

AtNSP1	1	MAQKLEAKGGEMGDVWDDGVYENVRKVVYVGOAQYGIAFVKFEYVNGSQVVVGEHGKKT
AtNSP2	1	MVQKVEARGGEIGDVWDDGAYDGVVRKVVYVGOEDGIAFVKFEYVNGSQEVVGD
BoESP	1	-----
AtESP	1	-----
LsTFP	1	-----
AtNSP5	1	-----
AtNSP1	61	LGVEEFEIDADDYIVYVEGYREKVNDMTS--EMITFLSIKTFKGKTSHPIEKRP
AtNSP2	61	LGAEFEVDPDDYIVYVEGYHEKVFVTTKEIISTLTFKTYKGTSPPFGI
BoESP	1	-----
AtESP	1	-----
LsTFP	1	-----
AtNSP5	1	-----
AtNSP1	120	GGKIVGFHGRSTDVHLHSLGAYVSLSSITKILCRWIKVEQKCEGPGLRCSHGIAOVGNKI
AtNSP2	121	GGKIVGFHGRSTDVHLHSLGAYISSPATPKIRCKWIKVEQKCEGPGPRCSHDIAOVGNKI
BoESP	1	-----MAPSVOGEWIKVEQKGGQTPCPRSSHGIAVVGDKL
AtESP	1	-----MAPTVOGEWIKVQKGGTGPGRSSHGIAVVGDKL
LsTFP	1	-----MALTVOGEWIKVEQKGGPAPGRSSHGIAVVGDKL
AtNSP5	1	-----MCPVENKWLKVEQKCEGPGARSSHAMTVVGNKV
AtNSP1	179	YSEGGELTPNQPIDKHLVYFDLETRTWSISPATGDPVPHLSCLGVRMVSIGSSTLYIFGGRD
AtNSP2	180	YSEGGELTPNQPIDKHLVYFDLETRTWSISPATGDPVPHLSCLGVRMVSIGSSTLYIFGGRD
BoESP	36	YSEGGELTPNISIDKDLVYFDLETRTWSISPSKGVAPDVKALGTRMVSIGTKLYIFGGRD
AtESP	36	YSEGGELTPNKHIDKDLVYFDLETRTWSIAQPKGDAPTVSCLGVRMVAVGTKLYIFGGRD
LsTFP	36	YMEGGELTPQFHLIDKHLVYFDLETRTWSIAEPKGEAPSLSCLGVRMVAVGTKLYIFGGRD
AtNSP5	34	YCFGGELKPTIHLIDNDLVYFDLETRQEWISAPATGEAPFPQFVSMVTIGSSTLYIFGGRD
AtNSP1	239	ASRQYNGFYSEDTTNEWKLLTPVEE--GPTPRSFHSMADENNVYVFGGVS-----AT
AtNSP2	240	ASRKYNGFYSEDTTNEWKLLTPVEQ--GPTPRSFHSMADENNVYVFGGVS-----AT
BoESP	96	ENKFDDEYSDTIVTNEWTKLTLIDQEGGEARTYHSMASDENNVYVFGGVS
AtESP	96	ENRNFENERSMDTIVTSEWTEFLKLDDEVGGEARTYHSMASDENNVYVFGGVS
LsTFP	96	ENRNYSDFYSDTIVKKEWKFLLKLDDEERVPEARSFPAAIADENHYVIFGGVS
AtNSP5	93	DKRRYNGLHSDTETNEWKLLAPVEE--GLPGRSYHSMAGDRRVYVFGGV-----AK
AtNSP1	291	ARLNTLDSYNIIVDKKWFHCSTPGD---SLTARGGAGLEVVGKLVVVVY-----GFN
AtNSP2	292	VRLKTLDAYNIIVDHKWVQCSTPGG---SCSVRGGAGLEVVGKLVVVVY-----GFN
BoESP	156	BRFRTEAAYNIADGKWSQLPDPEGEQFPRFERRGGAGFVVVGKLVVVVYGFATS
AtESP	156	TRFRTEAAYNIADGKWAQLPDPEGD---NFEKRGGAGFAVVVGKLVVVVYGFATS
LsTFP	156	ERFKSTIVYNIADGTWSQLPNPGP---DFEPRGGAGLAVTDKLVVVVCGFANS
AtNSP5	145	GRVNTLHAMDVVDCKWVEYPAAGE---ACKGRGAPGLVVVEGRIVVLF-----GFD
AtNSP1	339	GCEVDDVHYDYPVQDKWTOVEYFGVRPSESRVFAAIAIGKHLVIFGGEIAMDP
AtNSP2	340	GCEVDDVHCYDPAQDKWTOVEYFGGKPCARSVFAAIAVVGKHLVIFGGEIAMDP
BoESP	216	DYESDQVQFYDPATQKWTEVEYTKGDKPSARSVEGHAVVGKYLIFGGEETWPD
AtESP	213	DYESNAVQFYDPASKKWTEVEYTGAKPSARSVFAAIAVVGKYLIFGAGEVWP
LsTFP	212	DYNSNKVQYDYLVSQKWIYVKTSGVKPSGRSVFAAIAVIGKQIVYIFGGEIFR
AtNSP5	193	GNELGDIHCTDLASEQKAVEYTGDPVPAARSVEPAVSYGKYLIVYFGEIEPHE
AtNSP1	399	QITDGTALDTEITLWERTDKFEGEEETPSSRGWTASTTATIDCKKGLVMHGG
AtNSP2	400	QISGGTALDTEITLWEEKLIDKLGEEETPSIRGWSASTTGTIDCKKGLVMHGG
BoESP	276	TLSDDEGALDTEITLVWERFEGG--GAEPGQ---LGNPCYTTATVYCKKGLVMHGG
AtESP	273	TLSDNEGALDTEITLVWEKLGEEGAPAIPT---RGWTAYTAATVDCNGLVMHGG
LsTFP	272	TLSDNEGALDTEITLVWEKLVDCGEPMPPT---LGNWTANCTGTVYCKTGLVMHGG
AtNSP5	253	KVSGEVQLDTEITLVWERIVCGNEEEKP--SQRGWCAFTKAVKDCGEGLLVHGG
AtNSP1	459	FDDLFFYGIDSA---
AtNSP2	460	FGDLFFYGVDSA---
BoESP	332	TDELYFYAVNSA---
AtESP	330	TDDLFFYAVNSA---
LsTFP	329	TDDFFYFSF-----
AtNSP5	312	IDDLVFWGFSHLNVN

Fig. S2: Alignment of previously known specifier proteins for primer design. Protein names are as given in Tab. 1. Amino acid sequences were aligned with the ClustalW option implemented in MEGA 5.05 [49]. White letters on black background indicate amino acid residues that are identical in at least 80 % of the sequences, white letters on gray background indicate amino acid residues that are similar in at least 80 % of the sequences. In case of AtNSP1 and AtNSP2, partial amino acid sequences starting with amino acid 120 and 121, respectively, are shown. For all other proteins, full-length amino acid sequences are included. Green boxes indicate regions of high amino acid identity that were used to design degenerate primers P1, P2, P5, and P6 (Table S2).