methylC Track: Visual integration of single-base resolution DNA methylation data on the WashU EpiGenome Browser

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Supplementary note

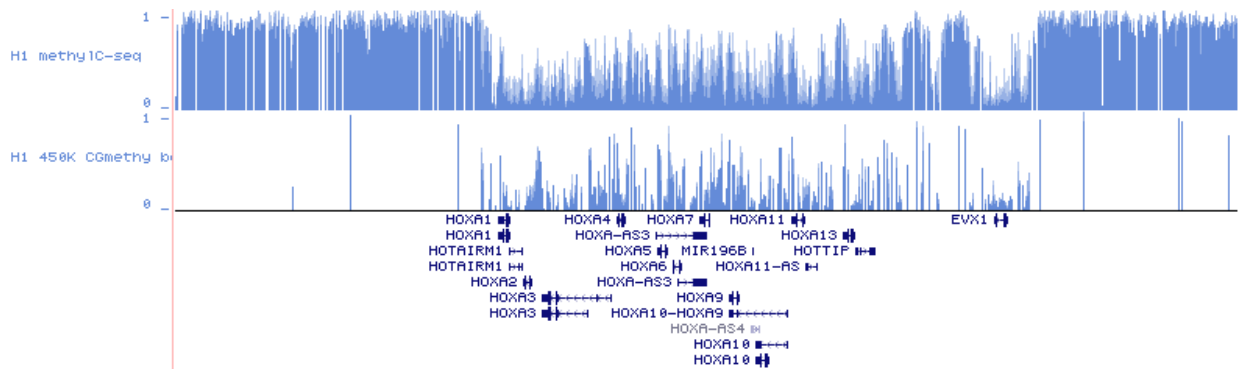
The most up-to-date descriptions and instructions about the methylC track can be found in this website: http://epigenomegateway.wustl.edu/+/cmtk/

Notes on the H1ES and IMR90 methylC-seq tracks used in this manuscript

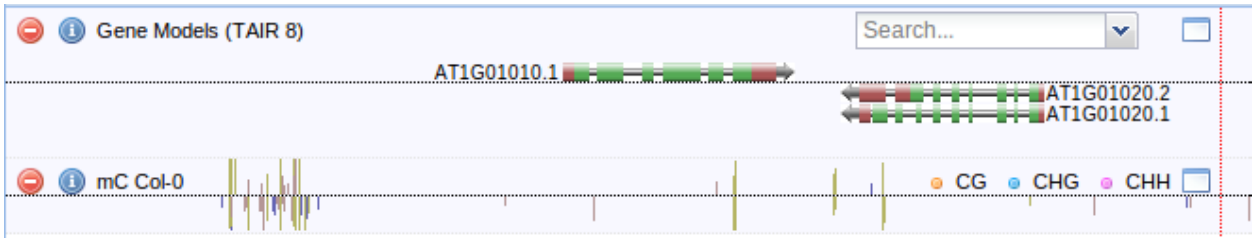
The H1ES and IMR90 methylC-seq experiment results are from the publication of Lister R. et. al., “Human DNA methylomes at base resolution show widespread epigenomic differences”, (doi: 10.1038/nature08514). We downloaded the cytosine methylation call data from the authors’ website (http://neomorph.salk.edu/human_methylome/data.html). For each cell line, we converted the data into 8 bedGraph files which were assembled into a methylC track for display (see Fig. 1a in main text). These methylC tracks can be accessed or downloaded from http://vizhub.wustl.edu/public/hg18/pmid19829295/hub.

For demonstration purpose we used methylation call data for all CG cytosines, but CHG/CHH cytosines, we only included methylated ones (methylation level >0). All unmethylated CHG/CHH cytosines were excluded. This is for demonstration purpose only, and is based on the fact that vast majority of CHG and CHH cytosines are unmethylated and are generally less biologically relevant compared to unmethylated CG cytosines. However, our methylC track is able to distinguish unmethylated cytosines from being lack of measurement in all contexts (CG, CHG, CHH), as described in main text. And we give full control to investigators over whether to include unmethylated CHG/CHH cytosines when preparing custom methylC tracks.

