SUPPLEMENTAL MATERIAL:

Table S1: Primers utilized in this study

Primer Name	Sequence (5' to 3')	Additional notes
Primers used to amplify promoters for EMSA assays		**Used to amplify promoter of**
p480-F	CTGACACGCAGGCCGGGGCACC	CKS-1750
p480-R	CTGTGCCGGACATCCGGCTG	
p711-F	CGTATGACGGTGTTCTGTCTGG	CKS-5296
p711-R	GCGCTATCTGTTGATTCTTGG	
PACCC-F	GGTCGTTAATCGCATCCCTGTG	*accC*
PACCC-R	GGCTTTTAGTCGGCTTCATCG	
PAHPF-F	GCAAAATCTAATTTCCGCATCGC	*ahpF*
PAHPF-F	GGTATCAAGCATAGTGAGTTCC	
PDEGP-F	GGCGGTGGAATAACCCGAG	*degP*
PDEGP-R	CTAAGCGCCAGGGCGCTTAAC	
PDKGA-F	GCTGACACAGTAAGTCGTGG	*dkgA*
PDKGA-R	CGCTGTGCTTAAGTCTAGC	
PESAR28F[a]	TCTTGCCTGTACTATAGTGCAGGTTAAG	*esaR* (as positive control)
PESAR28R[a]	CTTAACCTGCACTATAGTACAGGCAAGA	
PFABF-F	GGAAGAAGTGACCAACTCTGC	*fabF*
PFABF-R	CGCTTAGACACGTTCGTC	
PFABI-F	GCGTGGCAACGCCAGCGTTG	*fabI*
PFABI-R	CCTTATGGTCATGGTAGTTGGC	
PFKPA-F	GTCAGCAGACCTCGGCAGAGC	*fkpA*
PFKPA-R	CGGACTGAGGGCCCACAC	

FUSAF	GGCCTGGAAGCTTTTGAGGTTGC	*fusA*
FUSAR	GTA CGA GCC ATT TTA TTC CTC G	
PGALF-F	GAACCGTGGCTGTAAGTGTC	*galF, galE*
PGALF-R	GACATGCGTCAATTATGCCG	
PGALU-CDN	CTTACCCGCAAGACAGTGCCAGAAGTTAGC	*galU, CKS 2738*
PGALU-F	CGTCTGAGCAATAAACACCG	
PGLM-F	CGTTCTGGCCGATACCGCTATTCG	*glmU*
PGLM-R	CTGAGGAACGTTAAACGATTTAGC	
PGLPF-F	CCTGCAAGGCGTTGATGATGC	*glpF, glpK*
PGLPF-R	GTTGTTCCTGAAGCGAGG	
PHTPG-F	TGACATCAGCAAAGCCGATCG	*htpG*
PHTPG-R	CTGCACGTAGAGTTTCAGACC	
PLRHA-F	CAGAGAGCATCTTTAGTACAGG	*lrhA*
PLRHA-R	GCGGGAAGCTGTGTAGTTGTC	
PMGLB-F	GCGATTCCGCGATGTAACCG	*mglB*
PMGLB-R	GCTGCGTCAAGCCGCGGAAG	
PNEMR-F	CTGTCGCTGTATTGCAGCC	*nemR*
PNEMR-R	CATCCTGGTAGACCAATCG	
PNHAR-F	CCGTCCATTGCGCACCACTG	*nhaR*
PNHAR-R	GACATGCGTCAATTATGCCGGATG	
POMPF-F	CGCCTATGTCACAGGCGTAC	*ompA, down-stream of ompF*
POMPF-R	CCAGAATGTTGCGCTTCATC	
POSMY-F	CGCGTTTTCAGGGCCATTCTC	*osmY*
POSMY-R	CAACGCTACTGCGGCACAGG	

