

Supplementary Information

Identification and caste-dependent expression patterns of DNA methylation associated genes in *Bombus terrestris*

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AmDNMT1a : NNILQK--CEQKNENHDPKTDDEEYLDKHIDKRAKLTQVNIIP--TPQIK-----NINIFHNKSEYERKUN--EIKFPGHNGAVDEIATIPKIC : 134
AmDNMT1b : EKILCD-NKSDLTQKMQSDSSDESESNILKNNFENNINTEESKIMQ---QKPFNVHQKEYCKKTSIDKIPGHENAVBEMIALTPKIS : 211
ApDNMT1 : -----
EmDNMT1 : -----EVENKPYKNGDPIVVEIDNKRPGSVNNNHMDDDSETISNIRKSNIIIPDTEKNTICGFNNSDIYICQSGEADAVEBYIATINDRVI : 185
BtDNMT1a : -----KRVRFKDTTILS--TSKIK-----STNTFFHSKGEYCKKUND-DUKIKQGHENGAVNDEIATIPKIC : 71
BtDNMT1b : EEIICDSNTTDLVVEQKQSDSSDEPE-NILKRTTGGNDTINTESKILP---QKPVNVHQKEYCKKTSIDKIPGHENGAVBEMIALTPKIS : 209
CfDNMT1 : EANKNG--TVEFDKENHNPQINQDQENABKRMENNNEEISQLKSQVK---KTLTIERDYCKKUND-ETKIKQGHENGAVBEMIALTPKIC : 199
NvDNMT1a : -----NDEAGDRQATADHSSKRSFTELATKQSRPKMMHTGR---VAASRKEPVKEIKRKQDKDKFMAGHENDAVDYNVILPKIC : 162
NvDNMT1b : -----NDEAGDRQATADHSSKRSFTELATKQSRPKMMHTGR---VAASRKEPVKEIKRKQDKDKFMAGHENDAVDYNVILPKIC : 162
NvDNMT1c : QESKSLKIKLTKTSKSSKQSSSKSRSDRERKSKNKRKDDTATTSPDPYKVNKQDDISRIETETIN-YQLKFTTEPEENGYDDELATIPKIS : 499
PxDNMT1 : -----DSEIDEVNSDEDKISIDDENSNDVSEGEKMNCKEESNNAQDLN---NERONICRFNNSDIIFCQSGEADAVEBYIATINDRVI : 168
TcDNMT1 : -----MSLRNRFRESPAQETGDNTKKHKK---TSTHSDKKKFACTIN---QAVVTNFPDDYABESVAITSPKIN : 66
ZnDNMT1 : -----GKEEIEETDEMQVKKVLENGDVPARKKKKTVS-TPNTFKGIPSKQICRIIDDPDLHGHVEAVEBFVAITPKIS : 95

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AmDNMT1a : RNTSFSFHHSDRPPQNILYSSVLDKNHGLSFTGLIEKNVMYISGYIKATIEEA-SPEGGVETKDMGPINEWVYSGFDGGELALIGFNIAFAFYI : 233
AmDNMT1b : RTEPEIIVHSDRPPQNILHICVLDKNHGLSFTGLIEKNVMYISGYMKPIVEENS-CPGGVETKDMGPINEWVYSGFDGGELALIGFTIAFAFYI : 310
ApDNMT1 : -----MNEEINFLSVM---ISDVLNLS-----
EmDNMT1 : SSEDGDGM---RQTNIGFATIDEGHGLSPTGGIIVENDVRIMSGYLPS-CDSSEIDSESIIVKDVGPTEWFIHGDEGDRNCITLSEFGEN : 282
BtDNMT1a : RNNFSFHHSDRPPQNILYSSVLDKNHGLSFTGLIEKNVMYISGYIKATIEEA-SPEGGVETKDMGPINEWVYSGFDGGELALIGFNIAFAFYI : 170
BtDNMT1b : RTEPEAMHSDRPPQNILHICVLDKNHGLSFTGLIEKNVMYISGYMKPIVEENS-CPGGVETKDMGPINEWVYSGFDGGELALIGFTIAFAFYI : 308
CfDNMT1 : RTCDSFSFHHSDRPPQNILYSSVLDKNHGLSFTGLIEKNVMYISGYMKPIVEEDP-SPEGGVETKDMGPINEWVYSGFDGGELALIGFNIAFAFYI : 298
NvDNMT1a : RNEEPEHMHSDRAINKIIFNNVCRNGHGLSPTSGGLVEREAYIISGYVPIYSDS-SIEGAVESKDIGPIVEWFIHGDEGDAITVLSPIGEY : 261
NvDNMT1b : RNEEPEHMHSDRAINKIIFNNVCRNGHGLSPTSGGLVEREAYIISGYVPIYSDS-SIEGAVESKDIGPIVEWFIHGDEGDAITVLSPIGEY : 261
NvDNMT1c : RNEEENESREDDRAYNIISSSVLCNNHGLSPTSGGLVEREAYIISGYVPIYSDP-SIEGAVESKNGFPIVEWFIHGDEGDAITVLSPIGEY : 598
PxDNMT1 : AADSDGDM---RQTNIGFATIDEGHGLSPTGGIIVENDVRIMSGYLPS-CDSSEIDSESIIVKDVGPTEWFIHGDEGDMKNCTLSEFGEN : 265
TcDNMT1 : VNTEINISFEGDLPSHTICCSMDLNDHGLSPTGLICLQEVYHIGGYIKPIIDDDP-SPNGCATLDMGPIHEWFIHGDEGCKVIGITINVAQVY : 165
ZnDNMT1 : RTEDEYTHSDRPPQNILYSSVLDKEHGLSPTNGILERNVILSGYMKPIVEESP-DEEG-----

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AmDNMT1a : IMDSEEEIAFYDIVKPKIYMSLVIEFLIDE--INPSYEDLINKF-QTIVPPKNMSKFHDSILRHAQFICDQVLSFDNSAD-SEDTLLITSPCMRAIA : 329
AmDNMT1b : IMDAEVISEFIDSKPKIYMSLVIEFLIDE--INPTYEDLINKL-QTIVPPKGLSRFHDSILRYAQFICDQVLSFDASAG-PEDPLITSPCMRAIV : 406
ApDNMT1 : -----
EmDNMT1 : IIRSEANTILNNYKIKIWSKVVEIEEYHYLQPSYEDLIEVVRDFSIPELNNKKMHDEMHHKHAQFVCDQVLSLEIE---EDDEPLITSPCMREBI : 379
BtDNMT1a : IIMSEEEIAFYDIVKPKIYMSLVIEFLIDE--INSSYEDLINKL-QTIVPPKGIKPFHDSILRHAQFICDQVLSFDNSAS-AEDTLLITSPCMRAIA : 266
BtDNMT1b : IIMAEANAIFIDSKPKIYMSLVIEFLIDE--INPTYEDLINKL-QTIVPPKGLARFHDSILRYAQFICDQVLSFDASAR-PEDPLITSPCMRAIV : 404
CfDNMT1 : IIMSEEEIAFYDIVKPKIYMSLVIEFLIDE--ISPTYEDLINKL-QTIVPPKGMKPFHDSILRHAQFICDQVLSFDNSAD-VEBILITSPCMRAIA : 394
NvDNMT1a : IIMCSDDSSEFRCRKERTHSITVIGCLIDE--PNSEYEDLINKF-ETIPMPSGLPFRFHDSILRHAQFICDQVLSFDASAL-SDEPILHAPCVKRSI : 357
NvDNMT1b : IIMCSDDSSEFRCRKERTHSITVIGCLIDE--PNSEYEDLINKF-ETIPMPSGLPFRFHDSILRHAQFICDQVLSFDASAL-SDEPILHAPCVKRSI : 357
NvDNMT1c : IIMSEDEHSEFHSILIKILGIVIEVLYVEP--HATYEDLILNKLQSSSKYDILPNMHEDVILEYBFIYLVMSYDETAK-LNEPILHAPCVKRSI : 695
PxDNMT1 : IIMSEANTILNNYKIKIWSKVVEIEEYHYLQPTYEDLMEIIREATIPELDADKMHDEMHHKHAQFVCDQVLSLEAQD---EDDQILITSPCMREBI : 363
TcDNMT1 : IIMSELEIAFYISKCEHTVIFHFIIEILSNFSRAPSVEILAAV-----ENSDNPLLIEFLIQAQFVCDQVLSFDLAGNNNDMILLITPCVFTIA : 260
ZnDNMT1 : -----EVLIRHVKIR-----

