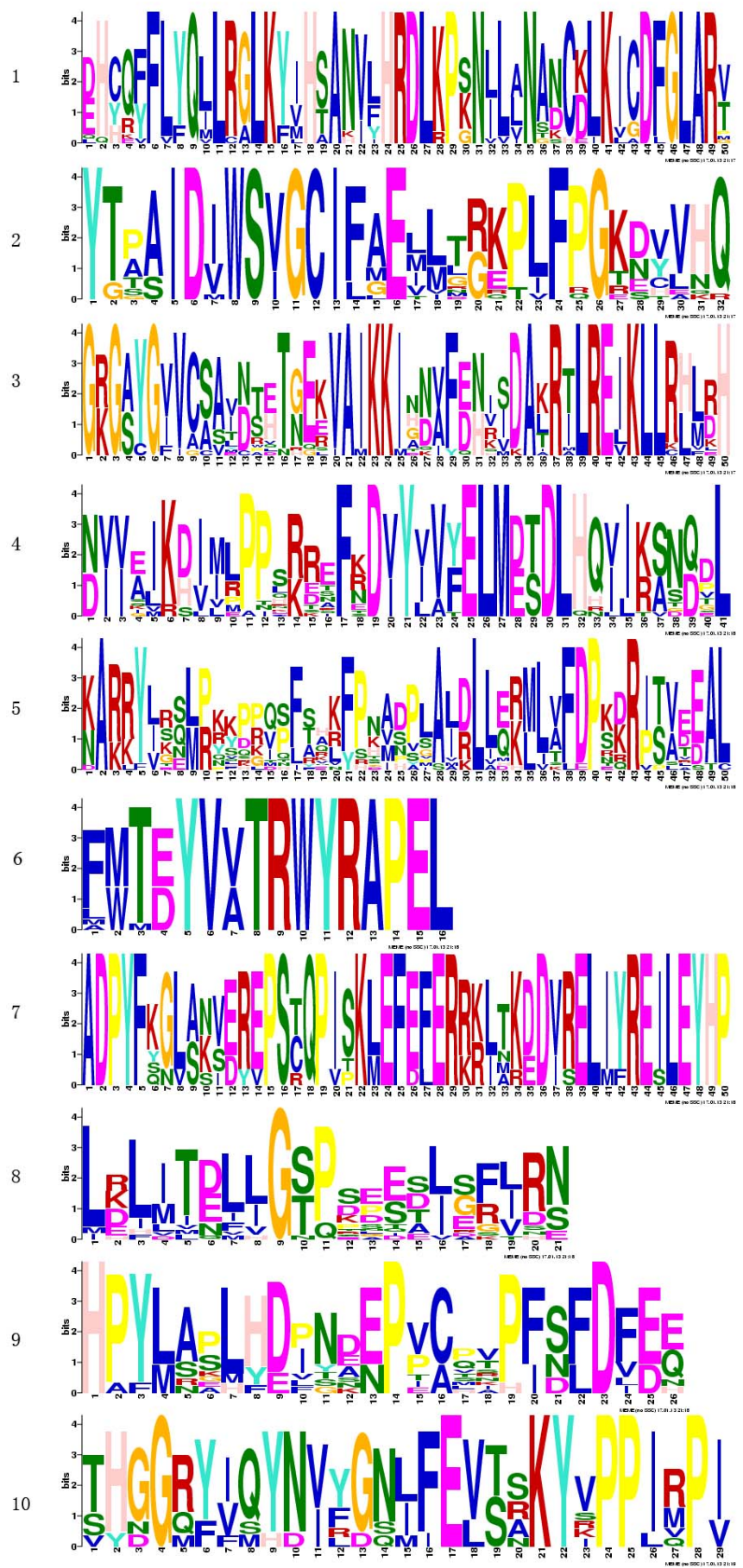


a

Motif



b

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BnaMPK8      1  MGGGGNLVDGVRRLWFQRPSSSSSSNNNNPQEPIKKSDTFSNPDHQSELVITEDLDFSGL
BnaMPK9      1  -----
BnaMPK17     1  -----
BnaMPK16     1  -----
BnaMPK19     1  -----
BnaMPK20     1  -----
BnaMPK1      1  -----MATPVD
BnaMPK2      1  -----MATPVD
BnaMPK3      1  -----MNNAGGQYP
BnaMPK6      1  -----MDGGTGQPAADTEMSEVTGGAAP
BnaMPK4      1  -----MSAENC
BnaMPK5      1  -----MSSETE
consensus    1

