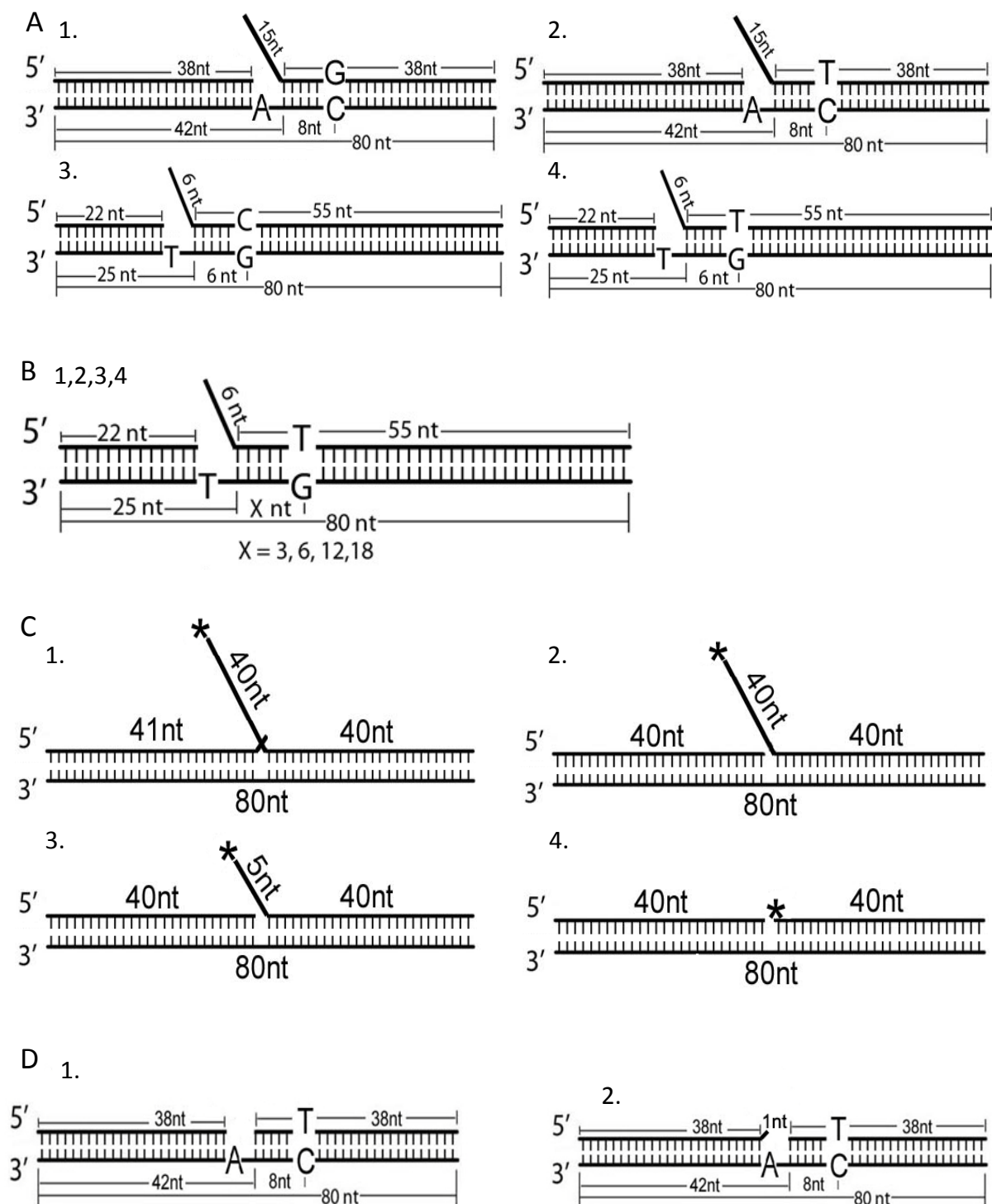


Figure S1.

