

CDKF1	-----AFREIDALTILNGSPNVVVVMHEY-----	80
AhCDKF1b	-----AFREIDALQILQGSPNVVVVLHEY-----	79
AhCDKF1a	-----AFREIDALQILQGAPNVVVVLHEY-----	79
AiCDKF1b	-----AFREIDALQILQGAPNVVVVLHEY-----	79
AdCDKF1	-----AFREIDALQILQGSPNVVVVLHEY-----	79
AiCDKF1a	-----AFREIDALQILQGSPNVVVVLHEY-----	83
CDKE1	-----VSPTAIREIMLLREISHENVV-KLVNVH-----	92
AhCDKE1a	-----VSPTAIREIMLLREITHENVV-KLVNVH-----	98
AhCDKE1b	-----VSPTAIREIMLLREITHENVV-KLVNVH-----	98
AdCDKE1	-----VSPTAIREIMLLREITHENVV-KLVNVH-----	98
AiCDKE1	-----VSPTAIREIMLLREITHENVV-KLVNVH-----	98
CDKG1	-----FPLTSLREINILLSFHNHPAIV-NVKEVV-----	367
CDKG2	-----FPLTSLREINILLSFHHPSIV-DVKEVV-----	472
AdCDKG2a	-----FPLTSLREINILLSFHHPSIV-DVKEVV-----	473
AhCDKG2a	-----FPLTSLREINILLSFHHPSIV-DVKEVV-----	473
AhCDKG2b	-----FPLTSLREINILLSFHHPSIV-DVKEVV-----	473
AiCDKG2a	-----FPLTSLREINILLSFHHPSIV-DVKEVV-----	518
AhCDKG2e	-----FPLTSLREINILLSFHNHPAIV-DVKEVV-----	307
AhCDKG2f	-----FPLTSLREINILLSFHNHPAIV-DVKEVV-----	307
AiCDKG2c	-----FPLTSLREINILLSFHNHPAIV-DVKEVV-----	307
AdCDKG2c	-----FPLTSLREINILLSFHNHPAIV-DVKEVV-----	307
AhCDKG2c	-----FPLTSLREINILLSFHDHPAIV-DVKEVV-----	338
AiCDKG2b	-----FPLTSLREINILLSFHDHPAIV-DVKEVV-----	338
AhCDKG2d	-----FPLTSLREINILLSFHDHPAIV-DVKEVV-----	339
AdCDKG2b	-----FPLTSLREINILLSFHDHPAIV-DVKEVV-----	339
AhCDKC1b	ILYRYFLSLFPITAIREIKILKKLHHENVIK-LKEIVT-----SPGT--	108
AdCDKC1	ILYRYFLSLFPITAIREIKILKKLHHENVIK-LKEIVT-----SPGT--	108
AhCDKC1a	-----FPITAIREIKILKKLHHENVIK-LKEIVT-----SPGP--	96
AiCDKC1	-----FPITAIREIKILKKLHHENVIK-LKEIVT-----SPD--	95
CDKC1	-----FPITAIREIKILKKLHHENVIQ-LKEIVT-----SPGR--	97
CDKC2	-----FPITAIREIKILKKLHHENVIH-LKEIVT-----SPGR--	97
CDKD1-1	-----VNVLTALREIKLLKELKHPHII-ELI-----	74
CDKD1-3	-----VNFTALREIKLLKELKHPHII-LLI-----	75
CDKD1-2	-----VNFTALREIKLLKELNHPHIV-ELI-----	76
AhCDKD1c	-----VNFTALREIKLLKELKDPNII-ELI-----	77
AiCDKD1a	-----VNFTALREIKLLKELKDPNII-ELI-----	77
AhCDKD1d	-----VNFTALREIKLLKELKDPNII-ELI-----	77
AdCDKD1b	-----VNFTALREIKLLKELKDPNII-ELI-----	77
AdCDKD1a	-----VNFTALREIKLLKELKDPNII-ELI-----	77
AiCDKD1b	-----VNFTALREIKLLKELKDPNII-ELI-----	77
AhCDKD1a	-----VNFTALREIKLLKELKDPNII-ELI-----	77
AhCDKD1b	-----VNFTALREIKLLKELKDPNII-ELI-----	77
CDKA1	-----VPSTAIREISLLKEMQHSNI-VK-----	65
AdCDKA1a	-----VPSTAIREISLLKEMQHRNI-VRYTSACFLVIGYLIINEVDFLNANSKAI	93
AhCDKA1a	-----VPSTAIREISLLKEMQHRNI-VR-----	65
AhCDKA1d	-----VPSTAIREISLLKEMQHRNI-VRYTSANCFVIGYLIINEVDFLNANSKAI	93
AhCDKA1b	-----VPSTAIREISLLKEMQHRNI-VR-----	65
AhCDKA1c	-----VPSTAIREISLLKEMQHRNI-VR-----	65
AdCDKA1b	-----VPSTAIREISLLKEMQHRNI-VR-----	65
AiCDKA1	-----VPSTAIREISLLKEMQHRNI-VR-----	65
AhCDKB1a	-----VPPTALREVSLLQMLSQSIYIVRLLSVE-----	71
AdCDKB1	-----VPPTALREVSLLQMLSQSIYIVRLLSVE-----	71
AiCDKB1	-----VPPTALREVSLLQMLSQSIYIVRLLSVE-----	71
AhCDKB1b	-----VPPTALREVSLLQMLSQSIYIVRLLSVE-----	71
CDKB1-1	-----IPPTALREISLLQMLSTSIYVVRLLCVE-----	71
CDKB1-2	-----IPPTALREISLLQMLSQSIYIVRLLCVE-----	71
AhCDKB2a	-----VPPTTLREVSILRMLSRDPHVVRMLMDVK-----	90
AdCDKB2	-----VPPTTLREVSILRMLSRDPHVVRMLMDVK-----	90
AhCDKB2b	-----VPPTTLREVSILRMLSRDPHVVRMLMDVK-----	90
AiCDKB2	-----VPPTTLREVSILRMLSRDPHVVRMLMDVK-----	90
CDKB2-1	-----VPSTTLREISILRMLARDPHVVRMLMDVK-----	81
CDKB2-2	-----VPPTTLREISILRMLARDPHIVRMLMDVK-----	83

::*: *

Fig. S1. Multiple alignments of cyclin-binding domains of CDKs. Group-wise alignment of *Arachis hypogaea*, *Arachis duranensis*, *Arachis ipaensis* and *Arabidopsis thaliana* represent the cyclin-binding domains of CDKs. CDKA-PSTAIRE motif, CDKB1-PPTALRE motif, CDKB2-PPTTLRE motif, CDKC-PITAIRE motif, CDKD-NFTALRE motif, CDKE-SPTAIRE motif, CDKG-PLTSLRE motif. Specific cyclin-binding domain is absent in CDKFs. * indicates highly conserved residues among all groups of CDKs.

