SUPPLEMENTARY DATA

Basu A., and Yap, M.-N. F. (2016) Ribosome hibernation factor promotes *Staphylococcal* survival and differentially represses translation.

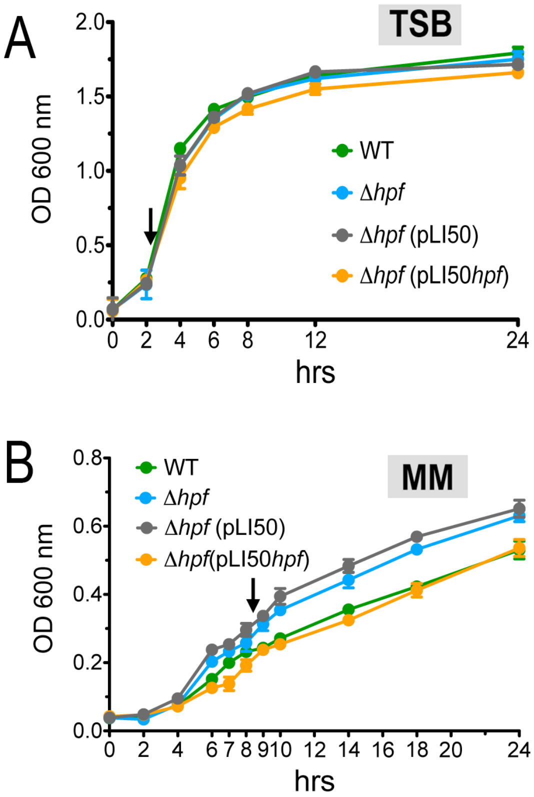

Figure S1. Growth curves of the wild-type and hpf_{Sa} mutant. (A) Tryptic soy broth (TSB) cultures. **(B)** Minimal medium (MM) cultures. No significant difference in growth rate was observed in TSB cultures, whereas the wild-type and complementing strain were delayed in entering the stationary phase compared with the hpf_{Sa} mutant. Error bars indicate the standard deviation of four independent experiments. An arrowhead denotes time point when cells were harvested for ribosome profiling.

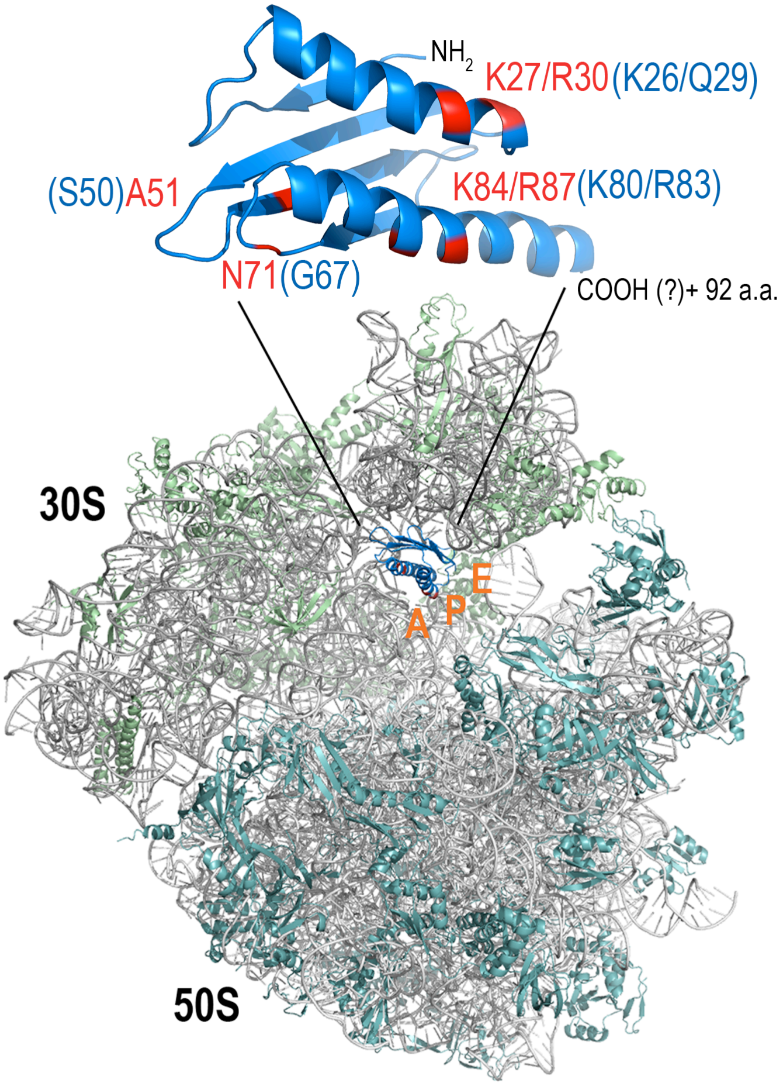

Figure S2. Illustration of the *E. coli* HPF$_{Ec}$ in complex with a *T. thermophilus* ribosome. The two conserved basic patches on the α-helices are highlighted in red. K27, R30, K84, R87 are the numbering of *S. aureus* HPF$_{Sa}$ equivalent to *E. coli* counterparts (blue). Additional non-essential residues (A51, N71) located outside of the α-helices are indicated. The fold of the HPF$_{Sa}$ C-terminal tail is unknown. Ribosomal A-, P-, and E-sites are highlighted in orange. Structural information was extracted from PDB 4V8H (1).

