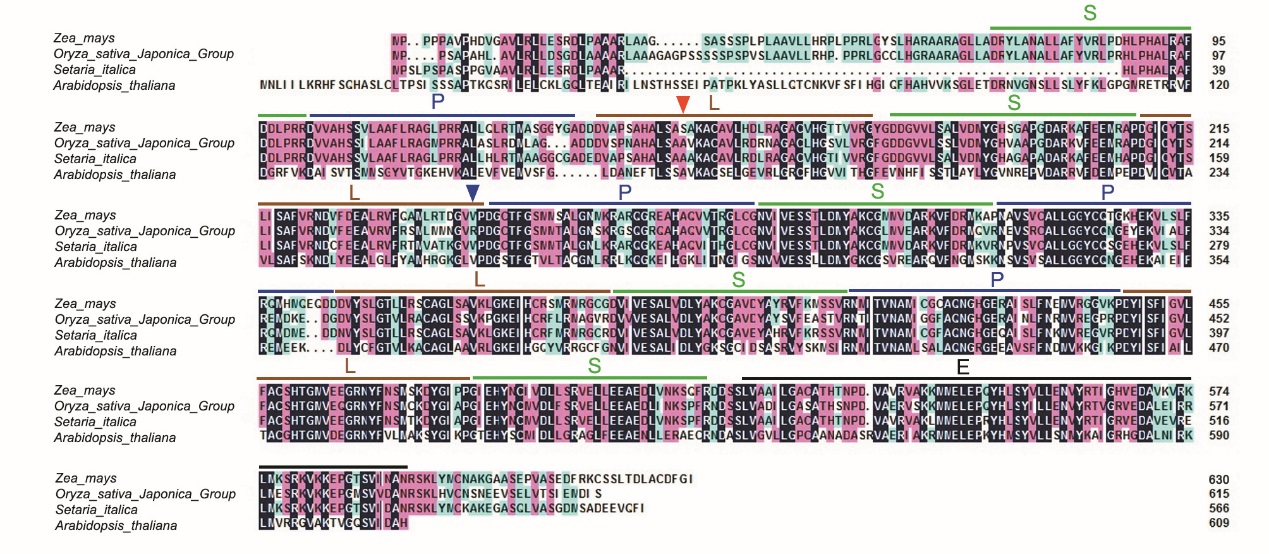
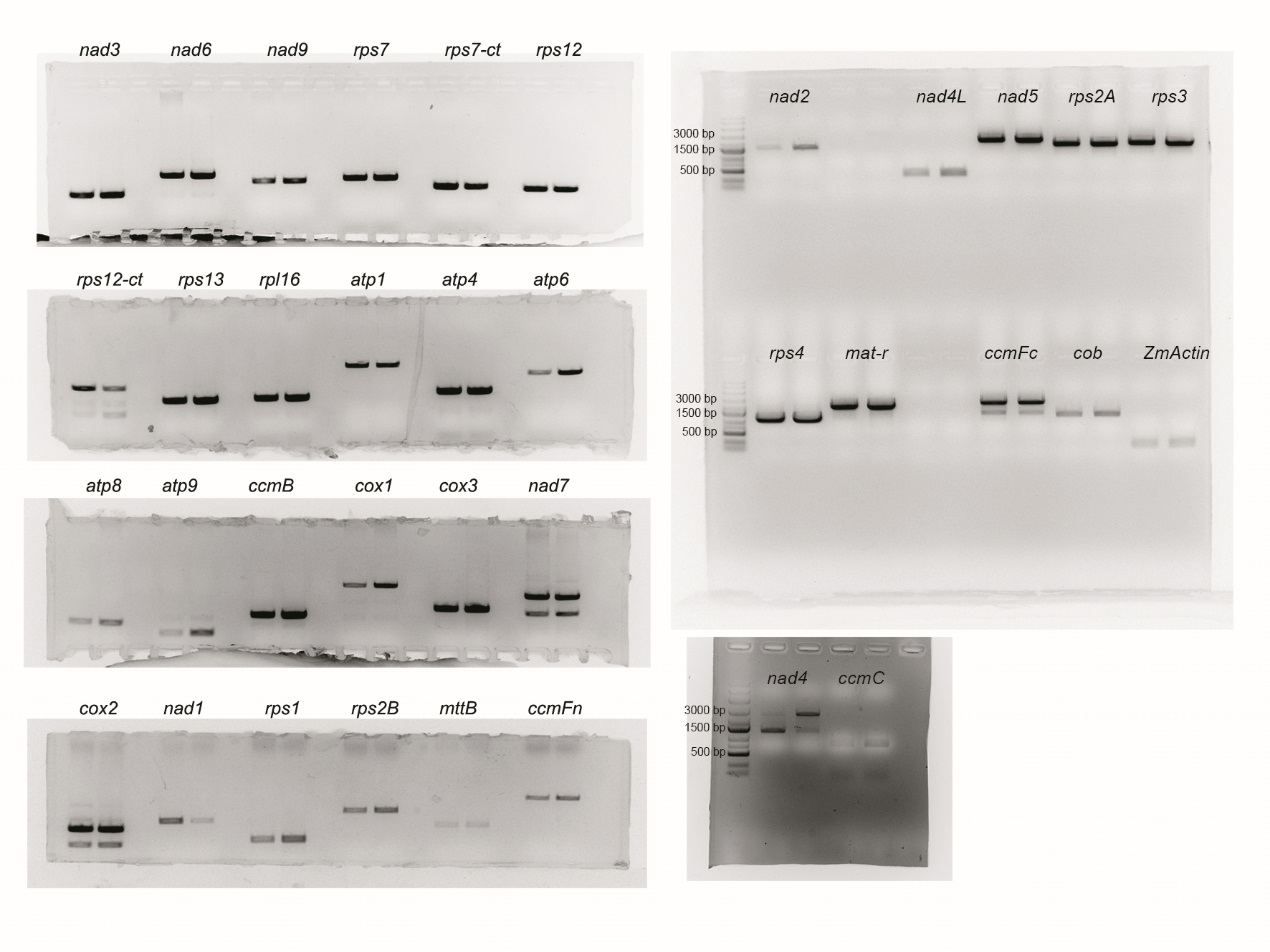
**Additional file 1**

