SUPPLEMENTARY INFORMATION
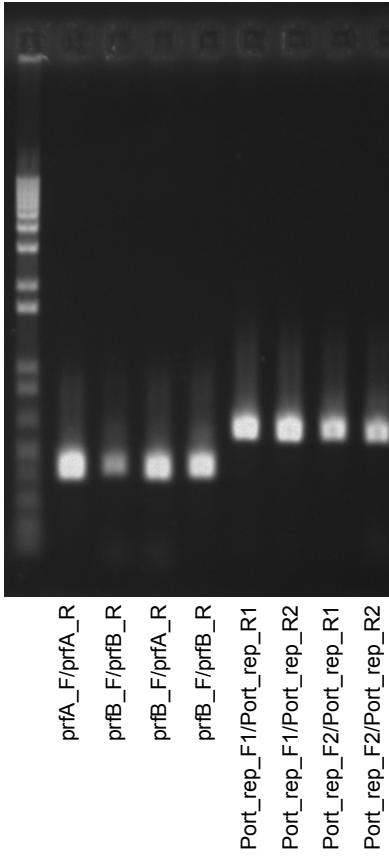

Figure S1. PCR-based evidence for the coexistence of alternative *Portiera* BT genome conformations in individual insects. DNA was extracted from a single *Bemisia tabaci* (biotype B) individual and successfully amplified with all four pairwise combinations of primers flanking the two sets of identical repeats found in the genome (see main text). Primer combinations are indicated below each lane and correspond to the sequences provided in Table S1.
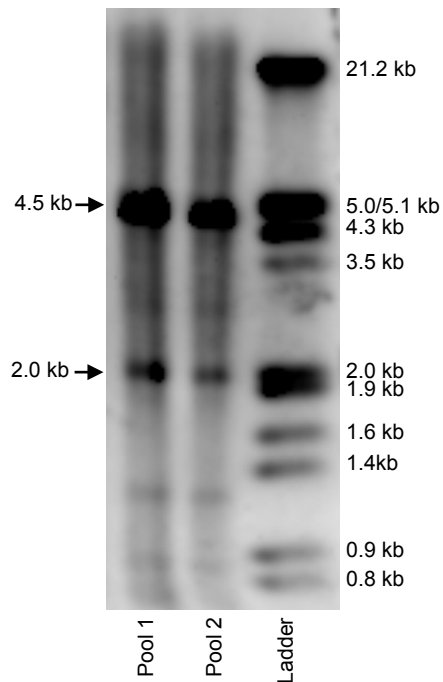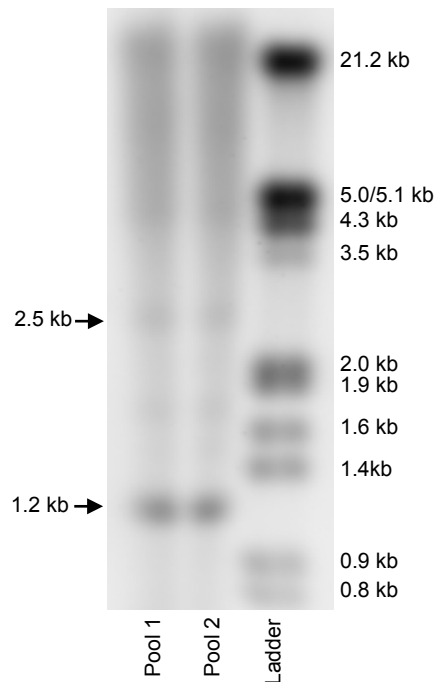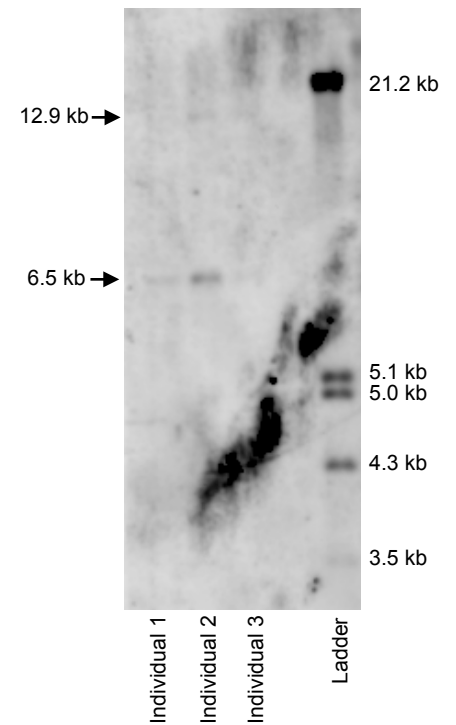
A. EcoRI Digest – *prfB* Probe

