STRUCTURAL GENOMIC VARIATION IN TRIPLOID PACIFIC OYSTERS:

Insight into differential physiology

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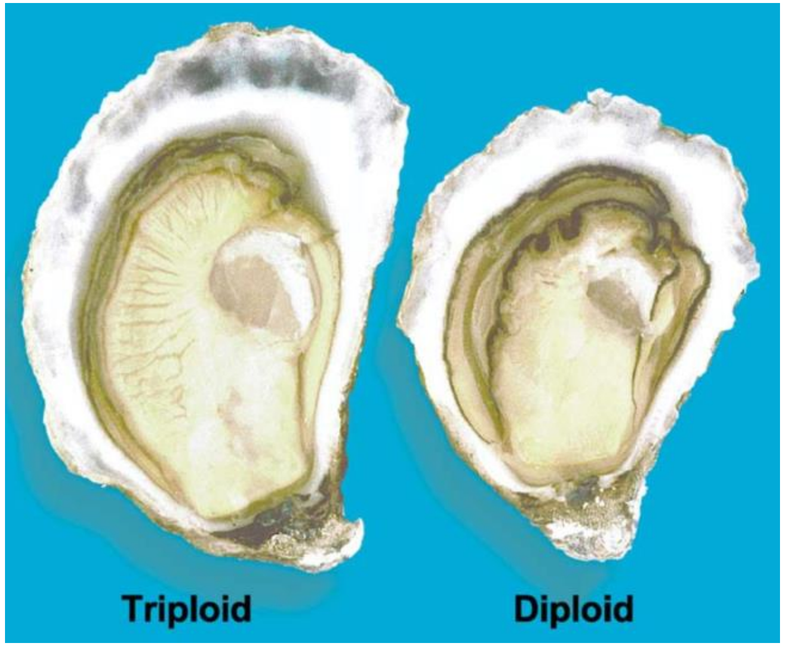
Oyster Tolerance

Pacific
Oyster

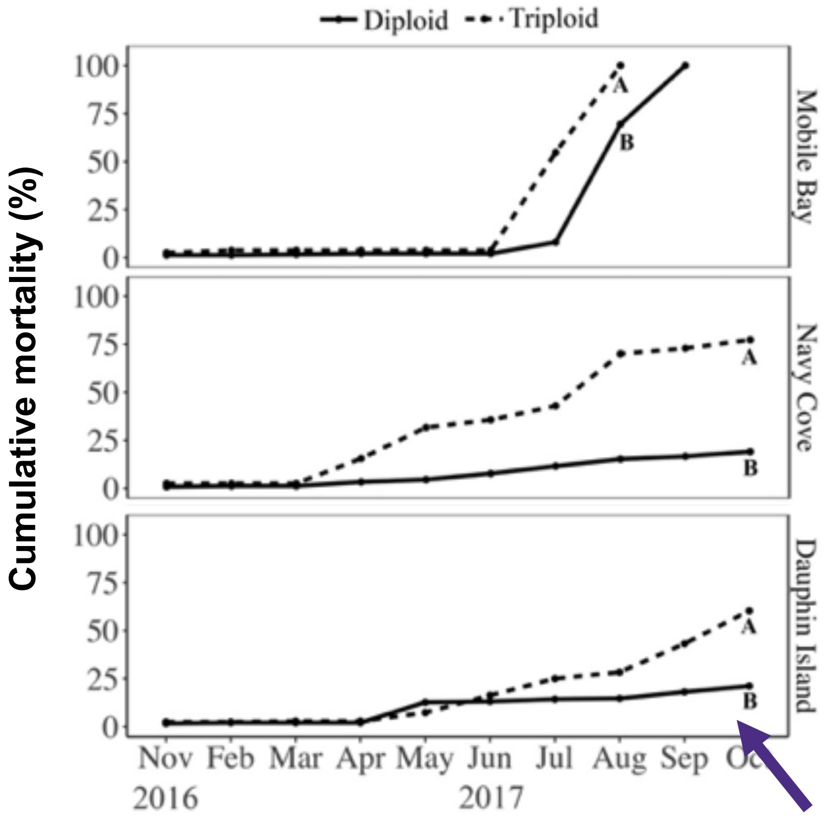
Reproductive control in Pacific oysters



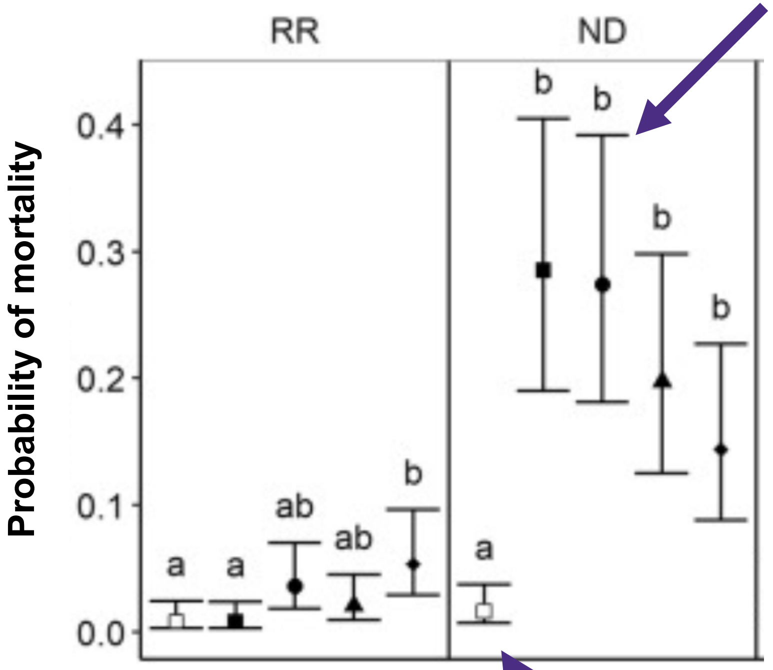
1. Various methods used to induce triploidy (tetraploid cross, heat-shock, pressure, etc.) developed in the late 1970’s.
2. Triploid oysters have an extra chromosome set (3n).
3. Triploidy **significantly reduces energetic investment in gonad production**.
4. Triploid oysters have **superior growth rates.**
5. Harvesting triploids in the summer **avoids the *unpleasant* taste of ‘spawny’ oysters**.

Diploid vs.
Triploid mortality in the field

Gulf of Mexico



Chesapeake Bay



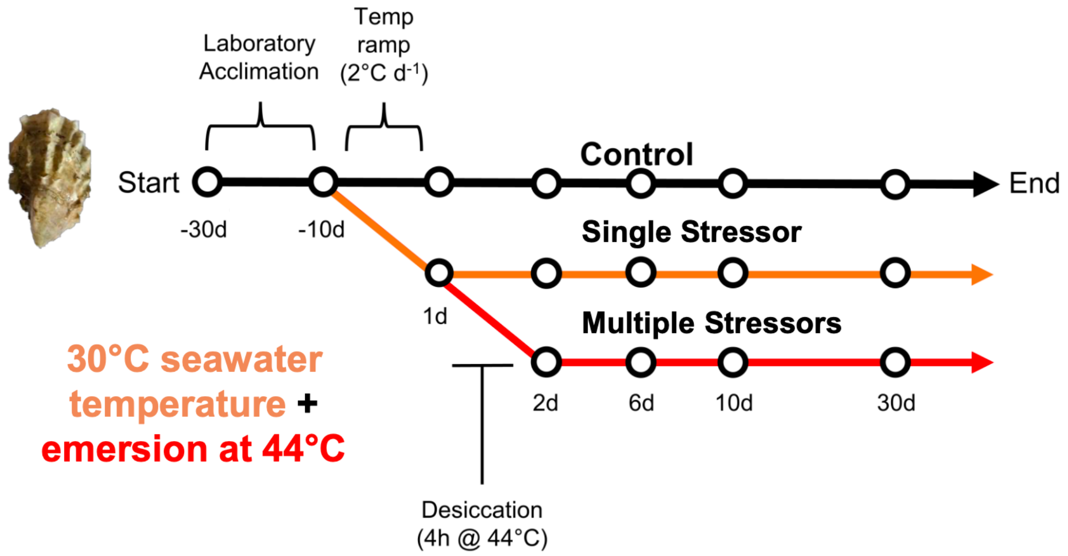
Triploid

Field mortality extending through the summer

Diploid

Wadsworth 2018; http://hdl.handle.net/10415/6074
Matt et al. 2020; doi: 10.1016/j.aquaculture.2020.735375

Controlled Experiment



Global Change Biology

RESEARCH ARTICLE | Full Access

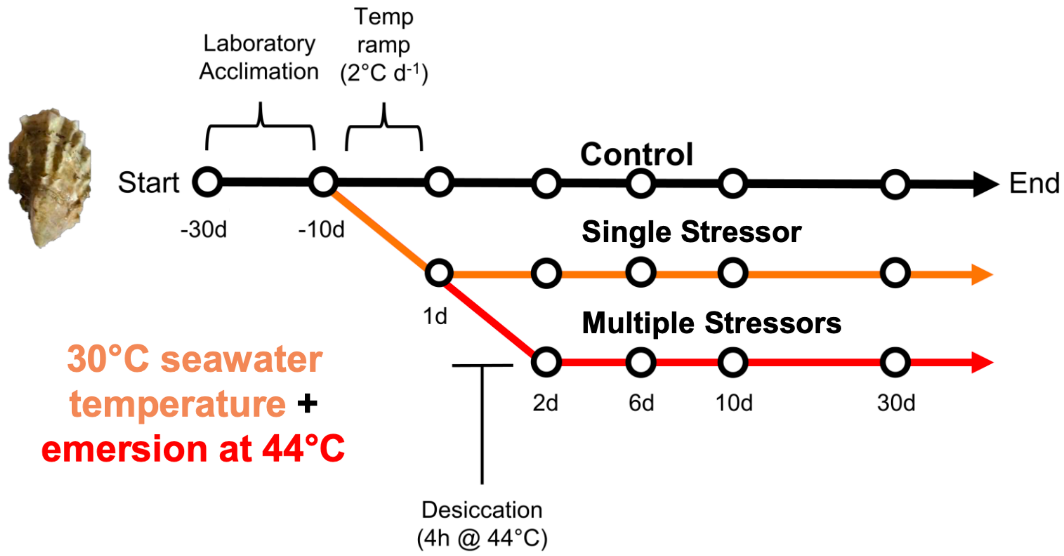
Triploid Pacific oysters exhibit stress response dysregulation and elevated mortality following heatwaves

