

Supplementary Data 6

IGV plots of ONT RRMS methylation and coverage track figures for each chromosome

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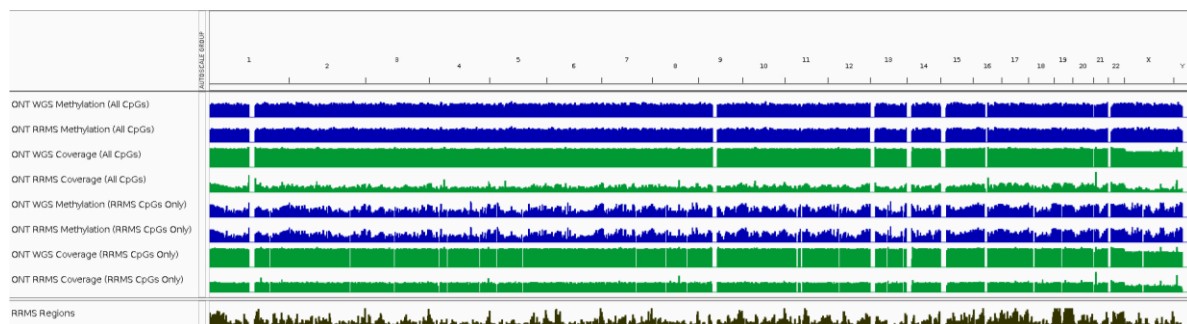
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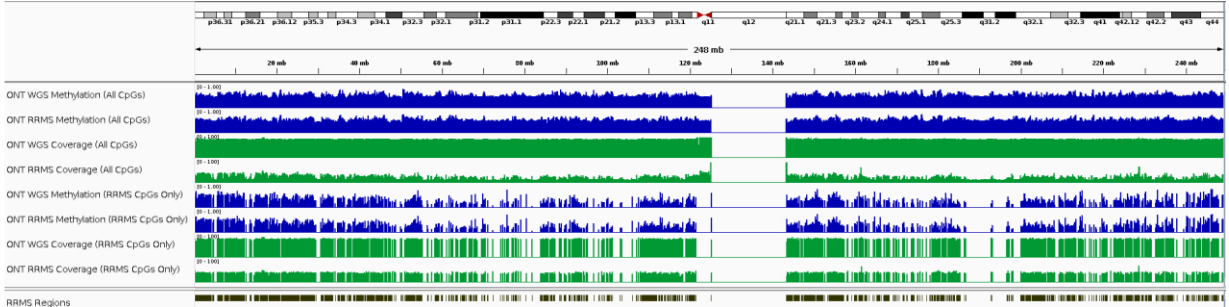
Each figure displays methylation levels of CpGs in blue track for HG002 ONT WGS and HG002 ONT RRMS, with corresponding coverage of each CpG site in green tracks, as viewed in IGV. "coverage" and

“mod_percentage” columns from aggregated per-site output of DeepMod2 were converted into BigWig format. In order to show a global view of BigWig tracks, IGV applies a mean function in a sliding window to simplify the view. We visualized the methylation and coverage for all CpG sites (shown by first four tracks in each figure) which shows enrichment of on-target regions compared to off-target regions as shown by coincidence of coverage peaks and RRMS track at the bottom. We separately visualized methylation and coverage for CpG sites only in RRMS regions, shown by next four tracks with “RRMS CpGs Only” in the description. We used bedtools intersect to select coverage and methylation from “All CpGs” tracks for only those CpGs that fell within on-target region used in RRMS. Comparison of methylation from RRMS and WGS for “RRMS CpGs” shows high correlation of methylation.

