**Supplementary:** **Genome-Wide Analysis and Cloning of the Apple Stress-Associated Protein Gene Family Reveals *MdSAP15*, Which Confers Tolerance to Drought and Osmotic Stresses in Transgenic *Arabidopsis***

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**A1. Genomic information for cloned MdSAPs**



>MdSAP7

CAGATTTTGTTCAAATGTAGGAAAATTTAAAGTTAAAGAGGAAGCAATATATTGCTTTTGAAGCATTCTTTTTATATAATAGCTTTTTATAGCAAATCATGATAATTTAAAATCCTCCTTCGGTTTTATATCATCATAATCATAAGAAGCTTTTTGCATGCGGGAGTGTTACTATTTGAACCATTCATCTTAATGGTTCGATAGGATAGTACAAGGAGAGGGTCCAAATATATACATTGAGCCGAGAATGAATCTTAACTTTCAAATTTTGTTTTTGCTTTCTAATGTTTATATTTTTGTAAAAGTAACAATTTGGCCTTACATATAGAGATTTAATAAATTTTTACAATGGTTAAATTTTACATAATACATGTATCACTCAATTTGTAGCCGGACCAGCTTTCTTATACTCCTTGTATCATTGATGAAAAATTACTAGAGCAAATTAAAAACTATAAATCAAAACATAACAAATCCATCTACGATATTTTGAGCTTCTATCGATTTTGAGCTACTAGATTGTCATAACTACTCACTTTAATCCCTGAAATTTAAAATATCACTGAGATTGTCAATTGTTAATCATTTTGATCAGTCCGTAAAAAAATCTTCGCTAAATAGAAAAAACTACAAATTCAAGTGAAGGGGTTGTTTGTGAGAATAATATCCATATGTTAACGAAAATTTTCATATAAAATCAAAATAATTGTCAATAAACAATCTAAGAACTATTATTTTAAATCGTAATAATAGAATTCCATAAAACTAGAGAAATTAGAACATGGGCAACCAATAGAATCAATCGGACGGCCGCATGTTGTAATACGCTGCATGTGGGTAAAAAATAGGGTCCCACCGTACCTTAAAATAAGCTTTGTCAGGATATTTACCTTTTCTCAATAATGACGATTATCCACGTCAAAACAACCAACCAATTTCAATGCGATCGTAATACGTGTGGTACACTCAGTATCACTATATAAATGATAAGATACGTGTGTTAAAAAATTAACAACTTAAAAAATATAACTTTTCACCAATTAAATAAAAACACGTAATGTACTATTCGTGTTCCGATTACAATACAGCAATACCACACCCAAGAACCCAAAAAAAATCAATTATTCCTTCTTTTTATTTAATTTTTTAAGCAAAAAGGTAATAGTAAAAGAAAAGTAGGAAGGGCATTTCGGTAAAACCGAAAGGCAAAAATGGATACGCGTCTCTATGTGGTCCATATTTTCTCGCCAGTACCCGACCTTTCACTCCCTCATATTATCCCCCTCCCCCATTTCTGTCTCCTCCATCGCCCACCCAAACCTCTCCTCTCCTCTCCTCTCTCTCTAAAAACCACAACTTTTTCTTCCTCTCTCTCTGTCTCTCTAGAAAACCACAACCTCCAATTTTCTTCCTTTCCATCCATCTATATCTCTGAAAAAAAACAGAAAAAAAAAAGAGAGAAGACGAGAGAGATCCATCTCTCGATTGTTCAAAATTTGAATGAAAAAAATGGCACAGAGAACGGAGAAGGAAGAGACGGAGTTCAAGGTCCCCGAAACGCTAACGCACTGCGTCAACAACTGCGGCGTCACCGGCAATCCCTCCACCAACAACATGTGCCAGAAGTGCTTCAACGCCGCATCGGCCGCCGCCGCCGCCGCCACTTCATCGTCGTCGTCAGCGGCGATTCTGAAGTTTTCAGCCGAGAAAAGTCCGAGATCTAGCTCATCTTTCAGCTTCGAGGCTGCTGCCGAGACCTGCCGTAAGACGACGGCATCAGAGATCGCGAGATCGGACGAAACGCCGAATCGGCGCGTGGTTAATCGGTGCTCCGGTTGTCGGAGGAAGGTCGGGTTGACCGGATTCAGGTGCCGGTGCGGCGAGCTTTTCTGCTCCGAACACCGGTACTCCGATCGCCACGTGTGCAGTTACGACTATAAGGCTGCCGGTCGCGAGGCCATCGCGAGAGAAAACCCCGTGGTCAAGGCCGCAAAGATCGTCCGGGTTTGATGATTTATATATCGATTGACTTTGTAGAAATGAAGCAACGCAAAAAGTGACGCGAAAATTTGAAGAGGAATTTGTGGCTCGATCGGTTCTCATGGCGCGTCTTTCTCTCGGAGACCAAAACGAAATTCAGAGACCGGGGAGAGATCGCTTCGTTTATCAAATTCTCTCTGATAAT

