

Supplemental Table S3
Decreased level of distribution of the *rpoZ* mutant RNAP

Position	Function	Left	D	RNAP site	D	Right	Function	WT	<i>rpoZ</i>
293446	prophage; DNA-binding protein	<i>yagL</i>	<	<i>yagM</i>	<	<i>yagN</i>	CP4-6 prophage; predicted pro	37.2	0.03
2558866	prophage; predicted integrase	<i>intZ</i>	>	<i>yffL</i>	>	<i>yffM</i>	CPZ-55 prophage; predicted pr	32.5	0.03
293168	prophage; DNA-binding protein	<i>yagL</i>	<		<	<i>yagM</i>	CP4-6 prophage; predicted pro	21.5	0.05
2103636	predicted acyl transferase	<i>wbbJ</i>	<	<i>wbbI</i>	<	<i>rfc</i>	O-antigen polymerase	20.7	0.05
279962	6 prophage; conserved protein	<i>yagB</i>	<		<	<i>yagA</i>	CP4-6 prophage; predicted DN	19.7	0.05
1687138	fumarase A monomer	<i>fumA</i>	<	<i>manA</i>	>	<i>ydgA</i>	conserved protein	18.6	0.05
296336	age; predicted phage integrase	<i>intF</i>	<		<	<i>yagP</i>	predicted transcriptional regulat	17.0	0.06
284632	ophage; predicted dehydratase	<i>yagF</i>	>		>	<i>yagG</i>	YagG GPH Transporter	16.6	0.06
278132	component of ABC superfamily	<i>afuC</i>	<	<i>afuB</i>	<	<i>insAB-2</i>	InsAB' transposase	15.9	0.06
2298346	ferredoxin-type protein	<i>napG</i>	<	<i>napA</i>	<	<i>napD</i>	signal peptide-binding chaperon	15.3	0.07
2106448	UDP-galactopyranose mutase	<i>glf</i>	<	<i>rfbX</i>	<	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-	15.2	0.07
2188970	outer membrane usher protein	<i>yehB</i>	<		<	<i>yehC</i>	putative fimbrial chaperone	14.7	0.07
3334932	binding transcriptional regulator	<i>yrbA</i>	<		<	<i>mIaB</i>	MlaB	14.0	0.07
1201330	e14 prophage; predicted protein	<i>ymlJ</i>	<		<	<i>ymlK</i>	e14 prophage; predicted repres	13.6	0.07
3192540	putative membrane protein	<i>yqIK</i>	>		<	<i>sibD</i>	SibD small RNA	12.2	0.08
4620444	DeoD	<i>deoD</i>	>	<i>yjiJ</i>	<	<i>lplA</i>	lipoyl-protein ligase A	12.1	0.08
1429566	redicted protein, C-ter fragment	<i>lomR_2</i>	>	<i>stfR</i>	>	<i>tfaR</i>	Rac prophage; predicted tail fib	12.1	0.08
4200248	zinc homeostasis protein	<i>zraP</i>	<	<i>zraS</i>	>	<i>zraR</i>	ZraR transcriptional activator	12.1	0.08
2784038	<i>Phantom Gen</i>		<		>	<i>ygaQ_1</i>	predicted protein	11.8	0.08
279646	predicted IS protein	<i>ykgN</i>	<	<i>yagB</i>	<	<i>yagA</i>	CP4-6 prophage; predicted DN	11.8	0.08
279738	predicted IS protein	<i>ykgN</i>	<	<i>yagB</i>	<	<i>yagA</i>	CP4-6 prophage; predicted DN	11.5	0.09
1544666	predicted lipoprotein	<i>yddL</i>	<	<i>yddG</i>	>	<i>fdnG</i>	formate dehydrogenase N, &alp	11.4	0.09
2558272	prophage; predicted integrase	<i>intZ</i>	>		>	<i>yffL</i>	CPZ-55 prophage; predicted pr	11.2	0.09
2106534	UDP-galactopyranose mutase	<i>glf</i>	<	<i>rfbX</i>	<	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-	11.2	0.09
1428072	redicted protein, C-ter fragment	<i>lomR_2</i>	>	<i>stfR</i>	>	<i>tfaR</i>	Rac prophage; predicted tail fib	10.8	0.09
3678430	2-keto-3-deoxygluconokinase	<i>kdgK</i>	>		<	<i>yhjJ</i>	predicted zinc-dependent peptid	10.7	0.09
4473768	toxin-antitoxin biofilm protein	<i>tabA</i>	>	<i>yjgL</i>	<	<i>argI</i>	ArgI	10.7	0.09
