

Supporting Information

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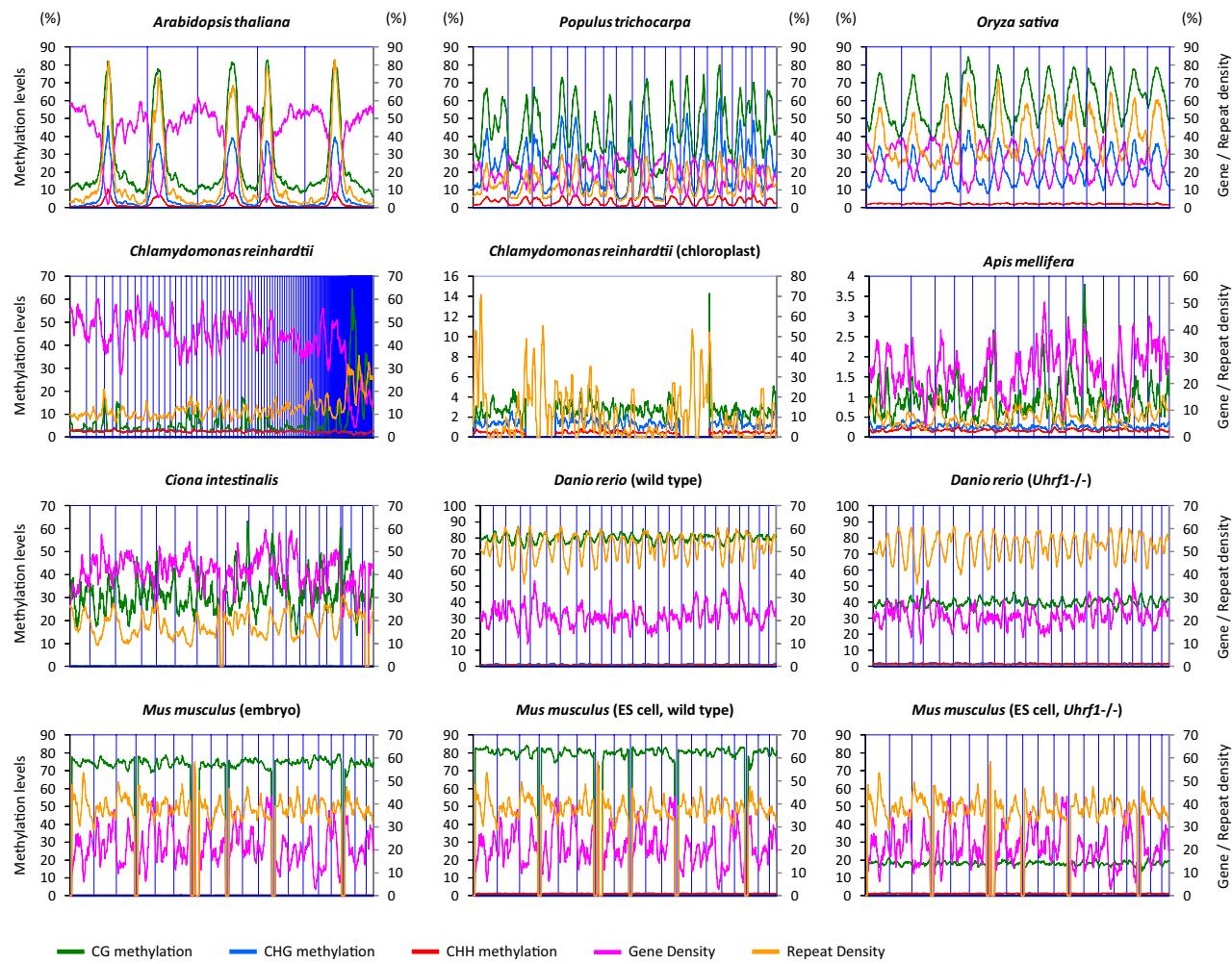


Fig. S1. Genome-wide distribution of methylation and correlation with genes and repeats in eight eukaryotic organisms. The x axis is divided into 1,000 bins, and the y axis indicates the running average of respective values in ± 5 consecutive bins. Data shown here are collected from the main chromosomes/linkage groups/scaffolds of each organism, unless labeled otherwise (Tables S1 and S2). Vertical blue lines mark boundaries of chromosomes/linkage groups/scaffolds. Gene and repeat density are the percentage of gene (earliest transcription start to latest transcription stop) and repetitive sequence in a given bin, respectively. Tissues are the same as in Fig. 1, unless labeled otherwise. Chlamydomonas methylation is high in short scaffolds (toward the right-hand side of its panel), coinciding with genome sequencing and assembly problems (Fig. S2), similar to what occurs with scaffolds in poplar (Fig. S2 and Fig. 1 legends).

