



Pangenome variation analysis uncovers the impacts of SNP-independent structural variations in modern European cattle breeding

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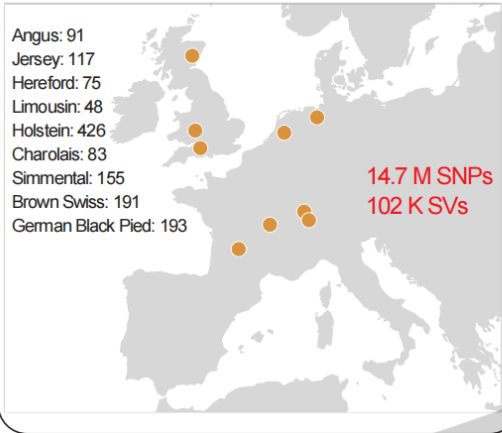
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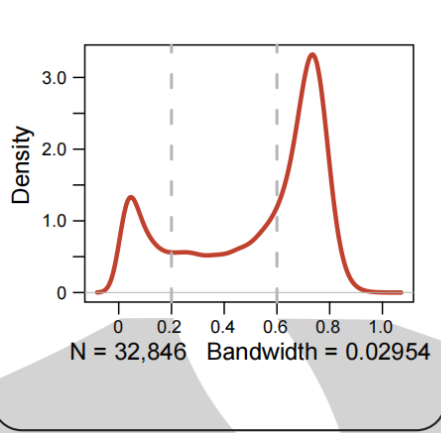
Shoulu Dai, Linjing Xu, Liu Yang, Pengju Zhao, Xin Li, Wei Huang, Wengang Zhang, et al. 2026. Pangenome variation analysis uncovers the impacts of SNP-independent structural variations in modern European cattle breeding. *iMetaOmics* 3:e70095. <https://doi.org/10.1002/imo2.70095>

Background

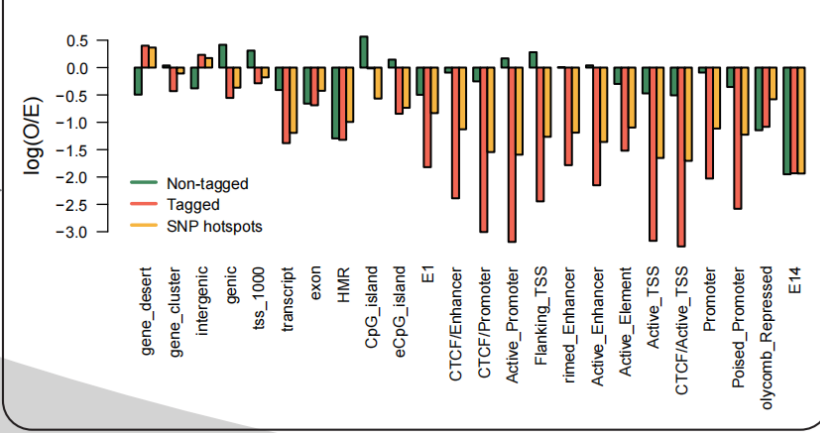
Pangenome variant catalogue for 1379 cattle



