

SUPPLEMENTAL DATA

Genes are listed in the order as shown in the Tables. For the seven genes that were analyzed for both hybrids S1/NS1 and S2/NS2, sequences of S1 and NS1 are listed first followed by those of S2 and NS2 if different from S1 and NS1. If allele sequences of the PCR fragments are the same between the two sets of inbred parents, only S1 and NS1 are listed. PCR primers are highlighted in yellow. PCR primers of S2 and NS2 are the same as those for S1 and NS1 for all 15 genes. Shaded areas are conserved regions between the two alleles. Allelic sequence polymorphisms (SNPS or InDels) are in bold face.

		1	50
NS1 <i>LTP</i>	(1)	TGTGTCATGCATCAGACTGGCACATAATAA	AGAAGTAGATCATGCACCCA
S1 <i>LTP</i>	(1)	TGTGTCATGCATCAGACTGGCACATAATAA	AGAAGTAGATCATGCACCCA
Consensus	(1)	TGTGTCATGCATCAGACTGGCACATAATAA	AGAAGTAGATCATGCACCCA
		51	100
NS1 <i>LTP</i>	(51)	CTAGTGATCACTTCGTCTAGTGCCCTCCGTTCAATGTC	CGTCGTCGTCGT
S1 <i>LTP</i>	(51)	CTAGTGATCACTTCGTCTAGTGCCCTCCGTTCAATGTC	CGTCGTCGTCGT
Consensus	(51)	CTAGTGATCACTTCGTCTAGTGCCCTCCGTTCAATGTC	CGTCGTCGTCGT
		101	150
NS1 <i>LTP</i>	(101)	CGT-----GTACCT--TACGTGACATGCTGTAGCACGTACGCTAGCAGA	
S1 <i>LTP</i>	(101)	CGT CGTGGT GTACCTCGTACGTGACATGCCGTAGCACGTACGCTAGCAGA	
Consensus	(101)	CGT GTACCT TACGTGACATGC GTAGCACGTACGCTAGCAGA	
		151	176
NS1 <i>LTP</i>	(143)	GCAGCACCTCAATGTCCTTGGGTTTG	
S1 <i>LTP</i>	(151)	GCAGCACCTCAATGTCCTTGGGTTTG	
Consensus	(151)	GCAGCACCTCAATGTCCTTGGGTTTG	
		1	50
NS2 <i>LTP</i>	(1)	TGTGTCATGCATCAGACTGGCACATAATAA	AGAAGTAGATCATGCACCCA
S2 <i>LTP</i>	(1)	TGTGTCATGCATCAGACTGGCACATAATAA	AGAAGTAGATCATGCACCCA
Consensus	(1)	TGTGTCATGCATCAGACTGGCACATAATAA	AGAAGTAGATCATGCACCCA
		51	100
NS2 <i>LTP</i>	(51)	CTAGTGATCACTTCGTCTAGTGCCCTCCGTT CGCTGTTGTCGT CGTCGT	
S2 <i>LTP</i>	(51)	CTAGTGATCACTTCGTCTAGTGCCCTCCGTT CAATGT -----CGTCGT	
Consensus	(51)	CTAGTGATCACTTCGTCTAGTGCCCTCCGTTCAATGT	CGTCGT
		101	150
NS2 <i>LTP</i>	(101)	CGTCGTGGTGTACCTCGTACGTGACATGCCGTAGCACGTACGCTAGCAGA	
S2 <i>LTP</i>	(95)	CGTCGT CGTGTACCT --TACGTGACATGCTGTAGCACGTACGCTAGCAGA	
Consensus	(101)	CGTCGT GTGTACCT TACGTGACATGC GTAGCACGTACGCTAGCAGA	
		151	176
NS2 <i>LTP</i>	(151)	GCAGCACCTCAATGTCCTTGGGTTTG	
S2 <i>LTP</i>	(143)	GCAGCACCTCAATGTCCTTGGGTTTG	
Consensus	(151)	GCAGCACCTCAATGTCCTTGGGTTTG	
		1	50
NS1 <i>GGT</i>	(1)	GGCCACAGCCAATGC GAGAATACAAGTCCAAGATTATGGTATCCCAACAT	
S1 <i>GGT</i>	(1)	GGCCACAGCCAATGC TAGAATACAAGTCCAAGATTATGGTATCCCAACAT	
Consensus	(1)	GGCCACAGCCAATGC AGAATACAAGTCCAAGATTATGGTATCCCAACAT	
		51	100
NS1 <i>GGT</i>	(51)	GTTCCCTGT-----AAATGATCCCCCTCAGCTATTCTCCGTCGA	
S1 <i>GGT</i>	(51)	GTTCCCTGT TTCCATGTAAAA ATGAT-CCCCCTCAGCTATTCTCCGTCGA	
Consensus	(51)	GTTCCCTGT AA TGAT CCCCCTCAGCTATTCTCCGTCGA	
		101	
NS1 <i>GGT</i>	(91)	AT	
S1 <i>GGT</i>	(100)	AT	
Consensus	(101)	AT	
		1	50
NS1 <i>GAB</i>	(1)	GCCACACCTACGACGAGT ACATCTGGGCGTCGGTTGGGCTGTACCTCGAC	
S1 <i>GAB</i>	(1)	GCCACACCTACGACGAGT ACATCTGGGCGTCGGTTGGGCTGTACCTCGAC	
Consensus	(1)	GCCACACCTACGACGAGTACATCTGGGCGTCGGTTGGGCTGTACCTCGAC	
		51	100
NS1 <i>GAB</i>	(51)	ATCCTGAACCTGTTCCCTCTCCATCCTGAACATGCTCAGGAGCATGCAATC	
S1 <i>GAB</i>	(51)	ATCCTGAACCTGTTCCCTCTCCATCCTGAACATGCTCAGGAGCATGCAATC	
Consensus	(51)	ATCCTGAACCTGTTCCCTCTCCATCCTGAACATGCTCAGGAGCATGCAATC	
		101	150
NS1 <i>GAB</i>	(101)	CGACA ACTAGCC GGTCAAAGCACCGCACCGGCC TCTTGA TA TCGAACA	

