Supplemental Table S4A

Position	Function	Left gene	D		D	Righ Gene	Function
41946	carnitine BCCT transporter	caiT	<		>	fixA	flavoprotein for anaerobic carnitine reduction
121966	Phe/Tyr/Trp APC transporter	aroP	<		>	pdhR	pyruvate dehydrogenase complex regulator
141230	glucose dehydrogenase	gcd	<		>	hpt	hypoxanthine-Gua phosphoribosyltransferase
243432	acyl-CoA dehydrogenase	fadE	<		>	lpcA	D-sedoheptulose 7-phosphate isomerase
328672	betaine operon transcriptional repressor	betI	<		>	betT	choline BCCT transporter
398634	inner membrane protein	yaiY	<		>	yaiZ	inner membrane protein
450964	cytochrome *bo* terminal oxidase	cyoA	<		>	ampG	muropeptide MFS transporter
478570	inner membrane protein	ylaC	<		<	maa	maltose acetyltransferase
629042	thioesterase for enterobactin biosynthesis	entH	>		>	cstA	peptide transporter
651244	citrate lyase synthetase	citC	<		>	dpiB	DpiBA TCS sensory histidine kinase
655330	DcuC dicarboxylate transporter	dcuC	<		>	pagP	lipid palmitoyltransferase
728256	K+ ion accessory transporter	kdpF	<		>	ybfA	predicted protein
741852	peptide POT Transporter	dtpD	<		>	ybgI	metal-binding hydrolase-oxidase
754030	citrate synthase monomer	gltA	<		>	sdhC	succinate dehydrogenase
770038	alpha-mannosidase	mngB	>		>	cydA	cytochrome *bd* terminal oxidase
840966	catecholate siderophore receptor	fiu	<		<	mcbA	protein involved in colanic acid production
847534	glutamine transporter	glnH	<		<	dps	stationary phase nucleoid iron-binding protein
953940	formate FNT transporter	focA	<		<	ycaO	conserved protein
996834	NAD(P)H-dependent FMN reductase	ssuE	<		>	ycbQ	fimbrial-like adhesin protein
1073354	pyrimidine oxygenase	rutA	<		>	rutR	pyrimidine/purine operon regulator
1084156	heme-containing peroxidase/deferrochelatase	efeB	>		>	phoH	ATP-binding protein
1165242	conserved protein	ycfP	>		>	ndh	NADH:ubiquinone oxidoreductase II
1194272	23S rRNA pseudouridine 2457 synthase	rluE	<		>	icd	isocitrate dehydrogenase
1236756	conserved protein	ycgB	<		>	dadA	D-amino acid dehydrogenase
1359040	glutamate-putrescine ligase	puuA	<		>	puuD	glutamyl-aminobutyrate hydrolase
1402642	*p*-aminobenzoyl-glutamate hydrolase	abgA	<		>	abgR	*p*-aminobenzoyl glutamate operon regulator
1445370	PEA operon transcriptional activator	feaR	<		>	feaB	phenylacetaldehyde dehydrogenase
1451850	oxepin-CoA hydrolase/CoA semialdehyde dehydrogenase	paaZ	<		>	paaA	ring 1,2-phenylacetyl-CoA epoxidase
1486148	conserved protein	ydcF	>		>	aldA	aldehyde dehydrogenase A
1493146	stress-response transcriptional regulator	ydcI	<		>	ydcJ	conserved protein
1561234	D-Ala-D-Ala dipeptidase	ddpX	<		<	dosP	c-di-GMP phosphodiesterase
1684632	fumarase C monomer	fumC	<		<	fumA	fumarase A monomer
1830072	acetylornithine delta-aminotransferase	astC	<		>	xthA	exonuclease III
1887768	acyl-CoA synthetase	fadD	<		<	yeaY	predicted lipoprotein
