



## Complementary DNA cloning, sequence analysis, and tissue transcription profile of a novel *U2AF2* gene from the Chinese Banna mini-pig inbred line

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**ABSTRACT.** U2 small nuclear RNA auxiliary factor 2 (*U2AF2*) is an important gene for pre-messenger RNA splicing in higher eukaryotes. In this study, the Banna mini-pig inbred line (BMI) *U2AF2* coding sequence (CDS) was cloned, sequenced, and characterized. The *U2AF2* complete CDS was amplified using the reverse transcription-polymerase chain reaction (RT-PCR) technique based on the conserved sequence information of cattle and known highly homologous swine expressed sequence tags. This novel gene was deposited into the National Center for Biotechnology Information database (Accession No. JQ839267). Sequence analysis revealed that the BMI *U2AF2* coding sequence consisted of 1416 bp and encoded 471 amino acids with a molecular weight of 53.12 kDa. The protein sequence has high sequence homology with *U2AF65* of 6 species - *Homo sapiens* (100%), *Equus caballus* (100%), *Canis lupus* (100%), *Macaca mulatta* (99.8%), *Bos taurus*

(74.4%), and *Mus musculus* (74.4%). The phylogenetic tree analysis revealed that BMI *U2AF65* has a closer genetic relationship with *B. taurus U2AF65* than with *U2AF65* of *E. caballus*, *C. lupus*, *M. mulatta*, *H. sapiens*, and *M. musculus*. RT-PCR analysis showed that BMI *U2AF2* was most highly expressed in the brain; moderately expressed in the spleen, lung, muscle, and skin; and weakly expressed in the liver, kidney, and ovary. Its expression was nearly silent in the spinal cord, nerve fiber, heart, stomach, pancreas, and intestine. Three microRNA target sites were predicted in the CDS of BMI *U2AF2* messenger RNA. Our results establish a foundation for further insight into this swine gene.

**Key words:** Banna mini-pig inbred line pig; China; *U2AF65*; *U2* small nuclear RNA auxiliary factor 2; Tissue expression analysis