This article relates to:

Matthew N. George, Olivia Cattau, Mollie A. Middleton, Delaney Lawson, Brent Vadopalas, Mackenzie Gavery, Steven B. Roberts

First published: 18 July 2023 | https://doi.org/10.1111/gcb.16880 | Citations: 2

Controlled Experiment



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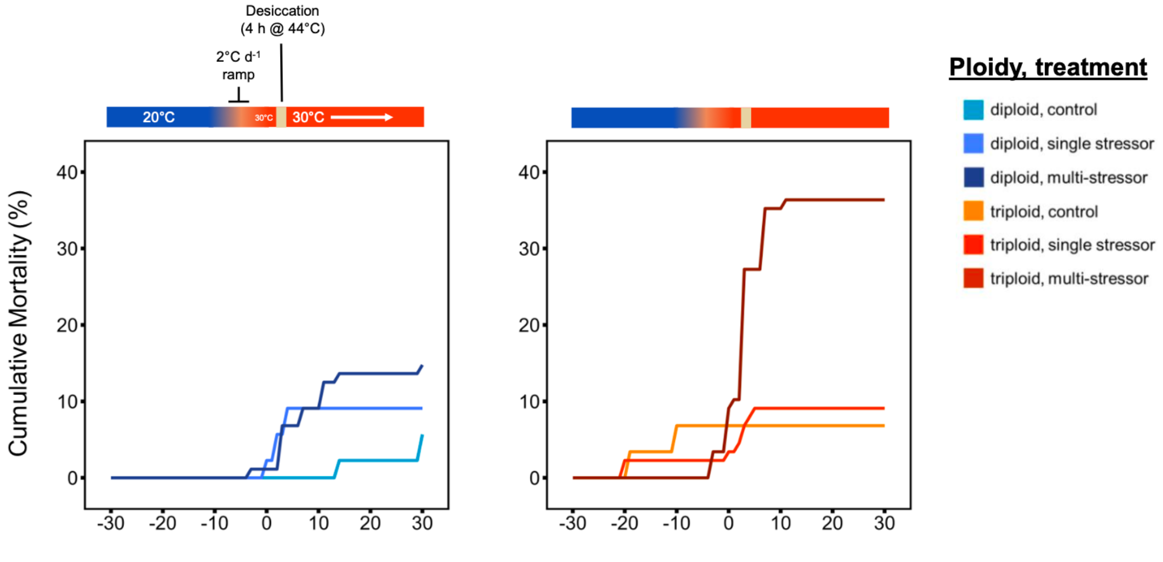
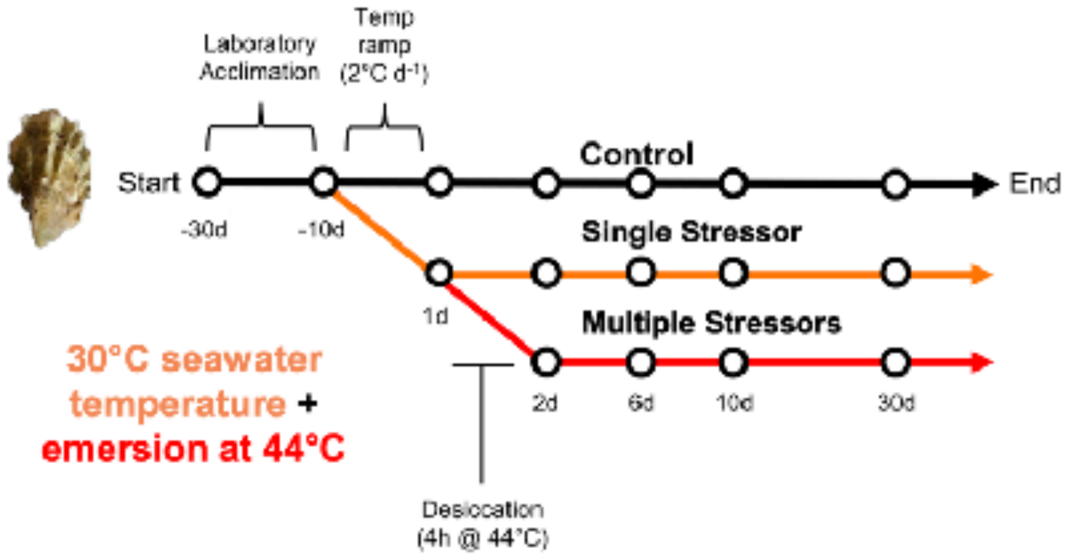


Diploid

Triploid

Controlled Experiment



30°C seawater temperature + emersion at 44°C

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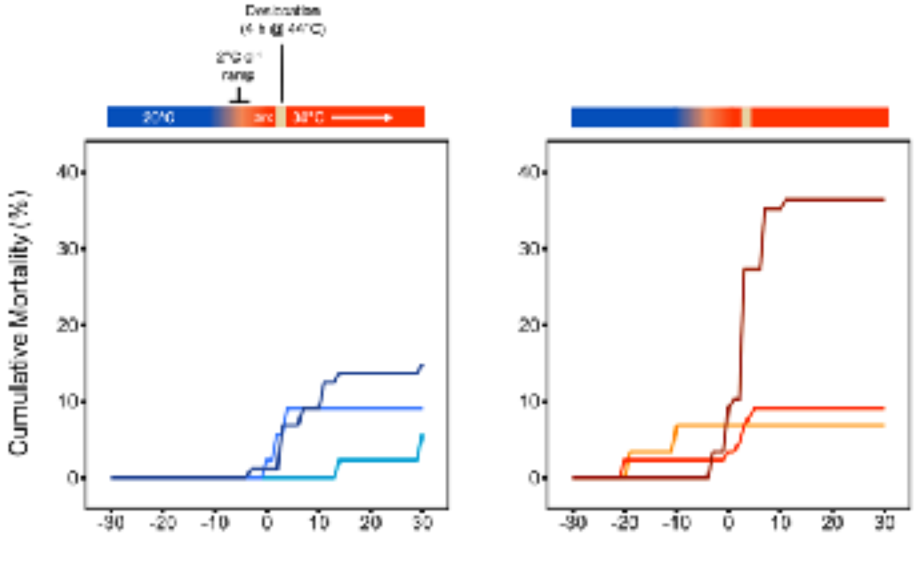

?

Gene Dysregulation

Triploids exhibited dysregulated expression of stress-related proteins following **multiple stress exposure**, including:

Heat Tolerance:
1. Heat Shock Proteins
2. Molecular Chaperones

Antiapoptotic proteins:
1. Inhibitor of apoptosis (IAP) proteins
2. E3 ubiquitin-protein ligases

Mitochondrial genes:
1. rRNA methyltransferases
2. NADH-ubiquinone oxidoreductase

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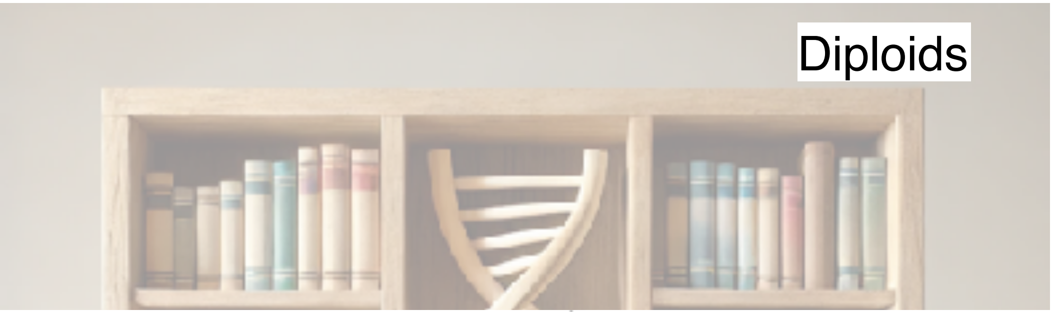
What is the Structural Variation Landscape?

Diploid and Triploids

Characteristics



	Diploids	Triploids
Genome Stability	More stable, with fewer genomic rearrangements.	Increased genomic instability due to **meiotic and mitotic challenges**.
Copy Number Variation (CNV)	More tightly controlled due to balanced gene dosage.	More **tolerant of CNVs** due to extra genome copies.
Deletions/Duplications	Deletions may be more detrimental, as there are only two copies of each gene.	**Triploids may buffer deletions** due to extra gene copies.
Inversions & Translocations	Occur at normal rates, with recombination acting as a repair mechanism.	**More frequent due to recombination suppression** and meiotic missegregation.
Gene Dosage Effects	Stronger, as a change in copy number directly affects expression.	Weaker, as multiple genome copies can buffer gene expression changes.

