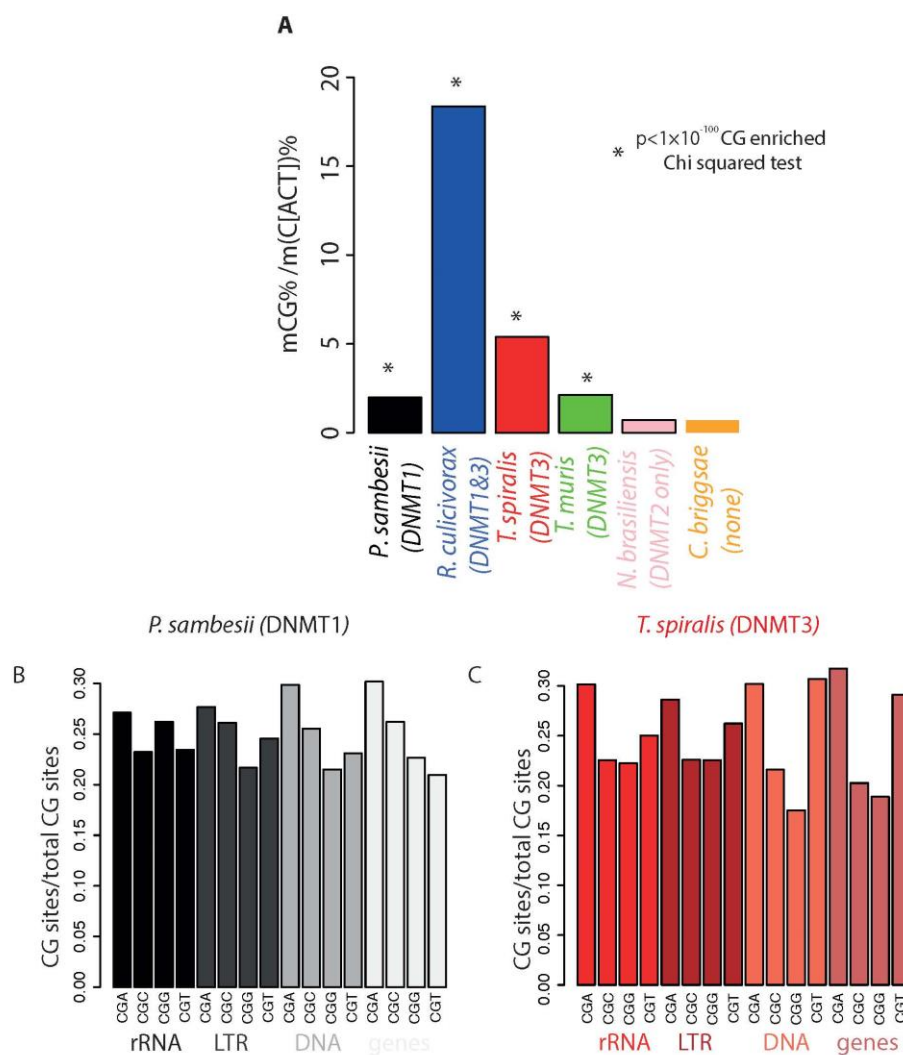


In the format provided by the authors and unedited.

Evolutionary analysis indicates that DNA alkylation damage is a byproduct of cytosine DNA methyltransferase activity

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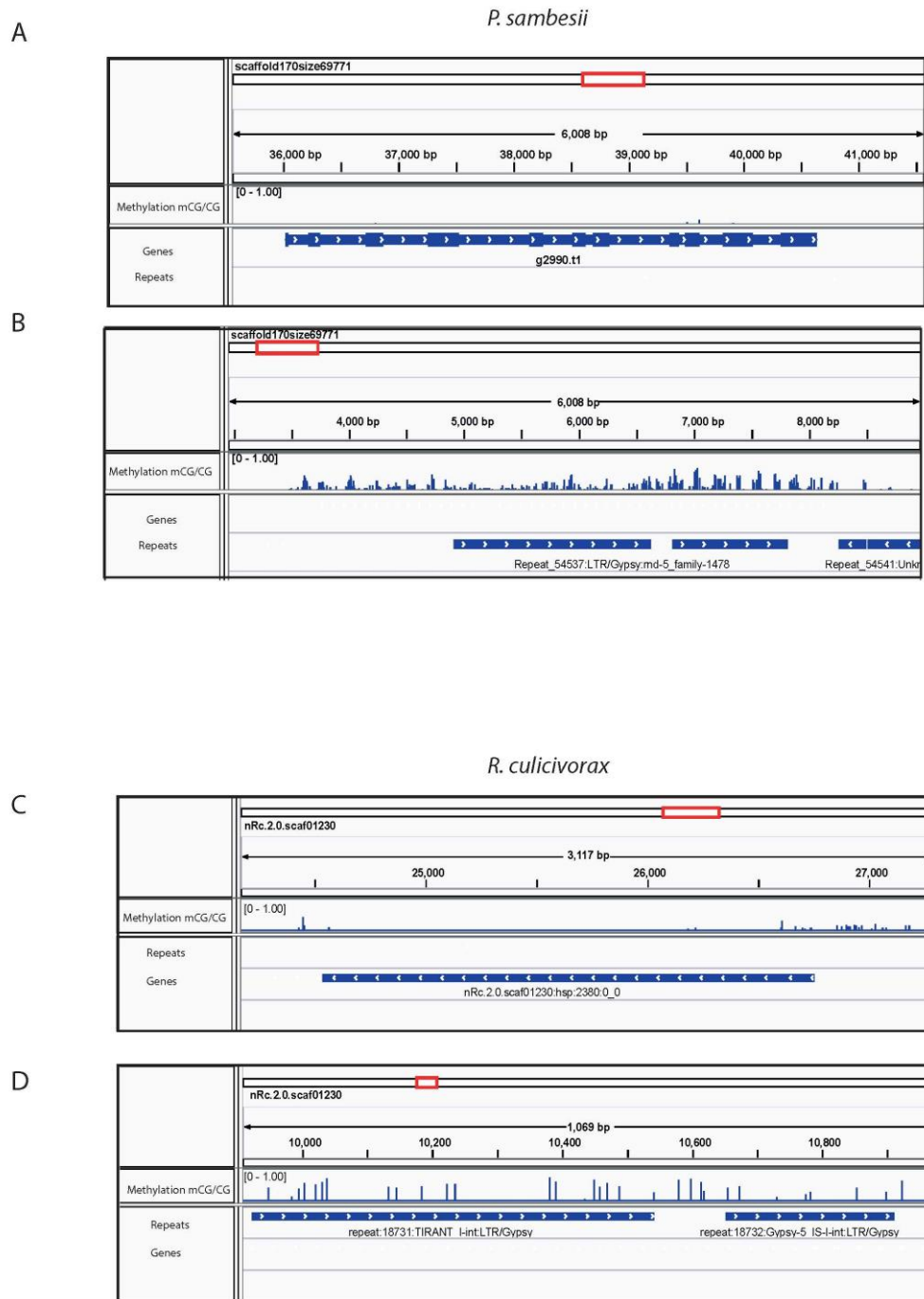
¹MRC London Institute of Medical Sciences, London, UK. ²Institute of Clinical Sciences, Imperial College London, London, UK. ³Institute of Biochemistry, Universität Stuttgart, Stuttgart, Germany. ⁴Department of Life Sciences, Imperial College London, London, UK. ⁵Department of Ecology and Evolution, University College London, London, UK. ⁶School of Biological Sciences and Wellcome Trust Centre for Cell Matrix Research, FBMH, MAHSC, University of Manchester, Manchester, UK. ⁷These authors contributed equally: Silvana Rošić, Rachel Amouroux and Cristina E. Requena. *e-mail: petra.hajkova@lms.mrc.ac.uk; psarkies@imperial.ac.uk



Supplementary Figure 1

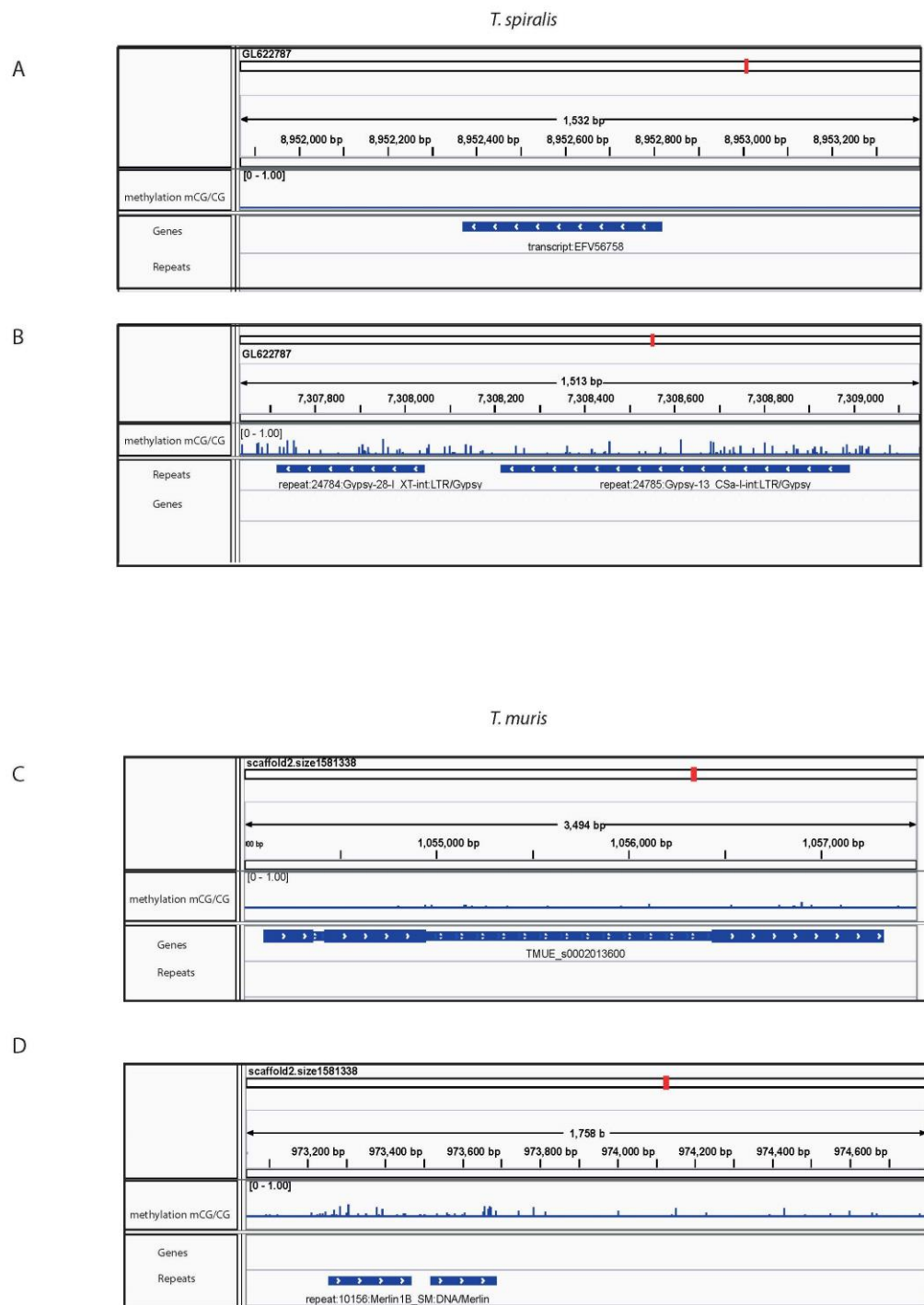
Extended analysis of the sequence context of DNA methylation in nematodes

a, Overall percentage methylation at CG and non-CG sites respectively for different nematodes. The chi-squared test P value is for a two-tailed test on a 2 by 2 table: meCG/non-meCG|meCX/non-meCX, where X is C, A or T. $P = 1 \times 10^{-100}$ is the minimum P value reported by the software used for calculation. See Supplemental Note 3 for the number of CGs in different contexts across the genome for all genomes analyzed. **b,c**, Enrichment of methylation for CG sites within different contexts for *P. sambesii* and *T. spiralis* respectively (nematodes with the most pronounced differences in CG[X] preferences; see Fig 2). See Supplemental Note 3 for the number of CGs in different contexts across the genome for all genomes analyzed.



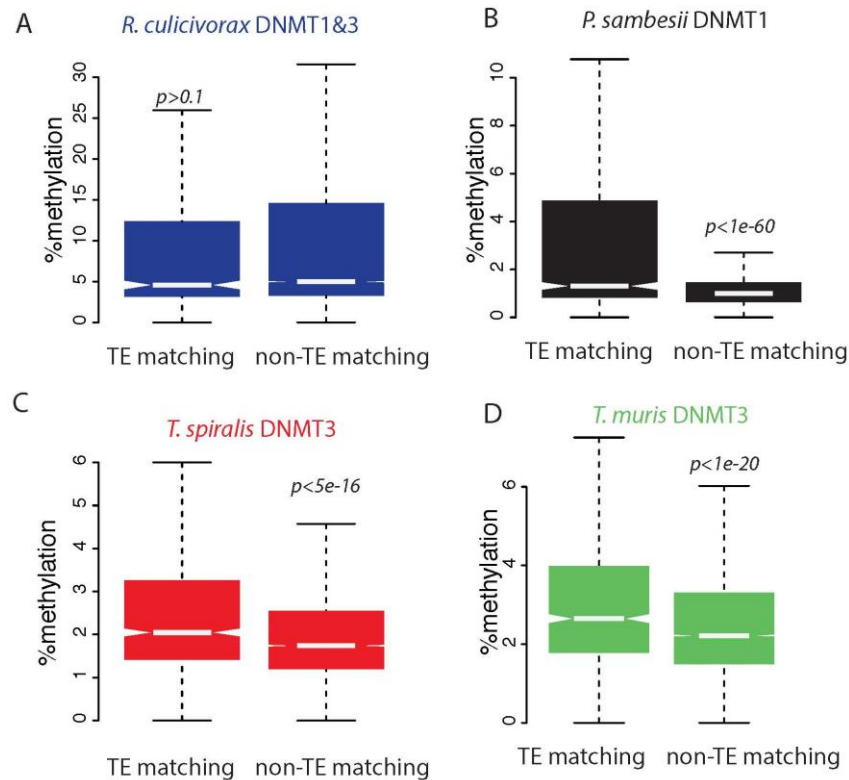
Supplementary Figure 2

Sample genome browser windows for *P. sambesii* and *R. culicivorax* showing lack of methylation on genes but high methylation on repeats



Supplementary Figure 3

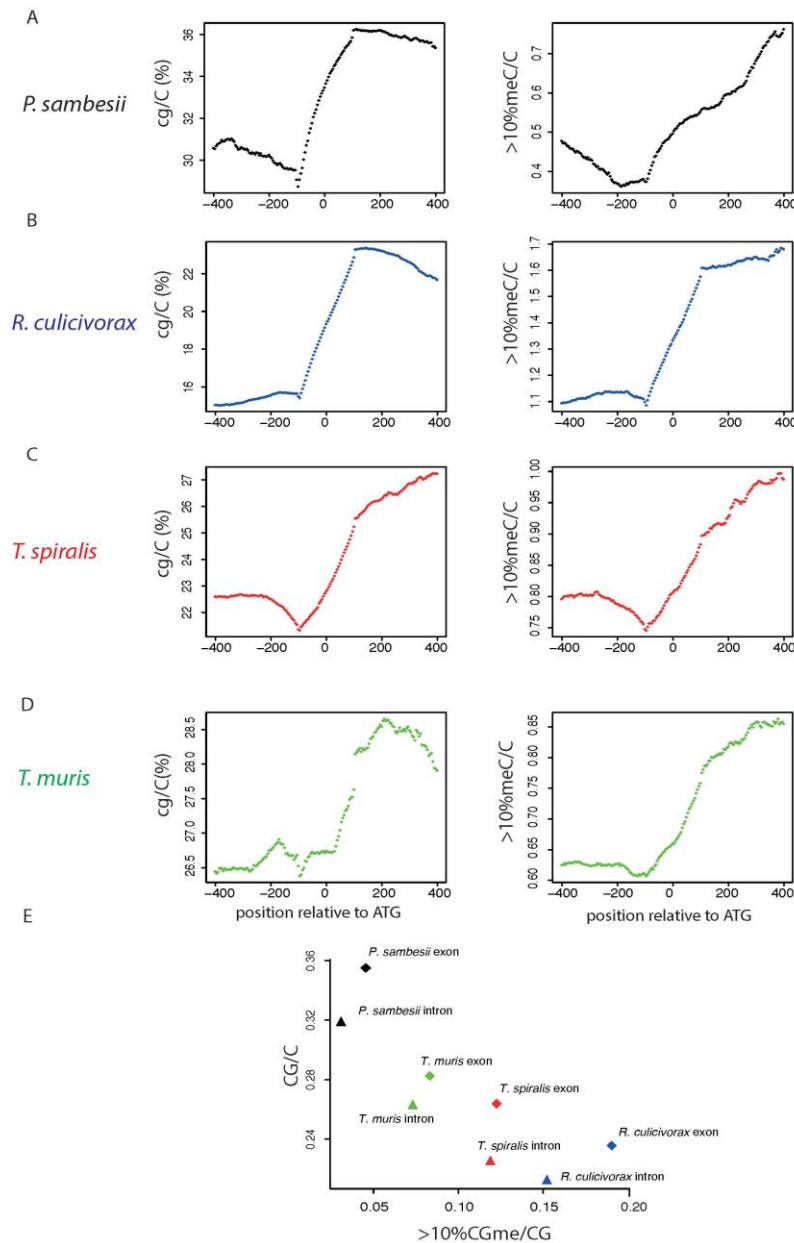
Sample genome browser windows for *T. spiralis* and *T. muris* demonstrating methylation prominence at repeats rather than genes



