Table 1S. Genes or operons whose expression is increased or decreased at least 4-fold by growth on sialic acid.

Gene or operon	Function	Gene	Fold increase or decrease
tnaA	tryptophan utilization	*tnaA*	-15.2
rbsDACBKR	D-ribose-transport system	*rbsD*	-13.1
		rbsB	-4.6
nrfABCDEFG	formate dependent nitrite reduction	*nrfE*	-10.4
melR	mellibiose regulated activator of *melAB* transcription	*melR*	-7.6
aldA	aldehyde dehydrogenase	*aldA*	-7.4
aceBAK	TCA cycle metabolism	*aceB*	-7.1
	isocitrate utilization, glyoxylate bypass	*aceK*	-4.4
mreBCD	shape determining factors	*mreC*	-6.9
ybfL	putative receptor protein	*ybfL*	-6.4
napFDAGHBC	iron/nitrate metabolism	*napG*	-5.8
gatYZABCDR	galactitol metabolism	*gatC*	-5.6
ackA	acetate kinase	*ackA*	-5.4
tktAB	transketolase	*tktB*	-5.4
pstSCABphoU	phosphate-specific transport	*phoU*	-5.3
dmsABC	dimethylsulfoxide reductase	*dmsB*	-5.2
cspD	stress induced DNA replication inhibition, cold shock protein homologue	*cspD*	-5.0
cspE	cold shock protein	*cspE*	-5.0
fldB	Flavodoxin I	*fldB*	-5.0
insA_6	IS1 transposon related function	*insA_6*	-4.9
yagG	putative permease	*yagG*	-4.9
acs	Acetyl CoA synthetase biosynthesis	*acs*	-4.6
yhiI	putative membrane protein	*yhiI*	-4.6
sdhCDAB	succinate-ubiquinone oxidoreductases	*sdhD*	-4.3
fliAZY	chemotaxis	*fliY*	-4.2
nuoA-N	NADH dehydrogenase	*nuoJ*	-4.2

hofH	putative general protein secretion protein	*hofH*	-4.1
malKlamBmalM	maltose and lambda receptor	*lamB*	-4.1
lplA	lipoate protein ligase	*lplA*	-4.1
rpsJrplCDWrpsSrplV	ribosomal subunit proteins	*rpsS*	4.0
rpsFpriBrpsRI	ribosomal proteins	*rpsF*	4.0
zraP	Zn-binding periplasmic protein	*zraP*	4.2
eutR	*eut* operon transcriptional activator, AraC family	*eutR*	4.3
pdhRaceEFlpd	pyruvate dehydrogenase complex	*aceE*	4.4
nrdI	putative zinc-resistance associated protein	*nrdI*	4.5
rpmUA	ribosomal proteins	*rpmA*	4.6
rluF	putative pseudouridine synthase	*rluF*	4.8
surA	periplasmic molecular chaperone	*surA*	5.3
yhbUVW	putative collagenases (*yhbUV)*	*yhbU*	5.8
yjiS	conserved protein	*yjiS*	5.8
csdE	CsdA-binding activator, Fe-S protein	*csdE*	6.5
nanCMS	porin	*nanC*	13.9
	mutarotase	*nanM*	8.4
	esterase	*nanS*	4.6
nanATEKyhcH	sialic acid metabolism, unknown	*yhcH*	10.5
yegS	phosphatidyl glycerol kinase, metal dependent	*yegS*	12.1
yjhBC	putative transport protein, dehydrogenase	*yjhC*	30.9

