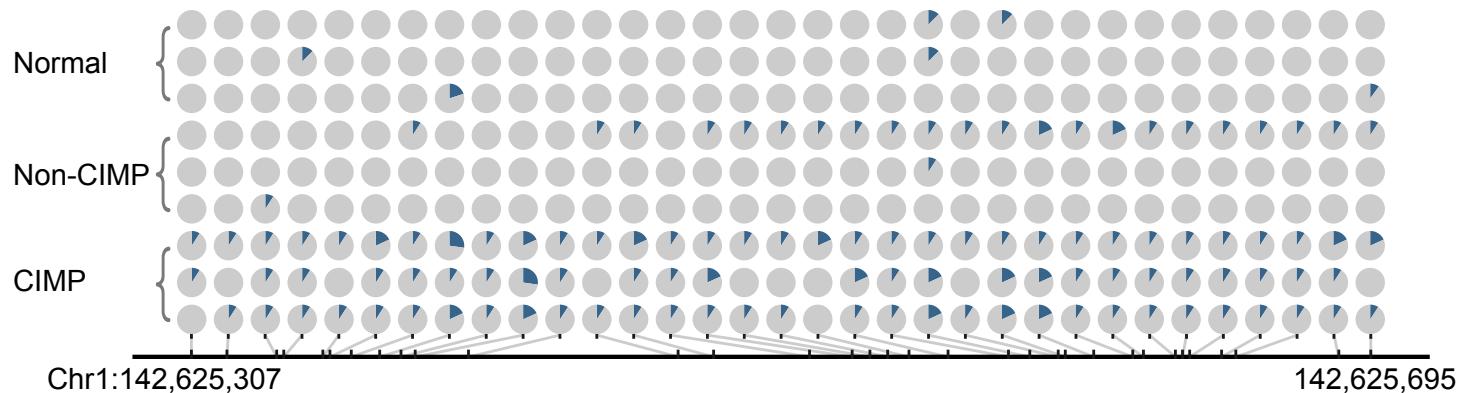
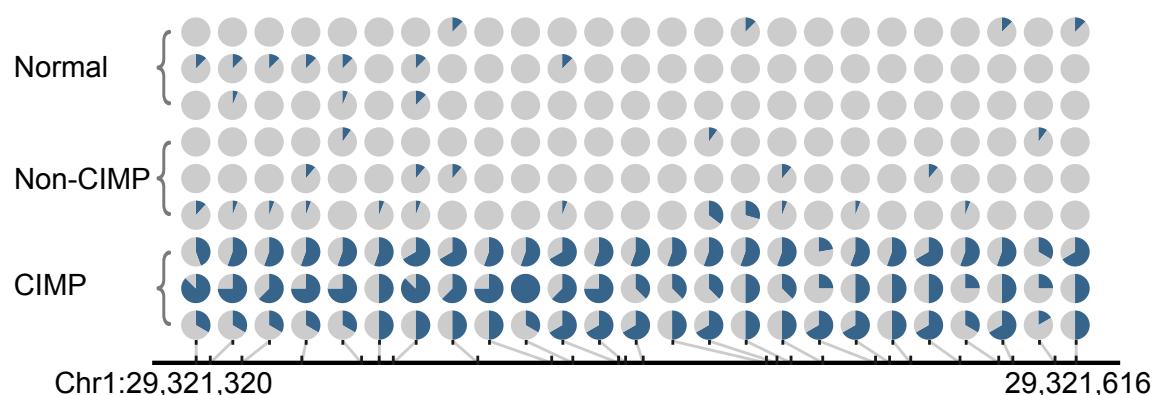


