

Figure S1. Biochemical analysis of WT and *dek10* endosperm.

A. SDS-PAGE analysis of total, zein, and nonzein proteins from WT and *dek10* mature endosperm.

B. Comparison of total, zein, and nonzein proteins from *dek10* and WT mature endosperm. The measurements were done on per mg of dried endosperm. Values are the mean values with standard errors, $n=3$ individuals.

C. Comparison of total starch and amylose content in WT and *dek10* mature endosperm. The measurements were done on per mg of dried endosperm. Values are the mean values with standard errors, $n=3$ individuals.

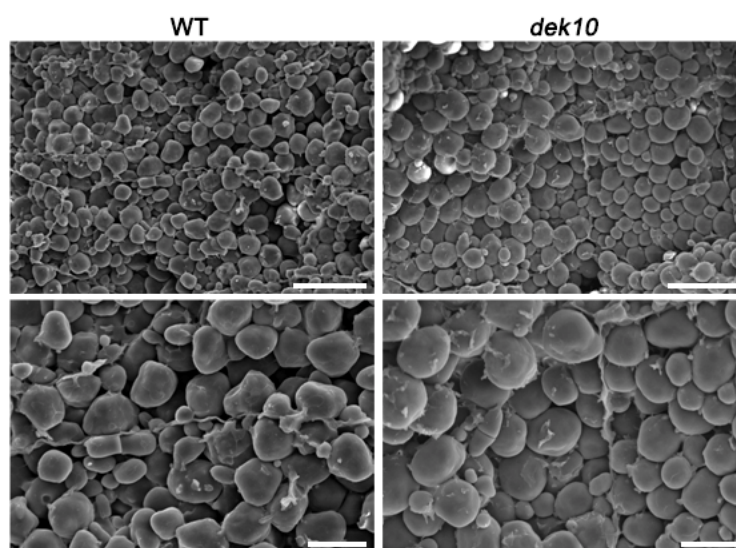


Figure S2. Scanning electron microscopy analysis of the peripheral regions of mature WT and *dek10* endosperm. Bars = 50 μ m (top), Lower, Bars=20 μ m (bottom).

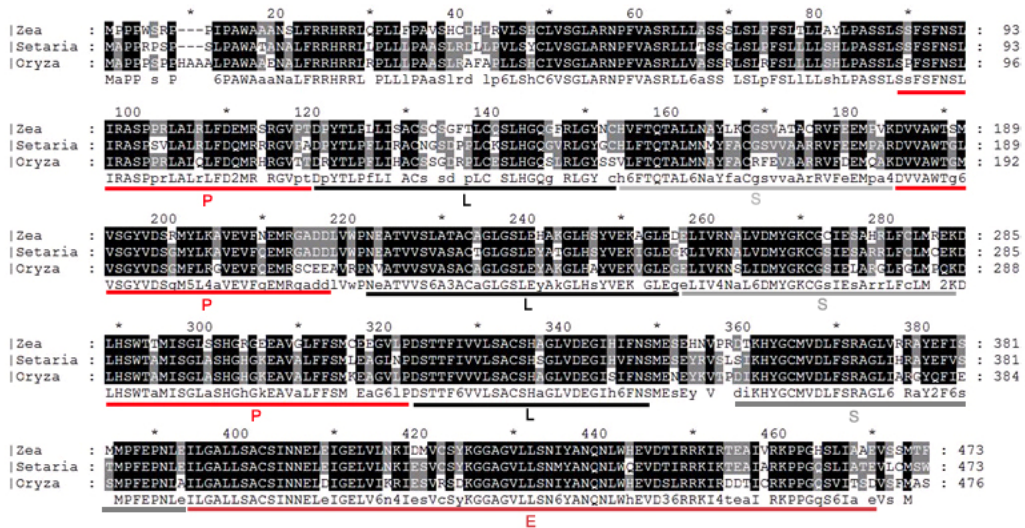


Figure S3. Alignment of Dek10 full length protein sequence and homologue protein sequences from *Setaria italica* and *Oryza sativa*.

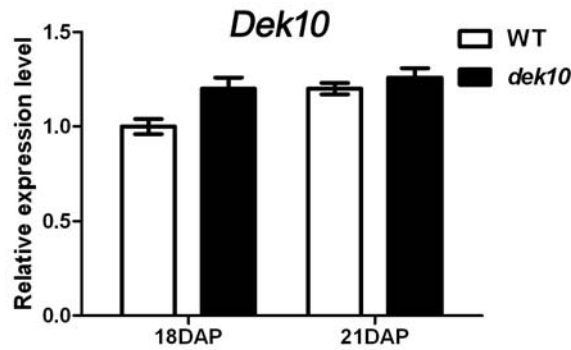


Figure S4. qRT-PCR comparing expression level of *Dek10* gene in the 18 DAP and 21 DAP *dek10* and WT kernels. Ubiquitin was used as internal control. Values are the mean values with standard errors, $n=3$ individuals.



Figure S5. Alignment of the Dek10 target sequences in *nad3* and *cox2*.