1977670	IS1 repressor	insA-5	<		>	uspC	universal stress protein
2102542	lipopolysaccharide biosynthesis protein	wbbK	<		<	wbbJ	predicted acyl transferase
2190388	fimbrial-like adhesin protein	yehD	<		<	yehE	predicted protein
2276340	predicted protein	yejG	<		<	bcr	multidrug MFS transporter
2304934	malate:quinone oxidoreductase	mqo	<		<	yojI	multidrug ABC superfamily transporter
2311260	antisense regulator sRNA for *ompF* synthesis	micF	>		>	rcsD	RcsD phosphotransferase
2384870	predicted peptidase	yfbL	>		>	yfbM	predicted protein
2403250	NADH:ubiquinone oxidoreductase	nuoA	<		<	lrhA	type-1 bimbriae operon regulator
2425944	Lys/Arg/ornithine transporter	argT	<		<	ubiX	flavin prenyltransferase
2576570	NADP-dependent malic enzyme	maeB	<		>	talA	transaldolase A
2643032	nucleoside diphosphate kinase	ndk	<		<	pbpC	peptidoglycan glycosyltransferase
2667070	HcaR transcriptional dual regulator	hcaR	<		>	hcaE	3-phenylpropionate dioxygenase
2723936	alpha-ketoglutarate MFS transporter	kgtP	<		<	rrfG	*rrfG* 5S ribosomal RNA
2786834	conserved protein	ygaQ	>		>	csiD	carbon starvation-induced protein
2983750	predicted acyltransferase	yqeF	<		>	yqeG	hydroxy/aromatic amino acid STP transporter
3126130	glycolate oxidase	glcD	<		>	glcC	glycolate operon regulator
3217432	aerotaxis sensor receptor flavoprotein	aer	<		>	ygjG	putrescine aminotransferase
3237758	membrane-bound redox modulator	alx	>		>	sstT	serine/threonine:Na+ symporter
3382536	malate dehydrogenase	mdh	<		>	argR	Arg/His operon regulator
3479338	K+-effulux ancillary protein	kefG	<		>	yheS	ABC superfamily transporter
3537960	transcriptional accessory protein	yhgF	>		>	feoA	ferrous iron transport
3590444	glycerol-3-phosphate transporter	ugpB	<		<	livF	branched chain amino acid ABC transporter
3656246	acid-resistance membrane protein	hdeD	>		>	gadE	glutamic acid operon transcriptional activator
3664032	GadX transcriptional dual regulator	gadX	<		<	gadA	glutamate decarboxylase A
3710232	oxalatae-formate MFS antiporter	yhjX	<		<	yhjY	putative lipase
3775254	conserved protein	yibL	>		>	lldP	dilactate/glycolate:H+ symporter
3921034	ATP-proton motive force interconversion	atpI	<		<	rsmG	16S rRNA G527 methyltransferase
4002730	conserved protein	yigI	<		>	pldA	phospholipase A1
4029138	3-hydroxybutyryl-CoA epimerase	fadB	<		>	pepQ	proline dipeptidase
4158830	pyridine nucleotide transhydrogenase	sthA	<		>	fabR	fatty acid biosynthesis operon regulator
4213436	homoserine O-succinyltransferase	metA	>		>	aceB	malate synthase A
4285548	acetyl-CoA synthetase	acs	<		>	nrfA	cytochrome C552
4323268	phosphonate ABC transporter	phnC	<		<	yjdN	conserved protein
4360056	CadC transcriptional activator	cadC	<		<	pheU	tRNA-Phe
4364850	dicarboxylate transporter	dcuA	<		<	aspA	aspartate ammonia-lyase