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**A2. Full-length amino acid sequences of 453 SAPs from 32 plant species**

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>RC29761G00070

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>TP5G05120

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>ZM07G24750

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>AL0G05070

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>AL1G12810

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>AL1G45860

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>AL3G13060

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>AL4G12660

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>AL5G22730

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>AL5G27260

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>AL7G19400

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>BR04G08650

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>BR06G09700

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>BR08G02710

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>CL02G22250

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>CL02G23340

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>CRU\_006G29960

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>CRU\_007G14770

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>CRU\_007G17560

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>CRU\_007G26930

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>CS00031G00350

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>CS00033G00100

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>CS00040G00770

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>CS00207G00150

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>CS05856G00010

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>CS09133G00010

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>EG0002G32530

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>EG0003G29380

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>EG0003G29390

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>EG0004G15980

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>EG0008G39620

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>FV0G51630

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>FV1G19700

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>FV1G23590

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>FV2G44220

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>FV3G42390

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>FV5G30030

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>FV6G18510

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>FV6G20940

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>FV7G02130

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>FV7G02150

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>FV7G11160

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>FV7G39980

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>FV7G40000

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>GM03G29662

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>GM12G36716

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>GM13G27410

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>GM15G03810

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>GM16G33180

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>GM17G14580

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>GR02G22920

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>GR02G24090

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>GR03G16780

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>GR04G17390

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>GR06G03130

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>GR06G13910

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>GR06G15620

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>GR06G21130

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>GR08G24090

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>GR09G08650

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>GR09G40470

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>GR13G25840

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>LJ1G049970

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>PT01G11500

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>PT01G26930

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>PT07G07850

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>PT09G14410

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>PT11G14360

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>PT15G13150

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>PT15G13190

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>ST03G009990

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>ST07G022130

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MTSCGKVENPILCAGGCGFYGTSSNHNLCSQCYKTFLKEEAKNIVVLSEKISSLTFHEGTTTENVDSTMKIKQRCMTCKKKVGLIGFSCRCEGMFCSVHKYPEEHSCTFDYKSFGRVTLAKENPPCRHDKLENRI\*

>ST07G022160

MTSCGKVENQILCARGCGFYGTSSNNNLCSQCYKAFLKEGEAKNVSYKKSSLIFHDDSEGTTKNVESTMKIKLRCMTCKKKVGLTGFSCRCEGMFCKVHRYPEEHACTYDFKSVGHVTLAKENPPCRSAKLENRI\*

>ST08G025520

MGSEGNKFNDGTSFSPADSILCSNGCGFFGAAATNGLCSKCHRDFKMKEDHAAMAKVAMDKLVISRPQVESIGKVDFCSSATVTAAEKPVVETAVAVEIAGSQPNRCLSCRKKVGVVGFKCRCGSTFCGTHRYPEKHDCTFDFKAKGKEEICKANPVVKADKIQRF\*

>ST09G010540

MAEEHEFQSPEGGRHQLCANNCGFFGNSTTENYCSKCYRDIEERKSDAKSIDCLFSPTKRVLEKMIVKPIVLTPDLVEAAVPLVTPQPNRCLVCKKKMGLMGFKCRCGTIFCGTHRYPEVHACTFDFKSMGREAIAKANPLIKAEKLKKI\*

