

Figure S1. Protein abundance compared with mRNA-seq and ribosome profile data

Three results of RNA quantification among 55 genes were compared with the amount of the corresponding protein, and their correlation coefficients are shown. RT-PCR (D =  $0.7 \text{ h}^{-1}$ ) and protein quantification data (D = 0.5 and  $0.7 \text{ h}^{-1}$ ) are as those from Ishii et al., and the values were converted to molecule/cell. RPKMcc for the genes analyzed using mRNA-seq and RP (D =  $0.6 \text{ h}^{-1}$ ) are those of the present study.

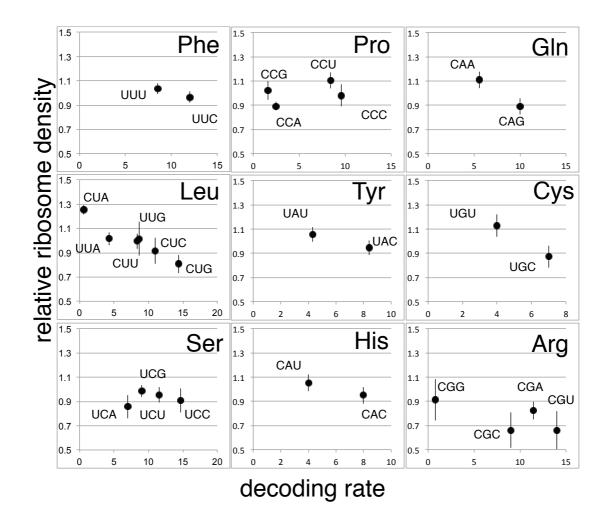


Figure S2. A-site ribosome density compared with decoding rate

The relative A-site ribosome density (shown in Figure 5, Y-axes) was compared with the RtRNA/Rshift value (decoding rate, Curran and Yarus [10], X-axes).

Only YNN codons that could be analyzed using their system are shown.



Figure S3 (1/4) Relative ribosome density of each codon at different locations.



Figure S3 (2/4) Relative ribosome density of each codon at different locations.

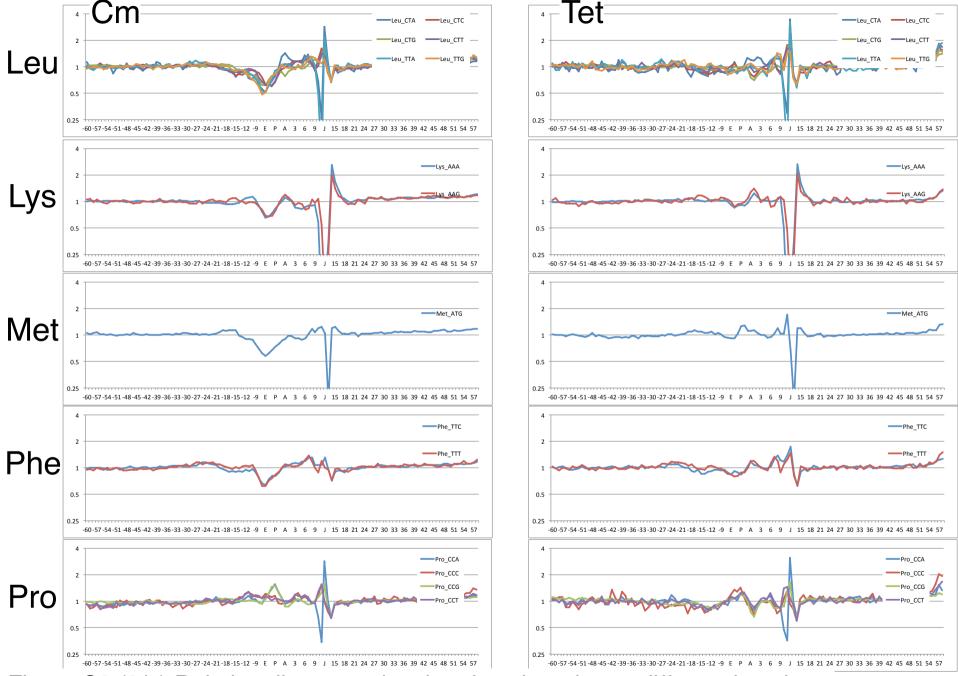


Figure S3 (3/4) Relative ribosome density of each codon at different locations.

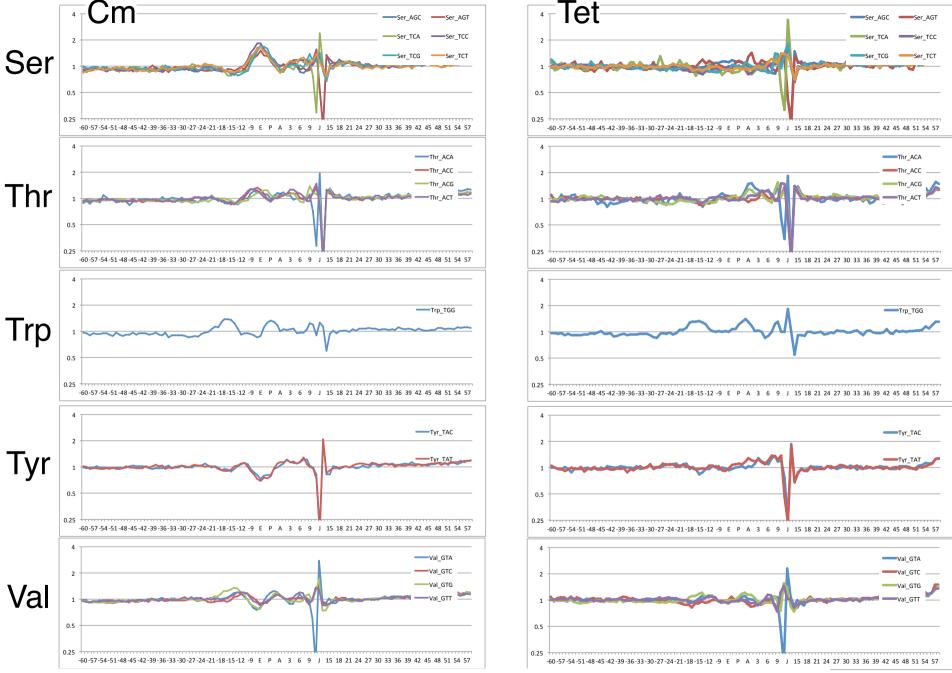


Figure S3 (4/4) Relative ribosome density of each codon at different locations.

