Supplementary Table S1-S4

Article title: **Pentatricopeptide repeat protein DEK40 is required for mitochondrial function and kernel development in maize**

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Table S1 Genetic analysis of the kernels in F$_2$ population of the segregating ears

F$_2$ population	Number of mutants	Number of WT	Actual ratio	Expected ratio	P
S162×*dek40-ref/+*	724	2134	1:2.95	1:3	0.68
V3b1×*dek40-ref/+*	446	1328	1:2.98	1:3	0.89
Mo17×*dek40-ref/+*	368	1130	1:3.07	1:3	0.70
Chang7-2×*dek40-ref/+*	803	2554	1:3.18	1:3	0.15

Table S2 Co-segregation analysis of the mutant sites and phenotypes of progenies from wild-type phenotype kernels segregated from self-pollinated *dek40-ref* heterozygous ears

No. of individuals	GRMZM2G304965 mutant site (+1719)	GRMZM2G005207 mutant site (+262)	Phenotype of the self-pollinated ear
16-1	G/G	G/G	No-Segregation
16-2	G/A	G/A	Segregation
16-3	G/A	G/A	Segregation
16-4	G/G	G/G	No-Segregation
16-5	G/G	G/G	No-Segregation
16-6	G/G	G/G	No-Segregation
16-7	G/G	G/G	No-Segregation
16-8	G/G	G/G	No-Segregation
16-9	G/A	G/A	Segregation
16-10	G/A	G/A	Segregation
16-11	G/A	G/A	Segregation
16-12	G/A	G/A	Segregation
16-13	G/G	G/G	No-Segregation
16-14	G/A	G/A	Segregation
16-15	G/A	G/A	Segregation
16-16	G/A	G/A	Segregation
16-17	G/A	G/A	Segregation
16-18	G/A	G/A	Segregation
16-19	G/G	G/G	No-Segregation
16-20	G/A	G/A	Segregation
16-21	G/A	G/A	Segregation
16-22	G/A	G/A	Segregation
16-23	G/A	G/A	Segregation
16-24	G/A	G/A	Segregation
16-25	G/G	G/A	No-Segregation
16-26	G/A	G/A	Segregation
16-27	G/A	G/A	Segregation
16-28	G/A	G/A	Segregation
16-29	G/A	G/G	Segregation
16-30	G/A	G/A	Segregation
16-31	G/G	G/G	No-Segregation
16-32	G/A	G/A	Segregation
16-33	G/A	G/A	Segregation
16-34	G/A	G/A	Segregation
16-35	G/A	G/A	Segregation
16-36	G/A	G/A	Segregation
16-37	G/G	G/G	No-Segregation
16-38	G/G	G/G	No-Segregation

16-39	G/A	G/A	Segregation
16-40	G/A	G/A	Segregation
16-41	G/A	G/A	Segregation
16-42	G/A	G/A	Segregation
16-43	G/A	G/A	Segregation
16-44	G/A	G/A	Segregation
16-45	G/A	G/A	Segregation
16-46	G/A	G/A	Segregation
16-47	G/A	G/A	Segregation
16-48	G/G	G/G	No-Segregation
16-49	G/G	G/G	No-Segregation
16-50	G/A	G/A	Segregation
16-51	G/A	G/A	Segregation
16-52	G/A	G/A	Segregation
16-53	G/A	G/A	Segregation
16-54	G/G	G/G	No-Segregation
16-55	G/A	G/A	Segregation
16-56	G/A	G/A	Segregation
16-57	G/A	G/A	Segregation
16-58	G/G	G/G	No-Segregation
16-59	G/A	G/A	Segregation
16-60	G/A	G/A	Segregation
16-61	G/G	G/G	No-Segregation
16-62	G/A	G/A	Segregation
16-63	G/G	G/G	No-Segregation
16-64	G/G	G/G	No-Segregation
16-65	G/A	G/A	Segregation
16-66	G/G	G/G	No-Segregation
16-67	G/A	G/A	Segregation
16-68	G/G	G/G	No-Segregation
16-69	G/A	G/A	Segregation
16-70	G/A	G/A	Segregation
16-71	G/A	G/A	Segregation
16-72	G/A	G/A	Segregation
16-73	G/G	G/G	No-Segregation
16-74	G/A	G/A	Segregation
16-75	G/A	G/A	Segregation
16-76	G/G	G/G	No-Segregation
16-77	G/G	G/G	No-Segregation
16-78	G/G	G/G	No-Segregation
16-79	G/G	G/G	No-Segregation
16-80	G/A	G/A	Segregation
16-81	G/G	G/G	No-Segregation
16-82	G/G	G/G	No-Segregation

