MINTIE is a catch-all cryptic variant finder for cancer RNA-seq data

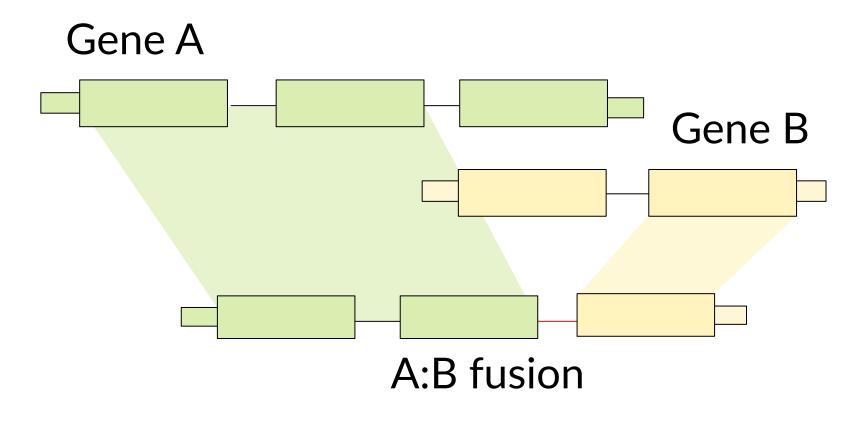
Marek Cmero, Breon Schmidt, Ian Majewski, Paul Ekert, Alicia Oshlack, Nadia Davidson

Motivation

- Cryptic variants are observed in cancers, and can create gain-of-function driver variants or disrupt tumour suppressor genes.
- Cryptic variants are difficult to detect in RNA-seq with current tools.

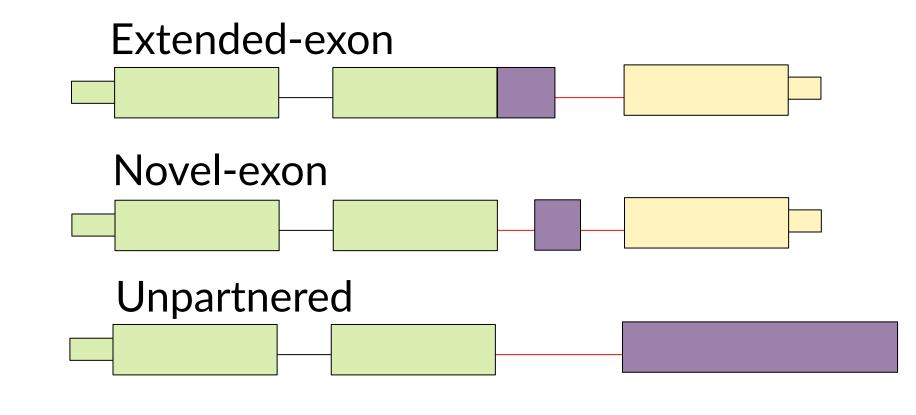
What are cryptic variants?

Let's consider the canonical fusion as a single gene product formed by two genes joined at an exon-exon boundary:



