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# Results interpretation

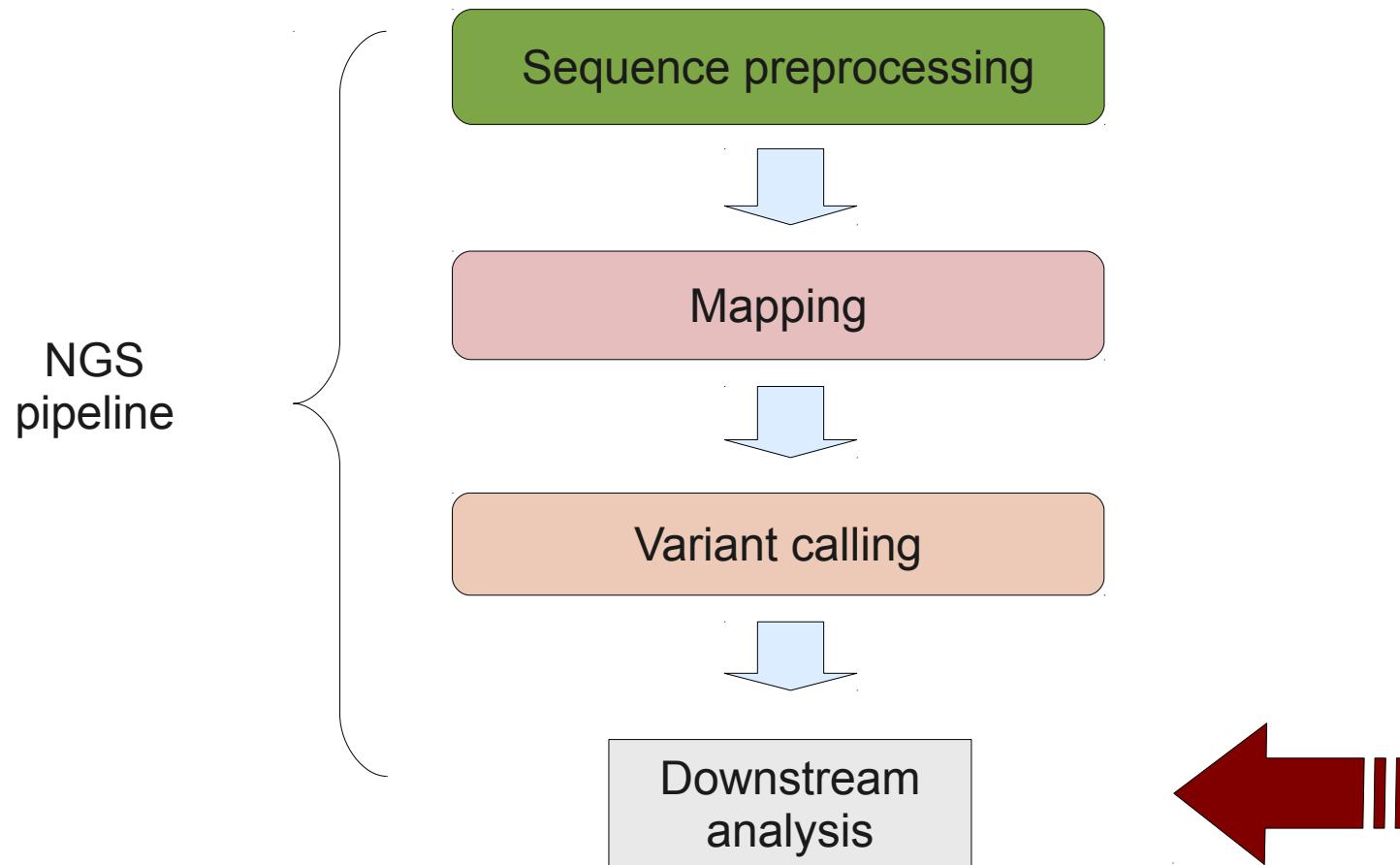
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BIER - CIBERER

Genomics Department  
Centro de Investigacion Principe Felipe (CIPF)  
(Valencia, Spain)



# NGS Sequence preprocessing

Where we are?