S1 GAB (101) CGACAACCTAGCC-----TCTTGA--TCGAACA
 Consensus (101) CGACAACCTAGCC TCTTGA TCGAACA
 151 194
 NS1 GAB (151) CGGTATACCCCC-----GCGGTCTGTGCTCTGGTTGTTA
 S1 GAB (126) CGGTATACCCCCATGGTAAATGCGGTCTGTGCTCTGGTTGTTA
 Consensus (151) CGGTATACCCCC GCGGTCTGTGCTCTGGTTGTTA

1 50
 NS1 AP2 (1) TACAACCTCCTGGACACAGCTAGCTAGCTGATTTTACAACATACAT---AC
 S1 AP2 (1) TACAACCTCCTGGACACAGCTAGCTAGCTGATTTTACAACATACATCATAC
 Consensus (1) TACAACCTCCTGGACACAGCTAGCTAGCTGATTTTACAACATACAT AC
 51 100
 NS1 AP2 (48) GGAGTACTACTGCTTGACAAGCATCTCCTTACATCACACCGTGCTGCTC
 S1 AP2 (51) GGAGTACTACTGCTTGACAAGCATCTCCTTACATCACACCGTGCTGCTC
 Consensus (51) GGAGTACTACTGCTTGACAAGCATCTCCTTACATCACACCGTGCTGCTC
 101
 NS1 AP2 (98) TTTACAA
 S1 AP2 (100) TTTACAA
 Consensus (101) TTTACAA

