Identification of host-associated genomic determinants in *Escherichia coli* using Genome-wide Association Study (GWAS)

Inaugural-Dissertation
to obtain the academic degree
Doctor rerum naturalium (Dr. rer. nat.)

Submitted to the Department of Biology, Chemistry, Pharmacy

of Freie Universität Berlin

By

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2021

This study was conducted between June 2017 and June 2021 under the guidance of Prof. Dr. Dr. h.c. Lothar H. Wieler at the Robert Koch Institute, 13353 Berlin, Germany.

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Date of oral defense: 30th November 2021

Acknowledgement

I’d like to sincerely thank Dr. Torsten Semmler for providing me the opportunity to work on such a huge collection and freedom to apply advance methods. From the day one in berlin, he helped me a lot. Thank you so much for your constant supervision, encouragement, and support on my research work.

I would like to thank Prof. Dr. Dr. h.c. Lothar H. Wieler for accepting me as his doctoral student and supervising my dissertation work. Apart from his core responsibilities he always made some time to investigate the work progress and provided guidance.

I would like to thank Prof. Dr. Stephan J. Sigrist for supervising my dissertation work. Thank you for your valuable suggestions and comments.

The research work is part of the consortium, and I would like to thank all the members of the HECTOR consortium for their contributions in this research and the associated funding agencies.

I would like to thank Prof. Dr. Niyaz Ahmed for providing me initial exposure to NGS analysis and the opportunity to pursue my doctorate in Germany & constant support.

I would like to thank Lennard and Silver for their constructive and supportive criticism on my work as well as the productive discussions and fun while working. Thank you for motivating and helping me time to time and maintaining healthy working environment. In addition to that thanks Silver for reading my thesis and providing valuable suggestions.

I would like to thank Rico for providing IT-support and extend my thanks to Felix, Johanna and Mustafa and other colleagues at the RKI for maintaining a friendly environment and support.

I would like to thank my former colleagues cum friends Dr. Narender, Dr. Ramani, Dr. Sabiha, Aditya, Dr. Kshitij and Arya for their guidance while learning the NGS analysis before starting my doctoral thesis. I would like to thank Dr. Amit, Dr. Arif, Dr. Nishant, Dr. Savita and Dr. Shamsul for helping me to understand the biology of the microbes. They all constantly guided and helped me in different possible ways.

Thanks to all my friends in Berlin and in India for their constant supports and all the teachers from schools to college for sharing their immense knowledge with me.

At last, but not the least, I would like to sincerely thanks my parents and family members for their abundant blessings and graces throughout life without them this journey would never been started.

Content

1. Introduction 11

2. Literature: 13

- 2.1) *Escherichia coli*: 13
  - 2.1.1) Classification of *Escherichia coli*: 13
  - 2.1.2) Genetic diversity and population structure of *E. coli*: 16
  - 2.1.3) Emergence of AMR and its transmission: 19
- 2.2) Population genomics of bacterial host-adaptation: 20
  - 2.2.1) Host-associated population structure: 20
  - 2.2.2) Mechanisms for host-adaptation: 22
  - 2.2.3) Signatures of adaptation: 24
- 2.3) Genome-wide Association Study (GWAS): 27
  - 2.3.1) Background: 27
  - 2.3.2) Introduction to bacterial GWAS: 28
  - 2.3.2) Confounding factors of bacterial GWAS: 29
  - 2.3.3) Tools for bacterial GWAS: 30

3. Material and Methods: 35

- 3.1) Strain selection: 35
- 3.2) DNA extraction and sequencing: 35
- 3.3) Quality control: 36
- 3.4) Genome assembly and annotation: 37
  - 3.3.1) Assembly: 37
  - 3.3.1) Gene prediction and annotation: 37
- 3.5) MLST and phylogroups: 37
- 3.6) Computation of pan-genome: 38
- 3.7) Reconstruction of phylogeny: 38
- 3.8) Identification of population structure: 38
- 3.9) Clustering of strains based on accessory-genome: 38
- 3.10) X^2-test for independence (by Boas C.L. van der Putten): 39
- 3.11) Genome-wide association analysis: 39
- 3.12) Prevalence of human-associated *nan* gene cluster: 42

4. Results: 45

- 4.1) Strain collection and distribution: 45
- 4.2) Phylogenetic analysis of strains: 48
- 4.3) Clustering of strains based on accessory-genome: 50

4.4) Host-associated clustering of strains: 51
4.5) Genome-wide association analysis: 53
4.3.1) *E. coli* genes associated with humans: 55
4.3.2) *E. coli* genes associated with cattle: 60
4.3.3) *E. coli* genes associated with chicken: 63
5. Discussion: 67
6. Summary: 73
7. Zusammenfassung: 75
8. References: 77
9. Supplement: 89

List of abbreviations

AMR:	Antimicrobial resistance
CDCV:	Common disease common variant
***E. coli*:**	*Escherichia coli*
ExPEC:	Extraintestinal pathogenic *E. coli*
GWAS:	Genome-wide Association Study
GTR:	General time-reversible
HGT:	Horizontal gene transfer
InPEC:	Intestinal pathogenic *E. coli*
INDELs:	Insertion/deletions
LD:	Linkage disequilibrium
LMM:	Linear mixed model
Lrt:	Logarithmic Ratio-test
MAF:	Minor allele frequency
MGE:	Mobile genetic element
MLEE:	Multi-locus enzyme electrophoresis
MRCA:	Most recent common ancestor
MLST:	Multi-locus sequence typing
PCR:	Polymerase chain reaction
OR:	Odds-ratio
SNP:	Single nucleotide polymorphism
ST:	Sequence type
t-SNE:	t-Distributed Stochastic Neighbor Embedding

Glossary

Genetic drift: A change in the frequency of an existing gene variant (allele) in the population over time due to random events (such as mutations).

Ecotypes: Genotypes adapted to a specific environmental condition, which is defined by the degree of the spread of an adaptive mutation.

Genetic hitchhiking: The process of change in the frequency of an allele linked to a gene under positive selection.

Selective sweep: The fixation of a beneficial allele in a population due to positive selection, which results in the loss of less fit, alternative alleles.

Core-genome: Genes present in all the members of a bacterial species. These also include housekeeping genes.

Accessory-genome: Genes that are present in only some members of a bacterial species. These also include strain-specific genes.

Pan-genome: The union of core- and accessory-genome.

Horizontal gene transfer: Transfer of genetic material between two microbes other than vertical transmission.

Heritability: The proportion of phenotypic variation due to inherited genetic variation.

Effect size (β): The standardized regression coefficient, derived from linear regressions in genome-wide association studies of continuous traits. It is reported as an estimate of the effect size of a single-nucleotide polymorphism (SNP) and reflects the change in phenotype expected from carrying a copy of the reference allele of the SNP.

Linkage-disequilibrium: Co-relation between variants due to co-inheritance.

k-mer: A sequence of bases of length k.

1. Introduction

The prevalence of antimicrobial resistance (AMR) is escalating worldwide. While the development of AMR is a natural process, it has become a major health problem for many nations. Intensive usage of antimicrobials in both the healthcare system and agricultural settings is attributing to this escalation. Every year approximately 700,000 people die due to infections caused by antimicrobial-resistant micro-organisms around the globe. As per the recent report released by the IACG (UN Interagency Coordination Group on Antimicrobial Resistance, 2020), drug-resistant diseases could cause up to 10 million deaths each year by 2050 [1]. This could result in an increased socioeconomic burden on many countries and force up to 24 million people into extreme poverty by 2030 [1]. Recent reports of plasmid-mediated colistin resistance, potentially associated with colistin usage in agriculture[2], [3], have further raised the fear of infections that have been untreatable due to AMR.

The prevalence of AMR has increased in both pathogenic bacteria and bacteria colonizing healthy human and animal populations. Natural environments may act as the reservoir of AMR genes and provide a medium through which resistant bacteria can spread between human and animal populations. Due to our current lack of understanding, it is still a matter of debate to what extent AMR commensal and pathogenic bacteria successfully spread and establish themselves in the human population due to transmission from animal and environmental reservoirs, and vice versa.

Commensal bacteria such as *Escherichia coli (E. coli)* can act as reservoirs of AMR genes in humans and animals[4]. As per the WHO Global Burden of Foodborne Disease report [5], annually,>300 million illnesses are reported, and approximately 200,000 deaths are caused by diarrheagenic *E. coli* globally each year. Multiple studies suggest that highly successful *E. coli* clones, such as the ST131 [6], [7] or *E. coli* belonging to CC87(ST58 and ST155), can infect both human and animal populations and are responsible for the spread of AMR [8]. However, there is a paucity of information to what extent lineages of *E. coli* are adapted to a particular host or have lost such specialization. Furthermore, genomic determinants contributing to this process are also currently unknown.

Although statistical analyses have shown that different lineages of AMR strains have varying spreading capacities, due to lack of data, modeling studies have not been able to investigate the relative importance of various host reservoirs and their potential impact on the transmission dynamics of resistant strains or the dissemination of resistance genes.

There is currently a massive gap in our understanding of the impact of host-adaptation on transmission dynamics of AMR *E. coli* between different reservoirs such as human and animal hosts. Although not mutually exclusive, identifying determinants contributing to host-adaptation may allow disentanglement of the different modes of AMR transmission (i.e., bacteria vs. MGE), which can help in designing more targeted interventions and reduce the transmission of AMR and may also help in better risk assessment for the transmission of highly resistant *E. coli* clones between different hosts. The research proposed here aims at closing these knowledge gaps.

Therefore, the thesis aimed to:

- Identify host-associated genomic determinants in *Escherichia coli* and their involvement in host-adaptation by performing an unbiased whole-genome sequence analysis with the emphasis on the following points:
  - Characterization of core- and accessory-genome of *E. coli* strains isolated from human and animal populations belonging to various geographical locations.
  - Analysis of potential association between *E. coli* strains with host and geographical locations based on core and accessory gene content.
  - Identification of host-associated genomic determinants in *E. coli* by performing a bacterial genome-wide association study.

2. Literature:

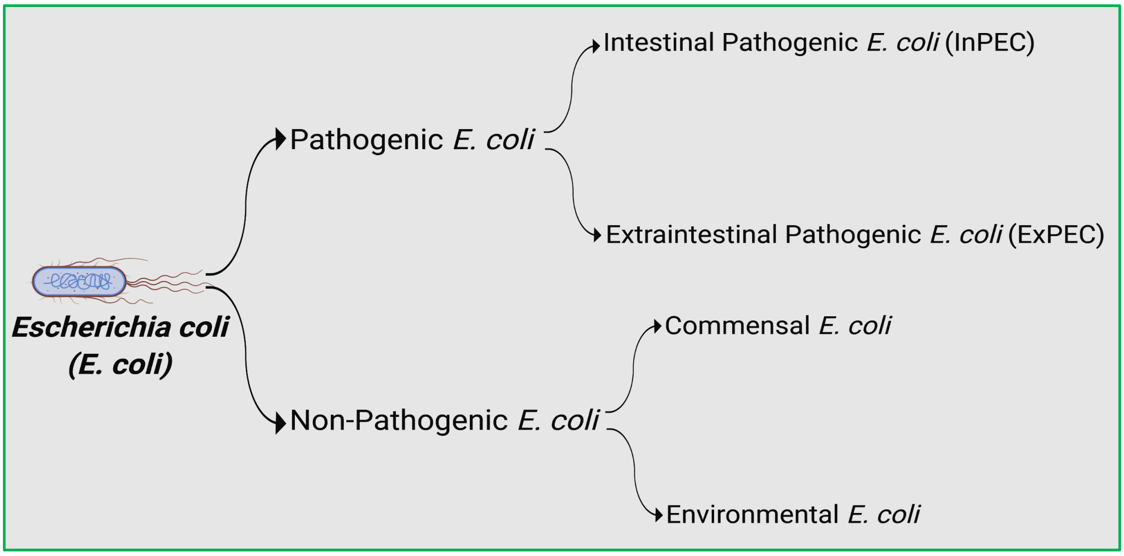
2.1) *Escherichia coli*:

Escherichia coli (E. coli) is a gram-negative, rod-shaped (1-5µm in length), facultative anaerobic bacterium belonging to the family of Enterobacteriaceae and the genus *Escherichia. E. coli* is the part of natural gut flora and is commonly found to be commensal within the gastrointestinal (GI) tracts of all warm-blooded and some cold-blooded organisms [9], [10]. *E. coli* typically colonizes the gut of these organisms within a short period after birth and co-exists throughout entire life [11]. The relationship between *E. coli* and its host is described as mutualism. *E. coli* benefits its mammalian hosts by producing vital vitamins such as K and B12 [12], [13]. It also consumes oxygen to facilitate a friendly environment for other anaerobic neighbors colonizing the gut [9]. *E. coli* has the interesting characteristic of being both a widespread gut commensal of vertebrates as well as versatile pathogen [14]. The normal microbiota of *E. coli* benefit its host by restricting the invasion of other pathogens through the secretion of bacteriocin or by competing for nutrients and niche as well as through other mechanisms [9], [10]. In contrast, its pathogenic form is reported to kill more than 2 million humans per year through intestinal and extraintestinal diseases [15], [16]. The diversity of *E. coli* has been enabled by various evolutionary events such as selective pressures within different hosts or environments, horizontal gene transfer (HGT), genomic rearrangements, and accumulation of mutations within the genome [17]. The versatile nature and ability to colonize a broad spectrum of hosts and environmental niches make *E. coli* a perfect microbe for studying the transition between commensalism and pathogenicity and genomic factors responsible for host-adaptation.

2.1.1) Classification of *Escherichia coli*:

E. coli are broadly classified into pathogenic and non-pathogenic (Figure 1) strains, based on their ability to cause infections in humans and other hosts. Non-pathogenic forms are commonly found in the environment and co-exist within humans and animals as commensal bacteria. The transition from commensal strain to pathogenic form involves the acquisition of virulence via HGT and/or accumulation of pathoadaptive mutations [18]–[20]. The acquisition of these new traits is crucial for the survival and fitness of any pathogen [21]. Pathogenic *E. coli* can cause a wide range of diseases, from gastroenteritis to extraintestinal infections of the urinary tract, bloodstream, and central nervous system [11] in humans, animals, or birds (Table 1). These pathovars are broadly classified into two groups (Figure 1) based on site of infection within the host: Extraintestinal pathogenic *E. coli* (ExPEC) and Diarrheagenic or Intestinal pathogenic *E. coli* (InPEC).

Figure 1: Broad classification scheme of pathogenic and non-pathogenic *E. coli*. (Created with BioRender.com)



Despite technological advancements, the problem of differentiating commensal *E. coli* from its pathogenic forms still persists. While there is increasing evidence that some pathogenic strains of *E. coli* evolved from respective commensal strains [22], it remains difficult to determine which genes or genetic changes are directly responsible for an *E. coli* to become pathogenic. This difficulty is driven by many traits such as the ability to colonize a given mucosal site, evade host defenses, and cause damage to host tissues.

Table 1*: Classification of *E. coli* pathovars and their host range as well as clinical manifestations.*

Name	**Host range**	**Diseases**
Intestinal Pathogenic *E. coli* (InPEC)		
Adherent invasive (AIEC)	Humans	Chronic diarrhea
Diffusely adherent (DAEC)	Humans, calves	Diarrhea
Enteroaggregative (EAEC)	Humans	Diarrhea
Enterohaemorragic (EHEC) Shigatoxin-producing (STEC)	Human (cattle)	Bloody diarrhea in humans, hemolytic-uremic syndrome (HUS), hemorrhagic colitis (HC)
Enteropathogenic (EPEC)	Humans, mammals	Diarrhea
Enteroinvasive (EIEC)	Humans, primates	Dysentery
Enterotoxigenic (ETEC)	Humans, pigs, cattle	Traveler's diarrhea; profuse neonatal diarrhea in babies, calves, piglets, and pups; post-weaning diarrhea in piglets
atypical EPEC (aEPEC)	Humans, mammals	Diarrhea
Edema disease (EDEC)	Pigs	Edema disease
Extraintestinal Pathogenic *E. coli* (ExPEC)		
Avian pathogenic (APEC)	Birds	General infections
New-born meningitis associated (NMEC)	Humans	Meningitis in babies
Uropathogenic (UPEC)	Humans, mammals	Cystitis, pyelonephritis
Necrotoxigenic (NTEC)	Humans, mammals, ruminants	Diarrhea, septicemia, urinary tract infections (UTIs)
Septicemia associated (SePEC)	Humans, mammals	Septicemia
Other ExPEC	Humans, mammals	Wound infections, respiratory tract infections

2.1.2) Genetic diversity and population structure of *E. coli*:

Escherichia coli is one of the most studied and well-characterized model micro-organisms. The reference strain *E. coli* K-12 and its derivatives have played a vital role in population genetics, genetic engineering, and functional analyses. The total population size of *E. coli* is estimated to be 10^{20} [23], with high within-species diversity. Hence, a single strain of *E. coli* cannot represent the entire population.

Revealing the genetic structure of *a* bacterial species on a global level might help to understand its evolution, global spread, and its ability to colonize different hosts and ecological niches. The population structure of any species of bacteria is predominantly defined by the interplay between recombination [24], [25], and mutation [26], [27]. They can move from a clonal structure in which all individuals are not potential recombination partners or having low or negligible recombination events to a panmictic population structure in which all individuals are potential recombination partners resulting in high rates of recombination [28], [29].

The population structure of *E. coli* is shaped by multiple factors such as the host environment, natural selection, recombination rate, and other environmental factors. Identification and sub-typing of lineages in *E. coli* or any bacterial species help to define its population structure. The sub-typing can also help to detect the real causative agent responsible for an outbreak. The first method to delineate *E. coli* and supports its clonal population structure is serotyping analysis. Serotyping scheme was established in the 1940s, based on O (somatic), K (capsular), and H (flagellar) antigens present on the outer membrane of the bacterial cell [30]–[32]. Today, a single serotype is defined by a combination of 173 O-antigens (somatic), 80 K-antigens (capsular), and 56 H-antigens (flagellar), which helps to provide a better resolution of population structure [33].

It was postulated that *E. coli* consists of stable lineages (called clones), among which little recombination between chromosomal genes occurred. In 1984, Ochman and Selander established the *E. coli* reference (ECOR) strain collection comprising of 72 strains based on Multilocus enzyme electrophoresis (MLEE) [34]. These strains were selected to represent the known diversity of *E. coli* (both pathogenic and commensal) from diverse hosts (mainly animals) and distinct geographical locations. Based on the MLEE data for 35 loci, these strains were later designated to phylogenetic groups A, B1, B2, C, D, and E [34]–[36]. This was followed by the development of a Clermont triplex polymerase chain reaction (PCR) based method, which allowed rapid and more accurate classification of *E. coli* strains into phylogenetic groups [37]. Currently, phylogroups A, B1, B2, D, E, F, G, and Clade I are recognized and assigned to *E. coli* based on this new PCR approach [38]. Clades I to V were characterized as cryptic lineages, which are highly divergent at the nucleotide level, but phenotypically similar to *E. coli* [39]–[41]. Recently, the clade V strains were re-examined and assigned to *Escherichia marmotae* sp. nov.,[42], [43].

After multiple advancements and the wider availability of sequencing technology, these began to supersede the traditionally existing methods for phylogenetic analysis due to their in-depth discrimination of *E. coli* strains. Multilocus sequence typing (MLST) involves sequencing of selected (historically seven) bacterial housekeeping genes and provide greater resolution. Variants within a gene sequence were referred to as alleles, and a unique number was assigned to each allele. These allele numbers of all seven genes form the allelic profile and define the Sequence Type (ST) of each strain unambiguously. Currently, there are two MLST schemes available for *E. coli* that use different sets of genes and are as follows*:*

a) In 2006, Mark Achtman developed the first MLST scheme based on sequence analysis of seven housekeeping genes: *adk* (adenylate)*, fumC* (fumarate hydratase)*, gyrB* (DNA gyrase)*, icd* (isocitrate dehydrogenase)*, mdh* (malate dehydrogenase)*, purA* (adenylosuccinate dehydrogenase) *and recA* (ATP/GTP-binding motif) (http://mlst.warwick.ac.uk/mlst/dbs/Ecoli) [44].

b) In 2008, Sylvain Brisse and Erik Denamur derived another MLST scheme based on eight housekeeping genes: *dinB* (DNA polymerase IV), *icdA* (isocitrate dehydrogenase), *pabB* (aminodeoxychorismate synthase component I), *polB* (DNA polymerase IV)*; putP* (proline permease), *trpA* (tryptophan synthase subunit alpha), *trpB* (Tryptophan synthase beta chain) and *uidA* (Beta-glucuronidase) (http://bigsdb.pasteur.fr/ecoli/) [45].

The high correlation between the results of both schemes indicates the robustness of the clonal structure of *E. coli* [17]. Later, the MLST scheme derived by Mark Achtman found to be highly correlated with the core-genome phylogeny derived from whole-genome sequences [44], [46]. These methods have different pitfalls and advantages, as shown in Table 2.

Table 2: Overview of strengths and weaknesses of different typing methods for *E. coli* (The table was adapted from [47]**)**

Typing method	**Strengths**	**Weaknesses**
Phenotypic		
Multilocus enzyme electrophoresis (MLEE)	❖ Most strains can be typed. ❖ Easy interpretation of results.	❖ Low throughput and intensive lab work are required. ❖ Low phylogenetic resolution compared to newer techniques.
Genotypic		
Multiplex PCR-based technique	❖ Rapid detection of STs and phylogroups. ❖ Potential application in clinical settings or during outbreaks. ❖ Relatively inexpensive, fast, and easy to interpret.	❖ It only allows detection of specific genomic targets as determined by primer mix.
Pulse-field gel electrophoresis (PFGE)	❖ Highly reproducible, profoundly discriminative technique with high phylogenetic resolution and epidemiological concordance. ❖ Cross-species comparison and interpretation possible.	❖ Slow, labor-intensive, and technically challenging. ❖ Limited resolution if DNA fragments are of similar sizes.
Multilocus sequence typing (MLST)	❖ Strong correlation with results produced by PFGE. ❖ Internationally standardized system and profoundly reproducible. ❖ Suitable for clinical settings and during outbreaks.	❖ Limited phylogenetic resolution. ❖ Expensive.
Whole Genome sequencing (WGS)	❖ Highest level of discrimination power and phylogenetic resolution. ❖ Allows cross-comparison by identifying MLST from WGS data. ❖ Lots of automated pipelines exist, current research is trying to implement this in	❖ Requires significant resources and bioinformatics expertise. ❖ Currently mostly used in research

	clinical settings.	

2.1.3) Emergence of AMR and its transmission:

Antimicrobial resistance (AMR) is a naturally occurring phenomenon and a major global health issue. In modern medicine, antibiotics or antimicrobials are being widely used to combat infections caused by many pathogens. The golden era of antibiotics ranged from the 1930s to the 1960s, which gave rise to many of our current antibiotics. However, this era ended soon after the emergence of antimicrobial-resistant enteric bacteria such as *Salmonella, Shigella, and E. coli* during the late 1950s and early 1960s. Intensive usage of antibiotics in both healthcare and agricultural settings has substantially increased the selection pressure on both commensal and pathogenic bacteria, thus favoring the development of resistant phenotypes of the bacteria [48], [49]. The genetic basis for antimicrobial resistance can be either intrinsic (i.e., the natural absence of the pathway targeted by the drug in the organism), a mutation associated, or resistance acquired via horizontal gene transfer (HGT) between different organisms [50]–[52].

The prevalence of AMR is increasing worldwide. This attributes to the substantial rise of mortality and epidemics due to infections caused by these AMR bacteria in both developed and developing nations. The recent reports of plasmid-mediated colistin resistance [2], [3], have further raised fears of an increase in the incidence of infections that might become untreatable with currently available antimicrobial therapy. This will result in the extensive loss of human life and may escalate the socio-economic burden around the world [53].

The prevalence of AMR has not only increased in pathogenic bacteria but also in their commensal forms. AMR bacteria can be transmitted within or across the human and animal populations, and AMR genes can be transmitted within or across different bacterial species through HGT. Natural environments may hereby act as reservoirs for AMR genes and provide the medium of transfer for resistant bacteria [54]–[56]. Due to our current lack of understanding, it is still a matter of debate to what extent commensal and pathogenic bacteria can successfully spread and establish themselves within the human population, possibly as a result of transmission from animal and environmental reservoirs and vice versa.

Commensal bacteria such as *E. coli* can act as reservoirs of AMR genes in both humans and animals [57]. Several studies suggested that highly successful *E. coli* clones, such as the ST131 [6], [7] or clonal complex 87 (CC87), are responsible for the spread of AMR *E. coli* within the human population [8]. Antimicrobial resistant *E. coli* strains can be transmitted within and between different host species or can also disseminate resistance traits [58], [59]. *E. coli* is intrinsically susceptible to almost all clinically relevant antimicrobial agents but has a great capacity to accumulate or disseminate resistance genes, mostly through horizontal gene transfer. However, there is a paucity of information on why certain lineages of *E. coli* are so dominant or successful in spreading AMR globally in comparison to others.

2.2) Population genomics of bacterial host-adaptation:

Host-adaption is the ability of a bacterium to colonize a new host by undergoing modifications required for its survival and successful proliferation [29], [60]. A bacterium colonizing a new host niche will have to compete with residential microbiota for survival [29], [61]. The new strains are likely to be less adapted as compared to resident strains and may often be out-competed [29], [61]. However, bacteria can survive and proliferate within a new host if selective phenotypes co-exist within an enormous *effective population size* (N_e), which can provide selective advantages [29], [62]. Bacteria often maintain homeostasis between the host and its microbiota, wherein the colonization of a novel strain inside the host may disrupt this homeostasis among commensal microbiota and can lead to the development of new diseases [29], [63]. To understand the genetic mechanisms of host-adaption by bacteria in a natural population, we have to first understand the host-associated genetic structure.

2.2.1) Host-associated population structure:

The genetic structure of bacterial species reflects host-ecology and population structure [29]. The traditional method to analyze the host-associated population structure is to construct a phylogenetic tree based on the variations present within the genomic sequences isolated from a selection of bacterial strains. The strains isolated from the same host are expected to cluster together on the phylogenetic tree with non-random topologies [26], [64], [65]. These host-associated lineages may also refer to obstacles for colonization or clonal expansion driven by genetic drift or natural selection [29]. Two theoretical models were used over the decade to explain the pattern of molecular evolution in bacteria. The first model emphasizes neutral diversification and the second model on ecotypes [66].

In the neutral evolutionary model (also known as neutral diversification), bacteria have the same fitness level, and all members of the population are derived from a single ancestral cell (the most recent common ancestor (MRCA)) through binary division and clonal descent [29]. In the case of binary division (entirely neutral model), multiple lineages colonize freely within hosts and expand to niches, whereas in clonal descent (diversification modulated by barriers), strains differentially colonize the host and give rise to multi-host and single-host lineages [29]. The host-associated clustering of isolates in natural populations on the resulting tree can be explained by a retrospective stochastic genetic model of how genetic diversity arises from a common ancestor, also known as coalescent theory [29], [66], [67]. This provides a null model for the rise of genetic diversity within a population due to genetic drift. In neutral models, the selection of adaptive traits influences the success of specific lineages within a particular host, but not the fitness [68].

Another way of describing the host-associated population structure is as *Ecotypes,* which provide an adaptive explanation. In the Ecotype model, clonal lineages carrying the host-adaptive trait will get fixed in the population by genetic hitchhiking [69] followed by selective sweep [70]. The fixation of a beneficial trait or allele within a population and the loss of less fit alternative allele increase the overall fitness of the clonal lineage carrying them and will allow them to out-compete coexisting lineages present in the same niche [71]. The independent host-associated clonal lineages would evolve if they were ecologically different.

Although adaptive explanations may be useful in understanding the population structure, but defining the host-adapted lineages can be difficult in a natural population of bacteria such as *Escherichia coli, Campylobacter jejuni,* and *Staphylococcus aureus* due to the following reasons:

i) Defining host-adapted lineages based on sequence types (ST), clonal complex and phylogroups may be an oversimplification [27], [64], [72], [29].

ii) Difficulties in defining host-restricted lineages or sub-lineages [29].

iii) Difficulties in quantifying host-range for a bacterial population [73], [29], as it depends upon the sampling strategies used results in a sampling and ascertainment biases.

iv) Due to genetic exchange between the bacteria [74], [29].

Recent advancements in high-throughput sequencing technologies revolutionized the field of microbiology. Next-generation sequencing (NGS) technology has facilitated the population-based comparative genome analysis of bacteria colonizing multiple hosts [75], [76]. Such studies reveal mechanisms and evolutionary processes driving bacterial adaptation to a new host. Identification of host-adaptive genetic determinants in combination with functional analysis could reveal the mechanism for successful host-switching as well as novel therapeutic candidates for controlling infections and may help in designing control interventions for the emergence of novel pathogens.

2.2.2) Mechanisms for host-adaptation:

The evolution of bacteria is mainly driven by DNA replication errors (or DNA damage) that generate point mutations, rearrangement, or deletions of different sizes and horizontal gene transfer followed by chromosomal recombination [29]. The relative rates of mutation and recombination shape the genetic structure of a bacterial population [29]. Both mutation and recombination lead to sequence variation within the bacterial genome (DNA). Consequently, influences the expression of a gene both at the level of transcription and translation and may eventually lead to host-adaptation [29]. Determination of genetic markers responsible for the bacterial host-adaptation is often challenging. The analysis of sequence variations in the core- and accessory-genome of a bacterial population revealed the importance of recombination and mutations in adapting a novel niche [75], [77], [78].

Mutations may occur both in the protein-coding region and non-coding regions (both promoters and non-coding RNAs) of the genomes. Mutations within a protein-coding region can diversify protein function or make genes non-functional [79], whereas a mutation in the non-coding region influences the gene expression or function of non-coding RNA [80], [81]. Both kinds of mutations can facilitate host or niche adaptation (Table 3) [82]. However, mutation rates in bacteria are generally low as mutations are usually deleterious [79], and natural selection drives improved DNA replication fidelity

[83]. The mutation rate varied a lot among bacteria due to differences in the drift barrier and bacterial ecology. Elevated mutation rates help bacteria to adapt to the sudden change in the environment, but the increased accumulation of deleterious mutation offsets this advantage under normal circumstances [29]. However, horizontal gene transfer (occurred via transformation, conjugation, and transduction) may lead to the introduction of intragenic sequences or genes by homologous or non-homologous recombination. In homologous recombination, homologous DNA is replaced with a sequence from a different lineage, whereas, in non-homologous recombination, foreign DNA is inserted into the chromosome at repetitive regions or by illegitimate recombination (Table 3). Like mutation, HGT can facilitate host and niche adaptation too. This was achieved through diversifying the gene-encoding regions (can be caused by frameshift mutations, duplications, or insertions/deletions) on the genome. HGT also has the potential to bring SNPs (Single nucleotide polymorphisms) together into the same genetic background by disrupting the linkage disequilibrium (LD) between sites, which may promote host-adaptation [29].

The rate of recombination can vary extremely, from clonal Mycobacterium *tuberculosis* bacterium to the highly recombining *Helicobacter pylori* [84]. Recombination can increase or decrease the genetic diversity when HGT occurred between strains in different lineages or within a clonal lineage, respectively [85]. It can ameliorate clonal interference [86], remove deleterious mutations (by purifying selection), and can facilitate a more rapid and effective adaptive evolution than spontaneous mutation [87]. The impact of recombination can be estimated by assessing the proportion of genetic diversity occurring between isolates as a result of recombination versus mutation (r/m) [85], [88].

Table 3: Genetic mechanisms of host or niche adaptation in bacteria. (The table was adapted from [29])

Genetic mechanism	Effect on genome	Effect on host-adaptation
a) Point mutation (Stochastic point mutation)	Nucleotide substitution (coding sequence)	New protein isoforms increase population phenotype variation and can promote adaptation
	Indel (coding sequence)	Loss of function associated with reductive evolution and may streamline genome
	Nucleotide substitution (intergenic region)	Variation in gene expression caused by mutations in promoter sequence or transcription associated with adaptation
	Nucleotide substitution (phase variable region)	Variation caused by activation or inactivation of gene expression is associated with adaptation
b) HGT (transformation, conjugation, transduction)	**Homologous recombination**	
	Replacement and inversion	Novel alleles increase population phenotypic variation and can promote adaptation
	Non-homologous recombination	
	Insertion	Novel genes increase phenotypic variation and can promote adaptation
	Deletion	Altered gene function may streamline the genome during adaptation
	Duplication	Production of new and/or more gene products promotes adaptation

2.2.3) Signatures of adaptation:

The identification of genomic signatures of adaptation inside a bacterial genome may lead to the mechanism responsible for host-adaption. However, not all genetic variation in strains leads to adaptation. These changes may arise due to bottleneck and genetic drift [29]. These genomic signatures might also reflect the timescale of host colonization, recent host-switching events, or more ancient events (signatures of reductive evolution), loss of redundant function, and positive selection [29]. Several approaches have been used to identify the signatures of host-adaption in the bacterial population by analyzing genomic sequences focusing on broad information on adaptive evolution (by estimating rates of amino-acid replacement) and specific group of genes (present on MGEs or allelic variations) involved in adaptation.

Rates of amino-acid replacement [29]**:** Measuring the rate of amino-acid substitution is often used for identifying adaptation. This quantifies the selective pressure by comparing the rate of substitutions at synonymous sites (dS), which results in no-change in amino-acid, with that on non-synonymous sites (dN), which results in a replacement of amino-acid. If dN/dS < 1, it indicates negative or purifying selection, which suppresses protein changes, while a dN/dS > 1 means positive selection, which promotes changes within the protein sequence [89]. The dN/dS analyses have been used widely in bacteria to investigate the selective pressure during adaptation, especially inside humans [90], [91]. Although dN/dS provides a qualitative estimate for host-adaption in bacteria, there is some limitation to its utilization:

a) Other than protein coding-sequence, genomic features like GC skew, gene order, distribution of coding sequence, and codon-usage are also maintained by selection, and these features are undetected by dN/dS analyses [29], [92].

b) Multiple genes interact at multiple levels during adaptation, which is untraceable by this approach [29], [93].

c) Strong LD between genes, frameshifts, and wrong interpretation of start codon can lead to false-positive and inaccurate estimation of dN/dS [29], [93].

d) The dN/dS estimates are inaccurate if polymorphisms are not fixed between independent lineages, and segregating variation in the population is likely weakly deleterious and destined to be purged in the future [29], [94], [95].

When genetic variations occur in different independent lineages, which is also known as convergent or parallel evolution [29], and might provide evidence for a role in adaptation. Convergent or parallel evolution leads to homoplasy, which occurs on multiple levels [29]. The most substantial evidence of adaptation through homoplasy was observed among genes having specific amino-acid changes associated with *S. aureus* complexes isolated from chicken but absent in human isolates [96].

MGEs, allelic variation, and reductive evolution [29] are associated with genes specific for adaptation. Bacteria have to face and overcome many new challenges while colonizing and proliferating inside a novel host species and evading the host immune response is one among them. The quick way of overcoming such a challenge is to acquire genes involved in host evasion, typically present on mobile genetic elements (MGEs), through HGT. The insertion of a prophage containing an immune evasion cluster in *S. aureus* isolated from humans [97] is one of the examples of MGEs associated host-adaptation. In addition to MGEs, there is evidence for host-adaptation associated with allelic variation in homologous sequences, which might also influence the fitness of bacteria within new host species. For example, a comparative genomics study on *Salmonellae enterica* subsp. *enterica* serovar Typhimurium revealed an amino acid substitution in FimH (type 1 fimbrin d-mannose-specific adhesin) responsible for enhanced binding to bovine enterocytes [98]. While reductive evolution is often associated with the loss of gene function, it may not be directly linked to adaptive evolution. Genetic drift leads to the accumulation of deleterious mutations, which ultimately leads to gene inactivation. Disruption of genes involved in metabolic pathways in *Salmonella enterica* subspecies *enterica* from distinct host-associated ecologies is an example of adaptation via reductive evolution [99].

Although these methods provide information about the genomic basis of host-adaptation; however, hosts reflect a complex ecosystem with numerous sub-niches with different selection pressures, and certain hosts are colonized by different lineages of the same bacterial species. In addition to that, temporal variability in colonizing strains can complicate the identification of adaptive signatures in species such as *E. coli,* where temporary infecting strains are unable to proliferate or displace native strains in the same hosts [100]. Such a level of complex phenotypic and genotypic variations in bacteria makes it challenging to characterize through traditional comparative genomics techniques. Recently, this problem was addressed by using genome-wide association studies (GWAS), which involves analyzing large number of strains of a bacterial species with the phenotype of interest.

2.3) Genome-wide Association Study (GWAS):

2.3.1) Background:

GWAS was developed based on the CDCV (common disease common variants) hypothesis [106], [101], which states that several high-frequency but low-effect variants contribute to disease. The main goal of a GWAS is to identify the common variants associated with complex illnesses and inheritance patterns observed for many phenotypes [102]. The GWAS was first applied in humans to understand disease aetiology and identify potential drug targets. It also confirmed the heritability of many human traits [103] and novel biological mechanisms [104].

In human GWAS (hGWAS), hundreds of thousands of SNPs are called across an individual's genome using genotyping chips [105]. Due to the segments' co-inheritance over the generations, the genetic variants in close proximity are in linkage disequilibrium (LD) [106]. The most common variants, such as SNPs, are identified. Those SNPs whose frequency is more than 1% in the population are analyzed using linear or logistic regression to determine whether one allele is significantly associated with the phenotype. The variants' effects for quantitative traits are reported as **beta** (β), also known as the **odds-ratio** for case-control studies. Typically, individual SNPs' main effects are determined, as the epistatic interaction between the SNPs and its environment is more challenging and requires additional multiple testing [107].

It's essential to perform quality control on SNPs prior to performing GWAS to reduce the false-positive associations. The standard quality control in human GWAS includes the removal of SNPs with low-quality, low minor allele frequency (MAF < 1-5%), high missingness (>1-5%), outliers in the genome-wide homozygosity, and the SNPs that are out of Hardy-Weinberg equilibrium (P<E-5 or E-6) [106].

Due to the successful implementation of GWAS in understanding the complex disease etiology and identifying potential drug targets in humans, it gained the interest of the clinical microbial researcher to implement GWAS on micro-organisms, especially bacteria, to determine the risk variants in the respective genomes. Microbial GWAS may reveal novel biological mechanisms that underlie clinical outcomes, such as drug resistance and pathogenesis. It may also lead to the identification of molecular targets for vaccine and drug development. Furthermore, it might enable the researchers to understand the evolution and track pathogenic strains' transmission dynamics through populations.

2.3.2) Introduction to bacterial GWAS:

Unlike human GWAS, bacterial GWAS focuses on the effects of gene presence or absence alongside SNPs' occurrence within the phenotype [106]. Since recombination in bacteria can introduce novel gene(s) which influences the phenotype. Bacterial GWAS uses whole-genome sequencing data, affecting several aspects, including SNP calling, which consists of allelic variants [108], [109]. Prior to applying GWAS, it’s important to perform a quality control using specific thresholds, which accounts for the sequencing quality, depth, and Phred scores of the bacterial genomes. Most human GWAS studies focused on the additive effects of variants. The likelihood of phenotype is increased linearly due to the carriage of each additional copy of an allele. Within-host diversity in some micro-organisms (for e.g., bacteria) will lead to non-discrete SNP calling, where the frequency of an allele is not an indicator of its presence or absence; instead, it reflects its frequency on the microbial genome within the host [106] Several other conceptual and analytical differences between human and bacterial GWAS are listed in detail in Table 4.

Table 4: Conceptual and analytical differences in human and bacterial GWAS (The table was adapted from [106])

Features	GWAS	
	Human	Bacterial
Heritability estimation	• Twin studies • Adoption studies • GREML analysis	• Within transmission pair correlations • Phylogenetic studies
Input data	SNPs from genotyping chips	WGS
Study design	• Case-control and Quantitative traits	• Binary and quantitative traits • Longitudinal sampling
Quality control	• Individual sample missingness • SNP missingness • Hardy-Weinberg equilibrium • MAF	• Sequencing depth • Poor assembly • MAF

Reference genomes for imputation and LD	• International HapMap project • 1000 genomes project	• RefSeq genomes • LD can be determined directly from the sample.
Confounding factors	• Ethnicity • Population stratification • Cryptic relatedness	• Subtypes or lineages • Selective sweeps • Recombination and HGT • Clonal expansion
Significance threshold	$P=5e^{-8}$	• No fixed thresholds and changes from species to species.
Replication	Required for publishing novel associations	• Not yet universal and possibility of *in-vitro* validation

2.3.2) Confounding factors of bacterial GWAS:

GWAS's main challenge is to enhance its statistical power and precision to identify true causal genomic elements while ignoring seemingly causative elements [110]. The major confounding factors in a bacterial population are genome-wide linkage disequilibrium (LD) and strong clonal population structure [106], [111].

Population structure refers to a condition in which subpopulations have systematic variations in alleles and the phenotype frequencies due to their shared ancestry [112]. Population structure may lead to false associations between phenotypes and genotypes rather than causal ones. Bacterial GWAS tools have applied single-locus approaches (adapted from human GWAS) and multi-locus approaches to control this confounding effect [111]. In single-locus approaches, models will test the association between a phenotype and a variant at a time. In contrast, models are fitted to the complete datasets at once by applying several machine learning approaches in multi-locus. Single-locus approaches include cluster-based techniques [113], [114], dimensionality reduction [109], [115], linear mixed models (LMMs) [116], [117] whereas artificial intelligence uses multi-locus models [118]. These models have been used successfully up to a certain extent, but population structure is still a challenge in bacterial GWAS [119].

In GWAS, false positive or type 1 errors in association tests are reported due to genome-wide LD [106], [111]. Genome-wide LD may lead to hitchhiking of linked non-causal mutations on the same genomic background as a causal mutation. In bacteria, LD can cover most of the genome, convoluting fine mapping of causal variants and posing an increased risk of type 1 errors. In humans, LD is broken down every generation by homologous recombination, allowing GWAS to map the causal variants even to a smaller genomic region.

Other factors like sample size and the distribution of effect sizes will also influence the GWAS power to identify the causal variants responsible for a phenotype. Due to the polygenicity of traits and shaping of many phenotypic traits in humans by neutral evolution, most of the causal variants have an odds ratio (OR) <1.5 [120]. In contrast, in bacteria, high selection pressure shapes many phenotypic traits, resulting in increased effect size (OR>10) for identifying causal elements [113], [121]. However, detecting the smaller effect sizes is challenging and requires further investigation.

2.3.3) Tools for bacterial GWAS:

Various tools were developed for performing the bacterial GWAS using different methods to handle the different bottlenecks. Traditionally these GWAS tools are broadly classified into three categories: (a) phylogeny, (b) non-phylogeny, and (c) hybrid tools that implement both combinations of statistical and phylogenetic methods [119]. An emerging fourth group comprises of tools that apply machine learning algorithms to predict the phenotype from the genotype data [119]. These tools implement different methods in order to overcome bottlenecks and pitfalls in bacterial GWAS [119].

1) ***CCTSWEEP and VENN*** [122] use phylogenetic trees to determine the correlation between statistically significant SNPs. Both VENN and CCTSWEEP use character optimization for handling missing data. They operate on apomorphy lists produced by popular phylogenetic tools. The significant difference between VENN and CCTSWEEP is that the former works well with a large number of SNPs, whereas later-one can be used even when no SNPs are completely penetrating the phenotype of interest. CCTSWEEP can also estimate the correlation between binary variables.

2) ***GWAMAR*** [123] is a tool used specifically for detecting mutations associated with

drug-resistance in bacteria. It computes several statistical scores, such as odds ratio, hypergeometric tests, and weighted support values. Despite promising results, it has the following limitations: (i) Epistatic interactions between mutations are not considered. (ii) It only considers genomic changes and ignores the gene expression levels.

3) ***Sequence Element Enrichment (SEER)*** [109] analysis is a *k-mer* based and standalone pipeline that counts *k-mers* of variable lengths using a distributed string-mining algorithm. It provides the option for clonal population correction and requires large data sets of tens of thousands of genomes, both *de-novo* assembled contigs or raw read data. The SEER output includes metadata such as effect sizes, direction, and standard error. SEER is a bit more complex to use and requires human interventions within different steps.

4) ***Scoary*** [108] is a python based standalone pan-GWAS tool for studying the association between the full complement of genes in a clade (i.e., the pan-genome) and any observed phenotypic traits. Each accessory gene is scored sequentially according to its apparent correlation to a predefined phenotype. The population structure correction is performed based on the phylogenetic structure inferred from the input data with minimal assumptions about the evolutionary process. No prior knowledge of the mutation rate is required. Scoary uses a *post-hoc* label switching permutation test to validate results. It supports binary or categorical phenotypic data and implements pairwise comparisons to control for spurious associations. These comparisons account for phylogenetic clustering and genetic difference. Scoary was not developed to handle thousands of genomes, but it provides a graphical user interface (GUI).

5) ***Bugwas*** [124] is implemented in R, Python, and C++. It uses principal components and linear mixed models (LMM, implemented in the Genome-wide Efficient Mixed Model Association) to infer and correct population structure. An independent R package for Bugwas method for controlling population structure is also available. Bugwas can be used to perform *K-mer*, SNP, and gene differential analysis. Bugwas effectively detects polySNP and polygenic effects when low penetrating variants are responsible for the phenotype, not a single high penetrating variant. It can Identify significant associations by considering both lineage effects and locus effects without losing detection power.

6) ***TreeWAS*** [112] is an R based GWAS tool and uses phylogeny to correct for confounding effects of clonal population structure and homologous recombination while also accounting for the statistical associations between a phenotype and genotype at all loci without losing power. The phenotypic data can be binary or discrete interval (categorical) and continuous. It can be applied to both bacterial and viral pan-genome. The recombination events in TreeWAS are detected with ClonalFrameML in the background.

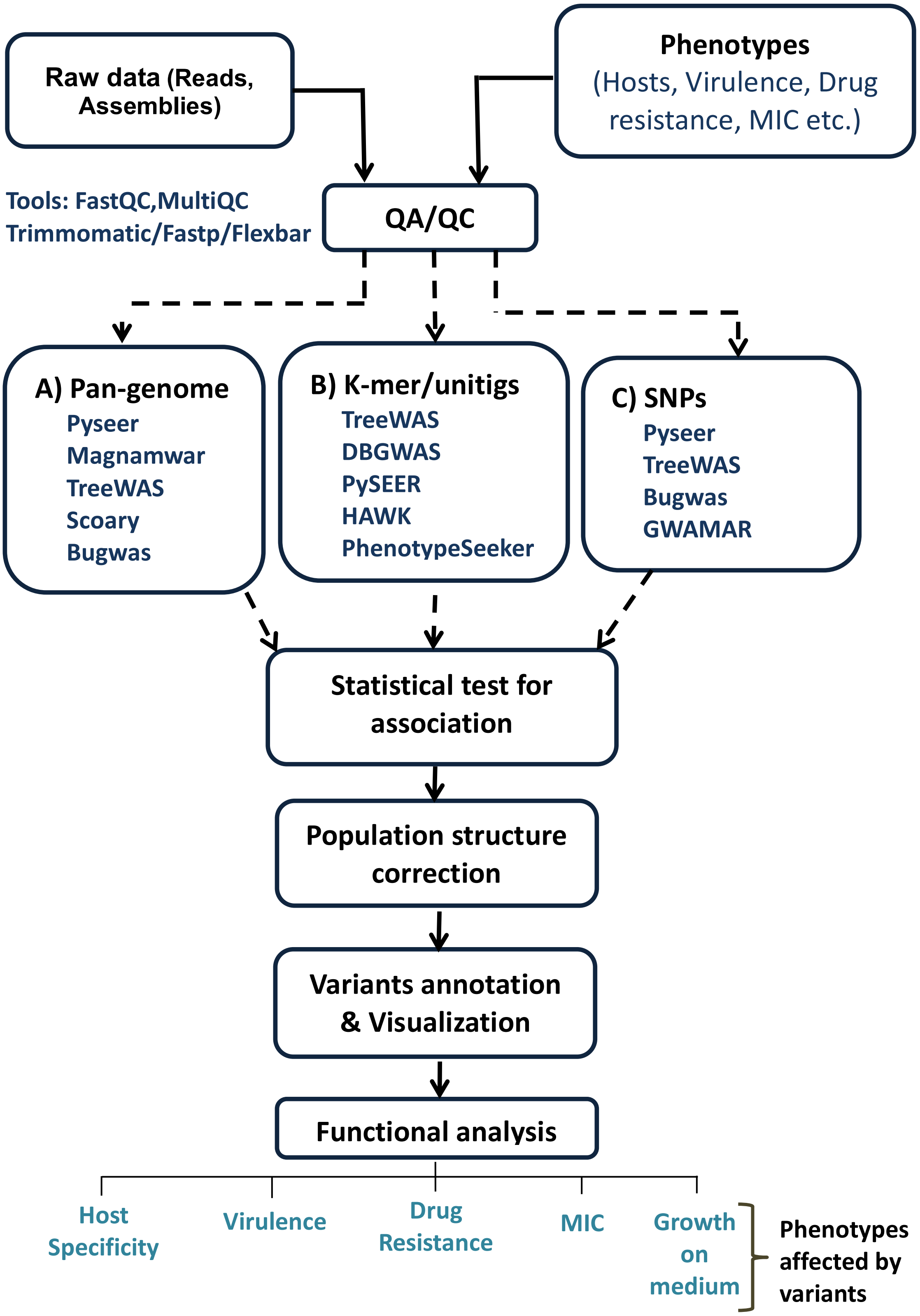
7) ***PhenotypeSeeker*** [125] is an easy-to-use and memory-efficient machine learning tool for identifying phenotype-specific *k-mers* and generates *k-mer* based prediction model for predicting the phenotype from the sequencing data of bacterial isolates. It consists of a modeling module *(PhenotypeSeeker modeling*) and a prediction module *(PhenotypeSeeker prediction).* The modeling module applies Welch's two-sample t-test if the phenotypic data is continuous and a chi-squared (X^2) test for binary phenotypic data. It then builds a regression or linear model used by the prediction module to predict phenotype. It optionally accounts for the clonal population structure by weighting strains based on the distance matrix created by Mash using shared *k-mers*.

8) ***pyseer*** [117] is a Python version of SEER with several enhancements. Each *k-mer (9-100bps)* is tested for associations to the phenotype using generalized linear models. It applies multi-dimensional scaling of a pairwise distance matrix to control for population structure. These components are included as fixed-effects within the model. The statistically significant *k-mers* can be annotated by mapping to a reference genome after adjusting for multiple testing. pyseer also allows testing for SNPs and indels' association against the reference(s). It also implements machine learning prediction with a regularized regression or elastic net and uses bugwas to estimate lineage effects.

9) ***Hitting Associations with k-mers (HAWK)*** [126] is another *k-mer* based GWAS tool implemented in C++ and uses logistic regression to determine the associations between *k-mers* and a phenotype of interest. It accepts raw read files as an input for each sample located in a separate directory. It uses principal component analysis (PCA) to detect and correct for population structure. The same pipeline can be used to map associations to SNPs, INDELs, and structural variation such as copy number variations (CNVs).

10) ***De Bruijn Graph GWAS (DBGWAS)*** [116] is an alignment-free, extended *k-mer* based GWAS used to produce interpretable genetic variants associated with various phenotypes. It bridges the gap between SNPs/gene-based and *k-mer* based GWAS, which lacks the suitable flexibility to cover complete genomic variations and may not be readily interpretable. It uses compacted De Bruijn Graphs (cDBGs) [127], [128], in which overlapping *k-mer*s are connected and yields a compact summary of all genomic variations. It eliminates local redundancy and characterizes the genomic environment of a *k-mer* at the population level. These cDBGs are known as unitigs. It uses Bugwas to test significant associations between these unitigs and a phenotype of interest while correcting the population structure. DBGWAS can identify both local polymorphisms and mobile genetic elements, reports expected and novel variants without prior knowledge. DBGWAS is memory-efficient and easily scalable to large datasets.

Figure 2: Workflow representing the critical steps involved in applying the GWAS. (The workflow was adapted from [119]**)**



3. Material and Methods:

3.1) Strain selection:

E. coli strains were isolated from five host-species (human, cattle, chicken, pig, and wild boar) between 2003 and 2018, selected from healthy and diseased hosts and belonging to four countries (Germany, Spain, UK, and Vietnam). These strains were selected from existing and newly isolated strain collections. The year of isolation was further classified into three time periods: 2003-2007, 2008-2012, and 2013-2018.

A unique combination of country, host, time-period, and host health status called strata (e.g., Germany, Human, 2003-2007 and healthy is considered one stratum). In total, 120 strata were possible, but only 42 strata could be filled with strains. Next, the strains were randomly selected from each stratum, with a maximum of 30 strains per stratum.

To reduce any sampling or ascertainment bias isolates that were too similar were excluded (e.g., part of an outbreak at a single location within a short timeframe/from a single farm/a single individual; one isolate per individual).

This selection procedure leads to a random selection of 1,213 *E. coli* strains from the current collection.

3.2) DNA extraction and sequencing:

The DNA of individual *E. coli* strains from Germany was extracted using QIAamp DNA Mini Kit (QIAGEN) by following the manufacturer's instructions. The DNA concentration was evaluated fluorometrically by using QubitTM 2.0 Fluorometer and the associated QubitTM dsDNA HS Assay Kit (0.2-100ng) and Qubit^{TM} BR Assay Kit (2-1000ng), respectively. The libraries were generated using Nextera DNA library preparation (Illumina). The sequencing was performed using the Illumina MiSeq and HiSeq system, generating 2 x 250 bp and 2 x 150 bp reads, respectively.

The DNA of individual *E. coli* strains from the UK was purified using a Promega DNA Wizard® genomic purification kit and quantified using Nanodrop. Libraries were generated using Nextera XT technology (Illumina, https://www.illumina.com), and DNA sequencing was performed at the Animal and Plant Health Agency (APHA, Surrey, UK, https://www.gov.uk/government/organisations/animal-and-plant-health-agency) using an Illumina MiSeq system generating 2 x 150 bp reads.

For *E. coli* strains from Spain, a single CFU was inoculated in BHI broth at 37ºC. DNA was then extracted using the DNA blood and tissue Qiagen kit (according to the manufacturer's instructions). The total amount of DNA was quantified using a Qubit fluorometer and frozen at -20ºC until further analyses. Libraries were prepared using Nextera XT DNA Library preparation (Illumina), and DNA samples were sequenced using a MiSeq platform (2 × 300 cycle V3 Kit)

The DNA of individual *E. coli* strains from Vietnam was extracted using the Wizard Genomic DNA purification kit (Promega, Madison, WI, USA) following the manufacturer's instructions. The concentration of the DNA was measured fluorometrically by using picogreen (Invitrogen). The sequencing was performed using an Illumina HiSeq 4000 system, generating 2 x 150bp reads.

3.3) Quality control:

Next-generation sequencing platforms such as Illumina generate enormous amounts of data (raw reads). However, these reads may consist of several technical artifacts, including base-calling errors, low-quality reads, and a primer/adapter contamination. These artifacts can significantly impact various downstream analyses such as assembly, mapping, and SNPs calling, which may lead to erroneous conclusions. Hence, these sequencing artifacts need to be removed before any downstream analysis.

To remove primer/adapter contamination within the reads, FLEXBAR [129] (v3.0.3) [130] was used. It is implemented in C++ using the Seqan library [131] and can detect target (adapter or barcodes) sequences within the raw reads by overlapping sequence alignments, based on the Needleman-Wunsch algorithm [132]. FLEXBAR allows five (ANY, LEFT, RIGHT, LEFT_TAIL and RIGHT_TAIL) different adapter/barcode recognition and removal modes.

An in-house collection of adapter/primer sequences was used to scan for their contamination within the raw reads and removed these using the trimming mode

ANY (adapter/barcode sequence is searched for any match within a read, the longer non-matching substring of the reads is retained).

FastQC [133] and MultiQC [134] were used to generate quality-control reports per sample and summarize all the reports into a single file, respectively, before and after the primer/adapter contamination removal.

3.4) Genome assembly and annotation:

3.3.1) Assembly:

Primer/adapter trimmed reads of each strain were *de-novo* assembled by using SPAdes v3.13.1 [135]. SPAdes uses BayesHammer for read-error correction (for Illumina data) [136] without any uniformity assumption before assembly. Any scaffolds smaller than 500bp were discarded. QUAST v5.0.0 [137] was used to assess the quality of these assemblies using default parameters. Draft assemblies were excluded if the N50 was below 40,000 bp, or the assembly consisted of more than 809 contigs. In total, 1,199 draft genomes were considered further for gene prediction.

3.3.1) Gene prediction and annotation:

The Prokka v1.13 [138] pipeline with a genus-specific blast enabled for *Escherichia* was used to predict and annotate genes in each draft genome. Prokka uses Prodigal [139], RNAmmer [140], Aragon [141], SignalP [142], and Infernal [143] for the prediction of coding sequences (CDS), ribosomal RNA genes (rRNA), transfer RNA genes (tRNA), signal leader peptides and non-coding RNAs (ncRNA) respectively.

3.5) MLST and phylogroups:

Sequence Types (STs) of all the strains were identified *in-silico* using the Achtman MLST scheme [44]. This scheme consists of seven housekeeping genes (*adk, fumC, gyrB, icd, mdh, and purA*) (http://mlst.warwick.ac.uk/mlst/dbs/Ecoli). For this, the “mlst” tool developed by Torsten Seemann (https://github.com/tseemann/mlst) was used, which assigned sequence types based on allelic profiles of those housekeeping genes available in the PubMLST database [144]. Later, a minimum spanning tree (MST) was constructed based on these STs' allelic profiles by using an improved MST algorithm called MSTreeV2 in GrapeTree [145]. The tree was labeled with STs and host metadata. *E. coli* phylogroups were also determined *in-silico* by using ClermonTyper v. 1.4 [146].

3.6) Computation of pan-genome:

Roary v3.12.0 [147] was used to define the pan-genome (consisting of both core- and accessory-genes) within the given strain collection. It requires annotated genomes (in GFF3 format) produced by Prokka as an input. Homologous genes were identified using a minimum of 95% sequence identity. Homologous groups containing paralogs were split into true-orthologous groups. Genes present in 99-100% of the total number of strains were considered core, and the rest is accessory genes. In addition, core-genes were aligned using a probabilistic multiple sequence alignment (MSA) program named prank [148] with default parameters. Prank aligns codon sequences using a codon substitution matrix that can produce better alignments for protein-encoding sequences.

3.7) Reconstruction of phylogeny:

SNPs were extracted from the core-genome alignment using snp-sites v2.4.1(-mc) [149]. These SNPs were used to reconstruct a phylogenetic tree with the maximum-likelihood method using RaxML v8.2.4 [150]. The tree was built by using the GTR-GAMMA nucleotide substitution model with ascertainment bias correction (-m ASC_GTRGAMMA) by Paul O. lewis (--asc-corr=lewis) [151], and the bootstrap value set to 100.

3.8) Identification of population structure:

The population structure within the *E. coli* genome collection was identified by hierBAPS [152] (Bayesian Analysis of Population structure implemented with hierarchical model-based clustering) based on the core-genome alignment. The R-implementation of the hierBAPS algorithm (rhierBAPS v1.1.3) [153] was used to delineate the phylogenetic clusters (also known as BAPS cluster) in R v3.6.1.

3.9) Clustering of strains based on accessory-genome:

Strains were clustered based on their accessory gene content by applying the Barnes-Hut implementation of the t-Distributed Stochastic Neighbor Embedding (t-SNE) [154], [155], which is a dimensionality reduction technique used for visualization of high-dimensional datasets. The tab-delimited binary file indicating the presence/absence of the genes within the strains was generated by Roary and used as an input to t-SNE. This analysis was performed in R v3.6.1 with the r-package Rtsne v0.15 [154], [155] at perplexity 30 with 5000 iterations.

iTOL [156] and Microreact [157] were used to visualize the core-genome phylogeny and clustering of strains based on the accessory-genome within the context of available metadata.

