В

•

MR766 Paraiba

KX156774 KU501215 FSS13025



С

Α

Mock

ZIKV



TCCACACTO

CTCCACACTO

AACAACAAAAAAGCACTG

AGAAGCACTGO

Peak 2

Peak 1

TABLE CONTRACT AND THE DATA CALL AND AND AND TANK TO CONTRACT AND THE CONTRACT AND THE TO CONTRACT AND THE C

Peak 3

1951 T191063194346C4490CT195174CT1950998991T1AT61CTC17CTC19764934A4806394794049444494CT146C41176TA7189 1951 T19105319434946C4490CT19517471745170598991T1AT61CC17C17C17494934A48064347947434494447446241176TA7189 1951 T1910531943496C4490CT195174CT195093991T1AT61CC17C17C1749394A480643479474494447446241176TA7189 1951 T1910531943496C4490CT195174CT195109991T1A51CC17C17C1749394A4806434794749447446241176TA7189	
10C110108C6108A846CA86CC110C1AC1150C586860111A105CC1C1C1C1GA8608AAA86GC40101GA8AA846AC11ACCA1105CA108 10C110108C6106A846CA86CC110C1AC1150C686800111A105CC1C1C1C1GA466GAAA86CA6105GA8A86AC11ACCA11105CA108 10C110108C01084A8C4369CC110C1AC1150C680800111A105CC1C1C1C1GA466GAAA86GCA8105GA8A846C11ACCA11105CA108	CCTGGGA
TIGCT TIGT GBCG TIGBAGAGCAGGCCT TIGCT ACT TIGCG GBGGG TT TA TIGCT CCT CT CT GAAGGGAAAAGGCAGT GT GAAGAAGAAGAACT TA CCAT TT GTCA TOG TIGCT TIGT GBCG TIGBAGAGCAGGCCT TIGCT ACT TIGCG GBGGG TT TA TIGCT CCT CT CT CT GAAGGGAAAAGGCAGT GT GAAGAA <mark>GAACT T</mark> A CCAT TT GTCA TOG	CCTGGGA
TGCTTGT66CGT66A6A6CA66CCTT6CTACTT6C566656GTTTAT6CTCCTCTCTCT6AA666AAA66GAA6T6T6AA6AA6AACTTACCATT6TCAT66	CCTGGGA
	CCTGGGA
TGCTCGTGGCATGGAGAGCG5GCCTGGCTACTTGTGGAGGGATCATGCTCCTCTCCCTGAAAGGGAAAGGTAGTGTGAAGAAGAAGAACCTGCCATGTGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	

Peak 4

05A GAGACCACAGA T05A GTGTACAGAGTGTACAGAGTGATCCCCAGACTGCTAGGTTCAACACAGGTT05A GTG5GAGTCTCCACAGAG5GGGGTCTTCCACACACTGAG5GAGCCCCCACTGAG5AGCGCGCGGG5AGG5AAGG5A
GSGGAGACCACAGA T GSAGTGTACAGAGTAAT GACTCGTAGACTGCTAGACTCAAGTT CAACACAAGT T GSAGTGGAGGT T AT GCAAGAGGGGGGCT T T CACACTA T GT GGCACGT CACAAAGGA T CCGCGCT GAGAAGCGGT GAAGAGGGGT CACAAAGGA T CCGCGCT GAGAAGCGGT GAAGGGGGGGACT T GA CAC
6565 <mark>635ACC</mark> ACA6AT65AGTGTACA6AGTAAT6ACTCGTA66CTGCTA69TTCAACACAA5TT65AGT65GAGTTAT6CAA6A6665GTCTTTCACACTATGT65CAC5TCACAAAA66ATCC5C5C5CT6A6AA65C6GT6AA656 <mark>A66ACTT</mark> GATC
950543454CCAC464166401614C46461444646454464646446446464464464464464446446
05060A5ACCACA6AT05A6T0TACA6A6TAAT6ACTCGTA6ACT6CTA66ATCAAA6TT05AA6T0506A6TCAT6CAA6A50656TCTTCCACACATT6A5C6C6CA6AAA666ATC05C6CT6A6AA6C66T6AA6656A5ACTT6ATC