Gene Copy Number Variation

Family 05

3n 2n

n = 16 (3n/2n)

Family 14

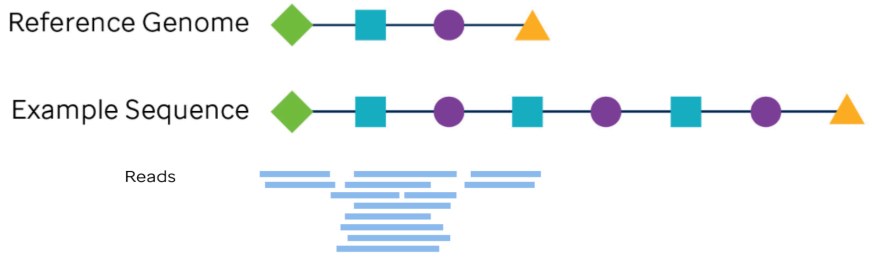
3n 2n

n = 16 (3n/2n)

Whole Genome Resequencing (WGR) – 30x

xbMagGiga1.1 Assembly
GCA_963853765.1

Copy Number Variations (CNVs)



Diploids and triploids were produced for each family using tetraploid crosses of parents

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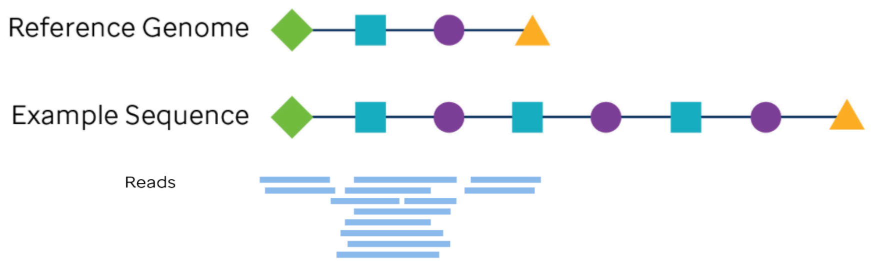
Triploid coverage compared to Diploid coverage per gene

Copy Number Variations (CNVs)



Diploids and triploids were produced for each family using tetraploid crosses of parents

Targeted Gene CNV (Energy)

Family 05

3n 2n

n = 16 (3n/2n)

Family 14

3n 2n

n = 16 (3n/2n)

Whole Genome Resequencing (WGR) – 30x

xbMagGiga1.1 Assembly
GCA_963853765.1

Mitochondrial and Ribosomal Gene CNV

Average coverage across the 12 mitochondrial genes

Average coverage across the large subunit, 5.8s, and small subunit rRNA

Nucleotide Structural Variation

Family 05

3n 2n

n = 16 (3n/2n)

Family 14

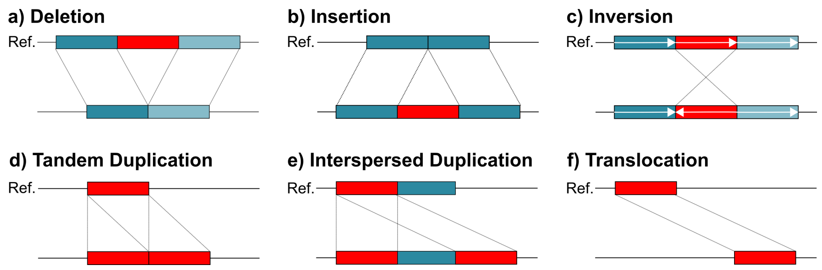
3n 2n

n = 16 (3n/2n)

Whole Genome Resequencing (WGR) – 30x

xbMagGiga1.1 Assembly
GCA_963853765.1

Nucleotide Variation



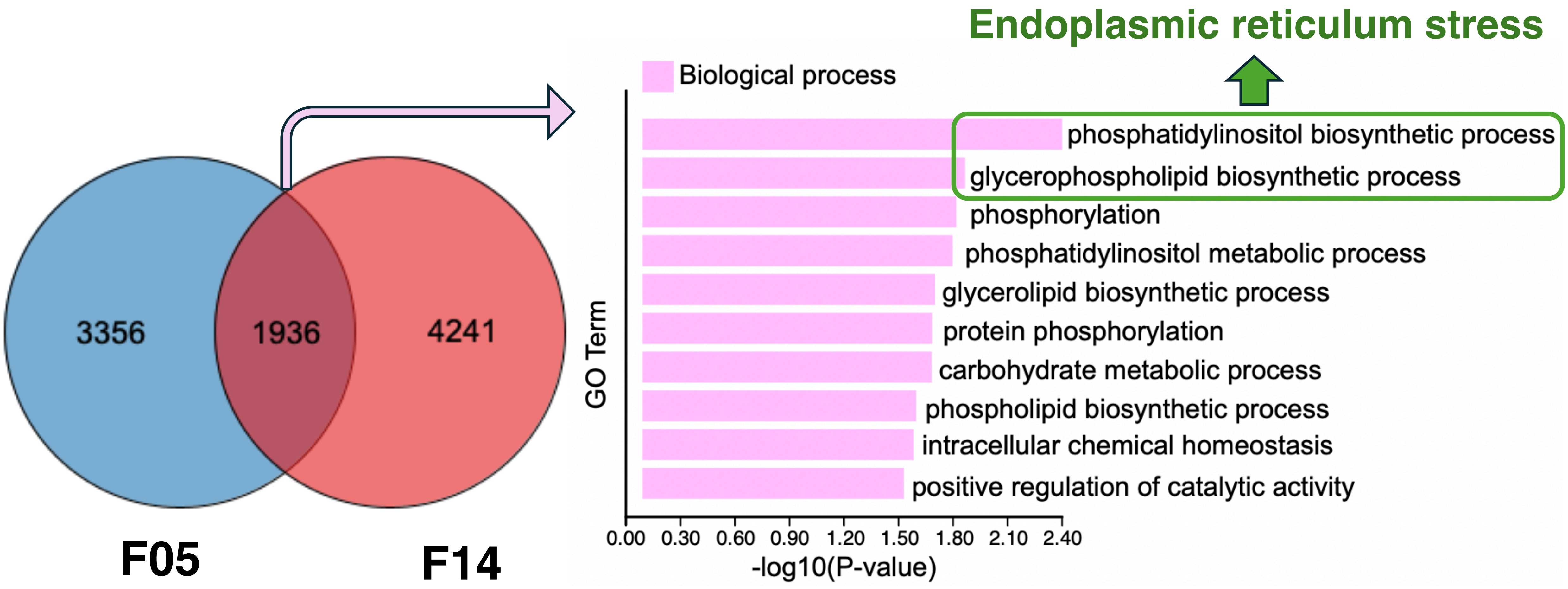
Gene Copy Number Variation

Triploid Properties per family

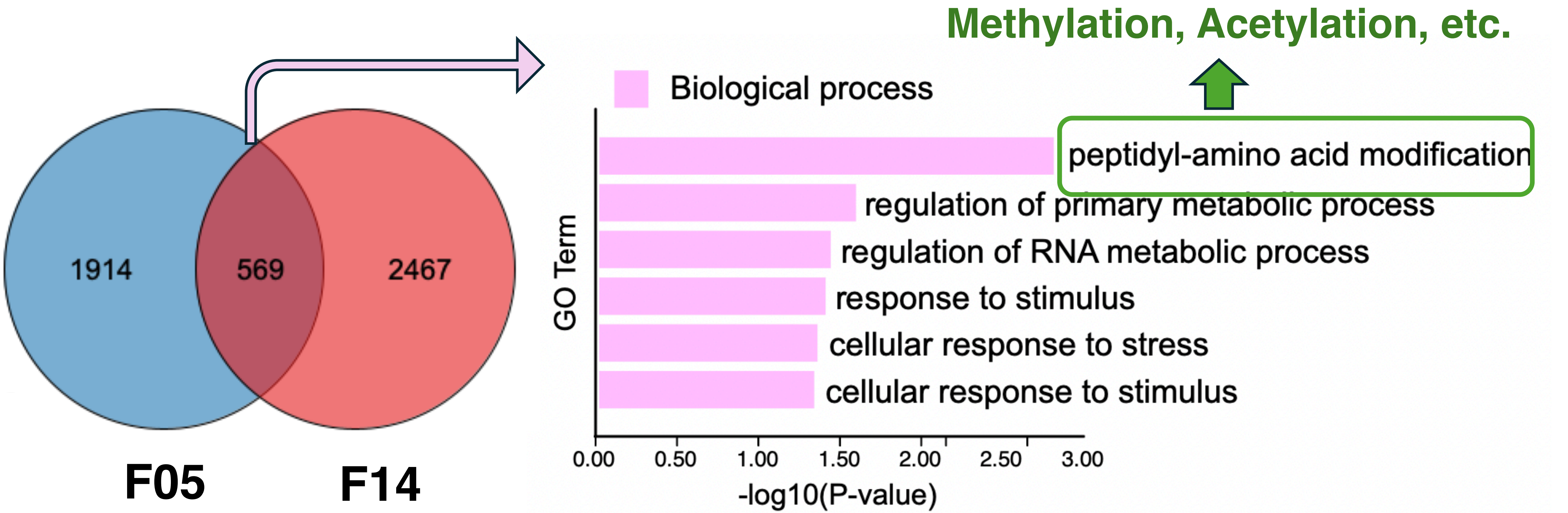
	Loss	Gain	Total
Region-Level CNV calls	5,131	2,099	7,220
Genes affected by CNV calls	5,294	2,483	7,777

	Loss	Gain	Total
Region-Level CNV calls	7,073	2,531	9,604
Genes affected by CNV calls	6,177	3,086	9,213