Supplementary Figure 4

Comparison of DNA methylation in genes and repeats

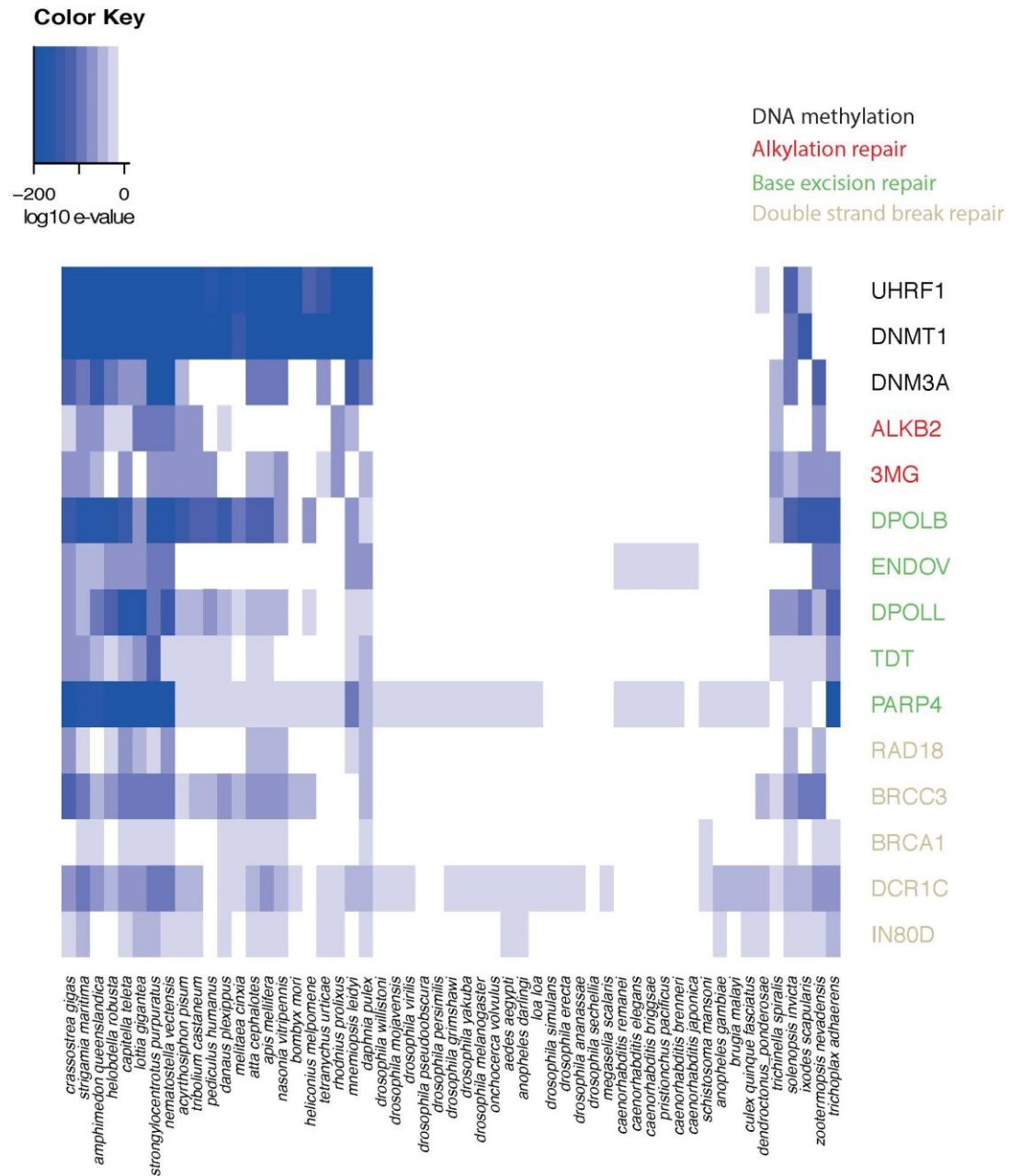
a–d, Methylation levels across genes for either genes with repeat homology or those without for the different nematode species with DNMT activity. *P* values shown are from two-tailed Wilcoxon unpaired tests. The box plot shows interquartile range, with a line at the median and whiskers extending to the most extreme point no more than 1.5 times the interquartile range from the box. The notch shows 95% confidence levels on the median (1.57 times the interquartile range/ $\sqrt{\text{number of samples}}$). *P* values are reported to the nearest significant figure. Analysis is based on the number of genes reported in Supplemental Note 3.



Supplementary Figure 5

Cytosine methylation and CG sequence content of genes in nematodes

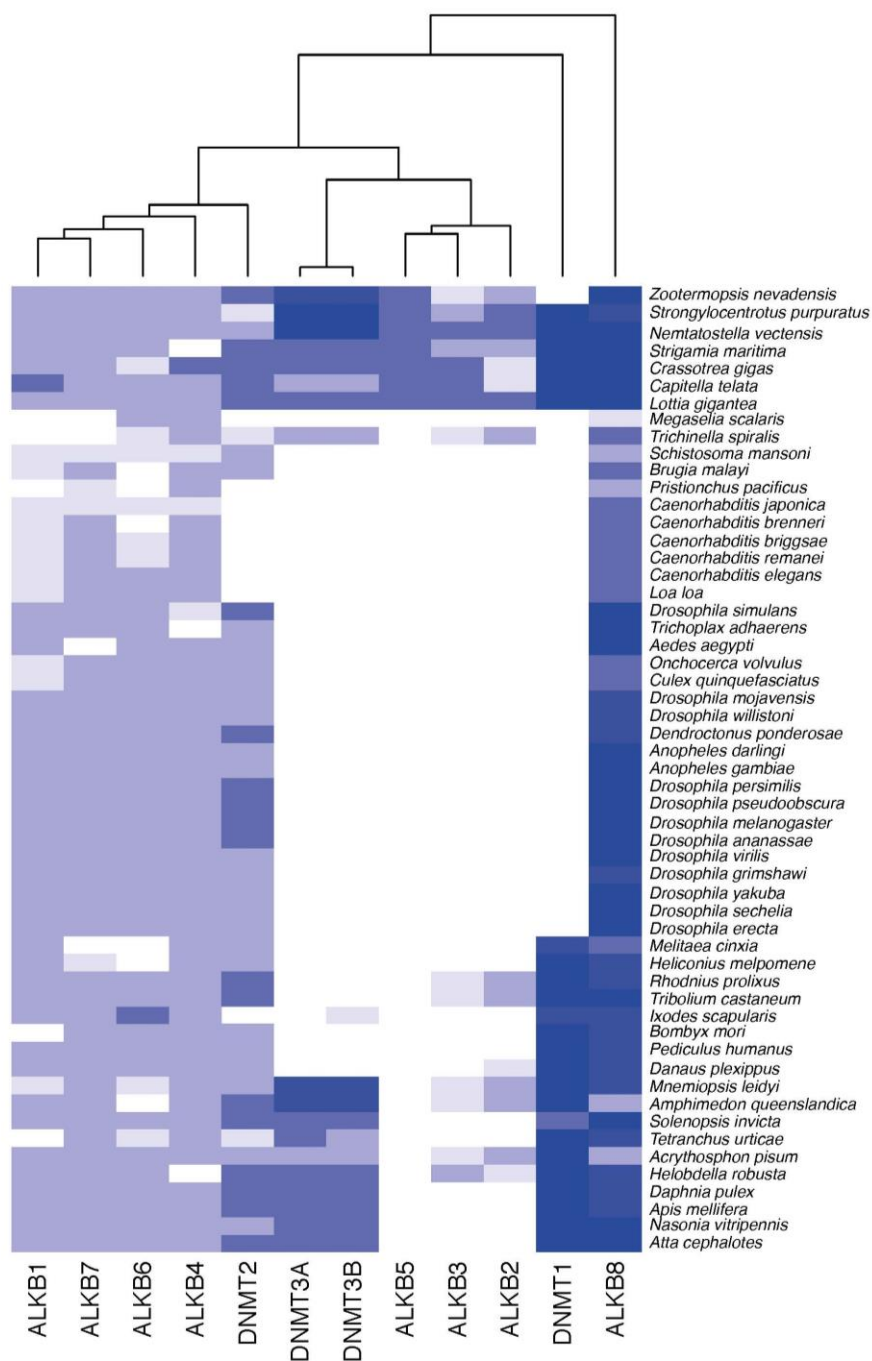
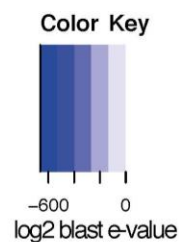
a–d, Comparison of methylation as a fraction of total cytosine (rather than CG) and CG levels upstream and downstream of the transcriptional start site for the different nematode species with cytosine DNMT activity. **e**, Variation of CG methylation normalized to CG content with overall CG content for exons (diamonds) or introns (triangles) in different nematodes. The number of CG sites analyzed for all plots is in Supplemental Note 3.



Supplementary Figure 6

Coevolution of DNA repair proteins with DNA methyltransferases

Heat map showing the conservation of different proteins with a GO term for DNA repair that coevolve with cytosine DNA methylation. DNMT1 and DNMT3 are shown for comparison. In addition to alkylation repair, this set of genes includes components of base excision repair, which is also involved in repairing DNA alkylation damage, and double-strand break repair, which would be required in the event of replication fork stalling, for instance at 3meC lesions if not repaired by ALKB2.



Supplementary Figure 7

ALKB2/3 coevolves with DNA methyltransferases across metazoa

Heat map showing the conservation of ALKB and DNMT family members across metazoans. ALKB2/3 are the only ALKB family members that show significant coevolution with DNA methyltransferases.

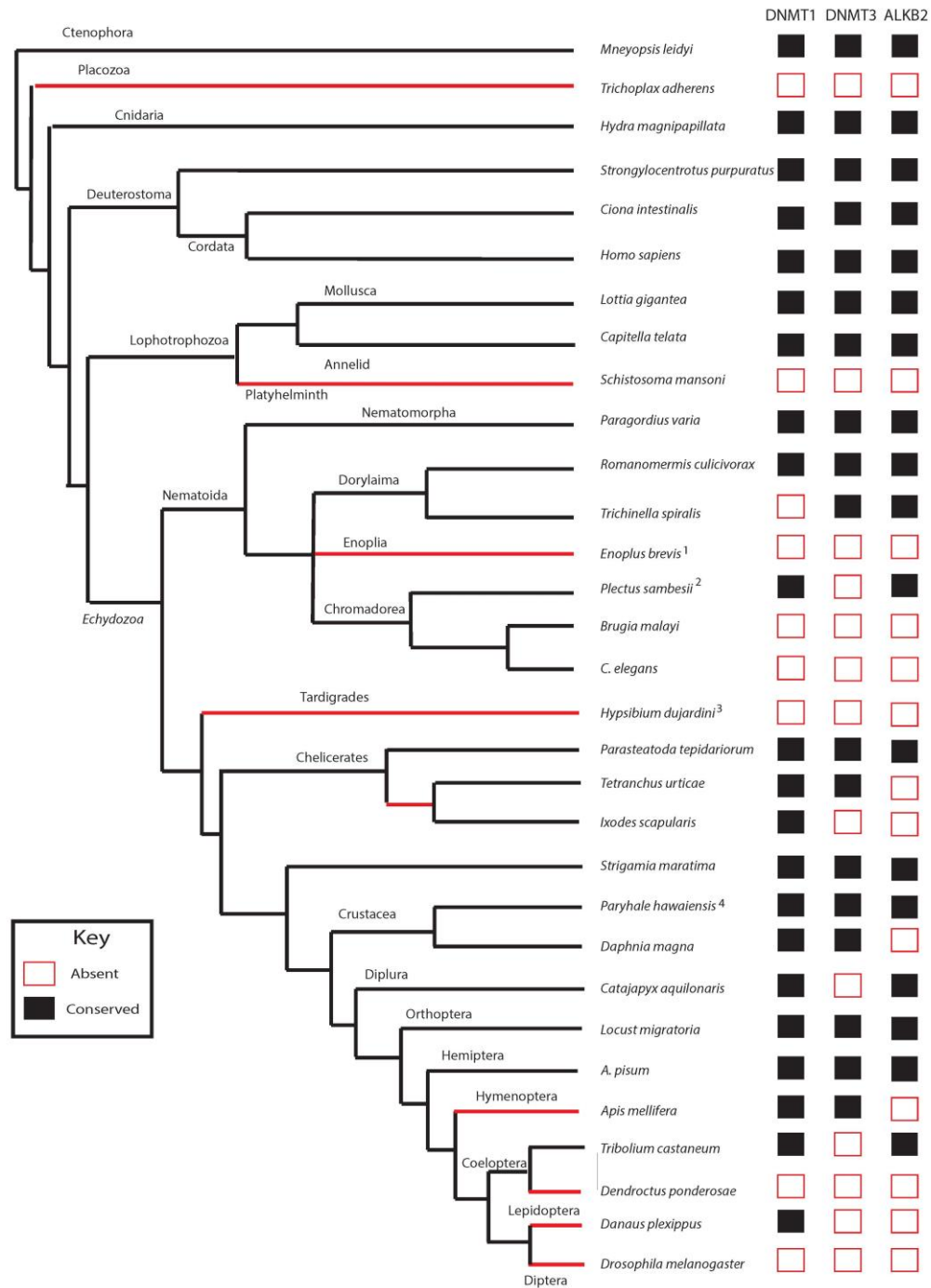
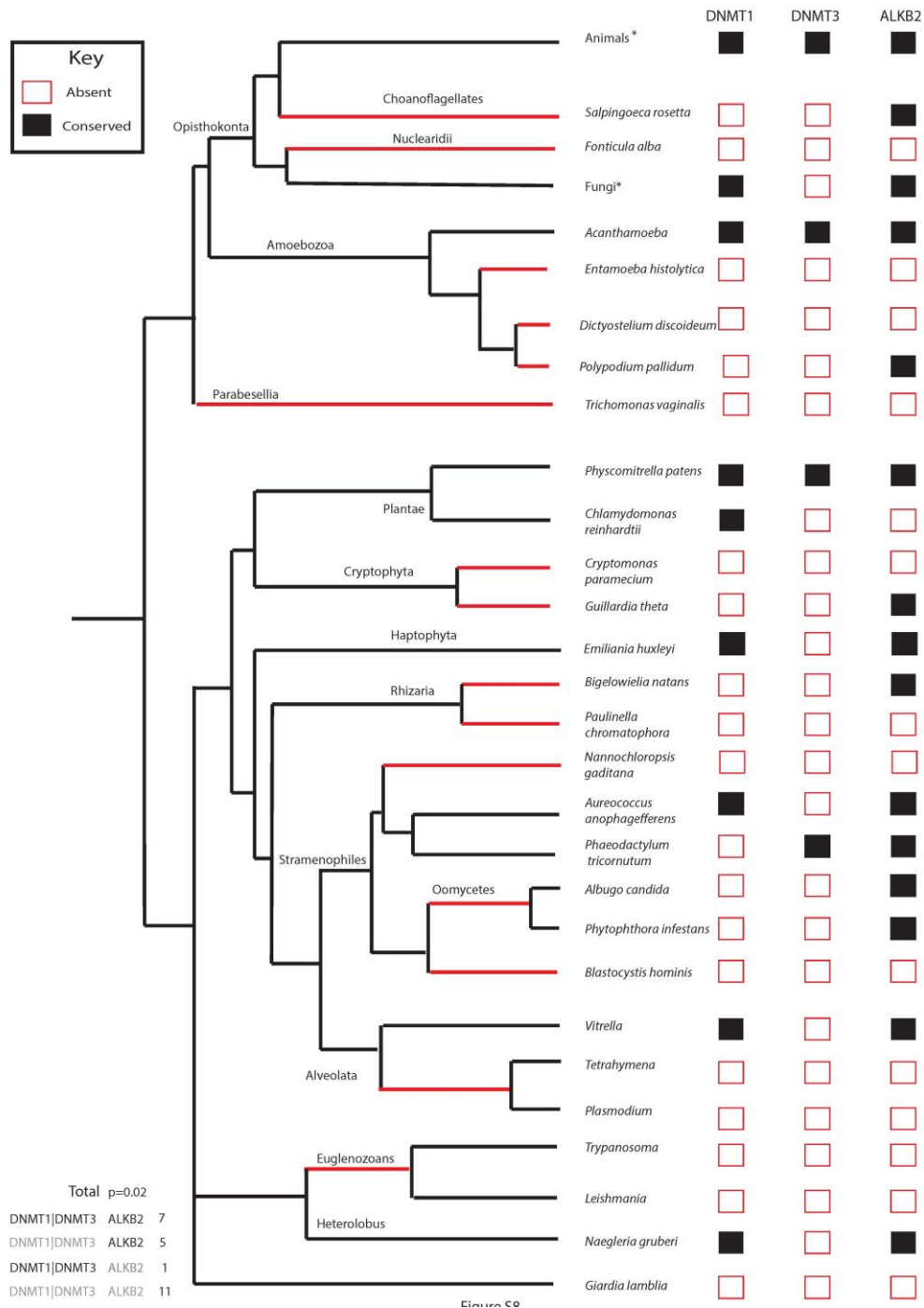


