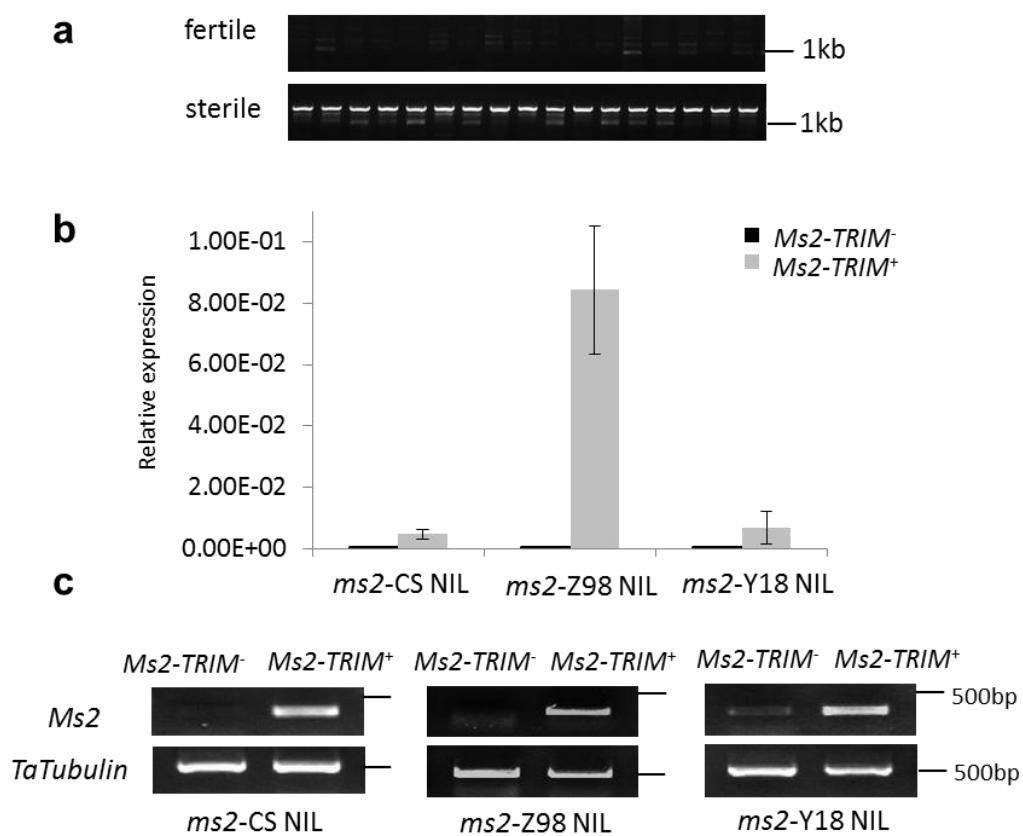


## Supplementary Figures

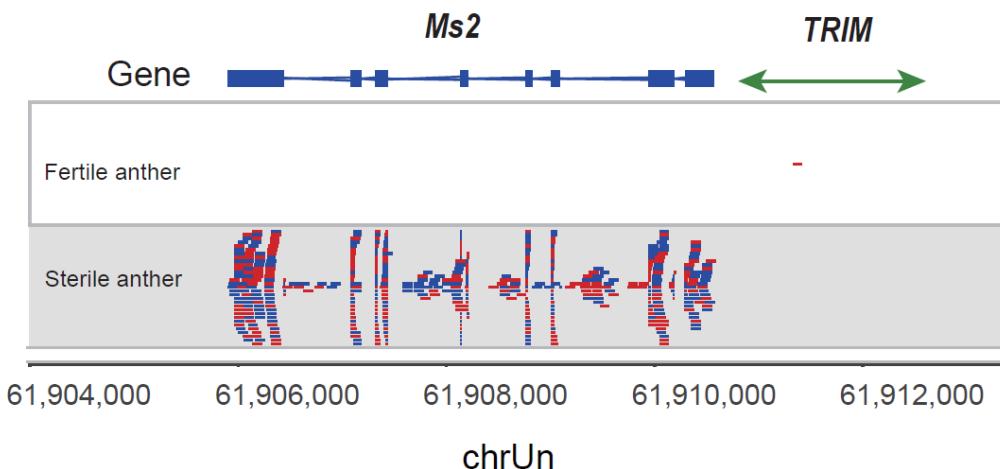
### Supplementary Fig. 1



### Supplementary Figure 1 | Ms2 polymorphism and expression pattern

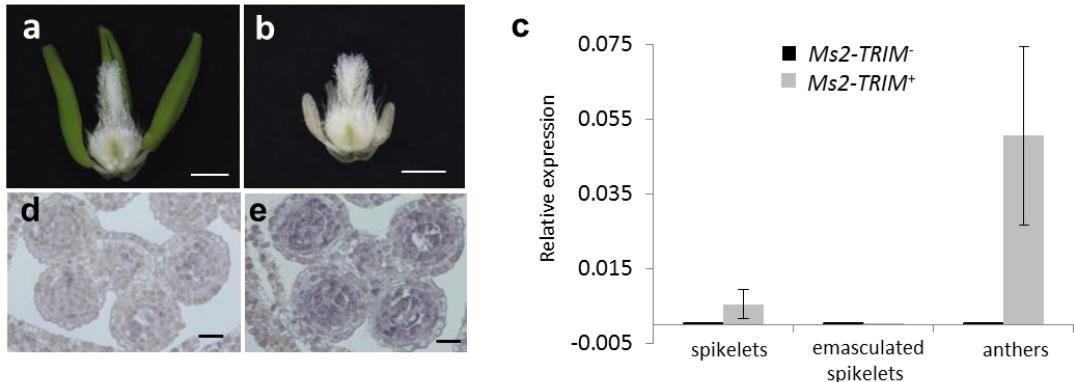
**analysis.** (a) TRIM insertion status in 17 different *ms2* NILs detected by a PCR marker amplifying a portion of the TRIM element sequence and *Ms2* promoter. (b, c) *Ms2* expression in the anthers of WT (*Ms2-TRIM*<sup>-</sup>, fertile) and *ms2* mutant (*Ms2-TRIM*<sup>+</sup>, sterile) NIL plants in three genetic backgrounds (Chinese Spring, Zhengmai98, and Yumai18).

## Supplementary Fig. 2



**Supplementary Figure 2 | The reads distribution across the TRIM element and gene no.14.** RNA-seq reads from the anther libraries from the ms2 mutant and wild type wheat were mapped to an artificial wheat genome (Chinese Spring) with the Ms2-TRIM sequence inserted in front of gene no.14. The plot is adopted from SeqMonk, and the red and blue blocks represent reads mapped to forward mapping and reverse strands, separately.