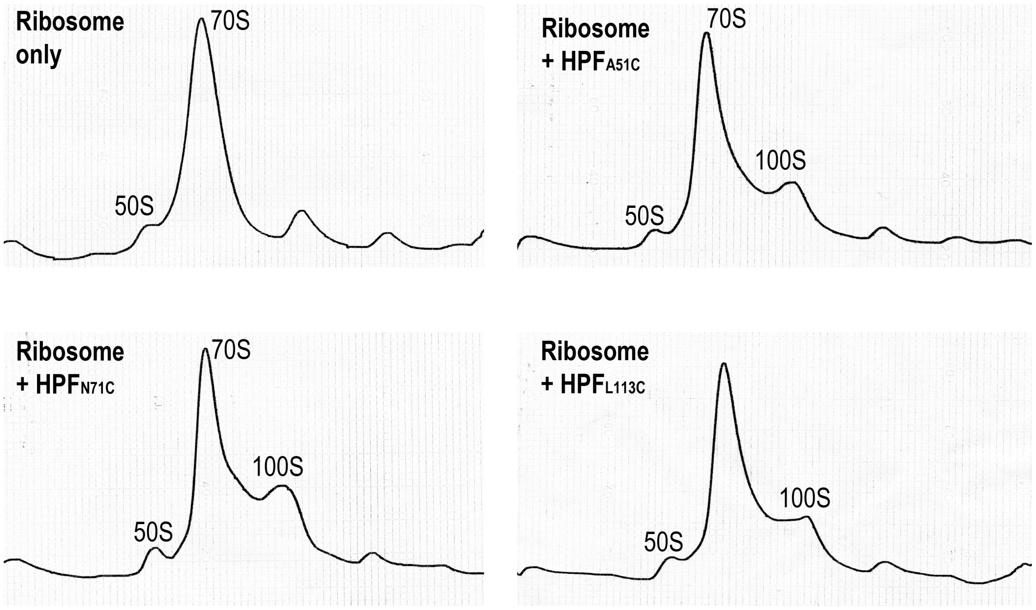

Figure S3. Mutations outside of the α-helices do not disrupt 70S dimerization. 5-25% sucrose density gradient profiles of salt-washed ribosome isolated from *S. aureus hpf* null strain with a mixture of 1:1 molar ratio of ribosomes to HPF$_{Sa}$ mutant variants. In vitro 100S complex formation of mutant variants is comparable to the wild-type HPF$_{Sa}$ (see Fig. 4). Residues A51 and N71 are predicted to locate on the β-sheet and flexible loop, respectively (see Fig. S2). The position of L113 is unknown as it resides at the C-terminal extension that is absent in HPF$_{Ec}$.

