SUPPLEMENTAL DATA

The following materials are available in the online version of this article.

Supplemental Figure S1. RPL10 sequences are highly conserved between different organisms at nucleotide and amino acid levels. Alignment of the nucleotide (A), coding (B) and amino acid (C) sequences of *Zea mays* and *A. thaliana* RPL10s. Start and stop codons are bold letters. D, Multiple sequence alignment of RPL10 proteins from different species. For protein accession numbers, see Methods. At, *A. thaliana*; Zm, *Zea mays*. The sequences were aligned using the Clustal W2 program. Dashes (-) indicate spaces introduced to promote optimal alignment, perfect matches are represented by an asterisk (*), high amino-acid similarities by double dots (:), and weak similarities by a single dot (·). Symbols are indicated below the sequences. Signature sequences (motifs) specific to Amidation are shaded grey, specific to Glycosylation pink, specific to Myristoylation yellow, specific to protein kinase C light blue and specific to casein kinase II green. Putative zif domain is bold-underlined.

Supplemental Figure S2. Coimmnunoprecipitation of RPL10 proteins in *A. thaliana*. A, Immunoblot analysis of *A. thaliana* recombinant RPL10 proteins. Partially purified recombinant RPL10 proteins were run on 12% SDS-PAGE and subjected to immunoblot analysis for RPL10. Ten micrograms of total proteins were loaded in all lanes. B, SDS-PAGE (10%) of RPL10-associated proteins. C, Classification of RPL10-associated proteins based on their cell functions. Proteins with percentage of coverage higher than 10% or at least two tryptic peptides were included in the diagram. Clustering was performed according to Usadel et al. (2006). D, Immunoblot analysis of RPL10-associated proteins. RPL10 proteins were immunoprecipitated from *A. thaliana* crude extracts with antibodies against *H. sapiens* QM protein. The immunocomplexes were solubilized, run on 12% SDS-PAGE and subjected to immunoblot analysis for RPL10, eukaryotic translation initiation factor 2 alpha (eIF2 alpha) and eukaryotic translation initiation factor 2 beta (eIF2 beta). The numbers indicate the molecular mass in kDa. CE: crude extract, IP: immunoprecipitate.

Supplemental Figure S3. Complementation of *A. thaliana* homozygous *rpl10B* mutants with WT At *RPL10B*. A, Presence of WT *RPL10B* transcript in transformed *A. thaliana rpl10B* mutant plants analyzed by PCR on genomic DNA. Lanes 1: negative control (without DNA); lane 2-4: genomic DNA from leaves of transformed plants; lanes 5: positive control (pCHF3-

RPL10B). B, At *RPL10B* expression level in Arabidopsis WT, *rpl10B* homozygous and complemented plants analyzed by RT-qPCR. Each reaction was normalized using the C_t values corresponding to the *POLYUBIQUITIN10* mRNA. The means of the results obtained using three independent biological experiments are shown, the error bars indicate the S.D. of the samples. WT levels were set at 1. C, 15-day-old WT (left), *rpl10B* mutant (middle) and complemented plants. Scale bar: 1 cm.

Supplemental Figure S4. Inhibition of protein synthesis by UV-B in *A. thaliana* WT and *rpl10* mutant plants. Fourty micrograms of total proteins were resolved by 12% SDS-PAGE after *in vivo* [^{35}S]Met labeling, visualized by autoradiography (A) and staining with Coomassie Blue (B) following the UV-B treatment and recovery period indicated.

Supplemental Figure S5. UV-B treatment is not lethal to *A. thaliana* plants. Chlorophyll a (A), Chlorophyll b (B), Flavonoids (C), Maximum Efficiency of PSII (D) and Total proteins (E) were measured after 4 h UV-B (4 h UV-B), 16 h post-treatment (16 h recovery) and in untreated controls (no UV-B). Measurements are the average of six adult leaves from four different plants. Statistical differences from the control are marked with an asterisk ($P<0.05$).

Supplemental Figure S6. Typical 2D gels of leaves from heterozygous *rpl10A-1* mutant and WT plants after a 4 h UV-B treatment. As examples of proteins with differential expression, the relative abundances of some but not all spots annotated by the number that appears in Supplemental Table S3 are shown. The graphs represent one example from at least three different gels used for the differential analysis. The first dimension was carried out using 17 cm immobilized pH gradient strips (pH 3–10); acidic side to the left; and the second dimension was on 12.5% (w/v) SDS–PAGE. The relative abundance of proteins was determined. The protein spots with changes in intensities (least 1.5-fold, $P <0.05$) were considered to be different.

Supplemental Figure S7. Hierarchical cluster analysis of proteins showing different levels in *rpl10A* mutant plants in comparison to WT plants under control conditions and after a 4 h UV-B treatment identified by MS. A, Proteins included show different levels in *rpl10A* mutants (at least 1.5-fold) in comparison to WT plants under control or UV-B conditions. B,

Proteins included show differential abundance (at least 1.5-fold) after a UV-B treatment; these proteins changed differentially in WT plants than in the *rpl10A* mutant. Red indicates higher protein levels than the reference, green indicates lower protein levels than the reference, and black indicates no significant change.

Supplemental Figure S8. Classification of proteins showing different levels in the *rpl10A* mutant in comparison to WT plants based on their cell functions. Proteins were identified by 2D Gel electrophoresis and those showing changes in abundances of at least 1.5-fold were included. A, Proteins changed in the *rpl10A* mutant under control (no UV-B) conditions. B, Proteins changed in the *rpl10A* mutant after 4 h of UV-B.

Supplemental Figure S9. *RPL10s* promoter sequences with predicted cis-elements. The transcription initiation site (referred to as +1) is indicated in bold letter and the ATG start codon is shown in bold and underlined letters. Numbers at the left refer to the positions of nucleotides relative to the putative transcription initiation site.

Supplemental Figure 1. RPL10 sequences are highly conserved between different organisms at nucleotide and amino acid levels. Alignment of the nucleotide (A), coding (B) and amino acid (C) sequences of *Zea mays* and *A. thaliana* RPL10s. D, Multiple sequence alignment of RPL10 proteins from different species.

