

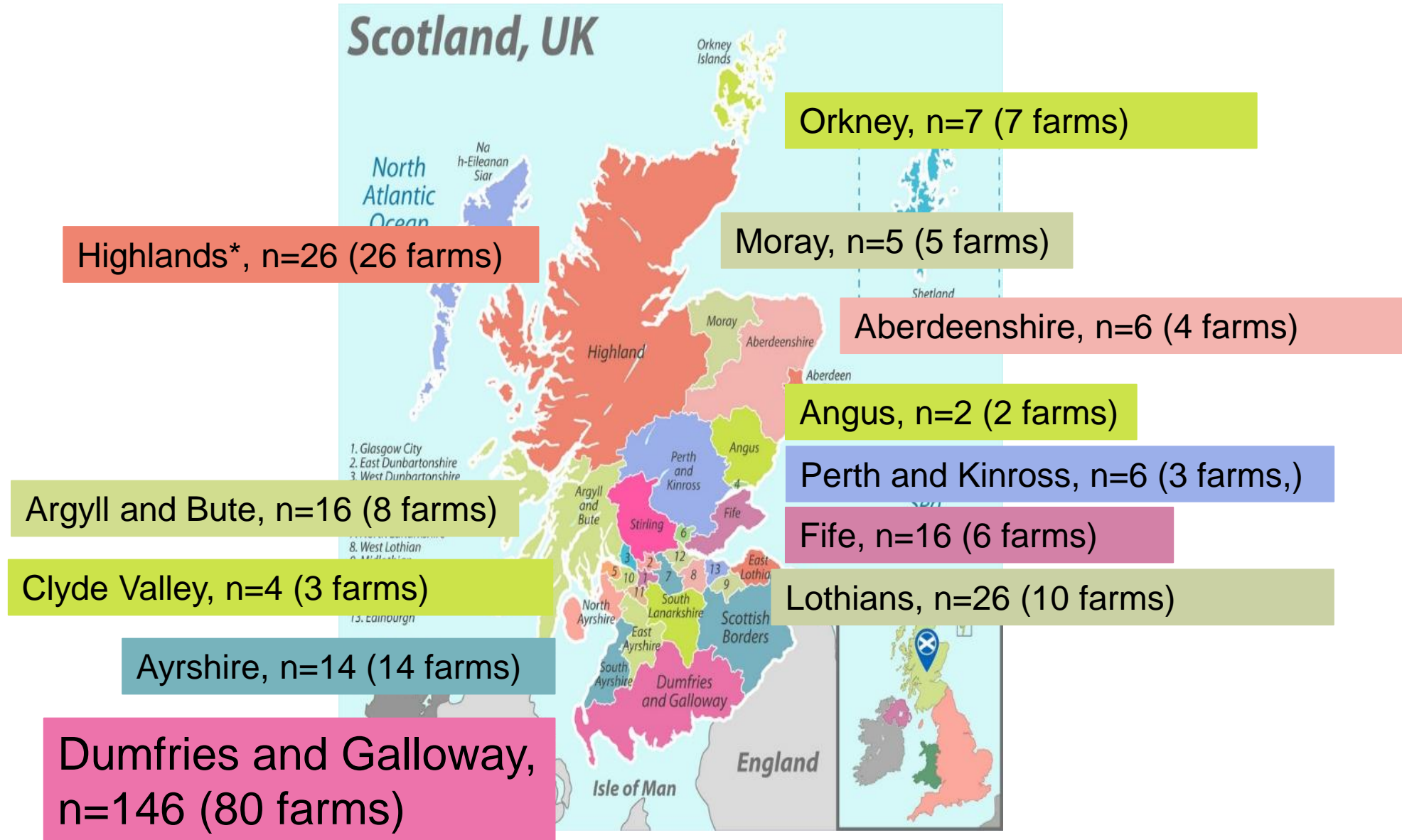


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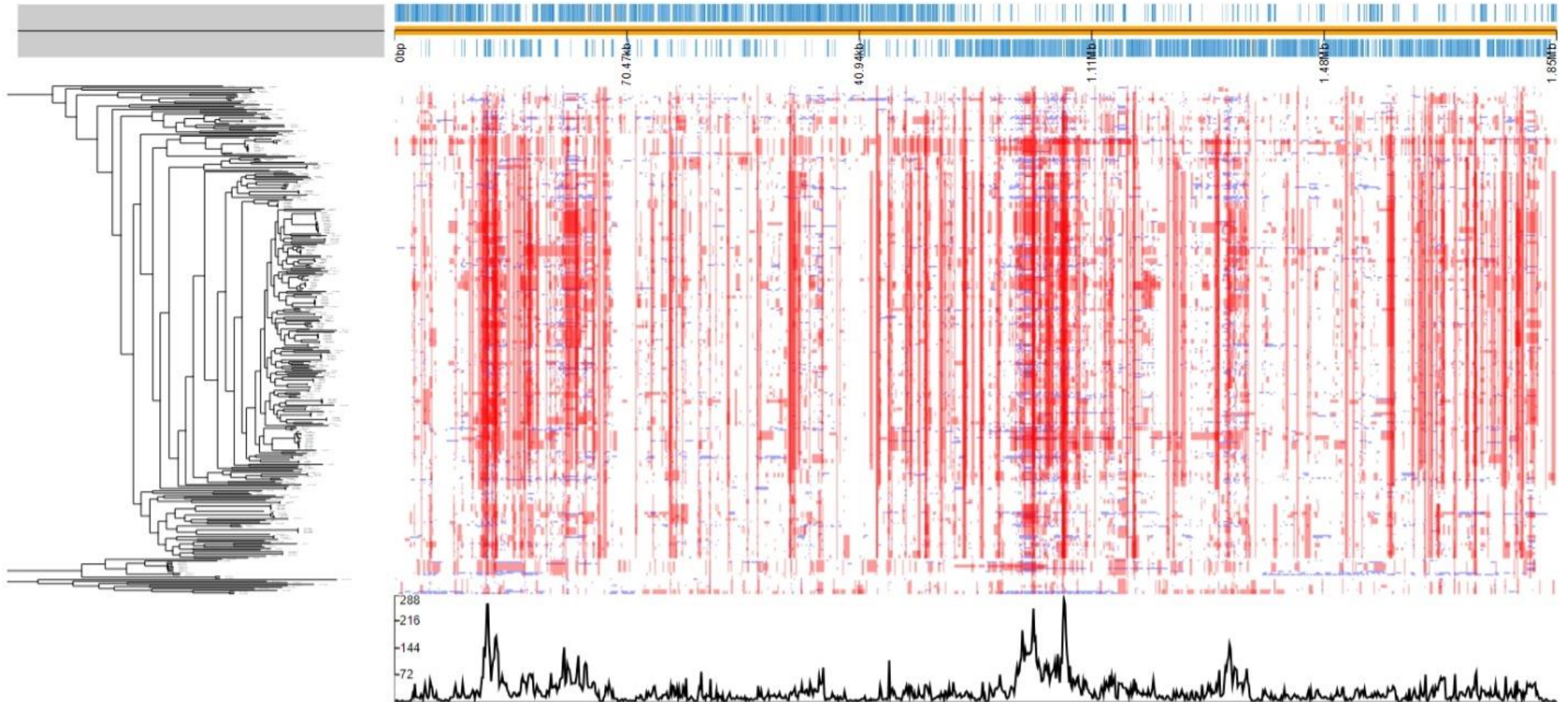
Dr Gavin Paterson

Genomic analysis of the bovine mastitis pathogen *Streptococcus uberis*

Sequenced isolates: 274 isolates from 168 premises (2007-2022)



