Supplementary Table 4 Utilization of various carbon sources by *Mannheimia succiniciproducens* MBEL55E [a].

Compounds	*In silico* prediction		Carbon source utilization[b]
	Transport	Catabolic pathway	
Xylitol	Negative	Negative	-
Inositol	Negative	Negative	-
Mannitol	Positive	Positive	+
Sorbitol	Negative	Negative	-
Glucose	Positive[c]	Positive	+
Fructose	Positive	Positive	+
Xylose	Positive	Positive	+
Sucrose	Positive	Positive	+
Maltose	Positive	Positive	+
Lactose	Positive	Positive	+
Trehalose	Negative[d]	Negative[d]	+
Xylan	Negative	Negative	-
Celullose	Negative	Negative	-

[a] Cells were grown anaerobically at 37°C for 24 h in MH medium (100 ml) containing a specified carbon source (10 g l^{-1}), polypeptone (10 g l^{-1}), yeast extract (5 g l^{-1}), K_2HPO_4 (3 g l^{-1}), NaCl (2 g l^{-1}), $(NH_4)_2SO_4$ (3 g l^{-1}), $CaCl_2 \cdot 2H_2O$ (0.2 g l^{-1}), $MgCl_2 \cdot 6H_2O$ (0.2 g l^{-1}), and $MgCO_3$ (10 g l^{-1}) with CO_2 as the gas phase.

[b] Utilization of carbon sources was examined by monitoring the decrease of the concentrations of carbon sources during the cultivation.

[c] Annotation results by COG database search, which we used throughout this study, suggested that there are two *ptsG* genes, which led us to assume that glucose is transported by the PTS system in this study. However, it should be noted that the annotation results for these genes by non-redundant database search were different; they were predicted as *treB* and *ptsB* by non-redundant database search. Identifying the true mechanism of glucose transport in *Mannheimia succiniciproducens* requires further study.

[d] This prediction was based on the annotation results obtained by COG database search, which were different from those obtained by non-redundant database search as well as cultivation experiment.