1 50
 NS1 Histone H2B (1) CGCGAGATCCAGACCTCCGTGCGCCTCGTCTCCAGGAGAGCTCGCCAA
 S1 Histone H2B (1) CGCGAGATCCAGACCTCCGTGCGCCTCGTCTCCAGGAGAGCTCGCCAA
 Consensus (1) CGCGAGATCCAGACCTCCGTGCGCCTCGTCTCCAGGAGAGCTCGCCAA
 51 100
 NS1 Histone H2B (51) ACACGCCGTCTCCGAGGGAACCAAGGCCGTACCAAGTTCACCAGCAATT
 S1 Histone H2B (51) ACATGCCGTCTCCGAGGGAACCAAGGCCGTACCAAGTTCACCAGCAATT
 Consensus (51) ACA GCCGTCTCCGAGGGAACCAAGGCCGTACCAAGTTCACCAGCAATT
 101 150
 NS1 Histone H2B (101) GAGCAGCCTCCAGCGTCCACGGATTGTTAGGTCTCCCCTTCTTACAAGG
 S1 Histone H2B (101) GAGCAGCCTCCAGCGTCCACGGATTGTTAGGTCTCCCCTTCTTACAAGG
 Consensus (101) GAGCAGCCTCCAGCGTCCACGGATTGTTAGGTCTCCCCTTCTTACAAGG
 151 200
 NS1 Histone H2B (151) GTTCTTCGTGCTGCTCTACCCCTCCCTCCCGCTATGTATGTGCTG
 S1 Histone H2B (151) GTTCTTCGTGCTGCTCTACCCCTC-----CCCGCTATGTATGTGCTG
 Consensus (151) GTTCTTCGTGCTGCTCTACCCCTC CCCGCTATGTATGTGCTG
 201 223
 NS1 Histone H2B (201) TGAATCGTTGATGTTCTCGTCTG
 S1 Histone H2B (196) TGAATCGTTGATGTTCTCGTCTG
 Consensus (201) TGAATCGTTGATGTTCTCGTCTG

1 50
 NS1 ARDA (1) GACGGCGGCAGCTACAAGCGGGCGCAGTCGACGCCGTGACCCCGACGAC
 S1 ARDA (1) GACGGCGGCAGCTACAAGCGGGCGCAGTCGATGCCGTGACCCCGACGAC
 Consensus (1) GACGGCGGCAGCTACAAGCGGGCGCAGTCGACGCCGTGACCCCGACGAC
 51 100
 NS1 ARDA (51) GCCGGTGACGCCGTGCTGCTG-----ACGACGCCGCGCGGCGCGG
 S1 ARDA (51) GCCGGTGACGCCGTGCTGCTGCTGCTGCTGCTGACGACGCCGCGCGGCGCGG
 Consensus (51) GCCGGTGACGCCGTGCTGCTGCTG ACGACGCCGCGCGGCGCGG
 101 123
 NS1 ARDA (92) GCAACGTGTGGCGCAGCGTCTTC
 S1 ARDA (101) GCAACGTGTGGCGCAGCGTCTTC
 Consensus (101) GCAACGTGTGGCGCAGCGTCTTC

1 50
 NS1 PRP (1) GGGCCAACGTCTGGGCATCAACCTCAACCTGCCATCAACCTCAGCCTC
 S1 PRP (1) GGGCCAACGTCTGGGCATCAACCTCAACCTGCCATCAACCTCAGCCTC
 Consensus (1) GGGCCAACGTCTGGGCATCAACCTCAACCTGCCATCAACCTCAGCCTC
 51 100
 NS1 PRP (51) CTCGTCAACTACTGCGGCAGGCGCGTCCCCTCGGGCTTCCAGTGCTTCTG
 S1 PRP (51) CTCGTCAACTACTGCGGCAGGCGCGTCCCCTCGGGCTTCCAGTGCTTCTG
 Consensus (51) CTCGTCAACTACTGCGGCAGGCGCGTCCCCTCGGGCTTCCAGTGCTTCTG
 101 121
 NS1 PRP (101) ACTATCACACGCCCATCGATC
 S1 PRP (101) AT-----CACGCCCATCGATC
 Consensus (101) A CACGCCCATCGATC