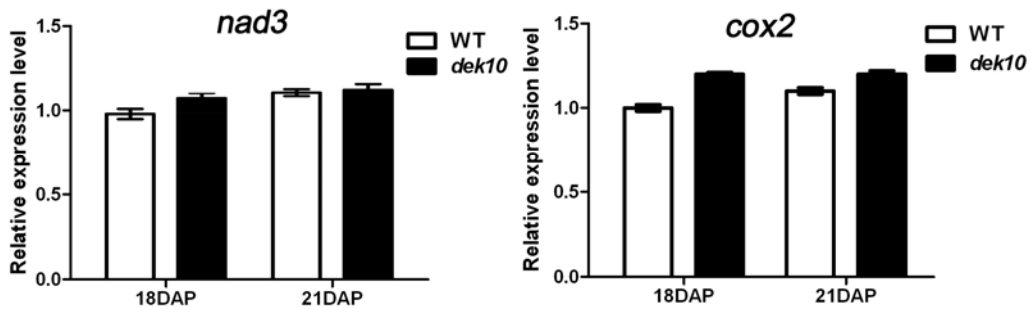


Figure S6. qRT-PCR comparing expression level of *nad3* and *cox2* gene in the 18 DAP and 21 DAP *dek10* and WT kernels. Ubiquitin was used as internal control. Values are the mean values with standard errors, $n=3$ individuals.

Table S1. Gene ontology classifications of DEGs with functional annotation.

GO ID	P-Value	Gene	Description	Fold change	P-Value
GO:0005740					
Mitochondrial envelope	5.00E-18	GRMZM2G157018	ATPase, F0 complex, subunit D Cytochrome c oxidase copper	3.53	1.62E-65
		GRMZM2G116517	chaperone	2.14	3.95E-06
		GRMZM2G051613	ETC complex I subunit Mitochondrial inner membrane	2.68	1.47E-11
		GRMZM2G144101	translocase complex	2.82	1.68E-15
		GRMZM2G540403	Ribosomal protein L4/L1e	2.04	4.92E-04
		GRMZM2G135186	Adenine nucleotide translocator 1 ETC complex I subunit conserved	2.84	8.00E-22
		GRMZM2G105207	region	2.51	2.79E-05
AC194341.4_FG002		GRMZM2G010933	ATPase, F0 complex, subunit G Cytochrome c oxidase 17	2.91	4.80E-20
		GRMZM2G157758	ATPase, F1 complex, epsilon subunit Mitochondrial inner membrane	3.41	7.05E-19
		GRMZM2G112640	translocase complex, subunit Tim17/22	2.22	3.44E-04
		GRMZM2G006704	Cytochrome c oxidase subunit Vc Mitochondrial inner membrane	2.32	3.66E-09
		GRMZM2G321404	translocase complex, subunit Tim17/22	3.85	1.28E-03
		GRMZM2G042078	ATPase, F0 complex, subunit G	2.86	2.11E-07
		GRMZM2G152827	Mitochondrial carrier domain	4.72	7.44E-19
		GRMZM2G064753	Cytochrome c oxidase, subunit Vb	2.95	3.52E-11
		GRMZM2G120876	Porin, eukaryotic type	3.76	2.55E-08
		GRMZM2G155021	Porin, eukaryotic type Mitochondrial inner membrane	2.31	9.96E-04
		GRMZM2G156848	translocase complex	2.04	8.66E-06
		GRMZM2G143234	ATPase, F1 complex, epsilon subunit Ubiquinol-cytochrome C reductase,	2.71	5.59E-17
		GRMZM2G171476	UQCRX/QCR9-like	3.05	1.12E-15
		GRMZM2G146670	Porin, eukaryotic type	3.66	2.65E-12
		GRMZM2G150616	Porin, eukaryotic type Mitochondrial inner membrane	3.90	2.84E-19
		GRMZM2G038375	translocase complex, subunit Tim17/22	2.61	7.32E-07
		GRMZM2G125669	Alternative oxidase 2 Mitochondrial inner membrane	366.17	3.65E-24
		GRMZM2G058432	translocase complex Ubiquinol-cytochrome C reductase,	6.04	1.89E-28
		GRMZM2G064896	UQCRX/QCR9-like	2.95	3.99E-11
		GRMZM2G048013	Cytochrome c oxidase, subunit VIIa	2.48	3.88E-10
		GRMZM2G412296	Cytochrome c oxidase, subunit VIIa Mitochondrial inner membrane	2.68	1.27E-04
		GRMZM5G801241	translocase complex	2.61	1.23E-08

