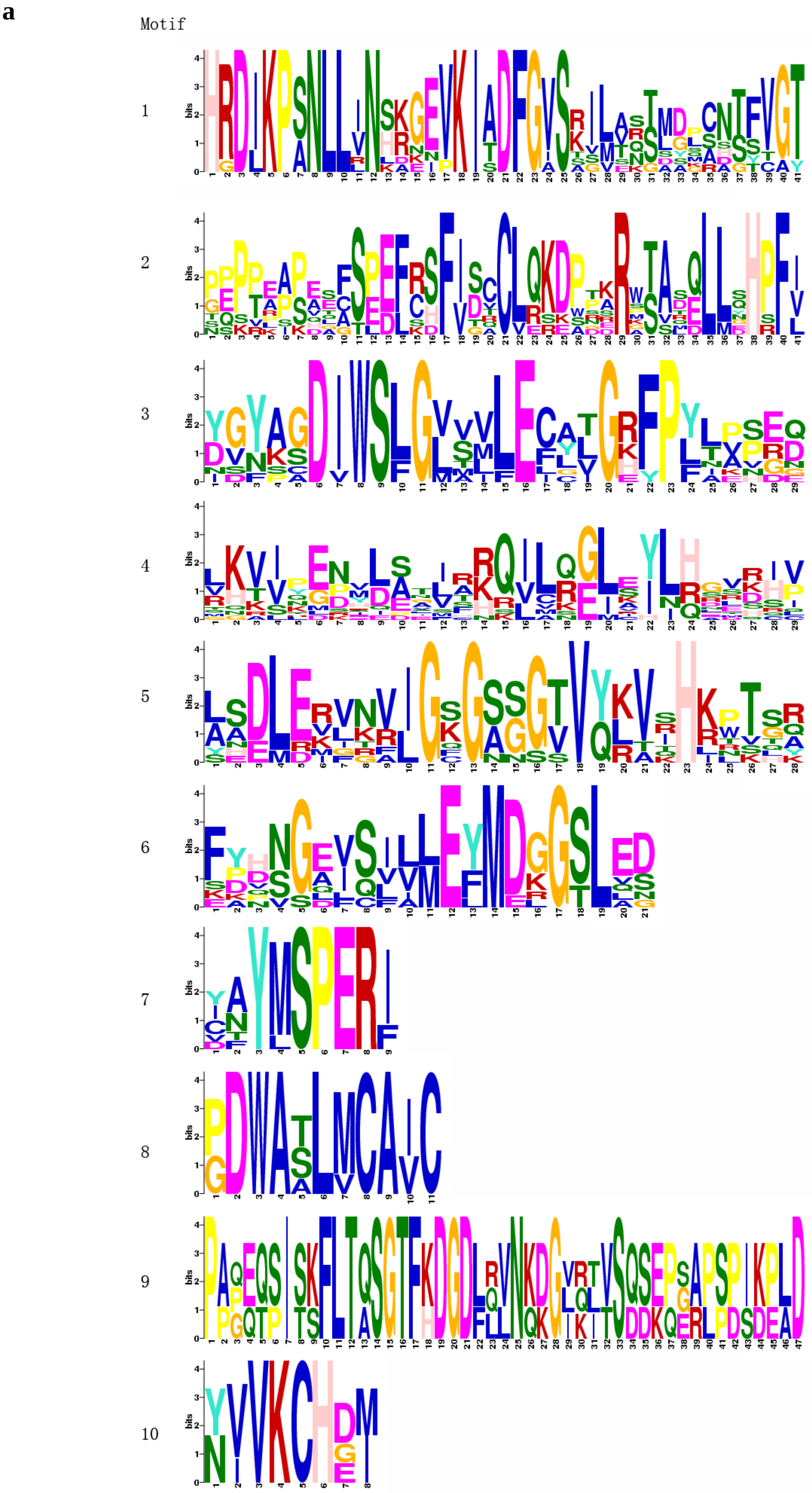
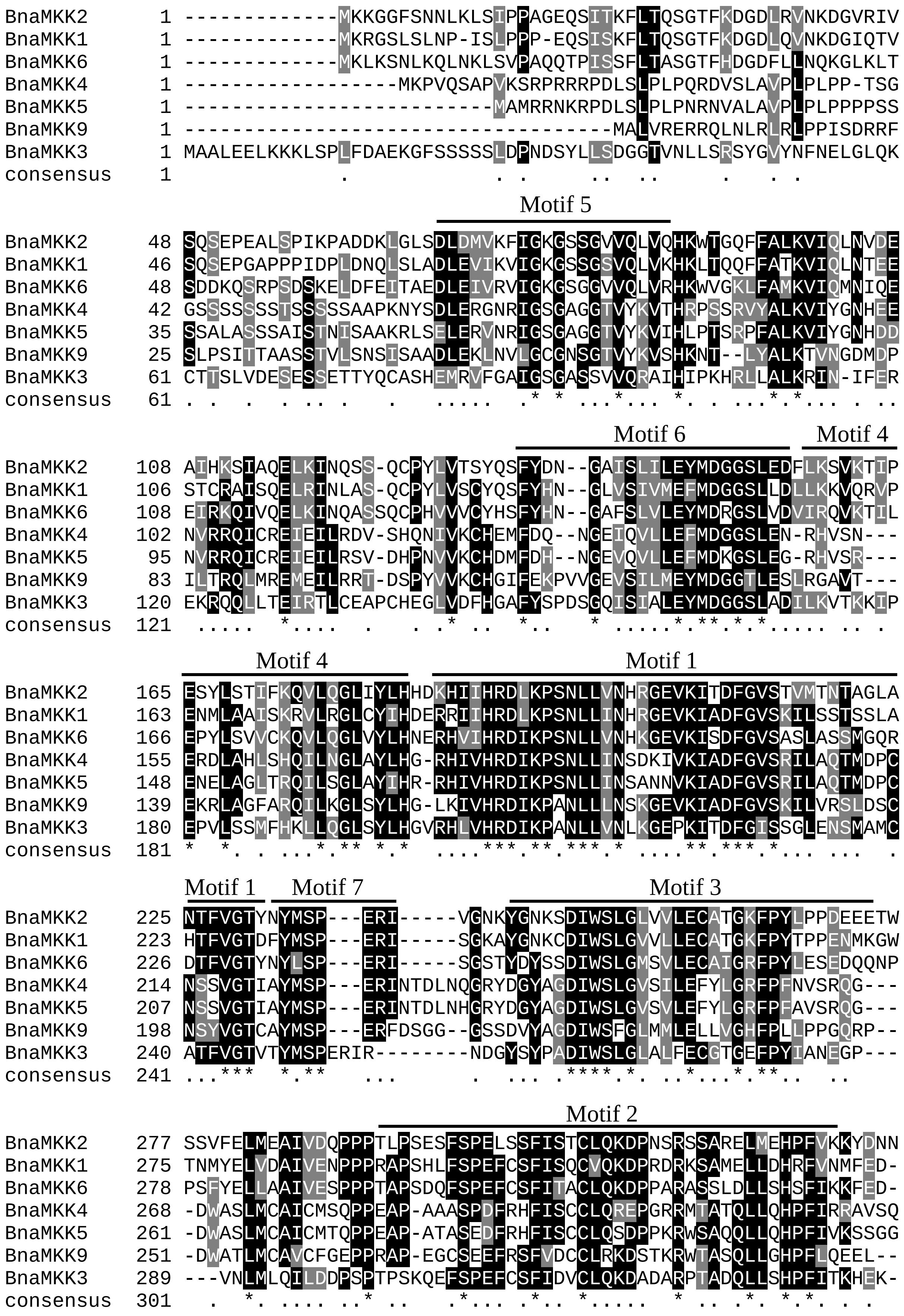

a
Motif
1
2
3
4
5
6
7
8
9
10
bits

b



```
                                           Motif 5
BnaMKK2      1 -------------MKKGGFSNNLKLSIPPAGEQSITKFLTQSGTFKDGDLRVNKDGVRIV
BnaMKK1      1 -------------MKRGSLSLNP-ISLPPP-EQSISKFLTQSGTFKDGDLQVNKDGIQTV
BnaMKK6      1 -------------MKLKSNLKQLNKLSVPAQQTPISSFLTASGTFHDGDFLLNQKGLKLT
BnaMKK4      1 ------------------MKPVQSAPVKSRPRRRPDLSLPLPQRDVSLAVPLPLPP-TSG
BnaMKK5      1 --------------------------MAMRRNKRPDLSLPLPNRNVALAVPLPLPPPPSS
BnaMKK9      1 ------------------------------------MALVRERRQLNLRLRLPPISDRRF
BnaMKK3      1 MAALEELKKKLSPLFDAEKGFSSSSSLDPNDSYLLSDGGTVNLLSRSYGVYNFNELGLQK
consensus    1              .            . .     ..  ..     .   . .