1 50
 NS1 Histone H4 (1) CCGTCACCTACACCGAGCACGCGCGCCGTAAGACCGTCACCGCCATGGAC
 S1 Histone H4 (1) CCGTCACCTACACCGAGCACGCGCGCCGTAAGACCGTCACCGCCATGGAC
 Consensus (1) CCGTCACCTACACCGAGCACGCGCGCCGTAAGACCGTCACCGCCATGGAC

51 100

NS1 *Histone H4* (51) GTCGTCTACGCGCTTAAGCGCCAGGGCCGCACCCTCTACGGCTTCGGCGG
 S1 *Histone H4* (51) GTCGTCTACGCGCTTAAGCGCCAGGGCCGCACCCTCTACGGCTTCGGCGG
 Consensus (51) GTCGTCTACGCGCTTAAGCGCCAGGGCCGCACCCTCTACGGCTTCGGCGG
 101 150

NS1 *Histone H4* (101) CTAGGCTGCCCAGCGCGCTTCGCCGTCGCTGCGGTTCTGGTGTGCTG
 S1 *Histone H4* (101) CTAGGCTGCCCAGCGCGCTTCGCCGTCGCTGCGGTTCTGGTGTGCTG
 Consensus (101) CTAGG CTGCCGCGCCGCGCTTCGCCGTCGCTGCGGTTCTGGTGTGCTG
 151 200

NS1 *Histone H4* (151) CAGTTCGCAAGTTGTTTGTGTGGG**GAAAAAATGCTAGCTACTGTTAGAAC**
 S1 *Histone H4* (151) CAGTTCGCAAGTTGTTTGTGTGGG**CGAAAAAATGCTAGATACTGTTAGAAC**
 Consensus (151) CAGTTCGCAAGTTGTTTGTGTGGG AAAAAATGCTAG TACTGTAGAAC
 201 213

NS1 *Histone H4* (201) **TGCAGTGCGGTAT**
 S1 *Histone H4* (201) **TGCAGTGCGGTAT**
 Consensus (201) TGCAGTGCGGTAT

1 50

NS1 *ZmPIP1-3* (1) **CCGTTCAAGAGCAGGTC**TTAAGCTGCCGCGG**GT**GTGCTGAGACATGCATG
 S1 *ZmPIP1-3* (1) **CCGTTCAAGAGCAGGTC**TTAAGCTGCCGCGG**CCGTGCCGAGACATGCCTG**
 Consensus (1) CCGTTCAAGAGCAGGTC**T**TAAGCTGCCGCGG GTGC GAGACATGC TG
 51 100

NS1 *ZmPIP1-3* (51) **CCAGTCCGGAAGGACGAGCGTCTTCCTGTGGGGGGGAATGCCTTGCTCTGC**
 S1 *ZmPIP1-3* (51) **CCAGTCCGGAAGGACGAGCGTCTTCCTGTGGG---GAATGCCCT-TCTGC**
 Consensus (51) CCAGT CGGAAGGACGAGCGTCTTCCTGTGGG GAATGCC T TCTGC
 101 145

NS1 *ZmPIP1-3* (101) **CCACGCCTAGTTTCTCTGCTGAATCTTCCATCTCTCTTCCCTTCA**
 S1 *ZmPIP1-3* (97) **CCACGCCTAGTTTCTCTGCTGAATCTTCCATCTCTCTTCCCTTCA**
 Consensus (101) CCACGCCTAGTTTCTCTGCTGAATCTTCCATCTCTCTTCCCTTCA

1 50

NS1 *Ribo-S29* (1) **GCAAACGCCAAGGACATT**GGCTTCATCAAGTACCGCTGAAGTCAGCTGGGC
 S1 *Ribo-S29* (1) **GCAAACGCCAAGGACATT**GGCTTCATCAAGTACCGCTGAAGTCAGCTGGGC
 Consensus (1) GCAAACGCCAAGGACATTGGCTTCATCAAGTACCGCTGAAGTCAGCTGGGC
 51 100