3.10) X^2-test for independence (by Boas C.L. van der Putten):

X^2-tests of independence were carried out on tables listing number of strains from each host belonging to specific phylogenetic clusters and phylogroups. The function "chisq.test" from the MASS library (version 7.3-51.1) was used in R (version 3.5.2) to perform the tests. Tests were carried out on the full dataset (14 phylogenetic clusters vs. five hosts and nine phylogroups vs. five hosts), and the analysis was subsequently repeated on isolates from individual countries to minimize geographical biases.

3.11) Genome-wide association analysis:

Genome-wide association studies developed for bacterial populations, as implemented in *pyseer*, was used to determine the host-specific/genomic determinants in this study. *pyseer* is a re-implementation of SEER in the python programming language and uses the fixed-effects model [109] or Factored Spectrally Transformed Linear Mixed Models (FaST-LMM) [158] for identifying associations of gene presence/absence, *k-mers* or SNPs/INDELs with a phenotype. These models use appropriate control for correcting the existing population structure.

K-mers allow parallel discovery of both short genetic variants and complete genes associated with a phenotype. Hence, we used *k-mers* of variable length from draft assemblies as input and assessed the association of each *k-mer* with the host-phenotype by using the linear mixed model. A variable *k-mer* length was selected as longer *k-mer*s provide higher specificity whereas shorter provide higher sensitivity. All *k-mers* of lengths >= 9 bases were counted and tested simultaneously. The step by step implementation of pyseer is described below and shown in Figures 4 and 5:

a) **Phenotype file:** A tab-delimited file with the first column containing sample names and the phenotype present in the last column in a binary format ('1' indicates positive for phenotype, '0' indicates absence, and 'NA' for missing phenotypes). For the current analysis, the host (i.e., Human, cattle, chicken, and pig) was chosen as the phenotype of interest. Four phenotypic files were created to compare each host with other hosts at a time.

b) ***K-mer* counting**: *K-mers* of variable length between 9 and 100 bp were counted by Frequency-based String Mining (fsm)-lite (https://github.com/nvalimak/fsm-lite) from each draft genome. *K-mers* were filtered out if they appeared with a prevalence, i.e., <1% or >99% of samples, or if the length of a *k-mer* was longer than 100 bp.

c) **Control for population structure:** To correct for population structure, *pyseer* required pairwise distance between all the samples. The pairwise distance between the samples can be estimated by three methods: i) mash ii) Phylogeny-based iii) Genotype matrix.

   i) **Mash:** Mash is an extension of the MinHash dimensionality-reduction technique to include a pairwise mutation distance and *p-value* significance test [159]. It first uses a 'sketch' function to shred each genome into *k-mers* of specific sizes called 'sketches.' The 'dist' function compares two sketches and estimates the fraction of shared *k-mers* (using the Jaccard index), a *p-value,* and the mash distance, which estimates the rate of sequence mutation under a simple evolutionary model [160]. The mash distance matrix as a control for population structure is mainly used with the fixed-effect model while testing associations.

   ii) **Phylogeny-based:** A distance matrix can be estimated by using a phylogeny. The phylogeny should be computed without recombination events and built with an accurate model of evolution. For testing the association with the fixed-effect model, the patristic distance between the samples will be estimated using the phylogeny, whereas, with the linear mixed model (FaST-LMM), the similarity is estimated based on the shared branch length between each pair's MRCA (Most recent common ancestor) and the root.

   iii) **Genotype matrix:** The genotype matrix can be constructed based on the SNPs retrieved from the core genomic regions and stored in a Variant Call Format (VCF). It uses the presence/absence of these variants to estimate a kinship matrix. Linear mixed models (LMMs) used in association mapping can also incorporate kinship into the models to correct genetic relatedness between individuals in a population.

Depending upon the model used for testing associations, a method for estimating the pairwise distance between the samples or genetic relatedness will be selected. In this analysis, we used the linear mixed model (FaST-LMM) for association testing together with the phylogeny-based similarity matrix for correcting the population structure. The general workflow for the implementation of *pyseer* is shown in Figure 3. GWAS analysis was carried out for each host. To reduce false-positive associations, strains from the host of interest were compared with an equal number of control strains from other hosts. This analysis was repeated 100 times (or runs) per host of interest by randomly selecting the control strains from other hosts in every iteration. The selection of control strains was stratified by phylogenetic clusters (or BAPS clusters identified in section 3.7) to minimize phylogenetic biases and to prevent the accumulation of the clonal group while subsampling (as shown in Figure 4). The statistical significance threshold (*p-value*) was estimated based on the number of unique *k-mer* patterns obtained per run. For each *k-mer* likelihood ratio test (lrt), a *p-value* was reported by *pyseer* per run, and if the lrt *p-value* was less than the estimated *p-value*, it was considered significant association with the phenotype in that run. Further, these *k-mers* from the individual runs were filtered based on their effect size (β)>0, and their prevalence was estimated across 100 runs. *K-mers,* which were present in more than 90% of the runs, were considered for annotation by mapping to the reference genomes using a fastmap algorithm in bwa [161]. The effect size of a *k-mer* represents whether presence ($\beta>0$) or absence ($\beta<0$) of the *k-mer* is associated with the phenotype. If the effect size is equal to zero, neither presence nor absence of the *k-mer* contributes to the phenotype.

3.12) Prevalence of human-associated *nan* gene cluster:

All available *E. coli* genomes were downloaded on Nov 29th, 2019, using NCBI-genome-download (https://github.com/kblin/ncbi-genome-download). A custom database using nine genes of the human-associated *nan* gene cluster was built. All 17,994 genomes were scanned against this custom database using ABRicate (https://github.com/tseemann/abricate) to identify the presence of human-associated *nan* gene cluster in these genomes at default settings. Sequence types of these genomes were determined, as mentioned in section 3.4.

Figure 3: Workflow of *pyseer* with three inputs a) Phenotype file, b) *K-mer* file and c) Distance matrix

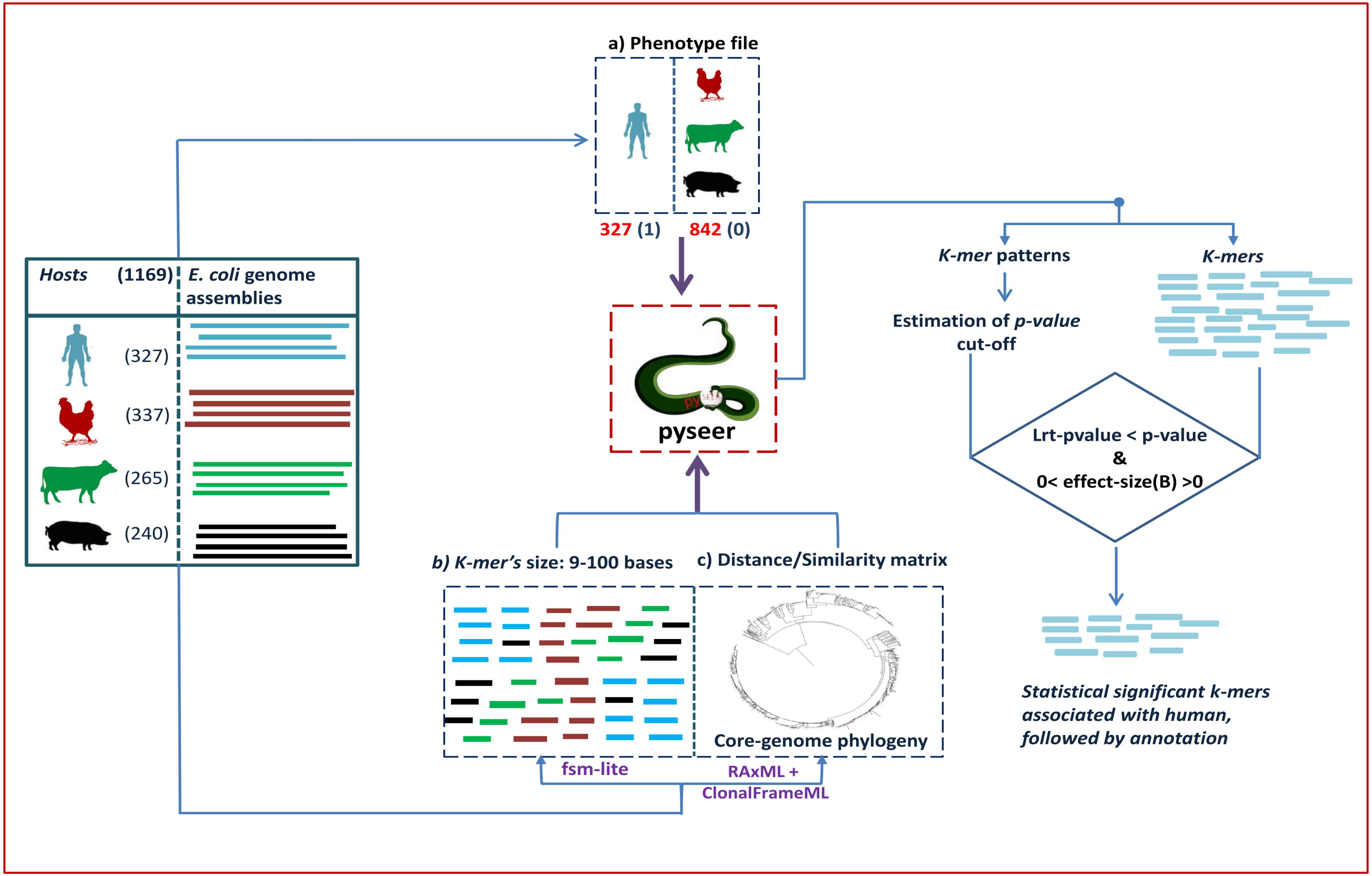
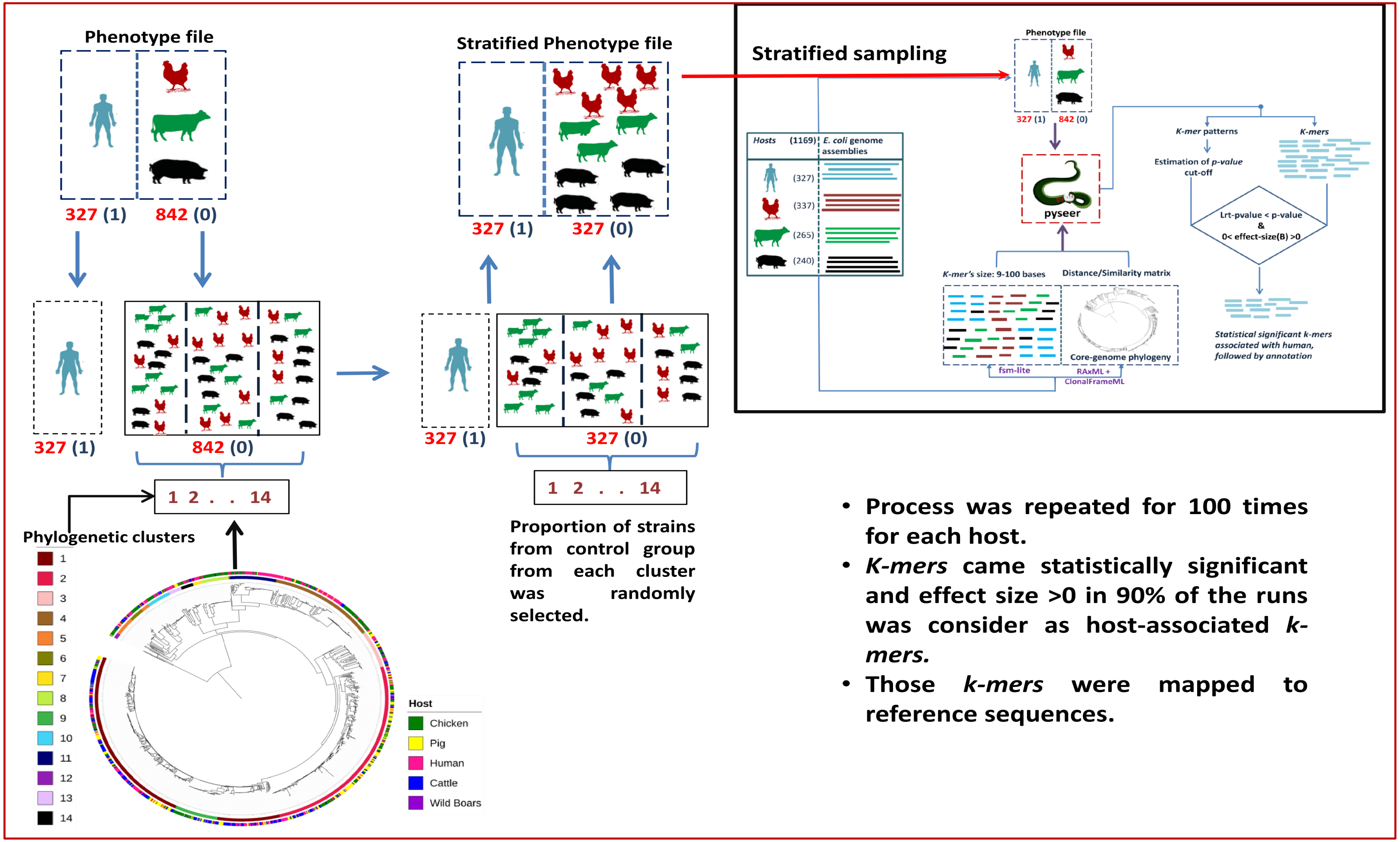


Figure 4: Stratifying and balancing the test-and-control groups in pyseer for each run per phenotyp



- Process was repeated for 100 times for each host.
- *K-mers* came statistically significant and effect size >0 in 90% of the runs was consider as host-associated *k-mers.*
- Those *k-mers* were mapped to reference sequences.

4. Results:

4.1) Strain collection and distribution:

In total, 14 genomes were discarded based on the quality control applied on whole-genome sequences. Also, one more strain was excluded since it was identified to be *Escherichia marmotae* (formerly cryptic clade V) [42], [43], a species commonly mistaken for *E. coli*. Hence, the final collection comprised of 1,198 *E. coli* whole-genome sequences and their metadata shown in Supplementary Table 9.1. The final collection also includes eight cryptic clade I strains, which could be considered *E. coli* based on the recommended species cut-off of 95-96% average nucleotide identity [43]. The collection consists of 22.1% (n=265) cattle, 28.1% (n=337) chicken, 27.3% (n=327) human, 20.3% (n=240) pigs and 2.4% (n=29) wild boar strains isolated from these hosts (Figure 5). Whereas 51.0% (n=612), 19.4% (n=233), 14.5% (n=174) and 14.94% (n=179) of these strains are from Germany, Spain, UK, and Vietnam respectively (Figure 6). There were no cattle, pig, and wild boar *E. coli* strains from the UK, no Spanish strains were from humans, no strains with wild boar as host from Germany, and there were no Vietnamese strains from cattle and wild boar hosts. In total, 35.5% (n=426) of the strains are from diseased hosts, whereas 62.0% (n=743) are from healthy, while 2.4% (n=29) of the host's health status was unknown.

To confirm that our collection covers most of the known diversity, a core-genome phylogeny of 1,344 *E. coli* strains (comprised of 67 *E. coli* strains from the ECOR collection, some well-known *E. coli* strains (n=69), and 10 *E. coli* cryptic clade reference genomes and our collection (n=1,198)) was built by applying the methods defined in section 3.5 and 3.6 above. The reference strains and the in-house strains are distributed over the phylogeny and share the same phylogenetic clusters (Figure 7). Our strain collection also consists of strains belonging to different known phylogroups A, B1, B2, C, D, E, F, and clade I, closely resembling the ECOR collection's diversity. Hence, our collection's population structure closely resembles the population structure of the reference strains collection, indicating the collection covers most of the known diversity of *E. coli sensu stricto* (Figure 7).

Figure 5: Distribution of strains: x-axis represents the hosts, and the y-axis represents the percentage of strains belonging to each country per host. The number on each bar represents the total number of strains per host. Note: WB= wild boar.

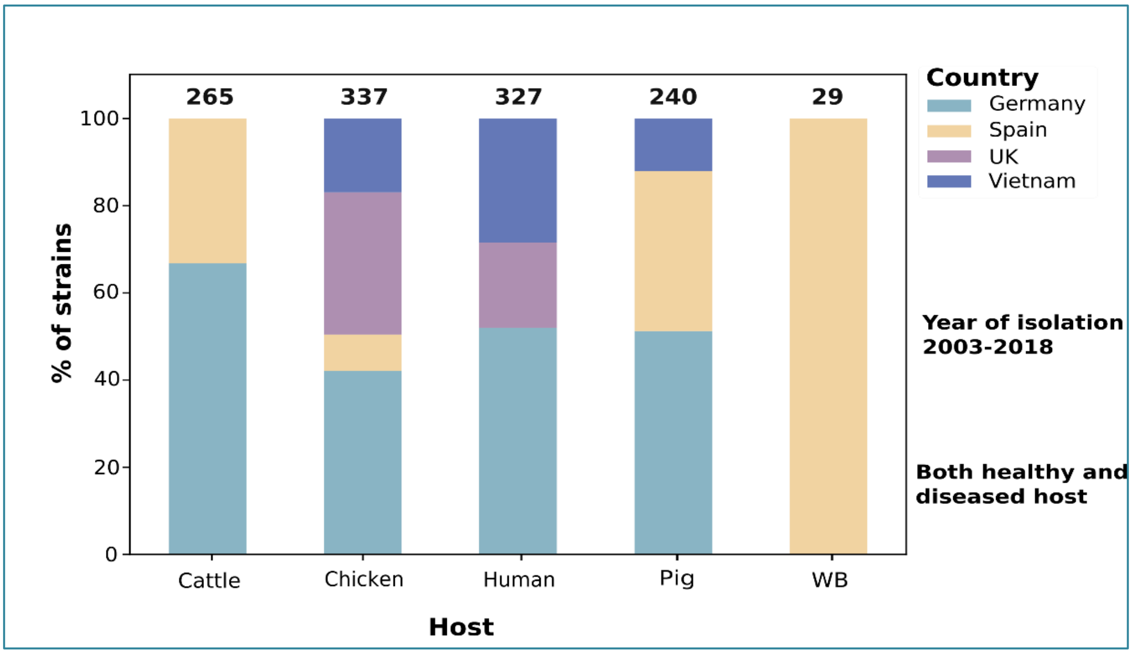


Figure 6: Distribution of strains: x-axis represents the country, and the y-axis represents the percentage of strains belonging to each host per country. The number on each bar represents the total number of strains per country. Note: WB= wild boar.

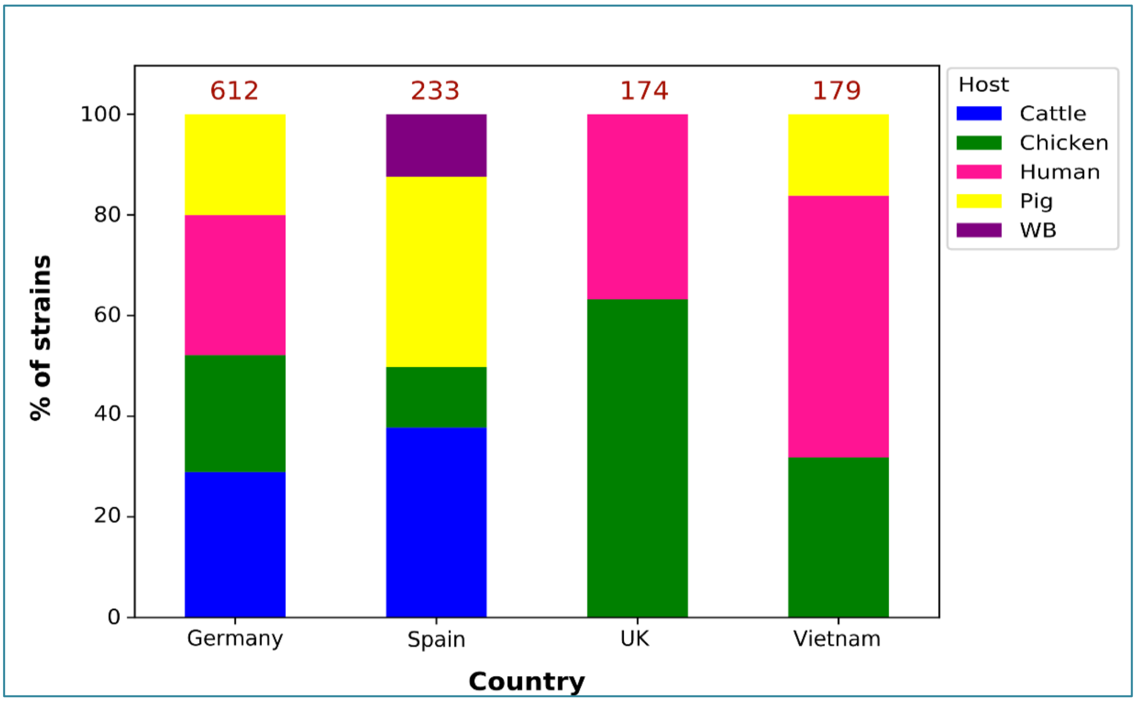
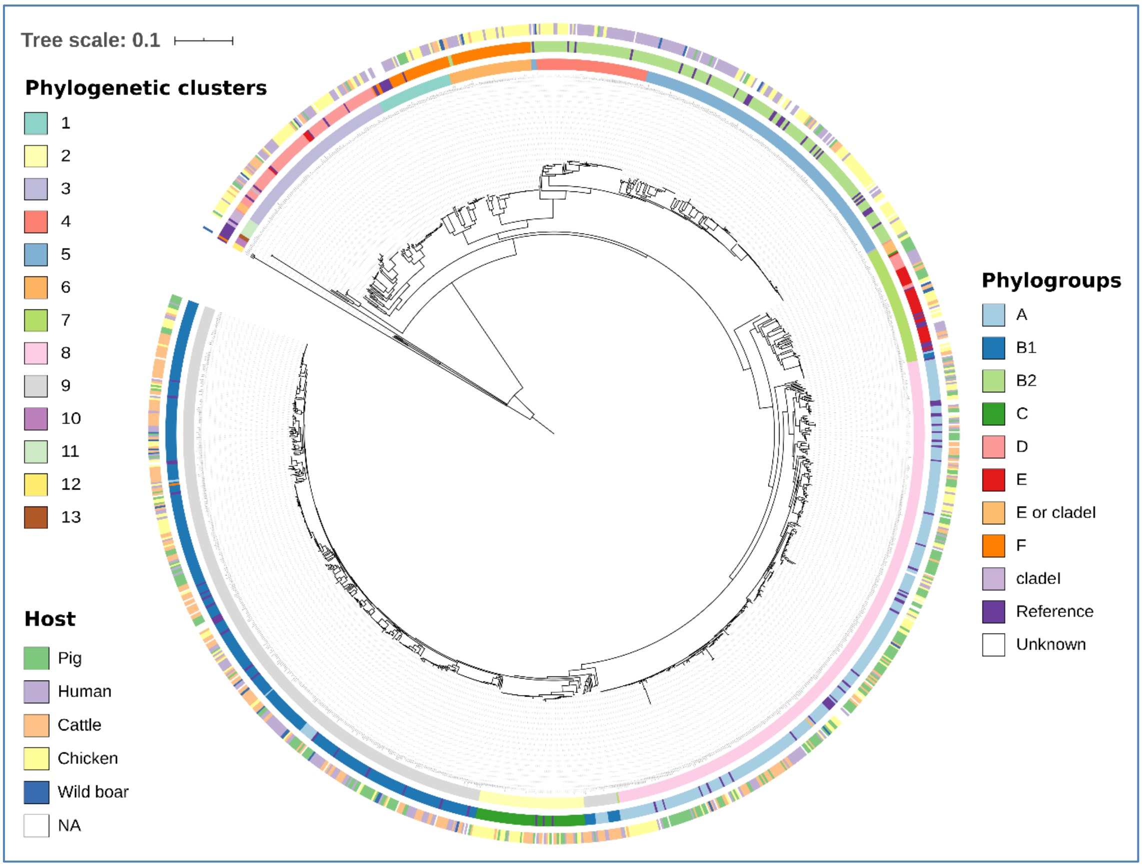


Figure 7: Core-genome phylogeny (n=1,344) consists of our strain collection, the ECOR collection, well known *E. coli* strains, and *E. coli* cryptic clade reference genome. The inner-ring represents the Phylogenetic clusters; the middle-ring represents the Phylogroups, and the outer ring represents the Host. (Performed by Boas C.L. van der Putten and Me)



4.2) Phylogenetic analysis of strains:

The pan-genome of the 1,198 strains of *E. coli* consists of 77,130 genes, of which 1,956 genes belong to the core-genome (i.e., found in at least 99% of strains), and 71,186 genes belong to the accessory-genome. The core-genome alignment consists of 110,920 core SNPs. The population structure of the collection was defined based on the core-genome alignment and by using a Bayesian analysis of population structure (BAPS), which assigned strains to 14 discrete phylogenetic clusters correlated well with core-genome phylogeny built using core SNPs, as shown in Figure 8.

Most of the isolates were assigned to phylogroups B1 (n=366, 30.6%), A (n=313, 26.1%) and B2 (n=213, 17.8%) in the collection. The remaining strains were distributed among phylogroups D (n=97, 8.1%), C (n=60, 5.0%), E (n=55, 4.6%), G (n=49, 4.1%), F (n=35, 2.9%) and clade I (n=8, 0.6%). Later these phylogroups were mapped back to the phylogeny, which was consistent with the phylogenetic clusters of the phylogeny (Figure 8). There were some discrepancies observed in the phylogroups assignment, which is corrected based on the phylogroup assignment of neighboring strains. Host species and country metadata were also plotted on the phylogeny to observe host-associated or country associated clusters on the phylogeny (Figure 8). *E. coli* strains from different hosts appeared to be evenly distributed across the phylogeny, but χ^2-tests for independence revealed a positive correlation between different phylogroups and hosts (p-value < $2.2e^{-16}$). This indicates that specific phylogroups (such as B1 with cattle, A with Pig, B2 with human & chicken, and G with Chicken) were enriched with different hosts in our collection (Figure 9).

Figure 8: Core-genome phylogeny (n=1,198) of *E. coli* strain collections (mid-point rooted on clade I strains): Distinct colors on clades represent Phylogroups, inner-ring represents Phylogenetic clusters, middle-ring represent Host whereas the outer-ring represents the Country.

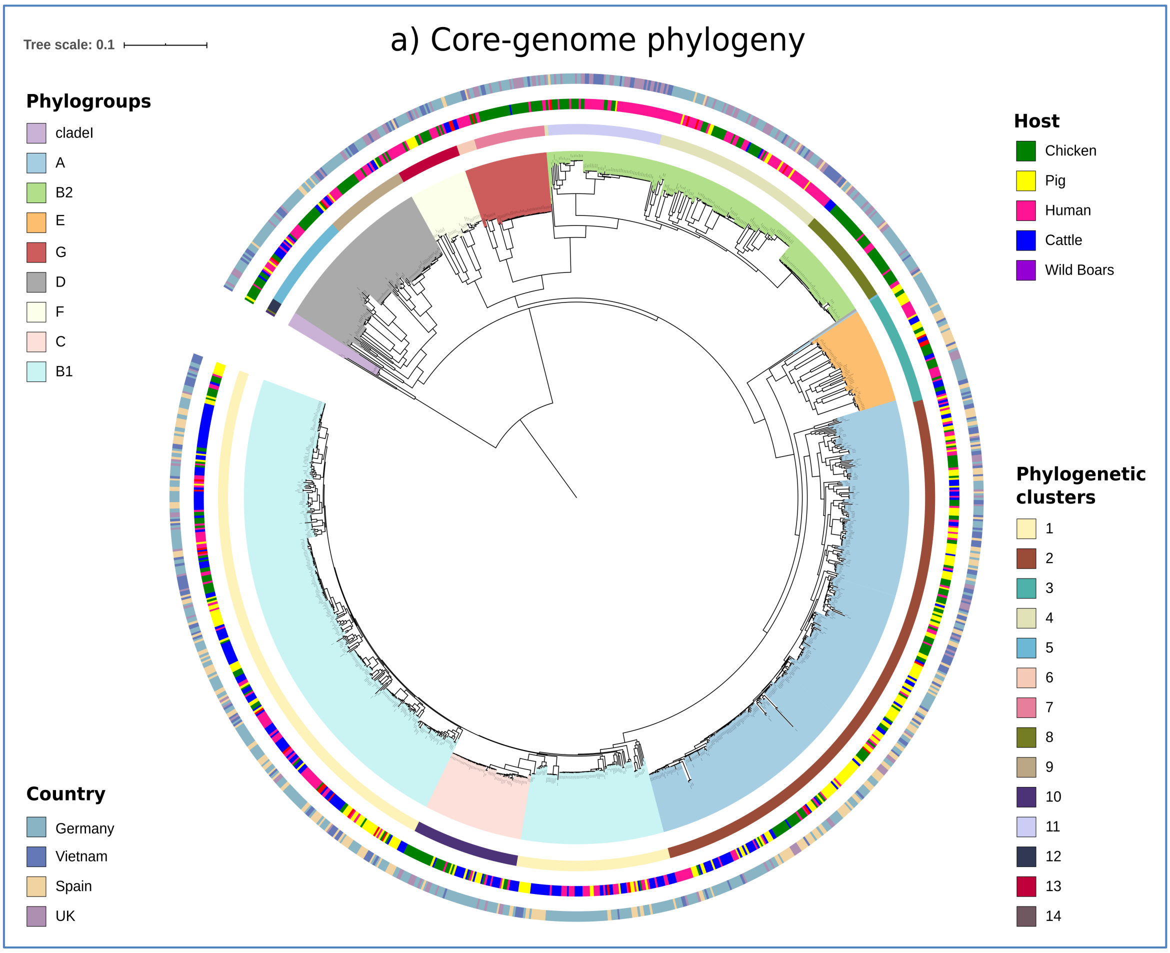
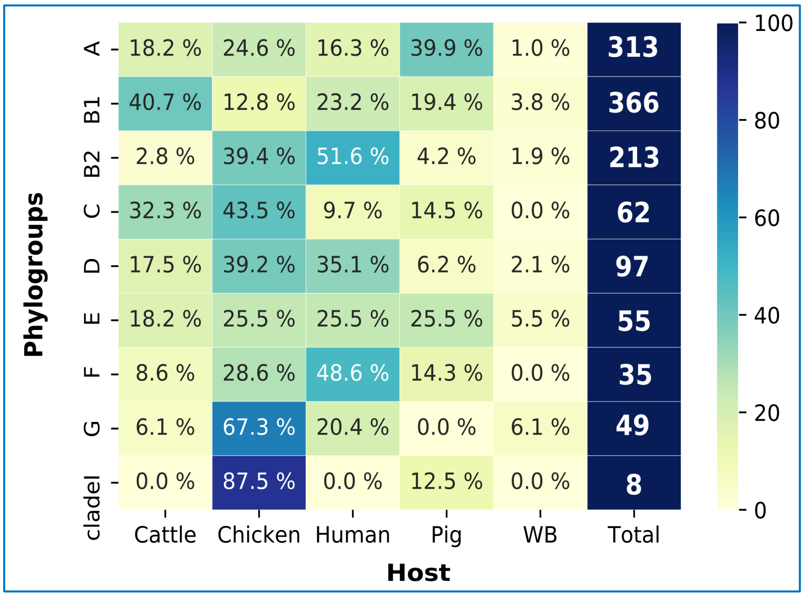


Figure 9: Heatmap showing the proportion of strains from each host per phylogroups. "Total" indicates total number of strains in each phylogroups.

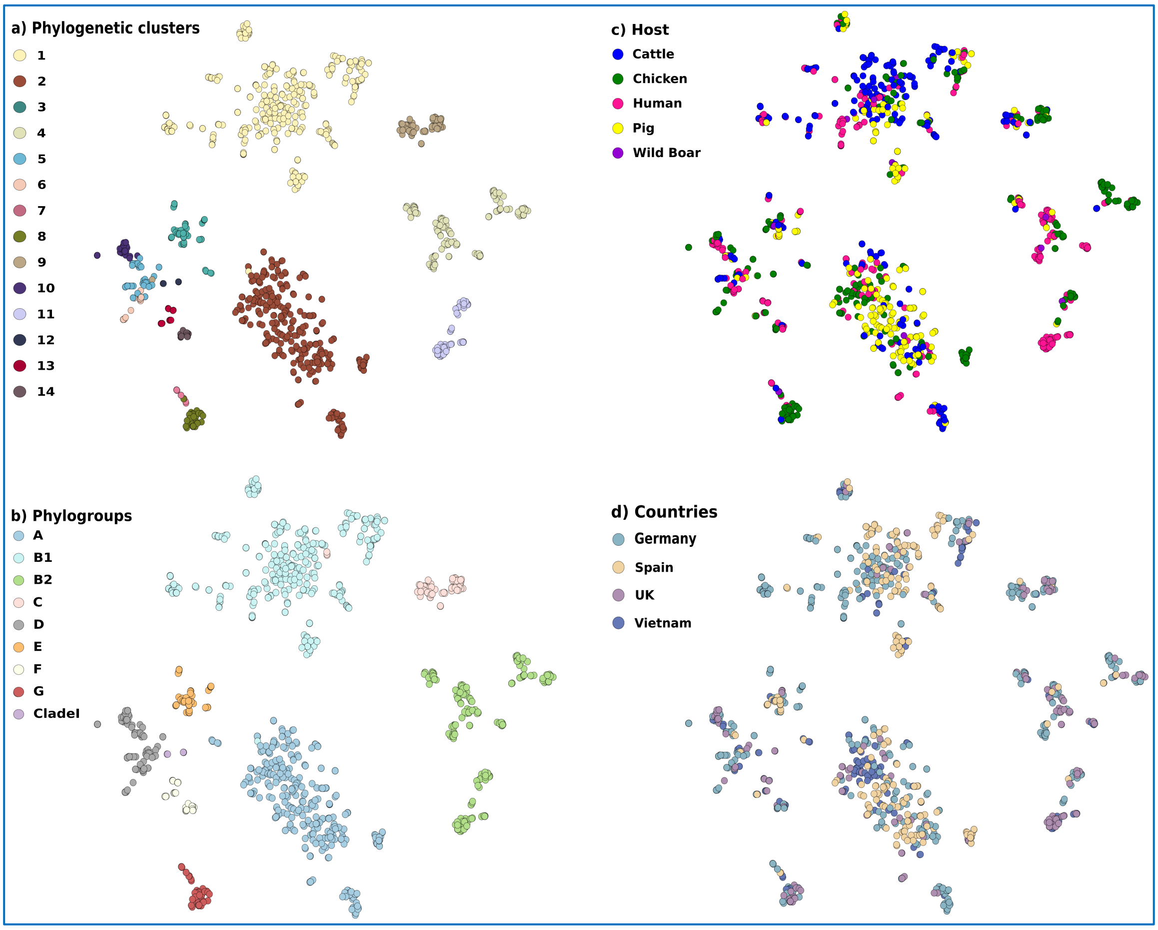


Phylogroups	Cattle	Chicken	Human	Pig	WB	Total
A	18.2 %	24.6 %	16.3 %	39.9 %	1.0 %	313
B1	40.7 %	12.8 %	23.2 %	19.4 %	3.8 %	366
B2	2.8 %	39.4 %	51.6 %	4.2 %	1.9 %	213
C	32.3 %	43.5 %	9.7 %	14.5 %	0.0 %	62
D	17.5 %	39.2 %	35.1 %	6.2 %	2.1 %	97
E	18.2 %	25.5 %	25.5 %	25.5 %	5.5 %	55
F	8.6 %	28.6 %	48.6 %	14.3 %	0.0 %	35
G	6.1 %	67.3 %	20.4 %	0.0 %	6.1 %	49
cladeI	0.0 %	87.5 %	0.0 %	12.5 %	0.0 %	8

4.3) Clustering of strains based on accessory-genome:

The clustering of strains based on the presence or absence of 71,130 accessory genes was strongly correlated with the phylogenetic clusters defined based on the core-genome (Figure 10a). This could indicate that the distinct population groups share a similar set of accessory genes. In general, the clustering of strains based on the core-genome and accessory gene content is highly similar. Hence, the clustering of strains based on phylogroups, hosts, or country would result in the same pattern on both core (Figure 8) and accessory gene content (Figure 10-b,c,d), and the same can be observed interactively on the Microreact platform (https://microreact.org/project/ouDOdcFxc).

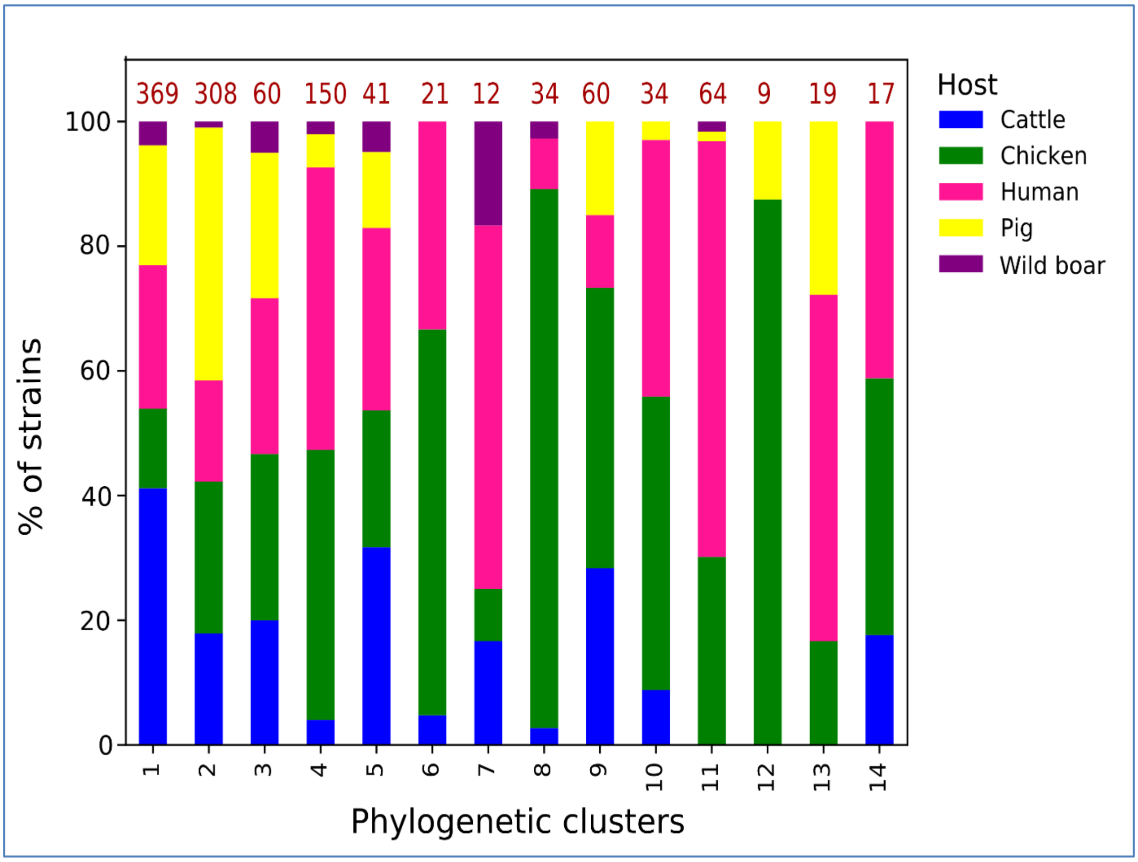
Figure 10: Clustering of strains (n=1,198) based on the accessory gene profile. Showing the distribution of strains based on a) Phylogenetic clusters, b) Phylogroups, c) Host, and d) Country.



4.4) Host-associated clustering of strains:

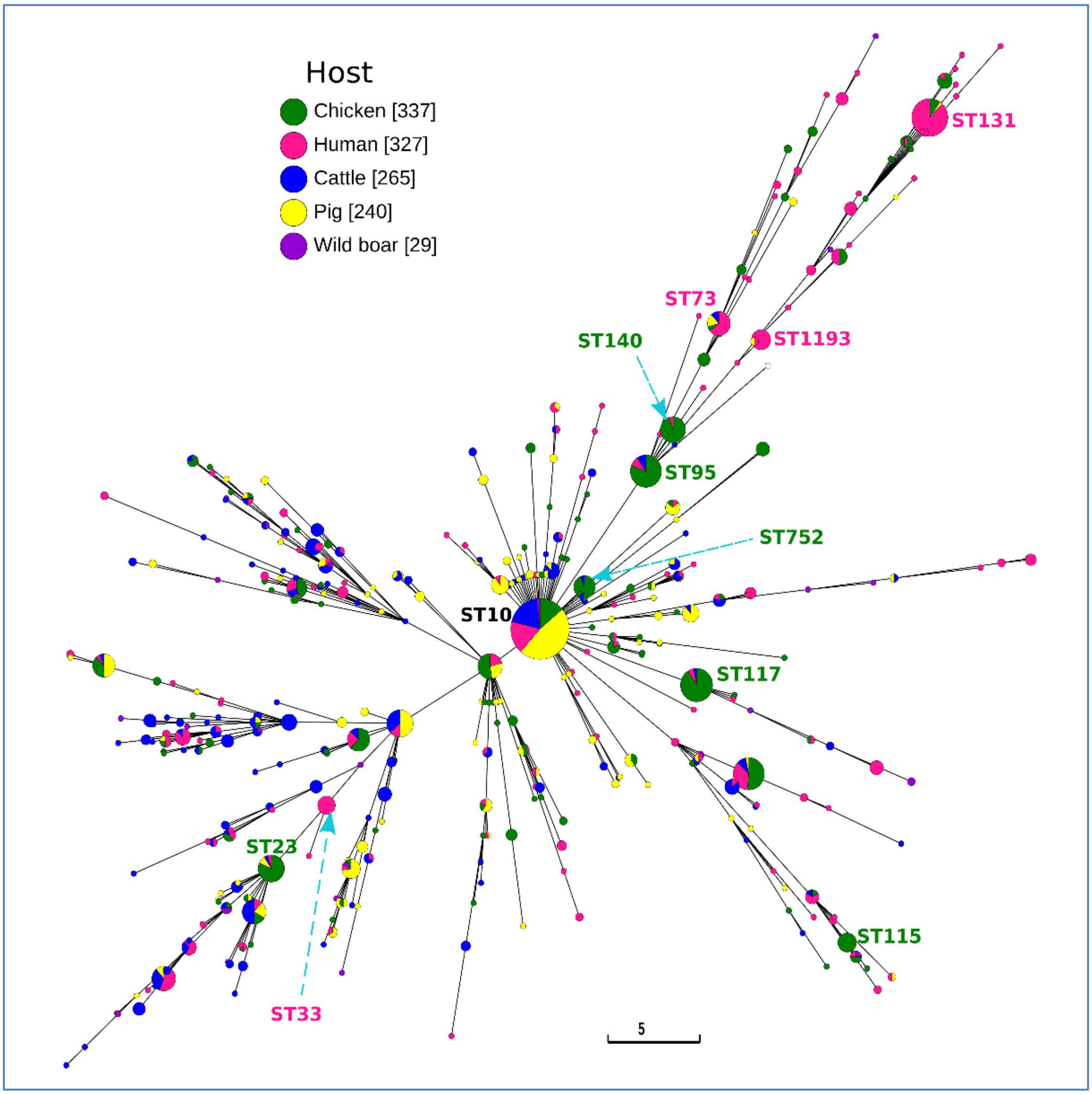
To test whether *E. coli* from specific phylogenetic clusters are more likely to be isolated from a particular host, χ^2-tests for independence were performed. Although all phylogenetic clusters contained strains from more than one host; however, the host distribution is not entirely independent of phylogenetic clusters (*p-value* $< 2.2e^{-16}$). The distribution of host in different phylogenetic clusters is shown in Figure 11. Also, when performing the χ^2-test for independence for isolates originating from a single country (to mitigate possible confounding effects by geographical origins) and hosts were found to be significantly dependent on each other (Germany: *p-value* $< 2.2e^{-16}$, Spain: *p-value* $< 2.2e^{-16}$, United Kingdom: *p-value* $= 6.523e^{-07}$, Vietnam: *p-value* $= 1.034e^{-10}$).

Figure 11: The proportion of strain isolated from different host-species constituting each phylogenetic cluster. The numeric value on the top of each bar indicates the total number strains in each phylogenetic cluster.



To further characterize the host-associated lineages, these strains were assigned to known sequence types. A total of 1,140 (out of 1,198) strains were grouped into 358 different sequence types, whereas 58 were not assigned to any known STs. ST1193 (n=12/12), ST33 (n=10/10), ST73 (n=11/17) and ST131 (n=37/42) appeared to be associated with human host (Figure 12). ST131 was predominantly reported in human strains, but the collection consists of ST131 from chicken (n=4/42) and pig (n=1/42) hosts too. ST115 (n=11/11), ST117 (n=30/33), ST140 (n=19/20), ST23 (n=18/22), ST752 (n=29/30) and ST95 (n=25/31) were found to be associated with chicken (Figure 12).

Figure 12: Minimum spanning tree of STs allelic profile: Representing the proportion of strains isolated from different hosts constituting each ST. Distances represent differences in their allelic profiles.

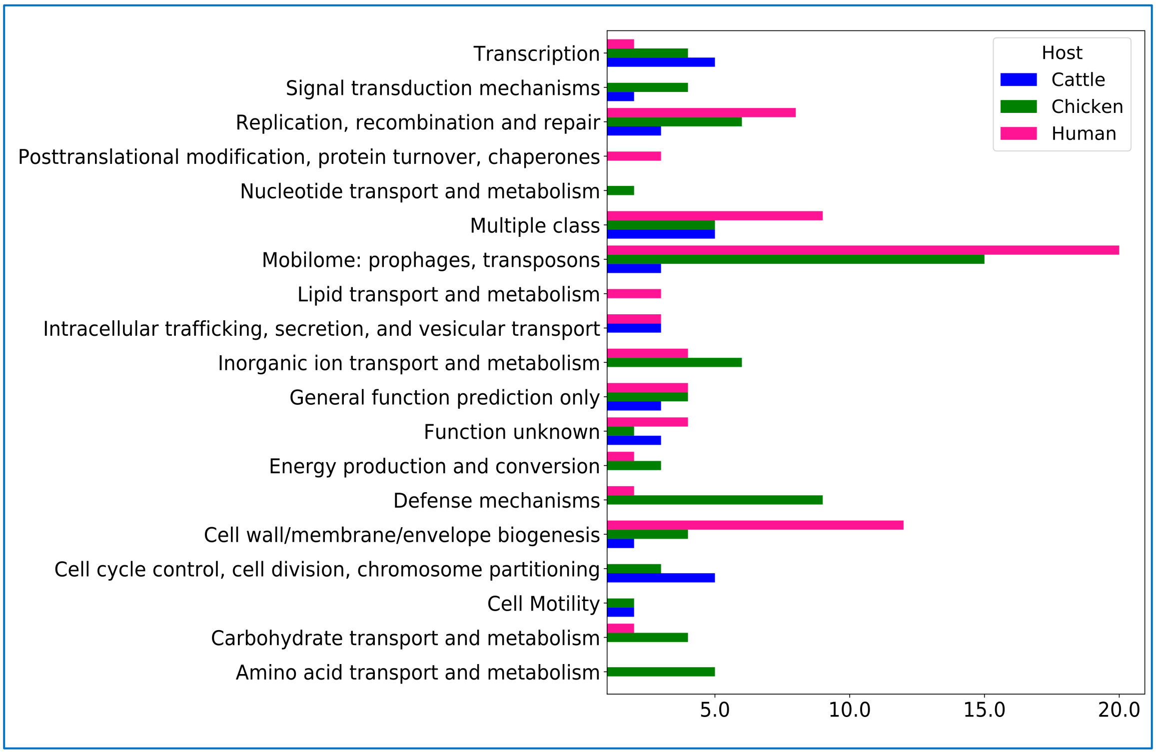


4.5) Genome-wide association analysis:

To determine the host-associated genomic determinants, a Genome-wide association study was carried out for *E. coli* strains isolated from cattle, chicken, human, and pig (i.e.1,169 strains in total). Genome-wide association analysis revealed the statistically significant association of 27,854, 16,164, and 69,307 *k-mers* with *E. coli* strains isolated from humans, cattle, and chicken. The average estimated *p-value* threshold across 100 runs was $1.87e^{-09}$, $2.16e^{-09,}$ and $1.9e^{-09}$ for humans, cattle, and chicken, respectively. These *k-mers* had an effect size (β)>0 and lrt-pvalue < estimated *p-value* in at least 90% of the runs with their respective host phenotype. No *k-mers* associated with the pig host phenotype were found significantly associated with at least 90% (90/100) of the runs.

These significant *k-mers* were mapped to their respective reference genomes (Supplementary Table 9.2) and accounted for 426, 179, and 915 *E. coli* genes from humans, cattle, and chicken (Supplementary Table: 9.3). An arbitrary cut-off of a minimum of 10 *k-mers* mapped per gene was chosen for *in-silico* functional characterization as well as COG assignment using Blast2GO [162] (Supplementary Table 9.4) and CD-search [163], [164]. Based on the functional characterization, these genes may be involved in a wide range of cellular activities. The biggest proportion of genes for humans and chicken belonged to the mobilome functional class, whereas in cattle, the maximum number of genes was involved in transcription, cell cycle regulation, and genes containing multiple domains (Figure 13). Further, genes associated with these hosts were analyzed for their involvement in specific cellular activity.

Figure 13: Molecular functions of genes associated with hosts: x-axis represents the number of genes, whereas the y-axis represents the molecular functional class.



4.3.1) *E. coli* genes associated with humans:

GWAS revealed an association of nine contiguous gene's cluster with the human host. The gene cluster annotated (*in-silico* using prokka) as *nan* (*nanA, nanC, nanK, nanM, nanR, nanS, nanT)* genes together with two *axeA1* genes (i.e., *axeA1_1* and *axeA1_2)* (Figure 14). Further analysis with Blast2GO and CD search confirms the *nan* genes annotations and revealed acetyl esterase domain (COG0657) in two *axeA1*-like genes. The proteins encoded by these two genes shows only shows ~19-20% similarity to known AxeA1 (UniProt id: D5EV35) present in *Prevotella ruminicola*. Further, the genomic location of two *axeA1*-like genes lies in between the *nan* genes (Figure 15a). Hence, these evidences leads to hypothesis that the proteins encoded by these *axeA1*-like genes are putative acetyl esterase and may be analogous to nanS (known as sialyl O-acetyl esterase [165], [166]). Hence, the novel gene cluster will refer as the "**human-associated *nan* gene cluster**" (Figure 15a).

Distinct *nan* genes were reported to be present in *E. coli*, together known as Sialoregulon (*nanR*, *nanATEKyhcH*, *yjhBC [nanXY]* and *nanCMS*) [167] (Figure 15b). Sialoregulon was known to metabolize sialic acids [168]–[170]. The prevalence of the human-associated *nan* gene cluster was estimated to be 7% (n=86/1198) of the strain collection, whereas in strains from humans is 24.4% (n=80/327) and 0.6% (n=6/871) in other host's strains. This human-associated *nan* gene cluster is found in different phylogroups consisting of strains belonging to specific STs and predominantly found in ST131 (n=35/42), ST73 (n=14/17), ST69 (n=6/31) strains, and 31 other STs (Figure 16). The orientation and order of the human-associated *nan* gene cluster are conserved in 82 (out of 85) strains. The gene cluster is flanked by IS-elements belonging to the IS66 and IS2 families. The sensitivity of the human-associated *nan* gene cluster within an external dataset consisting of 17,994 *E. coli* genomes (downloaded on 29th Nov 2019 from the NCBI reference sequence database called RefSeq) is 12%, and a correlation between its presence and lineages (ST131, ST73, and ST69) was observed (Table 5).

The prevalence of *nan* genes of Sialoregulon i.e., *yjhBC (nanXY) is ~15%, nanCMS is ~93%* and *nanRATEKyhcH* are found in almost all the strains of the collection (Figure 15*b*) and both are located on the chromosome. The Sialoregulon genes are found on three distinct chromosomal locations and shares several genes (based on gene annotation) with the novel human-associated *nan* gene cluster (but no significant sequence similarity with the *nan* genes of Sialoregulon at identity and coverage >= 70%). The presence of two copies of this regulon in some lineages of *E. coli* most likely helps them to metabolize host sialic acids efficiently and may provide a nutritional advantage over other bacteria in the human gut.

Figure 14: Bubble plot representing the genes or allelic variants associated to the human host. Each bubble on the plot represents an allele or gene, labelled according to their Prokka annotation. The bubble's size represents the number of *k-mers* mapped to an allele/gene, and the color gradient in the allele or gene quantifies the average effect size (β) of an allele/gene. The x-axis indicates the average frequency of the allele/gene in the collection, and the y-axis indicates the significant *p-value*.

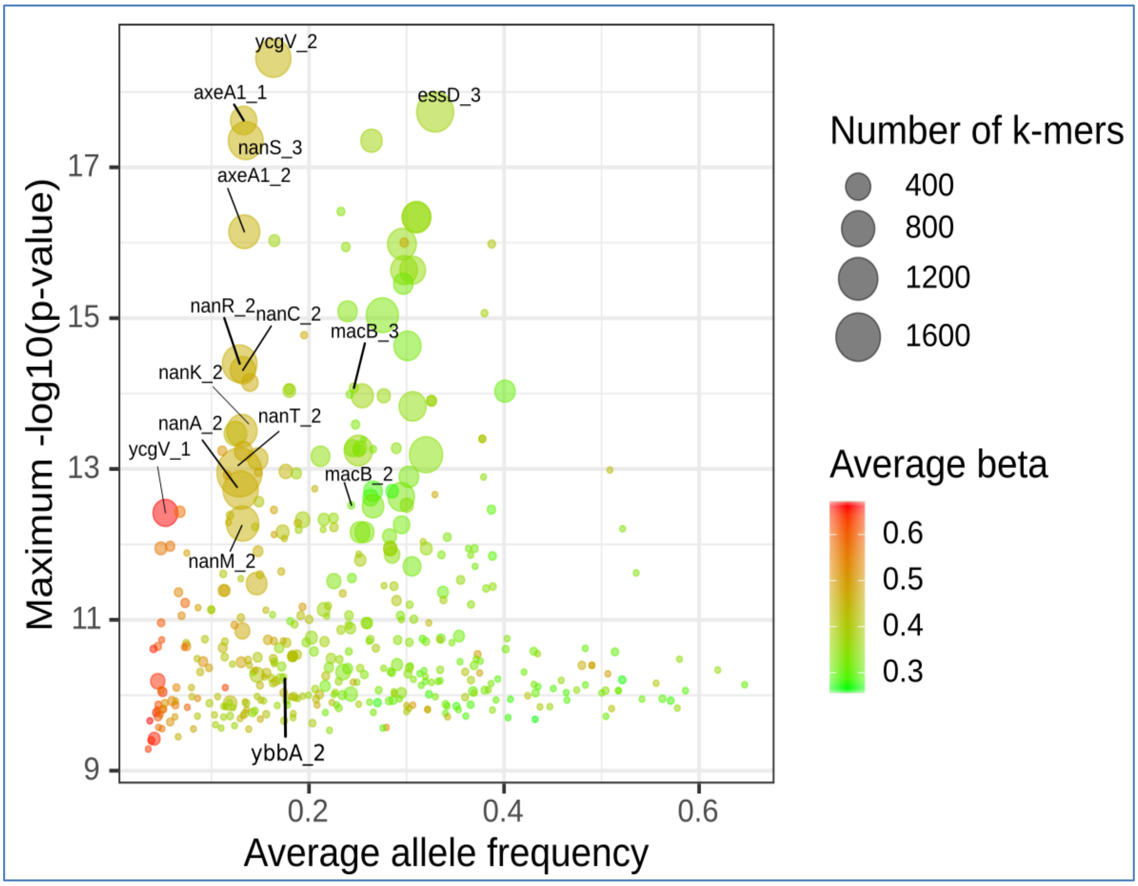


Figure 15: Genetic architecture of Sialic acid metabolic genes on *E. coli* chromosome: a) Human-associated *nan* gene cluster in *E. coli* strain EC-TO143 (accession number: NZ_LS999560.1). b) Sialoregulon (*E. coli* K-12 substr. MG1655, accession number: NC_000913).

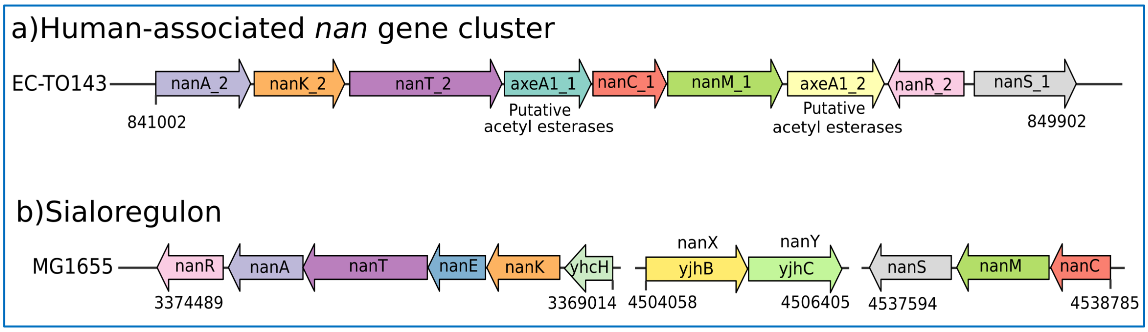
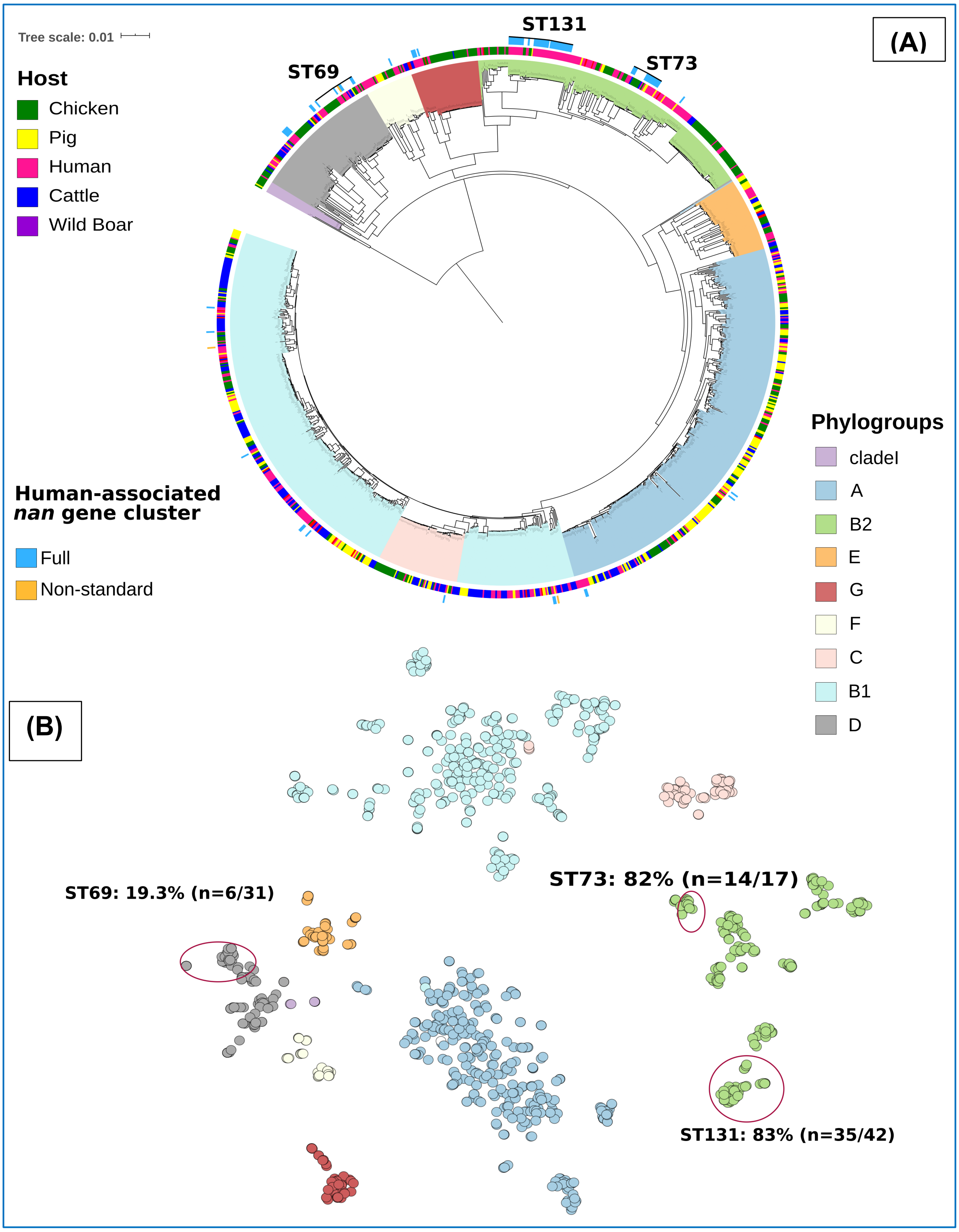


Table 5: Prevalence of human-associated *nan* gene cluster in different STs in our collection as well as in the *E. coli* genomes downloaded from the RefSeq (downloaded on 29th Nov 2019).

