

Supplementary Information for

**Distribution of adenylyl cyclase/cAMP phosphodiesterase gene, *CAPE*,
in streptophytes reproducing via motile sperm**

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This contains Supplementary Table S1-S3 and Figure S1-S3.

Table S1. Accession number of registered ACs and GCs in phylogenetic tree.

Species	Accession No.	Abbreviation
Viridiplantae		
<i>Adiantum capillus-veneris</i>	BAW35590.1	AdiantumCAPE
<i>Anthoceros agrestis</i>	LC588317 (in this study)	AnthocerosCAPE
<i>Azolla filiculoides</i>	Azfi_s0081.g038638	AzollaCAPE
<i>Chara braunii</i>	BAW35593.1	CharaCAPE
<i>Chara braunii</i>	GBG71085.1	Chara
<i>Chlamydomonas reinhardtii</i>	XP_001691280.1	Chlamydomonas-1
<i>Chlamydomonas reinhardtii</i>	PNW88988.1	Chlamydomonas-2
<i>Chlorella variabilis</i>	XP_005851659.1	Chlorella-1
<i>Chlorella sorokiniana</i>	PRW59677.1	Chlorella-2
<i>Coccomyxa subellipsoidea</i> C-169	XP_005649244.1	Coccomyxa-1
<i>Coccomyxa subellipsoidea</i> C-169	XP_005646174.1	Coccomyxa-2
<i>Coleochaete orbicularis</i>	GBSL01008739.1	ColeochaeteCAPE
<i>Coleochaete orbicularis</i>	GBSL01026055	Coleochaete
<i>Cryptomeria japonica</i>	LC588318 (in this study)	CryptomeriaCAPE cDNA
<i>Cycas revoluta</i>	LC588315 (in this study)	CycasCAPE
<i>Ginkgo biloba</i>	LC588316 (in this study)	GinkgoCAPE
<i>Gonium pectorale</i>	KXZ55438.1	Gonium
<i>Klebsormidium nitens</i>	GAQ89031.1	Klebsormidium-1
<i>Klebsormidium nitens</i>	GAQ78552.1	Klebsormidium-2
<i>Marchantia polymorpha</i>	PTQ35772.1	MarchantiaCAPE
<i>Marchantia polymorpha</i>	Mapoly0178s0022.1	Marchantia
<i>Mesostigma viride</i>	GBSK01038777.1	Mesostigma-1
<i>Mesostigma viride</i>	GBSK01037017	Mesostigma-2
<i>Micractinium conductrix</i>	PSC71265.1	Micractinium
<i>Pilgerodendron uviferum</i>	ETCJ_scaffold_2059111	PilgerodendronAC
<i>Physcomitrella patens</i>	XP_024382794.1	PhyscomitrellaCAPE
<i>Salvinia cucullata</i>	Sacu_v1.1_s0236.g026559	SalviniaCAPE
<i>Selaginella moellendorffii</i>	EFJ09864.1	SelaginellaCAPE
<i>Taxodium distichum</i>	FHST_scaffold_2061662	TaxodiumAC
<i>Tetrabaena socialis</i>	PNH10372.1	Tetrabaena
<i>Trebouxia</i> sp. A1-2	KAA6425186.1	Trebouxia
<i>Volvox carteri</i> f. nagariensis	XP_002949129.1	Volvox-1
<i>Volvox carteri</i> f. nagariensis	XP_002948497.1	Volvox-2
Stramenopile		
<i>Achlya hypogyna</i>	OQR90122.1	Achlya CAPE like
<i>Chattonella antiqua</i>	Chaan_24577_c0_g1_i1	Chattonella-C1
<i>Chattonella antiqua</i>	Chaan_24577_c0_g1_i1	Chattonella-C2
<i>Ectocarpus siliculosus</i>	CBJ26102.1	Ectocarpus-C1
<i>Ectocarpus siliculosus</i>	CBJ26102.1	Ectocarpus-C2
<i>Phaeodactylum tricornutum</i> CCAP 1055/1	XP_002177591.1	Phaeodactylum-C1
<i>Phaeodactylum tricornutum</i> CCAP 1055/1	XP_002177591.1	Phaeodactylum-C2
<i>Phaeodactylum tricornutum</i> CCAP 1055/1	XP_002186287.1	PhaeodactylumGC (GC)
<i>Phytophthora cactorum</i>	RAW37015.1	Phytophthora-1
<i>Phytophthora parasitica</i>	ETL50165.1	Phytophthora-2
<i>Pythium insidiosum</i>	GAX99050.1	Pythium-1
<i>Pythium insidiosum</i>	GAY06089.1	Pythium-2
<i>Saprolegnia diclina</i> VS20	XP_008616153.1	Saprolegnia-dCAPE like
<i>Saprolegnia parasitica</i> CBS 223.65	XP_012202270.1	Saprolegnia
<i>Saprolegnia parasitica</i> CBS 223.65	XP_012204290.1	Saprolegnia-pCAPE like
<i>Thalassiosira pseudonana</i> CCMP1335	XP_002289513.1	Thalassiosira-C1
<i>Thalassiosira pseudonana</i> CCMP1335	XP_002289513.1	Thalassiosira-C2
<i>Thraustotheca clavata</i>	OQS03511.1	Thraustotheca CAPE like

Table S1. Accession number of registered ACs and GCs in phylogenetic tree.

