Table 2. RNA expression ratios of iron-regulated genes identified by microarray analysis and biochemical verification of Fur binding by electrophoretic mobility shift assay (EMSA) with *Escherichia coli* and *Neisseria* Fur.

	EMSA [+]				Microarray relative quantification [#] (RNA expression ratios Fe/Df) at							
Transcriptional unit [*]	Fur box prediction	Tested region	*E. coli* Fur	*Neisseria* Fur	15m	30m	60m	90m	2h	3h	4h	5h
fbpA	+	-180/+5	+	+	0.40	0.51	0.60	0.63	0.69	0.52	0.65	0.84
NMB0034-0035	+	-145/-8	+	+	0.57-0.49	0.47-0.33	0.55-0.37	0.34-0.28	0.36-0.28	0.35-0.24	0.37-0.31	0.41-0.42
NMB0036	-	-157/-1	-	-	0.89	0.66	0.82	0.42	0.50	0.44	0.47	0.56
kat	+	-124/-6	+	+	1.62	2.71	1.32	1.37	1.44	1.36	0.93	0.99
nsgA	+	-99/+1	+	+	2.43	11.52	6.75	7.00	3.91	3.47	3.70	3.89
NMB0744	+	-135/-23	+	+	0.32	0.24	0.28	0.23	0.20	0.19	0.24	0.26
NMB0866-**0865-0864**	+	-127/-2	+	+	0.83-0.38-0.64	0.66-0.35-0.58	0.68-0.25-0.41	0.52-0.17-0.28	0.56-0.17-0.31	0.57-0.16-0.33	0.68-0.17-0.25	0.66-0.18-0.29
NMB1436-1437-1438	+	-345/-142	+	+	2.18-2.52-1.90	2.92-3.44-3.15	2.21-2.79-2.29	3.02-3.79-3.14	2.94-4.07-3.30	2.67-3.67-2.88	2.25-2.96-2.59	2.26-3.13-2.57
aniA	+	-58/+24	+	+	1.98	2.59	1.99	1.66	2.11	1.89	2.16	1.25
mdaB	+	-198/-18	+	+	1.02	0.64	0.63	0.49	0.37	0.44	0.45	0.56
NMB0101	+	-197/+19	nd	+	0.66	0.46	0.49	0.52	0.72	0.77	0.61	0.62
dsbA-2	-	-131/-33	+	+	0.71	0.51	0.56	0.58	0.61	0.52	0.50	0.60
NMB0317	+	-133/-17	+	+	0.81	0.25	0.37	0.33	0.45	0.40	0.53	0.78
lspA-***NMB0343***	+	-200/+20	nd	+	0.86-0.72	0.63-0.75	0.68-0.65	0.84-0.61	0.78-0.49	0.97-0.58	0.78-0.76	0.81-0.65
fnr	-	-200/+20	nd	-	0.85	0.68	0.56	0.67	0.64	0.61	0.48	0.53
nadA	+	-181/+28	+	+	1.03	1.14	0.75	0.47	0.53	0.40	0.31	0.31
nadC	+	-203/-46	+	+	1.01	0.91	0.85	0.63	0.71	0.57	0.50	0.70
NMB0584-0585	+	-109/+9	+	+	1.12-0.64	1.32-0.54	0.91-0.65	0.80-0.62	0.75-0.60	0.47-0.57	0.42-0.65	0.26-0.69
recN	+	-239/-15	+	+	1.12	1.32	0.91	0.80	0.75	0.47	0.42	0.26
NMB0808-**0807**-0806	-	-200/+19	nd	-	1.03-0.93-0.93	1.26-0.75-1.38	1.12-0.85-0.95	0.89-0.89-1.05	0.91-1.15-1.05	0.71-0.75-0.90	0.67-0.91-1.21	0.5-0.47-0.80
NMB0821	-	-200/+20	nd	-	1.55	1.11	1.00	0.72	0.76	0.54	0.50	0.39
NMB0977	-	-200/+20	nd	-	0.97	0.78	0.69	0.58	0.39	0.28	0.24	0.31
cysG1-cysH1-cysD1-cysN1-*cysJ1-ysl1*	-	-200/+20	nd	-	1.04-1.00-0.98-0.99-1.08-1.05	1.09-1.55-0.98-1.17-0.95-0.95	0.72-0.53-0.76-0.49-0.66-0.63	0.48-0.36-0.48-0.47-0.64-0.71	0.86-0.79-0.82-0.89-1.06-1.15	0.85-0.88-0.84-1.00-1.21-1.4	1.34-1.15-1.09-1.16-1.35-1.34	1.01-1.03-1.09-1.10-1.13-1.06
NMB1340-*pdhA*	+	-152/-40	+	+	0.66-0.97	1.30-1.11	0.60-1.34	0.46-1.03	0.60-0.98	0.71-0.70	0.60-0.82	0.67-0.98

