

File S1: Alignment file of all CAD enzymes used in this study

	<u>GHEXXGXXXXV</u>	<u>GDXXXXXXXXXXXXXX</u>
Rgu021554	SDMFAKEGVMPTPFPIVPGHEVVLVDVAVGEGVLGSWSAGDRVGVGVFGGACYHCDRCR	99
Gan031993	ADVIWTQNKHNDSMYPLVPGHEIVGVVRDVGSDVK-CFKVGDHVGVTYVNSCGDCENCN	122
OsCAD4_LOC_Os11g40690.1	ADVIWTRNMFNDISIYPLVPGHEIAGVVEVGADVK-GFKVGDH-----DCENCN	96
Bam015552.1	GDVIWTRNKHNSMYPLVPGHEIAGVVEVGSEVK-GFKVGDHVGVTYVNSCQDCENCN	114
OsCAD1.1_LOC_Os10g11810.1	ADVAVTRNLIINNSMYPLVPGHEIAGVVEVGADVK-SFKVGDHVGVTYVNSCRDCENCN	107
OsCAD1.3_LOC_Os10g11810.3	-----MKLCLNFNMRSHEIAGVVEVGADVK-SFKVGDHVGVTYVNSCRDCENCN	50
Ola036924.1	ADVAVTRNMLNNSMYPLVPGHEIAGVVEVGSDVK-GFKVGDHVGVTYVNSCRDCEYCD	107
Rgu012272	ADVAVTRNMLNNSMYPLVPGHEIAGVVEVGSNVK-GFKVGDHVGVTYVNSCRDCECCN	107
Bam025746.1	ADVAVTRNMHTDSMYPLVPGHEIAGVVEVGSAVE-RFKVGDHVGVTYVNSCRDCENCN	197
PH02Gene48685.t1	ADVAVTHNMLNNSMYPLVPGHEIAGVVEVGSDVK-GFKVGDHVGVTYVNSCRDCEICN	107
PH02Gene44682.t1	ADVWVTRNMHNDSMYPLVPGHEIAGVVEVGSDVK-GFKVGDHVGVTYVNSCRDCESC	107
PH02Gene46268.t1	ADVWVTRNMHNDSMYPLVPGHEIAGVVEVGSDVK-GFKVGDHVGVTYVNSCRDCESC	107
Ola035994.1	TDIHQAKNDLGASKYPMVPGHEVVGVEVVGPEVT-KFRAGEVVGVGIVGCCRCRCPCK	105
Rgu003339	TDIHQAKNDLGASKYPMVPGHEVVGVEVVGPEVT-KCRAGDVVGVGIVGCCRECRPCK	77
OsCAD2-1_Os02t0187800-01	TDIHQAKNHLGASKYPMVPGHEVVGVEVVGPEVT-KYSAGDVVGVGIVGCCRECHPCK	107
OsCAD2-2_Os02t0187800-02	TDIHQAKNHLGASKYPMVPGHEVVGVEVVGPEVT-KYSAGDVVGVGIVGCCRECHPCK	66
Gan017720	TDIHQAKNELGGSKYPMVPGHEVVGVEVVGPEVS-RYRAGDIVGVGIVGCCRECRPCK	98
Bam010499.1	TDIHQAKNELGASKYPMVPGHEVVGVEVVGPEVT-KYRAGDVVGVGIVGCCRECRPCK	107
PH02Gene39617.t1	TDIHQAKNELGASKYPMVPGHEVVGVEVVGPDVT-RYRAGDVVGVGIVGCCRECHPCK	107
PH02Gene04778.t1	TDIHQAKNELGASKYPMVPGHEVVGVEVVGPEVT-KYRAGDVVGVGIVGCCRECRPCK	107
Bam007854.1	TDIHQAKNELGASKYPMVPGHEVVGVEVVGPEVT-KYRAGDVVGVGIVGCCRECRPCK	107
OsCAD6_LOC_Os04g15920.1	TDLHFIHNDWGITMYPVVPGHEITGVTKVGTNVA-GFKVGDHVGVGICIAASCLDCEHCR	108
Ola016985.1	TDLHFIHNDWGITMYPVVPGHEITGVTKVGTNVS-GLKAGDRVGVGICIAASCLDCEHCR	92
Bam039144.1	SDLHFIHNDWGITMYPVVPGHEITGVTKVGTNVS-GFKVGDHVGVGICIAASCLDCEHCR	92
Bam034885.1	SDLHFIHNDWGITMYPVVPGHEITGVTKVGTNVS-GFKVGDHVGVGICIAASCLDCEHCR	108
Bam039795.1	TDLHFIHNDWGITMYPVVPGHEITGVTKVGTNVS-GFKVGDHVGVGICIAASCLDCEHCR	108
