

Characterization of 25 full-length *S-RNase* alleles, including flanking regions, from a pool of resequenced apple cultivars

Plant Molecular Biology

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Online resource 4 Alignment of the *S*₅₈-*RNase* allele from ‘Åkerö’ and ‘Antonovka Pamtorutka’ (MdS58) with *Malus* ‘Mt Blanc’ *S*₅₈ (MG262529), and *S*₃₉-*RNase* isolated from ‘Ijunscoe Raneé’ and ‘Young America’ (MdS39) with *S*₃₉ from *Malus sylvestris* (EU419871); A, C: genomic sequences (exons are highlighted in yellow); B, D: deduced protein sequences.

A)

MdS58	ATGGGGATTACGGGGATGATACATATAGTTACGATGGTATTTTCATTAATTGTATTAATA	60
MhS58_MG262529	-----	0
MdS58	TTGTCTTCCTCTACGGTGGGACACGATTATTTTCAATTTACGCAGCAATATCAGCCAGCT	120
MhS58_MG262529	-----CAGCT *****	5
MdS58	GTCTGCTACTTTAATCCTACTCCTTGTAAGGATCCTCCTGACAAGTTGTTTACGGTTCAC	180
MhS58_MG262529	GTCTGCTACTTTAATCCTACTCCTTGTAAGGATCCTCCTGACAAGTTGTTTACGGTTCAC *****	65
MdS58	GGTTTGTGGCCTTCAAACCTTGAATGGACCGCACCCAGAAAATGACGAATGCAACCGTG	240
MhS58_MG262529	GGTTTGTGGCCTTCAAACCTTGAATGGACCGCACCCAGAAAATGACGAATGCAACCGTG *****	125
MdS58	AATTCTCAGAGGTAATATTATTGATAATCAGATAGTCACTATTGTTTATTTTCATTTATG	300
MhS58_MG262529	AATTCTCAGAGGTAATATTATTGATAATCAGATAGTCACTATTATTATTTTCATTTATG *****	185
MdS58	TATTTGTGTATATATACATATACTCAACATAGATTTTCATGCACGCGTGTGCAAATATTA	360
MhS58_MG262529	TATTTGTGTATATATACATATACTCAACATAGATTTTCATGCACGCGTGTGCAAATATTA *****	245
MdS58	TAATAAATTTAAATTTAATCATAAATTTACCTAGCTATATTATATTATATTGTCAGATAA	420
MhS58_MG262529	TAATAAATTTAAATTTAATCATAAATTTACCTAGCTATATTATATTATATTGTCAGATAA *****	305
MdS58	CAAATATCCAAGCCCAGTTGAAAATTATTTGGCCGAACGTACTCGATCGAACCAATCATG	480
MhS58_MG262529	CAAATATCCAAGCCCAGTTGAAAATTATTTGGCCGAACGTACTCGATCGAACCAATCATG *****	365
MdS58	TAGGCTTCTGGAATAAACAGTGGATAAACATGGCAGCTGTGGGAATCCCCAATAATGA	540
MhS58_MG262529	TAGGCTTCTGGAATAAACAGTGGATAAACATGGCAGCTGTGGGAATCCCCAATAATGA *****	425
MdS58	ACGACACGCATTACTTTCAAACAGTAATCAACATGTACATAACCCAGAAACAAAATATCT	600
MhS58_MG262529	ACGACACGCATTACTTTCAAACAGTAATCAACATGTACATAACCCAGAAACAAAATATCT *****	485
MdS58	CTGGAATCCTCTCAAAGGCGAAGATTGAACCGGTGGGGGGAAAAGGCCACTGGTGGATA	660
MhS58_MG262529	CTGGAATCCTCTCAAAGGCGAAGATTGAACCGGTGGGGGGAAAAGGCCACTGGTGGATA *****	545

