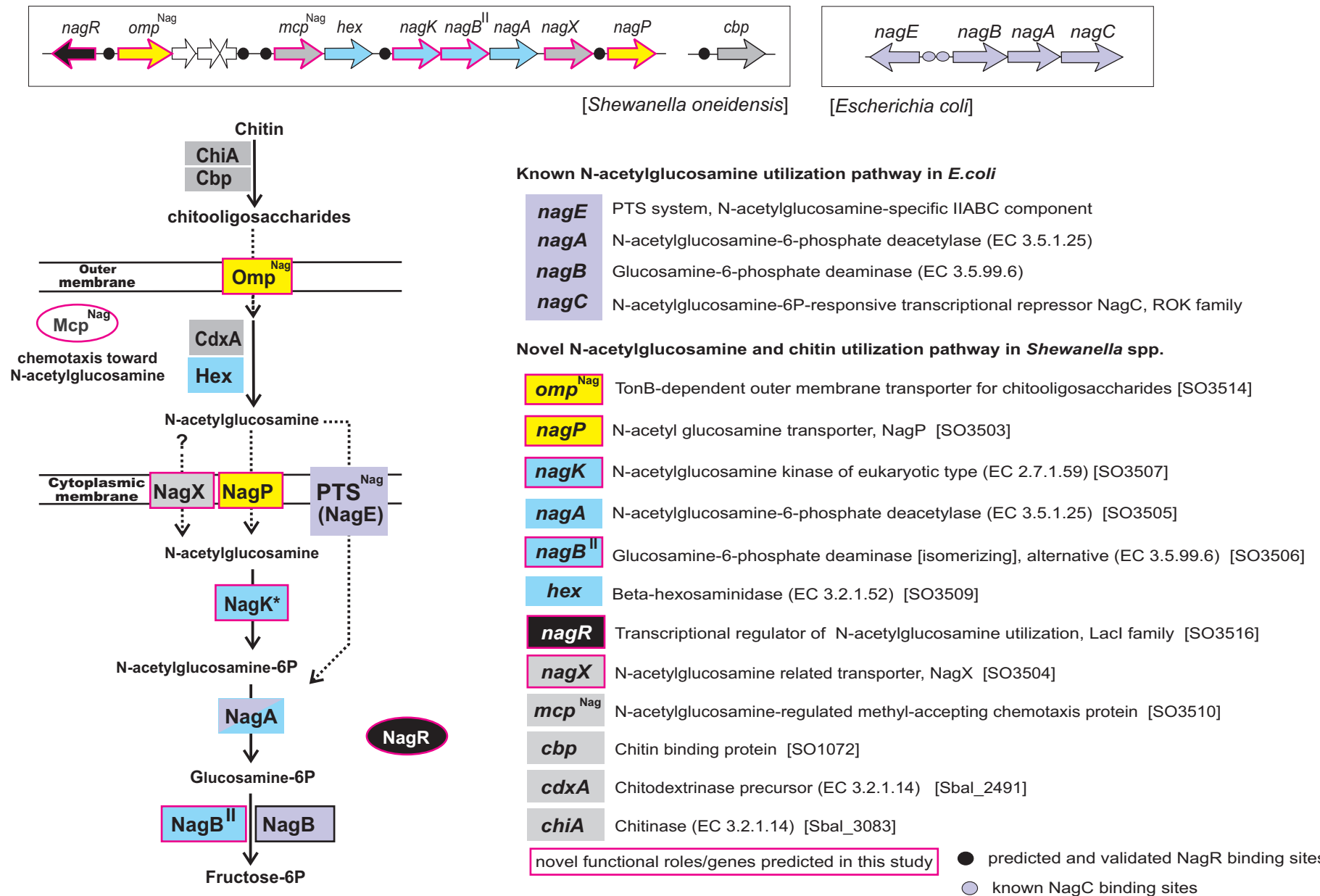
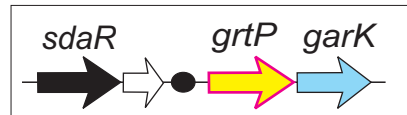


Additional file 9. Comparison of reconstructed sugar utilization pathways in *Shewanella* and Enterobacteria.

