

Table S1: Spectrum of spontaneous mutations generated in the *rpoB* gene in a *recA730 lexA(Def) ΔdinB ΔumuDC mutL^{+/-} rnhB^{+/-}* strains in the presence of *umuC_Y11A*^a.

Position ^b	bp change	<i>rnhB⁺ mutL</i>	<i>ΔrnhB mutL</i>	<i>rnhB⁺ mutL⁺</i>	<i>ΔrnhB mutL⁺</i>
1525	AT→CG			2	
1527	CG→AT			2	
	CG→GC			26	
1532	AT→CG			2	2
1532	AT→GC	23	11		6
1534	AT→GC	151	85	2	18
1535	CG→TA		2		
1535	CG→TA	88	4	7	
1536	AT→TA			2	
1537	CG→TA	1			
1537	CG→AT			7	
1538	AT→TA		2	72	30
1538	AT→GC	15	41		
1546	CG→AT	1	3	19	22
1546	CG→TA	33	56		6
1547	AT→TA			10	10
1547	AT→GC	11	54	17	10
1576	CG→AT	1	3	7	38
1577	AT→TA	1	20	17	36
1578	CG→AT			5	
1578	CG→GC			24	
1592	CG→AT				6
1592	CG→GC			5	4
1592	CG→TA	17	21	7	
1598	AT→TA			22	4
1600	CG→TA	5			
1691	CG→TA	8	20	2	18
1714	AT→CG			17	12
1714	AT→TA	19	53	7	88
1715	AT→CG			2	
1716	CG→GC			5	
	Transitions	352 (94%)	290 (77%)	36 (12%)	58 (19%)
	Transversions	22 (6%)	85 (23%)	253 (88%)	252 (81%)
	Total	374	375	290	310

^a: The data are the number of mutants found for each type of base substitution at a particular position

^b: The numbering system originates from Garibyan *et al.*, [57], where the A of the ATG initiation codon is #1.