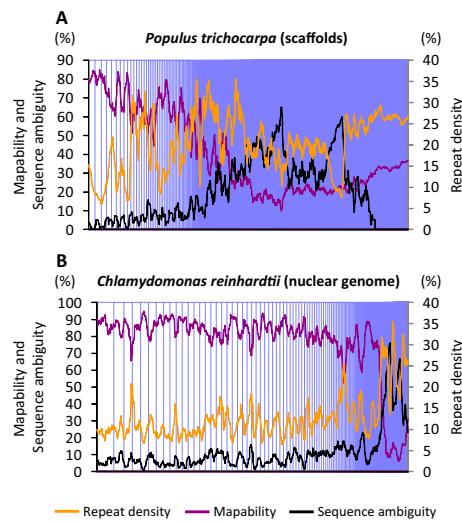


Fig. S2. Repeat density, mapability, and sequence ambiguity in poplar scaffolds not placed on any linkage group (*A*) and in *Chlamydomonas* main scaffolds (*B*). The x axis is divided into 1,000 bins, and the y axis indicates the running average of respective values in ± 5 consecutive bins. Vertical blue lines mark boundaries of scaffolds. Repeat density is the percentage of repetitive sequence in a given bin. Mapability is the fraction of genomic k-mers of the appropriate length starting within the bin that are uniquely BS mappable. Sequence ambiguity is the percentage of non-A/C/G/T nucleotides contained in the reference genome sequence in a given bin.

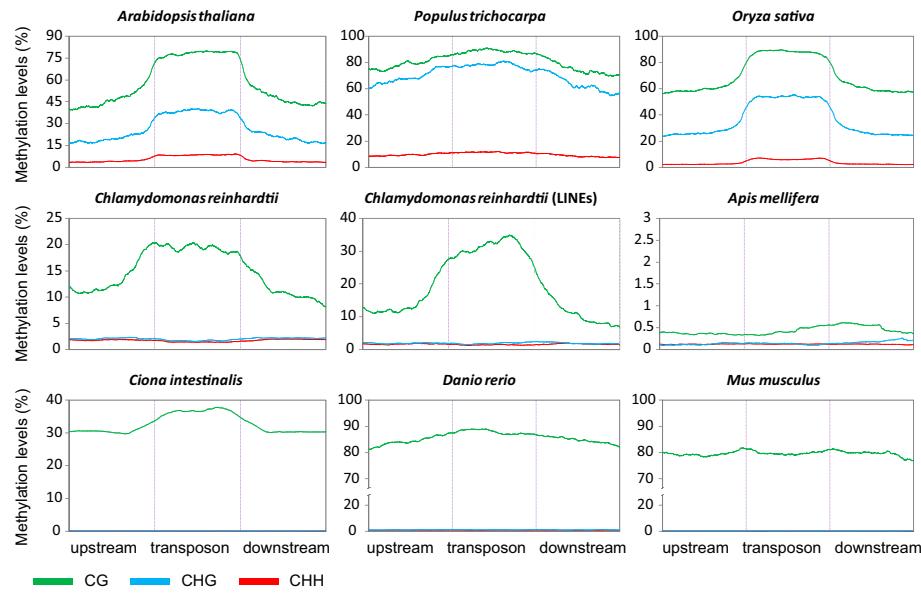


Fig. S3. Distribution of methylation along transposons. Upstream and downstream regions are the same length as the transposon. Only BS-Seq data up to halfway to the next nonoverlapping transposon are used in this analysis. Two vertical purple lines mark the repeat boundaries. The *Chlamydomonas* LINE elements are shown in addition to all transposons. Tissues are the same as in Fig. 1.



Fig. S4. Alignment of the catalytic domains of Arabidopsis CMT3 protein and its closest CMT homologs in rice, poplar, and Chlamydomonas. The methyltransferase catalytic motifs I, IV, VI, and VII-X (see markings along top) and the conserved amino acid residues (red asterisks) present in each motif are based on a previous report (1). Overall, the CMT proteins from flowering plants, Arabidopsis, rice, and poplar, are 100% conserved at these residues, whereas the candidate CMT protein from the green alga Chlamydomonas is more divergent. An initial alignment was obtained via ClustalW and the BOXSHADE functions within the Biology Workbench online application at the San Diego Supercomputer Center (<http://workbench.sdsc.edu>). Multiple alignment parameters were as follows: Gonnet Series with gap open penalty 10.00, gap extension penalty 0.20, and delay divergent sequences 30%. Alignment was inspected and modified manually for accuracy. Shading scheme is green for completely conserved, yellow for identical, and cyan for similar residues. Sequence accessions are: XP_002299134 (poplar), NP_177135 (Arabidopsis), NP_001049442 (rice), and XP_001693352 (Chlamydomonas).