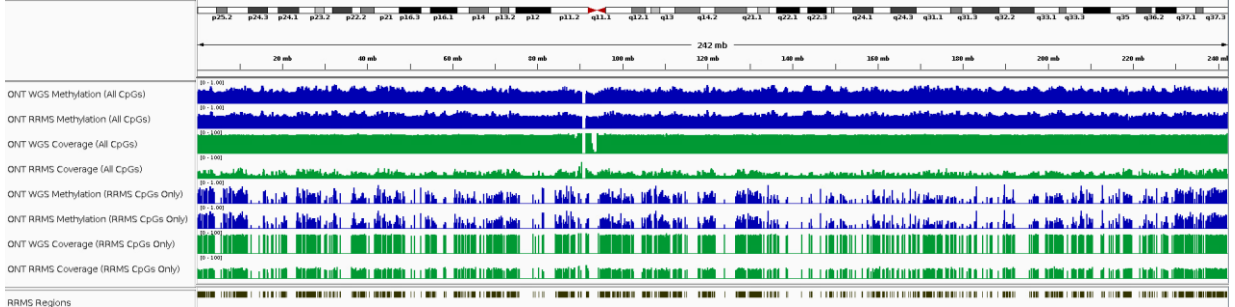
Whole Genome View



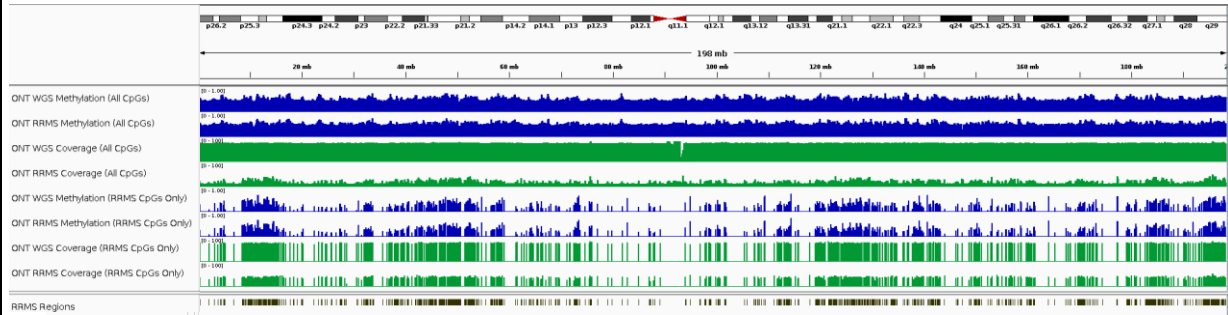
Chromosome 1



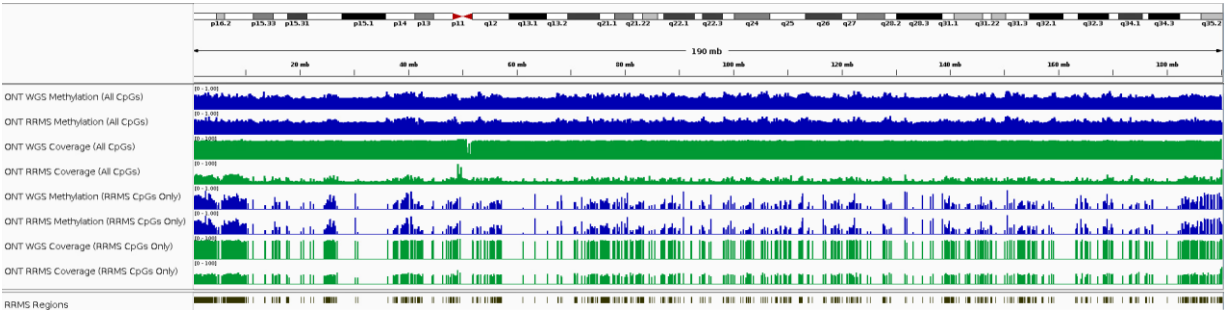
Chromosome 2



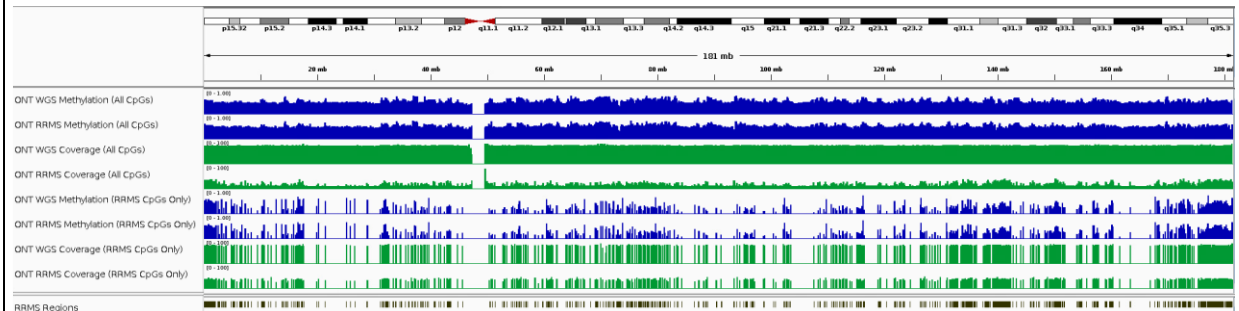
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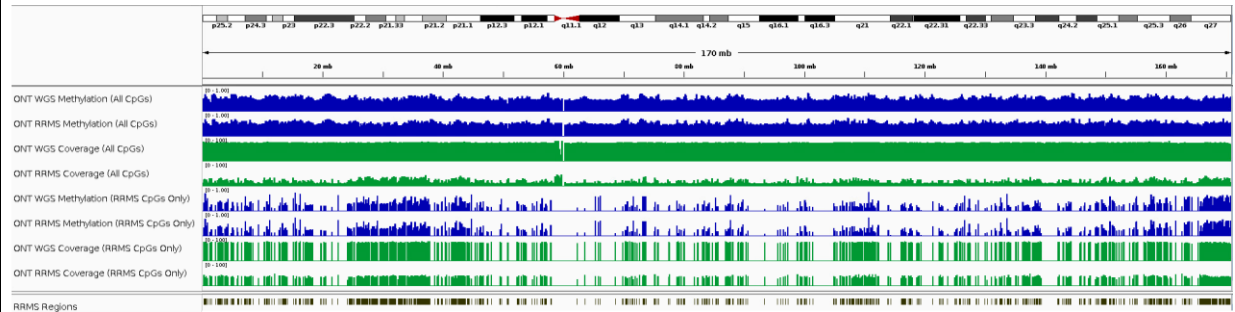
Chromosome 4



