

Supplementary Material



Genetic Transformation of Tobacco Serine Acetyltransferase 4 (NtSAT4) gene in *Brassica napus* L.

Hala Rajab¹, Muhammad Sayyar Khan^{1*}, Safdar Hussain Shah¹ and Syed Mehar Ali Shah²

¹Institute of Biotechnology and Genetic Engineering, The University of Agriculture Peshawar, Khyber Pakhtunkhwa, Pakistan, Postal code 25130; ²Department of Plant breeding and genetics, The University of Agriculture Peshawar, Khyber Pakhtunkhwa, Pakistan, Postal code 25130.

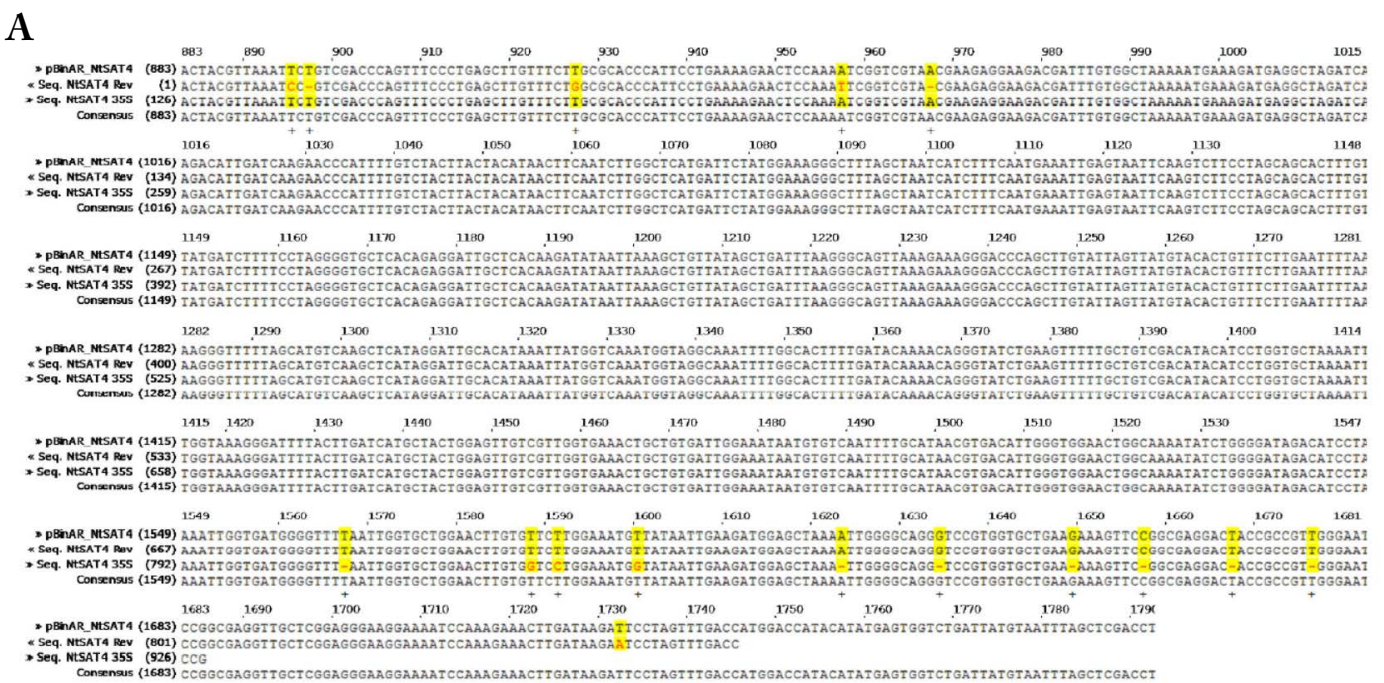
Received | August 27, 2019; Accepted | October 18, 2019; Published | November 25, 2019

*Correspondence | Muhammad Sayyar Khan, The University of Agriculture Peshawar; Email: sayyar@aup.edu.pk

Citation | Rajab, H., M.S. Khan, S.H. Shah and S.M.A. Shah. 2019. Genetic transformation of tobacco serine acetyltransferase 4 (NtSAT4) gene in *Brassica napus* L. *Sarhad Journal of Agriculture*, 35(4): 1224-1233.

