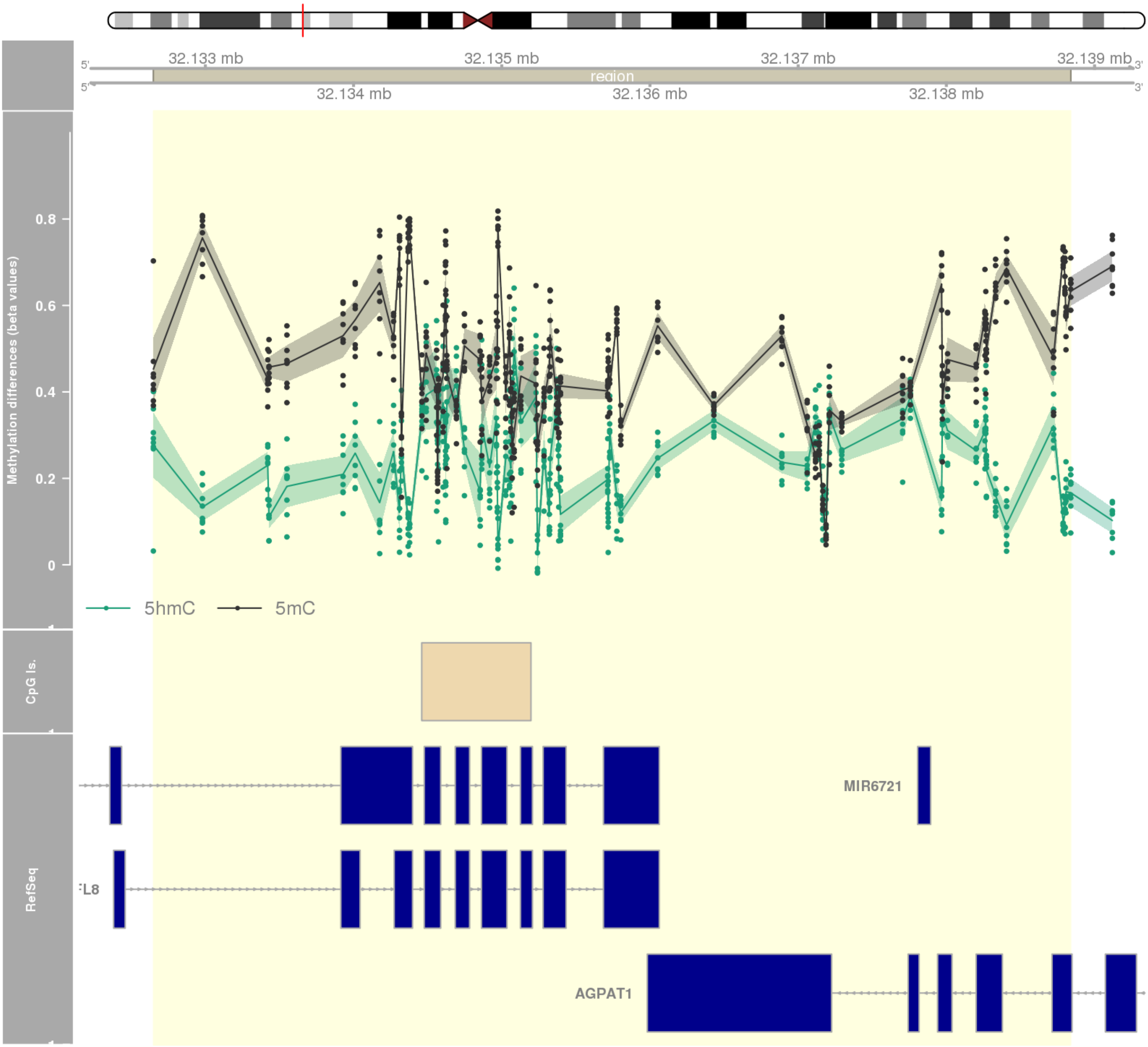
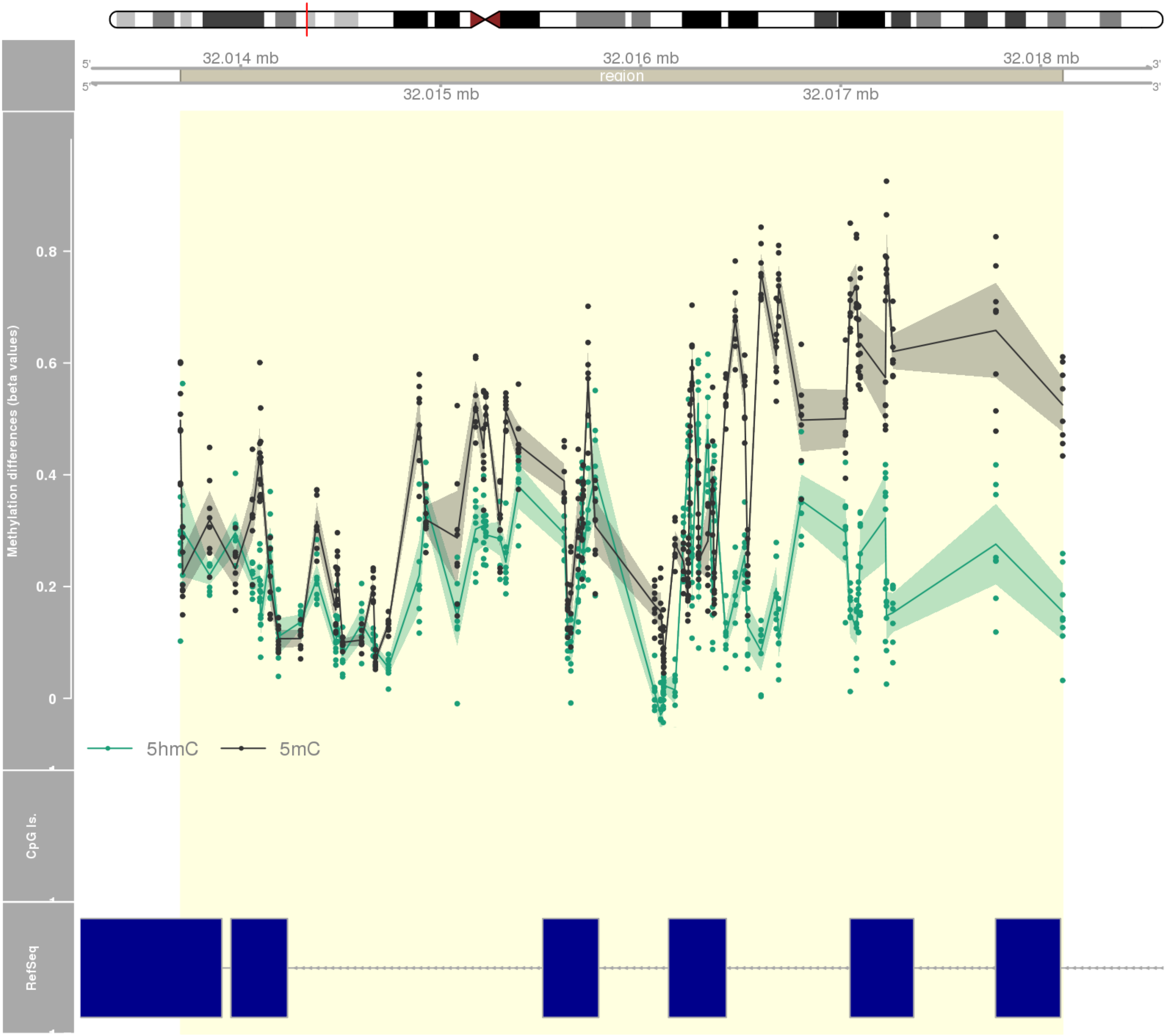
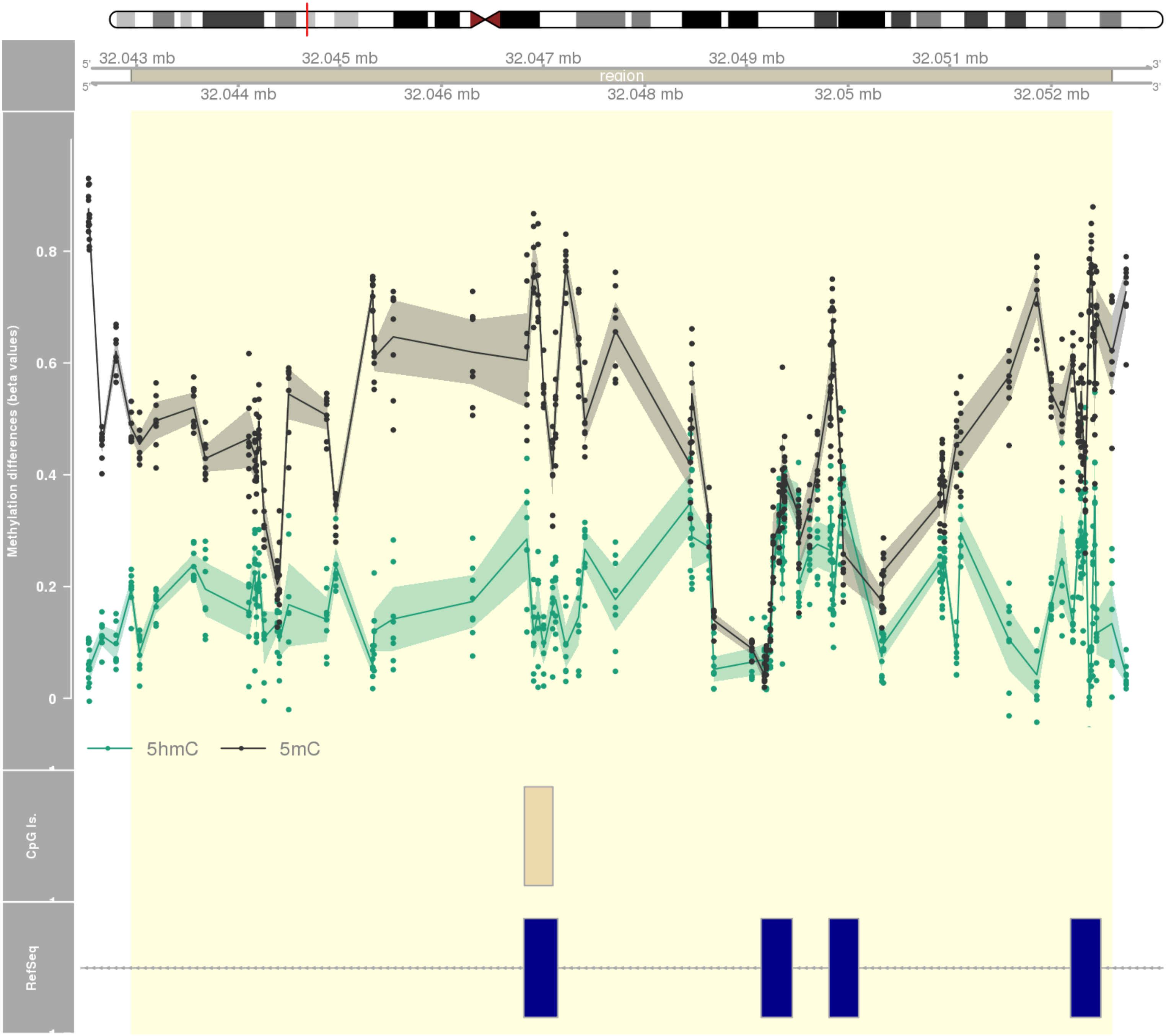
DMR 1 // chr6:32132649-32138839 // 6190 pb. (76 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: PPT2 / PPT2-EGFL8 / EGFL8 / AGPAT1 -



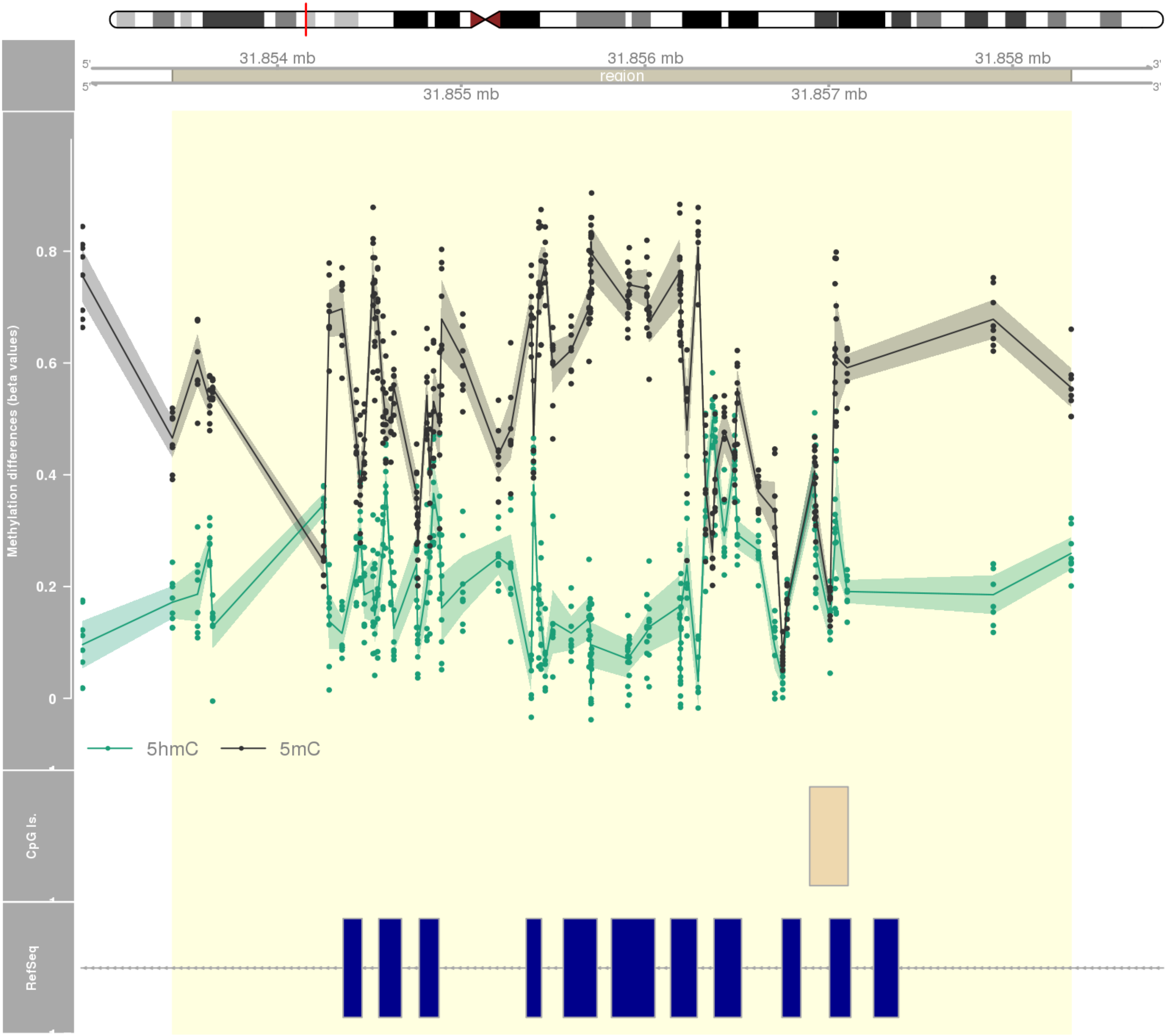
DMR 2 // chr6:32013699-32018110 // 4411 pb. (68 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: TNXB -



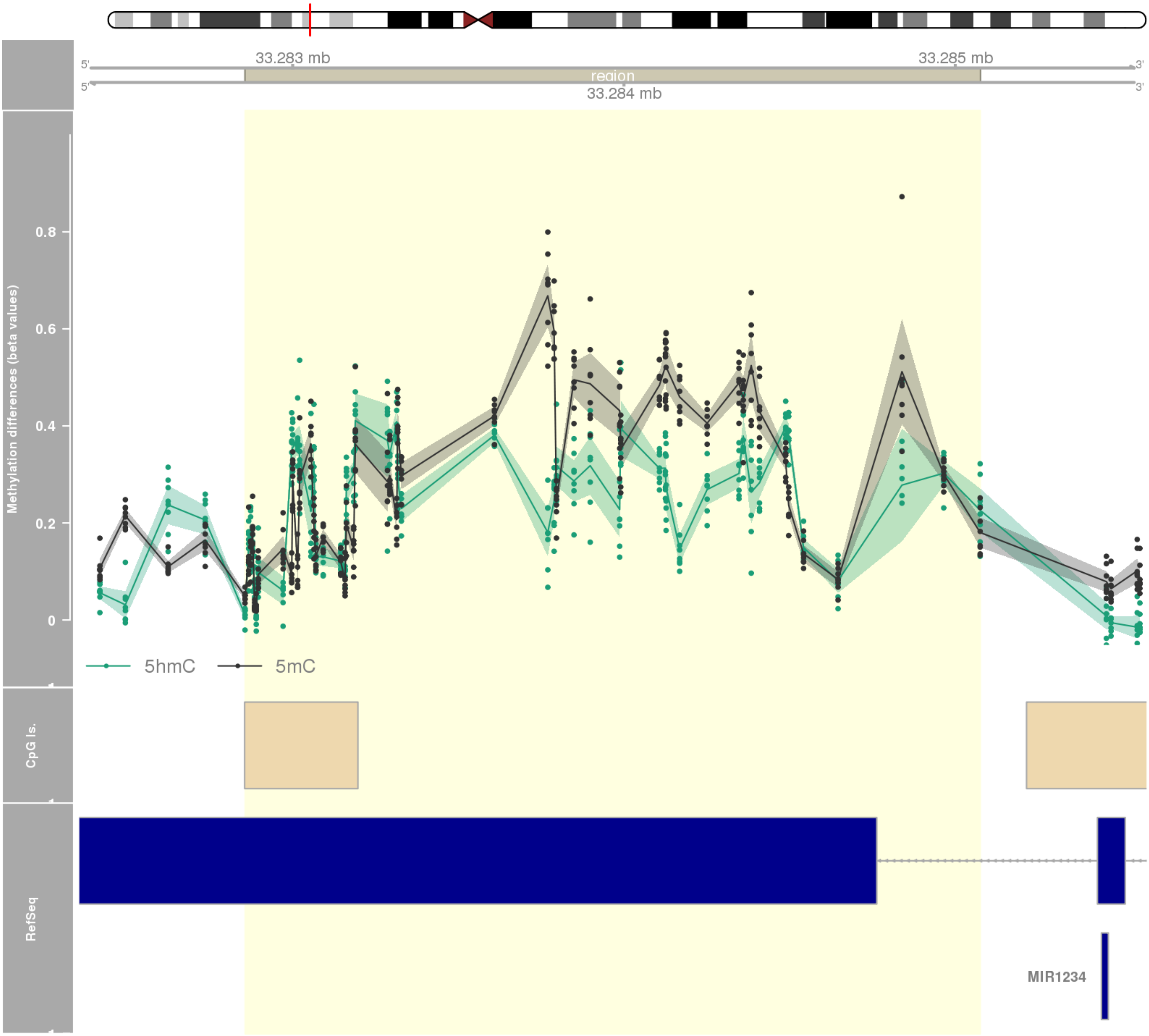
DMR 3 // chr6:32042947-32052596 // 9649 pb. (75 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: RNA5SP206 / TNXB -



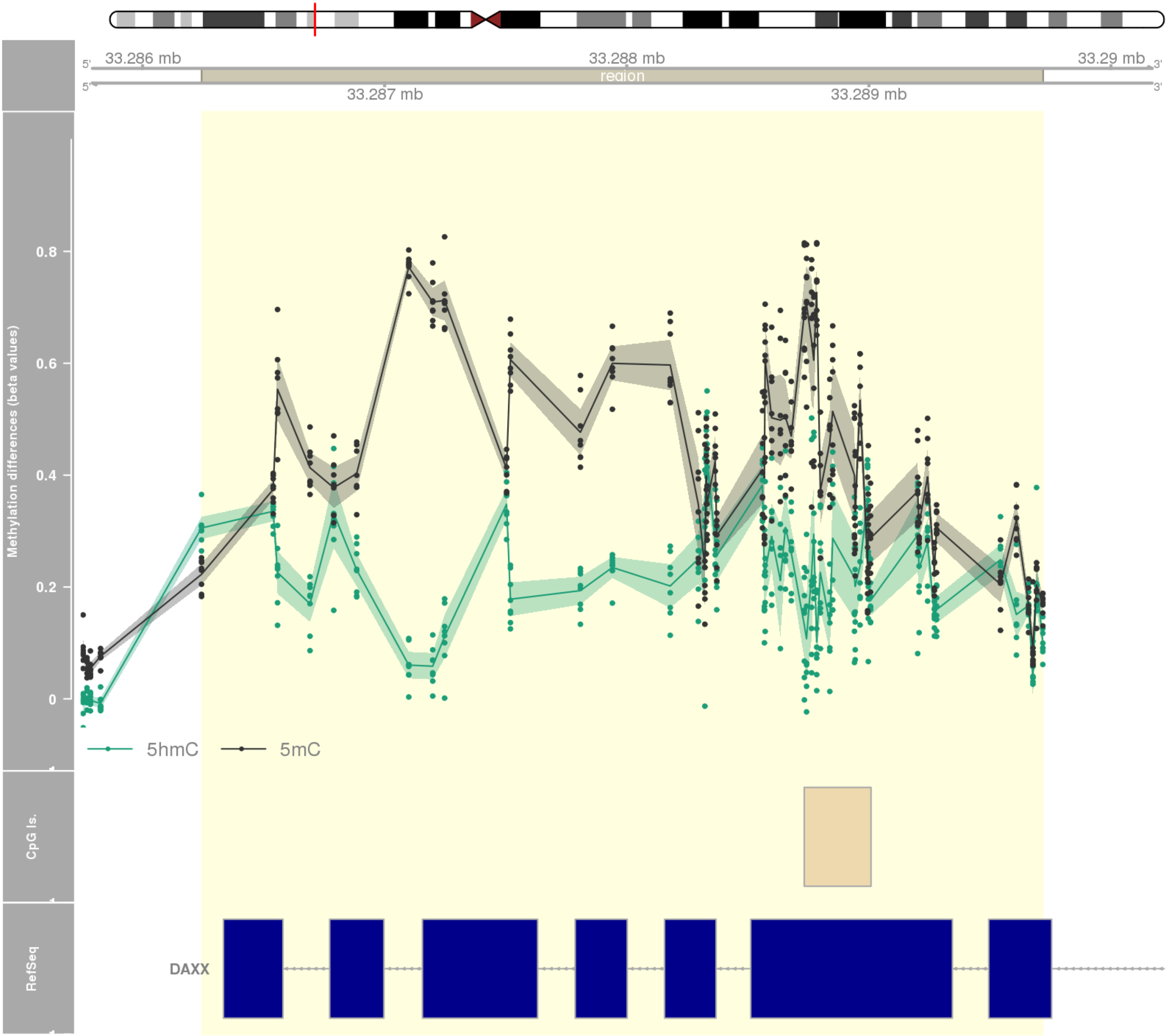
DMR 4 // chr6:31853428-31858319 // 4891 pb. (65 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: EHMT2 -



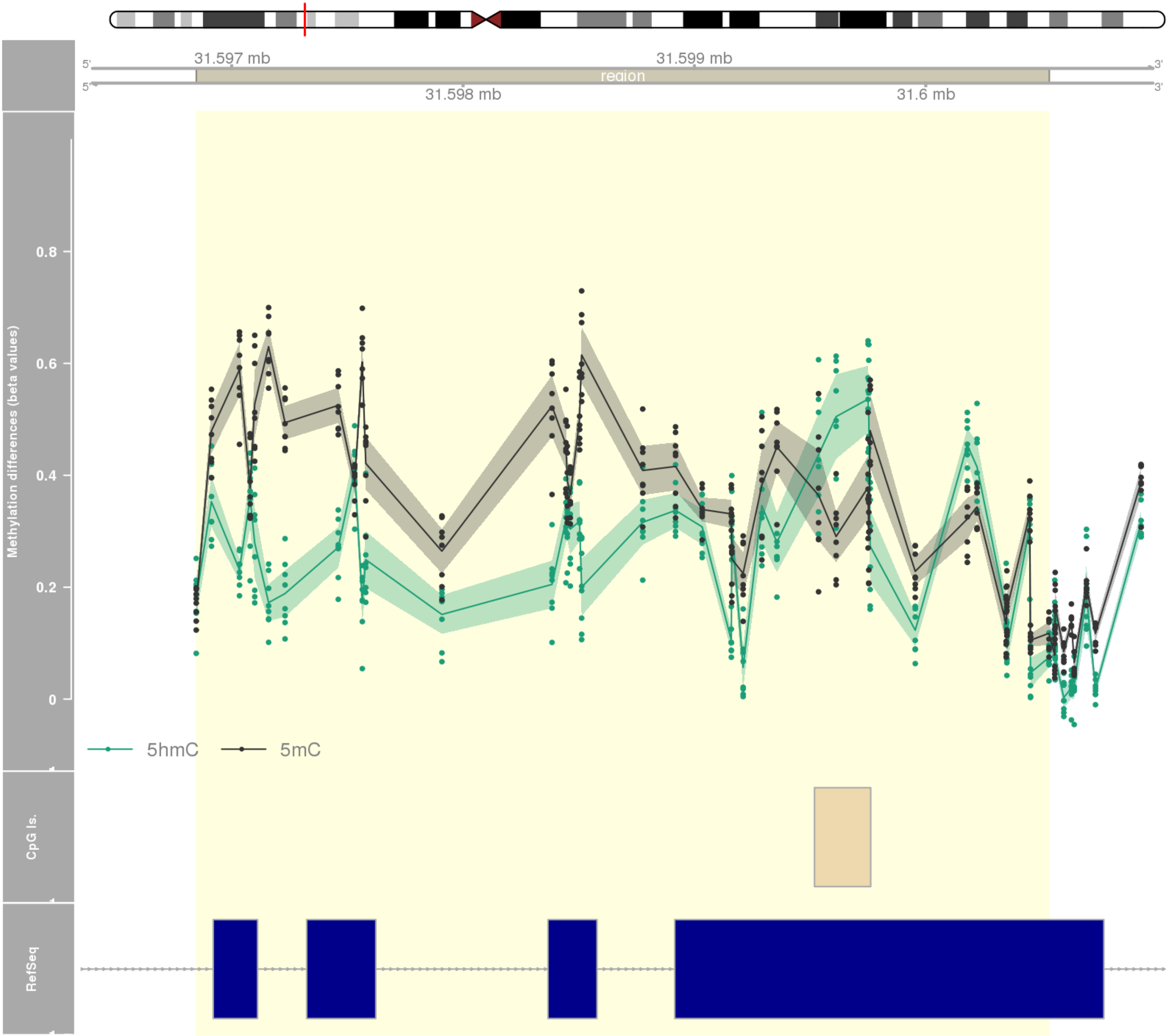
DMR 5 // chr6:33282856-33285075 // 2219 pb. (50 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: ZBTB22 -



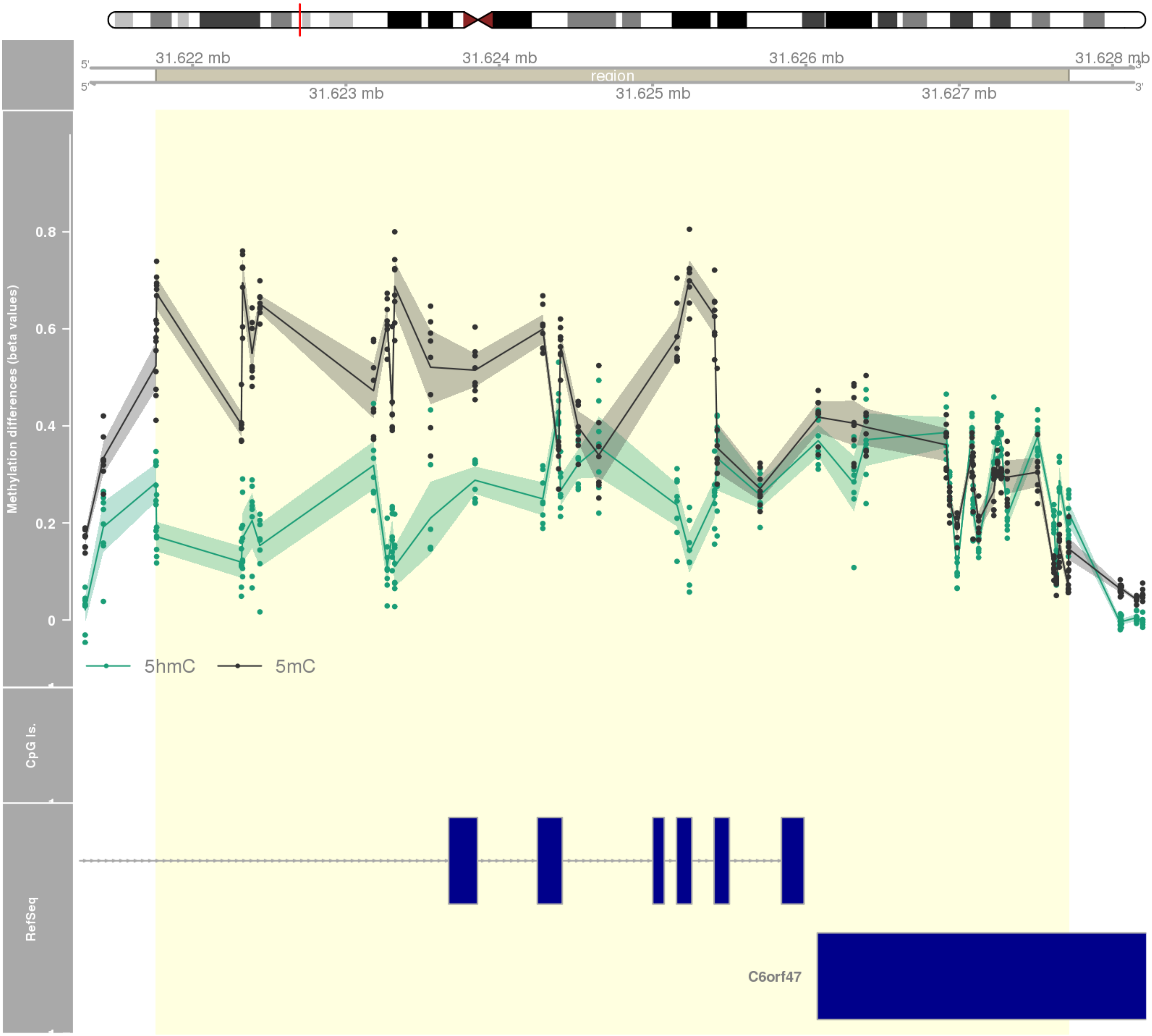
DMR 6 // chr6:33286244-33289719 // 3475 pb. (52 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: DAXX -



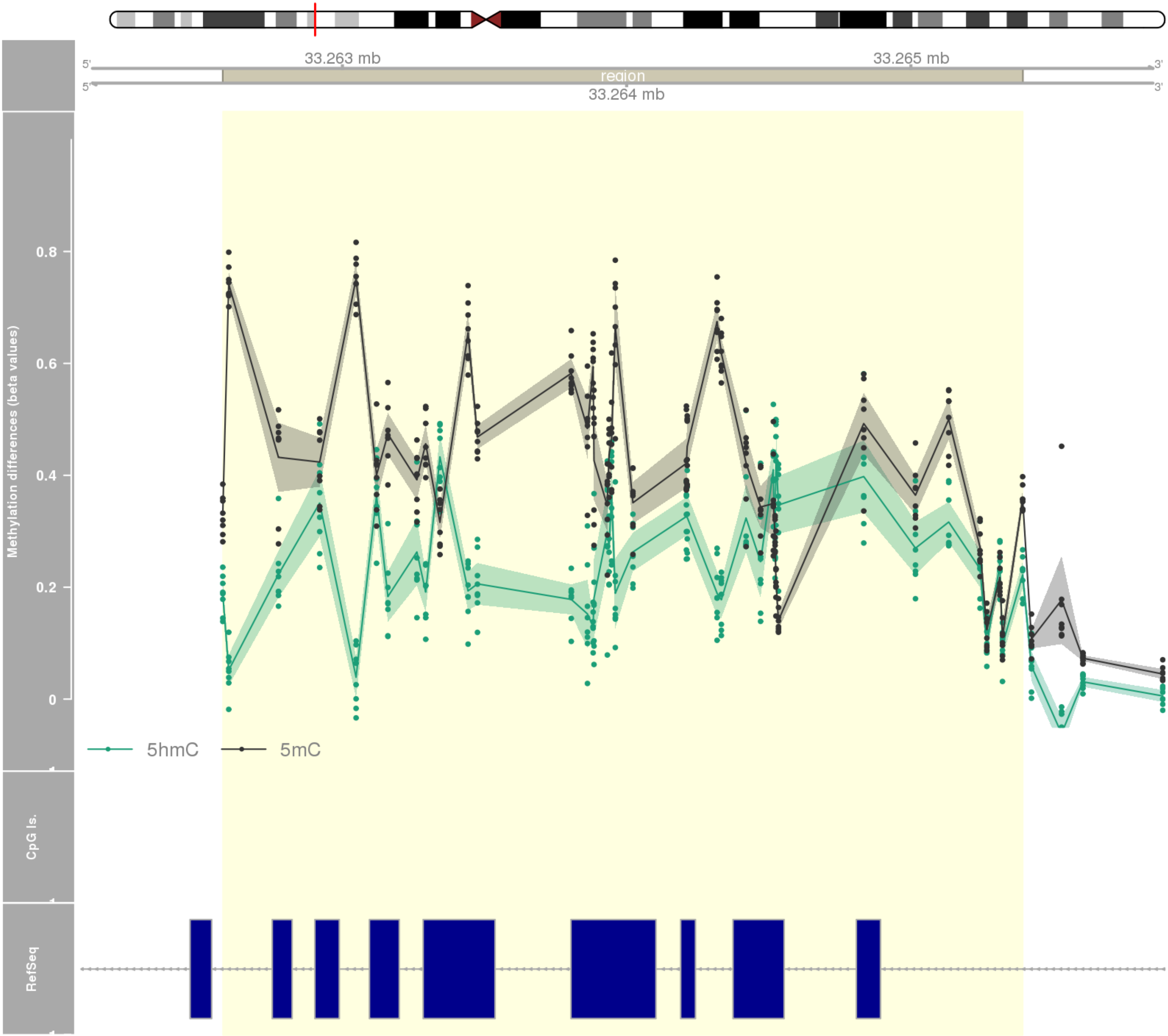
DMR 7 // chr6:31596847-31600533 // 3686 pb. (39 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: PRRC2A -



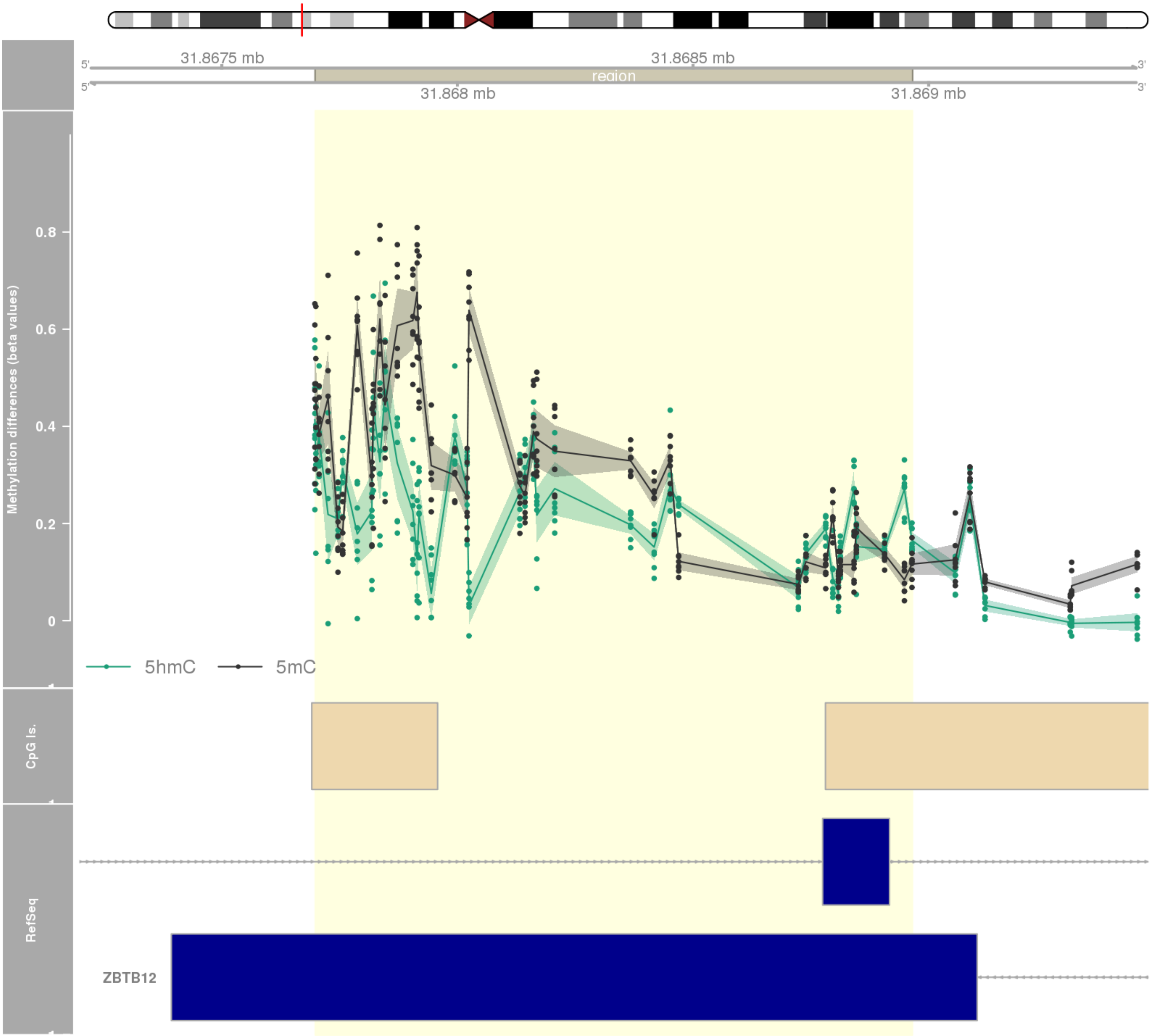
DMR 8 // chr6:31621761-31627714 // 5953 pb. (41 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: C6orf47-AS1 / APOM / C6orf47 -



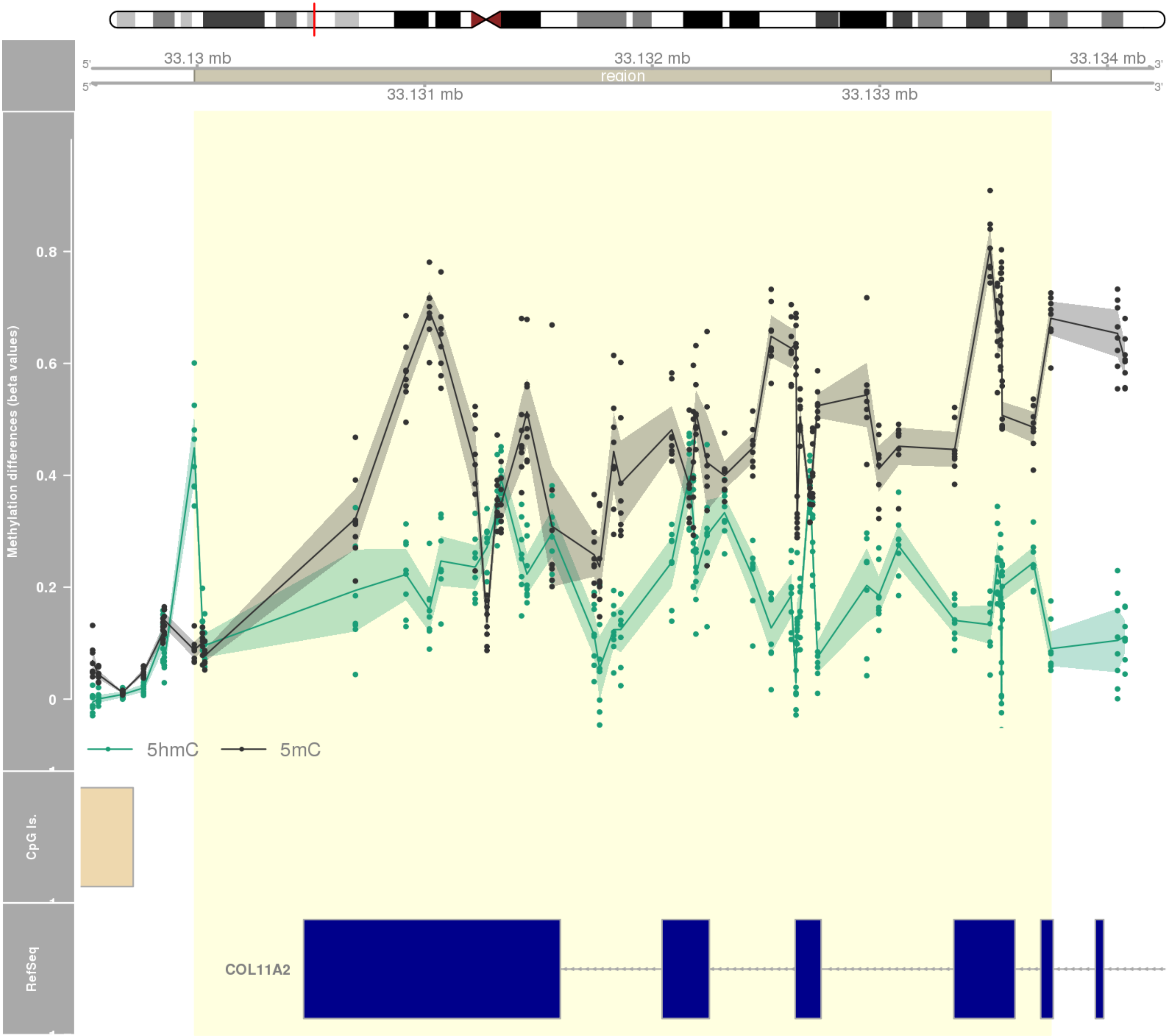
DMR 9 // chr6:33262579-33265393 // 2814 pb. (39 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0 // fwerArea: 0.111
- genes: PFDN6 / RGL2 -



