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Conventional and traditional livestock production systems – new challenges

Conservation genomics in the management of the Mouflon population from the hunting area Kalifront

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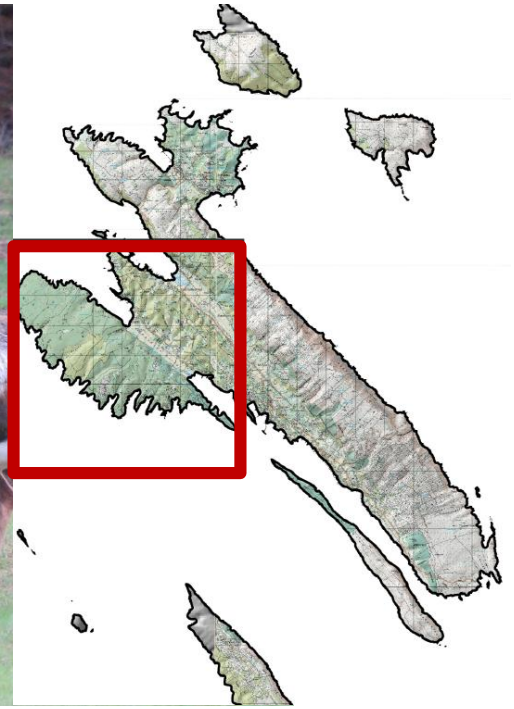
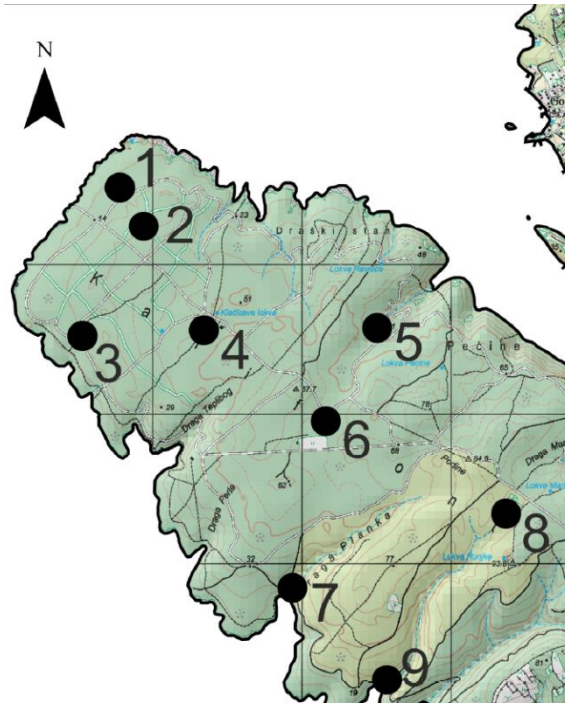
Kalifront - Rab: open state hunting area **(13,51 km²)**

1998 : **41** mouflons (**33 F** + **8 M**)

Current population size ≈ 270 mouflons (1.35 **F** : 1 **M**)

Observed decline in trophy values & body weight → last 10 years

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Aims of this study

1. To estimate genomic level of inbreeding
2. To estimate effective populations size
3. To analyse ticks paralysis lethality
   by autozygosity mapping

Materials & methods

Data and molecular analysis

- Our sample:

  32 Rab mouflons OvineSNP50 BeadChip (Illumina)

- Public data used:

