# Supplementary Material

## Title:

## RMBase v3.0: Decode the Landscape, Mechanisms and Functions of RNA Modifications

## Authors:

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# Figures

**Figure S1. Global map of the RNA modifications in humans. (A)** Heatmap of RNA modifications in different RNA species. The cell value represents the proportion of a particular RNA modification on an RNA to the total of that RNA modifications. Each row name represents one RNA modification type and its total number. Color bar shows the percentage. **(B)** Pie plot shows the abundance of clusters in five different RNA modifications. **(C)** Pie plot shows the distribution abundance of m$^6$A modification clusters on different RNA.

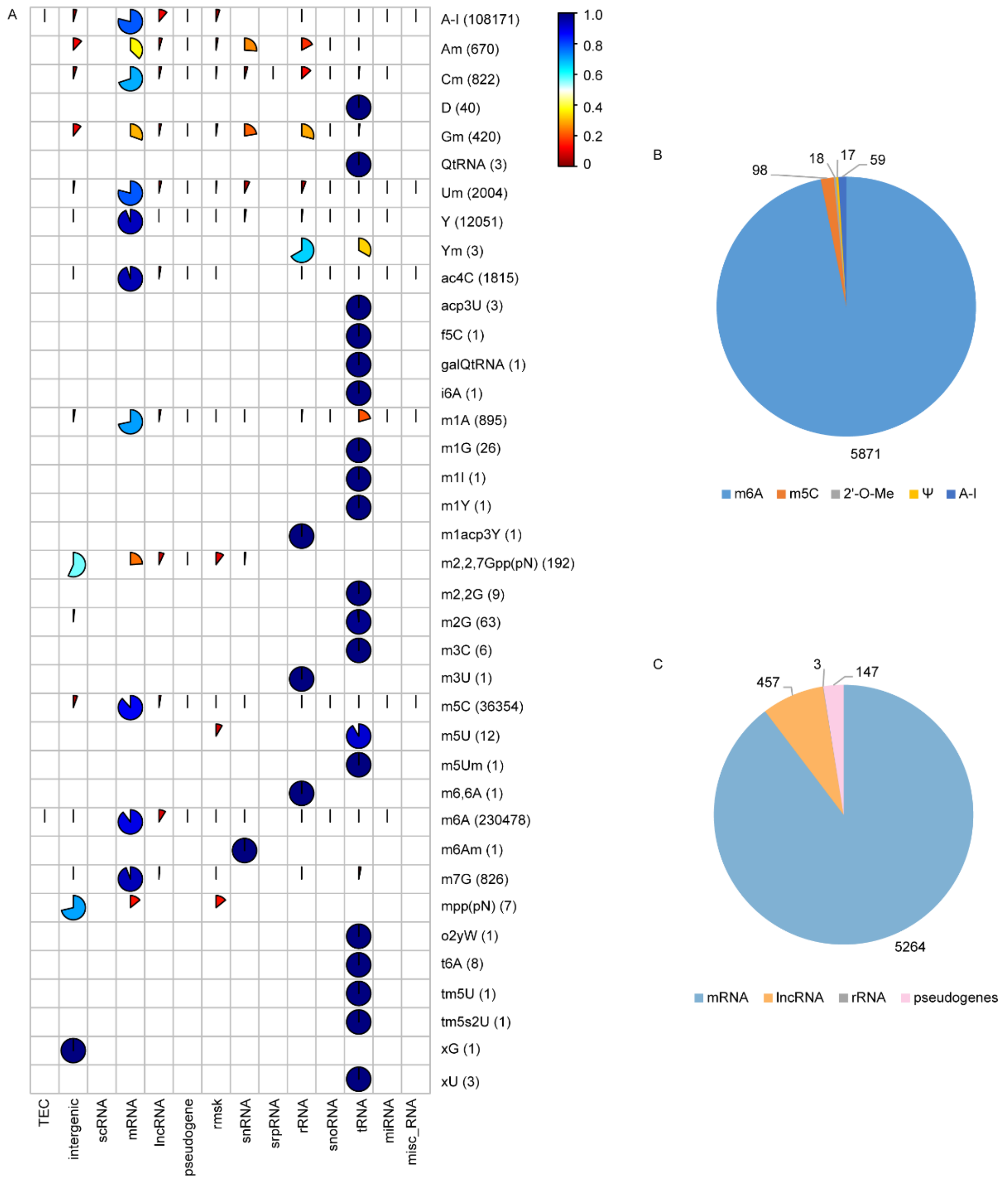


**Figure S2. The metagene plots of different RNA modifications.** These plots for $m^6A$ modification (A), A-I modification (B), Ψ modification (C) and $m^5C$ modification (D) in different species are generated using the "modMetagene" tool provided by RMBase v3.0.