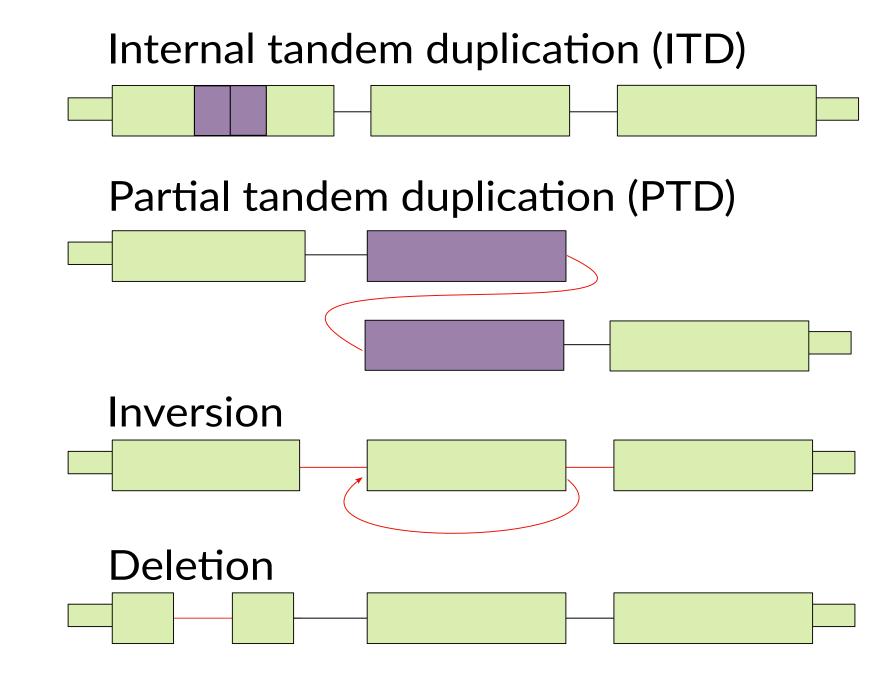
Fusion finders use very strict filters and do not consider non-standard fusions, such as:

Cryptic fusions

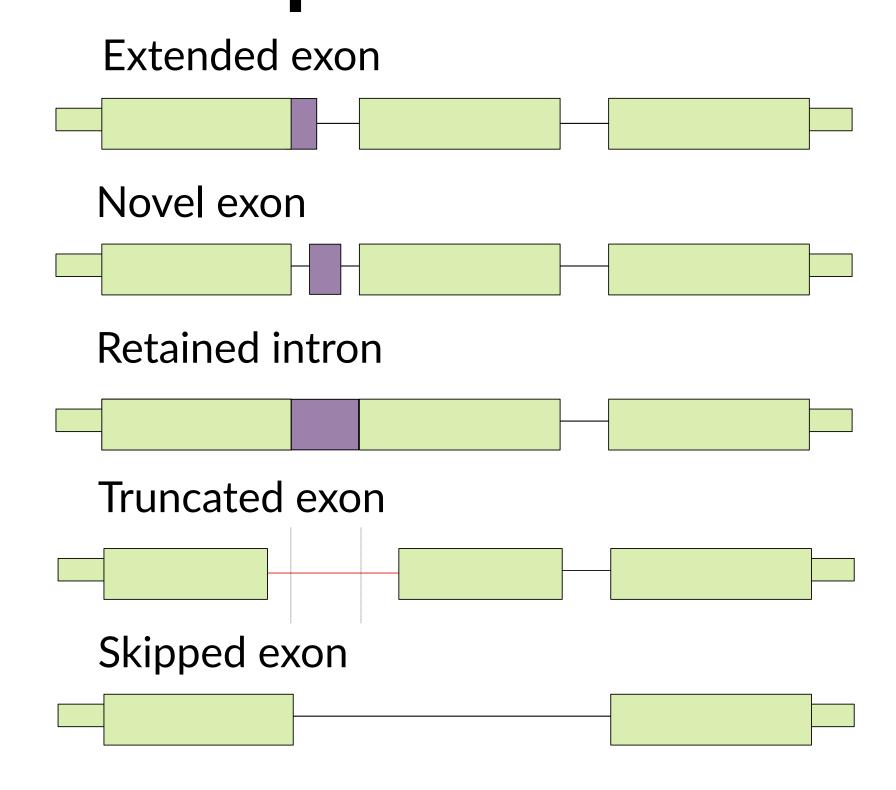


We also consider **cryptic variants** in singlegenes:

Transcribed structural variants

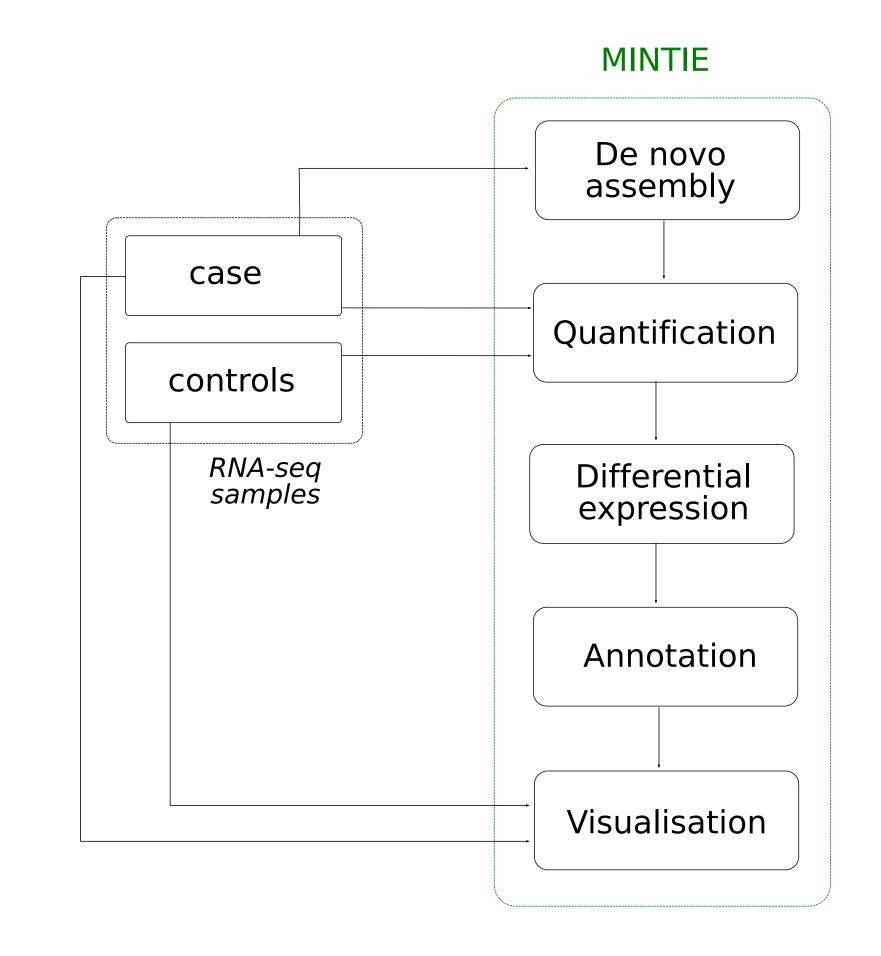


Novel splice variants



The MINTIE method

- 1. De novo assemble all transcripts in the case (cancer) sample.
- 2. Quantify all assembled transcripts in cancer and a set of controls (may be other cancer samples).
- 3. Perform differential expression on assembled transcripts (case vs. controls).
- 4. Align significant transcripts and identify novel regions.
- 5. Output IGV tracks for visualisation.



