

Table S1: Proteome analysis of *N. meningitidis* MC58 grown at 32°C and 37°C. Entries are organized hierarchically by localization (as annotated or predicted). overall significance level groups as assessed by Student's T-test ($P < 0.01$. dark grey; $P = 0.01$ to 0.05 . light gray; $P > 0.05$. white) and amplitude of differential regulation (ratio 32°C/37°C).

GI	protein*	name / function*	(predicted) localization**	32°C				37°C				ratio 32°C/37°C	P-value (T-test)
				A [#]	B [#]	C [#]	mean	A [#]	B [#]	C [#]	mean		
7227358	NMB2095	putative adhesin complex protein. ACP	outer membrane	1.013	0.964	1.246	1.075	0.233	0.227	0.317	0.259	4.150	0.0051
7226579	NMB1335	creA protein	outer membrane	0.819	0.879	1.100	0.933	0.470	0.597	0.801	0.623	1.498	0.0041
7226778	NMB1533	H.8 outer membrane protein	outer membrane	1.247	1.357	1.185	1.263	0.870	1.025	0.878	0.924	1.366	0.0037
7226166	NMB0928	outer membrane protein assembly protein BamC	outer membrane	0.577	0.688	0.635	0.633	0.723	0.853	0.787	0.788	0.804	0.0013
7225603	NMB0382	outer membrane protein class 4. RmpM	outer membrane	0.709	1.076	0.507	0.764	1.083	1.387	0.805	1.092	0.700	0.0050
7225687	NMB0461	transferrin-binding protein 1 TbpA	outer membrane	0.308	0.375	0.270	0.318	0.518	0.609	0.543	0.557	0.571	0.0059
7227230	NMB1969	autotransported serine protease NalP	outer membrane	0.806	1.018	0.919	0.914	1.538	1.996	1.742	1.758	0.520	0.0072
7413447	NMB0964	TonB dependent receptor. ZnuD	outer membrane	0.410	0.058	0.749	0.406	0.913	0.613	1.253	0.927	0.438	0.0011
7227388	NMB2132	Neisseria heparin binding antigen. NHBA	outer membrane	-	14.558	13.664	14.111	1.225	1.408	1.837	1.490	9.470	0.0337
7225291	NMB0071	polysialic acid capsule export outer-membrane lipoprotein CtrA	outer membrane	25.396	27.661	35.076	29.378	9.289	10.092	8.452	9.278	3.166	0.0257
7227353	NMB2091	BAM complex accessory protein	outer membrane	1.436	1.513	1.445	1.465	0.870	-	0.932	0.901	1.626	0.0313
7226815	NMB1567	probable FKBP-type peptidyl-prolyl cis-trans isomerase FkpA (MIP)	outer membrane	0.383	0.446	0.370	0.400	0.320	0.361	0.317	0.333	1.201	0.0195
7227261	NMB1998	autotransporter MspA (AusI)	outer membrane	1.009	1.388	0.725	1.041	1.273	1.786	1.005	1.354	0.768	0.0176
7227016	NMB1762	TpsA2 activation/secretion protein TpsB2	outer membrane	0.542	0.674	0.441	0.552	0.877	0.962	0.950	0.930	0.594	0.0303
7225401	NMB0182	outer membrane protein Omp85. BamA	outer membrane	0.414	0.473	0.389	0.425	0.775	0.777	0.882	0.811	0.524	0.0205
7226786	NMB1540	lactoferrin binding protein LbpA	outer membrane	0.317	0.241	0.152	0.237	0.565	0.437	0.471	0.491	0.482	0.0191
7227128	NMB1870	factor H binding protein fHbp	outer membrane	0.789	0.933	0.720	0.814	1.530	2.134	1.443	1.703	0.478	0.0297
7227205	NMB1946	putative D-methionine-binding lipoprotein MetQ	outer membrane	0.493	0.536	0.483	0.504	0.383	0.412	0.443	0.413	1.221	0.0723
7225253	NMB0033	putative membrane-bound lytic murein transglycosylase A	outer membrane	1.987	3.371	1.569	2.309	1.949	2.092	1.747	1.929	1.197	0.4909
7226110	NMB0873	outer-membrane lipoprotein LolB	outer membrane	0.753	0.844	0.716	0.771	0.759	0.651	0.837	0.749	1.029	0.8341
66731938	NMB1812	type IV pilus secretin PilQ	outer membrane	0.846	0.813	0.820	0.826	0.775	0.769	0.873	0.806	1.025	0.6426
7226550	NMB1309	type IV pilus biogenesis lipoprotein PilW	outer membrane	1.229	1.451	1.095	1.258	1.229	1.235	1.308	1.257	1.001	0.9952
7226969	NMB1714	multidrug efflux pump channel protein MtrE	outer membrane	1.053	1.036	1.085	1.058	0.996	1.025	1.176	1.066	0.993	0.8725
7227246	NMB1985	autotransporter App	outer membrane	0.736	0.973	0.872	0.860	0.846	1.080	0.679	0.868	0.991	0.9451
7227390	NMB2134	conserved hypothetical outer-membrane protein	outer membrane	0.815	1.103	0.635	0.851	0.771	1.013	0.819	0.867	0.981	0.8632
7225719	NMB0493	haemagglutinin/hemolysin-related protein TpsA1	outer membrane	2.181	2.705	1.213	2.033	2.186	2.592	1.489	2.089	0.973	0.6749
7225888	NMB0663	outer membrane protein NspA	outer membrane	2.018	2.902	1.559	2.160	2.119	3.387	1.511	2.339	0.923	0.3759
7225425	NMB0204	outer membrane protein assembly factor BamE	outer membrane	0.899	1.049	0.829	0.926	0.968	1.038	1.077	1.028	0.901	0.3138
7226294	NMB1053	class 5 outer membrane protein Opc	outer membrane	1.035	1.156	0.938	1.043	1.087	1.416	1.041	1.181	0.883	0.1586
7225691	NMB0464	putative phospholipase A1. pldA	outer membrane	0.930	1.031	0.867	0.943	1.008	1.034	1.217	1.086	0.868	0.3066
7225505	NMB0280	LPS-assembly protein LptD	outer membrane	0.507	0.580	0.445	0.511	0.569	0.605	0.656	0.610	0.837	0.2222
7225936	NMB0707	LPS-assembly lipoprotein LptE	outer membrane	0.969	1.009	0.915	0.964	1.115	1.113	1.249	1.159	0.832	0.1105
7226576	NMB1333	putative metalloproteinase	outer membrane	2.075	2.835	1.706	2.205	2.561	2.735	2.769	2.689	0.820	0.2865
7227250	NMB1988	TonB-dependent enterobactin receptor FetA (FrpB)	outer membrane	0.300	0.446	0.199	0.315	0.348	0.353	0.452	0.384	0.819	0.5619
7226921	NMB1668	hemoglobin receptor HmbR	outer membrane	0.573	0.625	0.602	0.600	0.668	1.021	0.561	0.750	0.800	0.3646
7227256	NMB1994	NadA autotransporter	outer membrane	0.110	0.112	0.118	0.113	0.134	0.122	0.172	0.143	0.795	0.1478
7226232	NMB0992	autotransporter NhHA	outer membrane	0.982	1.509	1.062	1.184	1.368	1.055	2.068	1.497	0.791	0.5373
7227251	NMB1989	enterobactin uptake system binding lipoprotein FetB	outer membrane	0.154	0.170	0.185	0.170	0.209	0.193	0.244	0.216	0.786	0.0553
7225265	NMB0044	peptide methionine sulfoxide reductase MrsAB	outer membrane	0.819	0.871	0.735	0.808	1.016	0.588	1.579	1.061	0.762	0.5196
7226452	NMB1214	haemagglutinin/hemolysin-related protein TpsA3	outer membrane	2.388	3.777	1.038	2.401	2.696	4.769	2.023	3.162	0.759	0.0784
7227022	NMB1768	haemagglutinin/hemolysin-related protein TpsA2	outer membrane	1.872	2.625	1.398	1.965	2.640	2.887	2.339	2.622	0.749	0.0843
7226739	NMB1497	TonB-dependent receptor	outer membrane	0.736	0.634	0.863	0.744	0.968	1.059	1.005	1.011	0.736	0.0856
7225306	NMB0088	hypothetical outer membrane protein P1	outer membrane	0.692	0.795	0.664	0.717	0.846	1.227	0.851	0.974	0.735	0.0988
7226669	NMB1429	major outer-membrane protein PorA	outer membrane	0.952	1.375	0.668	0.998	1.253	1.613	1.267	1.378	0.725	0.0760
7226992	NMB1737	putative TolC outer membrane protein	outer membrane	1.057	1.196	0.910	1.055	1.277	1.866	1.394	1.512	0.697	0.0726
7225928	NMB0700	IgA-specific serine endopeptidase	outer membrane	1.084	1.839	0.626	1.183	1.625	1.681	1.792	1.699	0.696	0.3098