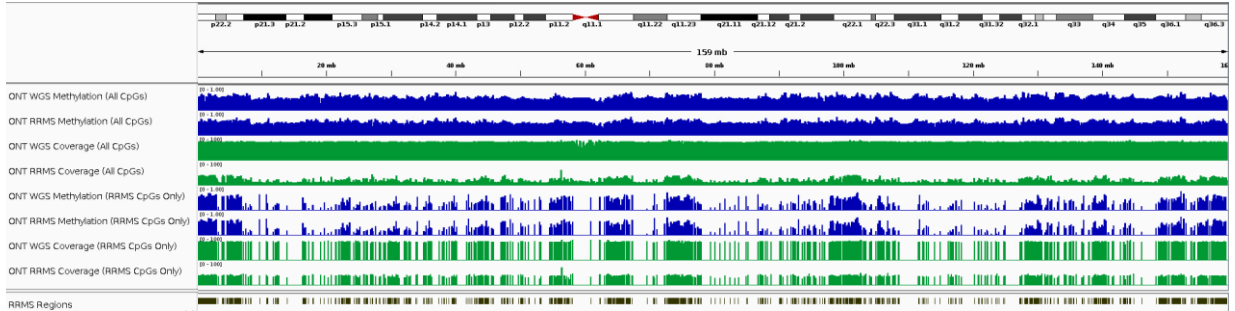
Chromosome 5



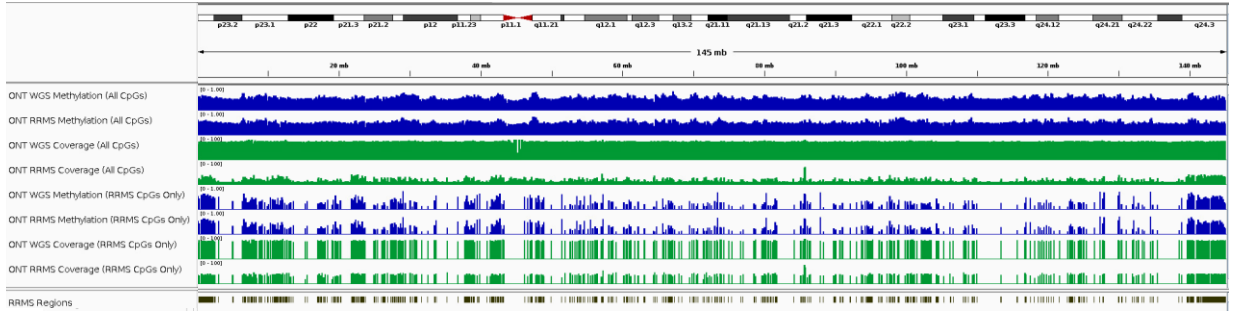
Chromosome 6



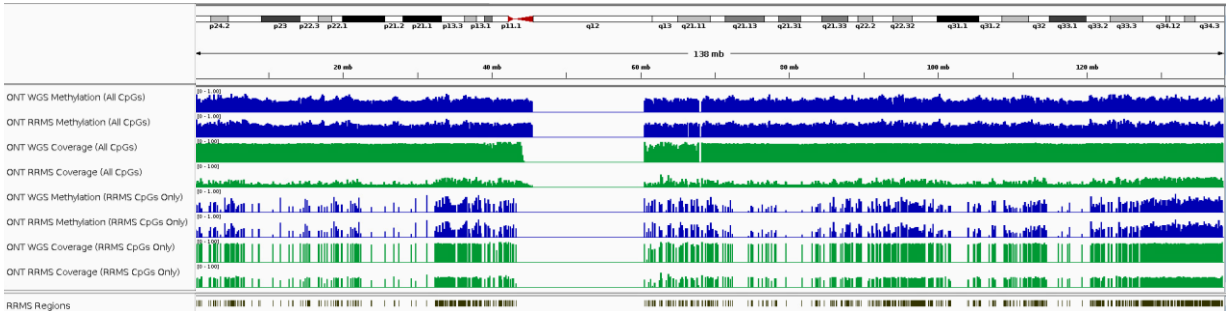
Chromosome 7



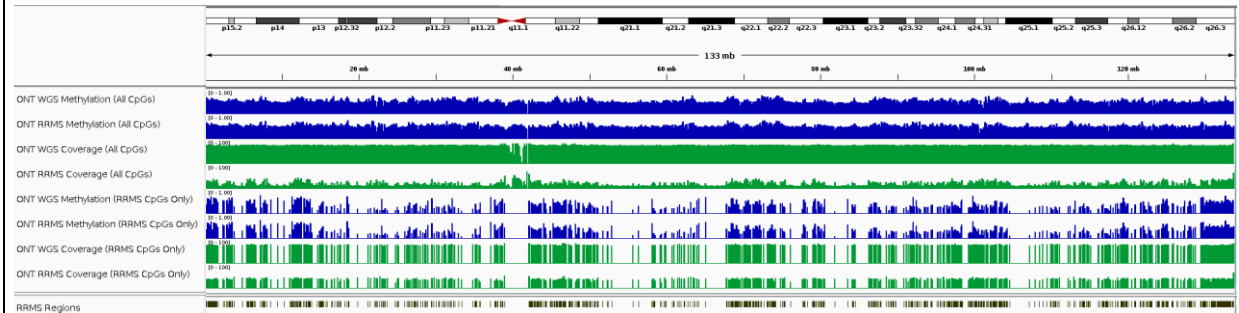
Chromosome 8



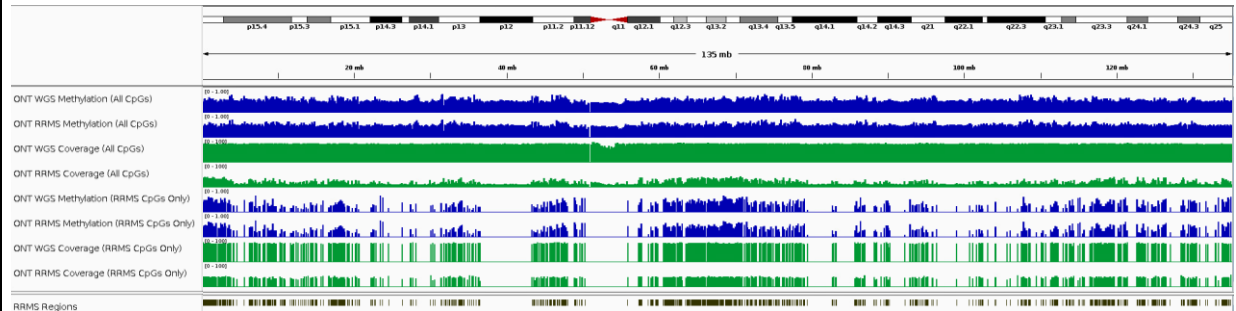