		GRMZM2G071071	Ras GTPase;EF hand associated Plant specific mitochondrial import	9.36	5.82E-60
		GRMZM2G100402	receptor subunit TOM20 Mitochondrial inner membrane	2.32	7.03E-04
		GRMZM2G167463	translocase complex	4.20	4.96E-08
		GRMZM2G015401	Mitochondrial carrier domain Mitochondrial inner membrane	4.00	1.28E-03
		GRMZM2G319878	translocase complex Mitochondrial inner membrane	5.54	2.62E-08
		GRMZM2G103771	translocase complex, subunit Tim17/22	0.19	3.63E-15
		GRMZM2G134738	Cytochrome c oxidase, subunit Vb	4.94	1.77E-18
		GRMZM2G069229	ATPase, F0 complex, subunit G Mitochondrial brown fat uncoupling	5.16	4.81E-04
		GRMZM2G000510	protein	2.22	2.21E-11
		GRMZM2G024823	Mitochondrial carrier domain	4.27	4.72E-04
		GRMZM2G067877	Mitochondrial carrier domain	3.71	3.01E-12
		GRMZM2G149480	Mitochondrial carrier domain	4.19	1.00E-04
		GRMZM2G122481	Cytochrome c oxidase subunit Vc	3.45	6.71E-04
		GRMZM2G018417	Porin, eukaryotic type	2.30	4.93E-04
		GRMZM2G115049	Porin, eukaryotic type	28.03	2.31E-181
		GRMZM2G018941	ETC complex I subunit Mitochondrial inner membrane	2.37	2.78E-12
		GRMZM2G064600	translocase complex, subunit Tim17/22	6.59	3.60E-08
GO:0015078					
Hydrogen ion					
transmembrane					
transporter activity	1.30E-13				
		GRMZM2G451281	Ubiquinol-cytochrome C reductase hinge	2.41	3.40E-11
		GRMZM2G157018	ATPase, F0 complex, subunit D Ubiquinol-cytochrome C reductase,	3.53	1.62E-65
		GRMZM2G064896	UQCRX/QCR9-like	2.95	3.99E-11
		GRMZM2G070360	ATPase, V1/A1 complex, subunit E	2.08	8.66E-06
		GRMZM2G171664	Rieske iron-sulphur protein, C-terminal Ubiquinol-cytochrome C reductase	2.55	6.63E-07
		GRMZM2G165483	hinge Cytochrome d ubiquinol oxidase,	2.73	1.16E-04
		GRMZM2G170457	14kDa subunit	3.99	2.93E-25
		GRMZM2G131434	Cytochrome c oxidase, subunit VIb	3.53	3.44E-04
		GRMZM2G131431	ATPase, V0 complex, subunit E ATPase, V0 complex, proteolipid	2.23	8.95E-07
		GRMZM2G101020	subunit C	2.30	2.04E-04
		AC194341.4_FG002	ATPase, F0 complex, subunit G ATPase, F1 complex, gamma subunit	2.91	4.80E-20
		GRMZM2G009638	conserved site	2.65	9.93E-17
		GRMZM2G157758	ATPase, F1 complex, epsilon subunit	3.41	7.05E-19

		GRMZM2G006704	Cytochrome c oxidase subunit Vc ATPase, F1 complex, delta/epsilon	2.32	3.66E-09
		GRMZM2G138220	subunit	2.71	4.95E-05
		GRMZM2G042078	ATPase, F0 complex, subunit G ATPase, F1/V1/A1 complex, alpha/beta	2.86	2.11E-07
		GRMZM2G021331	subunit	2.68	5.04E-11
		GRMZM2G064753	Cytochrome c oxidase, subunit Vb Ubiquinol-cytochrome C reductase	2.95	3.52E-11
		GRMZM2G152952	hinge ATPase, F1/V1/A1 complex, alpha/beta	2.52	1.13E-06
		GRMZM2G113408	subunit, N-terminal ATPase, F1 complex, gamma subunit	3.24	8.88E-32
		GRMZM2G321725	conserved site	2.32	3.62E-09
		GRMZM2G143234	ATPase, F1 complex, epsilon subunit Ubiquinol-cytochrome C reductase,	2.71	5.59E-17
		GRMZM2G171476	UQCRX/QCR9-like	3.05	1.12E-15
		GRMZM2G401139	UcrQ; Cytochrome b-c1 complex	2.60	5.24E-13
		GRMZM2G023194	Rieske iron-sulphur protein, C-terminal	2.26	4.96E-05
		GRMZM2G048013	Cytochrome c oxidase, subunit VIIa Cytochrome d ubiquinol oxidase,	2.48	3.88E-10
		GRMZM2G318346	14kDa subunit	3.47	4.35E-07
		GRMZM2G067707	UcrQ; Cytochrome b-c1 complex ATPase, F1 complex, OSCP/delta	2.24	5.18E-09
		GRMZM2G156068	subunit	3.88	6.54E-68
		GRMZM2G412296	Cytochrome c oxidase, subunit VIIa ATPase, F1 complex, gamma subunit	2.68	1.27E-04
		GRMZM2G069458	domain ATPase, F1/V1/A1 complex, alpha/beta	3.13	4.54E-17
		GRMZM2G041275	subunit, N-terminal ATPase, F1 complex, delta/epsilon	3.38	5.79E-11
		GRMZM2G171628	subunit	2.83	5.28E-17
		GRMZM2G067417	Cytochrome c oxidase, subunit VIb ATPase, V0 complex, proteolipid	3.94	1.05E-19
		GRMZM2G177005	subunit C	2.19	3.48E-06
		GRMZM2G134738	Cytochrome c oxidase, subunit Vb	4.94	1.77E-18
		GRMZM2G069229	ATPase, F0 complex, subunit G	5.16	4.81E-04
		GRMZM2G152925	Cytochrome c oxidase, subunit VIb	2.16	1.59E-05
		AC214350.3_FG007	Rieske iron-sulphur protein, C-terminal	2.26	1.21E-05
		GRMZM2G021635	ATPase, V1/A1 complex, subunit D	3.32	3.44E-04
		GRMZM2G122481	Cytochrome c oxidase subunit Vc	3.45	6.71E-04
		GRMZM2G118019	Na ⁺ /H ⁺ exchanger	0.02	2.04E-13
GO:0015992					
proton transport	7.00E-06	GRMZM2G157018	ATPase, F0 complex, subunit D	3.53	1.62E-65
		GRMZM2G070360	ATPase, V1/A1 complex, subunit E	2.08	8.66E-06