A

```
AtRPL10B        ------------------------------------------------------------
AtRPL10C        ------------------------------------------------------------
AtRPL10A        ------------------------------------------------------------
ZmRPL10-1       GCGAGTGGCGGGGAGAGGAGGCGGCGGCGGCAAGGGCGCGACGGGGGAGGATGATGTCGC 60
ZmRPL10-2       ------------------------------------------------------------


AtRPL10B        ------------------------------------------------------------
AtRPL10C        ------------------------------------------------------------
AtRPL10A        ------------------------------------------------------------
ZmRPL10-1       TGCAGCCTGCAGGAGTTGTGTTCTCTGGCCTTGAGAGAAAGGAGTCGCCAATTTTAGTGG 120
ZmRPL10-2       ------------------------------------------------------------


AtRPL10B        ------------------------------------------------------------
AtRPL10C        ------------------------------------------------------------
AtRPL10A        ------------------------------------------------------------
ZmRPL10-1       GCTCCTGTTGTGTTTTTCGGTCCATTCCTCCCAAGGCCCAGCATCTGCCAGTCGCATGCC 180
ZmRPL10-2       ------------------------------------------------------------


AtRPL10B        ------------------------------------------------------------
AtRPL10C        ------------------------------------------------------------
AtRPL10A        ------------------------------------------------------------
ZmRPL10-1       GTGACGCACAAAACCCACGGCGGCACGGCTCCATTCCGCGTCCGCACTCTCTATATAAAG 240
ZmRPL10-2       ------------------------------------GTCCACACTCTCTATATAAAG 21


AtRPL10B        ------------------------------CTTCTTCTTCTTCTTCTTCTTCTTCA 29
AtRPL10C        ------------------------------------------------AATTTCTAGGGT 12
AtRPL10A        --------------------------------AGTTTTTTCGTCGAGCAGCCGCGCTT 26
ZmRPL10-1       TGT-CCCTCTCTTCCCTCCAAGCCCTAGACGCACCCCTTCCTCGTTTCGCCGCCTCCGCC 299
ZmRPL10-2       TGTTCCCTCACTCCACTCCAAGCCCTAGCCGCATCCCTTCTTTCATTCGCCGCCGCCGCC 81


AtRPL10B        TTTCTAGGATTCGAAACAACAATC--AACGCG ATG GGACGAAGACCTGCGAGATGTTACC 87
AtRPL10C        TTTGCAAAACCAACACCGAAGATCC-AACACG ATG GGACGAAGACCTGCGAGATGTTACC 71
AtRPL10A        TTTGGCCGAGGAAGGATAAAGAGA--GACGCC ATG GGAAGAAGACCTGCGAGGTGTTACC 84
ZmRPL10-1       GACACCGACTGCCTACCTCAGCTGCCGTCGCC ATG GGCAGAAGGCCTGCTAGATGCTATC 359
ZmRPL10-2       TGC------------TCTCTGCTGCCGTCGCC ATG GGGAGAAGGCCTGCGAGATGCTATC 129
                                  * * *****  **** ***** ** ** ** *


AtRPL10B        GTCAAATTAAGGGAAAGCCATACCCTAAATCAAGATACTGTCGTGGTGTTCCCGATCCTA 147
AtRPL10C        GTCAGATTAAGGGAAAGCCATACCCGAAATCACGATACTGTCGTGGTGTGCCAGATCCCA 131
AtRPL10A        GTCAGATCAAGGGTAAGCCATACCCAAAGTCTCGCTACTGTCGTGGTGTGCCAGATCCAA 144
ZmRPL10-1       GCCAGATCAAGAACAAGCCGTACCCTAAGTCCAGGTACTGCCGTGGTGTCCCTGACCCCA 419
ZmRPL10-2       GCCAGATCAAGAACAAGCCATACCCCAAGTCCAGGTACTGCCGTGGTGTCCCTGACCCCA 189
                * ** ** ***   ***** ***** ** **  * ***** ******** ** ** ** *


AtRPL10B        AGATCAGGATTTACGATGTTGGTATGAAGAGGAAAGGAGTTGATGAGTTCCCTTACTGTG 207
AtRPL10C        AAATCAGGATCTACGATGTTGGTATGAAGAGGAAAGGTGTTGATGAGTTTCCATTCTGTG 191
AtRPL10A        AAATCAGGATCTACGATGTTGGTATGAAGAGGAAGGGTGTTGATGAGTTTCCATTCTGTG 204
ZmRPL10-1       AGATCAGGATCTACGATGTCGGGATGAAGAGGAAGGGTGTTGATGAGTTCCCCTACTGTG 479
ZmRPL10-2       AGATCAGGATCTACGATGTTGGCATGAAGAGAAAGGGTGTTGATGAGTTCCCCTACTGTG 249
                * ******** ******** ** ******** ** ** *********** ** * *****


AtRPL10B        TTCATTTGGTTTCATGGGAGAAAGAGAATGTTTCAAGTGAAGCTCTTGAAGCTGCTCGTA 267
AtRPL10C        TTCATTTGGTTTCATGGGAGAAAGAGAATGTGTCAAGTGAAGCACTTGAAGCAGCACGTA 251
AtRPL10A        TCCATTTGGTGTCATGGGAGAAGGAGAATGTGTCAAGTGAAGCACTTGAAGCTGCCCGTA 264
ZmRPL10-1       TGCACCTTGTCTCTTGGGAGAAGGAGAATGTCTCCAGTGAGGCGCTCGAGGCTGCCCGCA 539
ZmRPL10-2       TGCACCTTGTCTCTTGGGAGAAGGAGAATGTCTCCAGTGAGGCTCTTGAGGCTGCCCGTA 309
                * **  * ** ** ******** ******** ** ***** ** ** ** ** ** ** *
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AtRPL10B        TTGCTTGTAACA---------------------------------------------- 279
AtRPL10C        TTGCTTGCAACA---------------------------------------------- 263
AtRPL10A        TTGCTTGCAACA---------------------------------------------- 276
ZmRPL10-1       TTGCCTGCAACAAGTACATGACCAAGTCTGCAGGAAAGGATGCCTTCCACCTTAGGGTCC 599
ZmRPL10-2       TTGCCTGCAACA---------------------------------------------- 321
                **** ** ****

AtRPL10B        ------------AGTACATGGTGAAGTCTGCCGGGAAAGATGCGTTTCATCTCCGTATTA 327
AtRPL10C        ------------AGTATATGGTGAAATCTGCTGGGAAAGATGCTTTTCATTTGAGGATTA 311
AtRPL10A        ------------AGTACATGGTGAAGTCTGCTGGAAAAGATGCTTTTCATTTGAGGATTA 324
ZmRPL10-1       GTGCCTGCAACAAGTACATGACCAAGTCTGCAGGAAAGGATGCCTTCCACCTTAGGGTCC 659
ZmRPL10-2       ------------AGTACATGACCAAGTCTGCAGGAAAGGATGCCTTCCACCTTCGGGTCC 369
                            **** ***   ** ***** ** ** ***** ** **  *  *  *

AtRPL10B        GAGTTCATCCTTTCCATGTTCTTAGGATCAATAAGATGCTTTCTTGTGCTGGAGCTGATA 387
AtRPL10C        GGGTTCATCCTTTCCATGTTCTCAGGATTAACAAGATGCTTTCGTGTGCTGGAGCTGATA 371
AtRPL10A        GGGTTCATCCTTTCCATGTTCTCAGGATTAACAAGATGCTTTCGTGTGCTGGAGCTGATA 384
ZmRPL10-1       GGGTTCACCCGTTCCATGTCCTCCGTATCAACAAGATGCTTTCCTGTGCCGGGGCTGATA 719
ZmRPL10-2       GGGTTCACCCCTTCCATGTCCTTCGTATCAACAAGATGCTTTCGTGTGCTGGGGCTGATA 429
                * ***** ** ******** **  * ** ** *********** ***** ** *******

AtRPL10B        GACTTCAGACTGGTATGAGAGGTGCTTTTGGCAAAGCTCTTGGTACTTGTGCTAGAGTTG 447
AtRPL10C        GGCTTCAGACTGGAATGAGAGGTGCTTTTGGTAAAGCTCTTGGTACTTGTGCTAGAGTTG 431
AtRPL10A        GGCTTCAGACTGGTATGAGAGGTGCTTTTGGTAAAGCTTTGGGTACTTGTGCTCGTGTTG 444
ZmRPL10-1       GGCTCCAGACTGGAATGAGGGGTGCCTTTGGCAAGCCTCAGGGCACCTGTGCTAGGGTGG 779
ZmRPL10-2       GGCTCCAGACTGGAATGAGGGGTGCCTTTGGCAAGCCTCAGGGCACCTGTGCTAGGGTGG 489
                * ** ******** ***** ***** ***** **  **   ** ** ****** * ** *

AtRPL10B        CTATTGGACAGGTTCTTTTGTCTGTGAGGTGCAAAGATGCTCATGGTCATCATGCTCAGG 507
AtRPL10C        CGATTGGACAGGTTCTTTTGTCTGTTAGGTGTAAGGATAATCATGGAGTTCATGCTCAGG 491
AtRPL10A        CTATTGGACAGGTTCTTTTGTCTGTTCGTTGCAAGGATGCCCATGGTCACCATGCTCAAG 504
ZmRPL10-1       ACATTGGTCAGGTCCTCCTTTCCGTGCGATGCAAGGACAACAATGCTGCCCATGCCAGCG 839
