

SUPPLEMENTAL MATERIAL

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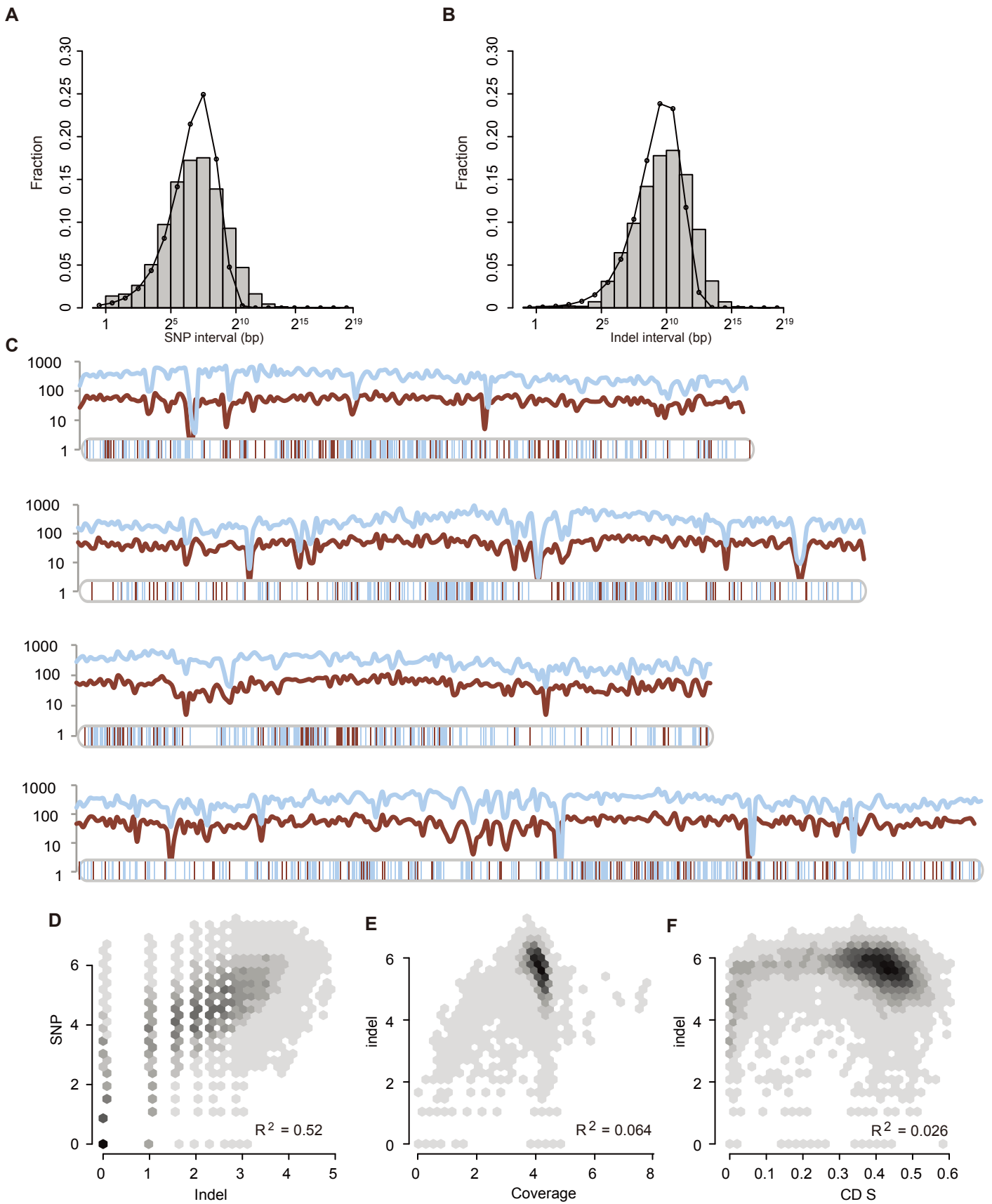
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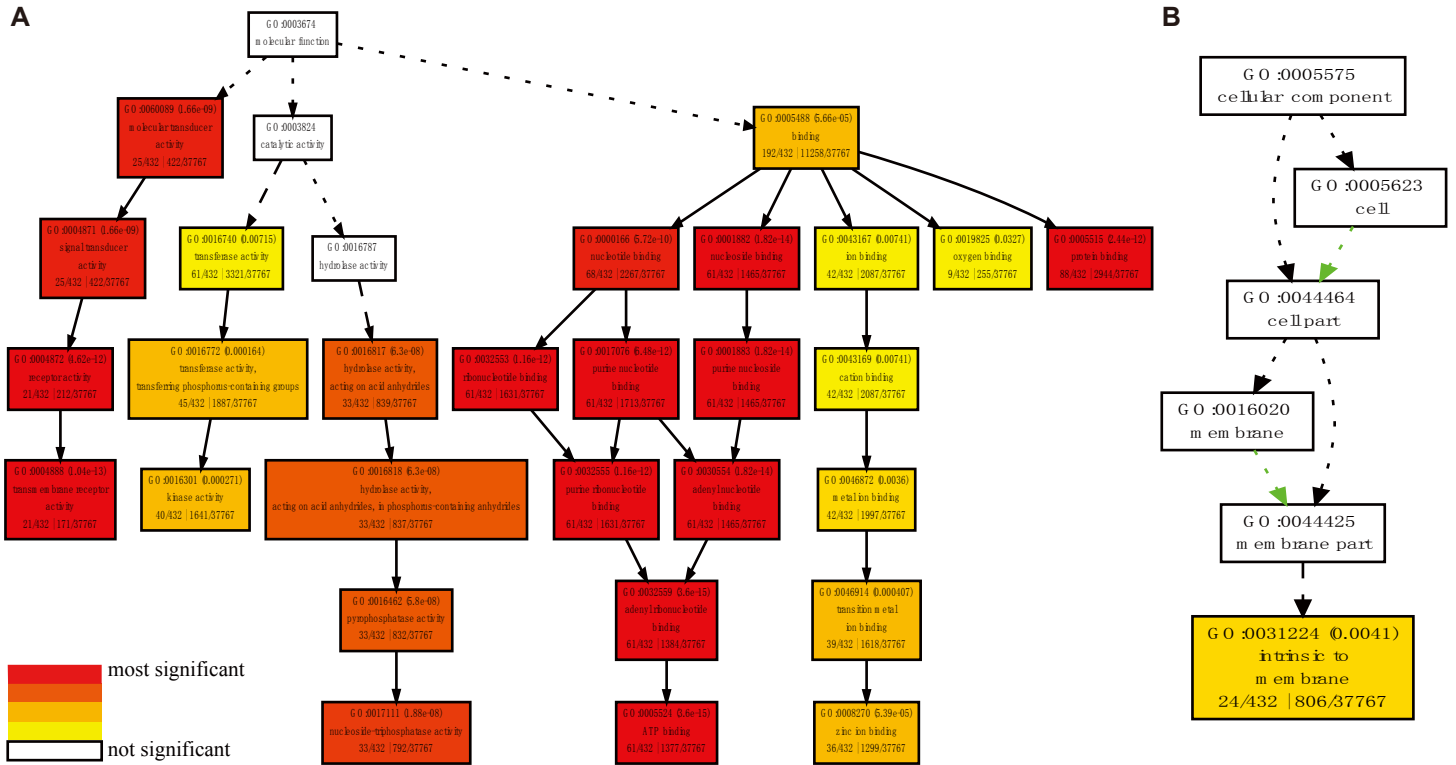
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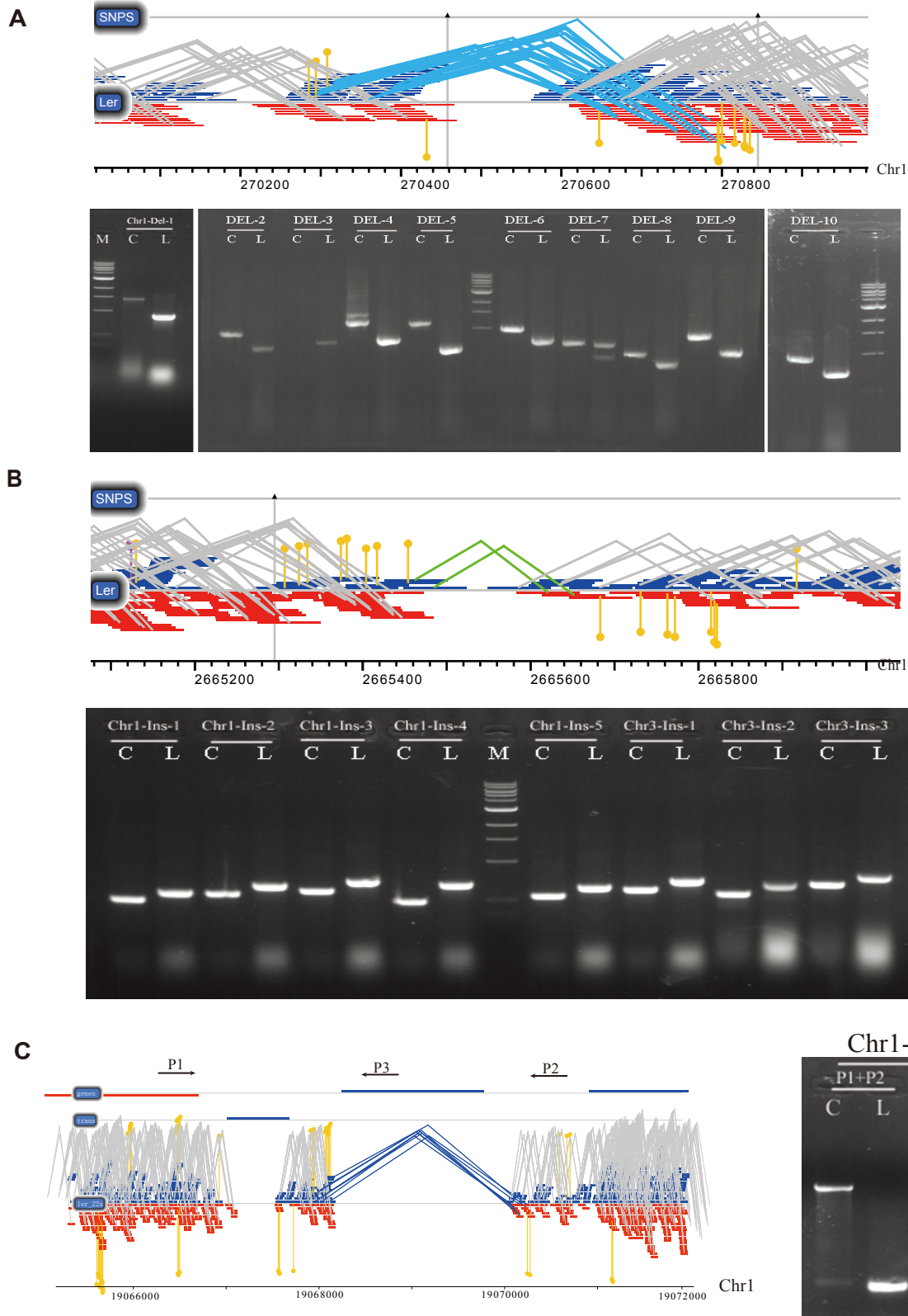
Supplemental Figure 1. The distribution of intervals between SNPs/indels and correlation of SNP and small indel densities.

(A, B) Histogram of interval between SNPs (A) or indels (B). The fraction of intervals in each length range was plotted. The curve shows the fraction from exponential distribution, as the length of intervals between SNPs/indels follows exponential distribution if SNPs/indels are randomly distributed across the genome. The actual distribution of interval length has heavier tail than exponential distribution. For either SNP or indel, the difference between actual distribution and exponential distribution is statistically different (Kolmogorov-Smirnov test, $p < 10e-10$) (C) Parallel change of SNP and small indel density on Chr2-5. The density was defined to be the number of SNPs/indels per 100 Kb. The blue curves represent SNP densities and the red curves for small indels. Blue and red vertical bars below show the locations of large deletions and insertions, respectively. (D) Linear regression of SNP and indel densities in 10 Kb sliding windows. (E, F) Linear regression of small indel densities with read coverage (E) or CDS fraction (F) in 100 Kb sliding window. SNP and indel densities are log2 transformed. Near zero R square value suggests read coverage or CDS fraction does not contribute much to the correlation.



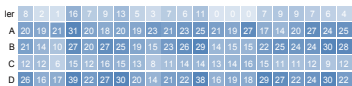
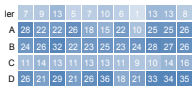
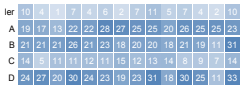
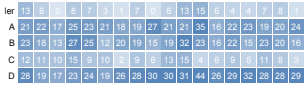
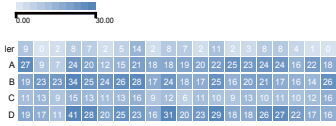
Supplemental Figure 2. Enriched GO groups in genes with 10 or more nonsynonymous SNPs.
 (A) Enriched groups of molecular function. (B) Enriched groups of cellular component.

Supplemental Figure 3. Genes affected by small or large indels. (A-C) Arabidopsis branch specific dN/dS values of genes affected by frameshift small indels (A), nonframeshift small indels (B) and large indels (C). (D-F) Expression level of affected genes in Col (x-axis) and Ler (y-axis). (D) Genes affected by frameshift small indels; (E) Genes affected by nonframeshift small indels; (F) Genes affected by large indels. Compared to genes with nonframeshift indel (E), more genes in (D) and (F) have decreased expression levels in Ler. (G-H) Enriched GO groups of cellular component (G) and molecular function (H) in genes affected by frameshift small indels. There is no enriched group of biological process. (I-J) Enriched GO groups of molecular function (I) and biological process (J) in genes affected by nonframeshift small indels. There is no enriched group of cellular component. For genes affected by large indels, none of three categories have any enriched GO groups.

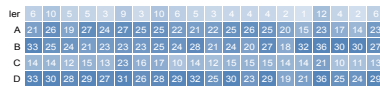
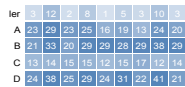
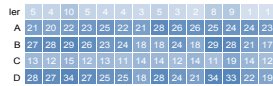
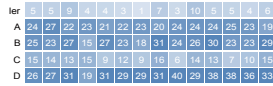
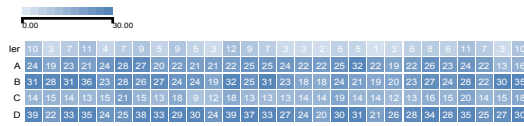


Supplemental Figure 4. The detection of indels using Illumina paired-end reads and verification by PCR. (A) Display of one ~200 bp deletion in Ler genome compared to Col reference (Chr1: 270,399-270,610 bp) (above). PCR and gel electrophoresis verification of bioinformatics detected Ler deletions (below). Ten deletions were randomly selected from the predicted dataset. (B) Display of one ~150 bp insertion in Ler genome (Chr1: 2,665,492-2,665,646 bp). PCR and gel electrophoresis verification of bioinformatics detected Ler insertions (below). Eight insertions were randomly selected from the predicted dataset. (C) Display of one deletion in Ler genome overlapped with At1g51430.1 (left). PCR and gel electrophoresis verification of bioinformatics detected Ler deletion (right). P1, P2 and P3 are the primers used for PCR with the arrow indicating the primer direction. Illumina paired-end reads from Ler mapped to the Col reference are displayed by blue (plus strand) bars and red bars (minus strand) correspondingly. Green polylines indicate distances of two ends are significantly shorter than their expected inserted sizes from DNA preparation, indicating there is an extra DNA fragment in Ler genome. Gray polylines between two ends of a read show that they are mapped with proper distances, while blue polylines indicate that distances of two ends are obviously longer than their inserted sizes from DNA preparation, suggesting there is a missing DNA fragment in Ler genome. Vertical yellow lines indicate only one end of a paired-end reads are mapped. M: DNA marker; C: Col genome; L: Ler genome. The detailed information for primers and locations are in the Supplemental Table 17.

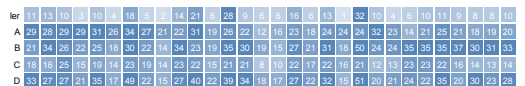
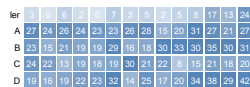
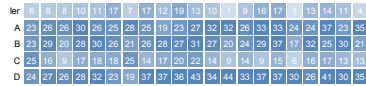
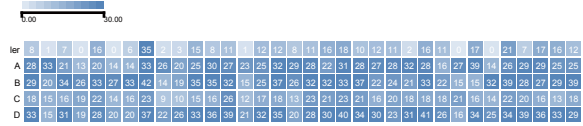
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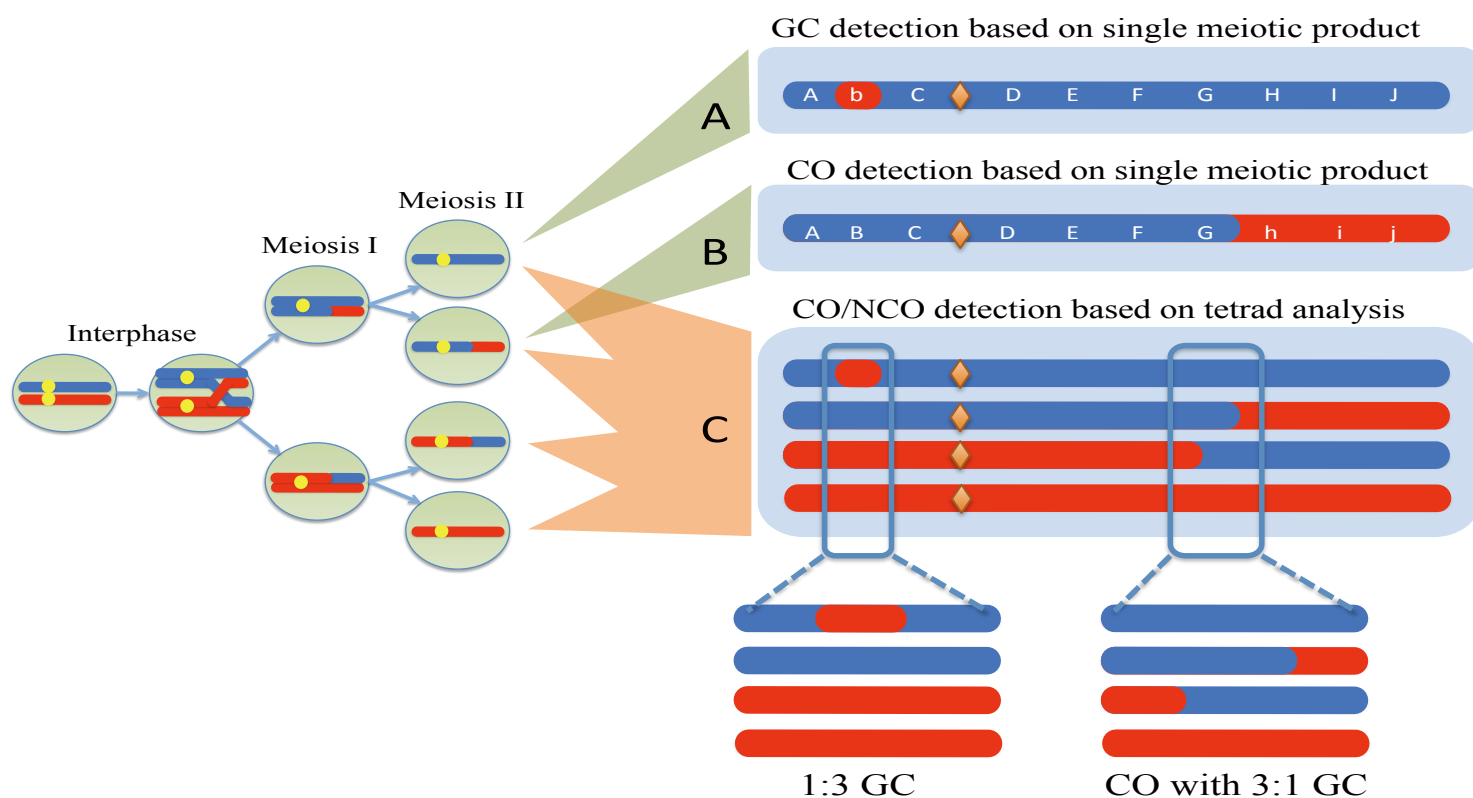
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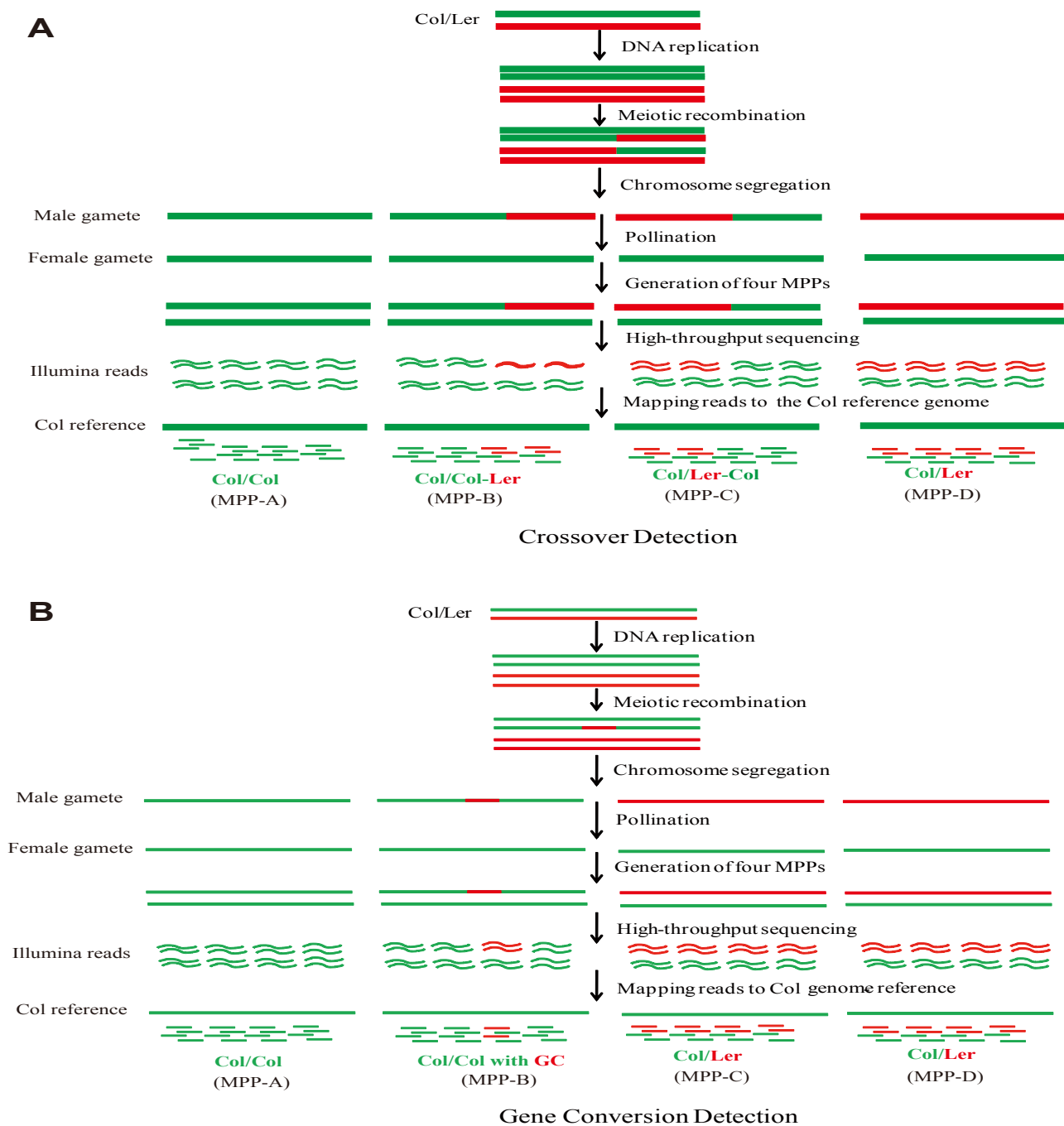
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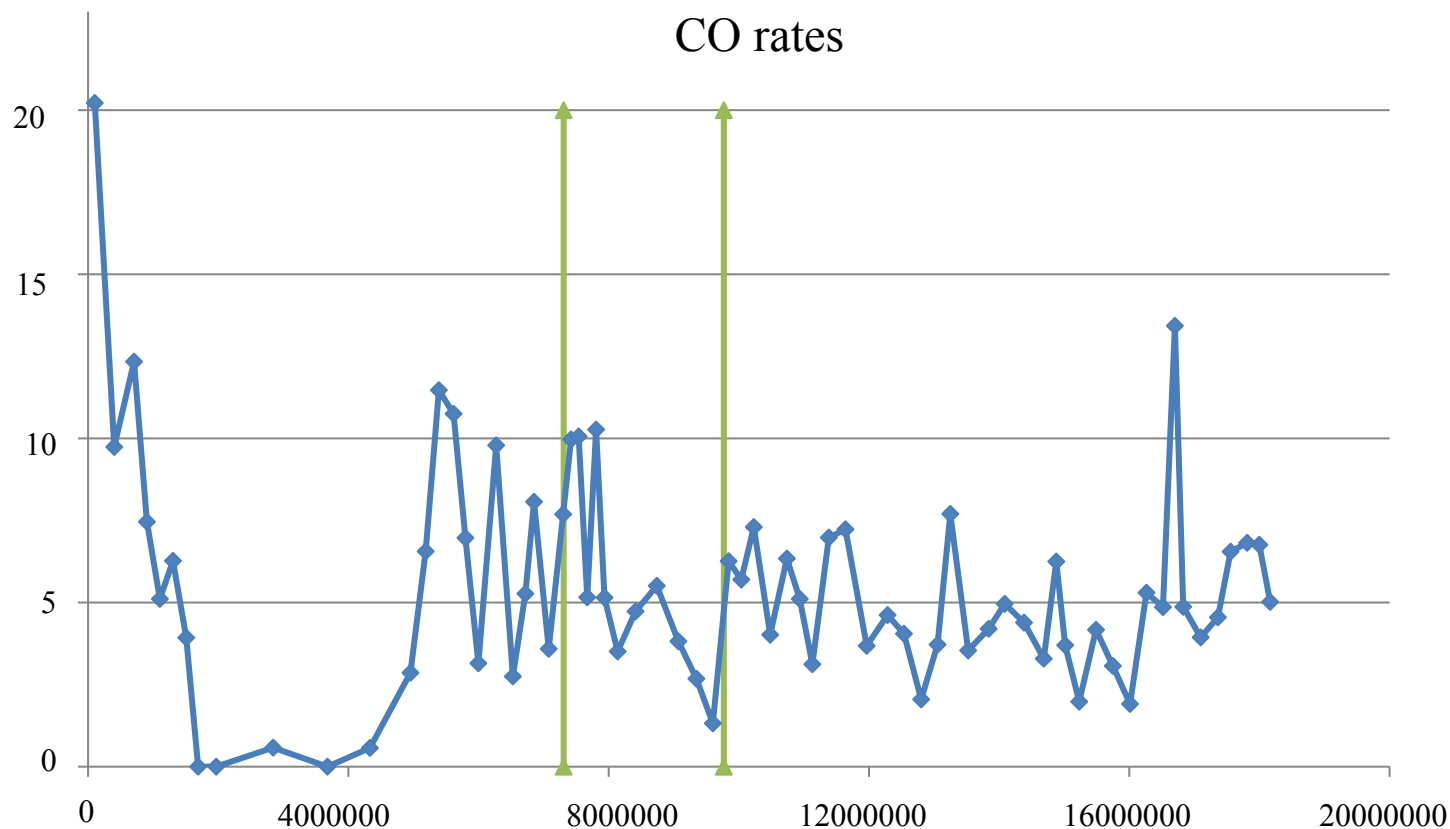
Supplemental Figure 5. CNVs verification of three transposon groups by using sequencing reads densities. Each block represents one transposon in either of five Col chromosomes from top the bottom, and the relative sequencing coverage are given by a number for Ler and four meiotic products marked by 'A', 'B', 'C' and 'D'. The coverage is calculated as number of reads per 100 bp in each segment. Considering different coverage of various samples, the numbers are normalized by using meiotic product 'B' as a calibration. (A) Display of read mapping densities of 84-copy ATREP1 transposons. (B) Display of 125-copy ATREP2 transposons. (C) Display of 85-copy ATREP3 transposons. Each block represents one transposon. The numbers in the blocks refer to the number of reads per 100 bp in each segment.



Supplemental Figure 6. Tetrad analysis for identification of meiotic CO and NCO. The comparison between analysis of single meiotic product and tetrad analysis. (A, B) GC and CO detection based on only single meiotic products. Without all four gametes, the tract length of CO cannot be determined. (C) GC and CO detection using tetrad analysis. With all four gametes included in the tetrad, we can find the length of CO tract and further distinguish GC within CO and GC independent of CO (NCO).



Supplemental Figure 7. A schematic illustration for detecting meiotic recombination using Illumina sequencing reads. Green bars represent Col genome, red bars show Ler genome. (A) Meiotic crossover was revealed by the reads from MPP-B and MPP-C plants. (B) Meiotic gene conversion was detected by the Ler reads in the MPP-B plant.

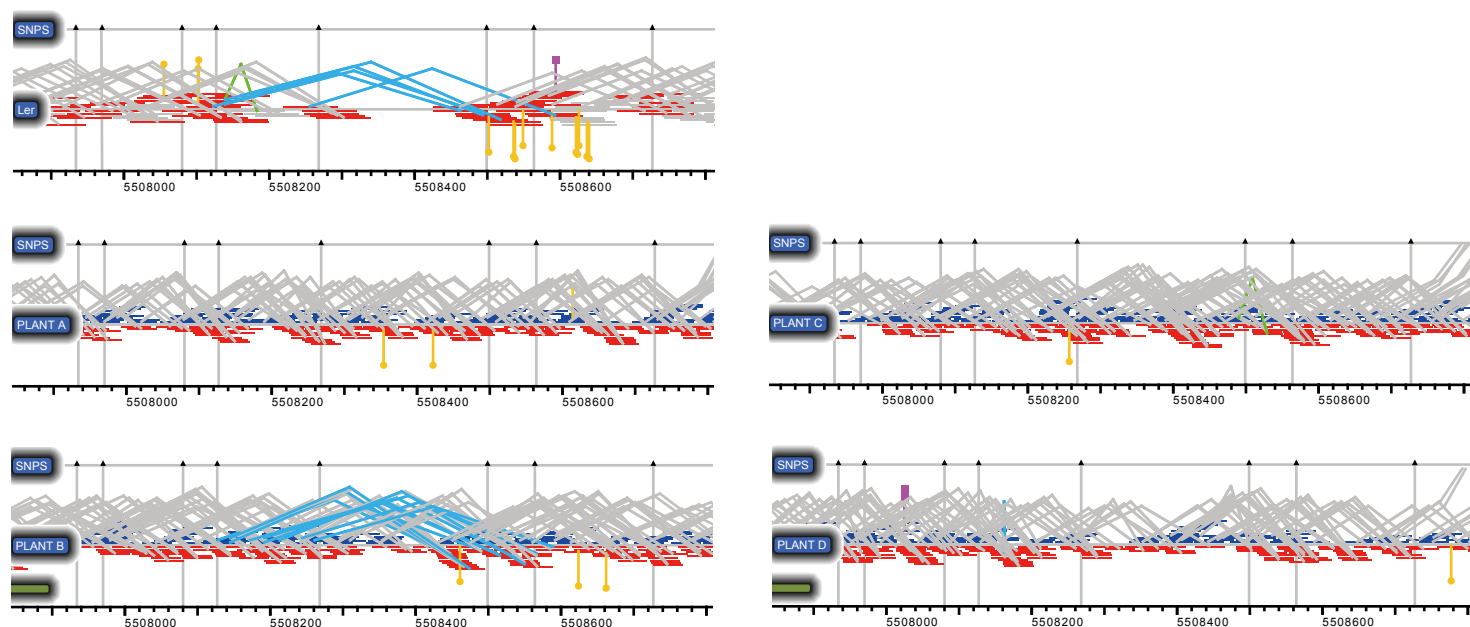


Supplemental Figure 8. The positions of two detected COs on chromosome 4 in this study among the high CO rates regions reported by Drouaud et al. (Drouaud et al. 2006). The CO rates, marked in blue, were evaluated from 1,404 meioses based on 71 genetic markers, the numbers of Y-axis refer to the average frequency of CO appearance (cM/Mb). Two vertical green lines are the COs detected in this study. Nucleolar organizer region is not included in the figure.

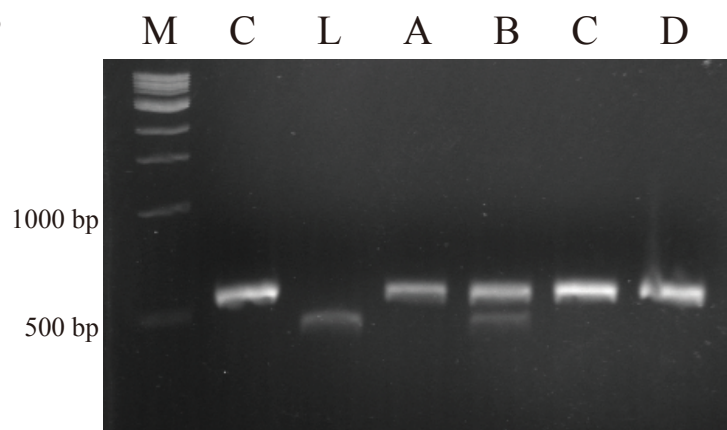
References

Drouaud J, Camilleri C, Bourguignon PY, Canaguier A, Berard A, Vezon D, Giancola S, Brunel D, Colot V, Prum B et al. 2006. Variation in crossing-over rates across chromosome 4 of *Arabidopsis thaliana* reveals the presence of meiotic recombination "hot spots". *Genome Res* **16**: 106-114.

A

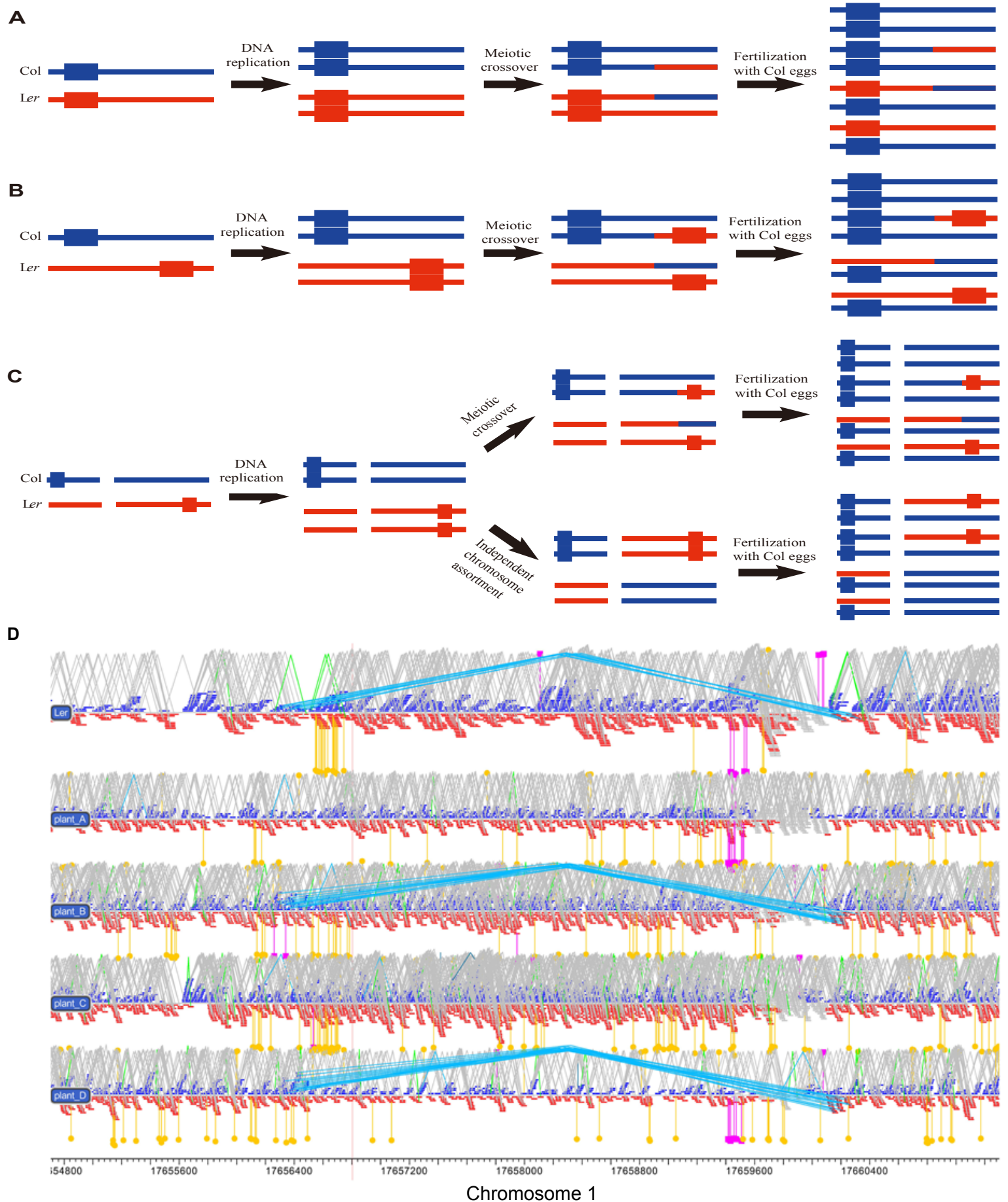


B



Supplemental Figure 9. The Ler deletion located inside the 1st meiosis CO-4 was replaced by Col DNA sequence after meiotic recombination.

(A) Mapping of Illumina paired-end sequencing reads reveal the 86 bp Ler deletion comparing to Col reference genome (Chr2: 5,508,341-5,508,426 bp), which overlaps with the 1st meiosis CO-4 (5,507,746-5,509,294 bp). MPP-A, MPP-C and MPP-D only produced Col genotype reads. MPP-B produced both Col and Ler genotype reads. (B) PCR and gel electrophoresis verification of the Ler deletion substituted by Col genotype. M: DNA marker; C: Col genome; L: Ler genome; A: MPP-A; B: MPP-B; C: MPP-C; D: MPP-D.



Supplemental Figure 10. Meiosis turns genomic transposition into copy number variations. (A) Blue (Col) and red (Ler) rectangles are represented two allelic regions. Without translocations, meiotic products have the same number of copies as parents. (B) In this case, blue and red rectangles are shown homologous regions with different locations on the same chromosome. After meiotic crossover, the second meiotic product obtained two copies, while the third meiotic product has none. (C) Blue and red rectangles are located in different chromosomes. Then either meiotic crossover and/or subsequently independent chromosome assortment can lead to copy number variation. (D) An example of identified genomic transposition between Col and Ler by sequencing reads. Illumina paired-end reads mapped to the Col reference are displayed by blue (plus strand) bars and red bars (minus strand) correspondingly. For the transposition region, paired-end reads from two boundaries of the Ler genome were mapped to the Col reference with a larger distance (light blue polylines); however, reads from inside of the transposition region were perfectly mapped to the reference, indicating this DNA fragment is located in Ler genome at different position with that in the Col genome.

Supplemental Table 1. Summary of read number and coverage.

		Total reads ^a	Mapped reads	Mapping quality ≥ 20	Coverage ^b
Ler ecotype		61,603,614	58,102,231	38,674,710	18.7
1st meiosis	Plant-1A	36,590,794	33,241,502	24,541,695	8.2
	Plant-1B	54,404,688	53,474,928	39,851,797	13.4
	Plant-1C	53,810,544	53,442,224	39,538,948	13.3
	Plant-1D	43,117,198	42,265,828	31,753,318	10.7
2nd meiosis	Plant-2A	48,220,664	45,774,118	34,705,911	16.5
	Plant-2B	50,370,054	47,877,914	33,159,674	16.6
	Plant-2C	45,102,640	43,347,370	32,485,254	13.8
	Plant-2D	39,898,699	38,375,746	27,887,166	10.0

- The number of total reads includes both single-end reads and paired-end reads. The two ends from paired-end technology are counted as two reads.
- Only take reads with mapping quality score ≥ 20 into account in calculating coverage.

Supplemental Table 2. The list of genes containing 10 or more nonsynonymous SNPs, nonsense SNPs, and potentially extended transcripts in Ler.

nonsynonymous

The list of genes containing 10 or more nonsynonymous SNPs in Ler.

Gene ID	Gene Model Description
AT1G55430.1	Cysteine/Histidine-rich C1 domain family protein
AT1G64210.1	Leucine-rich repeat protein kinase family protein
AT5G59260.1	Concanavalin A-like lectin protein kinase family protein
AT1G58400.1	Disease resistance protein (CC-NBS-LRR class) family
AT4G17880.1	Basic helix-loop-helix (bHLH) DNA-binding family protein
AT4G13992.1	Cysteine/Histidine-rich C1 domain family protein
AT3G44780.1	Cysteine proteinases superfamily protein
AT1G69550.1	disease resistance protein (TIR-NBS-LRR class)
AT5G47950.1	HXXXD-type acyl-transferase family protein
AT5G45113.1	mitochondrial transcription termination factor-related / mTERF-related
AT4G19570.1	Chaperone DnaJ-domain superfamily protein
AT2G05120.1	Nucleoporin, Nup133/Nup155-like
AT5G32613.1	Zinc knuckle (CCHC-type) family protein
AT4G08097.1	myosin heavy chain-related
AT3G45410.1	receptor-like kinase
AT5G45520.1	Leucine-rich repeat (LRR) family protein
AT4G03830.1	Protein of unknown function
AT1G67000.1	Protein kinase superfamily protein
AT4G28811.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G31820.1	Amino acid permease family protein
AT3G59130.1	Cysteine/Histidine-rich C1 domain family protein
AT3G11000.2	DCD (Development and Cell Death) domain protein
AT5G42710.1	unknown protein
AT3G47110.1	Leucine-rich repeat protein kinase family protein
AT2G04680.1	Cysteine/Histidine-rich C1 domain family protein
AT2G24700.1	Transcriptional factor B3 family protein
AT5G17740.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT2G40310.1	Pectin lyase-like superfamily protein
AT1G61210.1	Transducin/WD40 repeat-like superfamily protein
AT5G24830.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G18830.1	Transducin/WD40 repeat-like superfamily protein
AT1G43770.2	RING/FYVE/PHD zinc finger superfamily protein
AT1G43260.1	hAT transposon superfamily protein
AT4G21820.1	binding;calmodulin binding
AT3G10180.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G27230.1	Frigida-like protein
AT3G29830.1	F-box/RNI-like superfamily protein
AT3G57470.2	Insulinase (Peptidase family M16) family protein
AT4G19440.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G14250.1	structural constituent of ribosome
AT4G01350.1	Cysteine/Histidine-rich C1 domain family protein
AT3G25490.1	Protein kinase family protein
AT3G45800.1	Plant protein 1589 of unknown function
AT5G17680.1	disease resistance protein (TIR-NBS-LRR class)
AT3G42723.1	aminoacyl-tRNA ligases;ATP binding;nucleotide binding
AT1G62630.1	Disease resistance protein (CC-NBS-LRR class) family
AT4G05310.1	Ubiquitin-like superfamily protein
AT5G43745.1	Protein of unknown function (DUF1012)
AT4G02660.1	Beige/BEACH domain ;WD domain, G-beta repeat protein
AT3G25750.1	CONTAINS InterPro DOMAIN/s: F-box domain
AT2G31480.1	unknown protein

nonsynonymous

AT2G39580.1	CONTAINS InterPro DOMAIN/s: Putative zinc-finger domain (InterPro:IPR019607)
AT5G63020.1	Disease resistance protein (CC-NBS-LRR class) family
AT2G15042.1	Leucine-rich repeat (LRR) family protein
AT5G43740.1	Disease resistance protein (CC-NBS-LRR class) family
AT1G31670.1	Copper amine oxidase family protein
AT1G31840.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G51810.1	Leucine-rich repeat protein kinase family protein
AT1G31540.2	Disease resistance protein (TIR-NBS-LRR class) family
AT4G19990.2	FAR1-related sequence 1 (FRS1)
AT5G27140.1	NOP56-like pre RNA processing ribonucleoprotein
AT3G47200.1	Plant protein of unknown function (DUF247)
AT1G13410.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G42060.1	myosin heavy chain-related
AT5G32590.1	myosin heavy chain-related
AT5G07570.1	glycine/proline-rich protein
AT5G43300.1	PLC-like phosphodiesterases superfamily protein
AT3G26050.1	TPX2 (targeting protein for Xklp2) protein family
AT1G66620.1	Protein with RING/U-box and TRAF-like domains
AT1G17150.1	Pectin lyase-like superfamily protein
AT2G14080.1	Disease resistance protein (TIR-NBS-LRR class) family
AT4G05497.1	RNI-like superfamily protein
AT2G03360.2	Glycosyltransferase family 61 protein
AT3G07250.1	nuclear transport factor 2 (NTF2) family protein
AT3G44400.1	Disease resistance protein (TIR-NBS-LRR class) family
AT5G58120.1	Disease resistance protein (TIR-NBS-LRR class) family
AT5G45210.1	Disease resistance protein (TIR-NBS-LRR class) family
AT3G49510.1	F-box family protein
AT1G55928.1	Coiled-coil domain-containing protein 55 (DUF2040)
AT4G27870.1	Vacuolar iron transporter (VIT) family protein
AT3G45760.1	Nucleotidyltransferase family protein
AT3G44630.3	Disease resistance protein (TIR-NBS-LRR class) family
AT5G41750.1	Disease resistance protein (TIR-NBS-LRR class) family
AT2G03140.2	alpha/beta-Hydrolases superfamily protein
AT5G17250.1	Alkaline-phosphatase-like family protein
AT5G15980.1	Pentatricopeptide repeat (PPR) superfamily protein
AT5G65910.1	BSD domain-containing protein
AT3G55160.1	unknown protein
AT5G08010.1	unknown protein
AT5G66910.1	Disease resistance protein (CC-NBS-LRR class) family
AT4G01860.1	Transducin family protein / WD-40 repeat family protein
AT1G35150.1	General transcription factor 2-related zinc finger protein
AT5G38010.1	UDP-Glycosyltransferase superfamily protein
AT5G43310.1	COP1-interacting protein-related
AT5G17910.1	unknown protein
AT1G56540.1	Disease resistance protein (TIR-NBS-LRR class) family
AT1G29730.1	Leucine-rich repeat transmembrane protein kinase
AT1G80960.2	F-box and Leucine Rich Repeat domains containing protein
AT4G12780.1	Chaperone DnaJ-domain superfamily protein
AT3G49400.1	Transducin/WD40 repeat-like superfamily protein
AT1G50280.1	Phototropic-responsive NPH3 family protein
AT3G24780.1	Uncharacterised conserved protein UCP015417
AT1G63210.1	Transcription elongation factor Spt6
AT3G43148.1	Function unknown

nonsynonymous

AT4G04960.1	Concanavalin A-like lectin protein kinase family protein
AT5G43530.1	Helicase protein with RING/U-box domain
AT5G38386.1	F-box/RNI-like superfamily protein
AT3G45530.1	Cysteine/Histidine-rich C1 domain family protein
AT5G43240.1	Protein of unknown function (DUF674)
AT1G68980.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G08630.1	unknown protein
AT1G43020.1	Protein of unknown function, DUF547
AT5G42690.2	Protein of unknown function, DUF547
AT5G13380.1	Auxin-responsive GH3 family protein
AT4G17140.3	pleckstrin homology (PH) domain-containing protein
AT5G24360.2	inositol requiring 1-1 (IRE1-1)
AT1G65130.1	Ubiquitin carboxyl-terminal hydrolase-related protein
AT5G43390.1	Uncharacterised conserved protein UCP015417
AT5G45060.1	Disease resistance protein (TIR-NBS-LRR class) family
AT1G28180.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT2G06500.1	hAT family dimerisation domain
AT4G02710.1	Kinase interacting (KIP1-like) family protein
AT2G26470.1	unknown protein
AT1G50270.1	Pentatricopeptide repeat (PPR) superfamily protein
AT3G25060.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G00980.1	zinc knuckle (CCHC-type) family protein
AT4G02400.1	U3 ribonucleoprotein (Utp) family protein
AT1G58250.2	SABRE, putative gene of unknown function, homologous to maize apt1 gene
AT1G23880.1	NHL domain-containing protein
AT3G50420.1	Pentatricopeptide repeat (PPR) superfamily protein
AT3G29375.1	XH domain-containing protein
AT5G41630.1	F-box/RNI-like superfamily protein
AT3G27860.1	Tudor/PWWP/MBT superfamily protein
AT2G21090.1	Pentatricopeptide repeat (PPR-like) superfamily protein
AT5G20610.1	unknown protein
AT2G21800.2	Forms a complex with MUS81
AT3G60920.1	CONTAINS InterPro DOMAIN/s: Beige/BEACH (InterPro:IPR000409)
AT2G32590.1	Unknown protein
AT4G15890.1	binding
AT5G48690.1	CONTAINS InterPro DOMAIN/s
AT5G43620.1	Pre-mRNA cleavage complex II
AT1G57580.1	F-box family protein
AT1G64100.2	pentatricopeptide (PPR) repeat-containing protein
AT1G64255.1	MuDR family transposase
AT1G61840.1	Cysteine/Histidine-rich C1 domain family protein
AT1G40390.1	DNase I-like superfamily protein
AT1G64960.1	ARM repeat superfamily protein
AT1G56400.1	F-box family protein
AT3G43670.1	Copper amine oxidase family protein
AT5G38840.1	SMAD/FHA domain-containing protein
AT1G20060.1	ATP binding microtubule motor family protein
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AT3G46730.1	NB-ARC domain-containing disease resistance protein
AT3G46710.1	NB-ARC domain-containing disease resistance protein
AT5G44530.1	Subtilase family protein
AT1G42525.1	Cysteine proteinases superfamily protein

nonsynonymous

AT3G27473.1	Cysteine/Histidine-rich C1 domain family protein
AT1G59453.1	B-block binding subunit of TFIIC
AT3G48770.1	DNA binding;ATP binding
AT2G28970.1	Leucine-rich repeat protein kinase family protein
AT5G42840.1	Cysteine/Histidine-rich C1 domain family protein
AT4G14140.2	Encoding a DNA methyltransferase
AT3G55020.1	Ypt/Rab-GAP domain of gyp1p superfamily protein
AT3G28550.1	Proline-rich extensin-like family protein
AT1G53600.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G15340.1	Pentatricopeptide repeat (PPR) superfamily protein
AT5G02950.1	Tudor/PWWP/MBT superfamily protein
AT5G44230.1	Pentatricopeptide repeat (PPR) superfamily protein
AT1G22000.1	FBD, F-box and Leucine Rich Repeat domains containing protein
AT3G27870.1	ATPase E1-E2 type family protein
AT4G00440.2	Function unknown
AT5G24740.1	Calcium-dependent lipid-binding family protein
AT3G28780.1	Protein of unknown function (DUF1216)
AT3G27490.1	Cysteine/Histidine-rich C1 domain family protein
AT3G44090.1	F-box family protein
AT1G35710.1	Protein kinase family protein with leucine-rich repeat domain
AT2G16250.1	Leucine-rich repeat protein kinase family protein
AT2G18570.1	UDP-Glycosyltransferase superfamily protein
AT4G13820.1	Leucine-rich repeat (LRR) family protein
AT3G46650.1	UDP-Glycosyltransferase superfamily protein
AT5G66890.1	Leucine-rich repeat (LRR) family protein
AT5G17730.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G58390.1	Disease resistance protein (CC-NBS-LRR class) family
AT4G09780.1	TRAF-like family protein
AT4G14370.1	Disease resistance protein (TIR-NBS-LRR class) family
AT3G28415.1	ABC transporter family protein
AT2G07240.1	cysteine-type peptidases;cysteine-type peptidases
AT3G30230.1	myosin heavy chain-related
AT3G44710.1	Plant protein of unknown function (DUF247)
AT1G56040.1	HEAT/U-box domain-containing protein
AT5G47260.1	ATP binding;GTP binding;nucleotide binding;nucleoside-triphosphatases
AT1G57650.1	ATP binding;
AT2G21830.1	Cysteine/Histidine-rich C1 domain family protein
AT3G30770.1	Eukaryotic aspartyl protease family protein
AT3G45750.1	Nucleotidyltransferase family protein
AT4G11170.1	Disease resistance protein (TIR-NBS-LRR class) family
AT2G07760.1	Zinc knuckle (CCHC-type) family protein
AT4G04790.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G11730.1	Cation transporter/ E1-E2 ATPase family protein
AT1G51820.1	Leucine-rich repeat protein kinase family protein
AT2G04810.1	Protein of unknown function (DUF295)
AT1G55440.1	Cysteine/Histidine-rich C1 domain family protein
AT3G27510.1	Cysteine/Histidine-rich C1 domain family protein
AT3G50430.1	unknown protein
AT2G13690.1	PRLI-interacting factor, putative
AT1G18900.3	Pentatricopeptide repeat (PPR) superfamily protein
AT1G45100.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G60190.1	ARM repeat superfamily protein
AT3G25510.1	disease resistance protein (TIR-NBS-LRR class)

nonsynonymous

AT1G63670.1	Unknown function DUF3741
AT5G46260.1	disease resistance protein (TIR-NBS-LRR class) family
AT3G44770.1	Protein of unknown function (DUF626)
AT1G31430.1	Pentatricopeptide repeat (PPR-like) superfamily protein
AT2G17580.1	Polynucleotide adenylyltransferase family protein
AT5G38340.1	Disease resistance protein (TIR-NBS-LRR class) family
AT5G05750.1	DNAJ heat shock N-terminal domain-containing protein
AT5G64710.1	Putative endonuclease or glycosyl hydrolase
AT3G23370.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G51900.1	Regulator of Vps4 activity in the MVB pathway protein
AT3G47250.1	Plant protein of unknown function (DUF247)
AT2G29210.1	splicing factor PWI domain-containing protein
AT4G00990.1	Transcription factor jumonji (jmjC) domain-containing protein
AT5G07760.1	formin homology 2 domain-containing protein / FH2 domain-containing protein
AT1G09680.1	Pentatricopeptide repeat (PPR) superfamily protein
AT3G43990.1	Bromo-adjacent homology (BAH) domain-containing protein
AT5G50115.1	CONTAINS InterPro DOMAIN/s: Molecular chaperone, heat shock protein
AT5G48650.1	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain
AT1G27070.1	5'-AMP-activated protein kinase-related
AT3G28040.1	Leucine-rich receptor-like protein kinase family protein
AT3G25970.1	Pentatricopeptide repeat (PPR) superfamily protein
AT4G36150.1	Disease resistance protein (TIR-NBS-LRR class) family
AT1G52000.1	Mannose-binding lectin superfamily protein
AT1G36230.1	unknown protein
AT3G29580.1	Arabidopsis phospholipase-like protein (PEARL1 4) with TRAF-like domain
AT5G37570.1	Pentatricopeptide repeat (PPR-like) superfamily protein
AT5G45720.1	AAA-type ATPase family protein
AT4G36140.1	disease resistance protein (TIR-NBS-LRR class), putative
AT5G48310.1	unknown protein
AT5G41140.1	Myosin heavy chain-related protein
AT4G01925.1	Cysteine/Histidine-rich C1 domain family protein
AT5G05400.1	LRR and NB-ARC domains-containing disease resistance protein
AT2G28450.1	zinc finger (CCCH-type) family protein
AT3G29670.1	HXXXD-type acyl-transferase family protein
AT1G67450.1	F-box and associated interaction domains-containing protein
AT3G44230.1	unknown protein
AT4G36120.1	Plant protein of unknown function (DUF869)
AT4G16900.1	Disease resistance protein (TIR-NBS-LRR class) family
AT5G02390.1	Protein of unknown function DUF3741
AT3G25440.1	RNA-binding CRS1 / YhbY (CRM) domain protein
AT2G07280.1	unknown protein
AT1G23890.2	NHL domain-containing protein
AT5G16280.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G19050.1	NB-ARC domain-containing disease resistance protein
AT3G28330.1	F-box family protein-related
AT3G59120.1	Cysteine/Histidine-rich C1 domain family protein
AT3G32904.1	unknown protein
AT1G20400.1	Unknown protein
AT3G46920.1	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain
AT3G43930.1	BRCT domain-containing DNA repair protein
AT5G26160.1	unknown protein
AT4G16835.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G32120.1	FUNCTIONS IN: molecular_function unknown