OUR COLLECTION			RefSeq	
ST	**Presence/Total number of strains**	**%**	**Presence/Total number of strains**	**%**
131	35/42	83	1073/1256	85
73	14/17	82	253/372	68
69	6/31	19	155/302	51
38	3/6	50	57/196	29
10	4/109	4	66/1183	6
Other	24/993	2	512/14685	3
Total	**86/1198**	**7**	**2116/17994**	**12**

Figure 16: Distribution of human-associated *nan* gene cluster in different phylogroups having specific STs over A) the core-genome phylogeny and B) Genome clustering based on the accessory-genome.



In addition to human-associated *nan* gene cluster, our GWAS also revealed the significant association of *sat* gene, which encodes a serine protease sat autotransporter toxin (annotated by Prokka as ycgV_2) with the human host. The *sat* gene's prevalence in the *E. coli* strains isolated from the human host is 22.9% (n=75/327), and in other hosts, it is 0.59% (n=5/891). These strains belong to phylogroups A, B2, D, and F from healthy and diseased hosts (Supplementary Table 9.5). Sat contributes to cytotoxic activity in the urinary tract [171] and may also play a role in infection in niches other than the intestinal and urinary tract [172].

The prevalence of *sat* in *E. coli* strains isolated from the intestinal microbiota of healthy individuals suggests it may not act as a virulence factor in the human gut [173]. Nevertheless, the putative role of *sat* in adaptation of *E. coli* is still unknown [173]. Additionally, we found an association with macB_2 and macB_3 homologs of the macB protein, which is an ABC transporter [174] and has a multitude of roles, such as resistance to macrolide antibiotics [175], lipoprotein trafficking [176], and cell division [177]. The role of these genes in the adaptation of *E. coli* in humans is still unclear and needs further studies that mainly focus on this aspect of those proteins.

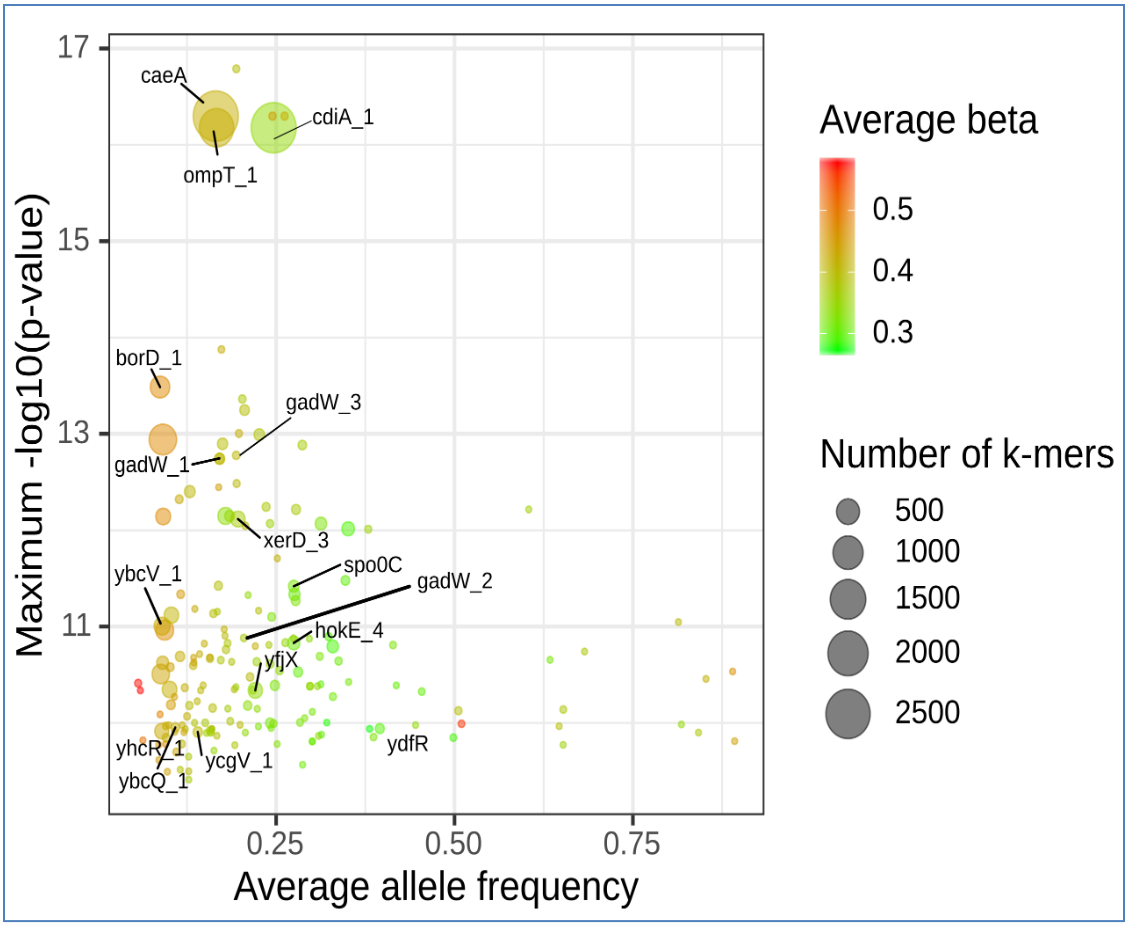
4.3.2) *E. coli* genes associated with cattle:

GWAS identified a significant association of protein belonging to the omptin family of proteases (Prokka annotated these as ompT_1, Figure 17). This protein was found to share 100% similarity with native OmpP protein (UniProt: P34210) and 70% similarity with ompT (uniport: P09169). The *ompP* gene's sensitivity in the entire collection is 8.2% where as its prevalence in cattle host is 32.5% (Table 6). Whereas this gene's presence in other hosts of the collection is 1.0% (n=12/933, including wild boar strains) but was not found in strains isolated from chicken. The cattle strains harboring the *ompP* gene belongs to different STs (no enrichment was observed in the individual sequence type). Most of the cattle strains harboring this gene belongs to phylogroup B1 (n=60/86) (Figure 18). On contrary, *ompT* gene appeared to be more prevalent in different hosts and phylogroups in comparative to *ompP* (Table 6 and Figure 18).

The protein encoded by *ompP* gene exhibits ompT-like substrate specificity and proteolytic activities [178], [179]. OmpP tended to function synergistically with OmpT to enhance *E. coli* ability to resist the action of cationic antimicrobial peptides in host species [180], [181]. Currently, there is no evidence of this gene being linked with any specific host species. Different homologs of the protein belonging to the omptin family of proteases were found to be associated with chicken and cattle host that might be responsible for host-adaptation and survival. These functions of the gene need to be further investigated in detail.

Apart from the enrichment of the omptin family of proteases, GWAS identified a *bor* gene homolog encoding for Bor protein (found within our *E. coli* strains collection) associated with cattle. This gene's prevalence in the entire collection was very low (4.3%, n=52/1198), whereas estimated to be 19.2% (n=51/265) in cattle hosts.

Figure 17: Bubble plot representing the genes or allelic variants associated with cattle host. (Note: All the definitions are same as described in the legend of Figure 14).



Bor is a lipoprotein of the cell envelope of *E. coli* lambda lysogens [182]. It shares homology with Iss (increased serum survival) with an identity of approximately 90% [182]. Bor appeared to confer complement resistance [183], [184]. However, unlike *iss, bor* is present on a cryptic prophage within the chromosome [185]–[187] and found to be associated with cattle hosts rather than APEC strains of *E. coli* (*iss* is known to be predominantly found in APEC strains [188], [189]). The expression of *bor* significantly increases the survival of *E. coli* in animal serum [190]. However, its potential role in adapting the host niches in cattle needs further examination.

Figure 18: Illustrating the distribution of *ompT* and *ompT-like* genes on the core-genome phylogeny across different hosts and phylogroups.

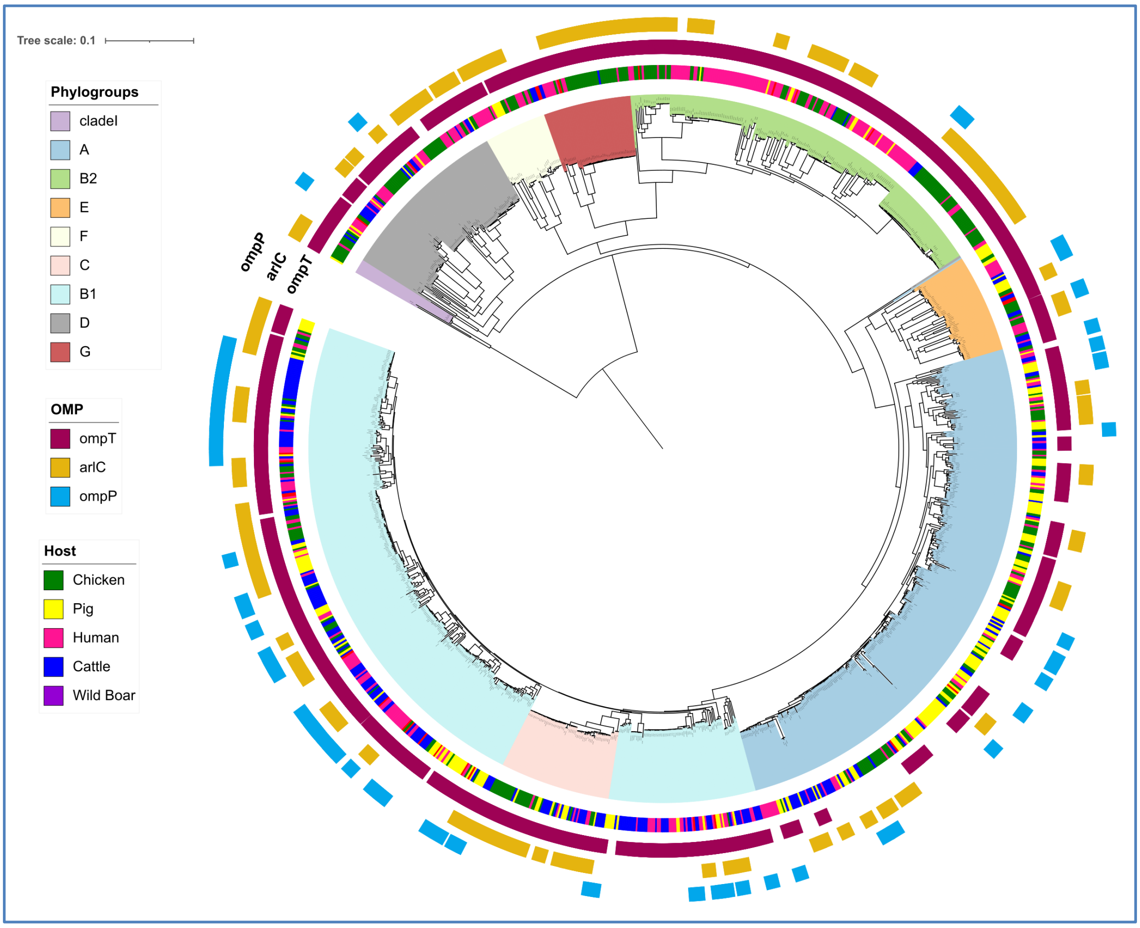


Table 6: The *ompT*, *arlC* and *ompP* gene's prevalence in different hosts.

Host	ompT	arlC	ompP	arlC+ompT	ompP+ompT	arlC+ompP +ompT
Cattle (n=265)	55.5% (147)	6.0% (16)	32.5% (86)	2.3% (6)	20.8% (55)	1.5% (4)
Chicken (n=337)	67.1% (226)	63.7% (208)	0	50.4% (170)	0	0
Pig (n=240)	42.1% (101)	13.7% (33)	2.1% (5)	12.5% (30)	0.8% (2)	0
Human (n=327)	72.8% (238)	7.6% (25)	1.5% (5)	6.1% (20)	0.9% (3)	0
WB (n=29)	62.1% (18)	0	6.9% (2)	0	3.4% (1)	0
Total (n=1198)	60.9% (730)	23.5% (282)	8.2% (98)	18.9% (226)	5.1% (61)	0.3% (4)

4.3.3) *E. coli* genes associated with chicken:

The genes associated with chicken hosts seems to be involved in acquiring metal ions. GWAS analysis revealed the association of the genes annotated by Prokka as elmGT, msbA_2, fes_2, besA and fepA_2 (Figure 19) to the chicken host species in contrast to other host species of this study. These genes are 99-100% identical with the *iroBCDEN* gene cluster in *E. coli* strain 536 (Figure 20), respectively. This was further confirmed by PSI-BLAST against RefSeq protein database and Blast2GO annotation server (Supplementary Table: 9.4). The entire gene cluster is found in 24.3% (n=291/1198) of the collection strains. The prevalence of the cluster in strains isolated from chicken hosts was 53.1% (n=179/327), whereas, in other hosts, it was found to be 13.1% (n=113/891). The gene cluster was found in different STs (Table 7), and some of these STs, such as ST117, ST95, ST23, and ST140, were enriched with strains isolated from chicken (Figure 12) and 96.9%, 67.7%, 90.9%, and 90.0% of these STs harbor the gene cluster respectively (Table 7)

Table 7: Abundance of the *iroBCDEN* gene cluster across different sequence types.

ST	Presence (# strains)	Total (# strains)	%
117	32	33	96.9
95	21	31	67.7
23	20	22	90.9
140	18	20	90.0
69	17	31	54.8
73	14	17	82.3
101	10	19	52.6
58	10	22	45.4
Other STs	149	447	33.3
Total	291	642	45.3

The chromosomally encoded *iroBCDEN* gene cluster was first characterized in *Salmonella enterica* and was involved in the uptake of catecholate-type siderophore-compounds. Siderophores (are high-affinity iron-chelating molecules) can contribute to bacterial survival during infection by absorbing iron (an essential trace element for most bacterial species) from their surroundings [191]. In *E. coli*, this cluster is located on a chromosomal pathogenicity island (PAI), although in ExPEC the cluster was found on ColV or ColBM virulence plasmids [192], [193]. The *iroBCDEN* gene cluster was also reported in uropathogenic (UPEC) and avian pathogenic *E. coli* (APEC) and is widely regarded as a virulence factor in *E. coli* [194]. In addition to this, homologs of these genes involved in zinc catabolism (*znuB*) and iron metabolism (*fes*) were also detected to be associated with the chicken host (Figure 19).

A gene called *arlC* (ompTp) belonging to the omptin family of proteases (Prokka annotated as ompT; Figure 19) also associated with chicken was revealed by GWAS. The protein encoded by this gene has appeared to be distinct from the previously cattle associated protein of the same family (amino-acid similarity of 69.40%) and also from reference protein sequence of ompT (uniport: P58603 and P09169; similarity 73.8 and 72.9% respectively) and ompP (P34210; amino-acid similarity 69.40%). The prevalence of *arlC* gene was found to be 23.5% (n=282/1198) across the entire collection. Whereas its prevalence in the strains isolated from chicken is 63.7% (n=208/337, Table 6) but there is no significant enrichment of this gene in certain phylogroups were observed (Figure 18).

Figure 19: Bubble plot representing genes or allelic variants associated with chicken host species. (Note: All the definitions are same as described in the legend of Figure 14)**.**

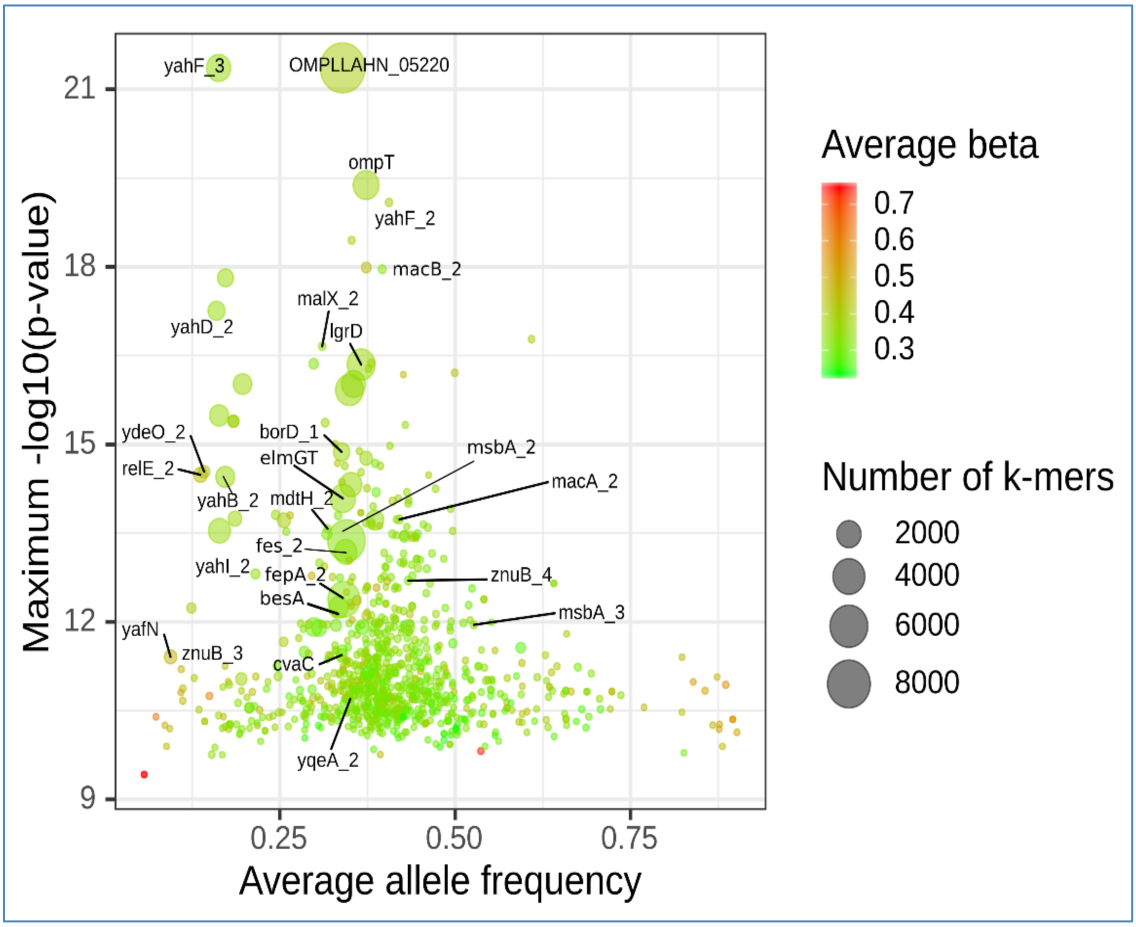
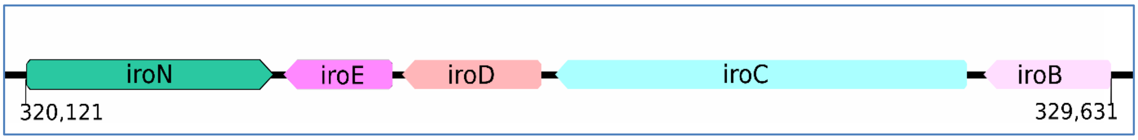


Figure 20: The salmochelin siderophore system (*iroBCDEN* gene cluster) on the reference genome *E. coli* strain 536 (NC_008253.1: 320,121-329,631 bps).



5. Discussion:

Escherichia coli (E. coli) is a diverse bacterium, having both commensal and pathogenic forms. The relationship between commensal *E. coli* and its host has been described as mutualism, whereas, on the other hand, pathogenic *E. coli* are involved in causing a wide range of infections at intestinal and extraintestinal sites (including moderate to severe symptoms). *E. coli* can be found in the natural environment, human and animal population. It can migrate between different host species and ecological niches. Its chromosomal plasticity helps *E. coli* to colonize and adapt to a wide range of selective pressures in different environments, including humans and animal hosts [46]. It gains various host-adaptive traits throughout this process. The remarkable ability of *E. coli* to adapt distinct environments provides an evolutionary advantage to acquire and disseminate antibiotic resistance traits within or across novel environments [46], [195]–[198]. In *E. coli*, mobile genetic elements play an essential role in acquiring or disseminating antimicrobial resistance. The ability to spread and disseminate AMR is driven by individual strains' fitness [199]. Commensal *E. coli* can act as a reservoir for AMR genes in both the human and animal populations.

In general, the escalating prevalence of AMR in both pathogenic and commensal bacteria is a significant concern for both developed and developing nations. The natural environment may hereby act as a reservoir of AMR genes or serve as a medium for disseminating resistant bacteria between human and animal populations. However, it is still a matter of debate to what extent resistant commensal and pathogenic bacteria successfully spread and establish themselves in the human population due to transmission from animal and environmental reservoirs and vice versa. Furthermore, to what extent *E. coli* lineages are adapted to a particular host species or have lost such specialization and the genomic determinants contributing to this host-adaptation are still unknown. Additionally, there is a considerable gap in our current understanding of the impact of host-adaptation on transmission dynamics of AMR *E. coli* between different reservoirs, such as human and animal hosts.

The characteristic of *E. coli* to colonize multiple hosts, the existence of commensal and pathogenic lineages, and involvement in the spreading of AMR make it a suitable organism to study in order to fulfill those knowledge gaps. Hence, this study was performed to shed some light on the genomic determinants associated with certain host species, and their potential role in different cellular activities was characterized *in-silico*. The analysis was performed with a diverse collection of 1,198 *E. coli* strains isolated between 2003 and 2018, from both healthy and diseased host-species (cattle, chicken, pig, human, and wild boar) belonging to four geographical locations (Germany, Spain, UK, and Vietnam). The collection closely resembles the population structure of ECOR and well characterized *E. coli* genomes, which indicates that this collection spans the known diversity of *E. coli*. This collection covers strains belonging to known phylogroups A, B1, B2, C, D, E, F, G, and clade I. These strains were further assigned to 358 different STs. This confirms further that the collection is quite diverse and should potentially reduce any sampling biases.

The core-genome phylogeny and clustering of strains based on their accessory-genome reveal 14 distinct phylogenetic clusters (Figure 8 and Figure 10). This indicates these strains probably share similar SNPs as well as accessory genes associated with the different phylogenetic clusters. The clustering pattern was also well correlated with the distribution of phylogroups and STs over the core-genome phylogeny and the clustering of strains based on their accessory- genome. In general, the hosts were distributed all over the core-genome phylogeny (Figure 8), and a similar pattern of host-distribution was observed on the accessory gene clustering as well (Figure 10c). However, the host-enrichment was observed among minor sub-clusters at the sub-population level. Further, a minimum-spanning tree (MST) was built based on the MLST profile, which revealed host-associated STs i.e., ST1193, ST33, ST73 and ST131 to be enriched with human host whereas ST115, ST117, ST140, ST23, ST752 and ST95 were enriched with the chicken host (Figure 12). The host-associated minor clusters observed on the core-genome phylogeny might most likely associated with these STs. χ^2-tests for independence revealed the enrichment of hosts in different phylogenetic clusters and phylogroups. Although the statistical test showed the strong dependence on the distribution of strains based on geographical location, it might be associated with the fact that approximately 51% of the strains were from one country (i.e., Germany).

A genome-wide association study (GWAS) on the strain collection was performed to identify the genomic determinants of *E. coli* associated with these hosts. A *k-mer* based GWAS method was implemented to capture the variations in the core and accessory genes as well as genes associated with the hosts. The GWAS, together with a stratified sampling approach, revealed accessory- genes and variations in the accessory genome associated with humans, cattle, and chicken hosts. These genes were found to be involved in different cellular activities leading to host-adaptation.

Sialic acids (neuraminic acid) is a family of over 40 diverse naturally occurring nine-carbon keto sugars acids derived from N-acetylneuraminic acid (Neu5Ac) found in both prokaryotes and eukaryotes [200]. In eukaryotes, sialic acid regulates innate immunity, whereas microbes have evolved various strategies to overcome this by molecular mimicry, scavenging host-derived intermediates, and modifying sialidases. Sialic acids are also used as a nutritional source (of carbon, nitrogen, energy) and precursors of cell wall biosynthesis in many microbes [200]. *In-vivo* studies indicate that in *E. coli*, they primarily act as a nutritional source [200]–[202], and might be involved in the regulation of type-1 fimbrial phase variation, which involved in colonization as well as pathogenesis (UPEC) [203]. The catabolism of Neu5Ac (N-acetylneuraminate, the most common sialic acid in humans) in *E. coli* is performed by *nanATEK-yhcH*, regulated by repressor protein nanR [167]. Earlier studies have shown that *nanCMS* is required for the growth of *E. coli* on O-acetylated sialic acids (prevalent in host mucin oligosaccharide) [165] whereas *yjhBC* (*nanXY*) are required for 2,7-anhydro-Neu5Ac uptake and utilization [170]. The expression of these genes is also regulated by NanR [204].

GWAS revealed the association of novel *nan* gene cluster together with two putative acetyl esterase encoding genes (probably *nanS* variants), which might metabolize the Sialic acid (Figure 15a). These strains were isolated mainly from the urine and stool of healthy and diseased individuals. The presence of two copies of these Sialic acid metabolic genes in these strains may provide them a nutritional advantage. This human-associated *nan* gene cluster might be involved in the metabolism of the most prominent and the other variants of host sialic acids. The operon was predominantly found in ST131, ST73 ST69, ST38, and ST10 in our collection and the RefSeq collection of *E. coli*. These lineages are known to be responsible for ExPEC infections [44], [205]–[207]. Hence, this could also play an essential role in the infection by controlling specific virulence genes' expression or helping *E. coli* to adapt to those extraintestinal sites. The human-associated *nan* gene cluster was found on the chromosome of *E. coli* complete genomes available in RefSeq and was not found in any other microbes. A detailed study needs to be performed in order to fully characterized the role of human-associated *nan* gene cluster in sialic acid metabolism.

In addition to the novel Sialic acid metabolic gene cluster, an association of a secreted autotransporter toxin (Sat) to the human host was also identified. The *sat* gene and its role in urinary tract infection (UTI) was first demonstrated in a mice model of ascending UTI with Sat-producing UPEC [171]. The presence of Sat was also reported in diarrheagenic *E. coli* (DAEC, EPEC, ETEC, and EAEC) [208]–[211]. However, the prevalence of the *sat* gene reported in previous studies [208]–[211] also confirms our finding of its association with the human host, but the function of this protein is not fully understood. Sat could play an essential role as a virulence factor for infection in both the gastrointestinal and urinary tract as well as other sites [172], [210], [212], [213].

On the other hand, studies have indicated that it does not act as a virulence factor in the intestine when present in commensal *E. coli* [173]. This could indicate that the action of Sat may depend upon the bacterial background. In our collection, strains harboring the *sat* gene were isolated from healthy and diseased humans belonging to different phylogroups. Further studies are required to fully understand the role of Sat (both as a virulence factor and as host-adaptation factor) in *E. coli* strains.

The ompT-like proteases OmpP (Outer membrane protease ompP) and ArlC (ompTp, OmpT family outer membrane protease) were previously described in *E. coli* [214]–[216]. The *ompT* gene is more prevalent in *E. coli* strains than *ompP* and *arlC*. Hence, the association of *ompP* and *arlC* (*ompTp*) genes with cattle and chicken hosts, respectively, revealed by GWAS is intriguing. Similar to ompT, *in-vitro* studies have shown that ompP and arlC are also involved in the cleavage and inactivation of cationic antimicrobial peptides (AMPs like defensins, cathelicidin, RNase 7) secreted by the hosts as a part of their innate immune response [178], [217]. The physiological substrates of ompP and arlC are unknown. Studies have shown that ompP cleaves the AMP protamine, whereas ArlC is associated with AMP resistance [214]–[216]. However, they have shown different substrate specificity and varied efficiency depending upon the size and secondary structure of AMPs [178], [217]. It was also reported that the catalytic activity of these genes for AMPs was higher in pathogenic strains than in commensal or strains isolated from healthy humans [178], [217]. The association of different omptin proteases to cattle and chicken might be linked to different AMPs secreted by these hosts. It would be interesting to explore the substrate specificity and catalytic efficiency of these proteins in the strains isolated from cattle and chicken. Due to functional similarity between ompT, ompP, and arlC, the AMPs inactivation mediated by ompP and arlC could also support the adaptation of *E. coli* in these hosts [180], [214]–[216]. The presence of either ompP and ompT or ArlC and ompT in the same strain may confer a fitness advantage by expanding the spectrum of targeted AMPs [217]. Additionally, AMPs are also being used as a substitute for antibiotics in animal farming [218]–[220]. It would be interesting to investigate further if ompT-like proteases play any role in resistance against AMPs used in animal farming.

Apart from the specificity for the omptin proteases in chicken and cattle hosts, strains isolated from these hosts also harbor different proteins for increased serum resistance. Serum resistance plays an essential role in phage and bacterial natural selection in animal hosts. *E. coli* genes encoding for BorD (Bacteriophage lambda Bor) protein was detected by GWAS to be associated with cattle host, whereas the *ISS* gene was already reported to be prevalent in APEC strains [188], [189]. The *bor* gene was also reported to share significant homology with the *ISS* gene [182]. Genes encoding both proteins are located on the outer membrane of the *E. coli* and have been related to virulence. These genes' expression was correlated with the *E. coli* strains' increased survival in animal serum [190]. The selective advantage of *bor* in *E. coli* strains isolated from healthy cattle needs further studies that can reveal more insights into the process of innate resistance.

The APEC and UPEC lineage of ExPEC are known to cause infections at extraintestinal sites in poultry and humans. Both share similar virulence factors for colonizing and invading their hosts, including toxins, adhesins, polysaccharide coatings, and unique iron acquisition systems [221], [222]. Iron plays a vital role in the survival of *E. coli*. However, the concentration of iron at extraintestinal sites is low. ExPEC strains have developed multiple strategies for sequestering iron from their hosts. One of them is by encoding the *iroBCDEN* gene cluster responsible for the salmochelin (high-affinity ferric iron chelators) biosynthesis and transport [223], [224]. Various studies have shown the direct involvement of this gene cluster in virulence within both human and chicken [194], [225]. The presented GWAS study also revealed the association of this gene cluster with *E. coli* strains from chicken host rather than other hosts. It might also support the previous thought about the possible zoonotic transmission of avian *E. coli* from poultry to humans [226], [227], or the transmission of this gene cluster from chicken to human. The gene cluster prevalence was significantly similar in strains isolated from healthy (47%) and diseased (51%) hosts in the collection. Hence, it would be interesting to see this gene cluster's role in host-adaptation in strains isolated from healthy hosts.

No association of *E. coli* genes was detected with the pig host after applying filtration criteria on the stratified GWAS approach. It could indicate that pigs are generally permissive hosts, and *E. coli* may not need specific genes to adapt the host, or the filtration criteria is too strict. Altogether various genes revealed by GWAS may indicate the evolution of different mechanisms in *E. coli* to adapt distinct niches within specific hosts by changing their accessory gene repertoire. Although the applied GWAS method uses *k-mer*, which should capture core- genome variations (e.g., SNPs) and accessory gene variations, we mainly identified the accessory genes associated with these hosts. This might indicate that host-adaptive genes are mainly encoded in the accessory-genome, which seems to be supported by the fact that only a few host-associated *E. coli* lineages were detected. The strains harboring these genes might have an adaptive and fitness advantage over others in the corresponding host. This fitness might play a crucial role in acquiring and disseminating the AMR across different human and animal populations.

6. Summary:

E. coli is a commensal bacterium, as well as a versatile pathogen. Its ability to colonize distinct environmental niches provides an evolutionary advantage to acquire and disseminate antibiotic resistance traits within or across the different populations. In this study, we analyzed a diverse collection of 1,198 strains of *E. coli* isolated from different hosts, and a microbial GWAS was applied to determine the host-associated genomic determinants leading to host-adaptation.

The *E. coli* were randomly distributed over the whole phylogeny, but small host-associated clusters (enriched with specific STs) were observed based on the core-genome phylogeny and clustering of strains based on their accessory genes. GWAS identified a novel *nan* gene cluster associated with *E. coli* strains isolated from humans. These *nan* genes were predicted to be responsible for the metabolism of sialic acid. It is located on the chromosome as inferred from the RefSeq complete genome collections of *E. coli* and was predominantly found in ST131 and ST73 ExPEC lineages; both are known multidrug-resistant and highly virulent lineages. On the other hand, a significant association of the omptin family of proteases with chicken and cattle hosts is also intriguing. The genes encoding for ompP and arlC (ompTp) proteases were associated with cattle and chicken hosts, respectively, instead of chromosomally encoded ompT protease. Preference for omptin proteases seems to correlate with the fact that both cattle and chicken have differences in innate immunity responses. In addition to that, GWAS also revealed the *bor* gene's (involved in increased serum resistance in animal serum) association with cattle and confirms the previous association of *iroBCDEN* gene cluster with chicken in contrast to humans or other hosts.

Here, we observed that host-associated genes belong to accessory-genome and these genes were found in few lineages of associated host. These determinants might play an essential role in adaptation and provide a fitness advantage over others in different host environments. To confirm their role in influencing a strain's AMR carrying ability and dissemination, additional *in-vitro* or *in-vivo* studies are required.

7. Zusammenfassung:

E. coli ist sowohl ein kommensales Bakterium als auch ein vielseitiges Pathogen. Seine Fähigkeit, verschiedene Umweltnischen zu kolonisieren, bietet einen evolutionären Vorteil, um Antibiotikaresistenz-Merkmale innerhalb oder zwischen den verschiedenen Populationen zu erwerben und zu verbreiten. In dieser Studie haben wir eine vielfältige Sammlung von 1.198 *E. coli* Stämmen untersucht, die aus verschiedenen Wirten isoliert wurden. Eine genomweite Assoziationstudie (GWAS) speziell adaptiert auf den Einsatz in mikrobiellen Genomen wurde angewendet, um die wirtsassoziierten genomischen Determinanten zu bestimmen, die zur Anpassung an die unterschiedlichen Wirte führen.

Die untersuchten *E. coli* Stämme waren weitgehend zufällig über die gesamte Phylogenie verteilt, es wurden jedoch kleine wirtsassoziierte Cluster (angereichert mit spezifischen STs) basierend auf der Kerngenom-Phylogenie und der Clusterung von Stämmen basierend auf ihrem akzessorischen Genom gefunden. Mit Hilfe der GWAS konnte ein neues *nan*-Gen-Cluster identifiziert werden, das mit von Menschen isolierten *E. coli* Stämmen assoziiert ist. Mittels *in silico* Vorhersage konnte gezeigt werden, dass diese *nan*-Gene wahrscheinlich für den Metabolismus von Sialinsäure verantwortlich sind. Eine Analyse der RefSeq-Gesamtgenomsammlungen von *E. coli* ergab, dass dieses *nan* Operon auf dem chromosomalen Genom der *E. coli* Stämme lokalisiert ist und vorwiegend in den ExPEC-Linien ST131 und ST73 gefunden wird. Diese beiden Linien sind sehr häufig mit Multiresistenz und Virulenz assoziiert. Auf der anderen Seite ist die Familie der Omptin Proteasen regelmäßig mit den Wirten Huhn und Rind assoziiert. Die Gene *ompP* und *arlC* (*ompTp*), die für die entsprechenden Proteasen kodieren, wurden oft in Stämmen gefunden, die aus Rindern und Hühnern isoliert wurden und ersetzen hier die im Chromosom häufig nicht vorhandene durch *ompT* kodierte Protease. Die Präferenz für Omptin-Proteasen scheint mit der Tatsache zu korrelieren, dass sowohl Rinder als auch Hühner Unterschiede in der angeborenen Immunantwort aufweisen. Darüber hinaus zeigte die GWAS auch die Assoziation des *bor*-Gens (beteiligt an der erhöhten Serumresistenz in tierischem Serum) mit Rindern und bestätigt auch die frühere Assoziation des *iroBCDEN*-Genclusters mit Hühnern im Gegensatz zu Menschen oder anderen Wirten.

Wir konnten in dieser Arbeit zeigen, dass wirtsassoziierte Gene zum akzessorischen Genom gehören und diese Gene nur in einigen Linien der wirtsassoziierten Stämme gefunden werden konnten. Diese Determinanten könnten eine wesentliche Rolle bei der Anpassung spielen und einen Fitnessvorteil gegenüber anderen Linien in verschiedenen Wirtsumgebungen bieten. In wieweit diese wirtsadaptiven genomischen Faktoren einen Einfluss auf die Fähigkeit eines Stammes haben antimikrobielle Resistenzfaktoren zu enthalten und zu deren Verbreitung beizutragen, erfordert zusätzliche *in-vitro* oder *in-vivo* Studien.

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9. Supplement:

Note: The complete work is formulated in the form of manuscript with a running title "**Genome-wide association study reveals host-adaptive genomic traits in *Escherichia coli***". (Not yet submitted)

9.1 Collected strains metadata (n=1,198). (Note: Not available [NA], Not Known [-], Genome-size in bp)

id	**Country**	**Host**	**Health-status**	**year**	**ST**	**BAPS**	**Phylogroup**	**# contigs**	**GC (%)**	**N50**	**Genome-Size**
8991	Germany	Chicken	Diseased	2003	95	4	B2	118	50.53	304144	5355136
9232	Germany	Chicken	Diseased	2004	95	4	B2	86	50.57	237131	5023000
9238	Germany	Chicken	Diseased	2004	10	2	A	109	50.67	237674	4854446
9242	Germany	Chicken	Diseased	2004	117	8	G	91	50.7	174758	5091782
11492	Germany	Chicken	Diseased	2005	140	4	B2	97	50.47	231010	5084846
11501	Germany	Chicken	Diseased	2005	140	4	B2	102	50.44	219194	5104973
11846	Germany	Chicken	Diseased	2006	355	4	B2	94	50.54	232290	5151909
11858	Germany	Chicken	Diseased	2006	117	8	G	153	50.75	120529	5262496
11863	Germany	Chicken	Diseased	2006	369	9	C	90	50.57	181210	5079456
11864	Germany	Chicken	Diseased	2006	117	8	G	91	50.83	250101	5081102
11889	Germany	Chicken	Diseased	2006	117	8	G	90	50.68	238432	5029119
12000	Germany	Chicken	Diseased	2006	95	4	B2	103	50.49	181752	5343574
12031	Germany	Chicken	Diseased	2006	23	9	C	61	50.62	212012	4960816
12045	Germany	Chicken	Diseased	2006	369	9	C	98	50.56	184759	5027254
12202	Germany	Chicken	Healthy	2006	937	1	B1	106	50.68	188255	5063587
12205	Germany	Chicken	Healthy	2006	937	1	B1	103	50.68	148433	5065100
12214	Germany	Chicken	Healthy	2006	1166	5	D	107	50.42	165927	5319920
12224	Germany	Chicken	Healthy	2006	69	10	D	168	50.38	180018	5645945
12226	Germany	Chicken	Healthy	2006	69	10	D	170	50.38	177688	5644581
12238	Germany	Chicken	Healthy	2006	1170	11	B2	49	50.5	271774	4967513

12244	Germany	Chicken	Healthy	2006	1166	5	D	62	50.42	241388	5283421
12246	Germany	Chicken	Healthy	2006	1166	5	D	66	50.42	224714	5284685
12514	Germany	Chicken	Diseased	2007	141	4	B2	78	50.57	442935	5103798
12517	Germany	Chicken	Diseased	2007	95	4	B2	76	50.56	265970	5037947
12518	Germany	Chicken	Diseased	2007	23	9	C	65	50.61	328582	5031623
12520	Germany	Chicken	Diseased	2007	131	11	B2	54	50.66	444487	5145939
13054	Germany	Chicken	Healthy	2007	770	12	cladeI	138	50.27	156163	5713128
13219	Germany	Chicken	Diseased	2007	355	4	B2	95	50.47	288708	5415664
13220	Germany	Chicken	Diseased	2007	38	6	D	93	50.5	208060	5423324
13682	Germany	Chicken	Healthy	2007	1049	1	B1	85	50.53	177514	5294779
13702	Germany	Chicken	Healthy	2007	115	6	D	154	50.53	140559	5584474
14107	Germany	Chicken	Healthy	2007	69	10	D	158	50.36	177708	5692274
14172	Germany	Chicken	Healthy	2007	69	10	D	191	50.38	165743	5715440
14182	Germany	Chicken	Healthy	2007	115	6	D	148	50.49	118482	5621387
14327	Germany	Chicken	Healthy	2007	115	6	D	161	50.49	117816	5622094
14348	Germany	Chicken	Healthy	2007	770	12	cladeI	138	50.25	157075	5627772
14726	Germany	Chicken	Healthy	2008	349	5	D	82	50.36	294914	5287015
14741	Germany	Chicken	Healthy	2008	115	6	D	155	50.48	110906	5624992
14756	Germany	Chicken	Healthy	2008	69	10	D	192	50.39	165743	5796042
14770	Germany	Chicken	Healthy	2008	770	12	cladeI	155	50.24	156164	5705058
14782	Germany	Chicken	Healthy	2008	69	10	D	200	50.4	163777	5786116
14783	Germany	Chicken	Healthy	2008	115	6	D	183	50.49	103852	5616399
14793	Germany	Chicken	Healthy	2008	69	10	D	210	50.4	165743	5793377
14800	Germany	Chicken	Healthy	2008	115	6	D	157	50.49	114288	5619856
14808	Germany	Chicken	Healthy	2008	115	6	D	168	50.49	118482	5621900
14815	Germany	Chicken	Healthy	2008	69	10	D	200	50.4	165743	5789828
14822	Germany	Chicken	Healthy	2008	69	10	D	196	50.39	165743	5791267
14835	Germany	Chicken	Healthy	2008	6807	2	A	168	50.58	88717	5073309
14863	Germany	Chicken	Healthy	2008	69	10	D	111	50.47	260705	5552633
14876	Germany	Chicken	Healthy	2008	302	3	E	75	50.19	342045	5251080
14885	Germany	Chicken	Healthy	2008	115	6	D	163	50.49	111014	5620903
14895	Germany	Chicken	Healthy	2008	115	6	D	176	50.48	108954	5619820
14911	Germany	Chicken	Healthy	2008	115	6	D	158	50.48	108954	5620307
14926	Germany	Chicken	Healthy	2008	95	4	B2	82	50.56	266057	5032191

14942	Germany	Chicken	Diseased	2008	95	4	B2	72	50.55	265970	5028212
15147	Germany	Chicken	Healthy	2008	429	11	B2	84	50.43	293281	5162651
15148	Germany	Chicken	Healthy	2008	428	11	B2	76	50.37	300517	5055847
15149	Germany	Chicken	Healthy	2008	429	11	B2	88	50.39	255690	5169657
15151	Germany	Chicken	Healthy	2008	420	4	B2	243	50.44	103332	5494249
15152	Germany	Chicken	Healthy	2008	428	11	B2	43	50.34	484921	5054952
15153	Germany	Chicken	Healthy	2008	429	11	B2	119	50.4	272444	5240554
17626	Germany	Chicken	Diseased	2008	140	4	B2	98	50.46	231010	5232572
18666	Germany	Chicken	Diseased	2009	11	3	E	174	50.29	160706	5344742
19038	Germany	Chicken	Diseased	2009	155	1	B1	65	50.54	194454	4828853
21065	Germany	Chicken	Diseased	2010	140	4	B2	102	50.55	231025	5025665
21066	Germany	Chicken	Diseased	2010	140	4	B2	96	50.48	231025	5099598
21070	Germany	Chicken	Diseased	2010	23	9	C	50	50.65	281944	4806140
21071	Germany	Chicken	Diseased	2010	95	4	B2	115	50.53	183103	5109760
21080	Germany	Chicken	Diseased	2010	23	9	C	79	50.56	148516	4902804
21083	Germany	Chicken	Diseased	2010	117	8	G	130	50.73	153327	5100279
21084	Germany	Chicken	Diseased	2010	95	4	B2	78	50.66	236855	4953273
21085	Germany	Chicken	Diseased	2010	117	8	G	115	50.68	238004	5139126
21088	Germany	Chicken	Diseased	2010	23	9	C	81	50.58	186760	5149063
21089	Germany	Chicken	Diseased	2010	23	9	C	60	50.66	279208	4904236
21090	Germany	Chicken	Diseased	2010	23	9	C	73	50.52	208637	5073221
21092	Germany	Chicken	Diseased	2010	131	11	B2	34	50.55	483809	5155064
21094	Germany	Chicken	Diseased	2010	95	4	B2	83	50.56	364116	5193045
21095	Germany	Chicken	Diseased	2010	141	4	B2	66	50.57	354382	5087817
21096	Germany	Chicken	Diseased	2010	140	4	B2	96	50.5	216941	5271506
21097	Germany	Chicken	Diseased	2010	95	4	B2	88	50.6	268834	5217989
21098	Germany	Chicken	Diseased	2010	95	4	B2	101	50.56	204544	5295587
21750	Germany	Chicken	Diseased	2010	1852	11	B2	48	50.49	387325	5099173
24887	Germany	Chicken	Diseased	2011	23	9	C	65	50.57	212015	4874609
28074	Germany	Chicken	Diseased	2011	-	9	C	58	50.42	226914	5035209
29394	Germany	Pig	Healthy	2011	2496	2	A	139	50.61	97079	4790262
29398	Germany	Pig	Healthy	2011	58	1	B1	141	50.67	131475	5211138
29401	Germany	Pig	Healthy	2011	58	1	B1	88	50.75	266203	4889112
29417	Germany	Pig	Healthy	2011	1684	2	A	57	50.57	293297	4920267

29449	Germany	Pig	Healthy	2011	1716	2	A	163	50.64	127010	4744747
29452	Germany	Pig	Healthy	2011	641	1	B1	100	50.62	106393	4825624
29459	Germany	Pig	Healthy	2011	2942	3	E	128	50.44	154170	5334913
29465	Germany	Pig	Healthy	2011	58	1	B1	102	50.74	148872	5050879
29489	Germany	Pig	Healthy	2011	131	11	B2	80	50.63	181610	5193523
30555	Germany	Pig	Healthy	2011	641	1	B1	116	50.6	106395	4740723
30565	Germany	Pig	Healthy	2011	58	1	B1	79	50.75	236254	4884330
30616	Germany	Pig	Healthy	2011	641	1	B1	72	50.69	196049	4884658
30787	Germany	Human	Diseased	2013	154	1	B1	56	50.62	294917	4718185
30916	Germany	Human	Diseased	2013	141	4	B2	61	50.6	354085	5069682
35110	Germany	Human	Diseased	2015	69	10	D	107	50.63	170319	5370242
39498	Germany	Pig	Healthy	2011	10	2	A	76	50.73	206676	4800087
39506	Germany	Pig	Healthy	2011	302	3	E	103	50.34	195830	5299342
39514	Germany	Pig	Healthy	2011	302	3	E	260	50	200740	5402507
39526	Germany	Pig	Healthy	2011	4423	2	A	138	50.65	142403	4734776
39533	Germany	Pig	Healthy	2011	410	9	C	309	50.07	233550	4997929
39541	Germany	Pig	Healthy	2011	641	1	B1	115	50.61	111722	4730541
04-06395	Germany	Human	Diseased	2004	20	1	B1	120	50.54	187956	5347804
04-07301	Germany	Human	Healthy	2004	10	2	A	133	51.08	95033	4829038
05-01317	Germany	Human	Healthy	2005	388	1	B1	124	50.64	205235	5193438
05-02486	Germany	Human	Healthy	2005	335	3	E	124	50.42	326761	5269227
05-02928	Germany	Human	Healthy	2005	2101	1	B1	108	50.68	396442	5018147
05-04624	Germany	Human	Healthy	2005	21	1	B1	339	50.42	104237	5730602
05-06037	Germany	Human	Healthy	2005	17	1	B1	191	50.59	134151	5204549
06-00703	Germany	Human	Healthy	2006	35	4	B2	51	50.52	335530	4727529
06-01677	Germany	Human	Diseased	2006	362	5	D	44	50.57	408617	4827374
06-01712	Germany	Human	Diseased	2006	21	1	B1	220	50.42	118064	5476354
06-03041	Germany	Human	Diseased	2006	38	6	D	139	50.49	167143	5417600
06-03230	Germany	Human	Diseased	2006	17	1	B1	173	50.59	134151	5167549
06-03514	Germany	Human	Healthy	2006	587	3	E	189	50.22	238786	5558726
06-05225	Germany	Human	Healthy	2006	7522	2	A	36	50.82	360292	4853193
07-06605	Germany	Human	Diseased	2007	589	4	B2	51	50.57	298091	4792615
07-06701	Germany	Human	Diseased	2007	-	2	A	74	50.6	212837	5000971
07-06796	Germany	Human	Diseased	2007	10	2	A	168	50.4	148139	5318509

07-06960	Germany	Human	Diseased	2007	40	1	B1	83	50.65	166867	5075689
07-07311	Germany	Human	Healthy	2007	40	1	B1	82	50.65	143508	5074200
07-08011	Germany	Human	Healthy	2007	335	3	E	87	50.44	401013	5293027
08-02745	Germany	Human	Diseased	2008	-	1	B1	205	50.89	108379	5351711
08-03995	Germany	Cattle	Healthy	2008	658	7	G	64	50.85	497766	4961922
08-03996	Germany	Cattle	Healthy	2008	11	3	E	178	50.32	181245	5426650
08-03997	Germany	Cattle	Healthy	2008	11	3	E	203	50.31	188586	5426093
08-04018	Germany	Cattle	Healthy	2008	21	1	B1	244	50.43	121718	5505810
08-04078	Germany	Cattle	Healthy	2008	445	1	B1	337	50.45	68435	5713349
08-04082	Germany	Cattle	Healthy	2008	445	1	B1	275	50.47	92816	5561072
08-04088	Germany	Cattle	Healthy	2008	16	1	B1	248	50.41	120129	5333575
08-04089	Germany	Cattle	Healthy	2008	445	1	B1	377	50.63	84735	5786344
08-04090	Germany	Cattle	Healthy	2008	445	1	B1	298	50.44	101022	5702064
08-04147	Germany	Cattle	Healthy	2008	21	1	B1	280	50.38	108500	5702263
08-04153	Germany	Cattle	Healthy	2008	21	1	B1	343	50.36	98144	5865440
08-04154	Germany	Cattle	Healthy	2008	21	1	B1	344	50.37	95600	5861888
08-04155	Germany	Cattle	Healthy	2008	21	1	B1	330	50.37	101162	5862211
08-04861	Germany	Human	Healthy	2008	738	7	G	212	50.59	115624	5524548
08-04862	Germany	Human	Healthy	2008	117	8	G	137	50.75	180236	5118658
08-04863	Germany	Human	Healthy	2008	35	4	B2	67	50.51	335530	4785773
08-04864	Germany	Human	Healthy	2008	297	1	B1	105	50.66	220228	4888854
08-05156	Germany	Human	Healthy	2008	5278	4	B2	183	50.38	136708	4897631
08-05529	Germany	Human	Diseased	2008	33	1	B1	170	50.73	168980	5532077
08-06237	Germany	Human	Healthy	2008	713	4	B2	72	50.49	425959	4743469
08-06238	Germany	Human	Healthy	2008	17	1	B1	201	50.5	165357	5211477
08-06418	Germany	Human	Healthy	2008	297	1	B1	95	50.55	288529	4927069
09-05726	Germany	Human	Diseased	2009	-	2	A	95	50.79	117469	4595453
10-01971	Germany	Human	Healthy	2010	137	3	E	334	50.25	251344	5548608
10-02734	Germany	Human	Healthy	2010	3494	1	B1	86	50.55	215206	4974911
10-02735	Germany	Human	Healthy	2010	25	1	B1	177	50.53	160496	5586867
10-02736	Germany	Human	Healthy	2010	33	1	B1	151	50.71	192693	5363223
10-03960	Germany	Human	Healthy	2010	40	1	B1	96	50.58	143749	5156315
10-04205	Germany	Human	Healthy	2010	137	3	E	178	50.36	251344	5343254
10-04206	Germany	Human	Healthy	2010	10	2	A	76	50.39	195504	4965433

10-06712	Germany	Human	Diseased	2010	21	1	B1	231	50.35	117495	5546836
10-07028	Germany	Human	Diseased	2010	29	1	B1	196	50.49	104349	5488685
10-07139	Germany	Human	Diseased	2010	21	1	B1	216	50.4	127118	5429766
11-00056	Germany	Human	Diseased	2011	33	1	B1	103	50.74	149302	5245073
11-00061	Germany	Human	Diseased	2011	58	1	B1	107	50.83	148872	4997958
11-08909	Germany	Human	Healthy	2011	33	1	B1	141	50.76	129509	5458899
11-08946	Germany	Human	Healthy	2011	28	4	B2	49	50.55	273991	4769487
11-08947	Germany	Human	Healthy	2011	28	4	B2	58	50.62	331012	4724197
11-08948	Germany	Human	Healthy	2011	28	4	B2	34	50.63	360466	4698841
11-08949	Germany	Human	Healthy	2011	738	7	G	285	50.58	129577	5652271
11-08950	Germany	Human	Healthy	2011	32	3	E	190	50.53	208264	5271205
11-08951	Germany	Human	Healthy	2011	32	3	E	187	50.53	207881	5273503
11844-2	Germany	Chicken	Diseased	2006	1158	5	D	178	50.41	272222	5765898
11887-1	Germany	Chicken	Diseased	2006	117	8	G	134	50.74	120846	5252787
12-01792	Germany	Human	Diseased	2012	1326	1	B1	78	50.84	187072	4987133
12-02111	Germany	Human	Diseased	2012	48	2	A	135	50.75	93828	4909616
12-05189	Germany	Human	Diseased	2012	86	1	B1	91	50.6	136284	4858298
12-05450	Germany	Human	Healthy	2012	21	1	B1	237	50.42	127118	5505915
12-05575	Germany	Human	Healthy	2012	4119	4	B2	36	50.62	559314	4700219
12-05576	Germany	Human	Healthy	2012	28	4	B2	45	50.51	460999	4877799
12-05705	Germany	Human	Healthy	2012	335	3	E	125	50.43	310153	5325134
12-05926	Germany	Human	Healthy	2012	1147	1	B1	46	50.64	220962	4640855
12-05927	Germany	Human	Healthy	2012	33	1	B1	138	50.66	151374	5484931
12-05928	Germany	Human	Healthy	2012	737	1	B1	164	50.42	118028	5538874
12042-4	Germany	Chicken	Diseased	2006	117	8	G	106	50.73	246413	5199373
13-00426	Germany	Human	Healthy	2013	40	1	B1	148	50.5	170017	5191231
13-00566	Germany	Human	Healthy	2013	4941	1	B1	180	50.51	161276	5186429
13-00570	Germany	Human	Healthy	2013	21	1	B1	295	50.27	112440	5582893
13-00810	Germany	Human	Healthy	2013	117	8	G	245	50.53	241650	5190163
13-00811	Germany	Human	Healthy	2013	21	1	B1	482	49.93	103683	5653986
13-01248	Germany	Human	Healthy	2013	335	3	E	149	50.38	326761	5328607
13-01899	Germany	Human	Healthy	2013	29	1	B1	308	50.36	125740	5629099
13-03293	Germany	Human	Healthy	2013	29	1	B1	325	50.29	118144	5647165
13-03609	Germany	Human	Healthy	2013	301	2	A	361	50.17	76137	5182785

13-03625	Germany	Human	Healthy	2013	21	1	B1	278	50.18	139539	5551210
13-05473	Germany	Human	Healthy	2013	25	1	B1	261	50.36	146957	5589812
13060-1	Germany	Chicken	Healthy	2007	770	12	cladeI	128	50.25	182350	5635436
14-03445	Germany	Human	Healthy	2014	62	13	F	472	50.07	84255	5752448
14-03756	Germany	Human	Healthy	2014	738	7	G	225	50.51	144014	5587398
14-04252	Germany	Human	Diseased	2014	975	2	A	216	50.16	301902	5043074
14-04504	Germany	Human	Diseased	2014	127	4	B2	229	50.26	288399	5338806
14-04585	Germany	Human	Diseased	2014	4674	8	G	247	50.54	128652	5097586
14-04785	Germany	Human	Diseased	2014	2813	4	B2	218	50.38	258477	4813630
14-05235	Germany	Human	Healthy	2014	6274	1	B1	199	50.6	158466	5510055
14-05648	Germany	Human	Healthy	2014	33	1	B1	313	50.37	88355	5514392
14-05649	Germany	Human	Healthy	2014	17	1	B1	291	50.39	135195	5243773
14-05823	Germany	Human	Healthy	2014	646	4	B2	126	50.34	363391	5271513
14-05824	Germany	Human	Healthy	2014	675	1	B1	249	50.37	207147	5512572
14-05953	Germany	Human	Healthy	2014	738	7	G	256	50.61	143600	5621905
14-05954	Germany	Human	Healthy	2014	32	3	E	262	50.4	192688	5364772
14154-1	Germany	Chicken	Healthy	2007	69	10	D	165	50.35	195507	5689656
15-02694	Germany	Human	Diseased	2015	582	4	B2	237	50.25	262390	5091835
15-02880	Germany	Human	Diseased	2015	388	1	B1	285	50.37	118980	5248133
15-02909	Germany	Human	Diseased	2015	583	4	B2	427	49.79	249084	5235865
15-03069	Germany	Human	Diseased	2015	5486	1	B1	384	50.24	96395	5158196
15-03070	Germany	Human	Diseased	2015	5486	1	B1	350	50.28	118775	5146225
15-03378	Germany	Human	Diseased	2015	99	1	B1	248	50.21	221845	5084311
15-04718	Germany	Human	Healthy	2015	73	4	B2	208	50.19	466447	5301647
15-04719	Germany	Human	Healthy	2015	442	1	B1	301	50.42	182809	5576579
16-01493	Germany	Human	Diseased	2016	33	1	B1	373	50.13	148775	5501747
16-01697	Germany	Human	Diseased	2016	3101	9	C	379	50.07	263584	5825910
16-02161	Germany	Human	Diseased	2016	640	11	B2	226	50.36	220900	5321122
16-02269	Germany	Human	Diseased	2016	11	3	E	261	50.2	147567	5374744
16-02351	Germany	Human	Diseased	2016	32	3	E	348	50.22	163349	5522213
16-02781	Germany	Human	Diseased	2016	1147	1	B1	150	50.58	244752	4739986
16-03948	Germany	Human	Diseased	2016	28	4	B2	188	50.32	197371	5174735
16-04045	Germany	Human	Diseased	2016	-	4	B2	151	50.56	511622	4796899
16-04050	Germany	Human	Diseased	2016	583	4	B2	202	50.5	252185	5130452