Species	Accession No.	Abbreviation
Alveolata		
<i>Besnoitia besnoiti</i>	PFH34891.1	Besnoitia
<i>Eimeria maxima</i>	XP_013333510.1	Eimeria
<i>Hammondia hammondi</i>	KEP62983.1	Hammondia
<i>Hepatocystis</i> sp. ex <i>Piliocolobus tephrosceles</i>	VWU49457.1	Hepatocystis
<i>Ichthyophthirius multifiliis</i>	XP_004024096.1	Ichthyophthirius
<i>Paramecium tetraurelia</i>	CAC81657.1	Paramecium-1
<i>Paramecium tetraurelia</i>	XP_001456616.1	Paramecium-2
<i>Plasmodium falciparum</i>	CAC81938.2	Plasmodium-f
<i>Plasmodium reichenowi</i>	CDO66529.1	Plasmodium-r
<i>Stentor coeruleus</i>	OMJ78156.1	Stentor
<i>Tetrahymena pyriformis</i>	CAC81658.1	Tetrahymena
<i>Toxoplasma gondii</i> ME49	XP_002368352.1	Toxoplasma
<i>Vitrella brassicaformis</i> CCMP3155	CEM03412.1	Vitrella
Cyanobacteria		
<i>Anabaena cylindrica</i> NIES-19 PCC 7122	BAA09511.1	AnabaenacCya
<i>Arthrospira platensis</i> NIES-39	BAA22996.1	ArthrospiraCyaA
<i>Arthrospira platensis</i> NIES-39	BAA22997.1	ArthrospiraCyaC
<i>Arthrospira platensis</i> NIES-39	BAB19924.1	ArthrospiraCyaG
<i>Nostoc</i> sp. PCC 7120	BAA13997.1	NostocCyaA
<i>Nostoc</i> sp. PCC 7120	BAA13998.2	NostocCyaB1
<i>Nostoc</i> sp. PCC 7120	BAA13999.1	NostocCyaB2
<i>Nostoc</i> sp. PCC 7120	BAA14000.1	NostocCyaC
<i>Nostoc</i> sp. PCC 7120	BAA14001.1	NostocCyaD
<i>Nostoc</i> sp. PCC 7120	WP_010994837.1	NostocCyaE
<i>Synechocystis</i> sp. PCC 6803	BAA17880.1	SynechocystisCya1
<i>Synechocystis</i> sp. PCC 6803	P72951	SynechocystisCya2
Bacteria		
<i>Chloroflexus aurantiacus</i>	WP_012258114.1	Chloroflexus-C1
<i>Chloroflexus aurantiacus</i>	WP_012258114.1	Chloroflexus-C2
<i>Mycobacterium tuberculosis</i> CDC1551_sp	P9WQ34.1	Mycobacterium
<i>Myxococcus xanthus</i>	BAC00918.1	Myxococcus
<i>Sinorhizobium meliloti</i>	AAA26247.1	SinorhizobiumAC3
Excavata		
<i>Euglena gracilis</i>	BAB85619.1	EuglenaPACa-C1
<i>Euglena gracilis</i>	BAB85619.1	EuglenaPACa-C2
<i>Euglena gracilis</i>	BAB85620.1	EuglenaPACb-C1
<i>Euglena gracilis</i>	BAB85620.1	EuglenaPACb-C2
<i>Euglena gracilis</i>	BAD20740.1	EgTAC1 (Excavata AC)
<i>Euglena gracilis</i>	BAD20741.1	EgTAC2 (Excavata AC)
<i>Leishmania donovani</i>	AAA74998.1	Leishmania (Excavata AC)
<i>Trypanosoma brucei brucei</i>	Q99279.1	TrypanosomaAC1 (Excavata AC)
<i>Trypanosoma brucei brucei</i>	AAA30158.1	TrypanosomaAC2 (Excavata AC)
<i>Trypanosoma brucei brucei</i>	CAA09951.1	TrypanosomaAC3 (Excavata AC)
<i>Trypanosoma congolense</i>	CAA91903.1	TcoAC (Excavata AC)
<i>Trypanosoma cruzi</i>	AAC61849.1	TcrAC1 (Excavata AC)
<i>Trypanosoma cruzi</i>	CAA09737.2	TcrAC2 (Excavata AC)
<i>Trypanosoma equiperdum</i>	CAA42029.1	TeAC (Excavata AC)
Amoebozoa		
<i>Dictyostelium discoideum</i>	AAA33163.1	DictyosteliumACA-C1
<i>Dictyostelium discoideum</i>	AAA33163.1	DictyosteliumACA-C2
<i>Dictyostelium discoideum</i>	AAD50121.1	DictyosteliumACB
<i>Dictyostelium discoideum</i>	AAA33164.1	DictyosteliumACG

Table S1. Accession number of registered ACs and GCs in phylogenetic tree.