Supplementary figures

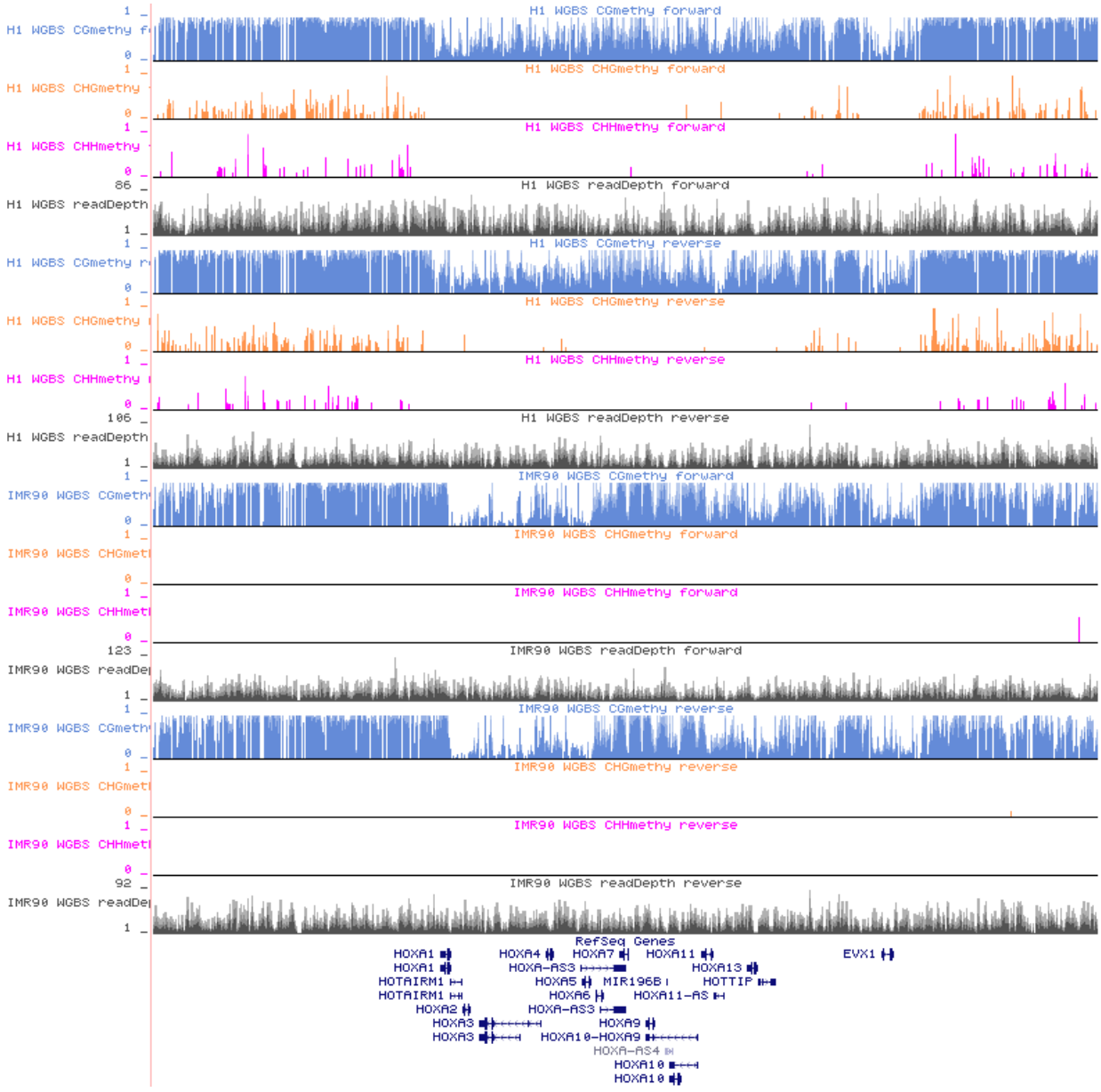


Supplementary figure 1: DNA methylation tracks displayed on the UCSC Genome Browser. Bar plots are used to indicate methylation levels at measured CpG sites. The track on the top is a methylC-seq experiment (GSM429321), the track on the bottom is an Infinium 450K array experiment (GSM999379). Both experiments are on human H1 embryonic stem cells. Data from two strands are combined