

Table 1 Suppl. Primer sequences of genes in qRT-PCR.

Acc. No.	Amplicon length [bp]	Forward primer	Reverse primer	Annealing temp. [°C]
CA684267	115	TACTAGCGATATTGCTGTGG	CATTGCTCAAGGGTTCAAAT	60
CK205485	173	GCCGCTGCCACTCCTATTTG	GTTCTGTGCCATTCGCTGCTC	60
CA664935	131	TGTAAGGGATACATACGCG	AAGTGCCTGTTTCTGACCT	60
CD863680	131	CGGGAGATAAGAGCCACAA	CGATCACTTCGGTAAGACGA	60
CA633933	94	TGATGAATCTGGGTCAACAAA	TCTCACTGGAGTGGTGGAAC	60
BQ168479	111	GCTTATTTAGGCATCTTCT	CCTCAAGTACCTGTGGAAG	60
CD890484	178	GCAAATAAACGCTGAACTGG	AAGTCTTTACAAGGACGAGGG	60
CD374038	143	ATGATGGGAAGGCAACGAAG	CCTCAATGATTCACGGCAAG	62
CA648596	133	AACAAGACGCCATTGACAAA	GTCGGCCAGGAAGTGTATGT	60
BJ272293	150	GGATGGGCACATTTCTTCAGTA	TTGAGTTCCATCTTTTCGCTGT	60
CA702371	119	CTGGTCAACAGCAGGCTAAG	ACCATGGCCTCATCAGTGTA	60
CA604317	143	AGTAGTGCACTGATACGTCCTTCT	GTTCCAACCGCATTATGCTA	60
CA659367	168	ATCGGCGCTTGCTTCTTTGT	CACTTCGGTCGCTGTCTTGC	58
BE591365	169	TCCGTGAACACTTGGCATT	CTTGGCAGCATTCTCGTAG	60
CA657773	100	CGGTGCTAGGTGATGACG	ATGCAGCCTTTGACGACAG	62
CA611901	94	GGGTGCTTCAGCAAGGAGT	CGGATCGGACCACATACAA	60
CA675924	93	ATGTCAGAGGCAAGAGGGA	TGTCGATGCGAAGTGGAGA	60
CA746306	90	GGCCAAGGACAACCTCAACT	CAGAACCTGGCGTTGACA	62
BJ229407	129	GGCATTTGTGGTCATTTAGTGT	GAGATTGATTCTTTGCTTTTCG	60
BJ262362	137	CTTGGGTTTCGCATTTCTTA	AGTGGCGGATTTATCTTCT	60
18S ribosomal RNA	151	GTGACGGGTGACGGAGAATT	GACACTAATGCGCCCGGTAT	60
β -actin	94	TGCTATCCTTCGTTTGGACCTT	AGCGGTTGTTGTGAGGGAGT	60

Table 2 Suppl. Primer sequences in constructing RNAi vector. The forward primer contains *Bam*HI site, the reverse primer contains *Xho*I site.

Accession No.	Amplicon length [bp]	Primer sequence (5'-3')
CK205485	395	F: CGCGGATCCCATAACCCGTAACAGTCCAA R: CCGCTCGAGAACCATGAAGGCAGTAGCAC
CA684627	204	F: CGGGATCCTACAAGCAAAGCAATG R: CCGCTCGAGGCAAAAATCCACATTG
CA664935	381	F: CGGGATCCTTCAAATGCTACTATAG R: CCGCTCGAGACAAGTAGTTATCAAT
CD863680	309	F: CGGGATCCAGTGGGAAAAGGCCTC R: CCGCTCGAGATGGACAACCTTCAGTT
CD890484	432	F: CGGGATCCAAATAAACGCTGAAACTGG R: CCGCTCGAGGATCATCTGATTGAA
BQ168479	294	F: CGGGATCCTAAGTAAGATATGTAG R: CCGCTCGAGAACCAACTTTTATAGG
CA633933	380	F: CGCGGATCCCTTAAGAAATAACAGATA R: CCGCTCGAGAAACAGGACATAACAT
BJ272293	291	F: CGGGATCCACTACAAGTCTACAAC R: CCGCTCGAGAGGTTTTCTTTTGCTA
CA648596	329	F: CGCGGATCCAATATTAATAAAGACATGGC R: CCGCTCGAGAAAGGATATGCAAACG
CD374038	351	F: CGGGATCCAACGATTTATAGAAGATTCTG R: CCGCTCGAGTTCCTGTCCCCATCA

