Supplementary Figure 4 | Most cancer-specific differential DNA methylation is located at CpG island shores. The top 50 C-DMRs, ordered by statistical significance. Displays are as in Fig. 1b. The upper panels are plots of *M* value versus genomic location for brain (grey), liver (pink), spleen (purple), normal colon (green), and colon cancer (orange). Each point (shown only for normal colon and colon cancer) represents the methylation level of an individual sample for a given probe. The curve represents averaged smoothed *M* values, described in detail in the Methods. Due to the scale and standardization used, *M* values which range from −0.5 to 0.5 represent unmethylated sites as defined by the control probes, and values from 0.5 to 1.5 represent baseline levels of methylation. The middle panels provide the location of CpG dinucleotides with black tick marks on the x-axis. CpG density was calculated across the region using a standard density estimator and is represented by the smoothed black line. The location of the CpG island is denoted on the x-axis as an orange line. The lower panels provide gene annotation for the genomic region. The thin outer grey line represents the transcript, the thin inner lines represent a coding region. Filled in grey boxes represent exons. On the y-axis, plus and minus marks denote sense and antisense gene transcription respectively.

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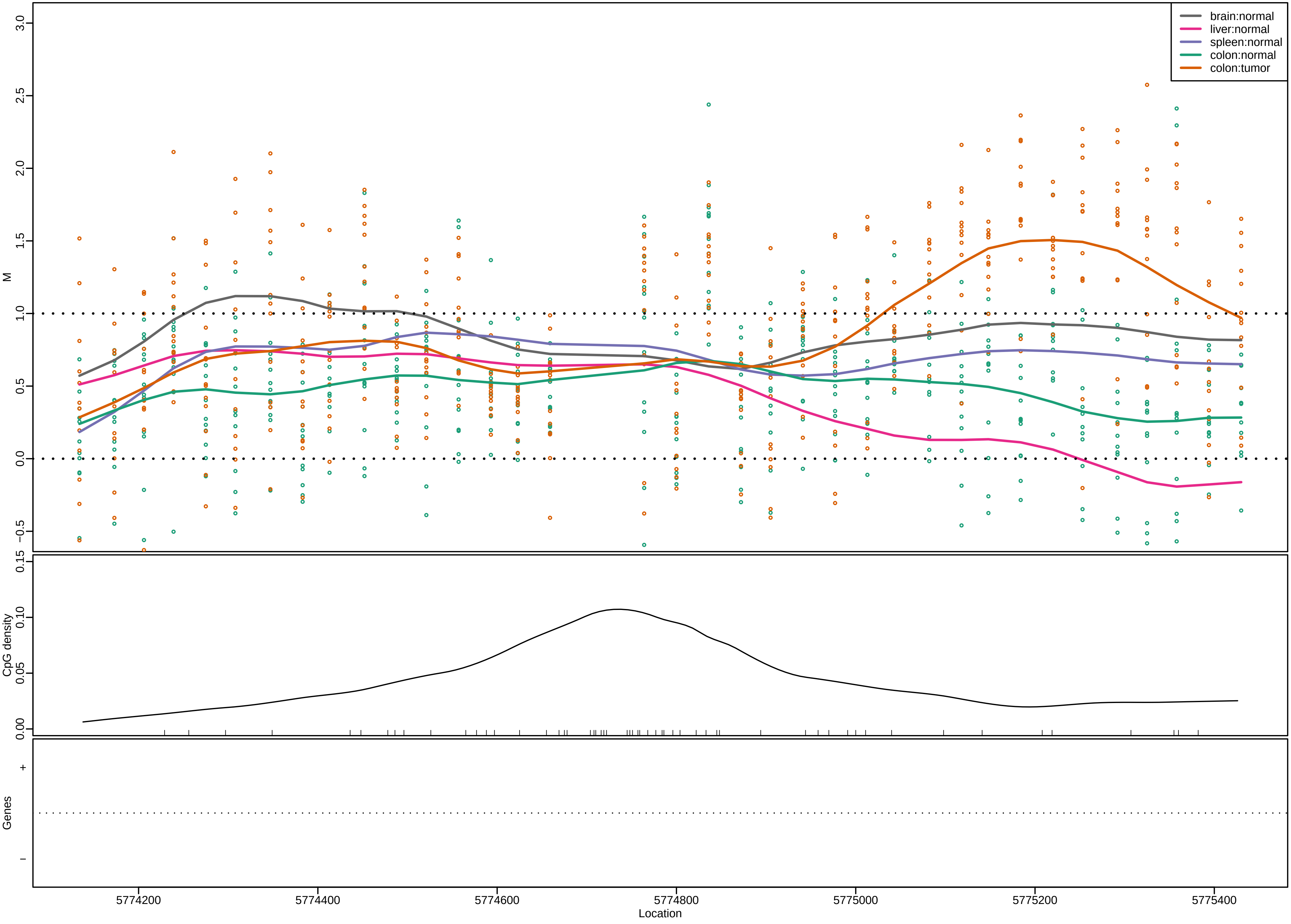

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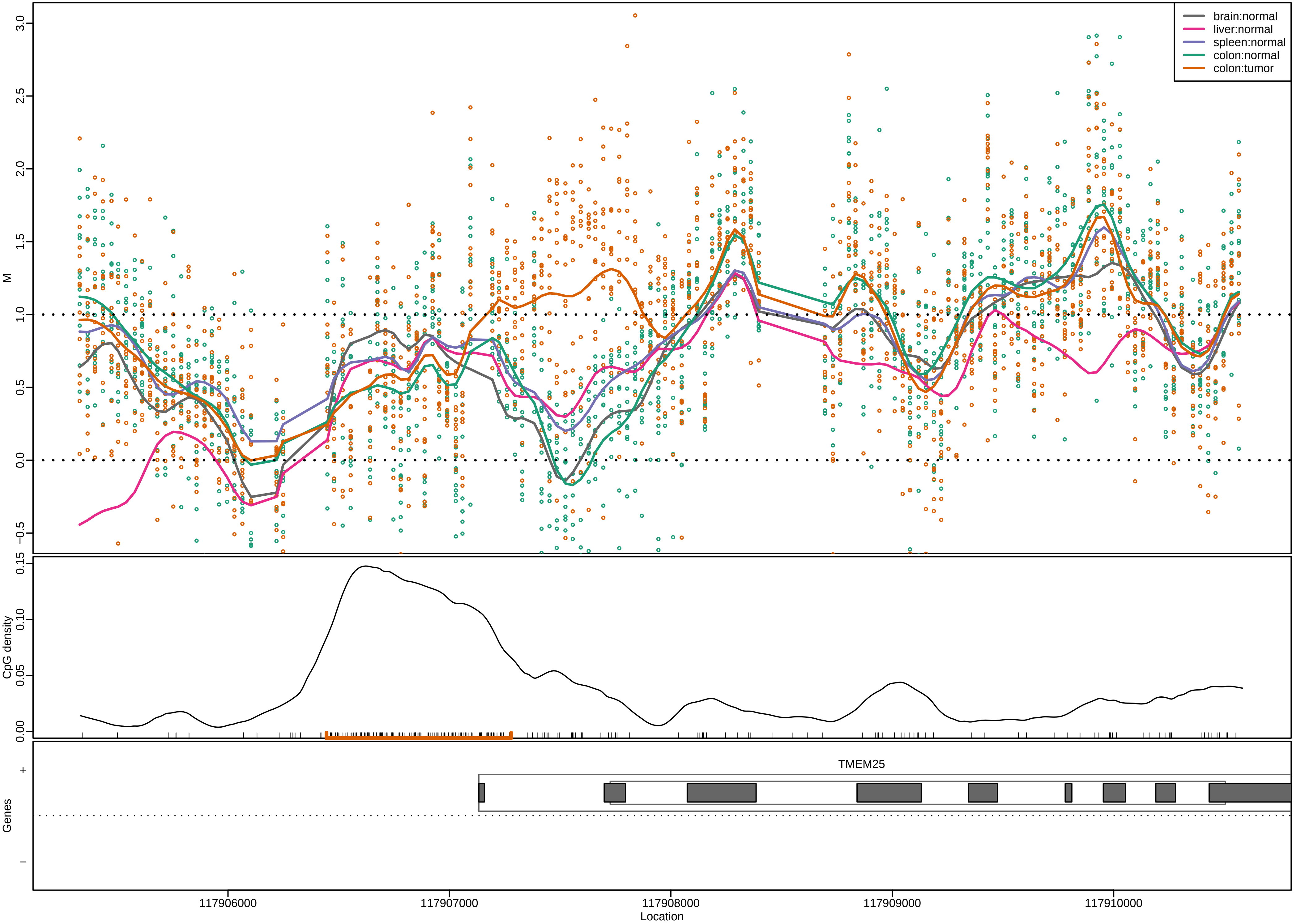

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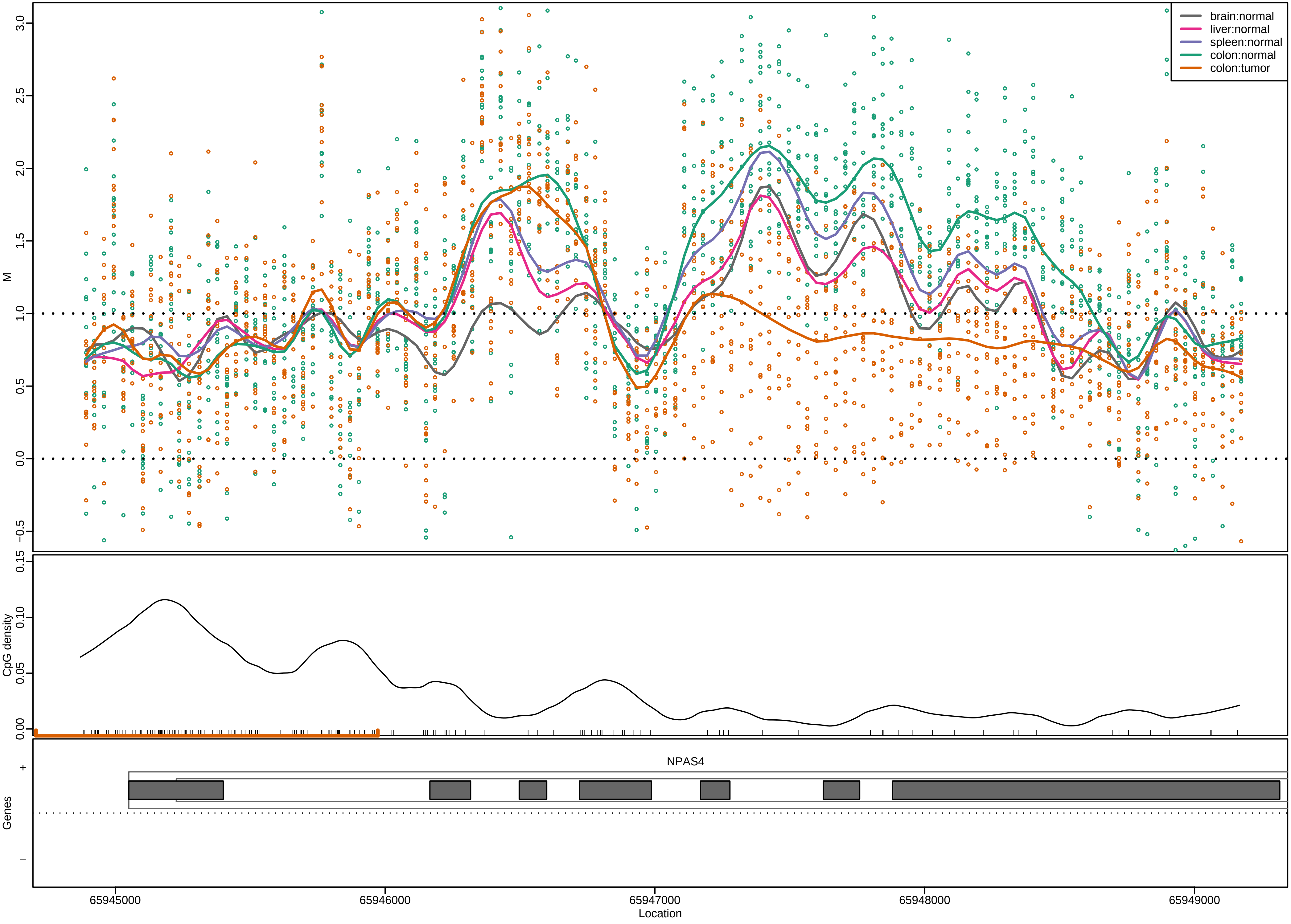

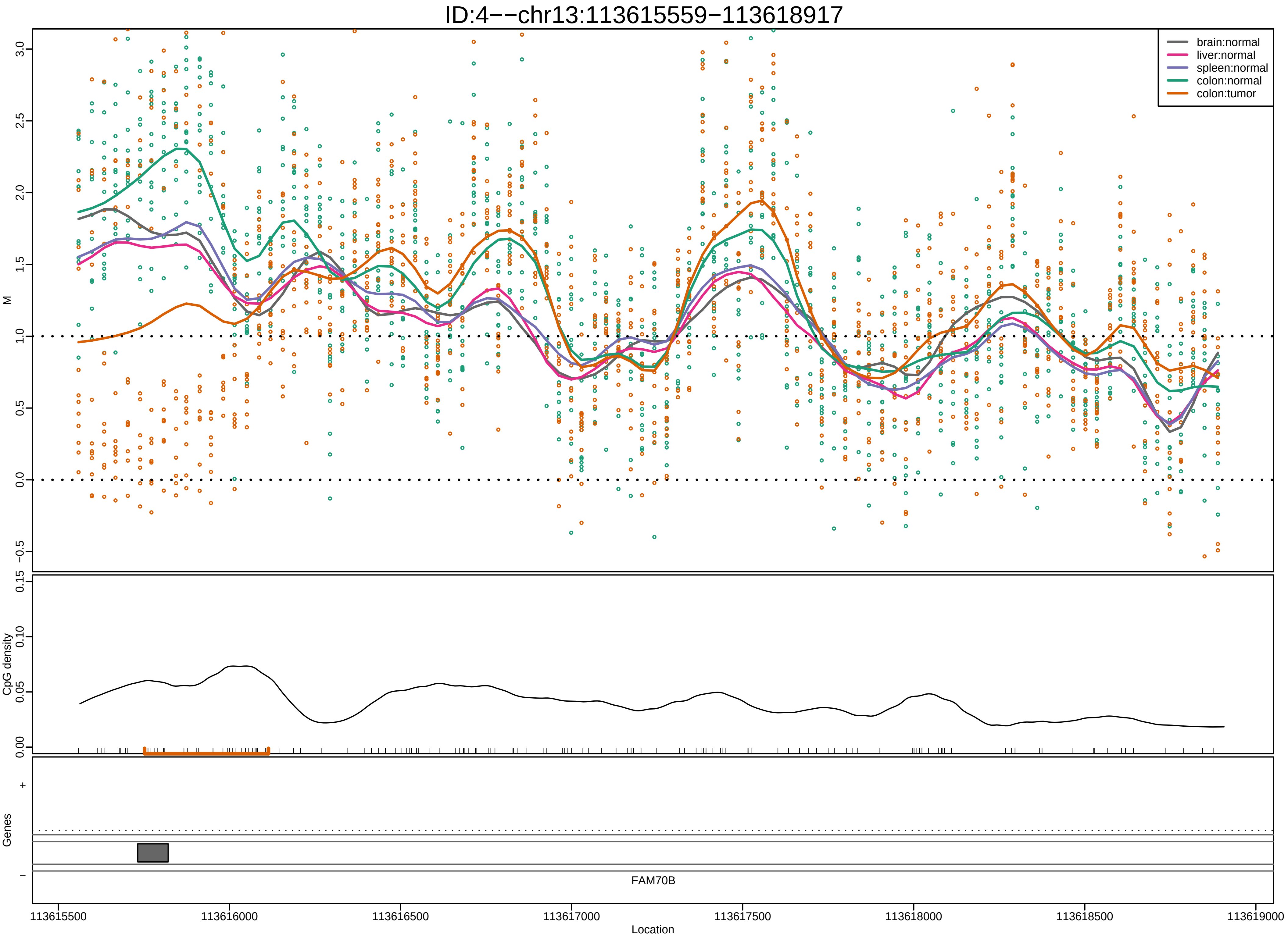
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spleen:normal
colon:normal
colon:tumor
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
FAM70B
113615500
113616000
113616500
113617000
113617500
113618000
113618500
113619000
Location

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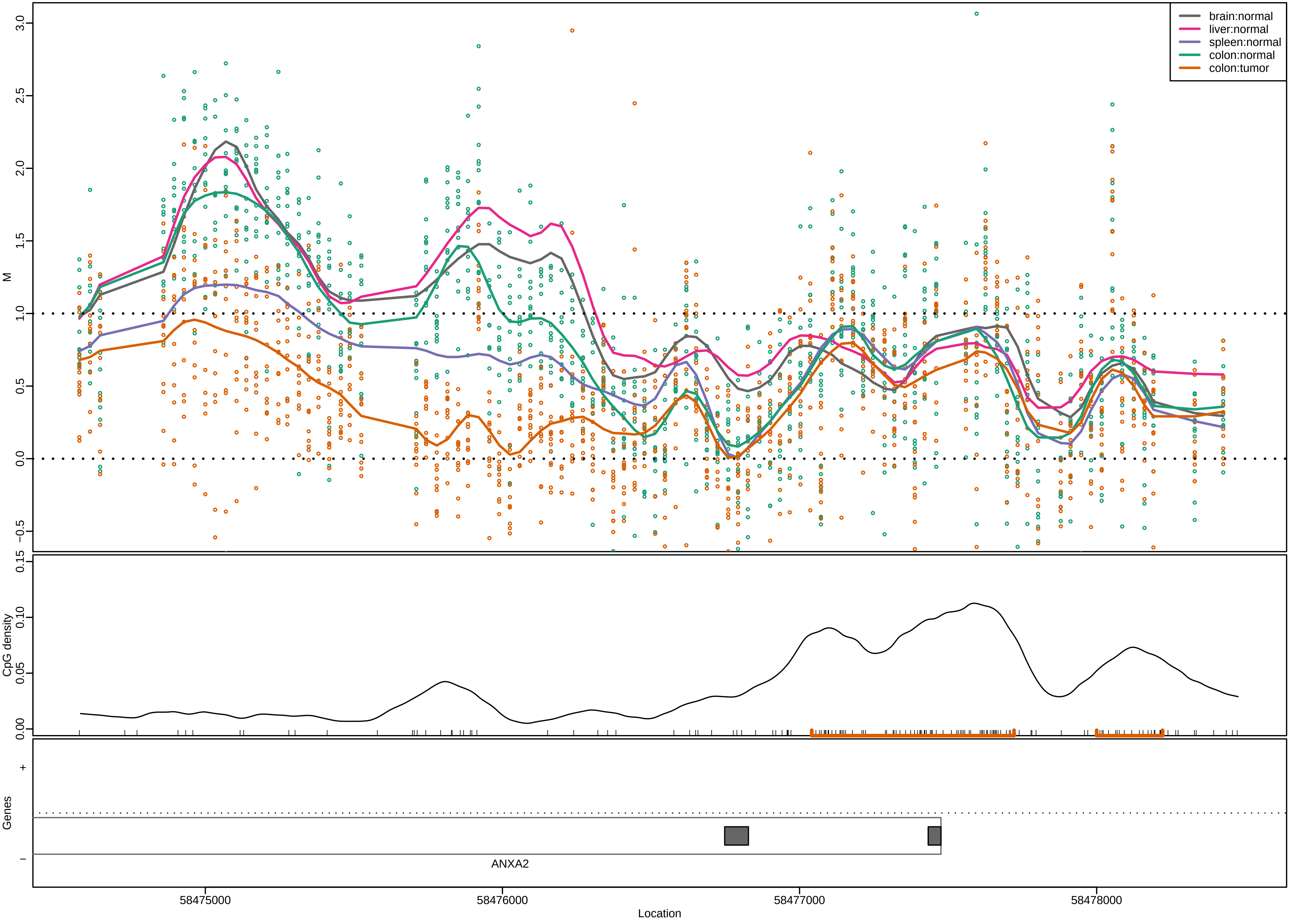

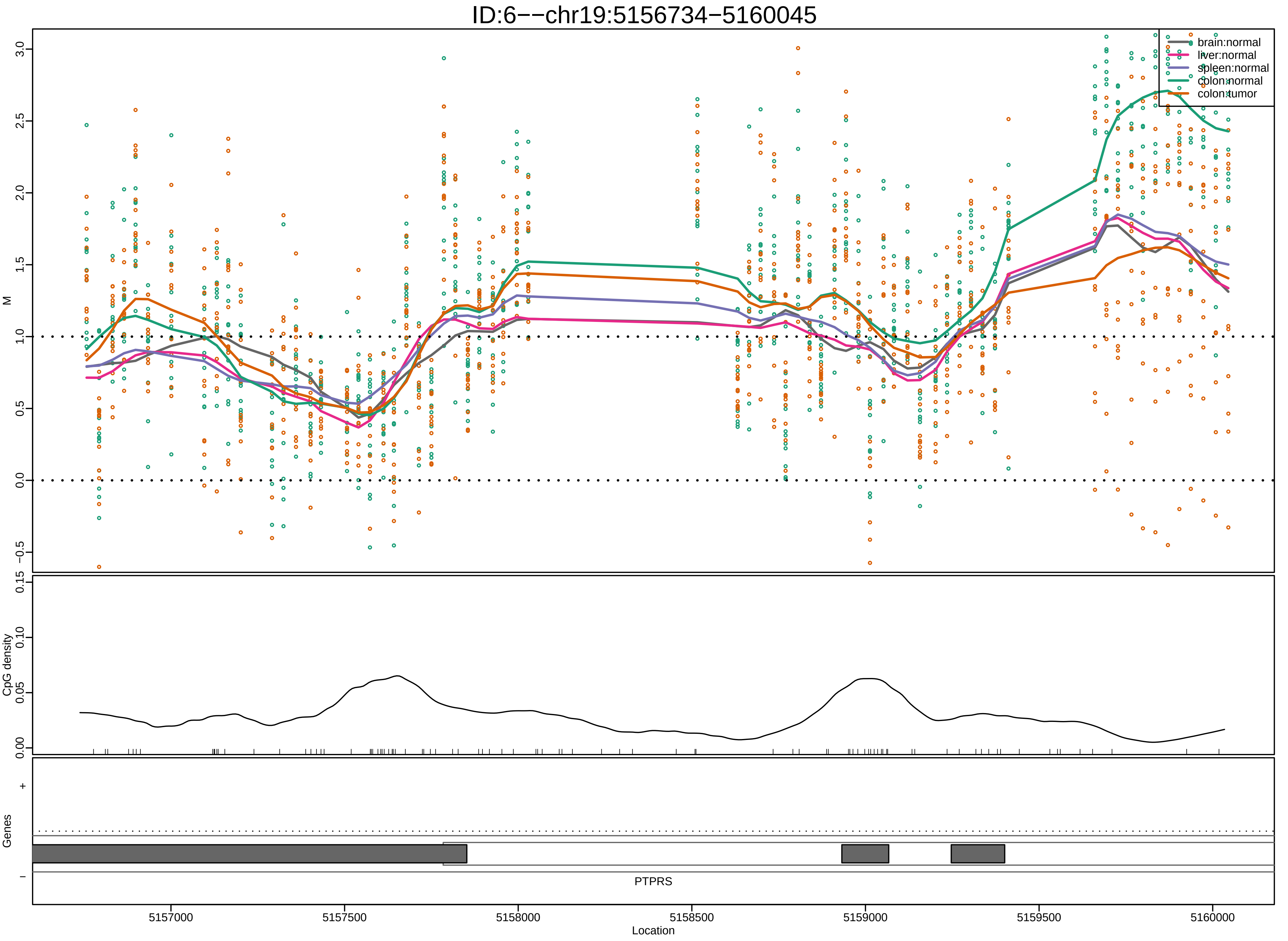
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−0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
brain:normal
liver:normal
spleen:normal
colon:normal
colon:tumor
CpG density
0.00
0.05
0.10
0.15
Genes
+
−
PTPRS
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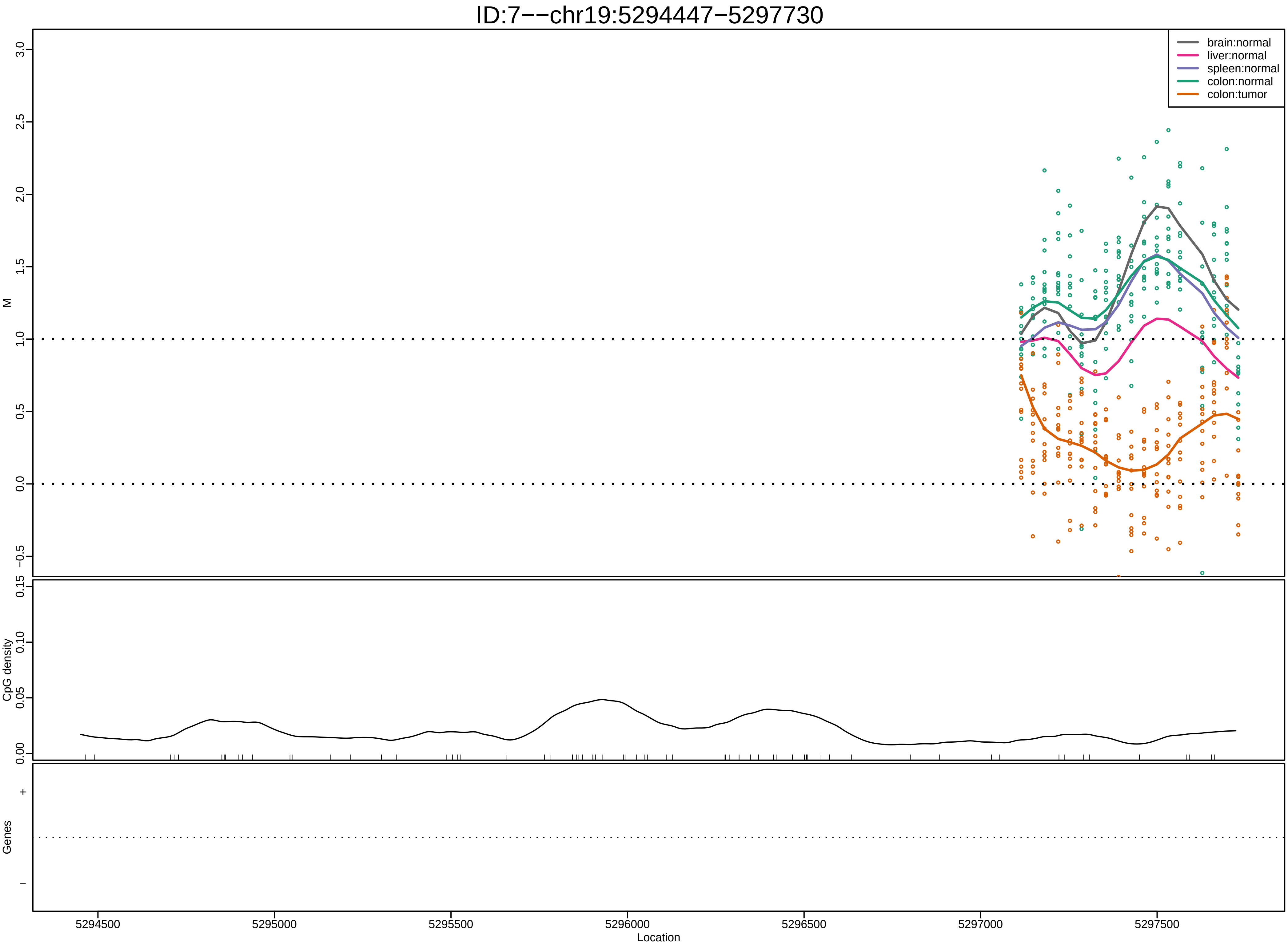
5159500
5160000
Location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liver:normal
spleen:normal
colon:normal
colon:tumor
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
5294500
5295000
5295500
5296000
5296500
5297000
5297500
Location

