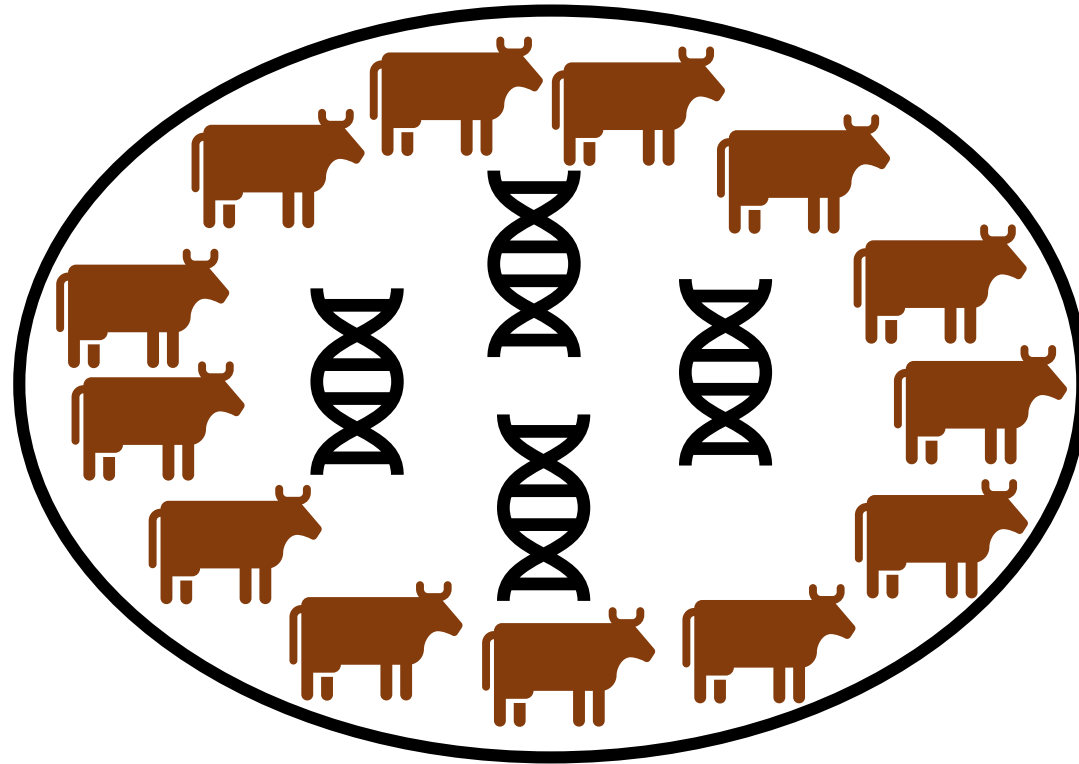


Investigating genetic redundancy as a source of genetic diversity and adaptability in the U.S. Holstein breed

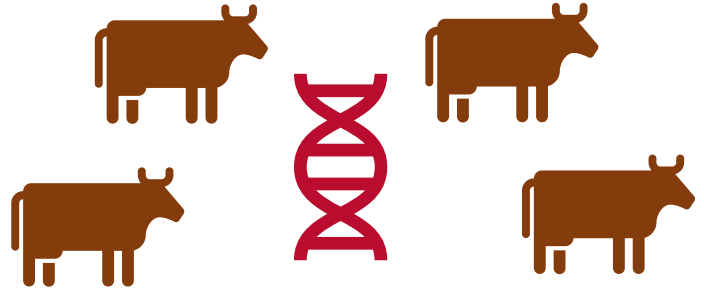
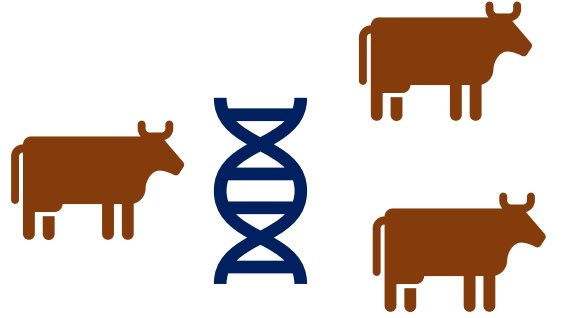
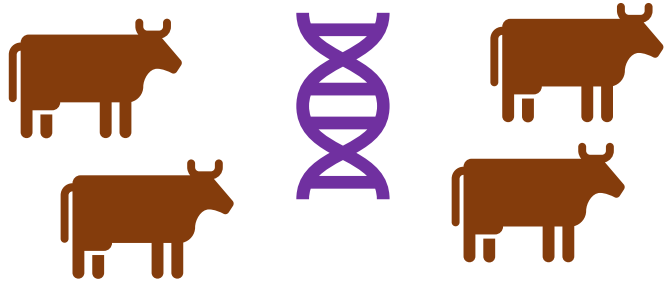
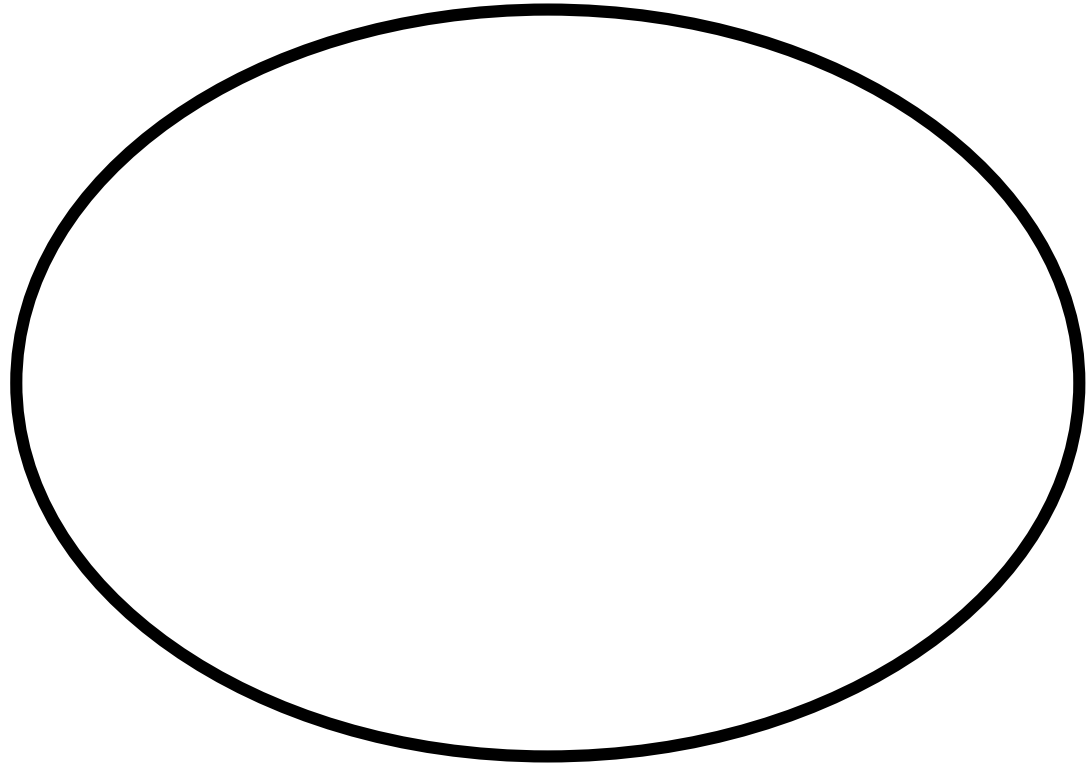
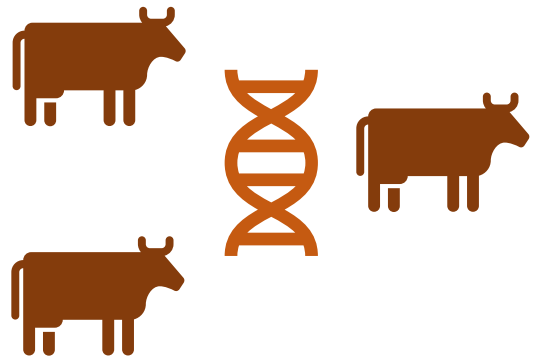
Yvette Steyn, T.J. Lawlor, S. Tsuruta, Y. Masuda, D.A.L. Lourenco, I. Misztal



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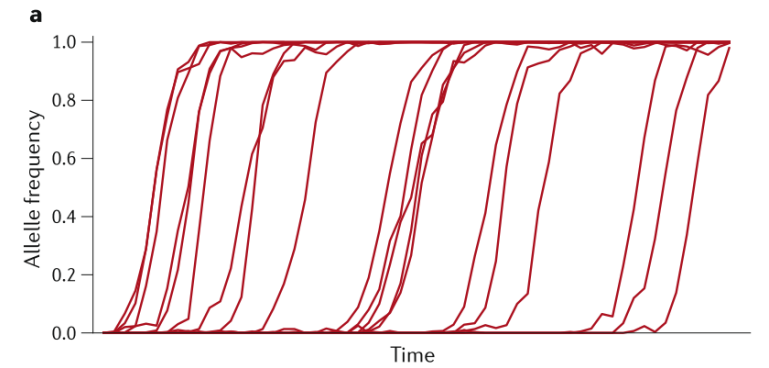
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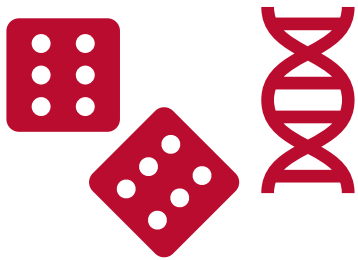


