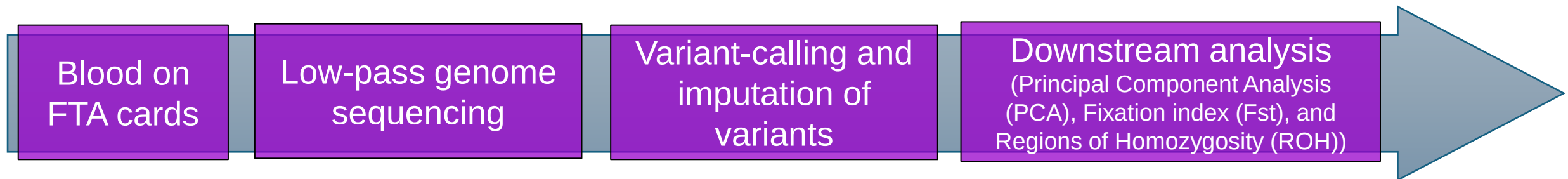


Genetic characterisation of indigenous chicken ecotypes from India and Bangladesh

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- 🔗 Genetic characterisation of the sampled chicken ecotypes/breeds/varieties
- 🔗 Association of the genomic region with the colonisation of *E. coli*



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🐔 Distinct genetic profiles of breeds (Figure 1)

🐔 Higher F_{st} values between groups of broilers and indigenous (Figure 2)

🐔 Regions with higher genetic variation between broilers and indigenous birds corresponded to growth, development and phenotypic appearance related genes (Figure 3)