PPGM-F	CGTCTGGATACGGCCGCGTTTGC	*pgm*
PPGM-R	GGCCATTGGCGCTTCTCC	
PPHES-F	CATACTTTACGGGCAGGCATAGC	*pheT, downstream of pheS*
PPHES-R	GTTCTGCTAGTTGGGACATG	
PRPSB-F	GAGATTGCCATTAAATTATTCCGC	*rpsB*
PRPSB-R	GTATCCCATACAACCGACCTC	
Primers for amplifying coding regions for qRT-PCR		**Gene amplified**
DKGA-CDNF	GGCAGCCTGAAAATTGTTAGC	*dkgA*
DKGA-CDNR	CGTATTAGCCGATAAACGTATCCG	
FABF-CDNF	GGAGGACGAACGTGTCTAAGC	*fabF*
FABF-CDNR	CGCCAGGTTTAGATTTTACGG	
RPSB-CDNF	GAGGTCGGTTGTATGGGATAC	*rpsB*
RPSB-CDNR	CAGAGCAAACCTTAATTAAGC	
LRHA-CDNF	CTTGTAATAACACCAGGATAGTAG	*lrhA*
LRHA-CDNR	GAAGACGGGATTTACTCTTCATCG	
GLPF-CDNF	CAACTATCATGAGTCAGACTACAACC	*glpF*
GLPF-CDNR	GAACTTACGCTTTACGTTCATGC	
MGLB-CDNF	CTTACCCGATGTTCTTCCGC	*mglB*
MGLB-CDNR	CTGAGACAGGTTTTCCTGATC	
27F	AGAGTTTGATCATGGCTCAG	*16S rRNA*
1429RLONG	ACCTTGTTACGACTTCACC	
qRT-PCR Primers		**Target gene**
DKGA-RTF	GCCCGGAGAAAGATCAGTACGTTG	*dkgA*
DKGA-RTR	GCTTTTGACCAGGCCTTGTTGC	

FABF-RTF	CGTCAATATGGTGGCGGGACATC	*fabF*
FABF-RTR	AGGCGGTCGCAATGGAAATGC	
RPSB-RTF	GCTCAAGGCTGGTGTTCACTTCG	*rpsB*
RPSB-RTR	ACGCGCACCGAAAATGAATGG	
LRHA-RTF	CGTCCGGTGGAGATGATGA	*lrhA*
LRHA-RTR	ATCCTTCTGCTGCACCCATT	
GLPF-RTF	TCTGGCCGGCATTTTCTC	*glpF*
GLPF-RTR	CCTGGCCCACGGAAATC	
MGLB-RTF	GATACGGCGATGTGGGATACCG	*mglB*
MGLB-RTR	GCGTTAGGGCCTGACAGC	
16S-RTF	GCCAGCAGCCGCGGTAAT	*16S rRNA*
16S-RTR	CGCTTTACGCCCAGTAATTCC	
DNase I footprinting assays		**Promoter amplified**
FAM-PDKGA-R2	/6-FAM/-TTGGTCTGCCATATCCTGC	P_{dkgA}
PDKGAF	GCTGACACAGTAAGTCGTGG	
FAM-PLRHA-R2	/6-FAM/-TCTGTCATACACACACGCTG	P_{lrhA}
PLRHA-F2	GCCGTGCATTAATCGTTAATACGG	
PGLPF-FAMF	/6-FAM/-CCTGCAAGGCGTTGATGATGC	P_{glpF}
PGLPF-R	GTTGTTCCTGAAGCGAGG	

