

1 **Supplementary table S1:** Summary of transcriptome comparison of *S. pneumoniae* strain  
2 D39 wild-type grown in LM17 (0.5% Lactose + M17) and GM17 (0.5% Glucose + M17).  
3 <sup>a</sup>Gene numbers refer to D39 locus tags. <sup>b</sup>D39 annotation/TIGR4 annotation (1-3), <sup>c</sup>Ratio  
4 represents the fold increase/decrease in the expression of genes in LM17 as compared to  
5 GM17.

<b>D39 tag<sup>a</sup></b>	<b>Function<sup>b</sup></b>	<b>Ratio<sup>c</sup></b>	<b>Predicted CcpA site</b>
<i>SPD_0088</i>	ABC transporter, permease protein	2.0	ATGTAATCGTTATCAA
<i>SPD_0265</i>	Alcohol dehydrogenase, zinc-containing	6.9	TGGAAAAGGCTTTCTT
<i>SPD_0277</i>	6-phospho-beta-glucosidase	8.5	AAGAATGCGTTTTTCAT
<i>SPD_0279</i>	PTS system, IIB component	1.8	
<i>SPD_0420</i>	Formate acetyltransferase	1.9	TTGAAATCGGTTACTA
<i>SPD_0559</i>	PTS system IIA component, putative	2.5	TTGACAACGGTTTTTCAT
<i>SPD_0560</i>	PTS system, IIB component, putative	4.5	
<i>SPD_0561</i>	PTS system, IIC component, putative	3.3	
<i>SPD_0580</i>	Glucokinase	1.9	CTGTAAGCATTTTCAA
<i>SPD_0621</i>	Lactate oxidase	1.7	AAGCAAACGCTTACTT
<i>SPD_1012</i>	Phosphopyruvate hydratase	3.1	AAGTAATCGCTTTCTT
<i>SPD_1300</i>	Thiamine biosynthesis protein ApbE, putative	2.8	ATGTAAGGGCTTCAAT
<i>SPD_1635</i>	Galactose operon repressor	2.2	AAGAAAACGATTACAC
<i>SPD_1634</i>	Galactokinase	1.9	
<i>SPD_1797</i>	Catabolite control protein A	-1.5	TTGAAAGTGTTTACAA
<i>SPD_1834</i>	Alcohol dehydrogenase, iron-containing	7.1	AATAATGCGTTATAAT ATGAAACTGTTTACAA
<i>SPD_1933</i>	4-alpha-glucanotransferase	2.0	TTAAAAACGCTTGCAA

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