<http://bioinfo.cipf.es/bierwiki>

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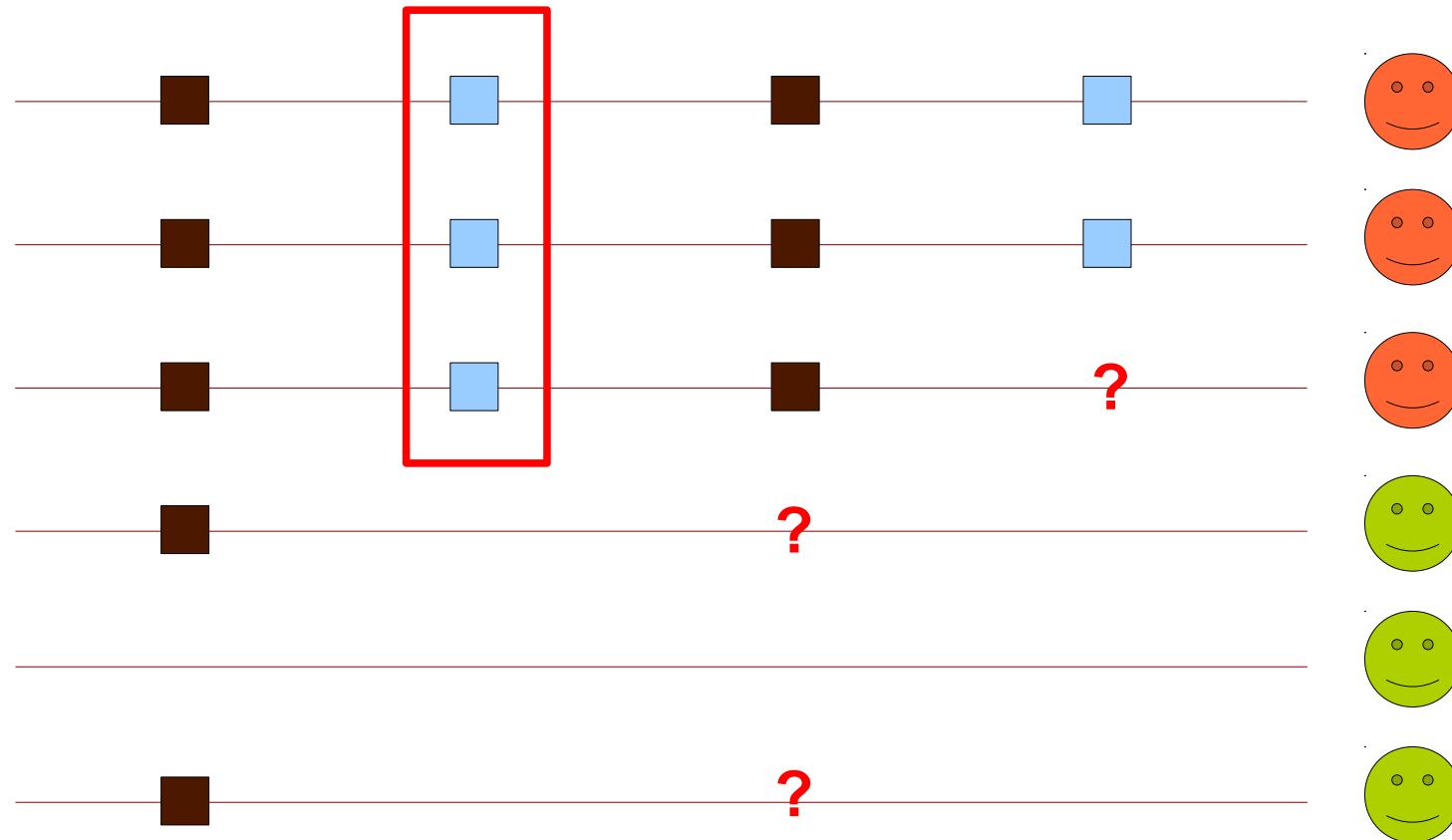
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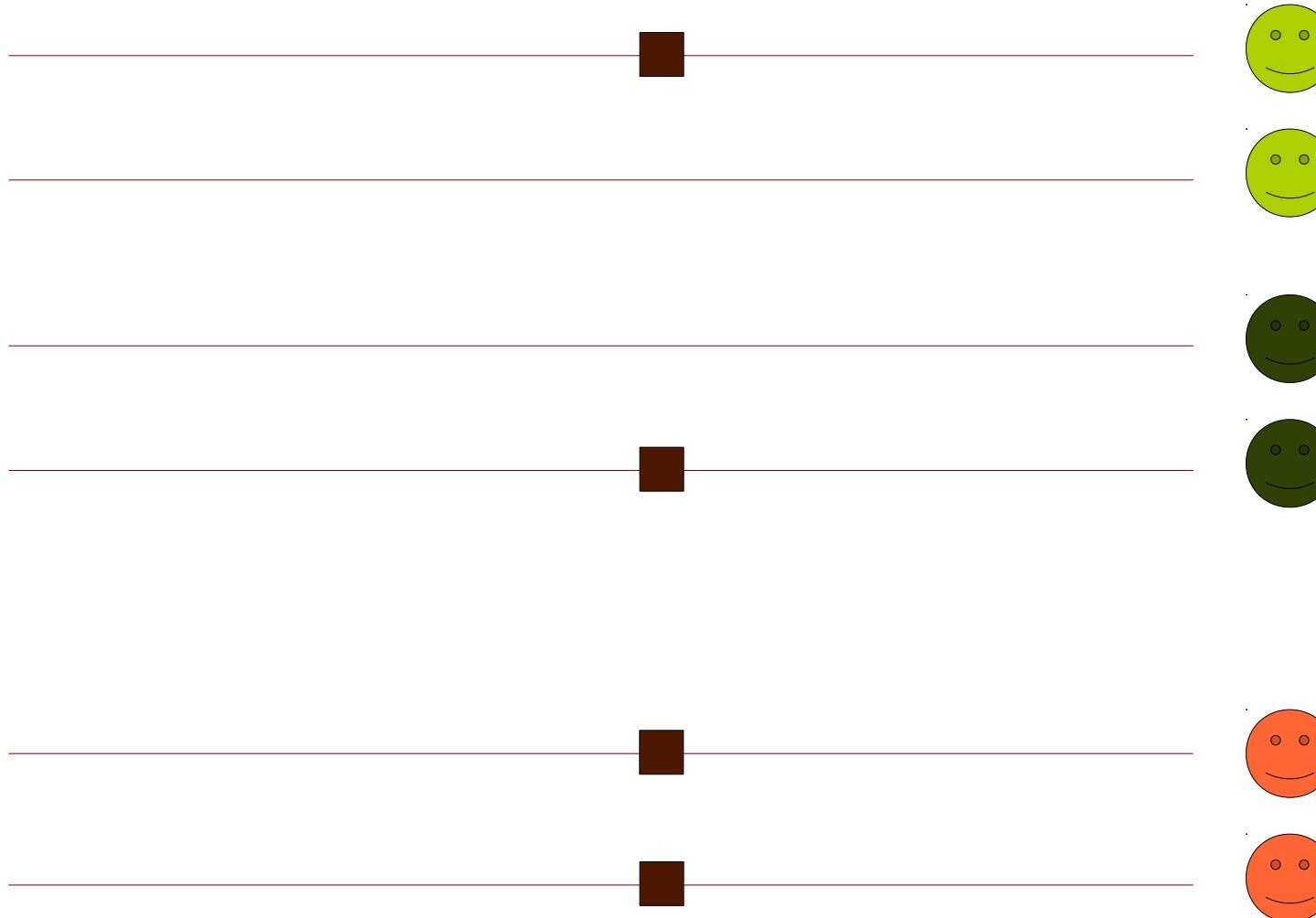
# Dominant

