Table S1: Number of genes significantly affected in D39 Δ*ccpA* as compared to the D39 wild-type grown in SM17 (0.5% sialic acid + M17) medium. Genes affected by more than 2-fold in D39 Δ*ccpA* as compared to the D39 wild type are selected.

Functional categories	**Total**	**Up**	**Down**
C: Energy production and conversion	14	3	11
D: Cell cycle control, cell division, chromosome partitioning	3	0	3
E: Amino acid transport and metabolism	34	12	22
F: Nucleotide transport and metabolism	8	4	4
G: Carbohydrate transport and metabolism	59	46	13
H: Coenzyme transport and metabolism	7	2	5
I: Lipid transport and metabolism	12	2	10
J: Translation, ribosomal structure and biogenesis	48	5	43
K: Transcription	21	15	6
L: Replication, recombination and repair	14	3	11
M: Cell wall/membrane/envelope biogenesis	14	6	8
O: Posttranslational modification, protein turnover, chaperones	13	10	3
P: Inorganic ion transport and metabolism	15	7	8
Q: Secondary metabolite biosynthesis, transport and catabolism	2	1	1
R: General function prediction only	31	13	18
S: Function unknown	21	13	8
T: Signal transduction mechanisms	10	6	4
U: Intracellular trafficking, secretion, and vesicular transport	5	3	2
V: Defense mechanisms	15	8	7
Total number of genes	**346**	**159**	**187**