

Table 1 Suppl. Real time quantitative PCR primers for soybean *NAC* genes.

Gene name	Forward primer	Reverse primer	Product size [bp]
<i>GmNAC02.7</i>	5'-ATTGAGAAAGCAGCAACCAGC-3'	5'-GAGTCGGAAGCCTCGAAGTA-3'	125
<i>GmNAC03.1</i>	5'-CGGTCAAAGAAAGCAAGAATA-3'	5'-CTGCCTGAGTTGTAGCTGTGA-3'	135
<i>GmNAC03.2</i>	5'-GATCGAAGCCTGAAACCTCT-3'	5'-TCCATAATGGCAGCAACAAT-3'	172
<i>GmNAC08.12</i>	5'-GAGCCACAAAATTCGGGTTAT-3'	5'-GCGTTAAGGATGAGGCGATA-3'	175
<i>GmNAC11.4</i>	5'-TGCTGCTAACTTGGGTTGT-3'	5'-CTTCTGGAATTGCTCGGCTA-3'	133
<i>GmNAC12.15</i>	5'-CAACAGCAGCACGAGGAGAA-3'	5'-CCCGATACGAAATCAACGAC-3'	107
<i>GmNAC13.7</i>	5'-CAACAGCACACGAGGAGAA-3'	5'-TAGGGACATAAAGGTCAATTGCA-3'	178
<i>GmNAC16.5</i>	5'-AAGTGTTCAGGCTCAGGTT-3'	5'-GCCCGTGTCTGTGAGTGGT-3'	139
<i>GmNAC17.5</i>	5'-TCAGTGGGTTCATGCACGAAT-3'	5'-GAAAGTTTGCTGCTACTAGAGGG-3'	149
<i>GmNAC19.5</i>	5'-AACTCAGGGGCAGAGCAAT-3'	5'-ATCTACGCCAGCCTCATCCA-3'	112
<i>ACT11</i>	5'-CTTCAGGCAATTCACGAGACAA-3'	5'-TAGAACCAACCGATCCAGACAC-3'	222

Glyma06g14250	GmNAC06.5
Glyma06g14260	GmNAC06.5
Glyma06g14290	GmNAC06.6
Glyma06g15840	GmNAC06.7
Glyma06g15990	GmNAC06.8
Glyma06g16440	GmNAC06.9
Glyma07g05350	GmNAC07.1
Glyma07g04140	GmNAC07.1G7.1
Glyma07g05360	GmNAC07.2
Glyma07g05370	GmNAC07.3
Glyma07g05660	GmNAC07.4
Glyma07g10240	GmNAC07.5
Glyma07g15180	GmNAC07.6
Glyma07g1220	GmNAC07.7
Glyma07g22250	GmNAC07.8
Glyma07g35630	GmNAC07.9
Glyma08g01280	GmNAC08.1
Glyma08g14260	GmNAC08.108.1
Glyma08g41990	GmNAC08.11
Glyma08g47220	GmNAC08.128.1
Glyma08g05590	GmNAC08.2
Glyma08g04610	GmNAC08.3
Glyma08g08010	GmNAC08.4
Glyma08g16620	GmNAC08.5
Glyma08g17140	GmNAC08.6
Glyma08g17350	GmNAC08.7
Glyma08g18470	GmNAC08.8

Glyma0g19300	Gm5AC08.9	MGDNVNLPGRGTHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma0g29760	Gm5AC09.1	MSVGLPGRGTHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma0g1650	Gm5AC09.2	MEHLNPGRGTHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma0g26600	Gm5AC09.3	QURDHFTQLPLLESPKLLQASAMPNPMEOYVDHVNHSITLSPLSLOHVQOQNOATYGNNSNLSQAVDPVTDWRVLDKFAVSODASKEFNGDTSNYSVRLHDQKLVPEQONASTSSNCSTHDLWK*	NAM
Glyma0g26620	Gm5AC09.4	ELDRFELALPYPHLQNPYSLFQSQPLQTOQWAVDYVSYSDTMMAKQATVRDCESSDGLVRYVSISGEMVESCPEMGTGREGNEWCVLDLVYSLHAGDESSQOREFANQSVHQVQSLRGEMDPAVAGQ*	NAM
Glyma0g17050	Gm5AC09.5	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g04350	Gm5AC10.1	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g049180	Gm5AC10.2	ADMDANSKQLPQGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g04130	Gm5AC10.3	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g02600	Gm5AC10.4	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g03630	Gm5AC10.5	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g03340	Gm5AC11.1	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g07990	Gm5AC11.2	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g10230	Gm5AC11.3	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g12170	Gm5AC11.4	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAC
