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#### ► To cite this version:

Riocreux-Verney Benjamin, Jocelyn Turpin, Rémi Diesler, Barbara Gineys, Christine Dolmazon, et al.. Diversity of b-retroviruses causing respiratory cancers in small ruminants. XXVèmes Journées Francophones de Virologie, Apr 2023, PARIS, France. hal-04727924

#### HAL Id: hal-04727924 https://hal.inrae.fr/hal-04727924v1

Submitted on 9 Oct 2024

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# Diversity of $\beta$ -retroviruses causing respiratory cancers in small ruminants

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## **CONTEXT AND OBJECTIVES**

Oncogenic β-retroviruses are responsible for respiratory cancers in small ruminants. While JSRV (Jaagsiekte Sheep RetroVirus) induces lung cancers in sheep, ENTV (Enzootic Nasal Tumor Virus) induces nasal tumors in sheep for (ENTV-1) and goats for (ENTV-2). The envelop (Env) glycoprotein, especially the intracytoplasmic tail of the transmembrane region, carries the transforming capacity and is referred as the main oncogenic determinant

- Multiples copies of highly related β-endogenous retroviruses (β-ERVs) resulting from ancestral infections of germinal cells during evolution are present in the small ruminant genomes
- ☑ JSRV and ENTV are endemic in many countries. As we observe in France, the clinical expression varies in terms of severity and morbidity/mortality rates in flocks, from isolated/ sporadic cases to cancer outbreaks

## OBJECTIVES

What is the diversity of retroviruses circulating in France and how does their diversity relate to the clinical expression?

We focused on the genetic characterization of the oncogenic  $\beta$  retroviruses (30 JSRV, 3 ENTV-1 and 21 ENTV-2) from various regions of France (31 flocks), and on their sequence analysis to identify specific strains associated with increased clinical expression in some flocks.

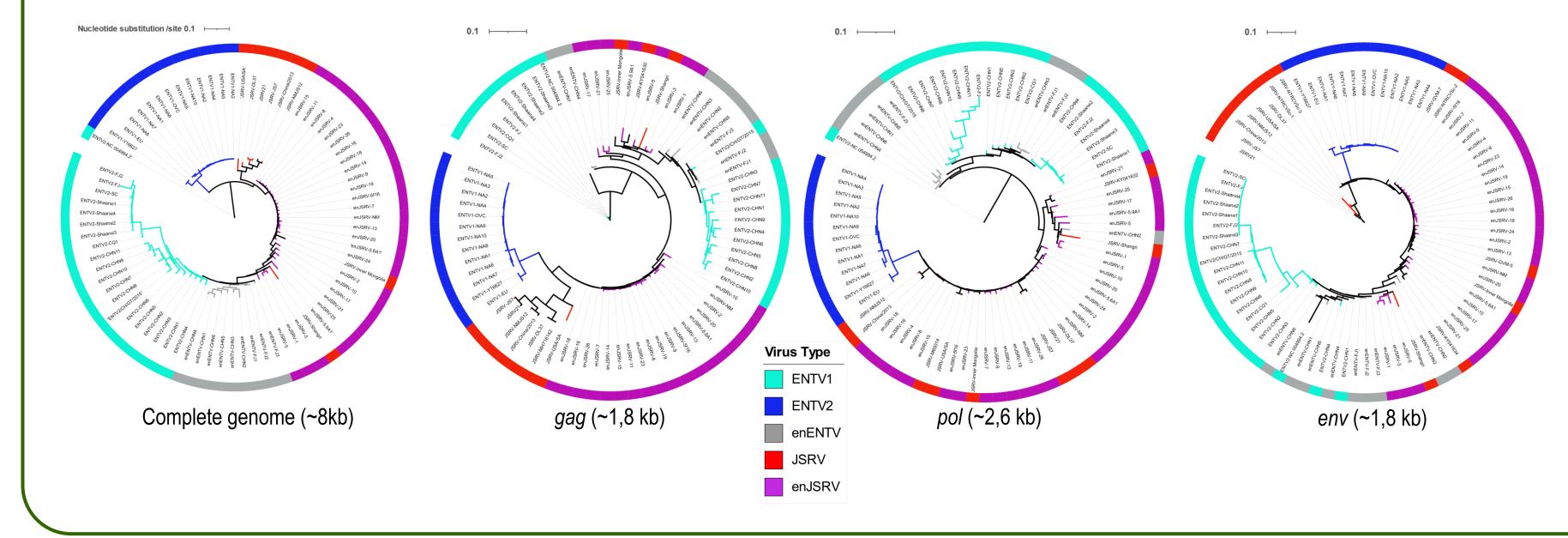
### METHODS AND RESULTS

Geographical localization of isolated strains

### (1) EXOGENOUS $\beta$ -RETROVIRUS ARE CLOSELY RELATED THEIR ENDOGENOUS COUNTERPARTS

Phylogenetic reconstruction based on JSRV, ENTV-1, ENTV-2 and small ruminant ERV (published in public databases)

