FIGURE 1

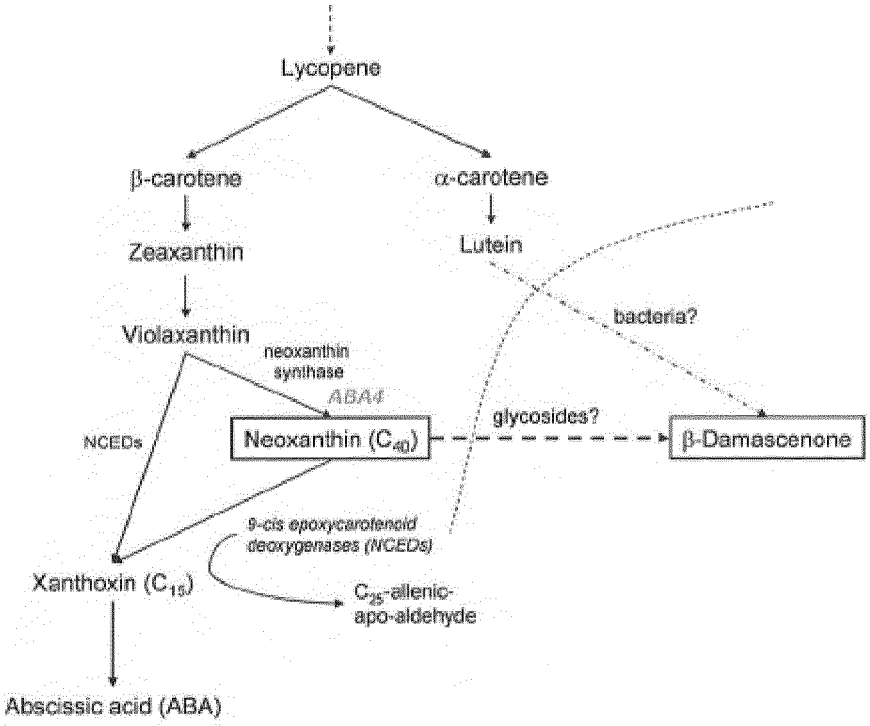

Lycopene
β-carotene
α-carotene
Zeaxanthin
Lutein
Violaxanthin
neoxanthin synthase
ABA4
bacteria?
NCEDs
Neoxanthin (C40)
glycosides?
β-Damascenone
9-cis epoxycarotenoid deoxygenases (NCEDs)
Xanthoxin (C15)
C25-allenic-apo-aldehyde
Abscissic acid (ABA)

FIGURE 2

A

atgtcactttcttttaattcttcttgtttttgttcccctcttaataagtcaagtatggacttctcttcttcttgcttctgctactc
tcacatctcactcaagatgaactgcagggcacctgccttgatgtccaggagaaaccagcctacctcttatacttttctagaaaaga
attctgacattgtaaatcaacaagtagtggaattcggaaccaagtttagaagtggagcgaatttcctgggaggatcaagagtcatt
attcaacttaatcttcaaacaactcttgctcaaagaaaaagctccagggtgactgcttgtttgccaagttctgaaattgcttctac
tgttttcacactgggaacagcagcagttcttccgttttatactctcatggttgtggctcctaaaactgaacttaccagaaaagtga
tgaaaagcagcatacccaatattggctttggacttctgtacacatatctagtatacctctcttggacaccagatacagttcggctg
atgtttgctagtaaatactggcttccggagctgcccggcataactaagatgttctccaacgagatgacattagcttctgcatggat
tcacttgttggctgtagatctttttgctgcaaggcaggtttatcatgatggattgcaaaatgatattgaaacccgccattctgtgt
ctctgtgcttgctgttttgccccgtcggaattgttactcacttcatcaccaaagctctagccagtagcccagaaaagagacagcat
aggactcattaa