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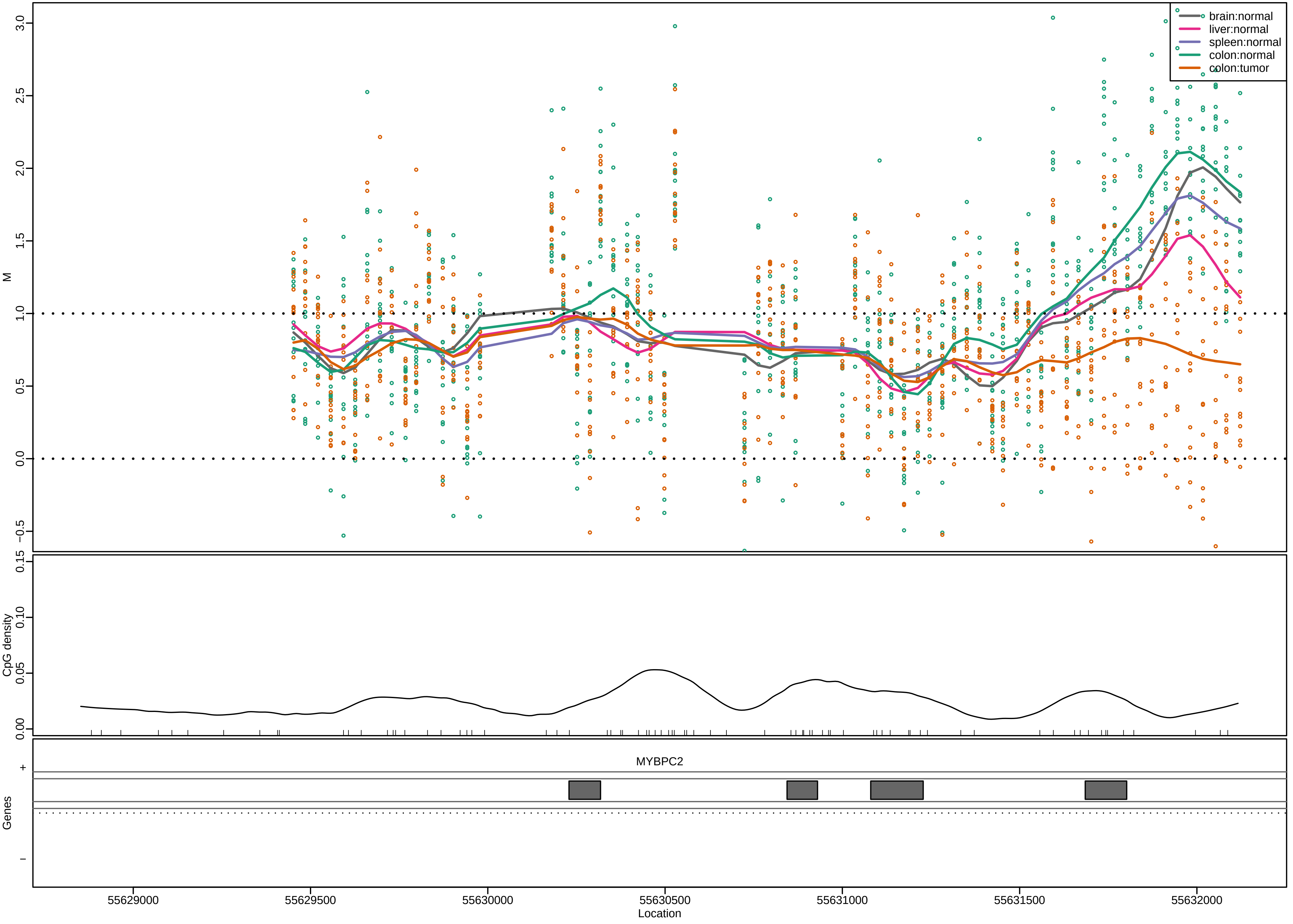

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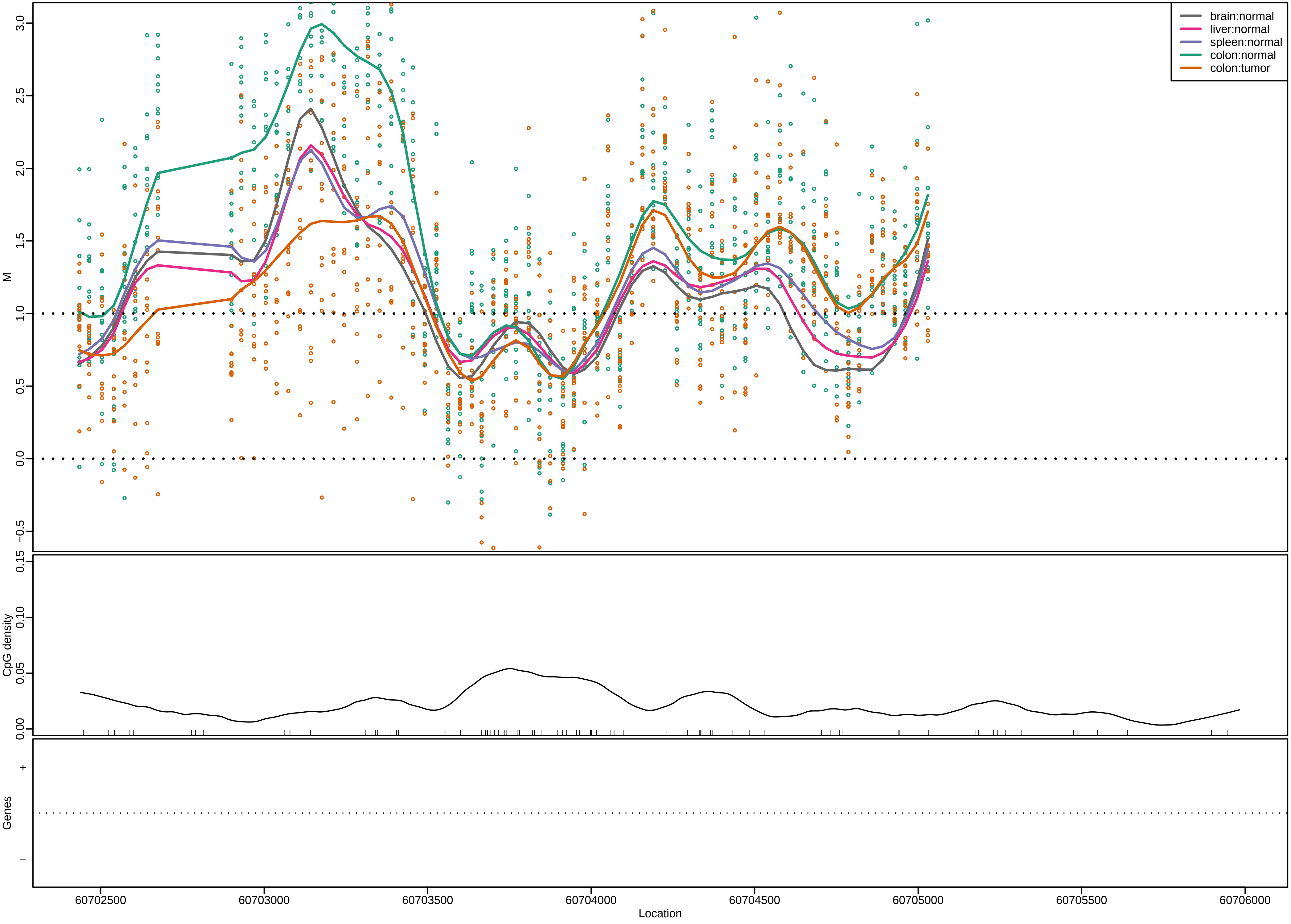

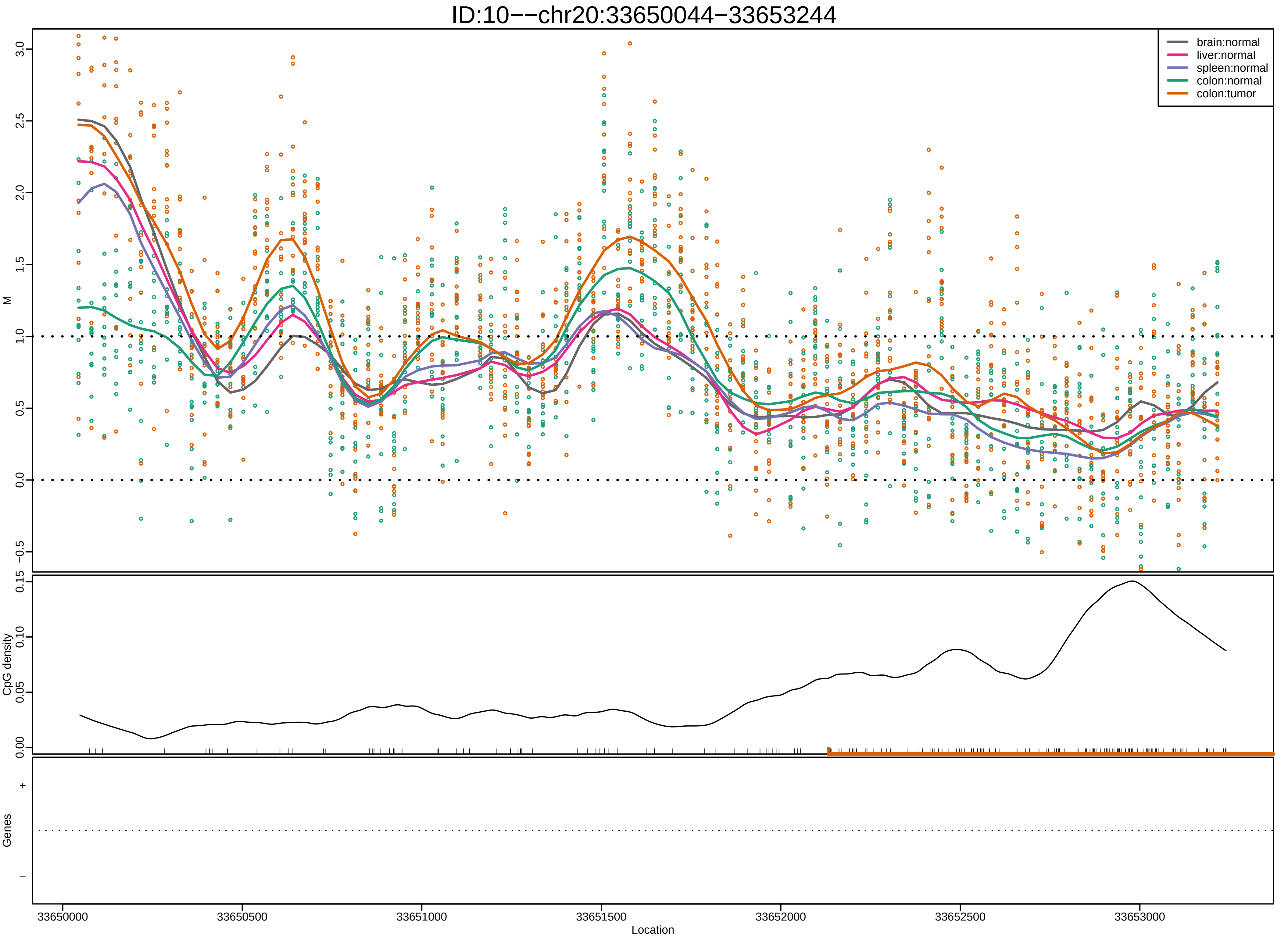
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liver:normal
spleen:normal
colon:normal
colon:tumor
M
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0.0
0.5
1.0
1.5
2.0
2.5
3.0
CpG density
0.00
0.05
0.10
0.15
Genes
+
−
33650000
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33651000
33651500
33652000
33652500
33653000
Location

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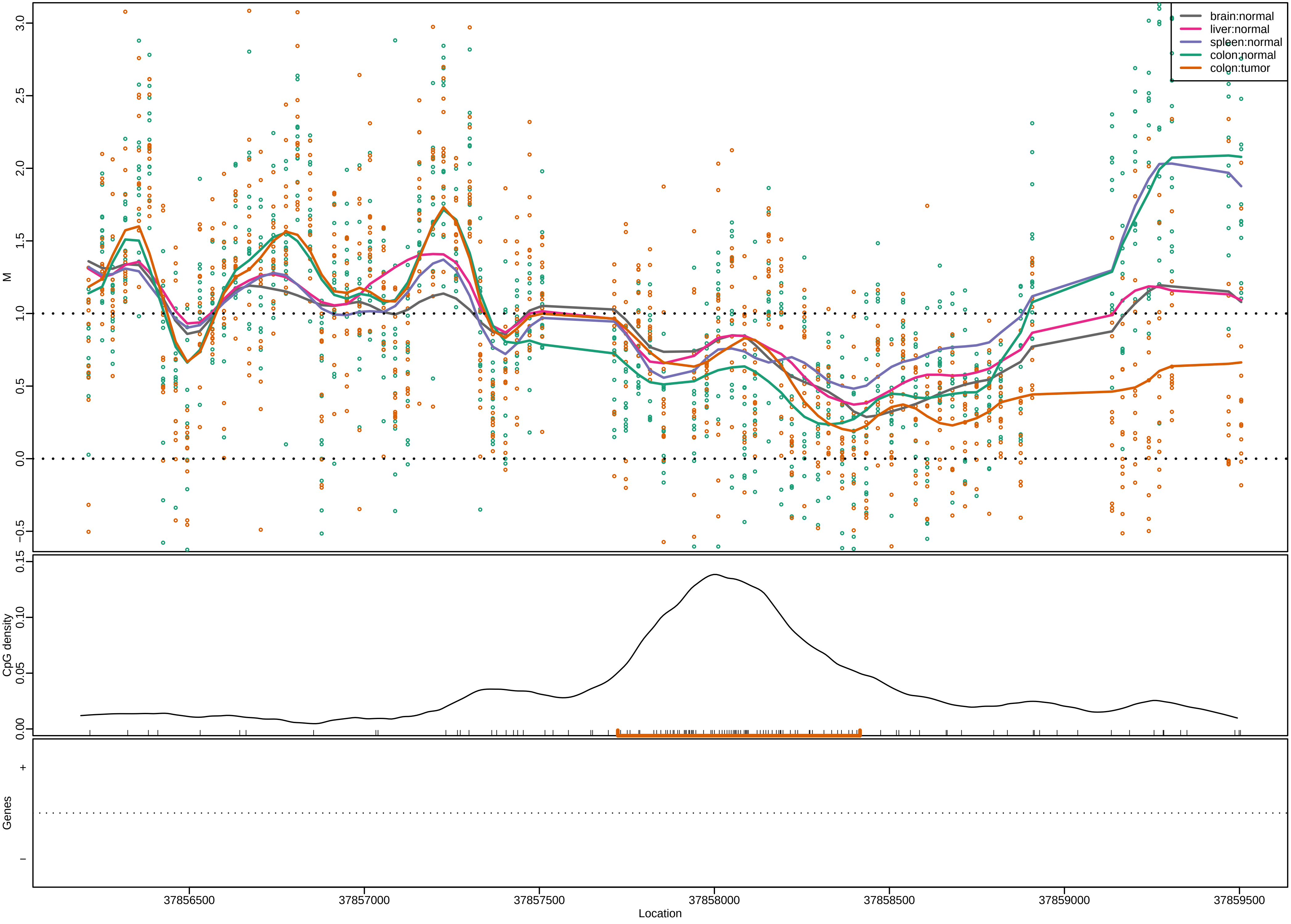

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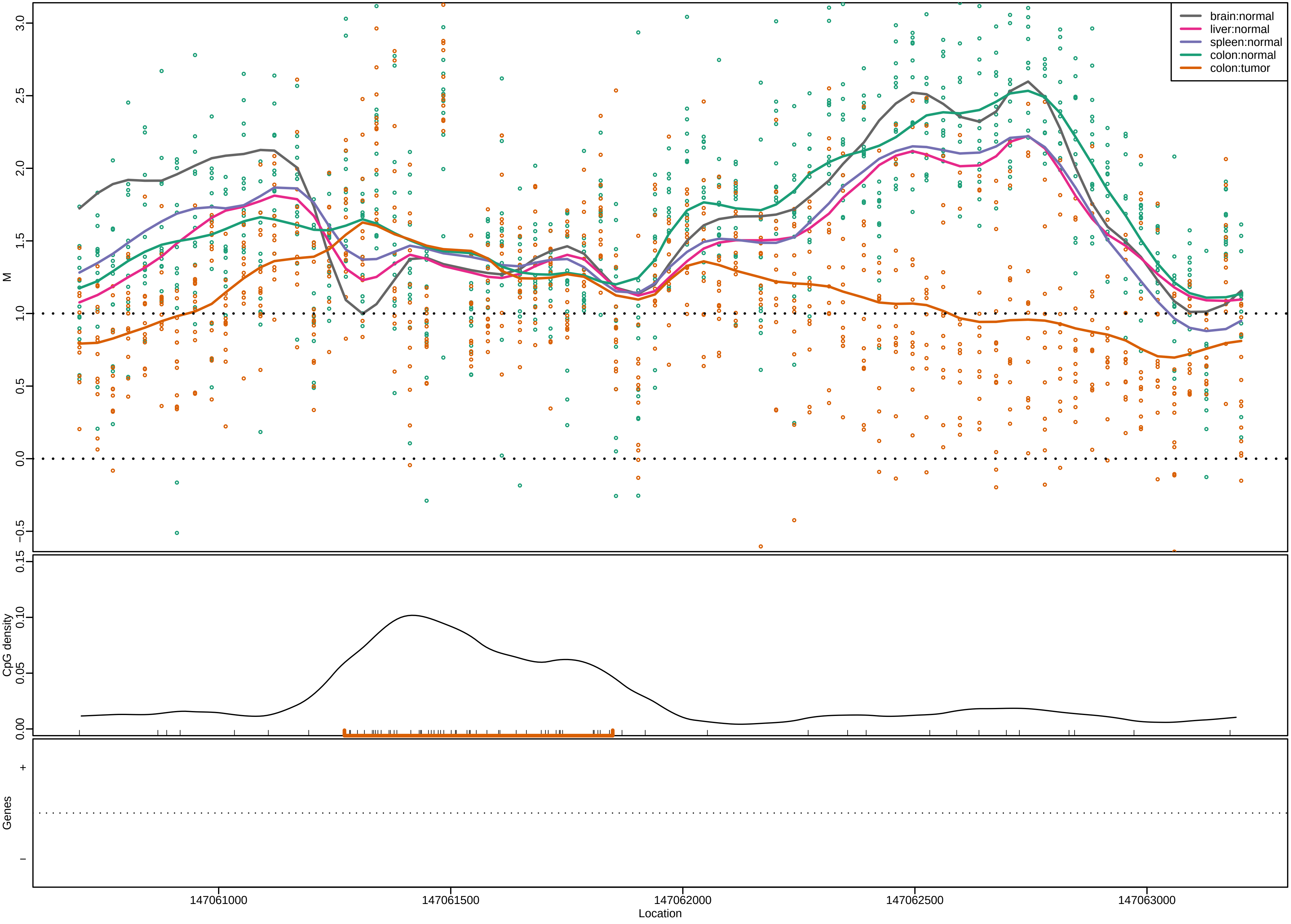

