

Supplementary Information

Genome-wide screening of antibiotic survival genes in *Escherichia coli* MG1655

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Table S1. The relative doubling time of AG1 strains expressing each candidate gene identified in this study. The relative doubling time was the ratio of the doubling time of each strain over the median doubling time of all ~4,200 AG1 strains in the ASKA library.

Gene name	Relative doubling time
aceK	1.455
agaS	0.681
ampC	0.875
araD	0.876
argF	1.163
ariR	0.816
aroD	0.504
astB	1.550
atoD	0.868
baeR	0.878
bcr	1.120
bglH	2.002
btuE	0.902
chbA	0.677
cspF	0.764
dctR	1.005
ecpC	0.860
etp	0.833
ettA	0.882
eutL	0.897
fabA	0.931
fabI	1.006
fadJ	0.956
fau	0.986
fhlA	1.034
flgC	0.811
folA	0.990
ftsA	0.837
ftsE	0.819
fucK	0.916
gadE	0.766
gadW	1.124
gadX	1.236

galE	0.888
gfcD	1.205
glpA	0.901
gmk	0.876
groL	0.776
grxC	1.061
gstB	0.625
hcp	0.708
hemF	0.811
hslJ	1.260
hyaA	0.726
hyfA	1.099
hyfH	0.957
hyfR	1.023
hypB	0.620
idnD	1.146
ilvH	0.844
ilvN	1.209
kduD	1.024
kefG	0.899
leuA	0.641
lolB	0.868
lrp	0.745
lsrA	1.106
marA	0.889
mgtA	1.762
minE	1.091
mlaB	1.233
mtfA	0.885
mutL	0.894
nanE	1.073
narH	1.064
nfsA	0.995
nikD	0.904
nikE	0.722
nrdH	0.874
oppD	0.918
osmC	0.875
oxc	0.508
paaB	1.173
paoC	0.880
paoD	0.939
patZ	0.835

pflA	0.552
ppiC	0.928
pptA	0.750
prpE	0.782
pspB	1.111
pspC	0.823
pspD	0.900
pspF	1.093
pstC	1.211
purL	1.006
pyrD	0.847
rarA	0.798
rdgB	0.945
recD	0.809
relA	0.682
rhoL	1.268
ribB	0.925
ribE	0.719
rihC	0.727
rph	0.770
rplI	0.800
rpmE	0.789
rpoN	0.858
rtcB	0.933
sbmC	0.628
sdhE	0.684
selB	0.969
sgbH	1.160
soxS	0.648
sspA	1.015
ssuE	0.710
sucC	1.111
sugE	0.800
tadA	0.747
tfaX	0.914
thiQ	0.743
tmaR	0.998
tnaC	1.214
treC	0.766
treF	0.785
trmJ	1.435
trmM	0.833
trpB	1.004

tus	1.250
tyrR	1.257
ubiX	0.910
umuD	1.386
upp	1.465
uvrY	0.858
wcaN	0.850
wzb	1.020
xapR	0.793
yacG	0.990
yagl	1.095
yaiE	0.749
ybcN	0.898
ybdO	0.641
ycaQ	0.650
ycgY	1.150
yciG	0.972
ycil	1.019
yciU	0.803
ycjV	0.801
ydaC	1.048
ydaE	0.685
ydfR	0.894
ydfW	0.890
ydiT	0.786
yeaD	1.033
yebK	1.056
yedR	1.048
yejF	0.831
yejG	0.901
yfcF	1.111
ygaC	0.955
ygbK	0.912
ygcO	0.938
yhdE	1.054
yhdZ	0.962
yheS	1.068
yhfW	0.808
yhhY	0.814
yiaG	1.114
yicC	0.691
yieE	1.164
yieH	0.887

yifK	1.535
yigB	0.527
yigZ	1.632
yjdN	0.790
ymjA	1.174
ynaK	1.057
ynjD	0.726
yoaC	1.060
ypdB	0.928
ypjJ	0.863