3803272	aride core biosynthesis protein	<i>rfaS</i>	<	<i>waaP</i>	<	<i>waaG</i>	lipopolysaccharide glucosyltran	10.5	0.09
294058	4-6 prophage; predicted protein	<i>yagM</i>	<		<	<i>yagN</i>	CP4-6 prophage; predicted pro	10.4	0.10
2765968	57 prophage; predicted protein	<i>yfjO</i>	>	<i>yfjP</i>	>	<i>yfjQ</i>	CP4-57 prophage; predicted pr	10.3	0.10
3467430	rioferritin-associated ferredoxin	<i>bfd</i>	<	<i>chiA</i>	<	<i>tufA</i>	elongation factor Tu	10.2	0.10
1311170	redicted inner membrane protein	<i>yciB</i>	<	<i>yciC</i>	>	<i>ompW</i>	OmpW, outer membrane protei	10.2	0.10
1736466	small membrane protein	<i>ynhF</i>	<	<i>purR</i>	<	<i>ydhB</i>	protein with similarity to transcr	10.1	0.10
293538	prophage; DNA-binding protein	<i>yagL</i>	<	<i>yagM</i>	<	<i>yagN</i>	CP4-6 prophage; predicted pro	9.9	0.10
3802572	ide-1,6-D-galactosyltransferase	<i>waaB</i>	<	<i>rfaS</i>	<	<i>waaP</i>	lipopolysaccharide core heptos	9.8	0.10
288440	inding transcriptional regulator	<i>yagI</i>	<		<	<i>argF</i>	ArgF	9.8	0.10
293372	prophage; DNA-binding protein	<i>yagL</i>	<	<i>yagM</i>	<	<i>yagN</i>	CP4-6 prophage; predicted pro	9.6	0.10
277762	omocysteine methyltransferase	<i>mmuM</i>	>	<i>afuC</i>	<	<i>afuB</i>	AfuB	9.5	0.11
294942	4-6 prophage; predicted protein	<i>yagN</i>	<		<	<i>intF</i>	CP4-6 prophage; predicted pha	9.2	0.11
2104144	1,6-galactofuranosyltransferase	<i>wbbI</i>	<	<i>rfc</i>	<	<i>glf</i>	UDP-galactopyranose mutase	9.2	0.11
284570	ophage; predicted dehydratase	<i>yagF</i>	>		>	<i>yagG</i>	YagG GPH Transporter	8.6	0.12
2989166	redicted protein	<i>ygeF</i>	>		>	<i>ygeG</i>	predicted chaperone	8.6	0.12
2106658	UDP-galactopyranose mutase	<i>glf</i>	<	<i>rfbX</i>	<	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-	8.6	0.12
293230	prophage; DNA-binding protein	<i>yagL</i>	<	<i>yagM</i>	<	<i>yagN</i>	CP4-6 prophage; predicted pro	8.5	0.12
277970	omocysteine methyltransferase	<i>mmuM</i>	>	<i>afuC</i>	<	<i>afuB</i>	AfuB	8.5	0.12
3798032	V; probably hexose transferase	<i>waaK</i>	<	<i>rfaZ</i>	<	<i>waaY</i>	lipopolysaccharide core heptos	8.4	0.12
2993554	redicted protein	<i>ygeL</i>	<	<i>ygeM</i>	<	<i>ygeN</i>	predicted protein	8.3	0.12
296170	4-6 prophage; predicted protein	<i>yagN</i>	<	<i>intF</i>	<	<i>yagP</i>	predicted transcriptional regulat	8.1	0.12
676832	redicted protein	<i>ybeR</i>	>	<i>djIB</i>	<	<i>ybeT</i>	conserved outer membrane pro	7.9	0.13
4429942	alanine/glycine APC transporter	<i>cycA</i>	>	<i>ytfE</i>	<	<i>ytfF</i>	inner membrane protein	7.9	0.13
546150	ureidoglycolate dehydrogenase	<i>allD</i>	<	<i>fdrA</i>	>	<i>ylbE_1</i>	predicted protein, N-ter fragmen	7.9	0.13
280064	6 prophage; conserved protein	<i>yagB</i>	<		<	<i>yagA</i>	CP4-6 prophage; predicted DN	7.9	0.13
294834	4-6 prophage; predicted protein	<i>yagN</i>	<		<	<i>intF</i>	CP4-6 prophage; predicted pha	7.8	0.13
3800232	alpha-1,2-glucosyltransferase	<i>waaJ</i>	<	<i>waal</i>	<	<i>waaB</i>	UDP-D-galactose:(glucosyl)lipo	7.7	0.13
293040	6 prophage; conserved protein	<i>yagK</i>	<	<i>yagL</i>	<	<i>yagM</i>	CP4-6 prophage; predicted pro	7.7	0.13