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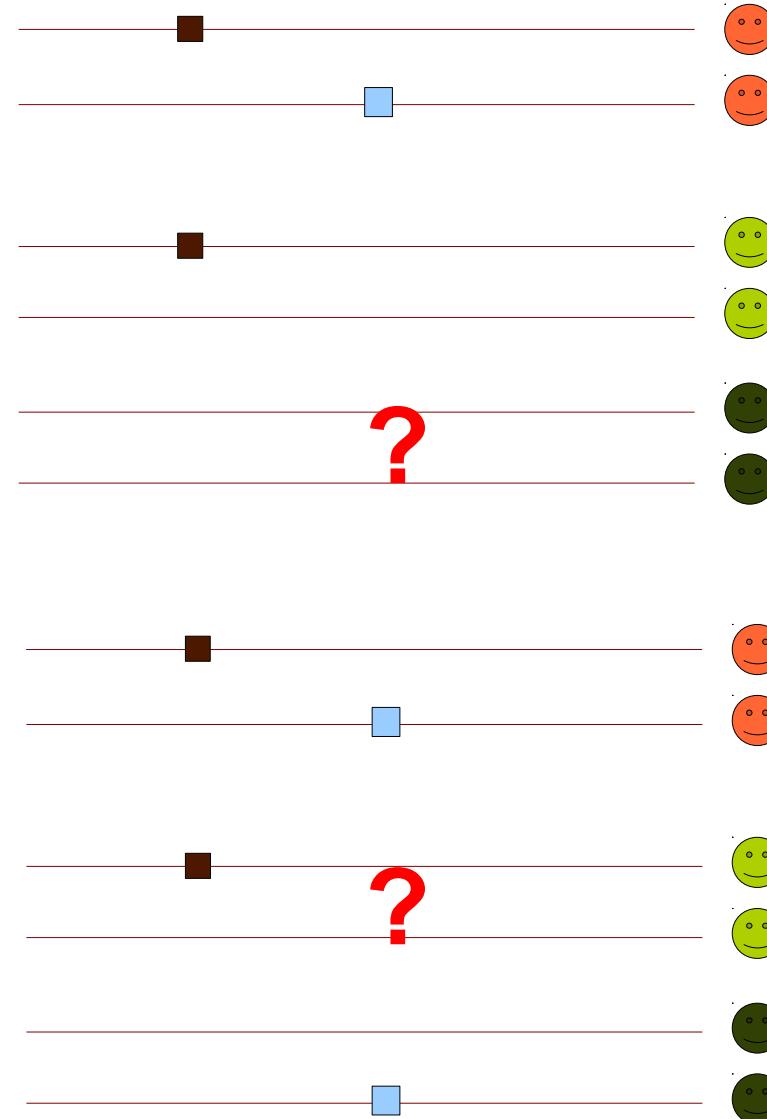
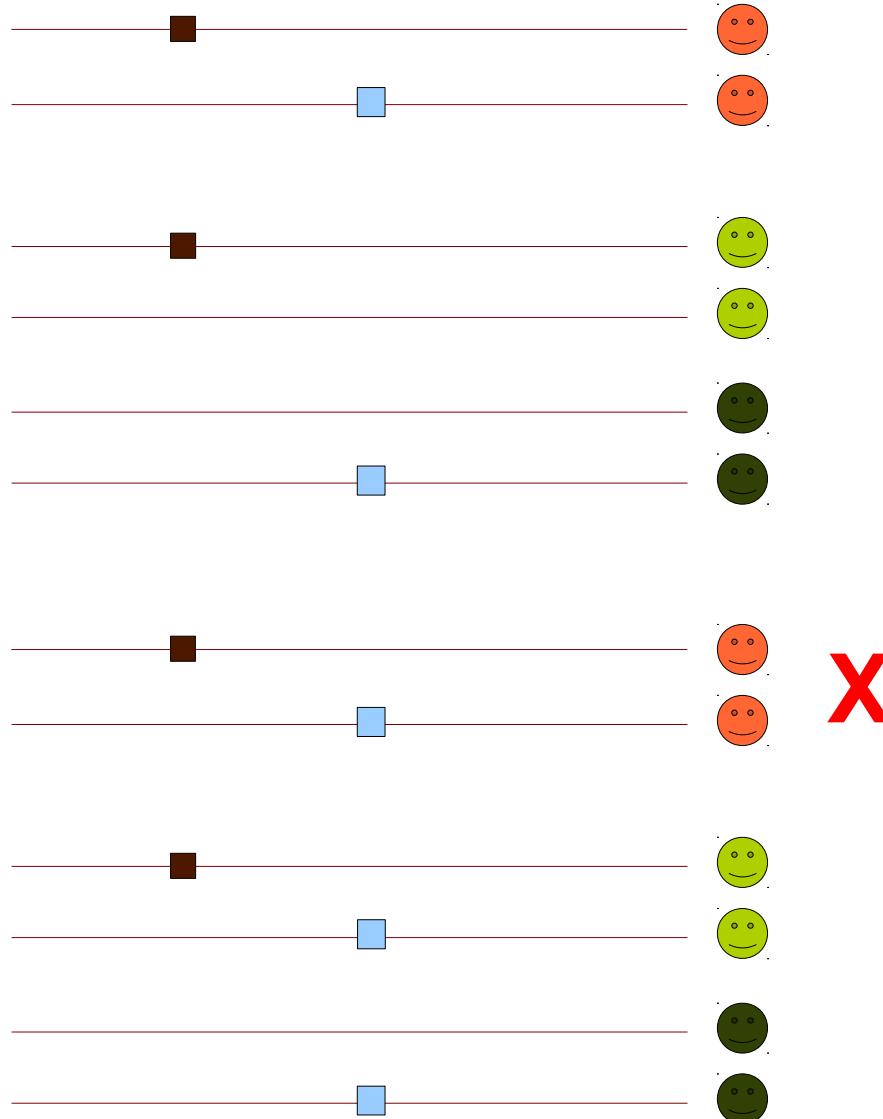


# Recessive - homozygous

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# Recessive – compound heterozygosity



# FILTERS

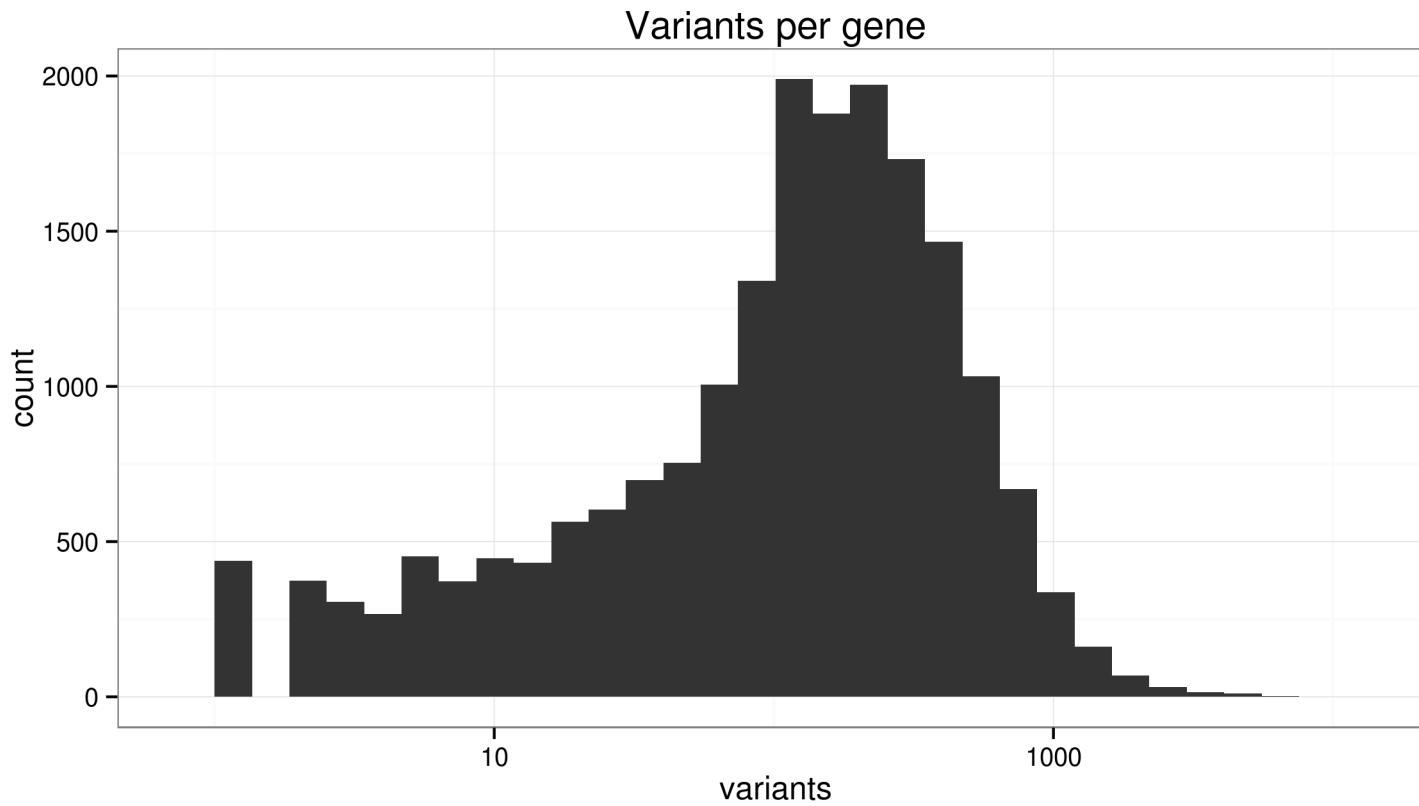
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## Available:

- Present in BIER samples (allele frequency)
- Consequence type
- % cases and controls with variant
- SNVs and indels
- 1000 genomes allele frequency
- Recessive: genes with deleterious variants
- De novo mutations: mark or delete
- present in dbSNP
- Regions

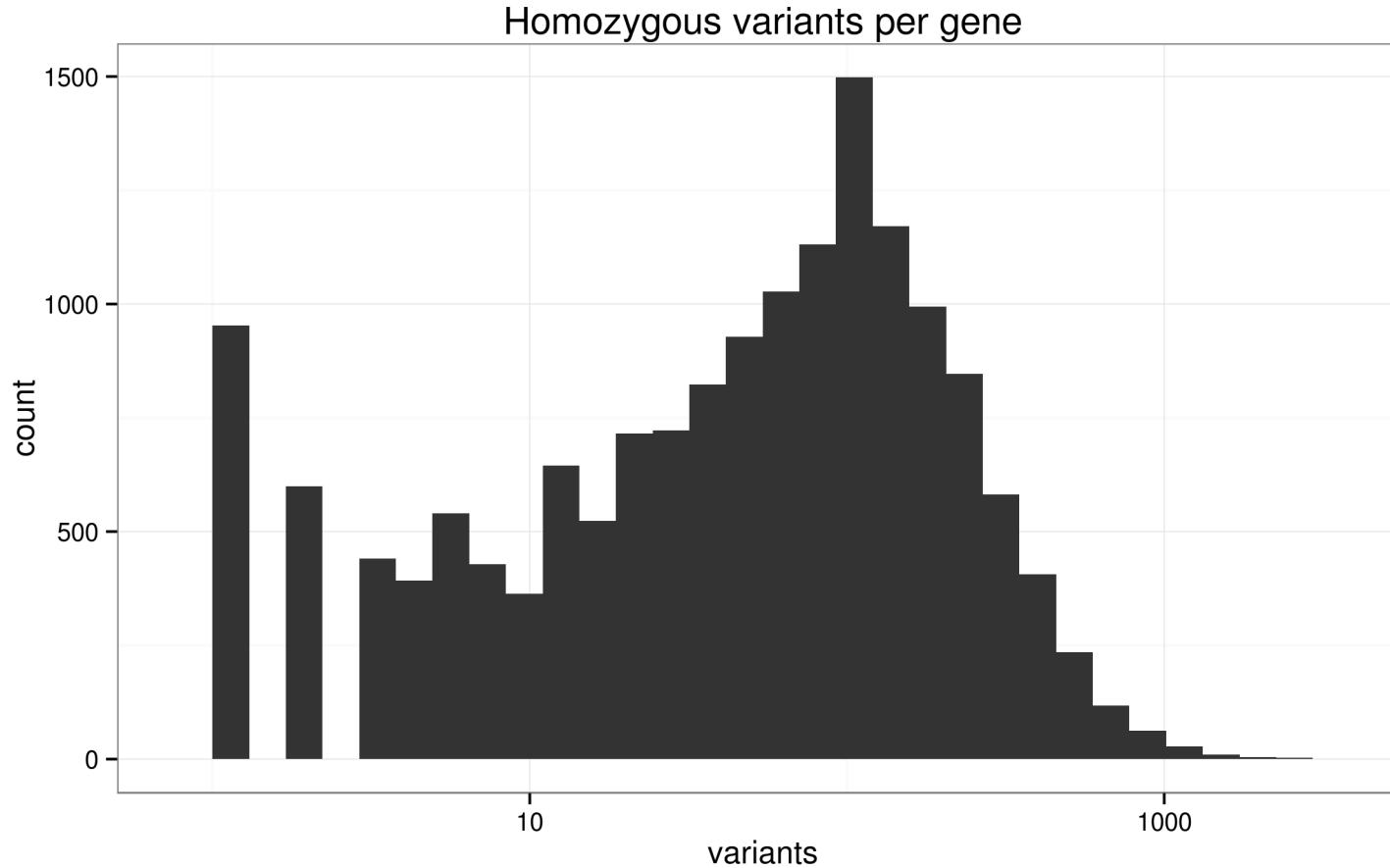
# Some statictics: Variants per gene

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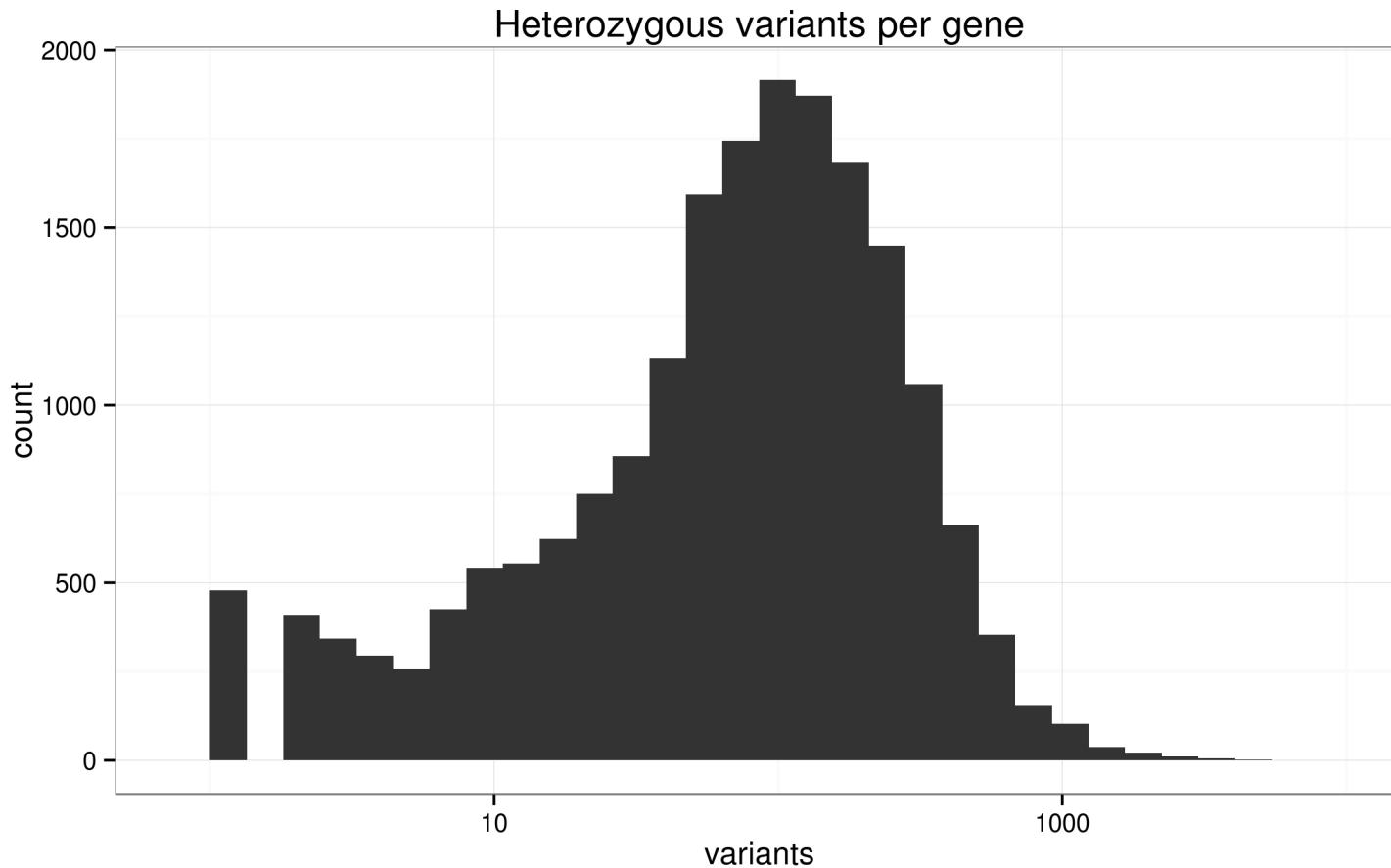
# Some statictics: Homozygous variants per gene