B

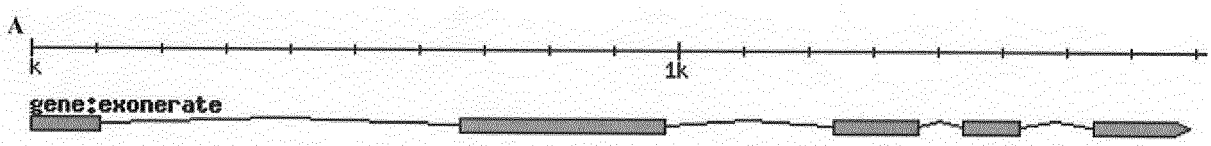
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IQLNLQTTLAQRKSSRVTACLPSSEIASTVFTLGTAAVLPFYTLMVVAPKTELTRKVMKSSIPNIGFGLLYTYLVYLSWTPDTVRL
MFASKYWLPELPGITKMFSNEMTLASAWIHLLAVDLFAARQVYHDGLQNDIETRHSVSLCLLFCPVGIVTHFITKALASSPEKRQH
RTH

C

NtABA4-F	caccatgtcactttcttttaattcttcttgt
NtABA4-R	ttaatgagtcctatgctgtctcttttc

FIGURE 3

3/8



B

```
Q    1 : ATGTCACTTTCTTTTAA---TTCTTCTTGTTTTTGTTCCCCTCTTAATAAGTCAAGTATGGA :   59
         ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
T    1 : ATGTCACTTTCTTTTAATTCTTCTTCTTGTTTTTGTTCCCCTCTTAATAAGTCAAGTATGGA :   62

    60 : CTTCTCTTCTTCTTGCTTCTGCTACTCTCACATCTCACTCAAG  >>>> Target Intro :  103
         ||||||||||||||||||||||||||||||||||||||||||||||||||||++          558 bp
    63 : CTTCTCTTCTTCTTGCTTCTGCTACTCTCACATCTCACTCAAGgt..................  :  108

   104 : n 1 >>>>  ATGAACTGCAGGGCACCTGCCTTGATGTCCAGGAGAAACCAGCCTACCTCTT :  154
                 ++|||||||||||||||||||||||||||||||||||||||||||||||||||||
   109 : ........agATGAACTGCAGGGCACCTGCCTTGATGTCCAGGAGAAACCAGCCTACCTCTT :  715

   155 : ATACTTTTCTAGAAAAGAATTCTGACATTGTAAATCAACAAGTAGTGGAATTCGGAACCAAG :  216
         |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
   716 : ATACTTTTCTAGAAAAGAATTCTGACATTGTAAATCAACGAGTAGTGGAATTCAGAACCAAG :  777

   217 : TTTAGAAGTGGAGCGAATTTCCTGGGAGGATCAAGAGTCATTATTCAACTTAATCTTCAAAC :  278
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   778 : TTTAGAAGTGGAGCGAATTTCCTGGGAGGATCAAGAGTCATTATTCAACTTAATCTTCAAAC :  839

   279 : AACTCTTGCTCAAAGAAAAAGCTCCAGGGTGACTGCTTGTTTGCCAAGTTCTGAAATTGCTT :  340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   840 : AACTCTTGCTCAAAGAAAAAGCTCCAGGGTGACTGCTTGTTTGCCAAGTTCTGAAATTGCTT :  901

   341 : CTACTGTTTTCACACTGGGAACAGCAGCAGTTCTTCCGTTTTATACTCTCATGGTTGTGGCT :  402
         |||||||||||||||||||||||||| |||||||||||||||| |||||||| ||||||
   902 : CTACTGTTTTCACACTGGGAACAGCAGCGGTTCTTCCGTTTTATACACTCATGGTAGTGGCT :  963

   403 : CCTAAAACTGAACTT  >>>> Target Intron 2 >>>>  ACCAGAAAAGTGATGAAA :  435
         ||||||| ||||||||++          261 bp          ++||||||||||||||||||
   964 : CCTAAAGCTGAACTTgt.........................agACCAGAAAAGTGATGAAA : 1257

   436 : AGCAGCATACCCAATATTGGCTTTGGACTTCTGTACACATATCTAGTATACCTCTCTTGGAC :  497
         |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
```

