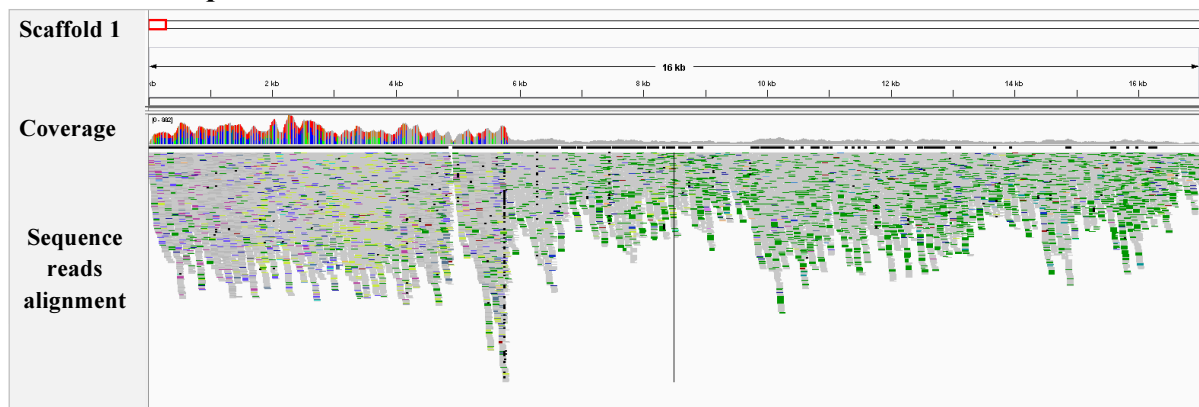


Supplementary File 2

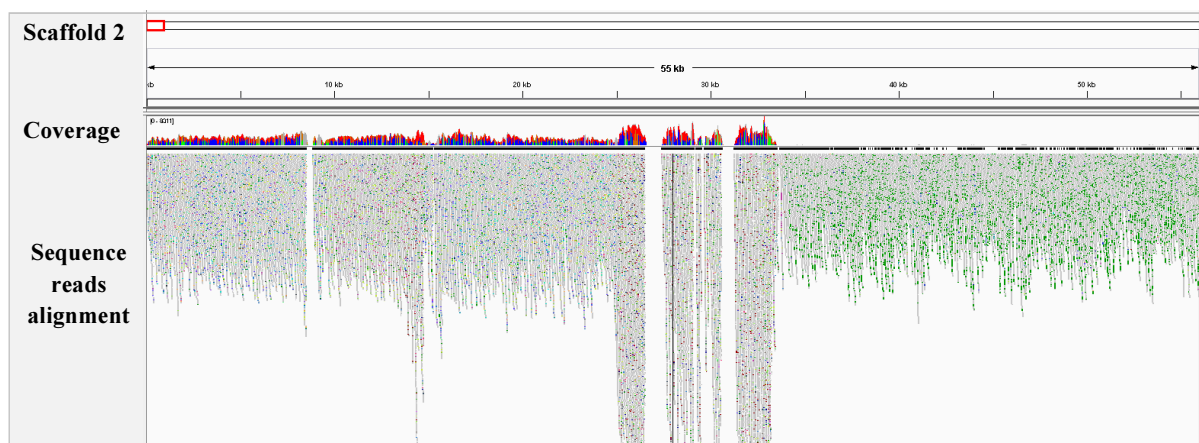
Examples of the sequence depth and number of mismatches across repetitive regions in *Knoxdaviesia capensis* and *K. proteae*.

Figures depict screenshots taken from the Integrative Genomics Viewer 2.3.97 (Robinson *et al.* 2011, Thorvaldsdóttir *et al.* 2013), showing trimmed raw sequence reads aligned to a portion of the *K. capensis* or *K. proteae* genome with bowtie2 version 2.2.6 (Langmead and Salzberg 2012). The coverage track displays a bar plot of the sequence depth at each nucleotide position. When more than 20% of aligned reads differ from the reference sequence at a certain position, the typically grey bar is coloured in proportion to the read count (A = green, C = blue, G = yellow, T= red). See the IGV user guide at <http://software.broadinstitute.org/software/igv/UserGuide> for more information.

