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SMALL RUMINANTS VERSUS ENDOGENOUS RETROVIRUSES: AN EVOLUTIVE SHOWDOWN STILL IN PROGRESS IN THE DOMESTIC GOAT GENOME

Marie Vernet^{1,2}, Caroline Leroux¹, Vincent Navratil³, Thomas Faraut⁴, Jocelyn Turpin^{1*}, Emmanuelle Lerat^{2*}

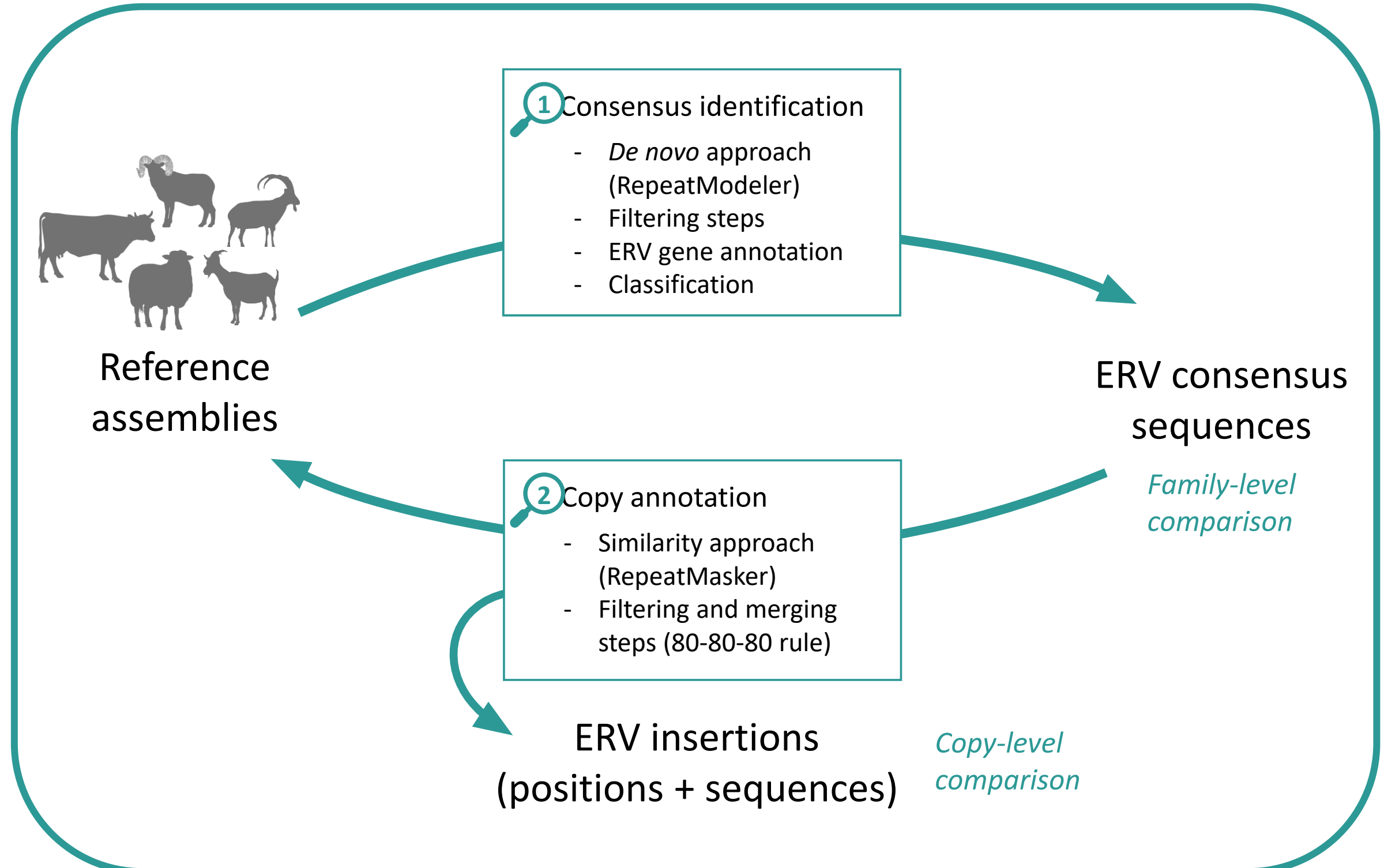
1- UMR754 INRAE-Lyon 1 Université-EPHE, "Viral Infections and Comparative Pathology", Lyon, France
 2- UMR5558 Lyon1 Université-CNRS-VetAgroSup, "Biometrics and Evolutionary Biology", Villeurbanne, France
 3- Bioinformatics Rhône Alpes Pole – Biological System Modeling and Analysis Platform, Villeurbanne, France
 4- UMR1388 INRAE-Toulouse INP-ENVT, "Genetics, Physiology and Breeding systems", Castanet-Tolosan, France
 *Equal contribution