16934_2#58	Germany	Chicken	Healthy	2012	648	14	F	100	50.42	242069	5442704
16934_2#59	Germany	Chicken	Healthy	2012	648	14	F	102	50.4	230750	5361172
16934_2#71	Germany	Cattle	Diseased	2013	648	14	F	77	50.46	230750	5100735
16934_2#74	Germany	Chicken	Diseased	2012	648	14	F	91	50.29	219727	5535529
16934_2#77	Germany	Chicken	Diseased	2010	648	14	F	77	50.46	230750	5099356
16934_2#78	Germany	Chicken	Diseased	2011	648	14	F	96	50.49	200043	5283058
16ZN_0001	Vietnam	Pig	Healthy	2015	101	1	B1	74	50.59	162301	4916553
16ZN_0002	Vietnam	Pig	Healthy	2015	48	2	A	135	50.76	126559	4743829
16ZN_0003	Vietnam	Pig	Healthy	2016	58	1	B1	106	50.56	173043	5085755
16ZN_0004	Vietnam	Pig	Healthy	2016	165	2	A	131	50.52	108854	4821545
16ZN_0005	Vietnam	Pig	Healthy	2016	898	1	B1	87	50.62	118692	4811169
16ZN_0006	Vietnam	Pig	Healthy	2016	971	1	B1	109	50.62	166624	5183252
16ZN_0007	Vietnam	Pig	Healthy	2015	3858	1	B1	64	50.65	202729	4779319
16ZN_0008	Vietnam	Pig	Healthy	2016	761	2	A	121	50.79	100806	4739925
16ZN_0009	Vietnam	Pig	Healthy	2016	-	2	A	157	50.81	59950	4520555
16ZN_0010	Vietnam	Pig	Healthy	2015	206	2	A	235	50.66	47823	5047277
16ZN_0011	Vietnam	Pig	Healthy	2016	10	2	A	107	50.66	117809	4923256
16ZN_0012	Vietnam	Pig	Healthy	2015	101	1	B1	129	50.22	120414	5037380
16ZN_0013	Vietnam	Pig	Healthy	2015	101	1	B1	82	50.6	137927	4915241
16ZN_0014	Vietnam	Pig	Healthy	2016	8165	1	B1	135	50.65	75832	4839732
16ZN_0015	Vietnam	Pig	Healthy	2016	224	1	B1	90	50.69	197279	5017213
16ZN_0016	Vietnam	Pig	Healthy	2016	453	1	B1	121	50.68	111363	4890643
16ZN_0017	Vietnam	Pig	Healthy	2016	603	1	B1	98	50.64	144205	5050747
16ZN_0018	Vietnam	Pig	Healthy	2016	603	1	B1	93	50.63	170812	5047662
16ZN_0019	Vietnam	Pig	Healthy	2016	8165	1	B1	135	50.64	78589	4848926
16ZN_0021	Vietnam	Pig	Healthy	2016	101	1	B1	88	50.54	148377	5060205
16ZN_0023	Vietnam	Pig	Healthy	2016	8165	1	B1	134	50.65	75832	4842145
16ZN_0024	Vietnam	Pig	Healthy	2016	-	2	A	162	50.8	59886	4508913
16ZN_0025	Vietnam	Pig	Healthy	2016	603	1	B1	93	50.64	170912	5050488
16ZN_0026	Vietnam	Pig	Healthy	2016	206	2	A	89	50.63	143844	4807396
16ZN_0028	Vietnam	Pig	Healthy	2016	3014	2	A	125	50.63	108194	4889238
16ZN_0030	Vietnam	Pig	Healthy	2015	10	2	A	166	50.14	115459	5205557
16ZN_0031	Vietnam	Pig	Healthy	2016	654	1	B1	63	50.79	186286	4755543
16ZN_0038	Vietnam	Pig	Healthy	2016	971	1	B1	116	50.62	154023	5173289

16ZN_0040	Vietnam	Pig	Healthy	2015	5471	2	A	190	50.53	66644	4977157
17-01273	Germany	Human	Healthy	2017	1040	4	B2	273	50.34	238707	5028702
17-01274	Germany	Human	Healthy	2017	33	1	B1	211	50.47	218870	5389385
17-01275	Germany	Human	Healthy	2017	738	7	G	220	50.65	129611	5393317
17-01338	Germany	Human	Healthy	2017	29	1	B1	287	50.39	131646	5603000
17-01713	Germany	Human	Healthy	2017	33	1	B1	267	50.49	157260	5468700
17-01714	Germany	Human	Healthy	2017	33	1	B1	299	50.32	175690	5298652
17-01717	Germany	Human	Healthy	2017	17	1	B1	319	50.39	135486	5478650
17-01866	Germany	Human	Healthy	2017	738	7	G	409	50.55	143565	5745979
17-04144	Germany	Human	Diseased	2017	88	9	C	287	50.21	149086	5379164
17-04145	Germany	Human	Diseased	2017	10	2	A	200	50.36	149094	4910726
17-04189	Germany	Human	Diseased	2017	1792	1	B1	266	50.35	122649	5382690
17-04317	Germany	Human	Diseased	2017	216	2	A	182	50.49	116753	4904454
17-04777	Germany	Human	Diseased	2017	21	1	B1	357	50.15	114035	5656995
17-05720	Germany	Human	Diseased	2017	17	1	B1	252	50.44	143557	5243566
17-05723	Germany	Human	Diseased	2017	17	1	B1	255	50.45	143557	5239652
17-05751	Germany	Human	Diseased	2017	416	4	B2	159	50.46	432931	5165794
17-06334	Germany	Human	Diseased	2017	4942	1	B1	246	50.28	109631	5321991
17-06461	Germany	Human	Diseased	2017	457	13	F	146	50.25	327898	5026309
18-1-1-4-D17	Germany	Pig	Healthy	2014	21	1	B1	190	50.39	138224	5440879
18-1-1-4-D3	Germany	Pig	Healthy	2014	567	4	B2	81	50.51	383945	5024658
18-1-1-4-D9	Germany	Pig	Healthy	2014	10	2	A	83	50.7	162037	4861762
18-1-1-4-M20	Germany	Pig	Healthy	2014	21	1	B1	207	50.38	127118	5438291
18-1-31-3-K17	Germany	Pig	Healthy	2014	-	2	A	80	50.48	204131	5101677
18-4-1-4-D14	Germany	Pig	Healthy	2014	88	9	C	69	50.62	291225	5015972
18-4-1-4-M18	Germany	Pig	Healthy	2014	88	9	C	67	50.63	196801	5015978
18-4-31-3-K20	Germany	Pig	Healthy	2014	34	2	A	162	50.64	139732	4918329
20-1-1-4-D15	Germany	Pig	Healthy	2014	10	2	A	131	50.82	95621	4687354
20-1-31-3-K11	Germany	Pig	Healthy	2014	3057	12	cladeI	88	50.41	217895	5150959
20-1-31-3-K8	Germany	Pig	Healthy	2014	34	2	A	148	50.56	175592	5102073
20-12-2-4-D18	Germany	Pig	Healthy	2014	10	2	A	139	50.82	89224	4685840
20-12-31-3-K1	Germany	Pig	Healthy	2014	34	2	A	109	50.53	178745	5070078
20-12-31-3-K6	Germany	Pig	Healthy	2014	58	1	B1	100	50.7	232601	4989150
20222_5#110	Vietnam	Chicken	Healthy	2012	1011	3	E	86	50.51	429137	5174800

20222_5#112	Vietnam	Chicken	Healthy	2012	101	1	B1	98	50.5	218016	4949083
20222_5#118	Vietnam	Chicken	Healthy	2012	101	1	B1	114	50.61	196311	4914839
20222_5#138	Vietnam	Human	Healthy	2012	354	13	F	77	50.49	295044	5190626
20222_5#173	Vietnam	Chicken	Healthy	2012	6751	2	A	161	50.75	67650	4692353
20222_5#240	Vietnam	Chicken	Healthy	2012	165	2	A	169	50.6	99467	4853025
20222_5#250	Vietnam	Chicken	Healthy	2012	48	2	A	172	50.63	89669	4839653
20222_5#264	Vietnam	Human	Healthy	2012	155	1	B1	111	50.58	114452	4979599
20222_5#309	Vietnam	Chicken	Healthy	2012	10	2	A	135	50.71	142769	5151033
20222_5#331	Vietnam	Chicken	Healthy	2012	206	2	A	171	50.49	104948	4885052
20222_5#349	Vietnam	Human	Healthy	2012	394	10	D	106	50.58	264901	5078001
20222_5#88	Vietnam	Human	Healthy	2012	607	2	A	113	50.71	207094	5001931
20222_6#107	Vietnam	Human	Healthy	2012	6697	2	A	169	50.72	84510	4821245
20222_6#135	Vietnam	Chicken	Healthy	2012	155	1	B1	120	50.29	219946	5242429
20222_6#136	Vietnam	Human	Healthy	2012	3570	1	B1	127	50.67	158306	5119974
20222_6#19	Vietnam	Human	Healthy	2012	1148	1	B1	103	50.43	334629	5083511
20222_6#190	Vietnam	Human	Healthy	2012	648	14	F	137	50.49	169474	5283127
20222_6#191	Vietnam	Human	Healthy	2012	648	14	F	124	50.3	198062	5444496
20222_6#199	Vietnam	Human	Healthy	2012	746	2	A	192	50.65	86024	4850992
20222_6#316	Vietnam	Chicken	Healthy	2012	6732	3	A	203	50.81	65785	4791913
20222_6#346	Vietnam	Chicken	Healthy	2012	48	2	A	633	50.66	89530	5075364
20222_6#353	Vietnam	Chicken	Healthy	2012	5273	12	cladeI	126	50.4	175422	5388193
20222_6#55	Vietnam	Chicken	Healthy	2012	117	8	G	143	50.77	174653	5035041
20222_6#57	Vietnam	Chicken	Healthy	2012	155	1	B1	137	50.4	197745	4972202
20222_6#61	Vietnam	Chicken	Healthy	2012	6720	2	A	614	50.27	70563	5451944
20222_7#240	Vietnam	Human	Healthy	2012	48	2	A	132	50.6	126489	4772112
20222_7#277	Vietnam	Human	Healthy	2012	131	11	B2	93	50.75	286760	5032141
20222_8#126	Vietnam	Human	Healthy	2012	73	4	B2	143	50.41	213809	5276642
20222_8#153	Vietnam	Human	Healthy	2012	93	2	A	131	50.54	130557	4964980
20222_8#158	Vietnam	Human	Healthy	2012	58	1	B1	91	50.71	219222	5016061
20222_8#214	Vietnam	Human	Healthy	2012	48	2	A	150	50.78	97433	4671105
20222_8#244	Vietnam	Human	Healthy	2012	1589	1	B1	116	50.54	175881	5125912
20222_8#292	Vietnam	Human	Healthy	2012	1380	10	D	169	50.48	186191	5370714
20222_8#299	Vietnam	Chicken	Healthy	2012	6792	2	A	165	50.62	100532	5014224
20222_8#332	Vietnam	Human	Healthy	2012	1674	13	F	86	50.54	299122	4954829

20222_8#74	Vietnam	Chicken	Healthy	2012	155	1	B1	123	50.51	173071	4881433
20222_8#75	Vietnam	Chicken	Healthy	2012	10	2	A	132	50.74	111096	4726904
20222_8#86	Vietnam	Chicken	Healthy	2012	70	5	D	70	50.32	288538	5066138
20275_1#114	Vietnam	Chicken	Healthy	2012	6798	3	A	233	50.82	84048	4634749
20275_1#16	Vietnam	Human	Healthy	2012	1684	2	A	217	50.66	192989	5005483
20275_1#21	Vietnam	Human	Healthy	2012	10	2	A	241	50.59	97124	5490046
20275_1#287	Vietnam	Chicken	Healthy	2012	48	2	A	202	50.74	94147	4812084
20275_1#323	Vietnam	Human	Healthy	2012	4598	3	A	76	50.75	262907	4791525
20275_1#37	Vietnam	Human	Healthy	2012	969	4	B2	236	50.46	237308	5292998
21224_2#116	Vietnam	Chicken	Healthy	2012	7118	3	E	102	50.62	445803	5399813
21224_2#135	Vietnam	Human	Healthy	2012	1163	7	G	102	50.8	206290	5048827
21224_2#17	Vietnam	Chicken	Healthy	2012	226	2	A	228	50.43	78915	5019628
21224_2#19	Vietnam	Human	Healthy	2012	1485	14	F	118	50.31	335237	5181842
21224_2#299	Vietnam	Human	Healthy	2012	101	1	B1	86	50.53	229831	4979908
21224_2#340	Vietnam	Human	Healthy	2012	131	11	B2	99	50.65	330035	4955122
21224_2#344	Vietnam	Human	Healthy	2012	131	11	B2	115	50.75	222123	5035269
21224_2#363	Vietnam	Human	Healthy	2012	155	1	B1	144	50.65	106059	5037939
21224_2#5	Vietnam	Chicken	Healthy	2012	3858	1	B1	114	50.72	191025	4894098
21224_2#88	Vietnam	Human	Healthy	2012	10	2	A	181	50.74	126161	5039002
21224_3#10	Vietnam	Human	Healthy	2013	1788	2	A	134	50.74	138726	4831409
21224_3#12	Vietnam	Human	Healthy	2013	2732	5	D	102	50.62	242315	4970777
21224_3#120	Vietnam	Human	Healthy	2013	48	2	A	504	50.75	131613	4980317
21224_3#16	Vietnam	Human	Healthy	2013	1638	2	A	245	50.91	61185	4580245
21224_3#168	Vietnam	Human	Healthy	2013	3177	14	F	103	50.44	240428	5383771
21224_3#190	Vietnam	Chicken	Healthy	2013	224	1	B1	113	50.81	328191	5035462
21224_3#20	Vietnam	Human	Healthy	2013	398	2	A	207	50.86	61386	4679468
21224_3#230	Vietnam	Chicken	Healthy	2013	155	1	B1	172	50.58	99155	5100246
21224_3#234	Vietnam	Chicken	Healthy	2013	6793	2	A	230	50.44	80129	4974683
21224_3#235	Vietnam	Chicken	Healthy	2013	539	1	B1	112	50.65	192890	5115441
21224_3#237	Vietnam	Human	Healthy	2013	31	5	D	127	50.64	208784	5163118
21224_3#256	Vietnam	Human	Healthy	2013	131	11	B2	113	50.63	246402	5110596
21224_3#267	Vietnam	Human	Healthy	2013	1177	6	D	156	50.53	147181	5403219
21224_3#275	Vietnam	Chicken	Healthy	2013	117	8	G	139	50.73	175634	5186906
21224_3#278	Vietnam	Chicken	Healthy	2013	1244	2	A	182	50.71	80345	4686987

21224_3#284	Vietnam	Chicken	Healthy	2013	48	2	A	159	50.82	87683	4742623
21224_3#285	Vietnam	Chicken	Healthy	2013	170	2	A	209	50.79	83760	4954708
21224_3#29	Vietnam	Human	Healthy	2013	405	5	D	145	50.72	145510	5223915
21224_3#294	Vietnam	Chicken	Healthy	2013	10	2	A	128	50.63	257430	4890313
21224_3#297	Vietnam	Human	Healthy	2013	155	1	B1	127	50.3	183782	5213665
21224_3#335	Vietnam	Human	Healthy	2013	206	2	A	163	50.88	104439	4580292
21224_3#34	Vietnam	Chicken	Healthy	2013	602	1	B1	130	50.59	176207	5073737
21224_3#352	Vietnam	Human	Healthy	2013	3014	2	A	156	50.75	106366	4710000
21224_3#354	Vietnam	Chicken	Healthy	2013	410	9	C	103	50.53	221195	4871121
21224_3#358	Vietnam	Chicken	Healthy	2013	752	2	A	202	50.45	140254	5153997
21224_3#361	Vietnam	Chicken	Healthy	2013	48	2	A	230	50.63	81104	4936909
21224_3#370	Vietnam	Human	Healthy	2013	1193	4	B2	108	50.62	376402	5070978
21224_3#46	Vietnam	Chicken	Healthy	2013	155	1	B1	116	50.7	181638	4906471
21224_3#62	Vietnam	Human	Healthy	2013	457	13	F	120	50.41	207416	5047282
21224_3#88	Vietnam	Chicken	Healthy	2013	7153	2	A	186	50.7	91924	4844507
21224_3#91	Vietnam	Chicken	Healthy	2013	7157	2	A	223	50.52	87360	5040156
21224_3#94	Vietnam	Chicken	Healthy	2013	2690	2	A	157	50.52	121793	4735947
21224_3#95	Vietnam	Chicken	Healthy	2013	6746	2	A	125	50.66	198533	4720824
21224_3#97	Vietnam	Chicken	Healthy	2013	155	1	B1	124	50.47	199216	5217307
21225_1#125	Vietnam	Chicken	Healthy	2012	226	2	A	96	50.73	152170	4754870
21225_1#165	Vietnam	Chicken	Healthy	2012	7177	2	A	58	50.53	430366	4880972
21225_1#224	Vietnam	Chicken	Healthy	2012	7122	2	A	155	50.74	87944	4745450
21225_1#278	Vietnam	Human	Healthy	2012	205	1	B1	111	50.67	155574	5031827
21225_1#350	Vietnam	Chicken	Healthy	2013	359	1	B1	49	50.74	222701	4737206
21225_2#108	Vietnam	Chicken	Healthy	2013	48	2	A	242	50.59	69413	4793918
21225_2#112	Vietnam	Chicken	Healthy	2013	1163	7	G	113	50.94	186649	4873260
21225_2#120	Vietnam	Chicken	Healthy	2013	117	8	G	120	50.61	187846	5168514
21225_2#129	Vietnam	Human	Healthy	2013	131	11	B2	483	50.35	100658	5651910
21225_2#143	Vietnam	Human	Healthy	2013	212	1	B1	154	50.62	161143	5114821
21225_2#162	Vietnam	Human	Healthy	2013	4995	2	A	97	50.66	209903	5072817
21225_2#178	Vietnam	Chicken	Healthy	2013	162	1	B1	90	50.66	242181	4932440
21225_2#179	Vietnam	Chicken	Healthy	2013	48	2	A	161	50.73	98042	4715648
21225_2#18	Vietnam	Human	Healthy	2013	1664	1	B1	154	50.48	106278	5418966
21225_2#181	Vietnam	Chicken	Healthy	2013	155	1	B1	116	50.58	119249	4976101

21225_2#205	Vietnam	Human	Healthy	2013	641	1	B1	118	50.74	132148	4725689
21225_2#214	Vietnam	Human	Healthy	2013	131	11	B2	145	50.56	244696	5236369
21225_2#239	Vietnam	Human	Healthy	2013	6803	2	A	172	50.82	92955	4716144
21225_2#249	Vietnam	Human	Healthy	2013	7204	2	A	142	50.83	126176	4691160
21225_2#274	Vietnam	Human	Healthy	2012	1177	6	D	149	50.53	142695	5329445
21225_2#28	Vietnam	Human	Healthy	2013	131	11	B2	149	50.7	204739	5436135
21225_2#31	Vietnam	Human	Healthy	2013	131	11	B2	147	50.69	222328	5448082
21225_2#38	Vietnam	Human	Healthy	2013	3014	2	A	197	50.51	105628	5012315
21225_2#41	Vietnam	Chicken	Healthy	2013	711	1	B1	145	50.64	154579	4921381
21225_2#44	Vietnam	Chicken	Healthy	2013	297	1	B1	109	50.52	182452	4959738
21225_2#48	Vietnam	Chicken	Healthy	2013	7194	2	A	132	50.66	133872	5174776
21225_2#50	Vietnam	Chicken	Healthy	2013	6706	2	A	216	50.7	100937	4851014
21225_2#74	Vietnam	Human	Healthy	2013	131	11	B2	97	50.68	403119	5126453
21225_2#8	Vietnam	Human	Healthy	2013	5229	1	B1	159	50.61	177293	4864128
21225_2#86	Vietnam	Human	Healthy	2013	5229	1	B1	124	50.54	150652	4886683
21225_2#89	Vietnam	Human	Healthy	2013	10	2	A	185	50.66	106866	5135131
21ZN-0026-2	Vietnam	Human	Diseased	2017	1193	4	B2	75	50.6	187918	5028082
21ZN-0034-1	Vietnam	Human	Diseased	2017	131	11	B2	118	50.61	158810	5316755
21ZN-0037-1	Vietnam	Human	Diseased	2017	453	1	B1	123	50.67	112725	4855695
21ZN-0037-2	Vietnam	Human	Diseased	2017	131	11	B2	83	50.58	191108	5138047
21ZN-0042-2	Vietnam	Human	Diseased	2017	131	11	B2	76	50.69	180896	5047413
21ZN-0049-2	Vietnam	Human	Diseased	2017	155	1	B1	104	50.71	161669	4982681
21ZN-0052-2	Vietnam	Human	Diseased	2017	1193	4	B2	73	50.64	237204	5096856
21ZN-0063-1	Vietnam	Human	Diseased	2017	10	2	A	131	50.75	148323	4880365
21ZN-0071-2	Vietnam	Human	Diseased	2017	69	10	D	114	50.63	191141	5155296
21ZN-0073-1	Vietnam	Human	Diseased	2017	131	11	B2	103	50.73	136555	5185668
21ZN-0089-1	Vietnam	Human	Diseased	2017	131	11	B2	112	50.7	172794	5202953
21ZN-0098-1	Vietnam	Human	Diseased	2017	95	4	B2	68	50.55	264122	5016294
21ZN-0105-1	Vietnam	Human	Diseased	2017	38	6	D	134	50.54	112508	5414727
21ZN-0114-2	Vietnam	Human	Diseased	2017	-	2	A	101	50.71	139476	4662513
21ZN-0134-1	Vietnam	Human	Diseased	2017	1193	4	B2	69	50.55	204034	5028472
21ZN-0147-1	Vietnam	Human	Diseased	2017	69	10	D	106	50.68	141523	5090399
21ZN-0151-1	Vietnam	Human	Diseased	2017	1193	4	B2	114	50.6	187935	5222538
21ZN-0152-1	Vietnam	Human	Diseased	2017	1193	4	B2	72	50.51	221544	5110166

21ZN-0154-2	Vietnam	Human	Diseased	2017	1193	4	B2	78	50.57	221632	5125327
21ZN-0157-1	Vietnam	Human	Diseased	2017	127	4	B2	69	50.46	254114	4981864
21ZN-0168-2	Vietnam	Human	Diseased	2017	131	11	B2	93	50.64	193067	5081410
21ZN-0175-1	Vietnam	Human	Diseased	2017	69	10	D	122	50.66	122192	5151798
21ZN-0188-1	Vietnam	Human	Diseased	2017	69	10	D	111	50.7	143436	5225542
21ZN-0188-2	Vietnam	Human	Diseased	2017	69	10	D	107	50.7	188867	5222148
21ZN-0196-2	Vietnam	Human	Diseased	2017	1193	4	B2	74	50.53	221813	5021876
21ZN-0198-2	Vietnam	Human	Diseased	2017	131	11	B2	93	50.66	195163	5251148
21ZN-0201-2	Vietnam	Human	Diseased	2017	131	11	B2	113	50.71	187419	5286225
21ZN-0203-1	Vietnam	Human	Diseased	2017	405	5	D	160	50.59	90452	5256390
21ZN-0205-1	Vietnam	Human	Diseased	2017	617	2	A	123	50.73	112914	4844354
21ZN-0206-2	Vietnam	Human	Diseased	2017	1193	4	B2	72	50.67	225617	5104179
21ZN-0220-2	Vietnam	Human	Diseased	2017	1193	4	B2	88	50.58	191248	5084447
22-6-2-4-D6	Germany	Pig	Healthy	2014	4577	1	B1	75	50.42	182451	4922328
22-6-2-4-M3	Germany	Pig	Healthy	2014	34	2	A	89	50.49	178745	5055712
22-7-3-4-D21	Germany	Pig	Healthy	2014	993	2	A	105	50.81	131267	5042027
22-7-3-4-D5	Germany	Pig	Healthy	2014	10	2	A	75	50.68	169901	5299984
22-7-31-3-K2	Germany	Pig	Healthy	2014	34	2	A	83	50.5	175502	5025300
23-1-2-4-D2	Germany	Pig	Healthy	2014	58	1	B1	98	50.87	177513	4692605
23-1-2-4-M9	Germany	Pig	Healthy	2014	58	1	B1	90	50.88	144736	4692084
23-3-3-4-D16	Germany	Pig	Healthy	2014	23	9	C	90	50.59	145440	4876699
23-3-3-4-M2	Germany	Pig	Healthy	2014	681	4	B2	71	50.68	235334	5066076
7738_5#10	Germany	Chicken	Healthy	2006	919	4	B2	166	50.64	141991	5239971
7738_5#11	Germany	Chicken	Diseased	2007	117	8	G	133	50.76	118721	5173228
7738_5#17	Germany	Pig	Diseased	2004	1	5	D	219	50.13	65856	5400522
7738_5#27	Germany	Chicken	Healthy	2008	302	3	E	78	50.16	224252	5205406
7738_5#36	Germany	Chicken	Healthy	2008	95	4	B2	121	50.57	174034	4900323
7738_5#48	Germany	Pig	Diseased	2004	720	5	D	37	50.56	251422	4931829
7738_5#5	Germany	Chicken	Healthy	2005	295	1	B1	104	50.5	130887	4769220
7738_5#9	Germany	Chicken	Healthy	2006	919	4	B2	183	50.73	102032	5178650
7738_6#50	Germany	Pig	Diseased	2004	13	1	B1	173	50.53	76547	5296077
7738_6#52	Germany	Pig	Diseased	2005	-	3	E	272	50.51	36706	4935018
7738_6#53	Germany	Pig	Diseased	2005	-	1	B1	179	50.47	74454	4986425
7738_6#55	Germany	Pig	Healthy	2010	724	5	D	164	50.64	106749	4832792

7738_6#65	Germany	Human	Healthy	2006	-	13	F	379	50.42	30656	4919177
7738_6#67	Germany	Human	Diseased	2006	-	11	B2	222	50.46	92910	4694222
7738_6#76	Germany	Chicken	Diseased	2009	1421	2	A	168	50.79	67548	4548152
7738_7#25	Germany	Pig	Healthy	2010	681	4	B2	68	50.66	197019	5058840
7738_7#28	Germany	Pig	Healthy	2010	1611	1	B1	62	50.58	176183	4849455
7738_7#3	Germany	Chicken	Diseased	2010	88	9	C	120	50.71	119760	5063995
7738_7#30	Germany	Pig	Healthy	2010	367	9	C	120	50.72	140754	4869039
7738_7#38	Germany	Chicken	Diseased	2004	95	4	B2	161	50.5	129533	4944592
8016_2#3	Germany	Cattle	Diseased	2008	29	1	B1	205	50.4	118000	5461526
8016_2#46	Germany	Human	Diseased	2010	648	14	F	74	50.49	189060	5008594
8016_2#53	Germany	Human	Diseased	2010	3177	14	F	115	50.47	187146	5367934
8016_2#60	Germany	Chicken	Healthy	2008	131	11	B2	62	50.56	218493	5047622
9352_7#13	Germany	Cattle	Diseased	2007	10	2	A	370	50.2	119121	5057557
9352_7#14	Germany	Cattle	Diseased	2005	10	2	A	252	50.55	129904	4969919
9352_7#15	Germany	Pig	Diseased	2004	10	2	A	93	50.51	158302	5026084
9352_7#16	Germany	Pig	Diseased	2004	10	2	A	126	50.41	147329	4932427
9352_7#18	Germany	Pig	Diseased	2007	10	2	A	174	50.4	137364	5250113
9352_7#28	Germany	Human	Healthy	2005	10	2	A	181	50.65	87289	5079187
9352_7#29	Germany	Human	Healthy	2004	10	2	A	160	50.74	102640	5132999
9352_7#30	Germany	Human	Healthy	2004	10	2	A	67	50.76	154987	4714070
9352_7#36	Germany	Pig	Diseased	2008	10	2	A	102	50.76	114295	4680737
9352_7#37	Germany	Pig	Diseased	2008	10	2	A	163	50.63	103888	5121229
9352_7#39	Germany	Pig	Diseased	2008	10	2	A	124	50.42	147813	5114551
9352_7#4	Germany	Chicken	Diseased	2004	10	2	A	160	50.59	93900	5055689
9352_7#48	Germany	Human	Healthy	2004	10	2	A	197	50.57	75791	5356922
9352_7#71	Germany	Pig	Diseased	2010	10	2	A	128	50.71	77920	4836375
9352_7#73	Germany	Pig	Diseased	2010	10	2	A	132	50.8	87812	4761531
9352_7#74	Germany	Pig	Diseased	2010	10	2	A	148	50.73	87577	4797485
9352_7#76	Germany	Pig	Healthy	2010	10	2	A	106	50.79	119195	4699416
9352_7#79	Germany	Pig	Healthy	2010	10	2	A	122	50.68	101958	4852610
9352_7#81	Germany	Pig	Diseased	2010	10	2	A	314	50.6	140370	4984411
9352_7#85	Germany	Pig	Healthy	2010	10	2	A	809	50.14	72917	5637945
9352_7#87	Germany	Pig	Healthy	2010	10	2	A	88	50.76	147855	4691727
9352_7#89	Germany	Pig	Healthy	2010	10	2	A	97	50.54	119056	4602211

9352_7#90	Germany	Pig	Diseased	2010	10	2	A	106	50.68	114449	4726603
9352_7#94	Germany	Pig	Healthy	2008	10	2	A	116	50.72	86310	4699519
9352_7#96	Germany	Pig	Healthy	2009	10	2	A	143	50.51	150034	4824866
9425_1#17	Germany	Pig	Healthy	2011	542	2	A	99	50.6	112137	4510922
9475_4#43	Germany	Cattle	Healthy	2011	648	14	F	79	50.46	207494	5017288
9475_4#44	Germany	Cattle	Diseased	2010	648	14	F	61	50.47	276933	4965828
C22773	Germany	Chicken	Healthy	2015	117	8	G	106	50.61	237726	5189206
C23281	Germany	Chicken	Healthy	2015	101	1	B1	93	50.36	285347	5037501
C25278	Germany	Chicken	Healthy	2015	95	4	B2	64	50.53	399648	5150640
C25286	Germany	Chicken	Healthy	2015	117	8	G	96	50.61	238532	5160437
C26516	Germany	Chicken	Healthy	2015	-	4	B2	79	50.6	471176	5259932
C26520	Germany	Chicken	Healthy	2015	1618	4	B2	56	50.63	475751	4934480
C26521	Germany	Chicken	Healthy	2015	131	11	B2	63	50.56	350578	5219357
C26970	Germany	Chicken	Healthy	2015	23	9	C	64	50.57	236021	4846344
C26988	Germany	Chicken	Healthy	2015	117	8	G	108	50.43	242326	5344191
C27108	Germany	Chicken	Healthy	2015	23	9	C	97	50.56	290237	4938848
C27348	Germany	Chicken	Healthy	2015	117	8	G	125	50.51	224372	5556569
C27354	Germany	Chicken	Healthy	2015	359	1	B1	97	50.38	219283	5269415
C27813	Germany	Chicken	Healthy	2015	140	4	B2	77	50.47	268925	5182022
C28212	Germany	Chicken	Healthy	2015	69	10	D	120	50.55	161634	5711150
C28213	Germany	Chicken	Healthy	2015	95	4	B2	59	50.56	390381	5050903
C28331	Germany	Chicken	Healthy	2015	95	4	B2	105	50.58	415263	5295045
C28333	Germany	Chicken	Healthy	2015	101	1	B1	58	50.42	287515	5035506
C28334	Germany	Chicken	Healthy	2015	4110	11	B2	36	50.4	705089	4959705
C28336	Germany	Chicken	Healthy	2015	95	4	B2	61	50.48	401100	5183589
C33031	Germany	Chicken	Healthy	2015	95	4	B2	88	50.41	236644	5354079
C33034	Germany	Chicken	Healthy	2015	428	11	B2	55	50.47	350992	4947200
C33037	Germany	Chicken	Healthy	2015	140	4	B2	80	50.57	219888	5116937
C33715	Germany	Chicken	Healthy	2015	117	8	G	107	50.7	238140	5127948
C34173	Germany	Chicken	Healthy	2015	140	4	B2	90	50.56	231025	5124681
C34551	Germany	Chicken	Healthy	2015	140	4	B2	99	50.42	255019	5213508
C34552	Germany	Chicken	Healthy	2015	23	9	C	57	50.67	283698	4810809
C34559	Germany	Chicken	Healthy	2015	140	4	B2	89	50.56	259427	5157877
C35609	Germany	Chicken	Healthy	2015	140	4	B2	89	50.56	259427	5152433

C35807	Germany	Chicken	Healthy	2015	140	4	B2	86	50.53	216941	5151584
DICM0900597-2EC	Spain	WB	NA	2009	130	5	D	152	50.48	89840	5286368
DICM0900608-2EC	Spain	WB	NA	2009	295	1	B1	82	50.54	140641	5113872
DICM0900621-2EC	Spain	WB	NA	2009	-	1	B1	128	50.75	108767	5224816
DICM0900823-2EC	Spain	WB	NA	2009	29	1	B1	205	50.49	112507	5498701
DICM0901114-2EC	Spain	WB	NA	2009	5949	1	B1	141	50.66	134631	5210242
DICM0901321-2EC	Spain	WB	NA	2009	6034	3	E	51	50.64	454980	5262938
DICM0901466-2EC	Spain	WB	NA	2009	641	1	B1	149	50.82	128968	4997861
DICM0901561-2EC	Spain	WB	NA	2009	2712	7	G	42	50.7	519886	4537486
DICM0901639-2EC	Spain	WB	NA	2009	5934	1	B1	81	50.74	198349	4946124
DICM0901645-2EC	Spain	WB	NA	2009	1583	4	B2	32	50.66	325901	4871145
DICM0901647-2EC	Spain	WB	NA	2009	2520	1	B1	102	50.54	227069	5217531
DICM1000037-2EC	Spain	WB	NA	2010	-	2	A	158	50.5	176258	5239913
DICM1000127-2EC	Spain	WB	NA	2010	1607	3	E	62	50.46	246366	5203614
DICM1000188-2EC	Spain	WB	NA	2010	2074	3	E	27	50.55	749522	4940524
DICM1000211-2EC	Spain	WB	NA	2010	2712	7	G	50	50.71	505789	4677832
DICM1000340-2EC	Spain	WB	NA	2010	68	5	D	89	50.5	190793	5109424
DICM1000520-2EC	Spain	WB	NA	2010	154	1	B1	114	50.5	189063	5087861
DICM1000521-2EC	Spain	WB	NA	2010	10	2	A	95	50.77	138605	4922769
DICM1000697-2EC	Spain	WB	NA	2010	10	2	A	78	50.6	169563	4899167
DICM1000906-2EC	Spain	WB	NA	2010	-	1	B1	238	50.56	195190	5515943
DICM1000924-2EC	Spain	WB	NA	2010	295	1	B1	91	50.66	133713	4911777
DICM1000957-2EC	Spain	WB	NA	2010	2244	1	B1	105	50.61	192315	5109844
DICM1001059-2EC	Spain	WB	NA	2010	657	8	G	196	50.86	102545	5191150
DICM1001064-2EC	Spain	WB	NA	2010	12	4	B2	83	50.47	288230	5096387
DICM1100135-2E	Spain	WB	NA	2011	-	1	B1	89	50.58	232713	5273056
DICM1100434-2EC	Spain	WB	NA	2011	1727	1	B1	104	50.69	145935	4962970
IMT10052	Germany	Pig	Diseased	2004	1109	2	A	142	50.69	135471	5100043
IMT10057	Germany	Cattle	Diseased	2004	88	9	C	101	50.71	192303	5065136
IMT10311	Germany	Human	Diseased	2005	95	4	B2	65	50.63	395109	5168301
IMT10336	Germany	Cattle	Diseased	2005	88	9	C	178	50.66	159358	5418715
IMT10447	Germany	Pig	Diseased	2005	10	2	A	90	50.75	117659	4758669
IMT10448	Germany	Pig	Diseased	2005	88	9	C	98	50.61	214470	5255503
IMT10752	Germany	Cattle	Diseased	2005	-	2	A	59	50.69	307835	4833293

IMT10899	Germany	Cattle	Diseased	2005	88	9	C	152	50.69	113587	5329143
IMT10902	Germany	Cattle	Diseased	2005	155	1	B1	118	50.87	328627	5080252
IMT10904	Germany	Cattle	Diseased	2005	399	2	A	187	50.73	102567	5100136
IMT10909	Germany	Cattle	Diseased	2005	448	1	B1	61	50.7	200817	4904688
IMT10911	Germany	Cattle	Diseased	2005	655	1	B1	136	50.44	193357	5225568
IMT10914	Germany	Cattle	Diseased	2005	38	6	D	67	50.65	260286	5008990
IMT11012	Germany	Cattle	Diseased	2005	617	2	A	86	50.74	176521	4817688
IMT11832	Germany	Cattle	Healthy	2006	949	1	B1	151	50.7	135792	5267140
IMT11833	Germany	Cattle	Healthy	2006	56	1	B1	128	50.6	236268	4939793
IMT11835	Germany	Cattle	Healthy	2006	117	8	G	132	50.75	126367	5263224
IMT12060	Germany	Pig	Diseased	2006	4214	2	A	79	50.7	189050	4710376
IMT12185	Germany	Human	Diseased	2006	131	11	B2	66	50.75	276810	5097616
IMT12208	Germany	Chicken	Healthy	2006	937	1	B1	105	50.65	211289	5087221
IMT12210	Germany	Chicken	Healthy	2006	68	5	D	83	50.41	201118	5438437
IMT12211	Germany	Chicken	Healthy	2006	68	5	D	85	50.41	271347	5437627
IMT12237	Germany	Chicken	Healthy	2006	1276	13	F	94	50.43	228158	5143585
IMT12243	Germany	Chicken	Healthy	2006	115	6	D	128	50.49	147251	5384544
IMT12295	Germany	Pig	Diseased	2006	42	5	D	210	50.42	108860	5837299
IMT12490	Germany	Chicken	Diseased	2007	73	4	B2	119	50.36	491469	5184599
IMT13326	Germany	Pig	Diseased	2007	354	13	F	166	50.78	140792	5032939
IMT13327	Germany	Pig	Diseased	2007	354	13	F	94	50.55	142483	4935799
IMT13328	Germany	Pig	Diseased	2007	354	13	F	113	50.57	104203	4931269
IMT13329	Germany	Pig	Diseased	2007	354	13	F	88	50.56	120631	4934098
IMT13330	Germany	Pig	Diseased	2007	354	13	F	69	50.55	144465	4931579
IMT13341	Germany	Cattle	Healthy	2007	167	2	A	148	50.41	122576	5300628
IMT13348	Germany	Cattle	Healthy	2007	301	2	A	261	50.49	103400	5710005
IMT13351	Germany	Cattle	Healthy	2007	10	2	A	47	50.72	325163	4718901
IMT13354	Germany	Cattle	Healthy	2007	-	1	B1	272	50.91	52048	4874191
IMT13363	Germany	Cattle	Healthy	2007	5289	3	E	97	50.44	282203	5352012
IMT13372	Germany	Cattle	Healthy	2007	167	2	A	178	50.52	126152	5285754
IMT13376	Germany	Cattle	Healthy	2007	88	9	C	155	50.85	110603	5226812
IMT13383	Germany	Cattle	Healthy	2007	167	2	A	110	50.77	137060	4957449
IMT13390	Germany	Cattle	Healthy	2007	937	1	B1	88	50.46	215150	5099378
IMT13394	Germany	Cattle	Healthy	2007	88	9	C	175	50.71	127952	5201856

IMT13404	Germany	Cattle	Healthy	2007	56	1	B1	161	50.6	119870	5218554
IMT13411	Germany	Cattle	Healthy	2007	362	5	D	300	50.82	66998	5461229
IMT13417	Germany	Cattle	Healthy	2007	446	1	B1	78	50.72	280303	5073075
IMT13422	Germany	Cattle	Healthy	2007	10	2	A	84	50.61	138754	4855832
IMT13427	Germany	Cattle	Healthy	2007	540	2	A	162	50.37	103171	5323022
IMT13430	Germany	Cattle	Healthy	2007	167	2	A	111	50.68	142398	5126938
IMT13435	Germany	Cattle	Healthy	2007	10	2	A	85	50.62	138611	4871757
IMT13445	Germany	Cattle	Healthy	2007	951	5	D	100	50.44	199870	5285475
IMT13448	Germany	Cattle	Healthy	2007	10	2	A	90	50.58	148811	4802721
IMT13457	Germany	Cattle	Healthy	2007	155	1	B1	159	50.83	317670	5160549
IMT13468	Germany	Cattle	Healthy	2007	973	5	D	160	50.54	158985	5410953
IMT13478	Germany	Cattle	Healthy	2007	10	2	A	133	50.61	116603	5069543
IMT13490	Germany	Cattle	Healthy	2007	783	9	C	124	50.48	206532	5541811
IMT13500	Germany	Cattle	Healthy	2007	362	5	D	60	50.44	256568	5170302
IMT13513	Germany	Cattle	Healthy	2007	167	2	A	128	50.69	138230	4929607
IMT13523	Germany	Cattle	Healthy	2007	167	2	A	147	50.73	139297	5244919
IMT13529	Germany	Cattle	Healthy	2007	88	9	C	88	50.66	346114	5141174
IMT13774	Germany	Human	Healthy	2007	10	2	A	86	50.53	158604	4799596
IMT13776	Germany	Human	Healthy	2007	162	1	B1	77	50.83	194266	4856807
IMT13784	Germany	Human	Healthy	2007	10	2	A	196	50.79	88379	5141427
IMT13792	Germany	Human	Healthy	2007	38	6	D	96	50.58	241086	5299599
IMT13794	Germany	Human	Healthy	2007	350	3	E	177	50.67	107282	5492808
IMT13798	Germany	Human	Diseased	2007	73	4	B2	52	50.49	533687	5007065
IMT13800	Germany	Human	Diseased	2007	73	4	B2	65	50.57	388859	5080259
IMT13819	Germany	Human	Diseased	2007	545	5	D	118	50.57	183274	5388499
IMT13824	Germany	Human	Diseased	2007	73	4	B2	110	50.38	412455	5340117
IMT13830	Germany	Human	Diseased	2007	130	5	D	78	50.5	267565	5329092
IMT13843	Germany	Human	Diseased	2007	69	10	D	39	50.64	403085	4903626
IMT13851	Germany	Human	Healthy	2007	141	4	B2	46	50.63	406768	4968463
IMT13852	Germany	Human	Healthy	2007	68	5	D	70	50.47	239591	5169195
IMT13857	Germany	Human	Healthy	2007	10	2	A	152	50.69	114220	5146699
IMT13859	Germany	Human	Healthy	2007	73	4	B2	69	50.42	388354	5103762
IMT13862	Germany	Human	Healthy	2007	428	11	B2	42	50.43	749382	4901407
IMT13879	Germany	Human	Healthy	2007	393	5	D	51	50.57	379702	5219072

IMT13882	Germany	Human	Healthy	2007	73	4	B2	109	50.44	276475	5247408
IMT13883	Germany	Human	Healthy	2007	88	9	C	94	50.74	179773	4875307
IMT13928	Germany	Cattle	Diseased	2007	10	2	A	81	50.83	181004	4651603
IMT13936	Germany	Cattle	Diseased	2007	10	2	A	77	50.58	214221	4826162
IMT13942	Germany	Cattle	Diseased	2007	10	2	A	128	50.87	153215	5012804
IMT13947	Germany	Cattle	Diseased	2007	101	1	B1	40	50.64	308596	4666830
IMT13956	Germany	Cattle	Diseased	2007	10	2	A	89	50.79	126495	4925161
IMT13962	Germany	Pig	Healthy	2007	118	3	E	84	50.63	261618	5028478
IMT13998	Germany	Cattle	Diseased	2007	295	1	B1	75	50.64	258693	4747596
IMT14007	Germany	Cattle	Diseased	2007	1148	1	B1	62	50.7	404814	4957840
IMT14019	Germany	Cattle	Diseased	2007	1301	3	E	46	50.45	428034	4976115
IMT14026	Germany	Cattle	Diseased	2007	398	2	A	98	50.75	138268	4721070
IMT14036	Germany	Cattle	Diseased	2007	58	1	B1	74	50.67	218970	5022103
IMT14041	Germany	Cattle	Diseased	2007	69	10	D	76	50.57	230103	5299617
IMT14047	Germany	Cattle	Diseased	2007	647	4	B2	67	50.48	246715	5367099
IMT15453	Germany	Pig	Diseased	2008	58	1	B1	108	50.83	161647	4957687
IMT15456	Germany	Pig	Diseased	2008	846	3	E	134	50.64	75853	4764299
IMT15459	Germany	Pig	Diseased	2008	101	1	B1	87	50.63	186079	4801488
IMT15464	Germany	Pig	Diseased	2008	58	1	B1	91	50.67	197744	4833394
IMT15469	Germany	Pig	Diseased	2008	101	1	B1	90	50.62	157581	4680801
IMT15474	Germany	Pig	Diseased	2008	393	5	D	53	50.64	391372	5172409
IMT15478	Germany	Pig	Diseased	2008	898	1	B1	105	50.66	159287	4849681
IMT15482	Germany	Pig	Diseased	2008	10	2	A	133	50.65	123017	5151753
IMT15485	Germany	Pig	Diseased	2008	868	2	A	160	50.88	67356	4598007
IMT15496	Germany	Pig	Diseased	2008	877	1	B1	86	50.58	129538	4812311
IMT15528	Germany	Pig	Diseased	2008	625	4	B2	81	50.59	321113	5161796
IMT15532	Germany	Pig	Diseased	2008	10	2	A	113	50.64	126835	4914208
IMT15913	Germany	Cattle	Diseased	2008	297	1	B1	98	50.69	260244	5134105
IMT15916	Germany	Cattle	Diseased	2008	445	1	B1	290	50.42	104775	5720110
IMT15918	Germany	Cattle	Diseased	2008	11	3	E	187	50.33	146927	5329588
IMT15922	Germany	Cattle	Diseased	2008	16	1	B1	280	50.44	119624	5452613
IMT15933	Germany	Cattle	Diseased	2008	58	1	B1	168	50.5	218910	5345493
IMT15937	Germany	Cattle	Diseased	2008	342	1	B1	216	50.45	101904	5261767
IMT15940	Germany	Cattle	Diseased	2008	17	1	B1	183	50.36	140031	5631345

IMT15942	Germany	Cattle	Diseased	2008	677	1	B1	151	50.71	179617	5269644
IMT15944	Germany	Cattle	Healthy	2008	677	1	B1	149	50.71	236007	5267664
IMT15947	Germany	Cattle	Healthy	2008	306	1	B1	216	50.37	126802	5519751
IMT15950	Germany	Cattle	Healthy	2008	659	1	B1	260	50.41	82508	5009552
IMT15952	Germany	Cattle	Healthy	2008	677	1	B1	165	50.73	165561	5255239
IMT15953	Germany	Cattle	Healthy	2008	306	1	B1	223	50.37	129632	5520452
IMT15955	Germany	Cattle	Healthy	2008	677	1	B1	113	50.7	179359	5158535
IMT15964	Germany	Cattle	Healthy	2008	306	1	B1	231	50.43	117284	5384887
IMT15967	Germany	Cattle	Healthy	2008	21	1	B1	297	50.35	100375	5594416
IMT15970	Germany	Cattle	Healthy	2008	677	1	B1	120	50.7	236007	5157989
IMT15971	Germany	Cattle	Healthy	2008	659	1	B1	264	50.4	82506	5012108
IMT16218	Germany	Pig	Healthy	2003	73	4	B2	138	50.76	345675	5106043
IMT16219	Germany	Pig	Healthy	2003	118	3	E	80	50.61	287557	5031423
IMT16220	Germany	Pig	Healthy	2003	73	4	B2	48	50.55	531442	5010354
IMT18157	Germany	Pig	Healthy	2004	23	9	C	63	50.69	208455	4932467
IMT18377	Germany	Human	Diseased	2009	80	4	B2	99	50.34	306984	5175355
IMT18378	Germany	Human	Healthy	2009	141	4	B2	73	50.46	384730	5226243
IMT18413	Germany	Human	Diseased	2009	357	11	B2	45	50.53	394206	4883235
IMT18433	Germany	Human	Diseased	2009	141	4	B2	59	50.57	399951	5081859
IMT18859	Germany	Cattle	Diseased	2009	10	2	A	112	50.59	147937	4879960
IMT19029	Germany	Human	Diseased	2009	80	4	B2	81	50.43	352867	5126330
IMT19221	Germany	Pig	Diseased	2009	10	2	A	71	50.57	168394	4643229
IMT19654	Germany	Pig	Diseased	2009	-	2	A	116	50.5	186446	5161132
IMT19655	Germany	Pig	Diseased	2009	799	3	E	163	50.29	159198	5413626
IMT20024	Germany	Cattle	Diseased	2009	73	4	B2	180	50.39	338728	5163910
IMT20253	Germany	Cattle	Healthy	2009	658	7	G	63	50.82	387104	4971306
IMT20255	Germany	Cattle	Healthy	2009	58	1	B1	125	50.69	177643	5008935
IMT20259	Germany	Cattle	Healthy	2009	376	1	B1	179	50.54	137616	5221716
IMT20261	Germany	Cattle	Healthy	2009	154	1	B1	101	50.66	220628	5057354
IMT20262	Germany	Cattle	Healthy	2009	20	1	B1	173	50.52	178120	5204579
IMT20265	Germany	Cattle	Healthy	2009	1890	1	B1	125	50.57	128219	4965903
IMT20520	Germany	Pig	Healthy	2005	10	2	A	122	50.74	91152	4840686
IMT20599	Germany	Cattle	Diseased	2010	73	4	B2	106	50.4	368483	5450036
IMT20730	Germany	Cattle	Diseased	2010	2230	9	C	80	50.5	256814	5186483

IMT20781	Germany	Cattle	Diseased	2010	949	1	B1	185	50.72	133546	5299058
IMT20785	Germany	Cattle	Diseased	2010	1615	9	C	110	50.54	188843	5156276
IMT21418	Germany	Cattle	Diseased	2010	1615	9	C	101	50.55	284576	5148577
IMT22456	Germany	Cattle	Diseased	2010	223	1	B1	132	50.51	177360	5135613
IMT22498	Germany	Cattle	Diseased	2010	642	1	B1	110	50.6	223252	5420805
IMT22634	Germany	Cattle	Diseased	2010	10	2	A	92	50.8	210330	4881887
IMT23976	Germany	Pig	Diseased	2010	100	2	A	131	50.7	180542	5525342
IMT24813	Germany	Cattle	Diseased	2011	88	9	C	145	50.76	178721	5281473
IMT24820	Germany	Cattle	Diseased	2011	1615	9	C	100	50.56	188843	5256683
IMT25261	Germany	Cattle	Diseased	2011	224	1	B1	91	50.77	362908	5021978
IMT26376	Germany	Human	Diseased	2011	678	1	B1	107	50.58	149053	5378531
IMT26377	Germany	Human	Diseased	2011	678	1	B1	139	50.59	149061	5344690
IMT26646	Germany	Cattle	Diseased	2011	1615	9	C	143	50.45	272207	5239848
IMT27294	Germany	Cattle	Diseased	2011	167	2	A	131	50.85	120618	4842710
IMT28138	Germany	Pig	Diseased	2011	206	2	A	140	50.57	102802	4866623
IMT28139	Germany	Pig	Diseased	2011	167	2	A	106	50.7	148155	5117351
IMT28508	Germany	Cattle	Diseased	2011	925	5	D	129	50.54	256287	5553622
IMT28628	Germany	Cattle	Diseased	2012	448	1	B1	134	50.66	135160	5355869
IMT28653	Germany	Cattle	Diseased	2012	617	2	A	163	50.62	107255	5146077
IMT29581	Germany	Human	Diseased	2012	95	4	B2	58	50.57	439657	5155483
IMT30909	Germany	Cattle	Diseased	2013	69	10	D	141	50.6	171870	5299219
IMT30910	Germany	Cattle	Diseased	2013	69	10	D	137	50.6	193292	5304027
IMT32380	Germany	Cattle	Diseased	2013	906	1	B1	52	50.74	375764	4809031
IMT32537	Germany	Cattle	Diseased	2013	2972	1	B1	65	50.72	240812	4956059
IMT32949	Germany	Cattle	Diseased	2014	10	2	A	70	50.54	312171	5010740
IMT33253	Germany	Cattle	Diseased	2014	95	4	B2	85	50.39	280250	5326559
IMT33363	Germany	Cattle	Diseased	2014	278	1	B1	95	50.51	147763	5278378
IMT33710	Germany	Cattle	Diseased	2014	392	1	B1	118	50.52	116438	5329818
IMT33921	Germany	Cattle	Diseased	2014	10	2	A	109	50.44	147937	5016005
IMT33932	Germany	Cattle	Diseased	2014	362	5	D	117	50.55	183274	5438858
IMT34135	Germany	Pig	Healthy	2014	10	2	A	119	50.68	119507	4857579
IMT34137	Germany	Pig	Healthy	2014	-	1	B1	76	50.8	262928	4932827
IMT34140	Germany	Pig	Healthy	2014	-	1	B1	65	50.79	280933	4946963
IMT34142	Germany	Pig	Healthy	2014	-	1	B1	64	50.8	280933	4933147

IMT34144	Germany	Pig	Healthy	2014	-	1	B1	60	50.8	280926	4931998
IMT34182	Germany	Cattle	Diseased	2014	-	5	D	56	50.61	282187	4838687
IMT34410	Germany	Cattle	Diseased	2014	362	5	D	139	50.64	223919	5380069
IMT34413	Germany	Cattle	Diseased	2014	362	5	D	130	50.64	223919	5360950
IMT34414	Germany	Cattle	Diseased	2014	88	9	C	54	50.76	352679	5011368
IMT34415	Germany	Cattle	Diseased	2014	744	2	A	141	50.46	126195	5035026
IMT34417	Germany	Cattle	Diseased	2014	1431	1	B1	84	50.85	173344	5027084
IMT37431	Germany	Cattle	Diseased	2015	442	1	B1	83	51	183080	4993674
IMT37433	Germany	Cattle	Diseased	2015	58	1	B1	81	50.79	226722	5012288
IMT37434	Germany	Cattle	Diseased	2015	2035	1	B1	68	50.62	154873	4604853
IMT37445	Germany	Cattle	Diseased	2015	-	1	B1	71	50.62	291980	4833601
IMT37451	Germany	Cattle	Diseased	2015	1148	1	B1	63	50.78	684383	4871588
IMT37462	Germany	Cattle	Diseased	2015	1415	2	A	88	50.68	202395	4640770
IMT37470	Germany	Cattle	Diseased	2015	1508	3	E	69	50.3	283049	5105482
IMT37703	Germany	Pig	Diseased	2015	69	10	D	53	50.64	349262	5096043
IMT38565	Germany	Cattle	Diseased	2016	362	5	D	98	50.55	198219	5261838
IMT38566	Germany	Cattle	Diseased	2016	361	2	A	112	50.53	131595	5003705
IMT38701	Germany	Pig	Healthy	2016	2067	1	B1	107	50.5	180489	5067897
IMT38723	Germany	Pig	Healthy	2016	641	1	B1	107	50.54	111168	4756292
IMT39234	Germany	Pig	Diseased	2016	361	2	A	72	50.74	135345	4730952
IMT39344	Germany	Cattle	Diseased	2016	361	2	A	103	50.69	131800	4926621
IMT39345	Germany	Cattle	Diseased	2016	783	9	C	116	50.67	188901	5338296
IMT39464	Germany	Pig	Diseased	2016	7986	2	A	156	50.83	63885	4439680
IMT39829	Germany	Chicken	Diseased	2016	3090	1	B1	105	50.68	135834	4938860
IMT40119	Germany	Pig	Diseased	2016	100	2	A	307	50.83	113612	5550496
IMT40120	Germany	Pig	Diseased	2016	100	2	A	156	50.63	123889	5434372
IMT40121	Germany	Pig	Diseased	2016	10	2	A	160	50.71	126141	5314764
IMT42104	Germany	Pig	Diseased	2017	5758	2	A	332	50.38	66463	5361916
IMT42105	Germany	Pig	Diseased	2017	345	1	B1	58	50.6	295791	4955843
IMT42106	Germany	Pig	Diseased	2017	73	4	B2	88	50.51	344427	5128164
IMT42107	Germany	Pig	Diseased	2017	2144	1	B1	41	50.77	300659	4834316
IMT8071	Germany	Pig	Diseased	2003	302	3	E	145	50.6	446097	5431118
IMT8072	Germany	Pig	Diseased	2003	48	2	A	268	50.46	58072	5178020
IMT9151	Germany	Cattle	Diseased	2004	540	2	A	76	50.66	179147	4828759

IMT9241	Germany	Chicken	Diseased	2004	95	4	B2	94	50.53	321816	5146047
IMT9267	Germany	Human	Diseased	2004	80	4	B2	76	50.32	344513	5114790
IMT9270	Germany	Human	Diseased	2004	62	13	F	165	50.49	109926	5368706
IMT9278	Germany	Human	Diseased	2004	2272	9	C	75	50.66	207778	5208618
IMT9285	Germany	Human	Diseased	2004	140	4	B2	100	50.42	262020	5259539
IMT9675	Germany	Human	Diseased	2004	1	5	D	123	50.31	92304	5041300
IMT9678	Germany	Human	Diseased	2004	5	1	B1	151	50.63	133369	5164813
IMT9679	Germany	Human	Diseased	2004	9	1	B1	256	50.45	89816	5422881
IMT9680	Germany	Human	Diseased	2004	2064	3	E	97	50.72	110403	4596141
IMT9682	Germany	Human	Diseased	2004	80	4	B2	103	50.38	192640	5129885
IMT9684	Germany	Human	Diseased	2004	21	1	B1	280	50.38	115633	5575807
IMT9687	Germany	Human	Diseased	2004	34	2	A	109	50.52	147936	5097286
IMT9795	Germany	Cattle	Diseased	2005	659	1	B1	330	50.42	68572	5379116
IMT9803	Germany	Cattle	Diseased	2005	56	1	B1	113	50.69	185700	4958583
IMT9872	Germany	Cattle	Diseased	2005	301	2	A	304	50.47	103388	5655626
IMT9877	Germany	Cattle	Diseased	2005	4085	2	A	149	50.46	105792	5157125
IMT9886	Germany	Pig	Diseased	2004	1153	1	B1	68	50.64	208109	5044208
IMT9901	Germany	Cattle	Diseased	2005	4038	1	B1	44	50.79	246860	4699159
IMT9904	Germany	Cattle	Diseased	2005	906	1	B1	148	50.57	161984	5009673
P3CEEC727728	Spain	Pig	Healthy	2003	-	1	B1	149	50.72	72693	4819497
P3ESEC699700	Spain	Pig	Healthy	2003	10	2	A	297	50.78	50956	5199927
P3EUEC125126	Spain	Pig	Healthy	2003	542	2	A	207	50.67	93167	5194865
P3EUEC151152	Spain	Pig	Healthy	2003	8449	2	A	144	50.5	125707	5259471
P3FGEC849850	Spain	Pig	Healthy	2003	4214	2	A	133	50.71	96081	4749533
P3FGEC853854	Spain	Pig	Healthy	2003	10	2	A	229	50.51	74742	4978957
P3FGEC919920	Spain	Pig	Healthy	2003	-	9	C	131	50.56	142598	5024037
P3FUEC141142	Spain	Pig	Healthy	2003	10	2	A	160	50.5	84736	4948456
P3FUEC525526	Spain	Pig	Healthy	2003	58	1	B1	181	50.69	90310	5054376
P3FUEC559560	Spain	Pig	Healthy	2003	1286	2	A	134	50.78	82927	4771677
P3GUEC747748	Spain	Pig	Healthy	2003	154	1	B1	116	50.59	108118	4766901
P3GUEC903904	Spain	Pig	Healthy	2003	10	2	A	201	50.71	56844	4749283
P3ICEC10301031	Spain	Pig	Healthy	2003	6617	2	A	783	50.87	38388	5595603
P3PREC237238	Spain	Pig	Healthy	2003	10	2	A	273	50.88	38996	4817935
P3SLEC338339	Spain	Pig	Healthy	2003	10	2	A	168	50.92	62150	4650493