PH02Gene48202.t1	SDLHFIHNDWGITMYPVVPGHEITGVTKVGTNVS-GFMVGDHVGVGICIAASCLDCEHCR	108
PH02Gene49901.t1	TDLHFIHNDWGITMYPVVPGHEITGVTKVGTNVS-GFMVGDHVGVGICIAASCLDCEHCR	108
Gan014390	TDLHFIHNDWGITMYPVVPGHEITGMVTKVGTNVS-GFMVGDHVGVGICIAASCLDCEHCR	108
Rgu008819	SDLSTIKNEWGNAKYPVVPGHEIVGVVTDVGPSVT-RFKAGDNVGVGYMASACRDCANCQ	113
OsCAD9_LOC_Os03g12270.1	SDLSTIKNEWGNAKYPVVPGHEIVGVVAVGVSSVA-RFAAGDTVGVGYIASTCRACANCQ	105
Gan006403	-----MVGVAEVSSTVT-RFNVDKVGVGVIASCTCRACPSQ	37
Ola001888.1	SDLSTIKNEWGNAKYPVVPGHEIVGVVTDVGASVT-RFKAGDNVGVGYIASACRACNTCL	104
PH02Gene26598.t1	TDLSTIKNEWGNAKYPVVPGHEIVGVVTEVGSSVT-RFKAGDKVGVGVIASCTCRACPNQ	104
Bam045387.3	SDLSTIKNEWGNAQYPVVPGHEIVGVVTEVGSSVT-RFKAGDKVGVGVIASCTCRACPNQ	712
OsCAD8B_LOC_Os09g23540.1	TDLHVVKNDWGNAMYPPVPGHEIVGVVTVGVAGVT-KFKAGDTVGVGFFVGSCTCDSCG	180
OsCAD8C1_LOC_Os09g23550.1	TDLHIVKNDWGNAMYPPVPGHEIVGVVTVGVAGVT-KFKAGDTVGVGFFVASCRCGCCG	180
OsCAD8C2_LOC_Os09g23550.2	-----MYPVVPGHEIVGVVTVGVAGVT-KFKAGDTVGVGFFVASCRCGCCG	46
Ola032369.1	TDLHVIKNDWGNALYPVVPGHEILGIVADVGSVVK-KFKAGDTVGVGFFVGSCTCDSCG	104
Rgu014373	TDLHVIKNDWGNALYPVVPGHEIVGVVAGVGSVVK-KFKAGDTVGVGFFVGSCTCDSCG	105
Gan002573	TDLHI IKNDWGNALYPVVPGHEILGVVVDVGSVVK-KFKAGDTVGVGFFVGSCTCDSCG	79
Gan004029	TDLHI IKNDWGNALYPVPGHEIVGVVADVGSVVK-KFKAGDTVGVGFFVGSCTCDSCG	77
PH02Gene13789.t1	TDLHI IKNDWGNALYPVVPGHEILGVVDVGSVVK-KFKAGDTVGVGFFVGSCTCDSCG	104
Bam027739.1	TDLHI IRNDWGNALYPVVPGHEILGVVAGVGSVVK-KFKAGDTVGVGFFVGSCTCDSCG	159
OsCAD8A_LOC_Os09g23530.1	TDLHTIKNEWGNAMYPPVPGHEIVGVVAGVAGVT-RFKAGDTVGVGFFVDSCTCDSCG	105
OsCAD8D_LOC_Os09g23560.1	TDLHI IKNEWGNAMYPPVPGHEIVGVVTVGVAGVT-KFKAGDTVGVGFFVGSCTCDSCG	105
Bam027740.1	TDLHI IKNEWGNAMYPPVPGHEVVGIVTDVGRGVK-NFKTGETVGVGFFVDSCTCDSCS	105
Bam040591.1	TDLHI IKNEWGNALYPVVPGHEVVGIVTDVGRGVK-NFKAGETVGVGFFVDSCTCDSCS	104
PH02Gene13790.t1	SDLHTIKNEWGNAMYPPVPGHEVVGIVTDVGRSVK-NFKAGETVGVGFFVDSCTCDSCS	219
PH02Gene13791.t1	TDLHTIKNEWGNAMYPPVPGHEVVGIVTDVGRGVK-NFKAGETVGVGFFVDSCTCDSCS	105
OsCAD3_LOC_Os10g29470.1	SDLHC IKNEWKHSIYPLVPGHEIAGVVEVGKNVT-RFKAGDRVGVGCMVNSCRSCECN	113
OsCAD5_LOC_Os08g16910.1	SDLHS IKNEWKNATYPLVPGHEIAGVVEAGKNVT-KFKGGDKVGVGCMVNSCHSCDSCN	103
