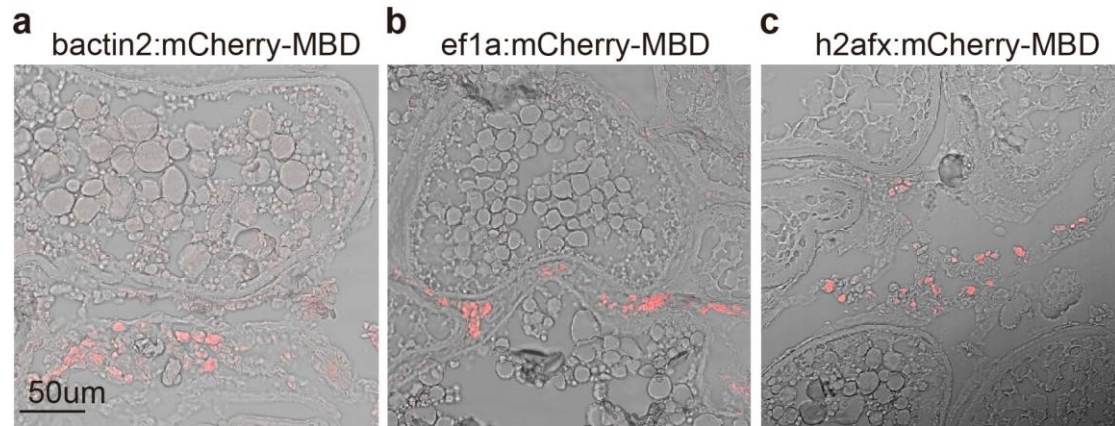


## High Resolution Imaging of DNA Methylation Dynamics using a Zebrafish Reporter

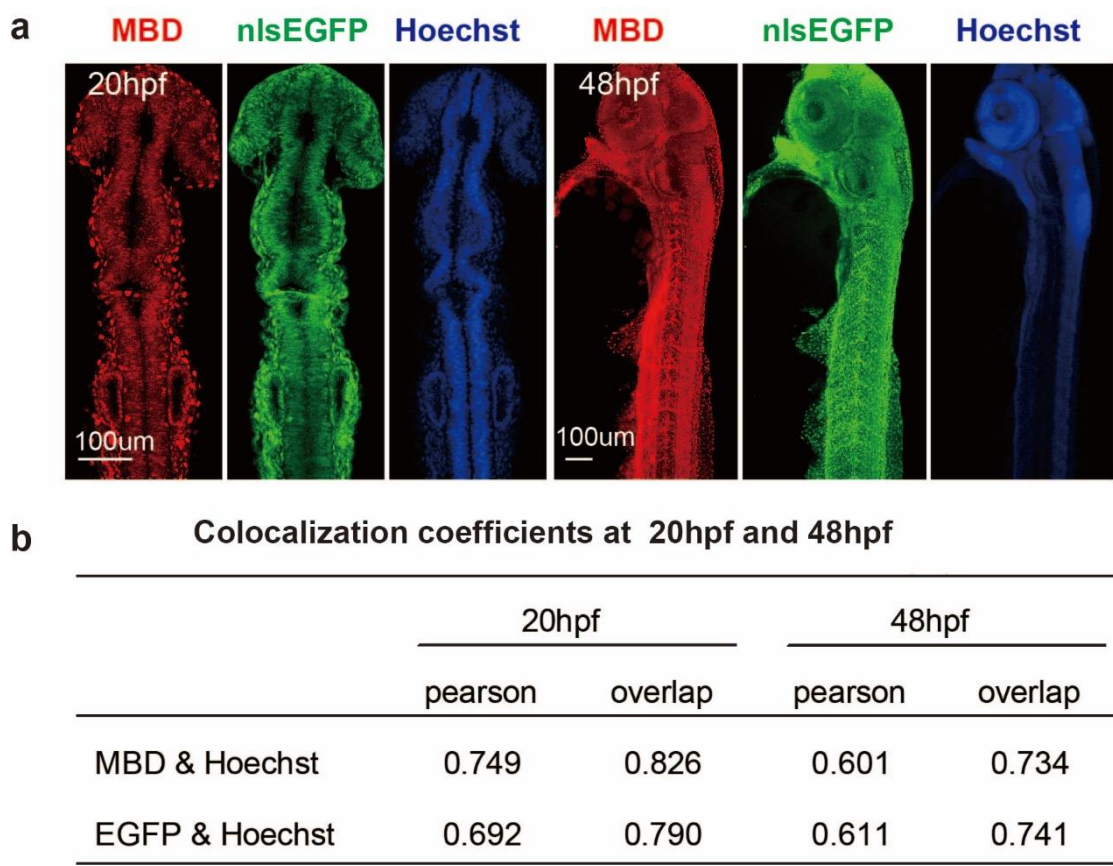
Ranran Zhang<sup>1</sup>, Lian Liu<sup>1</sup>, Yuxiao Yao<sup>2</sup>, Fei Fei<sup>2</sup>, Feng Wang<sup>1</sup>, Qian Yang<sup>1</sup>, Yonghao Gui<sup>1\*</sup>, Xu Wang<sup>2\*</sup>

