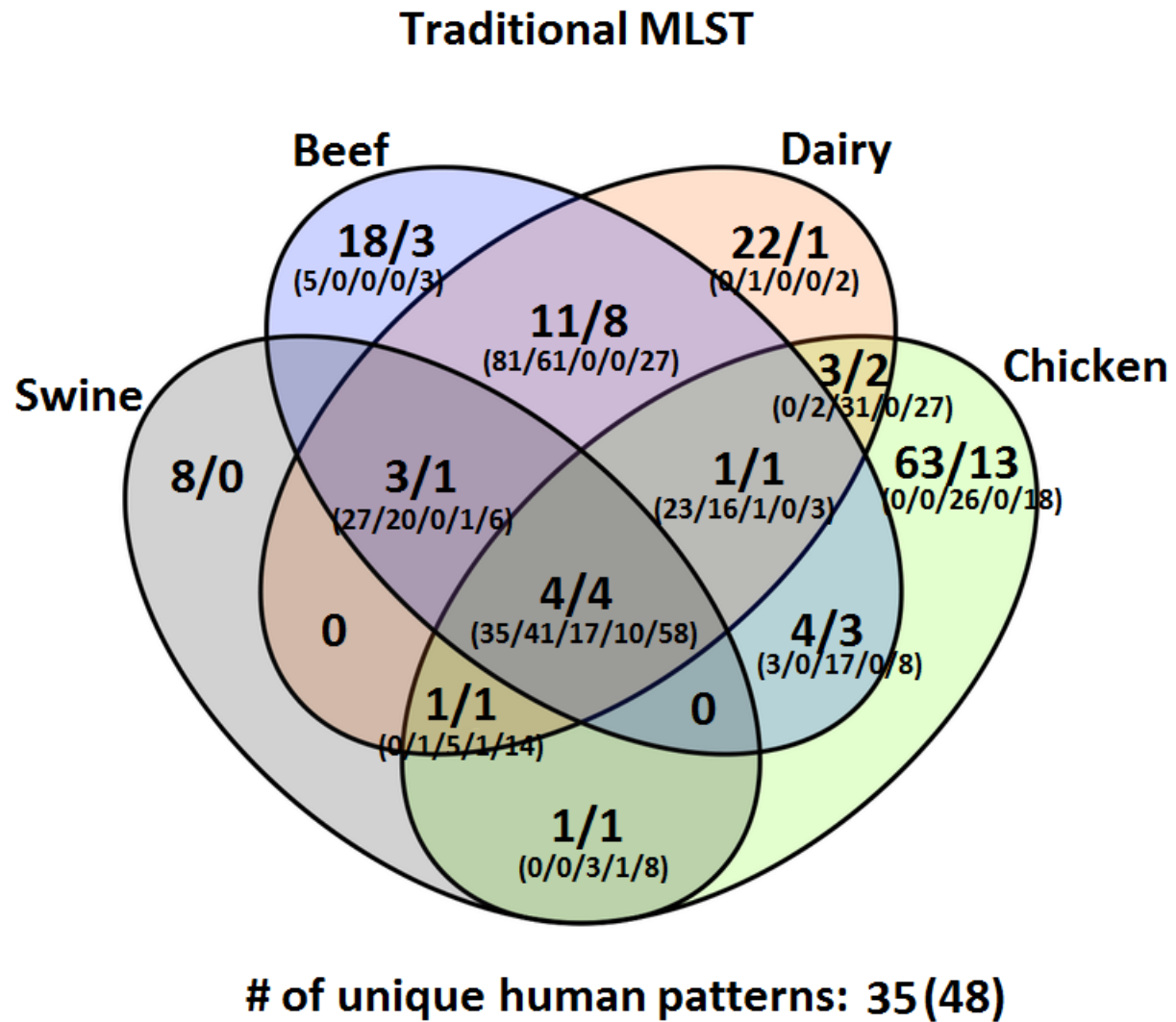