Table S2. MICs determined by the CLSI protocol for selected genes

Gene name	Antibiotics*	MIC by the CLSI protocol (µg/ml)	MIC reported in this study (µg/ml)
ycgY	TET	2	2
	NAL	300	600
	TMP	30	30
yciI	NIT	10	10
	TMP	60	60
yciU	DOX	1.5	1.5
	TOB	6	6
yejF	AMP	15	15
	CIP	1	2
yhfw	AMP	15	15
	ERY	150	150
yjeH	NAL	150	150
	NIT	10	10
ymjA	NAL	300	600
	TMP	60	60
ynaK	TET	2	2
	DOX	1.5	1.5
	NAL	150	300
	TOB	6	6
	NIT	10	10
	TMP	30	60

* Abbreviations for antibiotics: AMP (Ampicillin), TET (Tetracycline), DOX (Doxycycline), NAL (Nalidixic acid), CIP (Ciprofloxacin), TOB (Tobramycin), NIT (Nitrofurantoin), ERY (Erythromycin), TMP (Trimethoprim).

Figure S1. The STRING interaction map of potential survival genes for ampicillin. Clusters were indicated by different colors.

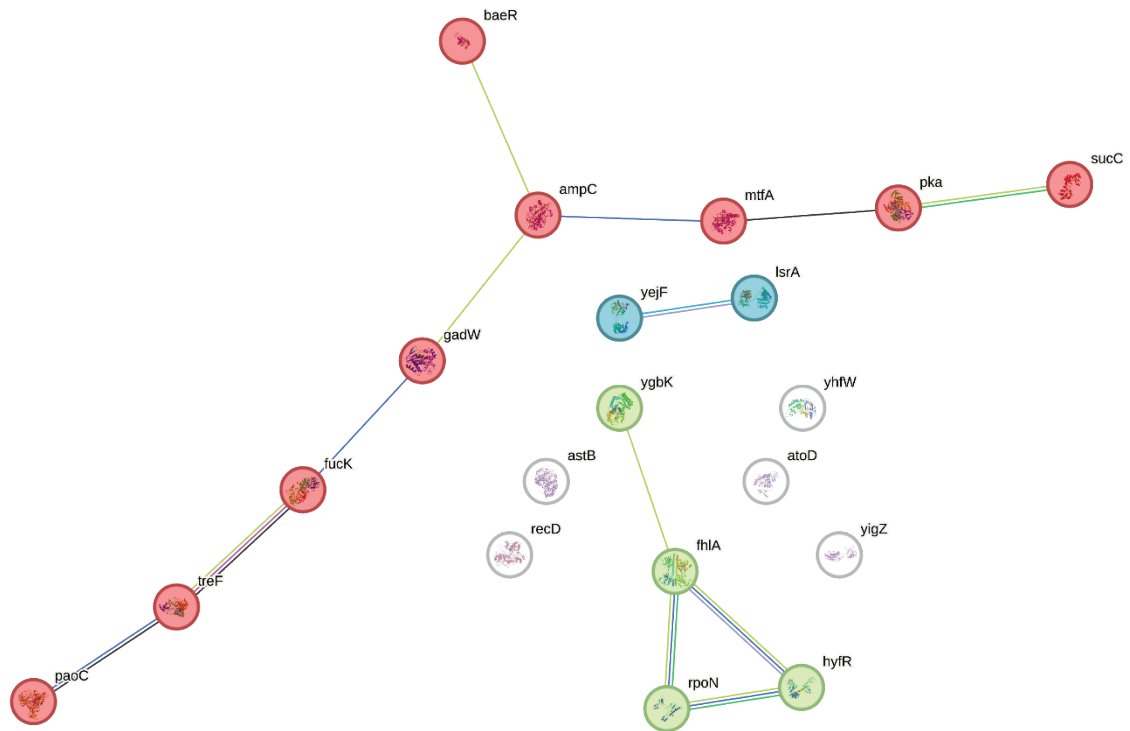


Figure S2. The STRING interaction map of potential survival genes for cefoxitin. Clusters were indicated by different colors.