Species	Accession No.	Abbreviation	
Fungi			
<i>Botrytis cinerea</i>	CAB77164.1	Botrytis	(Fungi AC)
<i>Candida albicans</i>	AAG18428.1	CandidaAC	(Fungi AC)
<i>Cryptococcus neoformans</i> var. <i>grubii</i>	AAG60619.1	CryptococcusAC	(Fungi AC)
<i>Lachancea kluyveri</i>	CAA39513.1	Lachancea	(Fungi AC)
<i>Madurella mycetomatis</i>	KXX82884.1	Madurella	(Fungi AC)
<i>Neurospora crassa</i>	XP_011393197.1	Neurospora	(Fungi AC)
<i>Saccharomyces cerevisiae</i>	CAA89295.1	Saccharomyces	(Fungi AC)
<i>Schizosaccharomyces pombe</i>	AAA35284.1	Schizosaccharomyces	(Fungi AC)
<i>Sordaria macrospora</i>	CAP09208.1	Sordaria	(Fungi AC)
<i>Ustilago maydis</i> 521_sp	P49606.1	Ustilago	(Fungi AC)
<i>Valsa mali</i>	KUI66200.1	Valsa	(Fungi AC)
Animal			
<i>Bos taurus</i>	AAA79957.1	BosAC-C1	(AnimalAC-C1)
<i>Bos taurus</i>	AAA79957.1	BosAC-C2	(AnimalAC-C2)
<i>Drosophila melanogaster</i>	AAA28844.1	DrosophilaAC-C1	(AnimalAC-C1)
<i>Drosophila melanogaster</i>	AAA28844.1	DrosophilaAC-C2	(AnimalAC-C2)
<i>Drosophila melanogaster</i>	AAA74408.1	DrosophilaGC	(GC)
<i>Homo sapiens</i>	NP_066939.1	HomoAC1-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_065433.2	HomoAC2-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_004027.2	HomoAC3-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_640340.2	HomoAC4-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_899200.1	HomoAC5-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_056085.1	HomoAC6-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_001105.1	HomoAC7-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_001106.1	HomoAC8-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_001107.2	HomoAC9-C1	(AnimalAC-C1)
<i>Homo sapiens</i>	NP_066939.1	HomoAC1-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_065433.2	HomoAC2-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_004027.2	HomoAC3-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_640340.2	HomoAC4-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_899200.1	HomoAC5-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_056085.1	HomoAC6-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_001105.1	HomoAC7-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_001106.1	HomoAC8-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	NP_001107.2	HomoAC9-C2	(AnimalAC-C2)
<i>Homo sapiens</i>	AAF01340.1	HomoGC-A	(GC)
<i>Homo sapiens</i>	NP_060887.2	Homo-sAC-C1	
<i>Homo sapiens</i>	NP_060887.2	Homo-sAC-C2	
<i>Mus musculus</i>	NP_033752.1	MusAC1-C1	(AnimalAC-C1)
<i>Mus musculus</i>	NP_705762.2	MusAC2-C1	(AnimalAC-C1)
<i>Mus musculus</i>	NP_001153008.1	MusAC3-C1	(AnimalAC-C1)
<i>Mus musculus</i>	NP_536683.1	MusAC4-C1	(AnimalAC-C1)
<i>Mus musculus</i>	NP_001012783.3	MusAC5-C1	(AnimalAC-C1)
<i>Mus musculus</i>	AAA37182.1	MusAC6-C1	(AnimalAC-C1)
<i>Mus musculus</i>	AAA57554.1	MusAC7-C1	(AnimalAC-C1)
<i>Mus musculus</i>	AAB41885.1	MusAC8-C1	(AnimalAC-C1)
<i>Mus musculus</i>	CAA90570.1	MusAC9-C1	(AnimalAC-C1)
<i>Mus musculus</i>	NP_033752.1	MusAC1-C2	(AnimalAC-C2)
<i>Mus musculus</i>	NP_705762.2	MusAC2-C2	(AnimalAC-C2)
<i>Mus musculus</i>	NP_001153008.1	MusAC3-C2	(AnimalAC-C2)
<i>Mus musculus</i>	NP_536683.1	MusAC4-C2	(AnimalAC-C2)
<i>Mus musculus</i>	NP_001012783.3	MusAC5-C2	(AnimalAC-C2)
<i>Mus musculus</i>	AAA37182.1	MusAC6-C2	(AnimalAC-C2)
<i>Mus musculus</i>	AAA57554.1	MusAC7-C2	(AnimalAC-C2)
<i>Mus musculus</i>	AAB41885.1	MusAC8-C2	(AnimalAC-C2)
<i>Mus musculus</i>	CAA90570.1	MusAC9-C2	(AnimalAC-C2)

Table S1. Accession number of registered ACs and GCs in phylogenetic tree.

Species	Accession No.	Abbreviation	
Animal			
<i>Mus musculus</i>	NP_766617.2	Mus-sAC10-1-C1	
<i>Mus musculus</i>	NP_766617.2	Mus-sAC10-1-C2	
<i>Oryctolagus cuniculus</i>	CAA82562.1	OryctolagusAC-C1	(AnimalAC-C1)
<i>Oryctolagus cuniculus</i>	CAA82562.1	OryctolagusAC-C2	(AnimalAC-C2)
<i>Rattus norvegicus</i>	AAA40682.1	RattusAC2-C1	(AnimalAC-C1)
<i>Rattus norvegicus</i>	AAB39764.1	RattusAC5-C1	(AnimalAC-C1)
<i>Rattus norvegicus</i>	AAA40682.1	RattusAC2-C2	(AnimalAC-C2)
<i>Rattus norvegicus</i>	AAB39764.1	RattusAC5-C2	(AnimalAC-C2)
<i>Rattus norvegicus</i>	AAA41201.1	RattusGC-C	(GC)
<i>Rattus norvegicus</i>	AAC52417.1	RattusksGC	(GC)
<i>Rattus norvegicus</i>	AAA41200.1	RattusGC-A	(GC)
<i>Rattus norvegicus</i>	AAB17953.1	RattusGC-Salpha1	(GC)
<i>Rattus norvegicus</i>	P20595.2	RattusGC-Sbeta1	(GC)
<i>Strongylocentrotus purpuratus</i>	AAA30051.1	StrongylocentrotusGC	(GC)

Table S2. Accession number of registered PDEs in phylogenetic tree.