[a] Primer pair annealed to form EsaR binding site in P_{esaR}

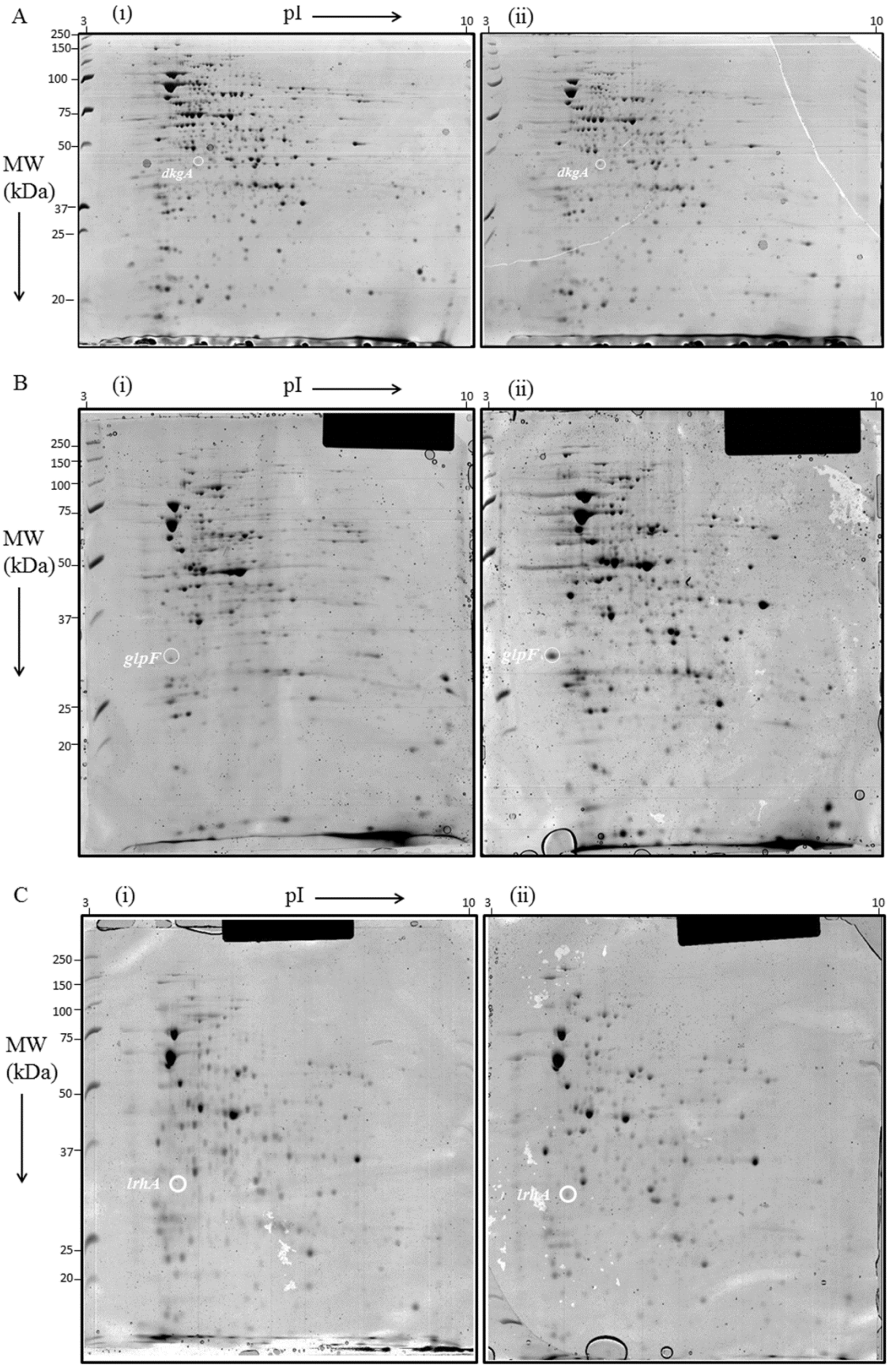
A
(i)
pI
3
10
(ii)
MW
(kDa)
250
150
100
75
50
37
25
20
dkgA
B
glpF
C
lrhA

Figure S1: Two-dimensional SDS PAGE experiments of *P. stewartii* DC283 strains. Panel A (i) ESN51 and (ii) ESN51 supplemented with 10 μM AHL; panels B and C (i) ESΔIR pBBR1MCS-3 (*esaR*$^{-}$/*esaI*$^{-}$) and (ii) ESΔIR pSVB60 (*esaR* complemented) depicting the three trials identifying differentially expressed protein spots. Locations of protein spots of DkgA, GlpF and LrhA are marked as examples in panel A, B and C, respectively. The positions of molecular weight standards are indicated on the left (in kDa) and the isoelectric pH (pI) gradient is indicated at the top from left to right.