Rgu015472	SDLHS IKNEWKNATYPLVPGHEIAGVVEVGKNVT-KFTAGEKVGVGCMVNSCHSCDSCN	126
Ola032840.1	SDLHS IKNDWKNTIYPIVPGHEIAGVVEVGKNVT-RLNVGDKVGVGIVNSCQSCESC	114
PH02Gene38471.t1	SDLHS IKNEWKNATYPIVPGHEIAGVVEVGKNVT-KFKAGDKVGVGCMVNSCQSCESC	113
Bam005700.1	SDLHS IKNDWKNAIYPIVPGHEIAGVVEVGKNVT-KFKAGDKVGVGCMVNSCQSCESC	114
Bam017920.1	SDLHS IKNDWKNAIYPIVPGHEIAGVVEVGKNVT-KFKAGDKVGVGCMVNSCQSCESC	114
PH02Gene38470.t1	SDLHS IQNEWKNATYPIVPGHEIAGVVEVGNNVT-KFKAGDKVGVGCMVNSCQSCESC	111
Bam032152.1	SDLHI IKNEWKNATYPIVPGHEIAGVVEVGKNVT-NFRAGDKVGVGCMVNSCQSCGSCN	114
Rgu021750	SDLHS IKNEWKNATYPIVPGHEIAGVVEVGKNVT-KFKAGDKVGVGCMVNSCQSCDNCN	66
Gan024020	SDLHS IKNEWKNATYPIVPGHEIAGVVEVGKNVT-KFKAGDKVGVGCMVNSCQSCDNCN	77
OsCAD7_Os04t0612700-01	SDLHTIKNEWKNATYPIVAGHEITGVVTEVGKNVA-RFKAGDEVVGCMVNTCGGCESC	120
Ola022375.1	SDLHTIKNEWKNATYPIVPGHEIVGVIAEVGEKVE-RFKAGDKVGVGCMVNTCQSCESC	116
Bam022082.1	SDLHTIKNEWRSATYPIVAGHEIVGLINEVGKNVQ-EFKVGDVGVGCMVNTCQSCESC	115
PH02Gene32740.t1	SDLHTIKNEWKNATYPIVAGHEIVGLITEVGKNVQ-MFKAGDKVGVGCMVNTCQSCESC	113
Bam044253.1	SDLHTIKNEWKNATYPIVAGHEIVGLITEVGKNVQ-KFKAGDKVGVGCMVNTCQSCESC	111
Rgu006342	TDLHHLRIT-ADSVFPLVPGHEFVGEVAAVGEVET-AHAVGDPVAVGNIVDSCGECRRR	78
Rgu008067	SDIHQVGEWGGETFFMPVPGHEIIGTVAEVGSDVT-EHAVGDTVGVGCFVDSCLECEACQ	180
Rgu021228	SDIHQARGEWGGESFFMPVPGHEIVGEVVEVGSVAVS-GHAVGDLVGVGCFVDSCLECEACQ	112
Rgu020259	SDIHTVKGDFGQPPFVPGHEIVGRVAVGVDEVT-THRVDGDRVGGLVNSCRECVNCR	102
Rgu021242	SDIHQARNEWGGSEFFMPVPGHEIAGTVSAVGAEVS-QYAVGDRVGVGCFVDSCRECDNCR	109

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 SFLENYCSN-TVFTFNRIID---TDGSVTMGGYSNHIVVRQRYCFKIPD-----GYPL 170
 SSLENHCSK-CVVITYNSVD---SDGTVTKGGYSSHILVHQRYCFKIPA-----DYPL 144
 SFLENHCSK-FVFTYNSID---TDGTVTKGGYSSHIVVHERYCHKIPD-----GYPL 162
 SSLENYCSQ-HVFTFNGVD---TDGTVTKGGYSTHIVVHERYCFKIPD-----GYPL 155
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 SFLENHCSK-HVFTFNGVD---TDGTVTKGGYSTHIVVHERYCFKIPD-----GYPL 155
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 ANVEQYCNK-RIWSYNDVY---TDGRPTQGGFSSAMVVDQKFVVKVPD-----GLAP 153
 ANVEQYCNK-RIWSYNDVY---TDGRPTQGGFSSAMVVDQKFVVKVPA-----GLAP 125
 ANVEQYCNK-RIWSYNDVY---TDGRPTQGGFASAMVVDQKFVVKIPA-----GLAP 155