P3SLEC381382	Spain	Pig	Healthy	2003	641	1	B1	253	50.68	52008	5096398
R27	Germany	Cattle	Healthy	2015	446	1	B1	101	50.46	261076	5040028
R28	Germany	Cattle	Healthy	2015	446	1	B1	81	50.5	261076	5024974
R29	Germany	Cattle	Healthy	2015	162	1	B1	97	50.55	232804	5017859
R30	Germany	Cattle	Healthy	2015	154	1	B1	84	50.4	217332	4969338
R31	Germany	Cattle	Healthy	2015	10	2	A	176	50.67	151571	5091548
R32	Germany	Cattle	Healthy	2015	2522	1	B1	169	50.54	165509	4996993
R33	Germany	Cattle	Healthy	2015	661	1	B1	90	50.67	198154	4937738
R34	Germany	Cattle	Healthy	2015	201	1	B1	102	50.55	205406	5194939
R35	Germany	Cattle	Healthy	2015	201	1	B1	101	50.54	194168	5197102
R36	Germany	Cattle	Healthy	2015	446	1	B1	75	50.59	214256	4963873
R37	Germany	Cattle	Healthy	2015	424	1	B1	90	50.74	198215	4989644
R38	Germany	Cattle	Healthy	2015	424	1	B1	85	50.75	211451	4988923
R39	Germany	Cattle	Healthy	2015	2217	1	C	173	50.61	185897	5240582
R40	Germany	Cattle	Healthy	2015	446	1	B1	72	50.6	261076	4927572
R41	Germany	Cattle	Healthy	2015	336	1	B1	171	50.51	92050	5158649
R42	Germany	Cattle	Healthy	2015	224	1	B1	51	50.9	711208	4760401
R43	Germany	Cattle	Healthy	2015	109	1	B1	56	50.73	703742	4945122
R45	Germany	Cattle	Healthy	2015	361	2	A	111	50.67	131801	4905851
R46	Germany	Cattle	Healthy	2015	23	9	C	93	50.6	124076	4820552
R55	Germany	Cattle	Healthy	2015	-	1	B1	118	50.52	167471	4724012
R59	Germany	Cattle	Healthy	2015	-	1	B1	104	50.61	214678	5050611
R61	Germany	Cattle	Healthy	2015	1301	3	E	60	50.5	615172	5047584
R65	Germany	Cattle	Healthy	2015	278	1	B1	59	50.57	198341	4929727
R66	Germany	Cattle	Healthy	2015	164	1	B1	68	50.62	276247	5035779
R67	Germany	Cattle	Healthy	2015	88	9	C	38	50.68	510949	4808347
R70	Germany	Cattle	Healthy	2015	1721	2	A	115	50.69	136959	5091030
R72	Germany	Cattle	Healthy	2015	1727	1	B1	93	51.05	452196	4669754
R84	Germany	Cattle	Healthy	2015	542	2	A	112	50.91	110970	4657017
R89	Germany	Cattle	Healthy	2015	154	1	B1	59	50.55	293829	4861038
R90	Germany	Cattle	Healthy	2015	906	1	B1	50	50.69	269156	4908056
SAP1372	UK	Human	Diseased	2017	131	11	B2	116	50.71	190456	5243433
SAP1468	UK	Human	Diseased	2017	394	10	D	80	50.49	190655	5215948
SAP1479	UK	Human	Diseased	2017	1858	4	B2	62	50.47	312057	5146606

SAP1492	UK	Human	Diseased	2017	-	9	C	37	50.75	359282	4862246
SAP1507	UK	Human	Diseased	2017	1677	4	B2	19	50.63	662075	4636755
SAP1515	UK	Human	Diseased	2017	73	4	B2	61	50.51	361979	5053567
SAP1541	UK	Human	Diseased	2017	569	4	B2	32	50.61	459061	4861029
SAP1597	UK	Human	Diseased	2017	69	10	D	137	50.59	286092	5395348
SAP1603	UK	Human	Diseased	2017	372	4	B2	48	50.4	302398	4863280
SAP1609	UK	Human	Diseased	2017	73	4	B2	81	50.42	361458	5048896
SAP1614	UK	Human	Diseased	2017	14	4	B2	94	50.47	252482	5162450
SAP1621	UK	Human	Diseased	2017	131	11	B2	94	50.65	166644	5272170
SAP1632	UK	Human	Diseased	2017	38	6	D	121	50.45	120744	5299885
SAP1664	UK	Human	Diseased	2017	131	11	B2	93	50.67	190734	5297708
SAP1710	UK	Human	Diseased	2017	636	4	B2	79	50.53	176475	4985890
SAP1766	UK	Human	Diseased	2017	127	4	B2	78	50.33	225960	5140482
SAP1773	UK	Human	Diseased	2017	12	4	B2	51	50.49	344210	5049730
SAP1781	UK	Human	Diseased	2017	8455	11	B2	75	50.61	202804	5171617
SAP1790	UK	Human	Diseased	2017	131	11	B2	84	50.72	189875	5151683
SAP1836	UK	Human	Diseased	2017	131	11	B2	92	50.64	195370	5303749
SAP1847	UK	Human	Diseased	2017	131	11	B2	67	50.73	231156	5091077
SAP1851	UK	Human	Diseased	2017	648	14	F	84	50.44	201502	5292260
SAP1852	UK	Human	Diseased	2017	131	11	B2	67	50.75	222117	5026207
SAP1858	UK	Human	Diseased	2017	131	11	B2	93	50.73	211816	5391560
SAP1873	UK	Human	Diseased	2017	131	11	B2	86	50.67	195275	5348516
SAP1876	UK	Human	Diseased	2017	4988	2	A	82	50.78	126388	4589527
SAP1879	UK	Human	Diseased	2017	131	11	B2	72	50.77	203050	5224450
SAP1887	UK	Human	Diseased	2017	131	11	B2	91	50.62	206883	5296583
SAP1888	UK	Human	Diseased	2017	131	11	B2	87	50.69	209516	5268326
SAP1913	UK	Human	Diseased	2017	1193	4	B2	74	50.61	354485	5111468
SAP1926	UK	Human	Diseased	2017	73	4	B2	85	50.44	362855	5196359
SAP1953	UK	Human	Diseased	2017	131	11	B2	64	50.74	216029	5038948
SAP1971	UK	Chicken	Healthy	2014	10	2	A	115	50.62	122255	4908237
SAP1973	UK	Chicken	Healthy	2014	373	2	A	97	50.62	150702	4944608
SAP1974	UK	Chicken	Healthy	2014	10	2	A	113	50.62	123231	4906747
SAP1975	UK	Chicken	Healthy	2014	3721	1	B1	53	50.72	343918	5178446
SAP1978	UK	Chicken	Healthy	2014	10	2	A	129	50.56	123231	5073338

SAP1979	UK	Chicken	Healthy	2014	373	2	A	92	50.63	150048	4900758
SAP1980	UK	Chicken	Healthy	2014	1638	2	A	127	50.63	96182	4782681
SAP1985	UK	Chicken	Healthy	2014	10	2	A	99	50.76	96388	4714940
SAP1987	UK	Chicken	Healthy	2014	770	12	cladeI	159	50.3	149345	5609818
SAP1988	UK	Chicken	Healthy	2014	3995	1	B1	107	50.87	135098	4995055
SAP1993	UK	Chicken	Healthy	2014	373	2	A	97	50.62	145720	4905338
SAP1995	UK	Chicken	Healthy	2014	919	4	B2	93	50.72	155962	5120750
SAP1996	UK	Chicken	Healthy	2014	155	1	B1	126	50.66	196965	5127199
SAP2000	UK	Chicken	Healthy	2014	2309	6	D	259	50.52	100777	5720263
SAP2001	UK	Chicken	Healthy	2014	355	4	B2	80	50.48	204824	5100203
SAP2004	UK	Chicken	Healthy	2017	117	8	G	117	50.74	167483	5187497
SAP2008	UK	Chicken	Healthy	2017	10	2	A	269	50.66	86000	5564091
SAP2012	UK	Chicken	Healthy	2017	-	5	D	123	50.46	125791	5076494
SAP2013	UK	Chicken	Healthy	2017	117	8	G	117	50.53	197511	5118510
SAP2016	UK	Chicken	Healthy	2017	-	14	F	147	50.18	135856	5489618
SAP2018	UK	Chicken	Healthy	2017	135	4	B2	48	50.68	445951	4833301
SAP2021	UK	Chicken	Healthy	2017	770	12	cladeI	95	50.4	155843	5376187
SAP2024	UK	Chicken	Healthy	2017	88	9	C	60	50.59	321259	5065400
SAP2026	UK	Chicken	Healthy	2017	752	2	A	133	50.24	134460	5162057
SAP2028	UK	Chicken	Healthy	2017	-	2	A	181	50.42	106974	5331326
SAP2030	UK	Chicken	Healthy	2017	752	2	A	162	50.29	147913	5240748
SAP2032	UK	Chicken	Healthy	2017	69	10	D	95	50.51	201592	5283355
SAP2034	UK	Chicken	Healthy	2017	752	2	A	144	50.3	142693	5244373
SAP2035	UK	Chicken	Healthy	2017	752	2	A	137	50.3	142693	5240938
SAP2036	UK	Chicken	Healthy	2017	1101	1	B1	85	50.72	167803	5183458
SAP2066	UK	Human	Healthy	2017	409	2	A	173	50.97	99854	5023935
SAP2067	UK	Human	Healthy	2017	69	10	D	76	50.76	188535	5169635
SAP2068	UK	Human	Healthy	2017	131	11	B2	59	50.61	272403	5237237
SAP2070	UK	Human	Healthy	2017	7892	5	D	57	50.55	292198	4937957
SAP2071	UK	Human	Healthy	2017	58	1	B1	148	50.73	125988	4876880
SAP2072	UK	Human	Healthy	2017	62	13	F	135	50.47	109796	5244119
SAP2077	UK	Human	Healthy	2017	540	2	A	63	50.7	148438	4725187
SAP2078	UK	Human	Healthy	2017	31	5	D	112	50.61	150899	5207636
SAP2079a	UK	Human	Healthy	2017	10	2	A	174	50.64	118890	5263120

SAP2079b	UK	Human	Healthy	2017	537	4	B2	66	50.27	393280	5159976
SAP2081	UK	Human	Healthy	2017	1193	4	B2	58	50.55	363154	5073623
SAP2082	UK	Human	Healthy	2017	10	2	A	171	50.68	115140	5168712
SAP2083	UK	Human	Healthy	2017	10	2	A	66	50.55	175277	4841532
SAP2085	UK	Human	Healthy	2017	23	9	C	87	50.64	196990	5108807
SAP2086	UK	Human	Healthy	2017	7670	9	D	95	50.46	210765	5560228
SAP2087	UK	Human	Healthy	2017	131	11	B2	55	50.72	233229	4902918
SAP2089	UK	Human	Healthy	2017	131	11	B2	77	50.74	340939	5194203
SAP2093	UK	Human	Healthy	2017	415	13	F	199	50.57	59263	5139287
SAP2096	UK	Human	Healthy	2017	131	11	B2	78	50.78	359897	5090987
SAP2097	UK	Human	Healthy	2017	69	10	D	48	50.68	260830	5064116
SAP2098	UK	Human	Healthy	2017	73	4	B2	62	50.52	363953	5209383
SAP2101	UK	Human	Healthy	2017	847	1	B1	57	50.79	271493	4937315
SAP2130	UK	Human	Healthy	2018	131	11	B2	93	50.69	156035	5179222
SAP2131	UK	Human	Healthy	2018	59	13	F	214	50.58	55331	5203125
SAP2134	UK	Human	Healthy	2018	569	4	B2	50	50.55	498328	4801017
SAP2135	UK	Human	Healthy	2018	2178	1	B1	38	50.84	321963	4611764
SAP2137	UK	Human	Healthy	2018	69	10	D	82	50.5	197689	5145664
SAP2139	UK	Human	Healthy	2018	10	2	A	159	50.72	124112	5120512
SAP2141	UK	Human	Healthy	2018	-	2	A	145	50.73	76284	4701553
SAP2142	UK	Human	Healthy	2018	963	6	D	115	50.66	171117	5148179
SAP2144	UK	Human	Healthy	2018	80	4	B2	33	50.34	514301	4961067
SAP2148	UK	Human	Healthy	2018	131	11	B2	50	50.77	284068	5164683
SAP453	UK	Chicken	Diseased	2012	117	8	G	133	50.66	217393	5305873
SAP454	UK	Chicken	Diseased	2013	1618	4	B2	90	50.56	413832	5178666
SAP456	UK	Chicken	Diseased	2012	140	4	B2	116	50.44	212816	5331033
SAP458	UK	Chicken	Diseased	2012	117	8	G	79	50.78	247944	5003000
SAP459	UK	Chicken	Diseased	2013	23	9	C	72	50.53	204672	5074894
SAP460	UK	Chicken	Diseased	2005	23	9	C	56	50.71	290237	4959146
SAP461	UK	Chicken	Diseased	2005	141	4	B2	63	50.69	344464	5069444
SAP463	UK	Chicken	Diseased	2008	140	4	B2	100	50.3	210112	5456226
SAP464	UK	Chicken	Diseased	2010	5924	11	B2	65	50.41	322668	5092459
SAP465	UK	Chicken	Diseased	2010	48	2	A	101	50.84	127094	4794451
SAP466	UK	Chicken	Diseased	2012	117	8	G	125	50.76	195023	5113385

SAP467	UK	Chicken	Diseased	2012	388	1	B1	117	50.72	125973	5208574
SAP468	UK	Chicken	Diseased	2012	69	10	D	70	50.53	318271	5316789
Sap469	UK	Chicken	Diseased	2013	69	10	D	124	50.36	221730	5364106
SAP470	UK	Chicken	Diseased	2013	69	10	D	83	50.37	309453	5409785
SAP471	UK	Chicken	Diseased	2013	297	1	B1	85	50.62	161517	5221284
SAP472	UK	Chicken	Diseased	2006	1618	4	B2	83	50.54	344163	5162116
SAP473	UK	Chicken	Diseased	2012	746	2	A	139	50.6	112008	5023308
SAP475	UK	Chicken	Diseased	2010	95	4	B2	75	50.48	299550	5367221
SAP477	UK	Chicken	Diseased	2012	48	2	A	93	50.89	107143	4607155
Sap481	UK	Chicken	Diseased	2003	140	4	B2	88	50.48	209530	5110745
Sap482	UK	Chicken	Diseased	2003	23	9	C	93	50.66	206428	5127754
Sap483	UK	Chicken	Diseased	2010	1056	1	B1	138	50.51	156624	5293095
SAP486	UK	Chicken	Diseased	2012	1638	2	A	177	50.74	71961	4724616
SAP488	UK	Chicken	Diseased	2010	23	9	C	80	50.56	187749	4889908
SAP492	UK	Chicken	Diseased	2006	4162	1	B1	107	50.67	130466	4905657
SAP493	UK	Chicken	Diseased	2012	1056	1	B1	114	50.52	208801	5314361
SAP496	UK	Chicken	Diseased	2006	420	4	B2	113	50.42	202357	5190004
SAP497	UK	Chicken	Diseased	2006	117	8	G	135	50.58	140331	4931041
SAP498	UK	Chicken	Diseased	2012	3580	1	B1	145	50.5	205520	5117408
SAP502	UK	Chicken	Diseased	2012	95	4	B2	153	50.38	171777	5499607
SAP503	UK	Chicken	Diseased	2013	23	9	C	99	50.53	173963	4993615
SAP505	UK	Chicken	Diseased	2013	117	8	G	142	50.51	118442	5137225
SAP506	UK	Chicken	Diseased	2013	5926	3	E	126	50.67	123522	5267945
SAP510	UK	Chicken	Diseased	2013	5926	3	E	161	50.66	114048	5212292
SAP511	UK	Chicken	Diseased	2013	48	2	A	141	50.78	99357	5038903
SAP515	UK	Chicken	Diseased	2011	140	4	B2	102	50.46	214107	5296867
SAP516	UK	Chicken	Diseased	2007	696	1	B1	130	50.66	149841	5223813
SAP521	UK	Chicken	Diseased	2012	428	11	B2	97	50.29	214070	5113588
SAP525	UK	Chicken	Diseased	2012	95	4	B2	76	50.64	201609	5150003
SAP526	UK	Chicken	Diseased	2012	1276	13	F	100	50.36	115618	5240487
SAP528	UK	Chicken	Diseased	2011	93	2	A	126	50.66	101533	4880461
SAP530	UK	Chicken	Diseased	2012	88	9	C	85	50.73	192549	4924268
SAP532	UK	Chicken	Diseased	2005	428	11	B2	90	50.28	219528	5109170
SAP533	UK	Chicken	Diseased	2012	5506	1	B1	66	50.66	185240	4928993

SAP539	UK	Chicken	Diseased	2012	1114	2	A	154	50.68	99765	4898218
SAP542	UK	Chicken	Diseased	2012	95	4	B2	79	50.64	268025	5150914
SAP543	UK	Chicken	Diseased	2013	23	9	C	83	50.58	187830	5251060
SAP548	UK	Chicken	Diseased	2013	140	4	B2	126	50.52	176639	5249657
SAP556	UK	Chicken	Diseased	2013	141	4	B2	90	50.56	343515	5250029
Sap561	UK	Chicken	Diseased	2006	-	8	G	208	50.65	57585	5427218
SAP562	UK	Chicken	Diseased	2008	23	9	C	96	50.68	185956	5158871
SAP563	UK	Chicken	Diseased	2006	371	3	E	123	50.43	125103	5461740
SAP565	UK	Chicken	Diseased	2007	117	8	G	81	50.54	139976	4963743
SAP568	UK	Chicken	Diseased	2011	357	11	B2	61	50.42	290650	5069458
SAP569	UK	Chicken	Diseased	2011	1304	1	B1	60	50.64	261066	4931726
SAP571	UK	Chicken	Diseased	2012	1618	4	B2	120	50.54	244955	5209513
SAP573	UK	Chicken	Diseased	2008	5928	2	A	130	50.57	172990	5112795
SAP574	UK	Chicken	Diseased	2012	1618	4	B2	91	50.51	325689	5156822
SAP575	UK	Chicken	Diseased	2010	2272	9	C	71	50.76	200477	5027417
SAP578	UK	Chicken	Diseased	2006	10	2	A	61	50.67	263979	4951330
SAP580	UK	Chicken	Diseased	2011	57	3	E	92	50.74	169133	5123360
SAP582	UK	Chicken	Diseased	2006	2705	2	A	59	50.54	185684	4784748
SAP616	UK	Chicken	Diseased	2013	140	4	B2	84	50.53	237500	5079923
SAP621	UK	Chicken	Diseased	2015	117	8	G	110	50.71	200565	5137069
SAP622	UK	Chicken	Diseased	2015	117	8	G	91	50.7	226971	5107722
SAP624	UK	Chicken	Diseased	2015	135	4	B2	106	50.55	286303	5353030
SAP627	UK	Chicken	Diseased	2015	1638	2	A	134	50.69	94767	4758020
Sap629	UK	Chicken	Diseased	2015	95	4	B2	116	50.5	177449	5305276
SAP630	UK	Chicken	Diseased	2015	117	8	G	121	50.52	148636	5147359
SAP632	UK	Chicken	Diseased	2015	428	11	B2	64	50.33	344619	5151305
SAP637	UK	Chicken	Diseased	2015	101	1	B1	86	50.43	218045	4950192
Sap638	UK	Chicken	Diseased	2015	648	14	F	178	50.37	148710	5535986
Sap639	UK	Chicken	Diseased	2015	1638	2	A	123	50.62	94767	4832348
Sap640	UK	Chicken	Diseased	2015	101	1	B1	98	50.34	151695	5168927
SAP641	UK	Chicken	Diseased	2015	117	8	G	107	50.57	153238	5127580
Sap646	UK	Chicken	Diseased	2015	-	8	G	114	50.7	194968	5108742
Sap650	UK	Chicken	Diseased	2015	117	8	G	118	50.7	148548	5103463
SAP653	UK	Chicken	Diseased	2015	429	11	B2	86	50.58	173990	5244519

SAP714	UK	Chicken	Diseased	2013	5925	9	C	71	50.61	194271	5070914
VE0600665EC	Spain	Pig	Healthy	2006	641	1	B1	228	50.25	62951	5304383
VE0600670EC	Spain	Pig	Healthy	2006	7450	2	A	167	50.73	66950	4842108
VE0600711EC	Spain	Pig	Healthy	2006	1141	2	A	207	50.73	65771	4775786
VE0600722EC	Spain	Pig	Healthy	2006	1286	2	A	148	50.71	82850	4864803
VE0600744EC	Spain	Pig	Healthy	2006	10	2	A	189	50.73	67856	4940983
VE0600834EC	Spain	Pig	Healthy	2006	846	3	E	146	50.61	73117	4817507
VE0600959EC	Spain	Pig	Healthy	2006	2035	1	B1	138	50.61	67835	4788795
VE0600987EC	Spain	Pig	Healthy	2006	1508	3	E	119	50.48	90020	4879237
VE0700906EC	Spain	Pig	Healthy	2007	10	2	A	108	50.66	129610	4819039
VE0700939EC	Spain	Pig	Healthy	2007	10	2	A	293	50.65	46817	4899179
VE0701436EC	Spain	Pig	Healthy	2007	542	2	A	126	50.92	120092	4765601
VE0701786EC	Spain	Pig	Healthy	2007	542	2	A	126	50.8	85754	4650497
VE0702121EC	Spain	Pig	Healthy	2007	4175	3	E	124	50.39	139551	5193378
VE0702142EC	Spain	Cattle	Healthy	2007	515	3	A	84	50.52	261218	5032471
VE0702144EC	Spain	Cattle	Healthy	2007	109	1	B1	152	50.74	89895	5020509
VE0702216EC	Spain	Cattle	Healthy	2007	278	1	B1	78	50.68	202427	4960288
VE0702242EC	Spain	Cattle	Healthy	2007	58	1	B1	176	50.76	109161	5114357
VE0702356EC	Spain	Cattle	Healthy	2007	2161	1	B1	80	50.76	410784	5126268
VE0702503EC	Spain	Cattle	Healthy	2007	2217	1	C	135	50.78	140055	5331337
VE0702719EC	Spain	Cattle	Healthy	2007	58	1	B1	340	50.88	35225	5011800
VE0702760EC	Spain	Pig	Healthy	2007	34	2	A	110	50.63	121815	4842579
VE0702785EC	Spain	Cattle	Healthy	2007	278	1	B1	98	50.74	145512	4969550
VE0703230EC	Spain	Cattle	Healthy	2007	-	2	A	92	50.8	132517	4660728
VE0703232EC	Spain	Cattle	Healthy	2007	164	1	B1	68	50.58	375780	5025097
VE0703480EC	Spain	Cattle	Healthy	2007	1080	1	B1	62	50.64	270188	5039854
VE0703639EC	Spain	Cattle	Healthy	2007	752	2	A	330	50.12	104077	5689380
VE0703802EC	Spain	Cattle	Healthy	2007	906	1	B1	97	50.72	120883	4872850
VE0703817EC	Spain	Cattle	Healthy	2007	392	1	B1	168	50.54	67790	5372609
VE0703842EC	Spain	Cattle	Healthy	2007	6186	1	B1	99	50.69	197026	5108751
VE0703955EC	Spain	Cattle	Healthy	2007	10	2	A	144	50.67	97028	4968838
VE0703997EC	Spain	Cattle	Healthy	2007	906	1	B1	108	50.63	160804	5183673
VE0703998EC	Spain	Cattle	Healthy	2007	442	1	B1	172	50.68	89087	5116351
VE0704187EC	Spain	Cattle	Healthy	2007	602	1	B1	108	50.71	111976	5183534

VE0704189EC	Spain	Cattle	Healthy	2007	925	5	D	132	50.66	126839	5079129
VE0704194EC	Spain	Cattle	Healthy	2007	164	1	B1	120	50.69	143645	4952632
VE0704232EC	Spain	Cattle	Healthy	2007	132	5	D	118	50.64	121734	4976932
VE0704415EC	Spain	Cattle	Healthy	2007	1122	2	A	121	50.68	129168	5003094
VE0704423EC	Spain	Cattle	Healthy	2007	1992	1	B1	123	50.62	205949	5149859
VE0704819EC	Spain	Cattle	Healthy	2007	441	1	B1	148	50.72	101544	5126565
VE0704864EC	Spain	Cattle	Healthy	2007	1145	2	A	190	50.1	90377	5129638
VE0705080EC	Spain	Cattle	Healthy	2007	278	1	B1	152	50.58	110722	5149511
VE0705167EC	Spain	Cattle	Healthy	2007	109	1	B1	90	50.85	148706	5091588
VE0705171EC	Spain	Cattle	Healthy	2007	906	1	B1	104	50.6	160954	4981144
VE0705213EC	Spain	Cattle	Healthy	2007	10	2	A	193	50.7	84494	4993680
VE0800879EC	Spain	Pig	Healthy	2008	10	2	A	255	50.52	61094	5377988
VE0800881EC	Spain	Pig	Healthy	2008	641	1	B1	114	50.71	161069	4989091
VE0800915EC	Spain	Pig	Healthy	2008	614	2	A	183	50.89	67544	4701974
VE0800922EC	Spain	Pig	Healthy	2008	101	1	B1	147	50.51	134428	5443636
VE0800924EC	Spain	Pig	Healthy	2008	542	2	A	100	50.82	105886	4750837
VE0800936EC	Spain	Pig	Healthy	2008	453	1	B1	131	50.68	112024	4997160
VE0800937EC	Spain	Pig	Healthy	2008	10	2	A	123	50.78	104360	4909175
VE0801370EC	Spain	Cattle	Healthy	2008	7459	3	E	103	50.44	201924	5147074
VE0801375EC	Spain	Cattle	Healthy	2008	109	1	B1	105	50.78	135024	5020216
VE0801570EC	Spain	Cattle	Healthy	2008	223	1	B1	309	50.73	55322	5352193
VE0801581EC	Spain	Pig	Healthy	2008	2628	1	B1	95	50.55	161889	5185343
VE0801588EC	Spain	Pig	Healthy	2008	10	2	A	174	50.55	99582	5182166
VE0801662EC	Spain	Cattle	Healthy	2008	3889	2	A	163	50.76	75997	5034096
VE0802046EC	Spain	Cattle	Healthy	2008	3021	2	A	164	50.72	95557	5110895
VE0802075EC	Spain	Cattle	Healthy	2008	10	2	A	156	50.55	78609	5034088
VE0802953EC	Spain	Pig	Healthy	2008	48	2	A	157	50.78	81369	4884098
VE0802961EC	Spain	Pig	Healthy	2008	1086	1	B1	126	50.63	96957	4996255
VE0802998EC	Spain	Pig	Healthy	2008	1081	1	B1	64	50.71	205163	5030760
VE0803001EC	Spain	Pig	Healthy	2008	75	1	B1	106	50.5	189454	5106137
VE0803070EC	Spain	Pig	Healthy	2008	4175	3	E	123	50.46	179784	5230644
VE0803090EC	Spain	Pig	Healthy	2008	-	2	A	133	50.67	103937	4800438
VE0803143EC	Spain	Pig	Healthy	2008	871	2	A	162	50.84	84209	4695425
VE0803145EC	Spain	Pig	Healthy	2008	542	2	A	155	50.83	68716	4690235

VE0803176EC	Spain	Pig	Healthy	2008	-	2	A	105	50.82	116930	4980168
VE0803182EC	Spain	Pig	Healthy	2008	86	1	B1	132	50.58	112285	4868239
ZTA0900668EC	Spain	Cattle	Healthy	2009	1252	1	B1	145	50.83	98863	5026370
ZTA0901077EC	Spain	Cattle	Healthy	2009	906	1	B1	195	50.69	79026	5169300
ZTA0901508EC	Spain	Cattle	Healthy	2009	223	1	B1	252	50.63	70265	5360513
ZTA0901539EC	Spain	Cattle	Healthy	2009	95	4	B2	177	50.57	94568	5252847
ZTA0902026EC	Spain	Pig	Healthy	2009	-	2	A	181	50.77	70286	4855949
ZTA0902079EC	Spain	Cattle	Healthy	2009	58	1	B1	131	50.65	112160	5030340
ZTA0902665EC	Spain	Cattle	Healthy	2009	1326	1	B1	46	50.71	251530	4962925
ZTA0902875EC	Spain	Cattle	Healthy	2009	1665	1	B1	158	50.73	95438	5120151
ZTA0902930EC	Spain	Pig	Healthy	2009	77	2	A	129	50.78	88394	4698223
ZTA0903219EC	Spain	Cattle	Healthy	2009	-	2	A	140	50.66	88320	4842456
ZTA0903229EC	Spain	Pig	Healthy	2009	1716	2	A	141	50.75	106397	4919372
ZTA0903328EC	Spain	Pig	Healthy	2009	10	2	A	141	50.63	105595	4955363
ZTA0903393EC	Spain	Pig	Healthy	2009	542	2	A	132	50.69	106038	4834597
ZTA0903452EC	Spain	Pig	Healthy	2009	43	2	A	91	50.63	292211	4768106
ZTA0903472EC	Spain	Cattle	Healthy	2009	2520	1	B1	173	50.71	74579	5065987
ZTA0903652-2EC	Spain	WB	NA	2009	8184	11	B2	44	50.48	481364	4867543
ZTA0903774EC	Spain	Pig	Healthy	2009	4175	3	E	107	50.5	109115	5071686
ZTA0903844EC	Spain	Cattle	Healthy	2009	56	1	B1	200	50.85	65912	4914978
ZTA0903848EC	Spain	Pig	Healthy	2009	-	1	B1	148	50.7	99191	4782512
ZTA0904060-2EC	Spain	WB	NA	2009	-	4	B2	57	50.52	314923	5173449
ZTA0904095EC	Spain	Cattle	Healthy	2009	109	1	B1	106	50.79	119962	4784441
ZTA0904100EC	Spain	Pig	Healthy	2009	388	1	B1	66	50.61	186022	4759055
ZTA0904262EC	Spain	Pig	Healthy	2009	10	2	A	188	50.83	60204	4692985
ZTA1000144-2EC	Spain	WB	NA	2010	1125	1	B1	42	50.32	276312	5100451
ZTA1100497EC	Spain	Cattle	Healthy	2010	1261	1	B1	125	50.64	112232	5244757
ZTA1100656EC	Spain	Cattle	Healthy	2010	3021	2	A	160	50.67	97845	5315445
ZTA1100804EC	Spain	Cattle	Healthy	2010	164	1	B1	158	50.61	88705	5102411
ZTA1100869EC	Spain	Cattle	Healthy	2011	-	1	B1	148	50.65	117322	5255881
ZTA1101269EC	Spain	Cattle	Healthy	2010	-	1	B1	156	50.55	69356	5012865
ZTA1101318EC	Spain	Cattle	Healthy	2011	-	1	B1	133	50.53	214556	5328024
ZTA1101327EC	Spain	Cattle	Healthy	2011	95	4	B2	115	50.48	139742	5329890
ZTA1101522EC	Spain	Cattle	Healthy	2010	392	1	B1	204	50.7	64014	5291101

ZTA1101529EC	Spain	Cattle	Healthy	2010	-	1	B1	138	50.53	149749	5319869
ZTA1101549EC	Spain	Cattle	Healthy	2011	58	1	B1	241	50.74	65808	5423251
ZTA1101973EC	Spain	Cattle	Healthy	2011	348	1	B1	127	50.74	131066	5166194
ZTA1102157EC	Spain	Cattle	Healthy	2010	-	1	B1	130	50.62	105656	5108183
ZTA1102423EC	Spain	Cattle	Healthy	2011	10	2	A	182	50.7	84864	4889316
ZTA1300319-1EC	Spain	Cattle	Healthy	2013	847	1	B1	91	50.45	173118	5354066
ZTA1300393-1EC	Spain	Cattle	Healthy	2013	109	1	B1	137	50.7	198281	5015805
ZTA1300505-1EC	Spain	Cattle	Healthy	2013	10	2	A	124	50.83	113260	5020054
ZTA1300668-1EC	Spain	Cattle	Healthy	2013	2217	1	C	149	50.71	90881	5325775
ZTA1300768-1EC	Spain	Cattle	Healthy	2013	-	2	A	95	50.65	163207	5141658
ZTA1300954-1EC	Spain	Cattle	Healthy	2013	906	1	B1	139	50.65	96548	5211846
ZTA1301531-1EC	Spain	Cattle	Healthy	2013	56	1	B1	144	50.72	116689	5084134
ZTA1302234-1EC	Spain	Cattle	Healthy	2013	-	1	B1	120	50.64	118545	5174978
ZTA1500170EC	Spain	Pig	Healthy	2015	10	2	A	129	50.59	113521	4692047
ZTA1500171EC	Spain	Pig	Healthy	2015	162	1	B1	86	50.72	193819	4947519
ZTA1500182-1EC	Spain	Cattle	Healthy	2015	7459	3	E	64	50.43	267691	5077860
ZTA1500188EC	Spain	Pig	Healthy	2015	101	1	B1	117	50.54	147039	5120506
ZTA1500195EC	Spain	Pig	Healthy	2015	871	2	A	143	50.94	87112	4648631
ZTA1500196EC	Spain	Pig	Healthy	2015	2325	2	A	117	50.67	198428	4847282
ZTA1500233EC	Spain	Pig	Healthy	2015	34	2	A	87	50.83	188573	4695856
ZTA1500235EC	Spain	Pig	Healthy	2015	93	2	A	123	50.29	141365	5279167
ZTA1500269EC	Spain	Pig	Healthy	2015	215	2	A	125	50.85	105088	4873522
ZTA1500270EC	Spain	Pig	Healthy	2015	154	1	B1	61	50.51	309474	4722224
ZTA1500280EC	Spain	Pig	Healthy	2015	2325	2	A	79	50.72	181675	4780040
ZTA1500311EC	Spain	Pig	Healthy	2015	34	2	A	93	50.76	159868	4731921
ZTA1500328-1EC	Spain	Cattle	Healthy	2015	1308	1	B1	81	50.64	142975	5009761
ZTA1500331-1EC	Spain	Cattle	Healthy	2015	2035	1	B1	83	50.63	133029	4781139
ZTA1500365-1EC	Spain	Cattle	Healthy	2015	327	1	B1	131	50.59	139772	4991325
ZTA1500374EC	Spain	Pig	Healthy	2015	-	2	A	186	50.79	70189	4642205
ZTA1500411-1EC	Spain	Cattle	Healthy	2015	164	1	B1	91	50.54	206483	5033927
ZTA1500426EC	Spain	Pig	Healthy	2015	93	2	A	90	50.43	201421	4949237
ZTA1500428EC	Spain	Pig	Healthy	2015	542	2	A	186	50.85	81295	4737306
ZTA1500446-1EC	Spain	Cattle	Healthy	2015	5289	3	E	94	50.41	316711	5455594
ZTA1500452EC	Spain	Pig	Healthy	2015	86	1	B1	93	50.56	145334	4871184

ZTA1500463EC	Spain	Pig	Healthy	2015	-	1	B1	187	50.62	94616	5163322
ZTA1500467EC	Spain	Pig	Healthy	2015	10	2	A	172	50.63	119501	5088714
ZTA1500525EC	Spain	Pig	Healthy	2015	10	2	A	129	50.71	85248	4829107
ZTA1500527EC	Spain	Pig	Healthy	2015	10	2	A	75	50.61	232587	4849188
ZTA1500580EC	Spain	Pig	Healthy	2015	195	2	A	90	50.58	156504	4794886
ZTA1500594EC	Spain	Pig	Healthy	2015	10	2	A	80	50.67	156638	4653933
ZTA1500630EC	Spain	Pig	Healthy	2015	48	2	A	96	50.75	147060	4660927
ZTA1500770-1EC	Spain	Cattle	Healthy	2015	5973	1	B1	136	50.6	145705	5243321
ZTA1500798EC	Spain	Pig	Healthy	2015	537	4	B2	117	50.39	258511	5322724
ZTA1500815-1EC	Spain	Cattle	Healthy	2015	642	1	B1	99	50.5	135316	5108657
ZTA1500822-1EC	Spain	Cattle	Healthy	2015	56	1	B1	158	50.59	111971	5251434
ZTA1500948-1EC	Spain	Cattle	Healthy	2015	515	3	A	58	50.64	234938	4552971
ZTA1501062-1EC	Spain	Cattle	Healthy	2015	29	1	B1	207	50.34	99571	5619684
ZTA1501068EC	Spain	Pig	Healthy	2015	48	2	A	148	50.78	75119	4747721
ZTA1501098-1EC	Spain	Cattle	Healthy	2015	1727	1	B1	109	50.7	200621	5036476
ZTA1501128-1EC	Spain	Cattle	Healthy	2015	1992	1	B1	158	50.64	109926	5146908
ZTA1501130-1EC	Spain	Cattle	Healthy	2015	109	1	B1	91	50.71	171797	4986540
ZTA1501134-1EC	Spain	Cattle	Healthy	2015	1248	1	B1	85	50.47	133994	4955896
ZTA1501142-1EC	Spain	Cattle	Healthy	2015	20	1	B1	226	50.59	97313	5412801
ZTA1501144-1EC	Spain	Cattle	Healthy	2015	109	1	B1	124	50.66	216483	5251457
ZTA1501147-1EC	Spain	Cattle	Healthy	2015	20	1	B1	165	50.53	129207	5368622
ZTA1501271-1EC	Spain	Cattle	Healthy	2015	-	2	A	122	50.4	109949	5194829
ZTA1501318EC	Spain	Pig	Healthy	2015	10	2	A	145	50.6	126026	4966754
ZTA1501349-1EC	Spain	Cattle	Healthy	2015	1955	5	D	99	50.55	102272	5182461
ZTA1501492EC	Spain	Pig	Healthy	2015	34	2	A	108	50.69	143042	4987098
ZTA1501616EC	Spain	Pig	Healthy	2015	88	9	C	178	50.53	127315	5250053
ZTA1502251EC	Spain	Pig	Healthy	2015	-	2	A	192	50.37	86035	5348381
ZTA1502332EC	Spain	Pig	Healthy	2015	1721	2	A	133	50.69	132228	4958786
ZTA1600785EC	Spain	Chicken	Healthy	2016	752	2	A	208	50.4	108311	5276418
ZTA1600789EC	Spain	Chicken	Healthy	2016	1403	1	B1	241	50.63	72030	4993223
ZTA1600790EC	Spain	Chicken	Healthy	2016	95	4	B2	97	50.56	187475	5162214
ZTA1600801EC	Spain	Chicken	Healthy	2016	10	2	A	125	50.46	107880	5088301
ZTA1600844EC	Spain	Chicken	Healthy	2016	189	2	A	269	50.39	57440	5379752
ZTA1600853EC	Spain	Chicken	Healthy	2016	752	2	A	327	50.06	104980	5710650

ZTA1600857EC	Spain	Chicken	Healthy	2016	-	1	B1	193	50.8	60052	4769096
ZTA1600887EC	Spain	Chicken	Healthy	2016	752	2	A	332	50.51	50681	5267234
ZTA1600908EC	Spain	Chicken	Healthy	2016	10	2	A	182	50.29	84691	5178746
ZTA1601050EC	Spain	Chicken	Healthy	2016	155	1	B1	120	50.57	95918	5104631
ZTA1601086EC	Spain	Chicken	Healthy	2016	997	3	E	146	50.52	103219	5195240
ZTA1601166EC	Spain	Chicken	Healthy	2016	752	2	A	256	50.47	73804	5226217
ZTA1601238EC	Spain	Chicken	Healthy	2016	752	2	A	249	50.22	94536	5503109
ZTA1601365EC	Spain	Chicken	Healthy	2016	5963	1	B1	166	50.72	74854	5004190
ZTA1601556EC	Spain	Chicken	Healthy	2016	752	2	A	266	50.45	66664	5162840
ZTA1601687EC	Spain	Chicken	Healthy	2016	641	1	B1	141	50.47	120332	5155869
ZTA1601769EC	Spain	Chicken	Healthy	2016	752	2	A	222	50.43	102879	5320173
ZTA1601912EC	Spain	Chicken	Healthy	2016	752	2	A	234	50.25	89925	5451666
ZTA1601917EC	Spain	Chicken	Healthy	2016	665	2	A	172	50.75	101387	5145894
ZTA1601942EC	Spain	Chicken	Healthy	2016	752	2	A	184	50.5	97836	5189268
ZTA1601967EC	Spain	Chicken	Healthy	2016	354	13	F	264	50.47	104000	5745393
ZTA1601993EC	Spain	Chicken	Healthy	2016	1011	3	E	106	50.63	126797	5072379
ZTA1601998EC	Spain	Chicken	Healthy	2016	10	2	A	172	50.64	69917	4975565
ZTA1602213EC	Spain	Chicken	Healthy	2016	997	3	E	175	50.38	111369	5364992
ZTA1602246EC	Spain	Chicken	Healthy	2016	-	2	A	143	50.35	122149	5006156
ZTA1602269EC	Spain	Chicken	Healthy	2016	10	2	A	239	50.34	84305	5163017
ZTA1602475EC	Spain	Chicken	Healthy	2016	997	3	E	150	50.47	120710	5222239
ZTA1602677EC	Spain	Chicken	Healthy	2016	997	3	E	129	50.5	125675	5235153

9.2: List reference genomes used for annotating host-associated *k-mers*.

Host	**Genome**
Human	21224_3#267
	15-04719
	21224_3#237
	14-03445
	21ZN-0147-1
Cattle	ZTA1500328-1EC
	IMT33253
	IMT13376
	IMT30910
Chicken	14756
	21225_2#181
	Sap638

9.3: *E. coli*'s genes associated with human. cattle and chicken host-species.

Host	locus_tag	gene	Reference	# *k-mers*	maxp	avg_af	avg_maf	avg_beta
Human	IIDENDNK_04903	nanT_2	21224_3#267	1655	12.95	0.13	0.13	0.46
Human	IIDENDNK_04034	essD_3	21224_3#267	1043	17.73	0.33	0.33	0.38
Human	IIDENDNK_04750	ycgV_2	21224_3#267	924	18.45	0.16	0.16	0.45
Human	IIDENDNK_04905	nanA_2	21224_3#267,15-04719	924	12.72	0.13	0.13	0.46
Human	IIDENDNK_04897	nanS_3	21224_3#267	902	17.35	0.14	0.14	0.46
Human	IIDENDNK_04898	nanR_2	21224_3#267	886	14.40	0.13	0.13	0.46
Human	IIDENDNK_05042	IIDENDNK_05042	21224_3#267	803	13.19	0.32	0.32	0.34
Human	IIDENDNK_04900	nanM_2	21224_3#267,15-04719	754	12.28	0.13	0.13	0.46
Human	IIDENDNK_05112	IIDENDNK_05112	21224_3#267	742	15.04	0.28	0.28	0.33
Human	IIDENDNK_04902	axeA1_2	21224_3#267,15-04719	680	16.15	0.13	0.13	0.46
Human	IIDENDNK_04904	nanK_2	21224_3#267	642	13.51	0.13	0.13	0.46
Human	IIDENDNK_04031	rrrQ_2	21224_3#267	579	16.34	0.31	0.31	0.36
Human	IIDENDNK_04996	IIDENDNK_04996	21224_3#267	569	15.98	0.30	0.30	0.35
Human	IIDENDNK_03988	intE_2	21224_3#267	543	13.24	0.25	0.25	0.37
Human	IIDENDNK_05036	rrrQ_4	21224_3#267	519	16.34	0.31	0.31	0.36
Human	IIDENDNK_04997	mec	21224_3#267	492	13.83	0.31	0.31	0.35
Human	IIDENDNK_05001	IIDENDNK_05001	21224_3#267	490	14.63	0.30	0.30	0.32
Human	IIDENDNK_05000	ynaA_3	21224_3#267	464	12.63	0.29	0.29	0.32
Human	IIDENDNK_05046	IIDENDNK_05046	21224_3#267	463	15.64	0.30	0.30	0.36
Human	IIDENDNK_04899	axeA1_1	21224_3#267	454	17.62	0.13	0.13	0.46
Human	IIDENDNK_04998	IIDENDNK_04998	21224_3#267	425	15.64	0.31	0.31	0.35
Human	IIDENDNK_04901	nanC_2	21224_3#267	405	14.31	0.13	0.13	0.46
Human	BNJMMDAK_03143	ycgV_1	15-04719	392	12.42	0.05	0.05	0.66
Human	IIDENDNK_04779	IIDENDNK_04779	21224_3#267	304	13.47	0.12	0.12	0.43
Human	IIDENDNK_05033	rzpD_5	21224_3#267,15-04719	285	13.97	0.25	0.25	0.37
Human	IIDENDNK_05002	IIDENDNK_05002	21224_3#267	262	12.51	0.27	0.27	0.32
Human	IIDENDNK_04035	nanS_2	21224_3#267,15-04719	257	17.35	0.26	0.26	0.37
Human	IIDENDNK_04756	IIDENDNK_04756	21224_3#267	237	11.48	0.15	0.15	0.46
Human	IIDENDNK_05053	IIDENDNK_05053	21224_3#267	224	14.03	0.40	0.40	0.30

Human	IIDENDNK_04749	IIDENDNK_04749	21224_3#267	223	13.13	0.15	0.15	0.46
Human	ALHKBHBA_01467	ALHKBHBA_01467	21224_3#237	205	12.90	0.30	0.30	0.32
Human	IIDENDNK_05045	IIDENDNK_05045	21224_3#267	201	12.16	0.25	0.25	0.33
Human	IIDENDNK_05054	IIDENDNK_05054	21224_3#267	198	15.46	0.30	0.30	0.32
Human	IIDENDNK_05051	IIDENDNK_05051	21224_3#267	194	15.09	0.24	0.24	0.33
Human	IIDENDNK_04999	IIDENDNK_04999	21224_3#267	188	12.16	0.26	0.26	0.33
Human	IIDENDNK_05089	IIDENDNK_05089	21224_3#267	178	13.17	0.21	0.21	0.35
Human	IIDENDNK_05012	IIDENDNK_05012	21224_3#267	173	12.71	0.27	0.27	0.28
Human	IIDENDNK_04745	IIDENDNK_04745	21224_3#267	156	13.24	0.13	0.13	0.47
Human	IIDENDNK_05055	IIDENDNK_05055	21224_3#267	151	11.71	0.31	0.31	0.32
Human	IIDENDNK_05044	IIDENDNK_05044	21224_3#267	119	12.26	0.29	0.29	0.32
Human	IIDENDNK_00715	yfjI_1	21224_3#267	115	14.15	0.14	0.14	0.47
Human	BNJMMDAK_05122	yhdJ_7	15-04719	99	13.28	0.24	0.24	0.34
Human	IIDENDNK_04039	yhdJ_2	21224_3#267,21224_3#237	97	11.86	0.29	0.29	0.34
Human	IIDENDNK_04939	IIDENDNK_04939	21224_3#267	96	12.62	0.26	0.26	0.28
Human	IIDENDNK_00716	IIDENDNK_00716	21224_3#267	88	10.85	0.13	0.13	0.48
Human	BNJMMDAK_05103	yhdJ_6	15-04719	81	10.31	0.23	0.23	0.33
Human	IIDENDNK_05043	lomR_1	21224_3#267,21224_3#237	80	12.33	0.19	0.19	0.38
Human	BNJMMDAK_04635	rep_2	15-04719	76	10.19	0.04	0.04	0.65
Human	IIDENDNK_05057	IIDENDNK_05057	21224_3#267	71	11.51	0.23	0.23	0.33
Human	IIDENDNK_04776	ybcY	21224_3#267	70	10.27	0.15	0.15	0.40
Human	IIDENDNK_05090	IIDENDNK_05090	21224_3#267	68	12.11	0.28	0.28	0.32
Human	IIDENDNK_04774	IIDENDNK_04774	21224_3#267	62	9.89	0.12	0.12	0.43
Human	BNJMMDAK_05082	yhdJ_4	15-04719,21224_3#237	60	13.28	0.25	0.25	0.34
Human	IIDENDNK_00713	flu	21224_3#267	58	12.97	0.18	0.18	0.45
Human	BNJMMDAK_05205	rzpD_4	15-04719	58	11.94	0.28	0.28	0.37
Human	BNJMMDAK_05403	rzpD_6	15-04719	58	11.94	0.28	0.28	0.37
Human	ALHKBHBA_01465	ALHKBHBA_01465	21224_3#237	57	10.01	0.24	0.24	0.32
Human	IIDENDNK_04030	rzpD_3	21224_3#267	56	13.97	0.28	0.28	0.36
Human	IIDENDNK_04805	insF-1_2	21224_3#267	55	12.52	0.30	0.30	0.36
Human	IIDENDNK_05074	IIDENDNK_05074	21224_3#267	55	12.16	0.17	0.17	0.42
Human	IIDENDNK_05034	IIDENDNK_05034	21224_3#267	51	11.14	0.22	0.22	0.37

Human	IIDENDNK_04934	IIDENDNK_04934	21224_3#267	49	14.04	0.18	0.18	0.37
Human	IIDENDNK_04938	IIDENDNK_04938	21224_3#267	45	12.71	0.29	0.29	0.27
Human	BNJMMDAK_05096	iraM	15-04719	40	10.76	0.20	0.20	0.36
Human	BNJMMDAK_04153	BNJMMDAK_04153	15-04719	39	11.95	0.05	0.05	0.56
Human	BNJMMDAK_01928	rzpD_2	15-04719	38	11.94	0.32	0.32	0.37
Human	BNJMMDAK_03600	yfjQ_3	15-04719	38	9.42	0.04	0.04	0.65
Human	IIDENDNK_05035	IIDENDNK_05035	21224_3#267	35	13.24	0.25	0.25	0.35
Human	IIDENDNK_04912	efeU_2	21224_3#267	34	12.33	0.22	0.22	0.36
Human	BNJMMDAK_01933	nanS_1	15-04719,21224_3#237	32	11.79	0.25	0.25	0.39
Human	BNJMMDAK_05138	BNJMMDAK_05138	15-04719	30	10.41	0.29	0.29	0.32
Human	IIDENDNK_04933	IIDENDNK_04933	21224_3#267	28	16.03	0.16	0.16	0.37
Human	BNJMMDAK_05230	BNJMMDAK_05230	15-04719	27	11.39	0.11	0.11	0.48
Human	IIDENDNK_03864	IIDENDNK_03864	21224_3#267	27	11.37	0.34	0.34	0.31
Human	IIDENDNK_04798	IIDENDNK_04798	21224_3#267	26	10.78	0.35	0.35	0.31
Human	BNJMMDAK_05197	BNJMMDAK_05197	15-04719	24	11.39	0.11	0.11	0.47
Human	BNJMMDAK_04626	BNJMMDAK_04626	15-04719	23	12.43	0.07	0.07	0.58
Human	IIDENDNK_05037	ydfR_3	21224_3#267	22	10.96	0.26	0.26	0.35
Human	IIDENDNK_04033	ydfR_2	21224_3#267	21	10.96	0.26	0.26	0.35
Human	IIDENDNK_03989	ompW	21224_3#267	21	10.89	0.24	0.24	0.37
Human	IIDENDNK_04936	IIDENDNK_04936	21224_3#267	20	12.94	0.19	0.19	0.38
Human	ALHKBHBA_01466	ALHKBHBA_01466	21224_3#237	20	10.12	0.22	0.22	0.32
Human	IIDENDNK_04753	iucC	21224_3#267	18	11.91	0.15	0.15	0.46
Human	IIDENDNK_05101	IIDENDNK_05101	21224_3#267	18	10.03	0.29	0.29	0.34
Human	BNJMMDAK_05292	BNJMMDAK_05292	15-04719	17	13.90	0.33	0.33	0.37
Human	BNJMMDAK_05140	BNJMMDAK_05140	15-04719	17	13.90	0.33	0.33	0.37
Human	BNJMMDAK_05102	yhdJ_5	15-04719	17	13.28	0.29	0.29	0.34
Human	IIDENDNK_00717	IIDENDNK_00717	21224_3#267	17	10.44	0.13	0.13	0.48
Human	BNJMMDAK_02617	BNJMMDAK_02617	15-04719	16	10.35	0.24	0.24	0.33
Human	IIDENDNK_04935	IIDENDNK_04935	21224_3#267	15	14.06	0.18	0.18	0.37
Human	IIDENDNK_04775	tfaX	21224_3#267	15	12.57	0.15	0.15	0.41
Human	BNJMMDAK_05353	BNJMMDAK_05353	15-04719	15	10.52	0.18	0.18	0.42
Human	BNJMMDAK_01932	BNJMMDAK_01932	15-04719	15	10.52	0.18	0.18	0.42

Human	BNJMMDAK_05198	BNJMMDAK_05198	15-04719	15	10.52	0.18	0.18	0.42
Human	BNJMMDAK_05231	BNJMMDAK_05231	15-04719	15	10.52	0.18	0.18	0.42
Human	IIDENDNK_00694	gfcE	21224_3#267	14	11.26	0.29	0.29	0.41
Human	IIDENDNK_04754	iucB	21224_3#267	14	10.49	0.22	0.22	0.37
Human	IIDENDNK_04915	macB_2	21224_3#267	13	12.35	0.23	0.23	0.36
Human	BNJMMDAK_04625	BNJMMDAK_04625	15-04719	13	11.98	0.06	0.06	0.57
Human	IIDENDNK_04851	IIDENDNK_04851	21224_3#267	13	10.71	0.22	0.22	0.38
Human	IIDENDNK_04920	agp_2	21224_3#267	13	10.63	0.17	0.17	0.36
Human	GHIANLFP_01018	tfaD_1	21ZN-0147-1	13	10.37	0.22	0.22	0.34
Human	BNJMMDAK_04629	BNJMMDAK_04629	15-04719	12	10.45	0.09	0.09	0.52
Human	IIDENDNK_04917	ybbA_2	21224_3#267	12	10.22	0.17	0.17	0.35
Human	IIDENDNK_04916	macB_3	21224_3#267	11	14.08	0.25	0.25	0.36
Human	ALHKBHBA_01457	stfR_2	21224_3#237	11	10.50	0.15	0.15	0.40
Human	BNJMMDAK_04621	BNJMMDAK_04621	15-04719	10	13.24	0.11	0.11	0.51
Human	IIDENDNK_00905	rep_1	21224_3#267	10	10.63	0.11	0.11	0.44
Human	IIDENDNK_04919	IIDENDNK_04919	21224_3#267	9	15.94	0.24	0.24	0.35
Human	IIDENDNK_04251	IIDENDNK_04251	21224_3#267	9	11.55	0.24	0.24	0.31
Human	IIDENDNK_00699	IIDENDNK_00699	21224_3#267	9	10.74	0.16	0.16	0.48
Human	IIDENDNK_04918	resA	21224_3#267	9	10.58	0.21	0.21	0.34
Human	IIDENDNK_05024	IIDENDNK_05024	21224_3#267	9	10.54	0.19	0.19	0.41
Human	IIDENDNK_00714	yeeP_1	21224_3#267	9	10.29	0.16	0.16	0.44
Human	IIDENDNK_05052	IIDENDNK_05052	21224_3#267	9	10.05	0.37	0.37	0.30
Human	BNJMMDAK_01925	BNJMMDAK_01925	15-04719	9	10.04	0.05	0.05	0.65
Human	IIDENDNK_01565	hyfI	21224_3#267	8	16.00	0.30	0.30	0.47
Human	BNJMMDAK_04627	BNJMMDAK_04627	15-04719	8	11.22	0.07	0.07	0.59
Human	IIDENDNK_04911	nqrC	21224_3#267	8	11.06	0.24	0.24	0.35
Human	IIDENDNK_04803	IIDENDNK_04803	21224_3#267	8	10.75	0.34	0.34	0.30
Human	IIDENDNK_05027	IIDENDNK_05027	21224_3#267	8	10.70	0.18	0.18	0.42
Human	IIDENDNK_05059	IIDENDNK_05059	21224_3#267	8	10.38	0.17	0.17	0.35
Human	ALHKBHBA_01469	ALHKBHBA_01469	21224_3#237	8	10.00	0.23	0.23	0.32
Human	IIDENDNK_04910	stoA	21224_3#267	7	13.59	0.25	0.25	0.33
Human	IIDENDNK_03654	betT_2	21224_3#267	7	12.46	0.39	0.39	0.30

Human	BNJMMDAK_05034	BNJMMDAK_05034	15-04719	7	12.23	0.23	0.23	0.41	
Human	BNJMMDAK_04613	BNJMMDAK_04613	15-04719	7	11.36	0.07	0.07	0.53	
Human	IIDENDNK_04281	traM	21224_3#267	7	10.73	0.29	0.29	0.34	
Human	IIDENDNK_04914	IIDENDNK_04914	21224_3#267	7	10.70	0.20	0.20	0.35	
Human	BNJMMDAK_04616	hcpA	15-04719	7	9.92	0.06	0.06	0.54	
Human	BNJMMDAK_04620	vgrG1_3	15-04719,21224_3#237	6	12.92	0.12	0.12	0.49	
Human	IIDENDNK_04081	flhA_3	21224_3#267	6	11.53	0.36	0.36	0.36	
Human	IIDENDNK_01110	yaiU	21224_3#267	6	11.45	0.29	0.29	0.39	
Human	IIDENDNK_03288	IIDENDNK_03288	21224_3#267	6	11.06	0.29	0.29	0.33	
Human	IIDENDNK_04755	iucA	21224_3#267	6	10.87	0.23	0.23	0.38	
Human	IIDENDNK_00670	yghJ	21224_3#267	6	10.37	0.30	0.30	0.36	
Human	IIDENDNK_01345	IIDENDNK_01345	21224_3#267	6	10.01	0.21	0.21	0.43	
Human	IIDENDNK_04967	IIDENDNK_04967	21224_3#267	5	16.41	0.23	0.23	0.34	
Human	IIDENDNK_03875	rspA_2	21224_3#267	5	12.10	0.34	0.34	0.33	
Human	IIDENDNK_03652	IIDENDNK_03652	21224_3#267	5	11.85	0.39	0.39	0.29	
Human	BNJMMDAK_04631	BNJMMDAK_04631	15-04719	5	10.65	0.07	0.07	0.53	
Human	IIDENDNK_03110	wcaI	21224_3#267	5	10.48	0.16	0.16	0.44	
Human	IIDENDNK_00749	hsdM_1	21224_3#267	5	10.28	0.30	0.30	0.34	
Human	IIDENDNK_03837	yeeJ_6	21224_3#267	5	10.26	0.22	0.22	0.42	
Human	IIDENDNK_00698	IIDENDNK_00698	21224_3#267	5	10.18	0.17	0.17	0.45	
Human	IIDENDNK_04804	insC-1_3	21224_3#267	5	9.93	0.29	0.29	0.30	
Human	BNJMMDAK_04615	yfiB_1	15-04719	5	9.72	0.05	0.05	0.61	
Human	IIDENDNK_03729	yadN	21224_3#267	4	15.98	0.39	0.39	0.41	
Human	IIDENDNK_04265	IIDENDNK_04265	21224_3#267	4	12.95	0.15	0.15	0.47	
Human	IIDENDNK_05022	IIDENDNK_05022	21224_3#267	4	11.06	0.19	0.19	0.43	
Human	IIDENDNK_00744	IIDENDNK_00744	21224_3#267	4	11.01	0.31	0.31	0.36	
Human	IIDENDNK_05026	IIDENDNK_05026	21224_3#267	4	11.01	0.20	0.20	0.41	
Human	IIDENDNK_04921	agp_3	21224_3#267	4	10.74	0.26	0.26	0.36	
Human	IIDENDNK_04139	rlmM	21224_3#267	4	10.70	0.30	0.30	0.34	
Human	IIDENDNK_03321	hemS	21224_3#267	4	10.40	0.48	0.48	0.46	
Human	IIDENDNK_02125	rrrQ_1	21224_3#267	4	10.39	0.37	0.37	0.33	
Human	GHIANLFP_01002	GHIANLFP_01002	21ZN-0147-1	4	10.27	0.26	0.26	0.34	