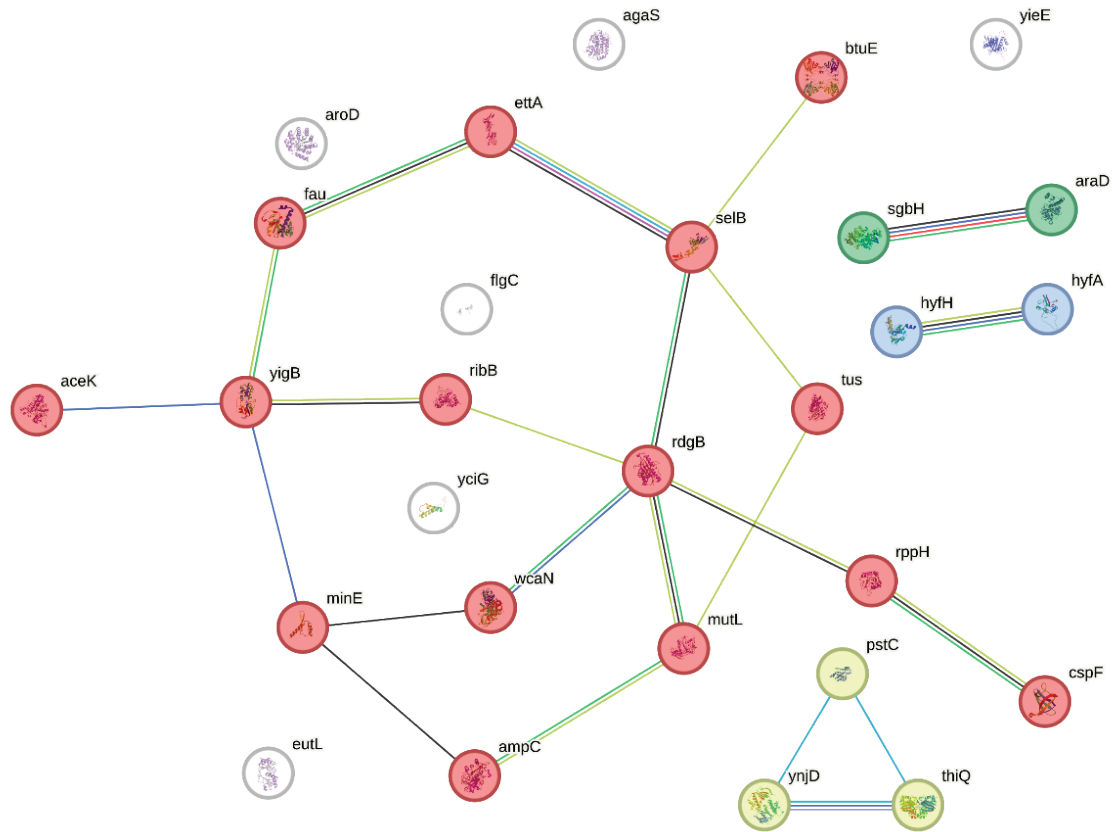


Figure S3. The STRING interaction map of potential survival genes for tetracycline. Clusters were indicated by different colors.

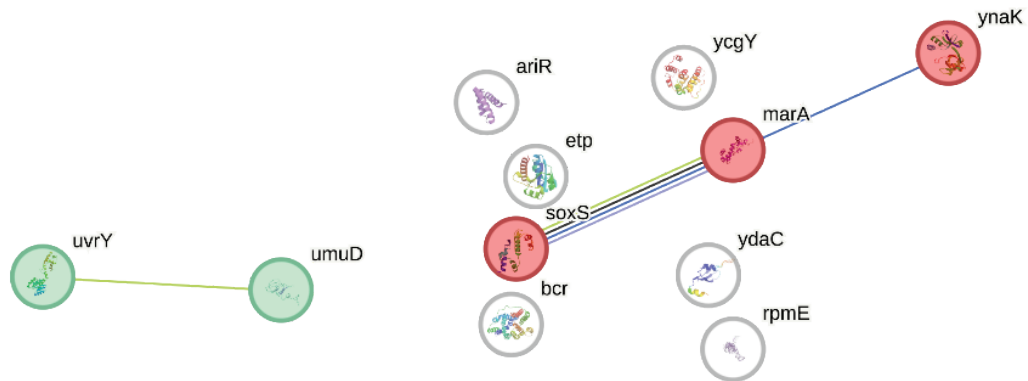


Figure S4. The STRING interaction map of potential survival genes for doxycycline. Clusters were indicated by different colors.