### Supplementary Fig.S1 The distribution of the probe mCherry-MBD in F0 mosaic's ovaries



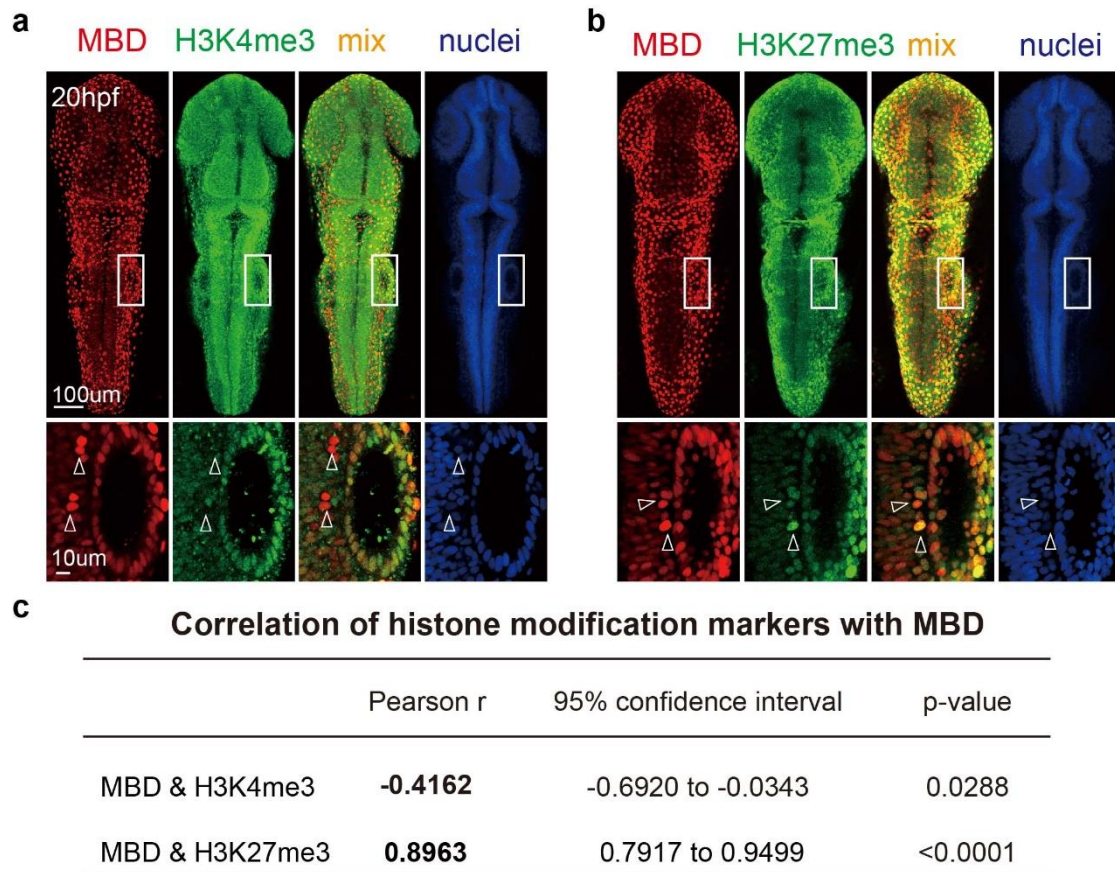
**Fig.S1 (a-c)** The distribution of the probe mCherry-MBD in the ovaries' section of adult *Tg(bactin2:mCherry-MBD-IRES-nlsEGFP)*, *Tg(ef1a:mCherry-MBD-IRES-nlsEGFP)*, and *Tg(h2afx:mCherry-MBD-IRES-nlsEGFP)* respectively.

Supplementary Fig.S2 The distribution pattern of the probes mCherry-MBD and nlsEGFP at 20hpf and 48hpf