nonsynonymous

AT5G59670.1	Leucine-rich repeat protein kinase family protein
AT2G12900.1	Basic-leucine zipper (bZIP) transcription factor family protein
AT5G27110.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G28823.1	FUNCTIONS IN: molecular_function unknown
AT4G11800.1	Calcineurin-like metallo-phosphoesterase superfamily protein
AT2G16040.1	hAT dimerisation domain-containing protein / transposase-related
AT1G24485.3	FUNCTIONS IN: molecular_function unknown
AT2G25650.1	DNA-binding storekeeper protein-related transcriptional regulator
AT5G18770.1	F-box/FBD-like domains containing protein
AT5G52800.3	DNA primases
AT1G34480.1	Cysteine/Histidine-rich C1 domain family protein
AT5G59130.1	Subtilase family protein
AT1G63530.1	Hydroxyproline-rich glycoprotein family protein
AT4G05523.1	Embryo defective 1745
AT3G29800.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G11362.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT2G15110.1	Protein of unknown function, DUF601
AT4G39952.1	Pentatricopeptide repeat (PPR) superfamily protein
AT1G62530.1	Plant protein of unknown function (DUF863)
AT2G23230.1	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT5G12430.1	Heat shock protein DnaJ with tetratricopeptide repeat
AT2G03000.1	RING/U-box superfamily protein
AT2G42480.1	TRAF-like family protein
AT5G28190.1	unknown protein
AT4G02540.1	Cysteine/Histidine-rich C1 domain family protein
AT5G27330.1	Prefoldin chaperone subunit family protein
AT3G49150.1	F-box/RNI-like superfamily protein
AT5G39770.1	Represents a non-function pseudogene homologous to AtMSU81 (At4g30870).
AT5G03360.1	DC1 domain-containing protein
AT3G45940.1	Glycosyl hydrolases family 31 protein
AT2G15710.1	TRAF-like family protein
AT4G20200.1	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT3G32940.1	RNA-binding KH domain-containing protein
AT3G49450.1	F-box and associated interaction domains-containing protein
AT1G30860.1	RING/U-box superfamily protein
AT1G61230.1	Mannose-binding lectin superfamily protein
AT5G38350.1	Disease resistance protein (NBS-LRR class) family
AT1G66450.1	Cysteine/Histidine-rich C1 domain family protein
AT3G56550.1	Pentatricopeptide repeat (PPR) superfamily protein
AT3G46800.1	Cysteine/Histidine-rich C1 domain family protein
AT1G43245.1	SET domain-containing protein
AT2G17600.1	Cysteine/Histidine-rich C1 domain family protein
AT1G24460.1	unknown protein
AT3G45670.1	Protein kinase superfamily protein
AT5G37430.1	Family of unknown function (DUF577)
AT2G10440.1	unknown protein
AT2G17050.1	disease resistance protein (TIR-NBS-LRR class), putative
AT2G27660.1	Cysteine/Histidine-rich C1 domain family protein
AT1G58050.1	RNA helicase family protein
AT3G21210.1	zinc ion binding
AT1G66235.1	unknown protein
AT3G26380.1	Melibiose family protein
AT1G10090.1	Early-responsive to dehydration stress protein (ERD4)

nonsynonymous

AT3G28880.1	Ankyrin repeat family protein
AT4G37380.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G01560.1	Protein of unknown function DUF1421
AT2G23360.1	Plant protein of unknown function (DUF869)
AT3G61380.1	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-related
AT3G29410.1	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT5G45510.1	Leucine-rich repeat (LRR) family protein
AT1G72270.1	Unknown protein
AT4G05360.1	Zinc knuckle (CCHC-type) family protein
AT4G11580.1	RNI-like superfamily protein
AT2G21350.1	RNA-binding CRS1 / YhbY (CRM) domain protein
AT4G00480.2	MYC-related protein
AT4G19560.1	CYCT1
AT5G45400.1	RPA70C
AT5G40840.2	Cohesion family protein SYN2 (SYN2).
AT5G42920.2	Encodes a component of the putative Arabidopsis THO/TREX complex
AT4G19490.1	Putative homolog of yeast Vps54
AT4G18600.1	Encodes a member of the SCAR family
AT1G58270.1	ZW9 mRNA, complete cds
AT2G20960.1	pEARL14
AT1G62340.1	Subtilisin-like serine protease
AT4G14400.1	encodes a novel protein with putative ankyrin and transmembrane regions.
AT1G36180.1	acetyl-CoA carboxylase 2 (ACC2)
AT5G26120.1	alpha-L-arabinofuranosidase 2 (ASD2)
AT3G11240.1	Encodes an arginyl-tRNA:protein arginyltransferase (ATE2)
AT5G40820.1	Encodes a Arabidopsis ortholog of the ATR protein kinase
AT3G47750.1	member of ATH subfamily
AT1G34170.3	AUXIN RESPONSE FACTOR 13 (ARF13)
AT4G21070.1	AtBRCA1
AT1G61215.1	Bromodomain protein with a DNA binding motif
AT2G21770.1	cellulose synthase, related to CESA6.
AT1G15660.1	Encodes a homologue of the human centromeric protein C (CENP-C)
AT4G19020.1	chromomethylase 2 (CMT2)
AT4G09680.1	Encodes CTC1 (Conserved Telomere Maintenance Component 1) involved in telomere maintenance.
AT4G11460.1	Encodes a cysteine-rich receptor-like protein kinase.
AT4G00970.1	Encodes a cysteine-rich receptor-like protein kinase.
AT1G55940.1	member of CYP708A
AT3G26150.1	putative cytochrome P450
AT3G26160.1	putative cytochrome P450
AT3G26290.1	putative cytochrome P450
AT3G26330.1	putative cytochrome P450
AT3G26280.1	cytochrome P450 monooxygenase
AT1G19630.1	member of CYP722A
AT3G25180.1	member of CYP82G
AT2G21910.1	member of CYP96A
AT5G40560.1	Encodes a putative DegP protease.
AT3G43920.2	Encodes a ribonuclease III family protein
AT5G23800.1	Member of the plant-specific DUF724 protein family
AT5G53870.1	early nodulin-like protein 1 (ENODL1)
AT5G48090.1	EDM2-like protein1 (ELP1)
AT2G28880.1	embryo defective 1997 (emb1997)
AT1G24340.1	A locus involved in embryogenesis
AT5G37630.1	EMBRYO DEFECTIVE 2656 (EMB2656)

nonsynonymous

AT1G61140.1	embryo sac development arrest 16 (EDA16)
AT3G48090.1	Component of R gene-mediated disease resistance
AT4G05130.1	equilibrative nucleoside transporter 4 (ENT4)
AT2G32250.1	FAR1-related sequence 2 (FRS2)
AT3G44560.1	fatty acid reductase 8 (FAR8)
AT1G52920.1	Encodes a plasma membrane-localized ABA receptor
AT5G44700.1	Encodes GASSHO2 (GSO2)
AT2G24720.1	member of Putative ligand-gated ion channel subunit family
AT1G28420.1	homeobox-1 (HB-1)
AT3G52890.1	KCBP-interacting protein kinase interacts specifically with the tail region of KCBP
AT1G62440.1	encodes a paralog of LRX1 (LEUCINE-RICH REPEAT/EXTENSIN 1)
AT1G62830.1	Encodes a homolog of human Lysine-Specific Demethylase1
AT4G08470.1	Encodes a member of the A1 subgroup of the MEKK (MAPK/ERK kinase kinase) family
AT3G16000.1	encodes a DNA-binding protein that binds to plastid DNA non-specifically
AT4G13610.1	maternal effect embryo arrest 57 (MEE57)
AT4G08480.1	Encodes a member of the A1 subgroup of the MEKK (MAPK/ERK kinase kinase) family
AT4G02070.1	encodes a DNA mismatch repair homolog of human MutS gene, MSH6
AT4G00540.1	Encodes a putative c-myb-like transcription factor
AT1G27460.1	encodes a calmodulin-binding protein
AT4G13750.1	Encodes NO VEIN (NOV)
AT2G15820.1	Encodes a protein that promotes splicing of type II introns
AT5G46540.1	P-glycoprotein 7 (PGP7)
AT3G28360.1	P-glycoprotein 16 (PGP16)
AT3G28390.1	P-glycoprotein 18 (PGP18)
AT1G52260.1	Encodes a protein disulfide isomerase-like (PDIL) protein
AT1G17750.1	Encodes PEPR2
AT2G33770.1	Encodes a ubiquitin-conjugating E2 enzyme
AT2G28830.1	PLANT U-BOX 12 (PUB12)
AT3G09400.1	Similar to POLTERGEIST (POL) protein phosphatase 2C
AT1G50840.1	DNA Polymerase gamma2
AT2G16650.1	proteinaceous RNase P 2 (PRORP2)
AT5G02310.1	Encodes PROTEOLYSIS6 (PRT6)
AT1G68210.1	Similar to ARR response regulator proteins
AT5G43090.1	Encodes a member of the Arabidopsis Pumilio (APUM) proteins
AT1G52940.1	purple acid phosphatase 5 (PAP5)
AT5G41820.1	RAB geranylgeranyl transferase alpha subunit 2 (RGTA2)
AT3G24560.2	novel gene involved in embryogenesis
AT1G74180.1	receptor like protein 14 (RLP14)
AT1G74190.1	receptor like protein 15 (RLP15)
AT2G15080.1	receptor like protein 19 (RLP19)
AT1G17240.1	Encodes a CLAVATA2 (CLV2)-related gene
AT2G25440.1	receptor like protein 20 (RLP20)
AT2G33060.1	receptor like protein 27 (RLP27)
AT3G23110.1	receptor like protein 37 (RLP37)
AT3G23120.1	receptor like protein 38 (RLP38)
AT3G24900.1	receptor like protein 39 (RLP39)
AT3G25010.1	receptor like protein 41 (RLP41)
AT5G40170.1	receptor like protein 54 (RLP54)
AT5G49290.1	receptor like protein 56 (RLP56)
AT1G47890.1	receptor like protein 7 (RLP7)
AT3G46530.1	Confers resistance to the biotrophic oomycete
AT1G60930.1	AtRECQ4B
AT2G03880.1	Pentatricopeptide repeat (PPR) superfamily protein

nonsynonymous

AT5G45260.1	Confers resistance to <i>Ralstonia solanacearum</i>
AT2G27070.1	member of Response Regulator: B- Type
AT5G45150.1	RNAse THREE-like protein 3 (RTL3)
AT1G12210.1	RFL1
AT4G15180.1	SET domain protein 2 (SDG2)
AT2G13800.1	somatic embryogenesis receptor-like kinase 5 (SERK5)
AT2G20850.1	STRUBBELIG-receptor family 1 (SRF1)
AT1G17770.1	Encodes a SU(VAR)3-9 homolog, a SET domain protein
AT5G59090.1	subtilase 4.12 (SBT4.12)
AT1G27720.1	TBP-associated factor 4B (TAF4B)
AT1G61120.1	Encodes a geranyllinalool synthase
AT2G27120.1	Encodes a protein with similarity to DNA polymerase epsilon catalytic subunit
AT1G35860.1	TOC75 pseudogene
AT5G05870.1	UDP-glucosyl transferase 76C1 (UGT76C1)
AT2G26480.1	UDP-glucosyl transferase 76D1 (UGT76D1)
AT1G78270.1	UDP-glucosyl transferase 85A4 (UGT85A4)
AT2G12940.1	unfertilized embryo sac 4 (UNE4)
AT5G17790.1	Encodes a 85.9 kDa protein containing novel repeats and zinc fingers described as protein interaction domains
AT1G56510.1	TIR-NB-LRR protein that confers resistance to four races of <i>Albugo candida</i> .
AT1G66550.1	member of WRKY Transcription Factor; Group III
AT2G21370.1	Similar to xylulose kinases

nonsense

The list of genes containing nonsense SNPs in *Ler*.

Gene ID	Gene Model Description
AT3G59750.1	Concanavalin A-like lectin protein kinase family protein
AT4G22730.1	Leucine-rich repeat protein kinase family protein
AT3G55670.1	F-box/RNI-like/FBD-like domains-containing protein
AT4G04925.1	unknown protein
AT3G24065.1	Plant self-incompatibility protein S1 family
AT1G12244.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT2G14800.1	unknown protein
AT5G32613.1	Zinc knuckle (CCHC-type) family protein
AT2G19240.1	Ypt/Rab-GAP domain of gyp1p superfamily protein
AT3G16820.1	F-box and associated interaction domains-containing protein
AT3G42780.1	unknown protein
AT3G25460.1	F-box and associated interaction domains-containing protein
AT1G52330.2	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT1G71300.1	Vps52 / Sac2 family
AT2G19360.1	Protein of Unknown Function (DUF239)
AT5G63180.1	Pectin lyase-like superfamily protein
AT3G30280.1	HXXXD-type acyl-transferase family protein
AT2G23171.1	unknown protein
AT1G20370.1	Pseudouridine synthase family protein
AT3G19515.2	Unknown protein
AT2G03110.1	RNA binding;nucleic acid binding
AT3G52680.1	F-box/RNI-like/FBD-like domains-containing protein
AT5G41660.1	unknown protein
AT5G40050.1	F-box/FBD-like domains containing protein
AT4G03945.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT1G33840.1	Protein of unknown function (DUF567)
AT3G30222.1	unknown protein
AT4G08878.1	Major facilitator superfamily protein
AT1G43260.1	hAT transposon superfamily protein
AT1G17340.1	Phosphoinositide phosphatase family protein
AT1G44020.1	Cysteine/Histidine-rich C1 domain family protein
AT5G49380.1	Protein of unknown function DUF625
AT1G22980.1	unknown protein
AT3G22057.1	unknown protein
AT3G45800.1	Plant protein 1589 of unknown function
AT1G31270.1	unknown protein
AT3G43970.1	unknown protein
AT3G42723.1	aminoacyl-tRNA ligases
AT4G04957.1	FUNCTIONS IN: molecular_function unknown
AT4G05310.1	Ubiquitin-like superfamily protein
AT3G47150.1	F-box and associated interaction domains-containing protein
AT4G23090.2	unknown protein
AT3G46160.1	Protein kinase superfamily protein
AT2G20170.1	Protein of Unknown Function (DUF239)
AT2G29780.1	Galactose oxidase/kelch repeat superfamily protein
AT2G43440.1	F-box and associated interaction domains-containing protein
AT2G15340.1	glycine-rich protein
AT1G62490.1	Mitochondrial transcription termination factor family protein
AT1G67623.1	F-box family protein
AT2G07505.1	zinc ion binding
AT5G32590.1	myosin heavy chain-related
AT2G27520.1	F-box and associated interaction domains-containing protein
AT4G22050.1	Eukaryotic aspartyl protease family protein
AT2G37680.1	Vacuolar import/degradation protein Vid24
AT4G29580.2	Cytidine/deoxycytidylate deaminase family protein
AT5G43580.1	Predicted to encode a PR (pathogenesis-related) peptide
AT5G03310.1	SAUR-like auxin-responsive protein family
AT4G37530.1	Peroxidase superfamily protein
AT3G14480.1	glycine/proline-rich protein
AT4G06688.1	Molecular_function unknown
AT3G30220.1	unknown protein
AT2G19420.1	unknown protein
AT1G47350.1	F-box associated ubiquitination effector family protein

nonsense

AT3G28130.2	nodulin MtN21 /EamA-like transporter family protein
AT1G28007.1	unknown protein
AT5G32460.1	Transcriptional factor B3 family protein
AT3G58820.1	F-box/RNI-like superfamily protein
AT4G10740.1	F-box and associated interaction domains-containing protein
AT4G18280.1	glycine-rich cell wall protein-related
AT2G17180.1	C2H2-like zinc finger protein
AT2G04037.1	Protein of unknown function (DUF784)
AT1G15180.1	MATE efflux family protein
AT1G62580.1	Flavin-binding monooxygenase family protein
AT1G35320.1	unknown protein
AT5G14160.1	F-box family protein
AT3G32960.1	Domain of unknown function DUF1985
AT3G44870.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT2G33160.1	glycoside hydrolase family 28 protein
AT5G28730.1	unknown protein
AT1G43320.1	unknown protein
AT5G34581.1	hydroxyproline-rich glycoprotein family protein
AT3G03776.1	hydroxyproline-rich glycoprotein family protein
AT4G20470.1	unknown protein
AT4G08895.1	inorganic phosphate transporter family protein
AT5G18740.1	Heat shock protein, Hsp40,
AT1G15610.1	unknown protein
AT2G10020.1	unknown protein
AT1G31319.1	unknown protein
AT2G10602.1	unknown protein
AT1G09730.1	Cysteine proteinases superfamily protein
AT3G43148.1	Molecular_function unknown
AT2G25590.1	Plant Tudor-like protein
AT3G29570.1	unknown protein
AT2G40745.1	unknown protein
AT3G51570.1	Disease resistance protein (TIR-NBS-LRR class) family
AT4G20920.1	double-stranded RNA-binding domain (DsRBD)-containing protein
AT5G25410.1	Protein of Unknown Function (DUF239)
AT4G33290.1	F-box and associated interaction domains-containing protein
AT1G28180.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G35926.1	Protein with RNI-like/FBD-like domains
AT1G44130.1	Eukaryotic aspartyl protease family protein
AT1G02300.1	Cysteine proteinases superfamily protein
AT5G28160.1	Galactose oxidase/kelch repeat superfamily protein
AT1G50870.1	F-box and associated interaction domains-containing protein
AT5G48550.1	F-box associated ubiquitination effector family protein
AT4G00980.1	zinc knuckle (CCHC-type) family protein
AT2G28401.1	unknown protein
AT4G04110.1	Toll-Interleukin-Resistance (TIR) domain family protein
AT3G29375.1	XH domain-containing protein
AT4G34690.1	unknown protein
AT5G38390.1	F-box/RNI-like superfamily protein
AT5G24355.1	unknown protein
AT3G17400.1	F-box family protein
AT2G20618.1	Encodes a Plant thionin family protein
AT3G19470.1	F-box and associated interaction domains-containing protein
AT5G18730.1	Unknown function (DUF3444)
AT3G28410.1	F-box/RNI-like superfamily protein
AT4G08640.1	ATP binding
AT1G71235.1	unknown protein
AT1G60380.1	NAC domain protein
AT3G03405.1	F-box associated ubiquitination effector family protein
AT3G17560.1	F-box and associated interaction domains-containing protein
AT1G58242.1	Plant thionin family protein
AT4G08876.1	pyrophosphate--fructose-6-phosphate 1-phosphotransferase-related
AT1G13990.3	unknown protein
AT5G07060.1	CCCH-type zinc fingerfamily protein with RNA-binding domain
AT5G31412.1	hAT transposon superfamily protein
AT1G23250.1	Caleosin-related family protein

nonsense

AT3G42628.1	phosphoenolpyruvate carboxylase-related / PEP carboxylase-related
AT2G46190.1	Mitochondrial glycoprotein family protein
AT3G18150.1	RNI-like superfamily protein
AT1G43145.1	unknown protein
AT3G01360.1	Family of unknown function (DUF716)
AT4G31520.1	SDA1 family protein
AT1G59630.1	F-box associated ubiquitination effector family protein
AT5G34870.1	zinc knuckle (CCHC-type) family protein
AT1G45165.1	Expressed protein
AT2G11010.1	Molecular function unknown
AT5G59050.1	unknown protein
AT1G55950.1	DNA-binding storekeeper protein-related transcriptional regulator
AT3G11380.1	Pentatricopeptide repeat (PPR) superfamily protein
AT1G38630.1	unknown protein
AT1G32600.1	F-box associated ubiquitination effector family protein
AT2G07240.1	cysteine-type peptidases;cysteine-type peptidases
AT4G08270.1	DNA binding
AT3G30230.1	myosin heavy chain-related
AT3G24070.1	Zinc knuckle (CCHC-type) family protein
AT5G51630.1	Disease resistance protein (TIR-NBS-LRR class) family
AT4G04632.1	Protein kinase superfamily protein
AT1G15165.1	RING/FYVE/PHD zinc finger superfamily protein
AT1G31835.1	unknown protein
AT5G26848.1	unknown protein
AT1G80865.1	unknown protein
AT5G48860.1	unknown protein
AT1G20967.1	unknown protein
AT5G55800.1	Cysteine/Histidine-rich C1 domain family protein
AT1G46912.1	F-box associated ubiquitination effector family protein
AT5G29613.1	unknown protein
AT1G72060.1	serine-type endopeptidase inhibitors
AT5G35230.1	unknown protein
AT3G30770.1	Eukaryotic aspartyl protease family protein
AT1G23670.2	Domain of unknown function (DUF220)
AT2G34240.1	Protein with domains of unknown function DUF627 and DUF632
AT1G31600.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT2G13550.1	unknown protein
AT5G24250.1	unknown protein
AT5G27890.1	Myosin heavy chain-related
AT5G17180.1	unknown protein
AT2G04810.1	Protein of unknown function (DUF295)
AT3G50430.1	unknown protein
AT2G07750.1	DEA(D/H)-box RNA helicase family protein
AT1G58235.1	unknown protein
AT3G63320.1	Protein phosphatase 2C family protein
AT5G16567.1	unknown protein
AT4G09647.1	Encodes a defensin-like (DEFL) family protein
AT5G66980.1	AP2/B3-like transcriptional factor family protein
AT3G44770.1	Protein of unknown function (DUF626)
AT2G06420.1	Domain of unknown function DUF1985
AT5G41690.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT2G04060.1	glycosyl hydrolase family 35 protein
AT3G23480.2	Cyclopropane-fatty-acyl-phospholipid synthase
AT1G53366.1	unknown protein
AT5G42504.1	unknown protein
AT3G59180.1	Protein with RNI-like/FBD-like domains
AT4G08760.1	Nucleolin like 1
AT3G43480.1	zinc ion binding;nucleic acid binding
AT3G44180.1	syntaxin-related family protein
AT3G27968.1	unknown protein
AT2G05420.1	TRAF-like family protein
AT4G32990.1	Transducin/WD40 repeat-like superfamily protein
AT5G41640.1	Protein of unknown function (DUF626)
AT5G66340.1	unknown protein
AT2G04235.1	unknown protein

nonsense

AT2G36815.1	Molecular_function unknown
AT1G12700.1	ATP binding;nucleic acid binding
AT4G12382.1	F-box family protein
AT2G04066.1	MATE efflux family protein
AT1G36230.1	unknown protein
AT3G32180.1	unknown protein
AT1G47497.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT4G26730.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT5G03600.1	SGNH hydrolase-type esterase superfamily protein
AT4G01925.1	Cysteine/Histidine-rich C1 domain family protein
AT4G09870.1	F-box and associated interaction domains-containing protein
AT5G52150.1	RING/U-box superfamily protein
AT3G04660.1	F-box and associated interaction domains-containing protein
AT1G69630.1	F-box/RNI-like superfamily protein
AT2G34800.1	unknown protein
AT5G02390.1	Protein of unknown function DUF3741
AT2G29654.1	unknown protein
AT5G56690.1	FBD, F-box and Leucine Rich Repeat domains containing protein
AT2G07280.1	unknown protein
AT1G33600.1	Leucine-rich repeat (LRR) family protein
AT1G02670.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G37860.1	SPT2 chromatin protein
AT3G32904.1	unknown protein
AT3G43682.1	unknown protein
AT2G32790.1	Ubiquitin-conjugating enzyme family protein
AT5G66830.1	F-box domain protein
AT2G12900.1	Basic-leucine zipper (bZIP) transcription factor family protein
AT1G43330.1	Homeodomain-like superfamily protein
AT4G05210.1	Trimeric LpxA-like enzymes superfamily protein
AT1G24485.3	Molecular_function unknown
AT3G58340.1	TRAF-like family protein
AT4G07825.1	unknown protein
AT2G27570.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G41840.1	F-box/RNI-like superfamily protein
AT4G13760.1	Pectin lyase-like superfamily protein
AT2G12935.1	unknown protein
AT5G34828.1	Encodes a Plant thionin family protein
AT4G10370.1	Cysteine/Histidine-rich C1 domain family protein
AT1G71370.1	DEA(D/H)-box RNA helicase family protein
AT1G61500.1	S-locus lectin protein kinase family protein
AT2G43730.1	Mannose-binding lectin superfamily protein
AT2G15110.1	Protein of unknown function, DUF601
AT2G05360.1	F-box associated ubiquitination effector family protein
AT3G05450.1	Cystatin-related
AT5G28190.1	unknown protein
AT5G18065.1	unknown protein
AT5G39770.1	Represents a non-function pseudogene homologous to AtMSU81 (At4g30870).
AT5G27790.1	Protein kinase superfamily protein
AT5G02700.1	F-box/RNI-like superfamily protein
AT1G47770.1	Beta-galactosidase related protein
AT1G59865.1	unknown protein
AT3G26085.2	CAAX amino terminal protease family protein
AT3G56870.1	unknown protein
AT1G61230.1	Mannose-binding lectin superfamily protein
AT1G30020.1	Protein of unknown function
AT5G30520.1	unknown protein
AT2G17970.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT3G28990.1	Plant protein 1589 of unknown function
AT1G53370.1	F-box and associated interaction domains-containing protein
AT2G06570.1	unknown protein
AT1G32970.1	Subtilisin-like serine endopeptidase family protein
AT2G27535.1	ribosomal protein L10A family protein
AT1G11590.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT2G30430.1	unknown protein
AT2G10440.1	unknown protein

nonsense

AT3G16970.1	Plant self-incompatibility protein S1 family
AT3G22421.1	F-box and associated interaction domains-containing protein
AT3G28370.1	unknown protein
AT3G46700.1	UDP-Glycosyltransferase superfamily protein
AT4G24600.1	unknown protein
AT5G44960.1	F-box/RNI-like/FBD-like domains-containing protein
AT1G62181.1	unknown protein
AT3G17265.1	F-box and associated interaction domains-containing protein
AT1G44740.1	unknown protein
AT4G19560.1	CYCT1;2;
AT3G25900.1	HMT-1
AT4G19000.1	Homology of the IWS1 proteins found in yeast and humans.
AT3G61940.1	member of Zinc transporter (ZAT) family
AT1G22400.1	UGT85A1
AT3G56450.1	member of alpha-SNAP Gene Family
AT5G23810.1	Encodes nonfunctional amino acid transporter
AT2G31780.1	ARIADNE 11 (ARI11)
AT1G35240.1	auxin response factor 20 (ARF20)
AT3G18070.1	beta glucosidase 43 (BGLU43)
AT4G26140.1	putative beta-galactosidase
AT4G38590.2	putative beta-galactosidase (BGAL14 gene)
AT3G44910.1	member of Putative Na ⁺ /H ⁺ antiporter family
AT5G39930.1	Encodes a protein with similarity to the CLP1 polyadenylation factor.
AT4G11480.1	Encodes a cysteine-rich receptor-like protein kinase.
AT3G45860.1	Encodes a cysteine-rich receptor-like protein kinase
AT4G20240.1	putative cytochrome P450
AT5G44480.1	mutant has Altered lateral root; UDP Glucose Epimerase
AT1G79760.1	Identified as target of the AGL15 binding motif CARG.
AT5G52460.1	embryo sac development arrest 41 (EDA41)
AT5G16320.1	family member of FRI-related genes
AT4G31710.1	member of Putative ligand-gated ion channel subunit family
AT5G50770.1	Encodes a putative hydroxysteroid dehydrogenase (HSD)
AT1G51780.1	Similar to IAR3.
AT1G23420.1	Essential for formation and asymmetric growth of the ovule outer integument.
AT3G05780.1	Encodes a member of the Lon protease-like proteins
AT2G04425.1	Encodes a member of a family of small,secreted, cysteine rich protein
AT3G43160.1	maternal effect embryo arrest 38 (MEE38)
AT2G01280.1	maternal effect embryo arrest 65 (MEE65)
AT2G23570.1	Encodes a protein with similarity to SABP2
AT2G38720.1	microtubule-associated protein 65-5 (MAP65-5)
AT5G07690.1	Encodes a putative transcription factor (MYB29).
AT2G26960.1	Member of the R2R3 factor gene family
AT3G63370.1	Encodes a chloroplast RNA editing factor.
AT3G55400.1	OVULE ABORTION 1 (OVA1)
AT5G24470.1	Encodes a pseudo-response regulator
AT3G46120.1	purple acid phosphatase 19 (PAP19)
AT1G52940.1	purple acid phosphatase 5 (PAP5)
AT4G04220.1	receptor like protein 46 (RLP46)
AT1G60930.1	AtRECQ4B
AT1G05760.1	Specifically restrict the long-distance movement of tobacco etch potyvirus (TEV)
AT5G45150.1	RNAse THREE-like protein 3 (RTL3)
AT3G55660.1	Encodes a member of KPP-like gene family
AT2G05117.1	Encodes a member of a family of small, secreted, cysteine rich proteins
AT3G61350.1	Encodes an SKP1 interacting partner (SKIP4).
AT1G67770.1	Similar to terminal ear1 in Zea mays
AT4G16730.1	No functional protein at this locus in Col
AT1G43640.1	Member of TLP family
AT1G47270.1	Member of TLP family
AT5G64510.1	unknown protein
AT3G21780.1	Encodes a protein with UDP-glucosyl transferase activity
AT4G25810.1	xyloglucan endotransglycosylase-related protein (XTR6)

extended

The list of genes containing potentially extended transcripts in Ler.

Gene ID	Gene Model Description
AT5G49050.1	Function unknown
AT2G03932.1	Encodes a defensin-like (DEFL) family protein
AT3G25620.2	ABC-2 type transporter family protein
AT5G01760.1	ENTH/VHS/GAT family protein
AT3G30456.1	unknown protein
AT2G38240.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT3G49270.3	function unknown
AT3G44630.3	Disease resistance protein (TIR-NBS-LRR class) family
AT1G18940.1	Nodulin-like / Major Facilitator Superfamily protein
AT1G58037.1	Cysteine/Histidine-rich C1 domain family protein
AT5G55131.1	Encodes a defensin-like (DEFL) family protein.
AT4G13730.1	Ypt/Rab-GAP domain of gyp1p superfamily protein
AT4G25160.1	U-box domain-containing protein kinase family protein
AT1G69550.1	disease resistance protein (TIR-NBS-LRR class)
AT1G49260.1	function unknown
AT5G67290.1	FAD-dependent oxidoreductase family protein
AT3G24700.1	F-box and associated interaction domains-containing protein
AT4G34170.1	Galactose oxidase/kelch repeat superfamily protein
AT2G02550.2	PIN domain-like family protein
AT2G24880.1	Plant self-incompatibility protein S1 family
AT5G22170.1	unknown protein
AT3G26870.1	Plant self-incompatibility protein S1 family
AT1G67000.1	Protein kinase superfamily protein
AT1G33970.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G16800.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G29630.1	Cytidine/deoxycytidylate deaminase family protein
AT1G11220.1	Protein of unknown function (DUF761)
AT5G30500.1	Nucleotide-diphospho-sugar transferases superfamily protein
AT4G30040.1	Eukaryotic aspartyl protease family protein
AT2G20590.1	Reticulon family protein
AT2G39650.1	Protein of unknown function (DUF506)
AT2G09840.1	nucleic acid binding;zinc ion binding
AT1G64020.1	Serine protease inhibitor (SERPIN) family protein
AT5G35200.1	ENTH/ANTH/VHS superfamily protein
AT3G49150.1	F-box/RNI-like superfamily protein
AT1G59885.1	unknown protein
AT1G49790.2	F-box associated ubiquitination effector family protein
AT1G50190.1	Cysteine/Histidine-rich C1 domain family protein
AT3G26860.2	Plant self-incompatibility protein S1 family
AT2G20820.2	unknown protein
AT1G16825.1	Reticulon family protein
AT2G33006.1	unknown protein
AT5G54030.1	Cysteine/Histidine-rich C1 domain family protein
AT3G46140.1	Protein kinase superfamily protein
AT5G44495.1	Encodes a ECA1 gametogenesis related family protein
AT2G20784.1	unknown protein
AT1G65541.1	unknown protein
AT5G41630.1	F-box/RNI-like superfamily protein
AT4G20250.1	unknown protein
AT4G08540.1	DNA-directed RNA polymerase II protein
AT2G05915.1	unknown protein
AT4G05540.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G25570.1	Adenosylmethionine decarboxylase family protein
AT3G47250.1	Plant protein of unknown function (DUF247)
AT3G43833.1	unknown protein
AT3G33528.1	unknown protein
AT4G03566.1	unknown protein
AT1G26890.1	FBD, F-box and Leucine Rich Repeat domains containing protein
AT1G23610.1	unknown protein
AT5G48950.1	Thioesterase superfamily protein
AT5G41740.2	Disease resistance protein (TIR-NBS-LRR class) family
AT4G25300.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT1G22490.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein

extended

AT5G65158.1	Lipase/lipoxygenase, PLAT/LH2 family protein
AT4G19730.1	Glycosyl hydrolase superfamily protein
AT3G10300.3	Calcium-binding EF-hand family protein
AT2G06960.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT3G27473.1	Cysteine/Histidine-rich C1 domain family protein
AT4G19360.1	SCD6 protein-related
AT3G13780.1	SMAD/FHA domain-containing protein
AT1G48730.1	unknown protein
AT5G52480.1	RNI-like superfamily protein
AT4G10670.1	Homologous to yeast SPT16, a general chromatin factor required for transcription
AT5G37415.1	Encodes a MADS-box gene AGL105 (AGAMOUS-LIKE 105).
AT1G62700.1	Encodes a NAC-domain transcription factor. Expressed in the vascular tissue.
AT3G51860.1	cation exchanger 3 (CAX3)
AT5G37630.1	EMBRYO DEFECTIVE 2656 (EMB2656)
AT1G69820.1	Note that conflicting nomenclature exists in the literature
AT3G07770.1	HEAT SHOCK PROTEIN 89.1 (Hsp89.1)
AT3G06230.1	member of MAP Kinase Kinase
AT3G02980.1	MEIOTIC CONTROL OF CROSSOVERS1 (MCC1)
AT4G04810.1	methionine sulfoxide reductase B4 (MSRB4)
AT1G66380.1	Encodes a member of the MYB family of transcription factors
AT5G45260.1	Confers resistance to Ralstonia solanacearum.
AT3G62670.1	member of Response Regulator: B- Type
AT1G23550.1	Encodes a protein with similarity to RCD1 but without the WWE domain.
AT1G63260.1	Member of TETRASPANIN family
AT2G28520.1	Vacuolar proton ATPase subunit VHA-a isoform 1
AT1G56510.1	TIR-NB-LRR protein that confers resistance to four races of Albugo candida.

Supplemental Table 3. Unknown genes and genetic variations*.

Variation type		Known genes	Unknown genes with expression data	Unknown gene without expressed data	Total	P-value (Chi-square)
SNPs	10 or more nonsynonymous	362 (331.5)	47 (56.9)	34 (54.6)	443	0.001923
	No such change	19996 (20026.5)	3448 (3438.1)	3319 (3298.4)	26763	
	Total	20358	3495	3353	27206	
SNPs	Nonsense	210 (238.7)	23 (41.0)	86 (39.3)	319	2.13e-15
	No such change	20148 (20119.3)	3472 (3454.0)	3267 (3313.7)	26887	
	Total	20358	3495	3353	27206	
Small Indels	Frame shift	593 (632.3)	88 (108.6)	164 (104.1)	845	7.41e-10
	No such change	19765 (19725.7)	3407 (3386.4)	3189 (3248.9)	26361	
	Total	20358	3495	3353	27206	
Small Indels	Nonframe shift	361 (345.7)	64 (59.4)	37 (56.9)	462	0.0169
	No such change	19997 (20012.3)	3431 (3435.6)	3316 (3296.1)	26744	
	Total	20358	3495	3353	27206	
Large Indels	Large indel	198 (236.5)	25 (40.6)	93 (38.9)	316	< 2.2e-16
	No such change	20160 (20121.5)	3470 (3454.4)	3260 (3314.1)	26890	
	Total	20358	3495	3353	27206	
All	All variation combined	1540 (1624.5)	231 (278.9)	400 (267.6)	2171	< 2.2e-16
	No such change	18818 (18733.5)	3264 (3216.1)	2953 (3085.4)	25035	
	Total	20358	3495	3353	27206	

* The numbers in brackets are the expected ones. The numbers above the brackets are the observed ones.

Supplemental Table 4. Expression of genes with 10 or more nonsynonymous mutation and genes with nonsense mutation based on plant ontology*.

Mutation type	Plant ontology categories		Genes with mutation	Genes without mutation	P value
10 or more nonsynonymous mutation	Growth stage	L mature pollen stage	22	3878	0.00022
		M germinated pollen stage	32	4557	0.0028
		petal differentiation and expansion stage	223	16298	0.014
		Seedling growth	3	884	0.017
	Structure component	Egg cell	6	166	0.016
		Guard cell	7	1811	0.00063
		Male gametophyte	111	12551	0.0026
		Pollen tube	31	4809	0.00036
Nonsense mutation	Growth stage	petal differentiation and expansion stage	78	16443	0.017
	Structure component	flower	79	16611	0.021
		Sperm cell	35	5380	0.0015

*PO categories with less than 3 mutated genes are not included.

Supplemental Table 5. The list of 50 genes with dN/dS >1.

Gene ID	dN/dS under different Codon Model				Annotation
	0	1	2	3	
AT1G10090.1	1.562	999	75.9	999	PRLI-interacting factor, putative
AT2G04810.1	999	999	999	999	Leucine-rich repeat protein kinase family protein
AT2G12900.1	999	999	999	3.47	Cysteine/Histidine-rich C1 domain family protein
AT2G13690.1	180.3	120.4	5	68.1	Disease resistance protein (TIR-NBS-LRR class) family
AT2G16650.1	999	999	999	999	Pentatricopeptide repeat (PPR) superfamily protein
AT2G17600.1	999	999	999	999	Mannose-binding lectin superfamily protein
AT2G18570.1	999	999	999	1.06	NHL domain-containing protein
AT1G23880.1	999	999	999	999	Putative endonuclease or glycosyl hydrolase
AT2G39580.1	999	999	999	999	UDP-Glycosyltransferase superfamily protein
AT2G42480.1	999	999	293	999	Pentatricopeptide repeat (PPR) superfamily protein
AT3G07250.1	373.8	999	70.4	999	Putative zinc-finger domain (InterPro:IPR019607)
AT3G23120.1	129.4	999	949	999	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G23370.1	999	999	999	999	Cysteine/Histidine-rich C1 domain family protein
AT3G25970.1	2.334	999	999	1.63	Protein kinase superfamily protein
AT3G26150.1	999	999	999	999	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G29830.1	999	999	999	999	Basic-leucine zipper (bZIP) transcription factor family protein
AT1G27720.1	6.534	3.861	999	1.08	TRAF-like family protein
AT3G44400.1	1.084	999	999	1.17	Molecular_function unknown
AT3G45670.1	999	36.3	26.4	748	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT3G45750.1	999	999	887	73.9	F-box/FBD-like domains containing protein
AT3G48090.1	3.448	660.5	999	768	unknown protein
AT3G56550.1	1.04	1.841	1.84	999	Early-responsive to dehydration stress protein (ERD4)
AT4G05497.1	999	999	999	999	Pentatricopeptide repeat (PPR) superfamily protein
AT4G09780.1	999	999	999	999	ATP binding
AT4G11460.1	999	999	999	999	RNI-like superfamily protein
AT4G11580.1	1.438	1.941	999	999	Exostosin family protein
AT4G19020.1	146	76.67	55.5	999	Nucleotidyltransferase family protein
AT4G19560.1	1.689	6.252	4.1	2.44	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein
AT4G21820.1	1.975	2.165	15.3	627	binding;calmodulin binding
AT4G28811.1	14.34	2.298	999	1.39	Disease resistance protein (TIR-NBS-LRR class) family
AT5G15980.1	999	999	438	1.08	TRAF-like family protein
AT5G17730.1	113.8	999	999	999	RNI-like superfamily protein
AT5G18770.1	5.274	5.575	6.58	999	F-box/RNI-like superfamily protein
AT5G28823.1	999	999	999	999	Protein of unknown function (DUF295)
AT5G39770.1	1.49	1.993	999	999	Represents a non-function pseudogene homologous to AtMSU81 (At4g30870).
AT5G40170.1	281.3	60.02	162	999	CYCT1;2
AT5G41250.1	999	999	999	999	RPA70C
AT5G41750.1	999	999	999	1.03	chromomethylase 2 (CMT2)
AT5G43090.1	1.852	3.998	1.06	1.07	Encodes a cysteine-rich receptor-like protein kinase.
AT5G45150.1	2.028	21.89	999	999	putative cytochrome P450
AT5G45400.1	17.77	999	953	999	Component of R gene-mediated disease resistance with homology to eukaryotic lipases.
AT5G59090.1	8.373	999	999	999	proteinaceous RNase P 2 (PRORP2)
AT5G64710.1	1.016	1.001	2.57	999	a member of the Arabidopsis Pumilio (APUM) proteins containing PUF domain
AT1G55430.1	999	999	999	1.71	receptor like protein 38 (RLP38)
AT1G57650.1	1.285	3.585	2.27	1.88	receptor like protein 54 (RLP54)
AT1G61120.1	999	999	574	276	RNase THREE-like protein 3 (RTL3)
AT1G61230.1	999	999	999	999	subtilase 4.12 (SBT4.12)
AT1G64210.1	2.883	83.74	170	23.9	TBP-associated factor 4B (TAF4B)
AT1G66235.1	999	1.022	48.8	2.37	a geranylinalool synthase that produces a precursor to TMTT, a volatile plant defense C16-homoterpene
AT1G66550.1	1.122	999	789	999	member of WRKY Transcription Factor

Supplemental Table 6. The lists of genes affected by frameshift and nonframeshift small indels.

frameshift

genes affected by frameshift small indels

Gene ID	Gene Model Description
AT5G05720.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G28958.1	Cupredoxin superfamily protein
AT3G59750.1	Concanavalin A-like lectin protein kinase family protein
AT3G29630.1	UDP-Glycosyltransferase superfamily protein
AT1G18940.1	Nodulin-like / Major Facilitator Superfamily protein
AT3G45820.1	unknown protein
AT5G52850.1	Pentatricopeptide repeat (PPR) superfamily protein
AT4G09090.1	Carbohydrate-binding X8 domain superfamily protein
AT1G51990.1	O-methyltransferase family protein
AT3G29050.1	receptor-like protein kinase-related
AT3G27906.1	unknown protein
AT4G24300.1	Peptidase C50, separase
AT1G16220.1	Protein phosphatase 2C family protein
AT2G40955.1	unknown protein
AT2G14800.1	unknown protein
AT5G32613.1	Zinc knuckle (CCHC-type) family protein
AT5G09430.1	alpha/beta-Hydrolases superfamily protein
AT5G39910.1	Pectin lyase-like superfamily protein
AT4G08406.1	unknown protein
AT5G28440.1	unknown protein
AT2G19940.1	oxidoreductases, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;copper ion binding
AT3G18530.1	ARM repeat superfamily protein
AT4G16045.1	TRAF-like superfamily protein
AT4G27360.1	Dynein light chain type 1 family protein
AT4G02000.1	unknown protein
AT3G19515.2	unknown protein
AT4G22280.1	F-box/RNI-like superfamily protein
AT5G03830.1	CDK inhibitor P21 binding protein
AT1G51830.1	Leucine-rich repeat protein kinase family protein
AT3G11325.1	Phospholipid/glycerol acyltransferase family protein
AT5G62580.1	ARM repeat superfamily protein
AT5G63820.1	Protein of unknown function (DUF626)
AT2G22942.1	growth factors
AT1G24480.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT5G60430.1	drug transmembrane transporters;antiporters
AT4G08878.1	Major facilitator superfamily protein
AT4G15070.1	Cysteine/Histidine-rich C1 domain family protein
AT3G09620.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G35200.1	ENTH/ANTH/VHS superfamily protein
AT1G73510.1	unknown protein
AT2G20970.2	unknown protein
AT2G29910.1	F-box/RNI-like superfamily protein
AT3G61560.2	Reticulon family protein
AT1G27870.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT3G45800.1	Plant protein 1589 of unknown function
AT1G79390.1	unknown protein
AT1G67270.1	Zinc-finger domain of monoamine-oxidase A repressor R1 protein
AT3G24580.1	F-box and associated interaction domains-containing protein
AT2G02440.1	unknown protein
AT3G43970.1	unknown protein

frameshift

AT3G42723.1	aminoacyl-tRNA ligases;ATP binding;nucleotide binding
AT5G46915.1	transcriptional factor B3 family protein
AT1G09300.1	Metallopeptidase M24 family protein
AT5G28070.1	unknown protein
AT1G20570.1	Spc97 / Spc98 family of spindle pole body (SBP) component
AT4G05540.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G47915.1	F-box family protein
AT4G10210.1	Protein of Unknown Function (DUF239)
AT3G52980.1	Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein
AT3G59840.1	unknown protein
AT5G48175.1	unknown protein
AT3G23955.2	F-box family protein
AT3G43490.1	Zinc knuckle (CCHC-type) family protein
AT1G27385.4	unknown protein
AT1G78470.1	unknown protein
AT5G07570.1	glycine/proline-rich protein
AT1G52270.1	unknown protein
AT3G46901.1	unknown protein
AT4G29580.2	Cytidine/deoxycytidylate deaminase family protein
AT1G36078.1	unknown protein
AT5G38260.1	Protein kinase superfamily protein
AT2G24870.1	Plant self-incompatibility protein S1 family
AT5G03495.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT5G10590.1	unknown protein
AT1G47350.1	F-box associated ubiquitination effector family protein
AT3G46910.1	Cullin family protein
AT2G19920.1	RNA-dependent RNA polymerase family protein
AT2G07200.1	Cysteine proteinases superfamily protein
AT4G14305.1	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
AT4G28590.1	unknown protein
AT1G32660.1	F-box and associated interaction domains-containing protein
AT1G44030.1	Cysteine/Histidine-rich C1 domain family protein
AT1G17710.1	Pyridoxal phosphate phosphatase-related protein
AT5G38850.1	Disease resistance protein (TIR-NBS-LRR class)
AT2G15770.1	Cupredoxin superfamily protein
AT2G04675.1	unknown protein
AT4G25410.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT3G13630.1	unknown protein
AT3G27610.2	Nucleotidyl transferase superfamily protein
AT2G25640.1	SPOC domain / Transcription elongation factor S-II protein
AT4G33600.1	unknown protein
AT3G53050.1	D-galactoside/L-rhamnose binding SUEL lectin protein
AT5G14160.1	F-box family protein
AT4G15056.1	unknown protein
AT1G80960.2	F-box and Leucine Rich Repeat domains containing protein
AT3G13700.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G11773.2	Thioredoxin superfamily protein
AT1G56520.2	Disease resistance protein (TIR-NBS-LRR class) family
AT4G35170.1	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT1G66610.1	TRAF-like superfamily protein
AT5G10620.1	methyltransferases
AT1G63350.1	Disease resistance protein (CC-NBS-LRR class) family

frameshift

AT4G15970.1	Nucleotide-diphospho-sugar transferase family protein
AT5G51730.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT2G10602.1	unknown protein
AT4G13180.1	NAD(P)-binding Rossmann-fold superfamily protein
AT3G43148.1	unknown protein
AT2G04020.1	GDSL-like Lipase/Acylhydrolase superfamily protein
AT3G63510.1	FMN-linked oxidoreductases superfamily protein
AT5G43530.1	Helicase protein with RING/U-box domain
AT1G78450.1	SOUL heme-binding family protein
AT1G49150.1	unknown protein
AT2G10550.1	unknown protein
AT2G06541.1	TTF-type zinc finger protein with HAT dimerisation domain
AT2G35580.1	Serine protease inhibitor (SERPIN) family protein
AT1G20790.1	F-box family protein
AT3G44760.1	unknown protein
AT3G59250.1	F-box/RNI-like superfamily protein
AT5G13380.1	Auxin-responsive GH3 family protein
AT4G22650.1	unknown protein
AT5G57570.1	GCK domain-containing protein
AT3G44850.1	Protein kinase superfamily protein
AT5G53780.1	Protein of unknown function (DUF295)
AT3G05520.2	Subunits of heterodimeric actin filament capping protein Capz superfamily
AT5G55010.1	unknown protein
AT5G32619.1	Defensin-like (DEFL) family protein
AT3G14452.1	unknown protein
AT5G48550.1	F-box associated ubiquitination effector family protein
AT5G10830.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G23270.1	unknown protein
AT1G30930.1	F-box family protein
AT4G35335.1	Nucleotide-sugar transporter family protein
AT4G16960.1	Disease resistance protein (TIR-NBS-LRR class) family
AT1G52180.1	Aquaporin-like superfamily protein
AT1G33940.1	unknown protein
AT2G03010.1	Family of unknown function (DUF577)
AT3G43950.1	Protein kinase superfamily protein
AT3G29796.1	unknown protein
AT3G28680.1	Serine carboxypeptidase S28 family protein
AT4G02850.1	phenazine biosynthesis PhzC/PhzF family protein
AT5G11400.2	Protein kinase superfamily protein
AT5G03250.1	Phototropic-responsive NPH3 family protein
AT4G03940.1	unknown protein
AT1G05780.1	Vacuolar ATPase assembly integral membrane protein VMA21-like domain
AT1G09400.1	FMN-linked oxidoreductases superfamily protein
AT3G57460.1	catalytics;metal ion binding
AT2G02498.1	unknown protein
AT1G32030.1	Domain of unknown function (DUF313)
AT1G22520.2	Domain of unknown function (DUF543)
AT3G30540.1	Glycosyl hydrolase superfamily protein
AT1G19470.1	Galactose oxidase/kelch repeat superfamily protein
AT5G35810.1	Ankyrin repeat family protein
AT5G04050.2	RNA-directed DNA polymerase (reverse transcriptase)
AT1G71235.1	unknown protein
AT1G60380.1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein

frameshift

AT4G02650.1	ENTH/ANTH/VHS superfamily protein
AT4G12850.1	Far-red impaired responsive (FAR1) family protein
AT5G36001.1	RING/U-box superfamily protein
AT4G15765.1	FAD/NAD(P)-binding oxidoreductase family protein
AT2G43930.1	Protein kinase superfamily protein
AT1G59453.1	B-block binding subunit of TFIIIC
AT1G22080.1	Cysteine proteinases superfamily protein
AT3G48770.1	DNA binding;ATP binding
AT5G35300.1	unknown protein
AT5G46873.1	Defensin-like (DEFL) family protein
AT4G10650.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G10695.1	CDC68-related
AT1G20730.1	Protein of unknown function (DUF833)
AT1G61400.1	S-locus lectin protein kinase family protein
AT5G36930.2	Disease resistance protein (TIR-NBS-LRR class) family
AT5G02950.1	Tudor/PWWP/MBT superfamily protein
AT3G62400.2	unknown protein
AT5G05430.1	RNA-binding protein
AT2G02870.1	Galactose oxidase/kelch repeat superfamily protein
AT2G46190.1	Mitochondrial glycoprotein family protein
AT1G52650.1	F-box/RNI-like superfamily protein
AT5G13940.1	aminopeptidases
AT5G35960.1	Protein kinase family protein
AT1G59630.1	F-box associated ubiquitination effector family protein
AT1G26762.1	unknown protein
AT4G05380.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G10500.1	Kinase interacting (KIP1-like) family protein
AT1G67880.1	beta-1,4-N-acetylglucosaminyltransferase family protein
AT5G48110.1	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT2G25530.1	AFG1-like ATPase family protein
AT2G13640.1	Transcription factor IIS family protein
AT4G34170.1	Galactose oxidase/kelch repeat superfamily protein
AT2G27505.1	FBD-like domain family protein
AT1G73200.1	Putative integral membrane protein conserved region (DUF2404)
AT4G16162.1	Leucine-rich repeat (LRR) family protein
AT3G43880.1	unknown protein
AT5G17730.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G52930.1	Protein of unknown function (DUF295)
AT1G79920.1	Heat shock protein 70 (Hsp 70) family protein
AT1G11460.1	nodulin MtN21 /EamA-like transporter family protein
AT2G31700.1	unknown protein
AT5G63340.1	unknown protein
AT3G54910.1	RNI-like superfamily protein
AT4G00070.1	RING/U-box superfamily protein
AT1G24230.1	Paired amphipathic helix (PAH2) superfamily protein
AT2G45870.1	Bestrophin-like protein
AT1G57650.1	ATP binding
AT5G41290.1	Receptor-like protein kinase-related family protein
AT1G12190.1	F-box and associated interaction domains-containing protein
AT1G46912.1	F-box associated ubiquitination effector family protein
AT3G52530.1	Protein kinase superfamily protein
AT3G05770.1	unknown protein
AT2G13550.1	unknown protein

frameshift

AT3G01325.1	Expressed protein
AT5G55150.1	Protein of unknown function (DUF295)
AT3G31350.1	unknown protein
AT1G19410.1	FBD / Leucine Rich Repeat domains containing protein
AT4G30380.1	Barwin-related endoglucanase
AT1G55440.1	Cysteine/Histidine-rich C1 domain family protein
AT1G45100.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G25510.1	disease resistance protein (TIR-NBS-LRR class), putative
AT5G37610.1	Eukaryotic porin family protein
AT1G47765.1	F-box and associated interaction domains-containing protein
AT1G19040.1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AT4G33565.1	RING/U-box superfamily protein
AT5G51090.1	unknown protein
AT1G05085.1	unknown protein
AT5G50940.1	RNA-binding KH domain-containing protein
AT4G11670.1	Protein of unknown function (DUF810)
AT2G34270.1	unknown protein
AT5G38540.1	Mannose-binding lectin superfamily protein
AT3G48290.2	cytochrome P450, family 71, subfamily A, polypeptide 24
AT5G57340.2	unknown protein
AT1G69030.1	BSD domain-containing protein
AT4G32030.1	unknown protein
AT3G29690.1	HXXXD-type acyl-transferase family protein
AT1G20290.1	SWI-SNF-related chromatin binding protein
AT3G43480.1	unknown protein
AT5G41765.1	DNA-binding storekeeper protein-related transcriptional regulator
AT4G34300.1	Cupredoxin superfamily protein
AT4G25710.1	Galactose oxidase/kelch repeat superfamily protein
AT2G06555.1	unknown protein
AT5G42170.1	SGNH hydrolase-type esterase superfamily protein
AT3G48620.1	Outer membrane OMP85 family protein
AT3G45443.1	unknown protein
AT5G62780.1	Chaperone DnaJ-domain superfamily protein
AT2G46200.1	unknown protein
AT1G23070.1	Protein of unknown function (DUF300)
AT1G36230.1	unknown protein
AT2G24950.1	Protein of Unknown Function (DUF239)
AT5G09720.1	Magnesium transporter CorA-like family protein
AT1G09260.1	Chaperone DnaJ-domain superfamily protein
AT4G02110.1	transcription coactivators
AT4G14368.1	Regulator of chromosome condensation (RCC1) family protein
AT1G31090.1	F-box family protein
AT5G50930.1	Histone superfamily protein
AT3G04190.1	RmlC-like cupins superfamily protein
AT1G28305.1	Plant self-incompatibility protein S1 family
AT5G56470.1	FAD-dependent oxidoreductase family protein
AT3G44240.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT2G05330.1	BTB/POZ domain-containing protein
AT4G12920.1	Eukaryotic aspartyl protease family protein
AT3G04660.1	F-box and associated interaction domains-containing protein
AT5G46010.1	Homeodomain-like superfamily protein
AT4G35680.1	Arabidopsis protein of unknown function (DUF241)
AT5G05020.1	Pollen Ole e 1 allergen and extensin family protein