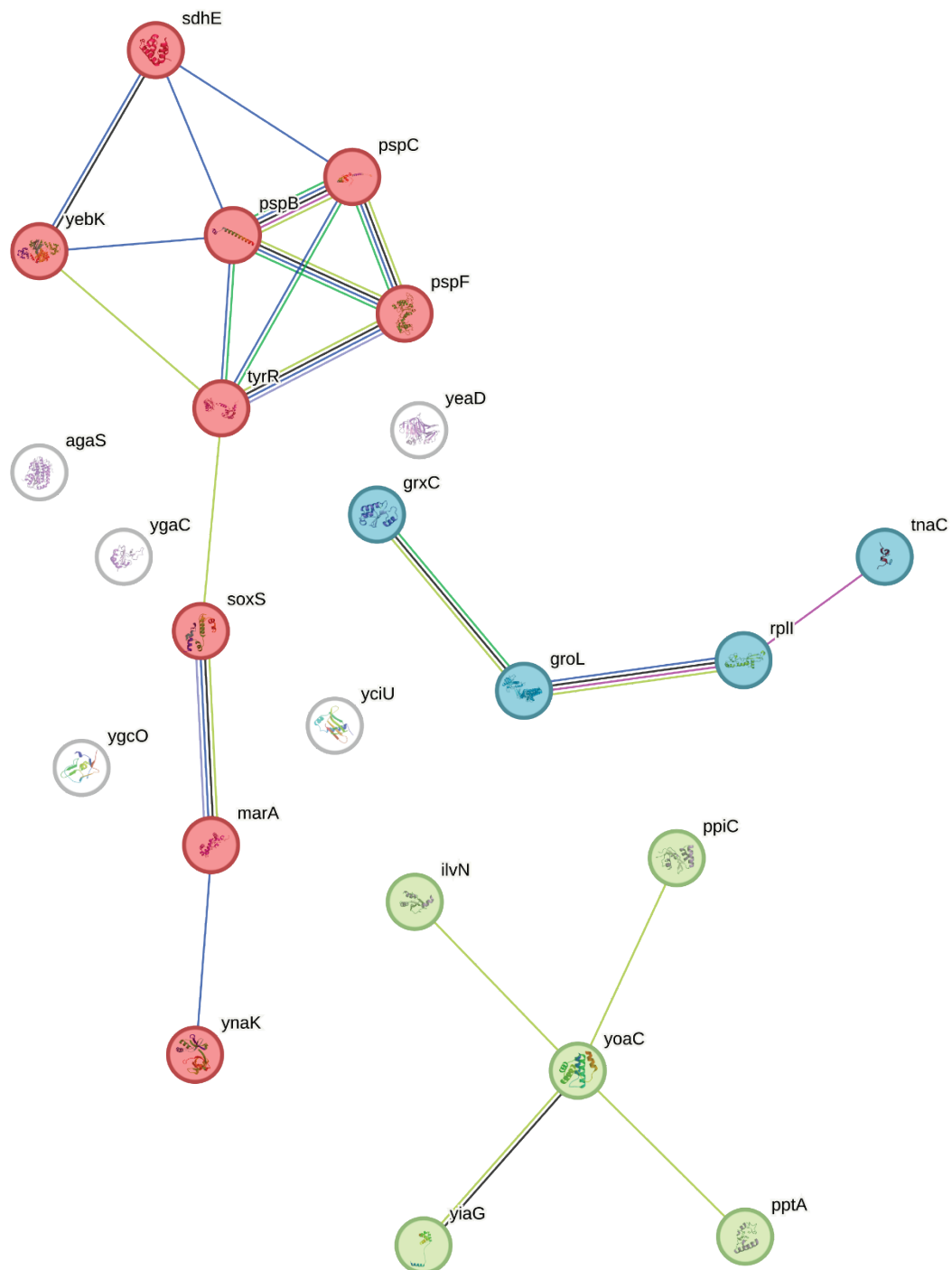


Figure S5. The STRING interaction map of potential survival genes for nalidixic acid. Clusters were indicated by different colors.