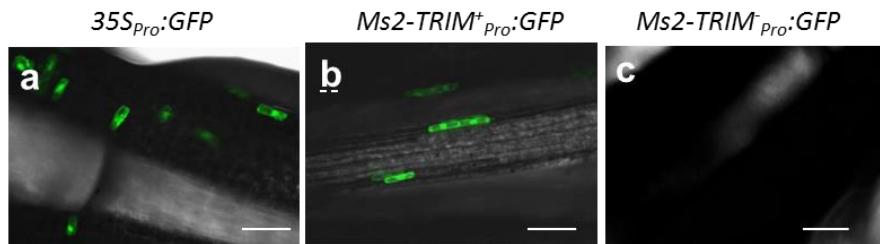
### Supplementary Fig. 3



**Supplementary Figure 3 | The phenotype of Ai-Bai wheat and *Ms2* expression analysis.** Phenotypes of floral organs, following the removal of the palea and lemma, of tall-fertile progeny of Ai-Bai wheat (-/Ms2-*TRIM*<sup>-</sup>) (a) and dwarf-sterile progeny of Ai-Bai wheat (*Rht-D1c*/Ms2-*TRIM*<sup>+</sup>) (b). (c) *Ms2* expression in three reproductive organs (spikelets, emasculated spikelets, anthers) of WT (Ms2-*TRIM*<sup>-</sup>, fertile) and *ms2* mutant (Ms2-*TRIM*<sup>+</sup>, sterile) plants in the Yanzhan1 genetic background. (d, e) *In situ* hybridization analysis (antisense probe) of *Ms2* in cross-sections of late prophase stage anthers from WT (d) and *ms2* mutant (e) plants.

Bars = 500 µm in (a) and (b), and 50 µm in (d) and (e).