1. Lindroth AM, et al. (2001) Requirement of CHROMOMETHYLASE3 for maintenance of CpXpG methylation. *Science* 292:2077–2080.

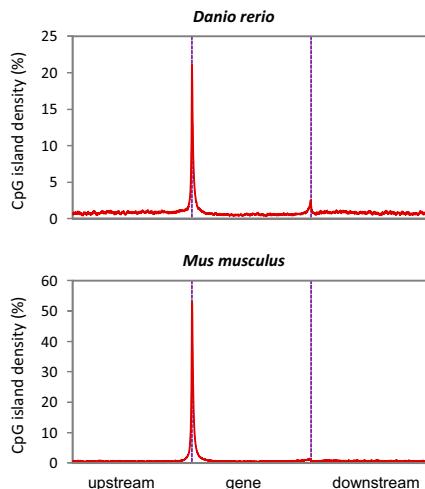


Fig. S5. CpG island density across genes in vertebrate animals. Upstream and downstream regions are the same length as the gene. Only CpG island density data up to half way to the next nonoverlapping gene are used in this analysis. Two vertical purple lines mark gene boundaries. The x axis is divided into 3,000 bins. CpG island density is the percentage of nucleotides in each bin that belong to CpG islands. CpG islands are defined using methods from a previous publication (1).

1. Irizarry RA, Wu H, Feinberg AP (2009) A species-generalized probabilistic model-based definition of CpG islands. *Mamm Genome* 20:674–680.

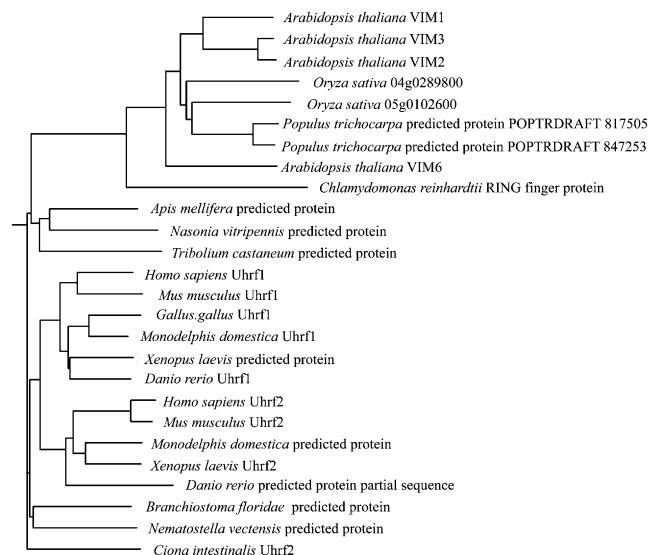


Fig. S6. Phylogenetic tree of candidate Uhrf proteins based on full-length sequences via ClustalW (EMBL-EBI; <http://www.ebi.ac.uk/Tools/clustalw2/index.html>) and DRAWGRAM (mobyl portal <http://mobyle.pasteur.fr/cgi-bin/portal.py?form=drawtree>). The multiple alignment parameters were as follows: Gonnet 250 matrix with gap open penalty 10, gap extension penalty 0.2, and gap separation penalty 4 sequences. For tree generation, gaps were excluded. No Uhrf homolog was identified in *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Caenorhabditis elegans*, or *Drosophila melanogaster*. Sequence accessions are as follows: *A. thaliana* VIM1: NP_176092.2; *A. thaliana* VIM3: NP_198771.1; *A. thaliana* VIM2: NP_176779.2; *O. sativa* 04g0289800: NP_001052387.1; *O. sativa* 05g0102600: NP_001054387.1; *P. trichocarpa* hypothetical protein: XP_002303746; *P. trichocarpa* hypothetical protein: XP_002299354; *A. thaliana* VIM6: NP_001078357; *C. reinhardtii* RING finger protein: XP_001703545; *A. mellifera* predicted: XM_001120707; *N. vitripennis* predicted: XM_001602155; *T. castaneum* predicted protein: XP_971012; *H. sapiens* Uhrf1: NP_001041666; *M. musculus* Uhrf1: NP_035061; *G. gallus* Uhrf1: XP_418269; *M. domestica* Uhrf1: XP_001365790; *X. laevis* hypothetical protein: NP_001129236; *D. rerio* Uhrf1: NP_998242; *H. sapiens* Uhrf2: NP_690856; *M. musculus* Uhrf2: NP_659122; *M. domestica*: hypothetical protein: XP_001365488; *X. laevis* Uhrf2: NP_001091384; *D. rerio* predicted partial: XP_001921120; *B. floridae* hypothetical protein: XP_002600554; *N. vectensis* predicted protein: XP_001632528; *C. intestinalis* Uhrf2: NP_001071846.