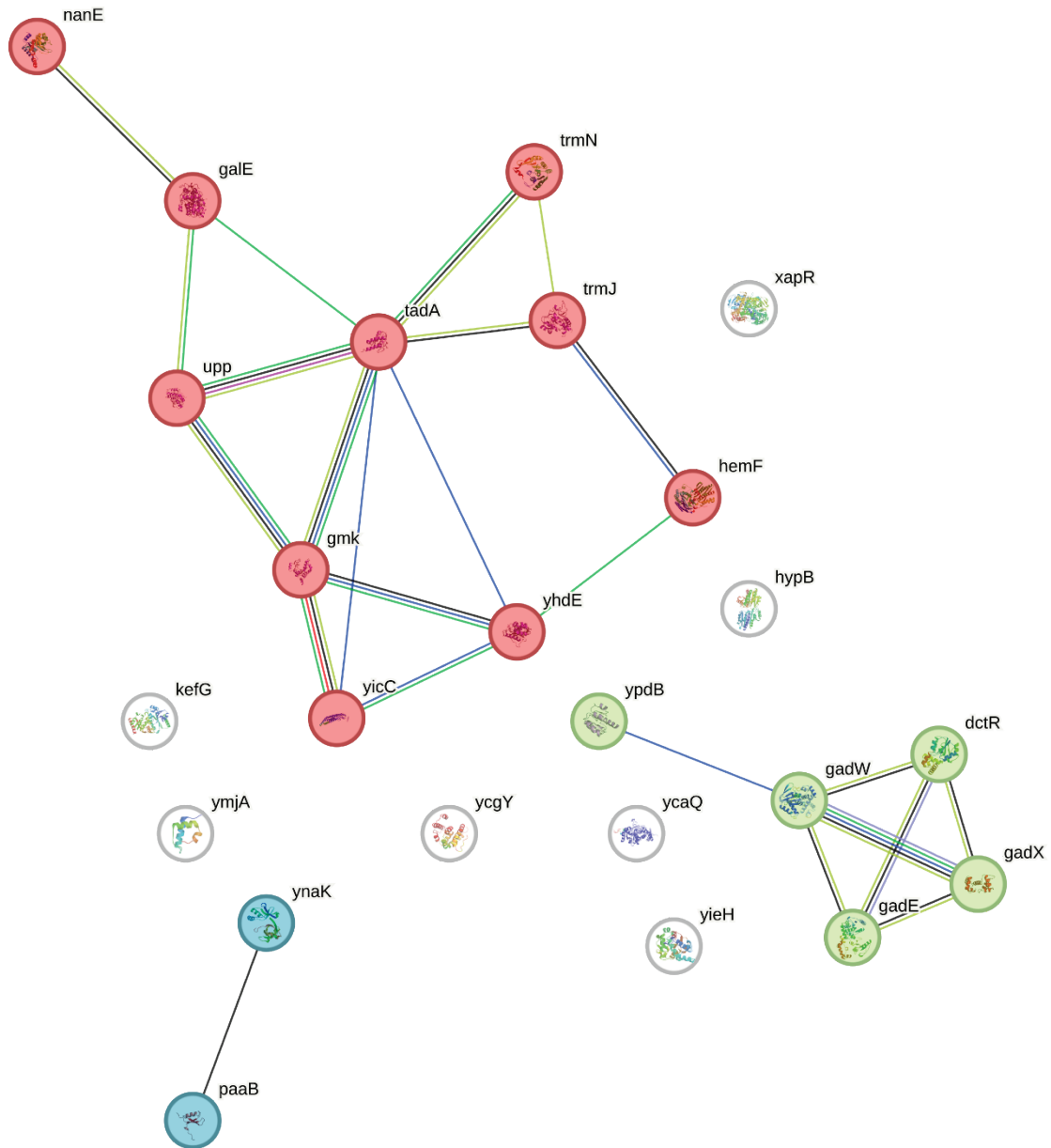


Figure S6. The STRING interaction map of potential survival genes for ciprofloxacin. Clusters were indicated by different colors.