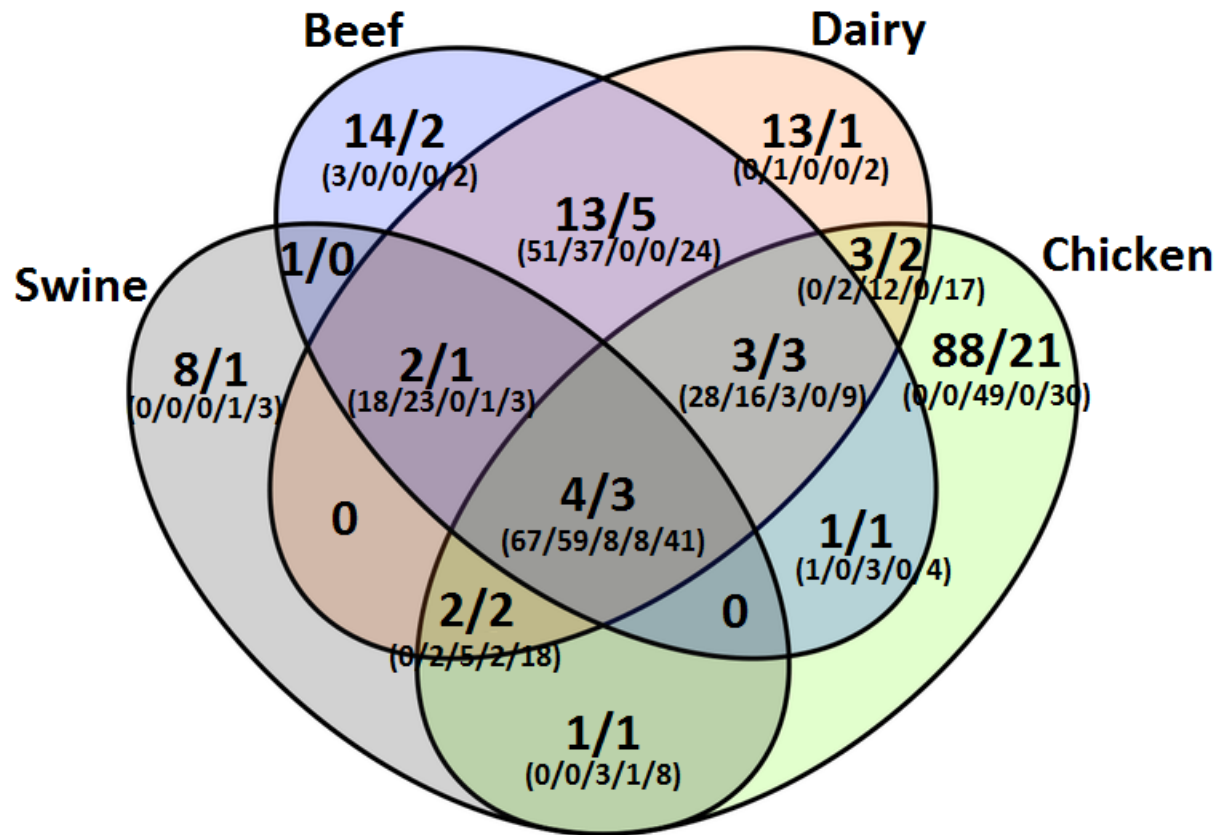


