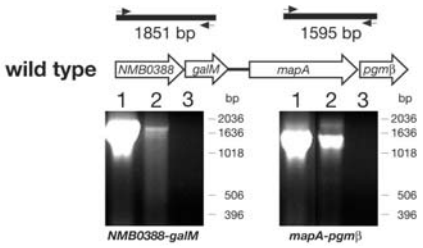

1851 bp
1595 bp
wild type
NMB0388
galM
mapA
pgmβ
1 2 3
bp
2036
1636
1018
506
396
NMB0388-galM
mapA-pgmβ

Fig. 1S

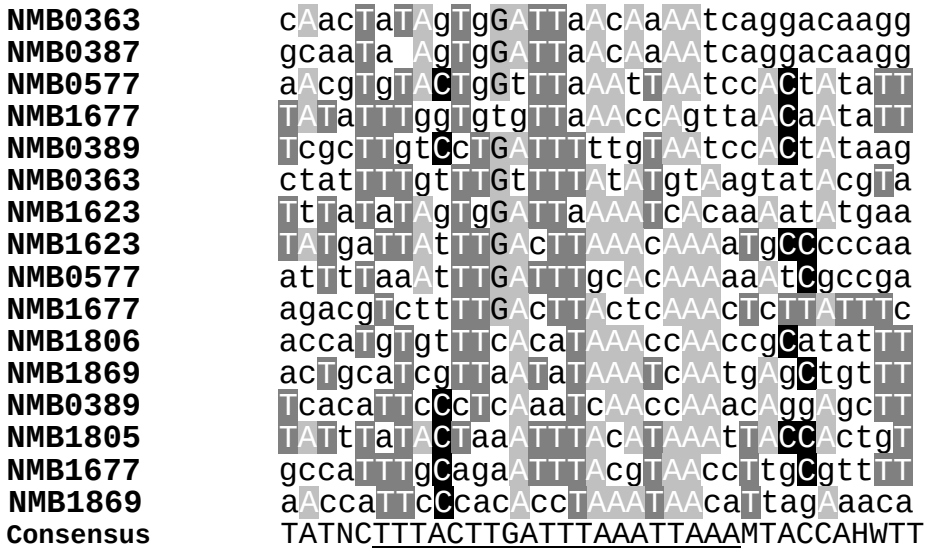

NMB0363
NMB0387
NMB0577
NMB1677
NMB0389
NMB0363
NMB1623
NMB1623
NMB0577
NMB1677
NMB1806
NMB1869
NMB0389
NMB1805
NMB1677
NMB1869
Consensus
TATNCTTTACTTGATTTAAATTAAAMTACCAHWTT

