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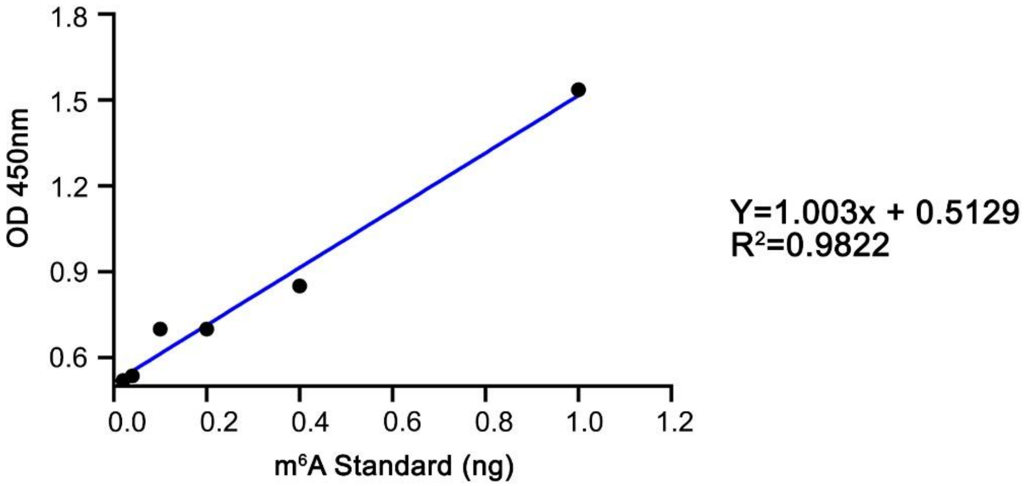
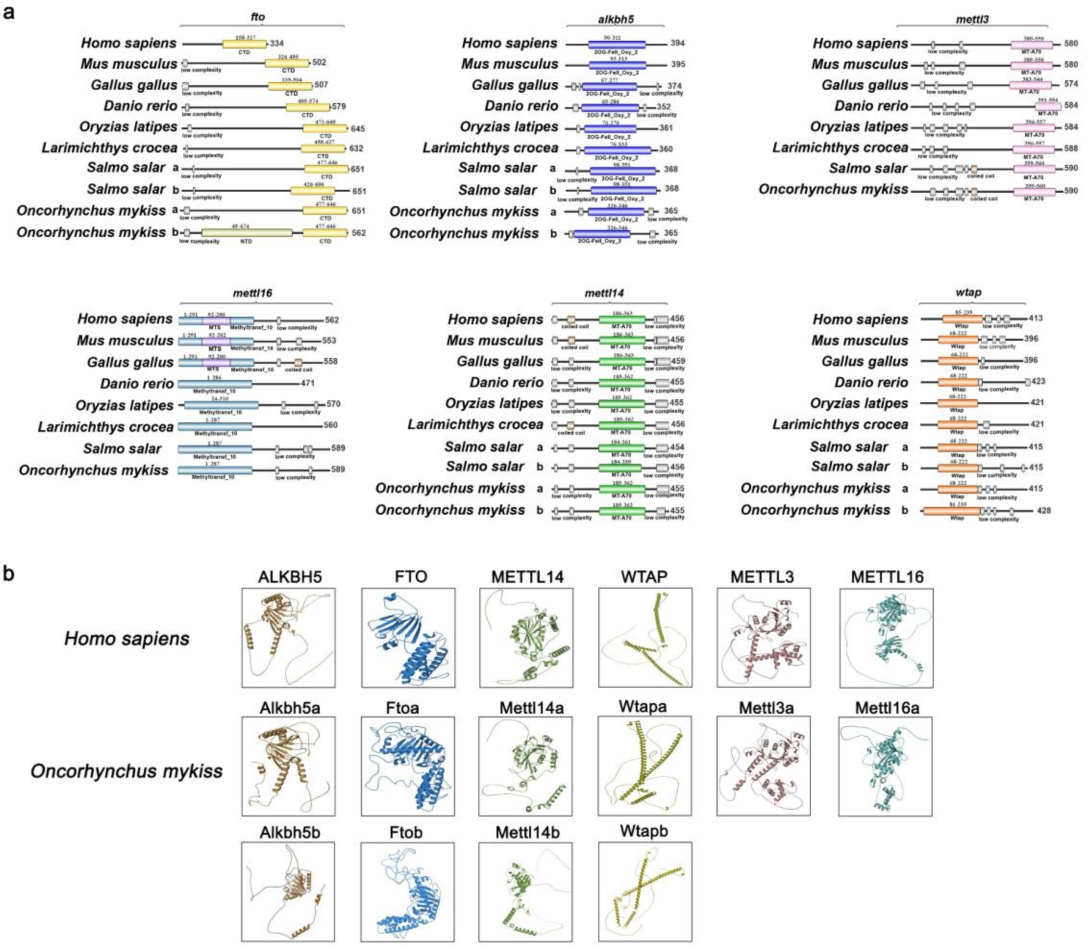


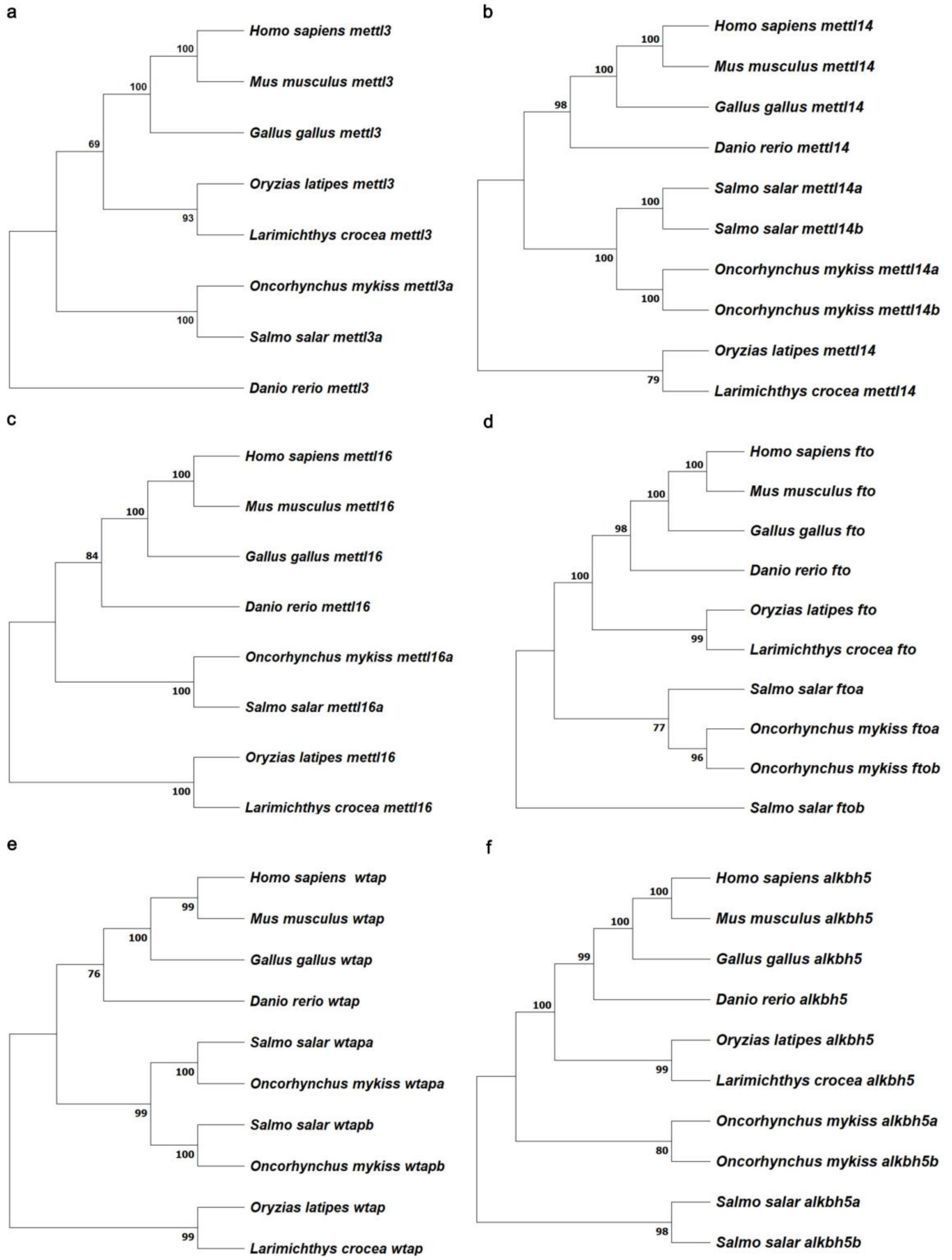
Supplementary Fig.1 Standard curve for m^{6}A quantification in *O. mykiss*.