for the methylC-seq track. Data is shown over the HOXA gene cluster same as Fig. 1b in the main text.

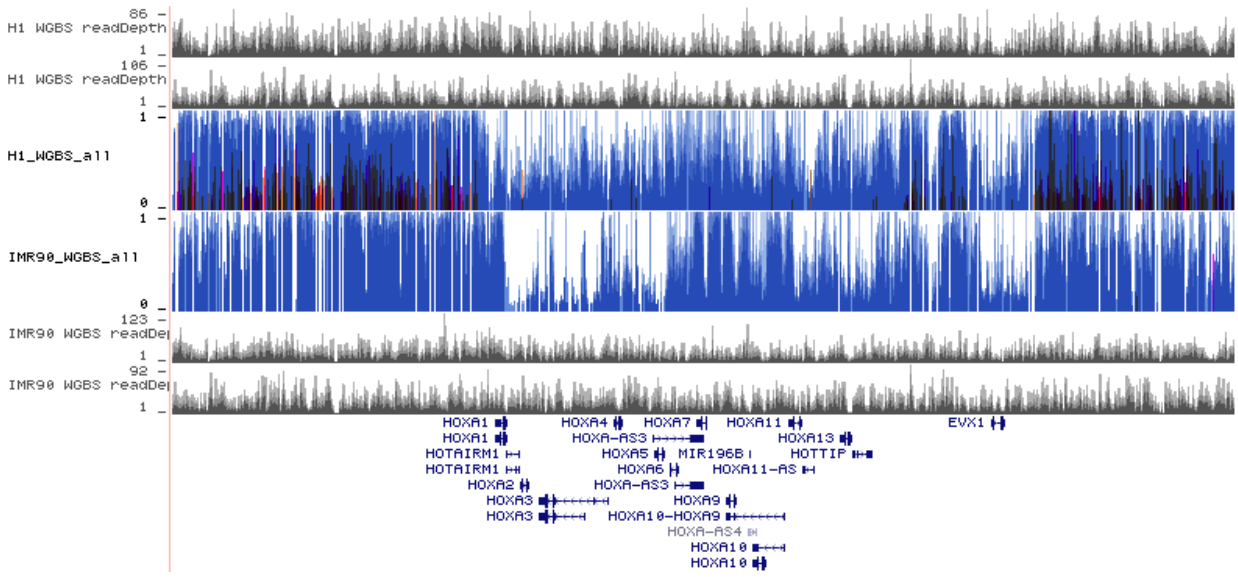


Supplementary figure 2: A whole genome bisulfite sequencing track is shown on the AnnoJ genome browser (http://neomorph.salk.edu/epigenome/epigenome.html). It displays strand-specific cytosine methylation levels, and distinguishes cytosines at different context (CG, CHG, CHH) with different bar colors.