Supplemental Data

Figure S3:

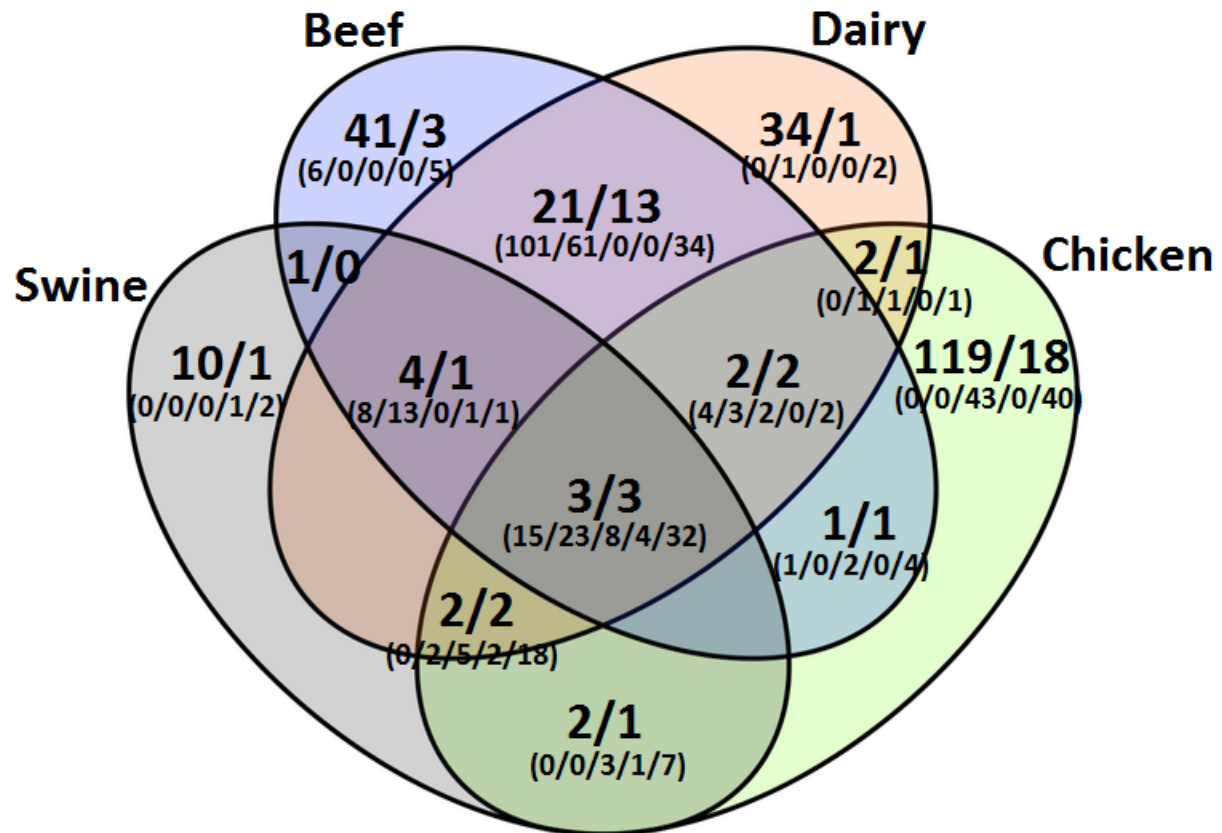


## Allelic Difference 200



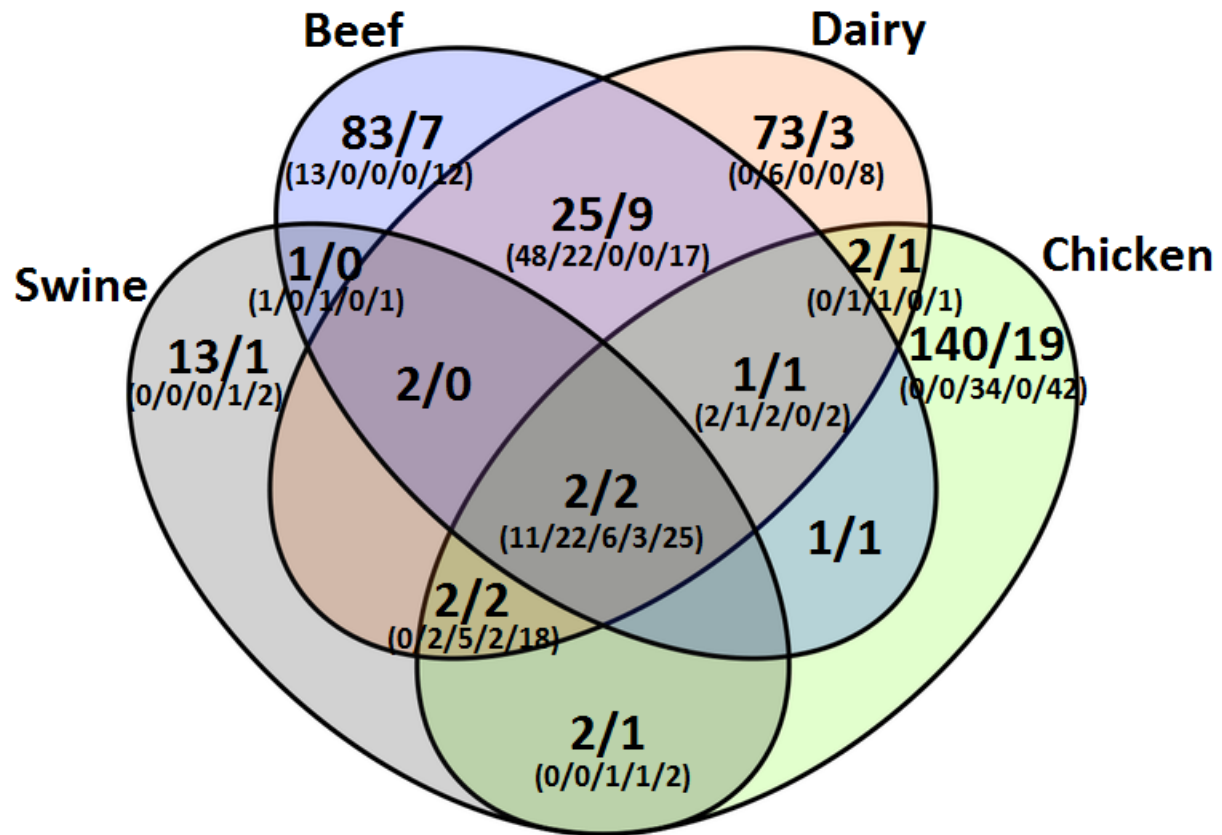
# of unique human patterns: 44 (61)