Figure S3. Local ribosome densities of codons located at each position Local ribosome density of each of 61 in-frame coding codons when that is located at each position was shown. One panel shows codons encoding an amino acid and samples taken from cultures treated with Cm or Tet. The x-axis shows the nucleotide position, and the first position of codon at A-site is designated as zero. Positions corresponding to ribosomal A, P, and E-site and the 3′ end of the sequence read (J) are marked.

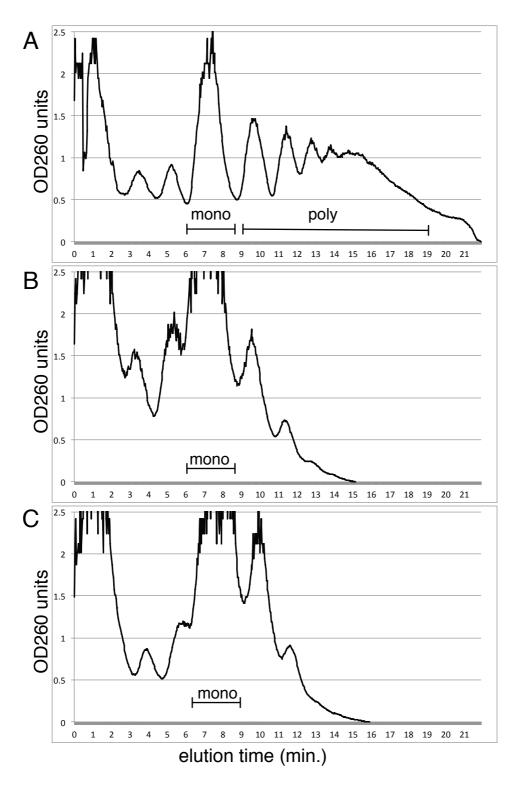


Figure S4. Sucrose density gradient pattern of ribosome fraction

Sucrose density gradient pattern of ribosome fraction without RNase treatment (A), or treated by RNaseI (B) or MNase (C). After the sucrose gradient centrifugation, solution was eluted from the top (light) and OD260 was monitored. Monosome (mono) and polysome (poly) sections were indicated.

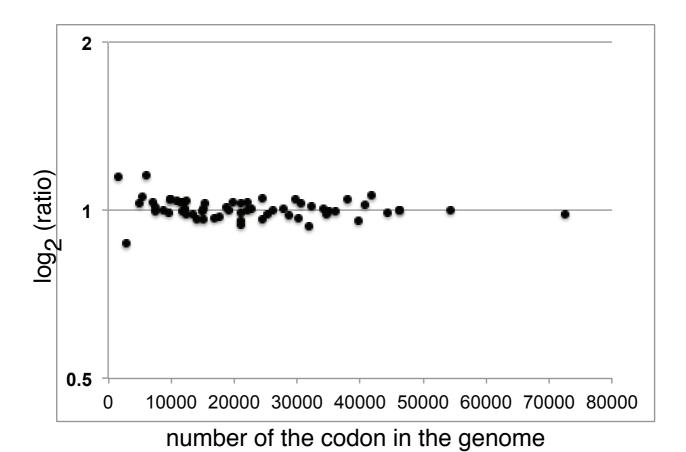


Figure S5. Ribosome density of each codon at A-site was calculated using all the sequence reads or reads whose 3'-end was not mapped to the position followed by A. Then the ratio of the two results for a codon was plotted against usage of the codon in the genome.

Table S1 RNA and protein abundance

Table S1	RNA and protein abundance								
	RNA (qRT-PCR, Ishii et al, D=0.7/h,	RNA (mRNA-seq, DPB, D=0.6/h)*2	RNA(RP, DPB, D=0.6/h)*2	protein(molecule/c ell, ishii et al,	ell, ishii et al,				
Gene	molecule/cell)*1			D=0.5/h )*1	D=0.7/h )*1				
aceA	73.57	2011.1	2268.6	23607.3	11076.0				
aceB	73.81	2226.0	1627.6	10445.3	9376.7				
aceE	69.88	1944.9	1626.7	3212.6	2490.8				
aceF	23.53	1375.2	1390.2	1015.0	1193.4				
ackA	10.75	192.4	408.8	6253.7	6899.4				
acnA	9.22	143.1	189.8	ND *3	209.7				
acnB	48.77	559.9	1311.5	834.9	938.2				
acs	6.02	46.8	54.6	ND	2399.7				
adhE	46.35	534.8	1333.6	192.1	705.6				
adk	47.70	1030.0	1749.0	719.2	1339.9				
eda	8.68	365.6	874.8	7629.5	6396.5				
eno	66.38	2685.6	4290.7	15018.2	27470.3				
fbaA -	46.20	2029.0	2787.7	3929.3	7244.8				
fbp	7.18	239.4	254.0	1152.2	1472.6				
frdA	1.73	39.6	38.4	531.3	129.9				
fumA	19.15	121.6	183.2	758.5	588.9				
fumB	0.35	3.7	6.1	85.9	656.9				
fumC	2.98	54.4	78.1	223.1	387.6				
galM	8.27	386.1	318.3	371.9	616.7				
gapA	143.33	3693.2	12608.2	33987.3	47941.4				
glcB	3.26	54.6	46.5	397.3	181.7				
g/tA	75.85	991.6	1284.2	3870.6	2494.3				
gnd	53.37	2305.5	2267.0	1593.2	1852.3				
gpmA 	31.80	2650.2	3411.7	9979.3	10017.4				
icd	122.67	3943.4	5741.2	8619.3	12662.7				
ldhA	4.00	137.0	194.1	716.8	1163.4				
lldD , ,	1.25	38.9	64.6	630.1	1233.9				
lpd "	67.61	1574.7	2074.7	7291.0	8810.4				
mdh	73.01	1755.4	3783.5	ND	2440.9				
pck pfkB	4.81	84.6	136.9 325.5	1650.8 385.8	533.9 1880.1				
pflA	6.96 2.94	57.7 103.8	162.1	96.5	224.7				
pfiA pflB	49.08	796.6	1185.2	1647.1	1291.0				
ľ	20.49	650.4	796.6	1097.5	2164.9				
pgi pgk	46.83	1126.6	2337.3	5043.8	6850.6				
pgm pgm	12.47	358.1	328.5	861.4	473.1				
ppc	40.05	581.9	767.0	1152.3	3597.3				
pps	8.08	175.1	169.3	258.7	418.3				
prpC	0.04	38.9	64.6	297.4	222.5				
pta	3.63	148.1	311.1	206.1	398.5				
pta ptsH	85.61	3005.3	7825.4	66387.7	86935.8				
ptsI	44.94	1458.7	1247.4	1686.8	2992.0				
pykA	9.06	200.6	427.3	943.7	584.0				
pykF	24.91	723.2	1425.3	1958.7	2862.1				
rpiA	7.52	681.9	1010.9	633.6	469.2				
sdhA	39.26	496.8	439.8	1890.3	3383.7				
sucB	65.25	624.7	1031.6	3214.0	3438.2				
sucC	65.32	846.4	1125.4	3589.7	4206.5				
sucD	18.06	833.5	1092.1	1387.3	1977.7				
talA	8.68	259.7	318.6	1425.0	2563.0				
talB	41.09	616.9	2016.6	2984.4	3127.9				
tktA	28.29	543.9	1011.5	726.8	1265.0				
tktB	7.48	212.0	184.5	1136.0	1574.2				
tpiA	13.22	1341.5	2077.8	2136.0	3304.8				
ybhE	11.13	171.2	395.3	281.1	270.2				
	al. 2007. <i>Science</i> 316		253.0	251	2.0.2				