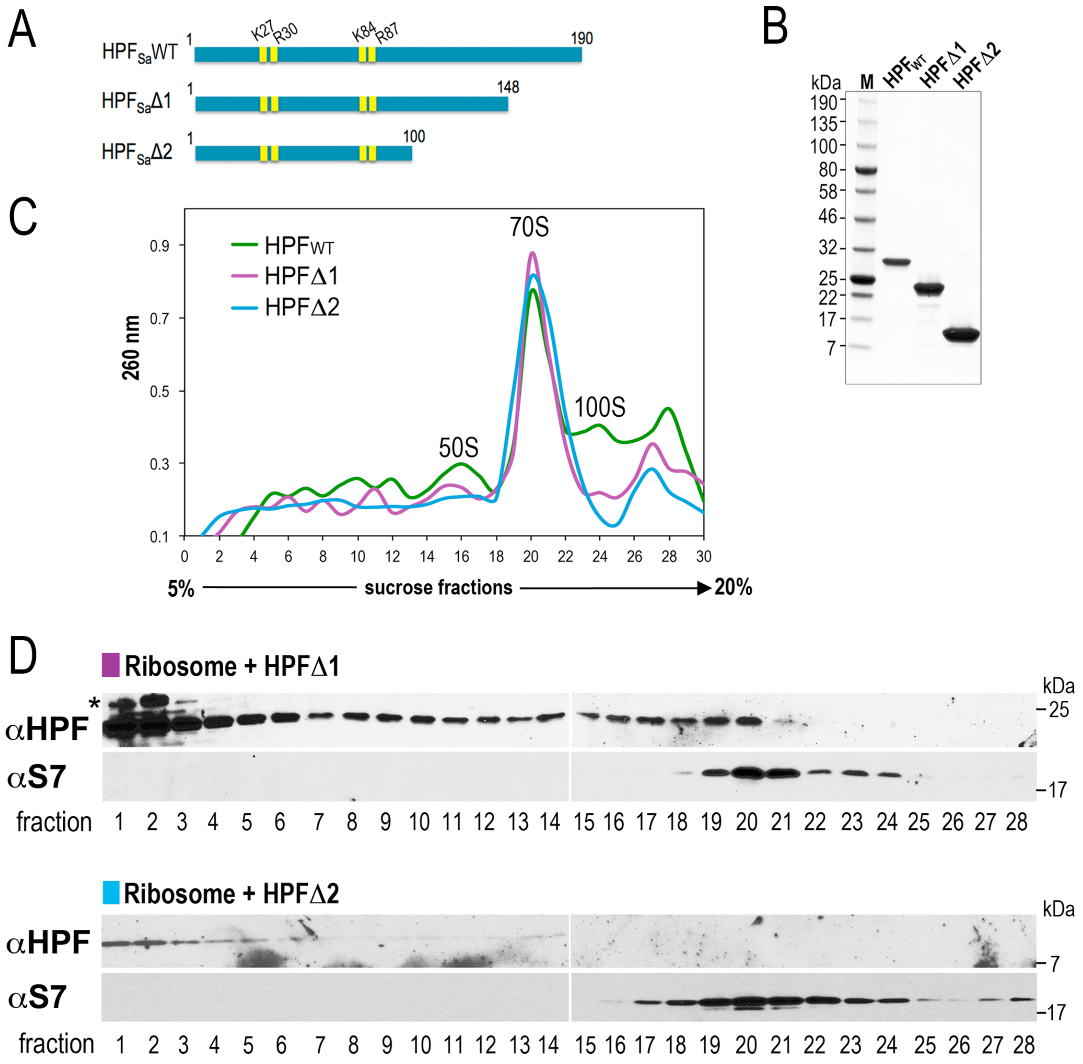

Figure S4. The C-terminal extended segment of HPF$_{\mathrm{Sa}}$ is necessary for ribosome binding. **(A)** Diagram showing the HPF$_{\mathrm{Sa}}$ deletion mutants. **(B)** SDS-PAGE showing the purity of affinity tag-free HPF$_{\mathrm{Sa}}$. **(C)** Sucrose density gradient fractionation confirms that both HPF$_{\mathrm{Sa}}$Δ1 and HPF$_{\mathrm{Sa}}$Δ2 failed to elicit 100S complex formation. An equimolar ratio of ribosome to HPF$_{\mathrm{Sa}}$ protein was used. **(D)** Western blots showing that HPF$_{\mathrm{Sa}}$Δ1 is loosely associated with the ribosome and HPF$_{\mathrm{Sa}}$Δ2 completely loses its binding to the ribosome. The large truncation reduces the antigenic reactivity to anti-HPF$_{\mathrm{Sa}}$, thus explaining the weaker signal. Anti-HPF$_{\mathrm{Sa}}$ was used in 1:1,000 and 1:500 dilutions for HPF$_{\mathrm{Sa}}$Δ1 and HPF$_{\mathrm{Sa}}$Δ2, respectively. Each fraction corresponds to the sucrose density fractions obtained in panel C. An asterisk denotes non-specific crossreaction.