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                                     Motif 10                               Motif 3
BnaMPK8      61  KLIKVPKRHLLPMDPQKKGVEKDFFFEYGEAN--RYQVQEVVGKGSYGVVASALDHTHTG
BnaMPK9      1  -----MDPQKQVTLLETEFFFEYGEAS--RYQIQEVIIGKGSYGVVASALDHTHTG
BnaMPK17     1  -----MLEKEFFFEYGEAS--QYQIQEVIIGKGSYGVVASAECPHTG
BnaMPK16     1  -----MQPDQKQKSSVELDFFFEYGEGL--RYRIEEVIIGKGSYGVVCSAYDHTHTG
BnaMPK19     1  -----MQQGQVKKNMKEVDFFFEYGEAN--RYQILEVIIGKGSYGVVCAALDHTHTG
BnaMPK20     1  -----MQQDPQKKNLEMEFFSDYGEAS--REKIQEVIIGKGSYGVVCSALDHTLTG
BnaMPK1      7  P-----PNGVRNQGKHIFT--MQQNLFEIDTKYMP--IKPIGRGAYGVVCSVNTDNN
BnaMPK2      7  P-----PNGVRNQGKHIFS--MQQTLFEIDTKYVP--IKPIGRGAYGVVCSVNTRETN
BnaMPK3      10 -----DFPAVQTHGGQFISYDIFGSLFEVTSKYRPPVPIGRGAYGIVCSVLDSETN
BnaMPK6      24  SQPMPGIENIPATLSHGGMFIQYNIFGNI FEVTAKYSPPIPIGKGYGIVCSAMNSETN
BnaMPK4      7  FGGGGGDQSTKGLATHGGQYVQYNVYGNIFEVTRKYVPLRPIGRGAYGIVCAATNSETG
BnaMPK5      7  S---ATENNIKGVLVHGGRYFQHNVYGNMFEVSNKYVPPPIRPIGRGAYGFVCAAVDSETH
consensus    61  ..*.***.***.***.***.***.***.***.***.***.***.***.***.***.***.***

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                                     Motif 3                               Motif 4
BnaMPK8      119 ERVAIKKINDVFEHVSADATRIILREIKLLRLLRHPDIVEIKHIMLPPSRREFRDIYVVFEL
BnaMPK9      47  EKVAIKKINDVFEHVSADATRIILREIKLLRLLRHPDIVEIKHVMLPPSRREFRDIYVVFEL
BnaMPK17     40  GKVAIKKMTNVFEHVSADATRIILREIKLLRLLRHPDIVEIKHIMLPPCRREFKDIYVVFEL
BnaMPK16     49  EKVAIKKINDVFEHVSADATRIILREIKLLRLLRHPDIVEIKHIMLPPSRREFRDIYVVFEL
BnaMPK19     49  EKVAIKKINDVFEHVSADATRIILREIKLLRLLRHPDIVEIKSIMLPPSRREFKDIYVVFEL
BnaMPK20     50  EKVAIKKIHDVFEHVSADATRIILREIKLLRLLRHPDIVEIKHIMLPPSRREFKDIYVVFEL
BnaMPK1      56  EKVAIKKIHNVEENRIDAALRTLREIKLLRHLRHLRHNVIKDKVMMPIHKRSFKDVYLVYEL
BnaMPK2      56  ERVAIKKIHNVEQNRIDAALRTLREIKLLRHLRHLRHNVIKDKVMMANHKRTFKDVYLVYEL
BnaMPK3      62  ELVAMKKIANAFDNHMDAKRTLREIKLLRHLRHLRHNVIKDKVMMANHKRTFKDVYLVYEL
BnaMPK6      84  ESVAIKKIANAFDNKIDAKRTLREIKLLRHLRHLRHNVIKDKVMMANHKRTFKDVYLVYEL
BnaMPK4      67  EEVAIKKIGNAFDNKIDAKRTLREIKLLRHLRHLRHNVIKDKVMMANHKRTFKDVYLVYEL
BnaMPK5      64  EEVAIKKIGKAFDNKIDAKRTLREIKLLRHLRHLRHNVIKDKVMMANHKRTFKDVYLVYEL
consensus    121 ...*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*