Table 3 Suppl. Primer sequences in RACE experiment. UPM - Universal Primer A mix (*Clontech*) long (0.4 μ M): 5'-CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT-3' and short (2 μ M): 5'-CTAATACGACTCACTATAGGGC-3'

Accession No.	5'-RACE primer (5'-3')	3'-RACE primer (5'-3')
BQ168479	F: GAGGGCCTATAAAAGTTGGTTCCACTGTC R: UPM	
CA648596	F: UPM R: GGCGTCTTGTTTATTCCAGAGTAGGTAGC	F: GGCCGAACGATCCACTTTATTTTCTC R: UPM

Table 4 Suppl. List of the transcripts expressed differentially in the three wheat cultivars. Average of the values measured at 24 and 48 hpi, control at 0 hpi. Means $\pm$ SE, $n = 3$. ^a - Expression estimates based on the Gene Chip analysis, values represent $\log_2FC$; ^b - mRNA level determined by qRT-PCR, values represent $\log_2FC$; ^c - Yumai 13 divided by HY at 0, 24 and 48 hpi, respectively; ^d - Yumai 13 divided by CYC at 0, 24 and 48 hpi, respectively.

Accession No.	Putative function	Yumai 13/ HY ^c		infected		Yumai 13/ CYC ^d		infected	
		control GC ^a	qPCR ^b	GC ^a	qPCR ^b	control GC ^a	qPCR ^b	GC ^a	qPCR ^b
CA684267	unknown	7.3	3.9 $\pm$ 0.4	7.3	3.4 $\pm$ 0.3	7.2	4.5 $\pm$ 0.6	6.9	2.7 $\pm$ 0.4
CK205485	glycosyltransferase	6.7	11.0 $\pm$ 0.5	7.4	12.6 $\pm$ 0.7	6.7	8.8 $\pm$ 0.1	7.3	9.9 $\pm$ 0.4
CA664935	unknown	6	8.4 $\pm$ 1.0	5.6	9.4 $\pm$ 0.6	5.3	8.6 $\pm$ 1.5	6.3	10.5 $\pm$ 0.9
CD863680	predicted protein	5.7	2.0 $\pm$ 0.2	5.6	2.3 $\pm$ 0.8	4.9	2.5 $\pm$ 0.3	5.6	3.1 $\pm$ 0.3
CA633933	unknown	5.3	5.6 $\pm$ 0.5	4.9	7.4 $\pm$ 0.6	5.5	5.8 $\pm$ 0.2	4.8	7.3 $\pm$ 0.4
BQ168479	unknown	5.3	4.0 $\pm$ 0.1	4.8	3.5 $\pm$ 0.4	4.9	4.5 $\pm$ 0.2	4.9	4.5 $\pm$ 0.5
CD890484	hypothetical protein	4.5	9.7 $\pm$ 0.9	4.5	13.0 $\pm$ 0.8	4.6	11.3 $\pm$ 0.4	5.1	11.3 $\pm$ 0.8
CD374038	metacaspase-1	4.1	5.7 $\pm$ 0.3	4.3	6.3 $\pm$ 0.2	4.1	4.5 $\pm$ 0.7	4.0	4.3 $\pm$ 0.5
CA648596	unknown	2.3	2.0 $\pm$ 1.1	4.1	3.5 $\pm$ 0.4	3.4	3.0 $\pm$ 0.3	3.6	2.9 $\pm$ 0.4
BJ272293	unknown	3.9	3.7 $\pm$ 0.7	3.8	2.7 $\pm$ 0.6	3.8	2.9 $\pm$ 0.8	3.8	3.9 $\pm$ 0.4
CA702371	hypothetical protein	4.9	2.3 $\pm$ 0.5	4.4	4.6 $\pm$ 0.6	4.0	3.2 $\pm$ 0.7	3.9	3.1 $\pm$ 0.3
CA604317	unknown	4.2	2.7 $\pm$ 0.3	5.2	3.3 $\pm$ 0.5	3.0	2.5 $\pm$ 0.8	3.7	3.0 $\pm$ 0.4
CA659367	Ca ²⁺ /H ⁺ -exchanging protein	3.9	5.2 $\pm$ 0.5	4.0	4.8 $\pm$ 0.2	3.6	4.3 $\pm$ 0.7	3.9	5.0 $\pm$ 0.4
BE591365	unknown	3.5	2.6 $\pm$ 0.8	3.8	3.8 $\pm$ 0.8	2.4	3.1 $\pm$ 1.0	4.1	3.3 $\pm$ 0.7
CA657773	unknown	2.9	3.0 $\pm$ 0.2	3	3.5 $\pm$ 0.4	4.2	6.7 $\pm$ 0.2	4.6	6.8 $\pm$ 0.5
CA611901	unknown	2.9	3.9 $\pm$ 0.8	3.3	3.7 $\pm$ 0.8	3.0	3.7 $\pm$ 0.5	2.8	2.9 $\pm$ 0.7
CA675924	unknown	2.8	3.2 $\pm$ 0.5	3.6	4.1 $\pm$ 0.5	3.1	4.0 $\pm$ 0.2	3.9	3.4 $\pm$ 0.4
CA746306	putative amino acid permease	2.4	5.8 $\pm$ 1.3	3.6	6.3 $\pm$ 0.7	2.8	5.5 $\pm$ 0.8	2.8	5.7 $\pm$ 0.5
BJ229407	unknown	2.4	1.4 $\pm$ 0.5	2.7	1.8 $\pm$ 0.4	3.0	0.7 $\pm$ 0.2	2.5	1.0 $\pm$ 0.3
BJ262362	unknown	1.8	2.6 $\pm$ 0.4	2.6	3.4 $\pm$ 0.5	3.6	5.4 $\pm$ 0.6	3.5	3.6 $\pm$ 0.5