Peak 5



Peak 6

TGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGG	GTGACAGACCATTCTGGGAAAACAGTTTGGTTCGT	TCCAAGCGTGAGAAACGGAAATGAAATCGCAGCCTGTCTGACA	AAAGGCTGGAAAGCGGGTCATACAGCTCAGCAGGAAGACT7	TTTGAGACAGAATTTCAGAAAACAAA
TGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGG	GTGACGGATCATTCTGGAAAAACAGTTTGGTTTGT	TCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACA	AAAGGCTGGAAAACGGGTCATACAGCTCAGCAGAAAGACTT	TTTGAGACAGAGTTCCAGAAAACAAA
TGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGG	GTGACGGATCATTCTGGAAAAACAGTTTGGTTTGT	TCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACA	AAAGGCTGGAAAACGGGTCATACAGCTCAGCAGAAAGACTT	TTTGAGACAGAGTTCCAGAAAACAAA
TGGAAGTCCCAGAGAGAGAGCCTGGAGCTCAGGCTTTGATTGG	GTGACGGATCATTCTGGAAAAACAGTTTGGTTTGT	TCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACA	AAAGGCTGGAAAACGGGTCATACAGCTCAGCAGAAAGACTT	TTTGAGACAGAGTTCCAGAAAACAA
TGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGG	GTGACGGATCATTCTGGAAAAACAGTTTGGTTTGT	TCCAAGCGTGAGGAATGGCAATGAGATCGCAGCTTGTCTGACA	AAAGGCTGGAAAACGGGTCATACAGCTCAGCAGAAAGACTT	TTTGAGACAGAGTTCCAGAAAACAAA

Peak 7

Peak 8

CITI CITUATE CONSIGNITION CONTRACTOR CONSIGNATION CONTRACTOR CONTR

Peak 9

TATTTGAAGAGGAAAAAGA	ATGGAAGAC	SCTOTOGAASCTO	TGAATGATCCAAGGTT	TIGGGCCCTAGTO	SATASSSASAS	ASAACACCACCTGA	GAGGAGAGTGTCAC	AGCTGTGTGTGTACAACA	150 T 655 00 0 0 0 50 500 00	GAAGCAAGGAG	AGTTCGGGAAAG
TATTTGAAGGGGGGAAAAAG	atagoogoci	CAGTOGA AGCTO	TAAACAATCCAAGATT	CTAGACTETIATO	30 C 00 G G 00 0 0	ABARCACCACCTRA	anagagagagagagagagagagagagagagagagagaga	ATTATATATATACAACA	001000000000000000000000000000000000000	000000000000000000000000000000000000000	AATTTGGAAAAGG
	GTOGAACAC	CONCTOCRACETO	TOAACOATCCAACOTT	CTOCOCTCTACTO	CACOLOGIALAG	ACACCACCACCTCA	CA COACA CTOCOACA	ACT TOTOTOTOTACAACA		GAAACAA COOCO	ATTTCCALAGE
TATTTGANGAGGAAAAAAGA	GT GGAAGACT	GCAGT GGAAGCTC	TGANCGATCCAAGGTT	CTOGGCTCTAGTO	SACAR GOARAG	AGAGCACCICA	CAGGAGAGAG TOCCAG	AGE TO	TOAT COOMAAAASA CAAAA	GAAACAA GGGGG	ATTTGGAAAOG
TATT TOAN ON OGNAMING	GIGGHAGACI	GCAGTOGAAGCTO	I GARCOATCCARGOTT	CIGGGCICIAGIO	JACAH GOAHAG	HUHULHLUHLLIUH	CHOCHOHOHO TOCOHO	HOLTOTOTOTACHACH		CHHACAHOOOG	HATTI GGHHAGG
TATT GAAGAGGAAAAAGA	GI GGAAGAC	GCAG TOGAAGC TO	I GAACGATCCAAGGTT	CIGGGCICIAGIG	SACAAGGAAAG	AGAGLALCALLIGA	CAGGAGAGAG IGCCAGA	AGCIGIGIGIACAACA	IGA I GEGAAAAAGAGAAAA	CAAACAA COOGG	AATTTOGAAAOGU