Colorimetrical method is performed for the m^{6}A quantification. Standard substance of m^{6}A methylation is selected for the construction of standard curve at 450 nm, with showing clear linear relationship (R^2=0.9822). Data are presented as mean ± SEM from 3 independent experiments.



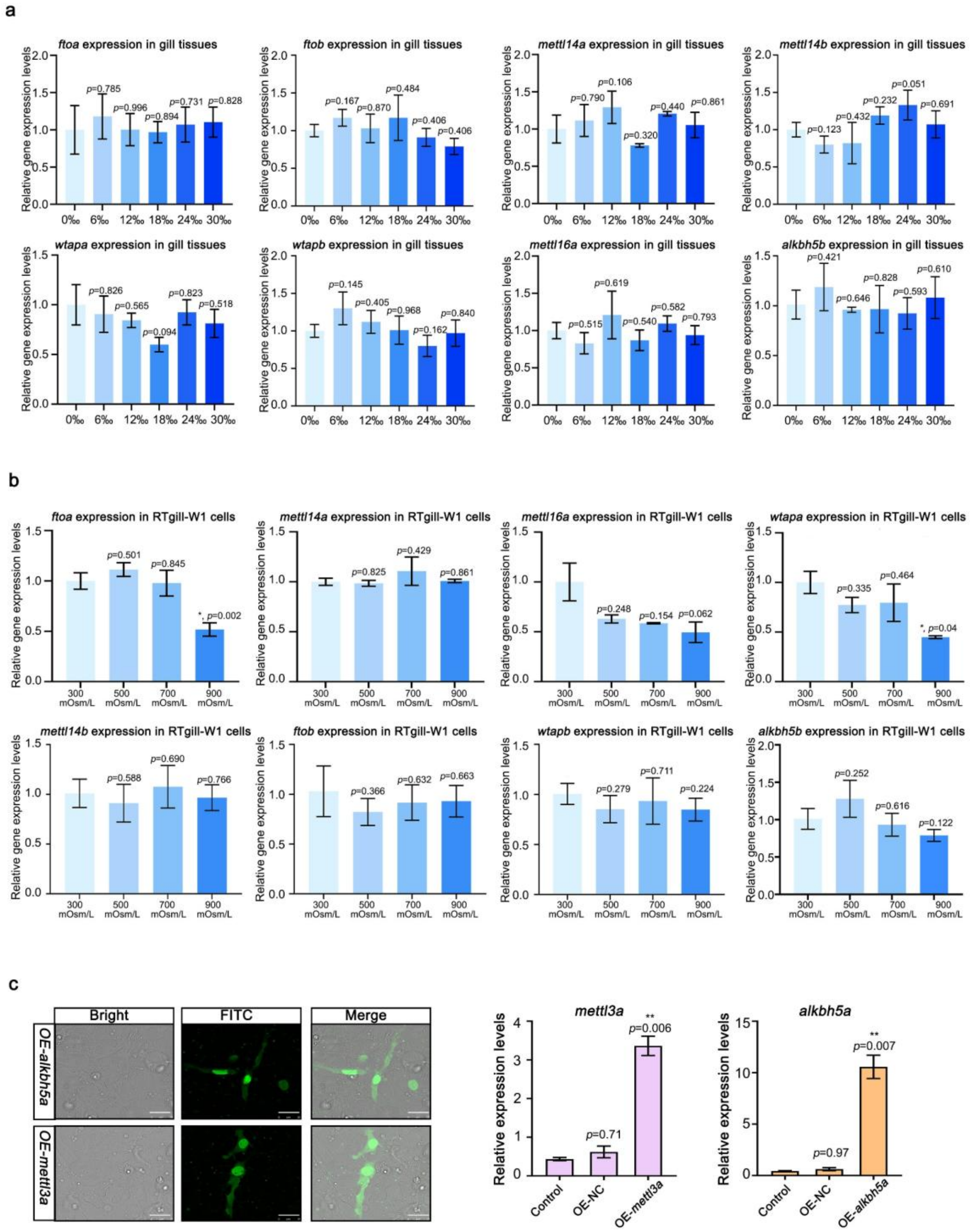
Supplementary Fig. 2 Comparative structural analysis of m^{6}A regulators genes in *O. mykiss*.

(a) Conserved domain organization of representative m^{6}A eraser and writer proteins across vertebrates, including human (*Homo sapiens*), mouse (*Mus musculus*), chicken (*Gallus gallus*), zebrafish (*Danio rerio*), Japanese medaka (*Oryzias latipes*), large yellow croaker (*Larimichthys crocea*), Atlantic salmon (*Salmo salar*) and rainbow trout (*Oncorhynchus mykiss*). Protein domains are predicted and displayed for *fto*, *alkbh5*, *mettl3*, *mettl16*, *mettl14* and *wtap* homologues. Domain positions and protein lengths are indicated above or beside each protein model; (b) Predicted three-dimensional structures of m^{6}A regulators from *O. mykiss* and Homo sapiens, generated using SWISS-MODEL and visualized in PyMOL.

