Supplementary Material

MeT-DB V2.0: Elucidating context-specific functions of N^6-methyl-adenosine methyltranscriptome

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[#] The authors wish it to be known that, in their opinion, the first 3 authors should be regarded as joint First Authors

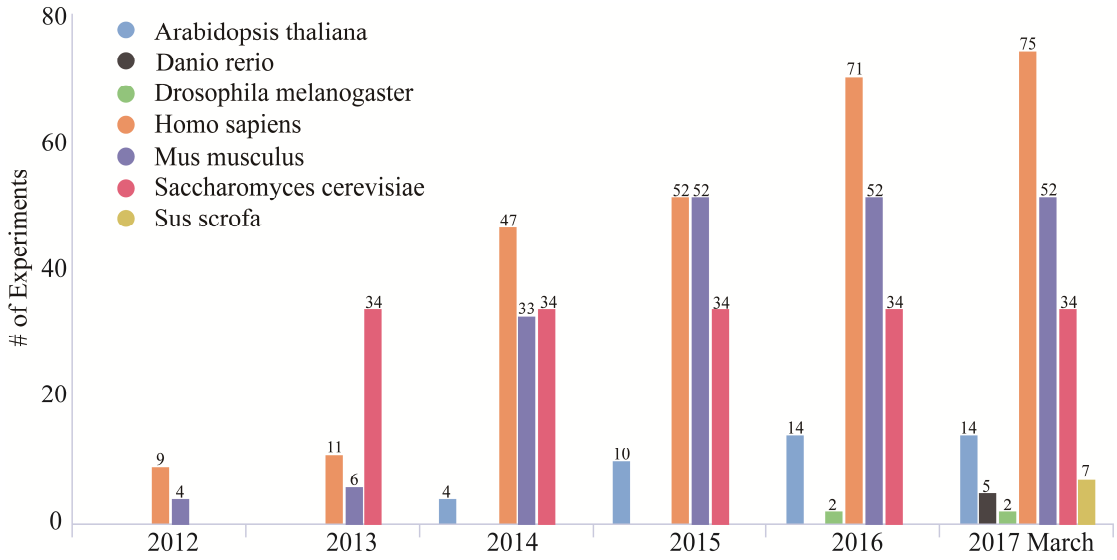

Figure S1. The number of MeRIP-seq samples by years. Published studies employed MeRIP-Seq experiments grew rapidly, while more and more species were enrolled.