Species	Accession No.	Abbreviation
Viridiplantae		
<i>Adiantum capillus-veneris</i>	BAW35590.1	AdiantumCAPE
<i>Anthoceros agrestis</i>	LC588317 (in this study)	AnthocerosCAPE
<i>Azolla filiculoides</i>	Azfi_s0081.g038638	AzollaCAPE
<i>Bathycoccus prasinus</i>	XP_007512124.1	Bathycoccus
<i>Chara braunii</i>	BAW35593.1	CharaCAPE
<i>Chlamydomonas reinhardtii</i>	PNW87509.1	Chlamydomonas
<i>Chloropicon primus</i>	QDZ24568.1	Chloropicon
<i>Coleochaete orbicularis</i>	GBSL01005997.1	Coleochaete
<i>Coleochaete orbicularis</i>	GBSL01008739.1	ColeochaeteCAPE
<i>Cryptomeria japonica</i>	LC588319 (in this study)	CryptomeriaCAPE
<i>Cycas revoluta</i>	LC588315 (in this study)	CycasCAPE
<i>Ginkgo biloba</i>	LC588316 (in this study)	GinkgoCAPE
<i>Gonium pectorale</i>	KXZ50318.1	Gonium
<i>Klebsormidium nitens</i>	GAQ77586.1	Klebsormidium
<i>Marchantia polymorpha</i>	PTQ35772.1	MarchantiaCAPE
<i>Mesostigma viride</i>	GBEK01001697.1	Mesostigma1
<i>Mesostigma viride</i>	GBEK01001701.1	Mesostigma2
<i>Mesostigma viride</i>	GBSK01059562.1	Mesostigma3
<i>Mesostigma viride</i>	GBEK01001659.1	Mesostigma4
<i>Ostreococcus tauri</i>	OUS44058.1	Ostreococcus
<i>Physcomitrella patens</i>	XP_024382794.1	PhyscomitrellaCAPE
<i>Salvinia cucullate</i>	Sacu_v1.1_s0236.g026559	SalviniaCAPE
<i>Selaginella moellendorffii</i>	EFJ09864.1	SelaginellaCAPE
<i>Volvox carteri</i> f. <i>nagariensis</i>	XP_002950511.1	Volvox
Stramenopile		
<i>Achlya hypogyna</i>	OQR90122.1	Achlya CAPE like
<i>Achlya hypogyna</i>	OQR94169.1	Achlya
<i>Chattonella antiqua</i>	Chaan_26589_c0_g1_i1_m61498	Chattonella1
<i>Chattonella antiqua</i>	Chaan_24326_c0_g1_i1_m36734	Chattonella2
<i>Dictyopteris undulata</i>	GFKK01054719.1	Dictyopteris
<i>Dinobryon</i> sp. LO226KS	HAGC01022162.1	Dinobryon
<i>Ectocarpus siliculosus</i>	CBJ33418.1	Ectocarpus
<i>Phytophthora kernoviae</i>	RLN60791.1	Phytophthora1
<i>Phytophthora kernoviae</i>	RLN54307.1	Phytophthora2
<i>Pythium oligandrum</i>	TMW64435.1	Pythium
<i>Saprolegnia diclina</i> VS20	XP_008616153.1	Saprolegnia-d CAPE like
<i>Saprolegnia parasitica</i> CBS 223.65	XP_012204290.1	Saprolegnia-p CAPE like
<i>Saprolegnia parasitica</i> CBS 223.65	XP_012195684.1	Saprolegnia
<i>Sargassum vulgare</i>	GFKX01008947.1	Sargassum1
<i>Sargassum vulgare</i>	GEHA01016282.1	Sargassum2
<i>Thraustotheca clavata</i>	OQS03511.1	Thraustotheca CAPE like
<i>Thraustotheca clavata</i>	OQS06861.1	Thraustotheca
<i>Thalassiosira oceanica</i>	EJK58346.1	Thalassiosira-o
<i>Thalassiosira rotula</i>	GGLQ01019201.1	Thalassiosira-r
Alveolata		
<i>Ichthyophthirius multifiliis</i>	XP_004037103.1	Ichthyophthirius1
<i>Ichthyophthirius multifiliis</i>	XP_004030322.1	Ichthyophthirius2
<i>Paramecium tetraurelia</i> strain d4-2	XP_001443417.1	Paramecium
<i>Plasmodium falciparum</i> 3D7	XP_001349954.1	Plasmodium1
<i>Plasmodium falciparum</i> 3D7	XP_002809026.1	Plasmodium2
<i>Plasmodium falciparum</i> 3D7	XP_024329151.1	Plasmodium3
<i>Plasmodium falciparum</i> 3D7	XP_001348846.2	Plasmodium4
<i>Stentor coeruleus</i>	OMJ67820.1	Stentor1
<i>Stentor coeruleus</i>	OMJ90718.1	Stentor2
<i>Tetrahymena thermophila</i> SB210	XP_001019765.3	Tetrahymena
<i>Theileria annulata</i>	XP_954120.1	Theileria
Excavata		
<i>Naegleria fowleri</i>	KAF0974972.1	Naegleria
<i>Trypanosoma cruzi</i>	AAL58095.1	TrypanosomaPDEA
<i>Trypanosoma cruzi</i>	AAM28249.1	TrypanosomaPDEB1
<i>Trypanosoma cruzi</i>	XP_803815.1	TrypanosomaPDEB2

Table S2. Accession number of registered PDEs in phylogenetic tree.

Species	Accession No.	Abbreviation
Amoebozoa		
<i>Planoprotostelium fungivorum</i>	PRP89163.1	Planoprotostelium
<i>Thecamonas trahens</i> ATCC 50062	XP_013757491.1	Thecamonas
Fungi		
<i>Powellomyces hirtus</i>	TPX62813.1	Powellomyces
<i>Spizellomyces punctatus</i> DAOM BR117	XP_016607590.1	Spizellomyces
Animal		
<i>Danio rerio</i>	XP_692892.6	DanioPDE1A
<i>Danio rerio</i>	XP_691883.4	DanioPDE3B
<i>Danio rerio</i>	XP_005165938.1	DanioPDE4B
<i>Danio rerio</i>	XP_005163431.3	DanioPDE4D
<i>Danio rerio</i>	NP_001116732.1	DanioPDE5A
<i>Danio rerio</i>	NP_957165.1	DanioPDE6C
<i>Danio rerio</i>	NP_002594.1	DanioPDE7A
<i>Danio rerio</i>	XP_009293456.1	DanioPDE8B
<i>Danio rerio</i>	XP_009302928.1	DanioPDE9A
<i>Danio rerio</i>	AAH49532.1	DanioPDE10A
<i>Danio rerio</i>	XP_697567.3	DanioPDE11
<i>Homo sapiens</i>	BAB20055.1	HomoPDE1A
<i>Homo sapiens</i>	NP_000915.1	HomoPDE1B
<i>Homo sapiens</i>	NP_005011.1	HomoPDE1C
<i>Homo sapiens</i>	AAH40974.1	HomoPDE2A
<i>Homo sapiens</i>	AAB18673.1	HomoPDE3A
<i>Homo sapiens</i>	NP_000913.2	HomoPDE3B
<i>Homo sapiens</i>	AAU82096.1	HomoPDE4A
<i>Homo sapiens</i>	NP_001032417.1	HomoPDE4B
<i>Homo sapiens</i>	AAB96875.1	HomoPDE4C
<i>Homo sapiens</i>	Q08499.2	HomoPDE4D
<i>Homo sapiens</i>	O76074.2	HomoPDE5A
<i>Homo sapiens</i>	NP_000431.2	HomoPDE6A
<i>Homo sapiens</i>	P35913.2	HomoPDE6B
<i>Homo sapiens</i>	P51160.2	HomoPDE6C
<i>Homo sapiens</i>	NP_002594.1	HomoPDE7A
<i>Homo sapiens</i>	NP_061818.1	HomoPDE7B
<i>Homo sapiens</i>	NP_002596.1	HomoPDE8A
<i>Homo sapiens</i>	NP_003710.1	HomoPDE8B
<i>Homo sapiens</i>	NP_002597.1	HomoPDE9A
<i>Homo sapiens</i>	NP_006652.1	HomoPDE10A
<i>Homo sapiens</i>	NP_058649.3	HomoPDE11A

Table S3. The PDE and AC domains of gymnosperms CAPE in the OneKP database.