**Supplementary figure**

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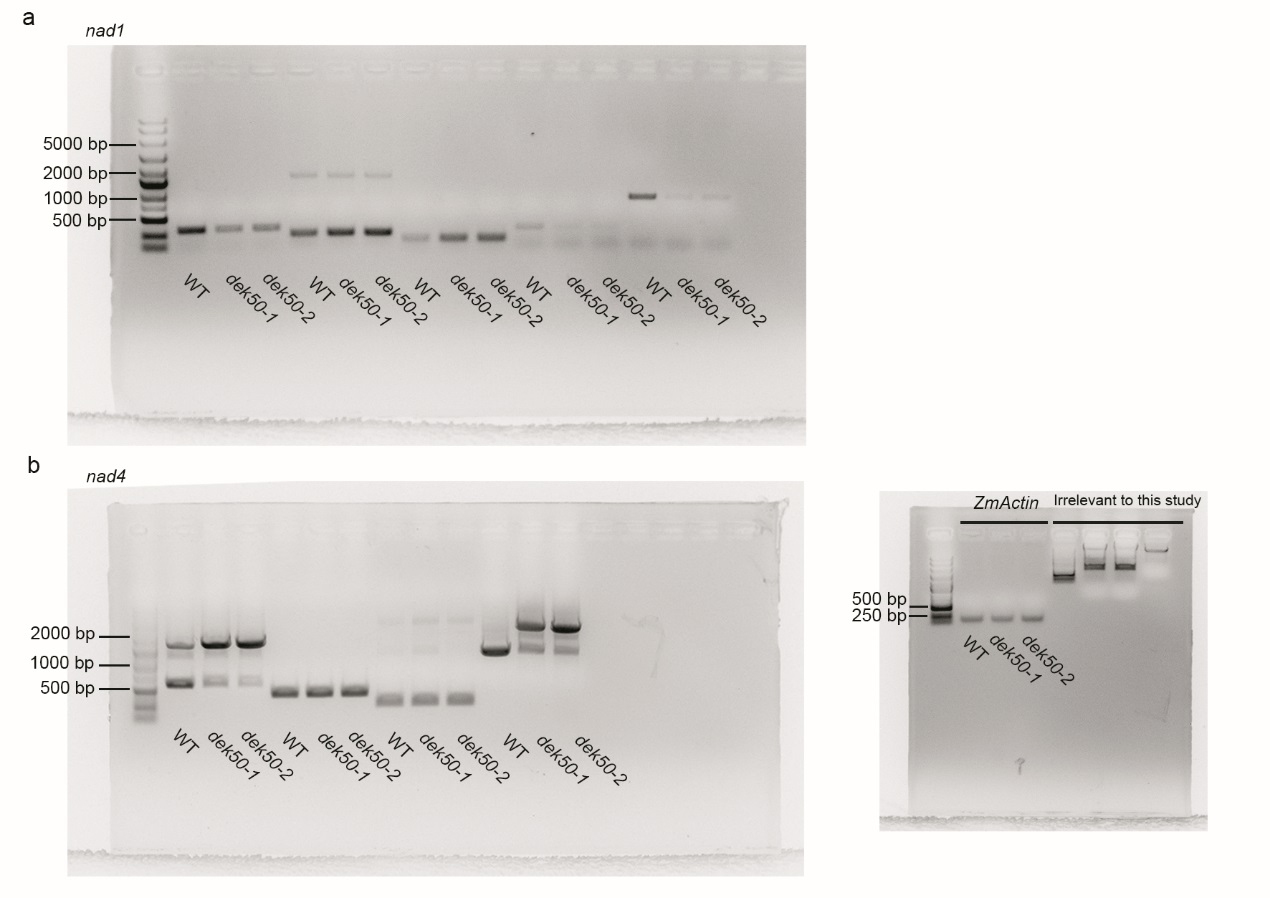
**Figure S1. Amino acid alignment of maize DEK55 with homologous PPR proteins of other plant species**