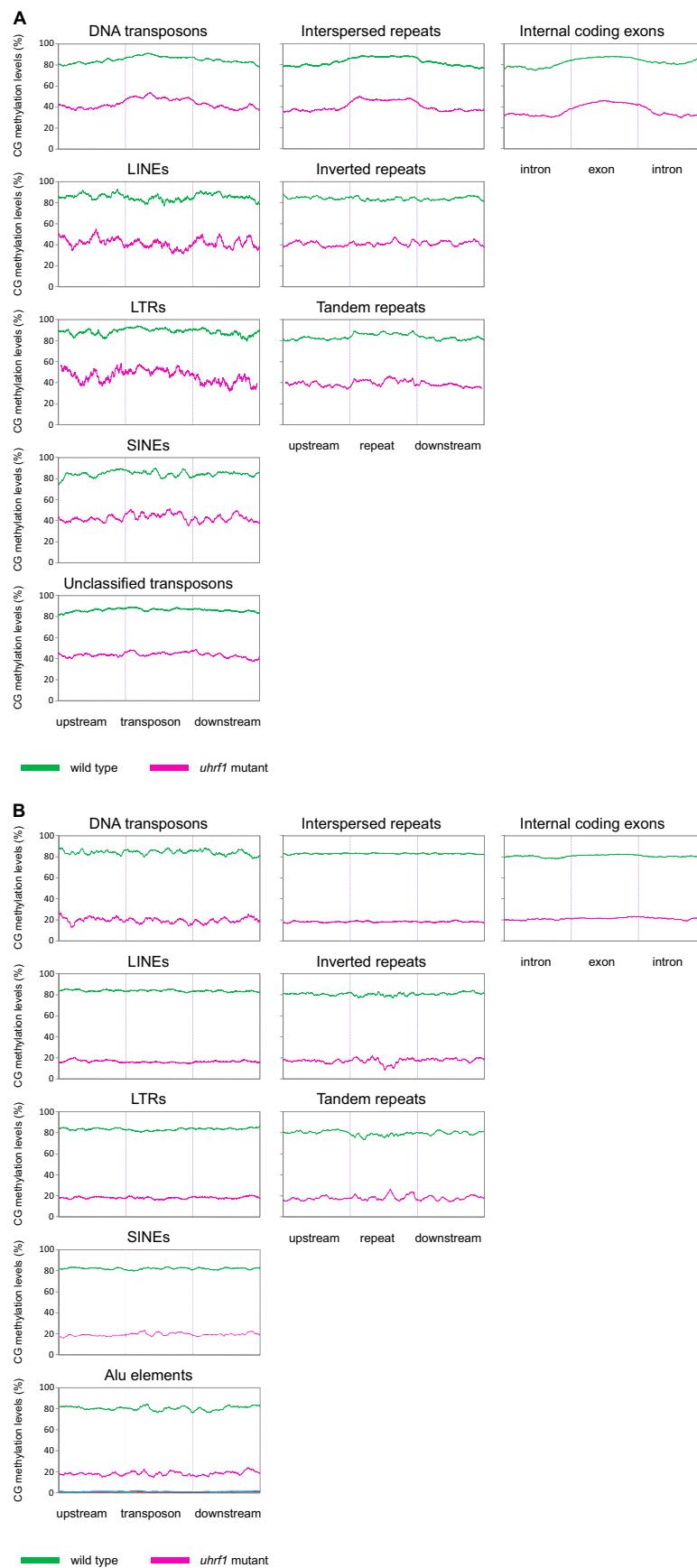


Fig. 57. UHRF1 is required for CG methylation. Distribution of methylation along various kinds of transposons and repeats, and across introns and exons, in zebrafish (A) and mouse (B). For transposons and repeats, upstream and downstream regions are the same length as the transposon/repeat. Only BS-Seq data

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up to half way to the next nonoverlapping transposon/repeat are used in this analysis. Two vertical purple lines mark repeat/transposon boundaries. For exons, only internal exons (flanked by introns on both ends) that do not contain any UTR bases are used. Upstream and downstream regions are the same length as the exon. Only BS-Seq data up to half way to the next exon are used in this analysis. Two vertical purple lines mark intron-exon and exon-intron boundaries. BS-Seq data annotated to at least one repeat and/or transposon are withheld from this analysis. Data from mouse ES cells and zebrafish embryos are shown here; classification of repeats and transposons are given in Table S3.