Family	Species	PDE*	AC*	Sequence ID
Cupressaceae	<i>Callitris gracilis</i> (taxid:214220)	○		IFLI_scaffold_2057545
	<i>Pilgerodendron uviferum</i> (taxid:103979)	○		ETCJ_scaffold_2051372
		○		ETCJ_scaffold_2056181
			●	ETCJ_scaffold_2059111
	<i>Taxodium distichum</i> (taxid:28982)		●	FHST_scaffold_2061662
	<i>Widdringtonia cedarbergensis</i> (taxid:13760)		○	AUDE_scaffold_2029632
		○	AUDE_scaffold_2034839	
Taxaceae	<i>Amentotaxus argotaenia</i> (taxid:25625)		○	IAJW_scaffold_2135942
	<i>Cephalotaxus harringtonia</i> (taxid:58029)	○		GJTI_scaffold_2038034
			○	GJTI_scaffold_2046253
			○	GJTI_scaffold_2056587
		○	○	GJTI_scaffold_2061849
			○	WYAJ_scaffold_2013049
			○	WYAJ_scaffold_2031765
		○	WYAJ_scaffold_2060862	
		○	WYAJ_scaffold_2082430	
	<i>Pseudotaxus chienii</i> (taxid:89481)	○		YLPM_scaffold_2066289
	<i>Torreya nucifera</i> (taxid:50189)		○	HQOM_scaffold_2031209
			○	HQOM_scaffold_2114042
Zamiaceae	<i>Stangeria eriopus</i> (taxid:34343)	○		KAWQ_scaffold_2021063

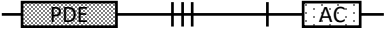
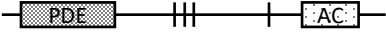
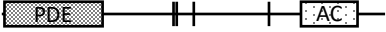
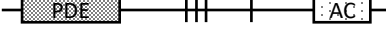
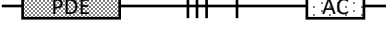
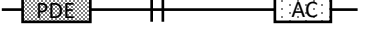
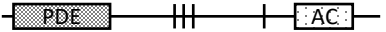
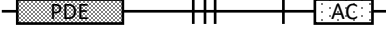
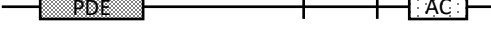
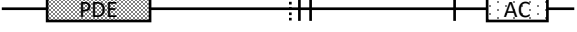
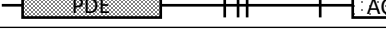
*Partial (○) or full length (●) sequences homologous to PDE or AC domains of CAPE are marked.