DOI | <http://dx.doi.org/10.17582/journal.sja/2019/35.4.1224.1233>

Keywords | *Brassica napus*, Transformation, Serine acetyltransferase, Cysteine, *Agrobacterium*



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359      370      380      390      400      410      420      430      440      450      460      470      480      491
* pBIN_AR_TKTP... (1) CCAATGCTATAACTACGTTAAATTCTGTGCGACCCA+GTTTCCCTGAGCTTGTTCCTTGGCGACCCATTCTCTGAAAAAGAACTCCAAAATCGGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAA
« Seq. TKTPNLSA... (44) CCAATGCTATAACTACGTTAAATTCTGTGCGACCCA+GTTTCCCTGAGCTTGTTCCTTGGCGACCCATTCTCTGAAAAAGAACTCCAAAATCGGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAA
» Seq. TKTPNLSA... (359) CCAATGCTATAACTACGTTAAATTCTGTGCGACCCA+GTTTCCCTGAGCTTGTTCCTTGGCGACCCATTCTCTGAAAAAGAACTCCAAAATCGGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAA
Consensus (359) CCAATGCTATAACTACGTTAAATTCTGTGCGACCCA+GTTTCCCTGAGCTTGTTCCTTGGCGACCCATTCTCTGAAAAAGAACTCCAAAATCGGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAA

492      500      510      520      530      540      550      560      570      580      590      600      610      624
* pBIN_AR_TKTP... (134) GATGAGGCTAGATCAGACATTTGATCAA+GAACCCATTTTGTCTACTTACTACATAA+CAATCTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTCAATGAAATTTGAGTAATTTCAAGTCT
« Seq. TKTPNLSA... (177) GATGAGGCTAGATCAGACATTTGATCAA+GAACCCATTTTGTCTACTTACTACATAA+CAATCTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTCAATGAAATTTGAGTAATTTCAAGTCT
» Seq. TKTPNLSA... (492) GATGAGGCTAGATCAGACATTTGATCAA+GAACCCATTTTGTCTACTTACTACATAA+CAATCTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTCAATGAAATTTGAGTAATTTCAAGTCT
Consensus (492) GATGAGGCTAGATCAGACATTTGATCAA+GAACCCATTTTGTCTACTTACTACATAA+CAATCTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTCAATGAAATTTGAGTAATTTCAAGTCT

625      630      640      650      660      670      680      690      700      710      720      730      740      757
* pBIN_AR_TKTP... (267) TCTTAGCAGCACITTTGTATGATCTTTTCTAGGGGTTGCTCACAGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATT+AGTTATGTACA
« Seq. TKTPNLSA... (310) TCTTAGCAGCACITTTGTATGATCTTTTCTAGGGGTTGCTCACAGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATT+AGTTATGTACA
» Seq. TKTPNLSA... (625) TCTTAGCAGCACITTTGTATGATCTTTTCTAGGGGTTGCTCACAGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATT+AGTTATGTACA
Consensus (625) TCTTAGCAGCACITTTGTATGATCTTTTCTAGGGGTTGCTCACAGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATT+AGTTATGTACA

758      770      780      790      800      810      820      830      840      850      860      870      880      890
* pBIN_AR_TKTP... (400) CTGTTTCTTGAATTTTAAAGGGTTTTT+TAGCATGTCAAGCTCATAGGATTTGCACATAA+TATGGTCAAATGGTAGGCAAA+TTTGGCACITTTGATACAAAACAGGCTATCTGAA+TTTTTGTCTGT+CGA
« Seq. TKTPNLSA... (443) CTGTTTCTTGAATTTTAAAGGGTTTTT+TAGCATGTCAAGCTCATAGGATTTGCACATAA+TATGGTCAAATGGTAGGCAAA+TTTGGCACITTTGATACAAAACAGGCTATCTGAA+TTTTTGTCTGT+CGA
» Seq. TKTPNLSA... (758) CTGTTTCTTGAATTTTAAAGGGTTTTT+TAGCATGTCAAGCTCATAGGATTTGCACATAA+TATGGTCAAATGGTAGGCAAA+TTTGGCACITTTGATACAAAACAGGCTATCTGAA+TTTTTGTCTGT+CGA
Consensus (758) CTGTTTCTTGAATTTTAAAGGGTTTTT+TAGCATGTCAAGCTCATAGGATTTGCACATAA+TATGGTCAAATGGTAGGCAAA+TTTGGCACITTTGATACAAAACAGGCTATCTGAA+TTTTTGTCTGT+CGA