Glyma1g12180	Gm5AC11.5	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAC
Glyma1g18770	Gm5AC11.6	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma1g33210	Gm5AC11.7	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g00540	Gm5AC12.1	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g29360	Gm5AC12.10	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g11150	Gm5AC12.11	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g31210	Gm5AC12.12	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g33460	Gm5AC12.13	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g34990	Gm5AC12.14	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g35000	Gm5AC12.15	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g35530	Gm5AC12.16	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM
Glyma12g00760	Gm5AC12.2	MGSTNGVPPGRHPTDEELVYVHFLHRKASLPLCHPDAIPDLEVYTPYDPWELGDALAGNQWYVYYSBRTQNRVITGONVKTGMPEEYVYSTSNRGMKKYVYHVHGAPTAGKTNWIMQVRLSDSASBRSKRQPQPKCEYNKVCYKRYERNDDNGTGLSCLDEVLSLDDDLDESLN*	NAM

Glyma 1g606480	GmbAC15.3	KATVGNDSRGRVREJSTPTPTTPTTDTGKLLTEIRITTCOSGGRNIEFGDQGHJHJLJCLPAQGVQDNPNDQJLEHLEKAVASDACKLHPLJDEHPITLEGNCIGITVHTPEKLPVCSKQDQGRHIFHRSPKAYTGTTRKRKRVTHTDQSGSTWHRWCTKTRAVAAAGAVKCFKKILVYTYNIGROKRPKTNWVWMOYHLGSTEELQGHLYVS KVYVQTPQRCQNTFKHCKYKEMKUNDSQGNINSILPKTALTDCTTAPYIDYVHVHSINRESSUQLPSSVYQVQSGYBRLTMDAKKARJESTGRK*	NAM
Glyma 1g606510	GmbAC15.4	MSNSVNAKLPGRFHRHDEELVCDYLMKKVAHINDSILMINVDLNKEPWPDEITACVGGKGFYFTORDRKTATGLRTNRATASCVWKA TGDKRSILKGTLVGMRRKTLVTPQGRAPKGNKTIEWVHIEFRIEGHPHGPKESSKDEWVLCRVFYPKNBEVAKPMKSCYEDTGSSEPALMDSYISFYDQTOTHADEFEQVPCPSIQN QTSPIFNHMTANATNAGVAPMLGYCLDWSCDRKMLKAVLWKTQTKMERNTNYSKLGSPGSLHGGNENYVWSPHFWNNV*	NAM
Glyma 1g606950	GmbAC15.5	MGNJENRQNDQYDIBHENVDDQVDPHJGRGHRHPTDEELVYVYQRLKDKPSEELJQKQYVDPWDLPKSTATGEGEYFVGRGHRKRSYRBNRPNKPTGSCVWKA TGUDKPVYSHGEGONDCQKALKVYTGSGAKGCKTDWAMHIEHRLPSTNDNNNTLSESKNYVDYVPEALWTLCHPRKENVSQRKHTPDLQKQAKOSKSHDKS SRMSVSNINQUESTINFGHYTEINQOPTNNTNSDKRSQVHYVHTHQLCAPVAQHQOQOQTPSSNWNPNPNDFETDNWDELGSLVKYAVDSLS*	NAM
Glyma 1g611830	GmbAC15.6	MAPMSLPGFHRHPTDEELVAYYLERKKTGHSIEDHAEVDVYKCEPWDLKPSKEDMWEYVTSPRDKPNGSRINATQAGVWKA TGKDRPVYLSQAKQVGMACKTLVYVYRGRAPHGRTNVMHIEVRLSVYGCATVLSLKGFEKQKRWQKEINSLSYTVSSVGYCLP*	NAM
Glyma 1g620290	GmbAC15.7	KAMPQNGQTLVPGFHRHPTDEELVYVYLRKASVYEVDDVADVEDLANKLEPWDLKQDQKQSGONQVWYTSUKDKKPTGTRTNWKA TGDRKSTVYTNSSKRGCMACKTLVPTTGRAPHGCKTDWIMHIEHRLDEDDADQEDQWVVCVFKKNSNSRGGFQGELEEEHILTHHRASGPCOVYLQKUILHMQGQPDHYNIDGT MILLPOFSPESAAPPTASSIPLASMANADILESQNLRLTTTEGGALNAQOQERISGRDSEWSELAKLSAHSHQMDQSCOPTNINHIAATVAGTSAQKPPHYVLCGDTHHDMKFSK*	NAM