PPR elements P, L and S are indicated by a green, blue and red bar, respectively. The mutant sites in *dek55-1* and *dek55-2* are indicated by red and blue arrow heads, respectively. E domain is indicated by black bar. *Arabidopsis thaliana*, sequence ID NP\_171853.1; *Oryza sativa Japonica Group*, sequence ID XP\_015643919.1; *Setaria italica*, sequence ID XP\_022681874.1. All data obtained from the NCBI (<https://www.ncbi.nlm.nih.gov/)>



**Figure S2. Original gel images** **for Fig. 5a.**

The RT-PCR products were detected by 1.0% agarose gel electrophoresis. The genes name were marked.



**Figure S3. Original gel images** **for Fig. 5c-d.**

**(a)** Original gel images of RT-PCR analysis of intron-splicing efficiency of *nad1* in WT, *dek55-1* and *dek55-2* mutant kernels.

**(b)** Original gel images of RT-PCR analysis of intron-splicing efficiency of *nad4* in WT, *dek55-1* and *dek55-2* mutant kernels. *ZmActin* gene (GRMZM2G126010) was used as an internal control and original gel image was also shown. Results irrelevant to this study were marked with “Irrelevant to this study”.



**Figure S4. Original gel images** **for Fig. 6a-b.**

**(a)** Original gel images of BN-PAGE analysis of mitochondrial complexes.

**(b)** Original gel images of in-gel NADH dehydrogenase activity analysis of complex I.

Results irrelevant to this study were marked with “Irrelevant to this study”.

**Supplementary Table**

**Table S1. Genetic analysis of the mutant kernels in the segregation ear.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Self-pollinated parents | Number of mutants | Number of WT | Actual ratio | Expected ratio | *P* |
| *dek55-1/+* | 411 | 1239 | 1:3.01 | 1:3 | 0.93 |
| F1 (C733×*dek55-1/+*) | 916 | 2821 | 1:3.07 | 1:3 | 0.49 |
| F1 (S162×*dek55-1/+*) | 457 | 1364 | 1:2.98 | 1:3 | 0.92 |