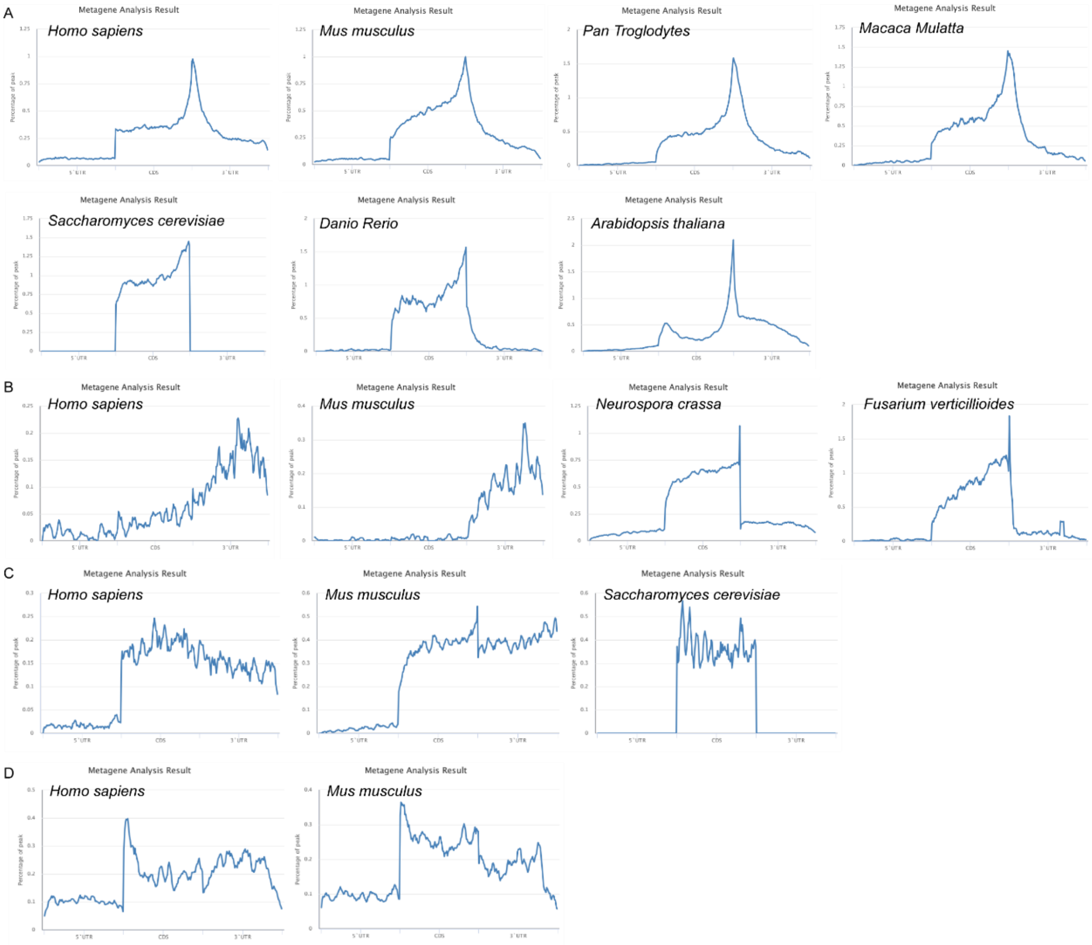


**Figure S3. Identification of 2'-O-Me modification sites guided by snoRNAs using sno2Nm. (A)** Flowchart of sno2Nm. **(B)** Pie plot shows that the distribution of known and novel snoRNA-guided 2'-O-Me sites on different gene biotypes.

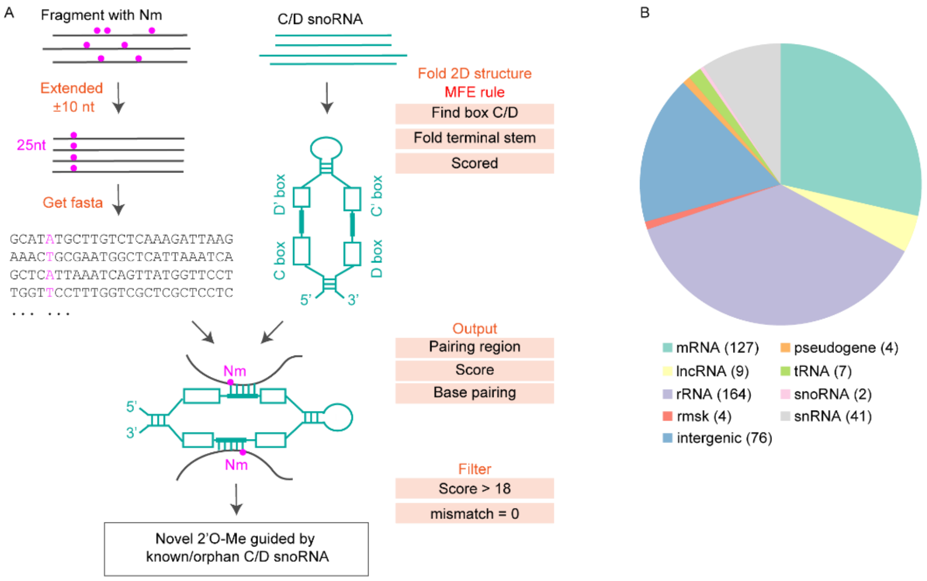


**Figure S4. Heatmap for differential expression of RMPs in 16 types of tumors.** "red" refers to up-regulated RMPs in tumors, while "blue" refers to down-regulated RMPs in tumors.

