Table S1 Summary of single-base 5mC and 5hmC sequencing using oxBS-seq and TAB-seq.

| | | Cortex | Olfactory bulb | Cerebellum |
|----------------|-----------------------------------|---------|----------------|------------|
| 5hmC (TAB-Seq) | Bisulfite conversion rate | 99.20% | 99.53% | 99.11% |
| | Tet oxidization rate | 98.38% | 98.45% | 98.11% |
| | Protection rate | 98. 93% | 99.31% | 99.14% |
| | Mapped depth | 23 | 26 | 21 |
| | #CpG covered > 5X | 20.02M | 20.23M | 19.55M |
| | Average 5hmC level in CpG context | 16.48% | 14.60% | 10.00% |
| 5mC (oxBS-Seq) | Bisulfite conversion rate | 99.85% | 99.86% | 99.85% |
| | Oxidization rate | 99.00% | 98.61% | 98.95% |
| | Mapped depth | 17 | 30 | 20 |
| | #CpG covered > 5X | 19.19M | 20.16M | 19.42M |
| | Average 5mC level in CpG context | 64.93% | 67.00% | 68.78% |

Both bisulfite conversion rate and oxidation rate by Tet was calculated by M. SsI treated spiked lambda DNA. Average 5hmC and 5mC level for all

CpG sites is calculated as C/(C+T) for TAB-seq and oxBS-seq, respectively. M means million.

| | Total reads | Uniquely mapped reads | Uniquely mapped rate |
|----------------------------|-------------|--------------------------|----------------------|
| Cortex replicate 1 | 12.15G | 9.27G | 76.30% |
| Cortex replicate 2 | 17.01 G | 14.68G | 86.30% |
| Olfactory bulb replicate 1 | 11.32G | 9.11G | 80.40% |
| Olfactory bulb replicate 2 | 12.53G | 10.39G | 82.90% |
| Cerebellum replicate 1 | 14.10G | 12.25G | 86.90% |
| Cerebellum replicate 2 | 8.60G | 6.751 | 78.50% |

Table S2 Summary of RNA-seq.

The raw FASTQ data files were mapped to the mouse reference sequence (mm10) for mRNA analysis and gencode version 9 for ncRNA analysis

using Tophat program. G means billion.