INTRODUCTION

- Endogenous retroviruses (ERVs) are remnants of ancient retroviral germline infections that have become permanently integrated into host genomes. ERVs are transmitted vertically and behave as LTR-retrotransposons.
- In small ruminants (sheep and goats), the exogenous JSRV (Jaagsiekte Sheep RetroVirus) and ENTV (Enzootic Nasal Tumor Virus) causing respiratory cancers are closely related to an ERV family previously designated as enJSRV (Leroux *et al.* 2008, DeMartini *et al.* 2003).
- Previous studies showed that some enJSRV insertions are providing to the host a potential protection against exogenous retrovirus infections *in vitro* (Mura *et al.* 2004), are playing a crucial role in sheep reproductive physiology (Dunlap *et al.* 2006) and are polymorphic in sheep population (Cumer *et al.* 2019).
- In cattle, an ERV family as been described as active with insertions causing cholesterol deficiencies (Tang *et al.* 2024).
- Apart from these specific families, the global ERV landscape in ruminants remains unclear, and the function of the other families are largely unknown.

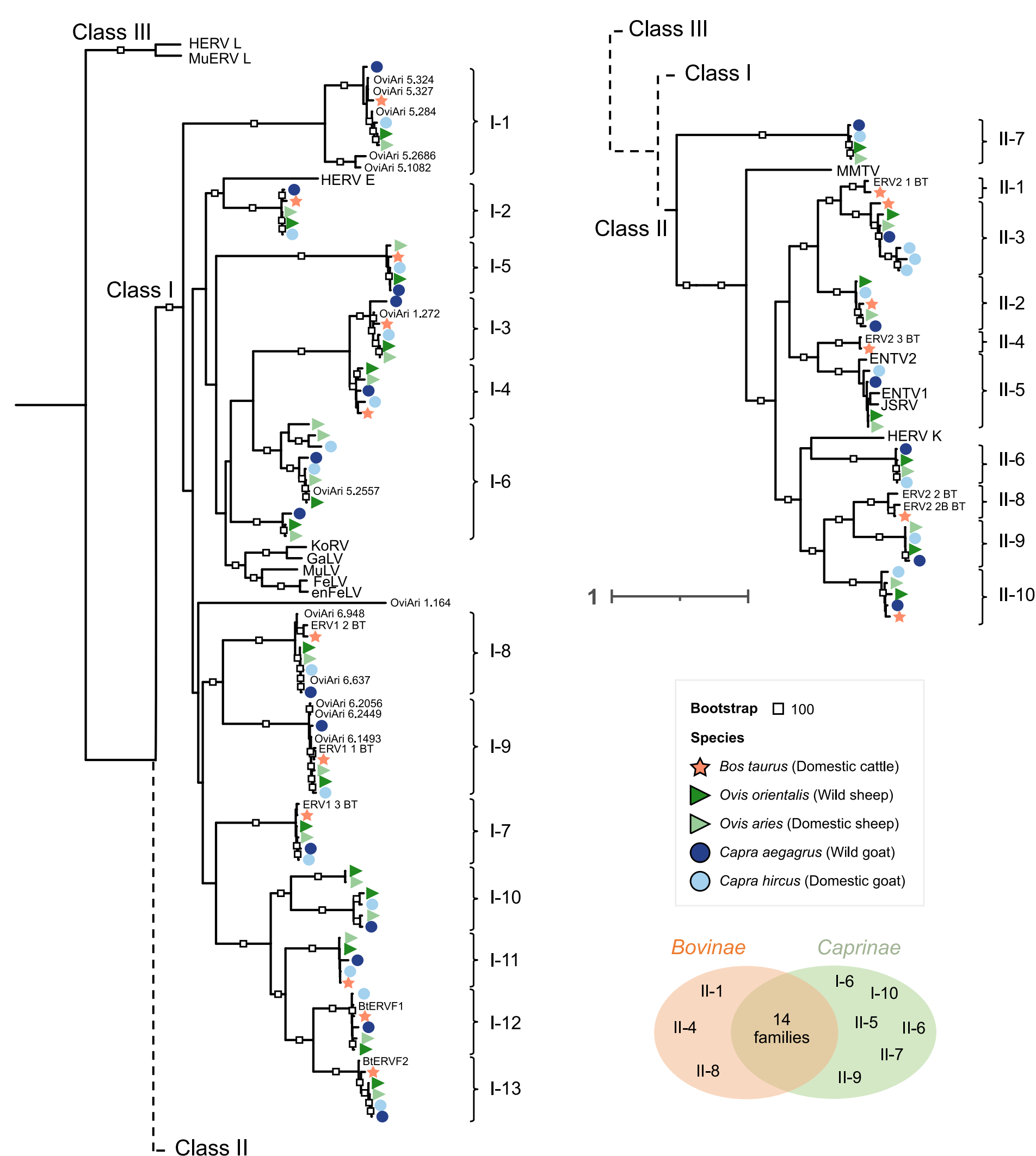
WHAT IS THE ERV LANDSCAPE IN RUMINANT GENOMES ?

