

# Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells

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5-hydroxymethylcytosine (5hmC) is a modified base present at low levels in diverse cell types in mammals<sup>1–5</sup>. 5hmC is generated by the TET family of Fe(II) and 2-oxoglutarate-dependent enzymes through oxidation of 5-methylcytosine (5mC)<sup>1,2,4–7</sup>. 5hmC and TET proteins have been implicated in stem cell biology and cancer<sup>1,4,5,8,9</sup>, but information on the genome-wide distribution of 5hmC is limited. Here we describe two novel and specific approaches to profile the genomic localization of 5hmC. The first approach, termed GLIB (glucosylation, periodate oxidation, biotinylation) uses a combination of enzymatic and chemical steps to isolate DNA fragments containing as few as a single 5hmC. The second approach involves conversion of 5hmC to cytosine 5-methylenesulphonate (CMS) by treatment of genomic DNA with sodium bisulphite, followed by immunoprecipitation of CMS-containing DNA with a specific anti-serum to CMS<sup>5</sup>. High-throughput sequencing of 5hmC-containing DNA from mouse embryonic stem (ES) cells showed strong enrichment within exons and near transcriptional start sites. 5hmC was especially enriched at the start sites of genes whose promoters bear dual histone 3 lysine 27 trimethylation (H3K27me3) and histone 3 lysine 4 trimethylation (H3K4me3) marks. Our results indicate that 5hmC has a probable role in transcriptional regulation, and suggest a model in which 5hmC contributes to the ‘poised’ chromatin signature found at developmentally-regulated genes in ES cells.

We developed two independent methods for precipitation of 5hmC in genomic DNA. The GLIB method (Fig. 1a) entails addition of a glucose molecule to each 5hmC with T4 phage  $\beta$ -glucosyltransferase (BGT)<sup>3</sup> (Supplementary Fig. 1a). The glucose moiety is oxidized with sodium periodate, which converts the vicinal hydroxyl groups to aldehydes<sup>10</sup>, and further modified with aldehyde-reactive probe, which adds two biotin molecules to each 5hmC (Fig. 1a). A related strategy, which uses a custom-synthesized UDP-glucose analogue (UDP-6-N<sub>3</sub>-glucose), was recently used to profile 5hmC distribution in mouse brain<sup>11</sup>. The second method uses an antibody against cytosine 5-methylenesulphonate (CMS)<sup>5</sup>, produced by reaction of 5hmC with sodium bisulphite (Fig. 1b)<sup>12</sup>. Anti-CMS antibodies are more sensitive and less density-dependent than anti-5hmC in DNA dot blot assays<sup>5</sup>. Both methods are specific for DNA containing 5hmC (Supplementary Fig. 1b)<sup>5</sup>.

We examined the ability of GLIB-treated (biotinylated) and bisulphite-treated 5hmC-containing DNA to be pulled down by streptavidin and anti-CMS antisera, respectively. Using varying ratios of dCTP:dhmCTP, we generated 201 base pairs PCR amplicons with differing incorporation of cytosine and 5hmC in identical sequence contexts (Supplementary Table 1). At each dhmCTP:dCTP ratio, the fraction of amplicons that contain no 5hmC, and therefore should not be precipitated, can be calculated using the binomial equation (Supplementary Table 2). Observed and calculated pull-down efficiencies

were very similar (Fig. 1c): even at low densities of 5hmC, more than 90% of DNA fragments calculated to contain a single 5hmC were precipitated after GLIB treatment. Anti-CMS pull-down showed increased density dependence compared to GLIB, but had very low background, such that there was still a strong preference for precipitation of sparsely hydroxymethylated amplicons over unmodified ones (Fig. 1d). The performance of a commercial polyclonal anti-hmC antiserum was inferior to that of anti-CMS, in terms of higher background pull-down of unmodified DNA (3.0% versus 0.06%) as well as greater density dependence (Fig. 1e). By testing PCR amplicons with varying 5mC, we confirmed that the methyl-DNA immunoprecipitation (MeDIP) technique, which uses a monoclonal antibody to 5mC, is extremely density-dependent (Fig. 1f).