FIGURE 3 Cont'd

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1258 : AGCAGCATACCCTATATTGGCTTTGGACTTCTGTACACATATCTAGTATACCTCTCTTGGAC : 1319

 498 : ACCAGATACAGTTCGGCTGATGTTTGCTAGTAAATACTGGCTTCCGGAG  >>>> Target :  547
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||++          7
1320 : ACCAGATACAGTTCGGCTGATGTTTGCTAGTAAATACTGGCTTCCGGAGgt..........  : 1371

 548 :  Intron 3 >>>>  CTGCCCGGCATAACTAAGATGTTCTCCAACGAGATGACATTAGCTT :  592
        0 bp          ++|||||||||||||||||||||||||||||||||||||||||||||||||||||
1372 : ..............agCTGCCCGGCATAACTAAGATGTTCTCCAACGAGATGACATTAGCTT : 1484

 593 : CTGCATGGATTCACTTGTTGGCTGTAGATCTTTTTGCTGCAAG  >>>> Target Intro :  636
        ||||||||||||||||||||| ||||||||||||||||||||++          114 bp
1485 : CTGCATGGATTCACTTGTTGGCCGTAGATCTTTTTGCTGCAAGgt.................  : 1530

 637 : n 4 >>>>  GCAGGTTTATCATGATGGATTGCAAAATGATATTGAAACCCGCCATTCTGTG :  687
                ++|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1531 : ........agGCAGGTTTATCATGATGGATTGCAAAATGATATTGAAACCCGCCATTCTGTG : 1693

 688 : TCTCTGTGCTTGCTGTTTTGCCCCGTCGGAATTGTTACTCACTTCATCACCAAAGCTCTAGC :  749
        ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |
1694 : TCTCTGTGCTTGCTGTTTTGCCCCTTCGGAATTGTTACTCACTTCATCACCAAAGCTCTAAC : 1755

 750 : CAGTAGCCCAGAAAAGAGACAGCATAGGACTCATTAA :  786
        |||||||||||||||||||||||||||||||||||
1756 : CAGTAGCCCAGAAAAGAGACAGCATAGGACTCATTAA : 1792
```

C

```
Query: 1   MSLSFNSSSCFCSPLNKSSMDFSSSCFCYSHISLKMNCRAPALMSRRNQPTSYTFLEKNS 60
           MSLSFNSS CFCSPLNKSSMDFSSSCFCYSHISLKMNCRAPALMSRRNQPTSYTFLEKNS
Sbjct: 1   MSLSFNSS-CFCSPLNKSSMDFSSSCFCYSHISLKMNCRAPALMSRRNQPTSYTFLEKNS 59

Query: 61  DIVNQRVVEFRTKFRSGANFLGGSRVIIQLNLQTTLAQRKSSRVTACLPSSEIASTVFTL 120
           DIVNQ+VVEF TKFRSGANFLGGSRVIIQLNLQTTLAQRKSSRVTACLPSSEIASTVFTL
Sbjct: 60  DIVNQQVVEFGTKFRSGANFLGGSRVIIQLNLQTTLAQRKSSRVTACLPSSEIASTVFTL 119

Query: 121 GTAAVLPFYTLMVVAPKAELTRKVMKSSIPYIGFGLLYTYLVYLSWTPDTVRLMFASKYW 180
           GTAAVLPFYTLMVVAPK ELTRKVMKSSIP IGFGLLYTYLVYLSWTPDTVRLMFASKYW
Sbjct: 120 GTAAVLPFYTLMVVAPKTELTRKVMKSSIPNIGFGLLYTYLVYLSWTPDTVRLMFASKYW 179