METHODS



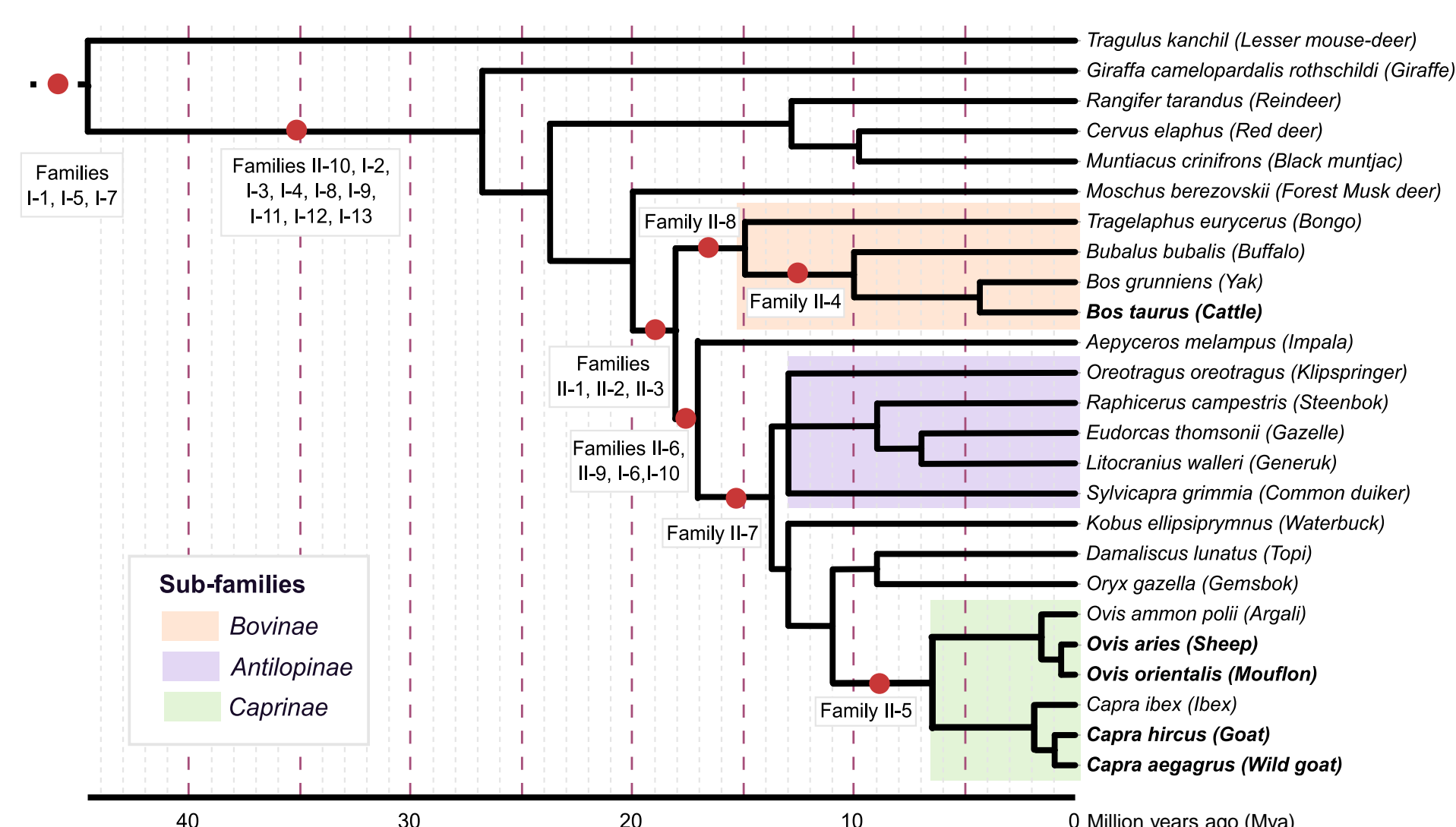
RESULTS

1 Sheep and goats share the same ERV families



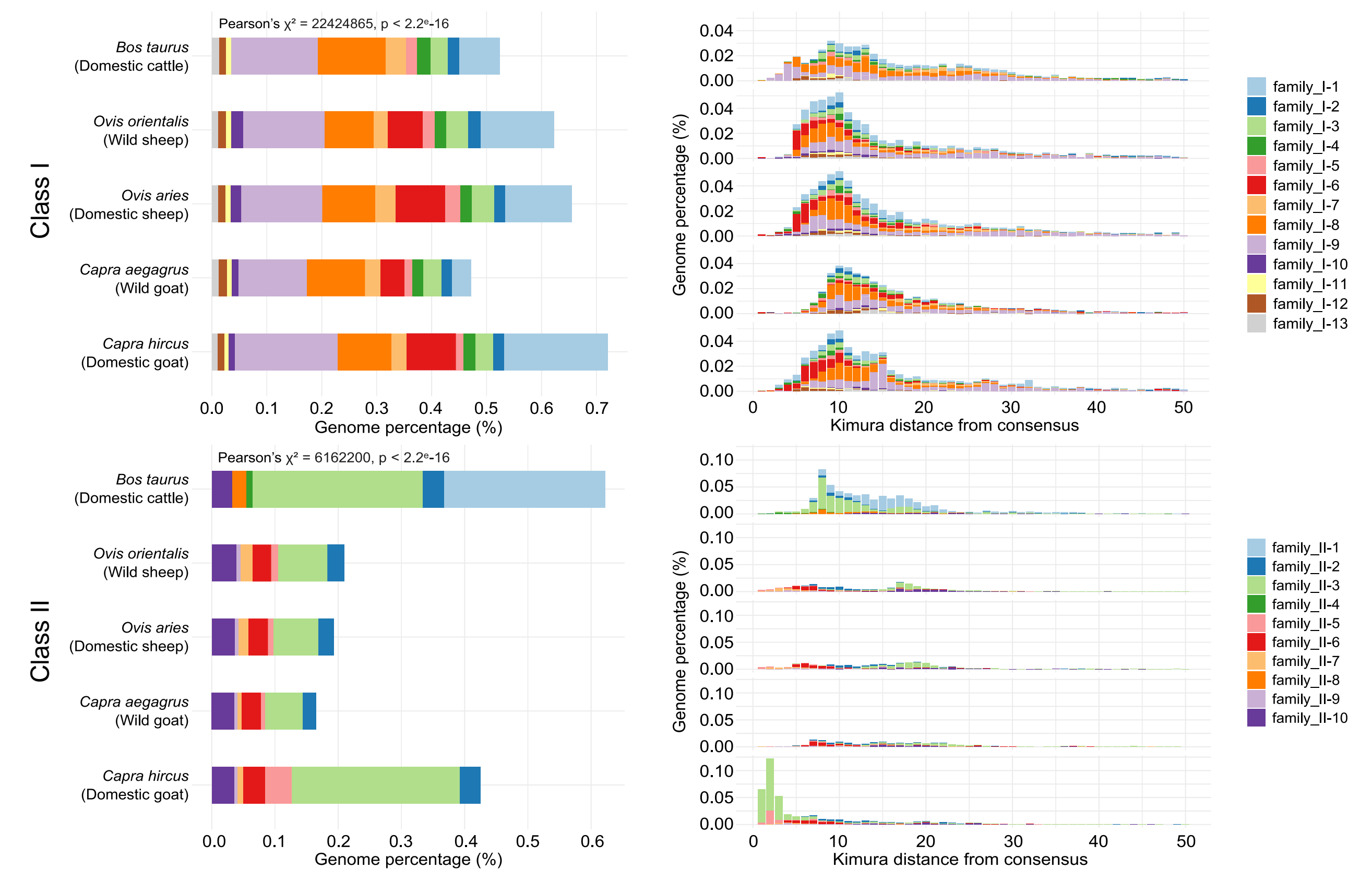
- 23 class I and II ERV families were characterized
- Bovinae and Caprinae reference families in Repbase were retrieved and we additionally discovered 9 and 15 new families in cattle and small ruminants respectively
- 3 ERV families were identified only in cattle, 6 only in small ruminants and 14 in common suggesting different integration events