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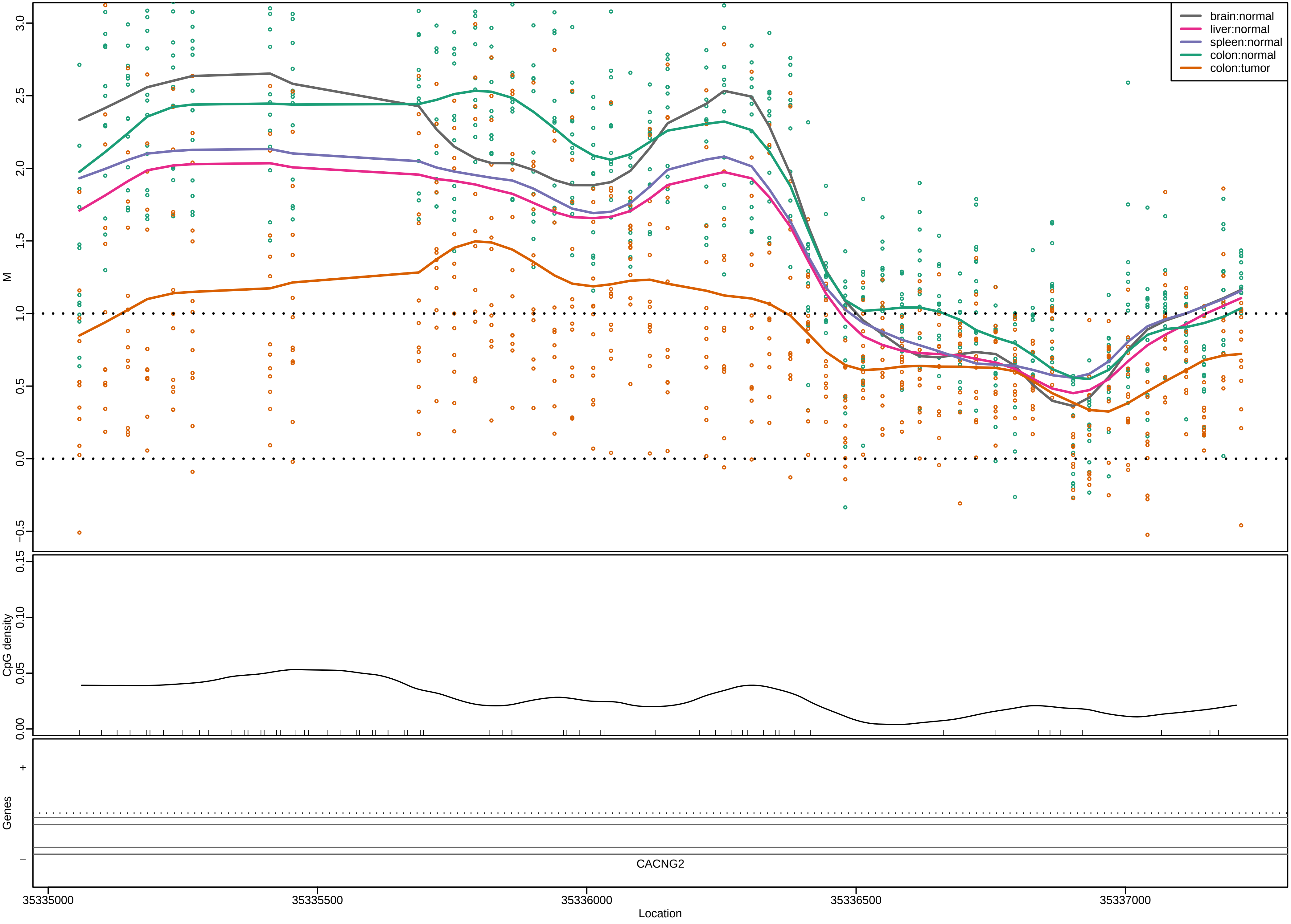

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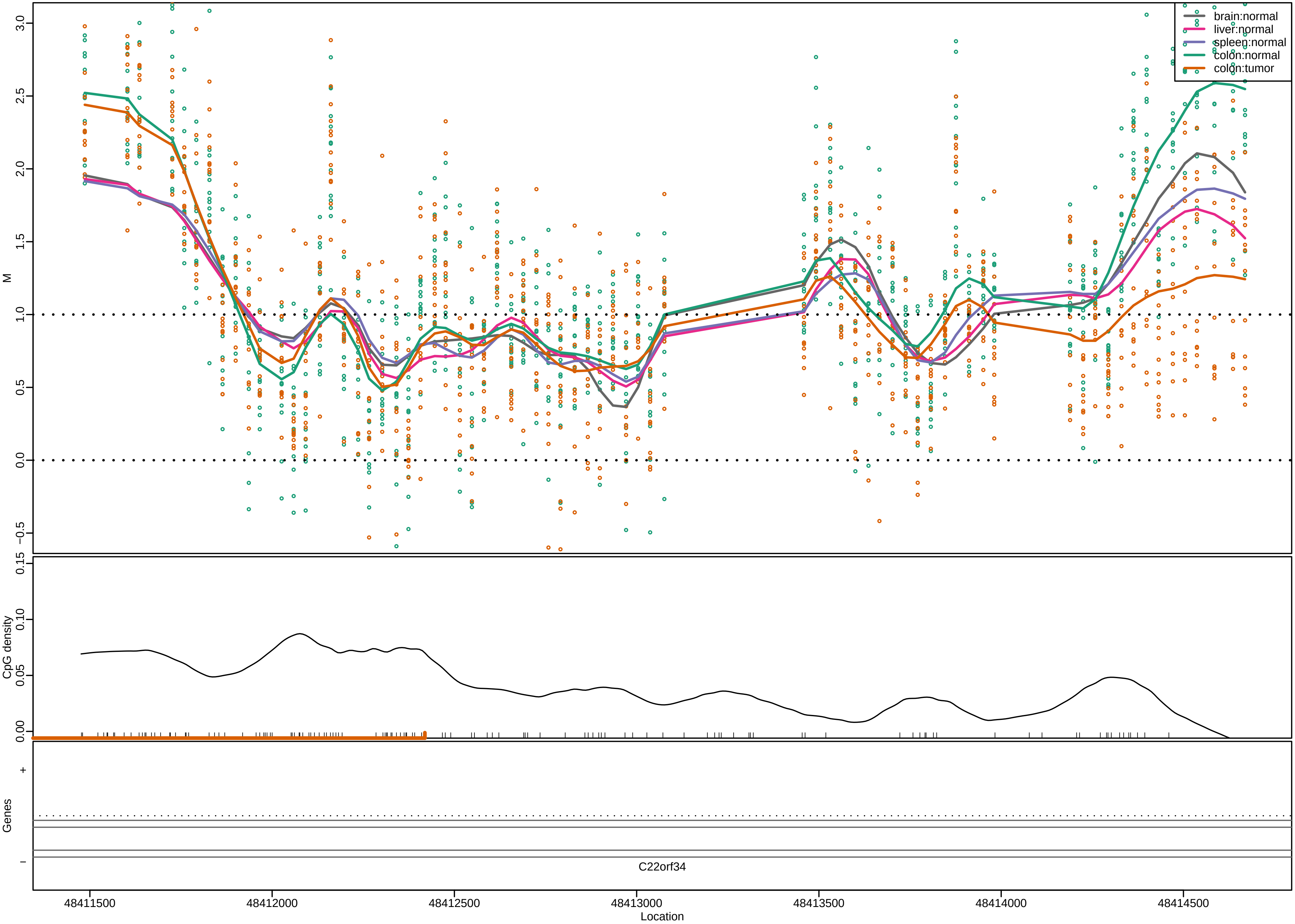

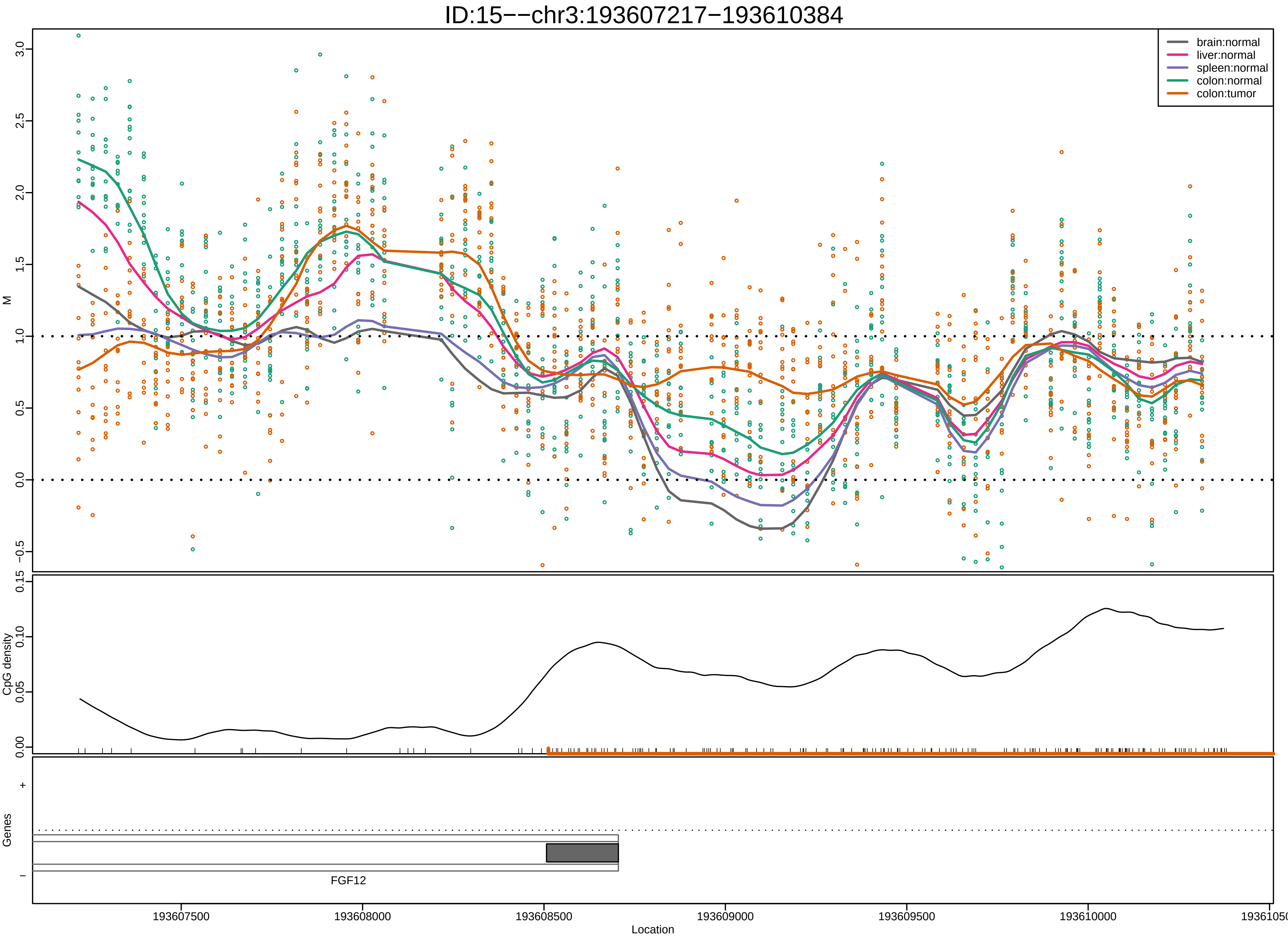
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spleen:normal
colon:normal
colon:tumor
M
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0.0
0.5
1.0
1.5
2.0
2.5
3.0
CpG density
0.00
0.05
0.10
0.15
Genes
+
−
FGF12
193607500
193608000
193608500
193609000
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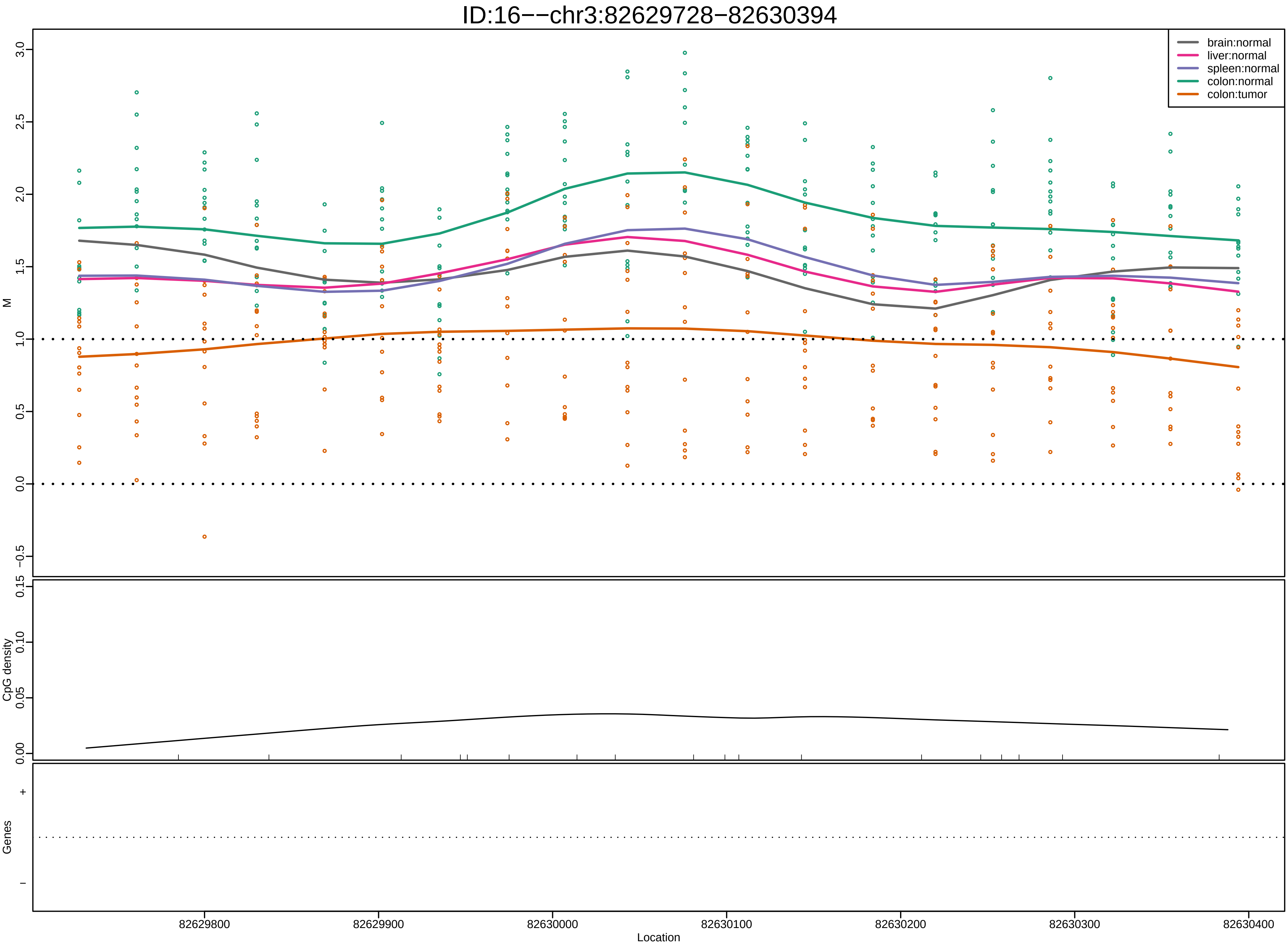
193610000
193610500
Location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liver:normal
spleen:normal
colon:normal
colon:tumor
M
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0.0
0.5
1.0
1.5
2.0
2.5
3.0
CpG density
0.00
0.05
0.10
0.15
Genes
+
−
82629800
82629900
82630000
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82630200
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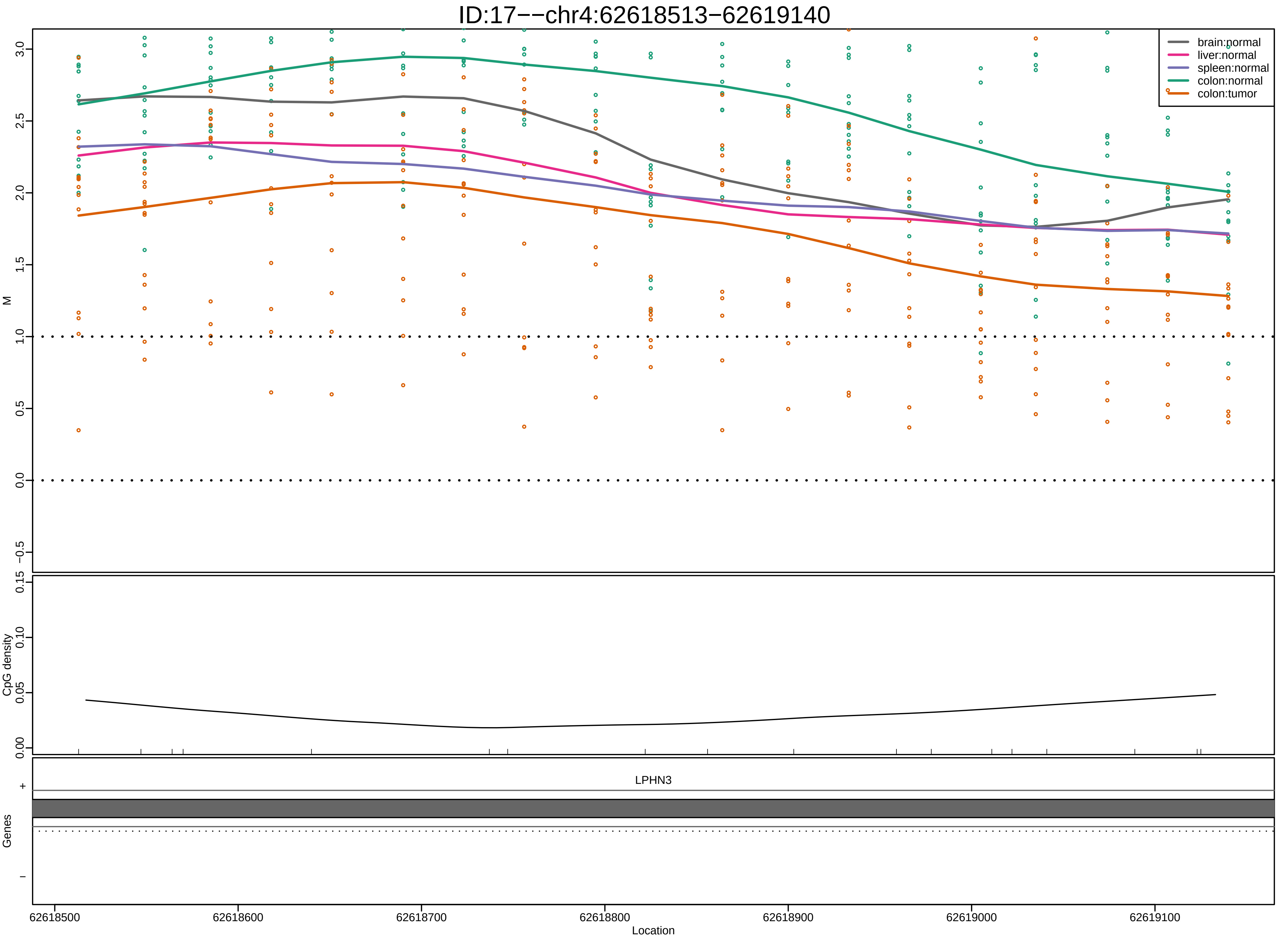
82630400
Location



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2.0
1.5
1.0
0.5
0.0
−0.5
brain:normal
liver:normal
spleen:normal
colon:normal
colon:tumor
CpG density
0.15
0.10
0.05
0.00
Genes
+
LPHN3
−
62618500
62618600
62618700
62618800
62618900
62619000
62619100
Location

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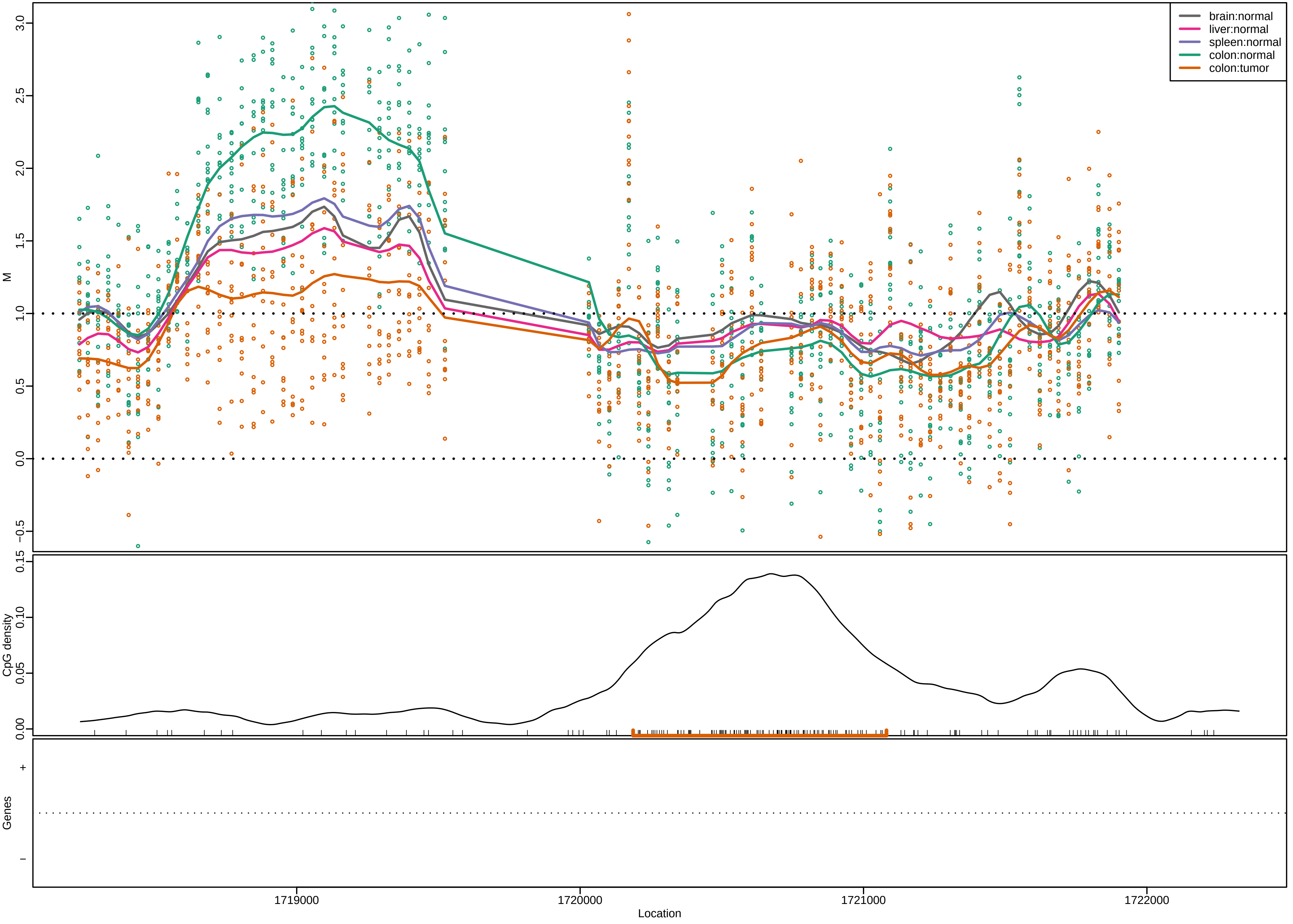