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AmDNMT1a : NAGVILGRVTFRRITQ-----R-EQVRKPAKTRKATIKVSDMFENITDQIKHDDKITMGPKRCQGVCEHQCPDCCGLNAKDMIRK : 416
AmDNMT1b : TAGVILNKRIALRITQ-----SRDQRNKKTTNTRKATIKVNNMFETFSQCATNNDKEISGPKRHRCGICETCQDCCVGTAKDMIRK : 494
ApDNMT1 : -----DDIIDFAEKKS-----
EmDNMT1 : KUMGKFKGK--IRTK-----IQYKIDKKKATKATIKVNRKTESFSNCKDKNHELVLK--RRRCGVCAQCPDCCGCAKRAKAK : 463
BtDNMT1a : NAGVITFGVGRQTR-----LKEQVRKPAKTRKATIKVNNMFENITDQIKHDDKITMGPKRCQGVCEHQCPDCCGLNAKDMIRK : 354
BtDNMT1b : TAGVILNKRIALRITQ-----SRDQSKKVTNTRKATIKVNNMFETFSQCATNNDKEVSGPKRHRCGICETCQDCCGCAKRAKAK : 492
CfDNMT1 : NAGVILGKAALRITR-----R-EQVRKPAKTRKATIKVNNMFENITDQIAKHDDRIPTGPKRCQGVCEHQCPDCCGCAKRAKAK : 481
NvDNMT1a : DLSGVTFRRKFRGRRRQFLENDEDWQGLRLSKQAPYNSKATIKQCHDFESFPPCDNTADRLKLK--RRRCGACAELETCCGCAKRAKAK : 455
NvDNMT1b : DLSGVTFRRKFRGRRRQFLENDEDWQGLRLSKQAPYNSKATIKQCHDFESFPPCDNTADRLKLK--RRRCGACAELETCCGCAKRAKAK : 455
NvDNMT1c : DLSGVTFVNRGVSRRG---FHXYQERRAGEIRKELLKVAENRGDSITSIDSLDPVEEKLITLSKPCTRDCGS-DRQRSSCKCE : 785
PxDNMT1 : KUMGKFKGK--TRTK-----IDYKIDKKKATKATIKVNRKTESFTHCKDKNDELVLK--RRRCGVCAQCPDCCGCAKRAKAK : 447
TcDNMT1 : TAGVSEFKKQLMRLLG---NQRTKLQSKATIKVNRKTESFTHCKDKNDELVLK--RRRCGVCAQCPDCCGCAKRAKAK : 344
ZnDNMT1 : ---IYKIVAMHQAQ---RKGFIRRAQSRATIP-LKVEYETFPBCKDKDQKENK-----VYIEYGLDCCGTVSQQDMK : 243

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AmDNMT1a : GEGRSKQACVRRCPENNAIQEADSSPENEDQYIEMENK-KVEEEKSKKKDKF---ELKDDIITIDQIANDNLK-TYKSVIIGDEEIGINIVLV : 510
AmDNMT1b : GEGRSKQACVRRCPENNAIQEADSSQEDDDFNDTIEN--TRITQKMLKEFK---HVEKEITVVEEPIINDGRR-TFYKSVIIGDEEIRANDVILV : 587
ApDNMT1 : -----RKPTEISNHF-----MYKILIER-----
EmDNMT1 : GEGRTKACVRRCPENNAIQEADSSPDDEDEYQISEKK-QDKIDDAVPVKLTG---SNKRNKRIEPIKADATK-IYVEKEIDGAEICNGDFVI : 558
BtDNMT1a : GEGRGKQACVRRCPENNAIQEADSSLENEDEQYDTR-----IEVEERKKVFG---ELTKDIVNIDQIASNNLK-TYKSVIIGDEEIRANDVILV : 444
BtDNMT1b : GEGRSKQACVRRCPENNAIQEADSSQEDDDFNDTIEN--VKITQKMLKEFK---HVEKEITVVEEPIINDGRR-TFYKSVIIGDEEIRANDVILV : 585
CfDNMT1 : GEGRSKQACVRRCPENNAIQEADSSPENEEQYDSIEN---QKVEEKPKDKF---ELKKNVVEEQDKIIDGQK-TYKSVIIGDEEIRANDVILV : 573
NvDNMT1a : GEGTSKQACVRRCPENNAIQEADSSDEYDEDDDDKANHES-SIEVHRKMIRALKK--KKSADVEMGEPIQS-ARG-DEYNAMNNHVDVKKNDVILV : 549
NvDNMT1b : GEGTSKQACVRRCPENNAIQEADSSDEYDEDDDDKANHES-SIEVHRKMIRALKK--KKSADVEMGEPIQS-ARG-DEYNAMNNHVDVKKNDVILV : 549
NvDNMT1c : PCSQXNYDDEPRRQFYREIQANEAQKDSVNLSQKSGNS-SISVFKKTINIFSS---FNAKIBLDCPIIVEGSGNTFNAKHEEETCVGDFVILV : 880
PxDNMT1 : GEGRTKQACVRRCPENNAIQEADSSPDDEEEYRNIAEKKEHDKIDDAVPVKLTG---AGSRKIVVEEPIKADATK-VYIDAEIDGAEIRANDVILV : 543
TcDNMT1 : GEDCNMKPKKIRCPENNVVQILDESDETVTVPARGREGRRPGRSVLSGDLQ---NFRSEIDILGGNDDDTG-ILLN---IRTKGDFVILV : 432
ZnDNMT1 : GEGRSKQACVRRCPENNAIQEADSSPENEDDYCLISEN---ATSDVTFANTHKGIRIREKRIIDTSLIKDDGSC-KYNTVYVNDDEIKPCGDMV : 339

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AmDNMT1a : RPRNPATSRVAKVIYMKENKNGIQ--FANKLHRENDTILGETSDIEILFISDDE--IFKSRSCCTVIFREIQRWNEICNMIDNFENDIKDLG : 607
AmDNMT1b : RSPNDPTVLLQAKVIYMKEDKNGAIL--CANWFRGSDTVLGETSDSLLEILLDQDA-VFTFSKSKATVYKTPRWNEICNADILPEDEIQNGG : 684
ApDNMT1 : RPN-----VSLRMH-----MTVNTGSS-----
EmDNMT1 : RPSQNTITVAKVIYMKKEIHNEISGYFGEVFRASDTVLGVSDEPREVILGRCHGALLSSLRKANERKETSADWFKLGKVED--DEHFEDG : 656
BtDNMT1a : RPRNPATSRVAKVIYMKENKNGIQ--FANKLHRENDTILGETSDIEILFISDDE--VFRAKRSCTVIFRNVPRAELICNMIDNSENEDVDIG : 541
BtDNMT1b : RSPNDPTVLLQAKVIYMKEDKNGAIL--CANWFRGSDTVLGETSDSLLEILLDQDA-VFTFSKSKATVYKTPRWNEIC--NVLPEDEIQNGG : 680
CfDNMT1 : RPRNPATLHVIKIMENKNGSVIQ--FANKLHRENDTILGETSDIEILFISDDE--VFTFSKSKATVIFKMPDWDIELICNMID--DEIKDILG : 668
NvDNMT1a : RPNSSVMOVIVKVMENKMGIL--LGTWLWRGSETILGETSIRELILVIGDQ--VELIYQAKANLVREYSNCTERCN-----IIDALKENS : 641
NvDNMT1b : RPNSSVMOVIVKVMENKMGIL--LGTWLWRGSETILGETSIRELILVIGDQ--VELIYQAKANLVREYSNCTERCN-----IIDALKENS : 641
NvDNMT1c : RSVDSQVACQVIVVMDENVGLAH--FANLYWKEHDTVGLGLARELILSINIKNA-LSVNCCTERINIDRYMNRQDVSTD-----EDDKA : 968
PxDNMT1 : RPSQNTITVAKVIYMKKEIHNEISGYFGEVFRASDTVLGVSDEPREVILGRCHGALLSSLRKAHREKREIPANWFKLGKVEE--DETLEDG : 641
TcDNMT1 : SPKSATKNTIARVYNTTATEPMVH---VYLFXRNEIRILGPVANQILASRDEE-QVAAVVGQAKVYATPDMADLGG-----IECLPSGD : 521
ZnDNMT1 : RPLDPTRALIARVYNTTADGTGAIR--GCHWFRGSDTVLGETSDSLLEILLDQDA-FDLSATGKATISQVIPSMAELIGVETQHEHAVED--G : 435

