

**S2 Table. Spontaneous *gtr6* mutations conferring phage Loki resistance**

<i>gtr6</i> mutation	residue changes	strain(s), this study	KL	additional strains (Genbank) <sup>b</sup>			additional strains (PATRIC) <sup>b</sup>		
				strain name	accession	KL	strain name	accession	KL
440A <sub>9→8</sub>	V142Gfs*8	JBA149 <sup>a</sup>	3	VB2107	CP051474.1	3	2015ZJAB25	WQMN01000013	3
			3	ABUH763	CP035051.1	22	2087	VMKD01000009	3
		JBA267 <sup>a</sup>	3	AC29	CP007535.2	3	208510	VMJJ01000010	3
			3	AC30	CP007577.1	3	24860_4	JFDE01000009	22
		JBA268 <sup>a</sup>	3	2018BJAB1	CP059351.1	3	4300STDY7045687	UFIZ01000012	3
				2018BJAB2	CP059350.1	3	4300STDY7045767	UFKE01000006	3
			3	2022CK-00784	CP117764.1	3	Ab83 strain D86	UEJK01000064	3
							C248	JAAZUG010000023	3
							PWa17_1044	JAJMQN010000011	3
							PWb12_715	JAJMPV010000012	3
							PWb48_2085	JAJMPN010000016	3
							PWb63_2087	JAJMPG010000011	3
							SP2107	JAAGSY010000002	3
		384A <sub>8→7</sub>	M150Cfs*22	JBA261 <sup>a</sup>	3	none			none
425::ISAba13	I131Ffs*6	EGA10	22	none			none		
		EGA65	22						

<sup>a</sup>ATCC 17978 background

<sup>b</sup>listed genomes had >75x sequencing coverage except C248 (24x), and no assembly anomalies