

Supplementary material

Acquisition and dissemination of cephalosporin-resistant *E. coli* in migratory birds sampled at an Alaska landfill as inferred through genomic analysis

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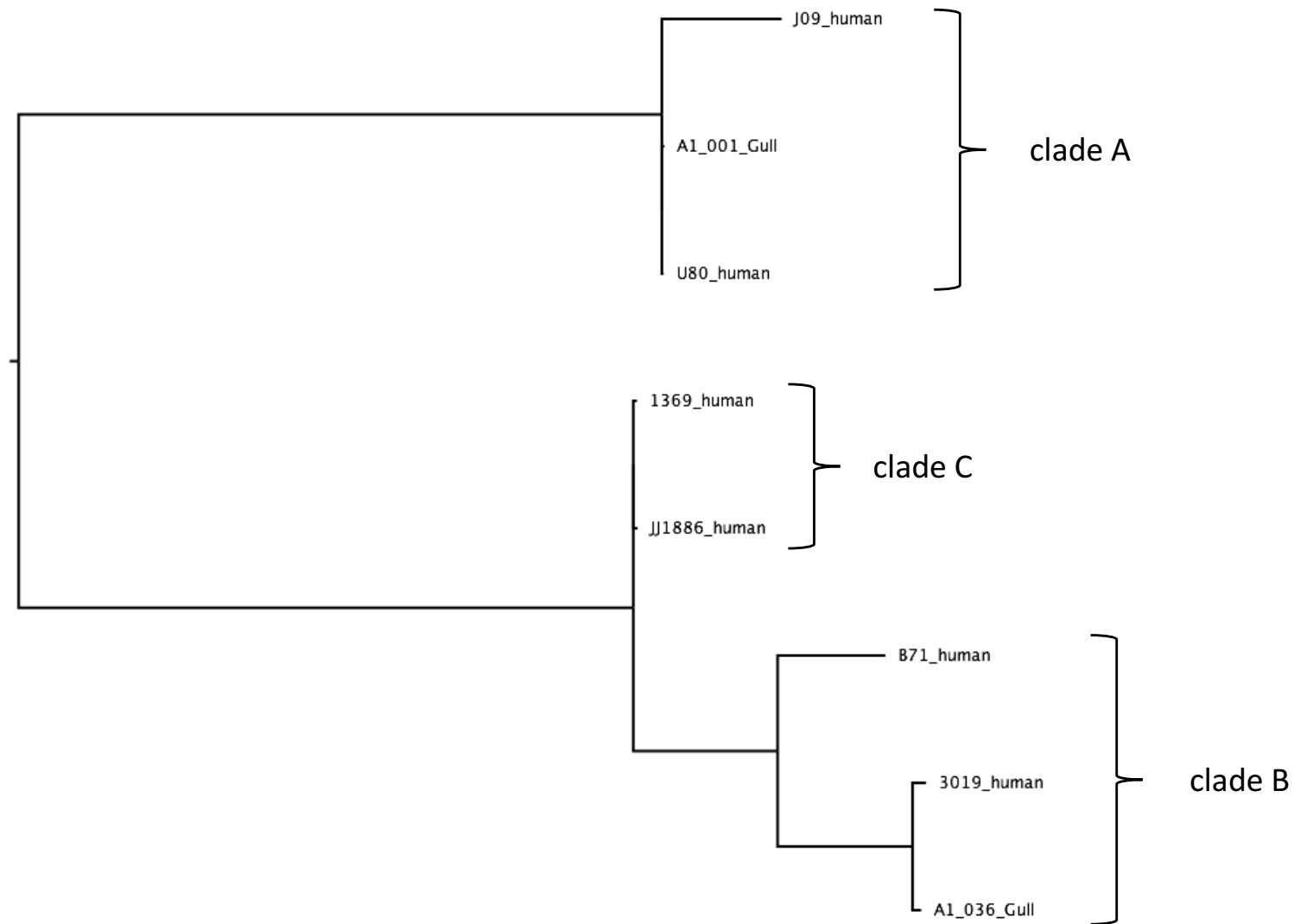


Fig. S1 Midpoint rooted clonal core genome phylogeny of ST131 *E. coli* isolates isolated from large-bodied gulls in this study and human clinical samples previously reported representing the three ST131 clades (McNalley et al., 2016).