7227083	NMB1829	TonB-dependent receptor	outer membrane	0.529	0.723	0.464	0.572	0.838	-	0.964	0.901	0.635	0.1469
7225686	NMB0460	transferrin-binding protein 2 TbpB	outer membrane	0.304	0.402	0.227	0.311	0.581	0.500	0.719	0.600	0.518	0.1263
7225932	NMB0703	outer membrane protein assembly factor BamD (ComL)	outer membrane	0.608	0.696	0.550	0.618	-	0.950	1.149	1.049	0.589	0.2457
7227300	NMB2039	major outer-membrane protein PorB	outer membrane	0.824	1.134	0.573	0.844	1.332	1.559	1.462	1.451	0.582	0.0510
7226874	NMB1623	copper-containing nitrite reductase AniA	outer membrane	2.833	1.696	3.379	2.636	5.123	12.307	6.095	7.841	0.336	0.1942
7226708	NMB1468	conserved hypothetical lipoprotein	inner/outer membrane	0.577	0.589	0.659	0.608	0.241	0.286	0.267	0.265	2.299	0.0056
7226089	NMB0853	conserved hypothetical TPR-containing membrane protein	inner/outer membrane	1.419	1.313	1.313	1.348	0.889	0.815	0.846	0.850	1.585	0.0013
7226450	NMB1212	hypothetical lipoprotein	inner/outer membrane	1.004	1.277	0.853	1.045	1.403	1.761	1.353	1.506	0.694	0.0046
7227208	NMB1949	putative lytic murein transglycosylase	inner/outer membrane	2.119	2.250	2.033	2.134	1.221	1.374	1.394	1.330	1.605	0.0104
7226287	NMB1047	conserved hypothetical lipoprotein	inner/outer membrane	1.308	1.451	1.270	1.343	0.889	0.899	0.932	0.907	1.481	0.0198
7226322	NMB1084	hypothetical protein	inner/outer membrane	0.308	0.308	0.318	0.311	0.209	0.193	0.258	0.220	1.414	0.0309
66731912	NMB1592	putative lipoprotein	inner/outer membrane	1.040	1.040	1.152	1.077	0.794	0.718	0.995	0.836	1.288	0.0372
7227155	NMB1898	meningococcal lipoprotein Mlp	inner/outer membrane	0.247	0.254	0.265	0.256	0.542	0.458	0.697	0.565	0.452	0.0428
7226345	NMB1107	hypothetical lipoprotein	inner/outer membrane	0.564	0.585	0.573	0.574	0.510	0.454	0.606	0.523	1.097	0.3962
7227396	NMB2139	conserved hypothetical lipoprotein	inner/outer membrane	1.855	2.179	1.768	1.934	1.806	2.046	1.674	1.842	1.050	0.0639
7226710	NMB1470	hypothetical lipoprotein	inner/outer membrane	0.463	0.415	0.398	0.425	0.514	0.550	0.480	0.515	0.826	0.0679
7225304	NMB0086	hypothetical lipoprotein	inner/outer membrane	0.344	0.344	0.332	0.340	0.324	0.378	0.602	0.435	0.781	0.3972
7226723	NMB1483	putative lipoprotein NlpD	inner/outer membrane	0.396	0.464	0.365	0.409	0.530	0.441	0.688	0.553	0.739	0.2859
7225274	NMB0054	hypothetical lipoprotein	inner/outer membrane	1.493	1.835	-	1.664	2.300	2.248	-	2.274	0.732	0.1988
7226275	NMB1035	hypothetical lipoprotein	inner/outer membrane	0.643	0.634	0.711	0.663	0.870	1.118	0.810	0.932	0.711	0.1399
7226925	NMB1672	conserved hypothetical lipoprotein	inner/outer membrane	1.938	1.116	1.573	1.543	2.253	1.643	2.864	2.253	0.685	0.1387
7227404	NMB2147	conserved hypothetical lipoprotein	inner/outer membrane	2.211	2.513	1.991	2.238	3.174	3.122	3.579	3.292	0.680	0.0667
7226451	NMB1213	hypothetical lipoprotein	inner/outer membrane	0.806	0.951	0.626	0.794	1.091	1.391	-	1.241	0.640	0.1343
7226076	NMB0841	hypothetical integral membrane protein	inner/outer membrane	0.590	0.558	0.659	0.602	1.107	0.513	1.344	0.988	0.610	0.2231
7225255	NMB0035	Efem/EfeO family lipoprotein	inner/outer membrane	0.075	0.071	0.095	0.080	0.162	0.097	0.222	0.160	0.502	0.1145
7226269	NMB1030	Neisseria ubiquinone-8 binding protein NUbp	periplasmic ⁺	1.405	1.469	1.564	1.479	0.285	0.340	0.308	0.311	4.759	0.0014
7225261	NMB0041	ABC transporter, periplasmic solute-binding protein	periplasmic	0.890	0.888	0.915	0.898	0.206	0.227	0.240	0.224	4.006	0.0001
7225774	NMB0548	AcrA/AcrE family protein	periplasmic	0.714	0.777	0.659	0.716	0.356	-	0.294	0.325	2.205	0.0059
7225566	NMB0345	Peptidylprolyl isomerase	periplasmic	0.661	0.683	0.668	0.671	0.300	0.261	0.367	0.309	2.170	0.0092
7226161	NMB0923	cytochrome c	periplasmic	0.485	0.522	0.464	0.490	0.340	0.412	0.348	0.367	1.337	0.0072
7227218	NMB1958	putative thioredoxin	periplasmic	0.366	0.424	0.379	0.390	0.281	0.349	0.281	0.303	1.285	0.0060
7226015	NMB0783	conserved hypothetical periplasmic protein	periplasmic	1.784	1.763	2.052	1.867	0.474	0.622	0.443	0.513	3.637	0.0100
7227223	NMB1963	conserved hypothetical periplasmic protein	periplasmic	1.480	1.161	1.213	1.285	0.395	0.454	0.416	0.422	3.046	0.0170
7226813	NMB1565	conserved hypothetical periplasmic protein	periplasmic	1.128	-	1.180	1.154	0.348	-	0.434	0.391	2.950	0.0143
7225777	NMB0550	thiol:disulfide interchange lipoprotein DsbC	periplasmic	3.018	2.393	2.469	2.627	0.945	0.975	0.792	0.904	2.906	0.0120
7225629	NMB0407	thiol:disulfide interchange protein DsbA3	periplasmic	1.176	0.987	1.308	1.157	0.451	0.454	0.525	0.476	2.428	0.0121
7225862	NMB0634	iron(III)-transport system iron-binding protein FbpB	periplasmic	0.432	0.429	0.502	0.454	0.225	0.130	0.330	0.229	1.987	0.0268
7226518	NMB1279	membrane-bound lytic murein transglycosylase B	periplasmic	1.322	1.237	1.550	1.369	0.771	0.782	0.846	0.799	1.713	0.0157
7225836	NMB0606	conserved hypothetical periplasmic protein	periplasmic	0.960	0.942	0.882	0.928	0.593	0.756	0.643	0.664	1.398	0.0393
7225533	NMB0313	conserved hypothetical TPR-containing periplasmic protein	periplasmic	0.396	0.518	0.303	0.406	0.708	0.815	0.814	0.779	0.521	0.0326
7225815	NMB0586	putative ABC transporter substrate-binding protein	periplasmic	0.489	0.188	0.758	0.478	0.209	0.227	0.240	0.225	2.122	0.2581
7226256	NMB1017	periplasmic sulfate-binding protein	periplasmic	0.035	0.031	0.043	0.036	0.028	0.017	0.018	0.021	1.744	0.0878
7227059	NMB1805	cytochrome c4	periplasmic	1.070	0.808	1.313	1.064	0.668	0.668	0.579	0.638	1.666	0.1316
7225681	NMB0456	N-acetylmuramoyl-L-alanine amidase AmiC	periplasmic	2.115	3.924	-	3.019	1.229	2.546	-	1.888	1.599	0.1364
7226716	NMB1475	conserved hypothetical periplasmic protein	periplasmic	0.361	0.045	0.730	0.379	0.253	0.176	0.376	0.268	1.411	0.5144
7227337	NMB2074	conserved hypothetical periplasmic protein	periplasmic	0.304	0.759	0.536	0.533	0.340	0.429	0.403	0.390	1.365	0.3108
7225400	NMB0181	periplasmic chaperone Skp (OmpH)	periplasmic	2.432	2.076	2.341	2.283	1.889	1.878	1.828	1.865	1.224	0.0632
7226681	NMB1440	conserved hypothetical TPR-containing periplasmic protein	periplasmic	4.004	4.451	2.161	3.539	2.542	3.735	2.801	3.026	1.170	0.4923
7225577	NMB0355	Lipopolysaccharide export system protein LptA	periplasmic	1.163	1.241	0.915	1.106	0.885	1.008	0.982	0.959	1.154	0.3056
7226109	NMB0872	conserved hypothetical TPR-containing periplasmic protein	periplasmic	2.370	3.455	1.668	2.498	1.941	1.706	2.887	2.178	1.147	0.7451
7225324	NMB0109	putative peptidoglycan-binding periplasmic protein	periplasmic	0.912	1.170	0.872	0.985	0.830	0.782	1.059	0.890	1.106	0.6271

7413435	NMB0643	MafB-related protein	periplasmic	1.172	1.013	1.678	1.288	1.166	1.092	1.285	1.181	1.090	0.5396
66731926	NMB0532	protease DO (DegQ)	periplasmic	1.203	0.857	1.261	1.107	1.115	1.025	1.059	1.066	1.038	0.7462
7226927	NMB1674	GDSL lipase family protein	periplasmic	0.802	1.000	0.654	0.819	0.708	1.000	0.661	0.789	1.037	0.4644
7225689	NMB0462	periplasmic spermidine/putrescine-binding protein	periplasmic	0.626	0.746	0.573	0.648	0.569	0.798	0.511	0.626	1.035	0.6171
7226084	NMB0848	conserved hypothetical periplasmic protein	periplasmic	1.198	1.259	1.047	1.168	1.036	0.777	1.620	1.144	1.021	0.9459
7225907	NMB0680	conserved hypothetical periplasmic protein	periplasmic	1.070	1.549	1.071	1.230	1.174	1.374	1.136	1.228	1.002	0.9809
7226804	NMB1557	conserved hypothetical periplasmic protein	periplasmic	0.916	0.839	1.095	0.950	0.877	1.172	0.864	0.971	0.978	0.9097
7226871	NMB1620	putative muramoyltetrapeptide carboxypeptidase	periplasmic	4.000	4.844	3.199	4.014	3.644	5.332	3.955	4.310	0.931	0.4700
7226019	NMB0787	putative amino acid ABC transporter binding lipoprotein	inner membrane	0.048	0.049	0.052	0.050	0.024	0.025	0.027	0.025	1.968	0.0002
7225402	NMB0183	Putative zinc metalloprotease	inner membrane	0.639	0.835	0.673	0.716	0.372	0.500	0.353	0.408	1.753	0.0044
7225558	NMB0338	conserved hypothetical integral membrane protein	inner membrane	0.436	0.509	0.431	0.459	0.265	0.340	0.308	0.304	1.508	0.0099
7226862	NMB1612	putative amino acid-binding lipoprotein (HBP)	inner membrane	0.700	0.768	0.678	0.715	0.545	0.651	0.561	0.586	1.221	0.0096
7225649	NMB0426	cell division protein FtsA	inner membrane	0.916	1.813	2.237	1.655	1.818	2.933	3.362	2.704	0.612	0.0049
7225281	NMB0060	putative oligopeptide transporter	inner membrane	0.595	0.692	0.564	0.617	0.292	0.357	0.389	0.346	1.782	0.0310
7226843	NMB1594	putative spermidine/putrescine-binding lipoprotein	inner membrane	1.608	1.951	1.460	1.673	0.905	1.046	0.891	0.948	1.765	0.0177
7226127	NMB0889	type IV pilus biogenesis protein PilK	inner membrane	1.097	1.339	-	1.218	0.640	0.807	0.851	0.766	1.590	0.0488
7225302	NMB0085	sodium/glutamate symporter	inner membrane	0.617	0.688	0.573	0.626	0.383	0.408	0.407	0.399	1.567	0.0206
7225854	NMB0623	putative spermidine/putrescine-binding lipoprotein	inner membrane	0.269	0.259	0.270	0.266	0.158	0.155	0.204	0.172	1.543	0.0207
7226031	NMB0798	cell division protease FtsH	inner membrane	1.542	1.692	1.900	1.711	1.055	1.063	1.489	1.202	1.423	0.0153
7226763	NMB1519	thiol:disulfide interchange protein DsbD	inner membrane	0.361	0.433	0.464	0.420	0.285	0.315	0.321	0.307	1.367	0.0284
7226971	NMB1716	membrane fusion protein mtrC	inner membrane	0.441	0.478	0.427	0.448	0.312	0.345	0.344	0.334	1.344	0.0191
7226970	NMB1715	multiple transferable resistance system protein MtrD	inner membrane	0.714	0.813	0.730	0.752	0.538	0.571	0.579	0.563	1.336	0.0196
7225628	NMB0406	putative cell division protein FtsN	inner membrane	0.529	0.567	0.550	0.548	0.419	0.445	0.466	0.443	1.237	0.0112
7227195	NMB1937	ATP-synthase F1. delta subunit	inner membrane	1.251	1.027	-	1.139	1.134	0.899	0.738	0.924	1.233	0.0284
7227315	NMB2053	ubiquinol-cytochrome c reductase. iron-sulfur subunit	inner membrane	0.573	1.000	0.431	0.668	1.206	1.450	1.199	1.285	0.520	0.0216
7225231	NMB0006	thioredoxin-related protein	inner membrane	1.295	1.201	1.431	1.309	-	0.336	0.294	0.315	4.154	0.0861
7226538	NMB1297	membrane-bound lytic murein transglycosylase D	inner membrane	2.203	3.040	2.299	2.514	1.233	0.782	2.041	1.352	1.860	0.1856
7225760	NMB0535	glucose/galactose transporter	inner membrane	1.000	0.670	0.654	0.775	0.451	0.597	0.452	0.500	1.549	0.1934
7225791	NMB0564	Na(+)-translocating NADH-quinone reductase. subunit F	inner membrane	3.145	5.321	2.171	3.546	2.241	2.332	2.579	2.384	1.487	0.3612
7227164	NMB1907	Membrane protein insertase YidC (OxA)	inner membrane	0.692	0.746	0.735	0.724	0.565	-	0.421	0.493	1.468	0.2562
7226203	NMB0963	phosphatidylserine decarboxylase precursor-related protein	inner membrane	0.811	0.768	0.540	0.706	0.447	0.676	0.403	0.509	1.389	0.1435
7225518	NMB0294	thiol:disulfide interchange lipoprotein DsbA2	inner membrane**	0.326	0.397	0.280	0.334	0.237	0.269	0.249	0.252	1.329	0.1003
66731937	NMB1809	type IV pilus biogenesis protein PilN	inner membrane	2.247	2.598	2.379	2.408	1.668	2.647	1.285	1.867	1.290	0.2431
7226478	NMB1238	peptidyl-prolyl cis-trans isomerase-related protein	inner membrane	0.894	1.085	0.929	0.969	0.680	0.987	0.661	0.776	1.249	0.0618
7226590	NMB1345	hypothetical protein	inner membrane	0.498	0.473	0.507	0.493	0.383	0.349	0.475	0.402	1.224	0.0911
7226734	NMB1493	carbon starvation protein A	inner membrane	-	1.272	1.104	1.188	0.901	1.441	0.597	0.980	1.213	0.7047
7226057	NMB0822	heat shock protein HtpX	inner membrane	0.207	0.228	0.185	0.207	0.162	0.185	0.172	0.173	1.194	0.0835
7225414	NMB0194	putative amino acid symporter	inner membrane	0.502	0.571	-	0.537	0.415	0.433	0.516	0.455	1.181	0.1427
7227063	NMB1810	type IV pilus biogenesis protein PilO	inner membrane	2.771	2.076	2.460	2.436	1.968	2.933	1.303	2.068	1.178	0.6139
7226575	NMB1332	carboxy-terminal peptidase	inner membrane	2.648	3.607	2.019	2.758	2.292	2.008	2.891	2.397	1.150	0.6635
7225840	NMB0610	spermidine/putrescine ABC transporter	inner membrane	0.674	0.737	0.630	0.680	0.522	0.676	0.584	0.594	1.145	0.1215
7227194	NMB1936	ATP synthase alpha chain	inner membrane	1.683	1.750	1.711	1.715	1.407	1.731	1.430	1.523	1.126	0.1568
7225838	NMB0608	protein-export membrane protein SecF	inner membrane	0.630	0.670	0.412	0.571	0.462	-	0.561	0.512	1.115	0.9623
7227193	NMB1935	ATP synthase F1. gamma subunit	inner membrane	1.581	1.946	1.758	1.762	1.462	1.819	1.502	1.595	1.105	0.0637
7225924	NMB0996	conserved hypothetical integral membrane protein	inner membrane	1.317	-	2.047	1.682	1.640	1.206	1.787	1.545	1.089	0.9314
7225598	NMB0378	putative phosphate permease	inner membrane	1.868	2.308	1.488	1.888	1.526	2.672	1.077	1.758	1.074	0.6528
7227192	NMB1934	ATP synthase F1. beta subunit	inner membrane	1.313	1.353	1.313	1.326	1.162	1.462	1.172	1.265	1.048	0.5499
7225837	NMB0607	protein-export membrane protein SecD	inner membrane	0.595	0.625	0.649	0.623	0.569	0.647	0.643	0.620	1.006	0.8282
7226009	NMB0778	putative heme biosynthesis protein HemX	inner membrane	0.392	0.473	0.355	0.407	0.494	0.458	0.294	0.415	0.980	0.8776
7227359	NMB2096	malate:quinone oxidoreductase	inner membrane	0.361	0.313	0.498	0.390	0.375	0.374	0.448	0.399	0.978	0.8127
7225562	NMB0341	TspA protein	inner membrane	0.921	0.929	0.900	0.917	0.854	1.088	0.882	0.941	0.974	0.7526