Polygenic shifts

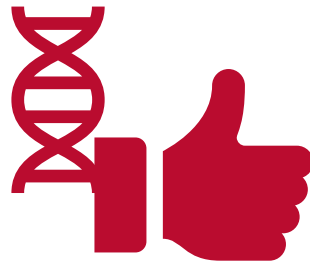
Methods of Change



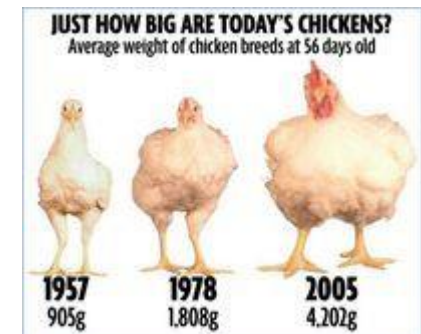
Selective sweeps



Random drift



Hitchhiking



Selection

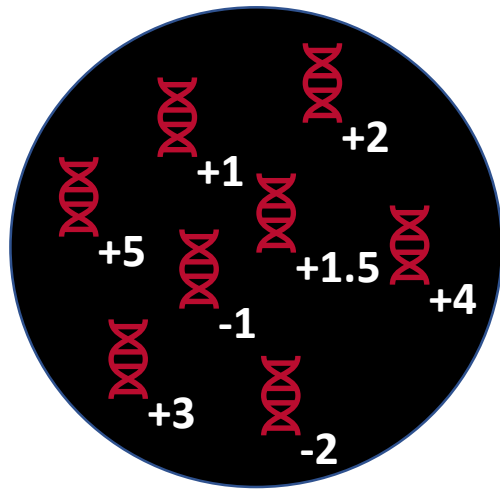
Genetic redundancy:

Many genotypic pathways to achieve the same phenotype.

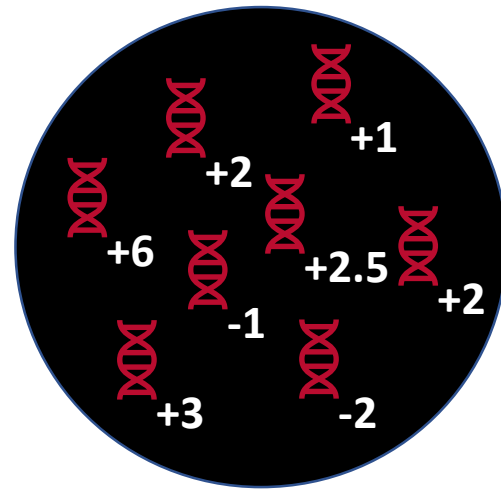
Thus, excess beneficial variants



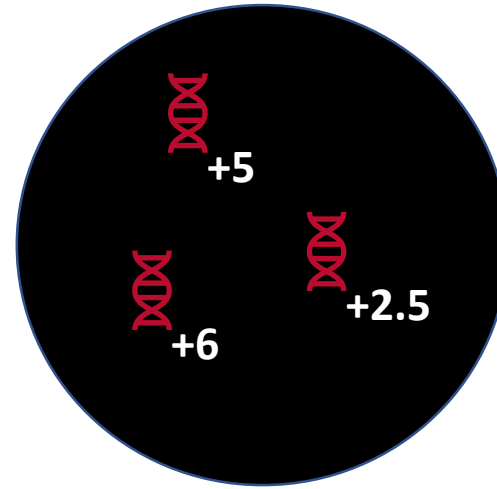
Highly polygenic



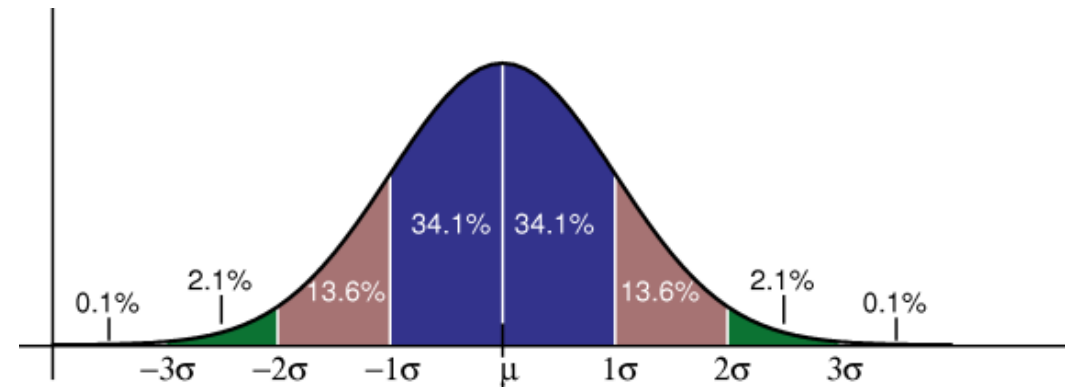
EBV: 13.5



EBV: 13.5



EBV: 13.5



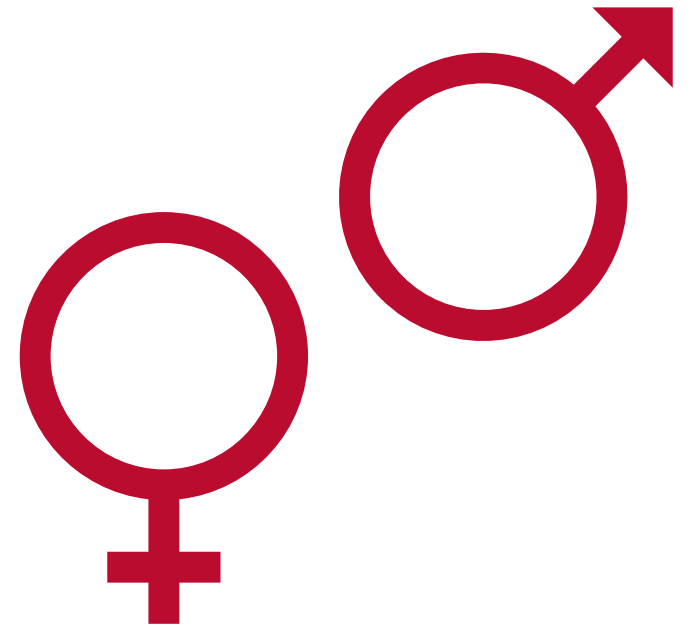
Objective

Investigate the presence of genetically different groups within the US Holstein population, and observe genetic changes within these groups over time



Data

- Up to 2014
- CDCB
- Sires of animals born after 2010 with at least 25 progeny
- Females measured after 2012
- 20,099 selected candidates