CDKL1	-----KIGQGTYSVFRAREVETGKMVALKKVFDNLQPE\$IRFMAREI	153
AhCDKL3	-----KIGQGTYSVFRAREVHSGRMVALKKVRFDFNQPE\$IRFMAREI	206
AdCDKL2	-----KIGQGTYSVFRAREVHSGRMVALKKVRFDFNQPE\$IRFMAREI	206
AhCDKL4	-----KIGQGTYSVFRAREVHSGRMVALKKVRFDFNQPE\$IRFMAREI	206
AiCDKL2	-----KIGQGTYSVFRAREVHSGRMVALKKVRFDFNQPE\$IRFMAREI	206
AdCDKL1	-----KIGQGTYSVFRAREVETGRMFALKKVRFDFNLQPE\$IRFMAREI	160
AhCDKL1	-----KIGQGTYSVFRAREVETGRMFALKKVRFDFNLQPE\$IRFMAREI	160
AhCDKL2	-----KIGQGTYSVFRAREVETGRMFALKKVRFDFNLQPE\$IRFMAREI	161
AiCDKL1	-----KIGQGTYSVFRAREVETGRMFALKKVRFDFNLQPE\$IRFMAREI	161
AiCDKL4	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	155
AdCDKL4	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	155
AhCDKL7	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	155
AhCDKL8	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	155
AdCDKL3	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	116
AiCDKL3	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	125
AhCDKL5	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	134
AhCDKL6	-----KIGQGTYSVFRARELETGKIVALKKVRFDFNFEPESVRFMAREI	134
CDKL2	-----KIGQGTYSNVFRARETETGRIVALKKVRFDFNFEPESVKFMAREI	169
CDKL3	-----KIGQGTYSNVFRARETETGRIVALKKVRFDFNFEPESVKFMAREI	179
CDKL7	-----KIGQGTYSNVYKADLLSGKIVALKKVRFDFNLEAESVKFMAREI	162
AhCDKL16	-----KIGQGTYSNVYKARDLLSGKIVALKKVRFDFNLEPESVKFMAREI	149
AiCDKL8	-----KIGQGTYSNVYKARDLLSGKIVALKKVRFDFNLEPESVKFMAREI	149
AhCDKL17	-----KIGQGTYSNVYKARDLLSGKIVALKKVRFDFNLEPESVKFMAREI	149
AdCDKL7	-----KIGQGTYSNVYKARDLLSGKIVALKKVRFDFNLEPESVKFMAREI	149
AhCDKL24	-----KIGQGTYSNVYKARDLVSGKIVALKKVRFDDLEGESVKFMAREI	104
AiCDKL11	-----KIGQGTYSNVYKARDLVSGKIVALKKVRFDDLEGESVKFMAREI	104
AhCDKL25	-----KIGQGTYSNVYKARDLVSGKIVALKKVRFDDHLEGESVKFMAREI	111
AdCDKL11	-----KIGQGTYSNVYKARDLVSGKIVALKKVRFDDHLEGESVKFMAREI	111
CDKL8	-----KIGSGTYSNVYKAKDSLGNIVALKKVRCDVNERESLKFMAREI	186
CDKL9	-----KIGQGTYSNVYKAKDMLTGKIVALKKVRFDFNLEPESVKFMAREI	166
AhCDKL10	-----KIGQGTYSNVYKARDTLTGKIVALKKVRFDFNLEPESVKFMAREI	161
AdCDKL6	-----KIGQGTYSNVYKARDTLTGKIVALKKVRFDFNLEPESVKFMAREI	161
AhCDKL11	-----KIGQGTYSNVYKARDTLTGKIVALKKVRFDFNLEPESVKFMAREI	160
AiCDKL6	-----KIGQGTYSNVYKARDTLTGKIVALKKVRFDFNLEPESVKFMAREI	160
AiCDKL12	-----KIGQGTYSNVYKAKDMMTGKIVALKKVRFDFNLEPESVKFMAREI	165
AdCDKL13	-----KIGQGTYSNVYKAKDMMTGKIVALKKVRFDFNLEPESVKFMAREI	166
AhCDKL12	-----KIGQGTYSNVYKAKDMMTGKIVALKKVRFDFNLEPESVKFMAREI	165
AhCDKL13	-----KIGQGTYSNVYKAKDMMTGKIVALKKVRFDFNLEPESVKFMAREI	166
AhCDKL14	-----KIGQGTYSNVYKAKDMLTGKIVALKKVRFDFNLEPESVKFMAREI	168
AiCDKL7	-----KIGQGTYSNVYKAKDMLTGKIVALKKVRFDFNLEPESVKFMAREI	168
AhCDKL15	-----KIGQGTYSNVYKAKDMLTGKIVALKKVRFDFNLEPESVKFMAREI	168
AdCDKL12	-----KIGQGTYSNVYKAKDMLTGKIVALKKVRFDFNLEPESVKFMAREI	168
CDKL4	-----QIGGGTFSKVFKARDLLRNKTVALKKIRFDINNSES\$IKCIAREI	151
CDKL5	-----KIGQGTYSNVYKARDLTNNKIVALKKVRFDFLSDLESVKFMAREI	185
CDKL6	-----KIGQGTYSNVYKARDLLHNKIVALKKVRFDFLNDMESVKFMAREI	261
AhCDKL19	-----KIGQGTYSTVYKARDITHQKIVALKKVRFDFNLDPE\$VKFMAREI	170
AhCDKL18	-----KIGQGTYSTVYKARDITQKIVALKKVRFDFNLDPE\$VKFMAREI	170
AdCDKL8	-----KIGQGTYSTVYKARDITQKIVALKKVRFDFNLDPE\$VKFMAREI	170
AiCDKL9	-----KIGQGTYSTVYKARDITHQKIVALKKVRFDFNLDPE\$VKFMAREI	170
AhCDKL20	-----KIGQGTYSTVYKARDVTNQKIVALKKVHFDSLNPES\$IKFMAREI	182
AiCDKL14	-----KIGQGTYSTVYKARDVTNQKIVALKKVHFDSLNPES\$IKFMAREI	164
AhCDKL21	-----KIGQGTYSTVYKARDVTNQKIVALKKVHFDSLNPES\$IKFMAREI	182
AdCDKL10	-----KIGQGTYSTVYKARDVTNQKIVALKKVHFDSLNPES\$IKFMAREI	182
CDKL10	-----MIGQGTYSNVYKARDLETNQIVALKKVRFANMDPE\$VRFMAREI	194
CDKL11	-----KIGQGTYSNVYKARDLETNQIVALKKVRFANMDPD\$VRFMAREI	211
AhCDKL22	-----DSKQIGQGTYSNVYKARDLETNKIVALKKVRFATMDPE\$VRFMAREI	155
AiCDKL10	-----DSKQIGQGTYSNVYKARDLETNKIVALKKVRFATMDPE\$VRFMAREI	155
AhCDKL26	-----ARDLETNKIVALKKVRFATMDPE\$VRFMAREI	149
AdCDKL9	-----IGQGTYSNVYKARDLETNKIVALKKVRFATMDPE\$VRFMAREI	180
AhCDKL28	-----QIGQGAYSSVHKALDLESGKFVALKKVRFLLSSDLAS\$VRFMAREI	203
AdCDKL14	-----QIGQGAYSSVHKALDLESGKFVALKKVRFLLSSDLAS\$VRFMAREI	203
AhCDKL27	-----QIGQGAYSSVHKALDLESGKFVALKKVRFLLSSDPAS\$VRFMAREI	203
AiCDKL13	-----QIGQGAYSSVHKALDLESGKFVALKKVRFLLSSDPAS\$VRFMAREI	203
CDKL15	-----KIGQGTYSNVYKARDLDQKKIVALKKVRFDFNLEPES\$VRFMAREI	182
AhCDKL23	VQYFAQISGILLMIDCEVLMKIGQGTYSNVYKARDLEQRKIVALKKVRFDFNLEPES\$VRFMAREI	238
AhCDKL9	-----KIGQGTYSNVYKARDLEQRKIVALKKVRFDFNLEPES\$VRFMAREI	179
AiCDKL5	-----KIGQGTYSNVYKARDLEQRKIVALKKVRFDFNLEPES\$VRFMAREI	179
AdCDKL5	-----KIGQGTYSNVYKARDLEQRKIVALKKVRFDFNLEPES\$VRFMAREI	179
CDKL12	-----KIGQGTYSNVYKARDLETKIVAMKKVRFVNMDPES\$VRFMAREI	195
CDKL13	-----MVAMKKVRFVNMDPES\$VRFMAREI	24
CDKL14	-----KIGQGTYSIVYKARDLETKIVAMKKVRFANMDPE\$VRFMAREI	189

.*:.*: : *.: :****

Fig. S2. Multiple alignments of cyclin-binding domains of CDKLs. Group-wise alignment of *Arachis hypogaea*, *Arachis duranensis*, *Arachis ipaensis* and *Arabidopsis thaliana* represent the cyclin-binding domains of CDKLs. CDK-like (CDKL)- (V/I/L)(R/K)(FM/CI)AREI motif. * indicates highly conserved residues among all groups of CDKLs.

CDK1 RVLHRDLKPFQMLLDRTNSLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 181

AhCDK1a RVLHRDLKPFQMLLDRTNSLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 240

AhCDK1a RVLHRDLKPFQMLLDRTNSLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 181

AhCDK1d RVLHRDLKPFQMLLDRTNSLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 214

AhCDK1b RVLHRDLKPFQMLLDRTNSLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 181

AhCDK1c RVLHRDLKPFQMLLDRTNSLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 181

AhCDK1b RVLHRDLKPFQMLLDRTNSLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 166

A1CDK1 R-----VVTWYRAPEILLGSHHY 140

* *****;

AhCDK1a IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 213

AhCDK1a IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 213

A1CDK1 IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 213

AhCDK1b IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 213

CDK1-1 IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 210

CDK1-2 IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 212

AhCDK2a IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 222

AhCDK2a IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 222

AhCDK2b IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 222

A1CDK2 IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 230

CDK2-1 IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 213

CDK2-2 IADLGLGRAFTVPLKSYTHEIVTLWYRAPEVLLGTHYSTGVDMNSVGCIFA----- 213

*****;

AhCDK1a LHRDIKGSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 227

AhCDK1a LHRDIKGSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 234

AhCDK1b LHRDIKGSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 234

A1CDK1 LHRDIKGSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 209

CDK1 LHRDIKGSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 220

CDK2 LHRDIKGSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 220

*****;

CDK1 MGDABEHGIVKIDPGLARIYQAPLPLSDMGVVVTIYRAPEILLGSHHYSAVDMKAV 222

AhCDK1a MGDABEHGIVKIDPGLARIYQAPLPLSDMGVVVTIYRAPEILLGSHHYSAVDMKAV 228

AhCDK1b MGDABEHGIVKIDPGLARIYQAPLPLSDMGVVVTIYRAPEILLGSHHYSAVDMKAV 228

AhCDK1c MGDABEHGIVKIDPGLARIYQAPLPLSDMGVVVTIYRAPEILLGSHHYSAVDMKAV 240

A1CDK1 MGDABEHGIVKIDPGLARIYQAPLPLSDMGVVVTIYRAPEILLGSHHYSAVDMKAV 228

*****;

CDK1 YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 473

CDK2 YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 579

AhCDK2a YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 580

AhCDK2a YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 580

AhCDK2b YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 580

A1CDK2a YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 623

AhCDK2a YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 413

AhCDK2c YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 413

A1CDK2c YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 413

AhCDK2c YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 444

A1CDK2b YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 444

AhCDK2d YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 445

AhCDK2b YLHTNWIHRDLKPSNLLIDNEGNLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 445

*****;

CDK1 LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 181

CDK1-3 LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 182

CDK1-2 LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 183

AhCDK1c LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 184

A1CDK1a LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 184

AhCDK1d LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 184

AhCDK1b LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 184

AhCDK1a LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 184

A1CDK1b LKGLAYCHKKWVLRDMKPFNLLIGSHGQLKLADPGLARAFGIPVRTFTHEVVTWYRAPEILLGSHHY 184

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CDK1 VVRDDTDKSDNVHDGDISCLATCTVSEMDODLGRNSFSYDADEAVDDTQGLMTCVGTNRFPPELL 304

