Functional annotation of CNV breakpoints in Holstein-Friesian cows

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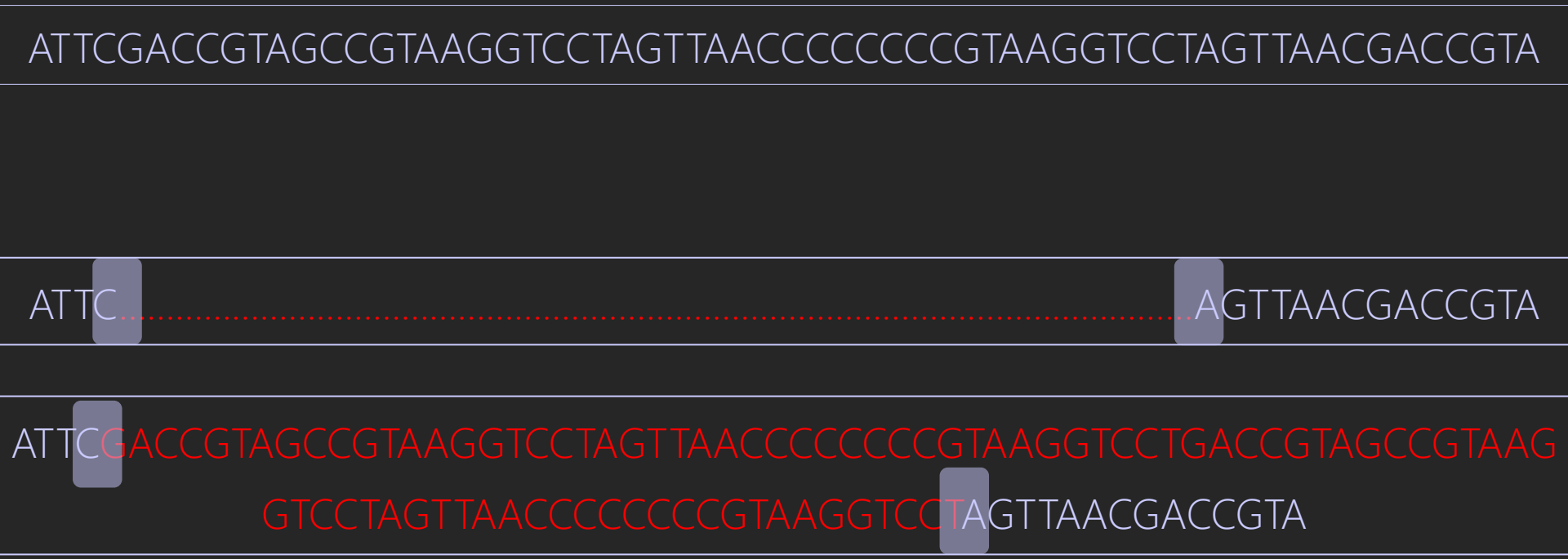
CNVs – Copy Number Variants



Why breakpoints ?

Are CNV breakpoints formed at random in the bovine genome ?

Outline

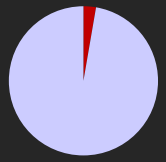
1. Material
2. CNV detection
3. Functional annotation of CNV breakpoints
   - SO terms
   - Gene functional category
   - All genes
4. Conclusions

Whole genome sequence data

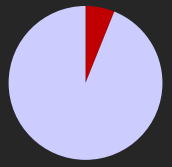
- 32 HF cows → 29 HF cows
- 16 paternal half-sibs
- WGS – Illumina HiSeq 2000
  - Paired end 100 bp
  - Raw reads 164,984,147 – 472,265,620
  - Coverage 5x – 17x

Copy Number Variation

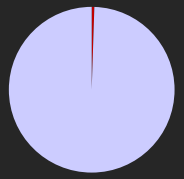
1. Alignment to UMD 3.1 – BWA.MEM
2. Read editing – SAMtools & Picard
3. CNV detection – CNVnator
   - Deletion 200 bp – 724,000 bp