## Identity plot (nt) along the β-retrovirus genome against a consensus sequence of related ERVs



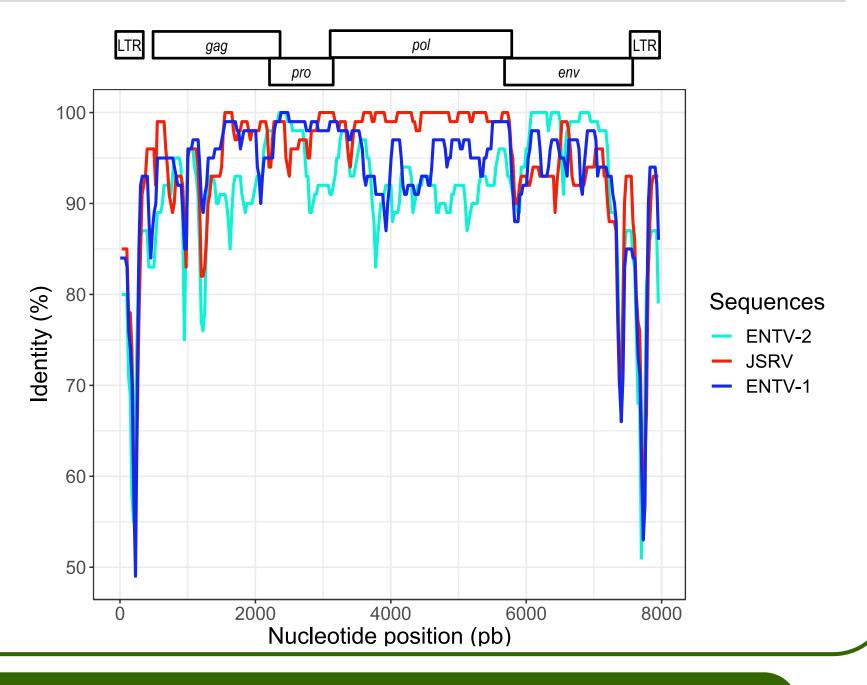
Compared to ERVs, only short and localized regions are specific of the exogenous β-retroviruses located in the terminal part of *env* and the U3 region of both LTRs

ENTV-2

ENTV-1

JSRV

 We have developed a highly specific strategy to selectively amplified the exogenous ENTV and JSRV genomes