Glyma 1g61900	GmbAC16.1	MPVGRFHRHPTDEELVYVYLRKLADDPVHHPHEDLCKVPSVDPQKSVYSDSDPWFHFTQWVYKYLKSKRPENETKAKQFVKWATQGNRKRIRGTFNGLTTLPHGQRVPRGAKTNVNHIEVHYHVAHSHESQRAYVLCRLMKAKKKNKGAEPSDIEGEPHSMVSDYQNPAPAEAGIASVYDQVYDMDHIEHVAQDAKSPVQHEN TFTNDVNYVLRWCKFKMGDWE	NAM
Glyma 1g626810	GmbAC16.10	KAMEFVAKSGEDVYDHRIDQDLRLJPGFHRHPTDEELVYVYLRKALASATACAGADKAPKCEHFWPKAKAGKAGKQWVYTCQDRKPTQGRAPNRATQGRVWKA TGCEGKQKGLKGRANVGMKATLVYVGRAPKATNWKVHIEHRLDEGFCVYLRKAAQDQVWVYKSHFESRTTINSKRVLPRNKRLLRANSSNGEHLDFP SSLPPIVYDPLTQDTSKHLHUKCTNTPSSSAAKLPSSSGYLTPNINNNNQMLMAKPELHEKVEHPNNYASTSGVDTTTPNMGISTSNMILLSPQRTQNSTVAPNMDQCYNHTHQKQCKAKMEQJSDISKQKPVYASQDTCLSSQTSVYAKGDNNDNGRKNALYEDNTEPSSVATTLSLECLWDDY*	NAM
Glyma 1g634310	GmbAC16.11	MSVGLPGFHRHPTDEELVYVYLRKKNQGELEDDHPVDLYKCEPWLEAKFSLPDSDEWYHFGPRDKVPNGRTNRATRAQYWKSTGRKRVKRSQRPCKMACKTLVYVYRGRAPQGRITDQVHIEHRLDDKECDTGLQDTYALCVFKKNGICSDIEQQGQCSJLIESQJTNCECTNSPDQKASSCLEEDKCDSDWMMQTTEDA WYSSNAAMVGGSESHVFTTN*	NAM
Glyma 1g619390	GmbAC16.2	MDVGVYGRPTDEELVYVYLRKHLDDKPCVHLLDVCLEPWPDLPLLDASAVRNGRWEHFPSPDYKVSNSKRVNRITKCEWKPFGKRGKRSQRTNNVETKTLTVYQGRVNSGVSNWVHIEVHYHVAHSHESQRTVLCRLMKPQKGTTEGTDALICBEGPGRSMVSDYENQATQDIPSGGTFTGMEITFGMHLAEKYF SPTQOSPTGHQEPSFTNYPNNAVFRNEDNEMQPTFEKDEAFASIVDENLVNESMHAFVNSSTQSESLRKYCESSDTDAEYVSEIRDNDVSDVTKCMEYPSDQYYSEREISSIKAVYQSLCCLSTNHEANQETMESLQNNWGMQSQYSTANKPLEINTYESSSPSTRRWNOYHPRPDYFTSOKTDEDLIRGRTQYMOY RM*	NAM
Glyma 1g61940	GmbAC16.3	MDDDVYLGRTPEQELVNYFLKHLGLDPRVHVIPVDYCDVEPWNVPVYLASSABRGDPDWFHSVDPKYLKSKRPNETKTCQFWKA TGKDRJDRJDTGTDNTVGTJTKTLVYVQGRVSGVSKNWVHIEVHYHVAHSHESQRTVLCRLMKPQKGTTEGTDALICBEGPGRSMVSDYENQATLEGASGETTIGEAFOATVPAKENTS PQOQSLTELEGASPNYAFNNAVFRNEDNEMQPTFEKDEFLNLILADSVNENKIDPNDNSTSELRKYCESSDTDAEYVSKLDDNDVSDTACNDYNSDPTSYSSKRFKSSHDAVHGGICHLPSNLEANQERKNSMDFQSGAETSDSTLDPLRINYDSSSPFTW*	NAM
Glyma 1g62200	GmbAC16.4	MPNNSMNSGQVQVGRFHRHPTDEELVYVYLRKSYKIDDLVQVQVQNLKLEPWDRKCKGTTPQVTRINATVAAQWKA TGDDKQVYNSGQRGRKMRKTLVYVYRGRAPHQKSDWIMHIEHRLDNNISDNNSNNAAGDAQGEHGWYVGRFKKNVHLKTLDPLASGEGRRSHMFPDQDEGALQQLQDM GRCKEESTLQNTSYGRFAMELNGGGQVQVQVQVQNLKLEPWDRKCKGTTPQVTRINATVAAQWKA TGDDKQVYNSGQRGRKMRKTLVYVYRGRAPHQKSDWIMHIEHRLDNNISDNNSNNAAGDAQGEHGWYVGRFKKNVHLKTLDPLASGEGRRSHMFPDQDEGALQQLQDM GRCKEESTLQNTSYGRFAMELNGGGQVQVQVQVQNLKLEPWDRKCKGTTPQVTRINATVAAQWKA TGDDKQVYNSGQRGRKMRKTLVYVYRGRAPHQKSDWIMHIEHRLDNNISDNNSNNAAGDAQGEHGWYVGRFKKNVHLKTLDPLASGEGRRSHMFPDQDEGALQQLQDM	NAM
Glyma 1g64720	GmbAC16.5	MEPIVYAKSGEDVYDHRIDQDLRLJPGFHRHPTDEELVYVYLRKALASATACAGADKAPKCEHFWPKAKAGKAGKQWVYTCQDRKPTQGRAPNRATQGRVWKA TGCEGKQKGLKGRANVGMKATLVYVGRAPKATNWKVHIEHRLDEGFCVYLRKAAQDQVWVYKSHFESRTTINSKRVLPRNKRLLRANSSNGEHLDFP SSLPPIVYDPLTQDTSKHLHUKCTNTPSSSAAKLPSSSGYLTPNINNNNQMLMAKPELHEKVEHPNNYASTSGVDTTTPNMGISTSNMILLSPQRTQNSTVAPNMDQCYNHTHQKQCKAKMEQJSDISKQKPVYASQDTCLSSQTSVYAKGDNNDNGRKNALYEDNTEPSSVATTLSLECLWDDY*	NAM