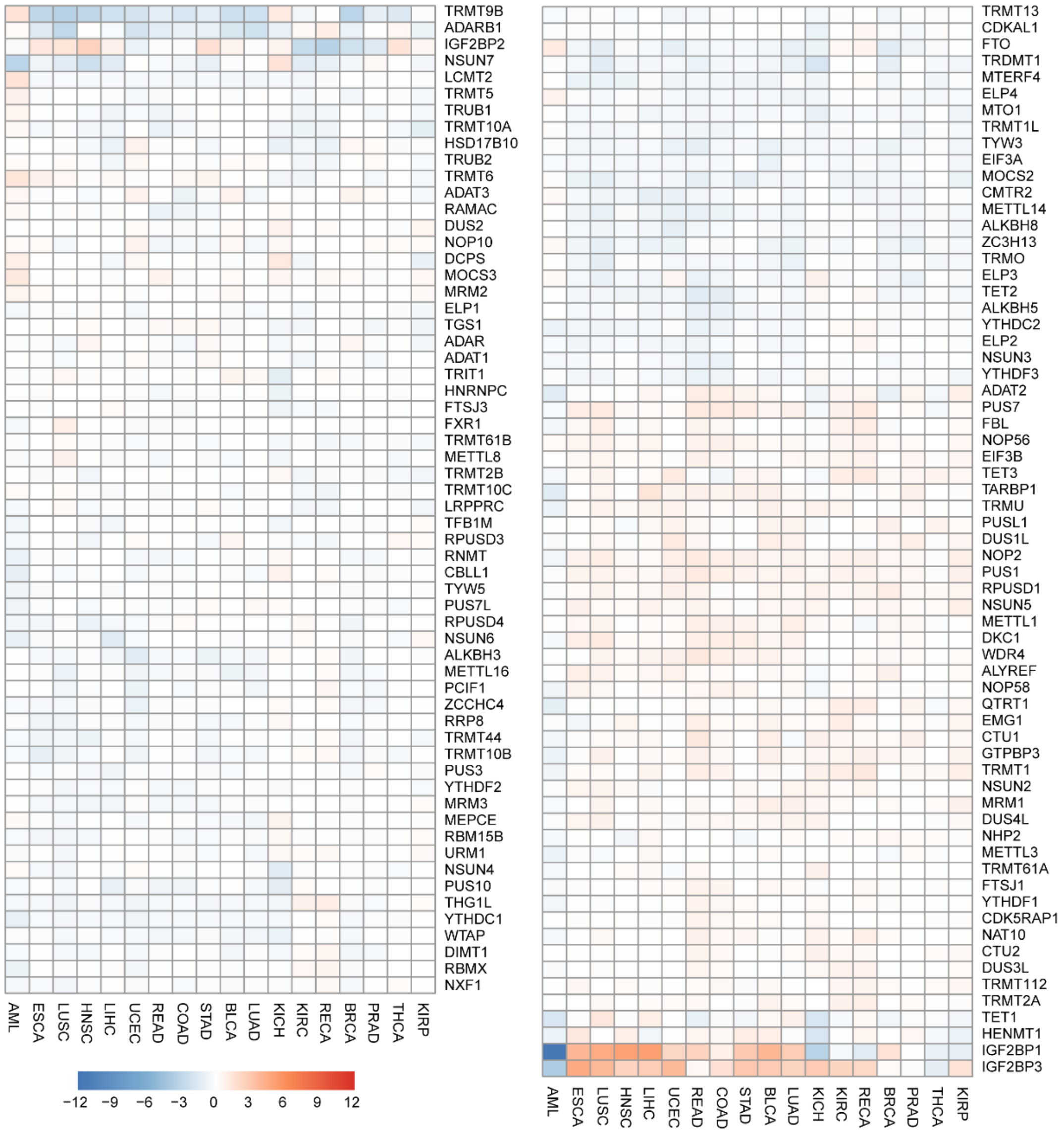
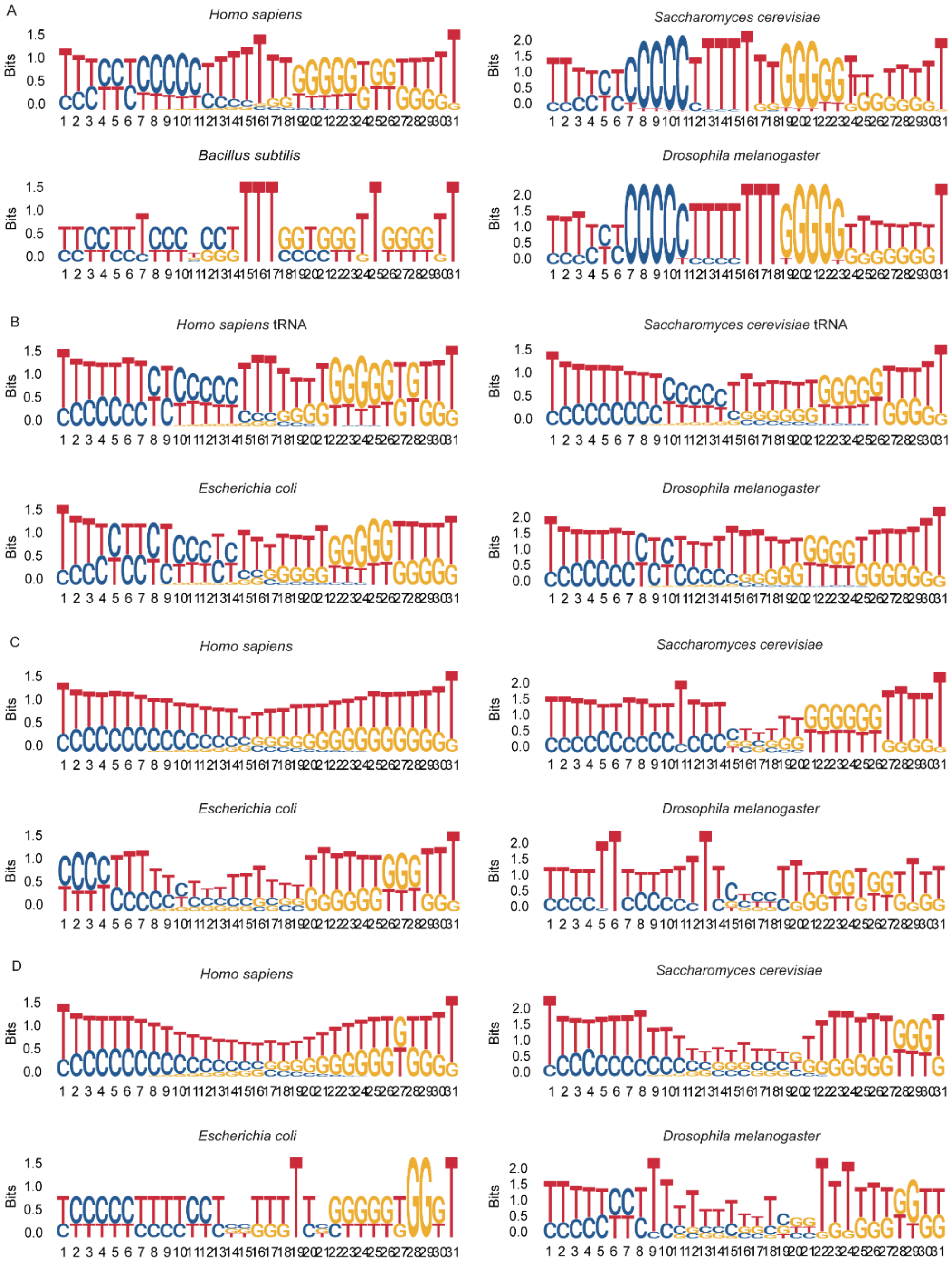


**Figure S5 The potential RNA structure motifs associated with specific RNA modifications.** The seqlogo plots show the RNA secondary structure features near the m$^1$A modification site (A), Ψ modification site (B), m$^7$G modification site (C) and m$^5$C modification site (D) across different species. Where, "C" stands for "(", "G" stands for ")", and "T" stands for "." in the MFE secondary structure (dot-bracket). The modification site is at the sixteenth position.



