SUPPLEMENTARY MATERIAL

Legends to supplementary figures:

Supplementary figure 1a: Distribution of genome coverage for *E. coli* isolates with confirmed ESBL and/or presence of *mcr*. The genome fraction of coverage of *E. coli* reference genome was set to 80% to ensure that only *Ec* isolates were analysed **Supplementary figure 1b: Ec-isolates filtering according to contigs.** Only samples with assemblies with less than 1,200 contigs were used for core genome analysis.

Supplementary Figure 2: Population structure of *Ec* with ESBL and *mcr* genes from Thailand

Phylogeny of *Ec* isolates was received from an alignment of 2,359 core genes. Core genome single nucleotide variants (cgSNVs) were extracted. We defined eight major sequence clusters (inner ring) and identified 146 distinct sequence types (ST). The STs were indicated with very small font sizes. The most common prevalent STs were ST10 (n=37), ST515 (n=21) and ST48 (n=18) and were labeled. The different farm sizes (middle ring) and hosts (outer ring) are indicated. SC; sequence cluster

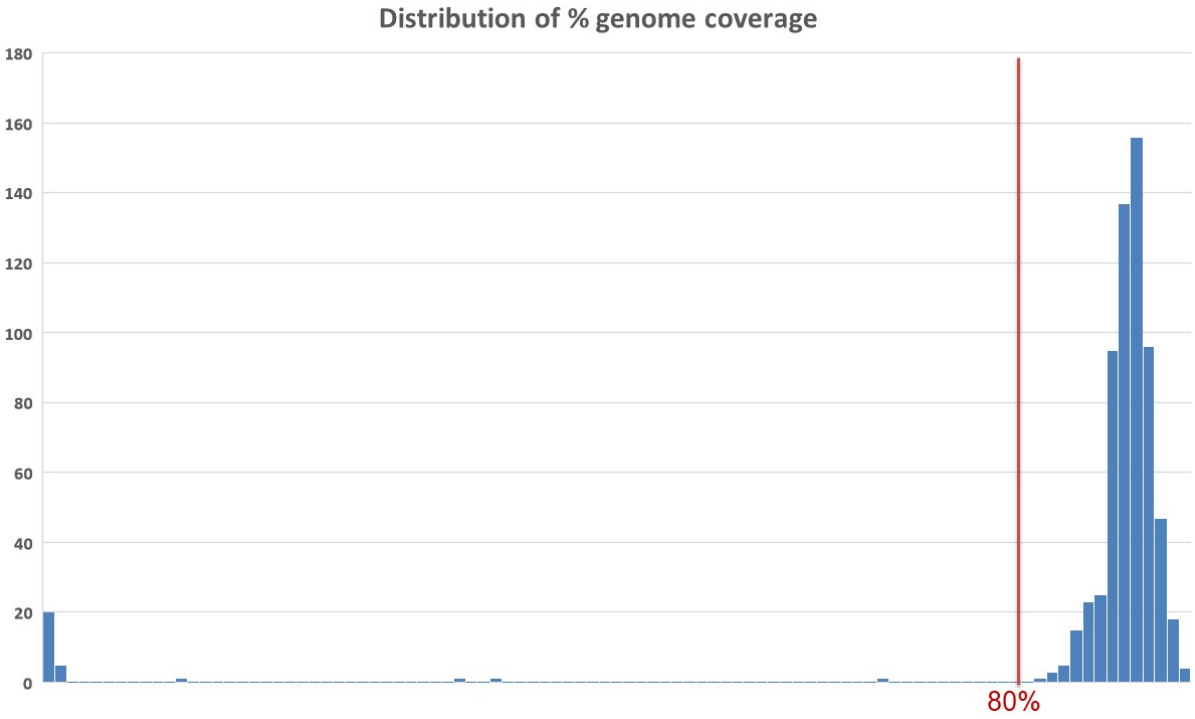
Supplementary figure 3: Characterization of *Ec* isolates by long and short read sequencing (hybrid assembly).

The same resistance gene ($bla_{\text{CTX-M-55}}$) was identified in the large (228,400 bp) plasmid IncHI1 for P188_1R and PMF6H0_1R (PMF06; **Supplementary figure 3A**). The hybrid sequences of the plasmids were visualized by BRIG.