Chromosome 9



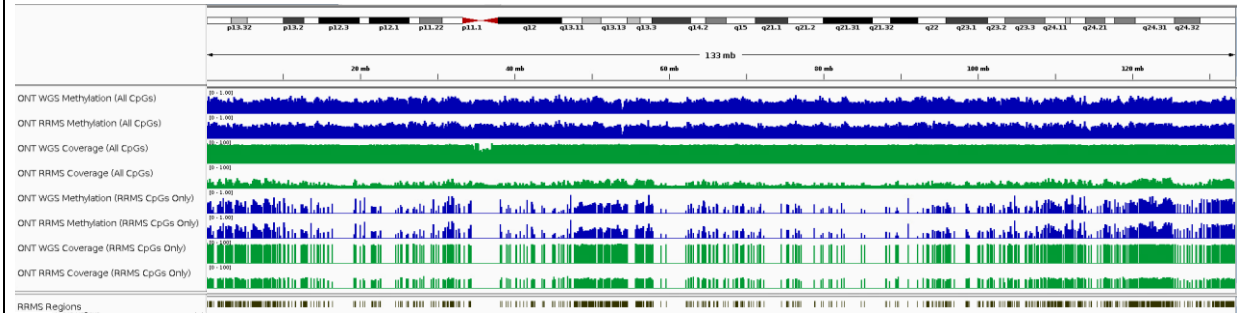
Chromosome 10



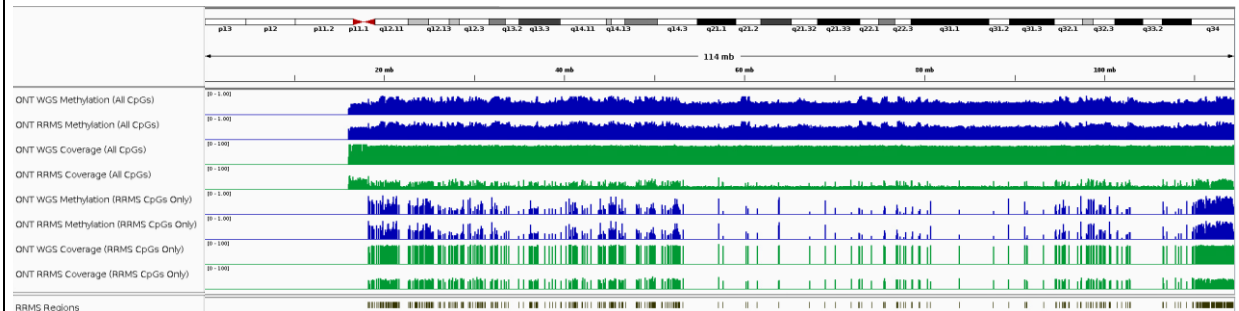
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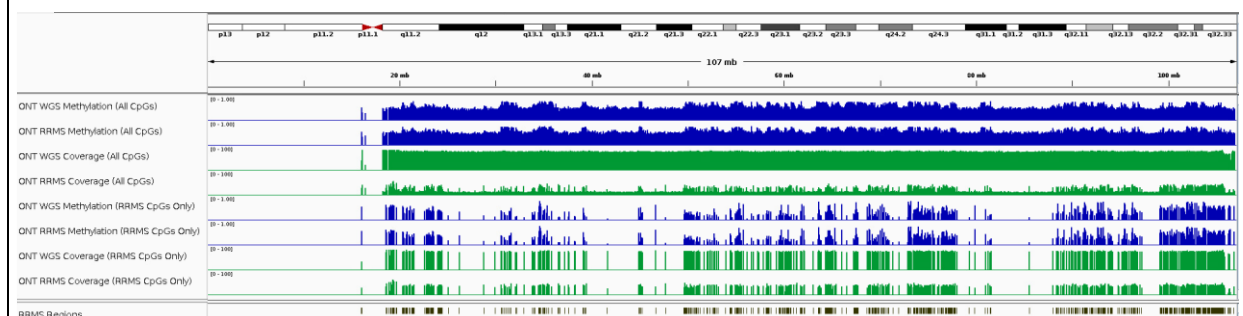
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