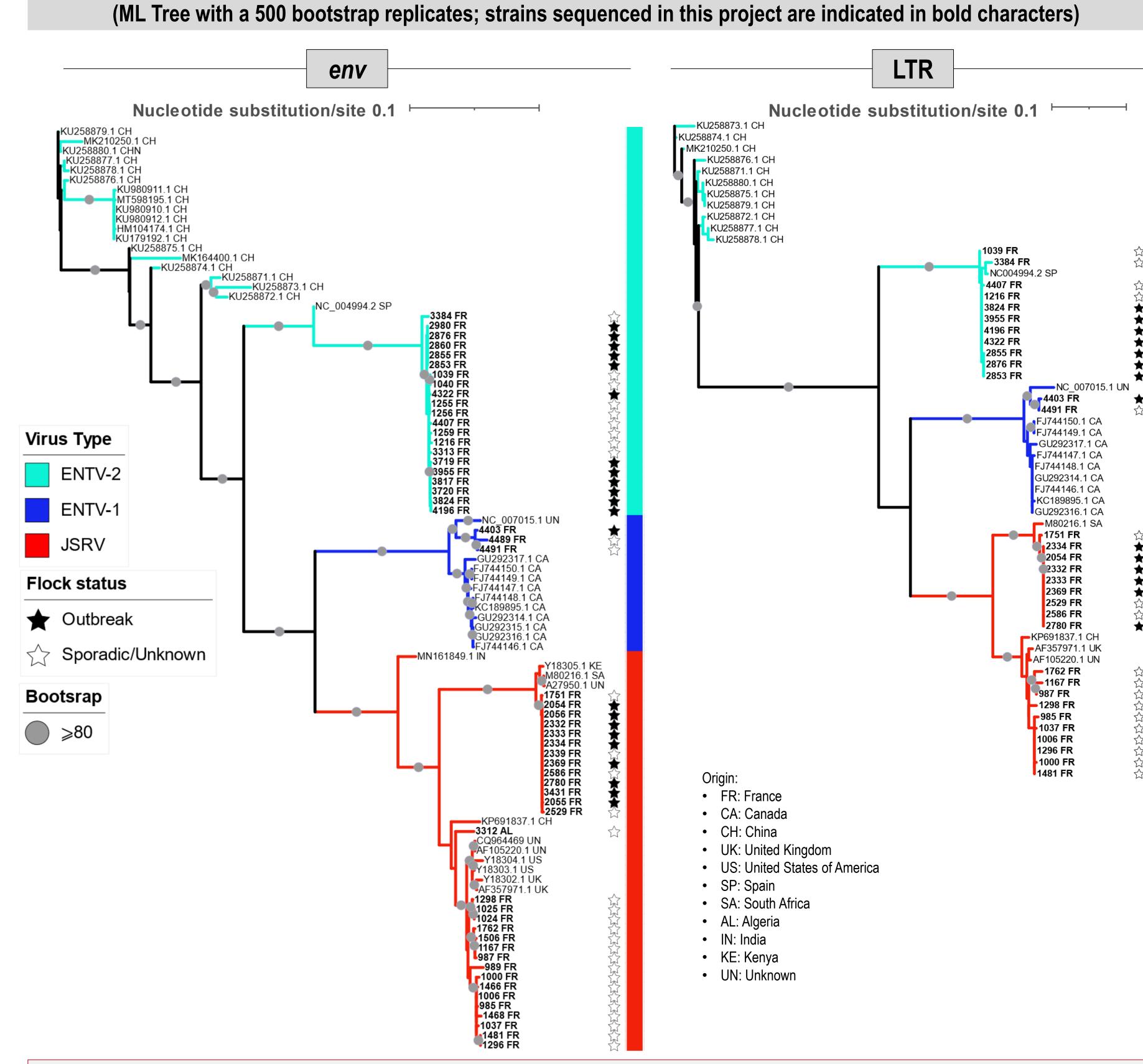


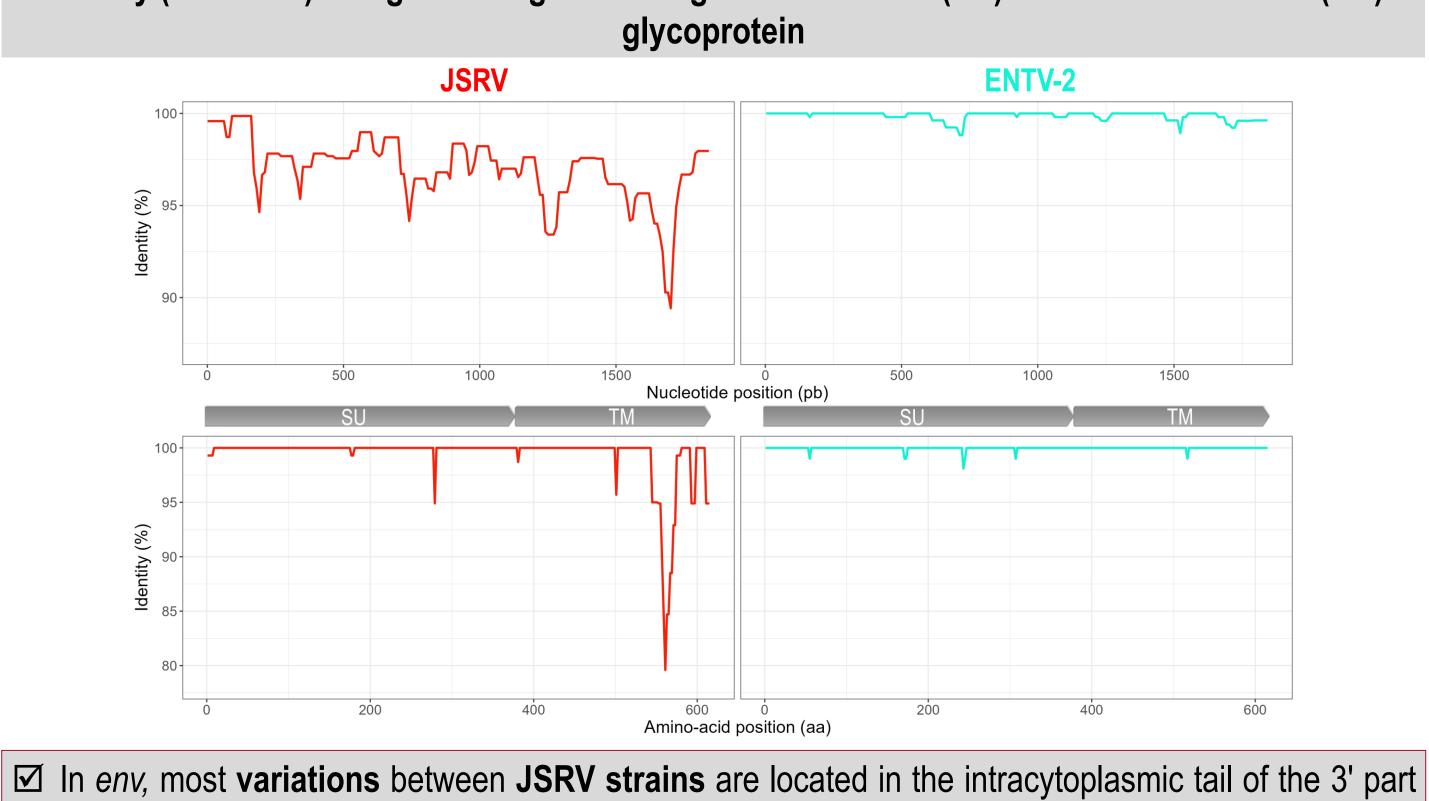
#### 2 DIVERSITY OF β-RETROVIRUSES CIRCULATING IN FRANCE