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AmDNMT1a : KTFEYQKRIPEIARFED PVPDVKYLHKKNYSRFPACATRLNMLEQFNTPKYERL-----EINSKEVINGLVYKKG--DYRVGTTFLQIDVENSKYKT : 702
AmDNMT1b : KTFEYQKRIPEIARFEDCSLDPECPKEISHRFOPACIRFTTLQCYITPKVEDRE-----EKNSEKVTNIVKYKNEEFKVGSAFIMGAIKMKYTS : 779
ApDNMT1 : -----EFTFSRI-----KTIKNRLTMTNEDRIN-----FIS : 108
BmDNMT1 : RTYFYSKYVDRFTSRFEDLPDPACPNALRKHRRFPSEKTKTRDARNIPKVEKILVKSEIVSEQNRSESYVYKQDFDYKKNCCGFPIKGTGFKLNKSM : 756
BtDNMT1a : KTFEYQKRIPEIARFEDPLPDICPFKEKSHRFOPACAHLREVEQNTPKYERL-----KEKSTKEVINGLVYKKGDFDYRVGTTFLQIDKAKNKKYKI : 636
BtDNMT1b : KTFEYQKRIPEIARFEDCTSDPECPKEISHRFOPACVRFTTLQCYITPKVENRE-----EESKNSEVTSVMYKKGDFEVRVGSTVFLMGAIAIKMKYTS : 775
CfDNMT1 : KTFEYQKRIPEIARFEDSLDPDECPKREKSHRFOPACARLRALEQNTPKYERL-----EESKSEKIVGVVYKKGDFEVRVGSAFVLYSAFKKQYKQ : 763
NvDNMT1a : MILEYQKRIPEIARFEDLLPELN--PPKGAEHCFSTCARDILSKMNRTPQLELD-----DTTDDKRKKGTLIRVLNDFEVRVGSAFVLYKKTTFTEFPN : 735
NvDNMT1b : MILEYQKRIPEIARFEDLLPELN--PPKGAEHCFSTCARDILSKMNRTPQLELD-----DTTDDKRKKGTLIRVLNDFEVRVGSAFVLYKKTTFTEFPN : 735
NvDNMT1c : NNIECEKSDPDSGSHLTKPEE--VSVLPTRHS--INIEGKHRRSERVEPTVDELG-----KKEGTLRAVLYKKGDFEVRVGSAFVLYKKTTFTEFPN : 1061
PxDNMT1 : KTYEYQKRIPEIARFEDLPDPACPNLQRHRRFPSEKTKTRDAKNIPIKIDKAEKSEFVTEANRTEPSLYVQDDHDFRGGGFLKGTGNTLNKSSL : 741
TcDNMT1 : DRFEYQKRIPEIARFEDLPDPACPNLQRHRRFPSEKTKTRDAKNIPIKIDKAEKSEFVTEANRTEPSLYVQDDHDFRGGGFLKGTGNTLNKSSL : 598
ZnDNMT1 : KTFEYQKRIPEIARFEDLPDPACPNLQRHRRFPSEKTKTRDAKNIPIKIDKAEKSEFVTEANRTEPSLYVQDDHDFRGGGFLKGTGNTLNKSSL : 530
f k y arfe fc c p 6 e g v5l p

AmDNMT1a : TYQDVLK--LKENVDEDMYPEYRKSSDHVKGSDFTDPPCIGYNTKANTNDMLVSPSDNIMNKLYRPENTHKSSSTMEQADLNMYVWSNEVCN : 800
AmDNMT1b : TYHISQK--YKKGVDMDMYPEYRKSSDHVKGSDFTDPPCHIGYNSYATNNKLVAASDMLKMKMYRPENTHKGLTMCQVDLNMYVWSNEVCN : 877
ApDNMT1 : -----VMSIESVOLDN : 119
BmDNMT1 : TKANTVAK--PEFEKVDRTYPEYRKNDNSNRGSDITDGPCCVGYIAATAASEGFLVPDLYLKUNVLRPENTSS--KFPQHEHTNLYLYTEHRE : 853
BtDNMT1a : IYDPAQK--YKKNVDEDMYPEYRKSSDHVKGSDFTDPPCIGYNSYATNDMLVSPSDNIMNKLYRPENTHKGLTMCQADLNMYVWSNEVCN : 734
BtDNMT1b : TYHISQK--YKKGVDMDMYPEYRKSSDHVKGSDFTDPPCHIGYNSYATNNKLVAASDMLKMKMYRPENTHKGLTMCQVDLNMYVWSNEVCN : 877
CfDNMT1 : MYQAEAK--PKKEVDEDMYPEYRKSEKAFNSVDTPDPPCHIGYNAIYASITDLVSSSDLYLKUNKMYRPENTHRDVTMEQADLNMYVWSNEVCN : 861
NvDNMT1a : MNQDTSRG--QKRIIVDEEKYPAAYRKFNDRVKGSDVTPDPPDICYTSTYSTSKSLAGVNAVYTKKMYRPENTHRGESKKKSDMNLVWSNEVCN : 834
NvDNMT1b : MNQDTSRG--QKRIIVDEEKYPAAYRKFNDRVKGSDVTPDPPDICYTSTYSTSKSLAGVNAVYTKKMYRPENTHRGESKKKSDMNLVWSNEVCN : 834
NvDNMT1c : LLDAKSGKISKIDDEKYPYLYRKAEDDAVIDKFMFAEDDICYTTEFTTT-----DKLYLKKKLYRPENTHRNEVLTKQNDMNLVWSNEVCN : 1153
PxDNMT1 : TYS-DTSK-PLENVDSVYPEYRKSDNNLRGSDVTPDPPCVCGLVAAAARGAGFLVPDLYLRVVRVCRPEHNAS--RFPQHEHTNLYLYTEHRE : 837
TcDNMT1 : ECTFDPAK--EENNSKYPEYRKREAN--ASCCKMOPPCIGLETCDG-----PAGLVARVFRPENTKGGSMYSQSDINLFWSTKFT : 684
ZnDNMT1 : TAAVTKDKS--DEKVDMDMYPEYRKSSDHVKGSDFTDPPCVCGLHKTFAKNTNDMLVSPSDNIMNKLYRPENTHRGCLMCQADLNMYVWSNEVCN : 630
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AmDNMT1a : KIKIVKGYCYIAASEN--LNQSEBWTAAAGYREYNAAINVOEKTDEPYHAISGKC--GKSGNLF-----GKKTSESEKRAIVNPIEYKXISE : 893
AmDNMT1b : KIKIVKGYCYIAASEN--LDQSEBWTAAAGYREYSAAINASEKTVDPIYAMNKGKSGKGGKAKAC-----SKKLETSKK--IIDKPINYCKYVK : 971
ApDNMT1 : ISDDHID-----KSRK : 136
BmDNMT1 : PLSSTVGHHLIDQNPONISDQELGNDICREYRMAVCKSTGSEPTDQNAISVGRDTRDKAGKGG-----STKTITETPAKVVEEKIR : 944
BtDNMT1a : KIKIVKGYCYIAASEN--LNQIVDEWTAAAGYREYNAAINVOEKTDEPYHAISGKS--GKSGNLF-----GKKTSESEKRAIVNPIEYKXISE : 893
BtDNMT1b : KIKIVKGYCYIAASEN--LDQSEBWTAAAGYREYSAAINASEKTVDPIYAMNKGKSGKGGKAKAC-----SKKLETSKK--IIDKPINYCKYVK : 971
CfDNMT1 : KIKIVKGYCYIAASEN--LSESVBWSLGTENRREYTAAMAKENSDPEPYVINIKGKS--GKSGKGGK-----AKKVGETENKPIVDKPIDHVPVIR : 964
NvDNMT1a : VRLNCKVGYCYIAASEN--LNQSEBWSASGSHREYSEAYLDNNESTTEPAHACSCTKSFKKDVAKSKS-----KVETIIEDIPVSLPQISH : 923
NvDNMT1b : VRLNCKVGYCYIAASEN--LNQSEBWSASGSHREYSEAYLDNNESTTEPAHACSCTKSFKKDVAKSKS-----KVETIIEDIPVSLPQISH : 923
NvDNMT1c : VSNVYVRYKYVAHAKD--FSKSEBWSNLSDREYEMMHDKKFTDIERNMGYCEDVLPDDIPYDPOVDAMT-----SSKASATT--ETSANASVR : 1225
PxDNMT1 : VPSAIV-----KTGKTEVPEAESGRIDKKEKGGK-----SSKASATT--ETSANASVR : 892
TcDNMT1 : VPRKVMKGYCYVWCSN--EQKAREYSEGSEYRYRROOPDPCGELVPTYSCTRLALR-----EGAGQDE-----RPFGR : 754
ZnDNMT1 : LNSVYVRYKYVAHAKD--VDFIAEWSHSEYRYFYCAALNSIKQTEPEPFHATNLGMYGKGGKGGK-----KKTWSETEEEKKKKMGKIEDWPQNHT : 728
6 f 6 gkc ew gp r yf y p k k k

AmDNMT1a : KLKTLDFVAGCGGLSEGLHQAGVAENL--WAIEKEESAHAVRLNPNPAVHIEPCNVLLKVVNGETTNEIGQKLPQKQGEVLLCGGPPCQGFSGMNR : 991
AmDNMT1b : KLKTLDFVAGCGGLSEGLHQAGVVDNQ--WAIEKDEPAALRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 1069
ApDNMT1 : -----FAGCGGLSEGLHQAGVVDNQ--WAIEKDEPAALRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 227
BmDNMT1 : FLRTLDVAGCGGLSEGLHQAGVAECK--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 1042
BtDNMT1a : KLKTLDFVAGCGGLSEGLHQAGVVDNQ--WAIEKEESAHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 925
BtDNMT1b : KLKTLDFVAGCGGLSEGLHQAGVVDNQ--WAIEKDEPAALRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 1065
CfDNMT1 : KLKTLDFVAGCGGLSEGLHQAGVAECK--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 966
NvDNMT1a : KLKTLDFVAGCGGLSEGLHQAGVAESL--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 1020
NvDNMT1b : KLKTLDFVAGCGGLSEGLHQAGVAESL--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 1020
NvDNMT1c : ---SLIEFAGCGGLSEGLHQAGVAESL--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 1320
PxDNMT1 : FLRTLDVAGCGGLSEGLHQAGVAESL--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 964
TcDNMT1 : FLKTLDFVAGCGGLSEGLHQAGVAESL--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 846
ZnDNMT1 : KLKTLDFVAGCGGLSEGLHQAGVAESL--WAIEENVEASHAVRLNPNPAVHIEPCNVLLKVVNGDLDNNGQRLPQKQGEVLLCGGPPCQGFSGMNR : 826
1 ld FAGCGls gl g wa e aa a lnn vf dc 1 g p kg v cggppc g sgmrnf

