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%).