

Supplementary Materials

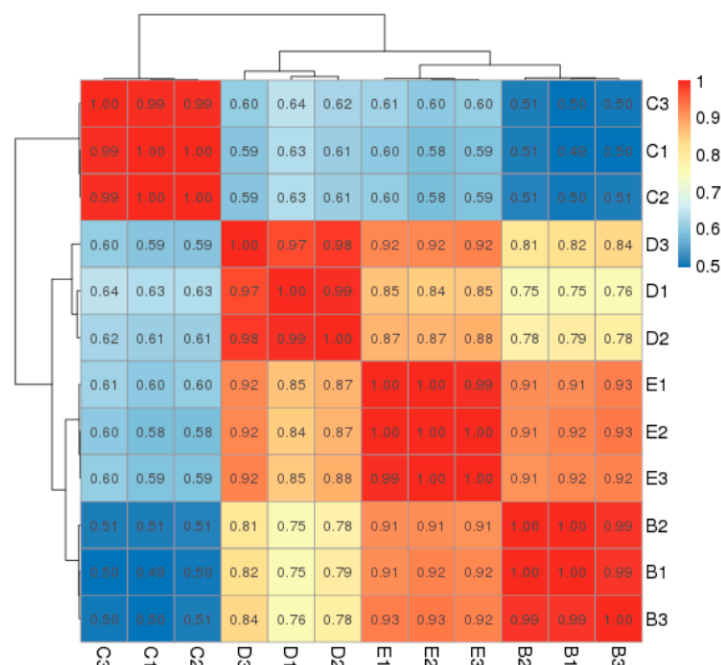


Figure S1. Correlation tests for the parental strain (Group B), strain 32M (1/2M) (Group C), strain 16M (1/8M) (Group D) and strain 8M (1/128M) (Group E) (triplicates in each group). The abscissa and ordinate in the figure are sample numbers. The closer the block value is to 1, the higher the similarity is.