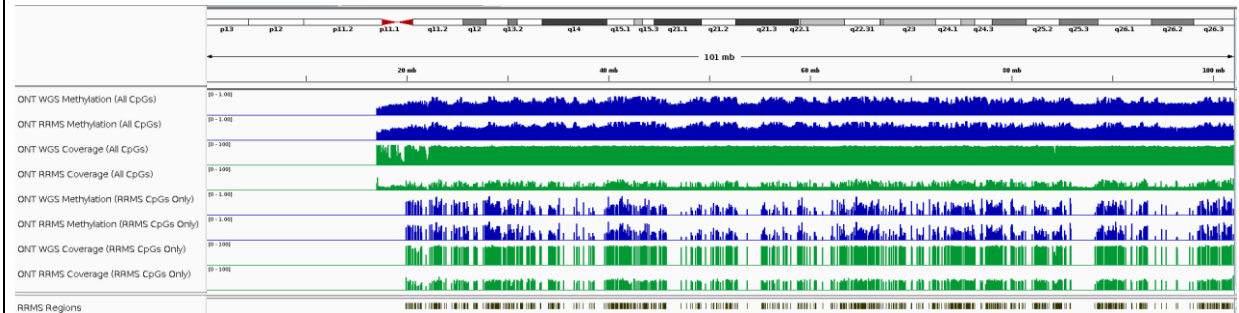
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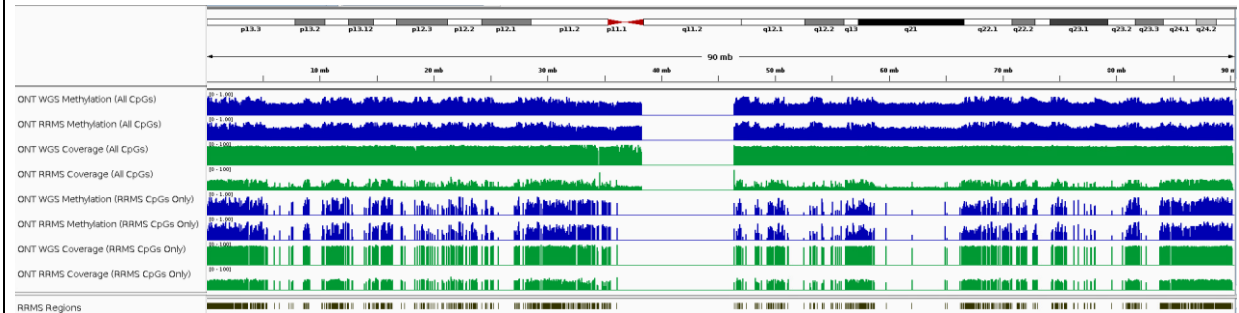
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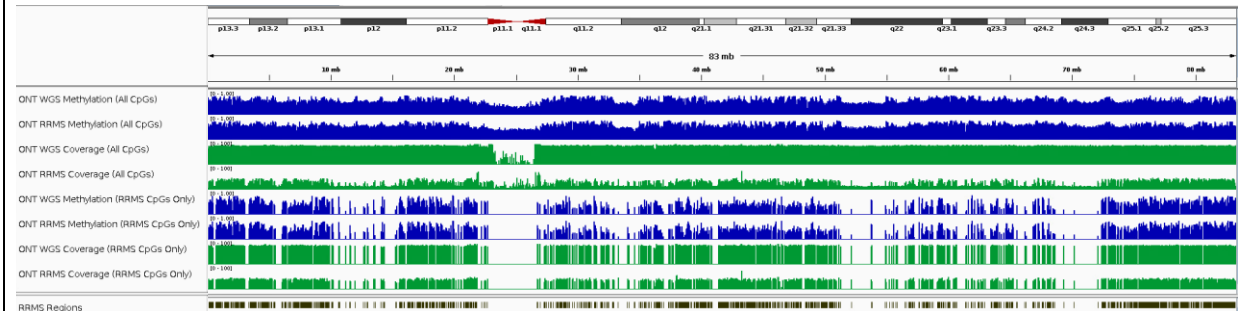