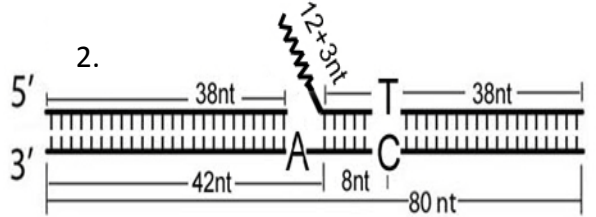
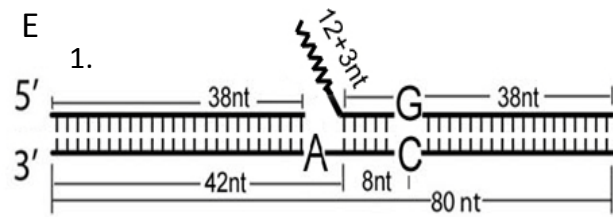
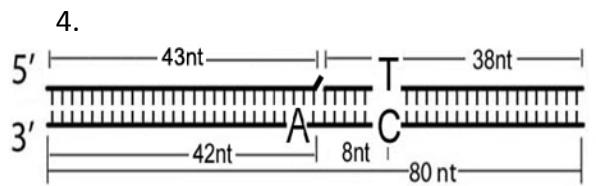
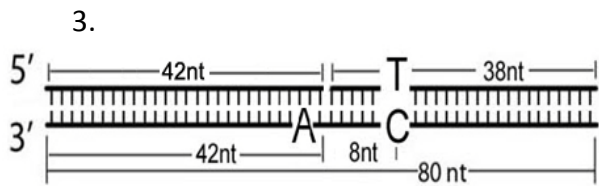


Figure S1 (continued)