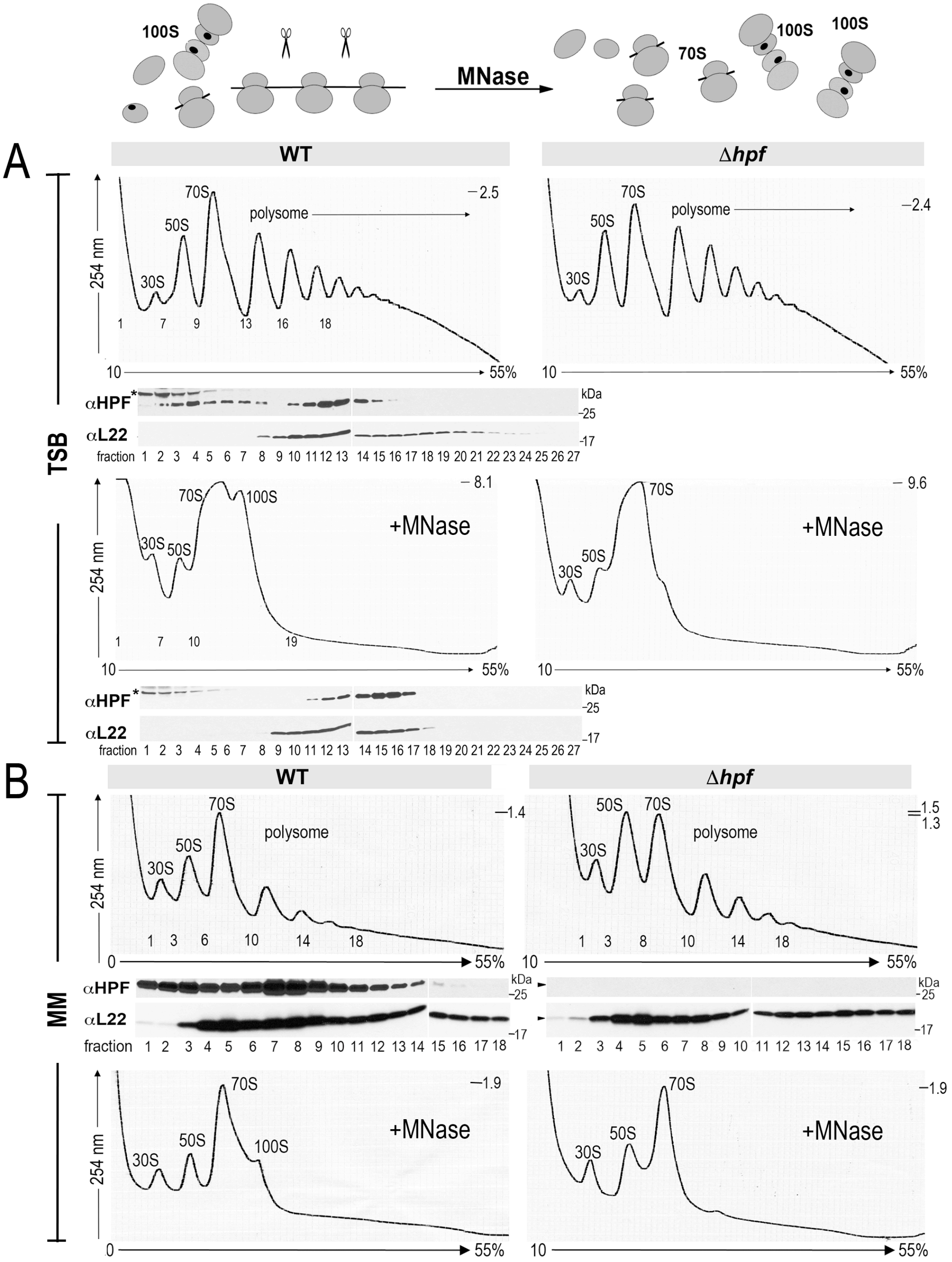

Figure S5. Sucrose density gradient plots of ribosome profiling samples before and after micrococcal nuclease (MNase) treatment. **(A)** Polysome profiles from TSB samples. **(B)** Polysome profiles from MM samples. 100S ribosomes are resistant to MNase digestion, showing as distinct peaks in the wild-type strain. In the MNase-free samples, the disome and the 100S ribosome peaks are indistinguishable on sucrose gradient due to near identical masses. Distributions of ribosomes and ribosomal subunits were analyzed on a 10-55% sucrose gradient. The middle panels between the plots are immunoblots showing the distribution of $\mathrm{HPF}_{\mathrm{Sa}}$. The 50S ribosomal subunit protein L22 is a marker control for fractionation. Anti-$\mathrm{HPF}_{\mathrm{Sa}}$ and anti-L22 were used in 1:8,000 and 1:1,500 dilutions, respectively. An asterisk indicates a non-specific band. Two-minute chloramphenicol pretreatment was conducted to capture polysomes. The treatment may artificially promote 30S-to-30S dimerization and produces a subpopulation of 30S dimers (0.85 MDa±0.15) that shares an overlapping peak with the 50S subunit (0.9 MDa±0.07), explaining the association of $\mathrm{HPF}_{\mathrm{Sa}}$ with the "50S peak" on the Western blots. The association of $\mathrm{HPF}_{\mathrm{Sa}}$ to the 30S monomer and 30S dimer may be more labile than to the 70S and 100S ribosomes, and dissociation may occur upon a low degree of rRNA cleavage by MNase (2). The elevated 30S and 50S peaks in the $\Delta \mathit{hpf}_{\mathrm{Sa}}$ MM culture may be the products of the post-termination disassembly of 70S ribosomes because a lack of $\mathrm{HPF}_{\mathrm{Sa}}$ (and 100S ribosomes) renders more ribosomes to engage in translation.