MdS58	TTGAAAAATGCCATACGGAAGAGTATCAACAATAAGAAACCAAAATTC AAGTGCCAAATGA	720
MhS58_MG262529	TTGAAAAATGCCATACGGAAGAGTATCAACAATAAGAAACCAAAATTC AAGTGCCAAATGA *****	605
MdS58	AGAATAAGGTGACTAAATTGGTTGAGATCAGTCTTTGCAGCGATGGCAGCTTAACTCAGT	780
MhS58_MG262529	AGAATAAGGTGACT----- *****	619
MdS58	TCATAAAATTGCCCCCGCCATTTCTACCAGGATCACCATATCTCTGCCCTTCCGATATTG	840
MhS58_MG262529	-----	619
MdS58	ATTATTAA	848
MhS58_MG262529	-----	619

B)

MdS58	MGITGMIHIVTMVFLIVLILSSSTVGHDFQFTQQYQPAVCYFNPTPCKDPPDKLFTVH	60
MhS58_MG262529	-----AVCYFNPTPCKDPPDKLFTVH *****	21
MdS58	GLWPSNLNGPHPENCTNATVNSQRITNIQAQLKI IWPNVLDRTNHVGFWNKQWIKHGSCG	120
MhS58_MG262529	GLWPSNFNPHPENCTNATVNSQRITNIQAQLKI IWPNVLDRTNHVGFWNKQWIKHGSCG *****:*****	81
MdS58	NPPIMNDTHYFQTVINMYITQKQNI SGILSKAKIEPVGGKRPLVDIENAIRKSINNKKPK	180
MhS58_MG262529	NPPIMNDTHYFQTVINMYITQKQNI SGILSKAKIEPVGGKRPLVDIENAIRKSINNKKPK *****	141
MdS58	FKCQMKNKVTKLVEISLCSDGSLTQFINCPRPFLPGSPYLCPSDIDY 227	
MhS58_MG262529	FKCQMKNKVT----- 151 *****	

c)

MdS39 ATGGGGATTATGGGGATGATAGATATGGTTACGATGGTATTTTCCTTAATGGTATTAATG
MsS39_EU419871 -----

MdS39 TTTTCTTCGCTCGCGGTGAAATACGATTATTTGCAATTTACGCAGCAATACCAGCCGGCT
MsS39_EU419871 -----TTTACGCAGCAATATCAGCCGGCT

MdS39 GCCTGCAACTCTAACCCCTACTCCTTGTAAACGATCCTACTGACAAGTTGTTTACGGTTCAC
MsS39_EU419871 GCCTGCAACTCTAACCCCTACTCCTTGTAAACGATCCTACTGACAAGTTGTTTACGGTTCAC

MdS39 GGATTGTGGCCTTCAAAGGTTAAAGGTCTGACCCACACGACTGCAAGACCAAAACCAAC
MsS39_EU419871 GGATTGTGGCCTTCAAAGGTTAAAGGTCTGACCCACACGACTGCAAGACCAAAACCAAC

MdS39 AAGTCTCAGACGGTAATATTAATAATCAAATAGTCAATATTGTTTAGGAAAAATTAGTAA
MsS39_EU419871 AAGTCTCAGACGGTAATATTAATAATCAAATAGTCAATATTGTTTAGGAAAAATTAGTAA

MdS39 TATGTTTCATATTTATTAATTTTCATTGACCGAAATTTTATTAGTTTTAGTTGATTGAAC
MsS39_EU419871 TATGTTTCATATTTATTAATTTTCATTGACTGAAATTTTATTAGTTTTAGTTGATTGAAC

MdS39 TTCCTATTATTAATGTATTAAAGTATTAACGAGTCAGTAACATTGGTTTTAAAAATAAAA
MsS39_EU419871 TTCCTATTATTAATGTATTAAAGTATTAATGAGTCAGTGACATTGTTTTAAAAATAAAA

MdS39 ATTAGCAATTAATTAGGATTTAATACTCACACATTTACTAACTCCTAATTAATTTTC
MsS39_EU419871 ATTAGCAATTAATCAGGATTTAATACTCACACATTTACTAACTCCTAATTAATTTTC