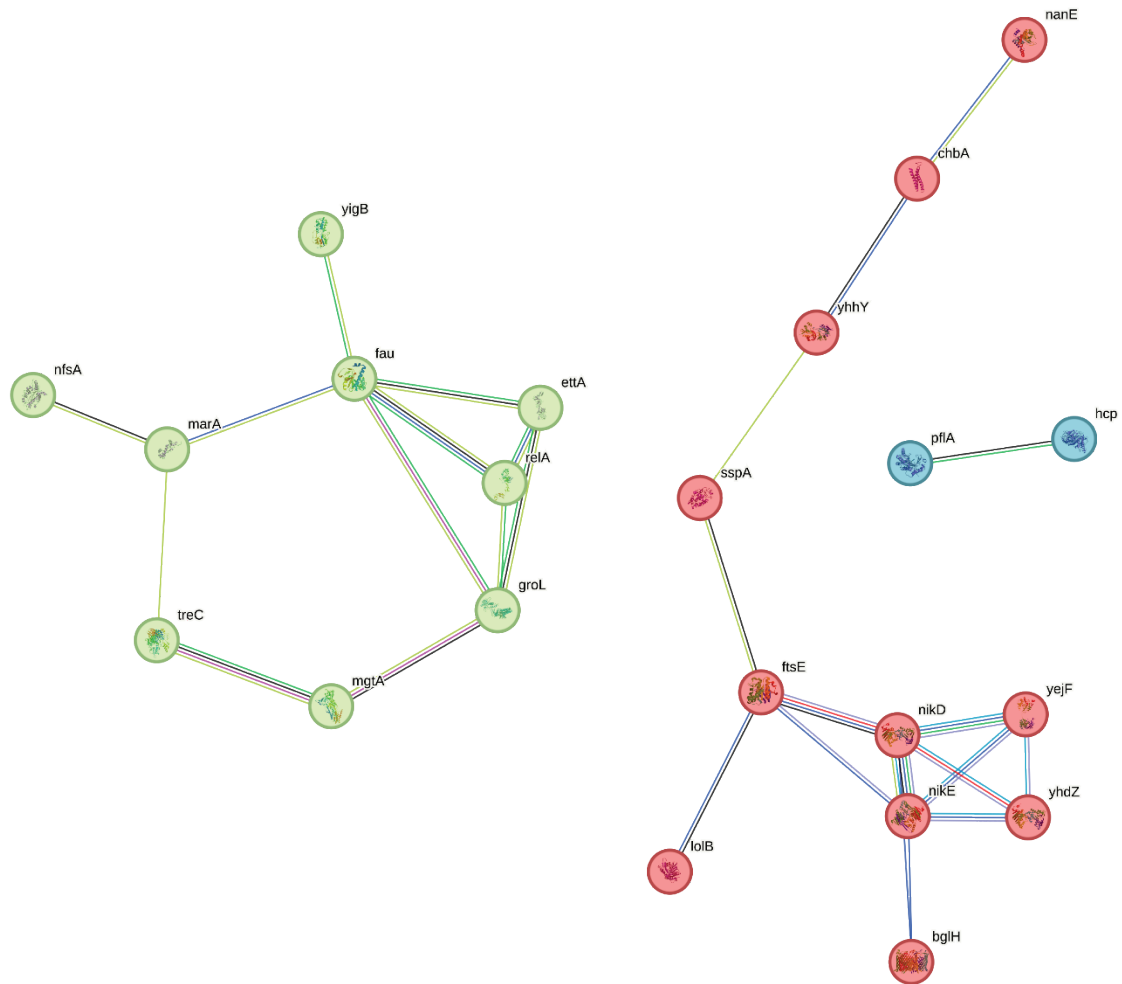


Figure S7. The STRING interaction map of potential survival genes for aminoglycosides. Clusters were indicated by different colors.