2 Multiple integration events of ERV families across evolution

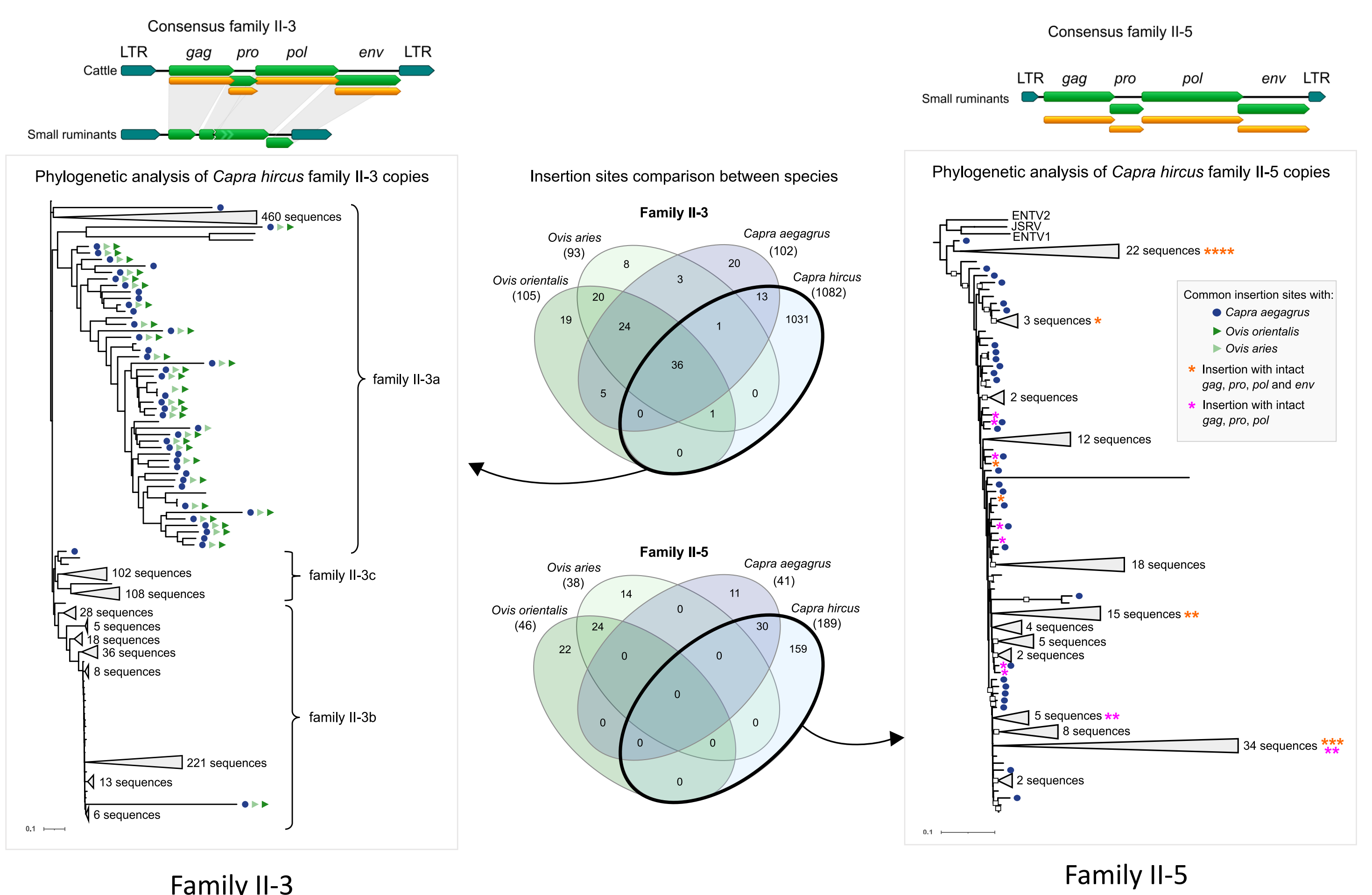


- The oldest ruminant ERV families integrated more than 40 Mya
- Family II-5 is the youngest and appeared between 6-11 Mya in Caprinae Family II-1 is maintained in Bovinae but degrading in Antilopinae and Caprinae species

3 Differential ERV insertion dynamics between ruminant species



- Between 18,000 to 25,000 copies were annotated as ERV → 0.65 to 1.15% of ruminant genomes are ERVs
- Different proportions are observed according to ERV families and classes
- Cattle has a different ERV landscape compared to small ruminants and wild and domestic sheep showed similar profiles
- Domestic goat genome contains two over-represented families with very conserved copies (II-3 and II-5)



- No copies identified with complete coding capacities in small ruminants
- 12 insertions identified with complete coding capacities in Capra hircus
- Shared insertion sites between Capra and Ovis mostly belong the subfamily II-3a → Ongoing transposition by trans-complementation ?
- Common insertion sites were found only within Capra or Ovis → Ongoing transposition or reinfection activity

CONCLUSIONS

- We propose the first high-resolution comprehensive repertoire of ERVs in cattle and small ruminant genomes
- The appearance and evolutionary dynamics of ERVs are different according to the ERV family and the ruminant species
- Most of the ruminant ERV insertions are silent but remain evidence of past infections and retrotransposon activity
- The identification of highly conserved and polymorphic copies from II-3 and II-5 families strongly suggest ongoing ERV activity in small ruminants especially in domestic goat where different mechanisms seem to be involved

Acknowledgments

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