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Comparison of the Polish and German Holstein-Friesian dairy cattle populations using SNP microarrays

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CONCLUSIONS

German and Polish HF dairy populations

- differ in LD pattern
- differ in additive effects of single SNPs
- generally no differences in effects of genomic regions of 0.25Mbp
- … except segments on BTA: 1, 6, 9, 14, 16

MATERIAL & METHODS

🇩🇪 2 294 German HF ♂

for 🇩🇪 and 🇵🇱 ♂

- genotypes → Illumina 50 K chip
- phenotypes (y) → deregressed breeding values
- LD → pairwise r^2 between SNPs
- SNP (q) estimates → SNP-BLUP model: $y = Zq + e$

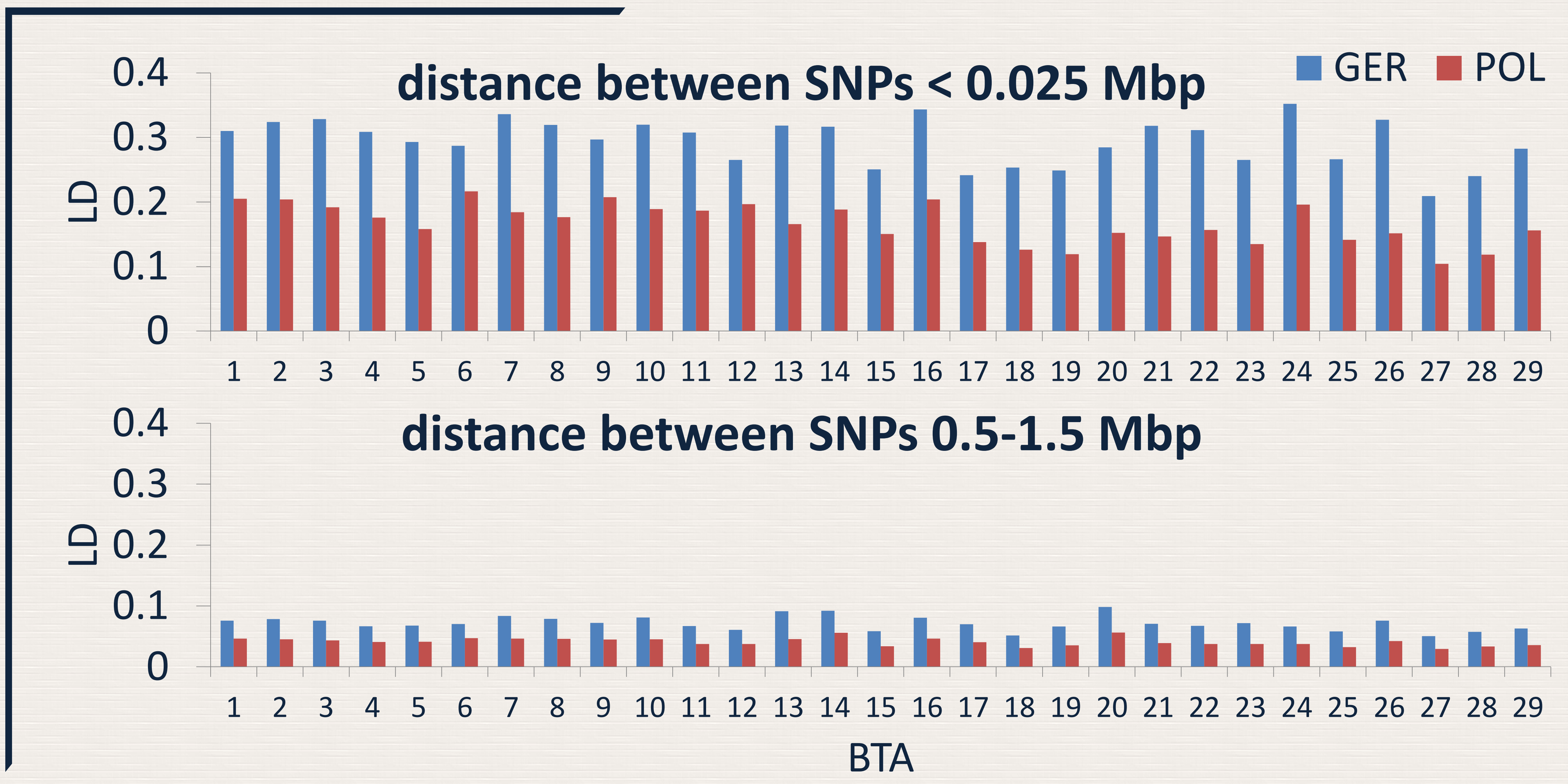
for 🇩🇪 against 🇵🇱 ♂

- 0.25 Mbp genomic region estimates → t test with SNP effects using: $2 \cdot MAF \cdot (1 - MAF) \cdot q^2$