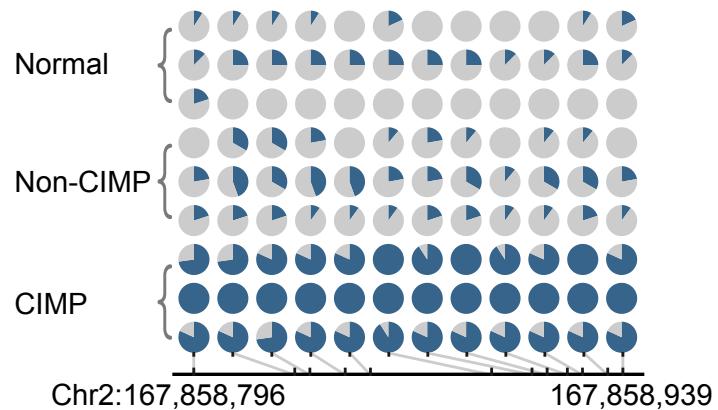
**Supplementary Figure 1:** Summary bisulfite sequencing results for the DMS located at chr1:142,624,050 -142,627,549. The bisulfite sequencing amplicon is located at chr1:142,625,307-142,625,695. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



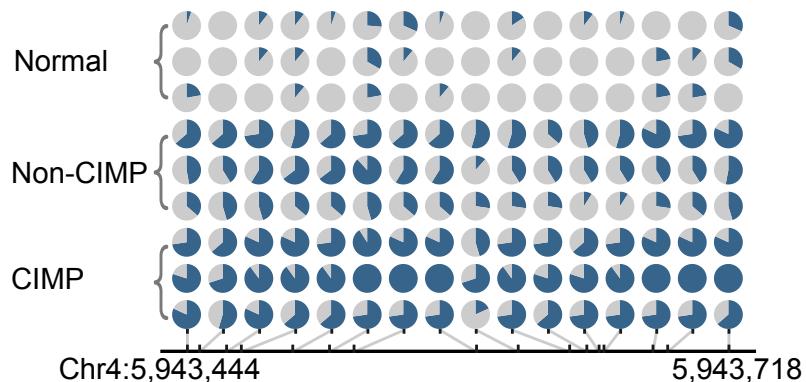
**Supplementary Figure 2:** Summary bisulfite sequencing results for the DMS located at chr1:29,320,550 -29,324,149. The bisulfite sequencing amplicon is located at chr1:29,321,320-29,321,616. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



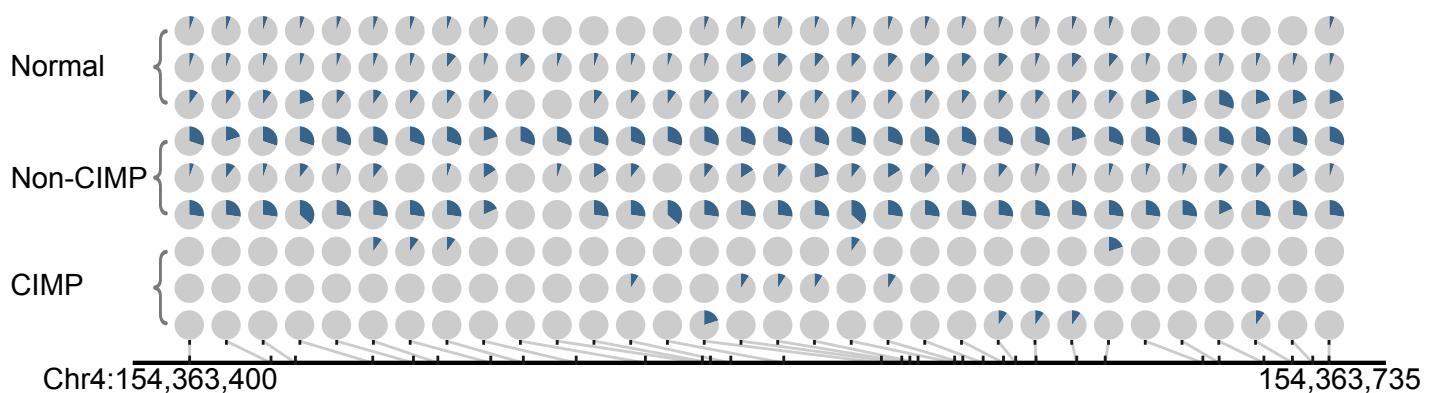
**Supplementary Figure 3:** Summary bisulfite sequencing results for the DMS located at chr2:167,857,150 -167,859,349. The bisulfite sequencing amplicon is located at chr2:167,858,796-167,858,939. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