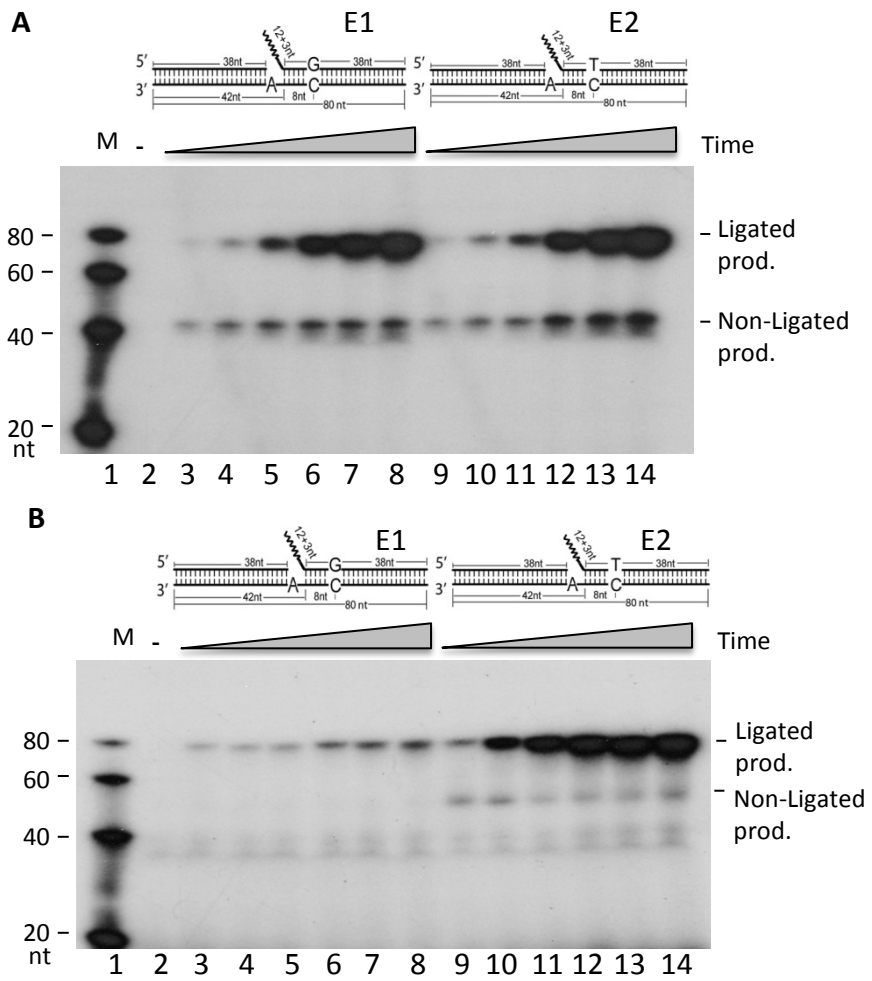


Figure S2

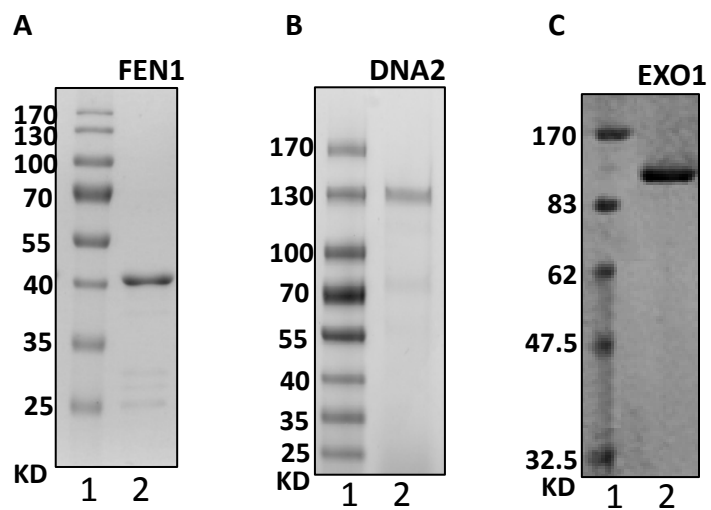


Figure S3.