		GRMZM2G131431	ATPase, V0 complex, subunit E	2.23	8.95E-07
			ATPase, V0 complex, proteolipid		
		GRMZM2G101020	subunit C	2.30	2.04E-04
		AC194341.4_FG002	ATPase, F0 complex, subunit G	2.91	4.80E-20
			ATPase, F1 complex, gamma subunit		
		GRMZM2G009638	conserved site	2.65	9.93E-17
		GRMZM2G157758	ATPase, F1 complex, epsilon subunit	3.41	7.05E-19
			ATPase, F1 complex, delta/epsilon		
		GRMZM2G138220	subunit	2.71	4.95E-05
		GRMZM2G042078	ATPase, F0 complex, subunit G	2.86	2.11E-07
		GRMZM2G069095	Inorganic H ⁺ pyrophosphatase	4.30	2.85E-11
			ATPase, F1/V1/A1 complex, alpha/beta		
		GRMZM2G021331	subunit	2.68	5.04E-11
			ATPase, F1/V1/A1 complex, alpha/beta		
		GRMZM2G113408	subunit	3.24	8.88E-32
			ATPase, F1 complex, gamma subunit		
		GRMZM2G321725	conserved site	2.32	3.62E-09
		GRMZM2G143234	ATPase, F1 complex, epsilon subunit	2.71	5.59E-17
		GRMZM2G144372	ATPase, V1 complex, subunit C	2.33	2.91E-04
			ATPase, F1 complex, OSCP/delta		
		GRMZM2G156068	subunit	3.88	6.54E-68
		GRMZM2G104419	Inorganic H ⁺ pyrophosphatase	4.57	8.11E-04
			ATPase, F1 complex, gamma subunit		
		GRMZM2G069458	domain	3.13	4.54E-17
			ATPase, F1/V1/A1 complex, alpha/beta		
		GRMZM2G041275	subunit	3.38	5.79E-11
			ATPase, F1 complex, delta/epsilon		
		GRMZM2G171628	subunit	2.83	5.28E-17
			ATPase, V0 complex, proteolipid		
		GRMZM2G177005	subunit C	2.19	3.48E-06
		GRMZM2G069229	ATPase, F0 complex, subunit G	5.16	4.81E-04
		GRMZM2G021635	ATPase, V1/A1 complex, subunit D	3.32	3.44E-04
GO:0006334					
Nucleosome assembly	5.40E-16	GRMZM2G121186	Nucleosome assembly protein (NAP)	2.23	2.97E-06
			Heavy metal transport/detoxification		
		GRMZM2G155281	protein	3.40	1.91E-26
		GRMZM2G047813	Histone H2A;Histone core;Histone-fold	5.37	1.72E-12
		GRMZM2G079089	Histone H2B;Histone core;Histone-fold	2.10	1.09E-03
		GRMZM2G401308	Histone H1/H5	2.19	6.90E-06
		GRMZM2G349651	Histone H4, conserved site	4.87	1.00E-04
		GRMZM2G421279	Histone H4, conserved site	3.80	6.93E-16
		GRMZM2G151826	Histone H2A;Histone core;Histone-fold	3.34	5.41E-04
		GRMZM2G479684	Histone H4, conserved site	3.37	2.04E-18
		GRMZM2G181153	Histone H4, conserved site	3.28	4.08E-05