  EU mouflon, Sardinian mouflon, Soay sheep,

  Finnsheep, Australian Merino, Churra and

  Sardinian White

  Dryad digital repository: http://dx.doi.org/10.5061/dryad.2p0qf

Genomic analysis

54,241 SNPs

Gap Size

mean = 50.9 kb

median = 42.6 kb

OvineSNP50 Genotyping BeadChip

Data editing and cleaning in PLINK

- GT score > 0.4
- GC score > 0.7
- Mind < 0.05
- Geno < 0.1

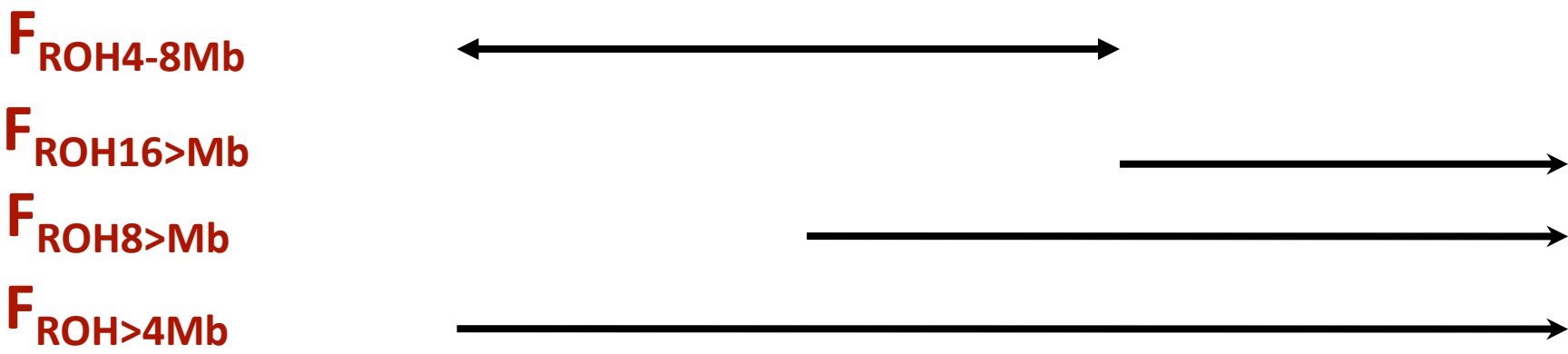
47708 polymorphic and **2549 monomorphic** loci on autosomes

Estimation of genomic (ROH) inbreeding

- Ferenčaković et al., 2013 GSE
- Software: SVS (SNP Variation Suite).

An **ROH** is defined as a continuous (uninterrupted) stretch of DNA sequence without heterozygosity in diploid state.

ROH length (*k*): >4Mb, >8Mb, >16Mb, 4-8Mb



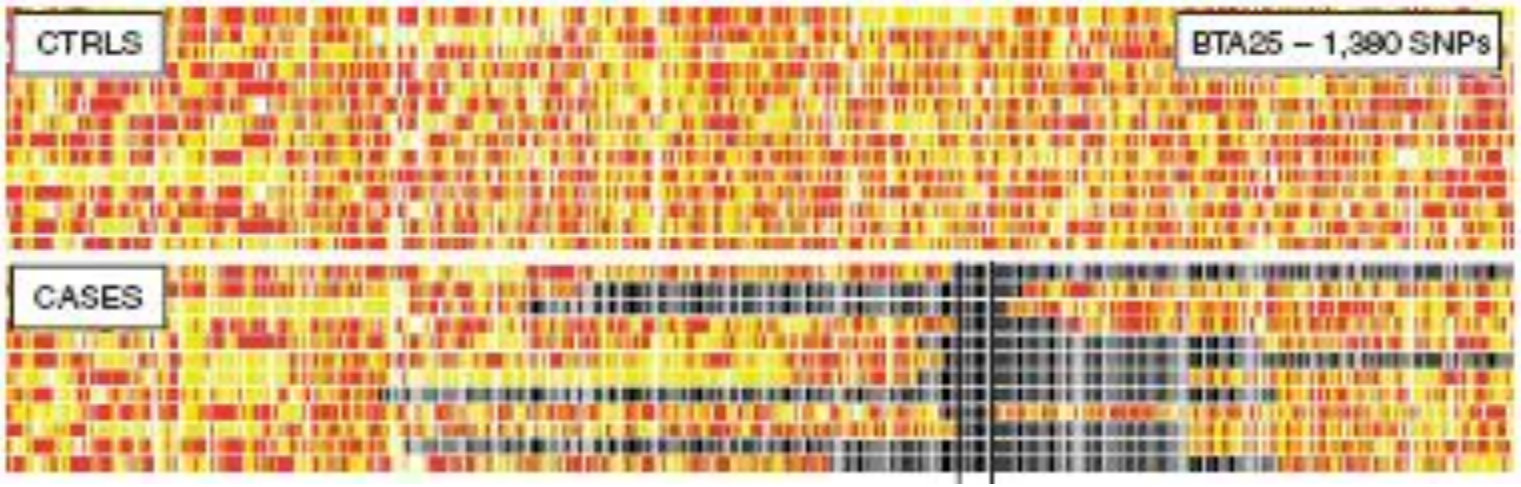
ROH (Mb)	4	8	16
E[common Ancestor]	12.5	6.25	3.13