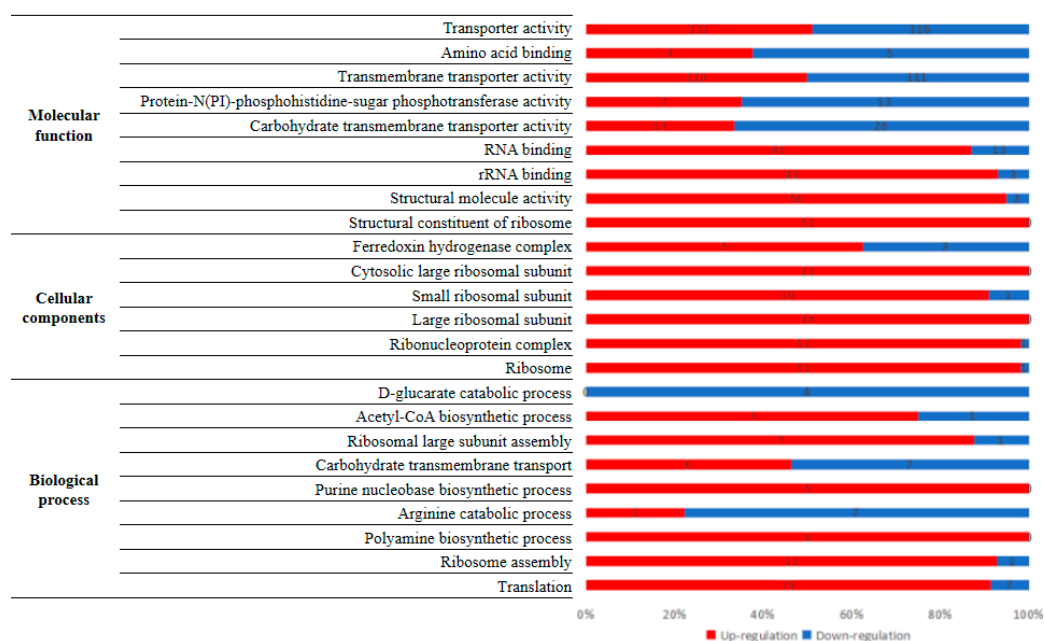
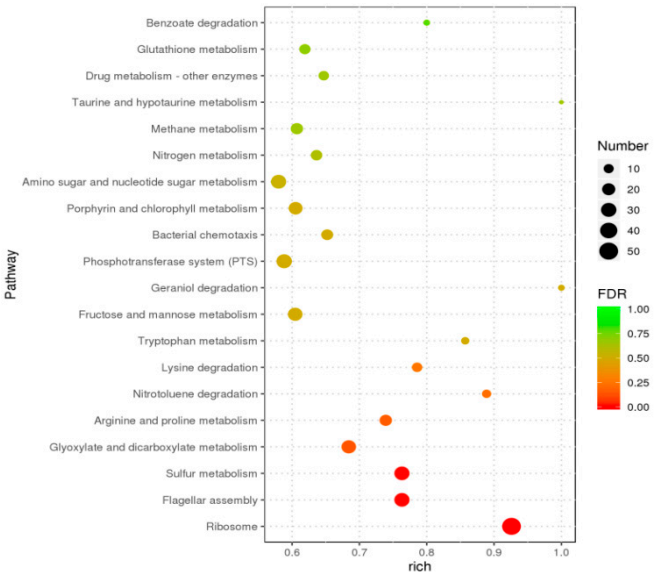
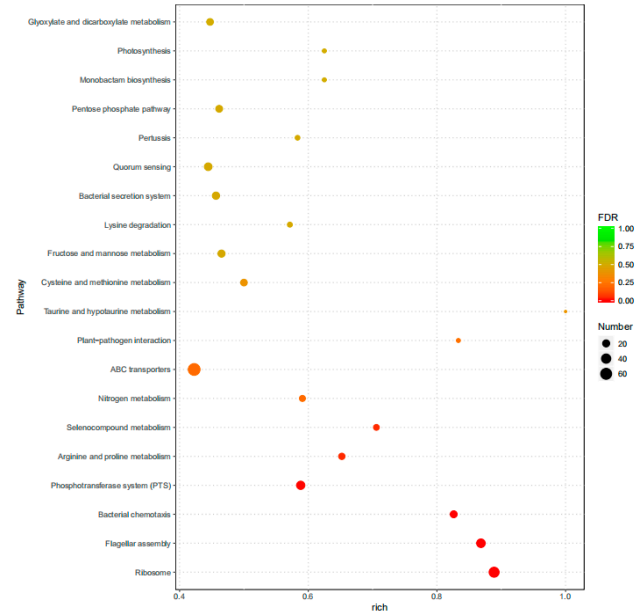


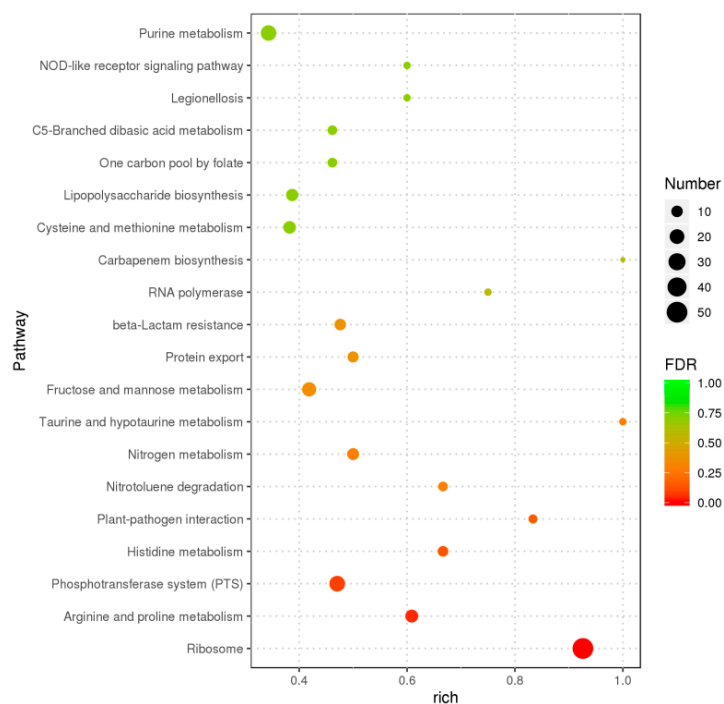
Figure S2. Enrichment of co-DEGs in GO Term.