19.3% SVs are not tagged by SNP



Non-tagged SVs are enriched in functional element region



Industrial Significance

➤ European cattle dominate beef and

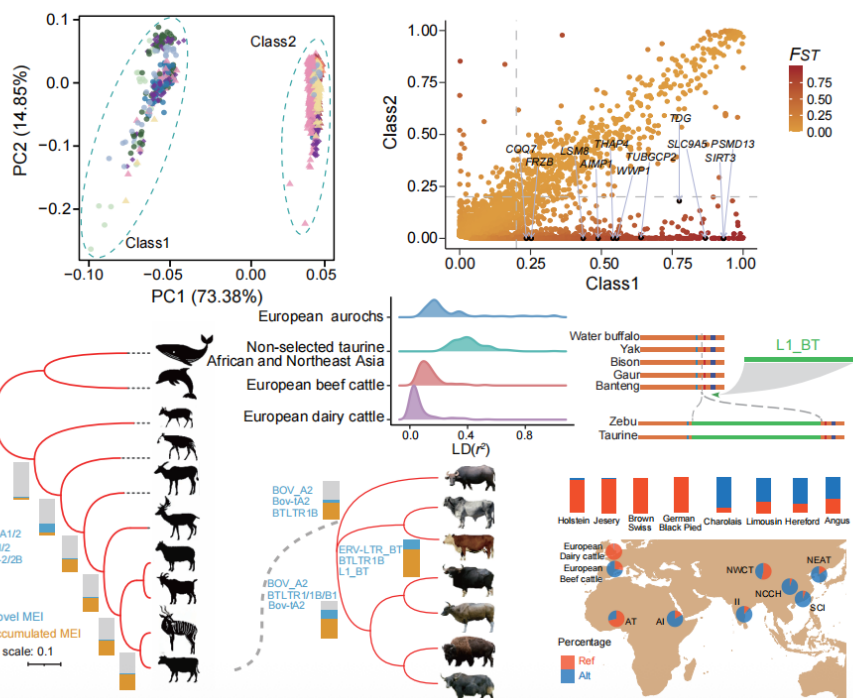
dairy production

➤ Key variants provide

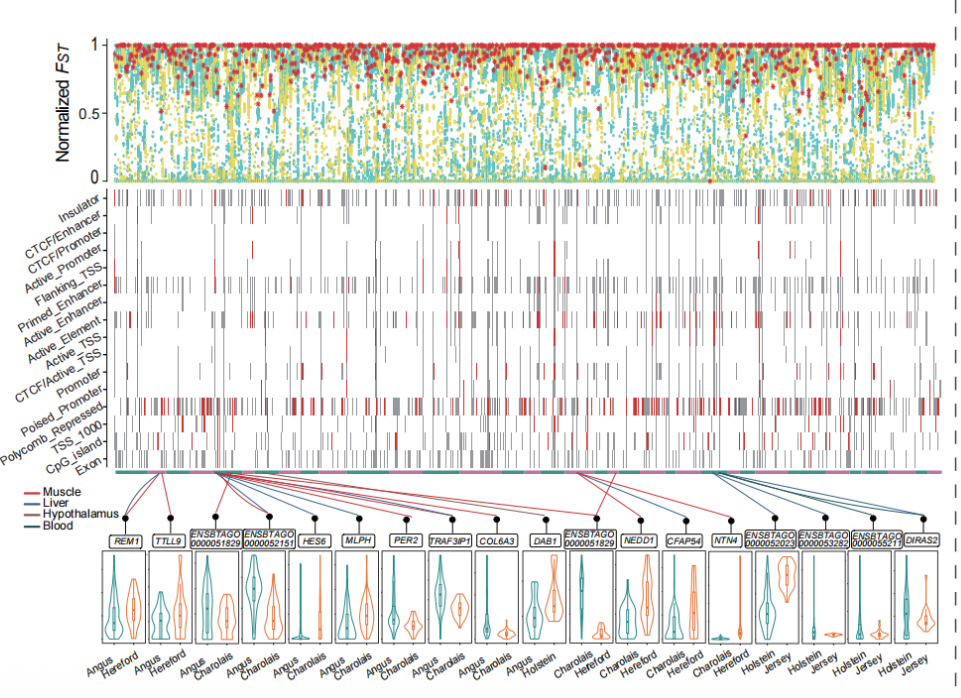
resources for global

trait improvement

Non-tagged SVs are crucial for selection, differentiation, and trait regulation



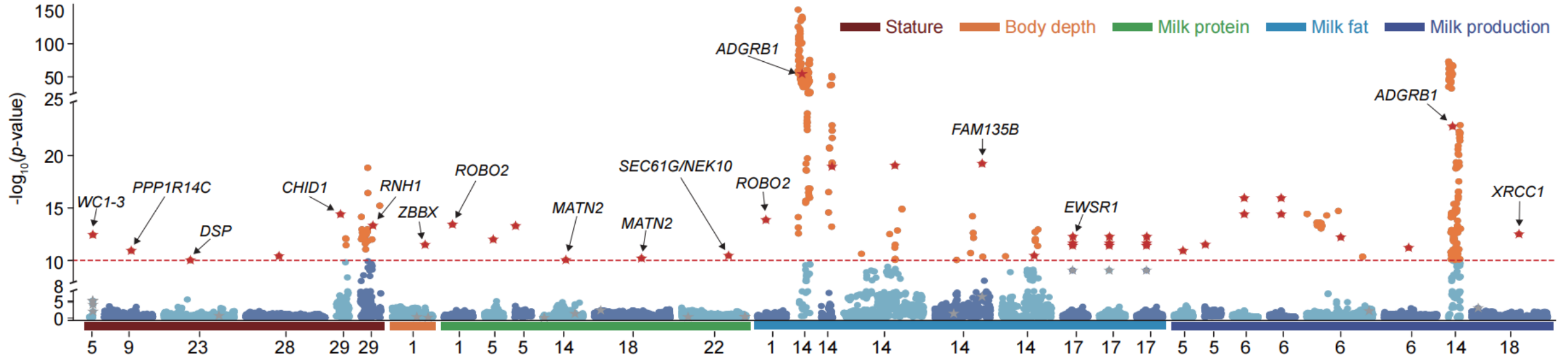
Tagged SVs dominate phenotypic regulation in haplotypes





Background

SNP + SV GWAS for 50,000 Holstein bulls reveals the essential role of structural variants in explaining phenotypic variation

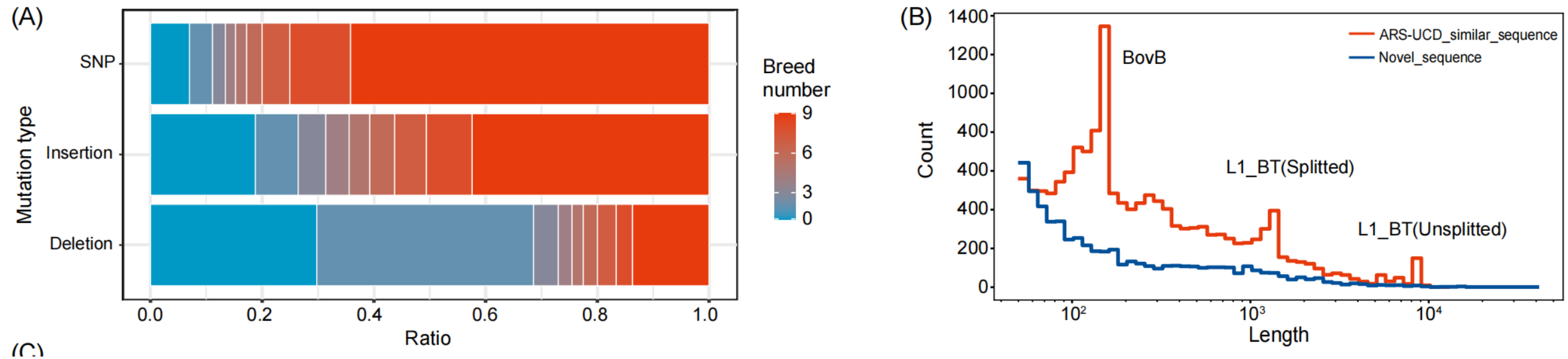


Research Status & Challenges

- SNP-based studies miss part of functional variation, leading to missing heritability
- Pan-genome enables more comprehensive analysis
- Some SVs cannot be tagged by SNPs and complement SNP effects
- Their distribution, origin, and functional roles remain unclear