**Table S2. The primers used in this study.**

|  |  |  |
| --- | --- | --- |
| umc1705-F | ATCTCACGTACGGTAATGCAGACA | For fine mapping |
| umc1705-R | CATGACCTGATAAACCCTCCTCTC |
| umc2302-F | GCATATGCGAGATCATATCGTTGA |
| umc2302-R | CTATACAGCCCTCAGCTCTGCTGT |
| M2-F | GTGCTATGCATGAGGGTAGAGT |
| M2-R | TGTATTGGGCGATACCGAGC |
| M3-F | ATCTGTAGTGCTTCCGTGCTCT |
| M3-R | GGCTCATTTGTAAGGTTGTGC |
| M4-F | GTTGAGATAACTATGCAAATCGTG |
| M4-R | CTTCCAACGTGCGTCTCTAC |
| M5-F | CGTCGTCGAGGTGATTAGGG |
| M5-R | GAACCCTCCTCCCGACTACT |
| M6-F | GGTTTCCAGAGCTAGGTGGG |
| M6-R | CGTCGTTTCCGTCGTCAATC |
| F148-F | GTTCGGTCGAGTTGGGATGA |
| F148-R | CAGACCAACCCTTCAGTCCC |
| DEK55-Full-F | GCCAGGTAGAATAGATGGAACC | Clone *DEK55* full length |
| DEK55-Full-R | CAAGAGCTGCTAAAATTTGTCAGTAC |
| ZmActin-F | ATGGTCAAGGCCGGTTTCG | qRT-PCR and RT-PCR primer of *ZmActin* |
| ZmActin-R | TCAGGATGCCTCTCTTGGCC |
| DEK55-qRT-F | CGATGACTGGTATAGCTTAGGG | qRT-PCR analysis of *DEK55* gene expression |
| DEK55-qRT-R | CGCATCCTCTCATCCTCATAG |
| nad1-1F | GCAACGTAGAAAGGGTCCTG | Test *nad1* introns splicing efficiency |
| nad1-2R | TGAGCTGCAGATCGTAATGC |
| nad1-2F | TCGAAATATGCCTTTCTAGGAG |
| nad1-3R | ATTCAGCTTCCGCTTCTGG |
| nad1-3F | GTCATGGCGCAAAAGCAGATATGG |
| nad1-4R | AGAGCAGACCCCATTGAAGA |
| nad1-4F | TCTTCAATGGGGTCTGCTCT |
| nad1-5R | AGGGAGCCATCGAAAGGTGA |
| nad4-1F | TTGATTGGTCTGTGCGTTTC | Test *nad4* introns splicing efficiency |
| nad4-2R | GGCTTCGGGTAACCAAATA |
| nad4-2F | TGCCGTCAAAGTGCCTAT |
| nad4-3R | GGTGCTCACTAAACCTCCATA |
| nad4-3F | CACTTTAGCCAATATGAGTTTACC |
| nad4-4R | ATGCAGTCCGGGAACACT |
| Aox1-qRT-F | AAGGTGCTGCTCGACAAGAT | qRT-PCR analysis of *Aox1* gene expression |
| Aox1-qRT-R | GTAGGCGTTGAAGAAGACGC |
| Aox2-qRT-F | GACATCTTCTTCCAGAGGCG | qRT-PCR analysis of *Aox2* gene expression |
| Aox2-qRT-R | TGACTACGTCCTTGAGCGTG |
| Aox3-qRT-F | CCAAGCTCGTGAAGGAAGAC | qRT-PCR analysis of *Aox3* gene expression |
| Aox3-qRT-R | GTAGGCGTTGAAGAAGACGC |
| DEK55-SC-F | CCGCGAATTCATGCCGCCGCCCCCAGCCG | Construct full length *DEK55-EGFP* vector |
| DEK55-SC-R | CCGCGGTACCGATACCAAAATCACAAGC |
| nad4-F1 | TTGATTGGTCTGTGCGTTTC | RT-PCR |
| nad4-R1 | ATGCAGTCCGGGAACACT |
| nad4-F | CAGTCACCCGGAGAAGATTT | Gene sequencing in RNA editing efficiency analysis |
| nad4-R | TAATTTGGCGCCTGATTGAC |
| nad2-F | GACGGAGGAGAGGAAATGAA | RT-PCR, Gene sequencing in RNA editing efficiency analysis |
| nad2-R | GCAGTCCACCCTTTCTTTGA |
| nad3-F | CTTTCCTATGTCCTTCCCCC |
| nad3-R | GAGGAGAGCGAGAGAACGAA |
| nad4L-F | CTGACATTCCATGTTTCCGA |
| nad4L-R | GAAGAGAACGAAAGGAGAACAGA |
| nad5-F | CGCTCGAACATTGTCTGATT |
| nad5-R | GTCCTGGCAAGCTCCTACAG |
| nad6-F | TGGAAAAACCAAACCCACAT |
| nad6-R | CAAGTTCCCTTGGCGTAGTC |
| nad7-F | GTTTTGGCTCGCAATAAAGC |