ZmRPL10-2       ACATTGGTCAGGTCCTCCTTTCTGTTCGATGCAAGGACAACAATGCTGCACATGCCAGTG 549
                  ***** ***** **  * ** **  * ** ** **     ***     *****    *

AtRPL10B        AGGCTCTTCGTCGTGCTAAGTTTAAGTTCCCTGGTCGTCAAAAGATCATTGTTAGCAGGA 567
AtRPL10C        AAGCTCTTCGTAGAGCTAAGTTTAAGTTCCCTGGTCGTCAAAAGATCATTGTTAGCAGGA 551
AtRPL10A        AGGCTCTTCGTCGTGCTAAGTTCAAGTTCCCTGGTCGTCAAAAGATTATTGTCAGCAGGA 564
ZmRPL10-1       AAGCTCTGCGTCGCGCTAAGTTCAAGTTCCCTGGCCGCCAAAAGATCATTGAGAGCAGAA 899
ZmRPL10-2       AAGCTCTGCGTCGCGCCAAGTTCAAGTTCCCTGGCCGCCAAAAGATTATTGAGAGCAGAA 609
                * ***** *** * ** ***** ********** ** ******** ****  ***** *

AtRPL10B        AATGGGGGTTCACCAAGTTTAACCGTGCTGATTACACAAAGCTAAGGCAAGAGAAGAGGA 627
AtRPL10C        AATGGGGATTCACTAAATTCAACCGTGCTGAGTACACGAAGCTGAGAGCGATGAAGAGGA 611
AtRPL10A        AATGGGGCTTCACGAAGTTTAACAGAGCTGACTTCACCAAGTTGAGGCAAGAGAAGCGTG 624
ZmRPL10-1       AGTGGGGCTTCACCAAGTTCAGCCGCGCTGACTACCTGAAGTACAAGAGCGAGGGCAGAA 959
ZmRPL10-2       AGTGGGGCTTCACCAAGTTCAGCCGTGCCGACTACCTGAAGTACAAGAGTGAGGGTAGAA 669
                * ***** ***** ** ** * * * ** ** * *   ***   *       *    *

AtRPL10B        TTGTCCCTGATGGTGTAAATGCCAAGTTCCTATCTTGCCATGGTCCGTTGGCTAACCGTC 687
AtRPL10C        TTGTGCCTGATGGTGTCAATGCTAAGTTTCTATCAAACCATGGTCCATTGGCTAACCGTC 671
AtRPL10A        TTGTCCCTGATGGTGTCAACGCTAAGTTCCTCTCATGCCATGGACCTTTGGCTAACCGTC 684
ZmRPL10-1       TTGTTCCTGATGGTGTCAACGCAAAGCTGCTCGGCAACCACGGCAGACTTGAGAAGCGTG 1019
ZmRPL10-2       TTGTTCCTGATGGTGTCAACGCAAAGCTGCTCGGTAACCATGGAAGACTTGAGAAGCGTG 729
                **** ********** ** ** *** * **      *** **     * *  ** ***

AtRPL10B        AGCCCGGAAGTGCGTTCTTGTCAG----CTGGTGCA-------------CAG<b>TGA</b>TGCAG 730
AtRPL10C        AACCTGGAAGTGCCTTCATATCAGCC-ACTAGCGAA-------------<b>TAA</b>GAATGAAG 717
AtRPL10A        AGCCGGGAAGTGCCTTTTTGCCAGCCCACTAC<b>TGA</b>AGAGTAT-------CAGAACTGAAG 737
ZmRPL10-1       CTCCTGGGAAGGCTTTCCTCGATGCC-GTTGCT<b>TAA</b>GTGC------------GGATGCGA 1066
ZmRPL10-2       CTCCTGGGAAGGCTTTCCTCGAGGCC-GTTGCT<b>TAA</b>GTCCAATCTACAGTTGGAATGCGA 788
                  ** ** *  ** **  *    *     *     *                     **

AtRPL10B        A----------------------TGACTTGTCGATG---TGGAGTTGATATCCTAGTTTT 765
AtRPL10C        AA-------------GATGATGATGATTTGTGGTTG---TAGAACCGATAATGTAGTTTC 761
AtRPL10A        TATCCTTCTCATTCCGGTGAAGAAGAATTATAATCAGCCTGAATCTTTTTACTTATCGTT 797
ZmRPL10-1       ATCCTGACGTTTTGCTTTAGCGTATCTTACTTTGCTTCGTGGAACATGAATTTCAAGTGT 1126
ZmRPL10-2       ATCCAGACGTTTTGGTTTAGCCTATCTTATTTTGCTTTGTGCAACATGAATTTTAAGTGT 848
                                      *  *        *  *          *

AtRPL10B        GGCAGATACTCAGTTTTTATTTTTTTGTTGGTAGTGACAGTTACAAACAATTCTCTTGCG 825
AtRPL10C        TGCTCTT-TTCTGTTTCAATTTTATTGT-AACAGTTGTAG--ACAAG-GATCCTCGTATG 816
AtRPL10A        ATCTCTGGTGTTGTTTTAAGTTTTTAGTTGGACACAATCAGTATTCTGAATCTTTTTGTG 857
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ZmRPL10-1       TTTGAGGGTATTACAGTGCCTTATGTGAACTTGCCTATCT-TGTGCTGAACATCGGAATG 1185
ZmRPL10-2       AT--GGGGTATTACAGTGCCTTGTGTGAACCTGCTTATCT-CGTGCTGAACATCGTTATG 905
                            **    *                     *        *

AtRPL10B        GTTCTG------TTGTTCATGGATAAGTTTTATGAAAGACTTGTTT---TGTTATC---- 872
AtRPL10C        ATTCCAAGACAATTGTTTCAACATGTGTTTCTTACTTTTATAATTC---CATCATCCAGT 873
AtRPL10A        ACTCTTTTGTTTAAGCTCTGAAATGATTTTGTTCCTTCGTT--CTT---GGCCATATATC 912
ZmRPL10-1       TATCCTC--CGAGTATGTTTAATCGCATTAATTTTATTGGAAATTG----GTTGCGGAAC 1239
ZmRPL10-2       CAT-------GGAAGTACTTATCT---TTTGTTCTGCTAAAAATTAAAGTGTTCTGCGAC 955
                  *                       **   *          *

AtRPL10B        ------------------------------------------------------------
AtRPL10C        TTCTCCTTT---------------------------------------------------- 882
AtRPL10A        TTTCATTTGCAAGTTTTATCATGGCTTTAGCTTTAAATATTTTAATTGAAGATTTGCTTG 972
ZmRPL10-1       AATGTCCAATTTACTCGAATTTGATTTCACCACGATCTTTTCTTATCCTTAAAATTTGTA 1299
ZmRPL10-2       TAAATATA-TCTTCTCAATCTGGATTGTCTC----TTTAATTTTATTGGAGATGGTTACA 1010


AtRPL10B        ------------------------------------------------------------
AtRPL10C        ------------------------------------------------------------
AtRPL10A        ------------------------------------------------------------
ZmRPL10-1       TAGAATACGTATTTGTGTGCCATCGCCTTTCCGGAGCTCACCAAACAGTCGTTCCTGCAG 1359
ZmRPL10-2       CAAA-------------------------------------------------------- 1014


AtRPL10B        ----------------------------------------
AtRPL10C        ----------------------------------------
AtRPL10A        ----------------------------------------
ZmRPL10-1       CAGCGTGAAACTGGACTTCAGAGAGAATATTGGGACGAGA 1399
ZmRPL10-2       ----------------------------------------
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B

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AtRPL10A        ATGGGAAGAAGACCTGCGAGGTGTTACCGTCAGATCAAGGGTAAGCCATACCCAAAGTCT 60
AtRPL10C        ATGGGACGAAGACCTGCGAGATGTTACCGTCAGATTAAGGGAAAGCCATACCCGAAATCA 60
AtRPL10B        ATGGGACGAAGACCTGCGAGATGTTACCGTCAAATTAAGGGAAAGCCATACCCTAAATCA 60
ZmRPL10-1       ATGGGCAGAAGGCCTGCTAGATGCTATCGCCAGATCAAGAACAAGCCGTACCCTAAGTCC 60
ZmRPL10-2       ATGGGGAGAAGGCCTGCGAGATGCTATCGCCAGATCAAGAACAAGCCATACCCCAAGTCC 60
                *****  **** ***** ** ** ** ** ** ** ***   ***** ***** ** **

AtRPL10A        CGCTACTGTCGTGGTGTGCCAGATCCAAAAATCAGGATCTACGATGTTGGTATGAAGAGG 120
AtRPL10C        CGATACTGTCGTGGTGTGCCAGATCCCAAAATCAGGATCTACGATGTTGGTATGAAGAGG 120
AtRPL10B        AGATACTGTCGTGGTGTTCCCGATCCTAAGATCAGGATTTACGATGTTGGTATGAAGAGG 120
ZmRPL10-1       AGGTACTGCCGTGGTGTCCCTGACCCCAAGATCAGGATCTACGATGTCGGGATGAAGAGG 120
ZmRPL10-2       AGGTACTGCCGTGGTGTCCCTGACCCCAAGATCAGGATCTACGATGTTGGCATGAAGAGA 120
                 * ***** ******** ** ** ** ** ******** ******** ** ********

AtRPL10A        AAGGGTGTTGATGAGTTTCCATTCTGTGTCCATTTGGTGTCATGGGAGAAGGAGAATGTG 180
AtRPL10C        AAAGGTGTTGATGAGTTTCCATTCTGTGTTCATTTGGTTTCATGGGAGAAAGAGAATGTG 180
AtRPL10B        AAAGGAGTTGATGAGTTCCCTTACTGTGTTCATTTGGTTTCATGGGAGAAAGAGAATGTT 180
ZmRPL10-1       AAGGGTGTTGATGAGTTCCCCTACTGTGTGCACCTTGTCTCTTGGGAGAAGGAGAATGTC 180
ZmRPL10-2       AAGGGTGTTGATGAGTTCCCCTACTGTGTGCACCTTGTCTCTTGGGAGAAGGAGAATGTC 180