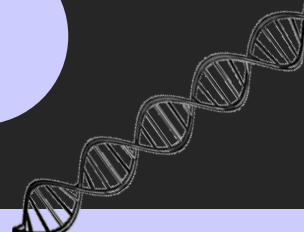
2.71 % – 6.09 %



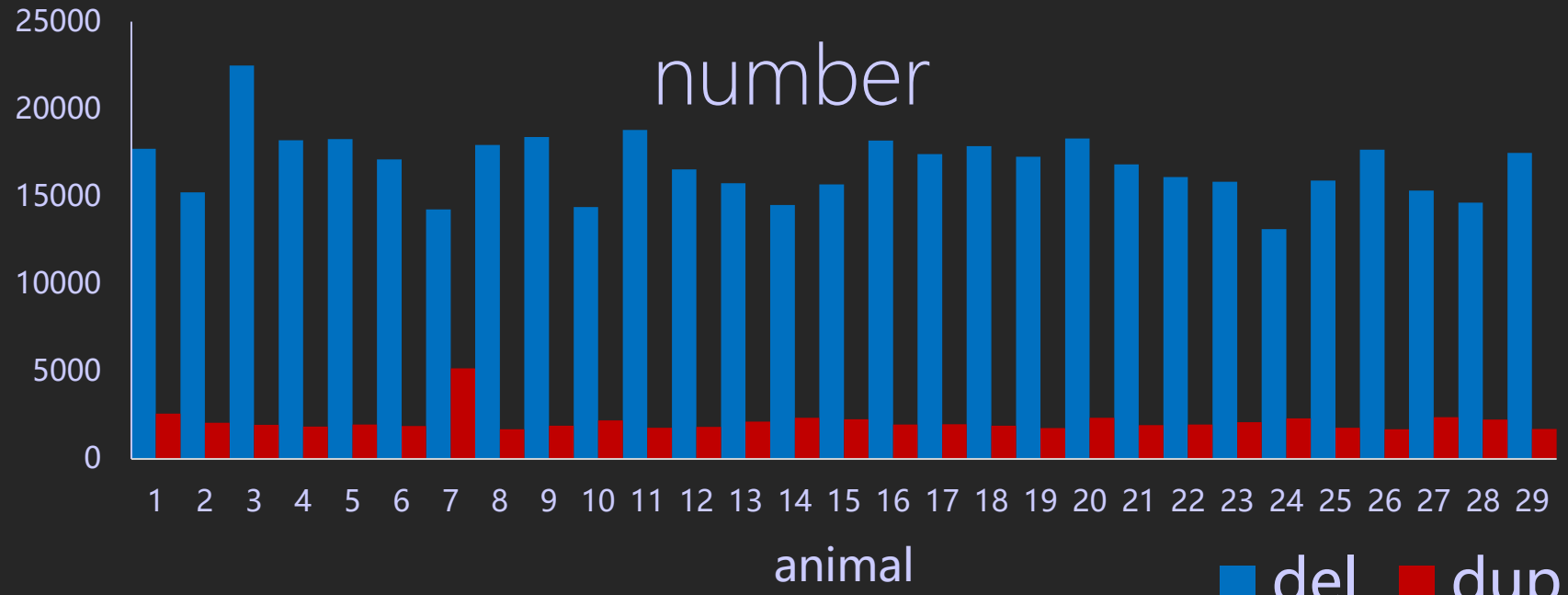
   - Duplication 200 bp – 439,300 bp

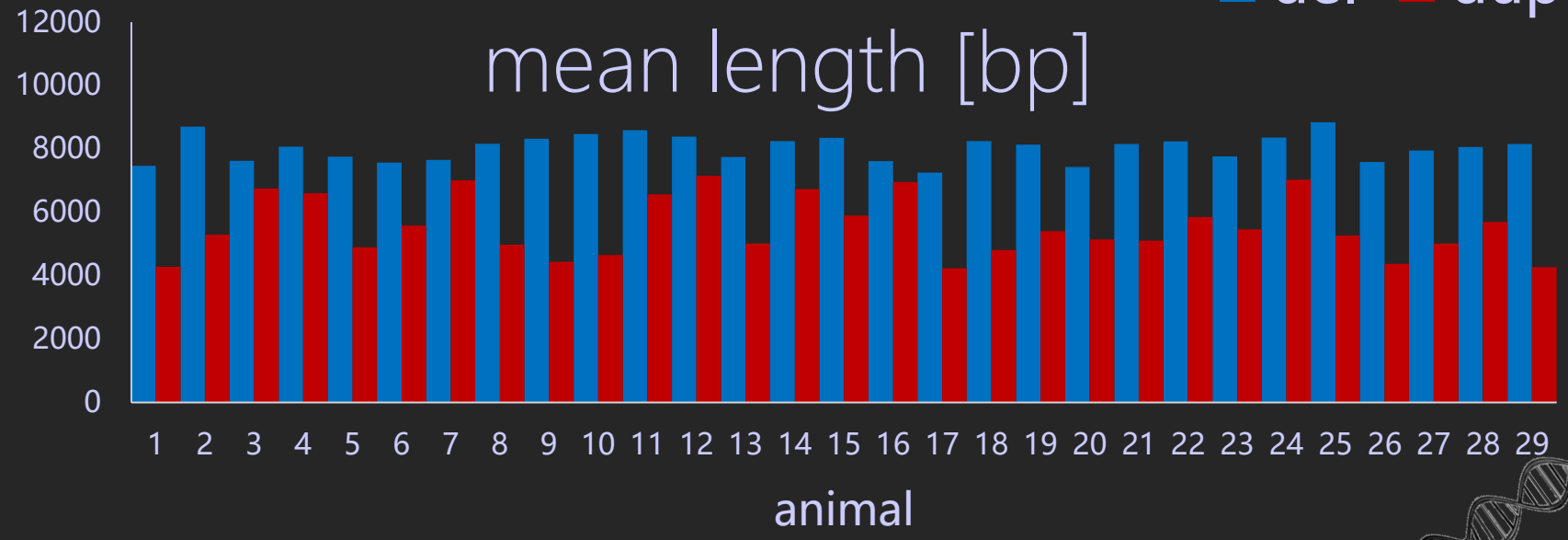


0.51 % – 1.58 %



Copy Number Variation





Functional annotation

Genome assembly UMD 3.1 (release 2011)

1. Sequence Ontology Terms
   - define consequences of DNA sequence point mutations