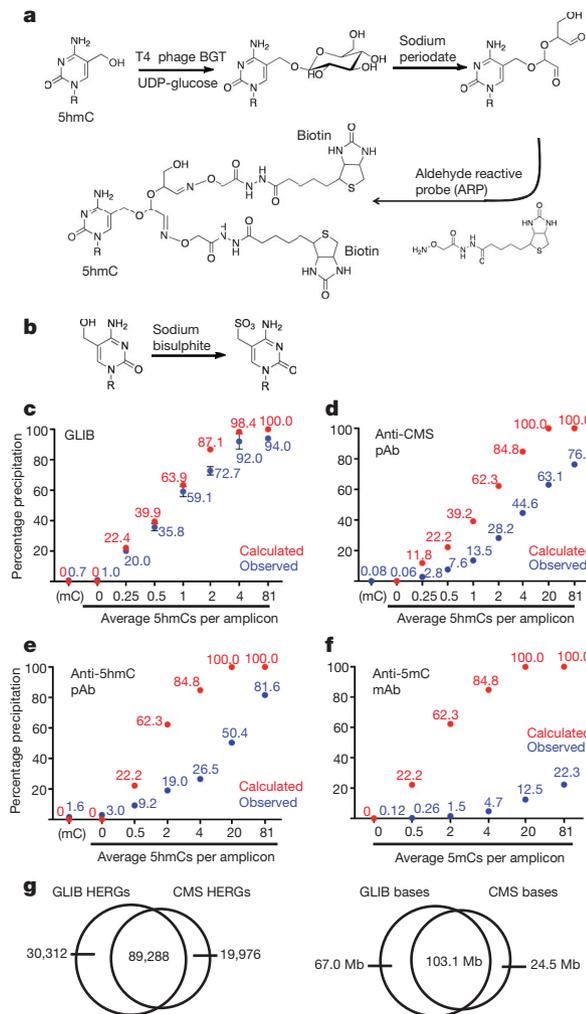
We applied the GLIB and anti-CMS techniques to enrich 5hmC-containing regions in genomic DNA using genomic DNA with low, intermediate and high levels of 5hmC (Supplementary Fig. 1c, left panel). For the GLIB and anti-CMS pull-downs, the amount of specifically precipitated genomic DNA was proportional to the relative amount of 5hmC (Supplementary Fig. 1c). The GLIB technique did not produce mutations (Supplementary Table 3), the biotinylated DNA could be efficiently eluted by heating with formamide (Supplementary Fig. 1d), and the biotinylated adduct had a minimal inhibitory effect on PCR at 5–25% hmC density (delay of approximately 0.1 cycles per converted 5hmC residue; Supplementary Fig. 1f). There was no PCR delay with CMS-containing PCR amplicons except at very high CMS levels (Supplementary Fig. 1e), consistent with our previous report that CMS inhibits PCR predominantly at biologically irrelevant sequences where multiple CMS adducts occur in a row<sup>13</sup>.

We investigated the genome-wide localization of 5hmC in murine V6.5 ES cells. For GLIB-treated DNA, we chose Helicos single molecule DNA sequencing, which does not require an amplification step and thus avoids PCR bias<sup>14,15</sup>. For CMS-enriched genomic DNA, we used an Illumina instrument, as longer read lengths are needed for efficient alignment of bisulphite-treated DNA to the genome<sup>16</sup>. With the GLIB method, 119,600 regions of the genome, averaging 1,422 bp in length, showed a substantially higher density of reads in the +BGT as opposed to the –BGT sample; with the CMS method, comparison of enriched to input DNA identified 109,264 enriched regions (average length 1,168 bp). There was high overlap in the enriched regions, here designated 5hmC-enriched regions of the genome (HERGs) (Fig. 1g). Comparing the number of HERGs retrieved by using different fractions of aligned reads yielded a curve that approached an asymptote, suggesting that a majority of hydroxymethylated regions had been identified (Supplementary Fig. 2a).

To determine whether HERGs overlapped with methylated DNA regions, we identified 62,991 5mC-enriched regions of the genome