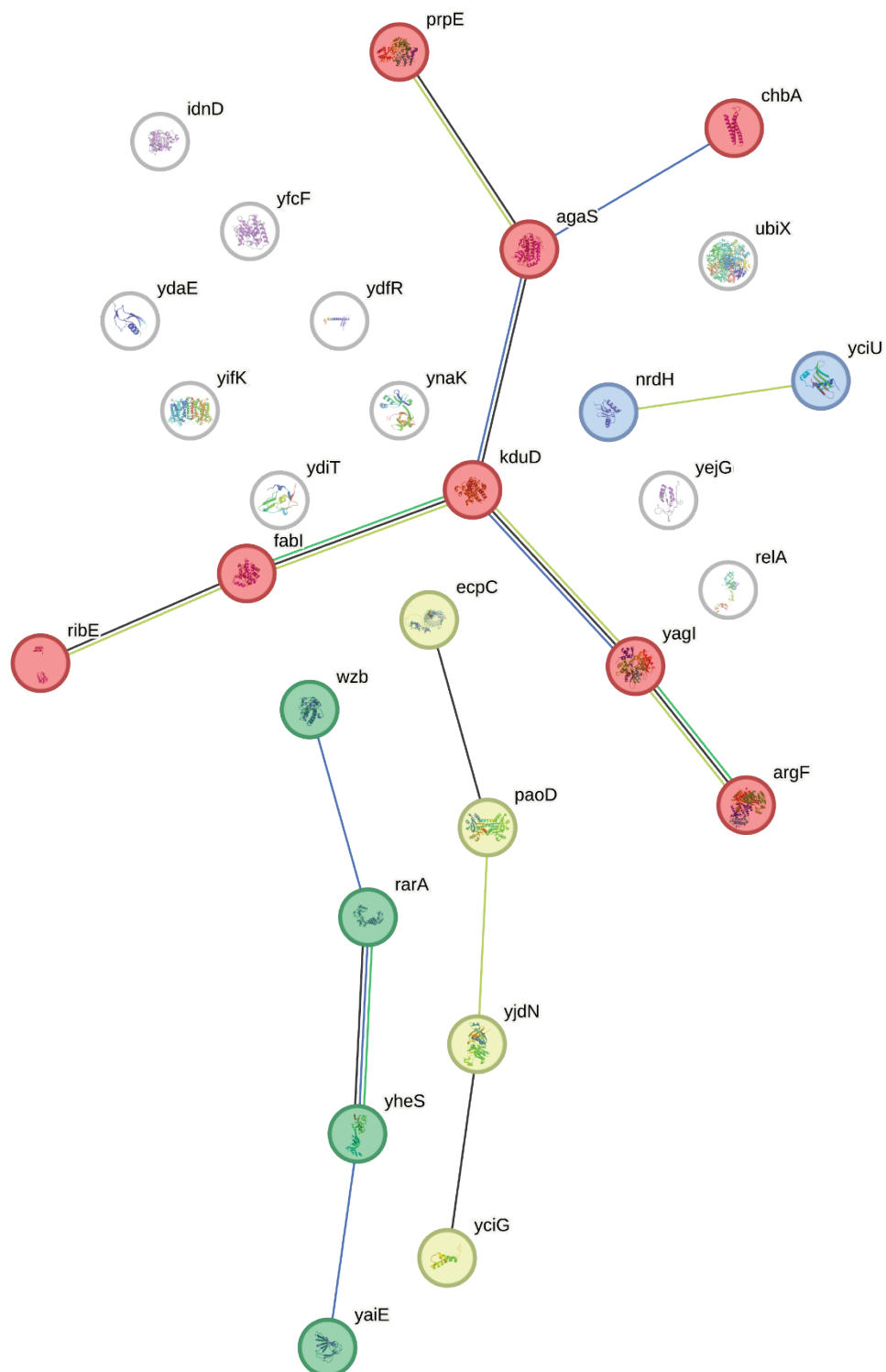


Figure S8. The STRING interaction map of potential survival genes for nitrofurantoin. Clusters were indicated by different colors.