Human	BNJMMDAK_04617	clpB_1	15-04719	4	10.03	0.17	0.17	0.45
Human	ALHKBHBA_03039	intE	21224_3#237	4	9.98	0.18	0.18	0.41
Human	IIDENDNK_05010	mobA_2	21224_3#267	4	9.90	0.27	0.27	0.27
Human	IIDENDNK_05102	yghO_2	21224_3#267	4	9.77	0.14	0.14	0.36
Human	IIDENDNK_04257	IIDENDNK_04257	21224_3#267	3	13.99	0.24	0.24	0.33
Human	BNJMMDAK_05017	BNJMMDAK_05017	15-04719	3	12.39	0.12	0.12	0.44
Human	IIDENDNK_04568	recE_2	21224_3#267	3	12.28	0.19	0.19	0.44
Human	IIDENDNK_04266	traC	21224_3#267	3	11.94	0.37	0.37	0.32
Human	IIDENDNK_04972	IIDENDNK_04972	21224_3#267	3	11.86	0.34	0.34	0.33
Human	IIDENDNK_05073	IIDENDNK_05073	21224_3#267	3	11.60	0.15	0.15	0.45
Human	IIDENDNK_04270	traV	21224_3#267	3	11.03	0.13	0.13	0.44
Human	BNJMMDAK_04628	BNJMMDAK_04628	15-04719	3	10.96	0.05	0.05	0.61
Human	BNJMMDAK_05028	yadA_6	15-04719	3	10.93	0.24	0.24	0.35
Human	IIDENDNK_00158	pheT	21224_3#267	3	10.71	0.32	0.32	0.33
Human	BNJMMDAK_04624	BNJMMDAK_04624	15-04719	3	10.65	0.05	0.05	0.61
Human	BNJMMDAK_05278	BNJMMDAK_05278	15-04719	3	10.62	0.27	0.27	0.40
Human	IIDENDNK_02047	yeeJ_2	21224_3#267	3	10.58	0.43	0.43	0.32
Human	IIDENDNK_03466	fadD_3	21224_3#267	3	10.58	0.51	0.49	0.30
Human	IIDENDNK_04778	ydfN	21224_3#267	3	10.51	0.11	0.11	0.41
Human	IIDENDNK_00747	IIDENDNK_00747	21224_3#267	3	10.48	0.23	0.23	0.36
Human	IIDENDNK_04907	IIDENDNK_04907	21224_3#267	3	10.36	0.25	0.25	0.36
Human	IIDENDNK_00686	malK_1	21224_3#267	3	10.31	0.28	0.28	0.33
Human	IIDENDNK_04746	insF-1_1	21224_3#267	3	10.20	0.52	0.48	0.27
Human	IIDENDNK_02877	arpA_3	21224_3#267	3	10.07	0.38	0.38	0.32
Human	IIDENDNK_00117	ynjC	21224_3#267	3	10.03	0.43	0.43	0.31
Human	IIDENDNK_02842	kup	21224_3#267	3	9.92	0.28	0.28	0.31
Human	BNJMMDAK_02573	ydfN_2	15-04719	3	9.77	0.04	0.04	0.65
Human	IIDENDNK_03355	bcsB	21224_3#267	3	9.76	0.13	0.13	0.41
Human	BNJMMDAK_04154	BNJMMDAK_04154	15-04719	3	9.65	0.06	0.06	0.52
Human	IIDENDNK_00051	rlmA	21224_3#267	2	15.07	0.38	0.38	0.38
Human	IIDENDNK_00648	gss	21224_3#267	2	14.77	0.19	0.19	0.46
Human	IIDENDNK_01832	tmk	21224_3#267	2	13.40	0.38	0.38	0.40

Human	IIDENDNK_02999	aroC	21224_3#267	2	13.40	0.38	0.38	0.40
Human	IIDENDNK_04246	traD	21224_3#267	2	13.26	0.27	0.27	0.34
Human	IIDENDNK_04260	IIDENDNK_04260	21224_3#267	2	12.52	0.24	0.24	0.31
Human	IIDENDNK_00941	psuK_1	21224_3#267	2	12.46	0.16	0.16	0.49
Human	BNJMMDAK_01952	BNJMMDAK_01952	15-04719	2	12.23	0.14	0.14	0.42
Human	IIDENDNK_01507	yphD	21224_3#267	2	12.20	0.19	0.19	0.38
Human	IIDENDNK_04742	IIDENDNK_04742	21224_3#267	2	11.64	0.17	0.17	0.45
Human	BNJMMDAK_04638	BNJMMDAK_04638	15-04719	2	11.61	0.11	0.11	0.41
Human	IIDENDNK_02927	yeeJ_3	21224_3#267	2	11.44	0.39	0.39	0.35
Human	IIDENDNK_00938	yeiI_1	21224_3#267	2	11.42	0.38	0.38	0.34
Human	IIDENDNK_01554	purN	21224_3#267	2	11.35	0.23	0.23	0.43
Human	IIDENDNK_04937	IIDENDNK_04937	21224_3#267	2	11.26	0.34	0.34	0.39
Human	IIDENDNK_02252	yrhB	21224_3#267	2	11.20	0.37	0.37	0.34
Human	IIDENDNK_04968	IIDENDNK_04968	21224_3#267	2	11.20	0.30	0.30	0.36
Human	IIDENDNK_02342	yicI_1	21224_3#267	2	11.18	0.22	0.22	0.39
Human	IIDENDNK_04293	xylF	21224_3#267	2	11.17	0.19	0.19	0.50
Human	IIDENDNK_04789	IIDENDNK_04789	21224_3#267	2	11.13	0.10	0.10	0.39
Human	IIDENDNK_04790	IIDENDNK_04790	21224_3#267	2	11.13	0.10	0.10	0.39
Human	BNJMMDAK_04612	BNJMMDAK_04612	15-04719	2	11.05	0.07	0.07	0.54
Human	IIDENDNK_00916	pduB	21224_3#267	2	10.98	0.18	0.18	0.32
Human	IIDENDNK_00899	IIDENDNK_00899	21224_3#267	2	10.94	0.19	0.19	0.37
Human	BNJMMDAK_04614	BNJMMDAK_04614	15-04719	2	10.93	0.12	0.12	0.51
Human	IIDENDNK_05009	IIDENDNK_05009	21224_3#267	2	10.75	0.32	0.32	0.30
Human	BNJMMDAK_05344	BNJMMDAK_05344	15-04719	2	10.74	0.09	0.09	0.41
Human	IIDENDNK_05025	IIDENDNK_05025	21224_3#267	2	10.72	0.16	0.16	0.47
Human	IIDENDNK_00849	IIDENDNK_00849	21224_3#267	2	10.71	0.11	0.11	0.42
Human	BNJMMDAK_03626	emrD	15-04719	2	10.69	0.07	0.07	0.43
Human	ALHKBHBA_04634	ALHKBHBA_04634	21224_3#237	2	10.61	0.04	0.04	0.65
Human	IIDENDNK_04558	yfdO_3	21224_3#267	2	10.61	0.40	0.40	0.32
Human	IIDENDNK_04535	IIDENDNK_04535	21224_3#267	2	10.58	0.24	0.24	0.33
Human	IIDENDNK_00004	aspS	21224_3#267	2	10.54	0.37	0.37	0.49
Human	IIDENDNK_02104	yfdS	21224_3#267	2	10.47	0.14	0.14	0.44

Human	IIDENDNK_04722	IIDENDNK_04722	21224_3#267	2	10.45	0.16	0.16	0.36
Human	IIDENDNK_02176	nirC	21224_3#267	2	10.36	0.10	0.10	0.49
Human	IIDENDNK_00485	mtr	21224_3#267	2	10.34	0.33	0.33	0.34
Human	IIDENDNK_00692	IIDENDNK_00692	21224_3#267	2	10.31	0.36	0.36	0.41
Human	BNJMMDAK_02555	BNJMMDAK_02555	15-04719	2	10.31	0.09	0.09	0.44
Human	IIDENDNK_04793	IIDENDNK_04793	21224_3#267	2	10.30	0.28	0.28	0.33
Human	IIDENDNK_02590	ygeQ	21224_3#267	2	10.24	0.17	0.17	0.38
Human	IIDENDNK_05068	papA	21224_3#267	2	10.23	0.16	0.16	0.41
Human	IIDENDNK_05048	stfR	21224_3#267	2	10.20	0.37	0.37	0.38
Human	IIDENDNK_03987	ydfE	21224_3#267	2	10.18	0.23	0.23	0.37
Human	IIDENDNK_04906	IIDENDNK_04906	21224_3#267	2	10.16	0.16	0.16	0.41
Human	IIDENDNK_04751	cirA_5	21224_3#267	2	10.13	0.15	0.15	0.44
Human	BNJMMDAK_04623	BNJMMDAK_04623	15-04719	2	10.10	0.06	0.06	0.54
Human	IIDENDNK_02695	intB_3	21224_3#267	2	10.08	0.21	0.21	0.38
Human	IIDENDNK_04713	IIDENDNK_04713	21224_3#267	2	10.07	0.27	0.27	0.33
Human	BNJMMDAK_04630	BNJMMDAK_04630	15-04719	2	10.07	0.05	0.05	0.57
Human	IIDENDNK_03231	emrB_2	21224_3#267	2	10.06	0.50	0.50	0.34
Human	IIDENDNK_03845	IIDENDNK_03845	21224_3#267	2	10.01	0.32	0.32	0.28
Human	IIDENDNK_01272	yohF	21224_3#267	2	9.97	0.36	0.36	0.39
Human	IIDENDNK_03470	entE_3	21224_3#267	2	9.95	0.56	0.44	0.30
Human	IIDENDNK_02638	fau	21224_3#267	2	9.95	0.21	0.21	0.42
Human	IIDENDNK_03836	IIDENDNK_03836	21224_3#267	2	9.93	0.57	0.43	0.28
Human	IIDENDNK_04913	tpd	21224_3#267	2	9.93	0.18	0.18	0.36
Human	ALHKBHBA_04625	ALHKBHBA_04625	21224_3#237	2	9.90	0.05	0.05	0.51
Human	BNJMMDAK_04880	ydcT	15-04719	2	9.89	0.10	0.10	0.40
Human	BNJMMDAK_01919	BNJMMDAK_01919	15-04719	2	9.89	0.14	0.14	0.39
Human	IIDENDNK_03295	IIDENDNK_03295	21224_3#267	2	9.88	0.34	0.34	0.31
Human	BNJMMDAK_00461	BNJMMDAK_00461	15-04719	2	9.88	0.37	0.37	0.28
Human	BNJMMDAK_04634	BNJMMDAK_04634	15-04719	2	9.87	0.05	0.05	0.62
Human	BNJMMDAK_01957	BNJMMDAK_01957	15-04719	2	9.87	0.06	0.06	0.57
Human	IIDENDNK_03653	IIDENDNK_03653	21224_3#267	2	9.86	0.35	0.35	0.28
Human	IIDENDNK_03831	IIDENDNK_03831	21224_3#267	2	9.83	0.23	0.23	0.33

Human	BNJMMDAK_01965	BNJMMDAK_01965	15-04719	2	9.82	0.05	0.05	0.56
Human	BNJMMDAK_01964	kilR_2	15-04719	2	9.82	0.05	0.05	0.56
Human	IIDENDNK_00689	IIDENDNK_00689	21224_3#267	2	9.79	0.14	0.14	0.36
Human	IIDENDNK_00072	yeaW	21224_3#267	2	9.75	0.16	0.16	0.41
Human	IIDENDNK_04932	IIDENDNK_04932	21224_3#267	2	9.72	0.12	0.12	0.38
Human	IIDENDNK_03913	ybfB	21224_3#267	2	9.66	0.17	0.17	0.40
Human	BNJMMDAK_00478	BNJMMDAK_00478	15-04719	2	9.63	0.20	0.20	0.40
Human	BNJMMDAK_01926	BNJMMDAK_01926	15-04719	2	9.40	0.04	0.04	0.65
Human	IIDENDNK_03224	ogt	21224_3#267	1	13.39	0.26	0.26	0.33
Human	IIDENDNK_03229	yeaM_2	21224_3#267	1	12.99	0.51	0.49	0.43
Human	IIDENDNK_01236	yeiR	21224_3#267	1	12.89	0.38	0.38	0.35
Human	IIDENDNK_01104	IIDENDNK_01104	21224_3#267	1	12.74	0.21	0.21	0.45
Human	IIDENDNK_04532	topB_2	21224_3#267	1	12.66	0.33	0.33	0.47
Human	HILLNCNG_01987	mleN_1	14-03445	1	12.29	0.12	0.12	0.45
Human	IIDENDNK_04965	srpC	21224_3#267	1	12.21	0.52	0.48	0.34
Human	IIDENDNK_05007	IIDENDNK_05007	21224_3#267	1	12.20	0.21	0.21	0.37
Human	IIDENDNK_01977	elfG	21224_3#267	1	12.13	0.16	0.16	0.48
Human	IIDENDNK_04343	ybgQ	21224_3#267	1	12.08	0.17	0.17	0.43
Human	IIDENDNK_04231	hrpA	21224_3#267	1	12.04	0.32	0.32	0.40
Human	IIDENDNK_04523	virD4	21224_3#267	1	11.94	0.36	0.36	0.32
Human	BNJMMDAK_05404	rnaJ	15-04719	1	11.89	0.07	0.07	0.48
Human	IIDENDNK_00792	mpl	21224_3#267	1	11.87	0.25	0.25	0.39
Human	IIDENDNK_03996	clsA	21224_3#267	1	11.86	0.37	0.37	0.33
Human	IIDENDNK_03006	yfcJ	21224_3#267	1	11.71	0.37	0.37	0.32
Human	IIDENDNK_03468	IIDENDNK_03468	21224_3#267	1	11.62	0.54	0.46	0.32
Human	BNJMMDAK_05079	tolA_2	15-04719	1	11.55	0.13	0.13	0.41
Human	IIDENDNK_04282	IIDENDNK_04282	21224_3#267	1	11.45	0.28	0.28	0.39
Human	IIDENDNK_04852	IIDENDNK_04852	21224_3#267	1	11.16	0.09	0.09	0.48
Human	IIDENDNK_04925	IIDENDNK_04925	21224_3#267	1	11.13	0.16	0.16	0.44
Human	BNJMMDAK_05172	BNJMMDAK_05172	15-04719	1	11.07	0.16	0.16	0.35
Human	BNJMMDAK_05136	BNJMMDAK_05136	15-04719	1	11.05	0.22	0.22	0.37
Human	IIDENDNK_04977	IIDENDNK_04977	21224_3#267	1	11.00	0.29	0.29	0.36

Human	IIDENDNK_02614	ygfT	21224_3#267	1	10.96	0.32	0.32	0.44
Human	IIDENDNK_01719	yabP_2	21224_3#267	1	10.75	0.40	0.40	0.33
Human	IIDENDNK_02107	yfdP	21224_3#267	1	10.74	0.33	0.33	0.41
Human	BNJMMDAK_04976	yadA_4	15-04719	1	10.73	0.05	0.05	0.62
Human	IIDENDNK_01147	menE	21224_3#267	1	10.72	0.17	0.17	0.45
Human	IIDENDNK_05058	IIDENDNK_05058	21224_3#267	1	10.72	0.26	0.26	0.34
Human	IIDENDNK_04108	IIDENDNK_04108	21224_3#267	1	10.70	0.35	0.35	0.33
Human	BNJMMDAK_05211	rhsD_5	15-04719	1	10.64	0.07	0.07	0.58
Human	IIDENDNK_00892	intB_2	21224_3#267	1	10.62	0.48	0.48	0.30
Human	IIDENDNK_01354	qmcA	21224_3#267	1	10.55	0.43	0.43	0.37
Human	BNJMMDAK_05204	dam_2	15-04719	1	10.49	0.09	0.09	0.43
Human	IIDENDNK_04974	elfC_2	21224_3#267	1	10.48	0.37	0.37	0.33
Human	IIDENDNK_01909	efeU_1	21224_3#267	1	10.48	0.58	0.42	0.35
Human	IIDENDNK_04245	traI	21224_3#267	1	10.45	0.38	0.38	0.31
Human	BNJMMDAK_02570	BNJMMDAK_02570	15-04719	1	10.44	0.35	0.35	0.30
Human	IIDENDNK_02259	ugpB	21224_3#267	1	10.42	0.16	0.16	0.41
Human	BNJMMDAK_03586	BNJMMDAK_03586	15-04719	1	10.41	0.12	0.12	0.40
Human	BNJMMDAK_00731	yghF	15-04719	1	10.40	0.14	0.14	0.43
Human	IIDENDNK_02212	yhgF	21224_3#267	1	10.40	0.49	0.49	0.48
Human	IIDENDNK_03173	pgpB	21224_3#267	1	10.40	0.49	0.49	0.48
Human	BNJMMDAK_02140	BNJMMDAK_02140	15-04719	1	10.39	0.30	0.30	0.32
Human	IIDENDNK_02312	ybhR	21224_3#267	1	10.36	0.28	0.28	0.35
Human	IIDENDNK_04250	IIDENDNK_04250	21224_3#267	1	10.33	0.62	0.38	0.36
Human	BNJMMDAK_05006	kbl_3	15-04719	1	10.33	0.14	0.14	0.46
Human	IIDENDNK_03851	nohB	21224_3#267	1	10.33	0.32	0.32	0.31
Human	IIDENDNK_02004	fucA_1	21224_3#267	1	10.31	0.42	0.42	0.31
Human	IIDENDNK_03283	ydaY	21224_3#267	1	10.30	0.14	0.14	0.36
Human	IIDENDNK_00838	aidB	21224_3#267	1	10.30	0.38	0.38	0.49
Human	IIDENDNK_04402	mfpA	21224_3#267	1	10.29	0.31	0.31	0.29
Human	IIDENDNK_04608	ubiE_1	21224_3#267	1	10.28	0.51	0.49	0.49
Human	IIDENDNK_04401	rhsD_4	21224_3#267	1	10.25	0.32	0.32	0.35
Human	IIDENDNK_03727	htrE	21224_3#267	1	10.24	0.15	0.15	0.43

Human	IIDENDNK_00897	lhr_2	21224_3#267	1	10.21	0.39	0.39	0.29
Human	IIDENDNK_01163	yfaU_1	21224_3#267	1	10.21	0.31	0.31	0.33
Human	IIDENDNK_02414	cydD	21224_3#267	1	10.20	0.46	0.46	0.36
Human	IIDENDNK_03531	frvR	21224_3#267	1	10.19	0.33	0.33	0.32
Human	IIDENDNK_04399	yhhI_5	21224_3#267	1	10.18	0.33	0.33	0.32
Human	BNJMMDAK_01917	BNJMMDAK_01917	15-04719	1	10.18	0.32	0.32	0.31
Human	IIDENDNK_03030	yfcC_2	21224_3#267	1	10.17	0.25	0.25	0.45
Human	IIDENDNK_04738	cirA_4	21224_3#267	1	10.17	0.25	0.25	0.34
Human	IIDENDNK_04050	IIDENDNK_04050	21224_3#267	1	10.17	0.33	0.33	0.33
Human	IIDENDNK_02488	acs	21224_3#267	1	10.16	0.56	0.44	0.41
Human	IIDENDNK_04887	rluD	21224_3#267	1	10.15	0.39	0.39	0.32
Human	IIDENDNK_02422	dmsB	21224_3#267	1	10.14	0.43	0.43	0.33
Human	IIDENDNK_04243	ycjY_4	21224_3#267	1	10.14	0.65	0.35	0.31
Human	IIDENDNK_01289	IIDENDNK_01289	21224_3#267	1	10.14	0.48	0.48	0.30
Human	IIDENDNK_02985	fadL	21224_3#267	1	10.13	0.32	0.32	0.31
Human	IIDENDNK_04961	ant1	21224_3#267	1	10.11	0.43	0.43	0.29
Human	BNJMMDAK_04622	BNJMMDAK_04622	15-04719	1	10.10	0.08	0.08	0.45
Human	IIDENDNK_03027	yfcF	21224_3#267	1	10.10	0.11	0.11	0.63
Human	IIDENDNK_04502	IIDENDNK_04502	21224_3#267	1	10.09	0.45	0.45	0.29
Human	IIDENDNK_00909	pduL	21224_3#267	1	10.07	0.47	0.47	0.35
Human	IIDENDNK_03631	recG	21224_3#267	1	10.07	0.38	0.38	0.34
Human	IIDENDNK_02971	envZ_9	21224_3#267	1	10.06	0.52	0.48	0.32
Human	IIDENDNK_03464	msbA_3	21224_3#267	1	10.06	0.52	0.48	0.32
Human	IIDENDNK_03469	pikAV	21224_3#267	1	10.06	0.59	0.41	0.29
Human	IIDENDNK_02179	IIDENDNK_02179	21224_3#267	1	10.04	0.29	0.29	0.35
Human	IIDENDNK_02969	yfdV	21224_3#267	1	10.04	0.23	0.23	0.37
Human	IIDENDNK_02111	IIDENDNK_02111	21224_3#267	1	10.03	0.46	0.46	0.29
Human	IIDENDNK_03589	cysE	21224_3#267	1	10.03	0.37	0.37	0.36
Human	IIDENDNK_03461	trpE_1	21224_3#267	1	10.03	0.50	0.50	0.32
Human	IIDENDNK_04006	adhE_2	21224_3#267	1	10.02	0.29	0.29	0.37
Human	IIDENDNK_04853	yhdJ_3	21224_3#267	1	10.01	0.23	0.23	0.34
Human	BNJMMDAK_02566	BNJMMDAK_02566	15-04719	1	10.00	0.20	0.20	0.36

Human	IIDENDNK_00695	IIDENDNK_00695	21224_3#267	1	9.99	0.42	0.42	0.41	
Human	IIDENDNK_01714	araA	21224_3#267	1	9.99	0.19	0.19	0.41	
Human	BNJMMDAK_01920	BNJMMDAK_01920	15-04719	1	9.98	0.15	0.15	0.39	
Human	IIDENDNK_04924	yfjI_2	21224_3#267	1	9.98	0.18	0.18	0.45	
Human	IIDENDNK_00939	yeiM_1	21224_3#267	1	9.98	0.11	0.11	0.42	
Human	HILLNCNG_05090	HILLNCNG_05090	14-03445	1	9.98	0.08	0.08	0.44	
Human	IIDENDNK_04975	yraI	21224_3#267	1	9.98	0.33	0.33	0.33	
Human	IIDENDNK_00911	IIDENDNK_00911	21224_3#267	1	9.97	0.19	0.19	0.41	
Human	BNJMMDAK_05022	BNJMMDAK_05022	15-04719	1	9.96	0.09	0.09	0.53	
Human	IIDENDNK_01409	cusF	21224_3#267	1	9.96	0.19	0.19	0.38	
Human	IIDENDNK_05029	IIDENDNK_05029	21224_3#267	1	9.95	0.29	0.29	0.32	
Human	IIDENDNK_03462	ampG_1	21224_3#267	1	9.95	0.54	0.46	0.31	
Human	IIDENDNK_04559	ydaT_3	21224_3#267	1	9.95	0.41	0.41	0.28	
Human	IIDENDNK_00611	fepB_1	21224_3#267	1	9.94	0.39	0.39	0.30	
Human	IIDENDNK_00334	ydeK	21224_3#267	1	9.94	0.46	0.46	0.29	
Human	IIDENDNK_04850	IIDENDNK_04850	21224_3#267	1	9.94	0.15	0.15	0.44	
Human	IIDENDNK_00858	yjeF	21224_3#267	1	9.93	0.15	0.15	0.38	
Human	BNJMMDAK_02554	BNJMMDAK_02554	15-04719	1	9.92	0.06	0.06	0.49	
Human	IIDENDNK_01171	IIDENDNK_01171	21224_3#267	1	9.91	0.13	0.13	0.46	
Human	IIDENDNK_04277	IIDENDNK_04277	21224_3#267	1	9.91	0.26	0.26	0.32	
Human	ALHKBHBA_04363	wcaA_2	21224_3#237	1	9.90	0.12	0.12	0.37	
Human	IIDENDNK_00080	yeaP	21224_3#267	1	9.90	0.22	0.22	0.43	
Human	IIDENDNK_04247	IIDENDNK_04247	21224_3#267	1	9.88	0.25	0.25	0.38	
Human	BNJMMDAK_03145	yadA_1	15-04719	1	9.87	0.23	0.23	0.32	
Human	IIDENDNK_04075	torZ	21224_3#267	1	9.87	0.18	0.18	0.34	
Human	IIDENDNK_02382	potH	21224_3#267	1	9.87	0.21	0.21	0.46	
Human	IIDENDNK_04051	IIDENDNK_04051	21224_3#267	1	9.87	0.31	0.31	0.50	
Human	IIDENDNK_00901	IIDENDNK_00901	21224_3#267	1	9.86	0.17	0.17	0.36	
Human	IIDENDNK_02652	IIDENDNK_02652	21224_3#267	1	9.86	0.30	0.30	0.44	
Human	IIDENDNK_05072	IIDENDNK_05072	21224_3#267	1	9.86	0.34	0.34	0.31	
Human	BNJMMDAK_05189	BNJMMDAK_05189	15-04719	1	9.85	0.11	0.11	0.39	
Human	IIDENDNK_03257	IIDENDNK_03257	21224_3#267	1	9.85	0.11	0.11	0.38	

Human	IIDENDNK_00691	IIDENDNK_00691	21224_3#267	1	9.85	0.45	0.45	0.37
Human	IIDENDNK_01037	ycjY_2	21224_3#267	1	9.85	0.44	0.44	0.40
Human	IIDENDNK_04582	mfd	21224_3#267	1	9.84	0.08	0.08	0.60
Human	BNJMMDAK_02141	BNJMMDAK_02141	15-04719	1	9.84	0.12	0.12	0.37
Human	IIDENDNK_04583	ycfS	21224_3#267	1	9.83	0.58	0.42	0.36
Human	IIDENDNK_02712	ypjA_1	21224_3#267	1	9.83	0.30	0.30	0.43
Human	IIDENDNK_01823	nagZ	21224_3#267	1	9.82	0.51	0.49	0.42
Human	BNJMMDAK_05052	epr	15-04719	1	9.81	0.32	0.32	0.46
Human	BNJMMDAK_05149	wprA	15-04719	1	9.81	0.32	0.32	0.46
Human	IIDENDNK_03590	gpsA	21224_3#267	1	9.81	0.14	0.14	0.46
Human	IIDENDNK_03350	yhjJ	21224_3#267	1	9.81	0.35	0.35	0.31
Human	IIDENDNK_01018	ycjZ_1	21224_3#267	1	9.80	0.39	0.39	0.35
Human	BNJMMDAK_04637	BNJMMDAK_04637	15-04719	1	9.80	0.04	0.04	0.62
Human	BNJMMDAK_03712	rhsD_3	15-04719	1	9.78	0.30	0.30	0.39
Human	IIDENDNK_05030	mobA_3	21224_3#267	1	9.77	0.27	0.27	0.32
Human	BNJMMDAK_00690	fucP_2	15-04719	1	9.77	0.22	0.22	0.31
Human	IIDENDNK_00487	yhbV	21224_3#267	1	9.76	0.34	0.34	0.30
Human	IIDENDNK_04317	yiaY	21224_3#267	1	9.75	0.18	0.18	0.42
Human	ALHKBHBA_04638	ALHKBHBA_04638	21224_3#237	1	9.75	0.05	0.05	0.58
Human	BNJMMDAK_04641	BNJMMDAK_04641	15-04719	1	9.74	0.10	0.10	0.41
Human	BNJMMDAK_05026	lomR_3	15-04719	1	9.73	0.13	0.13	0.44
Human	BNJMMDAK_03183	mutL	15-04719	1	9.72	0.36	0.36	0.28
Human	IIDENDNK_00940	psuG_1	21224_3#267	1	9.72	0.09	0.09	0.41
Human	IIDENDNK_01993	ycbB	21224_3#267	1	9.72	0.50	0.50	0.31
Human	ALHKBHBA_01459	ALHKBHBA_01459	21224_3#237	1	9.71	0.34	0.34	0.44
Human	ALHKBHBA_04712	ALHKBHBA_04712	21224_3#237	1	9.71	0.06	0.06	0.50
Human	HILLNCNG_05410	yedW_12	14-03445	1	9.71	0.11	0.11	0.38
Human	IIDENDNK_01304	yehB_1	21224_3#267	1	9.70	0.40	0.40	0.28
Human	IIDENDNK_04740	IIDENDNK_04740	21224_3#267	1	9.70	0.18	0.18	0.39
Human	IIDENDNK_04503	IIDENDNK_04503	21224_3#267	1	9.69	0.13	0.13	0.44
Human	IIDENDNK_00580	IIDENDNK_00580	21224_3#267	1	9.68	0.15	0.15	0.47
Human	IIDENDNK_03843	ybcQ_1	21224_3#267	1	9.68	0.43	0.43	0.27

Human	BNJMMDAK_01948	BNJMMDAK_01948	15-04719	1	9.66	0.04	0.04	0.66
Human	BNJMMDAK_00389	BNJMMDAK_00389	15-04719	1	9.61	0.10	0.10	0.39
Human	IIDENDNK_00362	pqqL	21224_3#267	1	9.60	0.12	0.12	0.37
Human	BNJMMDAK_01963	BNJMMDAK_01963	15-04719	1	9.57	0.05	0.05	0.57
Human	IIDENDNK_04864	ssb_3	21224_3#267	1	9.57	0.28	0.28	0.54
Human	ALHKBHBA_04343	ALHKBHBA_04343	21224_3#237	1	9.57	0.28	0.28	0.30
Human	ALHKBHBA_04424	pdxJ	21224_3#237	1	9.56	0.11	0.11	0.38
Human	BNJMMDAK_01966	BNJMMDAK_01966	15-04719	1	9.56	0.05	0.05	0.58
Human	BNJMMDAK_05033	BNJMMDAK_05033	15-04719	1	9.55	0.08	0.08	0.47
Human	IIDENDNK_00690	lacA_1	21224_3#267	1	9.55	0.14	0.14	0.44
Human	IIDENDNK_05082	mprA_2	21224_3#267	1	9.53	0.22	0.22	0.34
Human	BNJMMDAK_05371	fliC_2	15-04719	1	9.45	0.07	0.07	0.45
Human	BNJMMDAK_01935	stxB	15-04719	1	9.29	0.04	0.04	0.64
Cattle	NDEABJGN_03560	caeA	ZTA1500328-1EC,IMT33253	2613	16.30	0.17	0.17	0.42
Cattle	NDEABJGN_01576	cdiA_1	ZTA1500328-1EC	2605	16.18	0.25	0.25	0.34
Cattle	NDEABJGN_03561	ompT_1	ZTA1500328-1EC	1378	16.18	0.17	0.17	0.42
Cattle	NDEABJGN_03248	NDEABJGN_03248	ZTA1500328-1EC	796	12.94	0.09	0.09	0.47
Cattle	NDEABJGN_03247	borD_1	ZTA1500328-1EC	312	13.49	0.09	0.09	0.48
Cattle	NDEABJGN_03246	ybcV_1	ZTA1500328-1EC	246	10.96	0.09	0.09	0.47
Cattle	BBFLDBAN_03829	BBFLDBAN_03829	IMT33253	225	10.51	0.09	0.09	0.44
Cattle	BBFLDBAN_03830	finO	IMT33253	169	11.00	0.09	0.09	0.43
Cattle	NDEABJGN_03475	NDEABJGN_03475	ZTA1500328-1EC	151	12.15	0.18	0.18	0.34
Cattle	NDEABJGN_03249	NDEABJGN_03249	ZTA1500328-1EC	136	12.14	0.09	0.09	0.47
Cattle	BBFLDBAN_03826	BBFLDBAN_03826	IMT33253	133	10.35	0.10	0.10	0.42
Cattle	BBFLDBAN_03825	BBFLDBAN_03825	IMT33253	127	11.12	0.10	0.10	0.41
Cattle	NDEABJGN_03529	yfjX	ZTA1500328-1EC	119	10.34	0.22	0.22	0.34
Cattle	NDEABJGN_03559	xerD_3	ZTA1500328-1EC	118	12.12	0.20	0.20	0.37
Cattle	BBFLDBAN_03828	yhcR_1	IMT33253	113	9.91	0.09	0.09	0.43
Cattle	NDEABJGN_03532	NDEABJGN_03532	ZTA1500328-1EC	77	12.02	0.35	0.35	0.29
Cattle	NDEABJGN_03479	hokE_4	ZTA1500328-1EC	69	10.83	0.27	0.27	0.31
Cattle	BBFLDBAN_03824	BBFLDBAN_03824	IMT33253	63	10.63	0.09	0.09	0.43
Cattle	NDEABJGN_01575	shlB	ZTA1500328-1EC	54	12.07	0.31	0.31	0.32

Cattle	NDEABJGN_03533	NDEABJGN_03533	ZTA1500328-1EC	53	10.79	0.33	0.33	0.29
Cattle	NDEABJGN_04722	NDEABJGN_04722	ZTA1500328-1EC	46	11.33	0.28	0.28	0.31
Cattle	NDEABJGN_03545	rob_2	ZTA1500328-1EC	41	12.40	0.13	0.13	0.41
Cattle	NDEABJGN_03524	spo0C	ZTA1500328-1EC	39	11.42	0.27	0.27	0.32
Cattle	NDEABJGN_04718	NDEABJGN_04718	ZTA1500328-1EC	37	12.99	0.23	0.23	0.39
Cattle	NDEABJGN_03549	NDEABJGN_03549	ZTA1500328-1EC	33	12.90	0.17	0.17	0.39
Cattle	NDEABJGN_03251	gadW_3	ZTA1500328-1EC	28	12.74	0.17	0.17	0.40
Cattle	NDEABJGN_00114	gadW_1	ZTA1500328-1EC	28	12.74	0.17	0.17	0.40
Cattle	NDEABJGN_03476	NDEABJGN_03476	ZTA1500328-1EC	26	12.15	0.18	0.18	0.34
Cattle	NDEABJGN_00369	NDEABJGN_00369	ZTA1500328-1EC	24	13.25	0.21	0.21	0.39
Cattle	HEHKHGNK_02888	ycgV_1	IMT13376	22	9.91	0.14	0.14	0.40
Cattle	BBFLDBAN_03798	gadW_2	IMT33253	20	10.69	0.12	0.12	0.42
Cattle	NDEABJGN_03537	sopB	ZTA1500328-1EC	19	10.39	0.25	0.25	0.32
Cattle	NDEABJGN_03538	soj	ZTA1500328-1EC	17	10.00	0.24	0.24	0.32
Cattle	NDEABJGN_03550	NDEABJGN_03550	ZTA1500328-1EC	17	12.22	0.28	0.28	0.37
Cattle	NDEABJGN_04682	ydfR	ZTA1500328-1EC	17	9.94	0.40	0.40	0.29
Cattle	NDEABJGN_03528	NDEABJGN_03528	ZTA1500328-1EC	17	10.53	0.28	0.28	0.30
Cattle	NDEABJGN_03495	NDEABJGN_03495	ZTA1500328-1EC	16	11.27	0.28	0.28	0.32
Cattle	NDEABJGN_03250	NDEABJGN_03250	ZTA1500328-1EC	15	10.19	0.10	0.10	0.45
Cattle	NDEABJGN_03253	ybcQ_1	ZTA1500328-1EC	14	9.95	0.11	0.11	0.42
Cattle	NDEABJGN_03539	repE	ZTA1500328-1EC	13	11.48	0.35	0.35	0.30
Cattle	NDEABJGN_03551	NDEABJGN_03551	ZTA1500328-1EC	13	12.88	0.29	0.29	0.37
Cattle	NDEABJGN_03555	NDEABJGN_03555	ZTA1500328-1EC	11	10.18	0.21	0.21	0.33
Cattle	BBFLDBAN_03779	ypjA_2	IMT33253	9	11.42	0.17	0.17	0.39
Cattle	NDEABJGN_00249	NDEABJGN_00249	ZTA1500328-1EC	8	12.24	0.24	0.24	0.38
Cattle	NDEABJGN_00402	tfaD_1	ZTA1500328-1EC	7	12.32	0.11	0.11	0.43
Cattle	NDEABJGN_00403	nohA	ZTA1500328-1EC	7	10.58	0.10	0.10	0.44
Cattle	NDEABJGN_03496	NDEABJGN_03496	ZTA1500328-1EC	6	9.92	0.16	0.16	0.37
Cattle	BBFLDBAN_03827	hokE_3	IMT33253	6	9.85	0.10	0.10	0.42
Cattle	BBFLDBAN_03778	tibC	IMT33253	6	11.34	0.12	0.12	0.45
Cattle	NDEABJGN_00362	ydfN	ZTA1500328-1EC	6	10.61	0.24	0.24	0.35
Cattle	NDEABJGN_03478	NDEABJGN_03478	ZTA1500328-1EC	6	11.10	0.24	0.24	0.32

Cattle	NDEABJGN_03272	NDEABJGN_03272	ZTA1500328-1EC	5	13.36	0.20	0.20	0.38
Cattle	NDEABJGN_00400	NDEABJGN_00400	ZTA1500328-1EC	5	12.78	0.19	0.19	0.41
Cattle	NDEABJGN_04749	yhdJ_3	ZTA1500328-1EC,IMT33253	5	10.48	0.21	0.21	0.40
Cattle	NDEABJGN_01592	yjgZ	ZTA1500328-1EC	5	10.54	0.25	0.25	0.34
Cattle	NDEABJGN_00373	NDEABJGN_00373	ZTA1500328-1EC	5	10.15	0.16	0.16	0.39
Cattle	NDEABJGN_04564	rluA	ZTA1500328-1EC	4	16.30	0.26	0.26	0.42
Cattle	NDEABJGN_04721	NDEABJGN_04721	ZTA1500328-1EC	4	10.18	0.13	0.13	0.39
Cattle	NDEABJGN_04719	NDEABJGN_04719	ZTA1500328-1EC	4	10.67	0.16	0.16	0.40
Cattle	NDEABJGN_03484	vapB_1	ZTA1500328-1EC	4	10.90	0.32	0.32	0.29
Cattle	NDEABJGN_01602	NDEABJGN_01602	ZTA1500328-1EC	4	10.13	0.51	0.49	0.39
Cattle	NDEABJGN_01591	NDEABJGN_01591	ZTA1500328-1EC	4	10.60	0.13	0.13	0.41
Cattle	NDEABJGN_03489	NDEABJGN_03489	ZTA1500328-1EC	4	10.64	0.34	0.34	0.31
Cattle	NDEABJGN_01582	NDEABJGN_01582	ZTA1500328-1EC	4	12.07	0.24	0.24	0.35
Cattle	NDEABJGN_04770	NDEABJGN_04770	ZTA1500328-1EC	4	11.14	0.16	0.16	0.40
Cattle	NDEABJGN_00365	NDEABJGN_00365	ZTA1500328-1EC	4	10.76	0.18	0.18	0.39
Cattle	NDEABJGN_04563	hepA	ZTA1500328-1EC	4	16.30	0.24	0.24	0.45
Cattle	NDEABJGN_00078	stfR_1	ZTA1500328-1EC	4	10.64	0.22	0.22	0.35
Cattle	NDEABJGN_03273	NDEABJGN_03273	ZTA1500328-1EC	3	12.48	0.19	0.19	0.40
Cattle	BBFLDBAN_03781	ykgA_2	IMT33253	3	9.99	0.25	0.25	0.33
Cattle	NDEABJGN_03483	traI	ZTA1500328-1EC	3	10.69	0.31	0.31	0.32
Cattle	NDEABJGN_00083	NDEABJGN_00083	ZTA1500328-1EC	3	13.00	0.20	0.20	0.42
Cattle	NDEABJGN_00372	NDEABJGN_00372	ZTA1500328-1EC	3	12.01	0.38	0.38	0.36
Cattle	NDEABJGN_00404	NDEABJGN_00404	ZTA1500328-1EC	3	9.70	0.11	0.11	0.43
Cattle	BBFLDBAN_03797	BBFLDBAN_03797	IMT33253	3	9.78	0.12	0.12	0.41
Cattle	NDEABJGN_04771	NDEABJGN_04771	ZTA1500328-1EC	3	16.79	0.19	0.19	0.39
Cattle	HEHKHGNK_04552	fimD_1	IMT13376	3	10.37	0.12	0.12	0.42
Cattle	NDEABJGN_02922	NDEABJGN_02922	ZTA1500328-1EC	3	10.83	0.26	0.26	0.35
Cattle	NDEABJGN_01596	cpdA_1	ZTA1500328-1EC	3	10.34	0.22	0.22	0.35
Cattle	NDEABJGN_00090	NDEABJGN_00090	ZTA1500328-1EC	3	10.27	0.33	0.33	0.31
Cattle	BBFLDBAN_03749	umuC_2	IMT33253	3	10.41	0.06	0.06	0.58
Cattle	NDEABJGN_04686	cspF	ZTA1500328-1EC	2	9.85	0.50	0.50	0.29
Cattle	BBFLDBAN_03803	BBFLDBAN_03803	IMT33253	2	10.02	0.19	0.19	0.38

Cattle	NDEABJGN_00113	NDEABJGN_00113	ZTA1500328-1EC	2	10.38	0.30	0.30	0.34
Cattle	NDEABJGN_00371	NDEABJGN_00371	ZTA1500328-1EC	2	10.07	0.13	0.13	0.42
Cattle	NDEABJGN_00401	NDEABJGN_00401	ZTA1500328-1EC	2	13.88	0.17	0.17	0.42
Cattle	NDEABJGN_03271	intE	ZTA1500328-1EC	2	9.85	0.39	0.39	0.32
Cattle	NDEABJGN_03469	NDEABJGN_03469	ZTA1500328-1EC	2	9.90	0.16	0.16	0.36
Cattle	NDEABJGN_00368	NDEABJGN_00368	ZTA1500328-1EC	2	10.81	0.41	0.41	0.32
Cattle	NDEABJGN_02192	yadC	ZTA1500328-1EC	2	9.99	0.51	0.49	0.56
Cattle	NDEABJGN_01599	hsdM_1	ZTA1500328-1EC	2	10.65	0.17	0.17	0.38
Cattle	NDEABJGN_00383	NDEABJGN_00383	ZTA1500328-1EC	2	10.88	0.20	0.20	0.37
Cattle	HEHKHGNK_00677	HEHKHGNK_00677	IMT13376	2	10.14	0.65	0.35	0.38
Cattle	NDEABJGN_00513	ydcI_2	ZTA1500328-1EC	2	10.38	0.30	0.30	0.34
Cattle	NDEABJGN_01594	NDEABJGN_01594	ZTA1500328-1EC	2	10.83	0.18	0.18	0.38
Cattle	NDEABJGN_04694	ydfW	ZTA1500328-1EC	2	10.33	0.45	0.45	0.30
Cattle	NDEABJGN_00367	NDEABJGN_00367	ZTA1500328-1EC	2	10.01	0.28	0.28	0.32
Cattle	NDEABJGN_03468	yahA_2	ZTA1500328-1EC	2	10.00	0.15	0.15	0.37
Cattle	JANIAHEC_02514	fimD_2	IMT30910	2	9.97	0.10	0.10	0.42
Cattle	NDEABJGN_00376	NDEABJGN_00376	ZTA1500328-1EC	2	12.05	0.21	0.21	0.40
Cattle	NDEABJGN_01041	sdaB	ZTA1500328-1EC	1	12.22	0.60	0.40	0.36
Cattle	NDEABJGN_01253	glcA	ZTA1500328-1EC	1	9.87	0.31	0.31	0.35
Cattle	BBFLDBAN_03736	BBFLDBAN_03736	IMT33253	1	10.74	0.68	0.32	0.38
Cattle	NDEABJGN_02630	fliC_2	ZTA1500328-1EC	1	9.87	0.17	0.17	0.39
Cattle	BBFLDBAN_03795	cdtA	IMT33253	1	9.77	0.19	0.19	0.38
Cattle	NDEABJGN_04011	NDEABJGN_04011	ZTA1500328-1EC	1	10.53	0.89	0.11	0.47
Cattle	NDEABJGN_03019	NDEABJGN_03019	ZTA1500328-1EC	1	9.90	0.84	0.16	0.38
Cattle	BBFLDBAN_05075	BBFLDBAN_05075	IMT33253	1	9.97	0.65	0.35	0.39
Cattle	NDEABJGN_04769	NDEABJGN_04769	ZTA1500328-1EC	1	10.22	0.14	0.14	0.41
Cattle	NDEABJGN_02605	otsB	ZTA1500328-1EC	1	9.78	0.10	0.10	0.48
Cattle	BBFLDBAN_04705	BBFLDBAN_04705	IMT33253	1	10.39	0.15	0.15	0.41
Cattle	BBFLDBAN_05139	BBFLDBAN_05139	IMT33253	1	9.90	0.12	0.12	0.44
Cattle	NDEABJGN_02073	fliA_1	ZTA1500328-1EC	1	10.81	0.24	0.24	0.37
Cattle	NDEABJGN_01660	cpdA_2	ZTA1500328-1EC	1	9.81	0.89	0.11	0.44
Cattle	NDEABJGN_00391	NDEABJGN_00391	ZTA1500328-1EC	1	9.77	0.09	0.09	0.46

Cattle	NDEABJGN_04687	ydfT	ZTA1500328-1EC	1	10.66	0.63	0.37	0.32
Cattle	BBFLDBAN_04761	yeeJ_6	IMT33253	1	10.34	0.06	0.06	0.58
Cattle	NDEABJGN_01574	dgt_1	ZTA1500328-1EC	1	11.33	0.21	0.21	0.34
Cattle	BBFLDBAN_03802	toxA	IMT33253	1	10.27	0.11	0.11	0.45
Cattle	NDEABJGN_00087	NDEABJGN_00087	ZTA1500328-1EC	1	11.18	0.14	0.14	0.43
Cattle	NDEABJGN_00379	sohB_2	ZTA1500328-1EC	1	10.68	0.16	0.16	0.43
Cattle	NDEABJGN_03542	ccdA	ZTA1500328-1EC	1	10.88	0.27	0.27	0.36
Cattle	NDEABJGN_00361	tfaQ_1	ZTA1500328-1EC	1	9.90	0.15	0.15	0.36
Cattle	NDEABJGN_00363	lomR_1	ZTA1500328-1EC	1	10.00	0.14	0.14	0.38
Cattle	BBFLDBAN_04381	parM_3	IMT33253	1	10.37	0.19	0.19	0.36
Cattle	NDEABJGN_00099	NDEABJGN_00099	ZTA1500328-1EC	1	9.94	0.16	0.16	0.38
Cattle	NDEABJGN_01578	cdiA_2	ZTA1500328-1EC	1	9.41	0.13	0.13	0.37
Cattle	NDEABJGN_00082	NDEABJGN_00082	ZTA1500328-1EC	1	10.05	0.29	0.29	0.33
Cattle	NDEABJGN_00100	NDEABJGN_00100	ZTA1500328-1EC	1	9.94	0.16	0.16	0.38
Cattle	NDEABJGN_01580	cdiI	ZTA1500328-1EC	1	9.88	0.31	0.31	0.30
Cattle	BBFLDBAN_03773	ompT_2	IMT33253	1	9.98	0.12	0.12	0.42
Cattle	NDEABJGN_01601	NDEABJGN_01601	ZTA1500328-1EC	1	11.17	0.23	0.23	0.39
Cattle	NDEABJGN_02999	hycI	ZTA1500328-1EC	1	11.05	0.81	0.19	0.40
Cattle	NDEABJGN_03562	NDEABJGN_03562	ZTA1500328-1EC	1	9.90	0.21	0.21	0.34
Cattle	BBFLDBAN_03809	hlyA	IMT33253	1	9.95	0.24	0.24	0.32
Cattle	NDEABJGN_01589	cdiA4	ZTA1500328-1EC	1	9.57	0.29	0.29	0.31
Cattle	BBFLDBAN_04333	BBFLDBAN_04333	IMT33253	1	10.68	0.13	0.13	0.44
Cattle	NDEABJGN_03471	NDEABJGN_03471	ZTA1500328-1EC	1	9.94	0.12	0.12	0.38
Cattle	HEHKHGNK_01258	aegA	IMT13376	1	9.77	0.65	0.35	0.35
Cattle	NDEABJGN_04780	NDEABJGN_04780	ZTA1500328-1EC	1	9.98	0.10	0.10	0.42
Cattle	NDEABJGN_04032	stfR_2	ZTA1500328-1EC	1	9.81	0.30	0.30	0.31
Cattle	BBFLDBAN_03756	BBFLDBAN_03756	IMT33253	1	9.82	0.06	0.06	0.50
Cattle	NDEABJGN_01595	mupP	ZTA1500328-1EC	1	9.98	0.82	0.18	0.34
Cattle	NDEABJGN_00084	NDEABJGN_00084	ZTA1500328-1EC	1	10.39	0.42	0.42	0.30
Cattle	NDEABJGN_02107	fliN_1	ZTA1500328-1EC	1	10.87	0.30	0.30	0.34
Cattle	NDEABJGN_04448	NDEABJGN_04448	ZTA1500328-1EC	1	10.82	0.15	0.15	0.42
Cattle	BBFLDBAN_01791	dxs_2	IMT33253	1	9.52	0.12	0.12	0.39

Cattle	NDEABJGN_01581	NDEABJGN_01581	ZTA1500328-1EC	1	9.78	0.25	0.25	0.33
Cattle	HEHKHGNK_04910	HEHKHGNK_04910	IMT13376	1	10.34	0.14	0.14	0.40
Cattle	HEHKHGNK_04772	fimC_4	IMT13376	1	10.15	0.18	0.18	0.37
Cattle	NDEABJGN_00990	sgbU	ZTA1500328-1EC	1	10.35	0.19	0.19	0.40
Cattle	BBFLDBAN_03805	insN-2	IMT33253	1	9.91	0.11	0.11	0.43
Cattle	NDEABJGN_00381	NDEABJGN_00381	ZTA1500328-1EC	1	11.71	0.25	0.25	0.42
Cattle	NDEABJGN_00524	galS	ZTA1500328-1EC	1	9.98	0.20	0.20	0.40
Cattle	BBFLDBAN_03822	BBFLDBAN_03822	IMT33253	1	9.71	0.16	0.16	0.35
Cattle	NDEABJGN_04220	NDEABJGN_04220	ZTA1500328-1EC	1	10.46	0.85	0.15	0.42
Cattle	NDEABJGN_00374	NDEABJGN_00374	ZTA1500328-1EC	1	9.49	0.10	0.10	0.44
Cattle	NDEABJGN_00399	intZ	ZTA1500328-1EC	1	12.45	0.17	0.17	0.44
Cattle	NDEABJGN_04115	NDEABJGN_04115	ZTA1500328-1EC	1	10.97	0.18	0.18	0.41
Cattle	NDEABJGN_04112	NDEABJGN_04112	ZTA1500328-1EC	1	10.38	0.31	0.31	0.35
Cattle	NDEABJGN_00112	NDEABJGN_00112	ZTA1500328-1EC	1	10.15	0.22	0.22	0.34
Cattle	NDEABJGN_03252	NDEABJGN_03252	ZTA1500328-1EC	1	9.50	0.13	0.13	0.40
Cattle	NDEABJGN_04428	NDEABJGN_04428	ZTA1500328-1EC	1	9.98	0.45	0.45	0.35
Cattle	NDEABJGN_00102	NDEABJGN_00102	ZTA1500328-1EC	1	10.40	0.31	0.31	0.30
Cattle	NDEABJGN_00081	NDEABJGN_00081	ZTA1500328-1EC	1	9.96	0.23	0.23	0.32
Cattle	BBFLDBAN_03783	eamA_2	IMT33253	1	10.63	0.13	0.13	0.44
Cattle	NDEABJGN_01579	cdiA_3	ZTA1500328-1EC	1	9.65	0.13	0.13	0.38
Cattle	NDEABJGN_00397	NDEABJGN_00397	ZTA1500328-1EC	1	10.09	0.09	0.09	0.49
Cattle	NDEABJGN_02735	hflC	ZTA1500328-1EC	1	10.80	0.22	0.22	0.42
Cattle	BBFLDBAN_04366	BBFLDBAN_04366	IMT33253	1	9.62	0.09	0.09	0.45
Cattle	NDEABJGN_00370	NDEABJGN_00370	ZTA1500328-1EC	1	11.15	0.17	0.17	0.38
Cattle	NDEABJGN_04449	intF	ZTA1500328-1EC	1	10.90	0.18	0.18	0.40
Cattle	NDEABJGN_00079	NDEABJGN_00079	ZTA1500328-1EC	1	9.81	0.30	0.30	0.31
Cattle	HEHKHGNK_04529	cdiA	IMT13376	1	10.12	0.30	0.30	0.31
Cattle	BBFLDBAN_04723	yhdJ_2	IMT33253	1	10.63	0.19	0.19	0.38
Cattle	NDEABJGN_02664	mgtA	ZTA1500328-1EC	1	10.43	0.35	0.35	0.31
Cattle	NDEABJGN_00116	ybcO	ZTA1500328-1EC	1	9.94	0.38	0.38	0.27
Cattle	NDEABJGN_03485	vapC_1	ZTA1500328-1EC	1	10.00	0.32	0.32	0.28
Cattle	BBFLDBAN_05138	BBFLDBAN_05138	IMT33253	1	10.71	0.14	0.14	0.42

Chicken	OMPLLAHN_05220	OMPLLAHN_05220	14756	8890	21.36	0.34	0.34	0.40
Chicken	OMPLLAHN_05033	msbA_2	14756	5868	13.37	0.35	0.35	0.33
Chicken	OMPLLAHN_05036	fepA_2	14756.21225_2#181	4027	12.38	0.34	0.34	0.33
Chicken	OMPLLAHN_05110	lgrD	14756.21225_2#181	2860	16.35	0.37	0.37	0.36
Chicken	OMPLLAHN_05122	yjiA_2	14756.21225_2#181	2837	15.92	0.35	0.35	0.37
Chicken	OMPLLAHN_05111	ompT	14756.21225_2#181	2354	19.38	0.37	0.37	0.38
Chicken	OMPLLAHN_05032	elmGT	14756	2255	14.09	0.34	0.34	0.35
Chicken	OMPLLAHN_05352	yahF_3	14756	1978	21.36	0.16	0.16	0.36
Chicken	OMPLLAHN_05109	OMPLLAHN_05109	14756	1928	16.02	0.36	0.36	0.34
Chicken	OMPLLAHN_05034	fes_2	14756	1580	13.18	0.34	0.34	0.33
Chicken	OMPLLAHN_05351	OMPLLAHN_05351	14756	1539	13.54	0.16	0.16	0.36
Chicken	OMPLLAHN_05031	OMPLLAHN_05031	14756	1452	14.32	0.35	0.35	0.36
Chicken	OMPLLAHN_05035	besA	14756	1071	12.24	0.33	0.33	0.33
Chicken	OMPLLAHN_05353	yahE_3	14756	1001	15.49	0.16	0.16	0.36
Chicken	OMPLLAHN_05355	yahB_2	14756	983	14.45	0.17	0.17	0.36
Chicken	OMPLLAHN_05221	OMPLLAHN_05221	14756	932	16.02	0.20	0.20	0.37
Chicken	OMPLLAHN_05030	OMPLLAHN_05030	14756	808	13.72	0.39	0.39	0.34
Chicken	OMPLLAHN_05354	yahD_2	14756	729	17.26	0.16	0.16	0.36
Chicken	OMPLLAHN_04083	soj_1	14756	662	11.91	0.30	0.30	0.29
Chicken	OMPLLAHN_05029	borD_1	14756	648	14.87	0.34	0.34	0.37
Chicken	OMPLLAHN_05350	OMPLLAHN_05350	14756	596	17.81	0.17	0.17	0.36
Chicken	OMPLLAHN_04082	sopB	14756,21225_2#181	463	11.90	0.31	0.31	0.29
Chicken	OMPLLAHN_05641	OMPLLAHN_05641	14756	341	13.74	0.19	0.19	0.37
Chicken	OMPLLAHN_04024	relE_2	14756,21225_2#181	334	14.48	0.14	0.14	0.45
Chicken	OMPLLAHN_05107	OMPLLAHN_05107	14756	324	11.91	0.43	0.43	0.29
Chicken	FKALCOLL_04587	znuB_3	21225_2#181	307	11.91	0.37	0.37	0.29
Chicken	FKALCOLL_04468	FKALCOLL_04468	21225_2#181	306	13.72	0.26	0.26	0.39
Chicken	OMPLLAHN_05112	OMPLLAHN_05112	14756	258	14.77	0.37	0.37	0.36
Chicken	FKALCOLL_04466	yafN	21225_2#181	252	11.41	0.09	0.09	0.48
Chicken	FKALCOLL_04520	FKALCOLL_04520	21225_2#181	192	11.23	0.38	0.38	0.29
Chicken	OMPLLAHN_04467	ydeO_2	14756,21225_2#181	169	14.54	0.14	0.14	0.40
Chicken	FKALCOLL_04524	repB_3	21225_2#181	168	11.13	0.37	0.37	0.27