Total no. binding sites 69

Total no. regulatory targets 102

Supplemental Table S4B

Position	**Function**	***Gene***	**D**	**No**	**AI2**	**D**	***Gene***	**Function**
34072	carbamoyl-phosphate synthase	***carB***	**>**		🟧	**>**	***caiF***	carnitine operon regulator
264544	CP4-6 prophage protein	***yafX***	<	🟧		<	***ykfF***	CP4-6 prophage protein
313130	*rpmJ* (L36) paralog	***ykgM***	<	🟧	🟧	>	***insE***	IS3 element protein *InsE*
354170	propionyl-CoA synthetase	***prpE***	>	🟧		>	***codB***	cytosine transporter
407866	conserved protein	***yaiE***	>	🟧		<	***rdgC***	nucleoid-binding RecA regulator
527330	predicted protein	***ybbC***	>	🟧		<	***ybbB***	tRNA 2-selenouridine synthase
558062	fimbrial-like adhesin protein	***sfmA***	**>**		🟧	**>**	***sfmC***	pilin chaperone
636838	DNA-binding transcriptional regulator	***ybdO***	<	🟧	🟧	<	***dsbG***	periplasmic disulfide isomerase
660856	DNA-binding transcriptional regulator	***ybeF***	**<**		🟧	**<**	***lipB***	lipoyl-protein ligase
688452	IS5 transposase and trans-activator	***insH***	**<**		🟧	**<**	***lnt***	apolipoprotein N-acyltransferase
707052	glutamyl-tRNA synthetase	***glnS***	**>**		🟧	**>**	***ybfM***	outer membrane porin
728772	predicted protein	***ybfA***	>	🟧		>	***rhsC***	*rhsC* element core protein RshC
1084156	conserved protein	***efeB***	>	🟧	🟧	>	***phoH***	nucleoside triphosphate hydrolase
1200736	e14 prophage excisionase	***xisE***	<	🟧	🟧	>	***ymfI***	e14 prophage protein
1314070	predicted protein	***yciG***	<	🟧	🟧	<	***trpA***	tryptophan synthase
1332842	Cys synthesis operon regulator	***cysB***	>	🟧	🟧	>	***ymiA***	hypothetical protein
1342734	hypothetical protein	***yciZ***	<	🟧		<	***gmr***	modulator of RNase II stability
1926870	protease II	***ptrB***	<	🟧		<	***yebE***	conserved protein
2020940	flagellar biosynthesis protein	***fliQ***	**>**		🟧	**>**	***fliR***	flagellar export pore protein
2032840	ncRNA	***rseX***	**>**		🟧	**>**	***hchA***	Hsp31 molecular chaperone
2065942	IS5 transposase and trans-activator	***insH***	<	🟧		<	***insD***	KpLE2 IS2 insertion element transposase
2105234	O-antigen polymerase	***rfc***	**<**		🟧	**<**	***glf***	UDP-galactopyranose mutase
2175434	D-tagatose 1,6-bisphosphate aldolase 2	***gatY***	**<**		🟧	**<**	***fbaB***	fructose-bisphosphate aldolase class I
2331448	predicted protein	***yfaQ***	<	🟧		<	***yfaT***	predicted protein
2594748	conserved protein	***ypfJ***	<	🟧		<	***purC***	ribosylimidazole-succinocarboxamide synthase
2773032	CP4-57 prophage inner membrane protein	***yfjW***	**>**		🟧	**>**	***yfjX***	CP4-57 prophage antirestriction protein
2802570	ribonucleoside-diphosphate reductase 2	***nrdF***	**>**		🟧	**>**	***proV***	glycine betaine transporter subunit
2992436	pathogenesis-related protein	***ygeI***	>	🟧		<	***insD***	KpLE2 phage IS2 transposase
3110762	secretion pathway M-type protein	***yghD***	<	🟧		<	***yghG***	predicted protein
3132050	nucleoside triphosphate hydrolase domain	***yghS***	<	🟧	🟧	>	***yghT***	ATP-binding NTP hydrolase
3144758	predicted protein	***yghW***	<	🟧	🟧	>	***yghZ***	aldo-keto reductase
3517370	shikimate kinase I	***aroK***	**<**		🟧	**<**	***hofQ***	predicted fimbrial transporter
3537860	radiation-response translation control	***yhgF***	>	🟧	🟧	>	***feoA***	ferrous iron transporter
3597672	leucine/isoleucine/valine transportert	***livJ***	<	🟧		<	***rpoH***	RNA polymerase, sigma 32 (sigma H)
3664032	GAD-depend acid resistance regulator	***gadX***	<	🟧	🟧	<	***gadA***	glutamate decarboxylase A
3976654	acetamino-dideoxy-galactose transferase	***rffT***	>	🟧		>	***wzyE***	ECA polysaccharide chain elongation protein