<sup>\*1:</sup> Ishii N, et al. 2007. Science 316(5824): 593-597.

<sup>\*2:</sup> this work

<sup>\*3:</sup> not detected

Table S2 Read depth (DPB) and R/m ratio of the SAM selected genes.

Per	i abie		ead dept										
	gene		score									mRNA(GAII 6_1)*3	
Section		3.4					12.089	12.292		12.984		8.877	9.333
1969   1969													9.731
March   1909													
													11.325
	uspA	2.84	17 0.462	-4.023		0.700	12.233		12.049		9.124	8.917	9.232
Section   Sect													5.669
1969   1969													3.500
													5.582
May   May													7.816
Deal													5.046
field         -1,533         -1,701         2,861         1,814         3,961         -1,869         2,160         2,100         2,201         3,200         4,200         2,200         2,201         3,200         4,200         2,200         4,200         2,201         4,200         4,200         2,200         4,200													3.826
	ујіЕ												5.370
New   New							-0.520		0.310				
							1.910		0.789				4.453
	rimK	-1.64	48 -0.535	2.696	1.657	0.615		5.546	5.126	5.358	7.131	7.188	6.910
													6.158
													6.669
pmB         -2.221         O192         2.744         2.449         O.898         2.898         3.686         3.483         4.228         1.006         5.880         5.880           dwB         -2.295         -0.333         2.776         2.884         1.046         5.447         0.025         5.704         7.441         0.011         9.00           dwB         -2.295         -0.237         2.777         2.391         1.000         3.744         4.000         3.441         3.779         9.00           yeV         -2.295         2.227         2.783         3.139         1.159         -0.000         3.431         3.774         4.000         5.895         5.337         6.205           yeW         -2.449         -0.072         2.784         2.251         0.000         3.634         3.774         4.300         5.885         3.387         2.285         1.000         3.000         3.415         4.517         4.420         6.883         7.128         7.128         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279         7.279													6.554
yeld         -2828         -0848         2.756         3487         1285         0.148         2.741         4.445         4.107         400           abB         -2.299         0.383         2.377         2.284         1.106         5.447         0.295         3.041         3.379         3.338           abC         -2.279         -0.017         2.778         2.381         1.189													7.101
shell         -2985         0.333         2.787         2.884         1.046         5.447         6.025         3.704         7.441         9.031         9.107         9.00           spl         -2895         2.227         2.787         2.997         0.088         1.189         -         1.122         4.400         3.444         3.279           spl         -2.485         0.2237         2.783         2.129         0.080         0.354         3.774         4.300         6.985         5.337         2.221         1.221         1.221         1.221         1.222         1.222         1.221         1.222         1.222         1.223         1.223         0.080         0.080         0.000         2.838         1.736         0.020         0.084         0.037         4.156         0.037         0.238         1.736         0.020         0.030         0.481         0.037         0.020         0.288         1.736         0.020         0.030         0.030         0.132         0.038         0.237         0.020         0.030         0.030         0.030         0.030         0.030         0.030         0.030         0.030         0.030         0.030         0.030         0.030         0.030         0.030							2.586		3.463				
Sect							5.447		5.704				9.065
pc/m         -2.058         0.119         2.783         2.122         0.798         3.050         3.451         3.714         4.300         5.885         8.337         5.717           pc/m         -1.519         -0.428         2.784         2.310         0.002         -0.92         -1.581         -0.608         0.000         1.704         2.212         5.73           pc/m         -1.519         0.428         2.784         2.210         1.584         1.520         1.593         -0.850         0.000         8.000           pc/m         -2.880         0.002         2.288         1.516         0.020         6.000         6.300         6.132         6.161         6.937         6.125         6.018         1.518         0.020         6.000         6.300         6.122         6.019         3.300         3.360         3.360         3.360         3.300         3.360 </td <td></td> <td>3.474</td> <td></td> <td>3.393</td>											3.474		3.393
μαχ         -2.49         -0.702         2.784         2.310         0.902         -0.592         -1.590         0.000         1.704         2.121         1.272         <													3.249
Park   -3.619													5.713
ym/m         -2169         0.307         2.799         2.251         0.894         5.037         4.159         4.571         5.492         0.898         1.128         7.109           tn/H         -1.739         0.316         2.289         1.174         0.020         0.050         0.330         6.123         0.681         7.993         8.156         7.995           ym/m         -1.101         -0.038         2.289         1.157         0.584         2.437         2.298         3.150         0.584         2.430         2.182         3.380         3.880<													
rin B         -1.739         0.316         2.828         1.754         0.820         0.909         6.330         6.123         6.181         7.992         8.185         7.952           wish         -1.510         0.038         2.239         1.156         0.584         2.437         2.228         3.380         3.880         3.88           wish         -1.210         -0.038         2.293         1.738         0.822         4.081         5.339         4.887         7.004         7.015         6.582           wish         -2.281         -1.008         2.2082         1.235         0.810         0.822         4.087         5.242         0.489         8.042         2.080         1.035         2.005         1.035         2.035         2.035         2.035         2.035         2.035         2.035         2.035         2.032         2.035         2.035         2.022         2.045         2.035         0.202         0.035         2.252         0.004         3.035         2.232         0.004         3.035         2.232         0.004         3.035         3.232         0.004         3.035         3.232         0.004         3.035         3.232         0.004         3.035         3.232         0.004 </td <td></td> <td>7.081</td>													7.081
pine         -1512         00800         2839         1515         0534         2437         2288         2430         2182         3830         3800         3860         3860         386         4470         4881         5339         4857         7004         77015         6586         4470         4881         3239         4877         7004         77015         6586         4470         4881         3283         4877         7004         77015         6586         4470         4881         3281         3280         9878         4878         4212         3,868         4176         6907         797         497         4261         4088         2213         2296         0.770         1074         4082         0.386         2265         1901         3,349         5017         2258         542           mbmC         -2273         -0.143         2358         2.745         0.383         3.382         2.057         8.033         8.877         8.833         8.874         8.333           mbmC         -2.153         -0.043         2.949         3.041         1.725         0.838         0.186         0.428         3.049         3.041         1.725         0.838         8.837													1.114
													7.954
μαθ B         -1,786         -1,078         2,893         1,788         0,822         4,087         4,212         3,686         4,176         5,913         5,898         0,910         2,258         0,810         -1,176         0,966         -1,228         0,097         7,879         0,967         -2,228         0,089         2,913         2,229         0,000         1,092         -0,082         0,386         2,205         1,093         2,000         1,092         0,000         1,092         0,000         1,092         0,000         1,092         0,000         1,092         0,000         1,092         0,000         1,092         0,000         1,092         0,000         1,092         0,000         1,092         0,000         1,093         0,000													