The *S. uberis* genome is highly recombinogenic



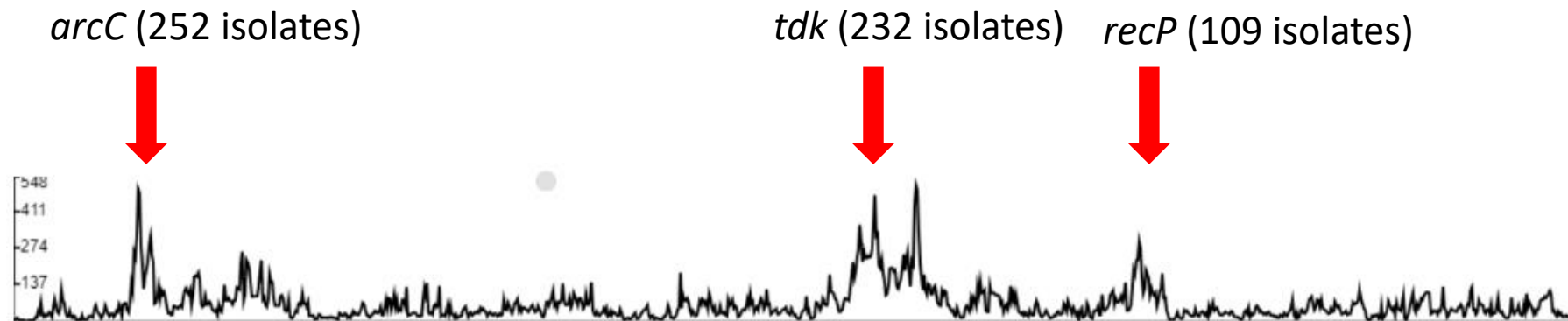
Recombination undermines the value of multilocus sequence typing

