

Supplementary Data

RMBase v2.0: Deciphering the Map of RNA Modifications from Epitranscriptome Sequencing Data

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Table S1. The source of genomes and annotations used in RMBase v2.0.

| Species | Build | Sequence | Genome annotation |
|----------------------|----------|--------------------|--------------------|
| Human | hg19 | UCSC | GENCODE v24 |
| Mouse | mm10 | UCSC | GENCODE vM11 |
| Rhesus | rheMac8 | Ensembl Release-87 | Ensembl Release-87 |
| Chimpanzee | panTro4 | Ensembl Release-87 | Ensembl Release-87 |
| Rat | rn5 | Ensembl Release-79 | Ensembl Release-79 |
| Pig | susScr3 | Ensembl Release-87 | Ensembl Release-87 |
| Zebrafish | danRer10 | Ensembl Release-87 | Ensembl Release-87 |
| <i>S. cerevisiae</i> | sacCer3 | Ensembl Release-87 | Ensembl Release-87 |
| Fly | BDGP6 | Ensembl Release-87 | Ensembl Release-87 |
| <i>A.thaliana</i> | TAIR10 | Ensembl Release-34 | Ensembl Release-34 |
| <i>S.pombe</i> | ASM294v2 | Ensembl Release-34 | Ensembl Release-34 |
| <i>E.coli</i> | ASM584v2 | Ensembl Release-34 | Ensembl Release-34 |
| <i>P.aetuginosa</i> | ASM676v1 | Ensembl Release-34 | Ensembl Release-34 |

Table S2. The data sets associated with modification sites.

| Data sets | Human | Mouse | Resource |
|---------------------|-----------|---------|-----------------------|
| RBP binding sites | 61179671 | 6418630 | starBase v2.0 |
| miRNA binding sites | 364878 | 61805 | starBase v2.0 |
| SNVs | 16782048 | / | COSMIC |
| | 4802718 | / | PMID23945592 |
| | 1644607 | / | PMID24390350 |
| SNPs | 155540826 | / | dbSNP 150 |
| | 314237 | / | GWASdb |
| | 1085981 | / | GTEX |
| | 279956 | / | ClinVar |
| | 808291 | / | CEU, CHB, JPT and YRI |

Table S3. The statistics of RNA modification sites associated with some RBPs.

| | Am | Cm | Gm | m1A | m5C | m6A | Um | Y | other | total |
|----------------|------------|------------|------------|-------------|-------------|----------------|------------|-------------|--------------|--------------|
| EIF4A3 | 996(0.49%) | 976(0.48%) | 829(0.41%) | 1645(0.81%) | 17(0.01%) | 197498(96.97%) | 445(0.22%) | 1229(0.6%) | 25(0.01%) | 203660 |
| ELAVL | 606(0.38%) | 509(0.32%) | 457(0.28%) | 721(0.45%) | 328(0.2%) | 155476(96.86%) | 355(0.22%) | 1844(1.15%) | 225(0.14%) | 160521 |
| AGO | 948(0.43%) | 870(0.39%) | 873(0.39%) | 1149(0.52%) | 668(0.3%) | 214176(96.16%) | 480(0.22%) | 3013(1.35%) | 543(0.24%) | 222720 |
| YTHDC1 | 159(1.4%) | 88(0.77%) | 125(1.1%) | 94(0.83%) | 271(2.38%) | 9770(85.91%) | 141(1.24%) | 494(4.34%) | 231(2.03%) | 11373 |
| YTHDF1 | 53(0.21%) | 54(0.21%) | 52(0.2%) | 30(0.12%) | 3(0.01%) | 25071(98.6%) | 36(0.14%) | 129(0.51%) | 0(0%) | 25428 |
| YTHDF2 | 0(0%) | 0(0%) | 1(0.06%) | 0(0%) | 0(0%) | 1670(99.64%) | 1(0.06%) | 4(0.24%) | 0(0%) | 1676 |
| WDR33 | 431(0.48%) | 362(0.4%) | 369(0.41%) | 520(0.58%) | 407(0.45%) | 86057(96.03%) | 253(0.28%) | 1003(1.12%) | 210(0.23%) | 89612 |
| NOP58 | 695(0.81%) | 483(0.56%) | 587(0.68%) | 1045(1.22%) | 527(0.61%) | 80732(94.21%) | 297(0.35%) | 1062(1.24%) | 269(0.31%) | 85697 |
| FBL | 635(0.83%) | 498(0.65%) | 577(0.75%) | 1000(1.31%) | 595(0.78%) | 71252(93.21%) | 321(0.42%) | 1151(1.51%) | 415(0.54%) | 76444 |
| FMR1 | 387(0.5%) | 459(0.59%) | 420(0.54%) | 364(0.47%) | 217(0.28%) | 74460(96%) | 287(0.37%) | 890(1.15%) | 82(0.11%) | 77566 |
| EIF3A | 2(2.15%) | 0(0%) | 0(0%) | 0(0%) | 0(0%) | 86(92.47%) | 1(1.08%) | 3(3.23%) | 1(1.08%) | 93 |
| EIF3B | 1(1.22%) | 0(0%) | 0(0%) | 1(1.22%) | 1(1.22%) | 70(85.37%) | 3(3.66%) | 3(3.66%) | 3(3.66%) | 82 |
| EIF3D | 2(1.72%) | 0(0%) | 1(0.86%) | 1(0.86%) | 1(0.86%) | 95(81.9%) | 5(4.31%) | 8(6.9%) | 3(2.59%) | 116 |
| EIF3G | 3(2.88%) | 0(0%) | 1(0.96%) | 1(0.96%) | 1(0.96%) | 83(79.81%) | 7(6.73%) | 5(4.81%) | 3(2.88%) | 104 |
| WTAP | 96(5.17%) | 87(4.68%) | 118(6.35%) | 30(1.62%) | 279(15.02%) | 431(23.21%) | 105(5.65%) | 426(22.94%) | 285(15.35%) | 1857 |
| METTL3 | 170(6.1%) | 146(5.24%) | 145(5.21%) | 38(1.36%) | 279(10.02%) | 1071(38.46%) | 110(3.95%) | 496(17.81%) | 330(11.85%) | 2785 |
| METTL14 | 169(7.23%) | 137(5.86%) | 127(5.44%) | 26(1.11%) | 234(10.02%) | 856(36.64%) | 126(5.39%) | 414(17.72%) | 247(10.57%) | 2336 |
| ALKBH5 | 9(1.68%) | 2(0.37%) | 7(1.3%) | 2(0.37%) | 2(0.37%) | 490(91.25%) | 12(2.23%) | 10(1.86%) | 3(0.56%) | 537 |