Peak 10



Peak 11

CACATGCCCTCAGGTTCTTGAATGACATGGGAAAAG	TTAGGAAAGACACACAGGAGTGGAAACCCTCGACTGGATG	GAGCAATTGGGAAGAAGTCCCGTTCTGCTCCCACCACTTCA	ACAAGCTGTACCTCAAGGATGGGAGATCCATTGTGGTC
CACATGCCCTCAGGTTCTTGAATGATATGGGAAAAA	ST TAGGAAGGACACACAAGAGTGGAAACCCTCAACTGGATG	GGACAACTGGGAAGAAGTTCCGTTTTGCTCCCACCACTTCA	ACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTT
CACATGCCCTCAGGTTCTTGAATGATATGGGAAAAG	ST TAGGAA <mark>GGACA</mark> CACAAGAGTGG <mark>AAACCC</mark> T CAACTGGATG	GGACAACTGGGAAGAAGTTCCGTTTTGCTCCCACCACTTCA	ACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTT
CACATGCCCTCAGGTTCTTGAATGATATGGGAAAAG	ST TAGGAA <mark>GGACA</mark> CACAAGAGTGG <mark>AAACCC</mark> T CAACTGGATG	GGACAACTGGGAAGAAGTTCCGTTTTGCTCCCACCACTTCA	ACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTT
CACATGCTCTCAGGTTCTTGAATGATATGGGAAAAG	TTAGGAAGGACACAAGAGTGGAAGCCCTCAACTGGATG	GGACAACTGGGAAGAAGTTCCGTTTTGCTCCCACCACTTCA	ACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTT

Peak 12

......





D







G

+ ZIKV

+ ZIKV







С

Β

Α





Figure S1. Related to Figure 1

(A) Correlation test between two biological replicates of vgRNA is shown.

(B) Alignment and m⁶A motif identity/conservation is shown for the 12 m⁶A peaks identified in ZIKV RNA among five ZIKV strains (MR766, Paraiba, KX156774, KU501215 and FSS13025). The DRACH, MGACK, and UGAC consensus motifs are highlighted in yellow.

(C) Nuclear and cytoplasmic localization of METTL3, METTL14 and ALKBH5 visualized by immunostaining of uninfected (Mock) and ZIKV-infected 293T cells at 24 h after infection. Cells were counterstained with DAPI. Scale bar, 100 µm. Arrows indicate cells with evident cytoplasmic localization of the indicated protein.

Figure S2. Related to Figure 2

(A) Silencing efficiency of shRNAs. METTL3, METTL14, and ALKBH5 expression in 293T cells expressing non-targeting shRNA (NTC) or the indicated gene-specific shRNAs, analyzed by qRT-PCR (left) or western blotting (right). N = 3.

(B, C) Viral titers (particle production) (B) and ZIKV RNA levels in supernatants (C) of 293T cells overexpressing METTL3, METTL14, or ALKBH5 proteins. N = 3.

(D) Western blot analysis of METTL3, METTL14, and ALKBH5 proteins in 293T cells expressing control pcDNA or the indicated overexpression vectors. GAPDH was probed as a loading control. All data are the mean \pm SEM of the indicated number of replicates. Student's t-test * p < 0.05, ** p < 0.005, *** p < 0.0005.

(E) Silencing efficiency of YTHDF1, 2, and 3 expression in 293T cells expressing indicated gene-specific shRNAs or non-targeting shRNA control (NTC) analyzed by qRT-PCR.

(F, G) Cell viability analyses by MTS assays in uninfected (F) and ZIKV infected (G) for specific shRNA knockdown (KD) or overexpression (OE) experiments as indicated.

Figure S3. Related to Figure 3

(A,B) Paired correlation analysis of the three biological replicates of (A) uninfected (control R1, R2, R3) and (B) ZIKV-infected samples (infect R1, R2, R3). Each paired results exhibit high correlation values, indicating good replicability.

(C) Relative mRNA level of genes listed in Suppl. Table 1 in mock or ZIKV-infected cells quantified by qRT-PCR.

