Fig. S1. Conserved direct and inverted elements in *PAL, CHI*, *CHS* and *PR-5* promoters. Elements conserved among seven UV-B inducible promoters (*MEB5.2*, *PyroA*, *Ubq3*, *CHI*, *CHS*, *PAL* and *PR-5*) identified in pairwise BLASTN comparisons are with solid arrows shown in their direct and inverted orientations, respectively, with slashes indicating single mismatches. Only those elements containing two or more guanosine and cytosine identities in a minimum of seven contiguous nucleotides are displayed. The regions in these promoters sharing the identities are designated with numbers following each gene designation. To further clarify orientation, the designation for inverted elements are underlined.

CHI

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                                    PAL-2                Ubq3-1
AATTATCTCAAATAACCAAAATATATAAAATCAATAATATGAAAGATAACGATAGAAAATATTTGAAATTATCCTAACTATGTGCTCTGCATATTTAAGG   -218

                CHS-3        CHS-4      Pyro-1  MEB-1 PAL-1        CHS-2
GCTCAAAGCTTCAACCACCAATTGTCAATGCATCTCCCAATCAAAATATAAAAAAAAGAGACGAAAACGAAAGTACACGTGCTTACACATCCAACACTCGT   -118

                        MEB-2     CHS-1              Pyro-3 Ubq3-3               MEB-3 Pyro-2
AATCGTAACTATTGCTACCTACCCTTCTCTCTTCTACTTAACCCCAAAGGCCCCAAAAACACAATCAAGAAAAGCTCTGTAACATTATTATCAATCGAAA    -18

       Ubq3-2
TTCCAACCGACTCAACAATG                                                                                     +3
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CHS

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ACTCTACGGCGTCTACGCCTCGCATGCCTATCATATTTAACCGTCAATAATGGATTGGCGGTTTTGGTAGGCCGGGTCAACCGGATTAAAAGAAAACGG   -989

TTTGGAGTCCTTCCTTGCAATTGAATTTTCACGCATCGGGTTTTGTGATTTCTCTGTCATAATGGGCCCGGCACATATGGTTCATAACCCATGTGGGCCT   -889

ATGGTATAATTTTTCCAATTAAAACTATTGTTAGGTCGATAAAACAAAAAACAATAAAAACGAGTGGAATACACATACCAAAAAGAATGTGATGAACATT   -789

                                          CHI-3
AGTAATTTTATTTTGATGGTTAATGAAAAACAAAATAATGCATCTTGACATCTTCCGTTGGAAAGCGCAAATAGGGCAGATTTTCAGACAGATATCACTA   -689

                                                PAL-1        Ubq3-1
TGATGGGGGTGGGAGAAAGAAAACGAGGCGTACCTAATGTAACACTACTTAATTAGTCGTTAGTTATAGGACTTTTTTTTTGTTTGGGCCTAGTTATAG    -589

                            CHI-1      CHI-2
GATCATAAGGTAAAAATGAAGAATGAATATTAGATTAGTAGGAGCTAATGATGGAGTTAAGTAGTATGCACGTGTAAGAACTGGGAAGTGAAACCTCCTG   -489

TATGGTGAAGAAACTATACAACAAAGCCCTTTGTTGGTGTATACGTATTAATTTTTATTCTTTTATCACAAGCGATACGTATCTTAAGCACATAATAAATA   -389

                    MEB-1
TATATCTTACTCATAATAAATATCTTAAGTATATATACAGTATACACCTGTATATATATAATAAATAGGCATATAGTAGAAATTAATATGAGTTGTTGT    -289

        CHI-4
TGTTGCAAATATATAAATCAATCAAAAGAATTAAAACCCACCATTCCAATCTTGGTAAGTAACGAAAAAACAGGGAAGCAAGAAGAACCACAGAAAAGGG   -189

GGCTAACAACTAGACACGTAGATCTTCATCTGCCCGTCCATCTAACCTACCACACTCTCATCTTCTTTTTCCCGTGTCAGTTTGTTATATAAGCTCTCAC    -89

TCTCCGGTATATTTCCAAATACACCTAACTTGTTTAGTACACAACAGCAACATCAAACTCTAATATACCCAAGTTGGTGTATACTATAATG           +3
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PAL

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TTTCACAAATTTTATACTCAATTACAAAATCAACGAAAATGTACATTTGTATCTTTAACTATTTACGTTTTTTTTTTACGTATCAACTTTCAGTTATATGTT   -937