     e.g. transcript ablation, stop gained, frameshift variant, …
   - cumulated to 8 categories: coding, intron, splice region, non-coding transcript, UTR, up/down stream gene, intergenic
2. Gene functional categories
3. All genes

Functional annotation

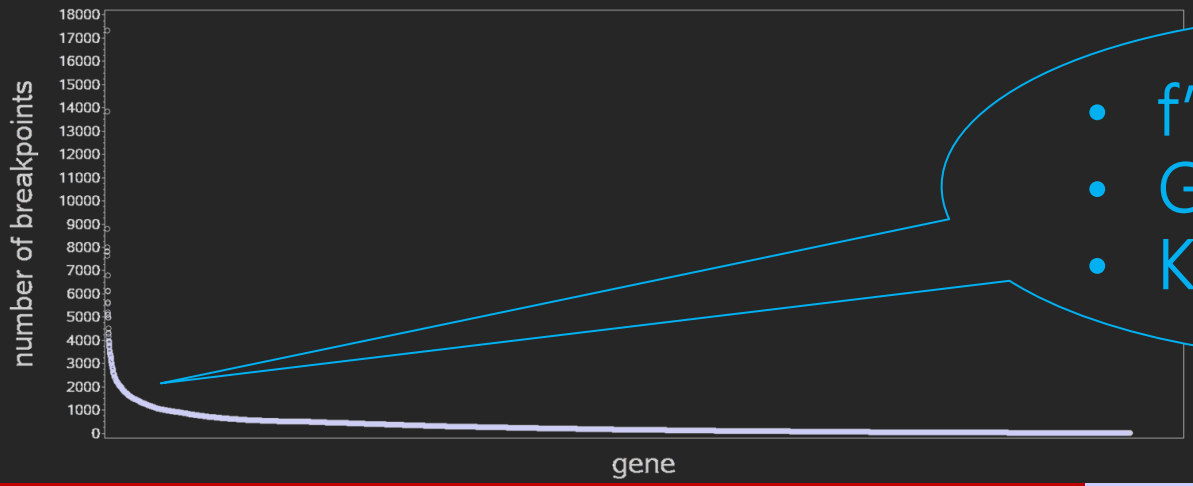
Genome assembly UMD 3.1 (release 2011)