Glyma 1g64740	GmbAC16.6	MGRPNSLPGRFHRHPTDEELVYVYLRKVASPIVYSIAEADVQVYKYLDPWDLPAKATIGERKVEYHFPSPDRKYPNGAKRNAAAGSYWKA TGDKTVYTLQVSGQVSGVKKALVYVYRGRKQVYKTNWIMHIEHRLVDNNRPKRLKDSMSRLDDWVLCRYKKSJHALISTEASHVGEVQDAEHLFQETLVLPKSPAPPPONTLISQKSVS PNSLDAMDLSLESHENHPTQVQSGAGNTGNDQKQSNPNNTNYPQKQVQVYSNMEHMRKQVYSDMDELTLPKSLTSSCHNTFNINSQYVENVWNTLAKQJLQJLQHPHQLQFQ*	NAM
Glyma 1g66620	GmbAC16.7	MEVLPHEKTYKLPVQGFREDSEELAGYLRKRMAORPNLDQCDVYQVWVPLPGGSKNLNWQRFHEHLTRFVLENKREAGNQWVTEKAOPELSEQVQVARKNVLAPEWAKGNESKSNWVHIEHRLVSKSPSVSMAVYVRFKTKKEGKGRKAKSEGETSSSSSEEEAADETPIVDITFMENGTVYCPSPATS EAS*	NAM
Glyma 1g624200	GmbAC16.8	MESZTPGRHPTDEELVYVYLRKVASQKDLVKREIDAYRWPDLQETVYRGVEQNEWYFHSIKDKYKTPGTRTNWATMAQFWKATGRKQSVYVETKLGMKRTLVYVYRGRAPNGOKTQDWMHIEHRLVETNPGQDEGWVCRKAFKRTKNGOKTKEGWHNRCKLVTDQQAQCGSVSTVYDPNDMLRQOQRFSGAQNMY KQEHEDANNLSMHAEQQVYLQHLSESLYLAQGSVYSPNDNNNDNNDQNGKSTNTKLTIDWALKYVYASQGEHHEGYSYFAHHHTTSDMVALLLQNSNENNNKNTFNSTBOLTYVYKIASALLOYAKELQKQWKAQYQPHIDKCLTLP*	NAM
Glyma 1g626740	GmbAC16.9	MGPATNSLPGRFHRHPTDEELVYVYLRKVASIPLVALAEVQYKTDWPDLPAKATGEKELVYFSPDRKYPNGAPRNAAAGSYWKA TGTDKNVIALAGYVREHFGVKKALVYVYRGRKQVYKTNWIMHIEHRLVDNNRPKRLKDSMSRLDDWVLCRYKFKKHVAPSPTEASLTQVNEQLDQAVVEEHQJDLTLPILKNNNTVP PQOATLMSQKSLSESNLLDATYSMLSTILSENHSNTPTSETLSLFNCEMLDQETQNTYINDTNSNNSTYLPQKNSMENAARKHLNMDHEDNMLYPLKKYHSSCNFTNLQNNQNNIMPKQLASHPVLRQ*	NAM
Glyma 1g60650	GmbAC17.1	MYMPGRHPTDEELVYVYLRKVEGRKRNLELITLMLYRYPDWELPALAAGFEHVLVYVYRPRDKYNGRDPNRKVTGSYWKATGADRMRITENRSPKIKTLVYVYSGAPKGRITSWIMNEYRLPQHETERYQAEISLCVYKKAQVDEHPSIPRCIPIRPPSSRASHDNNKRNINEMPTTEHVDKINETEASSDVNTALGLSKYAA YKAMGALSTMALVYPMHIEGLGMMHQQQQKQAAATVYHISAGVSTISLTLMAQSVYSLSPJLHPTPSILMLWVNHPPENQETSNMBSK*	NAM
Glyma 1g610970	GmbAC17.2	MEVNPVCKEDDQMDLPGRFHRHPTDEELVYVYLRKVADITKFCARAGEVLDNRSFMDLPWKAKMGEKVEYFCYRBRKYKTPGTRINRAATGYWKA TGDKKEHFGKSLVGMKRTLVYVYRGRAPKSGKSNWVHIEVYRLEGKSVINHLPKTAKEWVYCRVQKSGAGKTHSGIMLDSFADRLGSSALPPLSUSPSISGTRPNDT AYVPTCSNPDVQRQNGVDFDSFTSYAVSSNPMGLPRMPGSGSYTQGVQVAAANLPFGSVYTLQDHILRLTLENGTKPERDMINSYQETGLTDINAEITSNFDMGRPERPENNINIASVYVAILDLGLWNV*	NAM
Glyma 1g614700	GmbAC17.3	ANTSHVPPGRFHRHPTDEELVYVYLRKVASKRDLVDYDLYKRPDWLOELCKGTGDSWYFHSIKDKYKTPGTRINRAKAGFWKATGRKQVYKTLGOMKRTLVYVYRGRAPNGQSDWIMHIEHRLVETNPGQDEGWVYCRVTKKRTMTQKQVYGVYDQSPWYVYDEQVFSMQLESPPRISILPYASYHHHHHPKCPKL MEHQYNMHPHMLQLPQLSPKYTQSAACSVPYVYENNNNNNNNSITLQSSLTLEQLQTCNNQSHSLYGSNHAHVDQYTDWYLDKVTYASQSHNQDQVYSLKSTSSAPENVTYQSVYVANGKQKQVYQJYASTSYSTQJLWK*	NAM
Glyma 1g616500	GmbAC17.4	MGEATLPGRFHRHPTDEELVYVYLRKVEGELEHVPDLYKTDWPDLPEKSLPKEDLEWFEHCPGRKYPNGSRNRAKATAGYWKATGKDRKVVYQSNISTGYKTLVYVYLRAPLGRDRTWVHIEVRLCDDLDGQATCPQGEFALCVYRKKRNKANSIHATSRKYSSPTSPYVAPMGEFNQSVETTPNSNFWSPDMLDSKD YSQONMAECFPRYDPSVMAPWQSLHHPEITSSLSYNNGNEVADNLQJGCTQWNSMDLYGNDVYDQVDSNYSPEH*	NAM
Glyma 1g61740	GmbAC17.5	MGRFNIVYKGRILPGRFRCPTDEELVYVYLRKKAFAQQPASNISEDVTQTEPWKLGLERLNRNFTSNRSGNBRPAGSCWWSVYGEKQKHISESQVGMKTLVYVYRKSHEHRTQWVHIEHRLVASVPCOMPVADVYRIFOKNMKTRBSHKKPSSSKLQRLVYKASHTDFTVDFNIDDDGPTPCSPCLSECCSEBSSKLD *.	NAM