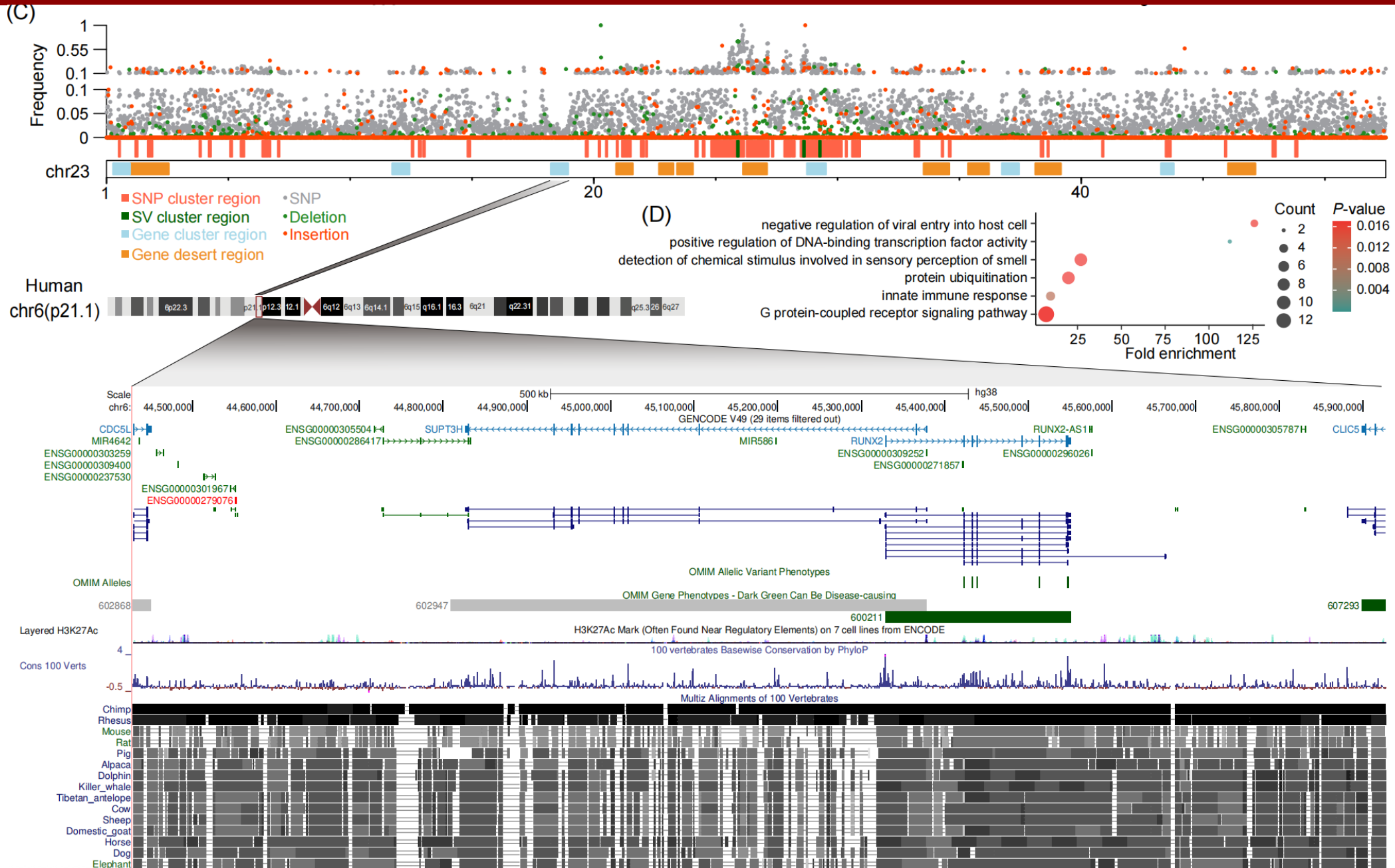


Result1: SNP and SV catalogue for nine European cattle breeds

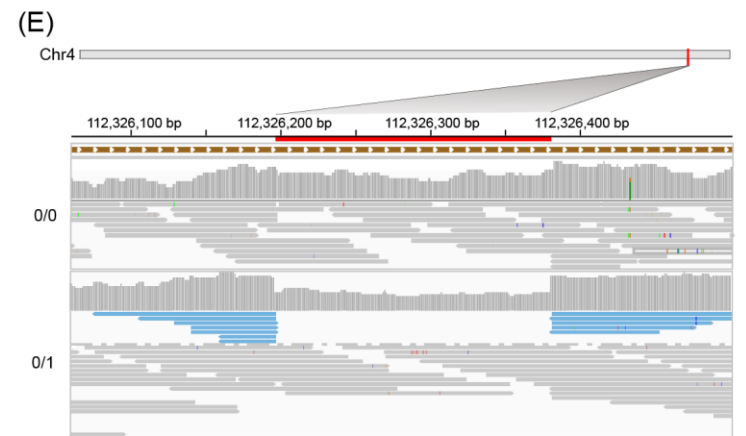
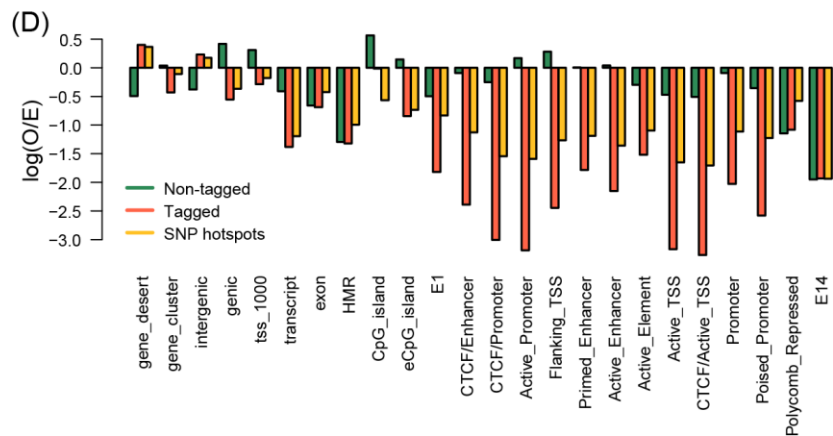
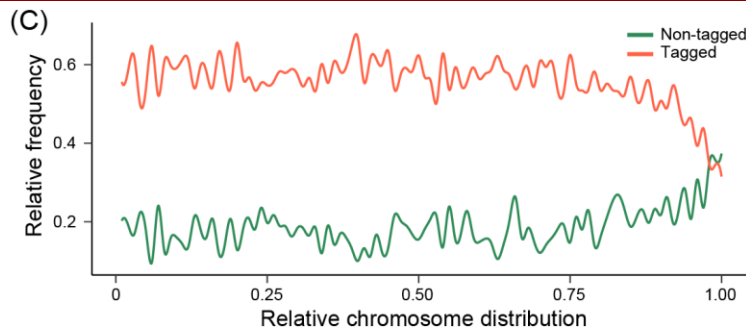
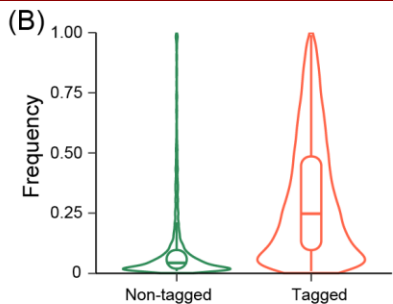
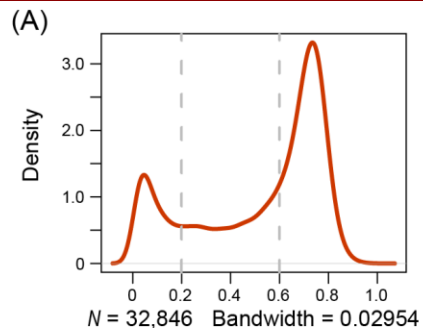