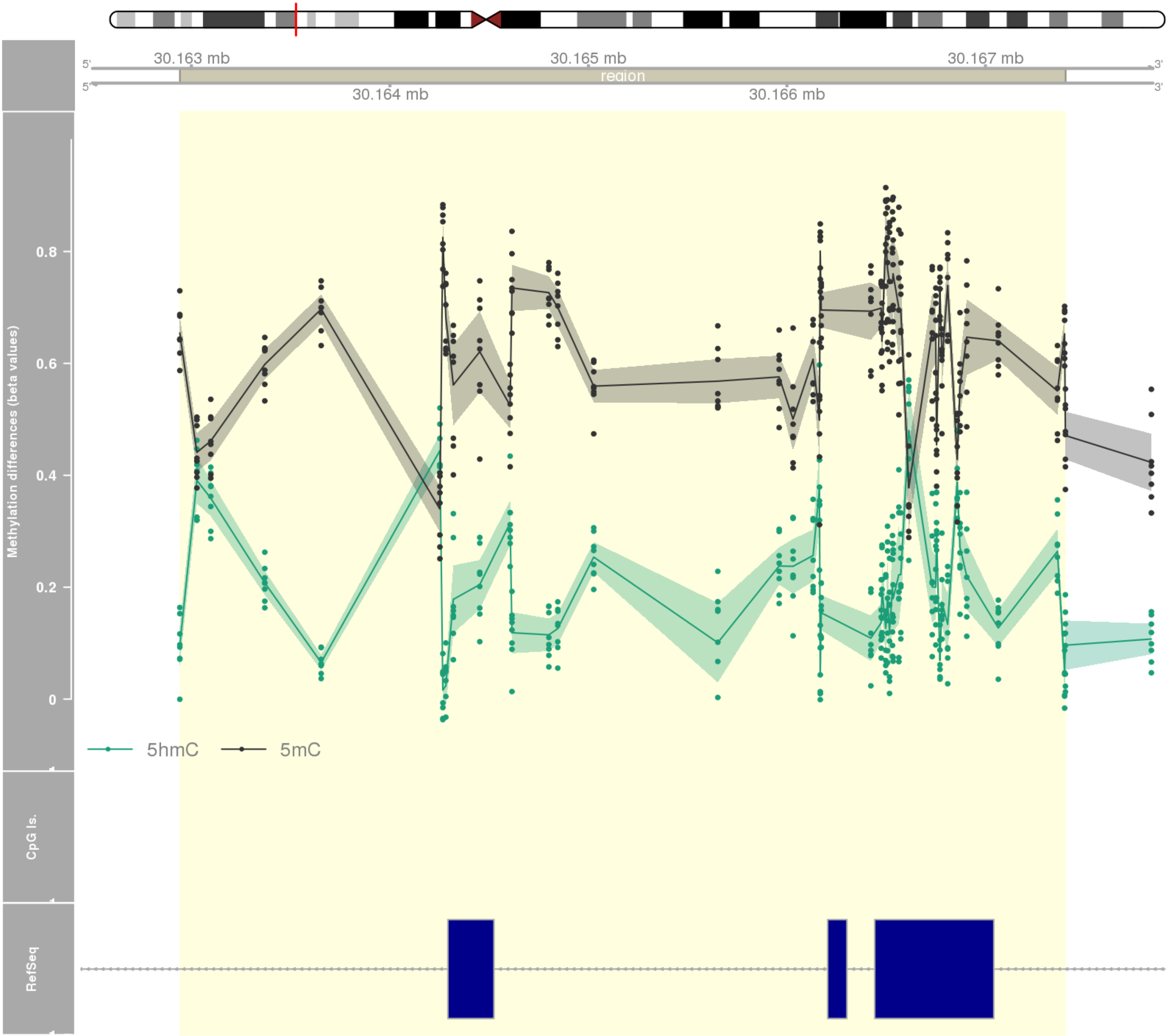
DMR 10 // chr6:31867698-31868965 // 1267 pb. (39 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: C2 / ZBTB12 -



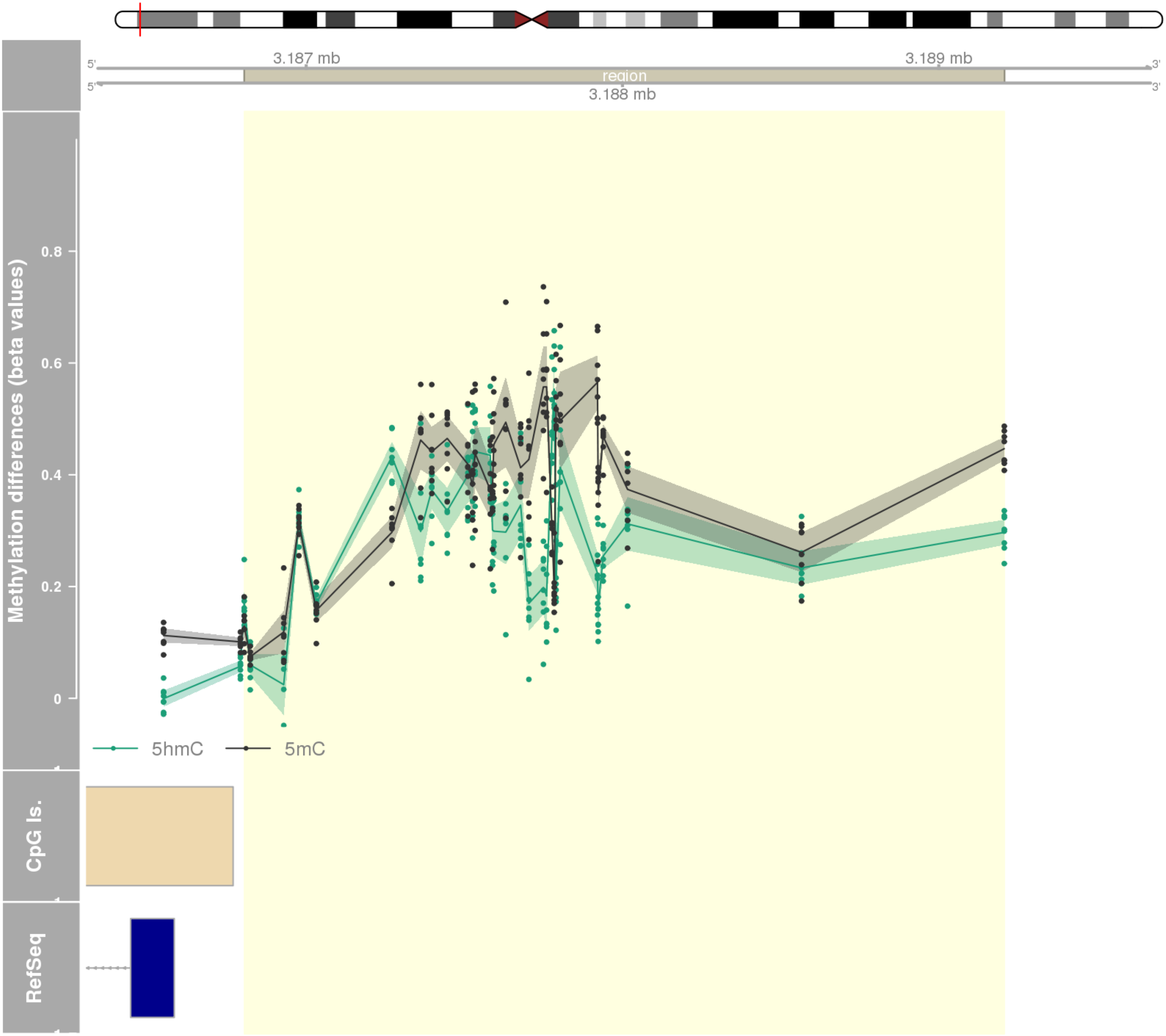
DMR 11 // chr6:33129988-33133752 // 3764 pb. (44 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: COL11A2 -



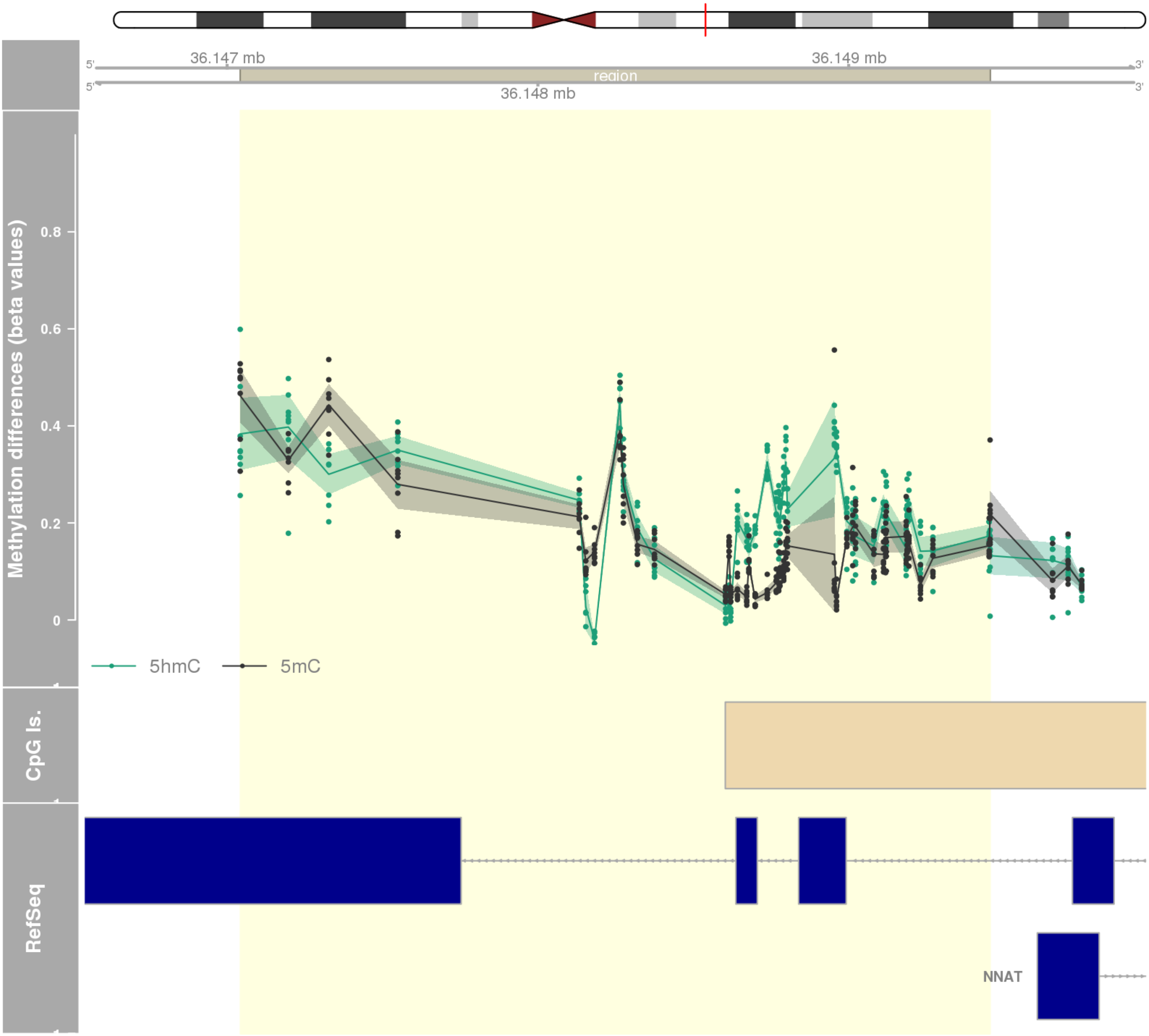
DMR 12 // chr6:30162942-30167403 // 4461 pb. (46 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: TRIM26 -



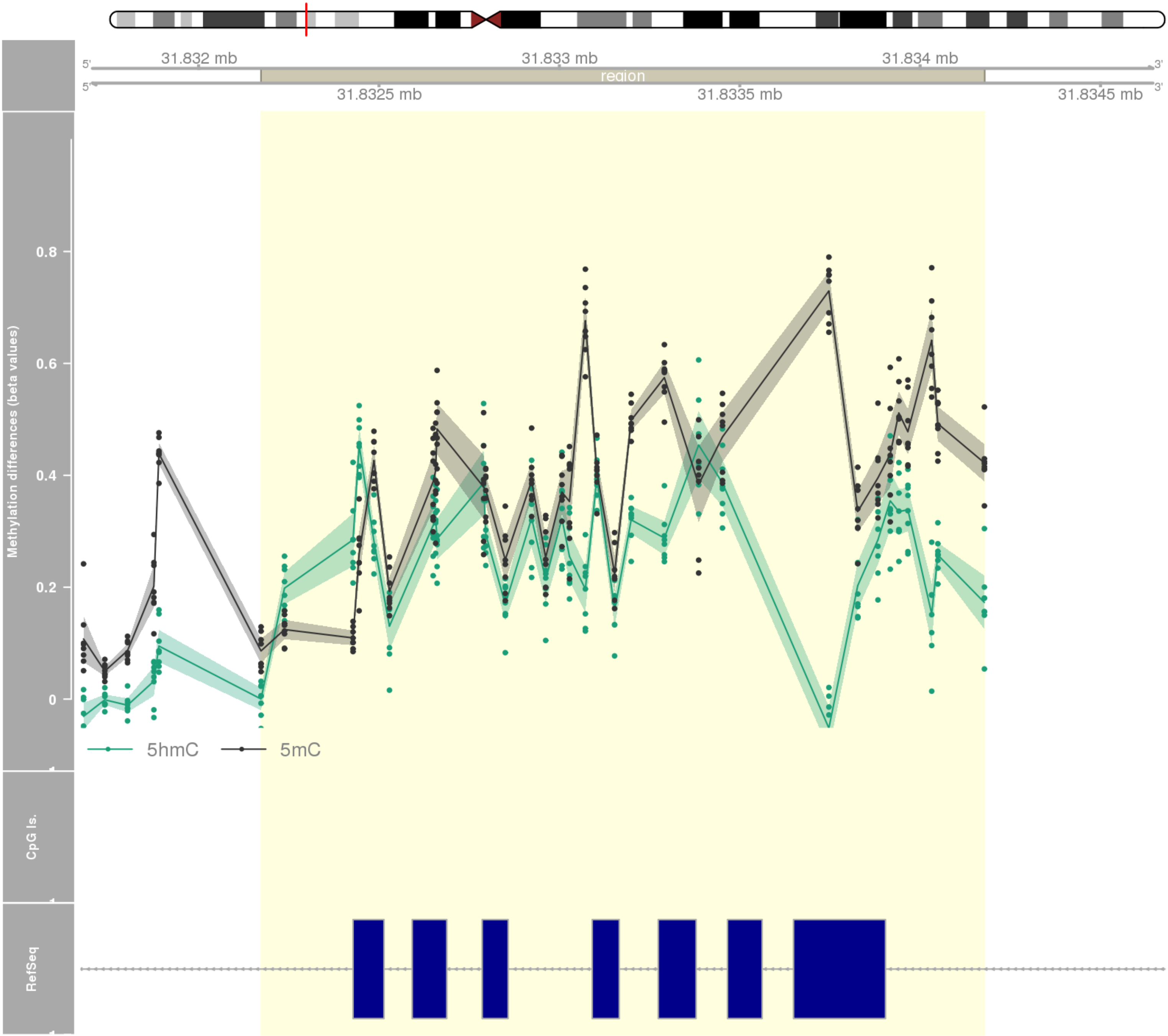
DMR 13 // chr11:3186804-3189207 // 2403 pb. (30 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: OSBPL5 -



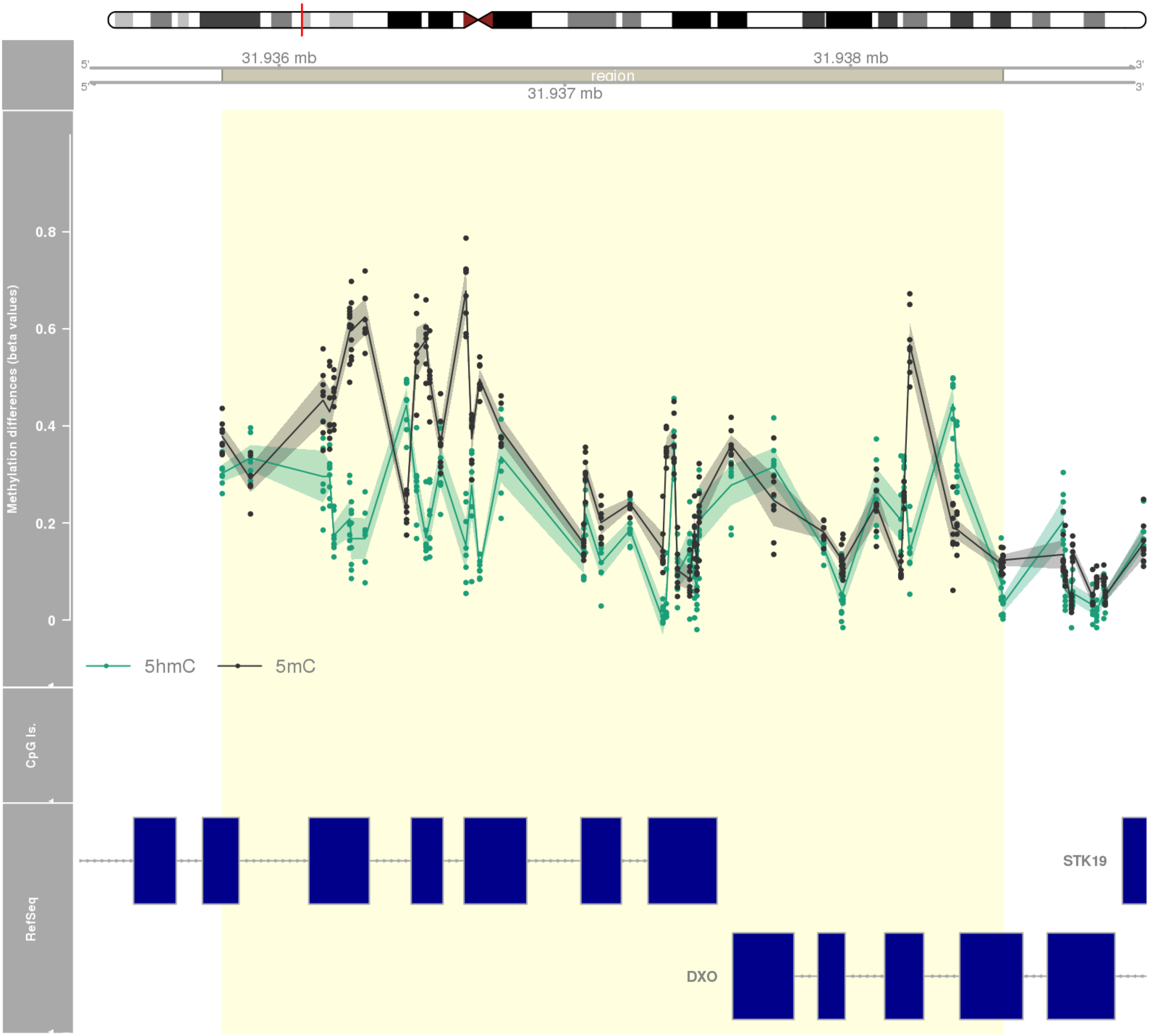
DMR 14 // chr20:36147042-36149455 // 2413 pb. (41 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: BLCAP -



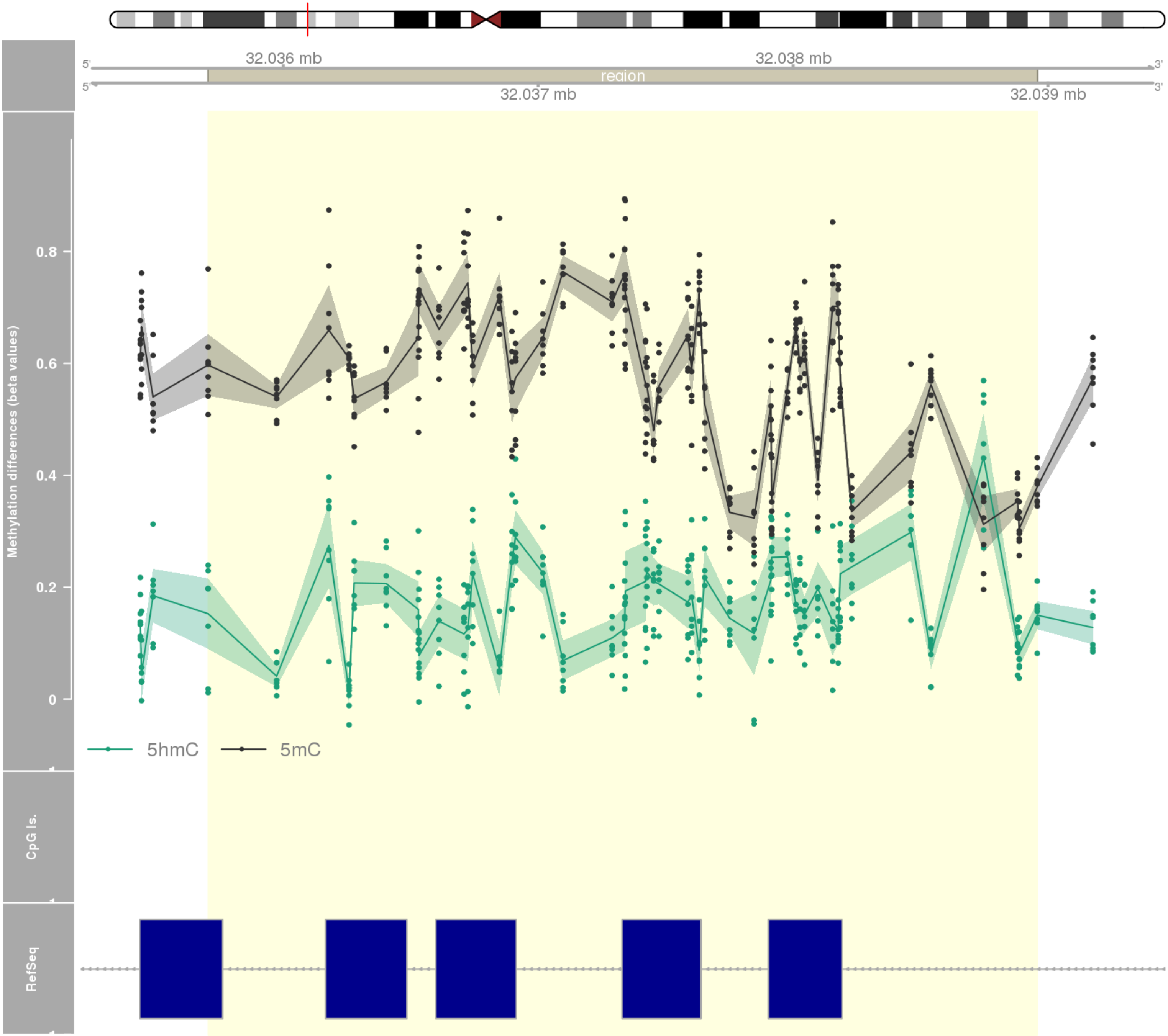
DMR 15 // chr6:31832173-31834178 // 2005 pb. (32 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: SLC44A4 -



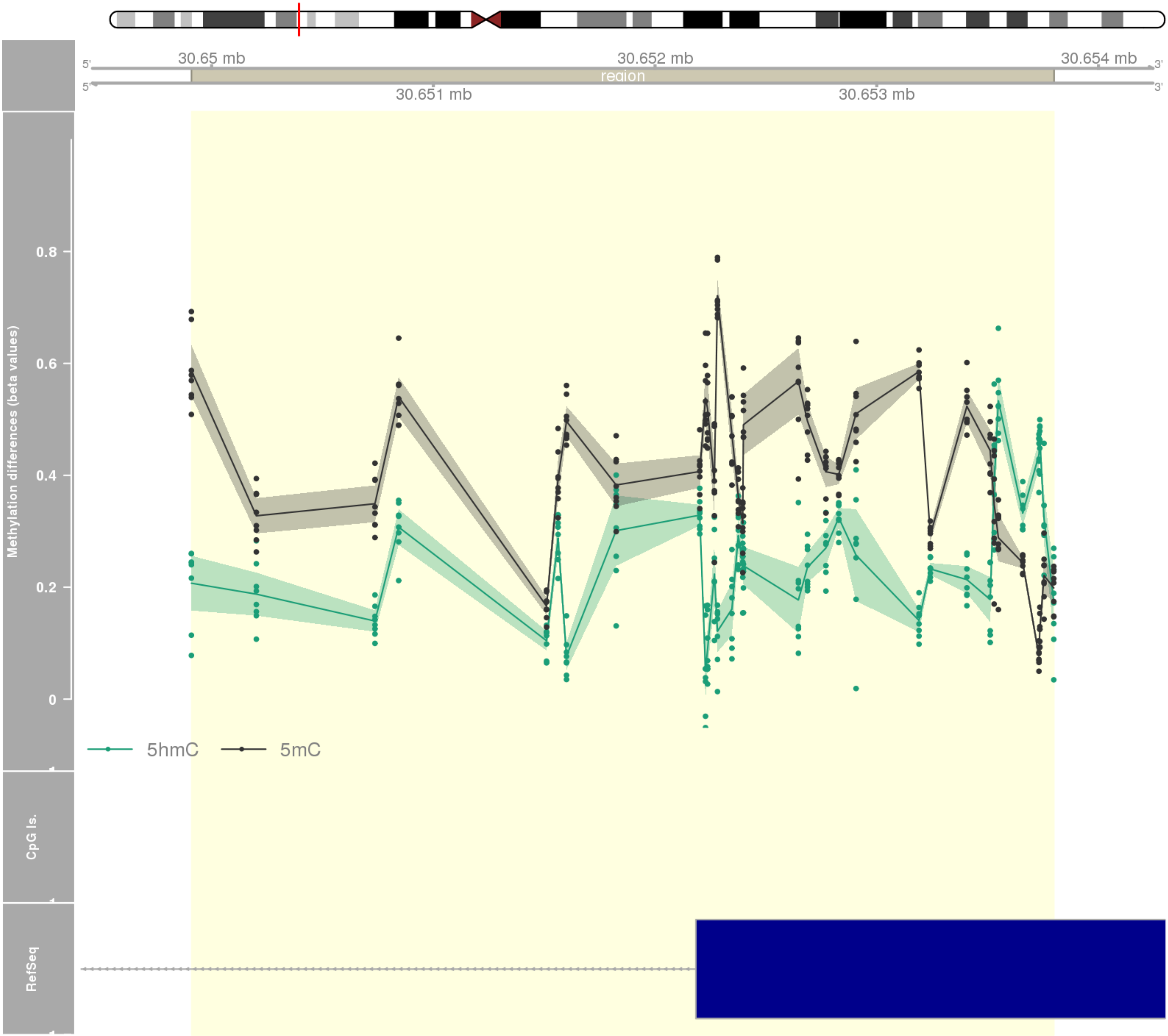
DMR 16 // chr6:31935801-31938533 // 2732 pb. (42 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: SKIV2L / DXO -



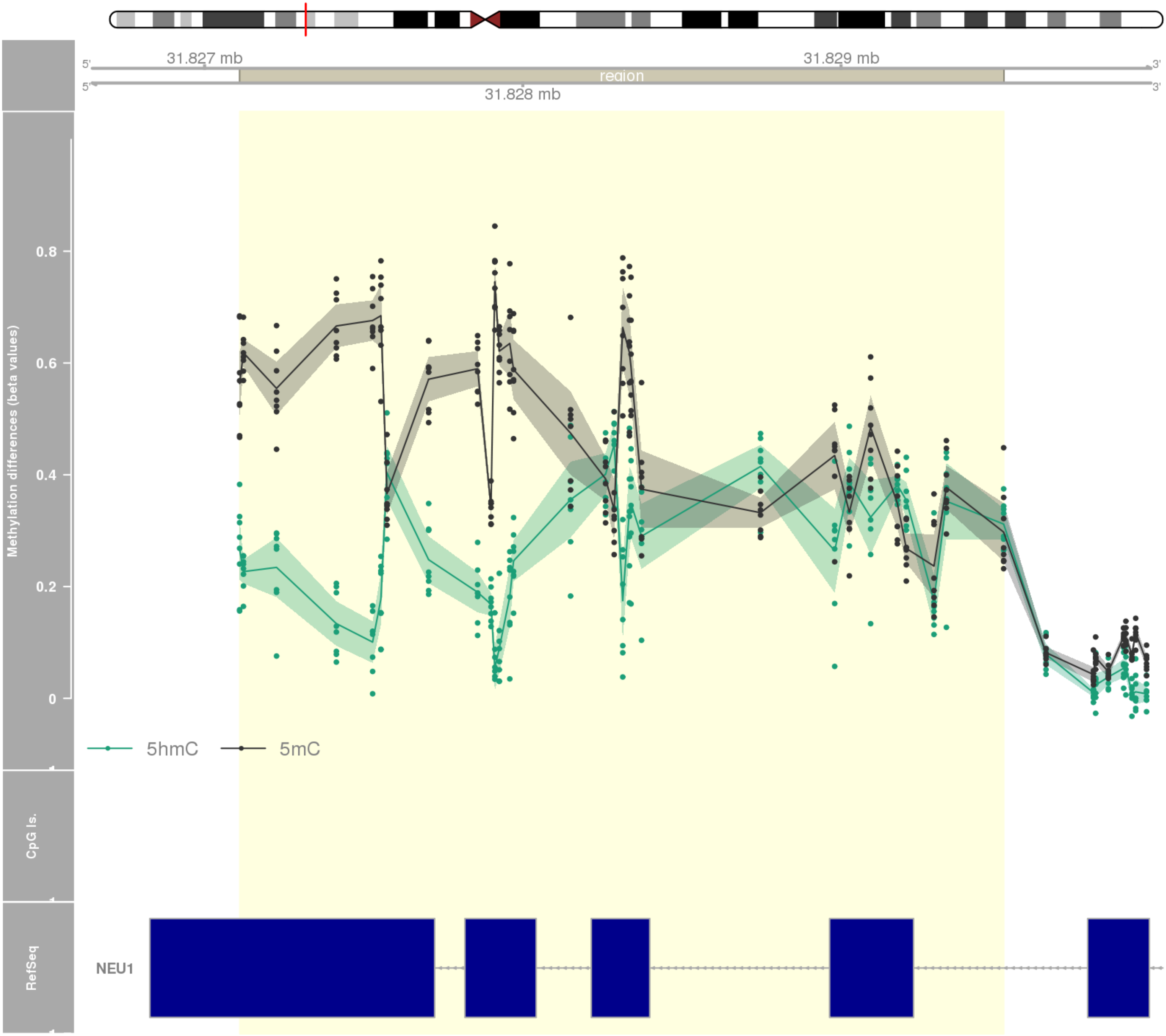
DMR 17 // chr6:32035705-32038958 // 3253 pb. (47 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: TNXB -



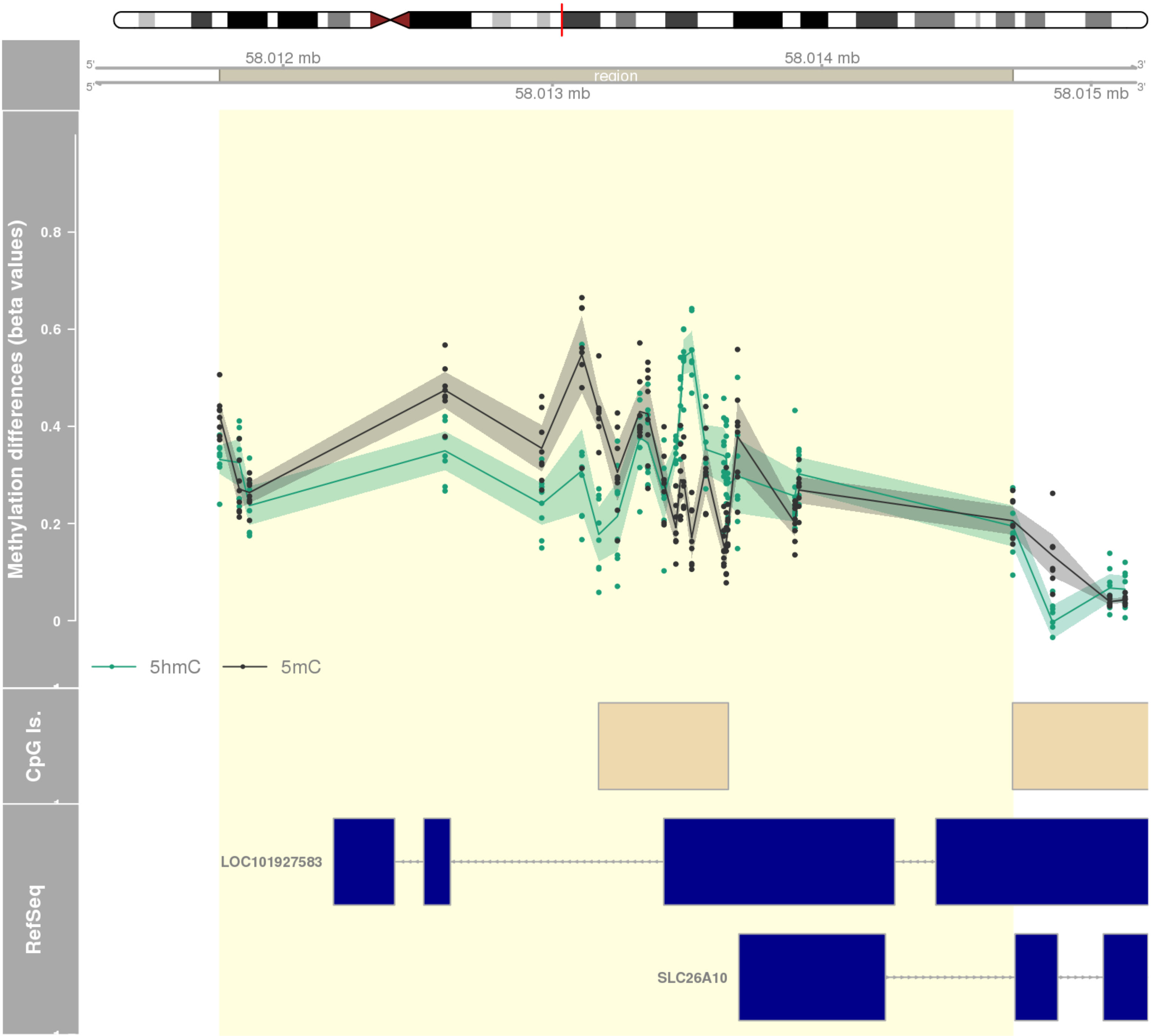
DMR 18 // chr6:30649909-30653799 // 3890 pb. (33 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: PPP1R18 -



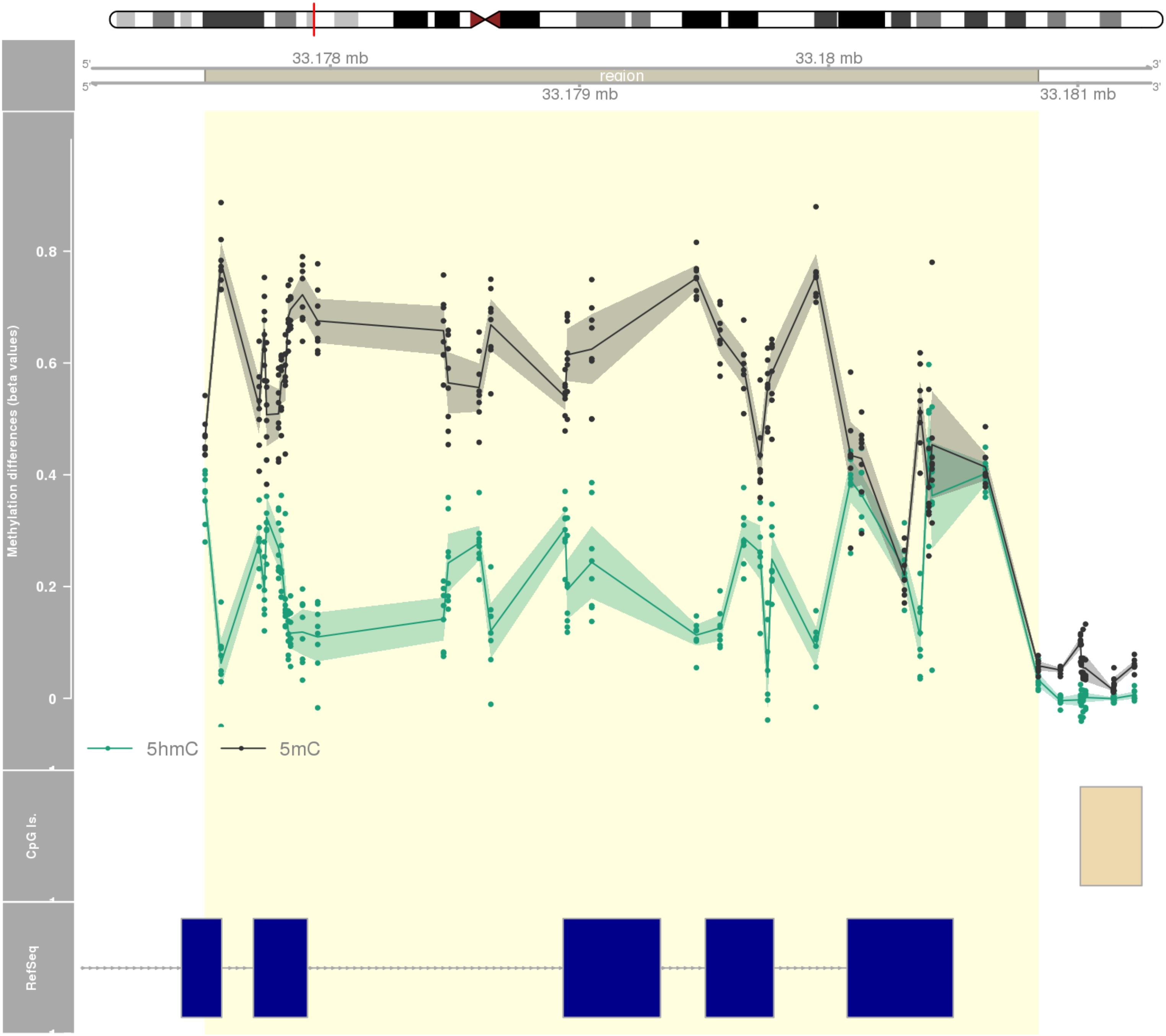
DMR 19 // chr6:31827110-31829511 // 2401 pb. (30 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: NEU1 -



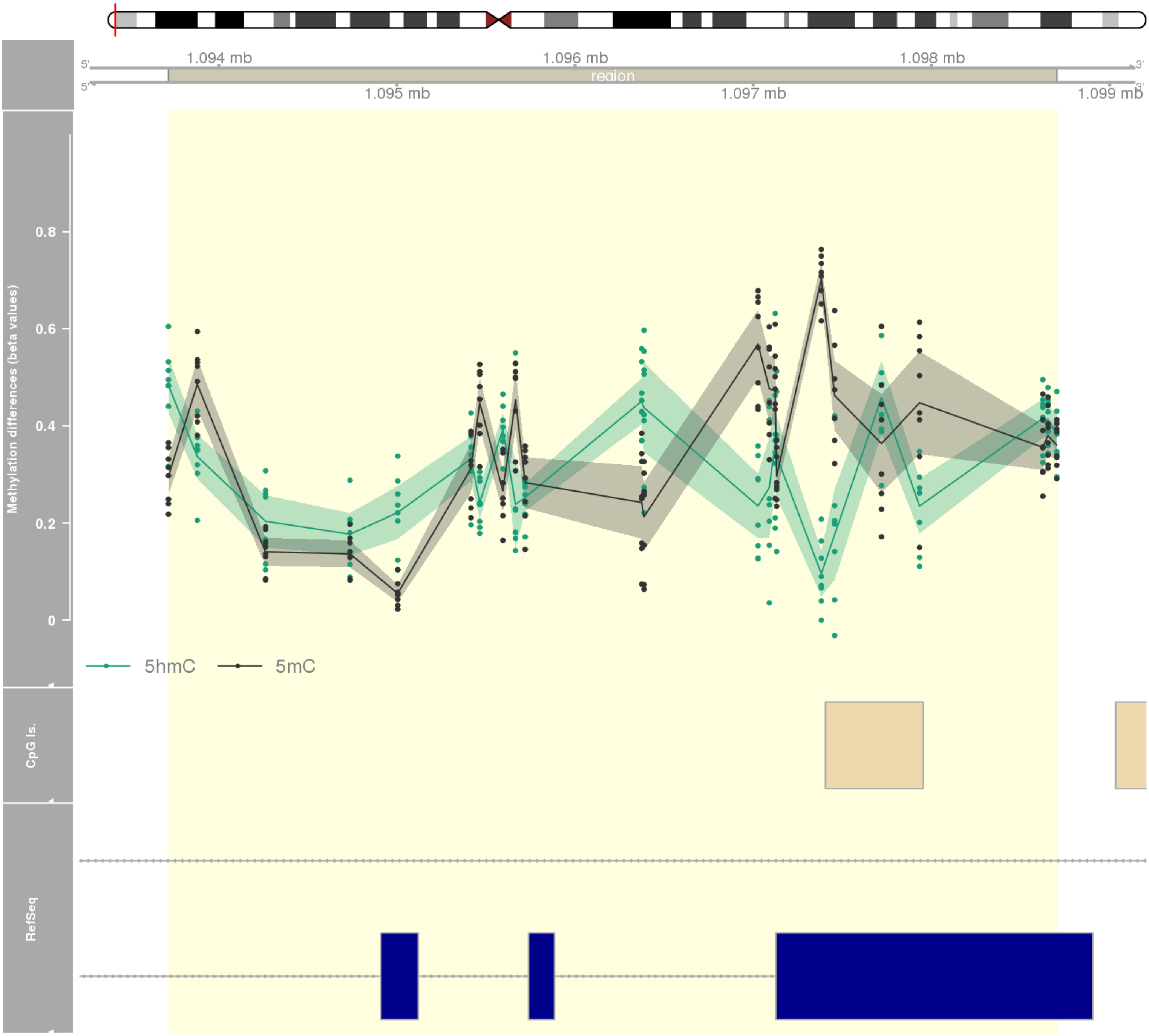
DMR 20 // chr12:58011764-58014709 // 2945 pb. (23 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: ARHGEF25 / SLC26A10 -