## Supplementary Fig. 4

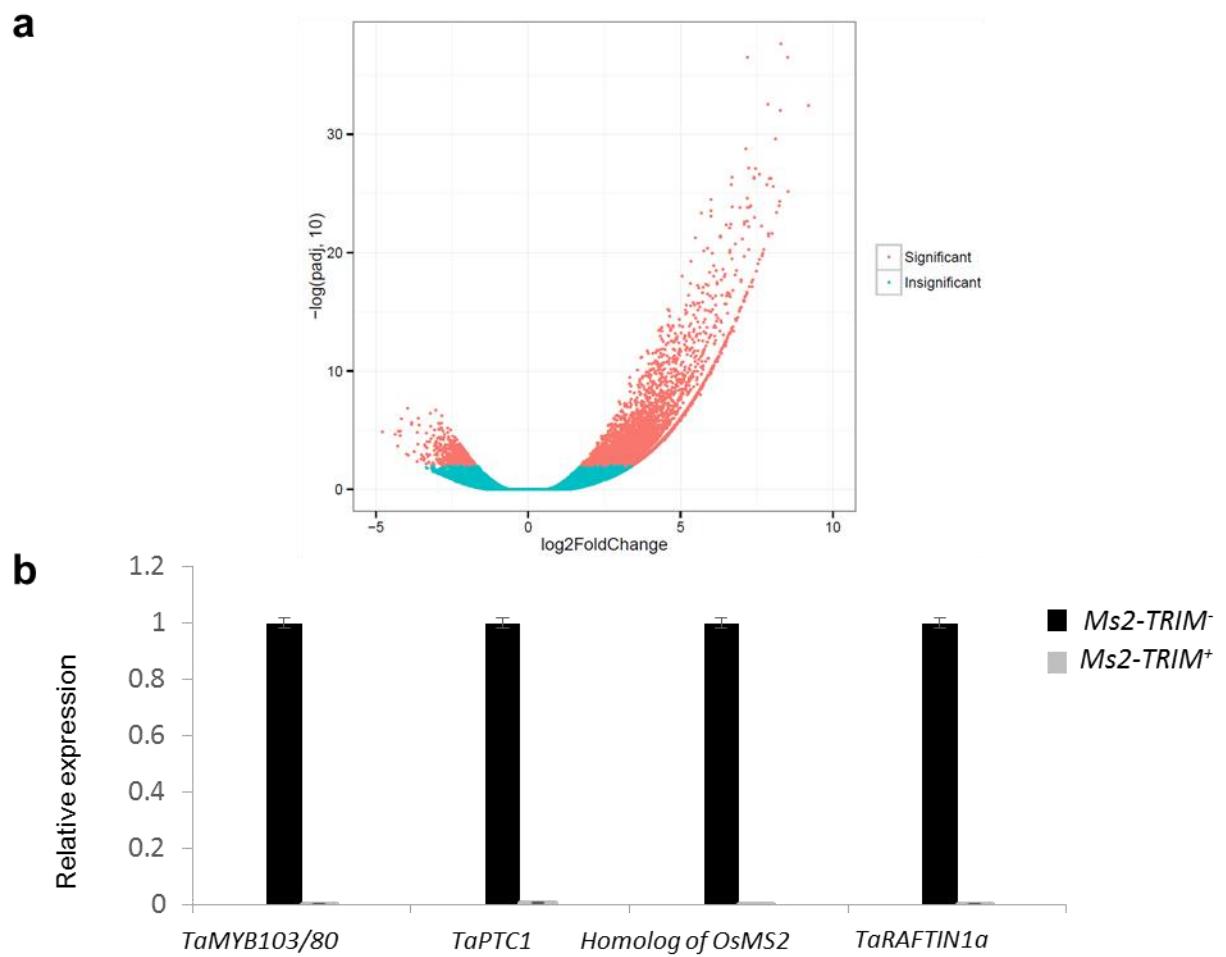


**Supplementary Figure 4 | Activity analysis of the *Ms2* promoter.**

(a-c) GFP fluorescence in anther transiently expressing  $35S_{Pro}:GFP$  (a),  $Ms2-TRIM^+_{Pro}:GFP$  (b), and  $Ms2-TRIM^-_{Pro}:GFP$  (c).

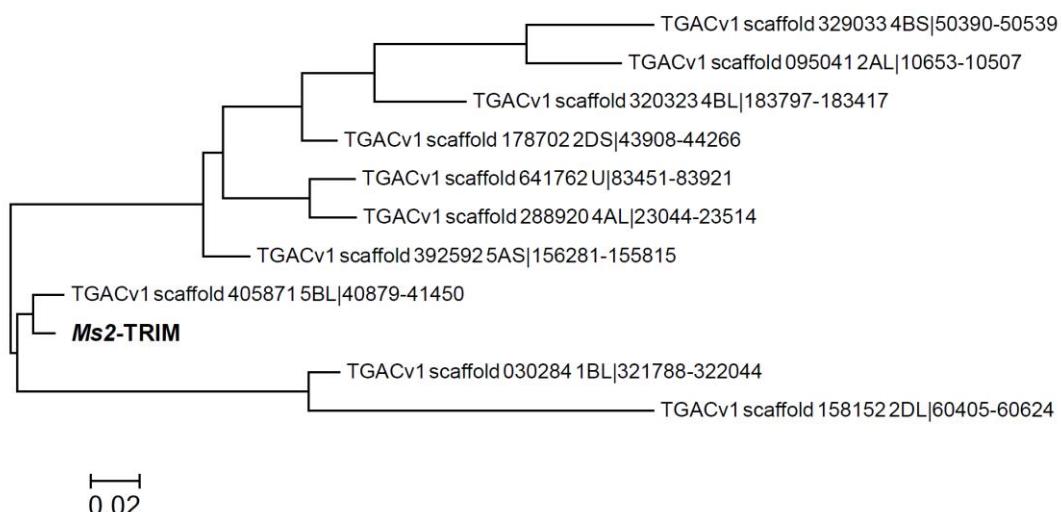
Bars = 100  $\mu$ m in (a) to (c).

## Supplementary Fig. 5



**Supplementary Figure 5 | Differentially expressed genes between *ms2* mutant vs. WT.** (a) Volcano plot of differentially expressed genes between *ms2* mutant vs. WT anthers. (b) The relative expression of *TaMYB80/MYB103*, *TaPTC1*, *Homolog of OsMS2* and *TaRAFTIN1* in WT and *ms2* mutant plants.