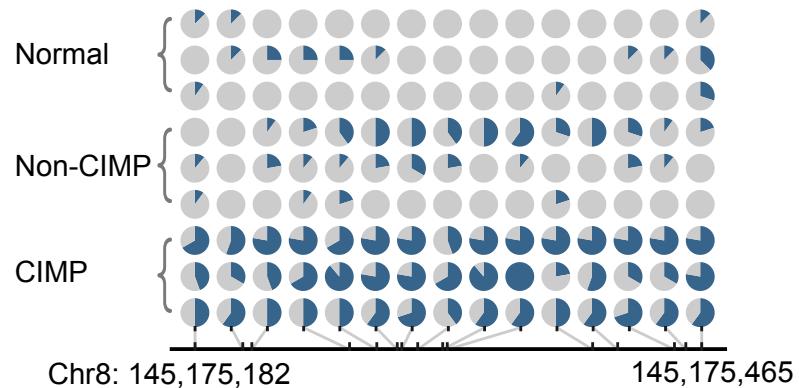
**Supplementary Figure 4:** Summary bisulfite sequencing results for the DMS located at chr4:5,942,850 -5,946,099. The bisulfite sequencing amplicon is located at chr4:5,943,444-5,943,718. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



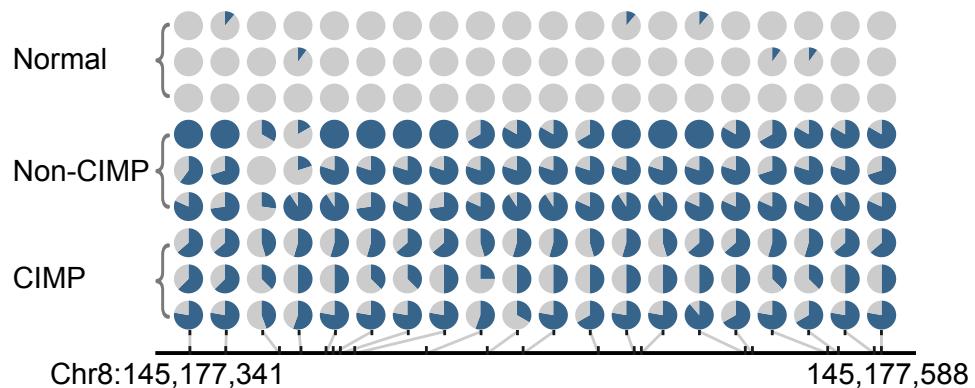
**Supplementary Figure 5:** Summary bisulfite sequencing results for the DMS located at chr4:154,363,050 -154,363,949. The bisulfite sequencing amplicon is located at chr4:154,363,400-154,363,735. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



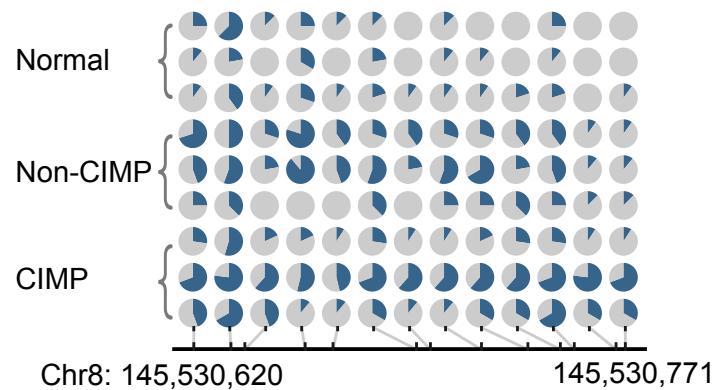
**Supplementary Figure 6:** Summary bisulfite sequencing results for the DMS located at chr8:145,175,200 -145,176,349. The bisulfite sequencing amplicon is located at chr8:145,175,182-145,175,465. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