# Tables

## Table S1. Datasets source of RNA modifications and their intersecting factors.

| Data | Datasets Source | Datasets List |
|---|---|---|
| $N^1$-methyladenosine ($m^1A$) | GEO, PubMed | m1A-seq, m1A-MAP |
| $N^5$-methylcytosine ($m^5C$) | GEO, PubMed | m5C-RIP, Bisulfite-seq |
| $N^6$-methyladenosine ($m^6A$) | GEO, PubMed | miCLIP, m6A-CLIP/IP, MAZTER-seq, DART-seq, m6A-REF-seq, m6A-seq, MeRIP-seq |
| $N^7$-Methylguanosine ($m^7G$) | GEO, PubMed | m7G-seq, BoRed-seq, m7G-RIP-seq |
| Pseudouridine (Ψ) | GEO, PubMed, snOPY, Yeast-snoRNADataBase, snoRNABase | Ψ-seq, CeU-seq, Pseudo-seq, PSI-seq, BID-seq, PRAISE |
| 2′-O-methylation (2'-O-Me) | GEO, PubMed, snOPY, Yeast-snoRNADataBase, snoRNABase | Nm-seq, RiboMeth-seq, RibOxi-seq, 2OMe-seq |
| $N^4$- acetylcytidine ($ac^4C$) | GEO | ac4C-seq, acRIP-seq |
| RNA-editing (A-I) | FairBase, REDIportal, RADAR and DARNED | / |
| Other modifications | MODOMICS | / |
| RNA binding proteins (RBP) | starBase (1), ENCODE and POSTAR2 (2) | eCLIP, HITS-CLIP, iCLIP, PARCLIP |
| miRNA targets | starBase | / |
| single-nucleotide variations (SNV) | COSMIC (3) and published literatures (4,5) | / |
| single-nucleotide polymorphisms (SNP) | Clinvar (6), GWAS (7) and GTEx (8) | / |

**Table S2. Source of genomes and gene annotations of 62 species.**

| Group | Species | Assembly | Genome and Annotations |
|---|---|---|---|
| Mammal | *Homo sapiens* | hg38 | gencode.v30, UCSC, miRBase v22 |
| | *Mus musculus* | mm10 | gencode.vM22, UCSC, miRBase v22 |
| | *Macaca mulatta* | rheMac8 | Ensembl v97, UCSC, miRBase v22 |
| | *Pan troglodytes* | panTro5 | Ensembl v97, UCSC, miRBase v22 |
| | *Rattus norvegicus* | rn6 | Ensembl v97, UCSC, miRBase v22 |
| | *Sus scrofa* | susScr11 | Ensembl v97, UCSC, miRBase v22 |
| | *Mesocricetus auratus* | MesAur1.0 | Ensembl v97 |
| | *Oryctolagus cuniculus* | OryCun2.0 | Ensembl v97, UCSC, miRBase v22 |
| | *Ovis aries* | Oar_v3 | Ensembl v97, UCSC, miRBase v22 |
| | *Bos taurus* | bosTau9 | Ensembl v97, UCSC, miRBase v22 |
| Plant | *Arabidopsis thaliana* | TAIR10 | Ensembl v44, GtRNAdb v18, miRBase v22 |
| | *Brassica napus* | AST_PRJEB5043_v1 | Ensembl v44 |
| | *Chlamydomonas reinhardtii* | CHLRE3 | NCBI |
| | *Cucumis sativus* | ASM407v2 | Ensembl v44 |
| | *Glycine max* | glyMax2.1 | Ensembl v44, GtRNAdb v18, miRBase v22 |
| | *Nicotiana tabacum* | Ntab-TN90 | NCBI |
| | *Phaseolus vulgaris* | PhaVulg1 | Ensembl v44, miRBase v22 |
| | *Solanum tuberosum* | SolTub3 | Ensembl v44, miRBase v22 |
| | *Spinacia oleracea* | ASM200726v1 | NCBI |
| | *Zea mays* | RefGenv4 | Ensembl v44 |
| Metazoa | *Bombyx mori* | ASM15162v1 | Ensembl v44 |
| | *Caenorhabditis elegans* | WBcel235 | Ensembl v97, UCSC, miRBase v22 |
| | *Xenopus laevis* | Xenopus_laevis_v2 | NCBI |
| Vertebrate | *Danio rerio* | danRer11 | Ensembl v97, UCSC, miRBase v22 |
| | *Gallus gallus* | GRCg6a | Ensembl v97, UCSC, miRBase v22 |
| Fungi | *Candida albicans* | Cand_albi_12C | Ensembl v44 |
| | *Fusarium graminearum* | ASM24013v3 | Ensembl v45, GtRNAdb v18 |
| | *Fusarium verticillioides* | ASM14955v1 | Ensembl v45, GtRNAdb v18 |
| | *Neurospora crassa* | NC12 | Ensembl v44 |
| | *Pichia jadinii* | Cybja1 | NCBI |
| | *Saccharomyces cerevisiae* | sacCer3 | Ensembl v97, GtRNAdb v18 |
| | *Schizosaccharomyces pombe* | ASM294v2 | Ensembl v44, GtRNAdb v18 |
| Insect | *Drosophila melanogaster* | BDGP6 | Ensembl v97, UCSC, miRBase v22 |
| Protists | *Tetrahymena thermophila* | JCVI-TTA1-2.2 | Ensembl v44 |
| Bacteria | *Bacillus subtilis* | ASM69118v1 | Ensembl v44 |

| | | | |
|---|---|---|---|
| | *Clostridium acetobutylicum* | ASM78585v1 | Ensembl v44 |
| | *Escherichia coli* | ASM584v2 | Ensembl v44, GtRNAdb v18 |
| | *Geobacillus stearothermophilus* | ASM74998v1 | Ensembl v44 |
| | *Halobacterium salinarum* | ASM680v1 | Ensembl v44, GtRNAdb v18 |
| | *Halococcus morrhuae* | ASM33669v1 | Ensembl v44 |
| | *Haloferax volcanii* | ASM2568v1 | Ensembl v44, GtRNAdb v18 |
| | *Lactococcus lactis* | ASM76111v1 | Ensembl v44, GtRNAdb v18 |
| | *Mycobacterium smegmatis* | ASM76770v1 | Ensembl v44, GtRNAdb v18 |
| | *Mycoplasma capricolum* | ASM83033v1 | Ensembl v44, GtRNAdb v18 |
| | *Mycoplasma mycoides* | ASM25307v1 | Ensembl v44, GtRNAdb v18 |
| | *Pseudomonas aeruginosa* | ASM676v1 | Ensembl v44, GtRNAdb v18 |
| | *Pyrococcus abyssi* | ASM19593v2 | Ensembl v45 |
| | *Rhodospirillum rubrum* | ASM1308v1 | Ensembl v44 |
| | *Salmonella typhimurium* | ASM553737v1 | NCBI |
| | *Spiroplasma citri* | ASM188685v1 | NCBI |
| | *Streptomyces coelicolor A3 (2)* | ASM20383v1 | Ensembl v44 |
| | *Streptomyces griseus* | ASM93222v1 | Ensembl v44 |
| | *Sulfolobus acidocaldarius* | ASM1228v1 | Ensembl v44, GtRNAdb v18 |
| | *Sulfolobus solfataricus* | ASM96839v1 | Ensembl v44 |
| | *Synechococcus elongatus PCC 6301* | ASM1006v1 | NCBI, GtRNAdb v18 |
| | *Synechococcus sp.PCC 7002* | ASM1948v1 | NCBI, GtRNAdb v18 |
| | *Synechocystis sp* | ASM34078v1 | NCBI |
| | *Thermoplasma acidophilum* | ASM19591v1 | Ensembl v44, GtRNAdb v18 |
| | *Thermotoga maritima* | ASM97857v1 | Ensembl v44, GtRNAdb v18 |
| | *Thermus thermophilus* | ASM812v1 | Ensembl v44, GtRNAdb v18 |
| Virus | *Enterobacteria phage T4* | ViralProj14044 | NCBI |
| | *Enterobacteria phage T5* | ASM292140v1 | NCBI |