Table S1, related to Fig 3 | Immune-Related Genes with Newly Gained or Lost m⁶A Peaks in ZIKV-Infected Cells

ZIKV-enriched m ⁶ A genes -	Immunity related
Gene	New m6A peak location
CREBBP	CDS
NCAM1	CDS
CLTC	CDS
KPNA2	CDS
IRF2	CDS
PML	CDS
IRF8	3'_UTR_junction
IFNAR2	3'_UTR
IFNAR1	3'_UTR
POM121	3'_UTR
SH2B1	CDS
IRS1	CDS
МАРЗКЗ	3'_UTR
KIF3C	CDS
HUWE1	CDS
UBE2E3	5'_UTR_junction
UBE2Z	3'_UTR
TRIM9	5'_UTR
UBR2	CDS
ASB3	5'_UTR
DZIP3	CDS
TAP2	CDS
AP1M1	CDS
DYNC1LI2	CDS
RAP1GAP2	CDS
IFIH1	5'_UTR
АРР	CDS
C4A	CDS
СЕВРВ	3'_UTR_junction
IKZF1	5'_UTR
TFE3	5'_UTR_junction
CACTIN	CDS
WNT5A	CDS
CSF1	CDS
ZBTB46	CDS
BMP4	CDS
PARP1	CDS
C4B	CDS
SUSD4	CDS

ZIKV-depleted m ⁶ A genes - Immunity related			
Gene	Lost m6A peak location		
TYRO3	Exon_junction		
GLI2	CDS		
PATZ1	CDS		
HMGB2	Exon_junction		
ITGB1	Exon_junction		
MOV10	CDS		
RFWD3	Exon_junction		
LRRC8A	CDS		
MYLK	Exon_junction		
HMGB2	Exon_junction		
GLI2	CDS		
SH3D19	Exon_junction		
TACC3	CDS		
ACTR1A	5'_UTR_junction		
SNRPB	5'_UTR		
KIF15	5'_UTR		
CD24	5'_UTR		
CD24	5'_UTR		
PAK1	3'_UTR		
MMP14	3'_UTR		
ERCC1	3'_UTR		
BRK1	3'_UTR		
ERCC1	3'_UTR		
BRK1	3'_UTR		
SP3	CDS		
RPS6KB2	Exon_junction		
IRS2	CDS		
MAFB	CDS		
ERCC2	Exon_junction		
LIG4	CDS		
NFKB1	Exon_junction		
CHD2	CDS		
КАТБА	CDS		
NFKB1	Exon_junction		
AGO4	Exon_junction		
IRS2	CDS		
ERCC2	Exon_junction		
ONECUT1	5'_UTR_junction		
SEC24C	5'_UTR_junction		

SUPPLEMENTAL EXPERIMENTAL PROCDURES

Lentiviral Preparation, Cell Transduction, and Viral RNA Quantification

293T cells (10⁶) were transfected with pLKO shRNA (1 µg), psPAX.2 (0.75 µg), and pMD2.G (0.25 µg) vectors using Lipofectamine 2000 and Opti-MEM (Invitrogen) according to the manufacturer's instructions. The medium was replaced with complete DMEM at 4 h post-transfection, and 48 h later, the supernatant was collected, filtered through a 0.22 µm membrane, and incubated with 293T cells in the presence of 1 µg/ml polybrene. After 12 h, the medium was removed and replaced with complete DMEM. At 3 days post-transduction, 293T cells were infected with MR766 virus at an MOI of 5. After 12 h, the medium was changed. Viral supernatants were collected and total cellular RNA was prepared at 48 h after infection. Viral titer was assessed as described above. Total RNA was extracted using TRIzol reagent (Invitrogen). mRNA expression was measured using iScript Reverse Transcription Supermix for RT-qPCR and iTaq Universal SYBR Green Supermix (Bio-Rad) for qPCR. Viral RNA released into the supernatant was measured using an iScript One Step RT-PCR kit.

Plaque-Forming Unit Assay

Confluent Vero cells were inoculated with four serial 10-fold dilutions of supernatants from infected cells. After 2 h, the cells were washed, overlaid with plaque medium containing 0.4% agarose, and cultured at 37°C for 4 days. Cells were then fixed with 3.7% formaldehyde, stained with 0.1% crystal violet in 20% ethanol, and plaques counted.