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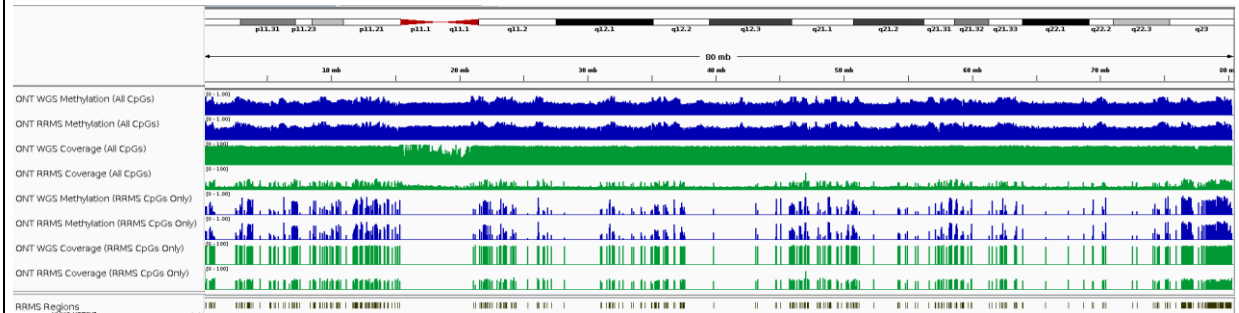
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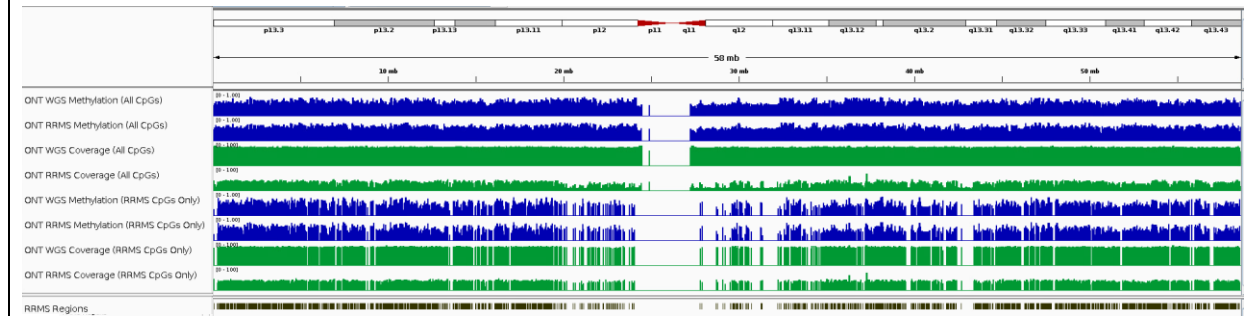
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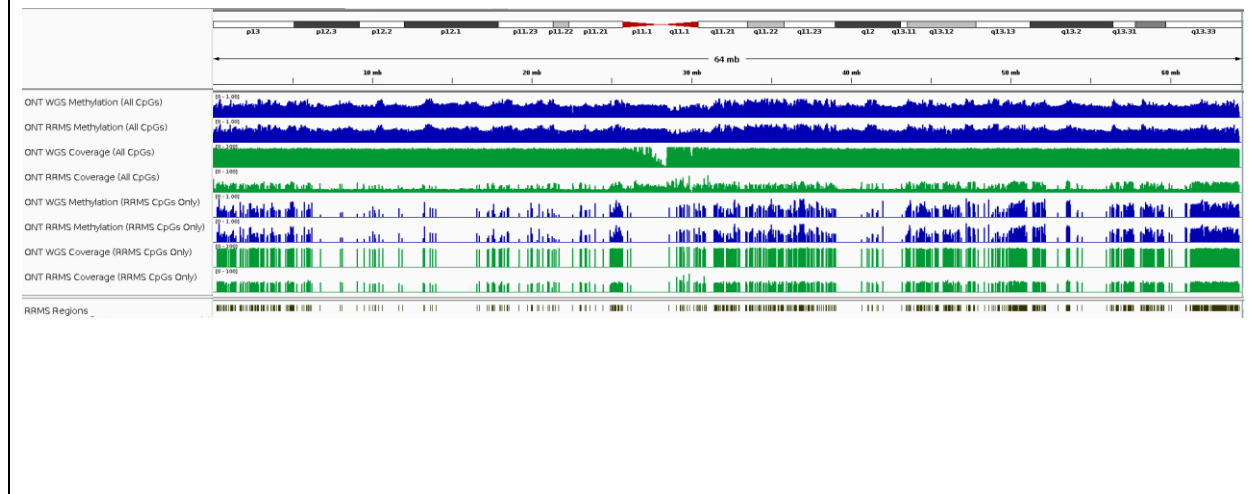
Chromosome 18