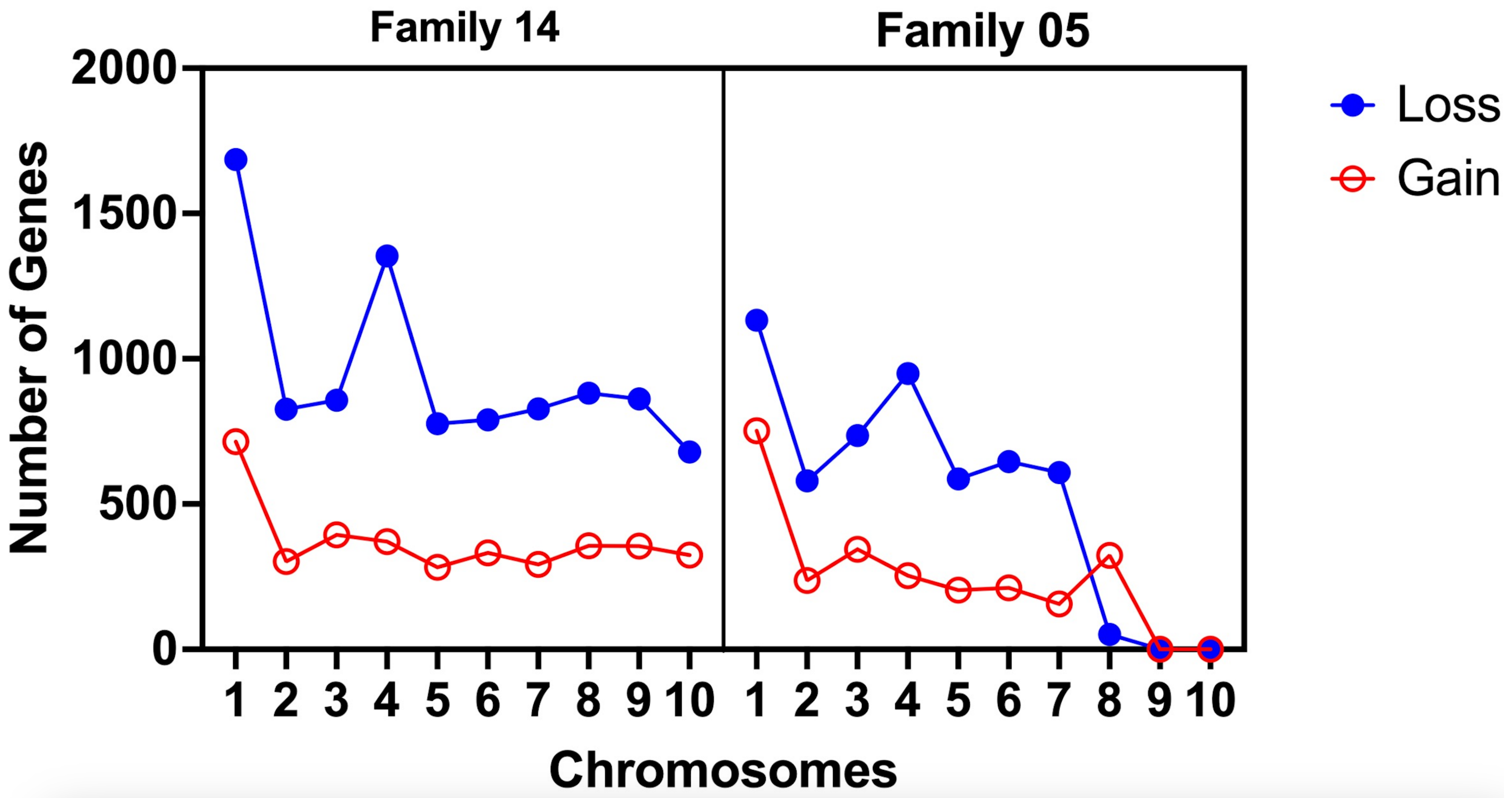
Gene copy number decrease / loss in triploids