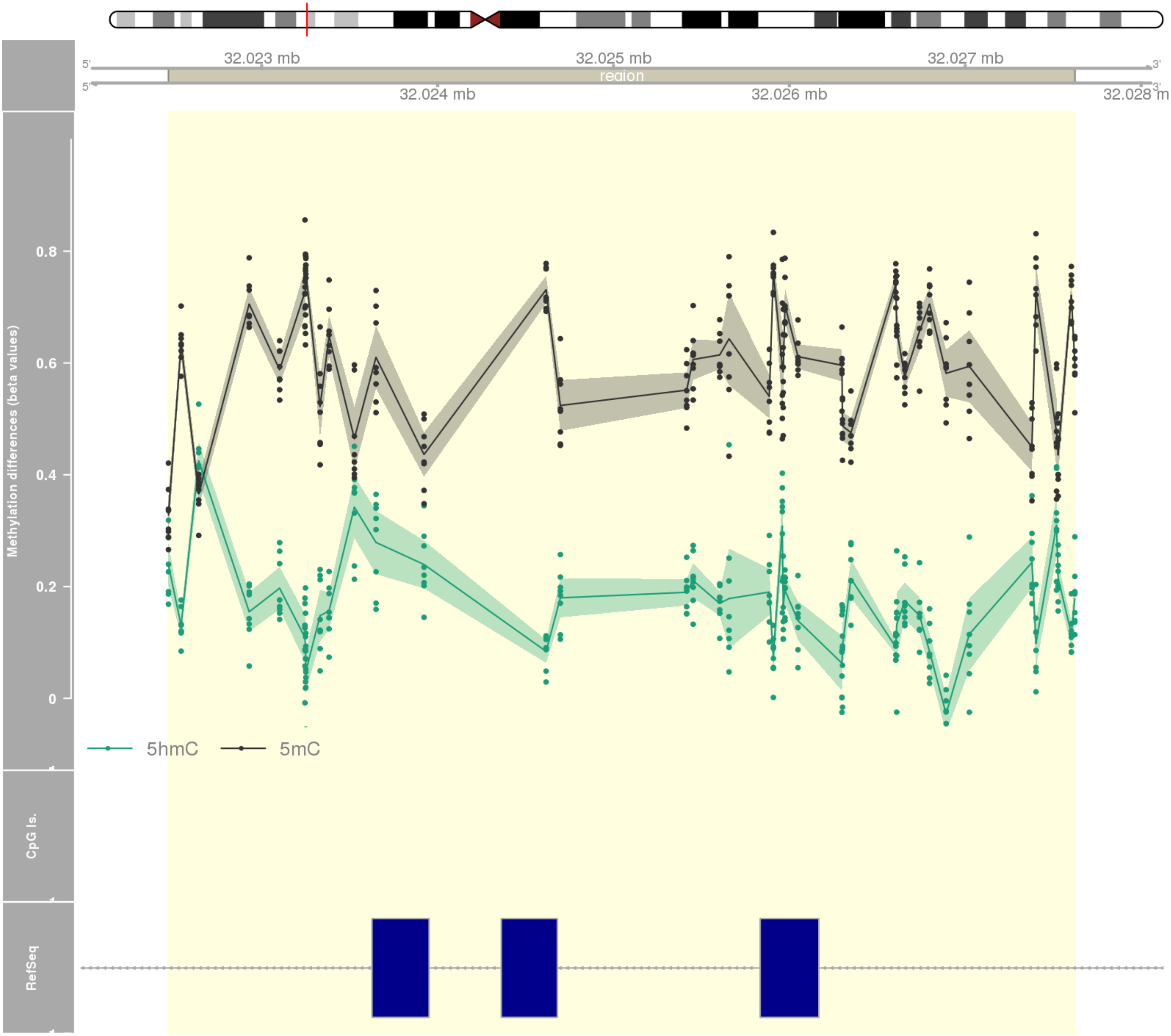
DMR 21 // chr6:33177497-33180841 // 3344 pb. (34 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: RING1 -



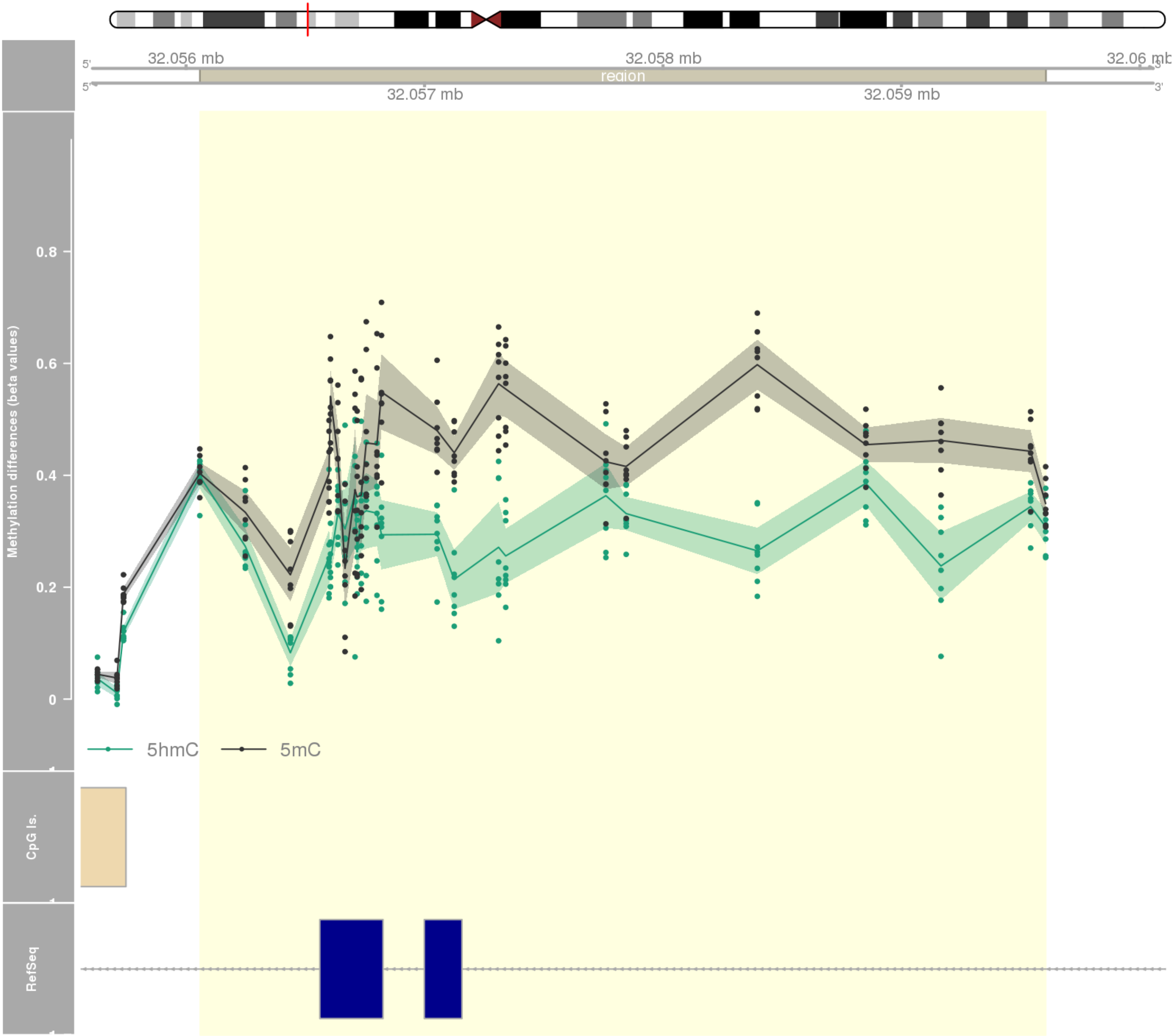
DMR 22 // chr7:1093718-1098703 // 4985 pb. (23 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: C7orf50 / GPR146 -



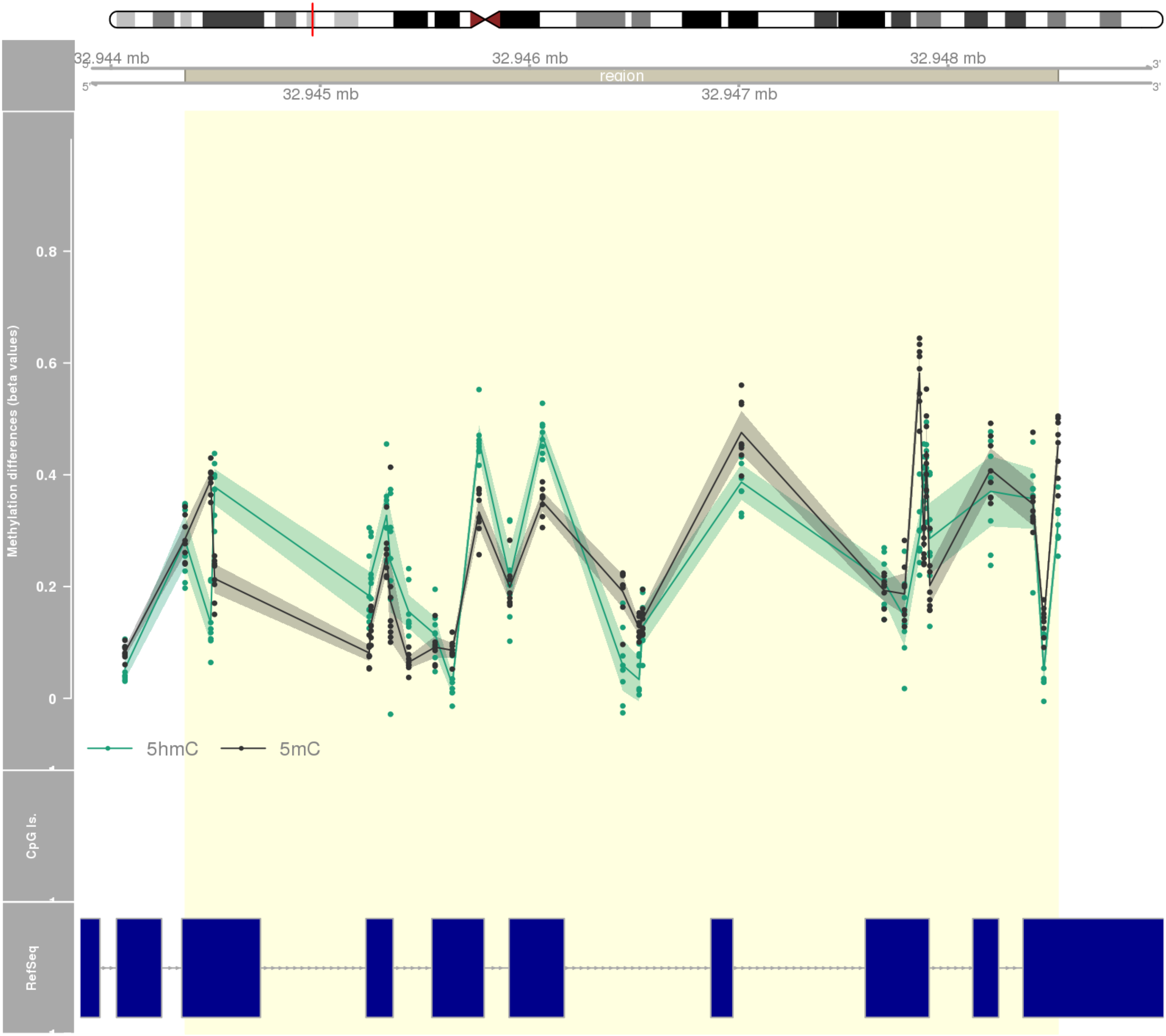
DMR 23 // chr6:32022470-32027623 // 5153 pb. (41 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: TNXB -



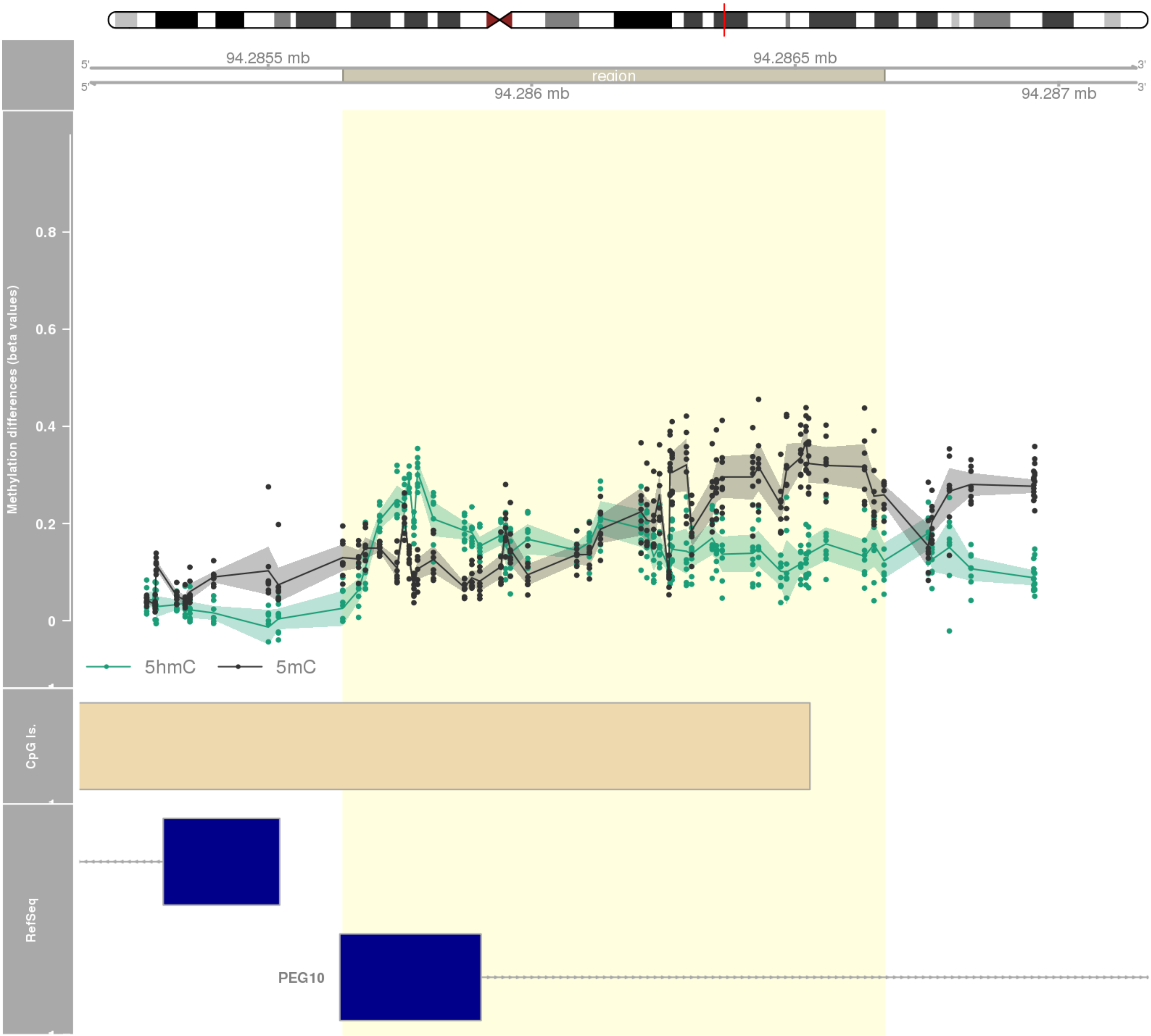
DMR 24 // chr6:32056058-32059605 // 3547 pb. (24 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.111
- genes: TNXB -



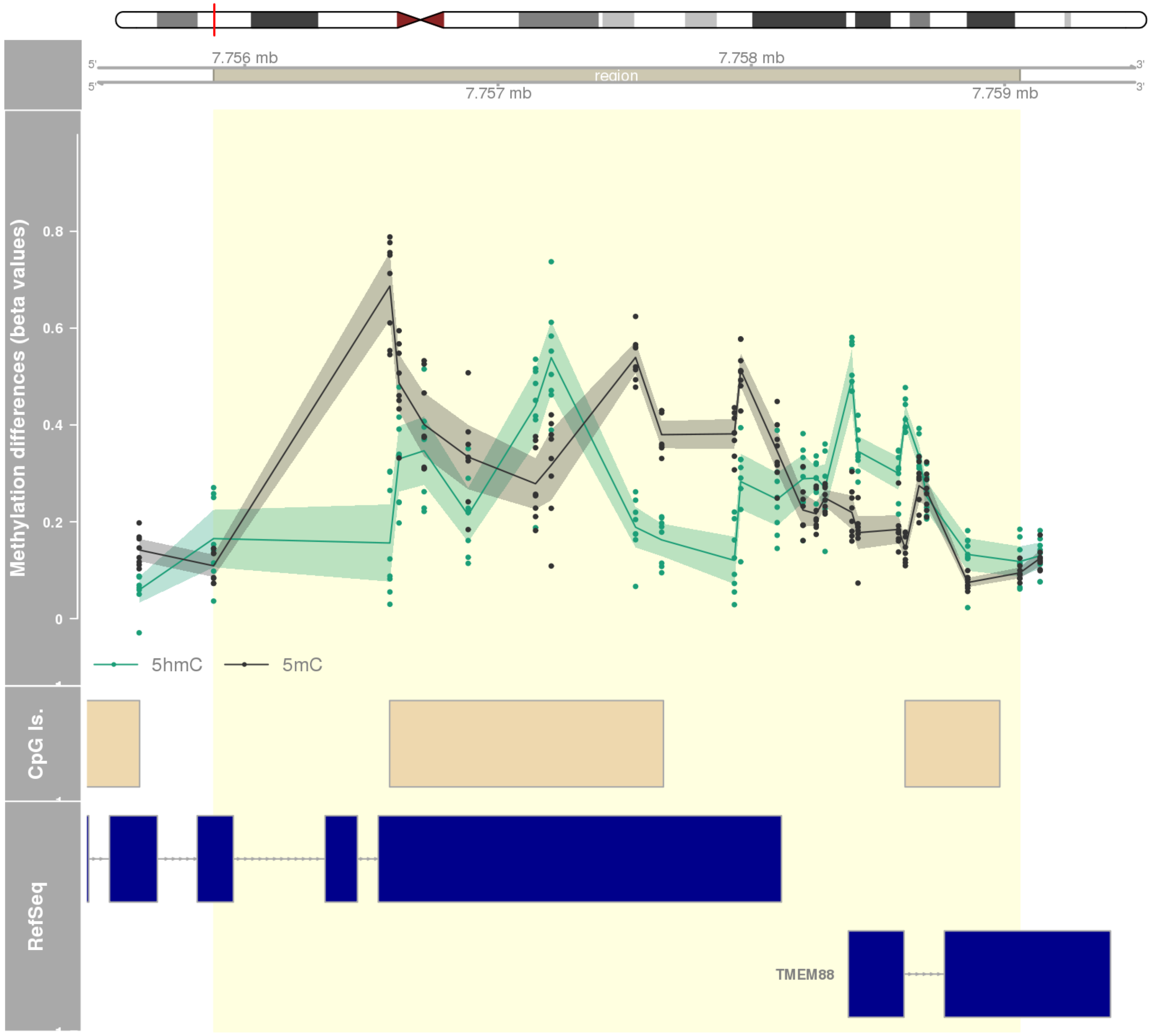
DMR 25 // chr6:32944354-32948526 // 4172 pb. (27 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.218
- genes: BRD2 -

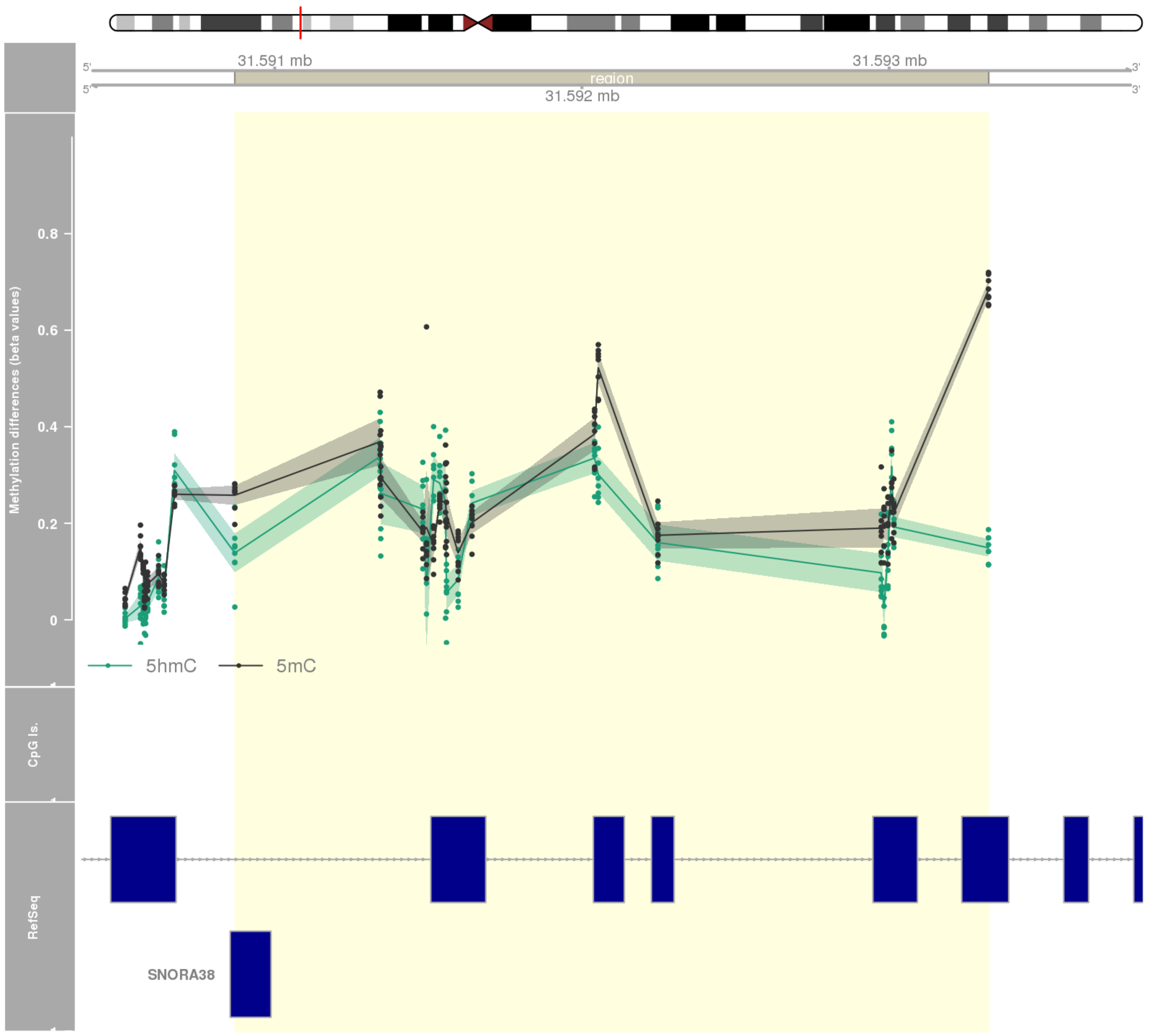


DMR 26 // chr7:94285642-94286669 // 1027 pb. (43 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.218
- genes: PEG10 -



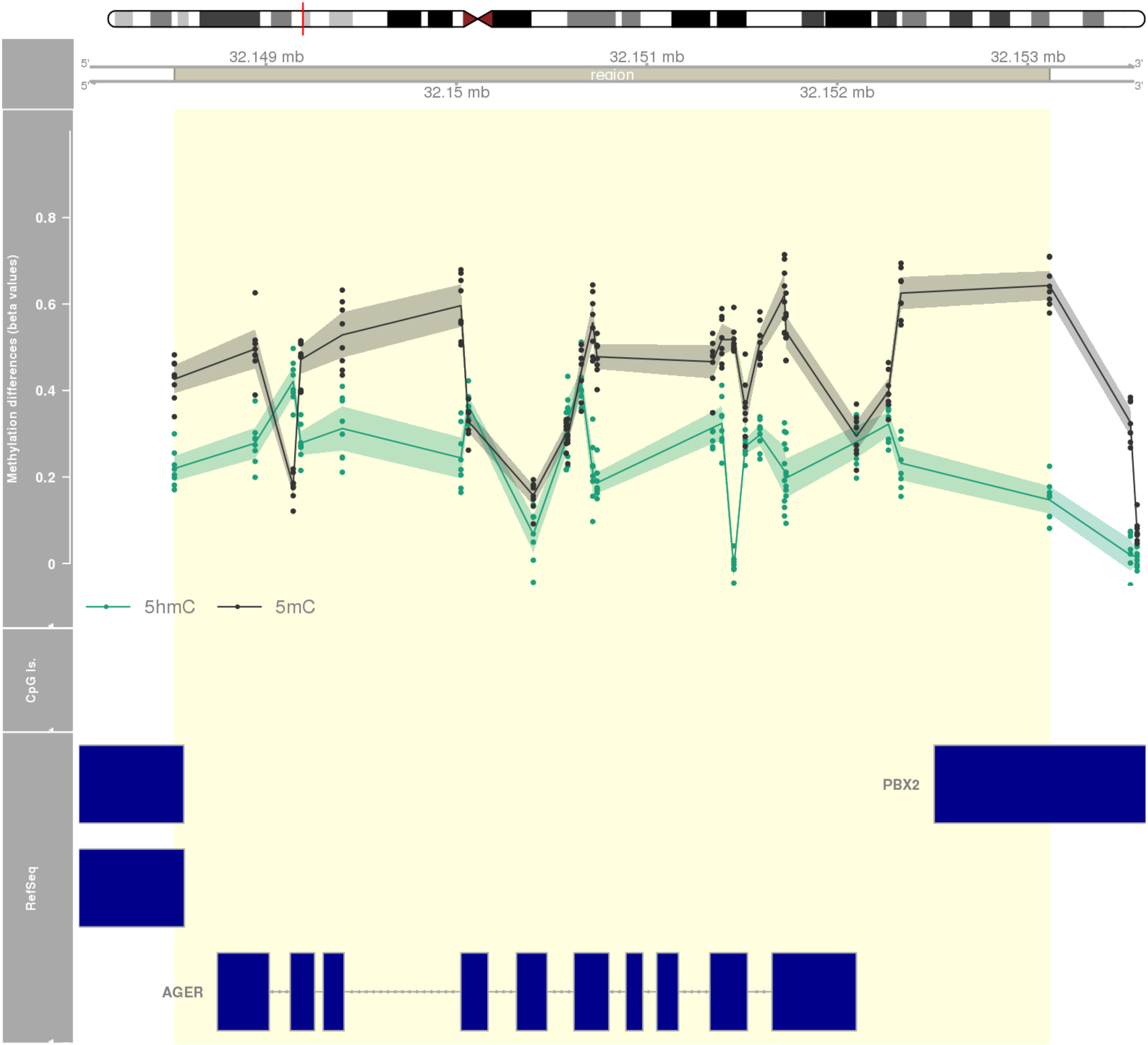
DMR 27 // chr17:7755877-7759060 // 3183 pb. (23 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.218
- genes: KDM6B / TMEM88 -



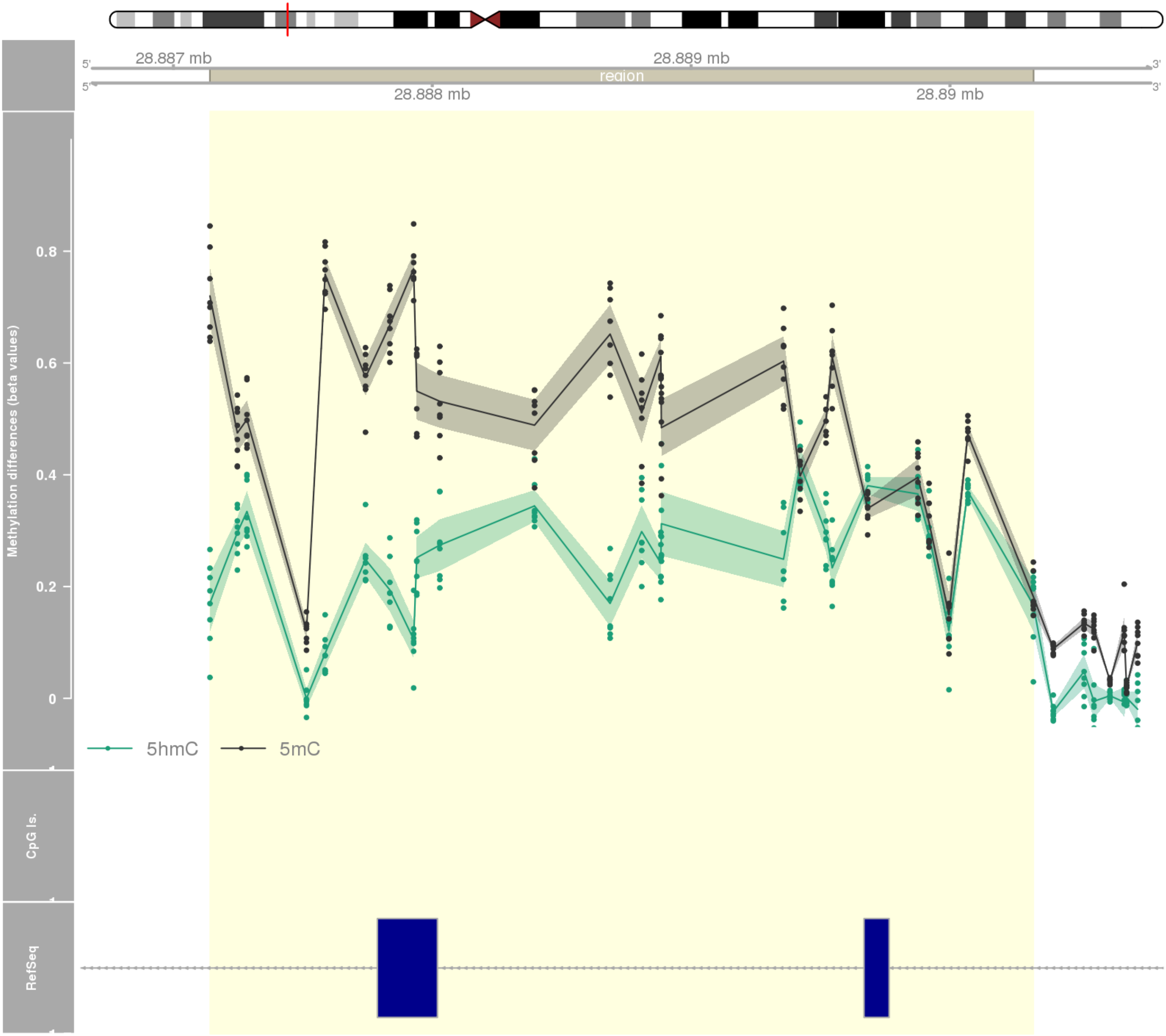


DMR 28 // chr6:31590870-31593323 // 2453 pb. (20 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.001 // fwerArea: 0.218
- genes: SNORA38 / PRRC2A -

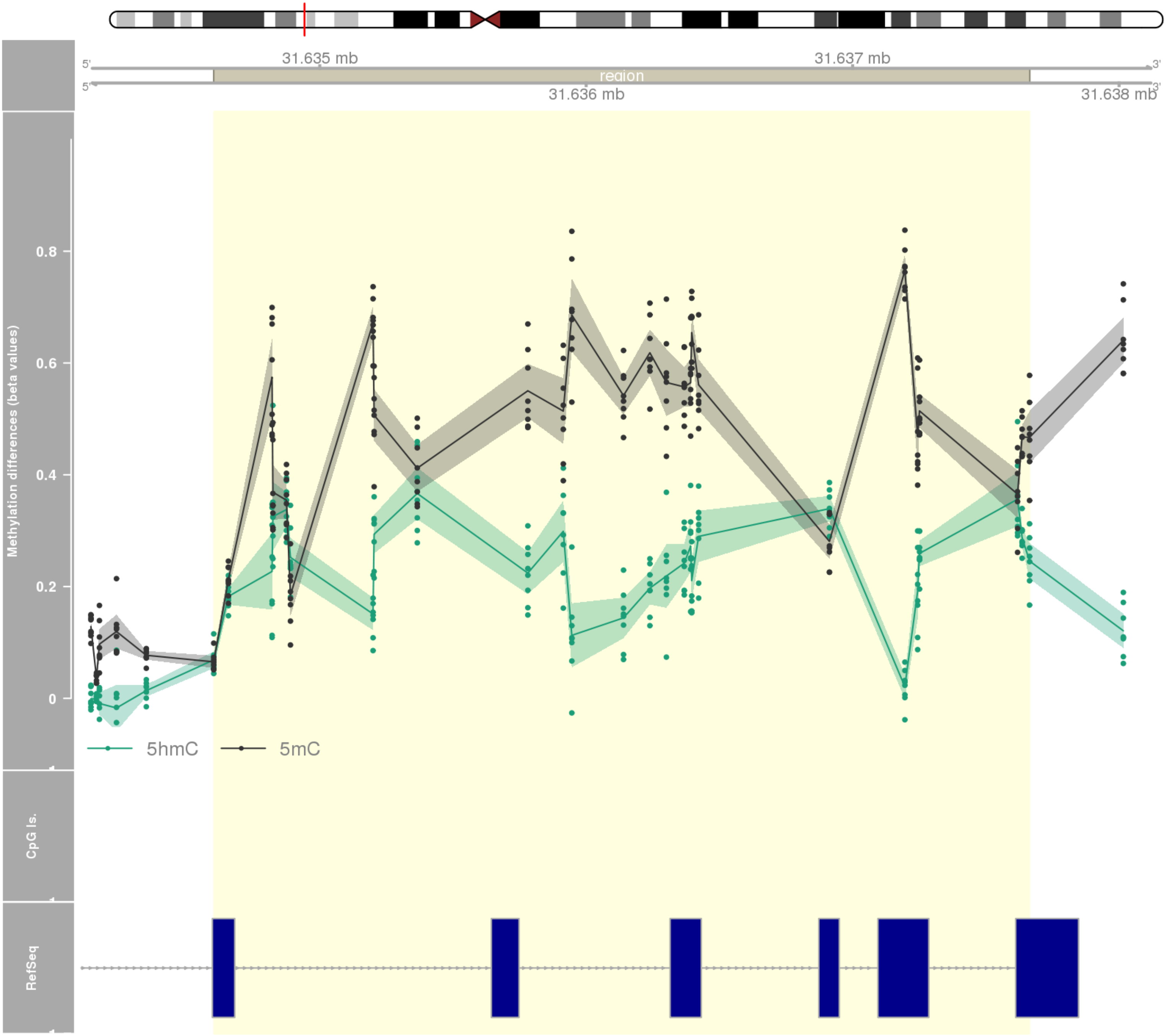
DMR 29 // chr6:32148519-32153115 // 4596 pb. (24 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: RNF5 / AGER / PBX2 -



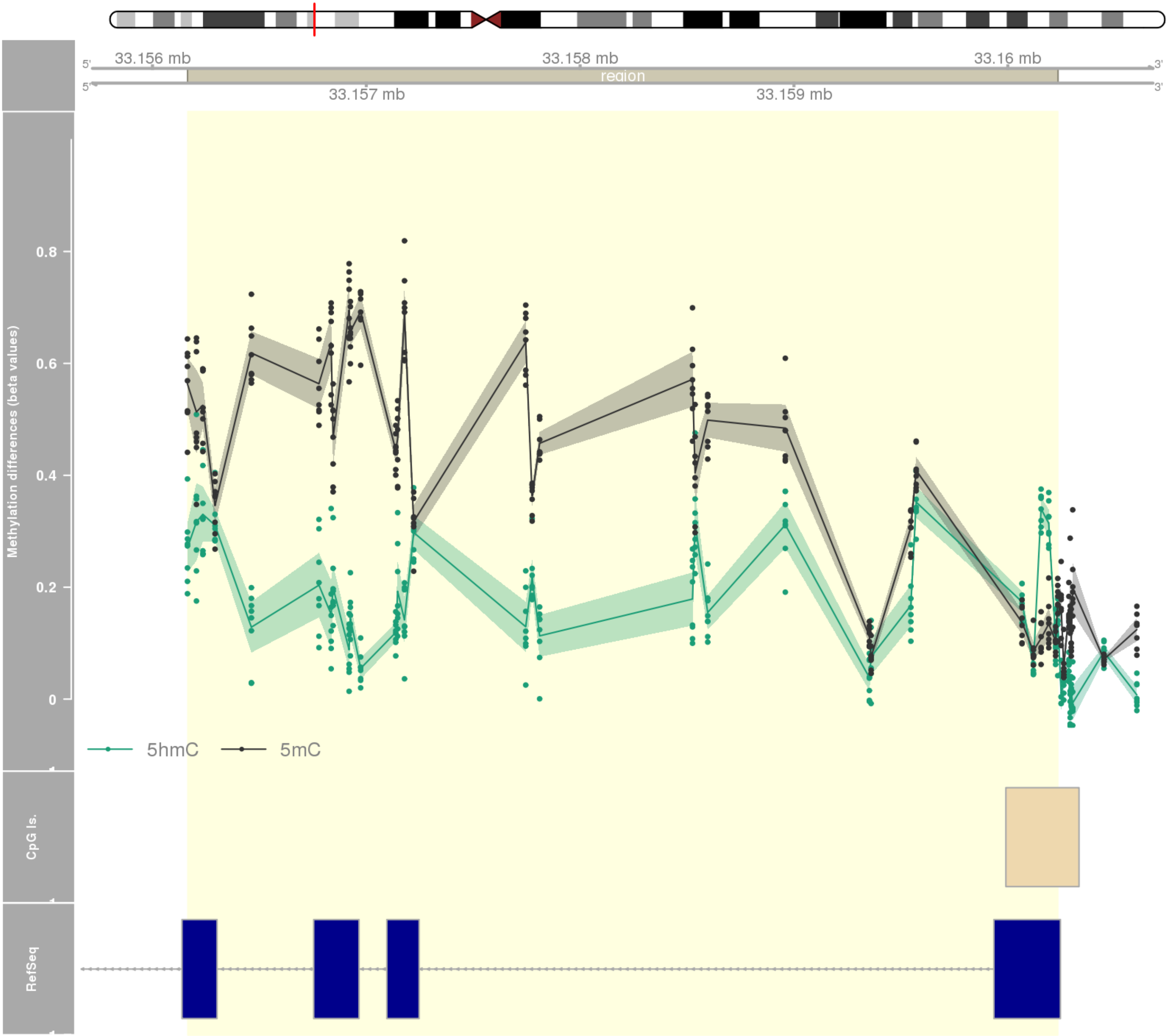
DMR 30 // chr6:28887141-28890322 // 3181 pb. (25 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: TRIM27 -