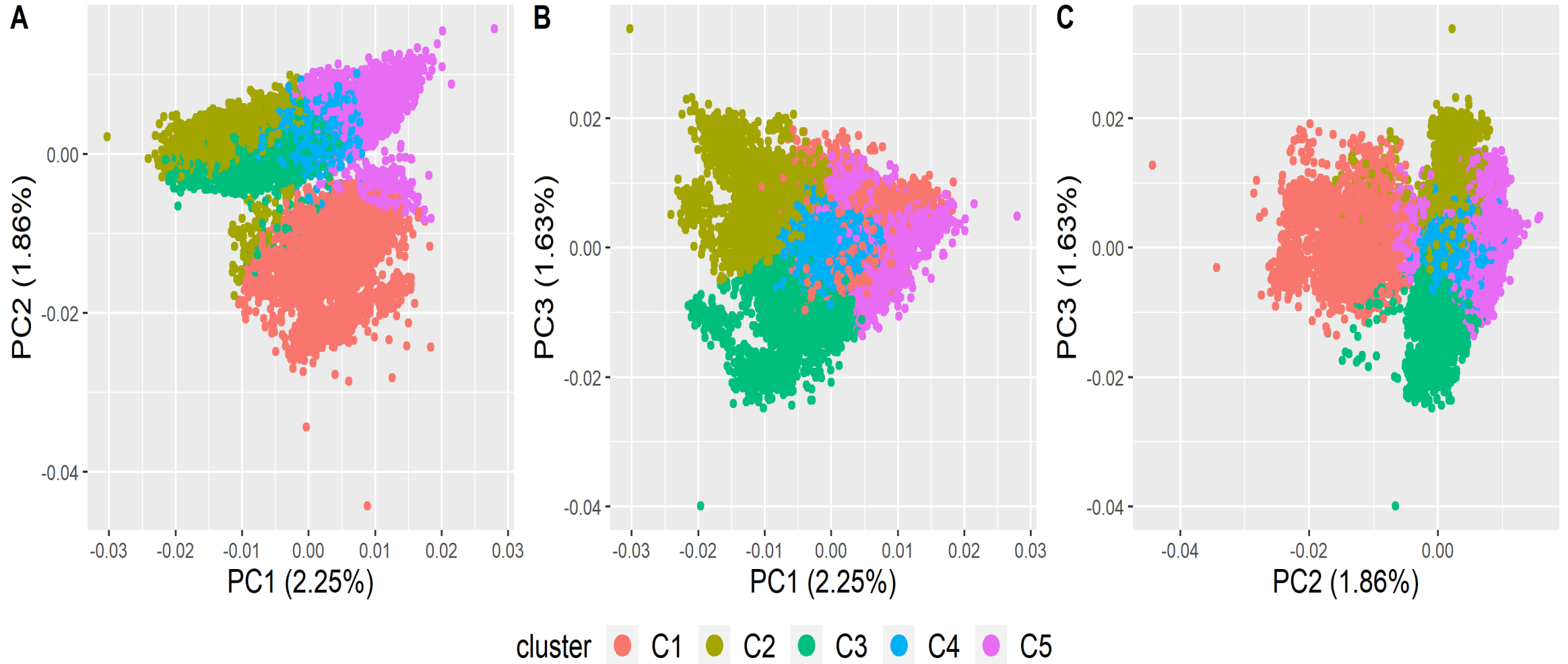
Approach

- 5 Clusters (K-means on G)
- Evaluate differences:
 - Expected inbreeding (Pedigree based)
 - F_{st}
 - Genetic correlations
- Measure non-parallel changes



PCA: Selected candidates

Principal Component Plots - 3 Dimensions

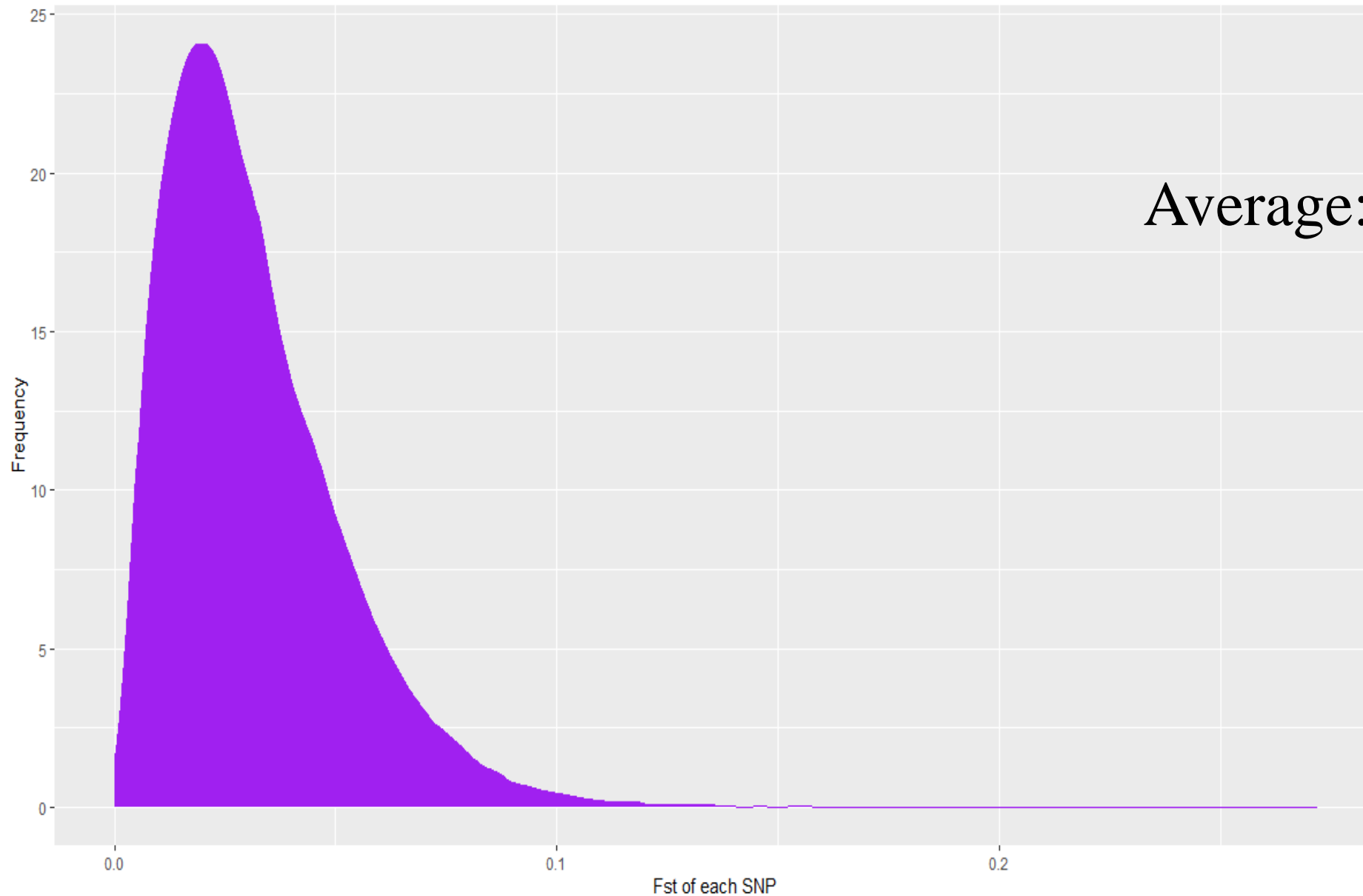


Expected inbreeding

Cluster	Average Inbreeding within Cluster	Average Inbreeding across Clusters
1	0.22	0.11
2	0.20	0.11
3	0.18	0.12
4	0.10	0.10
5	0.17	0.11



Distribution for F_{st}

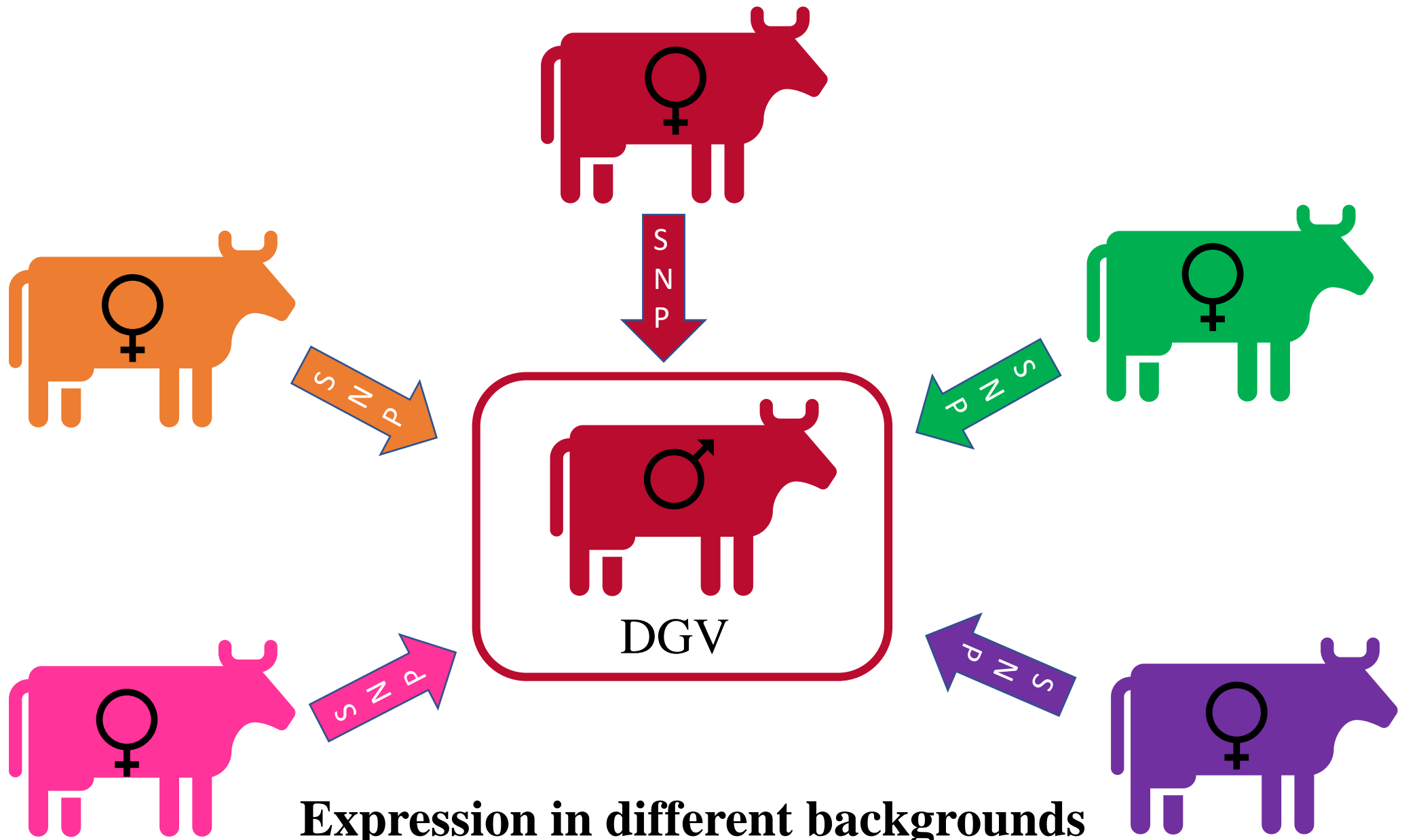


Additive genetic correlations

Expression of a genotype in genetic background of different populations

Duenk et al. 2020





Expression in different backgrounds

Adjustment

$$r_{A,B} = \frac{\sqrt{(\sum Rel_A)(\sum Rel_B)}}{\sum (Rel_A Rel_B)} r(BV_A, BV_B)$$