Query: 181 LPELPGITKMFSNEMTLASAWIHLLAVDLFAARQVYHDGLQNDIETRHSVSLCLLFCPFG 240
           LPELPGITKMFSNEMTLASAWIHLLAVDLFAARQVYHDGLQNDIETRHSVSLCLLFCP G
Sbjct: 180 LPELPGITKMFSNEMTLASAWIHLLAVDLFAARQVYHDGLQNDIETRHSVSLCLLFCPVG 239

Query: 241 IVTHFITKALTSSPEKRQHRTH 262
           IVTHFITKAL SSPEKRQHRTH
Sbjct: 240 IVTHFITKALASSPEKRQHRTH 261
```

FIGURE 4

A

ATGGAAACTCTTCTCAAACCTTTTCCATCTCCTTTACTTTTCACTCCTACACCTCACAGGTCTATTTTTCAACTGAAT
TCTACTTTTCTGAATCCAACCACCCAGAACTTTTCAAGAAAAGTTCATCGCAGAAACAAAAGTAGTAGTAACAAATTT
TGTAGCTTTCTTGACTTAGCACCCACATCAAAACCAGAGTCTTTAGATGTTGACATCTCATGGGTTGATCCTAATTCG
GGCCGGGCTCTATTCGACGTGATCATCATCGGAGCTGGTCCTGCGGGCCTCCGGCTAGCTGAGCAAGTATCAAGATAT
GGTATTAAGGTATGTTGTGTTGACCCTTCACCACTTTCCATGTGGCCAAATAATTATGGTGTTTGGGTTGATGAGTTT
GAGAAGTTAGGATTGGAAGATTGTTTAGATCATAAGTGGCCTATGACTTGTGTTCATATAAATGATAACAAGACTAAG
TATTTGGGAAGACCATATGGTAGAGTCAGTAGAAAAAAGTTGAAGTTGAAATTGTTGAATAGTTGTGTTGATAATGGA
GGGAAGTTTTATAAAGCCAAGGTTTGGAAAGTGGAGCATGAAGAATTTGAGTCTTCAGTTGTTTGTGATGATGGTAGG
AAGATAAGGGGTAGTTTGATTGTAGATGCAAGTGGTTTTGCTAGTCCTTTTATAGAATATGACAAGCCAAGAAACCAT
GGTTATCAAATAGCTCATGGGATTTTAGCACAAGTGGATAATCATCCATTTGATTTGGATAAAATGGTGCTTATGGAT
