Table 7. Putatively invertible regions on the BT strain VPI-5482 genome

Region	IR sequence [*]	Affected genes [†]	Description [‡]	Inversion type [§]	Recombinase [¶]
Class II IR (AGTTC{N$_5$}GAACT)					
1	IR-1:74-bp repeat IR-2:286-bp repeat	BT3239-BT3235	SusC / HP (family 1) / OMLP (family 1) / OMP (family 1) / OMLP (family 2)	1-b [‖]	-
		BT3240-BT3244	SusC / HP (family 1) / OMLP (family 1) / OMP (family 1) / OMLP (family 2)		
2	AGTTCTTGTAGAACT	BT4040-BT4038	Putative galactose oxidase / SusC / SusD	1-a	-
3	AGTTCTGTTAGAACT	BT4248-BT4244	Putative antisigma factor / SusC / SusD / IMP / OMP	1-c	-
		BT4249-BT4250	HP (N-terminal part of antisigma factor) / ECF-type sigma factor		
4	ATACTAAGTTCAAAGAGAACTTGGAAATTACA	BT4440-BT4441	Putative cell surface proteins	2	-
5	AGTTCATGGAGAACTTGGT	BT0867-BT0865	SusC / SusD / putative chitobiase	1-a	-
Class III IR (GTTAC{N$_7$}GTAAC)					
6	GTTACTTCTTAGGTAACGGAAGT	BT0376-BT0400	UpxYZ-PS-1	1-a	+
7	GTTACTTCTTAGGTAACGGA	BT0596-BT0614	UpxYZ-PS-3	1-a	+
8	CGTTACTTCTTAGGTAACG	BT1656-BT1642	UpxYZ-PS-5	1-a	+
9	CGTTACTTCTTAGGTAACG	BT1725-BT1707	UpxYZ-PS-6	1-a	+
10	GTTACTTTCTAGGTAACGG	BT4480-BT4481	HP / OMP (OmpA family)	1-a	+
11	TGTTACTTCTTAGGTAACGGAAA	BT0292-BT0294	OMP / HP / HP	1-a	+
12	GTTACTTCATAGGTAACGG	BT1502-	OMP (family 2) / OMP (OmpA	1-a	+

		BT1501	family)		
13	GTTACTTTGTAGGTAACGG	BT1507-BT1505	OMP (family 2) / IMP / OMP (OmpA family)	1-a	+
14	GTTACTCTGTAGGTAACGG	BT1512-BT1511	OMP / putative cell surface protein	1-a	+
15	GTTACTTTGTAGGTAACGGGAA	BT1792-BT1791	Putative cell surface protein / OMP	1-a	+
16	GTTACTTGGTAGGTAACGGG	BT1826	IMP	1-a	+
17	GTTACTTTGTAGGTAACGGGAA	BT1927	HP	1-a	+
18	GTTACTTCTTAGGTAACGG	BT2444	IMP	1-a	+
19	GTTACTTTGTAGGTAACGGG	BT2486-BT2485	IMP / OMP (OmpA family)	1-a	+
Class IV IR (TCTGCAAAGNCTTTGCAGA)					
20	TCTGCAAAGACTTTGCARA	BT2260-BT2259	SusC / IMP	4	+
		BT2264-BT2261	SusC / OMLP / OMLP / OMP		
		BT2268-BT2269	SusC / SusD		

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*Consensus motif sequences are underlined.

[†] Promoter orientations of each region in the final sequence assembly are indicated by red (on orientation) and blue (off-orientation) letters.

[‡] Gene products related to the synthesis of surface structures are indicated by green letters. IMP, putative inner membrane protein; OMP, putative outer membrane protein; OMLP, putative outer membrane lipoprotein; HP, hypothetical protein.

[§] Functional classification of DNA inversions is shown in Fig. 2.

[¶] Plus or minus indicates whether a site-specific recombinase gene is colocalized or not.

[||] IR-1 and IR-2 both located in the N-terminal parts of BT3239 and BT3240. The DNA inversions via these IRs exchange the N-terminal coding sequences of the two ORFs. However, because the N-terminal coding sequences of the two ORFs are highly conserved, the DNA inversions via IR-1 and IR-2 result in only three and no amino acids exchanges, respectively. Thus, the

DNA inversion in this region is categorized as type 1-b.