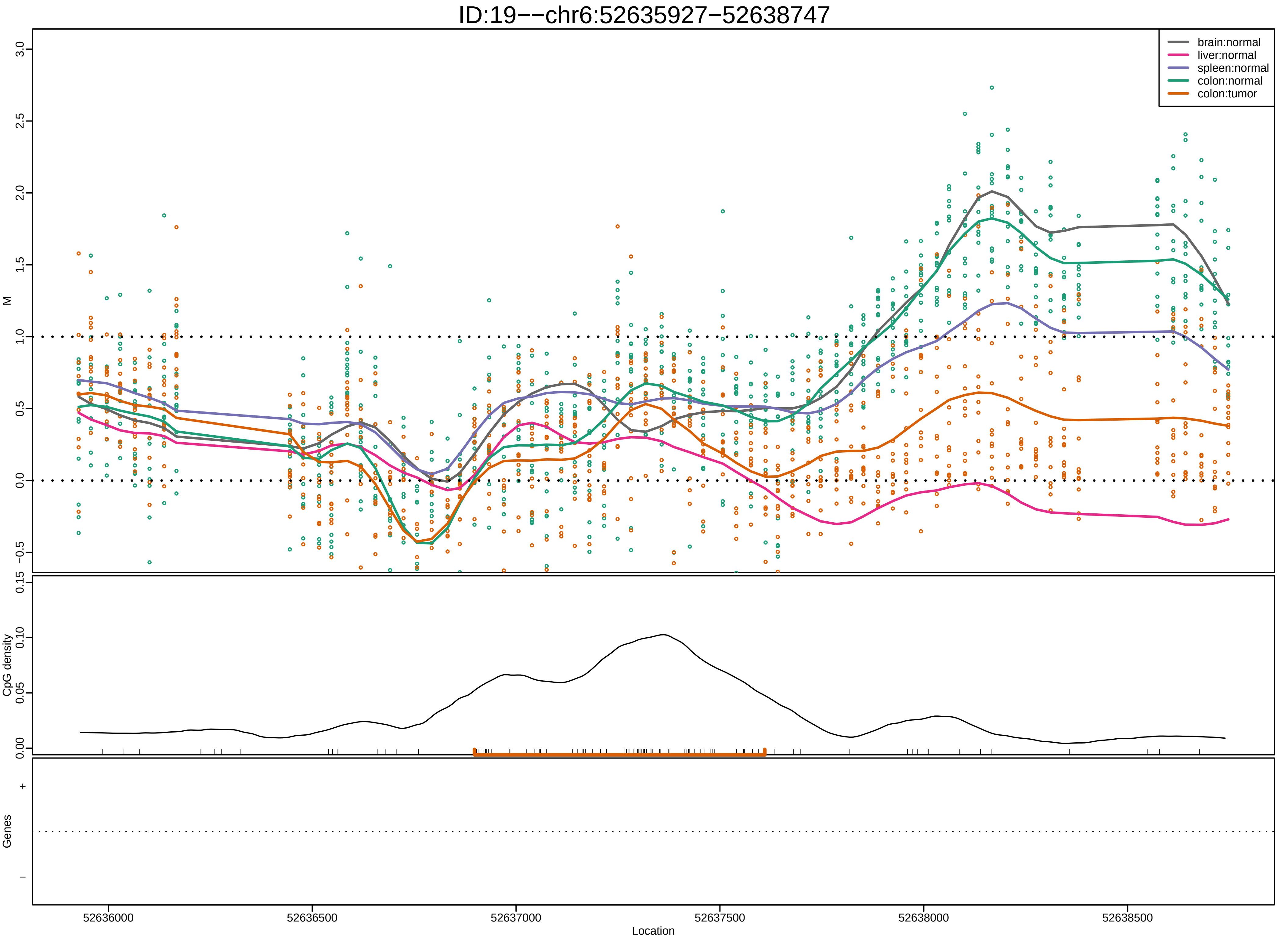
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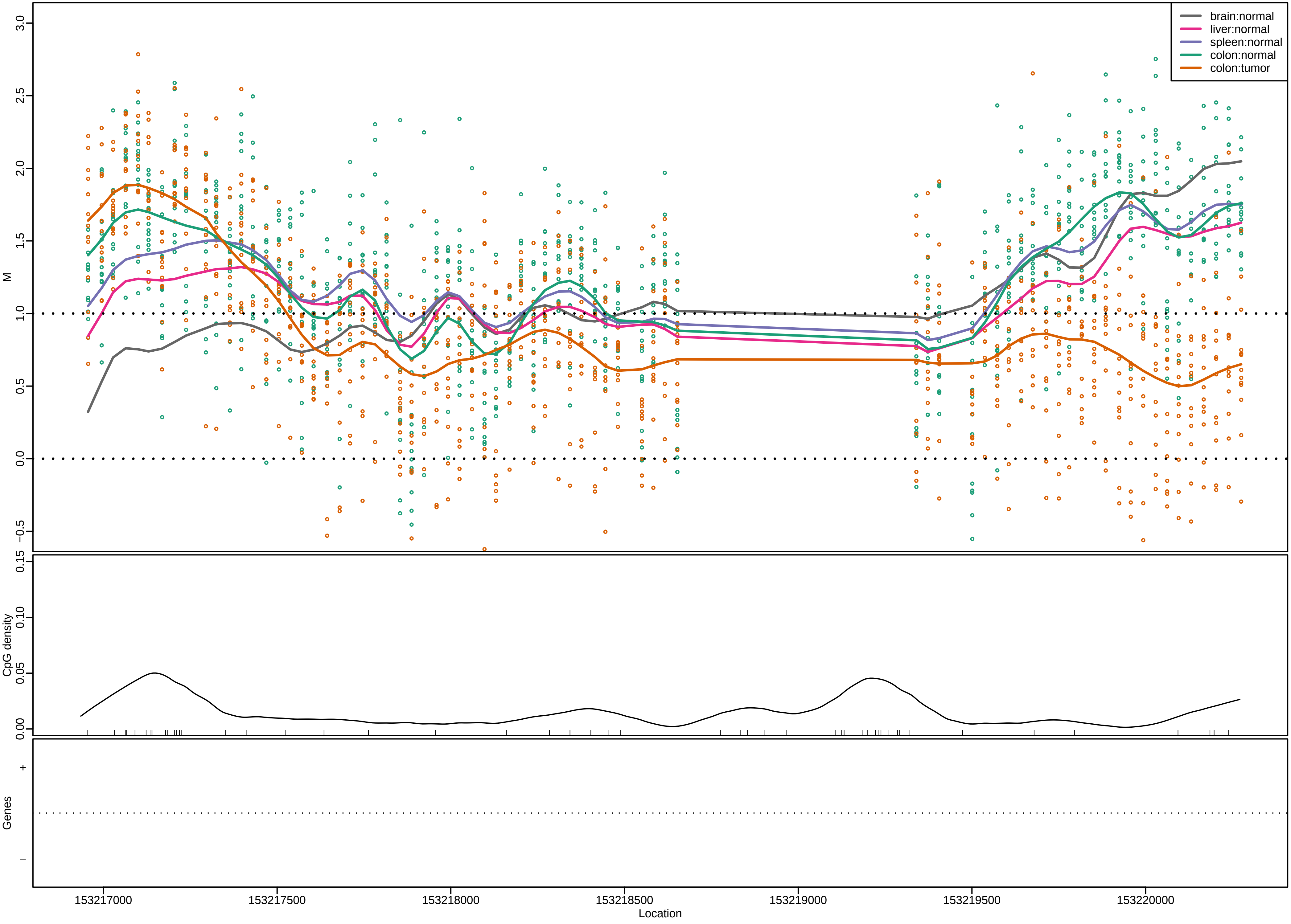
liver:normal
spleen:normal
colon:normal
colon:tumor
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
52636000
52636500
52637000
52637500
52638000
52638500
Location



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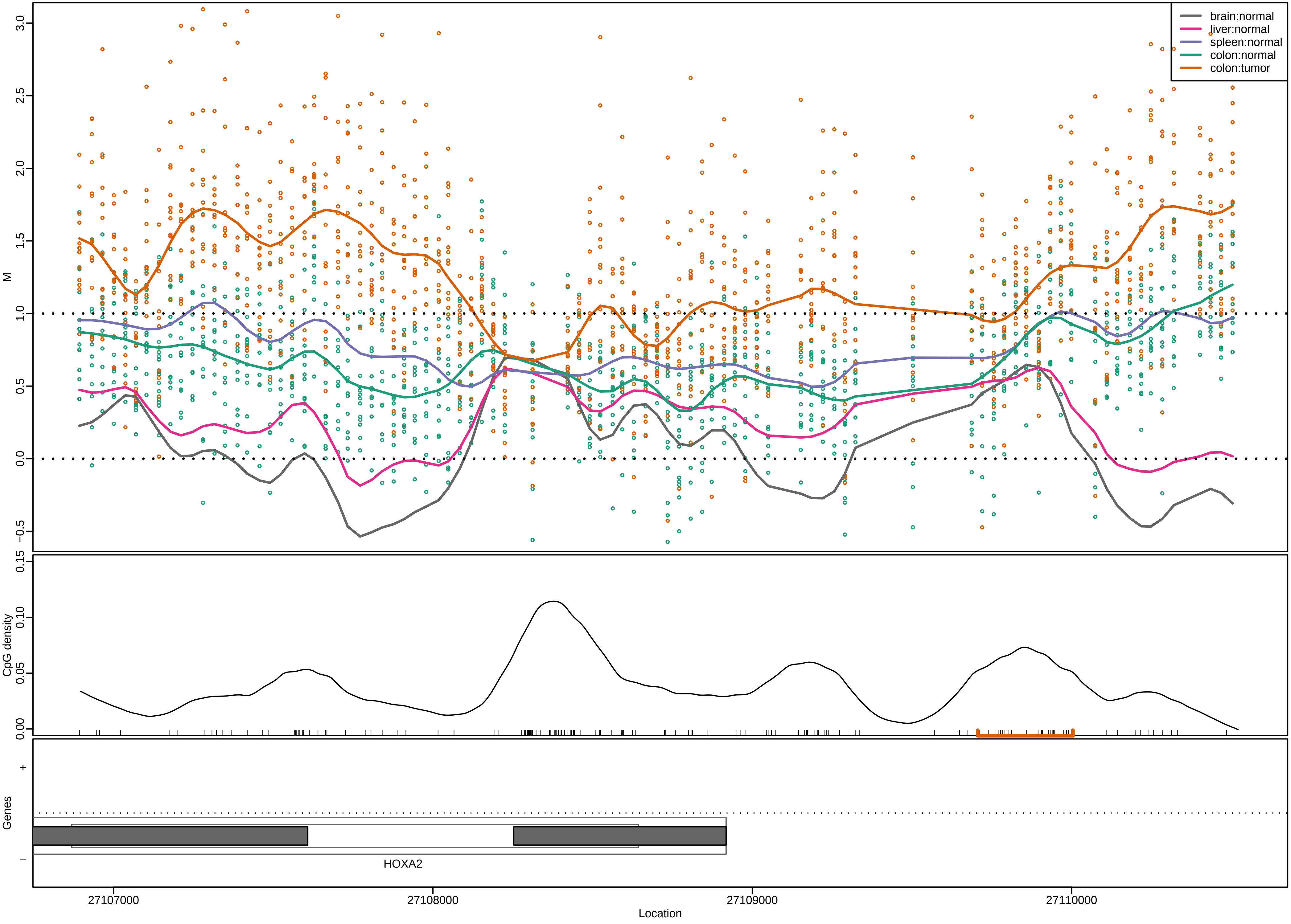

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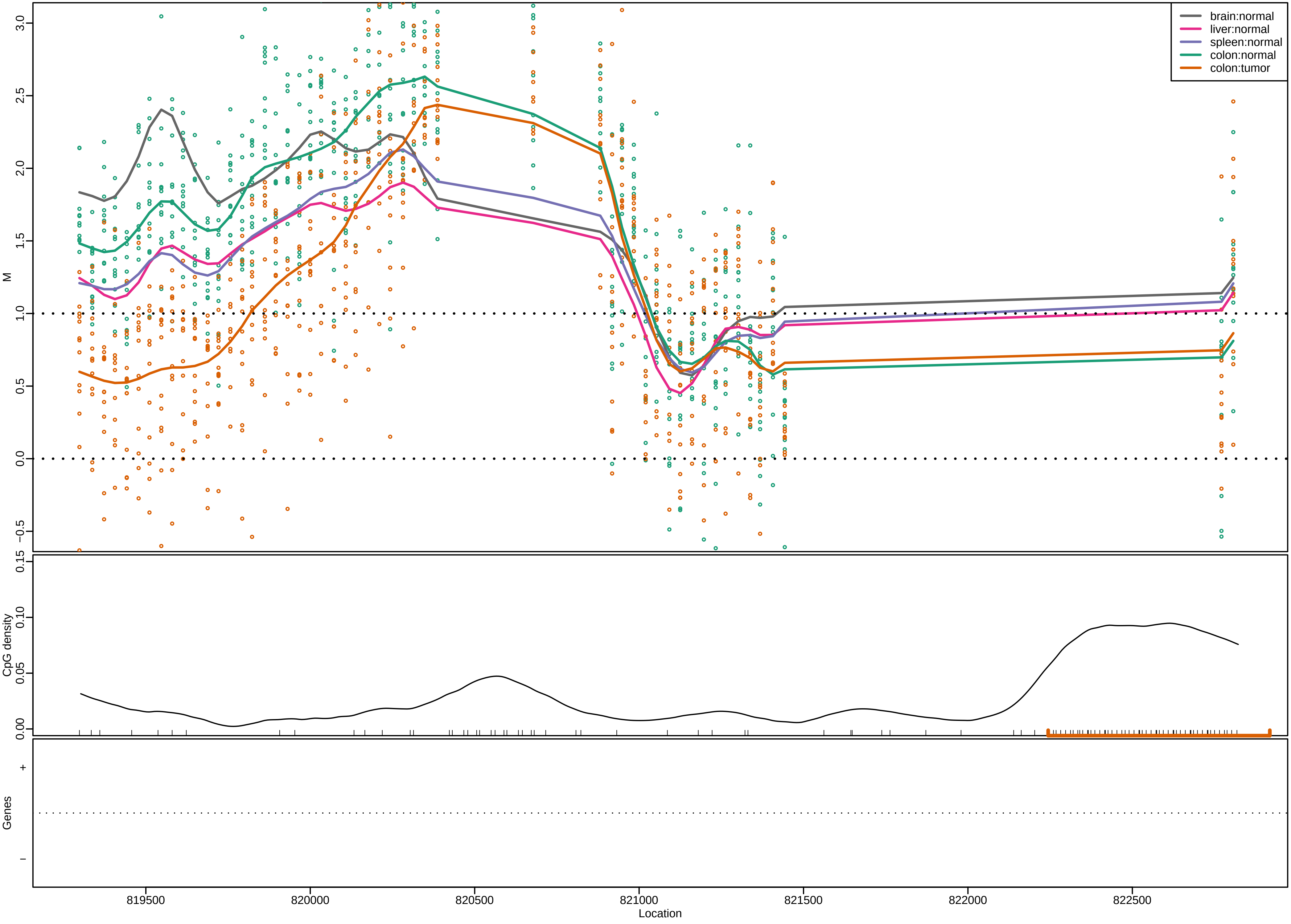

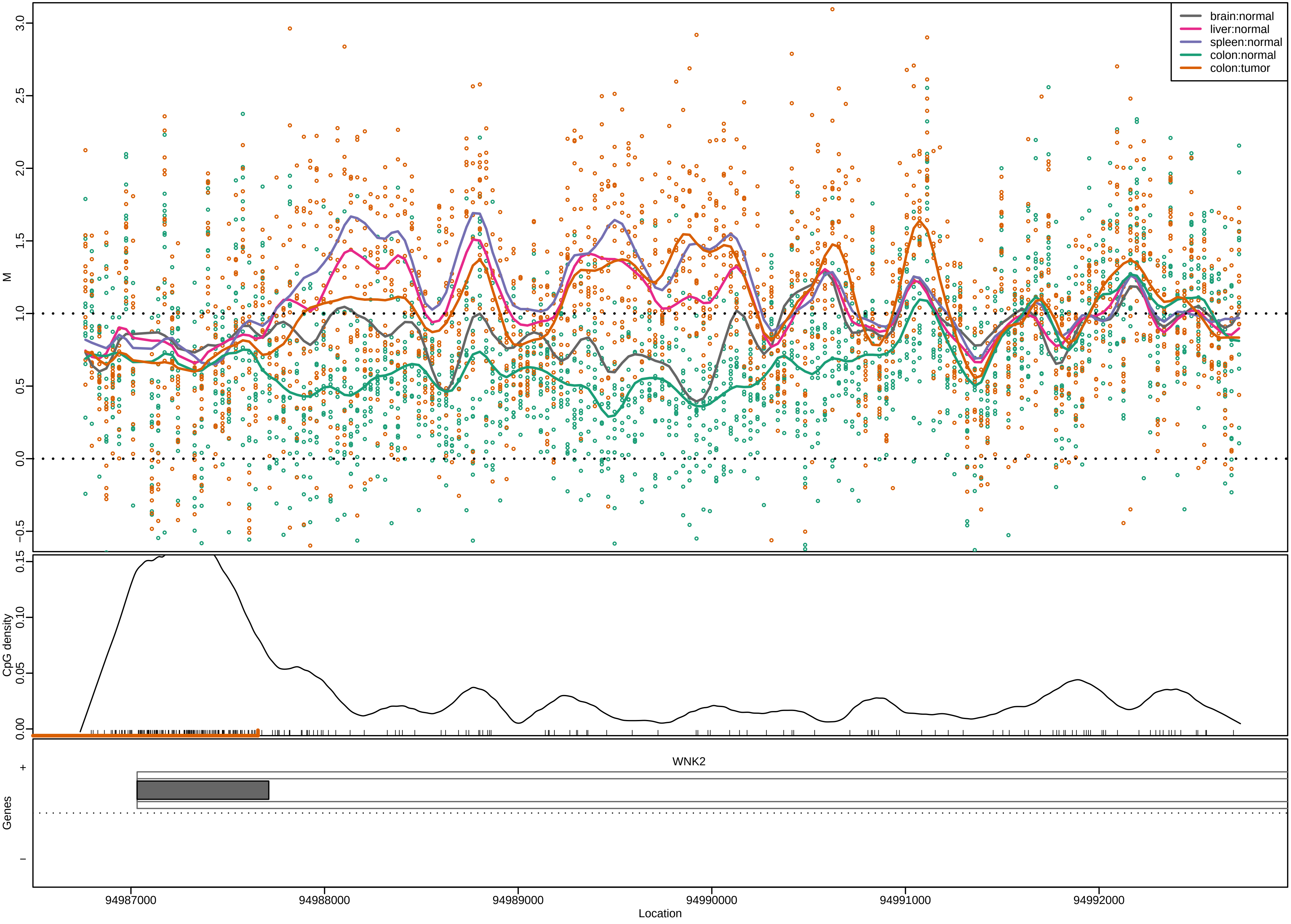
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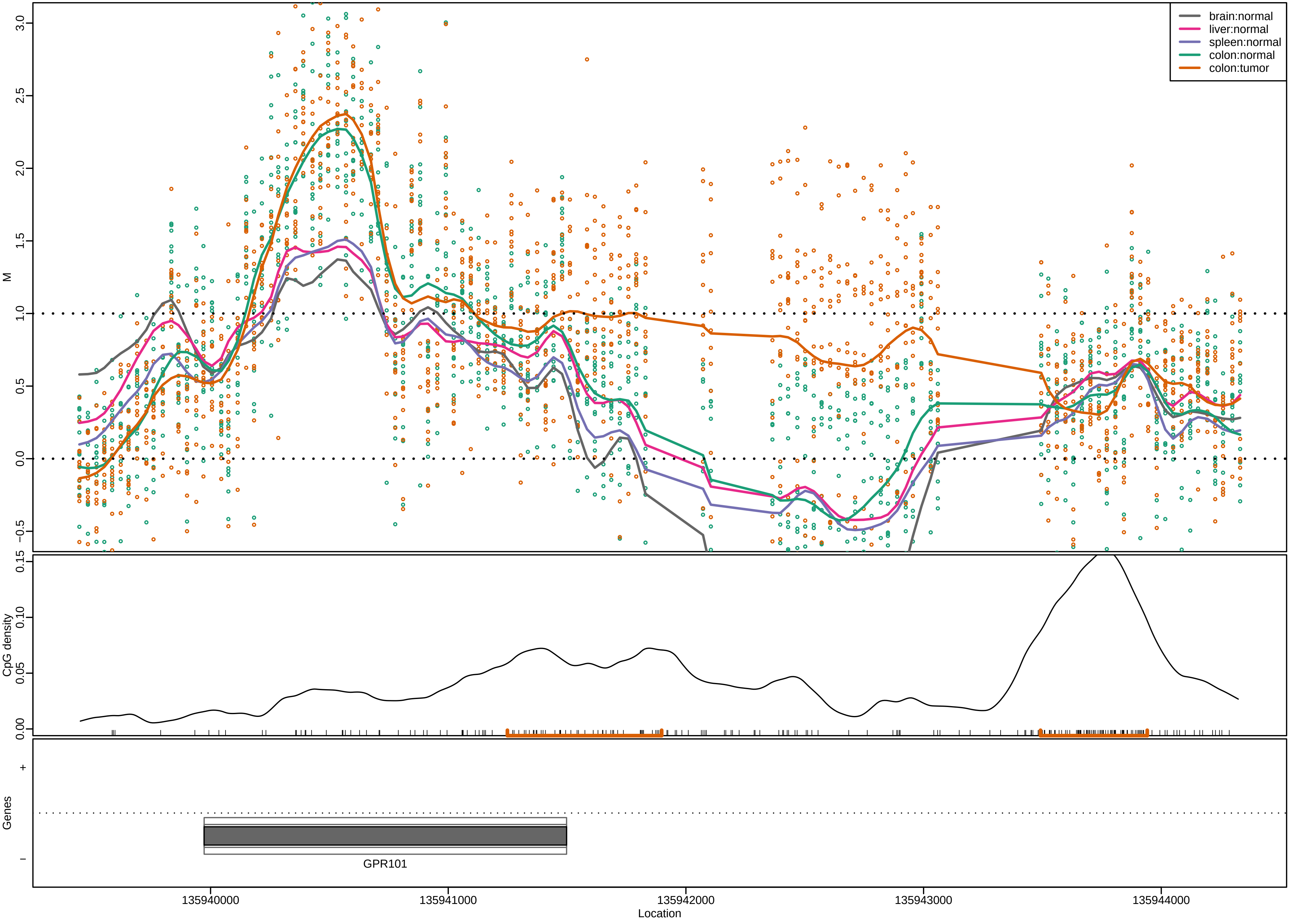