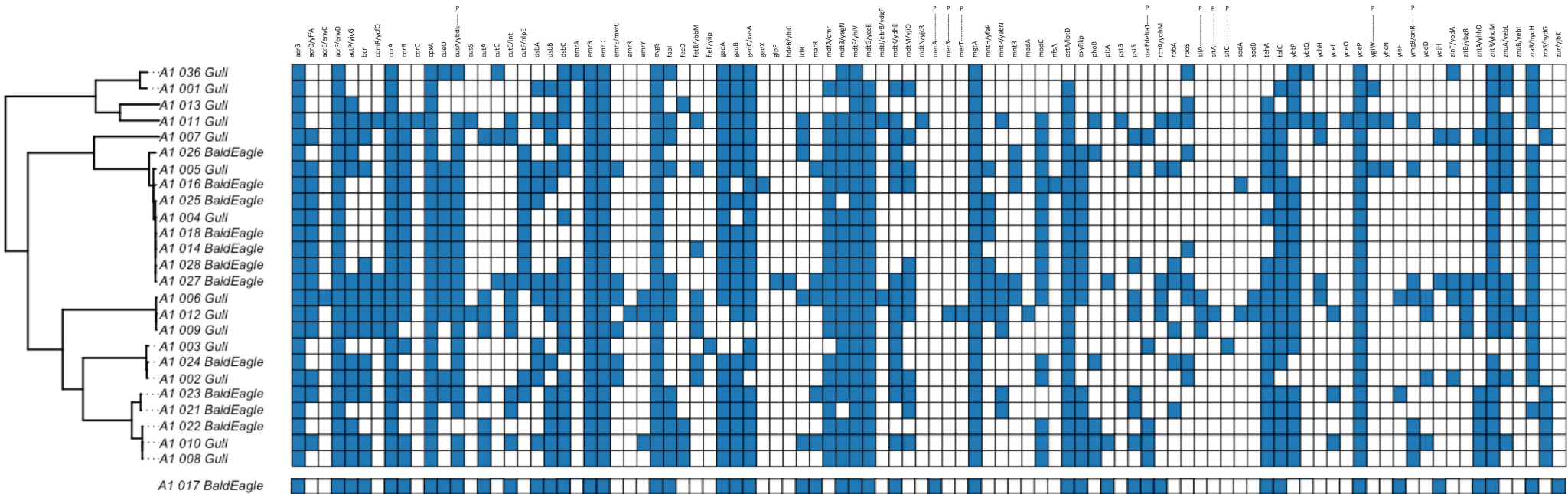


Fig. S2 Midpoint rooted clonal core genome phylogeny of 25 ESBL-producing *E. coli* isolates originating from large-bodied gulls and bald eagles in Alaska. Presence of each of 96 BacMet-identified biocide/heavy metal resistance genes is shown as a matrix, with colored squares indicating presence and white indicating that the gene was not found. The divergent A1_017_BaldEagle isolate is included at the bottom of the matrix. The letter “P” above the gene names indicates the gene has previously been found to be plasmid-borne.

