

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Repeat types of the five *P.australis* genome assemblies.

File name: Supplementary Data 2

Description: Genome assembly and quality statistics for the three contig-level genome assemblies obtained from genome assembly of Illumina sequencing data.

File name: Supplementary Data 3

Description: Results from scaffolding of the draft assemblies to chromosome level when using the reference assembly as template.

File name: Supplementary Data 4

Description: Chromosome sizes (in base pairs, bp) of each of the different lineages obtained from scaffolding.

File name: Supplementary Data 5

Description: Gene ontology (GO) enrichment analysis of subgenome A and subgenome B syntelogs. The statistics shows the enrichment results in subgenome A.

File name: Supplementary Data 6

Description: Gene ontology (GO) enrichment analysis of tandemly duplicated genes in subgenomes A and B. The statistics shows the GO enrichment in subgenome A.

File name: Supplementary Data 7

Description: The species used in gene family evolutionary analyses. The table lists the genomes of closely related species of *P. australis*, their annotation qualities and references to the original publications.

File name: Supplementary Data 8

Description: Gene ontology (GO) enrichment analysis of the genes specific to the PaEU invasive lineage.

File name: Supplementary Data 9

Description: Gene ontology (GO) enrichment analysis of the tandemly duplicated genes in the PaEU invasive lineage.

File name: Supplementary Data 10

Description: Accession numbers of the RNAseq libraries used for genome annotation, the last two columns state whether B chromosome genes were expressed and the numbers of alternatively spliced isoforms detected in B chromosomes.