Knoxdaviesia capensis:

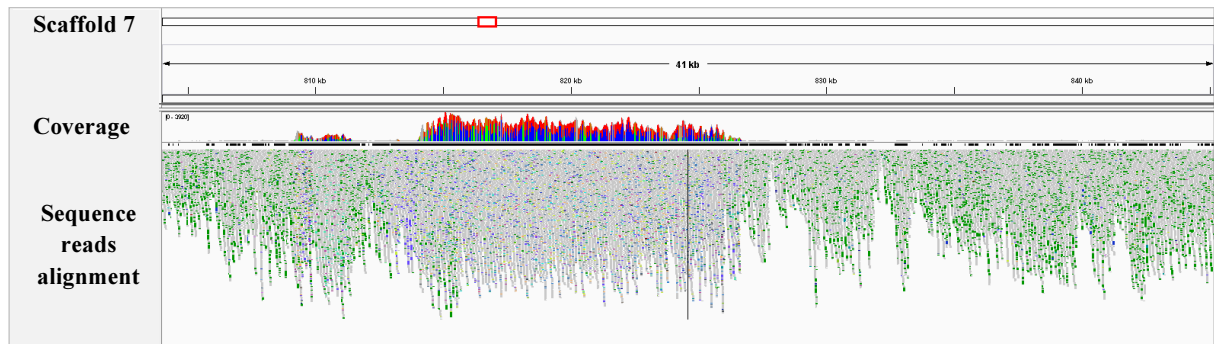


Scaffold 1, base position 1 – 17,001. The first 5,000 bases comprise a Class I LTR (long terminal repeat) retrotransposon.



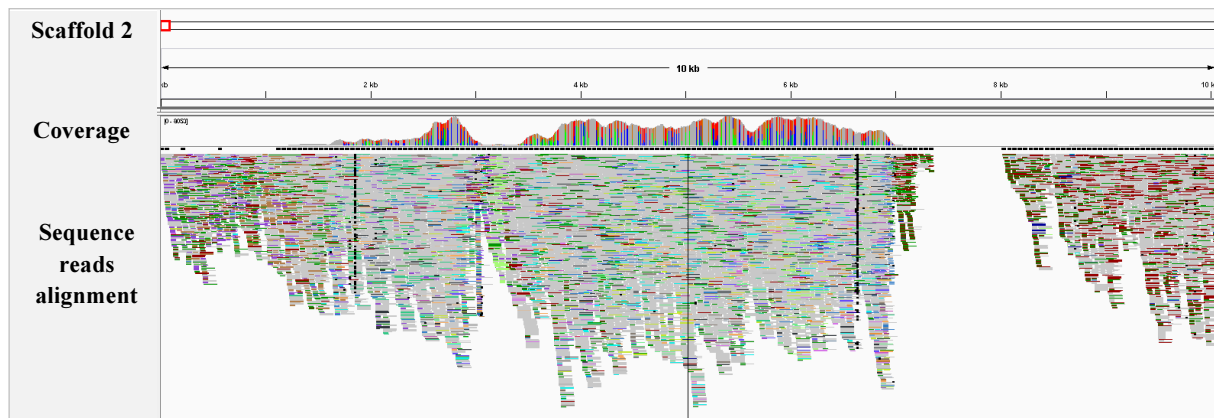
Scaffold 2, base position 1-56,015. The first 34,000 bases comprise two Class I LTR retrotransposons.

