```
                     *:*                 .                    : .:** .  ::.:**. *:   .  *:.:*    :::    .:*   : *:. :    :.  : *:*:  :   *   * :           . . *.*:*** **.*** *:****::.*:
AT3G15150.1          MASASSSDG------VAGRIQNASLVLVSDNSSTLADIRKAVAMMKNIAVQLEKENQTDKVKDLENSVAELLDLHSDCNHRSTAIQSVANRYQPVEQLTDFKKLLDDEFTKLKATPSSVPQNDHLMRQFREAVWNVHHAGEPMPGDDDED   144
POPTR_0011s14450.1   MASTSAPRGGGDVPSASGIMTTSASMLCSENQSLIVEMRKVFNMMKEIAVDLERENESAKVNELENTVAELLATYEDCTYQTSAIESVGNTYQPGAELTDFKKLLNDEFMKFKGNKSSAPQNHPLLRQFREAVWNVHHSGQPMPGEEHED   150
GSVIVT01014276001    MASPEDSGT----PLPLSTPITNLS---------LLKFRKAMILMKEVAVDLERDGQSQMVKELEDAVVELLGTSEDCTQFSAAIQSVGNEHQPRPELTDFKKLFEDEVAKLKASSSFAPQSHPLLRQFREAVWNVHHAGQPMPGDEQED   137
Solyc07g062780.1.1   MASTSGAGS----GVAAGRIRSHTSALYSDSQSLILEIRKSVTMMKDIAVHLERDERTQMVKDLEDGVVQLLAASDECMHLSEAIQSIGDTLEPGPEPTNFKKKFDEEIAKSKARSSSHTQNQSLLRKFREAVWHVHHEGQPMPGDEQED   146
LOC_Os05g48880_F     MSS------------VVNKLTNAAERESSEAETLIAEIRKAIGEMKSIAVDYERENKSDKVKQLEAAALELVASCEDCTCYADAIRKVPGAYQPSNQMTDFEKLIEAEVNKVKGNSSTSVENHLLIRQFREAVWNVHHAGQPMPGDEQED   138
Bradi2g16600.1       MSS------------AAMKLANAADASSEEAQSLIADMRKAVNTMRSIAVEFEKANMSDKVKEVEKEMLELLASYEDCAFLAEAVKAVPQIYQPSDQPTDFKRLIEAEVTKIKGNSRVSGHCQQLVRQFREAVWDVHHAGQPMPGDEQEE   138
Bradi2g16577.1       MSS------------AAMKLANAADTSSEESQSLIADMRKAVNTLRSIAVEYEKENRPDKVKEVEKEMLELLASYEDCAFLAEAVKAVPQIYQPSDQPTDFKKLIEAEVTKIKGNSRVSGHCQQLVRQFREVVWDVHHAGQPMPGDEQEE   138
Sb09g028460.1        MTS------------MATKLVNTAEVASSEAQTLVADMRKAINTMKSLAVDFERNGKSDKVNKLEEMVQEMVASYEDCAAMAQAIKAVPVVYQPSDQPTDFKTLIEVEVSKIKGASSASQQNHPLLRQFRESVWNVHHAGQPMPGEEQED   138
GRMZM2G022065_T01    MSS------------MATKLFNTAEVESSDAQALVADMRKAIGTMKSLAVDFERDGKSDKVKKLEETVLELVASYEDCAAMAQAIKAVPGVYQSSDQPTDFKTLIGVEASKIREASSASQQNHPLFRQFRESVWNVHHAGQPMPGEEQED   138
                     1.......10........20........30........40........50........60........70........80........90........100.......110.......120.......130.......140.......150

                     ::*****  :**:.**:: :*: :* :***             :*:*:*::  :: *:         .**::.*   *.  .* .*.:* .**:*.:*        .  ::  :   ::.
AT3G15150.1          IVMTSTQCPLLNMTCPLSGKPVTELADPVR----------SMDCRHVYEKSVILHYI-VNNPN--ANCPVAGCRGKLQNSKVICDAMLKFEIEEMRSLNKQSNRAEVIEDFTEDVDED---------------   249
POPTR_0011s14450.1   IVMTSTQSTILNITCPLSGKPITELAEPVR----------GVDCKHVYEKKAIMGYI-SLNAQ--AKCPVTGCPRYLRQDKVVSDPLLLVEIEEMRSMSKENMTATLVEDFTMTDDEEED-------------   257
GSVIVT01014276001    IVMTSTQCNLLNITCPLSGRPVTELADPVR----------SVDCKHIYEKKAILHYIKSKHGR--AQCPVAACPKILQAERVVCDALLQIEIDEMKSMSKQPGRTDVIEDFTELDDDDDEEEEDD--------   250
Solyc07g062780.1.1   IVMTSTQCNLLNVTCPLSGKPVIELVEPVR----------SMDCKHIYDRKAIMQYM-KKSKSTRGQCPVAGCPKILKAQRVLCDPFLLIEIDEVRSMNKQNARPDAIEDFTALDEDEDD-------------   255
LOC_Os05g48880_F     VLMTSTQTSILNVTCPLTGKPVIQLTEPVR----------CADCRHIYEKVPIMHYI-RNQKP--PKCPIAGCPRVLQVGRVTCDSLLQVEIDELRSSGPSAPDAENIEDLTDDEDDSNE-------------   245
Bradi2g16600.1       LVMTSTQRNVLNIKCPITMKPIIELTDPVR----------CTECRHIYDKNPIMSYI-RNNKP--PRCPIAGCPKMLHTGNVVCDSMLRVEIDEFRSSGAADSIASDVEDISDLNDDEEEPMDEDS----DHL   254
Bradi2g16577.1       LVMTSTQRNILNIKCPITMKPIIELTDPVRWKAVSALLGFITECRHIYDKNPIITYM-RNNKP--PRCPIAGCPKMLHIGNVKCDSMLRVEIDEFRSSGAADSIASDIEVISDLDDDEEEPMDEDNGDEYERR   268
Sb09g028460.1        IVMTSTQMSILNVTCPLTGKPVIELIDPVR----------CVDCKHIYEKDPVMQYI-RTKKP--PQCPIAGCPRVLERGKVICDPLLRIEIEELRSSETGAPNATNIDDLTDLLDDDEE-------------   245
GRMZM2G022065_T01    IVMTSTQMSILNVTCPLTGKPVIELMNPVR----------CVDCKHIYEKDPVMQYI-RTKKP--PQCPIAGCPRVLERGKVICDPFLLIEIEELRSSETAAPNATNIDDWTDLNDEDEE-------------   245
                     .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280...
```

Fig. S6 Alignment of SUMO ligase HPY2 type protein sequences