Supplementary Table 1. Adaptors and primers used in the pilot experiment

Primers and adaptors	Sequence(5'-3')
Ad1	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTT
Ad2	5'-Phosphate-AGAGATCG-amino-3'
Ad3	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGAT
Ad4	5'-Phosphate-TCTAGATCG-amino-3'
Ad5	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGTT
Ad6	5'-Phosphate-ACAAGATCG-amino-3'
Ad7	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGCT
Ad8	5'-Phosphate-GCCAGATCG-amino-3'
Ad9	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGAT
Ad10	5'-Phosphate-TCGAGATCG-amino-3'
TSP1-1	GCGTGCCTCCTTCCAGTCAATCTTT
TSP1-2	TATGGACAATCCTTCTGGTGACTTC
TSP1-3	TGTTTTGCTGTAGGAAATGATCGGA
TSP1-4	GAATGTGGTGTGGACTTCGCTCTAC
TSP1-5	GCTAAGGCACAGTTCGATCCAGCAT
TSP1-6	GGCGTTTCCCTGATAATTCCGGTGA
TSP1-7	AGCCAGGATGAGGTCTCGCAATTCA
TSP1-8	ACGCGCCAGAGTTGGAGATAGCTAT
TSP1-9	GGGATCGCATAAACTGGGGCATCTT
TSP1-10	TCTACCGGCTGTGATCCATGACCTA
TSP1-11	AAGATGTCTGGACGTGTTGAGGACG
TSP1-12	AGCCAGCAGGAGGTCTACAAGTTCA
TSP1-13	TGGCAAAGAGTTCGACATCCCGAAG
AP1	CATACGAGATCGTGATGTGACTGGAG
TSP2-1	TACACGACGCTCTTCCGATCTGAATATGTAGCTCTTCCCTT
TSP2-2	TACACGACGCTCTTCCGATCTGCAGAAAGTACCGTCACATA
TSP2-3	TACACGACGCTCTTCCGATCTTGGCCCCTTGTGTTATATGG
TSP2-4	TACACGACGCTCTTCCGATCTTGAGGGAGAGAGCTTTGGATAG
TSP2-5	TACACGACGCTCTTCCGATCTGAAAAGAAGTAAGCCAAAGTCAGTT
TSP2-6	TACACGACGCTCTTCCGATCTGATGACGGTGCCCATGTTT
TSP2-7	TACACGACGCTCTTCCGATCTGTCGCTTTTGATGTGGATTA
TSP2-8	TACACGACGCTCTTCCGATCTAAAGAAGTTGGCTACGACATC
TSP2-9	TACACGACGCTCTTCCGATCTTGACCACACTGACTCACTGC
TSP2-10	TACACGACGCTCTTCCGATCTGATCCATGACCTACACTCGAG
TSP2-11	TACACGACGCTCTTCCGATCTGGACCTGATAGACTCGACGTAC
TSP2-12	TACACGACGCTCTTCCGATCTAGGAGCAGTTCAGGTTCTTCAC
TSP2-13	TACACGACGCTCTTCCGATCTACAGGCTCCCTCACATCTTCA
AP2	GATGTGACTGGAGTTCAGACGTGT
AP3F	CAAGCAGAAGACGGCATACGAGATCGTGATGTGACTGGAGTTCAGACGT
AP3R	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

Ad: adaptor. TSP: target specific primer. AP: adaptor-derived primer. In the first round PCR, the forward primers of subpool1 consisted of TSP1-1 (target specific primer), TSP1-2 and TSP1-3; for subpool2, TSP1-1, TSP1-2, ... TSP1-5 were mixed as primers;

for subpool3, TSP1-1, TSP1-2, ... TSP1-7 were mixed as the primers; for subpool4, TSP1-1, TSP1-2, ... TSP1-10 were mixed as the primers; for subpool5, TSP1-1, TSP1-2, ... TSP1-13 were mixed as the primers.

Supplementary Table 2. Adaptors and primers used in mutation discovery from the sodium azide induced rice population

Primers and adaptors	Sequence(5'-3')
Ad25	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCATGAT
Ad26	5'-Phosphate-TCATGAGATCG-amino-3'
Ad27	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCATCTT
Ad28	5'-Phosphate-AGATGAGATCG-amino-3'
Ad29	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCATACT
Ad30	5'-Phosphate-GTATGAGATCG-amino-3'
Ad31	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAGAGT
Ad32	5'-Phosphate-CTCTGAGATCG-amino-3'
Ad33	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAGTCT
Ad34	5'-Phosphate-GACTGAGATCG-amino-3'
Ad35	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAGCTT
Ad36	5'-Phosphate-AGCTGAGATCG-amino-3'
Ad37	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCACTAT
Ad38	5'-Phosphate-TAGTGAGATCG-amino-3'
Ad39	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCACGTT
Ad40	5'-Phosphate-ACGTGAGATCG-amino-3'
Ad41	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCACTGT
Ad42	5'-Phosphate-CAGTGAGATCG-amino-3'
Ad43	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAGGT
Ad44	5'-Phosphate-CCTTGAGATCG-amino-3'
Ad45	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAACCT
Ad46	5'-Phosphate-GGTTGAGATCG-amino-3'
Ad47	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAGTT
Ad48	5'-Phosphate-ACTTGAGATCG-amino-3'
Ad49	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGAT
Ad50	5'-Phosphate-TCACTAGATCG-amino-3'
Ad51	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTCTT
Ad52	5'-Phosphate-AGACTAGATCG-amino-3'
Ad53	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTACT
Ad54	5'-Phosphate-GTACTAGATCG-amino-3'
Ad55	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGGATT
Ad56	5'-Phosphate-ATCCTAGATCG-amino-3'
Ad57	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGGTGT
Ad58	5'-Phosphate-CACCTAGATCG-amino-3'
Ad59	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGGCTT
Ad60	5'-Phosphate-AGCCTAGATCG-amino-3'
Ad61	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCATT
Ad62	5'-Phosphate-ATGCTAGATCG-amino-3'
Ad63	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCTAT
Ad64	5'-Phosphate-TAGCTAGATCG-amino-3'
Ad65	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCGTT

(*To be continued*)

Supplementary Table 2. Adaptors and primers used in mutation discovery from the sodium azide induced rice population (*continued*)