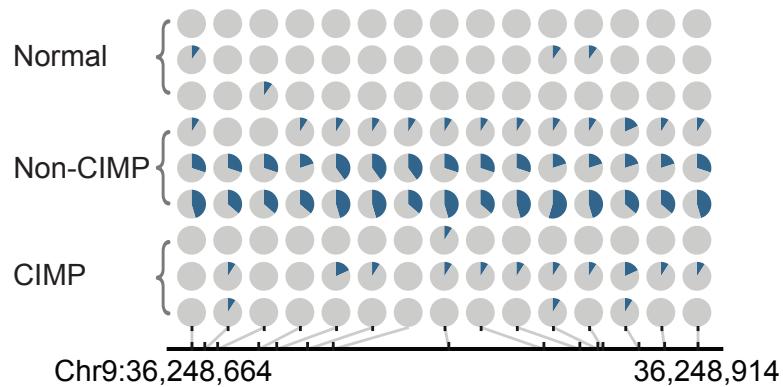
**Supplementary Figure 7:** Summary bisulfite sequencing results for the DMS located at chr8:145,176,650 -145,179,349. The bisulfite sequencing amplicon is located at chr8:145,177,341-145,177,588. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



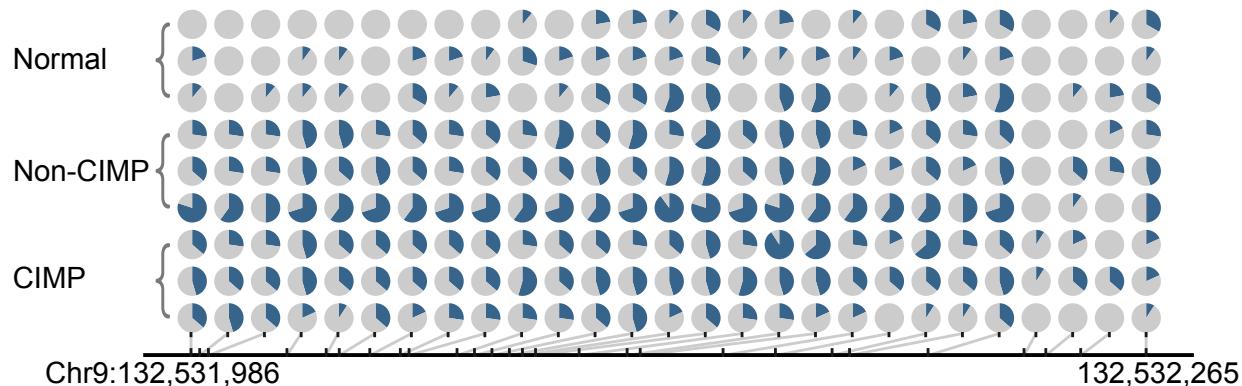
**Supplementary Figure 8:** Summary bisulfite sequencing results for the DMS located at chr8:145,530,450 - 145,530,849. The bisulfite sequencing amplicon is located at chr8:145,530,620-145,530,771. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



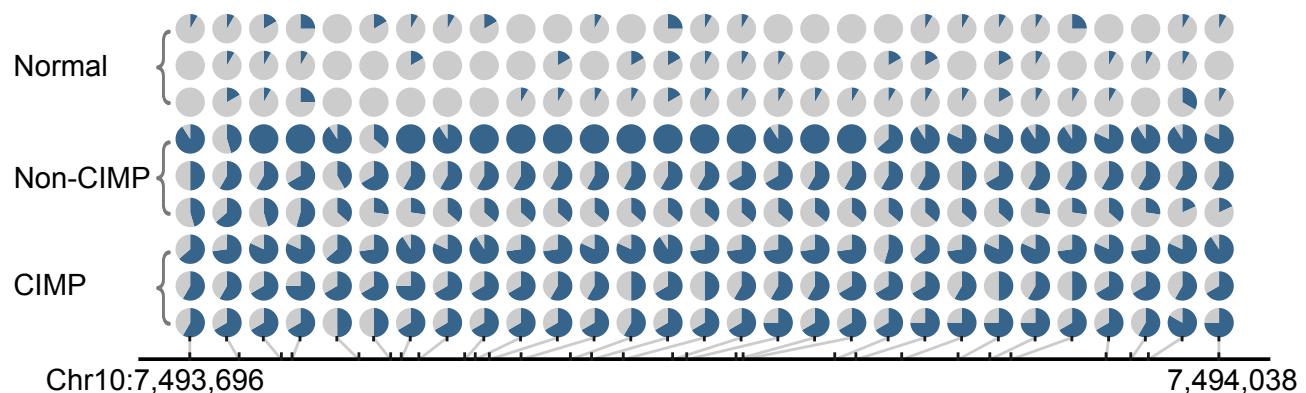
**Supplementary Figure 9:** Summary bisulfite sequencing results for the DMS located at chr9:36,248,100 -36,248,949. The bisulfite sequencing amplicon is located at chr9:36,248,664-36,248,914. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