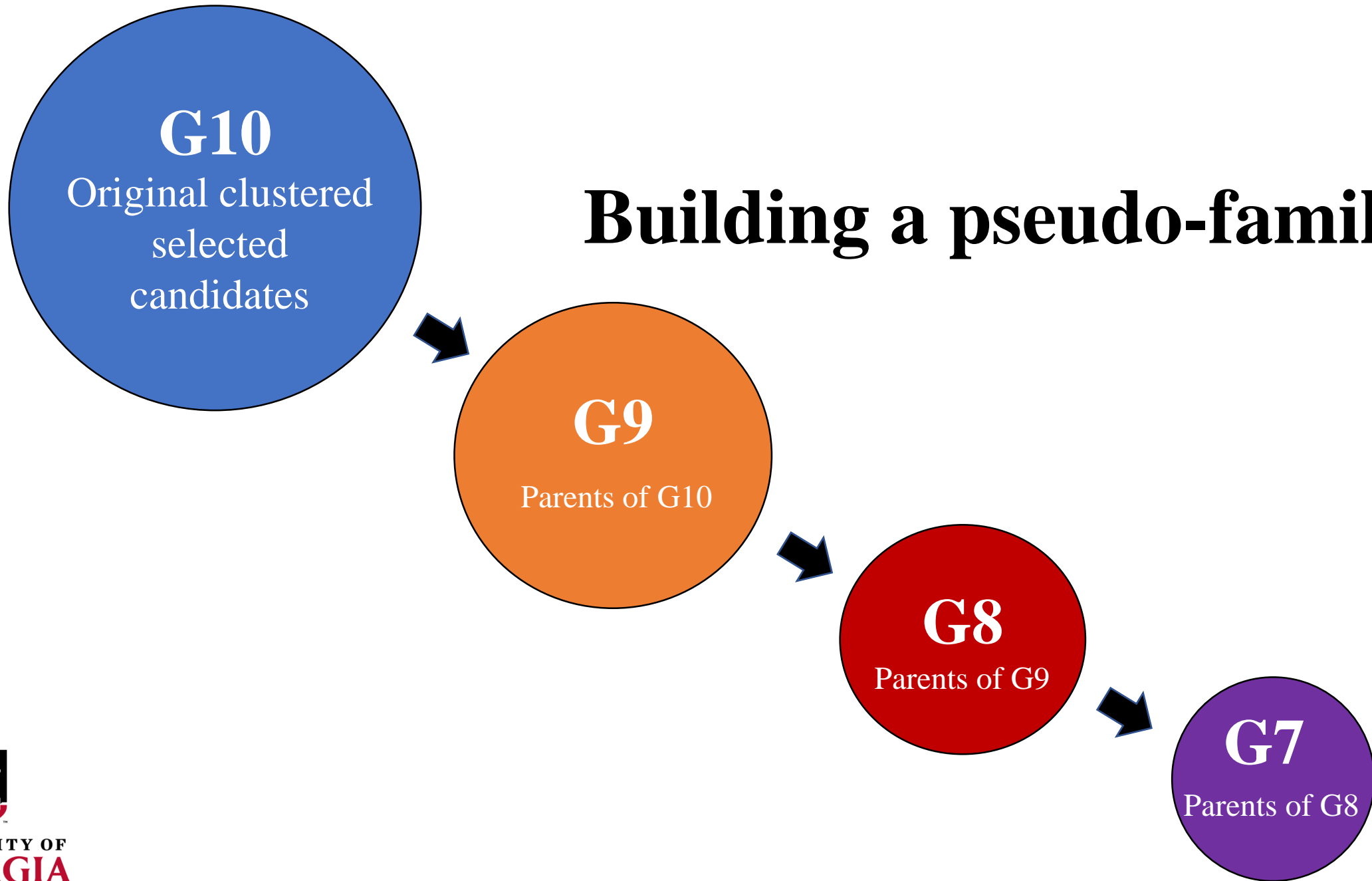
$$Adj = \frac{1}{h^2}$$

Adjusted correlations

SNP effects used	Cluster predicted				
	C1	C2	C3	C4	C5
C1	1.00	0.63	0.99	0.76	0.93
C2	0.77	1.00	0.62	0.59	0.51
C3	0.81	0.41	1.00	0.81	0.92
C4	0.80	0.74	0.93	1.00	0.90
C5	0.89	0.45	0.89	0.73	1.00



Building a pseudo-family



SNP to observe

- Selected genes (Ma et al. 2019)
- Variance
- Range

Selected marker

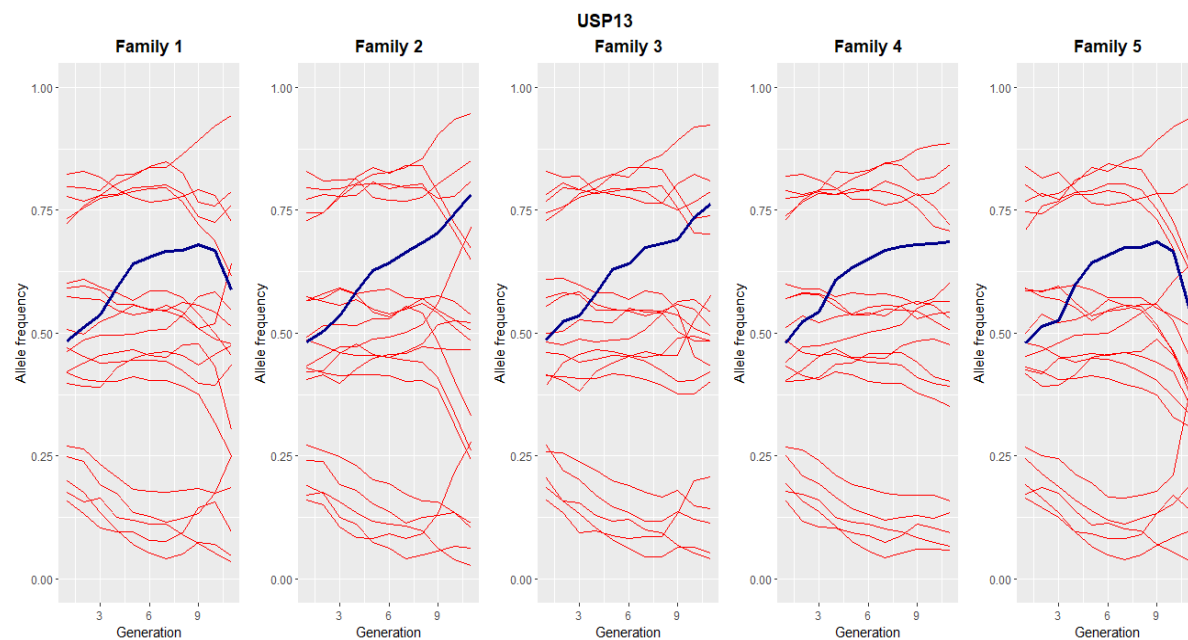
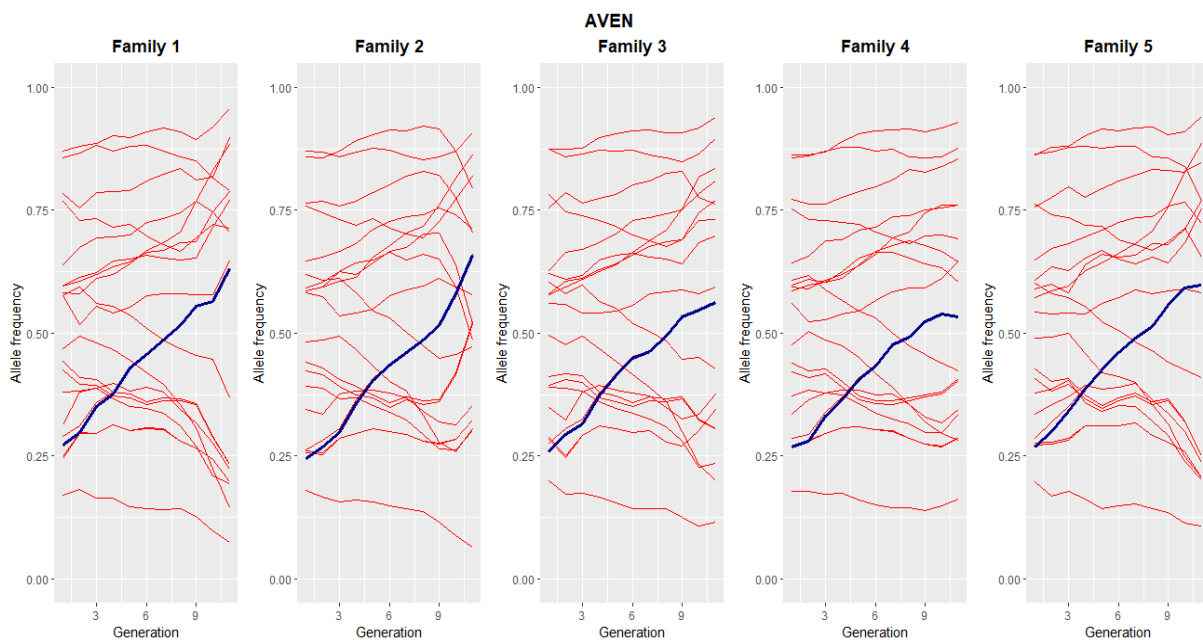
20 nearest markers