2562360	55 prophage; predicted protein	<i>yffQ</i>	>	<i>yffR</i>	>	<i>yffS</i>	CPZ-55 prophage; predicted pr	7.7	0.13
1199836	phage exclusion; e14 prophage	<i>lit</i>	>	<i>intE</i>	<	<i>xisE</i>	e14 prophage; predicted excisio	7.6	0.13
3796640	O-antigen ligase	<i>rfaL</i>	>	<i>waaK</i>	<	<i>rfaZ</i>	protein involved in KdoIII attach	7.5	0.13
2101934	ynthesis protein, N-ter fragment	<i>wbbL_1</i>	<	<i>wbbK</i>	<	<i>wbbJ</i>	predicted acyl transferase	7.4	0.13

294432	4-6 prophage; predicted protein	<i>yagM</i>	<	<i>yagN</i>	<	<i>intF</i>	CP4-6 prophage; predicted pha	7.4	0.14
291460	4-6 prophage; predicted protein	<i>yagJ</i>	>		<	<i>yagK</i>	CP4-6 prophage; conserved pro	7.4	0.14
2104264	1,6-galactofuranosyltransferase	<i>wbbl</i>	<	<i>rfc</i>	<	<i>glf</i>	UDP-galactopyranose mutase	7.3	0.14
1596458	predicted lipoprotein	<i>ydeK</i>	<		<	<i>lsrK</i>	autoinducer-2 kinase	7.3	0.14
294332	4-6 prophage; predicted protein	<i>yagM</i>	<		<	<i>yagN</i>	CP4-6 prophage; predicted pro	7.2	0.14
576232	1 protein; locus of qsr prophage	<i>nmpC</i>	<		>	<i>essD</i>	DLP12 prophage; predicted pha	7.1	0.14
3802172	de-1,6-D-galactosyltransferase	<i>waaB</i>	<		<	<i>rfaS</i>	lipopolysaccharide core biosynt	7.1	0.14
1639072	phage; predicted S lysis protein	<i>essQ</i>	<		<	<i>cspB</i>	Qin prophage; cold shock prote	7.0	0.14
2767872	57 prophage; predicted protein	<i>yfjQ</i>	>	<i>yfjR</i>	>	<i>ypjK</i>	CP4-57 prophage; predicted inr	7.0	0.14
2467506	actoprenyl glucosyl transferase	<i>yfdH</i>	>	<i>yfdI</i>	>	<i>tfaS</i>	CPS-53 (KpLE1) prophage; tail	7.0	0.14
4444030	outer membrane protein	<i>ytfM</i>	>	<i>ytfN</i>	>	<i>ytfP</i>	conserved protein	7.0	0.14
4091072	FrvA	<i>frvA</i>	<		<	<i>rhaM</i>	L-rhamnose mutarotase	7.0	0.14
4620636	DeoD	<i>deoD</i>	>	<i>yjiJ</i>	<	<i>lplA</i>	lipoyl-protein ligase A	6.9	0.14
292530	6 prophage; conserved protein	<i>yagK</i>	<	<i>yagL</i>	<	<i>yagM</i>	CP4-6 prophage; predicted pro	6.9	0.15
287836	putative β-xylosidase	<i>yagH</i>	>	<i>yagI</i>	<	<i>argF</i>	ArgF	6.9	0.15
2382656	deubiquitinase	<i>elaD</i>	>	<i>yfbK</i>	>	<i>yfbL</i>	predicted peptidase	6.9	0.15
1637130	in prophage; cold shock protein	<i>cspi</i>	<	<i>ydfP</i>	<	<i>ydfQ</i>	Qin prophage; predicted lysozy	6.8	0.15
284342	phage; predicted lyase/synthase	<i>yagE</i>	>	<i>yagF</i>	>	<i>yagG</i>	YagG GPH Transporter	6.8	0.15
4093968	-phosphate aldolase monomer	<i>rhaD</i>	<	<i>rhaA</i>	<	<i>rhaB</i>	L-rhamnulose kinase	6.8	0.15
2556732	ammonia-lyase, α subunit	<i>eutB</i>	<		>	<i>intZ</i>	CPZ-55 prophage; predicted int	6.8	0.15
3800158	α-1,2-glucosyltransferase	<i>waaJ</i>	<	<i>waal</i>	<	<i>waaB</i>	UDP-D-galactose:(glucosyl)lipo	6.7	0.15
4568572	predicted transposase	<i>yjiQ</i>	>	<i>yjiR</i>	>	<i>yjiS</i>	conserved protein	6.7	0.15
2993746	predicted protein	<i>ygeM</i>	<		<	<i>ygeN</i>	predicted protein	6.7	0.15
2763154	57 prophage; predicted protein	<i>yfjL</i>	<		<	<i>yfjM</i>	CP4-57 prophage; predicted pr	6.7	0.15
2185930	predicted protein	<i>yohN</i>	>	<i>yehA</i>	<	<i>yehB</i>	putative outer membrane usher	6.6	0.15
284448	phage; predicted dehydratase	<i>yagF</i>	>		>	<i>yagG</i>	YagG GPH Transporter	6.6	0.15