891      900      910      920      930      940      950      960      970      980      990      1000      1010      1023
* pBIN_AR_TKTP... (533) CATA+CATCTCTG+TCTAA+AAATTTGTA+AA+GGGATTTT+ACTTGA+TCATGCTACTG+GAGTTGCTGTTGCTGAACTGCTGATTTGGAATAATGTGCTCAATTTTGCATAACGTGACATTTGGTGGAACTG
« Seq. TKTPNLSA... (576) CATA+CATCTCTG+TCTAA+AAATTTGTA+AA+GGGATTTT+ACTTGA+TCATGCTACTG+GAGTTGCTGTTGCTGAACTGCTGATTTGGAATAATGTGCTCAATTTTGCATAACGTGACATTTGGTGGAACTG
» Seq. TKTPNLSA... (891) CATA+CATCTCTG+TCTAA+AAATTTGTA+AA+GGGATTTT+ACTTGA+TCATGCTACTG+GAGTTGCTGTTGCTGAACTGCTGATTTGGAATAATGTGCTCAATTTTGCATAACGTGACATTTGGTGGAACTG
Consensus (891) CATA+CATCTCTG+TCTAA+AAATTTGTA+AA+GGGATTTT+ACTTGA+TCATGCTACTG+GAGTTGCTGTTGCTGAACTGCTGATTTGGAATAATGTGCTCAATTTTGCATAACGTGACATTTGGTGGAACTG

1024      1030      1040      1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1156
* pBIN_AR_TKTP... (666) GCAAAATATCTGGGATGACATCTTAA+ATTTGGTGTGAGGGTTTTTAA+TGGTCTGGAAC+TTGTTCTTGGAAATGTTATAA+TGAAGTGGAGCTAAA+TTGGGCGAGGCTCGTGGTCTGGAAGAA+GT
« Seq. TKTPNLSA... (709) GCAAAATATCTGGGATGACATCTTAA+ATTTGGTGTGAGGGTTTTTAA+TGGTCTGGAAC+TTGTTCTTGGAAATGTTATAA+TGAAGTGGAGCTAAA+TTGGGCGAGGCTCGTGGTCTGGAAGAA+GT
» Seq. TKTPNLSA... (975) GCAAAATATCTGGGATGACATCTTAA+ATTTGGTGTGAGGGTTTTTAA+TGGTCTGGAAC+TTGTTCTTGGAAATGTTATAA+TGAAGTGGAGCTAAA+TTGGGCGAGGCTCGTGGTCTGGAAGAA+GT
Consensus (1024) GCAAAATATCTGGGATGACATCTTAA+ATTTGGTGTGAGGGTTTTTAA+TGGTCTGGAAC+TTGTTCTTGGAAATGTTATAA+TGAAGTGGAGCTAAA+TTGGGCGAGGCTCGTGGTCTGGAAGAA+GT

1156      1170      1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280
* pBIN_AR_TKTP... (798) TTCGCGCAGGACTACCCCGTTGGAAATCCCG+GAGTGTCTCGGAGGAAAGAAAATCCAAAGAACTGTATAAGATTCCTAGTTTGGACCATGACCATACATATGAGTGGTCTGATTTGTAATTTAGCT
« Seq. TKTPNLSA... (841) TTCGCGCAGGACTACCCCGTTGGAAATCCCG+GAGTGTCTCGGAGGAAAGAAAATCCAAAGAACTGTATAAGATTCCTAGTTTGGACCATGACCATACATATGAGTGGTCTGATTTGTAATTTAGCT
» Seq. TKTPNLSA... (975) TTCGCGCAGGACTACCCCGTTGGAAATCCCG+GAGTGTCTCGGAGGAAAGAAAATCCAAAGAACTGTATAAGATTCCTAGTTTGGACCATGACCATACATATGAGTGGTCTGATTTGTAATTTAGCT
Consensus (1156) TTCGCGCAGGACTACCCCGTTGGAAATCCCG+GAGTGTCTCGGAGGAAAGAAAATCCAAAGAACTGTATAAGATTCCTAGTTTGGACCATGACCATACATATGAGTGGTCTGATTTGTAATTTAGCT

