

Supplemental Table 5. CRISPR spacers in streptococcal isolates

	Isolate	Number of Sequences ^a	Number of spacers	Unique spacers	Average Length	Median Length	Different Repeats	Predicted Species
Subject 1	1Mut1	19	81	32	30	31	3	<i>S. salivarius</i>
	1Mut5	22	135	34	30	30	7	<i>S. salivarius</i>
	1Mut6	19	90	48	30	30	5	<i>S. salivarius</i>
	1Mut19	16	57	42	30	30	4	<i>S. salivarius</i>
	1Mut58	23	94	66	30	30	4	<i>S. salivarius</i>
	Subtotal	99	363	100^b			11^c	
Subject 2	2Mut9	17	48	31	30	30	2	<i>S. salivarius</i>
	2Mut22	20	74	46	30	30	2	<i>S. salivarius</i>
	2Mut37	19	77	21	30	30	1	<i>S. sanguinis</i>
	2Mut38	19	90	19	30	30	3	<i>S. mitis</i>
	2Mut53	18	115	60	30	30	5	<i>S. mitis</i>
	2Mut88	19	79	49	30	30	2	<i>S. salivarius</i>
	Subtotal	108	240	155^b			7^c	
Subject 3	3Mut13	15	65	16	30	30	3	<i>S. anginosus</i>
	3Mut21	13	32	31	30	31	6	<i>S. salivarius</i>
	3Mut32	21	60	53	30	31	3	<i>S. salivarius</i>
	3Mut47	10	26	26	30	31	4	<i>S. salivarius</i>
	Subtotal	70	183	119^b			9^c	
Subject 4	4Mut13	16	89	36	30	30	9	<i>S. salivarius</i>
	4Mut53	13	45	27	30	30	4	<i>S. mitis</i>
	4Mut54	12	24	14	31	30	4	<i>S. salivarius</i>
	4Mut79	10	17	16	30	30	3	<i>S. salivarius</i>
	4Mut94	13	16	16	33	31	3	<i>S. salivarius</i>
	Subtotal	76	134	63^b			11^c	

^aIncludes only sequences containing a minimum of 2 full repeats and 1 full spacer

^bIncludes only unique spacers across isolates for each subject

^cIncludes only unique repeat motifs across all isolates for each subject