Supplementary Tables/Figures

Title: Genomic diversity generated by a transposable element burst in a rice recombinant inbred population

Short title: *mPing* burst in a rice recombinant inbred population

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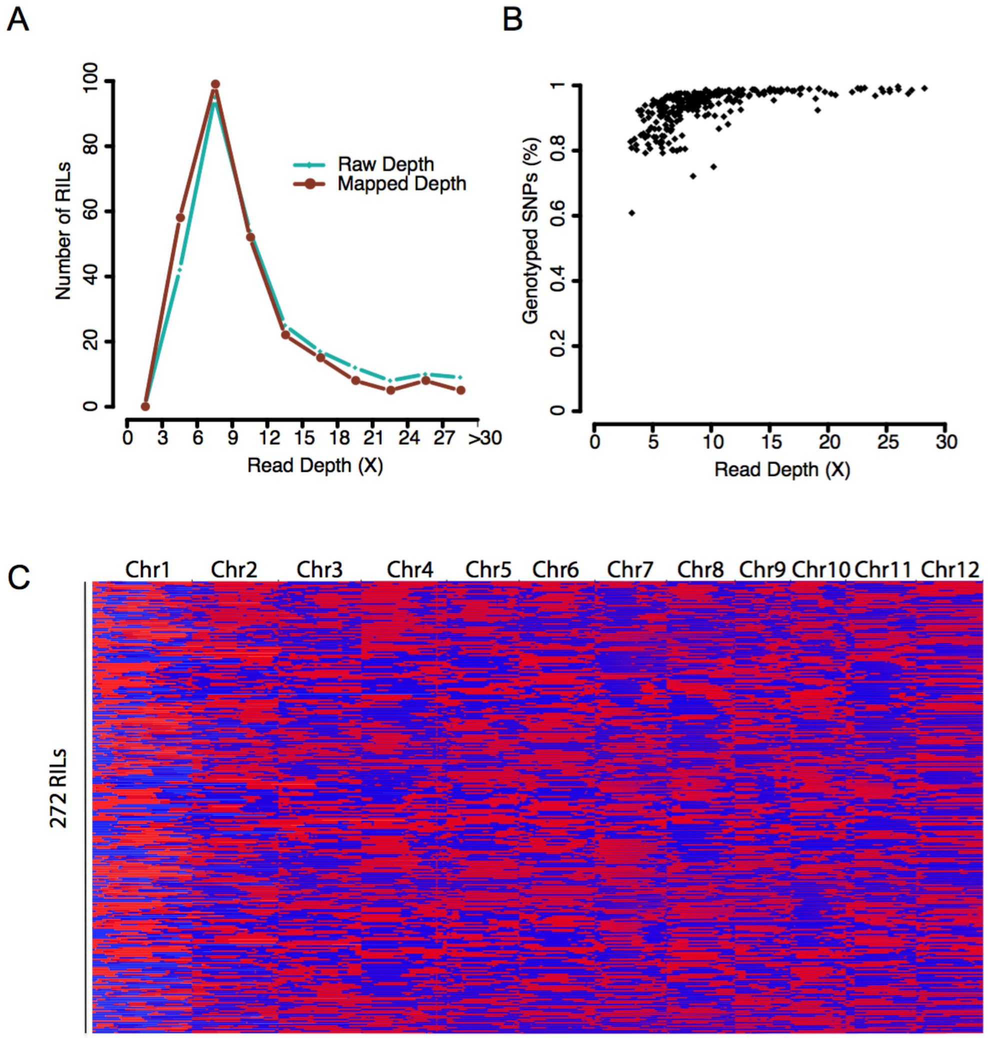
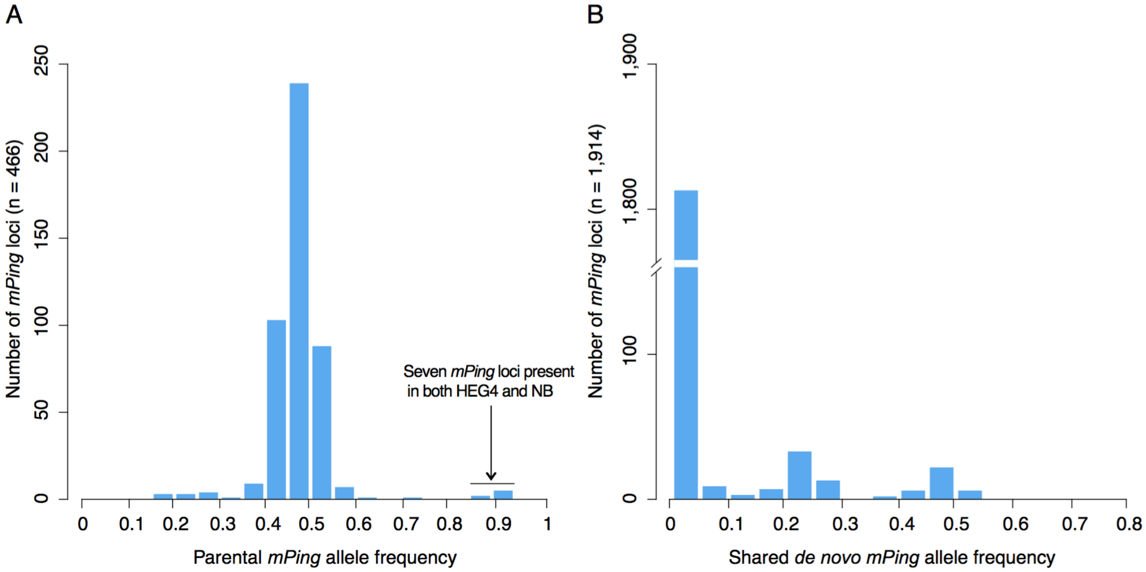
Keywords: *mPing*, active transposon, transposition, recombinant inbred lines, excision, sequence rearrangement, structural variation

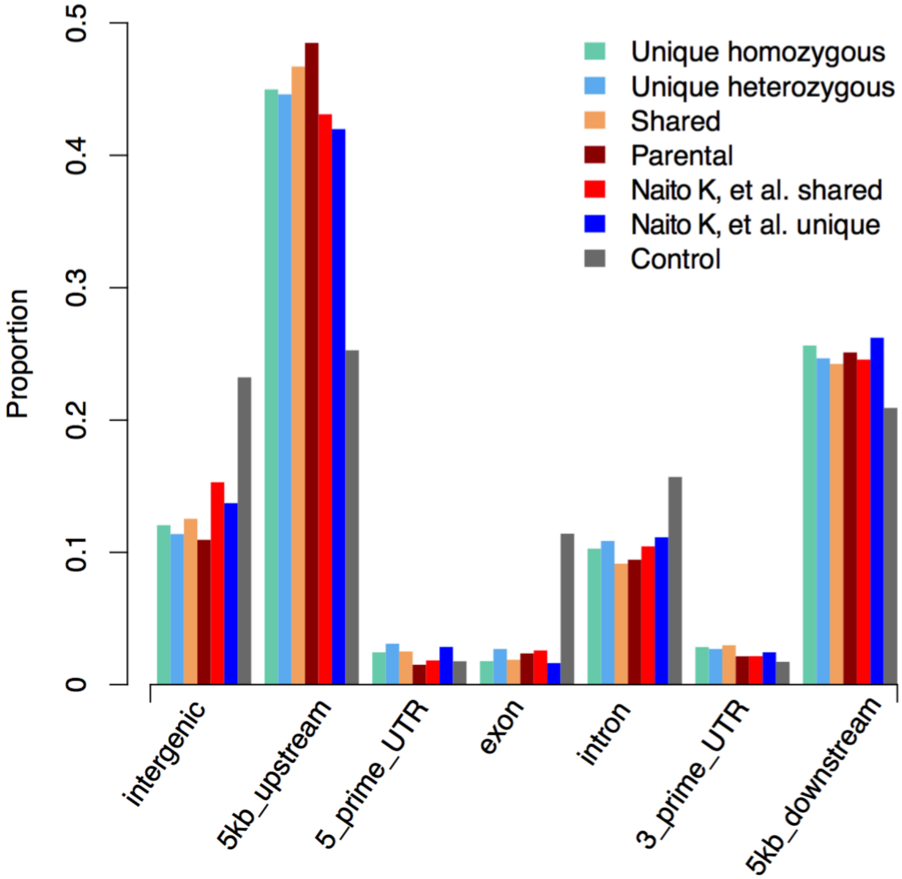
www.pnas.org/cgi/doi/10.1073/pnas.2015736117



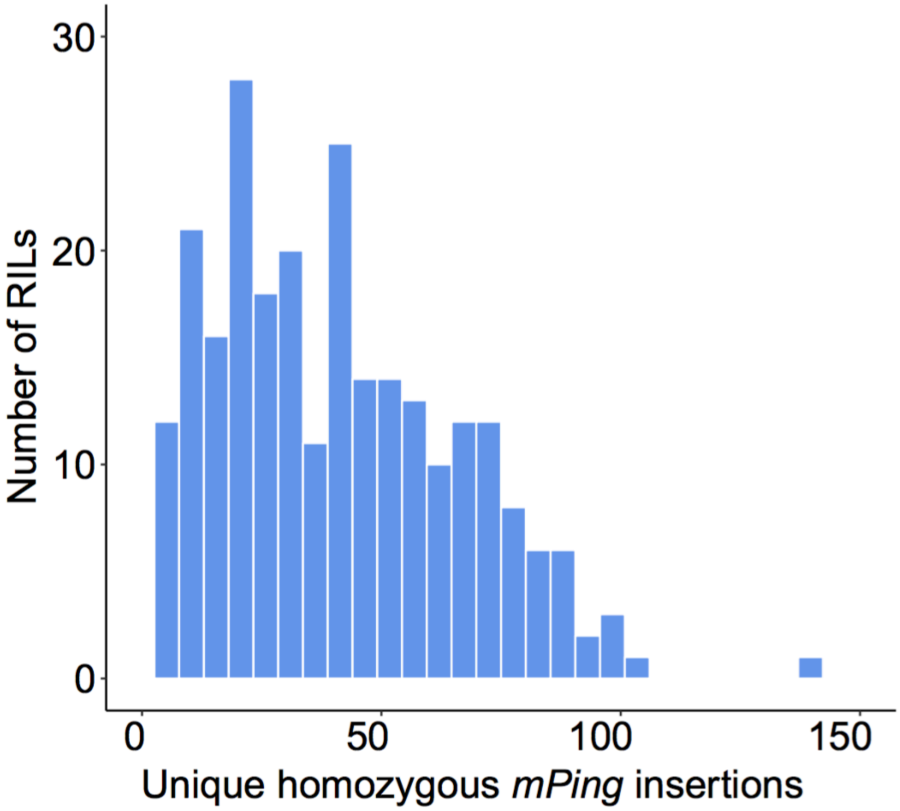
Supplementary Figure 1. Sequencing features and genotypes of 272 RILs. **A**, Sequence depth of 272 RILs. **B**, Genotyping rate of parental SNPs in the RILs. Reads were aligned to rice reference genome (MSUv7) by BWA and SNPs between parental strains were genotyped based on the alignments using GATK. **C**, Recombination map of RILs. Recombination bins were constructed using the high-quality genotype data in the RIL based on an HMM method. A comprehensive recombination map was constructed by imputation of missing makers and refining boundaries of the recombination bin using the R/qtl package. Blue and red represent parental accessions HEG4 and Nipponbare, respectively.



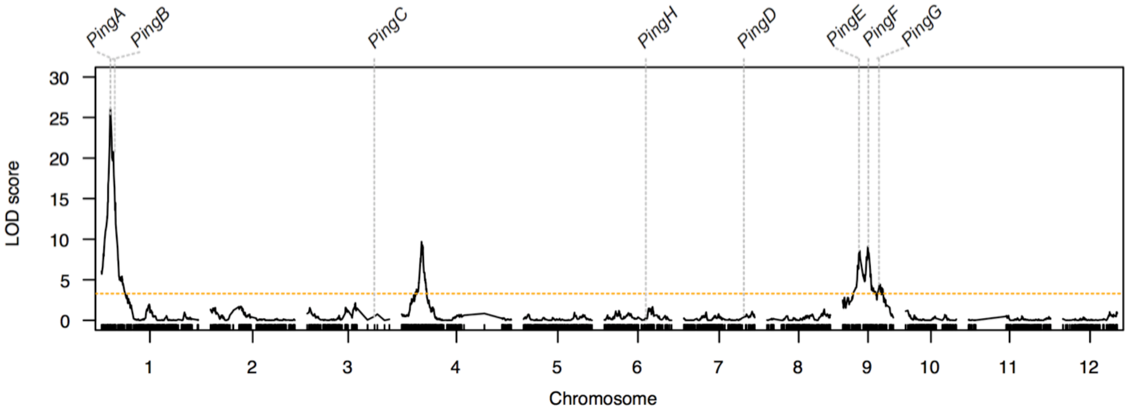
Supplementary Figure 2. Allele frequency of parental and shared *mPing* loci. A, Allele frequencies of parental *mPing* loci in 272 RILs. A total of 466 parental *mPing* loci (7 shared, 44 in NB, and 415 in HEG4) were used to calculate allele frequencies. **B**, Allele frequencies of shared *mPing* loci in 272 RILs. A total of 1,914 shared *de novo mPing* loci that are present in multiple RILs but not in HEG4 and NB were used to calculate the allele frequency.