Table S4. Putative diseases-related RNA modification Sites.

| | MEL | LUAD | UCEC | Stomach Cancer | CRC | BRCA | Hepatocellular Carcinomas | HNSC | LUSC | CLL | AML |
|--------------|----------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------------------|-----------------|-----------------|-----------------|------------------|
| Am | 56(0.31%) | 50(0.4%) | 58(0.48%) | 11(0.23%) | 49(0.41%) | 23(0.57%) | 25(0.52%) | 20(0.5%) | 15(0.44%) | 3(0.53%) | 5(0.33%) |
| Cm | 42(0.23%) | 46(0.37%) | 49(0.4%) | 14(0.29%) | 43(0.36%) | 9(0.22%) | 16(0.33%) | 17(0.43%) | 9(0.26%) | 3(0.53%) | 5(0.33%) |
| Gm | 40(0.22%) | 26(0.21%) | 36(0.3%) | 16(0.33%) | 35(0.3%) | 9(0.22%) | 16(0.33%) | 12(0.3%) | 9(0.26%) | 0(0%) | 2(0.13%) |
| m1A | 107(0.59%) | 88(0.7%) | 112(0.92%) | 37(0.76%) | 102(0.86%) | 34(0.84%) | 44(0.91%) | 36(0.9%) | 14(0.41%) | 5(0.89%) | 14(0.92%) |
| m5C | 0(0%) | 17(0.13%) | 0(0%) | 1(0.02%) | 0(0%) | 3(0.07%) | 8(0.17%) | 1(0.03%) | 0(0%) | 0(0%) | 0(0%) |
| m6A | 17657 (98%) | 12262 (97.36%) | 11798 (96.96%) | 4729 (97.69%) | 11540 (97.38%) | 3908 (96.68%) | 4696 (96.92%) | 3889 (97.3%) | 3355 (97.9%) | 544 (96.45%) | 1494 (97.84%) |
| Um | 20(0.11%) | 14(0.11%) | 27(0.22%) | 6(0.12%) | 18(0.15%) | 14(0.35%) | 7(0.14%) | 4(0.1%) | 7(0.2%) | 3(0.53%) | 3(0.2%) |
| Y | 95(0.53%) | 84(0.67%) | 85(0.7%) | 27(0.56%) | 64(0.54%) | 39(0.96%) | 27(0.56%) | 18(0.45%) | 18(0.53%) | 6(1.06%) | 4(0.26%) |
| other | 0(0%) | 7(0.06%) | 3(0.02%) | 0(0%) | 0(0%) | 3(0.07%) | 6(0.12%) | 0(0%) | 0(0%) | 0(0%) | 0(0%) |
| total | 18017 | 12594 | 12168 | 4841 | 11851 | 4042 | 4845 | 3997 | 3427 | 564 | 1527 |

Figure S1. The results page of various RNA modification sites in genes by filtering “lincRNA” in “modGene” interface.