Strains typed based on sequence of seven house-keeping genes

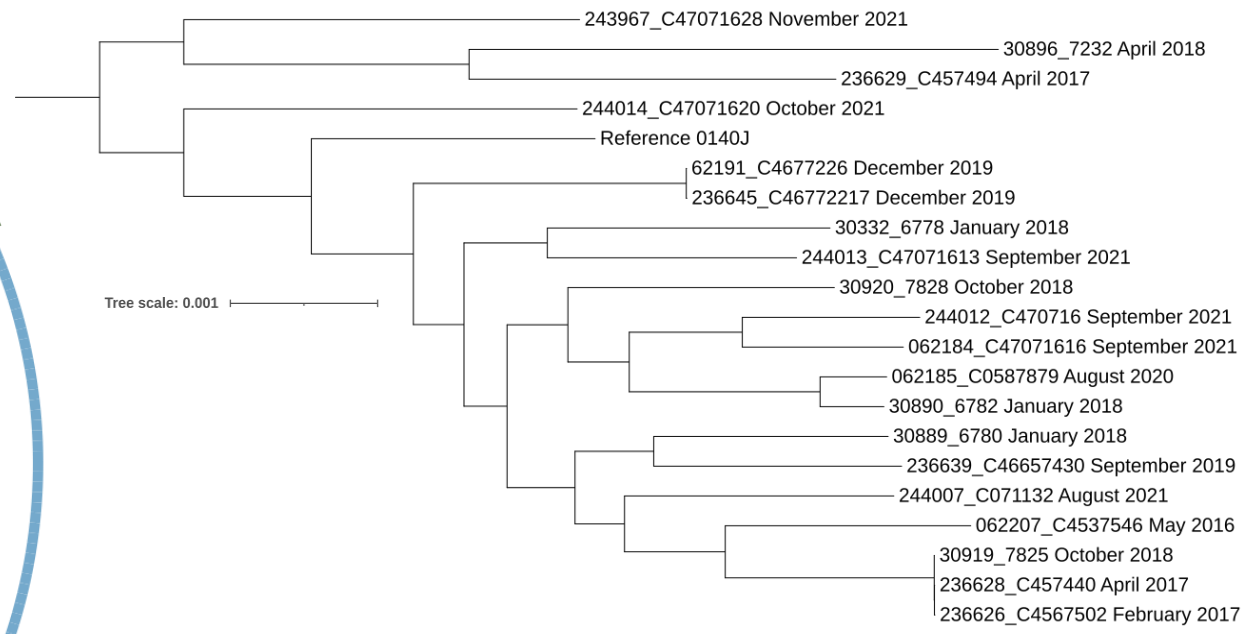
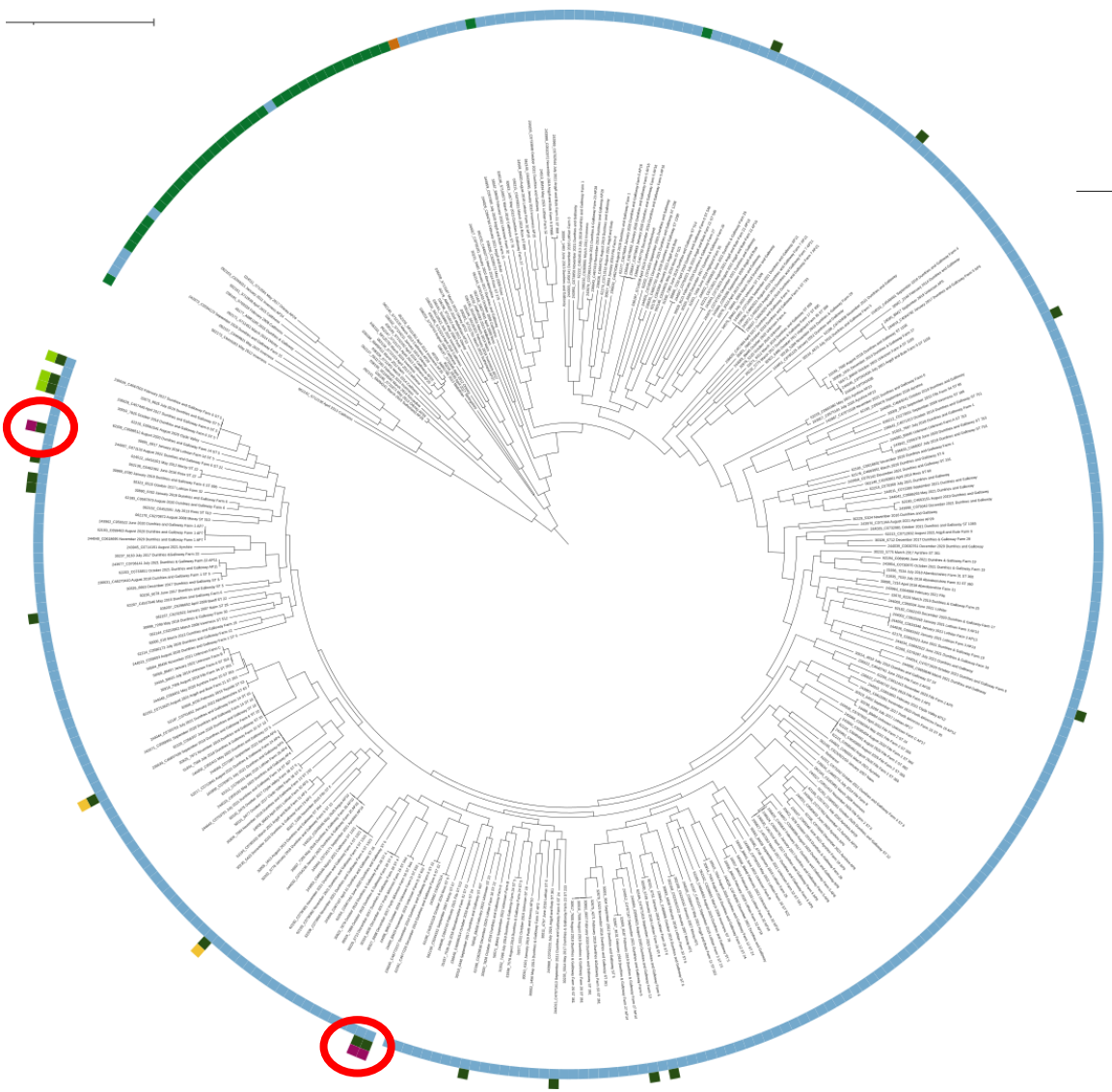
Each unique gene sequence (allele) given a number

Strains then given a seven-digit 'bar-code' denoting their allele profile

Each unique allele profile given a sequence type (ST) number which is assigned to strains matching that profile



Farm 6 (20 isolates)