Chicken	OMPLLAHN_05523	OMPLLAHN_05523	14756	165	11.03	0.20	0.20	0.37
Chicken	OMPLLAHN_05043	cvaC	14756	154	11.44	0.34	0.34	0.31
Chicken	OMPLLAHN_05348	OMPLLAHN_05348	14756	152	15.39	0.18	0.18	0.38
Chicken	OMPLLAHN_05509	OMPLLAHN_05509	14756	148	15.39	0.18	0.18	0.38
Chicken	OMPLLAHN_05113	OMPLLAHN_05113	14756	135	11.94	0.33	0.33	0.31
Chicken	OMPLLAHN_05106	repB_2	14756	117	13.44	0.43	0.43	0.30
Chicken	OMPLLAHN_05121	OMPLLAHN_05121	14756	116	11.51	0.34	0.34	0.30
Chicken	FKALCOLL_04039	finO	21225_2#181	106	11.49	0.28	0.28	0.29
Chicken	OMPLLAHN_05045	insO-2_1	14756	100	13.48	0.32	0.32	0.32
Chicken	OMPLLAHN_05126	codB_2	14756	87	17.99	0.37	0.37	0.45
Chicken	OMPLLAHN_04034	OMPLLAHN_04034	14756	84	11.56	0.59	0.41	0.27
Chicken	OMPLLAHN_04025	yafN_1	14756	77	16.36	0.30	0.30	0.32
Chicken	OMPLLAHN_05134	OMPLLAHN_05134	14756	73	10.55	0.21	0.21	0.32
Chicken	OMPLLAHN_04433	OMPLLAHN_04433	14756	69	10.55	0.21	0.21	0.32
Chicken	OMPLLAHN_04468	OMPLLAHN_04468	14756	68	12.23	0.12	0.12	0.40
Chicken	FKALCOLL_04521	FKALCOLL_04521	21225_2#181	59	10.84	0.37	0.37	0.30
Chicken	OMPLLAHN_05125	ydhB_2	14756	58	11.38	0.37	0.37	0.46
Chicken	OMPLLAHN_05349	yahI_2	14756	56	12.81	0.22	0.22	0.35
Chicken	OMPLLAHN_05132	rutB_2	14756	52	12.36	0.36	0.36	0.44
Chicken	FKALCOLL_04588	FKALCOLL_04588	21225_2#181	50	10.65	0.35	0.35	0.29
Chicken	OMPLLAHN_05131	yahE_2	14756	47	12.10	0.37	0.37	0.45
Chicken	OMPLLAHN_05339	stfR_2	14756	43	13.46	0.43	0.43	0.34
Chicken	OMPLLAHN_05443	OMPLLAHN_05443	14756	42	11.66	0.26	0.26	0.38
Chicken	OMPLLAHN_05046	insN-1_3	14756	37	13.81	0.24	0.24	0.36
Chicken	OMPLLAHN_05129	OMPLLAHN_05129	14756	35	10.81	0.36	0.36	0.43
Chicken	OMPLLAHN_05529	cydC_3	14756	35	14.19	0.39	0.39	0.29
Chicken	OMPLLAHN_05554	OMPLLAHN_05554	14756	33	11.64	0.50	0.50	0.28
Chicken	FKALCOLL_04043	FKALCOLL_04043	21225_2#181	29	10.86	0.30	0.30	0.29
Chicken	OMPLLAHN_05169	iucA	14756	28	11.61	0.39	0.39	0.30
Chicken	OMPLLAHN_05115	macB_2	14756	25	17.96	0.40	0.40	0.33
Chicken	OMPLLAHN_05114	macA_2	14756	24	13.73	0.42	0.42	0.36
Chicken	OMPLLAHN_05128	yqeA_2	14756	24	10.70	0.35	0.35	0.39

Chicken	OMPLLAHN_05240	OMPLLAHN_05240	14756	24	11.08	0.25	0.25	0.35
Chicken	OMPLLAHN_05609	insO-2_3	14756	23	13.48	0.45	0.45	0.30
Chicken	OMPLLAHN_05239	OMPLLAHN_05239	14756	22	15.37	0.31	0.31	0.38
Chicken	OMPLLAHN_05176	znuB_4	14756	21	12.70	0.43	0.43	0.32
Chicken	OMPLLAHN_05037	aroH_2	14756	20	11.92	0.41	0.41	0.35
Chicken	FKALCOLL_04530	FKALCOLL_04530	21225_2#181	19	11.25	0.25	0.25	0.31
Chicken	OMPLLAHN_05108	xerD_3	14756	17	10.64	0.48	0.48	0.27
Chicken	OMPLLAHN_04099	OMPLLAHN_04099	14756	16	14.04	0.41	0.41	0.41
Chicken	OMPLLAHN_05140	mdtH_2	14756	16	13.80	0.33	0.33	0.33
Chicken	OMPLLAHN_05168	OMPLLAHN_05168	14756	16	12.77	0.44	0.44	0.30
Chicken	OMPLLAHN_05302	malX_2	14756	16	16.66	0.31	0.31	0.34
Chicken	OMPLLAHN_00048	OMPLLAHN_00048	14756	15	11.58	0.39	0.39	0.34
Chicken	OMPLLAHN_05044	ntdC	14756	14	14.68	0.39	0.39	0.32
Chicken	OMPLLAHN_05086	OMPLLAHN_05086	14756	14	11.79	0.39	0.39	0.30
Chicken	OMPLLAHN_05130	yahF_2	14756	14	19.09	0.41	0.41	0.39
Chicken	OMPLLAHN_05253	recE	14756,21225_2#181	14	13.48	0.41	0.41	0.33
Chicken	OMPLLAHN_04429	hsdM_2	14756	13	16.38	0.38	0.38	0.37
Chicken	OMPLLAHN_05378	cea	14756	13	12.26	0.44	0.44	0.32
Chicken	OMPLLAHN_03886	yjhR_1	14756	12	12.04	0.41	0.41	0.31
Chicken	OMPLLAHN_03213	OMPLLAHN_03213	14756	11	11.99	0.39	0.39	0.33
Chicken	OMPLLAHN_04181	OMPLLAHN_04181	14756	11	12.77	0.40	0.40	0.35
Chicken	OMPLLAHN_04899	OMPLLAHN_04899	14756	11	11.25	0.38	0.38	0.32
Chicken	OMPLLAHN_05181	OMPLLAHN_05181	14756	11	10.83	0.34	0.34	0.32
Chicken	OMPLLAHN_00047	OMPLLAHN_00047	14756	10	13.00	0.31	0.31	0.33
Chicken	OMPLLAHN_03214	OMPLLAHN_03214	14756	10	13.64	0.38	0.38	0.33
Chicken	OMPLLAHN_04042	OMPLLAHN_04042	14756	10	11.23	0.68	0.32	0.31
Chicken	OMPLLAHN_04427	OMPLLAHN_04427	14756	10	12.91	0.45	0.45	0.35
Chicken	OMPLLAHN_04748	ydaV_1	14756	10	11.49	0.39	0.39	0.33
Chicken	OMPLLAHN_05042	msbA_3	14756	10	11.95	0.53	0.47	0.33
Chicken	OMPLLAHN_05460	dxs_2	14756	10	18.45	0.35	0.35	0.38
Chicken	OMPLLAHN_05547	tcpE_2	14756	10	11.29	0.42	0.42	0.33
Chicken	OMPLLAHN_05594	OMPLLAHN_05594	14756	10	13.58	0.32	0.32	0.35

Chicken	OMPLLAHN_05633	tfaE_3	14756	10	11.97	0.39	0.39	0.35
Chicken	FKALCOLL_04694	soj	21225_2#181	9	10.84	0.28	0.28	0.28
Chicken	OMPLLAHN_01507	OMPLLAHN_01507	14756	9	11.15	0.38	0.38	0.34
Chicken	OMPLLAHN_03026	OMPLLAHN_03026	14756	9	11.16	0.41	0.41	0.36
Chicken	OMPLLAHN_03219	smc_2	14756	9	12.18	0.43	0.43	0.36
Chicken	OMPLLAHN_03308	insF-1_1	14756	9	11.01	0.54	0.46	0.30
Chicken	OMPLLAHN_04535	yeeJ_4	14756	9	12.90	0.46	0.46	0.32
Chicken	OMPLLAHN_05116	cusC_2	14756	9	11.12	0.41	0.41	0.30
Chicken	OMPLLAHN_03285	nrdA_2	14756	8	12.04	0.41	0.41	0.33
Chicken	OMPLLAHN_04033	yhcR_1	14756	8	10.71	0.39	0.39	0.27
Chicken	OMPLLAHN_04131	OMPLLAHN_04131	14756	8	10.90	0.36	0.36	0.34
Chicken	OMPLLAHN_05127	atzF	14756	8	12.69	0.40	0.40	0.45
Chicken	OMPLLAHN_05145	OMPLLAHN_05145	14756	8	13.53	0.26	0.26	0.34
Chicken	OMPLLAHN_05171	iucC	14756	8	10.92	0.46	0.46	0.30
Chicken	OMPLLAHN_05230	hsdS_2	14756	8	12.75	0.41	0.41	0.32
Chicken	OMPLLAHN_05238	amiC_2	14756	8	11.46	0.29	0.29	0.42
Chicken	OMPLLAHN_05242	OMPLLAHN_05242	14756	8	11.96	0.29	0.29	0.37
Chicken	OMPLLAHN_05304	OMPLLAHN_05304	14756	8	11.52	0.33	0.33	0.33
Chicken	OMPLLAHN_05338	OMPLLAHN_05338	14756	8	12.59	0.37	0.37	0.37
Chicken	OMPLLAHN_05344	sacA_2	14756	8	11.71	0.42	0.42	0.34
Chicken	OMPLLAHN_05463	OMPLLAHN_05463	14756	8	11.38	0.34	0.34	0.33
Chicken	OMPLLAHN_05606	OMPLLAHN_05606	14756	8	13.59	0.46	0.46	0.36
Chicken	OMPLLAHN_03124	OMPLLAHN_03124	14756	7	13.68	0.38	0.38	0.36
Chicken	OMPLLAHN_03239	recG_1	14756	7	10.96	0.38	0.38	0.32
Chicken	OMPLLAHN_03602	OMPLLAHN_03602	14756	7	11.40	0.38	0.38	0.32
Chicken	OMPLLAHN_04157	OMPLLAHN_04157	14756	7	11.50	0.40	0.40	0.33
Chicken	OMPLLAHN_04187	OMPLLAHN_04187	14756	7	11.58	0.44	0.44	0.32
Chicken	OMPLLAHN_04416	xerC_5	14756	7	10.69	0.39	0.39	0.34
Chicken	OMPLLAHN_04426	hsdR_2	14756	7	11.18	0.36	0.36	0.34
Chicken	OMPLLAHN_04538	OMPLLAHN_04538	14756	7	10.72	0.28	0.28	0.33
Chicken	OMPLLAHN_04549	OMPLLAHN_04549	14756	7	11.40	0.38	0.38	0.32
Chicken	OMPLLAHN_04618	hsdM_6	14756	7	11.49	0.37	0.37	0.32

Chicken	OMPLLAHN_04656	ybcK	14756	7	11.98	0.51	0.49	0.32
Chicken	OMPLLAHN_04746	cdiA	14756	7	11.43	0.32	0.32	0.39
Chicken	OMPLLAHN_04749	cdiA2	14756	7	11.49	0.45	0.45	0.30
Chicken	OMPLLAHN_05087	OMPLLAHN_05087	14756	7	10.90	0.43	0.43	0.30
Chicken	OMPLLAHN_05144	pinR	14756	7	11.67	0.39	0.39	0.33
Chicken	OMPLLAHN_05170	iucB	14756	7	10.91	0.48	0.48	0.28
Chicken	OMPLLAHN_05226	OMPLLAHN_05226	14756	7	11.68	0.40	0.40	0.34
Chicken	OMPLLAHN_05342	rafA	14756	7	11.92	0.41	0.41	0.32
Chicken	OMPLLAHN_05409	cirA_7	14756	7	11.11	0.44	0.44	0.32
Chicken	OMPLLAHN_05462	ulaA_4	14756	7	11.96	0.31	0.31	0.35
Chicken	OMPLLAHN_05540	sodC_2	14756	7	10.71	0.30	0.30	0.45
Chicken	OMPLLAHN_05567	OMPLLAHN_05567	14756	7	10.95	0.32	0.32	0.40
Chicken	OMPLLAHN_05617	OMPLLAHN_05617	14756	7	11.12	0.30	0.30	0.34
Chicken	OMPLLAHN_01451	OMPLLAHN_01451	14756	6	11.04	0.39	0.39	0.34
Chicken	OMPLLAHN_01504	vgrG1_1	14756	6	11.69	0.44	0.44	0.39
Chicken	OMPLLAHN_01850	OMPLLAHN_01850	14756	6	11.44	0.44	0.44	0.34
Chicken	OMPLLAHN_01936	intA_1	14756	6	11.89	0.38	0.38	0.31
Chicken	OMPLLAHN_01979	OMPLLAHN_01979	14756	6	11.32	0.35	0.35	0.36
Chicken	OMPLLAHN_03268	OMPLLAHN_03268	14756	6	10.91	0.37	0.37	0.33
Chicken	OMPLLAHN_03315	yfjQ_1	14756	6	11.53	0.41	0.41	0.33
Chicken	OMPLLAHN_03514	OMPLLAHN_03514	14756	6	11.09	0.37	0.37	0.35
Chicken	OMPLLAHN_03878	arpA_2	14756	6	10.98	0.48	0.48	0.33
Chicken	OMPLLAHN_04125	xerC_3	14756	6	10.93	0.34	0.34	0.31
Chicken	OMPLLAHN_04136	cirA_3	14756	6	12.13	0.47	0.47	0.36
Chicken	OMPLLAHN_04138	OMPLLAHN_04138	14756	6	11.67	0.40	0.40	0.34
Chicken	OMPLLAHN_04182	dnaB_3	14756	6	13.17	0.40	0.40	0.35
Chicken	OMPLLAHN_04254	OMPLLAHN_04254	14756	6	11.09	0.37	0.37	0.35
Chicken	OMPLLAHN_04550	hsdM_3	14756	6	14.00	0.43	0.43	0.33
Chicken	OMPLLAHN_04606	upaG_1	14756	6	10.72	0.52	0.48	0.35
Chicken	OMPLLAHN_04615	hsdM_5	14756	6	10.97	0.35	0.35	0.35
Chicken	OMPLLAHN_04947	yadE_2	14756	6	13.91	0.49	0.49	0.34
Chicken	OMPLLAHN_05047	fadH_3	14756	6	12.75	0.34	0.34	0.31

Chicken	OMPLLAHN_05094	topB_3	14756	6	11.40	0.40	0.40	0.29
Chicken	OMPLLAHN_05142	fecD_5	14756	6	10.94	0.18	0.18	0.34
Chicken	OMPLLAHN_05248	cirA_5	14756	6	12.13	0.44	0.44	0.42
Chicken	OMPLLAHN_05267	OMPLLAHN_05267	14756	6	12.48	0.46	0.46	0.32
Chicken	OMPLLAHN_05293	OMPLLAHN_05293	14756	6	14.06	0.43	0.43	0.37
Chicken	OMPLLAHN_05309	insD_3	14756	6	10.47	0.39	0.39	0.32
Chicken	OMPLLAHN_05465	gntR_2	14756	6	16.21	0.50	0.50	0.43
Chicken	OMPLLAHN_05496	OMPLLAHN_05496	14756	6	11.34	0.45	0.45	0.32
Chicken	OMPLLAHN_05499	OMPLLAHN_05499	14756	6	13.06	0.45	0.45	0.34
Chicken	OMPLLAHN_05500	OMPLLAHN_05500	14756	6	13.06	0.45	0.45	0.34
Chicken	OMPLLAHN_05503	OMPLLAHN_05503	14756	6	10.88	0.32	0.32	0.37
Chicken	OMPLLAHN_05504	OMPLLAHN_05504	14756	6	14.64	0.34	0.34	0.37
Chicken	OMPLLAHN_05514	OMPLLAHN_05514	14756	6	13.16	0.47	0.47	0.33
Chicken	OMPLLAHN_05518	OMPLLAHN_05518	14756	6	11.56	0.46	0.46	0.33
Chicken	GEFDMLIC_04894	yahB_3	Sap638	5	9.76	0.15	0.15	0.34
Chicken	OMPLLAHN_01987	OMPLLAHN_01987	14756	5	11.27	0.37	0.37	0.36
Chicken	OMPLLAHN_02008	ygaQ_2	14756	5	11.22	0.41	0.41	0.35
Chicken	OMPLLAHN_02566	OMPLLAHN_02566	14756	5	11.97	0.44	0.44	0.35
Chicken	OMPLLAHN_02567	ydcM_1	14756	5	10.84	0.45	0.45	0.31
Chicken	OMPLLAHN_02644	OMPLLAHN_02644	14756	5	12.00	0.49	0.49	0.34
Chicken	OMPLLAHN_03123	OMPLLAHN_03123	14756	5	10.86	0.35	0.35	0.32
Chicken	OMPLLAHN_03125	glmM_2	14756	5	14.36	0.34	0.34	0.38
Chicken	OMPLLAHN_03142	wcaE	14756	5	13.02	0.43	0.43	0.33
Chicken	OMPLLAHN_03176	cobT_2	14756	5	13.01	0.42	0.42	0.31
Chicken	OMPLLAHN_03202	OMPLLAHN_03202	14756	5	13.06	0.41	0.41	0.33
Chicken	OMPLLAHN_03242	OMPLLAHN_03242	14756	5	10.87	0.36	0.36	0.32
Chicken	OMPLLAHN_03293	OMPLLAHN_03293	14756	5	10.57	0.21	0.21	0.31
Chicken	OMPLLAHN_03366	fecD_4	14756	5	11.10	0.37	0.37	0.37
Chicken	OMPLLAHN_03423	ppc	14756	5	11.82	0.43	0.43	0.34
Chicken	OMPLLAHN_03510	OMPLLAHN_03510	14756	5	12.58	0.39	0.39	0.51
Chicken	OMPLLAHN_03712	OMPLLAHN_03712	14756	5	11.30	0.40	0.40	0.36
Chicken	OMPLLAHN_03947	OMPLLAHN_03947	14756	5	12.93	0.31	0.31	0.41

Chicken	OMPLLAHN_04116	OMPLLAHN_04116	14756	5	11.55	0.43	0.43	0.37
Chicken	OMPLLAHN_04134	OMPLLAHN_04134	14756	5	14.64	0.39	0.39	0.37
Chicken	OMPLLAHN_04135	OMPLLAHN_04135	14756	5	11.25	0.53	0.47	0.33
Chicken	OMPLLAHN_04149	OMPLLAHN_04149	14756	5	11.11	0.39	0.39	0.33
Chicken	OMPLLAHN_04150	OMPLLAHN_04150	14756	5	10.60	0.42	0.42	0.34
Chicken	OMPLLAHN_04163	topB_2	14756	5	10.88	0.37	0.37	0.34
Chicken	OMPLLAHN_04476	OMPLLAHN_04476	14756	5	11.40	0.46	0.46	0.37
Chicken	OMPLLAHN_04485	OMPLLAHN_04485	14756	5	11.27	0.42	0.42	0.33
Chicken	OMPLLAHN_04501	OMPLLAHN_04501	14756	5	11.01	0.36	0.36	0.39
Chicken	OMPLLAHN_04747	OMPLLAHN_04747	14756	5	14.19	0.43	0.43	0.36
Chicken	OMPLLAHN_05041	cvaA	14756	5	12.28	0.52	0.48	0.30
Chicken	OMPLLAHN_05143	hmuT	14756	5	10.42	0.28	0.28	0.37
Chicken	OMPLLAHN_05202	OMPLLAHN_05202	14756	5	10.92	0.35	0.35	0.36
Chicken	OMPLLAHN_05243	OMPLLAHN_05243	14756	5	12.58	0.37	0.37	0.39
Chicken	OMPLLAHN_05311	OMPLLAHN_05311	14756	5	12.72	0.39	0.39	0.34
Chicken	OMPLLAHN_05420	OMPLLAHN_05420	14756	5	10.75	0.49	0.49	0.28
Chicken	OMPLLAHN_05464	ulaC_2	14756	5	14.26	0.37	0.37	0.37
Chicken	OMPLLAHN_05486	OMPLLAHN_05486	14756	5	10.63	0.19	0.19	0.33
Chicken	OMPLLAHN_05513	OMPLLAHN_05513	14756	5	13.73	0.42	0.42	0.35
Chicken	OMPLLAHN_05526	OMPLLAHN_05526	14756	5	11.81	0.38	0.38	0.31
Chicken	FKALCOLL_04518	bcsA_2	21225_2#181	4	10.57	0.30	0.30	0.38
Chicken	OMPLLAHN_00179	OMPLLAHN_00179	14756	4	10.93	0.38	0.38	0.31
Chicken	OMPLLAHN_00281	fepD	14756	4	11.71	0.37	0.37	0.35
Chicken	OMPLLAHN_00315	OMPLLAHN_00315	14756	4	12.04	0.40	0.40	0.32
Chicken	OMPLLAHN_00375	tolC_1	14756	4	11.00	0.47	0.47	0.33
Chicken	OMPLLAHN_00442	OMPLLAHN_00442	14756	4	11.23	0.54	0.46	0.35
Chicken	OMPLLAHN_01271	yddK_1	14756	4	10.51	0.45	0.45	0.30
Chicken	OMPLLAHN_01921	rlmG	14756	4	11.06	0.62	0.38	0.37
Chicken	OMPLLAHN_02311	OMPLLAHN_02311	14756	4	10.71	0.34	0.34	0.37
Chicken	OMPLLAHN_02885	OMPLLAHN_02885	14756	4	10.91	0.47	0.47	0.34
Chicken	OMPLLAHN_02972	OMPLLAHN_02972	14756	4	10.83	0.64	0.36	0.31
Chicken	OMPLLAHN_03032	elfG	14756	4	11.36	0.46	0.46	0.32

Chicken	OMPLLAHN_03126	cpsB_1	14756	4	12.32	0.38	0.38	0.34
Chicken	OMPLLAHN_03183	OMPLLAHN_03183	14756	4	10.53	0.29	0.29	0.29
Chicken	OMPLLAHN_03201	OMPLLAHN_03201	14756	4	13.95	0.38	0.38	0.35
Chicken	OMPLLAHN_03228	cgkA	14756	4	10.80	0.40	0.40	0.29
Chicken	OMPLLAHN_03232	OMPLLAHN_03232	14756	4	10.73	0.44	0.44	0.29
Chicken	OMPLLAHN_03238	parB	14756	4	10.86	0.40	0.40	0.30
Chicken	OMPLLAHN_03241	OMPLLAHN_03241	14756	4	11.09	0.47	0.47	0.31
Chicken	OMPLLAHN_03251	OMPLLAHN_03251	14756	4	11.63	0.37	0.37	0.30
Chicken	OMPLLAHN_03278	OMPLLAHN_03278	14756	4	12.96	0.44	0.44	0.33
Chicken	OMPLLAHN_03363	fhuA_2	14756	4	12.08	0.41	0.41	0.37
Chicken	OMPLLAHN_03376	plsC	14756	4	11.47	0.37	0.37	0.39
Chicken	OMPLLAHN_03823	ymfK_2	14756	4	12.24	0.49	0.49	0.30
Chicken	OMPLLAHN_04101	yqiG_1	14756	4	11.97	0.28	0.28	0.36
Chicken	OMPLLAHN_04106	intD_2	14756	4	10.65	0.40	0.40	0.33
Chicken	OMPLLAHN_04110	OMPLLAHN_04110	14756	4	10.75	0.49	0.49	0.28
Chicken	OMPLLAHN_04112	OMPLLAHN_04112	14756	4	16.28	0.38	0.38	0.38
Chicken	OMPLLAHN_04156	OMPLLAHN_04156	14756	4	10.39	0.42	0.42	0.30
Chicken	OMPLLAHN_04255	ogrK_2	14756	4	10.92	0.32	0.32	0.43
Chicken	OMPLLAHN_04420	OMPLLAHN_04420	14756	4	12.76	0.33	0.33	0.41
Chicken	OMPLLAHN_04422	OMPLLAHN_04422	14756	4	10.38	0.36	0.36	0.30
Chicken	OMPLLAHN_04428	hsdS_1	14756	4	12.98	0.43	0.43	0.37
Chicken	OMPLLAHN_04479	OMPLLAHN_04479	14756	4	12.92	0.40	0.40	0.33
Chicken	OMPLLAHN_04548	hsdR_3	14756	4	11.95	0.32	0.32	0.35
Chicken	OMPLLAHN_04552	OMPLLAHN_04552	14756	4	10.61	0.29	0.29	0.34
Chicken	OMPLLAHN_04560	ydiP_2	14756	4	10.26	0.18	0.18	0.35
Chicken	OMPLLAHN_04702	bfpB_3	14756	4	10.87	0.44	0.44	0.34
Chicken	OMPLLAHN_04735	OMPLLAHN_04735	14756	4	10.97	0.43	0.43	0.30
Chicken	OMPLLAHN_04762	yfjP_1	14756	4	10.70	0.50	0.50	0.27
Chicken	OMPLLAHN_04890	nuc	14756	4	10.58	0.38	0.38	0.31
Chicken	OMPLLAHN_04929	OMPLLAHN_04929	14756	4	14.53	0.37	0.37	0.36
Chicken	OMPLLAHN_04935	OMPLLAHN_04935	14756	4	10.48	0.35	0.35	0.31
Chicken	OMPLLAHN_05083	traL	14756	4	11.93	0.39	0.39	0.32

Chicken	OMPLLAHN_05085	OMPLLAHN_05085	14756	4	11.57	0.35	0.35	0.30
Chicken	OMPLLAHN_05120	OMPLLAHN_05120	14756	4	10.39	0.31	0.31	0.30
Chicken	OMPLLAHN_05179	znuA_3	14756	4	11.19	0.48	0.48	0.31
Chicken	OMPLLAHN_05223	OMPLLAHN_05223	14756	4	13.67	0.37	0.37	0.36
Chicken	OMPLLAHN_05244	OMPLLAHN_05244	14756	4	14.25	0.47	0.47	0.36
Chicken	OMPLLAHN_05247	OMPLLAHN_05247	14756	4	10.68	0.31	0.31	0.43
Chicken	OMPLLAHN_05299	OMPLLAHN_05299	14756	4	12.65	0.46	0.46	0.33
Chicken	OMPLLAHN_05301	nanE_2	14756	4	10.52	0.41	0.41	0.30
Chicken	OMPLLAHN_05328	neo_1	14756	4	11.95	0.43	0.43	0.30
Chicken	OMPLLAHN_05341	cytR_4	14756	4	13.54	0.50	0.50	0.37
Chicken	OMPLLAHN_05387	yagA_1	14756	4	12.56	0.41	0.41	0.36
Chicken	OMPLLAHN_05389	OMPLLAHN_05389	14756	4	16.78	0.61	0.39	0.41
Chicken	OMPLLAHN_05428	gpFI_3	14756	4	10.44	0.39	0.39	0.30
Chicken	OMPLLAHN_05461	tktA_2	14756	4	11.69	0.46	0.46	0.34
Chicken	OMPLLAHN_05485	OMPLLAHN_05485	14756	4	11.08	0.46	0.46	0.31
Chicken	OMPLLAHN_05502	OMPLLAHN_05502	14756	4	12.78	0.30	0.30	0.50
Chicken	OMPLLAHN_05507	OMPLLAHN_05507	14756	4	10.47	0.25	0.25	0.35
Chicken	OMPLLAHN_05539	OMPLLAHN_05539	14756	4	13.65	0.45	0.45	0.32
Chicken	OMPLLAHN_05550	OMPLLAHN_05550	14756	4	12.56	0.52	0.48	0.29
Chicken	OMPLLAHN_05612	OMPLLAHN_05612	14756	4	10.75	0.15	0.15	0.60
Chicken	FKALCOLL_01689	rzpD_2	21225_2#181	3	10.53	0.31	0.31	0.29
Chicken	GEFDMLIC_04905	GEFDMLIC_04905	Sap638	3	10.87	0.11	0.11	0.46
Chicken	OMPLLAHN_00056	OMPLLAHN_00056	14756	3	11.98	0.35	0.35	0.33
Chicken	OMPLLAHN_00060	OMPLLAHN_00060	14756	3	10.68	0.38	0.38	0.30
Chicken	OMPLLAHN_00094	OMPLLAHN_00094	14756	3	10.46	0.54	0.46	0.26
Chicken	OMPLLAHN_00370	cueR	14756	3	10.36	0.66	0.34	0.38
Chicken	OMPLLAHN_00371	prsE	14756	3	10.36	0.66	0.34	0.38
Chicken	OMPLLAHN_00476	adrA	14756	3	10.47	0.42	0.42	0.33
Chicken	OMPLLAHN_00622	elfC_1	14756	3	11.05	0.38	0.38	0.38
Chicken	OMPLLAHN_00727	slp	14756	3	10.94	0.89	0.11	0.58
Chicken	OMPLLAHN_00731	btuF_1	14756	3	10.33	0.49	0.49	0.34
Chicken	OMPLLAHN_00981	fhuA_1	14756	3	11.93	0.47	0.47	0.35

Chicken	OMPLLAHN_01256	ddpF	14756	3	11.01	0.36	0.36	0.37
Chicken	OMPLLAHN_02090	pphB	14756	3	10.86	0.38	0.38	0.37
Chicken	OMPLLAHN_02277	OMPLLAHN_02277	14756	3	10.59	0.41	0.41	0.33
Chicken	OMPLLAHN_02285	yehA	14756	3	11.44	0.36	0.36	0.35
Chicken	OMPLLAHN_02378	flhA_1	14756	3	10.90	0.42	0.42	0.36
Chicken	OMPLLAHN_02394	ygeM	14756	3	11.40	0.43	0.43	0.36
Chicken	OMPLLAHN_02471	OMPLLAHN_02471	14756	3	10.92	0.44	0.44	0.29
Chicken	OMPLLAHN_02727	OMPLLAHN_02727	14756	3	11.06	0.38	0.38	0.34
Chicken	OMPLLAHN_02964	ygeH_2	14756	3	10.63	0.45	0.45	0.37
Chicken	OMPLLAHN_02965	yeeJ_1	14756	3	10.91	0.38	0.38	0.35
Chicken	OMPLLAHN_03127	OMPLLAHN_03127	14756	3	11.80	0.35	0.35	0.30
Chicken	OMPLLAHN_03179	intA_3	14756	3	12.54	0.37	0.37	0.36
Chicken	OMPLLAHN_03181	yhcD	14756	3	13.04	0.35	0.35	0.39
Chicken	OMPLLAHN_03186	OMPLLAHN_03186	14756	3	13.46	0.42	0.42	0.34
Chicken	OMPLLAHN_03274	OMPLLAHN_03274	14756	3	10.64	0.39	0.39	0.31
Chicken	OMPLLAHN_03288	OMPLLAHN_03288	14756	3	10.85	0.38	0.38	0.33
Chicken	OMPLLAHN_03300	polA_1	14756	3	12.07	0.40	0.40	0.33
Chicken	OMPLLAHN_03321	cbeA_3	14756	3	14.97	0.41	0.41	0.36
Chicken	OMPLLAHN_03515	ogrK_1	14756	3	10.51	0.22	0.22	0.47
Chicken	OMPLLAHN_03599	ykgF_1	14756	3	11.27	0.48	0.48	0.36
Chicken	OMPLLAHN_03603	hsdM_1	14756	3	13.05	0.45	0.45	0.32
Chicken	OMPLLAHN_03609	glpT_3	14756	3	10.33	0.49	0.49	0.34
Chicken	OMPLLAHN_03610	OMPLLAHN_03610	14756	3	10.71	0.40	0.40	0.33
Chicken	OMPLLAHN_03744	hcaE	14756	3	10.79	0.45	0.45	0.35
Chicken	OMPLLAHN_03789	OMPLLAHN_03789	14756	3	10.84	0.40	0.40	0.30
Chicken	OMPLLAHN_03925	ytfR	14756	3	10.67	0.39	0.39	0.33
Chicken	OMPLLAHN_03946	xerD_2	14756	3	10.69	0.34	0.34	0.35
Chicken	OMPLLAHN_03956	OMPLLAHN_03956	14756	3	11.99	0.39	0.39	0.37
Chicken	OMPLLAHN_03959	OMPLLAHN_03959	14756	3	10.37	0.32	0.32	0.41
Chicken	OMPLLAHN_04026	OMPLLAHN_04026	14756	3	11.41	0.39	0.39	0.32
Chicken	OMPLLAHN_04113	OMPLLAHN_04113	14756	3	11.60	0.33	0.33	0.35
Chicken	OMPLLAHN_04114	OMPLLAHN_04114	14756	3	13.42	0.44	0.44	0.38

Chicken	OMPLLAHN_04129	OMPLLAHN_04129	14756	3	13.47	0.44	0.44	0.34
Chicken	OMPLLAHN_04140	OMPLLAHN_04140	14756	3	11.53	0.44	0.44	0.31
Chicken	OMPLLAHN_04162	OMPLLAHN_04162	14756	3	11.48	0.41	0.41	0.36
Chicken	OMPLLAHN_04250	OMPLLAHN_04250	14756	3	10.81	0.21	0.21	0.45
Chicken	OMPLLAHN_04257	OMPLLAHN_04257	14756	3	11.10	0.36	0.36	0.33
Chicken	OMPLLAHN_04283	OMPLLAHN_04283	14756	3	12.57	0.42	0.42	0.35
Chicken	OMPLLAHN_04417	OMPLLAHN_04417	14756	3	13.16	0.43	0.43	0.33
Chicken	OMPLLAHN_04421	bfpB_1	14756	3	11.07	0.32	0.32	0.35
Chicken	OMPLLAHN_04481	OMPLLAHN_04481	14756	3	10.68	0.52	0.48	0.28
Chicken	OMPLLAHN_04483	OMPLLAHN_04483	14756	3	12.27	0.44	0.44	0.37
Chicken	OMPLLAHN_04498	yafT	14756	3	10.56	0.36	0.36	0.34
Chicken	OMPLLAHN_04508	OMPLLAHN_04508	14756	3	11.02	0.44	0.44	0.41
Chicken	OMPLLAHN_04551	OMPLLAHN_04551	14756	3	12.35	0.39	0.39	0.29
Chicken	OMPLLAHN_04559	rbn_2	14756	3	11.25	0.42	0.42	0.39
Chicken	OMPLLAHN_04572	OMPLLAHN_04572	14756	3	11.73	0.28	0.28	0.38
Chicken	OMPLLAHN_04614	hsdM_4	14756	3	10.76	0.40	0.40	0.31
Chicken	OMPLLAHN_04619	recF_2	14756	3	12.42	0.39	0.39	0.36
Chicken	OMPLLAHN_04691	dinI_4	14756	3	12.03	0.46	0.46	0.33
Chicken	OMPLLAHN_04692	OMPLLAHN_04692	14756	3	14.09	0.42	0.42	0.37
Chicken	OMPLLAHN_04694	OMPLLAHN_04694	14756	3	10.86	0.55	0.45	0.32
Chicken	OMPLLAHN_04701	OMPLLAHN_04701	14756	3	11.03	0.38	0.38	0.33
Chicken	OMPLLAHN_04705	OMPLLAHN_04705	14756	3	10.44	0.40	0.40	0.32
Chicken	OMPLLAHN_04706	ptlF	14756	3	11.23	0.43	0.43	0.34
Chicken	OMPLLAHN_04715	OMPLLAHN_04715	14756	3	11.81	0.40	0.40	0.31
Chicken	OMPLLAHN_04751	shlB	14756	3	10.65	0.48	0.48	0.34
Chicken	OMPLLAHN_04886	OMPLLAHN_04886	14756	3	10.69	0.44	0.44	0.32
Chicken	OMPLLAHN_04915	OMPLLAHN_04915	14756	3	12.93	0.40	0.40	0.32
Chicken	OMPLLAHN_04938	OMPLLAHN_04938	14756	3	10.49	0.47	0.47	0.28
Chicken	OMPLLAHN_04940	OMPLLAHN_04940	14756	3	10.33	0.49	0.49	0.26
Chicken	OMPLLAHN_05003	OMPLLAHN_05003	14756	3	10.64	0.49	0.49	0.34
Chicken	OMPLLAHN_05050	paoC	14756	3	11.95	0.37	0.37	0.36
Chicken	OMPLLAHN_05090	OMPLLAHN_05090	14756	3	11.24	0.44	0.44	0.30

Chicken	OMPLLAHN_05103	stfE_1	14756	3	11.87	0.46	0.46	0.33
Chicken	OMPLLAHN_05141	fecE_1	14756	3	10.39	0.23	0.23	0.33
Chicken	OMPLLAHN_05182	OMPLLAHN_05182	14756	3	10.83	0.66	0.34	0.31
Chicken	OMPLLAHN_05184	OMPLLAHN_05184	14756	3	10.26	0.19	0.19	0.33
Chicken	OMPLLAHN_05197	OMPLLAHN_05197	14756	3	10.69	0.45	0.45	0.29
Chicken	OMPLLAHN_05246	OMPLLAHN_05246	14756	3	13.80	0.26	0.26	0.49
Chicken	OMPLLAHN_05257	ymfK_3	14756	3	11.56	0.40	0.40	0.32
Chicken	OMPLLAHN_05287	OMPLLAHN_05287	14756	3	10.78	0.39	0.39	0.30
Chicken	OMPLLAHN_05305	OMPLLAHN_05305	14756	3	10.67	0.52	0.48	0.31
Chicken	OMPLLAHN_05313	kgtP	14756	3	11.26	0.37	0.37	0.37
Chicken	OMPLLAHN_05343	lacY_3	14756	3	10.52	0.45	0.45	0.30
Chicken	OMPLLAHN_05432	OMPLLAHN_05432	14756	3	11.85	0.49	0.49	0.35
Chicken	OMPLLAHN_05441	ugpB_4	14756	3	11.31	0.37	0.37	0.36
Chicken	OMPLLAHN_05444	pagN_2	14756	3	10.91	0.36	0.36	0.30
Chicken	OMPLLAHN_05508	OMPLLAHN_05508	14756	3	11.07	0.22	0.22	0.43
Chicken	OMPLLAHN_05511	OMPLLAHN_05511	14756	3	13.07	0.48	0.48	0.33
Chicken	OMPLLAHN_05517	yfjP_3	14756	3	10.67	0.11	0.11	0.46
Chicken	OMPLLAHN_05570	OMPLLAHN_05570	14756	3	14.88	0.36	0.36	0.39
Chicken	OMPLLAHN_05584	OMPLLAHN_05584	14756	3	10.40	0.32	0.32	0.30
Chicken	OMPLLAHN_05586	OMPLLAHN_05586	14756	3	13.44	0.44	0.44	0.36
Chicken	OMPLLAHN_05587	OMPLLAHN_05587	14756	3	12.60	0.42	0.42	0.33
Chicken	OMPLLAHN_05590	OMPLLAHN_05590	14756	3	10.75	0.44	0.44	0.33
Chicken	OMPLLAHN_05613	tfaE_2	14756	3	10.61	0.40	0.40	0.32
Chicken	OMPLLAHN_05616	OMPLLAHN_05616	14756	3	13.44	0.44	0.44	0.36
Chicken	OMPLLAHN_05626	insD_4	14756	3	10.52	0.71	0.29	0.27
Chicken	OMPLLAHN_05651	OMPLLAHN_05651	14756	3	10.83	0.66	0.34	0.31
Chicken	FKALCOLL_01127	FKALCOLL_01127	21225_2#181	2	10.73	0.63	0.37	0.36
Chicken	FKALCOLL_01690	trkG	21225_2#181	2	10.51	0.34	0.34	0.28
Chicken	FKALCOLL_02941	ecfT	21225_2#181	2	10.50	0.39	0.39	0.29
Chicken	FKALCOLL_03988	FKALCOLL_03988	21225_2#181	2	10.87	0.23	0.23	0.30
Chicken	FKALCOLL_04478	FKALCOLL_04478	21225_2#181	2	10.74	0.26	0.26	0.29
Chicken	FKALCOLL_04517	bcsB_2	21225_2#181	2	11.05	0.13	0.13	0.40

Chicken	FKALCOLL_04527	FKALCOLL_04527	21225_2#181	2	10.12	0.19	0.19	0.31
Chicken	FKALCOLL_04564	malI_2	21225_2#181	2	10.84	0.36	0.36	0.28
Chicken	FKALCOLL_04656	yliE_2	21225_2#181	2	10.23	0.26	0.26	0.35
Chicken	OMPLLAHN_00001	pinE_1	14756	2	12.11	0.38	0.38	0.36
Chicken	OMPLLAHN_00049	OMPLLAHN_00049	14756	2	11.39	0.39	0.39	0.33
Chicken	OMPLLAHN_00050	OMPLLAHN_00050	14756	2	10.20	0.52	0.48	0.33
Chicken	OMPLLAHN_00058	OMPLLAHN_00058	14756	2	11.13	0.33	0.33	0.40
Chicken	OMPLLAHN_00059	OMPLLAHN_00059	14756	2	11.08	0.51	0.49	0.30
Chicken	OMPLLAHN_00092	OMPLLAHN_00092	14756	2	10.56	0.39	0.39	0.30
Chicken	OMPLLAHN_00292	ybdK	14756	2	10.93	0.50	0.50	0.42
Chicken	OMPLLAHN_00593	yhgE	14756	2	11.81	0.42	0.42	0.34
Chicken	OMPLLAHN_00597	greB	14756	2	10.22	0.38	0.38	0.34
Chicken	OMPLLAHN_00620	ycbV	14756	2	10.77	0.48	0.48	0.33
Chicken	OMPLLAHN_00623	fimC_1	14756	2	11.52	0.40	0.40	0.35
Chicken	OMPLLAHN_00665	tusA	14756	2	10.25	0.40	0.40	0.30
Chicken	OMPLLAHN_00670	OMPLLAHN_00670	14756	2	10.74	0.41	0.41	0.33
Chicken	OMPLLAHN_00673	OMPLLAHN_00673	14756	2	11.14	0.52	0.48	0.31
Chicken	OMPLLAHN_00759	OMPLLAHN_00759	14756	2	10.50	0.36	0.36	0.36
Chicken	OMPLLAHN_00783	OMPLLAHN_00783	14756	2	11.00	0.48	0.48	0.37
Chicken	OMPLLAHN_00855	yehB_1	14756	2	10.55	0.48	0.48	0.34
Chicken	OMPLLAHN_00891	yabP_1	14756	2	10.83	0.39	0.39	0.33
Chicken	OMPLLAHN_00967	yadC	14756	2	10.67	0.42	0.42	0.33
Chicken	OMPLLAHN_00968	yadK	14756	2	10.83	0.40	0.40	0.35
Chicken	OMPLLAHN_00970	htrE	14756	2	10.76	0.40	0.40	0.36
Chicken	OMPLLAHN_01063	ydiQ	14756	2	10.44	0.41	0.41	0.32
Chicken	OMPLLAHN_01160	pntA	14756	2	10.84	0.34	0.34	0.40
Chicken	OMPLLAHN_01288	slrP	14756	2	12.23	0.41	0.41	0.36
Chicken	OMPLLAHN_01295	btuB_1	14756	2	10.31	0.59	0.41	0.42
Chicken	OMPLLAHN_01491	lacA_1	14756	2	10.63	0.38	0.38	0.33
Chicken	OMPLLAHN_01547	dapE	14756	2	11.03	0.35	0.35	0.35
Chicken	OMPLLAHN_01708	nuoG	14756	2	10.80	0.38	0.38	0.32
Chicken	OMPLLAHN_01731	arnT	14756	2	11.32	0.46	0.46	0.29

Chicken	OMPLLAHN_01800	elbB	14756	2	11.30	0.60	0.40	0.45
Chicken	OMPLLAHN_01920	ygjP	14756	2	11.24	0.38	0.38	0.35
Chicken	OMPLLAHN_01939	OMPLLAHN_01939	14756	2	11.56	0.39	0.39	0.31
Chicken	OMPLLAHN_01998	ptsG_1	14756	2	11.06	0.37	0.37	0.34
Chicken	OMPLLAHN_02006	ypjB	14756	2	10.63	0.40	0.40	0.38
Chicken	OMPLLAHN_02135	ygcG_3	14756	2	10.94	0.34	0.34	0.37
Chicken	OMPLLAHN_02242	mglA	14756	2	11.02	0.55	0.45	0.44
Chicken	OMPLLAHN_02249	yohK	14756	2	10.47	0.53	0.47	0.36
Chicken	OMPLLAHN_02353	guaD	14756	2	10.33	0.46	0.46	0.33
Chicken	OMPLLAHN_02398	ygeH_1	14756	2	11.05	0.46	0.46	0.31
Chicken	OMPLLAHN_02401	OMPLLAHN_02401	14756	2	10.50	0.47	0.47	0.34
Chicken	OMPLLAHN_02576	zwf	14756	2	10.82	0.67	0.33	0.45
Chicken	OMPLLAHN_02630	intD_1	14756	2	11.09	0.49	0.49	0.29
Chicken	OMPLLAHN_02652	ssuC	14756	2	11.00	0.40	0.40	0.35
Chicken	OMPLLAHN_02876	ybjE	14756	2	10.50	0.42	0.42	0.30
Chicken	OMPLLAHN_02938	exuT_2	14756	2	10.49	0.37	0.37	0.34
Chicken	OMPLLAHN_02962	OMPLLAHN_02962	14756	2	11.50	0.37	0.37	0.34
Chicken	OMPLLAHN_02966	nepI_1	14756	2	11.35	0.51	0.49	0.40
Chicken	OMPLLAHN_02975	uhpB	14756	2	10.75	0.41	0.41	0.32
Chicken	OMPLLAHN_03174	dnaE_2	14756	2	10.73	0.57	0.43	0.30
Chicken	OMPLLAHN_03175	cobS_2	14756	2	11.00	0.45	0.45	0.32
Chicken	OMPLLAHN_03191	OMPLLAHN_03191	14756	2	12.68	0.35	0.35	0.38
Chicken	OMPLLAHN_03199	OMPLLAHN_03199	14756	2	11.33	0.39	0.39	0.33
Chicken	OMPLLAHN_03215	OMPLLAHN_03215	14756	2	10.76	0.74	0.26	0.34
Chicken	OMPLLAHN_03235	OMPLLAHN_03235	14756	2	10.41	0.42	0.42	0.31
Chicken	OMPLLAHN_03244	OMPLLAHN_03244	14756	2	10.69	0.27	0.27	0.33
Chicken	OMPLLAHN_03254	OMPLLAHN_03254	14756	2	10.59	0.39	0.39	0.33
Chicken	OMPLLAHN_03261	OMPLLAHN_03261	14756	2	10.49	0.36	0.36	0.28
Chicken	OMPLLAHN_03265	OMPLLAHN_03265	14756	2	10.38	0.29	0.29	0.32
Chicken	OMPLLAHN_03276	OMPLLAHN_03276	14756	2	10.59	0.42	0.42	0.31
Chicken	OMPLLAHN_03279	coaE_2	14756	2	12.30	0.40	0.40	0.36
Chicken	OMPLLAHN_03282	thyA_2	14756	2	11.00	0.37	0.37	0.36

Chicken	OMPLLAHN_03283	OMPLLAHN_03283	14756	2	10.23	0.38	0.38	0.32	
Chicken	OMPLLAHN_03284	nrdB_2	14756	2	11.14	0.34	0.34	0.31	
Chicken	OMPLLAHN_03296	OMPLLAHN_03296	14756	2	11.88	0.28	0.28	0.32	
Chicken	OMPLLAHN_03297	OMPLLAHN_03297	14756	2	11.88	0.43	0.43	0.37	
Chicken	OMPLLAHN_03298	recA_2	14756	2	10.41	0.43	0.43	0.32	
Chicken	OMPLLAHN_03303	OMPLLAHN_03303	14756	2	11.62	0.40	0.40	0.34	
Chicken	OMPLLAHN_03362	parE	14756	2	11.25	0.65	0.35	0.41	
Chicken	OMPLLAHN_03513	gpFI_1	14756	2	12.38	0.54	0.46	0.36	
Chicken	OMPLLAHN_03576	ampC	14756	2	11.13	0.39	0.39	0.37	
Chicken	OMPLLAHN_03601	hsdR_1	14756	2	10.84	0.43	0.43	0.31	
Chicken	OMPLLAHN_03606	ygeV_2	14756	2	10.28	0.40	0.40	0.30	
Chicken	OMPLLAHN_03661	phnL	14756	2	11.29	0.35	0.35	0.37	
Chicken	OMPLLAHN_03713	OMPLLAHN_03713	14756	2	10.43	0.45	0.45	0.39	
Chicken	OMPLLAHN_03751	yphC	14756	2	11.22	0.48	0.48	0.37	
Chicken	OMPLLAHN_03814	OMPLLAHN_03814	14756	2	10.81	0.54	0.46	0.31	
Chicken	OMPLLAHN_03876	metH	14756	2	10.22	0.63	0.37	0.35	
Chicken	OMPLLAHN_03888	OMPLLAHN_03888	14756	2	10.92	0.42	0.42	0.33	
Chicken	OMPLLAHN_03920	yjgA	14756	2	11.89	0.42	0.42	0.33	
Chicken	OMPLLAHN_03923	yjfF	14756	2	10.75	0.46	0.46	0.32	
Chicken	OMPLLAHN_03944	OMPLLAHN_03944	14756	2	11.07	0.40	0.40	0.37	
Chicken	OMPLLAHN_03951	OMPLLAHN_03951	14756	2	10.42	0.16	0.16	0.36	
Chicken	OMPLLAHN_03955	OMPLLAHN_03955	14756	2	11.22	0.40	0.40	0.35	
Chicken	OMPLLAHN_03957	OMPLLAHN_03957	14756	2	11.20	0.11	0.11	0.47	
Chicken	OMPLLAHN_03958	OMPLLAHN_03958	14756	2	10.66	0.28	0.28	0.35	
Chicken	OMPLLAHN_04041	OMPLLAHN_04041	14756	2	11.13	0.69	0.31	0.32	
Chicken	OMPLLAHN_04090	OMPLLAHN_04090	14756	2	10.48	0.40	0.40	0.30	
Chicken	OMPLLAHN_04105	OMPLLAHN_04105	14756	2	10.12	0.40	0.40	0.32	
Chicken	OMPLLAHN_04120	OMPLLAHN_04120	14756	2	10.54	0.35	0.35	0.33	
Chicken	OMPLLAHN_04143	OMPLLAHN_04143	14756	2	10.41	0.24	0.24	0.36	
Chicken	OMPLLAHN_04145	OMPLLAHN_04145	14756	2	11.87	0.40	0.40	0.33	
Chicken	OMPLLAHN_04153	OMPLLAHN_04153	14756	2	10.23	0.17	0.17	0.37	
Chicken	OMPLLAHN_04159	OMPLLAHN_04159	14756	2	10.41	0.37	0.37	0.32	

Chicken	OMPLLAHN_04169	OMPLLAHN_04169	14756	2	10.82	0.38	0.38	0.31
Chicken	OMPLLAHN_04179	OMPLLAHN_04179	14756	2	11.65	0.45	0.45	0.32
Chicken	OMPLLAHN_04185	cpsD	14756	2	10.86	0.38	0.38	0.35
Chicken	OMPLLAHN_04253	gpFI_2	14756	2	12.38	0.54	0.46	0.36
Chicken	OMPLLAHN_04335	cotSA	14756	2	10.84	0.55	0.45	0.33
Chicken	OMPLLAHN_04419	OMPLLAHN_04419	14756	2	10.44	0.29	0.29	0.34
Chicken	OMPLLAHN_04423	OMPLLAHN_04423	14756	2	13.61	0.43	0.43	0.33
Chicken	OMPLLAHN_04443	yhgA_2	14756	2	10.90	0.40	0.40	0.32
Chicken	OMPLLAHN_04477	OMPLLAHN_04477	14756	2	10.45	0.39	0.39	0.31
Chicken	OMPLLAHN_04480	bfpB_2	14756	2	10.74	0.42	0.42	0.28
Chicken	OMPLLAHN_04484	OMPLLAHN_04484	14756	2	13.42	0.44	0.44	0.39
Chicken	OMPLLAHN_04509	OMPLLAHN_04509	14756	2	10.42	0.37	0.37	0.35
Chicken	OMPLLAHN_04519	OMPLLAHN_04519	14756	2	10.72	0.35	0.35	0.39
Chicken	OMPLLAHN_04547	OMPLLAHN_04547	14756	2	10.64	0.47	0.47	0.30
Chicken	OMPLLAHN_04558	hpaB	14756	2	12.03	0.52	0.48	0.34
Chicken	OMPLLAHN_04567	ycgM_1	14756	2	10.70	0.71	0.29	0.36
Chicken	OMPLLAHN_04613	OMPLLAHN_04613	14756	2	15.01	0.33	0.33	0.39
Chicken	OMPLLAHN_04617	hsdR_4	14756	2	10.50	0.36	0.36	0.36
Chicken	OMPLLAHN_04644	insD_2	14756	2	10.21	0.69	0.31	0.26
Chicken	OMPLLAHN_04654	ybcM	14756	2	10.40	0.69	0.31	0.31
Chicken	OMPLLAHN_04693	yadA	14756	2	10.61	0.37	0.37	0.34
Chicken	OMPLLAHN_04695	outO_1	14756	2	11.72	0.43	0.43	0.31
Chicken	OMPLLAHN_04707	virB8	14756	2	11.47	0.40	0.40	0.31
Chicken	OMPLLAHN_04721	OMPLLAHN_04721	14756	2	11.98	0.39	0.39	0.34
Chicken	OMPLLAHN_04754	OMPLLAHN_04754	14756	2	10.61	0.47	0.47	0.29
Chicken	OMPLLAHN_04760	OMPLLAHN_04760	14756	2	10.85	0.36	0.36	0.33
Chicken	OMPLLAHN_04775	OMPLLAHN_04775	14756	2	10.75	0.55	0.45	0.27
Chicken	OMPLLAHN_04778	yjhR_2	14756	2	10.83	0.47	0.47	0.29
Chicken	OMPLLAHN_04866	fadH_2	14756	2	11.05	0.57	0.43	0.40
Chicken	OMPLLAHN_04882	ykgH	14756	2	10.48	0.39	0.39	0.35
Chicken	OMPLLAHN_04898	OMPLLAHN_04898	14756	2	10.77	0.59	0.41	0.33
Chicken	OMPLLAHN_04910	OMPLLAHN_04910	14756	2	12.75	0.35	0.35	0.37

Chicken	OMPLLAHN_04927	recD_2	14756	2	11.31	0.45	0.45	0.31
Chicken	OMPLLAHN_04931	OMPLLAHN_04931	14756	2	11.78	0.36	0.36	0.35
Chicken	OMPLLAHN_04946	OMPLLAHN_04946	14756	2	10.74	0.37	0.37	0.31
Chicken	OMPLLAHN_04951	intS_2	14756	2	10.52	0.13	0.13	0.42
Chicken	OMPLLAHN_05000	rhtB	14756	2	11.15	0.38	0.38	0.39
Chicken	OMPLLAHN_05059	phoE	14756	2	10.93	0.39	0.39	0.34
Chicken	OMPLLAHN_05084	OMPLLAHN_05084	14756	2	10.97	0.40	0.40	0.28
Chicken	OMPLLAHN_05095	OMPLLAHN_05095	14756	2	10.98	0.45	0.45	0.30
Chicken	OMPLLAHN_05096	OMPLLAHN_05096	14756	2	11.00	0.40	0.40	0.31
Chicken	OMPLLAHN_05099	OMPLLAHN_05099	14756	2	11.11	0.39	0.39	0.32
Chicken	OMPLLAHN_05100	intD_3	14756	2	15.33	0.43	0.43	0.35
Chicken	OMPLLAHN_05104	OMPLLAHN_05104	14756	2	10.33	0.44	0.44	0.30
Chicken	OMPLLAHN_05119	OMPLLAHN_05119	14756	2	11.39	0.39	0.39	0.31
Chicken	OMPLLAHN_05138	col	14756	2	11.13	0.34	0.34	0.30
Chicken	OMPLLAHN_05173	cirA_4	14756	2	10.19	0.18	0.18	0.38
Chicken	OMPLLAHN_05178	fhuC_5	14756	2	11.19	0.34	0.34	0.49
Chicken	OMPLLAHN_05180	OMPLLAHN_05180	14756	2	10.74	0.39	0.39	0.37
Chicken	OMPLLAHN_05227	OMPLLAHN_05227	14756	2	10.51	0.38	0.38	0.32
Chicken	OMPLLAHN_05229	hsdR_5	14756	2	10.72	0.47	0.47	0.30
Chicken	OMPLLAHN_05231	hsdM_7	14756	2	10.54	0.32	0.32	0.36
Chicken	OMPLLAHN_05237	OMPLLAHN_05237	14756	2	9.82	0.54	0.46	0.74
Chicken	OMPLLAHN_05262	OMPLLAHN_05262	14756	2	10.34	0.63	0.37	0.38
Chicken	OMPLLAHN_05272	borD_2	14756	2	10.60	0.47	0.47	0.28
Chicken	OMPLLAHN_05290	OMPLLAHN_05290	14756	2	10.85	0.38	0.38	0.32
Chicken	OMPLLAHN_05291	OMPLLAHN_05291	14756	2	10.84	0.86	0.14	0.50
Chicken	OMPLLAHN_05296	OMPLLAHN_05296	14756	2	11.10	0.38	0.38	0.31
Chicken	OMPLLAHN_05306	ugpB_2	14756	2	10.42	0.34	0.34	0.33
Chicken	OMPLLAHN_05307	OMPLLAHN_05307	14756	2	10.32	0.21	0.21	0.33
Chicken	OMPLLAHN_05314	yfiM	14756	2	11.26	0.36	0.36	0.38
Chicken	OMPLLAHN_05327	OMPLLAHN_05327	14756	2	10.13	0.56	0.44	0.31
Chicken	OMPLLAHN_05337	OMPLLAHN_05337	14756	2	10.31	0.38	0.38	0.32
Chicken	OMPLLAHN_05345	crr_2	14756	2	10.97	0.39	0.39	0.33

Chicken	OMPLLAHN_05346	frlD	14756	2	10.19	0.20	0.20	0.33
Chicken	OMPLLAHN_05347	lamB_2	14756	2	11.25	0.53	0.47	0.31
Chicken	OMPLLAHN_05379	OMPLLAHN_05379	14756	2	11.44	0.63	0.37	0.37
Chicken	OMPLLAHN_05380	OMPLLAHN_05380	14756	2	10.22	0.39	0.39	0.31
Chicken	OMPLLAHN_05419	OMPLLAHN_05419	14756	2	11.13	0.41	0.41	0.32
Chicken	OMPLLAHN_05435	OMPLLAHN_05435	14756	2	10.78	0.46	0.46	0.31
Chicken	OMPLLAHN_05457	OMPLLAHN_05457	14756	2	11.22	0.45	0.45	0.31
Chicken	OMPLLAHN_05473	pagN_3	14756	2	10.91	0.44	0.44	0.32
Chicken	OMPLLAHN_05510	OMPLLAHN_05510	14756	2	10.27	0.54	0.46	0.41
Chicken	OMPLLAHN_05527	proQ_4	14756	2	10.60	0.26	0.26	0.34
Chicken	OMPLLAHN_05542	stfR_3	14756	2	10.39	0.39	0.39	0.32
Chicken	OMPLLAHN_05545	OMPLLAHN_05545	14756	2	12.03	0.38	0.38	0.36
Chicken	OMPLLAHN_05546	OMPLLAHN_05546	14756	2	11.15	0.64	0.36	0.43
Chicken	OMPLLAHN_05551	OMPLLAHN_05551	14756	2	11.43	0.32	0.32	0.35
Chicken	OMPLLAHN_05553	yoeA_2	14756	2	10.52	0.68	0.32	0.26
Chicken	OMPLLAHN_05555	OMPLLAHN_05555	14756	2	10.41	0.31	0.31	0.34
Chicken	OMPLLAHN_05573	OMPLLAHN_05573	14756	2	11.13	0.37	0.37	0.33
Chicken	OMPLLAHN_05585	OMPLLAHN_05585	14756	2	10.83	0.42	0.42	0.34
Chicken	OMPLLAHN_05604	OMPLLAHN_05604	14756	2	10.78	0.56	0.44	0.32
Chicken	OMPLLAHN_05623	OMPLLAHN_05623	14756	2	12.32	0.35	0.35	0.34
Chicken	FKALCOLL_00393	FKALCOLL_00393	21225_2#181	1	10.99	0.18	0.18	0.43
Chicken	FKALCOLL_01667	sieB	21225_2#181	1	10.19	0.50	0.50	0.24
Chicken	FKALCOLL_01987	FKALCOLL_01987	21225_2#181	1	11.52	0.56	0.44	0.44
Chicken	FKALCOLL_02840	lhr_2	21225_2#181	1	10.17	0.29	0.29	0.29
Chicken	FKALCOLL_04462	FKALCOLL_04462	21225_2#181	1	10.29	0.22	0.22	0.30
Chicken	FKALCOLL_04475	FKALCOLL_04475	21225_2#181	1	11.02	0.27	0.27	0.30
Chicken	FKALCOLL_04539	FKALCOLL_04539	21225_2#181	1	11.91	0.49	0.49	0.31
Chicken	FKALCOLL_04562	yegT_2	21225_2#181	1	10.25	0.09	0.09	0.49
Chicken	FKALCOLL_04592	FKALCOLL_04592	21225_2#181	1	10.35	0.27	0.27	0.32
Chicken	FKALCOLL_04608	FKALCOLL_04608	21225_2#181	1	10.66	0.28	0.28	0.30
Chicken	FKALCOLL_04610	FKALCOLL_04610	21225_2#181	1	10.04	0.29	0.29	0.25
Chicken	FKALCOLL_04611	FKALCOLL_04611	21225_2#181	1	10.40	0.43	0.43	0.24