Genes

Blue lines: selected marker

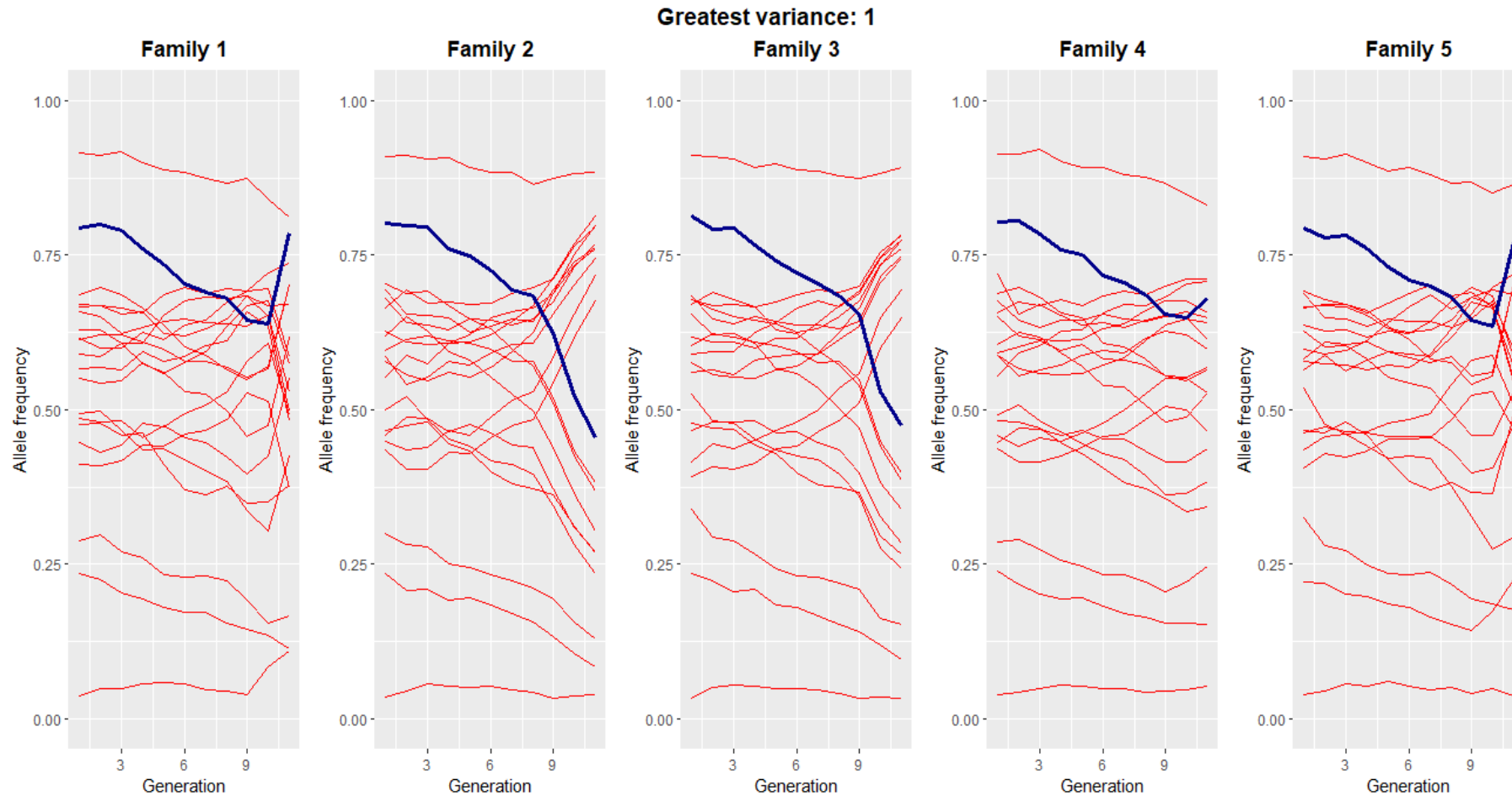
Red lines: 20 nearest markers



Variance

Blue lines: selected marker

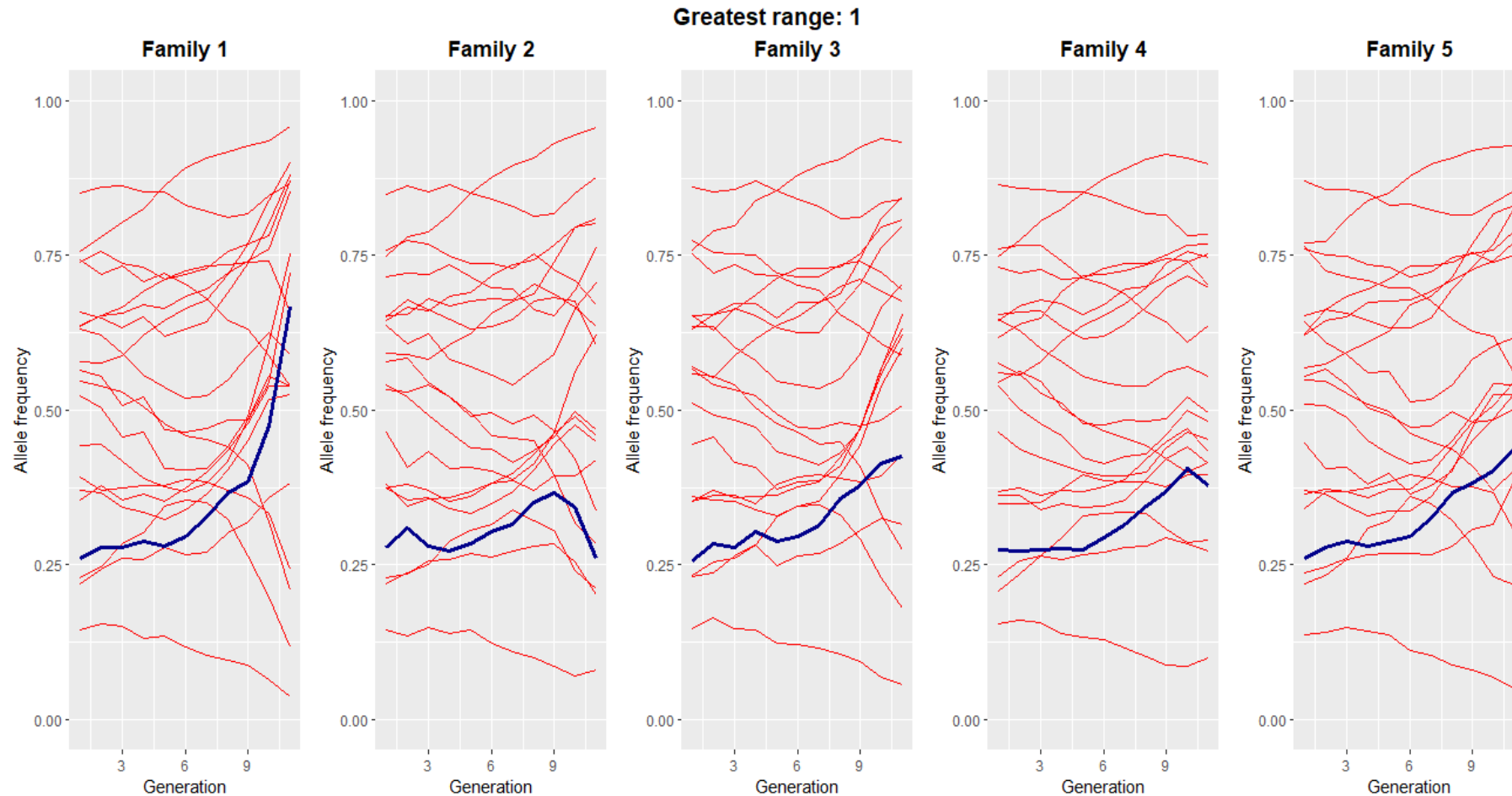
Red lines: 20 nearest markers



Range

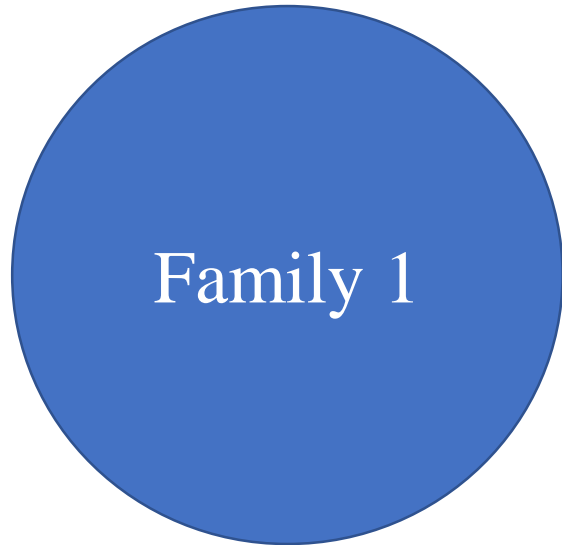
Blue lines: selected marker

Red lines: 20 nearest markers

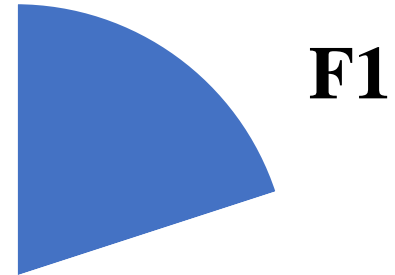


Replicate Frequency Spectrum