Farm 6

■ Farm 6

Farm 6 STs

■ ST5

■ ST10

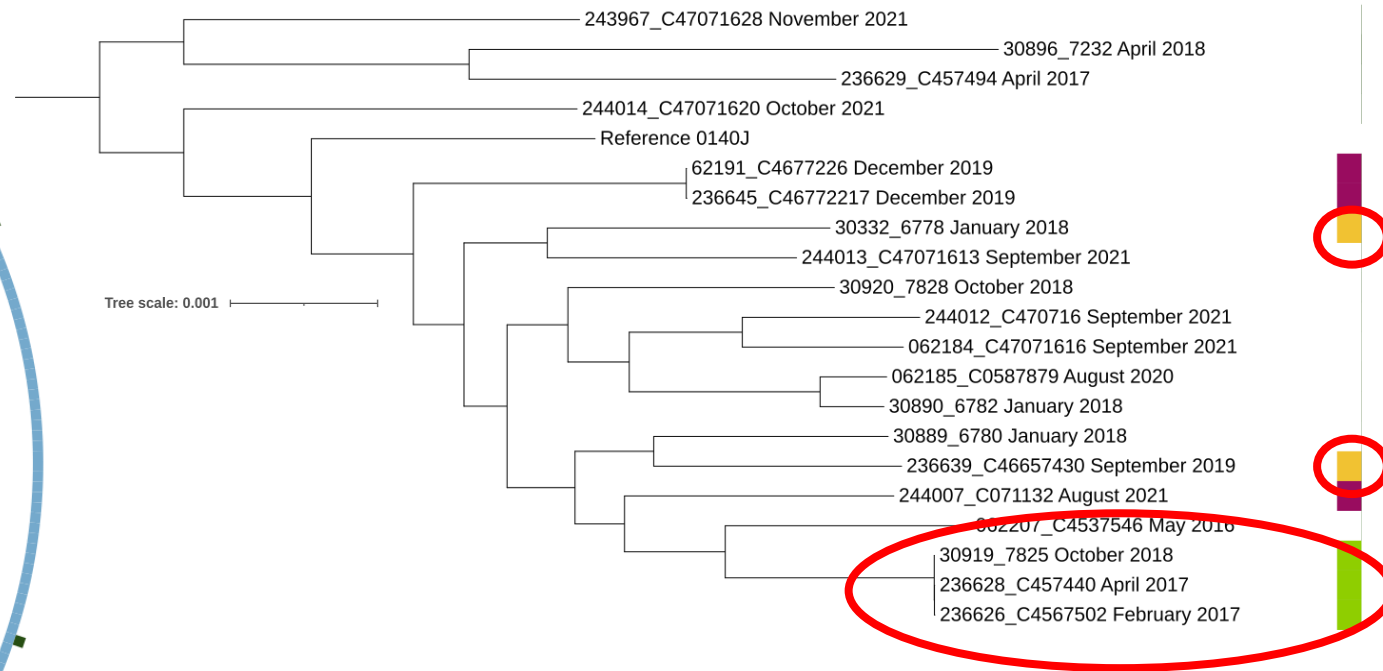
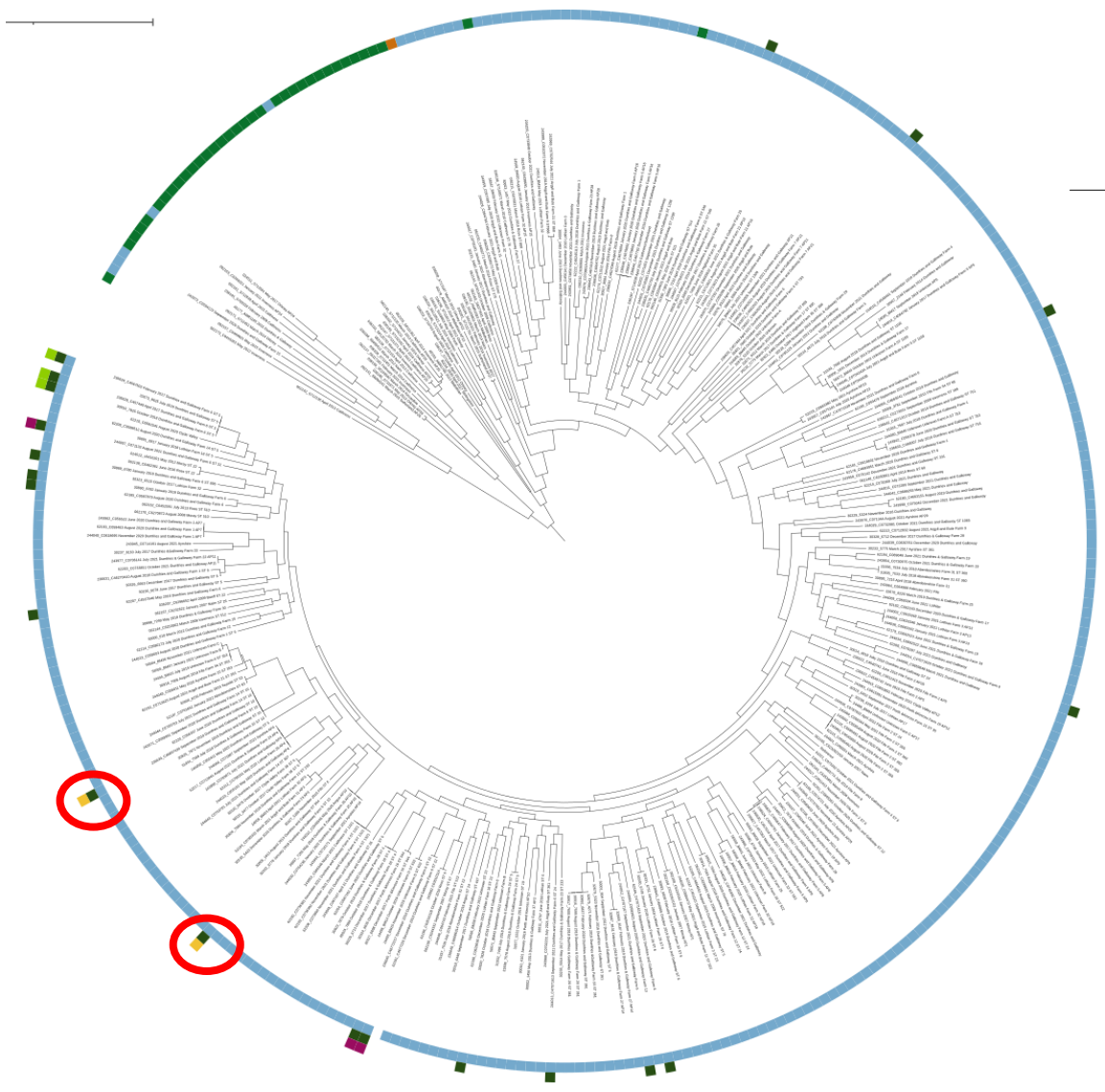
■ ST22