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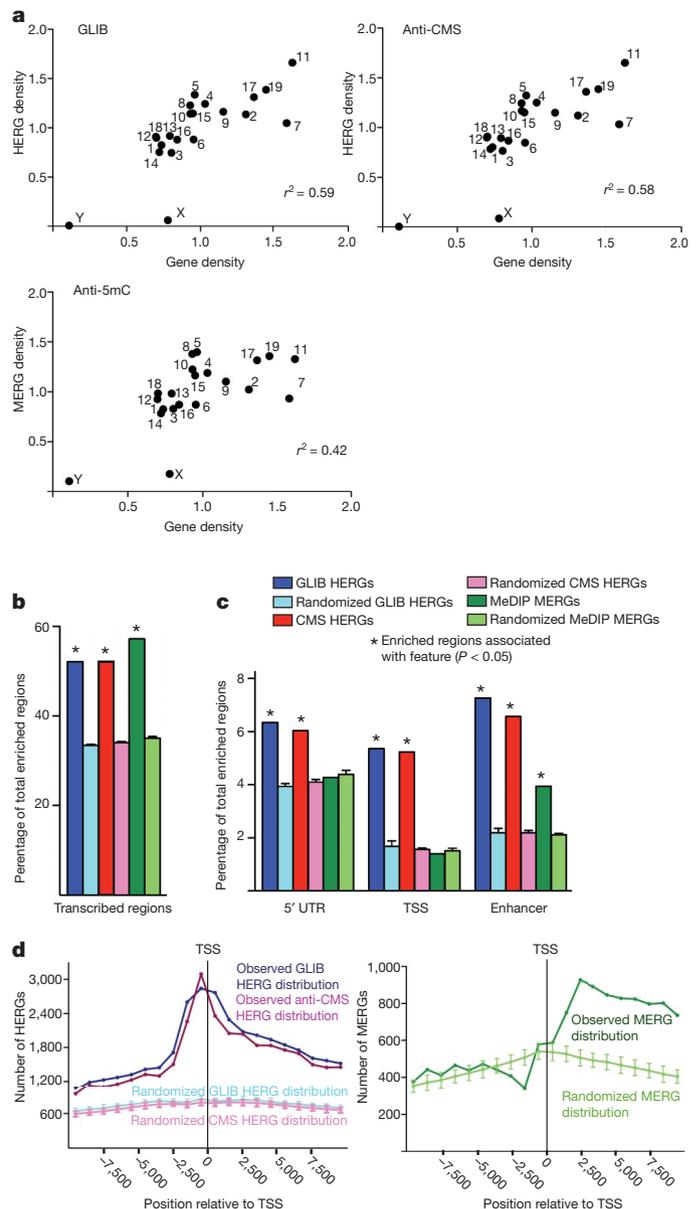
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**Figure 1 | Comparison of 5hmC enrichment methods.** **a**, The GLIB method. Glucose is added to 5mC by BGT, oxidized with sodium periodate to yield aldehydes, and reacted with the aldehyde reactive probe (ARP), yielding two biotins at the site of every 5hmC. **b**, 5hmC is converted to CMS by sodium bisulphite. **c–f**, Precipitation of PCR amplicons containing (1) varying amounts of 5hmC by GLIB methodology (**c**), anti-CMS methodology (**d**), or anti-5mC antibody (**e**); or (2) varying amounts of 5mC by anti-5mC antibody (**f**). pAb, polyclonal antibody; mAb, monoclonal antibody. Between 1 and 6 independent experiments per method, mean percentage input precipitated  $\pm$  s.d. is indicated. **g**, Overlap between HERGs identified by the GLIB and anti-CMS methodologies. Left panel, number of HERGs; right panel, number of base pairs contained within HERGs.

(MERGs) by MeDIP. The resulting 5mC profile does not represent a complete map of 5mC in mouse ES cells, but rather is biased towards regions of dense methylation. Statistics pertaining to the GLIB, anti-CMS and MeDIP enrichments are shown in Supplementary Figs 2b–d, the corresponding annotations are provided in Supplementary Tables 4–9, and reads and enrichment for the *Hoxb* locus are provided in Supplementary Table 10. As expected, both HERGs and MERGs contained a high frequency of CG sequences relative to the genome at large (Supplementary Fig. 3a). Intriguingly, HERGs also contained relatively high levels of CAG sequences, the most frequent site of non-CpG methylation in human ES cells<sup>16</sup>, and we confirmed that the TET1 catalytic domain is capable of hydroxylating 5mC in CHG and CHH (H = A, T or C) contexts *in vitro* (Supplementary Fig. 3b).