# Allelic Difference 100



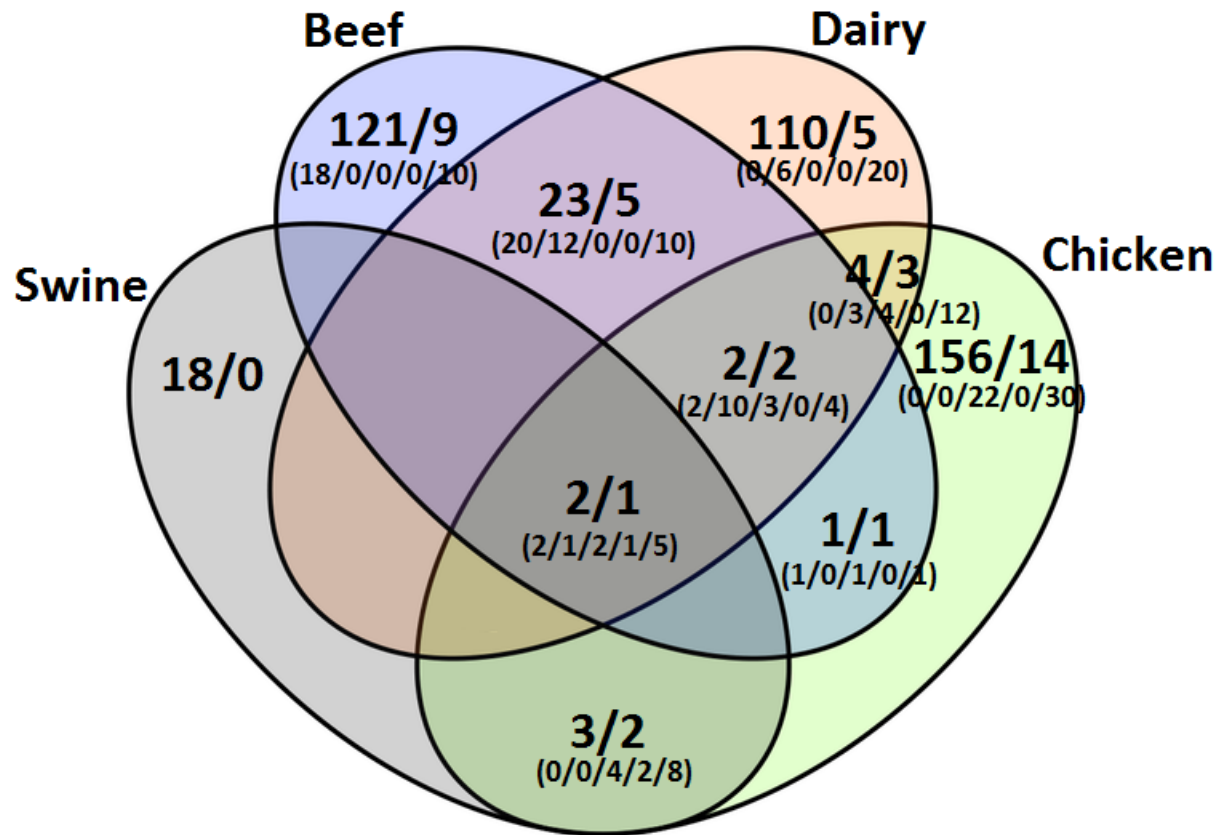
# of unique human patterns: 56 (74)