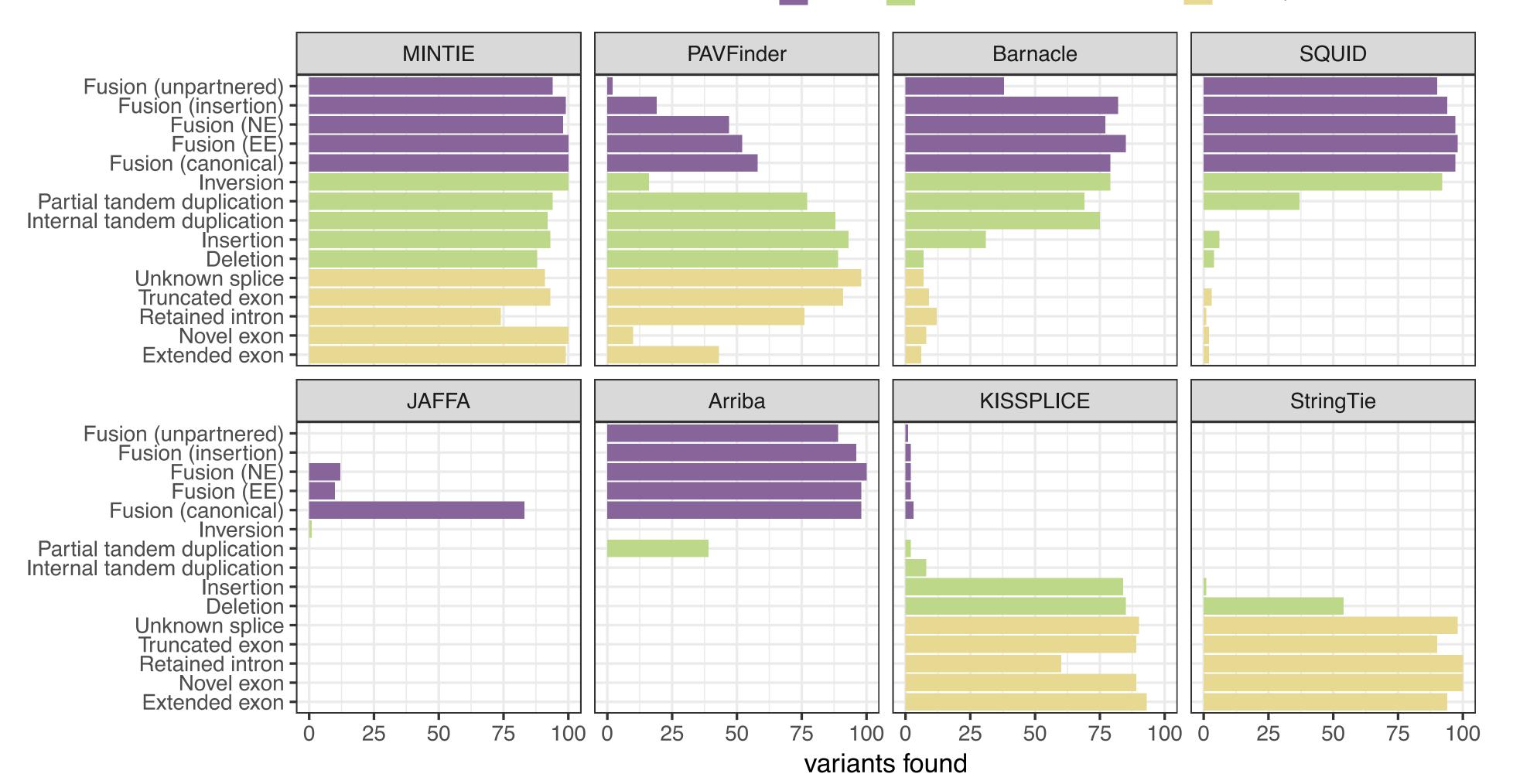
Simulation results

- We simulated 1500 variants across 15 types.
- MINTIE successfully found >93% of variants.
- We ran these simulations on 7 other tools and found that MINTIE could find and annotate more variants than any other method.