Estimation of inbreeding effective population size

- Gorjanc et al., (2018): presented within "Optimization of a genomic breeding program for small sized cattle populations”

Autozygosity mapping

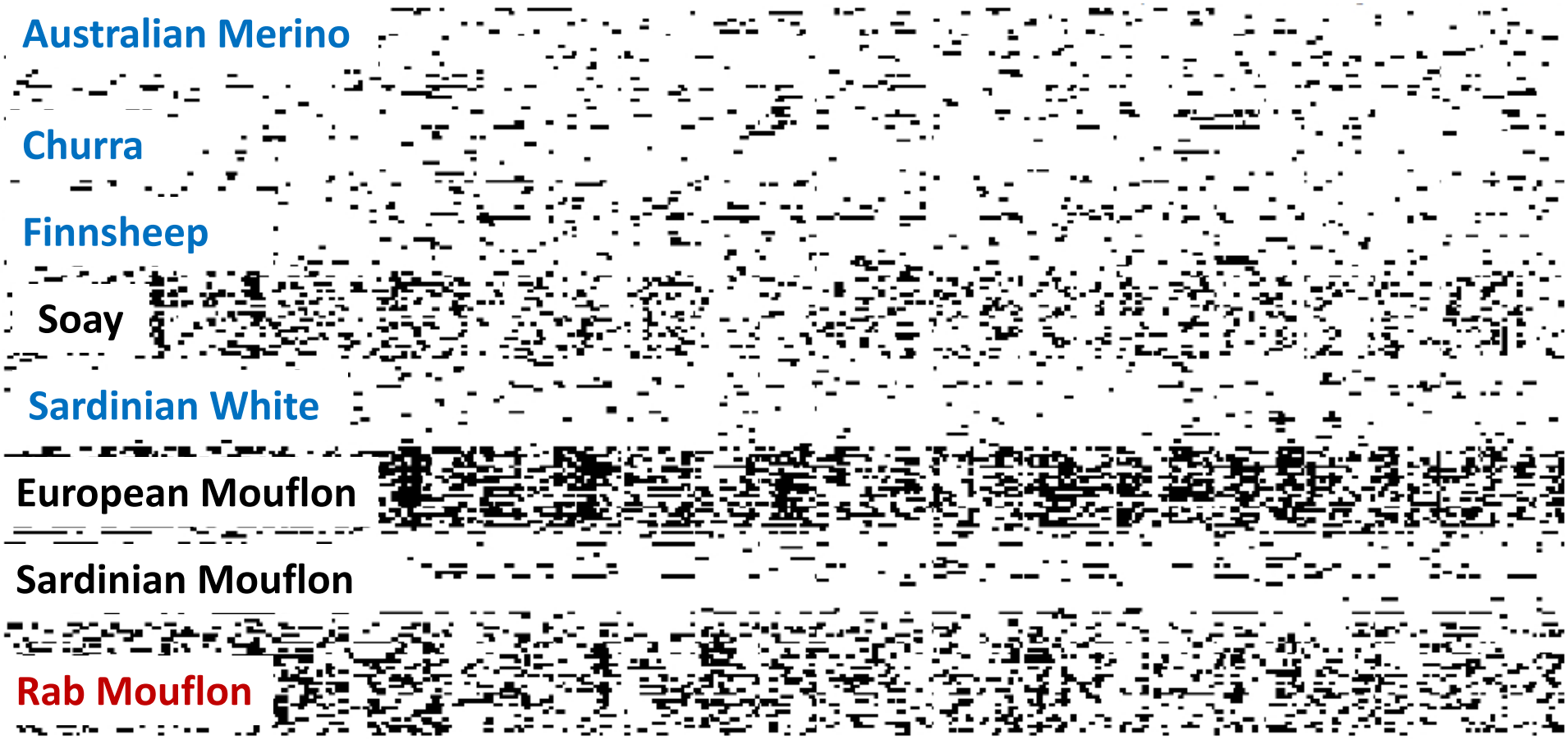
- Charlier et al., 2008; Drogemuller et al., 2011