Table S1. Basic statistics of the eight genomes used in this study

	Bases	Fraction bases	Genome version
<i>Apis mellifera</i>			Baylor 2
Total	228,583,940	100%	
16 Linkage groups	159,353,786	69.70%	
7,199 Unassembled and unoriented contigs	69,213,811	30.30%	
Mitochondrion	16,343	71.5 ppm	
<i>Ciona intestinalis</i>			JGI 2.0
Total	173,514,784	100%	
20 Chromosomal arms	93,809,953	54.10%	
4,370 Scaffolds	79,690,041	45.90%	
Mitochondrion	14,790	85.2 ppm	
<i>Arabidopsis thaliana</i>			TIGR 5
Total	119,707,898	100%	
5 Chromosomes	119,186,497	99.60%	
Chloroplast	154,478	1,290 ppm	
Mitochondrion	366,923	3,065 ppm	
<i>Oryza sativa</i>			TIGR 5.0
Total	372,702,860	100%	
12 Chromosomes	372,077,813	99.80%	
Chloroplast	134,526	361 ppm	
Mitochondrion	490,521	1,316 ppm	
<i>Populus trichocarpa</i>			JGI 1.1
Total	486,471,694	100%	
19 Linkage groups	307,840,768	63.30%	
21,993 Scaffolds	177,670,143	36.50%	
Chloroplast	157,033	323 ppm	
Mitochondrion	803,750	1,652 ppm	
<i>Chlamydomonas reinhardtii</i>			JGI 3.1
Total	118,433,693	100%	
1,266 scaffolds	118,214,107	99.80%	
Chloroplast	203,828	1,721 ppm	
Mitochondrion	15,758	133 ppm	
<i>Danio rerio</i>			Sanger Zv7
Total	1,440,582,308	100%	
25 Chromosomes	1,277,075,233	88.60%	
4,844 Unplaced contigs	117,689,868	8.20%	
166 Unplaced scaffolds	45,800,611	3.20%	
Mitochondrion	16,596	11.5 ppm	
<i>Mus musculus</i>			NCBI 37 C57BL/6J
Total bases	2,725,765,481	100%	
19 Autosomes	2,472,342,367	90.70%	
X chromosome	166,650,296	6.70%	
Y chromosome	15,902,555	0.60%	
Random contigs that cannot be assigned to a chromosome	5,900,358	0.20%	
Mitochondrion	16,299	6 ppm	
10 Random contigs that can be assigned to an autosome	4,486,070	0.20%	
Random contigs that can be assigned to X chromosome	1,785,075	0.10%	
Random contigs that can be assigned to Y chromosome	58,682,461	2.20%	

Table S2. Summary of bisulfite sequencing results and methylation estimates in each of the eight organisms

	Chromosome group*	No. of CHH observed methylated	No. of CHH observed	No. of CHG observed methylated	No. of CHG observed	No. of CG observed methylated	No. of CG observed	CHH methylation (ratio)	CHG methylation (ratio)	CG Methylation (ratio)
<i>Apis mellifera</i>	Linkage groups ("main")	13,008	7,711,277	5,230	1,989,668	52,529	5,670,507	0.17%	0.26%	0.93%
	Unassembled and unoriented contigs	4,707	3,877,111	1,182	720,017	39,393	1,275,761	0.12%	0.16%	3.09%
<i>Ciona intestinalis</i>	Chromosomal arms ("main")	3,546	2,855,409	1,315	786,602	229,973	739,569	0.12%	0.17%	31.10%
	Scaffolds	1,095	840,933	351	216,365	88,146	232,747	0.13%	0.16%	37.87%
<i>Arabidopsis thaliana</i>	Chromosomes ("main")	131,038	8,697,903	96,837	1,635,056	321,689	1,445,147	1.51%	5.92%	22.26%
	Chloroplast	830	298,742	269	53,338	282	62,524	0.28%	0.50%	0.45%
<i>Oryza sativa</i>	Chromosomes ("main")	97,593	4,475,002	239,292	1,154,861	668,815	1,126,122	2.18%	20.72%	59.39%
	Chloroplast	4	1,099	1	150	1	162	0.36%	0.67%	0.62%
<i>Populus trichocarpa</i>	Linkage groups ("main")	90,343	2,779,154	121,318	580,991	154,869	369,842	3.25%	20.88%	41.87%
	Scaffolds	40,819	825,083	80,528	191,786	94,424	145,166	4.95%	41.99%	65.05%
	Chloroplast	290	61,257	82	12,399	111	15,104	0.47%	0.66%	0.73%
<i>Chlamydomonas reinhardtii</i>	Scaffolds ("main")	90,526	3,638,962	107,383	4,146,574	365,037	6,790,031	2.49%	2.59%	5.38%
	Chloroplast	4,345	929,411	2,544	192,739	5,314	198,850	0.47%	1.32%	2.67%
<i>Danio rerio</i> (wild type)	Chromosomes ("main")	11,137	1,227,226	5,459	446,050	182,831	227,721	0.91%	1.22%	80.29%
	Unplaced contigs	944	98,428	503	39,027	20,342	24,265	0.96%	1.29%	83.83%
	Unplaced scaffolds	146	18,713	70	6,980	3,181	3,832	0.78%	1.00%	83.01%
<i>Danio rerio</i> (<i>Uhrf1</i> ^{-/-})	Chromosomes ("main")	22,492	1,475,722	8,217	468,673	79,302	200,211	1.52%	1.75%	39.61%
	Unplaced contigs	1,672	120,693	629	39,322	7,852	18,978	1.39%	1.60%	41.37%
	Unplaced scaffolds	354	22,218	171	7,131	1,320	3,219	1.59%	2.40%	41.01%
<i>Mus musculus</i> (embryo)	Autosomes ("main")	28,870	4,089,976	13,621	1,316,624	223,443	260,877	0.29%	0.30%	74.20%
	X chromosome	430	152,001	120	42,901	4,729	6,392	0.28%	0.28%	73.98%
	Y chromosome	1	640	1	185	25	35	0.16%	0.54%	71.43%
	Unplaced random contigs	38	3,294	4	1,180	312	499	1.15%	0.34%	62.53%
	Random contigs on an autosome	7	1,644	5	532	86	126	0.43%	0.94%	68.25%
	Random contigs on X chromosome	1	415	0	158	14	20	0.24%	0.00%	70.00%
	Random contigs on Y chromosome	7	1,237	2	336	57	74	0.57%	0.60%	77.03%
<i>Mus musculus</i> (ES cell, wild type)	Autosomes ("main")	93,557	9,159,964	38,528	2,876,969	411,105	512,608	1.02%	1.34%	80.20%
	X chromosome	2,764	281,165	1,011	77,329	8,695	10,730	0.98%	1.31%	81.03%
	Y chromosome	16	2,748	11	813	90	105	0.58%	1.35%	85.71%