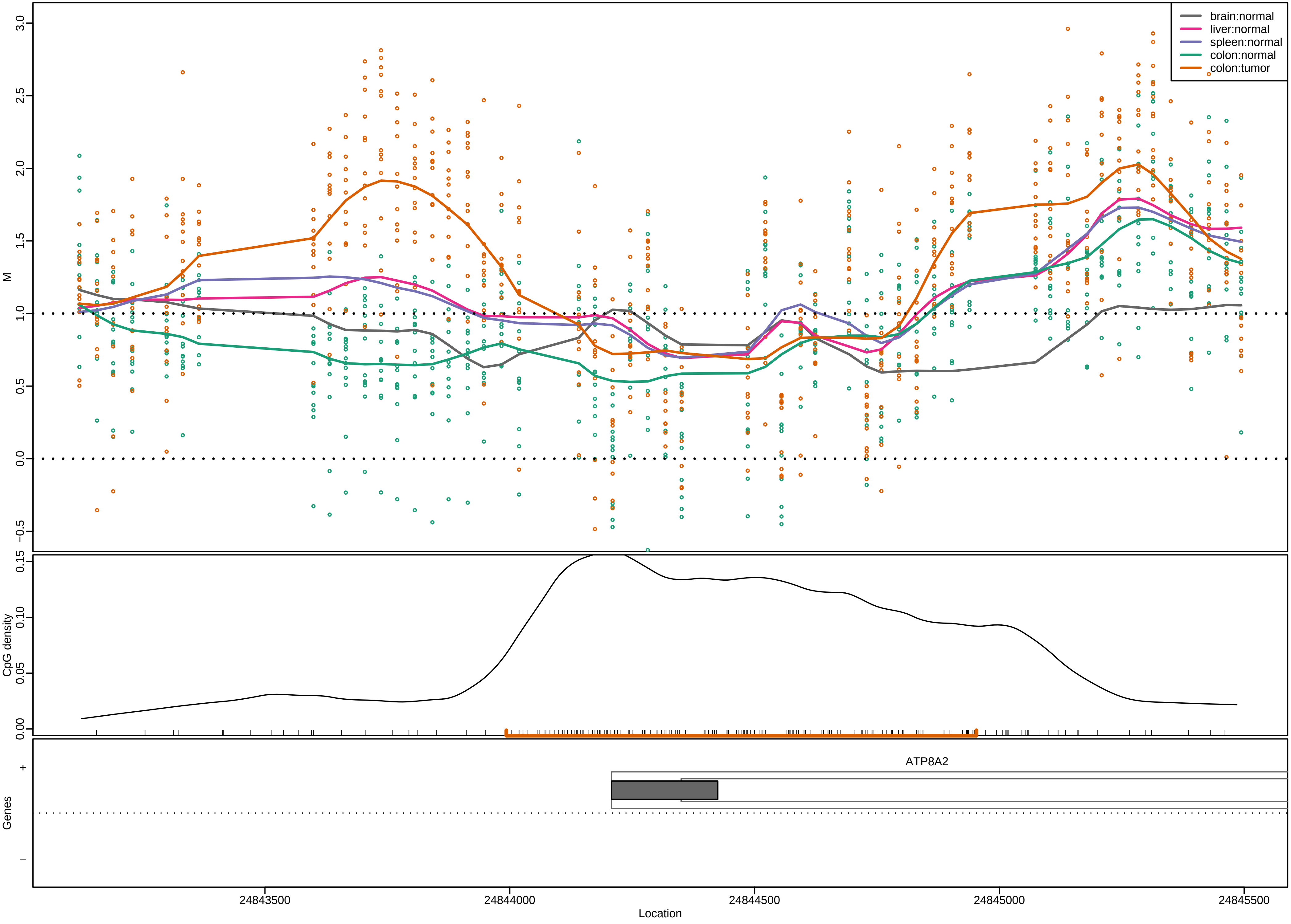

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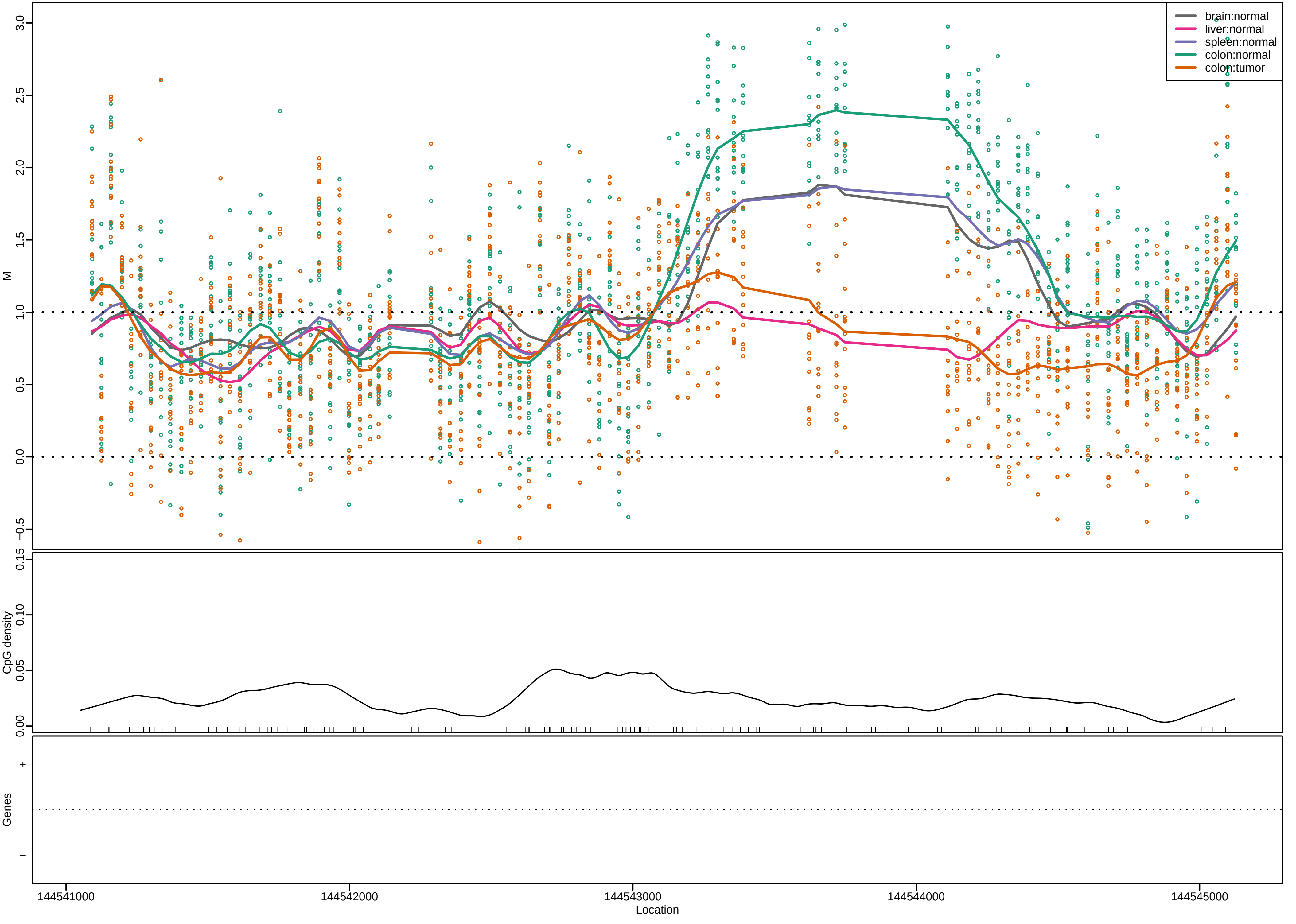

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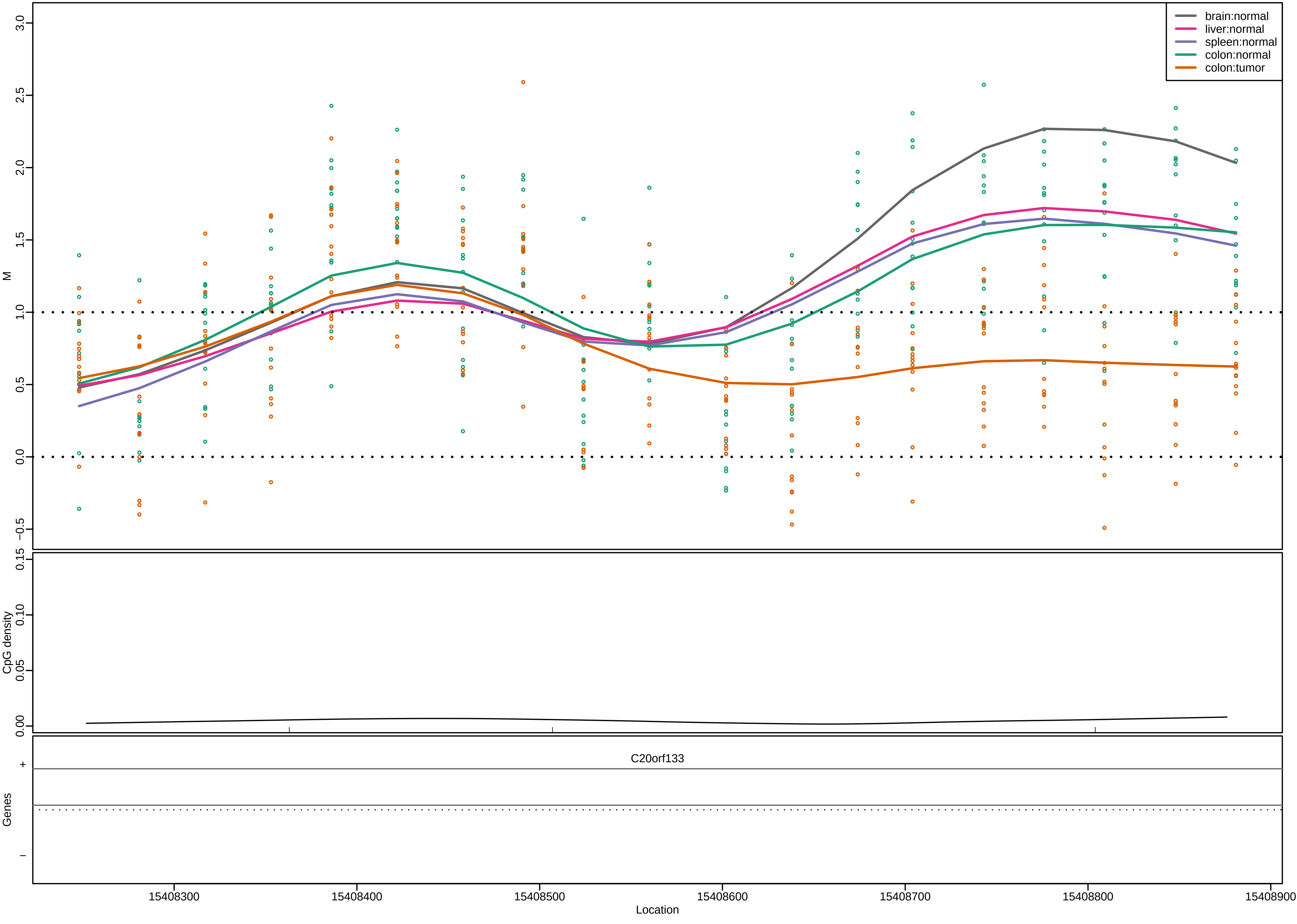

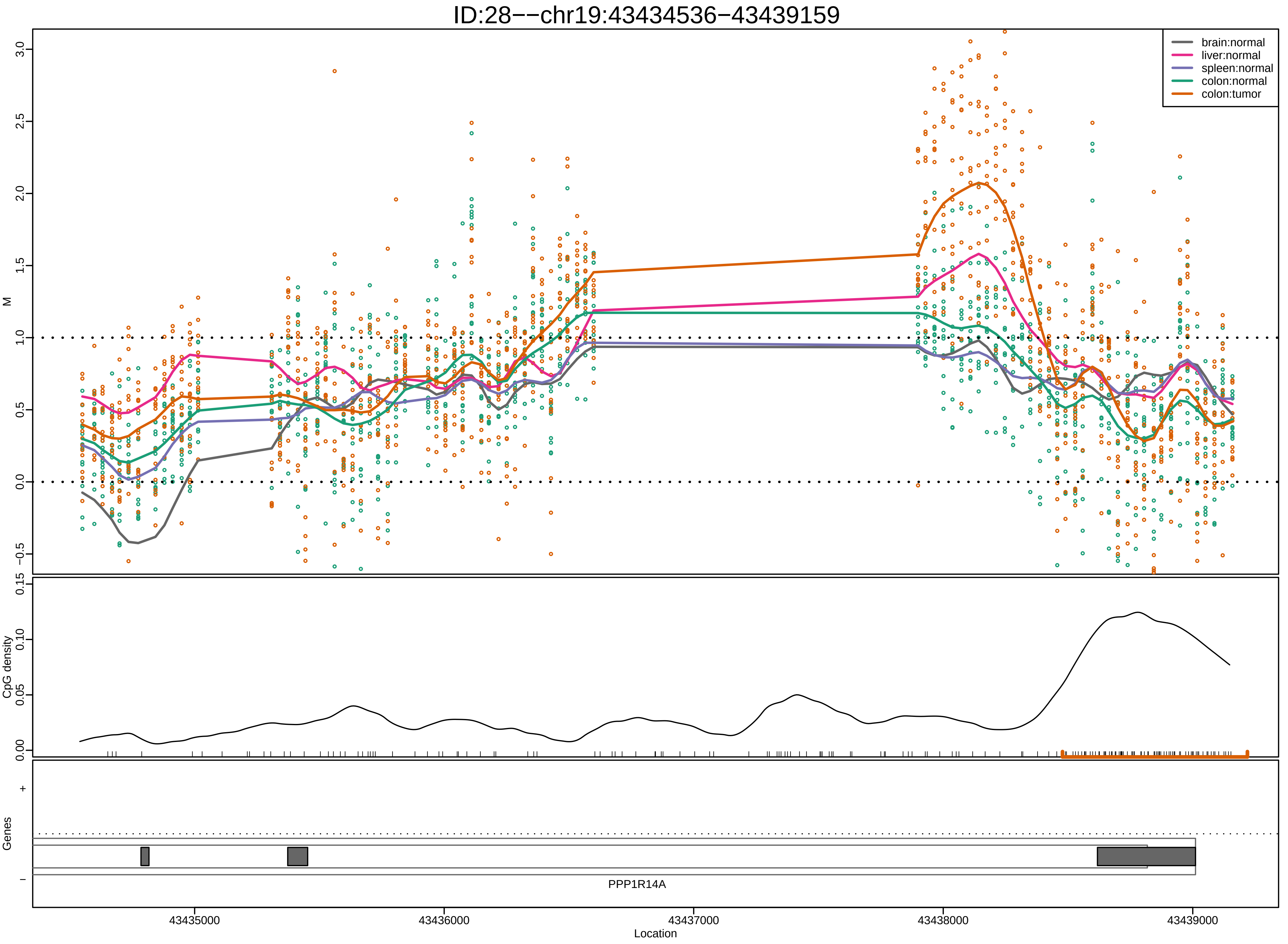
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liver:normal
spleen:normal
colon:normal
colon:tumor
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
PPP1R14A
43435000
43436000
43437000
43438000
43439000
Location

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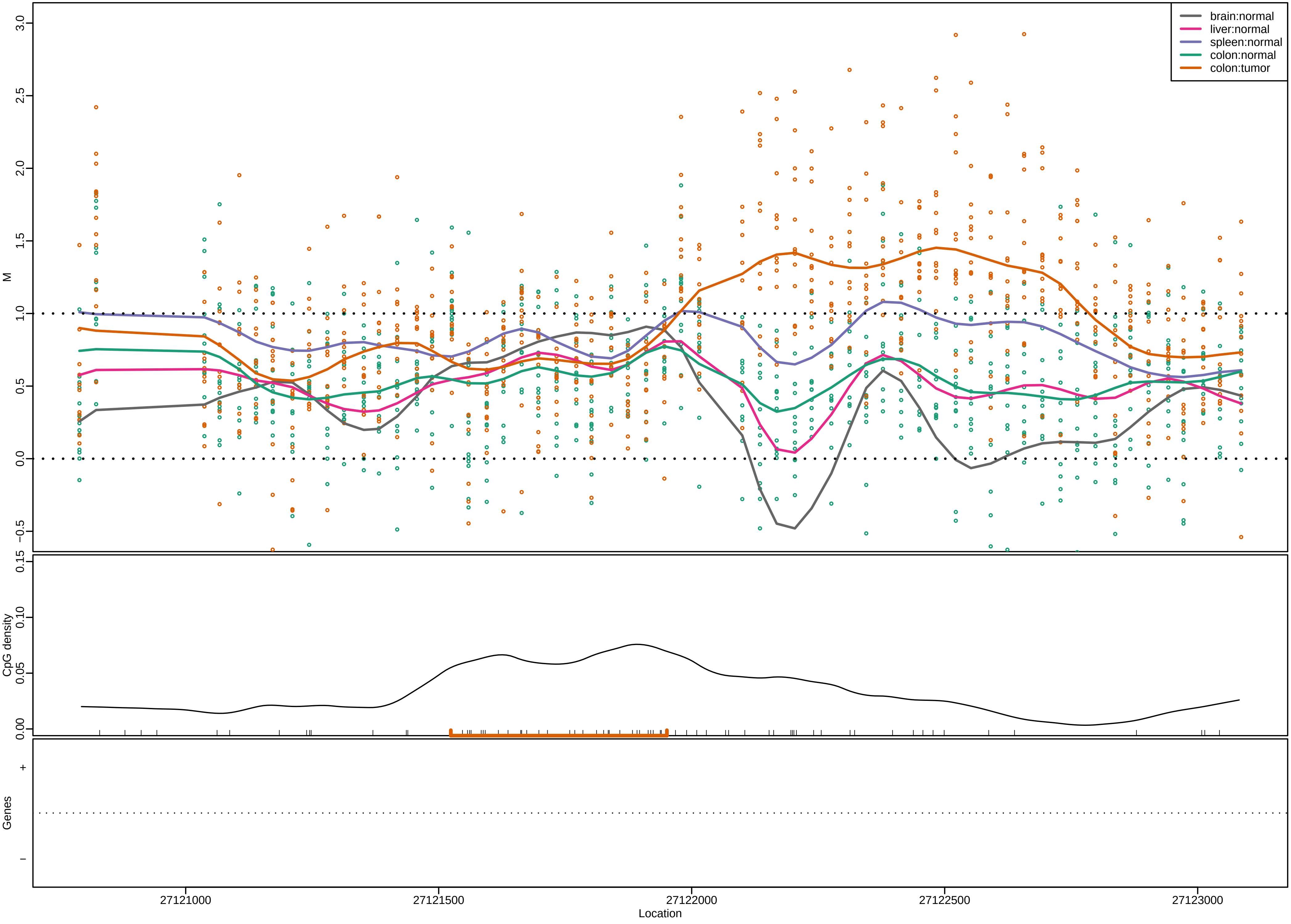

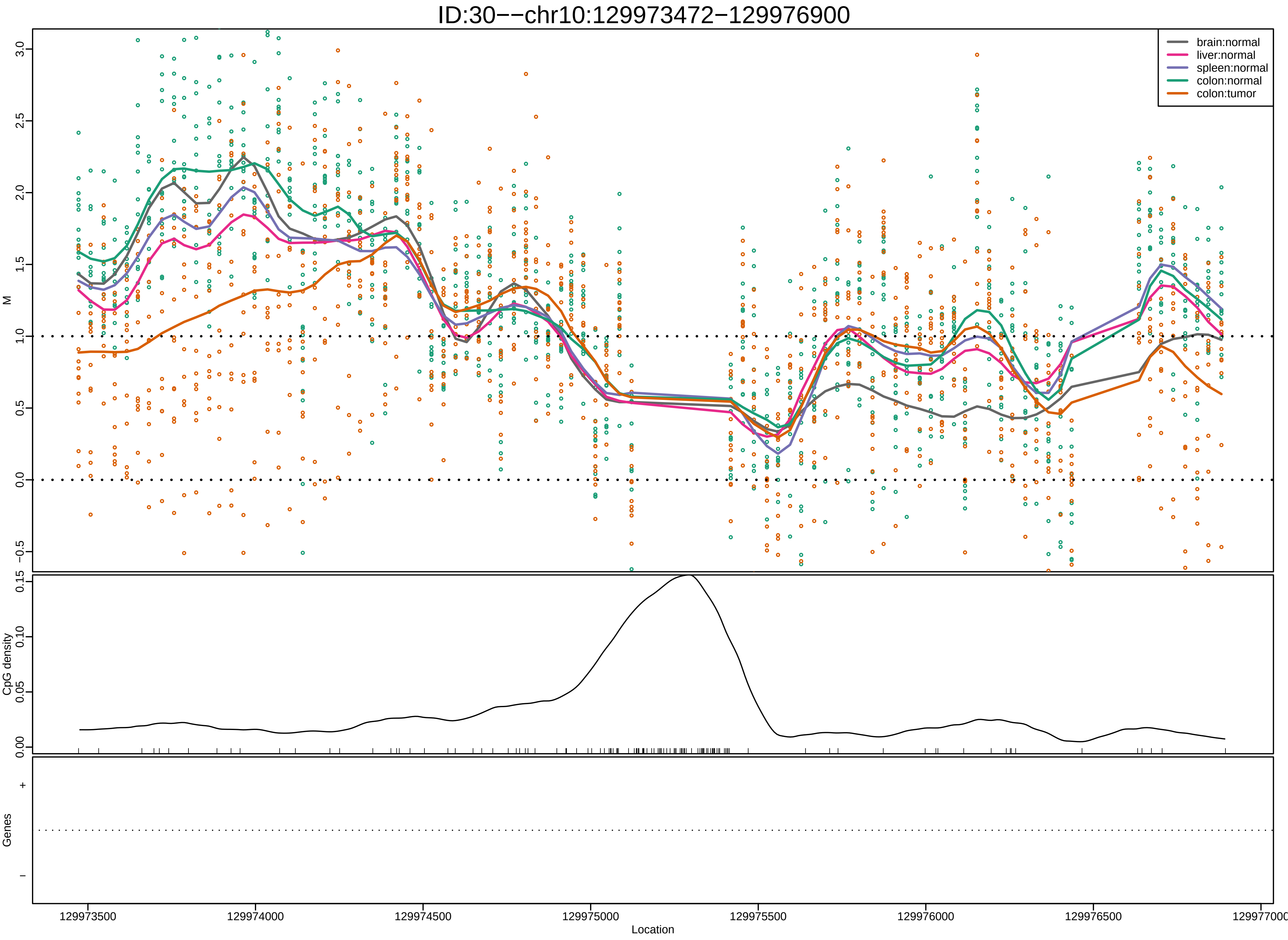
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liver:normal
spleen:normal
colon:normal
colon:tumor
M
−0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CpG density
0.00
0.05
0.10
0.15
Genes
+
−
129973500
129974000
129974500
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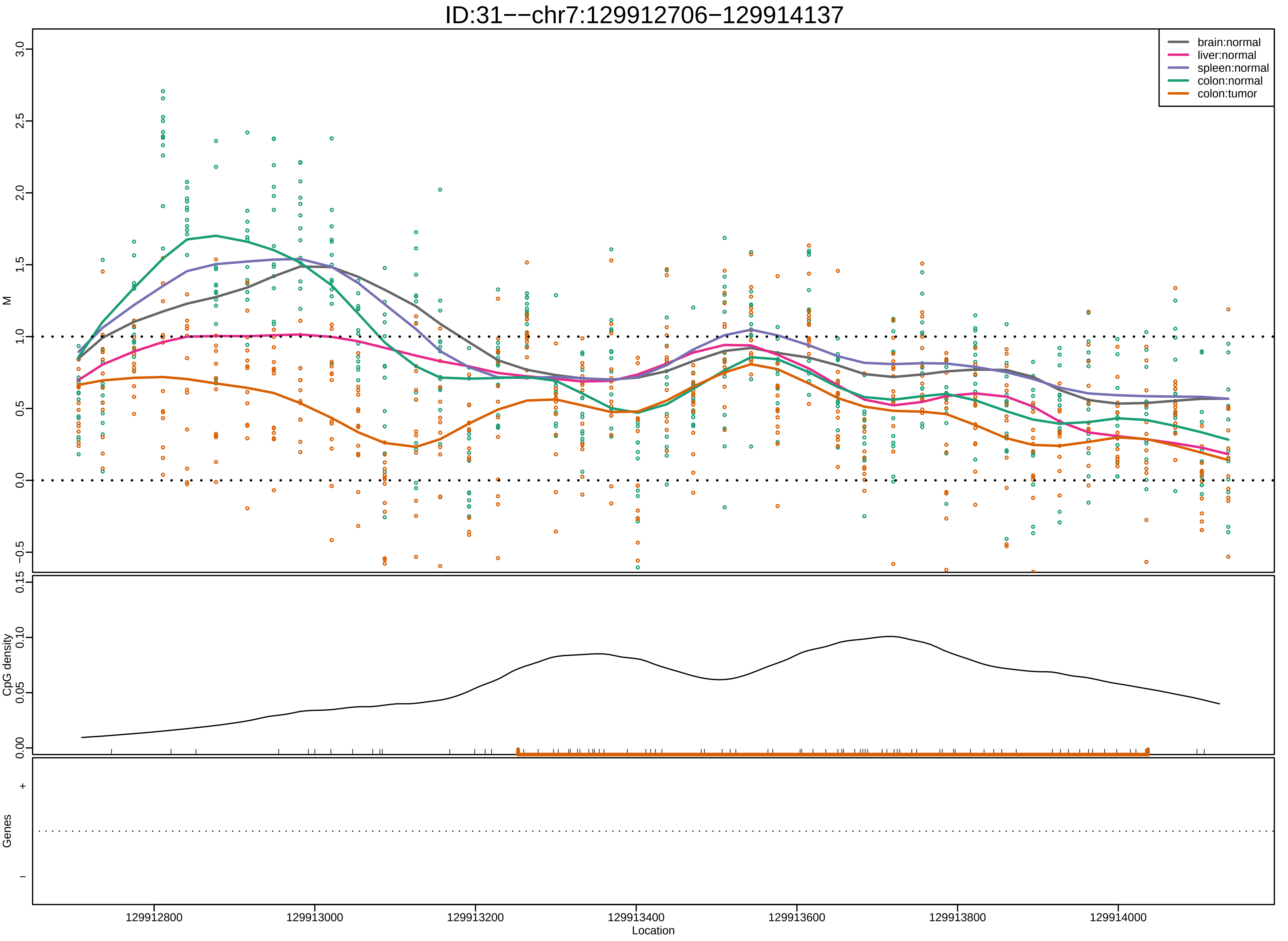
Location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liver:normal
spleen:normal
colon:normal
colon:tumor
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
129912800
129913000
129913200
129913400
129913600
129913800
129914000
Location

