SUPPLEMENTAL FIGURES

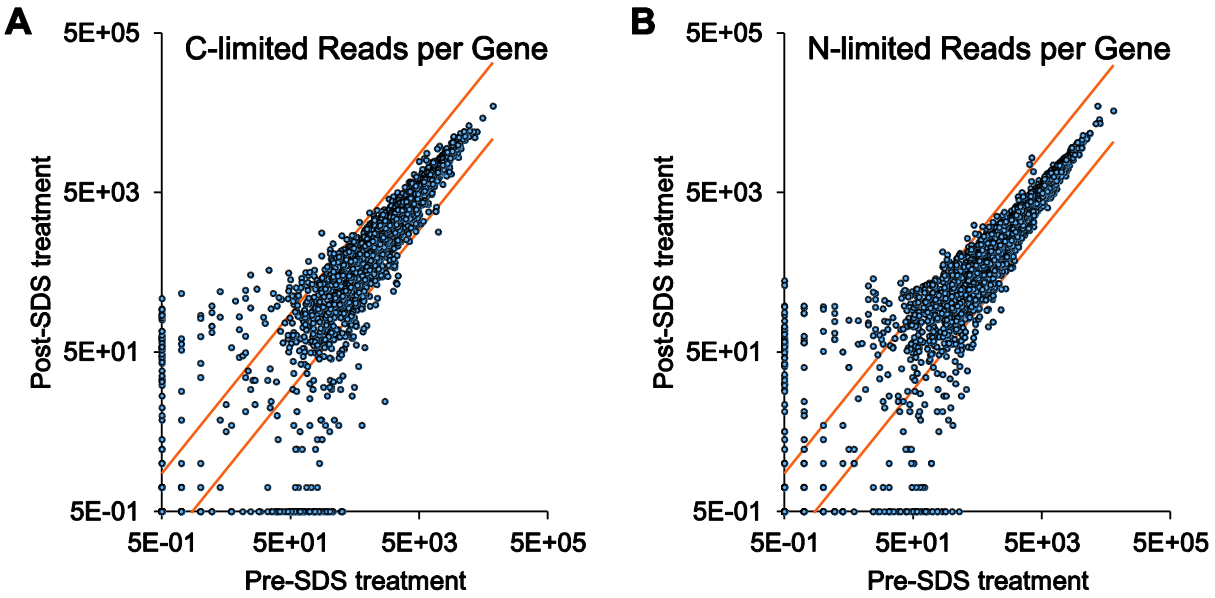

Figure S1. Comparison of sequencing reads per gene in pre- and post-treatment samples. The comparison of reads per gene in pre- and post-treatment for all genes is shown for carbon-limited samples (**A**) and for nitrogen-limited samples (**B**). Each data point represents a single gene. Orange lines represent a 3-fold change between pre- and post-treatment samples. For genes with zero reads, the value was replaced with 0.5 to allow display on a logarithmic scale.

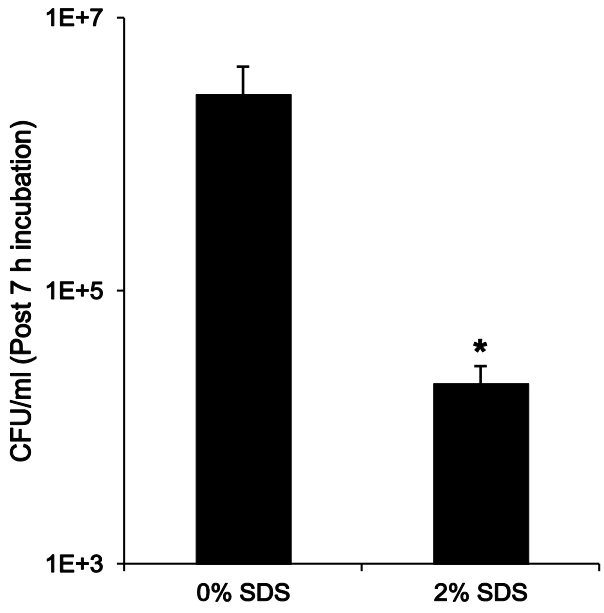

Figure S2. *wecE* mutant cells are SDS sensitive in exponential phase. Actively growing cells with a deletion of *wecE* were treated with SDS. Viability was assessed after 7 hours of treatment. * $p<0.05$ compared to untreated sample