TTGGATAATATATTTTTTTACTTTTGACTTTTCAGTTTTCACCTAATGATTGGGATATACATATGCATGCATAGTTCCCATTATTTAAATGTAAGCTAAG   -837

TGCATATGAACTGTTAGTCAAAATTACGAAGTTTATTTGTACATATATATAGTTATAACAAAATGGTACAGTAAATTAAACAGAACATCAAGAAAGTACA   -737

        MEB-2                                       Pyro-2                            Ubq3-3
AAAGACTGAACACAATAATTTACATGAAAACAAAACACTTAAAAAATCATCCGATAAAATCGAAATGATATCCCAAATGACAAAAATAACAATATAGAAA    -637

Ubq3-1 Ubq3-4 CHI-2
ATACAAAAACAAAAACAAAATATGAAAGAGTGTTATGGTGGGGACGTTAATTGACTCAATTACGTTCATACATTATACACACCTACTCCCATCACAATGA   -537

              Ubq3-5      CHS-1
AACGCTTTACTCCAAAAAAAAAAAAAAAACCCACTCTTCAAAAAAATCTCGTAGTCTCACCAACCGCGAAATGCAACTATCGTCAGCCACCAGCCACGACCA   -437

              CHI-1                           MEB-1
CTTTTACCACCGTGACGTTGACGAAAACCAAAGAAATTCACCACCGTGTTAAAATCAAATTAAAAATAACTCTCTTTTTGCGACTTAAACCAAATCCACG   -337

AATTATAATCTCCACCACTAAAATCCATCACTCACTCTCCATCTAACGGTCATCATTAATTCTCAACCAACTCCTTCTTTCTCACTAATTTTCATTTTTT    -237

                Ubq3-6
CTATAATCTTTATATGGAAGAAAAAAAGAAACTAGCTATCTCTATACGCTTACCTACCAACAAACACTACCACCTTATTTAAACCACCCTTCATTCATCT   -137

                                                      Ubq3-2
AATTTTCCTCAGGAACAAAATACAATTCCTTAACCAACAATATTACAAATAAGCTCCTATCTTCTTTCTTTCTTTTAGAGATCTTGTAATCTCCTCTTAGT    -37

TAATCTTCTATTGTAAAACTAAGATCAAAAGTCTAAATG                                                                  +3
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PR5

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AAAAGCAACCCTCATAGTCACGGCAAGATTCAATTACTTTTCCTCGGACCCAAAGTTGGTTCAATTTATGAACCAGTTTCTACGTCTAAGTCAGTCGTCT   -958

CACCTTATAATCTTTAAAGTCTCCCGCTGCACTAATCACTCCGTTTCATCGTTTTATATATCACTTGATTTTATTTTATTTCATAAAATATTTTTTTTTA   -858

AATACAGATTTTTCTTCAACTATGTTCTAGACTTCTAGAAGCCATAAAAGATTACAATATTATTAAAAATGCGGGACAAAACTACATAACGATACCATTTA   -758

ACGTACGAAATATTTCTAATTTACCTATTCGTTTATAACCAGATTTTATACCTGTTTAGATGTTTACTGTTTTAAAAACTACACATTCATGGTCATGGAG   -658

GATATGATATCTAAAACCTTAGGATTCAAGCTTTCGCGTTCAAGTAGCAAATCAGGCCTCTTATGTATGCATCTGTTCCGGTCTTATAATCGAGGATTCA   -558

CACCCAAATTAAAAAGCATCGATCTATTCGGGTTTCATACAATCATACTCATGGGTTACAACAGTCAACAAACACATCTATCTGGTCATCTGGATCTCAAA   -458

CTCGCACCTCACAACACAATATCTAACCGATCCGGATCTCATATTCAATTCGTGGATCACAATTAGACACATCTAATTGGATCTCATAGTCGCGGATCAC   -358

Ubq3-1
AATTAAATTCATCTATACAGATATCATACTCGCGGACCCACACATCACATGACATAAAACATCACACTGAACCCTAAGGTTTAGTGTAGTGTGCATCAGCC   -258

ATGGCCGAGTCAAAATGTTAAGATTTTTTTTTTTACCATTTATAGTAAACTAATGGAAGTAAAAACCAGTAATGCAAAGAAAATTCAGAGAACCAAAGGAA   -158

ATATCTATCAAGACACCAAAAATTCTAATTGATTAATCATGCAACATTACGTCGCTACCCCTCGAACCAACATCTATAAATAGAGGATCGGTGCCATTA    -58

ACATTCATCATCATCACCCACAGCACAGAGACACACACAAAAAACCCATAAAAAAAATATG                                          +3
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