100 SNP with most change



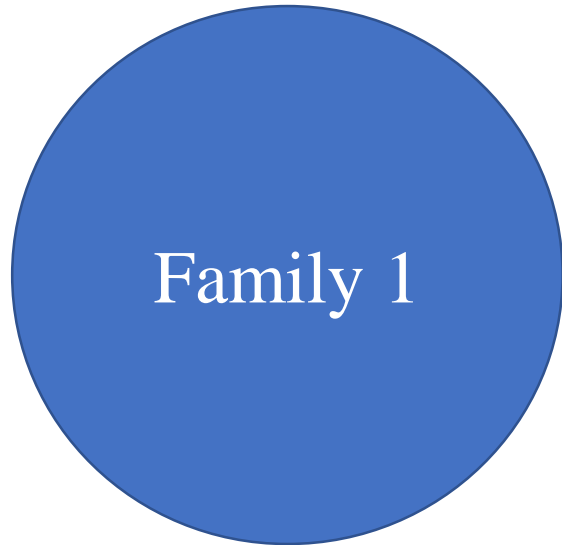
AF > 0.30



Replicate Frequency Spectrum

100 SNP with most change

AF > 0.30



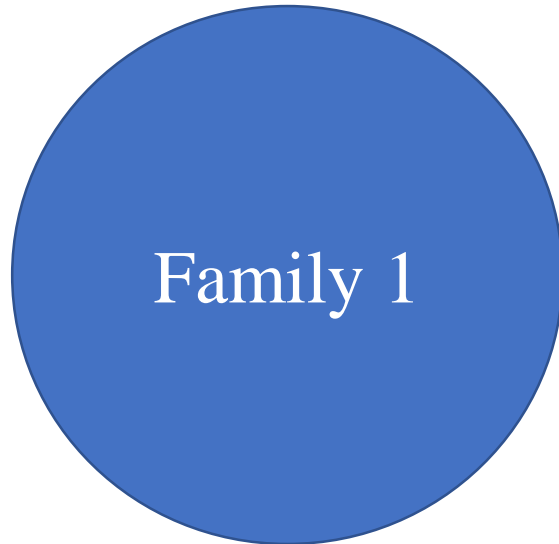
F2



Replicate Frequency Spectrum

100 SNP with most change

AF > 0.30



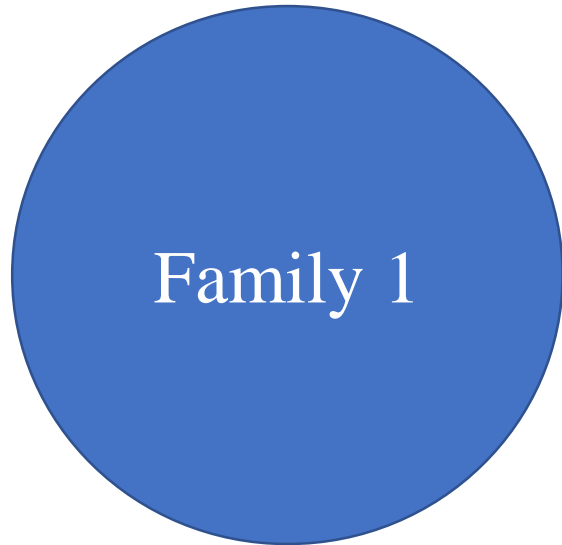
F3



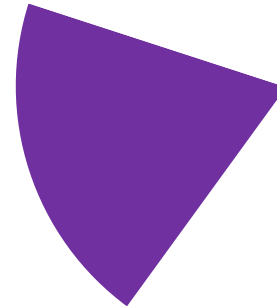
Replicate Frequency Spectrum

100 SNP with most change

AF > 0.30

