

Supplementary table S1: Summary of transcriptome comparison of *S. pneumoniae* strain D39 wild-type grown in FM17 (0.5% Fucose + M17) and GM17 (0.5% Glucose + M17).
^aGene numbers refer to D39 locus tags. ^bD39 annotation/TIGR4 annotation (1-3), ^cRatio represents the fold increase/decrease in the expression of genes in FM17 as compared to GM17.

Gene tag^a	Function^b	Ratio^c	Predicted CcpA site
<i>SPD_0063</i>	Beta-N-acetylhexosaminidase	7.36	ATATAATCGCTATCAA
<i>SPD_0088</i>	ABC transporter, permease protein	2.11	ATGTAATCGTTATCAA
<i>SPD_0089</i>	ABC transporter, permease protein	2.37	TTTGTATTCGTTATCATT
<i>SPD_0265</i>	Alcohol dehydrogenase, zinc-containing	2.78	TGGAAAAGGCTTTCTT
<i>SPD_0277</i>	6- phospho-beta-glucosidase	19.26	AAGAATGCGTTTTTAT
<i>SPD_0420</i>	Formate acetyltransferase	2.31	TGAAATCGGTTACTT
<i>SPD_0460</i>	Chaperone protein DnaK	3.47	AATGGAAAAGAATACACTC
<i>SPD_0657</i>	Acetoin utilization protein AcuB, putative	2.71	ATGTAAGCGTTTGATA
<i>SPD_1497</i>	N-acetylmannosamine-6-phosphate 2-epimerase 2, putative	2.68	TTGAAAGCGTTTTAAT
<i>SPD_1528</i>	ABC transporter, ATP-binding protein	2.43	ATTGTAAAGGCTATCAAAA
<i>SPD_1632</i>	Hypothetical protein	3.63	GTGTAATCGTTTTCTT
<i>SPD_1633</i>	Galactose-1-phosphate uridylyltransferase	3.73	
<i>SPD_1634</i>	Galactokinase	4.59	
<i>SPD_1834</i>	Alcohol dehydrogenase, iron-containing	2.84	ATGAAACTGTTTACAA
<i>SPD_1865</i>	Alcohol dehydrogenase, zinc-containing	3.53	ATGAAAGCCTATACTT
<i>SPD_1910</i>	Phosphate ABC transporter, phosphate-binding protein	5.43	ATTGACAACACTGCCAAAA
<i>SPD_1934</i>	Maltose/maltodextrin ABC transporter	3.23	AGGAAAACGTTTGCGT
<i>SPD_1985</i>	Alcohol dehydrogenase, iron-containing	2.75	TAAAAACGAATACAA
<i>SPD_2009</i>	Hypothetical protein	2.72	ATTGTTACCGCTTTCTTTT
<i>SPD_2012</i>	Alpha-glycerophosphate oxidase	2.29	TGTCAAAGCTTTCAT
<i>SPD_2013</i>	Glycerol kinase	2.12	AAGAAAGCGCTTTATT