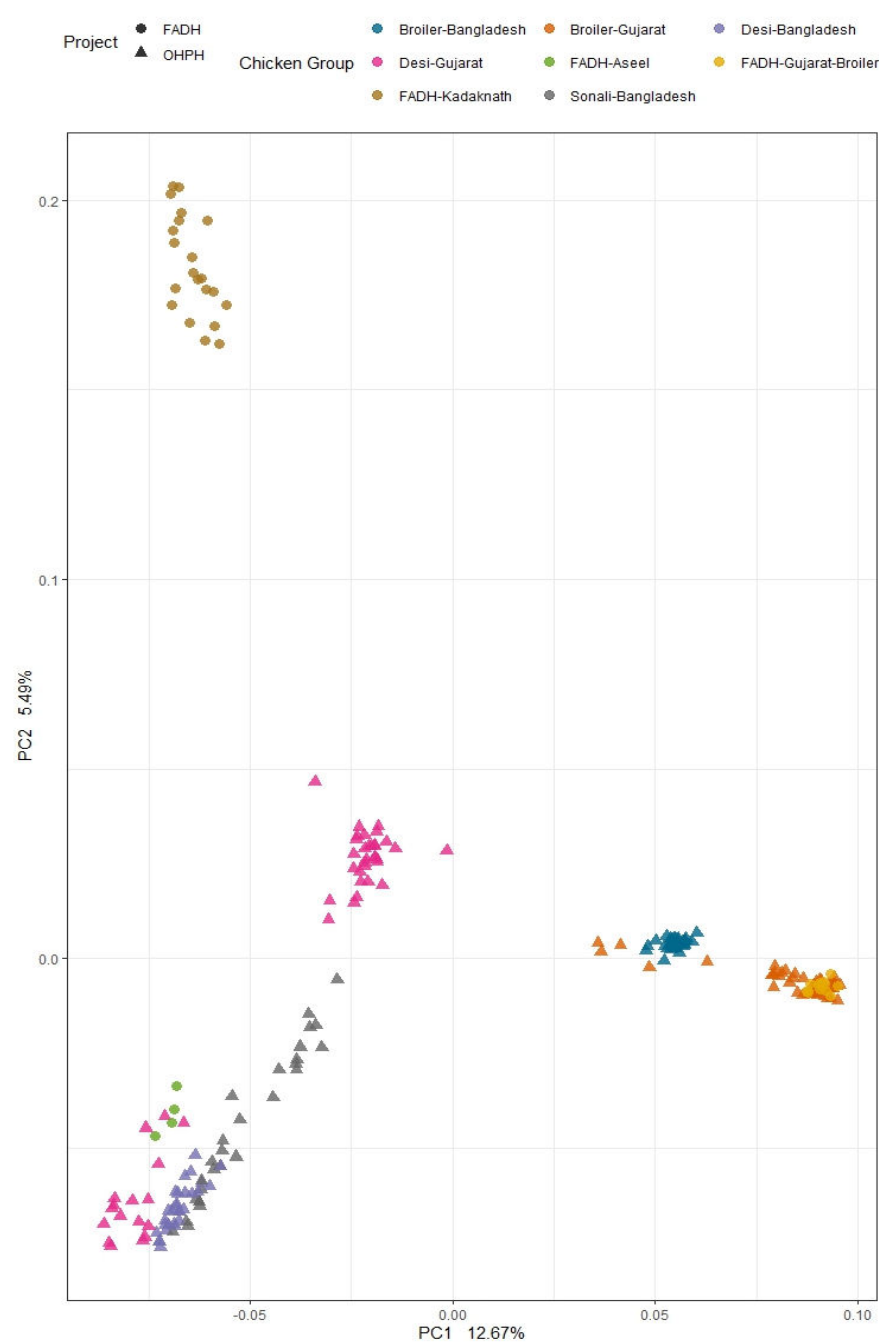


Figure 1: PCA based on Genomic Relationship matrix built using sequencing data

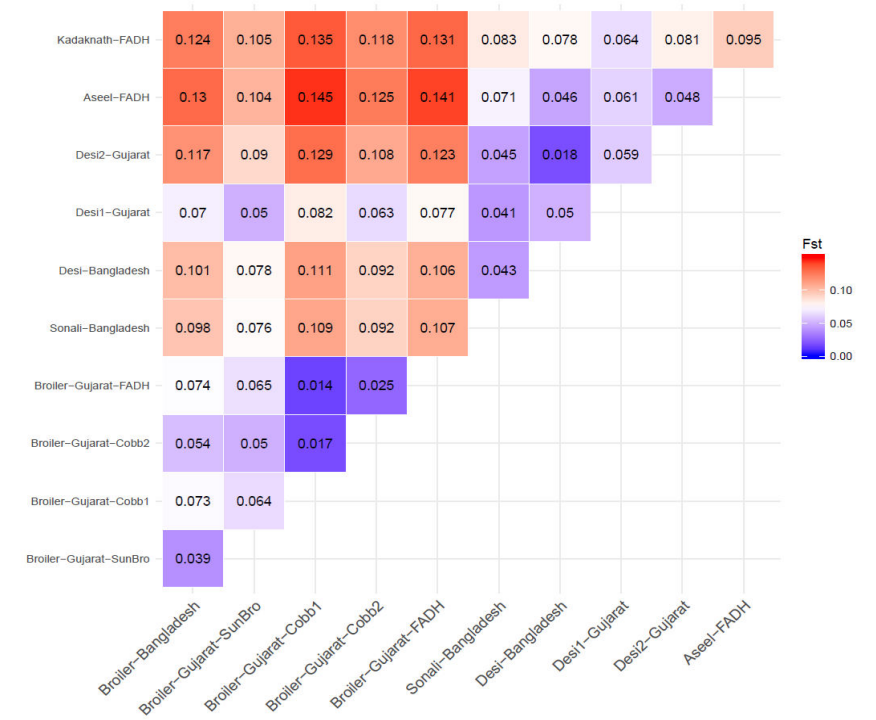


Figure 2: Pairwise F_{st} values between all groups of birds

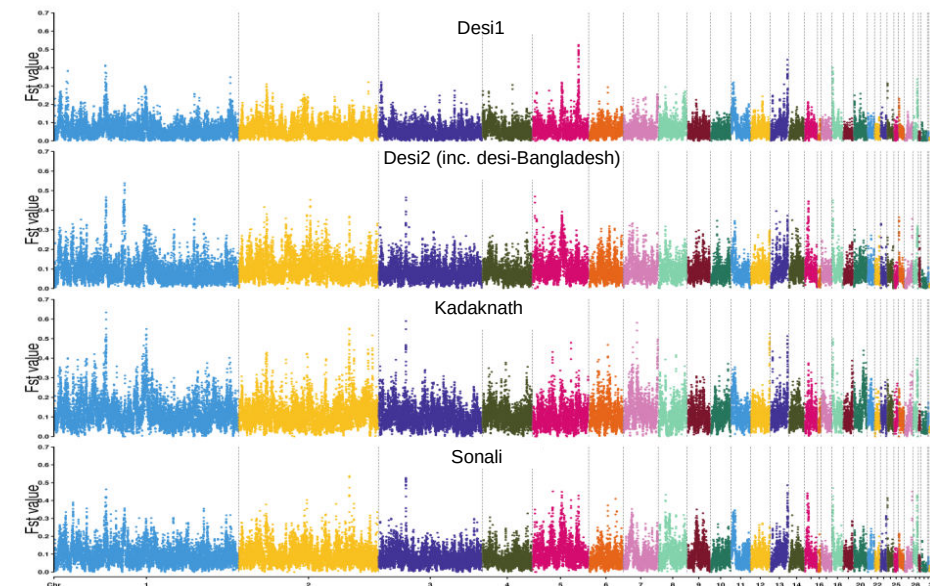


Figure 3: Manhattan plot highlighting peaks of interest with high F_{st} values from comparing broilers with individual indigenous

- Least ROHs in desi birds indicating more genetic diversity, higher number of ROHs in Kadaknath indicating higher levels of inbreeding (Figure 4)
 - Kadaknath had longer ROHs-recent inbreeding
- Overall lower F_{st} values for *E. coli* colonisation phenotype
 - Peaks contained immune-related genes and few previously associated with LPS (Figure 5)