Figure S6

Totals DNMT1|DNMT3 ALKB2 9 DNMT1|DNMT3 ALKB2 4
 DNMT1|DNMT3 ALKB2 0 DNMT1|DNMT3 ALKB2 7 p=0.004

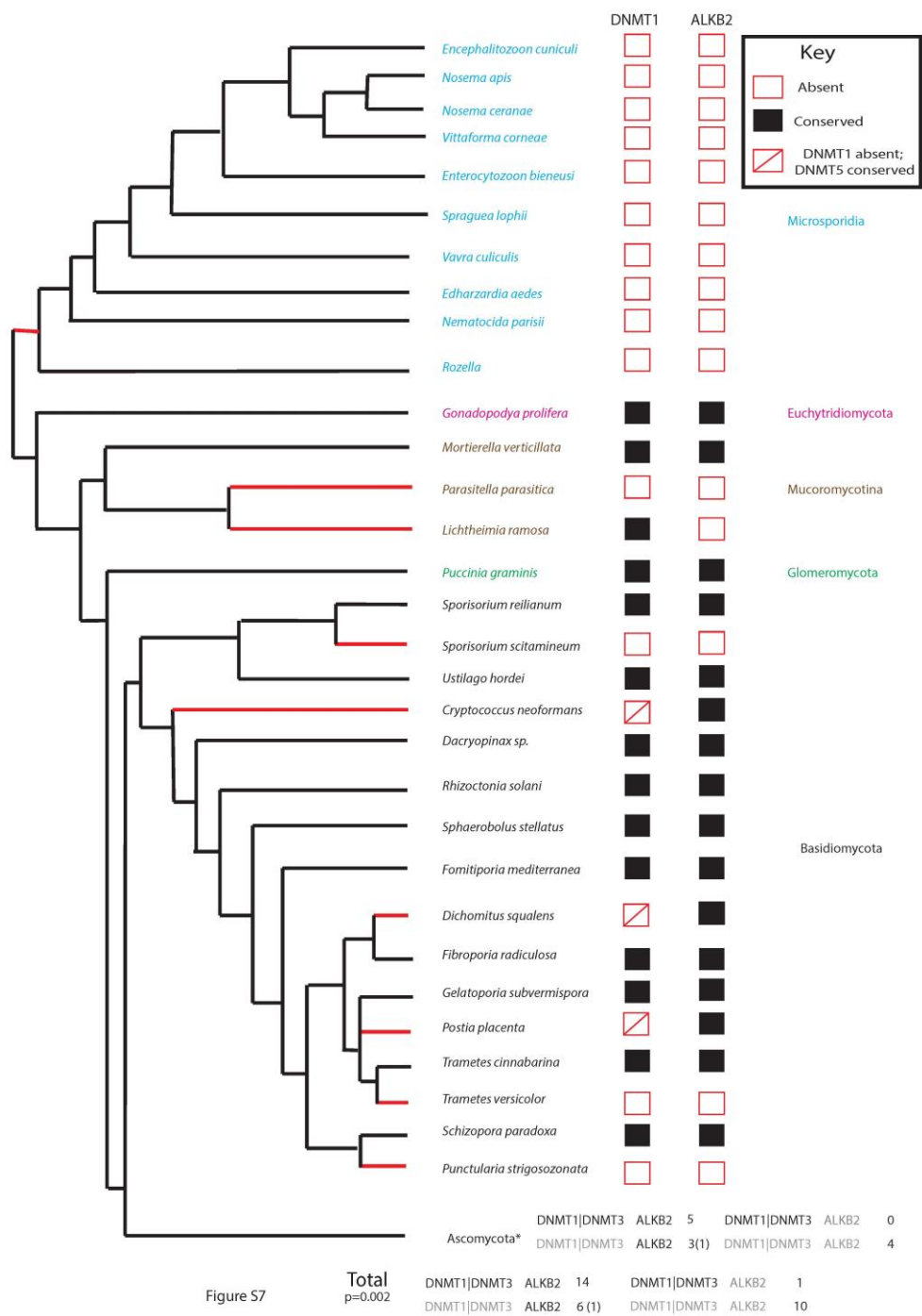
Supplementary Figure 8

ALKB2/3 and DNMT coevolution in metazoa



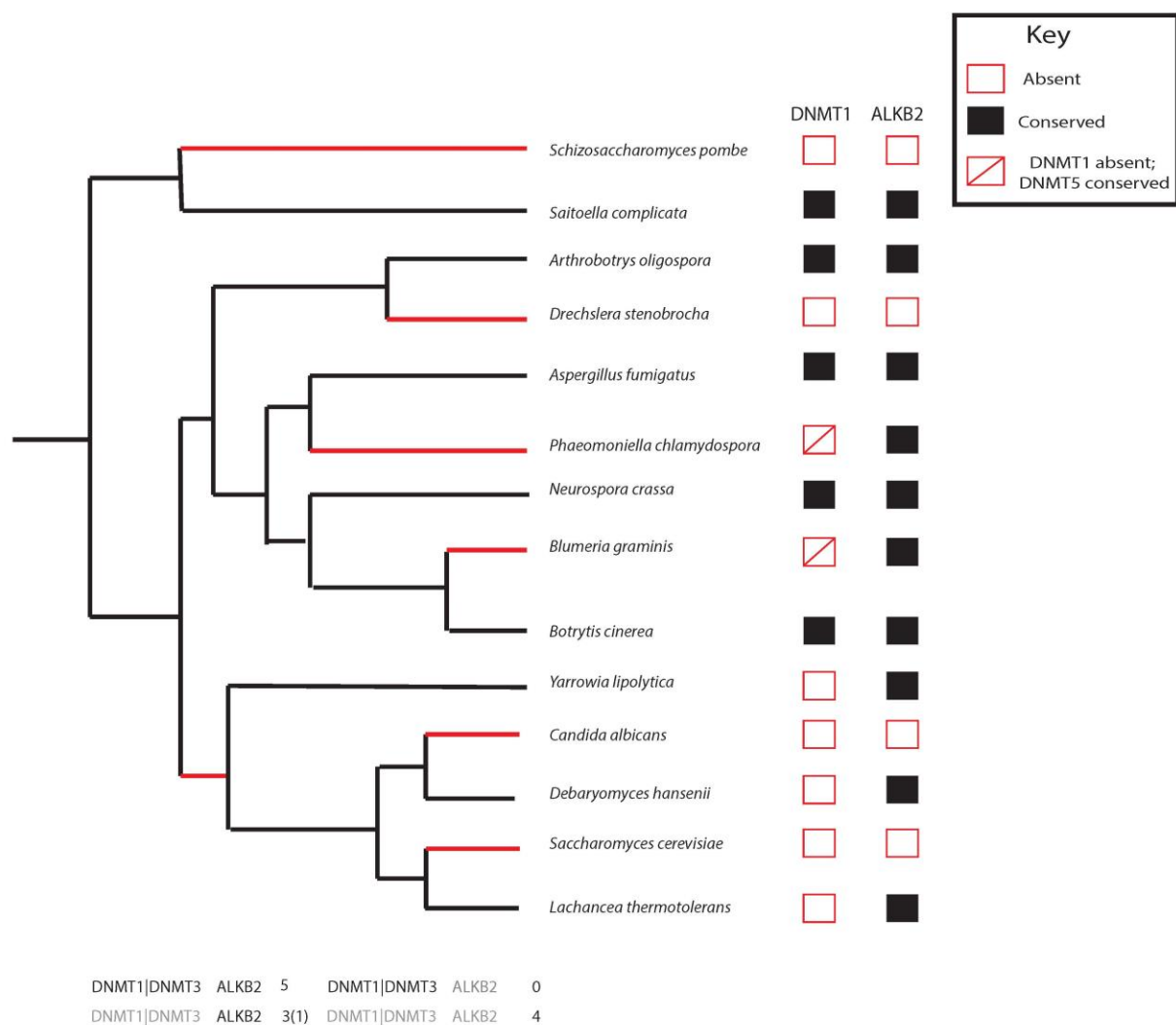
Supplementary Figure 9

DNA methylation and ALKB2/3 coevolution in protists



Supplementary Figure 10

DNA methylation and ALKB2/3 coevolution in fungi

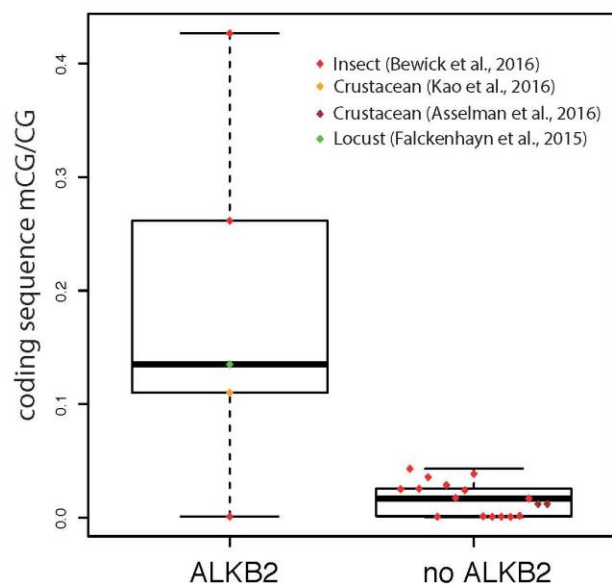


Supplementary Figure 11

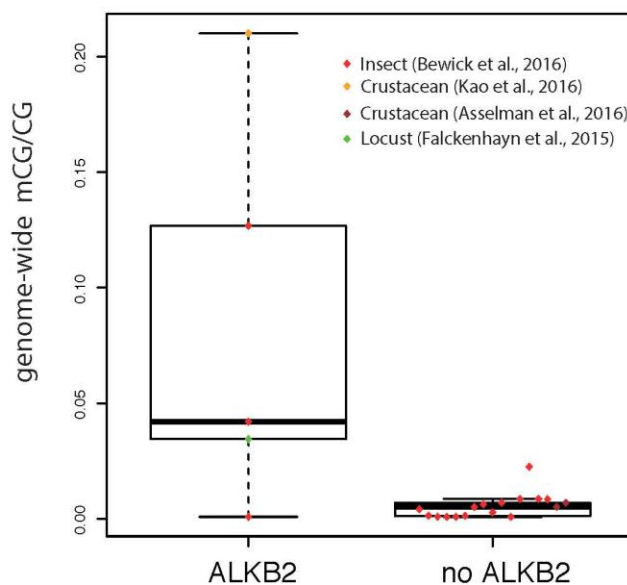
DNA methylation and ALKB2/3 coevolution in Ascomycota

See also Fig. 9.

A



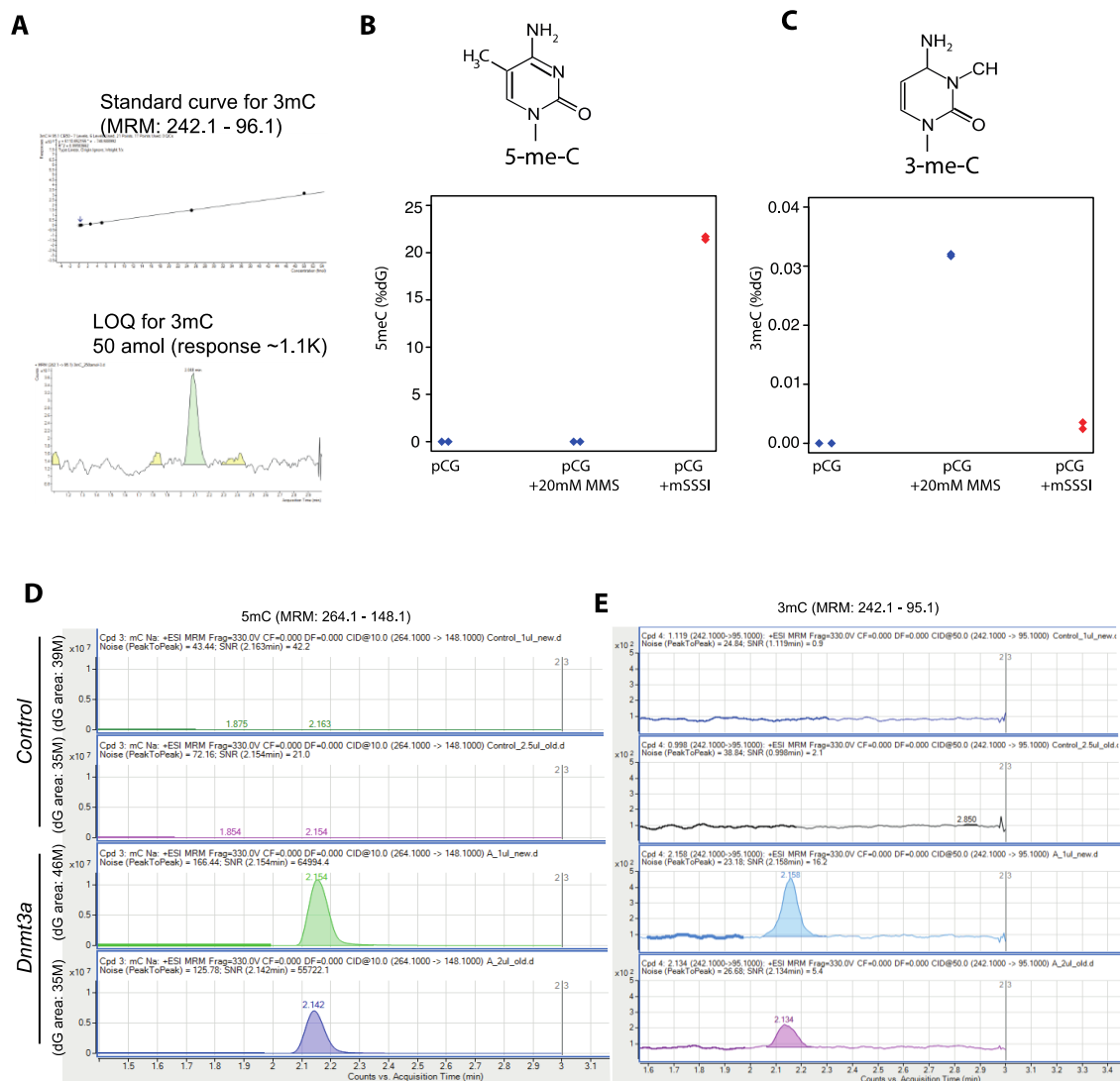
B



Supplementary Figure 12

ALKB2/3 supports higher DNA methylation levels in arthropods

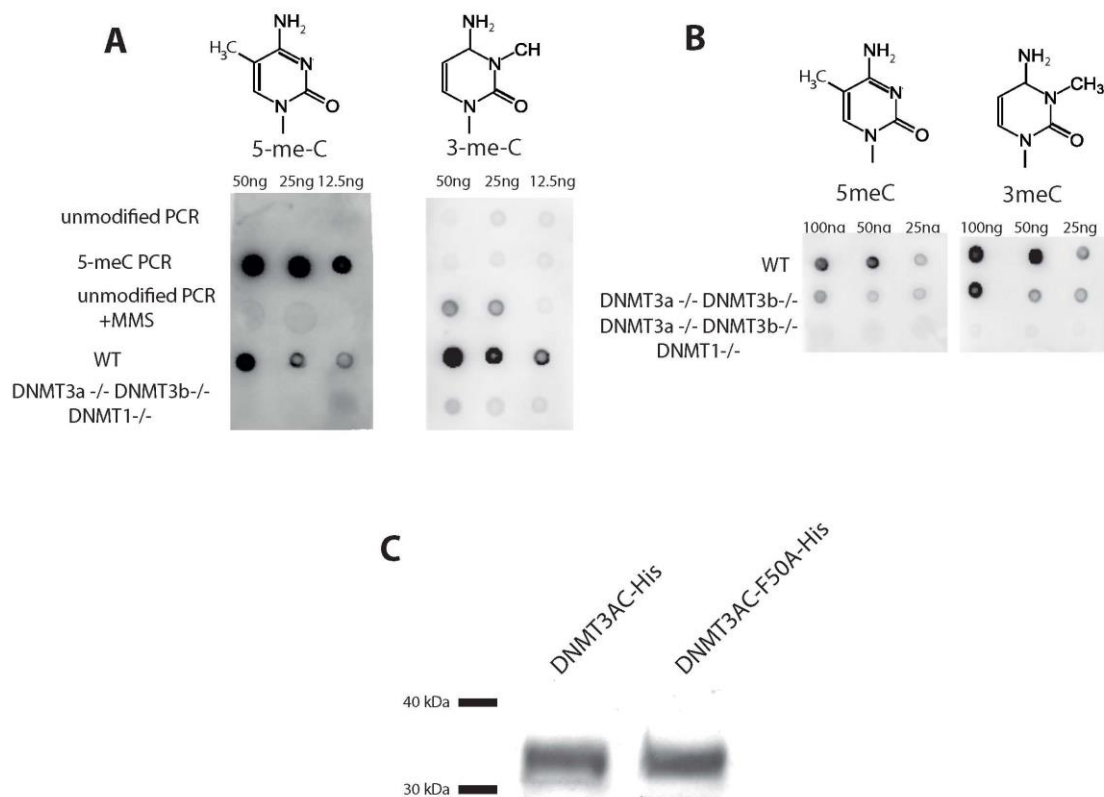
DNA methylation levels across arthropods comparing 4 species with ALKB2/3 and 17 species without ALKB2/3. A coding sequence B across the genome. The only species that has ALKB2/3 yet shows extremely low levels of detectable methylation is *T. castaneum*. The box plot shows a line at the median, the interquartile range as the box and whiskers extending to the greatest point that is less than 1.5 times the interquartile range. For the full list of arthropod species analyzed, see Supplemental Table 9.