1. Sequence Ontology Terms
2. Gene functional categories
   - housekeeping, under strong selection, neutral
3. All genes

Functional annotation

Genome assembly UMD 3.1 (release 2011)

1. Sequence Ontology Terms
2. Gene functional categories
3. All genes
   - genes with a large number of breakpoints

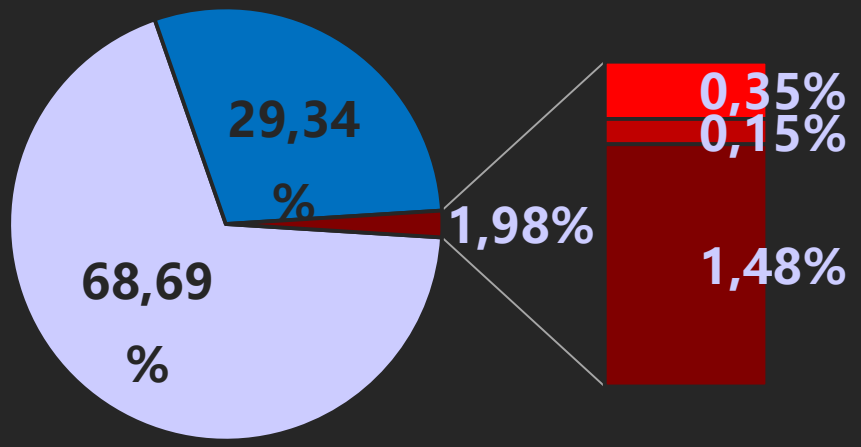


- f′(y=log*(x)) ≥ 1
- GO
- KEGG

Functional annotation – results

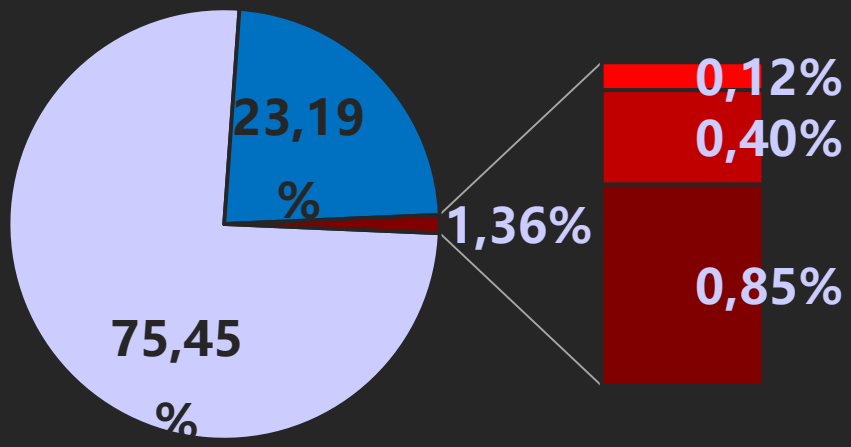
Annotation to SO terms

Deletions (487 746)



- intergenic
- intron
- non-coding regions of transcripts
- splice regions
- coding regions

Duplications (61 789)