Glyma 1g615930	GmbAC17.6	MEDHAAALPQVYHYPSEVLYGVYVYLRKNENHEFGYQSLDRLYDHDPTELDDAACVSYQVYGRKKHWFYKAKETRNRRKYNKSGFWLRKGLYRDSHDNGDDVYLGHTRIVYVYVGNLSKANAKTIDWLYYALVDHLEASVLYCRVYVPHKNSHSEGLSCCAEYSVYAVVHVYVQCDCAESDYEAKEVDEGVN RNEHAEVPSHGHOPVAVSVYAGSQHPSIANFCSCNLNLRVINTQNGSKCLDVLVPSFKRQ*	NAM
Glyma 1g616020	GmbAC18.1	KNMNAPSLPGRFHRHPTDEELVYVYLRKNGKKELEHBEVDYKACPWDLPEKSLPKEDLEWFEHCPGRKYPNGSRNRAKATAGYWKATGKDRKVVYQSNISTGYKTLVYVYLRAPLGRDRTWVHIEVRLCDDLDGQATCPQGEFALCVYRKKRNKANSIHATSRKYSSPTSPYVAPMGEFNQSVETTPNSNFWSPDMLDSKD CSPNINUSALNINNGHTRNNIGTWSHELAEIDNLPITASSFNTPCSMSPPSKVDALECARMOHRETMPPHLEVQDPPOVGMELMALQASCMGCGRRNNTDHLSEYLAHAEHJLNGSTYSRISOLGANNYAAPHESDFTPMQGNVKNVADNPNARSIEDGLDDGFKTERAVSNJAWYGMSSKNNE KGMHEOKVYPRHEBNTQNRNEEVQVQSGQHHNNKEINDDIPDSMGINGDHDNEDENGNSTNEVVEETKSHQMDVSTRQVADITHQJAPSTQVYQVLPNLAEDQSEENAVVYVMPHPRKFAVYVGMKLTKSNTIASALVYFALLMHCVTLKEQVEDLKSPKCFDGSANMKKINRQPAENIWNIEQENVSV GKCGKGSVYLLKKGHLELTSLALCTMVAHNVDS*	NAM
Glyma 1g613570	GmbAC18.2	MNVKVISSDDTKKDEEVLVYVYLRGHEHPTDEELVYVYLRKYDKKPKLKLKLYQVYKTPWDLPVNSNGEKWEYFCIRGKREYNSYRPNYTSFGFWKATGDKSYCYKEPHECGLKKSILVYVYRGSAGKGTDMWAMHIEHRLPNAKSPNDQAEALLYTCLSRGN*	NAM
Glyma 1g615020	GmbAC18.3	MEHNRHDEGLKSDMLPGRFHRHPTDEELVYVYLRKAKQORPILSHLQVLYKQVYDQWDSKMAATGTEKLEWVYVTECHDRKRVNSAPRNYTCAGWKA TGDRIPVNSSEKGTGLKKSILVYVYRGAAGKGTDMWAMHIEHRLPSLTPRSSDPKYVQKCTANESWAKHIEHRLTAQRAASHWSVSPLETTTSDHBDGQOLCOANMPTT KKSLSAQVYTHNESQSSTISTSTPTCDVAVSNVGNPLMILYRPSDLRPSNGDLPSKQSVISSLTSAKSDSTNAGDLNLSSTSSVLEDPKSGTEHTTNGELQHGNGVQPHLRDMMQGNENIDNALGRPNVAVVPRYQDQLETVRSIGEPFNGDVAWRPNMLWDTSSIL*	NAM
Glyma 1g619620	GmbAC18.4	MGBIENSKRKNKPELPGRFHRHPTDEELVYVYLRKVQNCQVCAIAGEVLDNKECPWDLPLAKMGEHTEWYFVCYRBRKPTGTRINRAIDQYWKATGDKDHENALGMKRTLVYVYRGRAPKGEKRTWVHIEVYRLEGKRNQPKGSEWVYCRVTEKSRCKGRKHPKCRFNRPNFGEPSGASLLPPLMDBSPYSSETRTTT AGEHSDVCTSDSPNQTEDONNTHDDVDSMETPLNSPFSRPSDNLAKATLSSASQASQAHQGEQSOPDYCYAPQERMLRMLHENHPEKCAQTKQKEPEGRDHPGDSMYSMDMINRGMQGHSSASGPDTHLWNV*	NAM
Glyma 1g62580	GmbAC19.1	MEHNRHDEGLKSDMLPGRFHRHPTDEELVYVYLRKAKQORPILSHLQVLYKQVYDQWDSKMAATGTEKLEWVYVTECHDRKRVNSAPRNYTCAGWKA TGDRIPVNSSEKGTGLKKSILVYVYRGAAGKGTDMWAMHIEHRLPSLTPRSSDPKYVQKCTANESWAKHIEHRLTAQRAASHWSVSPLETTTSDHBDGQOLCOANMPTT KKSLSAQVYTHNESQSSTISTSTPTCDVAVSNVGNPLMILYRPSDLRPSNGDLPSKQSVISSLTSAKSDSTNAGDLNLSSTSSVLEDPKSGTEHTTNGELQHGNGVQPHLRDMMQGNENIDNALGRPNVAVVPRYQDQLETVRSIGEPFNGDVAWRPNMLWDTSSIL*	NAM

Glyma	19g	44910	NAM
Glyma	19g	62850	NAM
Glyma	19g	62950	NAM
Glyma	19g	628520	NAM
Glyma	19g	620540	NAC and UBA_NACA_NACPI
Glyma	19g	605550	NAC and UBA_NACA_NACPI
Glyma	19g	64480	NAM
Glyma	19g	6210	NAM
Glyma	20g	64400	NAM
Glyma	20g	6210	NAM
Glyma	20g	62600	NAM
Glyma	20g	63300	NAM
Glyma	20g	63400	NAM

Table 3 Suppl. Duplicated *GmNAC* genes and the dates of the duplication blocks.

