**Additional file 2: File S1.** Sequences of Dof genes and coding proteins used in this research.

1. **CDS sequences**

>TaDof1.1-1A

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>TaDof8.15a-3D

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>TaDof8.17-3D

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>TaDof8.18-4A

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>TaDof8.20-4D

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1. **Protein sequences of wheat Dof**

>TaDof1.1

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>TaDof1.2

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>TaDof1.3

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>TaDof1.4

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>TaDof1.5

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>TaDof2.1

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>TaDof2.2

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>TaDof2.3

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LTWPLAAGN\*

>TaDof2.4

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>TaDof2.5

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>TaDof2.6

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>TaDof2.7

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>TaDof2.8

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>TaDof2.9

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>TaDof2.10

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>TaDof2.11

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>TaDof2.12

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>TaDof2.13

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>TaDof3.1

MIFPPSFLDSSSWNDNQHAHHQQVAAASCGGGAGDGGCNNHELLQPSIMQQGTLAEGGDGGGSGGQVVGPAKPMSMSERARLARVPLPEQGLKCPRCDSANTKFCYFNNYSLSQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRAKPKQAAAAAAAGAPAASGAASGGSTTSSTTSACTTMSNPAPVLPAMLQNGGGGNLSGLLPPLLRLADFDAMSLGSTFSGMGKPSPVDSPAGYYLGGGGGGAVPGLEQWRVQQMQGFPFFQAMADQQHTLTPAAAPAMAMPGMFHYLGLGNGGDGRGVHEDDGGDQQFHHAMPSKRECYPRSGSIAMYGGDHHLTAGAGYTSSYSNAATGNHLL\*

>TaDof3.2a

MIFPPSFLDSSSWNDNQVAAASCGGGAGDGGCNNHELLQPSIMQQGTLAEGGDGGGGGGGQVVGPVKPMSMSERARLARVPLPEQGLKCPRCDSANTKFCYFNNYSLSQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRAKPKQAAAAAAAGPLAANGAASGGSTTSSTTSACTTMSNPAPVLPAMLQNGGGGNLSGLLPPLLRLADFDAMSLGSTFSGMGKPSAVDSAAGYYLGGGGGGAVAGLEQWRVQQMQGFPFFQAMADQQHTLGPAAAPAMAMPGMFHYLGLGNGGDGRGGHEDDGGNQQFHHAMPSKREGYPRSGSIAMYGGDHHLAAGAGYTSSYSNAATGNHLL\*

>TaDof3.2b

MIFPPSFLDSSSWNDNQHAHHQQVAAASCGGGAGDGGCNNHELLQPSIMQQGTLAEGGDGGGGGGGQVVGPVKPMSMSERARLARVPLPEQGLKCPRCDSANTKFCYFNNYSLSQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRAKPKQAAAAAAAGPLAANGAASGGSTTSSTTSACTTMSNPAPVLPAMLQNGGGGNLSGLLPPLLRLADFDAMSLGSTFSGMGKPSAVDSAAGYYLGGGGGGAVAGLEQWRVQQMQGFPFFQAMADQQHTLGPAAAPAMAMPGMFHYLGLGNGGDGRGGHEDDGGNQQFHHAMPSKREGYPRSGSIAMYGGDHHLAAGAGYTSSYSNAATGNHLL\*

>TaDof3.2c

MIFPPSFLDSSSWNDNQLDFEQHAHHQQVAAASCGGGAGDGGCNNHELLQPSIMQQGTLAEGGDGGGGGGGQVVGPVKPMSMSERARLARVPLPEQGLKCPRCDSANTKFCYFNNYSLSQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRAKPKQAAAAAAAGPLAANGAASGGSTTSSTTSACTTMSNPAPVLPAMLQNGGGGNLSGLLPPLLRLADFDAMSLGSTFSGMGKPSAVDSAAGYYLGGGGGGAVAGLEQWRVQQMQGFPFFQAMADQQHTLGPAAAPAMAMPGMFHYLGLGNGGDGRGGHEDDGGNQQFHHAMPSKREGYPRSGSIAMYGGDHHLAAGAGYTSSYSNAATGNHLL\*

>TaDof3.3a

MIFPPSFLDSSSWNDNQHAHHQQVAAASCGGGAGDGGCNNHELLQPSIMQQGTLAEGGDGGGGGGQVVGPAKPMSMSERARLARVPLPEQGLKCPRCDSANTKFCYFNNYSLSQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRAKPKQAAAAAAAGAPAANGAASGGSTTSSTTSACTTVSNPAPVLPAMLQNGGGGNLSGLLPPLLRLADFDAMSLGSTFSGMGKPSPVDSAAGYYLGGGGGGAVAGLEQWRVQQMQGFPFFQAMADQQHTLAPAAAPAMAMPGMFHYLGLGNGGDGRGGHEDDGGDQQFHHAMPSKREGYPRSGSIAMYGGDHHLAAGAGYTSSYSNAATGNHLL\*

>TaDof3.3b

MIFPPSFLDSSSWNDNQLDFEQHAHHQQVAAASCGGGAGDGGCNNHELLQPSIMQQGTLAEGGDGGGGGGQVVGPAKPMSMSERARLARVPLPEQGLKCPRCDSANTKFCYFNNYSLSQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRAKPKQAAAAAAAGAPAANGAASGGSTTSSTTSACTTVSNPAPVLPAMLQNGGGGNLSGLLPPLLRLADFDAMSLGSTFSGMGKPSPVDSAAGYYLGGGGGGAVAGLEQWRVQQMQGFPFFQAMADQQHTLAPAAAPAMAMPGMFHYLGLGNGGDGRGGHEDDGGDQQFHHAMPSKREGYPRSGSIAMYGGDHHLAAGAGYTSSYSNAATGNHLL\*

>TaDof3.4

MIFPPAFLDSSSCWNTNHNQLQLQQIGCNTHVTTTPSPAGHGDGGGSNNNNHGQQEGLMATAGAGGGGGEGGGGDGDSAGGGNNKPMSMSERARLARVPQPEPGLNCPRCDSTNTKFCYFNNYSLTQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRSAKPKAGSAGSGSAAAGTSSATSTTPSTTACTTGTATAPPALQYSMFGSAPPHGSRFANSFDPASLGLSFPARLLFPDSGAYAADGGAQQQHHHHQGNGNGMEQWAAAQMQSFPFLHAMDHQMSGNQPPASAMPTTMAAMQGMFHLGLQSGGGGGNGDDGGNQQFHHPPAKRDYHQQQQQDYPSSRGMYGDVVNGNGGGFNFYSSTSNAAGN\*

>TaDof3.5

MAIMEIDRPRGGALLKRRRLASPAMIFLPAFLDSSDFWNTDHNQLQLQQIGTSTHSTTTSSPDGPGDGGCNNNNPKGFMATTGADYGVAGGGDDGCGGAGDGDCSRGRNNKSISMSERARLARLPHPVPGLNCPRCESTNTKFCYFNNYSLTQPRHFCRSCSRYWTRGGVLRNVPVGGGYRRHAKRRAKPKVVSATSRASTVGKSSVTPTMSSSTTYATGTDISPPRLQYPIFGSTPSHDSQFSGIFDPANLGLGFPVRLLFAESDAYTVDGCAHHHHHHAHGNGMEQLLEAQNSFPFMHAMDHHMSGLPAEAMPITMATMQGMFHLGLQSVRGGHGDEIAGQQLHYPPAKRNHKHQDYASSRGMHRDVVNGNGTGDYI\*

>TaDof3.6

MIFLPAFLDSSDFWNTDHNQLQLQQIGTSTHSTTTSSPDGPGDGGCNNNNPKGFMATTGADYGVAGGGDDGCGGAGDGDCSRGRNNKSISMSERARLARLPHPVPGLNCPRCESTNTKFCYFNNYSLTQPRHFCRSCSRYWTHGGVLRNVPVGGGYRRHAKRRAKPKVVSATSRASTVGKSSVTPTMSSSTTYATGTDISPPRLQYPIFGSTPSHDSQFSDIFDPANLGLGFPVRLLFAESDAYTVDGCAHHHHHHAHGNGMEQLFEAQNSFPFMHAMDHHMSGLPAEAMPITMATMQGMFHLGLQSVRGGHGDEIAGQQLHYPPAKRNHKHQDYASSRGMHRDVVNGNGTGGYI\*

>TaDof3.7

MAGGGGGDGGKLMSMCERARLAGVPQPESGLNCPRCDSTNTKFCYFNNYSLTQPRHFCRACRRSWTRGGALRNVPVGGRYRRHAKRSAKPKAASTASGDGAGTSSATSMTPNTTFTTTSSPALQYFMFGSAPPQDLLIDSFDPTSLGLSFPANLLFAEGGDYAVEGDVHHHQQGNETDMAQMQSFPHAMDHQMAGQLAVAMPTTMAAMQDMFQQVLQSGGNGDDGGDHHFHHHHQQDYASSRAIYRDVVNGNGGGGYNFYSSTSNAPGN\*

>TaDof3.8

MIFPPAFLDSSSCWNTNHNQLQLQQIGSNSHITTTPSPAGHGPGDGGGGNNNNHGQQEGLMATAGAGGGGGDGGGGGGGDGDSAGGGNNKPMSMSERARLARVPQPEPGLNCPRCDSTNTKFCYFNNYSLTQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRSTKPKAGSAGSGTAAAGTSSATSTTPSTTACTTGTATAPPALQYSMFGSAPPHGSRFADSFDPASLGLSFPARLLFPDNGAYAADGGAQQHHHHQGNGNGMEQWAAAHMQSFPFLHAMDHQMSGNPQSASAMPTTMAAMQGMFHLGLQSGGGGGNGDDGGNHQFHHQPAKRDYNQQQQQDYPSSRGMYGDVVNGNGGGFNFYSSTSNAAGN\*

>TaDof3.9

MIFLPAFLDSSNFWNTDHNQLQLQQIGTNTHSTTTSSPAGPGDGECKNSNKKRFMATAGAGSGAAGGGDDGCGGAVDGDCGGIGNKKSRSMSERARLARLPQPVPGLNCPRCDSTNTKFCYFNNYSLTQPRHFCRSCSRYWTRGGALRNVPVGGGCRRNTKRRAKPKVVSATSRAAMVGTSSVTSTMSSSTTYVTGTGTTPPRLQYPMFGSVPSHDSQFADSFDPANLGLIFPVRLLLADSDASAVDGCAQQHHHHAHGNGMEQLSVAQDSFPFMYAMDHQMSGLSAQAMPITMGTMQGMFHVGLQGIGGGNGDEIGGQQLHHPPAKRNHKQQDYPSSRDMYGDVVNANGGVGYI\*

>TaDof3.10

MIFLPAFLDSSNFWNTDNNQLQLQQIGTNTHSTTTPSPSGPGDGGCNSNNEEGFMATAGVGLVAGGGGNDGCSGAGDGDCSTNRNSKSMSMSERAQLVRLPQPVSGLNCPRCDSTNTKFCYFNNYSLTQPRHFCRSCRRYWTRGGALRNVPVGGGYRRHAKRRGKPNVVSNTSRSTAVGTSSVTTTMSSSTTYATGSGPVPPGLHSPMFGSAPSHDSQFAHSFDQASLRLSSPDRLLFADGGSCTVDGCAQHHHNHAHWNGMEQWSAAQMGSFQFMHAMDHQMSGAMPITMATMQGMFHLGLQSVAGGKDDNRGGHQLYHPSAKRNHKQQDYSSSRGMYEDMVNGNGGGGYI\*

>TaDof3.11

MIFLPAFLDSSNFWNTDHNQLQLQQIGTNTQSTTTPSPAGPGDGGCNNNNEEGFMATAGAGSVAGGGGNDGCSGAGDGDCSKSGNSKSMSMSERAQLAGLPQPVSGLNCPRCDSTNTKFCYFNNYSLIQPRHFCRSCRRYWTRGGTLRNVPVGGGYRRHAKRRGKPNVVSNTSRSTAVGTSSVTTTMSSNTTYATGTGPVPPGLQGPMLGSAPSHDSQFAHRIDPASLGLSFPDRLLFADGGSCAVDGCAQHHHNHAHWYGMEQWSAAQIGSFPFMHAMDHQMSGAMPITMATMQGMFHLGLQSVGGGKDDNRGGHLLHHKQQDYSSSRGMYGDMVNGELDQDLFLD\*