Table S2. Cont.

Chromosome group*	No. of CHH observed methylated	No. of CHH observed	No. of CHG observed methylated	No. of CHG observed	No. of CG observed methylated	No. of CG observed	CHH methylation (ratio)	CHG methylation (ratio)	CG Methylation (ratio)
Unplaced random contigs	209	13,839	43	5,315	1,462	2,211	1.51%	0.81%	66.12%
Random contigs on an autosome	30	3,911	17	1,226	202	239	0.77%	1.39%	84.52%
Random contigs on X chromosome	6	670	2	193	16	19	0.90%	1.04%	84.21%
Random contigs on Y chromosome	47	6,311	13	1,769	245	317	0.74%	0.73%	77.29%
<i>Mus musculus</i> (ES cell, <i>Uhrf1</i> ^{-/-})									
Autosomes ("main")	79,166	7,115,824	30,210	2,212,233	67,156	370,602	1.11%	1.37%	18.12%
X chromosome	2,588	241,772	894	66,855	1,283	8,629	1.07%	1.34%	14.87%
Y chromosome	21	2,294	5	624	5	81	0.92%	0.80%	6.17%
Unplaced random contigs	135	10,234	24	3,775	154	1,657	1.32%	0.64%	9.29%
Random contigs on an autosome	37	3,005	12	945	36	166	1.23%	1.27%	21.69%
Random contigs on X chromosome	8	615	1	153	1	16	1.30%	0.65%	6.25%
Random contigs on Y chromosome	42	6,301	20	1,679	16	347	0.67%	1.19%	4.61%

Shading indicates denominator <100.

*See Table S1 for details.