Primers and adaptors	Sequence(5'-3')
Ad66	5'-Phosphate-ACGCTAGATCG-amino-3'
Ad67	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGAGCT
Ad68	5'-Phosphate-GCTCTAGATCG-amino-3'
Ad69	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGACAT
Ad70	5'-Phosphate-TGTCTAGATCG-amino-3'
Ad71	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGAGTT
Ad72	5'-Phosphate-ACTCTAGATCG-amino-3'
Ad73	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCTGCT
Ad74	5'-Phosphate-GCAGAAGATCG-amino-3'
Ad75	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCTCAT
Ad76	5'-Phosphate-TGAGAAGATCG-amino-3'
Ad77	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCTAGT
Ad78	5'-Phosphate-CTAGAAGATCG-amino-3'
Ad79	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCGAGT
Ad80	5'-Phosphate-CTCGAAGATCG-amino-3'
Ad81	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCGTCT
Ad82	5'-Phosphate-GACGAAGATCG-amino-3'
Ad83	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCGCTT
Ad84	5'-Phosphate-AGCGAAGATCG-amino-3'
Ad85	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCCTAT
Ad86	5'-Phosphate-TAGGAAGATCG-amino-3'
Ad87	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCCGTT
Ad88	5'-Phosphate-ACGGAAGATCG-amino-3'
Ad89	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCCTGT
Ad90	5'-Phosphate-CAGGAAGATCG-amino-3'
Ad91	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCAGGT
Ad92	5'-Phosphate-CCTGAAGATCG-amino-3'
Ad93	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCACTT
Ad94	5'-Phosphate-AGTGAAGATCG-amino-3'
Ad95	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCAGCT
Ad96	5'-Phosphate-GCTGAAGATCG-amino-3'
Ad97	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTGAT
Ad98	5'-Phosphate-TCAACAGATCG-amino-3'
Ad99	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTCTT
Ad100	5'-Phosphate-AGAACAGATCG-amino-3'
Ad101	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTACT
Ad102	5'-Phosphate-GTAACAGATCG-amino-3'
Ad103	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGT
Ad104	5'-Phosphate-CTCACAGATCG-amino-3'
Ad105	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGTCT
Ad106	5'-Phosphate-GACACAGATCG-amino-3'

(*To be continued*)

Supplementary Table 2. Adaptors and primers used in mutation discovery from the sodium azide induced rice population (*continued*)

Primers and adaptors	Sequence(5'-3')
Ad107	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGCTT
Ad108	5'-Phosphate-AGCACAGATCG-amino-3'
Ad109	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTAT
Ad110	5'-Phosphate-TAGACAGATCG-amino-3'
Ad111	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTCGTT
Ad112	5'-Phosphate-ACGACAGATCG-amino-3'
Ad113	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTGT
Ad114	5'-Phosphate-CAGACAGATCG-amino-3'
Ad115	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTAGTT
Ad116	5'-Phosphate-ACTACAGATCG-amino-3'
Ad117	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTACAT
Ad118	5'-Phosphate-TGTACAGATCG-amino-3'
Ad119	CGAGATCGTGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTAGCT
Ad120	5'-Phosphate-GCTACAGATCG-amino-3'
TSP1-14	AATTGGTCGAGCAGACGACGACGAA
TSP1-15	CTCTAAGTGGGGAGAAAGTGGAACG
TSP1-16	CTACAGGTGCATCAAGGAGGCGCTC
TSP1-17	ACAGTCCGGCACTGTGAACATGAAG
TSP1-18	CACAGCTAACTCGACGCTCAATTCC
TSP1-19	TCAAGATGGGGAGATCAGGGTACGG
TSP1-20	TGTAAGCATCTGGACCGGTGTCCAC
TSP1-21	GTCTTCATCATTACACTAGCTGCGA
TSP1-22	TGGATCACGTGCTGATGCTGATCGC
TSP1-23	CACTTGTGTTAGCTAGGCTTGACCG
TSP1-24	GGCCACTGCAATTTGTAGGGCTACT
TSP1-25	GGATCGCATAAACTGGGGCATCTTG
TSP1-26	TCCTCTGATCTTACCTGCAAAACGC
TSP1-27	ACATACGGCACCCAGTCATTACAAG
TSP1-28	CGTCAGAAAACACGGCATCATCAAT
TSP1-29	TTGCTAATGGTCCTCTCGTAGTCCC
TSP1-30	ACAGGATTACTTTGCGAAATGGGGG
TSP1-31	GAATCACGGATGATCGCTACGGTTC
TSP1-32	GGCTGGTTGTTGTCATGGATCTTGT
TSP1-33	TGGGGAGAAAATGGCATAGTTGATA
TSP1-34	TGGATCATTTCTATGGTTTTTGCCG
TSP1-35	CGTACGTGTTGGTATGGACATGGCC
TSP1-36	CGCAGGAATATTTCGCGAAATGGGG
TSP1-37	GACATCGTACCCTAGCAAGTGCAAG
TSP1-38	GTTTTGGCCCAATAAGGTCCGAGTT
TSP1-39	TCCATGCATGTTACGGGAACGCTCG
TSP1-40	CCCTGGTATAAGAGCCTGCAATATG

(*To be continued*)

Supplementary Table 2. Adaptors and primers used in mutation discovery from the sodium azide induced rice population (*continued*)