4148470	inner membrane protein	***yijP***	<	🟧		<	***ppc***	phosphoenolpyruvate carboxylase
4151358	phosphoenolpyruvate carboxylase	***ppc***	**<**		🟧	**<**	***argE***	acetylornithine deacetylase
4166466	Glu tRNA	***gltT***	**>**		🟧	**>**	***rrlB***	23S ribosomal RNA of rrnB operon
4207870	Glu tRNA	***gltV***	**>**		🟧	**>**	***rrlE***	23S ribosomal RNA of *rrnE* operon
4259732	predicted protein	***yjbM***	>	🟧		>	***dusA***	tRNA-dihydrouridine synthase A
4267172	hypothetical protein	***yjbS***	<	🟧	🟧	>	***aphA***	acid phosphatase/phosphotransferase
			Total no. binding sites	**27**	**26**			
			Total no. regulatory targets	**38**	**37**			

Supplemental Table S4C

Position	**Function**	***Gene***	**D**		**D**	***Gene***	**Function**
19830	InsAB transposase	***insAB-1***	<		<	***insB-1***	IS1 protein InsB
384316	conserved protein	***yaiS***	<		>	***tauA***	taurine ABC transporter
582848	DLP12 prophage protein	***tfaX***	>		>	***appY***	DNA binding transcriptional activator
584962	outer membrane protease VII	***ompT***	<		<	***envY***	EnvY transcriptional activator
886556	predicted transporter	***ybjJ***	<		>	***rcdA***	DNA-binding transcriptional regulator
1020144	SOS cell division inhibitor	***sulA***	<		>	***sxy***	transcriptional coactivator for CRP
1102554	transcriptional dual regulator	***csgD***	<		>	***csgB***	curlin, minor subunit precursor
1104940	predicted protein	***ymdA***	>		>	***ymdB***	regulator of RNase III activity
1209454	e14 site-specific DNA recombinase	***pinE***	>		>	***mcrA***	restriction at 5-methylcytosine residues
1214962	blue light-responsive regulator of YcgE	***ycgF***	<		>	***ycgZ***	predicted protein
1321242	*trp* operon leader peptide	***trpL***	<		>	***yciV***	conserved protein
1622770	stress response protein	***ydeI***	<		>	***ydeJ***	conserved protein
1631666	Qin prophage transcriptional regulator	***ydfK***	>		>	***pinQ***	Qin prophage site-specific recombinase
1638666	Qin prophage S lysis protein	***essQ***	<		<	***cspB***	Qin cold shock transcriptional regulator
1669136	MFS transporter	***ynfM***	>		>	***asr***	acid shock protein
1669932	small membrane protein	***ydgU***	>		>	***ydgD***	predicted peptidase
1976556	InsAB' transposase	***insAB-5***	<		<	***insB-5***	IS1 protein
2066688	IS5 transposase and trans-activator	***insH-6***	<		>	***yoeA***	CP4-44 disrupted hemin or colicin receptor
2264250	NAD-dependent dehydrogenase	***yeiP***	>		>	***yeiQ***	predicted NAD-dependentdehydrogenase
2311454	antisense RNA against OmpF	***micF***	>		>	***rcsD***	RcsD phosphotransferase
2439732	β-ketoacyl-[acyl carrier prot] synthase I	***fabB***	<		>	***mnmC***	methylaminomethyl-thioU methyltransferase
2797030	nucleoid-protein with RNA chaperone activity	***stpA***	<		>	***ygaW***	predicted inner membrane protein
2989270	predicted protein	***ygeF***	>		>	***ygeG***	predicted chaperone
3651858	uncharacterized protein (pseudogene)	***yhiS_2***	<		>	***slp***	starvation lipoprotein
3766966	conserved protein	***yibG***	>		>	***yibV***	hypothetical protein
4042234	protein disulfide oxidoreductase	***dsbA***	>		>	***yihF***	putative GTP-binding protein
4328334	conserved protein	***yjcZ***	>		>	***proP***	osmolyte:H+ symporter
4336030	AdiY transcriptional activator	***adiY***	<		<	***adiA***	arginine decarboxylase
4477770	predicted acetyltransferase	***yjgM***	<		>	***yjgN***	conserved inner membrane protein
4502056	IS1 predicted transposase	***insG***	<		>	***yjhB***	MFS transporter
4538758	N-acetylneuraminic acid OM channel	***nanC***	<		>	***fimB***	regulator for *fimA*