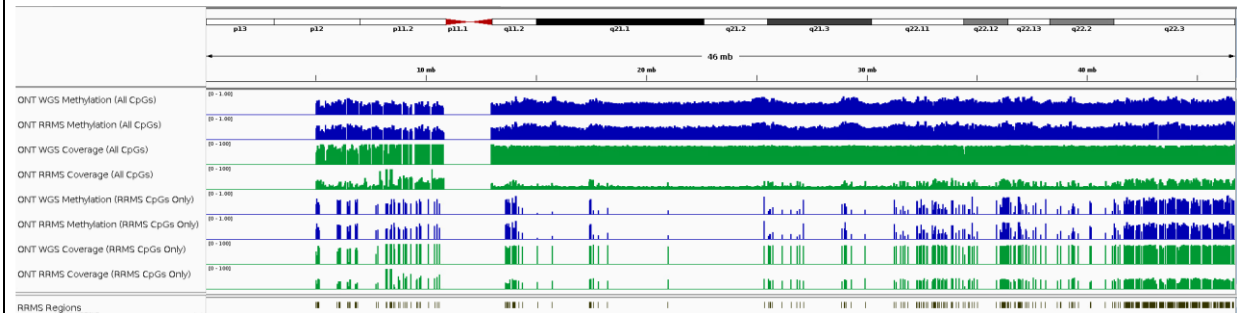
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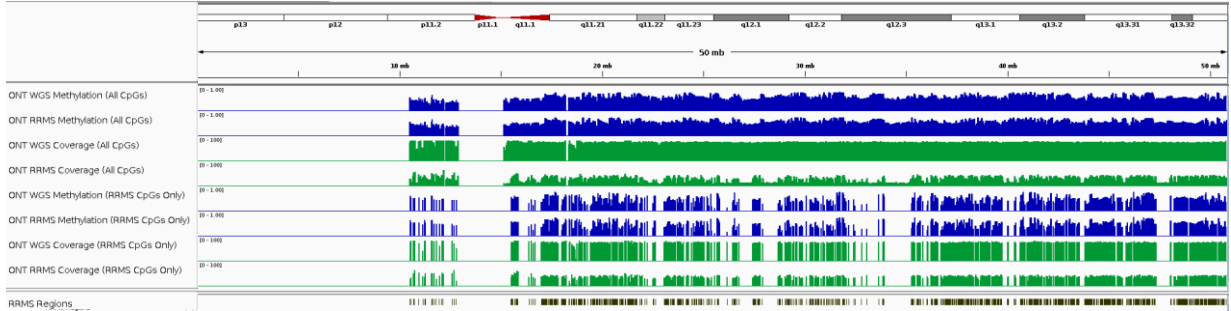
Chromosome 20