bab         -2281         -1008         2908         2355         0810         5.142         6.788         5.342         6.409         8.042         8.007         19.35         2.009           wish**         -2280         -0.328         2.937         3.080         1.052         1.074         0.368         -1.240         3.371         2.816         3.217           wish**         -22573         -0.143         2.938         2.485         0.848         3.085         2.855         1.901         3.341         5.371         2.818         3.84         8.83           wish**         -1.373         -0.017         2.938         1.285         0.942         4.466         4.386         3.331         4.177         6.022         6.274         8.83           wish**         -1.373         -0.017         2.938         1.886         0.942         4.466         4.386         3.331         4.177         6.022         6.274         4.042         2.00           wish**         -2.213         -0.350         2.990         3.054         1.022         -1.526         -1.582         -0.884         0.229         6.432         2.144         2.20           wish**         -2.213         -1.09													
yab         -2880         -0.328         2.927         3.080         1.052         1.074         0.386         -1.240         3.371         2.816         3.217           mulb         -2.539         -0.143         2.898         2.485         0.486         3.085         2.855         1.901         3.349         5.017         3.349         5.017         3.349         5.017         3.349         5.017         3.349         5.017         3.349         8.818         8.83         8.84         8.83         8.84         8.83         8.84         8.83         8.84         8.83         8.84         8.83         8.84         8.83         8.81         8.83         8.81         8.83         8.81         8.83         8.81         8.81         8.81         8.81         8.81         8.81         8.82         2.226         0.050         0.017         1.144         4.93           vor         -2.214         0.104         3.016         2.221         0.088         8.881         8.984         8.297         1.0317         1.198         1.1987         1.144         4.97           vor         -2.2561         -0.188         3.039         1.183         1.109         2.283         1.159         2.2710													7.979
	ylbF	-2.25	51 -0.689	2.913	2.269	0.779		-0.692		0.386	2.605	1.935	2.038
marge													3.219
yell   1,730													
													2.206
pmM	ycjT	-2.8	13 -0.350	2.990	3.054	1.022	-1.526	-1.582	-0.684	0.426	2.378	2.161	2.099
pends   -2.561   -0.057   3.027   2.710   0.895   -2.533   -1.589   -2.276   -0.903   0.300   0.345   0.875   astB   -2.561   -0.186   3.029   2.683   0.879   1.037   -0.090   -0.514   0.444   3.055   2.573   3.011   3.055   2.573   3.011   3.056   2.291   0.749   7.124   7.403   6.928   8.021   9.534   9.682   9.765   9.													4.970
													6.240
Pack   -1.643								7.403					9.763
	yjjN												1.560
	rpoA vahO								11.434		10.000	10.000	10.002
									2.324				5.419
rhcG         -2.336         0.340         3.134         2.353         0.751         0.482         0.841         0.739         1.424         3.588         2.927         3.15           ychA         -1.712         -0.381         3.160         3.345         1.059         0.162         -2.064         -1.166         -0.208         2.269         2.271         2.511           ychW         -2.652         -0.220         3.164         2.792         0.882         -0.359         -0.462         1.082         2.238         2.727         2.290           yfaE         -2.211         -0.025         3.170         2.250         0.710         4.949         5.234         4.884         5.765         7.623         7.327         7.42           spA         -2.201         0.877         3.210         2.671         0.832         3.381         4.286         4.747         4.504         7.164         6.706         6.833           ycaQ         -3.140         -0.508         3.240         3.434         1.060         0.354         1.035         0.610         2.598         4.682         4.634         4.434           ycaQ         -3.144         0.006         3.283         2.196         0.673													2.262
ychA         -1.712         -0.392         3.135         1.717         0.548         6.189         6.319         6.159         6.466         7.947         8.042         8.011           ycjS         -3.115         -0.351         3.160         3.345         1.059         0.162         -2.064         -1.166         -0.208         2.933         2.371         2.51           yfaE         -2.211         -0.025         3.170         2.250         0.710         4.949         5.234         4.884         5.765         7.623         7.327         7.422           xylG         -3.023         0.486         3.202         3.261         1.019         -1.086         -1.172         0.120         2.272         2.104         1.966           sapA         -2.601         0.877         3.210         2.671         0.832         3.381         4.286         4.174         4.504         7.164         6.706         6.833           ycaQ         -3.140         -0.623         3.241         1.060         0.354         1.035         0.610         2.598         4.682         4.632         4.634         4.43           ycaPA         -2.501         0.144         3.277         2.553         0.779													3.432
ycjis         -3.115         -0.351         3.160         3.345         1.059         0.162         -2.064         -1.166         -0.208         2.693         2.371         2.51           ydhW         -2.652         -0.220         3.164         2.792         0.882         -0.359         -0.462         1.082         2.938         2.727         2.90           ydG         -3.023         0.486         3.202         3.261         1.019         -1.969         -1.025         -1.712         0.120         2.272         2.104         1.961           aspA         -2.001         0.877         3.210         2.671         0.832         3.381         4.286         4.747         4.504         7.164         6.706         6.833           vaQ         -3.140         -0.508         3.244         3.444         1.000         0.354         1.035         0.610         2.599         4.682         4.634         4.444           holA         -2.024         -0.623         3.261         2.040         0.625         4.985         5.025         5.171         5.562         7.343         7.202         7.131           truA         -2.164         0.006         3.263         2.196         0.673													3.156
ydhW         -2.652         -0.220         3.164         2.792         0.882         -0.359         -0.462         1.082         2.938         2.727         2.90           yfaE         -2.211         -0.025         3.170         2.250         0.710         4.949         5.234         4.884         5.765         7.623         7.327         7.42           xylG         -3.023         0.486         3.202         3.261         1.019         -1.989         -1.025         -1.712         0.120         2.272         2.104         1.838           aspA         -2.601         0.877         3.210         2.671         0.832         3.381         4.286         4.747         4.504         7.164         6.706         6.83           ycaQ         -3.140         -0.508         3.240         3.434         1.060         0.535         5.925         5.171         5.562         7.343         7.022         7.133           truA         -2.164         0.006         3.263         2.196         0.673         5.183         5.347         5.189         5.920         7.687         7.622         7.491           truA         -2.164         0.006         3.253         3.275         0.573													8.010 2.514
yraE         -2.211         -0.025         3.170         2.250         0.710         4.949         5.234         4.884         5.765         7.623         7.327         7.422           xy/G         -3.023         0.486         3.202         3.2611         1.019         -1.869         -1.025         -1.712         0.120         2.272         2.104         1.968           aspA         -2.601         0.877         3.210         2.671         0.832         3.381         4.286         4.174         4.504         7.164         6.066         6.638           ycaQ         -3.140         -0.623         3.261         2.040         0.625         4.985         5.025         5.171         5.562         7.343         7.202         7.131           truA         -2.164         0.006         3.263         2.196         0.673         5.183         5.347         5.189         5.920         7.687         7.687         7.429           hydN         -2.501         0.144         3.277         2.553         0.779         0.936         0.792         2.591         8.406         8.55           intR         -3.087         0.339         3.291         3.295         1.010         3.336							J JE						2.907