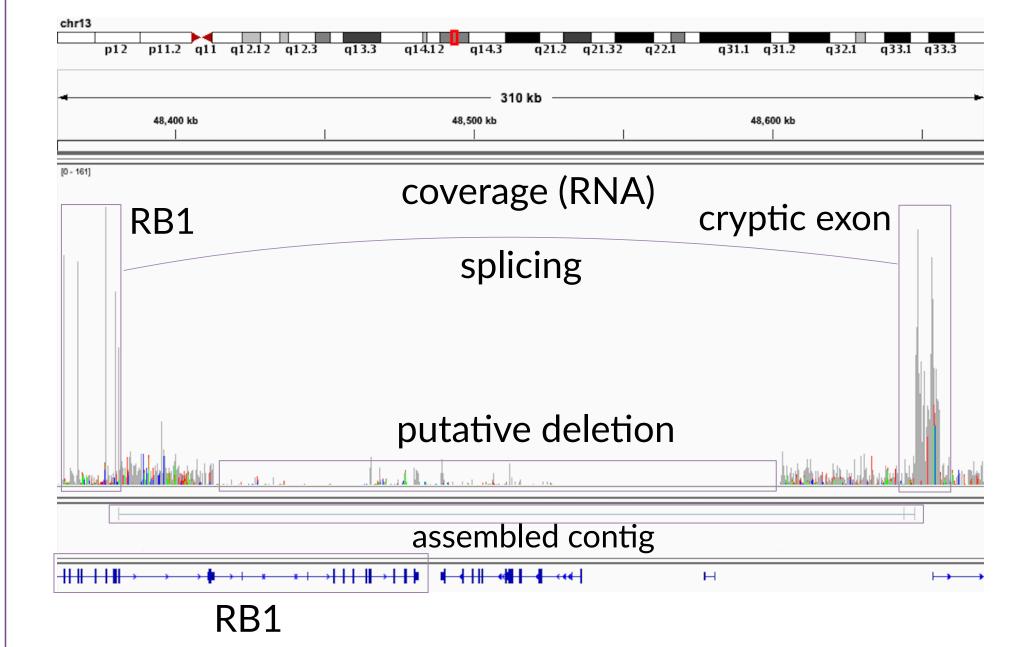
Novel splice variant

Transcribed structural variant

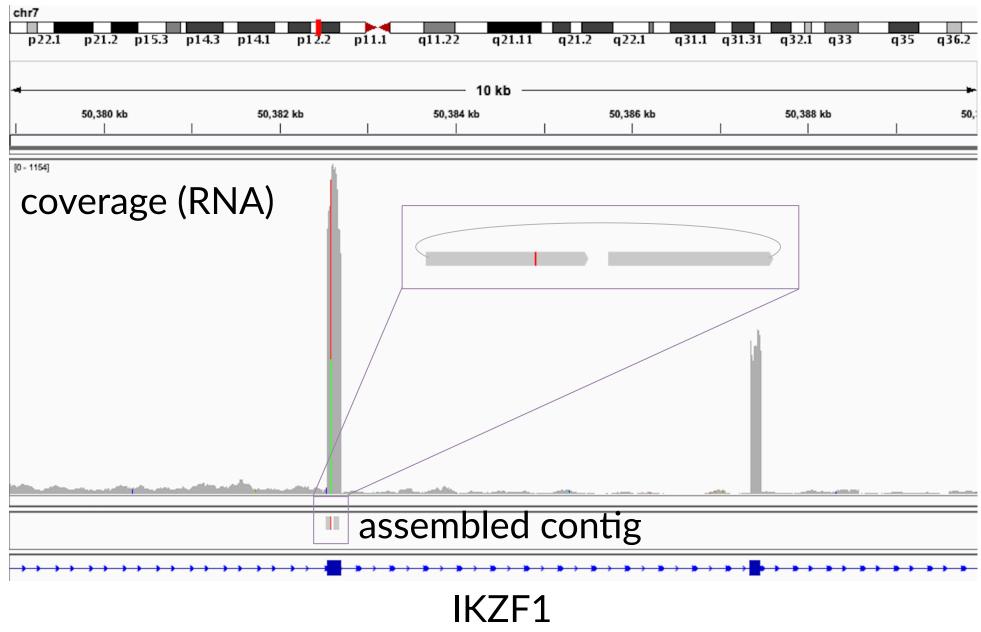


Candidate cryptic variants in paediatric leukaemia

We ran MINTIE on 97 B-ALLs from the Royal Children's Hospital, and found several clinically relevant cryptic variants, including the following in two patients with high risk disease and no previously detected relevant alterations.



Novel downstream exon reveals likely loss-offunction deletion in tumour suppressor RB1.



PTD found in IKZF1, known gene associated with B-cell acute lymphoblastic leukaemia and regulator of lymphocyte differentiation.



