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# The distribution of single nucleotide polymorphisms across consecutive exons and introns of the human genome

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## Conclusions

**distribution of SNPs among introns and exons is highly non uniform**

**1st exons → significantly more SNPs**

**1st introns → significantly more SNPs**

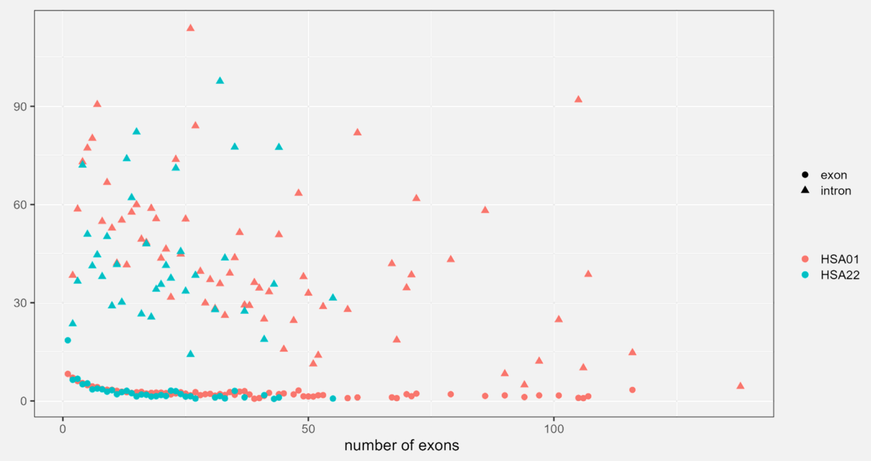
## Motivation

examine the **numers of SNPs** in consequtive introns / exons

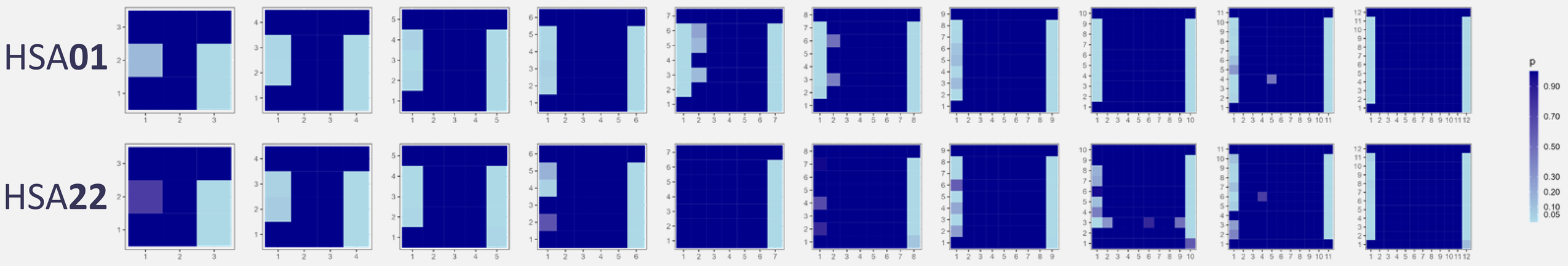
## Material

- 1,222 individuals of Polish origin
  → 41,836,187 SNPs from WGS

- HSA01 (5,177 genes ) & HSA22 (1,313 genes)
  → **1,705,575** SNPs

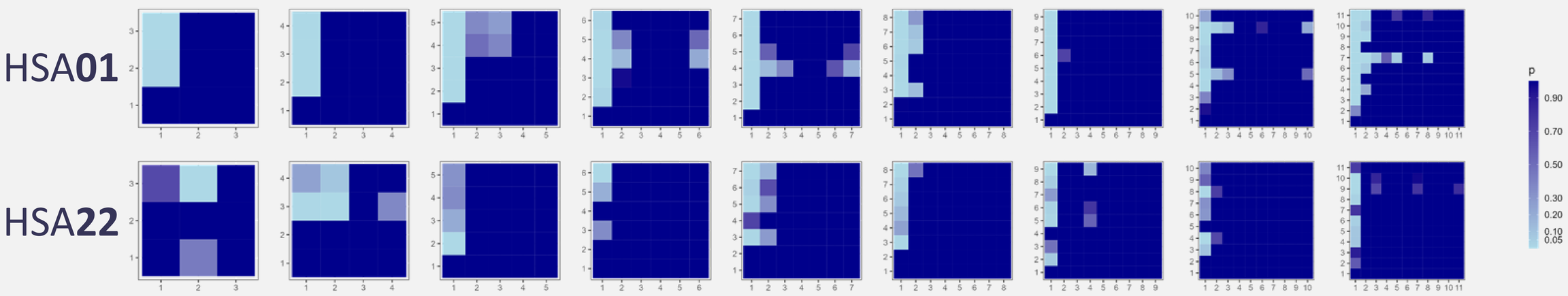



## Results




significance of pairwise comparisons of SNP counts in particular **exons**

P values → number of SNPs within the i-th exon (rows) < number of SNPs within the j-th exon (columns) → Conover test




significance of pairwise comparisons of SNP counts in particular **introns**

P values → number of SNPs within the i-th exon (rows) < number of SNPs within the j-th exon (columns) → Conover test