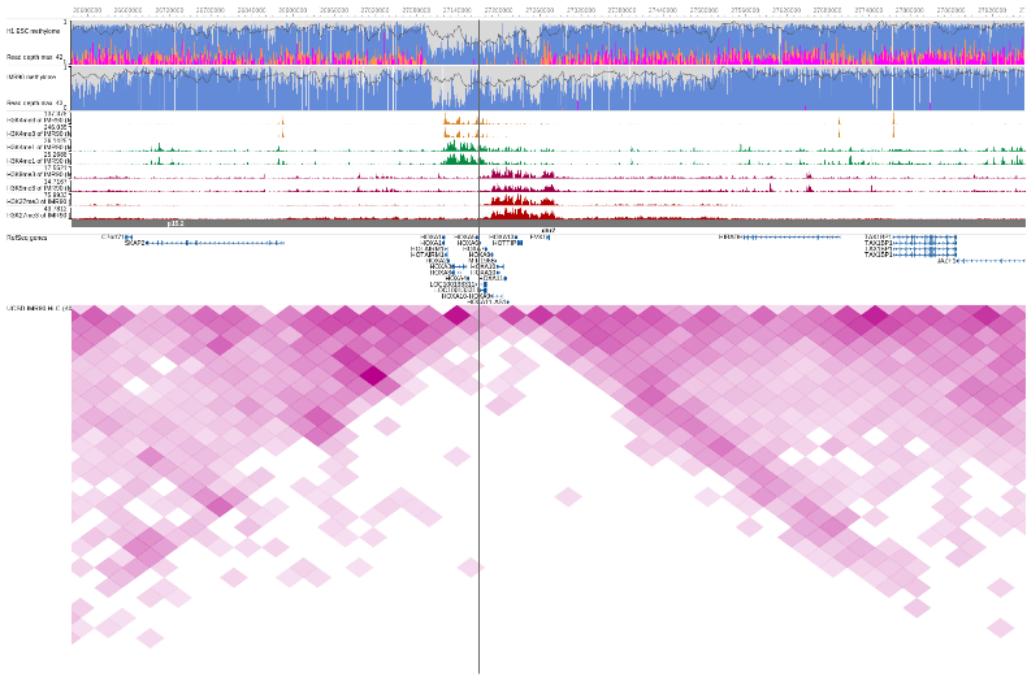
Supplementary figure 3a



Supplementary figure 3b



Supplementary figure 3: Display of the H1 ESC and IMR90 methylC-seq data in UCSC Genome Browser. The H1 ESC and IMR90 methylC-seq experiment data is the same as that used in Fig. 1b of main text. Cytosine methylation levels are presented on separate strands, and separate colors are used for different cytosine context (blue for CG, orange for CHG, magenta for CHH). Black color is used for read depth tracks. (a) Separate tracks were used to display strand-specific CG/CHG/CHH methylation data. (b) “multiWig” overlaying display method was used to display CG/CHG/CHH methylation levels from separate strands all in one track.

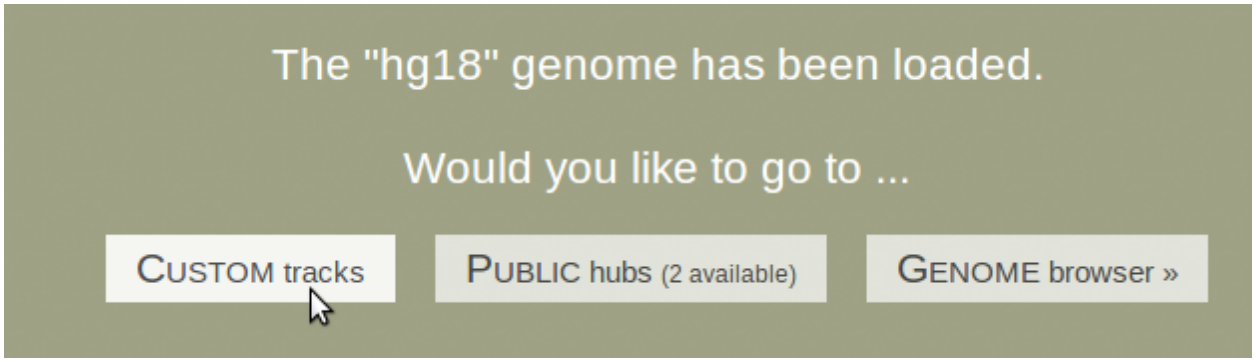


Supplementary figure 4: In IMR90 cells, HOXA gene cluster is characterized by bipartite chromatin status, and its center point lies at the boundary of two chromatin domains (black vertical line), correlating to the elevated CG methylation level observed in **Figure 1b** (marked by black box). The chromatin domain structure is revealed by the Hi-C experiment results on IMR90 cells (GSM892307). All the tracks are visualized using WashU EpiGenome Browser.