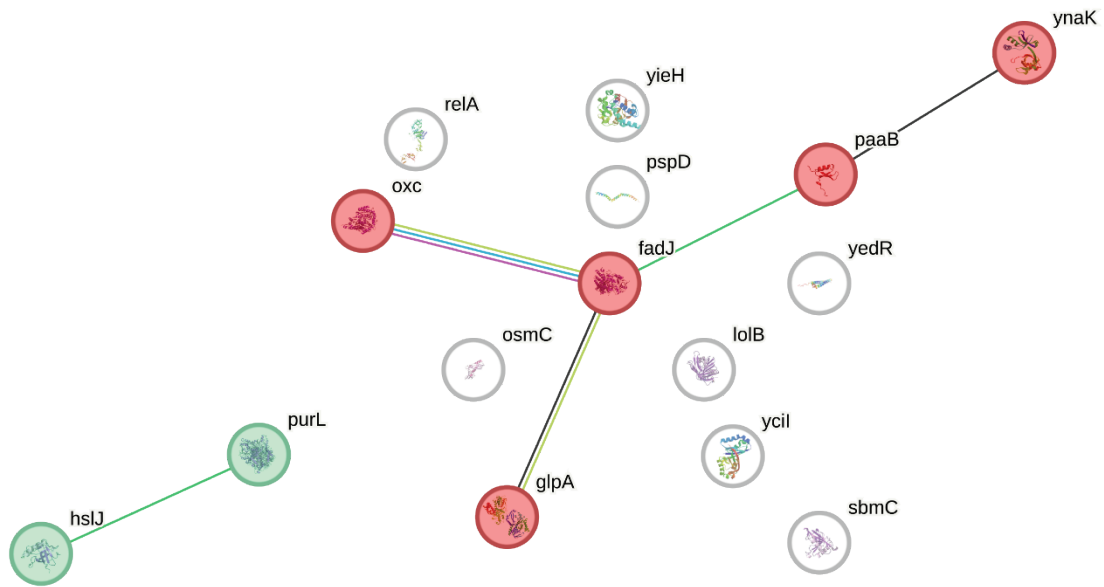


Figure S9. The STRING interaction map of potential survival genes for erythromycin. Clusters were indicated by different colors.

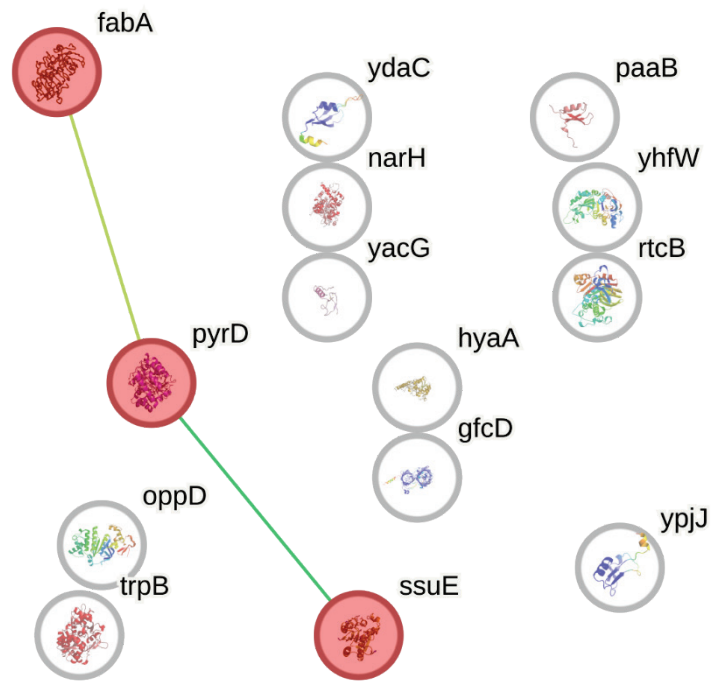


Figure S10. The STRING interaction map of potential survival genes for trimethoprim. Clusters were indicated by different colors.