Supplementary Figure 13

Establishment of a method to monitor 3meC by LC/MS

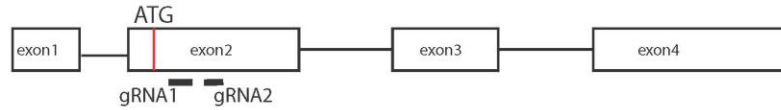
a. Example of a standard curve and LCQ for 3meC. The standard curve was repeated each time measurements were taken (5), with similar results. **b,c,** 5meC and 3meC levels measured in mSSSI methylated and unmethylated plasmid with or without exposure to MMS. Technical variation from two measurements is shown. Note low-level induction of 3meC by mSSSI alone in **c**. The signal-to-noise ratio for 3meC detection was 10 as per the Methods. **d,e,** Screenshots of LC/MS traces for two further independent replicate in vitro reactions containing the catalytic domain of DNMT3a and an unmethylated plasmid, showing induction of 5meC and 3meC.



Supplementary Figure 14

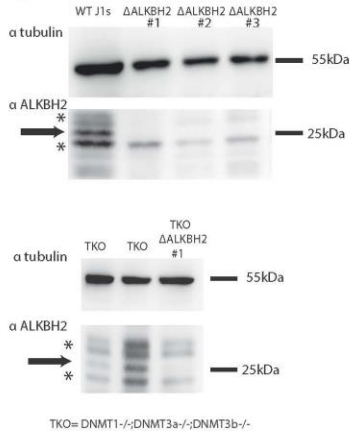
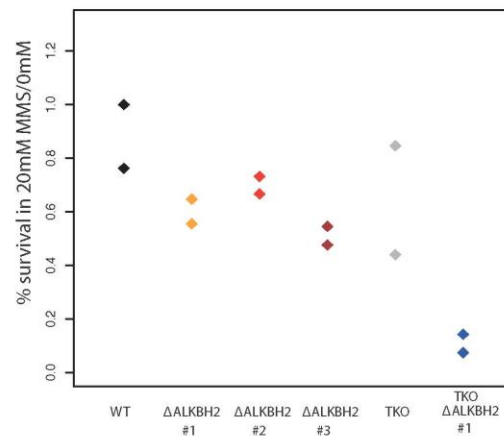
Analysis of alkylation damage caused by DNMTs

a, Dot blot demonstrating the specificity of 3meC antibody, which recognizes a DNA template alkylated in vitro and not a 5meC-containing template synthesized by PCR, in contrast to the anti-5meC antibody, which only recognizes the 5meC template. The experiment was repeated twice with similar results. **b**, Dot blot showing 3meC levels in WT ES cells and cells carrying either DNMT3a and DNMT3b deletion (DKO) or DNMT3a, DNMT3b and DNMT1 deletion (TKO). The experiment was repeated four times with similar results. **c**, Western blot showing comparable protein levels for both WT and mutant (F646A) DNMT3a catalytic domain expressed and purified from *E. coli*. The experiment was performed twice with similar results.

A**B**

WT J1s
 ΔALKBH2 #1 Allele1
 ΔALKBH2 #1 Allele2

TCCGCGACCTCCAAGGGGGAGGGGAGGAGCCCGCCCCGACGGGAGGAGCCTCGGGCGACCTGAAGAGCCCG
 TCCGCGACCTCC-----AAGAGCCCG
 TCCGCGACCTCCAAGGGGGAGGGGAGGAGCCCGCCCCGACGGGAGGAGCCCG-----TTGGAAGAGCCCG

C**D**

Supplementary Figure 15

Generation of clones carrying deletions in ALKBH2 in mouse ES cells

a, CRISPR strategy to generate disruptions in the first coding exon of mouse ALKBH2, the ortholog of ALKB2. **b**, Example of sequencing data showing out-of-frame deletion in both alleles, indicating successful disruption of the protein. **c**, Western blot confirming reduction of ALKB2 protein levels. Non-specific bands are indicated by an asterisk. Tubulin detection from the same membrane is shown as a control. The blot was performed three times for WT clones and two times for TKO clones. **d**, Sensitivity to 200 mM MMS. The y axis shows percentage surviving colonies relative to an untreated sample from the same line. The mean and range of two biological replicates are shown.

Supplementary Table 1: Library statistics

	Mapped reads	Mean Coverage	PCR duplicates (%)	Non-conversion(%)*
R. culicivorax	15100281.00	6.30	0.12	0.66
P. sambesii	17029848.00	10.30	0.10	0.71
T. spiralis	7589350.00	15.72	0.17	0.64
T.muris	19491243.00	24.78	0.10	0.61

*%mC/C unmethylated APC standard

Supplementary Table 2: methylated genes in *R. culicivora*x

Gene

nRc.2.0.1.t01079-RA;probable xaa-pro aminopeptidase 3 os=homo sapiens gn=xpnpep3 pe=1 sv=1
 nRc.2.0.1.t03560-RA;---NA---
 nRc.2.0.1.t44210-RA;ligand-gated ion channel 50 os=caenorhabditis elegans gn=lgc-50 pe=2 sv=2
 nRc.2.0.1.t22686-RA;homeobox protein hox-b1a os=danio rerio gn=hoxb1a pe=2 sv=2
 nRc.2.0.1.t16735-RA;somatostatin receptor type 1 os=homo sapiens gn=sstr1 pe=1 sv=1
 nRc.2.0.1.t41535-RA;---NA---
 nRc.2.0.1.t27186-RA;serine protease 27 os=homo sapiens gn=prss27 pe=1 sv=1
 nRc.2.0.1.t46500-RA;replication factor c subunit 1 os=drosophila melanogaster gn=gcnf1 pe=1 sv=2
 nRc.2.0.1.t45911-RA;---NA---
 nRc.2.0.1.t28252-RA;n-alpha-acetyltransferase 20 os=xenopus tropicalis gn=naa20 pe=2 sv=1
 nRc.2.0.1.t19193-RA;polymerase delta-interacting protein 2 os=mus musculus gn=poldip2 pe=2 sv=1
 nRc.2.0.1.t02098-RA;---NA---
 nRc.2.0.1.t45638-RA;---NA---
 nRc.2.0.1.t27084-RA;protein tag-256 os=caenorhabditis elegans gn=tag-256 pe=2 sv=1
 nRc.2.0.1.t06626-RA;---NA---
 nRc.2.0.1.t36671-RA;---NA---
 nRc.2.0.1.t26716-RA;---NA---
 nRc.2.0.1.t32382-RA;dehydrogenase reductase sdr family member 13 os=mus musculus gn=dhrs13 pe=1 sv=1
 nRc.2.0.1.t34523-RA;gag-pol polyprotein os=human immunodeficiency virus type 1 group o (isolate ant70) gn=gag-pol pe=3 sv=3
 nRc.2.0.1.t30178-RA;huntingtin os=takifugu rubripes gn=htt pe=3 sv=1
 nRc.2.0.1.t34697-RA;homeobox protein hox-b1 os=homo sapiens gn=hoxb1 pe=1 sv=2
 nRc.2.0.1.t02965-RA;wd repeat-containing protein 82 os=danio rerio gn=wdr82 pe=2 sv=1
 nRc.2.0.1.t25741-RA;muscarinic acetylcholine receptor gar-3 os=caenorhabditis elegans gn=gar-3 pe=1 sv=2
 nRc.2.0.1.t20407-RA;tyrosinase-like protein tyr-3 os=caenorhabditis elegans gn=tyr-3 pe=2 sv=5
 nRc.2.0.1.t14324-RA;pogo transposable element with krab domain os=homo sapiens gn=pogk pe=1 sv=2
 nRc.2.0.1.t31951-RA;ligand-gated ion channel 50 os=caenorhabditis elegans gn=lgc-50 pe=2 sv=2
 nRc.2.0.1.t18153-RA;---NA---
 nRc.2.0.1.t15625-RA;transposon ty3-i gag-pol polyprotein os=saccharomyces cerevisiae;(strain atcc 204508 s288c);gn=ty3b-l;pe=3
 nRc.2.0.1.t46595-RA;phosphorylase b kinase gamma catalytic skeletal muscle isoform os=homo sapiens gn=phkg1 pe=2 sv=3
 nRc.2.0.1.t37063-RA;kappa-type opioid receptor os=cavia porcellus gn=oprk1 pe=2 sv=1
 nRc.2.0.1.t38943-RA;tolloid-like protein 1 os=xenopus laevis gn=tl1 pe=1 sv=1
 nRc.2.0.1.t28502-RA;---NA---
 nRc.2.0.1.t07697-RA;retrovirus-related pol polyprotein from transposon 412 os=drosophila melanogaster gn=pol pe=4 sv=1
 nRc.2.0.1.t14707-RA;---NA---
 nRc.2.0.1.t20709-RA;---NA---
 nRc.2.0.1.t41025-RA;uncharacterized protein os=caenorhabditis elegans gn= pe=2 sv=1
 nRc.2.0.1.t23446-RA;transposon ty3-i gag-pol polyprotein os=saccharomyces cerevisiae;(strain atcc 204508 s288c);gn=ty3b-l;pe=3
 nRc.2.0.1.t09475-RA;uncharacterized protein os=caenorhabditis elegans gn= pe=2 sv=1
 nRc.2.0.1.t08338-RA;---NA---
 nRc.2.0.1.t24837-RA;---NA---
 nRc.2.0.1.t46402-RA;---NA---
 nRc.2.0.1.t28253-RA;bombesin receptor subtype-3 os=homo sapiens gn=brs3 pe=1 sv=1
 nRc.2.0.1.t34655-RA;zinc metalloproteinase nas-4 os=caenorhabditis elegans gn=nas-4 pe=2 sv=4
 nRc.2.0.1.t14443-RA;carbonyl reductase 1 os=bos taurus gn=cbr1 pe=2 sv=1
 nRc.2.0.1.t21879-RA;pol polyprotein os=feline endogenous virus ece1 gn=pol pe=3 sv=1

Supplementary Table 2: methylated genes in *R. culicivorax*

nRc.2.0.1.t17239-RA;protein-tyrosine sulfotransferase 2 os=bos taurus gn=tpst2 pe=2 sv=1
nRc.2.0.1.t02364-RA;potassium-transporting atpase alpha chain 2 os=cavia porcellus gn=atp12a pe=2 sv=1
nRc.2.0.1.t31882-RA;death-associated protein kinase 1 os=homo sapiens gn=dapk1 pe=1 sv=6
nRc.2.0.1.t32157-RA;retinol dehydrogenase 11 os=mus musculus gn=rdh11 pe=2 sv=2
nRc.2.0.1.t48314-RA;duoxa-like protein os=caenorhabditis elegans gn= pe=2 sv=2

Supplementary Table 3: Gene ontology terms associated with methylated genes in *R. culicivora*

number	Description
1	GO:0000003; reproduction; biological_process
4	GO:0000166; nucleotide binding; molecular_function
1	GO:0002119; nematode larval development; biological_process
7	GO:0003676; nucleic acid binding; molecular_function
1	GO:0003677; DNA binding; molecular_function
1	GO:0003689; DNA clamp loader activity; molecular_function
2	GO:0003700; transcription factor activity, sequence-specific DNA binding; molecular_function
1	GO:0003824; catalytic activity; molecular_function
1	GO:0004177; aminopeptidase activity; molecular_function
2	GO:0004222; metalloendopeptidase activity; molecular_function
1	GO:0004252; serine-type endopeptidase activity; molecular_function
1	GO:0004596; peptide alpha-N-acetyltransferase activity; molecular_function
2	GO:0004672; protein kinase activity; molecular_function
1	GO:0004930; G-protein coupled receptor activity; molecular_function
2	GO:0005230; extracellular ligand-gated ion channel activity; molecular_function
4	GO:0005488; binding; molecular_function
2	GO:0005515; protein binding; molecular_function
1	GO:0005516; calmodulin binding; molecular_function
3	GO:0005524; ATP binding; molecular_function
7	GO:0005622; intracellular; cellular_component
2	GO:0005634; nucleus; cellular_component
1	GO:0005663; DNA replication factor C complex; cellular_component
2	GO:0005667; transcription factor complex; cellular_component
3	GO:0005737; cytoplasm; cellular_component
1	GO:0005739; mitochondrion; cellular_component
1	GO:0005789; endoplasmic reticulum membrane; cellular_component
1	GO:0005794; Golgi apparatus; cellular_component
1	GO:0005829; cytosol; cellular_component
1	GO:0005886; plasma membrane; cellular_component
1	GO:0005980; glycogen catabolic process; biological_process
1	GO:0006006; glucose metabolic process; biological_process
6	GO:0006139; nucleobase-containing compound metabolic process; biological_process
1	GO:0006260; DNA replication; biological_process
2	GO:0006468; protein phosphorylation; biological_process
4	GO:0006508; proteolysis; biological_process
2	GO:0006811; ion transport; biological_process
1	GO:0006812; cation transport; biological_process
1	GO:0007165; signal transduction; biological_process
4	GO:0007186; G-protein coupled receptor signaling pathway; biological_process
2	GO:0008152; metabolic process; biological_process
1	GO:0008234; cysteine-type peptidase activity; molecular_function
2	GO:0008270; zinc ion binding; molecular_function
6	GO:0008408; 3'-5' exonuclease activity; molecular_function
1	GO:0009792; embryo development ending in birth or egg hatching; biological_process
1	GO:0009952; anterior/posterior pattern specification; biological_process

1	GO:0015031; protein transport; biological_process
7	GO:0015074; DNA integration; biological_process
1	GO:0015629; actin cytoskeleton; cellular_component
3	GO:0016020; membrane; cellular_component
7	GO:0016021; integral component of membrane; cellular_component
1	GO:0016491; oxidoreductase activity; molecular_function
1	GO:0016616; oxidoreductase, CH-OH group of donors, NAD or NADP acceptor; molecular_function
1	GO:0016740; transferase activity; molecular_function
4	GO:0016787; hydrolase activity; molecular_function
1	GO:0018149; peptide cross-linking; biological_process
1	GO:0019904; protein domain specific binding; molecular_function
1	GO:0021570; rhombomere 4 development; biological_process
1	GO:0021571; rhombomere 5 development; biological_process
1	GO:0021612; facial nerve structural organization; biological_process
1	GO:0021754; facial nucleus development; biological_process
1	GO:0022857; transmembrane transporter activity; molecular_function
1	GO:0030145; manganese ion binding; molecular_function
1	GO:0040007; growth; biological_process
1	GO:0042575; DNA polymerase complex; cellular_component
1	GO:0042967; acyl-carrier-protein biosynthetic process; biological_process
2	GO:0043565; sequence-specific DNA binding; molecular_function
1	GO:0045944; positive regulation of transcription from RNA polymerase II promoter; biological_process
1	GO:0046872; metal ion binding; molecular_function
1	GO:0046983; protein dimerization activity; molecular_function
1	GO:0048646; anatomical structure formation involved in morphogenesis; biological_process
1	GO:0048704; embryonic skeletal system morphogenesis; biological_process
1	GO:0070584; mitochondrion morphogenesis; biological_process
50	50

Supplementary Table 4: Gene ontology terms significantly enriched in genes coevolving with DNA methyltransferases

GO term	N observed	N expected	FT pvalue	FT odds	FT q (BH)
GO:0006281	639	18	1.45E-05	3.39	1.23E-02
GO:0090305	331	15	2.49E-07	5.54	2.16E-04
GO:0006302	197	14	2.31E-09	8.94	2.02E-06
GO:0070531	40	10	1.34E-12	38.89	1.18E-09
GO:0010212	78	9	2.53E-08	15.21	2.21E-05
GO:0071897	119	9	9.82E-07	9.54	8.42E-04
GO:0005694	145	8	3.93E-05	6.81	3.31E-02
GO:0006303	72	7	2.96E-06	12.55	2.53E-03
GO:1903874	8	7	2.58E-14	836.47	2.28E-11
GO:0003887	64	6	1.88E-05	12.05	1.59E-02
GO:0009008	10	6	7.80E-11	174.61	6.84E-08
GO:0010039	26	6	7.61E-08	34.96	6.63E-05
GO:0015093	8	6	1.06E-11	348.61	9.27E-09
GO:0031572	32	6	2.87E-07	26.87	2.49E-04
GO:0045739	52	6	5.57E-06	15.20	4.74E-03
GO:0005720	25	5	2.07E-06	29.13	1.77E-03
GO:0006306	30	5	5.36E-06	23.29	4.57E-03
GO:0006307	27	5	3.10E-06	26.46	2.65E-03

Supplementary Table 5: List of genes coevolving with DNA methyltransferases with DNA repair gene ontology term