Total no. binding sites **31**

Total no. regulatory targets **44**

Supplemental Table S4D

Position	Function	*Left gene*	D	N	A	F	K	D	*Right gene*	Function
11936	predicted protein	***yaaI***	<	🟧	🟧			>	***dnaK***	chaperone Hsp70, co-chaperone with DnaJ
29360	dihydrodipicolinate reductase	***dapB***	>	🟧	🟧			>	***carA***	carbamoyl P synthetase, Gln amidotransferase
84246	*leu* operon leader peptide	***leuL***	<	🟧	🟧	🟧	🟧	>	***leuO***	DNA-binding transcriptional activator
85462	Leu regulon transcriptional regulator	***leuO***	>	🟧	🟧	🟧	🟧	>	***ilvI***	acetolactate synthase III
89272	carbon metabolism transcriptional regulator	***cra***	>			🟧		>	***mraZ***	conserved protein
121872	aromatic amino acid transporter	***aroP***	<	🟧	🟧	🟧	🟧	>	***pdhR***	pyruvate dehydrogenase complex regulator
312342	*rpmJ* (L36) paralog	***ykgM***	<		🟧			>	***insE***	IS3 element protein InsE
317836	predicted protein	***ykgI***	<		🟧	🟧		<	***ykgC***	oxidoreductase FAD/NAD(P)-binding domain
440564	exonuclease VII small subunit	***xseB***	<	🟧				>	***thiI***	sulfurtransferase for thiamine/4-thiouridinesynthesis
454130	PBP regulator lactamase transcription	***bolA***	>		🟧	🟧		>	***tig***	peptidyl-prolyl cis/trans isomerase (trigger factor)
568022	DLP12 prophage multidrug resistance protein	***emrE***	>	🟧	🟧			>	***ybcK***	DLP12 prophage recombinase
576232	IS5 transposase and trans-activator	***insH***	<				🟧	>	***essD***	DLP12 prophage phage lysis protein
651244	citrate lyase synthetase	***citC***	<			🟧	🟧	>	***dpiB***	CitBA citrate operon TCS histidine kinase
655330	anaerobic C4-dicarboxylate transport	***dcuC***	<		🟧	🟧	🟧	>	***pagP***	palmitoyl transferase for Lipid A
660672	DNA-binding transcriptional regulator	***ybeF***	<	🟧	🟧			<	***lipB***	lipoyl-protein ligase
702948	glucosamine-6-phosphate deaminase	***nagB***	<	🟧	🟧	🟧		>	***nagE***	N-acetyl glucosamine specific PTS enzyme II
735540	predicted protein	***ybfC***	>				🟧	>	***ybfQ***	predicted transposase
735932	transposase	***ybfQ***	>		🟧			>	***ybfD***	conserved protein
770460	alpha-mannosidase	***mngB***	>	🟧		🟧	🟧	>	***cydA***	cytochrome d terminal oxidase, subunit I
832234	conserved protein	***ybiA***	<		🟧			>	***dinG***	ATP-dependent DNA helicase
840966	iron outer membrane transporter	***fiu***	<		🟧			<	***mcbA***	predicted protein
849470	threonine and homoserine efflux system	***rhtA***	<	🟧	🟧	🟧		>	***ompX***	outer membrane protein
953940	formate transporter	***focA***	<	🟧	🟧		🟧	<	***ycaO***	conserved protein
986332	outer membrane porin 1a	***ompF***	<			🟧	🟧	<	***asnS***	asparaginyl tRNA synthetase
996834	NAD(P)H-dependent FMN reductase	***ssuE***	<	🟧	🟧	🟧	🟧	>	***ycbQ***	fimbrial-like adhesin protein
1064672	predicted protein	***yccE***	>		🟧			>	***agp***	glucose-1-phosphatase/inositol phosphatase
1091836	outer membrane protein	***pgaA***	<	🟧		🟧		>	***ycdT***	predicted diguanylate cyclase
1120372	predicted protein	***bssS***	<	🟧	🟧	🟧	🟧	<	***dinI***	DNA damage-inducible protein I
1214838	FAD-binding phosphodiesterase	***ycgF***	<				🟧	>	***ycgZ***	predicted protein
1271162	calcium/sodium:proton antiporter	***chaA***	<		🟧			>	***chaB***	predicted cation regulator
1314248	predicted protein	***yciG***	<			🟧		<	***trpA***	tryptophan synthase
1402642	aminobenzoyl-glutamate utilization protein	***abgA***	<		🟧	🟧		>	***abgR***	aminoenzoyl-glutamate operon regulator
1431862	Rac prophage site-specific recombinase	***pinR***	<				🟧	<	***ynaE***	Rac prophage transcriptional regulator
1544148	predicted protein	***yddJ***	<			🟧	🟧	<	***yddG***	methyl viologen efflux pump
1570156	glutamate decarboxylase B, PLP-dependent	***gadB***	<		🟧		🟧	<	***pqqL***	predicted peptidase
1580646	conserved protein	***ydeN***	<		🟧			<	***ydeO***	acid response Gad cascade regulator
1585730	fimbrial-like adhesin protein	***ydeQ***	<	🟧	🟧	🟧		<	***ydeR***	fimbrial-like adhesin protein
1621964	conserved protein	***ydeH***	<			🟧		<	***ydeI***	conserved protein
1622654	conserved protein	***ydeI***	<				🟧	>	***ydeJ***	conserved protein
1631434	Qin prophage acid-response regulator	***ydfK***	>			🟧	🟧	>	***pinQ***	Qin prophage site-specific recombinase