2472336	E1) prophage; predicted protein	<i>yfdP</i>	>	<i>yfdQ</i>	>	<i>yfdR</i>	CPS-53 (KpLE1) prophage; ded	6.6	0.15
1644936	Qin prophage; predicted protein	<i>flxA</i>	>		<	<i>ydfW</i>	Qin prophage; predicted proteir	6.5	0.15
2190388	ted fimbrial-like adhesin protein	<i>yehD</i>	<		<	<i>yehE</i>	predicted protein	6.5	0.15
3095868		<i>rdgB</i>	>	<i>yggW</i>	<	<i>yggM</i>	conserved protein	6.4	0.16
2464466	tRNA^{argW}	<i>argW</i>	>		>	<i>intS</i>	CPS-53 (KpLE1) prophage; pro	6.4	0.16
2558668	5 prophage; predicted integrase	<i>intZ</i>	>	<i>yffL</i>	>	<i>yffM</i>	CPZ-55 prophage; predicted pr	6.4	0.16
1647062	Qin prophage; predicted protein	<i>rzpQ</i>	>		>	<i>dicF</i>	Qin prophage; DicF antisense F	6.3	0.16
575258		<i>insH-2</i>	<	<i>nmpC</i>	>	<i>essD</i>	DLP12 prophage; predicted pha	6.3	0.16
2559738	55 prophage; predicted protein	<i>yffM</i>	>	<i>yffN</i>	>	<i>yffO</i>	CPZ-55 prophage; predicted pr	6.3	0.16
4570170	conserved protein	<i>yjiS</i>	>		>	<i>yjiT</i>	conserved protein	6.2	0.16
295350	4-6 prophage; predicted protein	<i>yagN</i>	<	<i>intF</i>	<	<i>yagP</i>	predicted transcriptional regulat	6.2	0.16
4572350	conserved protein	<i>yjiT</i>	>	<i>yjiV</i>	<	<i>mcrC</i>	MrcC subunit of 5-methylcytosin	6.2	0.16
3359930	tamate synthase, small subunit	<i>gltD</i>	>	<i>gltF</i>	>	<i>yhxA</i>	predicted periplasmic chaperon	6.1	0.16
127764	droilipoamide acetyltransferase	<i>aceF</i>	>		>	<i>lpd</i>	E3 monomer	6.1	0.16
2882562	Cascade subunit A	<i>casA</i>	<		<	<i>cas3</i>	predicted fused HD nuclease a	6.1	0.17
2779238	ypjF-YfjZ toxin-antitoxin system	<i>ypjF</i>	>	<i>ypjA</i>	<	<i>pinH</i>	predicted invertase fragment	6.0	0.17
4089562	frv operon protein	<i>frvX</i>	<	<i>frvB</i>	<	<i>frvA</i>	FrvA	6.0	0.17
2601070	hydrogenase 4, component A	<i>hyfA</i>	>	<i>hyfB</i>	>	<i>hyfC</i>	hydrogenase 4, component C	6.0	0.17
1463152	peptide repeat acetyltransferase	<i>paaY</i>	>		<	<i>ynbG</i>	small protein	5.9	0.17
3801168	α-1,3-glucosyltransferase	<i>waal</i>	<	<i>waaB</i>	<	<i>rfaS</i>	lipopolysaccharide core biosynt	5.8	0.17
294172	4-6 prophage; predicted protein	<i>yagM</i>	<		<	<i>yagN</i>	CP4-6 prophage; predicted pro	5.7	0.17
4435856),5'-bisphosphate nucleotidase	<i>cysQ</i>	>	<i>ytfI</i>	<	<i>ytfJ</i>	conserved protein	5.7	0.18
4570068	conserved protein	<i>yjiS</i>	>		>	<i>yjiT</i>	conserved protein	5.7	0.18
2070240	IsrC small RNA	<i>isrC</i>	>	<i>flu</i>	>	<i>yeeR</i>	CP4-44 prophage; predicted me	5.6	0.18
293632	prophage; DNA-binding protein	<i>yagL</i>	<	<i>yagM</i>	<	<i>yagN</i>	CP4-6 prophage; predicted pro	5.6	0.18
4313832	-CoA N-acyltransferase domain	<i>phnO</i>	<	<i>phnN</i>	<	<i>phnM</i>	ATP-binding component of pho	5.6	0.18
2103554	predicted acyl transferase	<i>wbbJ</i>	<	<i>wbbl</i>	<	<i>rfc</i>	O-antigen polymerase	5.6	0.18
789330	galactokinase	<i>galK</i>	<	<i>galT</i>	<	<i>galE</i>	UDP-glucose 4-epimerase mon	5.5	0.18
2031954	of OmpA and OmpC expression	<i>rseX</i>	>		>	<i>yedS_1</i>	predicted protein, N-ter fragmen	5.5	0.18