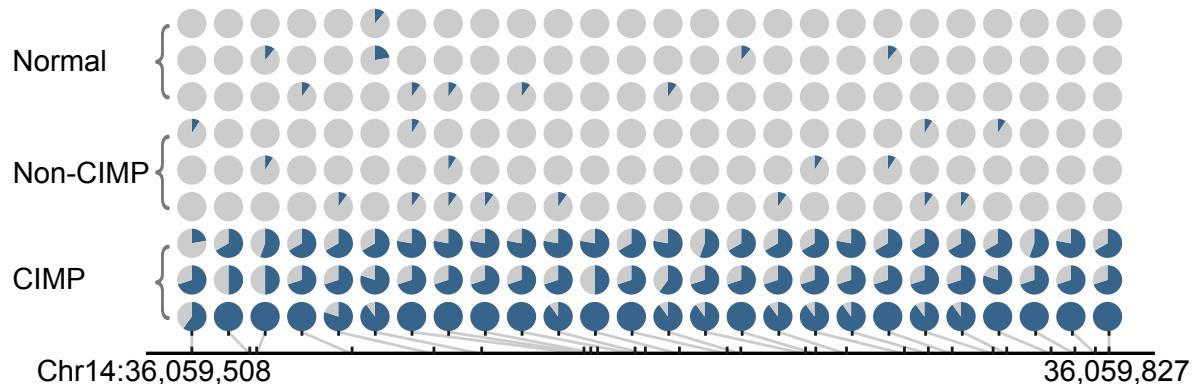
**Supplementary Figure 10:** Summary bisulfite sequencing results for the DMS located at chr9:132,530,850 - 132,532,199. The bisulfite sequencing amplicon is located at chr9:132,531,986-132,532,265. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