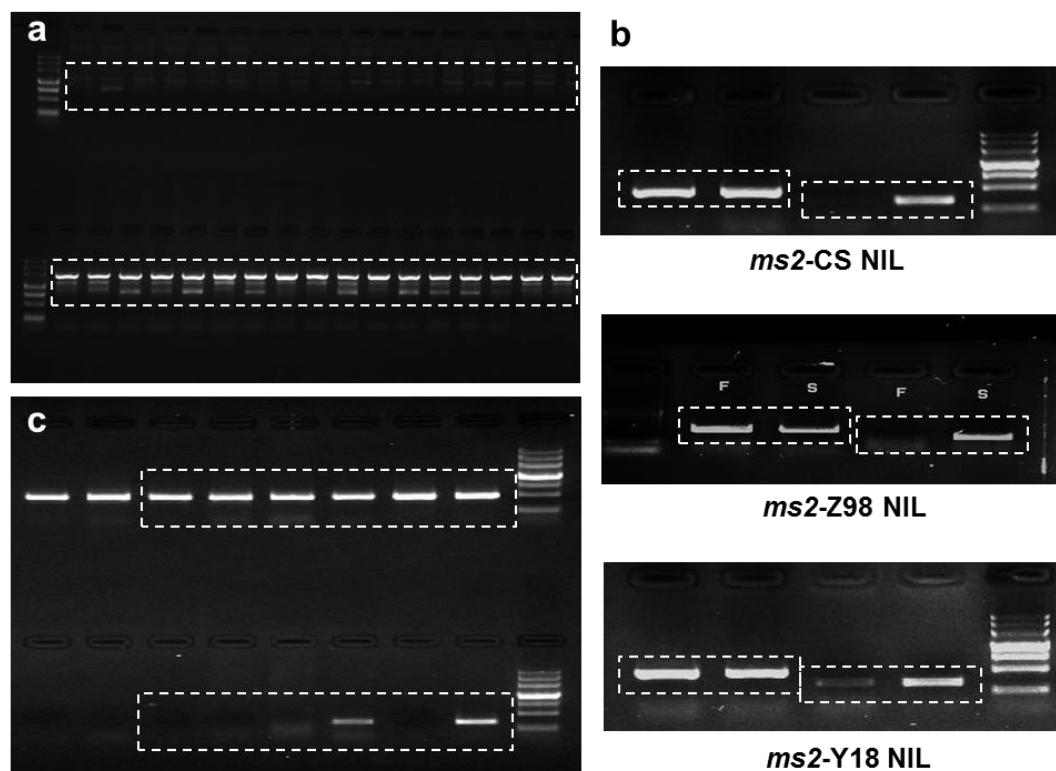
## Supplementary Fig. 6



**Supplementary Figure 6 | Phylogenetic tree of *MS2-TRIM* and its hits in the hexaploid wheat genome (Chinese Spring).**

Unrooted Neighbor-Joining phylogeny of the *Ms2* promoter TRIM based on the LTR region of the element in the wheat genome.

## Supplementary Fig. 7



**Supplementary Figure 7 | Uncropped gel images.** **(a)** Uncropped gel image of supplementary figure 1a. **(b)** Uncropped gel images for RT-PCR in supplementary figure 1c. **(c)** Uncropped gel image for expression pattern analysis in figure 2a.

## Supplementary Tables

**Supplementary Table 1.** Estimates of nucleotide diversity and test of statistics for selection in *Ms2*

	n	$\pi$ (per site)	$\theta$ (per site)	Tajima's D	Fu and Li's D
Wild	30	0.00615	0.00585	0.176 \$	0.381 \$
Landrace	28	0.00386	0.00233	2.026*	0.704 \$
Modern Variety	26	0.00302	0.00238	0.847 \$	0.720 \$

Note :  $\pi$  : nucleotide diversity ,  $\theta$ : Watterson's estimator of genetic diversity, Statistical significance: \$  $P>0.1$ , \*  $P <0.05$