>TaDof3.12

MIFPPAFLDSSSCWNTNHNQLQLQQIGSNTHVTTTPSPAGHGPGDGGGSNNNNHGQQEGLMATAGAGGGGGDGGGGGGGDGDSAGGGSNKPMSMSERARLARVPQPEPGLNCPRCDSTNTKFCYFNNYSLTQPRHFCRACRRYWTRGGALRNVPVGGGYRRHAKRSAKPKAGSAGSGTAAAGTSSATSTTPSTTACTTGTATAPPALQYSMFGSAPPHGSRFADSFDPASLGLSFPARLLFPDSGAYAADGGAQQHHHHHQGNGNGMEQWAAAQMQSFPFLHAMDHQMSGNQPPASAMPTTMAAMQGMFHLGLQSGGGGGGNGDDGGNHQFHHPPAKRDYQQQQDYPSSRGMYGDVVNGNGGGFNFYSSTSNAAGN\*

>TaDof3.13

MIFLPAFPDSSTFWNTDHNQLQLQQFGTNNHSTTTFSPASPSDGECSNNNNNNNNNNNNN

NNNNNNNNNNNNNKNNNQKRFMAMAKAGSCAAGGGDDGCGGAGDGDCGGNGKSKSMSMSERARLARLPQPVSGLNCPRCDSTNTKFCYFNNYSLTQPRHFCRSCRRYWTHGGMLRNVPVGGGYRRHAKRRAKPKVVSDTSRAAMVGTSSVTSTMSSSTTYVTGTGTAPPRLQYPMFSSAPSHDNQFVDSFDPANIGLSFPIRLLFADSDAYAMDDCAQNHHHHAHGNGMEQLSATRNSFPFIHVVDHQMSGLPAEAMPITMAAMEGMFHLRLQSVGGGTGDEIGGQQLHHPLAKRNHKRQDYPSSRGMYRDVVNGNCGGDYI\*

>TaDof3.14

MVFPPAAAYLDPPNWNNQQGQQQRATGGGGVGDAQHMPVDPTAGTAAGTPEVGGLPRSSAANEAAAGQQARPNSMTERARMARVPQPEPALKCPRCDSTNTKFCYYNNYSLSQPRHFCKACRRYWTRGGALRSVPVGGGCRRNKRSSKSSAGAASSSKPSSSSARQLPGGASSMPSTAASTTLGCDGASIPPGLSSMSHHLPFMGAMHPPGANLGLAFSAGLPQLAMQQHHHHMDGVDQFPLASGGGATFGASLEQWRVQQQQQQQFPFLELPPAPPMYQLGLQANRAAGSSAAAPAPSPAMFTLGQSSASTARRDEGSMKQADSKGQEMTLQRQFVMEALRQGDGVWGGNASDNNGNGSGSWTMNIPGFHSSSGGGDGGGLL\*

>TaDof3.15

MVFPPATAYLDPPNWNNQQGQQQRATGGGGVGDAQHMPEGPTAGTPEVGGLPRSSAANEAAAGQQARPNSMTERARMARVPQPEPALKCPRCDSTNTKFCYYNNYSLSQPRHFCKACRRYWTRGGALRSVPVGGGCRRNKRSSKSSAGAVSSSKPSSSSARQLPGVASSMPSTAASTTLGADGASIPPGLSSMSHHLPFMGAMHPPGANLGLAFSAGLPQLAMQQHHHHMDGVDQFPLASGGGATFGASLEQWRVQQQQQQFPFLELPPAPPMYQLGLQASRAAGSSAAAPAPSPAMFTLGQSSASIARRDEGSMKQADSKGQEMTLQRQFMMEALRQGDGVWGGNASDNNGNGSGSWTMNIPGFHSSSGGGDGGGLL\*

>TaDof3.16

MVFPPAAAYLDPPNWNNQQGQQQRTTGGGGVGDAQHMPVGPTAGTAAGTPEVGGLPRSSAANEAAAGQQARPNSMTERARMARVPQPEPALKCPRCDSTNTKFCYYNNYSLSQPRHFCKACRRYWTRGGALRSVPVGGGCRRNKRSSKSSAGAASSSKPSSSSARQLPGGASSMPSTTASTTLGADGASIPPGLSSMSHHLPFMGAMHPPGANLGLAFSAGLPQLAMQQQHHHMDGVDQFPLASGGGATFGASLEQWRVQQQQQFPFLELPPAPPMYQLGLQANRAAGSSAAAPAPSPAMFTLGQSSASTARRDEGSMKQADSKGQEMTLQRQFMMEALRQGDAVWGGNASDNNGNGSGSWTMNIPGFHSSSGGGDGGGLL\*

>TaDof3.17a

MVFSSFPIFLDPPSWTQMQQQPLQCFMGGGGGSEHQHHQLIPASSGQLAPLPDVPGSTAASAPAVAGSSSASLQLVVSGQQGNPGEQPPRPSVSMTERARMARVPLPEPGTLRCPRCDSANTKFCYFNNYSLSQPRHFCKACRRYWTRGGALRNVPVGGGCRRNTKRSSKKSSRQGQGGGGAVAAATSSSSTTSTSTTTSAAAATAADVIASMQALPHHLGGLPAAAALEASLEGYHSHSHHQHHNLPFLPPQFLQQGLHGYHFADGDIGSQLADGFPRGVASGLLAQLASIKMEEHGAGAAGAGGGFVGGHEQYWPGSGGGGGWPTEFLSGFSSSSSGNVM\*

>TaDof3.17b

MVFSSFPIFLDPPSWTQQPLQCFMGGGGGSEHQHHQLIPASSGQLAPLPDVPGSTAASAPAVAGSSSASLQLVVSGQQGNPGEQPPRPSVSMTERARMARVPLPEPGTLRCPRCDSANTKFCYFNNYSLSQPRHFCKACRRYWTRGGALRNVPVGGGCRRNTKRSSKKSSRQGQGGGGAVAAATSSSSTTSTSTTTSAAAATAADVIASMQALPHHLGGLPAAAALEASLEGYHSHSHHQHHNLPFLPPQFLQQGLHGYHFADGDIGSQLADGFPRGVASGLLAQLASIKMEEHGAGAAGAGGGFVGGHEQYWPGSGGGGGWPTEFLSGFSSSSSGNVM\*

>TaDof3.18

MVFSSVPLYHDPPNWNQNHNQQQQQQQLQQQQQQQQQQLSHHGQMFASGGGGGGVDMHHHHHQQQQQQQYQQQQQHQHQHQLRPPVPPPGALMAPRPDGMGSAVALSGAGGGGGGAGGGPTGGAVVRPGSMTDRARMAKIPQPEPGLKCPRCESTNTKFCYFNNYSLTQPRHFCKTCRRYWTRGGTLRNVPVGGGCRRNKRTKSSKSSSSAASASGGGTSSSTTSSTTTAGGANGNGNGNGNRNGSSAAAAAGAMMSSQGQGHAQMPFFGSLHPLGAGSGDHYGTGASRLGFPGLINSLDPVDYQLGGGGAAAAAMGLSEQWRLPQMQQFPFLGRADGMHQQQQQMAGLYPFDATDASGFAGEMMGGVGGSKQLVPGSAGLITQLASVKMEDNPPSNNAMAGAASAREFLGLPGNIQFWGGGNNGAGGNDNGGSHSSGTVAPGGAGGGGGWVDQLPGFNSSSSGNIL\*

>TaDof3.19a

MVFSSFPIFLDPPSWAQPLQCFMGGGGGSEHQHHQLIPASSGQLAPLPDVPGNTAASAPPVAGSSSASLQLVVSGQQGNPGEQPPRPSVSMTERARMARVPLPEPGTLRCPRCDSANTKFCYFNNYSLSQPRHFCKACRRYWTRGGALRNVPVGGGCRRNTKRSSKKSSRQGQGQGGGGAVAAATSSSSTTSTSTTTSAAAATAADVIASMQALPHHLGGLPAAAALEASLEGYHSHSHHQHHNLPFLPPQFLQQGLHGYHIADGDIGSQLADGFPRGVASGLLAQLASIKMEEHGAGAGGAGGGFVGAHEQYWPGSGGGGGWPTEFLSGFSSSSSGNVM\*

>TaDof3.19b

MVFSSFPIFLDPPSWAQQPLQCFMGGGGGSEHQHHQLIPASSGQLAPLPDVPGNTAASAPPVAGSSSASLQLVVSGQQGNPGEQPPRPSVSMTERARMARVPLPEPGTLRCPRCDSANTKFCYFNNYSLSQPRHFCKACRRYWTRGGALRNVPVGGGCRRNTKRSSKKSSRQGQGQGGGGAVAAATSSSSTTSTSTTTSAAAATAADVIASMQALPHHLGGLPAAAALEASLEGYHSHSHHQHHNLPFLPPQFLQQGLHGYHIADGDIGSQLADGFPRGVASGLLAQLASIKMEEHGAGAGGAGGGFVGAHEQYWPGSGGGGGWPTEFLSGFSSSSSGNVM\*

>TaDof3.19c

MVFSSFPIFLDPPSWAQMQQQPLQCFMGGGGGSEHQHHQLIPASSGQLAPLPDVPGNTAASAPPVAGSSSASLQLVVSGQQGNPGEQPPRPSVSMTERARMARVPLPEPGTLRCPRCDSANTKFCYFNNYSLSQPRHFCKACRRYWTRGGALRNVPVGGGCRRNTKRSSKKSSRQGQGGGGGAVAAATSSSSTTSTSTTTSAAAATAADVIASMQALPHHLGGLPAAAALEASLEGYHSHSHHQHHNLPFLPPQFLQQGLHGYHIADGDIGSQLADGFPRGVASGLLAQLASIKMEEHGAGAGGAGGGFVGAHEQYWPGSGGGGGWPTEFLSGFSSSSSGNVM\*

>TaDof3.20

MVFSSVPLYHDPPNWNQNHSQQQQQQLQQQQQQQLSQHGQMFASGGGGGGMEMHHHHQQQQHQQYQQQQLQQHQLRPPVPPSGALMAPRPDGMGSPVALSGAGGGGGGAGGGLTGGAVVRPGSMTDKARMAKIPQPEPGLKCPRCESTNTKFCYFNNYSLTQPRHFCKTCRRYWTRGGTLRNVPVGGGCRRNKRTKSSKSSSSAASASGGGTSSSTTSSTTTAGGGNGNGSTAAGAAGAMMSSQGQGHAQMPFFGSLHPLGAGSGDHYGTGASRLGFPGLINSLDPVDYQLGGGGAAAAAMALSEQWRLPQMQQFPFFGRADGMHQQQQQMAGLYPFDATDASGFAGEMMGGVGGSKQLVPGSAGLITQLASVKMEDNPPSNNSMAGAASAREFLGLPGNIQFWGGGNNGAGGNENGGSHSSGTVAPGGAGGGGGWVDQLPGFNSSSSGNIL\*

>TaDof3.21.1

MVFSSFPIFLDPPSWTQQQQPLQCFMGGGGGSEHQHHQLIPASTGQLAPLPDVPGNTAASAPAVAGSSSASLQLVVSGQQGNPGEQPPRPSVSMTERARMARVPLPEPGTLRCPRCDSANTKFCYFNNYSLSQPRHFCKACRRYWTRGGALRNVPVGGGCRRNTKRSSKKSSRQGQGQGGGGAVAAATSSSSTTSTSTTTSAAAATAADVIASMQALPHHLGGLPAAAALEASLEGYHSHSHHQHHNLPFLPPQFLQQGLHGYHFADGDIGSQLADGFPRGVASGLLAQLASIKMEEHGAGAGGTGGGFVGAHEQYWPGSGGGGGWPTEFLSGFSSNSSGNVM\*

>TaDof3.21.2

MVFSSFPIFLDPPSWTQMQQQQPLQCFMGGGGGSEHQHHQLIPASTGQLAPLPDVPGNTAASAPAVAGSSSASLQLVVSGQQGNPGEQPPRPSVSMTERARMARVPLPEPGTLRCPRCDSANTKFCYFNNYSLSQPRHFCKACRRYWTRGGALRNVPVGGGCRRNTKRSSKKSSRQGQGQGGGGAVAAATSSSSTTSTSTTTSAAAATAADVIASMQALPHHLGGLPAAAALEASLEGYHSHSHHQHHNLPFLPPQFLQQGLHGYHFADGDIGSQLADGFPRGVASGLLAQLASIKMEEHGAGAGGTGGGFVGAHEQYWPGSGGGGGWPTEFLSGFSSNSSGNVM\*