		GRMZM2G401147	Histone H2B;Histone core;Histone-fold	3.41	2.79E-12
		AC191069.3_FG004	IGR protein motif	3.85	8.64E-07
			Ribosomal biogenesis regulatory protein		
		GRMZM2G127312		2.31	1.44E-12
		GRMZM2G163939	Histone H2B;Histone core;Histone-fold	2.32	4.16E-05
		GRMZM2G003306	Histone H2A;Histone core;Histone-fold	4.49	2.56E-17
		GRMZM2G063896	Histone H4, conserved site	2.67	5.28E-04
		GRMZM2G305027	Histone H2B;Histone core;Histone-fold	2.57	1.62E-03
		GRMZM2G112912	Histone H2B;Histone core;Histone-fold	5.79	1.01E-12
		GRMZM2G034157	Heat shock protein Hsp20	7.08	6.54E-26
		GRMZM2G056231	Histone H2A;Histone core;Histone-fold	4.12	1.80E-08
			Histone core;Histone-fold;Histone H3;Longin;Synaptobrevin		
		GRMZM2G387076		3.33	1.23E-09
			Leucine-rich repeat;Ribosomal protein L19/L19e		
		GRMZM2G450937		2.85	1.67E-06
		GRMZM2G073275	Histone H4, conserved site	3.08	4.16E-10
		GRMZM2G118355	Histone core;Histone-fold;Histone H3	2.05	8.29E-13
		GRMZM2G106133	Histone H1/H5	2.65	8.57E-05
			Cyclophilin-type peptidyl-prolyl cis-trans isomerase		
		GRMZM2G084521		2.86	1.05E-10
		GRMZM2G305046	Histone H2A;Histone core;Histone-fold	9.29	2.95E-11
		GRMZM2G072855	Histone H4, conserved site	2.41	2.46E-03
		GRMZM2G472696	Histone H2B;Histone core;Histone-fold	2.41	1.21E-09
		GRMZM2G164020	Histone H1/H5	2.95	9.87E-06
		GRMZM2G332838	Histone H4, conserved site	4.70	3.18E-27
		GRMZM2G071959	Histone H2B;Histone core;Histone-fold	2.47	4.31E-13
			Ribosomal protein L19/L19e conserved site		
		GRMZM2G116135		2.00	2.99E-05
		GRMZM2G080274	Histone H4, conserved site	3.63	4.18E-04
		GRMZM2G447984	Histone core;Histone-fold;Histone H3	5.37	5.63E-05
		AC212565.3_FG001	Histone H4, conserved site	3.14	6.92E-12
		GRMZM2G342515	Histone H2B;Histone core;Histone-fold	4.96	1.75E-08
		AC196961.2_FG003	Histone H4, conserved site	4.46	1.28E-03
		GRMZM2G084195	Histone H4, conserved site	4.59	2.08E-10
		GRMZM2G016232	Histone H4, conserved site	2.69	3.83E-09
		GRMZM2G051879	Histone core;Histone-fold;Histone H3	2.04	2.18E-12
		GRMZM2G119071	Histone H2B;Histone core;Histone-fold	6.72	8.87E-05
		GRMZM2G046055	Histone H2A;Histone core;Histone-fold	4.42	4.34E-14
		GRMZM2G304575	Histone H2B;Histone core;Histone-fold	3.52	5.50E-10
		GRMZM2G078314	Histone core;Histone-fold;Histone H3	4.38	1.53E-09
		GRMZM2G306258	Histone H2B;Histone core;Histone-fold	4.16	4.61E-06
GO:0008652			Chorismate synthase, conserved site;Chorismate synthase		
Cellular amino acid biosynthetic process	6.00E-08	GRMZM2G164562		2.21	3.43E-05

	Dihydrodipicolinate reductase,		
GRMZM2G090241	N-terminal	2.36	1.44E-03
GRMZM2G013430	Serine acetyltransferase, N-terminal	8.18	6.43E-04
	Cysteine synthase/cystathionine		
	beta-synthase P-phosphate-binding		
GRMZM2G082185	site	3.28	1.70E-03
GRMZM2G161868	Dehydrogenase, multihelical	3.26	1.92E-33
GRMZM2G328893	Cysteine synthase K/M	3.63	8.54E-05
	RmlC-like jelly roll fold;"Acireductone		
GRMZM2G165998	dioxygenase, ARD"	2.00	1.94E-05
	Pyridoxal phosphate-dependent		
GRMZM2G170595	transferase	2.87	5.71E-06
GRMZM2G005887	Cysteine synthase K/M	3.43	3.91E-35
GRMZM2G165383	Phosphoserine phosphatase, domain 2	2.72	1.74E-04
	Aconitase/3-isopropylmalate		
GRMZM5G840002	dehydratase, swivel	7.57	2.43E-135
GRMZM2G407044	Acetolactate synthase, small subunit	2.24	4.11E-04
GRMZM2G055507	2-isopropylmalate synthase LeuA	4.87	5.94E-05
	Histidinol dehydrogenase, conserved		
GRMZM2G058584	site	2.44	2.36E-05
	Histidine biosynthesis HisG: ATP		
GRMZM2G068862	phosphoribosyltransferase	2.17	5.61E-05
GRMZM2G051219	Glycosyl transferase, family 3	2.77	1.04E-10
	Aconitase/3-isopropylmalate		
	dehydratase large subunit,		
GRMZM2G370852	alpha/beta/alpha	2.85	7.59E-21
	Isocitrate/isopropylmalate		
GRMZM2G104613	dehydrogenase	2.49	9.63E-08
	Cysteine synthase/cystathionine		
	beta-synthase P-phosphate-binding		
GRMZM2G165622	site	3.98	5.69E-07
	Histidine biosynthesis;Histidine		
GRMZM2G174589	biosynthesis, HisF	2.42	1.68E-05
	Delta 1-pyrroline-5-carboxylate		
GRMZM2G068665	reductase	3.69	1.05E-12
	Phosphoribosyl-ATP		
GRMZM2G082214	pyrophosphohydrolase-like	2.77	3.33E-05
GRMZM2G537291	2-isopropylmalate synthase LeuA	2.85	2.57E-05
GRMZM2G130332	Diaminopimelate epimerase	2.11	9.07E-04
	Semialdehyde dehydrogenase,		
GRMZM2G076885	dimerisation domain	3.31	5.69E-05
GRMZM2G010406	Argininosuccinate synthetase	3.45	1.87E-10
	Isocitrate/isopropylmalate		
GRMZM5G803490	dehydrogenase	2.32	1.45E-05