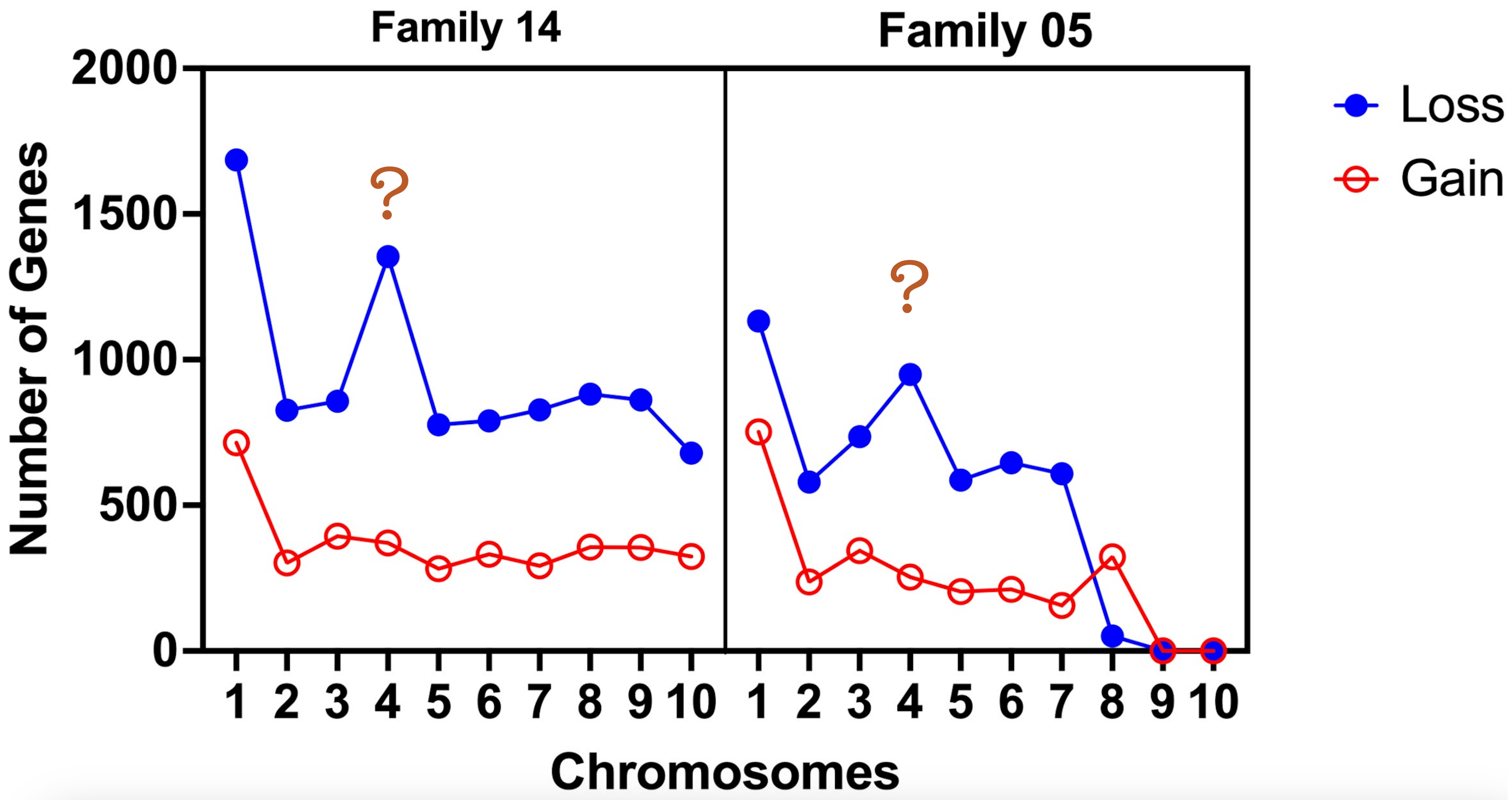
Gene copy number increase in triploids



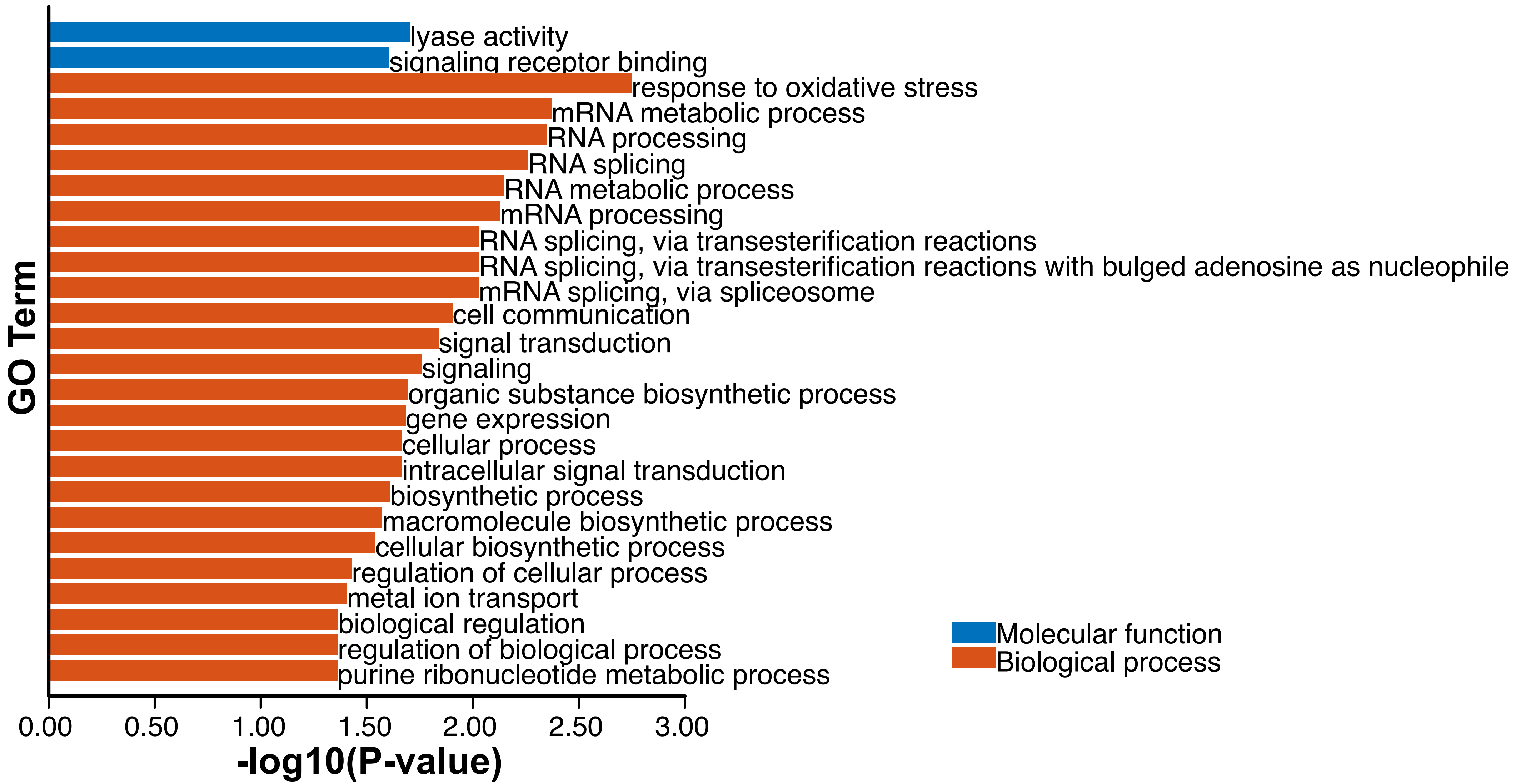
Chromosome Location of gene CNV



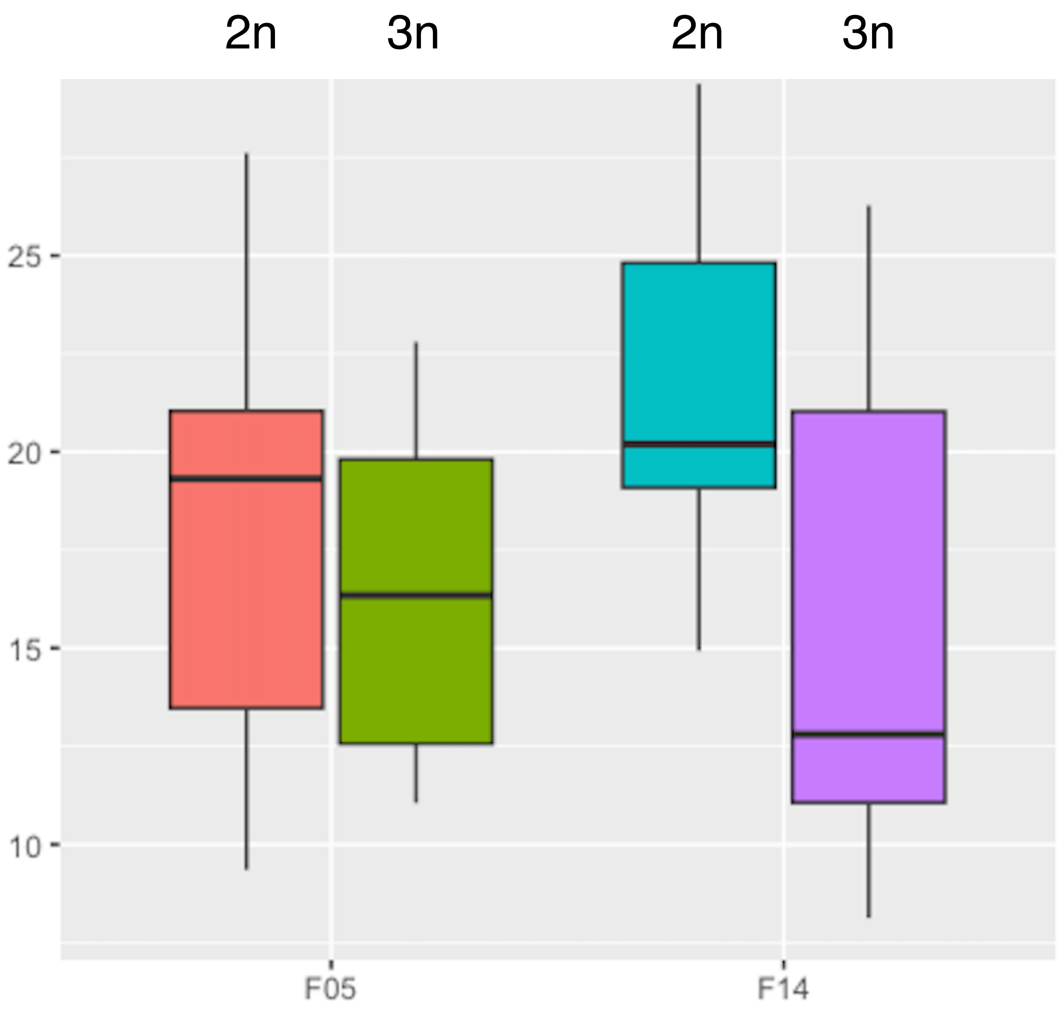