Protein (uniprot id)	pval DNMT1	pval DNMT3
sp P29372 3MG_HUMAN	7.18E-09	4.31E-07
sp Q9Y312 AAR2_HUMAN	3.43E-20	4.16E-02
sp Q96113 ABHD8_HUMAN	1.11E-09	4.60E-05
sp Q6UXC1 AEGP_HUMAN	5.90E-10	4.04E-08
sp Q6NS38 ALKB2_HUMAN	3.25E-07	3.15E-05
sp Q6AI12 ANR40_HUMAN	1.51E-08	2.99E-07
sp A1IGU5 ARH37_HUMAN	2.41E-08	8.00E-06
sp Q9NR81 ARHG3_HUMAN	6.40E-10	5.24E-09
sp Q7Z628 ARHG8_HUMAN	6.40E-10	5.24E-09
sp P15336 ATF2_HUMAN	2.64E-13	4.04E-08
sp P17544 ATF7_HUMAN	2.68E-11	2.99E-07
sp Q99933 BAG1_HUMAN	1.28E-07	7.58E-05
sp Q9NQY0 BIN3_HUMAN	1.19E-09	1.71E-05
sp P38398 BRCA1_HUMAN	1.28E-07	1.31E-03
sp P46736 BRCC3_HUMAN	1.12E-07	1.05E-11
sp Q14201 BTG3_HUMAN	1.11E-09	1.71E-06
sp Q9NY30 BTG4_HUMAN	2.29E-07	1.71E-06
sp Q2TBE0 C19L2_HUMAN	3.90E-20	4.76E-02
sp O75828 CBR3_HUMAN	5.33E-07	2.20E-09
sp Q96GN5 CDA7L_HUMAN	1.84E-07	1.11E-04
sp Q9BWT1 CDCA7_HUMAN	2.23E-08	5.99E-05
sp Q8N960 CE120_HUMAN	2.41E-08	8.00E-06
sp Q5TB80 CE162_HUMAN	5.79E-07	1.61E-04
sp O15078 CE290_HUMAN	2.41E-08	1.43E-03
sp A5D8W1 CFA69_HUMAN	2.81E-08	4.27E-06
sp Q5TON1 CFA70_HUMAN	3.25E-07	3.15E-05
sp Q9BRQ4 CK070_HUMAN	1.51E-08	1.18E-05
sp Q9H078 CLPB_HUMAN	2.71E-08	6.76E-11
sp Q8IY22 CMIP_HUMAN	1.51E-08	2.99E-07
sp Q96F85 CNRP1_HUMAN	1.28E-07	1.31E-03
sp Q9UBI1 COMD3_HUMAN	2.77E-07	1.86E-04
sp Q9NX08 COMD8_HUMAN	1.28E-07	7.58E-05
sp Q68DL7 CR063_HUMAN	1.83E-07	5.04E-05
sp Q14999 CUL7_HUMAN	2.23E-08	5.99E-05
sp Q96SD1 DCR1C_HUMAN	3.86E-07	6.69E-07
sp Q5TB30 DEP1A_HUMAN	2.77E-07	1.86E-04
sp Q8WUY9 DEP1B_HUMAN	2.77E-07	1.86E-04
sp O14521 DHSD_HUMAN	3.56E-07	2.78E-03
sp Q9UBC3 DNM3B_HUMAN	0.00E+00	2.99E-07
sp Q9UJW3 DNM3L_HUMAN	1.30E-15	4.27E-06
sp Q6XZF7 DNMBP_HUMAN	1.96E-08	2.13E-04
sp P26358 DNMT1_HUMAN	2.99E-07	1.00E+00
sp P06746 DPOLB_HUMAN	1.96E-08	3.18E-10
sp Q9UGP5 DPOLL_HUMAN	1.06E-10	6.54E-10
sp Q9NP87 DPOLM_HUMAN	7.18E-09	4.31E-07

Supplemental Table 5

sp Q6XUX3 DUSTY_HUMAN	3.25E-07	4.99E-07
sp Q0PNE2 ELP6_HUMAN	2.77E-07	2.09E-03
sp Q96AY2 EME1_HUMAN	2.54E-09	1.54E-05
sp Q8N8Q3 ENDOV_HUMAN	5.22E-07	2.07E-03
sp Q96EK7 F120B_HUMAN	2.29E-07	1.71E-06
sp Q8WW52 F151A_HUMAN	4.87E-20	3.68E-02
sp Q9GZU8 F192A_HUMAN	2.54E-20	4.74E-02
sp Q96BQ1 FAM3D_HUMAN	1.79E-20	4.46E-02
sp O94952 FBX21_HUMAN	3.25E-07	3.15E-05
sp Q8TB52 FBX30_HUMAN	4.87E-07	1.49E-03
sp Q9UH90 FBX40_HUMAN	3.25E-07	3.29E-03
sp Q5MNV8 FBX47_HUMAN	2.77E-07	6.55E-06
sp Q9BRP7 FDXA1_HUMAN	3.25E-07	7.24E-09
sp Q9UHY8 FEZ2_HUMAN	6.71E-20	1.43E-02
sp Q6ZNL6 FGD5_HUMAN	2.71E-08	4.57E-04
sp Q6MZW2 FSTL4_HUMAN	2.20E-10	5.66E-08
sp Q8N475 FSTL5_HUMAN	2.20E-10	5.66E-08
sp O95954 FTCD_HUMAN	3.43E-08	3.62E-05
sp Q96A11 G3ST3_HUMAN	5.22E-07	4.91E-07
sp Q2TAP0 GOG7B_HUMAN	2.22E-20	4.92E-02
sp Q86X24 HORM1_HUMAN	4.51E-09	4.70E-03
sp Q8N7B1 HORM2_HUMAN	2.23E-08	5.92E-03
sp O43301 HS12A_HUMAN	2.81E-08	4.27E-06
sp Q96MM6 HS12B_HUMAN	2.81E-08	4.27E-06
sp Q16270 IBP7_HUMAN	2.48E-13	1.71E-05
sp Q8WX77 IBPL1_HUMAN	1.28E-07	1.31E-03
sp Q53TQ3 IN80D_HUMAN	2.81E-08	1.07E-04
sp Q969R8 ITFG2_HUMAN	5.90E-10	5.70E-05
sp Q13572 ITPK1_HUMAN	5.33E-07	3.13E-12
sp Q7Z7F0 K0907_HUMAN	6.32E-07	2.52E-04
sp Q9P260 K1468_HUMAN	5.07E-07	2.73E-10
sp Q96I82 KAZD1_HUMAN	3.66E-11	4.27E-06
sp Q9P2K6 KLH42_HUMAN	2.23E-08	8.62E-04
sp Q9Y664 KPTN_HUMAN	5.48E-13	3.95E-06
sp Q9UHB6 LIMA1_HUMAN	2.77E-07	1.86E-04
sp Q9BT23 LIMD2_HUMAN	1.11E-09	2.11E-08
sp Q96E66 LRC51_HUMAN	1.28E-07	2.51E-06
sp Q9HCI5 MAGE1_HUMAN	2.62E-07	1.58E-03
sp Q9HAY2 MAGF1_HUMAN	5.32E-13	3.15E-05
sp Q9UNF1 MAGD2_HUMAN	8.27E-07	8.69E-03
sp Q9UJ55 MAGL2_HUMAN	4.47E-07	2.58E-05
sp Q9NZL9 MAT2B_HUMAN	2.77E-07	2.09E-03
sp Q14676 MDC1_HUMAN	2.99E-07	2.00E-08
sp Q9H8H3 MET7A_HUMAN	2.23E-08	5.99E-05
sp Q86V88 MGDP1_HUMAN	3.27E-09	3.43E-05
sp Q6ZRQ5 MMS22_HUMAN	3.25E-07	3.29E-03

Supplemental Table 5

sp P98088 MUC5A_HUMAN	3.84E-20	3.20E-02
sp P50539 MXI1_HUMAN	3.25E-07	7.24E-09
sp Q53F19 NCBP3_HUMAN	6.18E-07	2.26E-02
sp Q14934 NFAC4_HUMAN	0.00E+00	3.86E-02
sp Q6KC79 NIPBL_HUMAN	2.50E-20	4.16E-02
sp O15226 NKRF_HUMAN	2.29E-07	1.71E-06
sp Q9NP64 NO40_HUMAN	8.36E-08	3.55E-05
sp Q96MY1 NOL4L_HUMAN	2.97E-20	3.51E-02
sp P49281 NRAM2_HUMAN	5.71E-20	4.69E-02
sp Q9BRQ3 NUD22_HUMAN	6.34E-07	3.37E-04
sp Q6N063 OGFD2_HUMAN	1.83E-07	9.72E-05
sp Q96E52 OMA1_HUMAN	1.11E-09	1.71E-06
sp Q6GTS8 P20D1_HUMAN	2.81E-08	1.07E-04
sp Q8IVL6 P3H3_HUMAN	2.41E-08	8.00E-06
sp Q9UKK3 PARP4_HUMAN	1.28E-07	2.51E-06
sp Q9UHG3 PCYOX_HUMAN	1.12E-11	2.11E-04
sp Q8NBM8 PCYXL_HUMAN	1.12E-11	2.11E-04
sp Q9NTI5 PDS5B_HUMAN	2.50E-20	2.02E-02
sp Q504Y2 PKDCC_HUMAN	2.35E-08	6.39E-03
sp Q9NS91 RAD18_HUMAN	1.30E-15	4.27E-06
sp P78332 RBM6_HUMAN	1.28E-07	2.51E-06
sp Q9NWF9 RN216_HUMAN	2.41E-08	9.00E-07
sp Q5VYX0 RNLS_HUMAN	2.77E-07	1.86E-04
sp Q9BU20 RSG1_HUMAN	3.25E-07	3.15E-05
sp Q86VV8 RTTN_HUMAN	2.41E-08	8.00E-06
sp P0CK97 S35E2_HUMAN	1.28E-07	2.51E-06
sp Q7Z769 S35E3_HUMAN	2.23E-08	5.99E-05
sp A6NNN8 S38A8_HUMAN	1.85E-15	2.99E-07
sp Q6UVJ0 SAS6_HUMAN	1.28E-07	4.04E-08
sp P13866 SC5A1_HUMAN	7.18E-09	1.45E-05
sp P31639 SC5A2_HUMAN	3.25E-07	3.15E-05
sp P53794 SC5A3_HUMAN	3.25E-07	3.15E-05
sp Q8WU76 SCFD2_HUMAN	7.55E-07	3.98E-09
sp Q8NE22 SETD9_HUMAN	2.81E-08	2.78E-03
sp Q16533 SNPC1_HUMAN	5.22E-07	9.28E-06
sp Q5MJ70 SPDYA_HUMAN	7.67E-07	2.76E-04
sp Q8WWL2 SPIR2_HUMAN	2.62E-20	4.02E-02
sp P43307 SSRA_HUMAN	2.50E-20	4.16E-02
sp P49842 STK19_HUMAN	3.43E-08	1.08E-03
sp Q96EM0 T3HPD_HUMAN	4.56E-07	1.58E-04
sp Q2M2D7 TBC28_HUMAN	7.55E-07	4.31E-07
sp B5MCY1 TDR15_HUMAN	5.36E-10	1.86E-04
sp P04053 TDT_HUMAN	1.28E-07	2.51E-06
sp Q9H6L2 TM231_HUMAN	1.96E-08	6.09E-05
sp Q9ULQ1 TPC1_HUMAN	2.96E-08	5.67E-16
sp Q9NSU2 TREX1_HUMAN	6.43E-20	8.71E-03

Supplemental Table 5

sp Q12816 TROP_HUMAN	4.39E-08	1.45E-04
sp O14562 UBFD1_HUMAN	8.52E-07	7.52E-12
sp Q96T88 UHRF1_HUMAN	1.12E-07	0.00E+00
sp Q96PU4 UHRF2_HUMAN	1.12E-07	0.00E+00
sp C4AMC7 WASH3_HUMAN	2.48E-20	2.64E-02
sp O00401 WASL_HUMAN	2.57E-20	4.77E-02
sp Q96KV7 WDR90_HUMAN	3.25E-07	4.52E-04
sp Q8TEU8 WFKN2_HUMAN	2.77E-07	2.09E-03
sp Q9P2S5 WRP73_HUMAN	3.25E-07	3.15E-05
sp P49750 YLPM1_HUMAN	0.00E+00	4.44E-02
sp P59817 Z280A_HUMAN	1.28E-07	1.31E-03

Supplementary Table 6: DNMTs and ALKB2/3 in metazoans

	ALKB2/ALKB3	DNM3A/DNMT3B	DNMT1
<i>Amphimedon queenslandica</i>	1	1	1
<i>Trichoplax adhaerens</i>	0	0	0
<i>Mnemiopsis leidyi</i>	1	1	1
<i>Nematostella vectensis</i>	1	1	1
<i>Lottia gigantea</i>	1	1	1
<i>Crassostrea gigas</i>	1	1	1
<i>Capitella teleta</i>	1	1	1
<i>Helobdella robusta</i>	1	1	1
<i>Pediculus humanus</i>	0	0	1
<i>Acyrtosiphon pisum</i>	1	1	1
<i>Rhodnius prolixus</i>	1	0	1
<i>Zootermopsis nevadensis</i>	1	1	0
<i>Nasonia vitripennis</i>	0	1	1
<i>Solenopsis invicta</i>	0	1	1
<i>Atta cephalotes</i>	0	1	1
<i>Apis mellifera</i>	0	1	1
<i>Culex quinquefasciatus</i>	0	0	0
<i>Aedes aegypti</i>	0	0	0
<i>Anopheles darlingi</i>	0	0	0
<i>Anopheles gambiae</i>	0	0	0
<i>Drosophila willistoni</i>	0	0	0
<i>Drosophila pseudoobscura</i>	0	0	0
<i>Drosophila persimilis</i>	0	0	0
<i>Drosophila ananassae</i>	0	0	0
<i>Drosophila erecta</i>	0	0	0
<i>Drosophila melanogaster</i>	0	0	0
<i>Drosophila sechellia</i>	0	0	0
<i>Drosophila simulans</i>	0	0	0
<i>Drosophila yakuba</i>	0	0	0
<i>Drosophila grimshawi</i>	0	0	0
<i>Drosophila mojavensis</i>	0	0	0
<i>Drosophila virilis</i>	0	0	0
<i>Megaselia scalaris</i>	0	0	0
<i>Tribolium castaneum</i>	1	0	1
<i>Dendroctonus ponderosae</i>	0	0	0
<i>Melitaea cinxia</i>	0	0	1
<i>Heliconius melpomene</i>	0	0	1
<i>Danaus plexippus</i>	1	0	1
<i>Bombyx mori</i>	0	0	1
<i>Daphnia pulex</i>	0	1	1

Supplementary Table 6: DNMTs and ALKB2/3 in metazoans

<i>Paryhale hawaiiensis</i>	1	1	1
<i>Strigamia maritima</i>	1	1	1
<i>Ixodes scapularis</i>	0	0	1
<i>Tetranychus urticae</i>	0	1	1
<i>Hypsibium dujardini</i>	0	0	0
<i>Panagordius varius</i>	1	1	1
<i>Romanomermis culicivorax</i>	1	1	1
<i>Trichinella spiralis</i>	1	1	0
<i>Plectus sambesii</i>	1	0	1
<i>Enoplus brevis</i>	0	0	0
<i>Brugia malayi</i>	0	0	0
<i>Loa loa</i>	0	0	0
<i>Onchocerca volvulus</i>	0	0	0
<i>Caenorhabditis brenneri</i>	0	0	0
<i>Caenorhabditis briggsae</i>	0	0	0
<i>Caenorhabditis elegans</i>	0	0	0
<i>Caenorhabditis japonica</i>	0	0	0
<i>Caenorhabditis remanei</i>	0	0	0
<i>Pristionchus pacificus</i>	0	0	0
<i>Schistosoma mansoni</i>	0	0	0
<i>Strongylocentrotus purpuratus</i>	1	1	1

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Supplementary Table 7: DNMTs and ALKB2/3 in protists

Strain name	ALKB2/ALKB3	DNMT3A/DNMT3B	DNMT1
<i>Acanthamoeba castellanii</i> str. Neff	1	1	1
<i>Albugo candida</i>	0	0	0
<i>Albugo laibachii</i>	0	0	0
<i>Angomonas deanei</i>	0	0	0
<i>Aphanomyces astaci</i>	0	0	0
<i>Aphanomyces invadans</i>	0	0	0
<i>Aureococcus anophagefferens</i>	0	0	0
<i>Babesia bigemina</i>	0	0	0
<i>Babesia bovis</i>	0	0	0
<i>Babesia microti</i> strain RI	0	0	0
<i>Bigelowiella natans</i>	1	0	0
<i>Bigelowiella natans</i> (GCA_000002455)	0	0	0
<i>Blastocystis hominis</i>	0	0	0
<i>Bodo saltans</i>	0	0	0
<i>Capsaspora owczarzaki</i> ATCC 30864	1	0	0
<i>Chroomonas mesostigmatica</i> CCMP1168	0	0	0
<i>Cryptomonas paramecium</i>	0	0	0
<i>Cryptosporidium muris</i> RN66	0	0	0
<i>Cryptosporidium parvum</i>	0	0	0
<i>Cryptosporidium parvum</i> Iowa II	0	0	0
<i>Dictyostelium discoideum</i>	0	0	0
<i>Dictyostelium fasciculatum</i>	1	0	0
<i>Dictyostelium lacteum</i>	0	0	0
<i>Dictyostelium purpureum</i>	0	0	0
<i>Eimeria acervulina</i>	0	0	0
<i>Eimeria brunetti</i>	0	0	0
<i>Eimeria maxima</i>	0	0	0
<i>Eimeria mitis</i>	0	0	0
<i>Eimeria necatrix</i>	0	0	0
<i>Eimeria praecox</i>	0	0	0
<i>Eimeria tenella</i>	0	0	0
<i>Eimeria tenella</i> (GCA_000499545)	0	0	0
<i>Emiliana huxleyi</i>	1	0	1
<i>Entamoeba dispar</i> SAW760	0	0	0
<i>Entamoeba histolytica</i>	0	0	0
<i>Entamoeba histolytica</i> HM-1:IMSS-A	0	0	0
<i>Entamoeba histolytica</i> HM-1:IMSS-B	0	0	0
<i>Entamoeba histolytica</i> HM-3:IMSS	0	0	0
<i>Entamoeba histolytica</i> KU27	0	0	0
<i>Entamoeba invadens</i> IP1	0	0	0
<i>Entamoeba nuttalli</i> P19	0	0	0
<i>Fonticula alba</i>	0	0	0
<i>Giardia intestinalis</i>	0	0	0