>ST10G020750

MESSKETGCQAPEGPILCINNCGFFGSAATMNMCSKCHKDMILKQEQAKFAATSIENIVNGNSSSNGKEPIATGAINVQPGSADLKVISTEASSDLSSGPSSEVKPKEGPTRCTTCRKRVGLTGFNCKCGNLFCAAHRYSDKHECPFDYKNAGRDAIAKANPVVVAEKLNKI\*

>ST10G025720

MAEEHGFEAPEGHILCANNCGFFGSPTTQNFCSKCYNEVYIKGGQQKPIDSLFPPQLPIPSQSSSVLVLPEPAAVEEKPEVVIAAVTAAVQPMPAQSNRCSACRKKVGLIGFKCRCGTTFCGTHRYPEIHGCSFDFKSMGREAIAKANPVVKAEKLGKI\*

>ST11G011630

MAEEQRMQEGGGHRLCANNCGFFGSPTTLNLCSKCYKDHCMKEQQSRTAQLAMEKTRPQQQQSESTSTYIPCTKSLPILEVSQPRETEIATRAPQVQSDTAAEVPQVQLNTVADQTPQVQSNRCATCRKRIGLTGFKCRCGVTFCGSHRYPEHHGCTFDYKSMGKVAIAMANPLVKAEKLHKI\*

>ST11G016470

MEHDETGCQPHPEGPILCINNCGFFGSAANMNMCSKCYKDVILKQEQAKLAASSIENFVNGSTSQKGPVIVGSVDVQPALLESKSVIFSSPPSSSSGEAAELMAKEGPSRCSTCKKKVGLTGFKCRCGNFYCGSHRYSDKHDCQFDYRSAARNAIAKANPVVKAEKLDKI\*

>ST12G032310

MAAQKREKEETELKVPESIPLCSPTLPVPSPSPPPTTHLSVALISDLKRSDRSSTERVDLKVSSMDDQSRSTSAASPESTDLVGRKTGVKRQREANRCSGIGCRRKVGLMPFRCRCGEVFCSEHRYSDRHDCSYDYKAAGREAIAKENPVVKAAKILKV\*

>TC0001G08430

MANIDLPPLCAKGCGFYGSSETKNLCSKCYNDFLKELVSKSKSEPKVDTALTASCPSVPVDSSLASAPSKLKNRCESCNKKVGLMGFSCRCGKVLCDVHRYPQEHLCNFDFKKADRLILVKENPIIKADKLDSRI\*

>TC0001G40740

MEQNQRGCQAPKLCANNCGFFGTAATMNLCSKCHKDLVMKQQGDKLASSPNGSILDGSPGNNHEPVSVAVDPQSTSVKSTAITAQANSASISMNTGREEEVKRGPNKCSICGKRVGLTGFTCRCGDLFCAVHRYSDKHDCPYDYHCAARDAIAKANPVLKANKLDKI\*

>TC0001G40760

MAQRTEKEETEFKVPETLTLCINNCGVTGNPATNNMCQKCFNATTATPSSSSSSSSSATSPSATGGAIAGGASIPKFSDDQSSRSTPSRSQQNRSDSSPPTTAATVTNSRTTAWNRSGNDPAAAAEKKVVNRCSGCRKRVGLTGFRCRCGELFCAEHRYSDRHDCSYDYKTAGREAIARENPVVKAAKIIRV\*

>TC0003G16430

MESVESMDRKLCAKACSFNGSAQRNNLCSQCYKDFLVGEFQNHNPIGEPLIPTTDQPLNSCFTVPPYSVSHVNNSNGSVGFTFGWTNNSGGASLASTKNRCNSRNKRVGLTGFTCRCGNLFCGKHRYPEEHECCVDLKAIGREALVKENPDCKGVGPDNLIEVYGALTIAKNQMENSVFSNATFLHDQNLLGDYGFSSGIMFCQIRSDMAGESHSLKGAPELPSKGVVALPSKGAVVISFGGDLVLLDVEECQI\*

>TC0003G26090

MGSEQNEGTSFPPSEPKLCANGCGFFGTAANMNLCSKCYRDLRAGEEQAAKAKAAMEKSLSVKTKQEDVVVETILDVKPVEELPHVGSSSTAVEQPAVVAAGNEQAEPKVSNRCFICRKKVRLTGFKCRCGSTFCGEHRYPEKHECLFDFKGAGRDAIAKANPVVKADKVERF\*