| nad7-R | CAGGTGGGACAAGCTCTAGG |
| nad9-F | AGCAAGAAGCGGAACAAAAA |
| nad9-R | TATTGATTTGTCCCCTCCCC |
| cob-F | ATCAAGGCAAGGGGGTAAAT |
| cob-R | GGTGTGATCAGTCTCATCCG |
| cox1-F | GGCCCCTCTCTGATAAGGTT |
| cox1-R | GTTAAGGCAAAGCCCAAACA |
| cox2-F | GTCCTACTTCTGGTGCTGCC |
| cox2-R | GAGAATTGCATTTCCGCTTC |
| cox3-F | TCAATCCACTTATTCGTTCCC |
| cox3-R | GTTTACATACAACCGGGGCA |
| atp1-F | CGTTGCTGGTGAAGAAGCAT |
| atp1-R | AAAAGCGGATTTATCCATCG |
| atp4-F | AGCCACGTGCTCTAATCCTC |
| atp4-R | TCCCTTTCTCTTGGAGCAGA |
| atp6-F | CCAAGTCTCTTTTGGGAGCA |
| atp6-R | GGCTCCTCGTTTTTATGCAA |
| atp8-F | GGCAAGGATCCTCAGTCCTA |
| atp8-R | GAGGGTTGGTTTGATTGGAA |
| atp9-F | AGGGGCCTCGTCATCTCTAT |
| atp9-R | TAGTTGCGAAGGAAAAGCGT |
| ccmB-F | AGCCGTCGAAGTGAATGAAT |
| ccmB-R | AACGGCTTTTCCATGACTTG |
| ccmC-F | ACTTGCAAGGCAAGGAAAAA |
| ccmC-R | CCATGGATGCTTTAGCGAGT |
| ccmFc-F | GAGAAGCTCAAATCGAACGG |
| ccmFc-R | CGCAGCCACTATTTTGACTC |
| ccmFn-F | TGAAGATTGTAAGGCGTTTCC |
| ccmFn-R | GGATCATCCTGTGGTTACCG |
| rps1-F | AAGGTGGGCTTCGGATTATT |
| rps1-R | TCTTCAGTTTTACGCTTACGCT |
| rps2A-F | CAGGAAAGATATTTGCCCCA |
| rps2A-R | CCTGTATCTCCGGAAACGAA |
| rps2B-F | TCCATGGACCCACGTAAAAT |
| rps2B-R | GGCCCCTCTCTGATAAGGAA |
| rps3-F | GCAGAAAGGGGCAAAAGTAA |
| rps3-R | TCGCGACCCCTACTACATCT |
| rps4-F | AGAGTTGGGTTCGATTCCCT |
| rps4-R | AGCGACTAGGCCGATCTTTT |
| rps7-F | TTCGTTGGAAAAACCTACGC |
| rps7-R | ATGAGGAAGGCCGATTTTCT |
| rps7-ct-F | TTGAACCTCTTTCACGCTCA |
| rps7-ct-R | TTCCGATCGAGATGTATGGA |
| rps12-F | CTAGCTGCTTCCATATCGCC |
| rps12-R | CGGATCGGGAGTAACCACTA |
| rps12-ct-F | TGTACGGTTCTGTAGAGGGACA |
| rps12-ct-R | TCCGTTTTCTTTTTATAAGGGC |
| rps13-F | TCATGATGATTAAGGGAAGAGTGA |
| rps13-R | TTGAATTGAACAGTGTGATTGAT |
| rpl16-F | GGTTTTTCCCCACTAACCAA |
| rpl16-R | GGGTGCGGAAATAGCTAGAA |
| mat-r-F | AACGCCTGTTCGCTAAAATC |
| mat-r-R | AGGCTTTGCTCCCCTTTTT |
| mttB-F | TTGGTTTAGAATTGCTCGGG |
| mttB-R | AGGGGGAACCCTACCGAC |
| AD-Zmd049043F | CGGAATTCATGGCCCTCGCACTGCGCC | Yeast two-hybrid assay |
| AD-Zmd049043R | CGGGATCCTCATACCTGCCAGTTTCCTTG |
| AD-Zmd045528F | CGGAATTCATGGCCGCCGCCGCC |
| AD-Zmd045528R | CGGGATCCTCATCGCTGGTTCTCCCTC |
| AD-Zmd026307F | CGGAATTCATGGCAGCCGCATCAGCG |
| AD-Zmd026307R | CGGGATCCTCAGTGCTGCTCCTGATTC |
| AD-Zmd038760F | CGCATATGATGTATGCTTTTAGTACGAC |
| AD-Zmd038760R | CGGAATTCCTAGTCGCAGCTCCCAGTG |
| AD-Zmd026243F | CGGAATTCATGGCCACCGTAGCGCGC |
| AD-Zmd026243R | CGGGATCCTCATCTCTGGTAAGATTGG |
| AD-Zmd048291F | CGGAATTCATGGCGTCGGCGTCGCGTG |
| AD-Zmd048291R | CGGGATCCTCACTGGAAGTTGGAGTTGCC |
| AD-Zmd024674F | CGGAATTCATGGCCGCCTCCCTCCCGAC |
| AD-Zmd024674R | CGGGATCCTCACGAAGACGCGGACTCG |
| DEK55-BD-F | CGGAATTCGACCGCTACCTTGCTAACGCG |
| DEK55-BD-R | CGGGATCCTCAGATACCAAAATCACAAGC |