aspA         -2.601         0.877         3.210         2.671         0.832         3.381         4.286         4.747         4.504         7.164         6.706         6.833           yeaQ         -3.140         -0.508         3.240         3.434         1.060         0.554         1.035         0.610         2.598         4.682         4.634         4.43           holA         -2.024         -0.623         3.261         2.040         0.625         5.055         5.171         5.562         7.343         7.202         7.133           truA         -2.164         0.006         3.263         2.196         0.673         5.183         5.347         5.189         5.920         7.687         7.632         7.491           hydN         -2.501         0.144         3.277         2.553         0.779         0.936         0.792         2.818         2.836         3.25         3.25         3.25         1.001         0.935         0.709         0.929         2.591         8.436         8.155         intr         3.352         2.957         0.881         1.106         1.272         0.948         2.491         4.285         4.432         4.511         yagZ         2.2496         -0.863	yfaE	-2.2	11 -0.025	3.170	2.250	0.710		5.234	4.884	5.765	7.623	7.327	7.422
ycaQ         -3.140         -0.508         3.240         3.434         1.060         0.354         1.035         0.810         2.598         4.682         4.634         4.434           holA         -2.024         -0.623         3.261         2.040         0.625         4.985         5.025         5.171         5.562         7.343         7.202         7.132           truA         -2.164         0.006         3.263         2.186         0.673         5.183         5.547         5.189         5.920         7.687         7.632         7.748           hydN         -2.501         0.144         3.277         2.553         0.779         0.936         0.792         2.818         2.825         3.25           aceK         -3.133         0.767         3.278         3.312         1.010         3.836         4.993         5.411         5.981         8.436         8.106         8.551           intR         -3.087         -0.309         3.295         1.010         0.935         0.709         0.929         2.595         4.707         4.828         4.221           yagZ         -2.949         -0.068         3.365         2.957         0.881         1.106         1.272         <													1.968
hold         -2.024         -0.623         3.261         2.040         0.625         4.985         5.025         5.171         5.562         7.343         7.202         7.133           truA         -2.164         0.006         3.263         2.196         0.673         5.183         5.347         5.189         5.920         7.687         7.632         7.491           hydN         -2.501         0.144         3.277         2.553         0.779         0.336         0.792         2.2818         3.285         3.218           aceK         -3.133         0.767         3.278         3.312         1.010         0.935         0.709         0.929         2.595         4.707         4.828         4.22           mraZ         -2.496         -1.209         3.330         2.541         0.769         6.521         6.529         0.789         0.295         7.595         7.372         9.580         9.199         9.119         9.111         9.942         2.940         -0.068         3.360         2.943         0.876         0.206         1.062         3.825         2.640         3.317         9.942         9.241         4.285         4.432         4.511         4.511         4.922         4.942													6.832
truA         -2.164         0.006         3.263         2.196         0.673         5.183         5.347         5.189         5.920         7.687         7.632         7.494           hydN         -2.501         0.144         3.277         2.553         0.779         0.936         0.792         2.818         2.885         3.25           aceK         -3.133         0.767         3.278         3.312         1.101         0.935         0.709         0.929         2.595         4.707         4.828         4.255           intR         -3.087         -0.339         3.291         3.295         1.001         0.935         0.709         0.929         2.595         4.707         4.828         4.255           maZ         -2.496         -1.209         3.303         2.541         0.769         6.521         6.789         6.265         7.372         9.580         9.139         9.11           yagU         -2.816         -0.876         3.355         2.957         0.881         1.106         1.272         0.948         2.491         4.285         4.451         yagU         -2.816         -0.808         3.360         2.943         0.861         0.206         1.537         3.786													7.132
hydN         -2.501         0.144         3.277         2.553         0.779         0.936         0.792         2.818         2.885         3.25           aceK         -3.133         0.767         3.278         3.312         1.1010         3.836         4.993         5.411         5.981         8.436         8.106         8.559           inRR         -3.087         -0.339         3.291         3.295         1.001         0.935         0.0709         0.929         2.595         4.707         4.828         4.222           mraZ         -2.486         -1.209         3.303         2.541         0.769         6.521         6.789         6.265         7.372         9.580         9.139         9.111           yagJ         -2.816         -0.876         3.355         2.957         0.881         1.106         1.272         0.948         2.491         4.285         4.432         4.511           yegZ         -2.949         -0.068         3.361         3.170         0.943         -1.586         0.274         3.835         2.263         4.511           yegZ         -3.167         -1.154         3.397         3.288         0.968         -0.230         -1.558         0.274													7.132
intR         -3.087         -0.339         3.291         3.295         1.001         0.935         0.709         0.929         2.595         4.707         4.828         4.221           mraZ         -2.496         -1.209         3.303         2.541         0.769         6.521         6.789         6.265         7.372         9.580         9.139         9.11           yegZ         -2.816         -0.876         3.355         2.957         0.881         1.106         1.272         0.948         2.491         4.285         4.432         4.51           yegZ         -2.549         -0.068         3.360         2.943         0.876         0.006         1.062         3.825         2.494         3.61         3.170         0.943         0.066         1.052         3.825         2.640         3.317         0.746         0.074         3.167         3.167         3.177         0.943         0.068         -0.230         -1.558         0.274         3.163         3.029         2.533         3.029         2.533         3.766         3.032         2.53         3.741         4.528         4.958         7.306         7.141         6.776         6.844         2.471         3.872         4.774         6.626 <td>hydN</td> <td>-2.50</td> <td>0.144</td> <td>3.277</td> <td>2.553</td> <td>0.779</td> <td></td> <td>0.936</td> <td></td> <td>0.792</td> <td>2.818</td> <td>2.885</td> <td>3.251</td>	hydN	-2.50	0.144	3.277	2.553	0.779		0.936		0.792	2.818	2.885	3.251
mraZ         -2.496         -1.209         3.303         2.541         0.769         6.521         6.789         6.265         7.372         9.580         9.139         9.113           yagU         -2.616         -0.876         3.355         2.957         0.881         1.106         1.272         0.948         2.491         4.285         4.432         4.51           yeR         -2.949         -0.068         3.360         2.943         0.876         0.206         1.537         3.786         3.701         3.17           yeR         -3.167         -1.154         3.397         3.288         0.968         -0.230         -1.558         0.274         3.163         3.029         2.53           yeR         -2.716         0.235         3.413         2.779         0.814         3.949         3.741         4.528         4.958         7.306         7.141         6.77           smf         -2.251         0.249         3.552         2.348         0.661         1.447         1.221         1.440         1.814         4.103         3.848         3.53           dnaG         -2.721         0.280         3.660         2.784         0.763         5.032         5.165         5.2													8.559