AhCDK1b S-AEDIDKDTNIPDGNTSCLATCTTSDIDDDPLKSSFSYEAREDEGEESGCLTCVGTNRFPPELL 281

A1CDK1a S-AEDIDKDTNIPDGNTSCLATCTTSDIDDDPLKSSFSYEAREDEGEESGCLTCVGTNRFPPELL 283

A1CDK1b S-AEDIDKDTNIPDGNTSCLATCTTSDIDDDPLKSSFSYEAREDEGEESGCLTCVGTNRFPPELL 281

AhCDK1a S-AEDIDKDTNIPDGNTSCLATCTTSDIDDDPLKSSFSYEAREDEGEESGCLTCVGTNRFPPELL 281

AhCDK1b S-AEDIDKDTNIPDGNTSCLATCTTSDIDDDPLKSSFSYEAREDEGEESGCLTCVGTNRFPPELL 281

A1CDK1 S-AEDIDKDTNIPDGNTSCLATCTTSDIDDDPLKSSFSYEAREDEGEESGCLTCVGTNRFPPELL 281

*****;

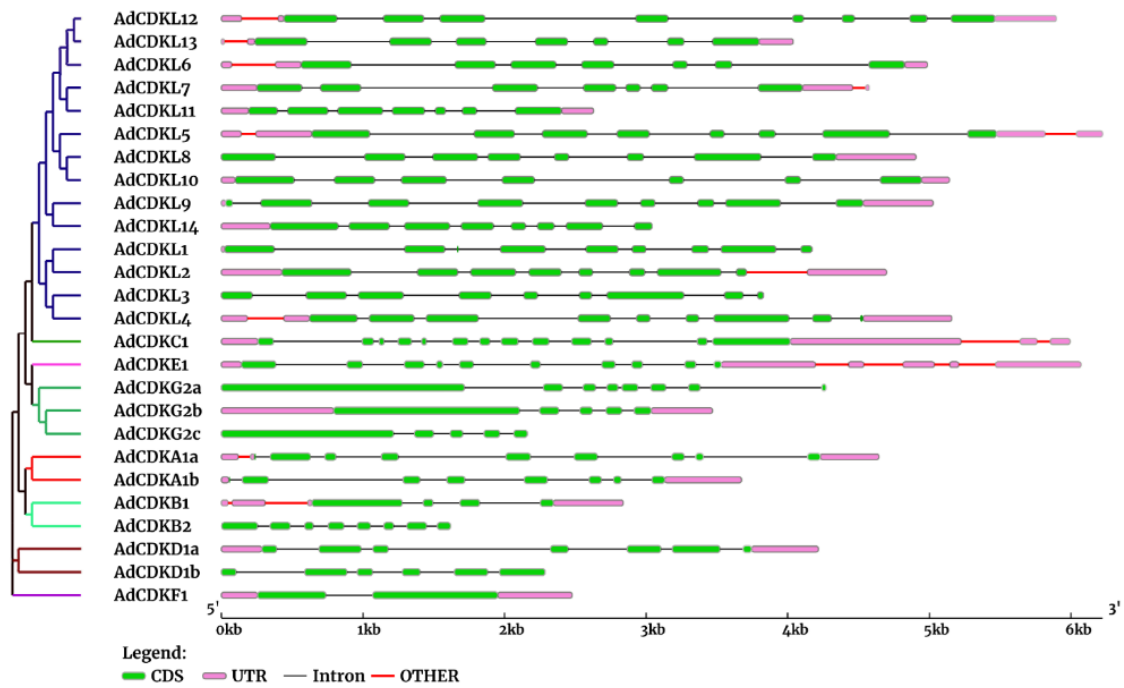
Fig. S3. Multiple alignments of T-loop regions of CDKs. Group-wise alignment of *Arachis hypogaea*, *Arachis duranensis*, *Arachis ipaensis* and *Arabidopsis thaliana* represent the T-loop regions of CDKs. Black line indicates T-loop region of each CDK group. Probable phosphorylated threonine residues are represented by red colour. * indicates highly conserved residues among all groups of CDKs.

