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gi|16507120|gb|AAL24047.1      MGRTPCCEKVG LKRGRWTA EEDQLLANYIAEHGEGSWRSLPKNAGLLRCG 50
P1-rr-p1p2                    MGRTPCCEKVG LKRGRWTA EEDQLLANYIAEHGEGSWRSLPKNAGLLRCG 50
*****
                                Myb DNA binding domain
KSCRLRWINYLRADVKRGNISKEEEDI I IKLHATLGNRWSLIASHLPGRT 100
P1-rr-p1p2                    KSCRLRWINYLRADVKRGNISKEEEDI I IKLHATLGNRWSLIASHLPGRT 100
*****

gi|16507120|gb|AAL24047.1      DNEIKNYWNSHLSRQ IHTYRRKYTAGPDDTAIAIDMSKLSADRRRGRT 150
P1-rr-p1p2                    DNEIKNYWNSHLSRQ IHTYRRKYTAGPDDTAIAIDMSKLSADRRRGRT 150
*****

gi|16507120|gb|AAL24047.1      PGRPPKASASRTKQADADQPGGEAKGPAAAASSPRHSDVVPNGPNQPNSS 200
P1-rr-p1p2                    PGRPPKTSASRTKHSADADQPGGEAKG--AAASSPRHSDAVNPGPNQPNSS 198
*****:*****:*****

                                Activation domain
SGSTGTAE EEPSS EDASGPWVLEPIELGDLVWGEADSEMDALMPIGPGG 250
P1-rr-p1p2                    SGSTGTAE EEPSS EDASGPWVLEPIELGDL-WGEADSEMDALMPIGPGG 247
*****:*****:*****

gi|16507120|gb|AAL24047.1      HDSAAL EGLGAVGCEAQVDDLFDMDWDGF AAHLWGGPEQDEHSAQLRQAA 300
P1-rr-p1p2                    HDSAALQGLGAVGCEAQVDDLFDMDWDGF AAHLWGGPEQDDHSAQLRQAA 297
*****:*****:*****

gi|16507120|gb|AAL24047.1      EPLE---VAAAAAATAARTPDDRELEAFETWLLSDFS 335
P1-rr-p1p2                    EPMEAAAVAAAAAATAACTPDDRELEAFETWLLSDFS 335
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Figure S2 Alignment of deduced amino acid sequences of P1 and P1P2 proteins. The alignment of maize Myb-like transcription factor P1 (AAL24047.1; upper) with deduced P1P2 amino acid sequence (lower). Myb-like DNA binding domains and putative Activation domains are boxed.