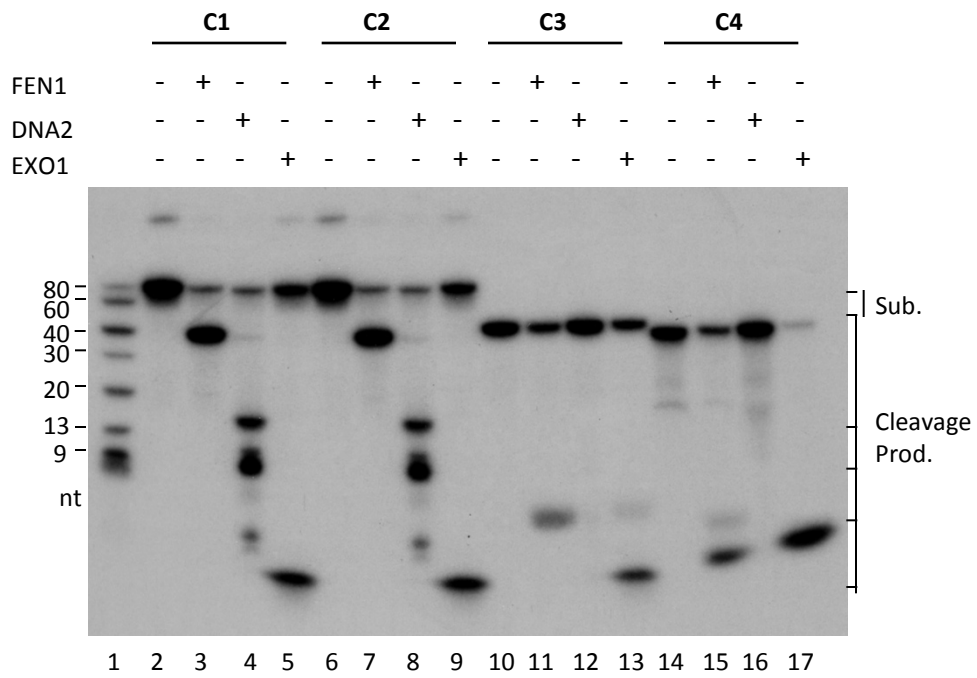


Figure S4