**Table S3. Overview of the top five clusters with the most abundant RNA modification sites of m$^6$A, m$^5$C, 2'-O-Me, Ψ, and A-I.** "Number" is the number of RNA modification sites in the cluster. "Density" refers to the average distance between RNA modification sites within a cluster.

| **Gene Name** | **Gene Type** | **Cluster** | **Number** | **Density** | **Modification** |
|---|---|---|---|---|---|
| MKI67 | mRNA | chr10:128105818-128109436:- | 113 | 32.0177 | m6A |
| MKI67 | mRNA | chr10:128103187-128105817:- | 83 | 31.6867 | m6A |
| PLIN4 | mRNA | chr19:4510671-4513028:- | 75 | 31.4267 | m6A |
| AL121827.2 | lncRNA | chr20:63256960-63258120:+ | 74 | 15.6757 | m6A |
| CREB3L3 | mRNA | chr19:4171681-4172987:+ | 71 | 18.3944 | m6A |
| CENPB | mRNA | chr20:3786441-3786639:- | 29 | 6.82759 | m5C |
| ANKRD9 | mRNA | chr14:102509599-102509799:- | 25 | 8 | m5C |
| ZSWIM6 | mRNA | chr5:61332733-61332870:+ | 24 | 5.70833 | m5C |
| BTBD2 | mRNA | chr19:2015393-2015714:- | 21 | 15.2857 | m5C |
| TBL1X | mRNA | chrX:9465148-9465351:+ | 20 | 10.15 | m5C |
| FP236383.1 | lncRNA | chr21:8400486-8401014:+ | 23 | 22.9565 | 2'-O-Me |
| FP236383.1 | lncRNA | chr21:8444718-8445246:+ | 23 | 22.9565 | 2'-O-Me |
| FP671120.2 | lncRNA | chr21:8217522-8217976:+ | 21 | 21.619 | 2'-O-Me |
| FP236383.1 | lncRNA | chr21:8401055-8401597:+ | 19 | 28.5263 | 2'-O-Me |
| FP236383.1 | lncRNA | chr21:8445287-8445829:+ | 19 | 28.5263 | 2'-O-Me |
| FP671120.2 | lncRNA | chr21:8218114-8218611:+ | 20 | 24.85 | Ψ |
| FP236383.1 | lncRNA | chr21:8401152-8401649:+ | 20 | 24.85 | Ψ |
| FP236383.1 | lncRNA | chr21:8445384-8445881:+ | 20 | 24.85 | Ψ |
| FP671120.2 | lncRNA | chr21:8210380-8211125:+ | 17 | 43.8235 | Ψ |
| FP236383.1 | lncRNA | chr21:8393415-8394160:+ | 17 | 43.8235 | Ψ |
| BMS1P10 | pseudogene | chr9:63302059-63302732:- | 59 | 11.4068 | A-I |
| OSMR-AS1 | lncRNA | chr5:38820960-38821768:- | 41 | 19.7073 | A-I |
| ISPD | mRNA | chr7:16089130-16089520:- | 38 | 10.2632 | A-I |
| TNFRSF14-AS1 | lncRNA | chr1:2556076-2556686:- | 32 | 19.0625 | A-I |
| OSMR-AS1 | lncRNA | chr5:38822949-38823463:- | 31 | 16.5806 | A-I |

**Table S4. The Ψ targets of H/ACA snoRNAs** (top 15 for guide H/ACA snoRNA and orphan H/ACA snoRNA respectively). “a” refers to known guide H/ACA snoRNA, “b” refers to orphan H/ACA snoRNA.