>TC0005G08290

MAEEHRCQAPEGHRLCVNNCGFFGSPATMNLCSKCYRDFRLKEQQEASSIKSSLSSSPTSSSTVVESVSQVPLLTLPEVNGESPVPAVEIAPATAEQRPQQQPNRCMVCRKRVGLTGFRCKCGITFCGSHRYPENHGCSFDFKTIGREEIARANPVVKAEKLEKI\*

>TC0005G16620

MILMSWRLEKMESHDETGCQAPEGPILCVNNCGFFGSAATMNMCSKCHKAMILKQEQVQLAASSIGSIVNGSSSGNGKEPTLAAALDVQSGIFESKNGSAEPSIDPSRMTFGGMKIKEGPNRCTTCRKRVGLTGFNCRCGNLFCAAHRYSDKHDCPFDYRTAARDAIAKANPVVRAEKLDKI\*

>TC0005G22760

MANANLPPLCAKGCGFYSSSQTKNLCSKCYNDFLKELIAKSTAEVKVDPSSAAPNPSVSVDSSSVPTPSKLKNRCESCNKKVGLMGFSCRCGKVLCGVHRYPKEHSCNFDFKTADRLILAEENSLVMADKLESRI\*

>TC0009G22510

MDEIIFACMSRRRGEEMDHEKTGCQAPPERPILCINNCGFFGSAATMNMCSKCHKDMILKQEQAKLAASSIDNIVNGSSTGNGNETVIATGVDVPNSVEPKTILVQTSCPSGSGESIEAKLKEGPIRCSTCKKRVGLTGFKCRCGNLFCTSHRYSDKHDCPFDYRTAARDAIAKANPVVKAEKLDKI\*

>TC0009G28100

MAEEYRSQAPQLCANNCGFFGIPATQNLCSKCYRDLQLKKQQSSSAKQAINQTLVPLSSPSSSLPSSSSISSSPFSGSLPMKEVETDEEVKVEEIQIQVRPNRCLACKKRVGLTGFTCRCGMVFCGTHRHPEQHDCTFDFKEMGKEQIAKANPVVKGEKLQKI\*

>TP1G11040

MGSEQNDSTSLSPSEPKLCVNGCGFFGTPSNMNLCSKCYRDIRATEEQAASAKAAVDKSLNPNKPHIKPQQSREIAPGVESGSSSSTSGGDSSAASSDPPKPTRTTRCLSCNKKVGVTGFKCRCGSTFCGAHRYPESHDCEFDFKGAAREAIAKANPLVKADKVERI\*

>TP1G37930

MDHDKTGCQSPPEGPKLCINNCGFFGSAATMNMCSKCHKAILFQQEQGAKFASAVSGTSSSSTIMKETFTSALVDVETKSVEPMVVAVQPSSVQVVAEVEAQEAAAKPKEGPSRCTTCNKRVGLTGFKCRCGDLFCGTHRYADIHNCSFNYHAAAQEAIAKANPVVKAEKLDKI\*

>TP2G01660

MGSEQNHSTSFSPSEQKLCVNGCGFFGTTANMNLCSKCYHDLRITEEQAASAKAALEKSLNPKPKTSLESAGASSSSTGSETAAFSESSPPPQTRAKKRCLSCNKKVGLMGFKCKCGSTFCGDHRYPENHECEFDFRGEGRDAIGKANPLVKAEKVDRV\*

>TP3G10770

MAQRTEKEETEFKVLETLTTPATTPTLCSNNCGVTANPATNNMCQKCFNASVAAAGVDSGSILKRSARSVNLRSTPAKVVIRTREIDPVKRDQQTVNRCSGCRKKVGLTGFRCRCGDLFCAEHRYSDRHDCSYDYKTAGREAIARENPVVKAAKMVKV\*

>TP4G10400

MAEEHRLQEPRLCANNCGFFGSTATQNFCSKCFRDLQHQQQNSSTAKHALNQTLASVSTGGVASSSVSSPTPPPPSPQADLTSSDPKEVNVTNAEKRVAAEEEEEKAPSQDPKRCLTCRRRVGITGFRCRCGFVFCGTHRYAEQHECSFDFKRVGKEKIAKANPIVKAEKLEKI\*