 ANVEQYCNK-RIWSYNDVY---TDGRPTQGGFASAMVVDQKFVVKIPA-----GLAP 114
 ANVEQYCNK-KIWSYNDVY---TDGRPTQGGFSSAMVVDQKFVVKVPA-----GLAP 146
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 RSEENYCDK-VTLTYNGIF---WDGSVTYGGYSSMLVAHKRFVVRIPD-----NLPL 140
 RSEENYCDK-VALTYNGIF---WDGSVTYGGYSNMLVAHKRFVVRIPD-----NLPL 140
 RSEENYCDK-VALTYNGIS---WDGSVTYGGYSNMLVAHKRFVVRIPD-----NLPL 156
 RSEENYCDK-VTLTYNGIF---WDGSVTYGGYSNMLVAHKRFVVRIPD-----NLPL 156
 SSEENYCDK-VTLTYNGIF---WDGSVTYGGYSNMLVSHKRFVVRIPD-----NLPL 156
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 DGFENYCNK-LVPSFNSAL---PDGATVHGGFSELAVVNQRYVVRIPG-----GGGGASPAPL 159
 EGFENYCNK-LVPSFNSAL---PDGTVKHGGFSELAVVHEHFVLRIPD-----ASPL 85
 EGFENYCNK-LVPSFNSAL---PDGATVHGGFSELAVVHEHFVLRIPD-----ASPL 152
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 NGYENYCNK-MVITTCNGVDHDHGGGAATQGGFSDAIVVNEHYVLRVPA-----GLPL 97
 KGYENYCNK-MVLTSGVDQEHG-GEVTKGGFSDVMVNVNEDYVVRVPD-----GLPL 154
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 KGYEQYCNK-VVFTSNGVDHDG-GAVTQGGFSDVMVNVNEDYVVRVPD-----GLPL 129
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DVAAPLLCAGITLYTPLHWGAG---PGKKVAVVGMGGGLGHVGVKIAHALGAEVTVLSQ 214

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SESKREEAINLLGADNFVIS---SDENQMESLKSSLHFIIDTASGDHQFDPYLSLLKVG 258
SESKRNEAINLLGADSFVIS---SDKEQMESLKSSLHFIIDTAAAGDHPFDPYLSLLKVG 276
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SLKKQEDG-KRLGADHYAT---SDPDTFEQLAGSFDLIVNTVSAHIDIAAYLGLLAVDG 263
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OsCAD1.1 LOC_Os10g11810.1	VMALLSFPEI-KVHPANLNLGGRSLGSGV-----	TGGTKDIQ	306
OsCAD1.3 LOC_Os10g11810.3	VMALLSFPEI-KVHPANLNLGGRSLGSGV-----	TGGTKDIQ	249
Ola036924.1	VMVLLSFPEI-KVHPANLNLGGRSLGSGV-----	TGGTKDTQ	306
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Rgu003339	KHVLGVIGQPLSFVSPMVLGRKSITGSF-----	IGSVDETA	277
OsCAD2-1_Os02t0187800-01	KLILMGVINQPLSFISPMVLGRKAITGSF-----	IGSMAETE	307
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Gan017720	KHILMGVIGQPLSFVTPMVLGRKSITGSF-----	IGSMDETA	298
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Ola016985.1	KLVLVGAPDKPELPSFPLIFGKRTVSGSM-----	TGGMRETQ	292