TGGAGGGATTCTCATCTGGGAAATGAGCCATATTTGAGGGTGAACAATACTAAAGAACCAACATTCTTGTATGTGATG
CCATTTGATAGGAATTTGGTATTCTTGGAAGAGACTTCTTTGGTGAGTCGGCCTGTGCTATCGTATAGGGAAGTGAAA
AATAGGATGGTGGCAAGGTTAAGGCATTTGGGGATCAAAGTGACAAGTGTTATTGAGGATGAGAAATGTGTGATCCCC
ATGGGAGGACCACTTCCGCGGATCCCTCAAAATGTTATGGCAATTGGTGGAAATTCAGGGATAGTTCATCCATCGACA
GGGTACATGGTGGCTCGGAGCATGGCATTGGCACCAGTTTTGGCTGAGGCCATTGCTGAGAGCCTCGGCACAACCAGA
ATGATAAGAGGATCTCCACTTTACCATAAAGTTTGGAATGGTTTGTGGCCTCTAGAGAGAAGAAGTGTGAGAGAATGT
TACTCTTTTGGGATGGAGACTTTGTTGAAGCTTGATTTGAAAGGGACTAGGAGATTGTTTGATGCTTTCTTTGATCTT
GATCCCAAATACTGGCAAGGGTTCCTTTCCTCAAGGTTGTCTGTCAAAGAACTTGCTATGCTTAGCTTGTACCTTTTT
GGGCATGCCTCAAATTTGGCTAGGTTGGATATTGTTACAAAATGCCCGGTGCCCTTGGTTAAAATGATGGAAATCTAG

B

METLLKPFPSPLLFTPTPHRSIFQLNSTFLNPTTQNFSRKVHRRNKSSSNKFCSFLDLAPTSKPESLDVDISWVDPNS
GRALFDVIIIGAGPAGLRLAEQVSRYGIKVCCVDPSPLSMWPNNYGVWVDEFEKLGLEDCLDHKWPMTCVHINDNKTK
YLGRPYGRVSRKKLKLKLLNSCVDNGGKFYKAKVWKVEHEEFESSVVCDDGRKIRGSLIVDASGFASPFIEYDKPRNH
GYQIAHGILAQVDNHPFDLDKMVLMDWRDSHLGNEPYLRVNNTKEPTFLYVMPFDRNLVFLEETSLVSRPVLSYREVK
NRMVARLRHLGIKVTSVIEDEKCVIPMGGPLPRIPQNVMAIGGNSGIVHPSTGYMVARSMALAPVLAEAIAESLGTTR