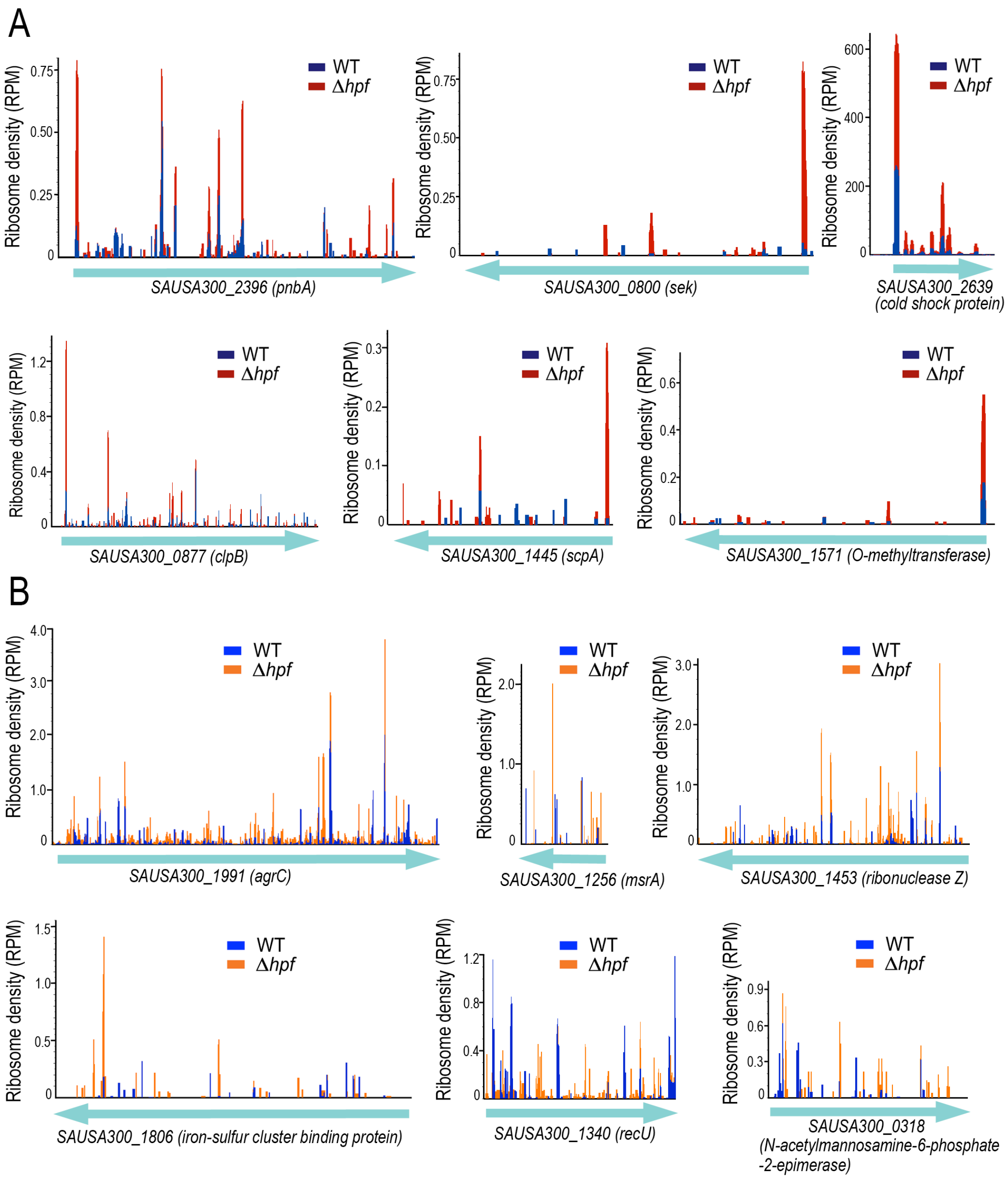

Figure S6. Examples of ribosome density plots showing differentially up-regulated translation in the hpf_{Sa} mutant. (A) Minimal medium (MM) samples. (B) Tryptic soy broth (TSB) samples. Ribosome occupancy around start codons is accentuated in MM samples.

SUPPLEMENTARY REFERENCES

1. Polikanov, Y.S., Blaha, G.M. and Steitz, T.A. (2012) How hibernation factors RMF, HPF, and YfiA turn off protein synthesis. *Science*, **336**, 915-918.
2. Del Campo, C., Bartholomaus, A., Fedyunin, I. and Ignatova, Z. (2015) Secondary structure across the bacterial transcriptome reveals versatile roles in mRNA regulation and function. *PLoS Genet*, **11**, e1005613.

Table S1. Summary of sixteen ribosome profiling and total mRNA sequencing libraries reported in this study.

Growth Media[a]	Replicate	Sequencing type[b]	Genotype[c]	Sample name	Mapped reads[d]	Replicates correlation	R square[e]
MM	**Rep 1**	RPF	WT	YP1	7,631,866	vs. YP5	0.892
			Δ*hpf*	YP2	41,393,905	vs. YP6	0.967
		Total mRNA	WT	YP3	39,255,811	vs. YP7	0.912
			Δ*hpf*	YP4	25,666,379	vs. YP8	0.923
	Rep 2	RPF	WT	YP5	9,723,245		
			Δ*hpf*	YP6	14,128,482		
		Total mRNA	WT	YP7	18,821,122		
			Δ*hpf*	YP8	22,170,673		
TSB	**Rep 1**	RPF	WT	YP10	3,593,733	vs. YP15	0.875
			Δ*hpf*	YP11	7,252,593	vs. YP16	0.845
		Total mRNA	WT	YP12	12,674,631	vs. YP17	0.939
			Δ*hpf*	YP13	23,767,550	vs. YP18	0.910
	Rep 2	RPF	WT	YP15	10,887,256		
			Δ*hpf*	YP16	4,580,635		
		Total mRNA	WT	YP17	26,776,849		
			Δ*hpf*	YP18	26,859,982		

[a] MM, minimal medium; TSB, tryptic soy broth

[b] RPF, ribosome-protected footprints

[c] All derived from *S. aureus* USA300 JE2

[d] unique reads that mapped to the *S. aureus* USA300 genome (GenBank CP000255.1) using Bowtie v.0.12.0, excluding rRNA and tRNA. Two mismatches were allowed.

[c] squared correlation coefficient of replicate 1 and 2 from the same sample type.

Table S2. List of genes whose translation efficiency (TE) is increased in MM grown Δhpf mutant relative to the wild-type.
Only genes that are translationally upregulated by ≥ 2-fold in the two independent biological replicates are confident.
Data shown is from replicate 2. Known virulence factors are highlighted in blue

Gene Locus	Δhpf_log2 TE	WT_log2 TE	log 2ΔTE (Δhpf-WT)	gene/ gene product
SAUSA300_2028	-1.681	-5.042	3.360	acpS
SAUSA300_0985	-0.806	-3.487	2.681	conserved hypothetical protein
SAUSA300_1461	2.571	0.073	2.499	conserved hypothetical protein hypothetical protein
SAUSA300_2294	2.132	-0.280	2.412	conserved hypothetical protein
SAUSA300_2211	-2.203	-4.593	2.390	putative membrane
SAUSA300_0427	-1.204	-3.520	2.316	conserved hypothetical protein hypothetical protein
SAUSA300_2295	0.487	-1.813	2.300	conserved hypothetical protein hypothetical protein
SAUSA300_0507	0.397	-1.862	2.259	ctsR
SAUSA300_1010	-1.153	-3.383	2.230	conserved hypothetical protein
SAUSA300_2647	-0.902	-3.050	2.148	rnpA
SAUSA300_1528	-0.552	-2.671	2.120	cdd
SAUSA300_2528	-0.136	-2.253	2.118	conserved hypothetical protein
SAUSA300_0800	-0.145	-2.213	2.068	sek enterotoxin
SAUSA300_1627	1.849	-0.215	2.065	infC, IF3
SAUSA300_0904	-1.285	-3.342	2.057	protozoan regulator
SAUSA300_2232	-0.778	-2.829	2.051	acetyltransferase
SAUSA300_1577	-0.643	-2.654	2.011	TPR(tetratricopeptide) family protein
SAUSA300_0493	-1.511	-3.522	2.011	folB, dihydroneopterin aldolase
SAUSA300_1176	-0.032	-1.979	1.947	pgsA, CDP-diacylglycerol--glycerol-3-phosphate
SAUSA300_2004	0.201	-1.743	1.943	conserved hypothetical protein
SAUSA300_1705	-1.289	-3.226	1.938	putative drug transporter
SAUSA300_1571	-1.792	-3.718	1.927	O-methyltransferase family
SAUSA300_0832	-0.094	-1.925	1.831	conserved hypothetical protein
SAUSA300_1361	-0.474	-2.299	1.826	conserved hypothetical protein
SAUSA300_0729	0.230	-1.578	1.808	integral membrane protein