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Bam034885.1	KLVLVGAPDKPELPSFPLIFGKRTVSGSM-----	TGGMKETQ	308
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Bam045387.3	KLVPVGPSPGKPVQLALYPLQSGGKVVAGSM-----	IGGMGDTQ	912
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OsCAD8C2 LOC_Os09g23550.2	QMVVVGAPTRPELPAIYVPGGKITGNC-----	VGGIRDQ	249
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Rgu014373	QMVVVGAPTRPELPAIYVPGGKITGNC-----	VGGVKDCQ	307
Gan002573	QMVVVGAPTRPELPAIYVPGGKITGNC-----	VGGIRDQ	281
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Ola032840.1	KMILVGLPENPLEVPAFSLVHGKRTLAGSC-----	IGGMRDQ	314
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Gan021750	KMILVGLPEKPLEVPAFALVQMNKTLAGSC-----	IGGMRDQ	266
Gan024020	KMILVGLPEKPLEIIPAFALVQMNKTLAGSC-----	IGGMRDQ	277
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Rgu008067	VMANLGAPSDNLEVSFAFSLPNRRSIAGSM-----	VGGLPETQ	379
Rgu021228	VMVNLGAPSDKLEVGAFSLPFRRSIEGSM-----	VGGLPETQ	311
Rgu020259	ALVNVGAPAEPTTVHAMTLVGGRRTFAGSM-----	IGGIAETQ	301
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OsCAD4 LOC_Os11g40690.1	EMINFCAANNVPDIEMIKIDYNEALQRLINRDVRFVRFVIDIENSFK*-----	343
Bam015552.1	EMLNFCAAANKIYPEIEIIKMDNINEALERLINRDVKYRFVGGVMALVGFPEIKVHPANL	373
OsCAD1.1 LOC_Os10g11810.1	EMINFCAANKIYPDIEMIKIDYINEALQRLVDRDVRFRFVIDIENSFK*-----	354
OsCAD1.3 LOC_Os10g11810.3	EMINFCAANKIYPDIEMIKIDYINEALQRLVDRDVRFRFVIDIENSFK*-----	297
Ola036924.1	EMINFCAANKIYPEIEIVKMDYINEALERLIKRDVRYRFVIDIENSFK-----	354
Rgu012272	EMINFCAANKIYPDIEMINIDYINEALDRLIKDVRYRFVIDIMENSFK-----	354
Bam025746.1	EMINFCAANKIYPDIEMIKIDYINEALERLINRDVRYRFVIDIETSFK-----	444
PH02Gene48685.t1	EMINFCAANKIYPDIEMIKIDYINEALERLINRDVRYRFVIDIENSFK-----	354
PH02Gene44682.t1	EMINFCAANKIYPDIEIIKIDYINEALERLINRDARYRFVIDIENSFK-----	354
PH02Gene46268.t1	QMLNFCAAANKIYPDIEMIKIDYINEALERLINRDVRYRFVIDIENSFK-----	354
Ola035994.1	EVLQFCVDKGLTSEIEVVVKMGYNQALERLERNDVRYRFVVDVAGSNLEDDAATDLA----	362
Rgu003339	EVLQFCVDKGLTSQIEVVVKMDYVNQALKRLERNDVRYRFVVDVAGSNLEASAADLP----	333
OsCAD2-1_Os02t0187800-01	EVLNFCVDKGLTSQIEVVVKMDYVNQALERLERNDVRYRFVVDVAGSNIDDDADAPPA*----	363