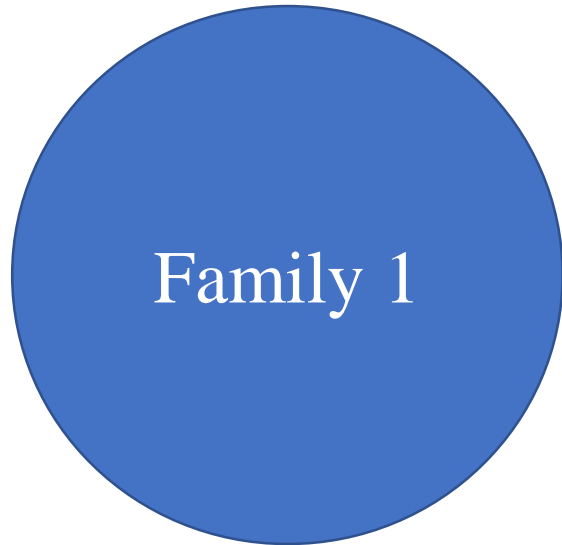


F4

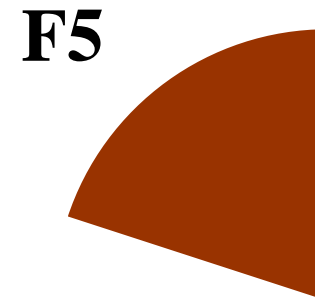


Replicate Frequency Spectrum

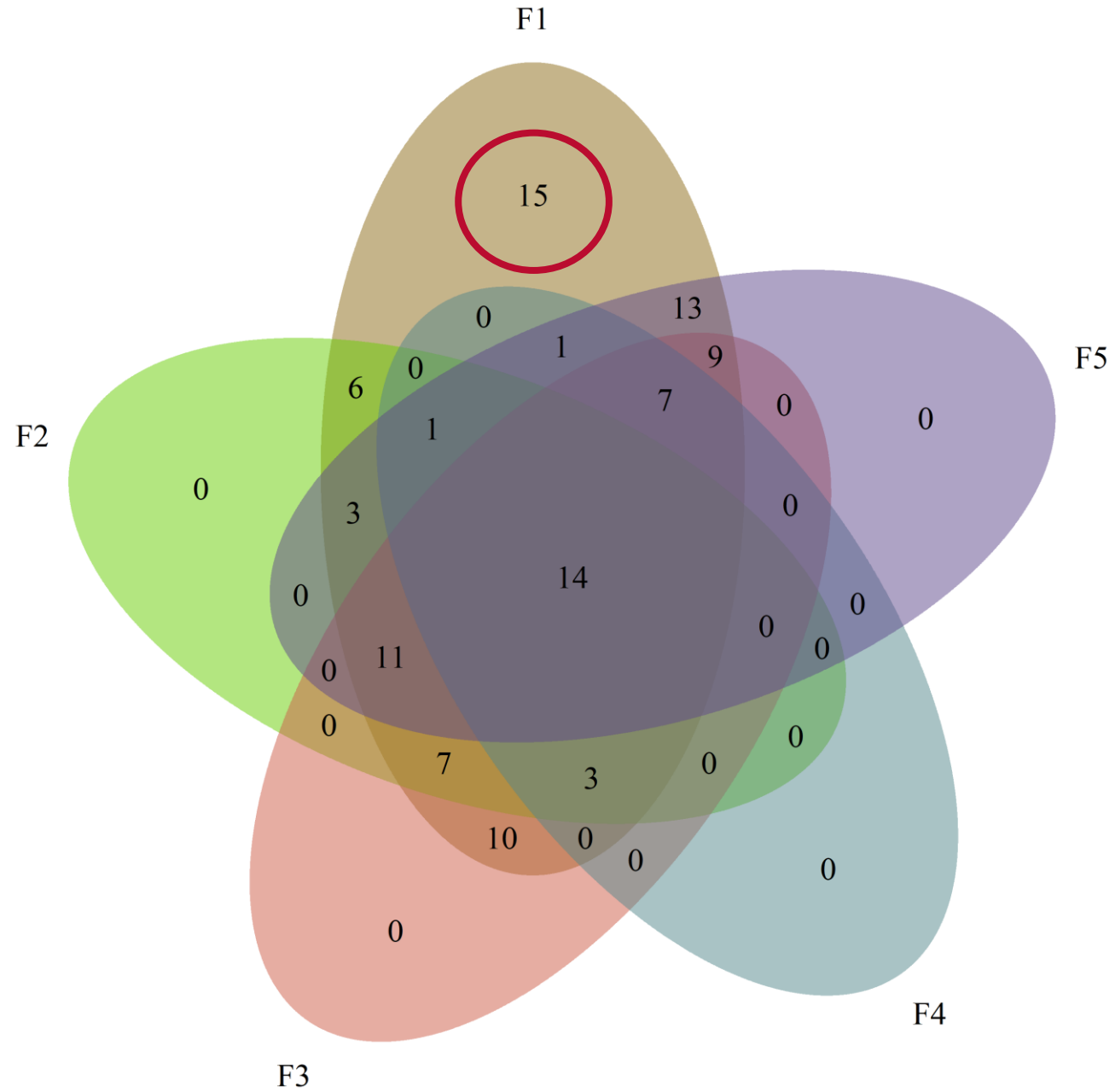
100 SNP with most change



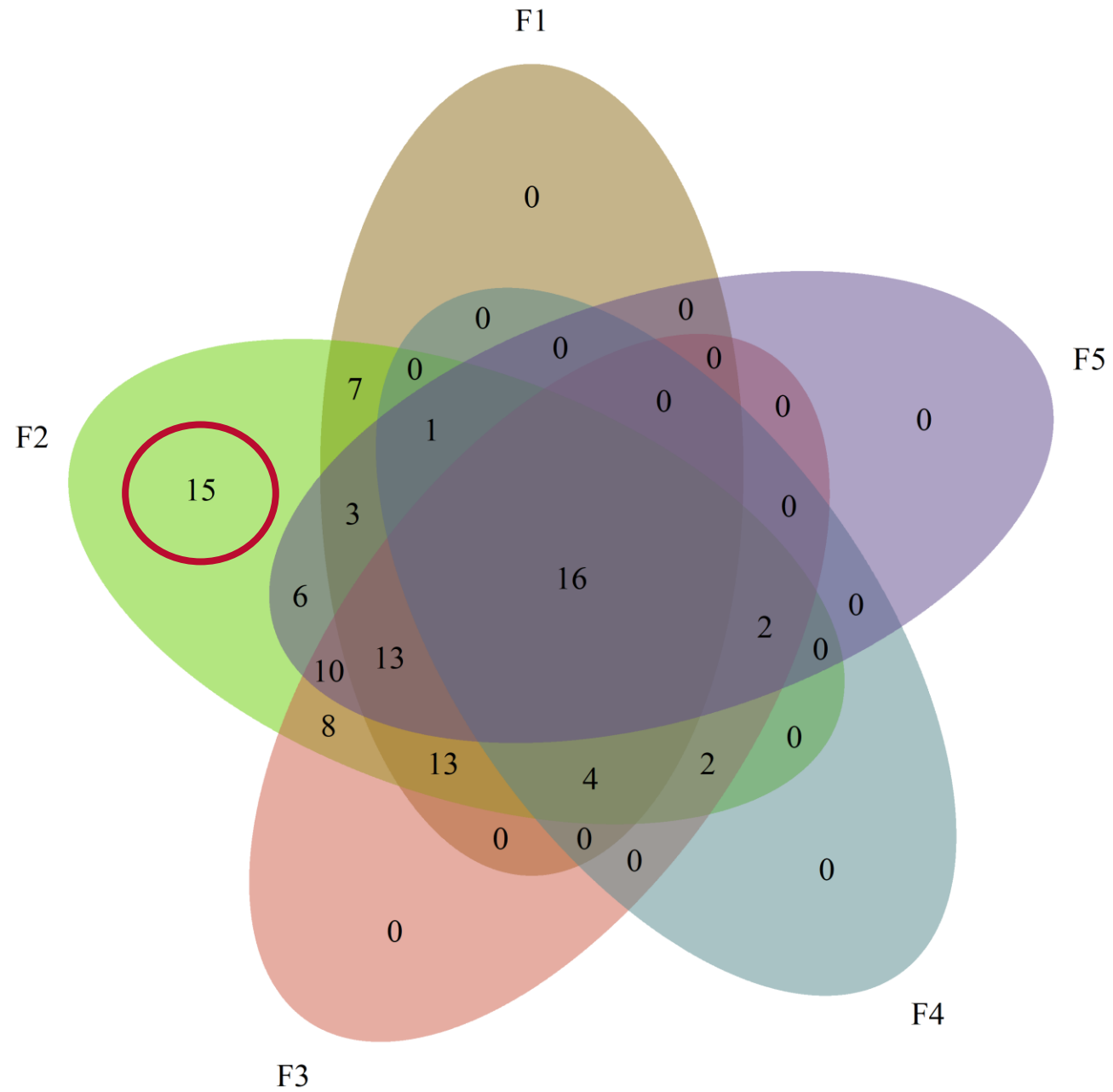
AF > 0.30



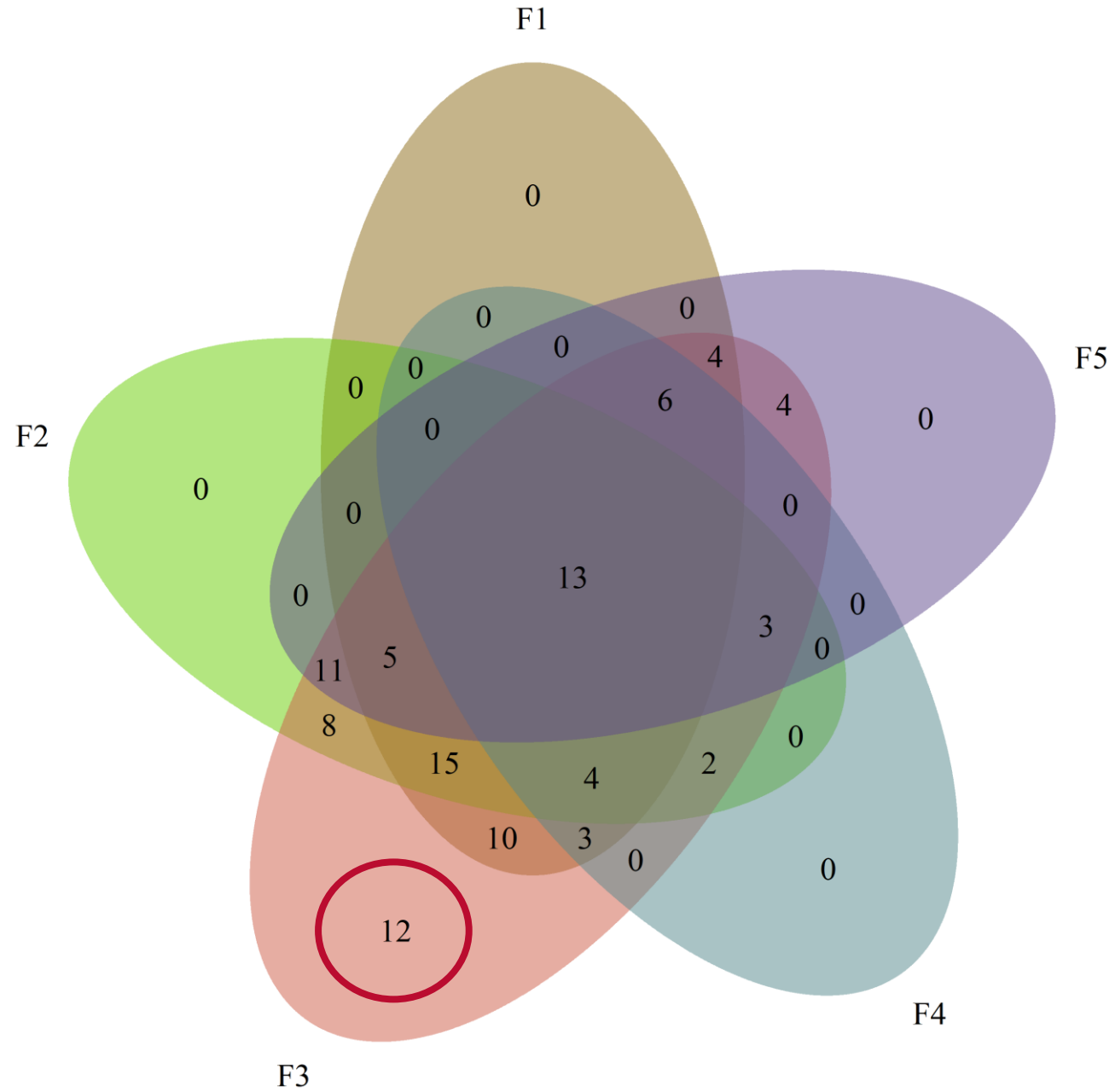
AF>0.30 of top 100 SNP in Family 1



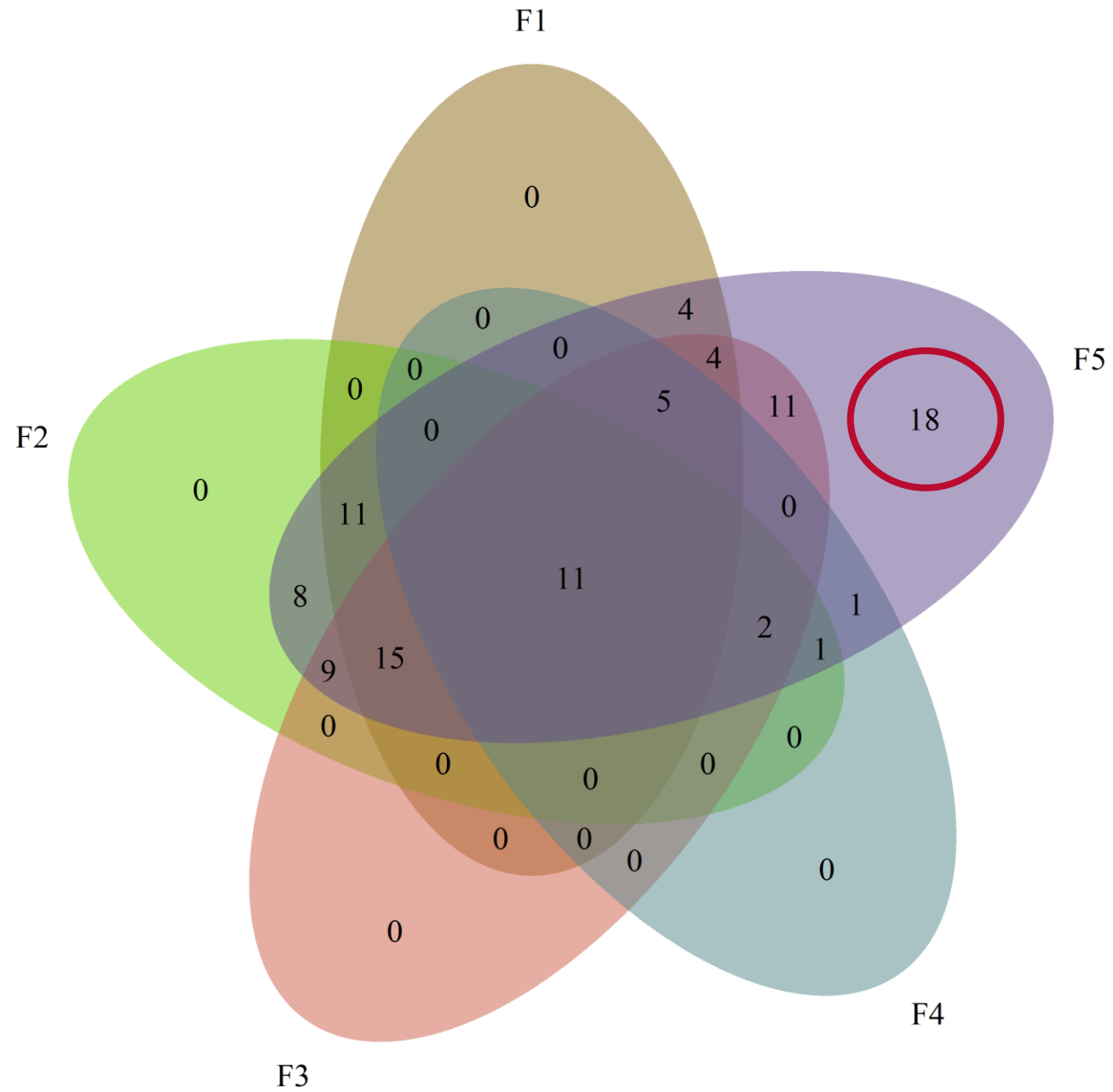
AF>0.30 of top 100 SNP in Family 2