| **snoRNA** | **Modification Site** | **Score** | **Target Type** | **Gene Type** | **Gene** | **Target Sequence** |
|---|---|---|---|---|---|---|
| SNORA16A [a] | 28S:4412 | 27.332 | known | rRNA | LSU-rRNA_Hsa | CGCUUUUUGAYCCUUCGAUGU |
| SNORA31 [a] | 28S:3713 | 26.462 | known | rRNA | LSU-rRNA_Hsa | AGAAAUUCAAYGAAGCGCGGG |
| SNORA17A [a] | 28S:4659 | 25.871 | known | rRNA | LSU-rRNA_Hsa | GGAUUAUGACYGAACGCCUCU |
| SNORA27 [a] | 28S:3694 | 25.392 | known | rRNA | LSU-rRNA_Hsa | GCUCUGAAUGYCAAAGUGAAG |
| SCARNA3 [a] | U6:40 | 24.733 | known | snRNA | U6 | AUUGGAACGAYACAGAGAAGA |
| SNORA8 [a] | 18S:1081 | 24.046 | known | rRNA | SSU-rRNA_Hsa | GUUCCGACCAYAAACGAUGCC |
| SNORA17A [a] | psi_2154 | 23.326 | unknow | rRNA | LSU-rRNA_Hsa | GGAUUAUGACYGAACGCCUUU |
| SNORA68B [a] | psi_2197 | 23.157 | unknow | lncRNA | MAGI2-AS3 | UUCUGUUUAAYAUCUUCAAGU |
| SNORA68 [a] | psi_2197 | 23.157 | unknow | lncRNA | MAGI2-AS3 | UUCUGUUUAAYAUCUUCAAGU |
| SNORA2A [a] | psi_2258 | 22.992 | unknow | mRNA | C9orf85 | UAGAUUUUGAYAUUGAUUUAG |
| SNORA10B [a] | psi_151 | 22.718 | unknow | mRNA | C11orf1 | ACCUGAGGAAYAUCGUGCAGC |
| SNORA10 [a] | psi_151 | 22.718 | unknow | mRNA | C11orf1 | ACCUGAGGAAYAUCGUGCAGC |
| SNORA30 [a] | 28S:4643 | 22.557 | known | rRNA | LSU-rRNA_Hsa | GAAGCUACCAYCUGUGGGAUU |
| SNORA3B [a] | 28S:3899 | 22.557 | known | rRNA | LSU-rRNA_Hsa | CCUGUUGAGCYUGACUCUAGU |
| SNORA30B [a] | 28S:4643 | 22.557 | known | rRNA | LSU-rRNA_Hsa | GAAGCUACCAYCUGUGGGAUU |
| SNORA2_3 [b] | psi_2258 | 22.992 | unknow | mRNA | C9orf85 | UAGAUUUUGAYAUUGAUUUAG |
| SNORA38B [b] | 28S:4269 | 22.869 | known | rRNA | LSU-rRNA_Hsa | UUGAUCUUGAYUUUCAGUACG |
| SNORA101B [b] | psi_1561 | 21.335 | unknow | snRNA | U2 | CUUCUCGGCCYUUUGGCUAAG |
| SNORA58B [b] | psi_2313 | 21.008 | unknow | mRNA | LAP3 | UGAAGUUCCCYAUCUACGGAA |
| SNORA15B-1 [b] | psi_2031 | 20.947 | unknow | mRNA | ZNF75D | AGCUGUCUGUYUUAUUCAGCA |
| SNORA15B-2 [b] | psi_2031 | 20.947 | unknow | mRNA | ZNF75D | AGCUGUCUGUYUUAUUCAGCA |
| SNODB2082 [b] | psi_319 | 20.936 | unknow | mRNA | PHGDH | CAGAGUGGAGYCUCCUCACAG |
| SNORA7 [b] | 28S:1779 | 20.368 | known | rRNA | LSU-rRNA_Hsa | UCUCAAACUUYAAAUGGGUAA |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| SNORA58B [b] | 28S:3823 | 20.342 | known | rRNA | LSU-rRNA_Hsa | CCACUGUCCCYACCUACUAUC |
| SNORA5 [b] | 18S:1625 | 19.842 | known | rRNA | SSU-rRNA_Hsa | UUGCAAUUAUYCCCCAUGAAC |
| SNORA5 [b] | psi_648 | 19.842 | unknow | rRNA | SSU-rRNA_Hsa | UUGCAAUUAUYCCCCAUGAAG |
| SNORA5 [b] | psi_1951 | 19.842 | unknow | rRNA | SSU-rRNA_Hsa | UUGCAAUUAUYCCCCAUGACC |
| SNORA38 [b] | psi_147 | 19.813 | unknow | mRNA | MRPS21 | UCCAUCUCUUYUCUUUGUACA |
| SNORA38 [b] | psi_1486 | 19.813 | unknow | mRNA | PEX1 | CUGCAUUCUUYUCUUUGAUGA |
| SNORA38 [b] | psi_1609 | 19.813 | unknow | mRNA | PPP4R1 | GACAGCUCUUYACUUUGUACU |

**Table S5. The 2'-O-Me targets of C/D snoRNAs (top 20).**

| snoRNA | Gene Type | Gene | Target Sequence | Score |
|---|---|---|---|---|
| SNORD57 | intergenic | intergenic | GCTCATTAAATCAGTTTTTTTGCCT | 45.236 |
| SNORD20 | rRNA | SSU-rRNA_Hsa | AACTTGACTATCTAGAGGAA | 36.508 |
| SNORD14E | rRNA | SSU-rRNA_Hsa | ACATCCAAGGAAGGTAG | 31.878 |
| SNORD59B | intergenic | intergenic | AAGAACGAAAGTCAGAA | 31.145 |
| SNORD91B | rRNA | LSU-rRNA_Hsa | ACAGGTTCAGACATTT | 29.355 |
| SNORD91B | rRNA | LSU-rRNA_Hsa | ACAGGTTCAGACATTT | 29.355 |
| SNORD57 | rRNA | SSU-rRNA_Hsa | GCTCATTAAATCAGTT | 28.968 |
| SNORD37 | intergenic | intergenic | GTCAAAGTGAAGAAAT | 28.912 |
| SNORD14A | intergenic | intergenic | ACATCCAAGGAAGGACT | 28.456 |
| SNORD14A | mRNA | KCTD10 | TCATCCAAGGAAGAAC | 28.274 |
| SNORD14B | rRNA | SSU-rRNA_Hsa | ACATCCAAGGAAGGT | 28.131 |
| SNORD14C | rRNA | SSU-rRNA_Hsa | ACATCCAAGGAAGGT | 28.131 |
| SNORD91B | rRNA | LSU-rRNA_Hsa | GCAGGTTCAGACATTT | 27.652 |
| SNORD91B | rRNA | LSU-rRNA_Hsa | CCAGGTTCAGACATTT | 27.652 |
| SNORD67 | snRNA | U6 | ATGGCCCCTGTGCA | 27.258 |
| SNORD37 | mRNA | CNTNAP5 | GTCAAAGTGAAGAAA | 27.255 |
| SNORD37 | pseudogene | AC109583.1 | GTCAAAGTGAAGAAA | 27.255 |
| SNORD45A | mRNA | CAMK2D | TGTAATTCTAGAGCTA | 27.214 |
| SNORD45C | mRNA | CAMK2D | TGTAATTCTAGAGCTA | 27.214 |
| SNORD105 | rRNA | SSU-rRNA_Hsa | AGCGTTTACTTTGAA | 27.168 |

**Table S6. Overview of SCNA regions**, consist of 36 amplification regions (Any-AP*) and 142 deletion regions (Any-DP*), that are identified from 146 RMPs in 16 types of tumors.