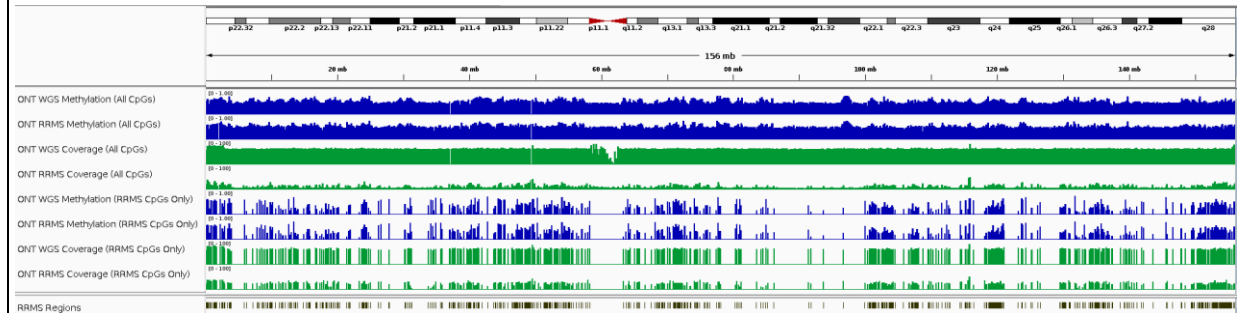
Chromosome 21



Chromosome 22



Chromosome X



Chromosome Y