yagU         -2.816         -0.876         3.355         2.957         0.881         1.106         1.272         0.948         2.491         4.285         4.432         4.511           yegZ         -2.949         -0.068         3.360         2.943         0.876         0.206         1.062         3.825         2.640         3.31           yieW         -3.017         0.984         3.361         3.170         0.943         -1.558         0.274         3.163         3.029         2.531           hofB         -3.167         -1.154         3.397         3.288         0.968         -0.230         -1.558         0.274         3.163         3.029         2.531           yggD         -2.716         0.235         3.413         2.779         0.814         3.949         3.741         4.528         4.958         7.306         7.141         6.77           smf         -2.509         0.361         3.531         2.558         0.724         3.872         4.774         6.626         6.766         6.644           yghF         -2.351         0.249         3.552         2.348         0.661         1.447         1.221         1.440         1.814         4.103         3.848         <													4.226 9.113
yegZ         -2.949         -0.068         3.360         2.943         0.876         0.206         1.062         3.825         2.640         3.31-1           yjeN         -3.017         0.894         3.361         3.170         0.943         -1.558         0.274         3.163         3.701         3.17           hofB         -3.167         -1.154         3.397         3.288         0.968         -0.230         -1.558         0.274         3.163         3.029         2.533           ygD         -2.716         0.235         3.413         2.779         0.814         3.949         3.741         4.528         4.958         7.306         7.141         6.775           smf         -2.509         0.361         3.531         2.558         0.724         3.843         4.271         3.872         4.774         6.626         6.766         6.844           yghF         -2.351         0.249         3.552         2.348         0.661         1.447         1.221         1.440         1.1814         4.103         3.848         3.531           dnaG         -2.721         0.280         3.660         2.074         0.763         5.032         5.165         5.207         6.107													4.517
yeN         -3.017         0.894         3.361         3.170         0.943         -1.537         3.786         3.701         3.177           hofB         -3.167         -1.154         3.397         3.288         0.998         -0.230         -1.558         0.274         3.163         3.029         2.53           yeD         -2.716         0.235         3.413         2.779         0.814         3.494         3.741         4.588         4.958         7.306         7.141         6.775           smf         -2.591         0.361         3.531         2.558         0.724         3.843         4.271         3.872         4.774         6.626         6.716         6.84           yebF         -2.251         0.249         3.552         2.348         0.661         1.447         1.221         1.440         1.814         4.103         3.848         3.53           dnaG         -2.721         0.280         3.661         2.784         0.763         5.032         5.165         5.207         6.107         8.325         8.188         7.99           yieR         -4.601         0.526         3.657         5.018         1.372         2.558         2.180         -0.508         2.							.=		•=				3.314
yggD         -2.716         0.235         3.413         2.779         0.814         3.949         3.741         4.528         4.958         7.306         7.141         6.776           smf         -2.509         0.361         3.531         2.558         0.724         3.843         4.271         3.872         4.774         6.626         6.766         6.844           ysh         -2.351         0.249         3.552         2.348         0.661         1.447         1.221         1.440         1.814         4.103         3.848         3.531           dnaG         -2.721         0.280         3.646         2.784         0.763         5.032         5.165         5.207         6.107         8.325         8.168         7.999           yiCR         -4.601         0.526         3.657         5.018         1.372         2.558         2.180         -0.508         2.820         6.80         6.623         6.831           dnaE         -2.094         -1.003         3.660         2.099         0.573         4.859         5.148         4.939         5.291         7.265         7.257         7.051           yiV         -2.997         -0.145         3.672         3.120         0	yjeN												3.177
smf         -2.509         0.361         3.531         2.558         0.724         3.843         4.271         3.872         4.774         6.626         6.776         6.844           yghF         -2.551         0.249         3.552         2.348         0.661         1.447         1.221         1.440         1.814         4.103         3.848         3.53           dnaG         -2.721         0.280         3.664         2.784         0.763         5.032         5.165         5.207         6.107         8.325         8.168         7.99           yieR         -4.601         0.526         3.657         5.018         1.372         2.558         2.180         -0.508         2.820         6.80         6.623         6.83           dnaE         -2.094         -1.003         3.660         2.099         0.573         4.959         5.148         4.939         5.291         7.255         7.255         7.05           vivC         -2.997         -0.145         3.672         3.120         0.850         4.879         5.040         5.060         6.290         8.526         8.419         8.36i           yiV         -2.998         1.275         3.706         3.103         0.83								0.744					2.537
yghF         -2.351         0.249         3.552         2.348         0.661         1.447         1.221         1.440         1.814         4.103         3.848         3.531           dnaG         -2.721         0.280         3.646         2.794         0.763         5.032         5.165         5.207         6.107         8.325         8.168         7.99           vicR         -4.601         0.526         3.657         5.018         1.372         2.558         2.180         -0.508         2.820         6.880         6.820         6.823         6.833         d6.83         d6.83         d6.86         6.23         6.833         d6.83         d6.86         6.23         6.833         d6.83         d6.80         6.890         6.890         6.890         6.80         6.890         6.890         6.80         6.890         6.890         6.820         6.80         6.890         6.890         6.890         8.481         8.361         7.057         7.057         7.057         7.057         7.057         7.057         7.057         7.057         7.057         7.059         7.059         8.228         8.290         8.407         4.384         7.057         7.057         7.057         7.057         7.057													6.774 6.842
dnaG         -2.721         0.280         3.646         2.784         0.763         5.032         5.165         5.207         6.107         8.325         8.168         7.99           yicR         -4.601         0.526         3.657         5.018         1.372         2.558         2.180         -0.508         2.820         6.880         6.623         6.83           dnaE         -2.094         -1.003         3.660         2.099         0.573         4.959         5.148         4.939         5.291         7.265         7.225         7.051           ruvC         -2.997         -0.145         3.672         3.120         0.860         4.879         5.040         5.060         6.290         8.526         8.491         8.848           yiV         -2.998         1.275         3.706         3.103         0.837         0.671         0.893         1.169         2.089         4.407         4.134         4.386           fdhF         -2.474         0.814         3.754         2.497         0.665         2.308         2.234         1.617         1.855         4.39         4.637         4.509           yceD         -2.522         -0.444         3.787         2.549													3.536