AmDNMT1a : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1091
AmDNMT1b : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1169
ApDNMT1 : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 327
BmDNMT1 : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1142
BtDNMT1a : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1025
BtDNMT1b : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1165
CfDNMT1 : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 974
NvDNMT1a : NSRAYSSFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1120
NvDNMT1b : NSRAYSSFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1120
NvDNMT1c : ---DTHVPSFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1415
PxDNMT1 : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 1064
TcDNMT1 : NEGEYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 946
ZnDNMT1 : NSROYSLFKNSLIVSLYSCDYRKNFFIMENVNRNFSFKRSMVLKLTIRCLIRMGYQCTFGILOAGNYGIPQTRRRILIAAAPGOMLEKVPPEHVS : 926
n y fksnl s cd y p f envrnf6 k lkltl c gyqctfg ag g pqttrr aaapg lp pep hvf

AmDNMT1a : KRAQOLSVLDNKKYSSCNWIDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1187
AmDNMT1b : KRAQOLSVLDNKKYSSCNWIDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1265
ApDNMT1 : RRSSTTVQGTGKKEKTNCKHDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 426
BmDNMT1 : RRACTTTTIDGKEKSTNHDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1238
BtDNMT1a : KRTCTLSVLDNKKYSSCNWIDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1121
BtDNMT1b : KRAQOLSVLDNKKYSSCNWIDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1261
CfDNMT1 : -----LILVSNVYDTSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1058
NvDNMT1a : KSTQCTVVDVNVNPEFTDTHESAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1217
NvDNMT1b : KSTQCTVVDVNVNPEFTDTHESAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1217
NvDNMT1c : KPLCEGVIDSKRTQCTTFTSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1510
PxDNMT1 : KRAQOLSVLDNKKYSSCNWIDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1160
TcDNMT1 : QRSGRDHYVDGKRYNGFNFTSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1041
ZnDNMT1 : KRAQOLSVLDNKKYSSCNWIDSAPRTISVBDAMSLEPEKNCWKKEMSYTN-BEPTHFQRMKG---KQYPLIRDHICKEMAPLVEARMHIFA : 1022
c 1 d 5 sAP R 6 DA DLP 1 g n Y p 3hfq4 6R 6 1H6CK 6 P662aR6 6P

AmDNMT1a : SGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1287
AmDNMT1b : SGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1365
ApDNMT1 : SGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 526
BmDNMT1 : FGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1338
BtDNMT1a : SGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1221
BtDNMT1b : SGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1361
CfDNMT1 : TGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1158
NvDNMT1a : TGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1317
NvDNMT1b : TGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1317
NvDNMT1c : VGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1610
PxDNMT1 : FGSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1242
TcDNMT1 : GSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1139
ZnDNMT1 : GSDWRDLPNIAVRLSDGTCKKLYTHDOKKACRSSVGYRGVCCCTEKSCDPTDRCENTLIPWCLHTEENRHHWAGLYGRLEBNGYSTTITNPEP : 1122
GSDWRDLPN6 6 Lsdg L Y dk g ss ga RG6C C g Cdp d4Q nt61PwCLpH3 4hnhWAGlygr w g f tt tt p p

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AmDNMT1a : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQNKDITEIDIKIQND----- : 1366
AmDNMT1b : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1444
ApDNMT1 : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 602
BmDNMT1 : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1412
BtDNMT1a : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1297
BtDNMT1b : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1442
CfDNMT1 : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1256
NvDNMT1a : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1399
NvDNMT1b : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1399
NvDNMT1c : LGPQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1682
PxDNMT1 : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : -
TcDNMT1 : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1208
ZnDNMT1 : MGKQGRVLHPVQTRVSVRECARSGGFPSFRFYC--NLDKKHRQIGNAVPPPLGVAIGHEIRNCQND--NILKTKIEDLHD----- : 1202
gkqgrv hp q r svrecarsqgfpd f g khrq gnavppp a g e

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Figure S1. Multiple sequence alignments of the deduced amino acid sequences of *AmDNMT1a*, *AmDNMT1b*, *ApDNMT1*, *BmDNMT1*, *BtDNMT1a*, *BtDNMT1b*, *CfDNMT1*, *NvDNMT1a*, *NvDNMT1b*, *NvDNMT1c*, *PxDNMT1*, *TcDNMT1* and *ZnDNMT1*. The numbering on the right represents the position of the last amino acid in that line. A black box indicates 100% identity, and a grey box presents 100% similarity. Taxon abbreviations: *Am*, *A. mellifera*; *Ap*, *A. pisum*; *Bm*, *B. mori*; *Bt*, *B. terrestris*; *Cf*, *C. floridanus*; *Nv*, *N. vitripennis*; *Px*, *P. xylostella*; *Tc*, *T. castaneum*; *Zn*, *Z. nevadensis*.

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TcDNMT2 : -----MELELYSGIGGMHWLKVSGVEGTTKKAVDINPTNSVYKHNEPHINLNRNVQSLTPQFNKLGVTILMSPPCOEPTENLQZE : 86
NvDNMT2 : -----MSDD-----DVPQINPDTLAALNEFY-OEREELEKO-FOAALEQEN-QDATFDEDWQLSQFWYDEETISTLTQSAVQ : 72
DmDNMT2 : -----MVFRVLELYSGIGGMHYLFNYAQLDGQIVAAIDVNTVNAWAHNYGSNLVKTRNIOGLVKEITKLGAMMLMSPPCOEHTQGLQR : 88
CfDNMT2 : -----MESDD-----EEPQLSSSTLAALOELCKERFEQQL-LELVSEEGQIPSNILFDENWQLSQFWYDDKTIEALVRALN : 74
BtDNMT2 : -----MRVLELYSGIGGMHYLQESGNGDVVAAVDINTVANSITRYNFPNVLLMNCITQSLAKLINDLNDITILMSPPCOEPTTRVQLQR : 86
BmDNMT2 : -----MEEKMEHRLLELYSGIGGMHCAWNESTKGGVVAADINTVANDVRYNFPETLLFTKNIOGLPIELEKYKIDITVLMSPPCQPTFRNKNL : 92
AmDNMT2 : -----MMRVLELYSGIGGMHYLQESGKGDVVAADINTVANSITRYNFPNVLLMNCITQSLAQENNLNIDITILMSPPCOEPTTRISLQK : 87
AgDNMT2 : FPRRNTMESTKSEPHRVLELYSGIGGMHMALEQAGKEFEIVSAIDVNPIDANVYRHNFAGAKTVRNGNLSLAERKVTKLKRVITILMSPPCOEPTFRNKN : 100
              le6 sgiggm a          aA6 n an y n          n sl          lmsppcqp tr G

TcDNMT2 : DINBERKSFHVLAIIPDKVTR-ILIENVKGFERRKMRDLLLETLEKCGENVCEFILTPTOIGIPNTHRYVGLAKKPPNVNFKTGVLKTEFPN--- : 182
NvDNMT2 : STEGNAKIALSCPTLYKQIVSAGERQVKLEFDKR-----FSIFGPDITFDYN-TPQDIEKDLYGQFLVICPPFFLS----- : 147
DmDNMT2 : DETEKSDALTHICGLPEQCQLEYILMENVKGFESQARNQFIESERSGHHREFILTPTOFNVPNTHRYVGLAKK-G-ADEFPAGKLTWEEMPG-- : 184
CfDNMT2 : STPANGKIALSCPTLYSKKKKCDKRQITLFEYDSR-----FKIFGVDITQDYK-SPLNVKCKMSSQFLVIADPPFFLS----- : 149
BtDNMT2 : DISDNRSSSLHVLSLIPQORTKHTLLENVKGFENEMRNAVLKCNMSGKNYKELLLSFCQFGIPNTHRYVGLAKKSDSEECEDHCLINFNLEPAVL : 186
BmDNMT2 : DENDPRTNSFYFIDIDKNTQYILMENVKGFECTVRNLFVEKITYCCVYQEFMLSPVSVGVPSNRLRYVGLAKKNWNWFKRKDELITCLPK--- : 189
AmDNMT2 : DMLDNRSSSLHVLSLIPQOKTKYILLENVKGFCKEMRNAVLKCNNTSGKNYKELLLSFCQFGIPNTHRYVGLAKKNLEFCFQSVINFLSDSIL : 187
AgDNMT2 : DINRRSDPFHICELDKPLKFLMENVKGFENQACEMYKARREASGHQYILSPHQFGVNTNTHRYVGLAKKHGADFKWKSE----- : 189
              d d r          6          il en6kg5e s          Gf 5          l p          6Pn r ry5 6a