Phylogenetic reconstructions based on French JSRVs and ENTVs in the env coding and LTR non-coding regions

#### **3 IDENTIFICATION OF GENETIC SIGNATURES POTENTIALLY ASSOCIATED** WITH DISEASE EXPRESSION IN FLOCKS

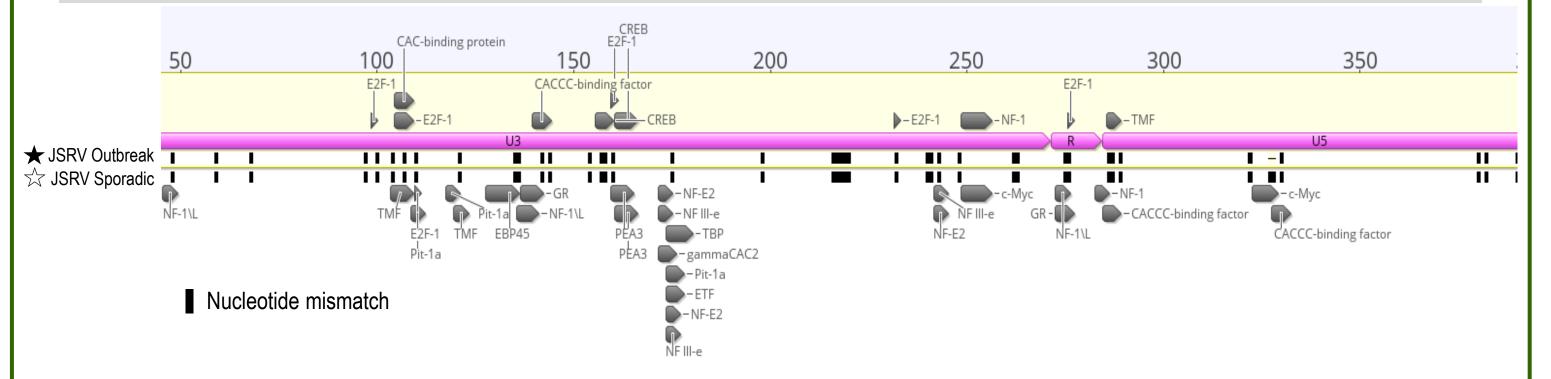
Identity (nt and aa) along the env gene coding for the Surface (SU) and Transmembrane (TM)





of the transmembrane domain (TM), implicated in the transformation process

# Differences in transcription factor binding-sites can be identified in JSRV LTRs, accordingly to the severity of the disease expression in a given flock (predicted by *tfscan*)



Based on their sequences in the LTR and *env* regions, we report on :

- ☑ the first genetic characterization of JSRV, ENTV-1 and ENTV-2 strains circulating in France
- ✓ the relative stability of JSRVs and ENTVs, sampled from geopgraphically distinct French areas with ~95% of nt similarity
- the stability of the circulating strain for a given ovine or caprine flock with over 98% similarity in nt sequences
  the circulation of two genetically distinct groups of JSRV, one being often associated to more severe clinical expression (in terms of morbidity/ mortality rates)

Identification of distinct transcription factor binding-sites between strains isolated from outbreaks and sporadic events

#### **CONCLUSIONS/ PERSPECTIVES**

- $\square$  First report on French strains of oncogenic  $\beta$ -retroviruses responsible for cancers in sheep and goats
- ☑ In France, low sequence diversity of ENTV while JSRV strains are more diverse
- ✓ Association of JSRV-genetic signatures with the severity of disease
- Perspectives : Test of the impact of the genetic signatures on the oncogenic properties of JSRV





Acknowledgments: The project is financed by INRAE and ANR. RVB is supported by a PhD grant of VetAgro Sup

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