METTL3, METTL14, and ALKBH5 Overexpression

METTL3, METTL14, and ALKBH5 overexpression plasmids were constructed by cloning the corresponding cDNAs into the mammalian expression vector pcDNA3 (Invitrogen). 293T cells were transfected using Lipofectamine 2000 and Opti-MEM. The medium was replaced with complete DMEM after 4 h, and 48 h later, the cells were infected with MR766 virus at an MOI of 5. Viral supernatants were collected and total cellular RNA was prepared at 24 h post-infection. Viral titer and RNA were quantified as described above.

FLAG-YTHDF1-3 Overexpression and Immunoprecipitation

293T cells (2 × 10^6) were transfected with 2 µg FLAG-YTHDF or control pcDNA plasmids using Lipofectamine 2000 and Opti-MEM. After 4 h, the medium was replaced with complete DMEM, and 20 h later, the cells were infected with ZIKV at an MOI of 5. At 24 h post-infection, cells

were lysed with Pierce IP lysis buffer supplemented with protease inhibitors and RNaseOUT. An aliquot of cleared lysate (5%) was saved as input. The remaining lysate was incubated overnight at 4°C with 2 µg of anti-FLAG antibody (clone M2, Sigma) and 50 µl of Protein G Dynabeads (Invitrogen). Beads were washed three times with lysis buffer and divided in half for RNA extraction and RT-qPCR analysis or for western blot analysis.

Liquid Chromatography–Tandem Mass Spectrometry

Genomic RNA from MR766 ZIKV was isolated from Vero cells as described previously (Dang et al., 2016), and modified nucleoside levels were quantified using LC-MS/MS as described (Jia et al., 2011). Briefly, 50 ng of viral genomic RNA was digested by nuclease P1 (2 U, Wako) in 25 μ I of buffer containing 25 mM NaCl and 2.5 mM ZnCl₂ at 42°C for 2 h, and then NH₄HCO₃ (1 M, 3 μ I) and alkaline phosphatase (0.5 U, Sigma) were added and the samples were incubated at 37°C for an additional 2 h. The samples were diluted to 50 μ I with nuclease-free water, filtered (0.22 μ m pore size, 4 mm diameter, Millipore), and 10 μ I aliquots were taken for analysis. Nucleosides were separated on a reverse phase ultra-performance liquid chromatography C18 column with in-line mass spectrometry detection using an Agilent 6410 QQQ triple-quadrupole LC mass spectrometer in positive electrospray ionization mode. Each modified nucleoside was quantified by the ratio of modified to unmodified nucleoside levels.

Data Analysis

For data analysis, after removing the adapter, the reads were mapped to human genome (hg38) and ZIKA genome (NC_012532) by using Tophat2 (Kim et al., 2013). The peak calling method was modified from the published method (Dominissini et al., 2012). To call m⁶A peaks, the longest isoform of each Human RefSeq gene (and the whole genome of ZIKV) was scanned using a 100 bp sliding window with 10 bp steps. To reduce bias from potential inaccurate gene structure annotation and the arbitrary use of the longest isoform, windows with read counts less than 1/20 of the top window in both m⁶A immunoprecipitate and input samples were excluded. For each gene, the read count in each window was normalized by the median count of all windows of that gene. A negative binomial model was used to identify the differential windows between immunoprecipitate and input samples by using the edgeR package (Robinson et al., 2010), for each and eventually combining information from all three replicates in the two groups. The window was called as positive if the FDR was <1% and the log₂ (enrichment score) was ≥1. Overlapping positive windows were merged. The following were calculated to obtain the enrichment score of each peak (or window): (a) read counts of the immunoprecipitate sample

in the current peak/window, (b) median read counts of the immunoprecipitated sample in all 100 bp windows on the current mRNA, (c) read counts of the input sample in the current peak/window, and (d) median read counts of the input sample in all 100 bp windows on the current mRNA. The enrichment score of each window was calculated as ([a × d])/([b × c]).