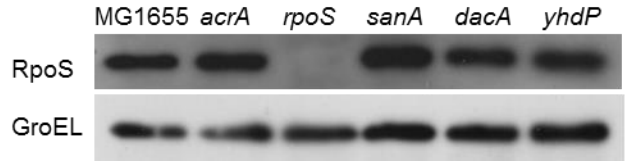

Figure S3. RpoS levels are not affected by *acrA*, *sanA*, *yhdP*, or *dacA* deletion. Protein levels of RpoS were determined by immunoblot analysis for the indicated strains in carbon-limited conditions as has been previously described with minor modifications (1): cells were lysed in sample loading buffer without protein precipitation and GroEL (Sigma G-6532, 1:10 000 dilution) was included as a loading control.

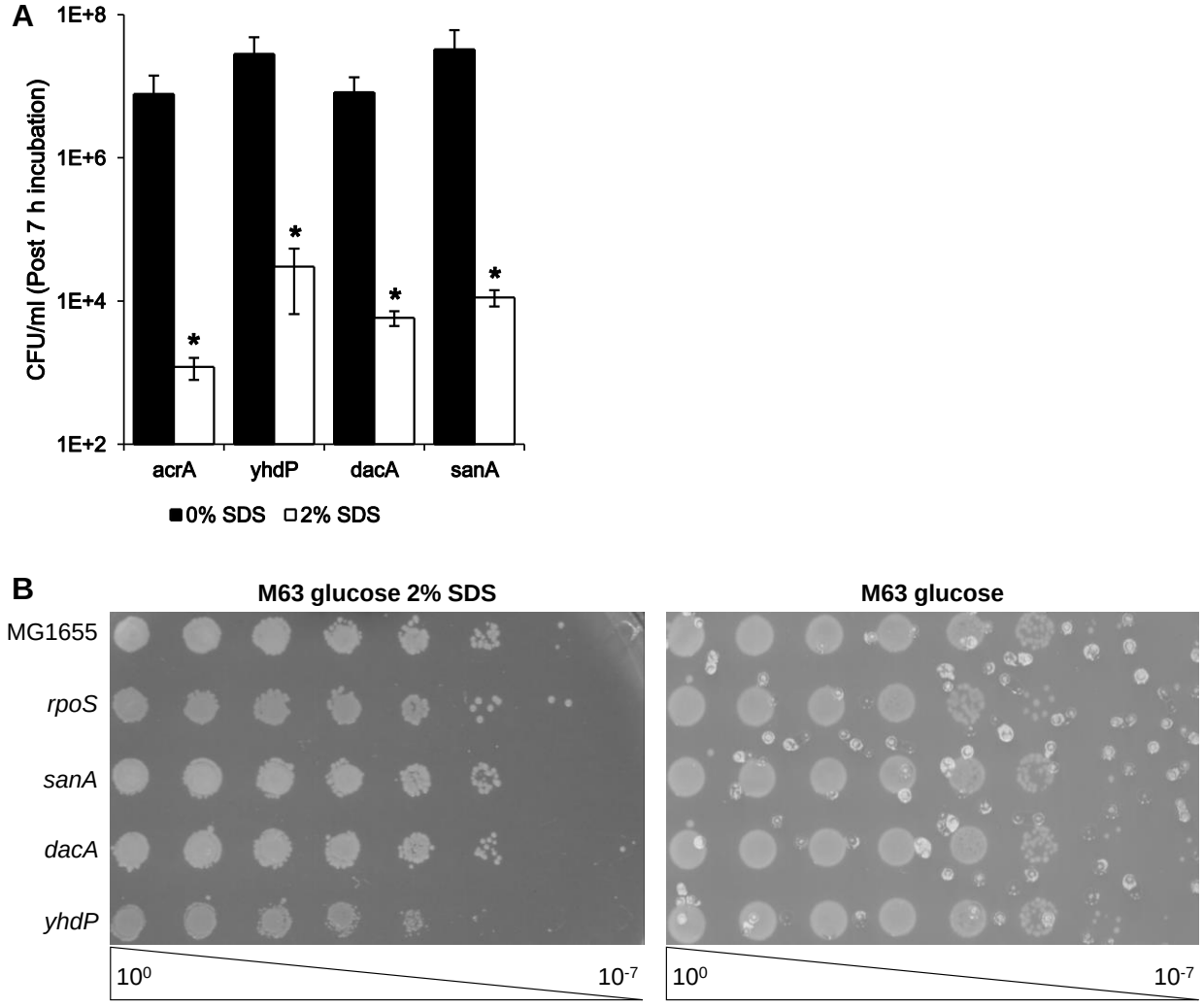

Figure S4. Genes identified in RpoS-dependent mechanism of SDS resistance have a small effect on SDS resistance in exponential phase. A. Actively growing cells with deletions of either *acrA*, *yhdP*, *dacA*, or *sanA* were treated with SDS and viability was assayed 7 h post-treatment. * $p<0.05$ against untreated sample. **B.** LB overnight cultures were serially diluted and plated on M63 glucose media with or without 2% SDS for an efficiency of plating assay.