                ** ** *********** ** * ****** **  * ** ** ******** ********

AtRPL10A        TCAAGTGAAGCACTTGAAGCTGCCCGTATT------------------------------ 210
AtRPL10C        TCAAGTGAAGCACTTGAAGCAGCACGTATT------------------------------ 210
AtRPL10B        TCAAGTGAAGCTCTTGAAGCTGCTCGTATT------------------------------ 210
ZmRPL10-1       TCCAGTGAGGCGCTCGAGGCTGCCCGCATTGCCTGCAACAAGTACATGACCAAGTCTGCA 240
ZmRPL10-2       TCCAGTGAGGCTCTTGAGGCTGCCCGTATT------------------------------ 210
                ** ***** ** ** ** ** ** ** ***

AtRPL10A        ------------------------------GCTTGCAACAAGTACATGGTGAAGTCTGCT 240
AtRPL10C        ------------------------------GCTTGCAACAAGTATATGGTGAAATCTGCT 240
AtRPL10B        ------------------------------GCTTGTAACAAGTACATGGTGAAGTCTGCC 240
ZmRPL10-1       GGAAAGGATGCCTTCCACCTTAGGGTCCGTGCCTGCAACAAGTACATGACCAAGTCTGCA 300
ZmRPL10-2       ------------------------------GCCTGCAACAAGTACATGACCAAGTCTGCA 240
                                    ** ** ******** ***   ** *****

AtRPL10A        GGAAAAGATGCTTTTCATTTGAGGATTAGGGTTCATCCTTTCCATGTTCTCAGGATTAAC 300
AtRPL10C        GGGAAAGATGCTTTTCATTTGAGGATTAGGGTTCATCCTTTCCATGTTCTCAGGATTAAC 300
AtRPL10B        GGGAAAGATGCGTTTCATCTCCGTATTAGAGTTCATCCTTTCCATGTTCTTAGGATCAAT 300
ZmRPL10-1       GGAAAGGATGCCTTCCACCTTAGGGTCCGGGTTCACCCGTTCCATGTCCTCCGTATCAAC 360
ZmRPL10-2       GGAAAGGATGCCTTCCACCTTCGGGTCCGGGTTCACCCCTTCCATGTCCTTCGTATCAAC 300
                ** ** ***** ** **  *  *  *  * ***** ** ******** **  * ** **

AtRPL10A        AAGATGCTTTCGTGTGCTGGAGCTGATAGGCTTCAGACTGGTATGAGAGGTGCTTTTGGT 360
AtRPL10C        AAGATGCTTTCGTGTGCTGGAGCTGATAGGCTTCAGACTGGAATGAGAGGTGCTTTTGGT 360
AtRPL10B        AAGATGCTTTCTTGTGCTGGAGCTGATAGACTTCAGACTGGTATGAGAGGTGCTTTTGGC 360
ZmRPL10-1       AAGATGCTTTCCTGTGCCGGGGCTGATAGGCTCCAGACTGGAATGAGGGGTGCCTTTGGC 420
ZmRPL10-2       AAGATGCTTTCGTGTGCTGGGGCTGATAGGCTCCAGACTGGAATGAGGGGTGCCTTTGGC 360
                *********** ***** ** ******** ** ******** ***** ***** *****

AtRPL10A        AAAGCTTTGGGTACTTGTGCTCGTGTTGCTATTGGACAGGTTCTTTTGTCTGTTCGTTGC 420
AtRPL10C        AAAGCTCTTGGTACTTGTGCTAGAGTTGCGATTGGACAGGTTCTTTTGTCTGTTAGGTGT 420
AtRPL10B        AAAGCTCTTGGTACTTGTGCTAGAGTTGCTATTGGACAGGTTCTTTTGTCTGTGAGGTGC 420
ZmRPL10-1       AAGCCTCAGGGCACCTGTGCTAGGGTGGACATTGGTCAGGTCCTCCTTTCCGTGCGATGC 480
ZmRPL10-2       AAGCCTCAGGGCACCTGTGCTAGGGTGGACATTGGTCAGGTCCTCCTTTCTGTTCGATGC 420
                **  **   ** ** ****** * ** *  ***** ***** **  * ** **  * **

AtRPL10A        AAGGATGCCCATGGTCACCATGCTCAAGAGGCTCTTCGTCGTGCTAAGTTCAAGTTCCCT 480
AtRPL10C        AAGGATAATCATGGAGTTCATGCTCAGGAAGCTCTTCGTAGAGCTAAGTTTAAGTTCCCT 480
AtRPL10B        AAAGATGCTCATGGTCATCATGCTCAGGAGGCTCTTCGTCGTGCTAAGTTTAAGTTCCCT 480
ZmRPL10-1       AAGGACAACAATGCTGCCCATGCCAGCGAAGCTCTGCGTCGCGCTAAGTTCAAGTTCCCT 540
ZmRPL10-2       AAGGACAACAATGCTGCACATGCCAGTGAAGCTCTGCGTCGCGCCAAGTTCAAGTTCCCT 480
                ** **     ***     *****    ** ***** *** * ** ***** *********

AtRPL10A        GGTCGTCAAAAGATTATTGTCAGCAGGAAATGGGGCTTCACGAAGTTTAACAGAGCTGAC 540
AtRPL10C        GGTCGTCAAAAGATCATTGTTAGCAGGAAATGGGGATTCACTAAATTCAACCGTGCTGAG 540
AtRPL10B        GGTCGTCAAAAGATCATTGTTAGCAGGAAATGGGGGTTCACCAAGTTTAACCGTGCTGAT 540
ZmRPL10-1       GGCCGCCAAAAGATCATTGAGAGCAGAAAGTGGGGCTTCACCAAGTTCAGCCGCGCTGAC 600
ZmRPL10-2       GGCCGCCAAAAGATTATTGAGAGCAGAAAGTGGGGCTTCACCAAGTTCAGCCGTGCCGAC 540
                ** ** ******** ****  ***** ** ***** ***** ** ** * * * ** **

AtRPL10A        TTCACCAAGTTGAGGCAAGAGAAGCGTGTTGTCCCTGATGGTGTCAACGCTAAGTTCCTC 600
AtRPL10C        TACACGAAGCTGAGAGCGATGAAGAGGATTGTGCCTGATGGTGTCAATGCTAAGTTTCTA 600
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AtRPL10B        TACACAAAGCTAAGGCAAGAGAAGAGGATTGTCCCTGATGGTGTAAATGCCAAGTTCCTA 600
ZmRPL10-1       TACCTGAAGTACAAGAGCGAGGGCAGAATTGTTCCTGATGGTGTCAACGCAAAGCTGCTC 660
ZmRPL10-2       TACCTGAAGTACAAGAGTGAGGGTAGAATTGTTCCTGATGGTGTCAACGCAAAGCTGCTC 600
                * *   ***   *       *    *  **** ********** ** ** *** * **

AtRPL10A        TCATGCCATGGACCTTTGGCTAACCGTCAGCCGGGAAGTGCCTTTTTGCCAGCCCACTAC 660
AtRPL10C        TCAAACCATGGTCCATTGGCTAACCGTCAACCTGGAAGTGCCTTCATATCAGCC-ACTAG 659
AtRPL10B        TCTTGCCATGGTCCGTTGGCTAACCGTCAGCCCGGAAGTGCGTTCTTGTCAGCT-GGTGC 659
ZmRPL10-1       GGCAACCACGGCAGACTTGAGAAGCGTGCTCCTGGGAAGGCTTTCCTCGATGCC-GTTGC 719
ZmRPL10-2       GGTAACCATGGAAGACTTGAGAAGCGTGCTCCTGGGAAGGCTTTCCTCGAGGCC-GTTGC 659
                     *** **     * *  ** ***   ** ** *  ** **  *    **    *

AtRPL10A        TGA---- 663
AtRPL10C        CGAATAA 666
AtRPL10B        ACAGTGA 666
ZmRPL10-1       TTAA--- 723
ZmRPL10-2       TTAA--- 663
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C

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AtRPL10A        MGRRPARCYRQIKGKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPFCVHLVSWEKENV 60
AtRPL10B        MGRRPARCYRQIKGKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPYCVHLVSWEKENV 60
AtRPL10C        MGRRPARCYRQIKGKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPFCVHLVSWEKENV 60
ZmRPL10-1       MGRRPARCYRQIKNKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPYCVHLVSWEKENV 60
ZmRPL10-2       MGRRPARCYRQIKNKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPYCVHLVSWEKENV 60
                ************.*******************************:************

AtRPL10A        SSEALEAARIACNKYMVKSAGKDAFHLRIRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
AtRPL10B        SSEALEAARIACNKYMVKSAGKDAFHLRIRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
AtRPL10C        SSEALEAARIACNKYMVKSAGKDAFHLRIRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
ZmRPL10-1       SSEALEAARIACNKYMTKSAGKDAFHLRVRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
ZmRPL10-2       SSEALEAARIACNKYMTKSAGKDAFHLRVRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
                ***************.***********:******************************

AtRPL10A        KALGTCARVAIGQVLLSVRCKDAHGHHAQEALRRAKFKFPGRQKIIVSRKWGFTKFNRAD 180
AtRPL10B        KALGTCARVAIGQVLLSVRCKDAHGHHAQEALRRAKFKFPGRQKIIVSRKWGFTKFNRAD 180
AtRPL10C        KALGTCARVAIGQVLLSVRCKDNHGVHAQEALRRAKFKFPGRQKIIVSRKWGFTKFNRAE 180