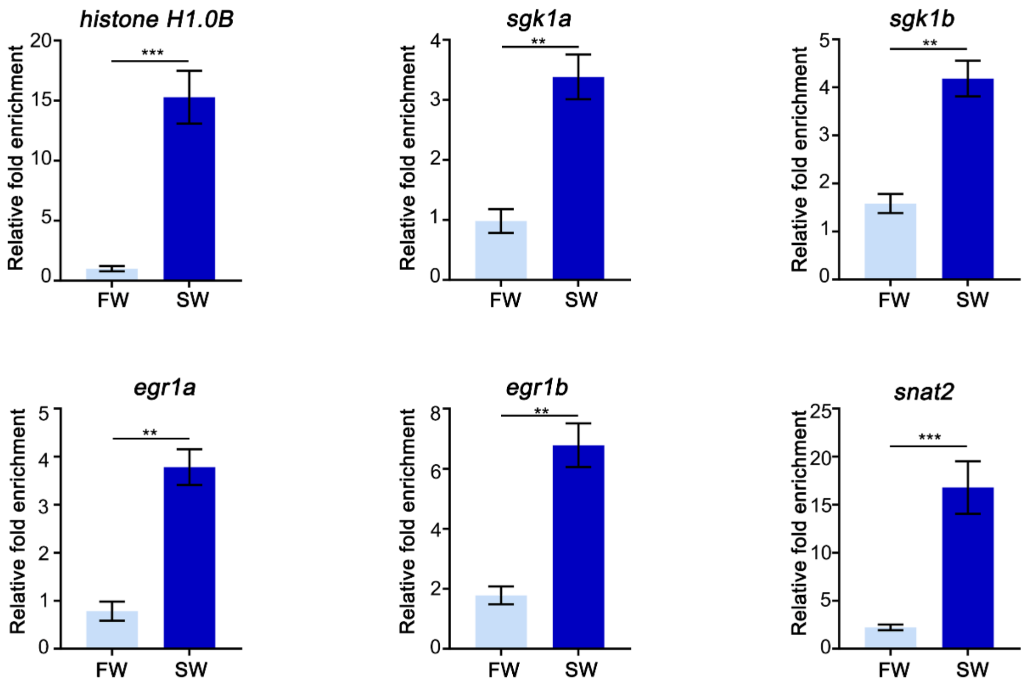


Supplementary Fig. 3 Phylogenetic analysis of representative m^{6}A writer and eraser genes across vertebrates.

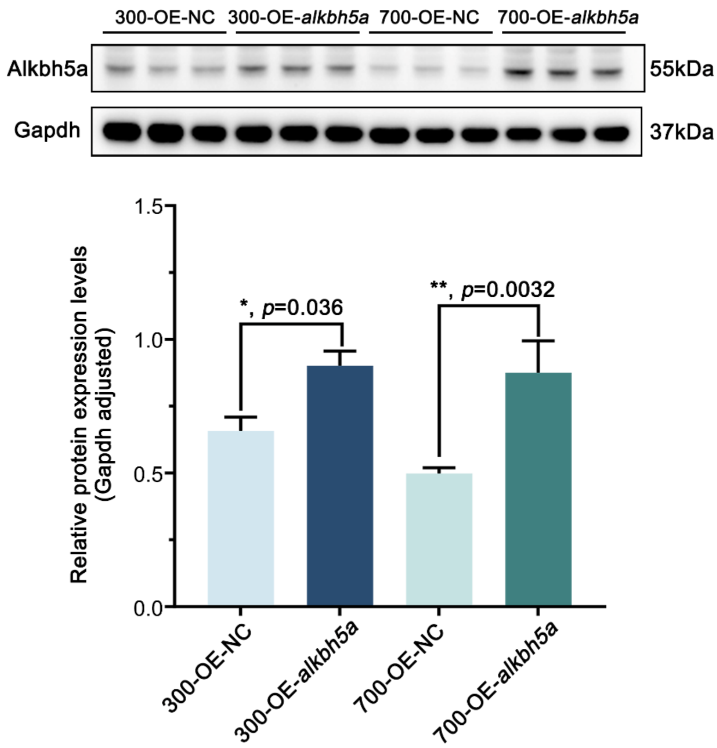
Maximum-likelihood phylogenetic trees were constructed using full-length amino acid sequences of selected m^{6}A writer and eraser genes from *Homo sapiens*, *Mus musculus*, *Gallus gallus*, *Danio rerio*, *Oryzias latipes*, *Larimichthys crocea*, *Salmo salar* and *Oncorhynchus mykiss*. Trees are shown for *mettl3* (a), *mettl14* (b), *mettl16* (c), *fto* (d), *wtap* (e) and *alkbh5* (f), respectively. There are duplicated *mettl3*, *mettl14*, *mettl16*, *fto*, *wtap* and *alkbh5* genes in *S. salar* and *O. mykiss*, due to the salmonid-specific whole genome duplication events. However, *mettl3* and *mettl16* may have undergone the pseudogenization, absent in the phylogenetic tree (a and c). Numbers at internal nodes indicate bootstrap support values from 1,000 replicates. *O. mykiss* and Atlantic salmon duplicated copies are labelled with paralogue suffixes where applicable. The phylogenies were used to support gene identity assignment and to infer orthology/paralogy relationships among conserved m^6A regulatory genes.