**Supplementary Table 2.** Materials were used to explore the nucleotide diversity of *Ms2*

Accession/Sample names	Species	Abbr. Population Name
TA1618	<i>Aegilops tauschii meyeri</i>	wild diploid D
TA2456	<i>Aegilops tauschii strangulata</i>	wild diploid D
TA2457	<i>Aegilops tauschii typica</i>	wild diploid D
TA2460	<i>Aegilops tauschii typica</i>	wild diploid D
TA2464	<i>Aegilops tauschii strangulata</i>	wild diploid D
TA2561	<i>Aegilops tauschii typica</i>	wild diploid D
TA1645	<i>Aegilops tauschii strangulata</i>	wild diploid D
TA1662	<i>Aegilops tauschii var.tauschii</i>	wild diploid D
TA2461	<i>Aegilops tauschii var.typica</i>	wild diploid D
TA2463	<i>Aegilops tauschii strangulata</i>	wild diploid D
TA2474	<i>Aegilops tauschii var.tauschii</i>	wild diploid D
TA2475	<i>Aegilops tauschii var.tauschii</i>	wild diploid D
TA2529	<i>Aegilops tauschii var.meyeri</i>	wild diploid D
CLAE1	<i>Aegilops tauschii</i>	wild diploid D
CLAE5	<i>Aegilops tauschii</i>	wild diploid D
CLAE17	<i>Aegilops tauschii</i>	wild diploid D
CLAE25	<i>Aegilops tauschii</i>	wild diploid D
PI 268210	<i>Aegilops tauschii</i>	wild diploid D
RL5214	<i>Aegilops tauschii</i>	wild diploid D
RL5257	<i>Aegilops tauschii</i>	wild diploid D
RL5261	<i>Aegilops tauschii</i>	wild diploid D
RL5263	<i>Aegilops tauschii</i>	wild diploid D
RL5272	<i>Aegilops tauschii</i>	wild diploid D
RL5392	<i>Aegilops tauschii</i>	wild diploid D
RL5422	<i>Aegilops tauschii</i>	wild diploid D
Y221	<i>Aegilops tauschii ssp.Stran gulata Eig.</i>	wild diploid D
Y222	<i>Aegilops tauschii ssp.strangulata EIG.</i>	wild diploid D
Y293	<i>Aegilops tauschii ssp.meyeri GRISEB.</i>	wild diploid D
Y294	<i>Aegilops tauschii ssp.meyeri GRISEB.</i>	wild diploid D
Y296	<i>Aegilops tauschii ssp.strangulata EIG.</i>	wild diploid D
sankecun	<i>Triticum aestivum</i>	landrace
zijuhong	<i>Triticum aestivum</i>	landrace
lanxizaoxiaomai	<i>Triticum aestivum</i>	landrace
heshangmai	<i>Triticum aestivum</i>	landrace
hongmangyouzimai	<i>Triticum aestivum</i>	landrace
tumangmai	<i>Triticum aestivum</i>	landrace
jiyumai	<i>Triticum aestivum</i>	landrace
changmangyingkemai	<i>Triticum aestivum</i>	landrace
nuomai	<i>Triticum aestivum</i>	landrace
wuxumai	<i>Triticum aestivum</i>	landrace
baihuamai	<i>Triticum aestivum</i>	landrace