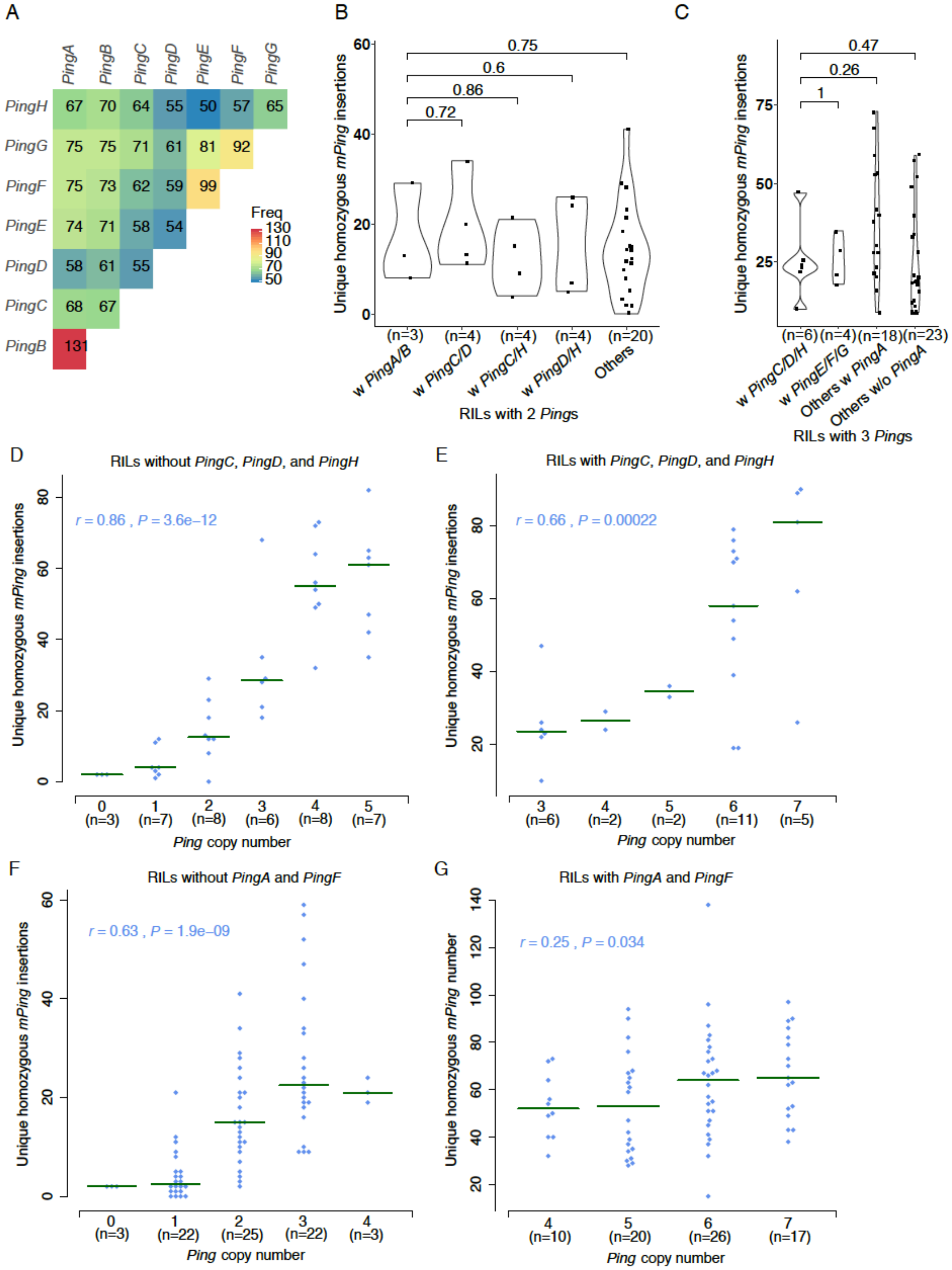
Supplementary Figure 3. Distribution of *mPing* insertion sites in RILs compared to Naito K, et al, 2009. *mPing* insertion sites are summarized according to their relative positions in and near protein-coding genes. Unique homozygous, unique heterozygous represent homozygous and heterozygous *mPing* insertion sites present exclusively in a single RIL. Shared represents insertion sites in multiple RILs but not in parents. Parental insertion sites are insertion sites shared in RILs and parents. Naito K, et al. shared are insertion sites in multiple individuals in Naito K, et al, 2009. Naito K, et al. unique are insertion sites in a single individual. Control is a random sampling from genomic sequence (n = 3,000).



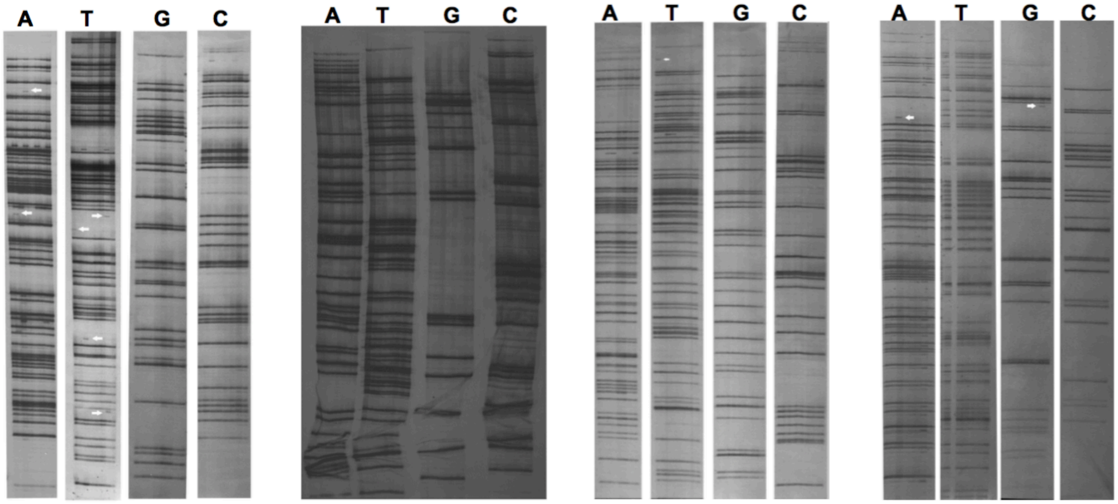
Supplementary Figure 4. Distribution of the number of unique homozygous *mPing* insertions vs. the number of RILs with that number of new insertions.



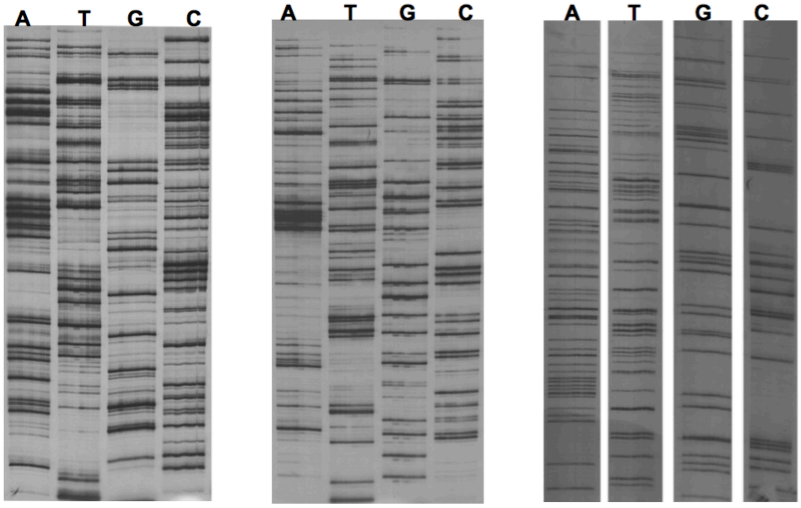
Supplementary Figure 5. Mapped genetic loci impacting *mPing* transposition activity in the RILs. Unique homozygous *mPing* insertions in RILs were used as the quantitative trait and recombination bins as markers. Markers along chromosomes are shown on the X axis and logarithm of the odds ratio (LOD score) of the QTL mapping along the Y axis. Orange dashed line indicates the threshold of the LOD score estimated by a permutation test (1,000 permutations, *P* = 0.05). *Ping* loci are shown (A -H).



Supplementary Figure 6. Comparison of unique homozygous *mPing* insertions in RILs with different *Ping* combinations. A, Number of pairwise *Ping* combination in RILs. **B-C,** Comparison of dosage effect of *PingC*, *PingD*, *PingH* on *mPing* transposition in RILs with 2 *Ping*s (**B**) or 3 *Ping*s (**C**). The difference between groups was tested by Mann-Whitney test and indicated by *P* value. **D**-**E**, Correlation between unique homozygous *mPing* insertions and *Ping* copy number in the RILs without (**D**) or with *PingC*, *PingD*, and *PingH* (**E**). **F**-**G**, Correlation between unique homozygous *mPing* insertions and *Ping* copy number in the RILs without (**F**) or with *PingA* and *PingF* (**G**). The 272 RILs were grouped by *Ping* copy number ranging from 0 to 7 and the scatterplot shows the number of unique *mPing* insertions in each group. The number of RILs in each group is in parentheses (n=). Green lines are the group median. The significance of correlation was tested by a two-tailed Pearson's correlation test and indicated by *P* value.