66731901	NMB0601	Sec-independent protein translocase protein TatA	inner membrane	0.405	0.402	0.412	0.406	0.383	0.462	0.421	0.422	0.963	0.5812
7225769	NMB0543	putative L-lactate permease	inner membrane	0.295	0.406	0.275	0.325	0.296	0.387	0.357	0.347	0.938	0.5636
7225503	NMB0278	thiol:disulfide interchange lipoprotein DsbA1	inner membrane**	0.449	0.509	0.450	0.470	0.510	0.664	0.439	0.538	0.873	0.2931
7226781	NMB1536	preprotein translocase SecA subunit	inner membrane	1.714	1.446	1.521	1.560	1.731	1.206	2.715	1.884	0.828	0.5398
7226984	NMB1729	biopolymer transport protein ExbB	inner membrane	0.485	0.469	-	0.477	0.478	0.504	0.810	0.597	0.798	0.6123
7227314	NMB2052	ubiquinol-cytochrome c reductase. cytochrome b	inner membrane	0.793	0.951	0.801	0.848	0.830	1.408	0.995	1.078	0.787	0.2017
7225553	NMB0333	pilus assembly protein PilG	inner membrane	1.608	2.000	1.194	1.601	1.711	-	2.439	2.075	0.771	0.4472
7226930	NMB1677	cytochrome c5	inner membrane	0.894	0.732	0.829	0.819	0.980	1.303	0.914	1.066	0.768	0.2662
7226977	NMB1723	cytochrome c oxidase. subunit III	inner membrane	0.744	0.906	0.649	0.767	1.063	-	1.059	1.061	0.723	0.0790
7227313	NMB2051	ubiquinol-cytochrome c reductase. cytochrome c1	inner membrane	-	1.031	0.682	0.857	1.083	1.542	1.050	1.225	0.700	0.1031
7226978	NMB1724	cytochrome c oxidase. subunit II	inner membrane	0.841	0.853	0.697	0.797	1.040	1.508	0.873	1.140	0.699	0.1590
7225608	NMB0387	phosphate permease PitA	inner membrane	3.163	-	5.445	4.304	3.573	5.248	10.511	6.444	0.668	0.4486
7226802	NMB1555	long-chain-fatty-acid-CoA ligase	inner membrane	2.480	2.442	2.611	2.511	3.514	3.479	5.557	4.183	0.600	0.1195
7226444	NMB1207	bacterioferritin A	cytoplasmic	0.617	0.679	0.626	0.640	0.352	0.433	0.380	0.388	1.649	0.0007
7226443	NMB1206	bacterioferritin B	cytoplasmic	0.551	0.625	0.583	0.586	0.316	0.420	0.339	0.359	1.635	0.0026
7227093	NMB1838	Ribosome-binding ATPase YchF	cytoplasmic	-	1.286	0.787	1.036	1.150	1.744	1.235	1.376	0.753	0.0066
7226965	NMB1710	NADP-specific glutamate dehydrogenase	cytoplasmic	0.132	0.129	0.175	0.146	0.182	0.185	0.231	0.199	0.731	0.0013
7226853	NMB1604	gpmA. phosphoglycerate mutase	cytoplasmic	0.956	1.179	0.791	0.975	1.909	2.412	1.833	2.051	0.476	0.0059
7226158	NMB0920	isocitrate dehydrogenase. NADP-dependent	cytoplasmic	0.366	0.384	0.318	0.356	0.190	0.197	0.226	0.204	1.740	0.0375
7225429	NMB0207	glyceraldehyde 3-phosphate dehydrogenase	cytoplasmic	6.921	8.844	9.137	8.301	4.605	5.496	5.145	5.082	1.633	0.0222
7226624	NMB1384	DNA gyrase subunit A	cytoplasmic	0.885	0.839	1.047	0.924	0.648	0.458	0.774	0.627	1.475	0.0205
7225988	NMB0758	polyribonucleotide nucleotidyltransferase	cytoplasmic	0.934	0.875	0.886	0.898	0.601	0.681	0.548	0.610	1.474	0.0257
7225344	NMB0127	50S ribosomal protein L11	cytoplasmic	0.846	0.696	0.853	0.798	0.514	0.479	0.638	0.544	1.469	0.0222
7226562	NMB1320	50S ribosomal protein L9	cytoplasmic	1.885	1.188	2.417	1.830	1.316	0.714	1.719	1.250	1.464	0.0123
7227094	NMB1839	formate-tetrahydrofolate ligase	cytoplasmic	0.824	0.942	0.754	0.840	0.518	0.756	0.475	0.583	1.440	0.0195
7226565	NMB1323	30S ribosomal protein S6	cytoplasmic	0.938	0.804	1.047	0.930	0.692	0.651	0.742	0.695	1.338	0.0342
7225690	NMB0463	30S ribosomal protein S20	cytoplasmic	1.097	1.054	1.066	1.072	0.794	0.891	0.796	0.827	1.296	0.0284
7227062	NMB1808	type IV pilus biogenesis protein PilM	cytoplasmic	3.388	3.938	3.341	3.555	2.443	3.416	2.683	2.847	1.249	0.0297
7226050	NMB0815	adenylosuccinate synthetase	cytoplasmic	0.436	0.504	0.455	0.465	0.502	0.559	0.552	0.538	0.865	0.0297
7226586	NMB1342	pyruvate dehydrogenase. E2 component	cytoplasmic	1.070	1.304	1.005	1.126	1.229	1.559	1.271	1.353	0.832	0.0220
7225946	NMB0720	threonyl-tRNA synthetase	cytoplasmic	6.837	5.991	6.024	6.284	7.715	7.294	7.891	7.634	0.823	0.0422
7225993	NMB0763	cysteine synthase A	cytoplasmic	0.269	0.326	0.256	0.284	0.340	0.445	0.339	0.375	0.756	0.0242
7413480	NMB2060	glycerol-3-phosphate dehydrogenase (NAD+)	cytoplasmic	0.383	0.487	0.379	0.416	0.545	0.571	0.570	0.562	0.740	0.0440
7226626	NMB1388	glucose-6-phosphate isomerase	cytoplasmic	3.436	3.531	3.469	3.479	5.130	4.870	4.538	4.846	0.718	0.0171
7226270	NMB1031	3-isopropylmalate dehydrogenase	cytoplasmic	0.441	0.558	0.327	0.442	0.565	0.739	0.561	0.622	0.710	0.0294
7226859	NMB1609	O-succinylhomoserine sulfhydrylase (OSH sulfhydrylase)	cytoplasmic	2.330	2.598	2.346	2.425	3.344	3.916	3.308	3.523	0.688	0.0101
7225510	NMB0286	conserved hypothetical protein	cytoplasmic	0.308	0.397	0.294	0.333	0.447	0.643	0.462	0.517	0.644	0.0290
7226931	NMB1678	aromatic-amino-acid aminotransferase	cytoplasmic	0.339	0.330	0.308	0.326	0.490	0.492	0.543	0.508	0.641	0.0204
7226800	NMB1554	CTP synthase	cytoplasmic	1.123	1.232	0.938	1.098	1.711	1.857	1.814	1.794	0.612	0.0165
7225468	NMB0246	NADH dehydrogenase I. F subunit	cytoplasmic	0.718	0.942	0.545	0.735	1.115	1.525	1.226	1.289	0.570	0.0220
7226806	NMB1559	glutathione synthetase	cytoplasmic	0.313	0.357	0.237	0.302	0.474	0.626	0.511	0.537	0.563	0.0236
7226525	NMB1285	Enolase	cytoplasmic	2.150	2.607	2.142	2.300	4.091	5.441	3.941	4.491	0.512	0.0212
7226313	NMB1073	putative carboxypeptidase	cytoplasmic	0.132	0.156	0.190	0.159	0.332	0.265	0.376	0.324	0.492	0.0285
7225307	NMB0089	pyruvate kinase	cytoplasmic	2.577	5.152	3.668	3.799	6.490	10.874	6.281	7.882	0.482	0.0455
7227144	NMB1885	protein-L-isoaspartate O-methyltransferase	cytoplasmic	0.379	1.000	0.223	0.534	1.249	2.248	0.959	1.485	0.359	0.0249
7225834	NMB0604	zinc containing alcohol dehydrogenase	cytoplasmic	0.308	0.455	0.223	0.329	0.850	1.248	0.805	0.968	0.340	0.0145
7413462	NMB1379	Cysteine desulfurase IscS (NifS protein homolog)	cytoplasmic	1.207	1.045	1.474	1.242	4.877	4.181	-	4.529	0.274	0.0499
7225370	NMB0152	50S ribosomal protein L14	cytoplasmic	1.943	3.379	3.256	2.859	1.024	0.971	1.303	1.099	2.601	0.0574
7225385	NMB0167	30S ribosomal protein S4	cytoplasmic	4.982	1.661	7.739	4.794	1.787	1.492	2.321	1.866	2.569	0.1942
7227088	NMB1833	isoleucyl-tRNA synthetase	cytoplasmic	10.850	6.563	4.445	7.286	5.123	2.651	1.964	3.246	2.245	0.0500
7225363	NMB0145	50S ribosomal protein L2	cytoplasmic	2.018	-	2.284	2.151	0.573	-	1.448	1.011	2.129	0.1659
7225376	NMB0158	50S ribosomal protein L18	cytoplasmic	1.423	0.634	1.479	1.179	-	0.492	0.679	0.585	2.014	0.3879