TcDNMT2 : -----QQNAPHCFEISKVLEQNELTPYYLTDKVLNTNYLETTDRYSTSRNTCCFTKAGRVKRGSGVYSLDLPITP-EIFNQLSD : 262
NvDNMT2 : -----EECTITAITVVKLAKKQIVL-----GCAMMSELAER-----LLNLKK : 186
DmDNMT2 : -----AIAQNQGLSQIAEIVENVSPDEFLVPDDVITRVLVMDIHFAQSRSMCFTKGYTHYTECGSAYPLSDESHRIFELVKE : 266
CfDNMT2 : -----AECITITAVTIKFLMKKNIVL-----GCAMMSELAER-----LLDVKR : 188
BtDNMT2 : KALPGSKHNLLLEG-----AKTDKNCKYLENILENVKSKQYLIPKLIQRAWLFDRTSQSDGSCCFTKAMSHVVECGSVSPYTBETIQQIFLEANK : 281
BmDNMT2 : TFAKPHC--LKDIENNVDPDDYLVPMKMRK-ANIFDCYADSNRSCCFTKAMTHVVECGSVFETSYDIOQYKILKANY : 267
AmDNMT2 : KILPKSKYNLLTKKSCTQNSKTDKNCTYLENILEHVEGSOYLIPKLIQRAWLFDRTSQSDGSCCFTKAMSHVVECGSVYCPYSKTIKEAFSEANK : 287
AgDNMT2 : -----DLITTPQS-----SCAKQLLVG-----TIVDT : 212
              l k          d          c          gtG v          e

TcDNMT2 : HEPGSSAYLK-----LAHGLKMRFEETPREGRIMSFEEDETFPENTSDKQKVMLLGNSINVRVVAELIKLLQ----- : 329
NvDNMT2 : CNFEPHHKNN-----LANEFWCNSNFDFDYIT----- : 214
DmDNMT2 : IDTSNQDASKSEKILQQRLLDLHQVRLRYETPREARLMSFPEEFPPETINRQKYRLLGNSINVRVVGELIKLLTIK----- : 345
CfDNMT2 : CDFTPGHRNN-----LANEFCCSNFNFDKME----- : 216
BtDNMT2 : YGQSLEASE-----VLQKIMLRMETPREVSRIMCFPEEFKFEPEHITCKQRYRLLGNSINRVVSRILIFLYTEKKIT : 354
BmDNMT2 : FEVGSDEFLQ-----TLKKILKLRMETPREVSRIMCFPEEFKFEPEHITCKQRYRLLGNSINRVVSRILIFLYTERKIT : 360
AmDNMT2 : YERQSLEVSK-----TLEKIMLRMETPREVSRIMCFPEEFKFEPEHITCKQRYRLLGNSINRVVSRILIFLYTERKIT : 360
AgDNMT2 : QQDALEQYG-----LKSATLLKHLPLMDICT----- : 238

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Figure S2. Multiple sequence alignments of the deduced amino acid sequences of *AmDNMT2*, *AgDNMT2*, *BmDNMT2*, *BtDNMT2*, *CfDNMT2*, *DmDNMT2*, *NvDNMT2*, and *TcDNMT2*. The numbering on the right represents the position of the last amino acid in that line. A black box indicates 100% identity, and a grey box presents 100% similarity. Taxon abbreviations: *Am*, *A. mellifera*; *Ag*, *A. gambiae*; *Bm*, *B. mori*; *Bt*, *B. terrestris*; *Cf*, *C. floridanus*; *Dm*, *D. melanogaster*; *Nv*, *N. vitripennis*; *Tc*, *T. castaneum*.

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ZnDNMT3 : -----ALITRAEDAGMTIPSEKINWSWIGESRISEINAK-CIDKFSNHLEERLIDNLTAT : -
NvDNMT3 : TPGKLVWGIVFRSGWGPDLNIVT-----ALITRAEDAGMTIPSEKINWSWIGESRISEINAK-CIDKFSNHLEERLIDNLTAT : 395
CfDNMT3 : -----ALITRAEDAGMTIPSEKINWSWIGESRISEINAK-CIDKFSNHLEERLIDNLTAT : -
BtDNMT3 : NNEELNRNGSRWGEYHEVRRVTRGSIKISKDLFVGKLVWGCGSGWMPALIIDADHVGMLSEAGKSWVYWIGEARISLSEKTOIEFFSYNKSRLTQNSN : 500
AmDNMT3 : -----MLSEEGKLWVYWIGEARISLLEKTOIEFFSCNLEKRLTQNLN : 43

ZnDNMT3 : -----SSLESRRKKIVAKRLLNPSD----- : 22
NvDNMT3 : NSKTKVTCCKQKDEACFKTIQLLKKHFTGALIVKPYIANIKNNILP-YKNKIDELHFPYPESSDRLNINLIVNSEKNEKIQEKEKRLC----SAFE : 490
CfDNMT3 : -----SKDNL---FCVTVDIIIPYPYKKNQPRLLDTREKNIKATEPFHSNORSSPSPTRKQAV : 58
BtDNMT3 : EARMRVID-----ATMQMLRRLLG-TLTKPYFTIENN-LQCAETIDELKYPYDKIQORLNLREKNAIITKVLDDKRENSQG----AKLA : 585
AmDNMT3 : VPRIRAIID-----ATMQMLRRLLG-TLTKPYFTIENLFPKNMIEMIDELKYPYDKIQORLNLREKNAIITKVLDDKRENSQG----AKLA : 129
n d fypyp l 6 n 4 6 q k

ZnDNMT3 : -----PFEGPEGLVWGKLRNFWPWPGLIIVDEHAIGSCIPSGFCFENFAERVRSGVQNKWMKPFKKHYEQCFPT--VQAL : 99
NvDNMT3 : PPNLIKIEKFEKPEKGGINIVDKYGMIVWAKMOYSWMPVIMDQHLNRKQHVHAWVWVWYGDYKYSOVQYRQITFPPTGDRMESKITATKDEL : 590
CfDNMT3 : E---CRDNTTSWKNVEDERLPIQNNGFIANAKIAGHGWPMAMIIDYRDCCLKEPSFCQWIMWYGDYKYSVVRHLELTFYKLGLEKMRDYIQNVKQC : 156
BtDNMT3 : E---AKDS-LQRGNVLDLTHPLKECNPGIITNAKIAGHGWPMAMIIDYRDCCMREPSFCQWIMWYGDYKYSVVRHLELTFYKLGLEKMRDYINNKHHI : 682
AmDNMT3 : E---SKDS-PQKVNVDLTLPLKECKEGLIANNKIAGHGWPMAMIIDYRDCCMREPSFCQWIMWYGDYKYSVVRHLELTFYKLGLEKMRDYINNKHHI : 226
k k q G 6 WaK6 g WWP 6I6y c p g qw6mW5gDy S V F kg e m d tk

ZnDNMT3 : VVSEVVEAVKLCARLGHNAESMKKEALCAQAGFORSANRKEEVTPIFVDPGVQDDLLIRCRKSNEINIKLEICGSSSFASSSQPSFQYDLEK : 199
NvDNMT3 : ECKAVVQAASKDYCKLGLLEPAKIKVVIHLIYK-----SKDIYKLKNAELTEPNEE---LVQOTKKQIRKQINIQEPSEPKKKL--ECKVLNL : 678
CfDNMT3 : VVDFVQAASKDYCSRIGCSNDNPLDVFEVPSN-----MNNIHVPYNYQ--LQVDSNKHIDKYSDLVKKINLEPKSKPNVDAEKNDK--TSALHR : 246
BtDNMT3 : VVDFVQAASKDYCSRIGCSNDNPLDVFEVPSN-----KEDSKRSCAQ---RKEDSVKHIDKYSDLVKKINLEPKSKPNVDAEKNDK--TSALHR : 771
AmDNMT3 : VVDFVQAASKDYCSRIGCSNDNPLDVFEVPSN-----PNHYDIASSANTWRREDSVKHIDKYSDLVKKINLEPKSKPNVDAEKNDK--TSALHR : 318
5 qv12A Kdyc 4LG t Wt f d kys i k n n r i d L

ZnDNMT3 : VKKSEMDIKSLCLCRSSKQVIGEHYPYKSLCLCMETVVEHIFTEGAGGIHMMCAICSNAGEVFGVGSNPQCKVYCHCTDLASEGAKNWIREKEP : 299
NvDNMT3 : LSEKPLSLOISCHESGE-EDEDHFFHASMCEKLEDSERIFALGNDAKCFYCTLCGGDDLVAVCGMSCHRVFCTACIRYIICPEFYEDILKHP : 777
CfDNMT3 : VVSECTVVKLCLCRFASKDKIEHFFHIGSLCRCSYAFKPCPMFVHNGGKCFYCTVCAATCTVLICTDDCHRVYCTACIRFLICPKAKDDMSDEP : 346
BtDNMT3 : ANNNNAFESLCLCLRVAEKGTIEHFFHIGSLCRCSYAFKPCPMFVHNGGKCFYCTVCAASGMMHICKEDECHRVYCTACIRFLICPKAKDDMSDEP : 871
AmDNMT3 : AKKSESFBSLCLCLRVSNDEMDIEHFFHIGSLCLCRCSERYKPCPMFVHNGGKCFYCTVCAASGMMHICKEDECHRVYCTACIRFLICPKAKDDMSDEP : 418
G e LC6 C1 HP5F gS6ck C kp 6F GnD kcf Ct6C g 6 6Cd Cp4V5CtaC6k 6 cp y 6l P