2993634	predicted protein	<i>ygeL</i>	<	<i>ygeM</i>	<	<i>ygeN</i>	predicted protein	5.5	0.18
2879966	Cascade subunit D	<i>casD</i>	<	<i>casC</i>	<	<i>casB</i>	Cascade subunit B	5.5	0.18
2108132	polysaccharide PST transporter	<i>rfbX</i>	<	<i>rfbC</i>	<	<i>rfbA</i>	dTDP-glucose pyrophosphoryla	5.4	0.18
292040	4-6 prophage; predicted protein	<i>yagJ</i>	>	<i>yagK</i>	<	<i>yagL</i>	CP4-6 prophage; DNA-binding	5.4	0.18
2882356	Cascade subunit A	<i>casA</i>	<		<	<i>cas3</i>	predicted fused HD nuclease a	5.4	0.19
2185770	predicted protein	<i>yohN</i>	>	<i>yehA</i>	<	<i>yehB</i>	putative outer membrane usher	5.4	0.19
1588350	predicted protein	<i>ydeT</i>	<		<	<i>yneL</i>	predicted transcriptional regulat	5.4	0.19

3800334	alpha;-1,2-glucosyltransferase	<i>waaJ</i>	<	<i>waal</i>	<	<i>waaB</i>	UDP-D-galactose:(glucosyl)lipo	5.4	0.19
2386672	predicted protein	<i>yfbN</i>	<	<i>yfbO</i>	>	<i>yfbP</i>	predicted protein	5.4	0.19
2885168	Cascade subunit A	<i>casA</i>	<	<i>cas3</i>	>	<i>sokX</i>	SokX	5.3	0.19
3805730	accharide glucosyltransferase I	<i>waaG</i>	<	<i>waaQ</i>	>	<i>waaA</i>	KDO transferase	5.3	0.19
2234632	imidine dehydrogenase subunit	<i>yeiA</i>	>		<	<i>mgIC</i>	MgIC	5.2	0.19
2755760	CP4-57 prophage; integrase	<i>intA</i>	>	<i>yfjH</i>	>	<i>alpA</i>	AlpA transcriptional activator; C	5.2	0.19
1470046	transposase of IS30	<i>insI-2</i>	>	<i>ydbA_2</i>	>	<i>ydbC</i>	predicted oxidoreductase, NAD	5.2	0.19
2992670	peptidoglycan-binding enzyme	<i>pbl</i>	>	<i>ygeK</i>	<	<i>ygeL</i>	predicted protein	5.2	0.19
1468846	transposase of IS30	<i>insI-2</i>	>	<i>ydbA_2</i>	>	<i>ydbC</i>	predicted oxidoreductase, NAD	5.2	0.19
296234	4-6 prophage; predicted protein	<i>yagN</i>	<	<i>intF</i>	<	<i>yagP</i>	predicted transcriptional regulat	5.2	0.19
636048	conserved protein	<i>ybdN</i>	<	<i>ybdO</i>	<	<i>dsbG</i>	DsbG_{reduced}	5.2	0.19
2765266	CP4-57 prophage; RNase LS	<i>rnlA</i>	>	<i>yfjO</i>	>	<i>yfjP</i>	CP4-57 prophage; predicted G	5.2	0.19
3416664	ted outer membrane lipoprotein	<i>yhdV</i>	>		>	<i>yhdW</i>	YhdW	5.2	0.19
1095368	predicted protein	<i>ymdE</i>	>	<i>ycdU</i>	<	<i>serX</i>	tRNA^{serX}	5.2	0.19
1643734	be the repressor activity of RelB	<i>relE</i>	<	<i>relB</i>	>	<i>ydfV</i>	Qin prophage; predicted protei	5.1	0.19
1635936	Qin prophage; predicted protein	<i>gnsB</i>	<		<	<i>ynfN</i>	Qin prophage; predicted protei	5.1	0.20
3796746	O-antigen ligase	<i>rfaL</i>	>	<i>waaK</i>	<	<i>rfaZ</i>	protein involved in KdoIII attach	5.1	0.20
2992436	peptidoglycan-binding enzyme	<i>pbl</i>	>		<	<i>ygeK</i>	predicted DNA-binding transcrip	5.1	0.20
2765354	57 prophage; predicted protein	<i>yfjO</i>	>		>	<i>yfjP</i>	CP4-57 prophage; predicted G	5.1	0.20
238730	C0067 small RNA	<i>C0067</i>	>		<	<i>yafU</i>	predicted inner membrane prote	5.0	0.20
2387730	predicted protein	<i>yfbO</i>	>	<i>yfbP</i>	<	<i>nuoN</i>	NADH:ubiquinone oxidoreducta	5.0	0.20
2988170	small protein	<i>yqeL</i>	<	<i>yqeK</i>	>	<i>ygeF</i>	predicted protein	5.0	0.20
927556	alanyl-tRNA-protein transferase	<i>aat</i>	<	<i>cydC</i>	<	<i>cydD</i>	CydD	5.0	0.20
