

**Table-S4:** Comparison of microarray- and real time qRT-PCR-based gene expression profiles

Gene	Gene Name	Gene function	Fold-Change (M1-SDH <sub>HBtail</sub> /M1-WT)	
			Micro-array	qRT-PCR
SPy0124	<i>rofA</i>	Regulatory protein	1.40	1.13
SPy0128		Pilin gene	-1.33	-1.36
SPy0148	<i>ntpl</i>	V-type Na <sup>+</sup> -ATPase subunit I	-5.56	-16.67
SPy0165	<i>nga</i>	NAD glycohydrolase precursor	-5.10	2.81
SPy0167	<i>slo</i>	Streptolysin O	-4.76	-1.28
SPy0252		Sugar-binding lipoprotein	-3.71	-1.48
SPy0336	<i>covR</i>	Control of virulence two-component regulator	N.D.	1.5
SPy0337	<i>covS</i>	Control of virulence two-component sensor kinase	1.28	-1.5
SPy0518		Putative ABC-transporter (ATP-binding protein)	-3.31	-1.42
SPy0631	<i>agaV</i>	PTS-dependent N-acetyl galactosamine-II B	N.D.	2.25
SPy0711	<i>speC</i>	Pyrogenic exotoxin C (Phage associated)	2.91	-1.85
SPy0712	<i>mf2</i>	Mitogenic factor (Phage associated)	3.23	-1.09
SPy0737	<i>epf</i>	Extracellular matrix-binding protein	10.92	1.85
SPy0738	<i>sagA</i>	Streptolysin S	-14.65	1.4
SPy1294		Maltose/maltodextrin-binding protein	-16.74	-3.03
SPy1295	<i>malF</i>	Maltose/maltodextrin ABC transport system	-14.42	-1.26
SPy1302	<i>amyA</i>	Cyclomaltodextrin glucanotransferase	-10.86	-2.17
SPy1306	<i>malX</i>	Maltose/maltodextrin-binding protein	-44.04	-2.77
SPy1373	<i>ptsH</i>	Phosphotransferase system phosphohistidine-containing protein	-3.03	-1.56
SPy1600		hyaluronidase	-1.82	1.82
SPy1625	<i>stk</i>	Eukaryote-type ser/thr kinase	1.35	1.25
SPy1626	<i>stp</i>	Eukaryote-type ser/thr phosphatase	1.39	1.4
SPy1718		Putative esterase	-3.95	1.2
SPy1755	<i>marR</i>	Transcriptional regulator ( <i>marR</i> family)	2.35	-1.53
SPy1815	<i>scrA</i>	Sucrose-specific PTS permease	1.48	2.61
SPy1979	<i>ska</i>	streptokinase	-2.82	-18.1
SPy2010	<i>scpA</i>	C5a peptidase	-1.31	-14.7
SPy2016	<i>sic</i>	Inhibitor of complement-mediated lysis	-4.38	-20.54
SPy2018	<i>emm1</i>	M protein type I	-2.19	-1.53
SPy2019	<i>mga</i>	M-protein transacting positive regulator	-1.01	-1.58
SPy2039	<i>speB</i>	Pyrogenic exotoxin B	-7.01	-3.22
SPy2042	<i>rgg/ropB</i>	Transcription regulator	-1.11	1.1
SPy2200	<i>hasA</i>	Hyaluronate synthase	-22.42	-909.0
SPy2201	<i>hasB</i>	UDP-glucose-6-dehydrogenase	-27.33	-1.58

Shaded area indicate the genes tested for the complemented strains. see Table-S6