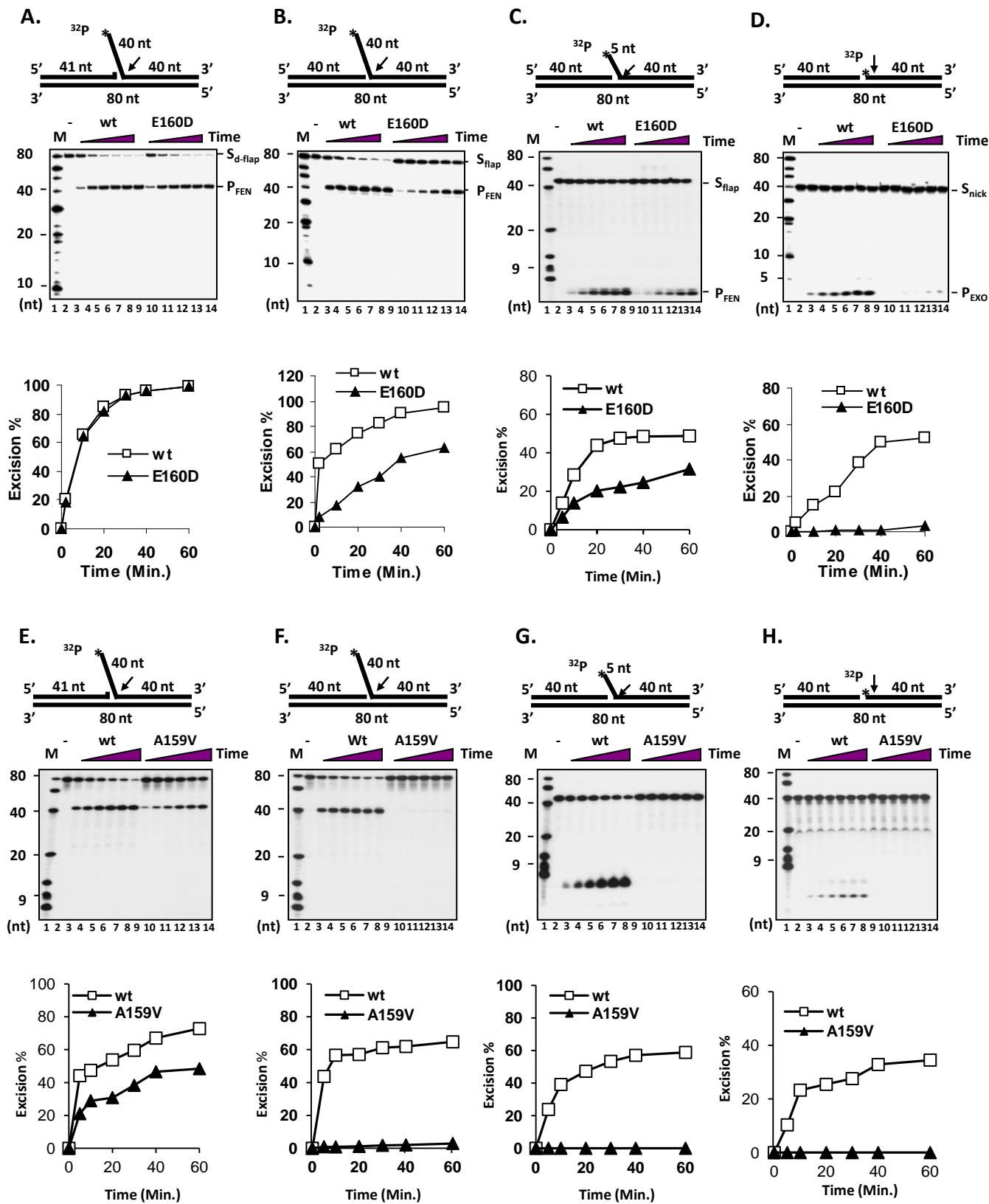


Figure S5