>TaDof3.22

MVFSSVPLYHDPPNWNQNHSQQQQQQQQQLQQQQQLSHHGQMFASGGGGGGMEMHHHHQQQQHQQYQQQQHHHQLRPPVPPSGALMAPRPDGMGSAVALSGAGGGGAGAGAGGGPTGGAVVRPGSMTDKARMAKIPQPEPGLKCPRCESTNTKFCYFNNYSLTQPRHFCKTCRRYWTRGGTLRNVPVGGGCRRNKRTKSSKSSSSAASASGGGGTSSSTTSSTTTAGGGNGNGSSAAAAAGAMMSSQGQGHAQMPFFGSLHPLGAGSGDHYGTGASRLGFPGLINSLDPVDYQLGGGGAAAAAMGLSEQWRLPQMQQFPFFGRADGMHQQQQQMAGLYQFDATDASGFAGEMMGGVGGSKQLVPGSAGLITQLASVKMEDNPPSNNAMAGAASAREFLGLPGNIQFWGGGNNGAGGNENGGSHSSGTVAPGGAGGGGGWVDQLPGFNSSSSGNIL\*

>TaDof4.1

MVNNFRNKSQCKFCGSQPMHTCIMQNGQDYNMQQTSIQNPSQAAGYCPVYQPLLARGQDQYTSFSNASSQLAFPNLSAYTTLNDIRQWTSIPEGEISVEDVHPLIVPTQIQETYGSFRCGQVLLQWDKPHMEPKEHWNFLDELMPLHSTQSRFYGESLPSTSLMDKAHKLLASTSSGDSVLKMITGVTSRATQTPQRRGVLIRPIEPYDSNADIFRPPVKKQRNAKYQLRFVNRVCNDYYTQEQIKSGDGSLLKVALYDENNRVVTSGPLSSASVEVVLLHGDFNVEGQDYWTSEEFSACLVHSQSLEEPPALGGDRVLALTDGEAALGNVSFQISSFHARTGKFKMGVEIKNVREESVQQGITSPFLVRVRQGEESSHHRITSPEALLRVRMELPKQVCGALQCDARERASSDQSSPERNVLVASKVEDHDSIVQSGSGVLLFPAPPPSSEQARVPQPEPGLKCPRCDSTNTMFCYFNNYSLTQPRHFCQACRRYWTRGGALRNVPSCHAKRSAKRSAKRCAKSKASAGEPAATATPSSALTATKPNTTSCIGAAPPGLHQYSMFCTKSESPHSNRFADNFDLASLRLGFPARLLFADGGVHHQPVLQGMFDLGLQSGGGNCEDGASSTTK\*

>TaDof4.2

MEEVFPSNSKSKAGQMAGEATAAAEKKPRPKPEQKVECPRCKSGNTKFCYYNNYSMSQPRYFCKACRRYWTHGGSLRNVPIGGGCRKPKRPGTSDAHKLGVASSSEPTVVMPPSTCTGMNFANVLPTFMSAGFEIPSSLSLTAFGSSSSSNTAAVMSPGGTTSFLDVLRGGAGGLLDGSLSQNNGYYYGGPATGSGIGMLMTPPVASFGIPGPMQQHGDLVVGGNGIGAATASIFQGGTGEEGDDGTGGVMGLQWQPQVGNGGGAGVVSGGVHHLGTGNNVTMGNNNIHNNNNNNSGGDDNNGASSRDCYWINNGGSNPWQSLLNNSSLMITQVEVPH\*

>TaDof4.3

MFCCWPQVLKMEEVFPSNSKSKAGQMAGEATAAAEKKPRPKPEQKVECPRCKSGNTKFCYYNNYSMSQPRYFCKACRRYWTHGGSLRNVPIGGGCRKPKRSGTSDAHKLGVASSSEHTAVMPPSTCTGINFANVLPTFMSAGFEIPRSLSLTTFGSSSSSNTTAVMSPGGTTSFLDVLRGGTGGLLDGNLGQNNGYYYGGSRSGIGMLMTPPAASFGIPGPMQQHGDLMVGGNGIGAATASIFQGGTGEEGDDGIGAMMGLQWQPHVGNGGGGGVVSGGVHHLGTGNNVTMGNNNINNNNNNGSHSDDNTGGSSRDCYWINNGGSNPWQSLLNSSSLM\*

>TaDof4.4

MRLLLHNLLQYRMEEVFPSNSKSKAGQMAGEAIAGAEKKPRPKPEQKVECPRCKSGNTKFCYYNNYSMSQPRYFCKACRRYWTHGGSLRNVPIGGGCRKPKRSGTSDAHKLGVASSPEPTTVVPPSTCTGMNFANVLPTFMSVGFEIPSSLSLTAFGSSSSSNTAAMMSPGGTTSFLDVLRGGAGGLLDGSLSQNNGYYYGGPAIGSGNGMLMTPPAVSFGIPVPMQQHGDLVVGGNGIGAATASIFQGATSEEGDDGMGGVMGLQWQPQVGNGGGGGGVSGGVHHLGTGNNVTMGNSNIHNNNNNDSGGDDNNGGSSRDCYWINNGGSNPWQSLLNSSSLM\*

>TaDof4.5

MMAGAAHPMHFCMDSDWLKGIVPEDQGGMGSSSPSEELIIACPEPMQAQQAADRRLRPQHDQPLKCPRCDSTHTKFCYYNNYSLSQPRYFCKTCRRYWTKGGSLRNVPVGGGCRKNKRASAAKKPSAAAVITPPISMMQQLHHGRHMAETGLHLSFSGMQPPAVSAADPLCSLGLFDWKYDHILSGSGGFESANSEAHFTGPGMMGIANGSGGGGAEYHALNALRYAAGLGEHLALPFGGATSRAERDSVVAEMKPQAERLLSLEWCGEASRAPTETSISSLGGLGLWSGMITGATHHHHGSSAAI\*

>TaDof4.6

MMAGAAHPMHFCMDSDWLKGIVPEDQGGMGSSSPSGELIIACPEPMQAQQAADRRLRPQHDQPLKCPRCDSTHTKFCYYNNYSLSQPRYFCKTCRRYWTKGGSLRNVPVGGGCRKNKRASAAKKPSAAAAIAPPISMMQQLHHGRHMAETGLHLSFSGMQPPAVSAADPLCSLGLFDWKYDHILSGSGGFESANSEAHFTGPGMMGIANGSGGGGAEYHALNALRYAAGLGEHLALPFGGATSRAERDSVVAEMKPQAERLLSLEWCGEASRAPTETSISSLGGLGLWSAMITGAAHHHHGSSAAI\*

>TaDof4.7

MMAGAAHPMHFCMDSDWLKGIVPEDQGGMGSSSPSGELIIACPEPMQAQQAADRRLRPQHDQPLKCPRCDSTHTKFCYYNNYSLSQPRYFCKTCRRYWTKGGSLRNVPVGGGCRKNKRASAAKKPSAAAAIAPPISMMQQLHHGRHMAETGLHLSFSGMPPPPVSAADPLCSLGLFDWKYDHILSGSGGFESANSEAHFTGPGMMGIANGSGGGGAEYHALNALRYAAGLGEHLALPFGGATSRAERDSVVAEMKPQAERLLSLEWCGEASRAPTETSISSLGGLGLWSGMVTGAAHHHHGSSAAI\*

>TaDof5.1

MLSSHCESMLAYAAAAGRRAMLVDPRRYRPNVEVAPNCPRCDSPNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKPVRSMAEADTASPSHGAAVFSHRFHGPVRPDLLLEGMVGNPAELAQPEPGEAEKPAGAADGPTIDLALLYSKFLSQQPLAEQGAVVPESAGPSSGSSTEMSPPALSSPGQHGLGEICGPASSTEPSATTMLQCADARAHALGEFNFSVDQSCYDSLGLPTDGADLTMLPPAWDQEAKYEPFSSLPDQEDAMSLHDAVPAGDDVWSKVLGCQGLEAALSAGLDRC\*

>TaDof5.2

MLSSHCESMLAYAAAAGRRAMLVDPRRYRPNVEVAPNCPRCDSPNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKPVRSMAEADTASPNHGAVVFSHRFHGPVRPDLLLEGMVGNPAELGQQPASAEADKPAGAADGPTIDLALLYSKFLSHQPLAEQCAVVPESADTSSGSSTEMSPPTLSGPSQHGPGEICGPASSTEPSATTMLQCADARAHALGEFNFSVDQSCYDSLGLPTDGGDLTMLPSAWDQEAKYEPFSSLPEEDAMSLHEGVPAGDDVWSKVLGCQGLEAALAAGLDRC\*

>TaDof5.3

MAYRGKHLVLASAALPPSHVYIRLPPLSPLASASFQILSHHRIPTFPRSPACLLISSSPIVAMLSSHSESMLAYAAAAGRRAMLVDPRRYRPNVEVAPNCPRCDSPNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKPVRSMAEADTASPNHGAAVFSHRFHGPVRPDLLLEGMVGNPAELGQPSSTEAEKPAGAADGPTIDLALLYSKFLSHQPLAEQCAVVPESADTSSGSSTEMSPPALSSPGQHRLGEICGPASSTEPSATTMLQCGDARAHALGEFNFSVDQSCYDSLGLPTDGGDLTMLPSAWDQEAKYEPFSSLPEEDAMSLHEGVPAGDDVWSKVLGCQGLEAALSAGLDRC\*

>TaDof5.4

MDAAHWPQGLGLVKPMEEMLMGAPSSNQQVQGSNPNPPAQAPSSAPGAGGPMRGGTPAMAVAASGVGAGSTERRPRPQKEKAINCPRCNSTNTKFCYYNNYSLQQPRYFCKTCRRYWTEGGSLRNVPVGGGSRKNKRSSSSSASASASAAASATASVANSSMLGAAPNKNPKLAHEGAAHDLNLAFPHHQGGMQAQADYMAFPSLESSSMCNPGGGGMAANGARAGGALSAMELLRSTGCYMPLQMPMQMPGEYGAAGFSLGEFRAPAPPQSQSLLGFSLDAHGSVGGASMAGYGSGAGMQGMQDRSGRLLFAFEDLKPTANSGAGGGESGGGSGAGVDGGDHQFEQGNKEQQGNGTPVGQPDTPGFWNGMIGGGGTW\*

>TaDof5.5

MDAAHWPQGLGLVKPMEEMLMGAPSANQQVQGSNPNPPAQAPSSAPGTGGPMRGGTPAMAVAGSGAGAGSTERRPRPQKEKAINCPRCNSTNTKFCYYNNYSLQQPRYFCKTCRRYWTEGGSLRNVPVGGGSRKNKRSSSSSASASASAAASATASVANSSMVGAAPNKNPKLAHEGAAHDLNLAFPHHQGGMQADYMAFPSLESSSMCNPGGGAMAGNGARAGGALSAMELLRSTGCYMPLQMPMQMPGEYGAAGFSLGEFRAPAPPQSQSLLGFSLDAHGPVGGASTAGYGSSAAMQGLQDRSGRLLFAFEDLKPTANSGAGGGESGGGSGAGVDGGDHQFEQGNKEQQGNGTPVGQPDTPGFWNGMIGGGGTW\*

>TaDof5.6

MDAAHWPQGLGLVKPMEEMLMGAPSANQQVQGSNPNPPAQAPSSAPGAGGPMRGGTPAMAVAGSGAGAGSTERRPRPQKEKAINCPRCNSTNTKFCYYNNYSLQQPRYFCKTCRRYWTEGGSLRNVPVGGGSRKNKRSSSSSASASASAAASTTASVANSSMLGAAPNKNPKLAHEGAAHDLNLAFPHHQGGMQAQADYMAFPSLESSSMCNPGGGGMAANGARAGGALSAMELLRSTGCYMPLQMPMQMPGEYGAAGFSLGEFRAPAPPQSQSLLGFSLDAHGPVGGASTAGYGSGAGMQGMQDRSGRLLFAFEDLKPTANSGAGGGESGGGSGAGVDGGDHQFEQGNKEQQGNGTPVGQPDTPGFWNGMIGGGGTW\*