Table S3. Repeats and transposons analyzed in this study

Type	Before size selection:			Size			Size selection threshold			After size selection			Size		
	No. of intervals	Total length (bp)	Min (bp)	Max (bp)	Mean (bp)	Median (bp)	5th percentile	95th percentile	No. of intervals	Total length (bp)	Min (bp)	Max (bp)	Mean (bp)	Median (bp)	
Interspersed repeat (Ame)	27,168	4,519,977	25	9,198	166.4	122	44	438	24,549	3,523,019	44	438	143.5	122	
Interspersed repeat (Ath)	25,470	17,715,213	26	55,951	695.5	218	60	2,929	22,961	10,647,534	60	2,929	463.7	218	
Interspersed repeat (Cin)	139,976	26,539,482	25	15,061	189.6	155	51	470	126,248	20,973,724	51	470	166.1	155	
Interspersed repeat (Cre)	25,793	8,784,462	27	13,494	340.6	136	45	1,262	23,258	5,868,147	45	1,262	252.3	136	
Interspersed repeat (Dre)	1,816,721	623,240,643	25	28,200	343.1	217	54	1,001	1,639,695	465,609,758	54	1,001	284.0	216	
Interspersed repeat (Mmu)	2,998,918	1,027,174,503	24	1,785,075	342.5	178	60	1,020	2,709,348	638,040,354	60	1,020	235.5	178	
Interspersed repeat (Osa)	252,566	140,588,653	25	22,651	556.6	217	63	2,431	227,316	76,272,215	63	2,431	335.5	217	
Interspersed repeat (Ptr)	77,007	52,542,205	25	13,180	682.3	384	77	2,195	69,315	38,488,061	77	2,195	555.3	384	
Inverted repeat (Ame)	107,672	11,821,442	20	4,873	109.8	71	26	313	97,329	8,910,236	26	313	91.5	71	
Inverted repeat (Ath)	10,373	2,297,624	20	14,889	221.5	64	24	889	9,381	1,214,846	24	889	129.5	63	
Inverted repeat (Cin)	57,664	8,141,579	20	10,000	141.2	99	27	352	52,154	6,064,933	27	352	116.3	98	
Inverted repeat (Cre)	37,363	3,947,942	20	9,448	105.7	64	27	258	33,851	2,576,158	27	258	76.1	64	
Inverted repeat (Dre)	892,699	117,648,414	20	32,215	131.8	75	28	384	810,157	85,670,122	28	384	105.7	75	
Inverted repeat (Mmu)	796,200	156,441,378	20	15,584	196.5	89	29	645	719,642	91,348,449	29	645	126.9	88	
Inverted repeat (Osa)	147,886	21,791,145	20	18,890	147.4	78	30	354	133,498	13,718,132	30	354	102.8	78	
Inverted repeat (Ptr)	115,926	14,478,698	20	13,565	124.9	67	25	388	105,160	9,321,033	25	388	88.6	67	
Tandem repeat (Ame)	124,347	12,903,131	25	15,160	103.8	42	26	494	112,457	7,091,782	26	494	63.1	42	
Tandem repeat (Ath)	19,401	2,987,958	25	71,744	154.0	55	27	402	17,519	1,469,681	27	402	83.9	55	
Tandem repeat (Cin)	36,004	6,653,731	25	12,967	184.8	77	30	650	32,455	4,736,162	30	650	145.9	77	
Tandem repeat (Cre)	70,973	5,158,151	25	5,808	72.7	47	26	156	65,283	3,603,590	26	156	55.2	47	
Tandem repeat (Dre)	655,074	100,599,139	25	174,973	153.4	56	27	575	592,352	55,167,172	27	575	93.1	56	
Tandem repeat (Mmu)	1,112,584	90,363,318	25	59,855	81.2	49	27	214	1,012,238	62,963,614	27	214	62.2	49	
Tandem repeat (Osa)	98,354	12,311,296	25	65,904	125.2	64	28	386	89,221	8,112,521	28	386	90.9	63	
Tandem repeat (Ptr)	130,024	16,700,466	25	20,716	128.9	49	26	445	119,309	9,783,516	26	445	82.0	48	
Transposons-DNA (Ath)	12,388	7,524,425	11	19,356	607.4	235	56	2,090	11,175	4,303,513	56	2,090	385.1	235	
Transposons-DNA (Cin)	45,298	8,386,987	11	3,582	185.2	181	61	391	40,794	6,749,665	61	391	165.5	181	
Transposons-DNA (Cre)	5,537	2,027,902	11	10,215	366.2	183	37	952	4,987	1,366,188	37	952	273.9	183	
Transposons-DNA (Dre)	1,418,146	309,117,119	11	18,662	218.0	131	46	688	1,277,184	235,421,102	46	688	184.3	131	
Transposons-DNA (Mmu)	129,380	22,375,778	11	2,077	172.9	156	57	358	116,683	18,570,444	57	358	159.2	155	
Transposons-DNA (Osa)	178,631	51,771,745	11	15,521	289.8	180	48	630	161,039	31,891,999	48	630	198.0	180	
Transposons-DNA (Ptr)	41,965	6,228,207	11	3,216	148.4	71	44	572	37,982	3,978,411	44	572	104.7	71	
Transposons-LINE (Ath)	1,778	1,280,398	15	6,835	720.1	269	57	3,589	1,605	859,713	57	3,589	535.6	268	
Transposons-LINE (Cin)	16,609	2,012,431	11	5,143	121.2	87	16	258	14,957	1,435,701	16	258	96.0	87	
Transposons-LINE (Cre)	12,064	4,685,982	11	9,710	388.4	159	40	1,394	10,862	3,235,343	40	1,394	297.9	159	
Transposons-LINE (Dre)	83,857	29,375,218	11	6,734	350.3	194	50	1,081	75,547	20,211,598	50	1,081	267.5	193	
Transposons-LINE (Mmu)	964,997	542,112,591	11	13,492	561.8	287	62	1,831	868,541	355,529,356	62	1,831	409.3	287	
Transposons-LINE (Osa)	4,987	2,861,405	11	9,122	573.8	226	48	2,422	4,490	1,550,582	48	2,422	434.4	226	
Transposons-LINE (Ptr)	1,484	310,847	27	1,168	209.5	109	41	726	1,337	251,350	41	726	188.0	109	
Transposons-LTR (Ath)	8,032	8,066,815	11	12,327	999.4	416	59	4,310	7,244	5,578,158	59	4,310	770.0	415	
Transposons-LTR (Cin)	353	118,133	26	3,452	334.7	238	42	1,192	319	85,626	42	1,192	268.4	238	
Transposons-LTR (Cre)	2,724	749,178	11	10,915	275.0	96	37	974	2,453	384,738	37	974	156.8	96	
Transposons-LTR (Dre)	42,918	31,836,292	11	9,867	741.8	227	50	4,152	38,886	20,128,772	50	4,152	517.6	226	

Table S3. Cont.

