Supplemental unit 1

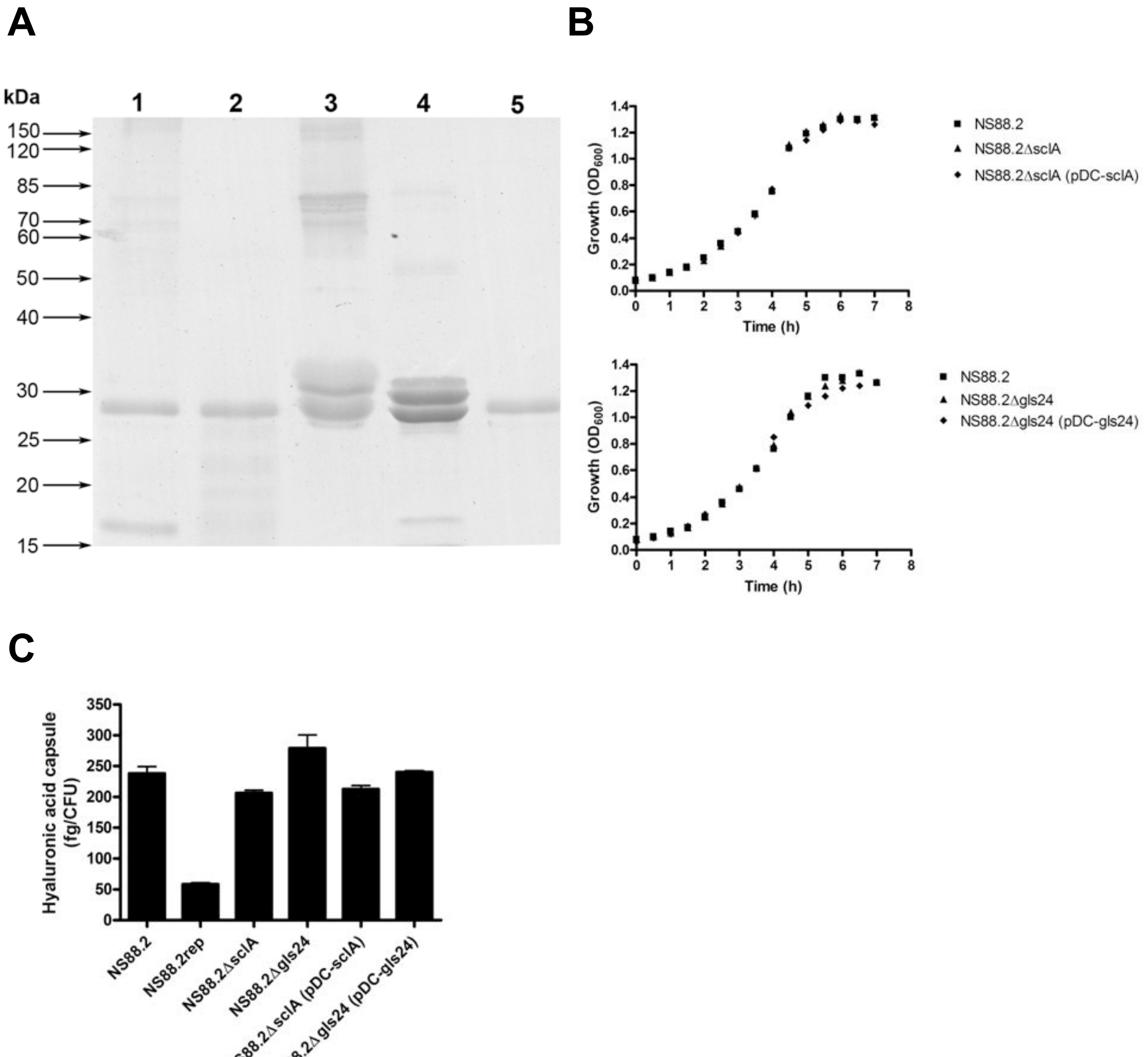

Fig. S1 **A** Gls24 protein is degraded by GAS cysteine protease SpeB *in vitro*. Lane 1: SpeB and Casein; Lane 2: SpeB and Gls24; Lane 3: Casein; Lane 4: Gls24; Lane 5: SpeB. Molecular weight markers are given in kilo-Daltons (kDa). **B** NS88.2, *sclA* and *gls24* isogenic knock-mutant mutants and complemented strains exhibit comparable growth kinetics in Todd-Hewitt broth. **C** NS88.2, *sclA* and *gls24* isogenic knock-out and complemented strains produce equivalent hyaluronic acid capsule. Capsule is expressed as femtograms of hyaluronic acid per colony forming unit (fg/CFU).

Supplemental unit 2

Table S1. List of proteins identified in the supernatant of NS88.2, NS88.2*rep* and NS88.2*covS*.

	Protein	pI[a]	Size (kDa)	Peptide Match[b]	Coverage[c]
1	Translation elongation factor G	4.83	76.5	9	22
2	Transketolase	4.98	71.4	3	6
3	Chaperone protein DnaK	4.62	64.9	8	19
4	Cell division trigger factor	4.48	47.1	3	16
5	Heat shock protein 60 family chaperone GroEL	4.75	42.1	8	32
6	Collagen-like surface protein A	5.39	32.2	3	13
7	Immunogenic secreted protein	5.42	54.1	4	10
8	Group B streptococcal surface immunogenic protein	4.62	40.8	4	18
9	Enolase	4.80	47.3	12	41
10	Pyruvate kinase	4.96	54.5	10	24
11	Xaa-His dipeptidase	4.87	51.3	6	19
12	SSU ribosomal protein S1p	4.90	43.8	7	20
13	Translation elongation factor Tu	4.89	43.9	9	36
14	Non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase	5.06	50.4	6	19
15	Arginine deiminase	4.99	46.3	6	18
16	Phosphoglycerate kinase	4.82	42.1	11	42
