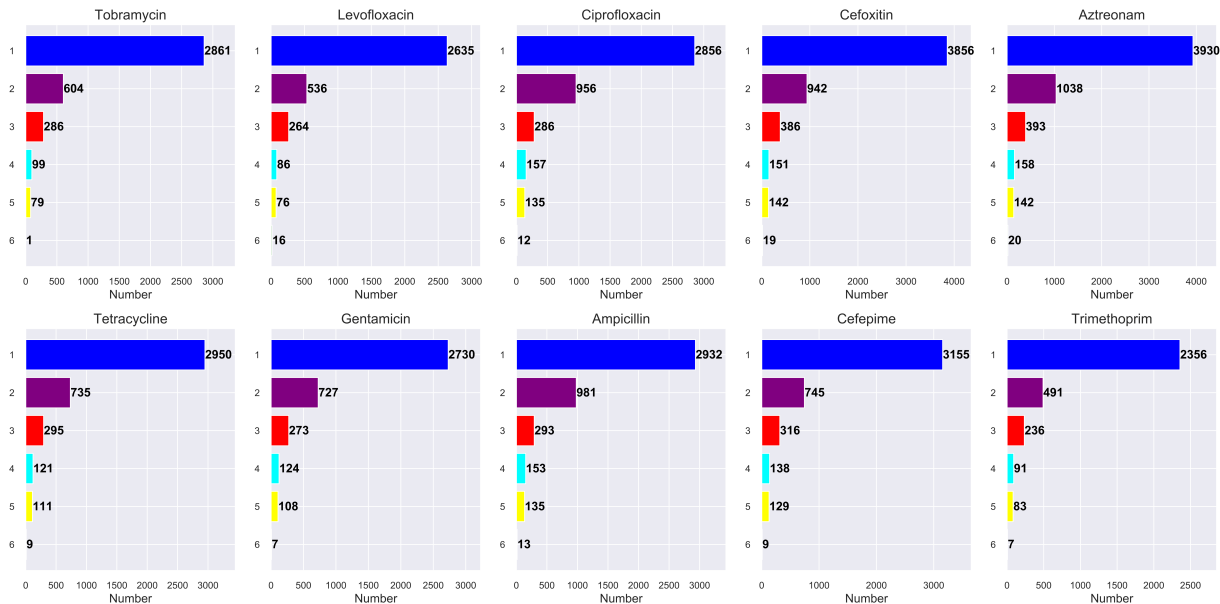
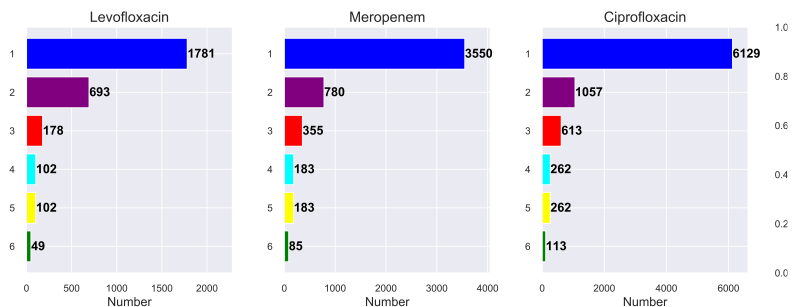


a)



b)



1. Total number of features (k-mer or SNP) in the AMR model
2. Number of unique genes corresponding to the features in the AMR model
3. Number of features in the top 10% of features in the AMR model
4. Number of unique genes corresponding to the top 10% of features in the AMR model
5. Number of genes with functional annotation which correspond to features in the top 10% of features in the AMR model
6. Number of genes in the genome scale model which correspond to features in the top 10% of features in the AMR model