Table 6. Invertible regions identified on the genome of BF strain YCH46

Region	IR sequence [*]	Affected genes [†]	Description [‡]	Inversion type [§]	Recombinase [¶]
Class I IR (ARACGTWCGT)					
1	AAACGTTCGTCTATTTGAAC	BF0803-BF0827	UpxYZ-PS-1	1-a	-
2	TGTTTCAAAAAACGTTCGT	BF1428-BF1445	UpxYZ-PS-3	1-a	-
3	AGTGTTTCAATAGACGTTCGTTTAA	BF1528-BF1551	UpxYZ-PS-4	1-a	-
4	TGTTTCAAAAAACGTTCGT	BF1828-BF1848	UpxYZ-PS-5	1-a	-
5	TGTTTCAAAARACGTTCGT	BF2585-BF2566	UpxYZ-PS-6	1-a	-
6	TGTTTCAAAAAACGTTCGT	BF3667-BF3644	UpxYZ-PS-8	1-a	-
7	AGTGTTTCAATARACGATCGTCT	BF3925-BF3925	UpxYZ-PS-9	1-a	-
8	TGTTTCAAAARACGTTCST	BF0074-BF0076	Putative electron transport protein / polysaccharide deacetylase/ IMP	1-b	-
		BF0077-BF0078	OMLP (family 1) / OMP		
9	TGTTTCAAAARACGTACGTCT	BF0160	OMLP (family 1)	1-a	-
10	ATGTGTTTTTAAACGTACGTTTA	BF1219-BF1220	Fe^{3+} ABC transporter, permease and ATP-binding protein	1-b	-
		BF1221-BF1224	HP / capsular polysaccharide export protein / HP / putative transcriptional regulator		
11	TGTTTCAAAAGACGTTCGTCT	BF4332	OMLP (family 1)	1-a	-

12	TGTTTCAAARGACGTACGT	BF4334-BF4335	HP similar to OMLP (family 1) / HP	1-a	-
13	TGTTTCAAAAGACGTTCST	BF4531	HP similar to OMLP (family 1)	1-a	-
14	TGTTTCAAAARACGTACGTCT	BF4533	OMLP (family 1)	1-a	-
Class II IR (AGTTC{N$_5$}GAACT)					
15	ATCGCCAAAGTTCTTCTGGAACTT	BF0388-BF0389	Two-component sensor histidine kinase/response regulator hybrid (one-component regulatory system)	2	-
16	AAGTYCTATCAGAACTT	BF0568-BF0569	SusC / SusD	1-d	-
17	IR-1:TGTTCTACTTAAGTTCTTCGAGAAC	BF0952-BF0953	SusC / SusD	4	-
		BF0948-BF0947	SusC / SusD		
	IR-2:TTCCTAAGTTCCGTATGAACTT	BF0946-BF0945	SusC / SusD		
	IR-3:439-bp inverted repeat	BF0944-BF0943	SusC / SusD		
18	AGTTCTCTTAGAACT	BF1893	HP	1-b	-
		BF1894-BF1895	OMP / IMP		
19	TCCTAGTTCTTACGGAACTTGGAAAA	BF2347-BF2353	CHP / HP / HP / IMP / HP / HP / HP	3	-
		BF2354-BF2355	HPs belonging same paralog family		
		BF2356	IMP		
20	AGTTCTAAAGGAACTA	BF3102-BF3105	Putative chitobiase / SusD / SusC / antisigma factor	1-c	-
		BF3106-BF3107	CHP (N-terminal part of antisigma factor) / ECF-type sigma factor		
21	AGTYCTTTCAGAACT	BF3436-BF3437	SusD / SusC	1-a	-

22	AGTTCCTGTAGAACTT	BF3784-BF3785	SusD / SusC	1-a	-
23	AGTTCTAACTGRACTT	BF4448-BF4449	SusC / SusD	1-a	-
24	AGTTCTCACGGAACTT	BF4460	SusC	1-a	-
Class III IR (GTTAC{N_7}GTAAC)					
25	GTTACTTTGTAGGTAACGGCA	BF3000-BF2992	HP / OMP (family 1) / CHP / OMLP / CHP / OMP / OMP / OMP / OMP	1-a	+
26	CCGTTACTTCGTAGGTAACGGGA	BF4031-BF4023	OMLP / IMP / OMP (family 1) / OMP / OMP / IMP / IMP / OMP / HP	1-a	+
27	GTTACTTTGTAGGTAAC	BF4281-BF4279	OMLP / OMP / OMLP	1-a	+
Class IV IR (TACTTANTAGGTAANAGAA)					
28	TCCCTTACTTATTAGGTAATAGAACA	BF2767-BF2769	Glycosyltransferase / polysaccharide export OMP / tyrosine-protein kinase	1-a	+
29	TACTTAATAGGTAAGAGAA	BF3395-BF3396 BF3397	10-kD chaperonine, GroES / 60-kD chaperonine, GroEL HP	1-b	-
Class V IR (TCTGCAAAGNCTTTGCAGA)					
30	TCTGCAAAGACTTTGCAGA	BF0665-BF0666 BF0668-BF0669 BF0670-BF0671	OMP / SusC SusC / SusD SusC / SusD	4	+
Class VI IR (ACTAAGTTCTATCGG)					
31	ACTAAGTTCTATCGG	BF1710-BF1712 BF1713-BF1714 BF1715-BF1717 BF1718-BF1720 BF1722-BF1723	SusC / SusD / HP SusC / SusD CHP / HP / putative ATPase SusC / SusD / α-L-fucosidase SusC / SusD	4	-

BF1724-BF1725	SusC / SusD

*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; CHP, conserved hypothetical protein; 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.