MIRGSPLYHKVWNGLWPLERRSVRECYSFGMETLLKLDLKGTRRLFDAFFDLDPKYWQGFLSSRLSVKELAMLSLYLF
GHASNLARLDIVTKCPVPLVKMMEI

C

NeSY-F	CACCATGGAAACTCTTCTCAAACCTTTTC
NeSY-R	CTAGATTTCCATCATTTTAACCAAG

FIGURE 5

A

ACACAAGCTTGGCTTTATTCGGAGGCAAACTATTCGCTCTTGGTGAATCTGATTTACCGTATGCAGTAAAATTAGCCCCAGATGGT
GATATTATTACCCTCGGCCGTTACGATTTCGACGGAAAACTTTTCATGAGCATGACGGCACATCCCAAAATTGACCCAGATACTAA
CGAGGCTTTTGCTTTCCGTTACGGTCCAATGCCTCCTTTTTTAACTTACTTTAGAATCGAACCAAATGGTACAAAAACACCAGACG
TGCCAATATTTTCTATGACACGTCCGTCATTTCTTCATGACTTTGCAATTACAAATAAATTTGCGATATTCTCGGACATACAAATA
GGAATGAACCCACTTGAGTTCATCACCGGTGGTTCACCGGTGAGTTCAGACTCGGGGAAAATC

B

NtCED2_RNAi-F: caccacacaagcttggctttattcg
NtCED2_RNAi-R: gattttccccgagtctgaact

FIGURE 6

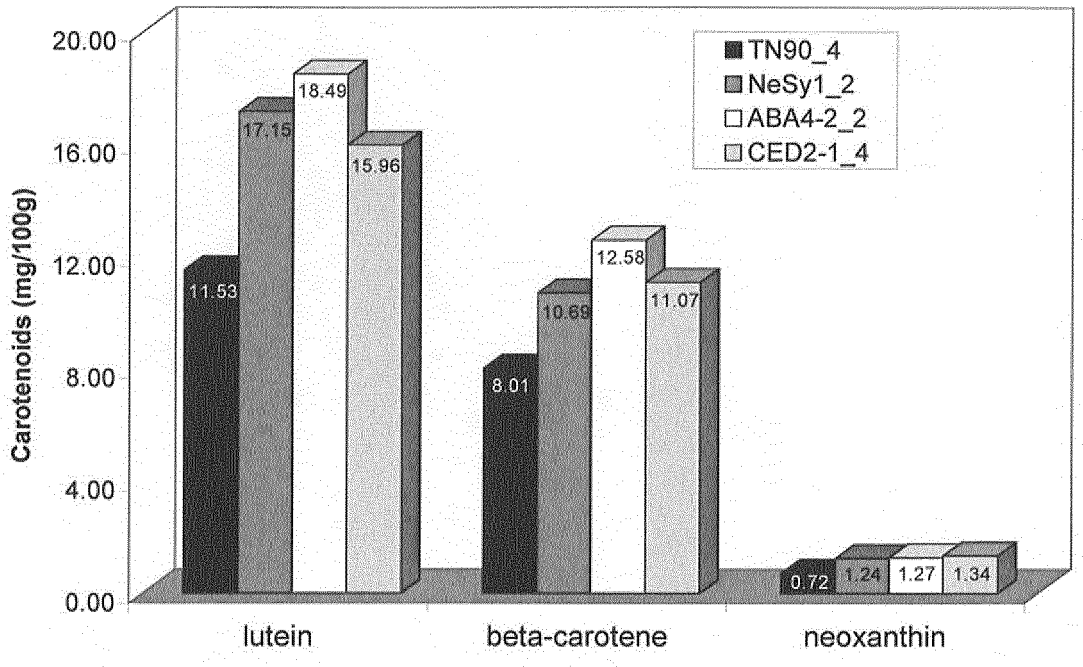
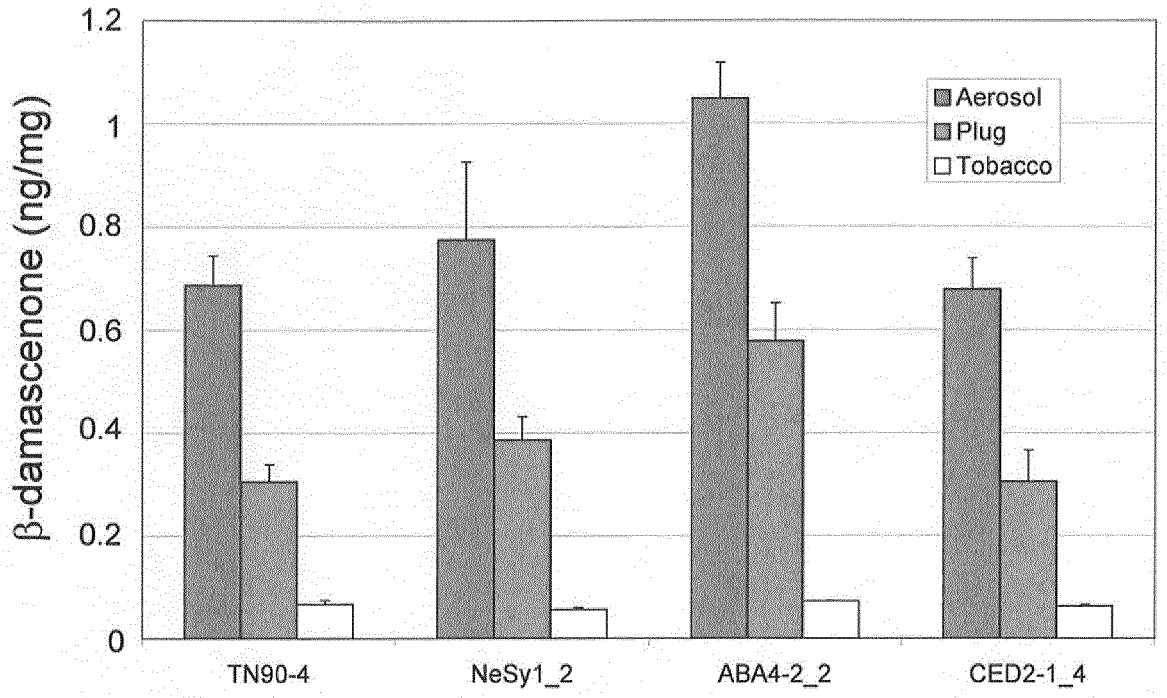

20.00
16.00
12.00
8.00
4.00
0.00
Carotenoids (mg/100g)
TN90_4
NeSy1_2
ABA4-2_2
CED2-1_4
11.53
17.15
18.49
15.96
8.01
10.69
12.58
11.07
0.72
1.24
1.27
1.34
lutein
beta-carotene
neoxanthin

FIGURE 7


β-damascenone (ng/mg)
1.2
1
0.8
0.6
0.4
0.2
0
Aerosol
Plug
Tobacco
TN90-4
NeSy1_2
ABA4-2_2
CED2-1_4