CDKL1	VLKIGDPGLANVTSP--SNKNQLTSRVVTWYRAPELLMGSTSYGVSVDLNSVGCVFPAEI	299
AhCDKL3	VLKIGDPGLANTLSP--NNKNPLTSRVVTWYRAPELLMGSTNYGVSVDLNSVGCVFPAEL	352
AdCDKL2	VLKIGDPGLANTLSP--NNKNPLTSRVVTWYRAPELLMGSTNYGVSVDLNSVGCVFPAEL	352
AhCDKL4	VLKIGDPGLANTLSP--NNKNPLTSRVVTWYRAPELLMGSTNYGVSVDLNSVGCVFPAEL	352
A1CDKL2	VLKIGDPGLANTLSP--NNKNPLTSRVVTWYRAPELLMGSTNYGVSVDLNSVGCVFPAEL	352
AdCDKL1	ILKIGDPGLANTISP--NNKHQLTSRVVTWYRPELLMGSTNYGVSVDLNSVGCVFPAEL	310
AhCDKL1	ILKIGDPGLANTISP--NNKHQLTSRVVTWYRPELLMGSTNYGVSVDLNSVGCVFPAEL	306
AhCDKL2	ILKIGDPGLANTISP--NNKHQLTSRVVTWYRPELLMGSTNYGVSVDLNSVGCVFPAEL	307
A1CDKL1	ILKIGDPGLANTISP--NNKHQLTSRVVTWYRPELLMGSTNYGVSVDLNSVGCVFPAEL	307
A1CDKL4	ILKVADPGLANFSSS-A-YRHPLTSRVVTWYRPELLLGSTDYGPVSVDLNSVGCVFPAEL	328
AdCDKL4	ILKVADPGLANFSSS-A-YRHPLTSRVVTWYRPELLLGSTDYGPVSVDLNSVGCVFPAEL	328
AhCDKL7	ILKVADPGLANFSSS-A-YRHPLTSRVVTWYRPELLLGSTDYGPVSVDLNSVGCVFPAEL	319
AhCDKL8	ILKVADPGLANFSSS-A-YRHPLTSRVVTWYRPELLLGSTDYGPVSVDLNSVGCVFPAEL	319
AdCDKL3	ILKVADPGLANWCNS-GN-KQPLTSRVVTWYRPELLLGSTDYSPSVDLNSVGCVFPAEL	262
A1CDKL3	ILKVADPGLANWCNS-GNNKQPLTSRVVTWYRPELLLGSTDYSPSVDLNSVGCVFPAEL	272
AhCDKL5	ILKVADPGLANWCNS-GNNKQPLTSRVVTWYRPELLLGSTDYSPSVDLNSVGCVFPAEL	281
AhCDKL6	ILKVADPGLANWCNS-GNNKQPLTSRVVTWYRPELLLGSTDYSPSVDLNSVGCVFPAEL	281
CDKL2	ILKVADPGLANFSSS-GHKKKPLTSRVVTWYRPELLLGATDYGASVDLNSVGCVFPAEL	317
CDKL3	ILKVADPGLANFCNASGN-KQPLTSRVVTWYRPELLLGATEYGASVDLNSVGCVFPAEL	326
CDKL7	ILK1ADPGLATFFDP--KQKQMTSRVVTWYRPELLLGATSYGTCVVDLNSAGC1MAEL	308
AhCDKL16	ILK1ADPGLATFFDP--KQKQVLTSRVVTWYRPELLLGATFFYGVCVDLNSAGC1LAEL	295
A1CDKL8	ILK1ADPGLATFFDP--KQKQVLTSRVVTWYRPELLLGATFFYGVCVDLNSAGC1LAEL	295
AhCDKL17	ILK1ADPGLATFFDP--KQKQVLTSRVVTWYRPELLLGATFFYGVCVDLNSAGC1LAEL	295
AdCDKL7	ILK1ADPGLATFFDP--KQKQVLTSRVVTWYRPELLLGATFFYGVCVDLNSAGC1LAEL	295
AhCDKL24	ILK1ADPGLAAFYDS--KQTRPMTSRVVTWYRPELLLGATFFYGVCIDLNSAGC1FAEL	250
A1CDKL11	ILK1ADPGLAAFYDS--KQTRPMTSRVVTWYRPELLLGATFFYGVCIDLNSAGC1FAEL	250
AhCDKL25	ILK1ADPGLAAFYDS--KQTRPMTSRVVTWYRPELLLGATFFYGVCIDLNSAGC1FAEL	257
AdCDKL11	ILK1ADPGLAAFYDS--KQTRPMTSRVVTWYRPELLLGATFFYGVCIDLNSAGC1FAEL	257
CDKL8	VLKIGDPGLATFFDA--SKRQEMTSRVVTWYRSPPELLHGVVEYSVGVVDLNSAGC1LAEL	332
CDKL9	VLK1ADPGLATIFDP--NKKRPMTSRVVTWYRAPELLLGATDYGVCIDLNSAGC1LAEL	312
AhCDKL10	VLK1ADPGLASFFDP--HHKHFMTSRVVTWYRPELLLGATEYGVGVVDLNSAGC1LAEL	307
AdCDKL6	VLK1ADPGLASFFDP--HHKHFMTSRVVTWYRPELLLGATEYGVGVVDLNSAGC1LAEL	307
AhCDKL11	VLK1ADPGLASFFDP--HHKHFMTSRVVTWYRPELLLGATEYGVGVVDLNSAGC1LAEL	306
A1CDKL6	VLK1ADPGLASFFDP--HHKHFMTSRVVTWYRPELLLGATEYGVGVVDLNSAGC1LAEL	306
A1CDKL12	ILK1ADPGLASLFDP--NKKHPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	291
AdCDKL13	ILK1ADPGLASLFDP--NKKHPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	280
AhCDKL12	ILK1ADPGLASLFDP--NKKHPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	311
AhCDKL13	ILK1ADPGLASLFDP--NKKHPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	312
AhCDKL14	VLK1ADPGLASFFDP--NRKQPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	314
A1CDKL7	VLK1ADPGLASFFDP--NRKQPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	314
AhCDKL15	VLK1ADPGLASFFDP--NRKQPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	314
AdCDKL12	VLK1ADPGLASFFDP--NRKQPMTSRVVTWYRPELLLGATDYGVCIDLNSAGC1LGE1	314
CDKL4	VLK1ADPGLATFFDP--HNSVPLTTHVATLWYRPELLLGASHYGTCVVDLNS1GCV1GE1	298
CDKL5	VLK1ADPGLATFFDP--QMCVPLTSRVVTWYRPELLLGACHYGVCVDLNS1GCC1LGE1	331
CDKL6	VLK1ADPGLATFFDP--AKSVPLTSRVVTWYRPELLLGASHYGVCVDLNS1GCC1LGE1	407
AhCDKL19	ILK1ADPGLANFLDP--HLNVPLTSRV-----TPELLLGASRYGVAVDLNS1GCC1LGE1	310
AhCDKL18	ILK1ADPGLANFLDP--HLNVPLTSRVVTWYRPELLLGASHYGVAVDLNS1GCC1LGE1	316
AdCDKL8	ILK1ADPGLANFLDP--HLNVPLTSRVVTWYRPELLLGASHYGVAVDLNS1GCC1LGE1	316
A1CDKL9	ILK1ADPGLANFLDP--HLNVPLTSRVVTWYRPELLLGASRYGVAVDLNS1GCC1LGE1	316
AhCDKL20	VLK1ADPGLASFFDP--HHS1PLTSRVVTWYRPELLLGANHYGVAVDLNS1GCC1LGE1	328
A1CDKL14	VLK1ADPGLASFFDP--HHS1PLTSRVVTWYRPELLLGANHYGVAVDLNS1GCC1LGE1	310
AhCDKL21	VLK1ADPGLASFFDP--HHS1PLTSRVVTWYRPELLLGANHYGVAVDLNS1GCC1LGE1	328
AdCDKL10	VLK1ADPGLASFFDP--HHS1PLTSRVVTWYRPELLLGANHYGVAVDLNS1GCC1LGE1	328
CDKL10	NLKIGDPGLANFYRC--QKQPLTSRVVTWYRPELLLGSTDYGVTVVDLNS1GCC1LAEL	340
CDKL11	NLKIGDPGLANFYRC--QKQPLTSRVVTWYRPELLLGSTDYGVTVVDLNS1GCC1LAEL	357
AhCDKL22	RLKIGDPGLATSFHP--SKGKPLTSRVVTWYRPELLLGATDYGVSVDLNS1GCC1LAEL	301
A1CDKL10	RLKIGDPGLATSFHP--SKGKPLTSRVVTWYRPELLLGATDYGVSVDLNS1GCC1LAEL	301
AhCDKL26	-----QP--SKGKPLTSRVVTWYRPELLLGATDYGVSVDLNS1GCC1LAEL	245
AdCDKL9	RLKIGDPGLATSFQP--SKGKPLTSRVVTWYRPELLLGATDYGVSVDLNS1GCC1LAEL	326
AhCDKL28	NLKIGDPGLATVYDP--EKNQQLTSRVVTWYRAPELLLGATEYGASIDMNSAGC1LAEL	349
AdCDKL14	NLKIGDPGLATVYDP--EKNQQLTSRVVTWYRAPELLLGATEYGASIDMNSAGC1LAEL	349
AhCDKL27	NLKIGDPGLATVYDP--EKNQQLTSRVVTWYRAPELLLGATEYGASIDMNSAGC1LAEL	349
A1CDKL13	NLKIGDPGLATVYDP--EKNQQLTSRVVTWYRAPELLLGATEYGASIDMNSAGC1LAEL	349
CDKL15	VLK1ADPGLASFFDP--RQTQPLTSRVVTWYRPELLLGATRYGAVDLNSAGC1LAEL	328
AhCDKL23	ILK1ADPGLASFFDP--NQIQPLTSRVVTWYRPELLLGATYYGTAVDLNS1GCC1LAEL	384
AhCDKL9	ILK1ADPGLASFFDP--NQIQPLTSRVVTWYRPELLLGATYYGTAVDLNS1GCC1LAEL	325
A1CDKL5	ILK1ADPGLASFFDP--NQIQPLTSRVVTWYRPELLLGATYYGTAVDLNS1GCC1LAEL	325
AdCDKL3	ILK1ADPGLASFFDP--NQIQPLTSRVVTWYRPELLLGATYYGTAVDLNS1GCC1LAEL	325
CDKL12	VLKIGDPGLANFYRC--DGDQLTSRVVTWYRAPELLLGATEYGPASIDLNSAGC1LTEL	341
CDKL13	VLKIGDPGLANIYHP--EQDQPLTSRVVTWYRAPELLLGATEYGPASIDLNSVGC1LTEL	170
CDKL14	VLKIGDPGLASFYKP--DQDQPLTSRVVTWYRAPELLLGSTGYGPASIDLNSVGC1LAEL	335

.* :* **** * *. :*: ** **:

Fig. S4. Multiple alignments of T-loop regions of CDKLs. Group-wise alignment of *Arachis hypogaea*, *Arachis duranensis*, *Arachis ipaensis* and *Arabidopsis thaliana* represent the T-loop regions of CDKLs. Black line indicates T-loop region of each CDK group. * indicates highly conserved residues among all groups of CDKLs.

A



B

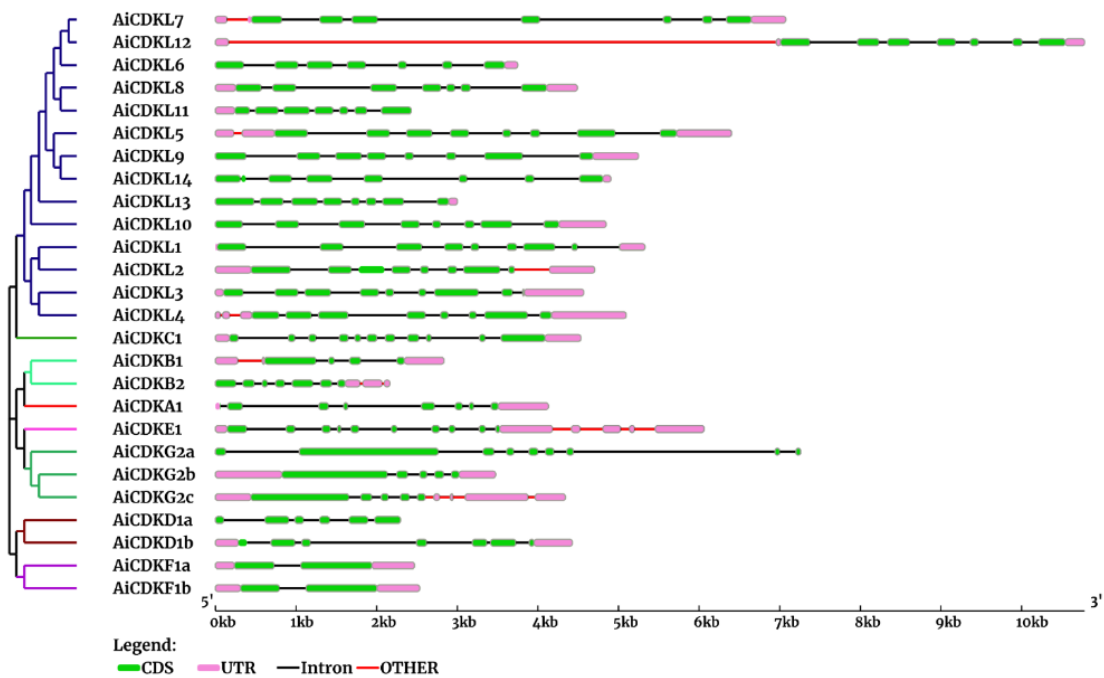


Fig. S5. Phylogenetic tree and gene structure analysis of 52 CDKs and CDKLs of *Arachis duranensis* and *Arachis ipaensis*. The phylogenetic tree was constructed using full-length amino acid sequences of CDKs and CDKLs proteins of *A. duranensis* (A) and *A. ipaensis* (B) using MEGA 7.0 with 1000 bootstrap replicates. Different colored lines indicate diverse groups. The exon-intron architecture highlights exons as green boxes and introns as black lines and magenta color box represents both 5' and 3' UTR regions.

