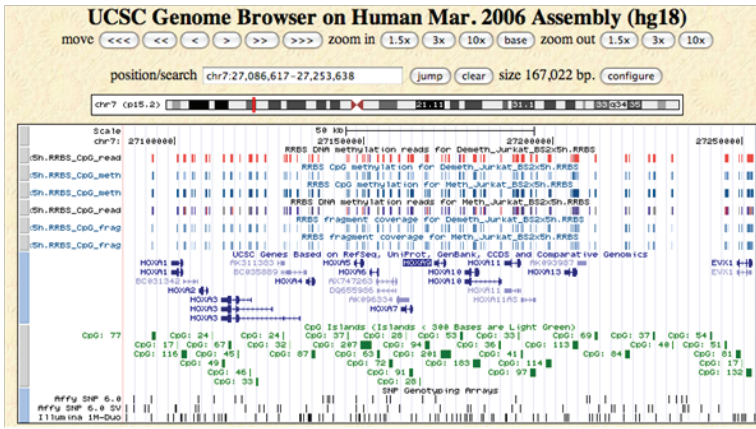


Overview of genomic region



HOXA Cluster

Tracks displayed:

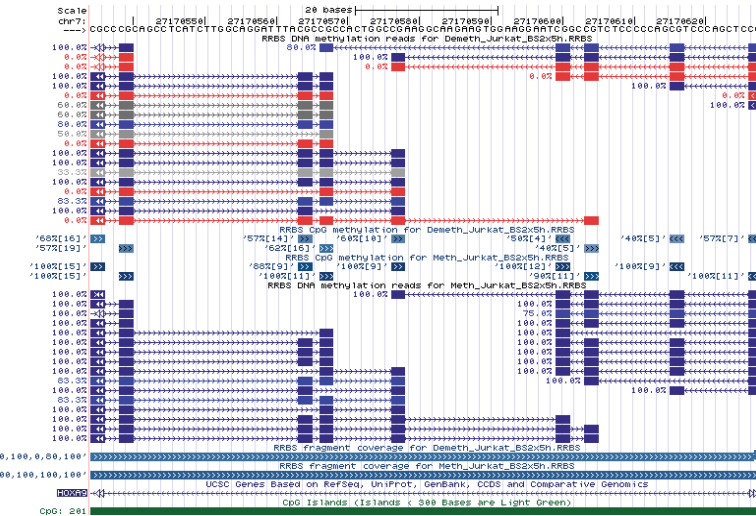
- Demethylated_Jurkat Read track
- Demethylated_Jurkat CpG Methylation track
- Methylated_Jurkat CpG Methylation track
- Methylated_Jurkat Read track
- Demethylated_Jurkat Fragment Coverage track
- Methylated_Jurkat Fragment Coverage track

Single gene (dense view)



HOXA9 zoomed in

Single gene (full view)



HOXA9 zoomed in further

'27:100,0,100,100,0,100,100,33,0,100,0,60,0,83,60,80,100,100,50,0,100,0,0,100,0,80,100'

'29:100,100,100,100,100,100,100,83,100,100,100,100,83,100,100,100,100,100,100,100,100,75,100,100,100,100,100,100,100'

The CpG Methylation track (genomeTrackUrl1)

- shows the mean DNA methylation level of each CpG (percentage value) and how often it was covered by sequencing reads
- darker shades of blue correspond to higher methylation levels
- the label on the left of a CpG, say '88%[9]', indicates a mean methylation level of 88% of a CpG with 9-fold sequencing read coverage (given in brackets)

The Fragment Coverage track (genomeTrackUrl2)

- shows how often a fragment was covered by sequencing reads
- darker shades of blue correspond to higher sequencing coverage
- the label on the left of the track (which also pops up when you hold the mouse pointer over the track) shows how many reads cover the fragment and what their mean methylation level is (as a percentage)
- track label example: '4: 50,50,25,50' means that the fragment was covered by 4 reads; 3 of these reads were 50% methylated and one read was 25% methylated

The Read track (genomeTrackUrl3)

- shows each read with the CpG positions it covers and the read's mean methylation level
- shades of blue correspond to high methylation levels; red corresponds to low methylation levels; grey is in between with darker shades of grey corresponding to higher methylation levels
- the CpGs of the read are represented as boxes; the connection line between them also indicates the strand (by arrow heads)
- the UCSC Genome Browser does not support separate colors for each CpG within a read, which is why only the mean methylation is shown for each read