>TaDof5.7

MLSSHPHEAAMLPYVPRPPSLLVDRRYSTGAEVAPNCPRCDSPNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKSSVRSASDSFSGVRDATFGHGGFPGPLRPDMVLEGMVGNPANPGQVMHDVPTAPDGSSIDLAMLYSKFLNNQQPAGDGSLVGSVTPESAGGHVDETFDTFSASSDMSPAGVLAPAQFDASPDGFLEWSRPVSSADPTCTASPATATTMLCTDESVQAALGELNFAMDQSCFDSLGLPTDGAAANLSSWCSIVPSLSTWEEPKYDSLDSFPDDTLSLHDGILAADHDWSADCQGLEALYMP\*

>TaDof5.8

MLSSHPHEAAMLPYVPRPPSLLVDRRYSTGAEVAPNCPRCDSPNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKSSVRSTSDSFSGVRDAAFGHGGFPGPLRPDMVLEGMVGNPANPGQAMHDVPTAPDGSSIDLAMLYSKFLNNQQPAGDGSLVGSVTPESAGGHVDETFDTFSASSDMSPGGVLAPAQFDASPDGFLEWSRPVSSADLNCTASPATATTMLCTDESVQAALGELNFAMDQSCFDSLGLPTDGAAANLSSWCSIVPSLSTWEEPKYDSLDSFPDDTLSLHDGILAADHDWSADCQGLEALYMP\*

>TaDof5.9

MLSSHPHEAAMLPYVPRPPSLLVDRRYSTGAEVAPNCPRCDSPNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKSSVRSASDSFSGVRDATFGHGGFPGPLRPDMVLEGMVGNPANPGQGMHDVPTAPDGSSIDLAMLYSKFLNNQQPAGDGNLVGSVTPESAGGHVDETFDTFSASSDMSPSGLLPPAQFDASPDGFVDWSRPVSSADPTSTASPATATTMLCTDESVQAALGELNFAMDQSCFDSLGLPTDGAAANLSSWCSIVPSLSTWEEPKYDSLDSFPDDTLSLHDGILAADHDWSADCQGLEALYMP\*

>TaDof5.10

MDAAQWHQGLGLVKPMEEMIMAGNPNPNPNSNGNPNPQPAPPSGAEAQRAPVPGPPAAGAGAAAGTGSTERKAARPQKEKAINCPRCNSTNTKFCYYNNYSLQQPRYFCKTCRRYWTEGGSLRNVPVGGGSRKNKRSSSSVVSSAAGAVSTSAAASGTVPVGGMGAKNPKLMHEGAHDLNLAFPHHHGRVLHPSEFAAFPSLESSSVCNPGGAMAANGAGGGRGMGAFSAMELLRSTGCYVPMPQVQLGMPPEYAAAGFALGEFRMPLQHQQHHQQQQQQQQHHQQQQQQVQNMLGFSLDTGGGGDAGGYGAGLQGAQESATGRMLFPFEDLKPGANPSGGGASGGDQFEHSKDQGGGGGGHETLGFWNNSMIGNGSSNDAGGGGGGGGGSW\*

>TaDof5.11

MDAAQWHQGLGLVKPMEEMIMAGNPNPNSNGNPNPQPAQPSGTEAQRAPVPGPPAAGAGAAAGTGSTERKAARPQKEKAINCPRCNSTNTKFCYYNNYSLQQPRYFCKTCRRYWTEGGSLRNVPVGGGSRKNKRSSSSVVSSAVGAVPTSAAVSGTVPVGGMAAKNPKLMHEGAHDLNLAFPHHHGRVLHPSEFAAFPSLESSSVCNPGGAMAANGAGGGRGMGAFSAMELLRSTGCYVPMPQVQLGMPPEYAAAGFALGEFRMPLQHQQHHHQQQQQQHHQQQQHQVHNMLGFSLDTGGGGDAGGYGAGLQGAQESATGRMLFPFEDLKPGANPNGGGASGGDQFEHSKDQGGGGGHETLGFWNNSMIGNGSSNDAGGGGGGGGGSSW\*

>TaDof5.12

MDAAQWHQGLGLVKPMEEMIMAGNPNPNPNPNGNPNPQPAPPSGAEAQRAPVPGPPAGGAGAAAGTGSTERKAARPQKEKAINCPRCNSTNTKFCYYNNYSLQQPRYFCKTCRRYWTEGGSLRNVPVGGGSRKNKRSSSSVVSSAAGAVSTSGAASGTVPIGGMAAKNPKLMHEGAHDLNLAFPHHHGRVLHPSEFAAFPSLESSSVCNPGGTMAANGAGGGRGMGAFSAMELLRSTGCYVPMPQVQLGMPPEYAAAGFALGEFRMPLQHQQHHQQQQQQQHQQHQQQVQNMLGFSLDTGGGGDAGGYGAGLQGAQESATGRMLFPFEDLKPGTNAGGGGASGGDQFEHSKDQGGGGGGGHETLGFWNNSMIGNGSSNDAGGGGGGGGGSW\*

>TaDof7.1

MVRITAMDQLEAEEVVVRAPAASGGVRRAGEPERLAQCPCPRCESTDTKFCYYNNYNLSQPRHFCRGCRRYWTRGGALRNVPVGGGTRKPNGSPAAVRRKRPSHSHSHSHHAVPAAAASQAAPVVPLSVSAPAPLPLPLLQPQPQPQPQQYELTFLPASLSAVDPDRRLLDLGGSFSSLLAPPAPLLPNFATSFVFGGAGAGMAMAHAHVPALPQPAPVASQALPESFWGMGWPDLSI\*

>TaDof7.2

MANLPTHATNADASAFKLFGQVIQPDAHRAASAPASTSISAGQSAAAPPPPPPPPPPPSTTQQAAVGGEPLPCPRCGSRETKFCYFNNYNVRQPRHLCRACRRYWTAGGALRRVATASPGRRRPRPSARSAAAAASATASASEEGAAAESVDSRS\*

>TaDof7.3

MDQLEAEEVVVRAPAPTAASGGVRRAGEPERLAQCPCPRCESTDTKFCYYNNYNLSQPRHFCKGCRRYWTRGGALRNVPVGGATRKPNGSPAGVRRKRPSHSHSNSHHAASSQAAPVVPLSVSAPAPLPLPLLPPPQPQPQQYELTFLPPSLSAVDPDRRLLDLGGSFSSLLAPPAPLLPNFATSFVFGGAGAGMAMAHAHVPALPQPAPVVSQALPESFWGMGWPDLSI\*

>TaDof7.4

MANLPTHATNADASAFKLFGQVIQPDAHRAASAPASTSISAGQSASAPPPPPPPPSTTQQAAVGGEPLPCPRCGSRETKFCYFNNYNVRQPRHLCRACRRYWTAGGALRRVATASPGRRRPRPSARSAAAAASATASASASEEGAAAESVDSRS\*

>TaDof7.5

MVRITAMDQLEGEEVVVRAPASGGVRRAGEPERLAQCPCPRCESTDTKFCYYNNYNLSQPRHFCKGCRRYWTRGGALRNVPVGGGTRKPNGSPAAVRRKRPSHSHSHHAAASSQAAPVVPLSVSAPAPLPLPLLPPPPQPQQYELTFLPPSLSAVDPDRRLLDLGGSFSSLLAPPAPLLPNFATSFMFGGAGAGMAMAHAHVPALPQQAPGVSQALPDGFWGMGWPDLSI\*

>TaDof7.6

MANLPTHATNADASGFKLFGQVIQPDAHRSAPASTSVSTGQSAAAPPPQPPPPPPSTTQPAAVGGEPLPCPRCGSRETKFCYFNNYNVRQPRHLCRACRRYWTAGGALRRVATASPGRRRPRPSARSAAAAASATASASEEGAAAESVDSRS\*

>TaDof7.7

MEAPLHQLAPMQQALLARPQNCKHDAAATMAATDMACLQQQQQLMQLQPAAANPNTPSGAAREQCPRCASHDTKFCYYNNYNTSQPRHFCRACRRYWTLGGSLRNVPIGGSTRKRLRPAPQQTMRRPPVHFGAPPPPPMPAQSHSQQAPQGGLLSSLFAFGAAPLFEGRVGFDLGLGLPGLSQVGLGGGAGEFGLHSLGLRGGHAGTSAPMLWPTAFLDNGNVDTWKVSGGGAAAMWAPEFSPAPTVAQVGGNGMFHGGAQIMGQL\*

>TaDof7.8

MEAPLHQLAPMQQALLAHPQNCKHDAAATMAATDMACVQQQQQLLQLQPAAANPNTPSAAAREQCPRCASHDTKFCYYNNYNTSQPRHFCRACRRYWTLGGSLRNVPIGGSTRKRLRPAPQQAMRRPPVHFGAPPPPMPAQSHSQQAPQGGLLSSLFALGGAPLFEGRVGFDLGLGLPGLSQVGLGGSAGEFGLHSLGLRGGHAGTSAPMLWPTAFLDNGNVDTWKVSGGGAAAMWAPEFSSAPTVAQVGGNGMFHGGAQIMGQL\*

>TaDof7.9

MEAPLHQLAPMQQALLAHPQNCKHDAAATMAATDMACLQQQQQQLMQLQPAAANPNTPSGAAREQCPRCASYDTKFCYYNNYNTSQPRHFCRACRRYWTLGGSLRNVPIGGSTRKRLRPAPQQAMRRPPVHFGAPPPPMPAQSHSQQAPQGGLLSSLFALGAAPLFEGRVGFDLGLGLPGLSQVGLGGSAGEFGLHSLGLRGGHAGTSAPMLWPTAFLDNGNVDTWKVSGGGAAAMWAPEFSPAPAVAQVGGNGMFHGGAQIM\*

>TaDof7.10

MQEPGRRPFAGAVDLRRPKGYPAPSATAQAEVGAAAAEEGEAHGDPCPRCESRDTKFCYYNNYNTSQPRHYCKSCRRYWTKGGTLRNVPVGGGSRKSSSSSSSSSSSPKRAKNSKRRRVAPAAPPAPEAEPGADASAAVAATTKEAAATEDVTAAEDPAAAPTADGCFAFTAGEPDAPPAKEGCFTLTAGEPDAPPAADGDGGFAFTAGEPDVPPAADRNGGLAFTDHPSVALGLGVADEAGGKELADPSPFEWPSGCDLGSYWVAGVFADTDPALFLSPP\*

>TaDof7.11

MIQELLGGTAMEQQQQQQQLKCAGNAANHHGSLPMVLQPISSNPSPTSSSTSSRSSTQRSPSAASSPQGQGQAQQGPPGPEQAPLRCPRCNSSNTKFCYYNNYNLTQPRHFCKTCRRYWTKGGALRNVPIGGGCRKPRPMPAPVAKAQPSSCKSVLGMGVGAAPSLGLGMGVGGGMSWASAPQTATAQLMALLNSARAGYAGSNMHRLLGLDTMGQLQVLPGSANGGQGMSPSLWPQATHRPTMPPPPMHLGMGSLGLGQGQGHHNLLSGLELKPPSSSPSPSSLAASYYSDQLNAVVSNGGAGRPHPYDTQASSYPCSTAMCSLPPSASTVSAAQSSHTVGMDQQPPTMSLGTQEMQYWSGGPASMMAWPDLPTLNGAFP\*

>TaDof7.12

MQEPGRRPFAGAVDLRRPKGYPAPLAAQAQAEAVAELATGEAHGDPCPRCESRDTKFCYYNNYNTSQPRHYCKSCRRYWTKGGTLRNVPVGGGSRKSSSSSSSSSSSPKRAKNSKRRRVAPAAPLEPEAEPGADAPAAVATTTKEAAATEDVTTAGDTAAAPAADGCFAFTAGEPDAPPAADRCFTFTSGEPDAPPAADGDGCFAFTAGEPDVPPAAKGDGGLAFTDHPSVALGLGVADDAGGKELADPSPFEWPSGCDLGSYWVAGVFADTDPALFLSPP\*