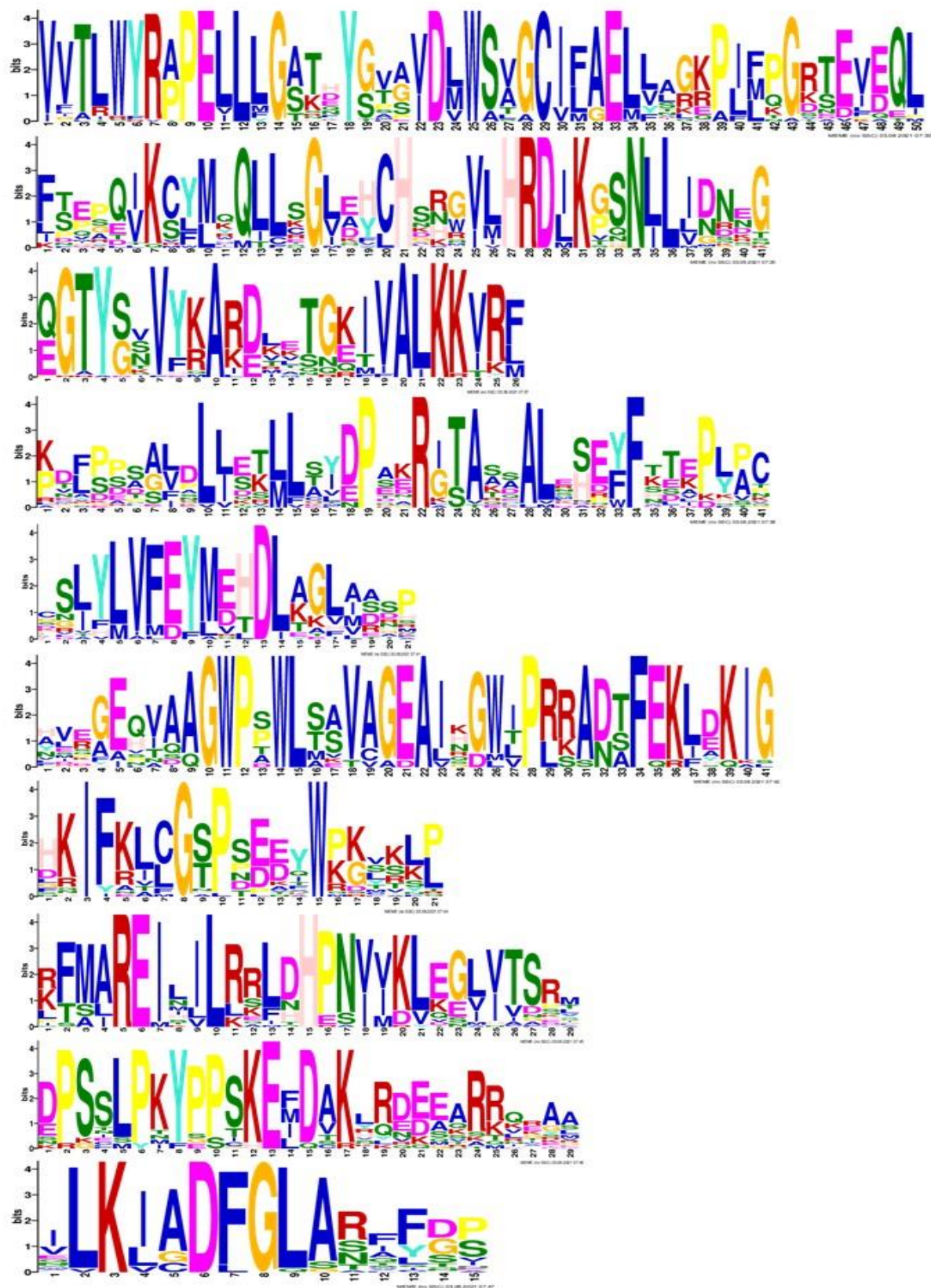


Fig. S6. Ten identified conserved protein motifs in *Arachis hypogaea*.

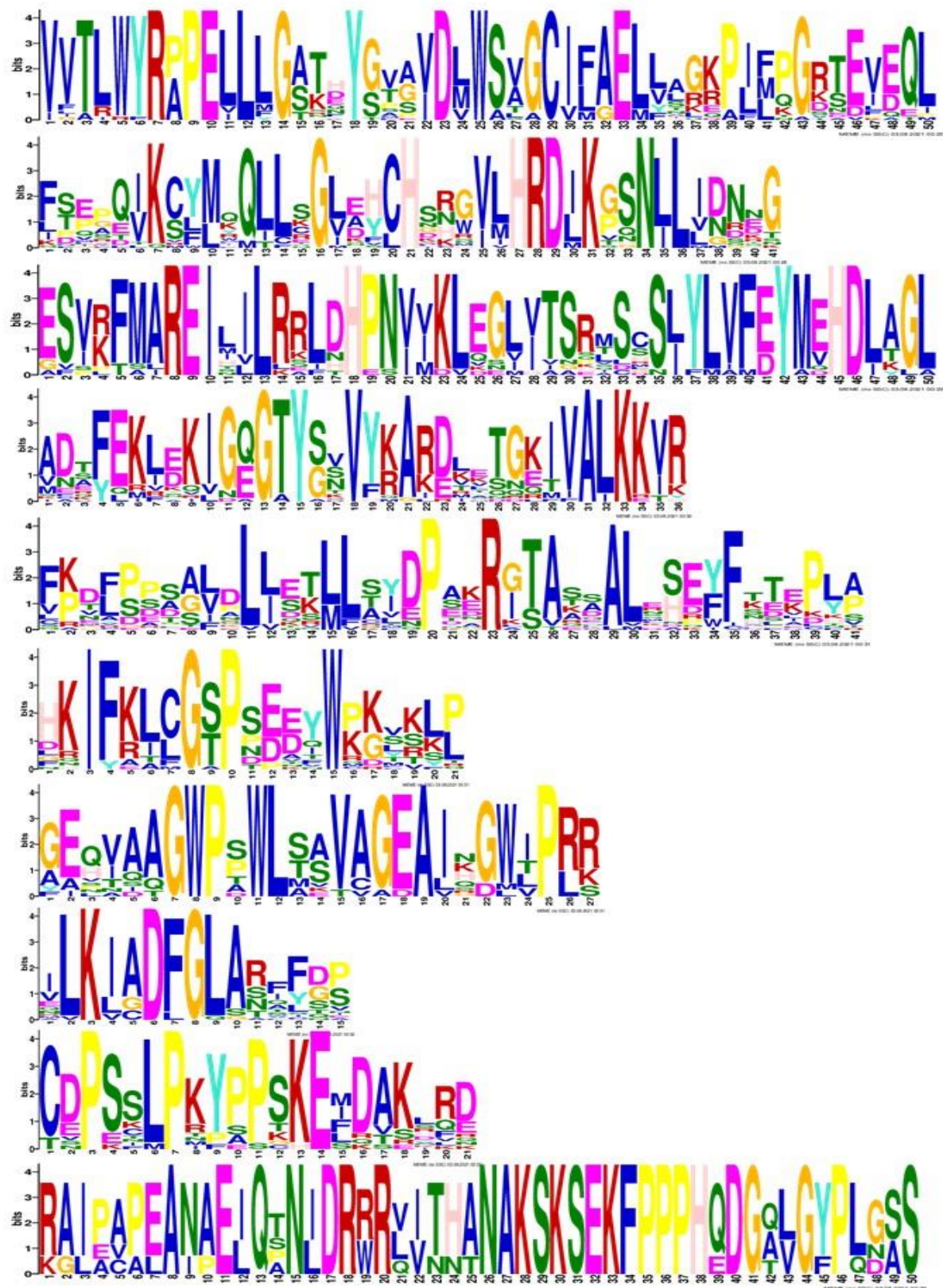


Fig. S7. Ten identified conserved protein motifs in *Arachis duranensis*.

