Supplemental Figure legends

Figure S1

Editing sites in psbA defined by differences in genomic and cDNA sequences.

The genomic sequence of the psbA gene and its derived amino acid sequence are shown in full, and only differences are shown for the cDNA sequences. An asterisk shows the only position in the sequenced where editing (C to T) does not result in an amino acid replacement.

Figure S2

Editing sites in petB defined by differences in genomic and cDNA sequences.

The genomic sequence of the petB gene and its derived amino acid sequence are shown in full, and only differences are shown for the cDNA sequences. The asterisk shows the only position in the sequence where editing changes a stop codon to instead encode an amino acid (lysine).

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                 10        20        30        40        50        60        70        80        90
DNA      GTATATTAATGTTCCCTCTCATTGGTTTGGCAATTGGTGCTTATATTTCAGCTTTTATTTTTGCTCCGCCAGTAGATATTGATGGAATTA
cDNA                                           C
            I  L  M  F  P  L  I  G  L  A  I  G  G  Y  I  S  A  F  I  F  A  P  P  V  D  I  D  G  I
                                                A

                100       110       120       130       140       150       160       170       180
DNA      GAGAACCAGTTGCTGGAAGTCTCTTGTATGGGAATAATATTATTACAGGAGCTGTTATACCAAGCTCAAATGCAATTGGTGTTCATTTTT
cDNA                                                              G
         R  E  P  V  A  G  S  L  L  Y  G  N  N  I  I  T  G  A  V  I  P  S  S  N  A  I  G  V  H  F
                                                                  V

                190       200       210       220       230       240       250       260       270
DNA      ATCCAATTTGGGAGTCACTAGGTTTTGATGAGTGGTTATATAATGGTGGTACATATCAATTTGTTGTTTTGCATTTTATTGTAGGTGTAT
cDNA          G
         Y  P  I  W  E  S  L  G  F  D  E  W  L  Y  N  G  G  T  Y  Q  F  V  V  L  H  F  I  V  G  V
               V

                280       290       300       310       320       330       340       350       360
DNA      CTTGTTGGATGGGTAGAGAATGGGAATTTAGTTTTAGATTAGGAATGCGTCCATGGATTTTTATAGCTTTTTCAGCACCTCTTATAGCAG
cDNA                                                                   G                    G
         S  C  W  M  G  R  E  W  E  F  S  F  R  L  G  M  R  P  W  I  F  I  A  F  S  A  P  L  I  A
                                                                        V                    V

                370       380       390       400       410       420       430       440       450
DNA      CTTCAGCTATTTTTATATTTTATCCAATTGGACAAGGAAGCTTTTCAGATGGTATGCCACTTGGTATTAGTGGCACATTTAATTTTATGT
cDNA                   G
         A  S  A  I  F  I  F  Y  P  I  G  Q  G  S  F  S  D  G  M  P  L  G  I  S  G  T  F  N  F  M
                        V

                460       470       480       490       500       510       520       530       540
DNA      TAGTATTTCAAGCAGAGCATAACATTTTAATGCATCCATTTCACATCTTAGGTGTGGCTGGTGTATTTGGAGGTTCATTATTCAGTGCAA
         L  V  F  Q  A  E  H  N  I  L  M  H  P  F  H  I  L  G  V  A  G  V  F  G  G  S  L  F  S  A

                550       560       570       580       590       600       610       620       630
DNA      TGCATGGTTCATTAGTATCATCTTCACTTTTAGCAGAAAGTTCTGGAGATGTCTCACTTAATGTTGGTTATAATTTTGGTCAAGAAGATG
cDNA                                                C
         M  H  G  S  L  V  S  S  S  L  L  A  E  S  S  G  D  V  S  L  N  V  G  Y  N  F  G  Q  E  D
                                                T

                640       650       660       670   *   680       690       700       710       720
DNA      AAACTTATAGTATCTCAGCTGCACATGGTTATTTTGGTCGTCTCATTTTTCAGTATGCAAGTTTTAACAACTCACGTAGTTTACATTTCT
cDNA                                                    T
         E  T  Y  S  I  S  A  A  H  G  Y  F  G  R  L  I  F  Q  Y  A  S  F  N  N  S  R  S  L  H  F