7225384	NMB0166	30S ribosomal protein S11	cytoplasmic	4.123	2.237	5.668	4.009	-	1.672	2.344	2.008	1.997	0.3929
7226114	NMB0876	50S ribosomal protein L25	cytoplasmic	1.053	-	1.379	1.216	0.589	0.466	0.810	0.622	1.956	0.0646
7226541	NMB1301	30S ribosomal protein S1	cytoplasmic	9.930	3.317	13.919	9.055	3.455	4.088	6.430	4.658	1.944	0.2330
7225361	NMB0143	50S ribosomal protein L4	cytoplasmic	3.220	1.634	5.204	3.353	1.704	1.324	2.199	1.742	1.925	0.1747
7227364	NMB2101	30S ribosomal protein S2	cytoplasmic	1.604	1.013	2.270	1.629	0.806	0.819	0.955	0.860	1.894	0.1410
7226223	NMB0983	bifunctional purine biosynthesis protein PurH	cytoplasmic	8.542	5.165	4.213	5.973	3.628	0.887	4.995	3.170	1.884	0.2601
7227318	NMB2056	30S ribosomal protein S9	cytoplasmic	2.062	1.022	2.863	1.982	1.032	0.824	1.321	1.059	1.872	0.1422
7225347	NMB0130	30S ribosomal protein S7	cytoplasmic	1.225	0.656	1.592	1.158	0.680	0.479	0.747	0.635	1.823	0.1139
7225379	NMB0161	50S ribosomal protein L15	cytoplasmic	4.189	1.688	4.204	3.360	1.170	2.685	1.860	1.905	1.764	0.3619
7225364	NMB0146	30S ribosomal protein S19	cytoplasmic	0.811	0.513	1.014	0.779	0.458	0.475	-	0.467	1.670	0.4305
7225366	NMB0148	30S ribosomal protein S3	cytoplasmic	3.423	2.210	5.062	3.565	1.858	2.097	2.462	2.139	1.667	0.1866
7225375	NMB0157	50S ribosomal protein L6	cytoplasmic	0.921	0.710	1.621	1.084	0.609	0.567	0.783	0.653	1.660	0.1758
7225360	NMB0142	50S ribosomal protein L3	cytoplasmic	1.220	0.946	1.882	1.349	0.755	0.811	0.905	0.824	1.638	0.1646
7227319	NMB2057	50S ribosomal protein L13	cytoplasmic	1.128	0.875	1.379	1.127	0.719	0.660	0.742	0.707	1.594	0.0748
7225373	NMB0155	30S ribosomal protein S14	cytoplasmic	1.626	0.964	2.427	1.672	-	0.870	1.231	1.050	1.592	0.4498
7225819	NMB0589	50s ribosomal protein L19	cytoplasmic	1.969	1.076	2.370	1.805	0.901	1.063	1.448	1.137	1.587	0.1805
7225372	NMB0154	50S ribosomal protein L5	cytoplasmic	1.427	0.893	1.829	1.383	0.862	0.777	0.982	0.874	1.583	0.1393
7225417	NMB0196	ribonuclease E	cytoplasmic	3.432	2.804	4.422	3.552	2.051	2.601	2.136	2.263	1.570	0.1659
7225950	NMB0723	50S ribosomal protein L20	cytoplasmic	0.841	0.754	0.910	0.835	0.518	0.592	0.493	0.534	1.563	0.0561
7225355	NMB0137	30S ribosomal protein S7	cytoplasmic	1.110	0.906	2.190	1.402	0.941	0.529	1.276	0.915	1.532	0.1594
7225387	NMB0169	50S ribosomal protein L17	cytoplasmic	0.714	0.589	0.853	0.719	0.490	0.538	0.457	0.495	1.452	0.1535
7225377	NMB0159	30s ribosomal protein S5	cytoplasmic	0.960	0.772	1.403	1.045	0.688	0.702	0.801	0.730	1.432	0.1788
7225358	NMB0140	30S ribosomal protein S10	cytoplasmic	0.987	0.804	1.028	0.940	0.676	0.710	0.611	0.666	1.412	0.1028
7225266	NMB0045	Signal recognition particle receptor FtsY	cytoplasmic	3.665	5.455	2.829	3.983	3.451	2.349	2.796	2.865	1.390	0.3781
7226277	NMB1037	glutamate-cysteine ligase	cytoplasmic	0.626	0.201	0.318	0.381	0.253	0.244	0.344	0.280	1.361	0.5340
7225345	NMB0128	50S ribosomal protein L1	cytoplasmic	0.687	0.563	0.844	0.698	0.486	0.508	0.566	0.520	1.342	0.1137
7227356	NMB2094	conserved hypothetical protein	cytoplasmic	0.727	0.674	0.787	0.729	0.502	0.588	0.548	0.546	1.336	0.0644
7225362	NMB0144	50S ribosomal protein L23	cytoplasmic	0.762	0.567	-	0.665	0.462	0.479	0.579	0.507	1.311	0.3182
7225839	NMB0609	30s ribosomal protein S15	cytoplasmic	0.833	0.759	1.047	0.880	0.617	0.735	0.692	0.681	1.291	0.1752
7225772	NMB0546	alcohol dehydrogenase. propanol-preferring	cytoplasmic	11.780	13.241	5.829	10.283	6.474	9.462	8.575	8.170	1.259	0.4822
7226295	NMB1055	serine hydroxymethyltransferase	cytoplasmic	5.220	5.147	4.517	4.961	3.771	3.681	4.462	3.971	1.249	0.1684
7226189	NMB0950	succinate dehydrogenase. flavoprotein subunit	cytoplasmic	1.581	2.286	1.488	1.785	1.538	1.227	1.656	1.474	1.211	0.4970
7226824	NMB1576	acetolactate synthase III. small subunit	cytoplasmic	0.176	0.156	-	0.166	0.138	0.092	0.186	0.139	1.198	0.1590
7225374	NMB0156	30S ribosomal protein S8	cytoplasmic	2.154	1.420	1.725	1.766	1.557	1.403	1.475	1.479	1.195	0.2301
7225343	NMB0126	transcription antitermination protein NusG	cytoplasmic	1.454	1.982	-	1.718	1.300	2.076	1.005	1.460	1.177	0.8485
7225560	NMB0340	lactoylglutathione lyase	cytoplasmic	0.727	1.004	-	0.866	0.692	0.739	0.783	0.738	1.173	0.4160
7225349	NMB0132	DNA-directed RNA polymerase. beta subunit	cytoplasmic	2.568	2.652	2.573	2.598	1.980	2.899	1.824	2.234	1.163	0.3605
7225386	NMB0168	DNA-directed RNA polymerase. alpha subunit	cytoplasmic	1.339	1.496	1.573	1.469	1.241	1.332	1.244	1.272	1.155	0.1033
7225859	NMB0629	hisA	cytoplasmic	1.489	2.335	1.938	1.921	1.573	1.382	2.086	1.680	1.143	0.5699
7226822	NMB1574	ketol-acid reductoisomerase	cytoplasmic	0.269	0.281	0.280	0.277	0.233	0.286	0.208	0.242	1.141	0.2595
7226618	NMB1372	ATP-dependent Clp protease. ATP-binding subunit ClpX	cytoplasmic	4.850	7.143	5.038	5.677	6.352	3.576	5.018	4.982	1.140	0.6889
7226143	NMB0906	conserved hypothetical protein	cytoplasmic	0.137	0.205	0.185	0.176	0.123	0.269	0.072	0.155	1.136	0.7204
7227196	NMB1938	ATP synthase F0. B subunit	cytoplasmic	1.476	1.531	1.498	1.502	1.182	1.655	1.154	1.330	1.129	0.3679
7225866	NMB0637	argininosuccinate lyase	cytoplasmic	1.445	1.603	1.251	1.433	1.150	1.504	1.167	1.274	1.125	0.1444
7225351	NMB0133	DNA-directed RNA polymerase. beta' subunit	cytoplasmic	2.643	2.862	2.464	2.656	2.217	2.983	1.914	2.372	1.120	0.3015
7225367	NMB0149	50S ribosomal protein L16	cytoplasmic	0.427	0.406	0.493	0.442	0.352	0.429	0.416	0.399	1.108	0.3178
7225519	NMB0295	signal recognition particle protein (fifty-four homolog)	cytoplasmic	1.507	1.500	1.896	1.634	1.328	1.479	1.620	1.476	1.107	0.1664
7225356	NMB0138	elongation factor G (EF-G)	cytoplasmic	4.771	5.415	5.408	5.198	4.115	4.487	5.484	4.695	1.107	0.2359
7226938	NMB1684	seryl-tRNA synthetase	cytoplasmic	4.749	5.375	3.863	4.662	6.601	-	1.851	4.226	1.103	0.9737
7226297	NMB1057	gamma-glutamyltranspeptidase	cytoplasmic	2.088	2.313	2.095	2.165	2.107	1.798	1.986	1.964	1.103	0.3369
7227117	NMB1860	biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP)	cytoplasmic	0.022	0.027	0.019	0.023	0.001	0.034	0.027	0.021	1.098	0.8525
7225825	NMB0595	DNA-binding response regulator	cytoplasmic	0.467	0.603	-	0.535	0.478	0.412	0.579	0.490	1.092	0.5376

