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Supplemental Information

**Comparison of RNA m⁶A and DNA
methylation profiles between mouse female
germline stem cells and STO cells**

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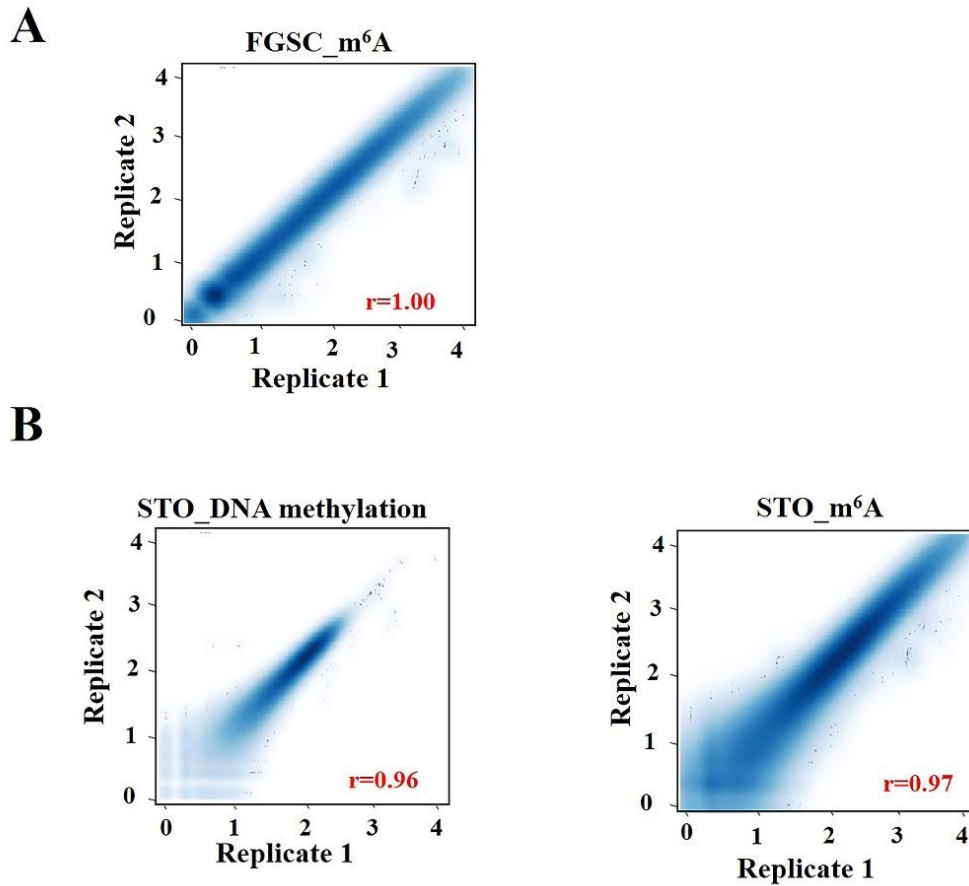


Figure S1. The repeatability and reliability of sequence data.

(A) Correlation analysis of replicate data, including MeRIP-Seq in FGSCs. (B) Correlation analysis of replicate data, including MeDIP-Seq and MeRIP-Seq in STO cells. Correlation was computed using whole-genome data.

Table S1: Sequence of primers used in RT-PCR:

Gene	Product Size(bp)	Primer Sequence (5' - 3')
<i>Mvh</i>	213bp	GGAAACCAGCAGCAAGTGAT TGGAGTCCTCATCCTCTGG
<i>Oct4</i>	430bp	GGAGGAAGCCGACAACAA AGCAGTGACGGGAACAGA
<i>Stella</i>	354bp	CCCAATGAAGGACCCTGAAAC AATGGCTCACTGTCCCGTTCA
<i>Fragilis</i>	295 bp	TCCGTGAAGTCTAGGGATCG TGTTACACCTGCGTGTAGGG
<i>Blimp-1</i>	483 bp	CGGAAAGCAACCCAAAGCAATAC CCTCGGAACCATAGGAAACATTC
<i>Gapdh</i>	458 bp	GTCCCGTAGACAAAATGGTGA TGCATTGCTGACAATCTTGAG

Table S2: Sequence of primers used in qRT-PCR:

Gene	Product Size(bp)	Primer Sequence (5'- 3')
<i>Mettl3</i>	173 bp	CTGGGCACTTGGATTTAAGGAA TGAGAGGTGGTGTAGCAACTT
<i>Mettl14</i>	105 bp	CTGAGAGTGCGGATAGCATTG GAGCAGATGTATCATAGGAAGCC
<i>Wtap</i>	67 bp	GAACCTCTTCCTAAAAAGGTCCG TTAACTCATCCCGTGCCATAAC
<i>Alkbh5</i>	144 bp	CGCGGTCATCAACGACTACC ATGGGCTTGAAGTGGAACTTG
<i>Fto</i>	137 bp	TTCATGCTGGATGACCTCAATG GCCAACTGACAGCGTTCTAAG
<i>Ythdf1</i>	128 bp	ACAGTTACCCCTCGATGAGTG GGTAGTGAGATACGGGATGGGA
<i>Ythdf2</i>	102 bp	GAGCAGAGACCAAAAAGGTCAAG CTGTGGGCTCAAGTAAGGTTT
<i>Ythdf3</i>	98bp	AACCAGGGGCATTAGGAAATACC TCCACTTGTTCCCATGTAGAG
<i>Ythdc1</i>	162bp	GTCCACATTGCCTGTAAATGAGA GGAAGCACCCAGTGTATAGGA
<i>Ythdc2</i>	154bp	ACCGACTAAGTCAATCTCTTGGT AGGCTCCTAACAGCATGTTTTG
<i>Gapdh</i>	123bp	AGGTCGGTGTGAACGGATTTG TGTAGACCATGTAGTTGAGGTCA
<i>Dnmt1</i>	178bp	AAGAATGGTGTGTCTACCGAC CATCCAGGTTGCTCCCTTG
<i>Dnmt3a</i>	176bp	CTGTCAGTCTGTCAACCTCAC GTGGAAACCACCGAGAACAC
<i>Dnmt3b</i>	72bp	AGCGGGTATGAGGA GGGAGCATCCTTCGTGTCTG