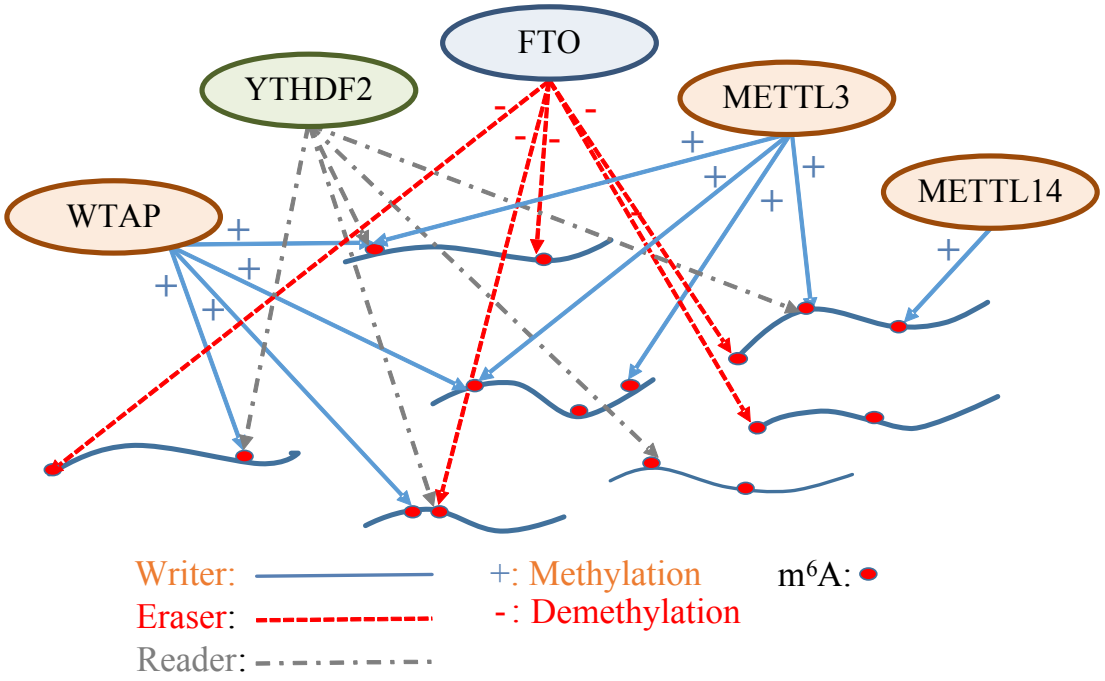

Figure S2. Illustration of m^{6}A readers, writers, and erasers in the TREW database. TREW is an acronym for the epitranscriptomic Target of Reader, Eraser and Writer. TREW collected ParCLIP-seq and MeRIP-seq samples for 8 regulator/reader proteins (including FTO, KIAA1429, METTL14, METTL3, WTAP, HNRNPC, YTHDC1, YTHDF1) from 10 published studies.

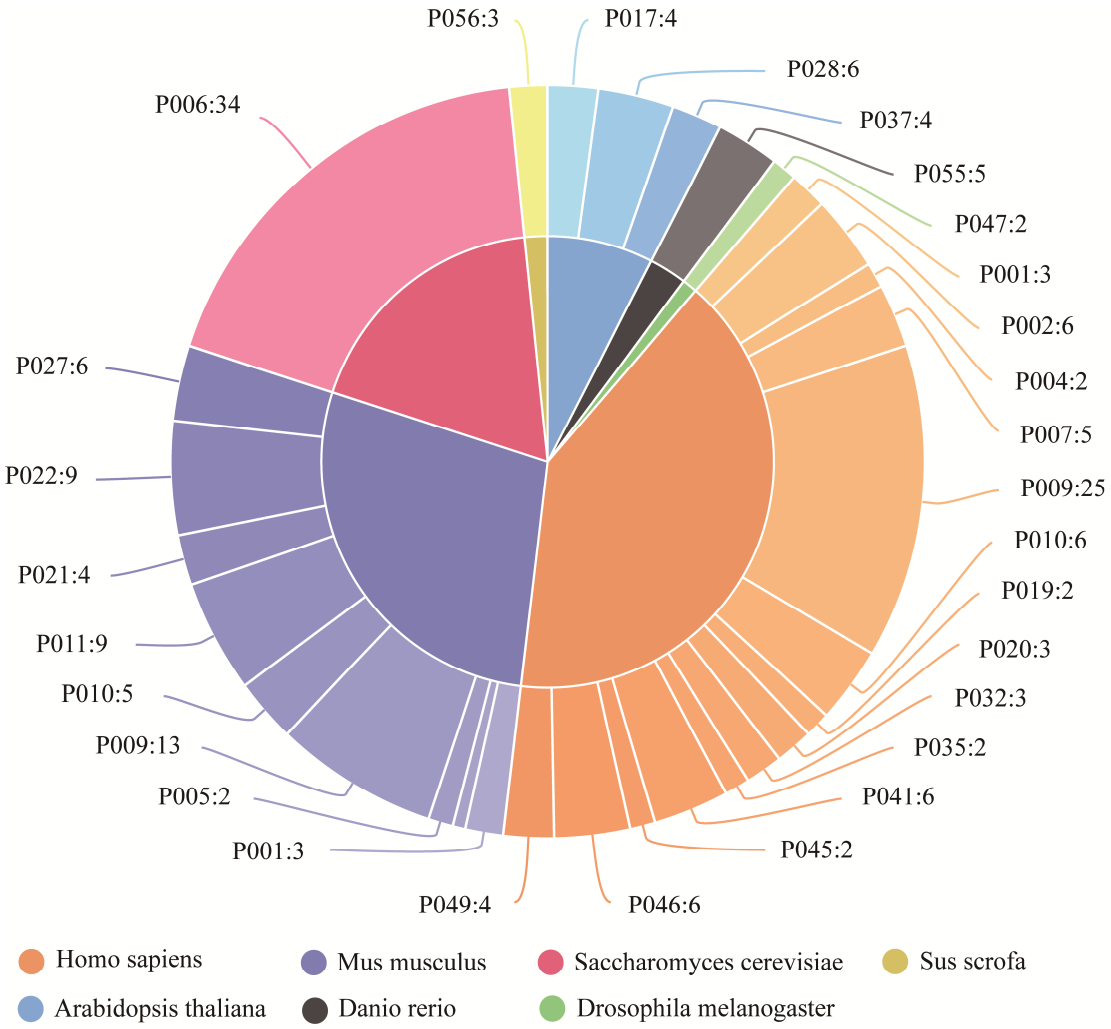

Figure S3. Distribution of MeRIP-seq samples by species and published papers. 26 independent studies and 185 MeRIP-Seq experiments were included in MeT-DB V2.0.