>TP4G18560

MAEEHRCKTPEGHRLCLNNCGFLGSSATMNLCSNCYGDLCLKQQQQASMKSSLSVASPLSSSEIDSIPSSSSSSSSTIAPVLENYAREKQIPTTATEQKEPQPPQRPNRCSLCRKRVGLTGFMCRCGTSFCGRHRYPEVHGCSYDFKSAGREEIAKANPLVIAAKLQKI\*

>TP5G09530

MAEEHRCQTPEGHRLCANNCGFLGSSATMNLCSNCYGDLCLKQQQQPSMKSTVESSLSTVSPPSPEIASISSPIIQPLVQNPSAELEVTVKNASKTVTTTEEQQQQKRPNRCTTCRKRVGLTGFKCRCGTTFCGAHRYPEVHGCTFDFKSAGREEIAKANPLVKAAKLQKI\*

>TP6G05470

MSSEQNNSTSFPPTEPKLCDNGCGFFGSPSNMNLCSKCYRSLRAEEDQTAVAKAAVEKSLKLPSCSLITTQEPKQPLETKPASVESVVVVSAETSSVPVATEQDEAEPSKPARPNRCFSCNKKVGVMGFKCKCGSTFCGSHRYPEKHECSFDFKEVGRDEIAKANPVIKADKVQRI\*

>TP7G12090

MTGEPSLCIKGCGFFSTSQTKNLCSKCYSGFKDESDRHLAALKDHTETVAEAAEEVTVAAEAEEAVVVRKESSRCNACKKKVGILGFRCRCGNVFCGSHRYPEEHSCPSDYKSAAINDLIIQNPIVNGDKLNRI\*

>TP7G20870

MGSEQNDSTSFTQSSDPKLCANGCGFFGSPSNMDLCSKCYRNICAEEAQTAVAKAAVEKSFKPSPPRTLFISEPAVKPSEPEKEKAVVAAVVVAEPSSIVGEGEEAAVPDQNEPSKPARPNRCLCCNKKVGIMGFKCKCGSTFCGEHRYPERHDCSFDFKEAGRGEIAKANPVIKADKLQSMRKSEIRIYLQTQLTQVDS\*

>TP7G23400

MVNASETEALPCAGGCGLFGTRKNNNLCSLCYKQSLLERVATLRLEPETERSTVCPPTSSPVAAEEPVKKRRCGTCQRKVGMLGFNCKCGHVFCGSHRYPEEHYCPFDYKQSGRLALARQLPLIRTEKLHKF\*

>VV02G07850

MSFNPKLLQENRTSSFSFLDTAGGVGGGDKSEPKVPNRCMSCNKKVGLTGFRCKCGSTFCGAHRYPEKHECTFDFKASGRDAIAKANPVVKADKLDRL\*

>VV02G07880

MQSPYGHEIQLSLETKSAFCGLSWSCVGGGDKSEPKVPNRCMSCNKKVGLTGFRCKCGSTFCGAHRYPEKHECTFDFKASGRDAIAKANPVVKADKLDRL\*

>VV06G06330

MDHDETGCQAHPEGPILCINNCGFFGSPATMNMCSKCHKDMMLKQEQAKLASSFSFGSEGSGEAKPKEGPNRCSTCKKRVGLTGFNCRCGHLFCATHRYSDKHDCPFDYRTAARDAIAKANPVVKAEKLDKI\*

>VV06G06360

MCRDLKVPQISTLKSRMAQKRENEQATETELKVPETLTLCVQTCGFSASDKPRSRSPSPPDDPDSTLENSDQGAVRRREVNRCSGCKRKLGLIGFRCRCGEMFCSKHRYSDRHECRFDYKAAGREMIAKENPVVRPAKILKV\*

>VV08G07910

MESHDETGCQAPEGPILCINNCGFFGSAATMNMCSKCHKDLALKQEQAKLAASSIGSIVNGSSSGNGKEPIEGPNRCTACRKRVGLTGFNCKCGNLFCAVHRYSDKHDCPFDYRTAARDAIAKANPVVKAEKLDKI\*