Primers and adaptors	Sequence(5'-3')
TSP1-41	GAGCCGGTGACATAGTATCAGAACG
TSP1-42	TTGGGACGAAGTAGTAGGTGGCACG
TSP1-43	TCTCCACAGATATTTGCCTTACATG
TSP1-44	TCTCCACACTGGACACCTTGAGCTC
TSP1-45	TCCCTTGATAGATCAGCCATCGTCG
TSP1-46	TTCGAGCTAACTGTAGAATCCACCG
TSP1-47	GTGGGGCCGATGAATTTCTTTCAGA
TSP1-48	CTCAAGGGACATGTTGGTGCTTTTC
TSP1-49	ATGCTGTCTTTGTTTCTGCTTGCAG
AP1	CATACGAGATCGTGATGTGACTGGAG
TSP2-14	TACACGACGCTCTTCCGATCTATGGATCTCGCCGACCCAAA
TSP2-15	TACACGACGCTCTTCCGATCTTCATCTTCCCCTACCTCCCA
TSP2-16	TACACGACGCTCTTCCGATCTTAATCATGCTGCTCCGCCAG
TSP2-17	TACACGACGCTCTTCCGATCTGAGTTTGAACAACTCGTCAC
TSP2-18	TACACGACGCTCTTCCGATCTAAGCATGGATCAGCTTACAA
TSP2-19	TACACGACGCTCTTCCGATCTTGGGAAAGGAGTTGCGAGAG
TSP2-20	TACACGACGCTCTTCCGATCTCTGAGCAGGATAGGTTGATG
TSP2-21	TACACGACGCTCTTCCGATCTGGTAAGATCATCAGTAACTC
TSP2-22	TACACGACGCTCTTCCGATCTAGAACATGTTCGACGAGGTT
TSP2-23	TACACGACGCTCTTCCGATCTCTGACCATCACTAGTCTCGT
TSP2-24	TACACGACGCTCTTCCGATCTATGGCGTAGTGGACATAAAG
TSP2-25	TACACGACGCTCTTCCGATCTAGATGACCACACTGACTCAC
TSP2-26	TACACGACGCTCTTCCGATCTACCCGTTGTGAATTGCATCG
TSP2-27	TACACGACGCTCTTCCGATCTGGCATCACCTACATGTTCTG
TSP2-28	TACACGACGCTCTTCCGATCTATCGTCACAGATCACTATGG
TSP2-29	TACACGACGCTCTTCCGATCTATTGCAAGAGGAGGAAGGAG
TSP2-30	TACACGACGCTCTTCCGATCTGGTGATGGGGACGATGTTTG
TSP2-31	TACACGACGCTCTTCCGATCTTGCATCAAGGAGACCCTACG
TSP2-32	TACACGACGCTCTTCCGATCTCAATTACCCTCAATCCAAAG
TSP2-33	TACACGACGCTCTTCCGATCTTCTCAGGCCATTGCCTACTC
TSP2-34	TACACGACGCTCTTCCGATCTAGCATGCCTACTAACTCATG
TSP2-35	TACACGACGCTCTTCCGATCTTCTGGTTCTCCGCCATAGCC
TSP2-36	TACACGACGCTCTTCCGATCTTGGATCTGAAACGCGAGCTC
TSP2-37	TACACGACGCTCTTCCGATCTTTCACCAAGCAGTACCACTG
TSP2-38	TACACGACGCTCTTCCGATCTAATTACTGAGGTCGTGGAAG
TSP2-39	TACACGACGCTCTTCCGATCTGTCGTCTTGTCATTGGAACA
TSP2-40	TACACGACGCTCTTCCGATCTGATCCTAAGAAGCGAGCCTT
TSP2-41	TACACGACGCTCTTCCGATCTTTGGTACAGGAAGATCTTCG
TSP2-42	TACACGACGCTCTTCCGATCTTAACCACTGGTTGGAGCTCC
TSP2-43	TACACGACGCTCTTCCGATCTTACGTGAGATATGCCGCTAC
TSP2-44	TACACGACGCTCTTCCGATCTCTGTTCACTCCCGTGTATAG

(*To be continued*)

Supplementary Table 2. Adaptors and primers used in mutation discovery from the sodium azide induced rice population (*continued*)

Primers and adaptors	Sequence(5'-3')
TSP2-45	TACACGACGCTCTTCCGATCTACCGACGGACGGATCGATAT
TSP2-46	TACACGACGCTCTTCCGATCTTCGCCTTCAGGTGGATGTTC
TSP2-47	TACACGACGCTCTTCCGATCTGCTCTCTATATCACTGGATC
TSP2-48	TACACGACGCTCTTCCGATCTTTTCCACAGGGCGATTCTGG
TSP2-49	TACACGACGCTCTTCCGATCTCGTTATCCGCGATCATTTGT
AP2	GATGTGACTGGAGTTCAGACGTGT
AP3F	CAAGCAGAAGACGGCATACGAGATCGTGATGTGACTGGAGTTCAGACGT
AP3R	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

In the first round PCR, the forward primers of the first primer set were TSP1-14, TSP1-15, ..., TSP1-25; the forward primers of the second set were TSP1-26, TSP1-27, ..., TSP1-37; the forward primers of the third set were TSP1-28, TSP1-29, ... TSP1-49. The reverse primer was AP1, which was universal for all of the first round PCRs. In the second round PCRs, the forward primers for each primer set were similar tothe first round PCRs, with TSP2-14 instead of TSP 1-14, TSP2-15 instead of TSP1-15, ..., TSP2-49 instead of TSP1-49. The reverse primer was AP2, which was universal for all of the second round PCRs.

Supplementary Table 3. Ratio of on-target reads

Bulks	Ratio(%)	Bulks	Ratio(%)	Bulks	Ratio(%)
AX1	57.50	AZ1	25.44	BY1	56.51
AX2	60.91	AZ2	60.16	BY2	60.70
AX3	63.17	AZ3	59.24	BY3	54.12
AX4	60.11	AZ4	56.85	BY4	54.53
AX5	62.62	AZ5	43.52	BY5	58.82
AX6	58.58	AZ6	25.67	BY6	65.34
AX7	63.03	AZ7	31.44	BY7	67.27
AX8	60.20	AZ8	54.43	BY8	64.67
AY1	16.88	BX1	65.39	BZ1	60.66
AY2	52.01	BX2	67.23	BZ2	42.20
AY3	13.44	BX3	65.30	BZ3	42.14
AY4	61.36	BX4	73.87	BZ4	51.75
AY5	64.33	BX5	67.51	BZ5	62.00
AY6	64.89	BX6	67.43	BZ6	54.52
AY7	64.45	BX7	67.67	BZ7	55.80
AY8	62.93	BX8	67.87	BZ8	60.83

Supplementary Table 4. Summary of the enriched fragment length of Pool A

		Bulks (bp)								Total (average) screened fragment length (bp)*
Fragments	Dimensions	1	2	3	4	5	6	7	8	
Os11g32240-1	X	0	105	122	105	117	115	105	113	16,584
	Y	0	114	0	99	85	113	99	109	(33)
	Z	0	113	128	118	0	0	0	91	
Os11g32240-2	X	114	160	162	162	184	162	162	162	17,584
	Y	86	117	0	0	174	169	147	160	(35)
	Z	68	133	135	108	0	0	0	0	
Os11g32240-3	X	154	201	209	201	237	217	197	202	66,697
	Y	139	185	124	152	190	227	185	192	(130)
	Z	148	218	251	222	137	131	134	135	
Os05g12040-1	X	171	178	193	195	188	200	197	204	65,736
	Y	126	171	120	200	160	174	169	174	(129)
	Z	135	187	197	147	204	134	131	178	
Os07g28110-1	X	106	106	111	106	108	108	106	111	46,532
	Y	106	111	101	114	106	107	106	108	(91)
	Z	106	111	108	94	106	103	106	120	
Os07g28110-2	X	152	154	152	154	161	159	169	220	56,719
	Y	98	178	63	232	169	156	154	159	(111)
	Z	118	179	243	163	231	99	128	220	
Os07g28110-3	X	110	114	128	112	178	116	175	210	16,214
	Y	108	202	105	247	178	178	177	183	(32)
	Z	110	209	246	183	229	110	112	210	
Os02g21810-1	X	0	0	0	0	0	0	0	0	0
	Y	0	99	0	195	0	0	0	0	(0)
	Z	0	0	193	32	99	0	0	87	
Os02g21810-2	X	180	183	182	183	182	182	188	210	66,850
	Y	110	214	99	239	188	185	185	188	(131)
	Z	134	214	251	193	224	122	134	215	
Os02g02230-1	X	148	142	159	144	160	173	169	187	61,208
	Y	119	194	111	229	167	161	155	149	(120)
	Z	125	173	216	160	213	124	125	194	
Os02g02230-2	X	127	115	127	109	131	134	128	156	43,587
	Y	94	155	0	198	132	124	123	129	(83)
	Z	99	145	212	127	167	95	100	150	
Os02g02230-3	X	146	161	151	146	168	172	183	197	62,740
	Y	120	194	111	230	189	171	146	153	(123)
	Z	135	192	236	193	216	114	135	201	
Subtotal of the first 12-plex nested PCR region										520,451 (1,017)