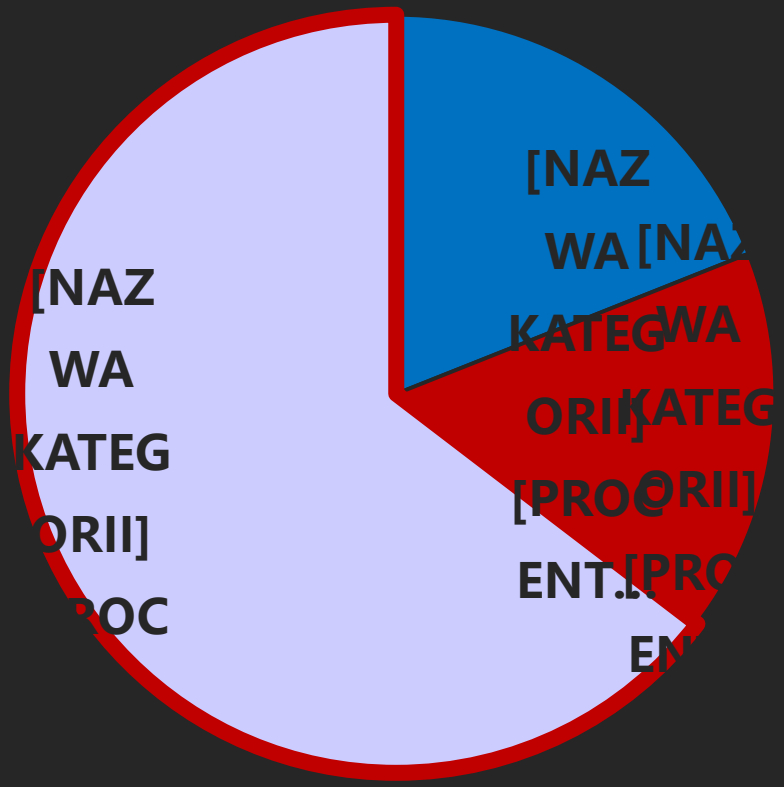


- intergenic
- intron
- non-coding regions of transcripts
- splice regions
- coding regions

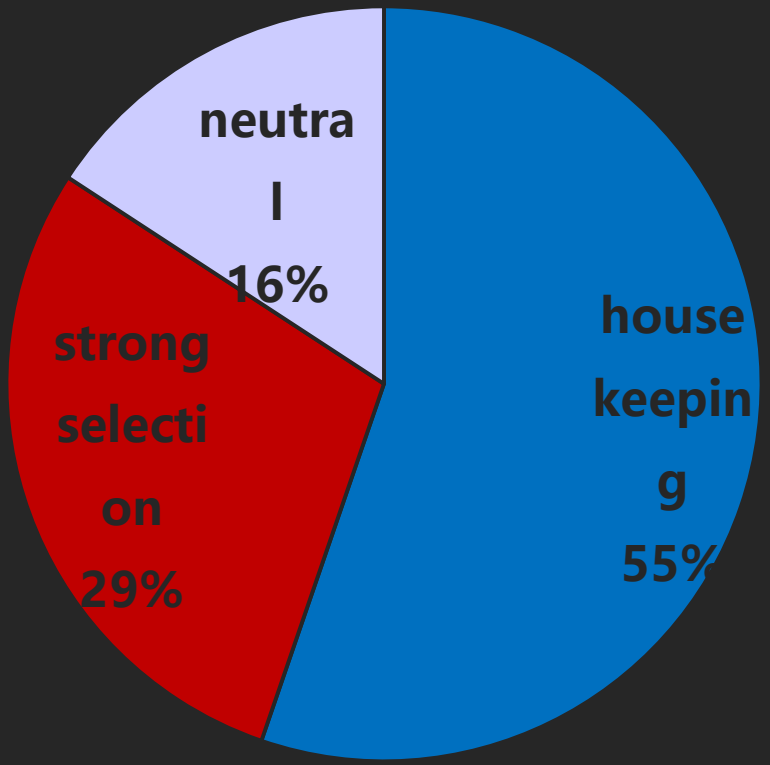
Functional annotation – results

Annotation to gene categories

Deletions (199)



Duplications (38)