Aylward *et al.* Genomic overview of closely related fungi with different *Protea* host ranges

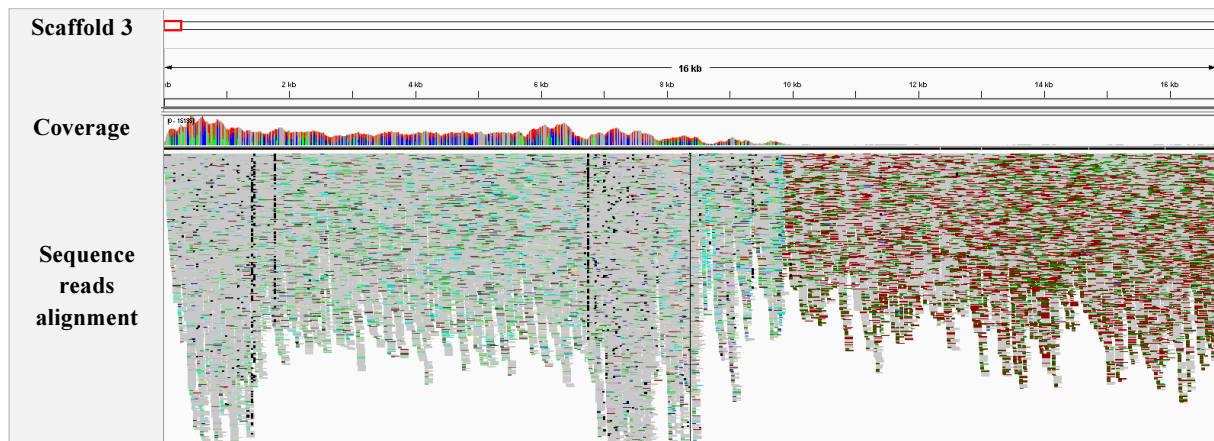


Scaffold 7, base position 803,980-845,202. Positions 813,134-814,024 and 823,860-826,684 each contain a Class I LTR retrotransposon.

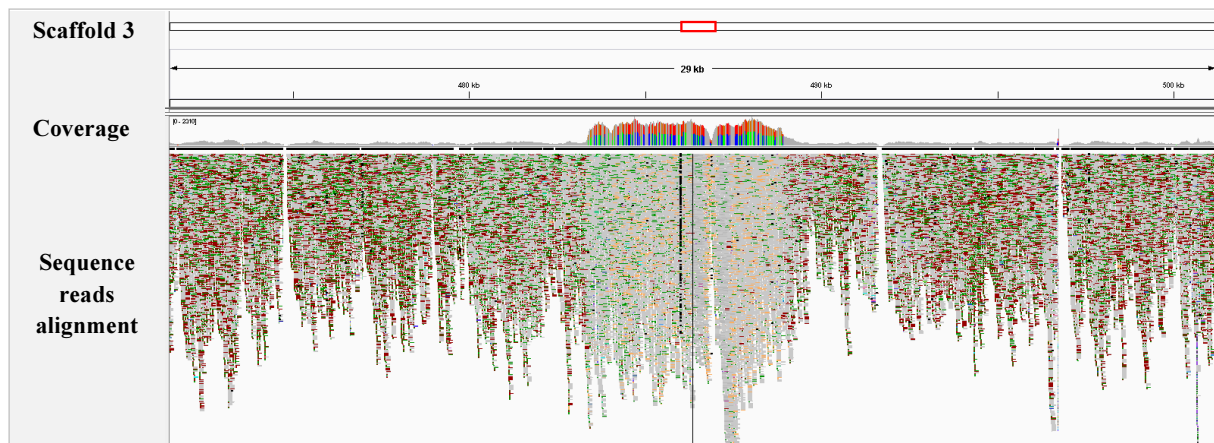
***Knoxdaviesia proteae*:**



Scaffold 2, base position 1-10,053. Position 1,626-6,998 comprises a Class I LTR retrotransposon.



Scaffold 3, base position 1-16,761. The first 8 kb comprises a minisatellite (low complexity) repeat, followed by a 1.5 kb Class I LTR retrotransposon.



Scaffold 4, base position 471,483-501,229. Position 483,331-488,976 comprises a Class I LTR retrotransposon.

REFERENCES

- Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. *Nat Methods* 2012;**9**: 357-9.
- Robinson JT, Thorvaldsdóttir H, Winckler W *et al.* Integrative genomics viewer. *Nat Biotechnol* 2011;**29**: 24-6.
- Thorvaldsdóttir H, Robinson JT, Mesirov JP. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Brief Bioinform* 2013;**14**: 178-92.