Chicken	FKALCOLL_04612	FKALCOLL_04612	21225_2#181	1	10.40	0.43	0.43	0.24
Chicken	GEFDMLIC_00314	GEFDMLIC_00314	Sap638	1	10.19	0.09	0.09	0.45
Chicken	OMPLLAHN_00057	OMPLLAHN_00057	14756	1	10.34	0.42	0.42	0.28
Chicken	OMPLLAHN_00063	OMPLLAHN_00063	14756	1	10.99	0.84	0.16	0.53
Chicken	OMPLLAHN_00070	rusA_1	14756	1	11.11	0.33	0.33	0.36
Chicken	OMPLLAHN_00078	OMPLLAHN_00078	14756	1	10.16	0.41	0.41	0.26
Chicken	OMPLLAHN_00079	OMPLLAHN_00079	14756	1	10.26	0.50	0.50	0.25
Chicken	OMPLLAHN_00080	OMPLLAHN_00080	14756	1	11.91	0.36	0.36	0.33
Chicken	OMPLLAHN_00082	ymfK_1	14756	1	10.14	0.39	0.39	0.30
Chicken	OMPLLAHN_00148	OMPLLAHN_00148	14756	1	10.44	0.52	0.48	0.31
Chicken	OMPLLAHN_00166	ybgQ	14756	1	10.66	0.41	0.41	0.43
Chicken	OMPLLAHN_00177	OMPLLAHN_00177	14756	1	10.74	0.44	0.44	0.37
Chicken	OMPLLAHN_00180	OMPLLAHN_00180	14756	1	10.90	0.63	0.37	0.42
Chicken	OMPLLAHN_00199	nagA	14756	1	11.40	0.82	0.18	0.47
Chicken	OMPLLAHN_00223	djlC	14756	1	10.67	0.46	0.46	0.31
Chicken	OMPLLAHN_00226	djlB	14756	1	10.17	0.38	0.38	0.33
Chicken	OMPLLAHN_00263	uspG	14756	1	11.15	0.41	0.41	0.33
Chicken	OMPLLAHN_00298	cusA	14756	1	11.37	0.43	0.43	0.35
Chicken	OMPLLAHN_00306	OMPLLAHN_00306	14756	1	11.25	0.34	0.34	0.36
Chicken	OMPLLAHN_00316	OMPLLAHN_00316	14756	1	10.63	0.39	0.39	0.31
Chicken	OMPLLAHN_00359	tesA	14756	1	10.09	0.50	0.50	0.33
Chicken	OMPLLAHN_00367	smc_1	14756	1	10.48	0.41	0.41	0.35
Chicken	OMPLLAHN_00372	cydC_1	14756	1	10.53	0.42	0.42	0.36
Chicken	OMPLLAHN_00373	OMPLLAHN_00373	14756	1	10.56	0.40	0.40	0.35
Chicken	OMPLLAHN_00374	OMPLLAHN_00374	14756	1	10.59	0.31	0.31	0.41
Chicken	OMPLLAHN_00449	yajI	14756	1	11.03	0.55	0.45	0.37
Chicken	OMPLLAHN_00462	envZ_1	14756	1	10.69	0.40	0.40	0.34
Chicken	OMPLLAHN_00549	yheS	14756	1	10.70	0.41	0.41	0.31
Chicken	OMPLLAHN_00576	gph	14756	1	10.15	0.49	0.49	0.30
Chicken	OMPLLAHN_00590	yrfG	14756	1	11.25	0.39	0.39	0.36
Chicken	OMPLLAHN_00598	yhgF	14756	1	10.86	0.36	0.36	0.37
Chicken	OMPLLAHN_00618	sfmH_2	14756	1	10.74	0.41	0.41	0.37

Chicken	OMPLLAHN_00621	ycbU	14756	1	11.22	0.45	0.45	0.32	
Chicken	OMPLLAHN_00638	OMPLLAHN_00638	14756	1	11.53	0.54	0.46	0.35	
Chicken	OMPLLAHN_00681	lolA_1	14756	1	10.16	0.37	0.37	0.33	
Chicken	OMPLLAHN_00698	gatB_1	14756	1	10.57	0.54	0.46	0.39	
Chicken	OMPLLAHN_00720	arsD	14756	1	12.17	0.37	0.37	0.37	
Chicken	OMPLLAHN_00743	mdtE	14756	1	10.27	0.36	0.36	0.33	
Chicken	OMPLLAHN_00758	OMPLLAHN_00758	14756	1	10.84	0.45	0.45	0.33	
Chicken	OMPLLAHN_00782	dppA	14756	1	10.83	0.33	0.33	0.38	
Chicken	OMPLLAHN_00787	mdoB	14756	1	10.75	0.35	0.35	0.37	
Chicken	OMPLLAHN_00788	OMPLLAHN_00788	14756	1	10.72	0.40	0.40	0.33	
Chicken	OMPLLAHN_00819	radA	14756	1	11.25	0.17	0.17	0.45	
Chicken	OMPLLAHN_00842	yaaA	14756	1	10.36	0.51	0.49	0.27	
Chicken	OMPLLAHN_00863	fkpB	14756	1	10.48	0.41	0.41	0.33	
Chicken	OMPLLAHN_00938	hofB_1	14756	1	10.91	0.60	0.40	0.43	
Chicken	OMPLLAHN_00972	yadN	14756	1	10.28	0.48	0.48	0.29	
Chicken	OMPLLAHN_00984	fhuB	14756	1	11.60	0.48	0.48	0.39	
Chicken	OMPLLAHN_00994	OMPLLAHN_00994	14756	1	10.01	0.46	0.46	0.30	
Chicken	OMPLLAHN_01023	nlpE	14756	1	10.13	0.43	0.43	0.32	
Chicken	OMPLLAHN_01041	arpA_1	14756	1	10.13	0.60	0.40	0.35	
Chicken	OMPLLAHN_01059	fadK	14756	1	10.41	0.42	0.42	0.32	
Chicken	OMPLLAHN_01077	sufA	14756	1	10.48	0.60	0.40	0.44	
Chicken	OMPLLAHN_01217	ydeK	14756	1	11.75	0.41	0.41	0.36	
Chicken	OMPLLAHN_01230	OMPLLAHN_01230	14756	1	11.48	0.42	0.42	0.33	
Chicken	OMPLLAHN_01249	dosC	14756	1	10.11	0.42	0.42	0.30	
Chicken	OMPLLAHN_01307	OMPLLAHN_01307	14756	1	10.35	0.90	0.10	0.56	
Chicken	OMPLLAHN_01320	kdsA	14756	1	10.52	0.36	0.36	0.35	
Chicken	OMPLLAHN_01382	acnA	14756	1	11.02	0.52	0.48	0.32	
Chicken	OMPLLAHN_01410	pspF	14756	1	10.27	0.46	0.46	0.34	
Chicken	OMPLLAHN_01413	pspC	14756	1	10.78	0.65	0.35	0.38	
Chicken	OMPLLAHN_01454	ynbA	14756	1	10.93	0.34	0.34	0.36	
Chicken	OMPLLAHN_01464	aldA	14756	1	10.33	0.38	0.38	0.34	
Chicken	OMPLLAHN_01508	OMPLLAHN_01508	14756	1	11.23	0.41	0.41	0.33	

Chicken	OMPLLAHN_01527	hyfR_1	14756	1	10.82	0.69	0.31	0.39
Chicken	OMPLLAHN_01560	eutT	14756	1	11.02	0.52	0.48	0.32
Chicken	OMPLLAHN_01567	eutH	14756	1	11.21	0.51	0.49	0.31
Chicken	OMPLLAHN_01569	eutB	14756	1	10.37	0.38	0.38	0.29
Chicken	OMPLLAHN_01618	ypdF	14756	1	10.35	0.51	0.49	0.30
Chicken	OMPLLAHN_01653	OMPLLAHN_01653	14756	1	12.20	0.42	0.42	0.37
Chicken	OMPLLAHN_01658	yfcO	14756	1	10.30	0.60	0.40	0.36
Chicken	OMPLLAHN_01673	OMPLLAHN_01673	14756	1	10.54	0.57	0.43	0.44
Chicken	OMPLLAHN_01707	nuoF	14756	1	10.90	0.63	0.37	0.42
Chicken	OMPLLAHN_01761	accB	14756	1	10.38	0.50	0.50	0.33
Chicken	OMPLLAHN_01794	OMPLLAHN_01794	14756	1	10.19	0.36	0.36	0.32
Chicken	OMPLLAHN_01796	gltD	14756	1	10.53	0.72	0.28	0.42
Chicken	OMPLLAHN_01797	gltB	14756	1	10.25	0.66	0.34	0.33
Chicken	OMPLLAHN_01849	OMPLLAHN_01849	14756	1	11.39	0.39	0.39	0.34
Chicken	OMPLLAHN_01852	yhbV	14756	1	10.14	0.43	0.43	0.34
Chicken	OMPLLAHN_01853	yhbU	14756	1	10.48	0.39	0.39	0.34
Chicken	OMPLLAHN_01882	garP	14756	1	10.26	0.39	0.39	0.36
Chicken	OMPLLAHN_01890	tdcB	14756	1	10.54	0.57	0.43	0.44
Chicken	OMPLLAHN_01893	pflB_1	14756	1	10.59	0.37	0.37	0.33
Chicken	OMPLLAHN_01913	uxaC	14756	1	10.27	0.88	0.12	0.50
Chicken	OMPLLAHN_01924	fadH_1	14756	1	10.56	0.40	0.40	0.32
Chicken	OMPLLAHN_01938	OMPLLAHN_01938	14756	1	10.19	0.50	0.50	0.26
Chicken	OMPLLAHN_01981	ligA_2	14756	1	10.56	0.39	0.39	0.36
Chicken	OMPLLAHN_01983	OMPLLAHN_01983	14756	1	10.45	0.35	0.35	0.33
Chicken	OMPLLAHN_02001	OMPLLAHN_02001	14756	1	10.78	0.43	0.43	0.32
Chicken	OMPLLAHN_02032	ygaY	14756	1	10.64	0.57	0.43	0.43
Chicken	OMPLLAHN_02115	cas3	14756	1	10.25	0.22	0.22	0.44
Chicken	OMPLLAHN_02162	yfaA	14756	1	10.53	0.42	0.42	0.36
Chicken	OMPLLAHN_02239	OMPLLAHN_02239	14756	1	10.82	0.72	0.28	0.45
Chicken	OMPLLAHN_02312	argO	14756	1	10.25	0.87	0.13	0.48
Chicken	OMPLLAHN_02321	bhsA_1	14756	1	11.08	0.29	0.29	0.41
Chicken	OMPLLAHN_02375	invF	14756	1	11.46	0.44	0.44	0.35

Chicken	OMPLLAHN_02382	spaO	14756	1	10.34	0.39	0.39	0.34
Chicken	OMPLLAHN_02389	prgH	14756	1	11.03	0.43	0.43	0.34
Chicken	OMPLLAHN_02396	OMPLLAHN_02396	14756	1	10.70	0.44	0.44	0.38
Chicken	OMPLLAHN_02404	yqeJ	14756	1	11.82	0.39	0.39	0.37
Chicken	OMPLLAHN_02420	ygdQ	14756	1	10.69	0.48	0.48	0.31
Chicken	OMPLLAHN_02448	fucR	14756	1	10.22	0.44	0.44	0.32
Chicken	OMPLLAHN_02475	OMPLLAHN_02475	14756	1	10.63	0.58	0.42	0.26
Chicken	OMPLLAHN_02485	selD	14756	1	11.07	0.39	0.39	0.35
Chicken	OMPLLAHN_02490	ydjE	14756	1	10.68	0.34	0.34	0.38
Chicken	OMPLLAHN_02632	OMPLLAHN_02632	14756	1	10.99	0.34	0.34	0.38
Chicken	OMPLLAHN_02634	OMPLLAHN_02634	14756	1	14.48	0.46	0.46	0.39
Chicken	OMPLLAHN_02637	OMPLLAHN_02637	14756	1	10.56	0.39	0.39	0.31
Chicken	OMPLLAHN_02646	OMPLLAHN_02646	14756	1	10.91	0.44	0.44	0.35
Chicken	OMPLLAHN_02649	OMPLLAHN_02649	14756	1	9.79	0.83	0.17	0.31
Chicken	OMPLLAHN_02721	OMPLLAHN_02721	14756	1	11.03	0.37	0.37	0.36
Chicken	OMPLLAHN_02779	OMPLLAHN_02779	14756	1	10.51	0.42	0.42	0.38
Chicken	OMPLLAHN_02798	fhuE	14756	1	10.08	0.37	0.37	0.32
Chicken	OMPLLAHN_02865	aat	14756	1	10.40	0.49	0.49	0.34
Chicken	OMPLLAHN_02895	ulaA_2	14756	1	11.51	0.37	0.37	0.36
Chicken	OMPLLAHN_02947	OMPLLAHN_02947	14756	1	10.75	0.36	0.36	0.33
Chicken	OMPLLAHN_02961	ipaB	14756	1	11.09	0.49	0.49	0.32
Chicken	OMPLLAHN_02971	ade	14756	1	10.19	0.88	0.12	0.52
Chicken	OMPLLAHN_02977	OMPLLAHN_02977	14756	1	10.47	0.25	0.25	0.43
Chicken	OMPLLAHN_02978	OMPLLAHN_02978	14756	1	10.31	0.32	0.32	0.35
Chicken	OMPLLAHN_02998	cbrA	14756	1	10.30	0.39	0.39	0.30
Chicken	OMPLLAHN_03010	dnaA	14756	1	10.54	0.52	0.48	0.41
Chicken	OMPLLAHN_03023	OMPLLAHN_03023	14756	1	10.78	0.46	0.46	0.34
Chicken	OMPLLAHN_03052	viaA	14756	1	10.52	0.43	0.43	0.34
Chicken	OMPLLAHN_03108	sbcB	14756	1	10.56	0.38	0.38	0.29
Chicken	OMPLLAHN_03113	hisD	14756	1	10.42	0.38	0.38	0.30
Chicken	OMPLLAHN_03133	wzxC	14756	1	10.32	0.45	0.45	0.29
Chicken	OMPLLAHN_03136	cpsB_2	14756	1	9.89	0.48	0.48	0.25

Chicken	OMPLLAHN_03185	OMPLLAHN_03185	14756	1	10.90	0.17	0.17	0.36
Chicken	OMPLLAHN_03193	OMPLLAHN_03193	14756	1	10.74	0.36	0.36	0.31
Chicken	OMPLLAHN_03195	lig	14756	1	10.83	0.38	0.38	0.33
Chicken	OMPLLAHN_03203	OMPLLAHN_03203	14756	1	11.99	0.55	0.45	0.32
Chicken	OMPLLAHN_03206	OMPLLAHN_03206	14756	1	10.21	0.31	0.31	0.30
Chicken	OMPLLAHN_03208	OMPLLAHN_03208	14756	1	10.13	0.37	0.37	0.32
Chicken	OMPLLAHN_03210	OMPLLAHN_03210	14756	1	10.49	0.57	0.43	0.26
Chicken	OMPLLAHN_03216	OMPLLAHN_03216	14756	1	13.84	0.37	0.37	0.41
Chicken	OMPLLAHN_03217	OMPLLAHN_03217	14756	1	13.84	0.37	0.37	0.41
Chicken	OMPLLAHN_03223	OMPLLAHN_03223	14756	1	11.35	0.34	0.34	0.32
Chicken	OMPLLAHN_03226	OMPLLAHN_03226	14756	1	10.78	0.35	0.35	0.36
Chicken	OMPLLAHN_03227	OMPLLAHN_03227	14756	1	10.78	0.35	0.35	0.36
Chicken	OMPLLAHN_03231	OMPLLAHN_03231	14756	1	10.74	0.30	0.30	0.34
Chicken	OMPLLAHN_03234	OMPLLAHN_03234	14756	1	10.76	0.52	0.48	0.31
Chicken	OMPLLAHN_03237	OMPLLAHN_03237	14756	1	10.87	0.40	0.40	0.32
Chicken	OMPLLAHN_03271	OMPLLAHN_03271	14756	1	10.55	0.37	0.37	0.37
Chicken	OMPLLAHN_03273	rnhA_1	14756	1	10.42	0.44	0.44	0.28
Chicken	OMPLLAHN_03275	OMPLLAHN_03275	14756	1	10.95	0.38	0.38	0.33
Chicken	OMPLLAHN_03280	folA_2	14756	1	10.36	0.45	0.45	0.30
Chicken	OMPLLAHN_03286	OMPLLAHN_03286	14756	1	11.13	0.42	0.42	0.30
Chicken	OMPLLAHN_03287	OMPLLAHN_03287	14756	1	11.02	0.37	0.37	0.31
Chicken	OMPLLAHN_03289	OMPLLAHN_03289	14756	1	10.62	0.43	0.43	0.33
Chicken	OMPLLAHN_03291	repB_1	14756	1	11.39	0.39	0.39	0.34
Chicken	OMPLLAHN_03302	OMPLLAHN_03302	14756	1	10.47	0.47	0.47	0.27
Chicken	OMPLLAHN_03317	yafX	14756	1	11.33	0.34	0.34	0.36
Chicken	OMPLLAHN_03319	yeeT_3	14756	1	10.83	0.20	0.20	0.40
Chicken	OMPLLAHN_03325	OMPLLAHN_03325	14756	1	10.11	0.48	0.48	0.26
Chicken	OMPLLAHN_03334	ttdA	14756	1	10.44	0.60	0.40	0.41
Chicken	OMPLLAHN_03352	dsbI	14756	1	11.16	0.45	0.45	0.48
Chicken	OMPLLAHN_03365	fecD_3	14756	1	10.40	0.31	0.31	0.28
Chicken	OMPLLAHN_03368	yebK_2	14756	1	10.29	0.46	0.46	0.40
Chicken	OMPLLAHN_03395	hybB	14756	1	10.29	0.46	0.46	0.33

Chicken	OMPLLAHN_03401	yghU	14756	1	10.43	0.38	0.38	0.36
Chicken	OMPLLAHN_03402	gss	14756	1	12.13	0.33	0.33	0.36
Chicken	OMPLLAHN_03403	pitB	14756	1	9.98	0.56	0.44	0.30
Chicken	OMPLLAHN_03427	pflC	14756	1	11.29	0.36	0.36	0.36
Chicken	OMPLLAHN_03438	ushA_2	14756	1	10.71	0.41	0.41	0.34
Chicken	OMPLLAHN_03512	OMPLLAHN_03512	14756	1	10.32	0.14	0.14	0.39
Chicken	OMPLLAHN_03516	OMPLLAHN_03516	14756	1	10.81	0.11	0.11	0.50
Chicken	OMPLLAHN_03523	yjfZ	14756	1	9.90	0.54	0.46	0.29
Chicken	OMPLLAHN_03549	rnr	14756	1	10.57	0.43	0.43	0.34
Chicken	OMPLLAHN_03566	orn	14756	1	9.90	0.88	0.12	0.47
Chicken	OMPLLAHN_03598	ykgE_1	14756	1	10.88	0.35	0.35	0.35
Chicken	OMPLLAHN_03600	ykgG_1	14756	1	10.81	0.40	0.40	0.34
Chicken	OMPLLAHN_03607	glnL_4	14756	1	10.94	0.42	0.42	0.30
Chicken	OMPLLAHN_03638	melA	14756	1	10.50	0.44	0.44	0.27
Chicken	OMPLLAHN_03686	actP	14756	1	10.63	0.40	0.40	0.35
Chicken	OMPLLAHN_03687	OMPLLAHN_03687	14756	1	10.41	0.42	0.42	0.35
Chicken	OMPLLAHN_03752	yphD	14756	1	10.91	0.39	0.39	0.33
Chicken	OMPLLAHN_03762	envZ_9	14756	1	10.45	0.55	0.45	0.38
Chicken	OMPLLAHN_03763	purL	14756	1	11.14	0.49	0.49	0.41
Chicken	OMPLLAHN_03793	OMPLLAHN_03793	14756	1	11.25	0.39	0.39	0.33
Chicken	OMPLLAHN_03819	yfdO_1	14756	1	10.68	0.40	0.40	0.30
Chicken	OMPLLAHN_03821	ymfL	14756	1	10.76	0.44	0.44	0.28
Chicken	OMPLLAHN_03822	dicC	14756	1	10.82	0.69	0.31	0.29
Chicken	OMPLLAHN_03837	OMPLLAHN_03837	14756	1	10.45	0.46	0.46	0.29
Chicken	OMPLLAHN_03840	OMPLLAHN_03840	14756	1	11.26	0.36	0.36	0.33
Chicken	OMPLLAHN_03861	yjbF	14756	1	10.46	0.50	0.50	0.33
Chicken	OMPLLAHN_03877	iclR	14756	1	10.67	0.35	0.35	0.36
Chicken	OMPLLAHN_03880	aceA	14756	1	10.72	0.40	0.40	0.33
Chicken	OMPLLAHN_03902	yjgL	14756	1	10.34	0.42	0.42	0.28
Chicken	OMPLLAHN_03912	treB	14756	1	10.70	0.42	0.42	0.33
Chicken	OMPLLAHN_03913	treC	14756	1	11.80	0.66	0.34	0.39
Chicken	OMPLLAHN_03952	OMPLLAHN_03952	14756	1	11.37	0.39	0.39	0.35

Chicken	OMPLLAHN_03968	yahA	14756	1	10.53	0.62	0.38	0.37
Chicken	OMPLLAHN_03977	OMPLLAHN_03977	14756	1	11.01	0.31	0.31	0.45
Chicken	OMPLLAHN_03992	prpE	14756	1	10.35	0.36	0.36	0.40
Chicken	OMPLLAHN_03995	cynR	14756	1	10.51	0.58	0.42	0.39
Chicken	OMPLLAHN_04027	OMPLLAHN_04027	14756	1	10.68	0.49	0.49	0.34
Chicken	OMPLLAHN_04055	OMPLLAHN_04055	14756	1	10.97	0.50	0.50	0.28
Chicken	OMPLLAHN_04085	glmU_2	14756	1	11.51	0.48	0.48	0.32
Chicken	OMPLLAHN_04089	cia	14756	1	12.31	0.40	0.40	0.37
Chicken	OMPLLAHN_04092	OMPLLAHN_04092	14756	1	11.35	0.35	0.35	0.41
Chicken	OMPLLAHN_04097	OMPLLAHN_04097	14756	1	10.43	0.33	0.33	0.31
Chicken	OMPLLAHN_04117	OMPLLAHN_04117	14756	1	11.17	0.34	0.34	0.34
Chicken	OMPLLAHN_04119	OMPLLAHN_04119	14756	1	10.21	0.39	0.39	0.33
Chicken	OMPLLAHN_04123	OMPLLAHN_04123	14756	1	11.00	0.40	0.40	0.32
Chicken	OMPLLAHN_04124	OMPLLAHN_04124	14756	1	10.35	0.39	0.39	0.34
Chicken	OMPLLAHN_04126	OMPLLAHN_04126	14756	1	10.86	0.44	0.44	0.30
Chicken	OMPLLAHN_04137	OMPLLAHN_04137	14756	1	16.18	0.43	0.43	0.45
Chicken	OMPLLAHN_04155	OMPLLAHN_04155	14756	1	10.31	0.38	0.38	0.35
Chicken	OMPLLAHN_04160	ssb_3	14756	1	10.47	0.82	0.18	0.44
Chicken	OMPLLAHN_04166	OMPLLAHN_04166	14756	1	10.65	0.46	0.46	0.30
Chicken	OMPLLAHN_04174	OMPLLAHN_04174	14756	1	11.24	0.41	0.41	0.31
Chicken	OMPLLAHN_04222	rffA	14756	1	10.55	0.77	0.23	0.47
Chicken	OMPLLAHN_04228	wzzE	14756	1	10.47	0.42	0.42	0.30
Chicken	OMPLLAHN_04237	ilvC	14756	1	10.68	0.44	0.44	0.35
Chicken	OMPLLAHN_04252	OMPLLAHN_04252	14756	1	10.32	0.14	0.14	0.39
Chicken	OMPLLAHN_04272	fliC	14756	1	10.23	0.35	0.35	0.34
Chicken	OMPLLAHN_04282	OMPLLAHN_04282	14756	1	10.46	0.40	0.40	0.34
Chicken	OMPLLAHN_04286	fliG	14756	1	10.06	0.42	0.42	0.29
Chicken	OMPLLAHN_04330	htrL	14756	1	10.35	0.90	0.10	0.56
Chicken	OMPLLAHN_04337	waaY	14756	1	10.27	0.54	0.46	0.32
Chicken	OMPLLAHN_04368	intS_1	14756	1	10.24	0.42	0.42	0.28
Chicken	OMPLLAHN_04382	OMPLLAHN_04382	14756	1	9.88	0.16	0.16	0.35
Chicken	OMPLLAHN_04395	yggR_1	14756	1	10.53	0.43	0.43	0.27

Chicken	OMPLLAHN_04412	nupG	14756	1	10.22	0.24	0.24	0.38
Chicken	OMPLLAHN_04413	speC	14756	1	10.13	0.90	0.10	0.52
Chicken	OMPLLAHN_04418	addA	14756	1	10.41	0.45	0.45	0.28
Chicken	OMPLLAHN_04424	insN-1_2	14756	1	10.09	0.49	0.49	0.24
Chicken	OMPLLAHN_04436	traI_2	14756	1	9.75	0.17	0.17	0.34
Chicken	OMPLLAHN_04446	OMPLLAHN_04446	14756	1	11.14	0.40	0.40	0.30
Chicken	OMPLLAHN_04457	yfjX_5	14756	1	12.65	0.64	0.36	0.34
Chicken	OMPLLAHN_04465	soj_2	14756	1	10.77	0.37	0.37	0.34
Chicken	OMPLLAHN_04469	proQ_2	14756	1	10.73	0.39	0.39	0.34
Chicken	OMPLLAHN_04474	OMPLLAHN_04474	14756	1	10.44	0.55	0.45	0.34
Chicken	OMPLLAHN_04488	dkgB	14756	1	10.51	0.43	0.43	0.32
Chicken	OMPLLAHN_04504	clpB_2	14756	1	10.82	0.72	0.28	0.45
Chicken	OMPLLAHN_04506	OMPLLAHN_04506	14756	1	10.39	0.23	0.23	0.40
Chicken	OMPLLAHN_04516	vgrG1_2	14756	1	10.30	0.42	0.42	0.35
Chicken	OMPLLAHN_04518	OMPLLAHN_04518	14756	1	10.55	0.33	0.33	0.38
Chicken	OMPLLAHN_04533	OMPLLAHN_04533	14756	1	10.75	0.36	0.36	0.33
Chicken	OMPLLAHN_04537	OMPLLAHN_04537	14756	1	11.07	0.87	0.13	0.46
Chicken	OMPLLAHN_04541	yjiM	14756	1	10.48	0.29	0.29	0.34
Chicken	OMPLLAHN_04543	mdtM	14756	1	10.15	0.50	0.50	0.29
Chicken	OMPLLAHN_04544	OMPLLAHN_04544	14756	1	10.35	0.35	0.35	0.28
Chicken	OMPLLAHN_04562	yfaU_2	14756	1	12.27	0.35	0.35	0.43
Chicken	OMPLLAHN_04589	yicJ_2	14756	1	12.03	0.35	0.35	0.46
Chicken	OMPLLAHN_04601	mtlD	14756	1	10.44	0.40	0.40	0.30
Chicken	OMPLLAHN_04616	OMPLLAHN_04616	14756	1	10.04	0.42	0.42	0.26
Chicken	OMPLLAHN_04636	uxuR	14756	1	12.59	0.40	0.40	0.38
Chicken	OMPLLAHN_04639	yjiE	14756	1	10.20	0.21	0.21	0.34
Chicken	OMPLLAHN_04658	renD	14756	1	11.33	0.46	0.46	0.31
Chicken	OMPLLAHN_04697	OMPLLAHN_04697	14756	1	10.49	0.41	0.41	0.30
Chicken	OMPLLAHN_04703	traG	14756	1	10.86	0.36	0.36	0.33
Chicken	OMPLLAHN_04710	OMPLLAHN_04710	14756	1	10.39	0.40	0.40	0.30
Chicken	OMPLLAHN_04712	virB1	14756	1	10.90	0.44	0.44	0.28
Chicken	OMPLLAHN_04718	traC_2	14756	1	10.38	0.42	0.42	0.28

Chicken	OMPLLAHN_04719	OMPLLAHN_04719	14756	1	9.76	0.39	0.39	0.45
Chicken	OMPLLAHN_04724	OMPLLAHN_04724	14756	1	10.08	0.56	0.44	0.26
Chicken	OMPLLAHN_04725	OMPLLAHN_04725	14756	1	9.94	0.47	0.47	0.30
Chicken	OMPLLAHN_04730	repA	14756	1	10.10	0.19	0.19	0.33
Chicken	OMPLLAHN_04733	proQ_3	14756	1	10.49	0.40	0.40	0.31
Chicken	OMPLLAHN_04739	OMPLLAHN_04739	14756	1	10.38	0.41	0.41	0.28
Chicken	OMPLLAHN_04761	OMPLLAHN_04761	14756	1	10.82	0.46	0.46	0.30
Chicken	OMPLLAHN_04773	OMPLLAHN_04773	14756	1	10.11	0.48	0.48	0.26
Chicken	OMPLLAHN_04789	hemE	14756	1	11.00	0.35	0.35	0.37
Chicken	OMPLLAHN_04823	OMPLLAHN_04823	14756	1	11.04	0.44	0.44	0.33
Chicken	OMPLLAHN_04828	znuA_2	14756	1	10.45	0.66	0.34	0.33
Chicken	OMPLLAHN_04867	ycjY_2	14756	1	10.71	0.38	0.38	0.35
Chicken	OMPLLAHN_04883	OMPLLAHN_04883	14756	1	10.28	0.18	0.18	0.34
Chicken	OMPLLAHN_04901	OMPLLAHN_04901	14756	1	10.89	0.41	0.41	0.31
Chicken	OMPLLAHN_04908	OMPLLAHN_04908	14756	1	10.79	0.33	0.33	0.29
Chicken	OMPLLAHN_04909	OMPLLAHN_04909	14756	1	10.22	0.50	0.50	0.30
Chicken	OMPLLAHN_04912	OMPLLAHN_04912	14756	1	11.36	0.32	0.32	0.31
Chicken	OMPLLAHN_04918	insF-1_3	14756	1	10.27	0.18	0.18	0.36
Chicken	OMPLLAHN_04923	OMPLLAHN_04923	14756	1	11.08	0.41	0.41	0.32
Chicken	OMPLLAHN_04932	OMPLLAHN_04932	14756	1	10.82	0.46	0.46	0.30
Chicken	OMPLLAHN_04943	yhbX_2	14756	1	10.35	0.42	0.42	0.29
Chicken	OMPLLAHN_04944	OMPLLAHN_04944	14756	1	10.82	0.38	0.38	0.32
Chicken	OMPLLAHN_04949	wcaL_2	14756	1	10.62	0.34	0.34	0.30
Chicken	OMPLLAHN_05008	xylA	14756	1	10.61	0.39	0.39	0.35
Chicken	OMPLLAHN_05082	OMPLLAHN_05082	14756	1	11.65	0.38	0.38	0.34
Chicken	OMPLLAHN_05098	yhcR_2	14756	1	11.58	0.47	0.47	0.31
Chicken	OMPLLAHN_05105	OMPLLAHN_05105	14756	1	9.93	0.49	0.49	0.34
Chicken	OMPLLAHN_05124	OMPLLAHN_05124	14756	1	10.82	0.38	0.38	0.32
Chicken	OMPLLAHN_05135	OMPLLAHN_05135	14756	1	10.75	0.47	0.47	0.30
Chicken	OMPLLAHN_05161	yihF	14756	1	10.44	0.42	0.42	0.34
Chicken	OMPLLAHN_05172	iucD	14756	1	11.01	0.63	0.37	0.35
Chicken	OMPLLAHN_05177	znuB_5	14756	1	10.40	0.17	0.17	0.44

Chicken	OMPLLAHN_05186	OMPLLAHN_05186	14756	1	10.48	0.33	0.33	0.35
Chicken	OMPLLAHN_05196	OMPLLAHN_05196	14756	1	10.64	0.38	0.38	0.28
Chicken	OMPLLAHN_05199	OMPLLAHN_05199	14756	1	10.58	0.39	0.39	0.33
Chicken	OMPLLAHN_05203	OMPLLAHN_05203	14756	1	9.90	0.09	0.09	0.46
Chicken	OMPLLAHN_05208	OMPLLAHN_05208	14756	1	10.20	0.17	0.17	0.35
Chicken	OMPLLAHN_05224	OMPLLAHN_05224	14756	1	12.50	0.35	0.35	0.38
Chicken	OMPLLAHN_05225	OMPLLAHN_05225	14756	1	11.12	0.35	0.35	0.37
Chicken	OMPLLAHN_05233	insB-1_2	14756	1	10.99	0.23	0.23	0.37
Chicken	OMPLLAHN_05241	OMPLLAHN_05241	14756	1	9.98	0.22	0.22	0.32
Chicken	OMPLLAHN_05250	potC	14756	1	10.72	0.40	0.40	0.32
Chicken	OMPLLAHN_05251	intE_3	14756	1	10.00	0.48	0.48	0.24
Chicken	OMPLLAHN_05259	ydaT_2	14756	1	11.08	0.59	0.41	0.28
Chicken	OMPLLAHN_05298	OMPLLAHN_05298	14756	1	10.26	0.35	0.35	0.31
Chicken	OMPLLAHN_05303	murR_3	14756	1	10.33	0.33	0.33	0.29
Chicken	OMPLLAHN_05310	cirA_6	14756	1	10.81	0.50	0.50	0.40
Chicken	OMPLLAHN_05361	OMPLLAHN_05361	14756	1	11.51	0.33	0.33	0.36
Chicken	OMPLLAHN_05367	dam_2	14756	1	10.56	0.37	0.37	0.31
Chicken	OMPLLAHN_05375	rop	14756	1	11.00	0.55	0.45	0.29
Chicken	OMPLLAHN_05385	OMPLLAHN_05385	14756	1	10.40	0.07	0.07	0.62
Chicken	OMPLLAHN_05386	OMPLLAHN_05386	14756	1	13.62	0.39	0.39	0.40
Chicken	OMPLLAHN_05392	OMPLLAHN_05392	14756	1	10.06	0.64	0.36	0.28
Chicken	OMPLLAHN_05404	OMPLLAHN_05404	14756	1	11.68	0.35	0.35	0.37
Chicken	OMPLLAHN_05405	dam_3	14756	1	10.56	0.37	0.37	0.31
Chicken	OMPLLAHN_05423	OMPLLAHN_05423	14756	1	10.32	0.61	0.39	0.30
Chicken	OMPLLAHN_05424	yggR_2	14756	1	10.71	0.42	0.42	0.28
Chicken	OMPLLAHN_05438	OMPLLAHN_05438	14756	1	10.51	0.35	0.35	0.32
Chicken	OMPLLAHN_05446	yjhB	14756	1	10.32	0.40	0.40	0.30
Chicken	OMPLLAHN_05447	yjhC	14756	1	10.41	0.36	0.36	0.33
Chicken	OMPLLAHN_05449	OMPLLAHN_05449	14756	1	10.94	0.38	0.38	0.34
Chicken	OMPLLAHN_05450	OMPLLAHN_05450	14756	1	10.94	0.38	0.38	0.34
Chicken	OMPLLAHN_05453	ycgV_2	14756	1	12.65	0.64	0.36	0.34
Chicken	OMPLLAHN_05458	OMPLLAHN_05458	14756	1	10.36	0.51	0.49	0.27

Chicken	OMPLLAHN_05459	yfjJ_2	14756	1	10.27	0.29	0.29	0.28
Chicken	OMPLLAHN_05471	papG	14756	1	11.09	0.40	0.40	0.33
Chicken	OMPLLAHN_05479	OMPLLAHN_05479	14756	1	10.16	0.23	0.23	0.35
Chicken	OMPLLAHN_05491	OMPLLAHN_05491	14756	1	10.16	0.23	0.23	0.35
Chicken	OMPLLAHN_05512	OMPLLAHN_05512	14756	1	10.25	0.31	0.31	0.24
Chicken	OMPLLAHN_05520	OMPLLAHN_05520	14756	1	10.46	0.49	0.49	0.28
Chicken	OMPLLAHN_05528	OMPLLAHN_05528	14756	1	10.55	0.50	0.50	0.31
Chicken	OMPLLAHN_05544	tfaD_3	14756	1	9.84	0.38	0.38	0.28
Chicken	OMPLLAHN_05559	OMPLLAHN_05559	14756	1	10.47	0.41	0.41	0.32
Chicken	OMPLLAHN_05561	OMPLLAHN_05561	14756	1	9.93	0.49	0.49	0.34
Chicken	OMPLLAHN_05568	OMPLLAHN_05568	14756	1	14.68	0.33	0.33	0.41
Chicken	OMPLLAHN_05576	nanE_3	14756	1	11.97	0.47	0.47	0.35
Chicken	OMPLLAHN_05577	OMPLLAHN_05577	14756	1	10.72	0.20	0.20	0.37
Chicken	OMPLLAHN_05588	OMPLLAHN_05588	14756	1	9.42	0.06	0.06	0.75
Chicken	OMPLLAHN_05591	tfaE_1	14756	1	10.55	0.42	0.42	0.31
Chicken	OMPLLAHN_05593	OMPLLAHN_05593	14756	1	10.32	0.67	0.33	0.26
Chicken	OMPLLAHN_05620	OMPLLAHN_05620	14756	1	10.32	0.52	0.48	0.28
Chicken	OMPLLAHN_05625	OMPLLAHN_05625	14756	1	10.75	0.47	0.47	0.30
Chicken	OMPLLAHN_05635	OMPLLAHN_05635	14756	1	9.42	0.06	0.06	0.75

9.4: *In-silico* characterization of *E. coli* genes associated to hosts using Blast2GO.

Host	Sequence Name	Gene annotation
Human	IIDENDNK_04031	lysozyme
Human	IIDENDNK_05074	inovirus Gp2 family protein
Human	IIDENDNK_04916	ABC transporter permease
Human	IIDENDNK_05034	Uncharacterised protein
Human	IIDENDNK_04753	IucA/IucC family siderophore biosynthesis protein
Human	IIDENDNK_05001	phage tail assembly protein T
Human	BNJMMDAK_05353	Protein of uncharacterised function (DUF826)
Human	IIDENDNK_04935	tonB family C-terminal domain protein
Human	BNJMMDAK_05205	endopeptidase
Human	IIDENDNK_04904	N-acetylmannosamine kinase
Human	IIDENDNK_04903	MFS transporter
Human	IIDENDNK_03864	phage tail assembly protein T
Human	IIDENDNK_00716	Uncharacterised protein
Human	IIDENDNK_05000	phage tail tape measure protein
Human	BNJMMDAK_04625	type VI secretion protein
Human	IIDENDNK_04999	phage tail protein
Human	IIDENDNK_04779	Uncharacterised protein
Human	IIDENDNK_04749	Uncharacterised protein
Human	BNJMMDAK_05102	DNA methylase
Human	IIDENDNK_04897	sialate O-acetylesterase
Human	IIDENDNK_04774	tail component
Human	BNJMMDAK_05096	anti-adapter protein IraM
Human	ALHKBHBA_01465	phage tail assembly protein T
Human	IIDENDNK_04899	alpha/beta hydrolase
Human	BNJMMDAK_05140	phage tail protein
Human	IIDENDNK_04998	phage minor tail protein L
Human	IIDENDNK_04938	Rep protein

Human	BNJMMDAK_05138	host specificity protein J
Human	IIDENDNK_05090	Uncharacterised protein
Human	BNJMMDAK_05230	DUF1378 domain-containing protein
Human	IIDENDNK_04754	N(6)-hydroxylysine O-acetyltransferase
Human	IIDENDNK_05036	lysozyme
Human	BNJMMDAK_04153	death-on-curing family protein
Human	IIDENDNK_04934	TonB-dependent receptor
Human	IIDENDNK_04745	Uncharacterised protein
Human	BNJMMDAK_05198	DUF826 domain-containing protein
Human	IIDENDNK_05042	phage tail protein
Human	BNJMMDAK_05292	tail assembly protein
Human	ALHKBHBA_01467	phage tail protein
Human	IIDENDNK_04996	phage tail protein
Human	IIDENDNK_04997	phage tail protein
Human	IIDENDNK_04756	MFS transporter
Human	IIDENDNK_05037	DUF1327 domain-containing protein
Human	IIDENDNK_05051	phage portal protein
Human	IIDENDNK_04920	glucose-1-phosphatase
Human	IIDENDNK_05045	phage tail protein
Human	IIDENDNK_04750	autotransporter outer membrane beta-barrel domain-containing protein
Human	IIDENDNK_04775	tail fiber assembly protein
Human	BNJMMDAK_01932	DUF826 domain-containing protein
Human	IIDENDNK_05046	phage minor tail protein L
Human	IIDENDNK_05089	phage tail protein
Human	IIDENDNK_05002	phage minor tail protein G
Human	IIDENDNK_05112	phage tail protein
Human	IIDENDNK_05035	Uncharacterised protein
Human	IIDENDNK_04798	transposase
Human	IIDENDNK_04936	iron-regulated protein
Human	BNJMMDAK_04626	type VI secretion protein VasK
Human	ALHKBHBA_01457	phage tail protein
Human	IIDENDNK_05053	phage terminase large subunit family protein

Human	IIDENDNK_04033	DUF1327 domain-containing protein
Human	IIDENDNK_04776	class I SAM-dependent methyltransferase
Human	IIDENDNK_05057	major capsid protein
Human	IIDENDNK_04034	holin
Human	IIDENDNK_04030	Endopeptidase
Human	IIDENDNK_03988	integrase
Human	IIDENDNK_05101	Uncharacterised protein
Human	IIDENDNK_04851	transposase
Human	BNJMMDAK_02617	transposase
Human	IIDENDNK_05012	plasmid replication protein
Human	BNJMMDAK_04629	type VI secretion system baseplate subunit TssG
Human	BNJMMDAK_03143	autotransporter outer membrane beta-barrel domain-containing protein
Human	IIDENDNK_00713	autotransporter adhesin Ag43
Human	BNJMMDAK_03600	DUF945 domain-containing protein
Human	BNJMMDAK_05122	site-specific DNA-methyltransferase
Human	ALHKBHBA_01466	phage minor tail protein G
Human	IIDENDNK_04898	transcriptional regulator nanR
Human	IIDENDNK_03989	outer membrane protein OmpW
Human	IIDENDNK_05055	phage tail protein
Human	IIDENDNK_04939	Rep protein
Human	BNJMMDAK_04635	DNA helicase UvrD
Human	IIDENDNK_04912	iron permease
Human	BNJMMDAK_05197	DUF1378 domain-containing protein
Human	IIDENDNK_04915	ABC transporter permease
Human	IIDENDNK_04917	ABC transporter ATP-binding protein
Human	BNJMMDAK_05231	DUF826 domain-containing protein
Human	IIDENDNK_00715	DUF3987 domain-containing protein
Human	BNJMMDAK_01928	endopeptidase
Human	IIDENDNK_05044	phage tail tape measure protein
Human	IIDENDNK_05054	phage tail protein
Human	GHIANLFP_01018	phage terminase large subunit family protein
Human	IIDENDNK_04805	Transposase

Human	BNJMMDAK_05103	site-specific DNA-methyltransferase
Human	BNJMMDAK_05403	lysis protein
Human	IIDENDNK_00717	AlpA family transcriptional regulator
Human	IIDENDNK_04933	putative enterotoxin protein SenB
Human	IIDENDNK_04901	N-acetylneuraminic acid channel protein
Human	IIDENDNK_00694	polysialic acid transporter KpsD
Human	IIDENDNK_05043	membrane protein
Human	IIDENDNK_04900	N-acetylneuraminic acid mutarotase
Human	BNJMMDAK_01933	DUF1737 domain-containing protein
Human	IIDENDNK_04905	N-acetylneuraminate lyase
Human	IIDENDNK_04902	peptidase S9
Human	IIDENDNK_04035	YjhS
Human	BNJMMDAK_05082	site-specific DNA-methyltransferase
Human	IIDENDNK_05033	lysis protein
Human	IIDENDNK_04039	DNA methylase
Cattle	NDEABJGN_03495	toxin ArtA
Cattle	HEHKHGNK_02888	autotransporter outer membrane beta-barrel domain-containing protein
Cattle	BBFLDBAN_03825	incFII family plasmid replication initiator RepA
Cattle	NDEABJGN_03550	phosphoadenosine phosphosulfate reductase
Cattle	BBFLDBAN_03824	Uncharacterised protein
Cattle	NDEABJGN_04718	autotransporter outer membrane beta-barrel domain-containing protein
Cattle	NDEABJGN_04682	DUF1327 domain-containing protein
Cattle	NDEABJGN_03561	outer membrane protease VII
Cattle	NDEABJGN_03247	lipoprotein bor
Cattle	NDEABJGN_03251	AraC family transcriptional regulator
Cattle	NDEABJGN_03528	DUF1380 domain-containing protein
Cattle	NDEABJGN_04722	transposase
Cattle	NDEABJGN_03532	DUF1380 domain-containing protein
Cattle	NDEABJGN_03533	putative cytoplasmic protein
Cattle	NDEABJGN_03545	AraC family transcriptional regulator
Cattle	NDEABJGN_03250	holin
Cattle	NDEABJGN_03529	antirestriction protein

Cattle	BBFLDBAN_03798	transcriptional activator
Cattle	NDEABJGN_03539	replication initiation protein
Cattle	NDEABJGN_03538	plasmid-partitioning protein SopA
Cattle	NDEABJGN_03248	Predicted lysozyme (DUF847)
Cattle	NDEABJGN_03249	phage holin family protein
Cattle	NDEABJGN_03537	protein sopB
Cattle	NDEABJGN_01575	ShlB/FhaC/HecB family hemolysin secretion/activation protein
Cattle	NDEABJGN_00369	phage tail tape measure protein
Cattle	NDEABJGN_03475	Uncharacterised protein
Cattle	BBFLDBAN_03829	Uncharacterised protein
Cattle	BBFLDBAN_03830	conjugal transfer protein
Cattle	NDEABJGN_03479	protein SrnB
Cattle	NDEABJGN_00114	AraC family transcriptional regulator
Cattle	BBFLDBAN_03826	replication protein
Cattle	NDEABJGN_01576	filamentous hemagglutinin N-terminal domain-containing protein
Cattle	NDEABJGN_03524	partitioning protein ParB
Cattle	NDEABJGN_03253	antitermination protein
Cattle	BBFLDBAN_03828	endonuclease
Cattle	NDEABJGN_03476	incFII family plasmid replication initiator RepA
Cattle	NDEABJGN_03559	site-specific recombinase
Cattle	NDEABJGN_03246	DUF1398 domain-containing protein
Cattle	NDEABJGN_03555	transposase
Cattle	NDEABJGN_03549	AidA-I family adhesin
Cattle	NDEABJGN_03551	transcriptional regulator
Cattle	NDEABJGN_03560	hydrolase
Chicken	FKALCOLL_04466	type II toxin-antitoxin system Phd/YefM family antitoxin
Chicken	OMPLLAHN_05353	DUF2877 domain-containing protein
Chicken	OMPLLAHN_05354	ankyrin repeat domain-containing protein
Chicken	OMPLLAHN_05128	carbamate kinase
Chicken	OMPLLAHN_04025	type II toxin-antitoxin system Phd/YefM family antitoxin
Chicken	OMPLLAHN_05443	PhoX family phosphatase
Chicken	OMPLLAHN_05086	MobA

Chicken	OMPLLAHN_05121	putative transposase
Chicken	OMPLLAHN_03214	DUF1983 domain-containing protein
Chicken	OMPLLAHN_03213	phage tail protein
Chicken	OMPLLAHN_05169	aerobactin synthase IucA
Chicken	OMPLLAHN_05029	lipoprotein bor
Chicken	OMPLLAHN_00048	phage tail protein
Chicken	OMPLLAHN_05131	DUF2877 domain-containing protein
Chicken	OMPLLAHN_05132	cysteine hydrolase
Chicken	OMPLLAHN_05115	MacB family efflux pump subunit
Chicken	OMPLLAHN_05044	dehydrogenase
Chicken	OMPLLAHN_05037	3-deoxy-7-phosphoheptulonate synthase
Chicken	OMPLLAHN_05240	transposase
Chicken	OMPLLAHN_05129	DUF1116 domain-containing protein
Chicken	OMPLLAHN_05034	catecholate siderophore esterase IroD
Chicken	OMPLLAHN_05035	catecholate siderophore esterase IroE
Chicken	OMPLLAHN_05181	IS200/IS605 family transposase
Chicken	OMPLLAHN_05032	salmochelin biosynthesis C-glycosyltransferase IroB
Chicken	OMPLLAHN_05633	tail fiber assembly protein
Chicken	OMPLLAHN_05045	IS3 family transposase
Chicken	OMPLLAHN_05106	RepFIB replication protein A
Chicken	OMPLLAHN_05107	Uncharacterised protein
Chicken	OMPLLAHN_05113	Uncharacterised protein
Chicken	OMPLLAHN_04099	nuclease PIN
Chicken	OMPLLAHN_05109	antimicrobial resistance protein Mig-14
Chicken	OMPLLAHN_04748	istB-like ATP binding family protein
Chicken	FKALCOLL_04587	metal ABC transporter permease
Chicken	OMPLLAHN_05641	Uncharacterised protein
Chicken	OMPLLAHN_05108	site-specific recombinase
Chicken	FKALCOLL_04039	conjugal transfer protein
Chicken	OMPLLAHN_05355	LysR family transcriptional regulator
Chicken	OMPLLAHN_05339	putative tail fiber protein from prophage
Chicken	OMPLLAHN_05609	IS3-like element ISEc31 family transposase

Chicken	OMPLLAHN_04899	conjugal transfer protein TraY
Chicken	OMPLLAHN_03886	DNA helicase
Chicken	OMPLLAHN_04433	transposase
Chicken	OMPLLAHN_05594	transposase
Chicken	FKALCOLL_04468	autotransporter outer membrane beta-barrel domain-containing protein
Chicken	OMPLLAHN_05046	transposase
Chicken	OMPLLAHN_05547	type II secretion protein F
Chicken	OMPLLAHN_05125	LysR family transcriptional regulator
Chicken	OMPLLAHN_05302	PTS glucose transporter subunit IIB
Chicken	OMPLLAHN_04427	DUF4268 domain-containing protein
Chicken	OMPLLAHN_05134	transposase
Chicken	OMPLLAHN_05176	iron/manganese ABC transporter permease subunit SitD
Chicken	FKALCOLL_04530	outer membrane protease
Chicken	OMPLLAHN_05460	transketolase family protein
Chicken	OMPLLAHN_05112	GlcNAc transferase
Chicken	OMPLLAHN_05348	putative transposase
Chicken	OMPLLAHN_05130	acyl-CoA synthetase FdrA
Chicken	OMPLLAHN_05351	DUF1116 domain-containing protein
Chicken	OMPLLAHN_05352	acyl-CoA synthetase FdrA
Chicken	OMPLLAHN_05509	putative transposase
Chicken	OMPLLAHN_04429	SAM-dependent DNA methyltransferase
Chicken	OMPLLAHN_05221	putative transposase protein
Chicken	OMPLLAHN_05033	salmochelin/enterobactin export ABC transporter IroC
Chicken	OMPLLAHN_05239	integrase
Chicken	OMPLLAHN_05030	putative DNA-binding protein
Chicken	FKALCOLL_04524	RepFIB replication protein A
Chicken	OMPLLAHN_04034	Uncharacterised protein
Chicken	OMPLLAHN_04042	conjugal transfer protein TraH
Chicken	FKALCOLL_04588	malate dehydrogenase
Chicken	OMPLLAHN_05350	xanthine permease
Chicken	OMPLLAHN_05031	integrase
Chicken	OMPLLAHN_04468	PerC family transcriptional regulator

Chicken	OMPLLAHN_05349	carbamate kinase
Chicken	OMPLLAHN_05554	IS21 family transposase
Chicken	OMPLLAHN_05220	autotransporter outer membrane beta-barrel domain-containing protein
Chicken	OMPLLAHN_05523	Uncharacterised protein
Chicken	OMPLLAHN_05042	peptidase domain-containing ABC transporter
Chicken	OMPLLAHN_05043	colicin V
Chicken	FKALCOLL_04520	transposase
Chicken	FKALCOLL_04043	incFII family plasmid replication initiator RepA
Chicken	OMPLLAHN_05529	IS2 element protein
Chicken	OMPLLAHN_05126	cytosine permease
Chicken	OMPLLAHN_05168	MFS transporter
Chicken	OMPLLAHN_04181	chromosome partitioning protein ParB
Chicken	OMPLLAHN_05140	MFS transporter
Chicken	OMPLLAHN_05114	efflux RND transporter periplasmic adaptor subunit
Chicken	OMPLLAHN_05378	colicin E1 protein
Chicken	OMPLLAHN_04083	plasmid-partitioning protein SopA
Chicken	FKALCOLL_04521	Uncharacterised protein
Chicken	OMPLLAHN_00047	putative membrane protein
Chicken	OMPLLAHN_04024	type II toxin-antitoxin system RelE/ParE family toxin
Chicken	OMPLLAHN_04082	ParB/RepB/Spo0J family plasmid partition protein
Chicken	OMPLLAHN_05122	cobalamin biosynthesis protein CobW
Chicken	OMPLLAHN_05110	NAD(P)H-binding protein
Chicken	OMPLLAHN_04467	AraC family transcriptional regulator
Chicken	OMPLLAHN_05036	siderophore salmochelin receptor IroN
Chicken	OMPLLAHN_05253	exonuclease
Chicken	OMPLLAHN_05111	omptin family outer membrane protease

9.5: The metadata of the strains harboring the *sat* gene in our collection.

Strain	Country	Health	Host	ST	Phylogroups
35110	Germany	Diseased	Human	69	D
06-03041	Germany	Diseased	Human	38	D
14-03445	Germany	Healthy	Human	62	F
14-04252	Germany	Diseased	Human	975	A
20222_6#191	Vietnam	Healthy	Human	648	F
20222_7#277	Vietnam	Healthy	Human	131	B2
20222_8#126	Vietnam	Healthy	Human	73	B2
21224_2#340	Vietnam	Healthy	Human	131	B2
21224_2#344	Vietnam	Healthy	Human	131	B2
21224_2#88	Vietnam	Healthy	Human	10	A
21224_3#256	Vietnam	Healthy	Human	131	B2
21224_3#267	Vietnam	Healthy	Human	1177	D
21224_3#370	Vietnam	Healthy	Human	1193	B2
21225_2#129	Vietnam	Healthy	Human	131	B2
21225_2#274	Vietnam	Healthy	Human	1177	D
21225_2#28	Vietnam	Healthy	Human	131	B2
21225_2#31	Vietnam	Healthy	Human	131	B2
21225_2#74	Vietnam	Healthy	Human	131	B2
21225_2#89	Vietnam	Healthy	Human	10	A
21ZN-0026-2	Vietnam	Diseased	Human	1193	B2
21ZN-0037-2	Vietnam	Diseased	Human	131	B2
21ZN-0052-2	Vietnam	Diseased	Human	1193	B2
21ZN-0071-2	Vietnam	Diseased	Human	69	D
21ZN-0073-1	Vietnam	Diseased	Human	131	B2

21ZN-0089-1	Vietnam	Diseased	Human	131	B2
21ZN-0105-1	Vietnam	Diseased	Human	38	D
21ZN-0134-1	Vietnam	Diseased	Human	1193	B2
21ZN-0147-1	Vietnam	Diseased	Human	69	D
21ZN-0151-1	Vietnam	Diseased	Human	1193	B2
21ZN-0152-1	Vietnam	Diseased	Human	1193	B2
21ZN-0154-2	Vietnam	Diseased	Human	1193	B2
21ZN-0188-1	Vietnam	Diseased	Human	69	D
21ZN-0188-2	Vietnam	Diseased	Human	69	D
21ZN-0196-2	Vietnam	Diseased	Human	1193	B2
21ZN-0198-2	Vietnam	Diseased	Human	131	B2
21ZN-0201-2	Vietnam	Diseased	Human	131	B2
21ZN-0206-2	Vietnam	Diseased	Human	1193	B2
21ZN-0220-2	Vietnam	Diseased	Human	1193	B2
9352_7#29	Germany	Healthy	Human	10	A
9352_7#48	Germany	Healthy	Human	10	A
IMT12185	Germany	Diseased	Human	131	B2
IMT12490	Germany	Diseased	Chicken	73	B2
IMT13784	Germany	Healthy	Human	10	A
IMT13798	Germany	Diseased	Human	73	B2
IMT13800	Germany	Diseased	Human	73	B2
IMT13882	Germany	Healthy	Human	73	B2
IMT15474	Germany	Diseased	Pig	393	D
IMT16218	Germany	Healthy	Pig	73	B2
IMT16220	Germany	Healthy	Pig	73	B2
IMT20024	Germany	Diseased	Cattle	73	B2
IMT9270	Germany	Diseased	Human	62	F
IMT9687	Germany	Diseased	Human	34	A
SAP1372	UK	Diseased	Human	131	B2
SAP1468	UK	Diseased	Human	394	D
SAP1515	UK	Diseased	Human	73	B2
SAP1597	UK	Diseased	Human	69	D

SAP1609	UK	Diseased	Human	73	B2
SAP1614	UK	Diseased	Human	14	B2
SAP1621	UK	Diseased	Human	131	B2
SAP1632	UK	Diseased	Human	38	D
SAP1781	UK	Diseased	Human	8455	B2
SAP1836	UK	Diseased	Human	131	B2
SAP1847	UK	Diseased	Human	131	B2
SAP1852	UK	Diseased	Human	131	B2
SAP1858	UK	Diseased	Human	131	B2
SAP1873	UK	Diseased	Human	131	B2
SAP1887	UK	Diseased	Human	131	B2
SAP1913	UK	Diseased	Human	1193	B2
SAP1926	UK	Diseased	Human	73	B2
SAP1953	UK	Diseased	Human	131	B2
SAP2068	UK	Healthy	Human	131	B2
SAP2072	UK	Healthy	Human	62	F
SAP2081	UK	Healthy	Human	1193	B2
SAP2082	UK	Healthy	Human	10	A
SAP2089	UK	Healthy	Human	131	B2
SAP2093	UK	Healthy	Human	415	F
SAP2096	UK	Healthy	Human	131	B2
SAP2098	UK	Healthy	Human	73	B2
SAP2131	UK	Healthy	Human	59	F
SAP2148	UK	Healthy	Human	131	B2

Declaration of independence

Hereby I declare that I have prepared my doctoral thesis entitled “**Identification of host-associated genomic determinants in *Escherichia coli* using Genome-wide Association Study (GWAS)**” independently and without impermissible help. Hereby I confirm that my doctoral thesis is not based on my Master thesis or has not been filed anywhere before.