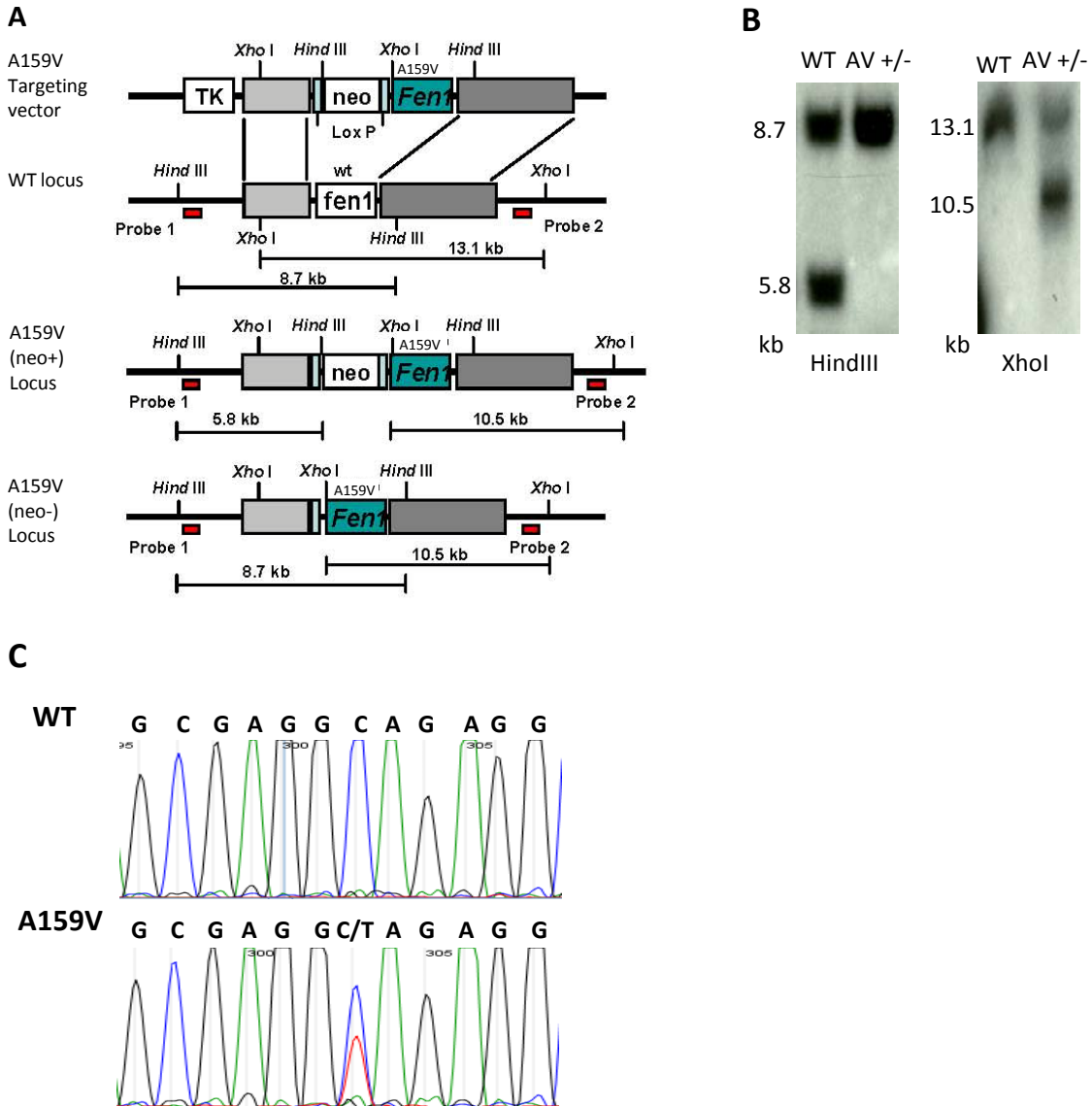
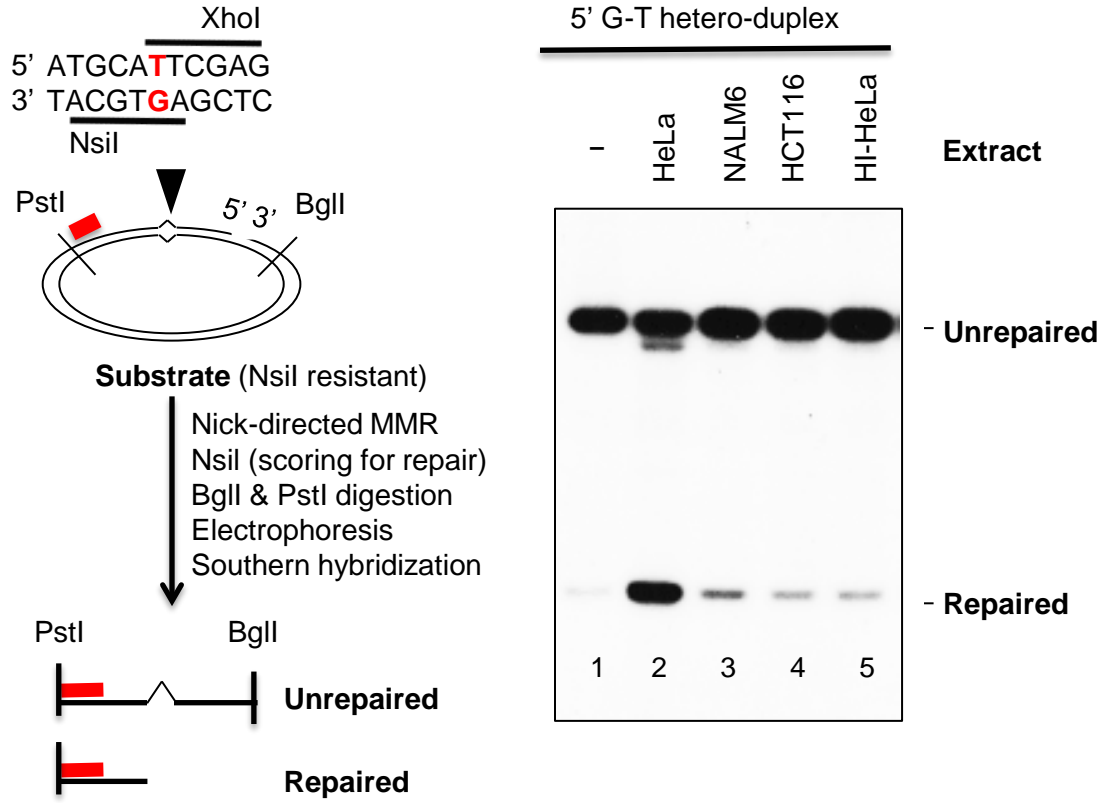


