Supplementary Table 2 (A) Functional categories of *M. succiniciproducens* MBEL55E genes based on the COG database.

Code	Description	Mannheimia succiniciproducens MBEL55E	Pasteurella multocida Pm70	Escherichia coli K-12	Bacillus subtilis
J	Translation, ribosomal structure and biogenesis	145 (6.08%)	148 (7.35%)	166 (3.87%)	151 (3.68%)
K	Transcription	104 (4.36%)	76 (3.77%)	245 (5.71%)	261 (6.37%)
L	DNA replication, recombination and repair	123 (5.16%)	101 (5.01%)	209 (4.87%)	127 (3.10%)
D	Cell division and chromosome partitioning	40 (1.68%)	22 (1.09%)	28 (0.65%)	32 (0.78%)
О	Posttranslational modification, protein turnover, chaperones	84 (3.52%)	80 (3.97%)	117 (2.73%)	90 (2.20%)
M	Cell envelope biogenesis, outer membrane	128 (5.37%)	130 (6.45%)	200 (4.66%)	160 (3.90%)
N	Cell motility and secretion	48 (2.01%)	44 (2.18%)	136 (3.17%)	87 (2.12%)
P	Inorganic ion transport and metabolism	86 (3.61%)	101 (5.01%)	172 (4.01%)	139 (3.39%)
T	Signal transduction mechanisms	35 (1.47%)	44 (2.18%)	140 (3.26%)	122 (2.98%)
С	Energy production and conversion	127 (5.33%)	107 (5.31%)	266 (6.20%)	161 (3.93%)
G	Carbohydrate transport and metabolism	167 (7.01%)	141 (7.00%)	333 (7.76%)	267 (6.51%)
Е	Amino acid transport and metabolism	167 (7.01%)	164 (8.14%)	342 (7.97%)	287 (7.00%)
F	Nucleotide transport and metabolism	57 (2.39%)	59 (2.93%)	88 (2.05%)	82 (2.00%)
Н	Coenzyme metabolism	80 (3.36%)	96 (4.77%)	117 (2.73%)	107 (2.61%)
I	Lipid metabolism	41 (1.72%)	45 (2.23%)	84 (1.96%)	84 (2.05%)
	Secondary metabolites				
Q	biosynthesis, transport and catabolism	39 (1.64%)	37 (1.84%)	89 (2.08%)	123 (3.00%)
R	General function prediction only	193 (8.10%)	180 (8.94%)	302 (7.04%)	326 (7.95%)
S	Function unknown	167 (7.01%)	165 (8.19%)	255 (5.95%)	212 (5.17%)
-	not in COGs	553 (23.20%)	274 (13.60%)	1000 (23.32%)	1282 (31.3%)
-	not in COGs Total		, ,	, ,	

Supplementary Table 2 (B) Analysis of the gene duplication in *M. succiniciproducens* genome.

Number of duplications (copies) and list of gene products.

# of duplication	# of genes	Gene products	
(copies)			
1 (2)	167	NqrA, TpiA, MtlD, PotC, LdhA and 162 more gene products	
2 (3)	39	OppF, DppD, DppC, DppB and 35 more gene products	
2 (4)	17	PtsN, AraH, EutG, NapF, CitT, WcaA, AcrA, OppA, CirA, GloA,	
3 (4)		NlpD, BtuC, Cof, MhpC, HybA, TbpA, MviM	
4.75	1.5	MglA, RbsB, SoxR, RbsK, ArtM, RluA, Gst, MdlB, RfaF, NrfG,	
4 (5)	15	MalK, NfnB, MdaB, Tra5, NemA	
5 (6)	8	XylB, DctP, AcrR, ArtI, GntT, BisC, TrxA, BaeS	
6 (7)	2	MutT, GlpR	
7 (8)	3	AraC, SmtA, RhaT	
9 (10)	1	PurR	
10 (11)	1	FabG	
11 (12)	1	ProP	
22 (23)	1	LysR	
Total	255		

Number of duplicated genes based on the COG categories.

Code	Description	Total genes	Genes with multiple copies
J	Translation, ribosomal structure and biogenesis	145 (6.08%)	31 (4.21%)
K	Transcription	104 (4.36%)	81 (11.01%)
L	DNA replication, recombination and repair	123 (5.16%)	40 (5.43%)
D	Cell division and chromosome partitioning	40 (1.68%)	4 (0.54%)
O	Posttranslational modification, protein turnover, chaperones	84 (3.52%)	36 (4.89%)
M	Cell envelope biogenesis, outer membrane	128 (5.37%)	49 (6.66%)
N	Cell motility and secretion	48 (2.01%)	17 (2.31%)
P	Inorganic ion transport and metabolism	86 (3.61%)	41 (5.57%)
T	Signal transduction mechanisms	35 (1.47%)	24 (3.26%)
C	Energy production and conversion	127 (5.33%)	65 (8.83%)
G	Carbohydrate transport and metabolism	167 (7.01%)	110 (14.95%)
E	Amino acid transport and metabolism	167 (7.01%)	107 (14.54%)
F	Nucleotide transport and metabolism	57 (2.39%)	6 (0.82%)
Н	Coenzyme metabolism	80 (3.36%)	16 (2.17%)
I	Lipid metabolism	41 (1.72%)	14 (1.90%)
Q	Secondary metabolites biosynthesis, transport and catabolism	39 (1.64%)	35 (4.76%)
R	General function prediction only	193 (8.10%)	48 (6.52%)
S	Function unknown	167 (7.01%)	12 (1.63%)
(No code)	Not in COGs	553 (23.20%)	0 (0.00%)
	Total	2384 (100%)	736 (100%)