		GRMZM2G141273	Prephenate dehydratase	3.42	6.71E-04
		GRMZM2G124059	Lyase 1, N-terminal HAD-like domain;Methylthioribulose-1-phosphate	3.21	1.02E-10
		GRMZM2G574782	dehydratase	2.31	2.11E-06
		GRMZM2G048740	Serine acetyltransferase, N-terminal Pyridoxal phosphate-dependent	2.95	3.31E-06
		GRMZM2G300801	transferase, major region	2.39	4.13E-05
GO:0006414					
Translational elongation	2.70E-13	GRMZM2G129804	Translation protein SH3-like, subgroup Translation elongation factor, IF5A	2.54	2.84E-03
		GRMZM2G113696	C-terminal Translation elongation factor	2.14	1.96E-24
		GRMZM2G110509	EFTu/EF1A, domain 2 UBA-like;Translation elongation factor	2.32	5.15E-09
		GRMZM2G095534	EFTs/EF1B Translation elongation factor	2.71	9.63E-06
		GRMZM2G153541	EFTu/EF1A	2.01	4.33E-28
		GRMZM2G157443	Ribosomal protein 60S	2.23	1.37E-13
		GRMZM2G022662	Nucleic acid-binding, OB-fold	2.79	7.85E-10
		GRMZM2G102891	Ribosomal protein 60S Translation elongation factor	2.02	4.98E-09
		GRMZM2G022269	EFTu/EF1A, domain 2 Translation elongation factor	2.44	4.08E-06
		AC233866.1_FG006	EFTu/EF1A, domain 2 Glutathione S-transferase, C-terminal-like	2.64	2.29E-18
		GRMZM2G439201	C-terminal-like	2.30	2.30E-35
		GRMZM2G059580	Translation elongation factor EF1B	2.09	9.00E-06
		GRMZM2G179976	Ribosomal protein L10 Translation elongation factor	2.87	1.79E-10
		GRMZM2G313678	EFTu/EF1A, domain 2 Signal recognition particle,	4.13	2.11E-05
		GRMZM2G058407	SRP9/SRP14 subunit	3.10	8.45E-04
		GRMZM2G119809	Ribosomal protein 60S	2.09	3.31E-10
		GRMZM2G136889	Glu-tRNAGln amidotransferase	2.86	7.46E-06
		GRMZM2G075630	Ribosomal protein 60S	2.33	1.42E-10
		GRMZM2G153569	Translation elongation factor EF1B	2.16	4.15E-06
		GRMZM2G010257	Ribosomal protein 60S	3.18	1.72E-07
		GRMZM2G077208	Ribosomal protein 60S	2.98	5.09E-36
		GRMZM2G105712	Ribosomal protein 60S	2.15	6.90E-06
		GRMZM2G032315	Ribosomal protein 60S	2.11	3.39E-14
		GRMZM2G320497	Glutathione S-transferase	2.13	4.72E-04
GO:0045735					
Nutrient reservoir activity	2.90E-11	GRMZM2G078441	Cupin 1	-3.64	1.64E-42