ZmRPL10-1       KPQGTCARVDIGQVLLSVRCKDNNAAHASEALRRAKFKFPGRQKIIESRKWGFTKFSRAD 180
ZmRPL10-2       KPQGTCARVDIGQVLLSVRCKDNNAAHASEALRRAKFKFPGRQKIIESRKWGFTKFSRAD 180
                *. ****** ************ :. **.**************** *********.**:

AtRPL10A        FTKLRQEKRVVPDGVNAKFLSCHGPLANRQPGSAFLPAHY- 220
AtRPL10B        YTKLRQEKRIVPDGVNAKFLSCHGPLANRQPGSAFLSAGAQ 221
AtRPL10C        YTKLRAMKRIVPDGVNAKFLSNHGPLANRQPGSAFISATSE 221
ZmRPL10-1       YLKYKSEGRIVPDGVNAKLLGNHGRLEKRAPGKAFLDAVA- 220
ZmRPL10-2       YLKYKSEGRIVPDGVNAKLLGNHGRLEKRAPGKAFLEAVA- 220
                : * :   *:********:*. ** * :* **.**: *
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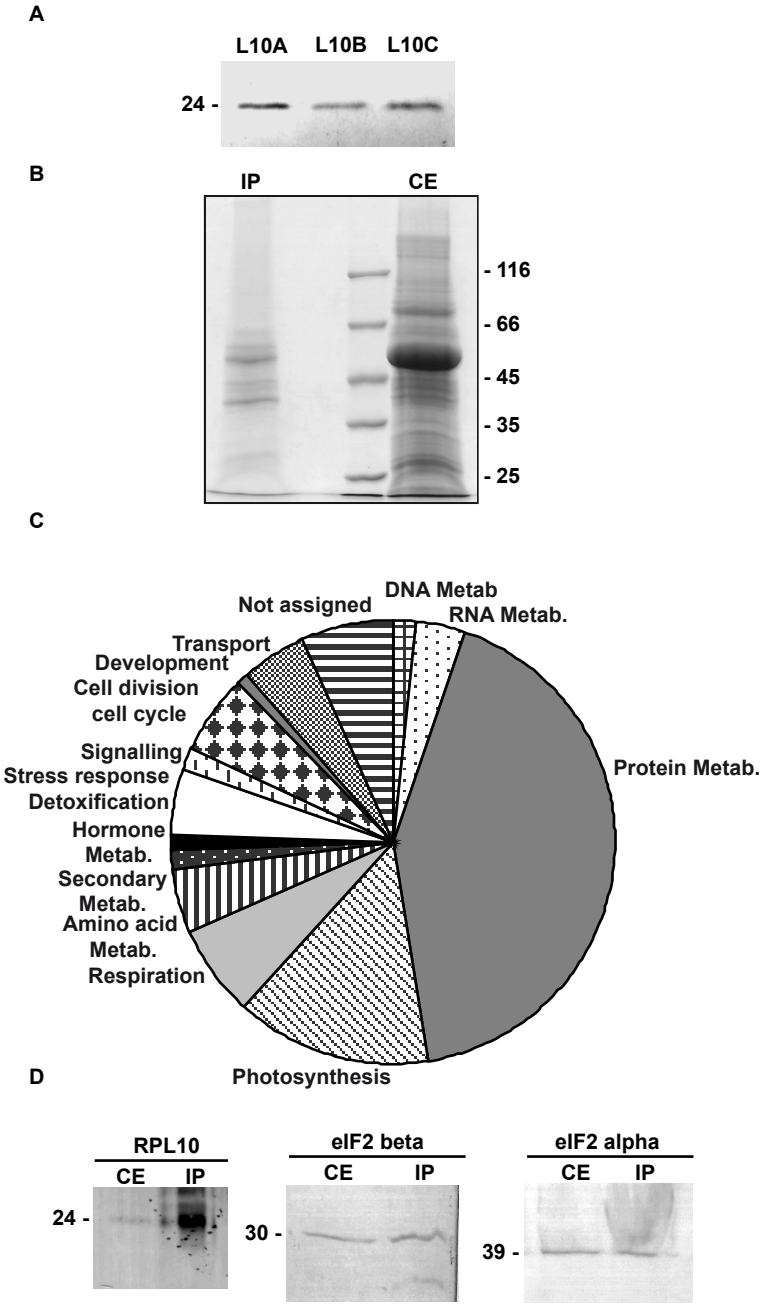
H. sapiens          MGRRPARCYRYCKNKPYPKSRFCRGVPDAKIRIFDLGRKKAKVDEFPLCGHMVSDEYEQL 60
M. musculus         MGRRPARCYRYCKNKPYPKSRFCRGVPDAKIRIFDLGRKKAKVDEFPLCGHMVSDEYEQL 60
G. gallus           -----PRCYRYCKNKPYPKSRFCRGVPDPKIRIFDLGRKKAKVDEFPLCGHMVSDEYEQL 55
C. elegans          MGRRPARCYRYIKNKPYPKSRFCRGVPDAKIRIFDLGNKRANVDTFPACVHMMSNEREHL 60
S. cerevisiae       MARRPARCYRYQKNKPYPKSRYNRAVPDSKIRIYDLGKKKATVDEFPLCVHLVSNELEQL 60
Z. mays-1           MGRRPARCYRQIKNKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPYCVHLVSWEKENV 60
Z. mays-2           MGRRPARCYRQIKNKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPYCVHLVSWEKENV 60
S. melongena        MGRRPARCYRQIKNKPYPKSRFCRGVPDPKIRIYDVGMKRKGVDEFPFCVHLVSWEKENV 60
L. esculetum        MGRRPARCYRQIKNKPYPKSRFCRGVPDPKIRIYDVGMKKKGVDEFPFCVHLVSWEKENV 60
A. thaliana-A       MGRRPARCYRQIKGKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPFCVHLVSWEKENV 60
A. thaliana-B       MGRRPARCYRQIKGKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPYCVHLVSWEKENV 60
A. thaliana-C       MGRRPARCYRQIKGKPYPKSRYCRGVPDPKIRIYDVGMKRKGVDEFPFCVHLVSWEKENV 60
P. taeda            MGRRPARCYRQIKNKPYPKSRYCRGVPDPKIRIFDVGAKKRLVDEFPFCVHLVSWEKENV 60
T. brucei           MARRPARCYRFCKNKPYPKSRFCRGVPDPRIRTFDIGKRRAPVDEFPVCVHVVSRELEQI 60
E. histolytica      MGRRPGRCYRLVRGHPYPKSKYCRGVPDPRIKLFDIGNRSAPCDDFPCCVHIVGLERENI 60
                          ****  :.:*****:: *.***.:*: :*:* :    * ** * *::. * *::

H. sapiens          SSEALEAARICANKYMVKSCGKDGFHIRVRLHPFHVIRINKMLSCAGADRLQTGMRGAFG 120
M. musculus         SSEALEAARICANKYMVKSCGKDGFHIRVRLHPFHVIRINKMLSCAGADRLQTGMRGAFG 120
G. gallus           SSEALEAARICANKYMVKSCGKDGFHIRVRLHPFHVIRINKMLSCAGADRLQTGMRGAFG 115
C. elegans          SSEALEAARICANKYMVKNCGKDGFHLRVRKHPFHVTRINKMLSCAGADRLQTGMRGAYG 120
S. cerevisiae       SSEALEAARICANKYMTTVSGRDAFHLRVRVHPFHVLRINKMLSCAGADRLQQGMRGAWG 120
Z. mays-1           SSEALEAARIACNKYMTKSAGKDAFHLRVRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
Z. mays-2           SSEALEAARIACNKYMTKSAGKDAFHLRVRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
S. melongena        SSEALEAARIACNKYMTKSAGKDAFHLRVRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
L. esculetum        SSEALEAARIACNKYMTKSAGKDAFHLRVRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
A. thaliana-A       SSEALEAARIACNKYMVKSAGKDAFHLRIRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
A. thaliana-B       SSEALEAARIACNKYMVKSAGKDAFHLRIRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
A. thaliana-C       SSEALEAARIACNKYMVKSAGKDAFHLRIRVHPFHVLRINKMLSCAGADRLQTGMRGAFG 120
P. taeda            SSEALEAGRIACNKYMVKFAGKDGFHLRVRVHPFHVLRSNKMLSCAGADRLQTGMRGAFG 120
T. brucei           SSEALEAARIQANKYMVKRANKECFHMRIRAHPFHVLRINKMLSCAGADRLQTGMRQSYG 120
E. histolytica      SSEAMEAARISINKNMLKYAGKDGFHVRIRIHPFHVLRINKMLSCAGADRLQTGMRGAWG 120
                   ****:**.**  ** * . ..:: **:*:* ***** * ************ *** ::*

H. sapiens          KPQGTVARVHIGQVIMSIRTKLQNKEHVIEALRRAKFKFPGRQKIHISKKWGFTKFNADE 180
M. musculus         KPQGTVARVHIGQVIMSIRTKLQNKEHVIEALRRAKFKFPGRQKIHISKKWGFTKFNADE 180
G. gallus           KPQGTVARVHMGQVIMSIRTKAQNKEHVVEALRRAKFKFPGRQKIHISKKWGFTKFNADA 175
C. elegans          KPQGLVARVDIGDILFSMRIKEGNVKHAIEAFRRAKFKFPGRQIIVSSRKWGFTKWDRED 180
S. cerevisiae       KPHGLAARVDIGQIIFSVRTKDSNKDVVVEGLRRARYKFPGQQKIILSKKWGFTNLDRPE 180
Z. mays-1           KPQGTCARVDIGQVLLSVRCKDNNAAHASEALRRAKFKFPGRQKIIESRKWGFTKFSRAD 180
Z. mays-2           KPQGTCARVDIGQVLLSVRCKDNNAAHASEALRRAKFKFPGRQKIIESRKWGFTKFSRAD 180
S. melongena        KPQGVCARVAIGQVLLSVRCKDGNSNHAQEALRRAKFKFPGRQKIIVSRKWGFTKFSRTD 180
L. esculetum        KPQGVCARVAIGQVLLSVRCKDGNANHAQEALRRAKFKFPGRQKIIVSRKWGFTKFSRTD 180
A. thaliana-A       KALGTCARVAIGQVLLSVRCKDAHGHHAQEALRRAKFKFPGRQKIIVSRKWGFTKFNRAD 180
A. thaliana-B       KALGTCARVAIGQVLLSVRCKDAHGHHAQEALRRAKFKFPGRQKIIVSRKWGFTKFNRAD 180
A. thaliana-C       KALGTCARVAIGQVLLSVRCKDNHGVHAQEALRRAKFKFPGRQKIIVSRKWGFTKFNRAE 180
P. taeda            KPQGTCARVAIGQVLLSVRSRDNHSNHAQEALRRAKFKFPGREKIIVNRKWGFTKYTRAD 180
T. brucei           KPNGTCARVRIGQILLSMRTKDTYVPQALESLRRAKMKFPGRQIIVISKYWGFTNILRNE 180
E. histolytica      KSYGSCARVKVGQVLISGRCKEQHLPAMIKSFRLACYKFAGRQKLVISNKWGFTKYTKEE 180
                   *. *  *** :*::::* * :       :.:* *  **.*:: :  .. ****:

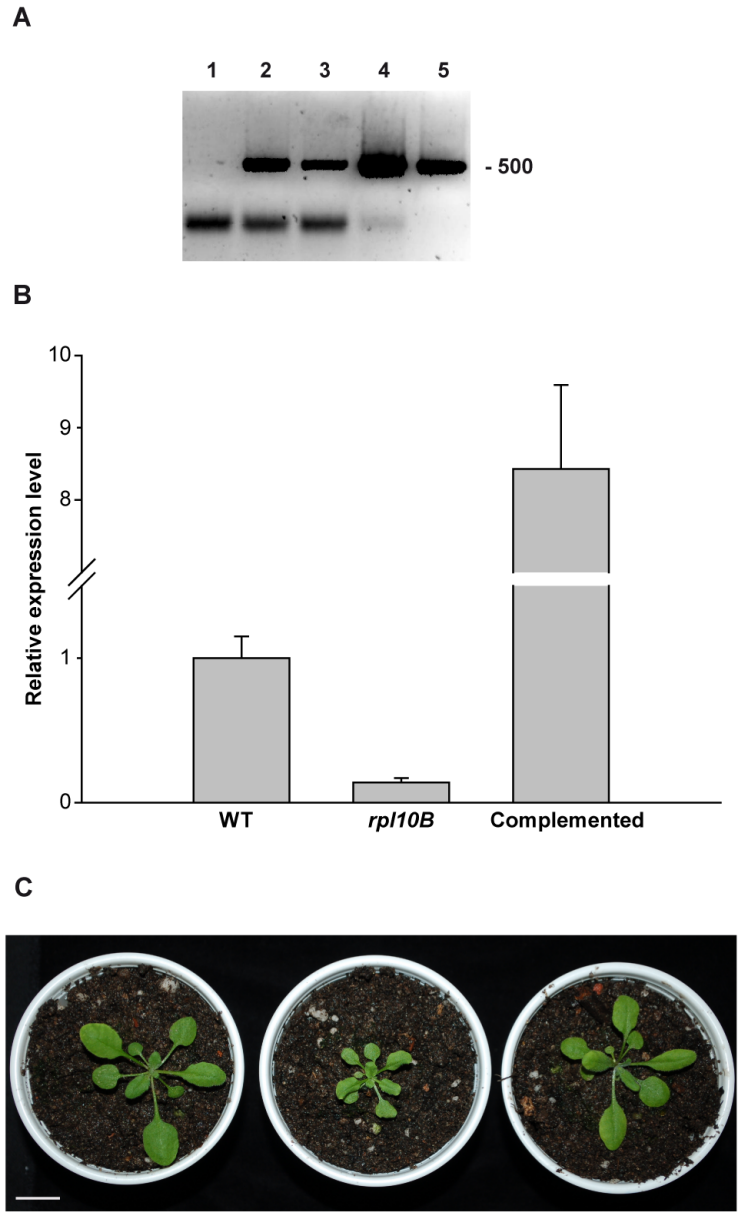
H. sapiens          FEDMVAEKRLIPDGCGVKYIPNRGPLDK-WRALHS-------------- 214
M. musculus         FEDMVAEKRLIPDGCGVKYIPNRGPLDK-WRALHS-------------- 214
G. gallus           FEEMVAQKRLIPDGCGVKYVPGRGPLDR-WRALHAA------------- 210
C. elegans          YERMRAEGRLRSDGVGVQLQREHGPLTK-WIENPI-------------- 214
S. cerevisiae       YLKKREAGEVKDDGAFVKFLSKKGSLENNIREFPEYFAAQA-------- 221
Z. mays-1           YLKYKSEGRIVPDGVNAKLLGNHGRLEK-RAPGKAFLDAVA-------- 220
Z. mays-2           YLKYKSEGRIVPDGVNAKLLGNHGRLEK-RAPGKAFLEAVA-------- 220
S. melongena        YLKYKSENRIVPDGVNAKLLGNHGPLAA-RQPGRAFLSSS--------- 219
L. esculetum        YLKYKSENRIVPDGVNAKLLGCHGRLAA-RQPGRAFLEAAN-------- 220
A. thaliana-A       FTKLRQEKRVVPDGVNAKFLSCHGPLAN-RQPGSAFLPAHY-------- 220
A. thaliana-B       YTKLRQEKRIVPDGVNAKFLSCHGPLAN-RQPGSAFLSAGAQ------- 221
A. thaliana-C       YTKLRAMKRIVPDGVNAKFLSNHGPLAN-RQPGSAFISATSE------- 221
P. taeda            YLKWKTENRIVPDGVNPKLLGCRGPLSN-RKPGQAFLKPAVVLSSDLVA 228
T. brucei           YEELRDAGKLQQRGLHVKLITPKGKITP--YNIMA------------- 213
E. histolytica      YQQLNKDGKIIADGCYFKLATTKGPLPK--VN---------------- 210
                   :       .:   *   :    :* :
```