Fig. 2S

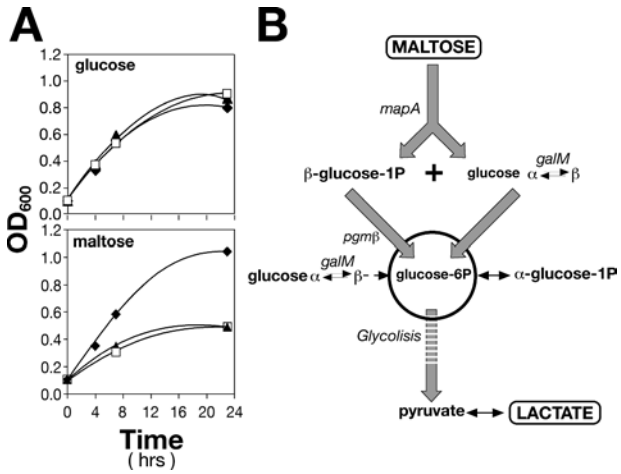
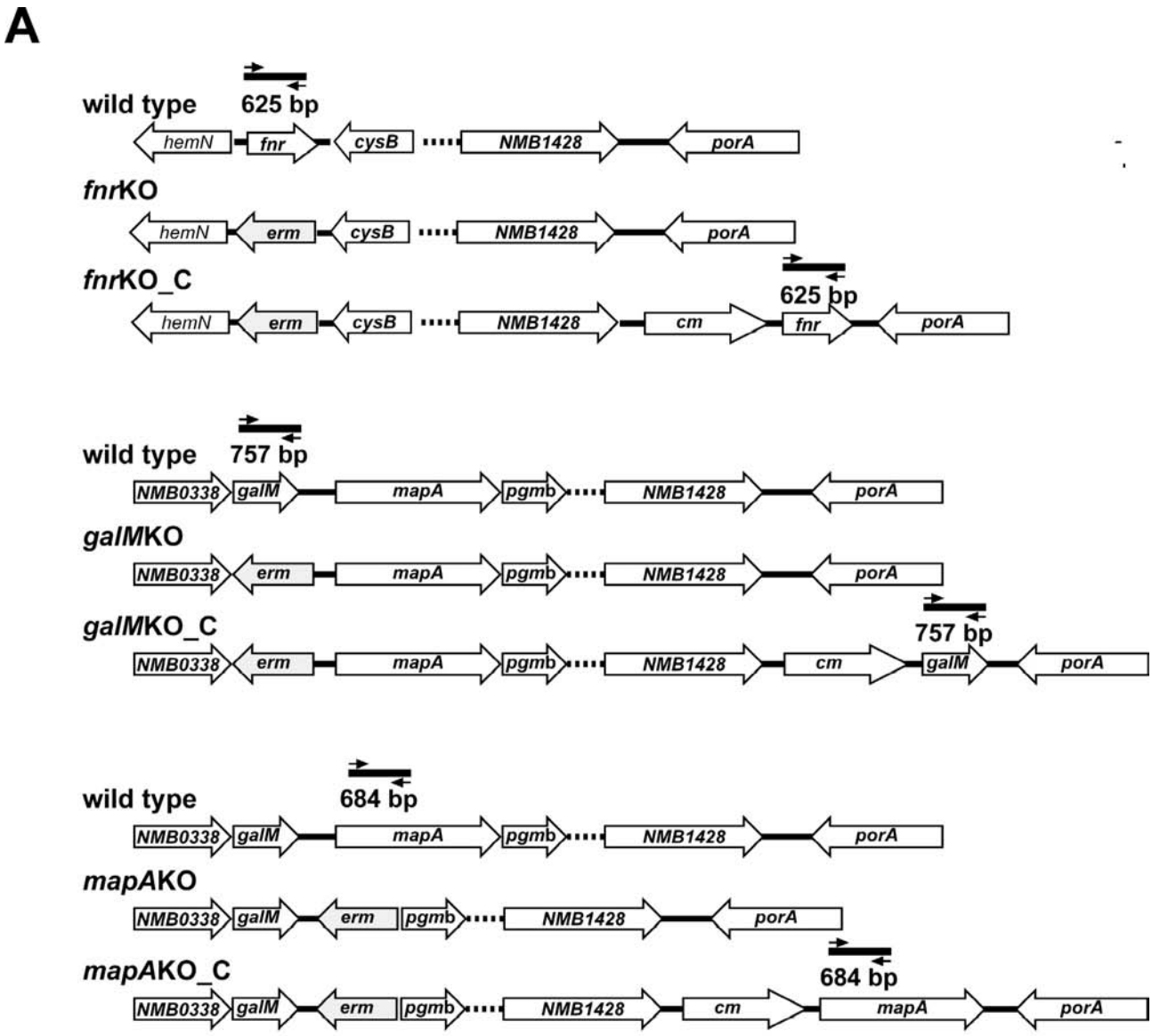

A
glucose
maltose
OD600
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0 4 8 12 16 20 24
Time
(hrs)
B
MALTOSE
mapA
β-glucose-1P
+
glucose α ◄► β
galM
pgmβ
galM
glucose α ◄► β-
glucose-6P
α-glucose-1P
Glycolisis
pyruvate
LACTATE