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247      260      270      280      290      300      310      320      330      340      350      360      379
* pBIN_AR_SHMT_N... (1) TTCCTGAGCTTGTTTTTCGCGACCCATTCTCTGAAAA+GAATCCAAAATCGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAAGATGAGGCTAGATCAGACATTTGATCAAGAACCCATTTTGT
« Seq. SHMTNLSA... (1) TTCCTGAGCTTGTTTTTCGCGACCCATTCTCTGAAAA+GAATCCAAAATCGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAAGATGAGGCTAGATCAGACATTTGATCAAGAACCCATTTTGT
» Seq. SHMTNLSA... (247) TTCCTGAGCTTGTTTTTCGCGACCCATTCTCTGAAAA+GAATCCAAAATCGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAAGATGAGGCTAGATCAGACATTTGATCAAGAACCCATTTTGT
Consensus (247) TTCCTGAGCTTGTTTTTCGCGACCCATTCTCTGAAAA+GAATCCAAAATCGGTCGTAACGAAGAGGAGACGATTTGTGGCTAAAAATGAAAGATGAGGCTAGATCAGACATTTGATCAAGAACCCATTTTGT

380      390      400      410      420      430      440      450      460      470      480      490      500      512
* pBIN_AR_SHMT_N... (134) CTACTTACTACATAA+CTCAACTTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTTCAATGAAATTTGAGTAATTTCAAGTCTTCTTAGCAGCACITTTGATGATCTTTTCTAGGGGTTGCTCAC
« Seq. SHMTNLSA... (134) CTACTTACTACATAA+CTCAACTTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTTCAATGAAATTTGAGTAATTTCAAGTCTTCTTAGCAGCACITTTGATGATCTTTTCTAGGGGTTGCTCAC
» Seq. SHMTNLSA... (380) CTACTTACTACATAA+CTCAACTTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTTCAATGAAATTTGAGTAATTTCAAGTCTTCTTAGCAGCACITTTGATGATCTTTTCTAGGGGTTGCTCAC
Consensus (380) CTACTTACTACATAA+CTCAACTTTGGCTCATGATTTCTATGGAAGGGCTTTAGCTAATCATCTTTTCAATGAAATTTGAGTAATTTCAAGTCTTCTTAGCAGCACITTTGATGATCTTTTCTAGGGGTTGCTCAC

513      520      530      540      550      560      570      580      590      600      610      620      630      645
* pBIN_AR_SHMT_N... (267) AGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATTAGTTATGTACACTGTTTCTTGAATTTTAAAGGGTTTTTACGATGTCAGGCTCAT
« Seq. SHMTNLSA... (267) AGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATTAGTTATGTACACTGTTTCTTGAATTTTAAAGGGTTTTTACGATGTCAGGCTCAT
» Seq. SHMTNLSA... (513) AGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATTAGTTATGTACACTGTTTCTTGAATTTTAAAGGGTTTTTACGATGTCAGGCTCAT
Consensus (513) AGAGGATTTGCTCACAGATATAA+TAAAGCTGTTATAGCTGATTTAAGGGCAGTTAAAGAAAGGGACCCAGCTTGTATTAGTTATGTACACTGTTTCTTGAATTTTAAAGGGTTTTTACGATGTCAGGCTCAT

646      660      670      680      690      700      710      720      730      740      750      760      778
* pBIN_AR_SHMT_N... (400) AGGATTTGCACATAA+ATGTTCAAATGGTAGGCAAA+TTTGGCAGCTTTTGTATACAAAACAGGGTATCTGAAAGTTTTTGGCTGCGACATACATCTCTGGTCTAAAATTTGGTAAAGGGATTTTACTTGATCATG
« Seq. SHMTNLSA... (400) AGGATTTGCACATAA+ATGTTCAAATGGTAGGCAAA+TTTGGCAGCTTTTGTATACAAAACAGGGTATCTGAAAGTTTTTGGCTGCGACATACATCTCTGGTCTAAAATTTGGTAAAGGGATTTTACTTGATCATG
» Seq. SHMTNLSA... (646) AGGATTTGCACATAA+ATGTTCAAATGGTAGGCAAA+TTTGGCAGCTTTTGTATACAAAACAGGGTATCTGAAAGTTTTTGGCTGCGACATACATCTCTGGTCTAAAATTTGGTAAAGGGATTTTACTTGATCATG
Consensus (646) AGGATTTGCACATAA+ATGTTCAAATGGTAGGCAAA+TTTGGCAGCTTTTGTATACAAAACAGGGTATCTGAAAGTTTTTGGCTGCGACATACATCTCTGGTCTAAAATTTGGTAAAGGGATTTTACTTGATCATG