frameshift

AT3G13760.1	Cysteine/Histidine-rich C1 domain family protein
AT4G16900.1	Disease resistance protein (TIR-NBS-LRR class) family
AT1G60970.1	SNARE-like superfamily protein
AT1G42700.1	unknown protein
AT1G12730.1	GPI transamidase subunit PIG-U
AT1G36100.1	myosin heavy chain-related
AT5G16280.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G32300.1	D-arabinono-1,4-lactone oxidase family protein
AT4G10200.1	TTF-type zinc finger protein with HAT dimerisation domain
AT1G08530.1	unknown protein
AT5G17720.1	alpha/beta-Hydrolases superfamily protein
AT5G37170.1	O-methyltransferase family protein
AT5G17130.1	cysteine-type peptidases
AT4G18840.1	Pentatricopeptide repeat (PPR-like) superfamily protein
AT2G19150.1	Pectin lyase-like superfamily protein
AT1G36925.1	unknown protein
AT5G48700.1	Ubiquitin-like superfamily protein
AT3G24890.2	vesicle-associated membrane protein 728
AT5G58820.1	Subtilisin-like serine endopeptidase family protein
AT5G28823.1	unknown protein
AT4G23370.1	unknown protein
AT4G15975.1	RING/U-box superfamily protein
AT1G57850.1	Toll-Interleukin-Resistance (TIR) domain family protein
AT2G27570.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G18870.1	E2F/DP family winged-helix DNA-binding domain
AT4G22170.1	F-box family protein with a domain of unknown function (DUF295)
AT3G56770.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G21920.1	unknown protein
AT2G44260.2	Plant protein of unknown function (DUF946)
AT1G54020.2	GDSL-like Lipase/Acylhydrolase superfamily protein
AT5G04885.1	Glycosyl hydrolase family protein
AT1G71370.1	DEA(D/H)-box RNA helicase family protein
AT3G66652.1	fip1 motif-containing protein
AT2G15110.1	Protein of unknown function, DUF601
AT3G45690.1	Major facilitator superfamily protein
AT1G70450.1	Protein kinase superfamily protein
AT1G30972.1	Plant thionin family protein
AT2G23230.1	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT5G39770.1	Restriction endonuclease, type II-like superfamily protein
AT1G26530.1	PIN domain-like family protein
AT3G22180.1	DHHC-type zinc finger family protein
AT4G20480.1	Putative endonuclease or glycosyl hydrolase
AT3G45910.1	unknown protein
AT1G61190.1	LRR and NB-ARC domains-containing disease resistance protein
AT1G65190.1	Protein kinase superfamily protein
AT3G28060.1	Nodulin MtN21 /EamA-like transporter family protein
AT1G06810.1	unknown protein
AT1G34560.1	Protein of unknown function (DUF1184)
AT4G17850.1	unknown protein
AT5G54030.1	Cysteine/Histidine-rich C1 domain family protein
AT2G26610.1	Transducin family protein / WD-40 repeat family protein
AT3G17320.1	F-box and associated interaction domains-containing protein
AT1G30020.1	Protein of unknown function, DUF538

frameshift

AT2G44210.2	Protein of Unknown Function (DUF239)
AT3G32030.1	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT2G06570.1	unknown protein
AT1G14270.1	CAAX amino terminal protease family protein
AT3G32920.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G38750.1	asparaginyl-tRNA synthetase family
AT1G32970.1	Subtilisin-like serine endopeptidase family protein
AT1G66540.1	Cytochrome P450 superfamily protein
AT5G38040.1	UDP-Glycosyltransferase superfamily protein
AT2G01780.1	Curculin-like (mannose-binding) lectin family protein
AT5G52770.1	Copper transport protein family
AT4G05040.1	ankyrin repeat family protein
AT3G48830.1	polynucleotide adenyllyltransferase family protein / RNA recognition motif (RRM)-containing protein
AT5G17750.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT2G11570.1	unknown protein
AT1G43665.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT2G05970.1	F-box family protein with a domain of unknown function (DUF295)
AT4G25300.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT3G21410.1	F-box and associated interaction domains-containing protein
AT2G34290.1	Protein kinase superfamily protein
AT3G10845.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G35560.1	TCP family transcription factor
AT4G39745.1	hydroxyproline-rich glycoprotein family protein
AT3G13677.1	unknown protein
AT1G33480.1	RING/U-box superfamily protein
AT1G05220.1	Transmembrane protein 97, predicted
AT4G01740.1	Cysteine/Histidine-rich C1 domain family protein
AT5G28590.1	DNA-binding family protein
AT1G59675.1	F-box family protein
AT4G07990.1	Chaperone DnaJ-domain superfamily protein
AT3G29255.1	catalytics;intramolecular transferases
AT2G17940.1	Plant protein of unknown function (DUF827)
AT4G28000.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G01450.1	Protein kinase superfamily protein
AT2G13150.1	Basic-leucine zipper (bZIP) transcription factor family protein
AT3G22961.1	Paired amphipathic helix (PAH2) superfamily protein
AT1G47800.1	F-box and associated interaction domains-containing protein
AT1G15680.1	F-box family protein
AT5G45460.1	unknown protein
AT1G27160.1	valyl-tRNA synthetase / valine--tRNA ligase-related
AT5G08080.3	syntaxin of plants 132
AT1G66640.1	RNI-like superfamily protein
AT5G03020.1	Galactose oxidase/kelch repeat superfamily protein
AT2G47690.1	NADH-ubiquinone oxidoreductase-related
AT5G23480.1	SWIB/MDM2 domain;Plus-3;GYF
AT1G76830.1	F-box and associated interaction domains-containing protein
AT2G05120.1	Nucleoporin, Nup133/Nup155-like
AT1G67130.1	F-box family protein
AT1G31510.1	F-box associated ubiquitination effector family protein
AT5G44520.1	NagB/RpiA/CoA transferase-like superfamily protein
AT1G52330.2	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family

frameshift

AT1G47390.1	F-box and associated interaction domains-containing protein
AT1G73050.1	Glucose-methanol-choline (GMC) oxidoreductase family protein
AT2G26810.1	Putative methyltransferase family protein
AT4G17700.1	unknown protein
AT4G04880.1	adenosine/AMP deaminase family protein
AT2G27320.1	Protein of Unknown Function (DUF239)
AT5G43730.1	Disease resistance protein (CC-NBS-LRR class) family
AT5G22180.1	unknown protein
AT2G25150.1	HXXXD-type acyl-transferase family protein
AT4G08430.1	Ulp1 protease family protein
AT4G19090.1	Protein of unknown function (DUF594)
AT1G27135.1	Maternally expressed gene (MEG) family protein
AT4G32970.1	unknown protein
AT2G42510.2	unknown protein
AT5G17740.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G27606.1	unknown protein
AT4G26170.1	unknown protein
AT2G36540.1	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AT3G28810.1	Protein of unknown function (DUF1216)
AT4G09012.1	Mitochondrial ribosomal protein L27
AT4G15140.1	unknown protein
AT4G05240.1	Ubiquitin-like superfamily protein
AT3G10180.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G14890.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT3G28870.1	unknown protein
AT5G20810.2	SAUR-like auxin-responsive protein family
AT1G61160.1	unknown protein
AT4G18540.1	unknown protein
AT1G20680.1	Protein of unknown function (DUF833)
AT1G44020.1	Cysteine/Histidine-rich C1 domain family protein
AT4G13620.1	Integrase-type DNA-binding superfamily protein
AT5G17950.1	unknown protein
AT1G77270.1	unknown protein
AT4G25920.1	Protein of unknown function (DUF295)
AT3G47150.1	F-box and associated interaction domains-containing protein
AT2G43440.1	F-box and associated interaction domains-containing protein
AT1G51810.1	Leucine-rich repeat protein kinase family protein
AT1G50340.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT4G30970.1	unknown protein
AT2G30925.1	unknown protein
AT2G15910.1	CSL zinc finger domain-containing protein
AT1G62270.1	F-box and associated interaction domains-containing protein
AT5G62660.1	F-box and associated interaction domains-containing protein
AT2G36920.1	unknown protein
AT1G29740.1	Leucine-rich repeat transmembrane protein kinase
AT3G44980.1	unknown protein
AT2G13430.1	unknown protein
AT1G61430.1	S-locus lectin protein kinase family protein
AT5G44940.1	F-box/RNI-like superfamily protein
AT3G27910.1	Galactose oxidase/kelch repeat superfamily protein
AT2G08986.1	unknown protein
AT5G65420.3	CYCLIN D4;1
AT5G23870.3	Pectinacetylesterase family protein

frameshift

AT5G48205.1	zinc ion binding
AT1G77650.1	F-box associated ubiquitination effector family protein
AT4G10740.1	F-box and associated interaction domains-containing protein
AT3G45760.1	Nucleotidyltransferase family protein
AT4G40100.1	GRAM domain family protein
AT4G11590.1	F-box associated ubiquitination effector family protein
AT1G30974.1	Plant thionin family protein
AT5G46720.1	ALG2-like (avirulence induced gene) family protein
AT1G67470.1	Protein kinase superfamily protein
AT3G09110.1	Protein of unknown function (DUF674)
AT5G48200.1	unknown protein
AT5G06040.1	self-incompatibility protein-related
AT5G03350.1	Legume lectin family protein
AT3G43170.1	unknown protein
AT1G03495.1	HXXXD-type acyl-transferase family protein
AT4G16970.1	Protein kinase superfamily protein
AT2G09970.1	Protein of unknown function (DUF1677)
AT1G43980.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G15360.1	unknown protein
AT5G40595.1	unknown protein
AT1G50980.1	F-box/RNI-like/FBD-like domains-containing protein
AT4G14272.1	Defensin-like (DEFL) family protein
AT1G20490.1	AMP-dependent synthetase and ligase family protein
AT4G18300.1	Trimeric LpxA-like enzyme
AT4G09965.1	unknown protein
AT2G44400.1	Cysteine/Histidine-rich C1 domain family protein
AT5G14140.1	zinc ion binding;nucleic acid binding;zinc ion binding
AT3G23325.1	Splicing factor 3B subunit 5/RDS3 complex subunit 10
AT2G18938.1	unknown protein
AT1G74620.1	RING/U-box superfamily protein
AT1G63860.1	Disease resistance protein (TIR-NBS-LRR class) family
AT3G49340.1	Cysteine proteinases superfamily protein
AT1G59722.1	unknown protein
AT1G47389.1	unknown protein
AT5G52870.1	unknown protein
AT3G49970.1	Phototropic-responsive NPH3 family protein
AT2G13950.1	Cysteine/Histidine-rich C1 domain family protein
AT4G15820.1	unknown protein
AT5G18040.1	unknown protein
AT3G16600.1	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related
AT2G30680.1	unknown protein
AT2G47570.1	Ribosomal protein L18e/L15 superfamily protein
AT2G18070.1	unknown protein
AT5G37920.1	Family of unknown function (DUF577)
AT1G43722.1	unknown protein
AT3G29375.1	XH domain-containing protein
AT3G14140.1	2-oxoglutarate-dependent dioxygenase family protein
AT5G37760.1	Chaperone DnaJ-domain superfamily protein
AT1G40083.1	unknown protein
AT5G21125.1	unknown protein
AT1G57580.1	F-box family protein
AT4G05136.1	unknown protein

frameshift

AT4G12334.1	Cytochrome P450 superfamily protein
AT5G55750.1	hydroxyproline-rich glycoprotein family protein
AT3G29195.1	unknown protein
AT4G26920.1	START (StAR-related lipid-transfer) lipid-binding domain
AT1G10990.2	unknown protein
AT1G27550.1	F-box family protein
AT5G46115.1	unknown protein
AT3G17140.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT5G48950.1	Thioesterase superfamily protein
AT5G18730.1	unknown protein
AT3G30380.1	alpha/beta-Hydrolases superfamily protein
AT3G22030.1	Receptor protein kinase-related
AT4G05018.1	unknown protein
AT3G23633.1	F-box associated ubiquitination effector family protein
AT4G03220.1	Protein with RNI-like/FBD-like domains
AT5G37150.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G30235.1	General transcription factor 2-related zinc finger protein
AT1G20800.1	F-box family protein
AT2G34185.2	unknown protein
AT2G37730.1	Protein of unknown function (DUF604)
AT5G25230.1	Ribosomal protein S5/Elongation factor G/III/V family protein
AT1G72840.2	Disease resistance protein (TIR-NBS-LRR class)
AT5G39580.1	Peroxidase superfamily protein
AT2G11626.1	unknown protein
AT5G31412.1	hAT transposon superfamily protein
AT4G11540.1	Cysteine/Histidine-rich C1 domain family protein
AT3G49440.1	F-box associated ubiquitination effector family protein
AT5G44680.1	DNA glycosylase superfamily protein
AT3G27490.1	Cysteine/Histidine-rich C1 domain family protein
AT3G44090.1	F-box family protein
AT1G11070.1	unknown protein
AT4G19910.1	Toll-Interleukin-Resistance (TIR) domain family protein
AT3G48630.1	unknown protein
AT5G01150.1	Protein of unknown function (DUF674)
AT2G27410.1	Domain of unknown function (DUF313)
AT4G29970.1	F-box and associated interaction domains-containing protein
AT4G08370.1	Proline-rich extensin-like family protein
AT5G52940.1	Protein of unknown function (DUF295)
AT4G33355.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G02410.1	DIE2/ALG10 family
AT2G11010.1	unknown protein
AT3G46650.1	UDP-Glycosyltransferase superfamily protein
AT2G32470.1	F-box associated ubiquitination effector family protein
AT3G09120.1	Protein of unknown function (DUF674)
AT2G02550.2	PIN domain-like family protein
AT3G10195.1	Putative membrane lipoprotein
AT3G11380.1	Pentatricopeptide repeat (PPR) superfamily protein
AT3G26020.4	Protein phosphatase 2A regulatory B subunit family protein
AT4G17565.1	F-box family protein with a domain of unknown function (DUF295)
AT1G32600.1	F-box associated ubiquitination effector family protein
AT2G07240.1	cysteine-type peptidases;cysteine-type peptidases
AT3G30230.1	myosin heavy chain-related

frameshift

AT3G44710.1	Plant protein of unknown function (DUF247)
AT3G11160.1	unknown protein
AT4G31690.1	Transcriptional factor B3 family protein
AT4G16150.1	calmodulin binding;transcription regulators
AT5G47260.1	ATP binding;GTP binding;nucleotide binding;nucleoside-triphosphatases
AT3G47130.1	F-box associated ubiquitination effector family protein
AT5G33406.1	hAT dimerisation domain-containing protein / transposase-related
AT5G22140.1	FAD/NAD(P)-binding oxidoreductase family protein
AT1G31835.1	unknown protein
AT4G14103.2	F-box/RNI-like superfamily protein
AT1G22290.2	14-3-3 family protein
AT3G27420.1	unknown protein
AT4G35295.1	homoserine kinase, putative / HSK, putative
AT5G45573.1	unknown protein
AT1G49450.1	Transducin/WD40 repeat-like superfamily protein
AT1G49180.1	protein kinase family protein
AT5G35050.1	Domain of unknown function (DUF1985)
AT3G29750.1	Eukaryotic aspartyl protease family protein
AT1G36580.1	unknown protein
AT5G24250.1	unknown protein
AT4G08800.1	Protein kinase superfamily protein
AT5G43480.1	unknown protein
AT1G47900.1	Plant protein of unknown function (DUF869)
AT4G05150.1	Octicosapeptide/Phox/Bem1p family protein
AT2G07750.1	DEA(D/H)-box RNA helicase family protein
AT5G01480.1	Cysteine/Histidine-rich C1 domain family protein
AT5G64390.3	RNA-binding KH domain-containing protein
AT5G49500.1	Signal recognition particle, SRP54 subunit protein
AT5G23770.2	DOMAIN OF UNKNOWN FUNCTION 724 8
AT4G03740.1	unknown protein
AT1G21730.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G06639.1	unknown protein
AT4G16230.1	GDSL-like Lipase/Acylhydrolase superfamily protein
AT5G05750.1	DNAJ heat shock N-terminal domain-containing protein
AT5G60310.1	Concanavalin A-like lectin protein kinase family protein
AT3G23480.2	Cyclopropane-fatty-acyl-phospholipid synthase
AT1G30780.1	F-box associated ubiquitination effector family protein
AT2G18200.1	unknown protein
AT1G51900.1	Regulator of Vps4 activity in the MVB pathway protein
AT1G64470.1	Ubiquitin-like superfamily protein
AT1G52415.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT1G72120.1	Major facilitator superfamily protein
AT2G38780.1	unknown protein
AT5G19170.1	Protein of Unknown Function (DUF239)
AT1G19260.1	TTF-type zinc finger protein with HAT dimerisation domain
AT3G45490.1	unknown protein
AT4G34550.1	unknown protein
AT5G40210.1	nodulin MtN21 /EamA-like transporter family protein
AT4G12380.1	unknown protein
AT1G61450.1	unknown protein
AT4G16530.1	Family of unknown function (DUF577)
AT4G17590.1	unknown protein

frameshift

AT5G43175.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G12382.1	F-box family protein
AT5G27980.1	Seed maturation protein
AT2G19200.1	unknown protein
AT1G62421.1	unknown protein
AT5G44316.1	Stabilizer of iron transporter SufD superfamily protein
AT3G11040.1	Glycosyl hydrolase family 85
AT5G51650.1	unknown protein
AT4G15953.1	Maternally expressed gene (MEG) family protein
AT4G09870.1	F-box and associated interaction domains-containing protein
AT1G74160.1	unknown protein
AT2G32170.2	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT3G44230.1	unknown protein
AT2G34800.1	unknown protein
AT1G67450.1	F-box and associated interaction domains-containing protein
AT3G03847.1	SAUR-like auxin-responsive protein family
AT5G45000.1	Disease resistance protein (TIR-NBS-LRR class) family
AT1G31530.1	DNAse I-like superfamily protein
AT5G04730.1	Ankyrin-repeat containing protein
AT2G06645.1	unknown protein
AT1G67760.1	TCP-1/cpn60 chaperonin family protein
AT5G55131.1	Protein of unknown function (PD694200)
AT5G38344.1	Toll-Interleukin-Resistance (TIR) domain family protein
AT4G27010.2	unknown protein
AT5G10040.1	unknown protein
AT3G59120.1	Cysteine/Histidine-rich C1 domain family protein
AT5G06980.4	unknown protein
AT1G34440.1	unknown protein
AT4G23000.1	Calcineurin-like metallo-phosphoesterase superfamily protein
AT2G36940.1	unknown protein
AT3G45510.1	RING/U-box protein
AT3G52510.1	F-box associated ubiquitination effector family protein
AT5G21030.1	PAZ domain-containing protein / piwi domain-containing protein
AT5G11870.2	Alkaline phytoceramidase (aPHC)
AT1G71280.1	DEA(D/H)-box RNA helicase family protein
AT3G17540.1	F-box and associated interaction domains-containing protein
AT4G39020.1	SH3 domain-containing protein
AT4G15715.1	Proteinase inhibitor I25, cystatin, conserved region
AT3G42565.1	ECA1 gametogenesis related family protein
AT3G28155.1	unknown protein
AT4G24410.1	unknown protein
AT2G30730.1	Protein kinase superfamily protein
AT2G42460.1	TRAF-like family protein
AT5G56700.1	FBD / Leucine Rich Repeat domains containing protein
AT1G58090.1	F-box and associated interaction domains-containing protein
AT5G22680.1	unknown protein
AT4G33585.1	unknown protein
AT4G15040.1	Subtilisin-like serine endopeptidase family protein
AT2G03870.2	Small nuclear ribonucleoprotein family protein
AT5G23900.1	Ribosomal protein L13e family protein
AT1G62590.1	pentatricopeptide (PPR) repeat-containing protein
AT3G31402.1	General transcription factor 2-related zinc finger protein
AT3G51915.1	unknown protein

frameshift

AT4G29930.3	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT5G56452.1	FBD-like domain family protein
AT3G15720.1	Pectin lyase-like superfamily protein
AT5G27570.1	Transducin/WD40 repeat-like superfamily protein
AT5G62400.1	unknown protein
AT3G17230.1	invertase/pectin methylesterase inhibitor family protein
AT5G09445.1	unknown protein
AT4G15150.1	glycine-rich protein
AT4G14165.1	F-box family protein-related
AT3G26820.1	Esterase/lipase/thioesterase family protein
AT4G15810.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G33393.1	unknown protein
AT1G63840.1	RING/U-box superfamily protein
AT1G62410.1	MIF4G domain-containing protein
AT3G47100.1	unknown protein
AT2G15710.1	TRAF-like family protein
AT1G20940.1	F-box family protein
AT3G21610.1	Acid phosphatase/vanadium-dependent haloperoxidase-related protein
AT3G31900.1	ATP-dependent helicase family protein
AT2G04700.1	ferredoxin thioredoxin reductase catalytic beta chain family protein
AT5G47380.1	Protein of unknown function, DUF547
AT3G44800.1	Meprin and TRAF (MATH) homology domain-containing protein
AT4G16810.1	VEFS-Box of polycomb protein
AT4G25980.1	Peroxidase superfamily protein
AT1G80200.1	unknown protein
AT1G30860.1	RING/U-box superfamily protein
AT1G61230.1	Mannose-binding lectin superfamily protein
AT4G04650.1	RNA-directed DNA polymerase (reverse transcriptase)-related family protein
AT4G10400.1	F-box/RNI-like/FBD-like domains-containing protein
AT3G46800.1	Cysteine/Histidine-rich C1 domain family protein
AT1G64260.1	MuDR family transposase
AT4G08540.1	DNA-directed RNA polymerase II protein
AT1G52990.1	thioredoxin family protein
AT5G67411.1	GRAS family transcription factor
AT3G29790.1	unknown protein
AT5G47300.1	F-box and associated interaction domains-containing protein
AT5G05530.1	RING/U-box superfamily protein
AT4G15060.1	unknown protein
AT3G29140.1	unknown protein
AT4G05080.1	F-box and associated interaction domains-containing protein
AT3G22421.1	F-box and associated interaction domains-containing protein
AT2G31390.1	pfkB-like carbohydrate kinase family protein
AT2G05370.1	unknown protein
AT5G27300.1	pentatricopeptide (PPR) repeat-containing protein
AT5G39870.1	Protein of unknown function (DUF1216)
AT1G49700.1	Plant protein 1589 of unknown function
AT2G33720.1	AP2/B3-like transcriptional factor family protein
AT3G32260.1	Nucleic acid-binding proteins superfamily
AT1G49730.1	Protein kinase superfamily protein
AT4G05360.1	Zinc knuckle (CCHC-type) family protein
AT3G24929.1	unknown protein
AT3G17265.1	F-box and associated interaction domains-containing protein
AT4G19740.1	Glycosyl hydrolase superfamily protein

frameshift

AT1G62780.1	unknown protein
AT1G77990.1	STAS domain / Sulfate transporter family
AT4G32200.1	DNA-binding HORMA family protein
AT4G21030.1	Dof-type zinc finger domain-containing protein
AT5G28770.2	bZIP transcription factor family protein
AT1G59620.1	Disease resistance protein (CC-NBS-LRR class) family
AT1G10920.1	NB-ARC domain-containing disease resistance protein
AT4G15950.1	RNA polymerase II, Rpb4, core protein
AT1G58520.2	lipases;hydrolases, acting on ester bonds
AT4G03205.2	Coproporphyrinogen III oxidase
AT3G20935.1	cytochrome P450, family 705, subfamily A, polypeptide 28
AT2G26250.1	3-ketoacyl-CoA synthase 10
AT1G69260.1	ABI five binding protein
AT1G69040.2	ACT domain repeat 4
AT3G18650.1	AGAMOUS-like 103
AT2G24840.1	AGAMOUS-like 61
AT5G39750.1	AGAMOUS-like 81
AT3G56450.1	alpha-soluble NSF attachment protein 1
AT5G10230.1	annexin 7
AT2G31760.1	RING/U-box superfamily protein
AT4G16144.1	associated molecule with the SH3 domain of STAM 3
AT3G47750.1	ATP binding cassette subfamily A4
AT1G34170.3	AUXIN RESPONSE FACTOR 13
AT1G35240.1	auxin response factor 20
AT1G34390.1	auxin response factor 22
AT4G15370.1	baruol synthase 1
AT4G36780.1	BES1/BZR1 homolog 2
AT5G42260.1	beta glucosidase 12
AT1G51490.1	beta glucosidase 36
AT1G59640.2	BIG PETAL P
AT4G14670.1	casein lytic proteinase B2
AT3G51860.1	cation exchanger 3
AT4G15320.1	cellulose synthase-like B6
AT1G44446.1	Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain
AT1G59720.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G69970.1	CLAVATA3/ESR-RELATED 26
AT1G09790.1	COBRA-like protein 6 precursor
AT3G23490.1	cyanase
AT1G44110.1	Cyclin A1;1
AT2G38620.2	cyclin-dependent kinase B1;2
AT4G21400.1	cysteine-rich RLK (RECEPTOR-like protein kinase) 28
AT4G04570.1	cysteine-rich RLK (RECEPTOR-like protein kinase) 40
AT3G45860.1	cysteine-rich RLK (RECEPTOR-like protein kinase) 4
AT4G15360.1	cytochrome P450, family 705, subfamily A, polypeptide 3
AT2G27010.1	cytochrome P450, family 705, subfamily A, polypeptide 9
AT4G12330.1	cytochrome P450, family 706, subfamily A, polypeptide 7
AT4G20240.1	cytochrome P450, family 71, subfamily A, polypeptide 27
AT3G26160.1	cytochrome P450, family 71, subfamily B, polypeptide 17
AT3G26270.1	cytochrome P450, family 71, subfamily B, polypeptide 25
AT5G04630.1	cytochrome P450, family 77, subfamily A, polypeptide 9
AT2G23220.1	cytochrome P450, family 81, subfamily D, polypeptide 6
AT3G10010.1	demeter-like 2
AT2G06210.1	binding

frameshift

AT5G48090.1	EDM2-like protein1
AT1G30610.1	pentatricopeptide (PPR) repeat-containing protein
AT2G18510.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G08910.1	zinc ion binding;zinc ion binding
AT1G59680.1	F-box associated ubiquitination effector family protein
AT1G61140.1	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related
AT5G05740.1	ethylene-dependent gravitropism-deficient and yellow-green-like 2
AT5G22420.1	fatty acid reductase 7
AT1G32550.2	2Fe-2S ferredoxin-like superfamily protein
AT5G63595.1	flavonol synthase 4
AT4G15200.1	formin 3
AT4G31380.1	FPF1-like protein 1
AT2G06005.1	FRIGIDA interacting protein 1
AT5G26930.1	GATA transcription factor 23
AT1G78220.1	general regulatory factor 13
AT1G30040.1	gibberellin 2-oxidase
AT5G07200.1	gibberellin 20-oxidase 3
AT1G60980.1	gibberellin 20-oxidase 4
AT3G07520.1	glutamate receptor 1.4
AT5G11180.1	glutamate receptor 2.6
AT4G09740.1	glycosyl hydrolase 9B14
AT4G38990.1	glycosyl hydrolase 9B16
AT1G07290.1	golgi nucleotide sugar transporter 2
AT4G30120.1	heavy metal atpase 3
AT2G26550.1	heme oxygenase 2
AT1G55970.1	histone acetyltransferase of the CBP family 4
AT5G23320.1	homolog of yeast STE14 A
AT1G23540.1	Protein kinase superfamily protein
AT1G16910.1	Protein of unknown function (DUF640)
AT1G15080.1	lipid phosphate phosphatase 2
AT5G65770.2	little nuclei4
AT5G47175.1	low-molecular-weight cysteine-rich 3
AT5G47077.1	low-molecular-weight cysteine-rich 6
AT3G43160.1	maternal effect embryo arrest 38
AT4G13610.1	DNA (cytosine-5-)-methyltransferase family protein
AT2G01280.1	Cyclin/Brf1-like TBP-binding protein
AT4G18120.1	MEI2-like 3
AT3G56100.1	meristematic receptor-like kinase
AT1G22310.2	methyl-CPG-binding domain 8
AT3G55270.1	mitogen-activated protein kinase phosphatase 1
AT4G15760.1	monooxygenase 1
AT3G60970.1	multidrug resistance-associated protein 15
AT3G44350.2	NAC domain containing protein 61
AT5G04400.1	NAC domain containing protein 77
AT5G39690.1	NAC domain containing protein 93
AT2G17420.1	NADPH-dependent thioredoxin reductase A
AT4G09590.1	NDR1/HIN1-like 22
AT1G08300.1	no vein-like
AT2G04430.1	nudix hydrolase homolog 5
AT3G57430.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G27080.2	PDI-like 5-4
AT4G00190.1	pectin methylesterase 38

frameshift

AT2G02360.1	phloem protein 2-B10
AT2G19670.1	protein arginine methyltransferase 1A
AT5G24470.1	pseudo-response regulator 5
AT1G68210.1	pseudo-response regulator 6
AT1G35750.1	pumilio 10
AT4G08560.1	pumilio 15
AT1G52940.1	purple acid phosphatase 5
AT4G36570.1	RAD-like 3
AT1G74180.1	receptor like protein 14
AT2G25440.1	receptor like protein 20
AT2G33080.1	receptor like protein 28
AT3G44480.1	Disease resistance protein (TIR-NBS-LRR class) family
AT4G16845.1	VEFS-Box of polycomb protein
AT5G53160.2	regulatory components of ABA receptor 3
AT5G42040.1	regulatory particle non-ATPase 12B
AT4G16110.1	response regulator 2
AT3G62670.1	response regulator 20
AT1G31650.1	RHO guanyl-nucleotide exchange factor 14
AT1G62670.1	rna processing factor 2
AT5G45150.1	RNase THREE-like protein 3
AT3G02240.1	unknown protein
AT1G34065.1	S-adenosylmethionine carrier 2
AT4G10767.1	SCR-like 21
AT5G15800.2	K-box region and MADS-box transcription factor family protein
AT3G53030.1	ser/arg-rich protein kinase 4
AT5G33210.1	SHI-related sequence 8
AT5G39510.1	Vesicle transport v-SNARE family protein
AT1G23550.1	similar to RCD one 2
AT3G53060.1	SKP1-like 6
AT2G42200.1	squamosa promoter binding protein-like 9
AT2G41300.1	strictosidine synthase-like 1
AT4G21326.1	subtilase 3.12
AT1G66570.1	sucrose-proton symporter 7
AT2G20610.1	Tyrosine transaminase family protein
AT4G17730.2	syntaxin of plants 23
AT1G61290.1	syntaxin of plants 124
AT3G05330.1	cyclin family
AT1G54360.2	TBP-ASSOCIATED FACTOR 6B
AT4G16730.1	terpene synthase 02
AT4G15870.1	terpene synthase 1
AT5G60220.1	tetraspanin4
AT5G48375.1	thioglucoside glucosidase 3
AT1G17000.1	trehalose-phosphatase/synthase 3
AT1G61940.1	tubby like protein 4
AT5G44340.1	tubulin beta chain 4
AT5G07350.2	TUDOR-SN protein 1
AT5G43380.1	type one serine/threonine protein phosphatase 6
AT3G08700.1	ubiquitin-conjugating enzyme 12
AT2G32780.1	ubiquitin-specific protease 1
AT1G07260.1	UDP-glucosyl transferase 71C3
AT2G18870.1	vernalization5/VIN3-like
AT4G15780.1	vesicle-associated membrane protein 724
AT2G32670.1	vesicle-associated membrane protein 725

frameshift

AT4G07400.1	VIER F-box proteine 3
AT1G16090.1	wall associated kinase-like 7
AT3G18010.1	WUSCHEL related homeobox 1
AT1G20710.1	WUSCHEL related homeobox 10
AT1G20700.1	WUSCHEL related homeobox 14
AT3G44990.1	xyloglucan endo-transglycosylase-related 8

nonframeshift

genes affected by nonframeshift small indels

Gene ID	Gene Model Description
AT3G07600.1	Heavy metal transport/detoxification superfamily protein
AT5G56990.1	unknown protein
AT1G04280.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G11521.1	Receptor-like protein kinase-related family protein
AT1G11230.2	Protein of unknown function (DUF761)
AT4G35940.1	unknown protein
AT1G34630.1	unknown protein
AT1G64180.1	intracellular protein transport protein USO1-related
AT2G03630.1	unknown protein
AT2G15560.1	Putative endonuclease or glycosyl hydrolase
AT5G07670.1	RNI-like superfamily protein
AT5G15430.1	Plant calmodulin-binding protein-related
AT1G12244.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT5G50270.1	F-box/RNI-like/FBD-like domains-containing protein
AT3G24450.1	Heavy metal transport/detoxification superfamily protein
AT2G42190.1	unknown protein
AT2G26810.1	Putative methyltransferase family protein
AT2G23100.1	Cysteine/Histidine-rich C1 domain family protein
AT5G55856.1	Ubiquitin-like superfamily protein
AT5G19750.1	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
AT3G59130.1	Cysteine/Histidine-rich C1 domain family protein
AT5G35910.1	Polynucleotidyl transferase, ribonuclease H fold protein with HRDC domain
AT3G61400.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT5G62360.1	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT5G58400.1	Peroxidase superfamily protein
AT1G01730.1	unknown protein
AT2G33400.1	unknown protein
AT1G79150.1	binding
AT3G13990.1	Kinase-related protein of unknown function (DUF1296)
AT4G14620.1	Protein of unknown function (DUF506)
AT4G26870.1	Class II aminoacyl-tRNA and biotin synthetases superfamily protein
AT3G42140.1	zinc ion binding;nucleic acid binding
AT5G53910.1	RING/U-box superfamily protein
AT3G28790.1	Protein of unknown function (DUF1216)
AT4G19920.1	Toll-Interleukin-Resistance (TIR) domain family protein
AT1G77550.1	tubulin-tyrosine ligases;tubulin-tyrosine ligases
AT1G24310.1	unknown protein
AT1G27210.1	ARM repeat superfamily protein
AT3G29075.1	glycine-rich protein
AT2G44730.1	Alcohol dehydrogenase transcription factor Myb/SANT-like family protein
AT1G52050.1	Mannose-binding lectin superfamily protein
AT3G53590.1	Leucine-rich repeat protein kinase family protein
AT3G46640.3	Homeodomain-like superfamily protein
AT1G77855.1	unknown protein
AT5G02460.1	Dof-type zinc finger DNA-binding family protein
AT1G62310.1	transcription factor jumonji (jmjC) domain-containing protein
AT2G31480.1	unknown protein
AT1G60300.1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AT5G02990.1	Galactose oxidase/kelch repeat superfamily protein
AT3G06340.1	DNAJ heat shock N-terminal domain-containing protein
AT4G10620.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein

nonframeshift

AT1G06210.1	ENTH/VHS/GAT family protein
AT5G28300.1	Duplicated homeodomain-like superfamily protein
AT1G49030.1	PLAC8 family protein
AT1G80610.1	unknown protein
AT5G42310.1	Pentatricopeptide repeat (PPR-like) superfamily protein
AT1G79950.1	RAD3-like DNA-binding helicase protein
AT1G69730.1	Wall-associated kinase family protein
AT5G37710.1	alpha/beta-Hydrolases superfamily protein
AT4G33160.1	F-box family protein
AT5G38620.1	MADS-box transcription factor family protein
AT1G02710.1	glycine-rich protein
AT4G08330.1	unknown protein
AT5G32460.1	Transcriptional factor B3 family protein
AT5G48420.1	unknown protein
AT3G54460.1	SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein
AT1G17710.1	Pyridoxal phosphate phosphatase-related protein
AT1G21830.1	unknown protein
AT3G45830.1	unknown protein
AT5G20470.1	myosin, putative
AT5G43140.1	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
AT4G39870.1	TLD-domain containing nucleolar protein
AT1G17850.2	Rhodanese/Cell cycle control phosphatase superfamily protein
AT3G24080.1	KRR1 family protein
AT5G65910.1	BSD domain-containing protein
AT5G22160.1	unknown protein
AT2G46980.2	unknown protein
AT1G30974.1	Plant thionin family protein
AT4G02920.2	unknown protein
AT5G08010.1	unknown protein
AT4G27930.1	unknown protein
AT4G01860.1	Transducin family protein / WD-40 repeat family protein
AT5G43310.1	COP1-interacting protein-related
AT4G22580.1	Exostosin family protein
AT1G73870.1	B-box type zinc finger protein with CCT domain
AT5G17910.1	unknown protein
AT4G27840.1	SNARE-like superfamily protein
AT5G54910.1	DEA(D/H)-box RNA helicase family protein
AT3G55240.1	Plant protein 1589 of unknown function
AT2G39795.1	Mitochondrial glycoprotein family protein
AT4G18070.1	unknown protein
AT4G39550.1	Galactose oxidase/kelch repeat superfamily protein
AT1G49880.1	Erv1/Alr family protein
AT4G20160.1	unknown protein
AT5G39380.1	Plant calmodulin-binding protein-related
AT5G07870.1	HXXXD-type acyl-transferase family protein
AT1G55550.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G46310.1	WRKY family transcription factor
AT2G04039.3	unknown protein
AT4G39690.1	unknown protein
AT3G42180.1	Exostosin family protein
AT4G26290.1	unknown protein
AT1G10120.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein

nonframeshift

AT5G17580.1	Phototropic-responsive NPH3 family protein
AT3G53380.1	Concanavalin A-like lectin protein kinase family protein
AT3G42800.1	unknown protein
AT3G57120.1	Protein kinase superfamily protein
AT5G42880.1	Plant protein of unknown function (DUF827)
AT2G43600.1	Chitinase family protein
AT3G27860.1	Tudor/PWWP/MBT superfamily protein
AT3G59680.2	unknown protein
AT4G09350.1	Chaperone DnaJ-domain superfamily protein
AT4G28300.1	Protein of unknown function (DUF1421)
AT1G01300.1	Eukaryotic aspartyl protease family protein
AT3G30820.1	Arabidopsis retrotransposon ORF-1 protein
AT1G53010.1	RING/U-box superfamily protein
AT3G25790.1	myb-like transcription factor family protein
AT1G23020.2	ferric reduction oxidase 3
AT5G43720.1	Protein of unknown function (DUF2361)
AT2G17650.1	AMP-dependent synthetase and ligase family protein
AT4G13190.1	Protein kinase superfamily protein
AT4G00467.1	Calcium-dependent lipid-binding (CaLB domain) family protein
AT1G63520.1	Protein of unknown function (DUF3527)
AT3G04160.2	unknown protein
AT4G02810.1	Protein of unknown function (DUF3049)
AT5G17120.1	Cystatin/monellin superfamily protein
AT3G16210.1	F-box family protein
AT3G52660.1	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G76780.1	HSP20-like chaperones superfamily protein
AT5G11930.1	Thioredoxin superfamily protein
AT2G25430.1	epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related
AT4G24910.1	Protein of unknown function (DUF579)
AT1G64430.1	Pentatricopeptide repeat (PPR) superfamily protein
AT5G65900.1	DEA(D/H)-box RNA helicase family protein
AT2G05400.1	Ubiquitin-specific protease family C19-related protein
AT4G35700.1	zinc finger (C2H2 type) family protein
AT2G31690.1	alpha/beta-Hydrolases superfamily protein
AT5G15120.1	Protein of unknown function (DUF1637)
AT3G03850.1	SAUR-like auxin-responsive protein family
AT3G28770.1	Protein of unknown function (DUF1216)
AT5G66815.1	unknown protein
AT2G17570.1	Undecaprenyl pyrophosphate synthetase family protein
AT5G06750.1	Protein phosphatase 2C family protein
AT3G03405.1	F-box associated ubiquitination effector family protein
AT3G27473.1	Cysteine/Histidine-rich C1 domain family protein
AT1G34320.1	Protein of unknown function (DUF668)
AT5G41020.1	myb family transcription factor
AT3G26730.1	RING/U-box superfamily protein
AT1G64050.1	unknown protein
AT5G41620.1	unknown protein
AT5G54150.1	unknown protein
AT3G13780.1	SMAD/FHA domain-containing protein
AT3G44716.1	unknown protein
AT1G60783.1	unknown protein
AT5G42330.1	unknown protein

nonframeshift

AT1G09600.1	Protein kinase superfamily protein
AT4G28340.1	unknown protein
AT3G45260.1	C2H2-like zinc finger protein
AT5G16160.1	unknown protein
AT1G25422.1	unknown protein
AT5G39410.1	Saccharopine dehydrogenase
AT1G23450.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G18450.1	PLAC8 family protein
AT2G40460.1	Major facilitator superfamily protein
AT5G51800.1	Protein kinase superfamily protein
AT2G16250.1	Leucine-rich repeat protein kinase family protein
AT1G05835.1	PHD finger protein
AT2G21530.1	SMAD/FHA domain-containing protein
AT1G24145.1	unknown protein
AT3G26020.4	Protein phosphatase 2A regulatory B subunit family protein
AT2G04495.1	unknown protein
AT2G31210.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT2G19130.1	S-locus lectin protein kinase family protein
AT5G38060.1	unknown protein
AT3G13480.1	unknown protein
AT2G20330.1	Transducin/WD40 repeat-like superfamily protein
AT5G17830.1	Plasma-membrane choline transporter family protein
AT2G30620.1	winged-helix DNA-binding transcription factor family protein
AT1G69610.1	Protein of unknown function (DUF1666)
AT1G16570.2	UDP-Glycosyltransferase superfamily protein
AT5G53080.1	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G30250.1	unknown protein
AT3G18940.1	clast3-related
AT1G12960.1	Ribosomal protein L18e/L15 superfamily protein
AT3G46890.1	unknown protein
AT1G79510.1	Uncharacterized conserved protein (DUF2358)
AT5G45410.1	unknown protein
AT4G14740.1	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region
AT2G46060.1	transmembrane protein-related
AT1G31620.1	unknown protein
AT1G74440.1	Protein of unknown function (DUF962)
AT4G17410.3	DWNN domain, a CCHC-type zinc finger
AT5G03330.1	Cysteine proteinases superfamily protein
AT2G34040.1	Apoptosis inhibitory protein 5 (API5)
AT5G66310.1	ATP binding microtubule motor family protein
AT4G15940.1	Fumarylacetoacetate (FAA) hydrolase family
AT3G43990.1	Bromo-adjacent homology (BAH) domain-containing protein
AT4G00420.2	Double-stranded RNA-binding domain (DsRBD)-containing protein
AT5G50115.1	unknown protein
AT5G02980.1	Galactose oxidase/kelch repeat superfamily protein
AT3G03550.1	RING/U-box superfamily protein
AT1G49380.1	cytochrome c biogenesis protein family
AT3G48800.1	Sterile alpha motif (SAM) domain-containing protein
AT1G49980.1	DNA/RNA polymerases superfamily protein
AT4G01897.1	unknown protein
AT3G14190.1	unknown protein
AT1G76880.1	Duplicated homeodomain-like superfamily protein

nonframeshift

AT3G27520.1	unknown protein
AT4G02990.1	Mitochondrial transcription termination factor family protein
AT4G08550.1	electron carriers;protein disulfide oxidoreductases
AT1G49120.1	Integrase-type DNA-binding superfamily protein
AT5G53970.1	Tyrosine transaminase family protein
AT3G15930.1	Pentatricopeptide repeat (PPR) superfamily protein
AT5G09850.1	Transcription elongation factor (TFIIS) family protein
AT1G25440.1	B-box type zinc finger protein with CCT domain
AT1G55310.3	SC35-like splicing factor 33
AT1G59550.1	UBX domain-containing protein
AT4G12810.1	F-box family protein
AT4G37860.1	SPT2 chromatin protein
AT1G27660.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT5G39090.1	HXXXD-type acyl-transferase family protein
AT5G44600.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT3G60370.1	FKBP-like peptidyl-prolyl cis-trans isomerase family protein
AT2G35430.1	Zinc finger C-x8-C-x5-C-x3-H type family protein
AT3G45460.1	IBR domain containing protein
AT5G37350.1	Serine/threonine-protein kinase Rio1
AT5G16500.1	Protein kinase superfamily protein
AT5G67130.1	PLC-like phosphodiesterases superfamily protein
AT5G14690.1	unknown protein
AT5G37140.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G54930.1	Protein phosphatase 2A regulatory B subunit family protein
AT3G01920.1	DHBP synthase RibB-like alpha/beta domain
AT1G12760.1	Zinc finger, C3HC4 type (RING finger) family protein
AT5G55507.1	hydroxyproline-rich glycoprotein family protein
AT1G03740.1	Protein kinase superfamily protein
AT1G49015.1	DPP6 N-terminal domain-like protein
AT5G60350.1	unknown protein
AT3G09130.1	unknown protein
AT5G12430.1	Heat shock protein DnaJ with tetratricopeptide repeat
AT2G41890.1	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein
AT5G55460.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT3G05450.1	unknown protein
AT3G45243.1	ECA1 gametogenesis related family protein
AT3G57480.1	zinc finger (C2H2 type, AN1-like) family protein
AT5G64430.1	Octicosapeptide/Phox/Bem1p family protein
AT5G24350.2	unknown protein
AT1G45015.1	MD-2-related lipid recognition domain-containing protein
AT5G22660.2	FBD, F-box, Skp2-like and Leucine Rich Repeat domains containing protein
AT3G26060.2	Thioredoxin superfamily protein
AT1G09910.1	Rhamnogalacturonate lyase family protein
AT3G06868.1	unknown protein
AT3G18890.1	NAD(P)-binding Rossmann-fold superfamily protein
AT4G02100.1	Heat shock protein DnaJ with tetratricopeptide repeat
AT5G11750.1	Ribosomal protein L19 family protein
AT2G47830.1	Cation efflux family protein
AT2G26600.1	Glycosyl hydrolase superfamily protein
AT3G26085.2	CAAX amino terminal protease family protein
AT1G23980.1	RING/U-box superfamily protein
AT2G19220.1	unknown protein

nonframeshift

AT5G61290.1	Flavin-binding monooxygenase family protein
AT2G41050.1	PQ-loop repeat family protein / transmembrane family protein
AT1G47980.1	unknown protein
AT1G01225.1	NC domain-containing protein-related
AT2G16270.1	unknown protein
AT1G13130.1	Cellulase (glycosyl hydrolase family 5) protein
AT5G04310.1	Pectin lyase-like superfamily protein
AT2G04620.1	Cation efflux family protein
AT4G00250.1	DNA-binding storekeeper protein-related transcriptional regulator
AT1G69280.1	unknown protein
AT3G45020.1	Ribosomal L18p/L5e family protein
AT2G17050.1	disease resistance protein (TIR-NBS-LRR class), putative
AT4G26288.1	unknown protein
AT4G13575.1	unknown protein
AT3G22920.1	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
AT3G21210.1	zinc ion binding
AT3G28880.1	Ankyrin repeat family protein
AT1G66810.1	Zinc finger C-x8-C-x5-C-x3-H type family protein
AT5G65500.1	U-box domain-containing protein kinase family protein
AT1G30920.1	F-box family protein
AT5G17780.2	alpha/beta-Hydrolases superfamily protein
AT1G63300.1	Myosin heavy chain-related protein
AT5G22320.1	Leucine-rich repeat (LRR) family protein
AT5G38565.1	F-box/FBD-like domains containing protein
AT1G61080.1	Hydroxyproline-rich glycoprotein family protein
AT5G10510.3	AINTEGUMENTA-like 6
AT5G18140.1	Chaperone DnaJ-domain superfamily protein
AT5G21170.2	5'-AMP-activated protein kinase beta-2 subunit protein
AT4G03070.1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT1G18150.2	Protein kinase superfamily protein
AT4G33260.1	Transducin family protein / WD-40 repeat family protein
AT2G29720.1	FAD/NAD(P)-binding oxidoreductase family protein
AT3G05210.1	nucleotide repair protein, putative
AT4G17460.1	Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein
AT1G55080.1	unknown protein
AT5G43990.2	SET-domain containing protein lysine methyltransferase family protein
AT3G59550.1	Rad21/Rec8-like family protein
AT5G43630.1	zinc knuckle (CCHC-type) family protein
AT2G20960.1	Arabidopsis phospholipase-like protein (PEARL1 4) family
AT2G31360.1	16:0delta9 desaturase 2
AT1G75660.1	5'-3' exoribonuclease 3
AT5G24420.1	6-phosphogluconolactonase 5
AT5G67030.1	zeaxanthin epoxidase (ZEP) (ABA1)
AT3G24650.1	AP2/B3-like transcriptional factor family protein
AT2G40220.1	Integrase-type DNA-binding superfamily protein
AT5G60440.1	AGAMOUS-like 62
AT1G69540.1	AGAMOUS-like 94
AT2G14170.1	aldehyde dehydrogenase 6B2
AT2G29990.1	alternative NAD(P)H dehydrogenase 2
AT3G05380.2	DIRP ;Myb-like DNA-binding domain
AT2G17390.1	ankyrin repeat-containing 2B
AT4G00730.1	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein

nonframeshift

AT1G54060.1	6B-interacting protein 1-like 1
AT4G29820.1	homolog of CFIM-25
AT5G47850.1	CRINKLY4 related 4
AT4G32980.1	homeobox gene 1
AT5G58580.1	TOXICOS EN LEVADURA 63
AT1G68725.1	arabinogalactan protein 19
AT4G16130.1	arabinose kinase
AT5G63730.1	IBR domain-containing protein
AT4G30080.1	auxin response factor 16
AT5G17430.1	Integrase-type DNA-binding superfamily protein
AT3G54620.1	basic leucine zipper 25
AT5G38800.1	basic leucine-zipper 43
AT2G27990.1	BEL1-like homeodomain 8
AT5G41410.1	POX (plant homeobox) family protein
AT1G26560.1	beta glucosidase 40
AT2G45880.1	beta-amylase 7
AT1G24470.1	beta-ketoacyl reductase 2
AT4G01840.1	Ca2+ activated outward rectifying K+ channel 5
AT1G56340.1	calreticulin 1a
AT3G26740.1	CCR-like
AT3G13784.1	cell wall invertase 5
AT3G63140.1	chloroplast stem-loop binding protein of 41 kDa
AT5G20420.1	chromatin remodeling 42
AT5G12990.1	CLAVATA3/ESR-RELATED 40
AT2G20190.1	CLIP-associated protein
AT3G44340.1	clone eighty-four
AT2G21660.1	cold, circadian rhythm, and rna binding 2
AT1G20610.1	Cyclin B2;3
AT4G11530.1	cysteine-rich RLK (RECEPTOR-like protein kinase) 34
AT3G20950.1	cytochrome P450, family 705, subfamily A, polypeptide 32
AT3G14640.1	cytochrome P450, family 72, subfamily A, polypeptide 10
AT1G64940.1	cytochrome P450, family 87, subfamily A, polypeptide 6
AT2G46310.1	cytokinin response factor 5
AT4G26150.1	cytokinin-responsive gata factor 1
AT5G45830.1	delay of germination 1
AT1G05800.1	alpha/beta-Hydrolases superfamily protein
AT2G27035.1	early nodulin-like protein 20
AT4G20090.1	Pentatricopeptide repeat (PPR) superfamily protein
AT1G48850.1	chorismate synthase, putative / 5-enolpyruvylshikimate-3-phosphate phospholyase, putative
AT1G12770.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G58210.1	kinase interacting family protein
AT5G62990.1	Ubiquitin carboxyl-terminal hydrolase family protein
AT2G45000.1	structural constituent of nuclear pore
AT5G15540.1	PHD finger family protein
AT4G02440.1	F-box family protein
AT4G39030.1	MATE efflux family protein
AT1G17440.1	Transcription initiation factor TFIID subunit A
AT3G56150.1	eukaryotic translation initiation factor 3C
AT3G26400.1	eukaryotic translation initiation factor 4B1
AT1G51640.1	exocyst subunit exo70 family protein G2
AT2G17230.1	EXORDIUM like 5
AT2G32250.1	FAR1-related sequence 2

nonframeshift

AT5G60490.1	FASCICLIN-like arabinogalactan-protein 12
AT5G67470.1	formin homolog 6
AT5G16320.1	FRIGIDA like 1
AT1G69200.1	fructokinase-like 2
AT5G55490.1	gamete expressed protein 1
AT5G25830.1	GATA transcription factor 12
AT3G06740.1	GATA transcription factor 15
AT5G65280.1	GCR2-like 1
AT1G09560.1	germin-like protein 5
AT1G14920.1	GRAS family transcription factor family protein
AT5G35790.1	glucose-6-phosphate dehydrogenase 1
AT1G33240.1	GT-2-like 1
AT3G24520.1	heat shock transcription factor C1
AT4G37200.1	Thioredoxin superfamily protein
AT5G22650.1	histone deacetylase 2B
AT2G18350.1	homeobox protein 24
AT5G65410.1	homeobox protein 25
AT3G60390.1	homeobox-leucine zipper protein 3
AT3G05720.1	importin alpha isoform 7
AT4G14750.1	IQ-domain 19
AT5G10470.2	kinesin like protein for actin based chloroplast movement 1
AT4G08150.1	KNOTTED-like from Arabidopsis thaliana
AT1G28300.1	AP2/B3-like transcriptional factor family protein
AT3G50510.1	LOB domain-containing protein 28
AT5G61960.1	MEI2-like protein 1
AT5G15460.1	membrane-anchored ubiquitin-fold protein 2
AT2G44180.1	methionine aminopeptidase 2A
AT4G04810.1	methionine sulfoxide reductase B4
AT1G33990.1	methyl esterase 14
AT3G45290.1	Seven transmembrane MLO family protein
AT3G52880.2	monodehydroascorbate reductase 1
AT2G11810.1	monogalactosyldiacylglycerol synthase type C
AT2G16640.1	multimeric translocon complex in the outer envelope membrane 132
AT5G57880.1	multipolar spindle 1
AT5G49330.1	myb domain protein 111
AT3G61250.1	myb domain protein 17
AT5G52260.1	myb domain protein 19
AT3G09370.2	myb domain protein 3r-3
AT5G65230.1	myb domain protein 53
AT4G05100.1	myb domain protein 74
AT5G66300.1	NAC domain containing protein 105
AT2G17750.1	NEP-interacting protein 1
AT2G15620.1	nitrite reductase 1
AT4G18910.1	NOD26-like intrinsic protein 1;2
AT5G20730.1	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related
AT3G59760.1	O-acetylserine (thiol) lyase isoform C
AT2G35720.1	DNAJ heat shock N-terminal domain-containing protein
AT4G25860.1	OSBP(oxysterol binding protein)-related protein 4A
AT3G54010.1	FKBP-type peptidyl-prolyl cis-trans isomerase family protein
AT1G68640.1	bZIP transcription factor family protein
AT2G02950.1	phytochrome kinase substrate 1
AT3G47640.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G08840.1	pumilio 11

nonframeshift

AT5G41160.1	purine permease 12
AT3G22310.1	putative mitochondrial RNA helicase 1
AT2G46860.1	pyrophosphorylase 3
AT5G63840.1	Glycosyl hydrolases family 31 protein
AT3G55510.1	Noc2p family
AT1G65800.1	receptor kinase 2
AT2G37710.1	receptor lectin kinase
AT3G24900.1	receptor like protein 39
AT3G24982.1	receptor like protein 40
AT5G19790.1	related to AP2 11
AT3G48430.1	relative of early flowering 6
AT4G16990.2	disease resistance protein (TIR-NBS class), putative
AT5G46470.1	disease resistance protein (TIR-NBS-LRR class) family
AT1G74890.1	response regulator 15
AT3G16130.1	RHO guanyl-nucleotide exchange factor 13
AT1G58470.1	RNA-binding protein 1
AT4G11130.1	RNA-dependent RNA polymerase 2
AT5G05940.1	ROP guanine nucleotide exchange factor 5
AT1G12210.1	RPS5-like 1
AT3G13570.1	SC35-like splicing factor 30A
AT2G24120.1	DNA/RNA polymerases superfamily protein
AT1G65113.1	SCR-like 2
AT1G12860.1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G24190.1	SIN3-like 3
AT5G16270.1	sister chromatid cohesion 1 protein 4
AT2G41290.1	strictosidine synthase-like 2
AT4G33030.1	sulfoquinovosyldiacylglycerol 1
AT2G31070.1	TCP domain protein 10
AT1G67770.1	terminal EAR1-like 2
AT1G18520.1	tetraspanin11
AT1G53300.1	tetratricopeptide-repeat thioredoxin-like 1
AT5G15900.1	TRICHOME BIREFRINGENCE-LIKE 19
AT1G78240.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G65350.1	ubiquitin 13
AT2G29750.1	UDP-glucosyl transferase 71C1
AT1G08190.1	vacuolar protein sorting 41
AT1G21240.1	wall associated kinase 3
AT4G26455.1	WPP domain interacting protein 1
AT3G54320.1	Integrase-type DNA-binding superfamily protein
AT1G55600.1	WRKY DNA-binding protein 10
AT5G52830.1	WRKY DNA-binding protein 27
AT2G03340.1	WRKY DNA-binding protein 3
AT2G21900.1	WRKY DNA-binding protein 59
AT1G80590.1	WRKY DNA-binding protein 66
AT3G56400.1	WRKY DNA-binding protein 70

