

1 **Supplementary Figure legends**

2 Fig. S1. Overview of CRISPR locus found from the genome of strain BD-a59. Repeats are
3 shown as black diamonds, spacers are numbered on open boxes, and the leader (L) is shown
4 on the box with slashes. The terminal repeat of the CRISPR locus is marked with a letter “T”
5 inside the last black diamond. *orf1* (DSC_15230) and *orf2* (DSC_15270) are coding genes of
6 uracil-DNA glycosylase and *O*-sialoglycoprotein endopeptidase. The nucleotide sequence in
7 bottom line represents the consensus palindromic repeated sequence. *cas*, CRISPR-associated
8 genes; *csd*, *cas* subtypes in *Desulfovibrio*.

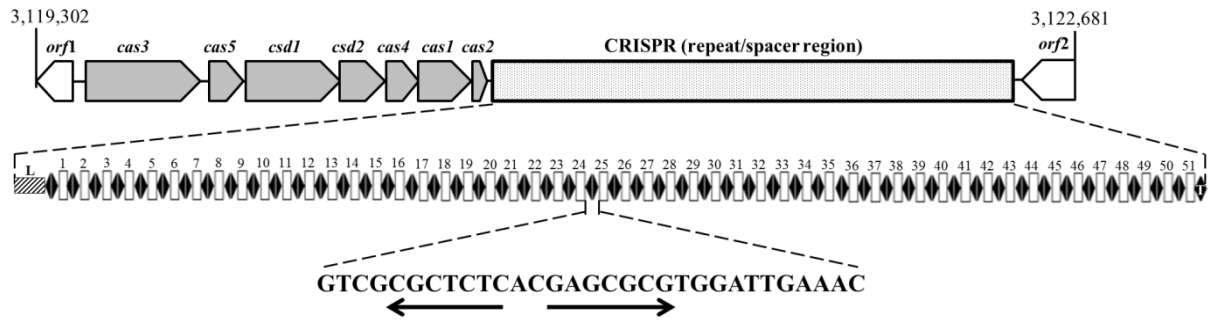
9 Fig. S2. Genomic alignment showing extensive genome-wide rearrangements in strains BD-
10 a59 and 11-1 in the form of reciprocal inversions. Boxes with identical colors represent local
11 colinear blocks (LCB), indicating homologous DNA regions. Regions that are inverted
12 relative to strain BD-a59 are shifted downward in the genome of strain 11-1.

13 Fig. S3. The GC/MS chromatograms documenting BTEX metabolites (analyzed as BSTFA
14 derivatives) of strain BD-a59 in MSB supplied with 250 ppm of (a) toluene, (b) benzene, (c)
15 *o*-xylene, (d) *m*-xylene, (e) *p*-xylene, and (f) ethylbenzene.

16

17 **Supplementary Figure S1**

18



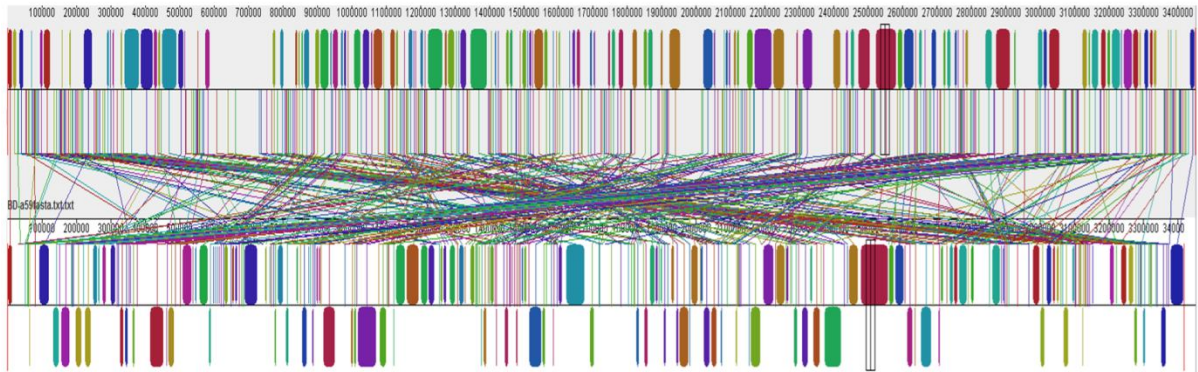
19

20

21

22 **Supplementary Figure S2**

Strain BD-a59



23 **Strain 11-1**

24

25