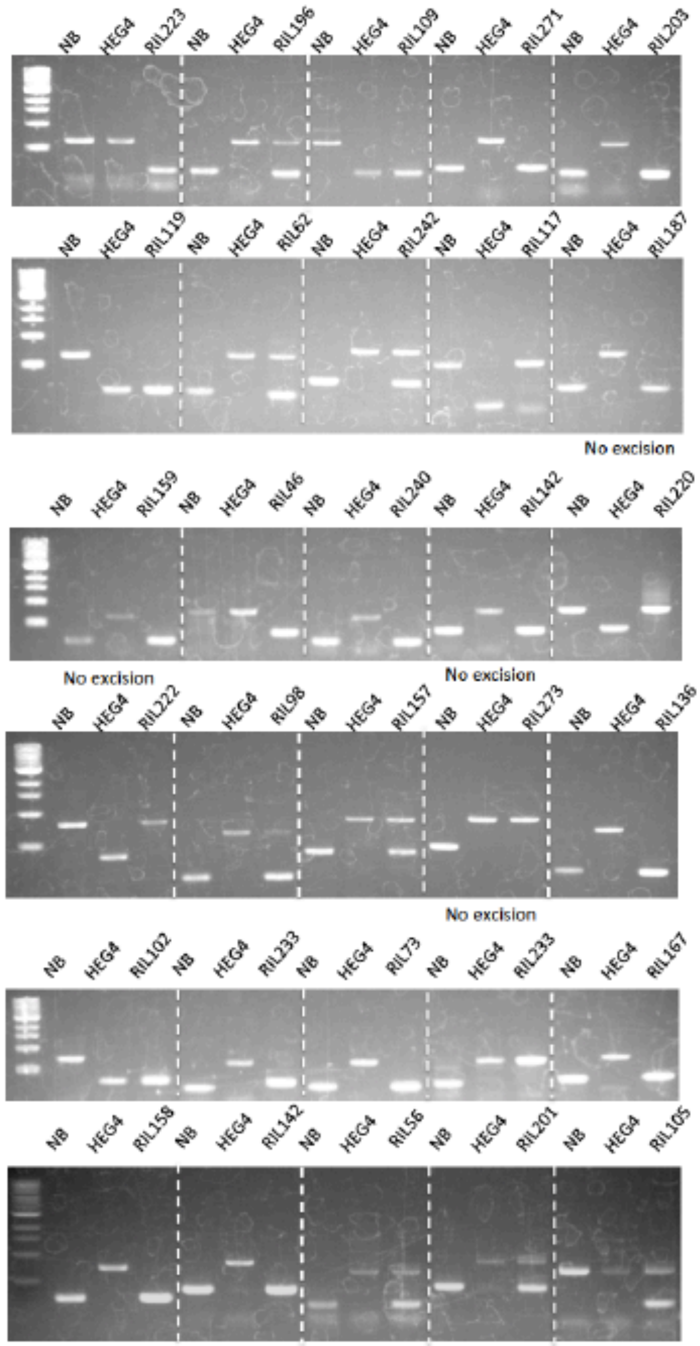


***PingA*: RIL60** ***PingB*: RIL179** ***PingC*: RIL234** ***PingD*: RIL100**

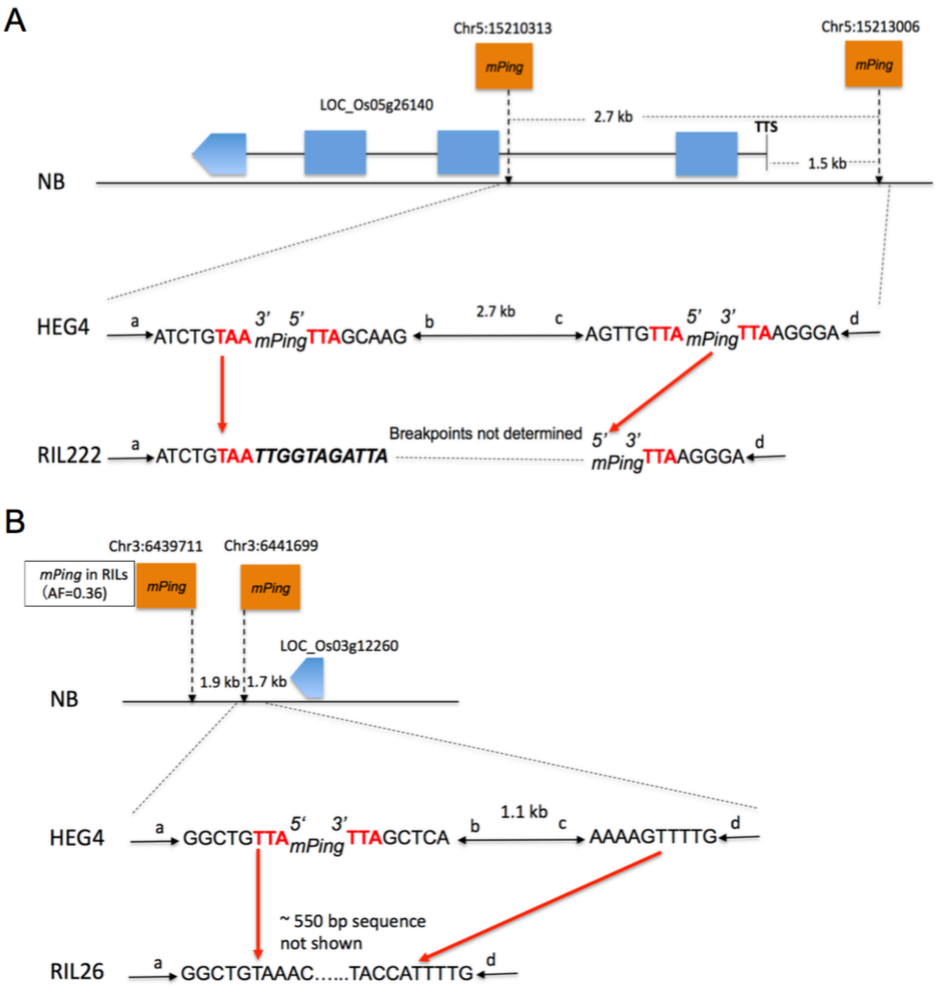


***PingE*: RIL45** ***PingG*: RIL12** ***PingH*: RIL156**

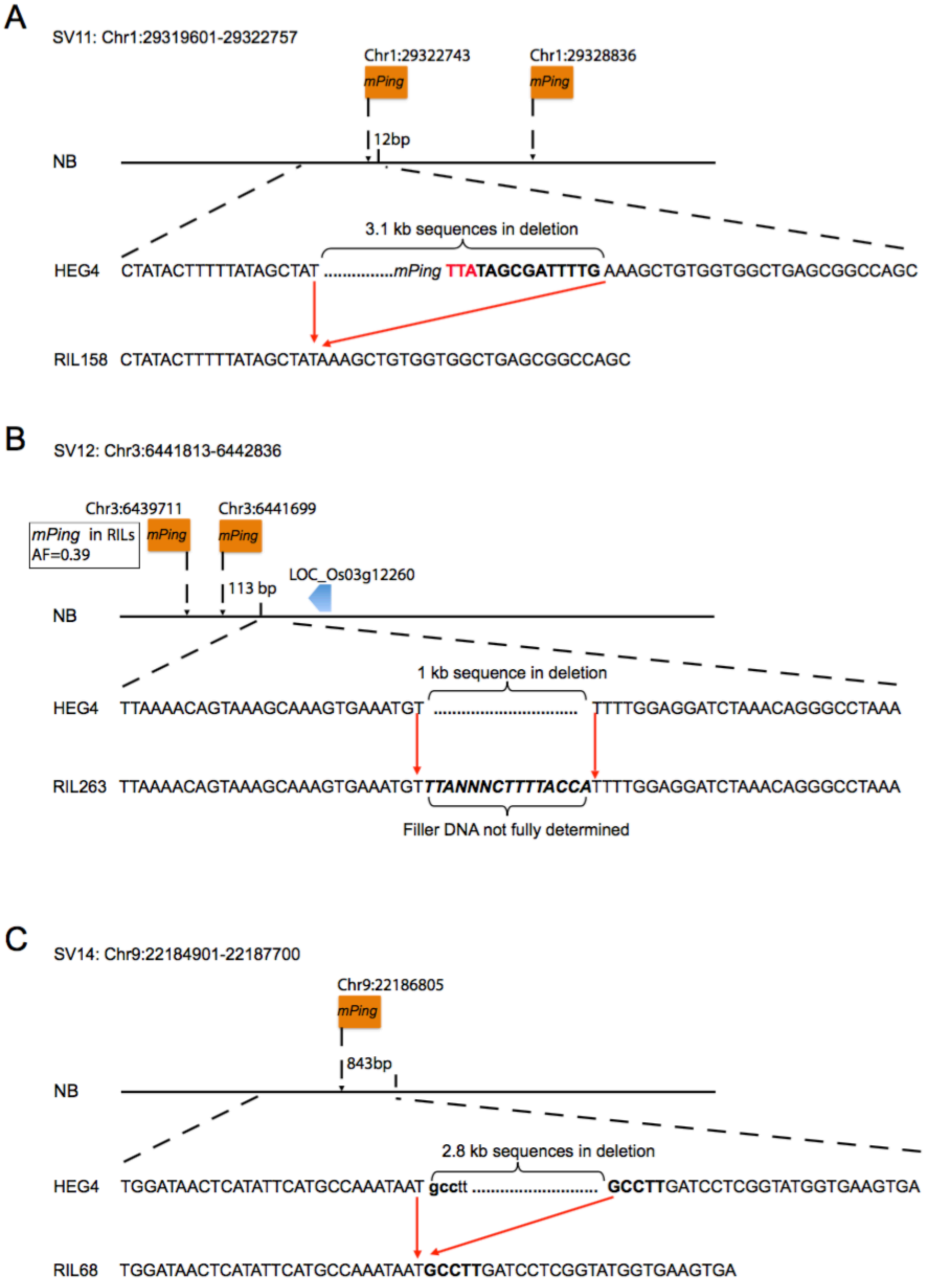
Supplementary Figure 7. Transposon display analysis of *mPing* transposition in single-*Ping* RILs. Genomic DNA of each plant was extracted and digested with *Mse*I, ligated with an adapter and two rounds of PCR amplification performed with preselective primers (*Mse*I + 0 and *mPing* P1) followed by four sets of selective primers (*Mse*I + A/T/G/C and *mPing* P2). Each panel contains 8 lanes – one for each plant analyzed. For each RIL, bands were compared within each selective primer set and new bands (indicated by white arrow) were counted if present in only one plant.



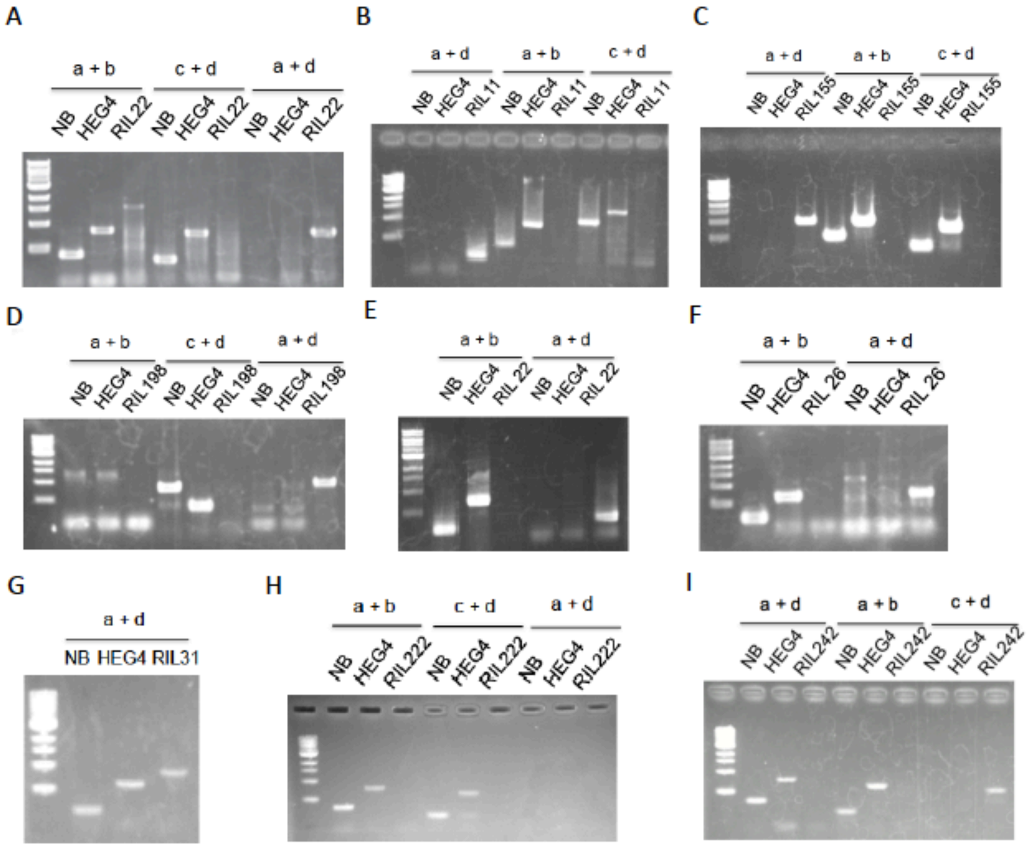
Supplementary Figure 8. PCR validation of 30 *mPing* excision events. Among excised *mPing* loci, 21 from HEG4 and 9 from NB (both specific and shared) were randomly selected to validate the accuracy of the excision identification method. Forward and reverse primers are in Supplementary Data 4.



Supplementary Figure 9. Structural variations mediated by *mPing* elements. A, SV5. **B**, SV3. *mPing*-associated structural variations in select RILs were aligned with either Nipponbare (NB) or HEG4 based on the chromosome of origin. Lines indicate DNA fragments flanking *mPing* insertions or the breakpoint of structural variation. Letters (a-d) on lines label the DNA fragment end. Orange boxes indicate *mPing* insertions. Blue boxes indicate exons of protein-coding genes. Target site duplications (TSDs) of *mPing* insertions are highlighted in red. Filler DNA at breakpoints is italicized. Red arrows indicate the breakpoints where structural variation occurred. Allele frequency (AF) is indicated if *mPing* is present in RILs but absent in parental accessions.



Supplementary Figure 10. Structural variations with *mPing* elements nearby but not at breakpoints*.* A, SV11. **B**, SV12. **C**, SV14. *mPing*-associated structural variations in select RILs were aligned with either Nipponbare (NB) or HEG4 based on the chromosome of origin. Orange boxes indicate *mPing* insertions. Blue boxes indicate exons of protein-coding genes. Target site duplications (TSDs) of *mPing* insertions are highlighted in red. Filler DNA at breakpoints are italicized. Red arrows indicate the breakpoints where structural variation occurred. Allele frequency (AF) is indicated if *mPing* is present in RILs but absent in parental accessions.



Supplementary Figure 11. PCR validation of *mPing*-associated sequence rearrangements shown in Figure 5 and Supplementary Figure 6. **A**, SV1. **B**, SV2. **C**, SV7. **D**, SV9. **E**, SV8. **F**, SV3. **G**, SV4. **H**, SV5. **I**, SV6. Forward and reverse primers are indicated by letters (a-d) as shown in Figure 5 and Supplementary Figure 6.

Supplementary Table 1. Recombination bin map of 272 RILs

Chromosome	Number of bins	Average bin size (kb)	Average genetic distance (cM)	Total genetic distance (cM)	Physical length (Mb)	Recombination rate (cM/Mb)
Chr1	343	119.81	0.57	196.25	43.27	4.54
Chr2	264	135.00	0.65	170.98	35.94	4.76
Chr3	163	209.20	1.02	166.90	36.41	4.58
Chr4	275	128.33	0.81	222.42	35.50	6.27
Chr5	217	137.64	0.64	138.91	29.96	4.64
Chr6	194	160.73	0.70	136.41	31.25	4.37
Chr7	248	119.26	0.58	143.77	29.70	4.84
Chr8	186	151.83	0.69	128.71	28.44	4.53
Chr9	122	187.18	0.84	102.68	23.01	4.46
Chr10	175	130.29	0.59	102.82	23.21	4.43
Chr11	220	131.89	0.76	166.42	29.02	5.73
Chr12	165	166.82	0.67	110.12	27.53	4.00
Mean (Total)	214 (2572)	142.76	0.69	148.86 (1786)	31.10 (373)	4.79

Supplementary Table 2. Genotypes of SNPs flanking *de novo mPing* insertion sites

Flanking SNP genotype[a]	Heterozygous *mPing*s	Homozygous *mPing*s
hom|hom	3129	8361
-NB	1312	3500
-HEG4	1429	3700
-NB+HEG4	123	315
-Not determined	265	846
hom|het	89	262
het|het	11	6
Not determined	778	1898
Total	4007	10527

[a], hom|hom is where SNPs flanking both ends of *mPing* are homozygous. hom+het is where SNPs flanking one end of *mPing* are homozygous while the other end is heterozygous. het|het is where SNPs flanking both ends of *mPing* are heterozygous.

Supplementary Table 3. *de novo Ping* insertions

New *Ping* locus	RIL	New homozygous (heterozygous) *mPing*	Nearest protein-coding genes	Location relative to closest protein-coding gene	Chromatin environment	All *Ping* loci in RIL where N = new *Ping*
Chr3:865992	3	43 (4)	LOC_Os03g02430.1	-3215	Euchromatin	7-NABCEFG
Chr1:34194379	14	48 (29)	LOC_Os01g59190.1	210	Euchromatin	6-NCEFGH
Chr8:18337647	26	42 (21)	LOC_Os08g29809.1	-7734 (intergenic)	TE island	5-NDEFG
Chr2:28343688	46	73 (46)	LOC_Os02g46490.1	-2292	Euchromatin	7-NABEFGH
Chr2:1188028	51	67 (25)	LOC_Os02g03020.1	-86	Euchromatin	6-NABDEF
Chr1:7258553	65	62 (18)	LOC_Os01g13040.1	-1231	Euchromatin	6-NABDEF
Chr3:36131662	93	21 (9)	LOC_Os03g63940.1	Intron	Euchromatin	4-NBGH
Chr7:5440360	104	44 (7)	LOC_Os07g10130.1	Intron	Euchromatin	4-NABH
Chr10:13635022	149	52 (15)	LOC_Os10g26290.1	-20820 (intergenic)	TE island	3-NGH
Chr1:23216637	174	43 (15)	LOC_Os01g41000.1	-1340	Euchromatin	7-NABDEFH
Chr5:4075298	175	81 (23)	LOC_Os05g07600.1	-707	Euchromatin	7-NABCDGH
Chr9:18957569	189	38 (10)	LOC_Os09g31458.1	76	Euchromatin	8-NABCEFGH
Chr11:22264027	211	73 (13)	LOC_Os11g37680.1	Intron	Euchromatin	5-NABDH
Chr7:22688057	221	70 (60)	LOC_Os07g37830.1	-841	Euchromatin	7-NABEFGH
Chr12:7386029	248	57 (20)	LOC_Os12g13280.1	Intron	Euchromatin	6-NABFGH
Chr11:4473183	270	96 (36)	LOC_Os11g08470.1	3436	TE island	6-NNEFGH
Chr11:5885534	270	96 (36)	LOC_Os11g10720.1	-4005	Euchromatin	6-NNEFGH

Supplementary Table 4. QTL loci contributing to *mPing* activity

Chromosome	Genetic map position	Genetic map interval	Interval on chromosome	Fitted LOD	Variance explained by QTL	QTL effect	Standard deviation of QTL effect
Chr1	17.92	17.18-20.40	2496808-3672310	29.65	28.19	14.02	1.06
Chr4	40.28	38.54-43.42	15520048-16724166	14.27	11.82	8.99	1.05
Chr9	50.95	31.88-54.16	10571059-14581359	10.93	8.79	7.81	1.06

Supplementary Table 5. *mPing* transposition estimated by the transposon display approach

Ping	RIL	Number of individuals	New *mPing* insertions	New *mPing* insertions per plant
PingA	RIL60	8	6	0.75
PingA	RIL60	8	8	1
PingA	RIL60	8	4	0.5
PingB	RIL179	8	0	0
PingB	RIL179	8	0	0
PingB	RIL179	8	0	0
PingC	RIL230	8	0	0
PingC	RIL230	8	0	0
PingC	RIL230	8	0	0
PingC	RIl234	8	1	0.125
PingC	RIl234	8	2	0.25
PingC	RIl234	8	3	0.375
PingD	RIL75	8	3	0.375
PingD	RIL75	8	2	0.25
PingD	RIL75	8	2	0.25
PingD	RIL100	8	2	0.25
PingD	RIL100	8	2	0.25
PingD	RIL100	8	2	0.25
PingE	RIL45	8	0	0
PingE	RIL45	8	0	0
PingE	RIL45	8	0	0
PingE	RIL268	8	2	0.25
PingE	RIL268	8	1	0.125

PingE	RIL268	8	1	0.125
PingG	RIl12	8	0	0
PingG	RIl12	8	0	0
PingG	RIl47	8	2	0.25
PingG	RIl47	8	2	0.25
PingG	RIl47	8	0	0
PingH	RIl156	8	0	0
PingH	RIl156	8	0	0
PingH	RIl166	8	0	0
PingH	RIl166	8	0	0
PingH	RIl166	8	0	0

Supplementary Table 6. *mPing* transposition estimated by the pooled-sequencing approach

Ping	RIL	Replicate	Number of individuals	New *mPing* insertions	New *mPing* insertions per plant
PingA	RIL60	Rep1	8	2	0.25
PingA	RIL60	Rep2	8	6	0.75
PingA	RIL60	Rep3	8	11	1.375
PingA	RIL60	Rep4	8	12	1.5
PingC	RIL230	Rep1	8	0	0
PingC	RIL230	Rep2	8	0	0
PingC	RIL230	Rep3	8	0	0
PingD	RIL99	Rep1	8	1	0.125
PingD	RIL99	Rep2	8	0	0
PingD	RIL99	Rep3	8	0	0
PingE	RIL268	Rep1	8	2	0.25
PingE	RIL268	Rep2	8	0	0
PingE	RIL268	Rep3	9	0	0
PingG	RIL12	Rep1	8	0	0
PingG	RIL12	Rep2	8	1	0.125
PingG	RIL12	Rep3	8	0	0
PingH	RIL156	Rep1	8	0	0
PingH	RIL156	Rep2	8	0	0
PingH	RIL156	Rep3	7	1	0.142857

Supplementary Table 7. Distance from high frequency excised *mPing* to nearest *mPing* insertion

mPing locus	# Excision event	Nearest *mPing* locus in HEG4 (kb)	Nearest *mPing* locus in RILs (kb)[a]
Chr1:29494572	5	165.7	165.7
Chr1:3444992	5	335.8	335.8
Chr1:36267659	5	2.8	2.8
Chr1:36270511	7	2.8	2.8
Chr1:6806761	7	9.6	9.6
Chr2:30934395	6	520.9	22.3
Chr3:6441699	8	70.3	1.9
Chr5:15210313	9	2.6	2.6
Chr5:15213006	10	2.6	2.6
Chr6.8316574	5	40	40
Chr8:13076782	6	26.3	26.3
Chr8:24622994	15	37.6	2.3

[a], 92 *mPing* loci are not parental but found in 10% or more of the RILs. These loci were also used to calculate the distance of *mPing* loci to their closest loci.