lldD	+	-80/+22	+	+	0.25	0.18	0.26	0.24	0.23	0.21	0.23	0.29
***nifU*-1381**	+	-79/-5	+	+	0.82-0.63	0.7-0.46	0.76-0.53	0.67-0.53	0.63-0.49	0.56-0.46	0.58-0.45	0.45-0.42
NMB1395	+	-200/+20	nd	+	0.53	0.59	0.41	0.39	0.50	0.57	0.63	0.73
NMB1402-1403-1404-**1405**	+	-111/-2	+	+	1.07-0.94-0.96-0.35	1.04-0.96-0.95-0.29	0.99-0.92-0.97-0.26	0.92-0.94-0.98-0.32	0.99-0.97-0.99-0.37	1.00-1.11-1.01-0.47	0.98-0.82-0.93-0.45	0.89-0.92-0.89-0.59
NMB1412	+	-109/+9	+	+	0.57	0.42	0.44	0.40	0.43	0.45	0.41	0.51
NMB1414-*frpC*	+	-132/-23	+	+	0.64-0.40	0.49-0.26	0.56-0.31	0.48-0.32	0.52-0.30	0.56-0.41	0.49-0.36	0.57-0.46
fumC	-	-107/-3	+	+	0.36	0.28	0.32	0.29	0.28	0.22	0.29	0.39
NMB1490	-	-200/+20	nd	-	0.74	1.00	0.53	0.46	0.40	0.52	0.74	0.77
NMB1492-**1491**	-	-200/+20	nd	+	0.95-0.93	1.28-1.26	1.15-1.15	1.02-1.02	1.03--0.98	0.81-0.91	0.53-0.51	0.51-0.46
NMB1727	-	-107/-1	nd	-	0.81	0.94	0.64	0.61	0.69	0.76	0.50	0.54
NMB1798	-	-200/+20	nd	+	0.59	0.31	0.39	0.50	0.64	0.73	0.68	0.52
mlp-1899	+	-153/-54	+	+	0.92-0.98	1.03-0.99	0.66-0.97	0.55-0.82	0.65-0.88	0.48-0.79	0.40-0.89	0.34-0.78
secY-infA-rpmJ	+	-37/+136	+	+	0.60-0.95-1.17	1.07-0.62-0.82	1.12-1.18-1.26	1.07-1.83-1.69	1.81-1.79-1.66	2.61-2.16-2.03	2.83-1.69-1.44	1.69-1.84-1.91
nuoA-***nuoB***-*nuoC*-***nuoD***-*nuoE*	+	-197/-14	+	+	1.21-1.50-1.16-2.11-1.10	1.27-2.65-1.42-3.36-1.42	1.25-1.65-1.16-2.09-1.16	1.42-2.14-1.41-2.84-1.54	1.46-2.28-1.24-2.72-1.43	1.22-2.15-1.10-2.96-1.47	1.32-2.36-1.36-3.30-1.46	1.14-1.88-1.19-2.53-1.38
NMB0296-0297-**0298**	+	-227/-49	+	+	0.98-1.03-1.94	1.02-1.24-1.37	0.76-0.80-2.85	0.83-0.94-2.82	0.88-1.01-2.08	0.77-1.32-2.33	0.66-1.24-2.43	0.60-1.14-3.67
sodB	-	-56/-241	+	+	3.43	6.52	5.62	5.69	4.38	4.31	4.56	3.91
NMB1804-**1803**	-	-159/-18	-	-	1.25-1.40	0.90-1.53	1.31-1.94	1.44-2.63	1.44-2.10	1.61-2.58	1.70-2.47	1.30-1.94
NMB1866	+	-190/-1	-	-	1.85	2.35	2.27	3.97	2.83	3.15	2.90	3.37

*) Transcriptional units found regulated in iron-replet vs. iron-starved cultures. The regulated genes, belonging to the transcriptional unit, are indicated in bold.

+) The 400-bp upstream regions of the regulated transcriptional units were searched search for the presence of a Fur-binding site, using the *E. coli* Fur consensus sequence, the *Neisseria* Fur consensus sequence , the (NATWAT)3 sequence, recently proposed as the *E. coli* Fur-box , and the Fur-binding sequences of the *Neisseria gonorrhoeae* fur and fbpA genes. In the table are reported the promoter regions tested by EMSA, with respect to ATG, and the binding ability of *E. coli* and *Neisseria* Fur.

#) Expression ratios of each gene composing the transcriptional units, in iron-repleted vs. iron-starved cultures at different time points.