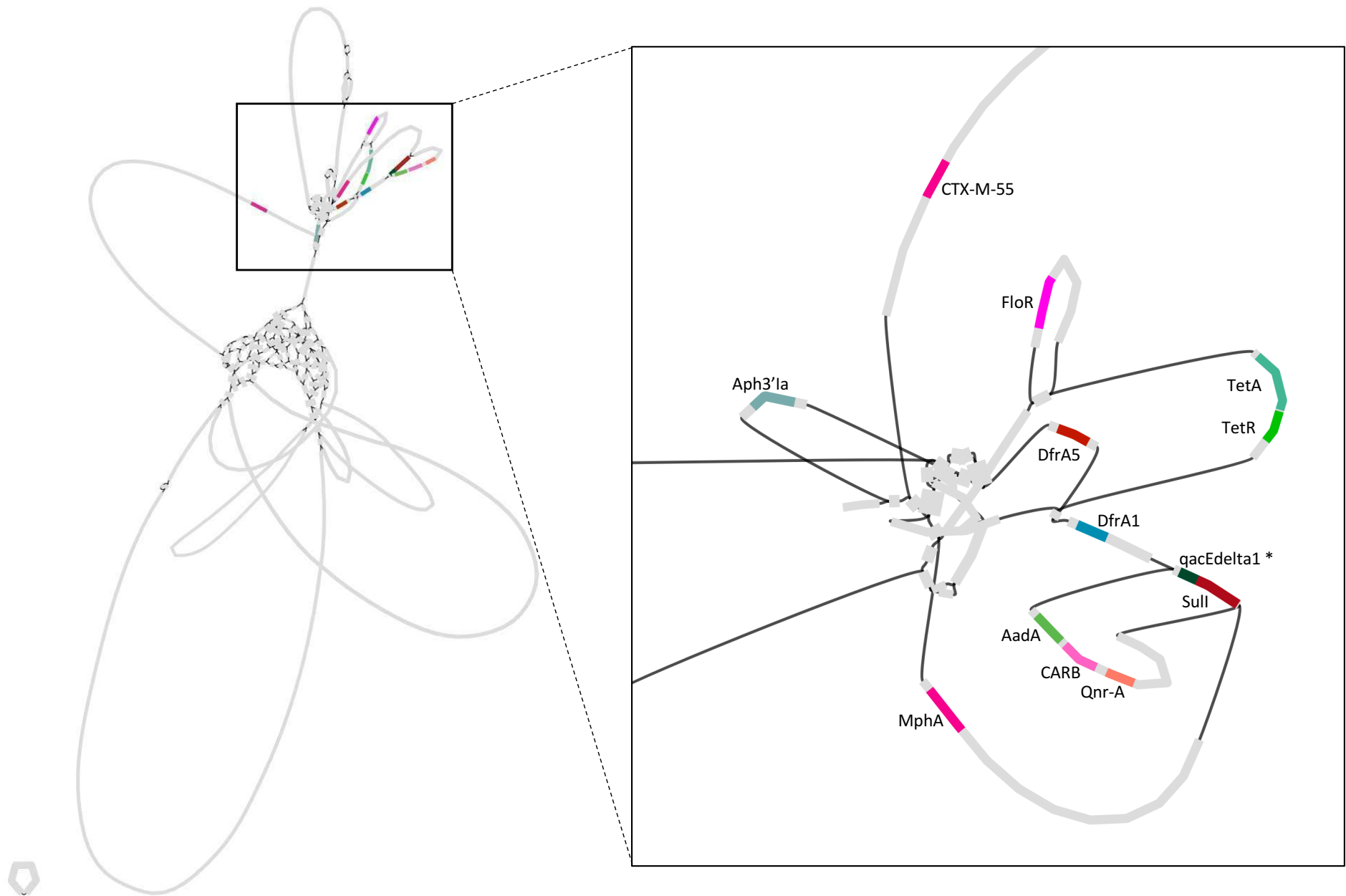


Fig. S3 Isolate A1_007_Gull putative plasmid contigs (grey rectangles) assembled by PlasmidSPAdes and visualized with Bandage. Likely connections between contigs are shown by black lines. The locations of AMR genes and biocide/heavy metal resistance genes are indicated by colored rectangles, labeled with the gene name. Biocide/heavy metal resistance genes are indicated by an asterisk (*).

Supplementary Table 1 Phenotypic resistance profiles to 18 antibiotic discs of ESBL-producing *E. coli* isolates originating from large-bodied gull and bald eagle fecal samples in Alaska.

Isolate ID	NAL	NIT100	PTZ36	TET	TR15	TSU25	MER10	CIP5	AMP10	CDR30	KLO	GEN10	MEC10	AMC	FEP	FOX	CFZ	CTX
A1_001_Gull	S	S	S	S	S	S	S	S	R	R	S	S	S	R	R	R	S	R
A1_002_Gull	S	S	S	S	S	S	S	S	R	R	S	S	S	S	R	S	S	R
A1_003_Gull	S	S	S	R	S	S	S	S	R	R	S	S	S	R	S	R	R	S
A1_004_Gull	S	S	R	S	S	S	S	S	R	R	S	S	S	R	S	R	R	S
A1_005_Gull	S	S	I	S	S	S	S	S	R	R	S	S	S	R	S	R	R	S
A1_006_Gull	S	S	S	R	S	S	S	S	R	R	S	S	S	R	S	R	S	S
A1_007_Gull	R	R	S	R	R	S	S	R	R	R	R	S	S	R	R	R	R	R
A1_008_Gull	S	S	S	S	R	R	S	S	R	R	S	S	S	R	S	R	R	S
A1_009_Gull	S	S	I	R	S	S	S	S	R	R	S	S	S	R	S	R	S	S
A1_010_Gull	S	S	S	S	R	R	S	S	R	R	S	S	S	R	S	R	R	S
A1_011_Gull	S	S	I	S	S	S	S	S	R	R	S	S	S	R	S	R	R	R
A1_012_Gull	S	S	S	R	S	S	S	S	R	R	S	S	S	R	S	R	S	S
A1_013_Gull	S	S	S	S	S	S	S	S	R	R	S	S	S	R	S	R	S	S
A1_014_BaldEagle	S	S	R	S	S	S	S	S	R	R	S	S	S	R	S	R	I	S
A1_016_BaldEagle	S	S	I	R	S	S	S	S	R	R	S	S	S	R	S	R	R	R
A1_017_BaldEagle	S	S	S	R	S	S	S	S	R	R	S	S	S	R	S	R	R	R
A1_018_BaldEagle	S	S	R	S	S	S	S	S	R	R	S	S	S	R	S	R	I	S
A1_021_BaldEagle	S	S	S	R	S	S	S	S	R	R	S	S	S	R	S	R	R	R
A1_022_BaldEagle	S	S	R	S	S	I	S	S	R	R	S	S	S	R	S	R	R	R
A1_023_BaldEagle	S	S	I	S	R	R	S	S	R	R	S	S	S	R	S	R	R	S
A1_024_BaldEagle	S	S	S	S	S	S	S	S	R	R	S	S	S	R	S	R	R	R
A1_025_BaldEagle	S	S	S	S	S	S	S	S	R	R	S	S	S	R	S	R	R	S
A1_026_BaldEagle	S	S	R	S	S	S	S	S	R	R	S	S	S	R	S	R	I	S
A1_027_BaldEagle	S	S	I	S	S	S	S	S	R	R	S	S	S	R	S	R	S	S
A1_028_BaldEagle	S	S	R	S	S	S	S	S	R	R	S	S	S	R	S	R	I	S
A1_036_Gull	S	S	R	S	S	S	S	S	R	R	S	S	S	R	S	R	R	S