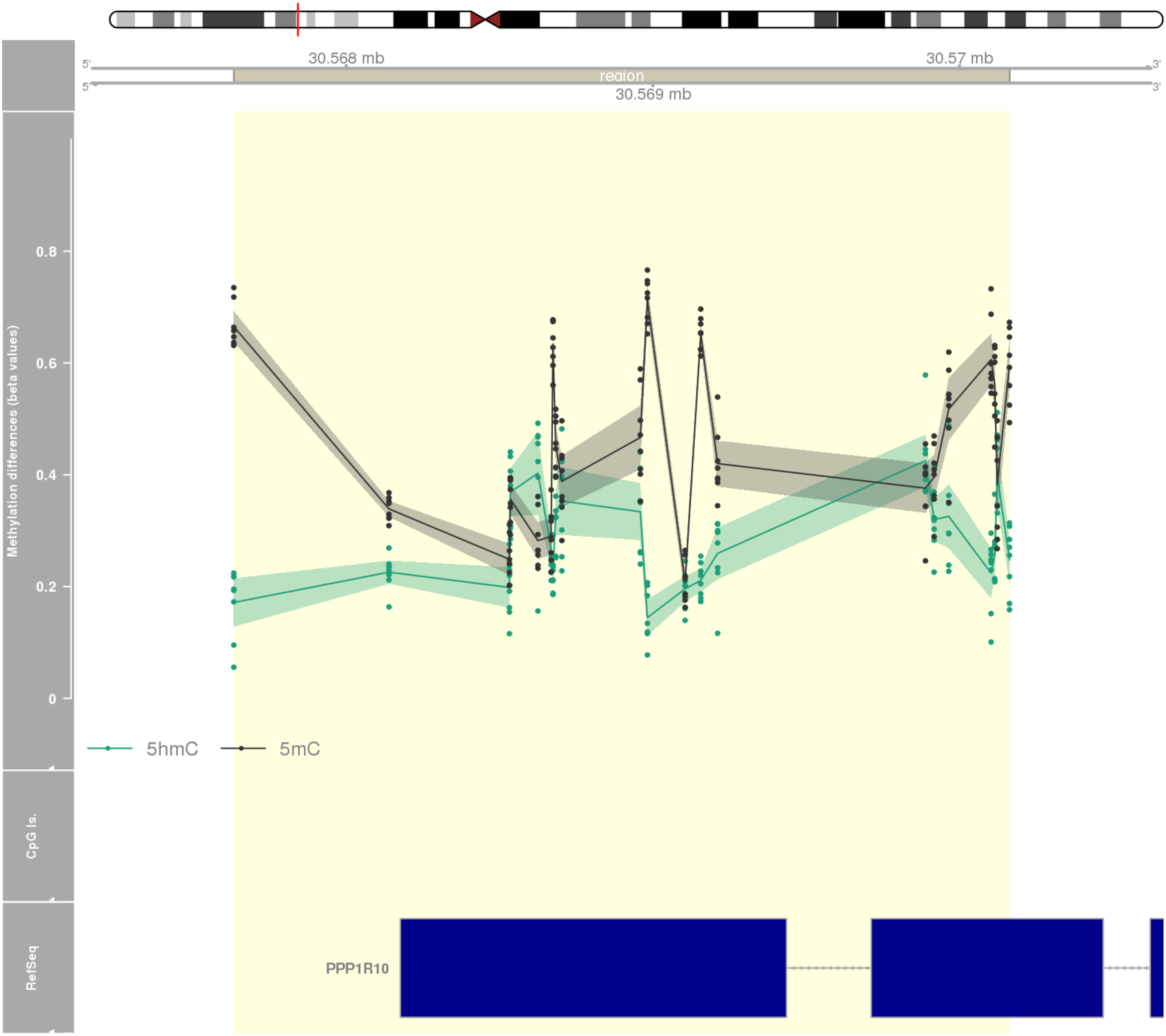
DMR 31 // chr6:31634602-31637664 // 3062 pb. (26 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: CSNK2B -



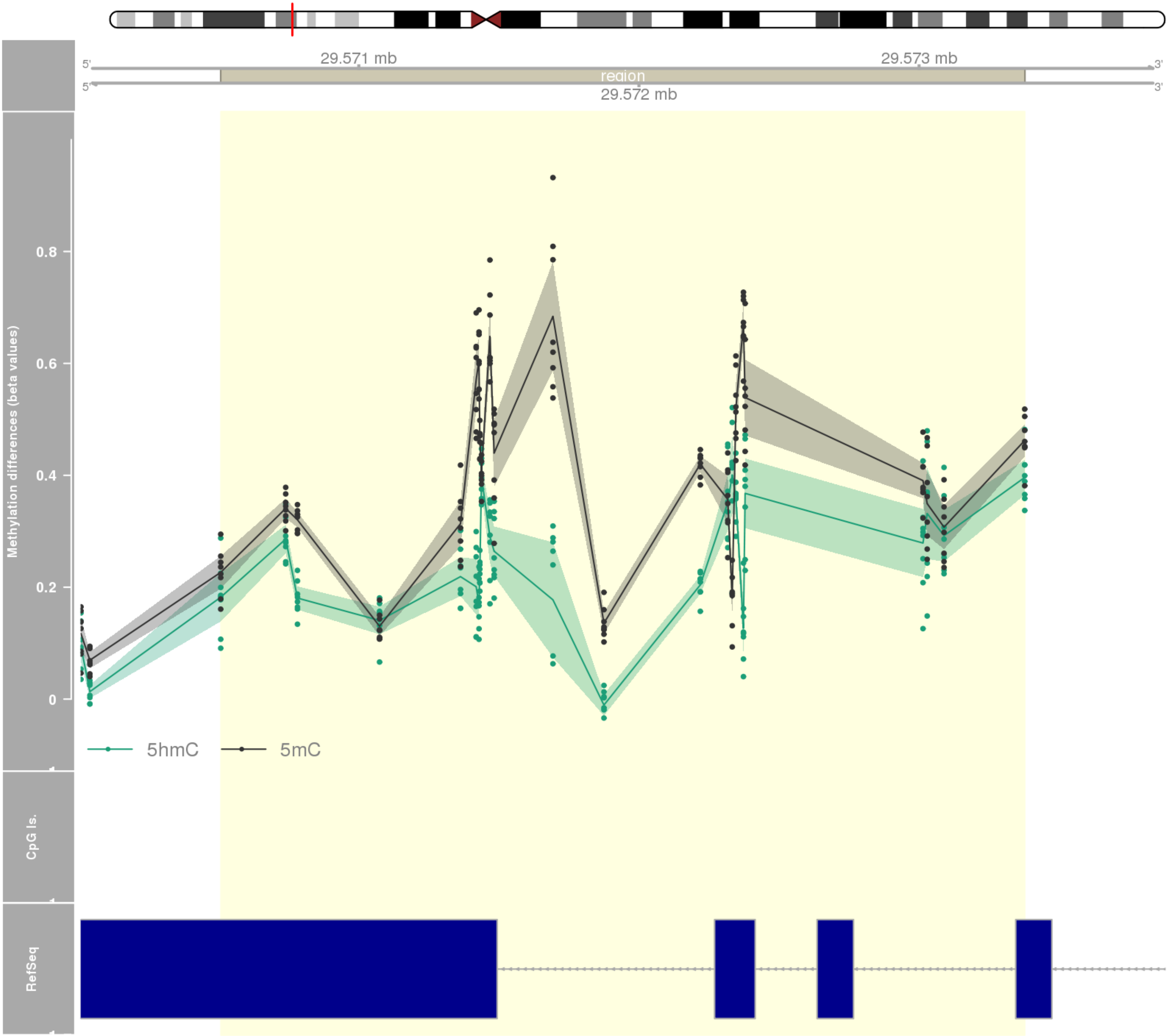
DMR 32 // chr6:33156164-33160234 // 4070 pb. (32 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: COL11A2 -



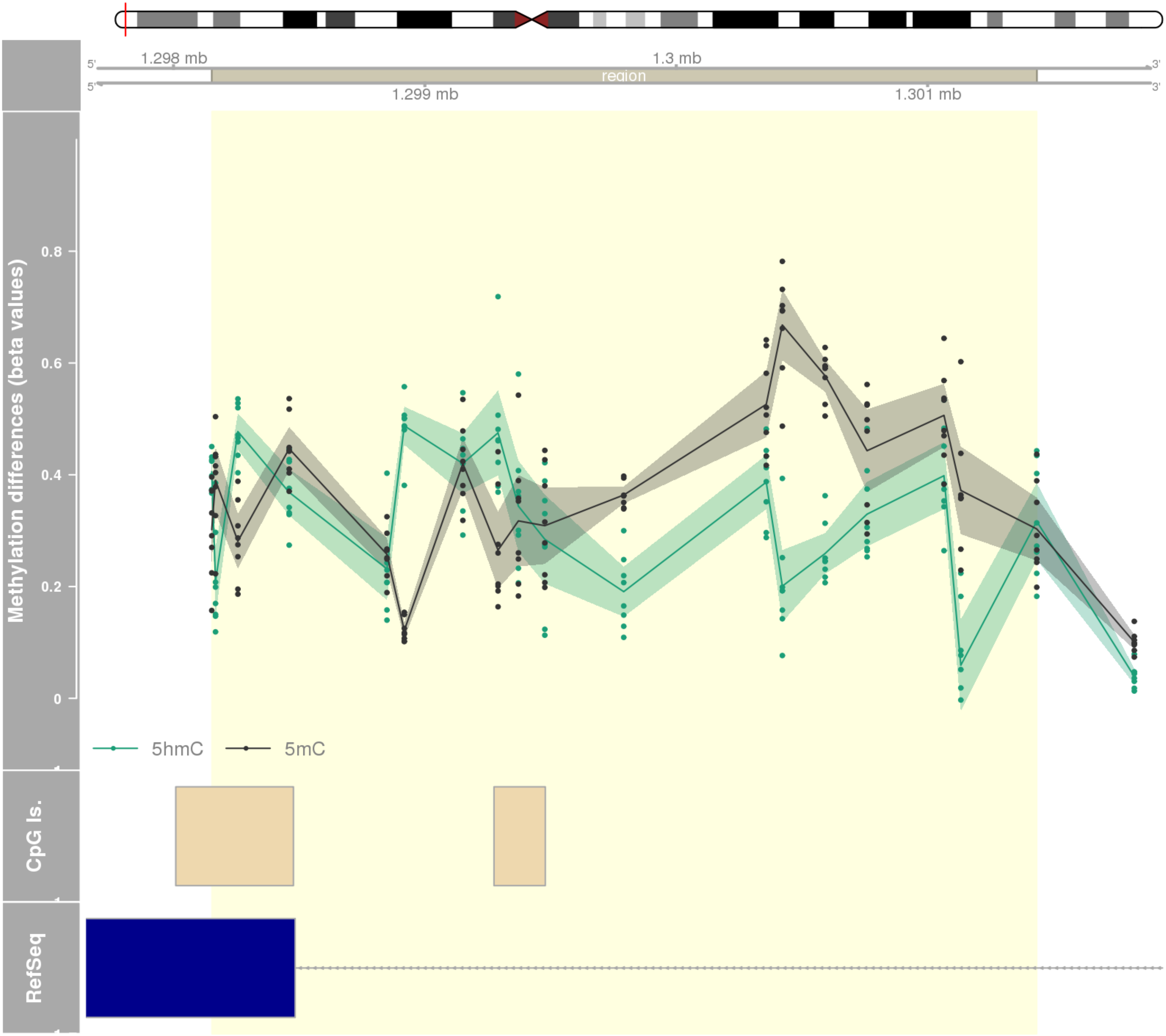
DMR 33 // chr6:30567633-30570163 // 2530 pb. (21 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: PPP1R10 -



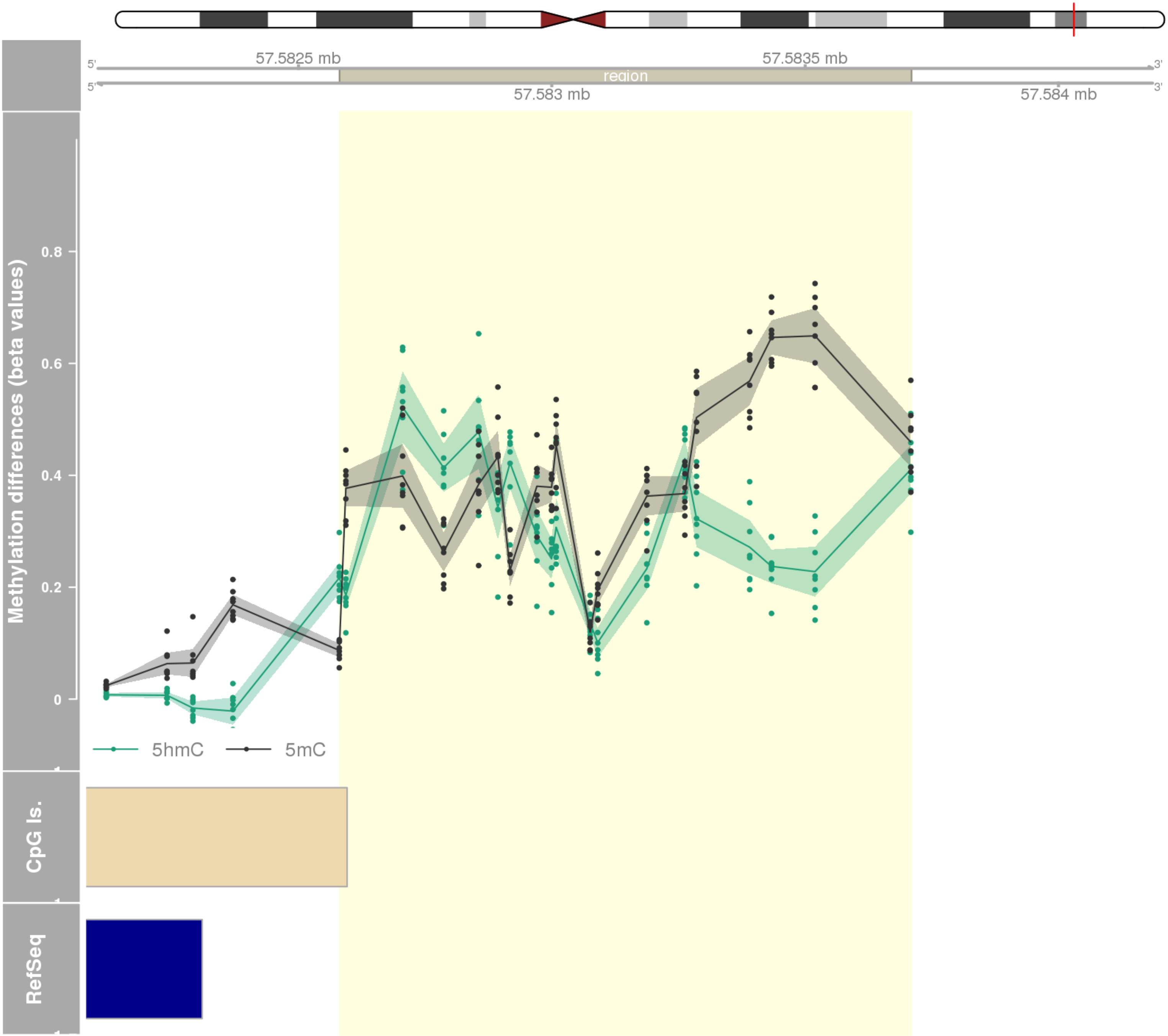
DMR 34 // chr6:29570507-29573377 // 2870 pb. (23 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: GABBR1 -



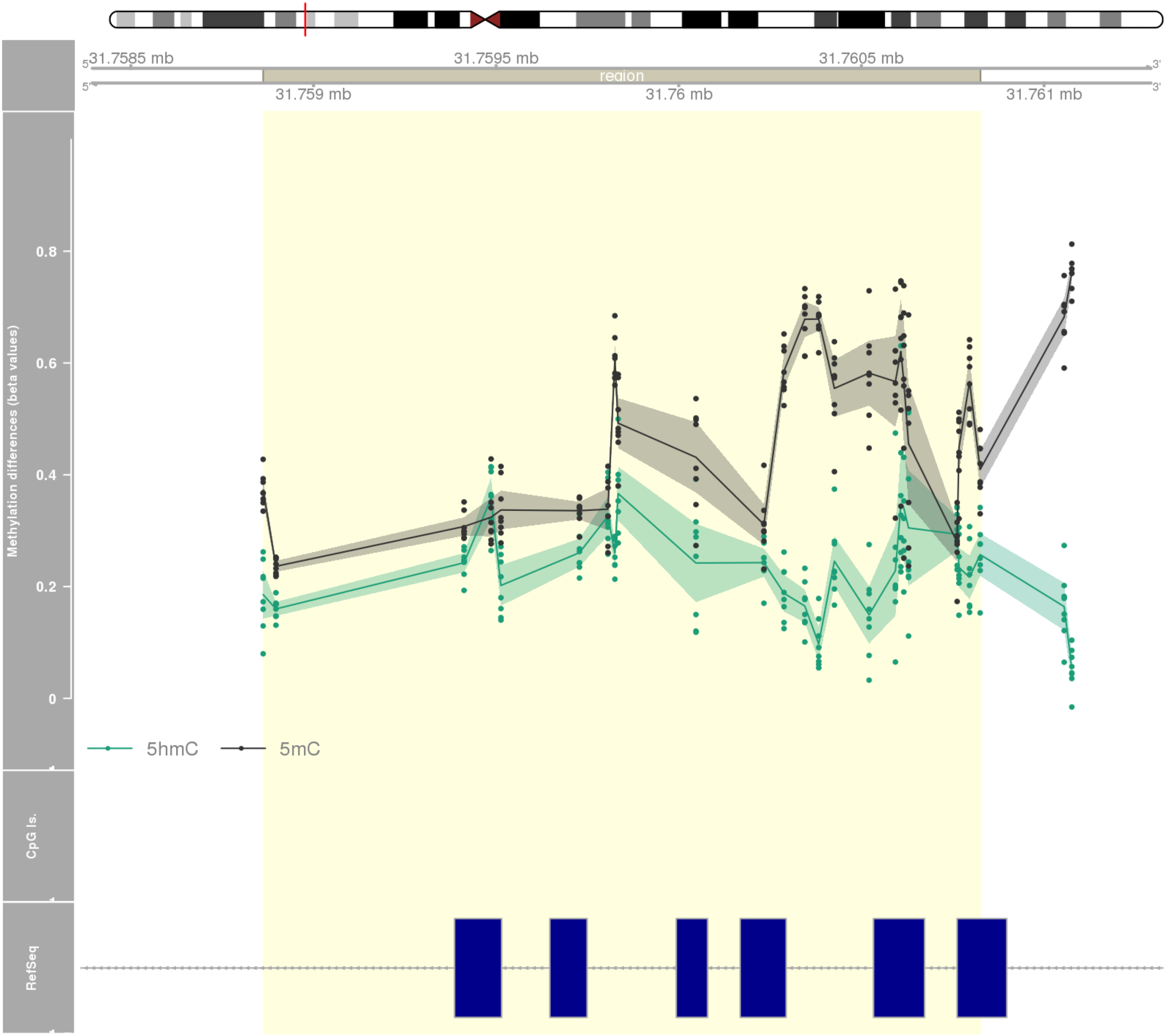
DMR 35 // chr11:1298152-1301434 // 3282 pb. (18 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: TOLLIP -



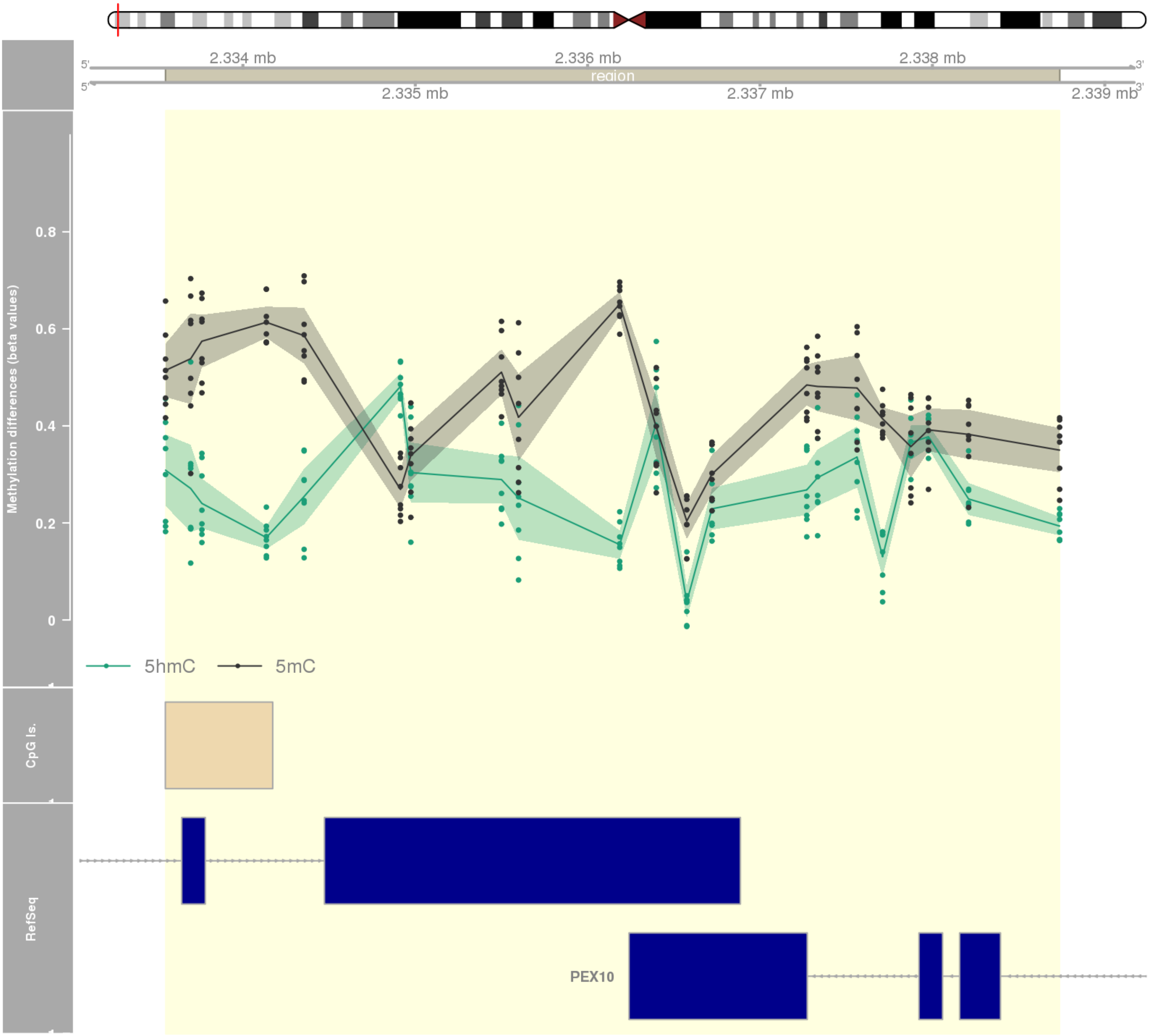
DMR 36 // chr20:57582581-57583709 // 1128 pb. (19 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218



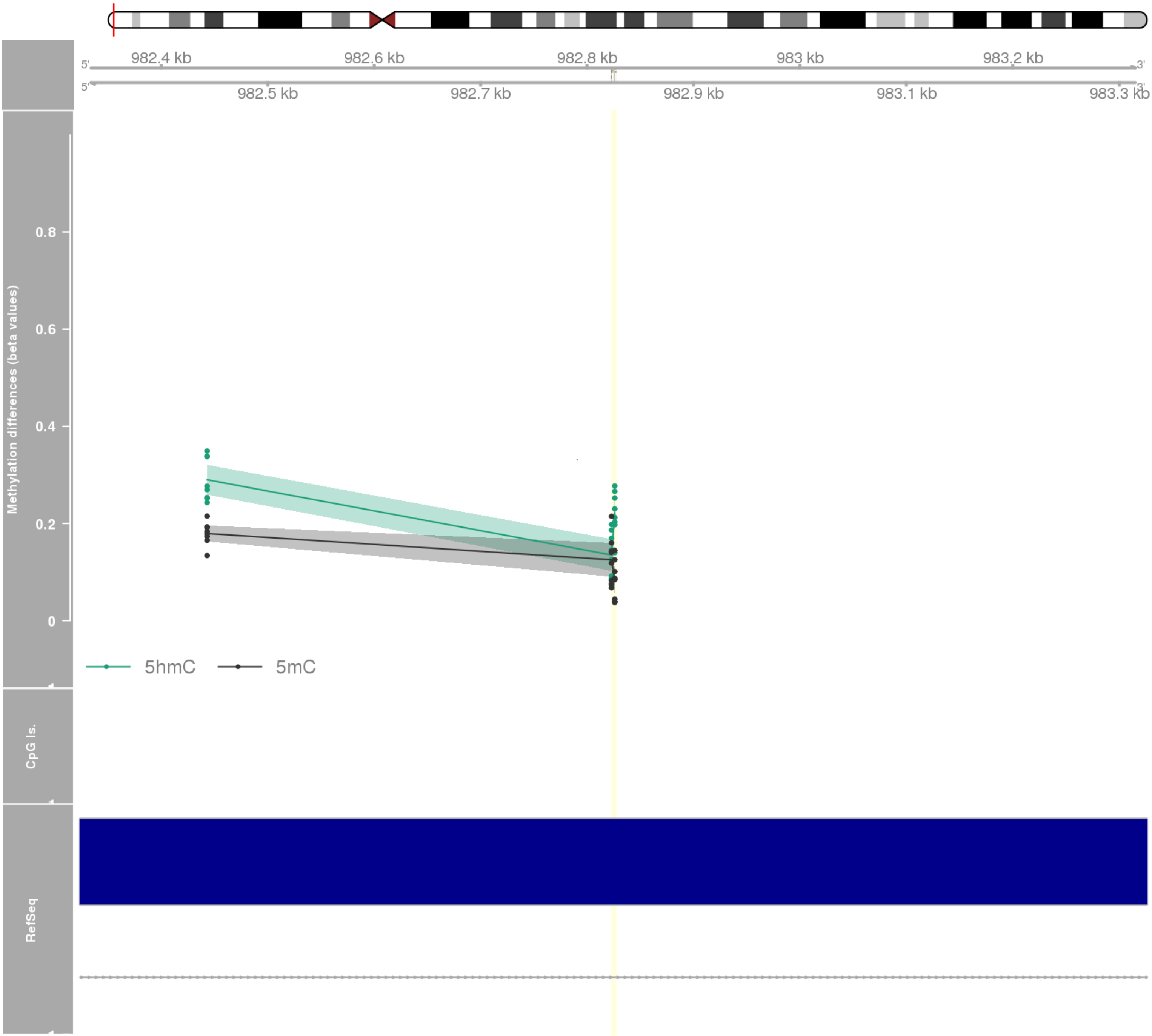
DMR 37 // chr6:31758862-31760825 // 1963 pb. (24 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: VARS -



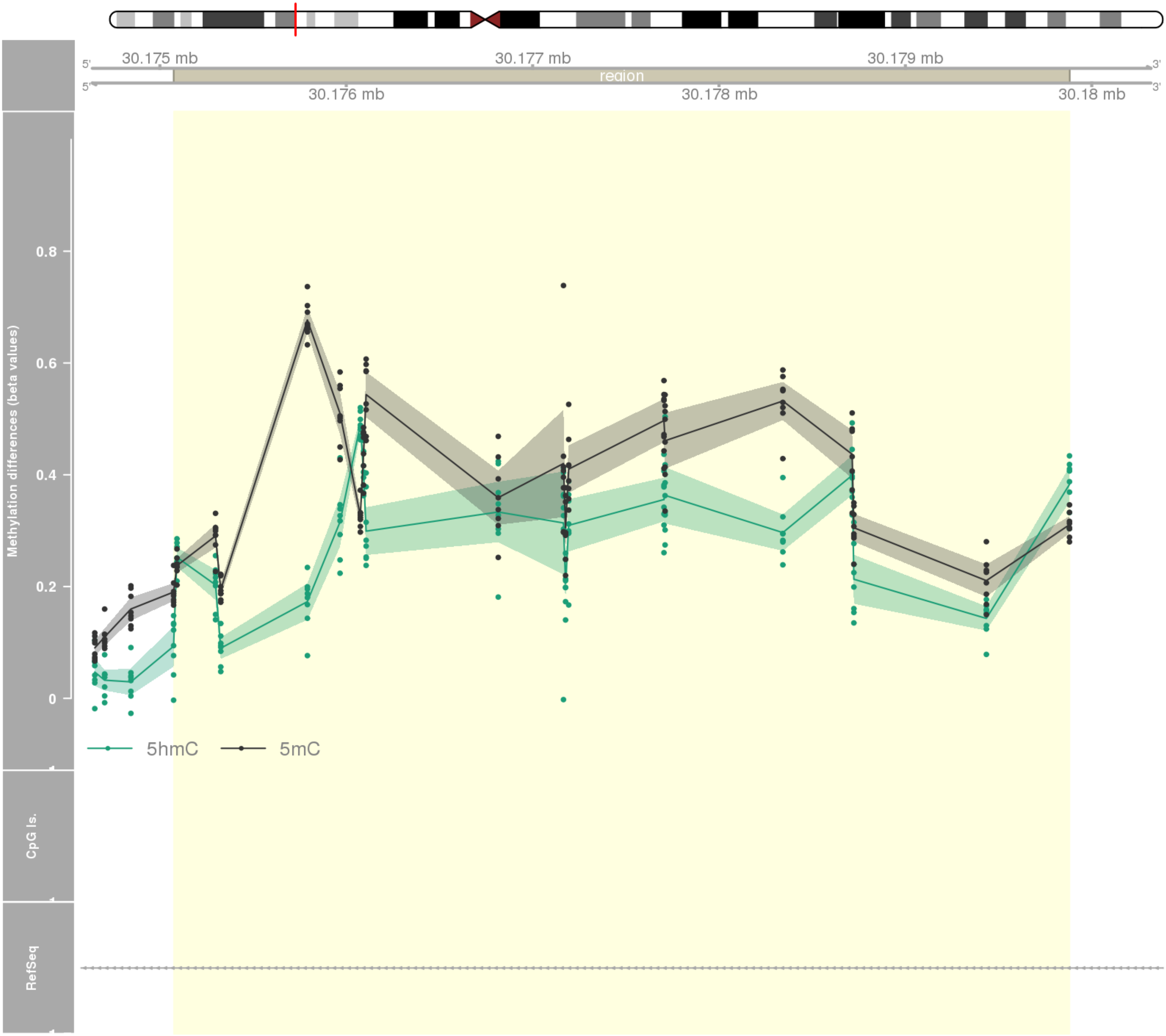
DMR 38 // chr1:2333551-2338738 // 5187 pb. (21 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: RER1 / PEX10 -



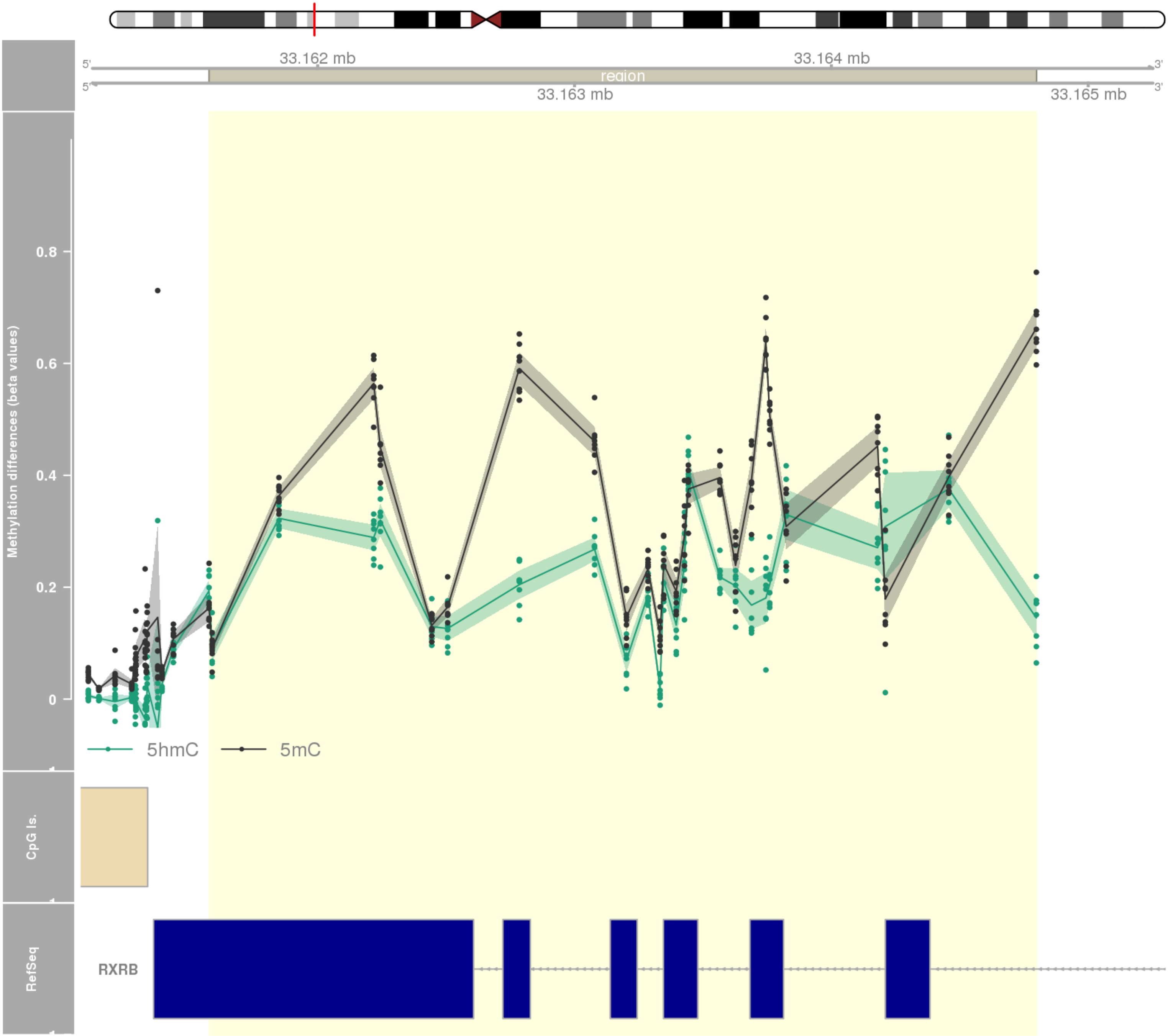
DMR 39 // chr4:982823-982826 // 3 pb. (2 probes) // pvalue: 0 // fwer: 0.218 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: SLC26A1 / IDUA -



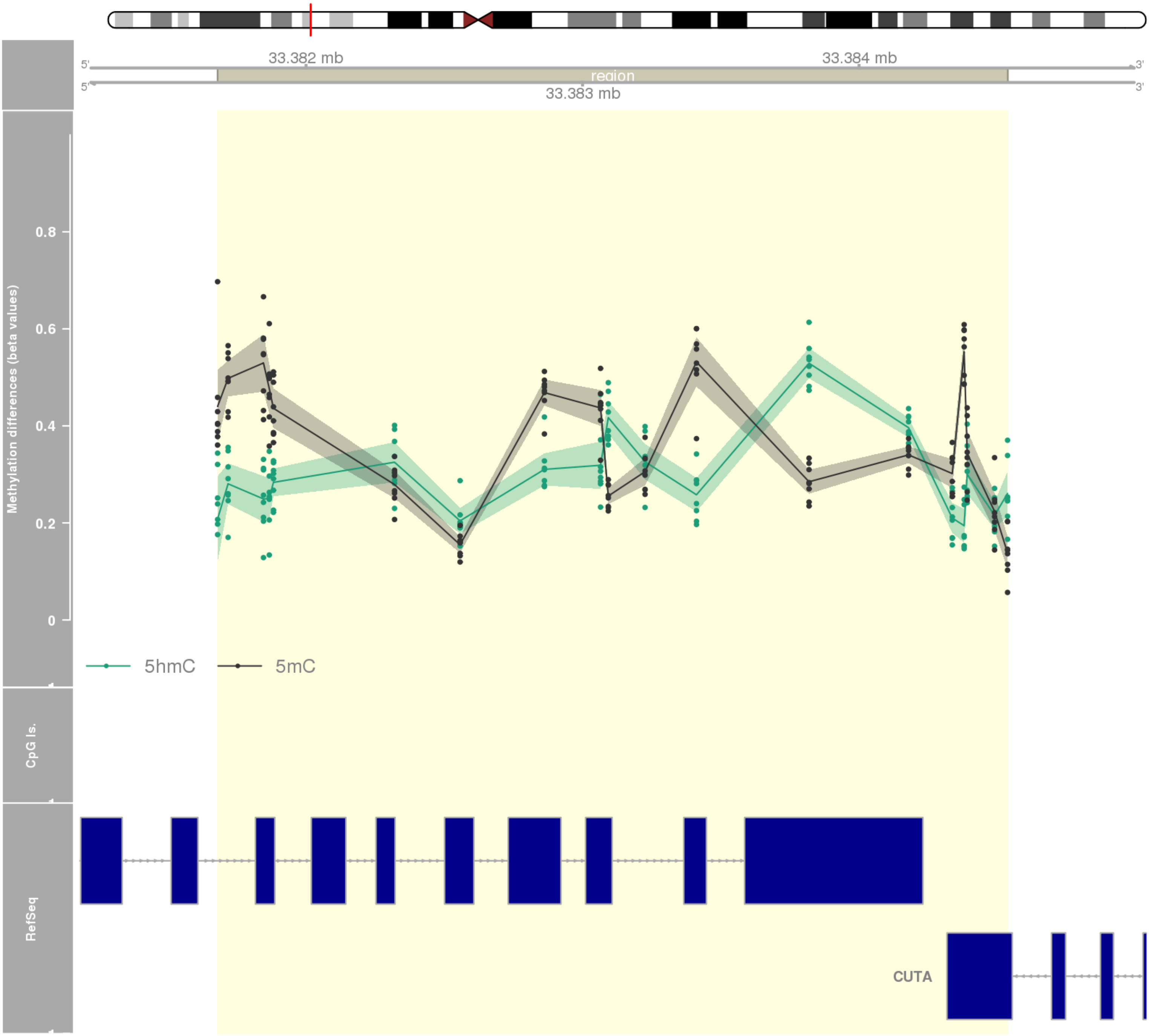
DMR 40 // chr6:30175074-30179881 // 4807 pb. (20 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: TRIM26 -



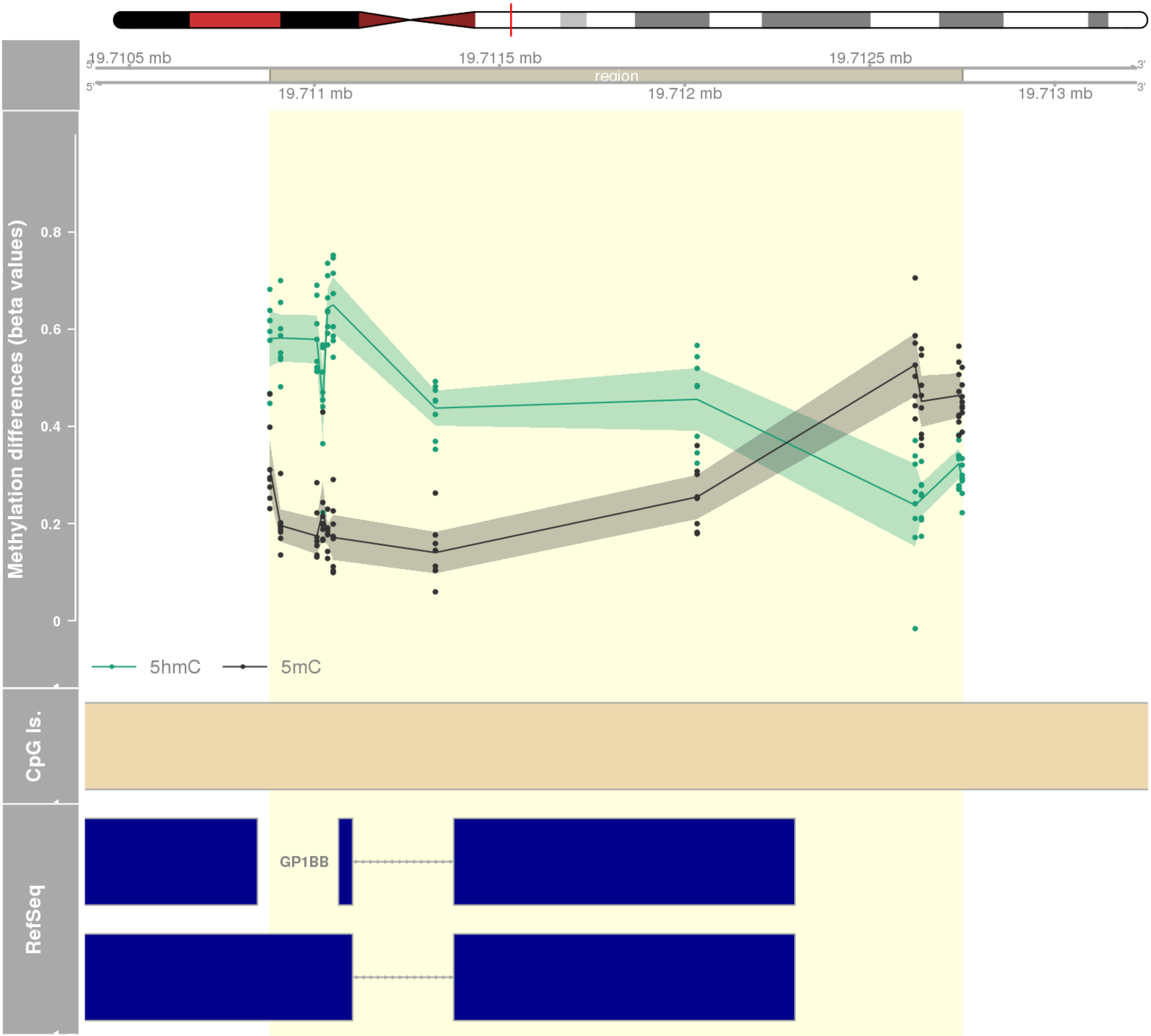
DMR 41 // chr6:33161577-33164798 // 3221 pb. (26 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: RXRB -