Supplemental Table 7. The list of 1,615 large deletions and 700 large insertions in *Ler* genome.

chromosome	type	size	start in col	end in col	confirm by Monsanto Ler contigs*	copy number in Col	TE driven	primarily affected gene	primarily affected gene ID	secondarily affected gene	secondarily affected gene ID	CNV
Chr1	deletion	103	270470	270572	Fully confirmed	2	No	intron	AT1G01725			Y
Chr1	deletion	96	440259	440354	Fully confirmed	1	No	intergenic				
Chr1	deletion	612	587482	588093	N/A	8	AT1TE01910	intergenic				Y
Chr1	deletion	1076	1160151	1161226	Fully confirmed	17	AT1TE03785	intergenic				Y
Chr1	deletion	809	1194311	1195119	Fully confirmed	34	AT1G04425	ncRNA	AT1G04425			Y
Chr1	deletion	172	1258207	1258378	Fully confirmed	1	No	intergenic				
Chr1	deletion	765	1430265	1431029	Fully confirmed	7	AT1TE04665	intergenic				Y
Chr1	deletion	679	1445753	1446431	N/A	2	No	intergenic				Y
Chr1	deletion	488	1617635	1618122	N/A	8	No	intergenic				Y
Chr1	deletion	1038	1705402	1706439	Fully confirmed	24	AT1TE05585	intergenic				Y
Chr1	deletion	2009	2029689	2031697	Fully confirmed	1	AT1TE06650	exon	AT1G06630			
Chr1	deletion	1353	2233813	2235165	Fully confirmed	29	AT1TE07300	intergenic				Y
Chr1	deletion	545	2493633	2494177	Fully confirmed	1	No	intergenic				
Chr1	deletion	12270	2788426	2800695	Fully confirmed	6	AT1TE09080	intergenic				Y
Chr1	deletion	247	2826076	2826322	Fully confirmed	1	No	intergenic				
Chr1	deletion	187	3196233	3196419	Fully confirmed	1	No	intron	AT1G09840			
Chr1	deletion	141	3198264	3198404	Partially confirmed	1	No	intron	AT1G09840			
Chr1	deletion	57	3239865	3239921	Fully confirmed	1	No	intergenic				
Chr1	deletion	268	3247327	3247594	Fully confirmed	4	AT1TE10550	intergenic				Y
Chr1	deletion	874	3250611	3251484	Partially confirmed	77	AT1TE10560	intergenic				Y
Chr1	deletion	2909	3262076	3264984	Fully confirmed	1	AT1TE10600	complete_gene	AT1G09995,AT1G10000			
Chr1	deletion	174	3297064	3297237	N/A	2	No	intergenic				Y
Chr1	deletion	1437	3728972	3730408	Partially confirmed	1	AT1TE12135	intergenic				
Chr1	deletion	763	3900259	3901021	Fully confirmed	1	No	intergenic				
Chr1	deletion	306	3933177	3933482	N/A	17	No	intergenic				Y
Chr1	deletion	920	4110103	4111022	Fully confirmed	14	AT1TE13365	intergenic				Y
Chr1	deletion	2342	4128398	4130739	Fully confirmed	1	AT1TE13430	complete_gene	AT1G12170	exon	AT1G12180	
Chr1	deletion	2912	4259496	4262407	Partially confirmed	1	No	complete_gene	AT1G12490			
Chr1	deletion	4498	4329895	4334392	Partially confirmed	1	AT1TE14085	intergenic				
Chr1	deletion	5115	4406006	4411120	Partially confirmed	19	AT1TE14315	intergenic				Y
Chr1	deletion	112	4599032	4599143	Fully confirmed	3	No	intergenic				Y
Chr1	deletion	1187	4741985	4743171	N/A	1	No	intergenic				
Chr1	deletion	1278	5044213	5045490	Fully confirmed	1	AT1TE16325	3'UTR	AT1G14685			
Chr1	deletion	4873	5351824	5356696	Fully confirmed	1	AT1TE17300	intergenic				
Chr1	deletion	677	5370132	5370808	Fully confirmed	1	No	3'UTR	AT1G15600			
Chr1	deletion	1269	5391422	5392690	Fully confirmed	13	AT1TE17415	3'UTR	AT1G15670			Y
Chr1	deletion	236	5394352	5394587	Fully confirmed	1	No	exon_3'_end	AT1G15680			
Chr1	deletion	469	5428128	5428596	N/A	1	No	exon	AT1G15770			
Chr1	deletion	135	5656262	5656396	N/A	1	No	intergenic				
Chr1	deletion	2605	5679268	5681872	Partially confirmed	3	AT1TE18370	intergenic				Y
Chr1	deletion	1120	5699960	5701079	Fully confirmed	14	No	intergenic				Y
Chr1	deletion	563	5862950	5863512	Fully confirmed	122	AT1TE18955	intergenic				Y
Chr1	deletion	231	5869457	5869687	N/A	1	No	intergenic				
Chr1	deletion	186	6135444	6135629	Partially confirmed	1	No	intergenic				
Chr1	deletion	2488	6156377	6158864	N/A	16	AT1TE19910	intergenic				Y
Chr1	deletion	264	6173303	6173566	Fully confirmed	8	No	intergenic				Y
Chr1	deletion	787	6262601	6263387	Partially confirmed	3	No	intergenic				Y
Chr1	deletion	5158	6538379	6543536	Fully confirmed	19	AT1TE21210	intergenic				Y
Chr1	deletion	5242	6704085	6709326	Fully confirmed	19	AT1TE21710	intergenic				Y
Chr1	deletion	117	6709619	6709735	Fully confirmed	1	AT1TE21715	intergenic				

Chr1	deletion	282	6715262	6715543	Fully confirmed	3	AT1TE21725	intron	AT1G19410	Y
Chr1	deletion	430	6912033	6912462	Fully confirmed	1	No	intergenic		
Chr1	deletion	990	7023545	7024534	Fully confirmed	3	AT1TE22695	complete_gene	AT1G20280	Y
Chr1	deletion	888	7024903	7025790	Fully confirmed	1	AT1TE22710	exon_3'_end	AT1G20290	
Chr1	deletion	207	7107609	7107815	Partially confirmed	1	No	intergenic		
Chr1	deletion	2271	7254958	7257228	Partially confirmed	7	AT1TE23420	intron	AT1G20860	Y
Chr1	deletion	12270	7352929	7365198	Fully confirmed	6	AT1TE23740	intergenic		Y
Chr1	deletion	103	7401056	7401158	N/A	1	No	intergenic		
Chr1	deletion	437	7457461	7457897	Partially confirmed	1	No	intergenic		
Chr1	deletion	154	7506006	7506159	Partially confirmed	2	AT1TE24170	intergenic		Y
Chr1	deletion	1045	7543913	7544957	Fully confirmed	1	No	intergenic		
Chr1	deletion	1280	7677045	7678324	Fully confirmed	1	No	complete_gene	AT1G21866	
Chr1	deletion	440	7714706	7715145	Fully confirmed	20	No	intergenic		Y
Chr1	deletion	57	7716522	7716578	Partially confirmed	1	No	intron	AT1G21940	
Chr1	deletion	5204	7717355	7722558	Fully confirmed	8	AT1TE24850	intergenic		Y
Chr1	deletion	541	7725326	7725866	Fully confirmed	70	AT1TE24855	intergenic		Y
Chr1	deletion	159	7726878	7727036	Fully confirmed	1	No	intergenic		
Chr1	deletion	265	7902609	7902873	Fully confirmed	1	No	intergenic		
Chr1	deletion	1977	7959351	7961327	N/A	1	AT1TE25610	intergenic		
Chr1	deletion	5255	7969346	7974600	Partially confirmed	1	AT1TE25645	intergenic		
Chr1	deletion	153	8016434	8016586	Fully confirmed	39	No	intergenic		Y
Chr1	deletion	255	8023994	8024248	Partially confirmed	1	AT1TE25820	intergenic		
Chr1	deletion	156	8140500	8140655	Fully confirmed	2	No	intergenic		Y
Chr1	deletion	644	8153880	8154523	Fully confirmed	1	No	intergenic		
Chr1	deletion	388	8228328	8228715	Fully confirmed	1	No	intron	AT1G23200	
Chr1	deletion	4505	8287516	8292020	Fully confirmed	1	AT1TE26705	intergenic		
Chr1	deletion	8673	8363224	8371896	Partially confirmed	1	No	complete_gene	AT1G23640	exon,5'UTR AT1G23660,AT1G23610
Chr1	deletion	808	8374343	8375150	N/A	1	AT1TE27030	intron	AT1G23670	
Chr1	deletion	8372	8453485	8461856	Partially confirmed	9	AT1TE27295	intergenic		Y
Chr1	deletion	2014	8488403	8490416	Fully confirmed	1	AT1TE27390	intergenic		
Chr1	deletion	2200	8490646	8492845	Partially confirmed	1	AT1TE27405	intergenic		
Chr1	deletion	478	8495259	8495736	N/A	1	No	intergenic		
Chr1	deletion	322	8515390	8515711	Fully confirmed	1	AT1TE27475	ncRNA	AT1G24068	
Chr1	deletion	1413	8538351	8539763	N/A	2	AT1TE27550	intergenic		Y
Chr1	deletion	3761	8644357	8648117	Partially confirmed	3	AT1TE27905	complete_gene	AT1G24380	Y
Chr1	deletion	640	8676342	8676981	N/A	1	No	complete_gene	AT1G24480	
Chr1	deletion	5623	8927602	8933224	N/A	1	AT1TE28830	intergenic		
Chr1	deletion	10879	9004835	9015713	Fully confirmed	11	AT1TE29060	intergenic		Y
Chr1	deletion	929	9147534	9148462	Partially confirmed	1	AT1TE29485	intergenic		
Chr1	deletion	2395	9276688	9279082	Partially confirmed	1	No	intergenic		
Chr1	deletion	461	9350490	9350950	Fully confirmed	1	No	intergenic		
Chr1	deletion	4961	9368348	9373308	Fully confirmed	1	AT1TE30195	intergenic		
Chr1	deletion	962	9384080	9385041	Partially confirmed	72	AT1TE30240	intergenic		Y
Chr1	deletion	310	9385284	9385593	Fully confirmed	1	AT1TE30250	intergenic		
Chr1	deletion	86	9393005	9393090	Partially confirmed	1	No	intron	AT1G27050	
Chr1	deletion	883	9418063	9418945	N/A	77	AT1TE30365	intergenic		Y
Chr1	deletion	949	9440360	9441308	Partially confirmed	1	AT1TE30440	intron	AT1G27180	
Chr1	deletion	5625	9475165	9480789	Partially confirmed	1	AT1TE30550	intergenic		
Chr1	deletion	14783	9676476	9691258	Fully confirmed	10	AT1TE31190	intergenic		Y
Chr1	deletion	313	9840458	9840770	Partially confirmed	1	No	intergenic		
Chr1	deletion	2117	9865345	9867461	Fully confirmed	84	AT1TE31775	intergenic		Y
Chr1	deletion	130	9883968	9884097	N/A	3	No	intergenic		Y
Chr1	deletion	149	9900441	9900589	Fully confirmed	1	AT1TE31905	intergenic		

Chr1	deletion	719	10021332	10022050	N/A	9	AT1TE32325	intergenic	Y
Chr1	deletion	97	10027428	10027524	Partially confirmed	1	No	intergenic	
Chr1	deletion	178	10339016	10339193	Partially confirmed	1	No	exon	AT1G29580
Chr1	deletion	3164	10339474	10342637	N/A	1	No	complete_gene	AT1G29590
Chr1	deletion	2245	10347110	10349354	Fully confirmed	4	AT1TE33455	intergenic	Y
Chr1	deletion	101	10434759	10434859	Fully confirmed	1	No	intron	AT1G29800
Chr1	deletion	253	10606312	10606564	Fully confirmed	1	No	exon_5'_end	AT1G30160
Chr1	deletion	324	10647995	10648318	Fully confirmed	1	No	intergenic	
Chr1	deletion	274	10964817	10965090	Fully confirmed	1	No	intergenic	
Chr1	deletion	950	10981930	10982879	N/A	2	AT1TE35460	intergenic	Y
Chr1	deletion	1950	11008409	11010358	Fully confirmed	1	No	exon_3'_end	AT1G30925
Chr1	deletion	94	11016727	11016820	Fully confirmed	1	No	intergenic	
Chr1	deletion	531	11023421	11023951	Partially confirmed	1	AT1TE35610	intergenic	
Chr1	deletion	3244	11153362	11156605	Fully confirmed	2	AT1TE36060	intergenic	Y
Chr1	deletion	178	11204458	11204635	N/A	16	AT1TE36215	intergenic	Y
Chr1	deletion	219	11212339	11212557	Fully confirmed	18	AT1TE36255	intergenic	Y
Chr1	deletion	148	11225228	11225375	N/A	1	No	intergenic	
Chr1	deletion	666	11226914	11227579	N/A	1	No	intergenic	
Chr1	deletion	1994	11228620	11230613	Fully confirmed	2	No	pseudo_gene	AT1G31355
Chr1	deletion	7448	11237838	11245285	Partially confirmed	1	AT1TE36340	complete_gene	AT1G31370,AT1G31380,AT1G31390
Chr1	deletion	748	11285782	11286529	Fully confirmed	1	No	intergenic	
Chr1	deletion	1017	11286653	11287669	Partially confirmed	40	AT1TE36510	intergenic	Y
Chr1	deletion	889	11351514	11352402	Partially confirmed	27	AT1TE36715	intron	AT1G31710
Chr1	deletion	93	11407244	11407336	N/A	1	AT1TE36890	intergenic	
Chr1	deletion	327	11421302	11421628	N/A	1	No	intergenic	
Chr1	deletion	637	11421815	11422451	Partially confirmed	2	AT1TE36945	intergenic	Y
Chr1	deletion	226	11440458	11440683	N/A	1	No	intergenic	
Chr1	deletion	902	11483284	11484185	Fully confirmed	1	No	intergenic	
Chr1	deletion	305	11500903	11501207	N/A	1	No	intergenic	
Chr1	deletion	148	11515098	11515245	Fully confirmed	1	No	exon_middle	AT1G32030
Chr1	deletion	674	11692500	11693173	N/A	1	AT1TE37870	intergenic	
Chr1	deletion	4627	11789452	11794078	Fully confirmed	3	AT1TE38210	intergenic	Y
Chr1	deletion	366	11804928	11805293	N/A	1	No	intergenic	
Chr1	deletion	905	11807618	11808522	Partially confirmed	1	No	intergenic	
Chr1	deletion	382	11957855	11958236	Fully confirmed	1	AT1TE38700	intergenic	
Chr1	deletion	773	11958316	11959088	Fully confirmed	11	AT1TE38705	intergenic	Y
Chr1	deletion	1051	12136632	12137682	Fully confirmed	1	AT1TE39360	intergenic	
Chr1	deletion	1083	12155771	12156853	N/A	1	AT1G33510	intergenic	
Chr1	deletion	1804	12160270	12162073	Partially confirmed	1	No	complete_gene	AT1G33530
Chr1	deletion	586	12183405	12183990	Fully confirmed	63	AT1TE39530	intergenic	Y
Chr1	deletion	750	12219670	12220419	Partially confirmed	2	No	intergenic	Y
Chr1	deletion	196	12228475	12228670	Fully confirmed	1	No	intergenic	
Chr1	deletion	875	12362073	12362947	Partially confirmed	1	AT1TE40230	intergenic	
Chr1	deletion	1912	12364081	12365992	Partially confirmed	80	AT1TE40240	intergenic	Y
Chr1	deletion	13578	12401964	12415541	Fully confirmed	1	AT1TE40340	complete_gene	AT1G34070,AT1G34095
Chr1	deletion	1374	12457084	12458457	Fully confirmed	1	AT1TE40525	3'UTR	AT1G34200
Chr1	deletion	481	12483094	12483574	N/A	2	AT1TE40640	intergenic	Y
Chr1	deletion	151	12654990	12655140	N/A	2	No	3'UTR	AT1G34570
Chr1	deletion	434	12666472	12666905	Partially confirmed	1	AT1TE41345	intergenic	
Chr1	deletion	10477	12674459	12684935	Fully confirmed	2	AT1TE41350	intergenic	Y
Chr1	deletion	874	12729446	12730319	N/A	1	AT1TE41465	intergenic	
Chr1	deletion	1691	12738314	12740004	Fully confirmed	1	AT1TE41525	intergenic	
Chr1	deletion	3586	12805025	12808610	Partially confirmed	1	No	complete_gene	AT1G34930,AT1G35030

Chr1	deletion	3620	12808990	12812609	N/A	1	AT1TE41725	complete_gene	AT1G35035	
Chr1	deletion	1167	12895329	12896495	Fully confirmed	2	AT1TE41995	intergenic		Y
Chr1	deletion	4049	12949828	12953876	N/A	1	AT1TE42225	intergenic		
Chr1	deletion	385	12968572	12968956	N/A	1	AT1TE42290	intergenic		
Chr1	deletion	274	12973442	12973715	Fully confirmed	1	No	intergenic		
Chr1	deletion	704	13067232	13067935	N/A	1	AT1TE42670	intergenic		
Chr1	deletion	892	13119392	13120283	Fully confirmed	2	AT1TE42850	intergenic		Y
Chr1	deletion	8733	13131275	13140007	Partially confirmed	4	AT1TE42890	intergenic		Y
Chr1	deletion	1092	13151833	13152924	Partially confirmed	1	AT1TE42930	intergenic		
Chr1	deletion	2065	13160804	13162868	Fully confirmed	2	AT1TE42950	intergenic		Y
Chr1	deletion	695	13164722	13165416	Fully confirmed	9	AT1TE42965	intergenic		Y
Chr1	deletion	1195	13166104	13167298	Partially confirmed	8	AT1TE42975	intergenic		Y
Chr1	deletion	638	13167652	13168289	N/A	1	AT1TE42975	intergenic		
Chr1	deletion	19439	13172922	13192360	Fully confirmed	1	AT1TE43010	intergenic		
Chr1	deletion	105	13201252	13201356	N/A	NULL	AT1TE43085	intergenic		
Chr1	deletion	618	13203994	13204611	Fully confirmed	1	AT1TE43115	intergenic		
Chr1	deletion	127	13217744	13217870	Partially confirmed	1	AT1TE43180	intergenic		
Chr1	deletion	721	13273051	13273771	Fully confirmed	1	AT1TE43355	intergenic		
Chr1	deletion	911	13329785	13330695	Fully confirmed	1	No	exon_5'_end	AT1G35850	
Chr1	deletion	58	13449932	13449989	N/A	1	AT1TE43985	intergenic		
Chr1	deletion	432	13453513	13453944	N/A	1	AT1TE44005	intergenic		
Chr1	deletion	7672	13482744	13490415	Fully confirmed	9	AT1TE44125	intergenic		Y
Chr1	deletion	302	13590869	13591170	Partially confirmed	1	No	intergenic		
Chr1	deletion	234	13616731	13616964	Fully confirmed	12	AT1TE44595	intergenic		Y
Chr1	deletion	9435	13658294	13667728	Fully confirmed	21	AT1TE44720	intergenic		Y
Chr1	deletion	681	14310769	14311449	N/A	9	AT1TE47020	intergenic		Y
Chr1	deletion	5142	15561951	15567092	Fully confirmed	1	AT1TE51245	intergenic		
Chr1	deletion	854	15580771	15581624	Fully confirmed	1	AT1TE51260	intergenic		
Chr1	deletion	11087	15703955	15715041	Fully confirmed	11	AT1TE51735	intergenic		Y
Chr1	deletion	220	15986295	15986514	N/A	1	No	intergenic		
Chr1	deletion	1263	16029466	16030728	N/A	2	AT1G42650	intergenic		Y
Chr1	deletion	998	16068979	16069976	Fully confirmed	1	AT1TE52920	intergenic		
Chr1	deletion	4184	16070136	16074319	Fully confirmed	1	AT1TE52925	intergenic		
Chr1	deletion	430	16149816	16150245	Partially confirmed	1	AT1TE53215	intergenic		
Chr1	deletion	1141	16180102	16181242	Fully confirmed	2	AT1TE53330	intergenic		Y
Chr1	deletion	5920	16311070	16316989	Fully confirmed	1	AT1TE53710	intergenic		
Chr1	deletion	5185	16319177	16324361	Fully confirmed	1	AT1TE53735	intergenic		
Chr1	deletion	1858	16325446	16327303	Fully confirmed	81	AT1TE53750	intergenic		Y
Chr1	deletion	535	16362015	16362549	N/A	4	AT1TE53925	intergenic		Y
Chr1	deletion	1804	16394350	16396153	Partially confirmed	4	AT1TE54005	intergenic		Y
Chr1	deletion	8713	16415358	16424070	Partially confirmed	1	AT1TE54110	intergenic		
Chr1	deletion	3129	16533825	16536953	Fully confirmed	1	AT1TE54515	intergenic		
Chr1	deletion	5351	16551720	16557070	Partially confirmed	2	AT1TE54585	intergenic		Y
Chr1	deletion	3675	16595419	16599093	Fully confirmed	1	AT1TE54710	intergenic		
Chr1	deletion	1444	16631697	16633140	Partially confirmed	19	AT1TE54805	intergenic		Y
Chr1	deletion	1314	16649736	16651049	Partially confirmed	1	AT1TE54880	intergenic		
Chr1	deletion	6577	16720758	16727334	Fully confirmed	1	AT1TE55255	intergenic		
Chr1	deletion	19362	16942836	16962197	Fully confirmed	4	AT1TE56135	intergenic		Y
Chr1	deletion	2912	16984569	16987480	Partially confirmed	1	AT1TE56235	intergenic		
Chr1	deletion	2282	16987669	16989950	Partially confirmed	26	AT1TE56255	intergenic		Y
Chr1	deletion	940	16999986	17000925	Fully confirmed	1	No	intron	AT1G44960	
Chr1	deletion	1495	17017028	17018522	Fully confirmed	2	AT1TE56365	intergenic		Y
Chr1	deletion	14957	17035063	17050019	Partially confirmed	4	AT1TE56420	intergenic		Y

Chr1	deletion	242	17121419	17121660	Fully confirmed	1	No	intergenic	
Chr1	deletion	169	17177656	17177824	Fully confirmed	1	No	intergenic	
Chr1	deletion	155	17280477	17280631	Partially confirmed	2	No	intergenic	Y
Chr1	deletion	205	17311753	17311957	Fully confirmed	1	No	intergenic	
Chr1	deletion	5765	17312052	17317816	Partially confirmed	2	AT1TE57380	intergenic	Y
Chr1	deletion	867	17318006	17318872	Partially confirmed	1	AT1TE57395	intergenic	
Chr1	deletion	100	17329154	17329253	Partially confirmed	1	No	intron	AT1G47271
Chr1	deletion	765	17332441	17333205	Partially confirmed	17	AT1TE57440	intron	AT1G47280 Y
Chr1	deletion	293	17342056	17342348	N/A	2	No	intergenic	Y
Chr1	deletion	762	17345627	17346388	Partially confirmed	1	AT1TE57480	intergenic	
Chr1	deletion	801	17347940	17348740	Partially confirmed	1	AT1TE57495	intergenic	
Chr1	deletion	3467	17594064	17597530	Partially confirmed	1	AT1TE58410	intergenic	
Chr1	deletion	1227	17620926	17622152	Fully confirmed	6	AT1TE58490	intergenic	Y
Chr1	deletion	2570	17624835	17627404	Fully confirmed	3	AT1TE58505	intergenic	Y
Chr1	deletion	112	17639365	17639476	N/A	NULL	No	intergenic	
Chr1	deletion	3617	17656702	17660318	Partially confirmed	2	AT1TE58625	intergenic	Y
Chr1	deletion	427	17663034	17663460	N/A	2	No	pseudo_gene	AT1G47930 Y
Chr1	deletion	1430	17666940	17668369	Fully confirmed	1	AT1TE58650	intergenic	
Chr1	deletion	1223	17713520	17714742	Fully confirmed	87	AT1TE58825	intergenic	Y
Chr1	deletion	89	17831161	17831249	Partially confirmed	1	AT1TE59195	intergenic	
Chr1	deletion	2975	17842313	17845287	N/A	1	AT1TE59235	intergenic	
Chr1	deletion	166	18010250	18010415	N/A	1	No	intergenic	
Chr1	deletion	5264	18013161	18018424	Fully confirmed	8	AT1TE59755	intergenic	Y
Chr1	deletion	1091	18058279	18059369	N/A	1	AT1TE59885	exon	AT1G48820
Chr1	deletion	426	18079438	18079863	Fully confirmed	1	No	intergenic	
Chr1	deletion	354	18126611	18126964	Fully confirmed	12	No	intergenic	Y
Chr1	deletion	285	18275404	18275688	Fully confirmed	1	No	pseudo_gene	AT1G49370
Chr1	deletion	872	18300270	18301141	N/A	78	AT1TE60645	intergenic	Y
Chr1	deletion	790	18320611	18321400	Fully confirmed	34	AT1TE60725	intergenic	Y
Chr1	deletion	1559	18338692	18340250	Partially confirmed	1	AT1TE60780	intergenic	
Chr1	deletion	177	18340368	18340544	N/A	1	No	intergenic	
Chr1	deletion	1089	18386407	18387495	N/A	2	AT1TE60920	intergenic	Y
Chr1	deletion	305	18548085	18548389	Partially confirmed	16	No	intron	AT1G50050 Y
Chr1	deletion	3363	18599503	18602865	Fully confirmed	1	AT1TE61640	intergenic	
Chr1	deletion	571	18626782	18627352	Fully confirmed	40	AT1TE61735	intergenic	Y
Chr1	deletion	802	18627544	18628345	Fully confirmed	1	AT1TE61735	intergenic	
Chr1	deletion	1659	18632143	18633801	Fully confirmed	1	AT1TE61755	intergenic	
Chr1	deletion	1106	18692134	18693239	Fully confirmed	1	AT1TE61940	intergenic	
Chr1	deletion	509	18700368	18700876	Fully confirmed	1	No	exon	AT1G50470
Chr1	deletion	732	18790117	18790848	N/A	84	AT1TE62285	intergenic	Y
Chr1	deletion	2009	18790924	18792932	N/A	83	AT1TE62285	intergenic	Y
Chr1	deletion	994	19052903	19053896	Partially confirmed	1	AT1TE63130	3'UTR	AT1G51402
Chr1	deletion	2223	19054343	19056565	N/A	1	AT1TE63140	intergenic	
Chr1	deletion	263	19067148	19067410	Fully confirmed	1	AT1TE63180	intergenic	
Chr1	deletion	1861	19068169	19070029	Fully confirmed	1	No	complete_gene	AT1G51430
Chr1	deletion	2999	19145625	19148623	N/A	2	AT1TE63440	intergenic	Y
Chr1	deletion	294	19251567	19251860	Partially confirmed	22	AT1TE63805	intergenic	Y
Chr1	deletion	9409	19336211	19345619	Fully confirmed	11	AT1TE64080	intergenic	Y
Chr1	deletion	636	19368175	19368810	Partially confirmed	1	No	intergenic	
Chr1	deletion	430	19405463	19405892	N/A	1	No	intergenic	
Chr1	deletion	4411	19446296	19450706	Partially confirmed	1	AT1TE64390	intergenic	
Chr1	deletion	195	19460277	19460471	Fully confirmed	1	No	intergenic	
Chr1	deletion	321	19463589	19463909	Partially confirmed	1	AT1TE64430	intergenic	

Chr1	deletion	2114	19464876	19466989	Partially confirmed	75	AT1TE64445	intergenic			Y
Chr1	deletion	1875	19496295	19498169	Fully confirmed	1	No	ncRNA	AT1G52347		
Chr1	deletion	780	19577841	19578620	Fully confirmed	1	No	intergenic			
Chr1	deletion	715	19602785	19603499	Partially confirmed	1	No	exon_5'_end	AT1G52618		
Chr1	deletion	315	19612487	19612801	Partially confirmed	1	No	3'UTR	AT1G52650		
Chr1	deletion	96	19620819	19620914	Fully confirmed	1	No	intron	AT1G52690		
Chr1	deletion	5644	19621667	19627310	N/A	1	AT1TE64905	complete_gene	AT1G52695		
Chr1	deletion	265	19641956	19642220	Partially confirmed	1	No	intergenic			
Chr1	deletion	11832	19724756	19736587	Fully confirmed	1	AT1TE65205	complete_gene	AT1G52950		
Chr1	deletion	3929	19741359	19745287	Partially confirmed	1	AT1TE65250	exon	AT1G52990	3'UTR	AT1G53000
Chr1	deletion	240	19898242	19898481	Fully confirmed	1	No	intergenic			
Chr1	deletion	5091	20085160	20090250	Fully confirmed	1	AT1TE66380	intergenic			
Chr1	deletion	276	20106640	20106915	Fully confirmed	2	No	intergenic			Y
Chr1	deletion	951	20141795	20142745	N/A	1	No	complete_gene	AT1G53935		
Chr1	deletion	258	20154055	20154312	N/A	44	AT1TE66570	3'UTR	AT1G54000		Y
Chr1	deletion	281	20206598	20206878	N/A	4	No	intergenic			Y
Chr1	deletion	585	20508837	20509421	Fully confirmed	63	AT1TE67755	intergenic			Y
Chr1	deletion	125	20908225	20908349	Fully confirmed	1	No	intron	AT1G55915		
Chr1	deletion	1392	20979442	20980833	Fully confirmed	6	AT1TE69285	exon	AT1G56100		Y
Chr1	deletion	2576	21108813	21111388	Partially confirmed	1	No	pseudo_gene	AT1G56390		
Chr1	deletion	4879	21244323	21249201	Fully confirmed	2	AT1TE70190	intergenic			Y
Chr1	deletion	4881	21346161	21351041	Fully confirmed	4	AT1TE70490	intergenic			Y
Chr1	deletion	193	21358567	21358759	Fully confirmed	1	No	intron	AT1G57670		
Chr1	deletion	162	21358919	21359080	Fully confirmed	1	No	intron	AT1G57670		
Chr1	deletion	407	21406776	21407182	Fully confirmed	1	No	intergenic			
Chr1	deletion	641	21428109	21428749	Partially confirmed	38	AT1TE70735	intergenic			Y
Chr1	deletion	116	21436896	21437011	N/A	1	No	intergenic			
Chr1	deletion	536	21463300	21463835	Fully confirmed	1	No	intergenic			
Chr1	deletion	447	21507597	21508043	Partially confirmed	1	AT1TE70985	intergenic			
Chr1	deletion	496	21509603	21510098	N/A	8	AT1TE70995	intergenic			Y
Chr1	deletion	329	21608226	21608554	Fully confirmed	1	AT1TE71300	intergenic			
Chr1	deletion	2348	21608810	21611157	Fully confirmed	1	AT1TE71310	complete_gene	AT1G58265		
Chr1	deletion	1001	21611377	21612377	Partially confirmed	1	No	3'UTR	AT1G58270		
Chr1	deletion	4904	21615296	21620199	Fully confirmed	1	AT1TE71330	intergenic			
Chr1	deletion	971	21681526	21682496	Fully confirmed	50	AT1TE71540	intergenic			Y
Chr1	deletion	1368	21697489	21698856	N/A	2	No	multi_exons	AT1G58400		Y
Chr1	deletion	245	21717800	21718044	Partially confirmed	1	No	intergenic			
Chr1	deletion	604	21731632	21732235	Fully confirmed	9	AT1TE71705	intron	AT1G58520		Y
Chr1	deletion	708	21911639	21912346	Fully confirmed	1	AT1TE72310	intergenic			
Chr1	deletion	930	22059346	22060275	Fully confirmed	2	AT1TE72845	complete_gene	AT1G59920		Y
Chr1	deletion	611	22069240	22069850	Fully confirmed	1	AT1TE72875	intron	AT1G59950		
Chr1	deletion	250	22075073	22075322	Fully confirmed	7	No	intergenic			Y
Chr1	deletion	706	22089159	22089864	Partially confirmed	2	AT1TE72930	intergenic			Y
Chr1	deletion	5996	22100644	22106639	Partially confirmed	1	AT1TE72970	intergenic			
Chr1	deletion	238	22107294	22107531	Partially confirmed	1	AT1TE72990	intergenic			
Chr1	deletion	1303	22111977	22113279	Partially confirmed	1	AT1TE73010	intergenic			
Chr1	deletion	264	22224557	22224820	Fully confirmed	16	AT1TE73400	intergenic			Y
Chr1	deletion	588	22303374	22303961	Fully confirmed	3	No	ncRNA	AT1G60545		Y
Chr1	deletion	1288	22356785	22358072	Fully confirmed	3	No	complete_gene	AT1G60720		Y
Chr1	deletion	158	22372617	22372774	Fully confirmed	1	No	intergenic			
Chr1	deletion	2767	22500110	22502876	Partially confirmed	1	AT1TE74230	exon	AT1G61093	5'UTR	AT1G61090
Chr1	deletion	364	22554737	22555100	Partially confirmed	7	No	intergenic			Y
Chr1	deletion	1118	22592593	22593710	N/A	1	AT1TE74530	3'UTR	AT1G61260		

Chr1	deletion	173	22604457	22604629	Fully confirmed	1	No	intergenic			
Chr1	deletion	241	22616629	22616869	Partially confirmed	1	No	intergenic			
Chr1	deletion	5384	22693954	22699337	Fully confirmed	1	AT1TE74860	intergenic			
Chr1	deletion	131	22714421	22714551	N/A	1	No	intergenic			
Chr1	deletion	301	22797714	22798014	Partially confirmed	1	No	intergenic			
Chr1	deletion	275	22827583	22827857	Partially confirmed	1	No	intergenic			
Chr1	deletion	159	22842236	22842394	Partially confirmed	1	No	intergenic			
Chr1	deletion	329	22862522	22862850	Partially confirmed	1	No	intergenic			
Chr1	deletion	914	22931656	22932569	Fully confirmed	2	AT1TE75580	intergenic			Y
Chr1	deletion	453	22945376	22945828	Partially confirmed	1	No	intergenic			
Chr1	deletion	7640	22950169	22957808	Fully confirmed	1	AT1TE75650	intergenic			
Chr1	deletion	2743	22972009	22974751	N/A	1	No	complete_gene	AT1G62160	exon	AT1G62170
Chr1	deletion	534	23062652	23063185	Fully confirmed	1	No	intergenic			
Chr1	deletion	4974	23118241	23123214	Fully confirmed	2	AT1TE76215	intergenic			Y
Chr1	deletion	640	23125062	23125701	Partially confirmed	106	AT1TE76235	intergenic			Y
Chr1	deletion	459	23156957	23157415	Partially confirmed	1	AT1TE76335	intergenic			
Chr1	deletion	207	23162820	23163026	Fully confirmed	1	No	intergenic			
Chr1	deletion	242	23167991	23168232	Fully confirmed	1	No	intergenic			
Chr1	deletion	2452	23171013	23173464	Fully confirmed	1	No	multi_exons	AT1G62570		
Chr1	deletion	951	23211759	23212709	Fully confirmed	1	AT1TE76520	intergenic			
Chr1	deletion	2957	23240234	23243190	Partially confirmed	2	AT1TE76620	intergenic			Y
Chr1	deletion	516	23276226	23276741	Fully confirmed	3	No	pseudo_gene	AT1G62860		Y
Chr1	deletion	276	23278861	23279136	Partially confirmed	1	AT1TE76730	intergenic			
Chr1	deletion	1601	23295658	23297258	Partially confirmed	4	AT1TE76780	intergenic			Y
Chr1	deletion	852	23320869	23321720	Fully confirmed	5	AT1TE76850	intergenic			Y
Chr1	deletion	238	23322314	23322551	Fully confirmed	4	No	intergenic			Y
Chr1	deletion	300	23368543	23368842	Fully confirmed	3	No	intergenic			Y
Chr1	deletion	1033	23565673	23566705	Partially confirmed	1	AT1TE77600	complete_gene	AT1G63535		
Chr1	deletion	188	23686158	23686345	Fully confirmed	1	No	intron	AT1G63830		
Chr1	deletion	5826	23708370	23714195	Partially confirmed	1	AT1TE78070	multi_exons	AT1G63870,AT1G63880		
Chr1	deletion	1093	23726547	23727639	Fully confirmed	1	AT1G63920	intergenic			
Chr1	deletion	384	23844210	23844593	Fully confirmed	1	No	intergenic			
Chr1	deletion	945	23850720	23851664	Fully confirmed	2	AT1TE78490	intergenic			Y
Chr1	deletion	7512	23925140	23932651	N/A	2	AT1TE78720	intergenic			Y
Chr1	deletion	322	24042817	24043138	Fully confirmed	1	AT1TE79075	intergenic			
Chr1	deletion	298	24043760	24044057	Fully confirmed	1	AT1TE79080	intergenic			
Chr1	deletion	258	24101057	24101314	Partially confirmed	1	No	intergenic			
Chr1	deletion	5681	24208793	24214473	Fully confirmed	1	No	exon	AT1G65170		
Chr1	deletion	1226	24221786	24223011	Partially confirmed	1	No	exon_5'_end	AT1G65200		
Chr1	deletion	480	24256162	24256641	Partially confirmed	1	No	intergenic			
Chr1	deletion	3994	24272590	24276583	Partially confirmed	1	AT1TE79810	intergenic			
Chr1	deletion	535	24327610	24328144	N/A	1	No	intergenic			
Chr1	deletion	288	24328291	24328578	N/A	2	No	intergenic			Y
Chr1	deletion	2505	24455910	24458414	Fully confirmed	1	AT1G65750	intergenic			
Chr1	deletion	655	24534535	24535189	Fully confirmed	1	AT1TE80590	intergenic			
Chr1	deletion	274	24611438	24611711	Fully confirmed	4	No	intergenic			Y
Chr1	deletion	164	24691672	24691835	N/A	1	No	intergenic			
Chr1	deletion	531	24732708	24733238	Fully confirmed	6	AT1TE81245	intergenic			Y
Chr1	deletion	534	24733422	24733955	Fully confirmed	1	AT1TE81245	intergenic			
Chr1	deletion	452	24744926	24745377	Fully confirmed	15	AT1TE81285	intergenic			Y
Chr1	deletion	863	24772181	24773043	Partially confirmed	15	No	intergenic			Y
Chr1	deletion	339	24776536	24776874	Fully confirmed	1	AT1TE81370	intergenic			
Chr1	deletion	325	24780625	24780949	Fully confirmed	1	No	intergenic			

Chr1	deletion	1008	24831629	24832636	N/A	13	AT1TE81560	intergenic		Y
Chr1	deletion	102	24857074	24857175	Fully confirmed	1	No	intergenic		
Chr1	deletion	1064	24907546	24908609	Fully confirmed	23	AT1TE81825	intergenic		Y
Chr1	deletion	4446	25159042	25163487	Fully confirmed	1	AT1TE82600	intergenic		
Chr1	deletion	670	25238354	25239023	Fully confirmed	1	No	ncRNA	AT1G67365	
Chr1	deletion	298	25267505	25267802	N/A	1	No	intergenic		
Chr1	deletion	164	25569891	25570054	N/A	1	No	intergenic		
Chr1	deletion	371	25619703	25620073	N/A	1	No	intergenic		
Chr1	deletion	259	25660005	25660263	Fully confirmed	16	No	intergenic		Y
Chr1	deletion	805	25962459	25963263	Fully confirmed	20	AT1TE85075	intergenic		Y
Chr1	deletion	758	25978463	25979220	Fully confirmed	1	No	exon_5'_end	AT1G69090	
Chr1	deletion	133	26053753	26053885	Fully confirmed	1	No	intergenic		
Chr1	deletion	109	26104228	26104336	Fully confirmed	1	No	intron	AT1G69440	
Chr1	deletion	1003	26110713	26111715	Partially confirmed	1	No	intergenic		
Chr1	deletion	279	26140024	26140302	Partially confirmed	3	AT1TE85640	intergenic		Y
Chr1	deletion	1999	26148452	26150450	Partially confirmed	1	No	exon	AT1G69545	
Chr1	deletion	151	26155230	26155380	Partially confirmed	1	No	intergenic		
Chr1	deletion	2158	26169395	26171552	Partially confirmed	85	AT1TE85730	intergenic		Y
Chr1	deletion	199	26245140	26245338	N/A	1	No	intergenic		
Chr1	deletion	451	26276441	26276891	Fully confirmed	1	No	intergenic		
Chr1	deletion	1596	26374366	26375961	Partially confirmed	7	AT1TE86375	intergenic		Y
Chr1	deletion	118	26582415	26582532	Fully confirmed	4	AT1TE87045	intergenic		Y
Chr1	deletion	73	26718055	26718127	Not confirmed	1	No	intergenic		
Chr1	deletion	122	26722324	26722445	N/A	21	No	pseudo_gene	AT1G70885	Y
Chr1	deletion	479	26724577	26725055	N/A	1	No	intergenic		
Chr1	deletion	153	26774483	26774635	Fully confirmed	1	No	intergenic		
Chr1	deletion	925	26887429	26888353	Fully confirmed	1	No	5'UTR	AT1G71340	
Chr1	deletion	116	26891728	26891843	Partially confirmed	1	No	intergenic		
Chr1	deletion	692	27117503	27118194	Partially confirmed	17	AT1TE88730	intergenic		Y
Chr1	deletion	1574	27439904	27441477	Fully confirmed	1	AT1TE89780	3'UTR	AT1G72930	
Chr1	deletion	202	27546991	27547192	Partially confirmed	1	No	intergenic		
Chr1	deletion	101	27916160	27916260	Fully confirmed	1	No	intron	AT1G74230	
Chr1	deletion	2574	27931099	27933672	Partially confirmed	1	AT1TE91400	3'UTR	AT1G74280	multi_exons AT1G74290
Chr1	deletion	287	28105499	28105785	Fully confirmed	5	No	intergenic		Y
Chr1	deletion	82	28326647	28326728	Partially confirmed	1	No	intergenic		
Chr1	deletion	618	28515394	28516011	Fully confirmed	1	AT1TE93275	intergenic		
Chr1	deletion	102	28537489	28537590	Fully confirmed	NULL	No	intergenic		
Chr1	deletion	3652	29377075	29380726	Partially confirmed	2	AT1TE96100	intergenic		Y
Chr1	deletion	268	29483360	29483627	N/A	1	No	intergenic		
Chr1	deletion	879	29774261	29775139	Fully confirmed	84	AT1TE97390	intron	AT1G79150	Y
Chr1	deletion	58	29873013	29873070	Fully confirmed	1	No	intron	AT1G79420	
Chr1	deletion	178	29900276	29900453	Partially confirmed	1	AT1TE97790	intergenic		
Chr1	deletion	1131	30068151	30069281	Fully confirmed	1	AT1TE98340	intergenic		
Chr1	deletion	5744	30418365	30424108	Fully confirmed	1	AT1TE99450	complete_gene	AT1G80970,AT1G80980	
Chr2	deletion	143	88642	88784	Fully confirmed	1	No	intergenic		
Chr2	deletion	1185	152015	153199	Partially confirmed	1	AT2TE00535	complete_gene	AT2G01310	
Chr2	deletion	1073	240847	241919	Partially confirmed	7	AT2TE00985	intergenic		Y
Chr2	deletion	5410	243803	249212	Fully confirmed	1	AT2TE01000	intergenic		
Chr2	deletion	393	337738	338130	N/A	1	No	exon_3'_end	AT2G01780	
Chr2	deletion	310	345933	346242	N/A	1	No	intergenic		
Chr2	deletion	7485	530249	537733	Partially confirmed	3	AT2TE02290	complete_gene	AT2G02103	Y
Chr2	deletion	1553	596285	597837	Partially confirmed	2	AT2TE02530	intergenic		Y
Chr2	deletion	278	612660	612937	Partially confirmed	8	AT2TE02595	intergenic		Y

Chr2	deletion	175	649588	649762	Fully confirmed	1	No	intron	AT2G02450	
Chr2	deletion	323	706913	707235	Partially confirmed	1	AT2TE03055	intergenic		
Chr2	deletion	2630	707443	710072	Fully confirmed	4	AT2TE03055	intergenic		Y
Chr2	deletion	1619	818913	820531	Partially confirmed	1	AT2TE03610	intergenic		
Chr2	deletion	1368	820693	822060	Partially confirmed	1	No	complete_gene	AT2G02835,AT2G02840	
Chr2	deletion	214	925142	925355	Fully confirmed	1	AT2G03291	3'UTR	AT2G03290	
Chr2	deletion	942	1000565	1001506	Fully confirmed	2	No	intergenic		Y
Chr2	deletion	260	1050143	1050402	N/A	17	No	intergenic		Y
Chr2	deletion	204	1061107	1061310	Partially confirmed	1	No	intron	AT2G03500	
Chr2	deletion	1647	1080055	1081701	Partially confirmed	1	No	complete_gene	AT2G03560	exon AT2G03565
Chr2	deletion	262	1184004	1184265	Fully confirmed	1	AT2TE05345	intergenic		
Chr2	deletion	278	1190064	1190341	Fully confirmed	1	No	intergenic		
Chr2	deletion	1364	1248856	1250219	Fully confirmed	1	No	intergenic		
Chr2	deletion	475	1250343	1250817	Fully confirmed	1	AT2TE05650	intergenic		
Chr2	deletion	105	1262566	1262670	Partially confirmed	1	No	intergenic		
Chr2	deletion	498	1262999	1263496	Partially confirmed	26	AT2TE05740	intergenic		Y
Chr2	deletion	8453	1263848	1272300	Fully confirmed	4	AT2TE05755	intergenic		Y
Chr2	deletion	106	1272535	1272640	Partially confirmed	1	No	intergenic		
Chr2	deletion	261	1318428	1318688	Partially confirmed	2	AT2TE06005	intergenic		Y
Chr2	deletion	680	1380617	1381296	N/A	18	AT2TE06330	intergenic		Y
Chr2	deletion	744	1392946	1393689	Fully confirmed	1	AT2TE06390	intergenic		
Chr2	deletion	4258	1395259	1399516	N/A	18	AT2TE06390	intergenic		Y
Chr2	deletion	313	1543013	1543325	Fully confirmed	1	No	intergenic		
Chr2	deletion	1215	1561645	1562859	Fully confirmed	1	AT2TE07175	intergenic		
Chr2	deletion	1340	1684736	1686075	N/A	5	AT2TE07805	intergenic		Y
Chr2	deletion	440	1763442	1763881	Partially confirmed	9	AT2TE08135	intergenic		Y
Chr2	deletion	4070	1793704	1797773	Partially confirmed	2	AT2TE08275	intergenic		Y
Chr2	deletion	2045	1876722	1878766	Fully confirmed	2	AT2TE08640	complete_gene	AT2G05185	Y
Chr2	deletion	134	1922699	1922832	Fully confirmed	1	AT2TE08840	intergenic		
Chr2	deletion	660	1968288	1968947	N/A	2	AT2TE09085	intergenic		Y
Chr2	deletion	4705	1970265	1974969	N/A	1	AT2TE09100	intergenic		
Chr2	deletion	202	1979237	1979438	N/A	1	No	intergenic		
Chr2	deletion	417	1980242	1980658	N/A	1	No	intergenic		
Chr2	deletion	146	2201891	2202036	N/A	1	No	intergenic		
Chr2	deletion	841	2211297	2212137	Partially confirmed	2	AT2TE10200	intergenic		Y
Chr2	deletion	277	2358742	2359018	N/A	1	AT2TE10880	intergenic		
Chr2	deletion	2958	2479564	2482521	Partially confirmed	1	AT2TE11300	intergenic		
Chr2	deletion	1642	2605354	2606995	Fully confirmed	1	No	intergenic		
Chr2	deletion	1570	2691572	2693141	Fully confirmed	65	AT2TE11955	intergenic		Y
Chr2	deletion	618	2711463	2712080	Partially confirmed	2	AT2TE12025	intergenic		Y
Chr2	deletion	8051	2712861	2720911	Fully confirmed	10	AT2TE12030	intergenic		Y
Chr2	deletion	1622	2721288	2722909	Fully confirmed	108	AT2TE12040	intergenic		Y
Chr2	deletion	140	2729445	2729584	N/A	1	No	intergenic		
Chr2	deletion	151	2758580	2758730	Partially confirmed	1	No	intergenic		
Chr2	deletion	241	2818588	2818828	Fully confirmed	4	AT2TE12385	intergenic		Y
Chr2	deletion	97	2822715	2822811	N/A	1	AT2TE12405	intergenic		
Chr2	deletion	17686	2846959	2864644	Fully confirmed	1	AT2TE12475	intergenic		
Chr2	deletion	4816	2902333	2907148	Partially confirmed	2	AT2TE12660	intergenic		Y
Chr2	deletion	406	3028363	3028768	Fully confirmed	1	No	exon	AT2G07280	
Chr2	deletion	589	3057685	3058273	Fully confirmed	6	AT2TE13315	intergenic		Y
Chr2	deletion	13498	3060811	3074308	Fully confirmed	1	AT2TE13335	intergenic		
Chr2	deletion	2046	3076201	3078246	Fully confirmed	2	AT2TE13350	intergenic		Y
Chr2	deletion	5567	3083903	3089469	Partially confirmed	1	AT2TE13385	intergenic		

Chr2	deletion	12506	3094966	3107471	Partially confirmed	2	AT2TE13440	intergenic	Y
Chr2	deletion	7237	3108155	3115391	Fully confirmed	1	AT2TE13445	intergenic	
Chr2	deletion	1424	3118280	3119703	Partially confirmed	3	AT2TE13505	intergenic	Y
Chr2	deletion	695	3120450	3121144	Partially confirmed	4	AT2TE13510	intergenic	Y
Chr2	deletion	1058	3133414	3134471	Fully confirmed	1	AT2TE13585	intergenic	
Chr2	deletion	1517	3143099	3144615	Fully confirmed	51	No	intergenic	Y
Chr2	deletion	5756	3160555	3166310	Fully confirmed	1	AT2TE13685	intergenic	
Chr2	deletion	5234	3225684	3230917	Fully confirmed	12	AT2TE13955	intergenic	Y
Chr2	deletion	2060	3533890	3535949	N/A	1	AT2TE15415	intergenic	
Chr2	deletion	391	3544144	3544534	Partially confirmed	36	AT2TE15440	intergenic	Y
Chr2	deletion	233	3562930	3563162	N/A	4	AT2TE15555	intergenic	Y
Chr2	deletion	718	3760853	3761570	Partially confirmed	3	AT2TE16235	intergenic	Y
Chr2	deletion	7525	4080278	4087802	Partially confirmed	1	AT2TE17245	intergenic	
Chr2	deletion	7741	4236657	4244397	Fully confirmed	8	AT2TE17875	intergenic	Y
Chr2	deletion	305	4244986	4245290	Fully confirmed	1	No	intergenic	
Chr2	deletion	104	4302087	4302190	Partially confirmed	3	AT2TE18050	ncRNA	AT2G10921
Chr2	deletion	904	4320824	4321727	Fully confirmed	1	AT2TE18155	intergenic	
Chr2	deletion	411	4371801	4372211	N/A	12	AT2TE18385	intergenic	Y
Chr2	deletion	121	4666799	4666919	Fully confirmed	1	No	pseudo_gene	AT2G11630
Chr2	deletion	5216	4703843	4709058	Fully confirmed	1	AT2TE19555	intergenic	
Chr2	deletion	580	4726055	4726634	Partially confirmed	1	AT2TE19600	intergenic	
Chr2	deletion	316	4837105	4837420	Partially confirmed	2	AT2TE20065	intergenic	Y
Chr2	deletion	1278	4896693	4897970	Fully confirmed	1	AT2TE20190	intergenic	
Chr2	deletion	95	5689782	5689876	Partially confirmed	1	No	intron	AT2G13650
Chr2	deletion	1872	5715422	5717293	Partially confirmed	1	AT2TE23140	intergenic	
Chr2	deletion	1661	5724272	5725932	Fully confirmed	1	AT2TE23175	complete_gene	AT2G13720
Chr2	deletion	197	5731207	5731403	Fully confirmed	1	AT2TE23185	intergenic	
Chr2	deletion	3857	5734466	5738322	Fully confirmed	3	AT2TE23240	complete_gene	AT2G13760,AT2G13770
Chr2	deletion	6423	5824944	5831366	Partially confirmed	1	AT2TE23730	complete_gene	AT2G13895
Chr2	deletion	585	5882511	5883095	Partially confirmed	1	AT2TE23940	intergenic	
Chr2	deletion	549	5885493	5886041	Fully confirmed	3	No	exon	AT2G14000
Chr2	deletion	1076	5904644	5905719	Fully confirmed	2	AT2TE24045	intergenic	Y
Chr2	deletion	122	5914366	5914487	Not confirmed	1	No	intergenic	
Chr2	deletion	162	5925881	5926042	Fully confirmed	1	AT2TE24140	intron	AT2G14080
Chr2	deletion	1877	6011516	6013392	Partially confirmed	1	AT2TE24460	intergenic	
Chr2	deletion	140	6041742	6041881	Fully confirmed	1	No	intron	AT2G14260
Chr2	deletion	653	6069152	6069804	Partially confirmed	11	AT2TE24680	intergenic	Y
Chr2	deletion	165	6088976	6089140	Fully confirmed	30	No	intergenic	Y
Chr2	deletion	1594	6231084	6232677	Fully confirmed	1	AT2TE25400	intergenic	
Chr2	deletion	113	6276789	6276901	N/A	1	No	intergenic	
Chr2	deletion	939	6306817	6307755	Partially confirmed	3	AT2TE25740	intergenic	Y
Chr2	deletion	1462	6350236	6351697	N/A	1	AT2TE25875	intergenic	
Chr2	deletion	670	6365842	6366511	Partially confirmed	1	AT2TE25935	intergenic	
Chr2	deletion	1310	6382744	6384053	Fully confirmed	29	AT2TE26020	intergenic	Y
Chr2	deletion	340	6391992	6392331	Partially confirmed	1	No	intergenic	
Chr2	deletion	220	6392954	6393173	N/A	1	No	intergenic	
Chr2	deletion	2915	6415115	6418029	Partially confirmed	1	AT2TE26190	intergenic	
Chr2	deletion	5093	6422212	6427304	Fully confirmed	1	AT2TE26230	intergenic	
Chr2	deletion	264	6485314	6485577	Fully confirmed	27	AT2TE26510	intergenic	Y
Chr2	deletion	2049	6508871	6510919	Partially confirmed	28	AT2TE26610	multi_exons	AT2G15042
Chr2	deletion	573	6551999	6552571	Fully confirmed	2	AT2TE26785	intergenic	Y
Chr2	deletion	404	6553881	6554284	Partially confirmed	3	AT2TE26785	intergenic	Y
Chr2	deletion	518	6554660	6555177	Fully confirmed	2	AT2TE26800	intergenic	Y