16-83	G/A	G/A	Segregation
16-84	G/A	G/A	Segregation
16-85	G/G	G/G	No-Segregation
16-86	G/A	G/A	Segregation
16-87	G/A	G/A	Segregation
16-88	G/G	G/G	No-Segregation
16-89	G/G	G/G	No-Segregation
16-90	G/A	G/A	Segregation
16-91	G/A	G/A	Segregation
16-92	G/A	G/A	Segregation
16-93	G/A	G/A	Segregation
16-94	G/G	G/G	No-Segregation
16-95	G/G	G/G	No-Segregation
16-96	G/A	G/A	Segregation
16-97	G/A	G/A	Segregation
16-98	G/G	G/G	No-Segregation
16-99	G/A	G/A	Segregation
16-100	G/G	G/G	No-Segregation
16-101	G/A	G/A	Segregation
16-102	G/G	G/G	No-Segregation
16-103	G/A	G/A	Segregation
16-104	G/A	G/A	Segregation
16-105	G/A	G/A	Segregation
16-106	G/G	G/G	No-Segregation
16-107	G/G	G/G	No-Segregation
16-108	G/A	G/A	Segregation
16-109	G/A	G/A	Segregation
16-110	G/A	G/A	Segregation
16-111	G/A	G/A	Segregation
16-112	G/A	G/A	Segregation
16-113	G/G	G/G	No-Segregation
16-114	G/G	G/G	No-Segregation
16-115	G/A	G/A	Segregation
16-116	G/A	G/A	Segregation
16-117	G/A	G/A	Segregation
16-118	G/A	G/A	Segregation
16-119	G/A	G/A	Segregation
16-120	G/A	G/A	Segregation
16-121	G/A	G/A	Segregation
16-122	G/A	G/A	Segregation
16-123	G/A	G/A	Segregation
16-124	G/G	G/G	No-Segregation
16-125	G/A	G/A	Segregation
16-126	G/G	G/G	No-Segregation

16-127	G/A	G/A	Segregation
16-128	G/G	G/G	No-Segregation
16-129	G/A	G/A	Segregation
16-130	G/G	G/G	No-Segregation
16-131	G/A	G/A	Segregation
16-132	G/G	G/G	No-Segregation
16-133	G/A	G/A	Segregation
16-134	G/G	G/G	No-Segregation
16-135	G/G	G/G	No-Segregation
16-136	G/A	G/A	Segregation
16-137	G/G	G/G	No-Segregation
16-138	G/G	G/G	No-Segregation
16-139	G/G	G/G	No-Segregation
16-140	G/G	G/G	No-Segregation
16-141	G/A	G/A	Segregation
16-142	G/G	G/G	No-Segregation
16-143	G/A	G/A	Segregation
16-144	G/A	G/A	Segregation
16-145	G/A	G/A	Segregation
16-146	G/G	G/G	No-Segregation
16-147	G/A	G/A	Segregation
16-148	G/A	G/A	Segregation
16-149	G/G	G/G	No-Segregation
16-150	G/G	G/G	No-Segregation
16-151	G/G	G/G	No-Segregation
16-152	G/A	G/A	Segregation
16-153	G/G	G/G	No-Segregation
16-154	G/A	G/A	Segregation
16-155	G/G	G/G	No-Segregation
16-156	G/G	G/G	No-Segregation
16-157	G/G	G/G	No-Segregation
16-158	G/A	G/A	Segregation

Note: One hundred fifty eight WT phenotype individuals that were segregated from the self-progenies of *dek40-ref* heterozygous ear (No.16) were selected for experiments because the *dek40* homozygous mutant was lethal. The genotypes of two mutation sites in GRMZM2G304965 (+1719) and GRMZM2G005207 (+262) were identified by PCR and DNA sequencing. The genotype GG in both sites was WT and GA was heterozygous site. After genotyping, these individuals were self-pollinated and the phenotypes of their progenies were further determined.

Table S3 Genotypes of kernels in the crosses between *dek40-ref* and *dek40-1* heterozygote's ear were identified by PCR-sequencing.