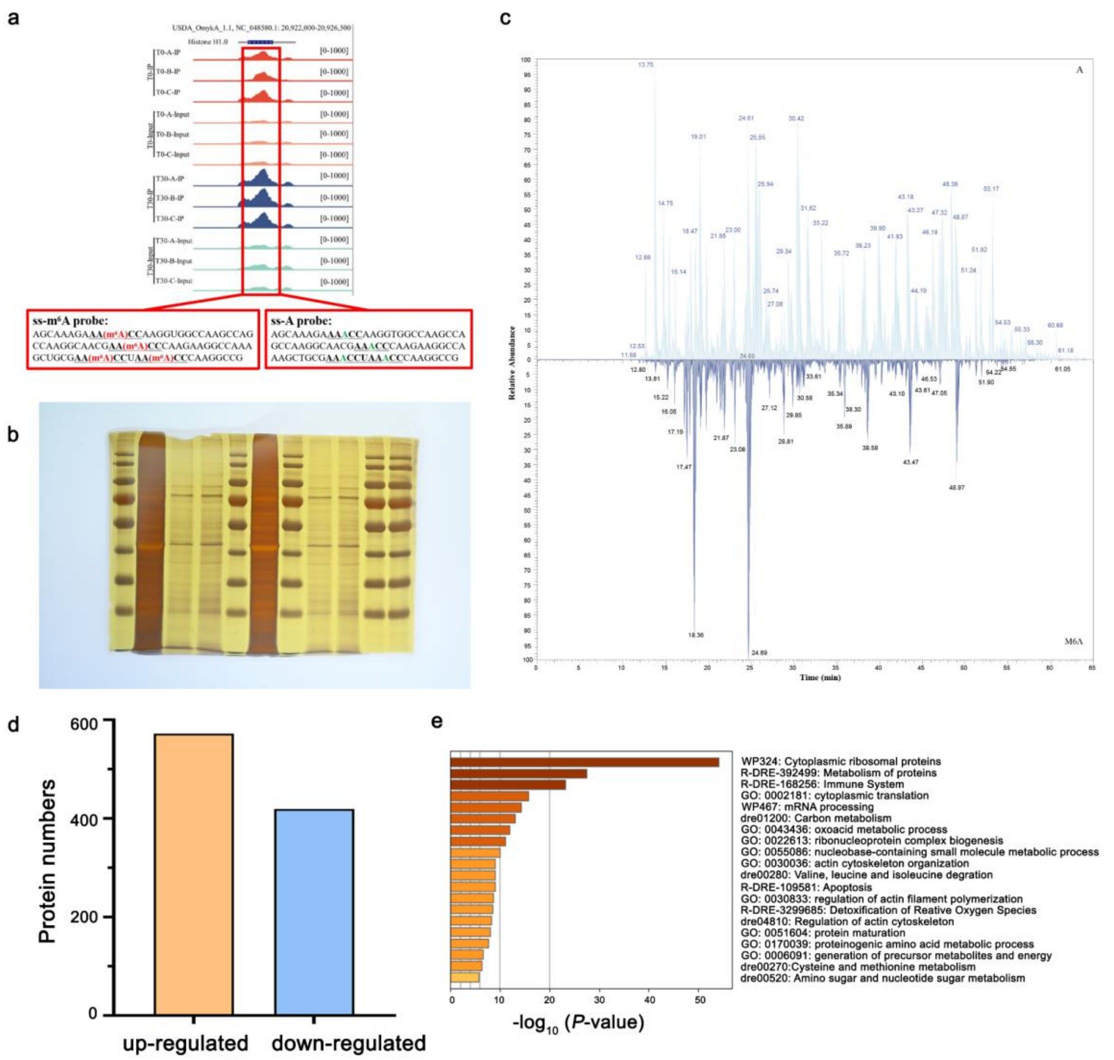
Supplementary Fig. 4 Relative expression levels of representative m^{6}A writer and eraser genes in gill tissues and gill epithelial cell line (RTgill-W1) of *O. mykiss* under different salinity conditions. (a) Expression of m^{6}A regulators in gill tissues (0‰–30‰); (b) Expression of m^{6}A regulators in RTgill-W1 cells (300–900 mOsm/L); (c) Overexpression of *alkbh5a* and *mettl3a* in RTgill-W1 cells. Left: fluorescence images of cells transfected with OE-*alkbh5a* and OE-*mettl3a* plasmids (scale bar, 20 μm). Right: validation of overexpression efficiency by RT–qPCR analysis. All qRT–PCR data are presented as mean ± SD ($n = 3$). Statistical significance was assessed using Student's t-test. ns, not significant; * $p < 0.05$; ** $p < 0.01$.



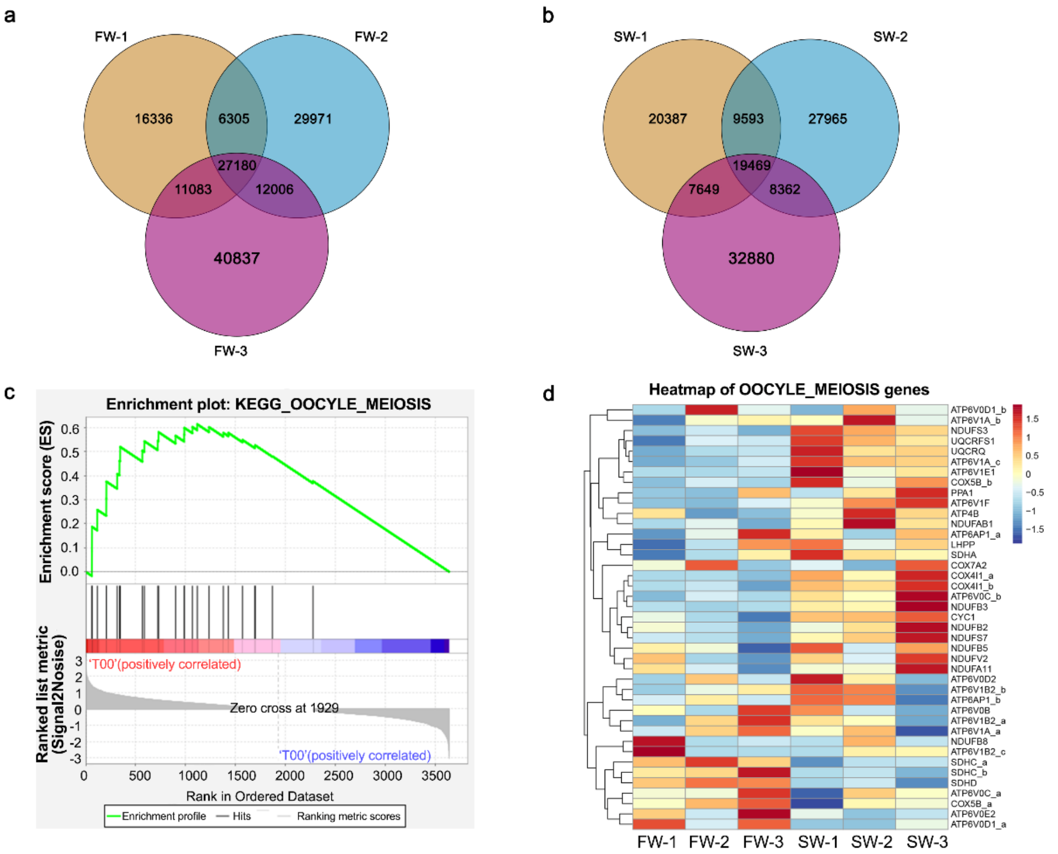
Supplementary Fig. 5 MeRIP-qPCR validation for the enrichment of m^{6A} methylation in several genes. A total of 6 genes are selected for the validation of different m^{6}A abundance between the FW and SW groups, detected by MeRIP-seq analysis, including *histone H1.0B*, *sgk1a*, *sgk1b*, *egr1a*, *egr1b*, and *snat2*. MeRIP-qPCR experiment is conducted based on the immunoprecipitation between m^{6}A antibody and mRNAs of target genes (n = 3 biologically independent experiments). Data are presented as mean ± SD. Statistical significance was evaluated using the Student's t test (*p<0.05, **p<0.01, ***p<0.001).