Fig. 1 Suppl. Contig 1 (1955 bp) of consensus length corresponding to *TaSl*. Contig tested primers: forward 5'-TGCCCAGTAGTATGTATT and reverse 5'-TTTATAGGCCCTCAAGTA

ACATGGGAAGGAGACCCGATGGCATGGCTGTACAAGTGGCACCCCTGGTCAGGTGGACGTTGGATGCTTTCTTCAGTGTT
TCTCTTTTCCCGCAGGCTTGATTTCCCTTGTTGGTTCGTAACCCAACTCCCAAAAGTCAACGCTTTCTTGGAGTCCTAATCCA
TCTACTTGTCCCCCTCTCTGTTCTTTCTATTGTAACGCGATCTTTCTTGGAGTCCTAATCCATCTACTTGCTCCCCCTCTC
TGAAGATATCATGCTATGGGACTTTTCGGCAGAACCTAAACTATGGTTTTACTTGCAGCTCAGTTTTTACATCCTTCCCA
GGTTTCAGAAAAACATAAACATGCTTGGATGTGTGTCCTTGCCGGCGACCTCGCTGTCTCCAACCCATCCGTCTGGACAG
GTAGCTTGCTATCCTCTCATCGTGTCTATTGGTGCAGTATCTCATATCCTCTCTCGAAGAGATGAGGTAAGGATTAAAGG
ACTACCAACTGAGTTCTACAGCTCACCTCACCAATAATGGAAGACATCCTCACCTACCTATAATGGAAGACATCCCGAG
TCATTATTTTGCATGCTAGAGAACAACAACATACAGTTGGTGATTTCCTGATATCTGGTTCTACAAGTGTGTCATATG
GACCAATGAAAGAAAAGATATTCCGGAGATAATAACTATATGGGCTACTCCAAATGGTCTGACAGTGGAACCAACACCTT
TTATAGGCCCTCAAGTACCTGTGGAAGTCTACCATGCAAGCATTATCCGACGATGACACTGCTTTTTTCGTACATATCATC
TTAAGACCATGGTCAGACTAAGAAGATGCCTAAATAAGCTGTGAGGCTGCCTATATATAAGTGTTTTTCTATAAACTGAT
CTAAGTCATTCTACTATCTGTAAACCAATTTAAGTTATTCTACTATTTGTAAACCCATCTAAGTCATTGTATTATCAGCA
ATACAATCCACATTGCATTATCTTTTATTCTACATATCTTACTTACTCACCCTAGCATCGCTTCTAACTCACTTTTTTGC
GCCATTGGCGCAACCGGGTCATCTAGTCTTCAGAATAACGCTTAAACGTCTACTACGTAATCCGAACCTATGCAACCATGC
GTGCTAGCCTAAAATGGCAGTGCTTCTTTAGTTTAGTAAATAGTACAATGGTAGATACAAAGATTAAGTCAATCATCAGA
TTTGGAAGACGTAATAAGAACAACCTCTGGTGAGCAGGCTCGCCATCAGATCCAATAGATTGAGAATGAATACTACACGT
TGTATGAGAGGAACATTGCACCTGGGGCGATATGATAAAAGGGGAGAATAAGAAATGTTTCTGATGAAAAGCAGCAGCCT
TGGTTTCTTTTCCAACCTAGATCGGAGTCGCGTCTTGGCGCGAGGGTGCCGGTGTCAACATTTTGATCAAGCAGGTAATGC
TAAGTAGTAGTAATTCAGGTTAAGCGTATGTTATTAATTTTGTATCACTGAGAGTGCCATGGCGCTCAGAGCCAGGTCC
TAATAGTTGTGCCTAAGCGTGTGTGCCAGGCGTGTGTAATTATGGGACAAGCTTAGCATGTTTCATAATACAATAATTT
GATTTTATGCCCATGATAAAACAGAAGTATTTTAGCTTGTTCAGAGCAATAGGACATGAAGTTCAGTGTGCAAGAGTAG
AGCCAGTGGCAGTGAGATTACAGGTGCATAGGAAGTCACATGTCATAGGACACATAGTTTTACATGACAAACACAATAGT
TAATCCATTGAAACATGACTAACACAGTAGTTAATCCATTGAAACACGACTAACACGGTAGTTAATCCTTTAAAATACAT
ACTACTGGGCAAAAGAAAGCATCAATTACATGTTAGATAAGATAGTAACCTTAGATAGCCAGATCGATGTACCATTATATT
TGACTCATTGACACCCCTATATATATATTTTGAAAG

