

**Table S5. Differentially expressed genes in *N. gonorrhoeae* wild-type FA1090 *modA13* ON versus the mutant strain FA1090 *modA13::kan*.**

Gene ID	Gene	Ratio	Qrt-per	B-stat
<b>Reduced expression in <i>N. gonorrhoeae modA13</i> mutant</b>				
NGO0055	PilC2	0.62		0.25
NGO0554	hypothetical protein	0.49		2.56
NGO0574	carbonic anhydrase	0.58		0.15
NGO0641	type III modI Modification methylase	0.55		3.02
NGO0714	6-phosphogluconate dehydratase	0.67		1.28
NGO0754	molybdopterin-guanine dinucleotide biosynthesis protein	0.55		3.91
NGO0794	bacterioferritin	0.59		1.59
NGO0867	Helix-turn-helix domain protein possible transcriptional regulator	0.57		1.26
NGO1247	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	0.63		1.22
NGO1258	phosphoglycerate mutase	0.64		1.28
NGO1318	haem utilisation protein	0.61		2.58
NGO1365	membrane fusion protein mtrc precursor	0.62		1.33
NGO1442	alcohol dehydrogenase, propanol-preferring (zn dependent)	0.52		3.21
NGO1581	phosphate permease, putative	0.29		8.53
NGO1587	adhesin MafB2	0.61		2.57
NGO1701	Tat (twin-arginine translocation) pathway signal sequence domain protein	0.6		1.40
NGO1931	glyceraldehyde-3-phosphate dehydrogenase, type I	0.37		5.10
NGO1947	putative periplasmic protein	0.67		1.12
NGO2062	truncated silent pilin gene	0.42		6.27
NGO2066	pilin silent gene cassette	0.41		5.11
<b>Increased expression in <i>N. gonorrhoeae modA13</i> mutant</b>				
NGO0057	thioredoxin	1.71		3.34
NGO0198	ammonium transporter	3.18		6.45
NGO0318	DNA repair protein RecN	1.98		2.02
NGO0340	cysteine synthase	2.23		4.20
NGO0372	amino acid ABC transporter, periplasmic amino acid-binding protein	2.27		3.28
NGO0373	amino acid ABC transporter, permease protein	3.01		5.47
NGO0374	amino acid ABC transporter, ATP-binding protein	2.81		7.14
NGO0376	peptidyl-prolyl cis-trans isomerase	1.77		2.00
NGO0584	ribosomal protein L9*	1.64		2.07
NGO0624	putative oxidoreductase	1.58		1.81
NGO0650	ATP-dependent RNA helicase, putative	3.14		6.62
NGO0655	exodeoxyribonuclease VII, large subunit	3.16		5.91
NGO0656	oxalate/formate antiporter	2.39		6.04
NGO0659	CDP-6-deoxy-delta-3,4-glucoseen reductase, putative	1.53		1.65
NGO0768	hypothetical protein	1.61		2.49
NGO0775	ATP-dependent protease La	1.87		1.37
NGO0878	sulfate ABC transporter, periplasmic sulfate-binding protein	1.62		0.54
NGO0927	Neisseria specific protein conserved hypothetical protein	2.93		2.46
NGO0928	5-methyltetrahydropteroyltriglutamate	3.01		6.59
NGO0929	5,10-methylenetetrahydrofolate reductase	4.92		8.32
NGO1046	ClpB protein endopeptidase	1.9		2.82
NGO1220	Membrane protein of unknown function (DUF340) family	1.84		1.41
NGO1355	sodium- and chloride-dependent transporter	2.17		2.21
NGO1368	efflux pump component MtrF	2.2		5.51
NGO1511	bicyclomycin resistance protein, putative	1.75		0.05
NGO1769	cytochrome c551 peroxidase	1.62		2.54
NGO1822	preprotein translocase SECY subunit	1.76		1.38
NGO1827	50S ribosomal protein L5	1.68		2.65
NGO1836	ribosomal protein L23*	1.52		0.74
NGO1843	translation elongation factor G	1.79		1.86
NGO1851	DNA-directed RNA polymerase, beta subunit*	1.58		1.69
NGO1901	chaperone protein dnaj	1.71		3.20
NGO2011	amino acid ABC transporter, permease protein glnM	1.51		1.45
NGO2012	amino acid ABC transporter, permease protein glnP	1.75		3.19

The genes listed are either down- or up- regulated in the *N. gonorrhoeae* FA1090 *modA13::kan* mutant strain. The identity of the gene is indicated with the gene ID in the annotation of the *N. gonorrhoeae* genome (TIGR). The average ratio presented is the mean of FA1090 *modA13::kan* mutant:wild-type FA1090 *modA13* ON from six replicate spots

on three independent microarrays, incorporating a dye swap. Only those genes with an expression value above 1.5-fold were included in this study. \*Genes have been shown to be Fur regulated [56].