>TaDof7.13

MIQELLGGTAMEQQQLKCAGNAANHHGSLPMALQPISSNPSPTSSSTSSRSSTQRSPSAASSPQGQGQQGQQGPPGPEQAPLRCPRCNSSNTKFCYYNNYNLTQPRHFCKTCRRYWTKGGALRNVPIGGGCRKPRPMPAPVAKAQPSSCKSVLGMGVGTAPSLGLGMGVGGGMSWASSPQTATAQLMALLNSARAGYAGSNMHRLLGLDTMGQLQVLPGSANGGPGMSPSLWPQATHRPTMPPPPMHLDSHLGMGSLGLGQGQGHHNLLSALELKPPSSSPSPSSLAASYYSDQLNAVVSNGGAGRPHPYDTPASSYPCSTAMCSLPPSASTVSAAQSSRTVGMDQQPPTMSLGTQEMQYWSGGPASMMAWPDLPTLNGAFP\*

>TaDof7.14

MQEPGRRPFAGAVDLRRPKGYPAPSATPQPQAEAGAGDAHGDPCPRCESRDTKFCYYNNYNTSQPRHYCKSCRRYWTKGGTLRNVPVGGGSRKSSSSSSSSSSSPKRAKNSKRRRVAPAAPPEPEAEHDADASAAAAVAARTKEAAATTEDVTTADDPAAAPAADGCFAFTAGEPDAPPAAEGCFTFLASELDAPPAAEGDRGLAFTAAEPDAPPAADGDGGLAFTDHPSVALGLGVADDAGGKELADPSPFEWPSGCDLGSYWVAGVFADTDPALFLSPP\*

>TaDof7.15

MIQELLGGTAMEQQQLKCAGNAANHHGSLPMVLQPISSNPSPTSSSTSSRSSTQRSPSAASSPQGQQGQQGPPGPEQAPLRCPRCNSSNTKFCYYNNYNLTQPRHFCKTCRRYWTKGGALRNVPIGGGCRKPRPMPAPVAKAQPSSCKSVLGMGVGGAPSLGLGMGVGGGMSWASAPQTATAQLMALLNSARAGYAGSNMHRLLGLDTMGQLQVLPGSANGGPGMSPSLWPQATHRPAMPPPPMHLDSHLGMGSLGLGQGQSHHNLLSGLELKPPSSSPSPSSLAASYYSDQLNAVVSNGGAGRPHPYDTQASSYPCSTAMCSLPPSASTVSAAQSSHSVGMDQQPPTMSLGSQEMQYWSGGPASMMAWPDLPTLNGAFP\*

>TaDof7.16

MQDFQSIPGLAGRLFGGAAAADIRRVQGPASRCGVFSQAASAQPEAAVKCPRCESTNTKFCYYNNYNLSQPRHFCKSCRRYWTKGGVLRNVPVGGGCRKAKRSSSSASAPSTPAATDAKSQRRASASSSSRSNSGSGSASPTAAAEETTTTETEPPPPPTPSSNSNSNAVSFANRMTNYPFAADVPPPAPIFADQAAALASLFAPPPPPPLPVFSFSAEPKMEEAIGSLLLPGQEASQEPEEPTCTSTVADMAPFMSLDAGIFELGDASPADYWNGGSCWTDVQDPSVYLP\*

>TaDof7.17

MQDFQSIPGLAGRLFGGAAAADIRRVQGPASRCGVFSQAASAQPEAAVKCPRCESTNTKFCYYNNYNLSQPRHFCKSCRRYWTKGGVLRNVPVGGGCRKAKRSSSSASAPSTPAATDAKSQRRASASSSSRSNNGSVSPTAAAEETTTTETDPPPPPTPSSNSNSNTVAFANRMTNYPFAADVPPPAPIFADQAAALASLFAPPPPPPLPVFNFSAEPKMEEAIGSLLLPGQVPAQETEEPTCTSTVADMAPFMSLDAGIFELGDASPADYWNGGSCWTDVQDPSVYLP\*

>TaDof7.18

MQDFQSIPGLAGRLFGGAAAADIRRVQGPASRCGVFSQAASAQPEAAVKCPRCESTNTKFCYYNNYNLSQPRHFCKSCRRYWTKGGVLRNVPVGGGCRKAKRSSSSASAPSTPAATDAKSQRRASSSSSSRSNSGSGSASPTANGEDTPTTTTDPPPATPSSNSNANAVSFASRMTNYPFAADVPPPAPIFADQAAALASLFAPPPPPPLPVFSFSAEPKMEEAIGSLLLPGQEPAQEPEEPTCTSTVADMAPFMSLDAGIFELGDASPADYWNGGSCWTDVQDPSVYLP\*

>TaDof7.19

MQEFQPIAGLAGRLFGGAAESAGLLRRGGAAAAAQEEVRCPRCDSANTKFCYYNNYNLSQPRHFCKGCRRYWTKGGLLRNVPVGGGCRKPKRKAAAASDVDKDVSSVNTEAKNARSGSSAGSSSLTSGPSSASTNTVNDVGACAAAHSSGGSTPFRGFGPSTFMADAPTLQPPAPMFADQAAAFATLFGTPLPAFTFAAQHKAEDDVAPAVTLTEQSSSATSTADMVPFSARSTGAATASASDWPPATMIDAGIFDLAGAVGSDTTSYWNTASWTDPDGTVYLP\*

>TaDof7.20

MESPGRAEQIDSKLRKLAPSSRQAPPSLRHVRAVHGMQEFQPIPGLAGRLFGGAADRPAGLLRHGGAPEEVRCPRCDSANTKFCYYNNYNLSQPRHFCKGCRRYWTKGGLLRNVPVGGGCRKPKRKAAAASSSDVDKDPSGANSEAKNARSGCSAGSSSLTSGASSASTNTVNDVGACAAAHSSGGSMPFTGLGPSTFIADAPPLQPPTAMFTDQAAAFASLFGTPLPAFTFSAQRKAEDDVAPAVTSTEQPSSASSTADLAPFSARSTGAATASASDWPPATMIDAGIFDIAGAVGSDTTSYWNTASWTDPDGTVYLP\*

>TaDof7.21

MQEFQSIPGLAGRLFGGAAESAGLLRRGGAAAAQEEVRCPRCDSANTKFCYYNNYNLSQPRHFCKGCRRYWTKGGLLRNVPVGGGCRKPKRKAAAASSDVEKDASSANSEAKNARSGCSAGSSSLTSAASSASTNTVIDAGACASAHSSGGSMPFTGLGPSTFMADAPPLQPPAPMFADQAAAFASLFGTPLPAFSFSAQRKAEDDVAPAVTLTEQPSSASSTADLAPFSARSTGAVTASASDWPPATVIEAGIFDIAGAVGSDTTSYWNTASWTDPDGTVYLP\*

>TaDof8.1

MGGAAGIKLFGKVITRQPTRTGADGGGGGVVVSKTQQAAPMSSSSSSSGRGSAEQLEEAARARAAAAEARLPCPRCRSEDTKFCYFNNYNVNQPRHFCRACHRYWTAGGAIRNVPVGSGRRKNRPVLHGASTVMSVADHHLAGPASPGMPNGLGFHPDHGWSQAVPPTAYLGHGEMEQCWWLVHQYPAQGQVNGDVQLSPSSLRINQYA\*

>TaDof8.2

MGGAAGIKLFGKVITRQPTRTGADGGGGVVVSKTQQAAPMSSSSSSSSGRGSAEQLEEAARARAAAAEARLPCPRCRSEDTKFCYFNNYNVNQPRHFCRACHRYWTAGGAIRNVPVGSGRRKNRPVLHGASTVMSVADHHLAGPASPGMPNGLGFHPDHGWSQVVPSPAYLGNAEMEQCWWLVHQYPAQGQVNGDVQLSPSSLRINQYA\*

>TaDof8.3

MVSHSHLEMGGAAGIKLFGKVITRQPTRTGADGGVVASKTQQAAPVSSSSSSSGRGSAEQLEEAARARAAAAEARLPCPRCRSEDTKFCYFNNYNVNQPRHFCRACHRYWTAGGAIRNVPVGSGRRKNRPVLHGASTVMSVADHHLAGPASPGMPNELGFHPDHGWSQAVPPPAYLGHGEMEQCWWLVHQYPAQGQVNGDVQLSPSSLRINQYS\*

>TaDof8.4

MASTTADDAGAGRRKAGTPPALPPPPAEQAVRCPRCDSPNTKFCYYNNYSLSQPRHFCKTCRRYWTKGGALRSVPVGGGCRKNKRSRSASSASRGLSLTTPAGGAADQDQHAARMGVGGFPGGGGDFRGVVGMLPVLHSPAVVGQYVPFGDWSSGETNGGGAARHATNGSGGAGNGAASSAIASSIESLSFINQDLHWKLQQQRVATMFLGPPSASSSSHPHAVGGGSNGMPAAAQFGGGGTFLQMAGLSGCMETLPAATTWFMDNSYALPSPPQPAAGVGAASSNINSSRSSGGGGDDNATSNDNNNCGGSIPSWGDISTFAMLP\*

>TaDof8.5

MELAGAAHPQPPESDVAPPRTPPQAPAEDSCKDTGDTRITEENSCTPPDLNLSQPNNSGLNSSSACENQTSNGDEMTEPESTLEAAKTEGDGSNKEKVLKKPDKILPCPRCNSMDTKFCYYNNYNIHQPRHFCRGCQRYWTAGGSMRNLPVGAGRRKSKSSSTNCNGILIPGDSLSAPGGDASVIPLPIKENQPAVKFGSDSTLPNSMASLLRVEEQNKNSNPASTAHPRNGENQTCPPSATTSDNPRIESVKVAVGVHQNGITGDCNGVTPMPPIPCFPGAPFMYPWNPAWNGVPAMAAPVCPVPAEPANCSENGHGGNIQWNFPPMVPMPGFCGPPIPFPVMPPSIWPLVSPWPNGAWSAPWLGPAYNMSAAPPTSSSTCSDSGSPVLGKHPRDSEPQGGEKAERSLWIPKTLRIDDPDEAAKSSIWTTLGIEPGERGMFRAFQPKSGGREQMSNAARVMQANPAAQSRFASFQETT\*

>TaDof8.6

MASTTADDAAAGRRKAGTPPALPPPPAEQAVRCPRCDSPNTKFCYYNNYSLSQPRHFCKTCRRYWTKGGALRSVPVGGGCRKNKRSRSGSSASASRGLSLTTPAGGAADQDQHAARMGVSGFPCGGGGGDFRGVVGMLPVLHSPAVVGQYVPFGDWSSGETNGGGAAGRATNGSAGAGNGAASSAIASSIESLSFINQDLHWKLQQQRVATMFLGPPSSSSSSHPHAVGGGSNGMPAAAQFGGGGTFLQMAGLSGCMETLPAATTWFMDNSYALPSPPRPTAGMGATSSNINSGRSSGGGGDDNATSDNNNNCGGSIPSWGDISTFAMLP\*

>TaDof8.7

MELAGAAHPQPPESDVAPPRTPPQAPAEDSCKDTGDTRITEENSCTPPDLNLSQPNNSGLNSSSACENQTSNSDEMTEPESTLEAAKTKGDGSNKEKVLKKPDKILPCPRCNSMDTKFCYYNNYNIHQPRHFCRGCQRYWTAGGSMRNLPVGAGRRKSKSSGTNCNGILIPGSSLAAPGGDASVIPLPIKENQPAVLFGSDATLPNSMASLLRVEEQNKNSNPASTAHPRNGENQTCPPSAATSDNPRIESVKVAVGVHQNGITGDCNGVTPMPPIPCFPGPPFMYPWNPAWNGVPAMAAPVCPVPAEPANCSENGHGGNIQWNFPSMVPMPGFCGPPIPFPLMPPSVWPLVSPWPNGAWSAPWLGPGYSMSAAPPTSSSTCSDSGSPVLGKHPRDSDPQGGEKAEKSLWIPKTLRIDDPDEAAKSSIWTTLGIEPGERGMFRPFQPKSGGREQMSNAARVMQANPAAQSRFASFQEMT\*