Chr2	deletion	11090	6620465	6631554	Fully confirmed	1	AT2TE26980	intergenic	
Chr2	deletion	1242	6644260	6645501	Fully confirmed	1	No	ncRNA	AT2G15292
Chr2	deletion	5201	6658917	6664117	Fully confirmed	1	AT2TE27165	intergenic	
Chr2	deletion	6309	6670982	6677290	Fully confirmed	1	AT2TE27220	complete_gene	AT2G15327
Chr2	deletion	6715	6778854	6785568	Fully confirmed	1	AT2TE27670	intergenic	
Chr2	deletion	3678	6942039	6945716	Partially confirmed	1	AT2TE28280	intergenic	
Chr2	deletion	451	6946137	6946587	N/A	25	No	intergenic	Y
Chr2	deletion	5011	6954028	6959038	N/A	1	AT2TE28325	intergenic	
Chr2	deletion	3197	7005167	7008363	Partially confirmed	1	AT2TE28555	intergenic	
Chr2	deletion	2232	7147961	7150192	Fully confirmed	1	AT2TE29090	intergenic	
Chr2	deletion	1096	7155514	7156609	Partially confirmed	15	AT2TE29120	intergenic	Y
Chr2	deletion	331	7246007	7246337	Partially confirmed	1	No	intergenic	
Chr2	deletion	497	7246547	7247043	Fully confirmed	12	AT2TE29500	intergenic	Y
Chr2	deletion	646	7247318	7247963	Partially confirmed	1	AT2TE29510	intergenic	
Chr2	deletion	699	7306935	7307633	Partially confirmed	1	AT2TE29775	intergenic	
Chr2	deletion	1080	7566538	7567617	Fully confirmed	9	AT2TE31140	intergenic	Y
Chr2	deletion	3598	7580549	7584146	N/A	1	AT2TE31215	intergenic	
Chr2	deletion	184	7585319	7585502	Partially confirmed	1	No	intron	AT2G17470
Chr2	deletion	122	7589671	7589792	Fully confirmed	1	No	intergenic	
Chr2	deletion	4018	7598599	7602616	N/A	1	AT2TE31290	intergenic	
Chr2	deletion	2802	7656237	7659038	Partially confirmed	1	AT2TE31545	intergenic	
Chr2	deletion	399	7680493	7680891	N/A	1	No	intergenic	
Chr2	deletion	7245	7777056	7784300	Fully confirmed	1	AT2TE32120	intergenic	
Chr2	deletion	235	7803476	7803710	Partially confirmed	1	No	exon_middle	AT2G17940
Chr2	deletion	66	7812635	7812700	N/A	2	No	intron	AT2G17960
Chr2	deletion	853	7856073	7856925	Partially confirmed	1	AT2TE32510	intergenic	
Chr2	deletion	1667	7890368	7892034	Fully confirmed	1	No	intergenic	
Chr2	deletion	733	7903929	7904661	Fully confirmed	1	AT2TE32725	intergenic	
Chr2	deletion	1757	7905786	7907542	Partially confirmed	2	AT2TE32755	intergenic	Y
Chr2	deletion	362	7956088	7956449	Fully confirmed	13	No	exon	AT2G18320
Chr2	deletion	417	8018453	8018869	Fully confirmed	1	No	intergenic	
Chr2	deletion	616	8090324	8090939	N/A	14	No	3'UTR	AT2G18660
Chr2	deletion	2779	8212099	8214877	N/A	1	AT2TE34160	intergenic	
Chr2	deletion	4812	8246676	8251487	Partially confirmed	1	AT2TE34310	exon_3'_end	AT2G19030
Chr2	deletion	88	8300876	8300963	N/A	1	AT2G19140	intergenic	
Chr2	deletion	5596	8343389	8348984	Partially confirmed	1	No	complete_gene	AT2G19230
Chr2	deletion	2776	8379698	8382473	Fully confirmed	2	AT2TE34910	intron	AT2G19360
Chr2	deletion	59	8410150	8410208	Fully confirmed	3	No	intergenic	Y
Chr2	deletion	2548	8420393	8422940	Fully confirmed	21	AT2TE35115	intergenic	Y
Chr2	deletion	1030	8464590	8465619	Partially confirmed	1	No	complete_gene	AT2G19550
Chr2	deletion	97	8515602	8515698	Fully confirmed	1	No	intron	AT2G19750
Chr2	deletion	400	8537659	8538058	Partially confirmed	2	AT2TE35720	intergenic	Y
Chr2	deletion	57	8561678	8561734	N/A	1	No	intergenic	
Chr2	deletion	4766	8562278	8567043	N/A	2	AT2TE35840	intergenic	Y
Chr2	deletion	1082	8590558	8591639	Fully confirmed	2	No	intergenic	Y
Chr2	deletion	1152	8621742	8622893	Fully confirmed	1	No	intergenic	
Chr2	deletion	5659	8815831	8821489	Fully confirmed	1	AT2TE37050	intergenic	
Chr2	deletion	265	8823434	8823698	N/A	1	No	intergenic	
Chr2	deletion	983	8869418	8870400	Fully confirmed	1	No	intergenic	
Chr2	deletion	667	8885590	8886256	Fully confirmed	1	AT2TE37390	exon_3'_end	AT2G20613
Chr2	deletion	2895	8913842	8916736	N/A	1	AT2TE37520	intergenic	
Chr2	deletion	332	8916921	8917252	N/A	1	AT2TE37521	intergenic	
Chr2	deletion	624	8996496	8997119	Fully confirmed	1	No	pseudo_gene	AT2G20910

Chr2	deletion	268	8997926	8998193	Partially confirmed	1	No	intergenic		
Chr2	deletion	266	9039006	9039271	N/A	13	AT2TE38150	intergenic		Y
Chr2	deletion	833	9047784	9048616	Fully confirmed	3	No	3'UTR	AT2G21100	Y
Chr2	deletion	2749	9057218	9059966	N/A	5	AT2TE38245	intergenic		Y
Chr2	deletion	1201	9063161	9064361	Fully confirmed	9	No	intergenic		Y
Chr2	deletion	1044	9091079	9092122	Fully confirmed	11	AT2TE38420	intergenic		Y
Chr2	deletion	3862	9121958	9125819	Fully confirmed	1	AT2TE38575	intergenic		
Chr2	deletion	7790	9187491	9195280	Fully confirmed	1	AT2TE38900	intergenic		
Chr2	deletion	168	9267471	9267638	Fully confirmed	1	No	intergenic		
Chr2	deletion	2887	9446501	9449387	Partially confirmed	1	AT2TE40165	intergenic		
Chr2	deletion	1523	9455004	9456526	Partially confirmed	2	AT2TE40200	intergenic		Y
Chr2	deletion	458	9564908	9565365	Fully confirmed	1	AT2TE40730	intergenic		
Chr2	deletion	922	9612020	9612941	Partially confirmed	3	AT2TE40975	intergenic		Y
Chr2	deletion	1576	9633547	9635122	Fully confirmed	1	AT2TE41090	intergenic		
Chr2	deletion	142	9668969	9669110	N/A	1	No	intergenic		
Chr2	deletion	286	9687800	9688085	Fully confirmed	1	No	intergenic		
Chr2	deletion	1114	9692111	9693224	Partially confirmed	1	AT2TE41350	intergenic		
Chr2	deletion	1242	9726910	9728151	Fully confirmed	1	AT2TE41525	intergenic		
Chr2	deletion	570	9807810	9808379	Partially confirmed	3	AT2TE41910	exon	AT2TE41910	Y
Chr2	deletion	191	9843863	9844053	Partially confirmed	1	No	intergenic		
Chr2	deletion	162	9888748	9888909	Fully confirmed	1	AT2TE42300	intergenic		
Chr2	deletion	229	9889676	9889904	Partially confirmed	1	No	intergenic		
Chr2	deletion	4944	9927657	9932600	N/A	1	AT2TE42485	intergenic		
Chr2	deletion	8178	10001480	10009657	Partially confirmed	6	AT2TE42810	intergenic		Y
Chr2	deletion	2757	10017784	10020540	Fully confirmed	19	AT2TE42855	intergenic		Y
Chr2	deletion	316	10047789	10048104	N/A	1	No	intron	AT2G23620	
Chr2	deletion	905	10075301	10076205	N/A	2	AT2TE43125	multi_exons	AT2G23690	Y
Chr2	deletion	8131	10085509	10093639	Fully confirmed	9	AT2TE43165	intergenic		Y
Chr2	deletion	1324	10279367	10280690	Fully confirmed	1	AT2TE43990	intergenic		
Chr2	deletion	364	10305377	10305740	Fully confirmed	1	AT2TE44110	intergenic		
Chr2	deletion	684	10315226	10315909	Fully confirmed	1	No	3'UTR	AT2G24255	
Chr2	deletion	526	10337683	10338208	N/A	1	AT2TE44280	intergenic		
Chr2	deletion	303	10343824	10344126	Fully confirmed	1	No	intergenic		
Chr2	deletion	2252	10433095	10435346	Fully confirmed	1	AT2TE44730	intergenic		
Chr2	deletion	1100	10436255	10437354	Fully confirmed	15	AT2TE44750	intergenic		Y
Chr2	deletion	489	10462867	10463355	Fully confirmed	1	No	complete_gene	AT2G24617,AT2G24620	
Chr2	deletion	868	10494092	10494959	Fully confirmed	1	No	multi_exons	AT2G24680	
Chr2	deletion	656	10506702	10507357	N/A	1	AT2TE45095	3'UTR	AT2G24693	
Chr2	deletion	114	10562001	10562114	N/A	1	AT2TE45325	intergenic		
Chr2	deletion	879	10565707	10566585	Fully confirmed	2	No	complete_gene	AT2G24780	Y
Chr2	deletion	16938	10592184	10609121	Fully confirmed	4	AT2TE45465	intergenic		Y
Chr2	deletion	686	10703435	10704120	Fully confirmed	1	No	multi_exons	AT2G25150	
Chr2	deletion	1387	10855233	10856619	N/A	1	No	5'UTR	AT2G25510	
Chr2	deletion	5660	10874582	10880241	Fully confirmed	3	AT2TE46755	intergenic		Y
Chr2	deletion	56	10932626	10932681	Partially confirmed	1	AT2TE47035	intergenic		
Chr2	deletion	695	11076692	11077386	Partially confirmed	1	AT2TE47765	intergenic		
Chr2	deletion	232	11231320	11231551	N/A	10	AT2TE48545	intergenic		Y
Chr2	deletion	196	11261452	11261647	Fully confirmed	1	No	intron	AT2G26470	
Chr2	deletion	2122	11285115	11287236	Fully confirmed	84	AT2TE48795	intergenic		Y
Chr2	deletion	6960	11436253	11443212	Fully confirmed	1	AT2TE49535	complete_gene	AT2G26820	
Chr2	deletion	900	11555402	11556301	Fully confirmed	26	AT2TE50120	exon	AT2G27070	Y
Chr2	deletion	55	11594438	11594492	Fully confirmed	1	No	intergenic		
Chr2	deletion	195	11734759	11734953	Fully confirmed	1	No	pseudo_gene	AT2G27440	

Chr2	deletion	1063	11867189	11868251	Fully confirmed	1	AT2TE51630	intergenic		
Chr2	deletion	262	11981724	11981985	N/A	6	No	intergenic		Y
Chr2	deletion	104	11995960	11996063	Fully confirmed	1	No	3'UTR	AT2G28140	
Chr2	deletion	338	12272810	12273147	Fully confirmed	1	No	3'UTR	AT2G28625	
Chr2	deletion	12342	12566154	12578495	Fully confirmed	6	AT2TE54910	intergenic		Y
Chr2	deletion	237	12717043	12717279	Partially confirmed	4	No	intergenic		Y
Chr2	deletion	2902	12740679	12743580	Fully confirmed	1	AT2TE55700	complete_gene	AT2G29870,AT2G29880	
Chr2	deletion	122	12768783	12768904	Fully confirmed	1	No	intergenic		
Chr2	deletion	632	12773701	12774332	Fully confirmed	2	AT2TE55860	intergenic		Y
Chr2	deletion	352	12780596	12780947	N/A	17	No	intergenic		Y
Chr2	deletion	235	12971847	12972081	N/A	1	No	intergenic		
Chr2	deletion	550	13101811	13102360	Fully confirmed	125	AT2TE57420	intergenic		Y
Chr2	deletion	3987	13223062	13227048	N/A	1	AT2TE58010	intergenic		
Chr2	deletion	801	13232820	13233620	Partially confirmed	2	No	intergenic		Y
Chr2	deletion	2054	13906667	13908720	N/A	84	AT2TE61325	intergenic		Y
Chr2	deletion	293	14296292	14296584	Fully confirmed	1	No	intergenic		
Chr2	deletion	3655	14402243	14405897	N/A	1	AT2TE63770	complete_gene	AT2G34120	multi_exons AT2G34110
Chr2	deletion	852	14571895	14572746	Fully confirmed	78	AT2TE64580	intergenic		Y
Chr2	deletion	1041	14682580	14683620	Fully confirmed	17	AT2TE65130	intergenic		Y
Chr2	deletion	919	14702089	14703007	Fully confirmed	1	AT2TE65230	multi_exons	AT2G34840	
Chr2	deletion	273	14812346	14812618	Fully confirmed	1	No	intergenic		
Chr2	deletion	247	14934707	14934953	Fully confirmed	1	No	intron	AT2G35580	
Chr2	deletion	3410	15050063	15053472	Fully confirmed	1	No	intergenic		
Chr2	deletion	272	15110052	15110323	Fully confirmed	3	AT2TE67240	intergenic		Y
Chr2	deletion	691	15134089	15134779	Fully confirmed	47	AT2TE67350	intergenic		Y
Chr2	deletion	407	15448702	15449108	N/A	18	AT2TE68900	intergenic		Y
Chr2	deletion	2065	15595120	15597184	N/A	2	AT2TE69630	intergenic		Y
Chr2	deletion	201	15722218	15722418	Fully confirmed	1	No	intergenic		
Chr2	deletion	137	15733538	15733674	Fully confirmed	8	No	intergenic		Y
Chr2	deletion	254	15972319	15972572	Fully confirmed	4	No	intergenic		Y
Chr2	deletion	124	15994740	15994863	Partially confirmed	1	No	intergenic		
Chr2	deletion	8303	16007424	16015726	Fully confirmed	1	AT2TE71670	intergenic		
Chr2	deletion	879	16125664	16126542	Partially confirmed	1	AT2TE72255	intergenic		
Chr2	deletion	921	16150385	16151305	Partially confirmed	15	AT2TE72380	intergenic		Y
Chr2	deletion	51	16184091	16184141	Not confirmed	1	No	intergenic		
Chr2	deletion	389	16373129	16373517	Fully confirmed	10	No	intergenic		Y
Chr2	deletion	1333	16379571	16380903	Partially confirmed	5	AT2TE73500	intergenic		Y
Chr2	deletion	424	16417656	16418079	N/A	1	AT2TE73690	multi_exons	AT2G39320	
Chr2	deletion	107	16453502	16453608	Fully confirmed	1	No	intron	AT2G39400	
Chr2	deletion	1059	16625760	16626818	Fully confirmed	3	AT2TE74725	intergenic		Y
Chr2	deletion	1298	16865549	16866846	N/A	1	No	intergenic		
Chr2	deletion	2836	17092687	17095522	Fully confirmed	2	AT2TE77005	intergenic		Y
Chr2	deletion	52	17106998	17107049	Fully confirmed	134	No	intergenic		Y
Chr2	deletion	6696	17270980	17277675	Fully confirmed	1	No	NULL		
Chr2	deletion	151	17687230	17687380	Partially confirmed	1	No	intron	AT2G42480	
Chr2	deletion	1314	18091977	18093290	Partially confirmed	1	AT2TE81930	intergenic		
Chr2	deletion	545	18165558	18166102	Fully confirmed	2	No	complete_gene	AT2G43865	Y
Chr2	deletion	429	18274979	18275407	Fully confirmed	1	No	exon_3'_end	AT2G44195	
Chr2	deletion	2279	18325223	18327501	Fully confirmed	1	No	complete_gene	AT2G44390,AT2G44400	
Chr2	deletion	458	18398508	18398965	N/A	1	AT2TE83440	intergenic		
Chr2	deletion	838	18470689	18471526	Partially confirmed	1	No	ncRNA	AT2G44798	
Chr2	deletion	1975	18709080	18711054	Fully confirmed	2	AT2TE84980	intergenic		Y
Chr2	deletion	234	18797807	18798040	Fully confirmed	1	No	intergenic		

Chr2	deletion	118	18902804	18902921	N/A	1	No	intergenic	
Chr2	deletion	128	18938654	18938781	Fully confirmed	1	AT2TE86120	intergenic	
Chr2	deletion	1346	19195410	19196755	Fully confirmed	29	AT2TE87415	intergenic	Y
Chr3	deletion	248	982095	982342	Partially confirmed	1	No	exon_3'_end	AT3G03847
Chr3	deletion	409	1143156	1143564	Fully confirmed	10	No	intergenic	Y
Chr3	deletion	559	1265729	1266287	Fully confirmed	1	No	exon_3'_end	AT3G04660
Chr3	deletion	241	1408193	1408433	Fully confirmed	2	No	intergenic	Y
Chr3	deletion	267	1447159	1447425	N/A	1	No	intergenic	
Chr3	deletion	5283	1555412	1560694	Fully confirmed	1	AT3TE06550	intergenic	
Chr3	deletion	774	1718635	1719408	N/A	1	No	multi_exons	AT3G05780
Chr3	deletion	299	1861345	1861643	Partially confirmed	1	No	intergenic	
Chr3	deletion	94	1874224	1874317	Partially confirmed	1	No	intergenic	
Chr3	deletion	611	1959413	1960023	Partially confirmed	2	AT3TE08235	intergenic	Y
Chr3	deletion	1766	2628484	2630249	Fully confirmed	26	AT3TE11080	intergenic	Y
Chr3	deletion	450	2805710	2806159	Fully confirmed	1	No	multi_exons	AT3G09160
Chr3	deletion	10474	2808421	2818894	Fully confirmed	2	AT3TE11850	intergenic	Y
Chr3	deletion	316	2849463	2849778	Fully confirmed	2	No	intergenic	Y
Chr3	deletion	916	2867395	2868310	Partially confirmed	1	No	exon	AT3G09340
Chr3	deletion	1569	2921721	2923289	Partially confirmed	4	AT3TE12275	complete_gene	AT3G09510
Chr3	deletion	582	3114980	3115561	Fully confirmed	5	AT3TE13060	intergenic	Y
Chr3	deletion	1013	3478252	3479264	Fully confirmed	2	AT3TE14615	intergenic	Y
Chr3	deletion	1050	3538065	3539114	N/A	1	AT3TE14865	intergenic	
Chr3	deletion	212	3549636	3549847	Partially confirmed	1	No	intergenic	
Chr3	deletion	157	3556090	3556246	Partially confirmed	1	No	intergenic	
Chr3	deletion	5594	3558543	3564136	Partially confirmed	1	No	complete_gene	AT3G11350,AT3G11370
Chr3	deletion	5340	3807305	3812644	Fully confirmed	2	AT3TE16035	intergenic	Y
Chr3	deletion	758	3987679	3988436	N/A	18	AT3TE16790	intergenic	Y
Chr3	deletion	1103	4724598	4725700	N/A	1	No	intergenic	
Chr3	deletion	136	4873157	4873292	Fully confirmed	3	No	intergenic	Y
Chr3	deletion	5038	4927416	4932453	Fully confirmed	1	AT3TE20780	complete_gene	AT3G14670
Chr3	deletion	162	5338738	5338899	N/A	1	No	intergenic	
Chr3	deletion	1023	5377195	5378217	Fully confirmed	1	AT3TE22580	intergenic	
Chr3	deletion	913	5379338	5380250	N/A	26	AT3TE22595	intergenic	Y
Chr3	deletion	2830	5390255	5393084	Fully confirmed	1	AT3TE22650	pseudo_gene	AT3G15935
Chr3	deletion	713	5493797	5494509	Fully confirmed	1	No	intergenic	
Chr3	deletion	101	5587146	5587246	Fully confirmed	1	No	intron	AT3G16440
Chr3	deletion	882	5590761	5591642	Fully confirmed	76	AT3TE23485	intergenic	Y
Chr3	deletion	1321	5651128	5652448	Fully confirmed	2	AT3TE23740	intergenic	Y
Chr3	deletion	1011	5839312	5840322	Partially confirmed	5	AT3TE24555	intergenic	Y
Chr3	deletion	96	5926989	5927084	N/A	1	No	intergenic	
Chr3	deletion	1279	5929425	5930703	Fully confirmed	6	AT3TE24910	intergenic	Y
Chr3	deletion	984	6342391	6343374	Fully confirmed	1	No	multi_exons	AT3G18485
Chr3	deletion	920	6486326	6487245	Fully confirmed	15	AT3TE27270	intergenic	Y
Chr3	deletion	761	7405426	7406186	Partially confirmed	1	No	5'UTR	AT3G21110
Chr3	deletion	159	7567185	7567343	Fully confirmed	1	No	intergenic	
Chr3	deletion	174	7637191	7637364	N/A	11	AT3TE32090	intergenic	Y
Chr3	deletion	4054	7693942	7697995	Partially confirmed	1	AT3TE32320	complete_gene	AT3G21850
Chr3	deletion	171	7846133	7846303	Fully confirmed	1	No	intron	AT3G22231
Chr3	deletion	79	7922674	7922752	Fully confirmed	1	No	intergenic	
Chr3	deletion	621	7936971	7937591	N/A	57	AT3TE33265	intergenic	Y
Chr3	deletion	288	7938288	7938575	Fully confirmed	1	AT3TE33275	intergenic	
Chr3	deletion	525	7999626	8000150	Fully confirmed	1	No	intergenic	
Chr3	deletion	2434	8093506	8095939	Fully confirmed	4	AT3TE33960	intergenic	Y

Chr3	deletion	1874	8101038	8102911	Fully confirmed	2	AT3TE33980	intergenic	Y
Chr3	deletion	1849	8129626	8131474	Fully confirmed	3	AT3TE34105	intergenic	Y
Chr3	deletion	1507	8247340	8248846	N/A	2	AT3TE34580	intergenic	Y
Chr3	deletion	335	8269111	8269445	Partially confirmed	1	No	intergenic	
Chr3	deletion	753	8344482	8345234	Partially confirmed	1	AT3TE34975	complete_gene	AT3G23320
Chr3	deletion	404	8612696	8613099	Partially confirmed	1	No	intergenic	
Chr3	deletion	7790	8654270	8662059	Partially confirmed	1	AT3TE36280, AT3TE36300	intergenic	
Chr3	deletion	175	8684948	8685122	Fully confirmed	12	AT3TE36405	intergenic	Y
Chr3	deletion	56	8805511	8805566	Partially confirmed	1	No	intergenic	
Chr3	deletion	15260	8842970	8858229	Fully confirmed	11	AT3TE37060	intergenic	Y
Chr3	deletion	136	8899567	8899702	Fully confirmed	1	No	intergenic	
Chr3	deletion	2755	8936332	8939086	Fully confirmed	1	AT3TE37380	complete_gene	AT3G24516,AT3G24517
Chr3	deletion	6260	9010932	9017191	Fully confirmed	1	AT3TE37690	intergenic	
Chr3	deletion	177	9102451	9102627	N/A	1	AT3TE38040	intergenic	
Chr3	deletion	236	9185350	9185585	Fully confirmed	1	No	pseudo_gene	AT3G25225
Chr3	deletion	156	9194021	9194176	Fully confirmed	1	No	intergenic	
Chr3	deletion	4746	9226632	9231377	Fully confirmed	1	AT3TE38565	intergenic	
Chr3	deletion	4221	9236765	9240985	Fully confirmed	1	AT3TE38595	intergenic	
Chr3	deletion	947	9471172	9472118	N/A	7	AT3TE39545	intergenic	Y
Chr3	deletion	789	9540460	9541248	Fully confirmed	17	AT3TE39820	intergenic	Y
Chr3	deletion	3986	9555749	9559734	Fully confirmed	1	AT3TE39890	intergenic	
Chr3	deletion	131	9646560	9646690	N/A	6	AT3TE40225	intergenic	Y
Chr3	deletion	12425	9723883	9736307	Fully confirmed	6	AT3TE40530	intergenic	Y
Chr3	deletion	1100	9808091	9809190	Fully confirmed	15	AT3TE40820	intergenic	Y
Chr3	deletion	681	9828709	9829389	Partially confirmed	18	AT3TE40900	intergenic	Y
Chr3	deletion	330	9981915	9982244	Fully confirmed	1	No	intergenic	
Chr3	deletion	2361	10166811	10169171	Partially confirmed	8	AT3TE42270	3'UTR	AT3G27470
Chr3	deletion	4129	10173740	10177868	Partially confirmed	1	AT3TE42300	intergenic	
Chr3	deletion	538	10181851	10182388	Partially confirmed	1	No	intergenic	
Chr3	deletion	2479	10200163	10202641	N/A	2	AT3TE42410	intergenic	Y
Chr3	deletion	544	10432536	10433079	Partially confirmed	44	AT3TE43325	intergenic	Y
Chr3	deletion	6617	10494354	10500970	Fully confirmed	1	AT3TE43605, AT3TE43635	complete_gene	AT3G28170
Chr3	deletion	270	10517678	10517947	Partially confirmed	21	AT3TE43690	intergenic	Y
Chr3	deletion	11467	10542617	10554083	Partially confirmed	1	AT3TE43800, AT3TE43875	intergenic	
Chr3	deletion	4669	10577157	10581825	Fully confirmed	3	AT3TE44000	exon	AT3G28310
Chr3	deletion	568	10588321	10588888	N/A	1	AT3TE44025	intergenic	
Chr3	deletion	467	10634573	10635039	Partially confirmed	1	No	intergenic	
Chr3	deletion	220	10665573	10665792	Fully confirmed	3	AT3TE44320	intergenic	Y
Chr3	deletion	581	10708599	10709179	N/A	121	AT3TE44490	intergenic	Y
Chr3	deletion	1249	10751116	10752364	Partially confirmed	8	AT3TE44695	intergenic	Y
Chr3	deletion	470	10752864	10753333	Partially confirmed	1	AT3TE44700	intergenic	
Chr3	deletion	1158	10834434	10835591	Partially confirmed	2	AT3TE45040	intergenic	Y
Chr3	deletion	88	10888277	10888364	Fully confirmed	1	AT3G28865	intergenic	
Chr3	deletion	612	10927517	10928128	N/A	1	AT3TE45405	intergenic	
Chr3	deletion	6906	10928283	10935188	Partially confirmed	1	AT3TE45415	intergenic	
Chr3	deletion	487	10992346	10992832	N/A	1	No	intergenic	
Chr3	deletion	215	11040272	11040486	N/A	1	No	intron	AT3G29050
Chr3	deletion	3556	11041052	11044607	Fully confirmed	1	AT3TE45900	intergenic	
Chr3	deletion	5946	11065429	11071374	N/A	1	AT3TE46000	complete_gene	AT3G29080
Chr3	deletion	2369	11097259	11099627	Partially confirmed	1	AT3TE46170	intergenic	
Chr3	deletion	4968	11122707	11127674	Partially confirmed	1	AT3TE46255	intergenic	
Chr3	deletion	616	11132130	11132745	Fully confirmed	103	AT3TE46270	intergenic	Y
Chr3	deletion	62	11150418	11150479	Fully confirmed	1	No	intron	AT3G29180

Chr3	deletion	321	11197512	11197832	N/A	1	AT3TE46630	intergenic	
Chr3	deletion	2276	11200443	11202718	Partially confirmed	2	AT3TE46655	intergenic	Y
Chr3	deletion	6336	11335561	11341896	Fully confirmed	4	AT3TE47235	intergenic	Y
Chr3	deletion	1552	11354159	11355710	N/A	2	AT3TE47280	intergenic	Y
Chr3	deletion	910	11369799	11370708	Partially confirmed	36	AT3TE47360	intergenic	Y
Chr3	deletion	231	11430057	11430287	N/A	29	AT3TE47630	intergenic	Y
Chr3	deletion	789	11438950	11439738	Fully confirmed	1	AT3TE47675	intergenic	
Chr3	deletion	297	11468926	11469222	Fully confirmed	1	AT3TE47805	intergenic	
Chr3	deletion	409	11575315	11575723	N/A	1	AT3TE48145	intergenic	
Chr3	deletion	122	11579544	11579665	Fully confirmed	1	No	intron	AT3G29750
Chr3	deletion	1445	11587846	11589290	N/A	1	AT3TE48180	intergenic	
Chr3	deletion	795	11619100	11619894	Partially confirmed	1	AT3TE48285	intergenic	
Chr3	deletion	2175	11646055	11648229	Partially confirmed	1	AT3TE48430	intergenic	
Chr3	deletion	4820	11664969	11669788	N/A	1	AT3TE48480	intergenic	
Chr3	deletion	566	11677845	11678410	Fully confirmed	1	AT3TE48525	intergenic	
Chr3	deletion	480	11736111	11736590	Partially confirmed	1	AT3TE48865	intergenic	
Chr3	deletion	5832	11826832	11832663	Fully confirmed	2	AT3TE49225	complete_gene	AT3G30200 Y
Chr3	deletion	5761	11846446	11852206	Fully confirmed	1	AT3TE49285	intergenic	
Chr3	deletion	1822	11859910	11861731	Partially confirmed	2	AT3TE49375	intergenic	Y
Chr3	deletion	1468	11863036	11864503	Fully confirmed	1	AT3TE49395	intergenic	
Chr3	deletion	1135	11883386	11884520	Partially confirmed	1	AT3TE49470	exon	AT3G30235
Chr3	deletion	10003	11935559	11945561	Partially confirmed	1	AT3TE49725	intergenic	
Chr3	deletion	909	11952918	11953826	Partially confirmed	1	AT3TE49765	intergenic	
Chr3	deletion	911	11959376	11960286	Fully confirmed	8	AT3TE49790	intergenic	Y
Chr3	deletion	5244	11962031	11967274	Partially confirmed	1	AT3TE49820	complete_gene	AT3G30370
Chr3	deletion	964	11967654	11968617	Partially confirmed	89	AT3TE49835	intergenic	Y
Chr3	deletion	1051	11971989	11973039	Partially confirmed	4	No	intergenic	Y
Chr3	deletion	231	12026528	12026758	Fully confirmed	3	AT3TE50125	intergenic	Y
Chr3	deletion	607	12068806	12069412	Fully confirmed	48	AT3TE50260	intergenic	Y
Chr3	deletion	1181	12196240	12197420	Fully confirmed	9	AT3TE50610	intergenic	Y
Chr3	deletion	99	12332674	12332772	N/A	1	No	intergenic	
Chr3	deletion	151	12348560	12348710	Fully confirmed	1	AT3TE51150	intergenic	
Chr3	deletion	136	12356953	12357088	N/A	1	No	intergenic	
Chr3	deletion	865	12373370	12374234	N/A	17	AT3TE51245	intergenic	Y
Chr3	deletion	172	12382194	12382365	Not confirmed	9	AT3TE51255	intergenic	Y
Chr3	deletion	2485	12487598	12490082	Fully confirmed	1	AT3TE51515	complete_gene	AT3G30805
Chr3	deletion	1035	12494997	12496031	Partially confirmed	18	AT3TE51535	intergenic	Y
Chr3	deletion	516	12634244	12634759	N/A	1	AT3TE51970	intergenic	
Chr3	deletion	111	12719083	12719193	Fully confirmed	2	AT3TE52365	intergenic	Y
Chr3	deletion	416	12725470	12725885	N/A	1	AT3TE52365	intergenic	
Chr3	deletion	377	12740090	12740466	Fully confirmed	3	AT3TE52420	intergenic	Y
Chr3	deletion	123	12977702	12977824	Partially confirmed	2	No	intergenic	Y
Chr3	deletion	11006	12982660	12993665	Fully confirmed	13	AT3TE53215	intergenic	Y
Chr3	deletion	715	13090177	13090891	Partially confirmed	1	AT3TE53605	intergenic	
Chr3	deletion	1007	13111152	13112158	N/A	36	AT3TE53665	intergenic	Y
Chr3	deletion	1632	13260519	13262150	Partially confirmed	10	AT3TE54245	intergenic	Y
Chr3	deletion	1428	13426577	13428004	Fully confirmed	79	AT3TE54740	intergenic	Y
Chr3	deletion	507	14540233	14540739	N/A	2	No	intergenic	Y
Chr3	deletion	1129	14676597	14677725	N/A	8	AT3TE60025	intergenic	Y
Chr3	deletion	1635	14686336	14687970	N/A	1	AT3TE60085	intergenic	
Chr3	deletion	266	14803829	14804094	N/A	12	AT3TE60460	intergenic	Y
Chr3	deletion	13957	14813279	14827235	Partially confirmed	11	AT3TE60510	intergenic	Y
Chr3	deletion	1102	14924397	14925498	N/A	1	AT3TE60875	intergenic	

Chr3	deletion	5292	14956987	14962278	Partially confirmed	19	AT3TE61000	intergenic			Y
Chr3	deletion	16061	14971501	14987561	Fully confirmed	1	AT3TE61035	intergenic			
Chr3	deletion	1144	15051501	15052644	Fully confirmed	1	AT3TE61335	intergenic			
Chr3	deletion	688	15061320	15062007	Partially confirmed	1	AT3TE61375	intergenic			
Chr3	deletion	1074	15064014	15065087	N/A	1	AT3TE61385	intergenic			
Chr3	deletion	291	15163926	15164216	N/A	4	AT3TE61650	intergenic			Y
Chr3	deletion	13322	15250477	15263798	Partially confirmed	18	AT3TE62025	intergenic			Y
Chr3	deletion	3720	15294694	15298413	N/A	1	AT3TE62190	intergenic			
Chr3	deletion	290	15309082	15309371	Fully confirmed	1	AT3TE62220	intergenic			
Chr3	deletion	578	15361978	15362555	N/A	1	AT3TE62395	intergenic			
Chr3	deletion	8952	15410889	15419840	Fully confirmed	1	AT3TE62570	intergenic			
Chr3	deletion	510	15428332	15428841	Not confirmed	5	AT3TE62595	intergenic			Y
Chr3	deletion	2726	15484295	15487020	Partially confirmed	1	AT3TE62750	intergenic			
Chr3	deletion	8841	15491888	15500728	Fully confirmed	1	AT3TE62785	intergenic			
Chr3	deletion	429	15525466	15525894	Partially confirmed	1	AT3TE62890	intergenic			
Chr3	deletion	9642	15644917	15654558	Fully confirmed	1	AT3TE63270	complete_gene	AT3G43750	multi_exons	AT3G43740
Chr3	deletion	306	15665314	15665619	Partially confirmed	1	No	intron	AT3G43810		
Chr3	deletion	99	15703194	15703292	Partially confirmed	1	AT3TE63505	intergenic			
Chr3	deletion	11217	15711475	15722691	Fully confirmed	15	AT3TE63540	intergenic			Y
Chr3	deletion	4962	15768787	15773748	Fully confirmed	1	AT3TE63765	intergenic			
Chr3	deletion	153	15774992	15775144	Partially confirmed	1	AT3TE63775	intron	AT3G43960		
Chr3	deletion	339	15782139	15782477	N/A	2	No	intergenic			Y
Chr3	deletion	381	15812831	15813211	Partially confirmed	1	AT3TE63930	intergenic			
Chr3	deletion	482	15972828	15973309	Fully confirmed	1	No	exon	AT3G44290		
Chr3	deletion	494	15980418	15980911	N/A	1	AT3TE64690	intergenic			
Chr3	deletion	313	16011205	16011517	Fully confirmed	1	No	intergenic			
Chr3	deletion	859	16037338	16038196	Fully confirmed	1	AT3TE64910	intergenic			
Chr3	deletion	593	16109549	16110141	Partially confirmed	1	No	intron	AT3G44510		
Chr3	deletion	271	16131645	16131915	N/A	1	AT3TE65295	intergenic			
Chr3	deletion	223	16152378	16152600	Fully confirmed	1	AT3TE65425	intron	AT3G44560		
Chr3	deletion	5900	16154498	16160397	Partially confirmed	1	AT3TE65435	complete_gene	AT3G44570		
Chr3	deletion	887	16162352	16163238	Fully confirmed	1	AT3TE65480	intergenic			
Chr3	deletion	1218	16172048	16173265	N/A	1	AT3TE65520	intergenic			
Chr3	deletion	10190	16173339	16183528	Fully confirmed	1	AT3TE65525	intergenic			
Chr3	deletion	594	16216059	16216652	Partially confirmed	2	No	intergenic			Y
Chr3	deletion	5702	16244608	16250309	Fully confirmed	1	AT3TE65835	intergenic			
Chr3	deletion	763	16274370	16275132	N/A	1	AT3TE65945	intergenic			
Chr3	deletion	1971	16277376	16279346	N/A	1	AT3TE65970	intergenic			
Chr3	deletion	251	16349629	16349879	Fully confirmed	1	No	intergenic			
Chr3	deletion	590	16351955	16352544	Partially confirmed	2	AT3TE66200	intergenic			Y
Chr3	deletion	1852	16450725	16452576	N/A	81	AT3TE66705	intergenic			Y
Chr3	deletion	984	16470308	16471291	Fully confirmed	4	AT3TE66765	intergenic			Y
Chr3	deletion	966	16500843	16501808	Fully confirmed	34	AT3TE66890	intergenic			Y
Chr3	deletion	1084	16553365	16554448	N/A	9	AT3TE67120	intergenic			Y
Chr3	deletion	1969	16561655	16563623	Partially confirmed	81	AT3TE67160	intergenic			Y
Chr3	deletion	570	16568176	16568745	Fully confirmed	9	AT3TE67180	intergenic			Y
Chr3	deletion	341	16625185	16625525	Partially confirmed	1	No	intergenic			
Chr3	deletion	315	16625935	16626249	Fully confirmed	1	No	intergenic			
Chr3	deletion	1094	16681866	16682959	N/A	5	No	intergenic			Y
Chr3	deletion	8715	16691854	16700568	Partially confirmed	1	AT3TE67635	complete_gene	AT3G45525		
Chr3	deletion	549	16724230	16724778	Fully confirmed	1	No	intergenic			
Chr3	deletion	530	16737595	16738124	Partially confirmed	16	AT3TE67835	intergenic			Y
Chr3	deletion	265	16770381	16770645	Partially confirmed	1	AT3TE67950	intergenic			

Chr3	deletion	472	16781217	16781688	Partially confirmed	1	AT3TE67980	intergenic	
Chr3	deletion	733	16797970	16798702	N/A	1	No	intergenic	
Chr3	deletion	1784	16798934	16800717	Partially confirmed	1	AT3TE68050	intergenic	
Chr3	deletion	1166	16801081	16802246	Partially confirmed	1	No	exon	AT3G45760
Chr3	deletion	952	16846943	16847894	Fully confirmed	3	AT3TE68240	intergenic	Y
Chr3	deletion	1007	16864184	16865190	Fully confirmed	1	No	multi_exons	AT3G45860
Chr3	deletion	553	16865741	16866293	Partially confirmed	1	No	exon	AT3G45860
Chr3	deletion	62	16946896	16946957	Fully confirmed	1	No	intergenic	
Chr3	deletion	525	16972288	16972812	Partially confirmed	1	No	intergenic	
Chr3	deletion	283	17018778	17019060	Partially confirmed	2	AT3TE68980	intergenic	Y
Chr3	deletion	700	17026271	17026970	N/A	1	No	exon	AT3G46340
Chr3	deletion	405	17087013	17087417	Fully confirmed	4	No	intergenic	Y
Chr3	deletion	203	17088209	17088411	N/A	1	No	intron	AT3G46430
Chr3	deletion	104	17103286	17103389	N/A	1	No	intron	AT3G46480
Chr3	deletion	918	17122508	17123425	Fully confirmed	1	No	5'UTR	AT3G46500
Chr3	deletion	2358	17145910	17148267	Fully confirmed	1	AT3TE69490	complete_gene	AT3G46570
Chr3	deletion	602	17150158	17150759	Partially confirmed	19	AT3TE69495	intergenic	Y
Chr3	deletion	224	17197258	17197481	Fully confirmed	10	AT3TE69690	intergenic	Y
Chr3	deletion	1128	17226019	17227146	Partially confirmed	29	AT3TE69815	intergenic	Y
Chr3	deletion	680	17270108	17270787	N/A	14	No	intergenic	Y
Chr3	deletion	2128	17299150	17301277	Fully confirmed	51	AT3TE70130	intergenic	Y
Chr3	deletion	1321	17395979	17397299	Partially confirmed	27	AT3TE70555	intergenic	Y
Chr3	deletion	1363	17449208	17450570	N/A	1	No	exon	AT3G47350
Chr3	deletion	497	17461417	17461913	Fully confirmed	1	No	intergenic	
Chr3	deletion	60	17570674	17570733	Partially confirmed	1	No	intergenic	
Chr3	deletion	3929	17575853	17579781	Fully confirmed	1	AT3TE71210	complete_gene	AT3G47675
Chr3	deletion	1251	17682939	17684189	Fully confirmed	3	No	complete_gene	AT3G47920
Chr3	deletion	96	17839757	17839852	Partially confirmed	1	AT3TE72275	intergenic	
Chr3	deletion	112	17875799	17875910	Not confirmed	1	No	intergenic	
Chr3	deletion	291	17947210	17947500	N/A	1	AT3TE72715	intergenic	
Chr3	deletion	890	17983130	17984019	Partially confirmed	1	AT3TE72850	intergenic	
Chr3	deletion	756	18055278	18056033	Fully confirmed	18	AT3TE73190	intergenic	Y
Chr3	deletion	94	18085968	18086061	N/A	1	AT3TE73330	intron	AT3G48770
Chr3	deletion	1153	18087048	18088200	Fully confirmed	4	No	intergenic	Y
Chr3	deletion	721	18107863	18108583	Fully confirmed	1	No	multi_exons	AT3G48830
Chr3	deletion	2370	18110240	18112609	Fully confirmed	7	AT3TE73435	intergenic	Y
Chr3	deletion	4939	18791151	18796089	Partially confirmed	1	AT3TE76225	intergenic	
Chr3	deletion	1013	18830912	18831924	Fully confirmed	3	AT3TE76350	intergenic	Y
Chr3	deletion	1215	18843490	18844704	N/A	8	AT3TE76405	intergenic	Y
Chr3	deletion	301	18873590	18873890	Fully confirmed	18	AT3TE76530	intergenic	Y
Chr3	deletion	262	18926130	18926391	N/A	33	AT3TE76765	intergenic	Y
Chr3	deletion	92	19011235	19011326	Partially confirmed	2	No	exon_middle	AT3G51171
Chr3	deletion	439	19027319	19027757	Fully confirmed	1	AT3TE77170	intergenic	
Chr3	deletion	586	19520642	19521227	Fully confirmed	63	AT3TE79240	intergenic	Y
Chr3	deletion	197	19534204	19534400	N/A	1	AT3TE79300	intergenic	
Chr3	deletion	620	19577850	19578469	Fully confirmed	3	No	complete_gene	AT3G52830
Chr3	deletion	199	19701000	19701198	N/A	2	AT3TE80000	intergenic	Y
Chr3	deletion	2983	19776682	19779664	Fully confirmed	5	AT3TE80315	intergenic	Y
Chr3	deletion	259	19783276	19783534	Fully confirmed	1	No	intergenic	
Chr3	deletion	777	19802580	19803356	Fully confirmed	1	No	intergenic	
Chr3	deletion	684	20090335	20091018	Partially confirmed	1	No	intergenic	
Chr3	deletion	95	20093001	20093095	Fully confirmed	1	No	intron	AT3G54280
Chr3	deletion	146	20277022	20277167	Fully confirmed	29	AT3TE82430	intergenic	Y

Chr3	deletion	229	20344274	20344502	N/A	1	No	5'UTR	AT3G54910	
Chr3	deletion	1215	20685604	20686818	Partially confirmed	1	AT3TE84110	intergenic		
Chr3	deletion	1330	20726136	20727465	Fully confirmed	2	AT3TE84280	intergenic		Y
Chr3	deletion	60	20763053	20763112	N/A	124	AT3TE84440	intergenic		Y
Chr3	deletion	2048	20786400	20788447	Partially confirmed	84	AT3TE84550	intergenic		Y
Chr3	deletion	476	21186145	21186620	Fully confirmed	1	No	intergenic		
Chr3	deletion	7475	21322158	21329632	Fully confirmed	2	AT3TE86800	5'UTR	AT3G57580	Y
Chr3	deletion	1293	21422541	21423833	Fully confirmed	1	No	intergenic		
Chr3	deletion	727	21898625	21899351	Fully confirmed	1	No	multi_exons	AT3G59240	
Chr3	deletion	2695	22112935	22115629	Fully confirmed	16	AT3TE90030	intergenic		Y
Chr3	deletion	2098	22118611	22120708	Fully confirmed	84	AT3TE90045	intergenic		Y
Chr3	deletion	5238	22237229	22242466	Partially confirmed	1	AT3TE90545	intergenic		
Chr3	deletion	93	22370239	22370331	Partially confirmed	2	No	intergenic		Y
Chr3	deletion	7798	22513422	22521219	Partially confirmed	2	AT3TE91745	intergenic		Y
Chr3	deletion	236	22521837	22522072	N/A	1	No	multi_exons	AT3G60940	
Chr3	deletion	509	22533236	22533744	Fully confirmed	10	AT3TE91790	intergenic		Y
Chr3	deletion	2286	22660299	22662584	Fully confirmed	2	AT3TE92345	intergenic		Y
Chr3	deletion	4956	22695566	22700521	Fully confirmed	8	AT3TE92525	3'UTR	AT3G61320	Y
Chr3	deletion	614	23085477	23086090	Fully confirmed	111	AT3TE94135	intergenic		Y
Chr3	deletion	1052	23109895	23110946	Partially confirmed	3	AT3TE94220	intergenic		Y
Chr3	deletion	557	23115818	23116374	Fully confirmed	1	AT3TE94220	intergenic		
Chr3	deletion	184	23377761	23377944	Fully confirmed	1	No	intergenic		
Chr4	deletion	190	194944	195133	Fully confirmed	1	No	intron	AT4G00440	
Chr4	deletion	2066	312202	314267	N/A	25	AT4TE01640	intergenic		Y
Chr4	deletion	816	378818	379633	Partially confirmed	4	AT4TE01975	intergenic		Y
Chr4	deletion	780	468526	469305	Partially confirmed	1	AT4TE02430	intergenic		
Chr4	deletion	171	513786	513956	Fully confirmed	2	No	intron	AT4G01220	Y
Chr4	deletion	69	514856	514924	Fully confirmed	2	No	intron	AT4G01220	Y
Chr4	deletion	1136	558355	559490	Partially confirmed	1	AT4TE02920	intergenic		
Chr4	deletion	928	571935	572862	Fully confirmed	3	AT4TE02995	intergenic		Y
Chr4	deletion	407	633630	634036	Fully confirmed	1	AT4TE03295	intergenic		
Chr4	deletion	279	687037	687315	Partially confirmed	1	No	intergenic		
Chr4	deletion	1835	690481	692315	Fully confirmed	1	AT4TE03560	complete_gene	AT4G01595	ncRNA AT4G01593_A T4G01593
Chr4	deletion	1231	697600	698830	Partially confirmed	13	AT4TE03595	intergenic		Y
Chr4	deletion	400	699790	700189	N/A	1	No	intergenic		
Chr4	deletion	2976	702116	705091	Partially confirmed	1	No	complete_gene	AT4G01640	multi_exons AT4G01650
Chr4	deletion	263	800834	801096	Partially confirmed	1	No	intergenic		
Chr4	deletion	9923	823501	833423	Partially confirmed	1	AT4TE04220	complete_gene	AT4G01910,AT4G01915,AT4G01920	
Chr4	deletion	980	993339	994318	Fully confirmed	16	No	intergenic		Y
Chr4	deletion	2085	999922	1002006	Fully confirmed	85	AT4TE05105	intergenic		Y
Chr4	deletion	219	1041939	1042157	Partially confirmed	1	No	intergenic		
Chr4	deletion	275	1094749	1095023	Partially confirmed	1	AT4TE05560	intergenic		
Chr4	deletion	2779	1097363	1100141	N/A	2	AT4TE05580	intergenic		Y
Chr4	deletion	2472	1114829	1117300	N/A	1	AT4TE06080	intron	AT4G02700	
Chr4	deletion	249	1190062	1190310	Fully confirmed	18	AT4TE06130	intergenic		Y
Chr4	deletion	912	1198713	1199624	Fully confirmed	71	No	intergenic		Y
Chr4	deletion	185	1294945	1295129	Fully confirmed	1	No	intergenic		
Chr4	deletion	275	1301142	1301416	Partially confirmed	1	AT4TE06645	intergenic		
Chr4	deletion	1016	1301948	1302963	N/A	25	AT4TE06655	intergenic		Y
Chr4	deletion	350	1305593	1305942	Fully confirmed	1	AT4TE06680	intergenic		
Chr4	deletion	4828	1312395	1317222	Partially confirmed	1	AT4TE06710	intergenic		
Chr4	deletion	624	1487511	1488134	Partially confirmed	1	AT4TE07570	intron	AT4G03380	
Chr4	deletion	268	1497260	1497527	Fully confirmed	1	No	intergenic		

Chr4	deletion	562	1521258	1521819	Fully confirmed	124	AT4TE07740	intergenic		Y
Chr4	deletion	4402	1544873	1549274	Partially confirmed	1	No	complete_gene	AT4G03480	
Chr4	deletion	7390	1550257	1557646	N/A	1	No	complete_gene	AT4G03500	multi_exons AT4G03490.A T4G03505
Chr4	deletion	114	1569640	1569753	Fully confirmed	1	No	intergenic		
Chr4	deletion	248	1624642	1624889	N/A	2	AT4TE08260	intergenic		Y
Chr4	deletion	1319	1667889	1669207	Fully confirmed	23	AT4TE08440	intergenic		Y
Chr4	deletion	1041	1774516	1775556	Fully confirmed	3	No	intergenic		Y
Chr4	deletion	1451	1806526	1807976	Partially confirmed	1	AT4TE08990	intergenic		
Chr4	deletion	8633	1838272	1846904	Partially confirmed	4	AT4TE09085	intergenic		Y
Chr4	deletion	2740	1850859	1853598	Fully confirmed	1	AT4TE09105	intergenic		
Chr4	deletion	1711	1996457	1998167	Fully confirmed	1	AT4TE09535	intergenic		
Chr4	deletion	695	2076051	2076745	Partially confirmed	2	No	intergenic		Y
Chr4	deletion	304	2108361	2108664	Fully confirmed	1	AT4TE09995	intergenic		
Chr4	deletion	347	2224695	2225041	Fully confirmed	1	No	intron	AT4TE09995	
Chr4	deletion	290	2253895	2254184	Fully confirmed	1	AT4TE10490	intergenic		
Chr4	deletion	109	2275798	2275906	Fully confirmed	2	AT4TE10585	intergenic		Y
Chr4	deletion	498	2321408	2321905	N/A	1	AT4TE10765	intergenic		
Chr4	deletion	130	2336801	2336930	N/A	1	No	intergenic		
Chr4	deletion	1534	2345775	2347308	Fully confirmed	1	AT4TE10910	intergenic		
Chr4	deletion	1766	2347830	2349595	Fully confirmed	1	AT4TE10925	intergenic		
Chr4	deletion	2117	2361334	2363450	Partially confirmed	28	AT4TE10985	intergenic		Y
Chr4	deletion	350	2376049	2376398	Fully confirmed	1	No	pseudo_gene	AT4G04692	
Chr4	deletion	11136	2396498	2407633	Partially confirmed	1	AT4TE11175	intergenic		
Chr4	deletion	2151	2443409	2445559	Partially confirmed	10	AT4TE11390	intergenic		Y
Chr4	deletion	179	2577017	2577195	Partially confirmed	4	No	intron	AT4G05030	Y
Chr4	deletion	468	2592290	2592757	Fully confirmed	15	AT4TE12145	intergenic		Y
Chr4	deletion	5660	2596990	2602649	N/A	1	AT4TE12175	intergenic		
Chr4	deletion	594	2636059	2636652	N/A	1	AT4TE12330	intergenic		
Chr4	deletion	1577	2639581	2641157	Fully confirmed	7	AT4TE12345	intergenic		Y
Chr4	deletion	1231	2641872	2643102	Partially confirmed	1	No	intergenic		
Chr4	deletion	5480	2643340	2648819	N/A	2	AT4TE12355	intergenic		Y
Chr4	deletion	1941	2648908	2650848	Partially confirmed	4	AT4TE12365	complete_gene	AT4G05136	Y
Chr4	deletion	1579	2771197	2772775	N/A	1	No	complete_gene	AT4G05490	
Chr4	deletion	4039	2789603	2793641	Fully confirmed	1	AT4TE13070	intergenic		
Chr4	deletion	261	2808437	2808697	Fully confirmed	1	No	intron	AT4G05523	
Chr4	deletion	7129	2809166	2816294	Fully confirmed	1	AT4TE13190	intergenic		
Chr4	deletion	1211	2878501	2879711	Fully confirmed	81	AT4TE13465	intergenic		Y
Chr4	deletion	193	2881391	2881583	Partially confirmed	16	AT4TE13465	intergenic		Y
Chr4	deletion	535	2899878	2900412	Fully confirmed	1	AT4TE13510	intergenic		
Chr4	deletion	576	2910829	2911404	Partially confirmed	21	AT4TE13555	intergenic		Y
Chr4	deletion	611	2997153	2997763	Fully confirmed	1	AT4TE13975	intergenic		
Chr4	deletion	164	3310933	3311096	Partially confirmed	48	AT4TE15130	intergenic		Y
Chr4	deletion	1835	4086837	4088671	Partially confirmed	3	AT4TE17710	intergenic		Y
Chr4	deletion	739	4191823	4192561	Partially confirmed	1	No	exon_3'_end	AT4G07380	
Chr4	deletion	95	4205596	4205690	Fully confirmed	1	No	intergenic		
Chr4	deletion	114	4205874	4205987	Partially confirmed	1	No	intergenic		
Chr4	deletion	303	4212346	4212648	Fully confirmed	2	AT4TE18165	intergenic		Y
Chr4	deletion	19199	4269499	4288697	Fully confirmed	1	AT4TE18315	intergenic		
Chr4	deletion	2782	4288996	4291777	Partially confirmed	1	AT4TE18335	intergenic		
Chr4	deletion	14555	4294664	4309218	Partially confirmed	1	AT4TE18365	intergenic		
Chr4	deletion	603	4312608	4313210	Fully confirmed	1	AT4TE18385	intergenic		
Chr4	deletion	603	4313938	4314540	Fully confirmed	1	AT4TE18385	intergenic		
Chr4	deletion	231	4454030	4454260	Not confirmed	36	AT4TE18825	intergenic		Y

