### Supporting information Legends G3

Figure S1.html

#### APSI\_primary and secondary\_v1 genome and transcriptome mapping to the NCBI fungal database and visualised with Krona/2.7. Available at <https://github.com/peritob/Myrtle-rust-genome-assembly>.

Figure S2.jpg

#### The GC content profile as identified by OcculterCut. of the *M. brunnea*, *R. commune*, *A.psidii*, *P. graminis* f. sp. *tritici*, *P. triticina*, *P. coronata* f. sp. *avenae*, *P. sorghi*, *P. striifomis* f. sp. *tritici*, *C.quercuum* f. sp. *fusiforme* and *M. larici-populina* genome. AT-rich isochores or regions can be observed in *M.brunnea*, *R.commune* and *A. psidii*, but peaks of the first two fungal species are more separated than that of *A. psidii*. Also, compared to other fungi here, *A. psidii* has the overall higher AT-content. AT-rich isochores cannot be detected in all other seven Pucciniomycetes.

Table S1.xlsx

#### (A) Annotation of rust genomes with 21 most abundant TE families using RepeatMasker. Initial annotation in the *A. psidii* genome was done using the REPET pipeline and might vary slightly from this annotation. The top 24 TE families were identified by deTEnovo from REPET. The top 24 repeats were identified previously and included in Repbase. (B) 5mC DNA MTases and 6mA DNA MTases annotations for *A. psidii*.

Table S2.xlsx

#### Pucciniales comparative statistics, including Pfam analysis of tree rust specific gene orthologs, and Interproscan (v.5) results from the primary and secondary annotated assemblies.

Table S3.docx

#### Hidden Markov model (HMMER) functional annotation of the predicted effectors within the primary assembly based on a reference proteome database (Potter et al. 2018). Listed are the 77 predicted effectors that had a functional annotation match.