Functional annotation – results

Annotation to genes with many breakpoints -

KEGG

Deletions

- olfactory transduction
- P=0.11
- breakpoints depleted
- Pr(0.001) vs Pr(0.010)

genes with many breakpoints

all genes

Duplications

- no significance

Functional annotation – results

Annotation to genes with many breakpoints –

GO term clusters

Deletions

highest enrichment

↓

regulation of cell adhesion

Duplications

highest enrichment

↓

binding of macromolecules

Conclusions

1. Dynamic landscape of CNVs
2. Variability across
3. CNV formation

Conclusions

1. Dynamic landscape of CNVs

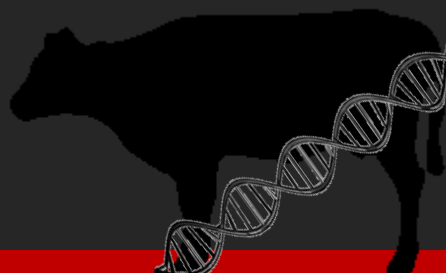
2. Variability across
   - Individuals
   - Chromosomes
   - Functional genome elements

3. CNV formation

Conclusions

1. Dynamic landscape of CNVs
2. Variability across
3. CNV formation
   - Supressed in coding regions
   - Deletions → supressed in housekeeping genes and genes under strong selection
   - Duplications → most common in housekeeping genes
   - More duplications → molecule binding → immune response

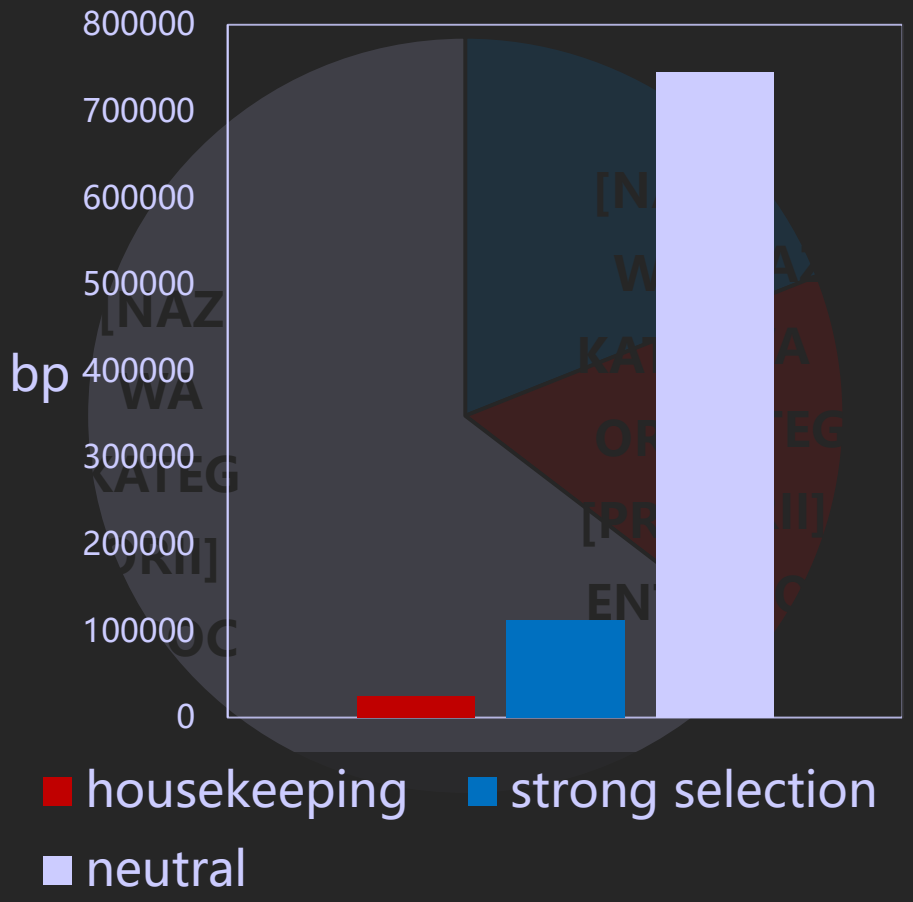
Thank you for attention



Functional annotation of CNV breakpoints

Annotation to gene categories

gene length



transcript length