| Search Results for Human modgenes | | | | | | | | | Help | | | | | | |
|--|--------------------|---|--------|---------|---------|----------|-------------|---------|---------------------|---|---|-----|-----|------|------|
| Show 10 entries | | | | | | | | | Search all columns: | | | | | | |
| Gene | Gene ID | Gene Type | Strand | m6A Num | m1A Num | m5C Num | 2'-O-Me Num | PseudoU | | | | | | | |
| NEAT1 | ENSG00000245532.5 | lincRNA | + | 106 | 1 | 0 | 3 | 0 | | | | | | | |
| RP1-140K8.5 | ENSG00000260604.2 | lincRNA | - | 96 | 0 | 0 | 0 | 0 | | | | | | | |
| XIST | ENSG00000229807.9 | lincRNA | - | 89 | 0 | 0 | 4 | 1 | | | | | | | |
| LINC00346 | ENSG00000255874.2 | lincRNA | - | 79 | 0 | 0 | 0 | 0 | | | | | | | |
| RP11-258F22.1 | ENSG00000198105.11 | lincRNA | - | 77 | 0 | 0 | 0 | 0 | | | | | | | |
| AL133493.2 | ENSG00000233922.2 | lincRNA | + | 62 | 0 | 0 | 0 | 0 | | | | | | | |
| RP11-284F21.9 | ENSG00000272068.1 | lincRNA | - | 58 | 0 | 0 | 0 | 0 | | | | | | | |
| CTC-559E9.1 | ENSG00000267581.1 | lincRNA | - | 57 | 0 | 0 | 0 | 0 | | | | | | | |
| SPATA13 | ENSG00000182957.15 | lincRNA,processed_transcript,protein_coding,retained_intron | + | 55 | 0 | 0 | 0 | 0 | | | | | | | |
| KBTBD11-OT1 | ENSG00000176595.3 | lincRNA | + | 55 | 0 | 0 | 0 | 0 | | | | | | | |
| <input type="button" value="Search"/> <input type="button" value="Search Gene I"/> <input type="text" value="lincRNA"/> <input type="button" value="Se"/> <input type="button" value="Search"/> <input type="button" value="Search"/> <input type="button" value="Search"/> <input type="button" value="Search 2'"/> <input type="button" value="Search"/> | | | | | | | | | | | | | | | |
| Showing 1 to 10 of 1,727 entries (filtered from 23,391 total entries) | | | | | First | Previous | 1 | 2 | 3 | 4 | 5 | ... | 173 | Next | Last |

Figure S2. The results of the list of RNA modification sites associated with “FMR1” in “modRBP” interface.

| Relationships between RNA modifications and RBP binding regions in Human Help | | | | | | | | | |
|---|----------------|---------|------------|---------|---------|------------|-------------------------------|--------------------------------------|--|
| RBPID | ModID | ModType | SupportNum | RBPname | RBPtype | ClipExpNum | GeneName | GeneType | |
| RBP_site_637605 | m6A_site_99966 | m6A | 3 | FMR1 | - | 1 | HOXC11 | protein_coding | |
| RBP_site_637585 | m6A_site_99956 | m6A | 5 | FMR1 | - | 1 | HOTAIR | antisense | |
| RBP_site_637365 | m6A_site_99889 | m6A | 34 | FMR1 | - | 1 | CALCOCO1,CALCOCO1 | retained_intron,protein_coding | |
| RBP_site_636954 | m6A_site_99840 | m6A | 2 | FMR1 | - | 2 | ATP5G2,ATP5G2,ATP5G2 | retained_intron,protein_coding,prote | |
| RBP_site_636903 | m6A_site_99839 | m6A | 1 | FMR1 | - | 2 | ATP5G2,ATP5G2,ATP5G2 | retained_intron,protein_coding,prote | |
| RBP_site_636846 | m6A_site_99838 | m6A | 2 | FMR1 | - | 2 | ATP5G2,ATP5G2,ATP5G2,ATP5G2 | processed_transcript,protein_coding | |
| RBP_site_636795 | m6A_site_99835 | m6A | 8 | FMR1 | - | 1 | ATF7,ATF7 | retained_intron,protein_coding | |
| RBP_site_636760 | m6A_site_99832 | m6A | 8 | FMR1 | - | 1 | RP11-793H13.10,ATF7,ATF7,ATF7 | protein_coding,retained_intron,prote | |
| RBP_site_636447 | m6A_site_99767 | m6A | 6 | FMR1 | - | 1 | RP11-793H13.10,ATF7,ATF7 | protein_coding,protein_coding,protei | |
| RBP_site_636406 | m6A_site_99762 | m6A | 22 | FMR1 | - | 1 | TARBP2,TARBP2,TARBP2 | protein_coding,nonsense-mediated_ | |

Showing 1 to 10 of 74,460 entries (filtered from 2,886,675 total entries)

First Previous 1 2 3 4 5 ... 7446 Next Last

[Search R](#)

[Search N](#)

[m6A](#)

[Search S](#)

[FMR1](#)

[Sear](#)

[Search C](#)

[Search GeneName](#)

[Search GeneType](#)