Results – Genomic inbreeding level

	<12.50G	<6.25G	<3.13G	6.25–12.50G
Population	**$F_{ROH>4Mb}$**	**$F_{ROH>8Mb}$**	**$F_{ROH>16Mb}$**	**$F_{ROH4-8Mb}$**
EU mouflon	**0.318**	**0.235**	**0.137**	0.083
Rab mouflon	0.205	0.120	0.050	**0.086**
Soay	0.126	0.056	0.017	0.071
Sardinia mouflon	0.073	0.062	0.046	0.011
Finnsheep	0.053	0.034	0.016	0.019
Australian Merino	0.052	0.033	0.016	0.019
Churra	0.043	0.030	0.017	0.012
Sardinian White	0.035	0.022	0.010	0.013

ROHoGram: >4 Mb, 26 autosomal chromosomes



Results – inbreeding effective population size

$$Ne_{FROH>LMb} = \frac{\#\ \text{generations as f(LROH)}}{2\sum_{gt0}^{gtb}\Delta F}$$

$F_{ROH>8Mb}$ = 0.120;

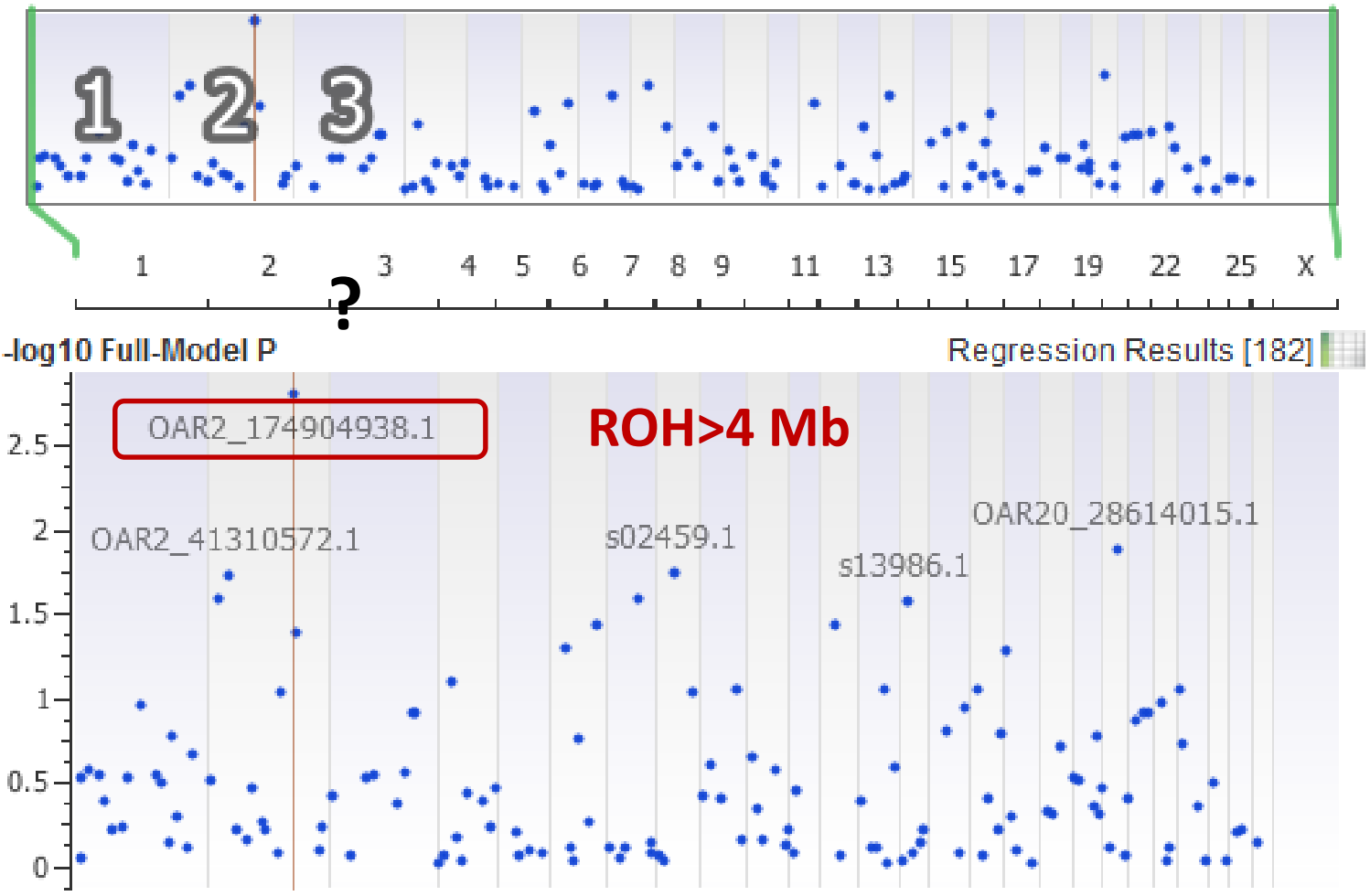
ΔF_{ROH} = 0.12/6.25 = 0.0192

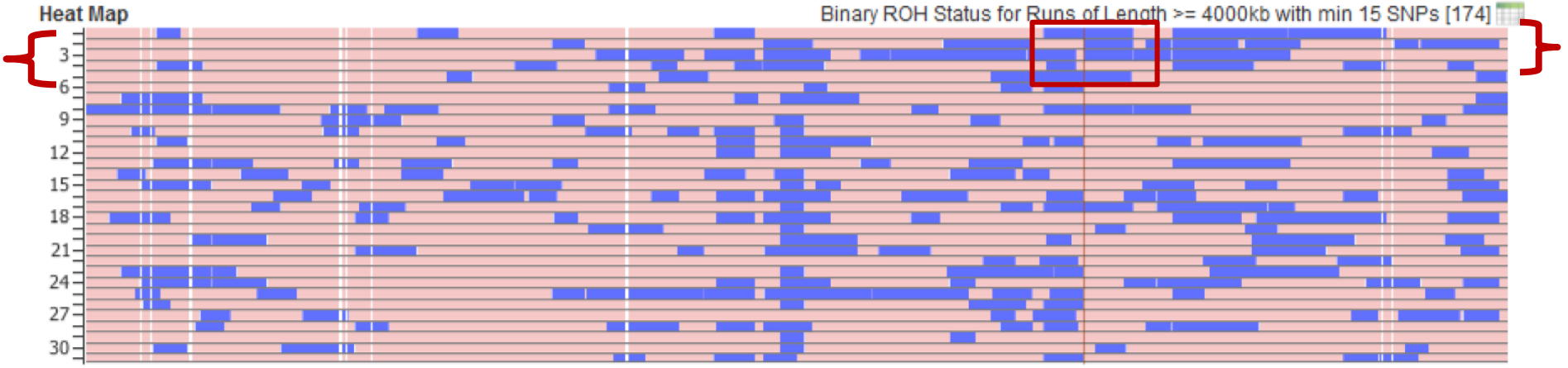
=> NeF_{ROH} = 1/(2ΔF_{ROH}) = **26.0**

Ne_X= $4N_{eM}N_{eF}/(N_{eM}+N_{eF})$ =(4 8 33)/(8+33) = **25.8**

Results – ticks paralysis deaths autozygosity mapping

5 tick paralysis dead versus 27 healthy mouflons





Tick paralysis deaths: no simple cause – lethal recessive homozygosity

Conclusions

1. High inbreeding estimated
2. High inbreeding effective population size estimated
3. Most likely recessive single gene lethality – not a cause of ticks paralysis lethality (more complex inheritance?)

Population refreshment needed/suggested!

This year new 33 animals (20 F + 13 M) were bought at XCell farm in Slovakia!

Genotyping of introduced mouflons (Illumina BeadChip) will enable evaluation of the introgression (refreshments) effects

Thank you for your attention !