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                                     Motif 4                               Motif 1
BnaMPK8      179  MESDLHQVIKANDDLTPDHYQFFLYQLLRGLKYVHAANVFHRDLKPKNILLANADCKLKIIC
BnaMPK9      107  MESDLHQVIKANDDLTPEHYQFFLYQLLRGLKFIHTANVFHRDLKPKNILLANSDCCLKIIC
BnaMPK17     100  MESDLHHVLKVNDDLTPQHQQFFLYQLLRGLKFMHSAHVHRDLKPKNILLANADCKIKIIC
BnaMPK16     109  MESDLHQVIKANDDLTPEHYQFFLYQLLRGLKYIHTANVFHRDLKPKNILLANADCKLKIIC
BnaMPK19     109  MESDLHQVIKANDDLTKEHHQFFLYQLLRALKYIHTANVYHRDLKPKNILLANANCKLKVIC
BnaMPK20     110  MESDLHQVIKANDDLTKEHYQFFLYQLLRALKYIHTANVYHRDLKPKNILLANANCKLKIIC
BnaMPK1      116  MDTDLHQIIRSNQQLSNDHCQYFLFQLLRGLKYIHSANILHRDLKPKGNLLINANCDLKIIC
BnaMPK2      116  MDTDLHQIIRSNQQLSNDHCQYFLFQLLRGLKYIHSANILHRDLKPKGNLLINANCDLKIIC
BnaMPK3      122  MDTDLHQIIRSNQQLSBEHCQYFLYQLLRGLKYIHSANILHRDLKPKSNLLINANCDLKIIC
BnaMPK6      144  MDTDLHQIIRSNQQLSBEHCQYFLYQLLRGLKYIHSANVLRDLKPKSNLLINANCDLKIIC
BnaMPK4      127  MDTDLHQIIRSNQPLTDDHCRCFFLYQLLRGLKYVHSANVLRDLKPKSNLLINANCDLKIIG
BnaMPK5      124  MDTDLHQIIRSDQPLTDDHCRCFFLYQLLRGLKYIHSANVLRDLKPKSNLLINANCDLKIIGA
consensus    181  *.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*

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| | | Motif 1 | Motif 6 | Motif 2 |
|-----------|-----|-------------------------------|----------------------------------|----------------------|
| BnaMPK8 | 239 | DFGLARVSFNDAPTAIFWTDYVATRWRAP | ELCGSFFFSKYTPAIDIWSVGCIFAEMILGK | |
| BnaMPK9 | 167 | DFGLARVSFNDAPSAIFWTDYVATRWRAP | ELCGSFFFSKYTPAIDIWSTGICIFAEMLTGK | |
| BnaMPK17 | 160 | DFGLARVSFTDSPAIFWTDYVATRWRAP | ELCGSFFYSNYTPAIDMWSVGCIFAEMLTGK | |
| BnaMPK16 | 169 | DFGLARVAFNDTPTAIFWTDYVATRWRAP | ELCGSFFFSKYTPAIDIWSTGICIFAELLTGK | |
| BnaMPK19 | 169 | DFGLARVSFNDTPITVFWTDYVATRWRAP | ELCGSFFCSKYTPAIDIWSTGICIFAELLGK | |
| BnaMPK20 | 170 | DFGLARVAFNDTPITVFWTDYVATRWRAP | ELCGSFFYSKYTPAIDIWSTGICIFAELVMGK | |
| BnaMPK1 | 176 | DFGLARTSN---TKCQLMTEYVVTRWRAP | ELL-LCCDNYGTSIDVWSVGCIFAELLGRK | |
| BnaMPK2 | 176 | DFGLARMSN---TKCQFMTEYVVTRWRAP | ELL-LCCDNYGTSIDVWSVGCIFAELLGRK | |
| BnaMPK3 | 182 | DFGLARPT---SENEFMTEYVVTRWRAP | ELL-LNSSDYTA AIDVWSVGCIFMELMNRK | |
| BnaMPK6 | 204 | DFGLARVN---SESEFMTEYVVTRWRAP | ELL-LNSSDYTA AIDVWSVGCIFMELMDRK | |
| BnaMPK4 | 187 | DFGLARTK---SETDFMTEYVVTRWRAP | ELL-LNCSEYTA AIDIWSVGCILGETMTRE | |
| BnaMPK5 | 184 | DFGLARTT---SETDLMTEYVVTRWRAP | ELL-LNSSEYTS AIDVWSVGCIFAELMTRE | |
| consensus | 241 | *.****. | * ** ***** | * . . . ** * |