>VV13G07540

MVKGNSHTRLYEAHIPSPLPTFESLKIPFSEPQIFILQTLDMAQKTEKEETEFKVPETLALCVNNCGFTGNPATNNMCQKCFSASASAAAAAAAGALKTNGLAGGDQPGSDEGRCLSCGASVHGSARVQLRLQDRRSRGYRAGKSGSESCEDRESLNIIGQKKKNQTKIVKFRGRGSRSRSLHLSEIVLSRSTLRESALERFVESFADIKMKKVSLVCSCWINLLFSFFLLFGFFVIHDPV\*

>VV13G07550

MDHNETGCQAPPEAPILCINNCGFFGSAATMNMCSKCHKDLVLKQEQAKLAASSFESIVEGSSNCNAKESMGPNRCSSCRKRVGLTGFNCRCGNIFCAVHRYSDKHACPFDYRTAARDAIAKSNPVIKPEKLDKI\*

>VV16G03240

MDPPLCVNGCGFFGTPATQNLCSKCYKDFLKEEEEAAKAKTKSMEKAMGSTVASTSSVDDVVTSMTQLSLSSENTKKTISDDSSTKKKVERCETCKKKVGIIGFKCRCGSMFCAEHRLPEKHECSFDYKTMGREILKKQIPLIKPDKLEGRV\*

>VV16G03440

MSQRVNKKKHFKRILAMTFKSNILGINLKRVGNMEDPILCANGCGFFGTTATRNLCSKCYRDFLKEEEESTKTKVMSMKKAMGPRVESTSSLDDEKEKNSESSANKRKPATRNLCSKCYGDYLKEEGESAKAKAMSMEKAMGPRVESTSSLDYVVTSMAQLSLSSENTNKVINGDLL\*

>ZM01G32310

MAQRDKKVEEPTELRAPELTLCANSCGFPGNPATNNLCQACFLAATASSSASASVSPPPPSSSSSSPAVLQFDEQQQQQNPRPRAPAASGPTEEPPRPARASAPAPAPASSSSVRRCQTCRKRVGLTGFRCRCGDLFCGAHRYSDRHDCCFDYRAAGRDAIARDNPVVRAAKIVRF\*

>ZM01G55640

MTQKRKSIGRGGVEDCGSPARAAACTSTTAASTSTTVEEKNTPAVFETTPPLWMTGPAETKKPKIASSSSSSSSSSSSSPDGGSNNAAVAQAQPQPPPANRCSACRKKVGLLGFRCCCGKTFCGAHRYAEKHACGFDYKHAGRGRIAKENPIIVADKIAKI\*

>ZM02G32660

MAQRDKKEEPTELRAPEITLCANNCGFPGNPATQNLCQSCFSASRSPSSPTSSSSSLASAASQPRPAALVVDAAAVEALAAPAAAAVGQATEAAARASASRCSSCRKRVGLTGFRCRCGELFCGAHRYSDRHGCSYDYRGAARDAIARENPVVRAAKVVRF\*

>ZM04G15730

MAEEQQHQRWQEGHRLCANNCGFFGSPATLDLCSKCYRDLYQQQPAGAAAGPSAPTASAFQHSSSAVSGAAAVSPDLEPPATAPAGAKAGRCSSCRKRVGLTGFACRCGATFCGVHRYPERHACAFDFRAAGRDAIARANPVVKGDKLKDKI\*

>ZM04G38190

MEHKEAGCQQPEGPILCINNCGFFGSAATMNMCSKCHKEMIMKQEQAQLAASSIDSIVNGGDNGKGPAIAATVGVAVPQVEEKTIAVQPMHVAETSEAAAVIAKAKEGPNRCATCRKRVGLTGFNCRCGNTYCSMHRYSDKHDCQFDYRTAARDAIAKANPVVKAEKLDKI\*

>ZM05G23560

MEHKEAGCQQPEGPILCINNCGFFGSAATMNMCSKCHKEMITKQEQAQLAASSIDSIVNGGDGGKGPVIAASVNVAVPQVEQKTIVVQPMLVAETSEAAAVIPKAKEGPDRCAACRKRVGLTGFSCRCGNMYCSVHRYSDKHDCQFDYRTAARDAIAKANPVVRAEKLDKI\*

