A) MIC, by classifer prediction

S
R

Number of genomes

Classifier prediction
- WT S
- NWT I
- NWT R

MIC (mg/L)

B) Disk zones, by classifer prediction

R
S

Number of genomes

Disk zone (mm)

C) Observed phenotype distribution, per genotype profile

Genotype profile		
0^ QRDR, 0 PMQR, aac6−	143 369 5168	
0 QRDR, 0 PMQR, aac6+	30 26 105	
0 QRDR, qnrB1, aac6−	69 61 30	
1 QRDR, 0 PMQR, aac6−	80 22 1	
1 QRDR, 0 PMQR, aac6+	20 1 2	
>1 QRDR, 0 PMQR	2150 2 15	
0 QRDR, 1 PMQR^, aac6−	423 94 29	
0 QRDR, 1 PMQR, aac6+	775 23 21	
0 QRDR, >1 PMQR	66 2	
>0 QRDR, >0 PMQR	2421 2 17	

Observed phenotype
- S
- I
- R

Proportion (%)