

**Fig. S1.** Screening the *LOC106302894* among common *Brassicaceae* vegetables in Taiwan. (a) Theory of ‘Triangle of U’ in *Brassica* species (U 1935). (b) and (c) PCR amplification results using LOC106302894 and BraTUB6 primer. Banding patterns were separated in 1.8% agarose gel. Genomic DNA of classic CC genome species *Brassica oleracea* such as broccoli (*B. oleracea* var. italica), cabbage (*B. oleracea* var. capitata), cauliflower (*B. oleracea* var. botrytis), and Chinese kale (*B. oleracea* var. alboglabra) were analyzed. Other *Brassicaceae* relatives including one AABB genome species leaf mustard (*B. juncea* (L.) Czern.), two AA genome species bok-choy (*B. rapa* var. Chinensis) and Chinese cabbage (*B. rapa* var. pekinensis), and white radish (*Raphanus sativus* var. Longipinnatus) were also investigated.