(A)



(B)



(C)

Figure S3. Pathway enrichment scatter plot of DEGs. (A) The top 20 KEGG pathway of B vs C group; (B) The top 20 KEGG pathway of B vs D group; (C) The top 20 KEGG pathway of B vs E group.

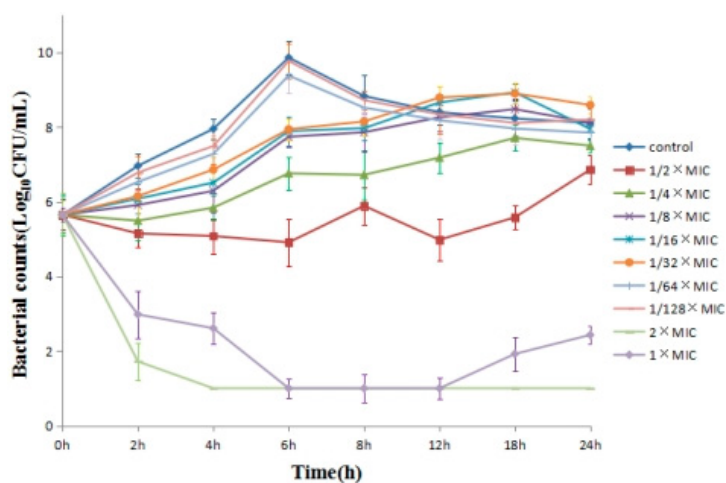


Figure S4. Growth curves of *Salmonella enterica* CICC 21527 in the TSB broth under sub-MIC of enrofloxacin.

Table S1. Primers used for identification OMPs and MDR efflux pumps of Salmonella.

Gene name	Primer	Sequences (5' -3')	Fragment size (bp)	Reference
<i>gapA</i>	gapA-F	CGCATCTCAGAACATCATC	130	This study
	gapA-R	AGGTCAACAACGGATACG		
<i>ompC</i>	ompC-F	GTGGATGGTCTGGACTTC	177	This study
	ompC-R	TTAGCGGTGTTGTTCTGAT		
<i>ompD</i>	ompD-F	TGTTGCCACCTACCGTAACA	200	Ivan et al. (2011)
	ompD-R	GGTCGCCAGGTAGATGTTGT		
<i>ompF</i>	ompF-F	GTTGAATCCTATACCGATATGG	300	This study
	ompF-R	GAGTTAATGCTGTGGTTGTC		
<i>acrB</i>	acrB-F	CAATATCCGACGATTGCGC	194	Kim et al. (2016)
	AcrB-R	TATCGATACCGTTCATATTCTGT		
<i>acrF</i>	AcrF-F	ATTCCTACCATCGCTGTTC	121	This study
	AcrF-R	CCACTATCGCATCGTCAA		
<i>emrB</i>	EmrB-F	CCTGTTGCTGAATAACTATCC	136	This study
	EmrB-R	CGATGCCAATCACCAGTA		
<i>mdfA</i>	MdfA-F	CGATATGAGTAAAGGAACGG	266	Sun et al. (2011)
	MdfA-R	AGCATCAGCAGTAGCCAAAGAA		
<i>mdtK</i>	MdtK-F	CGTCGGCATTGTATGGCTGT	94	Sun et al. (2011)
	MdtK-R	CACGACCTCAGGGTTGTCATTG		

Table S2. Differently expressed genes between groups of the Co-DEGs among three groups of mutants.