SAUSA300_1368	-0.205	-1.994	1.790	ansA
SAUSA300_1970	0.698	-1.072	1.770	putative exonuclease
SAUSA300_0359	-1.727	-3.486	1.759	transulforation enzyme
SAUSA300_2551	-1.054	-2.792	1.738	nrdD
SAUSA300_0017	-0.501	-2.235	1.734	purA
SAUSA300_2459	1.620	-0.095	1.715	marR
SAUSA300_1190	0.344	-1.371	1.715	glpP
SAUSA300_0521	0.043	-1.661	1.704	nusG
SAUSA300_2352	-1.835	-3.528	1.694	Txe/YoeB AT
SAUSA300_2396	0.830	-0.850	1.680	pnbA, para-nitrobenzyl esterase
SAUSA300_2252	0.453	-1.227	1.680	conserved hypothetical protein
SAUSA300_2266	2.727	1.062	1.666	conserved hypothetical protein
SAUSA300_2392	0.304	-1.359	1.663	OpuCb
SAUSA300_1796	0.212	-1.445	1.656	conserved hypothetical protein
SAUSA300_2527	0.406	-1.226	1.632	conserved hypothetical protein
SAUSA300_2402	2.508	0.879	1.628	conserved hypothetical protein
SAUSA300_2031	0.033	-1.567	1.600	conserved hypothetical protein
SAUSA300_1473	-1.852	-3.451	1.599	nusB
SAUSA300_1185	-1.830	-3.427	1.597	miaA
SAUSA300_2303	-3.300	-4.880	1.580	tcaR
SAUSA300_2430	0.373	-1.204	1.577	lipoprotein
SAUSA300_0730	-0.857	-2.414	1.556	GGDEF domainprotein
SAUSA300_1882	1.332	-0.214	1.545	gatB
SAUSA300_0542	0.657	-0.882	1.539	deoxynucleoside kinase
SAUSA300_0780	-0.523	-2.058	1.536	conserved hypothetical protein
SAUSA300_0695	-1.330	-2.836	1.506	radical activating enzyme
SAUSA300_2233	1.424	-0.075	1.499	BioY
SAUSA300_1152	0.860	-0.618	1.478	rrf
SAUSA300_0117	0.912	-0.562	1.474	sirA
SAUSA300_2300	-1.437	-2.905	1.468	tetR regulator

SAUSA300_2040	-1.838	-3.309	1.471	putative membrane protein
SAUSA300_1313	-1.879	-3.332	1.453	ctpA
SAUSA300_0910	-2.240	-3.690	1.450	mgtE
SAUSA300_1512	-2.198	-3.645	1.448	pbp3, penicillin binding
SAUSA300_2504	-3.354	-4.801	1.447	acyltransferase
SAUSA300_2064	-1.270	-2.710	1.440	atpB
SAUSA300_0536	1.218	-0.220	1.438	DJ-1/Pfp1 family protein
SAUSA300_0249	1.486	0.049	1.437	cytidinyltransferase
SAUSA300_0785	-0.993	-2.425	1.432	acetyltransferease
SAUSA300_0006	-2.218	-3.632	1.414	gyrA
SAUSA300_0671	-3.452	-4.852	1.400	ABC-transporter
SAUSA300_2258	-0.465	-1.862	1.398	formate dehydrogenase
SAUSA300_2422	1.886	0.514	1.372	oxidoreducatase
SAUSA300_1542	-1.226	-2.595	1.369	hrcA
SAUSA300_2067	0.388	-0.978	1.366	glyA
SAUSA300_0928	1.191	-0.172	1.363	comK
SAUSA300_1569	-1.603	-2.959	1.356	peptidease
SAUSA300_1665	1.103	-0.247	1.350	conserve
SAUSA300_1201	-0.581	-1.904	1.323	glnA
SAUSA300_1570	-1.050	-2.369	1.320	peptidase
SAUSA300_2353	0.806	-0.511	1.316	Txe/YoeB toxin-antitoxin
SAUSA300_1916	-1.131	-2.446	1.315	aminotransferase
SAUSA300_0963	-1.986	-3.300	1.313	qoxA
SAUSA300_1669	0.369	-0.939	1.308	aminotransferase
SAUSA300_1518	0.298	-1.007	1.305	ATP RNA helicase
SAUSA300_2130	-0.925	-2.224	1.299	UTP-glucose-1-phosphate uridyltransferase
SAUSA300_2066	0.940	-0.352	1.291	uracyl phosphosribosyltransferase
SAUSA300_2639	3.699	2.411	1.287	cold shock protein, csp
SAUSA300_1803	-1.768	-3.055	1.287	conserved hypothetical protein
SAUSA300_1445	-2.047	-3.328	1.281	scpA