Analysis of the GLIB and anti-CMS HERG sets gave very similar results. We observed a strong correlation between the densities of HERGs and genes on a given chromosome; this trend was less pronounced for MERGs (Fig. 2a). When we compared the distribution of



**Figure 2 | Genomic distribution of 5hmC or 5mC enriched regions of the genome.** **a**, Correlation of HERG or MERG density on each chromosome (*y*-axis) with gene density in the same chromosome (*x*-axis). Density is defined as frequency divided by chromosome length. **b**, **c**, Both HERGs and MERGs are enriched in transcribed regions (**b**), whereas HERGs are preferentially enriched at enhancers and the start sites of genes (**c**). The percentage of HERGs or MERGs mapping to the indicated genomic feature (darker bar) is compared with the percentage of randomly chosen sequences mapping to that feature (lighter bar). 5' UTR, 5' untranslated region. TSS, transcription start site (–800 bp to +200 bp relative to start of transcription). See Supplementary Methods for detailed definition of how HERGs or MERGs were classified as mapping to genomic features. **d**, Distribution of HERGs and MERGs relative to the TSS. The centre of each HERG was plotted relative to the nearest TSS in 1,000 bp increments from –10 kb to +10 kb surrounding the TSS.

HERGs and MERGs to the distribution of DNA fragments of equivalent length distributed randomly across the genome, both 5hmC and 5mC were enriched within transcribed regions, particularly exons, which are known to be sites of high CpG density<sup>17</sup> as well as high DNA methylation<sup>18</sup> (Fig. 2b and Supplementary Fig. 3c). However, only 5hmC was enriched at transcription start sites (TSSs) and within the 5' untranslated regions (UTRs) of genes (Fig. 2c). Moreover, 5hmC was relatively more enriched in enhancers (defined by H3K4me1 in the

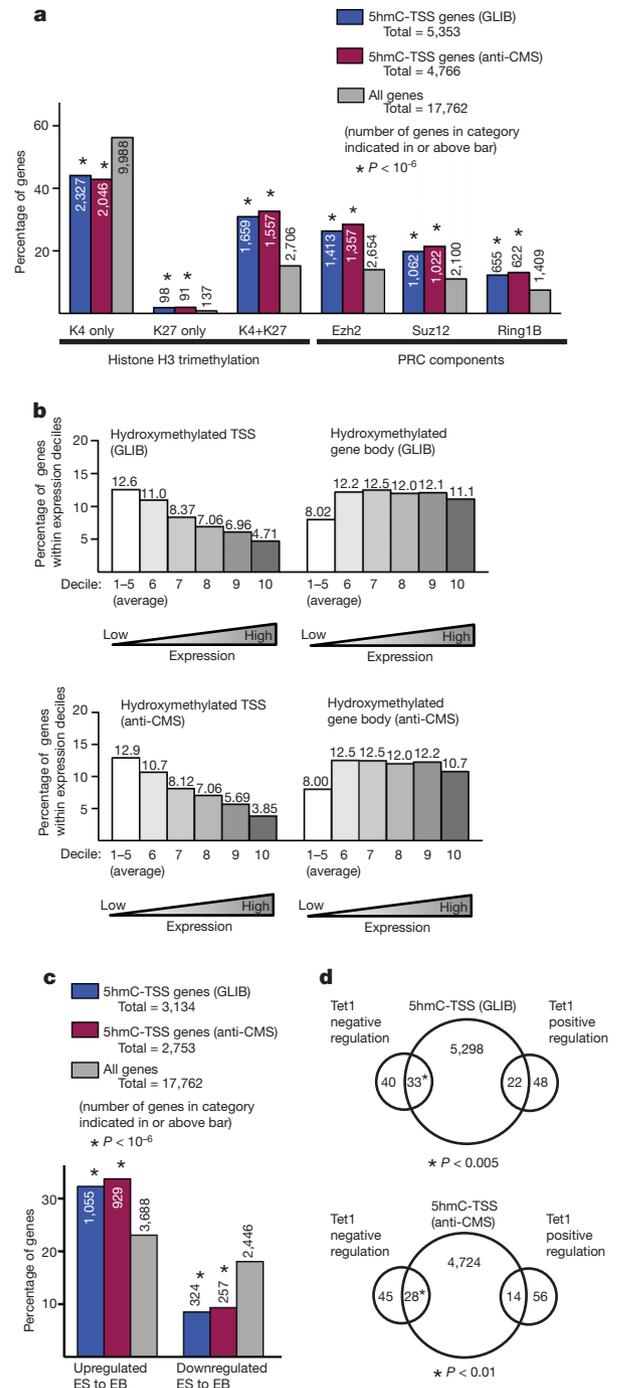
absence of H3K4me3)<sup>19</sup> than 5mC, strongly indicating a connection between 5hmC and regulatory elements (Fig. 2c). Plotting each HERG as a single point relative to the nearest TSS, we found that 5hmC is heavily enriched both 5' and 3' of the TSS, whereas 5mC is enriched primarily 3' of the TSS (Fig. 2d). These results show a unique distribution of 5hmC in regulatory elements of genes, one that is not explained simply by the distribution of 5mC, the substrate for TET enzymes.