dahongmai	<i>Triticum aestivum</i>	landrace
xinganxiaomai	<i>Triticum aestivum</i>	landrace
sanyuehuang	<i>Triticum aestivum</i>	landrace
dabaimai	<i>Triticum aestivum</i>	landrace
huangguaxian	<i>Triticum aestivum</i>	landrace
baiyoumai	<i>Triticum aestivum</i>	landrace
huajiechangbaican	<i>Triticum aestivum</i>	landrace
sanyuanmai	<i>Triticum aestivum</i>	landrace
shanmai	<i>Triticum aestivum</i>	landrace
sifangmai	<i>Triticum aestivum</i>	landrace
tuotuomai	<i>Triticum aestivum</i>	landrace
yangmai	<i>Triticum aestivum</i>	landrace
qigongmai	<i>Triticum aestivum</i>	landrace
chiyacao	<i>Triticum aestivum</i>	landrace
changgongfangxingmai	<i>Triticum aestivum</i>	landrace
yunnanxiaomai (YN3)	<i>Triticum aestivum</i>	landrace
paozimai	<i>Triticum aestivum</i>	landrace
bainong 791	<i>Triticum aestivum</i>	cultivated line
chuanmai 22	<i>Triticum aestivum</i>	cultivated line
chuanmai 42	<i>Triticum aestivum</i>	cultivated line
fengkang 7	<i>Triticum aestivum</i>	cultivated line
jinan 16	<i>Triticum aestivum</i>	cultivated line
jinan 4	<i>Triticum aestivum</i>	cultivated line
jinan 8	<i>Triticum aestivum</i>	cultivated line
jimai 23	<i>Triticum aestivum</i>	cultivated line
jingnong 79-13	<i>Triticum aestivum</i>	cultivated line
kefeng 6	<i>Triticum aestivum</i>	cultivated line
kehan 10	<i>Triticum aestivum</i>	cultivated line
liaochun 9	<i>Triticum aestivum</i>	cultivated line
longmai 33	<i>Triticum aestivum</i>	cultivated line
lumai 3	<i>Triticum aestivum</i>	cultivated line
mianyang 29	<i>Triticum aestivum</i>	cultivated line
neimai 19	<i>Triticum aestivum</i>	cultivated line
ningmai 13	<i>Triticum aestivum</i>	cultivated line
nongda 36	<i>Triticum aestivum</i>	cultivated line
shanhe 6	<i>Triticum aestivum</i>	cultivated line
shannong 1	<i>Triticum aestivum</i>	cultivated line
shijiazhuang 407	<i>Triticum aestivum</i>	cultivated line
wanmai 50	<i>Triticum aestivum</i>	cultivated line
xibei 612	<i>Triticum aestivum</i>	cultivated line
xiannong 39	<i>Triticum aestivum</i>	cultivated line
xiaoyan 4	<i>Triticum aestivum</i>	cultivated line
xiaoyan 759	<i>Triticum aestivum</i>	cultivated line

**Supplementary Table 3.** Primers used in map-based cloning and RT-qPCR

primer name	sequence 5' – 3'	type
M1-Forward	GGTATGCTCCTCATTATTCC	SSR
M1-Reverse	GACTAGTTCATCTGCATTAC	
M2-Forward	TAGTATTGAGAGAGAGGAGCTG	SSR
M2-Reverse	TTTGTTCGTCCTGATCTGA	
M3-Forward	TCGGATCCTTCACTGATGTGCT	SNP
M3-Reverse	TCCTGGCAAGTCTGCATCTCA	
M4-Forward	TGCACTTAGAGCTCTGCACCA	SNP
M4-Reverse	GGTGAGTGTGTGTTGTCAGCA	
M5-Forward	TTGGCTGCCATTGCCATCGTC	SNP
M5-Reverse	CAAACTTGCAGCCTCAACTTG	
M6-Forward	AGGGTGAGTAAGATCGTCAGCA	SNP
M6-Reverse	GAAGTACTGATTGATGTGAGGAC	
M7-Forward	GGCGTCCTCGTCTCCAAATA	Insertion
M7-Reverse	CGATGATGAACTCACCTGCTGTA	
M8-Forward	CCATACGAAAGCATAGCAATA	SSR
M8-Reverse	GTGATTGTGAGCAGTCCATT	
M9-Forward	CCACAAAATCAATGGTTCTA	SSR
M9-Reverse	AACATTTTAGACGTTGACG	
M10-Forward	GGAGGCATAATGGAGAATG	SSR
M10-Reverse	CGTCTGTTTCTCTCATCA	
M11-Forward	CTTACATGCAGATCCGTCTAAT	SSR
M11-Reverse	ATTTGTGTGTGTCTCTCT	
TaGAPDH-Forward	TTAGACTTGCAGGCCAGCA	
TaGAPDH-Reverse	AAATGCCCTTGAGGTTCCC	
TaTUBULIN-Forward	TGAGGACTGGTGCTTACCGC	
TaTUBULIN-Reverse	GCACCATCAAACCTCAGGGA	
Ms2-RT-Forward	CTGCTGCATCCGACTAACTATC	
Ms2-RT-Reverse	TGAGAATACTGTCCACCAAACTC	