GRMZM2G008341	Zein seed storage protein	-4.00	8.74E-17
GRMZM2G161097	Cupin 1	-3.46	7.01E-04
GRMZM2G045387	Zein seed storage protein	-3.87	2.72E-256
GRMZM2G034724	Cupin 1	-0.19	2.57E-18
GRMZM2G160739	Zein seed storage protein	-3.83	0.00E+00
GRMZM2G044152	Zein seed storage protein	-3.68	0.00E+00
AF546187.1_FG007	Zein seed storage protein	-7.54	0.00E+00
AF546187.1_FG002	Zein seed storage protein	-8.52	2.99E-18
AF546187.1_FG001	Zein seed storage protein	-9.86	0.00E+00
GRMZM2G088441	Zein seed storage protein	-3.91	0.00E+00
GRMZM2G044625	Zein seed storage protein	-3.51	0.00E+00
GRMZM2G088273	Zein seed storage protein	-22.58	2.29E-20
GRMZM2G053120	Zein seed storage protein	-4.68	3.80E-09
AF546188.1_FG005	Zein seed storage protein	-5.28	0.00E+00
AF546188.1_FG006	Zein seed storage protein	-5.72	1.19E-157
AF546188.1_FG007	Zein seed storage protein	-5.77	0.00E+00
AF546188.1_FG001	Zein seed storage protein	-6.99	0.00E+00
AF546188.1_FG003	Zein seed storage protein	-3.30	1.64E-11
GRMZM2G138689	Gliadin/LMW glutenin	-14.87	0.00E+00
GRMZM2G353268	Zein seed storage protein	-4.32	0.00E+00
GRMZM2G059620	Zein seed storage protein	-5.22	0.00E+00
GRMZM2G026703	Cupin 1	-364.00	4.50E-219
GRMZM2G008913	Zein seed storage protein	-4.07	0.00E+00
GRMZM2G026939	Zein seed storage protein	-3.34	1.93E-265
GRMZM2G067919	Cupin 1	-4.12	1.04E-39
GRMZM2G388461	Zein seed storage protein	-4.60	2.01E-239
GRMZM2G346897	Zein seed storage protein	-3.83	0.00E+00
GRMZM2G346895	Zein seed storage protein	-3.80	3.06E-79
GRMZM2G397687	Zein seed storage protein	-4.29	0.00E+00
GRMZM2G088365	Zein seed storage protein	-107.06	0.00E+00

Table S2. Primers used in this work.

	Primer name	Sequence
Mapping	AC196023.10	F:5'-TGTAATTGCGTTTGATTCGT-3'
		R:5'-AAAACGATACCTGGGAAATTAT-3'
	AC209356.12	F:5'-AAACTAATCCTAAGAGTGACGA-3'
		R:5'-CTCCCAGTTCATAGCTACAC-3'
	AC204567.28	F:5'-TGACGATGGTCCTTGATTCT-3'
		R:5'-CCGTGGTCCGTAGCTC-3'
	2G471304.4	F:5'-TTGATGACTATTGAGGCAGT-3'
		R:5'-TGAAATAGGGAAGACTGGGA-3'
	2G168984.7	F:5'-GTTTCACTTTCTACCCTCGC-3'
		R:5'-ATTAATTAAGAAGTGCAGCAGGA-3'
	AC202457.4	F:5'-CAGTAGTGGAGTTCCTTTGG-3'
		R:5'-ACGTACGGACATAGACCAAT-3'

Vector construction	2G087226.7	F:5'-ACAGATGCGATTGTGACTTGC-3'
		R:5'-TCCTGTCATCAGGAACCAAC-3'
	Gateway	F:5'-CACCATGCCGCCCATGGTCTCG-3'
		R:5'-GAAAGTCATGGAAGAACTTCTGC-3'
Genotyping	<i>BAR</i>	F:5'- GAAGTCCAGCTGCCAGAAAC-3'
		R:5'- GCACCATCGTCAACCACTAC-3'
	<i>Dek10</i>	F:5'- ACAGATGCGATTGTGACTTGC-3'
		R:5'- TCCTGTCATCAGGAACCAAC-3'
Real-time PCR	<i>Dek10</i>	F:5'-GCCAACTCCCTCTTCCGC-3'
		R:5'-CGAGGCAGTGGGACAGAAC-3'
	<i>cox2</i>	F:5'-AGACGCAGCAACACCTATGA-3'
		R:5'-CCATAAAGCGCGAACCAACA-3'
	GRMZM2G125669 (AOX2)	F:5'-ACAGGCTGCTTCCAACCATA-3'
		R:5'-GCTTCCAGAAACCCAGGAGG-3'
	GRMZM2G010933 (Cytochrome c oxidase 17)	F:5'- AACGAAAGTCGGCAGTTCT-3'
		R:5'- TTCACAGCTGGGGTTTCAGG-3'
	GRMZM2G115049 (Porin)	F:5'- ATCGGGAAGAAGGCCAGAGA-3'
		R:5'- AGTAATGGCAGCTCCGTTGG-3'
GRMZM2G064600 (Translocase subunit)	F:5'- GATACCTCCCCGCCCTCTAA-3'	
	R:5'- ATAACATCCACGCGACGAAA-3'	
GRMZM2G069229 (ATPase)	F:5'- ACGGAAGCCGTCTGAAGATT-3'	
	R:5'- GGTAGCCCGTGACGGTAAAA-3'	
RNA editing analysis	<i>nad3</i>	F:5'-CTTTCCTATGTCCTTCCCC-3'
		R:5'-GAGGAGAGCGAGAGAACGAA-3'
	<i>nad4L</i>	F:5'-CTGACATTCCATGTTTCCGA-3'
		F:5'-GAAGAGAACGAAAGGAGAACAGA-3'
	<i>nad6</i>	F:5'-TGAAAAACCAAACCCACAT-3'
		R:5'-CAAGTCCCTTGGCGTAGTC-3'
	<i>nad9</i>	F:5'-AGCAAGAAGCGGAACAAAA-3'
		R:5'-TATTGATTTGTCCCTCCCC-3'
	<i>nad7</i>	F:5'-GTTTTGGCTCGCAATAAAGC-3'
		R:5'-CAGGTGGGACAAGCTCTAGG-3'
	<i>nad4</i>	F:5'-CAGTCACCCGGAGAAGATTT-3'
		R:5'-TAATTTGGCGCCTGATTGAC-3'
	<i>nad1</i>	F:5'-GGCCCGATCATGAGTGAATA-3'
		R:5'-GCCCCCTTCAGAAGAACTT-3'
	<i>nad2</i>	F:5'-GACGGAGGAGAGGAAATGAA-3'
		R:5'-GCAGTCCACCCTTTCTTTGA-3'
	<i>nad5</i>	F:5'-CGCTCGAACATTGTCTGATT-3'
		R:5'-GTCCTGGCAAGCTCCTACAG-3'
<i>rps3</i>	F:5'-GCAGAAAGGGGCAAAAGTAA-3'	
	R:5'-TCGCGACCCCTACTACATCT-3'	
<i>rps13</i>	F:5'-TCATGATGATTAAGGGAAGAGTGA-3'	
	R:5'-TTGAATTGAACAGTGTGATTGAT-3'	
<i>rps12</i>	F:5'-CTAGCTGCTTCCATATCGCC-3'	
	R:5'-CGGATCGGGAGTAACCACTA-3'	
<i>rps7</i>	F:5'-TTCGTTGAAAAACCTACGC-3'	