# Allelic Difference 50



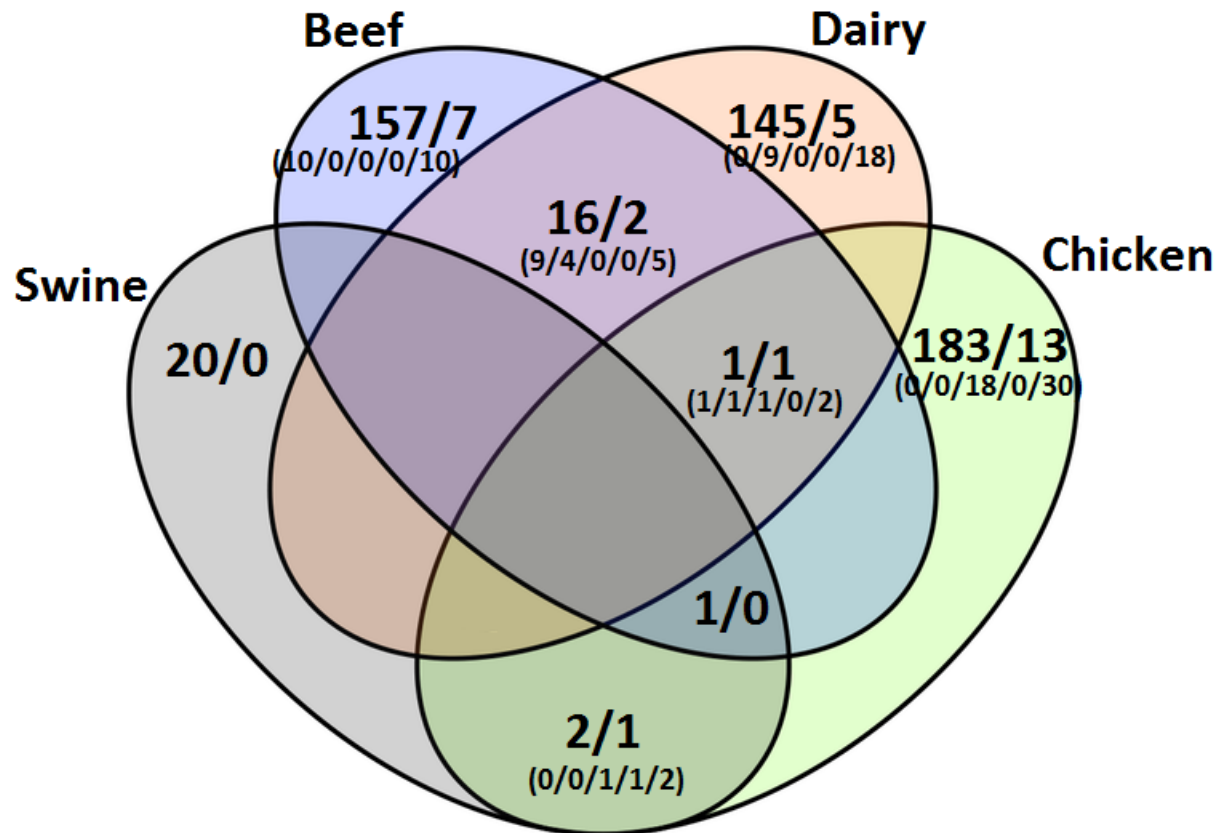
# of unique human patterns: 75(92)