Fig. 3S


A
wild type
625 bp
hemN
fnr
cysB
NMB1428
porA
fnrKO
hemN
erm
cysB
NMB1428
porA
fnrKO_C
625 bp
hemN
erm
cysB
NMB1428
cm
fnr
porA
wild type
757 bp
NMB0338
galM
mapA
pgmb
NMB1428
porA
galMKO
NMB0338
erm
mapA
pgmb
NMB1428
porA
galMKO_C
757 bp
NMB0338
erm
mapA
pgmb
NMB1428
cm
galM
porA
wild type
684 bp
NMB0338
galM
mapA
pgmb
NMB1428
porA
mapAKO
NMB0338
galM
erm
pgmb
NMB1428
porA
mapAKO_C
684 bp
NMB0338
galM
erm
pgmb
NMB1428
cm
mapA
porA

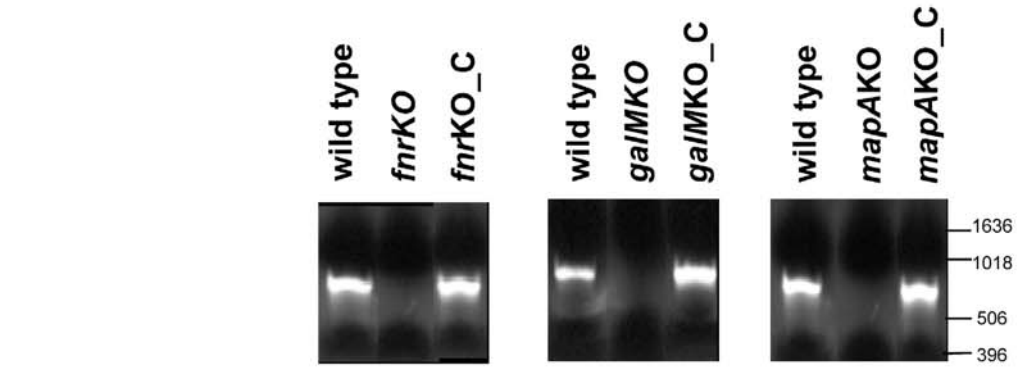

B
wild type
fnrKO
fnrKO_C
wild type
galMKO
galMKO_C
wild type
mapAKO
mapAKO_C
1636
1018
506
396

Fig. 4S

Table 2S. FNR binding to the upstream regions of the 9 FNR-regulated transcriptional units

Transcriptional unit [a]	EMSA-tested upstream region [b]	EMSA [c]	
		Ec FNR (nM)	Nm FNR (nM)
NMB0808	**-250/+20**	**>800**	**>800**
aniA	**-400/+20**	**50**	**400**
NMB0388-galM	**-400/+20**	**50**	**400**
mapA-pgmB	**-250/+20**	**>800**	**800**
NMB0363 (hypothetical)	**-250/+20**	**>800**	**100**
NMB1677 (cytocrome c5)	**-350/+20**	**200**	**400**
NMB1805 (cytocrome c4)	**-200/+20**	**>800**	**800**
NMB1806 (hypothetical)	**-200/+20**	**>800**	**800**
cbbA-**NMB1870**	**-200/+20**	**800**	**800**
nosR	**-250/+20**	**100**	**800**

FNR binding ability to the upstream regions was evaluated by Electrophoretic Mobility Shift Assay (EMSA) with increasing concentration of *E. coli* (Ec) and MenB (Nm) FNR proteins

[a] The genes found regulated in each transcriptional unit are indicated in bold. NMB0808 was used as a negative control.

[b] Numbers indicate the positions of primers used to amplify the DNA regions tested in EMSA with respect to the start codon (+1 position).

[c] Values indicate the lowest FNR dimer concentration at which binding was observed