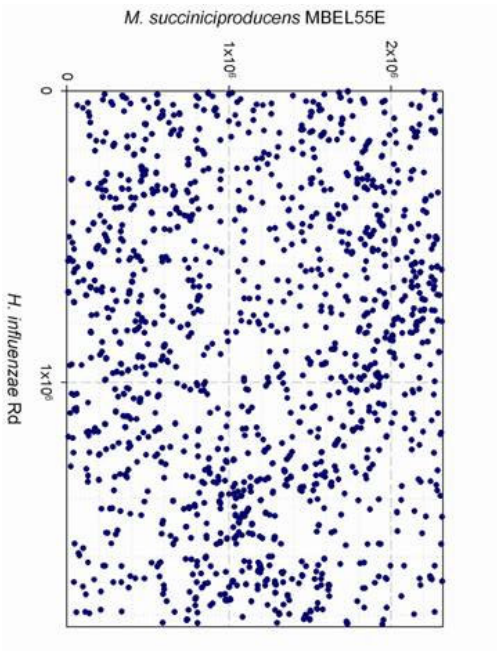




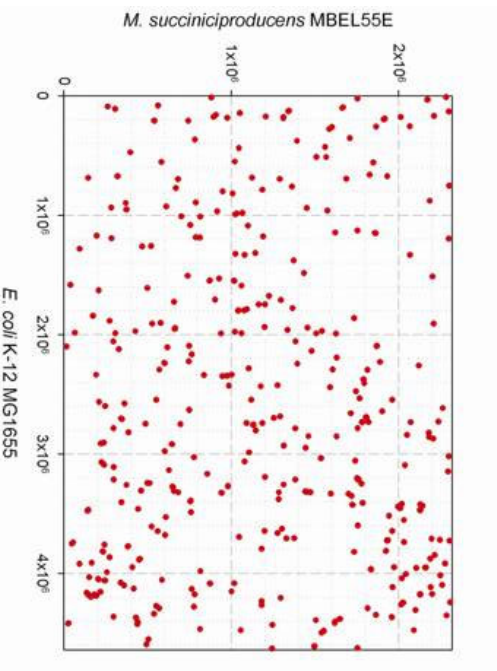
**Supplementary Figure 1 (A)** GC skew (red line) and cumulative GC skew (blue line) graph for the *M. succiniciproducens* MBEL55E genome. Calculation of the GC skew and cumulative GC skew values can be used as a basis for the prediction of the origin and termination of the replication of the genome.



**Supplementary Figure 1 (B)** Linear representation of *M. succiniciproducens* MBEL55E genome. The locations, directions, and the gene names are shown in the map. The colors used in the map represent the functional categories classified by the COG database. The detailed large size figure is available at our homepage (<http://mbel.kaist.ac.kr>).



Supplementary Figure 1 (C)-1



Supplementary Figure 1 (C)-2

Supplementary

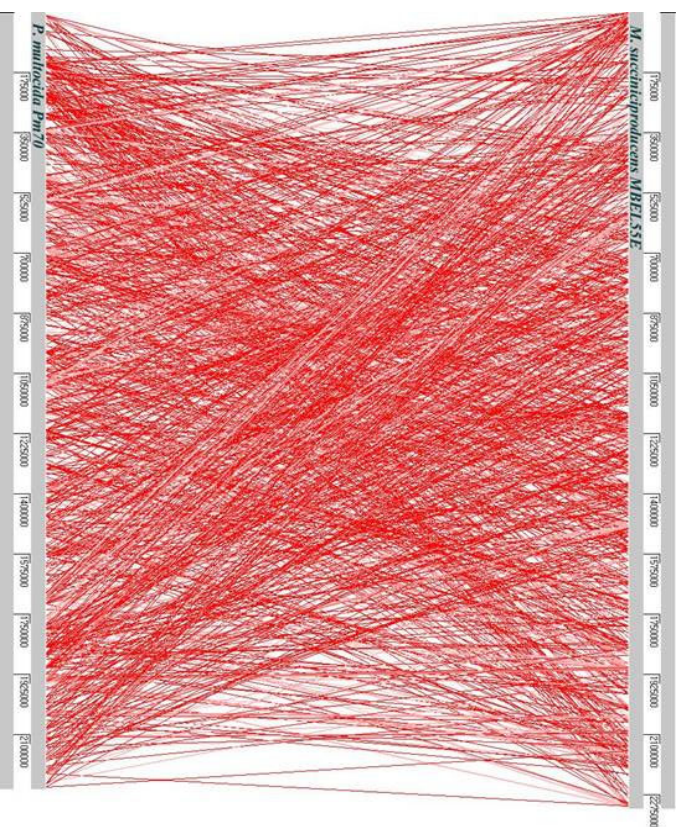


Figure 1 (C)-3

**Supplementary Figure 1 (C)** Dot plot and genome-genome comparison. Comparisons were made between the genome sequences of *M. succiniciproducens* and (C-1) *H. influenzae* Rd (dot plot), (C-2) *E. coli* K-12 (dot plot) or (C-3) *P. multocida* Pm70 (genome-genome). Minimum size for matching was 20 bp of nucleotide sequences. Genome sequences of *M. succiniciproducens* and *P. multocida* were compared by using the Artemis Comparison tool (<http://www.sanger.ac.uk/Software/ACT>).