**Supplementary Figures**

**Figure S1.** Genome completeness assessment of oomycete genomes using BUSCO with the alveolata-stramenopile set (234 BUSCOs in total).

**Figure S2.** PITG\_00248 and PPTG\_10928 (labelled with asterisks) were identified as orthologous using Syntenolog-Search. **(A)** Screenshot of OGOB showing that PITG\_00248 and PPTG\_10928 are syntenically conserved. (**B**) BLAST search results of PPTG\_10928 against the OGOB databases. PPTG\_10928 has a significant (1e-125) but not reciprocal best hit to PITG\_00248. **(C)** MUSCLE multiple sequence alignment of PITG\_00248 and PPTG\_10928.

**Figure S3.** Synteny information hosted by OGOB can be used to identify rapidly evolving tandem duplications and tandem duplicates that have undergone chromosomal rearrangement. In OGOB tandem duplicates are indicated with a orange coloured “b” button (**A**) A cluster of 4 tandemly duplicated elicitin proteins that are syntenically conserved in *Ph. infestans*, *Ph. parasitica*, *Ph. capsici* and *Ph. sojae*. 2 of the *Ph. capsici* proteins (PHYCA\_529852 and PHYCA\_509798) did not meet our initial BLAST criteria, however, they are obvious tandem duplicates when syntenic conservation is considered. (**B)** A cluster of 5 tandemly duplicated sugar efflux transporters that are syntenically conserved in *Ph. infestans*, *Ph. parasitica*, *Ph. capsici*, *Ph. sojae* and *Ph. ramorum*. However, 2 members of the *Ph. sojae* tandem cluster have relocated to another area on the same scaffold.

**Figure S4.** Distribution of oomycete proteins lengths across phylostrata for individual species housed in OGOB.

**Supplementary Tables**

**STable 1.** List of all tandem duplicates located by OGOB. Clusters for each species are labelled as well as the cluster size and constituent genes

**STable 2.** Enrichment analysis of secreted proteins and GO terms in oomycete tandem clusters, the oomycete paranome and core oomycete pillars.

**STable 3.** Analysis of the number of core and syntenolog oomycete, Peronosporales, *Pythium*, *Albugo* and Saprolegniales pillars. For the Peronosporales analysis we excluded *Pp. vexans*, despite it being a member of the Peronosporales, it is thought to be an intermediate between *Phytophthora* and *Pythium* species in terms of its gene content and genome organisation.

**STable 4.** Pairwise microsyntenic analysis of oomycete species. Counts of the number of orthologs and syntenologs shared by each possible pair of 20 oomycete species is shown. Also shown is the proportion of orthologs that were identified as syntenologs as well as the proportion of total genes identified as syntenologs.