4.5 kb →
2.0 kb →

21.2 kb
5.0/5.1 kb
4.3 kb
3.5 kb
2.0 kb
1.9 kb
1.6 kb
1.4kb
0.9 kb
0.8 kb

Pool 1   Pool 2   Ladder

B. EcoRV/SpeI Digest – 6.5kb_flank Probe

2.5 kb →
1.2 kb →

21.2 kb
5.0/5.1 kb
4.3 kb
3.5 kb
2.0 kb
1.9 kb
1.6 kb
1.4kb
0.9 kb
0.8 kb

Pool 1   Pool 2   Ladder

C. EcoRV Digest – 6.5kb Probe

12.9 kb →
6.5 kb →

21.2 kb
5.1 kb
5.0 kb
4.3 kb
3.5 kb

Individual 1   Individual 2   Individual 3   Ladder

Figure S2. DNA gel blot hybridizations confirming the existence of alternative *Portiera* BT genome structures. (A) Hybridizing EcoRI digested DNA with a probe immediately upstream of *prfB* verified that this gene exists in its "normal" conformation (4.5 kb fragment) as well as a chimeric form (2.0 kb fragment) resulting from recombination with an identical repeat in *prfA*. (B) Hybridizing EcoRV/SpeI digested DNA with a probe outside of the 349 bp identical repeat sequence confirmed that chromosomes lacking any copies of the 6.5 kb sequence (1.2 kb fragment) were more abundant than chromosomes with one or more copies of this sequence (2.5 kb fragment). (C) Hybridizations generated with low concentration DNA extracted from individual whiteflies showed that the same EcoRV 6.5/12.9 kb structural polymorphism observed in pooled DNA samples (fig. 2) could also be detected within a single host insect.

Table S1. PCR Primer Sequences

Purpose	Primer Name	Primer Sequence (5' to 3')
PCR-based detection of alternative genome conformations	prfA_F	CAGGTACACATCGAGTACAAAG
	prfA_R	CCTTGTGCAAAATTGTAAGTACG
	prfB_F	AAGGTATTCATCGCTTAGTTCG
	prfB_R	CTTTTATTCTCTGAGCATCTAACAC
	Port_rep_F1	CCTTTATTTTTCACAAAATCAAATAGCC
	Port_rep_R1	AAAAGTATCCAACTAATATGTTCAGC
	Port_rep_F2	AACATAAGACTTACACATACAGATAAC
	Port_rep_R2	GATGTTAATTTTTGCTTGTGTTCTG
Amplification of probes for DNA gel blots	6.5kb_blot_F	ATTGCCTATTGCCTCTTTCCTCT
	6.5kb_blot_R	AAAAAGGGCTATTTGATTTTGTGA
	6.5kb_flank_blot_F	TTAACAATCAAACTAACAGCAAAAA
	6.5kb_flank_blot_R	TGTATAATTCAATAACAACGAACATTT
	prfB_blot_F	CGGACATGCTGTGTTTATTTTT
	prfB_blot_R	TTTCAGTACGCATCCATCCA