Supplemental Figure 2



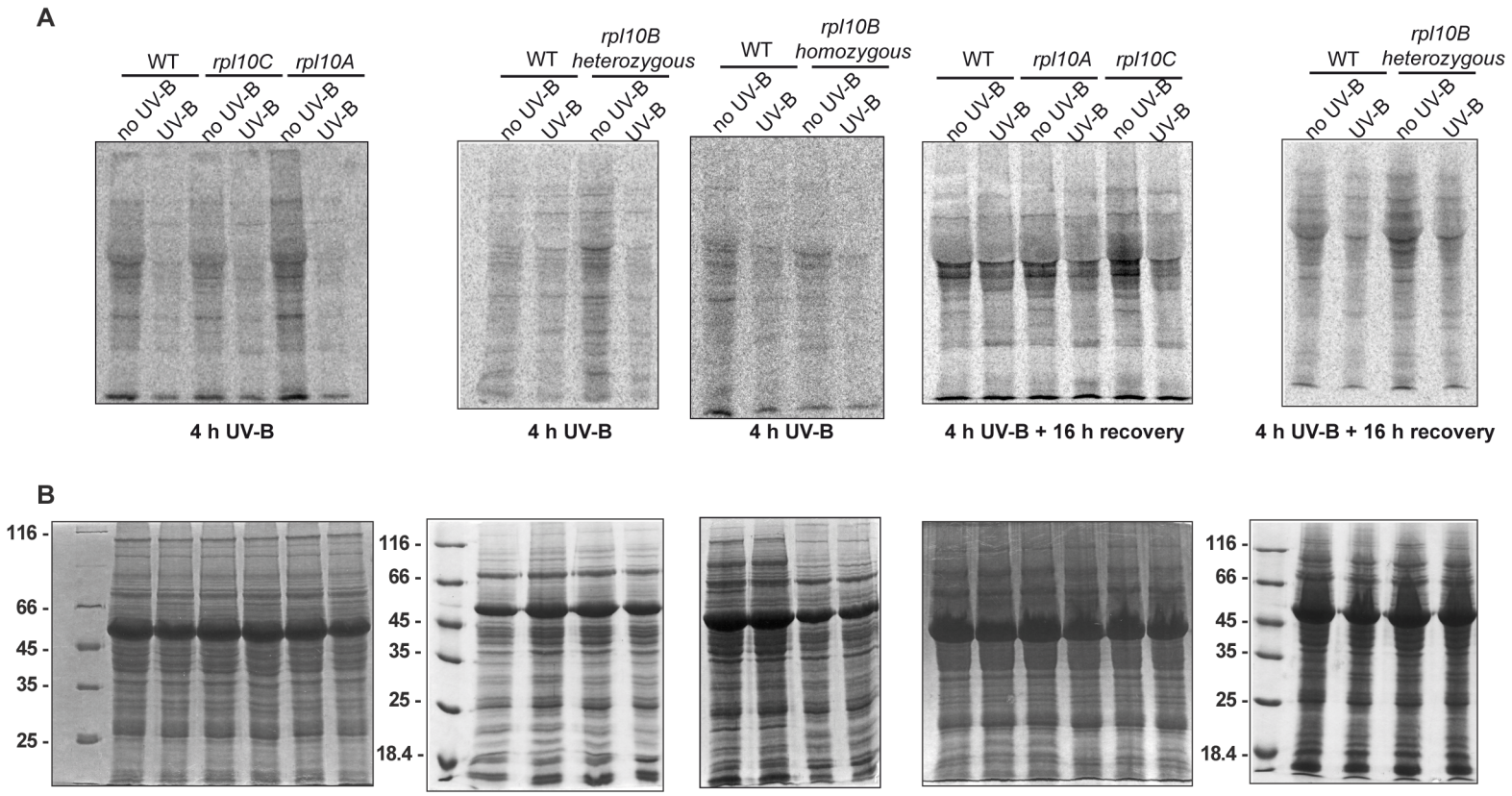
Coimmnunoprecipitation of RPL10 proteins in A. thaliana. A, Immunoblot analysis of A. thaliana recombinant RPL10 proteins. Partially purified recombinant RPL10 proteins were run on 12% SDS-PAGE and subjected to immunoblot analysis for RPL10. Ten micrograms of total proteins were loaded in all lanes. **B, SDS-PAGE (10%) of RPL10-associated proteins. C,** Classification of RPL10-associated proteins based on their cell functions. Proteins with percentage of coverage higher than 10% or at least two tryptic peptides were included in the diagram. Clustering was performed according to Usadel et al. (2006). D, **Immunoblot analysis of RPL10-associated proteins.** RPL10 proteins were immunoprecipitated from *A. thaliana* crude extracts with antibodies against *H. sapiens* QM protein. The immunocomplexes were solubilized, run on 12% SDS-PAGE and subjected to immunoblot analysis for RPL10, eukaryotic translation initiation factor 2 alpha (eIF2 alpha) and eukaryotic translation initiation factor 2 beta (eIF2 beta). The numbers indicate the molecular mass in kDa. CE: crude extract, IP: immunoprecipitate.

Supplemental Figure 3



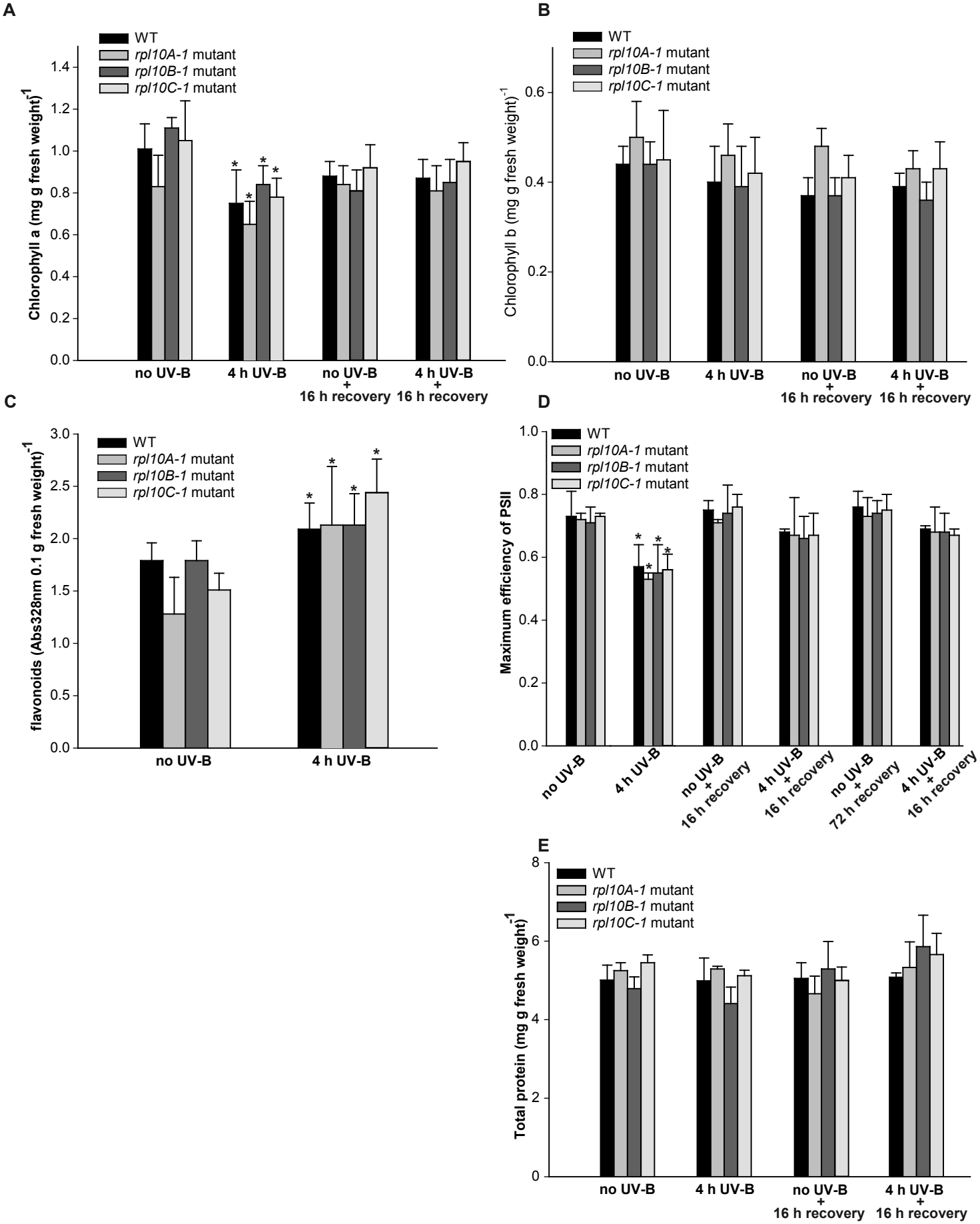
Complementation of *A. thaliana* homozygous *rpl10B* mutants with WT At *RPL10B*. A, Presence of WT *RPL10B* transcript in transformed *A. thaliana rpl10B* mutant plants analyzed by PCR on genomic DNA. Lanes 1: negative control (without DNA); lane 2-4: genomic DNA from leaves of transformed plants; lanes 5: positive control (pCHF3-*RPL10B*). B, At *RPL10B* expression level in Arabidopsis WT, *rpl10B* homozygous and complemented plants analyzed by RT-qPCR. Each reaction was normalized using the C_t values corresponding to the *POLYUBIQUITIN10* mRNA. The means of the results obtained using three independent biological experiments are shown, the error bars indicate the S.D. of the samples. WT levels were set at 1. C, 15-day-old WT (left), *rpl10B* mutant (middle) and complemented plants. Scale bar: 1 cm.

Supplemental Figure 4



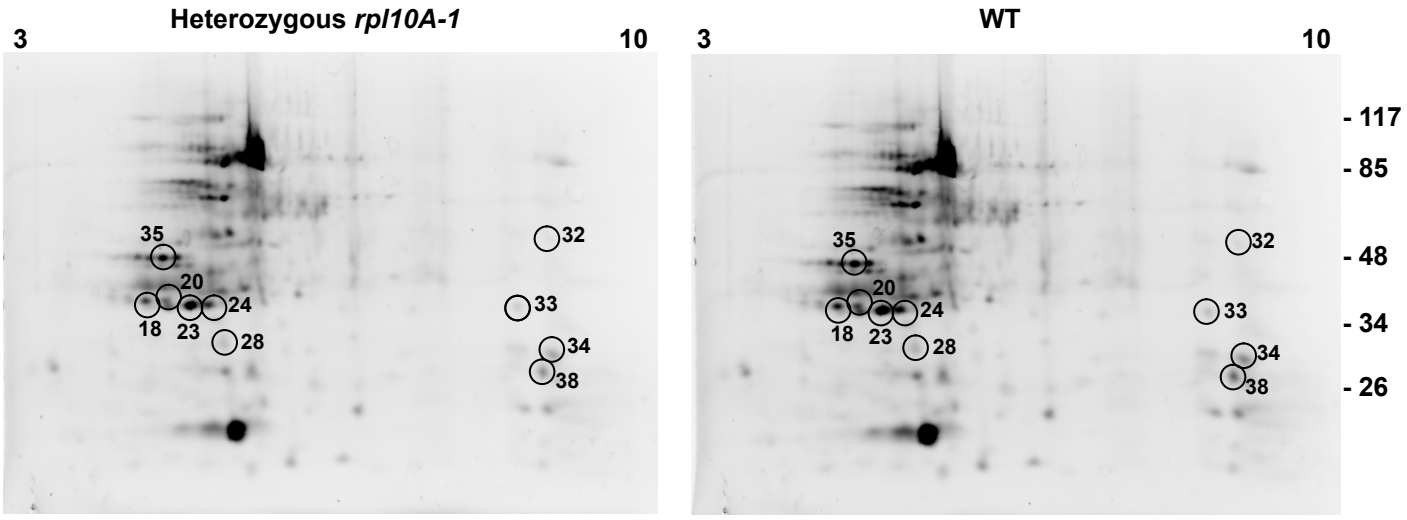
Inhibition of protein synthesis by UV-B in *A. thaliana* WT and *rpl10* mutant plants. Fourty micrograms of total proteins were resolved by 12% SDS-PAGE after *in vivo* [^{35}S]Met labeling, visualized by autoradiography (A) and staining with Coomassie Blue (B) following the UV-B treatment and recovery period indicated.