Chromosome Location of gene CNV



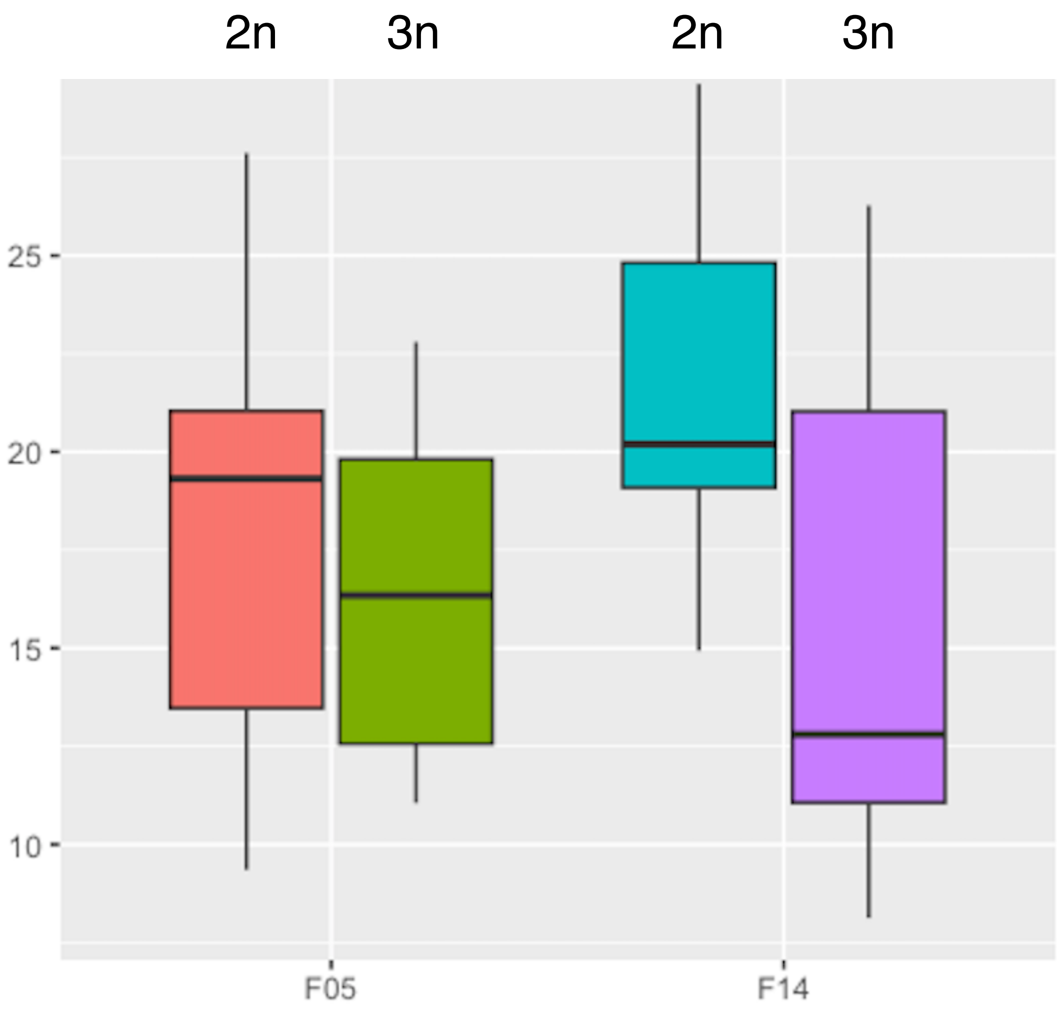
GO Processes: Genes loss Chromosome 4

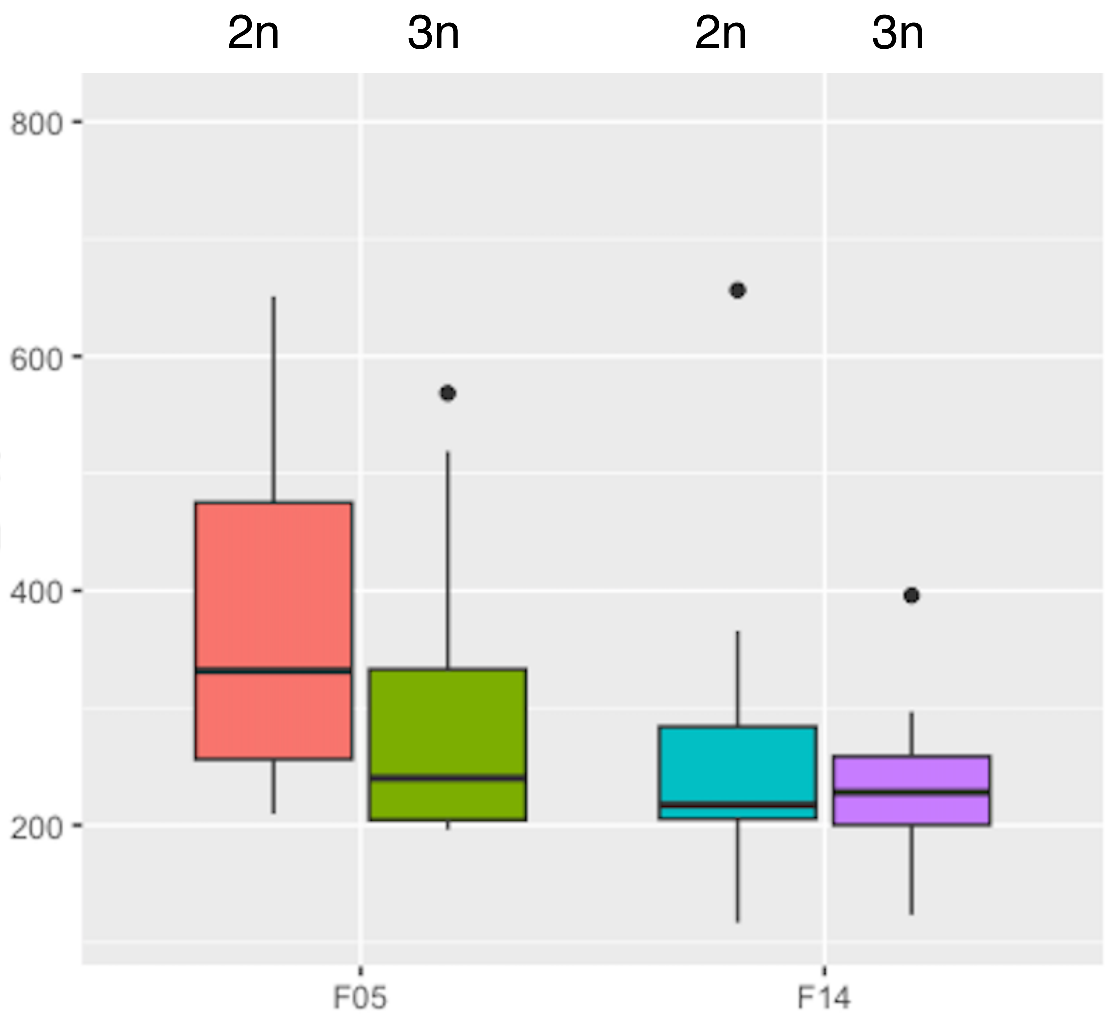


Mitochondrial and Ribosomal Genes

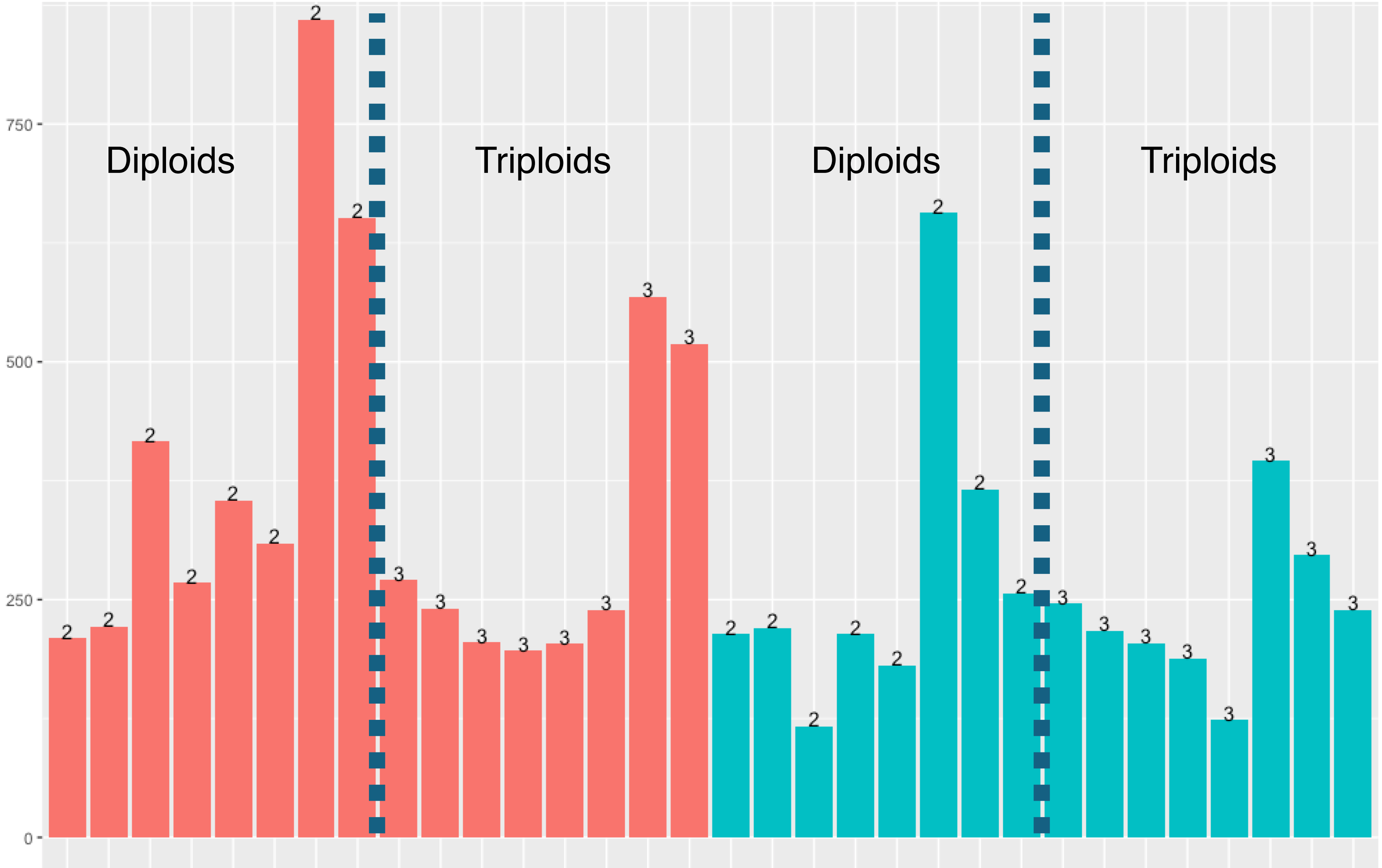