NS1 *Ribo-S29* (51) GGGCTATCTGAATGCCATCTCTT**GGACATGG**GACAGTGTAGTAGAGGCGAT
 S1 *Ribo-S29* (51) GGGCTATCTGAATGCCATCTCTT**G-----GACAGTGTAGTAGAGGCGAT**
 Consensus (51) GGGCTATCTGAATGCCATCTCTT GACAGTGTAGTAGAGGCGAT
 101 150

NS1 *Ribo-S29* (101) GCCACAATTTAATTACTGTCATTTAGATGTTCC**GTTTCAGAACTCTGCTA**
 S1 *Ribo-S29* (95) GCCACAATTTAATTACTGTCATTTAGATGTTCC**CTTCAGAACTCTGCTA**
 Consensus (101) GCCACAATTTAATTACTGTCATTTAGATGTTCC TTCAGAACTCTGCTA
 151 161

NS1 *Ribo-S29* (151) **TTTAAGTCCGC**
 S1 *Ribo-S29* (145) **TTTAAGTCCGC**
 Consensus (151) TTTAAGTCCGC

1 50

NS1 *UCR* (1) **CCTGCTGTGCTGTTATA**TTGTTTCTTCCATGACAGTTGGCTAGTGTTT
 S1 *UCR* (1) **CCTGCTGTGCTGTTATA**TTGTTTCTTCCATGACAGTTGGCTAGTGTTT
 Consensus (1) CCTGCTGTGCTGTTATA**T**TTTCTTCCATGACAGTTGGCTAGTGTTT
 51 100

NS1 *UCR* (51) **TTTTT--GCTCCACGAGGATCATTGCAATTCCTTGATGGTTCGACTGTTAT**
 S1 *UCR* (51) **TTTTTTTGCCCCACAAGGATCATTGCAATTCCTTAATGGCCGACGGTTAA**
 Consensus (51) TTTTT GC CCAC AGGATCATTGCAATTCCTT ATGG CGAC GTTA
 101 113

NS1 *UCR* (99) **ATGCCAAAGTGCG**
 S1 *UCR* (101) **ATGCCAAAGTGCG**
 Consensus (101) ATGCCAAAGTGCG

1 50

NS1 *PGS* (1) **GTTGAAAATGTAGGGAA**ACTCTTGTTTTCACTAAAAAGGAACCCCTGGAG
 S1 *PGS* (1) **GTTGAAAATGTAGGGAA**ACTCTTGTTTTCACTAAAAAGGAACCCCTGGAG
 Consensus (1) GTTGAAAATGTAGGGAAACTCTTGTTTTCACTAAAAAGGAACCCCTGGAG
 51 100

NS1 *PGS* (51) **GGGGGAGTAACGGTGTAGAAGTTTTATGTTGTCACAGTTGGCATGCATT**
 S1 *PGS* (51) **GGGGG-AGTAACGGTGTAGAAGTTTTATGTTGTCACAGTTGGCATGCATT**
 Consensus (51) GGGGG AGTAACGGTGTAGAAGTTTTATGTTGTCACAGTTGGCATGCATT
 101 128

NS1 *PGS* (101) **CAT---ATAGGAATAGCTAGGAGATGGC**
 S1 *PGS* (100) **CATCATATAGGAATAGCTAGGAGATGGC**

Consensus (101) CAT ATAGGAATAGCTAGGAGATGGC

1 50
NS1 *Ribo-S4* (1) GCTGCTGCCAAGGCATAAGTTCTCTGAATGTGCTGCTTGGAGCTTTTGGC
S1 *Ribo-S4* (1) GCTGCTGCCAAGGCATAAGTTCTCTGAATGTGCTGCTTGGAGCTTTTGGC
Consensus (1) GCTGCTGCCAAGGCATAAGTTCTCTGAATGTGCTGCTTGGAGCTTTTGGC
51 100
NS1 *Ribo-S4* (51) TATGTCTAGTTTAAATTTTTATCTGCAAGGATATAGAGCTACCTTCCCAAG
S1 *Ribo-S4* (51) TATGTCTAGTTTAAATTTTTATCTGCAAGGATATAGAGCTACCTTCCCAAG
Consensus (51) TATGTCTAGTTT AAATTTTTATCTGCAAGGATATAGAGCTACCTTCCCAAG
101 150
NS1 *Ribo-S4* (101) ACGTTTATCATCATGTTTTGTTGCTTTTGGTTCTTGAACAGCGTTTGCA
S1 *Ribo-S4* (101) AC--TTTATCATCATGTTTTGTTGCTTTTGGTTCTTGAACAGCGTTTGCA
Consensus (101) AC TTTATCATCATGTTTTGTTGCTTTTGGTTCTTGAACAGCGTTTGCA
151
NS1 *Ribo-S4* (151) GC
S1 *Ribo-S4* (149) GC
Consensus (151) GC