ZnDNMT3 : WCFCLCDDPLS---SMHGSIKERPDWMNCQRISSALFPANNIMSS---IPLSKKSSGLRVLSLFDGLSTGMVVLKMMELRVEKYASEVVKDINVSKV : 392
NvDNMT3 : WCFCLCDDPLS---ISNNVVIITRNDWR---YKMTSLYVINCDEEAPSNERLDR-NRR-IRVLSLFDGLSTGMVVLKMLNIEQYASEIIPDSMOVSEFF : 871
CfDNMT3 : WCFCLCDESK--QFAMULHFRBDWR---EKVSTMEFTASNPAASKDINFEYKNNKRPVRLSLFDGLSTGCLVLNLGLVVDVYASEIDKNALISSA : 442
BtDNMT3 : WCFCLCATNNKFRPSSSHIKERANWK---DKIIMMFTNCKNSPQELM-KHNWKKK-IRVLSLFDGLSTGCLVLNLGLVVDVYASEIDPALMVFAA : 967
AmDNMT3 : WCFCLCKSR---FATITVVRERANWK---DKIIMMFTSCDSNVEHLVAKHNSEKRS-IRVLSLFDGLSTGCLVLNLGLVVDVYASEIDPALMVFAA : 512
W CFLC 6 pR lW 46 65r 4k 6RVLSLFDG6 TG 6VL 6g 6 YIASE6D la6 63

ZnDNMT3 : NHGDSLEHIGDVELLSEPLSLRLCPIDLLIGGSPCTELSLVNPARKGLYDTEGSGYLFFDFYRVMTLQVHLG-KNIFWIFENTASMRYRLNVLIRSLG : 491
NvDNMT3 : NHGDSLEHIGDVELLSEPLSLRLCPIDLLIGGSPCTELSLVNPARKGLYDTEGSGYLFFDFYRVMTLQVHLG-KNIFWIFENTASMRYRLNVLIRSLG : 971
CfDNMT3 : HEGDRIVHLGNVKKIKELIQIAPIDLLIGGSPCNDLSLVNPRRGLHEDPKGTGLLFFEWCRICKLMMKANKDRELFWLYENVASMPSERVLEINKHLG : 542
BtDNMT3 : HEGDRIVHLGNVKKIKELIQIAPIDLLIGGSPCNDLSLVNPRRGLHEDPKGTGLLFFEWCRICKLMMKANKDRELFWLYENVASMPSERVLEINKHLG : 1067
AmDNMT3 : HEGDRIVHLGNVKKIKELIQIAPIDLLIGGSPCNDLSLVNPRRGLHEDPKGTGLLFFEWCRICKLMMKANKDRELFWLYENVASMPSERVLEINKHLG : 612
G1 I 6G1V 6 k6 e6aPIDLLIGGSPCn LSL NP R GL Dp G3G LF5 5 R6 16 k n h6FW65ENVASMP R I 4 LG

ZnDNMT3 : CDFVVIDASWLAAARRARFPWGNFGLGRTELPIINMKDECLMGMBEKAVYKINTVTQSSILQ---KNRTPVVRMMEADAVWITELEVIFGLFL : 589
NvDNMT3 : RFPKFLDSADFSAAHRRRIYGNFPWGFYQVN---NVVLQDVLKRCNQALVKKIYTVTRTNSINOT---KENLKPVMMDGKKMLWVTELEIFGFP : 1066
CfDNMT3 : RFPKFLDSADFSAAHRRRIYGNFPWGFYQVN---NVVLQDVLKRCNQALVKKIYTVTRTNSINOT---KENLKPVMMDGKKMLWVTELEIFGFP : 640
BtDNMT3 : QFPPTIDSADFSAAHRRRIYGNFPWGFYQVN---NVVLQDVLKRCNQALVKKIYTVTRTNSINOT---KENLKPVMMDGKKMLWVTELEIFGFP : 1165
AmDNMT3 : QFPPTIDSADFSAAHRRRIYGNFPWGFYQVN---NVVLQDVLKRCNQALVKKIYTVTRTNSINOT---KENLKPVMMDGKKMLWVTELEIFGFP : 712
eP 6D adfS QhR R15W N P 6qd L p R 6vkK6rTVtt nSL Qg K 6kp6 Mk e D 6W6TELE IFGfP

ZnDNMT3 : HYTDGILQLRERRQLLGRAWSVPVKHLIQFLKLYKEREKSVKQGKMTT----- : 641
NvDNMT3 : HYTDGILQLRERRQLLGRAWSVPVKHLIQFLKLYKEREKSVKQGKMTT----- : 1101
CfDNMT3 : HYTDVKNLSANNRKLLGKWSVQTLTAIRPLCFYKCKEDETSSNNISALHKDISLYRGKQF : 704
BtDNMT3 : HYTDVKNLSANNRKLLGKWSVQTLTAIRPLCFYKCKEDETSSNNISALHKDISLYRGKQF : 1210
AmDNMT3 : HYTDVKNLSANNRKLLGKWSVQTLTAIRPLCFYKCKEDETSSNNISALHKDISLYRGKQF : 758
H5TD nL R L6G4 WSvt6tai 6 5f

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Figure S3. Multiple sequence alignments of the deduced amino acid sequences of *AmDNMT3*, *BtDNMT3*, *CfDNMT3*, *NvDNMT3* and *ZnDNMT3*. The numbering on the right represents the position of the last amino acid in that line. A black box indicates 100% identity, and a grey box presents 100% similarity. Taxon abbreviations: Am, *A. mellifera*; Bt, *B. terrestris*; Cf, *C. floridanus*; Nv, *N. vitripennis*; Zn, *Z. nevadensis*.

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AgMBD3 : --MN--VSIRKRTDCAALKGQ--REEVLR--TGLSAG--KVDVYYY-- : 41
AmMBD3 : --MN--MSVEKKKYP--SALETN--PSREE--ASRKSQ--LSSTCKVDVYYY-- : 44
ApMBD3 : --MN--MPRIKKRSLETKARISRMKFAKRRREQILILK--TQAEEMEILC-- : 42
BmMBD3 : --MN--TSIRKRSDCSALEKQ--REEVVR--TGLSAG--KVDVYYY--SPTGKKFRSKPELVRYLGD-- : 59
BtMBD3 : --MN--MSVEKKKYP--SALETN--PIREE--ASRKSQ--LSSTCKVDVYYY-- : 44
CfMBD3 : --MN--MSVEKKKYP--SALETN--HAREE--PSRKSQ--LTSTCKD--YYG-- : 40
DmMBD3 : --MN--MSVEKKKYP--SALETN--HAREE--PSRKSQ--LTSTCKD--YYG-- : 40
NmMBD3 : --MN--MSVEKKKYP--SALETN--PIREE--ASRKSQ--LSSTCKVDVYYY-- : 47
PxMBD3 : --MN--TSIRKRSDCSALEKQ--REEVLR--TGLSAG--KVDVYYY-- : 40
TcMBD3 : MS--TSIRKRSYECALKQ--R--RDMLR--TGISVG--KVDVYYY-- : 41
ZnMBD3 : --MN--TSIRKRSYECALKQ--REEVLR--TGLSAG--KVDVYYY--SPNGKKFRSKPQLARYLGD-- : 57
      6 e4k4 alp w Ree kvdv yy

AgMBD3 : -----RANRS--TSLLPIPRQTASI : 60
AmMBD3 : -----RGVRNDASLVPPIRQTASI : 63
ApMBD3 : -----RGIRSEGLVPPIRQTASI : 61
BmMBD3 : -----SVDLSCFDQGGQINTMLLCKAKKARAQFDYRGVRNDASLVPPIRQTASI : 109
BtMBD3 : -----RGVRNDASLVPPIRQTASI : 63
CfMBD3 : -----R--ARNSSSLVPPIRQTASI : 58
DmMBD3 : ISLYRCSAMPLPIASGGGNGATSGSAANALKRKFARSQGGNAAGAAGAAPPAATASSAATAASASPSTANRQQQIELSRAIRTVSLVPPIRQTASI : 197
NmMBD3 : -----RGVRNDASLVPPIRQTASI : 66
PxMBD3 : -----RGVRNDASLVPPIRQTASI : 59
TcMBD3 : -----RGVRNDASLVPPIRQTASI : 60
ZnMBD3 : -----ALDLATDFRSGKINSLLRKNNKQRGTQFDYSRGVRNDASLVPPIRQTASI : 109
      R R d sL6PPIRQTASI

AgMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 146
AmMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 163
ApMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 143
BmMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 191
CfMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 163
DmMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 158
NmMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 283
PxMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 166
TcMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 141
ZnMBD3 : FKQPVTIKTQEGKVKDKHGNQEKPKQEGADKTLGMYCS--DKPKQLWEKRLEGLRACLDGCFDGMDLPSLRGPGYITEETILQSVATALHSSQ : 192
      FKQPVT6 4 qe K d k G q Kp4Q6fWEKRLEg6 Ac g e lp 64 GP T 6Qs6ATALH

AgMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 203
AmMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 223
ApMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 201
BmMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 249
CfMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 223
DmMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 218
NmMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 340
PxMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 226
TcMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 199
ZnMBD3 : FVVGQIGSKTSLKNTACGVFLNPGPLVNTVITFEDVKKQBERVQVAFRLKCLRA--- : 200
      p6tGQ 4 n gv5 p QPL6 V 6 eD64 QE RV AR 4Lq a6

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Figure S4. Multiple sequence alignments of the deduced amino acid sequences of *AmMBD3*, *ApMBD3*, *AgMBD3*, *BmMBD3*, *BtMBD3*, *CfMBD3*, *DmMBD3*, *NvMBD3*, *PxMBD3*, *TcMBD3* and *ZnMBD3*. The numbering on the right represents the position of the last amino acid in that line. A black box indicates 100% identity, and a grey box presents 100% similarity. Taxon abbreviations: Am, *A. mellifera*; Ap, *A. pisum*; Ag, *A. gambiae*; Bm, *B. mori*; Bt, *B. terrestris*; Cf, *C. floridanus*; Dm, *D. melanogaster*; Nv, *N. vitripennis*; Px, *P. xylostella*; Tc, *T. castaneum*; Zn, *Z. nevadensis*.

