The *OsNADK1*'s promoter sequence and cis-element analysis

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         10        20        30        40        50        60        70
....|....|....|....|....|....|....|....|....|....|....|....|....|...|
GGGCAAGTTCAAATCAGTGGAAATGTAGCTTCTTTTAGCGGTTCATGTCATTTGACATTTGACGAATACT
                                                          CGTCA-motif
         80        90       100       110       120       130       140
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CCCAGCTTCACTGATGAATTTTTCAGATAACGACTGAGATGTATACTTGTACGTTTGGTGGCTACCTAAT
                            TGA-element
        150       160       170       180       190       200       210
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CCAACGCTAGTTCAGAATGAAAGCAACTTTGAGTGCCCCAAAATACAAAGGCAAGTCACTGTACTCGTCA
                                                            CGTCA-motif
        220       230       240       250       260       270       280
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AGGGTATCTTTATACACGGAATATTGGTCGAGACAAGAGAATTCTAAAGCTTCAGATCCGATGCAAATCT
        290       300       310       320       330       340       350
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AACATAAGCCAACGAAATATACTTACTACGCAGCTATGTAAAAATGTTGTCTCTCATCTTGGAACATTTT
        360       370       380       390       400       410       420
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TTTTCCGCGAACGCGCAAAAAAATCGCACGTCAATATATTAGAAGAAAAGAGTTATAGTTACACAACACA
                            CGTCA-motif
        430       440       450       460       470       480       490
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ATTAGCTAGACCGGCTTATGCCAGGAGAAGAGAGAAAAAGTAAAATAAAAAGCTGAAGCTTATAAAACTA
        500       510       520       530       540       550       560
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CGGCAGCTAAACACAAACTCCAAGTAGCAGGAAGGGCCCGAGCCACGCTACACTCCCAACAAGTCTCCAA
        570       580       590       600       610       620       630
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AAGCGGCAATGCTAGTTAAAGACCACGTATGACCCTCTGAGTGGATGGATTTTCAGAACCACTGAGATTG
                            ABRE
        640       650       660       670       680       690       700
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AAGAGAGCGCAGAGTCGAAAACCCTAGTGTTTCGTTCCTTCCACAACTGCCAAGCGATCAAGAGCACTAG
                                                MBS
        710       720       730       740       750       760       770
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
GAAGTCAAAGCCAGCATGGAGATGCTCAACTAAGCAGGCCCTGAAGGACAGCCACCAATTCTGGAACCAG
        780       790       800       810       820       830       840
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CTGCCATGGGGAAGAGATAGCAGCCCAGCCAGGGAGGCGATAGCACACGCAACCAGACCTGCCGAGCAAA
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          850       860       870       880       890       900       910
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CACATAGTCGAGGAGGATGTGTTTCACCGTCTCAAGATCCTAAGGCCATTCCCAACCCATGACACTAGAC
          920       930       940       950       960       970       980
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ATAGTTTCCATAAACTCCACATCATCAAGAAACTAGTACTAGACACTACTCTTCCAATGCAAATACCACT
          990      1000      1010      1020      1030      1040      1050
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ATTCCATACTTAGATTTAATGCTATTTATCTCACATGATGCCTTGGATATTGTGTAGAAACCATTGTTTC
                                                          ARE
         1060      1070      1080      1090      1100      1110      1120
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CTTCTCTTTTCTCATTTATTCACTTGCCACATCATTTTTCATCCTAGGTGGTAGCTTATTTAATGCTATA
         1130      1140      1150      1160      1170      1180      1190
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
GACACTATCCTAGTCATTGGGTTGGAAATGGCCTAAACGCAAAAGGGGCACGCCGAGTGACTATCGATTC