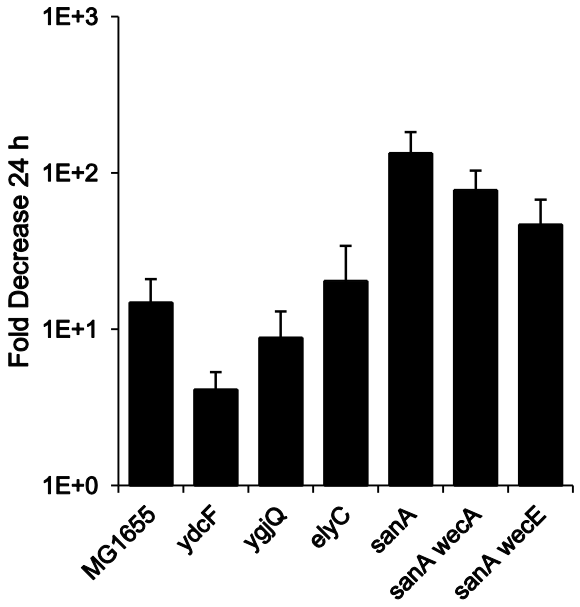

Figure S5. *sanA* acts in a different manner than its homologs, including *elyC*. Carbon-limited cells with the indicated genotype were treated with 2% SDS and incubated for 24 h before viability was assayed. The fold decrease of the SDS treated sample compared to the untreated sample is shown. No significant changes were observed between the parent (MG1655 for *ydcF*, *ygjQ*, and *elyC*, *sanA* for *sanA wecA* and *sanA wecE*) and mutant strains.

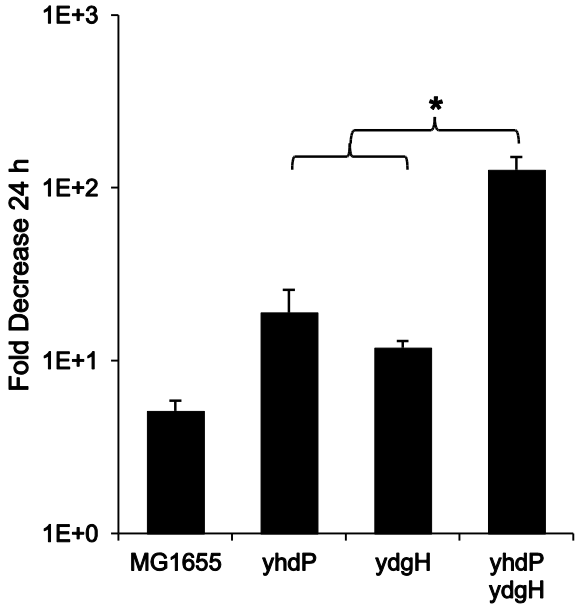

Figure S6. *ydhP* and *ydgH* are not epistatic. Carbon-limited cells from the indicated strains were treated with 2% SDS for 24 h and then viability was assayed. The fold decrease of the SDS treated sample compared to the untreated sample is shown. * $p<0.05$ against indicated samples