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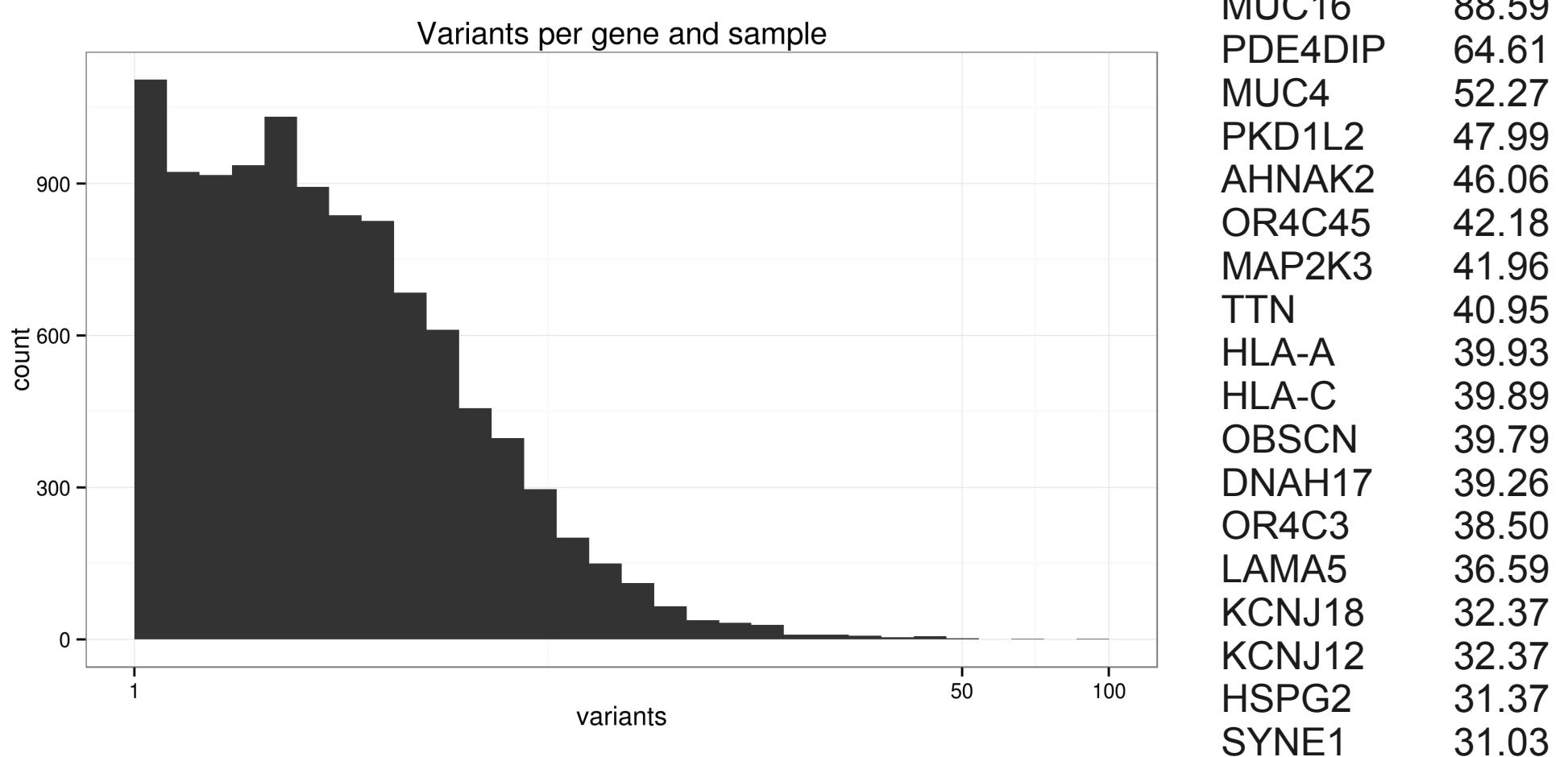


# Some statictics: Heterozygous variants per gene

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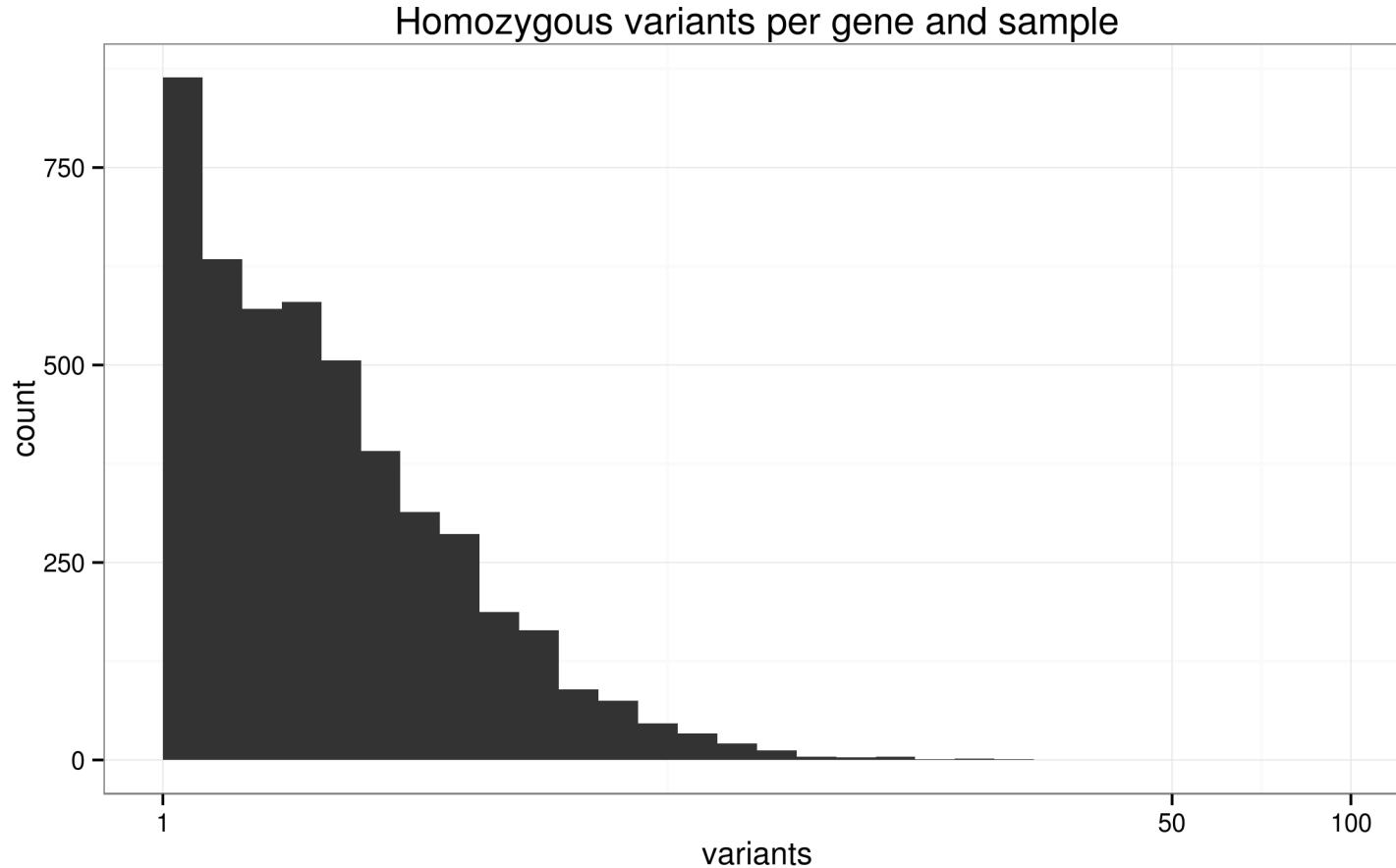