>TaDof8.8

MASTTADDAAAGRRKAGTPPALPPPPAEQAVRCPRCDSPNTKFCYYNNYSLSQPRHFCKTCRRYWTKGGALRSVPVGGGCRKNKRSRSGSSSSSRGLSLTTPAGGGADQDQQHAARMSMGGFPGGGGGDFRGVVGMLPVLHSPAVVGQYVPFGDWSSGETNGGGAAGRATNGSAGAGNGAASSAIASSIESLSFINQDLHWKLQQQRVATMFLGPPSASSSSHPHAVGGGSNGMPAAAQFGGGGAFLQMAGLSGCMETLPATTTWFMDNSYALPSPPRPAAGVGAASSNINSGRSSGGGGDDNATSDNNNCGGSIPSWGDISTFAMLP\*

>TaDof8.9

MGANLFPLCSRVANSTCRILPHMELAGAAHPQPPESDVAPPRTPPQAPVEDSCKDTGDTRITEENSCTPPDLNLSQPNNSGLNSSSACENQTSNGDEMTEPESTLEAAKTEGDGSNKEKVLKKPDKILPCPRCNSMDTKFCYYNNYNIHQPRHFCRGCQRYWTAGGSMRNLPVGAGRRKSKSSSTNCNGILIPGGSLAAPGGDSSVIPLSIKENQPAVKFGSDSTLPNSMASLLRVEEQNKNSNPASTAHPRNGENQTCPPSATTSDNPRIESVKAAVGVHQNGITGDCNGVTPMPPIPCFPGPPFMYPWNPAWNGVPAMAAPVCPVPAEPANCSENGHGGNIQWNFPPMVPMPGFCGPPIPFPLMPPSVWPLVSPWPNGAWSAPWLGPSYSMSAAPPTSSSTCSDSGSPVLGKHPRDSDPRGGEKAEKSLWIPKTLRIDDPDEAAKSSIWTTLGIEPGERGMFRAFQPKSGGREQMSNAARVMQANPAAQSRFASFQETT\*

>TaDof8.10

MSDQMDSGIKLFGRVIPLVPDAAPGPPEAEATAGSEHPPPPPPQESEAEAEADNNKEQHKETKDKGDSEMKVDAPEEKEDGGMKGDELRERKDDEMEVDAPQAKQNAETASSSTLDHKKDDQAQISNAEEKVASDPKEENEKKSNDESGQDKVLKKPDKIIPCPRCNSMDTKFCYYNNYNVNQPRHFCKNCQRYWTAGGSMRNVPVGAGRRKSKNSALHYRQLLMAPDCLLGSRVDISDTVNPEVLASLPSIPTQSASRNETVLKFGPEVPLCESMVSVLNIEEQNVTNAGSVPRDETREGNSCASTTTSNNGLPANAVPPGQNGAPVYCNGVGPVPQYYLGPPFMYPWSMGWNNLPVMVPGGSMPESASPSESCSTSSAPWMNSPMMPGSRLPAPPFPYPIVPPALWGCLPSWPAAAWNTPWVGTNGCISPSGSSNSSCSGNGSPTLGKHSRDPNPQKDDKEEKSLWVPKTLRIDDPDEAAKSSIWATLGIKPGDPGVFKPFQFKGESKGQPADARPARALQANPAAFSRSQSFQESS\*

>TaDof8.11

MAALRDRGDAAIKLFGRTIPLLDAAAEVVTKLGNDANSNDVMPCVSNKLLNVEATPFCSKNREQNDQAISKHGVEVRTGFKSEEIKTGSDGSGQDKVLKKPDIIVPCPRCNSMETKFCYFNNYNVSQPRHFCRNCQRYWTAGGNIRNVPVGSGRRRNKHASHFRHAMMSCDANIAAPGDVSNEIHHLALPLLPQVLPGPIKENKTVKEFGSQVPVCKPMSSIHNIEEQKDTYLVALASGDNSEEQSCPSPATVSGCSENQTPDSAVKKEPSNVLGYYNGITLPHPHGPALVFPWSPGWNSIAVMAAAQCSTEPIQGLENVKHGLPPWAPPLMMAAPGICTPVVPFPMMPPPLWSCIPGWPNGMWSSPCPGNNGPPNKITCSEDNSPTLGKHSRESDLQEENRENNVQVPKTLRIDDPSEATKSSVRDTLGIKPDEKGLFEPLQMKVLKNDKTPESPQALQANPAAFLRSQSFQERT\*

>TaDof8.12

MLSHVEMAPAGAGGGFKLFGKVITQCVEGTQASPSPAFAAQDEERRLHGETDRTTTAVKREAADTDSSQHQQQQQGAEASRRTQLQESAEARAAAAPLPCPRCRSRETKFCYFNNYNVNQPRHFCKACHRYWTAGGALRNVPIGAGRRKNRPLGPIATVAGHHHHHRAAAGFVLGFPSPSSSPTSPPPVYADRWQLGPDRRF\*

>TaDof8.13

MSDQMDSGIKLFGRVIPLVPDAAPGPPEAEATAGSEHPPPPPPPASEAEPEADNNKEQHKETEDKGDSEMKVDAPEEKEDSAMKGDEPRERKDNEMEVDAPQAKENAETASSSTLDHKKDDQAQISNTEEKAASDPKEENEKKSNDESGQVKVLKKPDKIIPCPRCNSMDTKFCYYNNYNVNQPRHFCKNCQRYWTAGGSMRNVPVGAGRRKSKNSALHYRQLLMAPDCLLGSRVHISNTVNPEVLASLPSIPTQSASRSETVLKFGPEVPLCESMVSVLNIEEQNVTNAGSVPRDETREDNSCTSSTTSNNGLPANAVLPGQNGAPVYCNGVGPVPQYYLGAPFMYPWSMGWNNLPVMVPGGSMPESASPSESCSTSSAPWMNSPMMPGSRLPAPPFPYPLVPPALWGCLPNWPAAAWNTPWIGTNGCISPSGSSNSSCSGNGSPTLGKHSRDSNPQKDDKEEKSLWVPKTLRIDDPDEAAKSSIWATLGIKPGDPGAFKPFQFKGESKGQPADARPARALQANPAAFSRSQSFQESS\*

>TaDof8.14

MLSHVEMAPAGAGGGFKLFGKVITQCVEGTQASPSPSPVFAAQDEERRLHGETDRTTTAVKREAADMDSSQQQQQQGAEASRRTQLQESAEARAAAAPLPCPRCRSRETKFCYFNNYNVNQPRHFCKACHRYWTAGGALRNVPIGAGRRKNRPLGPIATVAGHHHHHHRAAAGFVLGFPSPSSSPTSPPPVYADRWQLGPDGRF\*

>TaDof8.15.1

MMNFCRFLKAVLPWLNAHAMLVLEQHKEMEDKGDSEMKVDAPEEKEDSATKGDEPRERKDNEMEVDAPQAKEKAETASSSTLDHKKDDQAQISNTEEKAASDPKEGNEKKSNDESGQDKVLKKPDKIIPCPRCNSMDTKFCYYNNYNVNQPRHFCKNCQRYWTAGGSMRNVPVGAGRRKSKNSALHYRQLLMAPDCLLGSRVDISNTVNPEVLASLPSIPTQSASRSETVLKFGPEVPLCESMVSVLNIEEQNVTNAGSVPRDETREDNSCASSTTSNNGLPANAVLPGQNGAPAYCNGVGPVPQYYLGAPFMYPWSMGWNNLPVMVPGGSMPESASPSESCSTSSAPWMNSPMMPGSRLPAPPFPYPLVPPALWGCLPSWPAAAWNTPWVGTNGCISPSGSSNSSCSGNGSPTLGKHSRDPNPQKDDKEEKSLWVPKTLRIDDPDEAAKSSIWATLGIKPGDPGVFKPFQFKGESKGQPADARPARALQANPAAFSRLQSFQESS\*

>TaDof8.15.2

MSDQMDSGIKLFGRVIPLVPDAAPGPPEAEATAGSEHPPPPPPASEAEPEADNNKEQHKEMEDKGDSEMKVDAPEEKEDSATKGDEPRERKDNEMEVDAPQAKEKAETASSSTLDHKKDDQAQISNTEEKAASDPKEGNEKKSNDESGQDKVLKKPDKIIPCPRCNSMDTKFCYYNNYNVNQPRHFCKNCQRYWTAGGSMRNVPVGAGRRKSKNSALHYRQLLMAPDCLLGSRVDISNTVNPEVLASLPSIPTQSASRSETVLKFGPEVPLCESMVSVLNIEEQNVTNAGSVPRDETREDNSCASSTTSNNGLPANAVLPGQNGAPAYCNGVGPVPQYYLGAPFMYPWSMGWNNLPVMVPGGSMPESASPSESCSTSSAPWMNSPMMPGSRLPAPPFPYPLVPPALWGCLPSWPAAAWNTPWVGTNGCISPSGSSNSSCSGNGSPTLGKHSRDPNPQKDDKEEKSLWVPKTLRIDDPDEAAKSSIWATLGIKPGDPGVFKPFQFKGESKGQPADARPARALQANPAAFSRLQSFQESS\*

>TaDof8.16

MAALRDRGDAAIKLFGRTIPLLDAAAEVVTKLGNDANSNDVMPCVSNKLLNVEATPFCSKNREQNDQAISKHGVEVRTGFKSEEIKTGSDGSGQDKVLKKPDIIVPCPRCNSMETKFCYFNNYNVSQPRHFCRNCQRYWTAGGNIRNVPVGSGRRRNKHASHFRHAMMSCDANIAAPGDVSNEIHHLALPLLPQVLPGPIKENETVKEFGSQVPVCKPMSSIHNIEEQKDTHLVSLASGDNSEEQSCPSPATVSGCSENHTPDSAVKKEPSNVLGYYNGITLPHPHGPALVFPWSPGWNSIAVMAAAQCSTEPIQGLENVKHGLPPWAPPLMMAAPGICTPVVSFPMMPPPLWSCIPGWPNGMWSSPCPGSNGPPNKITCSEDNSPTLGKHSREADLQEEDRENNVQVPKTLRIDDPAETTKTSVRDTLGIKPDEKGMFEPFQMKVLKNDKTPESPQALQANPAAFSRSQSFQERT\*

>TaDof8.17

MAPAGAGGGFKLFGKVITQCVEGTQASPSPSPAFAAQDEERRLHGETDRTTTAVKREAADMDSSPQHQQQQGAEASRRTQLQESAEARAAAAPLPCPRCRSRETKFCYFNNYNVNQPRHFCKACHRYWTAGGALRNVPIGAGRRKNRPLGPIATVAGHHHHHHQRAAAGFVLGFPSPSSSPTSPPPVYADRWQLGPDRRF\*

>TaDof8.18

MGQLRAAPGGGGDCLIKLFGKTIPVPDAGDKDLQHRGSSATAEPKVQEIAPQDSTGSPPQQPEVVDVEDPSAAKNSAADQQDEEQGDTANQKEKLKKPDKILPCPRCSSMDTKFCYYNNYNINQPRHFCKNCQRYWTAGGAMRNVPVGAGRRKSKSLSAASHFLQRIRAALPGDPLCTPVNTNGTVLSFGSDASTLDVSEQMKHIKDLSSVTRTENTDAPSVGSSAEGWAKGEESSQMNPRERVAADRSANFVQHPCMNGAAMWPFSCAPPPAYFPSNVAIPFYPAAAAAYWGCMVPGAWNTPWQPQPQPQPQSQCQSSSPPSAASPVSTMSSCFQSRKHPRDGDEERDTKGNGKVWVPKTIRIDDVDEVARSSIWSLIGIKGDKEEKDDGKGCKLARVFDPKDEAKTSSHRGNNSLPFLKGNPAALSRSVNFHERS\*

>TaDof8.19

MGQLRAAAGAGGDCLIKLFGKTIPVPDAGAGDVHKDLQHRGSTTAEPKVQEIAPQDSMGSPQQPEVVDVEDPSAAKNSAADQQDEEQGDTANQKEKLKKPDKILPCPRCSSMDTKFCYYNNYNINQPRHFCKNCQRYWTAGGAMRNVPVGAGRRKSKSISAASHFLQRIRAALPGDPLCTPVNTNGTVLSFGSNASTLDVSEQMKHIKELNSVTRTENTDAPSVGSSAEGWAKGEESSQMNSRERVAAERSANCAQHPCMNGAAMWPFSCAPSPAYFASNVAIPFYPAAAAAYWGCMVPGAWNTPWQPQPQCQSSSLPSAASPVSTMSSCFQSRKHPRDGDEERDTKGNGKVWVPKTIRIDDVDEVARSSIWSLIGIKGDKVEKDDGKGCKLARVFDPKDEAKMSSHRGNNSLPFLKGNPAALSRSVNFQERS\*

