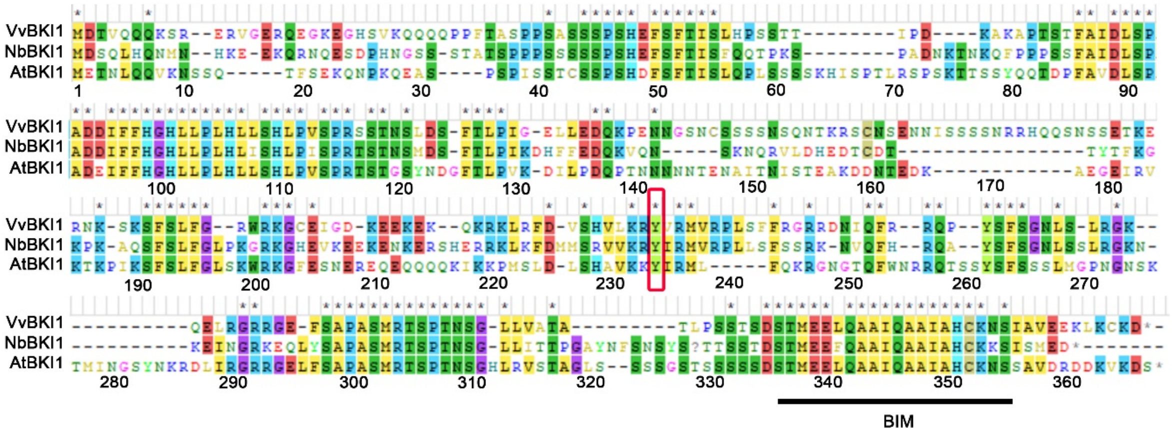
FIGURE S8



S8 Fig. Alignment of amino acid sequences of VvBKI1, NbBKI1, and AtBKI1.The alignment was conducted by using ClustalW in MEGA7 software. The conserved sites at 60% level are showed in background color. Conserved tyrosine site is labeled in red box.