CrCAPE	1	-----METRICTN-----	-----PMHTLPDEED-----	EIDCSNGCIQPSF	31	
GbCAPE	1	-----MEGNGMEQSRQMDLRIIN-----	-----PMQTLLEDE-----	ETECSDAYLESLL	41	
AaCAPE	1	-----	-----	MANFDEGTTKLS	13	
MpCAPE	1	MEKPELKDDKGKDQEEENDEAKNKRPRDLRLPLLNLERAREVVPASPTEKTSASDSEMLIISELPNIGQPDFSFSVPLREDSPKLPKAPSALDEAVQVQL			100	
CrCAPE	32	DGIKFLSFDIEVLDEDLDFKMMVERIFEDLGLFDIFSLDRCKERAFVDSMSACQVRATVPYHNFRHACDVIHAYVLLILTCAEAGKLLNDLEKLALVMASLCH			131	
GbCAPE	42	KGLKWSFDFIBEYIDEDLDFKMMVDFKFFADLGLFDLDFELDRCKERAFVDSMSACQVRATVPYHNFRHACDVIHAYVLLILTVEAGKLLNDLEMLALALALCH			141	
AaCAPE	14	KTIDWSFDFIDQIEDKDLDFEMVEMIFKKLLDFETELFQPKKERAFVDSMSACQVRATVPYHNFRHACDVIHAYVLLILTCAEAGKLLNDLEMLALALALCH			112	
MpCAPE	101	QGINSWTFDIEQLDDSLDFKMMVEKIFRELGLFDNFDLVDKVKRAFTNAMVMRQOPNPYHNFRHACDVIHAYVLLILTVEAGKLLNDLEMLALALALCH			199	
CrCAPE	132	DVDHPGLTNTFLVYCNCDPLAIRYNNISVLENHHASIAVKTLLDYKSMNVLSSTLEAEQQRHVRLKLMVALITATDMARHEEFIDSFKEFLNDPKPFECSSPY			231	
GbCAPE	142	DVDHPGLTNAFLVYCNCDPLAIRYNGISVLENHHASIAVKTLLLAYESTNLSNLTDAEQQRHVRLKLMVALITATDMQGAETMDRLEVRKIDLRPFECSS-PA			240	
AaCAPE	113	DVDHPGLTNSFLITTYDPLALRYNDISVLENHHASITFTITWSDENVDILSSFYEEKKIRKIVLSLTATDMQGHKIMSLMRSTSMQTFEKSQFI			212	
MpCAPE	200	DVDHPGLTNAFLVATYDPLALRYNDRAVLSSHHAATCFITMRGNDSLNLGLAGLSEEBQRHMRKLMIVLITATDMGEHARILREVGERVQDLRPFECSSPFY			299	
CrCAPE	232	ISQ-----REDFDCAIQGAQMKNSSGSTSVFVS-----	TKDVLILMKMLIKCADTNSIMKPFSLSKRWALLLTLEWFRQGDLEK		304	
GbCAPE	241	CAK-----REISDCPSN-----LVSASVEFVS-----	TKDALLMRMIKICADSNVVKPFSLSKRWALLLTLEWFRQGDLEK		307	
AaCAPE	213	QNVTN----FSSIIIQHDEERTTLQHERAQFSN-----	ISSDATILLQMIKICADSNVVKPFSLARRWASALLLEWFGQDLYER		289	
MpCAPE	300	TPPGCLSPILRDAESSSSGNTTAGAKSSDAFSSPKRLDPKVYKNPLSPSPPIQSTSDVMLLIQLLIKCADSNVVKPFSLSKRWALLLTLEWFRQGEIEK			399	
CrCAPE	305	RLCMPVSKHMDREDDSSALOSMNLGFLESVGRKEMFEMAELELKLQDEVLPTLWANRSEWTCFNSMGSS-SEKVVETILRTFDS-----			385	
GbCAPE	308	RLCMPVSKHMDREDDSSALOSMNLGFLESVGRKEMFEMAELELKLQDEVLPTLWANRSEWTCFNSMGSS-SEKVVETILRTFDS-----			388	
AaCAPE	290	KLGLPISIRFMRDASALISMTTGCIDILAKPMYEATFELKLHYDAIVLLSNRNDNMQLQNEFGQSVAQVETILGEYFPRN-----			373	
MpCAPE	400	QLGLPISIRFMRDREDETLTAMTCCGICIDYAKPMYEMVTMKLRLRMHENVLVNLNLRQMMSTFSTNGRRASETAQOILGPFAPPPIPKGEAVQEGYQQDHS			499	
CrCAPE	386	-----GLENFRDGGVCTKMET-----	QAIAARRSINGGNCMPGRRSFVS-----		424	
GbCAPE	389	-----GSVLKNQOQGMT-----	VQSINGETSMPLRSSLSLSPH-----		421	
AaCAPE	374	-----TMSFKLASNSFYQINKR-----	ISPNIVAHQDLNETSTKTED-----		411	
MpCAPE	500	KLEGKLVATFSGQYVSSDVPSRKLESSPSAKSLGSVSEDSEETVENVEDSPILSVTRDSSEFSLGSEAGSSVKTSPOFLSRAGTEAPSSPQSLQASQE			599	
CrCAPE	424	-----	-----	-----	424	
GbCAPE	421	-----	-----	-----	421	
AaCAPE	411	-----	-----	-----	411	
MpCAPE	600	QRGSPSPGVQYRLSPRGPGSPSPVPTQISGNPESPGYRETYGPGGSQPAAMEVVPVQKSPHEPVAVDVAASQQSADVIAPLSKPAQLQVQKQPVVPTVS			699	
CrCAPE	425	-----INSREKRDRPLSLLLG-----	FMELHAFCEAN-----	KAVPISESILTNR-----	465	
GbCAPE	422	-----VPMTPKAKNDRPLSLLLG-----	PMQHRTSVQSPDLARRVSVREASMSKSAFSETSLKRL-----		479	
AaCAPE	412	-----ILCKEADKTSMHASPSVS-----	PLLPTVVQATQNNDLPLSLLFGTASKEDSIIMVSDTARG-----		468	
MpCAPE	700	RGVHFDDSELTASERSELSSSIQSSSPFDLALRVSFVAINPDSDSVKVLIEQSDPLSTATIEQRDPDSPRMTGLEPFLLEEVAASSSESKAEPETEDEYNQ			799	
CrCAPE	466	-----SSSKPNLLSKVNG-----	SLTISPAVTERTRYSGFGSFRYSSEDRASILHHIAERN-----	SIDLSFKQSPBWK	532	
GbCAPE	480	-----STIR-TIQSPKDLG-----	SFNDTQSRTEVARSSV-FGPMHQ-----	SIFQRLAERN-----	SIDLSLKQPTWK	539
AaCAPE	469	-----TPLKESILHSLQL-----	VVKPTDSTSTCITSNIKNLSQSGLGEYPAFVISHSCSKLEG-----	KEGNKVLITICCHRLT	539	
MpCAPE	800	RYEAPLSLLFGATPREELMLPAKIKDKNASLVSALLPGANNLVNDRKQNAWEQMAFRSPSEQAASRGSILTTVPVSFANSDGDLEKSSSLRKGPPPEGEWE			899	