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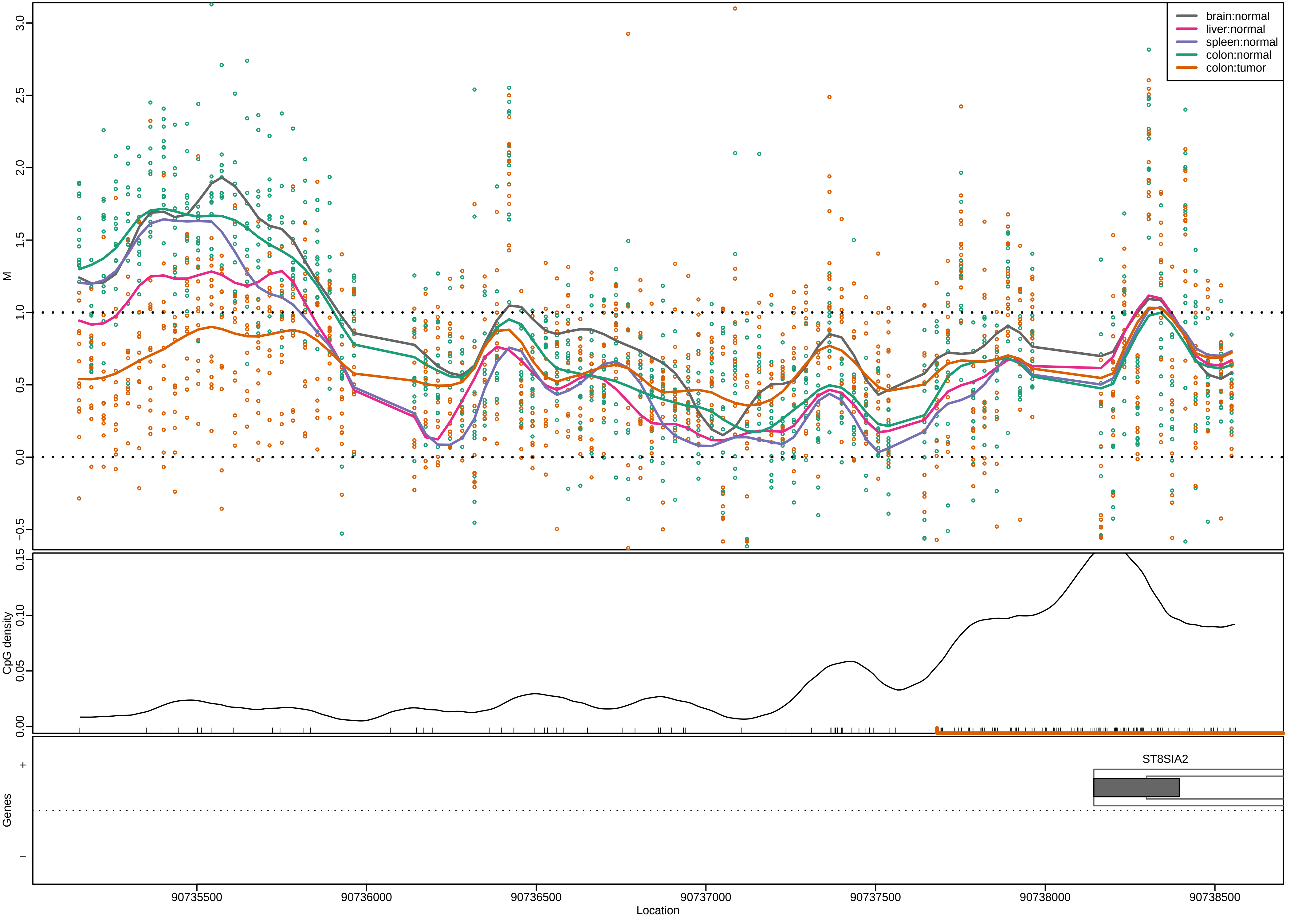

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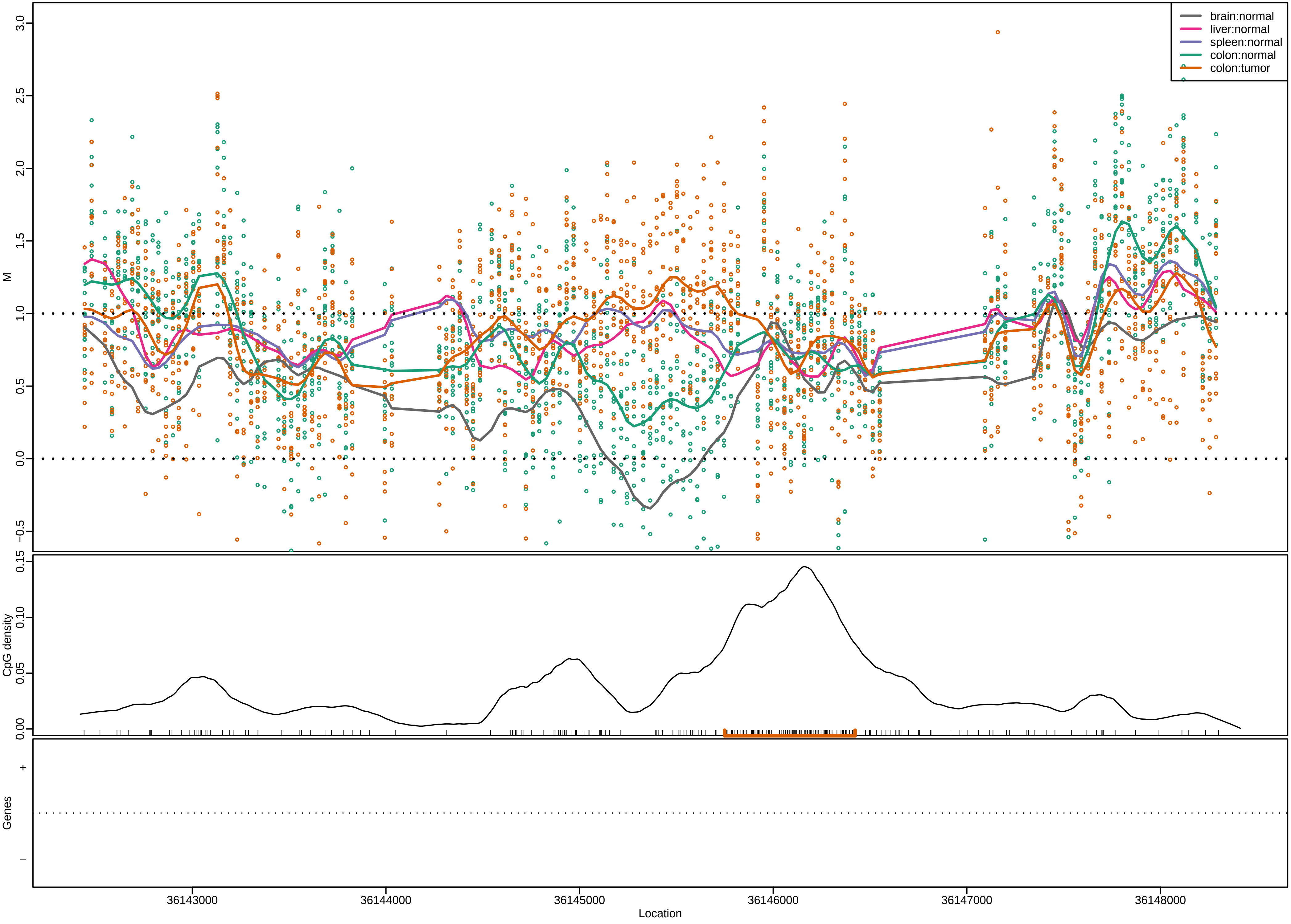

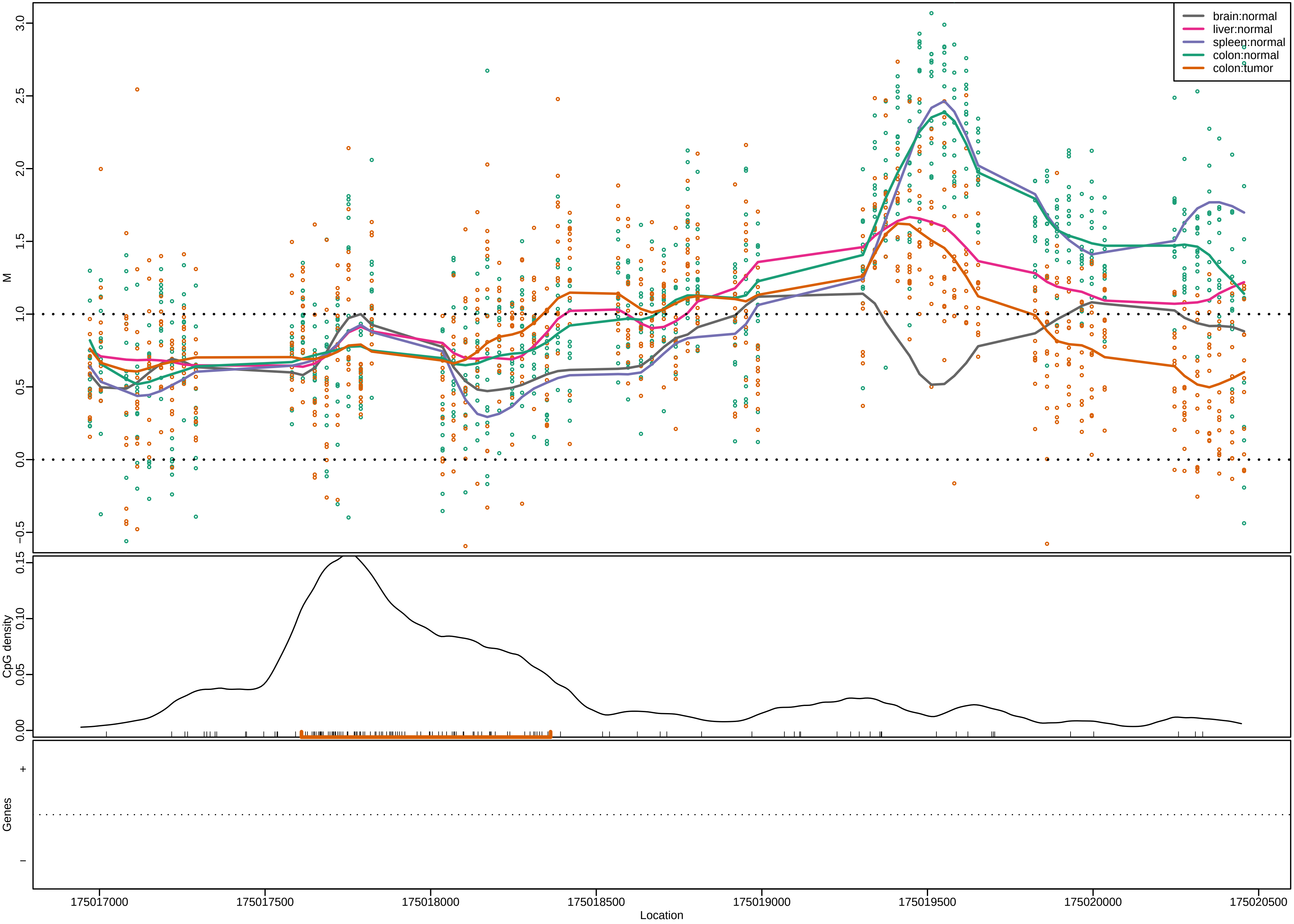
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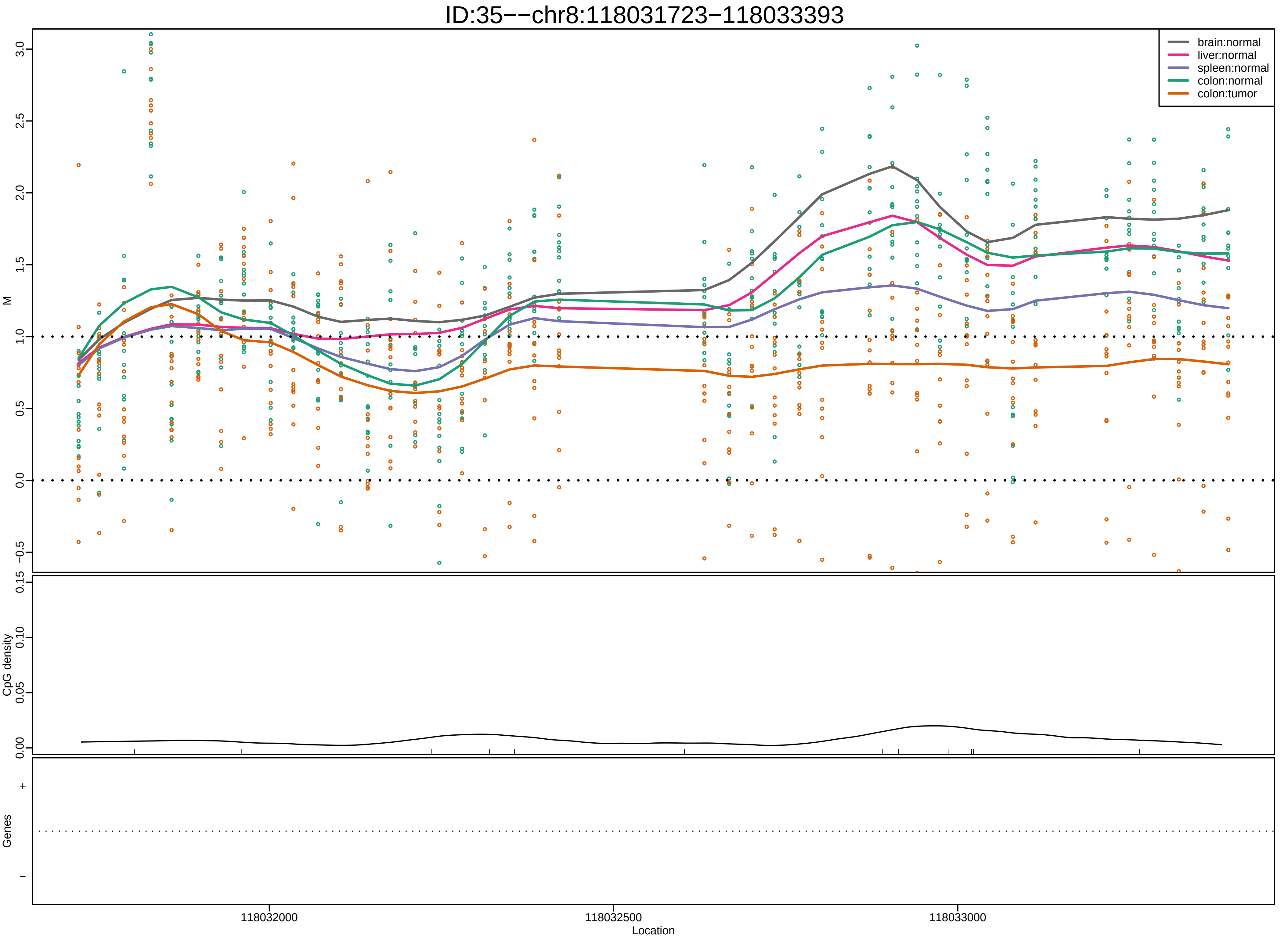
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M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
brain:normal
liver:normal
spleen:normal
colon:normal
colon:tumor
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
118032000
118032500
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Location

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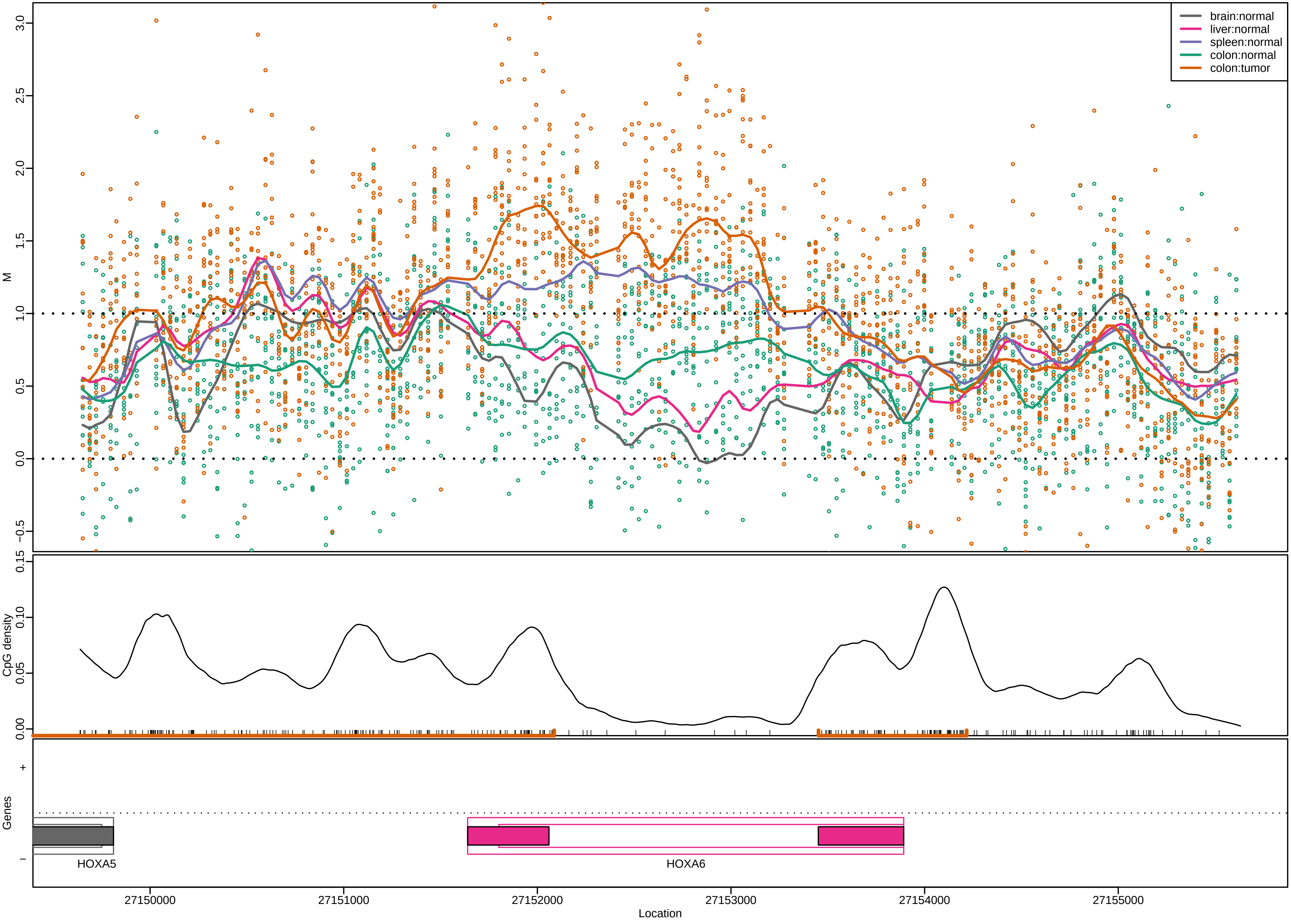

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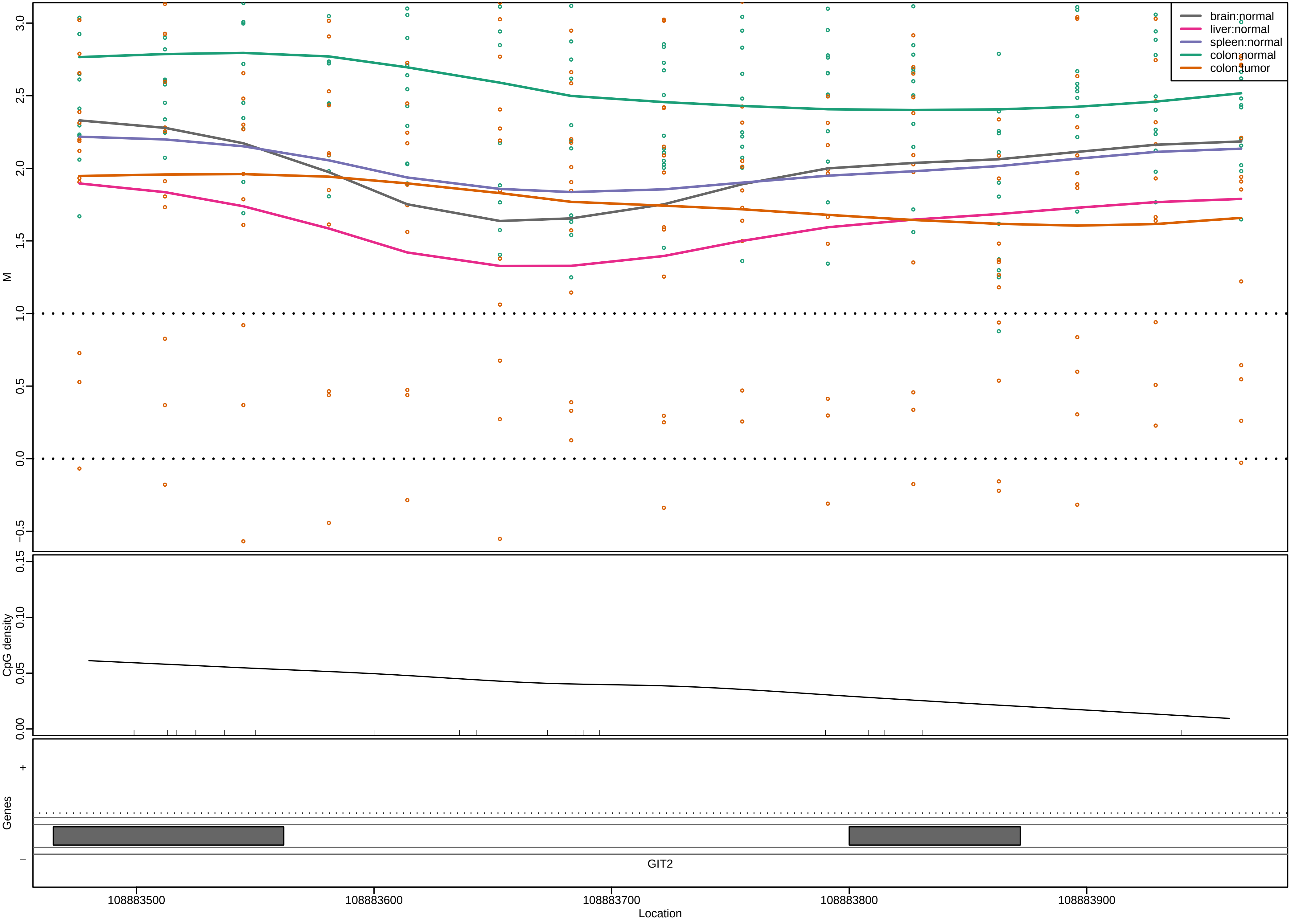