Supplementary Table 7: DNMTs and ALKB2/3 in protists

<i>Giardia intestinalis</i> (GCA_000498715)	0	0	0
<i>Giardia intestinalis</i> ATCC 50581	0	0	0
<i>Giardia intestinalis</i> assemblage B	0	0	0
<i>Giardia lamblia</i>	0	0	0
<i>Giardia lamblia</i> P15	0	0	0
<i>Gregarina niphandrodes</i>	0	0	0
<i>Guillardia theta</i> CCMP2712	0	0	0
<i>Hammondia hammondi</i>	0	0	0
<i>Hyaloperonospora arabidopsidis</i>	0	0	0
<i>Ichthyophthirius multifiliis</i>	0	0	0
<i>Leishmania braziliensis</i> MHOM/BR/75/M2904	0	0	0
<i>Leishmania donovani</i> BPK282A1	0	0	0
<i>Leishmania infantum</i> JPCM5	0	0	0
<i>Leishmania major</i>	0	0	0
<i>Leishmania mexicana</i> MHOM/GT/2001/U1103	0	0	0
<i>Leptomonas pyrrocoris</i>	0	0	0
<i>Leptomonas seymouri</i>	0	0	0
<i>Lotharella oceanica</i>	0	0	0
<i>Monosiga brevicollis</i> MX1	1	0	0
<i>Naegleria gruberi</i>	1	0	1
<i>Nannochloropsis gaditana</i>	0	0	0
<i>Nannochloropsis gaditana</i> CCMP526	0	0	0
<i>Oxytricha trifallax</i>	0	0	0
<i>Oxytricha trifallax</i> (GCA_000295675)	0	0	0
<i>Paramecium tetraurelia</i>	0	0	0
<i>Paulinella chromatophora</i>	0	0	0
<i>Perkinsella</i> sp. CCAP 1560/4	0	0	0
<i>Perkinsus marinus</i> ATCC 50983	1	0	0
<i>Phaeodactylum tricornutum</i>	1	0	0
<i>Phytomonas</i> sp. isolate EM1	0	0	0
<i>Phytomonas</i> sp. isolate Hart1	0	0	0
<i>Phytophthora infestans</i>	1	0	0
<i>Phytophthora kernoviae</i>	0	0	0
<i>Phytophthora lateralis</i>	0	0	0
<i>Phytophthora nicotianae</i>	0	0	0
<i>Phytophthora nicotianae</i> (GCA_001482985)	0	0	0
<i>Phytophthora parasitica</i>	1	0	0
<i>Phytophthora parasitica</i> (GCA_000509465)	1	0	0
<i>Phytophthora parasitica</i> (GCA_000509485)	1	0	0
<i>Phytophthora parasitica</i> (GCA_000509505)	1	0	0
<i>Phytophthora parasitica</i> (GCA_000509525)	1	0	0
<i>Phytophthora parasitica</i> CJ01A1	1	0	0
<i>Phytophthora parasitica</i> INRA-310	1	0	0
<i>Phytophthora parasitica</i> P10297	1	0	0

Supplementary Table 7: DNMTs and ALKB2/3 in protists

Phytophthora parasitica P1976	1	0	0
Phytophthora ramorum	0	0	0
Phytophthora sojae	0	0	0
Plasmodiophora brassicae	1	0	0
Plasmodium berghei	0	0	0
Plasmodium berghei (GCA_000005395)	0	0	0
Plasmodium berghei (GCA_900044335)	0	0	0
Plasmodium chabaudi	0	0	0
Plasmodium chabaudi chabaudi	0	0	0
Plasmodium cynomolgi strain B	0	0	0
Plasmodium falciparum	0	0	0
Plasmodium falciparum 7G8	0	0	0
Plasmodium falciparum CAMP/Malaysia	0	0	0
Plasmodium falciparum Dd2	0	0	0
Plasmodium falciparum FCH/4	0	0	0
Plasmodium falciparum HB3	0	0	0
Plasmodium falciparum IGH-CR14	0	0	0
Plasmodium falciparum MaliPS096_E11	0	0	0
Plasmodium falciparum NF135/5.C10	0	0	0
Plasmodium falciparum NF54	0	0	0
Plasmodium falciparum Palo Alto/Uganda	0	0	0
Plasmodium falciparum RAJ116	0	0	0
Plasmodium falciparum Santa Lucia	0	0	0
Plasmodium falciparum Tanzania (2000708)	0	0	0
Plasmodium falciparum UGT5.1	0	0	0
Plasmodium falciparum Vietnam Oak-Knoll (FVO)	0	0	0
Plasmodium fragile	0	0	0
Plasmodium gaboni	0	0	0
Plasmodium inui San Antonio 1	0	0	0
Plasmodium knowlesi	0	0	0
Plasmodium reichenowi	0	0	0
Plasmodium reichenowi (GCA_001601855)	0	0	0
Plasmodium vinckei petteri	0	0	0
Plasmodium vinckei vinckei	0	0	0
Plasmodium vivax	0	0	0
Plasmodium vivax Brazil I	0	0	0
Plasmodium vivax India VII	0	0	0
Plasmodium vivax Mauritania I	0	0	0
Plasmodium vivax North Korean	0	0	0
Plasmodium yoelii	0	0	0
Plasmodium yoelii (GCA_900002395)	0	0	0
Plasmodium yoelii 17X	0	0	0
Plasmodium yoelii yoelii	0	0	0
Plasmopara halstedii	1	0	0

Supplementary Table 7: DNMTs and ALKB2/3 in protists

<i>Polysphondylium pallidum</i> PN500	1	0	0
<i>Pseudocohnilembus persalinus</i>	1	0	0
<i>Pythium aphanidermatum</i>	1	0	0
<i>Pythium arrhenomanes</i>	0	0	0
<i>Pythium irregulare</i>	1	0	0
<i>Pythium iwayamai</i>	1	0	0
<i>Pythium ultimum</i>	1	0	0
<i>Pythium vexans</i>	1	0	0
<i>Reticulomyxa filosa</i>	1	0	0
<i>Salpingoeca rosetta</i>	1	0	0
<i>Saprolegnia diclina</i> VS20	0	0	0
<i>Saprolegnia parasitica</i> CBS 223.65	0	0	0
<i>Sphaeroforma arctica</i> JP610	0	0	0
<i>Spironucleus salmonicida</i>	0	0	0
<i>Strigomonas culicis</i>	0	0	0
<i>Stylonychia lemnae</i>	0	0	0
<i>Tetrahymena thermophila</i>	0	0	0
<i>Thalassiosira oceanica</i>	1	0	0
<i>Thalassiosira oceanica</i> CCMP1005	0	0	0
<i>Thalassiosira pseudonana</i>	1	0	0
<i>Thecamonas trahens</i> ATCC 50062	0	0	0
<i>Theileria annulata</i>	0	0	0
<i>Theileria equi</i> strain WA	0	0	0
<i>Theileria orientalis</i> strain Shintoku	0	0	0
<i>Theileria parva</i>	0	0	0
<i>Toxoplasma gondii</i>	0	0	0
<i>Toxoplasma gondii</i> ARI	0	0	0
<i>Toxoplasma gondii</i> FOU	0	0	0
<i>Toxoplasma gondii</i> GAB2-2007-GAL-DOM2	0	0	0
<i>Toxoplasma gondii</i> GT1	0	0	0
<i>Toxoplasma gondii</i> MAS	0	0	0
<i>Toxoplasma gondii</i> RUB	0	0	0
<i>Toxoplasma gondii</i> TgCatPRC2	0	0	0
<i>Toxoplasma gondii</i> VAND	0	0	0
<i>Toxoplasma gondii</i> VEG	0	0	0
<i>Toxoplasma gondii</i> p89	0	0	0
<i>Trichomonas vaginalis</i> G3	0	0	0
<i>Trypanosoma brucei</i>	0	0	0
<i>Trypanosoma cruzi</i>	0	0	0
<i>Trypanosoma cruzi</i> (GCA_000188675)	0	0	0
<i>Trypanosoma cruzi</i> Dm28c	0	0	0
<i>Trypanosoma cruzi</i> marinkellei	0	0	0
<i>Trypanosoma rangeli</i> SC58	0	0	0
<i>Vitrella brassicaformis</i> CCMP3155	1	0	1

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

Strain name	ALKB2/ALKB3	DNMT1
<i>Eremothecium cymbalariae</i> dbvpg 7215	1	1
<i>Coprinopsis cinerea</i> okayama7 130	1	1
<i>Allomyces macrogynus</i> atcc 38327	0	1
<i>Baudoinia panamericana</i> uamh 10762	1	1
<i>Spizellomyces punctatus</i> daom br117	1	0
<i>Gonapodya prolifera</i> jel478	1	1
<i>Rozella allomycis</i> csf55	0	0
<i>Acidomyces richmondensis</i> bfw	1	0
<i>Diplodia seriata</i>	1	0
<i>Macrophomina phaseolina</i> ms6	1	1
<i>Neofusicoccum parvum</i> ucrnp2	1	0
<i>Verruconis gallopava</i>	1	1
<i>Pseudocercospora fijiensis</i> cirad86	1	1
<i>Dothistroma septosporum</i>	1	1
<i>Mycosphaerella eumusae</i>	1	0
<i>Pseudocercospora musae</i>	1	1
<i>Sphaerulina musiva</i> so2202	1	1
<i>Zymoseptoria tritici</i>	1	0
<i>Zymoseptoria brevis</i>	1	1
<i>Aureobasidium namibiae</i> cbs 147 97	1	1
<i>Aureobasidium pullulans</i> exf 150	1	1
<i>Aureobasidium subglaciale</i> exf 2481	1	1
<i>Batrachochytrium dendrobatidis</i> jam81	1	1
<i>Leptosphaeria maculans</i>	1	1
<i>Phaeosphaeria nodorum</i>	1	1
<i>Bipolaris maydis</i> c5	1	1
<i>Bipolaris maydis</i> atcc 48331	1	1
<i>Bipolaris oryzae</i> atcc 44560	1	1
<i>Bipolaris sorokiniana</i> nd90pr	1	1
<i>Bipolaris victoriae</i> fi3	1	1
<i>Bipolaris zeicola</i> 26 r 13	1	1
<i>Pyrenophora teres</i>	1	1
<i>Pyrenophora tritici-repentis</i>	1	1
<i>Setosphaeria turcica</i> et28a	1	1
<i>Stemphylium lycopersici</i>	1	1
<i>Cyphellophora europaea</i> cbs 101466	1	1
<i>Capronia coronata</i> cbs 617 96	1	1
<i>Capronia epimyces</i> cbs 606 96	1	1
<i>Capronia semiimmersa</i>	1	1
<i>Cladophialophora bantiana</i> cbs 173 52	1	1
<i>Cladophialophora carrionii</i> cbs 160 54	1	1
<i>Cladophialophora psammophila</i> cbs 110553	1	1
<i>Cladophialophora yegresii</i> cbs 114405	1	1

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

<i>Cladophialophora immunda</i>	1	1
<i>Coniosporium apollinis</i> cbs 100218	1	1
<i>Exophiala aquamarina</i> cbs 119918	1	1
<i>Exophiala dermatitidis</i> nih ut8656	1	1
<i>Exophiala mesophila</i>	1	0
<i>Exophiala oligosperma</i>	1	1
<i>Exophiala sideris</i>	1	1
<i>Exophiala spinifera</i>	1	1
<i>Exophiala xenobiotica</i>	1	1
<i>Fonsecaea multimorphosa</i> cbs 102226	1	1
<i>Fonsecaea pedrosoi</i> cbs 271 37	1	1
<i>Phialophora attae</i>	1	1
<i>Rhinocladiella mackenziei</i> cbs 650 93	1	1
<i>Phaeomoniella chlamydospora</i>	1	0
<i>Endocarpon pusillum</i> z07020	1	1
<i>Aspergillus clavatus</i>	1	1
<i>Aspergillus flavus</i>	1	1
<i>Aspergillus flavus</i> af70	1	1
<i>Aspergillus fumigatus</i>	1	1
<i>Aspergillus fumigatus</i> z5	1	1
<i>Aspergillus fumigatus</i> a1163	1	1
<i>Aspergillus lentulus</i>	1	1
<i>Aspergillus nidulans</i>	1	1
<i>Aspergillus niger</i> atcc 1015	1	1
<i>Aspergillus nomius</i> nrri 13137	1	1
<i>Aspergillus ochraceoroseus</i>	1	1
<i>Aspergillus oryzae</i>	1	1
<i>Aspergillus oryzae</i> 3 042	1	1
<i>Aspergillus parasiticus</i> su 1	1	1
<i>Aspergillus rambellii</i>	1	1
<i>Aspergillus terreus</i>	1	1
<i>Aspergillus udagawae</i>	1	1
<i>Neosartorya fischeri</i>	1	1
<i>Aspergillus calidoustus</i>	1	1
<i>Aspergillus luchuensis</i>	1	1
<i>Aspergillus nidulans</i> fgsc a4	1	1
<i>Aspergillus niger</i>	1	1
<i>Aspergillus niger</i> gca 001515345	1	1
<i>Aspergillus oryzae</i> 100 8	1	1
<i>Aspergillus ruber</i> cbs 135680	1	1
<i>Aspergillus ustus</i>	1	1
<i>Aureobasidium melanogenum</i> cbs 110374	1	1
<i>Penicillium rubens</i> wisconsin 54 1255	1	1
<i>Penicillium chrysogenum</i>	1	1

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

Penicillium digitatum phi26	1	1
Penicillium digitatum pd1	1	1
Penicillium oxalicum 114 2	1	1
Penicillium roqueforti fm164	1	1
Penicillium brasilianum	1	1
Penicillium expansum	1	1
Penicillium expansum gca 000769745	1	1
Penicillium expansum gca 000769735	1	1
Penicillium freii	1	1
Penicillium griseofulvum	1	1
Penicillium italicum	1	1
Penicillium nordicum	1	1
Penicillium solitum	1	1
Byssosclamyces spectabilis no 5	1	1
Rasamsonia emersonii cbs 393 64	1	1
Talaromyces marneffeii pm1	1	1
Talaromyces marneffeii atcc 18224	1	1
Talaromyces stipitatus atcc 10500	1	1
Talaromyces islandicus	1	1
Blastomyces dermatitidis er 3	1	1
Blastomyces dermatitidis atcc 26199	1	1
Blastomyces dermatitidis atcc 18188	1	1
Blastomyces gilchristii slh14081	1	1
Emmonsia crescens uamh 3008	1	1
Histoplasma capsulatum nam1	1	1
Histoplasma capsulatum h88	1	1
Histoplasma capsulatum h143	1	1
Histoplasma capsulatum g186ar	1	1
Arthroderma benhamiae cbs 112371	1	1
Arthroderma otae cbs 113480	1	1
Microsporum gypseum cbs 118893	1	1
Trichophyton equinum cbs 127 97	1	1
Trichophyton interdigitale mr816	1	1
Trichophyton interdigitale h6	1	1
Trichophyton rubrum mr850	1	1
Trichophyton rubrum mr1459	1	1
Trichophyton rubrum mr1448	1	1
Trichophyton rubrum d6	1	1
Trichophyton rubrum cbs 735 88	1	1
Trichophyton rubrum cbs 289 86	1	1
Trichophyton rubrum cbs 288 86	1	1
Trichophyton rubrum cbs 202 88	1	1
Trichophyton rubrum cbs 118892	1	1
Trichophyton rubrum cbs 100081	1	1