7227209	NMB1950	30S ribosomal protein S21	cytoplasmic	1.048	0.924	-	0.986	0.842	1.004	0.869	0.905	1.090	0.7355
7227366	NMB2103	uridylate kinase	cytoplasmic	0.718	0.830	0.621	0.723	0.664	0.534	0.824	0.674	1.073	0.7647
7226982	NMB1727	conserved hypothetical protein	cytoplasmic	0.802	0.848	0.550	0.733	0.660	0.521	0.878	0.686	1.068	0.8322
7226872	NMB1621	glutathione peroxidase	cytoplasmic	3.687	3.054	-	3.370	3.838	2.563	-	3.200	1.053	0.6898
7227259	NMB1996	phosphoribosylformylglycinamide synthase	cytoplasmic	1.313	1.804	1.265	1.461	1.273	1.475	1.452	1.400	1.043	0.7242
7226831	NMB1583	imidazoleglycerol-phosphate dehydratase	cytoplasmic	2.057	1.446	3.095	2.199	1.791	2.727	1.810	2.109	1.043	0.9146
7226632	NMB1393	phosphogluconate dehydratase	cytoplasmic	0.859	1.156	0.872	0.962	0.854	1.050	0.891	0.932	1.033	0.5083
7226237	NMB0997	D-lactate dehydrogenase	cytoplasmic	0.559	0.576	0.607	0.581	0.466	0.765	0.466	0.566	1.026	0.8978
7227132	NMB1874	orotate phosphoribosyltransferase	cytoplasmic	0.912	1.067	-	0.989	0.866	0.987	1.041	0.965	1.026	0.1646
7226588	NMB1344	pyruvate dehydrogenase. E3 component	cytoplasmic	1.273	1.821	1.284	1.460	1.577	1.328	1.421	1.442	1.012	0.9483
7225259	NMB0039	putative HAD-superfamily hydrolase	cytoplasmic	1.233	2.214	1.104	1.517	1.372	1.832	1.317	1.507	1.007	0.9600
7226286	NMB1046	threonine synthase	cytoplasmic	1.493	1.790	1.341	1.542	1.292	1.466	1.842	1.534	1.005	0.9777
7226845	NMB1595	alanyl-tRNA synthetase	cytoplasmic	3.828	3.607	4.147	3.861	3.648	2.739	5.362	3.917	0.986	0.9357
7225507	NMB0281	peptidyl-prolyl cis-trans isomerase	cytoplasmic	2.013	2.040	1.725	1.926	1.787	2.109	2.023	1.973	0.976	0.7876
7226827	NMB1579	ATP phosphoribosyltransferase	cytoplasmic	8.749	4.969	6.161	6.626	8.281	6.597	5.498	6.792	0.976	0.8425
7226197	NMB0957	2-oxoglutarate dehydrogenase	cytoplasmic	0.264	0.286	0.232	0.261	0.233	-	0.303	0.268	0.972	0.7631
7227341	NMB2079	aspartate-semialdehyde dehydrogenase	cytoplasmic	0.912	0.897	0.886	0.898	0.905	0.798	1.090	0.931	0.965	0.7496
7226182	NMB0944	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	cytoplasmic	2.683	3.808	2.114	2.868	2.755	3.122	3.113	2.997	0.957	0.8168
7225572	NMB0351	transaldolase	cytoplasmic	0.185	0.219	0.152	0.185	0.178	0.172	0.235	0.195	0.949	0.8195
7226554	NMB1313	trigger factor	cytoplasmic	1.075	0.924	1.237	1.079	1.024	-	1.258	1.141	0.946	0.7474
7227316	NMB2054	GTP cyclohydrolase 1 type 2 homolog	cytoplasmic	1.115	1.121	1.109	1.115	1.103	1.097	1.344	1.181	0.944	0.5134
7225424	NMB0203	dihydrodipicolinate reductase	cytoplasmic	2.286	2.813	3.664	2.921	2.810	3.227	3.290	3.109	0.939	0.5743
7227170	NMB1913	fatty acid/phospholipid synthesis protein	cytoplasmic	1.282	1.951	1.682	1.638	1.411	2.382	1.462	1.752	0.935	0.6091
7226519	NMB1280	very long chain acyl-CoA dehydrogenase-related protein	cytoplasmic	1.665	1.982	1.327	1.658	1.613	1.538	2.204	1.785	0.929	0.7772
7226438	NMB1201	IMP dehydrogenase	cytoplasmic	0.529	0.679	0.427	0.545	0.526	0.790	0.448	0.588	0.926	0.3392
7226193	NMB0954	citrate synthase	cytoplasmic	0.630	0.920	0.592	0.714	0.731	0.706	0.882	0.773	0.923	0.7262
7227233	NMB1972	chaperonin. 60 kDa	cytoplasmic	0.361	0.375	0.374	0.370	0.375	0.517	0.326	0.406	0.912	0.5880
7225938	NMB0711	conserved hypothetical protein	cytoplasmic	0.379	0.442	0.346	0.389	0.411	0.471	0.407	0.430	0.905	0.0588
7225765	NMB0540	aspartate aminotransferase	cytoplasmic	0.714	1.411	0.682	0.936	0.870	1.311	0.932	1.038	0.902	0.4320
7227041	NMB1787	N-acetyl-gamma-glutamyl-phosphate reductase	cytoplasmic	0.264	0.344	0.318	0.309	0.281	0.391	0.357	0.343	0.900	0.0656
7225383	NMB0165	30S ribosomal protein S13	cytoplasmic	0.921	0.339	1.270	0.843	0.901	-	0.977	0.939	0.898	0.4576
7226717	NMB1476	glutamate dehydrogenase. NAD-specific	cytoplasmic	1.106	1.228	1.227	1.187	1.186	1.668	1.136	1.330	0.893	0.4583
7226435	NMB1199	GTP-binding protein TypA	cytoplasmic	10.128	5.737	7.270	7.712	8.277	8.563	9.240	8.693	0.887	0.5652
7226981	NMB1726	putative metalloproteinase	cytoplasmic	0.256	0.250	0.318	0.274	-	0.252	0.367	0.309	0.887	0.4727
7226284	NMB1044	ferredoxin-NADP reductase	cytoplasmic	0.520	0.513	0.408	0.480	0.506	0.567	0.552	0.542	0.887	0.3122
7226630	NMB1392	glucose-6-phosphate 1-dehydrogenase	cytoplasmic	6.441	6.299	6.886	6.542	9.953	4.025	8.176	7.385	0.886	0.6666
7226309	NMB1070	2-isopropylmalate synthase	cytoplasmic	2.903	0.813	2.171	1.962	1.787	2.269	2.706	2.254	0.871	0.7357
7227118	NMB1861	acetyl-CoA carboxylase. biotin carboxylase	cytoplasmic	2.485	2.241	2.355	2.360	2.352	3.235	2.584	2.724	0.867	0.3884
7225956	NMB0729	integration host factor. alpha subunit	cytoplasmic	0.982	0.768	-	0.875	0.953	0.706	1.394	1.017	0.860	0.2146
7226762	NMB1518	acetate kinase	cytoplasmic	1.696	1.826	1.332	1.618	1.783	2.004	1.878	1.888	0.857	0.1940
7226713	NMB1472	clpB protein	cytoplasmic	0.423	0.362	0.540	0.442	0.684	0.349	-	0.516	0.855	0.5314
7227365	NMB2102	elongation factor TS (EF-TS)	cytoplasmic	2.793	3.170	1.791	2.585	3.249	2.303	3.552	3.035	0.852	0.6133
7225436	NMB0214	oligopeptidase A	cytoplasmic	1.256	1.504	1.118	1.293	1.439	1.647	1.557	1.547	0.835	0.1105
7226892	NMB1642	transcription elongation protein nusA	cytoplasmic	2.352	2.799	2.365	2.505	2.838	2.908	3.294	3.013	0.832	0.1656
7226829	NMB1581	histidinol dehydrogenase	cytoplasmic	0.643	0.844	0.725	0.737	0.893	0.735	1.050	0.893	0.826	0.3649
7227228	NMB1968	aldehyde dehydrogenase A	cytoplasmic	0.344	0.397	0.322	0.354	0.423	0.345	0.520	0.429	0.826	0.4100
7225796	NMB0569	Na(+)-translocating NADH-quinone reductase. subunit A	cytoplasmic	1.872	1.205	7.829	3.636	3.791	5.046	-	4.418	0.823	0.2051
7227212	NMB1953	stringent starvation protein A	cytoplasmic	2.330	-	2.265	2.298	2.715	-	2.873	2.794	0.822	0.1406
7226783	NMB1538	RNA polymerase sigma factor RpoD	cytoplasmic	3.167	3.272	3.223	3.221	3.364	5.676	2.715	3.918	0.822	0.5099
7226819	NMB1572	aconitate hydratase 2	cytoplasmic	3.489	5.268	2.701	3.819	4.004	3.101	6.914	4.673	0.817	0.6898
7226748	NMB1505	nicotinate phosphoribosyltransferase	cytoplasmic	0.427	0.455	0.408	0.430	0.486	0.630	0.484	0.534	0.806	0.1032
7226686	NMB1445	recA protein	cytoplasmic	3.881	5.179	2.365	3.808	3.312	5.874	5.059	4.748	0.802	0.4266