Gene 1	Gene 2	Duplication	Fragment size	Ka	Ks	Ka/Ks	Date (Mya)
GmNAC02.3	GmNAC16.10	fragment	large	0.0336	0.0849	0.395759717	6.959016393
GmNAC16.5	GmNAC19.4	fragment	large	0.064	0.1564	0.409207161	12.81967213
GmNAC04.4	GmNAC06.10	fragment	large	0.0357	0.1341	0.266219239	10.99180328
GmNAC13.2	GmNAC19.2	fragment	large	0.0367	0.0907	0.40463065	7.43442623
GmNAC05.1	GmNAC17.2	fragment	large	0.0138	0.1191	0.115869018	9.762295082
GmNAC12.16	GmNAC13.6	fragment	large	0.0427	0.1771	0.241106719	14.51639344
GmNAC04.2	GmNAC06.2	fragment	large	0.0294	0.1419	0.207188161	11.63114754
GmNAC05.9	GmNAC08.3	fragment	large	0.0436	0.1386	0.314574315	11.36065574
GmNAC07.5	GmNAC09.2	fragment	large	0.0227	0.0742	0.305929919	6.081967213
GmNAC04.1	GmNAC06.1	fragment	large	0.0164	0.0768	0.213541667	6.295081967
GmNAC08.8	GmNAC15.4	fragment	large	0.0296	0.1102	0.268602541	9.032786885
GmNAC03.3	GmNAC19.7	fragment	large	0.006	0.1171	0.051238258	9.598360656
GmNAC09.4	GmNAC12.1	fragment	large	0.0086	0.0641	0.134165367	5.254098361
GmNAC07.4	GmNAC16.4	fragment	large	0.122	0.1976	0.617408907	16.19672131
GmNAC08.6	GmNAC15.7	fragment	large	0.0302	0.15	0.201333333	12.29508197
GmNAC01.6	GmNAC11.2	fragment	large	0.0217	0.1268	0.171135647	10.39344262
GmNAC02.1	GmNAC16.8	fragment	large	0.0372	0.095	0.391578947	7.786885246
GmNAC05.2	GmNAC17.3	fragment	large	0.0181	0.125	0.1448	10.24590164
GmNAC07.3	GmNAC16.3	fragment	large	0.0736	0.1449	0.507936508	11.87704918
GmNAC07.1	GmNAC16.1	fragment	large	0.0633	0.1519	0.416721527	12.45081967
GmNAC04.8	GmNAC06.6	fragment	large	0.0506	0.1456	0.347527473	11.93442623
GmNAC02.9	GmNAC14.5	fragment	large	0.0515	0.131	0.393129771	10.73770492
GmNAC12.12	GmNAC13.10	fragment	small	0.0754	0.2241	0.336456939	18.36885246
GmNAC04.7	GmNAC06.7	fragment	large	0.0648	0.1096	0.591240876	8.983606557
GmNAC10.3	GmNAC20.5	fragment	large	0.0769	0.1645	0.467477204	13.48360656
GmNAC10.5	GmNAC20.2	fragment	large	0.0284	0.1005	0.282587065	8.237704918
GmNAC05.4	GmNAC17.4	fragment	large	0.0249	0.1523	0.163493106	12.48360656