Primer List

Primer	Sequence
GAPDH Fwd	TGGCGGGGAAGTCAG
GAPDH Rev	CGGAGGAGAAATCGGGC
ZIKV Fwd	TTGGTCATGATACTGCTGATTGC
ZIKV Rev	CCCTCCACGAAGTCTCTATTGC
METTL3 Fwd	GACACGTGGAGCTCTATCCA
METTL3 Rev	GGAAGGTTGGAGACAATGCT
METTL14 Fwd	TCCCAAATCTAAATCTGACCG
METTL14 Rev	CTCTAAAGCCACCTCTTTCTC
ALKBH5 Fwd	AGGGACCCTGCTCTGAAAC
ALKBH5 Rev	TCCTTGTCCATCTCCAGGAT

shRNA Sequences

shRNA	Sequence
NTC	CCGCAGGTATGCACGCGT
METTL3-1	CCGGGCAAGTATGTTCACTATGAAACTCGAGTTTCATAGTGAACA
	TACTTGCTTTTTG
METTL3-2	CCGGGCCAAGGAACAATCCATTGTTCTCGAGAACAATGGATTGT
	TCCTTGGCTTTTTG
METTL14-1	CCGGCCATGTACTTACAAGCCGATACTCGAGTATCGGCTTGTAA
	GTACATGGTTTTT
METTL14-2	CCGGGCCGTGGACGAGAAAGAAATACTCGAGTATTTCTTCTCG
	TCCACGGCTTTTT
ALKBH5-1	CCGGGAAAGGCTGTTGGCATCAATACTCGAGTATTGATGCCAAC
	AGCCTTTCTTTTG
ALKBH5-2	CCGGCCACCCAGCTATGCTTCAGATCTCGAGATCTGAAGCATAG
	CTGGGTGGTTTTTG
FTO-1	CCGGCGGTTCACAACCTCGGTTTAGCTCGAGCTAAACCGAGGTT
	GTGAACCGTTTTTG
FTO-2	CCGGTCACCAAGGAGACTGCTATTTCTCGAGAAATAGCAGTCTC
	CTTGGTGATTTTTG
YTHDF1-1	CCGGCCCTACCTGTCCAGCTATTACCTCGAGGTAATAGCTGGAC
	AGGTAGGGTTTTTG
YTHDF1-2	CCGGCCCGAAAGAGTTTGAGTGGAACTCGAGTTCCACTCAAACT
	CTTTCGGGTTTTTG
YTHDF2-1	CCGGGCTACTCTGAGGACGATATTCCTCGAGGAATATCGTCCTC
	AGAGTAGCTTTTTG
YTHDF2-2	CCGGCGGTCCATTAATAACTATAACCTCGAGGTTATAGTTATTAA
	TGGACCGTTTTTG
YTHDF3-1	CCGGTAAGTCAAAGAAGACGTATTACTCGAGTAATACGTCTTCTT
	TGACTTATTTTTG
YTHDF3-2	CCGGGAAGTCTGTTGTGGACTATAACTCGAGTTATAGTCCACAA
	CAGACTTCTTTTG

SUPPLEMENTAL REFERENCES

Dang, J., Tiwari, S.K., Lichinchi, G., Qin, Y., Patil, V.S., Eroshkin, A.M., and Rana, T.M. (2016). Zika Virus Depletes Neural Progenitors in Human Cerebral Organoids through Activation of the Innate Immune Receptor TLR3. Cell Stem Cell *19*, 258-265.

Dominissini, D., Moshitch-Moshkovitz, S., Schwartz, S., Salmon-Divon, M., Ungar, L., Osenberg, S., Cesarkas, K., Jacob-Hirsch, J., Amariglio, N., Kupiec, M., *et al.* (2012). Topology of the human and mouse m6A RNA methylomes revealed by m6A-seq. Nature *485*, 201-206.

Jia, G., Fu, Y., Zhao, X., Dai, Q., Zheng, G., Yang, Y., Yi, C., Lindahl, T., Pan, T., Yang, Y.G., *et al.* (2011). N6-methyladenosine in nuclear RNA is a major substrate of the obesity-associated FTO. Nature chemical biology *7*, 885-887.

Kim, D., Pertea, G., Trapnell, C., Pimentel, H., Kelley, R., and Salzberg, S.L. (2013). TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. Genome Biol *14*, R36.

Robinson, M.D., McCarthy, D.J., and Smyth, G.K. (2010). edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics *26*, 139-140.