Supplemental Figure 5



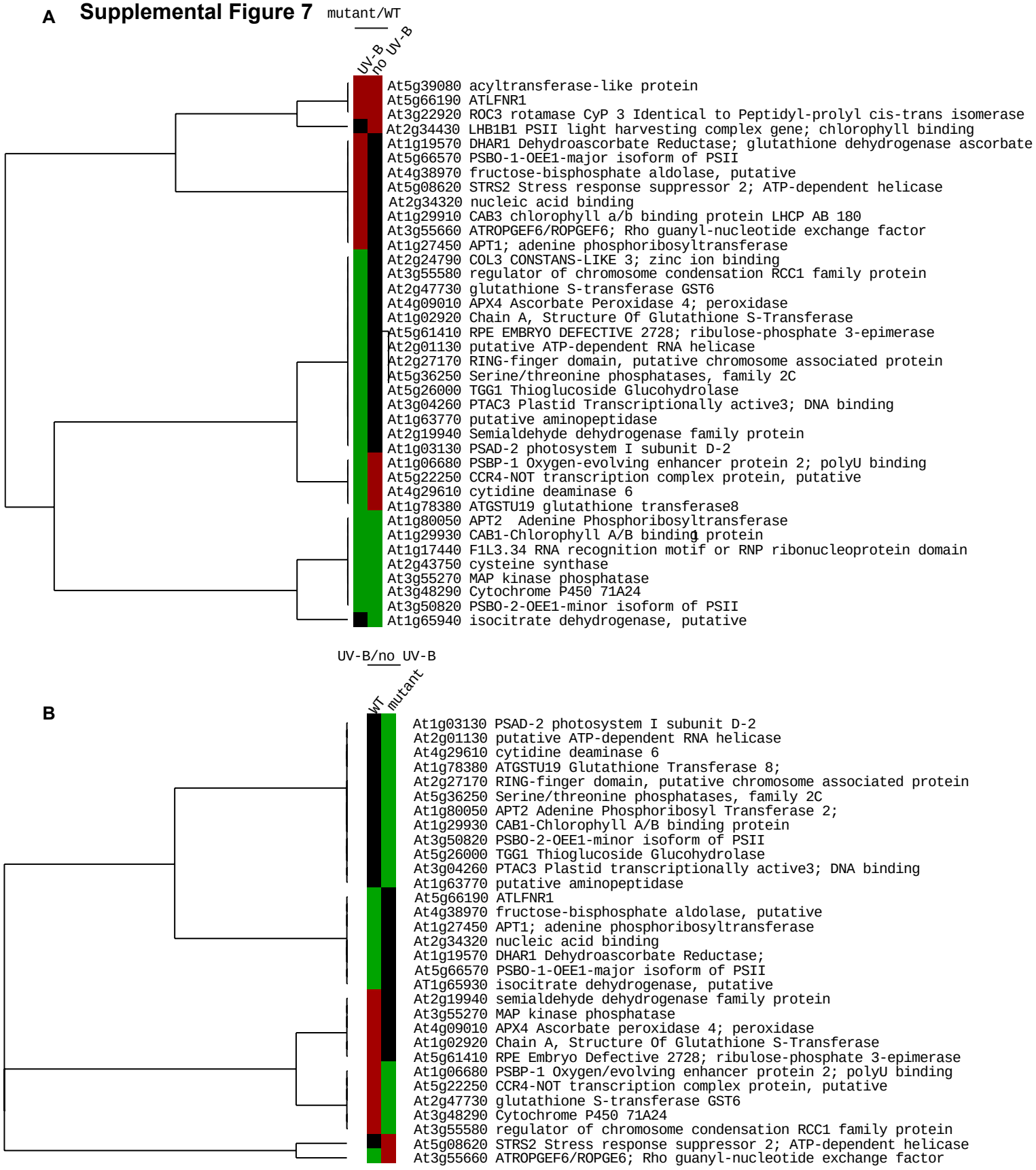
UV-B treatment is not lethal to *A. thaliana* plants. Chlorophyll a (A), Chlorophyll b (B), Flavonoids (C), Maximum Efficiency of PSII (D) and Total proteins (E) were measured after 4 h UV-B (4 h UV-B), 16 h post-treatment (16 h recovery) and in untreated controls (no UV-B). Measurements are the average of six adult leaves from four different plants. Statistical differences from the control are marked with an asterisk ($P<0.05$).

Supplemental Figure 6



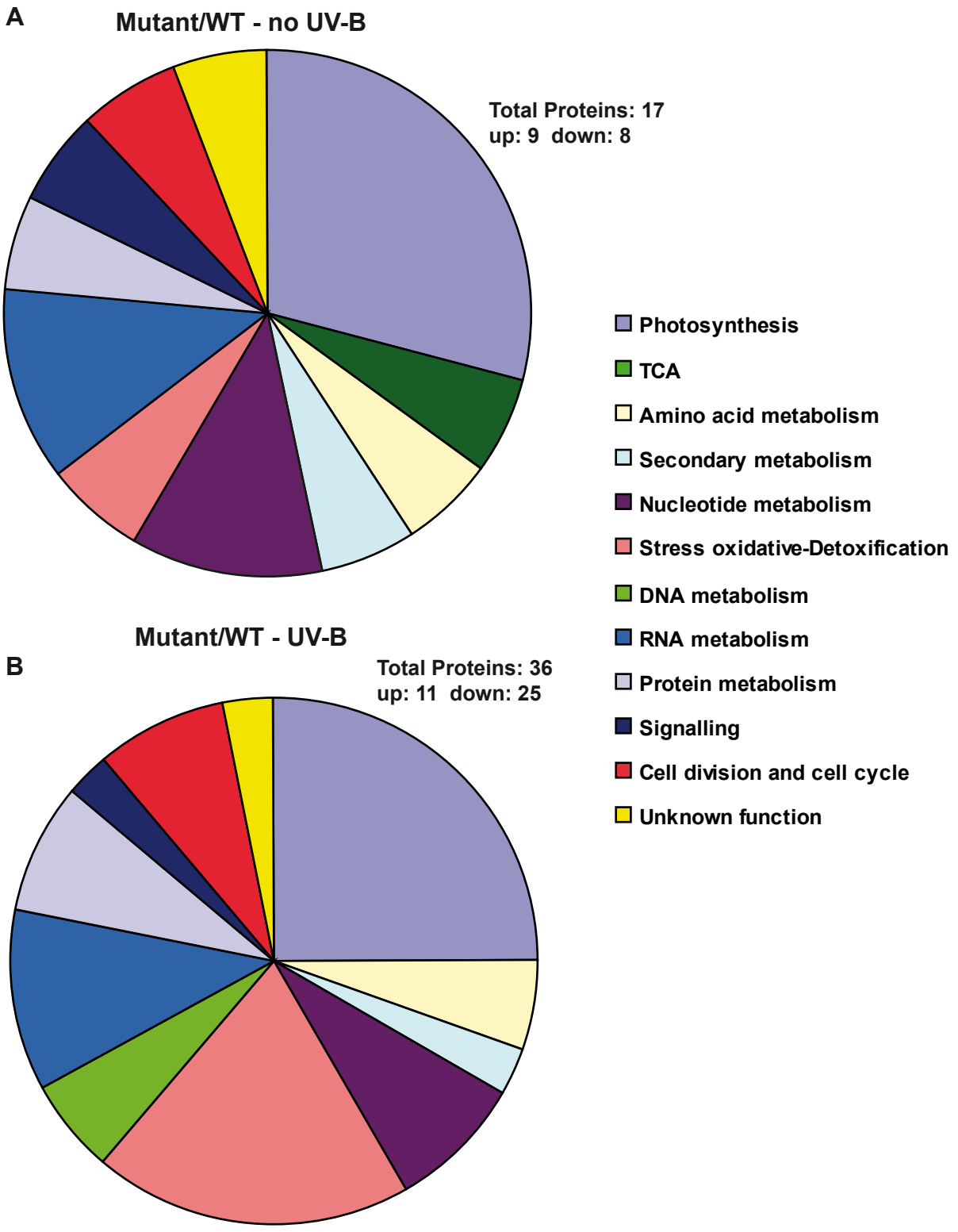
Typical 2D gels of leaves from heterozygous *rpl10A-1* mutant and WT plants after a 4 h UV-B treatment. As examples of proteins with differential expression, the relative abundances of some but not all spots annotated by the number that appears in Supplemental Table S3 are shown. The graphs represent one example from at least three different gels used for the differential analysis. The first dimension was carried out using 17 cm immobilized pH gradient strips (pH 3–10); acidic side to the left; and the second dimension was on 12.5% (w/v) SDS–PAGE. The relative abundance of proteins was determined. The protein spots with changes in intensities (least 1.5-fold, $P < 0.05$) were considered to be different.

Supplemental Figure 7



Hierarchical cluster analysis of proteins showing different levels in *rpl10A* mutant plants in comparison to WT plants under control conditions and after a 4h UV-B treatment identified by MS. A, Proteins included show different levels in *rpl10A* mutants (at least 1.5-fold) in comparison to WT plants under control or UV-B conditions. B, Proteins included show differential abundance (at least 1.5-fold) after a UV-B treatment; these proteins changed differentially in WT plants than in the *rpl10A* mutant. Red indicates higher protein levels than the reference, green indicates lower protein levels than the reference, and black indicates no significant change.

Supplemental Figure 8



Classification of proteins showing different levels in the *rpl10A* mutant in comparison to WT plants based on their cell functions. Proteins were identified by 2D Gel electrophoresis and those showing changes in abundances of at least 1.5-fold were included. A, Proteins changed in the *rpl10A* mutant under control (no UV-B) conditions. B, Proteins changed in the *rpl10A* mutant after 4 h of UV-B.

Supplemental Figure 9. *RPL10s* promoter sequences with predicted cis-elements. The transcription initiation site (referred to as +1) is indicated in bold letter and the ATG start codon is shown in bold and underlined letters. Numbers at the left refer to the positions of nucleotides relative to the putative transcription initiation site.