1653764	conserved inner membrane protein	***ynfA***	<		🟧			>	***ynfB***	predicted protein
1702472	predicted oxidoreductase	***ydgJ***	<		🟧			>	***blr***	beta-lactam resistance membrane protein
1719066	hemolytic protein-lke transcriptional regulator	***slyA***	<	🟧	🟧	🟧	🟧	>	***ydhI***	inner membrane protein
1752832	4Fe-4S ferridoxin-type protein	***ydhY***	<	🟧	🟧	🟧	🟧	<	***ydhZ***	predicted protein
1755332	pyruvate kinase I	***pykF***	>	🟧	🟧	🟧	🟧	>	***lpp***	murein lipoprotein
1801348	threonyl-tRNA synthetase	***thrS***	<	🟧	🟧	🟧		>	***yniD***	predicted protein
1804342	conserved protein	***ydiY***	<	🟧				>	***pfkB***	6-phosphofructokinase II
1811260	predicted protein	***ydjO***	<	🟧	🟧	🟧		<	***cedA***	cell division modulator
1821336	Gln-dependent NAD synthase	***nadE***	>			🟧		>	***cho***	endonuclease of nucleotide excision repair
1823762	β-ketoacyl-[acyl carrier protein] synthase I	***spy***	<			🟧	🟧	<	***astE***	succinylglutamate desuccinylase
1842870	inner membrane protein	***ynjI***	<			🟧	🟧	<	***topB***	DNA topoisomerase III
1906068	predicted protein	***yobF***	<	🟧	🟧			<	***yebO***	predicted protein
1944202	RuvABC resolvasome	***ruvA***	<		🟧	🟧	🟧	>	***yebB***	predicted protein
2033552	ncRNA	***rseX***	>	🟧	🟧	🟧	🟧	>	***hchA***	Hsp31 molecular chaperone
2051334	adhesin	***yeeJ***	>		🟧			>	***shiA***	shikimate transporter
2066456	IS5 transposase and trans-activator	***insH***	<	🟧	🟧			<	***insD***	KpLE2 IS2 transposase InsAB
2310860	outer membrane porin protein C	***ompC***	<	🟧	🟧			>	***micF***	ncRNA
2311260	ncRNA	***micF***	>	🟧	🟧		🟧	>	***rcsD***	RcbBC phosphotransfer intermediate protein
2347662	conserved protein	***inaA***	<		🟧	🟧		<	***glpQ***	glycerophosphodiester phosphodiesterase
2363766	conserved protein	***ais***	<				🟧	>	***arnB***	Uri-5' (pentapyranosyl-ulose PPi) aminotransferase
2467134	CPS-53 bactoprenol glucosyl transferase	***yfdH***	>	🟧	🟧		🟧	>	***yfdI***	CPS-53 (KpLE1) prophage IM protein
2475638	D-Ser operon transcriptional regulator	***dsdC***	<			🟧		>	***dsdX***	predicted transporter
2491366	formyl-CoA transferase,	***frc***	<				🟧	<	***yfdX***	predicted protein
2560064	CPZ-55 prophage protein	***yffN***	>			🟧		>	***yffO***	CPZ-55 prophage protein
2561242	CPZ-55 prophage protein	***yffP***	>	🟧	🟧			>	***yffQ***	CPZ-55 prophage protein
2627762	predicted protein	***yfgG***	>				🟧	>	***yfgH***	outer membrane lipoprotein
2714546	pyruvate formate lyase subunit	***yfiD***	<	🟧	🟧	🟧		>	***ung***	uracil-DNA-glycosylase
2729552	16S ribosomal RNA of *rrnG* operon	***rrsG***	<		🟧	🟧		<	***clpB***	protein disaggregation chaperone
2773032	CP4-57 prophage inner membrane protein	***yfjW***	>				🟧	>	***yfjX***	CP4-57 prophage antirestriction protein
2781672	adhesin-like autotransporter	***ypjA***	<	🟧	🟧		🟧	<	***ileY***	Ile tRNA
2784564	Ile tRNA	***ileY***	<		🟧		🟧	>	***csiD***	predicted protein
2796642	nucleoid-associated H-NS-like regulator	***stpA***	<	🟧	🟧		🟧	>	***ygaW***	inner membrane protein
2802658	ribonucleoside-diphosphate reductase 2	***nrdF***	>	🟧	🟧	🟧		>	***proV***	glycine betaine transporter
2816770	Ser tRNA	***serV***	<			🟧		<	***csrA***	carbon source metabolism regulator
2882356	predicted protein	***ygcL***	<				🟧	<	***ygcB***	DEAD box family protein
2925954	conserved protein	***ygdH***	>		🟧	🟧	🟧	>	***sdaC***	serine transporter
2931960	L-fuculose-1-phosphate aldolase	***fucA***	<	🟧	🟧	🟧		>	***fucP***	L-fucose transporter
2945334	murein transglycosylase A	***mltA***	<		🟧			>	***metZ***	Met tRNA
2985254	predicted transporter	***yqeG***	>		🟧			>	***yqeH***	conserved protein
3004034	AI2-induced transcriptional regulator	***ygeV***	<			🟧	🟧	>	***ygeW***	conserved protein
3077446	mannitol-specific PTS enzyme IIA	***cmtB***	<		🟧			<	***tktA***	transketolase 1, thiamin-binding
3117230	inner membrane lipoprotein	***yghJ***	<		🟧	🟧	🟧	<	***glcA***	glycolate transporter
3134540	phosphate transporter	***pitB***	<				🟧	<	***gsp***	glutathionylspermidine amidase
3144338	hydrogenase 2	***hybO***	<		🟧			<	***yghW***	predicted protein
3170266	inner membrane protein	***ygiZ***	<				🟧	>	***mdaB***	NADPH quinone reductase