- **Constructed representative European cattle SNP+SV reference panel via kinship filtering**
- **Provides significantly more insertion variants than previous studies**
- **SVs exhibit similar genomic distribution patterns to SNPs , enriching in immune loci and under selection in key functional genes**

Result1: SNP and SV catalogue for nine European cattle breeds



Result2: SVs not tagged by SNPs exhibit unique distribution patterns

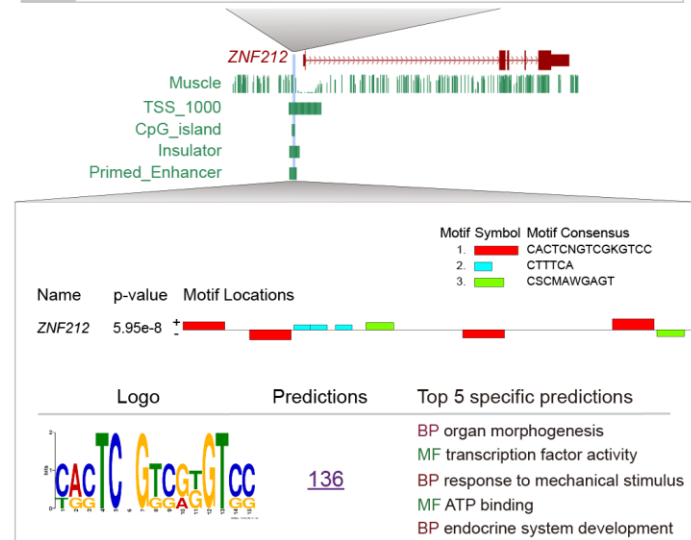
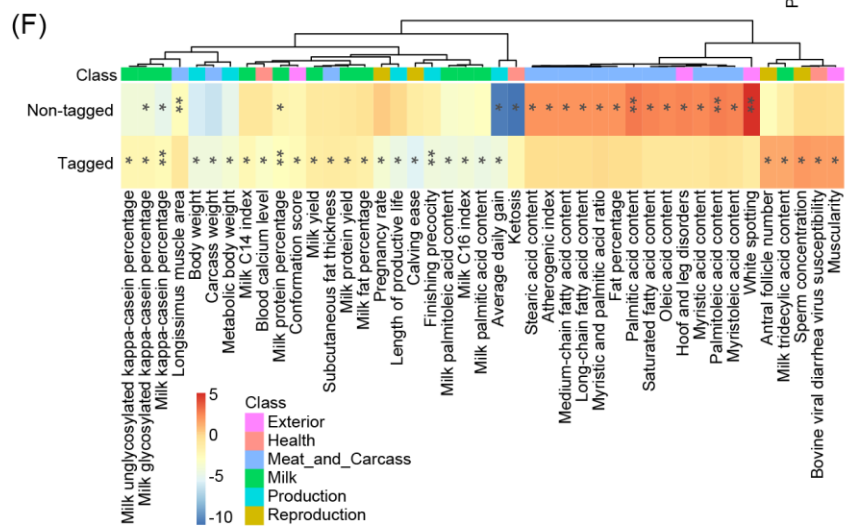


Non-tagged SVs:

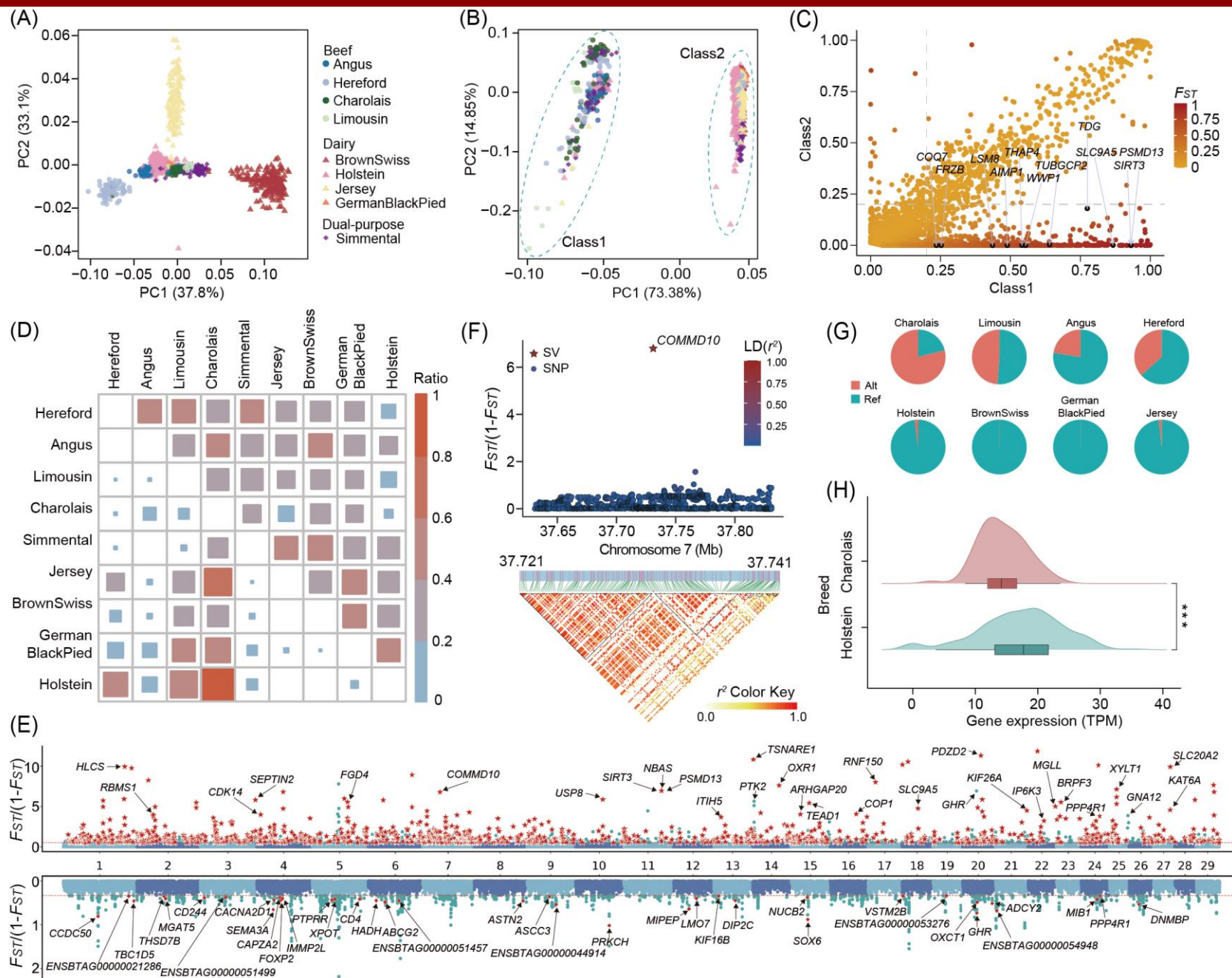
19.3% not tagged by SNPs

Features of Non-tagged SV:

- Lower mutation frequency
- Enriched at chromosome ends and promoter regions
- Associated with meat and milk QTLs



Result3: SVs not tagged by SNPs play a pivotal role in the recent directional selection of European dairy and beef cattle

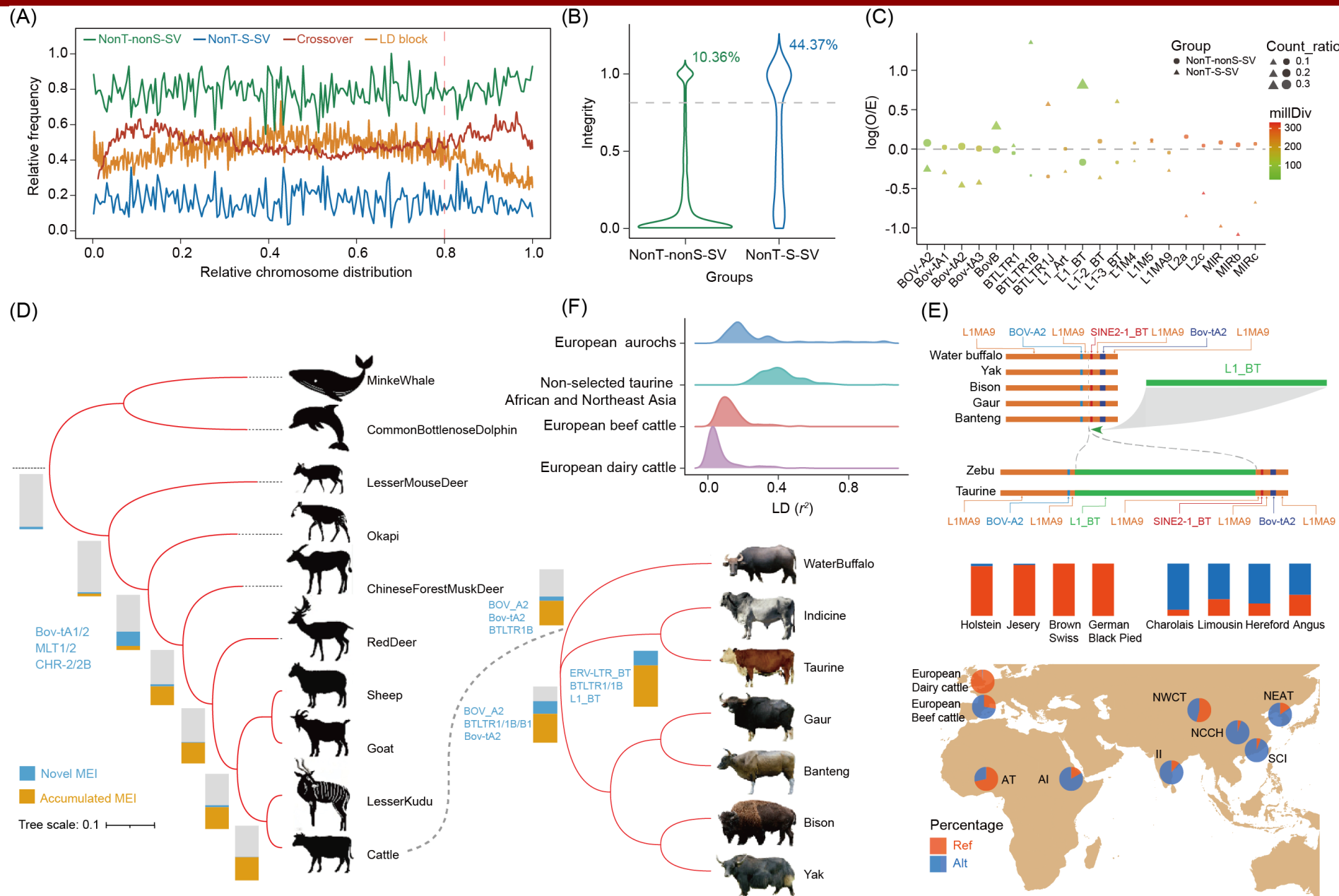


- Non-tagged SVs effectively distinguish European beef and dairy cattle
- Strongly selected non-tagged SVs enriched in meat/milk performance genes; higher proportion in selected SVs between breeds