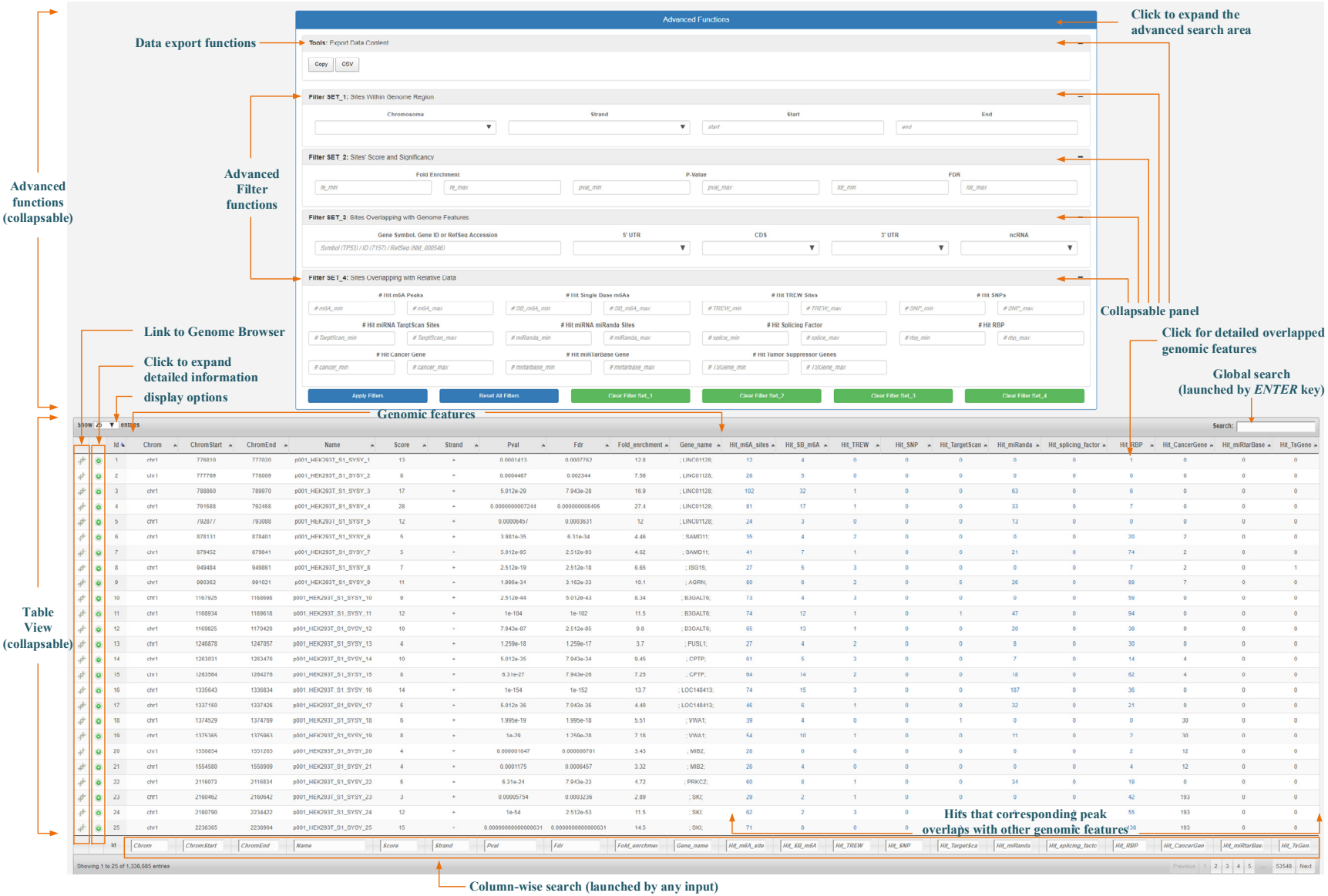

Figure S4. Illustration of table view. Table view is capable of displaying background data clearly and providing several search methods. To be more specific, global search can qurey input information within entire table. Column specific search, located in the footer of table, can perform search within corresponding column. More important, we designed variety of advance search functions for different tables to further assistance users to screen out most valuable elements among huge information stored in background database.Users can export data by clicking export buttons under any search conditions for following investigate. Besides, users are able to view detail information in genome browser of a specific entry by clicking the genome browser icon at the very left end of each row.