                                        P-box
          1200      1210      1220      1230      1240      1250      1260
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CACGCTGCTGAAATGCAAACCAAAGGATTCCGCAAAGTACTATAAAATATGTTTACCGGTTTTAATGATT
                 ARE
          1270      1280      1290      1300      1310      1320      1330
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TTGTAGTCCTTAAAAAGATATTAGAGCTACAAGTTTTTCTAGGATAATTTTAAGAAAAATAGTGTAAAAT
          1340      1350      1360      1370      1380      1390      1400
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ATAAGAATCTCGAGGTACGGCTCTCTCCTGCTATAAATACCTATAGAGAAGAGGTAACATTACCCTTTTT
         1410      1420      1430      1440      1450      1460      1470
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TTTCTTATATGAAATCAAACAAGATATCTACTGAAACAACTGGTGTTTAAGATAATATTAAGTTATAAAA
                                       MBS                          HSE
          1480      1490      1500      1510      1520      1530      1540
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TTTCAAAATTGAAATAATAACTAACCAAGTGACAGAAATATTCTGGTATATGATGGGATGAAAACGGGAA
   ERE
         1550      1560      1570      1580      1590      1600      1610
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CGGGAAAAGGAAAGGGAACAGACCCACCAACCAACCAACCAAACAAACCGGTTTAGCTTGCTGCTTGCCG
         1620      1630      1640      1650      1660      1670      1680
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
GCAGCAGTAACCACGAAAGCGCTCGGCTCCACACGCCACGCACACCCCACACCCCAACCCAAAGCGGCAT
                                    ABRE
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         1690      1700      1710      1720      1730      1740      1750
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CAGCGCACGCGTCAGTCGTAGCCTCACTGCGACCGGGACCCACCCACCCCCTGGCCCCACCTGTCAGCCC
       ABRE  CGTCA-motif
         1760      1770      1780      1790      1800      1810      1820
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
CCCGTTGGTGTCAACTCCCGGTGGCCTCCTGCTTCGCCGATAAATAACCGAATCGGGGGGAGGAGGTGGA
         1830      1840      1850      1860      1870      1880      1890
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
GGTGGTGCTCCTCCTCCTCAACAGCGTCGCCTCGCGTCGGCGTCGCCTCTCACCACCCAACCACCAGTCC
         1900      1910      1920      1930      1940      1950      1960
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ACCACCCACCTCTCTCCCTCCCCTCCCCTCCCCAAACCCAACCCGAGCCGAGGCCGGAATTTCCTTTTTG
          1970      1980      1990      2000 -1
....|....|....|....|....|....|....|....|....|....
GTGCGACGACGACGAGGTGAGGGTGAGCCAACCGCCGGATCGCGCCGCC（ATG:Start condon for
OsNADK1）
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Cis-elements analysis in OsNADK1's promoter

Plantcare element	Sequence	Position	Species	Function
CGTCA-motif	CGTCA	-320	*Hordeum vulgare*	involved in the MeJA-responsiveness
	CGTCA	-1631	*Hordeum vulgare*	involved in the MeJA-responsiveness
	TCAAG	-1802	*Hordeum vulgare*	involved in the MeJA-responsiveness
	TGACG	-1950	*Hordeum vulgare*	involved in the MeJA-responsiveness
ABRE	CGCACGCGTC	-326	*Hordeum vulgare*	involved in the abscisic acid responsiveness
	GCCACGCACA	-365	*Hordeum vulgare*	involved in the abscisic acid responsiveness
	CACGTA	-1426	*Arabidopsis thaliana*	involved in the abscisic acid responsiveness
ERE	ATTTCAAAA	-540	*Dianthus caryophyllus*	ethylene-responsive element
HSE	ATAAAATTTC	-545	*Brassica oleracea*	involved in heat stress responsiveness
MBS	CAACTG	-573	*Arabidopsis thaliana*	involved in drought-inducibility
	CAACTG	-1336	*Arabidopsis thaliana*	involved in drought-inducibility
ARE	AAACCA	-803	*Zea mays*	cis-acting regulatory element essential for the anaerobic induction
	AAACCA	-972	*Zea mays*	cis-acting regulatory element essential for the anaerobic induction
p-box	CAAAAGG	-850	*Oryza sativa*	gibberellin-responsive element
TGA-element	AACGAC	-1911	*Brassica oleracea*	auxin-responsive element