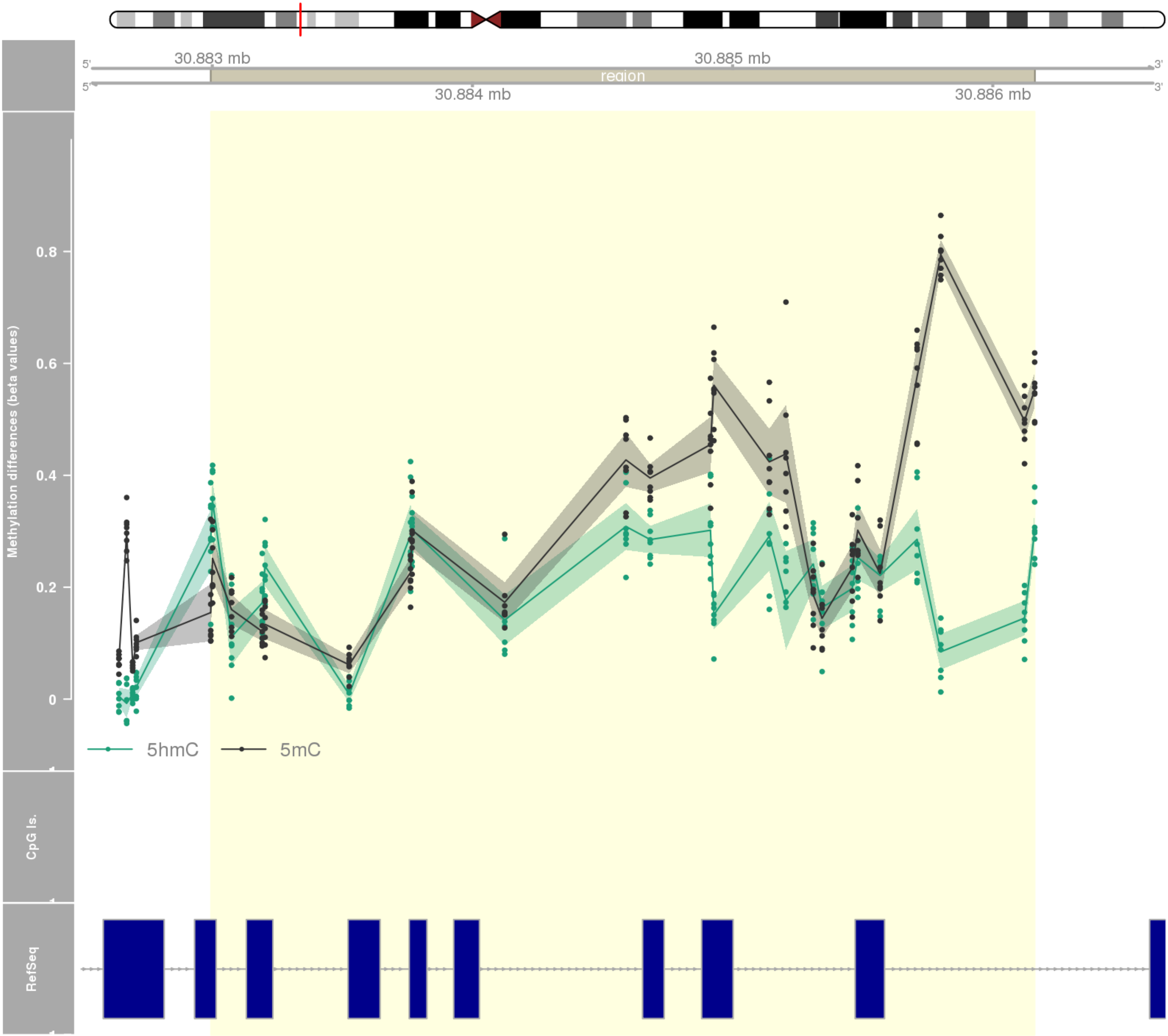
DMR 42 // chr6:33381680-33384537 // 2857 pb. (19 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: PHF1 / CUTA -



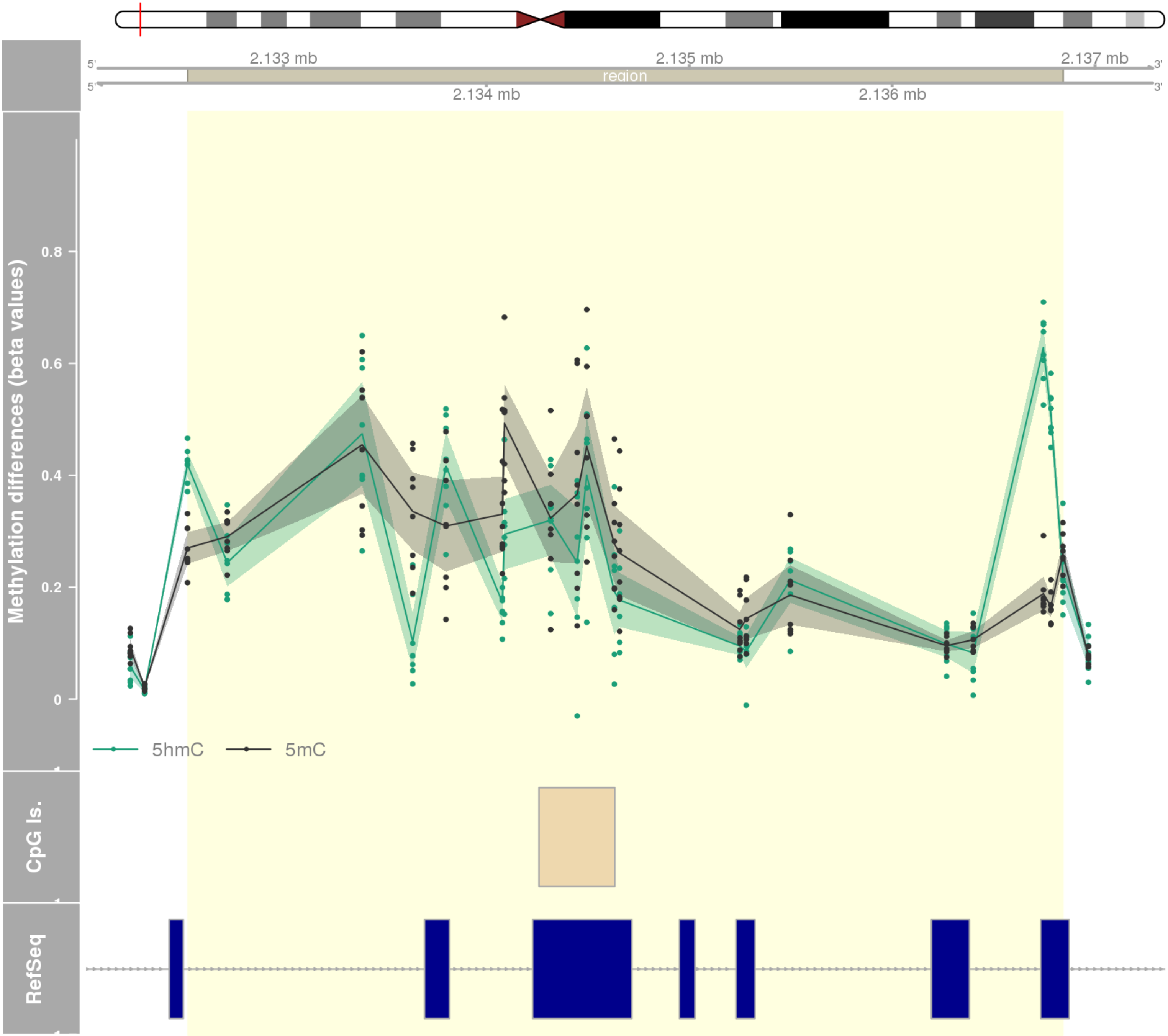
DMR 43 // chr22:19710880-19712750 // 1870 pb. (12 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.218
- genes: SEPT5 / GP1BB -



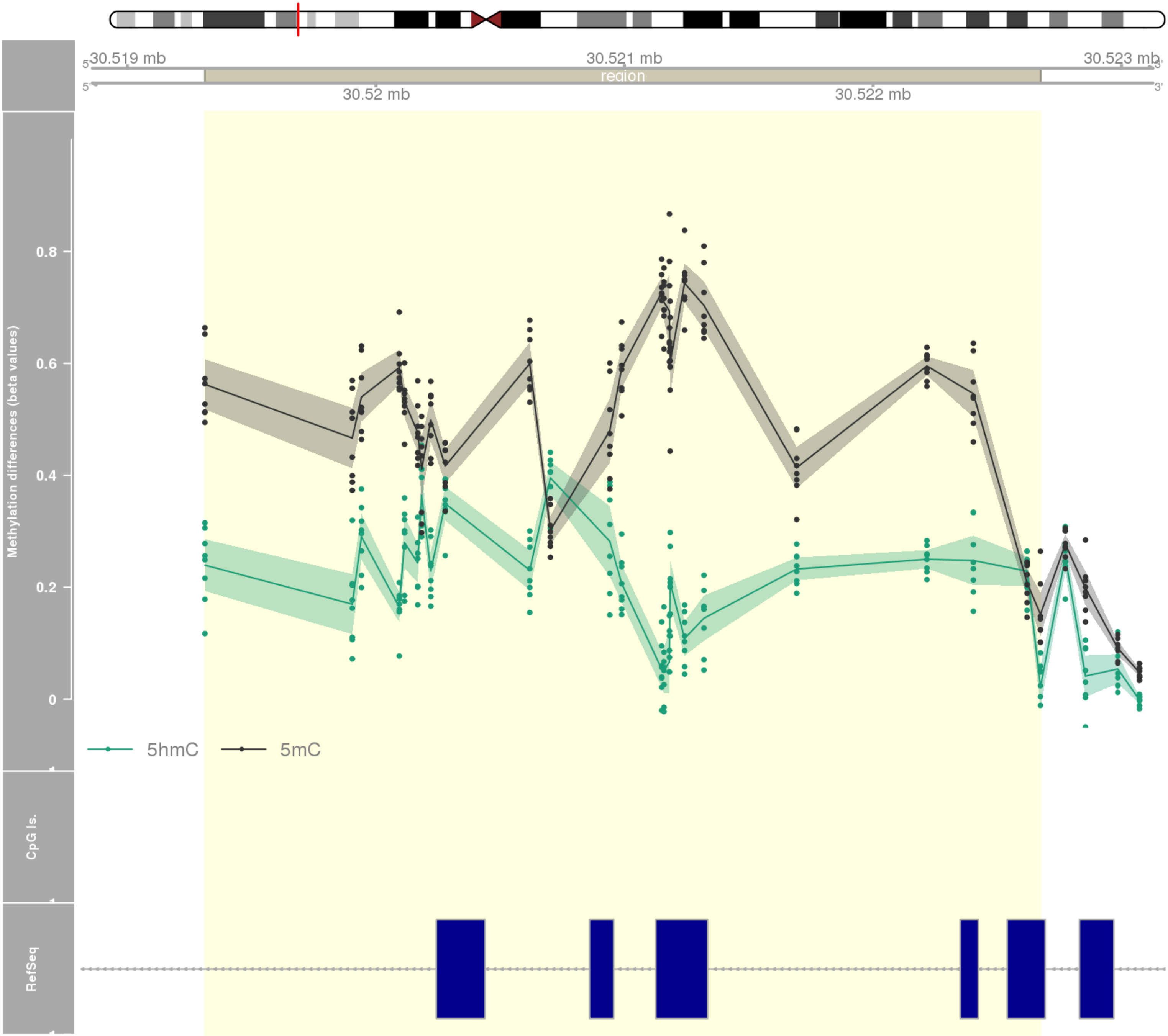
DMR 44 // chr6:30882994-30886161 // 3167 pb. (24 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.337
- genes: VARS2 -



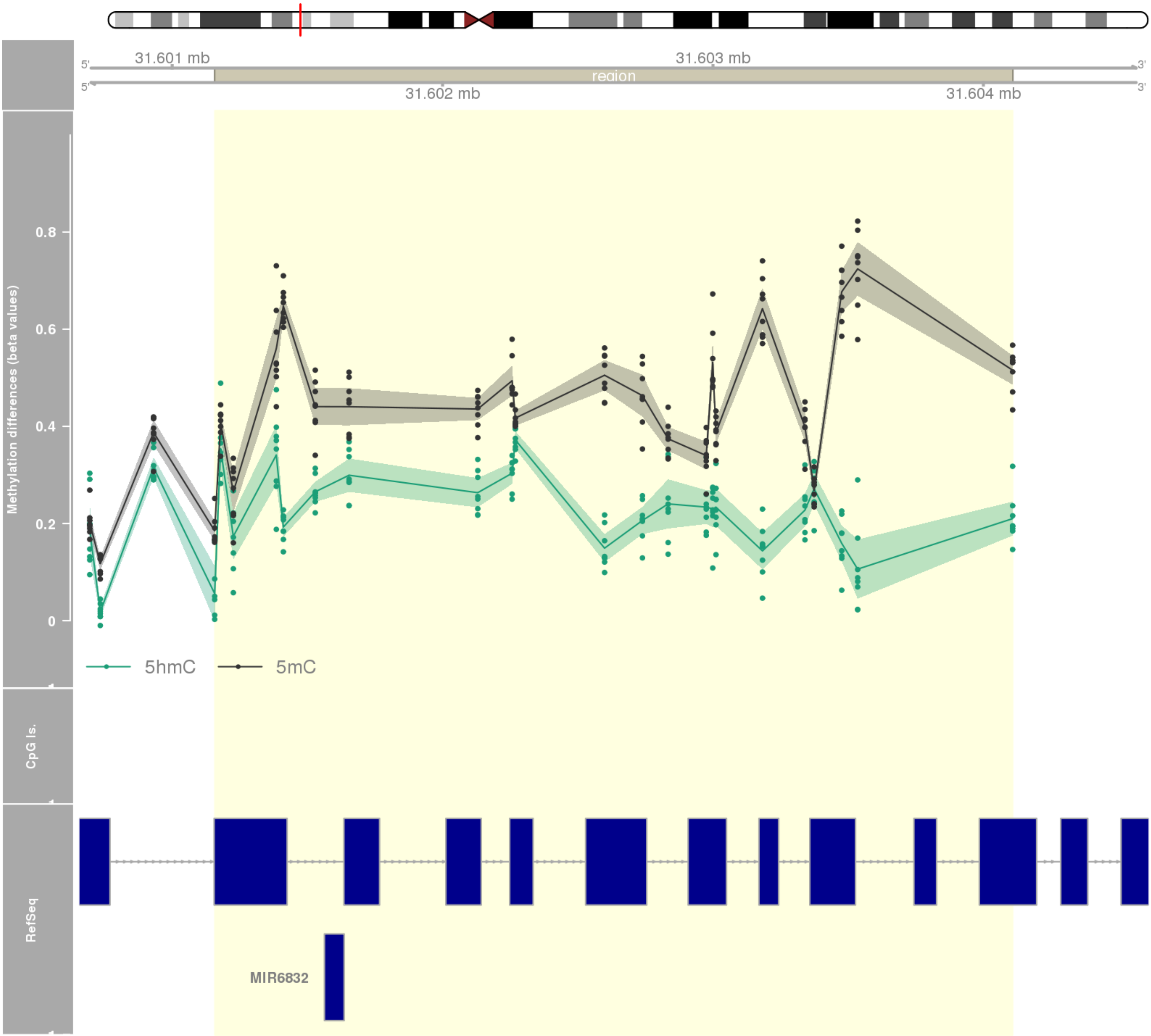
DMR 45 // chr16:2132527-2136842 // 4315 pb. (20 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.337
- genes: TSC2 -



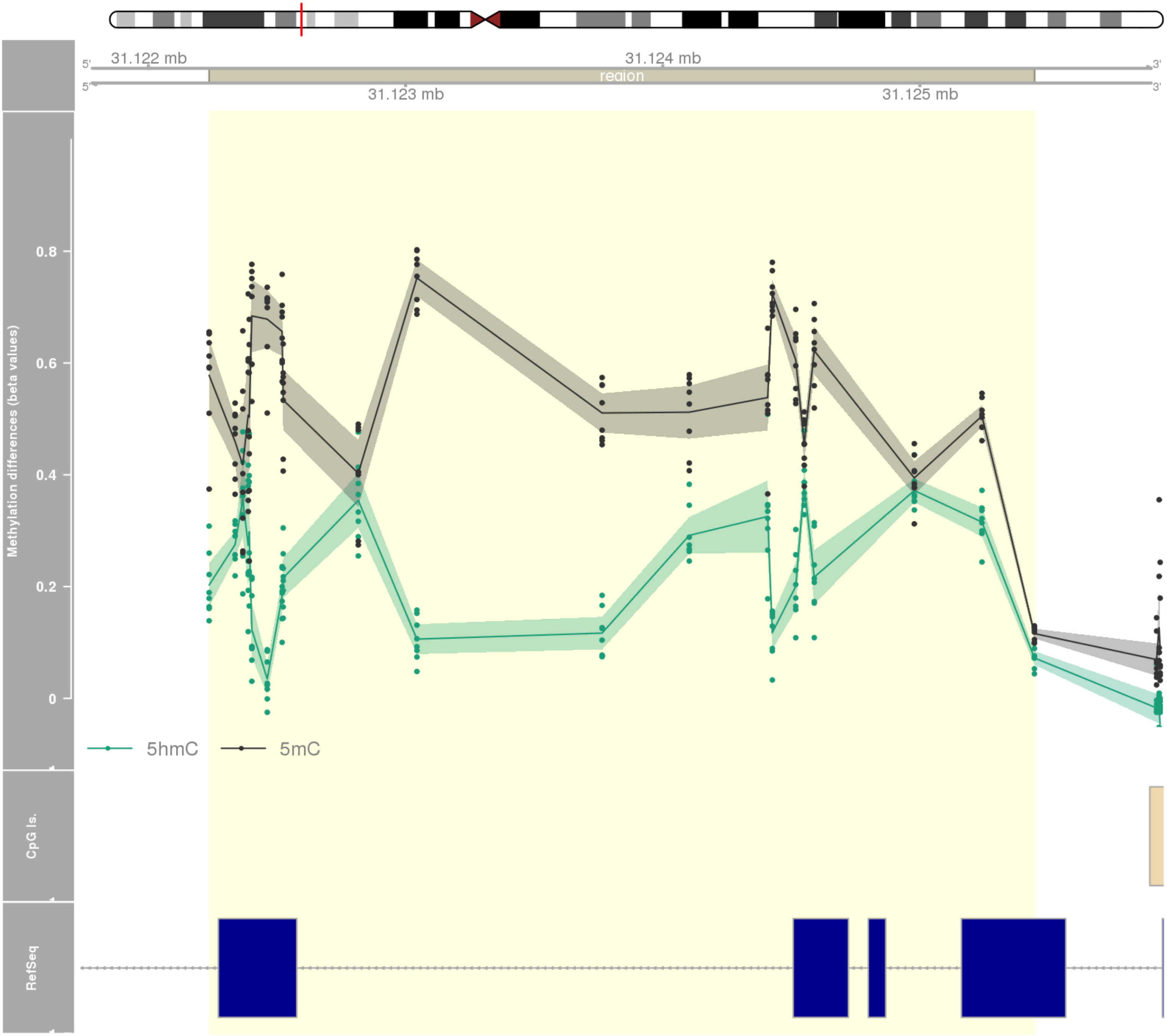
DMR 46 // chr6:30519312-30522674 // 3362 pb. (24 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.337
- genes: GNL1 -



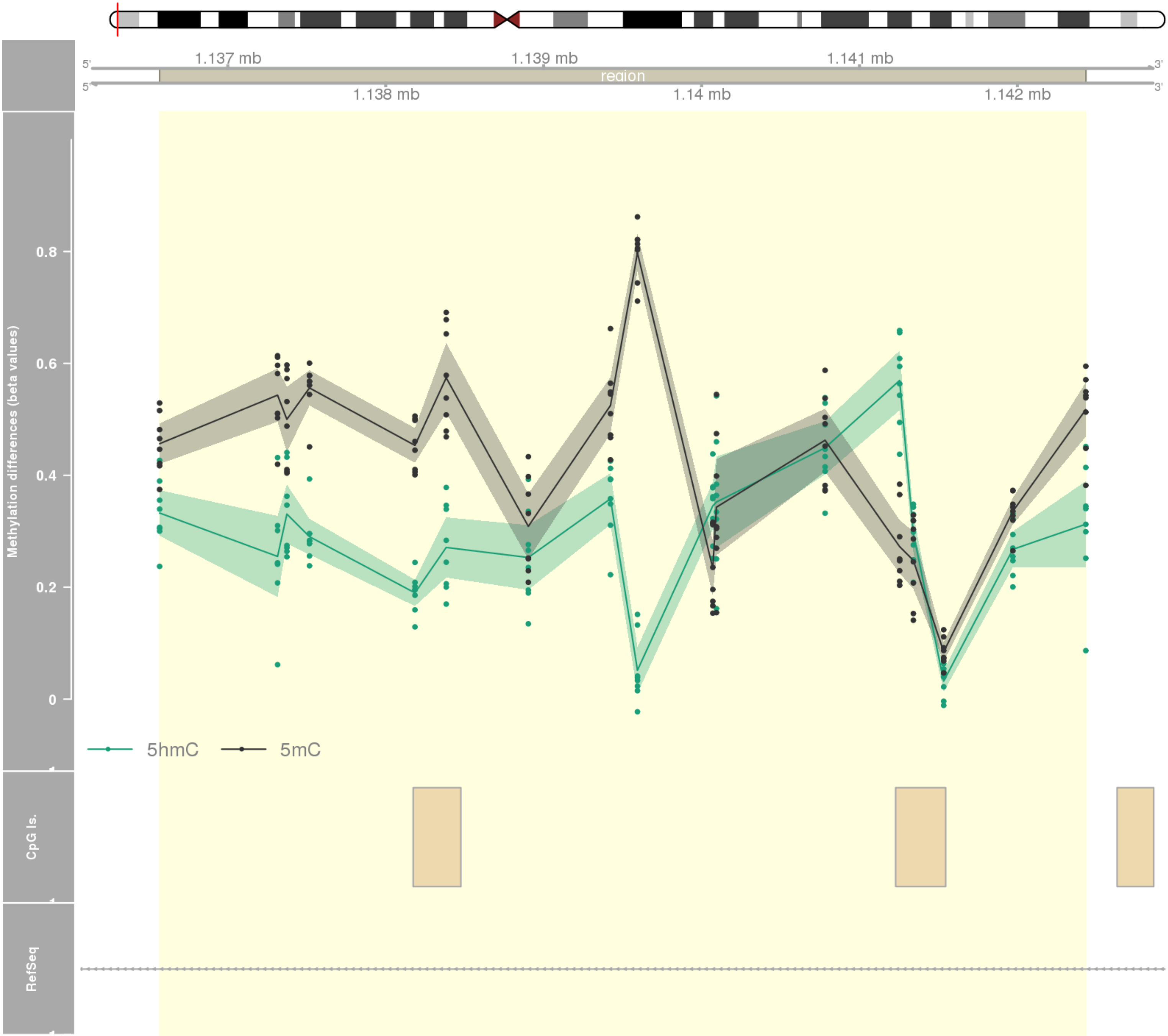
DMR 47 // chr6:31601157-31604108 // 2951 pb. (22 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.002 // fwerArea: 0.337
- genes: PRRC2A -



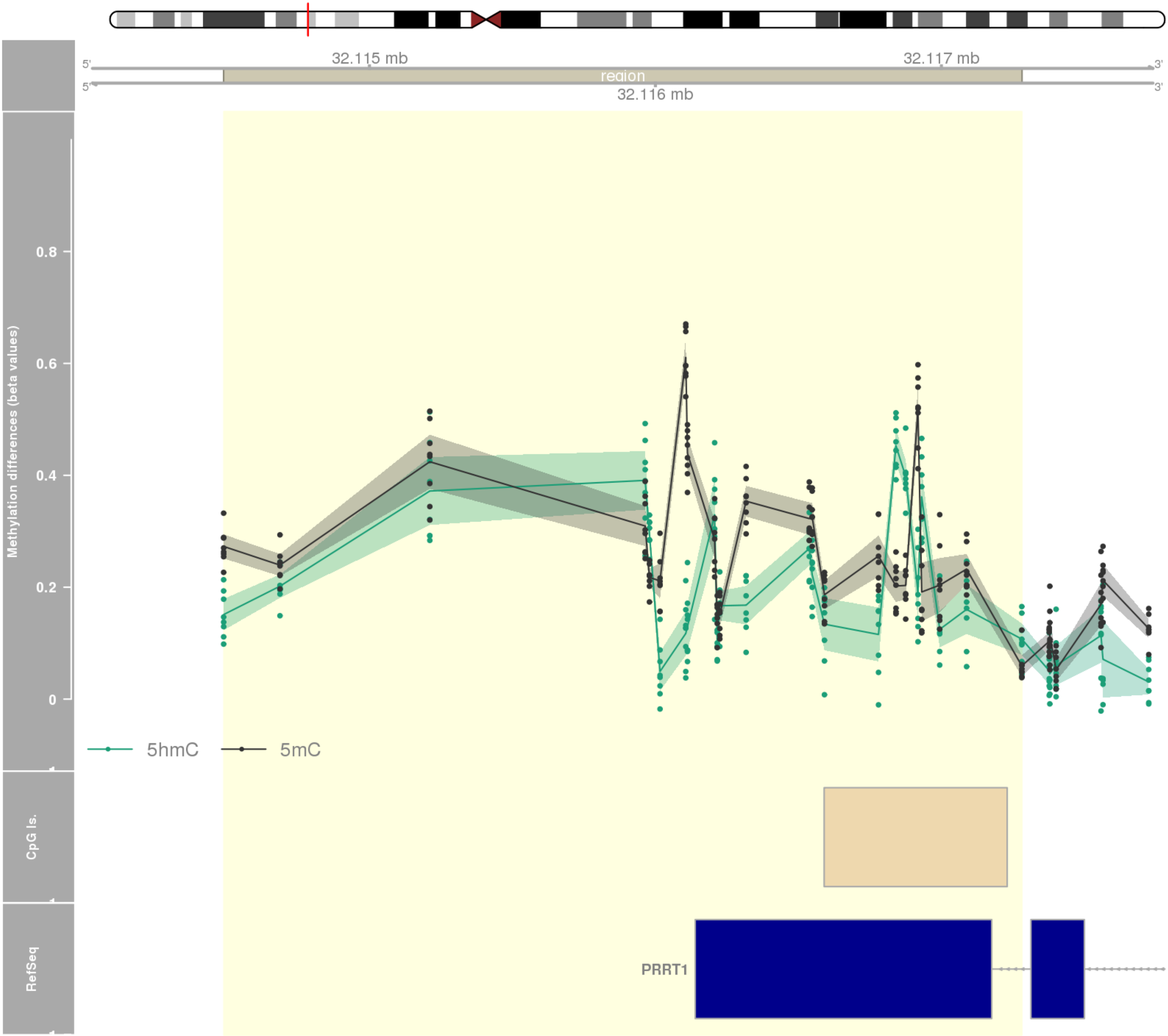
DMR 48 // chr6:31122236-31125445 // 3209 pb. (21 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: CCHCR1 -



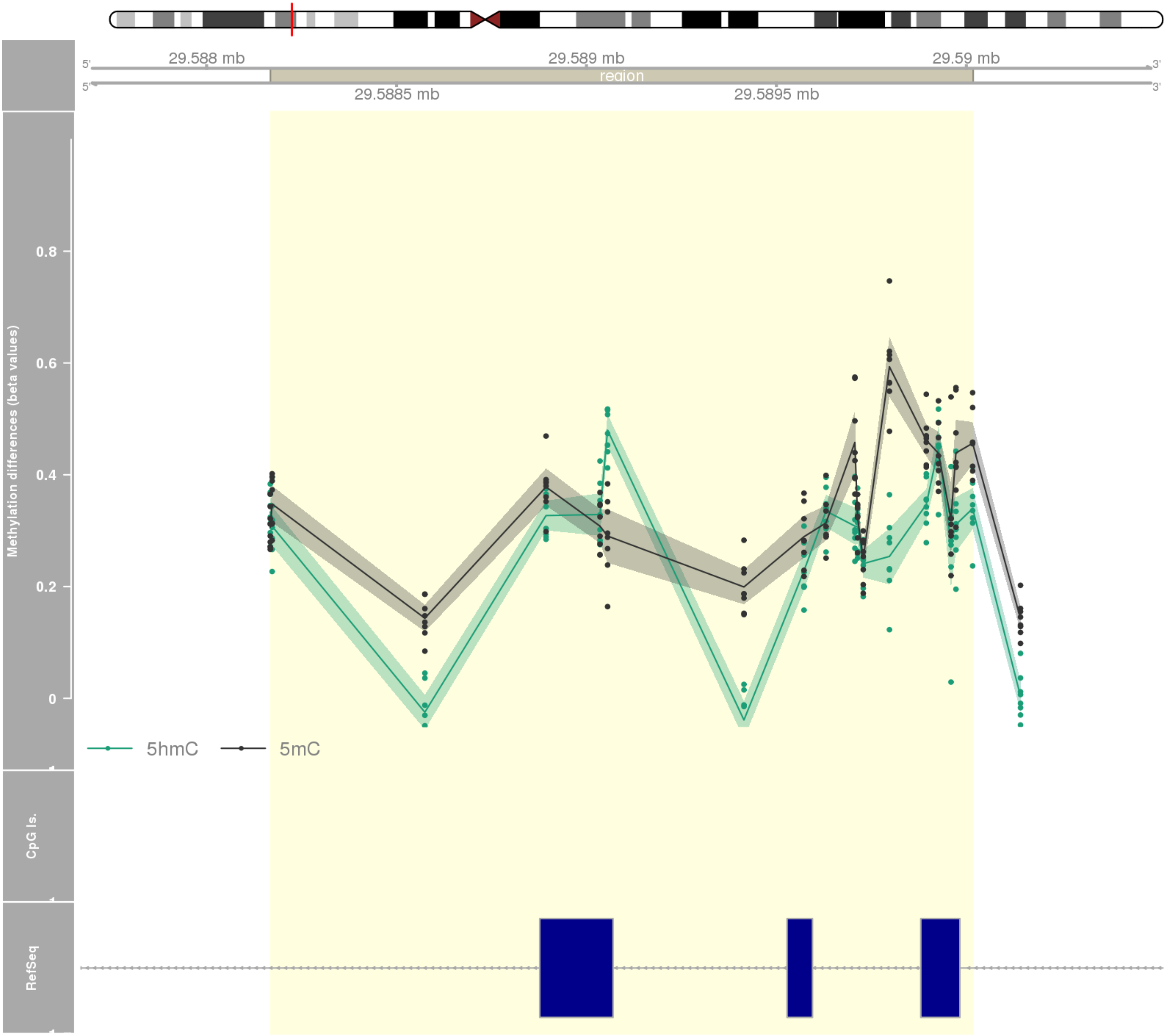
DMR 49 // chr7:1136568-1142433 // 5865 pb. (17 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: C7orf50 -



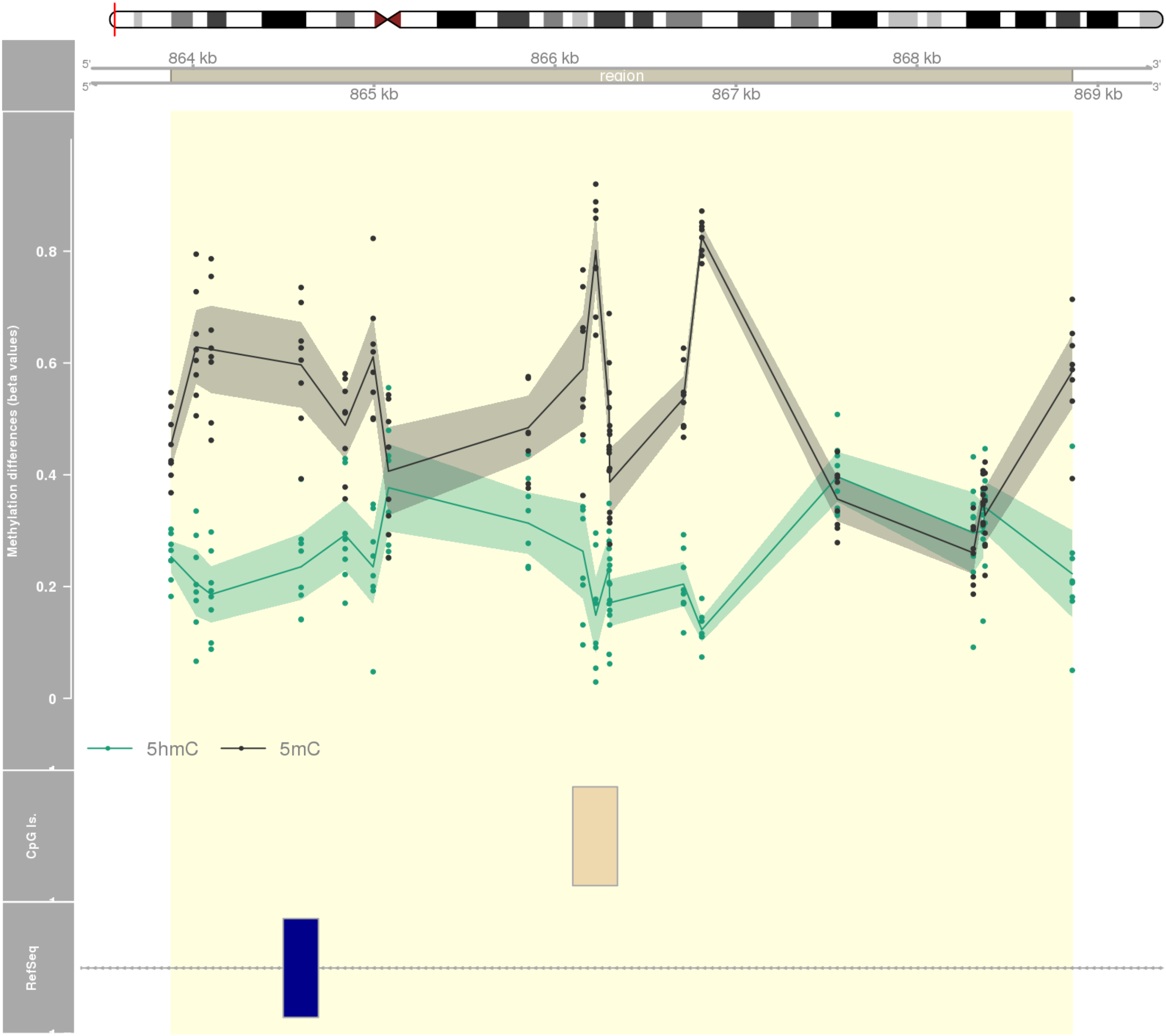
DMR 50 // chr6:32114490-32117281 // 2791 pb. (23 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: PRRT1 -



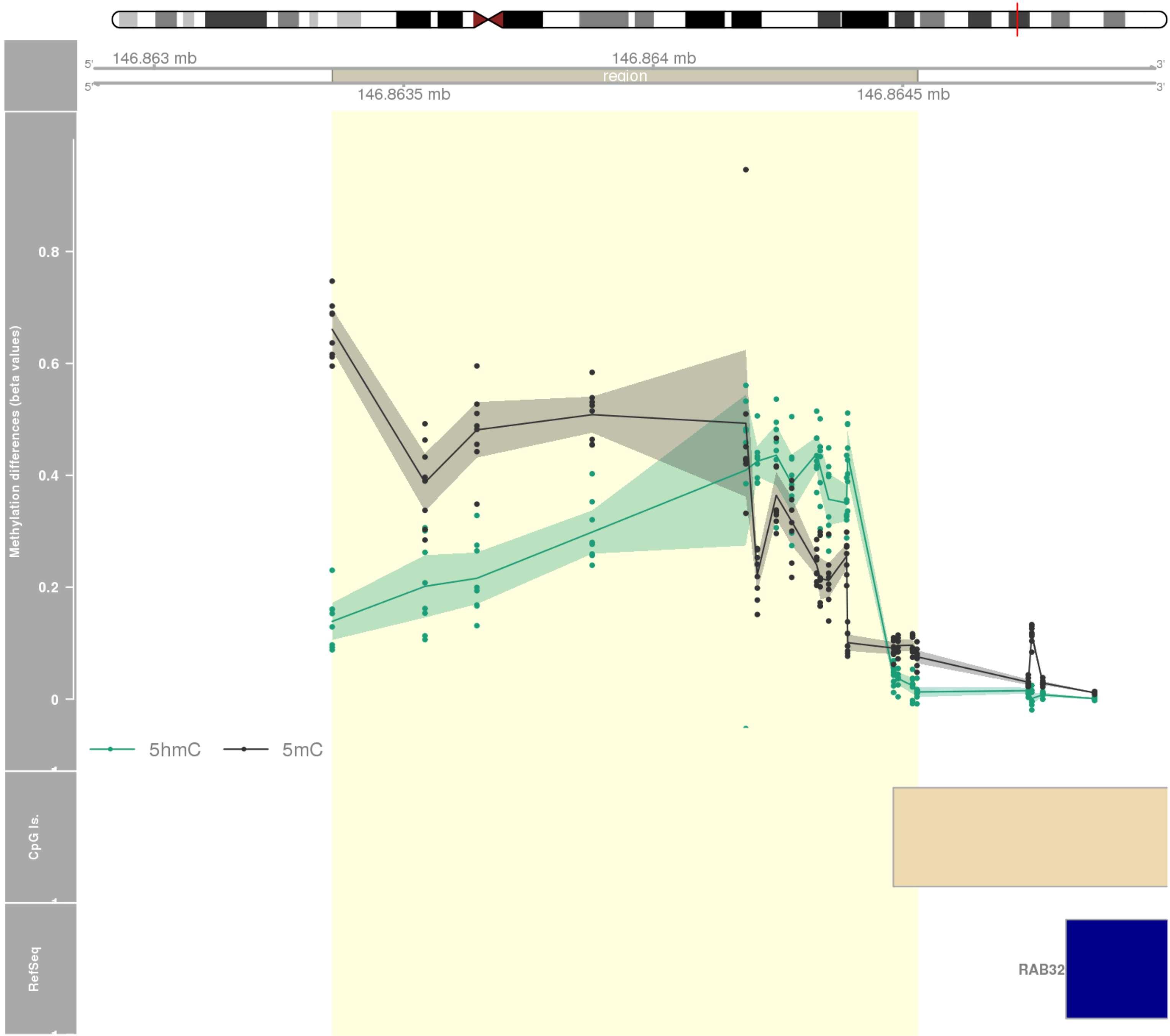
DMR 51 // chr6:29588168-29590017 // 1849 pb. (18 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: GABBR1 -



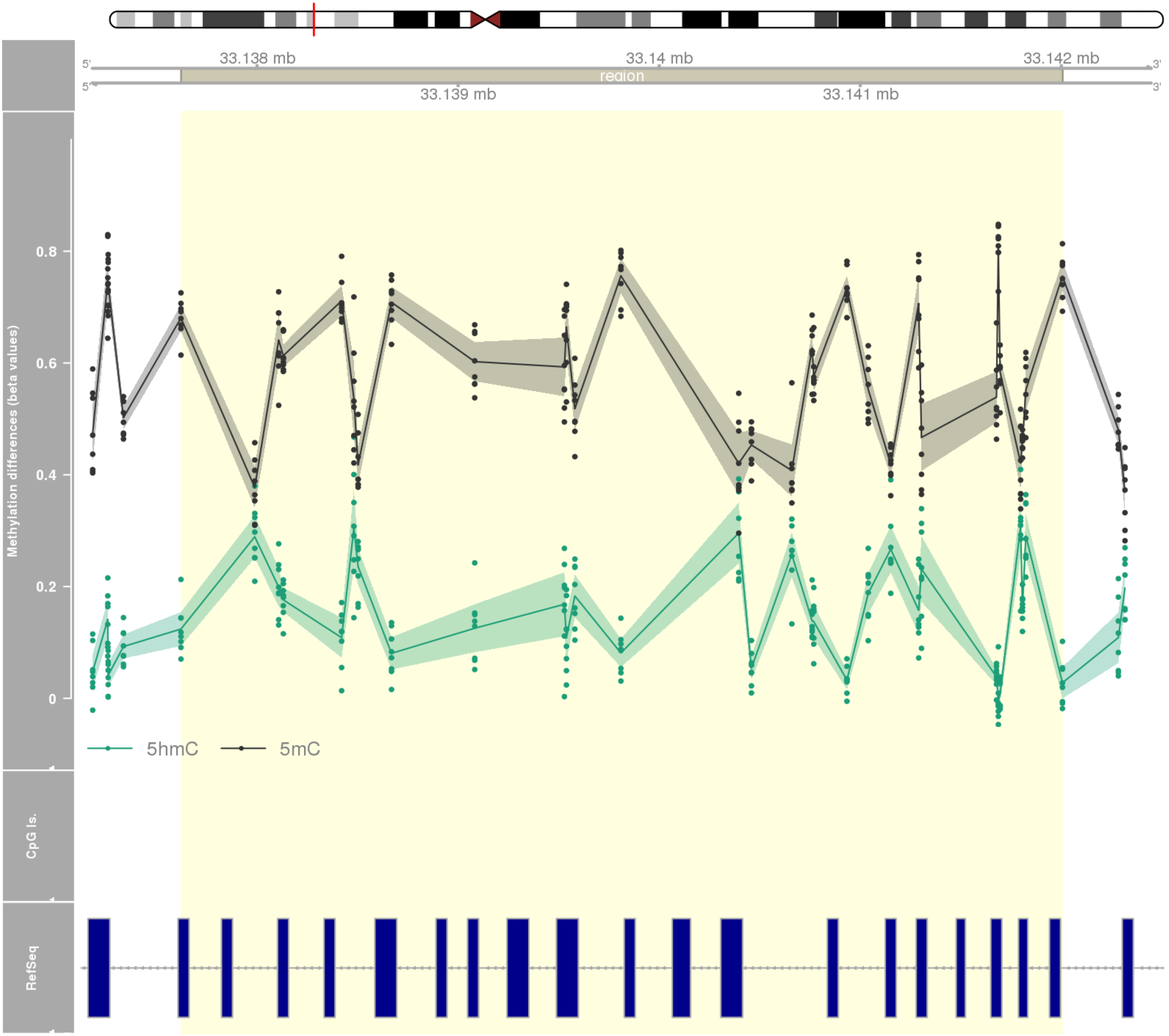
DMR 52 // chr4:863878-868858 // 4980 pb. (19 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: GAK -



