Supporting Information

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SI Text

Phylogenetic Analysis. The following proteins were used in this analysis: elongation factor Tu; initiation factor 2; leucyl-tRNA synthetase; phenylalanyl-tRNA synthetase, beta subunit; valyl-tRNA synthetase; RNA polymerase, beta subunit; and ribosomal protein subunits L2, S5 and S11. Amino acid sequences were obtained from the following genomes (Genbank accession numbers): *Bacillus subtilis str.* 168 (AL009126), *Bacteroides fragilis* NCTC 9343 (CR626927), *B. fragilis* YCH46 (AP006841), *B. thetaiotaomicron* VPI-5482 (AE015928), Candidatus *Sulcia muelleri* GWSS (CP000770), *Chlorobaculum parvum* NCIB 8327 (CP001099), *Chlorobium phaeobacteroides* BS1 (CP001101), *Cytophaga hutchinsonii* ATCC 33406 (CP000383), *Flavobacteriales bacterium* HTCC2170 (AAOC00000000), *Flavobacterium johnsoniae* UW101 (CP000685), *Gramella forsetii* KT0803 (CU207366), and *Salinibacter ruber* DSM 13855 (CP000159).

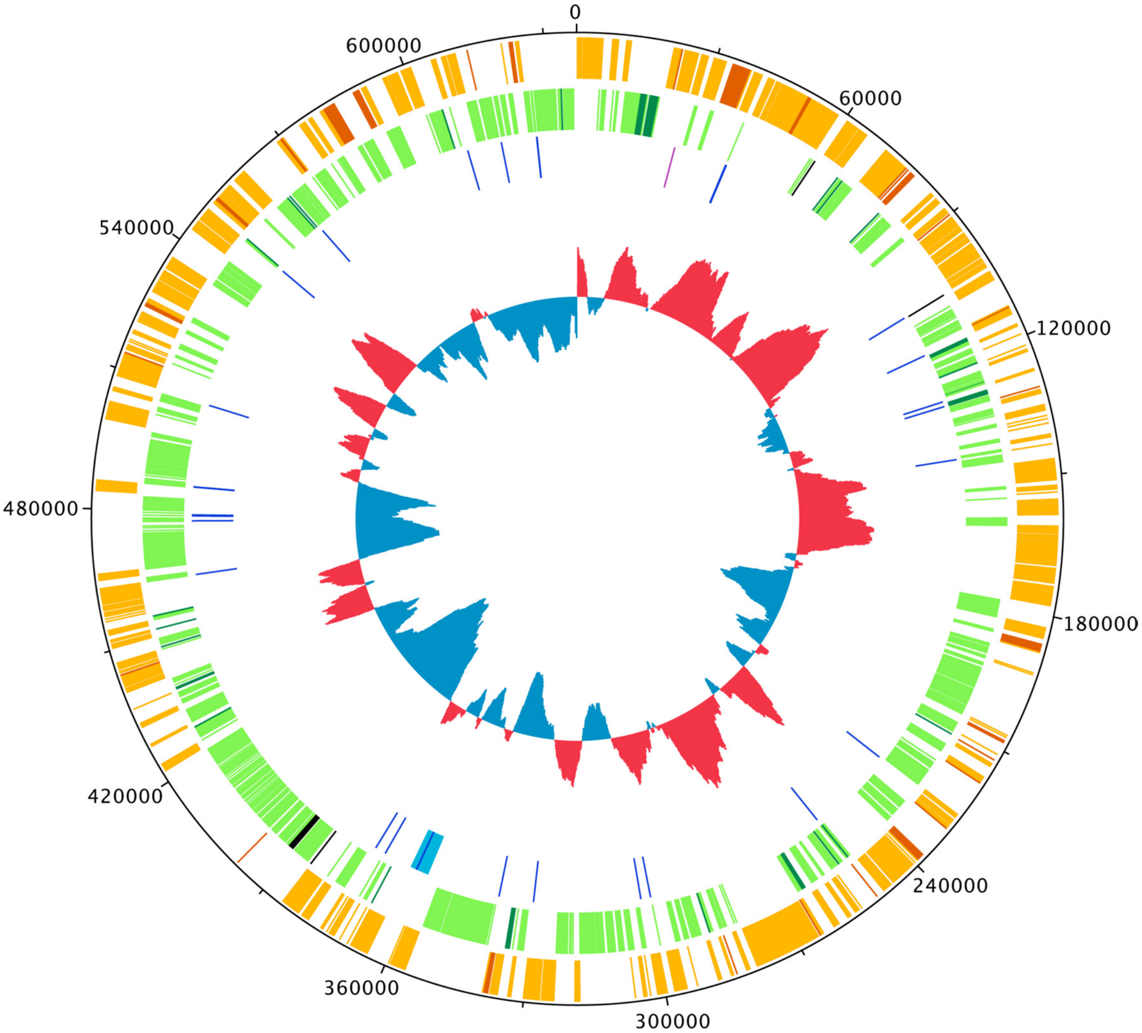

Fig. S1. Graphical representation of the *Blattabacterium* sp. BPLAN chromosome. The concentric rings illustrate the following features (from the outer ring to the innermost): (1) Numbered base pair ring (coordinates in bp); (2) Protein-coding genes, forward strand: goldenrod, proteins with assigned function; pumpkin, conserved hypothetical proteins; (3) Protein-coding genes, reverse strand: chartreuse, proteins with assigned function; dark green, conserved hypothetical proteins; black, pseudogenes; (4) RNA-encoding genes: light blue, rRNAs; royal blue, tRNAs; magenta, tmRNA; (5) GC skew: red, >0; blue, <0.