# Some statictics: Variants per gene and sample



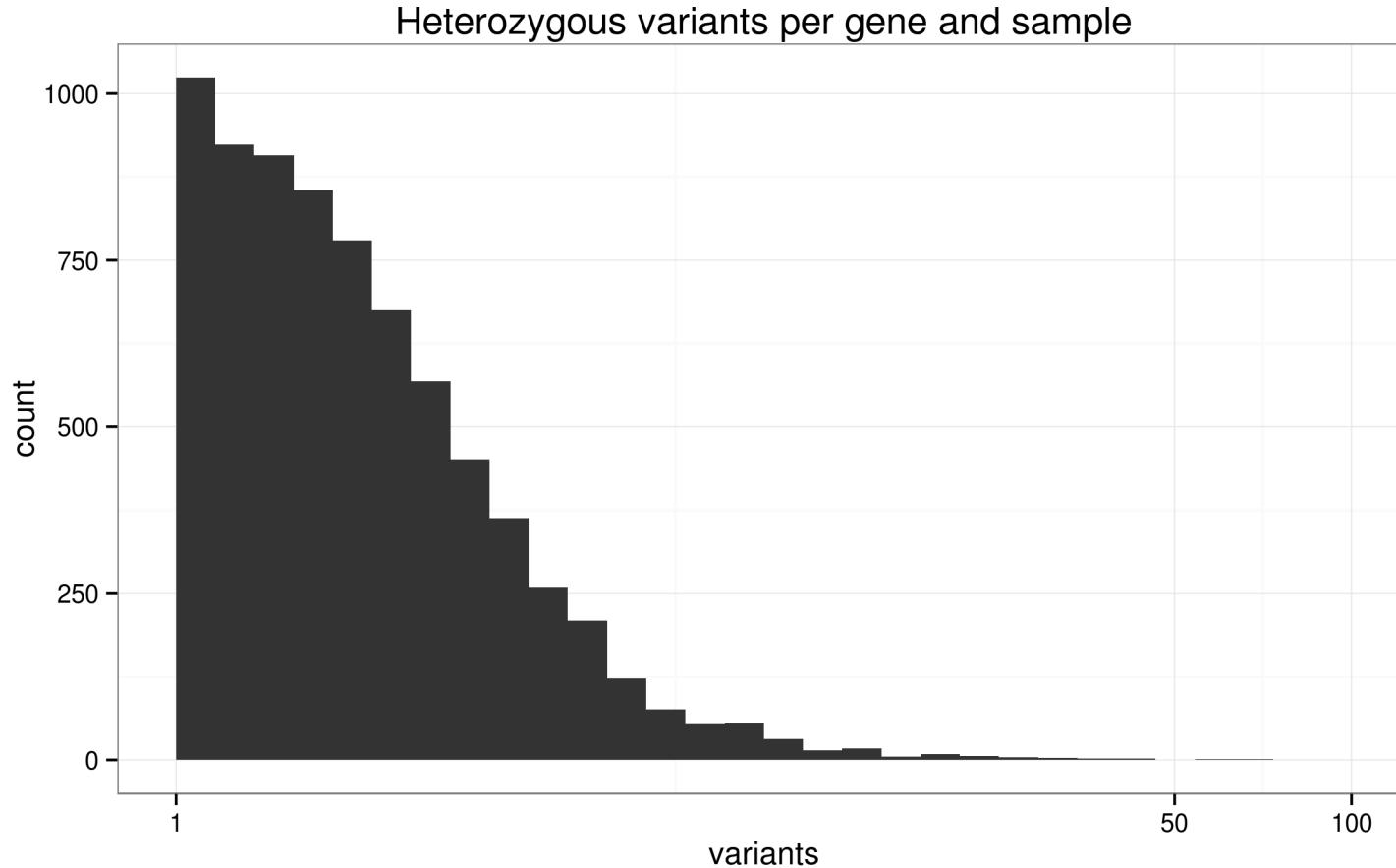
# Some statictics: Homozygous variants per gene and sample