>ZM07G17780

MAQRDKKEEPTELRAPEIALCANNCGFPGNPATQNLCQSCFSASRSSSSSSQPSPTSSPSASAPAAAVPQPRPALLDAALQLAPPAAAAGQPVEASARTSANRCSSCRKRVGLTGFRCRCGDLFCGAHRYSDRHGCRYDYRGAARDAIARENPVVRAAKIVRF\*

>ZM09G00120

MEHKEAGCQQPEGPILCINNCGFFGSAATMNMCSKCHKEMIMKQEQAQLAASSIDSIVNGGDNGKGPAIAATVGVAVPQVEEKTIAVQPMHVAETSEAAAVIAKAKEGPNRCATCRKRVGLTGFNCRCGNTYCSMHRYSDKHDCQFRLSNCS\*

>ZM09G15600

MEHKEAGCQAPEGPILCINNCGFFGSAATMNMCSKCHKEMITKQDQAKLAASSIDSIVNGSDAVMEPVVAGSNTVVAVAQVELQTMNVQQPADVAGPSEGVAAISKGGKVGPNRCSACRKRVGLTGFNCRCGNLYCALHRYSDKHDCKFDYRTAARDAIAKANPVVKADKLDKI\*

**A3. Sequence logo for the A20 domain in 26 MdSAP genes**

>MdSAP1

NMEPPRCAKGCGFFGSVTNMNMCSKCYRECLKE

>MdSAP2

MTERPCCANGCDFYGSVETKNLCSRCYXDYLKQ

>MdSAP3

.MEPPMCASGCGFYGTVENKNMCSKCYKDHLKH

>MdSAP4

.MEPPMCASGCGFYGTVENKNMCSKCYKDHLKH

>MdSAP5

PETLTHYVNNCGVTDNPSTNNLCQKCFNTATTS

>MdSAP6

PETLTHCVNNCGVTGNPSTNNMCQKCFNAASAA

>MdSAP7

PETLTHCVNNCGVTGNPSTNNMCQKCFNAASAA

>MdSAP8

PEAPKLCANNCGFFGSPATMNLCSKCHKDLVLK

>MdSAP9

PETLTHCVNNCGVTGNPSTNNMCQKCFNAASAA

>MdSAP10

PEGPILCVNNCGFFGSAATMNMCSKCHKDMMLK

>MdSAP11

PEGHHLCANNCGFFGSPATMNLCSKCYRDFCLK

>MdSAP12

PEGHHLCANNCGFFGSPATMNLCSKCYRDFCLK

>MdSAP13

PDRPILCVNNCGFFGRAATMNMCSKCYKDTLLK

>MdSAP14

PETLTHCVNNCGVTGNPSTNNMCQKCFNAASAA

>MdSAP15

PEAPKLCANNCGFFGSPATMNLCSKCHKDLVLK

>MdSAP16

PDRPILCVNNCGFFGRAATMNMCSKCYKDTLLK

>MdSAP17

NMEPPLCAKGCGFFGSVTNMNMCSNCYRQYLKE

>MdSAP18

CQAQQLCVNNCGFFGSPTTQNLCSKCYRDLQLK

>MdSAP19

CQAQQLCVNNCGFFGSPTTQNLCSKCYRDLQLK

>MdSAP20

CQAQQLCVNNCGFFGSPTTQNLCSKCYRDLQLK

>MdSAP22

PEGHHLCANNCGFFGSPATMNLCSKCYRDFCLK

>MdSAP23

PEGPILCVNNCGFFGSAATMNMCSKCHKDMMLK

>MdSAP24

PEGPILCVNNCGFFGSAATMNMCSKCHKDMMLK

>MdSAP26

PDRPILCVNNCGFFGRVATMNMCSXCYKDTLLK

>MdSAP29

PEGHHLCANNCGFXGSPATMNLCSKCYRDFCLK

>MdSAP30

PEGHHLCANNCGFXGSPATMNLCSKCYRDFCLK

**A4. Sequence logo for the AN1 domain in 28 MdSAP genes**

>MdSAP1

