

Table S4. Differentially expressed genes in *N. meningitidis* wild-type B6116/77 *modA12* ON versus the mutant strain B6616/77 *modA12::kan*

Gene ID	Gene	Ratio	Qrt-pcr	B-stat
Reduced expression in <i>N. meningitidis modA12</i> mutant				
NMA1203	hypothetical protein	0.58		6.39
<i>NMA1581</i>	<i>membrane lipoprotein</i>	<i>0.72</i>	<i>0.65± 0.14</i>	<i>4.35</i>
NMA1590	type III restriction/modification system modification methylase	0.13	0.07± 0.002	2.06
NMA1591	type III restriction/modification system enzyme	0.67		2.45
NMA1670	fumarate hydratase	0.64		5.28
NMB0292	conserved hypothetical protein	0.61		2.41
NMB0995	macrophage infectivity potentiator-related protein	0.65		2.99
NMB1017	sulfate ABC transporter, periplasmic sulfate-binding protein	0.59		4.40
NMB1070	2-isopropylmalate synthase	0.64		6.51
NMB1191	sulfate adenylyltransferase, subunit 1	0.67		1.92
NMB1426	hypothetical protein	0.44		7.78
NMB1458	fumarate hydratase, class II, aerobic	0.60		3.59
Increased expression in <i>N. meningitidis modA12</i> mutant				
NMA1623	hypothetical protein	1.72		6.09
NMA2088	nicotinate-nucleotide pyrophosphorylase	2.05		7.19
NMB0245	NADH dehydrogenase I, E subunit	1.57		4.45
NMB0246	NADH dehydrogenase I, F subunit	1.55		7.28
NMB0396	nicotinate-nucleotide pyrophosphorylase	1.62		3.36
NMB0950	succinate dehydrogenase, flavoprotein subunit	1.67		5.21
NMB0951	succinate dehydrogenase, iron-sulfur protein	1.83	2.61± 0.46	2.90
NMB0952	conserved hypothetical protein	1.68		2.46
NMB0953	hypothetical protein	1.76		6.87
NMB0954	citrate synthase	1.53		3.96
<i>NMB1206</i>	<i>bacterioferritin B</i>	<i>1.42</i>	<i>2.14± 0.35</i>	<i>2.48</i>
NMB1403	FrpA-C-related protein	1.65		5.40
NMB1405	FrpA-C-related protein	1.73	2.21± 0.49	4.25
NMB1424	hypothetical protein	1.54		3.57

The genes listed are either down- or up- regulated in the *N. meningitidis* B6116/77 *modA12::kan* mutant strain. The identity of the gene is indicated with the gene ID in the annotation of the *N. meningitidis* strain MC58 and Z2491 genome (TIGR). The average ratio presented is the mean of B6116/77 *modA12::kan* mutant:wild-type B6116/77 *modA12* ON from six replicate spots on seven independent microarrays, incorporating a dye swap. Only those genes with an expression value above 1.5-fold were included in this study except for NMA1581 and NMB1206, which are shown in italics.