2102040	ynthesis protein, N-ter fragment	<i>wbbL_1</i>	<	<i>wbbK</i>	<	<i>wbbJ</i>	predicted acyl transferase	5.0	0.20
3806064	accharide glucosyltransferase I	<i>waaG</i>	<	<i>waaQ</i>	>	<i>waaA</i>	KDO transferase	4.9	0.20
2559956	55 prophage; predicted protein	<i>yffM</i>	>	<i>yffN</i>	>	<i>yffO</i>	CPZ-55 prophage; predicted pr	4.9	0.20
3806372	de core heptosyl transferase III	<i>waaQ</i>	<		>	<i>waaA</i>	KDO transferase	4.9	0.20
2562046	55 prophage; predicted protein	<i>yffQ</i>	>	<i>yffR</i>	>	<i>yffS</i>	CPZ-55 prophage; predicted pr	4.9	0.20
2189932	putative fimbrial chaperone	<i>yehC</i>	<	<i>yehD</i>	<	<i>yehE</i>	predicted protein	4.9	0.20
2105234	O-antigen polymerase	<i>rfc</i>	<		<	<i>glf</i>	UDP-galactopyranose mutase	4.9	0.20
2988770	predicted protein	<i>yqeK</i>	<	<i>ygeF</i>	>	<i>ygeG</i>	predicted chaperone	4.9	0.20
3036248	RecJ	<i>recJ</i>	<	<i>dsbC</i>	<	<i>xerD</i>	site-specific recombinase	4.9	0.20
1471130	transposase of IS30	<i>insI-2</i>	>	<i>ydbA_2</i>	>	<i>ydbC</i>	predicted oxidoreductase, NAD	4.9	0.20
3700368	YhjV STP transporter	<i>yhjV</i>	>	<i>dppF</i>	<	<i>dppD</i>	DppD	4.9	0.21
2559840	55 prophage; predicted protein	<i>yffM</i>	>	<i>yffN</i>	>	<i>yffO</i>	CPZ-55 prophage; predicted pr	4.9	0.21
2106830	UDP-galactopyranose mutase	<i>glf</i>	<	<i>rfbX</i>	<	<i>rfbC</i>	dTDP-4-dehydroorhamnose 3,5-	4.8	0.21
582934	12 prophage; predicted protein	<i>tfaX</i>	>	<i>appY</i>	<	<i>ompT</i>	outer membrane protease VII (c	4.8	0.21
1991670	idylglycerophosphate synthase	<i>pgsA</i>	<	<i>uvrC</i>	<	<i>uvrY</i>	UvrY transcriptional regulator	4.8	0.21
3360048	periplasmic protein	<i>glTF</i>	>		>	<i>yhcA</i>	predicted periplasmic chaperon	4.8	0.21
238854	C0067 small RNA	<i>C0067</i>	>	<i>yafU</i>	>	<i>yafF</i>	conserved protein	4.8	0.21
2558970	55 prophage; predicted protein	<i>yffL</i>	>		>	<i>yffM</i>	CPZ-55 prophage; predicted pr	4.8	0.21
2838064	AscG transcriptional repressor	<i>ascG</i>	<	<i>ascF</i>	>	<i>ascB</i>	6-phospho-β-glucosidase;	4.8	0.21
2878270	predicted integrase	<i>cas1</i>	<	<i>casE</i>	<	<i>casD</i>	Cascade subunit D	4.7	0.21
292656	6 prophage; conserved protein	<i>yagK</i>	<	<i>yagL</i>	<	<i>yagM</i>	CP4-6 prophage; predicted pro	4.7	0.21
4057356	GlnA	<i>glnA</i>	<	<i>typA</i>	>	<i>yihL</i>	YihL putative transcriptional reg	4.7	0.21
2878936	crRNA endonuclease	<i>casE</i>	<	<i>casD</i>	<	<i>casC</i>	Cascade subunit C	4.7	0.21
2988240	small protein	<i>yqeL</i>	<	<i>yqeK</i>	>	<i>ygeF</i>	predicted protein	4.6	0.22
291064		<i>insA-3</i>	<	<i>yagJ</i>	<	<i>yagK</i>	CP4-6 prophage; conserved pro	4.6	0.22
2406734	hA transcriptional dual regulator	<i>lrhA</i>	<	<i>yfbQ</i>	>	<i>yfbR</i>	dCMP phosphohydrolase	4.6	0.22
2467692	actoprenyl glucosyl transferase	<i>yfdH</i>	>	<i>yfdI</i>	>	<i>tfaS</i>	CPS-53 (KpLE1) prophage; tail	4.6	0.22
1633262	icted tail fibre assembly protein	<i>tfaQ</i>	<	<i>ydfN</i>	<	<i>nohA</i>	Qin prophage; predicted packag	4.6	0.22
2101034		<i>insH-7</i>	<	<i>wbbL_1</i>	<	<i>wbbK</i>	predicted lipopolysaccharide bi	4.6	0.22
673772	rare lipoprotein LptE	<i>lptE</i>	<	<i>leuS</i>	>	<i>ybeL</i>	conserved protein	4.6	0.22