Supplementary Table 8. Nearest protein-coding gene from high frequency excised *mPing*

mPing	Nearest protein-coding gene	Location relative to closest protein-coding gene	Gene expression difference (FDR)
Chr1:29494572	LOC_Os01g51290.1	-2016	1
Chr1:3444992	LOC_Os01g07300.1	-165	0
Chr1:36267659	LOC_Os01g62630.1	402	1
Chr1:36270511	LOC_Os01g62630.1	-774	1
Chr1:6806761	LOC_Os01g12440.1	-6951	0.95
Chr2:30934395	LOC_Os02g50640.1	-104	0.75
Chr3:6441699	LOC_Os03g12260.1	1752	1
Chr5:15210313	LOC_Os05g26140.1	Intron	1
Chr5:15213006	LOC_Os05g26140.1	-576	1
Chr6:8316574	LOC_Os06g16740.1	Intron	1
Chr8:13076782	LOC_Os08g21840.1	721	1
Chr8:24622994	LOC_Os08g38960.1	-162	0.2

Supplementary Table 9. Features of structural variations in RILs

SV	Chromosome	Start	End	RIL[a]	SV Type	Length (bp)
SV1	Chr1	29494474	29496305	22	Deletion	1832
SV2	Chr2	28724476	28732623	11	Deletion	8148
SV3	Chr3	6441699	6442836	26	Deletion	1138
SV4	Chr3	6441699	6442399	31	Deletion + Duplication	701
SV5	Chr5	15210313	15213006	222	Deletion	2694
SV6	Chr5	15210313	15213006	242	Deletion	2694
SV7	Chr8	24622994	24625306	155	Deletion	2313
SV8	Chr8	24625306	24634547	22	Deletion	9242
SV9	Chr9	638901	694912	198	Deletion	56012
SV10	Chr1	10145801	10151500	274	Deletion	5700
SV11	Chr1	29319601	29322757	158	Deletion	3157
SV12	Chr3	6441813	6442836	263	Deletion	1024
SV13	Chr7	10749401	10760200	61	Deletion	10800
SV14	Chr9	22184901	22187700	68	Deletion	2800
SV15	Chr10	13066801	13068300	78	Deletion	1500
SV16	Chr10	17891753	17895900	78	Deletion	4148

[a], RILs where structural variations were characterized and validated

Supplementary Table 10. Presence or absence of structural variations in F1 progeny

SV	Location	# of RILs	F1 #26 progeny (RIL1-139)	F1 #27 progeny (RIL140-280)
SV1	Chr1:29494474-29496305	1	1	0
SV2	Chr2:28724476-28732623	1	1	0
SV3	Chr3:6441699-6442399	1	1	0
SV4	Chr3:6441699-6442836	1	1	0
SV5	Chr5:15210313-15213006	1	0	1
SV6	Chr5:15210313-15213006	1	0	1
SV7	Chr8:24622994-24625306	1	0	1
SV8	Chr8:24625306-24634547	1	1	0
SV9	Chr9:638901-694912	1	0	1
SV10	Chr1:10145801-10151500	67	0	67
SV11	Chr1:29319601-29322757	73	0	73
SV12	Chr3:6441813-6442836	1	0	1
SV13	Chr7:10749401-10760200	1	1	0
SV14	Chr9:22184901-22187700	1	1	0
SV15	Chr10:13066801-13068300	1	1	0
SV16	Chr10:17891753-17895900	1	1	0

Supplementary Table 11. SVs that do/do not include high excision *mPings*

mPing locus[a]	High frequency excision *mPing*	Structural variation-associated *mPing*
Chr1:29494572 (SV1)	+	+
Chr1:3444992	+	-
Chr1:36267659	+	-
Chr1:36270511	+	-
Chr1:6806761	+	-
Chr2:30934395	+	-
Chr3:6441699 (SV3 & SV4)	+	+
Chr5:15210313 (SV5 & SV6)	+	+
Chr5:15213006 (SV5 & SV6)	+	+
Chr6:8316574	+	-
Chr8:13076782	+	-
Chr8:24622994 (SV7)	+	+
Chr8:24625306 (SV7 & SV8)[b]	-	+
Chr1:29496305 (SV1)[c]	-	+
Chr8:28724476 (SV2)	-	+
Chr8:28732623 (SV2)	-	+
Chr3:6439711 (SV3 & SV4)[d]	-	+
Chr9:694483 (SV9)	-	+

[a], SVs in parentheses have *mPing* at breakpoints

[b], *mPing* locus Chr8:24625306 is in 97 RILs but not parents.

[c], *mPing* locus Chr1:29496305 is characterized by PCR (Supplementary Figure 7A) but is not detected by RelocaTE2.

[d], *mPing* locus Chr3:6439711 is in 107 RILs but not parents. It has 11 excision events and 10 of 11 with footprints.

Supplementary Table 12. Protein-coding genes associated with SVs

Genes affected by structural variation	Gene annotation	Affected regions	Associated structural variation
LOC_Os01g18110	cinnamoyl CoA reductase	exon and intron	SV10
LOC_Os01g18120	cinnamoyl CoA reductase	exon and intron	SV10
LOC_Os01g51040	transmembrane protein 16K	exon and intron	SV11
LOC_Os02g47060	WRKY66	full gene	SV2 (*mPing* associated)
LOC_Os05g26140	expressed protein	exon and intron	SV5 & SV6 (*mPing* associated)
LOC_Os07g18154	aldehyde oxidase	exon and intron	SV13
LOC_Os08g38970	transmembrane receptor	exon	SV8 (*mPing* associated)
LOC_Os09g01960	MYB family transcription factor	full gene	SV9 (*mPing* associated)
LOC_Os09g01970	expressed protein	full gene	SV9 (*mPing* associated)
LOC_Os09g02000	expressed protein	full gene	SV9 (*mPing* associated)

Supplementary Table 13. *mPing* excision events detected by conservative vs. standard methods

mPing	Conservative method		Standard method		Shared high frequency excision *mPing*
	Excision events	Event with footprint	Excision events	Event with footprint	
Chr8:24622994	15	14	28	14	+
Chr5:15213006	10	9	14	9	+
Chr5:15210313	9	8	18	9	+
Chr3:6441699	8	7	19	8	+
Chr1:36270511	7	6	19	7	+
Chr1:6806761	7	6	10	9	+
Chr2:30934395	6	5	8	5	+
Chr8:13076782	6	5	6	5	+
Chr1:36267659	5	4	18	4	+
Chr1:3444992	5	4	8	4	+
Chr1:29494572	5	4	7	4	+
Chr6:8316574	5	5	6	6	+
Chr2:14601853	4	3	11	3	-
Chr2:28732623	4	3	6	5	-
Chr7:29475470	4	3	6	4	-
Chr2:30104937	3	2	6	3	-
Chr5:23730117	3	2	6	2	-
Chr9:7117395	3	2	6	3	-
Chr7:25788368	2	1	10	1	-
Chr5:23730902	2	1	6	1	-
Chr4:33507343	2	1	6	3	-

Supplementary Data 1. Sequence and genotype quality of 272 RILs

RIL ID	Number of reads	Read depth	Insert size (bp)	Genotyped SNPs (%)	Genome coverage (%)
1	23383042	6.25	132	87.90	91.98
2	19649656	5.25	133	84.20	86.56
3	24519973	6.55	140	91.63	94.10
4	21499503	5.74	136	90.76	93.01
5	25126024	6.71	182	96.12	95.79
7	23157591	6.18	225	95.66	96.13
8	27594542	7.36	168	94.71	95.76
9	22707096	6.00	148	92.91	94.58
10	24009328	6.37	179	89.71	91.26
11	32377954	8.62	167	95.01	95.98
12	61108623	16.29	127	95.44	97.88
13	93999385	25.11	193	98.05	98.34
14	22645665	6.04	148	90.81	93.00
15	26750643	7.13	232	97.10	96.76
16	83610864	22.36	189	97.96	98.29
17	22677406	6.04	242	93.51	95.65
18	15322523	4.08	249	90.86	91.46
19	18847153	5.03	282	91.46	91.44
20	26666201	7.11	162	96.37	97.24
21	17508984	4.67	207	91.83	92.88
22	20275855	5.41	245	94.89	94.51
23	25951322	6.92	233	96.00	96.16
24	39005965	10.41	201	97.79	97.70
25	43441599	11.61	236	88.08	96.35
26	31456349	8.40	180	93.84	95.10
28	29421027	7.79	183	94.80	98.20
29	32682445	8.71	223	97.28	97.38
30	21871601	5.83	197	94.38	94.75
31	21698329	5.79	188	92.61	92.77
33	44575202	11.90	159	95.38	95.79
34	35150850	9.38	190	95.22	95.18
35	27468878	7.34	167	91.98	92.41
36	26072772	6.96	198	95.57	95.43
37	30617147	8.17	155	94.83	95.76
38	26079322	6.96	150	91.48	93.34
39	213561900	56.82	189	98.67	97.11
40	42973247	11.50	143	95.39	97.11
42	37841623	10.10	166	96.18	96.89
43	66951148	17.91	163	97.26	98.38

44	28406185	7.58	174	95.60	96.56
45	76868954	20.55	189	97.47	98.13
46	32165478	8.58	166	94.86	96.21
47	76637452	20.07	172	95.95	98.61
48	29784259	7.60	148	85.94	91.90
49	28659707	7.33	165	88.98	95.24
50	21456851	5.67	166	86.68	90.86
51	36269823	9.62	172	95.38	97.41
52	62261323	12.50	285	98.74	98.94
53	27295877	6.94	155	84.40	91.81
54	37373844	9.79	193	95.66	97.69
55	75974126	15.21	359	99.07	99.34
56	26394718	7.04	138	90.78	94.27
57	29682198	7.92	136	93.17	95.41
58	28436831	7.58	143	93.37	96.44
59	41356663	10.86	187	96.95	97.87
60	99703532	26.46	170	98.79	98.91
61	23932167	6.35	174	90.23	92.79
62	28110933	7.50	180	95.94	97.27
63	34190172	9.11	190	96.73	98.13
64	26400851	6.94	199	96.64	97.79
65	28549775	7.52	162	95.24	98.03
66	39729325	10.56	194	97.39	98.82
67	23763652	6.31	186	86.41	88.94
68	31098605	8.29	166	95.77	97.39
69	35833676	9.55	217	97.68	98.18
70	49843480	9.98	379	97.94	98.96
71	43276882	11.34	193	97.73	98.82
72	30513166	8.12	204	97.45	98.39
73	48059363	9.65	273	98.69	99.03
74	33101770	8.82	186	97.09	98.56
75	87991934	23.26	189	98.75	98.56
76	23262421	6.14	163	91.64	96.01
77	18102982	4.78	138	84.60	90.17
78	55845392	14.84	203	97.29	98.91
79	18152765	4.79	124	79.25	84.72
80	37519560	7.53	290	97.58	98.85
81	130949579	26.25	276	99.66	99.64
82	47660072	12.40	190	97.30	98.58
83	57229899	12.13	231	92.05	98.30
84	28838585	7.57	195	92.57	93.56
85	38269130	8.50	198	93.28	98.58

86	35582868	9.29	189	95.37	97.88
87	38459861	10.14	168	96.93	97.88
88	29336797	7.69	147	80.61	84.73
89	35671263	9.35	190	97.19	98.55
90	135772072	27.22	281	97.47	99.14
91	26782782	7.08	178	90.84	92.38
92	13667346	3.58	258	83.59	86.48
93	34419826	9.08	176	97.36	98.44
94	24833902	6.44	161	86.84	91.14
95	37113906	9.76	171	93.16	96.38
96	35001979	9.23	171	97.50	98.37
97	47737567	12.73	215	96.92	97.71
98	22765857	6.03	257	94.86	95.88
99	108250182	28.85	173	99.13	99.38
100	67700116	18.05	205	99.15	99.31
101	30323656	8.01	175	96.15	97.06
102	18224974	4.79	168	90.16	91.42
103	18232002	3.98	198	60.85	78.93
104	40963502	8.22	315	92.88	98.89
105	101828444	26.59	182	90.69	96.08
106	32429653	8.48	195	97.22	98.29
107	27792518	7.29	178	82.79	85.73
108	150092616	31.21	170	98.16	99.18
109	63629812	16.79	200	98.82	99.22
110	20892590	5.47	198	87.12	91.27
111	65263523	17.22	192	98.31	99.31
112	14453939	3.84	167	80.25	85.60
113	32373771	8.58	157	93.83	96.67
114	99296014	19.76	223	92.41	98.34
115	20481128	4.11	273	92.29	95.38
116	30640636	8.16	189	96.94	98.24
117	31272050	8.27	183	96.55	98.14
118	39308552	10.44	193	97.01	98.46
119	40099621	10.68	166	96.93	98.59
120	40916314	10.74	213	97.66	98.72
121	33081747	8.67	189	93.16	98.33
122	47346337	12.54	169	97.03	98.61
123	58596234	15.52	200	98.06	98.90
124	36484537	8.27	214	89.83	98.36
125	21837719	5.77	181	92.12	95.59
126	50553682	13.29	192	94.27	96.22
127	56502574	11.35	278	98.15	98.69