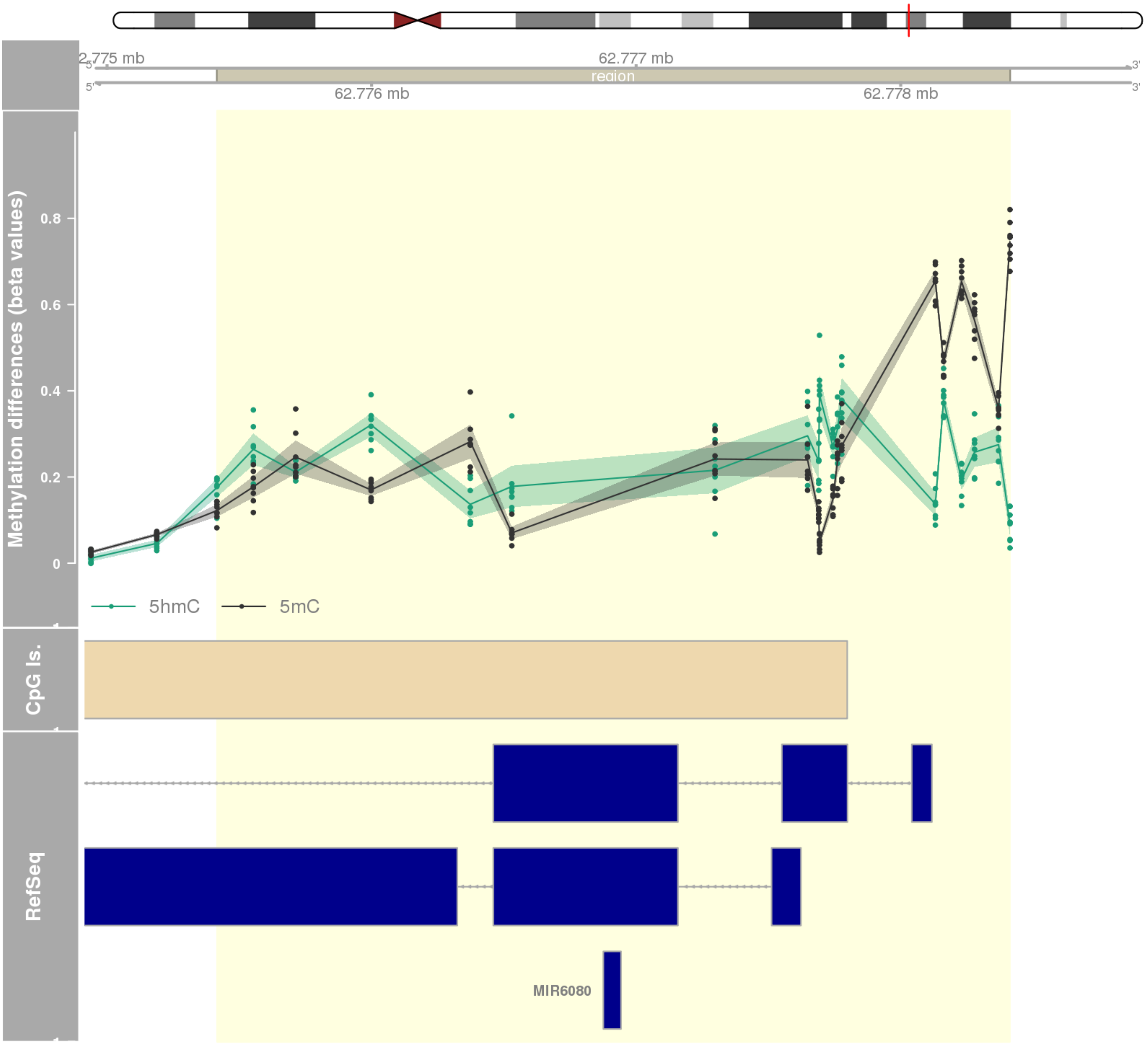
DMR 53 // chr6:146863357-146864529 // 1172 pb. (17 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337



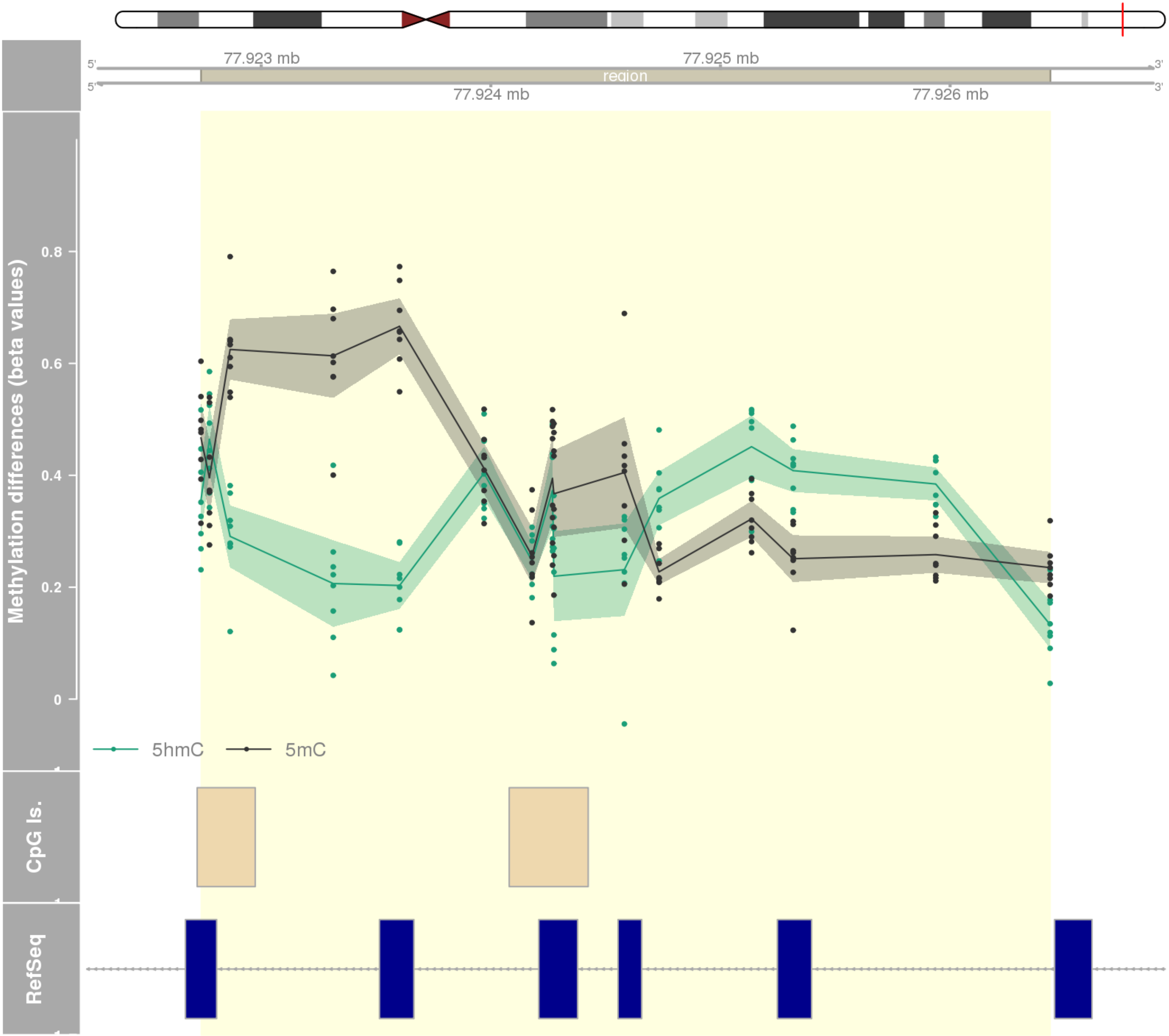
DMR 54 // chr6:33137622-33142006 // 4384 pb. (30 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: COL11A2 -

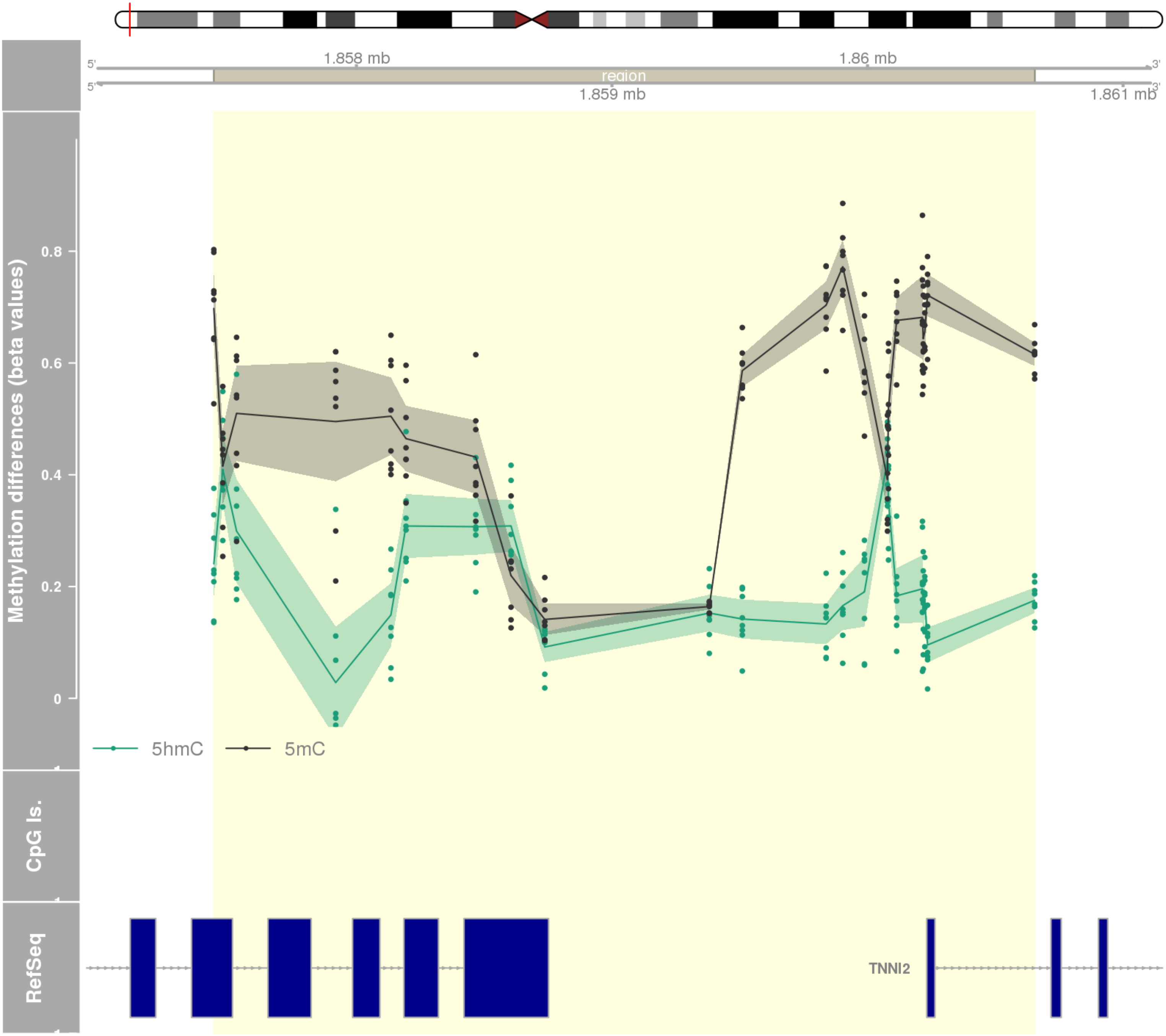


DMR 55 // chr17:62775415-62778413 // 2998 pb. (19 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: PLEKHM1P -



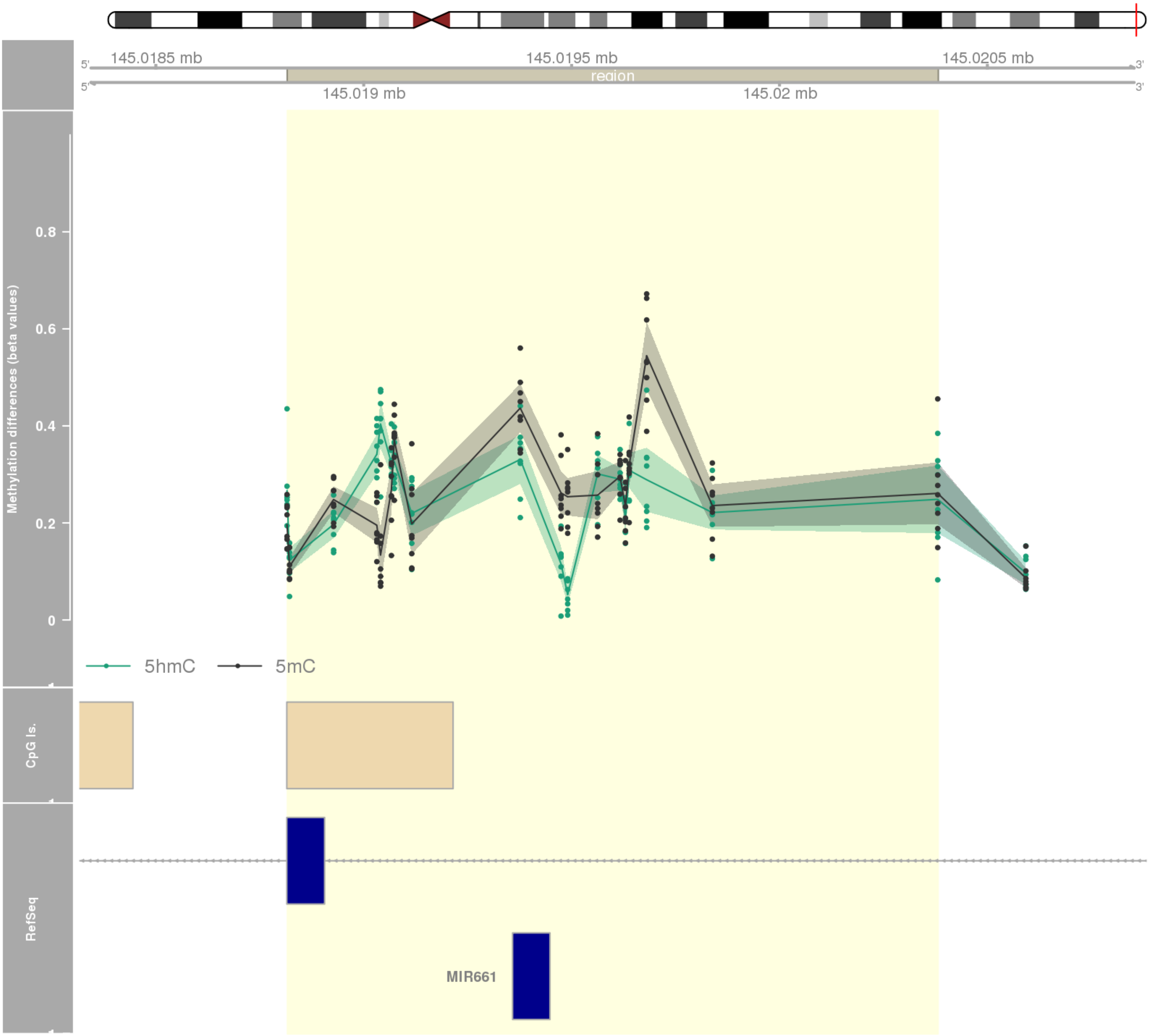
DMR 56 // chr17:77922738-77926436 // 3698 pb. (15 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: TBC1D16 -



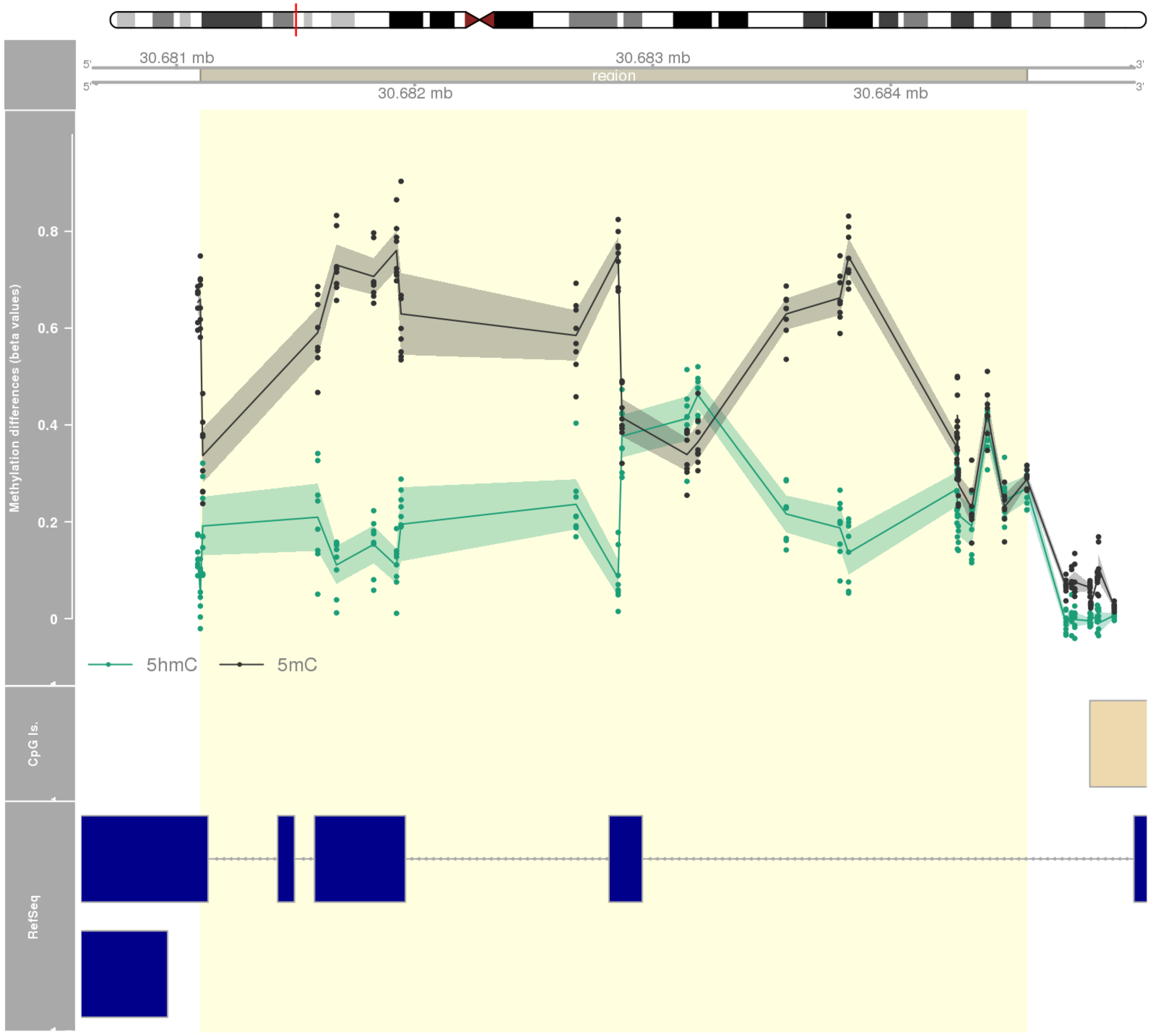


DMR 57 // chr11:1857442-1860654 // 3212 pb. (22 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: SYT8 / TNNI2 -

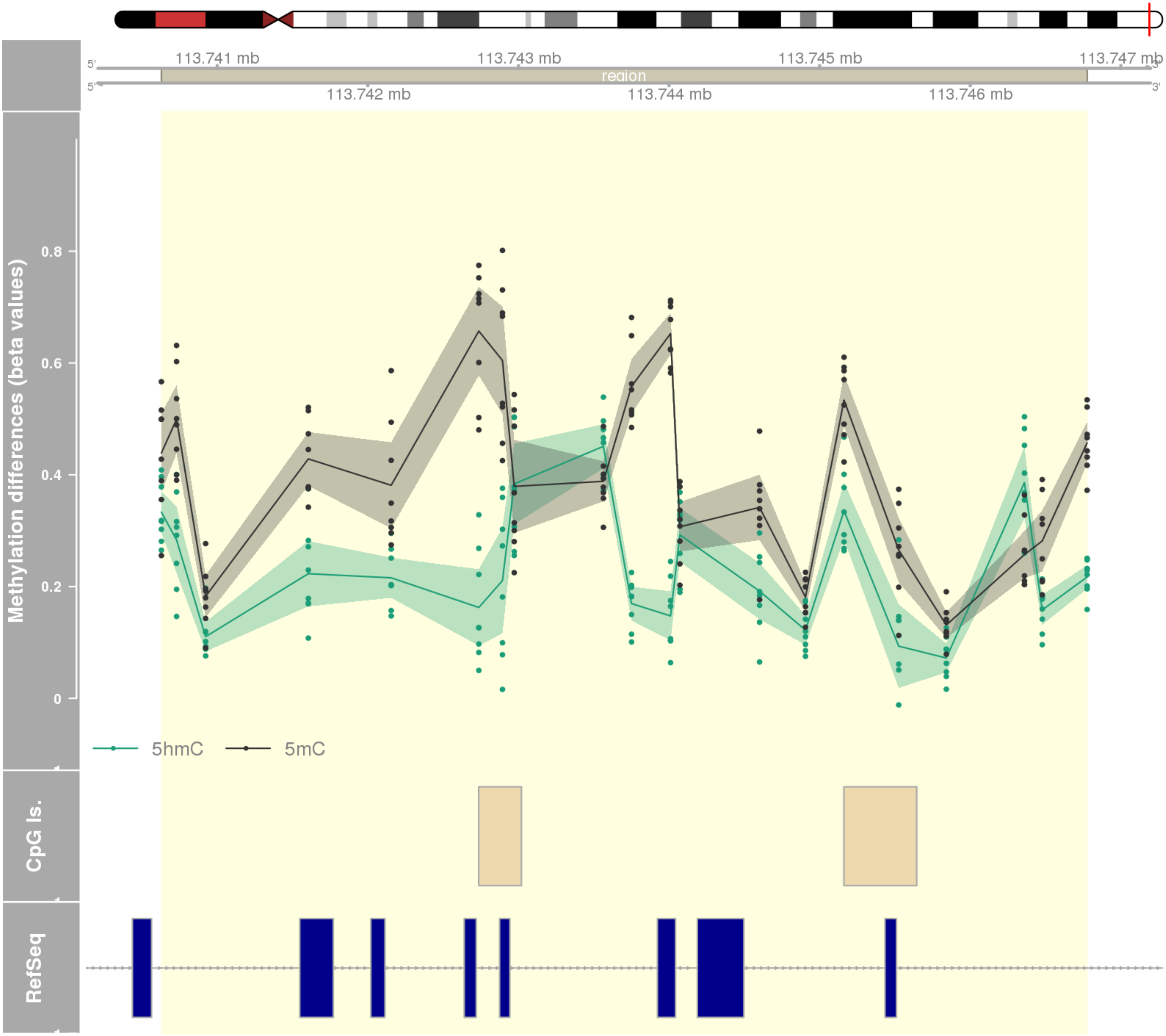
DMR 58 // chr8:145018816-145020381 // 1565 pb. (18 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: MIR661 / PLEC -



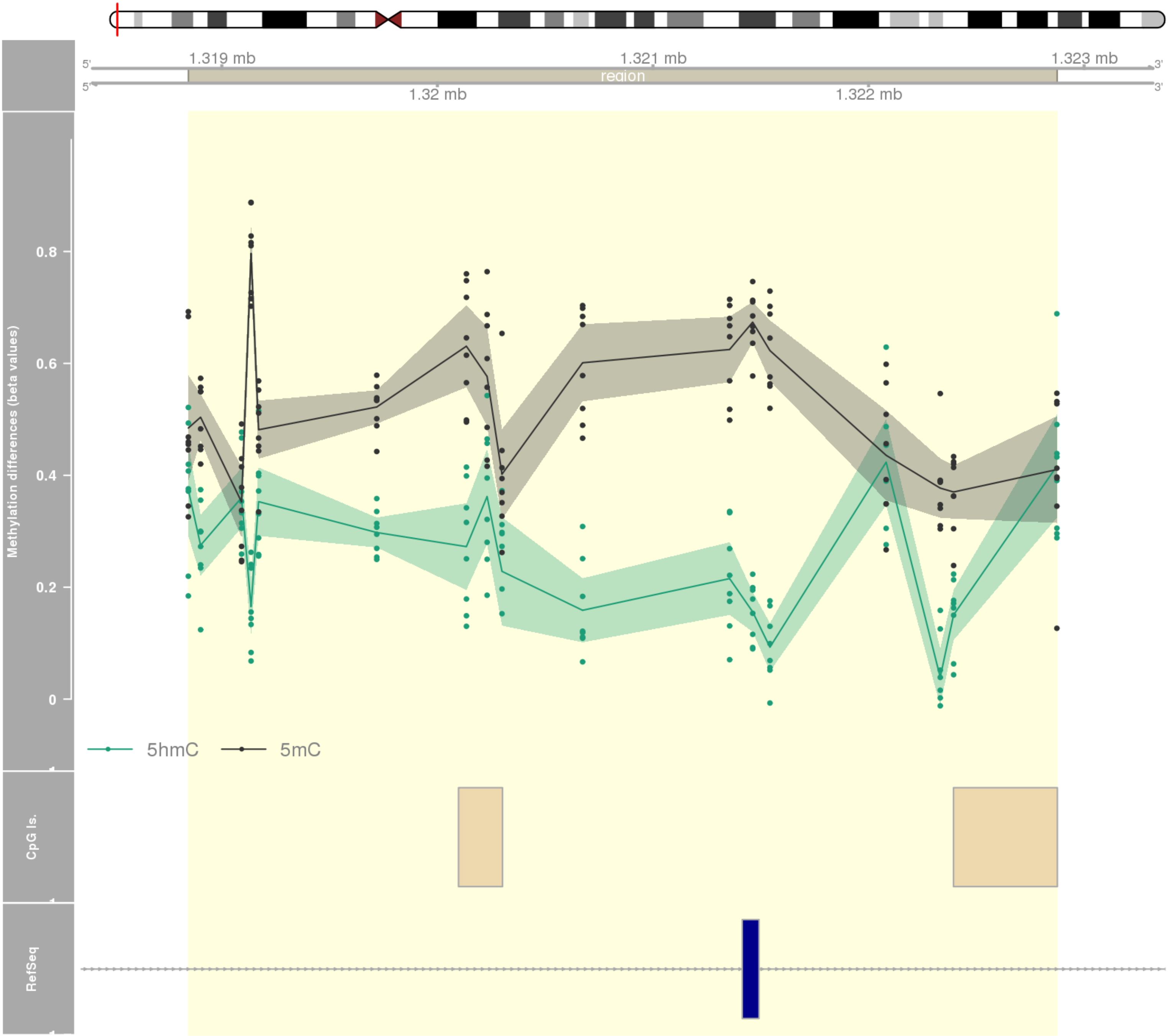
DMR 59 // chr6:30681100-30684572 // 3472 pb. (22 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: MDC1 -



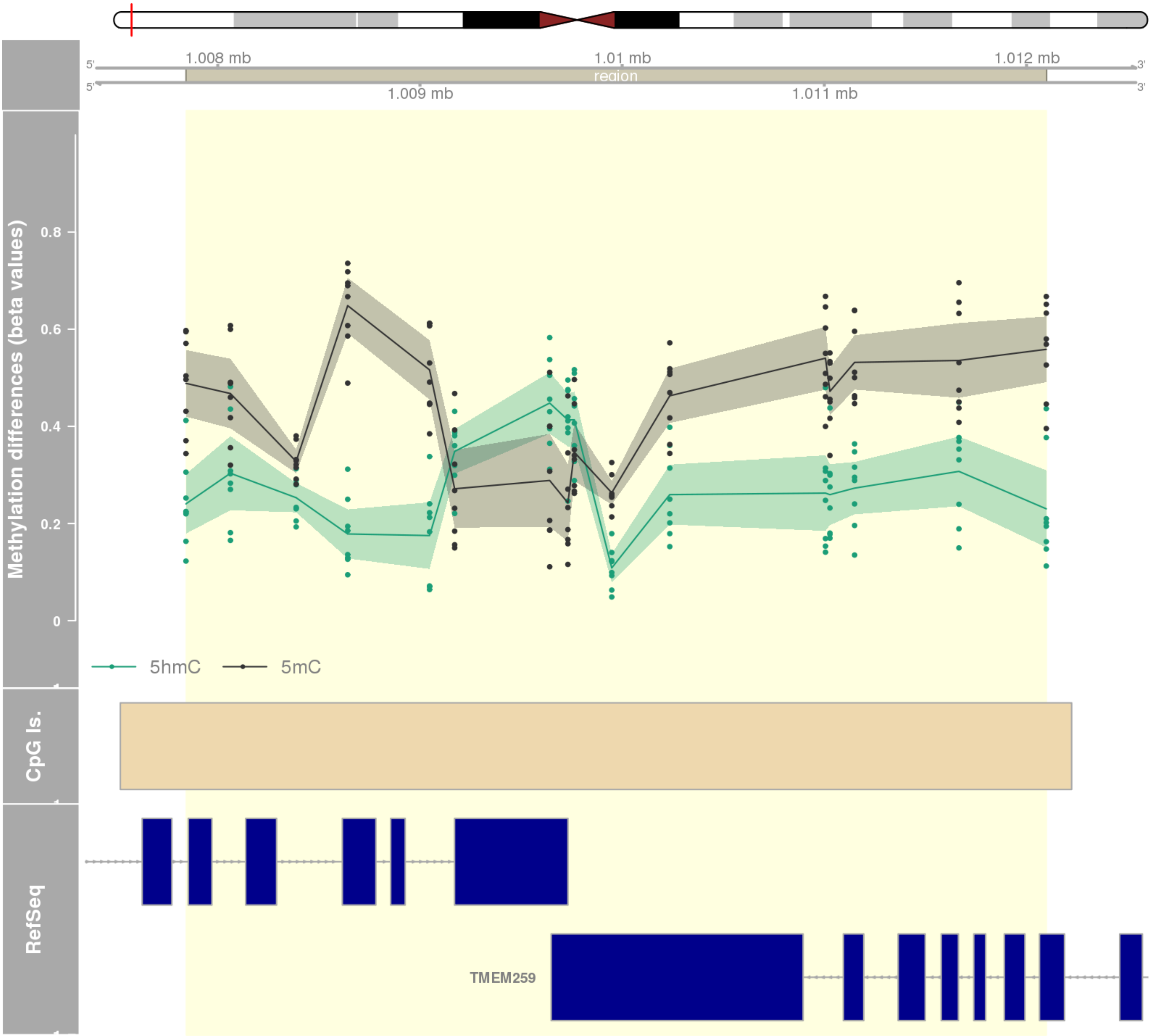
DMR 60 // chr13:113740629-113746776 // 6147 pb. (20 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: MCF2L -



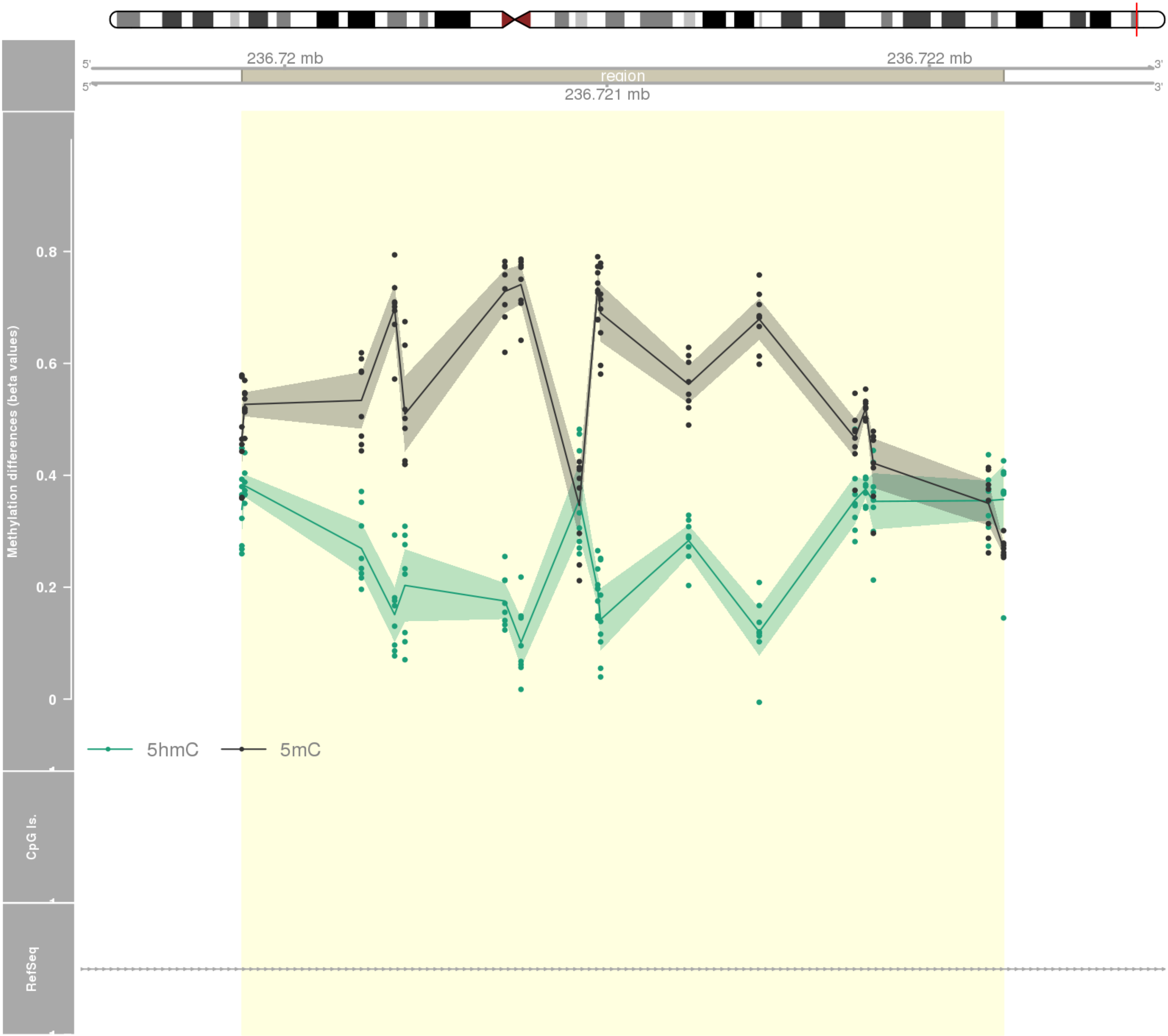
DMR 61 // chr4:1318845-1322874 // 4029 pb. (17 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: MAEA -



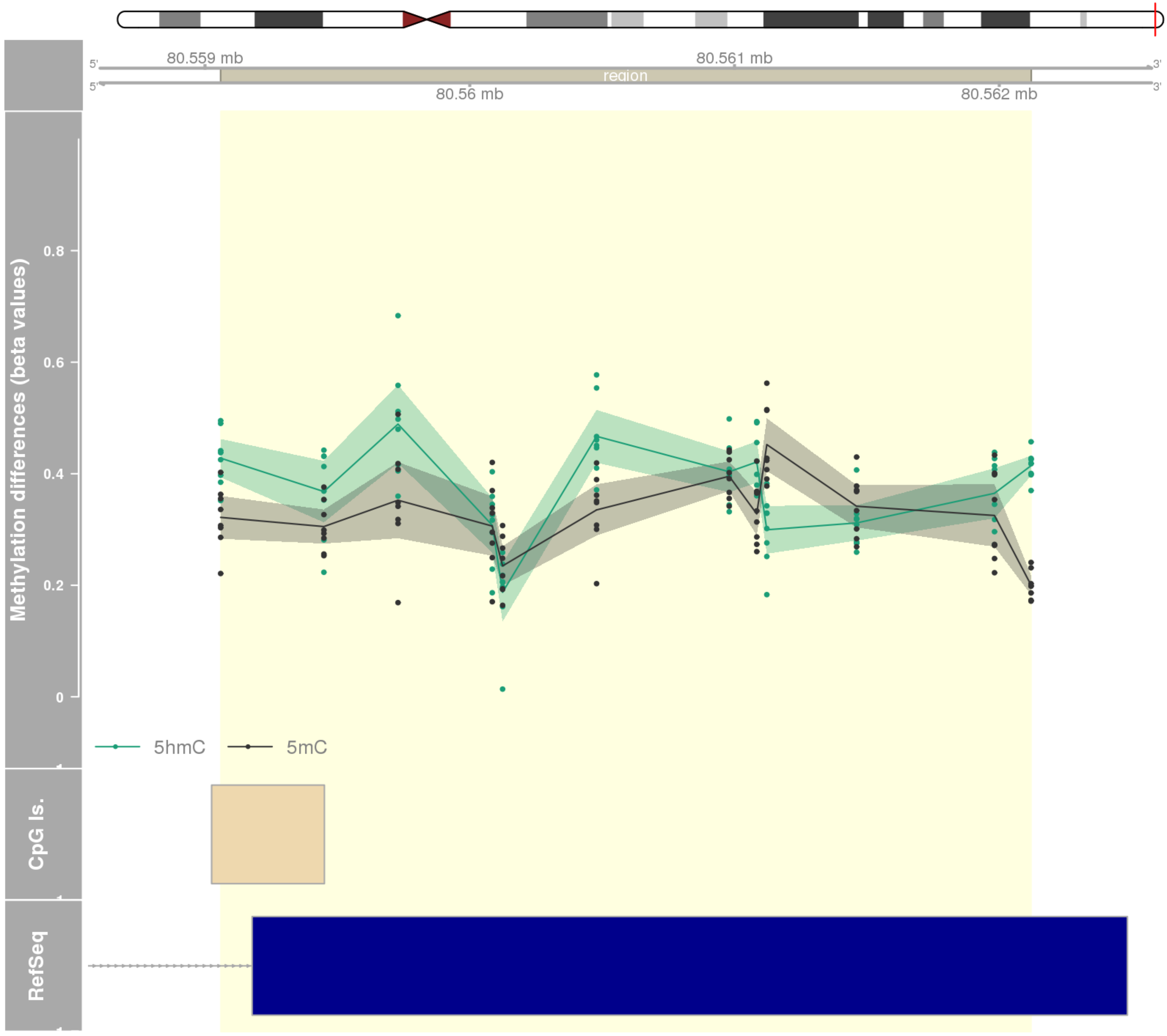
DMR 62 // chr19:1007843-1012098 // 4255 pb. (16 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.337
- genes: GRIN3B / TMEM259 -



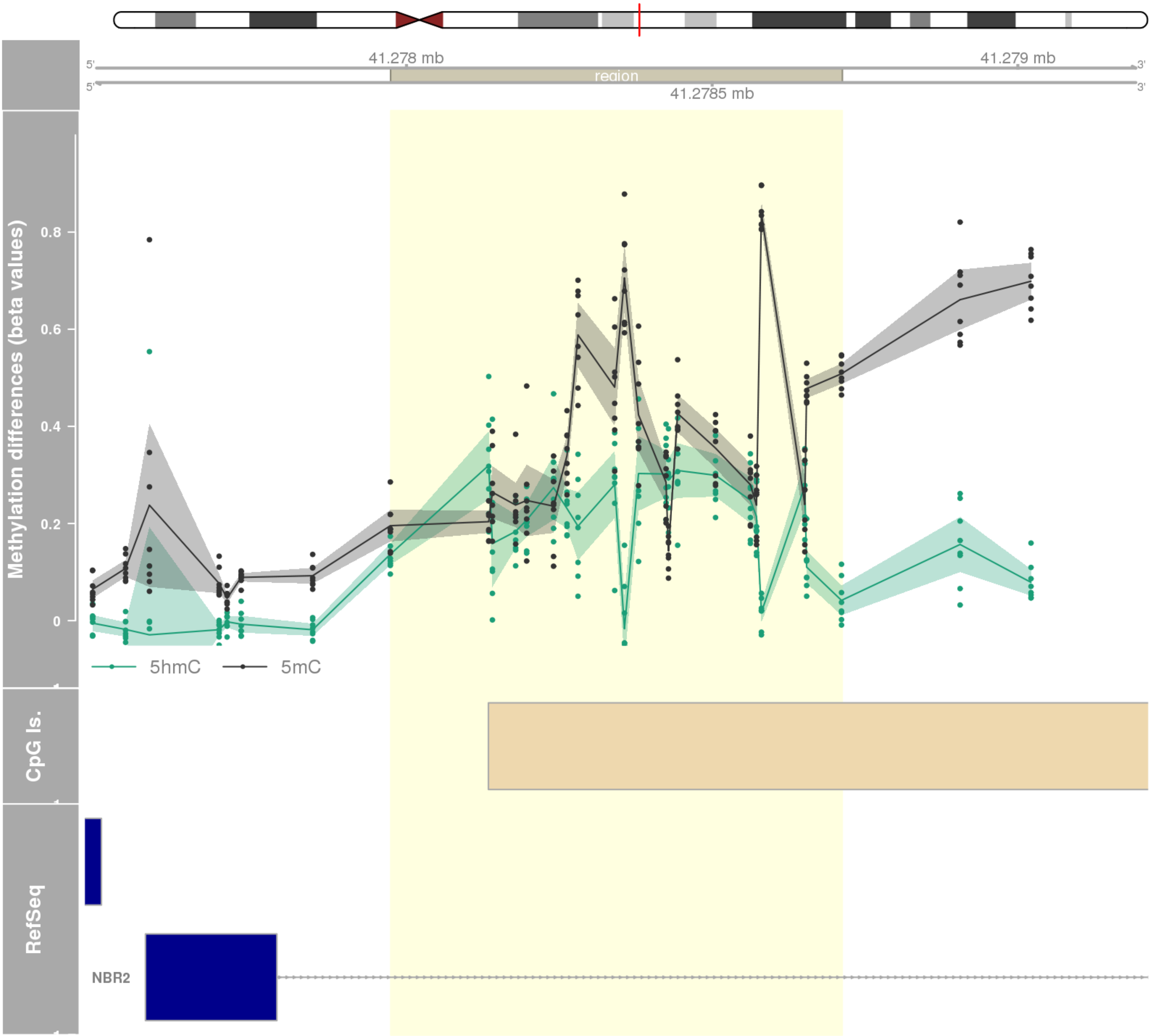
DMR 63 // chr2:236719867-236722230 // 2363 pb. (17 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.449
- genes: AGAP1 -