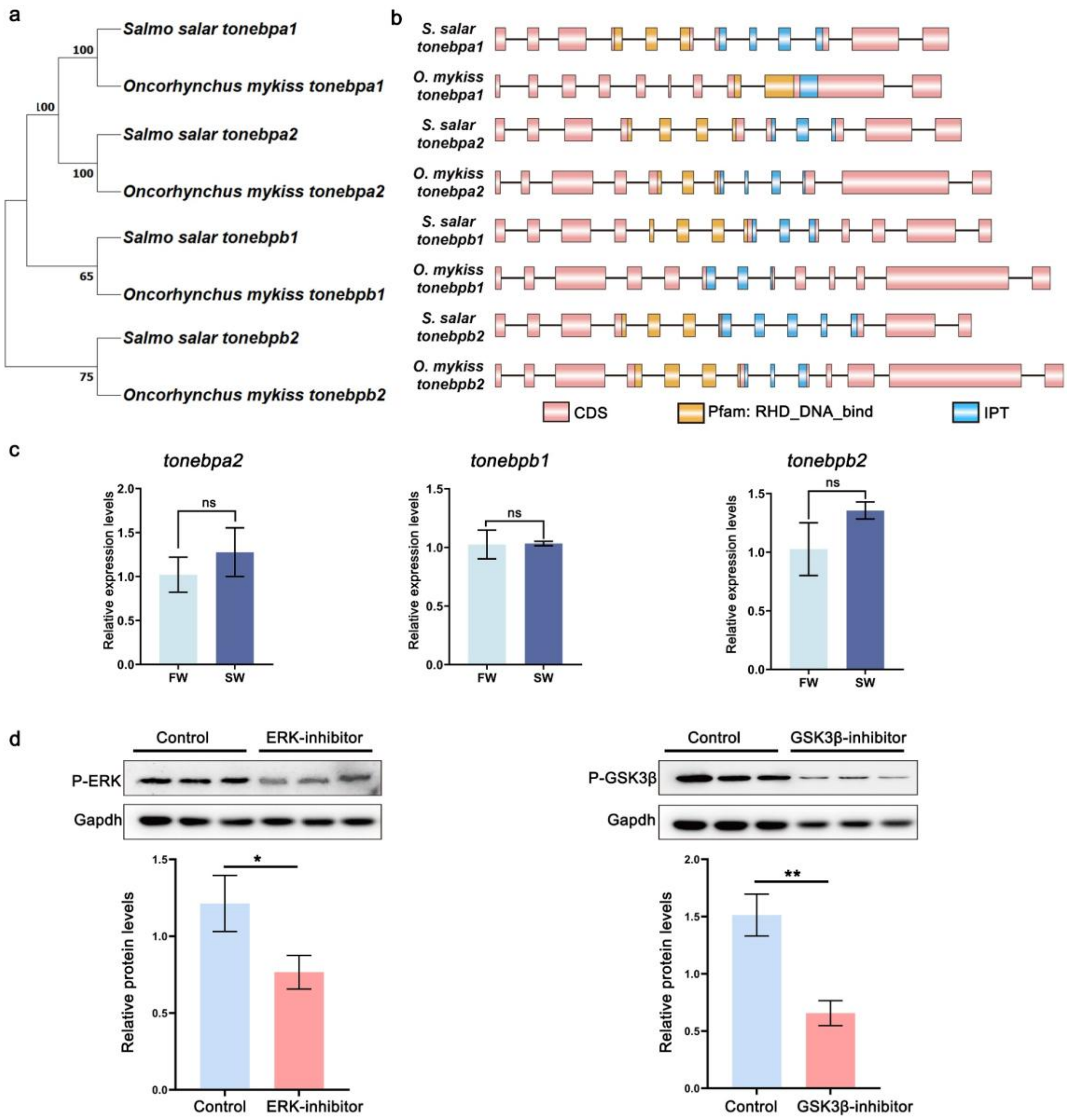
Supplementary Fig. 6 Overexpression experiment for master m^{6}A demethylase alkbh5a in the gill epithelium of *O. mykiss.* Overexpression vector of *alkbh5a* (OE-*alkbh5a* group) and empty vector (OE-NC group) are transfected into RTgill-W1 cell line under normal (300 mOsm/L) and hyper-osmotic (700 mOsm/L) conditions, respectively. Western blotting experiments are then conducted to detect the protein levels of Alkbh5a to confirm the success of transfection. Gapdh was used as the loading control. Quantification of relative protein levels is shown below representative western blot images. Data are presented as mean ± SEM. ns, not significant; *$p < 0.05$; **$p < 0.01$.



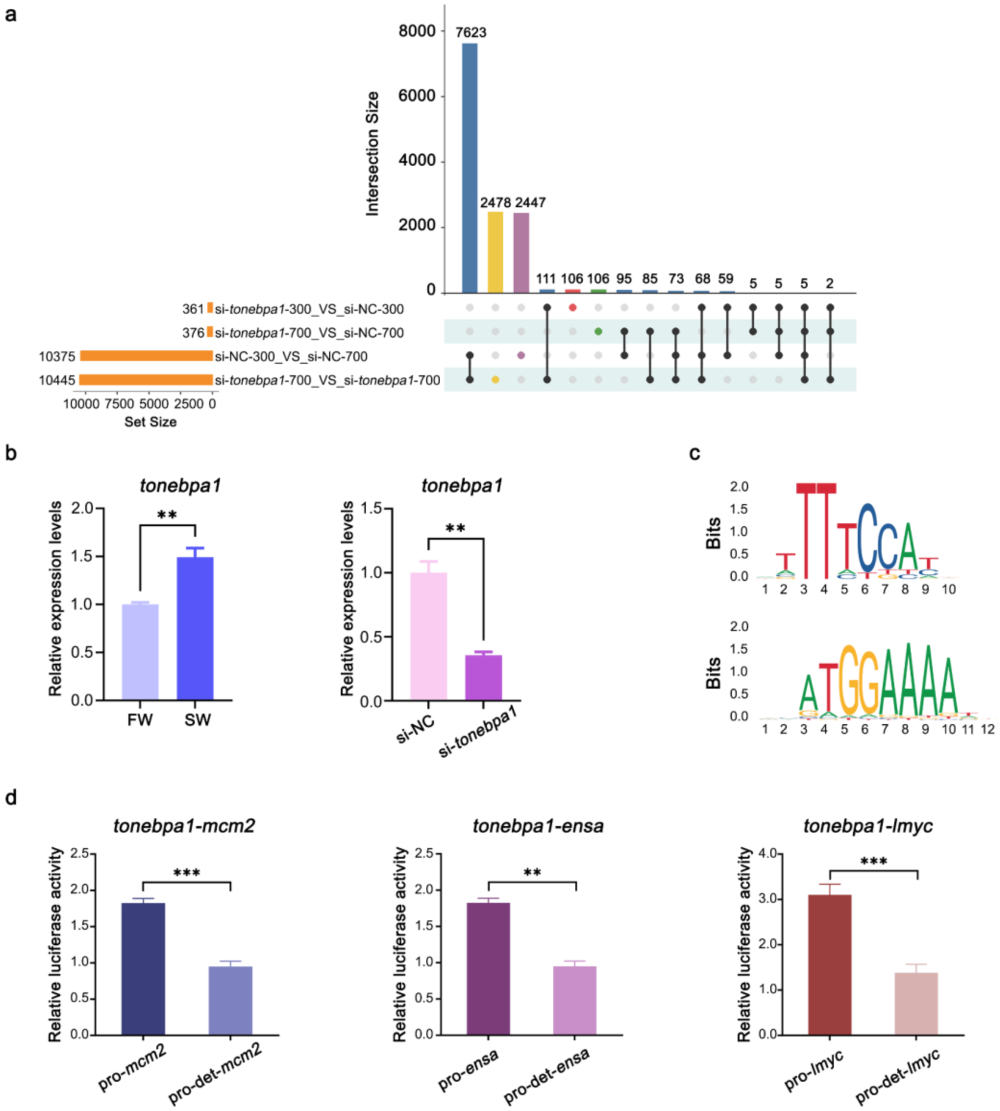
Supplementary Fig. 7 RNA pull-down and LC-MS/MS analysis for identifying the binding proteins of m^{6}A methylation on *histone H1.0B* mRNA. (a) Sequences of *histone H1.0B* ss-m^{6}A probe (positive probe) and ss-A probe (negative probe) for RNA pull-down analysis. Based on the different m^{6}A methylation abundance on *histone H1.0B* mRNAs detected by MeRIP-qPCR, biotin-labeled single-stranded RNA probes, containing m^{6}A (positive probe) or adenosine (negative probe), were biosynthesized for RNA pull-down experiment; (b) Silver staining of proteins pulled down by ss-m^{6}A probe and ss-A probe; (c) LC-MS/MS analysis identified and quantified proteins in eluents generated from RNA pull-down; (d) Different enriched proteins are pulled down between ss-m^{6}A probe and ss-A probe; (e) GO enrichment analysis reveals the potential functions of DEPs. Amino acid sequences of differentially enriched proteins are submitted to Metascape online tool for identification of their homologs so as to determine the enriched GO terms.