| SCNA ID | Genome Coordinate | SCNA ID | Genome Coordinate | SCNA ID | Genome Coordinate |
|---|---|---|---|---|---|
| Any-DP22 | chr10:18039971-38011171 | Any-DP30 | chr15:23687036-47187107 | Any-DP4 | chr2:234076904-242193529 |
| Any-AP10 | chr10:67553187-83045635 | Any-DP34 | chr15:33847092-43414476 | Any-DP1 | chr2:238550823-242193529 |
| Any-DP16 | chr10:84516936-133797422 | Any-DP31 | chr15:35232510-57223137 | Any-DP4 | chr2:238552211-242193529 |
| Any-DP25 | chr10:84517918-133797422 | Any-DP33 | chr15:37092607-43751053 | Any-DP4 | chr2:240605436-242193529 |
| Any-DP23 | chr10:99227306-133797422 | Any-DP35 | chr15:37099383-65387736 | Any-DP31 | chr22:43808440-50818468 |
| Any-DP25 | chr11:103083226-133786067 | Any-DP3 | chr1:54882224-146716040 | Any-DP45 | chr22:45147014-50818468 |
| Any-DP28 | chr11:104248923-135086622 | Any-DP3 | chr1:60968430-146716040 | Any-DP43 | chr22:45598443-50818468 |
| Any-DP17 | chr11:106051237-135086622 | Any-DP11 | chr16:1073224-90338345 | Any-DP40 | chr22:45842244-50818468 |
| Any-DP29 | chr11:107017966-122090888 | Any-DP34 | chr16:1-1772130 | Any-AP4 | chr2:27050024-31902797 |
| Any-DP2 | chr1:1-22273002 | Any-DP37 | chr16:1-860688 | Any-DP4 | chr2:29462731-119170220 |
| Any-DP2 | chr1:1-27537744 | Any-DP40 | chr16:31758063-70219917 | Any-DP5 | chr2:32038092-47339841 |
| Any-DP2 | chr1:1-27540195 | Any-AP27 | chr16:67051986-77286707 | Any-DP6 | chr2:40508595-45657277 |
| Any-DP3 | chr1:1-31503462 | Any-DP17 | chr16:74413389-90338345 | Any-AP3 | chr2:60217741-61040694 |
| Any-DP2 | chr1:1-32184201 | Any-DP18 | chr16:75653775-90338345 | Any-AP6 | chr3:162740552-198295559 |
| Any-AP17 | chr11:33521255-35407436 | Any-DP34 | chr16:85305209-90338345 | Any-AP1 | chr3:175206052-198295559 |
| Any-AP21 | chr11:34140379-35099383 | Any-DP35 | chr17:1-1921251 | Any-DP6 | chr3:183399451-198295559 |
| Any-DP1 | chr1:1-34868247 | Any-DP44 | chr17:1-4276191 | Any-DP5 | chr3:1-99843146 |
| Any-DP18 | chr11:37945516-49038091 | Any-DP12 | chr17:1-9804657 | Any-DP5 | chr3:42221061-64095595 |
| Any-AP1 | chr1:153772474-155317730 | Any-DP28 | chr17:40859914-83257441 | Any-DP5 | chr3:45787059-62264083 |
| Any-DP3 | chr1:1-5865449 | Any-AP10 | chr17:53482168-83257441 | Any-DP8 | chr4:1-12228847 |
| Any-DP2 | chr1:16449987-32474850 | Any-AP30 | chr17:58972171-82613252 | Any-DP8 | chr4:113024717-133099621 |
| Any-DP1 | chr1:1-8210429 | Any-AP22 | chr17:70437748-83257441 | Any-DP8 | chr4:68339322-99412774 |
| Any-DP13 | chr11:85844359-135086622 | Any-DP36 | chr17:80961398-83257441 | Any-DP10 | chr4:94736854-112153735 |

| | |
|---|---|
| Any-DP14 | chr11:96375540-135086622 |
| Any-DP25 | chr12:118416942-133275309 |
| Any-DP29 | chr12:121417330-133275309 |
| Any-DP20 | chr12:123244069-133275309 |
| Any-DP19 | chr12:23188659-133275309 |
| Any-DP1 | chr1:224734013-237051607 |
| Any-AP5 | chr1:234376848-235100677 |
| Any-AP17 | chr12:57692920-57857873 |
| Any-AP15 | chr12:57739474-57976149 |
| Any-DP30 | chr12:69954235-133275309 |
| Any-DP29 | chr12:72026299-133275309 |
| Any-DP25 | chr12:75427945-133275309 |
| Any-DP27 | chr12:98544935-133275309 |
| Any-AP15 | chr13:1-47260471 |
| Any-DP10 | chr13:22885862-86954491 |
| Any-DP21 | chr13:44548519-48305524 |
| Any-AP2 | chr1:38858493-43645853 |
| Any-AP2 | chr1:39574036-40078732 |
| Any-AP1 | chr1:39789450-40133402 |
| Any-DP21 | chr14:102722147-107043718 |
| Any-DP29 | chr14:103186698-107043718 |
| Any-DP19 | chr14:1-107043718 |
| Any-DP33 | chr14:1-28729025 |
| Any-DP20 | chr14:1-34433896 |
| Any-DP15 | chr14:1-34716226 |
| Any-DP30 | chr14:1-46069185 |
| Any-DP3 | chr1:78854116-146716040 |
| Any-DP19 | chr18:1-80373285 |
| Any-DP36 | chr18:36065361-74410170 |
| Any-DP2 | chr1:84139647-115055946 |
| Any-DP3 | chr1:89934392-102877252 |
| Any-DP36 | chr19:1100076-1943799 |
| Any-DP29 | chr19:1-11096366 |
| Any-DP41 | chr19:1-1912474 |
| Any-DP20 | chr19:1271276-4232571 |
| Any-DP41 | chr19:1293079-2233892 |
| Any-DP41 | chr19:1-3366418 |
| Any-DP13 | chr19:1-57774763 |
| Any-DP21 | chr19:1-58617616 |
| Any-AP43 | chr19:16565517-18004678 |
| Any-DP33 | chr19:1-7401250 |
| Any-DP42 | chr19:19351525-58617616 |
| Any-DP39 | chr19:45484771-58617616 |
| Any-DP1 | chr1:98271211-119712502 |
| Any-DP34 | chr20:1-64444167 |
| Any-AP46 | chr20:2586165-4402978 |
| Any-AP21 | chr20:43613202-50341857 |
| Any-DP37 | chr21:18220890-46709983 |
| Any-DP7 | chr2:121285113-181676580 |
| Any-DP2 | chr2:1-242193529 |
| Any-DP44 | chr21:37267476-46709983 |
| Any-DP41 | chr21:39347707-43612563 |
| Any-DP9 | chr5:103557581-114366226 |
| Any-DP14 | chr5:109877935-115172890 |
| Any-DP4 | chr5:1208683-136317879 |
| Any-AP6 | chr5:121373929-181538259 |
| Any-AP5 | chr5:151548708-181538259 |
| Any-DP11 | chr5:155014906-181538259 |
| Any-DP9 | chr5:31177078-181538259 |
| Any-DP10 | chr5:75487100-143813640 |
| Any-DP14 | chr5:78789805-135040865 |
| Any-DP18 | chr6:1-24429461 |
| Any-DP10 | chr6:128023474-170805979 |
| Any-DP13 | chr6:1-30499917 |
| Any-DP14 | chr6:149072252-170805979 |
| Any-DP12 | chr6:57309540-117487381 |
| Any-DP17 | chr6:57347010-132302870 |
| Any-DP13 | chr6:73828037-121080765 |
| Any-DP12 | chr6:79311053-98836429 |
| Any-DP14 | chr7:1-3302828 |
| Any-AP7 | chr7:21559416-37277484 |
| Any-AP8 | chr7:70337996-103926122 |
| Any-DP13 | chr8:11771885-51321318 |
| Any-AP13 | chr8:122611767-128894558 |
| Any-DP16 | chr8:15237757-29922546 |
| Any-DP15 | chr8:21895475-31643737 |
| Any-DP17 | chr8:22257058-28321147 |
| Any-DP6 | chr8:55763213-133244567 |