Type	Before size selection:			Size			Size selection threshold			After size selection			Size		
	No. of intervals	Total length (bp)	Min (bp)	Max (bp)	Mean (bp)	Median (bp)	5th percentile	95th percentile	No. of intervals	Total length (bp)	Min (bp)	Max (bp)	Mean (bp)	Median (bp)	
Transposons-LTR (Mmu)	811,241	272,489,502	11	7,752	335.9	270	58	832	731,302	202,097,270	58	832	276.4	270	
Transposons-LTR (Osa)	74,907	84,484,439	11	31,466	1,127.9	290	38	5,279	67,468	51,433,102	38	5,279	762.3	290	
Transposons-LTR (Ptr)	75,584	31,422,724	11	4,816	415.7	210	45	1,496	68,248	23,000,440	45	1,496	337.0	209	
Transposons-SINE (Ath)	653	117,295	33	1,422	179.6	149	53	351	589	92,184	53	351	156.5	149	
Transposons-SINE (Cin)	32,823	4,935,011	11	387	150.4	134	53	288	29,572	4,380,448	53	288	148.1	134	
Transposons-SINE (Cre)	324	124,140	18	539	383.1	426	71	535	306	122,338	71	535	399.8	440	
Transposons-SINE (Dre)	238,960	57,005,307	11	827	238.7	235	53	473	215,632	49,838,383	53	473	231.1	234	
Transposons-SINE (Mmu)	1,426,145	191,432,180	11	653	134.2	135	53	218	1,285,978	171,040,689	53	218	133.0	135	
Transposons-SINE (Osa)	10,034	1,524,417	11	1,646	151.9	131	34	352	9,093	1,328,389	34	352	146.1	131	
Transposons-SINE (Ptr)	105	5,889	28	144	56.1	53	31	97	98	5,192	31	97	53.0	53	
Transposons-LTR+DNA+LINE (Ame)	274	28,377	12	423	103.6	93	36	190	249	24,501	36	190	98.4	93	
Transposons-Unclassified (Ame)	21,999	2,843,894	25	8,655	129.3	83	41	336	19,841	2,084,394	41	336	105.1	83	
Transposons-Unclassified (Cin)	104,890	15,607,990	11	3,124	148.8	100	19	483	94,986	11,760,759	19	483	123.8	99	
Transposons-Unclassified (Cre)	1,511	352,923	11	1,051	233.6	98	38	679	1,369	294,885	38	679	215.4	97	
Transposons-Unclassified (Dre)	946,017	231,537,076	11	56,739	244.7	169	50	683	854,237	179,406,855	50	683	210.0	169	
Transposons-Alu (subset of SINEs) (Mmu)	537,328	62,984,532	11	653	117.2	125	56	149	488,879	58,499,259	56	149	119.7	126	
Transposons-Unclassified (Mmu)	5,949	2,119,957	11	2,945	356.4	190	27	1,580	5,364	1,588,504	27	1,580	296.1	190	
Transposons-Unclassified retroelement (Osa)	4,527	4,882,855	11	19,164	1,078.6	369	37	4,393	4,080	3,550,095	37	4,393	870.1	369	
Transposons-Unclassified others (Osa)	10,409	3,669,401	11	7,403	352.5	147	37	1,512	9,400	2,643,563	37	1,512	281.2	146	
Transposons-Unclassified retroelement (Ptr)	1,153	132,229	17	1,399	114.7	81	43	345	1,042	95,818	43	345	92.0	81	
Transposons-Unclassified others (Ptr)	2,294	216,757	14	664	94.5	71	44	237	2,080	157,597	44	237	75.8	71	

Key:
 Ame: *Apis mellifera*
 Ath: *Arabidopsis thaliana*
 Cin: *Ciona intestinalis*
 Cre: *Chlamydomonas reinhardtii*
 Dre: *Danio rerio*
 Mmu: *Mus musculus*
 Osa: *Oryza sativa*
 Ptr: *Populus trichocarpa*

Transposons are classified as:
 Class I transposons:
 LTR: long terminal repeat retrotransposons
 LINE: long interspersed nuclear elements (non-LTR retrotransposons)
 SINE: short interspersed nuclear elements (non-LTR retrotransposons)

Class II transposons:
 DNA: DNA transposons