RPL10A

```
-1000 TAACTTGAAAAGTTTCGGTGTGGAGATCTAACGCTAAAACTTTAATTTCTTTCTTCCCGGTTA
                                                 Homeobox
-937  ACCAATAAAGCGATCCATCTACATACAGAGCATGCCCCCGAGACGAGGAAGTATTAATCCGAT
      CCAAT-BOX
-874  AAGGAGAAGAAGGATTGATATACCTCCAAGTGTTGGTGCTAAAATCAAAAACTTCACATGTAG
                                  UVBox                          MYC2
-811  TAGCGTTTTCTAGGCCAAGTTCGGAAGAGTTATACATAACCAAACCGGTTTGTATATGCCACT
                     UVBox                                       ARF1
-748  GATTTTGTCTTTGCCAAATCCAAATTTAACGTGACTAAAATAACTTGGCTGCTCAAGACAGAT
                                    ACE           UVBox
-685  TTGTTGCAACCTGGAAACAGGGAAACGTCGATGCCATCGAGTGGCGGGATTATAAACAATGTT
                                  ACE
-622  GTTTAAGGTTTGGTAATCAAAGAGGCAAACAAGACCGTCACAACTATTGTGGAAAAGTTGGTA
          MRE
-559  AATATGATATCGTTCTGATGATATCAACAACACGTTAGTTTTAAGTGGAGGAGAATCAGCAGT
                                       ACE
-496  AACATGATGGGGCAACACCAACGTACTGGGTACTTCAGACACCAATACAAGATTTAGATCTTT
                               ACE                 CCAAT-BOX
-433  CCCGCCAGCTGAGCAGATCAACTGTTTCGCCTGGAAATATTGAGATTCGATTGTCAACTTCCA

-370  TTGTTTGCAAGCAGACTTGAATCTGAGCAGAGATTTCACCGGAACTCTCTCAAGAATATCCTC

-307  AACGGTGTCGTGGGGAAGCAATTGCATTATTTCTCTGTCTATTGAGAGGATTTTGTTCTGAGT

-244  GATGGATAACATGAAAGATATGCTTATTTGTATCAATTCAATCCAATGTTGATTTTTTCCTTG
                                                 CCAAT-BOX
-181  AGGAGGAAGATAAAAAAAAAAAAACGTATATACAATCGATGGGCCCTAACCCTATCCCTAACA
            GATA-BOX          ACE              SORLIP2
-118  AATCTCTTTAATATGTAATGCGCTTTAATAGTTAAAGCCCATTAGTTAAAAACCCAGAGCTAT

-55   ATTGTTGACCTAGCAAATTTCGGATCTATAAATTGAAGCCATTTTCTAGGTCATTAGTTTTTT
        W-BOX                                                    +1
      CGTCGAGCAGCCGCGCTTTTTGGCCGAGGAAGGATAAAGAGAGACGCCATG
                 I-BOX
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RPL10B

```
-1000 AGTTTTGCCGTACATCCCTATCAAAGCTGTGATTAAATGCAAGTCTAAATCAAGGCCAATCTT
                                                          CCAAT-BOX
-937  GATGCATAACACATGAGCAGATTCTGCTCCAGACAAATCTCCTAGATCACTAATAGCCGAAAG
            MYC2/DPBF1
-874  AAAAAGCTAAGCAACGTACTGACATTAACGACCACCTCACTTTTTCTCATAATCCTAAACAAA
                     ACE
-811  TCCAAAGCCAACGCTTTCTTAGAAACCTGAAGATACCCATTCATCAAAGTACTAAACGTAACA
                                                            ACE
-748  GCATCAACACTCTGCGGCATTTCGTCGAACACTTTCCGAGCATCACTAATCTTTCCACAAACA

-685  CAGTAAAAATGTATAAGAGCATTCCTCAAATCAGTAAAAACCATAAACCCAGATCTCAAAGCA

-622  ATCCCATGCAATCCCTCACCAATTGAAACACACAATTCACGAGAACATGATTTAAGAGTCGTG
                        CCAAT-BOX
-559  ATAAACGAGAATCGGTCCAAGGTCAAACCTTTAGCTCTCAATTGGTTGAAAACAGAAAATGCT
     GATA-BOX          UVBox       MRE
```

-496 CGCTCCGGCTCATCGCTAATCGAGTAACCTCTGATCATAGTGTTGAACATAAAGAGATTAGTG
GT1-motif
-433 TTGGAGACATGCTCGAAGATCGACGAAGCGTATCGAATGTCAAGTACAGAGGAAAAAGCAAGA

-370 AGCTTGCTCACTGCGAAATCGTCCTTGTCGAGTCCCGTTTTCACCATGTAACCATGAATTCGA

-307 GAAACTTCGACGGTGTCTCTGCAAGACCTTAGATCGTTGATAAGTTTCTGACATTGTGGAGAC
GATA-BOX
-244 AACAACGATTCAAGATTCCTACGACGGAACACGAAATTGCGCCTGAGCCGTGACGTAATCGCC
ACE
-181 AATGTCATCAGAAAGAAAAAAAAGTCGCCGGAATAAACACGGATTTGTTTTTTAAGCTTAAAA

-118 TATCAAATTGGGCTTTAGTTCCTTAATGGGCCTTATTTTGGTCCAAATCCAGTTACGTGGCAA
SORLIP2 ABRE/ACE
-55 AGAGAATTAGGGCTCTTTGTTCTTCTTATTTAAAAAAGTTACGCCTTTCTTCTTCTTCTTCTT
+1
CTTCTTCTTCTTCTTCTTCTTCATTTCTAGGATTCGAAACAACAATCAACGCGATG
I-BOX

RPL10C

-1000 GATGCTATCACGACAAATTAGTCCAAAATGGGCAGCGTATATTTTCTTATATGGGCCTAAACA
SORLIP2
-937 AAGGAAACTAACTAATTATAATCAACTTATGATCATCAGTCAATTATGAAAGGTTATATTTGA
MRE
-874 CAGGAGATTGTGTGTTTAAAACCATTTTGAGTATATCTGTTTTGAATCATTTGAGACAATTGT

-811 GATTTTTGCTTGTTCTGATCCCATTCTTTTAGTCTCGTGCATATGTGATCTTGTATTGTCTAA

-748 TAAGGATTATGATCTGTCCCCTAAACTTCAAAATTTGGAGGCCATGATCTGATTTTTGAATGT

-685 GGTTCTTATAGTTTTTTGCTTGATATTTTGCAGACGAATGATGGTGAATATCCATCTAAGTCA

-622 AATACAGATTCCATTTCTCTTTTAATACAAATCAAATAAGAAAACTGAAGCTTGCAAGCTCGC

-559 TTGTACTAAGTTTCTGAAAGTTTTTATTCTCGACTAAATAATGTCCAAGATGGAAGCAAGACA
UVBox
-496 TAAGCTCCATTGTTGATAGAATGGAGCTTATGTTGGCTTTTGTTTTTGTTTCAAAATGGTTTT

-433 TAACTTATGTGTGATTGCTTAGCCAAATGTGGACTCTGAAGATGGTTTTCAGTTTTTGGTTTT

-370 AATGTCCTTGTTACTATTGTTACACAGTCACACAGAGTTTACAAAAGATCATTCATCATTGTT

-307 TATAAGAGAACAAATTGATAACATATATCTTTTTGATGTGGATGGATTTGTTAACCCTCTAGA
GATA-BOX
-244 AGAACACCCAAATTTGGCTACAAAGTTGTCAACACATTGTTCTTCGTTCTTCTTTGACTTTGA
T-BOX
-181 CTAAAAATAAAAATAAACCTCGGCCTAAGAAAATAGCGTGTTCACATTGGATGATTAAGGCCT

-118 GGACCGAGTATCAAATAATATCTAAATGGGCCTAGCTAAGCAGTTACGTAAGCTAAATTTAGG
SORLIP2 ACE
-55 GTTTGTTTTTGCCGCACCTATAAAATAACAACACAGCTTCCCATTTGTAATTTCTAGGGTTTT
+1
GCAAAACCAACACCGAAGATCCAACACGATG

Supplemental Table S2. Segregation of *RPL10A* alleles

SALK 010170 line (n=47)

Heterozygote	WT
35 (74%)	12 (26%)

Progeny of *rpl10A* heterozygous plant (n=104)

Heterozygote	WT
68 (65%)	36 (35%)

SALK 106656 line (n=67)

Heterozygote	WT
57 (85%)	10 (15%)

Progeny of *rpl10A* heterozygous plant (n=32)

Heterozygote	WT
20 (63%)	12 (37%)

Supplemental Table S4. 5'UTR sequences in *A. thaliana RPL10* transcripts

RPL10	**AGI number**	**Sequence of the 5'UTR**	**Sequence of the putative 5'TOP**
RPL10A	At1g14320	AGTTTTTTCGTCGAGCAGCCGCGCTTTTTGGCCGAGGAAGGATAAAGAGAGACGCC	-
RPL10B	At1g26910	CTTCTTCTTCTTCTTCTTCTTCTTCTTCATTTCTAGGATTCGAAACAACAATCAACGCG	CTTCTTCTTCTTCTTCTTCTTCTTCTTC
RPL10C	At1g66580	AATTTCTAGGGTTTTGCAAAACCAACACCGAAGATCCAACACG	-

Supplemental Table S5. Primer Sequences used for PCR

Name	Sequence	Purpose
Zm thioredoxine-like-for	5'-GGACCAGAAGATTGCAGAAG-3'	qRT-PCR
Zm thioredoxine-like-rev	5'-ACGGATGTCCCATGAAGA-3'	qRT-PCR
Zm actine1-for	5'-CTTCGAATGCCCAGCAAT-3'	qRT-PCR
Zm actine1-rev	5'-CGGAGAATAGCATGAGGAAG-3'	qRT-PCR
Zm RPL10-1-for	5'-TGCAAGGACAACAATGC-3'	qRT-PCR
Zm RPL10-1-rev	5'-TCTGCCCTCGCTCTTGT-3'	qRT-PCR
Zm RPL10-2-for	5'-GCTCGGTAACCATGGAAGA-3'	qRT-PCR
Zm RPL10-2-rev	5'-GAGATAAGCAGGTTCACACA-3'	qRT-PCR
At UBQ10-for	5'-AAGCAGCTTGAGGATGGAC-3'	qRT-PCR
At UBQ10-rev	5'-AGATAACAGGAACGGAAACATAGT-3'	qRT-PCR
At CDPK3-for	5'-CGCTGAGAACCTTTCTGAAG-3'	qRT-PCR
At CDPK3-rev	5'-CCATCTCCATCCATATCAGC-3'	qRT-PCR
At RPL10A-for-1	5'-TCCTTCTCATTCCGGTGA-3'	qRT-PCR
At RPL10A-rev-1	5'-GCCAAGAACGAAGGAACA-3'	qRT-PCR screening
At RPL10B-for-1	5'-TGGTGTTCCCGATCCTAA3’	qRT-PCR
At RPL10B-rev-1	5'-ATCTTTCCCGGCAGACTT-3'	qRT-PCR screening
At RPL10C-for-1	5'-CCAACACCGAAGATCCAA-3'	qRT-PCR screening
At RPL10C-rev-1	5'-TTTTGGGATCTGGCACAC-3'	qRT-PCR screening
At RPL10A-for-2	5'-GCTTTGGGTACTTGTGCTC-3'	screening
At RPL10B-for-2	5'-GTCGCCGGAATAAACACG-3'	screening
At RPL10C-for-2	5'-GCCAAATGTGGACTCTGAAG-3'	screening
At RPL10B-for-3	5'-TAAATTGGTACCACAACAA TCAACGCGATGGGAC-3'	cloning
At RPL10B-rev-2	5'-ATTTAAGTCGACCTGTGCACCAGCTG	cloning

	ACAAGAAC-3'	
prom35-for	5'-CTATCCTTCGCAAGACCCTTC-3'	screening
LB-SALK	5'-GTCCGCAATGTGTTATTAAGTTGTC-3'	screening
LB3-SAIL	5'-TTCATAACCAATCTCGATACAC-3'	screening