

Supplemental Table S4. Potential P- variant forming sequences.

1-81-S2	G	C	A	AG	A	T	TC	AT	GAAAG	ACTTCT	TCCGCTTCAACA	A	C	GAAA	GAA	CGCAAAA	T	CA	GCTT	AC	GG	A	C	A	A	C	A	C	GA	T	AC	ACCGGCGACAACGACGACACCGTTGCCGACGCCAACAACGCC	G	C	A	C	TGAATCATCTGCCACC	
var	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17			20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	
nt location		162				176	180-181	187-188	195-199	205-210	223-234	239	253	255-258	262-264	267-273	282			301-302	304-305	315	322	326				355	358-359			400-441						
		1c5				2c1	2c1	1c4	1c4	1c5	1c3	1c5	1c5	1c5	1c5	1c5	1c5			1c5	1c5	6c1	1c5	6c1				1c5	1c5			1c1						
		6c1					3c2	1c5	1c5	2c1	1c5			6c1	6c1	6c1	6c1																					
							6c1	2c1	2c1	6c1	2c4																											
								2c2	2c4		3c2																											
								2c4	6c1		6c1																											
								2c5	6c2		6c2																											
								3c1			long repeats																											
								3c2			1c3																											
								6c1			1c4																											
											2c2																											

Footnotes: The parental sequence is displayed in the first row. The var region and nt location for all the regions of *pilE* is below. Each Var column then contains the pilS copies known to cause P- colony morphology at that specific position in the gene.