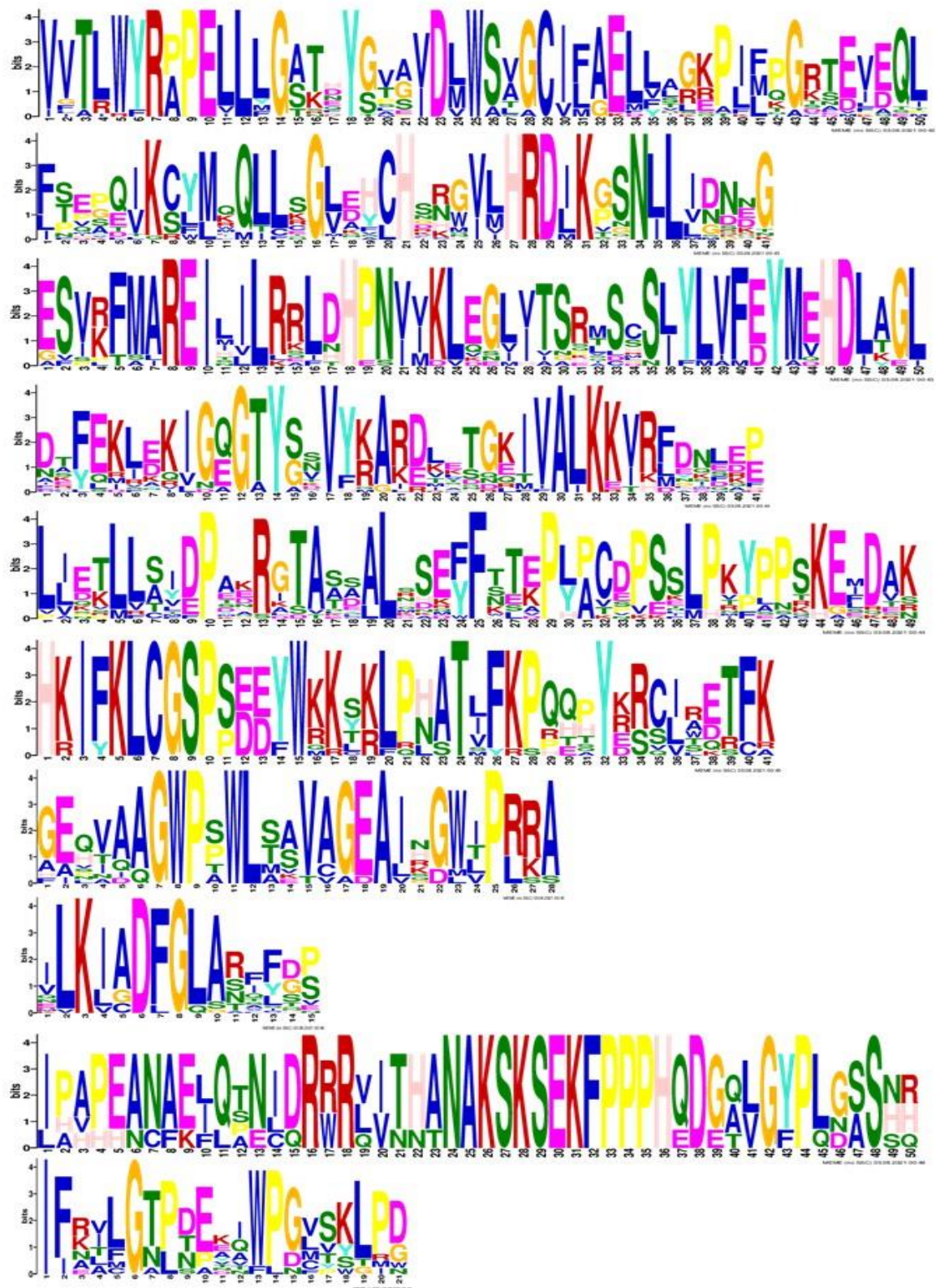
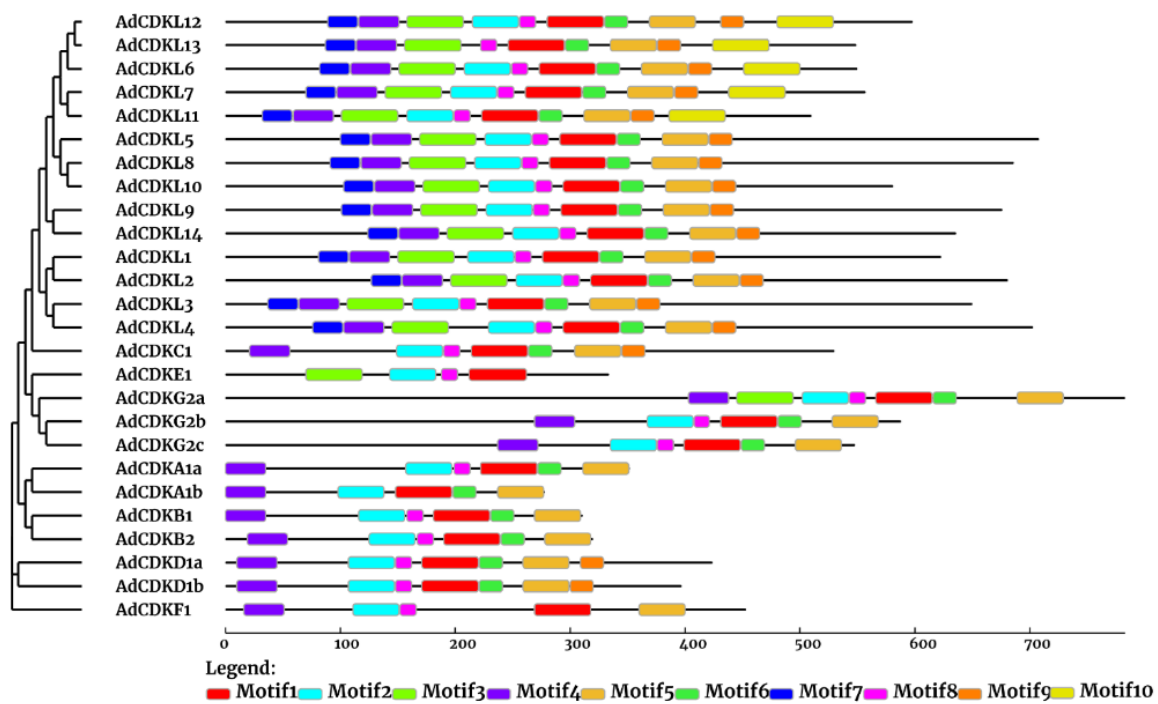


Fig. S8. Ten identified conserved protein motifs in *Arachis ipaensis*.

A



B

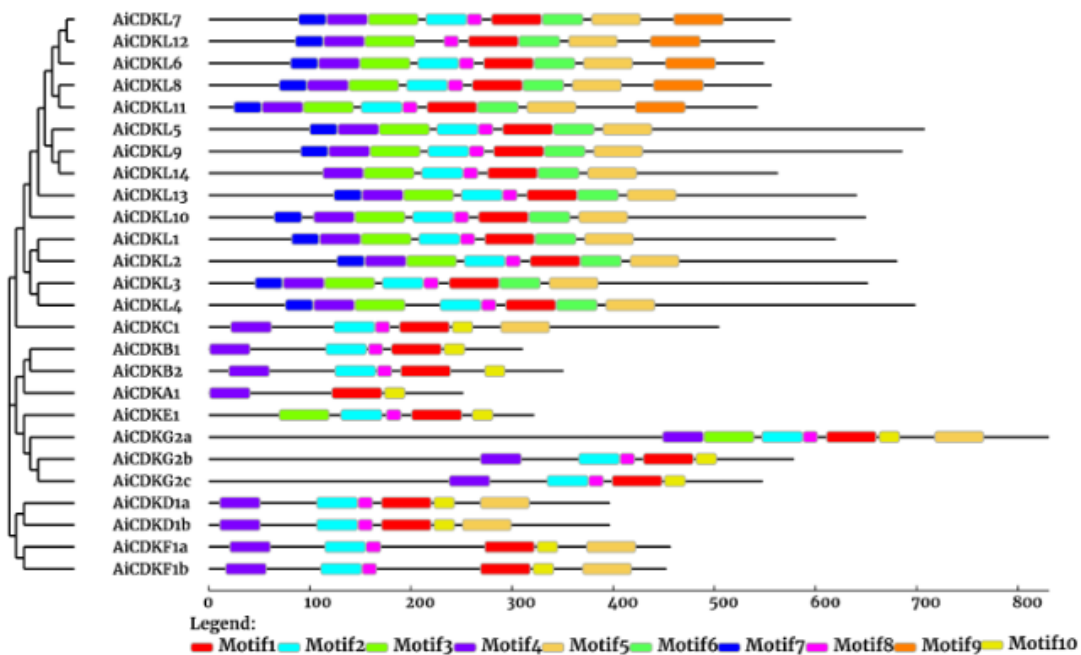


Fig. S9. Phylogenetic tree and protein motif structure analysis of CDK and CDKL proteins of *Arachis duranensis* and *Arachis ipaensis*. The phylogenetic tree was constructed using full-length amino acid sequences of CDKs and CDKLs proteins of *A. duranensis* (A) and *A. ipaensis* (B) using MEGA 7.0 with 1000 bootstrap replicates. The identified protein motifs are represented by colored boxes (Motif 1-Motif 10). Black lines indicate relative protein lengths.