MdS39 AATTCAAACATTTCCAAAATAAAAATAAAGTAAGTTGACTCATTAATTTTTTATAAAA
MsS39_EU419871 AATTCAAACATTTCCAAAATAAAAATAAAGTAAGTTGACTCATTAATTTTTTATAAAA

MdS39 AGATTTTTAAAAATTTTAAATATTAATGTACCCATTCATATAATATTTCAAACATTTAAT
MsS39_EU419871 AGATTTTTAAAAATTTTAAATCTTAAATGTACCCATTCATATAATATTTCAAACATTTAAT

MdS39 GTGTACTGTACACATTCCTAAATATTTCCAATTTGTTATATGTAAAATTTACAATTTTTTT
MsS39_EU419871 GTGTAGTGTACACATTCCTAAATATTTCCAATTTGTTATATGTAAAATTTACAATTTTTTAA

MdS39 TAAATATAAAATGTACCCATTTTCTTACAAAATCCATTCAATTTCTTTTAAATCCACTTT
MsS39_EU419871 AAAATATAAAATGTACCCATTTTCTTACAAAATCCATTCAATTTCTTTTAAATCCACTTT

MdS39 TGAACTTATACTGGTACATTCATCTCCGTAGGTACATTCCTTTTCATTTATTTGAGAATG
MsS39_EU419871 TGAACTTATATGGGTACATTCATCTCCGTAGGTACATTCCTTTTCATTTATTTGAGAATG

MdS39 TATCCATGCCAAGTTTAAATCGAAGAATTTACTAATGTACATGAAGCCTAGTATCTATTAT
MsS39_EU419871 TATCCATGCCAAGTTTAAATCGAAGAATTTACTAATGTACATGAAGCCTAGTATCTATTAT

MdS39 TTTGGTTTTGAAGAATGTACCCATGTTTATGTGTTAGTGTGTGTCGCGCATGTATGTGT
MsS39_EU419871 TTTGGTTTTGAAGAATGTACCCATGTTTATGTGTTAGTGTGTGTCGCGCATGTATATAT

MdS39 ATAT--ATATATAAAGCCTTTAAGGAAAGGTATCTCCATTTTTTATAAAAAATGGGATT
MsS39_EU419871 ATATATATATATAAAGCCTTTAAGGAAAGGTATCCCATTTTTTATAAAAAATGGGATT

MdS39 AGTTGTGGGGTCTACACCACATCGAACTTTAATGATCTGAACCGTCTATTTTTCAAGTTG
MsS39_EU419871 AGTTGTGGGGTCCACACCACATCAAACCTTTAATGATCCGAATCGTTTAT-TTCAAGTTG

MdS39 TACCTCATAGATCATCCTTACAAAATATTAGTCGAATTGGAAATATTTAAGACATCTAAT
MsS39_EU419871 TACCTCATAGATCATCCTTACAAAATATTAGTCGAATTGGAAATATTTAAGACATCTAAT

MdS39 TGGGTTCAAATAAATGAACGAATACTTTATTATATAAGAAACAATGAAATTTGATATTGA
MsS39_EU419871 TGGGTTCAAATAAATGAACGAATACTTTATTATATAAGAAACAATGAAATTTGATCTTGA

MdS39 TAATTAAGTAGGCAAAAATATTTAGATTGAATTGAATTTTTGTAAAGGATGATCTATGAAT
MsS39_EU419871 TAATTAAGTAGGCAAAAATATTTAGATTGAATTGAATTTTTGTAAAGGATGATCTATGAAT

MdS39 TGAGACTTACAAAATAGATGGTTCGGATCGTTGAAATTTGGGAGTGGGCCCCACTCCTAA
MsS39_EU419871 CGAGACTTACAAAATAGATGGTTCGGATCGTTGAAATTCAGGAGTGGGCCCCACTCCTAA

MdS39 TATCCATTTTTTTTCAAAAAATGGGGATCCCTTTGCATAAATGGCCTATATATATATGTGTG
MsS39_EU419871 TTTCCATTTGTTTTAAAAAATGGGGATCCCTTTGCATAAATGGCCTATATATATATGTGTG
* ***** **