Number	Genotype at +1719	Genotype at +2180
Mutant-1	G/A	G/A
Mutant-2	G/A	G/A
Mutant-3	G/A	G/A
Mutant-4	G/A	G/A
Mutant-5	G/A	G/A
Mutant-6	G/A	G/A
Mutant-7	G/A	G/A
Mutant-8	G/A	G/A
Mutant-9	G/A	G/A
Mutant-10	G/A	G/A
Mutant-11	G/A	G/A
Mutant-12	G/A	G/A
Mutant-13	G/A	G/A
WT-1	G/A	G/G
WT-2	G/G	G/G
WT-3	G/A	G/G
WT-4	G/G	G/G
WT-5	G/G	G/A
WT-6	G/G	G/A
WT-7	G/G	G/G
WT-8	G/A	G/G
WT-9	G/G	G/A
WT-10	G/A	G/G
WT-11	G/A	G/G
WT-12	G/A	G/G
WT-13	G/G	G/A

Table S4 Primer sequences used in this study

Primer Name	Sequence (5'-3')	
umc1380-F	CTGCTGATGTCTGGAAGAACCCT	
umc1380-R	AGCATCATGCCAGCAGGTTTT	
umc1152-F	CCGAAGATAACCAAACAATAATAGTAGG	
umc1152-R	ACTGTACGCCTCCCCTTCTC	
M2-F	GGTTGGAGGGGCAAATCTTG	
M2-R	ATATAGACAAATGGCGCGGC	
M3-F	ACTGTCTGTCTGTGAGCCAT	
M3-R	GGCCAGAGAGAGAGTGAGTG	
M4-F	GTGAAGGACAGAAGGAAG	
M4-R	CCGTATCTGTACGCTGGCTG	Fine mapping
M5-F	GTTGCAGGAGATGGAGGACT	
M5-R	AGACAAACTGCACGTCCATC	
M6-F	AGAAGCAGCCCCAGAGTTTA	
M6-R	CGGTTTGCTTTGGTGTCTTC	
M7-F	GTCCCGCCTGATTAACTTGC	
M7-R	CAGGAAACACGAAGACACCA	
M8-F	CAGAAGGCCAGAACGAAGC	
M8-R	GGCGTGCAAGTAAACTGGAT	
M9-F	TGATCGATGGCTCAATCAGT	
M9-R	ATCTGGAACACCGTCGTCTC	
dek40-ref-F	GATAACAGAGGCTCAGAAAC	Identify *dek40-ref*
dek40-ref-R	CGTCCCAGTATATCCACCA	mutant
dek40-1-F	CTGATGACAAGCCGCTACAAAC	Identify *dek40-1*mutant
dek40-1-R	CACCTCGATCCAGCTACAACC	
WRKY-F	CGTTCCTACCACCTCCTGC	Identify WRKY gene
WRKY-R	CTGCCCGTACTTCCTCCAC	mutant site
DEK40-SC-1F	AGATCTATGCCCCTGCCGCCCCACGC	Construct DKE40-GFP
DEK40-SC-1R	GGTACCACCACCAACGACTCTAACC	
DEK40-SC-2F	TCTAGAATGCCCCTGCCGCCCCACGC	Construct DKE40-RFP
DEK40-SC-2R	GGTACCACCACCAACGACTCTAACC	
Zmactin-qRT-F	ATGGTCAAGGCCGGTTTCG	
Zmactin-qRT-R	TCAGGATGCCTCTCTTGGCC	
ZmAox1-qRT-F	CCTATTGGACCGTCAAATTACTGC	
ZmAox1-qRT-R	CACTGTTTCCAGCATCATAGCAC	
ZmAox2-qRT-F	CCAAGACGCTGATGGATAAGGT	
ZmAox2-qRT-R	CCACGGTTTCCAGCATCAT	
ZmAox3-qRT-F	CGGCACCGAGAAGCATGA	qRT-PCR
ZmAox3-qRT-R	CTGGTCCACTTCCACTCCGT	
GRMZM2G456 217-qRT-F	ACGACGAGCTCTGAATTGC	

GRMZM2G456 217-qRT-R	ATTCACAGTCGGCGATGTTC	
GRMZM2G022 799-qRT-F	GACCAGGGGTTCCAACAAC	qRT-PCR
GRMZM2G022 799-qRT-R	CCTCTCCTTGCTCATTTGCT	
pGEX-4T-1- DEK40-F	TAAGATCTATGCCCCTGCCGCCCCACGC	REMSA
pGEX-4T-1- DEK40-R	GCCCCGGGACCACCAACGACTCTAACC	REMSA