## Allelic Difference 25



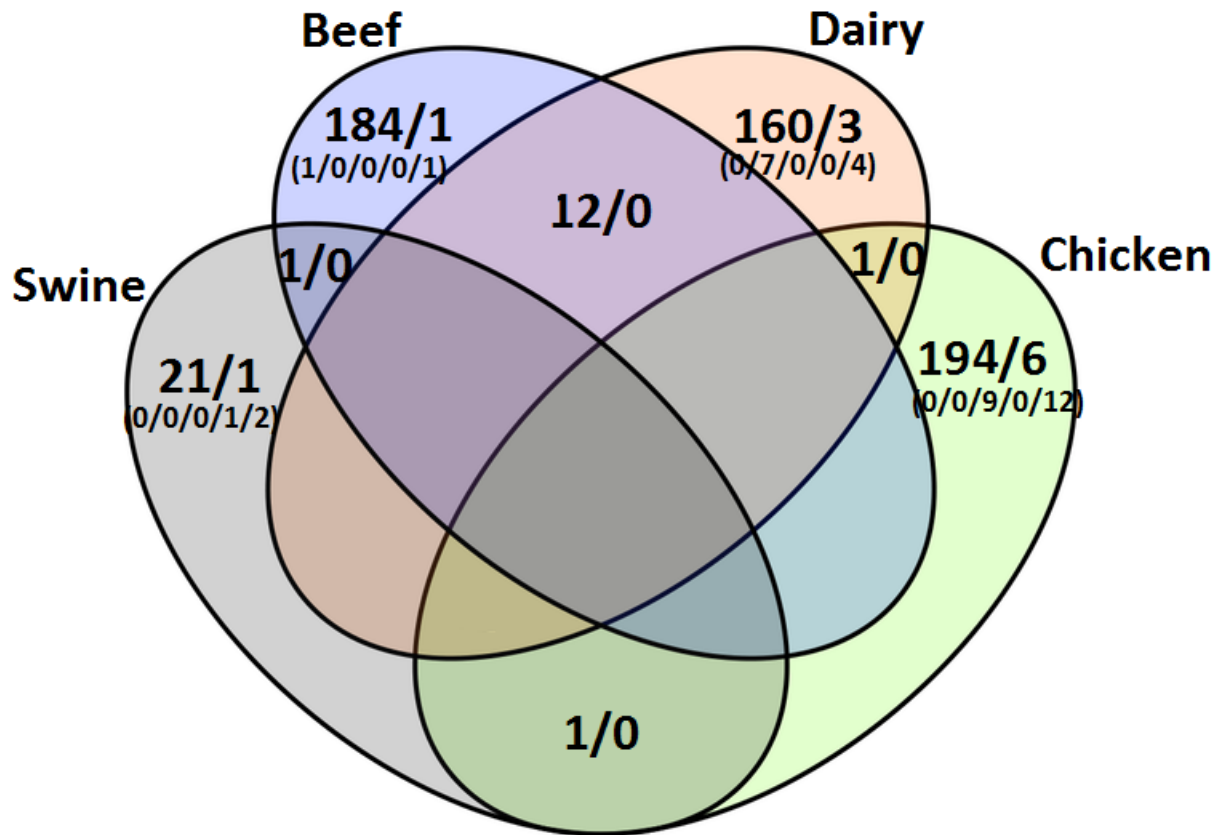
# of unique human patterns: 103(122)

## Allelic Difference 10



# of unique human patterns: 127 (155)

## Allelic Difference 5



**# of unique human patterns: 164(203)**

Figure S3. Distribution of sequence type groups (large lettering, above) and isolate composition of human-pathogenic groups (small lettering, below) across multiple food animal sources for different cgMLST thresholds. The total number of groups for each food source is shown to the left of the “/” and the number of groups that contain human pathogenic isolates are on the right. Isolate-level composition of human pathogenic groups below are displayed in the order of “a/b/c/d/e” corresponding to the number of isolates from a) beef cattle, b) dairy cattle, c) chicken, d) swine and e) human.