>TaDof8.20

MGQLRPAAGGGGDCLIKLFGKTIPVPDAGAGANAGDVDKDLQHRGGSTTAELKVQEIAPQDSTGSPQQPEVVDVEDPSAAKNSVADQQDEEQGDTANQKEKLKKPDKILPCPRCSSMDTKFCYYNNYNINQPRHFCKNCQRYWTAGGAMRNVPVGAGRRKSKSLSAASHFLQRIRAALPGDPLCTPVNTNGTVLSFGSDASTLDVSEQMKHIKELASVTRTENTDAPSVGSSAEGWAKGEESSQMNSRERVAADRSANFVQHPCMNGAAMWPFSCAPSPAYFPSNVAIPFYPAAAAAYWGCMVPGAWNTPWQPQPQPQSQCQSNSPPSAASPVSTMSSCFQSRKHPRDGDEERDTKGNGKVWVPKTIRIDDVDEVARSSIWSLIGIKGDKVEKDDGKGCKLARVFDPKDEAKTSSHRGNNSLPFLKGNPAALSRSVNFQERS\*

1. **Protein sequence of Arabidopsis, rice, and maize.**

>AT1G07640.1 MGGSMAERARQANIPPLAGPLKCPRCDSSNTKFCYYNNYNLTQPRHFCKGCRRYWTQGGALRNVPVGGGCRRNNKKGKNGNLKSSSSSSKQSSSVNAQSPSSGQLRTNHQFPFSPTLYNLTQLGGIGLNLAATNGNNQAHQIGSSLMMSDLGFLHGRNTSTPMTGNIHENNNNNNNENNLMASVGSLSPFALFDPTTGLYAFQNDGNIGNNVGISGSSTSMVDSRVYQTPPVKMEEQPNLANLSRPVSGLTSPGNQTNQYFWPGSDFSGPSNDLL

>AT1G21340.1

MLPYIGHNSYQQHQFPLPEMEIPEKWKLSYEQEAITAPACPRCASSNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNIPVGGGCRKRSRSRQNSHKRFGRNENRPDGLINQDDGFQSSPPGSDIDLAAVFAQYVTDRSPSSTDNTTGSDQDSPITTTTHALESLSWDICQETDVDLGFYGEFNNLTQKTKEDQEVFGQFLQEDREEIFEFQGLLDDKEIQEILECSFSEEPDQLVSQGSFMINGDNWSSTDLTRFGI

>AT1G26790.1

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>AT1G28310.1

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>AT1G29160.1 MATQDSQGIKLFGKTITFNANITQTIKKEEQQQQQQPELQATTAVRSPSSDLTAEKRPDKIIPCPRCKSMETKFCYFNNYNVNQPRHFCKGCQRYWTAGGALRNVPVGAGRRKSKPPGRVGGFAELLGAATGAVDQVELDALLVEEWRAATASHGGFRHDFPVKRLRCYTDGQSC

>AT1G47655.1 MPSEPNQTRPTRVQPSTAAYPPPNLAEPLPCPRCNSTTTKFCYYNNYNLAQPRYYCKSCRRYWTQGGTLRDVPVGGGTRRSSSKRHRSFSTTATSSSSSSSVITTTTQEPATTEASQTKVTNLISGHGSFASLLGLGSGNGGLDYGFGYGYGLEEMSIGYLGDSSVGEIPVVDGCGGDTWQIGEIEGKSGGDSLIWPGLEISMQTNDVK

>AT1G51700.1 MQDLTSAAAYYHQSMMMTTAKQNQPELPEQEQLKCPRCDSPNTKFCYYNNYNLSQPRHFCKNCRRYWTKGGALRNIPVGGGTRKSNKRSGSSPSSNLKNQTVAEKPDHHGSGSEEKEERVSGQEMNPTRMLYGLPVGDPNGASFSSLLASNMQMGGLVYESGSRWLPGMDLGLGSVRRSDDTWTDLAMNRMEKN

>AT1G64620.1 MDTAKWPQEFVVKPMNEIVTNTCLKQQSNPPSPATPVERKARPEKDQALNCPRCNSLNTKFCYYNNYSLTQPRYFCKDCRRYWTAGGSLRNIPVGGGVRKNKRSSSNSSSSSPSSSSSSKKPLFANNNTPTPPLPHLNPKIGEAAATKVQDLTFSQGFGNAHEVKDLNLAFSQGFGIGHNHHSSIPEFLQVVPSSSMKNNPLVSTSSSLELLGISSSSASSNSRPAFMSYPNVHDSSVYTASGFGLSYPQFQEFMRPALGFSLDGGDPLRQEEGSSGTNNGRPLLPFESLLKLPVSSSSTNSGGNGNLKENNDEHSDHEHEKEEGEADQSVGFWSGMLSAGASAAASGGSWQ

>AT1G69570.1 MSKSRDTEIKLFGRTITSLLDVNCYDPSSLSPVHDVSSDPSKEDSSSSSSSCSPTIGPIRVPVKKSEQESNKFKDPYILSDLNEPPKAVSEISSPRSSKNNCDQQSEITTTTTTSTTSGEKSTALKKPDKLIPCPRCESANTKFCYYNNYNVNQPRYFCRNCQRYWTAGGSMRNVPVGSGRRKNKGWPSSNHYLQVTSEDCDNNNSGTILSFGSSESSVTETGKHQSGDTAKISADSVSQENKSYQGFLPPQVMLPNNSSPWPYQWSPTGPNASFYPVPFYWGCTVPIYPTSETSSCLGKRSRDQTEGRINDTNTTITTTRARLVSESLRMNIEASKSAVWSKLPTKPEKKTQGFSLFNGFDTKGNSNRSSLVSETSHSLQANPAAMSRAMNFRESMQQ

>AT2G28510.1

DPEQEISNETLETILVSSTKGSNNNNKKMEEEMKKKVSRGELGGEAQNCPRCESPNTKFCYYNNYSLSQPRYFCKSCRRYWTKGGTLRNVPVGGGCRRNKRSSSSAFSKNNNNKSINFHTDPLQNPLITGMPPSSFGYDHSIDLNLAFATLQKHHLSSQATTPSFGFGGDLSIYGNSTNDVGIFGGQNGTYNNSLCYGFMSGNGNNNQNEIKMASTLGMSLEGNERKQENVNNNNNNSENPSKVFWGFPWQMTGDSAGVVPEIDPGRESWNGMVSSWNNGLLNTPLV

>AT2G28810.1 MVFSSVSSFLDPPINWPQSANPNNHPHHHQLQENGSLVSGHHQVLSHHFPQNPNPNHHHVETAAATTVDPSSLNGQAAERARLAKNSQPPEGALKCPRCDSANTKFCYFNNYNLTQPRHFCKACRRYWTRGGALRNVPVGGGCRRNKKGKSGNSKSSSSSQNKQSTSMVNATSPTNTSNVQLQTNSQFPFLPTLQNLTQLGGIGLNLAAINGNNGGNGNTSSSFLNDLGFFHGGNTSGPVMGNNNENNLMTSLGSSSHFALFDRTMGLYNFPNEVNMGLSSIGATRVSQTAQVKMEDNHLGNISRPVSGLTSPGNQSNQYWTGQGLPGSSSNDHHHQHLM

>AT2G34140.1 MATQDSQGIKLFGKTIAFNTRTIKNEEETHPPEQEATIAVRSSSSSDLTAEKRPDKIIACPRCKSMETKFCYFNNYNVNQPRHFCKGCHRYWTAGGALRNVPVGAGRRKSKPPGRVVVGMLGDGNGVRQVELINGLLVEEWQHAAAAAHGSFRHDFPMKRLRCYSDGQSC

>AT2G46590.1 MMNVKPMEQIMIPNNNTHQPNTTSNARPNTILTSNGVSTAGATVSGVSNNNNNTAVVAERKARPQEKLNCPRCNSTNTKFCYYNNYSLTQPRYFCKGCRRYWTEGGSLRNVPVGGSSRKNKRSSSSSSSNILQTIPSSLPDLNPPILFSNQIHNKSKGSSQDLNLLSFPVMQDQHHHHVHMSQFLQMPKMEGNGNITHQQQPSSSSSVYGSSSSPVSALELLRTGVNVSSRSGINSSFMPSGSMMDSNTVLYTSSGFPTMVDYKPSNLSFSTDHQGLGHNSNNRSEALHSDHHQQGRVLFPFGDQMKELSSSITQEVDHDDNQQQKSHGNNNNNNNSSPNNGYWSGMFSTTGGGSSW

>AT3G21270.1

KQQQQQQPQFAEQEQLKCPRCDSPNTKFCYYNNYNLSQPRHFCKSCRRYWTKGGALRNVPVGGGSRKNATKRSTSSSSSASSPSNSSQNKKTKNPDPDPDPRNSQKPDLDPTRMLYGFPIGDQDVKGMEIGGSFSSLLANNMQLGLGGGGIMLDGSGWDHPGMGLGLRRTEPGNNNNNPWTDLAMNRAEKN

>AT3G45610.1

MDYSSMHQNVMGVSSCSTQDYQNQKKPLSATRPAPPEQSLRCPRCDSTNTKFCYYNNYSLSQPRYFCKSCRRYWTKGGILRNIPIGGAYRKHKRSSSATKSLRTTPEPTMTHDGKSFPTASFGYNNNNISNEQMELGLAYALLNKQPLGVSSHLGFGSSQSPMAMDGVYGTTSHQMENTGYAFGNGGGGMEQMATSDPNRVLWGFPWQMNMGGGSGHGHGHVDQIDSGREIWSSTVNYINTGALL

>AT3G47500.1

MMMETRDPAIKLFGMKIPFPSVFESAVTVEDDEEDDWSGGDDKSPEKVTPELSDKNNNNCNDNSFNNSKPETLDKEEATSTDQIESSDTPEDNQQTTPDGKTLKKPTKILPCPRCKSMETKFCYYNNYNINQPRHFCKACQRYWTAGGTMRNVPVGAGRRKNKSSSSHYRHITISEALEAARLDPGLQANTRVLSFGLEAQQQHVAAPMTPVMKLQEDQKVSNGARNRFHGLADQRLVARVENGDDCSSGSSVTTSNNHSVDESRAQSGSVVEAQMNNNNNNNMNGYACIPGVPWPYTWNPAMPPPGFYPPPGYPMPFYPYWTIPMLPPHQSSSPISQKCSNTNSPTLGKHPRDEGSSKKDNETERKQKAGCVLVPKTLRIDDPNEAAKSSIWTTLGIKNEAMCKAGGMFKGFDHKTKMYNNDKAENSPVLSANPAALSRSHNFHEQI

>AT3G52440.1

MERAEALTSSFIWRPNANANAEITPSCPRCGSSNTKFCYYNNYSLTQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKSRRPKSSSGNNTKTSLTANSGNPGGGSPSIDLALVYANFLNPKPDESILQENCDLATTDFLVDNPTGTSMDPSWSMDINDGHHDHYINPVEHIVEECGYNGLPPFPGEELLSLDTNGVWSDALLIGHNHVDVGVTPVQAVHEPVVHFADESNDSTNLLFGSWSPFDFTADG

>AT3G61850.1

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>AT4G00940.1

MDHHQYHHHDQYQHQMMTSTNNNSYNTIVTTQPPPTTTTMDSTTATTMIMDDEKKLMTTMSTRPQEPRNCPRCNSSNTKFCYYNNYSLAQPRYLCKSCRRYWTEGGSLRNVPVGGGSRKNKKLPFPNSSTSSSTKNLPDLNPPFVFTSSASSSNPSKTHQNNNDLSLSFSSPMQDKRAQGHYGHFSEQVVTGGQNCLFQAPMGMIQFRQEYDHEHPKKNLGFSLDRNEEEIGNHDNFVVNEEGSKMMYPYGDHEDRQQHHHVRHDDGNKKREGGSSNELWSGIILGGDSGGPTW

>AT4G21030.1 MNNLNVFTNEDNEMNVMPPPRVCPRCYSDQTRFSYFNNNKKSQPRYKCKNCCRCWTHGGVLRNIPVTGICDKSNLPKIDQSSVSQMILAEIQQGNHQPFKKFQENISVSVSSSSDVSIVGNHFDDLSELHGITNSTPIRSFTMDRLDFGEESFQQDLYDVGSNDLIGNPLINQSIGGYVDNHKDEHKLQFEYES