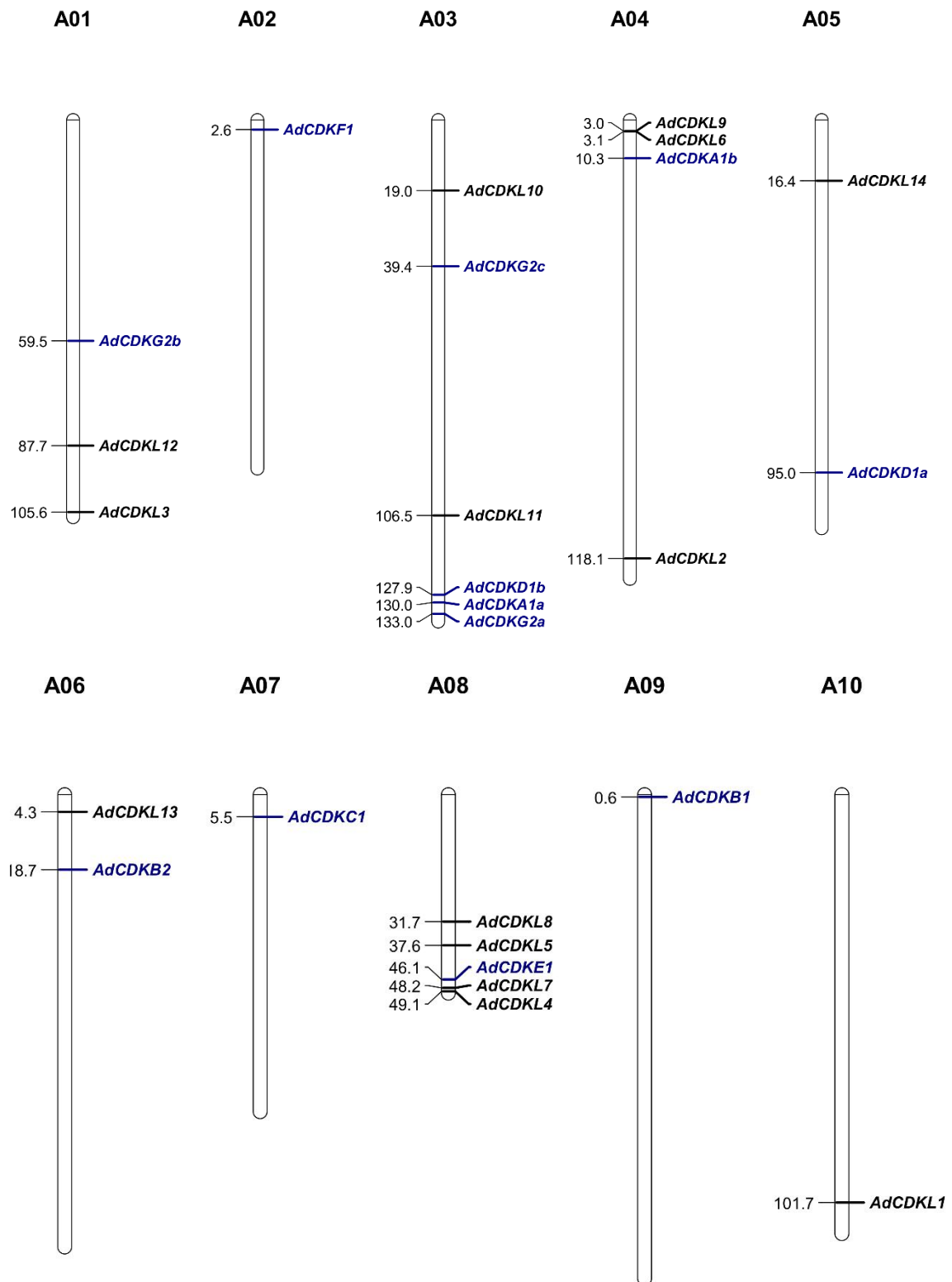


Fig. S10. The distributions of *CDK* and *CDKL* genes of *Arachis duranensis* across 10 chromosomes. The *CDKA-CDKG* group genes are depicted in blue, whereas the *CDKL* genes are highlighted in black. The values represent the relative start positions (Mbp) of each gene.

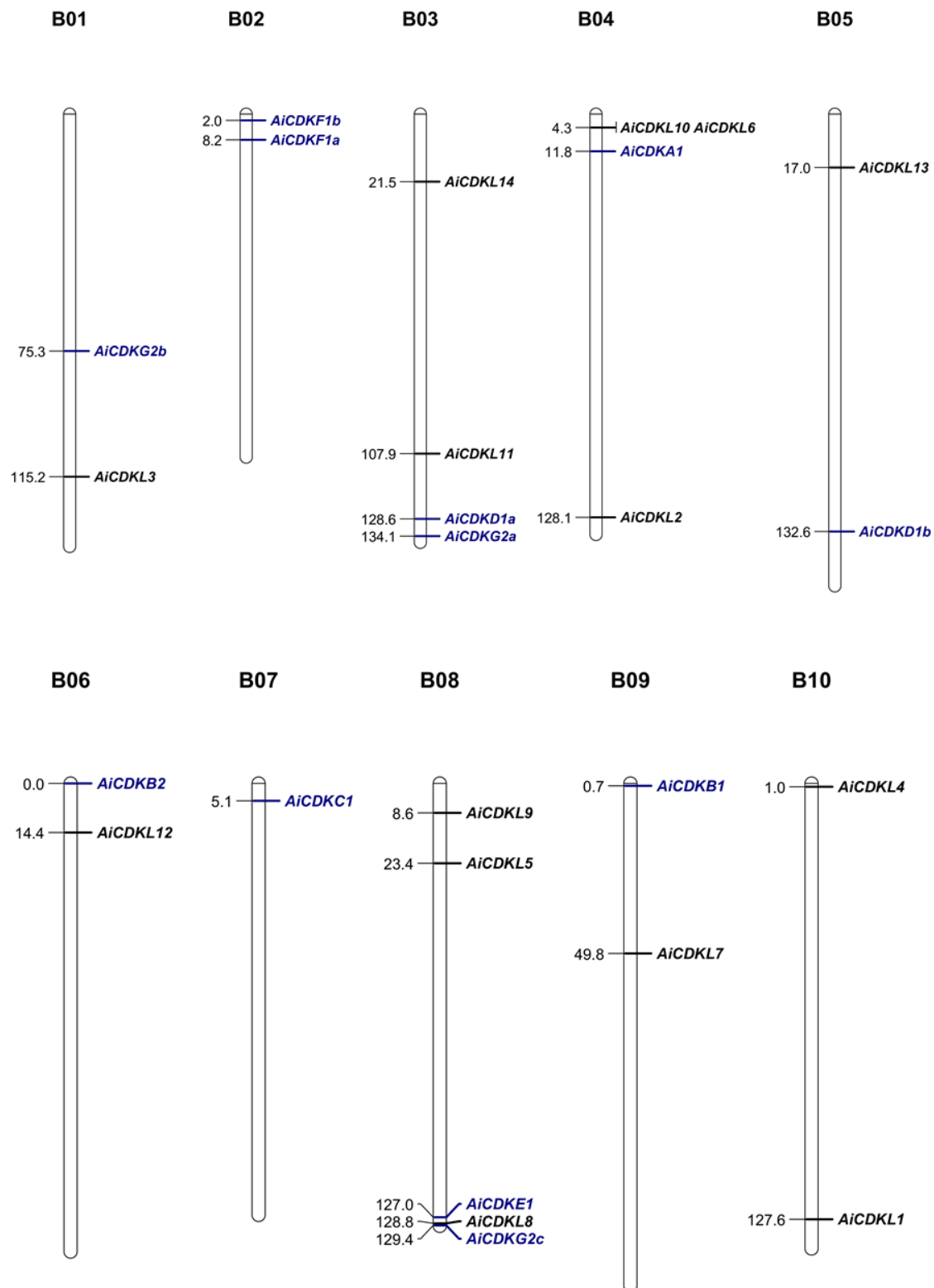


Fig. S11. The distributions of *CDK* and *CDKL* genes of *Arachis ipaensis* across 10 chromosomes. The *CDKA-CDKG* group genes are depicted in blue, whereas the *CDKL* genes are highlighted in black. The values represent the relative start positions (Mbp) of each gene.

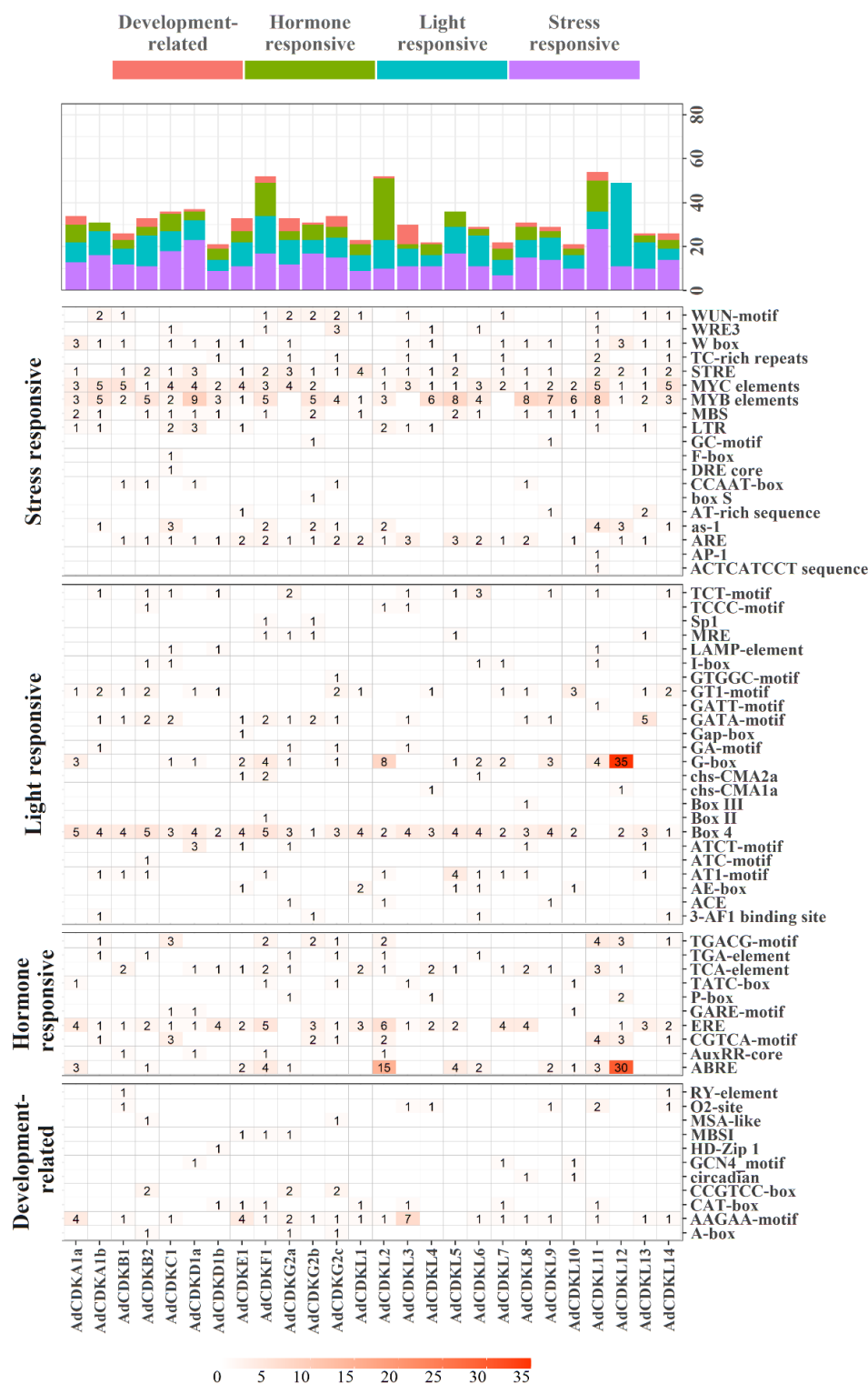


Fig. S12. The cis-elements distribution in the promoter of CDK and CDKL genes in *Arachis duranensis*. In upper panel, different colors was used to recognize various types of promoter cis-elements, like development related, phytohormone-responsive, light responsive and stress responsive. In lower panel, number of each cis-acting element of the CDK and CDKL genes promoter region (1.5 kb upstream of the translation start site).