3204358	anaerobic growth nucleoid protein	***dan***	<		▨			>	***ttdA***	L-tartrate dehydratase
3214730	siderophore interacting protein	***yqjH***	<	▨	▨	▨		>	***yqjI***	transcriptional regulator
3217358	aerotaxis signal transducer sensory	***aer***	<				▨	>	***ygjG***	putrescine:2-oxoglutaric acid aminotransferase
3265162	Thr/Ser regulonl regulator	***tdcA***	<	▨	▨			>	***tdcR***	Thr/Ser regulonl regulator
3279834	N-acetylgalactosamine-specific PTS	***agaV***	>			▨		>	***agaS***	tagatose-6-phosphate ketose/aldose isomerase
3359040	glutamate synthase, 4Fe-4S proteint	***gltD***	>	▨	▨		▨	>	***gltF***	periplasmic protein
3427154	16S ribosomal RNA of *rrnD* operon	***rrsD***	<	▨				>	***yrdA***	conserved protein
3316172	conserved protein	***yhbC***	<			▨		<	***metY***	Met tRNA
3348572	isoprenoid biosynthesis protein	***elbB***	<			▨		>	***ryhA***	ncRNA
3375554	stringent starvation protein A	***sspA***	<		▨	▨		<	***rpsI***	30S ribosomal subunit protein S9
3411666	drug-efflux regulon transcriptional regulator	***envR***	<				▨	>	***acrE***	cytoplasmic membrane lipoprotein
3427154	16S ribosomal RNA of rrnD operon	***rrsD***	<		▨			>	***yrdA***	conserved protein
3530664	inner membrane protein	***yhgE***	<		▨	▨		>	***pck***	phosphoenolpyruvate carboxykinase
3550864	maltodextrin phosphorylase	***malP***	<			▨		>	***malT***	maltotriose-ATP-binding transcription regulator
3581134	conserved protein	***yhhZ***	>				▨	>	***insA***	KpLE2 phage-like element; IS1 repressor InsA
3595724	leucine transporter subunit	***livK***	<		▨			>	***yhhK***	conserved protein
3597838	leucine/isoleucine/valine transporter	***livJ***	<			▨		<	***rpoH***	RNA polymerase sigma 32 (sigma H) factor
3622268	predicted protein	***yhhH***	>		▨			>	***yhhI***	predicted transposase
3632570	predicted protein	***yhiJ***	<			▨	▨	>	***yhiM***	inner membrane protein
3670238	YhjAB TCS response regulator	***yhjB***	<	▨	▨	▨		>	***yhjC***	DNA-binding transcriptional regulator
3706050	dipeptide transporter	***dppA***	<			▨	▨	<	***proK***	Pro tRNA
3728944	D-xylose isomerase	***xylA***	<			▨		>	***xylF***	D-xylose transporter subunit
3802172	UDP-D-galactose:LPS-galactosyltransferase	***rfaB***	<		▨	▨	▨	<	***rfaS***	LP core biosynthesis protein
3802986	UDP-D-galactose:LPS-galactosyltransferase	***rfaI***	<	▨	▨			<	***rfaB***	UDP-D-galactose:LP-1,6-D-galactosyltransferase
3803124	LPS core biosynthesis protein	***rfaS***	<				▨	<	***rfaP***	LP phosphorylates core heptose kinase
3806372	LPS core biosynthesis protein	***rfaQ***	<			▨		>	***waaA***	3-deoxy-D-manno-octulosonic-acid transferase
3834134	predicted transporter	***yicJ***	<	▨	▨	▨		>	***selC***	Sec tRNA
3841848	xanthine/uracil permase	***yicO***	<		▨	▨		>	***ade***	cryptic adenine deaminase
3886640	tryptophanase leader peptide	***tnaC***	>				▨	>	***tnaA***	tryptophanase/L-cysteine desulfhydrase
3904730	*bgl* operon transcriptional antiterminator	***bglG***	<				▨	<	***phoU***	PhoRB two-component regulator
3920768	membrane-bound ATP synthase	***atpI***	<	▨	▨	▨		<	***gidB***	SAM-dependent methyltransferase
3929268	transcriptional regulator: sigma-54 activator	***ravA***	<	▨	▨			>	***kup***	potassium transporter
4044850	predicted endonuclease	***yihG***	<			▨	▨	>	***polA***	DNA polymerase I
4076772	predicted acetyltransferase	***yiiD***	>	▨	▨	▨	▨	>	***yiiE***	DNA-depemdemt transcriptional regulator
4233870	glucosephosphate isomerase	***pgi***	>	▨	▨	▨		>	***yjbE***	predicted protein
4249834	maltose regulon periplasmic protein	***malM***	>				▨	>	***ubiC***	chorismate pyruvate lyase
4267058	hypothetical protein	***yjbS***	<			▨		>	***aphA***	acid phosphatase/phosphotransferase
4292346	heme lyase (NrfEFG)	***nrfG***	>			▨	▨	>	***gltP***	glutamate/aspartate:proton symporter
4324976	conserved protein	***yjdM***	<	▨	▨	▨	▨	>	***yjdA***	nucleoside triphosphate hydrolase kinase
4402644	inner membrane protein	***yjeT***	>	▨	▨			>	***purA***	adenylosuccinate synthetase
4539836	Tyr recombinase/inversion *fimA* on/off regulator	***fimB***	>	▨	▨	▨	▨	>	***fimE***	Tyr recombinase/inversion *fimA* on/off regulator
4554598	predicted protein	***yjiC***	<		▨			>	***yjiD***	DNA replication/recombination/repair protein
4589632	inner membrane protein	***yjiY***	<			▨		>	***tsr***	methyl-accepting chemotaxis Ser sensor
4601072	inner membrane protein	***yjjP***	<				▨	>	***yjjQ***	DNA-binding transcriptional regulator
	Total no. binding sites			**48**	**77**	**67**	**57**			
	Total no. regulatory targets			**70**	**##**	**97**	**78**			