MdS39 TGTACGCGCGCGTATGTGTATTGGAGAATATAATTTTTTTCATTTTTTCATCCACAAA
MsS39_EU419871 T-----GTGTGTATTGGAGAATATAATTTTTTGTATTTTTTCATCCACAAA
* *****

MdS39 TTATGGGTTTAAATTTAAAATCTCATTAATATAAACGACCACAAATTTAAATTTTTTATTT
MsS39_EU419871 TTATGGGTTTAAATTTAAAATCTCATTAATATAAACGACCACAAATTTCAATTTTTGATTT

MdS39 AAAATTATAATAACGTACATAGAAATACGTTATTACATTAATATCAGGAATTTCAATAAA
MsS39_EU419871 AAAATTATAATAACCTACATAGAAATACGTTATTACATTAATGTGAGGGATTTTCGATAAA

MdS39 AAATAAAAAGTCAACAAAAGTTTTAGTTAAAGAACATTTATAAATAGGGACCACATCTAAA
MsS39_EU419871 AAATAAAAATCAACAAAATTTAGTTAAAGAACATTTATAAATAGGGACCACATCTAAA

MdS39 GTCTATTGTTTTATTTTCAATTTATGCACCTTGTGTATATATACATATACACAACATAGATT
MsS39_EU419871 GTCTATTGTTTTATTTTCAATTTATGCACCTTGTGTATAT--ATACATATACACAACATAGATT

MdS39 TTCATGCACTCTTGTGTAATATTACAATTAATTTAAAATTTAATCATAAATTTTTCTAT
MsS39_EU419871 TTCATGCACTCTTGTGTAATATTACAATTAATTTAAAATTTAATCATAAATTTTTCTAT

MdS39 TGTATATATTGTATTGTCAGATAGATATATTACTCAAACCCAGTTGGAAATATTTGGC
MsS39_EU419871 TGTATATATTGTATTGTCAGATAGATATATTACTCAAACCCAGTTGGAAATGATTTGGC

MdS39 CGAACGTATTCAATCGAGCCGATAATGAAAGCTTCTGGGAAACACAGTGGGAAAAACATG
MsS39_EU419871 CGAACGT-----

MdS39 GCACCTGTGGATCTCCACAATAAAAGACAAGAACCATTACTTTGAAACAGTAATCAGAA
MsS39_EU419871 -----

MdS39 TGTACATAACCGAGAAAACAAACGTCTCTCATACCTATCCAAGGCCAACATCAATCCGG
MsS39_EU419871 -----

MdS39 ATGGTATAGCCAGGACACGGAAGGATATTGAAATTGCCATACGCAATAGTACTAACGATA
MsS39_EU419871 -----

MdS39 AGGAACCAAACTCAAGTGCCATAAGAAGAATGGGATAACTGAAATGGTGGAGTCACTC
MsS39_EU419871 -----

MdS39 TTTGCAGCAATTACTTCGAAAACAATTCATAAATTGCCCTAACAAAATTCAGAAAAAT

MsS39_EU419871 -----

MdS39
MsS39_EU419871 CACGATATTTCTGTCCCATCAAAGATATCCGGTATTAA

D)

MdS39 MGIMGMIDMVTMVFSMLVLMFSSSAVKYDYLQFTQQYQPAACNSNPTPCNDPTDKLFTVH
MsS39_EU419871 -----FTQQYQPAACNSNPTPCNDPTDKLFTVH

MdS39 GLWPSKVKGPDPHDCKTKTNKSQTIDILLKPQLEIIWPNVFNRADNESFWETQWEKHGTC
MsS39_EU419871 GLWPSKVKGPDPHDCKTKTNKSQTIDILLKPQLEMIWPNV-----
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MdS39 GSPTIKDKNHYFETVIRMYITEKQNVSHYLSKANINPDGIARTRKDIEIAIRNSTNDKEP
MsS39_EU419871 -----

MdS39 KLKCHKKNGITELVEVTLCSNYFGKQFINCPNKIPEKSRYFCPIKDIRY
MsS39_EU419871 -----