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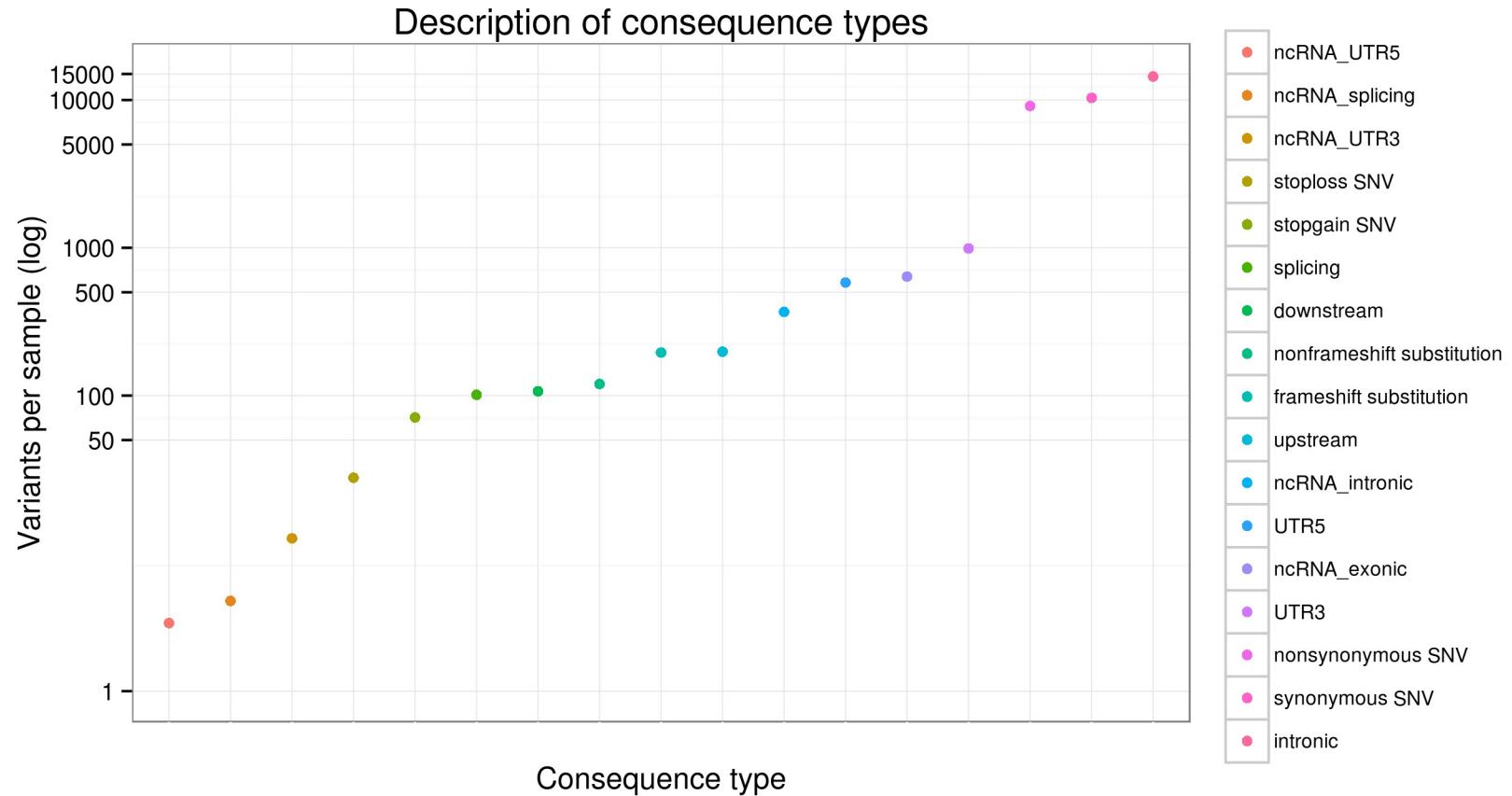
# Some statictics: Heterozygous variants per gene and sample

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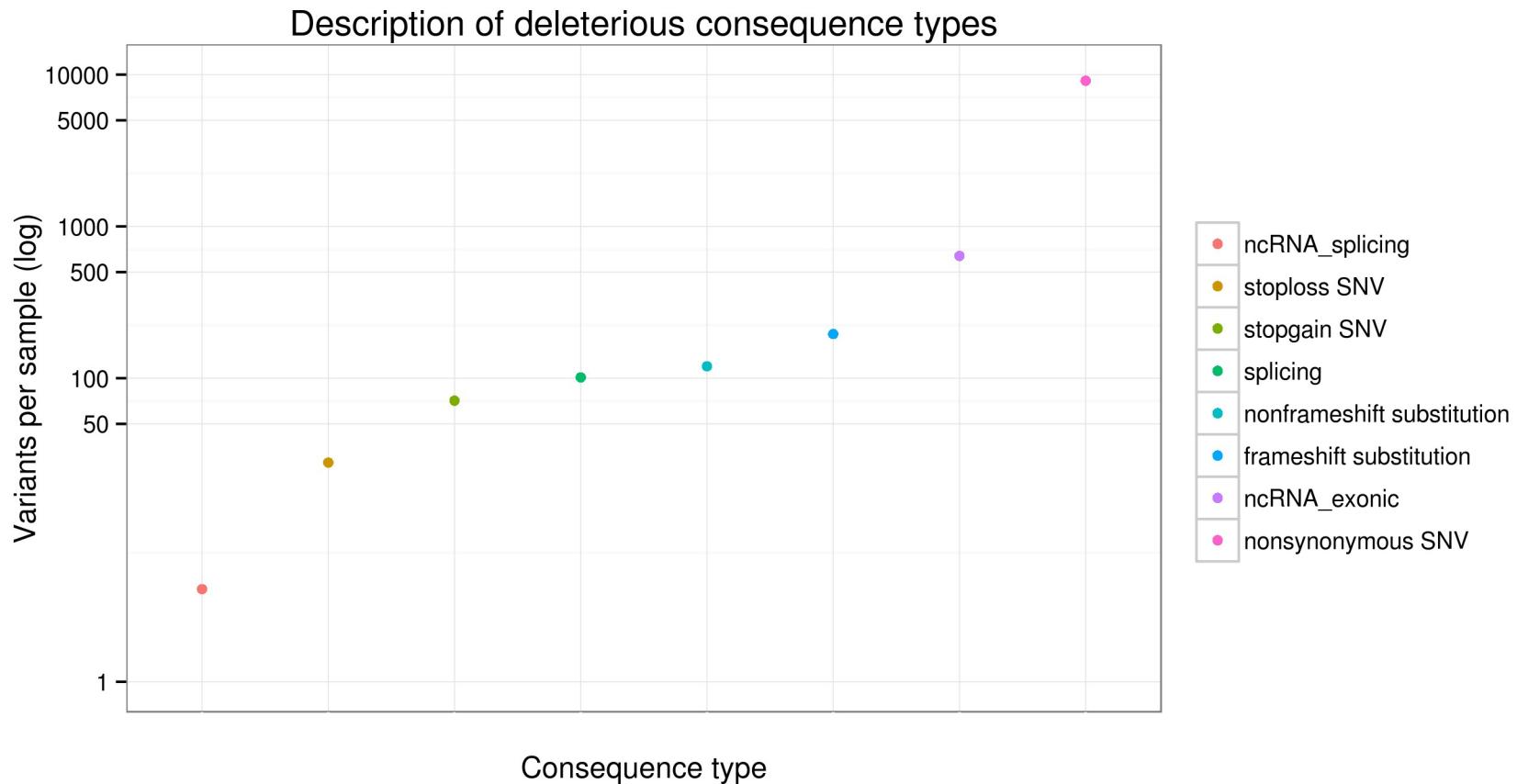
# Some statictics