Table S1. Studies from which the MeT-DB V2.0 core data samples were obtained

ID	Papa Abbr	Title	Species	Year
1	p001	Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3'UTRs and near Stop Codons	Human, Mouse	2012
2	p002	Topology of the human and mouse m^6A RNA methylomes revealed by m^6A -seq	Human, Mouse	2012
3	p004	RNA-Methylation-Dependent RNA Processing Controls the Speed of the Circadian Clock	Human	2013
4	p005	The fat mass and obesity associated gene (Fto) regulates activity of the dopaminergic midbrain circuitry	Muse	2013
5	p006	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis	Yeast	2013
6	p007	N6-methyladenosine-dependent regulation of messenger RNA stability	Human	2014
7	p009	Perturbation of m^6A writers reveals two distinct classes of mRNA methylation at internal and 5' sites	Human, Mouse	2014
8	p010	m^6A RNA modification controls cell fate transition in mammalian embryonic stem cells	Human, Mouse	2014
9	p011	FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipogenesis	Mouse	2014
10	p017	Unique features of the m^6A methylome in Arabidopsis thaliana	Thaliana	2014
11	p019	N6-methyladenosine marks primary microRNAs for processing	Human	2015
12	p020	N6-Adenosine Methylation in MiRNAs	Human	2015
13	p021	m^6A RNA methylation is regulated by microRNAs and promotes reprogramming to pluripotency	Mouse	2015
14	p022	m^6A mRNA methylation facilitates resolution of naive pluripotency toward differentiation	Mouse	2015
15	p027	Dynamic m^6A mRNA methylation directs translational control of heat shock response	Mouse	2015
16	p028	Transcriptome-wide high-throughput deep m^6A -seq reveals unique differential m^6A methylation patterns between three organs in Arabidopsis thaliana	Thaliana	2015
17	p032	The m^6A Methyltransferase METTL3 Promotes Translation in Human Cancer Cells	Human	2016
18	p035	Dynamics of the human and viral m^6A RNA methylomes during HIV-1 infection of T cells	Human	2016
19	p037	N6-Methyladenosine RNA Modification Regulates Shoot Stem Cell Fate in Arabidopsis	Thaliana	2016
20	p041	N6-methyladenosine of HIV-1 RNA regulates viral infection and HIV-1 Gag protein expression	Human	2016
21	p045	Dynamics of Human and Viral RNA Methylation during Zika Virus Infection	Human, Zika	2016
22	p046	N6-Methyladenosine in Flaviviridae Viral RNA Genomes Regulates Infection	Human	2016
23	p047	m^6A modulates neuronal functions and sex determination in Drosophila	Drosophila	2016
24	p049	FTO Plays an Oncogenic Role in Acute Myeloid Leukemia as a N 6-Methyladenosine RNA Demethylase	Mouse	2017
25	p055	Genome-wide mapping of 5-hydroxymethyluracil in the eukaryote parasite Leishmania	Zebrafish	2017
26	p056	mRNA N6-methyladenosine methylation of postnatal liver development in pig	Pig	2017

Table S2. Studies from which the TREW data samples were obtained

ID	Reference Title	Species	Techenic	Regulator Name	Regulator Type	Year
1	The fat mass and obesity associated gene (Fto) regulates activity of the dopaminergic midbrain circuitry	Mouse	MeRIP-seq	FTO	Eraser	2013
3	Perturbation of m^6A Writers reveals two distinct classes of mRNA methylation at internal and 5' sites	Human, Mouse	MeRIP-seq	WTAP,KIAA1429, METTL3,METTL14	Writer	2014
2	FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipogenesis	Mouse	MeRIP-seq	FTO	Eraser	2014
4	A METTL3-METTL14 complex mediates mammalian nuclear RNA N6-adenosine methylation	Human	MeRIP-seq, PAR-CLIP	WTAP,METTL3, METTL14	Writer	2014
5	Dynamic m^6A mRNA methylation directs translational control of heat shock response	Mouse	MeRIP-seq	FTO	Eraser	2015
6	m^6A mRNA methylation facilitates resolution of naive pluripotency toward differentiation	Mouse	MeRIP-seq	METTL3	Writer	2015
7	N6-methyladenosine-dependent RNA structural switches regulate RNA-protein interactions	Human	PAR-CLIP	METTL3,METTL14, HNRNPC	Writer	2015
8	N6-methyladenosine Modulates Messenger RNA Translation Efficiency	Human	PAR-CLIP	YTHDF1	Reader	2015
9	FTO Plays an Oncogenic Role in Acute Myeloid Leukemia as a N6-Methyladenosine RNA Demethylase	Human	MeRIP-seq	FTO	Eraser	2016
10	Structural basis for selective binding of m^6A RNA by the YTHDC1 YTH domain	Human	PAR-CLIP	YTHDC1	Reader	2016