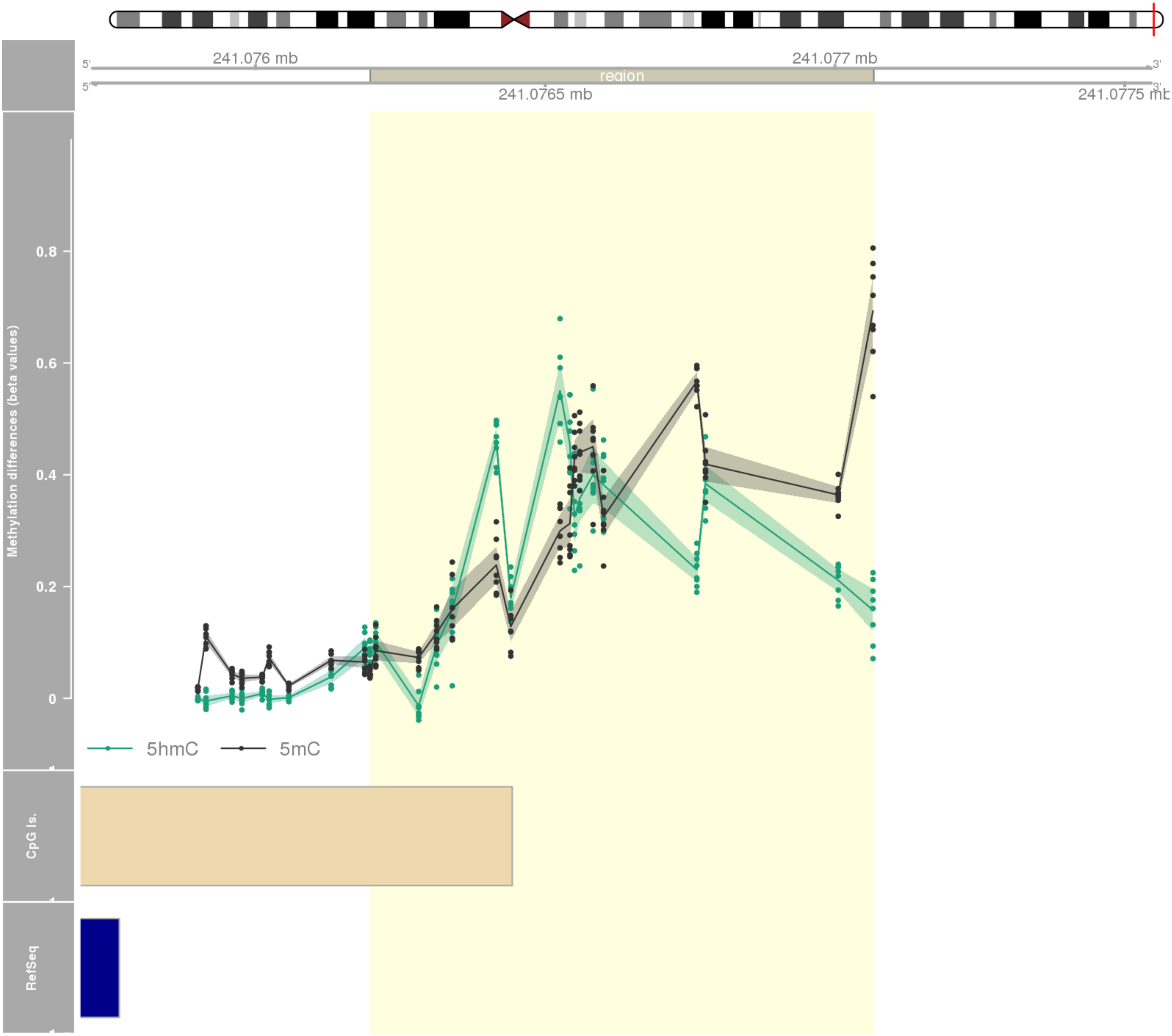
DMR 64 // chr17:80559059-80562120 // 3061 pb. (12 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.449
- genes: FOXK2 -



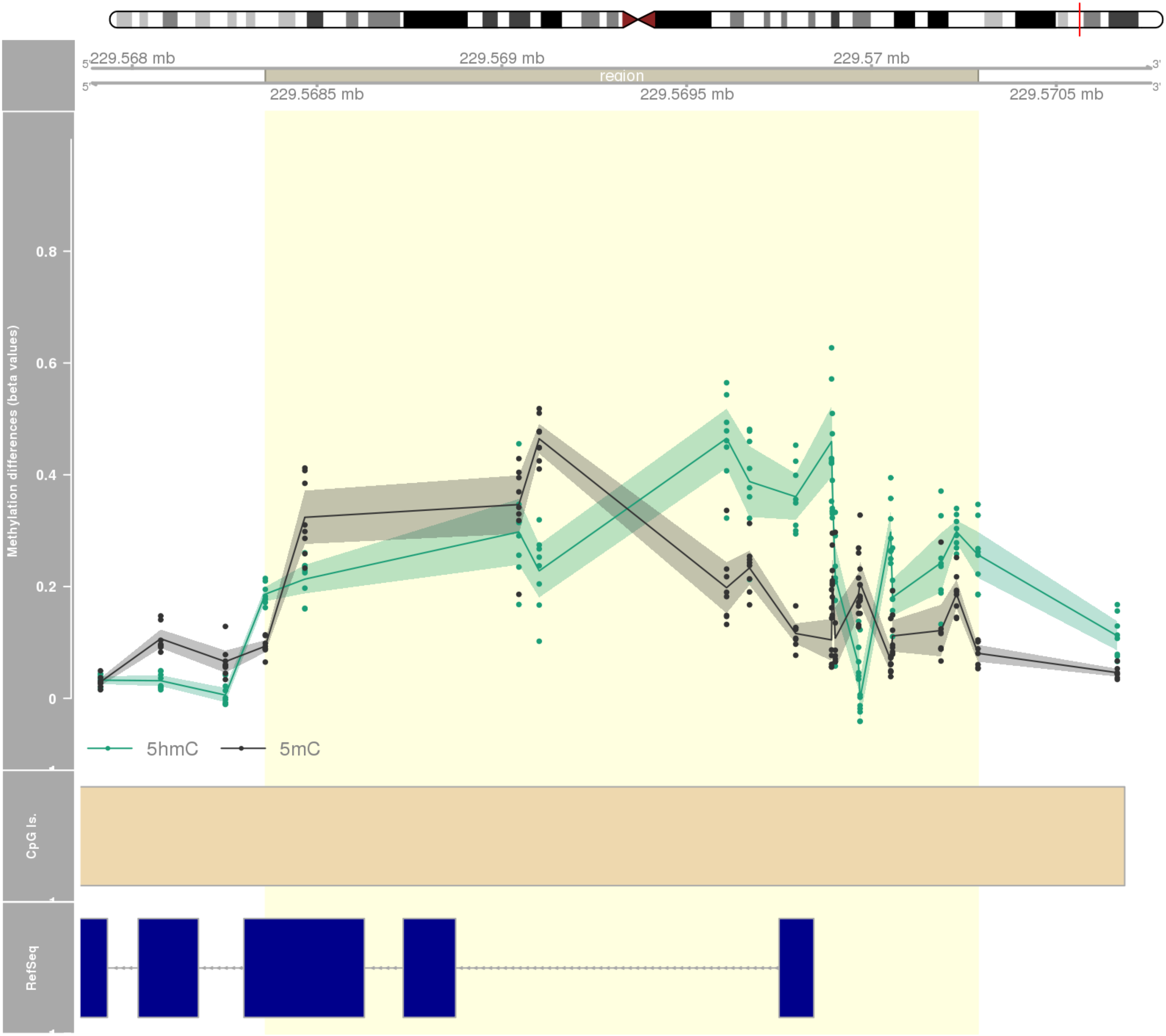
DMR 65 // chr17:41277974-41278712 // 738 pb. (21 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.449
- genes: NBR2 -



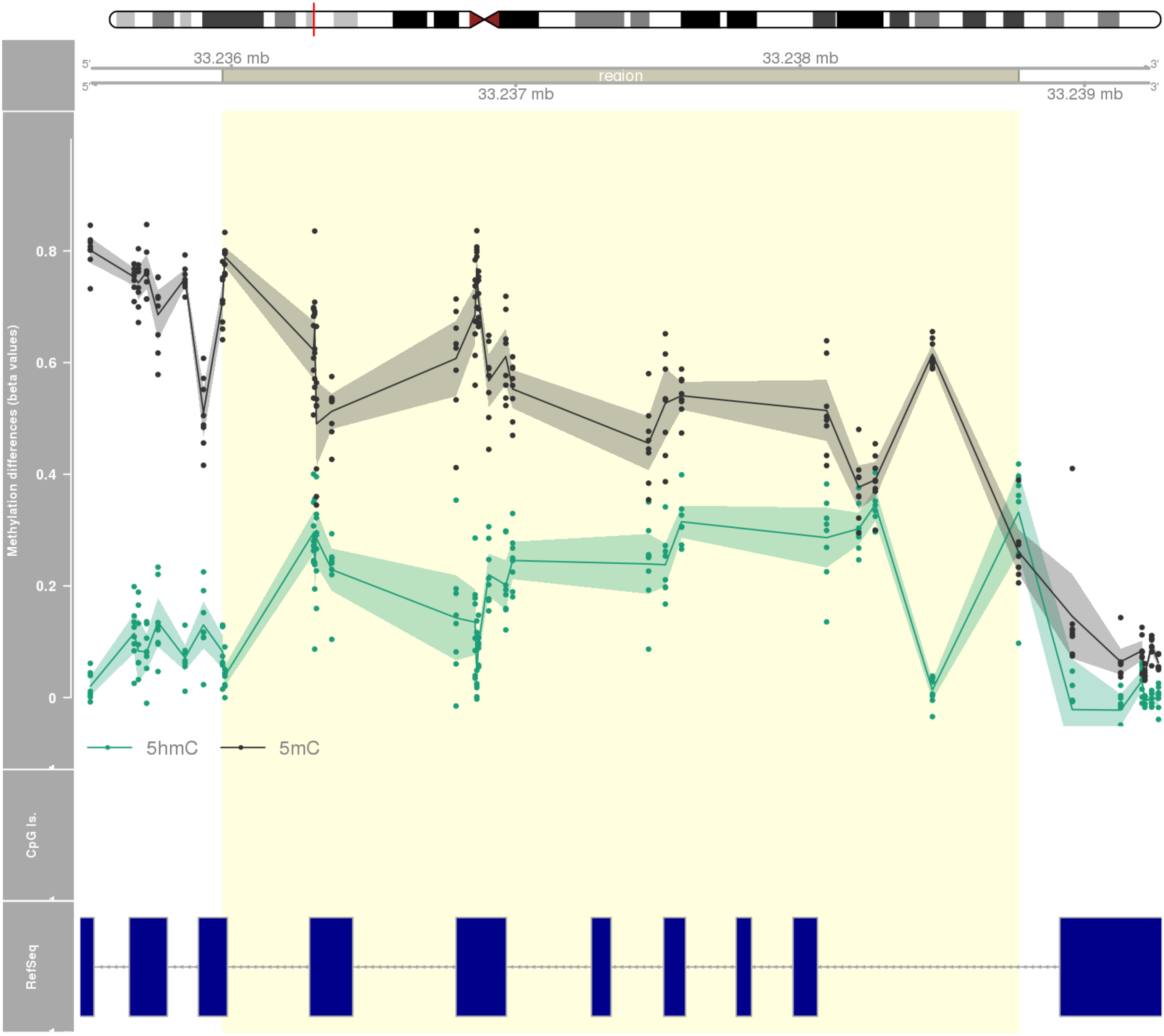
DMR 66 // chr2:241076198-241077066 // 868 pb. (17 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.003 // fwerArea: 0.449
- genes: MYEOV2 -



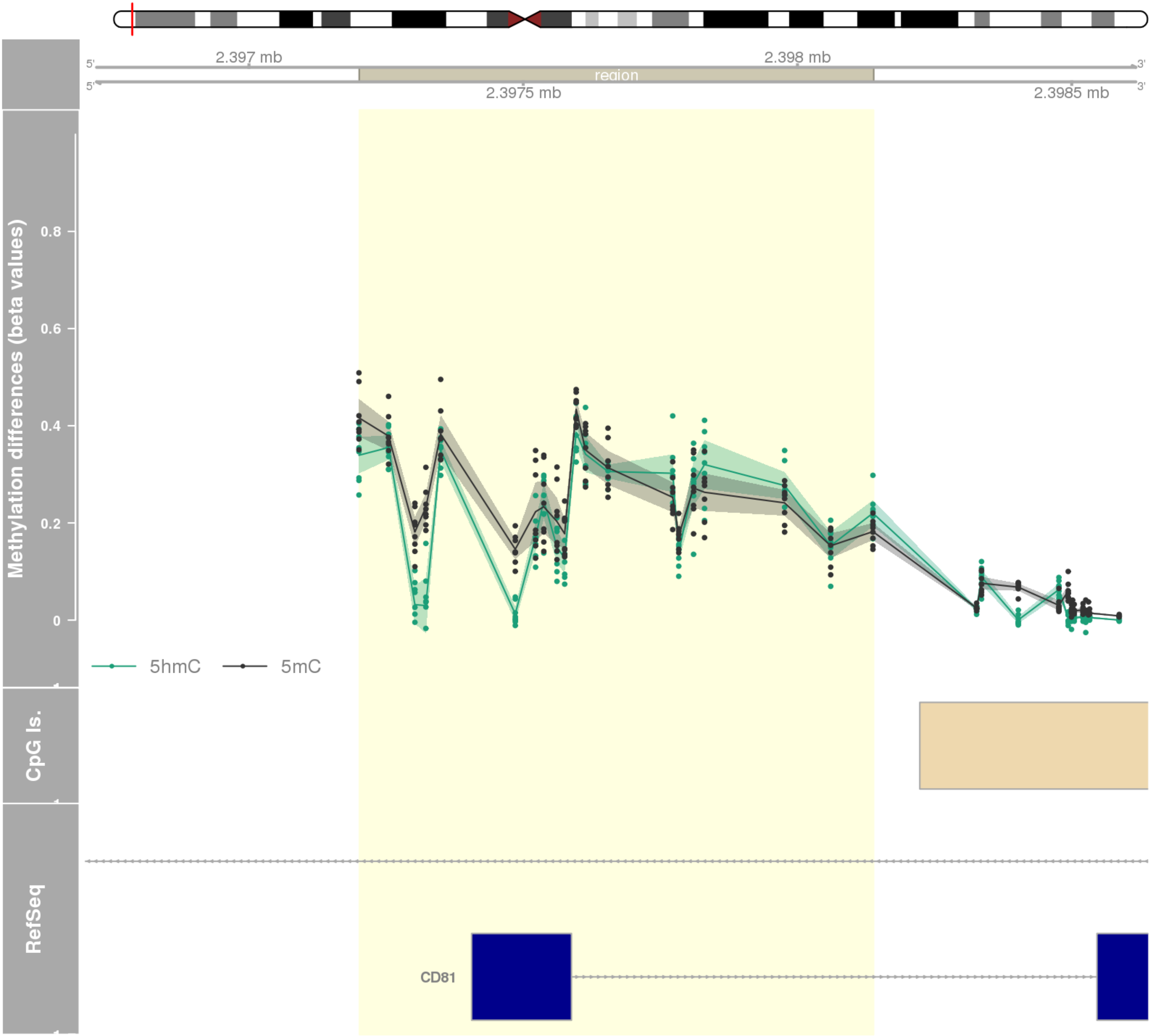
DMR 67 // chr1:229568360-229570288 // 1928 pb. (17 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: ACTA1 -



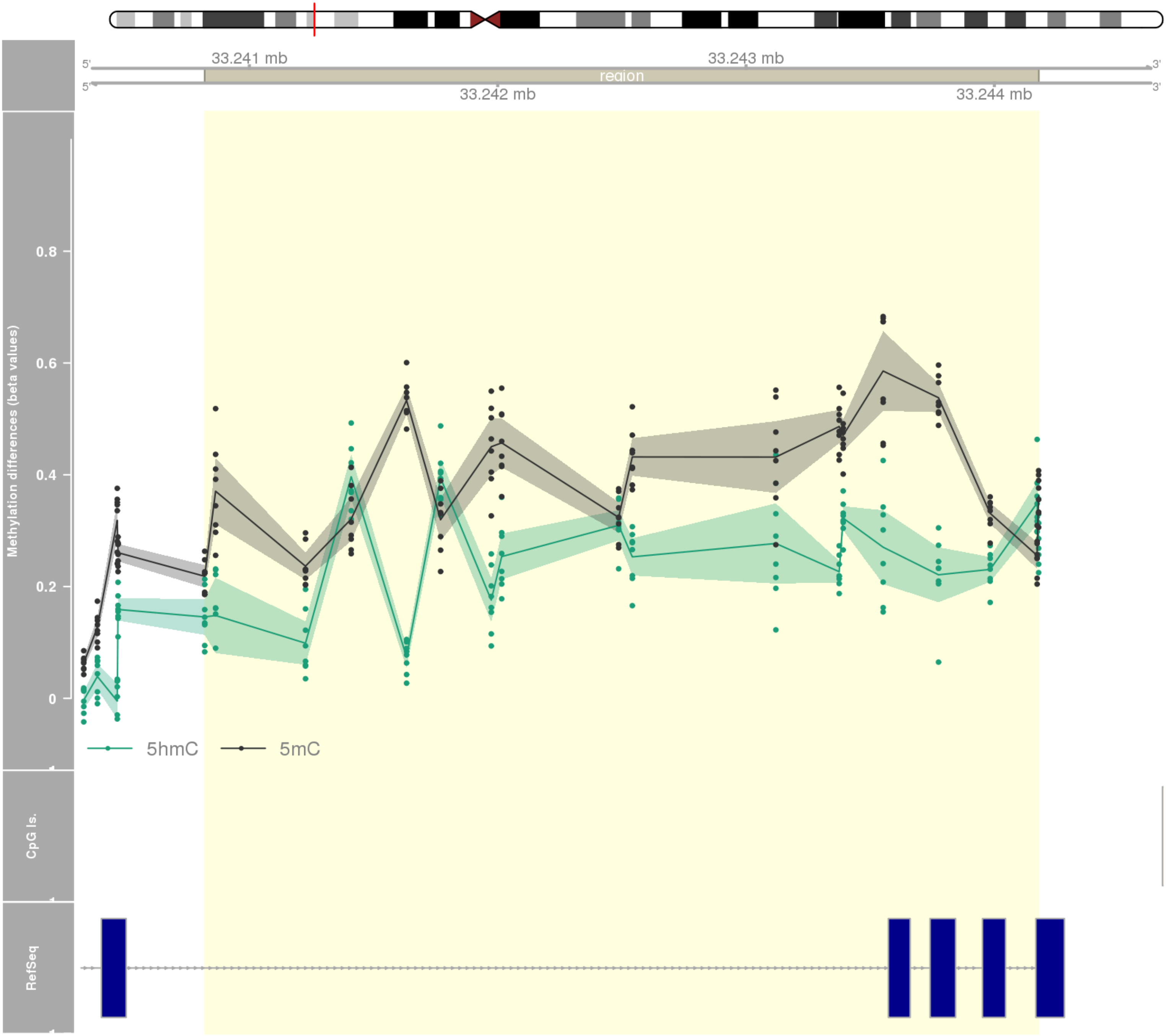
DMR 68 // chr6:33235969-33238768 // 2799 pb. (21 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: VPS52 -



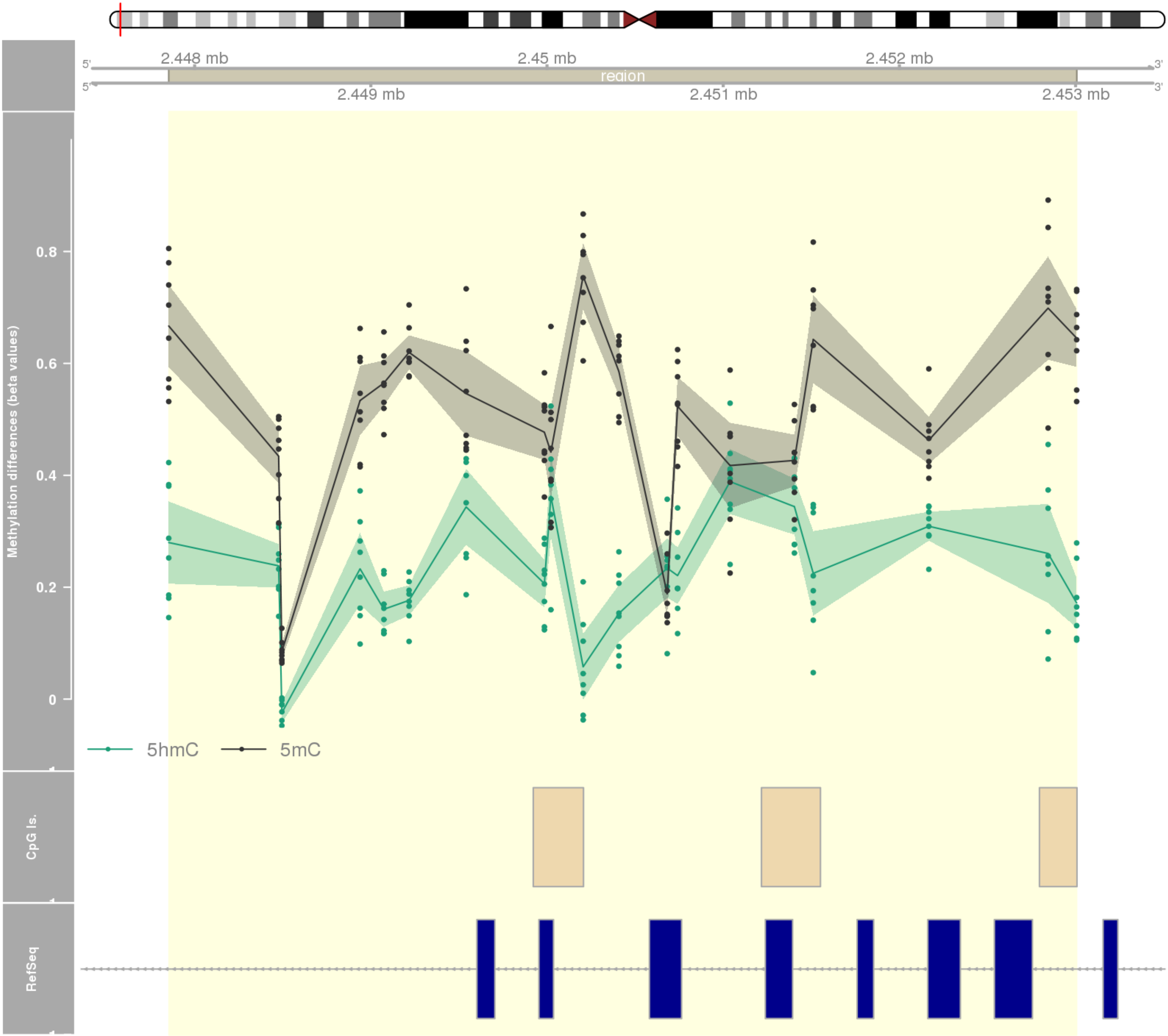
DMR 69 // chr11:2397201-2398138 // 937 pb. (20 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: CD81-AS1 / CD81 -



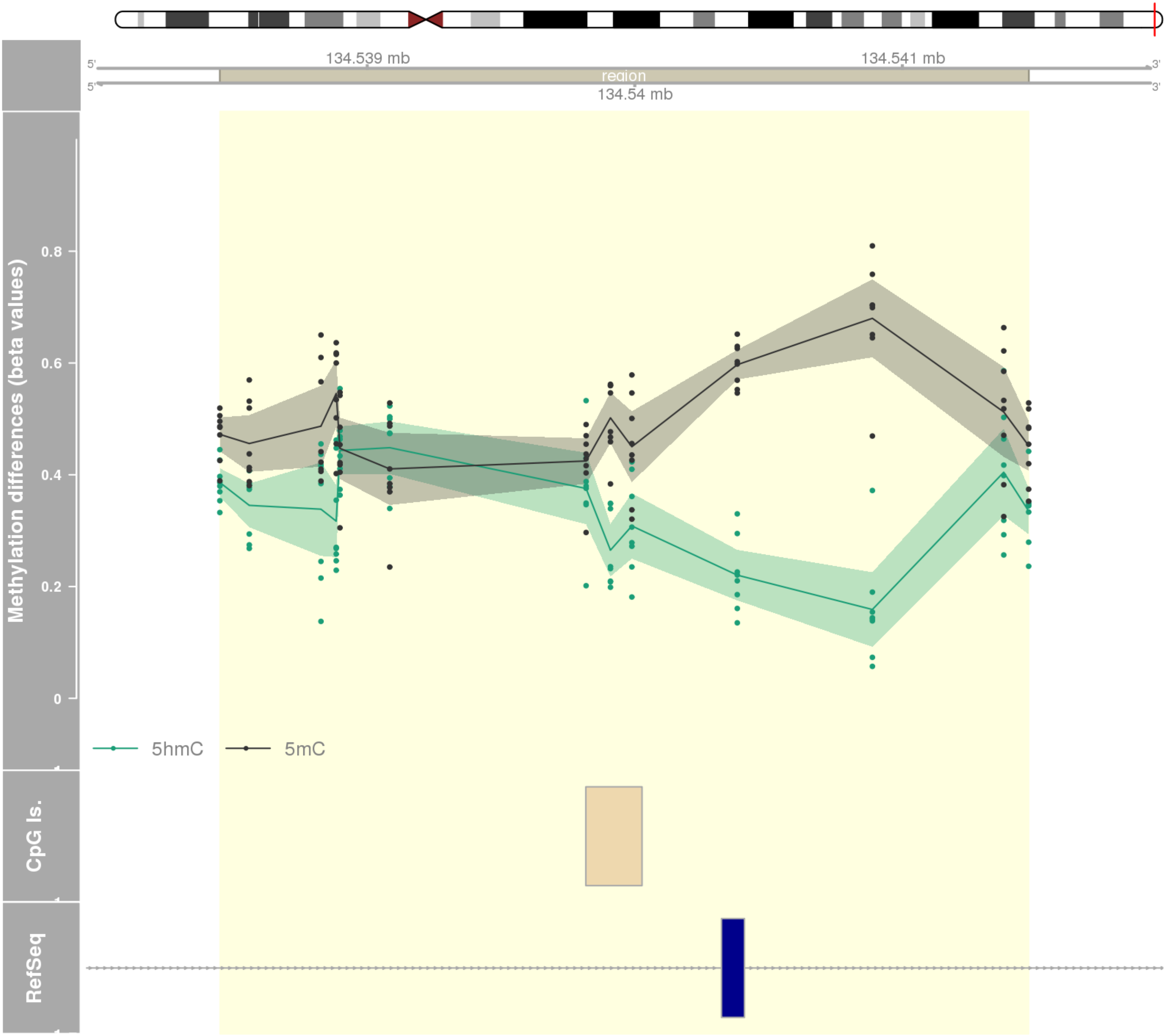
DMR 70 // chr6:33240820-33244178 // 3358 pb. (18 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: RPS18 -



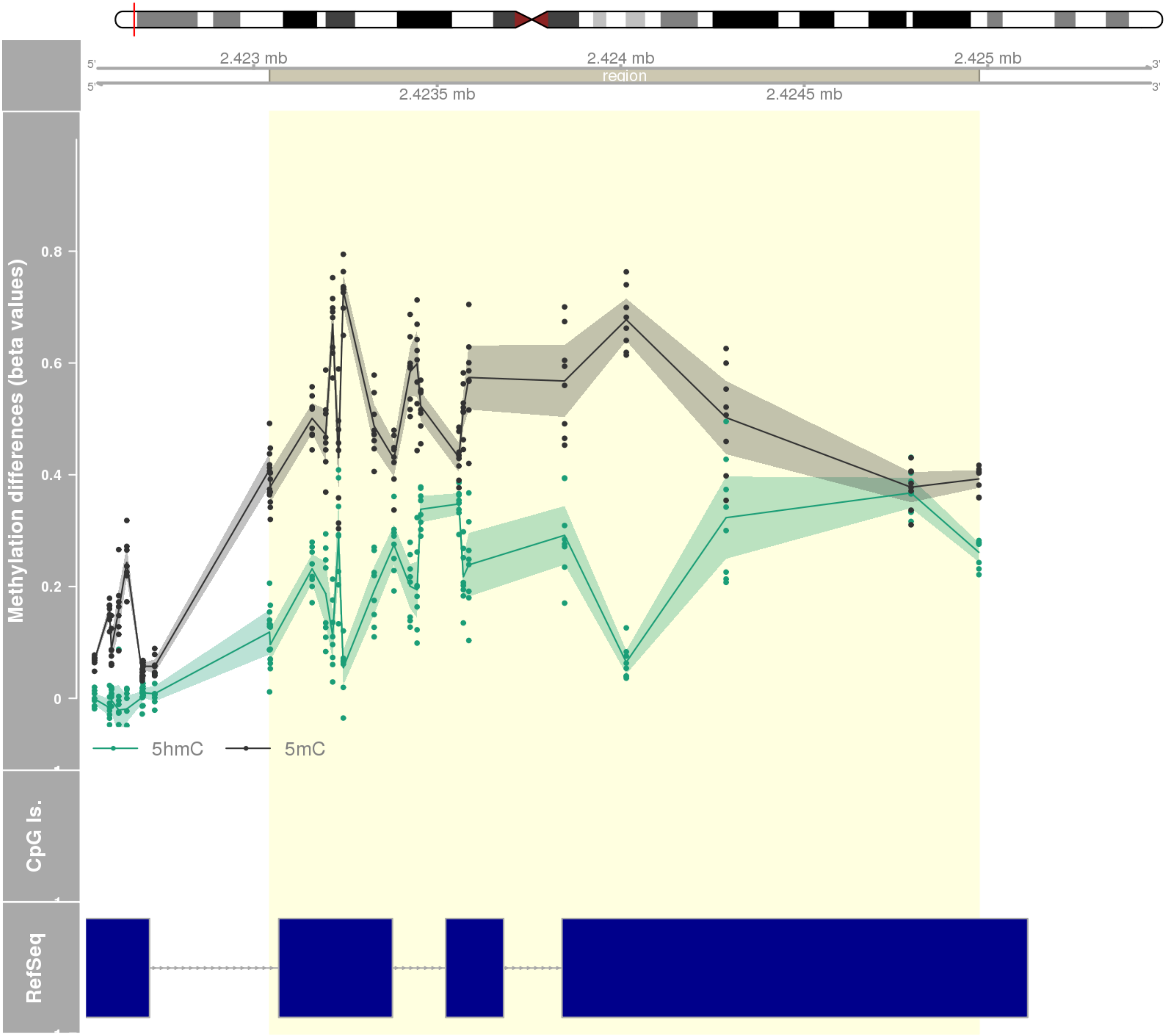
DMR 71 // chr1:2447853-2453006 // 5153 pb. (19 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: PANK4 -



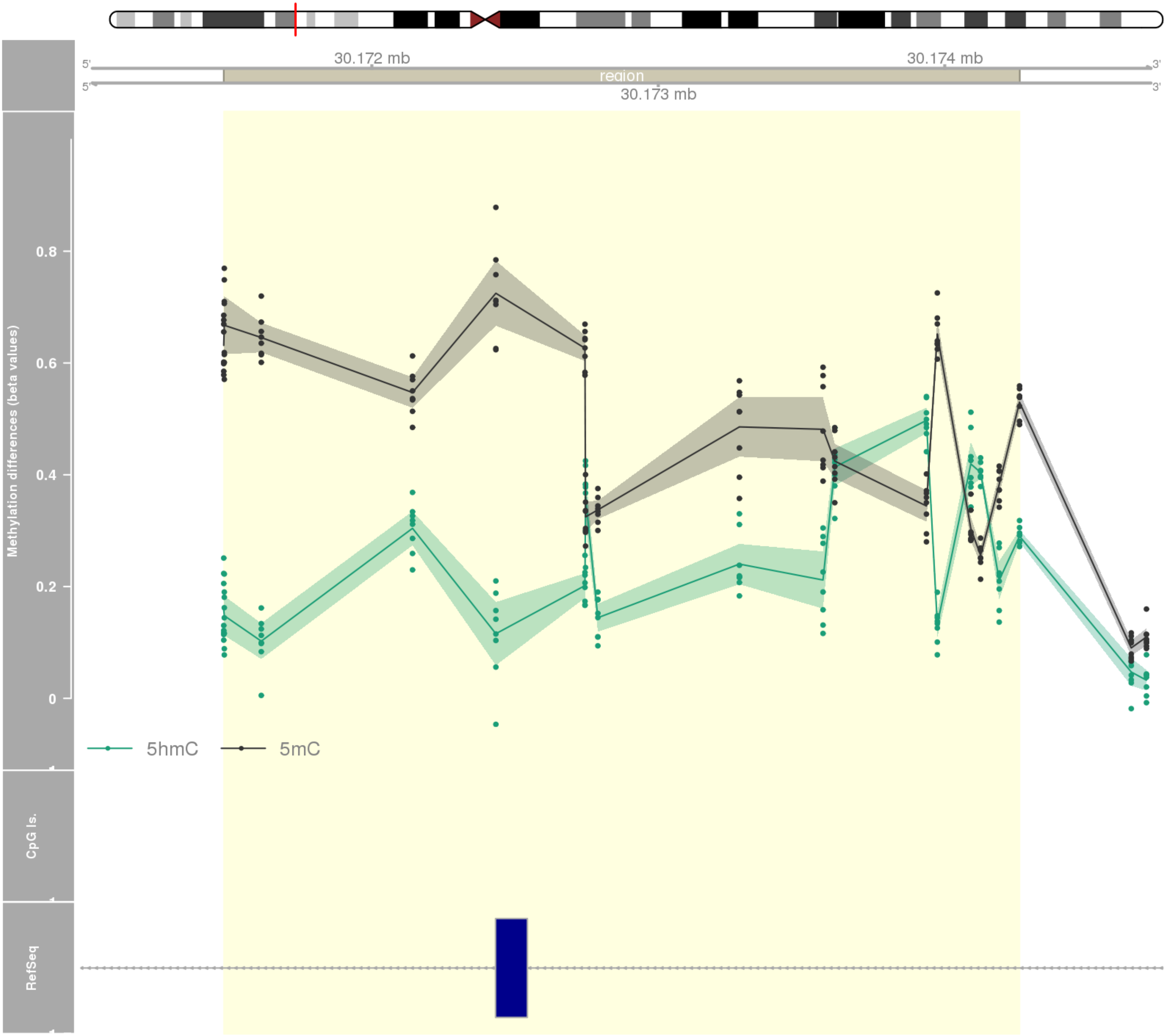
DMR 72 // chr10:134538449-134541472 // 3023 pb. (13 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: INPP5A -

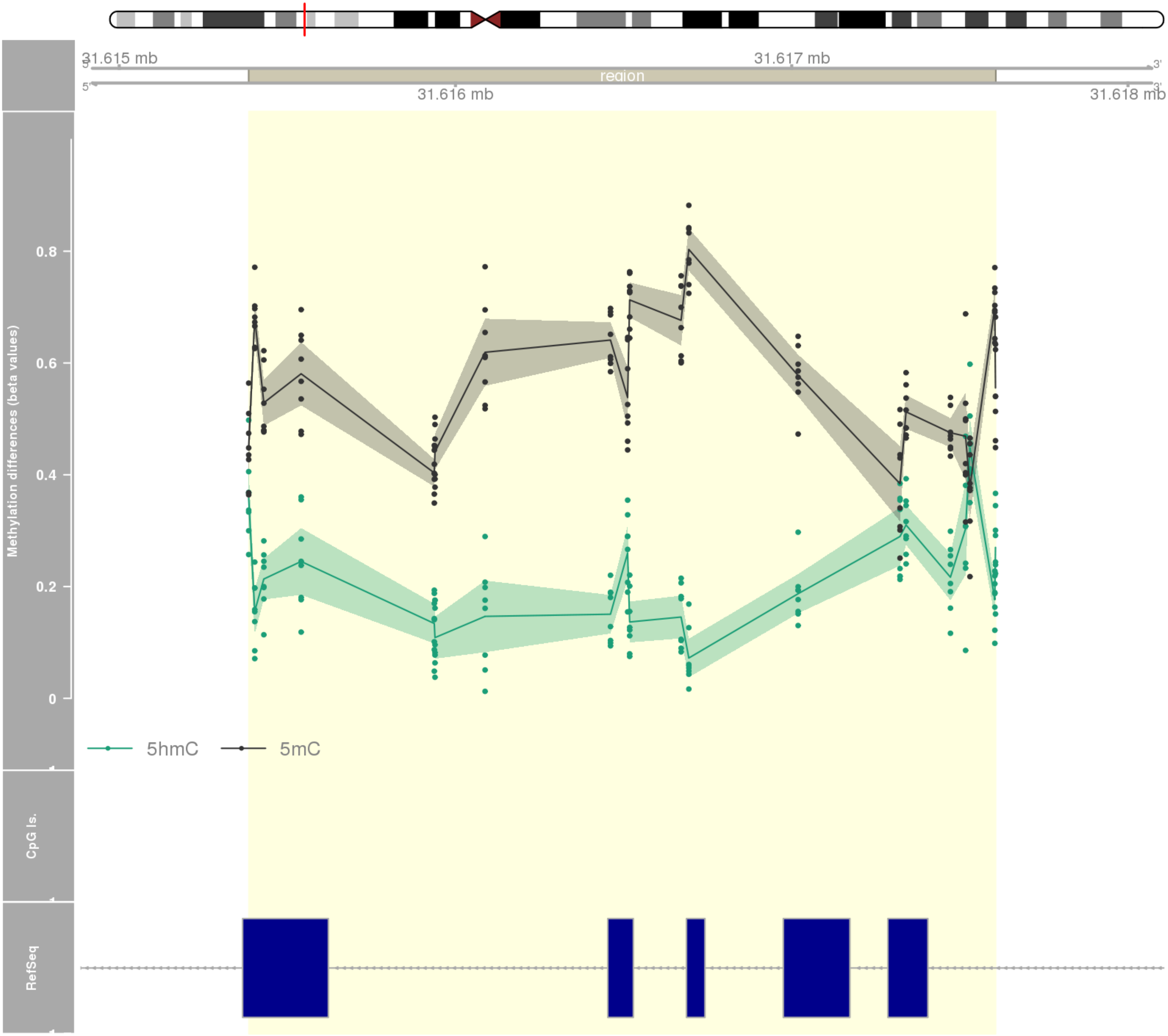


DMR 73 // chr11:2423043-2424976 // 1933 pb. (20 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: TSSC4 -