The enrichment of 5hmC at the TSS suggested a role for 5hmC in transcriptional regulation. To evaluate this possibility, we used published data sets on gene expression<sup>20,21</sup> and histone modification<sup>22,23</sup> profiles in mouse ES cells to compare the sets of genes with 5hmC or 5mC at their start sites (Supplementary Tables 11–13) to the set of all genes in the genome. 5hmC is preferentially found at promoters with high or intermediate CpG content (Supplementary Fig. 4a), even though high CpG promoters are hypomethylated in ES cells<sup>16,18,24</sup>. This distribution is consistent with the possibility that TET proteins are preferentially recruited to high CpG regions through their CpG-binding CXXC domains<sup>6,25</sup>.

In ES cells, genes with 'bivalent' H3K27 and H3K4 trimethylation are transcriptionally inactive but poised for expression upon differentiation to embryoid bodies<sup>20,26,27</sup>. We found that genes with 5hmC at their start sites were disproportionately likely to contain bivalent domains at their promoters; likewise, a majority (~60%) of genes reported to contain bivalent domains have 5hmC at their start sites (Fig. 3a). 5hmC was less likely to be found at genes with the activating 'H3K4me3 only' mark than is predicted by chance. Moreover, genes with 5hmC at their start sites showed lower expression in murine ES cells than other genes (Fig. 3b) and were more likely to be upregulated upon embryoid body differentiation (Fig. 3c). The correlation of 5hmC with bivalent domains holds even after adjusting for the known relation between promoter CpG content and bivalency<sup>22</sup> (Supplementary Fig. 5). Although 5mC at the TSS also correlates with lower gene expression in murine ES cells (Supplementary Fig. 4b), 5mC is not enriched at the promoters of genes with bivalent domains<sup>28</sup> (Supplementary Fig. 4c), and genes with high levels of 5mC did not tend to be upregulated upon embryoid body differentiation (Supplementary Fig. 4d). Thus 5hmC is preferentially enriched at the promoters of genes with bivalent histone marks in ES cells, indicating that 5hmC may contribute functionally to the 'poised' but inactive state of these genes in ES cells.

Genes with 5hmC at their start sites are also disproportionately enriched in the set of genes whose promoters bind polycomb repressor complex (PRC) components, and in a majority of genes with the 'H3K27me3' only mark (Fig. 3a). There is a statistically significant correlation between genes that had 5hmC at the TSS and genes that were upregulated upon small interfering RNA-mediated Tet1 depletion<sup>8</sup> (therefore, negatively regulated by Tet1) (Fig. 3d), indicating that 5hmC in the promoter region has a negative role in the transcription of some genes in ES cells. Unlike 5mC, however, 5hmC is not substantially enriched at sites of heterochromatic H3K9 or H4K20 trimethylation<sup>22</sup> (data not shown).

Collectively, our results support a model in which 5hmC and 5mC have different roles in transcription. Like 5mC<sup>28</sup>, 5hmC at promoters is predictive of lower levels of gene expression. However, 5hmC is uniquely associated with a 'poised' chromatin configuration and with genes that are upregulated upon differentiation, and may thus be involved in priming loci for rapid activation in response to appropriate signals. Activation of lineage-specific genetic loci upon differentiation could occur via a postulated 5mC 'demethylation' pathway (5mC to 5hmC to cytosine)<sup>1</sup> or through recruitment of transcriptional regulators that specifically recognize 5hmC and are activated in response to differentiation signals. The ability to profile 5hmC even at sparsely hydroxymethylated loci will allow a careful evaluation of these possibilities in differentiating cells.



**Figure 3 | Properties of HERGs at transcription start sites.** **a**, The percentage of genes with 5hmC at the TSS (blue and red bars) reported to contain histone H3 trimethylation (left) or PRC components (right) at their promoters is compared to the fraction of all genes (grey bars) with these promoter marks<sup>22</sup>. Number of genes in each category is indicated. **b**, HERGs are enriched at the TSSs of genes with low expression in ES cells. All genes were ranked by level of expression in ES cells<sup>21</sup> and sorted into deciles from lowest to highest. The percent of genes within the decile category with 5-hmC enriched at the TSS (left) or within gene bodies (right) are shown for each methodology. The first five deciles, which are comprised of genes lacking statistically significant expression, are pooled and averaged in this analysis. **c**, HERGs are enriched at the TSS of genes upregulated upon differentiation to embryoid bodies (EB)<sup>26</sup>. The percentage of genes with 5-hmC at their TSS (blue bars) that are substantially upregulated or downregulated upon differentiation to EB is compared with the percentage of total genes similarly regulated (grey bars). Number of genes in each category is indicated. **d**, Overlap between genes with 5hmC at the TSS and genes positively or negatively regulated by Tet1 (ref. 8).