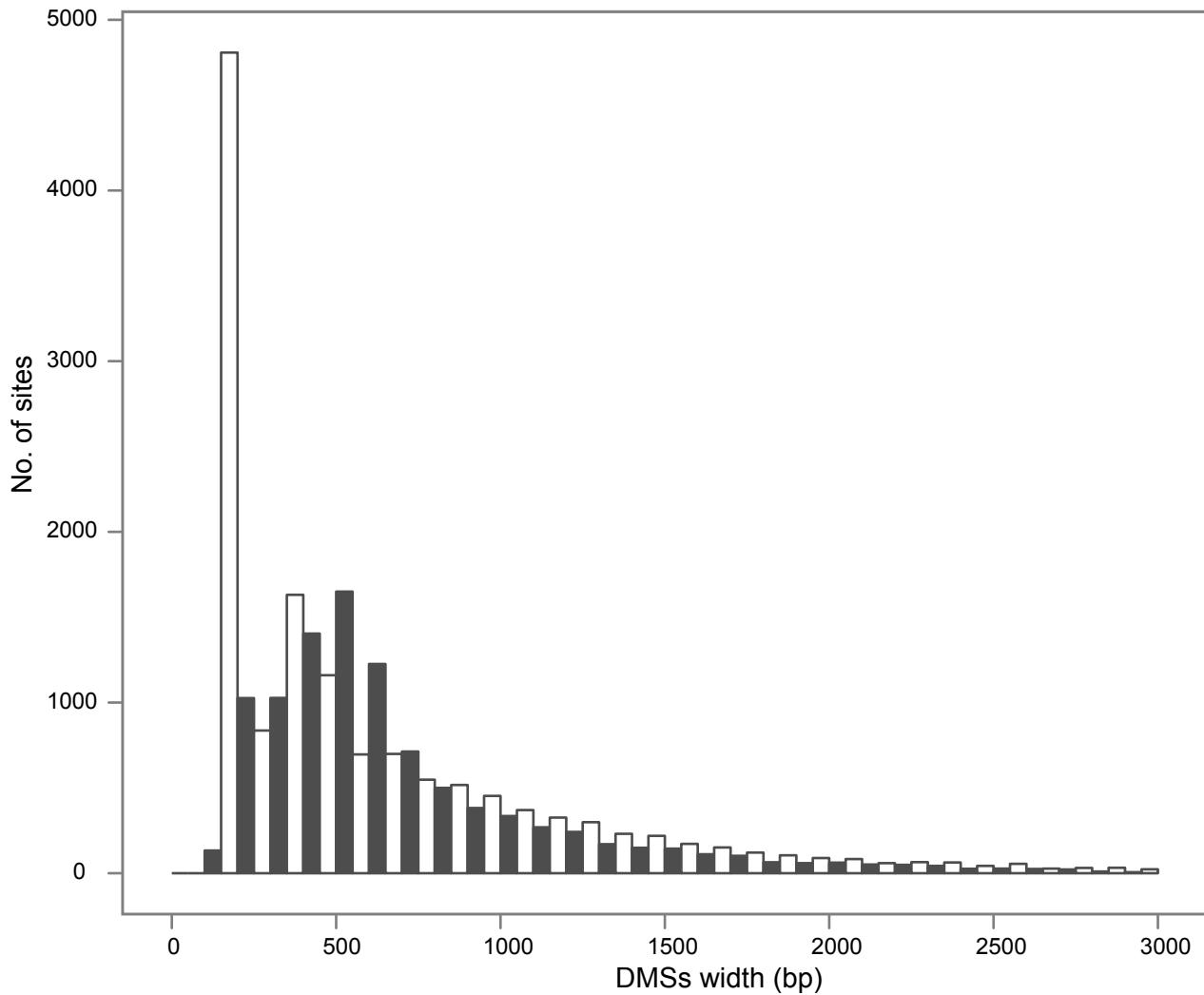
**Supplementary Figure 11:** Summary bisulfite sequencing results for the DMS located at chr10:7,489,900 -7,495,299. The bisulfite sequencing amplicon is located at chr10:7,493,696-7,494,038. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



**Supplementary Figure 12:** Summary bisulfite sequencing results for the DMS located at chr14:36,057,300 -36,060,349. The bisulfite sequencing amplicon is located at chr14:36,059,508-36,059,827. Each row represents one sample, and each circle represents a CpG site with the frequency of methylation expressed as a pie chart.



**Supplementary Figure 13:** Histogram of DMS widths between the Demonstration and the Evaluation datasets. The white bars represent the histogram of DMS widths from the Demonstration dataset while the grey bars represent the histogram of DMS widths from the Evaluation dataset. Only widths <3,000bp are shown.



**Supplementary Figure 14:** Overlap concordance of DMSs stratified by differential ratio ranges. Each white bar represents the total number of DMSs identified in the Demonstration dataset within the specified range of the absolute value of  $\log_2(\text{differential ratio})$  while a grey bar represents the number of DMSs among those in the white bar identified in the Evaluation dataset. The concordance rate of each range is denoted on top of the bar. For example, the white bar in the far left group represents 7,230 DMSs identified in the Demonstration dataset that have  $0.5 < |\log_2(\text{differential ratio})| \leq 1$ , and the grey bar represents 777 of those 7,230 DMSs also identified in the Evaluation dataset with the concordance rate of 10.7%.