(To be continued)

Supplementary Table 4. Summary of the enriched fragment length of Pool A (*continued*)

		Bulk (bp)								Total (average) screened fragment length (bp)*
Fragment	Dimension	1	2	3	4	5	6	7	8	
Os05g34325-1	X	150	162	167	152	175	170	185	203	65,246
	Y	120	206	114	247	158	162	162	176	(127)
	Z	136	196	262	183	229	141	138	213	
Os05g34325-2	X	194	202	210	194	208	215	217	230	80,537
	Y	152	221	144	232	202	208	200	208	(158)
	Z	174	223	289	209	258	152	173	228	
Os05g34325-3	X	136	142	145	142	142	150	142	191	50,815
	Y	92	207	46	254	156	148	142	146	(100)
	Z	102	192	258	192	234	90	104	188	
Os05g34330-1	X	92	135	147	142	173	147	149	145	41,435
	Y	104	147	83	105	147	155	117	139	(81)
	Z	116	168	173	168	102	82	0	100	
Os05g34330-2	X	150	213	211	205	237	211	205	205	57,673
	Y	125	150	106	110	205	211	196	205	(113)
	Z	136	170	196	154	104	101	157	115	
Os05g34330-3	X	152	184	188	212	222	210	212	193	61,190
	Y	147	184	126	161	212	217	184	188	(120)
	Z	157	221	228	210	141	132	134	140	
Os05g34380-1	X	0	0	101	71	124	101	101	101	6,315
	Y	85	119	0	0	75	116	0	68	(13)
	Z	0	135	134	125	0	0	0	0	
Os05g34380-2	X	153	159	167	172	194	177	172	168	54,103
	Y	138	153	107	138	172	167	155	167	(106)
	Z	144	155	156	153	104	85	95	112	
Os05g34380-3	X	102	122	117	136	182	154	145	141	21,094
	Y	95	117	0	82	168	154	112	117	(42)
	Z	106	121	136	117	0	0	0	0	
Os07g37970-1	X	0	93	106	98	107	98	88	99	10,928
	Y	0	99	0	99	0	99	72	99	(22)
	Z	0	103	112	101	0	0	0	100	
Os07g37970-2	X	155	200	221	210	228	221	210	214	73,552
	Y	154	211	146	169	200	217	195	208	(144)
	Z	157	219	238	222	154	151	140	157	
Os11g18194-1	X	159	159	167	161	161	151	158	139	36,937
	Y	36	143	75	0	153	161	158	158	(73)
	Z	0	164	164	160	95	130	79	142	
Subtotal of the second 12-plex nested PCR region										559,825 (1,094)

(*To be continued*)

Supplementary Table 4. Summary of the enriched fragment length of Pool A (*continued*)

Fragment	Dimension	Bulk (bp)								Total (average) screened fragment length (bp)*
		1	2	3	4	5	6	7	8	
Os11g18194-2	X	0	82	0	101	134	115	101	93	1,020
	Y	0	0	0	0	73	117	111	0	(2)
	Z	0	0	68	0	0	0	0	0	
Os11g18194-3	X	95	94	95	99	107	102	96	99	23,293
	Y	0	102	0	0	99	99	95	95	(46)
	Z	0	116	139	124	90	101	95	110	
Os11g18194-4	X	125	127	123	137	158	132	134	120	15,976
	Y	0	85	0	0	127	166	163	114	(32)
	Z	0	123	141	100	0	57	0	72	
Os11g18194-5	X	89	119	85	117	157	148	123	125	7,557
	Y	0	0	0	0	103	135	137	100	(15)
	Z	0	86	109	0	0	84	0	0	
Os11g18366-1	X	150	172	183	170	180	150	169	134	34,932
	Y	81	132	92	0	132	245	225	150	(69)
	Z	0	183	191	150	98	123	0	131	
Os11g18366-2	X	0	0	0	93	102	0	81	72	2,532
	Y	0	0	0	0	95	98	47	0	(5)
	Z	0	115	133	100	0	0	0	101	
Os11g18366-3	X	53	86	106	124	126	126	118	107	12,970
	Y	0	106	0	0	119	122	111	73	(26)
	Z	0	128	138	126	0	0	0	101	
Os06g28820-1	X	83	116	120	120	162	124	116	120	10,803
	Y	0	103	0	0	116	124	114	116	(22)
	Z	0	110	113	99	0	0	0	0	
Os06g28820-2	X	166	171	176	182	182	180	182	162	39,690
	Y	120	122	107	0	180	203	196	166	(78)
	Z	119	160	157	140	79	101	0	102	
Os06g28820-3	X	99	106	103	112	145	126	110	123	18,533
	Y	0	100	0	0	105	111	111	105	(37)
	Z	0	110	145	105	27	88	0	100	
Os06g28820-4	X	116	120	124	134	145	139	134	116	35,579
	Y	100	109	90	0	132	143	140	114	(70)
	Z	87	130	132	111	99	106	0	111	
Os06g28820-5	X	147	147	147	169	159	146	162	142	49,344
	Y	99	139	89	58	162	177	164	142	(97)
	Z	83	189	209	185	107	135	111	142	
Subtotal of the third 12-plex nested PCR region										252,229 (493)
Total										**1,332,505** **(2603)**

* The total screened fragment length for a particular fragment was calculated by adding the length of the enriched fragments of each of the 512 individuals for this fragment. An individual was presented in 3 bulks, 1 in X, 1 in Y and 1 in Z. In each bulk, the fragment had a starting base position and an ending base position, which indicated the region of the enriched fragment. The valid screened fragment length of this individual for this fragment was calculated by using the minimum value of the 3 ending base positions (1 in X, 1 in Y and 1 in Z) minus the maximum value of the 3 starting base positions. In this way, the resulting length represents the number of bases, of this individual for this fragment, that were presented in all of the 3 bulks, which were the premise to determine whether a base was mutated or not.

