BamHI fragment	dir	tag position	3′ end offset	# tags in genome	# tags sampled	seq
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307	f	2080293	119	1	2	GGCTCTTGCACAGGTAA
308	r	2080603	185	1	5	AGGTTTGAAGTGCTAAA
308	f	2092438	525	1	3	AGTACCATTGATATTAA
309	r	2093046	77	1	2	GGTCACAATAACCATTG
309	f	2106132	133	1	1	GATAATCGCTTGATATT
310	r	2106890	619	1	5	GGTTTGTATGGCGTTTT
310	f	2120014	86	1	2	TTGTACGGGGGAAGTAA
311	r	2120182	76	1	3	GTCTGTACTTCCGATGA
311	f	2129488	88	1	2	CCCGAATTTGGCAGCAA
312	r	2129969	387	1	3	CACAGTGACGTGCAGCG
312	f	2130738	304	1	5	CGGTAGGTTACGCCTCT
313	r	2131064	16	1		CAAAGGTGTTCTGGATC
313	f	2134087	267	1	5	ATCAGGTAGAAGCGATG
314	r	2134555	195	1	3	GTGCGCCGGTATCATAA
314	**f**	**2172626**	**155**	**1**		**GTACTGCCATTGCTATC**
315	**r**	**2172984**	**197**	**1**		**AACACATCCCCCATCAC**
315	**f**	**2175158**	**29**	**1**		**ATAGCCTGATAACCCGA**
316	**r**	**2175558**	**365**	**1**		**TTACCCGAATCGCAACG**
316	**f**	**2175554**	**171**	**1**		**CGATCATCTGTTGACAG**
317	**r**	**2175753**	**22**	**1**		**TGGCGTTTTCGTCAGCA**
317	**f**	**2178777**	**94**	**1**		**CAGGCATTCATTCCCGC**
318	**r**	**2179119**	**242**	**1**		**TTGATGATGAACGGCTG**
318	**f**	**2180595**	**136**	**1**		**TTTTTAACTACGGCGTC**
319	**r**	**2180781**	**44**	**1**		**GATATCAATAACGTCGG**
319	**f**	**2180777**	**305**	**1**		**CGGTCTTCACGGGTCAT**
321	**r**	**2181536**	**26**	**1**		**TTGAAGTTCGTAGCAAA**
321	**f**	**2183946**	**107**	**1**		**GCAAAAGTGAAAACAGA**
322	**r**	**2184222**	**163**	**1**		**TCCCTTTGATTGAGATG**
322	**f**	**2195480**	**345**	**1**		**GTAGCGACAATCGAGAG**
323	**r**	**2195891**	**60**	**1**		**ATACGGGTTACCACAAA**
323	**f**	**2216837**	**169**	**1**		**TTGATTTGGATTATCTC**
324	**r**	**2217541**	**529**	**1**		**CTTCGCTTTCTGGTTCT**
324	**f**	**2226652**	**345**	**1**		**CCGTTCGGTTCAGCATT**
325	**r**	**2227109**	**106**	**1**		**GTGGCCCCCATTGGGTT**
325	**f**	**2229741**	**78**	**1**		**ACCTCTCTACCACAAAA**
326	**r**	**2230734**	**909**	**1**		**ACGTGCTGGCTCATCGT**
326	**f**	**2230730**	**87**	**1**		**TTTAACGCGGTATTGTC**
327	**r**	**2230891**	**68**	**1**		**GCAGGCCAGAGTCACAT**
327	**f**	**2254414**	**33**	**1**		**CCAGAGTCAGTTTTTCA**
328	r	2254501	48	1	3	GCAAGCGGATGAAATTA
328	f	2267812	51	1	2	TGCGACCTTGTAAGAAA
329	r	2268386	517	1	2	AACGCGACTCAAGCTGT
329	f	2271255	24	1		CCAGTGTTTAACACCCG
330	r	2271393	108	1	6	GCACACGCATCCCCTTG
330	f	2273387	202	1		ACTCGTCTGTCGCACCG
331	r	2273759	164	1	1	ATTAAGCGTTCTATCTC
331	f	2280614	341	1	7	GGATCTGTATCTGGCAT
332	r	2281344	383	1	7	TGGCCGCCGCGCTTAAA
332	f	2287128	88	1	2	TCACCCCATTTTGTTGG
333	r	2287254	32	1	3	TCCATCCCACTGGAAAG
333	f	2289939	1057	1	3	TTAACACCACCGATTCA
334	r	2291018	16	1	2	AGCCAACCGCCGGGATC
334	f	2305777	20	1		AAGTGAAAAATGGTCTG
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While statistical fluctuations lead to sporadic zero counts for some tags, a long contiguous stretch indicates a deletion in our sample with respect to the CO92 sequence. In this case, the missing DNA is a pathogenicity island