S = Susceptible, I = Intermediate, R = Resistant

NAL = nalidixic acid, NIT100 = nitrofurantoin, PTZ36 = piperacillin-tazobactam, TET = tetracycline, TR15 = trimethoprim, TSU25 = trimethoprim-sulfamethoxazole, MER10 = meropenem, CIP5 = ciprofloxacin, AMP10 = ampicillin, CDR30 = cefadroxil, KLO = chloramphenicol, GEN10 = gentamicin, MEC10 = mecillinam, AMC = Amoxicillin/clavulanic acid, FEP = Cefepime, FOX = Ceftaxime, CFZ = Ceftazidime, CTX = Cefotaxime

Supplementary Table 2 WGS *de novo* assembly metrics of 27 ESBL-producing *E. coli* isolates originating from large bodied gull and bald eagle fecal samples in Alaska.

Isolate ID	mean # contigs >500bp
A1_001_Gull	104
A1_002_Gull	81
A1_003_Gull	84
A1_004_Gull	82
A1_005_Gull	179
A1_006_Gull	206
A1_007_Gull	108
A1_008_Gull	146
A1_009_Gull	90
A1_010_Gull	241
A1_011_Gull	170
A1_012_Gull	372
A1_013_Gull	89
A1_014_BaldEagle	74
A1_016_BaldEagle	120
A1_017_BaldEagle	107
A1_018_BaldEagle	100
A1_020_BaldEagle	931
A1_021_BaldEagle	139
A1_022_BaldEagle	263
A1_023_BaldEagle	231
A1_024_BaldEagle	212
A1_025_BaldEagle	92
A1_026_BaldEagle	160
A1_027_BaldEagle	256
A1_028_BaldEagle	122
A1_036_Gull	52

File S1: Command line arguments for programs used

Arguments:

\$1= prefix for each isolate ID

\$2= path to SPAdes-assembled contigs

ConDeTri

```
perl condetri.pl -fastq1=$1_R1.fastq -fastq2=$1_R2.fastq -prefix=$1 -sc=33
```

```
perl filterPCRDupl.pl -fastq1=$1_trim1.fastq -fastq2=$1_trim2.fastq -prefix=$1
```

SPAdes

```
python spades.py -k 21,33,55,77,99,127 --cov-cutoff 'auto' --careful -1 $1_uniq1.fastq -2 $1_uniq2.fastq
```

PlasmidSPAdes

```
python spades.py -k 21,33,55,77,99,127 --cov-cutoff 'auto' --plasmid --careful -1 $1_uniq1.fastq -2 $1_uniq2.fastq
```

Parsnp

```
parsnp -r ! -d $2 -c
```

ClonalFrameML

```
./ClonalFrameML "path to parsnp nwk tree file" "path to parsnp xmfa file" -xmfa_file true
```

in silico phylotyping (Kaas et al., 2012)

```
perl Ks_phylotyper.pl -t Phylotyping_products.txt -r rules_table.txt -l results.txt $2
```

SRST2 MLST typing

```
python srst2.py --input_pe $1_uniq1.fastq $1_uniq2.fastq --log --mlst_db Escherichia_coli1.fasta --mlst_definitions ecoli.txt --forward _uniq1 --reverse _uniq2
```

SRST2 AMR gene detection

```
python srst2.py --input_pe $1_uniq1.fastq $1_uniq2.fastq --log --gene_db srst2/data/ARGannot.r1.fasta --forward _uniq1 --reverse _uniq2 --report_all_consensus
```

```
python srst2.py --prev_output "path to srst2 AMR gene detection results" --output compiled_AMR_results
```

```
python consensus_alignment.py --in "path to srst2 AMR gene detection results" *.all_consensus_alleles.fasta --type gene
```

BacMet biocide/heavy metal resistance gene detection

```
perl BacMet-Scan.pl -i $2 -d BacMet_EXP.704
```

Seqpoet *in silico* PCR

```
seqpoet --pcr --out $1_insilicoPCR_results.fasta $2.fasta primers.txt
```

LS-BSR

```
python ls_bsr.py -d $2 -c usearch
```

```
python filter_BSR_variome.py --bsr_matrix= bsr_matrix.txt
```