The sequence of *TaSl* *long* amplified by 5'RACE. A 320 bp EST sequence is *underlined*.

TTTTTTTTTTTTTTTTTTTTTAAGTAAGATATGTAGAATGAAAGATAATGCAATGTGGATTGTATTGCAGGTAATACAATGA
CTTAGATGGGTTTACAAATAGTAGAATAACTTAAATTGGTTTACAGATAGTAGAATGACTTAGATCAGTTTATAGAAAAA
CACTTATATATAGGCAGCCTCATGGCTTATTTAGGCATCTTCTTAGTCTGACCATGGTCTTAAGATGATATGTACGAAAA
AGCAGTGTCTATCGTCGGATAATGCTTGCATGGTAGACTTCCACAGGTACTTGAGGGCCTATAAAAGTTGGTTCCACTGTC
AGACCATTTGGAGTAGCCCATATAGTTATTATCTCCGAAATATCTTTTCTTTTATTGGTCCATATGACACACTTGTAGAA
CCAGATATCAGGGAAATCACCAACGTGATAGTTGTTGTTCTCTAGCATGCAAAACAATGACTCGGGATGTCTTCATTAT
AGGTGAGGTGAGGATGTCTTCATTATTGGTGAGGTGAGCTGTAGAACTCAGTTGGTAGTCCTTTAATCCTTACCTCATC
TCTTCGAGAGAGGATATGAGATACTGCACCAATAGACACGATGAGAGGATAGCAAGCTACCTGTCCAGACGGATGGGTTG
GAGACAGCGAGGTGCGCGGAAGGACACACATCCAAGCATGTTTATGTTTTTCTGAAACCTGGGAAGGATGTGAAAACCTG
AGCTGCAAGTAAAACCATAGTTTGGTTCTGCCGAAAAGTCCCATAGCATGATATCTTCAGAGAGGGGAGCAAGTAGATG
GATTAGGACTCCAAGAAAGATCGCGTTACAATAGAAAGAACAGAGAGGGGGACAAGTAGATGGATTAGGACTCCAAGAAA
GCGTTGACTTTTGGGAGTTGGGTTACGACCACAAGGAAATCAAGCCTGCGGAAAAGAGAAACACTGAAGAAAGCATCCA
ACGTCCACCTGACCAGGGTGCCACTTGTACAGCCATGCCATCGGGTCTCCTTCCCATGT

Fig. 2 Suppl. Contig 2 (1 226 bp) of consensus length corresponding to *TaS2*.