yicR         -4.601         0.526         3.657         5.018         1.372         2.558         2.180         -0.508         2.820         6.80         6.623         6.831           dnaE         -2.094         -1.003         3.660         2.099         0.573         4.959         5.148         4.939         5.291         7.265         7.225         7.057           yiV         -2.997         -0.145         3.672         3.120         0.850         4.879         5.040         5.060         6.290         8.526         8.419         8.368           yiV         -2.998         1.275         3.706         3.103         0.837         0.671         0.089         1.169         2.089         4.407         4.134         4.386           fdhF         -2.474         0.814         3.754         2.497         0.665         2.308         2.234         1.817         1.855         4.359         4.637         4.50           yeeD         -2.522         -0.444         3.787         2.549         0.673         9.779         9.938         9.223         9.905         12.177         12.306         12.07           yiM         -2.284         0.048         3.911         2.295 <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>7.991</td></th<>													7.991
ruvC         -2.997         -0.145         3.672         3.120         0.850         4.879         5.040         5.060         6.290         8.526         8.419         8.36i           yiV         -2.998         1.275         3.706         3.103         0.837         0.671         0.893         1.169         2.099         4.407         4.134         4.38           fdhF         -2.474         0.814         3.754         2.497         0.665         2.308         2.234         1.617         1.855         4.359         4.607         4.500           yeac         -2.522         -0.444         3.787         2.549         0.673         9.479         9.938         9.223         9.905         12.177         12.306         12.07         xy/A         -2.888         0.485         3.911         2.955         0.756         1.422         1.611         1.316         2.405         4.715         4.560         4.651           yffM         -2.264         0.043         4.016         2.267         0.564         0.038         0.309         2.335         2.472         2.255           mbhA         -3.010         -9.933         4.225         3.011         0.713         -0.941         -0.582	yicR	-4.60	0.526	3.657	5.018	1.372	2.558	2.180	-0.508	2.820	6.880	6.623	6.839
yiV         -2.998         1.275         3.706         3.103         0.837         0.671         0.893         1.169         2.089         4.407         4.134         4.384           fdhF         -2.474         0.814         3.754         2.497         0.665         2.308         2.234         1.617         1.855         4.39         4.637         4.50           yceD         -2.522         -0.444         3.787         2.549         0.673         9.479         9.938         9.223         9.905         12.177         12.306         12.07           xylA         -2.888         0.485         3.911         2.955         0.756         1.422         1.811         1.316         2.405         4.715         4.560         4.566           yffM         -2.264         0.043         4.016         2.267         0.564         0.038         0.309         2.335         2.472         2.255           mbhA         -3.010         -0.933         4.225         3.011         0.713         -0.941         -0.582         -0.684         -1.311         2.300         1.746         2.359           ybaJ         -3.142         -0.730         4.280         3.165         0.739         5.428													7.059
fahr         -2.474         0.814         3.754         2.497         0.665         2.308         2.234         1.817         1.855         4.359         4.637         4.509           yceD         -2.522         -0.444         3.787         2.549         0.673         9.479         9.938         9.223         9.905         12.177         12.306         12.078           yfM         -2.288         0.485         3.911         2.955         0.766         1.422         1.611         1.316         2.405         4.715         4.560         4.656         4.650         4.656         4.650         4.656         4.650         4.656         4.650         4.656         4.650         4.65													8.368
yceD         -2.522         -0.444         3.787         2.549         0.673         9.479         9.938         9.233         9.905         12.177         12.306         12.07           xy/A         -2.888         0.485         3.911         2.955         0.756         1.422         1.611         1.316         2.405         4.715         4.560         4.550           yfM         -2.264         0.043         4.016         2.267         0.564         0.038         0.309         2.335         2.472         2.255           mbhA         -3.010         -0.933         4.225         3.011         0.713         -0.941         -0.582         -0.844         -1.311         2.300         1.746         2.359           ybaJ         -3.142         -0.730         4.280         3.165         0.739         5.428         5.015         5.882         5.08         8.327         8.889         1.321           tmD         -4.096         0.103         4.346         4.339         0.998         7.008         7.448         6.397         8.889         1.1930         11.920         11.872           mokB         -5.955         -0.312         6.273         5.964         0.951         2.814													4.384
xylA         -2.888         0.485         3.911         2.955         0.756         1.422         1.611         1.316         2.405         4.715         4.560         4.650           yffM         -2.264         0.043         4.016         2.267         0.564         0.038         0.398         2.335         2.472         2.255           mbhA         -3.010         -0.933         4.225         3.011         0.713         -0.941         -0.582         -0.684         -1.311         2.300         1.746         2.359           ybaJ         -3.142         -0.730         4.280         3.165         0.739         5.428         5.015         5.882         5.682         5.682         8.271         8.853         8.851           trmD         -4.096         0.103         4.346         4.339         0.998         7.008         7.448         6.937         8.89         11.920         11.926         11.926           mokB         -5.955         -0.312         6.273         5.964         0.951         2.814         2.588         1.486         2.859         8.792         8.743         7.666													12.075
mbhA         -3.010         -0.933         4.225         3.011         0.713         -0.941         -0.582         -0.884         -1.311         2.300         1.746         2.351           ybaJ         -3.142         -0.730         4.280         3.165         0.739         5.428         5.015         5.882         5.058         8.327         8.853         8.351           tmD         -4.096         0.103         4.346         4.339         0.998         7.008         7.448         6.937         8.899         11.930         11.926         11.872           mokB         -5.955         -0.312         6.273         5.964         0.951         2.814         2.588         1.486         2.859         8.792         8.743         7.666	xylA	-2.88	38 0.485	3.911	2.955	0.756		1.611		2.405	4.715	4.560	4.656
ybaJ         -3.142         -0.730         4.280         3.165         0.739         5.428         5.015         5.882         5.058         8.327         8.853         8.35           trmD         -4.096         0.103         4.346         4.339         0.998         7.008         7.448         6.937         8.889         11.930         11.926         11.87           mokB         -5.955         -0.312         6.273         5.964         0.951         2.814         2.588         1.486         2.859         8.792         8.743         7.669													2.253
trmD -4.096 0.103 4.346 4.339 0.998 7.008 7.448 6.937 8.889 11.930 11.926 11.87 mokB -5.955 -0.312 6.273 5.964 0.951 2.814 2.588 1.486 2.859 8.792 8.743 7.666													
mokB -5.955 -0.312 6.273 5.964 0.951 2.814 2.588 1.486 2.859 8.792 8.743 7.665													11.873
													7.669
*1: R/m ratio in logalithm base 2, *2: the results from SAM analysis, *3: DPB of the gene in each sample (logalithm base 2) sample names are shown in Table S3.	yjhD	-4.74	1.097	6.307	4.712	0.747				-0.600	4.426	5.078	4.181