7225392	NMB0174	valyl-tRNA synthetase	cytoplasmic	3.291	5.402	3.171	3.954	4.806	4.042	6.068	4.972	0.795	0.5022
7226220	NMB0990	NAD(P) transhydrogenase. alpha subunit	cytoplasmic	0.335	0.469	-	0.402	0.553	0.416	0.557	0.509	0.790	0.6509
7225556	NMB0336	enoyl-(acyl-carrier-protein) reductase	cytoplasmic	0.348	0.201	0.284	0.278	0.344	-	0.367	0.355	0.782	0.5321
7227179	NMB1921	3-oxoacyl-(acyl-carrier-protein) reductase	cytoplasmic	0.692	1.138	0.545	0.792	0.889	1.139	1.018	1.015	0.780	0.2444
7225897	NMB0671	malate oxidoreductase (NAD)	cytoplasmic	0.211	0.353	0.190	0.251	0.289	0.374	0.317	0.326	0.770	0.1332
7226199	NMB0959	succinyl-CoA synthetase. beta subunit	cytoplasmic	2.251	2.924	1.754	2.310	2.980	2.168	3.864	3.004	0.769	0.4897
7227050	NMB1796	putative oxidoreductase	cytoplasmic	1.101	1.567	0.924	1.197	1.613	1.160	1.905	1.559	0.768	0.4686
7225555	NMB0335	2.3.4.5-tetrahydropyridine-2.6-dicarboxylate N-succinyltransferase	cytoplasmic	0.194	0.277	0.123	0.198	0.261	0.197	0.317	0.258	0.766	0.5235
7226672	NMB1432	3-phosphoshikimate 1-carboxyvinyltransferase	cytoplasmic	3.965	6.647	4.152	4.921	7.162	8.403	4.104	6.556	0.751	0.2236
7225509	NMB0284	adenylosuccinate lyase	cytoplasmic	1.185	1.549	0.953	1.229	1.561	1.647	1.814	1.674	0.734	0.1842
7226749	NMB1506	arginyl-tRNA synthetase	cytoplasmic	3.498	2.330	3.559	3.129	2.526	-	6.036	4.281	0.731	0.7381
7225547	NMB0326	octaprenyl-diphosphate synthase	cytoplasmic	0.670	1.080	-	0.875	0.960	1.126	1.529	1.205	0.726	0.4008
7226194	NMB0955	2-oxoglutarate dehydrogenase. E1 component	cytoplasmic	1.150	2.152	3.303	2.202	2.810	-	3.258	3.034	0.726	0.5174
7227154	NMB1897	leucyl-tRNA synthetase	cytoplasmic	0.617	0.804	0.474	0.631	0.802	0.874	0.937	0.871	0.725	0.1759
7226492	NMB1252	phosphoribosylformylglycinamide cyclo-ligase	cytoplasmic	0.379	0.563	0.265	0.402	0.498	0.655	0.511	0.555	0.725	0.0838
7226467	NMB1228	homoserine dehydrogenase	cytoplasmic	1.493	1.621	1.104	1.406	1.996	1.324	2.511	1.944	0.723	0.3888
7225848	NMB0618	phosphoenolpyruvate synthase	cytoplasmic	0.467	0.518	0.441	0.475	0.573	0.832	0.570	0.658	0.722	0.1084
7226585	NMB1341	pyruvate dehydrogenase. E1 component	cytoplasmic	0.304	0.295	0.327	0.309	0.391	0.521	0.376	0.429	0.719	0.1548
7227127	NMB1869	fructose-bisphosphate aldolase	cytoplasmic	3.617	6.308	3.185	4.370	5.249	6.718	6.683	6.217	0.703	0.1759
7226024	NMB0791	peptidyl-prolyl cis-trans isomerase	cytoplasmic	4.300	5.317	2.038	3.885	4.130	5.542	7.000	5.557	0.699	0.4171
7226740	NMB1498	aspartokinase. alpha and beta subunits	cytoplasmic	3.511	1.991	1.573	2.359	-	0.849	5.937	3.393	0.695	0.6630
7227323	NMB2061	phosphoenolpyruvate carboxylase	cytoplasmic	1.308	1.205	1.341	1.285	1.763	1.466	2.371	1.867	0.688	0.1280
7227187	NMB1930	glycyl-tRNA synthetase. beta chain	cytoplasmic	3.599	-	3.493	3.546	8.277	4.147	3.145	5.190	0.683	0.5473
7227385	NMB2129	argininosuccinate synthase	cytoplasmic	3.119	4.241	2.517	3.292	4.862	4.244	5.376	4.827	0.682	0.2061
7226702	NMB1460	single-strand binding protein	cytoplasmic	0.458	0.643	0.308	0.470	0.621	0.685	0.765	0.690	0.681	0.2155
7226531	NMB1291	ribonucleoside-diphosphate reductase. alpha subunit	cytoplasmic	0.855	0.978	0.512	0.781	-	1.303	1.014	1.158	0.675	0.1342
7226628	NMB1390	glucokinase	cytoplasmic	0.159	0.161	0.213	0.178	0.277	0.261	0.253	0.264	0.674	0.0674
7226063	NMB0828	ADP-L-glycero-D-mannoheptose-6-epimerase	cytoplasmic	1.366	-	1.261	1.313	2.028	1.803	2.077	1.969	0.667	0.0662
7227417	NMB2159	GAPDH	cytoplasmic	2.150	2.214	2.171	2.178	2.822	4.752	2.339	3.305	0.659	0.2585
7226035	NMB0802	cystathionine gamma-synthase	cytoplasmic	1.079	1.022	1.175	1.092	1.407	1.882	1.715	1.668	0.655	0.0652
7226601	NMB1356	Glu-tRNA(Gln) amidotransferase. subunit A	cytoplasmic	0.687	0.888	0.578	0.718	1.087	0.853	1.371	1.104	0.651	0.2482
7225581	NMB0359	glutamate-ammonia ligase	cytoplasmic	0.198	0.210	0.185	0.198	0.225	0.374	0.312	0.304	0.650	0.1221
7225441	NMB0219	3-oxoacyl-(acyl-carrier-protein) synthase II	cytoplasmic	5.427	5.214	5.322	5.321	8.182	9.786	6.638	8.202	0.649	0.0924
7226678	NMB1437	conserved hypothetical protein	cytoplasmic	1.278	-	2.000	1.639	1.648	-	3.416	2.532	0.647	0.3370
7225249	NMB0030	methionyl-tRNA synthetase	cytoplasmic	3.194	5.022	3.284	3.834	6.937	-	5.100	6.018	0.637	0.2125
7226090	NMB0854	histidyl-tRNA synthetase	cytoplasmic	1.731	2.487	0.597	1.605	1.672	0.828	5.077	2.526	0.636	0.6663
7225544	NMB0323	UbiH family protein	cytoplasmic	3.661	1.719	2.412	2.597	4.494	3.702	-	4.098	0.634	0.2467
7227157	NMB1900	polyphosphate kinase	cytoplasmic	0.273	-	0.422	0.347	0.530	0.492	0.633	0.552	0.630	0.0608
7225780	NMB0554	dnaK protein	cytoplasmic	0.872	0.763	0.877	0.837	1.269	1.088	1.643	1.333	0.628	0.0683
7227105	NMB1849	carbamoyl-phosphate synthase. small subunit	cytoplasmic	1.119	1.036	0.896	1.017	1.660	1.235	1.964	1.620	0.628	0.1397
7227124	NMB1867	1-deoxyxylulose-5-phosphate synthase	cytoplasmic	3.573	2.598	2.773	2.981	6.486	3.450	4.489	4.808	0.620	0.0925
7226833	NMB1584	3-hydroxyacid dehydrogenase	cytoplasmic	0.207	0.237	0.142	0.195	0.134	0.105	0.706	0.315	0.620	0.6442
7225695	NMB0468	biosynthetic arginine decarboxylase	cytoplasmic	0.256	0.313	0.251	0.273	0.462	0.391	0.480	0.444	0.615	0.0675
7226186	NMB0947	dihydrolipoyl dehydrogenase	cytoplasmic	-	0.286	0.190	0.238	-	0.269	0.520	0.395	0.602	0.5323
7227111	NMB1855	carbamoyl-phosphate synthase. large subunit	cytoplasmic	0.991	1.308	0.905	1.068	1.565	1.294	2.575	1.811	0.590	0.2709
7226583	NMB1339	prolyl-tRNA synthetase	cytoplasmic	4.969	4.973	-	4.971	10.565	6.151	8.656	8.458	0.588	0.3679
7225235	NMB0010	phosphoglycerate kinase	cytoplasmic	2.115	2.339	2.152	2.202	3.134	4.996	3.163	3.764	0.585	0.1038
7226268	NMB1029	aspartate ammonia-lyase	cytoplasmic	0.916	1.040	1.223	1.060	1.779	1.223	2.443	1.815	0.584	0.1313
7226603	NMB1358	Glu-tRNA(Gln) amidotransferase. subunit B	cytoplasmic	0.537	0.701	0.469	0.569	0.980	0.782	1.303	1.022	0.557	0.1730
7226034	NMB0801	delta-aminolevulinic acid dehydratase	cytoplasmic	0.493	1.170	0.498	0.720	1.399	1.147	1.344	1.297	0.555	0.1946
7226668	NMB1428	putative metallopeptidase	cytoplasmic	0.145	0.205	0.147	0.166	0.304	0.214	0.398	0.306	0.543	0.1864
7227044	NMB1789	protein-export protein SecB	cytoplasmic	0.326	0.406	0.275	0.336	0.605	0.466	0.810	0.627	0.535	0.1678

7226679	NMB1438	putative ferredoxin-like protein	cytoplasmic	1.366	-	2.592	1.979	4.478	-	2.986	3.732	0.530	0.4198
7225927	NMB0699	tryptophane synthase	cytoplasmic	1.806	1.804	1.313	1.641	2.601	3.504	3.222	3.109	0.528	0.0502
7226698	NMB1457	transketolase	cytoplasmic	0.414	0.531	0.308	0.418	0.822	0.727	1.036	0.862	0.485	0.1031
7225651	NMB0427	cell division protein FtsZ	cytoplasmic	2.018	3.799	1.863	2.560	5.024	5.256	6.756	5.679	0.451	0.0882
7225623	NMB0401	proline dehydrogenase	cytoplasmic	-	0.826	1.100	0.963	1.794	1.601	3.027	2.141	0.450	0.2567
7226184	NMB0946	peroxiredoxin 2 family protein/glutaredoxin	cytoplasmic	1.141	2.527	1.218	1.629	3.455	2.487	4.941	3.628	0.449	0.2101
7225240	NMB0015	6-phosphogluconate dehydrogenase	cytoplasmic	3.498	2.786	1.412	2.565	5.696	-	5.964	5.830	0.440	0.2136
7226200	NMB0960	succinyl-CoA synthetase, alpha subunit	cytoplasmic	1.577	2.058	1.512	1.716	3.573	-	4.231	3.902	0.440	0.0969
7226680	NMB1439	phosphoribosylaminoimidazole carboxylase	cytoplasmic	0.101	0.183	-	0.142	0.336	0.277	0.412	0.342	0.416	0.2568
7225861	NMB0631	putative phosphate acetyltransferase Pta	cytoplasmic	0.705	-	0.517	0.611	1.411	1.336	1.683	1.477	0.414	0.1535
7225693	NMB0466	aspartyl-tRNA synthetase	cytoplasmic	3.075	1.911	3.919	2.968	6.178	-	8.348	7.263	0.409	0.1109
7225612	NMB0390	maltose phosphorylase	cytoplasmic	-	2.893	1.853	2.373	5.996	6.202	14.018	8.739	0.272	0.3309
7227269	NMB2005	glutamate N-acetyltransferase/amino-acid acetyltransferase	cytoplasmic	0.502	-	0.502	0.502	1.498	-	2.321	1.910	0.263	0.1811
7226839	NMB1590	alkyl hydroperoxide reductase AhpD	no prediction	0.846	0.799	0.834	0.826	0.470	0.504	0.416	0.464	1.782	0.0097
7225567	NMB0346	hypothetical protein	no prediction	0.445	0.571	0.412	0.476	0.095	0.113	0.145	0.118	4.046	0.0228
7226903	NMB1652	conserved hypothetical protein	no prediction	0.326	0.406	0.303	0.345	0.387	0.437	0.376	0.400	0.863	0.0478
7225626	NMB0404	conserved hypothetical protein	no prediction	0.449	0.509	0.540	0.500	0.589	0.630	0.620	0.613	0.815	0.0236
7225329	NMB0113	conserved hypothetical protein	no prediction	1.273	1.143	-	1.208	0.862	0.929	-	0.895	1.350	0.1943
7226459	NMB1220	stomatin/Mec-2 family protein	divergent ⁺⁺⁺	2.586	2.772	2.635	2.664	2.107	6.958	2.824	3.963	0.672	0.4668

* according to Tettelin *et al.*. 2000

** according to NeMeSys (Rusniok *et al.*. 2009), UniProt (The UniProt Consortium. 2015) or pSORTb (Yu *et al.*. 2010), respectively

+ according to (Donnarumma *et al.*. 2015)

** according to (Tinsley *et al.*. 2004)

+++ divergent results by NeMeSys, UniProt and pSORTb

Values were obtained as the signal ratio between the sample (*i.e.* protein preparation of MC58 grown at either 32°C or 37°C) and the corresponding internal control (*i.e.* protein preparation of metabolically ¹⁵N-labeled MC58) which was added in equal amounts to each sample prior to sample preparation and measurement (see Materials and Methods). Values in A, B, or C represent the results of each of the three independent experiments for each protein.

References:

Tettelin, *et al.* (2000) Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58. *Science* 287: 1809-1815.

Rusniok C. *et al.* (2009) NeMeSys: a biological resource for narrowing the gap between sequence and function in the human pathogen *Neisseria meningitidis*. *Genome biology* 10(10):R110. The UniProt Consortium (2015) UniProt: a hub for protein information. *Nucleic Acids Res.* 43: D204-12.