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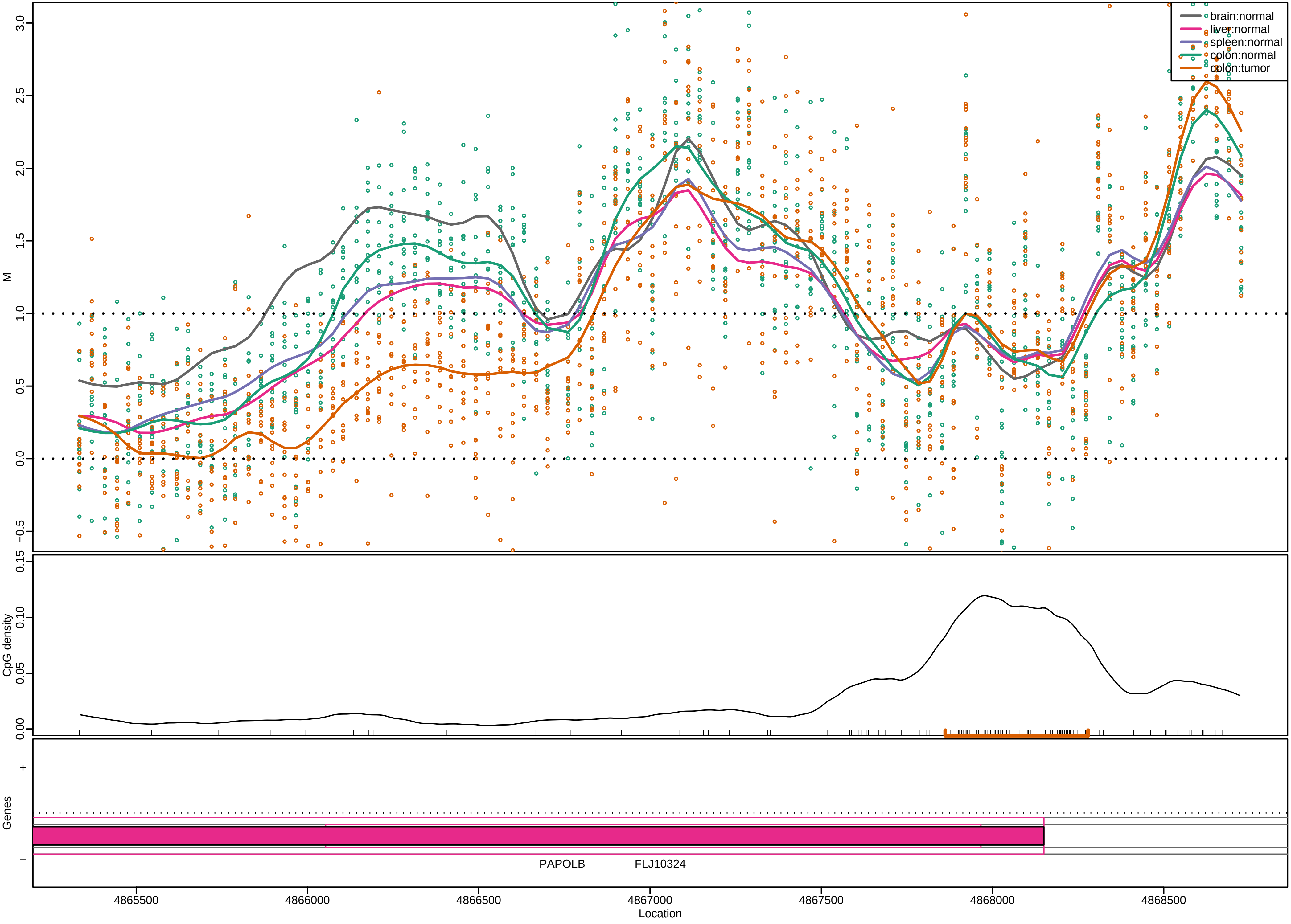

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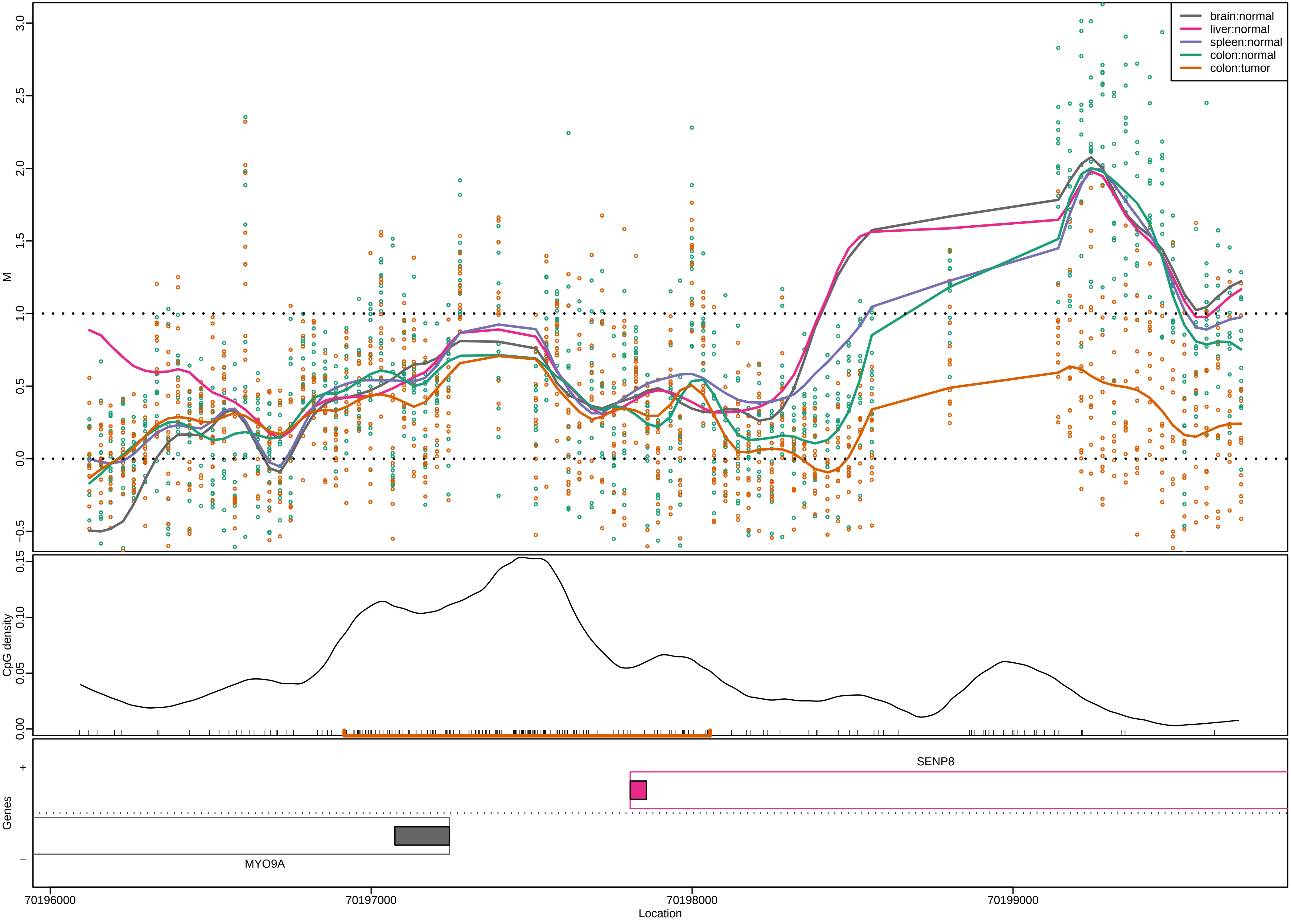

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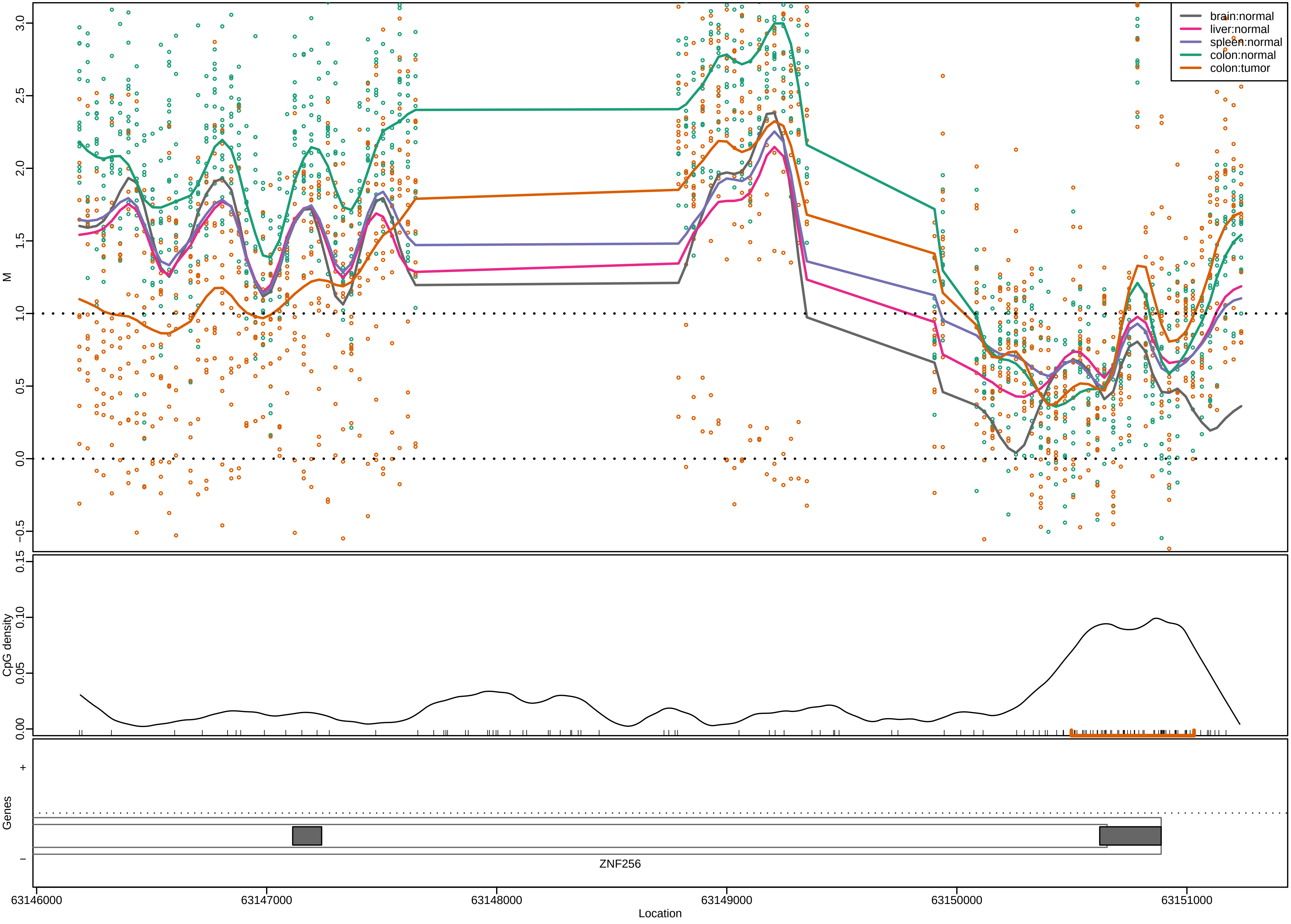

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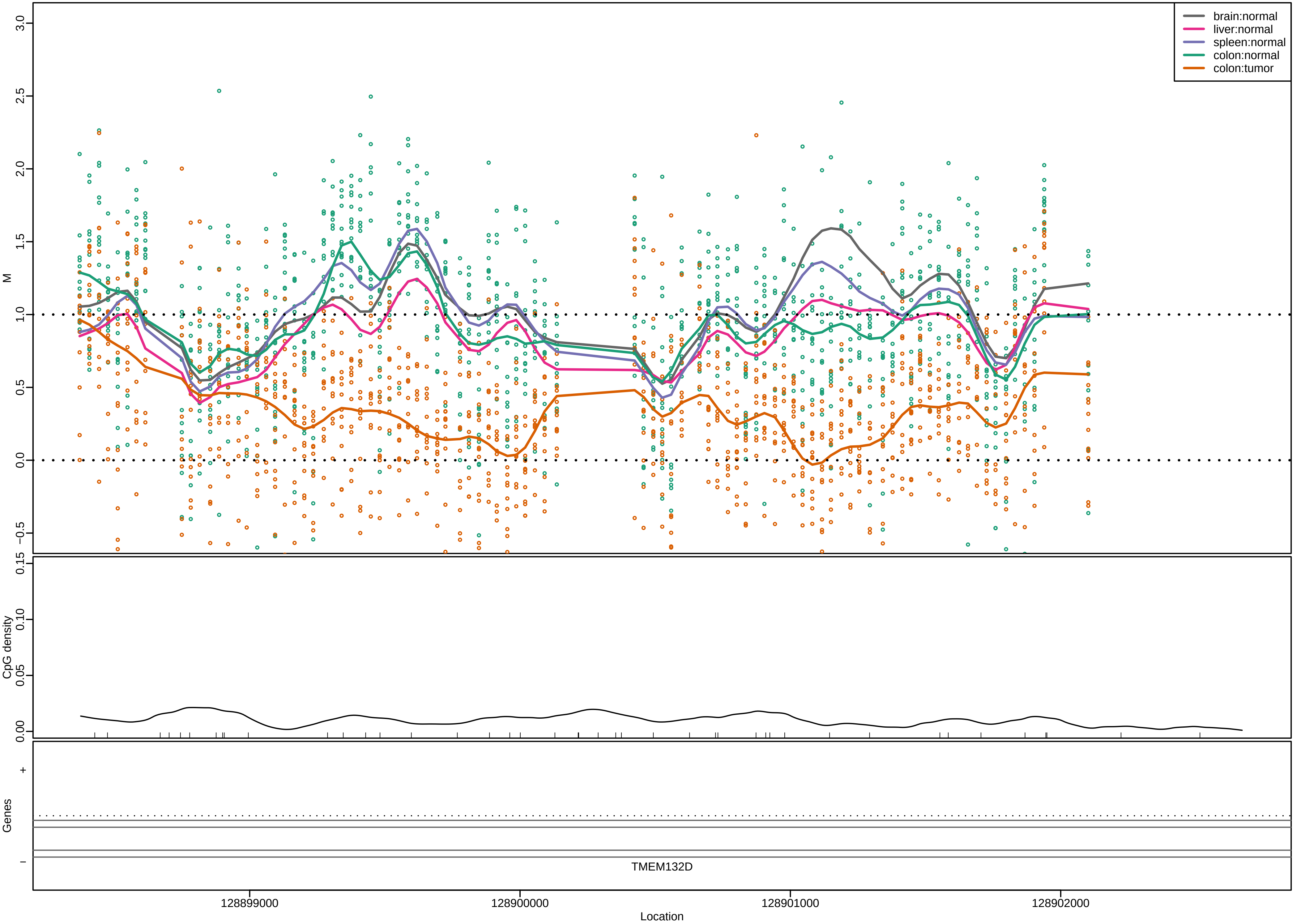

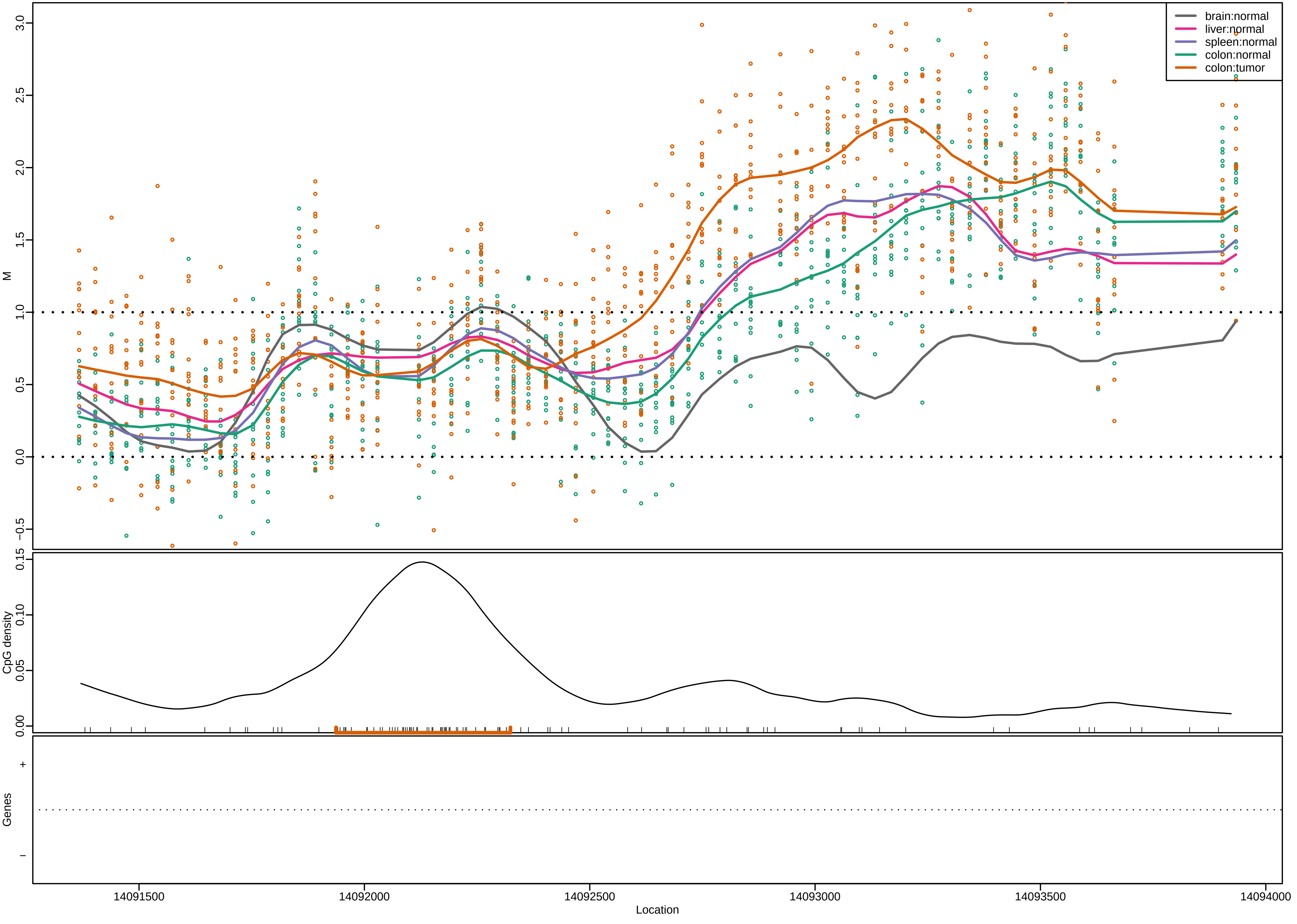

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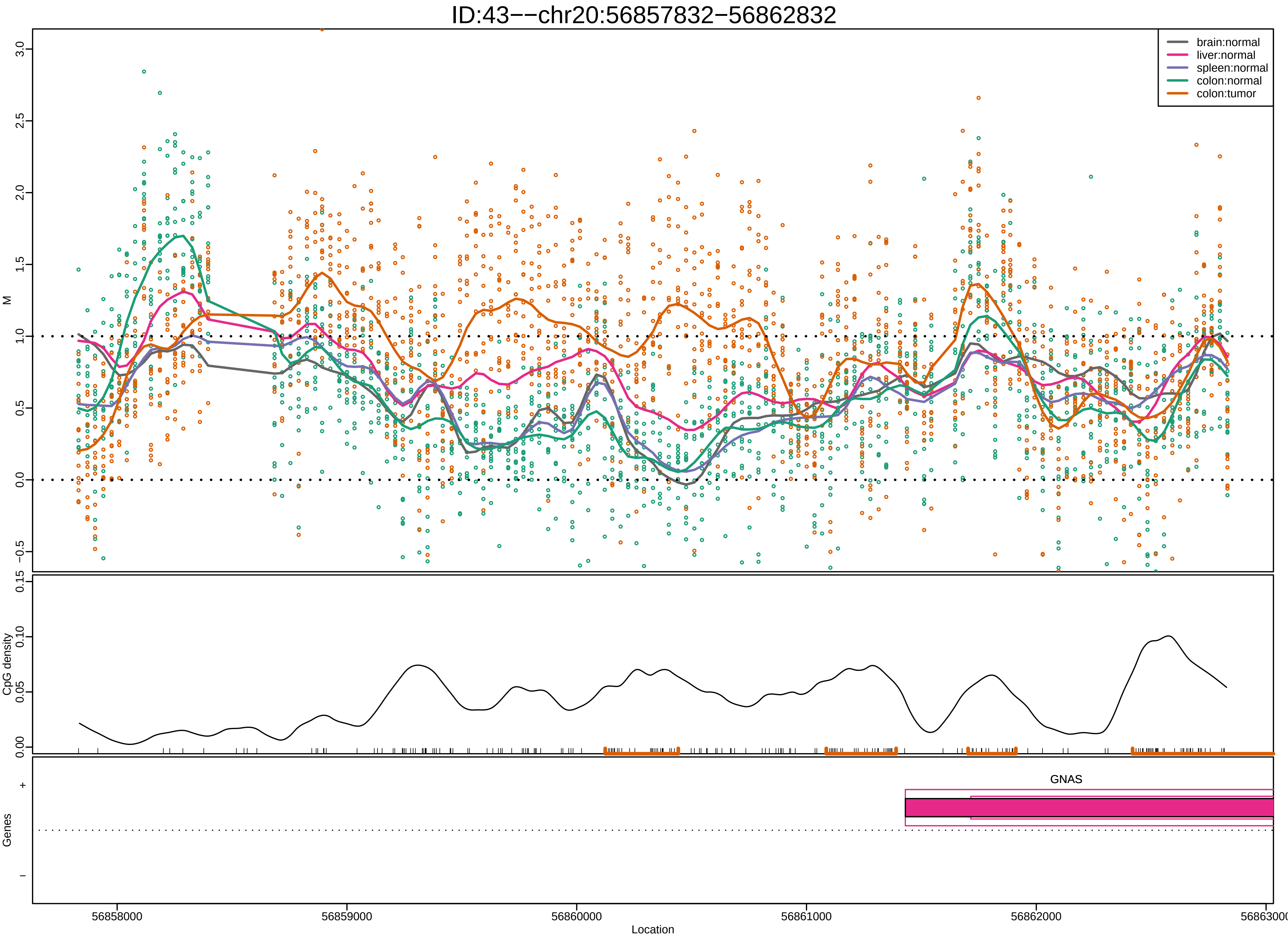
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brain:normal
liver:normal
spleen:normal
colon:normal
colon:tumor
M
−0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
CpG density
0.00
0.05
0.10
0.15
Genes
+
−
GNAS
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56859000
56860000
56861000
56862000
5686300
Location

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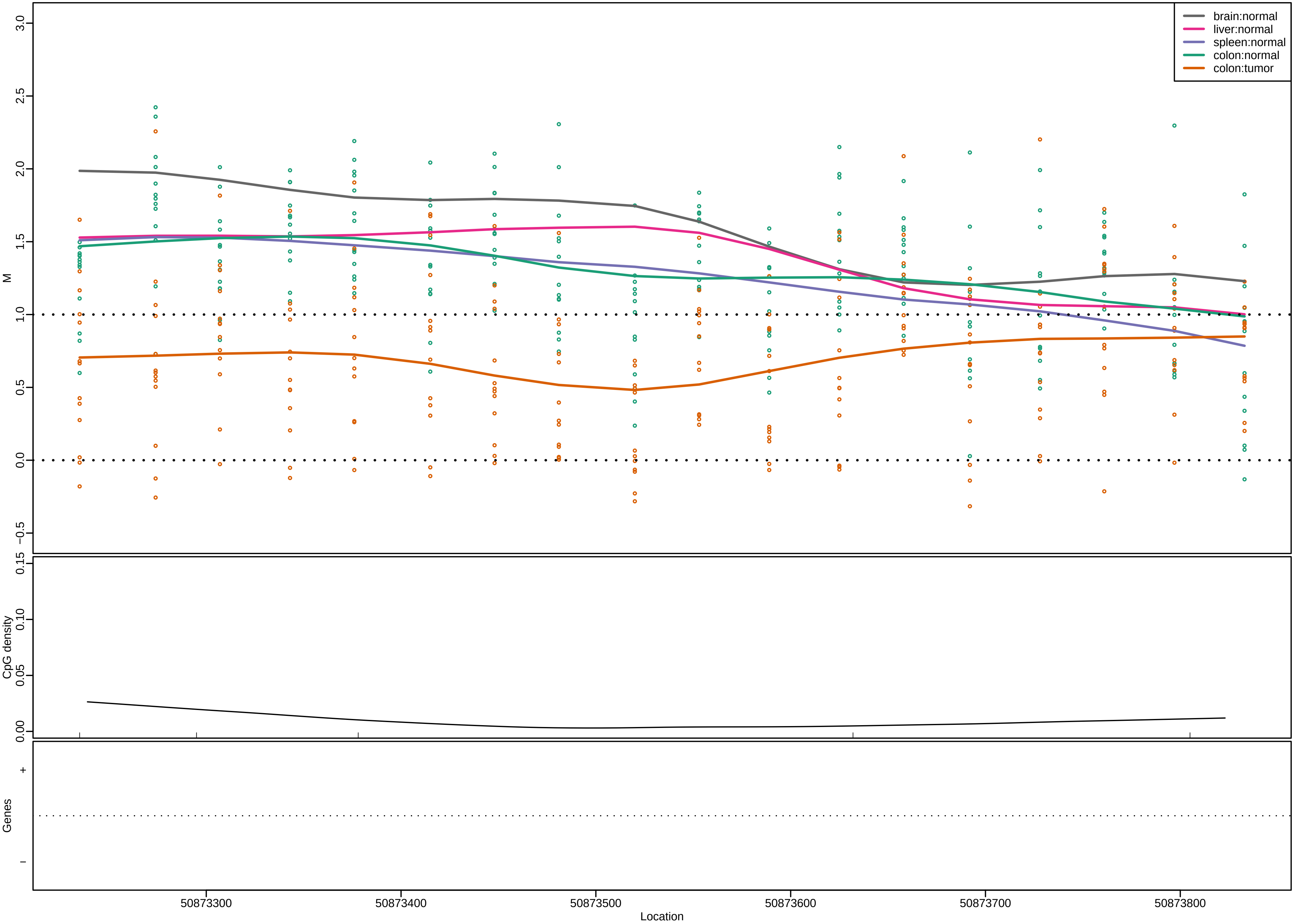