Example:

- Non-tagged SV at *COMMD10* (milk-related) under strong selection between beef and dairy

Result4: High recombination rates and strong selection drive the decoupling of SVs from SNP markers



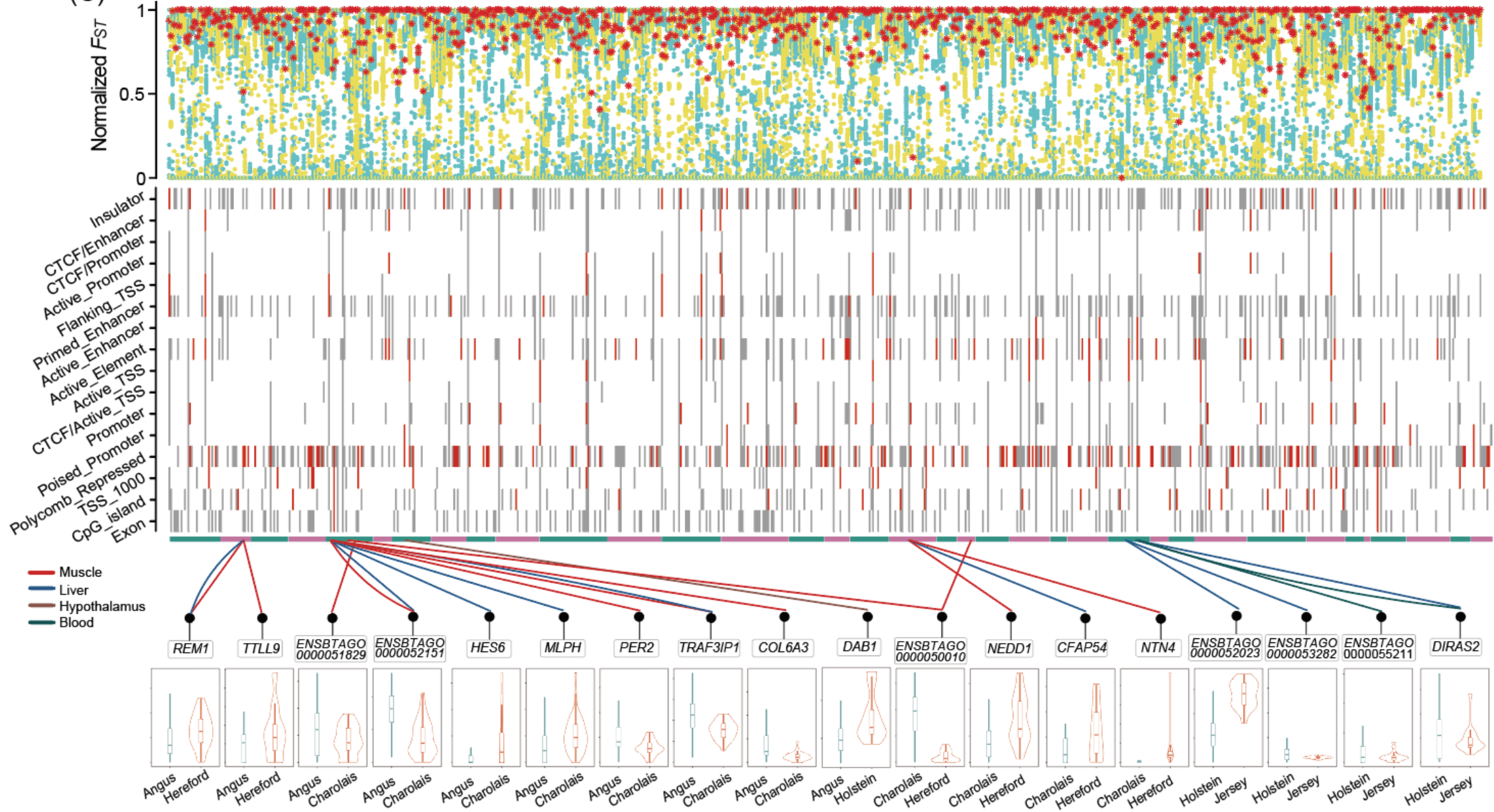
Reasons why SVs not tagged by SNPs

- High-frequency chromosome breakage and recombination
- Strong selection on young SVs



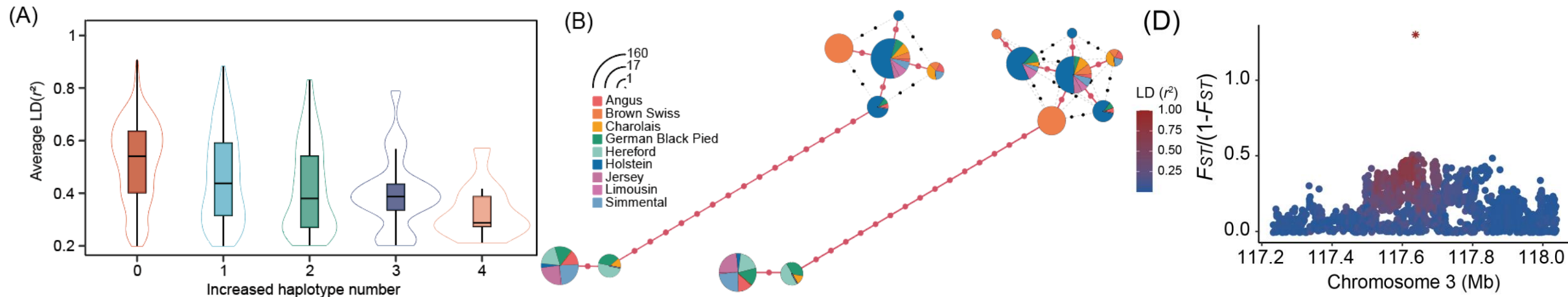
Result5: SNP-tagged SVs dominate haplotype structure and function in cattle breed differentiation