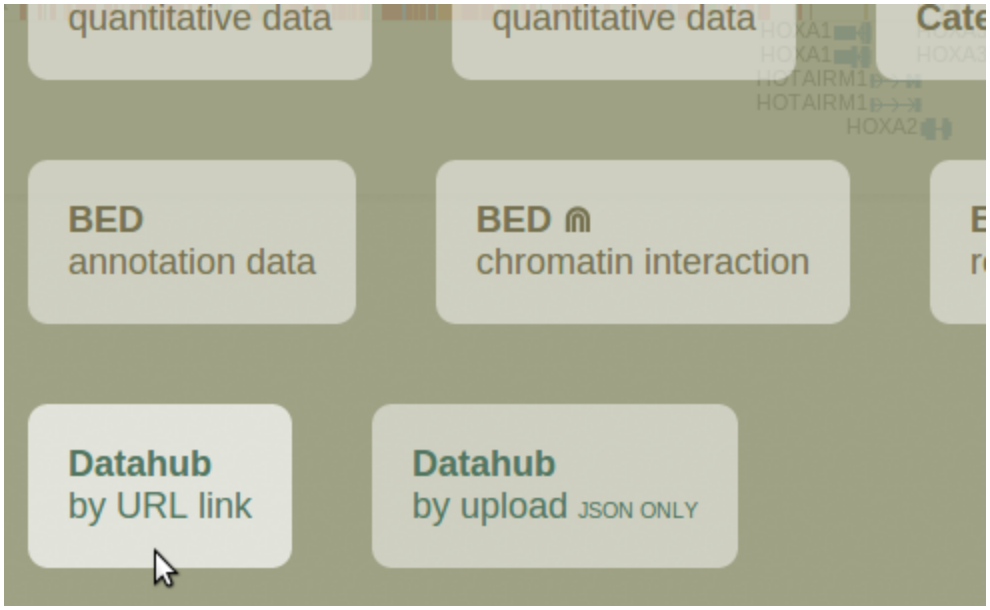
Supplementary tutorial: steps to display sample methylC tracks on WashU EpiGenome Browser

Note: sample methylC tracks are described in this datahub file: http://vizhub.wustl.edu/public/hg18/methylC_sample. It should be displayed in human hg18 genome.

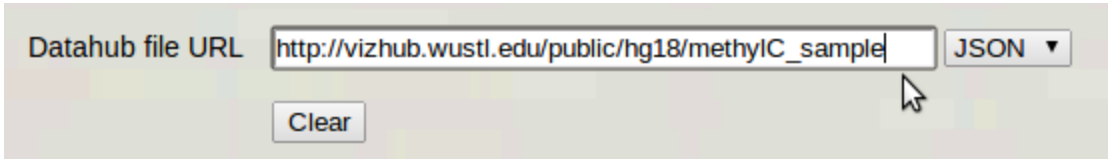
1. Go to the browser at http://epigenomegateway.wustl.edu/browser/. Choose human hg18. Then click “CUSTOM tracks”:



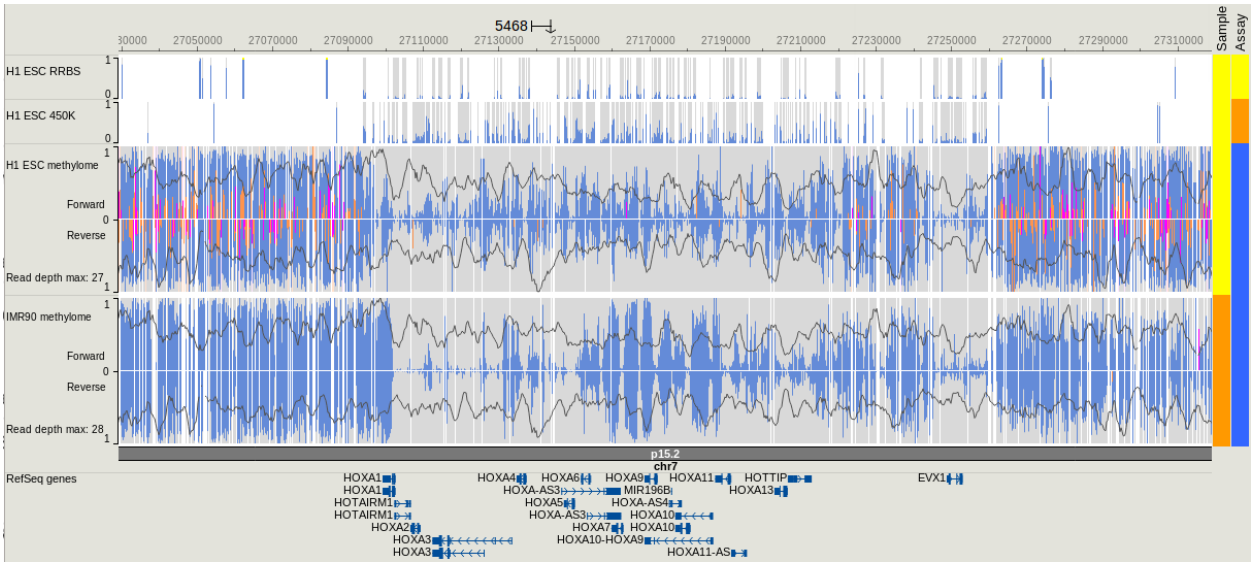
2. Choose "Datahub" from the options:



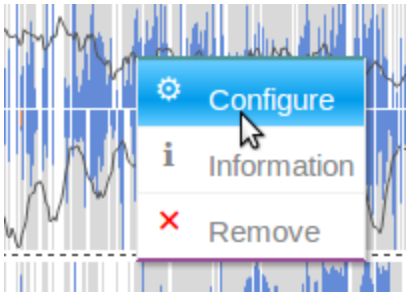
3. Enter the URL http://vizhub.wustl.edu/public/hg18/methylC_sample into the text field. Choose "JSON" from the dropdown menu and submit:



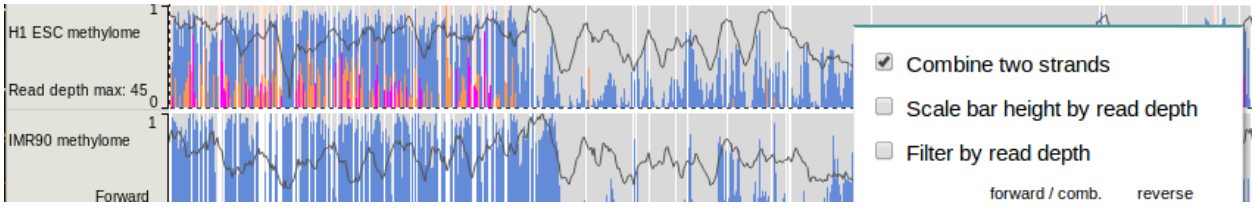
4. Now the methylC tracks are displayed. The two WGBS experiments are displayed as full blown methylC tracks, showing strand-specific information on position and methylation levels of CG/CHG/CHH cytosines, together with read depth across the whole region. Mouse over the track to see details about methylation status at specific position from the tooltip:



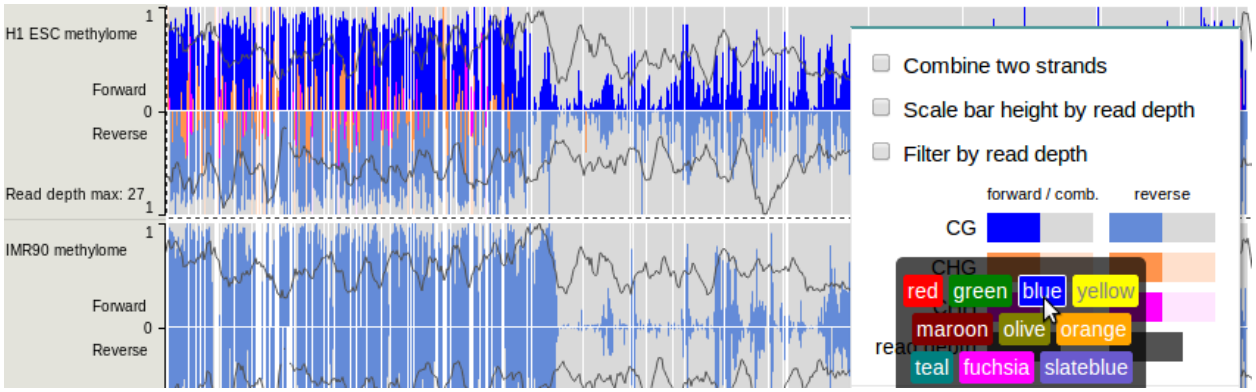
5. To update the track right click and select "Configure", options will appear in the menu:



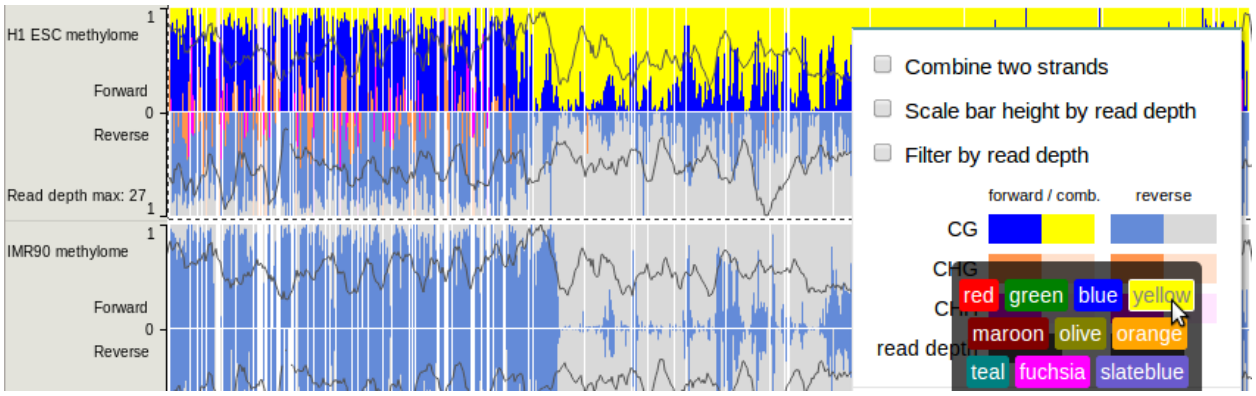
6. By default the methylC-seq data is shown in separate strands. To merge the two strands, check the first checkbox in the menu:



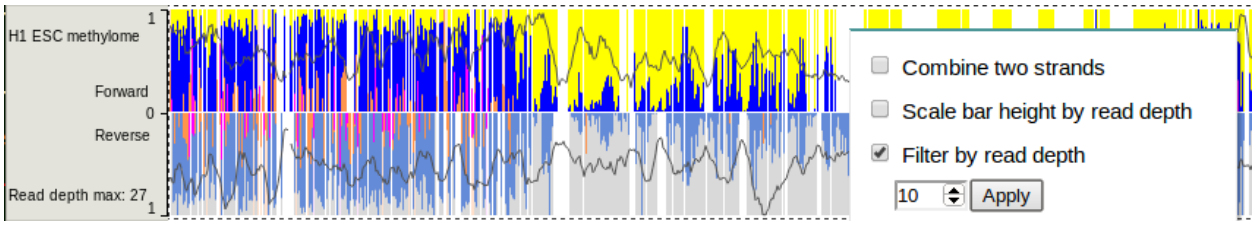
7. The methylC track allows you to configure rendering colors of all components. For instance click the top left color cell to change forward strand CG cytosine methylation level:



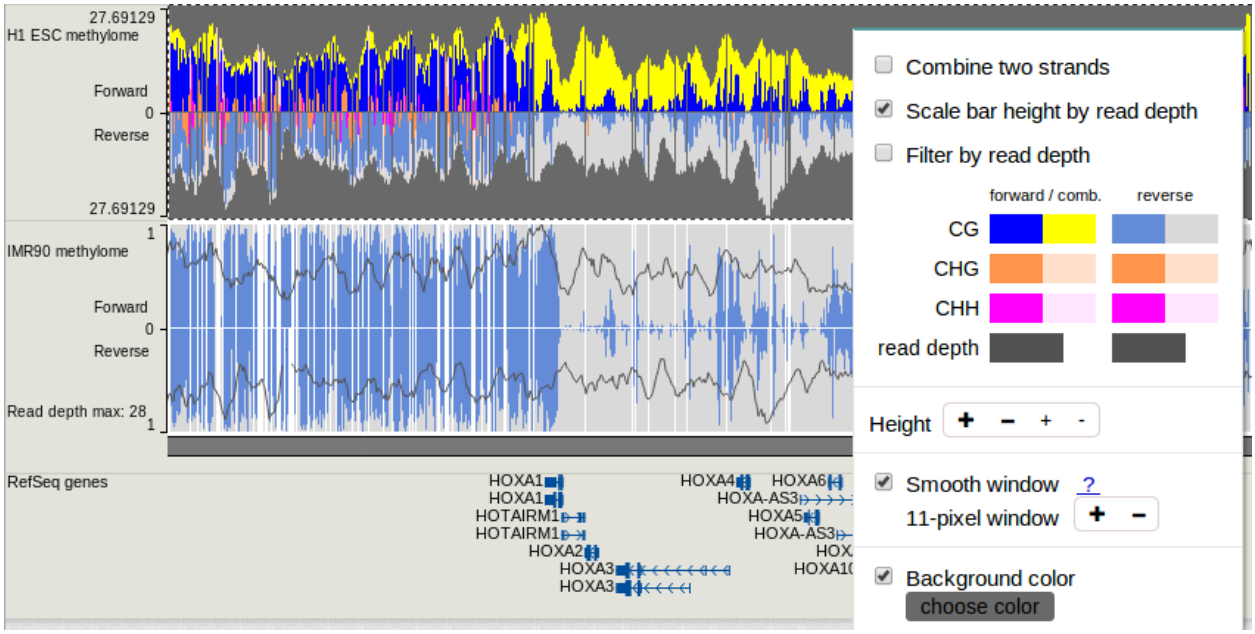
8. Similarly, click the color cell next to this one to assign yellow background for all CG di-nucleotides in the forward strand:



9. A minimum read depth cutoff can be applied, so that methylation calls will be filtered out if their underlying read depth is lower than minimum:



10. Finally you can tune the methylC track into a very different look compared with default style. Check the second checkbox in the menu to scale bar heights by read depth, and assign contrasting colors for CG background (yellow) and track background (dark gray):


27.69129
H1 ESC methylome
Forward
0
Reverse
27.69129
1
IMR90 methylome
Forward
0
Reverse
Read depth max: 28
1
RefSeq genes
HOXA1
HOXA1
HOTAIRM1
HOTAIRM1
HOXA2
HOXA3
HOXA3
HOXA4
HOXA6
HOXA-AS3
HOXA5
HOXA-AS3
HOX
HOXA10
Combine two strands
Scale bar height by read depth
Filter by read depth
forward / comb.
reverse
CG
CHG
CHH
read depth
Height
+
−
+
-
Smooth window
?
11-pixel window
+
−
Background color
choose color