Chr4	deletion	1530	4609217	4610746	N/A	98	AT4TE19380	intergenic	Y
Chr4	deletion	5588	4637750	4643337	Partially confirmed	1	AT4TE19495	intergenic	
Chr4	deletion	543	4644207	4644749	N/A	1	No	exon_3'_end	AT4G07825
Chr4	deletion	3511	4645309	4648819	Partially confirmed	27	AT4TE19530	intergenic	Y
Chr4	deletion	5349	4705787	4711135	Fully confirmed	1	AT4TE19780	intergenic	
Chr4	deletion	340	4855628	4855967	Partially confirmed	3	AT4TE20205	intergenic	Y
Chr4	deletion	693	4897646	4898338	Partially confirmed	2	AT4TE20400	intergenic	Y
Chr4	deletion	192	4954190	4954381	Fully confirmed	1	AT4TE20705	intergenic	
Chr4	deletion	595	5094172	5094766	Fully confirmed	6	AT4TE21135	intergenic	Y
Chr4	deletion	1400	5118131	5119530	N/A	2	AT4TE21255	intergenic	Y
Chr4	deletion	897	5140103	5140999	N/A	3	AT4TE21325	intergenic	Y
Chr4	deletion	1992	5174257	5176248	N/A	3	AT4TE21500	intergenic	Y
Chr4	deletion	327	5264077	5264403	Fully confirmed	1	AT4TE21900	intergenic	
Chr4	deletion	1244	5292980	5294223	Fully confirmed	1	AT4TE22040	intergenic	
Chr4	deletion	5275	5303776	5309050	Fully confirmed	1	AT4TE22095	intergenic	
Chr4	deletion	693	5391697	5392389	Fully confirmed	60	AT4TE22535	intergenic	Y
Chr4	deletion	543	5394479	5395021	N/A	1	AT4TE22545	complete_gene	AT4G08485
Chr4	deletion	5042	5581566	5586607	Fully confirmed	5	AT4TE23410	multi_exons	AT4G08760
Chr4	deletion	1089	5618038	5619126	Fully confirmed	1	AT4TE23545	intergenic	
Chr4	deletion	94	5634735	5634828	Fully confirmed	1	No	intergenic	
Chr4	deletion	593	5673141	5673733	N/A	1	No	complete_gene	AT4G08874
Chr4	deletion	434	5727819	5728252	Partially confirmed	6	AT4TE23995	intergenic	Y
Chr4	deletion	149	5742337	5742485	Fully confirmed	1	AT4TE24085	intergenic	
Chr4	deletion	984	5772262	5773245	N/A	1	AT4TE24230	intergenic	
Chr4	deletion	4874	5822426	5827299	Partially confirmed	2	AT4TE24480	intergenic	Y
Chr4	deletion	62	5848276	5848337	Fully confirmed	1	No	intron	AT4G09180
Chr4	deletion	2981	5851694	5854674	Fully confirmed	1	AT4TE24645	intergenic	
Chr4	deletion	374	5979310	5979683	Fully confirmed	1	AT4TE25170	intergenic	
Chr4	deletion	4976	5987002	5991977	Fully confirmed	2	AT4TE25200	intergenic	Y
Chr4	deletion	12446	6002550	6014995	Partially confirmed	1	AT4TE25295	complete_gene	AT4G09466
Chr4	deletion	106	6016175	6016280	Partially confirmed	1	No	intron	AT4G09490
Chr4	deletion	83	6040826	6040908	Fully confirmed	1	No	intergenic	
Chr4	deletion	849	6046707	6047555	Partially confirmed	1	AT4TE25495	intergenic	
Chr4	deletion	5239	6067398	6072636	Partially confirmed	3	AT4TE25590	intergenic	Y
Chr4	deletion	720	6109176	6109895	Partially confirmed	5	AT4TE25780	intergenic	Y
Chr4	deletion	1222	6110310	6111531	Fully confirmed	2	AT4TE25785	intergenic	Y
Chr4	deletion	3119	6113367	6116485	Partially confirmed	1	AT4TE25805	intergenic	
Chr4	deletion	746	6124401	6125146	Partially confirmed	1	No	exon_5'_end	AT4G09690
Chr4	deletion	6963	6125914	6132876	Partially confirmed	1	AT4TE25865	intergenic	
Chr4	deletion	64	6133897	6133960	Not confirmed	1	No	intron	AT4G09720
Chr4	deletion	196	6142349	6142544	Partially confirmed	1	AT4TE25925	intergenic	
Chr4	deletion	241	6153747	6153987	N/A	1	No	intergenic	
Chr4	deletion	1127	6178449	6179575	Fully confirmed	28	AT4TE26155	intergenic	Y
Chr4	deletion	1532	6183610	6185141	Partially confirmed	2	AT4TE26180	intron	AT4G09820
Chr4	deletion	2249	6197691	6199939	Fully confirmed	6	AT4TE26270	intergenic	Y
Chr4	deletion	645	6203665	6204309	N/A	1	No	intergenic	
Chr4	deletion	101	6222348	6222448	Fully confirmed	1	No	intron	AT4G09900
Chr4	deletion	1944	6226307	6228250	Fully confirmed	1	No	intergenic	
Chr4	deletion	1910	6365765	6367674	Partially confirmed	2	AT4TE27130	complete_gene	AT4G10230
Chr4	deletion	746	6393431	6394176	Partially confirmed	1	No	intron	AT4G10310
Chr4	deletion	219	6395801	6396019	Fully confirmed	1	No	3'UTR	AT4G10310
Chr4	deletion	69	6422800	6422868	Fully confirmed	1	No	intergenic	
Chr4	deletion	5657	6467412	6473068	Fully confirmed	1	AT4TE27640	intergenic	

Chr4	deletion	8873	6499714	6508586	Partially confirmed	1	AT4TE27775	intergenic	
Chr4	deletion	424	6586902	6587325	Partially confirmed	1	No	intergenic	
Chr4	deletion	5084	6588726	6593809	N/A	1	AT4TE28200	intergenic	
Chr4	deletion	812	6632716	6633527	Fully confirmed	2	AT4TE28405	intergenic	Y
Chr4	deletion	6267	6634291	6640557	Partially confirmed	1	AT4TE28445	complete_gene	AT4G10780
Chr4	deletion	140	6676898	6677037	Fully confirmed	1	No	3'UTR	AT4G10850
Chr4	deletion	2824	6684577	6687400	N/A	1	AT4TE28670	complete_gene	AT4G10880
Chr4	deletion	792	6814867	6815658	Partially confirmed	1	AT4TE29300	intron	AT4G11170
Chr4	deletion	2384	6827472	6829855	Partially confirmed	1	AT4TE29380	intergenic	
Chr4	deletion	291	6861500	6861790	Fully confirmed	2	No	intergenic	Y
Chr4	deletion	316	6877328	6877643	Partially confirmed	1	No	intergenic	
Chr4	deletion	870	6953478	6954347	Partially confirmed	1	AT4TE30000	complete_gene	AT4G11430
Chr4	deletion	573	6977665	6978237	Fully confirmed	4	No	intergenic	Y
Chr4	deletion	108	6980582	6980689	N/A	1	No	intron	AT4G11490
Chr4	deletion	1757	6992608	6994364	N/A	2	AT4TE30225	intergenic	Y
Chr4	deletion	283	7006099	7006381	Partially confirmed	1	No	intergenic	
Chr4	deletion	792	7099847	7100638	N/A	2	AT4TE30820	intergenic	Y
Chr4	deletion	1436	7101221	7102656	N/A	2	AT4TE30830	intergenic	Y
Chr4	deletion	264	7149946	7150209	Fully confirmed	1	AT4TE31060	intergenic	
Chr4	deletion	274	7169824	7170097	Partially confirmed	2	AT4TE31165	intergenic	Y
Chr4	deletion	331	7216504	7216834	Fully confirmed	1	No	intergenic	
Chr4	deletion	132	7227861	7227992	N/A	1	No	intergenic	
Chr4	deletion	2263	7275815	7278077	Partially confirmed	2	AT4TE31680	intergenic	Y
Chr4	deletion	131	7280975	7281105	N/A	1	No	intergenic	
Chr4	deletion	373	7298994	7299366	Partially confirmed	1	No	intron	AT4G12270
Chr4	deletion	1270	7300395	7301664	Fully confirmed	1	AT4TE31790	intergenic	
Chr4	deletion	294	7335197	7335490	Not confirmed	2	No	intergenic	Y
Chr4	deletion	1710	7346926	7348635	Partially confirmed	8	AT4TE32010	intergenic	Y
Chr4	deletion	1074	7639375	7640448	Fully confirmed	1	No	intergenic	
Chr4	deletion	1375	7812745	7814119	Fully confirmed	1	No	pseudo_gene	AT4G13442
Chr4	deletion	4986	7816821	7821806	Fully confirmed	16	AT4TE34305	intergenic	Y
Chr4	deletion	122	7833499	7833620	Fully confirmed	1	No	intergenic	
Chr4	deletion	730	7838213	7838942	Fully confirmed	12	AT4TE34395	intergenic	Y
Chr4	deletion	729	7848236	7848964	N/A	1	No	intergenic	
Chr4	deletion	661	7852872	7853532	N/A	10	AT4TE34490	intergenic	Y
Chr4	deletion	259	7922687	7922945	Fully confirmed	1	No	intergenic	
Chr4	deletion	1147	7950299	7951445	Partially confirmed	1	AT4TE34980	multi_exons	AT4G13670
Chr4	deletion	103	7954729	7954831	N/A	1	No	intron	AT4G13690
Chr4	deletion	2306	8063399	8065704	Partially confirmed	59	AT4TE35580	intergenic	Y
Chr4	deletion	1034	8141771	8142804	N/A	1	AT4TE35980	intergenic	
Chr4	deletion	6070	8313836	8319905	Partially confirmed	1	AT4TE36845	intergenic	
Chr4	deletion	2079	8327637	8329715	N/A	2	AT4TE36905	intergenic	Y
Chr4	deletion	409	8458376	8458784	N/A	3	No	pseudo_gene	AT4G14743
Chr4	deletion	556	8717996	8718551	Partially confirmed	2	No	intergenic	Y
Chr4	deletion	3383	8740918	8744300	Fully confirmed	2	AT4TE39035	exon	AT4G15320
Chr4	deletion	240	8762485	8762724	Fully confirmed	1	No	intergenic	
Chr4	deletion	3276	8807027	8810302	N/A	1	AT4TE39350	intron_type1	AT4G15396
Chr4	deletion	363	8858702	8859064	Fully confirmed	18	AT4TE39595	intergenic	Y
Chr4	deletion	939	8899078	8900016	Fully confirmed	70	AT4TE39800	intergenic	Y
Chr4	deletion	5916	8901449	8907364	Fully confirmed	1	AT4TE39815	intergenic	
Chr4	deletion	415	8946382	8946796	Fully confirmed	5	AT4TE40040	intergenic	Y
Chr4	deletion	759	8947174	8947932	Partially confirmed	1	AT4TE40050	intergenic	
Chr4	deletion	1055	8959464	8960518	N/A	1	AT4TE40115	intergenic	

Chr4	deletion	272	9035250	9035521	Partially confirmed	32	AT4TE40525	intergenic		Y
Chr4	deletion	379	9042153	9042531	Fully confirmed	1	No	intergenic		
Chr4	deletion	1694	9186894	9188587	Fully confirmed	1	No	intergenic		
Chr4	deletion	166	9215599	9215764	Partially confirmed	1	No	exon_3'_end	AT4G16295	
Chr4	deletion	651	9368717	9369367	Fully confirmed	30	AT4TE42280	5'UTR	AT4G16640	Y
Chr4	deletion	278	9401719	9401996	Fully confirmed	2	AT4TE42450	intergenic		Y
Chr4	deletion	427	9424166	9424592	N/A	1	AT4TE42560	intergenic		
Chr4	deletion	2005	9432385	9434389	Fully confirmed	1	AT4TE42605	intergenic		
Chr4	deletion	216	9466190	9466405	Fully confirmed	1	No	intergenic		
Chr4	deletion	5109	9570497	9575605	Partially confirmed	19	AT4TE43250	intergenic		Y
Chr4	deletion	5138	9732597	9737734	Fully confirmed	2	AT4TE44080	intergenic		Y
Chr4	deletion	2017	9761797	9763813	Fully confirmed	2	AT4TE44220	intergenic		Y
Chr4	deletion	4246	9794358	9798603	N/A	1	AT4TE44390	intergenic		
Chr4	deletion	182	9800360	9800541	Fully confirmed	1	No	intergenic		
Chr4	deletion	1917	9840691	9842607	N/A	2	AT4TE44650	intergenic		Y
Chr4	deletion	543	9860632	9861174	Fully confirmed	33	AT4TE44745	intergenic		Y
Chr4	deletion	204	9890106	9890309	Fully confirmed	1	No	intergenic		
Chr4	deletion	1212	9980882	9982093	Fully confirmed	2	AT4TE45320	intergenic		Y
Chr4	deletion	289	10020180	10020468	N/A	1	No	intergenic		
Chr4	deletion	398	10123719	10124116	Partially confirmed	1	No	intergenic		
Chr4	deletion	3774	10171524	10175297	Fully confirmed	1	AT4TE46305	intergenic		
Chr4	deletion	384	10179475	10179858	N/A	1	No	intergenic		
Chr4	deletion	3273	10283831	10287103	Fully confirmed	5	AT4TE46875	complete_gene	AT4G18692	Y
Chr4	deletion	238	10317068	10317305	Partially confirmed	1	AT4TE47040	intergenic		
Chr4	deletion	394	10341385	10341778	Partially confirmed	1	No	intergenic		
Chr4	deletion	626	10344878	10345503	N/A	1	No	exon_3'_end	AT4G18860	
Chr4	deletion	197	10427140	10427336	N/A	53	AT4TE47620	intergenic		Y
Chr4	deletion	2440	10537173	10539612	Partially confirmed	2	AT4TE48190	complete_gene	AT4G19270	Y
Chr4	deletion	187	10599334	10599520	N/A	1	No	intergenic		
Chr4	deletion	445	10605730	10606174	Fully confirmed	1	AT4TE48500	intergenic		
Chr4	deletion	718	10613061	10613778	Fully confirmed	1	No	exon	AT4G19470	
Chr4	deletion	154	10622451	10622604	N/A	1	No	intron	AT4G19490	
Chr4	deletion	173	10668723	10668895	Fully confirmed	1	No	intron	AT4G19580	
Chr4	deletion	201	10682675	10682875	Fully confirmed	1	No	exon	AT4G19620	
Chr4	deletion	1128	10684656	10685783	Partially confirmed	1	No	5'UTR	AT4G19630	pseudo_gene AT4G19633
Chr4	deletion	111	10743287	10743397	Fully confirmed	1	AT4TE49210	intergenic		
Chr4	deletion	631	10744551	10745181	Fully confirmed	1	AT4TE49220	intergenic		
Chr4	deletion	349	10766966	10767314	Fully confirmed	1	No	intergenic		
Chr4	deletion	795	10803136	10803930	Fully confirmed	1	AT4TE49505	exon_5'_end	AT4G19930	
Chr4	deletion	160	10817653	10817812	Fully confirmed	1	No	intergenic		
Chr4	deletion	128	10825623	10825750	Fully confirmed	7	No	intergenic		Y
Chr4	deletion	541	10839861	10840401	Fully confirmed	1	AT4TE49680	intergenic		
Chr4	deletion	5125	10992995	10998119	Fully confirmed	1	AT4TE50435	intergenic		
Chr4	deletion	1047	10999801	11000847	Partially confirmed	35	AT4TE50445	3'UTR	AT4G20370	Y
Chr4	deletion	557	11208794	11209350	Partially confirmed	2	No	intergenic		Y
Chr4	deletion	4231	11257415	11261645	Fully confirmed	1	No	multi_exons	AT4G21090,AT4G21100	
Chr4	deletion	567	11416572	11417138	Fully confirmed	1	No	pseudo_gene	AT4G21437	
Chr4	deletion	4521	11834128	11838648	Fully confirmed	2	AT4TE54750	intergenic		Y
Chr4	deletion	330	11928645	11928974	Partially confirmed	1	No	intergenic		
Chr4	deletion	5132	11930899	11936030	Partially confirmed	1	AT4TE55215	intergenic		
Chr4	deletion	2653	12002228	12004880	Partially confirmed	1	AT4TE55595	intergenic		
Chr4	deletion	2333	12129313	12131645	Partially confirmed	1	AT4TE56270	multi_exons	AT4G23160	
Chr4	deletion	7844	12152592	12160435	Fully confirmed	1	No	complete_gene	AT4G23220,AT4G23230	pseudo_gene AT4G23215

Chr4	deletion	875	12217309	12218183	N/A	1	No	exon_3'_end	AT4G23390	miRNA	AT4G23387
Chr4	deletion	125	12625375	12625499	Fully confirmed	1	No	miRNA	AT4G24415		
Chr4	deletion	848	12847579	12848426	Fully confirmed	1	No	multi_exons	AT4G24980		
Chr4	deletion	449	12892311	12892759	Fully confirmed	17	AT4TE60280	intron	AT4G25120		Y
Chr4	deletion	547	12948909	12949455	Partially confirmed	6	AT4TE60590	intergenic			Y
Chr4	deletion	17375	13619972	13637346	Fully confirmed	1	AT4TE64180	complete_gene	AT4G27190,AT4G27220		
Chr4	deletion	859	13887250	13888108	Partially confirmed	7	AT4TE65510	intron	AT4G27890		Y
Chr4	deletion	114	13960435	13960548	Fully confirmed	1	No	intron	AT4G28085		
Chr4	deletion	394	14031563	14031956	Fully confirmed	2	No	intergenic			Y
Chr4	deletion	8127	14280182	14288308	Fully confirmed	9	AT4TE67560	intergenic			Y
Chr4	deletion	89	14602167	14602255	Fully confirmed	1	No	intron	AT4G29860		
Chr4	deletion	4645	14977037	14981681	Fully confirmed	1	AT4TE71140	intergenic			
Chr4	deletion	2384	15012482	15014865	Partially confirmed	8	AT4TE71340	intergenic			Y
Chr4	deletion	952	15397744	15398695	Fully confirmed	2	AT4TE73405	intergenic			Y
Chr4	deletion	273	15566552	15566824	N/A	2	No	intron	AT4G32230		Y
Chr4	deletion	1212	15922833	15924044	Fully confirmed	13	AT4TE76155	intergenic			Y
Chr4	deletion	130	16396438	16396567	Partially confirmed	1	No	3'UTR	AT4G34250		
Chr4	deletion	100	16754768	16754867	Partially confirmed	1	No	intergenic			
Chr4	deletion	721	16830739	16831459	Partially confirmed	3	AT4TE80960	intergenic			Y
Chr4	deletion	1807	16863263	16865069	Fully confirmed	81	AT4TE81120	intergenic			Y
Chr4	deletion	245	16920949	16921193	Fully confirmed	1	No	intergenic			
Chr4	deletion	145	16951533	16951677	Fully confirmed	41	No	intergenic			Y
Chr4	deletion	336	17555586	17555921	Fully confirmed	1	No	3'UTR	AT4G37300		
Chr4	deletion	1145	17654864	17656008	N/A	11	AT4TE85270	intergenic			Y
Chr4	deletion	571	17674153	17674723	Partially confirmed	1	AT4TE85370	intergenic			
Chr4	deletion	130	17681683	17681812	N/A	1	No	intergenic			
Chr4	deletion	4816	17712150	17716965	Fully confirmed	1	AT4TE85580	intergenic			
Chr4	deletion	240	18087204	18087443	Fully confirmed	1	AT4TE87560	intron	AT4G38750		
Chr4	deletion	107	18100443	18100549	Partially confirmed	1	No	intergenic			
Chr4	deletion	56	18133442	18133497	Fully confirmed	1	No	intron	AT4G38870		
Chr4	deletion	4047	18247688	18251734	Partially confirmed	1	AT4TE88410	intron	AT4G39180		
Chr4	deletion	1771	18517136	18518906	Fully confirmed	1	No	complete_gene	AT4G39930		
Chr4	deletion	230	18526368	18526597	N/A	1	No	intron	AT4G39950		
Chr5	deletion	6496	64772	71267	Fully confirmed	4	AT5TE00230	intergenic			Y
Chr5	deletion	94	163116	163209	Not confirmed	1	No	exon_middle	AT5G01400		
Chr5	deletion	1030	250091	251120	Fully confirmed	5	AT5TE00870	intergenic			Y
Chr5	deletion	3156	353874	357029	Fully confirmed	1	AT5TE01245	intergenic			
Chr5	deletion	2781	681763	684543	Fully confirmed	1	No	complete_gene	AT5G02930		
Chr5	deletion	358	875031	875388	Partially confirmed	2	No	5'UTR	AT5G03495		Y
Chr5	deletion	579	876022	876600	Partially confirmed	1	No	3'UTR	AT5G03500		
Chr5	deletion	2014	1013761	1015774	Partially confirmed	1	No	intergenic			
Chr5	deletion	572	1026497	1027068	N/A	9	AT5TE03750	intergenic			Y
Chr5	deletion	7546	1349153	1356698	Partially confirmed	1	No	intergenic			
Chr5	deletion	314	1366103	1366416	Fully confirmed	1	No	intron	AT5G04730		
Chr5	deletion	1142	1515163	1516304	Partially confirmed	1	AT5TE05480	intergenic			
Chr5	deletion	3170	1687787	1690956	Partially confirmed	1	AT5TE06110	complete_gene	AT5G05657		
Chr5	deletion	168	1732023	1732190	Partially confirmed	2	No	intergenic			Y
Chr5	deletion	176	1738493	1738668	Fully confirmed	1	No	intergenic			
Chr5	deletion	8380	1962067	1970446	Partially confirmed	1	No	intergenic			
Chr5	deletion	130	2062890	2063019	Fully confirmed	1	No	intergenic			
Chr5	deletion	576	2066882	2067457	Fully confirmed	1	No	intergenic			
Chr5	deletion	357	2088918	2089274	Fully confirmed	1	No	complete_gene	AT5G06755	5'UTR	AT5G06750
Chr5	deletion	2164	2105886	2108049	Partially confirmed	1	AT5TE07650	intergenic			

Chr5	deletion	268	2242903	2243170	N/A	1	No	intergenic	
Chr5	deletion	5590	2257343	2262932	Fully confirmed	1	AT5TE08220	intergenic	
Chr5	deletion	57	2611775	2611831	Fully confirmed	1	No	intergenic	
Chr5	deletion	2527	2896502	2899028	Partially confirmed	1	AT5TE10540	intergenic	
Chr5	deletion	825	3161603	3162427	Fully confirmed	18	No	intergenic	Y
Chr5	deletion	57	3314170	3314226	N/A	1	No	intergenic	
Chr5	deletion	430	3723249	3723678	Partially confirmed	1	No	intergenic	
Chr5	deletion	5004	4208082	4213085	Fully confirmed	8	AT5TE15240	3'UTR	AT5G13200 Y
Chr5	deletion	3618	4286126	4289743	Fully confirmed	1	No	intergenic	
Chr5	deletion	6077	4320161	4326237	Fully confirmed	1	AT5TE15640	intergenic	
Chr5	deletion	224	4402589	4402812	N/A	1	No	3'UTR	AT5G13650
Chr5	deletion	867	4970260	4971126	N/A	16	AT5TE17955	intergenic	Y
Chr5	deletion	594	5007980	5008573	Partially confirmed	2	No	complete_gene	AT5G15420 Y
Chr5	deletion	103	5029427	5029529	Fully confirmed	1	No	intron	AT5G15490
Chr5	deletion	66	5255088	5255153	Fully confirmed	1	No	intergenic	
Chr5	deletion	833	5288316	5289148	Fully confirmed	1	No	intergenic	
Chr5	deletion	1136	5383156	5384291	Fully confirmed	1	No	complete_gene	AT5G16486
Chr5	deletion	839	5442302	5443140	Fully confirmed	3	AT5TE19690	intergenic	Y
Chr5	deletion	2931	5643931	5646861	N/A	2	AT5TE20430	intron	AT5G17165 Y
Chr5	deletion	2004	5776110	5778113	Partially confirmed	1	No	intergenic	
Chr5	deletion	2830	5848253	5851082	Fully confirmed	1	AT5TE21155	intergenic	
Chr5	deletion	89	5902449	5902537	Fully confirmed	1	No	3'UTR	AT5G17860
Chr5	deletion	333	5906035	5906367	Fully confirmed	1	No	intergenic	
Chr5	deletion	97	5938728	5938824	Fully confirmed	1	No	intron	AT5G17920
Chr5	deletion	6821	6205806	6212626	Fully confirmed	3	AT5TE22500	complete_gene	AT5G18636 Y
Chr5	deletion	285	6364286	6364570	Fully confirmed	1	No	intergenic	
Chr5	deletion	5144	6403053	6408196	Partially confirmed	1	AT5TE23185	intergenic	
Chr5	deletion	698	6460695	6461392	N/A	1	AT5TE23375	3'UTR	AT5G19200
Chr5	deletion	4755	6630718	6635472	Fully confirmed	1	AT5TE24040	intergenic	
Chr5	deletion	217	6789420	6789636	N/A	6	No	intergenic	Y
Chr5	deletion	167	6889655	6889821	Fully confirmed	1	No	intron	AT5G20380
Chr5	deletion	2188	6910220	6912407	Fully confirmed	1	No	complete_gene	AT5G20450,AT5G20447
Chr5	deletion	450	6926015	6926464	N/A	9	AT5TE25115	intergenic	Y
Chr5	deletion	1333	6982213	6983545	Partially confirmed	3	AT5TE25310	intergenic	Y
Chr5	deletion	1001	7034218	7035218	Fully confirmed	1	AT5TE25460	intergenic	
Chr5	deletion	2444	7056138	7058581	N/A	1	AT5TE25535	intergenic	
Chr5	deletion	528	7069990	7070517	N/A	114	AT5TE25585	intergenic	Y
Chr5	deletion	108	7090221	7090328	N/A	1	No	intergenic	
Chr5	deletion	361	7300695	7301055	Fully confirmed	1	No	intergenic	
Chr5	deletion	56	7505868	7505923	N/A	1	No	intergenic	
Chr5	deletion	117	7614638	7614754	N/A	6	No	intergenic	Y
Chr5	deletion	1006	7684598	7685603	N/A	1	No	intergenic	
Chr5	deletion	2092	7711132	7713223	N/A	25	AT5TE27905	intergenic	Y
Chr5	deletion	261	7739127	7739387	N/A	1	No	intergenic	
Chr5	deletion	377	7752817	7753193	Fully confirmed	4	No	intergenic	Y
Chr5	deletion	233	7825728	7825960	Fully confirmed	4	No	3'UTR	AT5G23230 Y
Chr5	deletion	1357	7828927	7830283	Fully confirmed	1	AT5TE28340	intergenic	
Chr5	deletion	904	7833876	7834779	Fully confirmed	26	AT5TE28355	intergenic	Y
Chr5	deletion	1757	8033514	8035270	N/A	1	No	complete_gene	AT5G23830
Chr5	deletion	76	8048050	8048125	N/A	1	No	intron	AT5G23870
Chr5	deletion	208	8171308	8171515	Fully confirmed	1	No	intergenic	
Chr5	deletion	164	8187000	8187163	Fully confirmed	1	No	intergenic	
Chr5	deletion	132	8219480	8219611	N/A	1	No	3'UTR	AT5G24210

Chr5	deletion	296	8241282	8241577	Partially confirmed	1	No	intergenic	
Chr5	deletion	327	8322623	8322949	Fully confirmed	1	No	intergenic	
Chr5	deletion	6921	8385135	8392055	Partially confirmed	1	AT5TE30340	intergenic	
Chr5	deletion	304	8398080	8398383	Fully confirmed	11	No	intergenic	Y
Chr5	deletion	495	8400174	8400668	Fully confirmed	1	AT5TE30375	intergenic	
Chr5	deletion	1093	8400987	8402079	Fully confirmed	1	No	pseudo_gene	AT5G24557
Chr5	deletion	2121	8419467	8421587	Fully confirmed	1	AT5TE30460	complete_gene	AT5G24593
Chr5	deletion	415	8442889	8443303	N/A	1	No	intergenic	
Chr5	deletion	531	8447710	8448240	Partially confirmed	2	No	5'UTR	AT5G24670 Y
Chr5	deletion	4340	8502770	8507109	Fully confirmed	1	AT5TE30775	intergenic	
Chr5	deletion	109	8507359	8507467	Fully confirmed	1	No	intergenic	
Chr5	deletion	6379	8571468	8577846	Partially confirmed	1	AT5TE31020	intergenic	
Chr5	deletion	1423	8585647	8587069	Fully confirmed	1	AT5TE31060	intergenic	
Chr5	deletion	875	8601819	8602693	Partially confirmed	81	AT5TE31125	intron	AT5G24960 Y
Chr5	deletion	4873	8624510	8629382	Fully confirmed	4	AT5TE31200	intergenic	Y
Chr5	deletion	5715	8664270	8669984	Fully confirmed	1	AT5TE31340	intergenic	
Chr5	deletion	1190	8675303	8676492	N/A	23	AT5TE31350	intergenic	Y
Chr5	deletion	950	8741906	8742855	Fully confirmed	2	No	multi_exons	AT5G25230 Y
Chr5	deletion	110	8743260	8743369	Fully confirmed	1	No	intron	AT5G25230
Chr5	deletion	1310	8769365	8770674	Partially confirmed	3	AT5TE31745	intergenic	Y
Chr5	deletion	140	8803847	8803986	Fully confirmed	1	No	intergenic	
Chr5	deletion	870	8819316	8820185	Fully confirmed	1	AT5TE31920	intergenic	
Chr5	deletion	3426	8826688	8830113	Partially confirmed	1	AT5TE31945	intergenic	
Chr5	deletion	1965	8836278	8838242	N/A	1	No	multi_exons	AT5G25415
Chr5	deletion	149	8910957	8911105	N/A	1	No	intergenic	
Chr5	deletion	152	9271247	9271398	Fully confirmed	1	No	intergenic	
Chr5	deletion	3824	9272019	9275842	N/A	1	AT5TE33540	intergenic	
Chr5	deletion	131	9315913	9316043	Partially confirmed	1	AT5TE33720	intergenic	
Chr5	deletion	2060	9461349	9463408	Fully confirmed	3	AT5TE34340	intergenic	Y
Chr5	deletion	1848	9557659	9559506	Fully confirmed	4	AT5TE34715	intergenic	Y
Chr5	deletion	275	9560687	9560961	N/A	1	No	intergenic	
Chr5	deletion	4231	9601050	9605280	Partially confirmed	2	AT5TE34840	complete_gene	AT5G27247,AT5G27260 Y
Chr5	deletion	7729	9609749	9617477	Partially confirmed	1	AT5TE34865	intergenic	
Chr5	deletion	892	9631793	9632684	Fully confirmed	17	No	intergenic	Y
Chr5	deletion	3629	9640954	9644582	Partially confirmed	1	AT5TE34980	intergenic	
Chr5	deletion	139	9652602	9652740	Partially confirmed	1	AT5TE35010	intron	AT5G27350
Chr5	deletion	139	9909295	9909433	Fully confirmed	2	AT5G27895	intergenic	Y
Chr5	deletion	354	9910235	9910588	Fully confirmed	1	AT5TE36095	intergenic	
Chr5	deletion	1329	9915469	9916797	Fully confirmed	1	AT5TE36115	intergenic	
Chr5	deletion	225	9918400	9918624	Partially confirmed	9	AT5TE36125	intergenic	Y
Chr5	deletion	13614	9920345	9933958	Partially confirmed	1	AT5TE36160	intergenic	
Chr5	deletion	2076	9962941	9965016	Partially confirmed	85	AT5TE36260	intergenic	Y
Chr5	deletion	562	10041812	10042373	N/A	59	AT5TE36570	intergenic	Y
Chr5	deletion	11259	10048056	10059314	Partially confirmed	1	AT5TE36620	intergenic	
Chr5	deletion	1059	10067089	10068147	Partially confirmed	1	AT5TE36680	intergenic	
Chr5	deletion	1658	10071499	10073156	Partially confirmed	1	AT5TE36700	intergenic	
Chr5	deletion	677	10084166	10084842	Fully confirmed	1	No	intergenic	
Chr5	deletion	1144	10087607	10088750	Fully confirmed	108	AT5TE36790	intergenic	Y
Chr5	deletion	661	10095076	10095736	Fully confirmed	1	AT5TE36805	intergenic	
Chr5	deletion	727	10221249	10221975	Partially confirmed	1	AT5G28250	intergenic	
Chr5	deletion	1263	10225174	10226436	Partially confirmed	1	AT5TE37300	intergenic	
Chr5	deletion	501	10614270	10614770	Fully confirmed	1	No	intergenic	
Chr5	deletion	766	10632799	10633564	Fully confirmed	10	AT5TE38725	intergenic	Y

Chr5	deletion	680	10676747	10677426	Partially confirmed	1	AT5TE38860	3'UTR	AT5G28646	
Chr5	deletion	421	10733701	10734121	N/A	3	AT5TE39080	intergenic		Y
Chr5	deletion	115	10749772	10749886	Fully confirmed	1	No	intergenic		
Chr5	deletion	161	10797658	10797818	N/A	1	No	intron	AT5G28770	
Chr5	deletion	586	10801725	10802310	Fully confirmed	1	AT5TE39275	intergenic		
Chr5	deletion	153	10844069	10844221	Fully confirmed	3	No	intron	AT5G28824	Y
Chr5	deletion	221	10894351	10894571	Partially confirmed	1	AT5TE39590	intergenic		
Chr5	deletion	1252	10897809	10899060	N/A	1	No	exon	AT5G28885	
Chr5	deletion	264	11416265	11416528	Fully confirmed	2	AT5TE41310	intergenic		Y
Chr5	deletion	843	11454150	11454992	Partially confirmed	2	AT5TE41415	intergenic		Y
Chr5	deletion	1009	11558499	11559507	N/A	2	AT5TE41795	intergenic		Y
Chr5	deletion	388	11593640	11594027	Fully confirmed	13	AT5TE41875	intergenic		Y
Chr5	deletion	6726	11599318	11606043	Fully confirmed	16	AT5TE41900	intergenic		Y
Chr5	deletion	1220	11654862	11656081	Partially confirmed	2	AT5TE42025	intergenic		Y
Chr5	deletion	104	11662500	11662603	Partially confirmed	6	AT5TE42045	intergenic		Y
Chr5	deletion	551	11667806	11668356	N/A	49	No	intergenic		Y
Chr5	deletion	11323	11810270	11821592	Partially confirmed	6	AT5TE42440	intergenic		Y
Chr5	deletion	1270	12027029	12028298	N/A	37	No	intergenic		Y
Chr5	deletion	215	12195138	12195352	N/A	9	AT5TE43370	intergenic		Y
Chr5	deletion	518	12514529	12515046	Fully confirmed	1	AT5TE44345	intergenic		
Chr5	deletion	2348	12524983	12527330	Partially confirmed	26	AT5TE44370	intergenic		Y
Chr5	deletion	722	12601008	12601729	Fully confirmed	2	AT5TE44640	intergenic		Y
Chr5	deletion	428	12934892	12935319	Partially confirmed	46	AT5TE46055	intergenic		Y
Chr5	deletion	1158	12987486	12988643	Fully confirmed	2	AT5TE46190	intergenic		Y
Chr5	deletion	351	13056891	13057241	Fully confirmed	1	AT5TE46435	intergenic		
Chr5	deletion	715	13081012	13081726	N/A	1	AT5TE46565	intergenic		
Chr5	deletion	5525	13666697	13672221	Partially confirmed	1	No	complete_gene	AT5G35450	
Chr5	deletion	103	13775522	13775624	N/A	1	No	intergenic		
Chr5	deletion	13736	13776973	13790708	Partially confirmed	1	AT5TE49075	complete_gene	AT5G35603,AT5G35604	
Chr5	deletion	970	13795010	13795979	Partially confirmed	1	AT5TE49110	intergenic		
Chr5	deletion	157	13808024	13808180	Fully confirmed	1	AT5TE49170	intergenic		
Chr5	deletion	1685	13815898	13817582	Fully confirmed	5	AT5TE49245	intergenic		Y
Chr5	deletion	151	13853245	13853395	Fully confirmed	1	No	exon_middle	AT5G35660	
Chr5	deletion	124	13945543	13945666	Partially confirmed	3	AT5TE49700	intergenic		Y
Chr5	deletion	104	13947222	13947325	Fully confirmed	1	AT5TE49700	intergenic		
Chr5	deletion	4546	13949457	13954002	N/A	1	AT5TE49725	intergenic		
Chr5	deletion	238	13978143	13978380	Fully confirmed	18	AT5TE49810	intergenic		Y
Chr5	deletion	5319	13982136	13987454	Partially confirmed	1	AT5TE49855	intergenic		
Chr5	deletion	5498	13994795	14000292	Fully confirmed	2	AT5TE49915	intergenic		Y
Chr5	deletion	1186	14012276	14013461	Fully confirmed	1	AT5TE49950	intergenic		
Chr5	deletion	7196	14055651	14062846	N/A	1	AT5TE50130	complete_gene	AT5G35920	
Chr5	deletion	1186	14289399	14290584	N/A	3	No	intergenic		Y
Chr5	deletion	559	14521132	14521690	Partially confirmed	1	No	exon	AT5G36870	
Chr5	deletion	287	14544976	14545262	Partially confirmed	1	No	intron	AT5G36890	
Chr5	deletion	2002	14557737	14559738	Partially confirmed	1	AT5TE52345	intergenic		
Chr5	deletion	226	14560393	14560618	N/A	1	No	intergenic		
Chr5	deletion	239	14563875	14564113	Partially confirmed	1	No	intergenic		
Chr5	deletion	1766	14567969	14569734	Fully confirmed	1	No	multi_exons	AT5G36930	
Chr5	deletion	387	14680198	14680584	Fully confirmed	2	AT5G37125	intergenic		Y
Chr5	deletion	650	14693438	14694087	Fully confirmed	11	AT5TE52920	intergenic		Y
Chr5	deletion	518	14739917	14740434	Partially confirmed	1	No	intergenic		
Chr5	deletion	1725	14770325	14772049	N/A	1	AT5TE53250	intergenic		
Chr5	deletion	107	14773761	14773867	Partially confirmed	1	No	intron	AT5G37310	

Chr5	deletion	528	14896191	14896718	Fully confirmed	1	No	intergenic	
Chr5	deletion	531	15007225	15007755	Fully confirmed	1	No	intergenic	
Chr5	deletion	164	15096992	15097155	N/A	1	No	intron	AT5G37910
Chr5	deletion	1336	15105702	15107037	Partially confirmed	7	AT5TE54615	intergenic	Y
Chr5	deletion	1324	15109015	15110338	Fully confirmed	1	AT5TE54635	intergenic	
Chr5	deletion	776	15110765	15111540	Partially confirmed	1	AT5TE54635	intergenic	
Chr5	deletion	239	15126473	15126711	N/A	4	No	intergenic	Y
Chr5	deletion	1445	15183234	15184678	Partially confirmed	8	AT5TE54925	intergenic	Y
Chr5	deletion	3579	15194500	15198078	N/A	2	AT5TE54980	intergenic	Y
Chr5	deletion	2680	15202648	15205327	N/A	1	AT5TE55010	pseudo_gene	AT5TE55010
Chr5	deletion	426	15212897	15213322	N/A	25	No	intergenic	Y
Chr5	deletion	1191	15236738	15237928	Partially confirmed	2	AT5TE55140	multi_exons	AT5G38190
Chr5	deletion	595	15291231	15291825	Fully confirmed	16	AT5TE55330	intergenic	Y
Chr5	deletion	176	15312553	15312728	Partially confirmed	1	No	intergenic	
Chr5	deletion	172	15325640	15325811	Fully confirmed	1	No	intergenic	
Chr5	deletion	6151	15334061	15340211	N/A	1	AT5TE55490	intergenic	
Chr5	deletion	1482	15341214	15342695	N/A	30	AT5TE55500	intergenic	Y
Chr5	deletion	248	15343214	15343461	N/A	1	No	intergenic	
Chr5	deletion	325	15409028	15409352	Partially confirmed	1	AT5TE55735	intergenic	
Chr5	deletion	205	15443365	15443569	Fully confirmed	1	No	intergenic	
Chr5	deletion	261	15505797	15506057	N/A	1	No	intergenic	
Chr5	deletion	2960	15636218	15639177	N/A	2	AT5TE56560	intergenic	Y
Chr5	deletion	311	15643179	15643489	Partially confirmed	1	AT5TE56580	intergenic	
Chr5	deletion	5021	15646197	15651217	Fully confirmed	1	AT5TE56585	intergenic	
Chr5	deletion	947	15696528	15697474	Partially confirmed	15	AT5TE56685	intergenic	Y
Chr5	deletion	380	15699111	15699490	Fully confirmed	1	AT5TE56690	intergenic	
Chr5	deletion	161	15704300	15704460	Fully confirmed	2	AT5TE56725	intergenic	Y
Chr5	deletion	518	15725824	15726341	Fully confirmed	1	No	intergenic	
Chr5	deletion	921	15741623	15742543	Partially confirmed	1	No	intergenic	
Chr5	deletion	1539	15764245	15765783	Fully confirmed	1	No	complete_gene	AT5G39390
Chr5	deletion	778	15779045	15779822	Fully confirmed	17	AT5TE56960	intergenic	Y
Chr5	deletion	621	15791114	15791734	N/A	48	AT5TE57005	intergenic	Y
Chr5	deletion	112	15793443	15793554	Partially confirmed	1	AT5TE57010	intergenic	
Chr5	deletion	127	15795341	15795467	Partially confirmed	1	No	exon_middle	AT5G39471
Chr5	deletion	372	15798970	15799341	Fully confirmed	1	No	pseudo_gene	AT5G39473
Chr5	deletion	5894	15867512	15873405	Partially confirmed	1	No	intergenic	
Chr5	deletion	1134	15982207	15983340	N/A	1	No	complete_gene	AT5G39920
Chr5	deletion	5653	16259101	16264753	Partially confirmed	1	AT5TE58755	intergenic	
Chr5	deletion	408	16267846	16268253	Partially confirmed	1	No	intergenic	
Chr5	deletion	386	16310014	16310399	Fully confirmed	1	No	intergenic	
Chr5	deletion	113	16515847	16515959	Fully confirmed	2	No	intron	AT5G41300
Chr5	deletion	6525	16547154	16553678	Fully confirmed	1	No	intergenic	
Chr5	deletion	1016	16602727	16603742	Partially confirmed	1	No	pseudo_gene	AT5G41494
Chr5	deletion	3036	16604621	16607656	Fully confirmed	1	AT5TE59955	intergenic	
Chr5	deletion	1299	16681243	16682541	N/A	3	AT5TE60220	intergenic	Y
Chr5	deletion	591	16712849	16713439	Partially confirmed	114	AT5TE60325	intergenic	Y
Chr5	deletion	742	16721196	16721937	Fully confirmed	16	AT5TE60370	intergenic	Y
Chr5	deletion	241	16826316	16826556	Fully confirmed	17	AT5TE60750	intergenic	Y
Chr5	deletion	397	16828721	16829117	Fully confirmed	2	No	intergenic	Y
Chr5	deletion	203	16859302	16859504	N/A	1	AT5TE60880	intergenic	
Chr5	deletion	2218	16908095	16910312	Partially confirmed	4	AT5TE61035	intergenic	Y
Chr5	deletion	3138	16979101	16982238	Partially confirmed	1	AT5TE61280	complete_gene	AT5G42460
Chr5	deletion	2356	16996012	16998367	Fully confirmed	1	AT5TE61340	intergenic	

Chr5	deletion	494	17033961	17034454	Fully confirmed	1	No	intergenic				
Chr5	deletion	147	17063316	17063462	Partially confirmed	1	No	intron	AT5G42610			
Chr5	deletion	209	17071687	17071895	Fully confirmed	1	No	intergenic				
Chr5	deletion	1367	17085554	17086920	Fully confirmed	6	AT5TE61705	intergenic				Y
Chr5	deletion	4907	17090769	17095675	Fully confirmed	1	AT5TE61735	intergenic				
Chr5	deletion	472	17123285	17123756	Partially confirmed	1	No	intron	AT5G42700			
Chr5	deletion	1797	17132873	17134669	N/A	2	No	pseudo_gene	AT5G42730			Y
Chr5	deletion	279	17175141	17175419	Fully confirmed	1	AT5TE62050	intergenic				
Chr5	deletion	478	17212710	17213187	Partially confirmed	1	No	intron	AT5G42930			
Chr5	deletion	447	17236715	17237161	Fully confirmed	1	No	complete_gene	AT5G42965			
Chr5	deletion	3802	17251250	17255051	Partially confirmed	3	AT5TE62350	intergenic				Y
Chr5	deletion	10184	17258210	17268393	Fully confirmed	1	AT5TE62380	complete_gene	AT5G43030,AT5G43040	5'UTR	AT5G43050	
Chr5	deletion	2157	17274785	17276941	Fully confirmed	1	AT5TE62440	intergenic				
Chr5	deletion	2026	17278180	17280205	N/A	1	AT5TE62455	intergenic				
Chr5	deletion	188	17288652	17288839	N/A	1	No	intergenic				
Chr5	deletion	1134	17291738	17292871	Partially confirmed	4	No	intergenic				Y
Chr5	deletion	219	17327182	17327400	N/A	8	No	intergenic				Y
Chr5	deletion	1033	17343955	17344987	Fully confirmed	1	No	pseudo_gene	AT5G43196			
Chr5	deletion	393	17358372	17358764	Partially confirmed	1	No	intergenic				
Chr5	deletion	839	17359296	17360134	Fully confirmed	33	AT5TE62730	intergenic				Y
Chr5	deletion	2957	17364488	17367444	Partially confirmed	2	AT5TE62750	intergenic				Y
Chr5	deletion	172	17393305	17393476	Fully confirmed	1	No	intergenic				
Chr5	deletion	797	17403494	17404290	N/A	1	No	intergenic				
Chr5	deletion	9426	17404438	17413863	N/A	1	AT5TE62865	complete_gene	AT5G43360			
Chr5	deletion	2003	17430144	17432146	N/A	1	No	ncRNA	AT5G43403			
Chr5	deletion	6261	17439675	17445935	N/A	1	AT5TE63020	intergenic				
Chr5	deletion	242	17573537	17573778	Fully confirmed	1	No	intron	AT5G43745			
Chr5	deletion	1104	17578479	17579582	Fully confirmed	19	AT5TE63560	intergenic				Y
Chr5	deletion	9084	17596763	17605846	Partially confirmed	1	AT5TE63610	intergenic				
Chr5	deletion	221	17630116	17630336	Fully confirmed	1	AT5TE63690	intergenic				
Chr5	deletion	259	17638643	17638901	N/A	15	No	intergenic				Y
Chr5	deletion	574	17726423	17726996	Partially confirmed	121	AT5TE64040	intergenic				Y
Chr5	deletion	647	17796138	17796784	N/A	10	AT5TE64270	intergenic				Y
Chr5	deletion	2072	17811678	17813749	N/A	5	AT5TE64325	intergenic				Y
Chr5	deletion	179	17847387	17847565	N/A	1	No	intergenic				
Chr5	deletion	193	17893273	17893465	N/A	1	No	intergenic				
Chr5	deletion	7990	17893547	17901536	Partially confirmed	9	AT5TE64600	intergenic				Y
Chr5	deletion	1619	17955559	17957177	Partially confirmed	2	AT5TE64790	intergenic				Y
Chr5	deletion	537	17974799	17975335	N/A	1	No	5'UTR	AT5G44575			
Chr5	deletion	4737	18142156	18146892	Fully confirmed	1	AT5TE65370	intergenic				
Chr5	deletion	224	18181219	18181442	Fully confirmed	1	AT5G45050	intergenic				
Chr5	deletion	1750	18207322	18209071	N/A	1	No	complete_gene	AT5G45095			
Chr5	deletion	5018	18233442	18238459	N/A	1	AT5TE65640	intergenic				
Chr5	deletion	1890	18258404	18260293	Fully confirmed	2	AT5TE65710	intergenic				Y
Chr5	deletion	936	18387141	18388076	Fully confirmed	3	AT5TE66180	intergenic				Y
Chr5	deletion	2539	18413671	18416209	Fully confirmed	1	AT5TE66280	complete_gene	AT5G45450			
Chr5	deletion	4629	18490607	18495235	Partially confirmed	3	AT5TE66565	intergenic				Y
Chr5	deletion	752	18500735	18501486	N/A	18	AT5TE66580	intergenic				Y
Chr5	deletion	1131	18549683	18550813	N/A	1	AT5TE66760	intergenic				
Chr5	deletion	426	18558301	18558726	N/A	5	No	intergenic				Y
Chr5	deletion	2598	18667375	18669972	Partially confirmed	1	AT5TE67210	intergenic				
Chr5	deletion	2621	18702496	18705116	Partially confirmed	1	AT5TE67330	intergenic				
Chr5	deletion	594	18758262	18758855	N/A	1	No	intergenic				

Chr5	deletion	330	18786541	18786870	N/A	1	No	exon	AT5G46310	
Chr5	deletion	5844	18933096	18938939	Fully confirmed	4	AT5TE68140	intergenic		Y
Chr5	deletion	1330	18980160	18981489	Partially confirmed	6	AT5TE68275	intergenic		Y
Chr5	deletion	5470	18993749	18999218	Partially confirmed	1	AT5TE68330	complete_gene	AT5G46820	
Chr5	deletion	940	19018620	19019559	Partially confirmed	28	AT5TE68420	intergenic		Y
Chr5	deletion	559	19101550	19102108	Partially confirmed	123	AT5TE68695	intergenic		Y
Chr5	deletion	101	19148946	19149046	Fully confirmed	1	No	intergenic		
Chr5	deletion	1326	19152418	19153743	Fully confirmed	8	AT5TE68915	intergenic		Y
Chr5	deletion	436	19197379	19197814	Fully confirmed	1	AT5TE69060	intergenic		
Chr5	deletion	111	19199254	19199364	Fully confirmed	1	No	exon_3'_end	AT5G47300	
Chr5	deletion	155	19199964	19200118	Fully confirmed	1	No	intergenic		
Chr5	deletion	5735	19358335	19364069	Fully confirmed	1	AT5TE69650	intergenic		
Chr5	deletion	548	19390983	19391530	N/A	42	AT5TE69755	intergenic		Y
Chr5	deletion	747	19488600	19489346	Fully confirmed	1	No	3'UTR	AT5G48090	
Chr5	deletion	855	19493754	19494608	Fully confirmed	1	AT5TE70150	intergenic		
Chr5	deletion	2180	19542721	19544900	Partially confirmed	3	No	complete_gene	AT5G48190	Y
Chr5	deletion	259	19574175	19574433	Fully confirmed	1	No	intergenic		
Chr5	deletion	2041	19670802	19672842	Fully confirmed	24	AT5TE70785	intergenic		Y
Chr5	deletion	636	19682124	19682759	Partially confirmed	1	No	intergenic		
Chr5	deletion	287	19830048	19830334	Fully confirmed	1	No	intergenic		
Chr5	deletion	1268	20048359	20049626	N/A	1	AT5TE72200	complete_gene	AT5G49440	
Chr5	deletion	151	20096659	20096809	Fully confirmed	4	No	intergenic		Y
Chr5	deletion	681	20233156	20233836	Fully confirmed	17	AT5TE72870	intergenic		Y
Chr5	deletion	5457	20265303	20270759	Partially confirmed	1	AT5TE72990	intergenic		
Chr5	deletion	312	20296500	20296811	N/A	1	AT5TE73100	3'UTR	AT5G49900	
Chr5	deletion	1146	20386990	20388135	Fully confirmed	1	AT5TE73430	intergenic		
Chr5	deletion	8838	20393145	20401982	Fully confirmed	1	AT5TE73495	complete_gene	AT5G50140,AT5G50136	
Chr5	deletion	135	20493811	20493945	Fully confirmed	1	No	intron	AT5G50340	
Chr5	deletion	1316	20803358	20804673	Fully confirmed	1	No	complete_gene	AT5G51195	
Chr5	deletion	177	20983614	20983790	Fully confirmed	1	No	intron	AT5G51660	
Chr5	deletion	802	21015768	21016569	Fully confirmed	12	AT5TE75710	intergenic		Y
Chr5	deletion	355	21179167	21179521	Fully confirmed	1	No	intron	AT5G52120	
Chr5	deletion	409	21421990	21422398	Fully confirmed	1	AT5TE77145	intergenic		
Chr5	deletion	2088	21530090	21532177	Partially confirmed	75	AT5TE77565	intergenic		Y
Chr5	deletion	3869	21542908	21546776	Fully confirmed	1	AT5TE77610	intergenic		
Chr5	deletion	116	21600952	21601067	N/A	1	No	intergenic		
Chr5	deletion	171	21680499	21680669	Partially confirmed	1	No	intron	AT5G53430	
Chr5	deletion	923	21814649	21815571	Fully confirmed	3	AT5TE78580	exon	AT5G53740	Y
Chr5	deletion	360	21959499	21959858	Fully confirmed	7	No	intron	AT5G54110	Y
Chr5	deletion	4869	22002016	22006884	Fully confirmed	4	AT5TE79225	intergenic		Y
Chr5	deletion	307	22013127	22013433	Fully confirmed	1	No	intergenic		
Chr5	deletion	153	22226871	22227023	Fully confirmed	1	No	intergenic		
Chr5	deletion	512	22228548	22229059	Fully confirmed	1	No	intron	AT5G54710	
Chr5	deletion	1674	22230980	22232653	Partially confirmed	1	AT5TE80015	intergenic		
Chr5	deletion	117	22439717	22439833	N/A	1	No	intergenic		
Chr5	deletion	652	22444316	22444967	N/A	1	No	exon_5'_end	AT5G55360	
Chr5	deletion	754	22509451	22510204	N/A	1	No	3'UTR	AT5G55565	
Chr5	deletion	3458	22627984	22631441	Fully confirmed	1	AT5TE81425	intergenic		
Chr5	deletion	3790	22829957	22833746	Fully confirmed	3	AT5TE82140	intergenic		Y
Chr5	deletion	242	22835929	22836170	Partially confirmed	1	No	3'UTR	AT5G56370	
Chr5	deletion	192	22837944	22838135	Partially confirmed	1	No	intergenic		
Chr5	deletion	3088	22838434	22841521	Fully confirmed	1	No	complete_gene	AT5G56380	
Chr5	deletion	889	22868882	22869770	N/A	1	No	complete_gene	AT5G56470	

Chr5	deletion	282	23024593	23024874	N/A	20	AT5TE82820	intergenic	Y
Chr5	deletion	1273	23026046	23027318	Partially confirmed	10	AT5TE82825	intergenic	Y
Chr5	deletion	241	23037434	23037674	N/A	1	No	intergenic	
Chr5	deletion	219	23336611	23336829	Fully confirmed	1	No	intergenic	
Chr5	deletion	1341	23431544	23432884	Partially confirmed	8	AT5TE84250	intergenic	Y
Chr5	deletion	150	23750262	23750411	Not confirmed	1	No	pseudo_gene	AT5G58810
Chr5	deletion	1403	23774301	23775703	Fully confirmed	6	AT5TE85500	intergenic	Y
Chr5	deletion	480	23844278	23844757	Fully confirmed	1	No	complete_gene	AT5G59060
Chr5	deletion	150	23995939	23996088	Fully confirmed	1	AT5TE86330	intergenic	
Chr5	deletion	99	24139803	24139901	Partially confirmed	1	No	intergenic	
Chr5	deletion	988	24254886	24255873	Fully confirmed	1	No	multi_exons	AT5G60260
Chr5	deletion	102	24304001	24304102	N/A	1	AT5TE87420	intergenic	
Chr5	deletion	128	24734804	24734931	Partially confirmed	1	No	intron	AT5G61500
Chr5	deletion	1411	24818769	24820179	Fully confirmed	3	AT5TE89325	intergenic	Y
Chr5	deletion	309	24970899	24971207	Partially confirmed	3	No	intergenic	Y
Chr5	deletion	144	25193091	25193234	Fully confirmed	1	No	intron	AT5G62720
Chr5	deletion	1095	25844605	25845699	Fully confirmed	1	AT5TE93020	intergenic	
Chr5	deletion	577	25846513	25847089	Fully confirmed	1	AT5TE93030	intergenic	
Chr5	deletion	94	25848000	25848093	Partially confirmed	1	No	intergenic	
Chr5	deletion	2143	25855945	25858087	Partially confirmed	2	AT5TE93055	intergenic	Y
Chr5	deletion	1052	26069813	26070864	N/A	4	AT5TE93845	intergenic	Y
Chr5	deletion	976	26209503	26210478	Fully confirmed	1	AT5TE94375	intergenic	
Chr5	deletion	419	26233116	26233534	Fully confirmed	16	No	intergenic	Y
Chr5	deletion	1956	26414972	26416927	Fully confirmed	1	AT5TE95125	intergenic	
Chr5	deletion	228	26611248	26611475	Fully confirmed	1	No	3'UTR	AT5G66670
Chr5	deletion	103	26682383	26682485	Fully confirmed	1	No	intergenic	
Chr5	deletion	1748	26891652	26893399	N/A	1	AT5TE96875	intergenic	
Chr5	deletion	176	26926310	26926485	Fully confirmed	2	No	intergenic	Y
Chr1	insertion	91	822678	822679	Partially confirmed	0	No	3'UTR	AT1G03350
Chr1	insertion	53	2420882	2420887	Fully confirmed	0	No	intergenic	
Chr1	insertion	185	2665500	2665557	Partially confirmed	0	No	intergenic	
Chr1	insertion	887	2769275	2769287	Partially confirmed	0	No	intron	AT1G08695
Chr1	insertion	1202	2951430	2951444	N/A	0	No	intergenic	
Chr1	insertion	403	3186590	3186595	Partially confirmed	0	No	intergenic	
Chr1	insertion	4275	3300751	3301143	N/A	0	No	exon	AT1G10100
Chr1	insertion	113	3314004	3314047	Not confirmed	0	No	intron	AT1G10130
Chr1	insertion	98	3714498	3714500	Partially confirmed	0	No	intergenic	
Chr1	insertion	100	3830401	3830401	N/A	0	No	intron	AT1G11370
Chr1	insertion	214	3899968	3899971	Partially confirmed	0	No	intergenic	
Chr1	insertion	1458	4301160	4301874	Partially confirmed	0	No	intergenic	
Chr1	insertion	649	5172654	5172681	Partially confirmed	0	No	exon	AT1G15015
Chr1	insertion	1339	5453059	5453154	Fully confirmed	0	No	intergenic	
Chr1	insertion	452	5611415	5611478	Partially confirmed	0	No	intergenic	
Chr1	insertion	110	5854011	5854014	Partially confirmed	0	No	intergenic	
Chr1	insertion	231	5869262	5869262	N/A	0	No	3'UTR	AT1G17160
Chr1	insertion	100	6506993	6507003	Not confirmed	0	No	intergenic	
Chr1	insertion	404	6941847	6941852	Partially confirmed	0	No	intergenic	
Chr1	insertion	958	7295107	7295122	N/A	0	AT1TE23550	intergenic	
Chr1	insertion	126	7732141	7732144	Partially confirmed	0	No	intergenic	
Chr1	insertion	192	7855706	7855715	N/A	0	No	intergenic	
Chr1	insertion	4640	8161460	8161464	N/A	0	AT1TE26270	intergenic	
Chr1	insertion	105	8177696	8177711	Partially confirmed	2	No	intergenic	Y
Chr1	insertion	113	8226989	8227039	Partially confirmed	0	No	intergenic	

