

Fig. S1. The screenshot of the main functionality of GCevobase.

(A) and (B) display the distribution of GC content. (C) and (D) indicate two dimensional plot for GC content versus effective length. (E) and (F) show the scatter plot for mean GC against standard deviation GC. (G) and (H) denote the analysis of orthologs for *OS01G0541900* and paralogs for *GLYMA0175S50*, respectively. For (E), (F) and (G), the colors are chosen to differentiate a variety of taxonomical levels: black (species), red (family), orange (order), yellow (class), green (phylum) and blue (kingdom). In particular, the color code for (H) is defined based on the protein identity: red (0-20%), green (20%-40%), blue (40%-60%), orange (60%-80%) and yellow (80%-100%).