\*1: R/m ratio in logalithm base 2, \*2: the results from SAM analysis, \*3: DPB of the gene in each sample (logalithm base 2) sample names are shown in Table S3.

Table S3 Sequenced samples and number of reads mapped to CDS

Name	source strain	library*1	${ m CDS\ reads}^{*2}$
$GAII05_3$	$\mathrm{BW}25113\;smpB$	RP(Cm)	2,538,972
$GAII05\_5$	BW25113	RP(Cm)	3,959,115
GAII_9_4	BW25113	RP(Cm)	2,124,985
$GAII_9_2$	BW25113	RP(Cm)(Mnase)	6,562,793
GAII06_1	$\mathrm{BW}25113\;smpB$	RNA-seq	5,127,408
GAII05_8	BW25113	RNA-seq	1,611,231
GAII_8_10	BW25113	RNA-seq	5,967,668
$GAII05_4$	BW25113	RP(Tet)	1,027,370
$GAII07_4$	BW25113	RP(Tet)	3,357,792
GAII07_5	BW25113	RP(Tet)	4,498,133

<sup>\*1</sup> Type of library used (RNA-seq or RP), antibiotics used to stop translation (Cm or Tet), and nuclease used for polysome digestion (MNase: if specified, or RNaseI: if not indicated) are shown

<sup>\*2</sup> Total number of the sequence reads mapped to CDSs