128	45337178	11.97	196	97.91	98.89
129	56819652	15.03	179	97.82	98.81
130	34315106	9.03	187	93.56	95.26
131	24875332	4.89	199	88.63	88.45
132	115347450	23.13	274	99.09	99.06
133	39141197	8.71	190	72.15	88.29
134	35144802	9.30	169	96.83	98.35
135	55150684	11.07	286	98.25	98.87
136	26893243	7.10	162	95.82	97.59
137	31624850	8.36	164	95.53	97.54
138	43939999	11.46	155	88.94	93.83
139	27085793	7.15	166	95.80	97.46
140	61930077	16.43	164	97.96	98.75
141	30137263	7.98	169	97.15	98.22
142	29439814	7.70	193	84.61	86.06
143	31020939	8.16	189	92.54	93.05
144	39331854	10.31	199	96.85	98.86
145	19352702	3.88	296	92.28	94.79
146	32568107	8.57	182	92.51	95.78
147	53529738	10.75	281	98.67	99.14
148	36252712	7.28	275	92.04	98.18
149	22639197	5.90	192	82.98	86.06
150	47411849	12.51	193	80.23	89.69
151	20854354	5.51	165	94.34	96.31
153	63862983	13.71	182	75.03	82.98
154	26702546	5.36	311	84.10	97.35
155	27643954	7.30	157	93.48	96.42
156	105291759	27.85	170	98.59	99.30
157	33463390	8.77	197	96.49	98.20
158	35287979	9.25	187	97.45	98.78
159	40340788	10.68	179	97.56	98.23
160	33340181	8.78	185	94.25	96.93
161	43348624	11.26	202	90.68	94.79
162	69416120	18.56	171	94.38	95.96
163	18894011	5.01	202	92.41	94.58
164	68030315	13.66	271	98.74	99.26
165	24573464	6.43	239	96.32	97.82
166	73402701	19.45	187	98.98	98.99
167	51338378	13.59	203	96.66	97.87
168	57539178	15.23	238	98.44	99.19
169	88933904	17.82	278	98.91	98.80
170	64007878	12.85	290	98.70	99.04

172	22520554	5.96	194	84.55	89.00
173	48172756	12.67	189	94.92	96.45
174	70466470	18.39	184	94.88	96.68
175	26465110	6.95	183	80.14	82.88
176	46950500	12.23	186	87.70	92.72
177	78760465	20.95	223	97.07	97.93
178	19785124	5.22	205	94.68	96.01
179	19188073	5.12	210	95.51	96.77
180	156030354	31.28	288	99.48	99.16
181	42745264	11.06	194	86.71	90.54
182	40862025	10.58	192	80.51	83.72
183	26448467	6.99	194	83.57	83.18
184	32929204	6.61	279	96.89	98.11
185	29689283	7.85	172	80.46	83.28
186	18390542	4.81	191	81.75	86.37
187	43806955	11.56	261	97.96	98.54
188	29004974	5.82	290	95.39	97.70
189	17735883	4.69	182	89.27	91.52
190	31285034	6.27	381	96.16	98.02
191	16746728	4.41	198	93.88	94.89
192	43191518	8.67	279	97.93	98.99
193	20183774	5.21	210	86.10	92.70
194	131726771	26.41	266	98.76	98.95
195	34338281	8.98	177	86.51	88.90
196	44872044	9.01	282	97.29	98.93
197	50478900	13.32	183	97.20	98.05
198	34917371	9.24	181	97.09	98.35
199	54282739	14.38	188	97.20	98.15
200	22975778	6.05	184	79.26	81.08
201	39087788	7.85	278	97.55	98.59
203	34036807	9.02	189	90.72	94.58
204	19091866	5.01	197	93.80	95.31
205	37126800	9.86	185	98.01	98.61
206	44748927	11.80	269	98.47	98.97
207	45718101	12.15	193	97.72	98.91
208	13896308	3.50	256	82.73	88.20
209	69461358	13.95	308	98.65	98.81
210	24036211	6.32	204	96.75	97.34
211	35380498	9.31	189	92.23	94.29
212	93023734	19.73	218	97.10	99.12
213	23203247	6.13	171	93.58	95.16
214	21635749	5.72	199	93.28	95.50

215	23810036	6.27	199	91.94	95.10
216	97717902	26.01	206	95.70	98.00
217	24242436	6.26	172	90.39	94.33
218	37325947	9.87	169	90.65	92.65
219	39216524	10.28	181	95.11	97.66
220	35666562	7.16	330	79.94	98.40
221	39362569	10.40	245	97.46	98.56
222	58183878	12.90	184	97.32	98.63
223	116416542	23.38	290	99.24	99.17
224	34256204	8.92	187	82.54	85.35
225	99788611	26.23	221	90.43	92.72
226	33673524	8.85	199	97.40	98.00
227	26964409	7.17	187	96.99	97.87
228	69982302	14.05	291	98.37	98.76
229	32073645	8.47	179	95.77	98.46
230	62384302	12.52	286	98.64	98.94
231	80771086	16.21	295	98.78	98.97
232	81102867	16.29	267	98.25	98.82
233	83562405	22.08	184	94.46	96.28
234	73428554	19.47	202	99.06	99.03
235	31506873	8.33	193	84.76	86.43
236	90866634	19.34	230	98.13	98.97
237	93911578	24.92	162	99.02	99.29
238	43254548	8.68	285	96.64	98.46
239	46700347	12.36	193	96.43	97.50
240	113833688	22.80	282	99.14	99.20
241	44190816	11.66	174	98.48	98.60
242	77344062	15.53	286	98.77	99.18
244	79107401	15.88	279	98.43	99.29
245	56549727	14.96	177	96.27	98.62
246	85056700	22.52	186	98.05	98.99
247	37941521	10.03	174	96.52	98.39
248	36349018	7.29	291	97.45	98.31
249	23975384	6.36	151	93.24	96.80
250	31455139	6.31	318	96.40	98.19
251	28102454	7.45	181	97.42	98.44
252	122206896	32.37	183	98.03	99.26
253	95174019	25.07	187	92.53	98.33
254	97603758	25.75	155	98.03	99.02
255	31158156	8.26	174	97.42	98.31
256	41501020	10.57	215	95.64	98.28
257	16892124	4.47	156	85.22	89.97

258	16653675	4.42	177	80.85	84.17
259	65572096	17.40	180	98.39	98.86
260	45829502	12.20	173	95.24	97.57
261	78556264	16.69	193	93.91	97.96
262	20682120	5.46	199	88.74	93.63
263	24724949	6.53	189	82.24	83.32
264	16894657	4.47	188	84.01	89.05
265	25682293	6.48	234	93.67	97.12
266	52930674	14.06	166	98.72	99.16
267	22090084	5.83	179	82.05	84.65
268	25680448	10.18	206	94.56	98.63
269	57990233	15.23	208	86.65	88.98
270	34207974	9.06	156	95.99	98.29
271	28432635	7.54	180	89.70	94.75
272	50939281	11.08	208	91.96	97.93
273	106479958	28.15	163	96.83	99.00
274	19922818	5.22	208	94.28	96.23
275	17847361	4.72	166	81.90	87.97
276	24062940	6.14	155	80.86	84.70
277	150041504	39.31	191	98.41	98.59
278	41017018	10.87	211	93.67	98.47
279	99205070	21.70	211	91.17	96.77
280	92958817	18.65	285	98.85	98.86

RIL IDs are assigned using plant numbers (1 to 280) of the F2 generation. Five lines have been lost during the process of breeding and three lines have been removed because they are duplicates of other RILs. The lines that has been lost during breeding are 27, 32, 41, 171, and 202. The lines that are duplicates and have been removed are 6 (duplicate of 5**)**, 152 (duplicate of 145), and 243 (duplicate of 278).

Supplementary Data 2. List of *mPing* and *Ping* copy numbers in the RILs

RIL ID	Total number of *mPing*	Number of shared parental *mPing*	Number of other shared *mPing*	Number of unique *mPing*	Number of unique homozygous *mPing*	Number of unique heterozgyous *mPing*	*Ping* copy number	*Pong* copy number	*Ping* code
1	253	176	49	28	19	9	6	1	CDEFGH
2	163	131	20	12	10	2	3	4	CDH
3	303	206	50	47	43	4	7	3	*ABCEFG
4	234	167	41	26	23	3	5	4	CDEFG
5	211	156	32	23	18	5	3	4	FGH
7	247	203	35	9	9	0	3	3	FGH
8	274	190	34	50	40	10	4	3	ABDF
9	214	160	29	25	16	9	4	3	CEFH
10	344	238	56	50	39	11	5	4	ABCDF
11	435	257	66	112	97	15	7	3	ABDEFGH
12	264	231	32	1	1	0	1	4	G
13	464	223	66	175	105	70	4	4	ABGH
14	325	198	50	77	48	29	6	3	*CEFGH
15	375	210	56	109	75	34	5	4	DEFGH
16	283	247	35	1	0	1	2	3	EF
17	229	183	26	20	14	6	2	4	DG
18	260	214	30	16	13	3	3	4	DFG
19	236	175	40	21	18	3	2	4	EG
20	226	176	34	16	15	1	2	4	BD
21	309	207	45	57	38	19	7	3	ABCEFGH
22	309	229	52	28	21	7	3	3	ABC
23	292	219	38	35	28	7	5	3	ABDEF
24	414	248	60	106	73	33	6	4	ABCDFH
25	261	227	33	1	1	0	1	3	D
26	371	256	52	63	42	21	5	2	*DEFG

28	217	169	32	16	15	1	2	4	CH
29	286	199	43	44	22	22	3	4	CDH
30	306	203	45	58	55	3	6	3	ABEFGH
31	263	201	39	23	21	2	5	3	CEFGH
33	273	212	47	14	11	3	2	3	CD
34	473	279	84	110	82	28	7	4	ABCDEFG
35	258	209	41	8	8	0	2	3	FH
36	311	254	45	12	8	4	2	3	AB
37	230	176	29	25	16	9	3	3	ABH
38	281	222	36	23	19	4	6	3	CDEFGH
39	234	190	42	2	2	0	0	3	No *Ping*
40	291	238	48	5	5	0	1	4	D
42	307	246	45	16	12	4	3	4	DEF
43	294	234	38	22	21	1	1	4	C
44	354	210	59	85	76	9	6	3	ABCEFG
45	237	199	34	4	4	0	1	3	E
46	385	212	54	119	73	46	7	3	*ABEFGH
47	252	224	25	3	3	0	1	4	G
48	288	173	48	67	54	13	4	1	ABFG
49	338	209	47	82	63	19	4	3	ABEH
50	295	212	42	41	39	2	6	3	ABCDGH
51	377	222	63	92	67	25	6	3	*ABDEF
52	338	273	42	23	16	7	3	4	CDE
53	249	179	41	29	28	1	3	4	ABD
54	423	255	57	111	71	40	6	4	ABCDGH
55	278	205	39	34	21	13	4	3	DFGH
56	375	201	57	117	78	39	6	4	ABDEFG
57	415	256	74	85	54	31	6	3	CDEFGH
58	309	216	51	42	29	13	5	3	CDEFG
59	371	284	55	32	21	11	3	4	CDG

60	241	202	35	4	4	0	1	3	A
61	288	188	42	58	56	2	5	2	CDEFG
62	392	233	49	110	76	34	5	4	ACEFG
63	388	253	60	75	53	22	3	4	ABC
64	346	218	56	72	53	19	7	4	ABCEFGH
65	352	223	49	80	62	18	6	4	*ABDEF
66	467	276	71	120	87	33	6	3	ABDEFG
67	200	166	29	5	2	3	2	3	CG
68	349	217	54	78	56	22	4	3	AEFG
69	423	257	68	98	79	19	7	3	ABCDEFG
70	368	270	56	42	27	15	4	4	ABDG
71	358	229	61	68	44	24	4	4	ABCE
72	407	241	69	97	68	29	6	4	ABCEFG
73	280	194	48	38	30	8	5	4	ABCFH
74	307	224	55	28	23	5	3	4	ADH
75	321	274	47	0	0	0	1	3	D
76	283	211	45	27	19	8	4	3	BCGH
77	315	185	56	74	52	22	4	1	ABCD
78	411	215	74	122	73	49	4	3	ABCH
79	166	137	21	8	7	1	2	1	DH
80	312	208	51	53	41	12	2	4	BC
81	235	189	32	14	4	10	2	4	CH
82	259	199	37	23	18	5	3	4	EFG
83	399	237	66	96	67	29	5	4	ABCEF
84	305	245	45	15	11	4	4	3	CEFH
85	217	155	29	33	29	4	3	3	EFG
86	353	257	54	42	26	16	5	4	BCEFG
87	375	244	52	79	58	21	4	4	ABCG
88	330	229	48	53	51	2	5	3	ABDEH
89	290	183	42	65	47	18	4	3	EFGH

90	395	247	57	91	58	33	6	3	CDEFGH
91	332	265	43	24	20	4	3	4	CGH
92	341	187	64	90	61	29	5	4	ABEFG
93	288	214	44	30	21	9	4	4	*BGH
94	341	218	51	72	63	9	5	4	ABEFG
95	341	258	52	31	31	0	5	4	ABFGH
96	380	214	54	112	89	23	7	3	ABCDEFH
97	373	275	59	39	28	11	3	4	ABG
98	382	265	61	56	47	9	3	3	CDH
99	303	259	41	3	2	1	1	4	D
100	215	192	22	1	0	1	1	3	D
101	262	174	45	43	33	10	5	3	CDFGH
102	165	110	31	24	21	3	2	4	CH
103	216	155	39	22	20	2	3	2	ABH
104	317	212	54	51	44	7	4	4	*ABH
105	356	202	52	102	83	19	6	3	ABEFGH
106	283	239	41	3	2	1	0	4	No *Ping*
107	260	169	38	53	44	9	4	1	ABDH
108	298	231	37	30	26	4	3	3	CDH
109	278	203	42	33	23	10	3	4	CDH
110	366	288	55	23	20	3	3	3	ABC
111	305	204	57	44	34	10	3	4	EGH
112	254	155	48	51	34	17	5	3	ABEFH
113	345	227	64	54	38	16	3	4	ABC
114	245	190	31	24	23	1	2	4	EF
115	233	176	27	30	28	2	3	3	BDG
116	281	201	41	39	24	15	3	3	CDH
117	384	197	71	116	82	34	5	4	ABEFG
118	375	223	60	92	70	22	6	3	CDEFGH
119	357	212	59	86	42	44	4	3	ABCH

120	485	235	72	178	96	82	6	3	ABCEFG
121	359	188	50	121	86	35	5	4	ABCGH
122	373	213	65	95	68	27	5	3	ACEFG
123	261	202	37	22	13	9	2	4	AB
124	270	191	58	21	15	6	6	4	ABEFGH
125	274	211	42	21	18	3	3	3	BCD
126	354	231	51	72	53	19	5	3	ABCGH
127	406	252	56	98	69	29	6	3	ABCDEG
128	358	241	63	54	42	12	3	4	ABC
129	240	212	26	2	2	0	0	4	No *Ping*
130	331	220	55	56	40	16	5	3	ABCGH
131	328	239	48	41	29	12	5	3	ABDFG
132	368	267	54	47	19	28	3	3	CDF
133	404	263	72	69	65	4	7	3	ABCDEFG
134	427	257	59	111	76	35	6	3	ABCDEH
135	386	232	63	91	51	40	6	3	ABCEFG
136	466	271	75	120	90	30	5	4	ABDEF
137	416	262	75	79	59	20	3	3	ABH
138	287	208	47	32	30	2	5	4	ABCGH
139	239	195	32	12	11	1	2	4	CG
140	275	239	27	9	9	0	1	3	H
141	289	222	31	36	28	8	2	4	DG
142	380	216	62	102	72	30	6	2	ABDEFH
143	373	299	48	26	21	5	5	3	CDEFG
144	462	201	65	196	138	58	6	4	ABDEFG
145	204	147	26	31	27	4	4	3	ABEH
146	415	239	70	106	83	23	4	4	ABDE
147	291	214	37	40	19	21	3	3	DEG
148	374	242	55	77	49	28	3	4	CFG
149	303	182	54	67	52	15	3	4	*GH