1 50
NS2 *Ribo-S4* (1) GCTGCTGCCAAGGCATAAGTTCTCTGAATGTGCTGCTTGGAGCTTTTGGC
S2 *Ribo-S4* (1) GCTGCTGCCAAGGCATAAGTTCTCTGAATGTGCTGCTTGGAGCTTTTGGC
Consensus (1) GCTGCTGCCAAGGCATAAGTTCTCTGAATGTGCTGCTTGGAGCTTTTGGC
51 100
NS2 *Ribo-S4* (51) TATGTCTAGTTTAAATTTTTATCTGCAAGGATATAGAGCTACCTTCCCAAG
S2 *Ribo-S4* (51) TATGTCTAGTTTAAATTTTTATCTGCAAGGATATAGAGCTACCTTCCCAAG
Consensus (51) TATGTCTAGTTT AAATTTTTATCTGCAAGGATATAGAGCTACCTTCCCAAG
101 150
NS2 *Ribo-S4* (101) AC--TTTATCATCATGTTTTGTTGCTTTTGGTTCTTGAACAGCGTTTGCA
S2 *Ribo-S4* (101) ACGTTTATCATCATGTTTTGTTGCTTTTGGTTCTTGAACAGCGTTTGCA
Consensus (101) AC TTTATCATCATGTTTTGTTGCTTTTGGTTCTTGAACAGCGTTTGCA
151
NS2 *Ribo-S4* (149) GC
S2 *Ribo-S4* (151) GC
Consensus (151) GC

1 50
NS1 *ZmPIP2-1* (1) AGGCGACCCGAACCAACCACCGGCACCCAAGTCGATCGATGA----TGTC
S1 *ZmPIP2-1* (1) AGGCGACCCGAACCAACCACCGGCACCCAAGTCGATCGATGAATGATGGC
Consensus (1) AGGCGACCCGAACCAACCACCGGCACCCAAGTCGATCGATGA TG C
51 95
NS1 *ZmPIP2-1* (47) ATTCTCCTCGCTCACGACTTCCCCCGCCC GTAGGTCGCCCGCCAT
S1 *ZmPIP2-1* (51) ATTCTCCTCGCTCACGGC--CCCCCGCCC GTAGGTCGCCCGCCAT
Consensus (51) ATTCTCCTCGCTCACG C CCCCCGCCGTAGGTCGCCCGCCAT

1 50
NS1 *MSP* (1) CGGTACCTGTTTTACTACTCT--GTTTGGTGGTTTCTGAGGCAAGTTGCC
S1 *MSP* (1) CGGTACCTGTTTTACTACTCTCTGTTTGGTGGTTTCTGAGG-AAGTTGCC
Consensus (1) CGGTACCTGTTTTACTACTCT GTTTGGTGGTTTCTGAGG AAGTTGCC
51 100
NS1 *MSP* (49) CGTGTACTTGTATCGTAAAAACCGAGTGGGACATCTGCATCGTTTCATCT
S1 *MSP* (50) CGTGTACTTGTATCGTAAAAACCGAGTGGGACATCTGCATCGTTTCATCT
Consensus (51) CGTGTACTTGTATCGTAAAAACCGAGTGGGACATCTGCATCGTTTCATCT
101
NS1 *MSP* (99) GC
S1 *MSP* (100) GC
Consensus (101) GC