**SUPPLEMENTAL DATA**

# Genome-wide alteration of 5-hydroxymethylcytosine in a mouse model of fragile X-associated tremor/ataxia syndrome

By

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**Supplementary Figure 1. Chromosome-wide 5hmC densities in wild-type and rCGG mice cerebella.** Chromosome-wide densities were determined as reads per chromosome divided by the total number of reads in millions. Expected values were determined by dividing $10^6$ by the total genome length and multiplying by chromosome length.

**Supplementary Figure 2**. **Differential 5hmC distribution on various CpG density promoters. (A-C)** Normalized 5hmC read densities on promoters with differential CGI abundance. Wild-type and rCGG 5hmC were separately plotted **(A-B)** or combined together **(C)**.

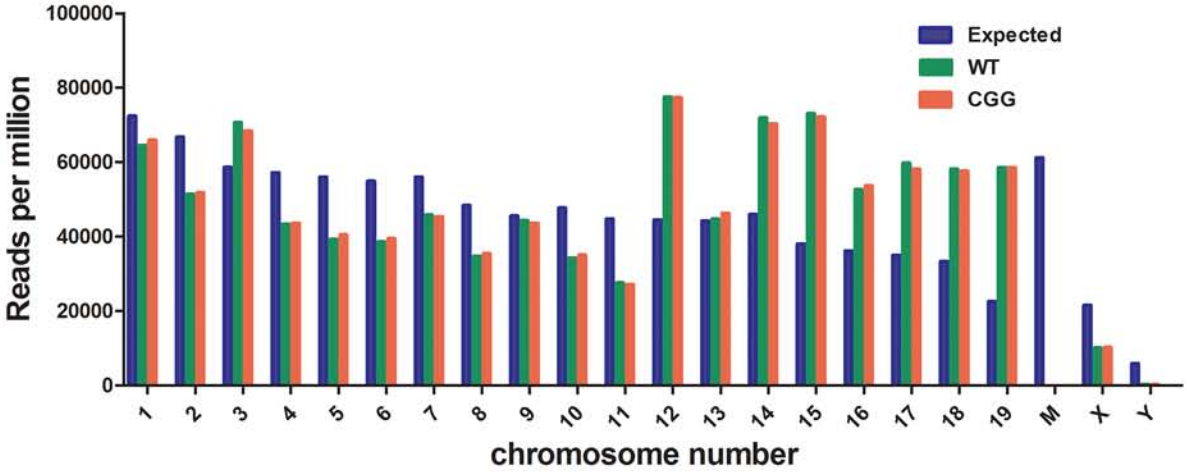
**Supplementary Figure 3**. **Mouse phenotype predictions for defined DhMRs. (A-B)** Identified DhMRs were predicted for associated mouse genotypes using the GREAT tool.

**Supplementary Table 1.** Sequencing information for each biological replicate and combined samples.

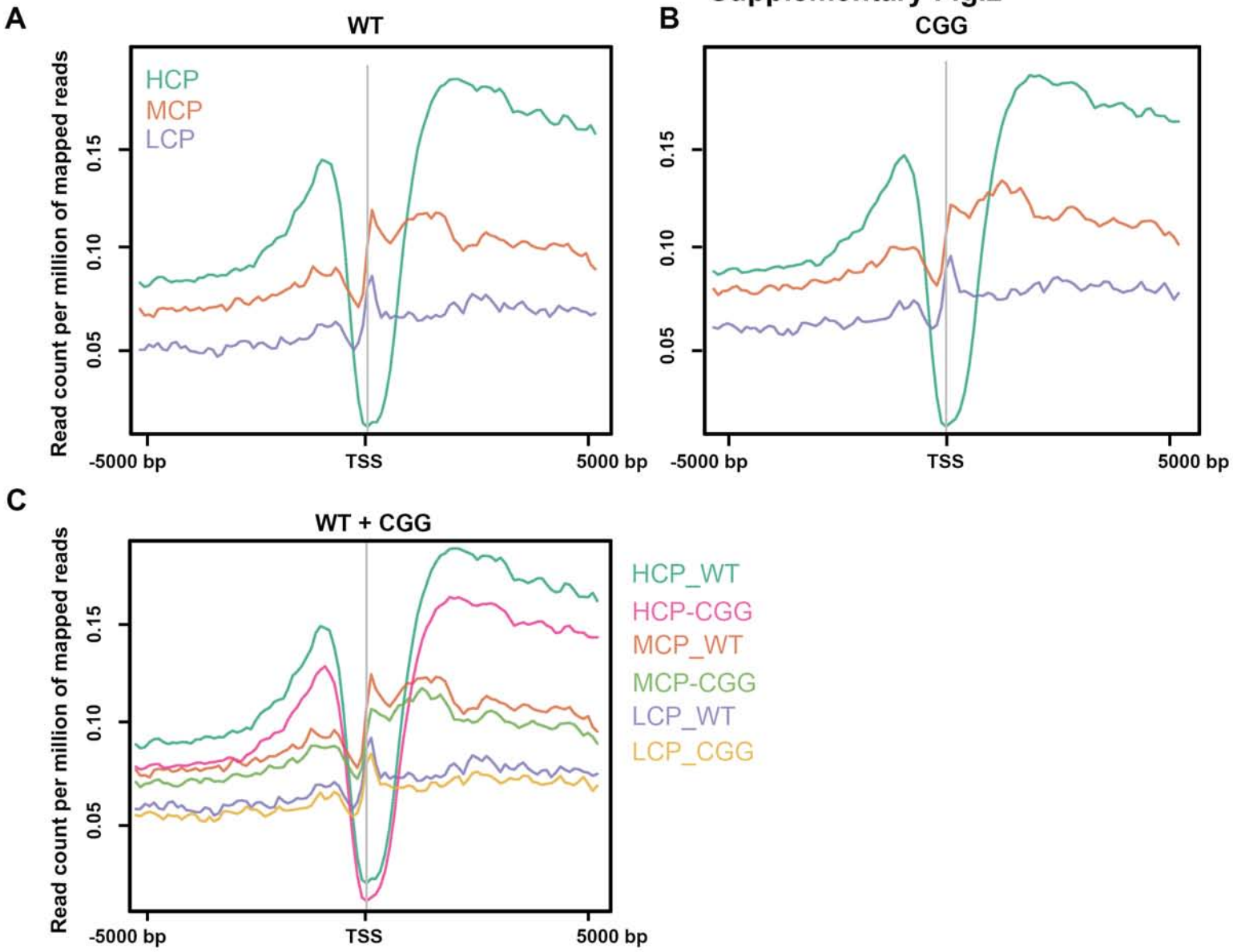
**Supplementary Table 2-3.** Wild-type- or rCGG-specific DhMRs identified by MACS.