| | | Motif 2 | Motif 8 | Motif 5 |
|-----------|-----|---------------------------|-----------------------------|---------------------|
| BnaMPK8 | 299 | PLFPGEDVVHQLDHTDFHGNPPPE | ESISRIRNEKARRYLSMRKQHPDSFYH | KFKADPL |
| BnaMPK9 | 227 | PLFPGKNVVHQLDHTDMLGTPSPE | AISRIRNEKARRYLGNMRRKPPVPTH | KFPVDP |
| BnaMPK17 | 220 | PLFPGKNVVHQLDHTDLLGTPSPIT | LSRIRNEKARKYLSNMRRKDPVPTH | KFPNIDPV |
| BnaMPK16 | 229 | PLFPGKNVVHQLDHTDMLGTPSAE | ATGRVNEKARRYLSMRKKKPIPF | SHKFPHADPL |
| BnaMPK19 | 229 | PLFPGKSVVHQLDHTDMLGTPKSE | TIAGVRNEKARKYLGEMRKKSLV | PFTQKFPNADPS |
| BnaMPK20 | 230 | PLFPGKNVVHQLDHTDMLGTPSLD | TISRVRNEKARRYLSMRKKKPIPF | TQKFPNADPL |
| BnaMPK1 | 232 | PIFQGTCLNQLKLIIVNILGSQR | DELEFIDNPKAKRYIRSLPYS | PGMSLSRLYPGAHV |
| BnaMPK2 | 232 | PIFPGTECLNQLKLIINILGSQK | EDELEFIDNPKAKRYIESLPYS | PGMSLSRLYPNANV |
| BnaMPK3 | 237 | PLFPGKDHVHQLRLITELIGTP | TESDLGFTHNEAKRYIRQLPN | FPRQLAKLFSHVNP |
| BnaMPK6 | 259 | PLFPGRDHVHQLRLITELIGTP | SEQEVFN-ENAKRYIRQLPPY | PRQSIDKFPNVHPL |
| BnaMPK4 | 242 | PLFPGKDYVHQLRLITELIGSP | DDSSLGFIRSENARRYVKQL | PQYPRQNF AARFPNMSAG |
| BnaMPK5 | 239 | PLFPGKDYVHQLRLITELIGSP | DGTSLEFIRSENARKYVKEL | PKLPRQSF AARFPMSSSI |
| consensus | 301 | *.*.*. . . . * | * | * * |

| | | Motif 5 | Motif 9 | Motif 7 |
|-----------|-----|---------------------|-----------------------|-----------------------|
| BnaMPK8 | 359 | ALRLLERLITFDPKDRVSA | ADDALADPYFSGLSNS | ERV PSTQPI SKLEFDLERK |
| BnaMPK9 | 287 | ALRLLHRLIAFDPKDRPTA | EALADPYFYGLANVD | REPSTQPIPKLEFEFERRK |
| BnaMPK17 | 280 | ALKLLQHLVAFDPKDRPSA | EALADPYFQGLANVD | YEPSRQPI SKLEFEFERRK |
| BnaMPK16 | 289 | ALRLLKMLSFDPKDRPTSE | EALADPYFKNLAKVERE | PSCQPVTKLEFEFERRIT |
| BnaMPK19 | 289 | ALRLLQRLIAFDPKDRPTA | EALADPYFKGLAKVERE | PSCQPI SKMEFEFERRL |
| BnaMPK20 | 290 | SLKLLERLIAFDPKDRP | -PLRSTCDPYFKDCESG | EG-ASCQPIR-DEFEFERRK |
| BnaMPK1 | 292 | AIDLQKMLVDFPSKRISV | TEALQHPYMAPLYDPNAN | PPAQQVPIDLDVDEEEL |
| BnaMPK2 | 292 | AIDLQKMLVDFPSKRISV | VEALQHPYMAPLYDPNAN | PPAQQVPIDLDVDEEED |
| BnaMPK3 | 297 | AIDLVDRLTFDPNKRITV | EEALNHPYLAKLHDPN | DEPICLPKPFSDFEQ |
| BnaMPK6 | 318 | AIDLIEKMLTFDPRRITV | LDALAHPYLNSLHDIS | DEPECTIPFNDFEQ |
| BnaMPK4 | 302 | AADLLEKMLVDFPSRRITV | DEALCHPYLAPLHDIN | EEPVCVRPFNFDFEQ |
| BnaMPK5 | 299 | AIDLLEKMLVDFPEKRITV | EEALCHPFLSALHDIN | DEPVCNSHFSDFEN |
| consensus | 361 | ...* * | * | * |