150	358	231	77	50	40	10	3	2	ABH
151	339	229	35	75	45	30	4	3	ABCG
153	354	219	54	81	67	14	6	4	ABDFGH
154	338	250	64	24	9	15	3	3	DGH
155	376	269	40	67	49	18	7	3	ABDEFGH
156	261	228	25	8	8	0	1	3	H
157	382	276	60	46	41	5	4	3	CFGH
158	374	224	62	88	73	15	3	3	ACH
159	485	251	93	141	95	46	5	4	ABCDG
160	378	285	42	51	41	10	6	3	ABCEFH
161	258	204	32	22	20	2	2	3	CD
162	319	238	38	43	35	8	3	4	EFG
163	269	202	32	35	32	3	6	4	ABCEFG
164	306	216	40	50	32	18	4	4	AEFG
165	289	227	36	26	21	5	3	4	EFG
166	237	213	24	0	0	0	1	3	H
167	455	280	57	118	94	24	5	4	ABDFG
168	266	206	39	21	9	12	3	4	CGH
169	309	223	40	46	29	17	4	4	ACDH
170	351	262	44	45	33	12	5	3	CDEFG
172	307	236	38	33	24	9	4	4	DEFG
173	283	222	32	29	24	5	2	3	DH
174	233	138	37	58	43	15	7	4	*ABDEFH
175	432	269	59	104	81	23	7	1	*ABCDGH
176	448	290	59	99	79	20	4	3	ABCE
177	270	196	36	38	22	16	4	4	CEFG
178	336	228	49	59	42	17	5	3	CDEFG
179	178	147	29	2	2	0	1	4	B
180	368	271	43	54	33	21	4	3	ABCH
181	335	227	43	65	53	12	3	3	ABH

182	294	220	35	39	33	6	3	3	EGH
183	281	197	35	49	40	9	4	2	ABFH
184	309	200	38	71	55	16	5	3	ABCGH
185	321	192	50	79	39	40	6	4	ABDFGH
186	316	215	45	56	45	11	6	2	ABCFGH
187	335	216	46	73	40	33	3	4	BCH
188	283	236	33	14	9	5	3	3	DGH
189	309	223	38	48	38	10	8	3	*ABCEFGH
190	312	231	35	46	30	16	4	4	ABDH
191	303	234	39	30	23	7	5	3	CEFGH
192	341	250	33	58	40	18	4	3	ABCE
193	262	224	33	5	5	0	2	3	CF
194	417	272	51	94	66	28	6	4	ACDEFG
195	261	209	32	20	15	5	2	3	CG
196	392	234	56	102	65	37	5	3	ABEFG
197	359	228	50	81	54	27	6	3	ACDEFG
198	426	291	58	77	63	14	7	4	ABCDEFG
199	227	186	24	17	12	5	2	3	EG
200	296	230	36	30	25	5	4	3	BDEF
201	421	249	60	112	81	31	6	3	ABCEFG
203	315	223	39	53	41	12	5	4	BDEFG
204	325	271	38	16	11	5	3	3	CDF
205	343	237	44	62	39	23	5	4	DEFGH
206	232	194	24	14	14	0	2	4	CF
207	498	284	72	142	86	56	7	3	ABDEFGH
208	163	117	23	23	19	4	3	2	BDH
209	448	280	50	118	72	46	4	3	ABFG
210	189	159	23	7	5	2	2	4	DH
211	360	210	64	86	73	13	5	4	*ABDH
212	349	229	43	77	59	18	3	4	BDH

213	281	213	28	40	30	10	4	3	ABCD
214	312	211	44	57	49	8	4	4	ABEF
215	299	232	35	32	24	8	4	4	CDGH
216	439	241	102	96	79	17	6	3	ABCDGH
217	372	241	40	91	61	30	5	3	ABCEG
218	371	242	54	75	62	13	4	3	ABCH
219	298	196	41	61	50	11	4	4	ABEF
220	440	261	110	69	26	43	7	4	ABCDEGH
221	429	235	64	130	70	60	7	3	*ABEFGH
222	346	209	55	82	37	45	5	4	ABFGH
223	360	195	56	109	49	60	6	3	CDEFGH
224	318	209	40	69	57	12	3	4	DGH
225	317	264	40	13	13	0	2	3	CD
226	312	254	34	24	9	15	3	3	ABD
227	216	178	26	12	10	2	2	4	DE
228	357	262	49	46	31	15	6	4	BDEFGH
229	392	276	53	63	41	22	4	4	ABCG
230	239	206	31	2	1	1	1	3	C
231	189	162	24	3	3	0	1	4	H
232	417	278	51	88	64	24	4	3	ABEF
233	374	245	42	87	68	19	3	4	ABE
234	284	241	33	10	4	6	1	4	C
235	359	257	49	53	42	11	5	3	ABEFG
236	332	225	51	56	47	9	5	3	ABEFG
237	216	185	28	3	2	1	1	3	H
238	302	256	34	12	12	0	1	4	G
239	299	174	50	75	52	23	7	3	ABDEFGH
240	297	225	38	34	29	5	4	4	CDFG
241	271	170	36	65	41	24	5	3	CEFGH
242	436	237	65	134	69	65	4	4	ABCH

244	310	236	37	37	29	8	2	3	AB
245	379	264	42	73	42	31	4	4	CEFH
246	285	220	31	34	26	8	4	4	EFGH
247	381	247	52	82	59	23	5	4	ABDEF
248	350	214	59	77	57	20	6	4	*ABFGH
249	312	246	42	24	21	3	2	3	DE
250	345	205	48	92	67	25	4	4	ABDH
251	257	216	28	13	12	1	2	3	EF
252	347	246	46	55	36	19	5	3	CDFGH
253	351	210	65	76	55	21	5	4	ABCEH
254	261	226	30	5	5	0	1	4	D
255	324	212	53	59	51	8	6	4	ABCDEF
256	284	220	32	32	26	6	2	4	DH
257	276	191	41	44	35	9	5	1	ABEFG
258	252	201	26	25	23	2	4	3	ABDG
259	217	184	32	1	0	1	1	3	H
260	339	230	52	57	47	10	6	3	ABCEFH
261	409	267	64	78	62	16	7	4	ABCDFGH
262	311	239	37	35	29	6	2	4	BD
263	324	236	44	44	38	6	4	3	ABDH
264	333	250	40	43	37	6	6	4	ABCEFG
265	208	187	18	3	2	1	1	4	H
266	257	202	39	16	9	7	2	4	CH
267	368	250	49	69	42	27	3	3	ADE
268	240	205	24	11	11	0	1	3	E
269	351	272	43	36	34	2	2	3	CD
270	411	197	82	132	96	36	6	4	**EFGH
271	397	222	63	112	90	22	7	3	ABCDEFH
272	266	228	31	7	3	4	2	4	EH
273	369	209	69	91	73	18	4	4	ABEF

274	287	211	30	46	30	16	3	3	ABH
275	294	225	38	31	25	6	4	3	ABDG
276	370	200	61	109	80	29	4	1	CEFH
277	282	243	34	5	2	3	2	3	AD
278	444	239	81	124	86	38	8	4	ABCDEFGH
279	362	224	53	85	61	24	6	3	ABCEGH
280	432	291	68	73	57	16	4	4	ABCG

Ping code: Chr1:2640500..2640502 (*PingA*); Chr1:4220010..4220012 (*PingB*); Chr3:28019800..28019802 (*PingC*); Chr7:26460307..26460309 (*PingD*); Chr9:10863118..10863120 (*PingE*); Chr9:13736141..13736143 (*PingF*); Chr9:16690612..16690614 (*PingG*); Chr6:23521641..23526981 (*PingH*, Nipponbare *Ping*); New *Ping* (*)

Supplementary Data 3. List of excisions and footprints at parental *mPing* loci

mPing loci	Number of excisions	Number of excisions with footprints	Number of RILs with excisions	Number of RILs with footprints	Footprints (number of RILs)
Chr1:10903901	0	0	0	0	NA
Chr1:11226135	1	0	1	0	Perfect(1)
Chr1:1132975	0	0	0	0	NA
Chr1:12249228	1	0	1	0	Perfect(1)
Chr1:13935275	0	0	0	0	NA
Chr1:14047376	0	0	0	0	NA
Chr1:1715117	1	0	1	0	Perfect(1)
Chr1:17513834	1	1	1	1	I_TGTGACACAG(1)
Chr1:18989742	2	2	2	2	D_4-D_2(1);I_GACC(1)
Chr1:21351851	0	0	0	0	NA
Chr1:21565700	0	0	0	0	NA
Chr1:22415370	0	0	0	0	NA
Chr1:23332547	2	1	2	1	D_22(1);Perfect(1)
Chr1:24082898	0	0	0	0	NA
Chr1:24610175	0	0	0	0	NA
Chr1:24779771	2	1	2	1	I_A(1);Perfect(1)
Chr1:25256701	1	1	1	1	D_2(1)
Chr1:25261112	0	0	0	0	NA
Chr1:25680936	0	0	0	0	NA
Chr1:28356229	0	0	0	0	NA
Chr1:28924285	0	0	0	0	NA
Chr1:29276379	0	0	0	0	NA
Chr1:29322743	1	1	1	1	I_AAAACGAGGAT(1)
Chr1:29328836	2	1	2	1	D_7(1);Perfect(1)

Chr1:29494572	5	4	7	4	D_17(1);D_6(1);I_A(1);I_AA(1);Perfect(3)
Chr1:29926801	1	0	1	0	Perfect(1)
Chr1:29931517	2	1	3	2	D_9(2);Perfect(1)
Chr1:30895565	0	0	0	0	NA
Chr1:31556970	0	0	0	0	NA
Chr1:32293360	1	0	1	0	Perfect(1)
Chr1:34086312	1	0	1	0	Perfect(1)
Chr1:34281436	0	0	0	0	NA
Chr1:3444992	5	4	8	4	D_8(1);D_5(1);I_TTTTC-I_TC-I_CTTG(1);D_2(1);Perfect(4)
Chr1:34897489	0	0	0	0	NA
Chr1:35465445	0	0	0	0	NA
Chr1:35607599	1	1	1	1	D_2(1)
Chr1:36114224	0	0	0	0	NA
Chr1:36149918	0	0	0	0	NA
Chr1:36267659	5	4	57	43	D_5(40);D_12(1);D_2(1);D_9(1);Perfect(14)
Chr1:36270511	7	6	50	38	D_31(1);D_20(32);D_23(2);D_16(1);D_4(1);I_T(1);Perfect(12)
Chr1:3780849	0	0	0	0	NA
Chr1:37828361	0	0	0	0	NA
Chr1:38092038	0	0	0	0	NA
Chr1:38674212	0	0	0	0	NA
Chr1:38859876	2	1	2	1	D_5(1);Perfect(1)
Chr1:38898352	1	1	1	1	D_17(1)
Chr1:39147394	1	0	1	0	Perfect(1)
Chr1:39212320	2	1	2	1	D_8(1);Perfect(1)
Chr1:3929765	2	2	2	2	D_5(1);I_AC(1)
Chr1:39543338	2	1	2	1	D_2-D_9(1);Perfect(1)

Chr1:39957257	0	0	0	0	NA
Chr1:40469772	0	0	0	0	NA
Chr1:40641754	0	0	0	0	NA
Chr1:4076464	3	2	3	2	D_4(1);D_2(1);Perfect(1)
Chr1:40818575	0	0	0	0	NA
Chr1:40832862	0	0	0	0	NA
Chr1:4101860	2	2	2	2	D_19(1);I_A(1)
Chr1:41148511	0	0	0	0	NA
Chr1:41818259	0	0	0	0	NA
Chr1:42156581	0	0	0	0	NA
Chr1:42599829	0	0	0	0	NA
Chr1:42930250	0	0	0	0	NA
Chr1:6172233	2	1	2	1	D_16(1);Perfect(1)
Chr1:6806761	7	6	10	9	D_2-D_19-I_A(1);D_13(1);D_12(1);D_4(1);D_3(4);I_TTA(1);Perfect(1)
Chr1:6816415	4	3	4	3	D_10(1);D_2(1);D_3(1);Perfect(1)
Chr1:6846279	1	0	2	0	Perfect(2)
Chr1:6864904	3	2	3	2	D_9(1);D_20(1);Perfect(1)
Chr1:7514412	1	0	1	0	Perfect(1)
Chr1:8479732	0	0	0	0	NA
Chr1:8750744	0	0	0	0	NA
Chr1:9142465	0	0	0	0	NA
Chr1:9581605	1	0	1	0	Perfect(1)
Chr10:11955070	0	0	0	0	NA
Chr10:13102744	0	0	0	0	NA
Chr10:13370541	0	0	0	0	NA
Chr10:14020306	0	0	0	0	NA
Chr10:16851282	2	1	4	1	D_1-D_1-D_3-D_1(1);Perfect(3)
Chr10:17496871	0	0	0	0	NA

Chr10:18044214	0	0	0	0	NA
Chr10:18765103	1	1	1	1	I_T(1)
Chr10:21163118	0	0	0	0	NA
Chr10:21361206	0	0	0	0	NA
Chr10:21716391	1	1	1	1	D_1(1)
Chr10:22510407	0	0	0	0	NA
Chr10:22578379	0	0	0	0	NA
Chr10:2734624	0	0	0	0	NA
Chr10:2854153	0	0	0	0	NA
Chr10:2854243	0	0	0	0	NA
Chr10:4007946	3	2	3	2	I_TAAG(1);I_AA(1);Perfect(1)
Chr10:4320421	0	0	0	0	NA
Chr10:6566243	0	0	0	0	NA
Chr10:6896566	0	0	0	0	NA
Chr10:9169250	1	1	1	1	D_7-D_4(1)
Chr11:10797353	0	0	0	0	NA
Chr11:10863129	1	1	1	1	D_11(1)
Chr11:14340125	0	0	0	0	NA
Chr11:14578665	0	0	0	0	NA
Chr11:14670786	1	1	1	1	D_2(1)
Chr11:16397045	1	1	1	1	D_7(1)
Chr11:16894772	0	0	0	0	NA
Chr11:19084257	0	0	0	0	NA
Chr11:19939294	1	0	1	0	Perfect(1)
Chr11:20490425	0	0	0	0	NA
Chr11:21176364	0	0	0	0	NA
Chr11:21459184	0	0	0	0	NA
Chr11:22474609	0	0	0	0	NA
Chr11:22938098	0	0	0	0	NA
Chr11:23200105	0	0	0	0	NA