CrCAPE	533	TARSNPYAVKONRALSTVWQCVIVPISCHAFADDLVRAAFPKYIDSYAAKTYLVCLALFLELIMLSLVRNHYFASISFWLDDLGSLSLVPFTMGATQ			632	
GbCAPE	540	IVRSHPYAVNANRLDSRIWQCVIVPISCHAFADDLVRAAFPKYIDSYAAKTYLVCLALFLELIMLSLVRNHYFASISFWLDDLGSLSLVPFTMGATQ			639	
AaCAPE	540	TIRKYTRIMKINKALSKAWSIISATLHALFIDDFTRKALLPKADVYETHLLIICFTLEFVLDILALSLMRBEEYFAGFFWDLDLGLTSLIPTICETMS			639	
MpCAPE	900	ALRTHRVNRNRLRALSCKTNALLIVATLVLEADDDVVGKFLPKHADVYESHILTACLSLELAESALLCIFDRYFSSFFFWLMDLGSLSLVPFTMGATQ			999	
CrCAPE	633	VNLIITARSIKTAKTFFRAAKMONGDYKLFRLAN-VMMVMVRCRNSASSDDDEETVPDPDHHCQKPSQVWTRSELTSOKLVIGMLTIIVVVPDLVHTD			731	
GbCAPE	640	ANLIITARSIKTAKTFFRAAKMONGGGYMKLFQFSN-VLRLVRRRGSVSSNDDEDETEHENDHHYQKPSQVWTRSELTSOKLVIGMLTIIVVVPDLRTS			738	
AaCAPE	640	PNLMIATKGRAAKSVTRASKLMOASRFSNLLISIR-FMKIIVYQKPSILNIEN-KVRNDENELIISKPSQVWSTLAEITTOKLETGLVLIVITPILLSKC			736	
MpCAPE	1000	QNLVIATGRAAKTVTRFSKTLQASHIQQIVHIFVLEVFVKFFG-FKRDTSLSPSEYEEEEKFLSKPSOKLVIGMLTIIVVVPDLVHTD			1098	
CrCAPE	732	ISDVGFVTSLESLDHQPLYSLSYFNSSLNKILQFYKHLKVELLYLGVGRDGLPPEYISLEYCSVTNMSSTCQGVDEGGTTYHOVVEEKKERMNAKEDAEK			831	
GbCAPE	739	PNDLGFVTSLESLDHQPLYSYMFVNSLTNLLHFYKHLNKKLYLGVGDGLLYPESILLKNCASATSTSTCKGVEGD-ATYNQVIPAITHQEDAKTNAEMK			837	
AaCAPE	737	EKDLAPVMSLNTFEDVELTQBFESILHYAIKFYNNMHNKLYLGVKPHQDLVG----TFQNTT-----	YHOVFNSTIKNEEKNEIEKK		817	
MpCAPE	1099	EKLAPLVSLDPLDDYLIGSPNFNLTVERNVMTKRHCQNLNLYLGVKASRISIKEGGYSYGLGIDVAGVEK-----YQOILPNVDEEDPGRQAQEE			1190	
CrCAPE	832	YRITELLKVSNSKRSEAYESVKKETQIYHAYDLATITIIILILSAMSFFLSRDSNKLIIQPIERMVNFVKELADDPVSFAGKVLPOQ-CDG---KVMET			927	
GbCAPE	838	YRDSLELLVTSQSRSEAYESVKKETQLYHAFDLATITIIILILSAMSFFLSRDSNKLIIQPIERMVNFVKELADDPVSFAGKVLPOQCDG---KVMET			934	
AaCAPE	818	YRQVELLIASSDDGRSEAYETIKKSSVKYIMNMCCOTIILLVLAACWFFLSRDSNKLIIQPIERMVNFVKELADDPVSFAGKFSQETKPAPMGRVMT			917	
MpCAPE	1191	FRPTELISVTSDDSRQAQAYSIKKSRFKYGMNIAMTVLILLLAANCFLLSRDSNKLIIQPIERMVNFVKELADDPVSFAGKVVVKPTGDS--KIMET			1288	
CrCAPE	928	RFIEAALLKIASLTQKVALGDAGMDILSNLKGSEFNPMPPGKKVRACYGFCDIRNFTDATECLOQEEVMMFVNRIADLIHNKVMHGGFPNKNIGDAFLIV			1027	
GbCAPE	935	RFIEAALLKIASLTQKVALGDAGMDILSNLKGSEFNPMPPGKKVRACYGFCDIRNFTDATECLOQEEVMMFVNRIADLIHNKVMHGGFPNKNIGDAFLIV			1034	
AaCAPE	918	RFVEAALLKIASLTQKVALGDAGMDILSNLKGSEFNPMPPGKKVRACYGFCDIRNFTDATECLOQEEVMMFVNRIAEVHNKVLHGGFPNKNIGDAFLIV			1017	
MpCAPE	1289	FVVEAALLKIASLTQKVALGDAGMDILSNLKGSEFNPMPPGKKVRACYGFCDIRNFTDATECLOQEEVMMFVNRIADVHNKVLHGGFPNKNIGDAFLIV			1388	
CrCAPE	1028	WKKTISDAASKHFVQSGTSFADRALRSFLDIIHVSVETSKALQESAMHPSIQKRMPPGYRIRLGFGLHVGWAIEGAIGSSHKVDPSPYLSPHVNMASRLEAAT			1127	
GbCAPE	1035	WKKTISDAASKHFVQSGTSFADRALRSFLDIIHAVETSQALQESAMHPSIQKRMPPGYRIRLGFGLHVGWAIEGAIGSSHKVDPSPYLSPHVNMASRLEAAT			1134	
AaCAPE	1018	WKKTISDNTSS--KTRGISFADRALRSFLDIIQAVETSQTLADAKHPAQORMPGYRIHMGFGLHVGWAIEGAIGSSHKVDPSPYLSPHVNMASRLEAAT			1115	
MpCAPE	1389	WKKTISDNTNK---SRATSFADRALRSFLDIQSIETSSQSAEABAKHPAQORMPGYRIHMGFGLHVGWAIEGAIGSSHKVDPSPYLSPHVNMASRLEAAT			1485	
CrCAPE	1128	KQYGVMLISETVIANLTKSSLRDSRCRLDRVTVKGSAPFLTYTYDMPSFOKDLKGNQODYKNLFEAAVDQVYIYGNHSHESCDLKECARLWPSDKPFSI			1227	
GbCAPE	1135	KQYGVMLISETVIANLTKSSLRDSRCRLDRVTVKGSAPFLTYTYDMPSFOKDLKGNQODYKNLFEAAVDQVYIYGNHSHESCDLKECARLWPSDKPFSI			1234	
AaCAPE	1116	KQYGVMLISETVISHLTKSSLRDSRCRLDRVTVKGSAPFLTYTYDMPSFOKDLKGNQODYKNLFEAAVDQVYIYGNHSHESCDLKECARLWPSDKPFSI			1215	
MpCAPE	1486	KQYGVMLISETVIAHLTSTLDRSRLDRVTVKGSQPMVLYTFDIEFLFODLQAGNQBQYRDIFFBAVDSYIGDNDIALEFLQECQTLWPTDKPATV			1585	
CrCAPE	1228	LLDFMASHRNIVPSNWKKGRELTEK			1252	
GbCAPE	1235	IADFMASYKNVVPENWKKGRELTEK			1259	
AaCAPE	1216	LMSYMASNYRSPENWLKGRRELTEK			1240	
MpCAPE	1586	LLTFMASHNNAIPENWNAKGRRELTEK			1610	