17	Translation elongation factor Ts	4.86	37.3	7	28
18	glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	5.34	35.9	5	15
19	L-lactate dehydrogenase	5.14	35.3	5	22
20	Phosphate acetyltransferase	4.85	35.9	4	15
21	6-phosphofructokinase	5.34	35.7	4	11
22	Manganese-dependent inorganic pyrophosphatase	4.47	33.9	4	20
23	Fructose-bisphosphate aldolase class II	4.98	31.2	5	32
24	Protein serine/threonine phosphatase PrpC	4.60	27	5	31
25	Adenylate kinase	4.74	23.7	4	29
26	Translation elongation factor P	4.85	20.4	4	27
27	Manganese superoxide dismutase	4.87	22.7	6	45
28	Phosphoglycerate mutase	5.10	26	7	41
29	Ribosomal subunit interface protein	4.45	21.1	4	34
30	Peptidoglycan hydrolase, Autolysin2	4.66	25.5	4	31
31	Alkyl hydroperoxide reductase protein C	4.65	20.5	3	22
32	Sortase A, LPXTG specific	9.17	27.7	5	18
33	Transcription elongation factor GreA	4.67	17.6	3	31
34	General stress protein, Gls24 family	4.93	12.6	5	50
35	Peptide deformylase	5.50	22.9	2	13
36	Streptodornase B; Mitogenic factor 1	8.61	28.7	6	33
37	Triosephosphate isomerase	4.57	26.6	6	33
38	Ribosome recycling factor	5.58	20.6	4	22
39	Streptokinase	5.58	50.2	9	28
40	Secreted antigen GbpB/SagA/PcsB, putative peptidoglycan hydrolase	8.42	42	3	15
41	Streptococcal pyrogenic exotoxin B (SpeB)	8.76	43.2	8	28
42	M1_SPy_1686 (PepSY)	4.40	12.6	2	24

[a] Isoelectric point calculated using Expasy compute pI/Mw tool

[b] Number of tryptic peptides from mass spectrum matched to theoretical tryptic digest of protein sequence

[c] Percentage coverage of protein sequence covered by Petide Matches