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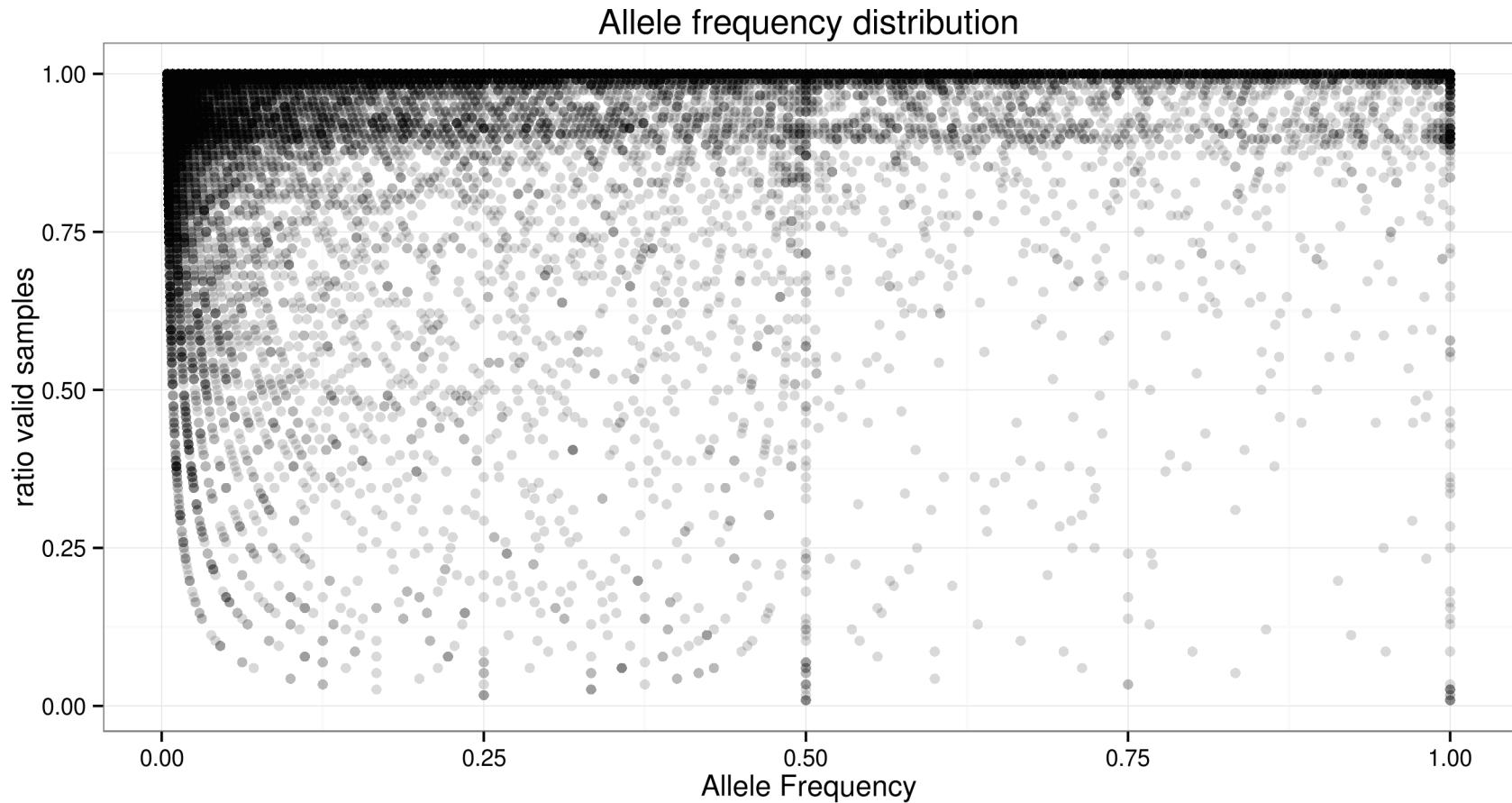
# Some statictics

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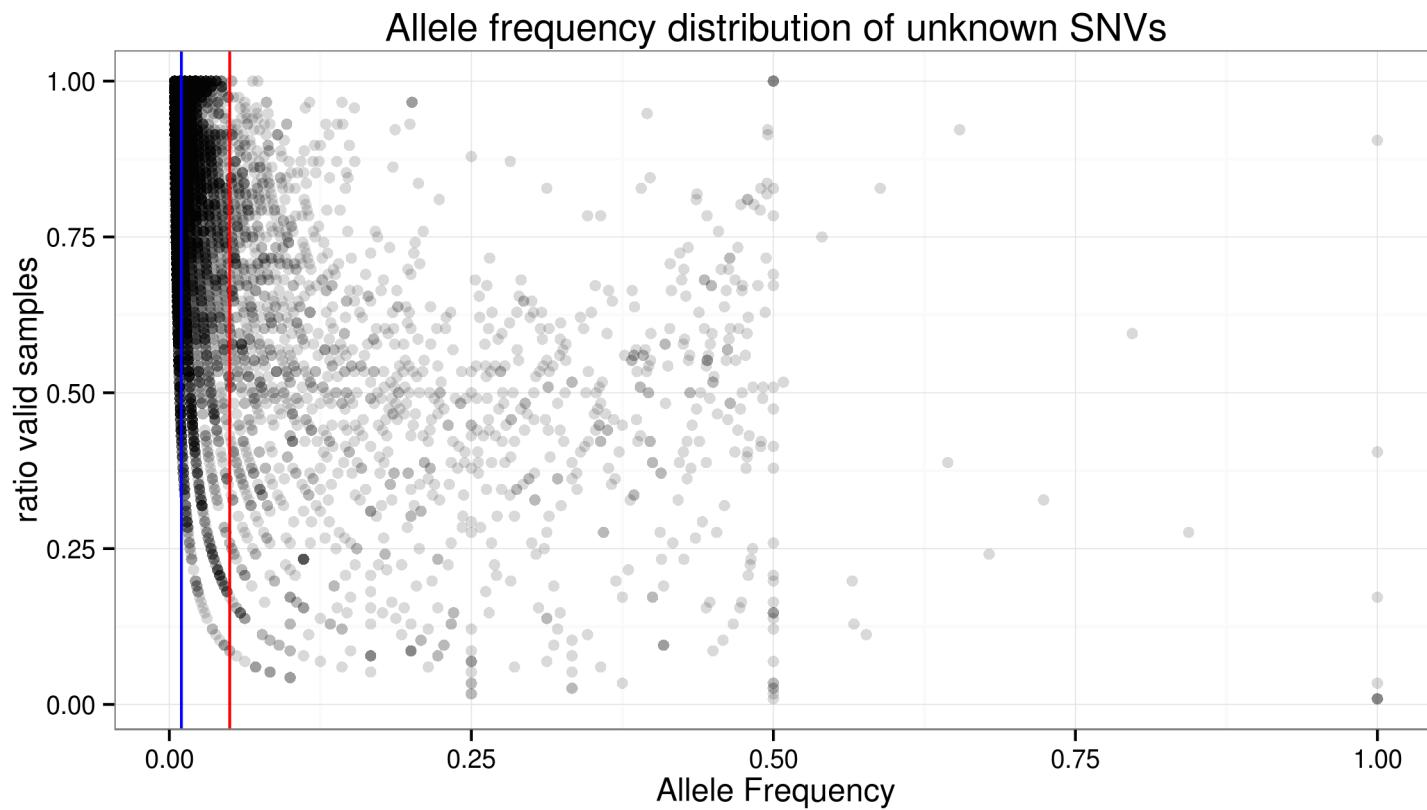
# Some statictics

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# Some statictics

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# Questions?

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