SAUSA300_1881	-0.849	-2.128	1.278	gatA
SAUSA300_2467	-0.065	-1.342	1.277	sortase A, srtA
SAUSA300_1238	0.743	-0.531	1.274	conserved hypothetical protein
SAUSA300_0306	-1.998	-3.260	1.262	brnQ
SAUSA300_2622	-0.029	-1.286	1.257	conserved hypothetical protein
SAUSA300_2544	0.982	-0.269	1.252	conserved hypothetical protein
SAUSA300_0816	3.391	2.141	1.250	csbD-like protein
SAUSA300_1475	-2.192	-3.441	1.250	accC
SAUSA300_0178	-2.780	-4.026	1.246	conserved hypothetical protein
SAUSA300_2070	-1.069	-2.314	1.245	conserved hypothetical protein
SAUSA300_1110	-2.208	-3.443	1.235	sun, ribosome methyltransferase
SAUSA300_1295	3.292	2.071	1.222	cold shock protein, CSD family
SAUSA300_1449	1.488	0.274	1.214	mutT/nudix family
SAUSA300_0877	0.124	-1.087	1.211	ClpB
SAUSA300_1689	-1.219	-2.429	1.210	conserved hypothetical protein
SAUSA300_1690	0.842	-0.366	1.208	putative therodoxin
SAUSA300_0986	-1.140	-2.346	1.206	cytochrome ubiqunol oxidase subunit
SAUSA300_0668	0.934	-0.270	1.205	conserved hypothetical protein
SAUSA300_2037	-0.250	-1.448	1.198	RNA helicase
SAUSA300_0541	0.108	-1.089	1.197	deoxynucleoside kinase family
SAUSA300_0981	0.002	-1.191	1.193	conserved hypothetical protein
SAUSA300_0468	-1.367	-2.556	1.189	TatD family hydrolase
SAUSA300_2249	0.385	-0.799	1.185	ssaA
SAUSA300_2648	2.289	1.109	1.181	rpmH
SAUSA300_1982	0.417	-0.762	1.179	groL
SAUSA300_1548	0.277	-0.888	1.166	comE
SAUSA300_2327	0.707	-0.458	1.165	conserved hypothetical protein
SAUSA300_2315	0.958	-0.205	1.163	putative lipoprotein
SAUSA300_0377	1.257	0.101	1.156	putative lipoprotein
SAUSA300_1685	0.775	-0.376	1.151	conserved hypothetical protein

SAUSA300_0865	0.629	-0.521	1.150	pgi, glucose6-phosphate isomerase
SAUSA300_2297	-1.326	-2.475	1.149	conserved hypothetical protein
SAUSA300_1850	-1.440	-2.580	1.140	conserved hypothetical protein
SAUSA300_1880	-1.172	-2.309	1.137	gatB
SAUSA300_1182	-1.876	-3.013	1.137	pyruvate ferredoxin oxidoreductaase, alpha subunit
SAUSA300_2531	0.706	-0.430	1.136	hydrolase
SAUSA300_1277	0.616	-0.512	1.129	conserved hypothetical protein
SAUSA300_2529	1.056	-0.070	1.126	conserved hypothetical protein
SAUSA300_1144	-1.576	-2.688	1.112	gid
SAUSA300_0959	-1.431	-2.541	1.110	fmt
SAUSA300_1103	2.286	1.178	1.108	rpoZ
SAUSA300_1167	0.617	-0.491	1.108	pnpA
SAUSA300_1086	0.632	-0.472	1.105	putative cell division initiation protein
SAUSA300_1647	-0.596	-1.700	1.104	accD
SAUSA300_1659	2.010	0.912	1.098	tpx
SAUSA300_1508	1.359	0.264	1.094	conserved hypothetical protein
SAUSA300_2002	-1.076	-2.169	1.093	glycoprotein endopeptidase
SAUSA300_1844	1.696	0.611	1.085	bacterioferritin
SAUSA300_1364	0.004	-1.079	1.083	engA
SAUSA300_2057	-1.511	-2.587	1.075	atpC
SAUSA300_1911	0.482	-0.585	1.068	ABC transporter
SAUSA300_0839	1.024	-0.040	1.064	conserved hypothetical protein hypothetical protein
SAUSA300_0619	-1.954	-3.010	1.056	ABC transporter
SAUSA300_0556	-3.242	-4.295	1.053	SIS domain protein
SAUSA300_1080	1.110	0.058	1.052	ftsZ
SAUSA300_1476	0.044	-1.007	1.051	accB
SAUSA300_0790	1.739	0.690	1.049	putative arsenate reductase
SAUSA300_1686	-2.191	-3.238	1.047	murC
SAUSA300_0709	-2.041	-3.069	1.027	5'(3')deoxyribonucleotidase
SAUSA300_1889	-0.918	-1.936	1.019	purB

SAUSA300_1579	-1.452	-2.466	1.014	aminotransferase, classV
SAUSA300_0380	1.514	0.510	1.005	ahpC
SAUSA300_1197	0.800	-0.200	1.000	gluthathione peroxidase
SAUSA300_0912	-0.002	-0.995	0.993	trans-2-enoyl-ACP-reductase

Table S3. List of genes whose translation efficiency (TE) is increased in TSB grown Δhpf mutant relative to the wild-type.
Only genes that are translationally upregulated by ≥ 2-fold in the two independent biological replicates are confident.
Data shown is from replicate 2. Known virulence factors are highlighted in blue