>AT4G21040.1 MDNFNVVANEDNQVNDVKPPPPPPRVCARCDSDNTKFCYYNNYSEFQPRYFCKNCRRYWTHGGALRNVPIGGSSRAKRTRINQPSVAQMVSVGIQPGSHKPFFNVQENNDFVGSFGASSSSFVAAVGNRFSSLSHIHGGMVTNVHPTQTFRPNHRLAFHNGSFEQDYYDVGSDNLLVNQQVGGYVDNHNGYHMNQVDQYNWNQSFNNAMNMNYNNASTSGRMHPSHLEKGGP

>AT4G21050.1

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>AT4G21080.1 MDNLNVFANEDNQVNDVKPPPPPPRVCARCDSDNTKFCYYNNYCEFQPRYFCKNCRRYWTHGGALRNIPIGGSSRAKRARVNQPSVARMVSVETQRGNNQPFSNVQENVHLVGSFGASSSSSVGAVGNLFGSLYDIHGGMVTNLHPTRTVRPNHRLAFHDGSFEQDYYDVGSDNLLVNQQVGGYGYHMNPVDQFKWNQSFNNTMNMNYNNDSTSGSSRGSDMNVNHDNKKIRYRNSVIMHPCHLEKDGP

>AT4G24060.1

MDTAQWPQEIVVKPLEEIVTNTCPKPQPQPLQPQQPPSVGGERKARPEKDQAVNCPRCNSTNTKFCYYNNYSLTQPRYFCKGCRRYWTEGGSLRNIPVGGGSRKNKRSHSSSSDISNNHSDSTQPATKKHLSDHHHHLMSMSQQGLTGQNPKFLETTQQDLNLGFSPHGMIRTNFTDLIHNIGNNTNKSNNNNNPLIVSSCSAMATSSLDLIRNNSNNGNSSNSSFMGFPVHNQDPASGGFSMQDHYKPCNTNTTLLGFSLDHHHNNGFHGGFQGGEEGGEGGDDVNGRHLFPFEDLKLPVSSSSATINVDINEHQKRGSGSDAAATSGGYWTGMLSGGSWC

>AT5G02460.1

MVFSSFPTYPDHSSNWQQQHQPITTTVGFTGNNINQQFLPHHPLPPQQQQTPPQLHHNNGNGGVAVPGGPGGLIRPGSMAERARLANIPLPETALKCPRCDSTNTKFCYFNNYSLTQPRHFCKACRRYWTRGGALRSVPVGGGCRRNKRTKNSSGGGGGSTSSGNSKSQDSATSNDQYHHRAMANNQMGPPSSSSSLSSLLSSYNAGLIPGHDHNSNNNNILGLGSSLPPLKLMPPLDFTDNFTLQYGAVSAPSYHIGGGSSGGAAALLNGFDQWRFPATNQLPLGGLDPFDQQHQMEQQNPGYGLVTGSGQYRPKNIFHNLISSSSSASSAMVTATASQLASVKMEDSNNQLNLSRQLFGDEQQLWNIHGAAAASTAAATSSWSEVSNNFSSSSTSNI

>AT5G39660.1 MADPAIKLFGKTIPLPELGVVDSSSSYTGFLTETQIPVRLSDSCTGDDDDEEMGDSGLGREEGDDVGDGGGESETDKKEEKDSECQEESLRNESNDVTTTTSGITEKTETTKAAKTNEESGGTACSQEGKLKKPDKILPCPRCNSMETKFCYYNNYNVNQPRHFCKKCQRYWTAGGTMRNVPVGAGRRKNKSPASHYNRHVSITSAEAMQKVARTDLQHPNGANLLTFGSDSVLCESMASGLNLVEKSLLKTQTVLQEPNEGLKITVPLNQTNEEAGTVSPLPKVPCFPGPPPTWPYAWNGVSWTILPFYPPPAYWSCPGVSPGAWNSFTWMPQPNSPSGSNPNSPTLGKHSRDENAAEPGTAFDETESLGREKSKPERCLWVPKTLRIDDPEEAAKSSIWETLGIKKDENADTFGAFRSSTKEKSSLSEGRLPGRRPELQANPAALSRSANFHESS

>AT5G62430.1

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>AT5G62940.1 MGLTSLQVCMDSDWLQESESSGGSMLDSSTNSPSAADILAACSTRPQASAVAVAAAALMDGGRRLRPPHDHPQKCPRCESTHTKFCYYNNYSLSQPRYFCKTCRRYWTKGGTLRNIPVGGGCRKNKKPSSSNSSSSTSSGKKPSNIVTANTSDLMALAHSHQNYQHSPLGFSHFGGMMGSYSTPEHGNVGFLESKYGGLLSQSPRPIDFLDSKFDLMGVNNDNLVMVNHGSNGDHHHHHNHHMGLNHGVGLNNNNNNGGFNGISTGGNGNGGGLMDISTCQRLMLSNYDHHHYNHQEDHQRVATIMDVKPNPKLLSLDWQQDQCYSNGGGSGGAGKSDGGGYGNGGYINGLGSSWNGLMNGYGTSTKTNSLV

>AT5G65590.1

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>AT5G66940.1

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>AT2G37590.1

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>AT3G50410.1

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>AT4G38000.1 MMTSSHQSNTTGFKPRRIKTTAKPPRQINNKEPSPATQPVLKCPRCDSVNTKFCYYNNYSLSQPRHYCKNCRRYWTRGGALRNVPIGGSTRNKNKPCSLQVISSPPLFSNGTSSASRELVRNHPSTAMMMMSSGGFSGYMFPLDPNFNLASSSIESLSSFNQDLHQKLQQQRLVTSMFLQDSLPVNEKTVMFQNVELIPPSTVTTDWVFDRFATGGGATSGNHEDNDDGEGNLGNWFHNANNNALL

>AT5G60850.1

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>LOC\_Os01g09720.1

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>LOC\_Os01g48290.1

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>LOC\_Os01g55340.1

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>LOC\_Os02g45200.1

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>LOC\_Os02g49440.1

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>LOC\_Os03g38870.1

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>LOC\_Os03g55610.1 MIQELLGGTTMDQLKGASALNHASLPVVLQPIVSNPSPTSSSSTSSRSSAQATQQRSSSATSSPHGQGQGGGAAEQAPLRCPRCNSSNTKFCYYNNYNLTQPRHFCKTCRRYWTKGGALRNVPIGGGCRKPRPMPAPVAKPPMSCKAAPPLGLGGGPVSWASGQQAATAHLMALLNSARGVQGHGGSNVHRLLGLDTMGHLQILPGAPNGAGAGTAASLWPQSAPRPVTPPPPHMDSQLGMGTLGHHDVLSSLGLKLPSSASSSPAASYYSDQLHAVVSNAGRPQAPYDVATASLPCTTAVTSLPSALSSVSAAAPTSNTVGMDLPPVSLAAPEMQYWNGPAAMSVPWPDLPTPNGAFP\*

>LOC\_Os03g60630.1

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>LOC\_Os04g47990.1 MDAAHWHQGLGLVKPMEEMLMAANAAAGANPNPAATAPSSVTGGALRGGGGGGAPPVAGGAGAGSTERRARPQKEKALNCPRCNSTNTKFCYYNNYSLQQPRYFCKTCRRYWTEGGSLRNVPVGGGSRKNKRSSSSAASASPASASTANSVVTSASMSMSMASTGGGASKNPKLVHEGAQDLNLAFPHHGGLQAPGEFPAFPSLESSSVCNPGGPMGTNGRGGGALSAMELLRSTGCYMPLQVPMQMPAEYATPGFALGEFRAPPPPPQSSQSLLGFSLDAHGSVGGPSAAGFGSSAGLQGVPESTGRLLFPFEDLKPTVSSGTGGGGASGGGAGVDGGHQFDHGKEQQAGGGGGGPGGHDTPGFWNGMIGGGSGTSW\*

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>LOC\_Os08g38220.1 MQEQQPETGRRPAQQFATVDLRRPKGYAAAPATPQPGSAATAAAAAGPAATAAAAAAGEGDPCPRCESRDTKFCYYNNYNTSQPRHFCKCCRRYWTKGGTLRNVPVGGGTRKKSSSSSSSSSSSSAAAAAPAAKRQKTSKKRRVTTPEPLAATTPVLTEAAADSAAKTTTEATSEKKTTTSTTTTTPPAPDTTSEITTELVVPAVEEDSFTDLLQPDSAAVTLGLDFSDYPSITKSLADPDLHFEWPPPAFDMASYWPAGAGFADPDPTAVFLNLP\*

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>LOC\_Os03g07360.1

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>LOC\_Os01g15900.1 MCDKDPGIKLFGRVIPLAPEAEAAAAADGSDQPEAAAAAAAEVEPAAQDEDHHKETEERKYDEMKVDVPQEEEDNEMKVDAPQEKKDNEVTADVPEEKGNDEMRVDASESIESIEPVSRSTLDNKKEDQGQMNNVEEKAASDSKDENEKTANDESGQDKVLKKPDKILPCPRCNSMDTKFCYYNNYNVNQPRHFCKNCQRYWTAGGTMRNVPVGAGRRKSKSSSLHYRHLLMAPDCMMGSRVEISKSMNPEAFASAHSTPIQPIGRNETVLKFGPEVPLCESMASVLNIQEQNGTNAAAVPTGENQEDNSCISSITSHNVLPENAAQVDKNSTPVYCNGVGPVPQYYLGAPYMYPWNIGWNNVPMMVPGTSMPESASQSESCSTSSAPWMNMNSPMMPVASRLSAPPFPYPLVPPALWGCLSSWPATAWNIPWIRTNGGCMSPSSSSNSSCSGNGSPLGKHSRDSSLPLKEDKEEKSLWVPKTLRIDDPDEAAKSSIWATLGIKPGDPGIFKPFQSKGESKGQAASETRPARALKANPAALSRSQSFQETS\*

>LOC\_Os01g17000.1 protein|expressed protein

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>LOC\_Os05g02150.1 protein|expressed protein

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**Additional file 2: File S2.** Sequences of Dof genes with experimentally supported functions.

>GAI

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FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI

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>AtDof3.6

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>MaDof23

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NKRPSLSSAAATTSATSATTSSTAATSSIVSNPKKLPIDLIPPRVSLSASQKFHDGQDLN

LAFPHHGLPEFNGFPGLESSTVNSNSSGTGNCSNPCNAVGALSAMELLRSGMTMRGLSPF

VTMPLPEYPTGFELQEFRAPALNFPMEAIAGGEGREGSSGGYGALQGVQESAGGRLLFPF

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>OsDof15

MIQELLGGTTMDQLKGASALNHASLPVVLQPIVSNPSPTSSSSTSSRSSAQATQQRSSSA

TSSPHGQGQGGGAAEQAPLRCPRCNSSNTKFCYYNNYNLTQPRHFCKTCRRYWTKGGALR

NVPIGGGCRKPRPMPAPVAKPPMSCKAAPPLGLGGGPVSWASGQQAATAHLMALLNSARG

VQGHGGSNVHRLLGLDTMGHLQILPGAPNGAGAGTAASLWPQSAPRPVTPPPPHMDSQLG

MGTLGHHDVLSSLGLKLPSSASSSPAASYYSDQLHAVVSNAGRPQAPYDVATASLPCTTA

VTSLPSALSSVSAAAPTSNTVGMDLPPVSLAAPEMQYWNGPAAMSVPWPDLPTPNGAFP\*

>ZmDOF36

MDMNSNANNSTAAAASAPINNQQEAVVSSPTRKEQARNPKKARAAPQQAGGSGEPRPRPP

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SSSSSPFPGPSSTAATSAAMEKTVSTRLMLMATSTMAMPSPTAGLFVPDDMSPAFTPTTG

GSGFDDLAGMDEQHQQGFLPFSPLSLSDQAPELAPGGGGDTTPSFLDMLTGGYLDGGGYG

GMSGGSDAMDMPFSLPEMGPPTTDPMPFQLQWTSSELDNYINDDGGYAAGPAAGVQQQQQ

QQQQQINGGDHQKQDENKEAGNGKGNDDGGGGSSSVYSFWMNTSGSDGAEG