Supplementary Table 5. Summary of the enriched fragment length of Pool B

		Bulks (bp)								Total (average) screened fragment length (bp)*
Fragments	Dimensions	1	2	3	4	5	6	7	8	
Os11g32240-1	X	89	105	102	109	105	105	105	99	10,254
	Y	0	0	0	0	0	105	102	80	(20)
	Z	107	0	0	60	106	102	0	89	
Os11g32240-2	X	120	152	135	181	145	127	146	108	19,236
	Y	0	0	0	0	108	146	137	120	(38)
	Z	180	124	0	150	180	170	0	76	
Os11g32240-3	X	185	193	186	215	190	185	189	173	62,151
	Y	122	129	131	126	145	190	190	182	(122)
	Z	198	179	102	185	198	198	125	138	
Os05g12040-1	X	171	174	171	173	171	171	171	171	68,538
	Y	176	169	150	145	195	205	175	169	(134)
	Z	171	126	149	144	172	147	171	171	
Os07g28110-1	X	110	110	106	109	107	110	106	106	47,552
	Y	109	107	107	106	106	110	107	106	(93)
	Z	107	106	106	105	108	107	107	110	
Os07g28110-2	X	220	215	218	249	229	229	227	220	59,140
	Y	156	177	130	104	227	220	220	221	(116)
	Z	227	70	128	99	177	130	157	159	
Os07g28110-3	X	221	221	210	260	236	236	227	231	29,193
	Y	179	196	116	113	217	236	218	239	(57)
	Z	212	110	113	111	190	114	172	178	
Os02g21810-1	X	112	162	0	99	59	11	0	99	741
	Y	0	0	0	0	0	124	171	222	(2)
	Z	59	0	0	0	0	0	0	0	
Os02g21810-2	X	238	242	233	244	242	241	233	224	67,634
	Y	195	210	133	112	224	242	242	251	(132)
	Z	224	108	138	110	224	134	188	181	
Os02g02230-1	X	185	177	181	223	210	189	189	185	63,423
	Y	164	182	129	125	183	189	189	185	(124)
	Z	194	115	140	125	171	130	155	161	
Os02g02230-2	X	149	149	146	221	171	162	163	163	51,423
	Y	131	149	107	99	158	163	149	157	(101)
	Z	159	93	108	100	140	106	129	131	
Os02g02230-3	X	203	199	199	239	214	208	207	206	62,726
	Y	169	189	126	105	201	204	201	201	(122)
	Z	206	110	133	111	191	133	169	154	
Subtotal of the first 12-plex nested PCR region										542,011 (1,059)

(*To be continued*)

Supplementary Table 5. Summary of the enriched fragment length of Pool B (*continued*)

		Bulks (bp)								Total (average) screened fragment length (bp) *
Fragments	Dimensions	1	2	3	4	5	6	7	8	
Os05g34325-1	X	215	209	206	262	247	245	247	229	57,345
	Y	167	206	148	144	216	235	220	229	(112)
	Z	219	123	147	143	189	148	160	162	
Os05g34325-2	X	230	225	223	292	245	230	245	231	55,780
	Y	197	225	179	152	230	234	225	225	(109)
	Z	253	142	196	161	218	185	194	194	
Os05g34325-3	X	222	216	196	265	235	222	226	239	49,699
	Y	150	166	109	90	222	232	222	235	(97)
	Z	212	0	110	92	168	108	142	145	
Os05g34330-1	X	102	114	111	152	133	111	123	111	26,382
	Y	0	85	92	80	55	106	114	101	(52)
	Z	154	111	0	145	143	154	0	100	
Os05g34330-2	X	182	205	196	224	197	177	205	163	59,267
	Y	110	119	124	113	154	203	196	163	(116)
	Z	222	168	104	194	208	205	109	133	
Os05g34330-3	X	166	188	183	222	188	165	188	161	60,931
	Y	124	120	130	121	159	187	187	161	(119)
	Z	220	169	102	178	217	212	126	141	
Os05g34380-1	X	0	0	0	86	0	0	0	0	0
	Y	0	0	0	0	0	0	0	0	(0)
	Z	119	0	0	118	97	128	0	0	
Os05g34380-2	X	147	167	162	180	167	167	167	143	55,035
	Y	107	120	116	112	144	167	155	153	(108)
	Z	193	147	83	160	172	167	111	140	
Os05g34380-3	X	102	112	112	175	121	112	117	102	24,124
	Y	0	75	0	77	104	112	112	102	(47)
	Z	170	112	0	125	147	152	0	100	
Os07g37970-1	X	92	100	78	99	95	98	94	98	10,369
	Y	0	0	67	0	0	99	99	78	(21)
	Z	59	0	0	64	96	97	0	95	
Os07g37970-2	X	169	203	188	212	197	177	203	183	69,492
	Y	144	154	154	154	154	199	198	177	(136)
	Z	210	164	131	188	210	205	141	157	
Os11g18194-1	X	134	130	122	139	120	115	103	109	53,624
	Y	138	158	139	147	149	153	156	157	(105)
	Z	156	157	158	157	157	158	161	158	
Subtotal of the second 12-plex nested PCR region										522,048 (1020)

(*To be continued*)

Supplementary Table 5. Summary of the enriched fragment length of Pool B (*continued*)

Fragments	Dimensions	Bulks (bp)								Total (average) screened fragment length (bp) *
		1	2	3	4	5	6	7	8	
Os11g18194-2	X	120	134	147	164	142	153	154	177	17,087
	Y	147	170	156	161	111	93	115	126	(34)
	Z	76	0	0	0	0	0	101	153	
Os11g18194-3	X	100	100	100	102	99	110	105	110	43,908
	Y	99	127	100	138	99	95	99	99	(86)
	Z	124	99	99	92	99	99	99	114	
Os11g18194-4	X	181	175	177	221	181	189	194	217	56,292
	Y	175	210	193	214	157	157	181	181	(110)
	Z	120	88	112	122	118	118	153	185	
Os11g18194-5	X	138	139	150	167	147	160	163	181	18,332
	Y	148	165	165	159	122	115	137	151	(36)
	Z	0	0	0	73	0	0	115	151	
Os11g18366-1	X	191	188	183	229	186	189	183	191	77,410
	Y	202	265	207	208	169	190	233	233	(152)
	Z	172	144	150	180	183	183	240	268	
Os11g18366-2	X	115	105	107	121	106	123	113	178	32,622
	Y	102	189	106	139	102	103	104	103	(64)
	Z	115	95	92	0	102	99	102	121	
Os11g18366-3	X	114	114	126	138	124	132	133	142	46,515
	Y	130	138	135	138	107	80	105	120	(91)
	Z	126	85	107	111	100	103	119	138	
Os06g28820-1	X	99	117	111	140	115	110	115	99	12,491
	Y	0	0	0	95	83	116	112	99	(25)
	Z	140	106	0	109	140	120	0	0	
Os06g28820-2	X	211	205	209	235	209	230	227	244	76,493
	Y	202	234	219	224	200	188	209	209	(150)
	Z	166	148	160	171	166	160	188	225	
Os06g28820-3	X	105	107	118	139	111	136	135	149	45,418
	Y	135	136	141	148	96	89	94	102	(89)
	Z	148	93	101	101	102	105	110	140	
Os06g28820-4	X	150	152	151	173	149	173	153	164	57,588
	Y	147	184	164	169	143	144	146	146	(113)
	Z	116	109	120	134	134	124	142	163	
Os06g28820-5	X	178	175	183	195	182	191	192	228	70,501
	Y	183	217	191	217	171	156	174	169	(138)
	Z	170	149	147	147	150	150	175	194	
Subtotal of the third 12-plex nested PCR region										554,657 (1084)
Total										**1,618,716** **(3162)**