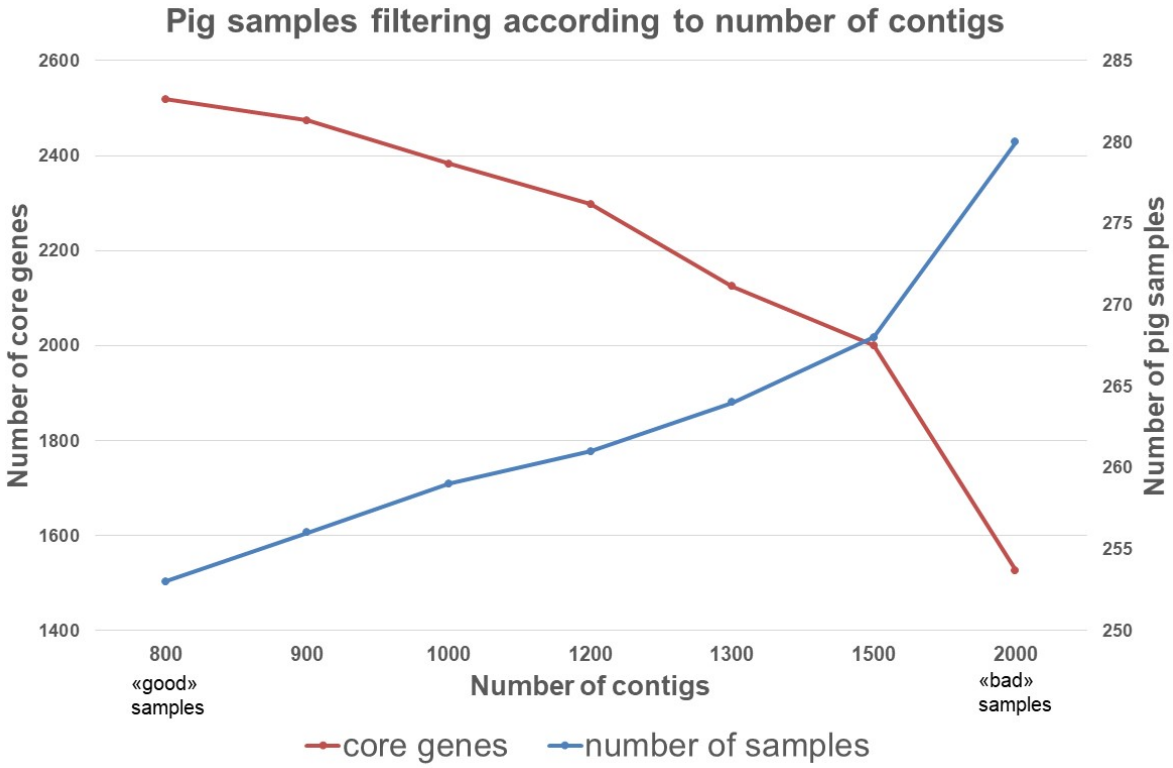
mcr-1's chromosomal environment was identified in two pig farmers and one pig from farm ID PMF02 (**Supplementary figure 3B)**

Supplementary figures:

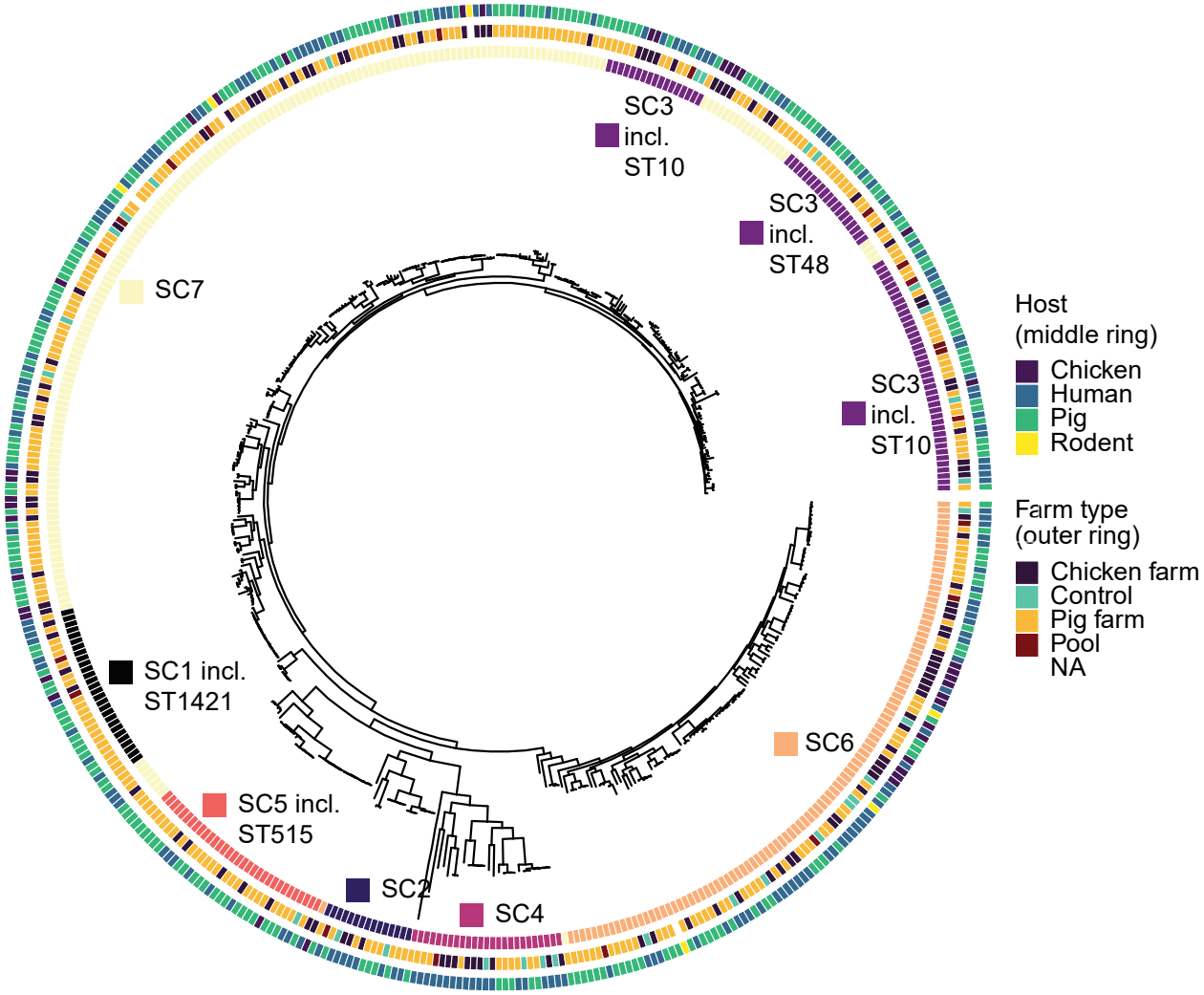
Supplementary figure 1a



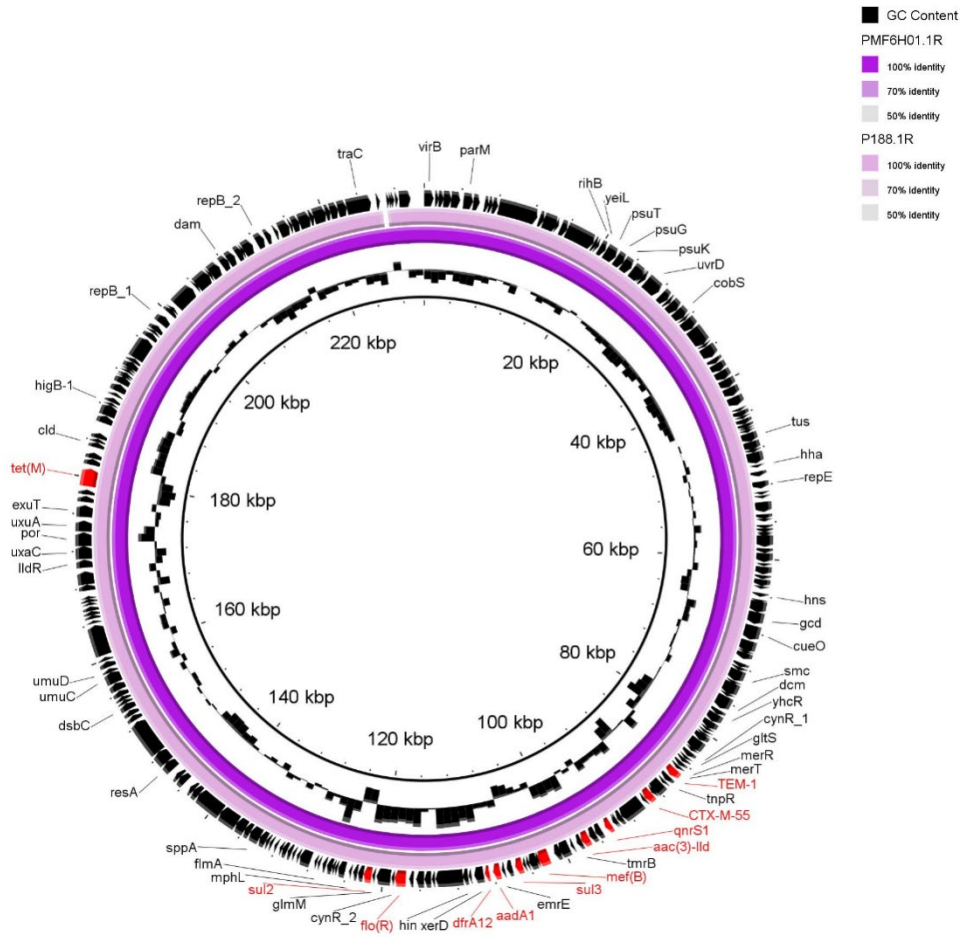
Supplementary figure 1b



Supplementary figure 2



Supplementary figure 3A: Plasmid for PMF6



Supplementary figure 3B: *mcr-1*'s chromosomal environment in two pig farmers and one pig from farm PMF02