■ ST5

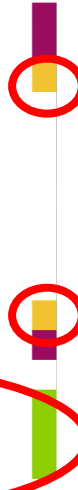
■ ST10

■ ST22

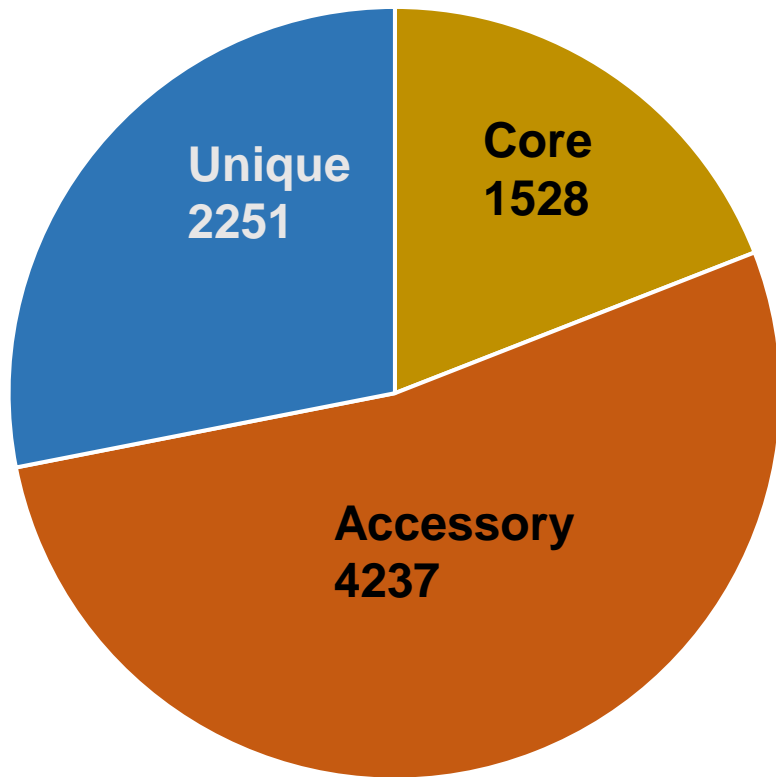
Farm 6 (20 isolates)