* The total screened fragment length for a particular fragment was calculated by adding the length of the enriched fragments of each of the 512 individuals for this fragment. An individual was presented in 3 bulks, 1 in X, 1 in Y and 1 in Z. In each bulk, the fragment had a starting base position and an ending base position, which indicated the region of the enriched fragment. The valid screened fragment length of this individual for this fragment was calculated by using the minimum value of the 3 ending base positions (1 in X, 1 in Y and 1 in Z) minus the maximum value of the 3 starting base positions. In this way, the resulting length represents the number of bases, of this individual for this fragment, that were presented in all of the 3 bulks, which were the premise to determine whether a base was mutated or not.

Supplementary Table 6. Number of candidate mutations remaining after each filtering step in Pool A

Fragments	Raw	MiSD (512)	MiMR ($3.02x10^{-3}$)	1X1Y1Z	Candidate mutations	*t*-test of significance	Mutation types
Os11g32240-1	1,386	767	1	0	0	0	C to T
Os11g32240-2	1,843	870	1	0	0	0	C to T
Os11g32240-3	2,613	1,547	3	3	1	1	C to T
Os05g12040-1	1,982	1,458	7	0	0	0	C to T
Os07g28110-1	1,028	696	1	0	0	0	C to T
Os07g28110-2	1,986	1,059	3	0	0	0	C to T
Os07g28110-3	2,172	1,062	3	0	0	0	C to T
Os02g21810-1	1,950	208	1	0	0	0	C to T
Os02g21810-2	2,278	1,268	0	0	0	0	C to T
Os02g02230-1	1,984	920	2	0	0	0	C to T
Os02g02230-2	1,984	648	0	0	0	0	C to T
Os02g02230-3	1,982	1,295	4	3	1	1	C to T
Os05g34325-1	2,166	1,183	0	0	0	0	C to T
Os05g34325-2	2,670	1,275	9	0	0	0	C to T
Os05g34325-3	2,111	1,150	4	3	1	1	C to T
Os05g34330-1	1,584	853	2	0	0	0	C to T
Os05g34330-2	2,569	1,148	4	0	0	0	C to T
Os05g34330-3	1,743	1,293	3	3	1	1	C to T
Os05g34380-1	1,261	362	6	0	0	0	C to T
Os05g34380-2	1,676	917	0	0	0	0	C to T
Os05g34380-3	1,235	451	3	0	0	0	C to T
Os07g37970-1	1,236	469	5	0	0	0	C to T
Os07g37970-2	2,793	1,717	9	0	0	0	C to T
Os11g18194-1	1,267	806	1	0	0	0	C to T
Os11g18194-2	913	184	0	0	0	0	C to T
Os11g18194-3	529	175	0	0	0	0	C to T
Os11g18194-4	984	441	16	0	0	0	C to T
Os11g18194-5	809	249	0	0	0	0	C to T
Os11g18366-1	1,974	894	2	0	0	0	C to T
Os11g18366-2	940	143	2	0	0	0	C to T
Os11g18366-3	917	327	1	0	0	0	C to T
Os06g28820-1	1,315	418	0	0	0	0	C to T
Os06g28820-2	1,299	773	35	0	0	0	C to T
Os06g28820-3	1,059	524	0	0	0	0	C to T
Os06g28820-4	841	417	15	0	0	0	C to T
Os06g28820-5	1,092	623	0	0	0	0	C to T
Os11g32240-1	1,002	561	43	4	2	0	G to A
Os11g32240-2	1,403	630	178	0	0	0	G to A
Os11g32240-3	1,970	987	301	14	6	0	G to A
Os05g12040-1	1,725	1,195	316	0	0	0	G to A

(*To be continued*)

Supplementary Table 6. Number of candidate mutations remaining after each filtering step in Pool A (*continued*)

Fragments	Raw	MiSD (512)	MiMR ($3.02x10^{-3}$)	1X1Y1Z	Candidate mutations	*t*-test of significance	Mutation types
Os07g28110-1	1,038	664	51	0	0	0	G to A
Os07g28110-2	2,357	1,251	327	7	3	0	G to A
Os07g28110-3	2,328	1,204	273	0	0	0	G to A
Os02g21810-1	2,227	236	36	0	0	0	G to A
Os02g21810-2	2,346	1,315	349	0	0	0	G to A
Os02g02230-1	1,821	925	188	8	4	0	G to A
Os02g02230-2	1,917	833	66	0	0	0	G to A
Os02g02230-3	1,759	841	199	0	0	0	G to A
Os05g34325-1	2,614	1,318	423	0	0	0	G to A
Os05g34325-2	2,472	1,431	531	4	2	0	G to A
Os05g34325-3	2,109	1,005	205	3	1	0	G to A
Os05g34330-1	1,491	643	127	0	0	0	G to A
Os05g34330-2	2,372	1,031	87	0	0	0	G to A
Os05g34330-3	2,061	1,137	308	7	3	0	G to A
Os05g34380-1	1,460	314	34	3	1	0	G to A
Os05g34380-2	1,582	902	128	0	0	0	G to A
Os05g34380-3	1,399	511	120	0	0	0	G to A
Os07g37970-1	1,673	626	106	0	0	0	G to A
Os07g37970-2	2,082	1,194	309	0	0	0	G to A
Os11g18194-1	1,729	1,086	271	0	0	0	G to A
Os11g18194-2	912	175	12	0	0	0	G to A
Os11g18194-3	824	207	9	0	0	0	G to A
Os11g18194-4	1,238	446	80	0	0	0	G to A
Os11g18194-5	1,037	381	46	0	0	0	G to A
Os11g18366-1	1,960	924	278	0	0	0	G to A
Os11g18366-2	1,012	80	12	0	0	0	G to A
Os11g18366-3	927	373	43	0	0	0	G to A
Os06g28820-1	2,055	794	100	3	1	1	G to A
Os06g28820-2	1,223	726	209	0	0	0	G to A
Os06g28820-3	1,038	301	12	0	0	0	G to A
Os06g28820-4	1,103	663	103	0	0	0	G to A
Os06g28820-5	1,204	623	170	0	0	0	G to A
Sum	117,641	56,123	6,193	65	27	5	