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AmTET2 : VPSSTATSRDDCASKAIKSEPDQKSQEGNNYKFRDGGPAKVSFVGWSWCCRRGGCTEQPTPEHLRECCQ--GLQTRDEILADG---TDKSD-VKNEG : 1089
BmTET2 : YYIEQIKSEHSPGPHKIYKNMYS--PPRDEPYLFPDGGPTAIKNEVYSSCCRQGSTTKKPPPEHLRDACP--GYOTKDEVLDEPETTDKNDPKM-QKA : 1380
BtTET2 : VPSPTVVSKSDGCKASKIKSEPDQRAQESNNYKFRDGGPAKVSFVGWSWCCRRGGCTEQPTPEHLRECCQ--GLQTRDEILADS---AEKSD-VKNEG : 1512
PxTET2 : YVVEQIKSEHSPGPHKIYK--SSFGHLSKSEPYLFRDGGPVIRNEVYSSCCRQGSTTKKPPPEHLRADACP--GLQTKDEVIEDDDPDATDRNDPKCQKGP : 781
NvTET2 : LSVRSEEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHAHRDLHNMNNGCTVVSVLTKHRSFSKPDDEQL : 1800
TcTET2 : TSVS-SPNYSNGSNGAQPYPQVNSPQLASHSSSYFSGSQFSG-TSQEMWQEESSVWQEEAKPEQNDRVN-LNTRIKTMLSQKQENSEKKVENTTGH : 771
ApTET2 : -----LPGIDDPRTVQ-----KNGYVFCNGGSENPIDVVAIPWCCRMGGTDTPTTKHLSDECGH--GLKTLDEG-----IDPVEMKQENGL : 219
AgTET2 : PPPTKKEKSKSKSKSSAASTASSGASTANSVASPGPGSGSGTGAAGSGSGSGSGSPRAHTPGSQKSTSGKGGSGSGSGSSNAALDLVTGLTEKHSSPL : 1800
DmTET2 : ALGHGAPPLSHHGMLEPKIEDMGLHGCGGYAILESEKPLNN--GFSCCRQGGTRPPTAEHLKDTCLGLGTPKEELIDEDELIDTHGNGLKPIGG : 1594
ZnTET2 : NSNCNSQNDVRTATPPDKVTESTKVKTEQLSYLFAIDGGLPLEKTKGSSWCCRQGGIETPTPEHLRADCCQ--GFQTADEQDTKQWPSPQPPASTGDGC : 688
CfTET2 : -----DTSIAENEESRKIVP-----DYKFRDGGPAKVSFETGSWCCRRGGTKQPSPEHLKDCCCQ--GLQTKDEMLADS---PQAAE-LKNEG : 402
                                     g      g                                     g

AmTET2 : QSPR-----NGGAPSTTKLQDHLEKLNKNVRSEVPDCNFFADICPPEPGSYYYTHLGAANASLPDLNDLERRTGLKENAIFEKVIVYTGKEGK : 1177
BmTET2 : TAPTPD-----VTKPKENQFNYSKEYLENLERLTNSRTEVPDCNFFADINPPEPGSYYYTHLGSASSPAELRRELEARTGLSSKELRIEKICYTGKEGK : 1475
BtTET2 : QSPR-----TGSVPSTTKLQDHLDEKLNKNVRSEVPDCNFFADICPPEPGSYYYTHLGAANASLPDLNDLERRTGLKENAIFEKVIVYTGKEGK : 1600
PxTET2 : PTPGPDA-LAKVTKFVFNQFNYSKEDLENLEKLNKNRTEVPDCNFFADINPPEPGSYYYTHLGAANASLPDLRRELEARTGLSSKELRIEKICYTGKEGK : 880
NvTET2 : HVLPLIIMDDSEDFSGKEGQEAIKSGAIEVLTKYPCVVRVRSVPLOCRSHGKKRKEDEPDASNKKDTKSPAEFVDNRRQMYQDPSFPLRDSOLS : 1900
TcTET2 : FLWYSHHRRFIVNGGGGAKLTTEKPKQLPKKYSSPYENEFPYCNVVRAGGAESPCTFYTHLGCANNINLHDLERTGTGKERATIEKIRNTGKEGR : 871
ApTET2 : NNSQ : -----CSDNLD-----NOKTNIKATLPDCNFFADICPPEPGSYYYTHLGSAYSLEITNENMMSGIRENGHEKVLIVYTGKEGK : 299
AgTET2 : HGQAGGAGGALVAAGGGNGGTGSSAFTAPNTINSPNLANNGANNNTSLIDMASMIDNFTDAQLOSNQSSSTLDSPYSYDYNTGOYIDNRQYNNW : 1900
DmTET2 : VGKAKGKKQDEIPIEIVVKHEKINPMFDTTDRLEKGNKTEPECEFTQSDINPPEPGSYYYTHLGTASSIMDLRREPERCNLTGROLRIEKIVYTGKEGK : 1694
ZnTET2 : HNTN-K-----GFGGMSAKEFQDHLERLNKNVRSEVPDCNFFADICPPEPGSYYYTHLGAANASLPDLNDLERRTGLKENAIFEKVIVYTGKEGK : 777
CfTET2 : HSPRTP-----ASAATTTTKLQDHLDEKLNKNVRSEVPDCNFFADICPPEPGSYYYTHLGAANASLPDLNDLERRTGLKENAIFEKVIVYTGKEGK : 492
                                     p c c      epg yth g l r e      g r e      ytgk gk

AmTET2 : TTAGCCPMKAKWILRRSGLEPKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 1277
BmTET2 : TTAGCCPMKAKWILRRSGLEPKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 1575
BtTET2 : TTAGCCPMKAKWILRRSGLEPKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 1700
PxTET2 : TTAGCCPMKAKWILRRSGLEPKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 980
NvTET2 : LEMTSM-EGMDAQLOQSSQVSSVLDSPVSMYQSWNYQTEQWRSFGWDRQKRSWMNPWTEYGFPGGLDREVVDPDSTSLDSSRPASVAVSOEDYRPAAR : 2000
TcTET2 : TTAGCCPIAKWILRRSGSDPEKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 971
ApTET2 : TTAGCCPLAKWILRRSGSDPEKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 399
AgTET2 : PTDYDGNRGDPSLAGLAGRNEETPTTTPRGSNSNSAFSPSPDPTKTPTTHMDYDGSKLGQGOVHHHHHQLQQOQQOQQOQQOQQOQQOQQOQQO : 2000
DmTET2 : TTAGCCPMKAKWILRRSGLEPKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 1794
ZnTET2 : TTAGCCPLAKWILRRSGSDPEKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 877
CfTET2 : TTAGCCPMKAKWILRRSGMDPEKILTLVHHQGHKOPTAVIVVAMVAMEGVPTHEADRIYSLLSHKLNRFLPTTRRCATNEPRTCACQGLDETCGASFSFG : 592
t ggcg akw r ek l vk r gh c iv w g y l kln g rc tn tcacqgl p gas sfg

AmTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 1377
BmTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 1675
BtTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 1800
PxTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 1080
NvTET2 : QNSNSESPRANTCSRGHPISPRASLPSTPVSESYSTPPRTCPSTPHEPHDQRLISPRSSGYGSAPSEFSLSSPSFRNYQNSLDGRONISPRAYONS : 2100
TcTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 1071
ApTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 499
AgTET2 : QQQHQQQSQOQTQNYTHLQOPEQGFVKPKPPDYNPAGYGYHHNTPMGYGYHHHHHPHHHTPYDPYQNYNYYPQSYHHHHHTTYNMYPAASAAAA : 2100
DmTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 1894
ZnTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 977
CfTET2 : CSWSMYNGCKYARSTVRKFRISVRSSEQVEEERMHVLATLLSPLYLSLAPEAFNNQTOFEREASECRLGFKPGRPFSGVTACTIDFCAHSHRDLHNMNN : 692
cswsmyngck r3k vrkfrl v ee e at l p p nq e crlg pg Pf vtac dfcah h d hnm

AmTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 1475
BmTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEEDSGDSANNSTNTPQOS : 1773
BtTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 1898
PxTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 1178
NvTET2 : SYNLESPORTNTPSNNQHTSTPIGSEAARRNOSPMMNQLRSPSLNSDSYSSNISSPRYEVVDHNOFPFGSMAQNIAMQDSKSTPKAPISQIPQQSSENS : 2200
TcTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 1134
ApTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 583
AgTET2 : AAAQTQLPGTGAPPPPPPTAVIPAPPPSNWNLYPPHGLAPSTAQLHVAAAAAGALGKQSEGGAVGAGMMSQSAVVPQAPAPPSAPLPKETLGEVT : 2200
DmTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 1994
ZnTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 1075
CfTET2 : GCTAVVVTIAK--HRTLSKPEDEQLHVLPLYIMDTTDEYGSKEGDEKVASFALEILDKYPMVVRVSVPLQPCRRHGKKRKEDEPDITSSKKDSKKNVNE : 790
gct v k w r eq hvlp ly de q k g l e r r

```

Figure S5. Multiple sequence alignments of the deduced amino acid sequences of *AmTET2*, *ApTET2*, *AgTET2*, *BmTET2*, *BtTET2*, *CfTET2*, *DmTET2*, *NvTET2*, *PxTET2*, *TcTET2* and *ZnTET2*. The numbering on the right represents the position of the last amino acid in that line. A black box indicates 100% identity, and a grey box presents 100% similarity. Taxon abbreviations: Am, *A. mellifera*; Ap, *A. pisum*; Ag, *A. gambiae*; Bm, *B. mori*; Bt, *B. terrestris*; Cf, *C. floridanus*; Dm, *D. melanogaster*; Nv, *N. vitripennis*; Px, *P. xylostella*; Tc, *T. castaneum*; Zn, *Z. nevadensis*.

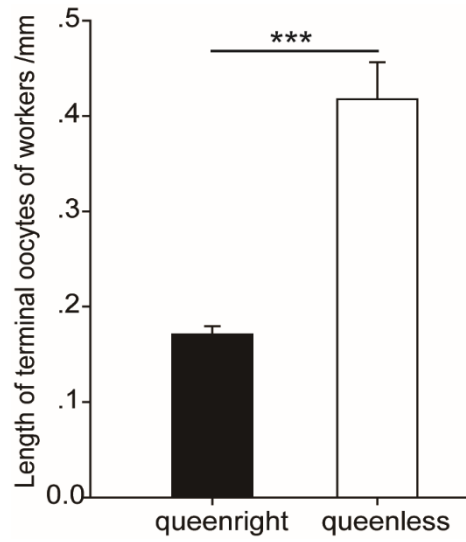


Figure S6. Length of the terminal oocytes of workers in queenright and queenless colonies. Data in the figure represent mean $\pm$ SM of four biological replicates, and the asterisks indicate significant difference between two treatments by independent sample T-test ($P < 0.001$).

Table S1. Primers used for qRT-PCR.

Primer name	Primer sequence (5'→3')
<i>DNMT1a</i> F	CATATTCCGACTGCGAGTG
<i>DNMT1a</i> R	ACGCCACGATGTGCTCC
<i>DNMT1b</i> F	GTGGGTTATCCGAAGGT
<i>DNMT1b</i> R	TGTTGCATTAGGGTTGT
<i>DNMT2</i> F	ATAGTGGTATTGGTGGA
<i>DNMT2</i> R	TAAGGTTGACATGGAGG
<i>DNMT3</i> F	ACTATAAGCCCTGCATGTTCC
<i>DNMT3</i> R	ATCATGCCAGAGGCTGCG
<i>TET2</i> F	CACTCCGCTACCTTACATAC
<i>TET2</i> R	GCACGGTTCTTGCTCAT
<i>MBD3</i> F	CCGATTAGGGAAGAAGC
<i>MBD3</i> R	CGTATTTGCCATCAGTTTT
<i>EF1a</i> F	CGTTTACCGCTTCAGGACGT
<i>EF1a</i> R	GCATGCCTGGTTTCAGAATACC

Table S2. Sequences analysis of genes involved in DNA methylation in *Bombus terrestris*.

Gene	Open Reading Frame	Number of amino acid	Relative molecular weight of protein	Isoelectric point of protein
<i>DNMT1a</i>	4,329 bp	1,442 aa	163.62 KDa	6.56 pH
<i>DNMT1b</i>	3,894 bp	1,297 aa	148.48 KDa	8.42 pH
<i>DNMT2</i>	1,065 bp	354 aa	40.73 KDa	8.82 pH
<i>DNMT3</i>	3,633 bp	1,210 aa	138.47 KDa	7.87 pH
<i>TET2</i>	8,268 bp	2,755 aa	306.77 KDa	6.93 pH
<i>MBD3</i>	672 bp	223 aa	24.87 KDa	9.21 pH

Table S3. Gene names, species names and GenBank accession numbers used for the phylogenetic analysis.

Gene	Species	GenBank accession number
<i>DNMT1a</i>	<i>Bombus terrestris</i>	XP_008181290.1
<i>DNMT1b</i>	<i>Bombus terrestris</i>	XP_012167869.1
<i>DNMT1a</i>	<i>Apis mellifera</i>	NP_001164522.1
<i>DNMT1b</i>	<i>Apis mellifera</i>	XP_006562865.1
<i>DNMT1a</i>	<i>Nasonia vitripennis</i>	NP_001164521.1
<i>DNMT1b</i>	<i>Nasonia vitripennis</i>	XP_008217946.1
<i>DNMT1c</i>	<i>Nasonia vitripennis</i>	XP_001607336.1
<i>DNMT1</i>	<i>Camponotus floridanus</i>	XP_011257755.1
<i>DNMT1</i>	<i>Zootermopsis nevadensis</i>	XP_021941799.1
<i>DNMT1</i>	<i>Bombyx mori</i>	BAP86925.1
<i>DNMT1</i>	<i>Plutella xylostella</i>	XP_011556728.1
<i>DNMT1</i>	<i>Acyrtosiphon pisum</i>	XP_008181290.1
<i>DNMT1</i>	<i>Tribolium castaneum</i>	KYB29654.1
<i>DNMT2</i>	<i>Bombus terrestris</i>	XP_003400893.1
<i>DNMT2</i>	<i>Apis mellifera</i>	XP_006563008.1
<i>DNMT2</i>	<i>Nasonia vitripennis</i>	NP_001129999.1
<i>DNMT2</i>	<i>Camponotus floridanus</i>	EFN60586.1
<i>DNMT2</i>	<i>Bombyx mori</i>	NP_001036934.1
<i>DNMT2</i>	<i>Tribolium castaneum</i>	EFA09160.1
<i>DNMT2</i>	<i>Drosophila melanogaster</i>	NP_477475.2
<i>DNMT2</i>	<i>Anopheles gambiae</i>	XP_306830.2
<i>DNMT3</i>	<i>Bombus terrestris</i>	XP_003393693.2
<i>DNMT3</i>	<i>Apis mellifera</i>	NP_001177350.1
<i>DNMT3</i>	<i>Nasonia vitripennis</i>	XP_008204446.1
<i>DNMT3</i>	<i>Camponotus floridanus</i>	EFN74862.1
<i>DNMT3</i>	<i>Zootermopsis nevadensis</i>	XP_021915979.1
<i>MBD3</i>	<i>Bombus terrestris</i>	XP_003396187.1
<i>MBD3</i>	<i>Apis mellifera</i>	XP_392422.2
<i>MBD3</i>	<i>Nasonia vitripennis</i>	NP_001164526.1
<i>MBD3</i>	<i>Camponotus floridanus</i>	EFN64427.1
<i>MBD3</i>	<i>Zootermopsis nevadensis</i>	XP_021933495.1
<i>MBD3</i>	<i>Bombyx mori</i>	XP_004929675.1
<i>MBD3</i>	<i>Plutella xylostella</i>	XP_011549226.1
<i>MBD3</i>	<i>Acyrtosiphon pisum</i>	NP_001156167.1
<i>MBD3</i>	<i>Tribolium castaneum</i>	XP_969537.1
<i>MBD3</i>	<i>Drosophila melanogaster</i>	NP_001262421.1
<i>MBD3</i>	<i>Anopheles gambiae</i>	XP_318432.4
<i>TET2</i>	<i>Bombus terrestris</i>	XP_012169992.1
<i>TET2</i>	<i>Apis mellifera</i>	XP_016770977.1
<i>TET2</i>	<i>Nasonia vitripennis</i>	XP_008203340.1

<i>TET2</i>	<i>Camponotus floridanus</i>	EFN73124.1
<i>TET2</i>	<i>Zootermopsis nevadensis</i>	KDR09818.1
<i>TET2</i>	<i>Bombyx mori</i>	XP_012544637.1
<i>TET2</i>	<i>Plutella xylostella</i>	XP_011554443.1
<i>TET2</i>	<i>Acyrtosiphon pisum</i>	XP_008183450.1
<i>TET2</i>	<i>Tribolium castaneum</i>	XP_008193024.1
<i>TET2</i>	<i>Drosophila melanogaster</i>	NP_001246581.1
<i>TET2</i>	<i>Anopheles gambiae</i>	XP_001688023.1