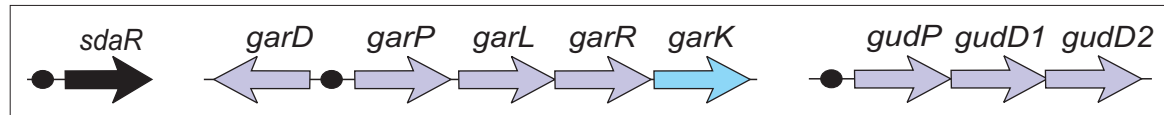
A. N-acetylglucosamine (Nag) and chitin utilization pathways.



B. D-glycerate (Grt) and D-glucarate/D-galactarate utilization pathways.



[*Shewanella oneidensis*]



[*Escherichia coli*]

Known D-glucarate/D-galactarate utilization pathway in *E. coli*

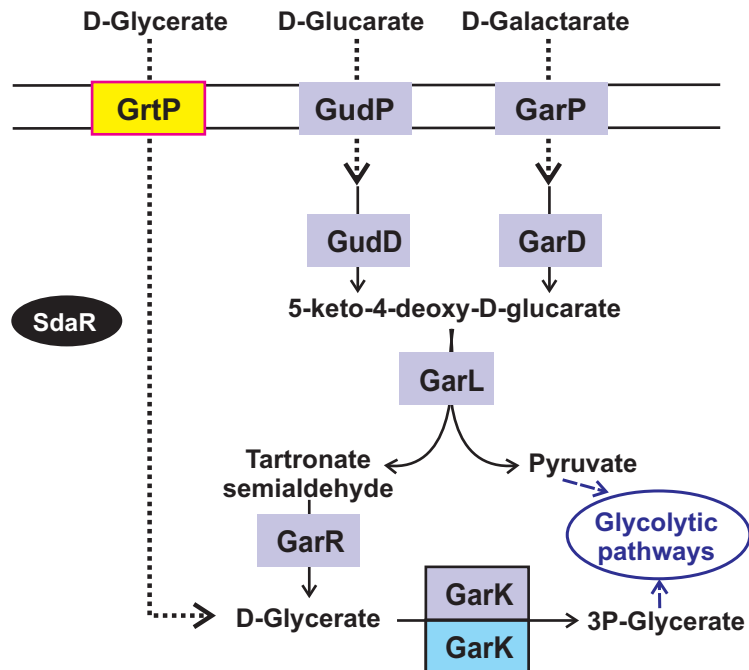
<i>gudD</i>	Glucarate dehydratase (EC 4.2.1.40)
<i>garD</i>	D-galactarate dehydratase (EC 4.2.1.42)
<i>gudP</i>	D-glucarate permease
<i>garP</i>	D-galactarate permease
<i>garL</i>	2-dehydro-3-deoxyglucarate aldolase (EC 4.1.2.20)
<i>garR</i>	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)
<i>garK</i>	Glycerate kinase (EC 2.7.1.31)

Predicted D-glycerate utilization pathway in *Shewanella* spp.

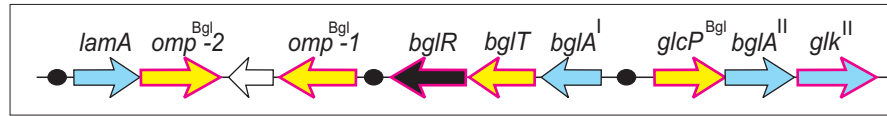
<i>grtP</i>	D-glycerate transporter [SO1771]
<i>garK</i>	Glycerate kinase (EC 2.7.1.31) [SO1770]
<i>sdaR</i>	Sugar diacid utilization regulator SdaR [SO1774]