Figure S6

A



B

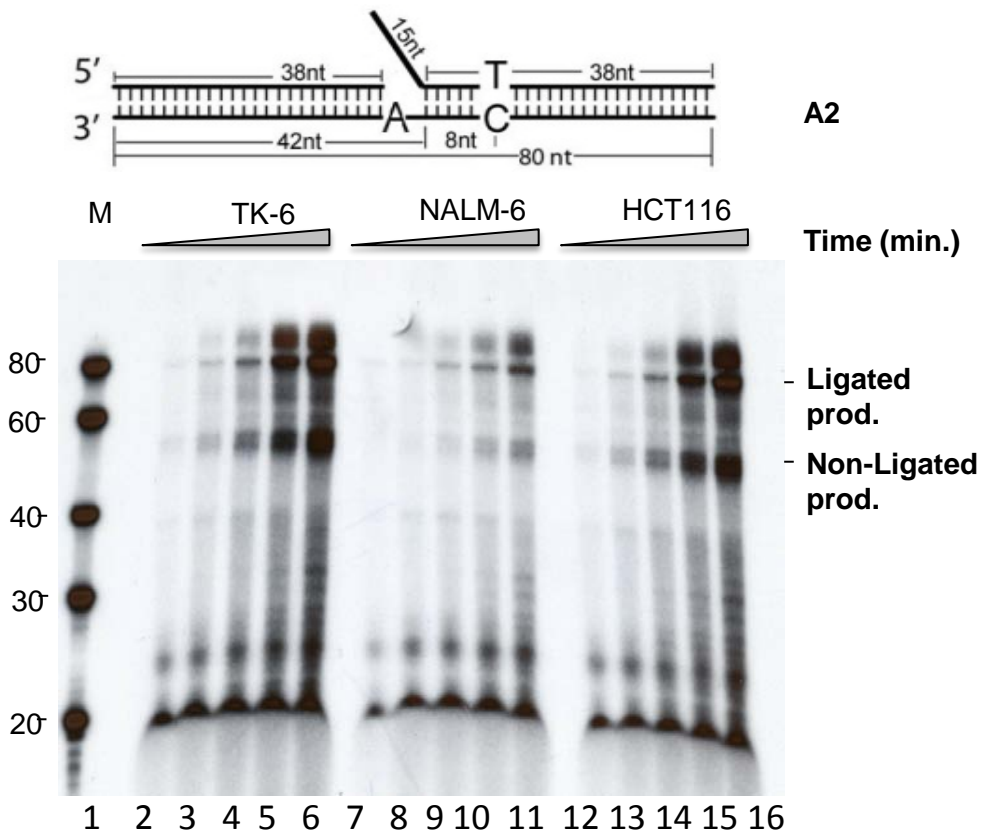


Figure S7

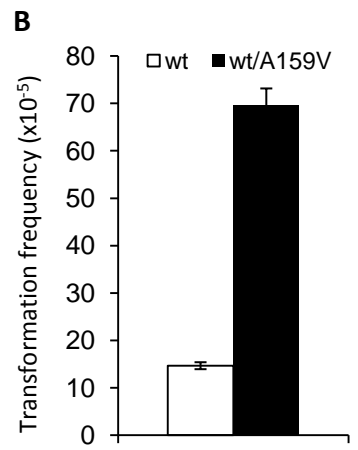
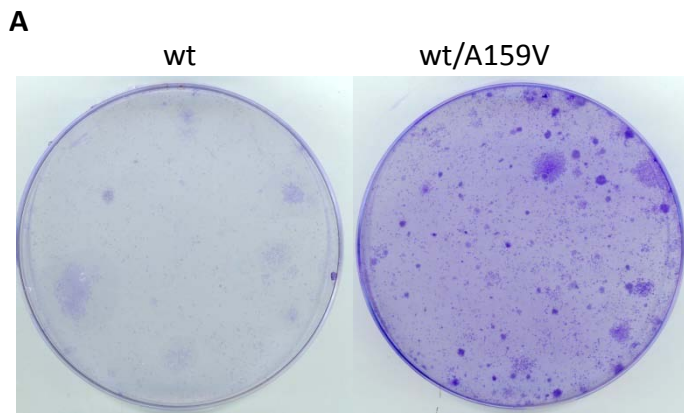