GGGTACGTCGCGGGCCGGACTGGGGGAGGGCAGGGGCAAAGACCATCCTACCCTTTTTTAAGTTTTTCAGGCGAAGGGGTA
TAGGACGATCTGGACCGTTGATGTTTTTCAGGGGGTTGTACCGAAGAAGAAGTGCATATCACCACCATTACCGTACCAC
TCACACACACTTATGTGCACACACACACACACAGACTTCATATCATCTCCACCCCAACACTCACACATACACACATCTTC
AATCCTCGACTGGCGTTTTTCCCTCCGTGGCCGGCGTCCATGGCACAGCCATATGGTGAGTAAATCATATGAAGGTTGCAT
ATGATCATTATCTCTTTTTATTATTTTTCTTCTCTTTGTTCACTTCTTTTTGTGGCATCTCGCGGCTCTACATGGCGATC
TAATCGTCGCGGTGGATGTCTCATCGTTTGATCTACAACAAAAATCGGCGGTGTCCGCGGCTCTACATGACGATCTAGT
CGTCGCGGTGGATATCTCATCGTTGAAACGTACAACGAAAAATCGGCGGTGTCCGCGGCTCTACATGACGATCTAATCG
TCGCGGTGGATATCTCATCGTTTGATCTACAACAAAAATCGGCGGTGTCCGCGGCTCTACATGGCGATCTAATCGTCGT
CGCGGTGTTTTCTTTGTTTGATCTATAGAAAGAATTCGGCGGCATCCGCGGCTCTACATGACGATCTAATCGTCGCGCG
GACGTTCTATCACCCGATCTACAGAAAAACAGTTTGATGGCATCCCGTGGCTCTACATGGCGATCAAGTCGTCGCCACGG
ATGTTTATGGTTTGATCAGTAAAGGAAAGGAAGGTTATGATGTTTCGTGGCTCTACCTGACGCTTCAATCGTCGCGGTAA
ACATTTTCATGGTGTGGAGTCACAAGGGAAAGCAATATAGCTGTACAAAAAGAATCAACATCATCGTCCAGCATACATAAT
ATATTCAGAGGTAGCAAGGGGGTCACGTGATATACAAAGGATGGTTTCTCATCATGAGATAATCCAATATTAATAAAGAC
ATGGCTACCTACTCTGGAATAAACAGACGCCATTGACAAAATTCTGCAGAACCATGTTTCTCAATCAGATGAGGGTTCA
TCTTCAAGTCCATGCTCAATACACTTCTTCCGCGACCGACGAGGCCGAACTTACATACACTTCTGGCCGACGAGGCA
GGATACATCATGTTTCGTGACCGACGA

The sequence of *TaS2_long* amplified by 5'RACE. A 587 bp EST sequence is *underlined*.

ACATGGGTCGATGGCACAGCCATATGGTGAGTAAATCATATGAAGGTTGCATATGATCATTATCTCTTTTATTTATTTT
TCTTCTCTTTGTTCACTTCTTTTTGTGGCATCTCGCGGCTCTACATGGCGATCTAATCGTCGCGGTGGATGTCTCATCGT
TTGATCTACAACAAAAATCGGCGGTGTCCGCGGCTCTACATGACGATCTAGTCGTCGCGGTGGATATCTCATCGTTTGA
TCTACAACAAAAATCGGCGGTGTCCGCGGCTCTACATGACGATCTAGTCGTCGCGGTGGATATCTCATCGTTTGA
CAACAAAAATCGGCGGTGTCCGCGGCTCTACATGGCGATCTAATCGTCGTCGCGGTGTTTCTTTGTTTGATCTATAGA
AAGAATTCGGCGGCATCCGCGGCTCTACATGGCGATCTAATCGTCGCGCGGACGTTCTATCACCCGATCTACAGAAAA
CAGTTTGATGGCATCCCGTGGCTCTACATGGCGATCAAGTCGTCGCCACGGATGTTTATGGTTTGATCAGTAAAGGAAA
AGGGAAGGTTATGATGTTTTCGTGGCTCTACCTGACGCTTCAATCGTCGCGGTAAACATTTTCATGGTGTGGAGTCACAAAG
GAAAGCAATATAGCTGTACAAAAAGAATCAACATCATCGTCCAGCATACATCATATATTCAGAGGTAGCAAGGGGGTCAC
GTGATATACAAAGGATGGTTTCTCATCATGAGATAATCCAATATTAATAAAGACATGGCTACCTACTCTGGAATAAACAA
GACGCCATTGACAAAATTCTGCAGAACCATGTTTCTCCATCAGATGAGGGTTCATCTTCAAGTCCATGCTCAATACACTT
TCTTCCGCGACCGACGAGGCCGAACTTACATACACTTCTTGGCCGACGAGGCAGGATACATCATGTTTCGTGGCCGACGA
GGCCGAACGATCCACTTTATTTTCTCTTTGAGACTTGATCTATATCCCTTGTTTGATTTGGTGCATGAATCCATAAATTT
TTAACATGGCGAGATTATTGTTTTGCTCANAGCGTTTGATATCCTTTGGCCTGGNGACAGAAGCCAAGNAGTTTGGATA
ATGATGATGACCGTTTGANGCAGCTTAATCGGAGTCTTTCATAGATATGCTATGATGTAATAACTANAGTNCCTTCNAGG
TCCAGGANCCAGATACCNATGTCCTTTAAAGTANGTGCATNCNAGNCAGTAAATNGATGTTACCTNCANTAAGNTAAANT
CNCGCAAAAAAAAAA