779      790      800      810      820      830      840      850      860      870      880      890      900      911
* pBIN_AR_SHMT_N... (533) CTACTGGAGTTGTCGTTGGTGAACCTGCTGTGATTTGGAATAATGTTGCAATTTTGCATAA+CTGACATTTGGTGGAACTGGCAAAATATCTGGGGATAGACATCTTAAATTTGGTGTGAGGGTTTTTAA+TTGG
« Seq. SHMTNLSA... (533) CTACTGGAGTTGTCGTTGGTGAACCTGCTGTGATTTGGAATAATGTTGCAATTTTGCATAA+CTGACATTTGGTGGAACTGGCAAAATATCTGGGGATAGACATCTTAAATTTGGTGTGAGGGTTTTTAA+TTGG
» Seq. SHMTNLSA... (779) CTACTGGAGTTGTCGTTGGTGAACCTGCTGTGATTTGGAATAATGTTGCAATTTTGCATAA+CTGACATTTGGTGGAACTGGCAAAATATCTGGGGATAGACATCTTAAATTTGGTGTGAGGGTTTTTAA+TTGG
Consensus (779) CTACTGGAGTTGTCGTTGGTGAACCTGCTGTGATTTGGAATAATGTTGCAATTTTGCATAA+CTGACATTTGGTGGAACTGGCAAAATATCTGGGGATAGACATCTTAAATTTGGTGTGAGGGTTTTTAA+TTGG

912      920      930      940      950      960      970      980      990      1000      1010      1020      1030      1044
* pBIN_AR_SHMT_N... (666) TGTGGAACTTGGTTCTTGGAAATGTTATAA+TTGAAGATGGAGCTAAA+TTGGGGCAGGGTCCGTGGTGTCTGAAAGAAAGTTCCGGCAGGACTACCCCGTTGGGAATCCGGCAGGTTGCTCGGAGGGAA+G
« Seq. SHMTNLSA... (666) TGTGGAACTTGGTTCTTGGAAATGTTATAA+TTGAAGATGGAGCTAAA+TTGGGGCAGGGTCCGTGGTGTCTGAAAGAAAGTTCCGGCAGGACTACCCCGTTGGGAATCCGGCAGGTTGCTCGGAGGGAA+G
» Seq. SHMTNLSA... (912) TGTGGAACTTGGTTCTTGGAAATGTTATAA+TTGAAGATGGAGCTAAA+TTGGGGCAGGGTCCGTGGTGTCTGAAAGAAAGTTCCGGCAGGACTACCCCGTTGGGAATCCGGCAGGTTGCTCGGAGGGAA+G
Consensus (912) TGTGGAACTTGGTTCTTGGAAATGTTATAA+TTGAAGATGGAGCTAAA+TTGGGGCAGGGTCCGTGGTGTCTGAAAGAAAGTTCCGGCAGGACTACCCCGTTGGGAATCCGGCAGGTTGCTCGGAGGGAA+G

1045      1050      1060      1070      1080      1090      1100      1110      1121
* pBIN_AR_SHMT_N... (799) GAAAAATCCAAAGAAACTTGTATAAGATTCCTAGTTTGGACCATGGACCATACATATGAGTGGTCTGATTTGTAATTTAG
« Seq. SHMTNLSA... (799) GAAAAATCCAAAGAAACTTGTATAAGATTCCTAGTTTGGACCATGGACCATACATATGAGTGGTCTGATTTGTAATTTAG
» Seq. SHMTNLSA... (959) GAAAAATCCAAAGAAACTTGTATAAGATTCCTAGTTTGGACCATGGACCATACATATGAGTGGTCTGATTTGTAATTTAG
Consensus (1045) GAAAAATCCAAAGAAACTTGTATAAGATTCCTAGTTTGGACCATGGACCATACATATGAGTGGTCTGATTTGTAATTTAG

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Supplementary Figure 1: Cloning and sequencing analysis of NtSAT4 gene overexpression constructs; Sequencing result using 35S forward and NtSAT4 reverse primers for the (A) Cytosolic targeted NtSAT4 (B) Plastid targeted NtSAT4 (C) Mitochondrial targeted NtSAT4 sequences.