Chr11:24682792	0	0	0	0	NA
Chr11:25523876	0	0	0	0	NA
Chr11:26077404	1	1	1	1	D_13(1)
Chr11:28625682	0	0	0	0	NA
Chr11:3851785	0	0	0	0	NA
Chr11:393598	0	0	0	0	NA
Chr11:4179066	1	0	2	0	Perfect(2)
Chr11:6969696	2	1	4	1	D_1-D_2-I_A(1);Perfect(3)
Chr11:714790	0	0	0	0	NA
Chr11:7473250	1	1	1	1	D_2(1)
Chr11:7503886	2	1	3	1	D_2(1);Perfect(2)
Chr12:1045463	1	0	1	0	Perfect(1)
Chr12:10612331	0	0	0	0	NA
Chr12:10822439	0	0	0	0	NA
Chr12:19177973	0	0	0	0	NA
Chr12:23877483	1	0	1	0	Perfect(1)
Chr12:24595103	1	1	1	1	D_11(1)
Chr12:26261130	0	0	0	0	NA
Chr12:26642870	0	0	0	0	NA
Chr12:2734541	0	0	0	0	NA
Chr12:3119686	1	1	1	1	I_CCTCC-I_CT(1)
Chr12:3285787	0	0	0	0	NA
Chr12:332029	0	0	0	0	NA
Chr12:3373257	0	0	0	0	NA
Chr12:3616590	0	0	0	0	NA
Chr12:4097962	0	0	0	0	NA
Chr12:4965478	0	0	0	0	NA
Chr12:6625424	0	0	0	0	NA
Chr12:7210157	0	0	0	0	NA
Chr12:839604	1	1	1	1	I_TTA(1)

Chr12:8852564	0	0	0	0	NA
Chr12:9350665	1	0	2	0	Perfect(2)
Chr12:9951106	0	0	0	0	NA
Chr2:10076667	1	1	1	1	D_11(1)
Chr2:1161811	0	0	0	0	NA
Chr2:12467700	2	1	3	1	D_3-D_5(1);Perfect(2)
Chr2:13161938	0	0	0	0	NA
Chr2:13200714	1	0	2	0	Perfect(2)
Chr2:14601853	4	3	51	43	D_6(1);D_6(41);D_1-D_5(1);Perfect(8)
Chr2:15727562	1	0	56	0	Perfect(56)
Chr2:1583547	1	0	1	0	Perfect(1)
Chr2:18534787	1	0	1	0	Perfect(1)
Chr2:18569683	1	1	2	2	D_8(2)
Chr2:20000327	1	0	1	0	Perfect(1)
Chr2:20144823	0	0	0	0	NA
Chr2:2025376	1	1	1	1	D_12(1)
Chr2:20589717	2	1	2	1	D_28(1);Perfect(1)
Chr2:20722279	0	0	0	0	NA
Chr2:21001168	0	0	0	0	NA
Chr2:21319934	1	0	1	0	Perfect(1)
Chr2:21443360	0	0	0	0	NA
Chr2:214437	0	0	0	0	NA
Chr2:223440	2	1	2	1	D_2(1);Perfect(1)
Chr2:22478977	0	0	0	0	NA
Chr2:22549115	0	0	0	0	NA
Chr2:23882557	0	0	0	0	NA
Chr2:24014618	2	1	2	1	D_1(1);Perfect(1)
Chr2:25548875	0	0	0	0	NA
Chr2:25969392	0	0	0	0	NA

Chr2:26510355	0	0	0	0	NA
Chr2:27162235	0	0	0	0	NA
Chr2:27244610	0	0	0	0	NA
Chr2:27685185	1	1	1	1	D_3(1)
Chr2:28008341	1	0	1	0	Perfect(1)
Chr2:28376797	0	0	0	0	NA
Chr2:28662452	0	0	0	0	NA
Chr2:28724476	3	3	4	4	D_10(1);D_3(2);I_A(1)
Chr2:28732623	4	3	6	5	D_14(1);D_12(2);D_9(2);Perfect(1)
Chr2:29244327	0	0	0	0	NA
Chr2:29429219	0	0	0	0	NA
Chr2:29547915	2	2	2	2	D_22(1);D_2-D_1(1)
Chr2:29576700	0	0	0	0	NA
Chr2:30104937	3	2	6	3	D_3(2);I_TT(1);Perfect(3)
Chr2:30104997	1	1	1	1	D_1-D_6(1)
Chr2:30934395	6	5	8	5	D_1(1);D_3(1);I_TT(1);I_TTA(1);I_TTAAC(1);Perfect(3)
Chr2:31455301	1	0	1	0	Perfect(1)
Chr2:31636377	0	0	0	0	NA
Chr2:32397174	1	0	2	0	Perfect(2)
Chr2:32572258	0	0	0	0	NA
Chr2:32858536	0	0	0	0	NA
Chr2:32895944	0	0	0	0	NA
Chr2:33871069	0	0	0	0	NA
Chr2:34670530	1	1	1	1	D_21(1)
Chr2:3502594	0	0	0	0	NA
Chr2:3639031	0	0	0	0	NA
Chr2:4314535	1	1	1	1	D_16(1)
Chr2:617949	0	0	0	0	NA
Chr2:7113420	1	0	1	0	Perfect(1)

Chr2:8187917	0	0	0	0	NA
Chr2:8898160	0	0	0	0	NA
Chr2:913613	0	0	0	0	NA
Chr3:10593111	0	0	0	0	NA
Chr3:10990369	0	0	0	0	NA
Chr3:11329080	1	0	1	0	Perfect(1)
Chr3:11781493	0	0	0	0	NA
Chr3:11922190	1	0	1	0	Perfect(1)
Chr3:12036120	0	0	0	0	NA
Chr3:12067613	0	0	0	0	NA
Chr3:12409837	1	0	2	0	Perfect(2)
Chr3:1247288	0	0	0	0	NA
Chr3:12735756	2	2	2	2	D_12(1);I_TTA(1)
Chr3:1299651	0	0	0	0	NA
Chr3:13027116	1	1	1	1	D_15(1)
Chr3:13281744	1	0	1	0	Perfect(1)
Chr3:13683979	0	0	0	0	NA
Chr3:14597027	0	0	0	0	NA
Chr3:15487801	1	0	1	0	Perfect(1)
Chr3:15698486	0	0	0	0	NA
Chr3:16222140	0	0	0	0	NA
Chr3:17195960	1	0	1	0	Perfect(1)
Chr3:17575717	0	0	0	0	NA
Chr3:17642391	0	0	0	0	NA
Chr3:198572	0	0	0	0	NA
Chr3:21026572	1	0	1	0	Perfect(1)
Chr3:21360120	0	0	0	0	NA
Chr3:22701631	2	1	17	16	D_25(16);Perfect(1)
Chr3:24436164	1	0	1	0	Perfect(1)
Chr3:24855529	2	1	2	1	D_7(1);Perfect(1)

Chr3:24920217	0	0	0	0	NA
Chr3:26028786	0	0	0	0	NA
Chr3:26753248	0	0	0	0	NA
Chr3:2675912	1	0	36	0	Perfect(36)
Chr3:28088459	1	0	3	0	Perfect(3)
Chr3:28365657	0	0	0	0	NA
Chr3:29404858	0	0	0	0	NA
Chr3:29404901	0	0	0	0	NA
Chr3:30784687	0	0	0	0	NA
Chr3:31364757	0	0	0	0	NA
Chr3:31683285	1	1	1	1	D_1(1)
Chr3:31890843	1	1	1	1	I_TTC(1)
Chr3:33362073	0	0	0	0	NA
Chr3:34077806	0	0	0	0	NA
Chr3:34592545	1	1	1	1	D_3(1)
Chr3:35176773	0	0	0	0	NA
Chr3:35894895	0	0	0	0	NA
Chr3:35945979	0	0	0	0	NA
Chr3:3623527	0	0	0	0	NA
Chr3:3804370	0	0	0	0	NA
Chr3:399055	1	0	1	0	Perfect(1)
Chr3:4377252	0	0	0	0	NA
Chr3:511329	0	0	0	0	NA
Chr3:5504299	0	0	0	0	NA
Chr3:6154020	0	0	0	0	NA
Chr3:6328408	1	0	1	0	Perfect(1)
Chr3:6441699	8	7	19	8	D_18(2);D_6(1);D_2(1);D_7(1);I_TTAT(1);I_AAATACA(1);D_26(1);Perfect(11)
Chr3:6512009	1	0	1	0	Perfect(1)

Chr3:6513589	0	0	0	0	NA
Chr3:7296367	0	0	0	0	NA
Chr3:9014023	2	1	2	1	D_1-D_11-D_10(1);Perfect(1)
Chr3:9162954	0	0	0	0	NA
Chr3:9240074	1	0	1	0	Perfect(1)
Chr3:9427120	0	0	0	0	NA
Chr3:9568670	0	0	0	0	NA
Chr3:982231	0	0	0	0	NA
Chr4:13471891	0	0	0	0	NA
Chr4:15070775	0	0	0	0	NA
Chr4:18566524	0	0	0	0	NA
Chr4:1877633	0	0	0	0	NA
Chr4:19021060	0	0	0	0	NA
Chr4:19471782	0	0	0	0	NA
Chr4:19922773	0	0	0	0	NA
Chr4:19999252	0	0	0	0	NA
Chr4:20249932	0	0	0	0	NA
Chr4:21600764	1	1	1	1	I_A(1)
Chr4:21673101	0	0	0	0	NA
Chr4:21998764	2	2	2	2	D_23(1);I_TTTAAGATCTAATC(1)
Chr4:23199000	0	0	0	0	NA
Chr4:23439376	1	0	1	0	Perfect(1)
Chr4:23571130	0	0	0	0	NA
Chr4:24208721	0	0	0	0	NA
Chr4:25029910	0	0	0	0	NA
Chr4:26020117	0	0	0	0	NA
Chr4:26982348	0	0	0	0	NA
Chr4:27475745	0	0	0	0	NA
Chr4:28289923	0	0	0	0	NA
Chr4:28739797	0	0	0	0	NA

Chr4:28903396	0	0	0	0	NA
Chr4:29218325	0	0	0	0	NA
Chr4:29603863	1	1	1	1	D_1-D_4-D_8(1)
Chr4:30320688	1	0	1	0	Perfect(1)
Chr4:30513997	0	0	0	0	NA
Chr4:31677002	0	0	0	0	NA
Chr4:31997420	1	1	1	1	D_8(1)
Chr4:32326935	1	0	1	0	Perfect(1)
Chr4:33017281	0	0	0	0	NA
Chr4:33021868	0	0	0	0	NA
Chr4:33507343	2	1	6	3	D_8(3);Perfect(3)
Chr4:33861550	1	0	1	0	Perfect(1)
Chr4:34302847	0	0	0	0	NA
Chr4:34688306	0	0	0	0	NA
Chr4:35244614	0	0	0	0	NA
Chr4:35421806	0	0	0	0	NA
Chr4:35422419	0	0	0	0	NA
Chr5:14154610	1	0	1	0	Perfect(1)
Chr5:1441039	0	0	0	0	NA
Chr5:14654628	0	0	0	0	NA
Chr5:14878712	1	0	1	0	Perfect(1)
Chr5:15210313	9	8	18	9	D_25(1);D_12(1);D_15(1);I_A-D_3(1);D_17(2);I_CAATCAAATT(1);I_TT(1);I_A(1);Perfect(9)
Chr5:15213006	10	9	14	9	D_11-D_23(1);D_23(1);D_15(1);D_9(1);D_7(1);D_9(1);D_12(1);I_TTA(1);D_1(1);Perfect(5)
Chr5:15488460	0	0	0	0	NA
Chr5:15586258	0	0	0	0	NA

Chr5:15698449	0	0	0	0	NA
Chr5:16364136	0	0	0	0	NA
Chr5:16615709	0	0	0	0	NA
Chr5:18747498	0	0	0	0	NA
Chr5:19143339	1	0	1	0	Perfect(1)
Chr5:19328618	1	0	1	0	Perfect(1)
Chr5:19961220	2	1	2	1	D_6(1);Perfect(1)
Chr5:20117985	1	0	1	0	Perfect(1)
Chr5:21633282	0	0	0	0	NA
Chr5:22056644	0	0	0	0	NA
Chr5:22235594	1	0	1	0	Perfect(1)
Chr5:22646609	1	0	1	0	Perfect(1)
Chr5:226600	1	0	1	0	Perfect(1)
Chr5:23257994	0	0	0	0	NA
Chr5:23730117	3	2	6	2	I_A(1);I_ATTG(1);Perfect(4)
Chr5:23730902	2	1	6	1	D_29(1);Perfect(5)
Chr5:24878619	0	0	0	0	NA
Chr5:25474861	1	1	1	1	D_1(1)
Chr5:25536621	0	0	0	0	NA
Chr5:25546566	2	1	2	1	D_3-D_1-I_A-I_C(1);Perfect(1)
Chr5:26247575	0	0	0	0	NA
Chr5:28151164	0	0	0	0	NA
Chr5:28927631	0	0	0	0	NA
Chr5:4249078	0	0	0	0	NA
Chr5:5370456	1	0	1	0	Perfect(1)
Chr5:6164428	2	1	2	1	D_4(1);Perfect(1)
Chr5:772694	2	1	2	1	I_TTATCTCTGAATGT(1);Perfect(1)
Chr6:10360943	0	0	0	0	NA
Chr6:13737618	0	0	0	0	NA
Chr6:14533008	2	1	3	1	I_G(1);Perfect(2)

Chr6:14790333	1	0	1	0	Perfect(1)
Chr6:17106306	1	0	1	0	Perfect(1)
Chr6:18136422	0	0	0	0	NA
Chr6:18886270	0	0	0	0	NA
Chr6:2035335	2	2	2	2	D_11(1);I_AATCAGTGTCTG(1)
Chr6:20717707	0	0	0	0	NA
Chr6:21010525	0	0	0	0	NA
Chr6:22646015	0	0	0	0	NA
Chr6:23126474	0	0	0	0	NA
Chr6:23535331	0	0	0	0	NA
Chr6:24594639	0	0	0	0	NA
Chr6:25002506	0	0	0	0	NA
Chr6:26083883	0	0	0	0	NA
Chr6:27840591	0	0	0	0	NA
Chr6:2856376	1	0	1	0	Perfect(1)
Chr6:29048879	0	0	0	0	NA
Chr6:30049593	0	0	0	0	NA
Chr6:30099538	2	2	2	2	D_5(1);D_2(1)
Chr6:30293899	0	0	0	0	NA
Chr6:30450783	0	0	0	0	NA
Chr6:4093156	0	0	0	0	NA
Chr6:4729737	0	0	0	0	NA
Chr6:5711665	0	0	0	0	NA
Chr6:6151042	1	1	1	1	D_14(1)
Chr6:6356702	0	0	0	0	NA
Chr6:6521725	0	0	0	0	NA
Chr6:6848916	0	0	0	0	NA
Chr6:7690782	0	0	0	0	NA
Chr6:8042613	1	1	1	1	I_TT(1)