                730       740       750       760       770       780       790       800       810
DNA      TTTTAGCTGGTTGGCCAGTTATTGGTATCTGGTTTACAGCACTTGGTGTTAGTACAATGGCTTTCAATTTAAATGGGTTGAATTTTAATC
cDNA              C
         F  L  A  G  W  P  V  I  G  I  W  F  T  A  L  G  V  S  T  M  A  F  N  L  N  G  L  N  F  N
                  A

                820       830       840       850       860       870       880       890       900
DNA      AGTCCATAATTGATTCATCAGGTCATCTTATAAATAGTTGGGCTGATATAATTAATAGAGCAGATTTGGGTATGGAGGTTATGCATGAAC
cDNA                                                       G
         Q  S  I  I  D  S  S  G  H  L  I  N  S  W  A  D  I  I  N  R  A  D  L  G  M  E  V  M  H  E
                                                            V

DNA      GAAATG
         R  N
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Figure S1

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              10        20        30        40        50        60        70        80        90
DNA   TGATTGGTGTGAAGAAAGATTAGAGATTCAGTCTATTTCAGATGATGTTTTAGCTAAATTCGTACCATCTCATGTAAATATATTTTATTG
cDNA                                                A
       D  W  C  E  E  R  L  E  I  Q  S  I  S  D  D  V  L  A  K  F  V  P  S  H  V  N  I  F  Y  C
                                                    I

             100       110       120       130       140       150       160       170       180
DNA   TTTTGGAGGTATTATATTGACATCTTTTATATTTCAAGTTGCTACAGGTTTTGCTCTTACAATTTATTATCAACCTACAGTAGTTGAAGC
cDNA               G                                                         G
        F  G  G  I  L  T  S  F  I  F  Q  V  A  T  G  F  A  L  T  I  Y  Y  Q  P  T  V  V  E  A
                    V                                                        R

             190       200       210       220       230       240       250       260       270
DNA   TTTCTCAAGTATTGAAAATATTTTATATCATGTGAATTTAGGCTGGTTTATTAAATCTGTTCATCGTTGGTCTTCAGGAGTTATGGTTCT
cDNA                                                       G
        F  S  S  I  E  N  I  L  Y  H  V  N  L  G  W  F  I  K  S  V  H  R  W  S  S  G  V  M  V  L
                                                           R

             280       290       300       310       320       330       340       350       360
DNA   TATATTAGCCCTTCATATAAATAGGGTTTATTTAACAGGAGGTTCTTAAAAACCAAGAGAATTAATTTGGATTACAGGTACAATATTAGC
cDNA   G                                          T A                                GT
        I  L  A  L  H  I  N  R  V  Y  L  T  G  G  S  *  K  P  R  E  L  I  W  I  T  G  T  I  L  A
        V                                         F  K                                V

             370       380       390       400       410       420       430       440       450
DNA   TGTCACCTCTATATCATTTGGTGTAACTGGTTATTCATTACCTTGGGACACAATTGGTTATTGGGCTTGTAAAATTGTGACAGCTGTTCC
        V  T  S  I  S  F  G  V  T  G  Y  S  L  P  W  D  T  I  G  Y  W  A  C  K  I  V  T  A  V  P

             460       470       480       490       500       510       520       530       540
DNA   GGAAGCATTAGATAATTTAATCCCAGGTGTTGGGAAAATATCTGTTATAATTTTGAGAGGAGGGTTTAGTGTCAATCAAATTACTTTGAC
cDNA               G                                                            G    GC
        E  A  L  D  N  L  I  P  G  V  G  K  I  S  V  I  I  L  R  G  G  F  S  V  N  Q  I  T  L  T
                    D                                                           S     A

             550       560       570       580       590       600
DNA   AAGATTTTACAGTATTCATACATTTATTTTGCCATTAGCGACTTTAATTTTAGTAGTAGTTCATTTTTC
cDNA                           G                    G           A
        R  F  Y  S  I  H  T  F  I  L  P  L  A  T  L  I  L  V  V  V  H  F  S
                                V                    V           I
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Figure S2