

Figure. S1 The phylogenetic tree of B3 family members. The tree was constructed by using the Neighbor-Joining (NJ) method on TreeBeST (version 1.9.2) and visualized in iTOL. Five color blocks represent five subfamilies. The number on the tree branches represents the bootstrap value.

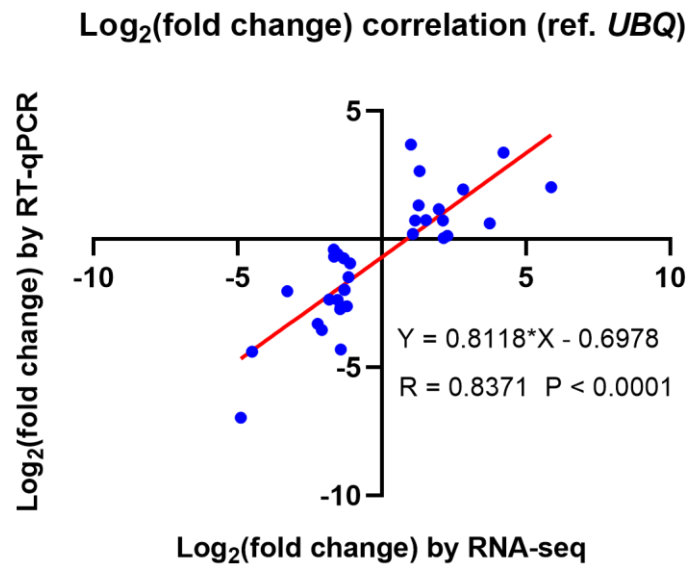


Figure. S2 RT-qPCR validation of the expression levels of B3 genes. The correlation between log₂(fold changes) of B3 genes were analyzed by RNA-seq and by RT-qPCR. RT-qPCR results were expressed on the basis of *UBQ*.