

Supplemental Table 1. *E. coli* chromosomal integration sites obtained using a RAM-targetron library with randomized target site recognition sequences.

Target gene	Target gene function	Integration site	Annotation
	intergenic region	3553453o	
	intergenic region	3643872o	
	intergenic region	3773856o	
	intergenic region	3851225i	
	intergenic repeats	2902301o	
agaZ	putative tagatose 6-phosphate kinase 2	3276627o	
argE	acetylornithine deacetylase	4151651i	
b1452	putative receptor	1521597i	
b2520	unknown	2647574i	
b3814	unknown	3998023o	
bisC	biotin sulfoxide reductase	3711727o	
cdh	CDP-diacylglycerol phosphotidylhydrolase	4107960i	
cyaA	adenylate cyclase	3988770o	
deaD	ATP-independent RNA helicase	3304206o	
deoB	phosphopentomutase	4617331o	
ebgA	evolved beta-D-galactosidase, alpha subunit	3220453o, 3221497i	
eutH	putative transport protein	2565489i	
fadB	4-enzyme protein	4027811i	
flhA	flagellar structural component	1962889i	
fliC	flagellin	2000818i	
fpr	ferredoxin-NADP reductase	4111553o	2 different introns
frvB	transport of small molecules (carbohydrates, organic acids, alcohols)	4089543i	
FrwD	PTS system fructose-like IIB component 2	4144880i	
glnL	histidine protein kinase sensor for GlnG regulator	4052894i	
gltS	transport of small molecules (amino acids & amines)	3826182o	
hofQ	putative transport protein	3517567i	
hsdR	endonuclease R	4582348o	
hybF	may modulate levels of hydrogenase-2	3138104o	
ilvB	acetolactase synthase I	3849472i	
ilvD	dihydroxyacid dehydratase	3952908i	
ilvG_2	acetolactate synthase II	3949387o	
ilvY	positive regulator for ilvC	3955169i	
katG	catalase	4132746i	
malM	periplasmic protein of mal regulon	4247678i	
malT	positive regulator of mal regulon	3552527i	
metL	aspartokinase II and homoserine dehydrogenase II	4129267i	
modF	ATP-binding component of molybdate transport system	792101o	
nfnB	oxygen-insensitive NAD(P)H nitroreductase	604329i	
nrdE	ribonucleoside-diphosphate reductase 2, alpha subunit	2801360o	
nrfA	periplasmic cytochrome C	4286662i	
ppiA	peptidyl-prolyl cis-trans isomerase (rotamase A)	3489568o	
ppx	exopolyphosphatase	2624459o	
ptsI	pEP-protein phosphotransferase system enzyme I	2533081o	
recQ	ATP-dependent DNA helicase	4003683o	
rhaB	rhamnulokinase	4094828o	
rhsA	rhsA protein in rhs element; Transposon-related functions	3759887o	
sela	selenocysteine synthase	3758861o, 3757911i	

selB	selenocysteinyl-tRNA-specific translation factor	3756822i	
ubiB	ferrisiderophore reductase/flavin reductase	4024371o	
ugpB	sn-glycerol 3-phosphate transport system; periplasmic binding protein	3589389o	
uhpB	sensor histidine protein kinase	3847413i	
wecE	putative regulator	3973830o, 3973099o	
wzxE	putative cytochrome	3974108i	
yfbS	putative transport protein	2408241i	
yfeN	putative sugar hydrolase	2523510o	
yggM	unknown	3096577o, 3097264o	
ygjE	unknown	3206400i	
ygjO	putative enzyme	3232638i	
yhcD	putative outer membrane protein	3362694o	
yhcP	unknown	3384118o	
yhiQ	unknown	3640733o	5 different introns
yhjK	unknown	3681887i	
yhjS	putative protease	3694887o	
yhjW	unknown	3706205i	
yiaM	unknown	3742411i	
yiaY	putative oxidoreductase	3754545o	
yibK	unknown	3778886i	
yicO	unknown	3840463o, 3840519i	
yidJ	unknown, similar to arylsulfatases	3854924o	2 identical introns
yidR	unknown	3866768i	
yidZ	putative transcriptional regulator LYSR-type	3890889o, 3890949i	
yieG	putative membrane / transport protein	3893761i, 3893459i	
yieK	putative isomerase	3896317i	
yieL	putative xylanase	3897502o	
yigB	putative phosphatase	3994809o	
yigZ	unknown	4030395o	
yihO	putative permease	4063262o	
yihU	putative dehydorgenase	4070425i	
yjbC	unknown	4228328i	
yjgR	unknown	4487174i	
yqjB	unknown	3246378o	
yraR	unknown	3296369o	
ysgA	unknown	4013570i	

Integration sites are numbered according to the genome sequence of *E. coli* K-12 MG1655 (Genbank accession number U00096), followed by o or i, indicating the outside (presented) or inside DNA strand.