GenomeScope Profile len:1,023,540,636bp uniq:48.7% het:0.0584% kcov:17.5 err:0.165% dup:0.368% k:19 3.0e+07 observed full model unique sequence errors kmer-peaks 2.0e+07 Frequency 1.0e+07 0.0e+00 0 20 40 80 60 100 Coverage

Figure S1. Genome characteristics information of *G. elata* using GenomeScope.



**Figure S2.** Kimura distance-based copy divergence analysis of TEs in the Orchidaceae family genomes (*G. elata, A. shenzhenica, D. catanatum* and *P. equwstris*). The graphs represent genome coverage (y-axis) for each type of TEs (DNA transposons, SINE, LINE, and LTR retrotransposons) in Kimura distances to their corresponding consensus sequence (x axis, K-value from 0 to 50).



**Figure S3.** Estimated insertion time (mya) of LTRs in *G. elata* and the density of elements at each insertion time.



**Figure S4.** GO annotation of the predicted genes of the *G. elata* genome. The horizontal axis indicates classes of the second-level GO-annotation, and the vertical level axis indicated the number of genes in each class.