Supplementary Fig. 8 ATAC-seq profiling of chromatin accessibility in gill tissues of *O. mykiss* under freshwater (FW) and seawater (SW) groups. (a) Venn diagram showing the intersections of accessible chromatin regions (peaks) among 3 biological replicates of ATAC-seq (FW-1, FW-2, FW-3) in the FW group; (b) Intersections of accessible peaks among biological replicates of ATAC-seq (SW-1, SW-2, SW-3) in the SW group; (c) Gene set enrichment analysis (GSEA) of genes associated with differentially accessible chromatin regions, showing enrichment of the oocyte meiosis pathway (KEGG_OOCYTE_MEIOSIS); (d) Expression patterns of genes involved in the oocyte meiosis pathway across FW and SW samples.



Supplementary Fig. 9 Functional validation of *tonebp* paralogs in *O. mykiss.* (a) Maximum-likelihood phylogenetic tree of *tonebp* paralogs between *S. salar* and *O. mykiss*. Numbers at internal nodes indicate supporting values by 1000 bootstrap replicates. The topology reveals the close evolutionary relationships of *tonebp* genes between *S. salar* and *O. mykiss*; (b) Gene structure of four tonebp paralogs (*tonebpa1*, *tonebpa2*, *tonebpb1*, and *tonebpb2*) in *S.salar* and *O. mykiss*, showing coding sequences, conserved Pfam domains (RHD_DNA_bind) and IPT domains; (c) Relative mRNA expression levels of *tonebpa2*, *tonebpb1* and *tonebpb2* between freshwater (FW) and seawater (SW) groups. No significant differences were detected in any these *tonebp* paralogs between FW and SW groups; (d) ERK and GSK3β inhibition experiments. The experiments are performed to further validate the regulatory relationships between kinases and *tonebpa1* genes. ERK and GSK3β inhibitors are added to the culture medium of RTgill-W1 cells, and then Western blot analysis is performed for the effectiveness of inhibitors. Inhibitors significantly reduced phosphorylated levels of ERK1/2 and GSK3β. The *tonebpa1* expression is repressed as shown in Fig. 4l-m. Gapdh was used as the loading control. Quantification of relative protein levels is shown below representative western blot images. Data are presented as mean ± SEM. ns, not significant; *$p < 0.05$; **$p < 0.01$.



Supplementary Fig. 10 Expression patterns of *tonebpa1* knockdown in RTgill-W1 cells. (a) Intersections of differentially expressed genes (DEGs) among different pairwise comparisons. The si-RNAs are designed for *tonebpa1* knockdown, which are transfected into RTgill-W1 cells under normal (300 mOsm/L) and hyper-osmotic (700 mOsm/L) conditions, resulting into 4 different groups, namely si-NC-300, si-NC-700, si-tonebpa1-300, si-tonebpa1-700, respectively. Then, total RNAs of these groups were extracted and submitted for RNA-seq. DEGs were identified based on the different pairwise comparisons and strict thresholds; (b) Comparative gene expression levels of *tonebpa1*. The qPCR experiment is performed for the detection of *tonebpa1* gene expression in gill epithelium between FW and SW groups, and in RTgill-W1 between si-NC and si-*tonebpa1* groups (n = 3 biologically independent experiments); (c) Binding motifs of *tonebpa1*. As a transcription factor, *tonebp* genes are able to bind the neighbor regions of target genes. Their binding motif sequences are acquired from the JASPER database.

(d) Dual-luciferase reporter assays demonstrating the regulatory relationships between *tonebpa1* and several target genes. Three target genes, including *mcm2*, *ensa*, and *lmyc*, are selected for the validation experiment. The *tonebp* overexpression vector and reference vector (Renilla Luciferase) are co-transfection into RTgill-W1 cells. Mutating of promoter sequences directly changes their expression levels, showing by the luciferase activity. Data are mean ± SD of three independent experiments. Statistical significance was evaluated using Student's t test (**$p < 0.01$).

Supplementary Table 1 Gene information of m^{6}A regulator genes in representative vertebrate species.

Gene name	Gene ID	Chr	Genomic location	Species
mettl3	56339	14	NC_000014.9: 21498138-21511340	*Homo sapiens*
mettl3	56335	14	NC_000080.7: 52532298-52548555	*Mus musculus*
mettl3	107050363	35	NC_052566.1: 5728-28055	*Gallus gallus*
mettl3	100004398	7	NC_133182.1: 21861395-21873008	*Danio rerio*
mettl3	101169238	18	NC_136254.1: 17781145-17790359	*Oryzias latipes*
mettl3	104927608	contigs	NW_017608411.1: 50351-55950	*Larimichthys crocea*
mettl3a	139416030	18	NC_138308.1: 80553025-80559532	*Salmo salar*
mettl3b	106608831	7	NC_138297.1: 25918524-25922373	*Salmo salar*
mettl3a	110531644	9	NC_092155.1: 18254770-18260807	*Oncorhynchus mykiss*
mettl3b	110500847	21	NC_048585.1: 43405498-43409042	*Oncorhynchus mykiss*
mettl14	57721	4	NC_000004.12: 118685392-118715430	*Homo sapiens*
mettl14	210529	3	NC_000069.7: 123161944-123179639	*Mus musculus*
mettl14	422684	4	NC_052535.1: 54492812-54516443	*Gallus gallus*
mettl14	404603	1	NC_133176.1: 21568577-21573220	*Danio rerio*
mettl14	101170004	1	NC_019859.2: 14174760-14186490	*Oryzias latipes*
mettl14	104930832	contigs	NW_017608065.1: 344760-355828	*Larimichthys crocea*
mettl14a	123733213	contigs	NW_025548665.1: 15820-51503	*Salmo salar*
mettl14b	123732938	contigs	NW_025548359.1: 518260-544059	*Salmo salar*
mettl14a	110519301	contigs	NW_023493710.1: 219895-246493	*Oncorhynchus mykiss*
mettl14b	118947005	contigs	NW_023493659.1: 2462613-2483098	*Oncorhynchus mykiss*
mettl16a	110503873	24	NC_048588.1: 16763694-16798239	*Oncorhynchus mykiss*
mettl16	79066	17	NC_000017.11: 2415715-2511888	*Homo sapiens*
mettl16	67493	11	NC_000077.7: 74661658-74716649	*Mus musculus*
mettl16	431184	1	NC_052532.1: 79468206-79479158	*Gallus gallus*
mettl16	445217	15	NC_133190.1: 27686796-27745937	*Danio rerio*
mettl16	101169471	13	NC_136249.1: 19699838-19721775	*Oryzias latipes*
mettl16	104935454	contigs	NW_017608255.1: 1692-25634	*Larimichthys crocea*
mettl16a	100195164	9	NC_059450.1: 128942309-128973388	*Salmo salar*
mettl16b	110507704	27	NC_048591.1: 19522166-19537134	*Oncorhynchus mykiss*
wtap	9589	6	NC_000006.12: 159726693-159756319	*Homo sapiens*
wtap	60532	17	NC_000083.7: 13185686-13211430	*Mus musculus*
wtap	421588	3	NC_052534.1: 45292520-45316337	*Gallus gallus*
wtap	334058	20	NC_133195.1: 33718018-33724795	*Danio rerio*
wtap	101154997	24	NC_136260.1: 17672146-17678483	*Oryzias latipes*
wtap	104922544	contigs	NW_017609274.1: 1181963-1188460	*Larimichthys crocea*
wtapa	100194790	15	NC_059456.1: 55849486-55857223	*Salmo salar*
wtapb	100196682	1	NC_059442.1: 43740239-43746579	*Salmo salar*
wtapa	110522352	4	NC_048568.1: 27201542-27218948	*Oncorhynchus mykiss*
wtapb	110529887	8	NC_048572.1: 37793008-37801035	*Oncorhynchus mykiss*
fto	790682	16	NC_000016.10: 53703963-54121941	*Homo sapiens*
fto	26383	8	NC_000074.7: 92039995-92395061	*Mus musculus*