2763338	57 prophage; predicted protein	<i>yfjL</i>	<		<	<i>yfjM</i>	CP4-57 prophage; predicted pr	4.6	0.22
2558062	5 prophage; predicted integrase	<i>intZ</i>	>		>	<i>yffL</i>	CPZ-55 prophage; predicted pr	4.6	0.22
4436036),5'-bisphosphate nucleotidase	<i>cysQ</i>	>	<i>ytfI</i>	<	<i>ytfJ</i>	conserved protein	4.5	0.22
2103932	predicted acyl transferase	<i>wbbJ</i>	<	<i>wbbI</i>	<	<i>rfc</i>	O-antigen polymerase	4.5	0.22
2101836	ynthesis protein, N-ter fragment	<i>wbbL_1</i>	<	<i>wbbK</i>	<	<i>wbbJ</i>	predicted acyl transferase	4.5	0.22
292260	6 prophage; conserved protein	<i>yagK</i>	<		<	<i>yagL</i>	CP4-6 prophage; DNA-binding	4.5	0.22
2988054	small protein	<i>yqeL</i>	<	<i>yqeK</i>	>	<i>ygeF</i>	predicted protein	4.5	0.22
3801248	alpha;-1,3-glucosyltransferase	<i>waal</i>	<	<i>waaB</i>	<	<i>rfaS</i>	lipopolysaccharide core biosynt	4.5	0.22
3798254	lysaccharide core biosynthesis	<i>rfaZ</i>	<		<	<i>waaY</i>	lipopolysaccharide core heptos	4.5	0.22

2252332	rimidine nucleoside transporter	<i>nupX</i>	<	<i>rihB</i>	>	<i>yeiL</i>	YeiL transcriptional activator	4.5	0.22
2140654	Dcd	<i>dcd</i>	<	<i>udk</i>	>	<i>yegE</i>	predicted diguanylate cyclase	4.5	0.22
2385530	predicted protein	<i>yfbM</i>	>		<	<i>yfbN</i>	predicted protein	4.4	0.22
265132	CP4-6 prophage; predicted protein	<i>ykfF</i>	<	<i>ykfB</i>	<	<i>yafY</i>	CP4-6 prophage; inner membrane	4.4	0.23
3805672	disaccharide glucosyltransferase I	<i>waaG</i>	<	<i>waaQ</i>	>	<i>waaA</i>	KDO transferase	4.4	0.23
2987942	small protein	<i>yqeL</i>	<		<	<i>yqeK</i>	predicted protein	4.4	0.23
798130	6-phosphofructose 1,6-bisphosphatase	<i>ybhA</i>	<	<i>pgl</i>	<	<i>ybhD</i>	predicted DNA-binding transcription factor	4.4	0.23
280360	CP4-6 prophage; conserved protein	<i>yagB</i>	<	<i>yagA</i>	>	<i>yagE</i>	CP4-6 prophage; predicted lysin	4.4	0.23
2069334	predicted GTP-binding protein	<i>yeeP</i>	>		>	<i>isrC</i>	IsrC small RNA	4.4	0.23
1643558	CP4-6 prophage; small toxic polypeptide	<i>hokD</i>	<	<i>relE</i>	<	<i>relB</i>	RelB Qin prophage; antitoxin of	4.4	0.23
2878344	predicted integrase	<i>cas1</i>	<	<i>casE</i>	<	<i>casD</i>	Cascade subunit D	4.4	0.23
3800548	UDP-galactose 4-epimerase	<i>waaJ</i>	<	<i>waal</i>	<	<i>waaB</i>	UDP-D-galactose:(glucosyl)lipid	4.3	0.23
2987772	predicted transcriptional regulator	<i>yqeI</i>	>	<i>yqeJ</i>	<	<i>yqeL</i>	small protein	4.3	0.23
3803540	lipopolysaccharide core biosynthesis protein	<i>rfaS</i>	<	<i>waaP</i>	<	<i>waaG</i>	lipopolysaccharide glucosyltransferase	4.3	0.23
2107634	polysaccharide PST transporter	<i>rfbX</i>	<		<	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	4.3	0.23
2385772	predicted protein	<i>yfbM</i>	>	<i>yfbN</i>	>	<i>yfbO</i>	predicted protein	4.3	0.23
2763272	CP4-57 prophage; predicted protein	<i>yfjL</i>	<		<	<i>yfjM</i>	CP4-57 prophage; predicted protein	4.3	0.23
2755870	CP4-57 prophage; integrase	<i>intA</i>	>	<i>yfjH</i>	>	<i>alpA</i>	AlpA transcriptional activator; C	4.3	0.24
586152	EnvY transcriptional activator	<i>envY</i>	<		<	<i>ybcH</i>	predicted protein	4.3	0.24