SUPPLEMENTAL TABLES

Table S1. Strains used in this study

Strain Name	Genotype
MG1655	K-12 F^- λ^- *rph-1* (Coli Genetic Stock Center 6300)
AM102	MG1655 Δ*acrA*
AM103	MG1655 Δ*acrB*
AM144.5	MG1655 *sprE*:Tn10
AM145	MG1655 Δ*acrA sprE*:Tn10
AM104	MG1655 Δ*rpoS*
AM146	MG1655 Δ*rpoS sprE*:Tn10
AM136	MG1655 Δ*acrA* Δ*rpoS*
AM137	MG1655 Δ*acrB* Δ*rpoS*
AM163	MG1655 *ydgH*::Kan
AM172	MG1655 *bssR*::Kan
AM173	MG1655 *tatB*::Kan
AM174	MG1655 *wecA*::Kan
AM175	MG1655 *ompA*::Kan
AM176	MG1655 *dacA*::Kan
AM144	MG1655 *sanA*::Kan
AM177	MG1655 *yftK*::Kan
AM179	MG1655 *wecE*::Kan
AM180	MG1655 *rfaH*::Kan
AM178	MG1655 *yhdP*::Kan
AM187	MG1655 Δ*rpoS yhdP*::Kan
AM190	MG1655 Δ*rpoS dacA*::Kan
AM149	MG1655 Δ*rpoS sanA*::Kan
AM184	MG1655 Δ*rpoS ydgH*::Kan
AM193	MG1655 Δ*rpoS rfaH*::Kan
AM186	MG1655 Δ*acrA yhdP*::Kan
AM189	MG1655 Δ*acrA dacA*::Kan
AM148	MG1655 Δ*acrA sanA*::Kan
AM183	MG1655 Δ*acrA ydgH*::Kan
AM192	MG1655 Δ*acrA rfaH*::Kan
AM182	MG1655 Δ*yhdP*
AM197	MG1655 Δ*dacA*
AM196	MG1655 Δ*yhdP sanA*::Kan
AM200	MG1655 Δ*yhdP* Δ*dacA*
AM199	MG1655 Δ*dacA sanA*::Kan
AM201	MG1655 Δ*yhdP* Δ*dacA sanA*::Kan
AM198	MG1655 Δ*yhdP ydgH*::Kan
AM215	MG1655 *ydcF*::Kan
AM216	MG1655 *ygjQ*::Kan
AM217	MG1655 *elyC*::Kan
AM158	MG1655 Δ*sanA*
AM221	MG1655 Δ*sanA wecA*::Kan
AM222	MG1655 Δ*sanA wecE*::Kan

Table S2. Tn-Seq reads per gene

	Reads per gene	
Data Set	**Average**	**Median**
Carbon-limited pre-treatment	3017	1740
Carbon-limited post-treatment	3077	1813
Nitrogen-limited pre-treatment	2673	1443
Nitrogen-limited post-treatment	2713	1439

Table S3. Descriptive statistics for Tn-Seq data

	Log2 Fold Post/Pre treatment	
Statistic	**Carbon-limited**	**Nitrogen-limited**
Average	-0.04	0.06
Median	0	0
Standard Deviation	1.43	1.35
Max	8.87	9.61
Min	-9.35	-9.01

Table S4. Non-envelope related Tn-Seq hits causing SDS sensitivity only in carbon-limited cells

	Carbon-limited Reads per Kbp[b]		Log2 Fold Post/Pre treatment[c]	
Gene[a]	**Pre-treatment**	**Post-treatment**	**Carbon-limited**	**Nitrogen-limited**
dam	1338	174	-2.2	0.9
paaD	1739	231	-2.2	0.3
ccmC	4352	735	-1.9	0.2
bioA	1552	274	-1.8	0.2
argH	1539	298	-1.7	1.1
aceA	6995	1386	-1.6	-0.1
xerC	1216	241	-1.6	-0.2
rluC	1385	282	-1.6	0.8

[a] Genes with at least 700 sequence reads, decreasing at least 3-fold during treatment in carbon-limiting conditions, and changing less than 3-fold in nitrogen limiting conditions

[b] The number of sequence reads for each gene was normalized to the length of the gene

[c] The fold change in read number before and after SDS treatment in either carbon- or nitrogen-limiting conditions

SUPPLEMENTAL REFERENCES

1. Mandel, M. J., and T. J. Silhavy. 2005. Starvation for different nutrients in *Escherichia coli* results in differential modulation of RpoS levels and stability. Journal of Bacteriology 187:434-442.