		R:5'-ATGAGGAAGGCCGATTTTCT-3'
	rps4	F:5'-AGAGTTGGGTTTCGATTCCCT-3' R:5'-AGCGACTAGGCCGATCTTTT-3'
	rps2B	F:5'-TCCATGGACCCACGTAAAAT-3' R:5'-GGCCCCTCTCTGATAAGGAA-3'
	rps2A	F:5'-CAGGAAAGATATTTGCCCA-3' R:5'-CCTGTATCTCCGAAACGAA-3'
	rps1	F:5'-AAGGTGGGCTTCGGATTATT-3' R:5'-TCTTCAGTTTTACGCTTACGCT-3'
	rpl16	F:5'-GGTTTTTCCCCACTAACCA-3' R:5'-GGGTGCGGAAATAGCTAGAA-3'
	atp1	F:5'-CGTTGCTGGTGAAGAAGCAT-3' R:5'-AAAAGCGGATTTATCCATCG-3'
	atp4	F:5'-AGCCACGTGCTCTAATCCTC-3' R:5'-TCCCTTCTCTTGGAGCAGA-3'
	atp6	F:5'-CCAAGTCTCTTTGGGAGCA-3' R:5'-GGCTCCTCGTTTTTATGCAA-3'
	atp8	F:5'-GGCAAGGATCCTCAGTCCTA-3' R:5'-GAGGGTTGGTTTGATTGGAA-3'
	atp9	F:5'-AGGGCCTCGTCATCTCTAT-3' R:5'-TAGTTGCGAAGGAAAAGCGT-3'
	ccmB	F:5'-AGCCGTGCAAGTGAATGAAT-3' R:5'-AACGGCTTTTCCATGACTTG-3'
	ccmC	F:5'-ACTTGCAAGGCAAGGAAAAA-3' R:5'-CCATGGATGCTTTAGCGAGT-3'
	ccmFC	F:5'-GAGAAGCTCAAATCGAACGG-3' R:5'-CGCAGCCACTATTTGACTC-3'
	ccmFN	F:5'-TGAAGATTGTAAGGCGTTTCC-3' R:5'-GGATCATCCTGTGGTTACCG-3'
	cob	F:5'-ATCAAGGCAAGGGGTAAAT-3' R:5'-GGTGTGATCAGTCTCATCCG-3'
	cox1	F:5'-GGCCCCTCTCTGATAAGGTT-3' R:5'-GTAAAGCAAAGCCCAAACA-3'
	cox2	F:5'-GTCCTACTTCTGGTCTGCC-3' R:5'-GAGAATTGCATTTCCGCTTC-3'
	cox3	F:5'-TCAATCCACTTATTCGTTCCC-3' R:5'-GTTTACATACAACCGGGGCA-3'
	Mat-r	F:5'-AACGCCTGTTTCGCTAAAATC-3' R:5'-AGGCTTTGCTCCCCTTTTT-3'
	mttB(orfX)	F:5'-TTGGTTTAGAATTGCTCGGG-3' R:5'-AGGGGAACCCACCGAC-3'
	rps12-ct	F:5'-TGTACGGTCTGTAGAGGGACA-3' R:5'-TCCGTTTTCTTTTATAAGGGC-3'
	rps7-ct	F:5'-TTGAACCTCTTTCACGCTCA-3' R:5'-TTCCGATCGAGATGTATGGA-3'