(C)

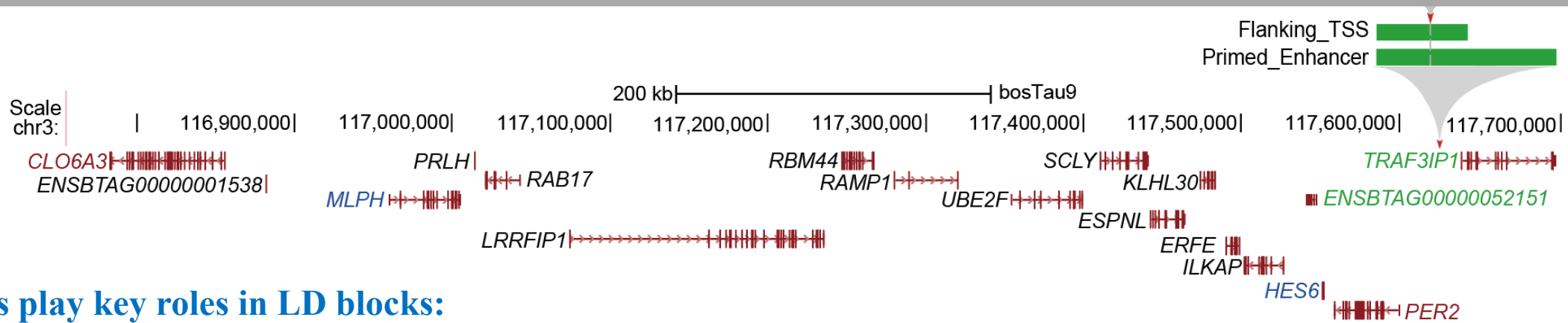




Result5: SNP-tagged SVs dominate haplotype structure and function in cattle breed differentiation



(E) DNA sequence alignment showing a selected SV in the *TRAF3IP1* enhancer region. The sequence is shown in a box with the SV highlighted in red. The sequence is: AAGGTATCTGTGGGGAGCGAGCTCCGCCCATGGCAAAGGTCATGAGGAAGGAGGCTTGACATACGCAAAAGGGGGATCAAGCCTCAGGAGTCTCCCTGAAAATCTCGAGCAATCTACCCCAAAACCAGAGTCIGCCTACTTTCTACTTTGTGCTTTACCTACACCTCTGACTTTACGGGGCTGTCCCCACACCTCTCTGAAAAAGAGTTAGCTTACAGCTCCAGTTAATAATCTTGGGTGTGACAGTGTTCACCTACAAACCTCTTTGAAAGTCCCTAGCCTGCCTGAATAGGTTTTCCGGCCACATGTGATTGTTTCAGAGCCTCCCACTGTGAGAGGCCAGGAGATGTTCTAACTGTCCAAACACAGATTCTTTGAGTAGTTAAAAGATTGATTAGAAATGTATTGGTGAAGGATTTTCACTTGTGGGCCAATGTTGCTGCTAAGTTCCATATCCCTTACTGCTGTGCCCTGGCAGTGTATTGATTAATAATTTGGTGTAAATAGTAGCTTTAATGTTGTAACCTGGGACCCTTAATCTTTTCTGTATAGCCACACACCTTTGCTCTGTAGGAATGCAACTTTATCTAATGCTTTTGGAGGGTGGCTCTGACCAATCACCTTTAGAGAAAAATAAGTTTCTGAAGAAAAGGCTTAAATGTTAACAGGCCTCCGGCCAGAAAGATGATGCAATCACCTAAGCTTTTGCATATGATAAGTTGCAGGAAGAAAGCCTGGCTTGTGCTGCTGACTACTACCCTTCCCCCATATCCTCTATGCA TAACTTAAGGTATAAAAATACTTTGGAAAATAAGTGCGGGCCCTTGTCCACCGAAACTTGGTCTCACCATGTCGTTCTTCTTACCTTCTGGCTGAATATTCAGCCCTCTTTCTCCACTGAATTTCCCTACTGAGCTATCCTTATTCAGCCCTCTTTCTTCACTGAATTTACTGAGCTATCCTCATTCTATTACTCTTTATATCCTTAATTAACGTTTAATAAGCAATGTTTCTGATCCTCGCCGACGCCATCCCGCTTCGAATTCCTGGATCCACCAGGGCTGGACCCCGGC.