| | | Motif 7 |
|-----------|-----|-----------------------|
| BnaMPK8 | 419 | SELIFREILEYHPQMMQ |
| BnaMPK9 | 347 | RELIYREILEYHPRMQ |
| BnaMPK17 | 340 | RELMYREILEYHPRMQ |
| BnaMPK16 | 349 | RELIYRESLEYHPKML |
| BnaMPK19 | 349 | RELIYREILEYHPQLL |
| BnaMPK20 | 347 | RELISREILEYHPQLL |
| BnaMPK1 | 349 | REMMWNEMLHYHPQ |
| BnaMPK2 | 351 | RELMWEEVMHYHPET |
| BnaMPK3 | 355 | KEMIYREAIALNP |
| BnaMPK6 | 376 | KELIYREALAFNPE |
| BnaMPK4 | 360 | KELIYRETVKFN |
| BnaMPK5 | 357 | KELVWLESVKFN |
| consensus | 421 | * * * |

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BnaMPK8      477 RSTAMHRHHASLPRERVPAQSGETAEESS-----
BnaMPK9      399 RSAPLQQRHASLPRERVPAPKEENRPAAT-----
BnaMPK17     396 NSPPIQRKYTSLPRERVCSSEDEGGDSVH-----
BnaMPK16     402 HNPPEQQHASLPRACVLYSDNNHAAAQSSVEVTDGLSKCSIRDTERPRGADRRVPINV
BnaMPK19     401 PIIPPERKHASLPRSTVHPGVVTTSSNAQPPESRRHVSFDPSRNVVPSTSTKPLGPPPRIP
BnaMPK20     399 PVAPLERKHASLPRSTVIHSTGVARGGQPKLMNSTNTLNPETTRNIPLNHATLQAQQRN
BnaMPK1      -----
BnaMPK2      -----
BnaMPK3      -----
BnaMPK6      -----
BnaMPK4      -----
BnaMPK5      -----
consensus    481      . . . . .

BnaMPK8      506 -----DVERR-----AAAVASTLESEEEAD-
BnaMPK9      428 -----LATTP-----ESPQSSQHEGSNYMNG
BnaMPK17     425 -----AQLPS-----SSVFTPPQTPNTETG
BnaMPK16     462 PQTIQGAAVAR-----PGKVVGSVLRYNNCGA
BnaMPK19     461 SGRPGRAVESSSLTYENNRNLKESSYDARTSYYRTTPQQNTVSPNCFNPNTTMNQEKR
BnaMPK20     459 LSAAKPSAFMG--PVAPFDNGRSSRDAYDPRSFIRSTTTSLPFQQSASTAAMGKQQERR
BnaMPK1      -----
BnaMPK2      -----
BnaMPK3      -----
BnaMPK6      -----
BnaMPK4      -----
BnaMPK5      -----
consensus    541

BnaMPK8      526 -NGGGYSARSLMKS-----SSISGSKCIGVQSKTDKEDTIAEEGDGESVSAELT
BnaMPK9      449 MSQTGYSARSLLKS-----ASISASKCIGVKQRNQSE---HGESNSDATDALS
BnaMPK17     446 LSSKKTAQVDKAAA-----TPVKRSACLVR-----SDSICASRCV
BnaMPK16     489 ATGVEAIEQQRRM-----VRNPAGAAQYPKRTPQCKSNRGDEDSEGSSRLK
BnaMPK19     521 LGTEAAASQSKPQF-----VPTQCNSAKPAELNPNYVQQTQHKVGIDAKLLH
BnaMPK20     517 TTTTMESEKQARQISQYNIYAQPDVAINIDNNPFIMARTGMHKAENMSDHRIIIDTNLLQ
BnaMPK1      -----
BnaMPK2      -----
BnaMPK3      -----
BnaMPK6      -----
BnaMPK4      -----
BnaMPK5      -----
consensus    601

BnaMPK8      573 DRV-ASLRNS-----
BnaMPK9      494 QKA-AALHT-----
BnaMPK17     481 GVS-SAVS-----
BnaMPK16     537 QNP-QYIPQKVGGAQDTATSRWY-----
BnaMPK19     569 AQS-QYGPAGAAAVAVAAHRSVGTVGYGMS---
BnaMPK20     577 ATAGIGVAAAAAAAPGGSAHRKVGGVRYGMSKMY
BnaMPK1      -----
BnaMPK2      -----
BnaMPK3      -----
BnaMPK6      -----
BnaMPK4      -----
BnaMPK5      -----
consensus    661

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Figure S5. A detailed motif analysis and multiple alignment of canola MPKs.

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 BnaMPKs with 10 motifs shown as overbars.