Supplemental Table S4E

Function	Gene	D		D	Gene	Function
leu operon leader peptide	***leuL***	<		>	***leuO***	*leu* regulon regiator
Asp tRNA	***aspV***	>		>	***yafT***	predicted aminopeptidase
predicted protein	***yaiA***	>		>	***aroM***	conserved protein
predicted protein	***tomB***	<		<	***acrB***	multidrug efflux system protein
IS5 transposase and trans-activator	***insH***	<		>	***essD***	DLP12 prophage phage lysis protein
predicted protein	***ybfA***	>		>	***rhsC***	*rhsC* element core protein RshC
citrate synthase	***gltA***	<		>	***sdhC***	succinate dehydrogenase
alpha-mannosidase	***mngB***	>		>	***cydA***	cytochrome *d* terminal oxidase
periplasmic protein	***tolB***	>		>	***pal***	peptidoglycan-associated OM lipoprotein
Rossmann-fold domain transferase	***ybhK***	<		>	***moaA***	molybdopterin biosynthesis protein A
aquaporin	***aqpZ***	<		>	***ybjD***	nucleoside triphosphate hydrolase
formate transporter	***focA***	<		<	***ycaO***	conserved protein
ferric-rhodotorulic acid OM transporter	***fhuE***	<		>	***hinT***	purine nucleoside phosphoramidase
hemolysin E	***hlyE***	<		>	***umuD***	DNA polymerase V
ABC superfamily MD transporter	***yddA***	<		<	***ydeM***	conserved protein
predicted lipoprotein	***ydeK***	<		<	***lsrK***	autoinducer-2 (AI-2) kinase
predicted protein	***ynfD***	>		>	***ynfE***	oxidoreductase
autogeneous regulation	***slyA***	<		>	***ydhI***	inner membrane protein
predicted transporter	***ydhC***	>		>	***cfa***	cyclopropane fatty acyl phospholipid synthase
threonyl-tRNA synthetase	***thrS***	<		>	***yniD***	predicted protein
predicted protein	***yoaI***	<		>	***yeaL***	conserved inner membrane protein
conserved protein	***yoaB***	>		>	***yoaC***	predicted protein
predicted protein	***yobF***	<		<	***yebO***	predicted protein
flagellar regulon transcriptional regulator	***flhD***	<		<	***insB***	IS1 transposase InsAB'
cell division control transcriptional activator	***sdiA***	<		<	***yecC***	ABC superfamily transporter
IS5 transposase and trans-activator	***insH***	<		<	***insD***	KpLE2 IS2 transposase InsAB'
predicted protein	***yegR***	<		>	***yegS***	phosphatidylglycerol kinase
ncRNA	***micF***	>		>	***rcsD***	RcsBC TCS phosphotransfer intermediate
adhesin	***yfaL***	<		<	***ypaB***	hypothetical protein
outer membrane porin protein	***yfaZ***	<		>	***nudI***	predicted NUDIX hydrolase
CPS-53 (KpLE1) prophage protein	***yfdP***	>		>	***yfdQ***	CPS-53 (KpLE1) prophage protein
Mur-NAC cell wall regulator	***murR***	<		>	***murQ***	predicted PTS component
predicted inner membrane protein	***yfgF***	<		>	***yfgG***	predicted protein
Ile tRNA	***ileY***	<		>	***csiD***	predicted protein
predicted protein	***ygdR***	>		>	***tas***	NADP(H)-dependent oxidoreductase
arabinose transporter	***araE***	<		<	***kduD***	2-deoxy-D-gluconate 3-dehydrogenase
predicted transporter	***yqeG***	>		>	***yqeH***	conserved protein
ABC superfamily transporter	***ygiS***	<		<	***mqsA***	MqsRA T-AT antitoxin regulator
KpLE2 phage IS2 transposase InsAB'	***insD***	>		>	***yqiH***	predicted periplasmic pilin chaperone
predicted glycogen synthesis protein	***glgS***	<		>	***yqiJ***	predicted inner membrane protein
arg operon transcriptional dual regulator	***argR***	>		>	***yhcN***	conserved protein
predicted outer membrane protein	***yhdV***	>		>	***yhdX***	predicted amino-acid transporter
DNA-binding transcriptional dual regulator	***gadX***	<		<	***gadA***	glutamate decarboxylase A
predicted glutathione S-transferase	***yibF***	<		>	***rhsA***	*rhsA* element core protein RshA
bifunctional enzyme/transcriptional regulator	***yifB***	<		>	***ilvL***	*ilvG* operon leader peptide
ilvG operon leader peptide	***ilvL***	>		>	***ilvM***	acetolactate synthase II
predicted endonuclease	***yihG***	<		>	***polA***	DNA polymerase I
predicted acetyltransferase	***yiiD***	>		>	***yiiE***	transcriptional regulator
glyoxylate bypass operon regulator	***iclR***	<		>	***metH***	homoCys-methyltetrahydrofolate transmethylase
biodegradative arginine decarboxylase	***adiA***	<		<	***melR***	DNA-binding transcriptional dual regulator
PAPS-bisphosphate nucleotidase	***cysQ***	>		>	***ytfI***	predicted protein
trehalose transport catabolism regulator	***treR***	<		>	***mgtA***	magnesium transporter
KpLE2 RNAP sigma 19 factor	***fecI***	<		>	***insA***	KpLE2 phage IS1 repressor protein InsA
conserved protein	***yjhX***	<		<	***yjhS***	conserved protein
N-acetylnuraminic acid OM channel protein	***nanC***	<		>	***fimB***	tyrosine recombinase/inversion *fimA* regulator
tyrosine recombinase/*fimA on-off* regulator	***fimB***	>		>	***fimE***	tyrosine recombinase/inversion *fimA* regulator
predicted protein	***yjiC***	<		>	***yjiD***	DNA replication/recombination/repair protein

Total no. binding sites	**56**
Total no. regulatory targets	**80**