fto	415718	11	NC_052542.1: 4295663-4518110	*Gallus gallus*
fto	553363	7	NC_133182.1: 36218728-36450533	*Danio rerio*
fto	101162356	3	NC_136239.1: 33188470-33311741	*Oryzias latipes*
fto	104918019	VIII	NC_040018.1: 21965821-22080500	*Larimichthys crocea*
fto	106587595	26	NC_138316.1: 29703289-29881240	*Salmo salar*
ftob	106587580	11	NC_138301.1: 30253154-30417161	*Salmo salar*
ftoa	110526968	6	NC_048570.1: 76827001-77038395	*Oncorhynchus mykiss*
ftob	110506743	26	NC_048590.1: 37021575-37243475	*Oncorhynchus mykiss*
alkbh5	54890	17	NC_000017.11: 18183828-18209954	*Homo sapiens*
alkbh5	268420	11	NC_000077.7: 60428509-60449338	*Mus musculus*
alkbh5	770703	14	NC_052545.1: 5043695-5061240	*Gallus gallus*
alkbh5	770703	1	NC_133176.1: 9940665-9949717	*Danio rerio*
alkbh5	101168432	1	NC_136237.1: 18758509-18764990	*Oryzias latipes*
alkbh5	104921183	contigs	NW_017608462.1: 1424210-1429959	*Larimichthys crocea*
alkbh5a	106594281	2	NC_059443.1: 93319743-93325755	*Salmo salar*
alkbh5b	106593210	12	NC_059453.1: 2182228-2191788	*Salmo salar*
alkbh5b	118949617	contigs	NW_023493746.1: 68819-76888	*Oncorhynchus mykiss*
alkbh5a	118947576	contigs	NW_023493669.1: 380651-386909	*Oncorhynchus mykiss*

Supplementary Table 2 Primer sequences for RT-qPCR and MeRIP-qPCR experiments.

Gene name	Primer sequence (5’ - 3’)
mettl3a	Forward (F): ATTGGAAGGCTGGAGGAGGAAGG
	Reverse (R): TGCTGGTTCAGGAGGCTCTCTATC
mettl14a	Forward (F): CGCCAGATGAGAGCAACCCTTATG
	Reverse (R): GATGAAGTTCTGTGGTCGGTGTCC
mettl14b	Forward (F): GGACACCGACCACAGAACTTCA
	Reverse (R): GGCTCCAGCAGGATCACATCA
mettl16a	Forward (F): TATCGGTACTGGAGCGTCCTGTATC
	Reverse (R): TGGTGGCATAGTCAAAGCAGATGTC
wtapa	Forward (F): CTGCTGTGGTTGCCATCGTCTC
	Reverse (R): CCAGTATGTGTTGACCGCCTTAGC
wtapb	Forward (F): ACGATGTGACTGGGCTGAAGGA
	Reverse (R): GGTTGCTGGACTTGCTTGAGGTA
ftoa	Forward (F): CCAGGAATGCTCTAATCTC
	Reverse (R): TCCCATAATACGGCTCTT
ftob	Forward (F): GTCAAGACACGGCGACGAGAT
	Reverse (R): GCCACTCTGCTGGTCTTCATCC
alkbh5a	Forward (F): GTCATTGAGGGCAAGATAAA
	Reverse (R): CGCCTGGTTGGTAGTCGT
alkbh5b	Forward (F): CGTAGCAACAGCTCCGAGAA
	Reverse (R): ATCCAGTCCGGTGTTCAGTG
18S rRNA	Forward (F): ATGGCCGTTCTTAGTTGGTG
	Reverse (R): TCAGTCTCGTGTGGCTGAAC
OE-*mettl3a*	Forward (F): CAAAGAGGAGTGTACGCGGT
	Reverse (R): GGGGCGTCGATCTCATAGTG
OE-*alkbh5a*	Forward (F): GGCGGGGTTACAGTAAGACT
	Reverse (R): AGTCTTCACGTTGTGGTTCTCT
Histone H 1.0B	Forward (F): CGGGAATACTTGAACTGAACC
	Reverse (R): CATGGACGGCTGCCTTAA
serine/threonine-protein kinase Sek 1a (sgk1a)	Forward (F): CTCCTATGGACCCGCTGAC
	Reverse (R): GCAAACCTCCTAAACTGCTCTAA
serine/threonine-protein kinase Sek 1b (sgk1b)	Forward (F): CCACTCTGGGTTAGGATT
	Reverse (R): TTTACTAACTAGGACGGACTC
early growth response protein 1a (egr1a)	Forward (F): CCGGTTTCAACTCTGGCTCT
	Reverse (R): CGTCAAGGACTGGGCAAAGA
early growth response protein 1b (egr1b)	Forward (F): CCTTTCCATCCTCTGTCGCT
	Reverse (R): AGTCCACCCTCTCTCCAAAGA
sodium-coupled neutral amino acid transporter2 (snat2)	Forward (F): TGGATCAACAACGCCTCACA
	Reverse (R): TTGGGTAGCAGTCTTAGCGG
hnrnpab1	Forward (F): ATGAAGCCGAGGAAGAACTGAA
	Reverse (R): AACAAGATGAACCCAAACCCAC
tonebpa1	Forward (F): AACGGTTGTCTGGGTCCATT

	Reverse (R): CCAACGAACATTAGCGGGCA
tonebpa2	Forward (F): CCAGACTCAGCAGATAAGTCCC
	Reverse (R): CAGGGTCAGAGGCCAGATAA
tonebpb1	Forward (F): TGCCAAATAGCGTTTTGTTTGTT
	Reverse (R): CCCTCAGATATGAACGTCGCT
tonebpb2	Forward (F): AGCGTGTTACACAGGCTAAT
	Reverse (R): ACCGTCGTTGAGCTAGCAA

Supplementary Table 3 Statistics of MeRIP-seq data.