Chr6:8316574	5	5	6	6	D_14(1);D_21(2);I_TTA(1);D_10(1);D_5(1)
Chr6:8356631	0	0	0	0	NA
Chr6:844779	0	0	0	0	NA
Chr6:986514	0	0	0	0	NA
Chr7:11852825	0	0	0	0	NA
Chr7:13481675	1	1	1	1	D_19(1)
Chr7:14975641	0	0	0	0	NA
Chr7:16023232	0	0	0	0	NA
Chr7:17125850	0	0	0	0	NA
Chr7:18920532	0	0	0	0	NA
Chr7:20152299	1	1	1	1	D_2(1)
Chr7:20204538	0	0	0	0	NA
Chr7:20615708	1	1	1	1	D_9(1)
Chr7:21376225	0	0	0	0	NA
Chr7:22060085	1	0	1	0	Perfect(1)
Chr7:22679547	0	0	0	0	NA
Chr7:23009797	1	1	1	1	I_T(1)
Chr7:23272150	0	0	0	0	NA
Chr7:23752427	0	0	0	0	NA
Chr7:23852999	2	2	2	2	D_13(1);I_TAGTA(1)
Chr7:23898253	0	0	0	0	NA
Chr7:24937108	0	0	0	0	NA
Chr7:25772025	0	0	0	0	NA
Chr7:25788368	2	1	33	24	D_16(24);Perfect(9)
Chr7:26090554	2	1	2	1	D_20(1);Perfect(1)
Chr7:26156682	1	0	1	0	Perfect(1)
Chr7:27443190	0	0	0	0	NA
Chr7:28151483	0	0	0	0	NA
Chr7:28821663	0	0	0	0	NA

Chr7:29015072	0	0	0	0	NA
Chr7:29475470	4	3	6	4	I_TA(1);D_25(2);I_AA(1);Perfect(2)
Chr7:29484349	0	0	0	0	NA
Chr7:3667745	3	2	4	2	D_17(1);D_2(1);Perfect(2)
Chr7:4019952	0	0	0	0	NA
Chr7:4560975	0	0	0	0	NA
Chr7:7314674	1	0	1	0	Perfect(1)
Chr7:7972038	1	0	1	0	Perfect(1)
Chr7:8879928	0	0	0	0	NA
Chr8:1019672	0	0	0	0	NA
Chr8:11403145	0	0	0	0	NA
Chr8:13076782	6	5	6	5	D_15(1);D_14(1);I_C(1);I_AA(1);I_TGAAG(1);Perfect(1)
Chr8:13103108	1	0	1	0	Perfect(1)
Chr8:14721482	0	0	0	0	NA
Chr8:15387727	1	0	1	0	Perfect(1)
Chr8:16683588	0	0	0	0	NA
Chr8:19197271	0	0	0	0	NA
Chr8:19452248	0	0	0	0	NA
Chr8:20442416	0	0	0	0	NA
Chr8:20628372	0	0	0	0	NA
Chr8:20674237	0	0	0	0	NA
Chr8:22948360	4	4	4	4	D_13(1);D_37(1);I_A(1);I_AGAATAGAGGG(1)
Chr8:23290289	0	0	0	0	NA
Chr8:23802328	0	0	0	0	NA
Chr8:24585356	0	0	0	0	NA

Chr8:24622994	15	14	28	14	D_9(1);D_8(1);D_20(1);D_15(1);D_8(1);D_13(1);D_11(1);D_3(1);D_4-D_29(1);I_T(1);I_TT(1);D_14-D_4-I_C(1);D_2(1);D_1(1);Perfect(14)
Chr8:24830426	0	0	0	0	NA
Chr8:24965704	0	0	0	0	NA
Chr8:25236840	1	0	1	0	Perfect(1)
Chr8:25278859	0	0	0	0	NA
Chr8:25881178	1	1	1	1	I_TAA(1)
Chr8:27109715	0	0	0	0	NA
Chr8:27153071	1	0	1	0	Perfect(1)
Chr8:28186241	0	0	0	0	NA
Chr8:458415	0	0	0	0	NA
Chr8:4712970	1	1	1	1	D_4(1)
Chr8:737334	0	0	0	0	NA
Chr8:8581520	1	0	1	0	Perfect(1)
Chr8:8655022	0	0	0	0	NA
Chr8:9385127	1	0	1	0	Perfect(1)
Chr8:973880	0	0	0	0	NA
Chr8:9778572	1	1	1	1	D_10(1)
Chr9:14118723	0	0	0	0	NA
Chr9:15394515	0	0	0	0	NA
Chr9:15441738	1	1	1	1	I_TT(1)
Chr9:15873914	0	0	0	0	NA
Chr9:16024218	0	0	0	0	NA
Chr9:16330820	1	1	1	1	D_3(1)
Chr9:16698141	0	0	0	0	NA
Chr9:17452747	0	0	0	0	NA
Chr9:17901601	0	0	0	0	NA
Chr9:18354394	0	0	0	0	NA

Chr9:18705899	2	1	2	1	I_T(1);Perfect(1)
Chr9:19596969	1	1	1	1	I_T(1)
Chr9:19832667	2	1	55	1	D_1(1);Perfect(54)
Chr9:20177227	1	0	1	0	Perfect(1)
Chr9:2094378	1	0	1	0	Perfect(1)
Chr9:21458344	0	0	0	0	NA
Chr9:21744263	0	0	0	0	NA
Chr9:21859387	1	1	1	1	D_7(1)
Chr9:21884649	0	0	0	0	NA
Chr9:22186805	0	0	0	0	NA
Chr9:22706823	1	0	1	0	Perfect(1)
Chr9:6030900	0	0	0	0	NA
Chr9:643091	0	0	0	0	NA
Chr9:694483	0	0	0	0	NA
Chr9:7117395	3	2	6	3	I_A-D_19(1);D_3(2);Perfect(3)
Chr9:7248751	1	0	2	0	Perfect(2)
Chr9:968867	1	1	1	1	D_3(1)

Footprints are represented by insertions (I) or deletions (D) followed by base pairs inserted or length of base pairs deleted. Numbers in parentheses are number of RILs have the same footprint at this locus.

Supplementary Data 4. Primers used in this study

Primers	Sequence (5'-3')
Primers for transposon display	
MseI+0	GACGATGAGTCCTGAGTAA
MseI+T/A/G/C	GACGATGAGTCCTGAGTAAT/A/G/C
mPing P1	GTAGCCGTGCAATGACACTAG
mPing P2	TGACACTAGCCATTGTGACTG
Primers for qRT-PCR	
PingORF1_F	CAACAAGACCCAAATTCATGTTTG
PingORF1_R	ACTTGGTGGCTGTGGAGATATTGG
PingTPASE_F	TACGTATTGTGGACGCATTAGGC
PingTPASE_R	CATCAGCACCACTACCAGTAGCC
Actin_F	CCAGTGGTCGTACCACAGGTATTG
Actin_R	AGTAACCACGCTCCGTCAGG
Primers for validation of excisions	
RME1F	ATAAGCAAGCTAGTTTGGGCCT
RME1R	AAAGCTCTAGATTGACGGCCAA
RME2F	TGACACTACTGTGACAGCATCC
RME2R	TAACTCACTCACCATGTGGCAA
RME3F	TGGGAAGTGATGAGGAGGAGAT
RME3R	GCGCGGGGGATTAGAATACTTA
RME4F	GCACTCCGAAGAAGCAAAAAGT
RME4R	GGCCCCGCGATTAGTTACTAAT
RME5F	CACTACTCATCAGCAAGGTGGT
RME5R	GCTACATGCTACAGTGACGAGA
RME6F	GCCGTACGTGGTTTCAGAAAAA
RME6R	GGAGAAAAAGGACTAGCTGGCT
RME7F	ATCCGATTCTCAGCTCAGCTTC
RME7R	CACCATCAGCCAGTACCTTCTT
RME8F	TAAACACAACCTTTGTCACGGC
RME8R	CCGCAATCAATACCGCATTCAT
RME9F	CCATCCCTTGATCACCCCTAAG
RME9R	AACACGAAACAACAGAACACCT
RME10F	CAAGATAACTGCCACCAGGAGT
RME10R	TGAAGGGTGTTGCATGGGATAA
RME11F	ATGTTCCATGGGCCAGAGAATT
RME11R	TGTGGCCGAGTATATTGGGATG
RME12F	CTGTTGTACTCCTTTCGTCCCA
RME12R	TACCGTGCCAAGTGATGAATGA
RME13F	AACAAACGATGCTTTCTGCTCC
RME13R	ATTTTCTGTGTGCACCGTTCTG
RME14F	GCCTCGTCAGAAAAACAGCTTT

RME14R	TGATGAATGGAGTGCTGCTGAT
RME15F	TCAAACACACCTACACGCTGAT
RME15R	GAACTTCCTGTCTCTGCACTCA
RME16F	ATTCTCTTTTCGCTTTGTCGGC
RME16R	TTAATACATGGCCCCACCTGTC
RME17F	GGTGACGTGTTACCAAATACCG
RME17R	GCAGTCTGCGTCCATGATAAAC
RME18F	TGAATGAACCATCTCTCGTGCA
RME18R	TGAATTGGAGCCAGTAGTTGACT
RME19F	GGACAGGTGGAGTATTCCCTTG
RME19R	ATTCTTCTCTCCTGCTTGTGGG
RME20F	CAACTTTCCATCAGTTGCAGGA
RME20R	GAGGTTGGGAAGAGAGAATGGG
RME21F	ATTTAGGGGAGTGTGTCGTGTC
RME21R	TTCTTCTCCGGGTGTGATGAAG
RME22F	CCAATGGAAGCAGAGGAGGAAT
RME22R	CCACGATCGATGTCACACATTG
RME23F	CTTCCTCTAGATCTAGCCCCGA
RME23R	CATCAACGGATGCAGATGGAAC
RME24F	AATGAGATGAGACAGTGCAGCA
RME24R	TCACTGGCACACACTAGCTTAG
RME25F	TGGGCTCACATGCTAATCAACT
RME25R	CAACCCAGATCTCTTCAGCCTT
RME26F	ACAACCTAGGGTTTAGTGTGCT
RME26R	GATGACACGAGGCTAGGTGAAA
RME27F	AATCAAGTTCGGGAGCTTGGAT
RME27R	TCCATCCAGAACGGCCAATA
RME28F	GCCGCTGCTTTGTTTTACTCTT
RME28R	TTGCATCAATGATGACATGGCA
RME29F	GTTGTCAAGTCGTCAGTTGTCG
RME29R	ACGATACAATTGCCTGGACAGT
RME30F	GTGCGTCCAAAAGGTAGCTTTT
RME30R	ACGATACGAAGGAAGCAGGATC

Primers for validation of structrual variations associated with *mPing* loci

SV22_C1F	GTGGCATTTTATCCGGTGCATT
SV22_C1R	TGTGAGAGTGTGAGTGCTTTGT
SV_R26_2F	TCAGTGAACATGGAGAGGGTTG
SV_R26_2R	GCAGACATGGCAGTTTCACTTT
SV_R26R	TAGCAGACATGGCAGTTTCACT
SV_R22F	ATGACAAAAGCAGGCAACACTC
SV_R22R	TATCCTCCAATTTGCCGTCGAA

SV198_C9aF	ACCTCTGTCTCCATACCATCCA
SV198_C9aR	CGGGTGAGAAGGTACATCGAAA
SV198_C9bF	ACGTGGACCGAATAGGAAACAT
SV198_C9bR	AGCAACCGTGTTATAGCTGGAA
SV_C1_29LF	TGCTTGCAGTATACGAGGGTTT
SV_C1_29LR	ACTCCGGCAAGTCCTAATCAAG
SV_C1_29RF	GATTTTGAAAGCTGTGGTGGCT
SV_C1_29RR	GAACACATTATCCGAACCAGCG
SV_C7_10LF	TGCCACGAAATAGTTAACCCGA
SV_C7_10LR	CTCACCTGATGCCTGAACGATA
SV_C7_10RF	GACCAGTGAACAAACAGCAACT
SV_C7_10RR	TGGAATTGCTAGTGCTGTCTGT
SV_C10_13LF	CCTTGTACTTTTGGCTGGTTCG
SV_C10_13LR	GAGTGATTGATGCCCCGAAAAC
SV_C10_13RF	AGTACTTTGTACTTCCCTGTGCT
SV_C10_13RR	TCATGCAAGCGTGTGTTTTGAT
SV_C10_17LF	AACTAAGCGGAGGTAGAAGCAC
SV_C10_17LR	CACAAGCGAAGAAACACTCTGG
SV_C10_17RF	TGGCTGTTCCTCTTGTCTCTTG
SV_C10_17RR	TGACGGCCGATAGTTTAACGAA
SV_C9_22LF	AAACTGTCGCATCCGATTCTCT
SV_C9_22LR	TGTCCCCTTTGTCGATAACTGG
SV_C9_22RF	TAGGTCCAACGCTATGCTGAAG
SV_C9_22RR	AAAGATGAGGTCCAACGTCACA

Primers for genotyping RILs using genome-wide markers developed using *mPing* polymorphysim between HEG4 and Nipponbare

C1_29MF	AATGTCACCATGGCTCCTGTAG
C1_29MR	GCTTGGGCGTTGTCAAACTAAT
C4_26MF	CTCCTCTCATCTTGCGCCTATG
C4_26MR	GATTCCCGCTTATCCTCCAGTT
C6_27MF	ATGAATCATGGCACTGTCTCGT
C6_27MR	CTGGGAAAGCAGAGTAGTGGTT
C7_7MF	TGGCCGGAGTAGTTTTACAGAG
C7_7MR	CAACTTCTCTCAGGACACGGAA
C10_6MF	GTTGCGGATTTCCCTATCATGC
C10_6MR	AGGCTGAAGTTACTGCTTTGGT
C11_7MF	GTTGCAAGACACAATCCTCCAC
C11_7MR	ATGGCTTTGATCCTCCACTAGC
C12_3MF	AAATTCCGACACTCTCTGGCAT
C12_3MR	GGATGTGCTCCGAATGATGTTG
C12_19MF	AGAGACATAGACTTGGCCAACG

C12_19MR	GAGTACATATGACCGGGGGAAC
MADS50F	AAAAGTGGGTAGTGTTGGCTCT
MADS50R	CTGCTCTTCTTCTTGTCCCCAT
37180F	GCAGGAGAGTGAACACCAGTAA
37180R	AACCTTGAATCGGTCGACATGA
3850bF	ACAGACAGATCGTGATGATGCA
3850bR	TCAAACCGGCTGAAGATTAGCT