QSSQGSSDSSEKKRCLSCKKRVGPTG.FECR.CGGVFCGKHRYPEEHSCCVDYKK

>MdSAP2

CSKSSSGSTSVKNRCESCNRKVGVLG.FSCR.CGGVFCGTHRYPEKHCCHVDFKM

>MdSAP3

NMGTSSVGVIKKNRCQSCSRKVGVLG.FQCR.CGGVFCGTHRYPEEHSCDVDLKQ

>MdSAP4

NMGTSSVGVIKKNRCQSCSRKVGVLG.FQCR.CGGVFCGTHRYPEEHSCDVDLKQ

>MdSAP6

ARSDESPNRRVVNRCSGCRRKVGLTG.FRCR.CGELFCSEHRYSDRHVCSYDYKA

>MdSAP7

ARSDETPNRRVVNRCSGCRRKVGLTG.FRCR.CGELFCSEHRYSDRHVCSYDYKA

>MdSAP8

NIKREEKVKETPTRCGTCRKRVGLTG.FSCR.CGDLFCAVHRYSDKHNCPHDYRT

>MdSAP9

ARSDETPNRRVVNRCSGCRRKVGLTG.FRCR.CGELFCSEHRYSDRHVCSYDYKA

>MdSAP10

SGSSGEPRPEGPKRCNTCNKRVGLTG.FNCR.CGHQFCAVHRYSDKHDCPYDYRT

>MdSAP11

RAPEVATVVSQPNRCTVCRKRVGLTG.FKCR.CGTTFCGVHRYPEKHACSFDFKT

>MdSAP12

RAPEVATVVSQPNRCTVCRKRVGLTG.FKCR.CGTTFCGVHRYPEKHACSFDFKT

>MdSAP13

SMKIEMKENKGPSRCTTCRKRVGLTG.FNCK.CGNTFCASHRYSDKHDCPFDYRT

>MdSAP14

ARSDESPNRRVVNRCSGCRRKVGLTG.FRCR.CGELFCSEHRYSDRHVCSYDYKA

>MdSAP15

NIKSEEKVKETPTRCGTCRKRVGLTG.FSCR.CGDIFCAVHRYSDKHKCPYDYRT

>MdSAP16

SMKIEMKENKGPSRCTTCRKRVGLTG.FNCK.CGNTFCASHRYSDKHDCPFDYRT

>MdSAP17

QSSQGSSDLSQKKRCLSCKKRVGPTG.FECR.CGGVFCGKHRYPEEHSCSVDYKK

>MdSAP18

EKEAAPSAGAQANRCTTCRRRVGLTG.FKCR.CGMTFCGTHRYPEQHACGFDFRG

>MdSAP19

EKEAAPSAGAQANRCTTCRRRVGLTG.FKCR.CGMTFCGTHRYPEQHACGFDFRG

>MdSAP20

EKEAAPSAGAQANRCTTCRRRVGLTG.FKCR.CGMTFCGTHRYPEQHACGFDFRG

>MdSAP21

GNCDPKNKKKPTCPVRRCKETLTFSNTSTCKTCQIKVCLKHRFPADHVCRKQTAA

>MdSAP23

SGSSGEPKPEGPKRCNTCNKRVGLTG.FNCR.CGHLFCAVHRYSDKHDCSYDYLT

>MdSAP24

SGSSGEPKPEGPKRCNTCNKRVGLTG.FNCR.CGHLFCAVHRYSDKHDCSYDYLT

>MdSAP25

PSNYEKATKKKKCPIPGCKEILTFSNTIKCRDCMVDHCLKHRFGPDHKCPGPKKP

>MdSAP26

SMKIEVKEKKGPSKCTTCRKRVGLTG.FNCK.CGNTXCASHRYSDKHDCPFDYKT

>MdSAP27

GNCDPRKKKKPTCPVRRCKEILTFSNTSTCKTCKIKVCLKHRFPADHVCQKQTAA

>MdSAP28

GNCDPRKKKKPTCPVRRCKEILTFSNTSTCKTCKIKVCLKHRFPADHVCQKQTAA

>MdSAP29

RAREVAEVVSQPNRCTVCRKRVGLTG.FKCR.CGTTFCGVHRYPEKHACSFDFKT

>MdSAP30

RAREVAEVVSQPNRCTVCRKRVGLTG.FKCR.CGTTFCGVHRYPEKHACSFDFKT