GmNAC09.1	GmNAC16.11	fragment	large	0.0072	0.0938	0.076759062	7.68852459
GmNAC08.7	GmNAC15.6	fragment	large	0.0658	0.171	0.384795322	14.01639344
GmNAC02.10	GmNAC14.6	fragment	large	0.1206	0.1819	0.663001649	14.90983607
GmNAC11.7	GmNAC18.1	fragment	large	0.0298	0.1117	0.266786034	9.155737705
GmNAC05.11	GmNAC08.1	fragment	large	0.0325	0.0977	0.332650972	8.008196721
GmNAC01.2	GmNAC02.5	fragment	small	0.031	0.0966	0.320910973	7.918032787
GmNAC08.10	GmNAC18.3	fragment	small	0.0372	0.1919	0.193850964	15.7295082
GmNAC13.1	GmNAC19.1	fragment	large	0.0228	0.1168	0.195205479	9.573770492
GmNAC02.11	GmNAC14.1	fragment	large	0.0637	0.1083	0.588180979	8.87704918
GmNAC08.11	GmNAC18.2	fragment	small	0.0587	0.1928	0.304460581	15.80327869
GmNAC07.10	GmNAC17.1	fragment	large	0.0149	0.0581	0.256454389	4.762295082
GmNAC11.3	GmNAC12.3	fragment	large	0.0117	0.1293	0.090487239	10.59836066
GmNAC03.4	GmNAC19.8	fragment	small	0.0256	0.0698	0.366762178	5.721311475
GmNAC11.6	GmNAC12.5	fragment	large	0.0921	0.1994	0.461885657	16.3442623
GmNAC12.11	GmNAC13.11	fragment	small	0.0393	0.1155	0.34025974	9.467213115
GmNAC04.11	GmNAC06.3	fragment	large	0.0401	0.1733	0.231390652	14.20491803
GmNAC04.5	GmNAC06.9	fragment	large	0.0239	0.1454	0.16437414	11.91803279
GmNAC06.12	GmNAC12.8	fragment	small	0.0466	0.2377	0.196045435	19.48360656
GmNAC12.15	GmNAC13.7	fragment	large	0.0233	0.2075	0.112289157	17.00819672
GmNAC01.3	GmNAC02.6	fragment	small	0.0156	0.0947	0.164730729	7.762295082
GmNAC07.9	GmNAC20.1	fragment	small	0.0237	0.1057	0.224219489	8.663934426
GmNAC02.2	GmNAC16.9	fragment	large	0.036	0.1002	0.359281437	8.213114754
GmNAC06.13	GmNAC12.7	fragment	small	0.0762	0.1485	0.513131313	12.17213115
GmNAC13.5	GmNAC15.2	fragment	large	0.0596	0.1427	0.417659425	11.69672131
GmNAC12.14	GmNAC13.8	fragment	large	0.0164	0.0809	0.202719407	6.631147541
GmNAC04.6	GmNAC06.8	fragment	large	0.0449	0.1268	0.354100946	10.39344262
GmNAC05.5	GmNAC08.4	fragment	large	0.023	0.0748	0.307486631	6.131147541
GmNAC08.9	GmNAC15.1	fragment	small	0.0137	0.0988	0.138663968	8.098360656
GmNAC14.2	GmNAC17.6	fragment	large	0.1148	0.162	0.708641975	13.27868852