Chr1	insertion	308	8495133	8495147	Partially confirmed	0	No	intergenic	
Chr1	insertion	200	8516654	8516697	Partially confirmed	0	No	intron	AT1G24070
Chr1	insertion	2412	8541470	8541518	Partially confirmed	0	No	exon	AT1G24145
Chr1	insertion	183	8588191	8588224	Not confirmed	0	No	intergenic	
Chr1	insertion	178	8639456	8639499	Partially confirmed	0	No	intron	AT1G24350
Chr1	insertion	221	9849195	9849239	Fully confirmed	1	No	intergenic	
Chr1	insertion	473	9882634	9882714	Partially confirmed	0	No	intergenic	
Chr1	insertion	510	10199550	10199553	N/A	0	No	intron	AT1G29179
Chr1	insertion	718	10456761	10456854	Partially confirmed	1	AT1TE33790	intergenic	
Chr1	insertion	176	10587076	10587121	Fully confirmed	0	No	intergenic	
Chr1	insertion	190	10703476	10703558	Not confirmed	0	No	intergenic	
Chr1	insertion	142	10851292	10851294	Partially confirmed	0	AT1TE35050	intergenic	
Chr1	insertion	644	10965938	10965942	Fully confirmed	0	No	intergenic	
Chr1	insertion	163	11010834	11010839	Partially confirmed	0	No	intron	AT1G30925
Chr1	insertion	152	11068182	11068192	Partially confirmed	0	No	intergenic	
Chr1	insertion	507	11090919	11090924	Partially confirmed	0	No	intergenic	
Chr1	insertion	156	11341593	11341630	N/A	0	No	intron	AT1G31670
Chr1	insertion	227	11429765	11429813	Partially confirmed	0	No	intergenic	
Chr1	insertion	57	11434047	11434050	N/A	0	No	intergenic	
Chr1	insertion	122	11441197	11441199	Partially confirmed	0	No	intergenic	
Chr1	insertion	621	11484884	11484962	N/A	0	No	intergenic	
Chr1	insertion	418	11524090	11524102	Partially confirmed	0	No	intergenic	
Chr1	insertion	163	11641966	11641969	Fully confirmed	0	AT1TE37670	intergenic	
Chr1	insertion	323	12080714	12080721	Partially confirmed	0	AT1TE39150	intergenic	
Chr1	insertion	266	12127579	12127671	Fully confirmed	0	No	3'UTR	AT1G33440
Chr1	insertion	806	12150415	12150428	Fully confirmed	0	No	intergenic	
Chr1	insertion	1569	12159335	12159599	N/A	0	No	intergenic	
Chr1	insertion	255	12467289	12467293	N/A	0	AT1TE40560	intergenic	
Chr1	insertion	174	12475265	12475345	Partially confirmed	0	AT1TE40615	intergenic	
Chr1	insertion	119	12565227	12565229	N/A	1	AT1TE40930	intergenic	
Chr1	insertion	222	12602213	12602279	Partially confirmed	0	No	intergenic	
Chr1	insertion	95	12933839	12933839	N/A	0	No	intron	AT1G35250
Chr1	insertion	223	13047967	13047992	N/A	0	No	intergenic	
Chr1	insertion	5196	13128825	13128835	Partially confirmed	0	AT1TE42880	intergenic	
Chr1	insertion	994	13155896	13156292	Partially confirmed	0	AT1TE42935	intergenic	
Chr1	insertion	306	13460584	13460731	Partially confirmed	0	No	intergenic	
Chr1	insertion	155	13532023	13532098	Partially confirmed	0	No	intergenic	
Chr1	insertion	333	14212672	14212699	N/A	0	AT1TE46660	intergenic	
Chr1	insertion	58	14304821	14304823	N/A	0	AT1TE46990	intergenic	
Chr1	insertion	168	15587770	15587806	Partially confirmed	27	No	intergenic	Y
Chr1	insertion	112	15900535	15900569	Partially confirmed	0	No	intergenic	
Chr1	insertion	302	15911524	15911536	N/A	0	AT1TE52420	intergenic	
Chr1	insertion	297	16156438	16156506	Partially confirmed	0	No	intron	AT1G43020
Chr1	insertion	162	16178486	16178487	N/A	0	AT1TE53330	intergenic	
Chr1	insertion	269	16237540	16237542	Partially confirmed	0	AT1TE53465	intergenic	
Chr1	insertion	291	16397294	16397300	Partially confirmed	0	AT1TE54005	intergenic	
Chr1	insertion	939	16509688	16509688	Partially confirmed	0	No	exon	AT1G43730
Chr1	insertion	202	16558855	16558859	N/A	0	AT1TE54600	intergenic	
Chr1	insertion	1719	16667897	16667899	Partially confirmed	0	AT1TE54940	intergenic	
Chr1	insertion	1417	16728916	16728994	N/A	0	AT1G44040	intergenic	
Chr1	insertion	1109	16729138	16729142	N/A	0	No	intergenic	
Chr1	insertion	773	16925571	16925572	N/A	0	AT1TE56040	intergenic	
Chr1	insertion	489	16983032	16983033	Partially confirmed	0	No	3'UTR	AT1G44920

Chr1	insertion	69	17279217	17279219	N/A	0	No	intergenic	
Chr1	insertion	223	17381574	17381635	Not confirmed	9	AT1TE57565	intergenic	Y
Chr1	insertion	93	17443660	17443660	N/A	0	AT1TE57805	intergenic	
Chr1	insertion	215	17662943	17662945	Partially confirmed	0	No	pseudo_gene	AT1G47930
Chr1	insertion	102	18626687	18626691	Partially confirmed	0	AT1TE61730	intergenic	
Chr1	insertion	658	18645392	18645499	Partially confirmed	0	No	intergenic	
Chr1	insertion	846	18819793	18819793	Partially confirmed	0	No	intron	AT1G50770
Chr1	insertion	129	18880038	18880038	Fully confirmed	0	No	intergenic	
Chr1	insertion	671	19319184	19319231	Partially confirmed	0	No	intergenic	
Chr1	insertion	346	19431351	19431395	N/A	0	No	intergenic	
Chr1	insertion	336	19467376	19467496	Partially confirmed	0	AT1TE64445	intergenic	
Chr1	insertion	610	19740762	19740766	Partially confirmed	0	No	intron	AT1G52990
Chr1	insertion	147	19804910	19804937	Partially confirmed	0	No	intergenic	
Chr1	insertion	51	19820358	19820362	Partially confirmed	0	No	intergenic	
Chr1	insertion	115	20010481	20010481	N/A	0	No	intergenic	
Chr1	insertion	805	20079100	20079105	Fully confirmed	0	No	intergenic	
Chr1	insertion	217	20153041	20153110	Partially confirmed	0	No	intergenic	
Chr1	insertion	159	20475428	20475430	N/A	0	No	intergenic	
Chr1	insertion	108	21124502	21124507	N/A	0	No	intergenic	
Chr1	insertion	501	21221127	21221235	Partially confirmed	0	No	intergenic	
Chr1	insertion	382	21326534	21326673	Partially confirmed	0	No	intergenic	
Chr1	insertion	177	21327296	21327301	Fully confirmed	0	No	intergenic	
Chr1	insertion	351	21430952	21430983	Partially confirmed	0	No	intergenic	
Chr1	insertion	159	21512361	21512361	Fully confirmed	0	No	intergenic	
Chr1	insertion	192	21620442	21620492	Partially confirmed	0	No	3'UTR	AT1G58280
Chr1	insertion	171	21688663	21688725	Fully confirmed	0	No	intergenic	
Chr1	insertion	245	21694509	21694513	Fully confirmed	1	No	intergenic	
Chr1	insertion	816	21694769	21694774	Partially confirmed	1	No	intergenic	
Chr1	insertion	156	21726221	21726283	Partially confirmed	0	AT1TE71690	intergenic	
Chr1	insertion	113	21913555	21913555	N/A	0	No	intergenic	
Chr1	insertion	261	22059072	22059077	Partially confirmed	0	AT1TE72840	intergenic	
Chr1	insertion	138	22091285	22091289	Fully confirmed	0	No	intron	AT1G59990
Chr1	insertion	397	22108893	22108924	N/A	0	AT1TE72995	intergenic	
Chr1	insertion	381	22113665	22113761	Fully confirmed	0	No	intergenic	
Chr1	insertion	342	22187210	22187345	Fully confirmed	0	No	intergenic	
Chr1	insertion	134	22283083	22283098	Partially confirmed	0	AT1TE73570	intergenic	
Chr1	insertion	361	22317245	22317408	Partially confirmed	0	No	intergenic	
Chr1	insertion	442	22334289	22334304	Fully confirmed	0	No	intergenic	
Chr1	insertion	148	22601106	22601106	Partially confirmed	1	No	intron	AT1G61270
Chr1	insertion	179	22716218	22716245	Partially confirmed	1	No	intergenic	
Chr1	insertion	162	22743959	22744009	N/A	0	No	intergenic	
Chr1	insertion	441	22828359	22828365	N/A	0	AT1TE75240	intergenic	
Chr1	insertion	199	22914191	22914228	Fully confirmed	0	No	intergenic	
Chr1	insertion	1407	22914500	22914501	Partially confirmed	0	No	intergenic	
Chr1	insertion	255	22959896	22959923	Fully confirmed	0	No	intergenic	
Chr1	insertion	1339	23058556	23058573	Partially confirmed	0	No	intergenic	
Chr1	insertion	313	23109479	23109625	Partially confirmed	0	No	intergenic	
Chr1	insertion	131	23125810	23125835	N/A	0	AT1TE76235	intergenic	
Chr1	insertion	131	23164842	23164844	Partially confirmed	0	No	intergenic	
Chr1	insertion	406	23223380	23223515	N/A	0	No	intergenic	
Chr1	insertion	201	23294962	23294990	Fully confirmed	1	AT1TE76775	3'UTR	AT1G62880
Chr1	insertion	127	23368248	23368249	Fully confirmed	0	No	intron	AT1G63030
Chr1	insertion	152	23478779	23478793	Partially confirmed	0	No	intergenic	

Chr1	insertion	174	23822918	23822919	Partially confirmed	0	No	exon	AT1G64180
Chr1	insertion	779	23835497	23835691	Partially confirmed	0	No	intergenic	
Chr1	insertion	712	24043418	24043467	Fully confirmed	0	No	intergenic	
Chr1	insertion	140	24111662	24111664	Fully confirmed	0	AT1TE79290	intergenic	
Chr1	insertion	249	24201231	24201231	Fully confirmed	0	No	intergenic	
Chr1	insertion	549	24215524	24215709	N/A	0	No	intergenic	
Chr1	insertion	176	24217981	24217992	Partially confirmed	0	No	intergenic	
Chr1	insertion	58	24355339	24355341	Partially confirmed	0	No	intergenic	
Chr1	insertion	397	24365035	24365076	N/A	0	No	intron	AT1G65540
Chr1	insertion	136	24370428	24370453	Partially confirmed	0	No	intron	AT1G65550
Chr1	insertion	197	24669901	24669928	Fully confirmed	0	No	intergenic	
Chr1	insertion	191	24686217	24686258	Fully confirmed	0	No	intergenic	
Chr1	insertion	462	24922211	24922400	N/A	0	No	intergenic	
Chr1	insertion	105	25138725	25138725	N/A	0	AT1TE82540	intergenic	
Chr1	insertion	362	25273655	25273658	Partially confirmed	0	No	intergenic	
Chr1	insertion	76	25359065	25359067	N/A	0	No	intergenic	
Chr1	insertion	953	25407156	25407158	N/A	0	No	intron	AT1G68980
Chr1	insertion	142	25656359	25656364	Partially confirmed	0	No	intergenic	
Chr1	insertion	129	25800074	25800087	N/A	0	No	intergenic	
Chr1	insertion	58	25934892	25934894	Fully confirmed	0	No	intergenic	
Chr1	insertion	122	25963747	25963784	Not confirmed	0	No	intergenic	
Chr1	insertion	60	26079910	26079923	N/A	0	No	intergenic	
Chr1	insertion	267	26245985	26246063	Partially confirmed	0	No	intergenic	
Chr1	insertion	6615	26247797	26247800	Partially confirmed	0	No	intergenic	
Chr1	insertion	1075	26284346	26284346	Partially confirmed	0	No	intergenic	
Chr1	insertion	197	26310241	26310309	Partially confirmed	0	No	intron	AT1G69860
Chr1	insertion	663	26740764	26740765	Partially confirmed	0	No	intergenic	
Chr1	insertion	51	27100235	27100239	Fully confirmed	0	No	intergenic	
Chr1	insertion	100	27160899	27160904	Fully confirmed	0	No	intergenic	
Chr1	insertion	255	27527717	27527826	Partially confirmed	0	AT1TE90070	intergenic	
Chr1	insertion	122	27835157	27835159	Partially confirmed	0	No	intergenic	
Chr1	insertion	239	28938707	28938750	N/A	0	No	intergenic	
Chr1	insertion	54	29065740	29065762	Fully confirmed	0	No	intergenic	
Chr1	insertion	708	29358508	29358533	Partially confirmed	0	No	3'UTR	AT1G78070
Chr1	insertion	202	29471324	29471324	N/A	0	No	pseudo_gene	AT1G78330
Chr1	insertion	110	29531951	29531960	Partially confirmed	0	No	intron	AT1G78500
Chr1	insertion	153	29610021	29610025	Partially confirmed	0	No	intergenic	
Chr1	insertion	150	29787741	29787813	Not confirmed	0	No	intergenic	
Chr1	insertion	89	29807396	29807405	N/A	0	No	pseudo_gene	AT1G79245
Chr1	insertion	98	29897136	29897136	Fully confirmed	0	No	intergenic	
Chr1	insertion	177	30189823	30189900	Fully confirmed	0	No	intergenic	
Chr1	insertion	145	30297571	30297606	N/A	0	No	intergenic	
Chr1	insertion	4551	30345514	30345518	Partially confirmed	0	No	exon	AT1G80740
Chr1	insertion	1169	30415876	30416073	Partially confirmed	0	No	intergenic	
Chr1	insertion	93	30417405	30417405	Fully confirmed	0	No	exon	AT1G80960
Chr2	insertion	268	153339	153343	Fully confirmed	0	No	intergenic	
Chr2	insertion	229	345715	345716	Partially confirmed	0	No	intergenic	
Chr2	insertion	157	610357	610384	Partially confirmed	0	No	intergenic	
Chr2	insertion	209	610477	610574	N/A	0	No	3'UTR	AT2G02320
Chr2	insertion	123	679972	679984	Partially confirmed	46	No	intergenic	Y
Chr2	insertion	408	755869	756020	Partially confirmed	0	No	intergenic	
Chr2	insertion	87	792296	792300	N/A	0	AT2TE03485	intergenic	
Chr2	insertion	2192	874805	874990	Partially confirmed	0	No	intergenic	

Chr2	insertion	131	924279	924284	N/A	0	No	intergenic	
Chr2	insertion	281	931632	931632	Partially confirmed	0	AT2TE04135	intergenic	
Chr2	insertion	510	936070	936073	N/A	1	No	intron	AT2G03110
Chr2	insertion	269	1198725	1198732	Fully confirmed	0	No	intergenic	
Chr2	insertion	347	1310540	1310548	N/A	0	AT2TE05965	intergenic	
Chr2	insertion	236	1540082	1540125	N/A	0	No	intron	AT2G04430
Chr2	insertion	150	1619600	1619632	Partially confirmed	0	No	intron	AT2G04630
Chr2	insertion	4811	1951596	1952546	Partially confirmed	0	No	exon	AT2G05350
Chr2	insertion	125	1961016	1961019	N/A	1	No	intron	AT2G05370
Chr2	insertion	379	2257630	2257642	N/A	0	No	exon	AT2G05900
Chr2	insertion	4529	2336379	2336531	Partially confirmed	0	No	intergenic	
Chr2	insertion	438	2608131	2608154	Partially confirmed	0	AT2TE11725	intergenic	
Chr2	insertion	686	2689813	2689818	N/A	0	No	intergenic	
Chr2	insertion	158	2885875	2885875	Fully confirmed	0	AT2TE12575	intergenic	
Chr2	insertion	645	3026690	3026703	N/A	1	No	intron	AT2G07280
Chr2	insertion	203	3046973	3046974	Fully confirmed	1	No	intergenic	
Chr2	insertion	272	3134622	3134639	Partially confirmed	1	No	intergenic	
Chr2	insertion	365	3141407	3141407	Partially confirmed	2	No	intergenic	Y
Chr2	insertion	59	3570745	3570748	Fully confirmed	0	AT2TE15565	intergenic	
Chr2	insertion	1141	4137311	4137320	N/A	0	AT2TE17480	intergenic	
Chr2	insertion	454	4215745	4215751	Partially confirmed	0	AT2TE17780	intergenic	
Chr2	insertion	636	4255855	4255857	Partially confirmed	0	AT2TE17925	intergenic	
Chr2	insertion	222	4372453	4372493	N/A	0	AT2TE18385	intergenic	
Chr2	insertion	847	4646259	4646279	Partially confirmed	0	AT2TE19280	intergenic	
Chr2	insertion	161	4784974	4785019	N/A	0	No	intergenic	
Chr2	insertion	972	4826414	4826415	Partially confirmed	5	AT2TE20015	intergenic	Y
Chr2	insertion	960	4826748	4826749	Partially confirmed	5	AT2TE20015	intergenic	Y
Chr2	insertion	92	5100505	5100505	N/A	20	AT2TE20960	intergenic	Y
Chr2	insertion	678	5384097	5384098	Partially confirmed	2	AT2TE21805	intergenic	Y
Chr2	insertion	112	5875820	5875825	N/A	0	No	intergenic	
Chr2	insertion	538	5901485	5901485	N/A	1	AT2TE24035	intergenic	
Chr2	insertion	180	5927997	5928001	Fully confirmed	1	No	intron	AT2G14080
Chr2	insertion	185	6132030	6132036	Partially confirmed	0	No	intergenic	
Chr2	insertion	350	6246246	6246340	Fully confirmed	0	No	intergenic	
Chr2	insertion	3635	6298154	6298168	Partially confirmed	0	AT2TE25695	intergenic	
Chr2	insertion	507	6361699	6361703	N/A	0	No	intergenic	
Chr2	insertion	524	6366687	6366746	N/A	0	AT2TE25940	intergenic	
Chr2	insertion	594	6390418	6390520	Partially confirmed	0	AT2TE26070	intergenic	
Chr2	insertion	133	6394121	6394122	N/A	0	No	intron	AT2G14880
Chr2	insertion	344	6502846	6502888	Partially confirmed	0	No	intergenic	
Chr2	insertion	509	6550569	6550570	Partially confirmed	2	AT2TE26785	intergenic	Y
Chr2	insertion	605	6579708	6579809	Partially confirmed	0	AT2TE26875	intergenic	
Chr2	insertion	120	6953877	6953932	N/A	0	AT2TE28325	intergenic	
Chr2	insertion	366	6966826	6966828	Partially confirmed	0	No	intergenic	
Chr2	insertion	109	7019991	7020017	Partially confirmed	0	AT2TE28565	intergenic	
Chr2	insertion	270	7080000	7080108	Fully confirmed	0	No	pseudo_gene	AT2G16367
Chr2	insertion	1453	7165568	7165749	Partially confirmed	0	No	intergenic	
Chr2	insertion	172	7319888	7319888	N/A	0	No	pseudo_gene	AT2G16895
Chr2	insertion	315	7326486	7326526	Partially confirmed	0	AT2TE29900	intergenic	
Chr2	insertion	285	7382707	7382745	Partially confirmed	0	No	intergenic	
Chr2	insertion	78	7405065	7405076	Fully confirmed	0	No	intron	AT2G17036
Chr2	insertion	244	7492615	7492625	Partially confirmed	0	No	intergenic	
Chr2	insertion	12149	7598158	7598166	Partially confirmed	0	No	intergenic	

Chr2	insertion	465	7643879	7643943	Partially confirmed	0	No	intergenic	
Chr2	insertion	167	7944053	7944117	Fully confirmed	0	No	intergenic	
Chr2	insertion	255	8402681	8402724	Partially confirmed	0	No	intergenic	
Chr2	insertion	495	8473508	8473709	Partially confirmed	0	No	intron	AT2G19580
Chr2	insertion	68	8528063	8528069	Fully confirmed	0	No	intron	AT2G19790
Chr2	insertion	344	8776345	8776348	Fully confirmed	0	No	intergenic	
Chr2	insertion	112	8874432	8874450	N/A	0	AT2TE37325	intergenic	
Chr2	insertion	926	8891735	8891736	Partially confirmed	0	No	intergenic	
Chr2	insertion	183	8973857	8973860	Partially confirmed	0	No	intron	AT2G20840
Chr2	insertion	626	9337443	9337650	N/A	0	No	intergenic	
Chr2	insertion	336	9844890	9845021	N/A	0	No	intron	AT2G23130
Chr2	insertion	489	10241457	10241458	Fully confirmed	0	No	intergenic	
Chr2	insertion	239	10248556	10248565	Fully confirmed	0	No	pseudo_gene	AT2G24110
Chr2	insertion	741	10272683	10272685	Partially confirmed	0	No	pseudo_gene	AT2G24165
Chr2	insertion	129	10403933	10403935	Partially confirmed	0	No	intergenic	
Chr2	insertion	774	10404105	10404107	Partially confirmed	0	No	intergenic	
Chr2	insertion	703	10432200	10432289	Partially confirmed	0	No	intron	AT2G24560
Chr2	insertion	3706	10505344	10505344	Partially confirmed	0	No	intergenic	
Chr2	insertion	5044	10521464	10521874	N/A	0	AT2TE45145	intergenic	
Chr2	insertion	4828	10522460	10522539	Partially confirmed	0	No	intergenic	
Chr2	insertion	185	10697176	10697185	Fully confirmed	0	No	intergenic	
Chr2	insertion	114	10738230	10738260	Partially confirmed	0	No	intron	AT2TE46070
Chr2	insertion	390	11195066	11195228	Partially confirmed	0	No	intergenic	
Chr2	insertion	395	11225798	11225870	Partially confirmed	0	No	intron	AT2G26370
Chr2	insertion	275	11259027	11259143	N/A	0	No	intergenic	
Chr2	insertion	181	11449675	11449681	Fully confirmed	0	No	intron	AT2G26850
Chr2	insertion	977	11699232	11699232	Partially confirmed	0	No	intergenic	
Chr2	insertion	360	11835807	11835807	N/A	0	No	intergenic	
Chr2	insertion	245	12204094	12204108	Partially confirmed	0	No	intergenic	
Chr2	insertion	630	12404431	12404442	Partially confirmed	0	No	intergenic	
Chr2	insertion	973	12557616	12557628	Fully confirmed	0	No	intergenic	
Chr2	insertion	255	12971671	12971686	Partially confirmed	0	No	intergenic	
Chr2	insertion	128	13152803	13152820	Not confirmed	0	No	intergenic	
Chr2	insertion	613	13300244	13300479	Partially confirmed	0	No	intergenic	
Chr2	insertion	471	13409047	13409106	Fully confirmed	0	No	3'UTR	AT2G31480
Chr2	insertion	574	13447227	13447493	Partially confirmed	0	No	intron	AT2G31590
Chr2	insertion	131	13717181	13717184	Fully confirmed	0	No	intergenic	
Chr2	insertion	100	13852103	13852157	Not confirmed	0	No	intron	AT2G32645
Chr2	insertion	1533	13959050	13959056	Partially confirmed	0	No	exon	AT2G32905
Chr2	insertion	143	13986547	13986551	N/A	0	No	intergenic	
Chr2	insertion	221	14030355	14030372	Partially confirmed	0	No	intron	AT2G33070
Chr2	insertion	115	14232844	14232846	Not confirmed	0	AT2TE62955	intergenic	
Chr2	insertion	1678	14559527	14559532	Partially confirmed	0	No	intergenic	
Chr2	insertion	112	15047324	15047328	Fully confirmed	0	No	intron	AT2G35800
Chr2	insertion	979	15115157	15115167	Partially confirmed	0	No	intron	AT2G35990
Chr2	insertion	414	15253719	15253722	N/A	0	No	intergenic	
Chr2	insertion	110	15690936	15690958	Partially confirmed	0	No	intergenic	
Chr2	insertion	98	16441906	16441906	N/A	0	No	intergenic	
Chr2	insertion	286	16588261	16588280	Fully confirmed	0	No	intergenic	
Chr2	insertion	101	17102929	17102936	Fully confirmed	0	No	intron	AT2G40980
Chr2	insertion	704	17203825	17203825	Partially confirmed	0	No	intergenic	
Chr2	insertion	868	17676960	17676962	Partially confirmed	0	No	intron	AT2G42460
Chr2	insertion	312	18089613	18089616	N/A	0	No	intergenic	

Chr2	insertion	799	18114775	18114786	Fully confirmed	0	No	intergenic	
Chr2	insertion	321	18288393	18288393	Partially confirmed	0	No	intergenic	
Chr2	insertion	604	18439568	18439573	Partially confirmed	0	No	intron	AT2G44735
Chr2	insertion	168	18511381	18511437	Partially confirmed	0	No	intergenic	
Chr2	insertion	454	19624820	19624831	N/A	0	No	intergenic	
Chr3	insertion	457	370671	370686	Fully confirmed	0	No	intergenic	
Chr3	insertion	150	1000929	1000960	Fully confirmed	0	No	intron	AT3G03890
Chr3	insertion	2684	1250360	1250565	Fully confirmed	0	AT3TE05245	intergenic	
Chr3	insertion	59	1676418	1676422	Fully confirmed	0	No	intergenic	
Chr3	insertion	141	1714819	1714820	Fully confirmed	0	No	intergenic	
Chr3	insertion	127	2099812	2099827	Partially confirmed	0	No	intergenic	
Chr3	insertion	207	2223812	2223905	N/A	0	No	intron	AT3G07030
Chr3	insertion	266	2337458	2337470	Fully confirmed	0	No	intron	AT3G07330
Chr3	insertion	115	2563520	2563521	Fully confirmed	0	No	intergenic	
Chr3	insertion	144	2794222	2794223	Partially confirmed	0	No	3'UTR	AT3G09110
Chr3	insertion	198	3040752	3040810	Fully confirmed	0	No	intron	AT3G09920
Chr3	insertion	452	3551645	3551664	Fully confirmed	0	No	intergenic	
Chr3	insertion	1085	3565795	3566212	Partially confirmed	0	No	intergenic	
Chr3	insertion	68	3996956	3996968	Partially confirmed	0	No	intron	AT3G12590
Chr3	insertion	90	4075276	4075276	Partially confirmed	0	No	intron	AT3G12820
Chr3	insertion	64	4259252	4259254	N/A	0	No	intron	AT3G13225
Chr3	insertion	143	4400628	4400645	Fully confirmed	0	No	intergenic	
Chr3	insertion	6009	4939991	4940008	Partially confirmed	0	No	intergenic	
Chr3	insertion	169	5603819	5603819	Partially confirmed	3	No	intergenic	Y
Chr3	insertion	58	6000407	6000408	Partially confirmed	0	No	intergenic	
Chr3	insertion	86	6795058	6795059	Partially confirmed	0	No	intergenic	
Chr3	insertion	123	7132252	7132282	Not confirmed	0	AT3TE29960	intergenic	
Chr3	insertion	216	7637470	7637563	N/A	0	No	intergenic	
Chr3	insertion	160	7671756	7671826	Partially confirmed	0	No	intergenic	
Chr3	insertion	167	7727360	7727383	Partially confirmed	0	No	intergenic	
Chr3	insertion	415	7994322	7994326	N/A	0	No	intergenic	
Chr3	insertion	1048	8122241	8122628	N/A	0	No	intergenic	
Chr3	insertion	161	8140597	8140598	Fully confirmed	0	No	intron	AT3G22960
Chr3	insertion	134	8301857	8301891	Fully confirmed	0	No	intergenic	
Chr3	insertion	401	8940627	8940770	N/A	0	No	intron	AT3G24518
Chr3	insertion	1415	9001258	9001501	Partially confirmed	0	No	intergenic	
Chr3	insertion	476	9218255	9218353	Partially confirmed	0	No	intron	AT3G25420
Chr3	insertion	167	9288918	9288934	N/A	0	No	intron	AT3G25572
Chr3	insertion	180	9585419	9585421	N/A	1	No	intergenic	
Chr3	insertion	651	9634852	9634861	Partially confirmed	0	No	intergenic	
Chr3	insertion	136	9713017	9713026	Fully confirmed	0	No	intergenic	
Chr3	insertion	566	10155275	10155282	N/A	0	No	3'UTR	AT3G27430
Chr3	insertion	124	10181548	10181554	N/A	0	No	intergenic	
Chr3	insertion	163	10330665	10330744	N/A	0	No	intergenic	
Chr3	insertion	382	10337766	10337785	Partially confirmed	0	No	intergenic	
Chr3	insertion	76	10713088	10713089	Not confirmed	0	No	intergenic	
Chr3	insertion	1130	10885282	10885286	Fully confirmed	0	AT3TE45260	intergenic	
Chr3	insertion	940	10967716	10968048	Partially confirmed	0	AT3TE45610	intergenic	
Chr3	insertion	65	11117792	11117794	Fully confirmed	1	AT3TE46245	intergenic	
Chr3	insertion	350	11172273	11172278	Fully confirmed	0	AT3TE46490	intergenic	
Chr3	insertion	405	11275584	11275604	Partially confirmed	0	No	intergenic	
Chr3	insertion	771	11300844	11300885	N/A	0	No	intergenic	
Chr3	insertion	816	11463110	11463115	Partially confirmed	0	No	intergenic	

Chr3	insertion	282	11575035	11575038	Fully confirmed	0	AT3TE48135	intergenic	
Chr3	insertion	181	11618906	11618925	Partially confirmed	0	AT3TE48285	intergenic	
Chr3	insertion	2051	11691621	11691627	Partially confirmed	0	AT3TE48555	intergenic	
Chr3	insertion	5590	11717075	11717096	Partially confirmed	0	AT3TE48790	intergenic	
Chr3	insertion	750	11735444	11735445	Partially confirmed	0	No	intergenic	
Chr3	insertion	93	11740036	11740038	N/A	0	AT3TE48875	intergenic	
Chr3	insertion	280	11834279	11834279	Partially confirmed	0	No	intergenic	
Chr3	insertion	783	11882950	11882953	Partially confirmed	1	No	intron	AT3G30235
Chr3	insertion	1143	12663103	12663165	Partially confirmed	1	AT3TE52110	intergenic	
Chr3	insertion	1112	12976674	12976718	Partially confirmed	1	AT3TE53185	intergenic	
Chr3	insertion	556	13148826	13148826	Partially confirmed	9	AT3TE53765	intergenic	Y
Chr3	insertion	107	14117851	14117854	N/A	0	AT3TE57860	intergenic	
Chr3	insertion	132	14288140	14288193	N/A	0	AT3TE58670	intergenic	
Chr3	insertion	343	14317988	14317989	N/A	0	AT3TE58815	intergenic	
Chr3	insertion	525	14468412	14468614	N/A	0	AT3TE59295	intergenic	
Chr3	insertion	1115	14735508	14735627	Partially confirmed	0	No	intergenic	
Chr3	insertion	95	14738148	14738148	Partially confirmed	0	AT3TE60270	intergenic	
Chr3	insertion	881	15233860	15233872	Fully confirmed	0	No	intergenic	
Chr3	insertion	161	15248314	15248314	Fully confirmed	0	AT3TE62000	intergenic	
Chr3	insertion	347	15265203	15265257	N/A	0	AT3TE62035	intergenic	
Chr3	insertion	105	15561338	15561340	N/A	0	AT3TE62975	intergenic	
Chr3	insertion	111	15603878	15603881	Partially confirmed	0	AT3TE63075	intergenic	
Chr3	insertion	450	15692262	15692285	Fully confirmed	0	AT3TE63465	intergenic	
Chr3	insertion	347	15958455	15958457	Partially confirmed	1	AT3TE64590	intergenic	
Chr3	insertion	536	16050766	16050774	Partially confirmed	0	No	intergenic	
Chr3	insertion	416	16075918	16076028	Partially confirmed	0	No	intergenic	
Chr3	insertion	506	16153427	16153435	Fully confirmed	0	No	intron	AT3G44560
Chr3	insertion	274	16163687	16163737	Partially confirmed	0	AT3TE65490	intergenic	
Chr3	insertion	143	16264445	16264446	N/A	12	AT3TE65875	intergenic	Y
Chr3	insertion	313	16265157	16265158	N/A	12	AT3TE65875	intergenic	Y
Chr3	insertion	970	16318297	16318656	Fully confirmed	0	No	intron	AT3G44770
Chr3	insertion	124	16350092	16350092	Fully confirmed	1	No	intergenic	
Chr3	insertion	194	16350953	16350954	Partially confirmed	1	No	intron	AT3G44805
Chr3	insertion	176	16559616	16559678	N/A	0	AT3TE67140	intergenic	
Chr3	insertion	228	16650465	16650466	Fully confirmed	0	No	intergenic	
Chr3	insertion	206	17025866	17025868	Partially confirmed	0	No	intergenic	
Chr3	insertion	275	17088812	17088820	Partially confirmed	0	No	intergenic	
Chr3	insertion	285	17088930	17088930	Partially confirmed	0	No	intergenic	
Chr3	insertion	803	17145202	17145266	Partially confirmed	0	AT3TE69475	intergenic	
Chr3	insertion	4033	17225381	17225383	Partially confirmed	0	No	intergenic	
Chr3	insertion	108	17231730	17231731	Fully confirmed	0	No	intergenic	
Chr3	insertion	155	17503927	17503972	N/A	0	AT3TE70915	intergenic	
Chr3	insertion	915	17508492	17508747	Partially confirmed	0	No	intergenic	
Chr3	insertion	390	17510077	17510239	Partially confirmed	0	No	intergenic	
Chr3	insertion	110	17637629	17637629	Partially confirmed	0	No	intron	AT3G47810
Chr3	insertion	51	17687114	17687115	Partially confirmed	0	No	intron	AT3G47930
Chr3	insertion	122	18079170	18079184	Fully confirmed	0	No	intron	AT3G48770
Chr3	insertion	125	18176074	18176076	Partially confirmed	0	AT3TE73705	intergenic	
Chr3	insertion	3156	18731494	18732010	N/A	0	No	intergenic	
Chr3	insertion	630	18744443	18744721	Partially confirmed	0	No	intergenic	
Chr3	insertion	220	18744915	18744916	Partially confirmed	0	No	intron	AT3G50510
Chr3	insertion	181	18895049	18895050	Fully confirmed	0	No	intron	AT3G50830
Chr3	insertion	227	18967774	18967774	Fully confirmed	0	No	intergenic	

Chr3	insertion	141	19030001	19030001	Fully confirmed	0	No	intron	AT3G51250	
Chr3	insertion	377	19443339	19443369	Partially confirmed	0	No	intergenic		
Chr3	insertion	77	19584741	19584757	Not confirmed	0	No	intron	AT3G52840	
Chr3	insertion	406	19806984	19806993	Partially confirmed	0	No	intergenic		
Chr3	insertion	292	20244387	20244387	Partially confirmed	0	No	intergenic		
Chr3	insertion	230	20668427	20668428	N/A	0	No	3'UTR	AT3G55690	
Chr3	insertion	129	20809190	20809191	Partially confirmed	0	No	intergenic		
Chr3	insertion	786	20951706	20951898	Partially confirmed	0	No	exon	AT3G56540	
Chr3	insertion	91	21718486	21718501	Partially confirmed	0	No	intergenic		
Chr3	insertion	174	21735332	21735349	Partially confirmed	0	No	intergenic		
Chr3	insertion	350	22340176	22340182	Partially confirmed	0	No	intergenic		
Chr3	insertion	364	22506527	22506536	Partially confirmed	0	No	intron	AT3G60920	
Chr3	insertion	338	22652306	22652423	Partially confirmed	0	No	intergenic		
Chr3	insertion	176	23068328	23068328	Partially confirmed	0	AT3TE94070	intergenic		
Chr3	insertion	309	23068444	23068529	N/A	0	AT3TE94070	intergenic		
Chr3	insertion	449	23071793	23071794	Partially confirmed	0	No	intergenic		
Chr3	insertion	654	23359599	23359611	Fully confirmed	0	No	intergenic		
Chr4	insertion	703	199483	199677	N/A	0	No	intergenic		
Chr4	insertion	1700	412549	412557	N/A	0	No	exon	AT4G00955	
Chr4	insertion	322	513216	513266	N/A	0	No	intergenic		
Chr4	insertion	130	858607	858607	Partially confirmed	0	No	intergenic		
Chr4	insertion	147	910742	910776	N/A	0	No	intron	AT4G02070	
Chr4	insertion	2006	920957	921091	Partially confirmed	0	AT4TE04685	intergenic		
Chr4	insertion	810	1081357	1081374	Partially confirmed	0	No	intron	AT4G02465	
Chr4	insertion	209	1188583	1188633	Partially confirmed	0	No	intergenic		
Chr4	insertion	143	1191736	1191806	Fully confirmed	0	No	intron	AT4G02700	
Chr4	insertion	472	1257106	1257284	Fully confirmed	0	No	intergenic		
Chr4	insertion	552	1268701	1268764	Partially confirmed	0	No	intergenic		
Chr4	insertion	58	1278477	1278485	N/A	0	No	intergenic		
Chr4	insertion	144	1318786	1318788	N/A	2	No	intron	AT4G02970	Y
Chr4	insertion	288	1342392	1342405	Partially confirmed	0	AT4TE06840	intron	AT4G03040	
Chr4	insertion	234	1342941	1342948	N/A	0	AT4TE06840	intron	AT4G03040	
Chr4	insertion	646	1446756	1446950	Partially confirmed	0	No	intron	AT4G03298	
Chr4	insertion	4990	1540192	1542308	Partially confirmed	0	AT4TE07840	intergenic		
Chr4	insertion	246	1560355	1560395	Partially confirmed	0	No	intergenic		
Chr4	insertion	574	1572106	1572266	Partially confirmed	0	No	intergenic		
Chr4	insertion	1049	1648014	1648412	Partially confirmed	1	No	intergenic		
Chr4	insertion	99	1885229	1885246	N/A	15	AT4TE09255	intergenic		Y
Chr4	insertion	66	2105076	2105077	Fully confirmed	0	AT4TE09990	intergenic		
Chr4	insertion	283	2233379	2233390	Fully confirmed	1	No	intron	AT4G04490	
Chr4	insertion	431	2275270	2275271	Partially confirmed	0	AT4TE10585	intergenic		
Chr4	insertion	220	2344012	2344053	Partially confirmed	1	No	intergenic		
Chr4	insertion	394	2532741	2532776	Partially confirmed	0	No	intergenic		
Chr4	insertion	95	2591384	2591385	N/A	0	No	intron	AT4G05060	
Chr4	insertion	232	2849676	2849679	N/A	2	AT4G05581	intergenic		Y
Chr4	insertion	517	2852546	2852549	Fully confirmed	0	AT4TE13370	intergenic		
Chr4	insertion	279	3050682	3050779	Partially confirmed	0	AT4TE14130	intergenic		
Chr4	insertion	211	4234432	4234438	N/A	0	AT4TE18215	intergenic		
Chr4	insertion	270	4889424	4889517	Fully confirmed	0	AT4TE20370	intergenic		
Chr4	insertion	1358	5292723	5292738	Partially confirmed	0	AT4TE22030	intergenic		
Chr4	insertion	78	5315469	5315472	Fully confirmed	0	No	exon	AT4G08390	
Chr4	insertion	225	5374667	5374668	Fully confirmed	0	No	intergenic		
Chr4	insertion	1330	5449091	5449462	N/A	0	AT4TE22825	intergenic		

Chr4	insertion	4956	5751635	5753183	Partially confirmed	0	No	exon	AT4G08967
Chr4	insertion	245	5780030	5780083	Fully confirmed	0	AT4TE24265	intergenic	
Chr4	insertion	979	5923263	5923265	Partially confirmed	0	AT4TE24950	intergenic	
Chr4	insertion	174	5959455	5959455	Not confirmed	5	AT4TE25065	intergenic	Y
Chr4	insertion	929	6159628	6159761	Partially confirmed	0	No	intron	AT4G09780
Chr4	insertion	296	6459118	6459244	Fully confirmed	0	No	intergenic	
Chr4	insertion	305	6483642	6483723	Fully confirmed	0	AT4TE27670	intergenic	
Chr4	insertion	816	6554151	6554165	Partially confirmed	0	No	intergenic	
Chr4	insertion	420	6594719	6594871	Partially confirmed	0	No	intergenic	
Chr4	insertion	175	6688244	6688277	N/A	0	No	intergenic	
Chr4	insertion	285	6750121	6750183	Partially confirmed	0	No	intron	AT4G11050
Chr4	insertion	778	6763463	6763463	Partially confirmed	0	No	intergenic	
Chr4	insertion	312	6859741	6859747	Partially confirmed	0	AT4TE29540	intergenic	
Chr4	insertion	108	6912942	6912947	N/A	0	AT4TE29820	intergenic	
Chr4	insertion	126	6978538	6978538	Fully confirmed	0	No	intergenic	
Chr4	insertion	1214	6982676	6982773	Partially confirmed	0	No	pseudo_gene	AT4G11500
Chr4	insertion	830	7056008	7056015	Partially confirmed	0	No	intergenic	
Chr4	insertion	513	7069474	7069474	Partially confirmed	0	No	exon	AT4G11730
Chr4	insertion	496	7159460	7159575	Partially confirmed	0	No	intergenic	
Chr4	insertion	330	7159913	7159923	Partially confirmed	0	No	intergenic	
Chr4	insertion	410	7275379	7275393	Fully confirmed	0	AT4TE31680	intergenic	
Chr4	insertion	165	7278286	7278346	N/A	0	AT4TE31680	intergenic	
Chr4	insertion	282	7279795	7279866	Partially confirmed	0	AT4TE31685	intergenic	
Chr4	insertion	374	7344028	7344030	N/A	0	No	intergenic	
Chr4	insertion	121	7605298	7605320	Fully confirmed	0	No	intron	AT4G13020
Chr4	insertion	295	7643916	7643920	Partially confirmed	0	No	intergenic	
Chr4	insertion	318	7659172	7659289	N/A	0	No	intergenic	
Chr4	insertion	275	7672179	7672226	Partially confirmed	0	No	intron	AT4G13210
Chr4	insertion	88	7716200	7716202	Fully confirmed	0	No	intergenic	
Chr4	insertion	96	7756575	7756575	Not confirmed	0	No	intergenic	
Chr4	insertion	956	7936661	7936686	Partially confirmed	0	No	3'UTR	AT4G13640
Chr4	insertion	2323	7956971	7957122	N/A	0	No	intergenic	
Chr4	insertion	1977	8069660	8069679	Partially confirmed	0	No	intron	AT4G13968
Chr4	insertion	158	8099898	8099954	Fully confirmed	0	No	intron	AT4G14030
Chr4	insertion	753	8110097	8110099	Partially confirmed	0	No	intergenic	
Chr4	insertion	183	8156975	8156976	Partially confirmed	0	No	intergenic	
Chr4	insertion	215	8213551	8213552	Partially confirmed	0	No	intergenic	
Chr4	insertion	237	8587822	8587934	Partially confirmed	0	AT4TE38260	intergenic	
Chr4	insertion	476	8717085	8717094	N/A	0	No	intron	AT4G15270
Chr4	insertion	70	8765823	8765825	Fully confirmed	0	No	intergenic	
Chr4	insertion	1175	8785910	8785918	Partially confirmed	0	No	intergenic	
Chr4	insertion	176	8890450	8890451	Partially confirmed	0	No	intergenic	
Chr4	insertion	294	9015369	9015455	Partially confirmed	0	No	intron	AT4G15880
Chr4	insertion	1043	9022896	9023176	Partially confirmed	0	No	intergenic	
Chr4	insertion	54	9035870	9035882	Not confirmed	0	No	intergenic	
Chr4	insertion	556	9343615	9343616	Fully confirmed	0	No	intergenic	
Chr4	insertion	135	9345766	9345767	N/A	0	AT4TE42160	intron	AT4G16590
Chr4	insertion	209	9399020	9399115	Partially confirmed	0	No	intron	AT4G16710
Chr4	insertion	83	9454341	9454347	Not confirmed	0	No	intergenic	
Chr4	insertion	627	9799964	9799967	Partially confirmed	0	No	intergenic	
Chr4	insertion	150	9859586	9859641	Fully confirmed	0	No	intergenic	
Chr4	insertion	304	10090630	10090631	Partially confirmed	0	No	intron	AT4G18250
Chr4	insertion	143	10101155	10101156	Fully confirmed	0	No	intron	AT4G18270

Chr4	insertion	149	10182953	10182956	Partially confirmed	0	No	intergenic	
Chr4	insertion	173	10183456	10183461	Partially confirmed	0	No	intergenic	
Chr4	insertion	126	10281878	10281883	Fully confirmed	0	No	intergenic	
Chr4	insertion	111	10481347	10481363	Not confirmed	0	No	intergenic	
Chr4	insertion	237	10576865	10576897	Partially confirmed	0	No	intergenic	
Chr4	insertion	241	10582556	10582624	Partially confirmed	0	No	intron	AT4G19410
Chr4	insertion	130	10605231	10605274	Not confirmed	0	No	intergenic	
Chr4	insertion	249	10609384	10609430	Fully confirmed	0	No	intergenic	
Chr4	insertion	178	10618187	10618260	Not confirmed	0	No	intron	AT4G19490
Chr4	insertion	111	10638582	10638596	Fully confirmed	0	No	intron	AT4G19510
Chr4	insertion	216	10737486	10737564	N/A	0	AT4TE49195	intergenic	
Chr4	insertion	86	10826385	10826386	Fully confirmed	0	No	intergenic	
Chr4	insertion	384	10937391	10937395	Partially confirmed	0	No	intergenic	
Chr4	insertion	127	10938098	10938107	N/A	0	No	intron	AT4G20250
Chr4	insertion	179	12836689	12836693	N/A	0	No	intergenic	
Chr4	insertion	96	12933605	12933607	Fully confirmed	0	No	3'UTR	AT4G25240
Chr4	insertion	587	13294002	13294037	N/A	0	No	intron	AT4G26255
Chr4	insertion	428	13880899	13880963	Fully confirmed	0	No	intron	AT4G27870
Chr4	insertion	122	14796222	14796222	Fully confirmed	0	No	intergenic	
Chr4	insertion	1887	15698652	15699192	N/A	0	AT4TE74930	intergenic	
Chr4	insertion	415	15908297	15908309	Partially confirmed	0	No	intergenic	
Chr4	insertion	1320	16256271	16256920	N/A	0	No	intron	AT4G33910
Chr4	insertion	197	16257592	16257653	Partially confirmed	0	No	intergenic	
Chr4	insertion	91	16741217	16741217	Partially confirmed	0	No	intergenic	
Chr4	insertion	494	17217933	17217967	Fully confirmed	0	No	intergenic	
Chr4	insertion	164	17236584	17236638	Partially confirmed	0	No	intergenic	
Chr4	insertion	98	17339276	17339298	N/A	0	AT4TE83650	intergenic	
Chr4	insertion	112	17348263	17348279	Not confirmed	0	No	intergenic	
Chr4	insertion	64	18272098	18272099	Fully confirmed	0	No	intergenic	
Chr4	insertion	597	18448377	18448393	N/A	0	No	intergenic	
Chr4	insertion	226	18505573	18505647	Partially confirmed	0	No	intergenic	
Chr4	insertion	287	18522682	18522780	N/A	0	No	intergenic	
Chr5	insertion	122	996	997	Fully confirmed	1	No	intergenic	
Chr5	insertion	163	446852	446880	Partially confirmed	0	No	intergenic	
Chr5	insertion	139	795650	795682	Partially confirmed	0	No	intron	AT5G03290
Chr5	insertion	287	1208150	1208184	Partially confirmed	0	No	intergenic	
Chr5	insertion	422	1979062	1979083	Fully confirmed	0	AT5TE07190	intergenic	
Chr5	insertion	359	2081984	2082104	N/A	0	No	intergenic	
Chr5	insertion	809	2082384	2082678	N/A	0	No	intergenic	
Chr5	insertion	85	2250152	2250153	N/A	0	AT5TE08195	intergenic	
Chr5	insertion	95	2564592	2564594	Partially confirmed	0	No	intron	AT5G08000
Chr5	insertion	86	3460355	3460357	Fully confirmed	0	No	intron	AT5G10950
Chr5	insertion	52	3717161	3717163	Partially confirmed	0	No	intron	AT5G11570
Chr5	insertion	673	4004252	4004510	Partially confirmed	1	No	intron	AT5G12370
Chr5	insertion	154	4027669	4027732	Not confirmed	0	No	intergenic	
Chr5	insertion	78	4501274	4501286	Partially confirmed	0	No	intergenic	
Chr5	insertion	273	5331711	5331838	Partially confirmed	0	No	intergenic	
Chr5	insertion	141	5332028	5332043	Fully confirmed	0	No	intergenic	
Chr5	insertion	441	5675117	5675251	Fully confirmed	0	No	intergenic	
Chr5	insertion	121	6057419	6057471	N/A	0	No	intergenic	
Chr5	insertion	125	6224585	6224592	Fully confirmed	0	No	intergenic	
Chr5	insertion	721	6361451	6361460	Partially confirmed	0	No	intergenic	
Chr5	insertion	182	6570031	6570032	N/A	0	No	intron	AT5G19473

Chr5	insertion	168	6827813	6827875	Fully confirmed	0	No	intergenic	
Chr5	insertion	228	6976479	6976486	Partially confirmed	1	No	intergenic	
Chr5	insertion	177	7192910	7192980	Partially confirmed	0	No	intron	AT5G21150
Chr5	insertion	121	7608537	7608542	Fully confirmed	1	No	intron	AT5G22794
Chr5	insertion	124	7836874	7836924	N/A	0	No	intron	AT5G23260
Chr5	insertion	552	8065663	8065893	N/A	0	No	intergenic	
Chr5	insertion	302	8166208	8166298	Fully confirmed	0	No	intron	AT5G24140
Chr5	insertion	6416	8198846	8198861	Partially confirmed	0	AT5TE29650	intergenic	
Chr5	insertion	568	8396662	8396861	N/A	0	No	intergenic	
Chr5	insertion	188	8455417	8455437	Partially confirmed	0	No	3'UTR	AT5G24680
Chr5	insertion	1707	8509437	8510038	Partially confirmed	0	No	intergenic	
Chr5	insertion	186	8529598	8529650	Partially confirmed	0	No	intergenic	
Chr5	insertion	192	8582298	8582379	N/A	0	No	intergenic	
Chr5	insertion	206	8636452	8636452	Fully confirmed	0	No	intron	AT5G25060
Chr5	insertion	265	8698305	8698322	Partially confirmed	2	No	intergenic	Y
Chr5	insertion	77	9077177	9077191	Partially confirmed	0	No	intron	AT5G25990
Chr5	insertion	467	9135139	9135178	N/A	0	AT5TE33045	intergenic	
Chr5	insertion	566	9142676	9142765	Fully confirmed	0	No	intergenic	
Chr5	insertion	220	9858345	9858359	N/A	0	AT5TE35890	intergenic	
Chr5	insertion	522	9918178	9918193	Partially confirmed	0	No	intergenic	
Chr5	insertion	103	9918981	9918997	Not confirmed	0	AT5TE36130	intergenic	
Chr5	insertion	497	9941675	9941724	Fully confirmed	0	No	intron	AT5G27990
Chr5	insertion	297	10017556	10017646	Partially confirmed	0	No	intergenic	
Chr5	insertion	811	10018595	10018677	Partially confirmed	0	No	intergenic	
Chr5	insertion	99	10027497	10027502	N/A	0	No	intron	AT5G28020
Chr5	insertion	1796	10061370	10061373	Partially confirmed	0	AT5TE36645	intergenic	
Chr5	insertion	1172	10073463	10073511	N/A	0	AT5TE36710	intergenic	
Chr5	insertion	219	10123654	10123684	Partially confirmed	0	AT5TE36895	intergenic	
Chr5	insertion	58	10220493	10220494	N/A	0	AT5TE37275	intergenic	
Chr5	insertion	554	10567787	10567790	N/A	0	No	intergenic	
Chr5	insertion	547	10596754	10596853	N/A	0	AT5TE38665	intergenic	
Chr5	insertion	184	10796317	10796323	Fully confirmed	0	AT5TE39250	intergenic	
Chr5	insertion	252	11740070	11740071	Fully confirmed	0	AT5G31821	intergenic	
Chr5	insertion	751	12251213	12251213	Partially confirmed	2	AT5TE43520	intergenic	Y
Chr5	insertion	251	12275405	12275408	Partially confirmed	0	No	intergenic	
Chr5	insertion	6061	12512565	12512579	Partially confirmed	0	No	intergenic	
Chr5	insertion	143	12566883	12566942	Partially confirmed	0	AT5TE44525	intergenic	
Chr5	insertion	438	12603806	12603834	Partially confirmed	0	No	intron	AT5G33370
Chr5	insertion	292	12934062	12934065	Partially confirmed	35	AT5TE46055	intergenic	Y
Chr5	insertion	696	12985545	12985545	Partially confirmed	0	AT5TE46190	intergenic	
Chr5	insertion	100	13055350	13055351	Fully confirmed	0	AT5TE46425	intergenic	
Chr5	insertion	798	13137876	13137878	Partially confirmed	0	AT5TE46770	intergenic	
Chr5	insertion	333	13818717	13818785	N/A	0	AT5TE49260	intergenic	
Chr5	insertion	162	13993109	13993145	Partially confirmed	0	AT5TE49905	intergenic	
Chr5	insertion	472	14007535	14007653	Partially confirmed	0	No	intergenic	
Chr5	insertion	864	14567241	14567345	Partially confirmed	0	No	intergenic	
Chr5	insertion	377	14677082	14677085	N/A	0	AT5TE52830	intergenic	
Chr5	insertion	602	14690406	14690406	N/A	0	No	intergenic	
Chr5	insertion	604	14744076	14744076	Partially confirmed	0	No	intergenic	
Chr5	insertion	486	14767038	14767151	Partially confirmed	0	No	intergenic	
Chr5	insertion	122	15033116	15033117	N/A	0	AT5TE54265	intergenic	
Chr5	insertion	1232	15033313	15033313	Partially confirmed	0	No	intergenic	
Chr5	insertion	186	15033499	15033499	Partially confirmed	0	No	intergenic	