Yu NY. *et al.* (2010) PSORTb 3.0: improved protein subcellular localization prediction with refined localization subcategories and predictive capabilities for all prokaryotes. *Bioinformatics* 26(13):1608-1615.

Donnarumma *et al.* (2015) *Neisseria meningitidis* GNA1030 is a ubiquinone-8 binding protein. *FASEB J* 29(6): 2260-7

Tinsley *et al.* (2004) Three homologues, including two membrane-bound proteins, of the disulfide oxidoreductase DsbA in *Neisseria meningitidis*: effects on bacterial growth and biogenesis of functional type IV pili. *J Biol Chem* 279 (26): 27078-87

Table S2: *Neisseria meningitidis* strains used in this study

Strain designation	Strain and genotype	Relevant phenotypic characteristic	Plasmid(s)	Resistance**	Reference or source
WUE2135	MC58 (WT)	B:15:P1.7,16-2:F1-5: ST-74, ST-32 complex	-	-	provided by E.R. Moxon
WUE3240 (MC58cps ⁻)	MC58Δ <i>csb</i>	polysialyltransferase mutant, no capsule expression	pGH15	CM	(Lappann <i>et al.</i> , 2006)
WUE4939	MC58Δ <i>pile</i>	Deficient in pilin, unable to produce pilus	pTL1-pilE-SmR	spec	This study
WUE4749	MC58Δ <i>pilT</i>	Deficient in pilT, unable to retract pilus, hyperpiliated	pTL1-pilT-SmR	spec	This study
WUE5013	MC58Δ <i>nalP</i>	Autotransporter protease NalP mutant	pDS2	kan	This study
WUE5014	MC58Δ <i>csb</i> Δ <i>nalP</i>	Double mutant of polysialyltransferase and autotransporter protease NalP	pGH15, pDS2	CM, kan	This study
WUE5030	MC58Δ <i>nhbA</i>	Mutant of heparin binding protein NHBA	pDS6	kan	This study
WUE5031	MC58Δ <i>csb</i> Δ <i>nhbA</i>	Double mutant of polysialyltransferase and heparin binding protein NHBA	pGH15, pDS6	CM, kan	This study
WUE5036	MC58ΔNMB1030	Mutant of hypothetical gene NMB1030	pDS7	ery	This study
WUE5037	MC58Δ <i>csb</i> ΔNMB1030	Double mutant of polysialyltransferase and hypothetical gene NMB1030	pGH15, pDS7	CM, ery	This study
WUE5042	MC58ΔNMB2095	Mutant of the Adhesin Complex Protein ACP (NMB2095)	pDS8	ery	This study
WUE5043	MC58Δ <i>csb</i> ΔNMB2095	Double mutant of polysialyltransferase and Adhesin Complex Protein ACP (NMB2095)	pGH15, pDS8	CM, ery	This study
WUE4833	MC58Δ <i>rpoE</i>	Mutant of the alternative Sigma factor E (NMB2144)	pKB8	kan	This study
WUE5060	MC58Δ <i>csb</i> Δ <i>rpoE</i>	Double mutant of polysialyltransferase and the alternative Sigma factor E (NMB2144)	pEWHRE1.1, pKB8	Kan, ery	This study
	MC58Δ <i>mseR</i>	Mutant of the anti-Sigma E factor (NMB2145)	pNMB1	kan	This study
WUE5071	MC58Δ <i>csb</i> Δ <i>mseR</i>	Double mutant of polysialyltransferase and the anti-Sigma E factor (NMB2145)	pGH15, pMB1	CM, kan	This study
WUE5053	MC58ΔNMB2091	Mutant of the Bam complex accessory factor NMB2091	pDS10	kan	This study
	MC58Δ <i>csb</i> ΔNMB2091	Double mutant of NMB2091 and polysialyltransferase	pGH15, pDS10	CM, kan	This study
WUE4294	MC58Δ <i>csb</i> Δ <i>lst</i> Δ <i>fHbp</i>	Mutant of serogroup B strain α16 (ST-41) lacking <i>lst</i> , <i>csb</i> and <i>fHbp</i>	pMP1, pGH7, pMF32.35:T5	kan, CM, spec	as described in (Hubert <i>et al.</i> , 2012)
WUE4321	WUE4294 <i>hfq</i> ⁺	Overexpression mutant of <i>hfq</i> by transformation with plasmid pAB3	pMP1, pGH7, pMF32.35:T5, pAB3	kan, CM, spec, ery	This study
WUE4353	WUE4294 <i>fnr</i> ⁺	Overexpression mutant of <i>fnr</i> by transformation with plasmid pAB2	pMP1, pGH7, pMF32.35:T5, pAB2	kan, CM, spec, ery	This study
WUE4547	WUE4294 <i>rpoH</i> ⁺	Overexpression mutant of <i>rpoH</i> by transformation with plasmid pAB1	pMP1, pGH7, pMF32.35:T5, pAB1	kan, CM, spec, ery	This study
WUE5058	MC58Δ <i>csb</i> Δ <i>relA</i>	Double mutant of polysialyltransferase and stringent response factor <i>relA</i>	pKE1, pEWHRE1.1	Kan, ery	This study
	MC58Δ <i>csb</i> Δ <i>hfq</i>	Double mutant of polysialyltransferase and RNA-chaperone <i>hfq</i>	pSS2, pEWHRE1.1	CM, ery	This study
WUE5061	MC58Δ <i>csb</i> Δ <i>misR</i>	Double mutant of polysialyltransferase and two-component sensor kinase	pLK3, pEWHRE1.1	CM, ery	This study
WUE2668 (WUE2594cps ⁻)	A:4:P1.9:ST-5	capsule mutant of strain WUE2594	pNT5	CM	(Lappann <i>et al.</i> , 2006)
WUE2517 (WUE2120cps ⁻)	C:NT:P1.5,2:F3-9:ST-11	capsule mutant of strain WUE2120	pHC10	CM	(Lappann <i>et al.</i> , 2006)
WUE4511 (DE11340cps ⁻)	C:P1.5-1,10-8:F3-6:ST-11	capsule mutant of strain DE11340	pHC10	CM	(Lappann <i>et al.</i> , 2006)
WUE3494 (α111cps ⁻)	Y:P1.5-2,10-1:F4-1:ST-23	capsule mutant of strain α111	pHC4Th	CM	(Lappann <i>et al.</i> , 2006)
WUE3495 (α143cps ⁻)	Y:P1.5-2,10-1:F4-1:ST-23	capsule mutant of strain α143	pHC4Tu	CM	(Lappann <i>et al.</i> , 2006)
α284	(B):P1.22-1,14:F3-3:ST-32	unencapsulated isolate, ST-32 complex	-	-	(Weber <i>et al.</i> , 2006)

α376	(B):P1.5-1,10-1:F3-3:ST-32	unencapsulated isolate, ST-32 complex	-	-	(Weber et al., 2006)
α688	(C):P1.18-3,1:F5-2:ST-337	unencapsulated isolate, ST-41/44 complex	-	-	(Weber et al., 2006)
α822	(B):P1.18:F2-28:ST-957	unencapsulated isolate, ST-41/44 complex	-	-	(Weber et al., 2006)
α60	<i>cnf</i> :P1.7-36,30-2:F1-2:ST-53	unencapsulated isolate, ST-53 complex	-	-	(Claus et al., 2002)
α225	<i>cnf</i> :P1.7,30-2:ST-53	unencapsulated isolate, ST-53 complex	-	-	(Claus et al., 2002)
WUE3491 (α278cps)	E:P1.5,2-59:F1-7:ST-60	capsule mutant of strain α278, ST-60 complex	pNB10	kan	(Lappann et al., 2006)
WUE3492 (α378cps)	E:P1.5-2,12-59:ST-60	capsule mutant of strain α378, ST-60 complex	pNB10	kan	(Lappann et al., 2006)
α5	<i>cnf</i> :P1.18,25:ST-198	unencapsulated isolate, ST-198 complex	-	-	(Claus et al., 2002)
α134	<i>cnf</i> :P1.18,25:F5-5:ST-198	unencapsulated isolate, ST-198 complex	-	-	(Claus et al., 2002)
WUE5221	Y92-1009 (<i>Neisseria lactamica</i>)	ST-3493	-	-	(Oliver et al., 2002)
WUE5220	020-06 (<i>Neisseria lactamica</i>)	ST-640	-	-	(Bennett et al., 2005)
WUE2136	FA1090 (<i>Neisseria gonorrhoeae</i>)	ST-1899	-	-	(Nachamkin et al., 1981)

*ST, sequence type

**CM, chloramphenicol; kan, kanamycin; ery, erythromycin; spec, spectinomycin

References:

- Bennett, J. S., D. T. Griffiths, N. D. McCarthy, K. L. Sleeman, K. A. Jolley, D. W. Crook & M. C. Maiden, (2005) Genetic diversity and carriage dynamics of *Neisseria lactamica* in infants. *Infection and immunity* **73**: 2424-2432.
- Claus, H., M. C. Maiden, R. Maag, M. Frosch & U. Vogel, (2002) Many carried meningococci lack the genes required for capsule synthesis and transport. *Microbiology* **148**: 1813-1819.
- Hubert, K., M. C. Pawlik, H. Claus, H. Jarva, S. Meri & U. Vogel, (2012) Opc expression, LPS immunotype switch and pilin conversion contribute to serum resistance of unencapsulated meningococci. *PloS one* **7**: e45132.
- Lappann, M., J. A. Haagensen, H. Claus, U. Vogel & S. Molin, (2006) Meningococcal biofilm formation: structure, development and phenotypes in a standardized continuous flow system. *Mol Microbiol* **62**: 1292-1309.
- Nachamkin, I., J. G. Cannon & R. S. Mittler, (1981) Monoclonal antibodies against *Neisseria gonorrhoeae*: production of antibodies directed against a strain-specific cell surface antigen. *Infection and immunity* **32**: 641-648.
- Oliver, K. J., K. M. Reddin, P. Bracegirdle, M. J. Hudson, R. Borrow, I. M. Feavers, A. Robinson, K. Cartwright & A. R. Gorrington, (2002) *Neisseria lactamica* protects against experimental meningococcal infection. *Infection and immunity* **70**: 3621-3626.
- Weber, M. V., H. Claus, M. C. Maiden, M. Frosch & U. Vogel, (2006) Genetic mechanisms for loss of encapsulation in polysialyltransferase-gene-positive meningococci isolated from healthy carriers. *International journal of medical microbiology* : *IJMM* **296**: 475-484.