Figure S1. Multiple sequence alignment of CAPE

The amino acid sequences of CrCAPE, GbCAPE, AaCAPE, and MpCAPE are shown. Amino acid residues that were identical in the majority of the sequences are shown in gray. Fully identical amino acids in all sequences are shown in black. The catalytic domains of PDE and AC are shown as gray and dotted underlines, respectively.

Aa, *Anthoceros agrestis*; Cr, *Cycas revoluta*; Gb, *Ginkgo biloba*; Mp, *Marchantia polymorpha*

Species*	Number of transmembrane regions in CAPE**	Domain structures of CAPE***
Gymnosperms		
<i>Cycas revoluta</i> *	4	
<i>Ginkgo biloba</i> *	4	
Ferns		
<i>Adiantum capillus-veneris</i>	4	
<i>Azolla filiculoides</i>	4	
<i>Salvinia cucullata</i>	4	
Lycophytes		
<i>Selaginella moellendorffii</i>	2	
Bryophytes		
<i>Anthoceros agrestis</i> *	4	
<i>Physcomitrella patens</i>	4	
<i>Marchantia polymorpha</i>	2	
Streptophyte algae		
<i>Chara braunii</i>	3 (4)	
<i>Coleochaete orbicularis</i>	4	

*DATA were obtained in this study.

**The transmembrane regions of CAPE were predicted with the TMHMM v2.0 program. In *Chara braunii*, the transmembrane region was predicted with the SOSUI engine ver. 1.11 program, and the predicted number was shown in parenthesis.

***The transmembrane regions are shown as vertical lines. In *Chara braunii*, the additional transmembrane region by SOSUI program is shown as a dotted vertical line.

Figure S2. Number of transmembrane regions and domain structures of CAPE

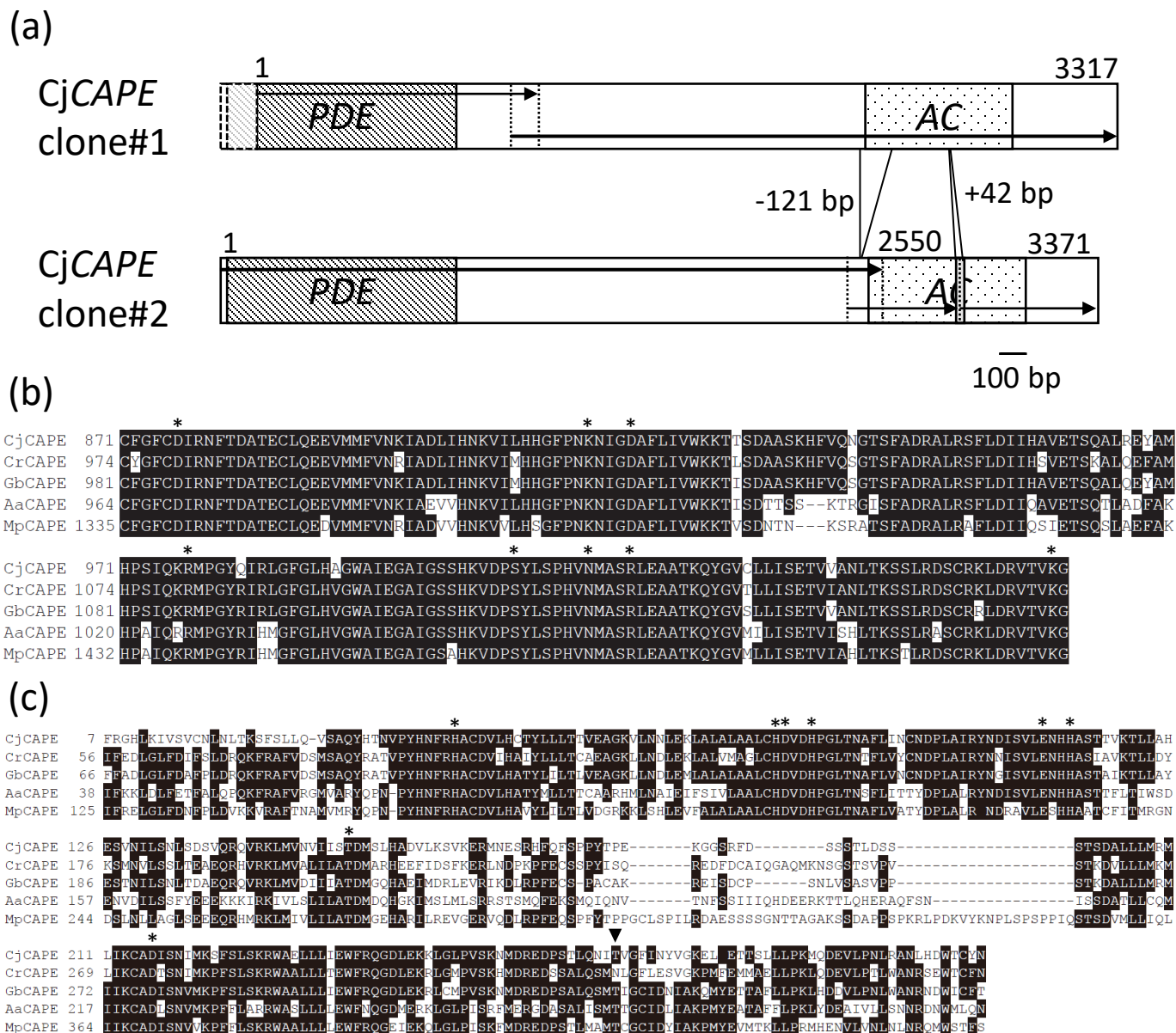


Figure S3. CAPE cDNA clones obtained from *Cryptomeria japonica*

(a) Schematic representation of CjCAPE. CjCAPE clone#1 encoded a partial PDE domain that lacks 14 amino acids at the N-terminus and complete AC domain. CjCAPE clone#2 encoded PDE domain and an incomplete AC domain caused by the deletion of 121 bp just before the AC domain and insertion of 42 bp at the middle of the AC-coding sequence. Open reading frames are shown by arrows.

(b) Multiple alignment of the AC domain of CAPE. Amino acids involved in binding the substrate ATP are indicated by asterisks. Amino acid residues that were identical in the majority of the sequences are shown in black. The amino acids sequence for CjCAPE was used from clone#1.

(c) Multiple alignment of the PDE domain of CAPE. Amino acids involved in metal ion binding are indicated by asterisks. Arrowhead shows amino acid residues involved in the recognition of purine bases. Amino acid residues that were identical in the majority of the sequences are shown in black. The amino acids sequence for CjCAPE was used from clone#2.

Aa, *Anthoceros agrestis*; Cj, *Cryptomeria japonica*; Cr, *Cycas revoluta*; Gb, *Ginkgo biloba*; Mp, *Marchantia polymorpha*