OsCAD2-2_Os02t0187800-02	EVLNFCVDKGLTSQIEVVVKMDYVNQALERLERNDVRYRFVVDVAGSNIDDDADAPPA*----	322
Gan017720	EVLQFCVDKGLTSQIEVVVKMDYVNQALERLERNDVRYRFVVDVAGSNIEDAA-----	350
Bam010499.1	EVLQFCVDKGLTSQIEVVVKMDYVNQALERLERNDVRYRFVVDVAGSNIVDAA-----	359
PH02Gene39617.t1	EVLQFCVDKGLTSQIEVVVKMDYVNQALERLERNDVRYRFVVDVAGSNIEDAA-----	359
PH02Gene04778.t1	EVLQFCVDKGLTSQIEVVVKMDYVNQAFERLERNDVRYRFVVDVAGSNIEDAA-----	359
Bam007854.1	EVLQFCVDKGLTSQIEVVVKMDYVNQALERLERNDVRYRFVLDVAGSNIEDAA-----	359
OsCAD6 LOC_Os04g15920.1	EMMDICGEHNITCDIEIVSTDRINDALARLARNDVRYRFVINVGGS SKL*-----	360
Ola016985.1	EMMDLCGQHNTAQVEVIGIEDVNAAMERLQKGDVRYRFVVDIESS SKL-----	341
Bam039144.1	EMMDLCGEHDITCDIELVSTDRINEALGRLARNDVRYRFVIDIGKNSKL-----	341
Bam034885.1	EMMDLCGEHDITCDIELVSTDRINEALGRLARNDVRYRFVIDIGKNSKL-----	357
Bam039795.1	EMMDMCGEHNITCDIELVSTDRINEALGRLARNDVRYRFVIDIGKNPKL-----	357
PH02Gene48202.t1	EMMDLCGEHNITCDIELVSTDRINEALGRLARNDVRYRFVVDIGKNSKLQ-----	361
PH02Gene49901.t1	EMMDLCGEHNITCDIELVSTDRINEALGRLARNDVRYRFVVDIGKNSKL-----	357
Gan014390	EMMDLCGEHNITCDIELVSTDRINEALGRLARNDVRYRFVVDIAKNSKL-----	357
Rgu008819	EMIDFAAEHNITAQVEVIGIEDVNAAMERLQKGDVRYRFVIDIANTIARA-----	363
OsCAD9 LOC_Os03g12270.1	EMVDFAVEHGVAAAEVEVIGMEDVNGAMERLQKGDVRYRFVIDVANTMARAR*-----	362
Gan006403	EMIDFAAEHNITAAAEVEVIGIEDVNAAMERLQKGDVRYRFVIDVANTMARAY-----	310
Ola001888.1	EMIDFAAEHNITAQVEVIGMEDVNAAMERLQKGDVRYSSTAIKGEKKGWR-----	354
PH02Gene26598.t1	EMIDFAAEHSAAEAEVEVIGIDVNAAMERLQKGDVRYRFVIDIANTMARA-----	354
Bam045387.3	EMIDFAAEHNITAAAEVEVIGIDVNAAMERLQKGDVRYRFVIDVANTMARAY-----	963
OsCAD8B LOC_Os09g23540.1	AMLDFAGEHGITAEEVEVIMKDYVNTAMERLEKNDVRYRFVIDVAGSSLGGSGDDKI*----	436
OsCAD8C1 LOC_Os09g23550.1	AMLDFAGEHGITAEEVEVIMKDYVNTAMERLEKNDVRYRFVIDVAGSSLAGSGDAKI*----	439
OsCAD8C2 LOC_Os09g23550.2	AMLDFAGEHGITAEEVEVIMKDYVNTAMERLEKNDVRYRFVIDVAGSSLAGSGDAKI*----	305
Ola032369.1	AMLDFAAAHGITAEEVEVVKMDYVNTALERLEKNDVRYRFVIDVAGSLGSTA-----	357
Rgu014373	AMLDFAAEHGITAEEVEVIMKDYVNTALERLEKNDVRYRFVVDVAGSLGSDA-----	358
Gan002573	AMLDFAGEHGVTADVEVIMKDYANKALERLEKNDVRFVVIDVAGSLGSTS-----	332
Gan004029	AMLDFAGEHGITAEEVEVIMKDYVNTALERLEKNDVRYRFVIDIAGSLGSAA-----	330