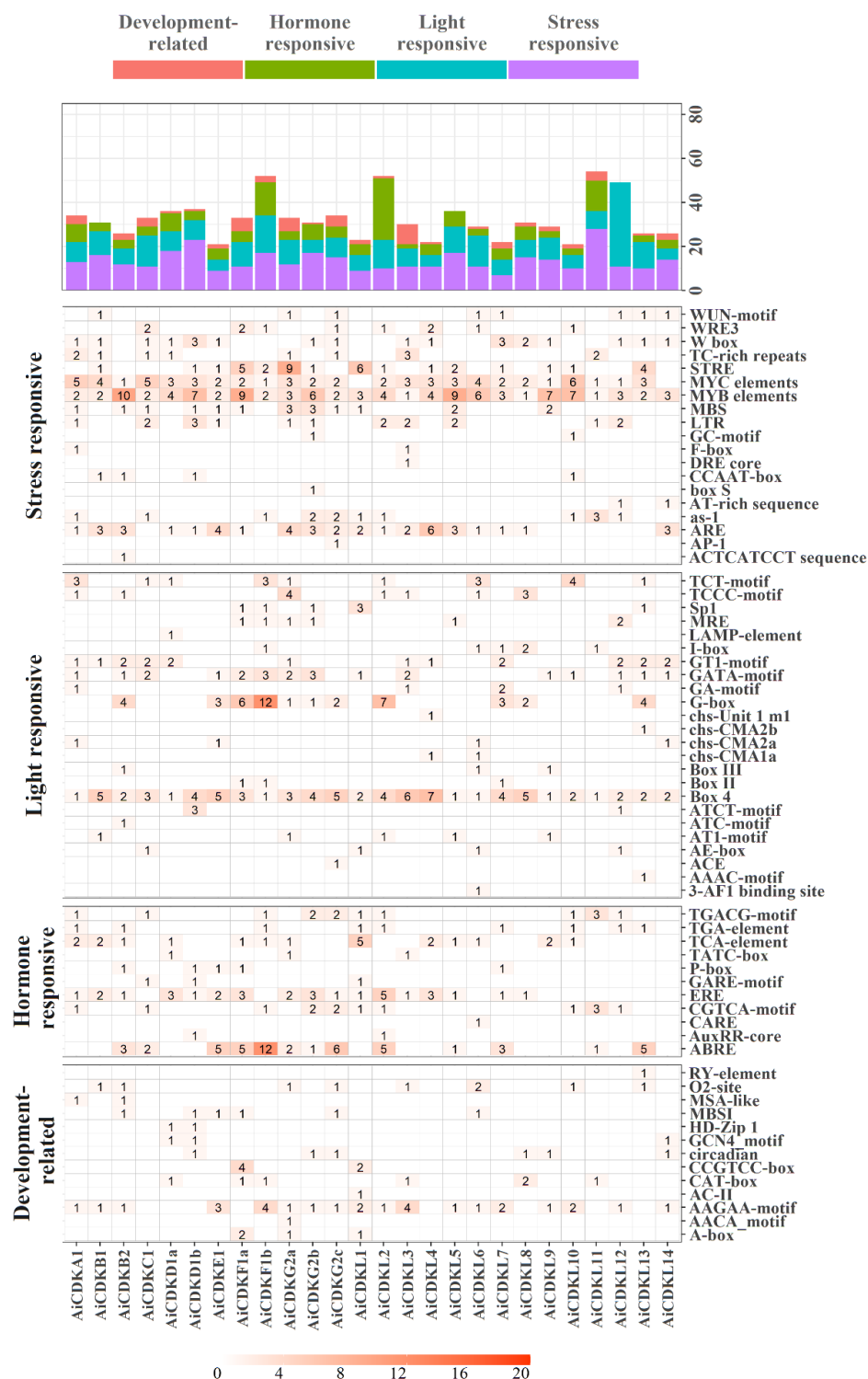


Fig. S13. The cis-elements distribution in the promoter of CDK and CDKL genes in *Arachis ipaensis*. In upper panel, different colors was used to recognize various types of promoter cis-elements, like development related, phytohormone-responsive, light responsive and stress responsive. In lower panel, number of each cis-acting element of the CDK and CDKL gene promoter region (1.5 kb upstream of the translation start site).

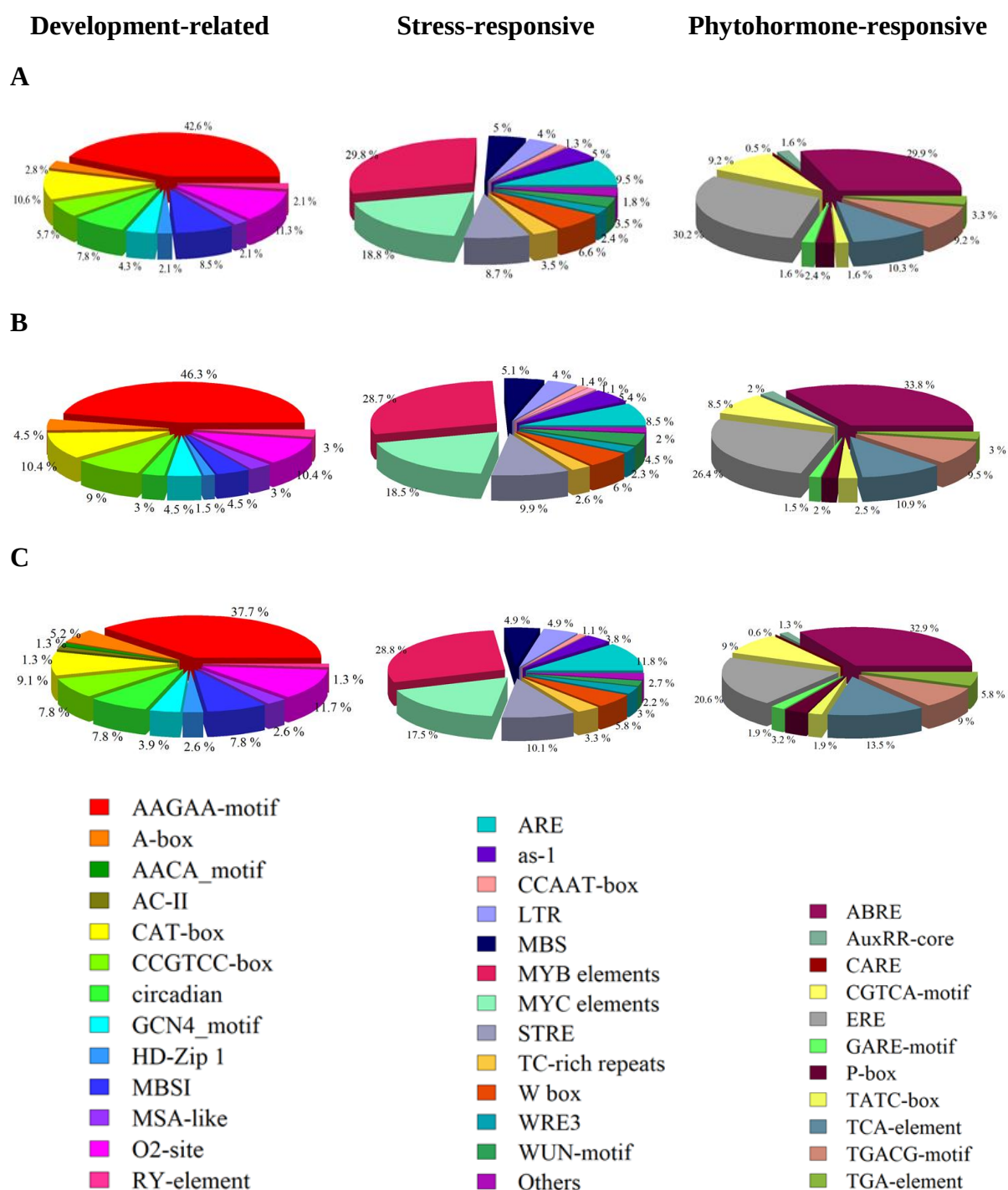


Fig. S14. Percentage of promoter cis-elements in cultivated peanut and its diploid parents.
(A) *Arachis hypogaea* (B) *Arachis duranensis* and (C) *Arachis ipaensis*.