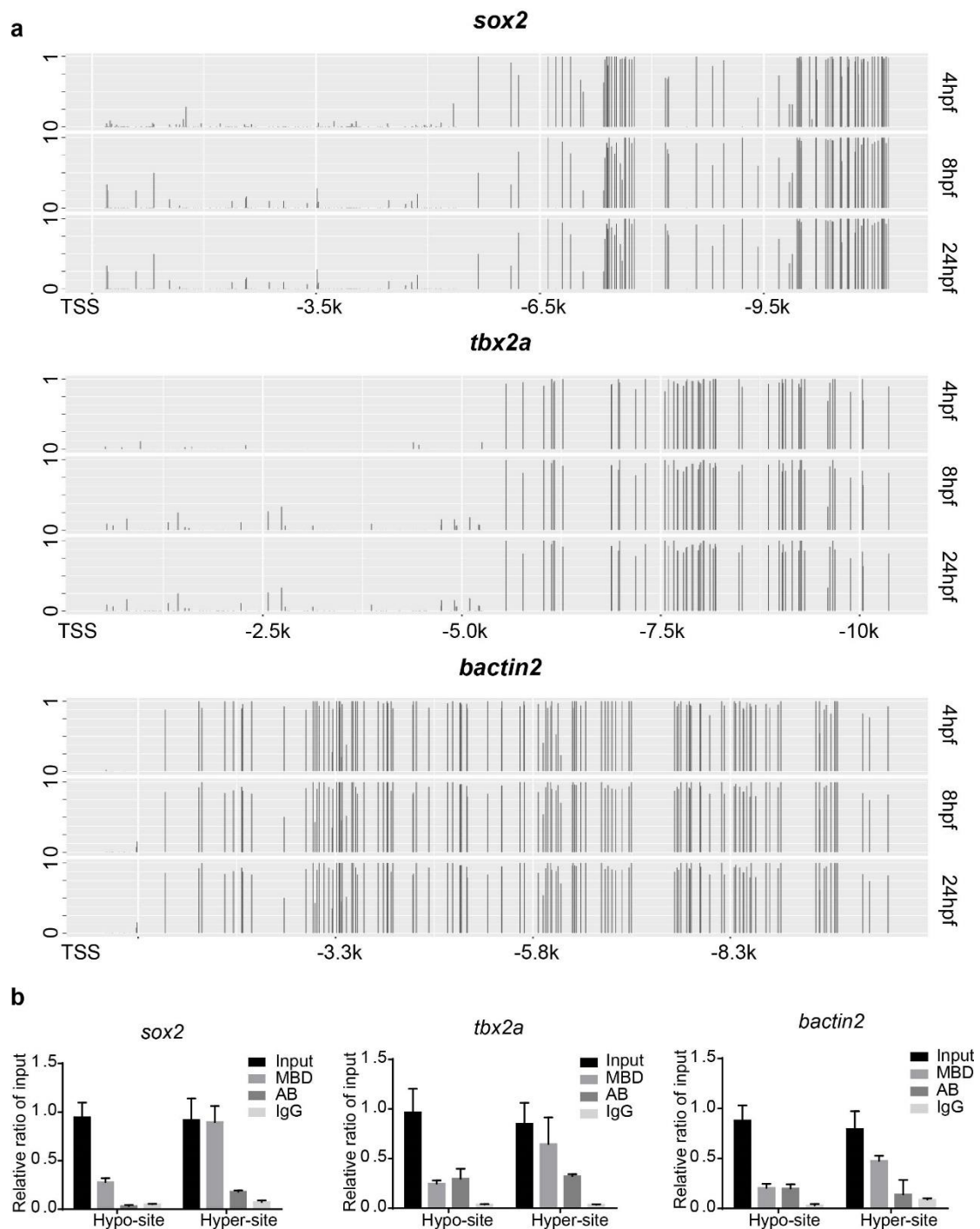
**Fig.S2 (a)** The distribution pattern of the probe mCherry-MBD and the probe nlsEGFP in embryos at 20hpf and 48hpf. **(b)** The pearson's correlation and overlap coefficient of chromosome and mCherry-MBD.

Supplementary Fig.S3 The correlation of tri-methylated H3K4/H3K27 with mCherry-MBD at 20hpf



**Fig.S3 (a)** The correlation between mCherry-MBD and H3K4me3 at 20hpf. The images in white boxes are magnified below. White arrowheads denote overlapping cells. **(b)** The correlation between mCherry-MBD and H3K27me3 at 20hpf. **(c)** The pearson's correlation and overlap coefficient of trimethylated H3K4/H3K27 and mCherry-MBD in general view.

**Supplementary Fig.S4 Specific genes' methylation status and the enrichment in mCherry-Chip DNA.**



**Fig.S4 (a)** DNA methylation status in the upstream of TSS from genes *sox2*, *tbx2a*, *bactin2* at 4hpf, 8hpf and 24hpf. TSS, transcriptional start site. **(b)** The enrichment of hypo-/hyper-methylated sites from genes *sox2*, *tbx2a*, *bactin2* through mCherry-mediated Chip-qPCR. Columns represent the enrichment level of specific sites in different group. The columns were normalized to their input group. Hypo-site, hypomethylated site; Hyper-site, hypermethylated site.

Supplementary Table 1 Primers for Chip-qPCR

primer name	primer sequence
sox2 hypo F	ACCCCCACCAAACATAATGA
sox2 hypo R	AAAAAGCCAGCCCATTACCT
sox2 hyper F	GGCCTGGATTGCTGATGTAT
sox2 hyper R	CATTGAGGGTTTGCAGGAGT
tbx2 hypo F	AGCCATTAATTCCACATTGC
tbx2 hypo R	ACCGACAGGCAGAGGAAAAT
tbx2 hyper F	CCCTGAATGATCAGCTCCAT
tbx2 hyper R	CAGTTTCGACCTTGCAGTGA
bactin2 hypo F	TGGAATTTGCCAAAAACAAA
bactin2 hypo R	TGTGCTTGAGCAGCAGTGAT
bactin2 hyper F	GCTTCCCCTTCTTTCACTCTC
bactin2 hyper R	CATACCCGGCTCTAGCCATA