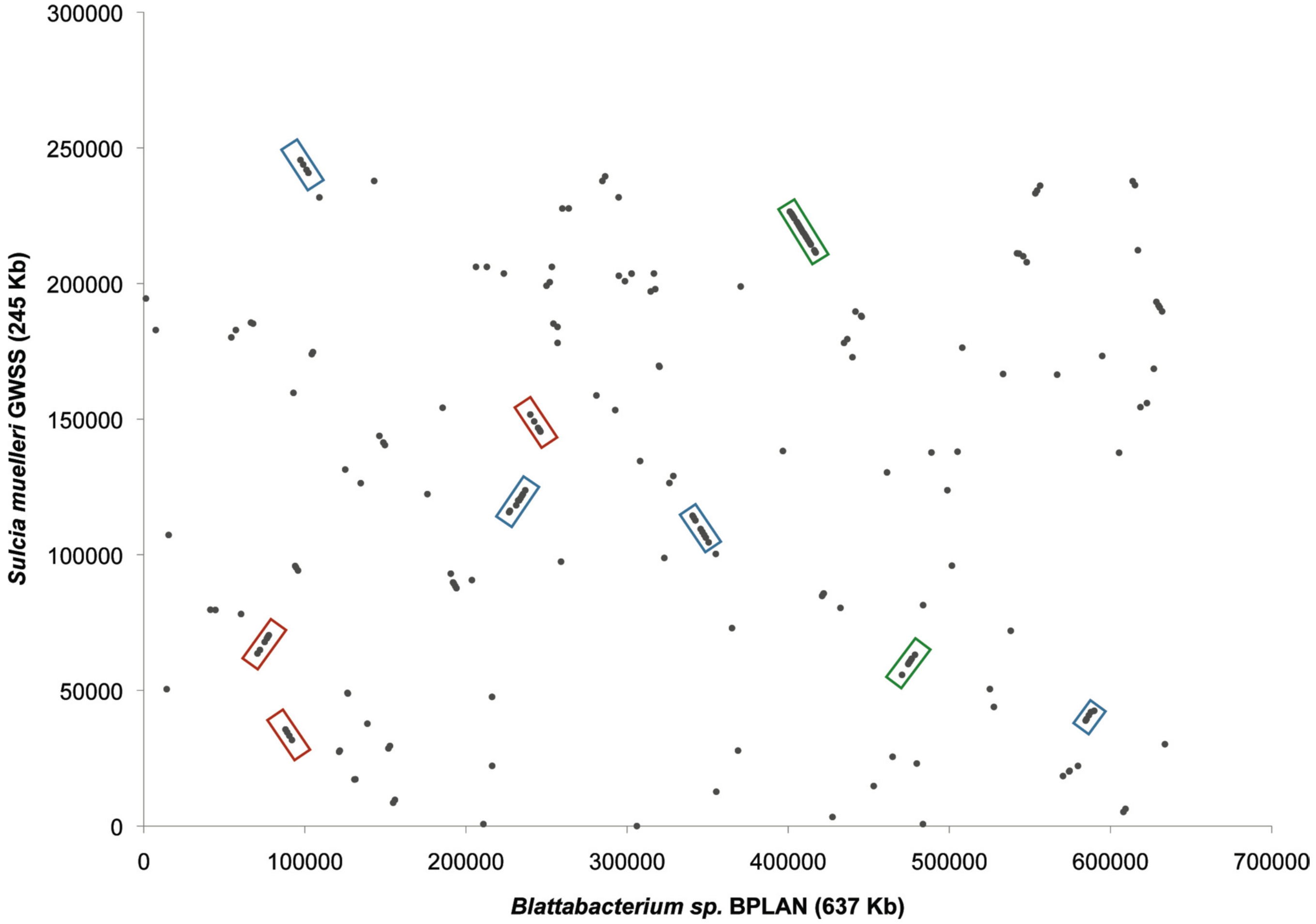

Fig. S2. Gene order dot-plot comparison of homologous proteins from *Blattabacterium* sp. BPLAN and *Sulcia muelleri* GWSS. Genes encoding proteins involved in translation and ribosome structure (green), amino acid biosynthesis (blue), and energy production (red) pathways are indicated.

Table S1. COG distribution of chromosomal and plasmid-encoded *Blattabacterium* sp. BPLAN genes compared with those of other Flavobacteriales

	Blattabacterium sp. BPLAN (563)	*Sulcia muelleri* GWSS (226)	*Flavobacterium johnsonii* UW101 (3,481)
Amino acid transport and metabolism	13.14	20.35	7.35
Carbohydrate transport and metabolism	3.55	1.33	7.04
Cell cycle control, cell division, and chromosome partitioning	1.60	1.33	0.57
Cell motility and secretion	0.18	<1	0.26
Cell wall, envelope, and outer membrane biogenesis	6.39	2.65	7.99
Coenzyme metabolism	7.82	4.42	3.96
Defense mechanisms	0.71	–	1.95
DNA replication, recombination, and repair	5.33	3.54	4.91
Energy production and conversion	7.10	11.95	4.77
Function unknown	2.31	0.44	8.56
General function prediction only	7.64	3.54	12.90
Inorganic ion transport and metabolism	2.66	0.88	5.75
Intracellular trafficking, secretion, and vesicular transport	2.66	3.54	1.41
Lipid metabolism	3.55	0.88	3.76
Nucleotide transport and metabolism	5.86	1.33	2.10
Posttranslational modification, protein turnover, and chaperones	5.15	6.64	3.85
Secondary metabolite biosynthesis, transport, and catabolism	1.24	0.88	2.84
Signal transduction mechanisms	0.36	<1	6.75
Transcription	2.84	2.21	8.45
Translation, ribosomal structure, and biogenesis	19.89	34.07	4.83

The COG distributions are represented as percentages of coding sequences assigned to a category. The values in parentheses represent the number of ORFs assigned to COGs in the genome.