PH02Gene13789.t1	AMLNFAGEHGITAEEVEVIMKDYVNTALERLEKNDVRYRFVIDVAGSLGSTA-----	357
Bam027739.1	AMLDFAGEHGITAEEVEVIMKDYVNTALERLEKNDVRYRFVIDVAGSLGSTA-----	412
OsCAD8A LOC_Os09g23530.1	AMLDFAGEHGIAADVEVVAMGDVNAALGRLERNDVRYRFVIDVAGTLHAAAAAPS*-----	359
OsCAD8D LOC_Os09g23560.1	AMLDFAGEHGIAADVEVVAMDVNAALGRLERNDVRYRFVVDVAGTMHAAAAAASS*-----	362
Bam027740.1	AMLDFAGEHGVTADVEVIMKDYVNTAVERLERNDVRYRFVVDVAGSLGAAA-----	329
Bam040591.1	AMLDFAGQHGITADVEIVKMDYVNTAVERLERNDVRYRFVVDVAGSLGAAA-----	355
PH02Gene13790.t1	AMLDFAGENGITADVEVVVKMDYVNTAVERLERNDVRYRFVLDVAGSLGAAA-----	470
PH02Gene13791.t1	AMLDFAGKHGITADVEVVVKMDYVNTAVERLERNDVRYRFVLDVAGSLGAAA-----	356
OsCAD3 LOC_Os10g29470.1	EMIELAAKHGVTADIEVIGADDVNTAMERLAKADVRYRFVIDVGNTLHAAAAE*-----	366
OsCAD5 LOC_Os08g16910.1	-----SKHGVTAEIEVIGADYVNTAMERLAKADVRYRFVIDIGNTLKDAIE*-----	332
Rgu015472	EMMDLAAEHGVTADVEVISADYVNAAMERLAEADVRYRFVIDVGNTLKSTV-----	377
Ola032840.1	EMIDLAAKHGVTADVEVISADYVNTAMERLAKADVRYRFVIDVGNTLTNTE-----	365
PH02Gene38471.t1	EMIDLAAKHGVTADIEVISANYVNTAMERLAKADVRLRLIL-----	336
Bam005700.1	EMIDLAAKHGVTADIEVIGADYVNTAMERLARADVSTGDDDVVIKILYCGICHSDLHSI	374
Bam017920.1	-----	304
PH02Gene38470.t1	EMIDLAAKHGVTADIEVISANYVNTAMERLAKADVRYRFVIDIGNTLENTE-----	362
Bam032152.1	EMIDLAAKHGVTADIEVIGAEYVNTALERLAKADVRYRFVIDIGNTLKNTA-----	365
Gan021750	EMINLAAKHGVTADVEVIGADYVNTAMERLAKADVRYRFVIDIGNTLKDTE-----	317
Gan024020	EMIDLAAKHGVTADVEVIGADYVNTAMERLAKADVRYRFVIDIGNTLKDTE-----	328
OsCAD7_Os04t0612700-01	EMIDFAAEHGVAAADIELIGADEVNTAMERLAKGDVRYRFVVDIGNTLRSD*-----	379
Ola022375.1	EMIDFAAEHGVAAADIELVGAGGVNAAMERLAKGDVRYRFVIDVGDTLKSSD-----	367
Bam022082.1	EMIDFAAKHGVTADIELIGADGVNTAMERLAKGDIRYRFVIDVGNTLKSD-----	365
PH02Gene32740.t1	EMIDFAAKHGVTADIELVGADGVNTAMERLAKGDVRYRFVIDVGNTLKSD-----	363
Bam044253.1	EMIDFAAKHGVTADIELIGADSNTAMERLAKGDIRYRFVIDVGNTLKSD-----	361
Rgu006342	ELLAFCGEHGITADVEVLPASEVATALDRLARNDVRYRFVLDTTAL-----	322
Rgu008067	EMMDFCAEHGVTADVEVITADQVDEYYDKVVSGDVRYRAVIDTSSLA-----	426
Rgu021228	EMLDFCAEHGVTATVEVIDADDVDAYYDKVVSGDVRYRAVIDTATFG-----	358
Rgu020259	EMLDFCAEHGIGSDVEVIGAEQVNEAYERVLASDVRYRFVIDTASLA-----	348
Rgu021242	KMLDFCAEHHIGAEIETIGVDDVNKAYDRVVDSDVRYRFVIDTATFGG-----	356