2107730	polysaccharide PST transporter	<i>rfbX</i>	<	<i>rfbC</i>	<	<i>rfbA</i>	dTDP-glucose pyrophosphorylase	4.2	0.24
3800958	UDP-galactose 4-epimerase	<i>waaJ</i>	<	<i>waal</i>	<	<i>waaB</i>	UDP-D-galactose:(glucosyl)lipid	4.2	0.24
576360	phage protein; locus of qsr prophage	<i>nmpC</i>	<		>	<i>essD</i>	DLP12 prophage; predicted phage	4.2	0.24
273772	CP4-6 prophage; conserved protein	<i>ykfC</i>	>	<i>insH-1</i>	>	<i>mmuP</i>	MmuP APC transporter	4.2	0.24
1646036	transcriptional regulator for DicB	<i>dicC</i>	<	<i>dicA</i>	>	<i>ydfA</i>	Qin prophage; predicted protein	4.2	0.24
3803124	lipopolysaccharide core biosynthesis protein	<i>rfaS</i>	<		<	<i>waaP</i>	lipopolysaccharide core heptose	4.2	0.24
1461572	phenylacetate-CoA ligase	<i>paaK</i>	>		>	<i>paaX</i>	PaaX	4.2	0.24
4395832	muramoyl-L-alanine amidase 2	<i>amiB</i>	>	<i>mutL</i>	>	<i>miaA</i>	tRNA(i⁶A37) synthetase	4.2	0.24
1599036	autoinducer-2 kinase	<i>lsrK</i>	<	<i>lsrR</i>	>	<i>lsrA</i>	LsrA	4.2	0.24
1644664	Qin prophage; predicted protein	<i>ydfV</i>	>	<i>flxA</i>	<	<i>ydfW</i>	Qin prophage; predicted protein	4.1	0.24
58658	chaperone with DnaK	<i>djlA</i>	>	<i>yabP</i>	>	<i>yabQ</i>	predicted protein	4.1	0.24
1645350	Qin prophage; predicted protein	<i>ydfW</i>	<		<	<i>ydfX</i>	Qin prophage; predicted protein	4.1	0.24
3796534	O-antigen ligase	<i>rfaL</i>	>	<i>waaK</i>	<	<i>rfaZ</i>	protein involved in KdoIII attachment	4.1	0.24
3780254	predicted rRNA methylase	<i>yibK</i>	>	<i>cysE</i>	<	<i>gpsA</i>	GpsA	4.1	0.24
4570370	conserved protein	<i>yjiS</i>	>		>	<i>yjiT</i>	conserved protein	4.1	0.24
1633630	predicted tail fibre assembly protein	<i>tfaQ</i>	<	<i>ydfN</i>	<	<i>nohA</i>	Qin prophage; predicted packaging	4.1	0.25
690530	polipoprotein N-acyltransferase	<i>Int</i>	<	<i>ybeX</i>	<	<i>ybeY</i>	conserved protein involved in trans	4.1	0.25
2092660		<i>hisB</i>	>	<i>hisH</i>	>	<i>hisA</i>	N-(5'-phospho-L-ribosyl)-formimidate	4.0	0.25
4476964	phosphonuclease E inhibitor protein B	<i>rraB</i>	>		>	<i>yjgM</i>	predicted acetyltransferase	4.0	0.25
2988370	predicted protein	<i>yqeK</i>	<		>	<i>ygeF</i>	predicted protein	4.0	0.25
2845070	hydrogenase 3, large subunit	<i>hycE</i>	<	<i>hycD</i>	<	<i>hycC</i>	hydrogenase 3, membrane subunit	4.0	0.25
3799872	lipopolysaccharide core heptose (II) kinase	<i>waaY</i>	<	<i>waaJ</i>	<	<i>waal</i>	UDP-D-glucose:(glucosyl)LPS kinase	4.0	0.25
2763970	CP4-57 prophage; predicted protein	<i>yfjM</i>	<	<i>rmlA</i>	>	<i>yfjO</i>	CP4-57 prophage; predicted protein	4.0	0.25
2387644	predicted protein	<i>yfbO</i>	>	<i>yfbP</i>	<	<i>nuoN</i>	NADH:ubiquinone oxidoreductase	4.0	0.25

Chip-chip assay was performed for *E. coli* K-12 wild-type and its *rpoZ*-defective mutant strains. After tiling array analysis, the level of RNAP binding was compared between two strains. The ratio between the binding of RpoZ-defective RNAP and that of wild-type RNAP was calculated for the entire probe along the genome. This value is aligned in the increasing order in the *rpoZ* column (shown in bold). Top 31 genes of low-level distribution of the RpoZ-defective RNAP are described in Table 2.