novel functional roles/genes predicted in this study

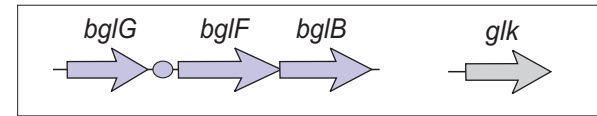
● predicted SdaR binding sites



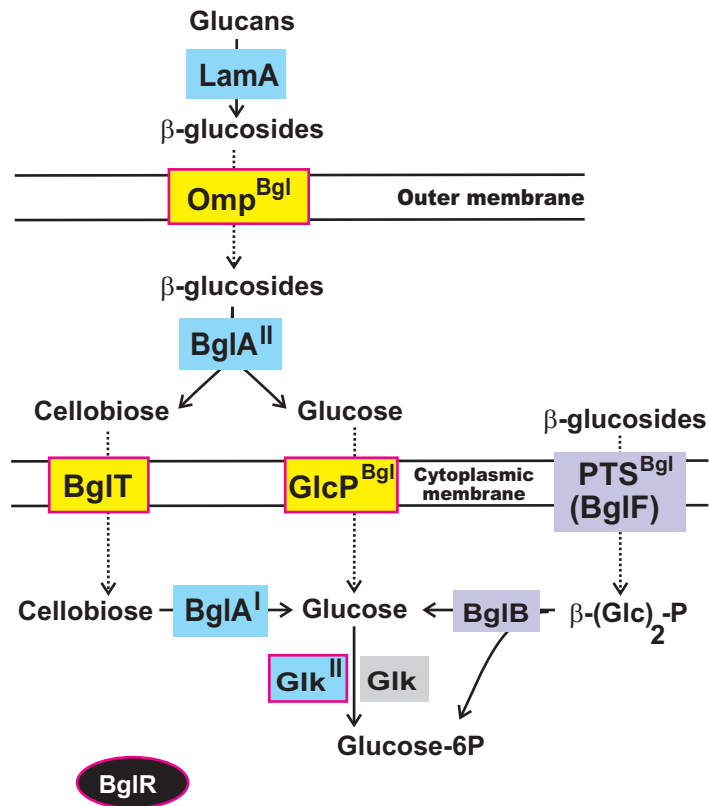
C. β -glucoside (Bgl) utilization pathway.



[*Shewanella amazonensis*]



[*Escherichia coli*]



Known cellobiose utilization pathway in Enterobacteria (cryptic operon in *E.coli*)

bglG	Beta-glucoside <i>bgl</i> operon antiterminator, BglG family
bglF	PTS system, β -glucoside-specific IIABC component
bglB	6-phospho- β -glucosidase (EC 3.2.1.86)
glk	Glucokinase (EC 2.7.1.2)

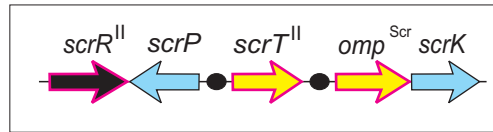
Predicted β -glucoside/cellobiose utilization pathway in *Shewanella* spp.

omp<sup>Bgl</sup>	TonB-dependent outer membrane transporter for β -glucosides [Sfri_1313]
bglT	β -glucoside transporter, GPH family [Sfri_1315]
glcP<sup>Bgl</sup>	Glucose transporter in β -glucoside utilization gene cluster [Sfri_1317]
lamA	β -glucanase precursor (EC 3.2.1.73) [Sfri_1319]
bglA<sup>II</sup>	Periplasmic β -glucosidase (EC 3.2.1.21) [Sfri_1318]
bglA<sup>I</sup>	Cytoplasmic β -glucosidase (EC 3.2.1.21) [Sfri_1317]
bglR	Transcriptional regulator of β -glucosides utilization, LacI family [Sfri_1314]
glk<sup>II</sup>	Glucokinase, ROK family (EC 2.7.1.2) [Sfri_1321]

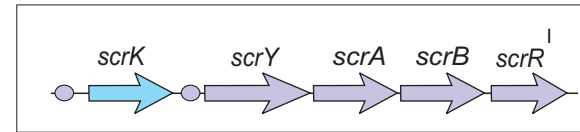
novel functional roles/genes predicted in this study