Table S3: Primers used in this study

Primer	Sequence (5'-3')*	Restriction site	Coordinates referring to NMB genome**
Cloning primers:			
NMB1030 knock-out:			
NMB1030_up_F	gcgcgGATATCTACGTCGACAACGCCGCC	EcoRV	1046176-1046159
NMB1030_up_R	gcgcgGAATTCGTGGGCCGGTAAAGCGC	EcoRI	1045619-1045636
NMB1030_down_F	gcgcgGAATTCGCGAATCAGCACAAATGCCG	EcoRI	1045031-1045012
NMB1030_down_R	gcgcgGGATCCTTGCTGTGCCGTCGCC	BamHI	1044401-1044418
NMB1030_F	ACGCCCGTTTCGCCATCG	-	1045515- 1045498
NMB1030_R	TGGGTGATGGTGGTGC	-	1045126- 1045143
NMB2091 knock-out :			
NMB2091_up_F	gcgcgCGGCCCGCCGTACAGGCTGCCG	NotI	2211294-2211308
NMB2091_up_R	gcgcgGGATCCGTCTCTCTTTTGGGC	BamHI	2211859-2211842
NMB2091_down_F	gcgcgGGATCCCTCTACCAAAATCACGTCC	BamHI	2212443-2212463
NMB2091_down_R	gcgcgGATAICTGTTTTCGGGGTGCC	EcoRV	2213067-2213051
NMB2091_F	GCCATTTTCAGCCTTGCCC	-	2211902- 2211920
NMB2091_R	TACGTTGCCGTAGGTAACG	-	2212354- 2212336
NMB2095 knock-out:			
NMB2095_up_F	gcgcgGATATCCAAACCTGAAACCGGACG	EcoRV	2213921-2213939
NMB2095_up_R	gcgcgGAATTCGGAAATGAAAAATGTCGGGC	EcoRI	2214421-2214401
NMB2095_down_F	gcgcgGAATTCATCAGGCAACAAAAACAGCG	EcoRI	2214996-2215016
NMB2985_down_R	gcgcgGGATCCCGAGGCAACCCCGACG	BamHI	2215518-2215501
NMB2095_F	CCGCAATCCTGTCTCCGC	-	2214638- 2214656
NMB2095_R	GATTTGGTTGTCAGGTGCGG	-	2214969- 2214950
NMB2132 (NHBA) knock-out:			
NMB2132_up_F	gcgcgGATATCGCGGCACACGCAAGG	EcoRV	2240487-2240471
NMB2132_up_R	gcgcgGAATTCCTTCATCGTATTTCTTTGG	EcoRI	2239952-2239973
NMB2132_down_F	gcgcgGAATTCCTGCTGAAGCAGGGCGC	EcoRI	2238467-2238450
NMB2132_down_R	gcgcgCTAGAGTTGGCAATAAGCAATAAGG	XbaI	2237884-2237904
NMB2132_F	TGCACCTGCGAATGGCGG	-	2239364- 2239347
NMB2132_R	CGAATCCGCCCTTTCCGC	-	2238508- 2238526
NMB1969 knock-out:			
NMB1969_up_F	gcgcgACTAGTCCGAACAGACCTAGATCC	SpeI	2060987-2061006
NMB1969_up_R	gcgcgGGATCCCTCTTGAATCTGACAAT	BamHI	2061444-2061427
NMB1969_down_F	gcgcgGGATCCACAGCCGCAAAAGTACAGG	BamHI	2064716-2064734
NMB1969_down_R	gcgcgCTCGAGGTTAATCCGTATAAAGACCG	XhoI	2065355-2065335
NMB1969_F2	AAAATGCGCCGAGTACCC	-	2063964- 2063982
NMB1969_R3	GCGTCCGTTACAGTCCGC	-	2064491- 2064474
NMB2145 knock-out:			
NMB2145_up_F	gcgcgCGGCCCGCACCCCTGATTTGGC	NotI	2256935-2256950
NMB2145_up_R	gcgcgGGATCCGCCATTTTTTATAACG	BamHI	2257456-2257442
NMB2145_down_F	gcgcgGGATCCCGGCATAAGCTGACGG	BamHI	2257649-2257664
NMB2145_down_R	gcgcgGAGCTCGCGGAGGGAAGAGGC	SacI	2258237-2258223
NMB2145_F	ATATCGCCCTGCTCTTTCC	-	2257462-2257481
NMB2145_R	GAAGTTCTGGTTGTTTTGCC	-	2257618-2257598
NMB2144 knock-out:			
NMB2144_up(F)	gcgcgAAGCTTTGTATACCGAAACGCTGCAA	HinDIII	2256228-2256249
NMB 2144_Up(R)	gcgcgGAATTCAGTATCGGGAACAAGGTAATTT	EcoRI	2256852-2256831
NMB 2144_Down(F)	gcgcgGAATTC ACGTTATGAAAAATGCCGC	EcoRI	2257441- 2257460
NMB 2144_Down(R)	gcgcgGGATCCATCTTGAAAAATCATCAGAT	BamHI	2258057-2258038
NMB0052 (pilT) knock-out:			
pilT fwd	gcgcgCTAGAACAAAGCATCCGACCTTCAC	XbaI	57842-57862
pilT rev	gcgcgCTCGAGACCAGCGATTGCAGCGATT	XhoI	56925-56943
pilT_AvrII_inv_fwd	tgggtcCCTAGGTGCTGTCCGAATCGCTGAC	AvrII	57116-57136
pilT_AvrII_inv_rev	tgcggaCCTAGGCGCGTTGGCGAAGCTGAG	AvrII	57336-57352
NMB0018 (pilE) knock-out:			
pilE fwd	gcgcgCTAGAGTACCAACAAGGCTGGATTC	XbaI	18267-18286
pilE rev	gcgcgCTCGAGCGTTGCCTCGGCTTAGCTC	XhoI	16656-16674
pilE_AvrII_inv_fwd	gtaaaaCCTAGGTGCGGACAGCGGTTACG	AvrII	17345-17353
pilE_AvrII_inv_rev	tgttcCCTAGGATTCGCCGTGATTCAGG	AvrII	17552-17568
qPCR-primers:			
NMB2132-fwd	ATTGTGATGGGGAAGCGG		target: NMB2132 (NHBA)
NMB2132-rev	CGCCTTTTGGCGTTCCG		target: NMB2132 (NHBA)
NMB1030-fwd	CACTCGCAGCCCGCC		target: NMB1030
NMB1030-rev	CTTGGTGAACCTCGACGG		target: NMB1030
NMB2095-fwd	CACCGGACAGGTCGCCG		target: NMB2095 (ACP)
NMB2095-rev	GTGGAGTTTGCCTGTTCCG		target: NMB2095 (ACP)
NMB1969-fwd	GCACCTATGAAGCAAGCG		target: NMB1969 (NalP)
NMB1969-rev	GTACGCAGTTGTGCTTGC		target: NMB1969 (NalP)
rpoE-fwd	ATACAGAGCAGGCGACAGTTTTCA		target: rpoE (sigma E)
rpoE-rev	GCTTATCCAGTAGCTGTCATCCA		target: rpoE (sigma E)
NMB1392 -fwd	CGTGCAGGAAATATCC		target: zwf
NMB1392 -rev	TAGAAGGGAACCCCTCC		target: zwf

*Restriction sites used for cloning of the PCR products are underlined. Small letters: 5'-extension of primers to ensure restriction.

** (Tettelin *et al.*, 2000):

Tettelin, H., N. J. Saunders, J. Heidelberg, A. C. Jeffries, K. E. Nelson, J. A. Eisen, K. A. Ketchum, D. W. Hood, J. F. Peden, R. J. Dodson, W. C. Nelson, M. L. Gwinn, R. DeBoy, J. D. Peterson, E. K. Hickey, D. H. Haft, S. L. Salzberg, O. White, R. D. Fleischmann, B. A. Dougherty, T. Mason, A. Ciecko, D. S. Parksey, E. Blair, H. Cittone, E. B. Clark, M. D. Cotton, T. R. Utterback, H. Khouri, H. Qin, J. Vamathevan, J. Gill, V. Scarlato, V. Massignani, M. Pizza, G. Grandi, L. Sun, H. O. Smith, C. M. Fraser, E. R. Moxon, R. Rappuoli & J. C. Venter, (2000) Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58. *Science* **287**: 1809-1815.

Table S4: Plasmids used in this study

plasmid	description	origin
pAB1	Plasmid for overexpression of <i>rpoH</i> under control of PorA promotor, containing erythromycin resistance cassette. A 873bp PCR fragment containing <i>rpoH</i> was introduced via <i>SpeI</i> and <i>EcoRV</i> into plasmid pAP1 (Lappann <i>et al.</i> , 2006)	This study
pAB2	Plasmid for overexpression of <i>fmr</i> under control of PorA promotor, containing erythromycin resistance cassette. A 735bp PCR fragment containing <i>fmr</i> was introduced via <i>SpeI</i> and <i>EcoRV</i> into plasmid pAP1 (Lappann <i>et al.</i> , 2006)	This study
pAB3	Plasmid for overexpression of <i>hfq</i> under control of PorA promotor, containing erythromycin resistance cassette. A 294bp PCR fragment containing <i>hfq</i> was introduced via <i>SpeI</i> and <i>EcoRV</i> into plasmid pAP1 (Lappann <i>et al.</i> , 2006)	This study
pBluescript®II SK(+)	cloning vector	Stratagen
pCR-XL-Erm1	Vector comprising the gene encoding rRNA methyltransferase conferring erythromycin resistance cassette	This study
pEWHRE1.1	Replaces <i>siaB-D</i> with <i>rpsL</i> and erythromycin resistance cassette	(Unkmeir <i>et al.</i> , 2002, Johnston & Cannon, 1999)
pDS2	kanamycin resistance gene cloned between <i>nalP</i> (NMB1969) upstream and downstream regions	This study
pDS6	kanamycin resistance gene cloned between <i>NHBA</i> (NMB2132) upstream and downstream regions	This study
pDS7	erythromycin resistance gene cloned between NMB1030 upstream and downstream regions	This study
pDS8	erythromycin resistance gene cloned between NMB2095 upstream and downstream regions	This study
pDS10	kanamycin resistance gene cloned between NMB2091 upstream and downstream regions	This study
pKB8	kanamycin resistance gene cloned between <i>rpoE</i> (sigma-factor E; NMB2144) upstream and downstream regions	This study
pKE1	kanamycin resistance gene cloned between <i>relA</i> (NMB1735) upstream and downstream regions	This study
pLK3	Chloramphenicol resistance cassette cloned between <i>misR</i> (NMB0595) upstream and downstream regions	This study
pMB1	erythromycin resistance gene cloned between <i>mseR</i> (anti-Sigma factor E; NMB2145) upstream and downstream regions	This study
pSS2	Chloramphenicol resistance cassette cloned between <i>hfq</i> (NMB0748) upstream and downstream regions	This study
pUC4K	Vector containing an aminoglycoside 3'-phosphotransferase conferring resistance to kanamycin	GE Healthcare
pTL1-pilE-SmR	disruption of <i>pilE</i> (NMB0018) by insertion of spectinomycin cassette via <i>AvrII</i> -mediated ligation; <i>AvrII</i> -site was introduced via inverse PCR into <i>pilE</i> -construct	This study
pTL1-pilT-SmR	disruption of <i>pilT</i> (NMB0052) by insertion of spectinomycin cassette via <i>AvrII</i> -mediated ligation; <i>AvrII</i> -site was introduced via inverse PCR into <i>pilT</i> -construct	This study

References:

- Johnston, D. M. & J. G. Cannon, (1999) Construction of mutant strains of *Neisseria gonorrhoeae* lacking new antibiotic resistance markers using a two gene cassette with positive and negative selection. *Gene* **236**: 179-184.
- Lappann, M., J. A. Haagensen, H. Claus, U. Vogel & S. Molin, (2006) Meningococcal biofilm formation: structure, development and phenotypes in a standardized continuous flow system. *Molecular microbiology* **62**: 1292-1309.
- Unkmeir, A., K. Latsch, G. Dietrich, E. Wintermeyer, B. Schinke, S. Schwender, K. S. Kim, M. Eigenthaler & M. Frosch, (2002) Fibronectin mediates Opc-dependent internalization of *Neisseria meningitidis* in human brain microvascular endothelial cells. *Molecular microbiology* **46**: 933-946.