

```

ZmHb1      MALAEADDGAVVFGEEQEALVLKSWAVMKKDAANLGLRFFFLKVF EIAPSAKQMFSEFLRDS 60
ZmHb2      -----MGFSEAQEELVLRSWKAMKSDSESTALKFFLRIFEIAPGAKQMFSEFLRDA 50
           : * . * ** ***: ** . ** . *: . . *: ***: : ***** . *****:

ZmHb1      -DVPLEKNPKLKTHAMSVFVMTCEAAAQLRKAGKVTVRETTLKRLGATHLRYGVADGHFE 119
ZmHb2      GDAPLEKHPKLKAHAVTVFVMACE SATQLRSTGDVKVREATLKRLGATHARAGVADAHFE 110
           * . *****: *****: ** : : *****: ** : * : *** . : * . * . ***: ***** * ***** . ***

ZmHb1      VTGFALLETIKEALPADMWSLEMKKAWAEAYSQLVAAIKREMKPDA----- 165
ZmHb2      VVKTALLDTIRDVP-DMWTPEMKAWE EAYDQLAAVIKEEMKNAAA AEEQTKNAATAAE 169
           * .   ***: ** : : * : * ***: *** ** *** . ** . * . ** . *** *

ZmHb1      -----
ZmHb2      ETTNAAA AEEETTNA AAAVDAS 191

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Supplemental Figure 1. Amino acid sequence alignment of ZmHb1 and ZmHb2 with Clustal W using BLOSUM protein weight matrix (Larkin et al., 2007).