Supplementary Table 7. Number of candidate mutations remaining after each filtering step in Pool B

Fragments	Raw	MiSD (512)	MiMR ($3.02x10^{-3}$)	1X1Y1Z	Candidate mutations	*t*-test of significance	Mutation types
Os11g32240-1	1,284	637	2	0	0	0	C to T
Os11g32240-2	1,843	868	1	0	0	0	C to T
Os11g32240-3	2,367	1,438	6	6	2	2	C to T
Os05g12040-1	1,834	1,430	5	3	1	1	C to T
Os07g28110-1	1,020	692	0	0	0	0	C to T
Os07g28110-2	2,024	1,184	4	0	0	0	C to T
Os07g28110-3	2,253	1,199	12	3	1	0	C to T
Os02g21810-1	2,035	333	0	0	0	0	C to T
Os02g21810-2	2,256	1,397	1	0	0	0	C to T
Os02g02230-1	2,120	973	3	3	1	1	C to T
Os02g02230-2	2,259	718	0	0	0	0	C to T
Os02g02230-3	2,132	1,355	4	0	0	0	C to T
Os05g34325-1	2,190	1,302	1	0	0	0	C to T
Os05g34325-2	2,703	1,363	7	0	0	0	C to T
Os05g34325-3	2,211	1,294	0	0	0	0	C to T
Os05g34330-1	1,459	696	0	0	0	0	C to T
Os05g34330-2	2,331	1,248	1	0	0	0	C to T
Os05g34330-3	1,650	1,220	0	0	0	0	C to T
Os05g34380-1	1,094	135	2	0	0	0	C to T
Os05g34380-2	1,557	917	3	3	1	1	C to T
Os05g34380-3	1,110	418	1	0	0	0	C to T
Os07g37970-1	853	442	8	3	1	0	C to T
Os07g37970-2	2,417	1,591	4	0	0	0	C to T
Os11g18194-1	1,166	913	5	0	0	0	C to T
Os11g18194-2	1,314	474	1	0	0	0	C to T
Os11g18194-3	850	289	3	0	0	0	C to T
Os11g18194-4	1,077	782	22	0	0	0	C to T
Os11g18194-5	1,008	416	0	0	0	0	C to T
Os11g18366-1	2,072	1,377	0	0	0	0	C to T
Os11g18366-2	1,324	446	3	0	0	0	C to T
Os11g18366-3	1,171	498	1	0	0	0	C to T
Os06g28820-1	1,200	442	1	0	0	0	C to T
Os06g28820-2	1,457	1,079	52	3	1	1	C to T
Os06g28820-3	1,304	702	2	0	0	0	C to T
Os06g28820-4	1,056	556	24	0	0	0	C to T
Os06g28820-5	1,430	766	0	0	0	0	C to T
Os11g32240-1	892	481	44	4	2	0	G to A
Os11g32240-2	1,399	604	176	3	1	1	G to A
Os11g32240-3	1,731	896	233	0	0	0	G to A

(*To be continued*)

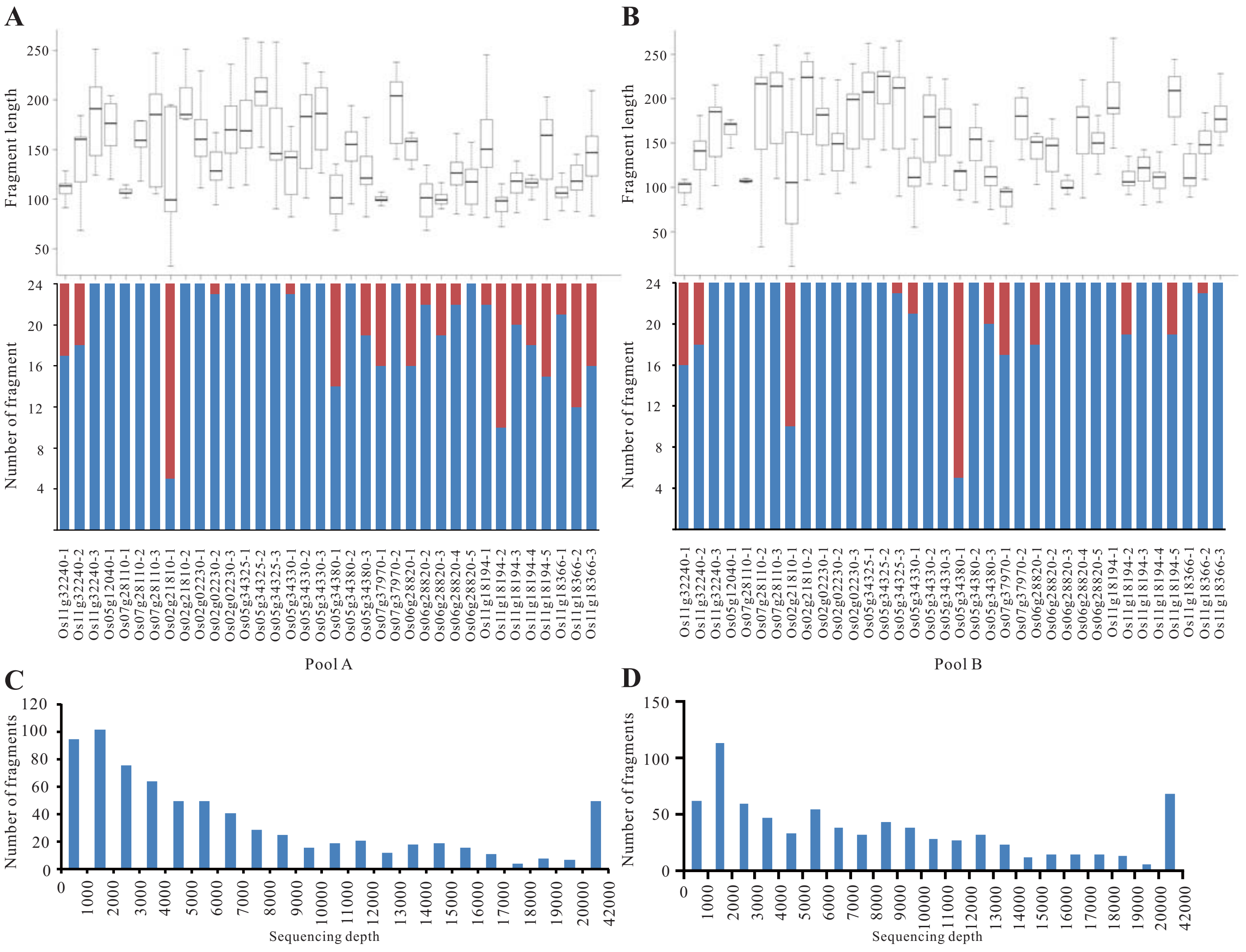
Supplementary Table 7. Number of candidate mutations remaining after each filtering step in Pool B (*continued*)