● predicted BglR binding sites ● known BglG binding sites

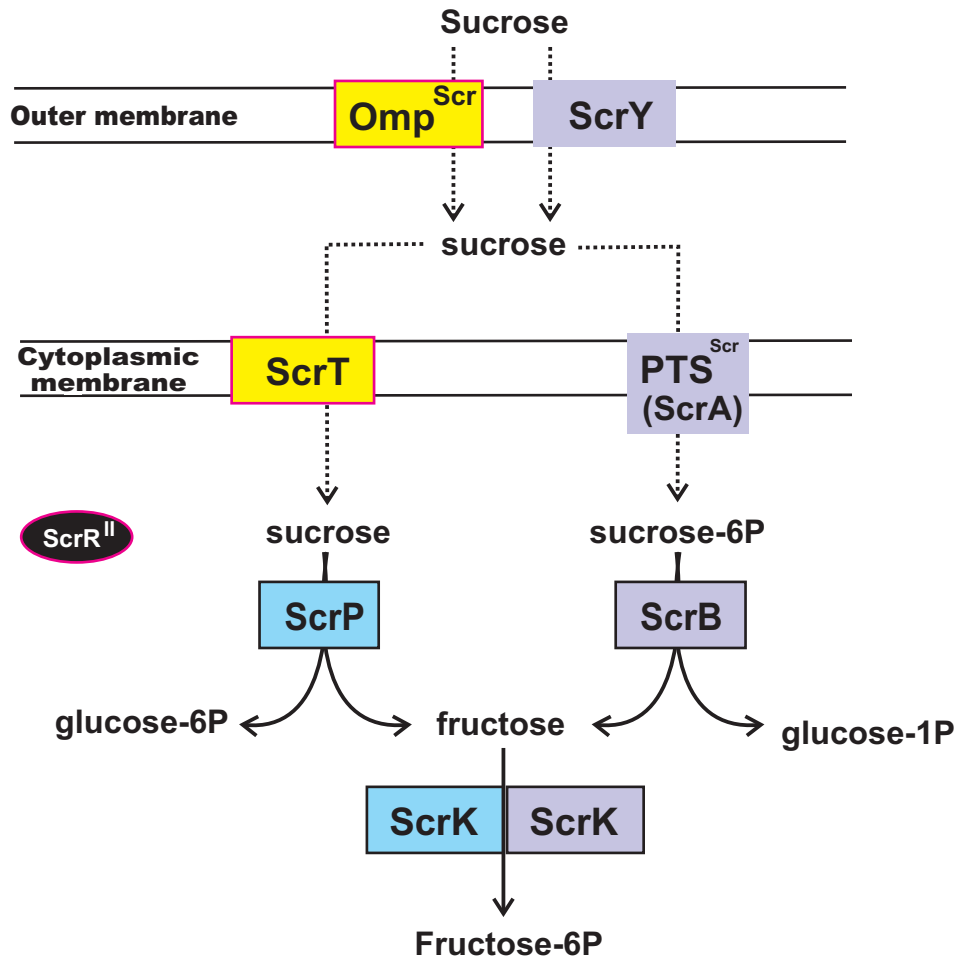
D. Sucrose (Scr) utilization pathway.



[*Shewanella frigidimarina*]



[*Klebsiella pneumoniae*; *Erwinia amylovora*; *Salmonella* spp.]



Known sucrose utilization pathway in Enterobacteria

scrY	Sucrose-specific outer membrane porin
scrA	PTS system, sucrose-specific IIBC component
scrB	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)
scrK	Fructokinase (EC 2.7.1.4)

Predicted sucrose utilization pathway in *Shewanella* spp.

omp^{Scr}	TonB-dependent outer membrane transporter for sucrose [Sfri_3988]
scrT	sucrose permease, MFS family, FucP subfamily [Sfri_3989]
scrP	Sucrose phosphorylase (EC 2.4.1.7) [Sfri_3990]
scrK	Fructokinase (EC 2.7.1.4) [Sfri_3987]
scrR^{II}	Sucrose repressor, LacI family [Sfri_3991]

novel functional roles/genes predicted in this study

- predicted ScrR^{II} binding sites
- known ScrR^I binding sites

E. L-arabinose (Ara) and arabinosides utilization pathways.