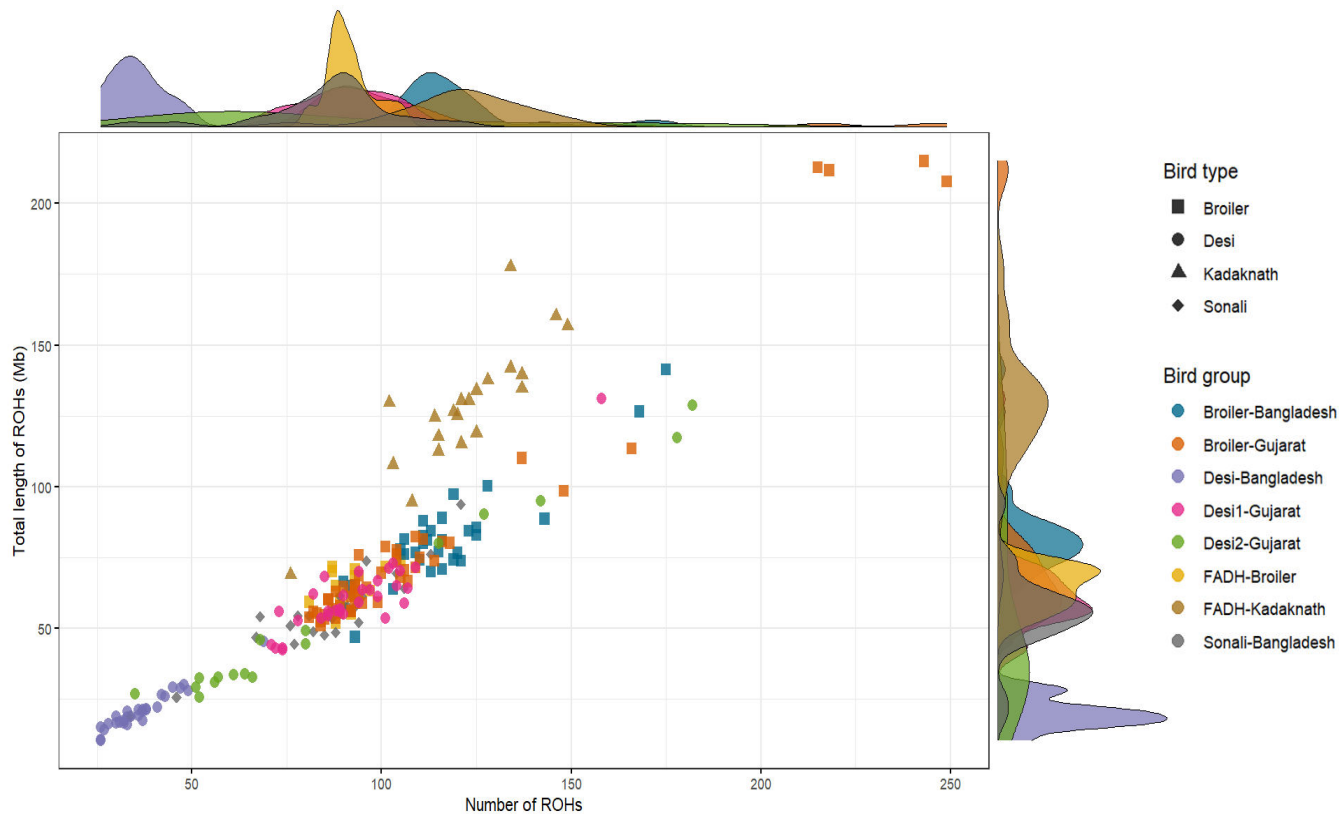


Figure 4: Distribution of ROHs by number and length per chicken

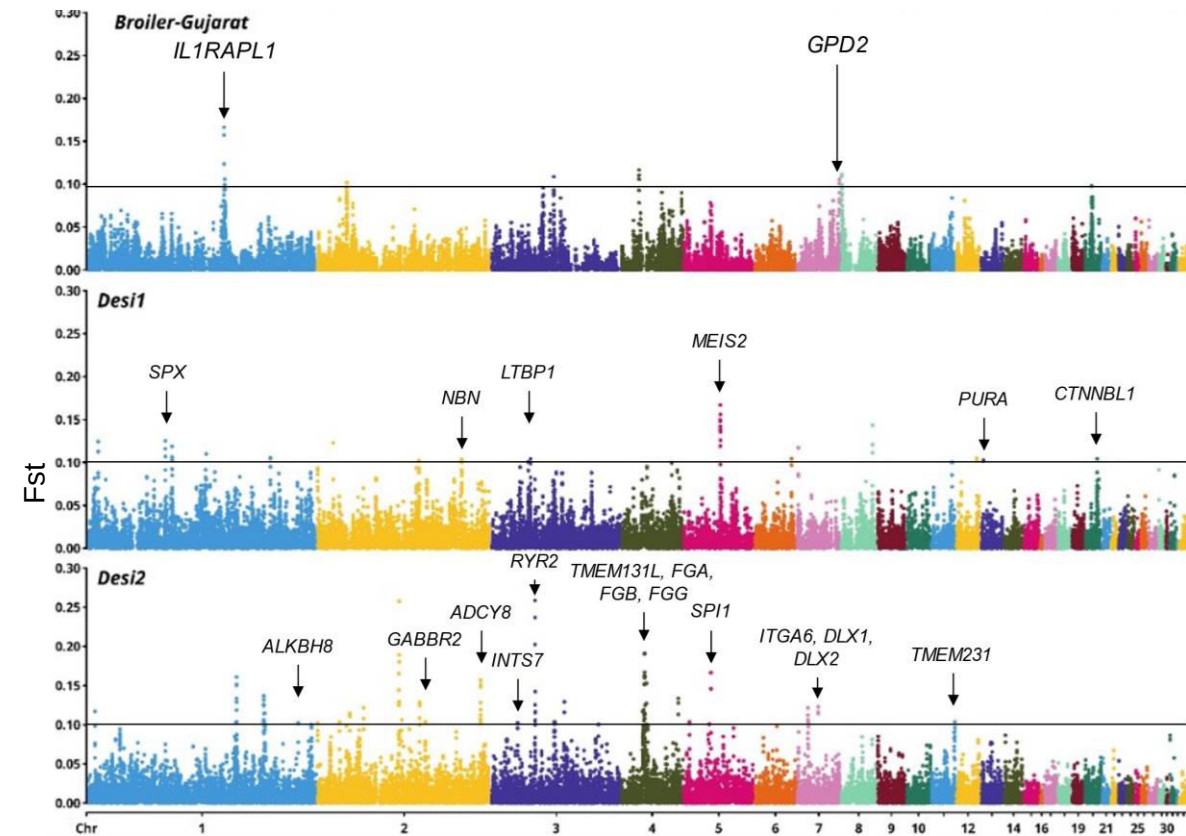


Figure 5: Manhattan plot highlighting genes from top F_{st} values from *E. coli* colonisation