Gene name	Fold change CvsB	Fold change DvsB	Fold change EvsB	NR
<i>deaD</i>	28.30	4.62	6.74	DEAD/DEAH family ATP-dependent RNA helicase
<i>purD</i>	20.78	6.28	5.10	Phosphoribosylamine--glycine ligase
<i>acrR</i>	2.02	-5.26	-4.17	TetR-family transcriptional regulator
<i>rhlE</i>	20.16	3.85	6.05	ATP-dependent RNA helicase RhlE
<i>rsxD</i>	18.11	6.91	4.03	Electron transport complex subunit RsdD
<i>marA</i>	14.52	6.24	47.54	Transcriptional activator RamA
<i>infB</i>	12.44	3.70	3.09	Initiation factor IF2-alpha
<i>priB</i>	12.40	9.15	9.60	Primosomal replication protein N
<i>aceF</i>	12.40	2.95	2.22	Pyruvate dehydrogenase complex dihydrolipoyllysine-residue acetyltransferase
<i>purH</i>	11.70	3.14	2.92	Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
<i>rsxC</i>	11.52	2.98	3.13	Electron transport complex subunit RsdC
<i>purF</i>	10.04	3.49	3.97	Amidophosphoribosyltransferase
<i>fusA</i>	9.80	5.49	4.45	Elongation factor G
<i>speD</i>	9.06	5.88	4.10	Adenosylmethionine decarboxylase
<i>nusA</i>	8.83	2.3	2.54	Transcription termination/antitermination protein NusA
<i>purB</i>	8.76	3.15	3.06	Adenylosuccinate lyase
<i>codA</i>	8.37	3.45	2.38	Cytosine deaminase
<i>fis</i>	8.18	5.43	14.00	DNA-binding transcriptional regulator Fis

<i>speE</i>	7.84	7.16	4.03	Polyamine aminopropyltransferase
<i>purL</i>	6.94	3.43	3.92	Phosphoribosylformylglycinamidine synthase
<i>lepB</i>	6.52	3.86	3.66	Signal peptidase I
<i>rapA</i>	5.71	2.05	2.45	RNA polymerase-associated protein RapA
<i>gyrA</i>	4.98	3.38	2.24	DNA topoisomerase (ATP-hydrolyzing) subunit A
<i>pnp</i>	4.87	2.99	2.13	Polynucleotide phosphorylase
<i>soxR</i>	3.58	-3.45	-3.57	Redox-sensitive transcriptional activator SoxR
<i>purR</i>	3.42	4.72	5.73	HTH-type transcriptional repressor PurR
<i>apt</i>	3.40	7.33	7.78	Adenine phosphoribosyltransferase
<i>cdd</i>	2.94	-2.27	-4.76	Cytidine deaminase
<i>cedA</i>	2.30	2.50	5.81	Cell division activator CedA
<i>cpxP</i>	-2.17	2.65	14.14	Cell-envelope stress modulator CpxP
<i>sodB</i>	-2.22	3.42	2.98	Superoxide dismutase, partial
<i>phsB</i>	-5.00	2.60	2.31	Thiosulfate reductase electron transport protein PhsB
<i>fumC</i>	-6.67	-3.57	-2.33	Fumarate hydratase class II
<i>sucC</i>	-7.69	-4.55	-2.17	ADP-forming succinate--CoA ligase subunit beta
<i>rhaS</i>	-16.67	2.91	3.58	HTH-type transcriptional activator RhaS
<i>aceA</i>	-25.00	-2.17	-2.78	Isocitrate lyase
<i>prpD</i>	-33.33	-3.33	-7.14	Bifunctional 2-methylcitrate dehydratase/aconitate hydratase
<i>aceK</i>	-33.33	-2.56	-2.44	Bifunctional isocitrate dehydrogenase kinase/phosphatase
<i>prpC</i>	-50.00	-4.00	-5.56	2-methylcitrate synthase
<i>prpB</i>	-100.00	-3.70	-5.56	Methylisocitrate lyase