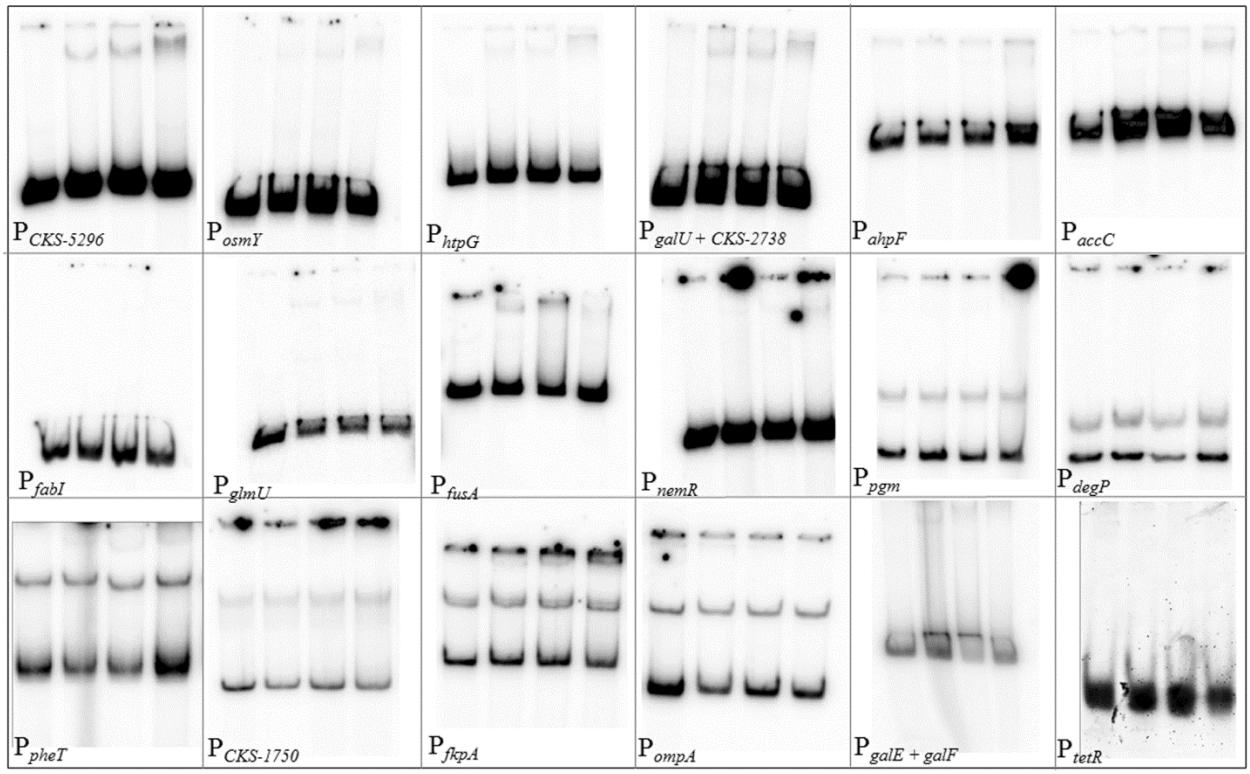

Figure S2: Electrophoretic mobility shift assays on the promoters of genes in the QS regulon. Concentration of DNA probe in all lanes is 1 nM. Lanes within each panel labeled with gene promoters consist of (left to right): DNA probe, DNA probe with 50 nM HMGE, DNA probe with 100 nM HMGE, and DNA probe with 100 nM HMGE plus 100 nM unlabeled DNA probe. The identity of the second band produced during PCR amplification of the gene promoters $P_{pgm,}$ $P_{degP,}$ $P_{pheT,}$ $P_{CKS\text{-}1750,}$ $P_{fkpA,}$ and P_{ompA} is not known.

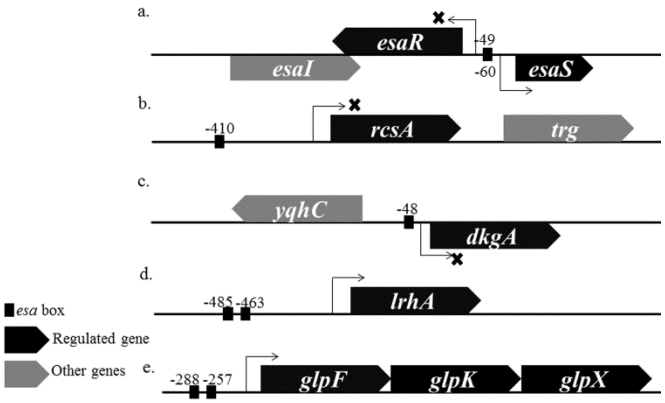

Figure S3: Relative positions of *esa* box on the promoters of the direct targets of EsaR. Numbers above or below the *esa* boxes denote base pairs from translational (ATG) start sites of the downstream open reading frames. The 'x' in front of the directional arrows indicates repression, absence of 'x' indicates activation. Model not drawn to scale.