| | |
|---|---|
| Any-DP30 | chr14:1-49579565 |
| Any-DP1 | chr1:4418360-31368947 |
| Any-DP21 | chr14:57863913-107043718 |
| Any-DP29 | chr14:58274934-107043718 |
| Any-DP29 | chr14:81617875-107043718 |
| Any-DP34 | chr14:81618928-107043718 |
| Any-DP33 | chr14:92740008-107043718 |
| Any-DP32 | chr15:1-40693915 |
| Any-DP16 | chr15:1-56262145 |
| Any-DP23 | chr15:1-61854397 |
| Any-DP35 | chr15:1-82096090 |
| Any-DP5 | chr2:208822783-242193529 |
| Any-DP44 | chr22:1-21741481 |
| Any-DP4 | chr2:212536940-242193529 |
| Any-DP1 | chr2:213742524-242193529 |
| Any-DP14 | chr22:1-50818468 |
| Any-DP4 | chr2:217939472-242193529 |
| Any-AP36 | chr22:18124604-26431626 |
| Any-AP30 | chr22:18131163-21785126 |
| Any-DP2 | chr2:224394640-242193529 |
| Any-DP3 | chr2:227147251-242193529 |
| Any-DP5 | chr2:228174428-242193529 |
| Any-AP11 | chr8:64714595-113387382 |
| Any-AP12 | chr9:124783428-129198374 |
| Any-DP21 | chr9:38617174-111900370 |
| Any-DP15 | chrX:1-156040895 |
| Any-AP24 | chrX:133367616-156040895 |
| Any-AP30 | chrX:133560672-156040895 |
| Any-AP28 | chrX:152108541-156040895 |
| Any-AP28 | chrX:152576712-155653639 |
| Any-AP50 | chrX:153530695-155653639 |

**Table S7. Improvements of RMBase v3.0 against previous versions.**

This table describes the major improvements of data features and web-based functionalities in updated RMBase v3.0 by comparing to previous version. ([a] is Curated Data, [b] is Main Results, [c] is Web-based Functionalities)

| **Items** | **RMBase v3.0** | **previous version** |
|---|---|---|
| Species [a] | 62 species (9 clades) | 13 species (6 clades) |
| Types of RNA Modifications [a] | 73 | 47 |
| Datasets of RNA Modifications [a] | 1,886 datasets (834 WT datasets), 6 databases | 604 datasets, 3 databases |
| Datasets of $m^6A$ [a] | 689 datasets, modomics | 507 datasets, modomics |
| Datasets of $m^1A$ [a] | 72 datasets, modomics | 72 datasets, modomics |
| Datasets of $m^5C$ [a] | 38 datasets, modomics | 4 datasets, modomics |
| Datasets of pseudo [a] | 19 datasets, modomics, snoRNABase, snOPY | 16 datasets, modomics, snoRNABase, snOPY |
| Datasets of 2'-O-Me [a] | 6 datasets, modomics, snoRNABase, snOPY | 5 datasets, modomics |
| Datasets of $m^7G$ [a] | 6 datasets, modomics | modomics |
| Datasets of $ac^4C$ [a] | 4 datasets, modomics | modomics |
| Datasets of RNA-editing [a] | modomics, REDIportal, DARNED, RADAR, FairBase | modomics |
| RBP Datasets [a] | 1,439 (6 species) | (2 species) |
| RBP Biding Sites (Raw Data) [a] | 108,320,121 | 67,598,301 |
| SNV Sites [a] | 19,437,720 | 19,087,089 |
| SNP Sites [a] | 46,735,114 | 2,052,046 |
| Types of miRNA Targets [a] | 5 | 1 |
| miRNA Targets (circRNA) [a] | 1,229,615 | 0 |
| miRNA Targets (lincRNA) [a] | 83,759 | 0 |
| miRNA Targets (mRNA) [a] | 3,170,237 | 426,683 |
| miRNA Targets (pseudogene) [a] | 105,326 | 0 |
| miRNA Targets (sncRNA) [a] | 23,578 | 0 |
| Histone Modifications [a] | 14 | 0 |
| RNA Modifications Sites [b] | 2,545,031 (1,103,583 high accuracy sites) | 1,397,244 |
| RNA Modification Clusters [b] | 6,068 | 0 |
| Regularory Pairs of mod-mirTar (circRNA) [b] | 258,111 | 0 |
| Regularory Pairs of mod-mirTar (lincRNA) [b] | 10,657 | 0 |
| Regularory Pairs of mod-mirTar (mRNA) [b] | 314,520 | 45,423 |

|  |  |  |
|---|---|---|
| Regularory Pairs of mod-mirTar (pseudogene) [b] | 7,746 | 0 |
| Regularory Pairs of mod-mirTar (sncRNA) [b] | 1,684 | 0 |
| Regularory Pairs of mod-RBP binding sites [b] | 7,178,019 | 3,261,544 |
| Regularory Pairs of mod-SNVs [b] | 971,808 | 192,283 |
| Regularory Pairs of mod-SNPs [b] | 3,904 | 1,862 |
| Co-localization of RNA modifications and histone modification [b] | 13 cells, 6 RNA modifications * 32 histone modifications | 0 |
| Expression profiles of RMPs in cancers [b] | Yes | No |
| somatic mutation-driver RMPs [b] | 16 | 0 |
| SCNA-driver RMPs [b] | 38 | 0 |
| Mechanism (snoRNA-guided Ψ and 2'-O-Me) [b] | Yes | No |
| Motif [b] | 11 RNA modifications | $m^6A$ and $m^1A$ |
| RNA secondary structures [b] | Yes | No |
| Web-based Tools [c] | 3 | 2 |
| Cell/Tissues Information [c] | Yes | No |
| Evolutionary Conservation [c] | Yes | No |

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