- Farm 6**
- Farm 6
- Farm 6 STs**
- ST5
 - ST10
 - ST22

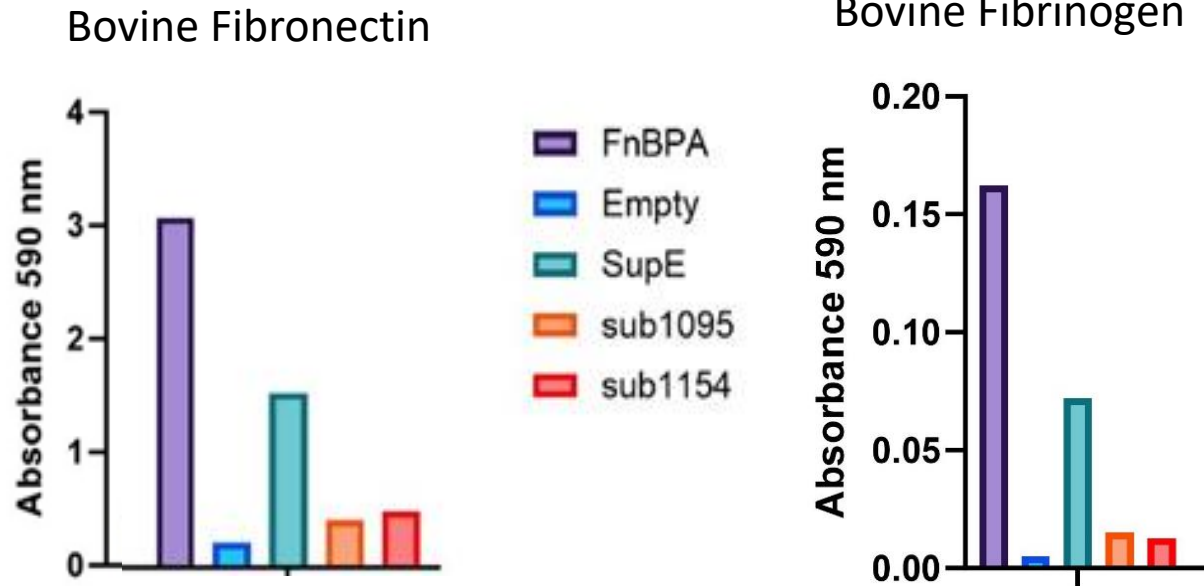
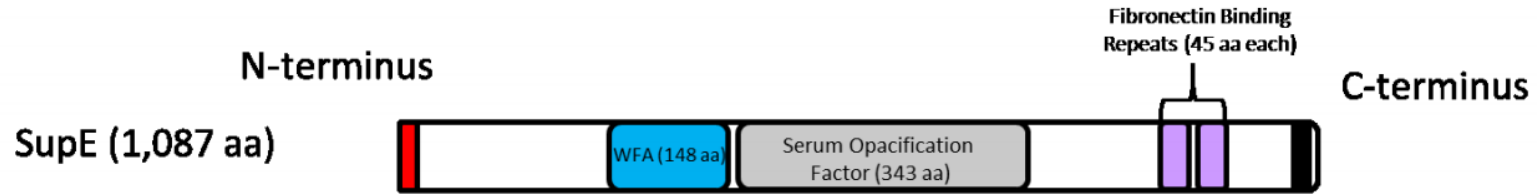


Pangenome (All sequenced *S. uberis* isolates)



- Pangenome (all genes found within population/collection of isolates): **8016 genes**
- Core genes (found in $\geq 95\%$ of isolates): **1528**
- **992** genes found in 100% of isolates
- Accessory genes (found in >1 isolate but $<95\%$ of isolates): **4237**
- Unique genes (found in **one** isolate): **2251**
- 5475/8016 genes = “hypothetical protein” (68.3%)

Using the genome to understand disease pathogenesis: the example of cell-wall-anchored proteins



SupE identified as novel bacterial adhesin binding bovine fibronectin and fibrinogen

Thank you!

- **University of Edinburgh:** Logan Newstead, Tom Smith-Zaitlik, Jennifer Harris, Alastair Macrae & Ross Fitzgerald
- **SRUC:** Geoff Foster, Colin Mason & Katrina Henderson
- **Moredun Research Institute:** Nuno Silva



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