Gene Locus	Δhpf_log2 TE	WT_log2 TE	log 2ΔTE (Δhpf-WT)	gene/ gene product
SAUSA300_2437	2.079	-0.414	2.494	sarT
SAUSA300_1573	-2.074	-4.558	2.485	conserved hypothetical protein hypothetical protein
SAUSA300_0363	-0.655	-3.001	2.346	conserved hypothetical protein hypothetical protein
SAUSA300_0529	-2.271	-5.757	3.486	conserved hypothetical protein
SAUSA300_2481	-2.936	-6.050	3.114	conserved hypothetical protein
SAUSA300_1891	-1.269	-3.280	2.011	conserved hypothetical protein
SAUSA300_1599	-1.786	-3.768	1.983	PheB
SAUSA300_1602	-2.079	-4.019	1.940	conserved hypothetical protein
SAUSA300_0840	1.024	-0.884	1.908	conserved hypothetical protein
SAUSA300_1326	2.264	0.367	1.897	EbsB, cell wall enzyme
SAUSA300_1200	-1.614	-3.486	1.872	glnR
SAUSA300_2514	2.398	0.621	1.777	conserved hypothetical protein
SAUSA300_0810	1.165	-0.591	1.757	conserved hypothetical protein
SAUSA300_2511	2.777	1.046	1.731	conserved hypothetical protein
SAUSA300_2071	-2.361	-4.083	1.722	HemK methyltransferase family
SAUSA300_1091	0.263	-1.451	1.714	pyrR (bifunctional protein)
SAUSA300_0771	2.305	0.622	1.684	acetyltransferase
SAUSA300_1915	0.321	-1.335	1.657	conserved hypothetical protein
SAUSA300_1256	-1.038	-2.675	1.637	msrA, peptide methionine sulfoxide reductase
SAUSA300_1334	-0.116	-1.671	1.555	putative membrane protein
SAUSA300_1343	-0.141	-1.692	1.551	nth, endonuclease III
SAUSA300_1050	0.970	-0.569	1.539	purine NTP pyrophasphatase
SAUSA300_1097	0.235	-1.237	1.472	pyrF
SAUSA300_2043	0.440	-1.032	1.472	conserved hypothetical protein
SAUSA300_1340	-1.910	-3.370	1.460	recU

SAUSA300_0767	0.479	-0.968	1.447	conserved hypothetical protein
SAUSA300_2143	0.268	-1.163	1.431	conserved hypothetical protein
SAUSA300_0518	-1.287	-2.712	1.425	conserved hypothetical protein
SAUSA300_0070	1.742	0.370	1.371	lysophospholipase
SAUSA300_1991	-2.688	-4.079	1.391	agrC, accessory gene regulator C
SAUSA300_0432	0.405	-0.964	1.369	sodium transporter
SAUSA300_1196	0.463	-0.898	1.361	hfq
SAUSA300_2065	-1.888	-3.246	1.358	UDP..epimerase
SAUSA300_1236	-1.811	-3.157	1.346	conserved hypothetical protein
SAUSA300_1026	-0.853	-2.192	1.339	conserved hypothetical protein
SAUSA300_2547	1.392	0.056	1.336	conserved hypothetical protein
SAUSA300_0552	0.542	-0.787	1.329	conserved hypothetical protein
SAUSA300_0657	1.459	0.180	1.278	conserved hypothetical protein
SAUSA300_1909	2.282	1.010	1.273	conserved hypothetical protein
SAUSA300_1806	-1.160	-2.421	1.261	putative iron-sulfur cluster binding protein
SAUSA300_2355	-0.106	-1.367	1.261	putative lipoprotein
SAUSA300_1198	-0.050	-1.306	1.256	putative GTP-binding protein
SAUSA300_1872	0.229	-1.014	1.243	conserved hypothetical protein
SAUSA300_1453	-0.134	-1.372	1.238	ribonuclease Z
SAUSA300_0223	1.610	0.388	1.222	conserved hypothetical protein
SAUSA300_1099	-0.433	-1.654	1.221	conserved hypothetical protein
SAUSA300_1222	1.102	-0.114	1.217	nuc, thermonuclease
SAUSA300_0318	0.774	-0.427	1.201	N-acetylmannosamine-6-phosphate-2-epimerase
SAUSA300_2503	1.745	0.545	1.199	ssaA, secretory antigen precursor
SAUSA300_2331	0.380	-0.804	1.183	marR
SAUSA300_1316	0.586	-0.585	1.171	msrB
SAUSA300_1632	0.941	-0.209	1.149	conserved hypothetical protein
SAUSA300_1800	0.600	-0.544	1.145	RluD family protein, pseudouridine synthease
SAUSA300_1795	2.733	1.597	1.136	conserved hypothetical protein
SAUSA300_0224	0.981	-0.137	1.118	coa,staphylocoagulase precursor

SAUSA300_1021	0.690	-0.424	1.115	conserved hypothetical protein
SAUSA300_1594	2.601	1.493	1.109	yajC
SAUSA300_0003	1.241	0.136	1.106	conserved hypothetical protein
SAUSA300_1904	2.382	1.281	1.101	conserved hypothetical protein
SAUSA300_2644	-0.785	-1.881	1.096	gidB, glucose-inhibited division protein
SAUSA300_1305	0.382	-0.713	1.095	sucB
SAUSA300_1101	0.129	-0.966	1.095	fibronectin
SAUSA300_1801	1.190	0.095	1.095	fumC
SAUSA300_1596	-1.005	-2.092	1.088	queA
SAUSA300_2504	-1.331	-2.417	1.086	acyltransferase
SAUSA300_1534	-1.282	-2.364	1.081	conserved hypothetical protein
SAUSA300_1452	1.383	0.302	1.081	proC
SAUSA300_0993	2.055	0.974	1.080	pdhA
SAUSA300_0367	-1.103	-2.184	1.080	ssb, single strand binding protein
SAUSA300_2219	-0.419	-1.432	1.013	moaA
SAUSA300_1605	0.546	-0.464	1.010	mreC
SAUSA300_1505	-1.336	-2.334	0.997	conserved hypothetical protein
SAUSA300_1597	-1.176	-2.169	0.993	ruvB
SAUSA300_2252	1.286	0.294	0.992	conserved hypothetical protein