                                                   Motif 6          Motif 4
BnaMKK2     48 SQSEPEALSPIKPADDKLGLSDLDMVKFIGKGSSGVVQLVQHKWTGQFFALKVIQLNVDE
BnaMKK1     46 SQSEPGAPPPIDPLDNQLSLADLEVIKVIGKGSSGSVQLVKHKLTQQFFATKVIQLNTEE
BnaMKK6     48 SDDKQSRPSDSKELDFEITAEDLEIVRVIGKGSGGVVQLVRHKWVGKLFAMKVIQMNIQE
BnaMKK4     42 GSSSSSSSTSSSSSAAPKNYSDLERGNRIGSGAGGTVYKVTHRPSSRVYALKVIYGNHEE
BnaMKK5     35 SSALASSSAISTNISAAKRLSELERVNRIGSGAGGTVYKVIHLPTSRPFALKVIYGNHDD
BnaMKK9     25 SLPSITTAASSTVLSNSISAADLEKLNVLGCGNSGTVYKVSHKNT--LYALKTVNGDMDP
BnaMKK3     61 CTTSLVDESESSETTYQCASHEMRVFGAIGSGASSVVQRAIHIPKHRLLALKRIN-IFER
consensus   61 . .  .  . .. .   .   .....  .* * ...*... *. . ...*.*... . ..

BnaMKK2    108 AIHKSIAQELKINQSS-QCPYLVTSYQSFYDN--GAISLILEYMDGGSLEDFLKSVKTIP
BnaMKK1    106 STCRAISQELRINLAS-QCPYLVSCYQSFYHN--GLVSIVMEFMDGGSLLDLLKKVQRVP
BnaMKK6    108 EIRKQIVQELKINQASSQCPHVVVCYHSFYHN--GAFSLVLEYMDRGSLVDVIRQVKTIL
BnaMKK4    102 NVRRQICREIEILRDV-SHQNIVKCHEMFDQ--NGEIQVLLEFMDGGSLEN-RHVSN---
BnaMKK5     95 NVRRQICREIEILRSV-DHPNVVKCHDMFDH--NGEVQVLLEFMDKGSLEG-RHVSR---
BnaMKK9     83 ILTRQLMREMEILRRT-DSPYVVKCHGIFEKPVVGEVSILMEYMDGGTLESLRGAVT---
BnaMKK3    120 EKRQQLLTEIRTLCEAPCHEGLVDFHGAFYSPDSGQISIALEYMDGGSLADILKVTKKIP
consensus  121  .....  *....  .   .. * ..  *..   * .....*.**.*.*..... .. .

                     Motif 4                         Motif 1
BnaMKK2    165 ESYLSTIFKQVLQGLIYLHHDKHIIHRDLKPSNLLVNHRGEVKITDFGVSTVMTNTAGLA
BnaMKK1    163 ENMLAAISKRVLRGLCYIHDERRIIHRDLKPSNLLINHRGEVKIADFGVSKILSSTSSLA
BnaMKK6    166 EPYLSVVCKQVLQGLVYLHNERHVIHRDIKPSNLLVNHKGEVKISDFGVSASLASSMGQR
BnaMKK4    155 ERDLAHLSHQILNGLAYLHG-RHIVHRDIKPSNLLINSDKIVKIADFGVSRILAQTMDPC
BnaMKK5    148 ENELAGLTRQILSGLAYIHR-RHIVHRDIKPSNLLINSANNVKIADFGVSRILAQTMDPC
BnaMKK9    139 EKRLAGFARQILKGLSYLHG-LKIVHRDIKPANLLLNSKGEVKIADFGVSKILVRSLDSC
BnaMKK3    180 EPVLSSMFHKLLQGLSYLHGVRHLVHRDIKPANLLVNLKGEPKITDFGISSGLENSMAMC
consensus  181 *  *. . ...*.** *.*  ....***.**.***.* ....**.***.*... ...  .

