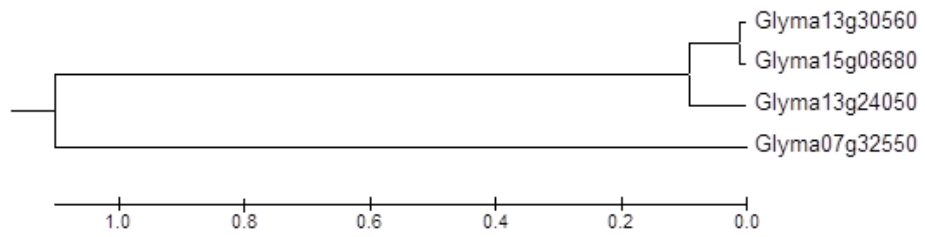


Figure S6



**Figure S6** The inferred evolutionary history for the four Glycine Max ChII subunits calculated using the UPGMA method. The UPGMA neighbor joining tree shows the close sequence similarity of Glyma13g30560 with Glyma15g08680. The optimal tree with the sum of branch length = 2.30757376 is shown.