**Supplementary Table 4-5.** Wild-type- or rCGG-specific DhMRs annotation results by HOMER.

**Supplementary Fig.1**

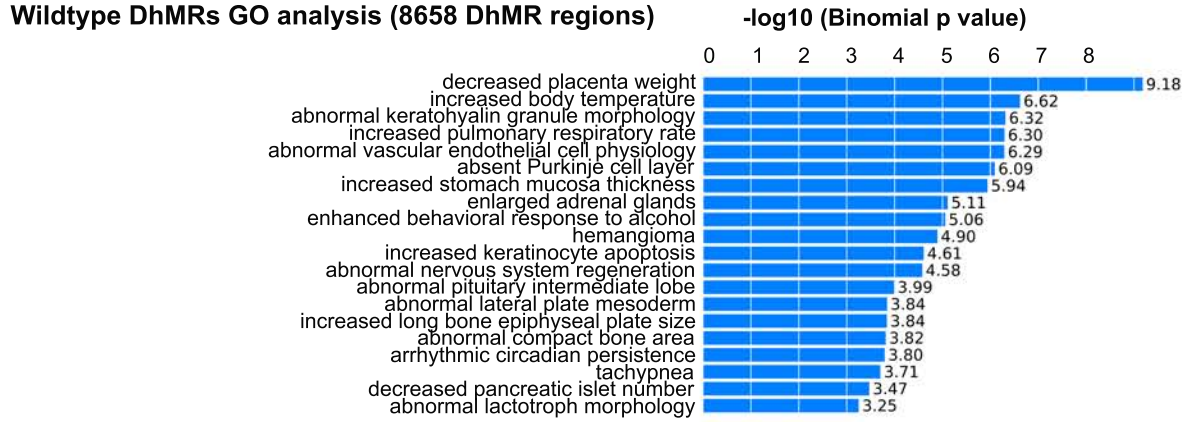


Supplementary Fig.2

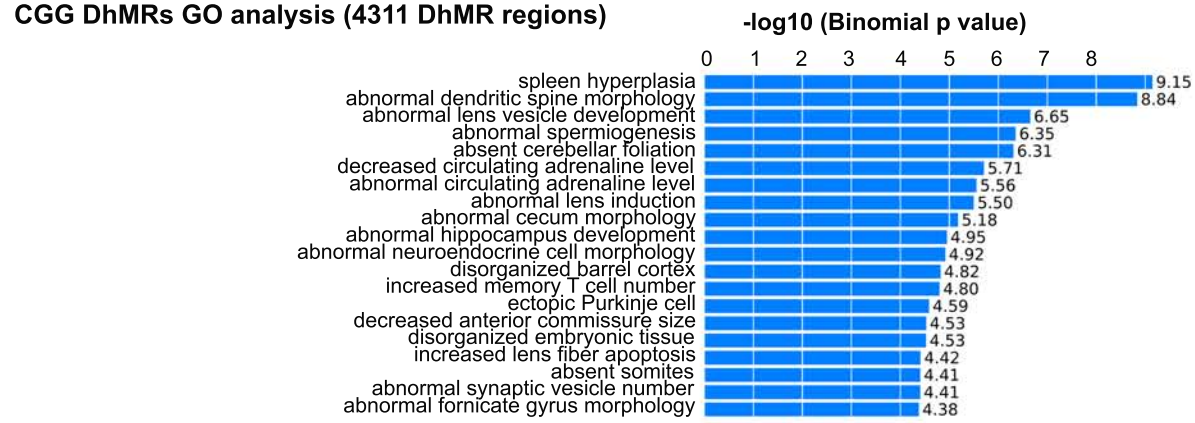


# Supplementary Fig.3

**A**




**B**



**Supplementary Table 1**

| replicates | Monoclonal reads | Number of peaks called to input | Number of negative peaks called (enrich in input) |
|---|---|---|---|
| 16wkWT-1 | 6,568,046 | 80877 | 207 |
| 16wkWT-2 | 4,597,660 | 57118 | 140 |
| 16wkWT-3 | 9,194,192 | 90508 | 290 |
| 16wkCGG-1 | 13,429,874 | 114476 | 350 |
| 16wkCGG-2 | 12,328,423 | 114032 | 370 |
| 16wkCGG-3 | 8,309,064 | 76635 | 210 |

| Combined samples | Monoclonal reads | Number of peaks called to input | DhMRs in WT or CGG |
|---|---|---|---|
| 16wkWT | 20,359,898 | 95116 | 8658 |
| 16wkCGG | 46,744,882 | 77846 | 4311 |