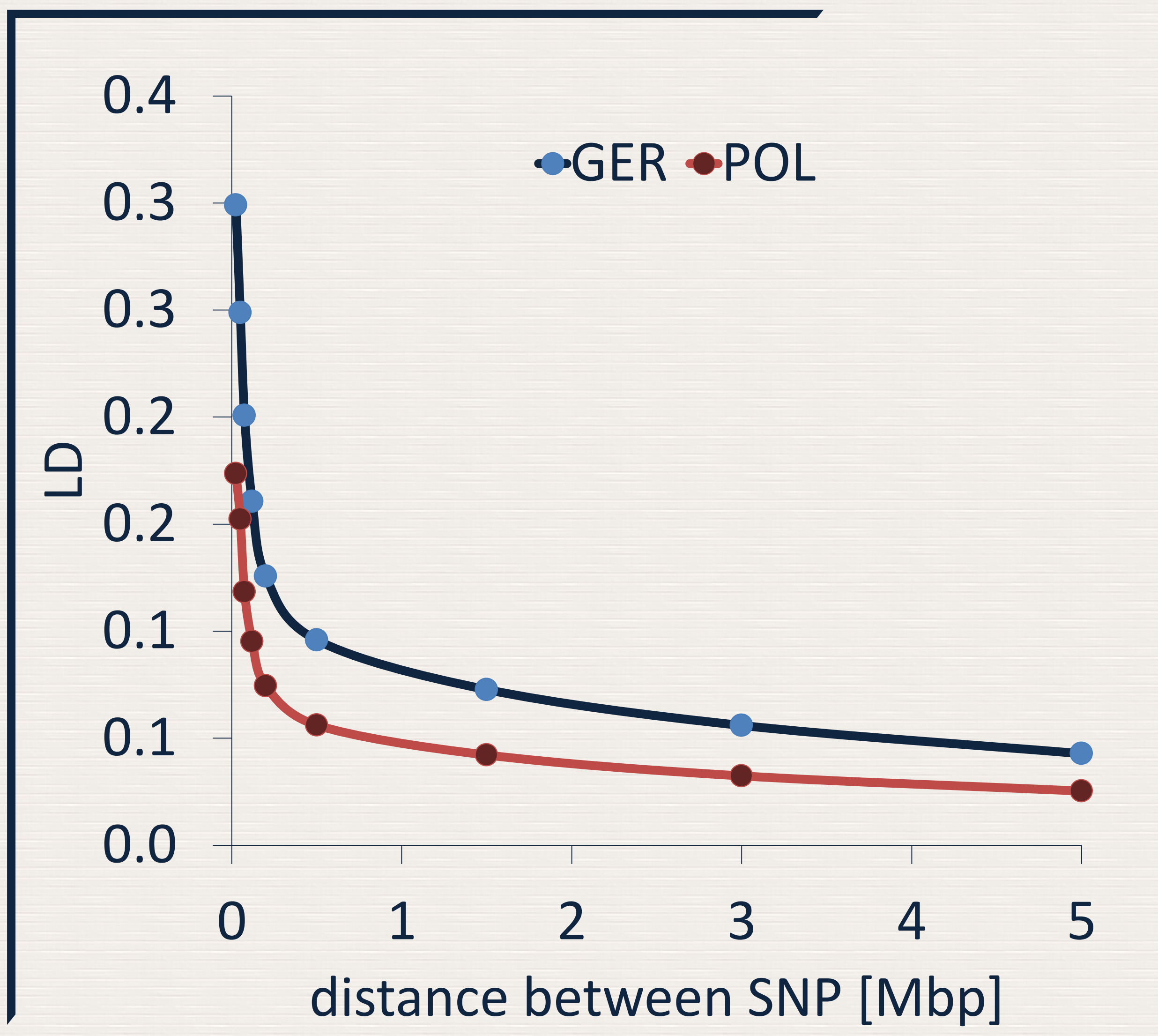
🇵🇱 2 243 Polish HF ♂

RESULTS

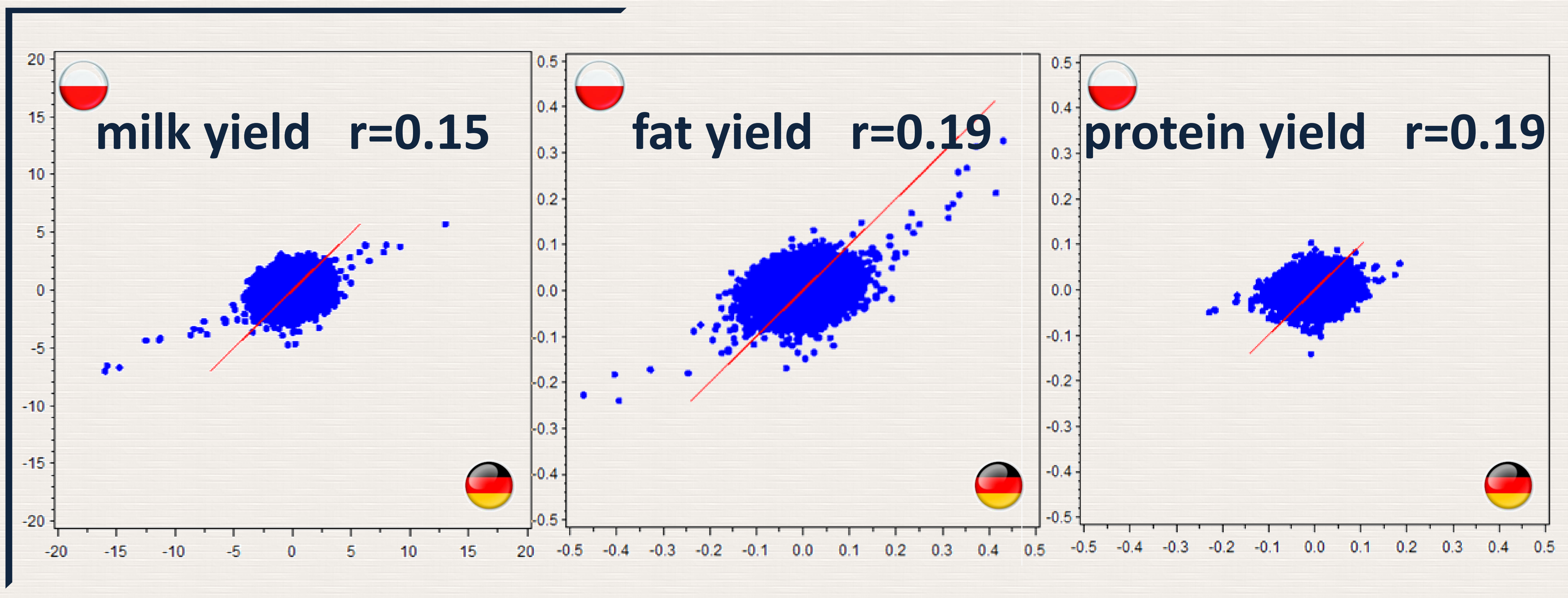
average LD



LD decay



SNP effect estimates



differentially estimated regions

- milk yield: BTA14 → ~Csmd3
- fat yield: BTA09 → LOC100138409
- protein yield: BTA16 → LOC781542
  BTA14 → ~Csmd3
  BTA06 → FTH1
  BTA01 → EPHA6
  BTA09 → ARID1B
- SCS: BTA14 → CTHRC1