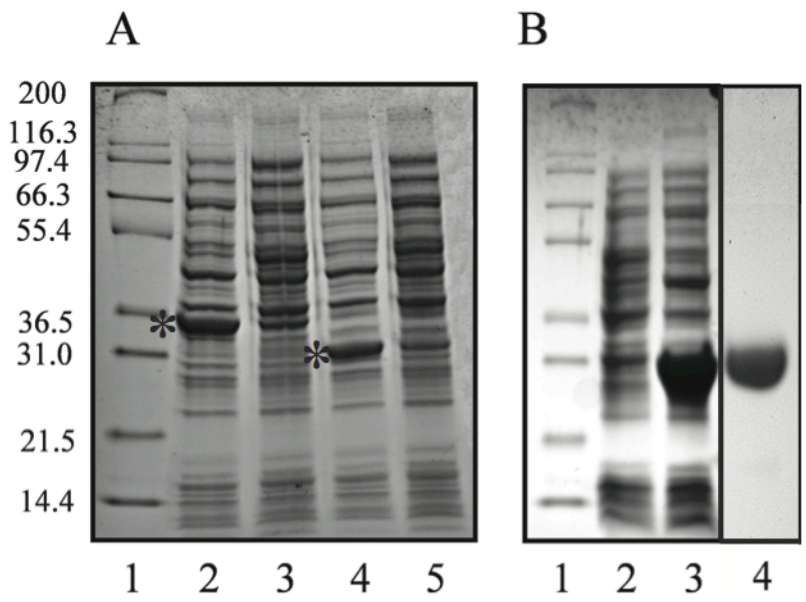

Figure S1

FIG. S1. Purification of native recombinant NanR. Strain BL21 (DE3) Star harboring either pSX674 expressing histidine-tagged *nanR* or pSX800 expressing the native form of the gene were either uninduced or induced with IPTG prior to cell disruption and SDS-PAGE of the soluble supernatant fractions. A. Lanes 2 and 3, induced and uninduced extracts from cells harboring pSX674 respectively. Lanes 4 and 5, induced and uninduced extracts from cell harboring pSX800. Asterisks indicate positions of the overproduced NanR polypeptides. Lane 1 shows molecular weight markers with sizes in kDa mass units given by the numbers at the left. B. Lanes 2 and 3 are uninduced and induced extracts respectively from cells harboring pSX800 as described in the text. Lane 4 shows 14 µg of purified native NanR from the heparin chromatography step. The black vertical line indicates the result is from a separate gel included to show the purity of NanR after the heparin step. Lane 1 shows molecular weight markers.

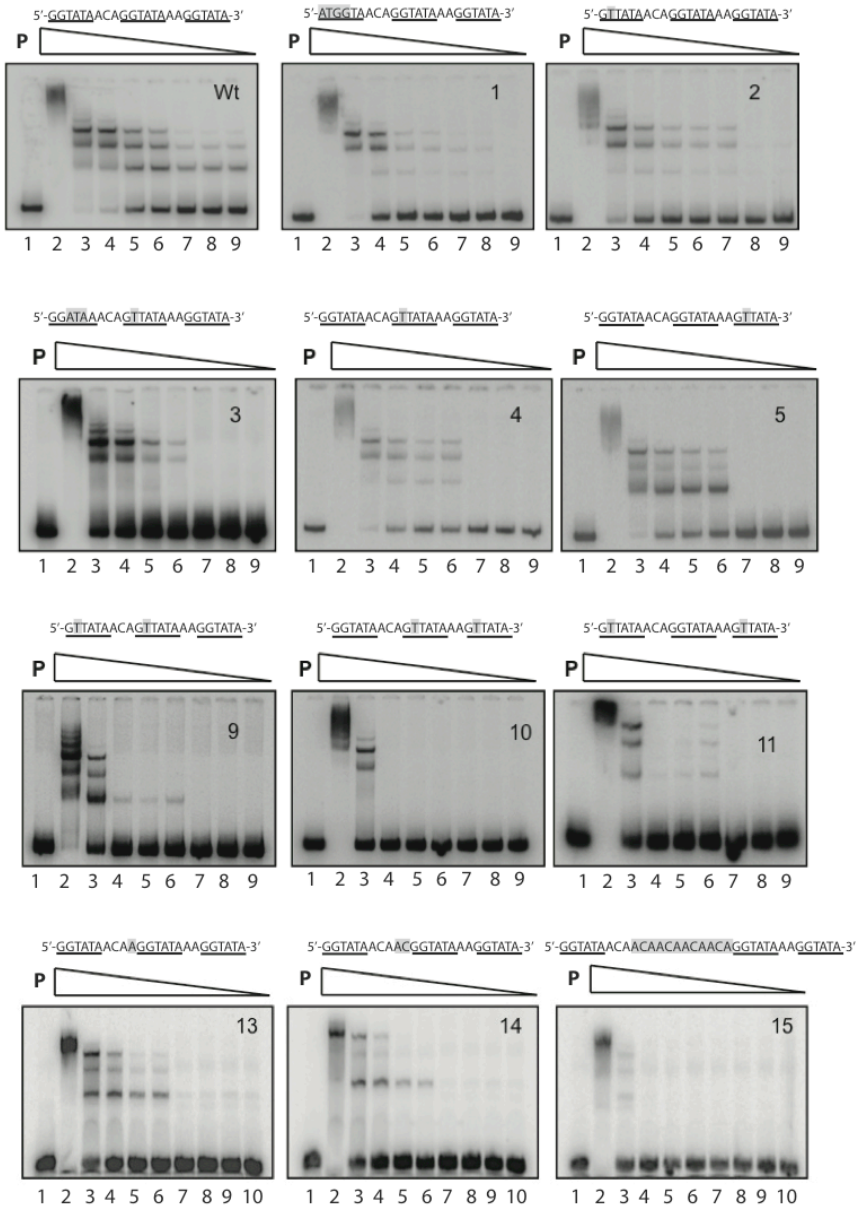

FIG. S2. Representative EMSA of NanR binding to wild type and mutant operators. The corresponding operator sequence and mutation if any (shaded in gray) is given above each EMSA gel and corresponds to the wild type (WT) or mutant numbers (in upper right corner) in Table 2. P means the promoter fragment alone (lane 1) and the triangles indicate decreasing NanR concentration. Lanes 2-9 for the wild type (WT) EMSA and mutant operators 1-5, 9-11, and 13-15 represent 550, 55, 28, 14, 7, 5.5, 3.7 and 2.75 mM NanR, respectively, used for the gel-shift analyses.

Figure S2