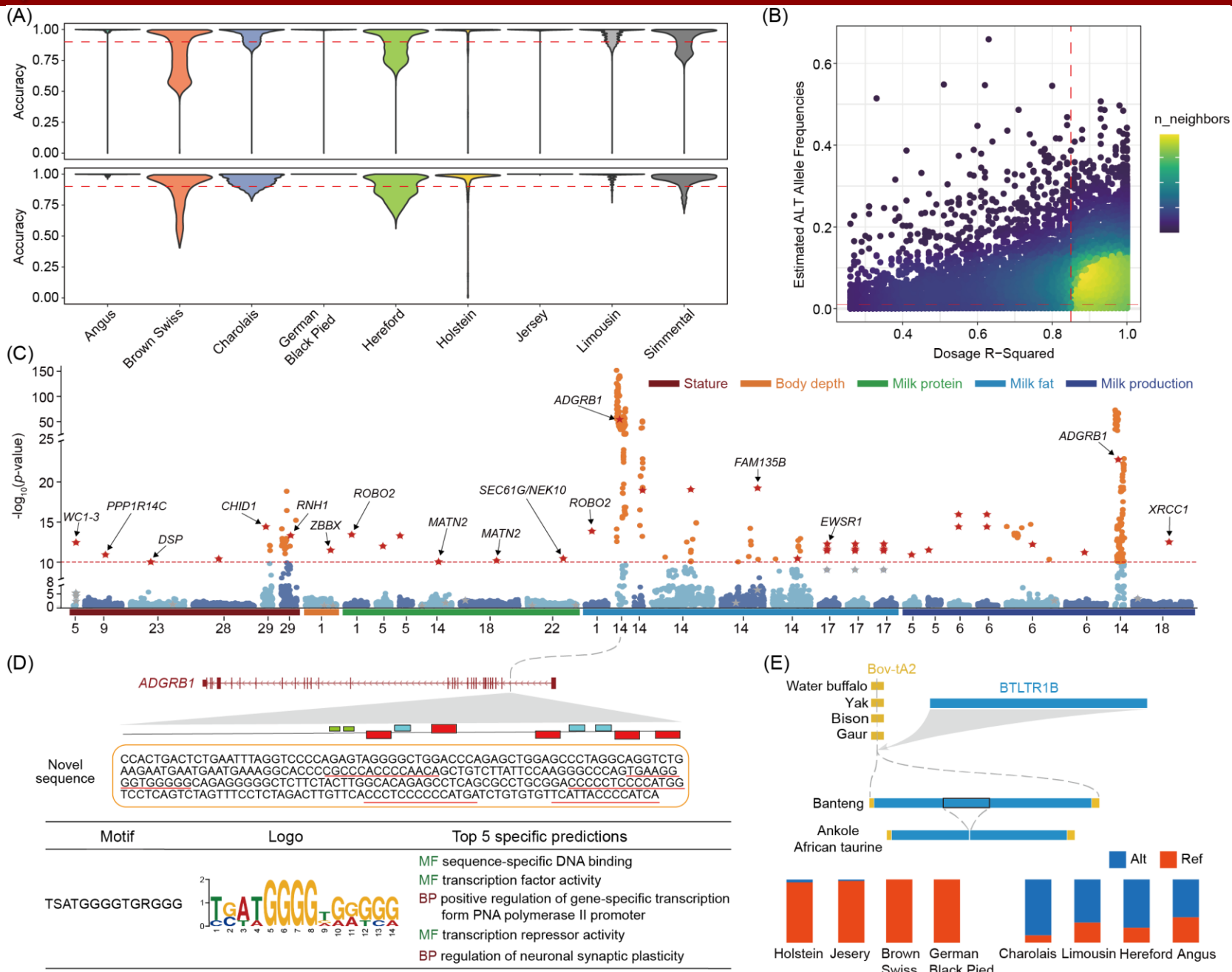


SVs play key roles in LD blocks:

- SVs can increase haplotype diversity and generate breed-specific haplotypes
- SVs exert dominant regulation via disrupting key genomic elements

- **Example:** Selected SV in *TRAF3IP1* enhancer region (Angus vs. Charolais)

Result6: Large-scale GWAS in Holstein cattle reveals pivotal role of SVs



➤ The imputation panel enables accurate SV prediction using SNPs

➤ Imputed SNP+SV genotypes for 50,000 bulls from SNP array data

➤ SNP+SV GWAS revealed non-tagged SVs linked to dairy production traits

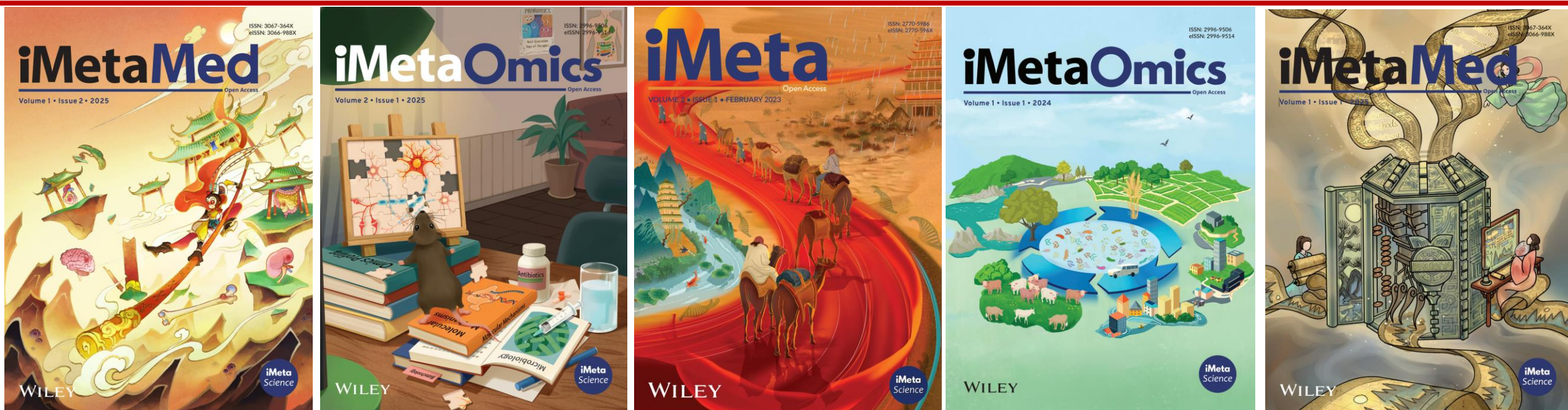
总结

- **Constructed a representative European cattle SNP+SV imputation panel**
- **19.3% of SVs are not tagged by SNPs and are enriched in key regulatory regions**
- **Non-tagged SVs play key roles in the selection of European dairy and beef cattle**
- **High recombination and strong selection on young SVs explain non-tagged SVs**
- **Tagged SVs may dominate phenotypic regulation within LD blocks**
- **Pioneered SNP-based SV imputation; large-scale GWAS demonstrated SVs complement SNPs in explaining phenotypic variation**

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