## METHODS SUMMARY

**GLIB precipitation.** V6.5 ES cells were lysed and proteins digested by treatment with Proteinase K at 55 °C. DNA was purified by phenol-chloroform extraction and then precipitated with ethanol. RNA was removed with RNase A (Qiagen). Samples were treated with 20 ng BGT per 1 µg DNA at 30 °C for 3 h (50 mM HEPES pH 8.0, 25 mM MgCl<sub>2</sub>, 50 µM UDPG for 3 h at 30 °C), then oxidized with 23 mM sodium periodate 16 h at 22 °C in 0.1 M sodium phosphate pH 7.0. Periodate was quenched by the addition of 46 mM sodium sulphite at room temperature for 10 min, then exchanged into 1× PBS and incubated with 2 mM Aldehyde Reactive Probe (Invitrogen) for 1 h at 37 °C. DNA was sequenced with a HeliScope Single Molecule Sequencer. See Supplementary Methods for detailed protocol.

**CMS precipitation.** The generation of the anti-CMS antibody is described elsewhere<sup>5</sup>. DNA fragments were ligated with methylated adaptors and treated with sodium bisulphite (Qiagen). The DNA was then denatured for 10 min at 95 °C (0.4 M NaOH, 10 mM EDTA), neutralized by addition of cold 2 M ammonium acetate pH 7.0, incubated with anti-CMS antiserum in 1× immunoprecipitation buffer (10 mM sodium phosphate pH 7.0, 140 mM NaCl, 0.05% Triton X-100) for 2 h at 4 °C, and then precipitated with Protein G beads. Precipitated DNA was eluted with Proteinase K, purified by phenol-chloroform extraction, and amplified by 4–6 cycles PCR using Pfu TurboC<sub>x</sub> hotstart DNA polymerase (Stratagene). DNA sequencing was carried out using Illumina/Solexa Genome Analyzer II and HiSeq sequencing systems.

Received 4 December 2010; accepted 11 April 2011.

Published online 8 May 2011.

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Supplementary Information is linked to the online version of the paper at [www.nature.com/nature](http://www.nature.com/nature).

**Acknowledgements** We thank B. Ren for assistance in next generation sequencing using the Illumina platform. We thank M. Guttman for making his RNASeq data set available to us. W.A.P. is supported by a predoctoral graduate research fellowship from the National Science Foundation, and Y.H. by a postdoctoral fellowship from the Leukemia and Lymphoma Society. R.L. is supported by a California Institute for Regenerative Medicine Training Grant. This study was supported by the National Institute of Health grants RC1 DA028422, R01 AI44432 and 1 R01 HD065812-01A1 and a grant from the California Institute of Regenerative Medicine (to A.R.), a pilot grant from Harvard Catalyst, The Harvard Clinical and Translational Science Center (NIH Grant 1 UL1 RR 025758-02) and NIH K08 HL089150 (to S.A.), and a grant from the Mary. K. Chapman Foundation (to J.R.E.).

**Author Contributions** W.A.P., Y.B. and S.A. devised the GLIB method. W.A.P., S.A., H.R.H. and E.M.M. optimized the GLIB method. Y.H. generated the anti-CMS antiserum, and Y.H. and W.A.P. optimized the anti-CMS pull-down. W.A.P. and Y.H. grew ES cells. W.A.P. prepared GLIB samples for sequencing, Y.H. prepared CMS samples, H.R.H. performed MedIPs. Helicos sequencing and mapping was performed by P.K. and P.M.M., Illumina sequencing and mapping was performed by R.L. and J.R.E., and U.J.P. was responsible for bioinformatic analysis. M.K. performed the anti-5hmC dot blot. W.A.P. and M.T. performed anti-5hmC pull-downs. H.R.H. and S.M. performed and optimized *in vitro* tests of Tet substrate specificity. W.A.P., S.A. and A.R. wrote the manuscript. S.A. and A.R. coordinated research.

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