Mitochondrial and Ribosomal Genes

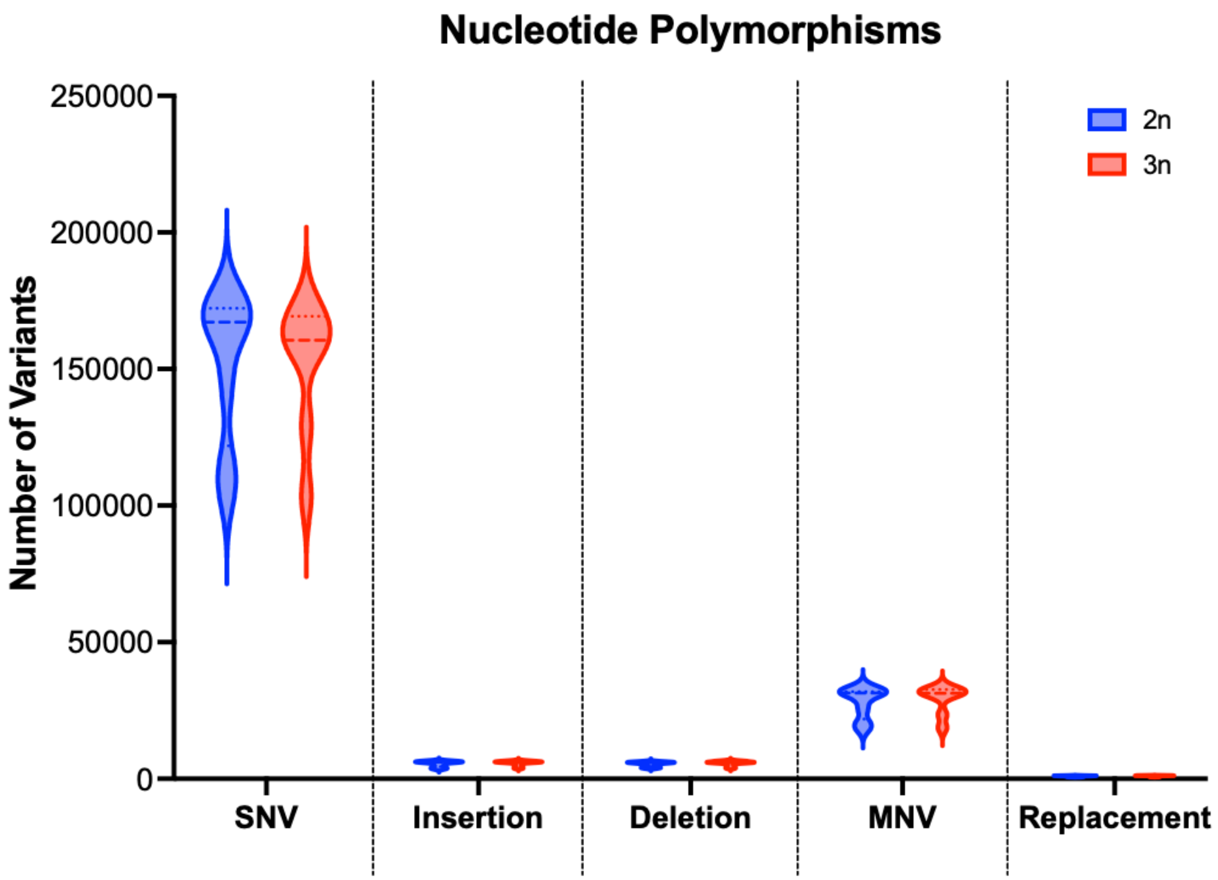


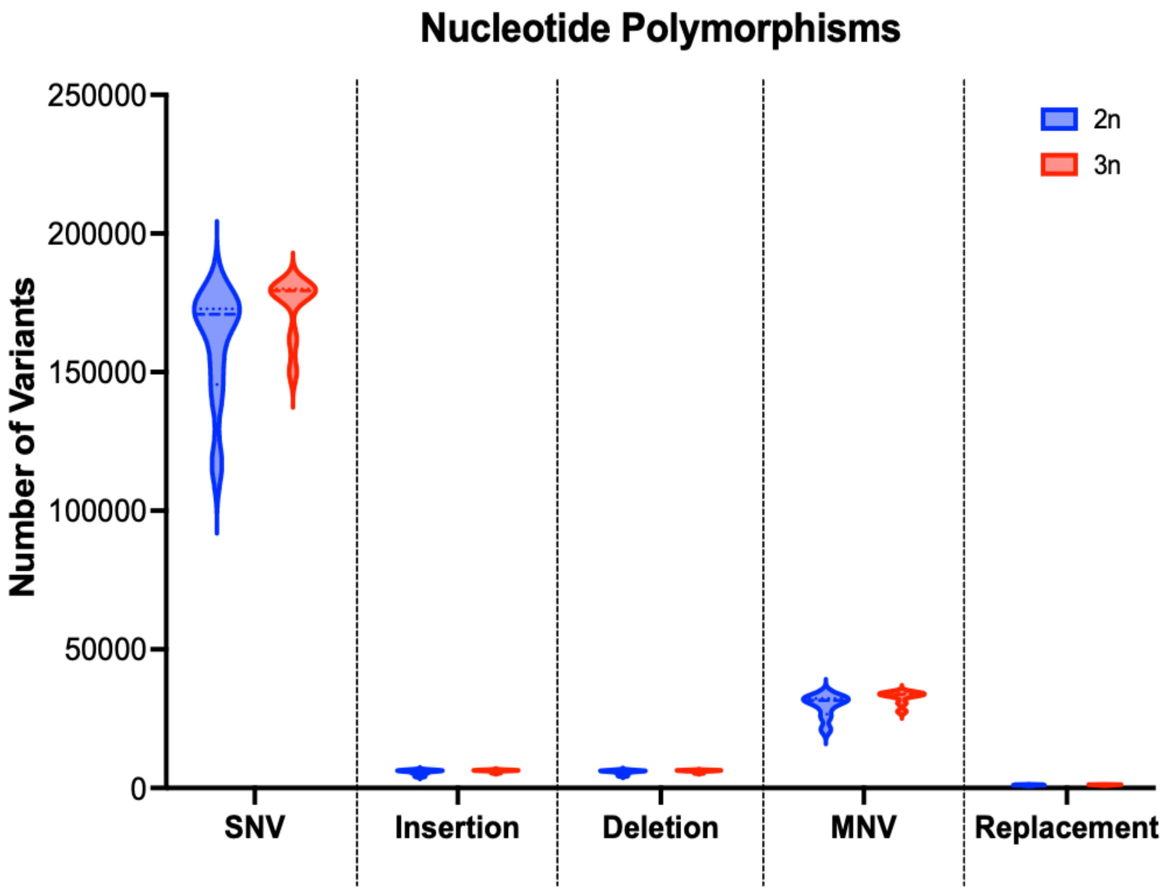


Ribosomal CNV across individuals



Structural Variation (bp)





Conclusions?

