create database MTB_variants; use MTB_variants;

create variants table

create table variants (variant_id int not null, chromosome int not null, position int not null, ref varchar(100) not null, alt varchar(100) not null, consq varchar(100) not null, impact varchar(100), symbol varchar(100), gene varchar(100) not null, feature_type varchar(100), feature varchar(100), biotype varchar(100), exon varchar(100), intron varchar(100), HGCSc varchar(100), HGVSp varchar(100), cDNA_position int, CDS_position int, protein_position int, amino_acids varchar(100), codons varchar(100), existing_variation varchar(100), distance int, strand varchar(100), flags int, pick int, variant_class varchar(100), symbol_source varchar(100), HGNC_ID varchar(100), mutation varchar(100) not null, PRIMARY KEY (variant_id)

) MAX_ROWS=1310000

create isolates table:

Create table isolates (

```
isolate varchar(30) not null,
lineage varchar(100),
metadata varchar(100),
PRIMARY KEY(isolate)
create table DST:
Create table DST (
drug_id int not null,
full_name varchar(30),
drug_abrv varchar(30),
PRIMARY KEY(drug_id)
create the "have" relationship (isolates have variants):
create table have (
isolate varchar(30) not null,
variant_id int not null,
qual float,
DP int,
filter varchar(20),
foreign key (isolate) references isolates(isolate) on delete cascade,
foreign key (variant_id) references variants(variant_id) on delete cascade
)
create the "susceptible_to" relationship (isolates susciptble/resistant to which drug):
create table resistance profile (
isolate varchar(30) not null,
drug_id varchar(30) not null,
R_S varchar(5) not null,
foreign key (isolate) references isolates(isolate) on delete cascade,
foreign key (drug_id) references DST(drug_id) on delete cascade
)
upload files:
load data infile 'variants_table' into table MTB_variants.variants
fields terminated by ','
```

lines terminated by '\n'

load data infile 'have_table' into table MTB_variants.have fields terminated by ',' lines terminated by '\n';