Chr5	insertion	378	15053327	15053339	Partially confirmed	0	AT5TE54365	intergenic	
Chr5	insertion	313	15136090	15136128	Partially confirmed	0	No	intergenic	
Chr5	insertion	136	15139324	15139336	N/A	0	AT5TE54750	intergenic	
Chr5	insertion	1360	15211104	15211105	Partially confirmed	0	No	intergenic	
Chr5	insertion	104	15235940	15235953	Not confirmed	0	No	exon	AT5G38190
Chr5	insertion	740	15306978	15306987	Partially confirmed	0	No	3'UTR	AT5G38300
Chr5	insertion	143	15330374	15330444	N/A	0	No	intron	AT5G38350
Chr5	insertion	107	15450256	15450257	Fully confirmed	1	No	intron	AT5G38570
Chr5	insertion	752	15505438	15505507	N/A	0	AT5TE56045	intergenic	
Chr5	insertion	288	15540634	15540713	Partially confirmed	0	No	intron	AT5G38810
Chr5	insertion	219	15645165	15645260	Partially confirmed	1	No	intergenic	
Chr5	insertion	376	15645668	15645677	Fully confirmed	1	No	intergenic	
Chr5	insertion	226	15890734	15890745	Partially confirmed	0	No	intergenic	
Chr5	insertion	276	16068232	16068237	Fully confirmed	0	No	intergenic	
Chr5	insertion	761	16142312	16142313	Partially confirmed	0	No	intergenic	
Chr5	insertion	235	16148313	16148342	N/A	0	No	intron	AT5G40370
Chr5	insertion	1236	16224946	16225164	Partially confirmed	0	No	intergenic	
Chr5	insertion	206	16246542	16246576	Partially confirmed	0	No	intergenic	
Chr5	insertion	140	16508818	16508818	Fully confirmed	0	No	intron	AT5G41270
Chr5	insertion	287	16603851	16603894	Partially confirmed	0	No	intergenic	
Chr5	insertion	299	16623560	16623572	N/A	0	No	intergenic	
Chr5	insertion	277	16679268	16679269	Fully confirmed	0	AT5TE60210	intergenic	
Chr5	insertion	533	16683364	16683365	N/A	0	No	exon	AT5G41720
Chr5	insertion	384	16740356	16740478	Fully confirmed	0	No	intergenic	
Chr5	insertion	243	16801044	16801044	Partially confirmed	0	No	intergenic	
Chr5	insertion	111	16805329	16805331	Partially confirmed	0	No	intergenic	
Chr5	insertion	240	16921027	16921130	Partially confirmed	0	No	intron	AT5G42320
Chr5	insertion	652	16975365	16975367	Partially confirmed	0	No	intergenic	
Chr5	insertion	537	16991213	16991218	Partially confirmed	0	No	exon	AT5G42490
Chr5	insertion	711	17023405	17023410	Partially confirmed	0	No	intergenic	
Chr5	insertion	81	17112477	17112483	Fully confirmed	0	No	intergenic	
Chr5	insertion	254	17129337	17129340	Fully confirmed	0	No	intergenic	
Chr5	insertion	155	17176928	17176992	Partially confirmed	0	No	intron	AT5G42830
Chr5	insertion	599	17273232	17273329	Partially confirmed	0	AT5TE62425	intergenic	
Chr5	insertion	1001	17290600	17290636	Partially confirmed	0	AT5TE62495	intergenic	
Chr5	insertion	604	17323416	17323590	Fully confirmed	0	No	intergenic	
Chr5	insertion	622	17326942	17326942	Partially confirmed	0	No	intergenic	
Chr5	insertion	297	17332059	17332060	Partially confirmed	0	No	intergenic	
Chr5	insertion	799	17348699	17348832	Partially confirmed	0	No	intergenic	
Chr5	insertion	174	17376715	17376716	N/A	0	No	intergenic	
Chr5	insertion	189	17571971	17572015	N/A	0	No	intron	AT5G43745
Chr5	insertion	104	17632355	17632355	Fully confirmed	0	No	intergenic	
Chr5	insertion	436	17811142	17811145	Fully confirmed	0	No	exon	AT5G44220
Chr5	insertion	529	17913555	17913590	N/A	0	No	intergenic	
Chr5	insertion	278	17948506	17948508	N/A	0	AT5TE64770	intergenic	
Chr5	insertion	289	17968782	17968785	Partially confirmed	0	No	intron	AT5G44572
Chr5	insertion	218	18081133	18081133	N/A	0	AT5TE65210	intergenic	
Chr5	insertion	115	18162732	18162734	Fully confirmed	0	No	intergenic	
Chr5	insertion	495	18220129	18220133	Fully confirmed	0	No	intergenic	
Chr5	insertion	1554	18298576	18299248	N/A	0	No	intergenic	
Chr5	insertion	155	18381169	18381242	Partially confirmed	0	AT5TE66160	intergenic	
Chr5	insertion	211	18392465	18392564	Partially confirmed	0	No	intron	AT5G45380
Chr5	insertion	204	19192046	19192142	Partially confirmed	0	No	intron	AT5G47260

Chr5	insertion	324	19573800	19573808	Fully confirmed	0	No	intergenic	
Chr5	insertion	229	19647142	19647152	Partially confirmed	0	No	intergenic	
Chr5	insertion	166	19647316	19647360	Partially confirmed	0	No	intergenic	
Chr5	insertion	245	19651152	19651202	N/A	0	No	intergenic	
Chr5	insertion	434	19849375	19849417	Partially confirmed	0	No	intergenic	
Chr5	insertion	96	19929934	19929935	Fully confirmed	0	AT5TE71730	intergenic	
Chr5	insertion	82	19966446	19966451	Fully confirmed	0	AT5TE71880	intergenic	
Chr5	insertion	1346	20080338	20080344	Partially confirmed	0	No	intergenic	
Chr5	insertion	850	20323900	20323901	Partially confirmed	0	No	intergenic	
Chr5	insertion	701	20365493	20365493	Partially confirmed	0	No	intergenic	
Chr5	insertion	459	20381061	20381062	Fully confirmed	0	No	intergenic	
Chr5	insertion	214	20787520	20787535	Fully confirmed	3	No	intergenic	Y
Chr5	insertion	236	20884459	20884543	Partially confirmed	0	No	intergenic	
Chr5	insertion	104	20979549	20979557	N/A	0	No	intergenic	
Chr5	insertion	279	20989988	20989992	Fully confirmed	0	No	intergenic	
Chr5	insertion	153	21135799	21135808	N/A	0	No	intergenic	
Chr5	insertion	1021	21497704	21497713	N/A	0	No	intergenic	
Chr5	insertion	332	21814032	21814034	Partially confirmed	0	No	exon	AT5G53740
Chr5	insertion	74	22014808	22014818	Partially confirmed	0	No	intergenic	
Chr5	insertion	565	22233220	22233223	Fully confirmed	0	No	intergenic	
Chr5	insertion	208	22360998	22361037	Fully confirmed	0	No	intergenic	
Chr5	insertion	444	22385132	22385181	Partially confirmed	0	No	intergenic	
Chr5	insertion	615	22579876	22579951	Partially confirmed	0	No	intergenic	
Chr5	insertion	129	22962841	22962846	Fully confirmed	0	No	intergenic	
Chr5	insertion	275	22978237	22978238	N/A	0	No	intergenic	
Chr5	insertion	166	23991883	23991955	Fully confirmed	0	No	intron	AT5G59520
Chr5	insertion	97	24614431	24614437	Fully confirmed	0	No	intergenic	
Chr5	insertion	92	24836430	24836431	Fully confirmed	0	No	intron	AT5G61820
Chr5	insertion	267	25279715	25279715	N/A	0	No	intergenic	
Chr5	insertion	371	25303643	25303657	Fully confirmed	0	No	intergenic	
Chr5	insertion	157	25535892	25535894	Fully confirmed	0	No	intergenic	
Chr5	insertion	146	25645017	25645023	Fully confirmed	0	No	intergenic	
Chr5	insertion	194	25766051	25766142	Fully confirmed	0	No	intron	AT5G64440
Chr5	insertion	200	26098052	26098143	N/A	0	No	intergenic	
Chr5	insertion	574	26119987	26119988	N/A	0	No	3'UTR	AT5G65360
Chr5	insertion	278	26325117	26325206	Fully confirmed	0	No	intergenic	
Chr5	insertion	559	26353931	26354110	Fully confirmed	0	No	intergenic	
Chr5	insertion	86	26740043	26740045	Fully confirmed	0	No	intergenic	
Chr5	insertion	475	26742873	26743025	Fully confirmed	0	No	intergenic	

* An indel is "Fully confirmed" if it is fully covered and supported by Monstanto contig. An indel is "Partially confirmed" if it is patially covered by Monstanto contig and partially supported. "N/A" means this indel is not covered by Monstan contig, due to the low coverage of Monsanto sequences.

Supplemental Table 8. The list of 130 genes with full CDS deleted in the *Ler* genome.

Gene ID	Description
AT1G09995	DNA repair DEAD helicase RAD3/XP-D subfamily protein
AT1G10000	Ribonuclease H-like superfamily protein
AT1G12170	F-box family protein
AT1G12490	F-box associated ubiquitination effector family protein
AT1G20280	homeobox-leucine zipper protein-related
AT1G21866	Encodes a Plant thionin family protein
AT1G23640	unknown protein
AT1G24380	unknown protein
AT1G24480	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G29590	eukaryotic translation Initiation Factor 4E3 (eIF4E3)
AT1G31370	Ubiquitin-specific protease family C19-related protein
AT1G31380	TRAF-like family protein
AT1G31390	TRAF-like family protein
AT1G33530	F-box family protein
AT1G34070	Retrotransposon gag protein
AT1G34095	unknown protein
AT1G34930	Encodes a Plant thionin family protein
AT1G35030	unknown protein;
AT1G35035	Encodes a Plant thionin family protein
AT1G51430	unknown protein
AT1G52695	alpha/beta-Hydrolases superfamily protein
AT1G52950	Nucleic acid-binding, OB-fold-like protein
AT1G53935	unknown protein
AT1G58265	Cytochrome P450 superfamily protein
AT1G59920	MADS-box family protein
AT1G60720	RNA-directed DNA polymerase (reverse transcriptase)-related family protein
AT1G62160	Serine protease inhibitor (SERPIN) family protein
AT1G63535	Encodes a defensin-like (DEFL) family protein. protein_coding
AT1G80970	XH domain-containing protein
AT1G80980	unknown protein
AT2G01310	Cyclin-dependent protein kinase 3 related
AT2G02103	unknown protein
AT2G02835	unknown protein
AT2G02840	nucleic acid binding;zinc ion binding
AT2G03560	F-box domain, cyclin-like
AT2G05185	unknown protein
AT2G13720	DNA topoisomerase (ATP-hydrolyzing)s;ATP binding;DNA binding
AT2G13760	unknown protein
AT2G13770	Putative harbinger transposase-derived nuclease
AT2G13895	Cysteine/Histidine-rich C1 domain family protein
AT2G15327	unknown protein
AT2G19230	Leucine-rich repeat transmembrane protein kinase protein
AT2G19550	alpha/beta-Hydrolases superfamily protein
AT2G24617	unknown protein
AT2G24620	S-locus glycoprotein family protein
AT2G24780	unknown protein
AT2G26820	phloem protein 2-A3 (PP2-A3)
AT2G29870	Aquaporin-like superfamily protein
AT2G29880	unknown protein
AT2G34120	Cytochrome C oxidase polypeptide VIB family protein
AT2G43865	unknown protein

AT2G44390	Cysteine/Histidine-rich C1 domain family protein
AT2G44400	Cysteine/Histidine-rich C1 domain family protein
AT3G09510	Ribonuclease H-like superfamily protein
AT3G11350	Pentatricopeptide repeat (PPR) superfamily protein
AT3G11370	Cysteine/Histidine-rich C1 domain family protein
AT3G14670	unknown protein
AT3G21850	one of Arabidopsis SKP1 homologues
AT3G23320	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT3G24516	unknown protein
AT3G24517	unknown protein
AT3G28170	unknown protein
AT3G29080	unknown protein
AT3G30200	Plant transposase (PttA/En/Spm family)
AT3G30370	Transposase, MuDR, plant
AT3G30805	Class II aminoacyl-tRNA and biotin synthetases superfamily protein
AT3G43750	RING/U-box protein with C6HC-type zinc finger domain
AT3G44570	Arabidopsis retrotransposon ORF-1 protein
AT3G45525	RING/U-box protein with C6HC-type zinc finger related
AT3G46570	Glycosyl hydrolase superfamily protein
AT3G47675	unknown protein;
AT3G47920	unknown protein
AT3G52830	Ankyrin repeat family protein
AT4G01595	Protein kinase superfamily protein
AT4G01640	F-box associated ubiquitination effector family protein
AT4G01910	Cysteine/Histidine-rich C1 domain family protein
AT4G01915	unknown protein
AT4G01920	Cysteine/Histidine-rich C1 domain family protein
AT4G03480	Ankyrin repeat family protein
AT4G03500	Ankyrin repeat family protein
AT4G05136	unknown protein
AT4G05490	RNI-like superfamily protein
AT4G08485	Encodes a defensin-like (DEFL) family protein
AT4G08874	Beta-galactosidase related protein
AT4G09466	Carbohydrate-binding X8 domain superfamily protein
AT4G10230	unknown protein
AT4G10780	LRR and NB-ARC domains-containing disease resistance protein
AT4G10880	unknown protein;
AT4G11430	hydroxyproline-rich glycoprotein family protein
AT4G18692	unknown protein
AT4G19270	unknown protein
AT4G23220	Encodes a cysteine-rich receptor-like protein kinase
AT4G23230	Encodes a cysteine-rich receptor-like protein kinase.
AT4G27190	NB-ARC domain-containing disease resistance protein
AT4G27220	NB-ARC domain-containing disease resistance protein
AT4G39930	unknown protein
AT5G02930	F-box/RNI-like superfamily protein
AT5G05657	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT5G06755	unknown protein
AT5G15420	unknown protein
AT5G16486	RNA-directed DNA polymerase (reverse transcriptase)-related family protein
AT5G18636	unknown protein;
AT5G20447	unknown protein
AT5G20450	Myosin family protein with Dil domain

AT5G23830	MD-2-related lipid recognition domain-containing protein
AT5G24593	unknown protein
AT5G27247	unknown protein
AT5G27260	unknown protein
AT5G35450	Disease resistance protein (CC-NBS-LRR class) family
AT5G35603	Protein of unknown function
AT5G35604	Myosin heavy chain-related
AT5G35920	a cytochrome P450 pseudogene
AT5G39390	Leucine-rich repeat protein kinase family protein
AT5G39920	CLP1-similar protein 5 (TAIR:AT5G39930.1)
AT5G42460	F-box and associated interaction domains-containing protein
AT5G42965	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT5G43030	Cysteine/Histidine-rich C1 domain family protein
AT5G43040	Cysteine/Histidine-rich C1 domain family protein
AT5G43360	Encodes Pht1;3, a member of the Pht1 family of phosphate transporters
AT5G45095	unknown protein
AT5G45450	Oligopeptide transporter OPT superfamily protein
AT5G46820	Protein of Unknown Function
AT5G48190	Domain of unknown function (DUF23)
AT5G49440	unknown protein
AT5G50136	unknown protein
AT5G50140	Ankyrin repeat family protein
AT5G51195	unknown protein
AT5G56380	F-box/RNI-like/FBD-like domains-containing protein
AT5G56470	FAD-dependent oxidoreductase family protein
AT5G59060	RNA-directed DNA polymerase (reverse transcriptase)-related family protein

Supplemental Table 9. The list of 186 genes with partially deleted in the *Ler* genome.

gene ID	deletion position	annotation
AT1G03350	3'UTR	BSD domain-containing protein
AT1G06630	exon	F-box/RNI-like superfamily protein
AT1G10100	exon	unknown protein
AT1G12180	exon	HSP20-like chaperones superfamily protein
AT1G14685	3'UTR	BASIC PENTACYSSTEINE 2 (BPC2)
AT1G15015	exon	F-box family protein
AT1G15600	3'UTR	unknown protein
AT1G15670	3'UTR	Galactose oxidase/kelch repeat superfamily protein
AT1G15680	exon_3'_end	F-box family protein
AT1G15770	exon	unknown protein
AT1G17160	3'UTR	pfkB-like carbohydrate kinase family protein
AT1G20290	exon_3'_end	SWI-SNF-related chromatin binding protein
AT1G23610	5'UTR	unknown protein
AT1G23660	exon	Unkown protein
AT1G24145	exon	unknown protein
AT1G29580	exon	unknown protein
AT1G30160	exon_5'_end	Unkown protein
AT1G30925	exon_3'_end	phospholipase Cs
AT1G32030	exon_middle	regulation of transcription, DNA-dependent
AT1G33440	3'UTR	Major facilitator superfamily protein
AT1G34200	3'UTR	Glyceraldehyde-3-phosphate dehydrogenase-like family protein
AT1G34570	3'UTR	Essential protein Yae1, N-terminal
AT1G35850	exon_5'_end	Encodes a member of the Arabidopsis Pumilio (APUM)
AT1G43730	exon	RNA-directed DNA polymerase (reverse transcriptase)-related family protein
AT1G44920	3'UTR	unknown protein
AT1G48820	exon	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT1G50470	exon	F-box associated ubiquitination effector family protein
AT1G51402	3'UTR	unknown protein
AT1G52618	exon_5'_end	unknown protein
AT1G52650	3'UTR	F-box/RNI-like superfamily protein
AT1G52990	exon	thioredoxin family protein
AT1G53000	3'UTR	Encodes a putative CMP-KDO synthetase
AT1G54000	3'UTR	GDLS-like Lipase/Acylhydrolase superfamily protein
AT1G56100	exon	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT1G58270	3'UTR	ZW9 mRNA, complete cds protein_coding (ZW9) (ZW9)
AT1G58280	3'UTR	Phosphoglycerate mutase family protein
AT1G58400	multi_exons	Disease resistance protein (CC-NBS-LRR class) family;
AT1G61090	5'UTR	unknown protein
AT1G61093	exon	unknown protein
AT1G61260	3'UTR	Unkown protein
AT1G62170	exon	Serine protease inhibitor (SERPIN) family protein
AT1G62570	multi_exons	belongs to the flavin-monooxygenase (FMO) family
AT1G62880	3'UTR	Cornichon family protein
AT1G63870	multi_exons	Disease resistance protein (TIR-NBS-LRR class) family
AT1G63880	multi_exons	Encodes a TIR-NBS-LRR class of disease resistance protein
AT1G64180	exon	intracellular protein transport protein USO1-related
AT1G65170	exon	Ubiquitin carboxyl-terminal hydrolase family protein

AT1G65200	exon_5'_end	Ubiquitin carboxyl-terminal hydrolase-related protein
AT1G69090	exon_5'_end	Protein of unknown function
AT1G69550	exon	disease resistance protein
AT1G71340	5'UTR	PLC-like phosphodiesterases superfamily protein
AT1G72930	3'UTR	Toll/interleukin-1 receptor-like protein (TIR) mRNA
AT1G74280	3'UTR	alpha/beta-Hydrolases superfamily protein
AT1G74290	multi_exons	alpha/beta-Hydrolases superfamily protein
AT1G78070	3'UTR	Transducin/WD40 repeat-like superfamily protein
AT1G80740	exon	ecotype Kl-0 chromomethylase (CMT1).
AT1G80960	exon	F-box and Leucine Rich Repeat domains containing protein
AT2G01780	exon_3'_end	Curculin-like (mannose-binding) lectin family protein
AT2G02320	3'UTR	phloem protein 2-B7 (PP2-B7)
AT2G03290	3'UTR	emp24/gp25L/p24 family/GOLD family protein
AT2G03565	exon	unknown protein
AT2G05350	exon	unknown protein
AT2G05900	exon	Predicted to encodes a SU(VAR)3-9 homolog, a SET domain protein.
AT2G07280	exon	unknown protein
AT2G14000	exon	Arabidopsis retrotransposon ORF-1 protein
AT2G15042	multi_exons	Leucine-rich repeat (LRR) family protein
AT2G17940	exon_middle	Plant protein of unknown function
AT2G18320	exon	F-box associated ubiquitination effector family protein
AT2G18660	3'UTR	Encodes PNP-A (Plant Natriuretic Peptide A).
AT2G19030	exon_3'_end	RALF-LIKE 11 (RALFL11)
AT2G20613	exon_3'_end	DNA-binding storekeeper protein-related transcriptional regulator
AT2G21100	3'UTR	Disease resistance-responsive (dirigent-like protein) family protein
AT2G23690	multi_exons	unknown protein
AT2G24255	3'UTR	unknown protein
AT2G24680	multi_exons	transcriptional factor B3 family protein
AT2G24693	3'UTR	Encodes a defensin-like (DEFL) family protein.
AT2G25150	multi_exons	HXXXD-type acyl-transferase family protein
AT2G25510	5'UTR	unknown protein
AT2G27070	exon	member of Response Regulator B-Type
AT2G28140	3'UTR	Protein of unknown function (DUF1635)
AT2G28625	3'UTR	unknown protein
AT2G31480	3'UTR	unknown protein
AT2G32905	exon	Unkown protein
AT2G34110	multi_exons	Forkhead-associated (FHA) domain-containing protein
AT2G34840	multi_exons	Coatomer epsilon subunit
AT2G39320	multi_exons	Cysteine proteinases superfamily protein
AT2G44195	exon_3'_end	CBF1-interacting co-repressor CIR, N-terminal
AT2TE41910	exon	
AT3G03847	exon_3'_end	SAUR-like auxin-responsive protein family
AT3G04660	exon_3'_end	F-box and associated interaction domains-containing protein
AT3G05780	multi_exons	Encodes a member of the Lon protease-like proteins
AT3G09110	3'UTR	Protein of unknown function
AT3G09160	multi_exons	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G09340	exon	Transmembrane amino acid transporter family protein
AT3G18485	multi_exons	Encodes a novel protein
AT3G21110	5'UTR	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole synthetase

AT3G27430	3'UTR	Encodes 20S proteasome beta subunit PBB1 (PBB1)
AT3G27470	3'UTR	Unkown protein
AT3G28310	exon	Protein of unknown function
AT3G30235	exon	General transcription factor 2-related zinc finger protein
AT3G43740	multi_exons	Leucine-rich repeat (LRR) family protein
AT3G44290	exon	NAC domain containing protein 60 (NAC060)
AT3G45760	exon	Nucleotidyltransferase family protein
AT3G45860	multi_exons	Encodes a cysteine-rich receptor-like protein kinase.
AT3G46340	exon	Leucine-rich repeat protein kinase family protein
AT3G46500	5'UTR	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT3G47350	exon	Encodes a putative hydroxysteroid dehydrogenase (HSD).
AT3G48830	multi_exons	polynucleotide adenylyltransferase family protein
AT3G51171	exon_middle	F-box and associated interaction domains-containing protein
AT3G54910	5'UTR	RNI-like superfamily protein
AT3G55690	3'UTR	unknown protein
AT3G56540	exon	alpha/beta-Hydrolases superfamily protein
AT3G57580	5'UTR	F-box and associated interaction domains-containing protein
AT3G59240	multi_exons	RNI-like superfamily protein
AT3G60940	multi_exons	Putative endonuclease or glycosyl hydrolase
AT3G61320	3'UTR	Bestrophin-like protein
AT4G00955	exon	Unkown protein
AT4G01650	multi_exons	Polyketide cyclase / dehydrase and lipid transport protein
AT4G03490	multi_exons	Ankyrin repeat family protein
AT4G03505	multi_exons	Ankyrin repeat family protein
AT4G07380	exon_3'_end	unknown protein
AT4G07825	exon_3'_end	unknown protein
AT4G08390	exon	Encodes a chloroplastic stromal ascorbate peroxidase sAPX.
AT4G08760	multi_exons	nucleolin like 1
AT4G08967	exon	unknown protein
AT4G09690	exon_5'_end	Cysteine/Histidine-rich C1 domain family protein
AT4G10310	3'UTR	encodes a sodium transporter (HKT1) expressed in xylem parenchyma cells.
AT4G10850	3'UTR	Nodulin MtN3 family protein
AT4G11730	exon	Cation transporter/ E1-E2 ATPase family protein
AT4G13640	3'UTR	unfertilized embryo sac 16 (UNE16)
AT4G13670	multi_exons	plastid transcriptionally active 5 (PTAC5)
AT4G15320	exon	encodes a gene similar to cellulose synthase
AT4G16295	exon_3'_end	self-incompatibility (S) protein homolog
AT4G16640	5'UTR	Matrixin family protein
AT4G18860	exon_3'_end	unknown protein
AT4G19470	exon	Leucine-rich repeat (LRR) family protein
AT4G19620	exon	unknown protein
AT4G19630	5'UTR	winged-helix DNA-binding transcription factor family protein
AT4G19930	exon_5'_end	F-box and associated interaction domains-containing protein
AT4G20370	3'UTR	Encodes a floral inducer that is a homolog of FT
AT4G21090	multi_exons	MITOCHONDRIAL FERREDOXIN 2 (MFDX2);
AT4G21100	multi_exons	DAMAGED DNA BINDING PROTEIN 1 B (DDB1B)
AT4G23160	multi_exons	CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 8 (CRK8)
AT4G23390	exon_3'_end	Protein of Unknown Function
AT4G24980	multi_exons	nodulin MtN21 /EamA-like transporter family protein

AT4G25240	3'UTR	Encodes GPI-anchored SKU5-like protein.
AT4G34250	3'UTR	KCS16, a member of the 3-ketoacyl-CoA synthase family
AT4G37300	3'UTR	maternal effect embryo arrest 59 (MEE59);
AT5G01400	exon_middle	ENHANCED SILENCING PHENOTYPE 4 (ESP4)
AT5G03495	5'UTR	RNA-binding (RRM/RBD/RNP motifs) family protein
AT5G03500	3'UTR	Mediator complex, subunit Med7
AT5G06750	5'UTR	Protein phosphatase 2C family protein
AT5G13200	3'UTR	GRAM domain family protein
AT5G13650	3'UTR	elongation factor family protein
AT5G17860	3'UTR	calcium exchanger 7 (CAX7)
AT5G19200	3'UTR	NAD(P)-binding Rossmann-fold superfamily protein
AT5G23230	3'UTR	nicotinamidase 2 (NIC2)
AT5G24210	3'UTR	alpha/beta-Hydrolases superfamily protein
AT5G24670	5'UTR	Cytidine/deoxycytidylate deaminase family protein
AT5G24680	3'UTR	Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2
AT5G25230	multi_exons	Ribosomal protein S5/Elongation factor G/III/V family protein
AT5G25415	multi_exons	Protein of Unknown Function
AT5G28646	3'UTR	WAVE-DAMPENED 2 (WVD2)
AT5G28885	exon	unknown protein
AT5G35660	exon_middle	Glycine-rich protein family
AT5G36870	exon	encodes a gene similar to callose synthase
AT5G36930	multi_exons	Disease resistance protein (TIR-NBS-LRR class) family;
AT5G38190	multi_exons	Myosin heavy chain-related (TAIR:AT1G32010.1)
AT5G38300	3'UTR	Unknown protein
AT5G39471	exon_middle	Cysteine/Histidine-rich C1 domain family protein
AT5G41720	exon	F-box protein-related
AT5G42490	exon	ATP binding microtubule motor family protein
AT5G43050	5'UTR	Chloroplast localized YCF20-like gene involved in nonphotochemical quenching
AT5G44220	exon	F-box family protein
AT5G44575	5'UTR	unknown protein
AT5G46310	exon	WRKY family transcription factor
AT5G47300	exon_3'_end	F-box and associated interaction domains-containing protein
AT5G48090	3'UTR	EDM2-like protein1 (ELP1)
AT5G49900	3'UTR	Beta-glucosidase, GBA2 type family protein
AT5G53740	exon	unknown protein
AT5G55360	exon_5'_end	MBOAT (membrane bound O-acyl transferase) family protein
AT5G55565	3'UTR	Encodes a defensin-like (DEFL) family protein
AT5G56370	3'UTR	F-box/RNI-like/FBD-like domains-containing protein
AT5G60260	multi_exons	unknown protein
AT5G65360	3'UTR	Histone superfamily protein;
AT5G66670	3'UTR	Protein of unknown function (DUF677)

Supplemental Table 10. Gene duplication followed by reciprocal loss between Col and Ler

Deleted Gene in Col	Chromosome	Start	End	Inserted in Ler	Chromosome	Start	End
AT4G03480	Chr4	1546024	1548871	insert	Chr4	1540192	1542308
AT4G03500	Chr4	1553092	1556571	insert	Chr4	1540192	1542308
AT4G03490	Chr4	1549345	1552784	insert	Chr4	1540192	1542308
AT4G03505	Chr4	1556888	1557319	insert	Chr4	1540192	1542308
AT5G16486	Chr5	5383597	5384226	insert	Chr4	412549	412557
AT1G43730	Chr1	16508723	16509784	insert	Chr4	412549	412557
AT1G60720	Chr1	22357072	22357941	insert	Chr4	412549	412557
AT5G59060	Chr5	23844301	23844777	insert	Chr4	412549	412557
AT1G10000	Chr1	3263877	3264788	insert	Chr3	4939991	4940008
AT3G09510	Chr3	2921804	2923258	insert	Chr3	4939991	4940008
AT5G18636	Chr5	6211268	6212371	insert	Chr3	4939991	4940008
AT4G23220	Chr4	12153956	12157091	insert	Chr4	6982676	6982773
AT4G23230	Chr4	12157569	12160270	insert	Chr4	6982676	6982773
AT5G50140	Chr5	20395856	20398197	insert	Chr3	1250360	1250565
AT2G02103	Chr2	530241	531636	insert	Chr1	26247797	26247800
AT3G23320	Chr3	8344629	8345204	insert	Chr5	12512565	12512579
AT1G12490	Chr1	4260783	4261869	insert	Chr1	5172654	5172681
AT4G01640	Chr4	702563	703600	insert	Chr1	5172654	5172681
AT5G42460	Chr5	16979773	16981115	insert	Chr1	5172654	5172681
AT1G34070	Chr1	12402283	12403209	insert	Chr1	30345514	30345518
AT4G11430	Chr4	6952799	6954242	insert	Chr1	30345514	30345518
AT3G47920	Chr3	17682952	17683854	insert	Chr3	11717075	11717096

Supplemental Table 11. The list of meiotic crossovers detected in the two meioses.

Meiosis Sample	Crossover	Chromosome	Offspring	Maximal Length	Minimal Length	Containing GC
1st meiosis	CO-1	Chr1	A,B	1166	0	No
	CO-2	Chr1	A,B	562	143	Yes
	CO-3	Chr1	A,B	1514	1	Yes
	CO-4	Chr2	C,D	1549	1209	Yes
	CO-5	Chr3	A,B	1305	0	No
	CO-6	Chr4	A,B	568	0	No
	CO-7	Chr5	A,B	3099	0	No
	CO-8	Chr5	A,B	306	0	No
	CO-9	Chr5	A,C	1064	1	Yes
2nd meiosis	CO-1	Chr1	B,C	129508	0	No
	CO-2	Chr1	B,C	980	0	No
	CO-3	Chr2	A,D	873	0	No
	CO-4	Chr3	A,D	926	0	No
	CO-5	Chr3	A,B	977	0	No
	CO-6	Chr3	A,B	829	0	No
	CO-7	Chr4	A,D	3288	141	Yes
	CO-8	Chr5	A,B	2026	150	Yes
	CO-9	Chr5	B,C	1749	0	No

Supplemental Table 12. The list of gene conversions detected in the two meioses.

Meiosis Sample	Chromosome	Min Start	Min End	Min Length	Max Start	Max End	Max Length	# Supporting SNPs
1st meiosis	Chr1	13957178	13958976	1799	13955540	13959511	3972	3
	Chr1	17235790	17235790	1	17232765	17236663	3899	1
	Chr5	121436	121436	1	120397	123474	3078	1
2nd meiosis	Chr5	4114437	4114437	1	4109948	4116643	6696	1

Supplemental Table 13. Redistribution of SNPs and indels by crossing over meiotic crossovers and independent chromosome assortment *

Genotype		Chr1	Chr2	Chr3	Chr4	Chr5	Total
SNP	<i>Ler</i>	82392	63075	66040	55579	82085	349171
	Meiosis I	Plant A	26422	0	15184	27630	91913
		Plant B	55967	63075	50855	27949	255360
		Plant C	0	40776	0	1893	42669
		Plant D	82392	22290	66040	55579	308386
	Meiosis II	Plant A	0	17266	42417	36510	113563
		Plant B	54391	63075	20134	0	179602
		Plant C	28001	0	66040	55579	172329
		Plant D	82392	45809	3489	19067	232842
	<i>Ler</i>	14399	9536	10772	9648	13730	58085
	Meiosis I	Plant A	5534	0	3239	5955	19496
		Plant B	8864	9536	7532	3693	38209
		Plant C	0	6974	0	377	7351
		Plant D	14399	2559	10772	9648	51108
Small Indel	Meiosis II	Plant A	0	3421	6159	5583	18556
		Plant B	8524	9536	3865	0	27677
		Plant C	5872	0	10772	9648	30874
		Plant D	14399	6115	748	4064	39056
	<i>Ler</i>	588	396	402	397	532	2315
	Meiosis I	Plant A	170	0	80	175	556
		Plant B	417	396	322	222	1751
		Plant C	0	274	0	7	281
		Plant D	588	122	402	397	2041
	Meiosis II	Plant A	0	87	277	287	732
		Plant B	409	396	113	0	1231
		Plant C	179	0	402	397	1116
		Plant D	588	309	12	110	1551

* All SNPs and indels were using the Col sequence as reference. Pure Col sequence has 0 in the table.

Supplemental Table 14. The locations of genetic structure variations between Col and Ler resulting in CNVs in two meiotic offspring.

					PCR verification results	
					Col	Ler
CNVs generated in the first meiosis offspring	Regions in Col		Regions in Ler			
	CNV1	Chr1 4330003	Chr1 17710647		Confirmed	No band obtained
		4334114			Confirmed	No band obtained
	CNV2	Chr1 5352243	Chr3 20946049		Confirmed	No band obtained
		5356410			Confirmed	No band obtained
	CNV3	Chr1 17257556	Chr4 8946707	Potential	Not experimented	Not experimented
		17258027			Not experimented	Not experimented
	CNV4	Chr1 17657005	Chr2 1422365		Not experimented	Not experimented
		17659473			Not experimented	Not experimented
	CNV5	Chr1 26366833	Chr5 9532137		Confirmed	No band obtained
		26371395			Confirmed	No band obtained
	CNV6	Chr2 5894104 (5886400)	Chr1 13476708		Not experimented	Not experimented
		5899880			Not experimented	Not experimented
	CNV7	Chr2 6422827			Not experimented	Not experimented
		6426873			Not experimented	Not experimented
	CNV8	Chr2 8816488	Chr1 18055255	Potential	Not experimented	Not experimented
		8820784	Chr3 23299167	Potential	Not experimented	Not experimented
	CNV9	Chr2 9124731(9122639)			Not experimented	Not experimented
		9125291			Not experimented	Not experimented
	CNV10	Chr2 12449625	Chr2 1945640		Confirmed	No band obtained
		12454241	Chr2 1945913		Confirmed	No band obtained
	CNV11	Chr3 9227606			Not experimented	Not experimented
		9230460	Chr3 3046811		Not experimented	Not experimented
	CNV12	Chr3 9435026	Chr4 7856247		Confirmed	No band obtained
		9436262			Confirmed	No band obtained
	CNV13	Chr3 14278567	Chr4 14272984		Not experimented	Not experimented
		14281298			Not experimented	Not experimented
	CNV14	Chr3 18791447	Chr4 12123803	Potential	Confirmed	No band obtained
		18795367			Confirmed	No band obtained
	CNV15	Chr3 21322317	Chr5 24635715		Not experimented	Not experimented
		21329562			Not experimented	Not experimented
	CNV16	Chr3 22232853	Chr3 6009704		Confirmed	No band obtained
		22235543	Chr3 6009637		Confirmed	No band obtained
	CNV17	Chr4 13625333			Not experimented	Not experimented
		13629630			Not experimented	Not experimented
	CNV18	Chr5 9641291	Chr1 2870468		Confirmed	No band obtained
		9644406			Confirmed	No band obtained
	CNV19	Chr5 9922025	Chr5 1375595		Not experimented	Not experimented
	CNV20	Chr5 10350412	Chr2 5666717		Confirmed	No band obtained
		10356295	Chr1 1194357/18632298/5	Potential	Confirmed	No band obtained
	CNV21	Chr5 17597594	Unknown			
		17602890				
	CNV1	Chr1 3729164	Chr3 7094540			
		3730139				
	CNV2	Chr1 4330003				
		4333985				
	CNV3	Chr1 5352243	Chr3 20946025			
		5356410				
	CNV4	Chr1 11028429	Chr3 16854585			
		11028658				
	CNV5	Chr1 12273345				
		12276038				
	CNV6	Chr1 15715267				
		15716273				
	CNV7	Chr1 18338925	Chr3 16322530			
		18340184				
	CNV8	Chr1 26366833				
		26371357				
	CNV9	Chr2 3224635	Chr1 28830587			
		3232061				
	CNV10	Chr2 4704163				
		4705404				
	CNV11	Chr2 5888098	Chr1 10467677			
		5899880	Chr1 13476708			
	CNV12	Chr3 9236916	Chr1 19399421			
		9237528				
	CNV13	Chr3 9435026	Chr4 7856144			
		9438515				
	CNV14	Chr3 9614087	Chr1 10467702			
		9625248				

CNVs generated in the second meiosis offspring	CNV15	Chr3	13099798 13103754	Chr2	859100	Not experimented
	CNV16	Chr3	16799136 16800466			
	CNV17	Chr3	21322444 21328184	Chr5	24535716	
	CNV18	Chr3	22232853 22235543	Chr3	6009637	
	CNV19	Chr4	1458753 1462400	Chr1	24224902	
	CNV20	Chr4	2790064 2791708	Chr2	9634085	
	CNV21	Chr4	5966100 5970550	Chr5	15601183	
	CNV22	Chr4	13624800 13632000	Chr2	2955131	
	CNV23	Chr4	17712514 17715406	Chr3	16887993	
	CNV24	Chr5	5217542 5220900	Chr1	8640512	
	CNV25	Chr5	6403273 6407808			
	CNV26	Chr5	7027929 7039146	Chr3	12448495	
	CNV27	Chr5	7829136 7830097	Chr3	21471927	
	CNV28	Chr5	9641392 9644005			
	CNV29	Chr5	10350525 10356164	Chr1	5798860/18632298/1194357	
	CNV30	Chr5	14557784 14559637	Chr3	16352725	
	CNV31	Chr5	15581932 15582401			
	CNV32	Chr5	18387234 18388038	Chr2 Chr5	1241219 18387514/10527661	

Numbers indicated the positions of the reference genome. For PCR verification, primers were designed according to the Col reference sequence. The PCR products cover the predicted boundaries in Col. "Potential" means there are many sequencing reads supporting that, but not all. "Unknow" means the position cannot be defined by sequencing reads.

Supplemental Table 15. Gene families enriched for genomic variations.

	Gene family	10 or more nonsynonymous SNPs (443/27206)	Nonsense SNPs (319/27206)	Frameshift indels (845/27206)	Nonframeshift indels (462/27206)	Large indels (316/27206)	All variations (2171/27206)
Not/moderately enriched	MADS	-	-	-	-	-	-
	Myb	-	-	-	0.01115 (6/132)	-	-
	bHLH	-	-	-	-	-	-
	AP2/EREBP	-	-	-	0.01572 (6/138)	-	-
	WD repeat	-	-	-	-	-	-
Strongly enriched	WRKY	-	-	-	1.57e-5 (6/73)	-	-
	F-box	-	<2.2e-16 (36/656)	<2.2e-16 (63/656)	-	1.18e-7 (22/656)	<2.2e-16 (134/656)
	LRR-RLK	3.61e-8 (14/223)	-	-	-	-	-
	LRR-RLP	<2.2e-16 (37/57)	-	-	-	-	2.1e-8 (16/57)
	NBS-LRR	<2.2e-16 (37/147)	-	6.55e-16 (15/147)	-	1.19e-6 (8/147)	<2.2e-16 (58/147)
	Receptor kinase-like	3.97e-13 (21/307)	-	-	-	-	8.89e-5 (43/307)

Supplemental Table 16. Correlation of genome size and genetic distance among various species.

Species	Genome size (Mb)	Chromosome number	Genetic distance (cM)	Physical distance/ morgan	COs /per cell	CO/per Chromosome	Kb/ per CO	References
Budding Yeast	12	16	4,395	0.27	91	5.7	131	(Goffeau et al. 1996; Qi et al. 2009)
Fission Yeast	14	3	1700	0.82	-	-	-	(Gygax and Thuriaux 1984)
C. elegans	97	6	300	32	6	1	16,100	(CSC 1998)
Arabidopsis	120	5	469	25	10	2	12,000	(AGI 2000)
Rice	389	12	1,521	25.6	20.8	2.1	18,700	(Anderson et al. 2003; 2005; Wang et al. 2009)
Maize	2,300	10	1,856	123	28	2.8	82,100	(Maguire and Riess 1994; Anderson et al. 2003; Schnable et al. 2009)
Zebrafish	1700	25	2297	74	-	-	-	(Shimoda et al. 1999)
Mouse	2,500	20	1,361	183.6	23-26	1.1-1.3	96,153-108,695	(Baker et al. 1995; Dietrich et al. 1996; Waterston et al. 2002)
Human	3,000	23	2,545	118	50.9	2.2	58,939	(Barlow and Hulten 1998)

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Supplemental Table 17. The list of primers used for PCR-based verification of some predicted indels between Col and Ler .

PCR verification for predicted deletions in Ler :						
Deletion	primer name	primer sequence	Start (Col)	End (Col)	Deletion length	Col size
Chr1-Del-1	oMC6784	TCAGCTTTCACAGTTGATCTGAC	270399	270610	211	917
	oMC6726	TTCTGGGCCCATATTTGAAG				
Chr1-Del-2	oMC6727	CAGCAAGTGATTGGCAAAAG	1258134	1258377	243	846
	oMC6728	TCAACATCCAACGGTCTGAA				
Chr1-Del-3	oMC6729	TCCTCCGAATTTGAGCATT	1430170	1431039	869	1545
	oMC6730	CCAAGGAACCAAGGTTTGAA				
Chr1-Del-4	oMC6731	GGACTACGGTGAAGATTCTGT	1445508	1446064	556	1195
	oMC6732	ATCCAACCTCAAGGATCTCG				
Chr1-Del-5	oMC6733	GGAGGCCCACTCTTTCTTTC	1617564	1618155	591	1158
	oMC6734	AACCTGAACCAATTGATCG				
Chr1-Del-6	oMC6735	TGCAAATATGCAATATACGTTCC	6795296	6795629	333	1032
	oMC6736	ACGACCAACAAAGGACTCG				
Chr1-Del-7	oMC6737	ATTGGTGGCATTGGCATATC	9588388	9588643	255	750
	oMC6738	TTCTTGATTGACCACCGAAC				
Chr1-Del-8	oMC6739	GGCTCGACGTTAAGCATCAT	10027348	10027535	187	586
	oMC6740	GGAGATATTGGCAAGGAAGG				
Chr1-Del-9	oMC6741	TTTCGGCCAAAAAGATTTACA	10606239	10606569	330	858
	oMC6742	CGGTTTGGCCAGAGTACATT				
Chr1-Del-10	oMC6743	CACCACACAGAATCCGAAAA	11212178	11212568	390	951
	oMC6744	GCGCCAAATGCTATTGTTT				
Chr1-Del-11	oMC6805	ACAGCAGTTTGGCTACACG				
	oMC6806	TTGGTGTGAACGAAACCTCA				
	oMC6807	ACCTGTGTCTCCAGGGATTG				

PCR verification for predicted insertion in Ler :						
Insertion name	primer name	primer sequence	Start (Col)	End (Col)	Insertion length	Col size
Chr1-Ins-1	oMC6785	GGGGAGGGGACTAATCATGT	2665492	2665646	222	508
	oMC6786	GCCACCTAAGGGCTAAGTGC				
Chr1-Ins-2	oMC6787	CTCATCAGCCTTTGGAGGAA	5853924	5854042	269	575
	oMC6788	CCATGTGCGCTGTTTCTTCT				
Chr1-Ins-3	oMC6789	TTGGTCACGACGAAAATGAA	18879974	18880075	223	612
	oMC6790	GTCGTGATCCCACTTTGCTT				
Chr1-Ins-4	oMC6791	TGAGAGCTTCCCAAAATTCG	24217943	24218015	273	496
	oMC6792	TCTCGAGCTTCCAAAAGTTTC				
Chr1-Ins-5	oMC6793	TCGGGTGCAATAAATGATGG	24370325	24370502	258	542
	oMC6794	CACCCGGTGAAAGAACAAC				
Chr3-Ins-1	oMC6795	CTTTGGGATGCTTGGCTAAA	1000896	1000987	272	602
	oMC6796	CATATGCGGTATGCTTTCCA				
Chr3-Ins-2	oMC6797	CCTGCCGCTATATGTGACT	2563426	2563597	226	558
	oMC6798	TTGTGGCCTTTTATTGGT				
Chr3-Ins-3	oMC6799	CGGACTCCGACTAATAAATAGCTG	4400594	4400683	274	672
	oMC6800	GGCCTTTCATCCAATTTCTG				
Chr3-Ins-4	oMC6801	CATAAATCCCGTGGCTCAAT	9232291	9232373	233	494
	oMC6802	GATGCCAGAAGCTCCAGAGG				
Chr3-Ins-5	oMC6803	GCTCATCCGTTGTCAATTCCT	12164675	12164818	236	589
	oMC6804	TGTGCCTTTTCTTGTATCTTTG				

Supplemental Table 18. The list of primers for PCR-based verification of predicted COs and NCOs.

The primers for PCR amplification and conventional sequencing for the 1st meiosis COs:

CO name	Primer name	Primer sequence	
1st meiosis-CO-1	CO-1-1 (F)	ACGAATCACATGGGGTCAAT	
	CO-1-1 (R)	TGGCTATTCGTTGGATGTCA	
	CO-1-2 (F)	TCTCGCAACAACACAAGAGC	
	CO-1-2 (R)	ACGAATCATCAGGACCAAGG	
1st meiosis-CO-2	CO-2-1 (F)	ACGAATCATCAGGACCAAGG	
	CO-2-1 (R)	AAGGCTGTGATTTACTTTGACCA	
1st meiosis-CO-3	CO-3-1 (F)	CACCTCCTTTGGTTGCCTCT	
	CO-3-1 (R)	TTGTGTTGCCAAGTTTGGGA	
	CO-3-2 (F)	TTGAATACTGGTGATATTCAATCG	
	CO-3-2 (R)	TTTAAGGCTAAGAATTTTCAACAGC	
1st meiosis-CO-4	CO-4-1 (F)	TTTTGTTACCCCGATTCTGC	
	CO-4-1 (R)	ACACCGCACATGGAATCTTT	
	CO-4-2 (F)	AAAGATTCCATGTGCGGTGT	
	CO-4-2 (R)	TGGAAGACTCGAACCACAAA	
	CO-4-3 (F)	TTGTGGTTCGAGTCTTCCA	
	CO-4-3 (R)	GGCATTTCCAATTGACAACA	
	CO-4-4 (F)	CCCACCAAAGGAAAACGTAG	Deletion verification
	CO-4-4 (R)	CGGGCATCAGGATATCATCT	Deletion verification
1st meiosis-CO-5	CO-5-1 (F)	CAGAGTGGTAGAACCAAGCTGAA	
	CO-5-1 (R)	CTGAAAACTCGCCGAAAAG	
	CO-5-2 (F)	ATTCATAGTTATATGTCTCGCAGA	
	CO-5-2 (R)	CTGCTCCTCCACCAAAGTTC	
1st meiosis-CO-6	CO-6-1 (F)	GCTACACCGGCACAAATTCT	
	CO-6-1 (R)	TCGGTGAAAGCAGAGGAGAT	
1st meiosis-CO-7	CO-7-1 (F)	CCACCTTCAACCACATTTC	
	CO-7-1 (R)	TGTGTTGCAACGAACAATGA	
	CO-7-2 (F)	AAAGATTTCTTATGAAAGACTTGGAA	
	CO-7-2 (R)	AGGTTTTGTAACCTTAAATGGGTCT	
1st meiosis-CO-8	CO-8-1 (F)	GTGAAGGAGGAGGAGCTGGT	
	CO-8-1 (R)	TATCTCAACAGGGCCAGAC	
1st meiosis-CO-9	CO-9-1 (F)	CCCAATGCGACTTCTTGATT	
	CO-9-1 (R)	CGATGACGACTTACCATCCA	
	CO-9-2 (F)	ACCGACCGAAGCCTTATTCT	
	CO-9-2 (R)	CACACACCGTGTGAAAAGT	

The primers for PCR amplification and conventional sequencing for the 1st meiosis NCOs:

1st meiosis-GC-1	GC-1-1 (F)	TGGCTTAATCGAAAACCTGGA	
	GC-1-1 (R)	AAGGCGGGCTTTGAATCTTAC	
	GC-1-2 (F)	CTCGTCTGATTGGCCTATG	
	GC-1-2 (R)	AGCTTAACCGGCTCCAATACC	
	GC-1-3 (F)	GAGCTTATAGACGCCGCAAC	
	GC-1-3 (R)	GACCGTCTCCACCTTCATGT	
	GC-1-4 (F)	GTGCGTGCAGGAGTAGTTGA	
	GC-1-4 (R)	GCCCAGATGACCAAGAAAAA	
1st meiosis-GC-2	GC-2-1 (F)	CAATCTTGCTTCCCTCCAAG	
	GC-2-1 (R)	TTGACTCTCGCAAGTGGTTG	
	GC-2-2 (F)	TTGAACACTGTGGTCCGTA	
	GC-2-2 (R)	GGCAGCACACAAAACCTCTCA	
	GC-2-3 (F)	GGTCTACCCCTTTTCAACG	
	GC-2-3 (R)	TGTGTGGTTCAAGTTGGAGA	

1st meiosis-GC-3	GC-3-1 (F)	GATTCGGACCCGTCAAGTTA
	GC-3-1 (R)	GCTTTGGTGGTGGGAAGACAT
	GC-3-2 (F)	GGTTTTGGGTGGTAGGGAAT
	GC-3-2 (R)	TTCGTGGAACATACGGATCA
	GC-3-3 (F)	CGTGAGCCGTTTAAACCAAT
	GC-3-3 (R)	AAAAAGTCCCGACCATTGA

The primers for PCR amplification and conversional sequencing for the 2nd meiosis COs:

2nd meiosis-CO-1

2nd meiosis-CO-2	CO-2-1 (F)	TGATTGTTTTGTATAAACCGCATA
	CO-2-1 (R)	TGGATGTGAGTTTTCGGACA
	CO-2-2 (F)	TTAATGAGAACGACGCAACG
	CO-2-2 (R)	AAAACGTCTCGCACATCCTT
	CO-2-3 (F)	CGATAGCGATTCCGATGTTT
	CO-2-3 (R)	CTGCATGAACGGGCACTACT
2nd meiosis-CO-3	CO-3-1 (F)	CGCATGTCTACGATGGAGTG
	CO-3-1 (R)	CCACCGGAGTACTTGGAGAA
	CO-3-2 (F)	ATCAATCTTCCCCATCCTC
	CO-3-2 (R)	GCAATGATTACATCAGCGAAC
2nd meiosis-CO-4	CO-4-1 (F)	GCAGTGATCCTCGTGGGTAT
	CO-4-1 (R)	ACGCCATTTATGTCCTACC
	CO-4-2 (F)	GATAAATACCCCGCAACCAA
	CO-4-2 (R)	CGGAGACGGATACAAAGGAA
	CO-4-3 (F)	CGTTGTCGGTTACACGAATG
	CO-4-3 (R)	TGCATCTTCCACAATTCA
	CO-4-4 (F)	GAGCCACGTATTGCCTTACC
	CO-4-4 (R)	TCGGATTTTGATCTAGATTACTGTTG
2nd meiosis-CO-5	CO-5-1 (F)	TTGCCCAGTTGACAAGTTGA
	CO-5-1 (R)	ATATGTACTCGCCGGCACTC
	CO-5-2 (F)	TCACCTCGCATAGTCGCATA
	CO-5-2 (R)	TTGTTACTTGGTTTGGTGCAA
	CO-5-3 (F)	TTTGAGCGTGGGGTTATTTT
	CO-5-3 (R)	ATATGTACTCGCCGGCACTC
2nd meiosis-CO-6	CO-6-1 (F)	GACGAGCCGCTTTTCTTTTT
	CO-6-1 (R)	TCTTCGGATTCGTTTTACTAGG
	CO-6-2 (F)	CCTTTGGGGATGGAGAGTAA
	CO-6-2 (R)	AAACGCAAATCATCAAGGAA
2nd meiosis-CO-7	CO-7-1 (F)	ACTTCGGCTCCAAGATACGA
	CO-7-1 (R)	TGATGGAGATAGGGCAGGAC
	CO-7-2 (F)	CTGTGTATGGGGGTCAAACT
	CO-7-2 (R)	TCGTTTGTGATGGCAAAATC
	CO-7-3 (F)	TTGGCTTCTAACAACGCTGT
	CO-7-3 (R)	TGAATCACCACCATGCTGT
	CO-7-4 (F)	ATTGGGGAACCACTCAGGAT
	CO-7-4 (R)	TCCACCTTGGAACCACTC
2nd meiosis-CO-8	CO-8-1 (F)	TACCGGCGAAAAATCAGAAG
	CO-8-1 (R)	GGAGCACAACGTCATCTCT
	CO-8-2 (F)	TCTCGTCGTAGAGCACATGG
	CO-8-2 (R)	GTGCGTACACAGTCGCCTAA
	CO-8-3 (F)	TGTCCAGGAGAACCATGAGA
	CO-8-3 (R)	TTTCGTCATCAGGACCATTG
	CO-8-4 (F)	TGCAACATTGGGTCATCATT
	CO-8-4 (R)	GCAAATCAAGGTGTGAACGA
2nd meiosis-CO-9	CO-9-1 (F)	TCAGGGTGTCTGTCTTGA
	CO-9-1 (R)	AACGATGTTGCGGTTCTAGC
	CO-9-2 (F)	GCGGGAATGAGCAGTACAGT
	CO-9-2 (R)	AGTCTTCGCTCCCAAAGTCA

The primers for PCR amplification and conventional sequencing for the 2nd meiosis NCOs:

2nd meiosis-GC-1	GC-1-1 (F)	ACTTCACCCGCTCAAGAAAA
	GC-1-1 (R)	AGCTGTTTGCATCCTCAGGT
	GC-2-1 (F)	AAGGTGAAAGTTCCGGGTTT
	GC-2-1 (R)	AGTTCCAAACGCGTATGCTC
	GC-3-1 (F)	CATTCCCAGTGTCGAATCT
	GC-3-1 (R)	ACCATGTTCTGGGTGTTGCT