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Trichophyton soudanense cbs 452 61	1	1
Trichophyton tonsurans cbs 112818	1	1
Trichophyton verrucosum hki 0517	1	1
Uncinocarpus reesii 1704	1	1
Coccidioides immitis rs	1	1
Coccidioides immitis rmscc 3703	1	1
Coccidioides immitis rmscc 2394	1	1
Coccidioides immitis h538 4	1	1
Coccidioides posadasii str silveira	1	1
Coccidioides posadasii rmscc 3488	1	1
Coccidioides posadasii c735 delta sowgp	1	1
Paracoccidioides brasiliensis pb18	1	1
Paracoccidioides brasiliensis pb03	1	1
Paracoccidioides sp lutzii pb01	1	1
Blumeria graminis	1	0
Blumeria graminis f sp tritici 96224	1	0
Erysiphe necator	1	0
Marssonina brunnea f sp multigermtubi mb m1	1	0
Glarea lozoyensis atcc 20868	1	1
Glarea lozoyensis 74030	1	1
Phialocephala scopiformis	1	0
Botrytis cinerea	1	1
Botrytis cinerea t4	1	1
Botrytis cinerea bcdw1	1	1
Sclerotinia borealis f 4157	1	1
Sclerotinia sclerotiorum	1	1
Oidiodendron maius zn	1	1
Pseudogymnoascus destructans 20631 21	1	1
Pseudogymnoascus sp vkm f 4520 fw 2644	1	1
Pseudogymnoascus sp vkm f 4519 fw 2642	1	1
Pseudogymnoascus sp vkm f 4518 fw 2643	0	1
Pseudogymnoascus sp vkm f 4517 fw 2822	1	1
Pseudogymnoascus sp vkm f 4516 fw 969	1	1
Pseudogymnoascus sp vkm f 4515 fw 2607	1	1
Pseudogymnoascus sp vkm f 4514 fw 929	1	1
Pseudogymnoascus sp vkm f 4513 fw 928	1	1
Pseudogymnoascus sp vkm f 4281 fw 2241	1	1
Pseudogymnoascus sp vkm f 4246	1	1
Pseudogymnoascus sp vkm f 3808	1	1
Pseudogymnoascus sp vkm f 3557	1	1
Pseudogymnoascus sp vkm f 103	1	1
Colletotrichum fioriniae pj7	1	1
Colletotrichum gloeosporioides	1	1
Colletotrichum gloeosporioides cg 14	1	1

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<i>Colletotrichum graminicola</i>	1	1
<i>Colletotrichum nymphaeae</i> sa 01	1	1
<i>Colletotrichum orbiculare</i>	1	1
<i>Colletotrichum higginsianum</i>	1	1
<i>Colletotrichum incanum</i>	1	1
<i>Colletotrichum salicis</i>	1	1
<i>Colletotrichum simmondsii</i>	1	1
<i>Colletotrichum sublineola</i>	1	1
<i>Colletotrichum tofieldiae</i>	1	1
<i>Verticillium alfalfae</i> vams 102	1	1
<i>Verticillium dahliae</i>	1	1
<i>Verticillium dahliae</i> jr2	1	1
<i>Verticillium longisporum</i>	1	1
<i>Verticillium longisporum</i> gca 001268165	1	1
<i>Metarhizium acridum</i> cqma 102	1	1
<i>Metarhizium album</i> arsef 1941	1	1
<i>Metarhizium anisopliae</i>	1	1
<i>Metarhizium anisopliae</i> brip 53293	1	1
<i>Metarhizium anisopliae</i> brip 53284	1	1
<i>Metarhizium anisopliae</i> arsef 549	1	1
<i>Metarhizium brunneum</i> arsef 3297	1	1
<i>Metarhizium guizhouense</i> arsef 977	1	1
<i>Metarhizium majus</i> arsef 297	1	1
<i>Metarhizium anisopliae</i> arsef 23	1	1
<i>Metarhizium robertsii</i>	1	1
<i>Torrubiella hemipterigena</i>	1	1
<i>Beauveria bassiana</i> d1 5	1	1
<i>Beauveria bassiana</i> arsef 2860	1	1
<i>Cordyceps militaris</i> cm01	1	1
<i>Trichoderma atroviride</i> imi 206040	1	1
<i>Trichoderma reesei</i>	1	1
<i>Trichoderma reesei</i> rut c 30	1	1
<i>Trichoderma virens</i>	1	1
<i>Trichoderma gamsii</i>	1	1
<i>Trichoderma harzianum</i>	1	1
<i>Acremonium chrysogenum</i> atcc 11550	1	1
<i>Ustilaginoidea virens</i>	1	1
<i>Fusarium verticillioides</i>	1	1
<i>Fusarium oxysporum</i>	1	1
<i>Fusarium oxysporum</i> fosc 3 a	1	1
<i>Fusarium oxysporum</i> fo47	1	1
<i>Fusarium oxysporum</i> f sp vasinfectum 25433	1	1
<i>Fusarium oxysporum</i> f sp raphani 54005	1	1
<i>Fusarium oxysporum</i> f sp radicis lycopersici 2638	1	1

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<i>Fusarium oxysporum</i> f sp pisi hdv247	1	1
<i>Fusarium oxysporum</i> f sp melonis 26406	1	1
<i>Fusarium oxysporum</i> f sp lycopersici mn25	1	1
<i>Fusarium oxysporum</i> f sp cubense tropical race 4	1	1
<i>Fusarium oxysporum</i> f sp conglutinans race 2 54	1	1
<i>Fusarium oxysporum</i> f sp cubense race 4	1	1
<i>Fusarium oxysporum</i> f sp cubense race 1	1	1
<i>Fusarium pseudograminearum</i>	1	1
<i>Fusarium solani</i>	1	1
<i>Fusarium fujikuroi</i>	1	1
<i>Fusarium fujikuroi</i> gca 001023065	1	1
<i>Fusarium fujikuroi</i> gca 001023045	1	1
<i>Fusarium fujikuroi</i> gca 001023035	1	1
<i>Fusarium graminearum</i>	1	1
<i>Fusarium graminearum</i> gca 000599445	1	1
<i>Fusarium langsethiae</i>	1	1
<i>Neonectria ditissima</i>	1	1
<i>Drechmeria coniospora</i>	1	1
<i>Hirsutella minnesotensis</i> 3608	1	1
<i>Ophiocordyceps sinensis</i> co18	1	1
<i>Ophiocordyceps unilateralis</i>	1	1
<i>Tolypocladium ophioglossoides</i> cbs 100239	1	1
<i>Stachybotrys chartarum</i> ibt 7711	1	1
<i>Stachybotrys chartarum</i> ibt 40293	1	1
<i>Stachybotrys chartarum</i> ibt 40288	1	1
<i>Stachybotrys chlorohalonata</i> ibt 40285	1	1
<i>Ceratocystis platani</i>	1	0
<i>Thielaviopsis punctulata</i>	1	1
<i>Diaporthe ampelina</i>	1	1
<i>Gaeumannomyces graminis</i>	1	1
<i>Magnaporthe oryzae</i>	1	1
<i>Magnaporthe poae</i>	1	1
<i>Grosmannia clavigera</i> kw1407	1	1
<i>Ophiostoma piceae</i> uamh 11346	1	1
<i>Sporothrix brasiliensis</i> 5110	1	1
<i>Sporothrix schenckii</i> atcc 58251	1	1
<i>Sporothrix schenckii</i> 1099 18	1	1
<i>Chaetomium thermophilum</i> var <i>thermophilum</i> d	1	1
<i>Chaetomium globosum</i> cbs 148 51	1	1
<i>Myceliophthora thermophila</i> atcc 42464	1	1
<i>Thielavia terrestris</i> nr1 8126	1	1
<i>Podospora anserina</i> s mat	1	1
<i>Neurospora crassa</i> gca 000786625	1	1
<i>Neurospora tetrasperma</i> fgsc 2509	1	1

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<i>Neurospora tetrasperma</i> fgsc 2508	1	1
<i>Neurospora crassa</i>	1	1
<i>Sordaria macrospora</i>	1	1
<i>Madurella mycetomatis</i>	1	1
<i>Phaeoacremonium minimum</i> ucrpa7	1	1
<i>Eutypa lata</i> ucrel1	1	1
<i>Microdochium bolleyi</i>	1	1
<i>Pestalotiopsis fici</i> w106 1	1	1
<i>Rosellinia necatrix</i>	1	1
<i>Xylona heveae</i> tc161	1	1
<i>Dactylellina haptotyla</i> cbs 200 50	1	1
<i>Drechslerella stenobrocha</i> 248	0	0
<i>Arthrobotrys oligospora</i> atcc 24927	1	1
<i>Pyronema omphalodes</i> cbs 100304	1	1
<i>Tuber melanosporum</i>	1	1
<i>Candida albicans</i> wo 1	0	0
<i>Candida albicans</i> sc5314	0	0
<i>Candida albicans</i> sc5314 gca 000784655	0	0
<i>Candida albicans</i> sc5314 gca 000784635	0	0
<i>Candida albicans</i> p94015	0	0
<i>Candida albicans</i> p87	0	0
<i>Candida albicans</i> p78048	0	0
<i>Candida albicans</i> p78042	0	0
<i>Candida albicans</i> p76067	0	0
<i>Candida albicans</i> p76055	0	0
<i>Candida albicans</i> p75063	0	0
<i>Candida albicans</i> p75016	0	0
<i>Candida albicans</i> p75010	0	0
<i>Candida albicans</i> p60002	0	0
<i>Candida albicans</i> p57072	0	0
<i>Candida albicans</i> p57055	0	0
<i>Candida albicans</i> p37039	0	0
<i>Candida albicans</i> p37037	0	0
<i>Candida albicans</i> p37005	0	0
<i>Candida albicans</i> p34048	0	0
<i>Candida albicans</i> l26	0	0
<i>Candida albicans</i> gc75	0	0
<i>Candida albicans</i> ca6	0	0
<i>Candida albicans</i> 19f	0	0
<i>Candida albicans</i> 12c	0	0
<i>Candida dubliniensis</i> cd36	0	0
<i>Candida maltosa</i> xu316	0	0
<i>Candida orthopsilosis</i> co 90 125	0	0
<i>Candida tropicalis</i> mya 3404	0	0

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<i>Candida parapsilosis</i> cdc317	0	0
<i>Lodderomyces elongisporus</i> nrri yb 4239	0	0
<i>Debaryomyces hansenii</i> cbs767	1	0
<i>Debaryomyces fabryi</i>	0	0
<i>Meyerozyma guilliermondii</i> atcc 6260	1	0
<i>Millerozyma farinosa</i> cbs 7064	0	0
<i>Scheffersomyces stipitis</i> cbs 6054	0	0
<i>Spathaspora passalidarum</i> nrri y 27907	0	0
<i>Candida tenuis</i> atcc 10573	0	0
<i>Geotrichum candidum</i>	1	0
<i>Yarrowia lipolytica</i>	1	0
<i>Candida auris</i>	0	0
<i>Clavispora lusitaniae</i> atcc 42720	0	0
<i>Cyberlindnera jadinii</i>	1	0
<i>Komagataella pastoris</i>	1	0
<i>Komagataella pastoris</i> cbs 7435	1	0
<i>Wickerhamomyces ciferrii</i>	1	0
<i>Brettanomyces bruxellensis</i> awri1499	0	0
<i>Ogataea parapolyomorpha</i> dl 1	1	0
<i>Pichia kudriavzevii</i>	1	0
<i>Ashbya gossypii</i>	0	0
<i>Ashbya gossypii</i> fdag1	0	0
<i>Eremothecium sinicaudum</i>	0	0
<i>Kazachstania africana</i> cbs 2517	0	0
<i>Kazachstania naganishii</i> cbs 8797	0	0
<i>Kluyveromyces marxianus</i>	0	0
<i>Kluyveromyces lactis</i>	0	0
<i>Kluyveromyces marxianus</i> dmku3 1042	0	0
<i>Lachancea thermotolerans</i> cbs 6340	1	0
<i>Lachancea lanzarotensis</i>	1	0
<i>Candida glabrata</i>	0	0
<i>Candida glabrata</i> gca 001466685	0	0
<i>Candida glabrata</i> gca 001466635	0	0
<i>Candida glabrata</i> gca 001466575	0	0
<i>Candida glabrata</i> gca 001466565	0	0
<i>Candida glabrata</i> gca 001466535	0	0
<i>Candida glabrata</i> gca 001466525	0	0
<i>Naumovozyma castellii</i> cbs 4309	0	0
<i>Naumovozyma dairenensis</i> cbs 421	0	0
<i>Saccharomyces arboricola</i> h 6	0	0
<i>Saccharomyces cerevisiae</i>	0	0
<i>Saccharomyces cerevisiae</i> yjm996	0	0
<i>Saccharomyces cerevisiae</i> yjm993	0	0
<i>Saccharomyces cerevisiae</i> yjm990	0	0

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Saccharomyces cerevisiae yjm987	0	0
Saccharomyces cerevisiae yjm984	0	0
Saccharomyces cerevisiae yjm981	0	0
Saccharomyces cerevisiae yjm978	0	0
Saccharomyces cerevisiae yjm975	0	0
Saccharomyces cerevisiae yjm972	0	0
Saccharomyces cerevisiae yjm969	0	0
Saccharomyces cerevisiae yjm789	0	0
Saccharomyces cerevisiae yjm693	0	0
Saccharomyces cerevisiae yjm689	0	0
Saccharomyces cerevisiae yjm683	0	0
Saccharomyces cerevisiae yjm682	0	0
Saccharomyces cerevisiae yjm681	0	0
Saccharomyces cerevisiae yjm627	0	0
Saccharomyces cerevisiae yjm555	0	0
Saccharomyces cerevisiae yjm554	0	0
Saccharomyces cerevisiae yjm541	0	0
Saccharomyces cerevisiae yjm470	0	0
Saccharomyces cerevisiae yjm456	0	0
Saccharomyces cerevisiae yjm453	0	0
Saccharomyces cerevisiae yjm451	0	0
Saccharomyces cerevisiae yjm450	0	0
Saccharomyces cerevisiae yjm428	0	0
Saccharomyces cerevisiae yjm326	0	0
Saccharomyces cerevisiae yjm320	0	0
Saccharomyces cerevisiae yjm271	0	0
Saccharomyces cerevisiae yjm270	0	0
Saccharomyces cerevisiae yjm248	0	0
Saccharomyces cerevisiae yjm244	0	0
Saccharomyces cerevisiae yjm195	0	0
Saccharomyces cerevisiae yjm193	0	0
Saccharomyces cerevisiae yjm189	0	0
Saccharomyces cerevisiae yjm1615	0	0
Saccharomyces cerevisiae yjm1592	0	0
Saccharomyces cerevisiae yjm1574	0	0
Saccharomyces cerevisiae yjm1573	0	0
Saccharomyces cerevisiae yjm1549	0	0
Saccharomyces cerevisiae yjm1527	0	0
Saccharomyces cerevisiae yjm1526	0	0
Saccharomyces cerevisiae yjm1479	0	0
Saccharomyces cerevisiae yjm1478	0	0
Saccharomyces cerevisiae yjm1477	0	0
Saccharomyces cerevisiae yjm1463	0	0
Saccharomyces cerevisiae yjm1460	0	0

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

<i>Saccharomyces cerevisiae</i> yjm1450	0	0
<i>Saccharomyces cerevisiae</i> yjm1447	0	0
<i>Saccharomyces cerevisiae</i> yjm1444	0	0
<i>Saccharomyces cerevisiae</i> yjm1443	0	0
<i>Saccharomyces cerevisiae</i> yjm1439	0	0
<i>Saccharomyces cerevisiae</i> yjm1434	0	0
<i>Saccharomyces cerevisiae</i> yjm1433	0	0
<i>Saccharomyces cerevisiae</i> yjm1419	0	0
<i>Saccharomyces cerevisiae</i> yjm1418	0	0
<i>Saccharomyces cerevisiae</i> yjm1417	0	0
<i>Saccharomyces cerevisiae</i> yjm1415	0	0
<i>Saccharomyces cerevisiae</i> yjm1402	0	0
<i>Saccharomyces cerevisiae</i> yjm1401	0	0
<i>Saccharomyces cerevisiae</i> yjm1400	0	0
<i>Saccharomyces cerevisiae</i> yjm1399	0	0
<i>Saccharomyces cerevisiae</i> yjm1389	0	0
<i>Saccharomyces cerevisiae</i> yjm1388	0	0
<i>Saccharomyces cerevisiae</i> yjm1387	0	0
<i>Saccharomyces cerevisiae</i> yjm1386	0	0
<i>Saccharomyces cerevisiae</i> yjm1385	0	0
<i>Saccharomyces cerevisiae</i> yjm1383	0	0
<i>Saccharomyces cerevisiae</i> yjm1381	0	0
<i>Saccharomyces cerevisiae</i> yjm1356	0	0
<i>Saccharomyces cerevisiae</i> yjm1355	0	0
<i>Saccharomyces cerevisiae</i> yjm1342	0	0
<i>Saccharomyces cerevisiae</i> yjm1341	0	0
<i>Saccharomyces cerevisiae</i> yjm1338	0	0
<i>Saccharomyces cerevisiae</i> yjm1336	0	0
<i>Saccharomyces cerevisiae</i> yjm1332	0	0
<i>Saccharomyces cerevisiae</i> yjm1326	0	0
<i>Saccharomyces cerevisiae</i> yjm1311	0	0
<i>Saccharomyces cerevisiae</i> yjm1307	0	0
<i>Saccharomyces cerevisiae</i> yjm1304	0	0
<i>Saccharomyces cerevisiae</i> yjm1273	0	0
<i>Saccharomyces cerevisiae</i> yjm1252	0	0
<i>Saccharomyces cerevisiae</i> yjm1250	0	0
<i>Saccharomyces cerevisiae</i> yjm1248	0	0
<i>Saccharomyces cerevisiae</i> yjm1244	0	0
<i>Saccharomyces cerevisiae</i> yjm1242	0	0
<i>Saccharomyces cerevisiae</i> yjm1208	0	0
<i>Saccharomyces cerevisiae</i> yjm1202	0	0
<i>Saccharomyces cerevisiae</i> yjm1199	0	0
<i>Saccharomyces cerevisiae</i> yjm1190	0	0
<i>Saccharomyces cerevisiae</i> yjm1133	0	0