Figure S8

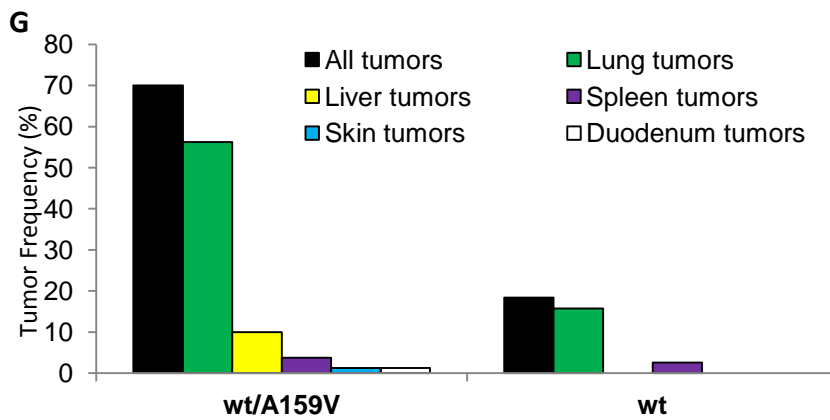
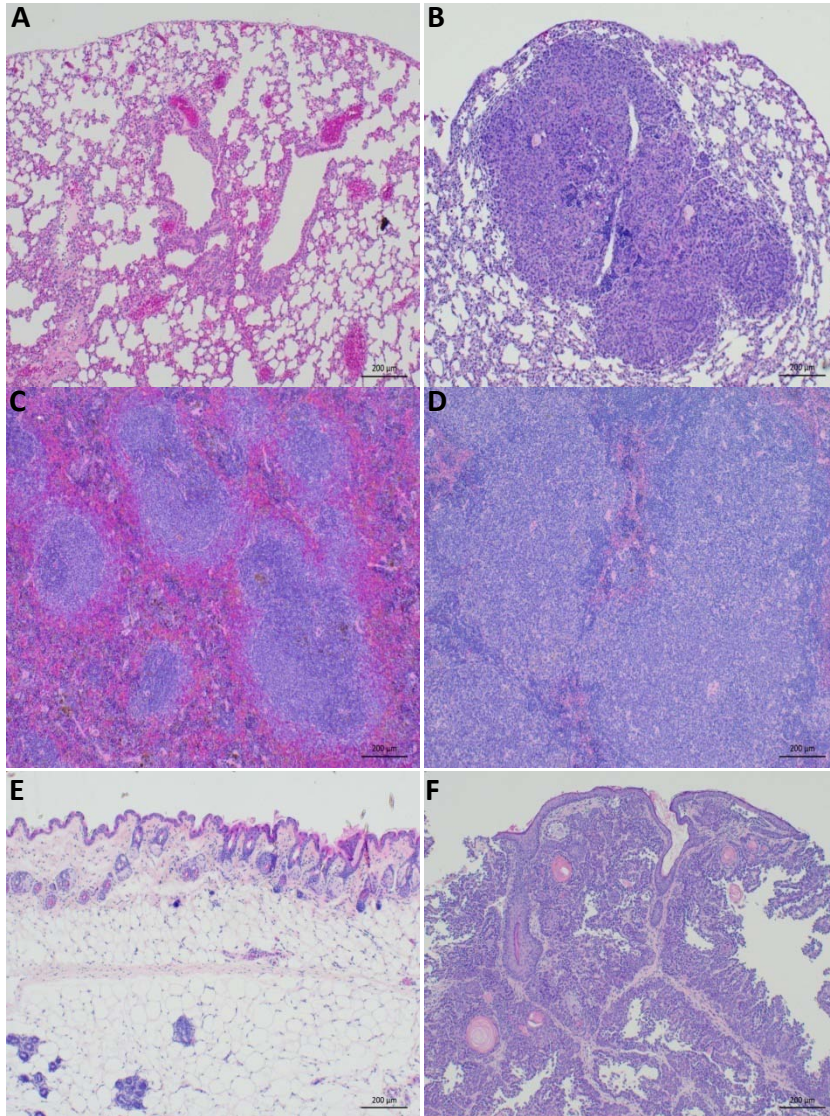


Figure S9