Sample ID	Raw reads	Raw bases (Gb)	Clean reads	Clean bases (Gb)	Clean base percentage (%)	Q20	Q30	Aligned reads
FW_A_IP	36,380,770	5.46	35,864,342	5.14	94.15	97.96	94.31	33,054,956 (92.17%)
FW_B_IP	42,665,344	6.40	41,826,482	5.74	89.72	97.55	93.66	36,572,134 (87.44%)
FW_C_IP	39,779,548	5.97	39,143,460	5.58	93.52	97.79	93.99	35,570,325 (90.87%)
SW_A_IP	39,455,494	5.92	38,844,038	5.51	93.18	97.88	94.17	35,490,370 (91.37%)
SW_B_IP	40,600,906	6.09	39,865,770	5.68	93.34	97.72	93.86	36,076,365 (90.50%)
SW_C_IP	39,394,694	5.91	38,682,478	5.54	93.67	97.74	93.92	35,070,278 (90.66%)
FW_A_input	43,432,834	6.51	43,130,074	6.00	92.08	98.32	95.01	40,255,203 (93.34%)
FW_B_input	51,458,960	7.72	51,085,382	7.10	91.98	98.26	94.88	47,302,137 (92.59%)
FW_C_input	46,685,974	7.00	46,364,812	6.47	92.36	98.25	94.86	43,129,341 (93.02%)
SW_A_input	39,685,724	5.95	39,408,788	5.50	92.32	98.27	94.9	36,806,038 (93.40%)
SW_B_input	51,513,130	7.73	51,171,186	7.14	92.42	98.29	94.96	47,529,949 (92.89%)
SW_C_input	46,950,068	7.04	46,634,446	6.50	92.37	98.32	95.02	43,027,179 (92.27%)

Supplementary Table 4 Characteristics of *histone H1.0B* gene in *O. mykiss.*

Gene name	Gene ID	Chr	Genomic location	Species
histone H1.0B	110491606	16	NC_048580.1: 20924087-20925551	*Oncorhynchus mykiss*

Supplementary Table 5 Sequences for *histone H1.0B* m^{6}A probes.

name	Probe sequence (5’ - 3’)
ss-m^{6}A	AGCAAAGAAA**m^{6}A**CCAAGGUGGCCAAGCCAGCCAAGGCAACGAA**m^6**
Positive probe	**A**CCCAAGAAGGCCAAAGCUGCGAA**m^{6}A**CCUAA**m^{6}A**CCCAAGGCCG
ss-A	AGCAAAGAAA**A**CCAAGGUGGCCAAGCCAGCCAAGGCAACGAA**A**CCC
Negative probe	AAGAAGGCCAAAGCUGCGAA**A**CCUAA**A**CCCAAGGCCG

Supplementary Table 6 Characteristics of *hnrnpab* paralog genes in *O. mykiss.*

Gene name	Gene ID	Chr	Genomic location	Species
hnrnpab1	110537820	12	NC_048576.1: 56575548-56581114	*Oncorhynchus mykiss*
hnrnpab2	110504804	31	NC_050571.1: 23844402-23848266	*Oncorhynchus mykiss*
hnrnpab3	110533317	10	NC_048574.1: 8302180-8308063	*Oncorhynchus mykiss*
hnrnpab4	110488598	14	NC_048578.1: 4963367-4969132	*Oncorhynchus mykiss*

Supplementary Table 7 Characteristics of *tonebp* paralog genes in *O. mykiss.*

Gene name	Gene ID	Chr	Genomic location	Species
tonebpa1	106561332	10	NC_138300.1: 98286056-98309736	*Salmo salar*
tonebpa1	110496711	2	NC_048566.1: 77697226-77716788	*Oncorhynchus mykiss*
tonebpa2	106573386	16	NC_138306.1: 24229993-24251784	*Salmo salar*
tonebpa2	110521983	1	NC_048565.1: 35709824-35731063	*Oncorhynchus mykiss*
tonebpb1	106562092	11	NC_138301.1: 19957225-20021754	*Salmo salar*
tonebpb1	110506508	26	NC_048590.1: 26344232-26404304	*Oncorhynchus mykiss*
tonebpb2	106587185	26	NC_138316.1: 19198743-19251578	*Salmo salar*
tonebpb2	110526388	6	NC_048570.1: 66506911-66565353	*Oncorhynchus mykiss*

Supplementary Table 8 Probe sequences for fluorescence in situ hybridization of *nka* and *tonebpa1.*

Gene name	Primer sequences (5’ - 3’)
tonebpa1	Forward (F): ATTTAGGTGACACTATAGCTCGAGATGCCCTCTGATTTTATATCCCTC Reverse (R): TAATACGACTCACTATAGGGGAATTCTCACTGCTCCTGTAGGCTC
nka	Forward (F): ATTTAGGTGACACTATAGGGAAGGCTGGAGGAGGAAGG Reverse (R): TAATACGACTCACTATAGGGATGAACCCAAACCCAAGCCTCTTA

Supplementary Table 9 Sequences of siRNAs for *tonebpa1* knockdown in *O. mykiss.*

Gene name	Sequences (5’ - 3’)
si-*tonebpa1*-s	CGACCAGACCUCUGCUCAU
si-*tonebpa1*-a	AUGAGCAGAGGUCUGGUCG

Supplementary Table 10 Primer sequences for dual-luciferase assays.

Gene name	Primer sequences (5' - 3')
tonebpa1	Forward (F): CTCGAGATGCCCTCTGATTTTATATCCCTC
	Reverse (R): GAATTCTCACTGCTCCTGTAGGCTC
mcm2	Forward (F): GAGCTCAGGAGCATGCCATAGCTACAAT
	Reverse (R): CTCGAGATATGAGACCCGATCCAGTCGATC
ensa	Forward (F): GAGCTCCGCACCAATAACCAACCAACTGTC
	Reverse (R): CTCGAGACCGCGCTTAGCTACTTTGTTGCTC
lmyc	Forward (F): GGTACCTGACTGGCAAATCGAGGCA
	Reverse (R): CTCGAGCAGCCCATCTGTAAATAGCCCA
mcm-det	Forward (F): CTTACCATCTCTCCACTGCCTTTTCCATGACCTGACCAG
	Reverse (R): CTGGTCAGGTCATGGAAAAGGCAGTGGAGAGATGGTAAG
ensa-det	Forward (F): GGTATTTATCTGAATGTTACCGGAAAACCATCCCAGATAG
	Reverse (R): CTATCTGGGATGGTTTTCCGGTAACATTCAGATAAATACC
lmyc-det	Forward (F): ATAAATACATTTTATTTAACCGGAAAATTCTGTGAACTGGC
	Reverse (R): GCCAGTTCACAGAATTTTCCGGTTAAATAAAATGTATTTAT