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Title: Application of high-throughput sequencing to whole rabies viral genome characterisation and its use for phylogenetic re-evaluation of a raccoon strain incursion into the province of Ontario



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Application of high-throughput sequencing to whole rabies viral genome characterisation and its use for phylogenetic re-evaluation of a raccoon strain incursion into the province of Ontario

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Highlights of manuscript by Nadin-Davis et al.

- A protocol for high throughput whole genome sequencing (WGS) of raccoon rabies virus
- WGS vastly improves phylogenetic resolution of virus isolates
- New insights from a re-examination of the spread of raccoon rabies in Ontario
- Methodology has broad application to many rabies virus variants

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