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

<i>Saccharomyces cerevisiae</i> yjm1129	0	0
<i>Saccharomyces cerevisiae</i> yjm1083	0	0
<i>Saccharomyces cerevisiae</i> yjm1078	0	0
<i>Saccharomyces cerevisiae</i> x <i>saccharomyces kudr</i>	0	0
<i>Saccharomyces cerevisiae</i> vl3	0	0
<i>Saccharomyces cerevisiae</i> vin13	0	0
<i>Saccharomyces cerevisiae</i> rm11 1a	0	0
<i>Saccharomyces cerevisiae</i> r103	0	0
<i>Saccharomyces cerevisiae</i> r008	0	0
<i>Saccharomyces cerevisiae</i> p301	0	0
<i>Saccharomyces cerevisiae</i> p283	0	0
<i>Saccharomyces cerevisiae</i> lalvin qa23	0	0
<i>Saccharomyces cerevisiae</i> kyokai no 7	0	0
<i>Saccharomyces cerevisiae</i> gca 000091065	0	0
<i>Saccharomyces cerevisiae</i> fosterso	0	0
<i>Saccharomyces cerevisiae</i> fostersb	0	0
<i>Saccharomyces cerevisiae</i> ec1118	0	0
<i>Saccharomyces cerevisiae</i> awri796	0	0
<i>Saccharomyces kudriavzevii</i> ifo 1802	0	0
<i>Saccharomyces cerevisiae</i> cen pk113 7d	0	0
<i>Saccharomyces eubayanus</i>	0	0
<i>Saccharomyces</i> sp <i>boulardii</i> gca 001413975	0	0
<i>Saccharomyces</i> sp <i>boulardii</i>	0	0
<i>Saccharomycetaceae</i> sp <i>ashbya aceri</i>	0	0
<i>Tetrapisispora blattae</i> cbs 6284	0	0
<i>Tetrapisispora phaffii</i> cbs 4417	0	0
<i>Torulaspora delbrueckii</i>	0	0
<i>Vanderwaltozyma polyspora</i> dsm 70294	0	0
<i>Zygosaccharomyces bailii</i> isa1307	1	0
<i>Zygosaccharomyces rouxii</i>	1	0
<i>Kuraishia capsulata</i> cbs 1993	1	0
<i>Hanseniaspora uvarum</i> dsm 2768	0	0
<i>Pneumocystis carinii</i> b80	0	0
<i>Pneumocystis jirovecii</i> ru7	0	0
<i>Schizosaccharomyces cryophilus</i>	0	0
<i>Schizosaccharomyces japonicus</i>	0	0
<i>Schizosaccharomyces octosporus</i>	0	0
<i>Schizosaccharomyces pombe</i>	0	0
<i>Saitoella complicata</i> nr1 y 17804	1	1
<i>Botryobasidium botryosum</i> fd 172 ss1	1	1
<i>Rhizoctonia solani</i> ag 8 wac10335	1	1
<i>Rhizoctonia solani</i> ag 1 ia	1	1
<i>Rhizoctonia solani</i> ag 3 rhs1ap	1	1
<i>Rhizoctonia solani</i> ag 1 ib	1	1

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

<i>Rhizoctonia solani</i> 123e	1	1
<i>Tulasnella calospora</i> mut 4182	1	1
<i>Cylindrobasidium torrendii</i> fp15055 ss 10	1	1
<i>Schizopora paradoxa</i>	1	1
<i>Punctularia strigosozonata</i> hhb 11173 ss5	0	0
<i>Gloeophyllum trabeum</i> atcc 11539	1	1
<i>Fomitiporia mediterranea</i> mf3 22	1	1
<i>Gelatoporia subvermispora</i> b	1	1
<i>Postia placenta</i> mad 698 r	0	1
<i>Trametes versicolor</i> fp 101664 ss1	0	0
<i>Trametes cinnabarina</i>	1	1
<i>Fomitopsis pinicola</i> fp 58527 ss1	1	1
<i>Phanerochaete carnosae</i> hhb 10118 sp	1	1
<i>Phlebiopsis gigantea</i> 11061 1 cr5 6	1	1
<i>Dichomitus squalens</i> lyad 421 ss1	1	0
<i>Fibroporia radiculosa</i>	1	1
<i>Heterobasidion irregulare</i> tc 32 1	1	1
<i>Stereum hirsutum</i> fp 91666 ss1	0	0
<i>Piriformospora indica</i> dsm 11827	1	1
<i>Serendipita vermifera</i> maff 305830	1	1
<i>Agaricus bisporus</i> var <i>burnettii</i> jb137 s8	1	1
<i>Agaricus bisporus</i> var <i>bisporus</i> h97	1	1
<i>Leucoagaricus</i> sp symc cos	1	1
<i>Plicaturopsis crispa</i> fd 325 ss 3	1	0
<i>Amanita muscaria</i> koide bx008	1	1
<i>Hebeloma cylindrosporum</i> h7	1	1
<i>Fistulina hepatica</i> atcc 64428	1	1
<i>Hypsizygus marmoreus</i>	1	1
<i>Termitomyces</i> sp j132	1	1
<i>Moniliophthora perniciosa</i> fa553	1	1
<i>Moniliophthora roreri</i>	1	1
<i>Moniliophthora roreri</i> mca 2997	1	1
<i>Gymnopus luxurians</i> fd 317 m1	1	1
<i>Pleurotus ostreatus</i> pc15	1	1
<i>Schizophyllum commune</i> h4 8	1	1
<i>Galerina marginata</i> cbs 339 88	1	1
<i>Hypholoma sublateritium</i> fd 334 ss 4	1	1
<i>Laccaria amethystina</i> laam 08 1	1	1
<i>Laccaria bicolor</i> s238n h82	1	1
<i>Fibulorhizoctonia</i> sp cbs 109695	1	1
<i>Piloderma croceum</i> f 1598	1	1
<i>Coniophora puteana</i> rwd 64 598 ss2	1	1
<i>Serpula lacrymans</i> var <i>lacrymans</i> s7 9	1	1
<i>Serpula lacrymans</i> var <i>lacrymans</i> s7 3	1	1

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

Hydnomerulius pinastri md 312	1	1
Paxillus involutus atcc 200175	1	1
Paxillus rubicundulus ve08 2h10	1	1
Pisolithus microcarpus 441	1	1
Pisolithus tinctorius marx 270	1	1
Scleroderma citrinum foug a	1	1
Suillus luteus uh slu lm8 n1	1	1
Jaapia argillacea mucl 33604	1	1
Sphaerobolus stellatus ss14	1	1
Dacryopinax sp djm 731 ss1	1	1
Xanthophyllomyces dendrorhous	0	0
Cryptococcus gattii wm276	1	0
Cryptococcus gattii ru294	1	0
Cryptococcus gattii ram5	0	0
Cryptococcus gattii r265	0	0
Cryptococcus gattii nt 10	1	0
Cryptococcus gattii mmrl2647	0	0
Cryptococcus gattii la55	0	0
Cryptococcus gattii ind107	1	0
Cryptococcus gattii ejb2	1	0
Cryptococcus gattii e566	1	0
Cryptococcus gattii cbs 10090	0	0
Cryptococcus gattii ca1873	1	0
Cryptococcus gattii ca1280	1	0
Cryptococcus gattii ca1014	0	0
Cryptococcus gattii 99 473	0	0
Cryptococcus gattii 2001 935 1	0	0
Cryptococcus neoformans	0	0
Cryptococcus neoformans var neoformans b 350	1	0
Cryptococcus neoformans var grubii h99	0	0
Tremella mesenterica dsm 1558	0	0
Trichosporon asahii var asahii cbs 8904	1	1
Trichosporon asahii var asahii cbs 2479	1	1
Trichosporon oleaginosus	1	1
Wallemia ichthyophaga exf 994	0	0
Wallemia mellicola cbs 633 66	1	0
Rhodotorula sp jg 1b	1	1
Microbotryum violaceum	1	1
Rhodotorula glutinis atcc 204091	1	0
Rhodotorula graminis wp1	1	0
Rhodotorula toruloides	1	1
Rhodotorula toruloides np11	1	1
Sporidiobolus salmonicolor	1	0
Mixia osmundae iam 14324	1	0

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

Mixia osmundae iam 14324 gca 000708205	1	0
Melampsora laricipopulina	1	1
Puccinia graminis	1	1
Puccinia graminisug99	1	1
Puccinia striiformis f sp tritici pst 78	1	1
Puccinia triticina	0	1
Puccinia sorghi	1	1
Ceraceosorus bombacis	1	1
Tilletiaria anomala ubc 951	1	0
Malassezia sympodialis atcc 42132	1	1
Malassezia pachydermatis	0	0
Anthracozytis flocculosa pf 1	0	1
Kalmanozyma brasiliensis ghg001	1	1
Moesziomyces aphidis dsm 70725	1	1
Moesziomyces antarcticus	0	1
Pseudozyma hubeiensis sy62	1	0
Sporisorium reilianum	1	1
Sporisorium scitamineum	0	0
Ustilago maydis	1	0
Ustilago hordei	1	1
Conidiobolus coronatus nrri 28638	0	1
Mortierella verticillata nrri 6337	1	1
Lichtheimia corymbifera jmrc fsu 9682	0	1
Lichtheimia ramosa	0	1
Mucor circinelloides f circinelloides 1006phl	0	0
Mucor ambiguus	0	0
Parasitella parasitica	0	0
Rhizopus delemar ra 99 880	0	0
Rhizophagus irregularis daom 197198w	1	1
Rhizophagus irregularis daom 181602	1	1
Enterocytozoon bieneusi h348	0	0
Nosema apis brl 01	0	0
Nosema bombycis cq1	0	0
Nosema ceranae	0	0
Nosema ceranae brl01	0	0
Vittaforma corneae atcc 50505	0	0
Spraguea lophii 42 110	0	0
Anncaliia algerae pra339	0	0
Anncaliia algerae pra109	0	0
Encephalitozoon cuniculi gb m1	0	0
Encephalitozoon cuniculi ecuniii l	0	0
Encephalitozoon intestinalis atcc 50506	0	0
Edhazardia aedis usnm 41457	0	0
Mitosporidium daphniae	0	0

Supplementary Table 8: DNMTs and ALKB2/3 in Fungi

Nematocida parisii ertm3	0	0
Nematocida parisii ertm1	0	0
Nematocida sp 1 ertm6	0	0
Nematocida sp 1 ertm2	0	0
Ordospora colligata oc4	0	0
Pseudoloma neurophilia	0	0
Trachipleistophora hominis	0	0
Vavraia culicis subsp floridensis	0	0

Supplemental Table 9: ALKB2/3 in insects

	ALKB2
<i>Blattella germanica</i>	1
<i>Nicrophorus vespilloides</i>	0
<i>Tribolium castaneum</i>	1
<i>Aedes aegypti</i>	0
<i>Aedes albopictus</i>	0
<i>Anopheles gambiae str. PEST</i>	0
<i>Culex quinquefasciatus</i>	0
<i>Drosophila melanogaster</i>	0
<i>Acyrtosiphon pisum</i>	1
<i>Apis mellifera</i>	0
<i>Camponotus floridanus</i>	0
<i>Copidosoma floridanum</i>	0
<i>Harpegnathos saltator</i>	0
<i>Microplitis demolitor</i>	0
<i>Nasonia vitripennis</i>	0
<i>Polistes canadensis</i>	0
<i>Solenopsis invicta</i>	0
<i>Bombyx mori</i>	0
<i>Parhyale hawaiiensis</i>	1
<i>Daphnia pulex</i>	0
<i>Daphnia magna</i>	0
<i>Schistocerca gregaria</i>	1

***Plectus sambesii* assembly methods: Supplementary Note 1**

We acquired ~250M 150bp paired-end genome sequencing read pairs with 550bp insert size through Edinburgh Genomics. Quality control of the genome sequencing data was performed using Fastqc v0.10.1 (Andrews, 2010), and reads were quality trimmed using skewer v0.2.2 (Jiang et al., 2014) with parameters `-q 30 -l 51`. K-mer plots were generated with kmc, which revealed extensive heterozygosity. A preliminary single-end assembly was generated with Velvet (Zerbino and Birney, 2008) to screen for contaminants but no significant hits were found using Blobtools (Kumar et al., 2013; Laetsch, 2016). The dataset was digitally normalised to 40x coverage and assembly was carried out with SPAdes v3.5.1 (Bankevich et al., 2012) with parameters `--k 21,33,55,77,99 --cov-cutoff auto --careful`. Error correction of the sequencing reads was done with BayesHammer that runs as part of the SPAdes pipeline. Examination of the resulting distribution of contig coverages revealed a bimodal distribution of coverage indicating again heterozygosity. Haplocontigs were collapsed and postprocessed with Redundans (Pryszcz and Gabaldón, 2016), that runs SSPACE3 (Boetzer et al., 2011) and SOAPdenovo Gapcloser internally. The identity percentage for the collapse of redundant contigs was chosen to be of 90%, ensuring the presence of 95.97% of CEGMA KOGs (Parra et al., 2007). Lower identity percentage values did not result in an appreciable reduction of the span suggesting that most heterozygous regions are collapsed at that threshold. Blobplot analysis after postprocessing revealed ~20Mb of bacterial contaminant sequence at 60% GC and lower coverage than the nematode contigs, which we therefore excluded from the final assembly.

To annotate genes, we first masked repeats in the assembly. We used RepeatModeler v1.0.8 (Smit and Hubley, 2008) to generate a species-specific repeat library that was concatenated with a nematode repeat library extracted from RepBase RepeatMasker edition update 27-01-2017. The combined library was used to mask the genome with RepeatMasker v4.0.7 (Smit et al., 2013). To annotate the genome, we acquired ~100M RNA-seq reads from rRNA-depleted paired-end RNA-seq libraries generated in the LMS Genomics Facility. Quality control of the RNA-seq reads was performed with Fastqc and Skewer with parameters `-q 30 -l 50`. Spliced alignment of the reads to the masked assembly was done with STAR v2.5.2 (Dobin et al., 2013) with default parameters except for `--twopassMode Basic`. RNA-seq alignments were used for automated HMM training and annotation using BRAKER v1.9 (Hoff et al., 2016) with parameters `--softmasking 1 --UTR off --gff3`, running internally GeneMark-ET v4.21 (Lomsadze et al., 2014) and augustus v2.3.2 (Stanke and Morgenstern, 2005).

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Supplementary Note 2: Phylogeny References

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Supplementary Note 3: sample numbers for genome-wide comparisons

CGs covered by >10 reads used for significance testing in Figure 1c

Plectus sambesii

gene 1230239

rRNA 1193

LTR 7069

DNA 1599

unannotated 727548

Romanomermis culicivorax

gene 656710

rRNA 561

LTR 4897

DNA 1830

unannotated 124399

Trichuris muris

gene 2115909

rRNA 3183

LTR 79067

DNA 51875

unannotated 1247125

Trichinella spiralis

gene 738591

rRNA 291

LTR 21480

DNA 3540

unannotated 193453

Caenorhabditis briggsae

gene 82526

rRNA 708

LTR 590

DNA 3725

unannotated 59570

Nippostrongylus brasiliensis

Gene 20765

rRNA 926

DNA 1199

LTR 2879

unannotated 12940

Analysed genomes: number of genome-wide Cs and CGs

P. sambesii

total_C	29615596
total_CG	7728644
total_CGA	2355653
total_CGC	2169535
total_CGG	1402387
total_CGT	1793453

R. culicivora

total_C	48473942
total_CG	7829396
total_CGA	2785794
total_CGC	1457635
total_CGG	1529381
total_CGT	2050824

T. spiralis

total_C	9943967
total_CG	1710706
total_CGA	539942
total_CGC	348898
total_CGG	309852
total_CGT	511933

T. muris

total_C	18839135
total_CG	4505970
total_CGA	1184822
total_CGC	1125042
total_CGG	921658
total_CGT	1274273

N. brasiliensis

total_C	58220992
total_CG	12740122
total_CGA	4131434
total_CGC	2803568
total_CGG	2582339
total_CGT	3221088

C. briggsae

total_C	19684666
total_CG	3455622
total_CGA	1266130
total_CGC	588973
total_CGG	765446
total_CGT	834762

B. mori
total_C 79039767
total_CG 16946963
total_CGA 4852595
total_CGC 3693029
total_CGG 3551168
total_CGT 4848034

M. musculus
total_C 38179275
total_CG 1428189
total_CGA 354635
total_CGC 299758
total_CGG 374931
total_CGT 398865

Analysed genomes: CGs within ± 1000 bp of TSS with sufficient coverage to estimate methylation (see Supplemental Figure 3)

P. sambesii 2002411
R. culicivora 6231622
T. spiralis 1055855
T. muris 1632567

CGs in 1st exon vs introns analysed (Supplemental Figure 3)

P. sambesii 480833e,4352323i
R. culicivora 2506380e,5629056i
T. spiralis 502608e,1992647i
T. muris 287818e,2699672i

total number of genes analysed with DNA methylation coverage for repeat homology (Supplemental Figure 2)

P. sambesii 38467
R. culicivora 43622
T. spiralis 12913
T. muris 10932