               Motif 1  Motif 7                  Motif 3
BnaMKK2    225 NTFVGTYNYMSP---ERI-----VGNKYGNKSDIWSLGLVVLECATGKFPYLPPDEEETW
BnaMKK1    223 HTFVGTDFYMSP---ERI-----SGKAYGNKCDIWSLGVVLLECATGKFPYTPPENMKGW
BnaMKK6    226 DTFVGTYNYLSP---ERI-----SGSTYDYSSDIWSLGMSVLECAIGRFPYLESEDQQNP
BnaMKK4    214 NSSVGTIAYMSP---ERINTDLNQGRYDGYAGDIWSLGVSILEFYLGRFPFNVSRQG---
BnaMKK5    207 NSSVGTIAYMSP---ERINTDLNHGRYDGYAGDIWSLGVSVLEFYLGRFPFAVSRQG---
BnaMKK9    198 NSYVGTCAYMSP---ERFDSGG--GSSDVYAGDIWSFGLMMLELLVGHFPLLPPGQRP--
BnaMKK3    240 ATFVGTVTYMSPERIR--------NDGYSYPADIWSLGLALFECGTGEFPYIANEGP---
consensus  241 ...***  *.**   ...      .  ... .****.*. ..*...*.**..  ..

                                Motif 2
BnaMKK2    277 SSVFELMEAIVDQPPPTLPSESFSPELSSFISTCLQKDPNSRSSARELMEHPFVKKYDNN
BnaMKK1    275 TNMYELVDAIVENPPPRAPSHLFSPEFCSFISQCVQKDPRDRKSAMELLDHRFVNMFED-
BnaMKK6    278 PSFYELLAAIVESPPPTAPSDQFSPEFCSFITACLQKDPPARASSLDLLSHSFIKKFED-
BnaMKK4    268 -DWASLMCAICMSQPPEAP-AAASPDFRHFISCCLQREPGRRMTATQLLQHPFIRRAVSQ
BnaMKK5    261 -DWASLMCAICMTQPPEAP-ATASEDFRHFISCCLQSDPPKRWSAQQLLQHPFIVKSSGG
BnaMKK9    251 -DWATLMCAVCFGEPPRAP-EGCSEEFRSFVDCCLRKDSTKRWTASQLLGHPFLQEEL--
BnaMKK3    289 ---VNLMLQILDDPSPTPSKQEFSPEFCSFIDVCLQKDADARPTADQLLSHPFITKHEK-
consensus  301   .  *. .... ..* ..   .*... .*.. *.....  * .. .*. *.*. . .
```

```
BnaMKK2    337 SEINLASYFTNAGSPLATLKNLSGTFSV--------------------------------
BnaMKK1    334 VDVDLSSYFTAAGSLIPPLANS--------------------------------------
BnaMKK6    337 MDIDLGILVGTLEPPVNCLR----------------------------------------
BnaMKK4    326 GLNRSPQNLHQLLPPPPPRTLSSSSSSSPTT-----------------------------
BnaMKK5    319 ------PNLRQMLPPPPPAS----------------------------------------
BnaMKK9        ------------------------------------------------------------
BnaMKK3    345 ESVDLAAFVRSIFDPTQRLKDIADMLTIHYYSLFDGYDDLWHHARSLYTETSVFSFSGKQ
consensus  361   . .   .  .  .   .

BnaMKK2        ------------------------------------------------------------
BnaMKK1        ------------------------------------------------------------
BnaMKK6        ------------------------------------------------------------
BnaMKK4        ------------------------------------------------------------
BnaMKK5        ------------------------------------------------------------
BnaMKK9        ------------------------------------------------------------
BnaMKK3    405 YTGSTEILSQLSNIRNTLAGDLPSEKLVHVVEKLQCKPHGVGGVMIRAIGSFIVGNQFLI
consensus  421


BnaMKK2        ------------------------------------------------------
BnaMKK1        ------------------------------------------------------
BnaMKK6        ------------------------------------------------------
BnaMKK4        ------------------------------------------------------
BnaMKK5        ------------------------------------------------------
BnaMKK9        ------------------------------------------------------
BnaMKK3    465 CGDGVQAEGLPSFKDLGFDLGTRRVGRFQEQFVVESGDLIGRYFIAKQELYITS
consensus  481
```

Figure S2. A detailed motif analysis and multiple alignment of canola MKKs.

a, The analysis is from MEME 4.9.0 (Release date: Wed Oct 3 11:07:26 EST 2012).
Stack heights represent conservation at a position, and symbol heights within a stack represent the relative frequency of each residue.
b, Multiple alignment of BnaMKKs with 7 motifs shown as overbars.