GmNAC16.7	GmNAC19.3	fragment	large	0.0535	0.1141	0.468886941	9.352459016
GmNAC01.5	GmNAC02.4	fragment	small	0.0622	0.158	0.393670886	12.95081967
GmNAC12.13	GmNAC13.9	fragment	large	0.0163	0.1186	0.137436762	9.721311475
GmNAC07.8	GmNAC13.3	fragment	large	0.0253	0.1256	0.201433121	10.29508197
GmNAC13.4	GmNAC15.3	fragment	large	0.0367	0.1573	0.233312142	12.89344262
GmNAC11.5	GmNAC12.4	fragment	large	0.0027	0.1495	0.018060201	12.25409836
GmNAC04.9	GmNAC06.5	fragment	large	0.02	0.1149	0.174064404	9.418032787
GmNAC04.10	GmNAC06.4	fragment	large	0.0193	0.1511	0.12772998	12.3852459
GmNAC19.9	GmNAC19.10	tandem repeat		0.0114	0.0371	0.307277628	3.040983607
GmNAC19.5	GmNAC19.6	tandem repeat		0.0128	0.1418	0.090267983	11.62295082

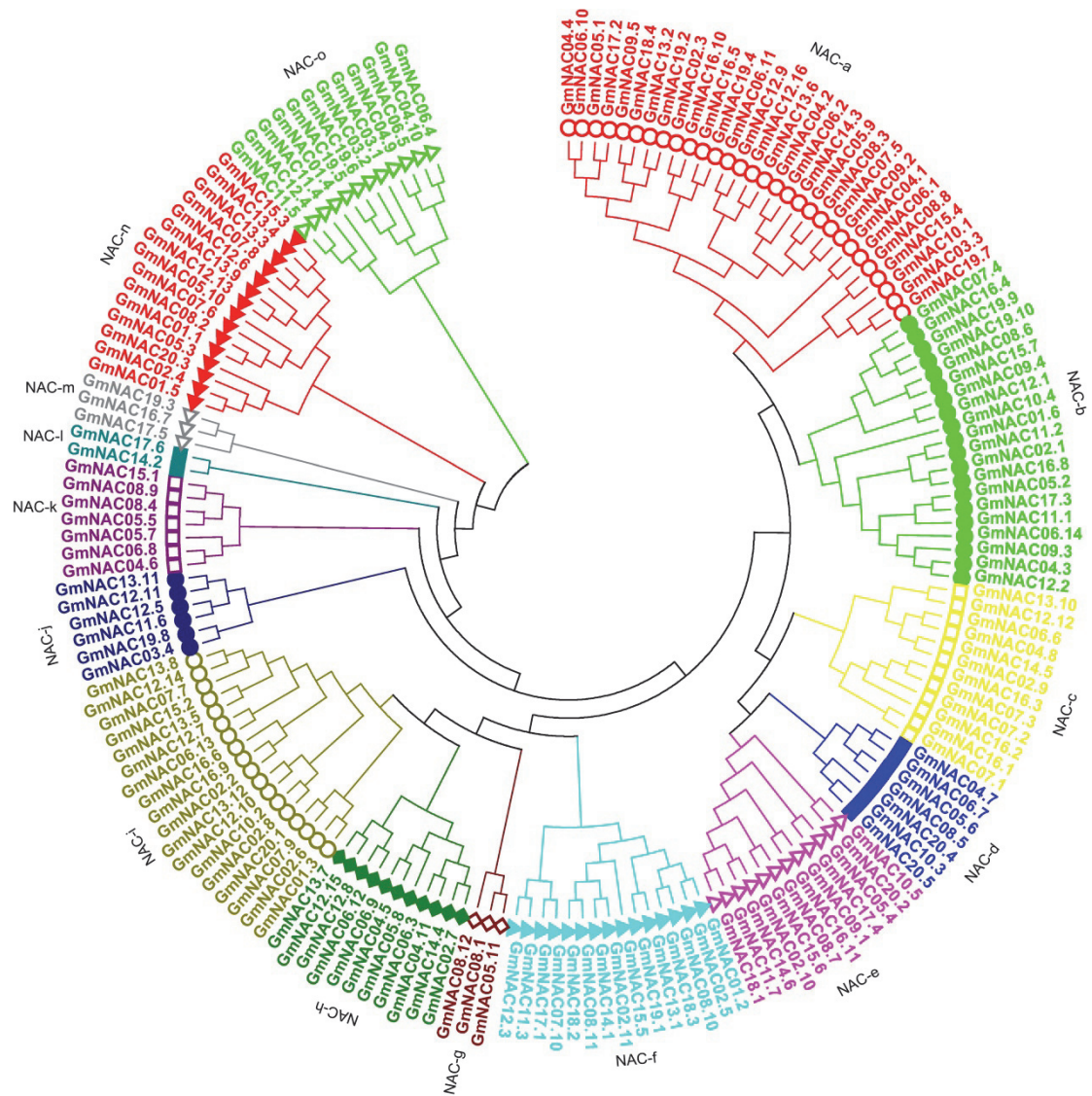


Fig. 1 Suppl. Phylogenetic relationships and gene structure of GmNAC proteins. The phylogenetic tree of GmNAC proteins constructed from a complete alignment of 173 full-length GmNAC proteins using *MEGA 5.0* by the neighbor-joining method. The bootstrap consensus tree inferred from 1 000 replicates is taken to represent the evolutionary history of the taxa analyzed. Fifteen major phylogenetic subgroups (designated as NAC-a to NAC-o) are indicated.

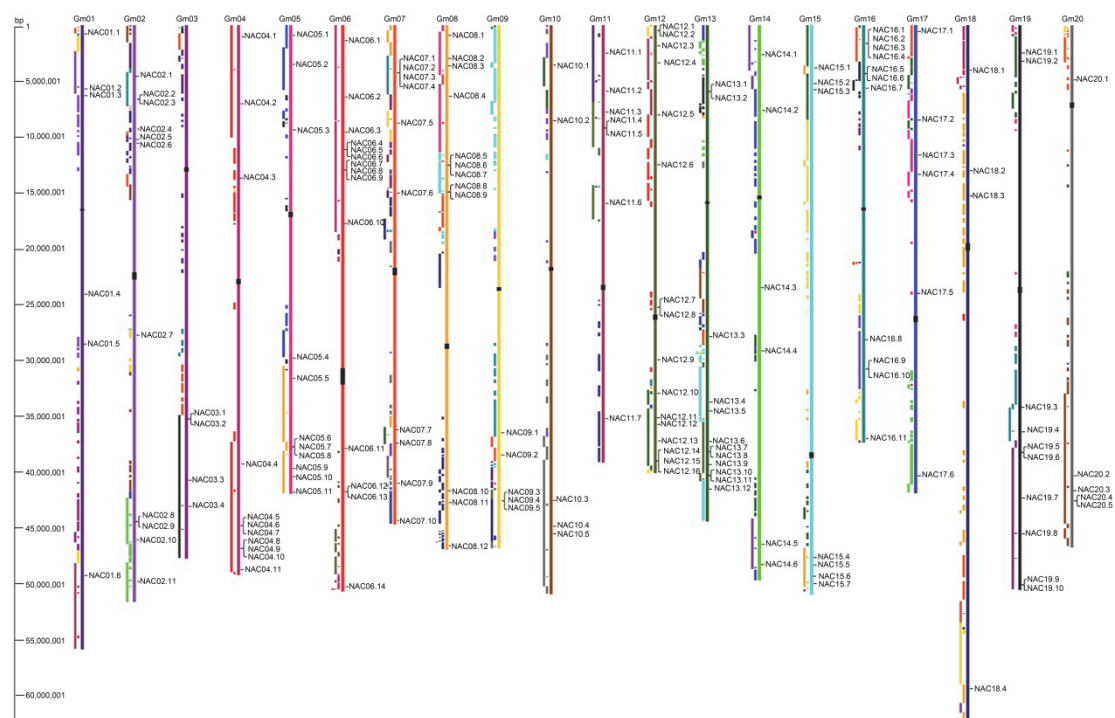


Fig. 2 Suppl. Chromosomal locations and region duplication of *GmNAC* genes. The schematic diagram of genome-wide chromosome organization and segmental duplication arising from the genome duplication event in soybean was made from the *CViT* genome search and *Syteny* viewer at the *Legume Information System* (<http://comparative-legumes.org>). The chromosome numbers are indicated at the top of each bar and sizes/length of chromosomes are represented by the vertical scale on the left. *Coloured blocks* to the left of each chromosome show duplications with chromosomes of the same colour. The locations of centromeric repeats are shown as *black rectangles* over the chromosomes.

Fig. 3 Suppl. Expression of *NAC* gene family in different soybean tissues.