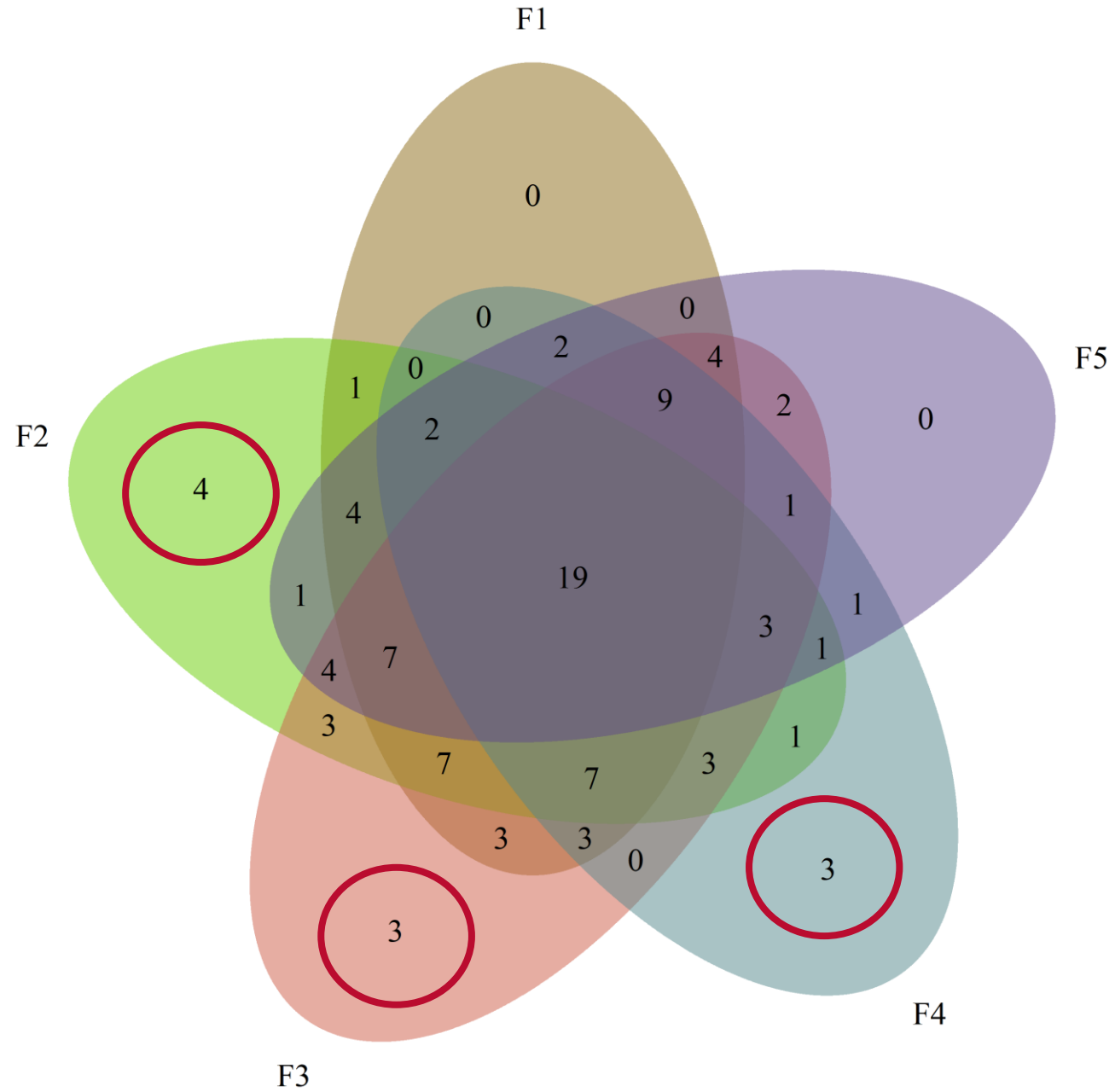
AF>0.30 of top 100 SNP in Family 3



AF>0.30 of top 100 SNP in Family 5



AF>0.30 of top 100 SNP in Family 4



Conclusion

- Diversity exists within the breed
- Observed non-parallel changes
- Allows continuous improvement
- Further research for application
- More recent data required
- Potential for gene searches



Thank you



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