Fragments	Raw	MiSD (512)	MiMF ($3.02x10^{-3}$)	1X1Y1Z	Candidate mutations	*t*-test of significance	Mutation types
Os05g12040-1	1,541	1,115	274	3	1	1	G to A
Os07g28110-1	1,028	663	55	0	0	0	G to A
Os07g28110-2	2,438	1,400	392	0	0	0	G to A
Os07g28110-3	2,432	1,376	371	0	0	0	G to A
Os02g21810-1	2,276	381	60	0	0	0	G to A
Os02g21810-2	2,331	1,469	448	0	0	0	G to A
Os02g02230-1	1,992	941	195	4	2	0	G to A
Os02g02230-2	2,140	877	93	3	1	1	G to A
Os02g02230-3	1,894	872	203	0	0	0	G to A
Os05g34325-1	2,674	1,488	543	3	1	0	G to A
Os05g34325-2	2,470	1,437	534	3	1	0	G to A
Os05g34325-3	2,241	1,121	282	4	2	0	G to A
Os05g34330-1	1,370	484	58	3	1	0	G to A
Os05g34330-2	2,150	1,105	74	0	0	0	G to A
Os05g34330-3	1,893	1,034	248	0	0	0	G to A
Os05g34380-1	1,222	121	13	0	0	0	G to A
Os05g34380-2	1,489	897	133	0	0	0	G to A
Os05g34380-3	1,258	480	90	0	0	0	G to A
Os07g37970-1	1,208	576	86	0	0	0	G to A
Os07g37970-2	1,708	1,108	284	0	0	0	G to A
Os11g18194-1	1,566	1,202	326	4	2	0	G to A
Os11g18194-2	1,215	471	74	0	0	0	G to A
Os11g18194-3	1,238	335	8	0	0	0	G to A
Os11g18194-4	1,407	872	230	0	0	0	G to A
Os11g18194-5	1,251	609	125	0	0	0	G to A
Os11g18366-1	2,046	1,441	544	4	2	0	G to A
Os11g18366-2	1,506	286	69	0	0	0	G to A
Os11g18366-3	1,164	562	82	3	1	1	G to A
Os06g28820-1	1,900	834	98	0	0	0	G to A
Os06g28820-2	1,484	974	366	0	0	0	G to A
Os06g28820-3	1,459	423	41	3	1	1	G to A
Os06g28820-4	1,285	872	219	4	2	0	G to A
Os06g28820-5	1,380	757	247	0	0	0	G to A
Sum	120,109	62,154	7,497	72	28	11	

Supplementary Table 8. The confirmed genuine and false positive mutations by Sanger sequencing

Candidate mutations	Fragments	Positions	Types	Coordinates in 3D pool	TRUE or FALSE*	Pool
No.1	Os11g32240-F3	3,458	C to T	X3Y6Z6	TRUE	A
No.2	Os02g02230-F3	2,367	C to T	X8Y5Z1	TRUE	A
No.3	Os05g34325-F3	2,342	C to T	X5Y3Z4	TRUE	A
No.4	Os05g34330-F3	5,417	C to T	X6Y7Z5	TRUE	A
No.5	Os06g28820-F1	279	G to A	X8Y8Z2	TRUE	A
No.6	Os07g28110-F2	1,209	G to A	X2Y6Z2	FALSE	A
No.7	Os02g02230-F1	277	G to A	X6Y1Z1	FALSE	A
No.8	Os02g02230-F1	277	G to A	X6Y1Z3	FALSE	A
No.9	Os05g34325-F2	1,498	G to A	X3Y3Z3	FALSE	A
No.10	Os05g34325-F2	1,498	G to A	X2Y3Z3	FALSE	A
No.11	Os11g32240-F3	3,449	C to T	X5Y4Z2	TRUE	B
No.12	Os11g32240-F3	3,498	C to T	X5Y5Z7	TRUE	B
No.13	Os05g12040-F1	1,094	C to T	X8Y6Z7	TRUE	B
No.14	Os02g02230-F1	230	C to T	X7Y1Z5	TRUE	B
No.15	Os05g34380-F2	1,017	C to T	X8Y6Z6	TRUE	B
No.16	Os06g28820-F2	8,307	C to T	X4Y6Z1	TRUE	B
No.17	Os11g32240-F2	3,026	G to A	X5Y8Z2	TRUE	B
No.18	Os05g12040-F1	1,018	G to A	X7Y8Z2	TRUE	B
No.19	Os02g02230-F2	1,808	G to A	X7Y7Z1	TRUE	B
No.20	Os11g18366-F3	12,453	G to A	X7Y5Z3	TRUE	B
No.21	Os06g28820-F3	8,768	G to A	X2Y4Z2	TRUE	B
No.22	Os07g28110-F3	1,634	C to T	X5Y2Z1	FALSE	B
No.23	Os02g02230-F1	279	G to A	X1Y3Z2	FALSE	B
No.24	Os02g02230-F1	279	G to A	X1Y3Z7	FALSE	B
No.25	Os05g34325-F1	745	G to A	X2Y2Z3	FALSE	B
No.26	Os05g34325-F2	1,564	G to A	X1Y6Z6	FALSE	B
No.27	Os11g18366-F1	276	G to A	X5Y2Z5	FALSE	B
No.28	Os11g18366-F1	276	G to A	X7Y2Z5	FALSE	B

* TRUE indicates the genuine mutation. FALSE indicates the false positive mutation.



Supplementary Fig. 1. Summary of the enriched products in Pools A and B. (a & b) The fragment length of each enriched target fragment (shown by the box plot) and the number of successfully enriched (blue) or non-enriched (red) fragments (shown in the histogram). (c & d) The distribution of sequencing depth among the enriched fragments.