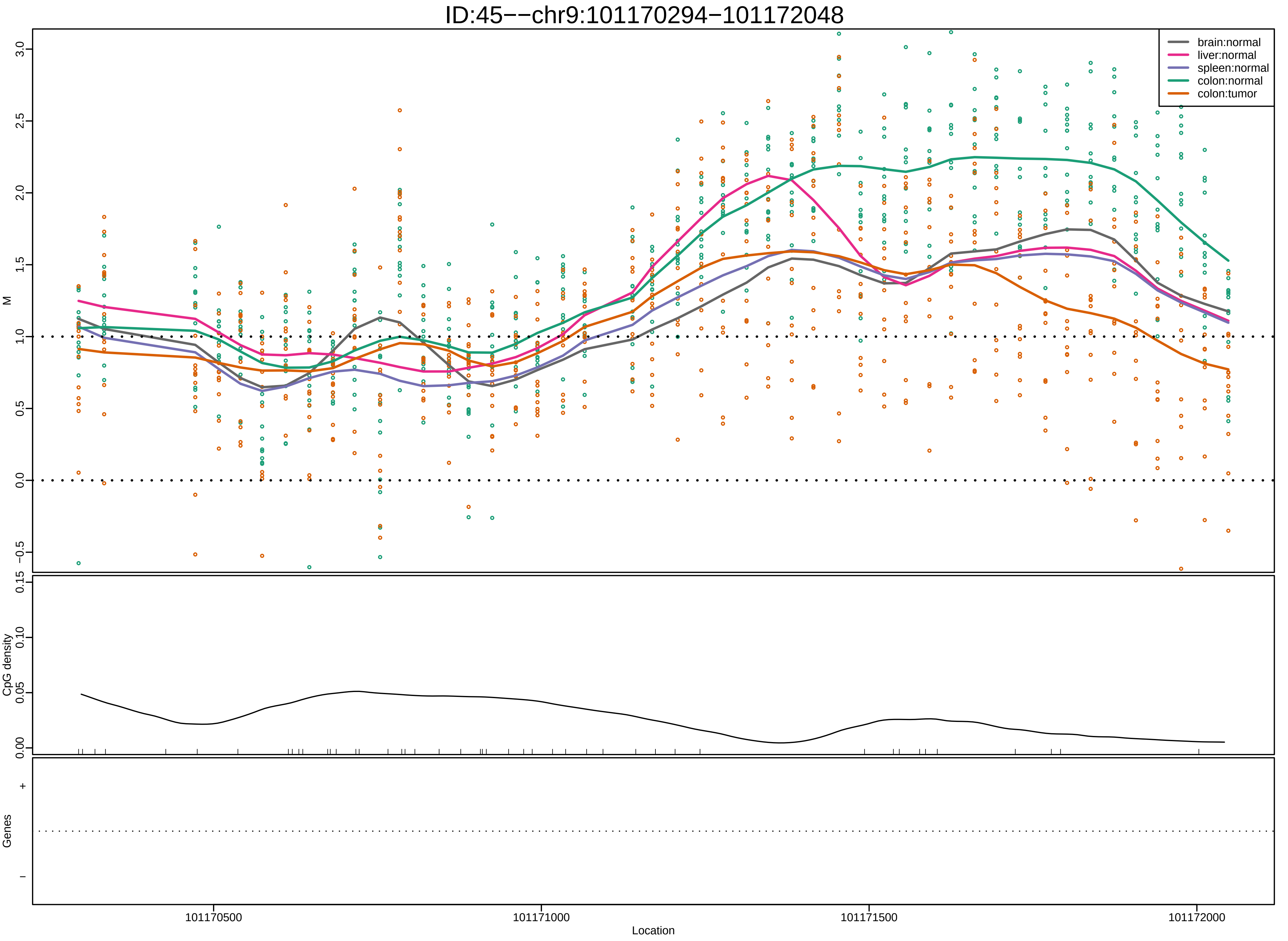
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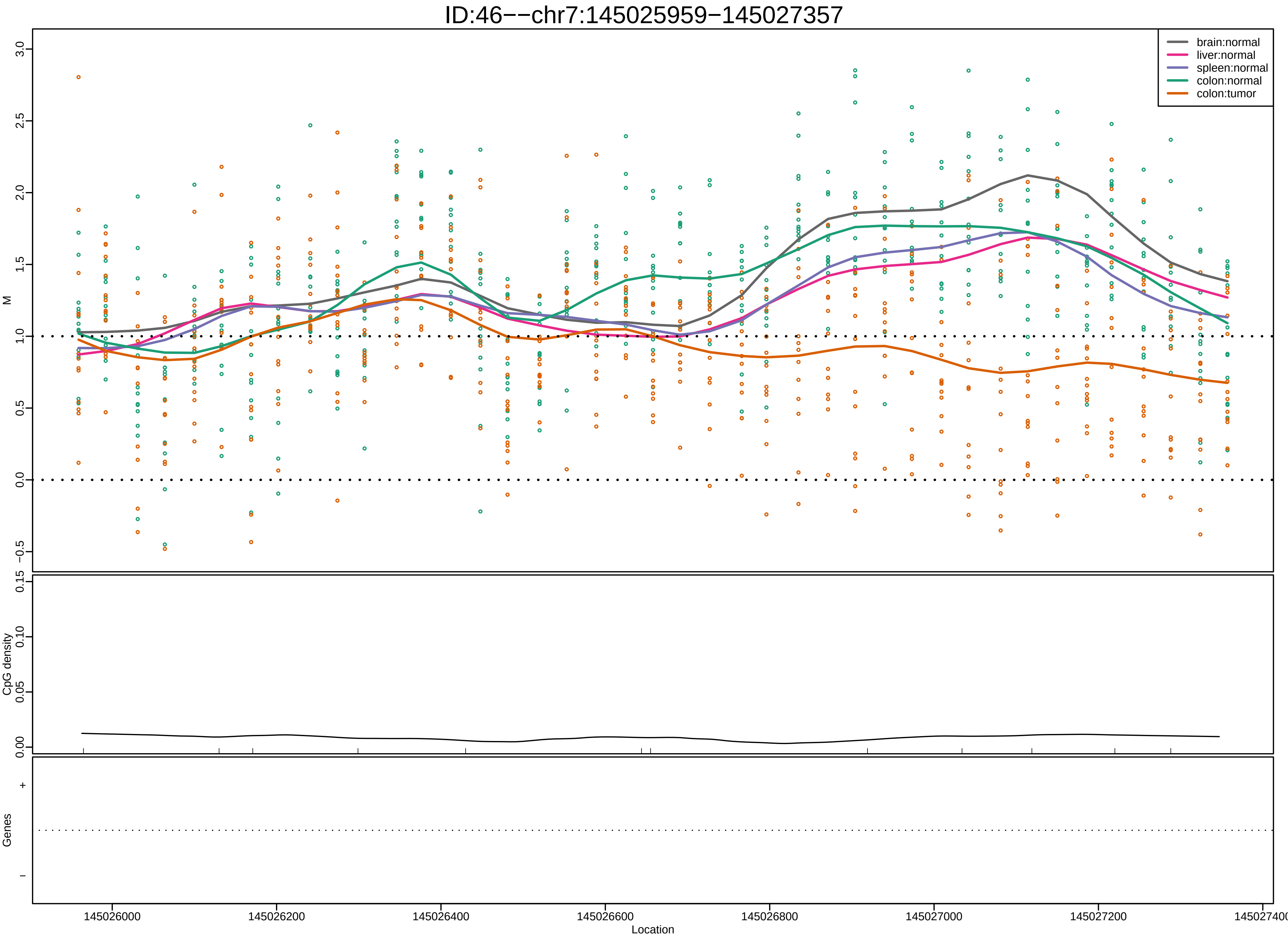
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
brain:normal
liver:normal
spleen:normal
colon:normal
colon:tumor
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
101170500
101171000
101171500
101172000
Location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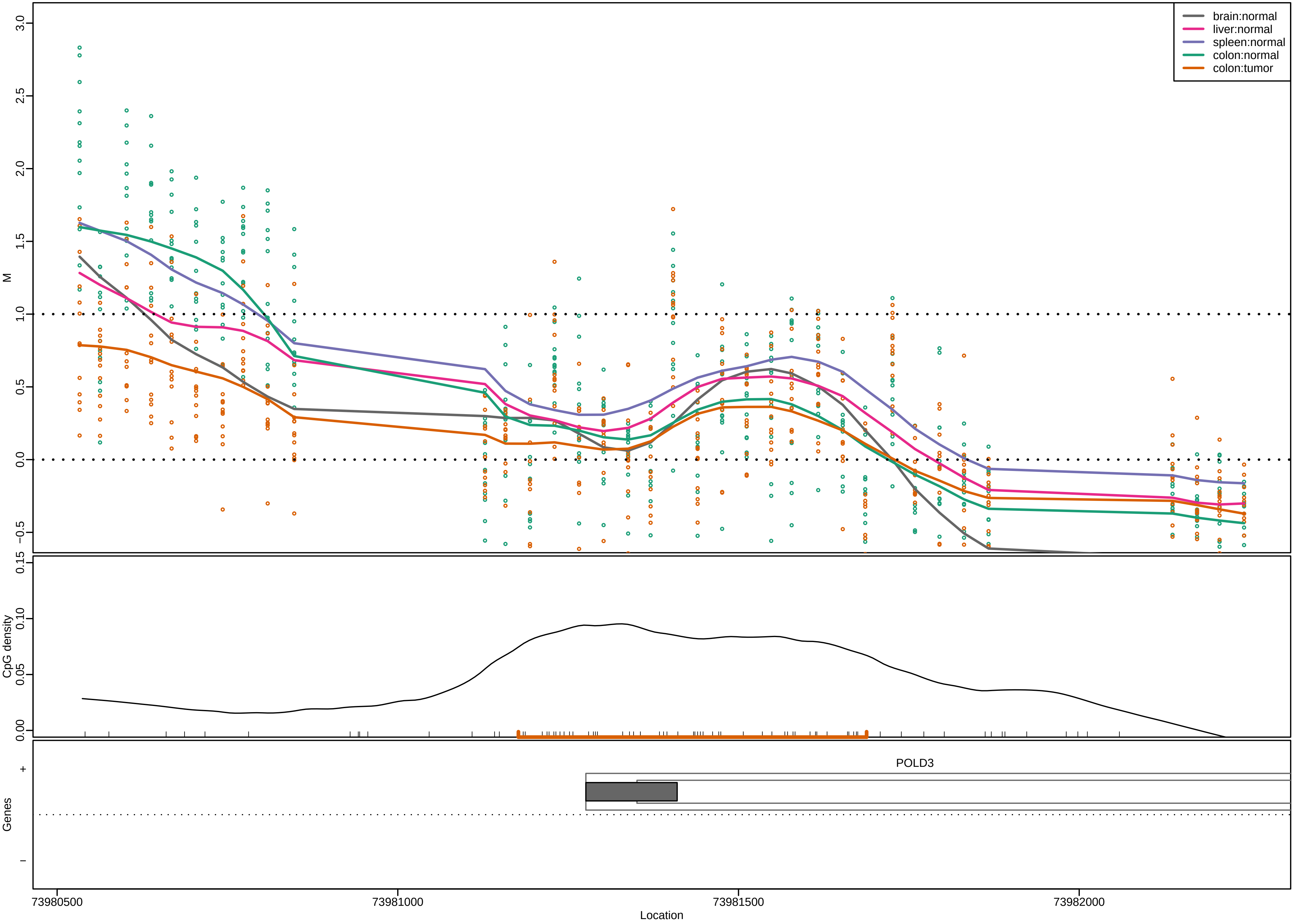
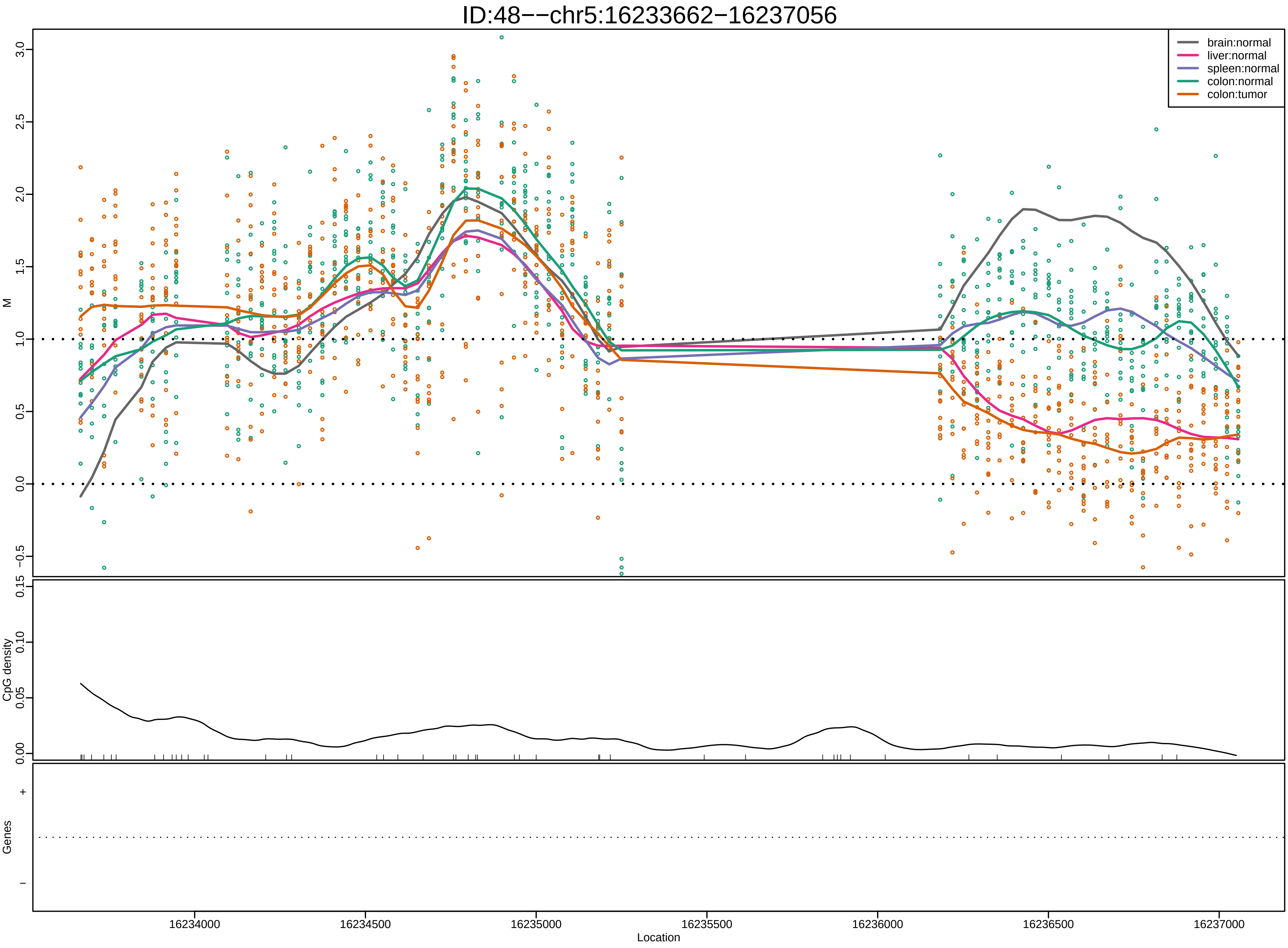
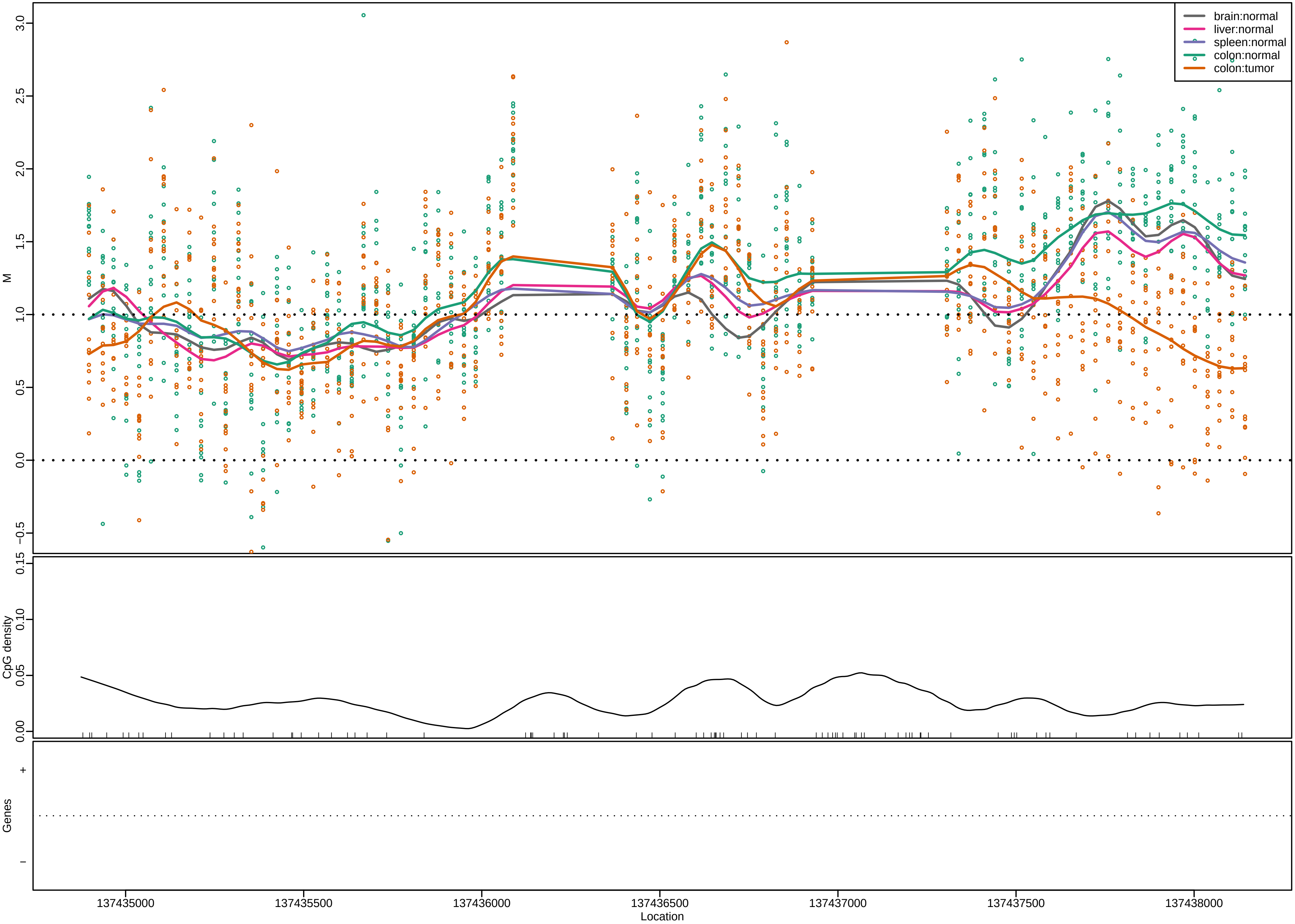
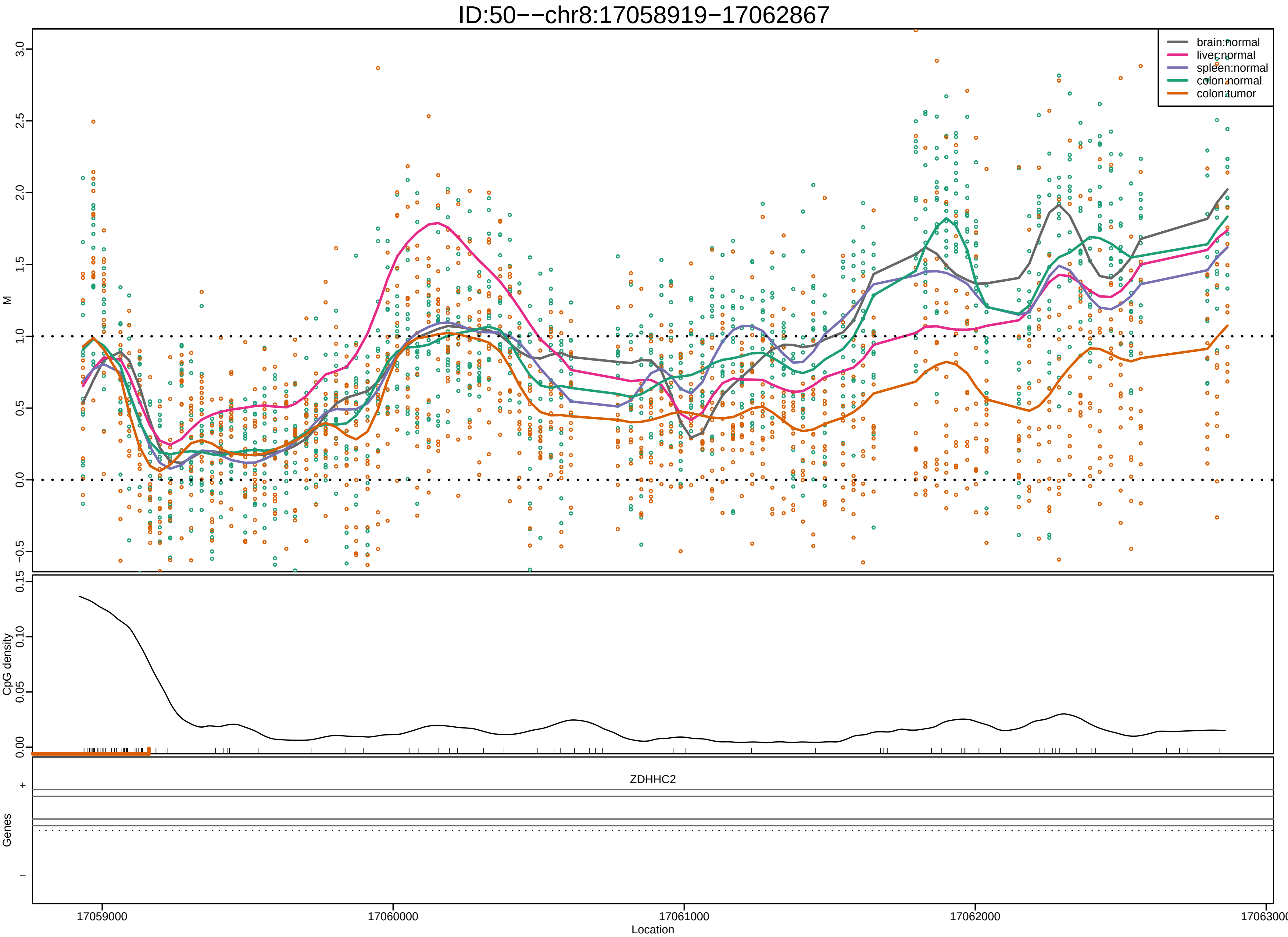
ID:47−−chr11:73980533−73982242




ID:48−−chr5:16233662−16237056
brain:normal
liver:normal
spleen:normal
colon:normal
colon:tumor
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
16234000
16234500
16235000
16235500
16236000
16236500
16237000
Location

ID:49−−chr9:137434871−137438143




ID:50−−chr8:17058919−17062867
M
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
brain:normal
liver:normal
spleen:normal
colon:normal
colon:tumor
CpG density
0.15
0.10
0.05
0.00
Genes
+
−
ZDHHC2
17059000
17060000
17061000
17062000
17063000
Location