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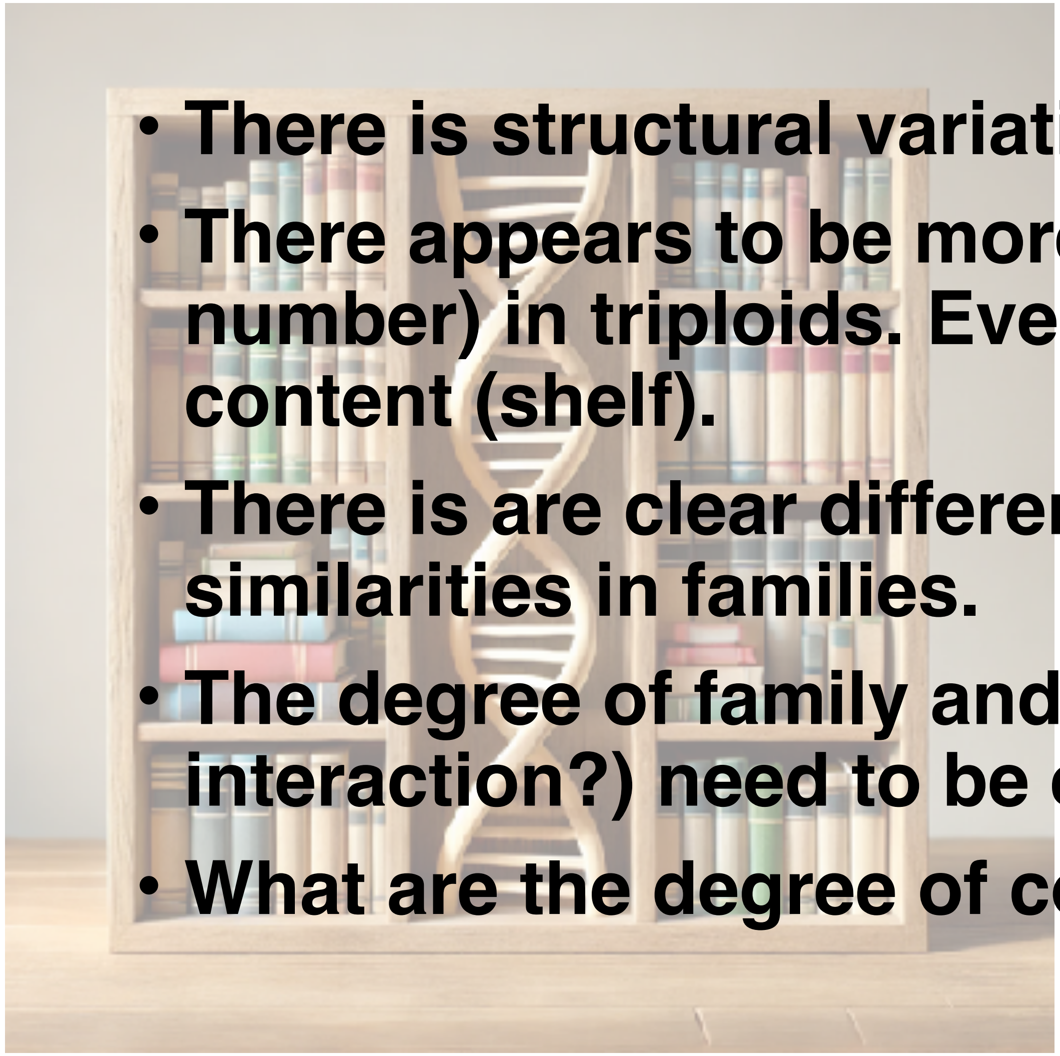
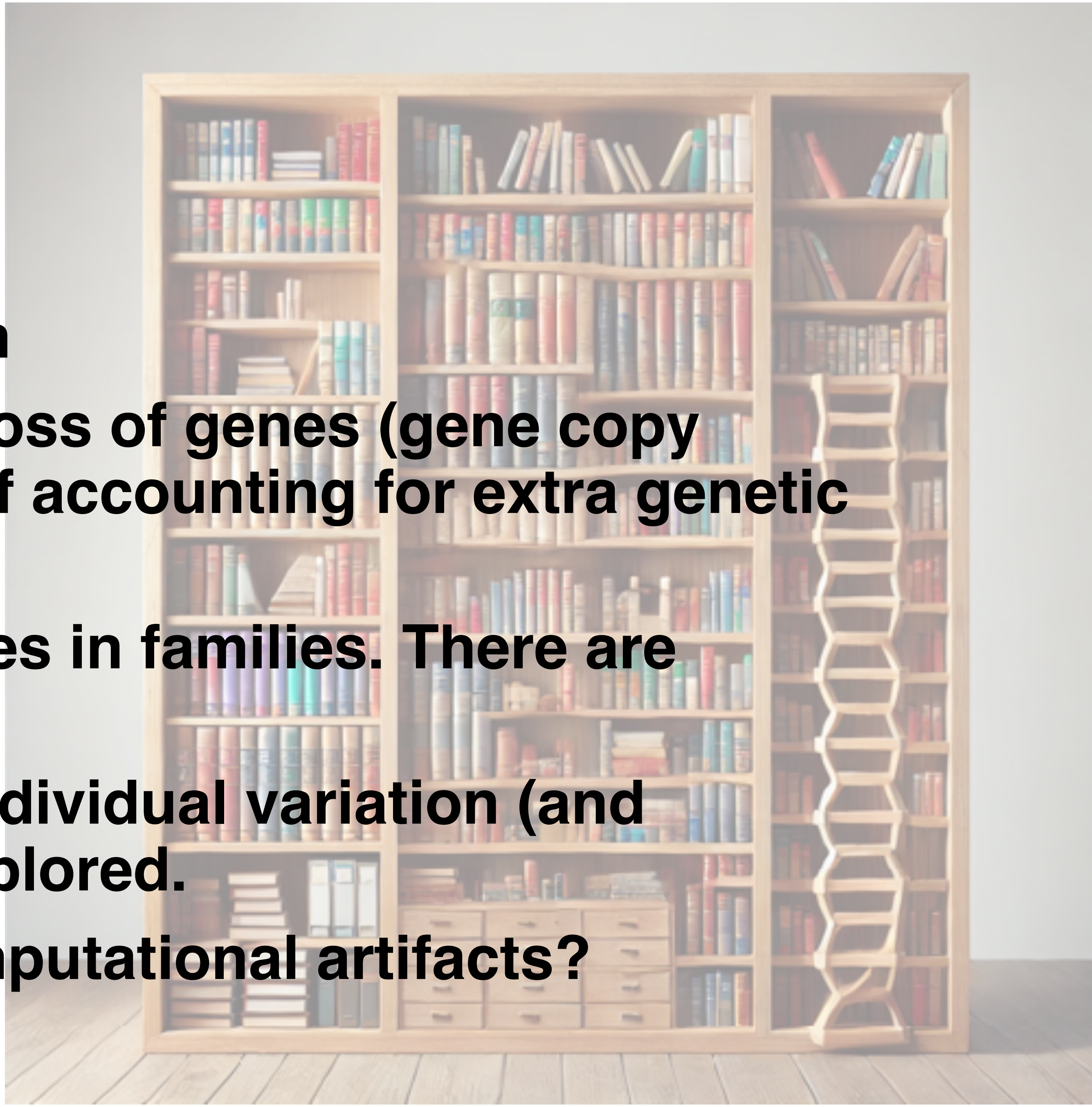
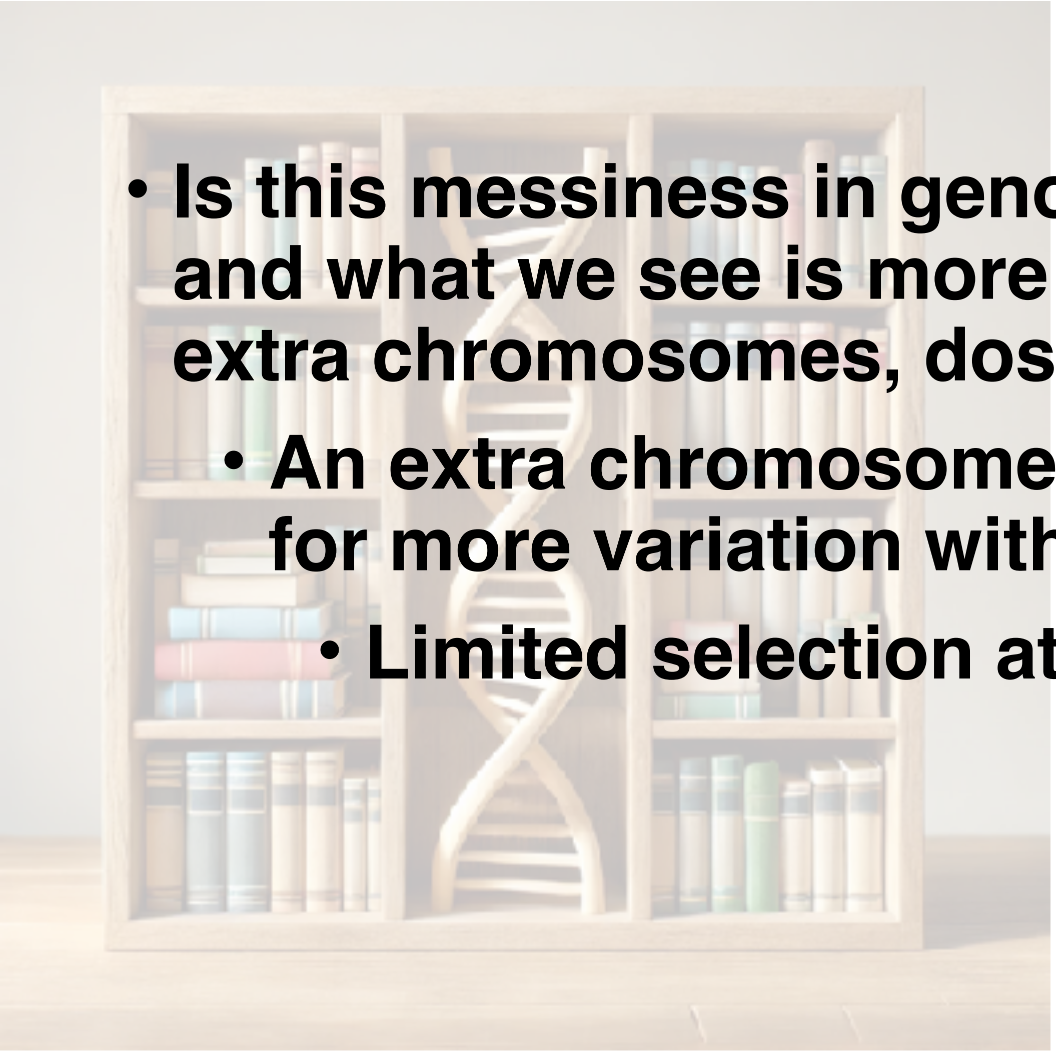
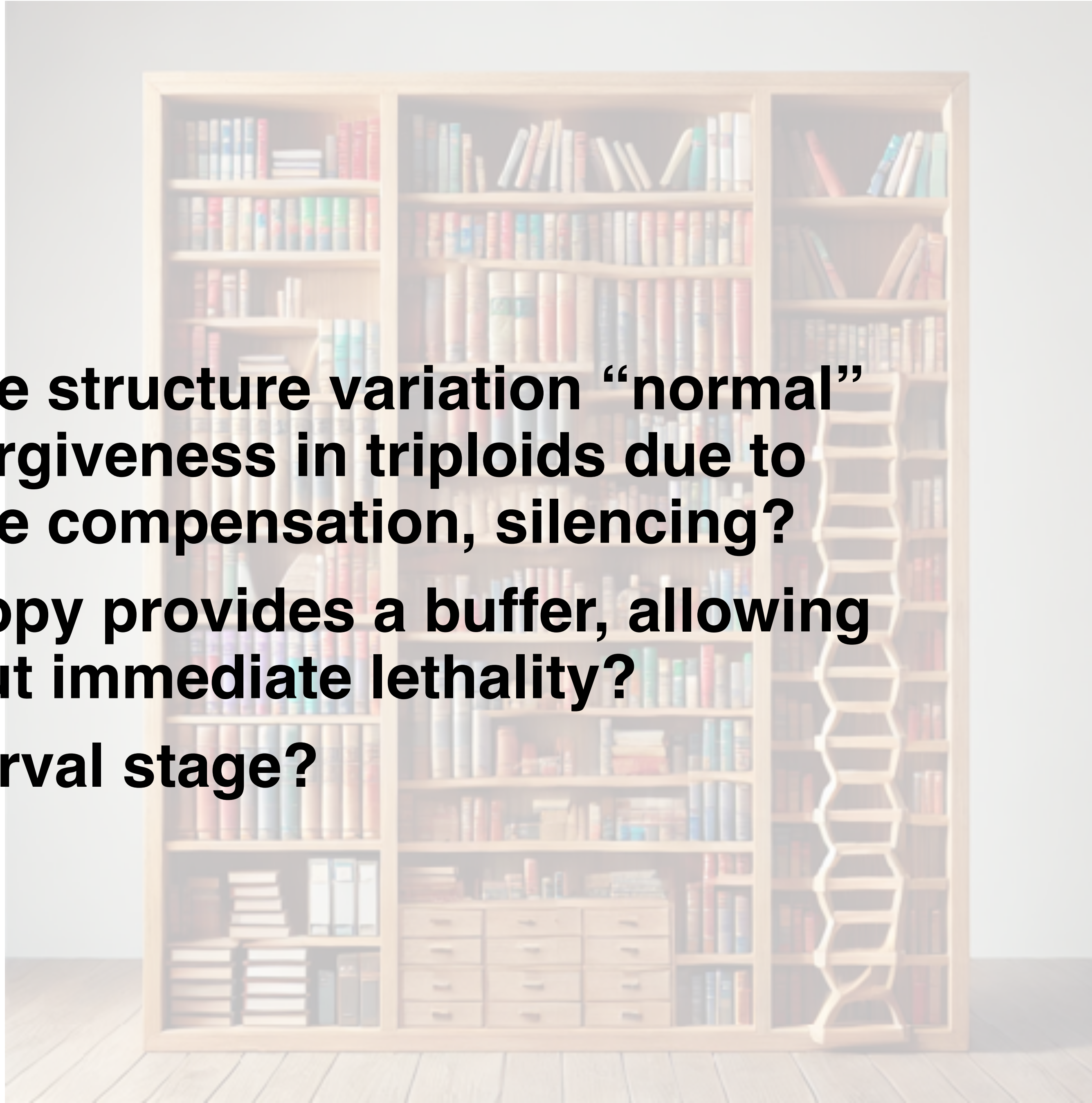




- There is structural variation
- There appears to be more loss of genes (gene copy number) in triploids. Even if accounting for extra genetic content (shelf).
- There is are clear differences in families. There are similarities in families.
- The degree of family and individual variation (and interaction?) need to be explored.
- What are the degree of computational artifacts?

Conclusions?





- Is this messiness in genome structure variation "normal" and what we see is more forgiveness in triploids due to extra chromosomes, dosage compensation, silencing?
  - An extra chromosome copy provides a buffer, allowing for more variation without immediate lethality?
    - Limited selection at larval stage?

Acknowledgements

- **NRSP8- Aquaculture Animal Genome Program**

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