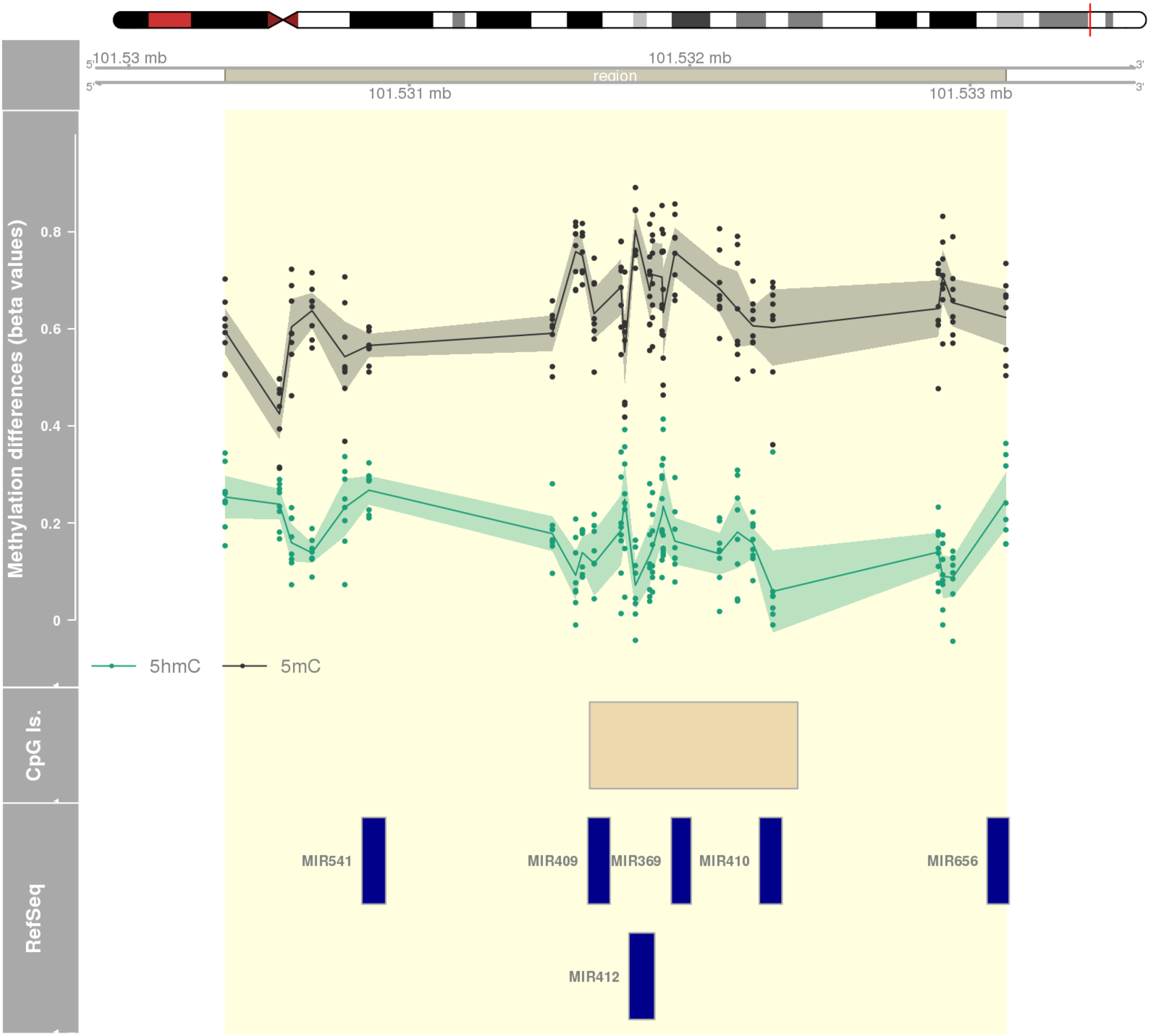
DMR 74 // chr6:30171483-30174261 // 2778 pb. (17 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: TRIM26 -



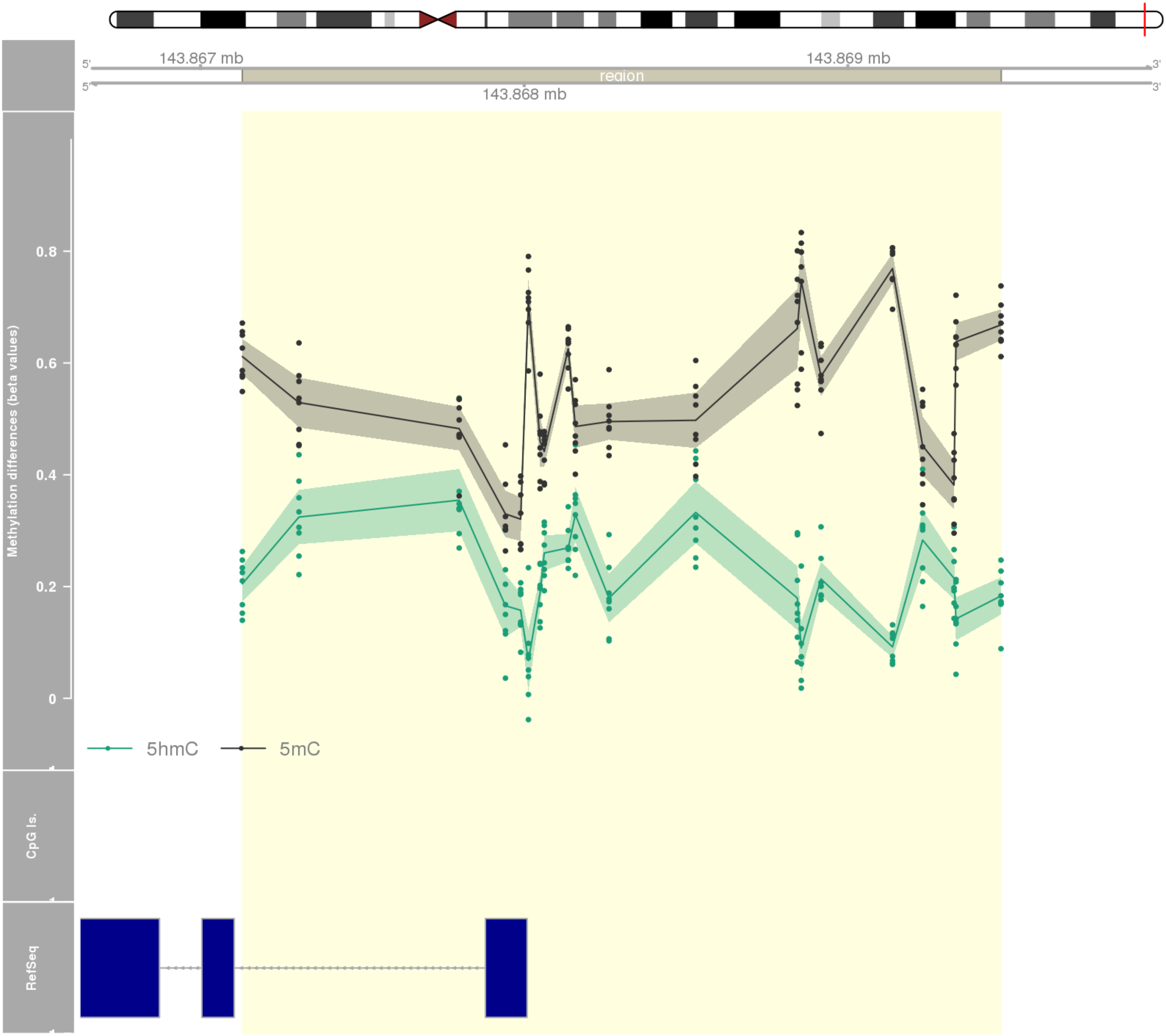


DMR 75 // chr6:31615385-31617606 // 2221 pb. (20 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: BAG6 -

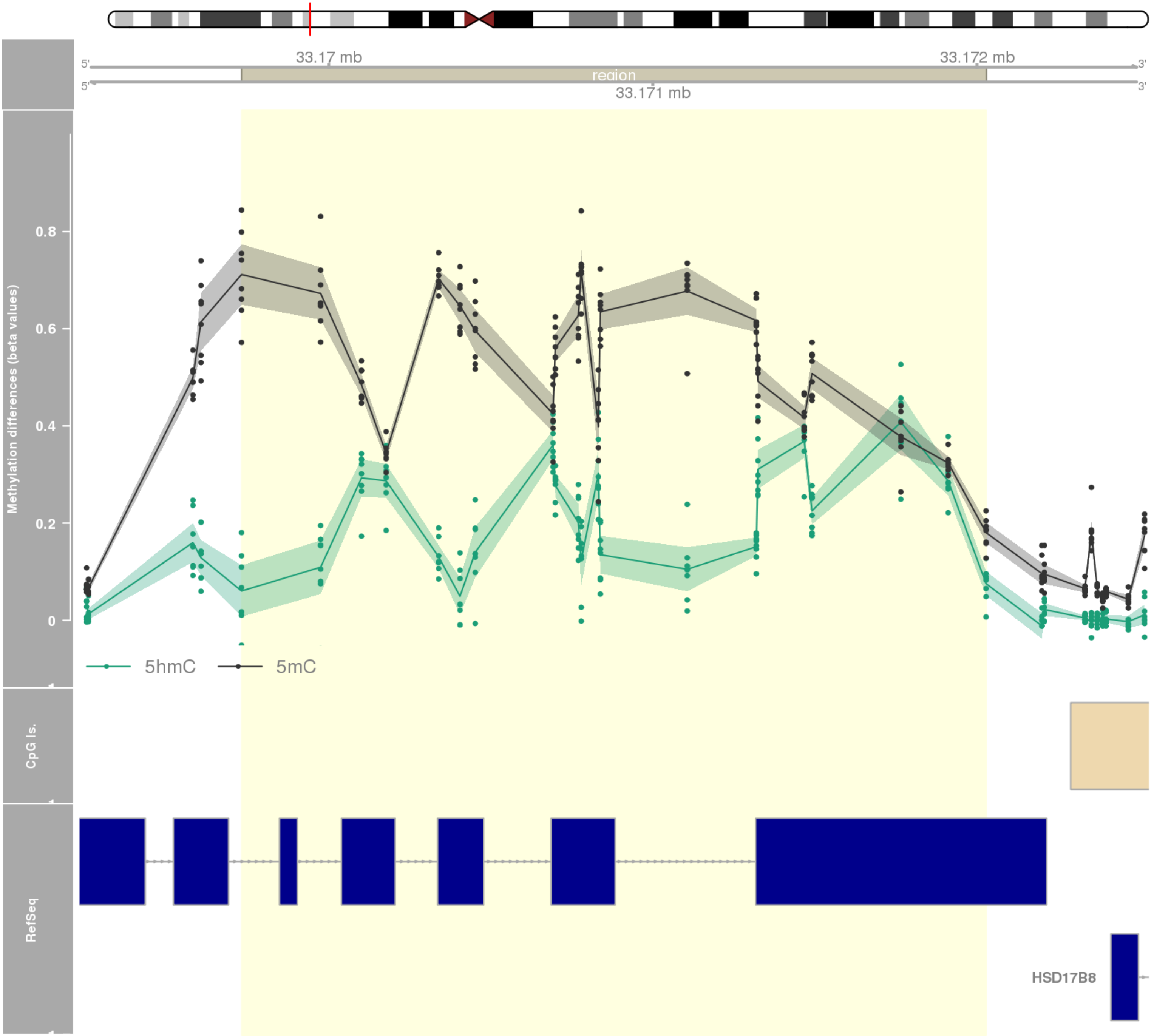
DMR 76 // chr14:101530343-101533127 // 2784 pb. (26 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: MIR541 / MIR409 / MIR412 / MIR369 / MIR410 / MIR656 -



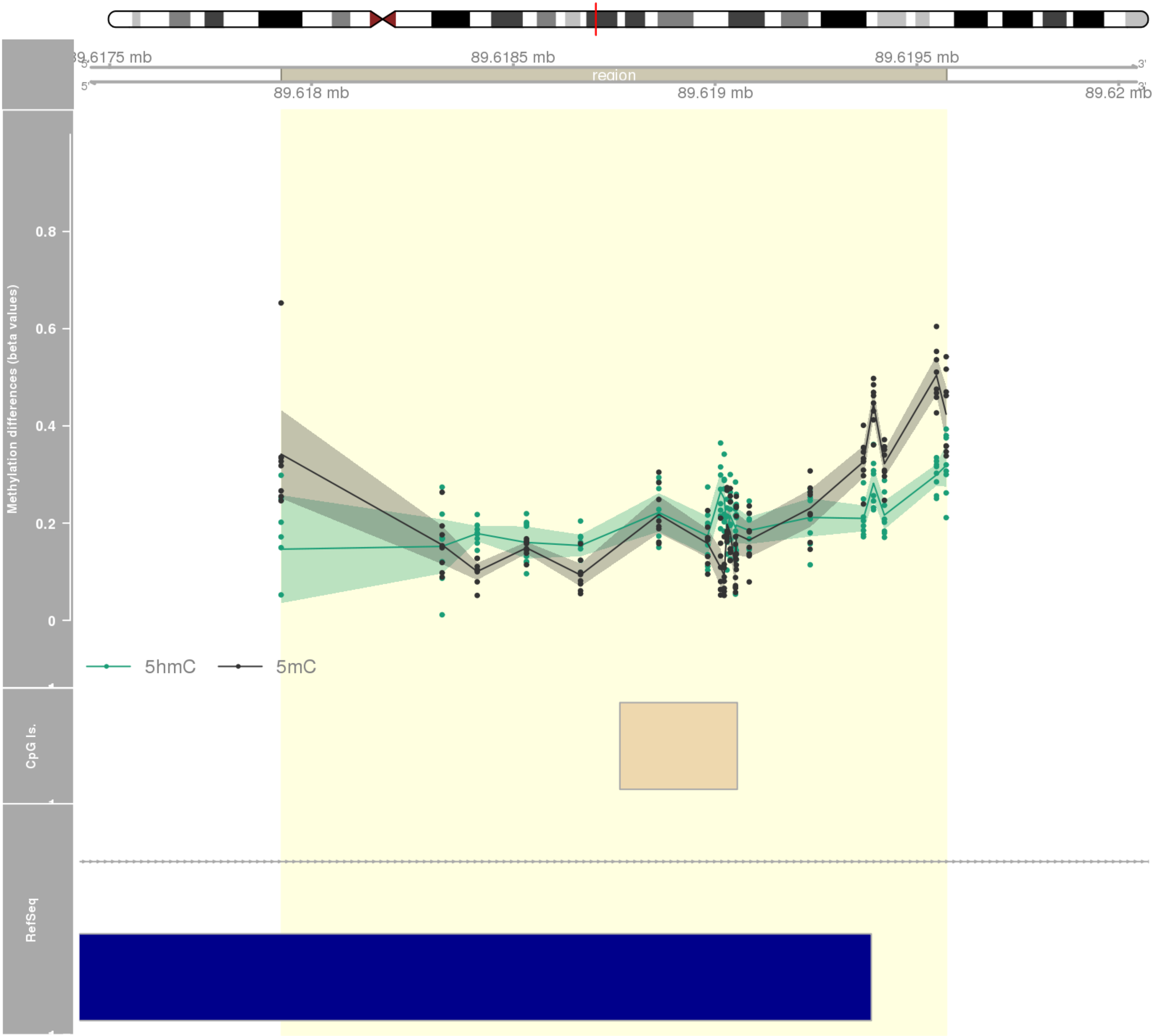
DMR 77 // chr8:143867129-143869473 // 2344 pb. (20 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: LY6D -

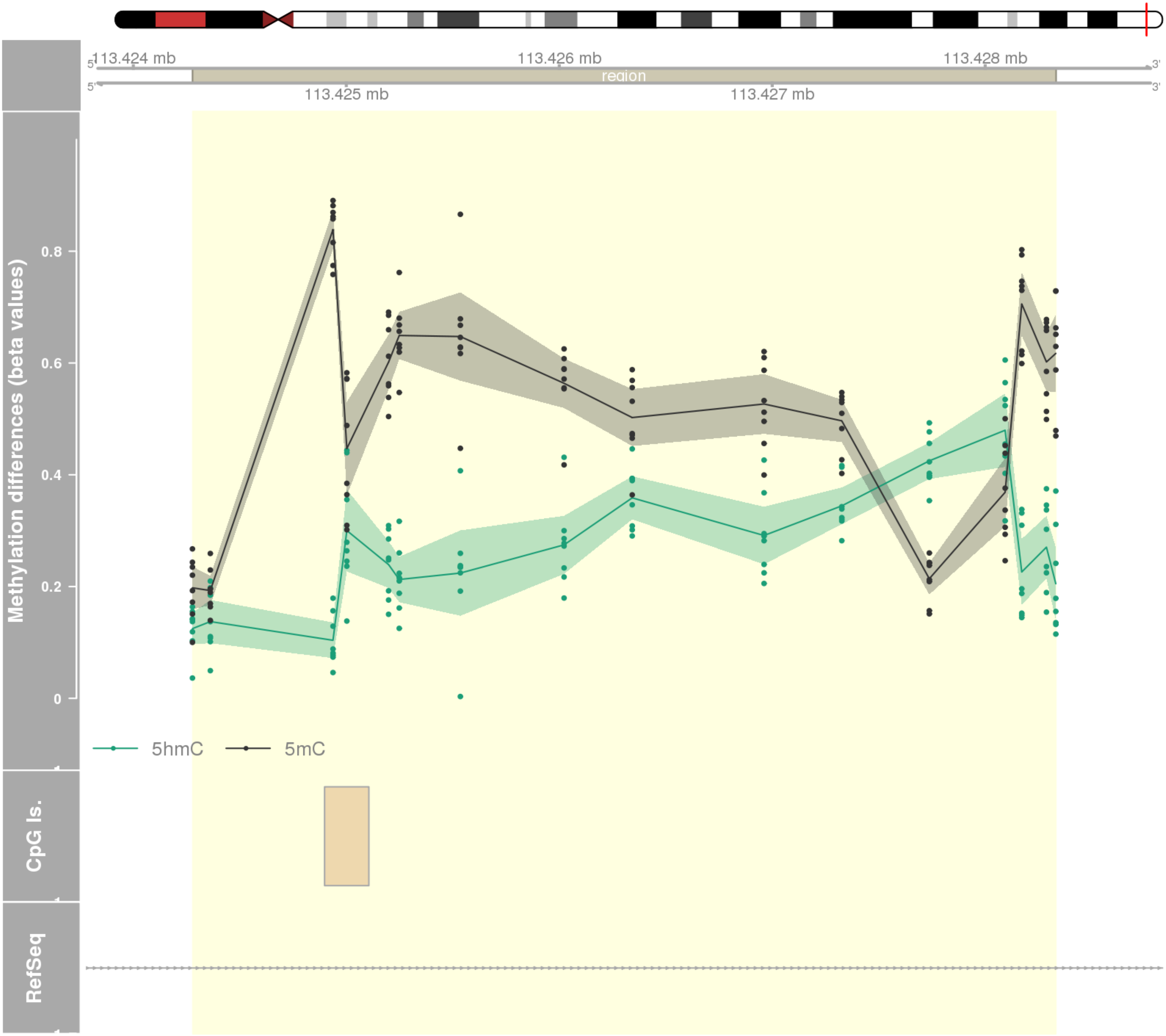


DMR 78 // chr6:33169731-33172028 // 2297 pb. (21 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: SLC39A7 -



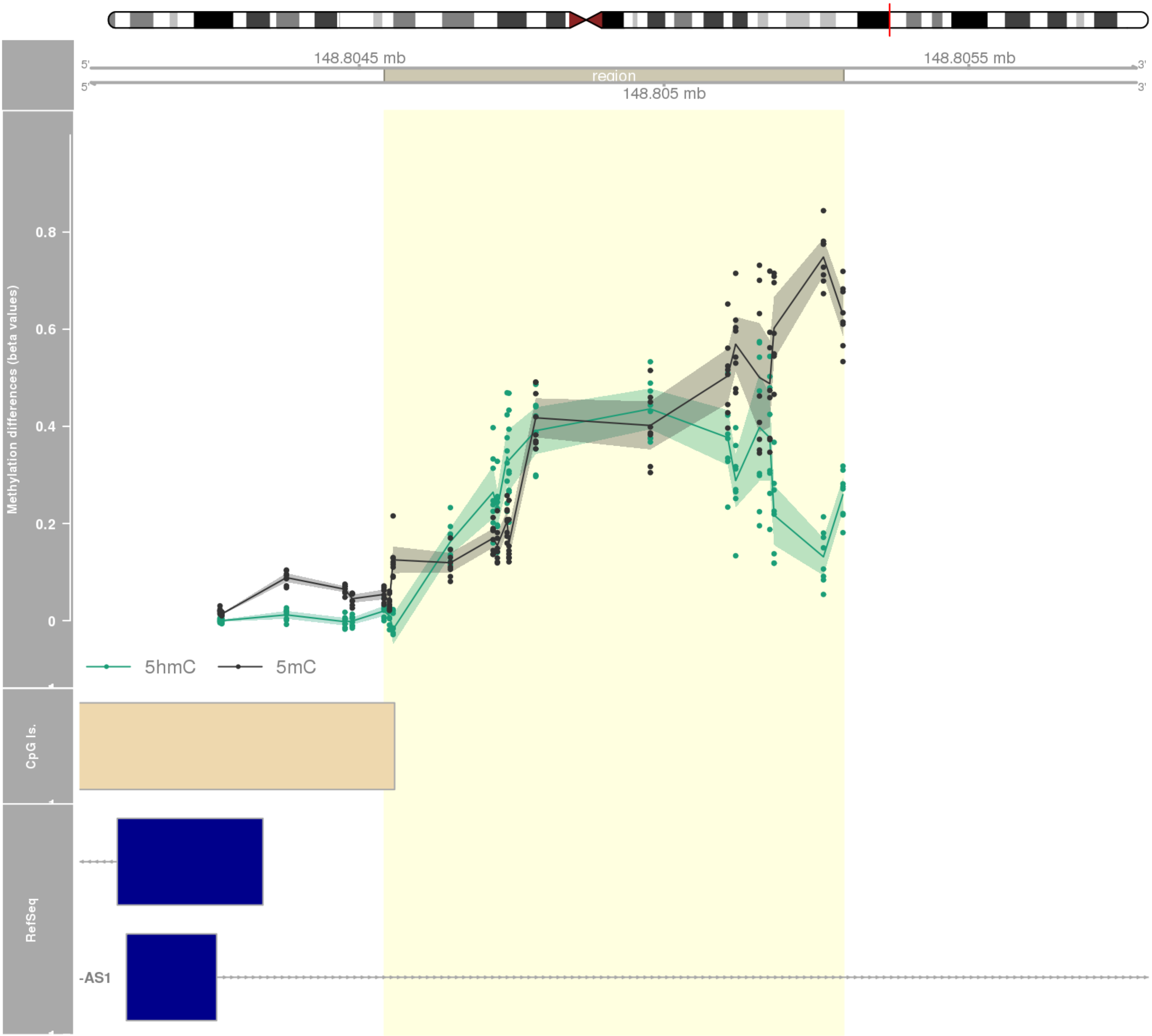
DMR 79 // chr4:89617925-89619573 // 1648 pb. (20 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: HERC3 / NAP1L5 -



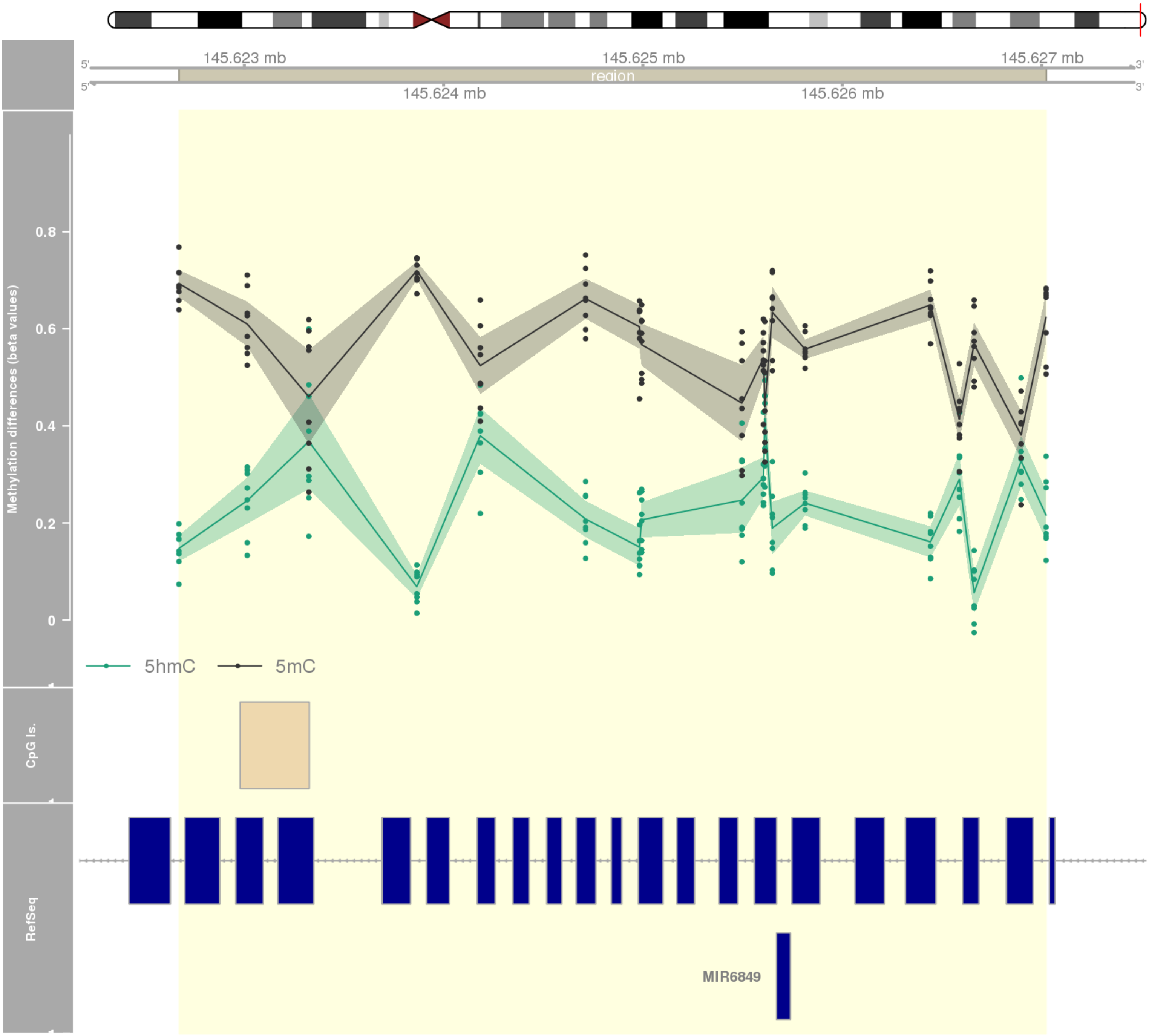


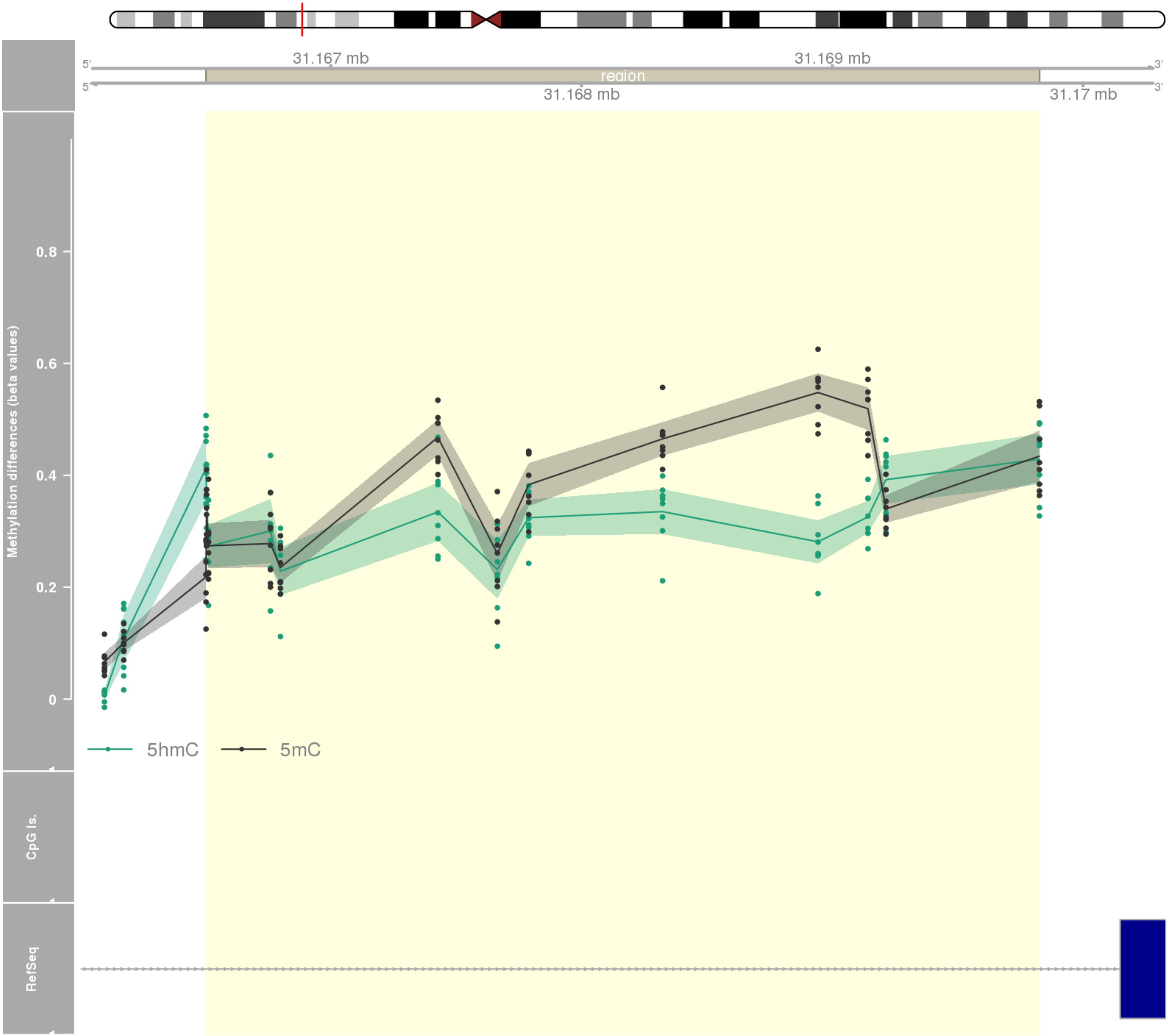
DMR 80 // chr13:113424278-113428332 // 4054 pb. (16 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: ATP11A -

DMR 81 // chr3:148804541-148805294 // 753 pb. (17 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: HLTF-AS1 -



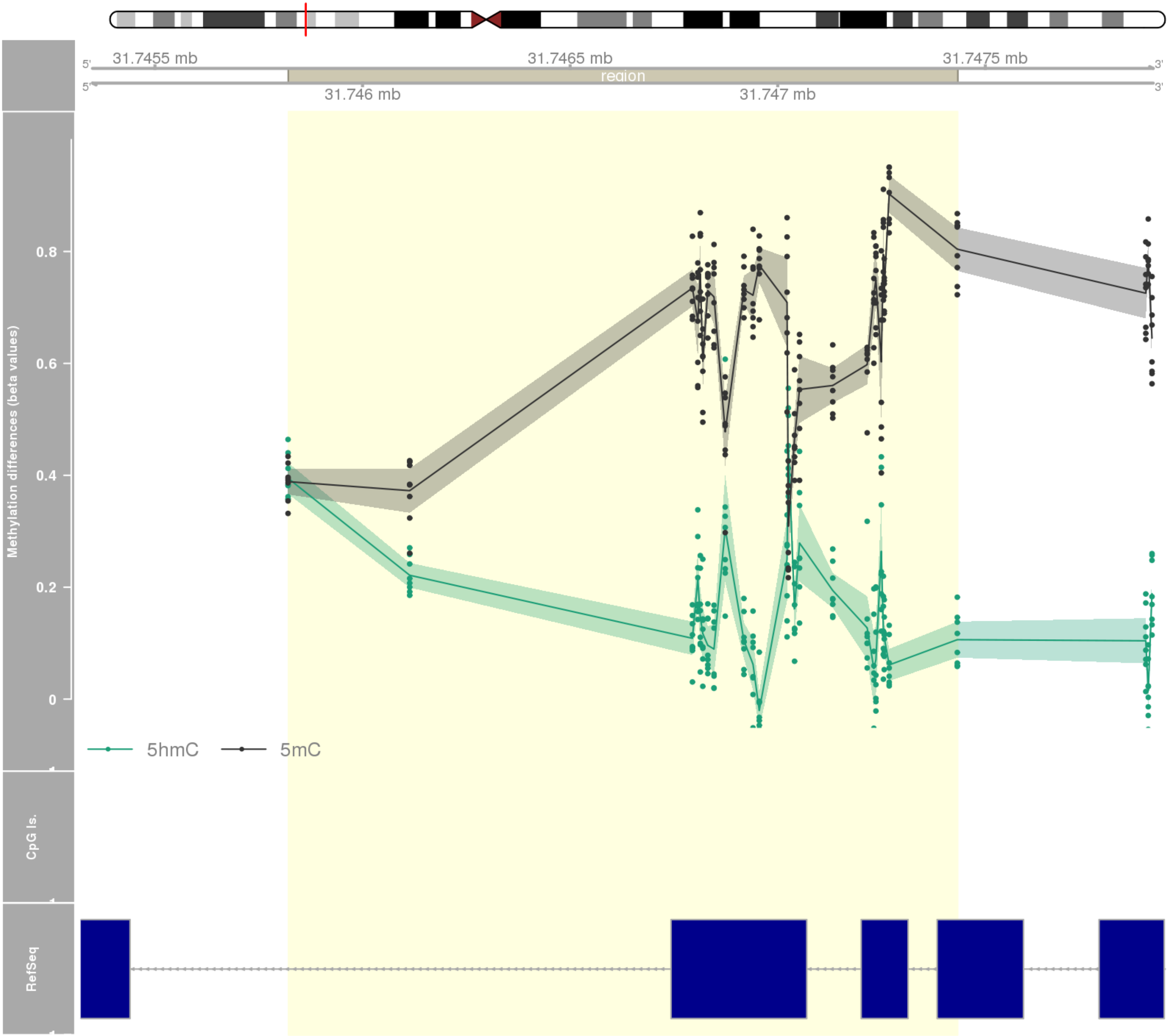
DMR 82 // chr8:145622672-145627023 // 4351 pb. (18 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: MIR1234 / CPSF1 -



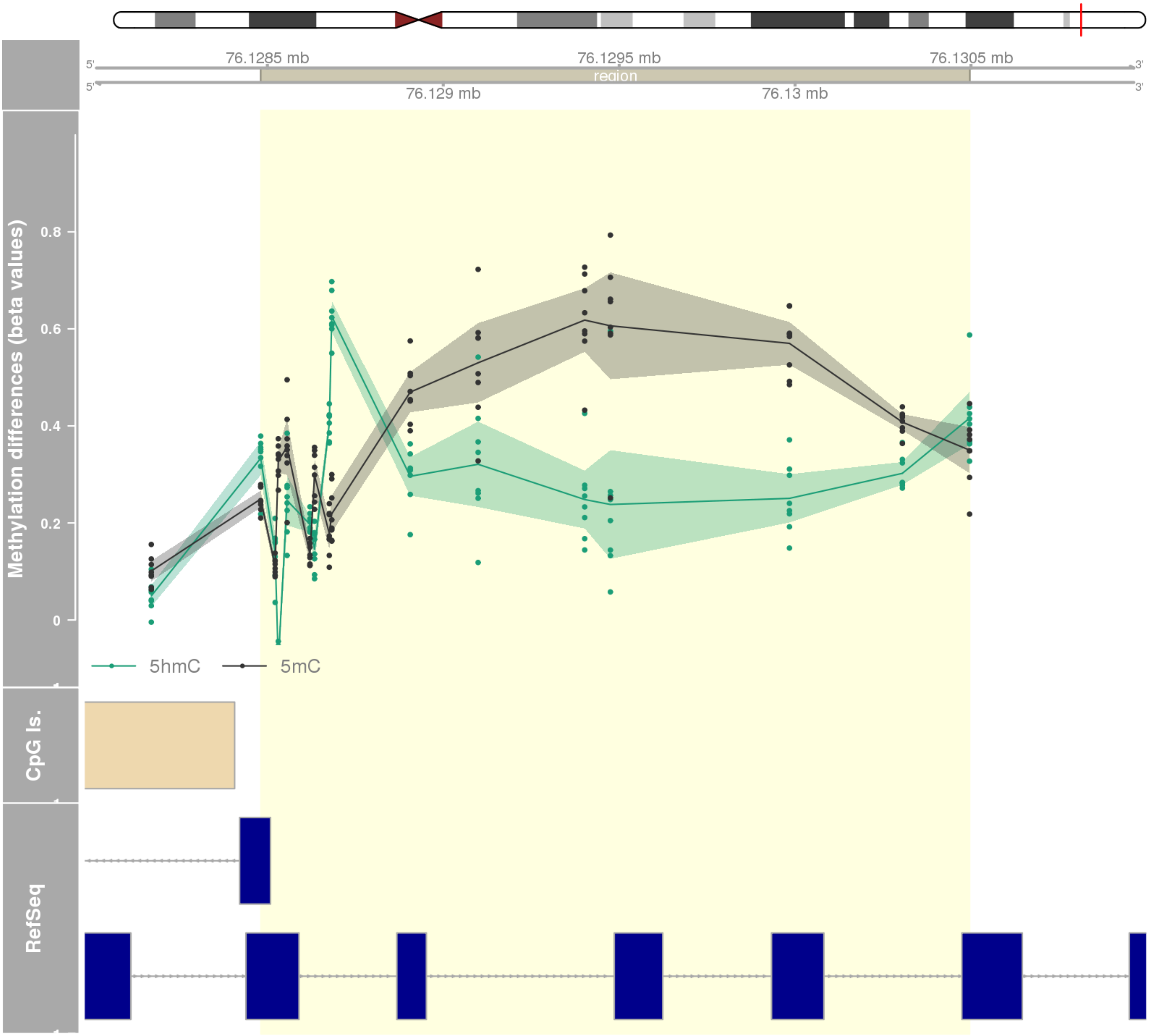


DMR 83 // chr6:31166502-31169826 // 3324 pb. (13 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: HCG27 -

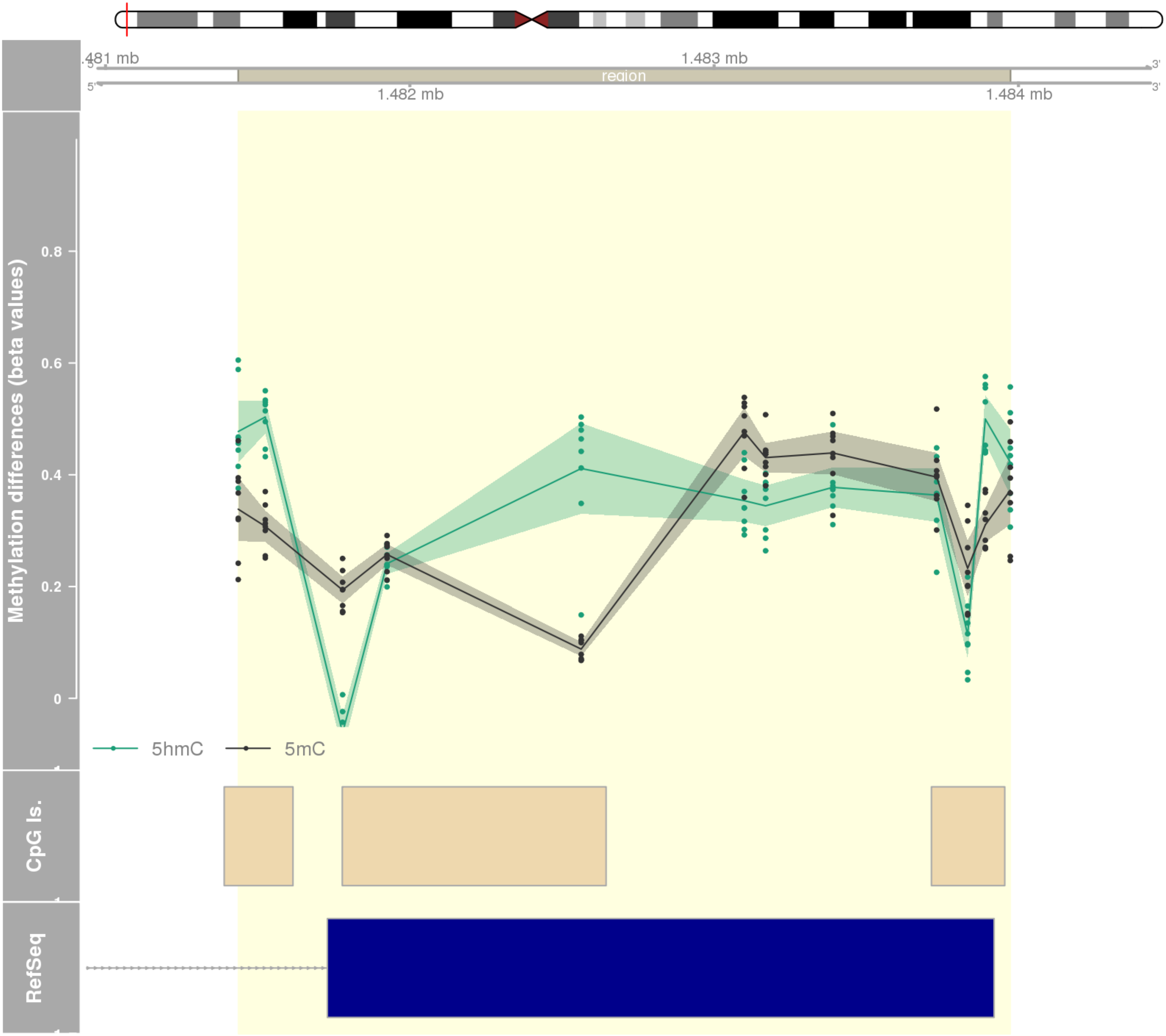
DMR 84 // chr6:31745821-31747433 // 1612 pb. (25 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: VARS -



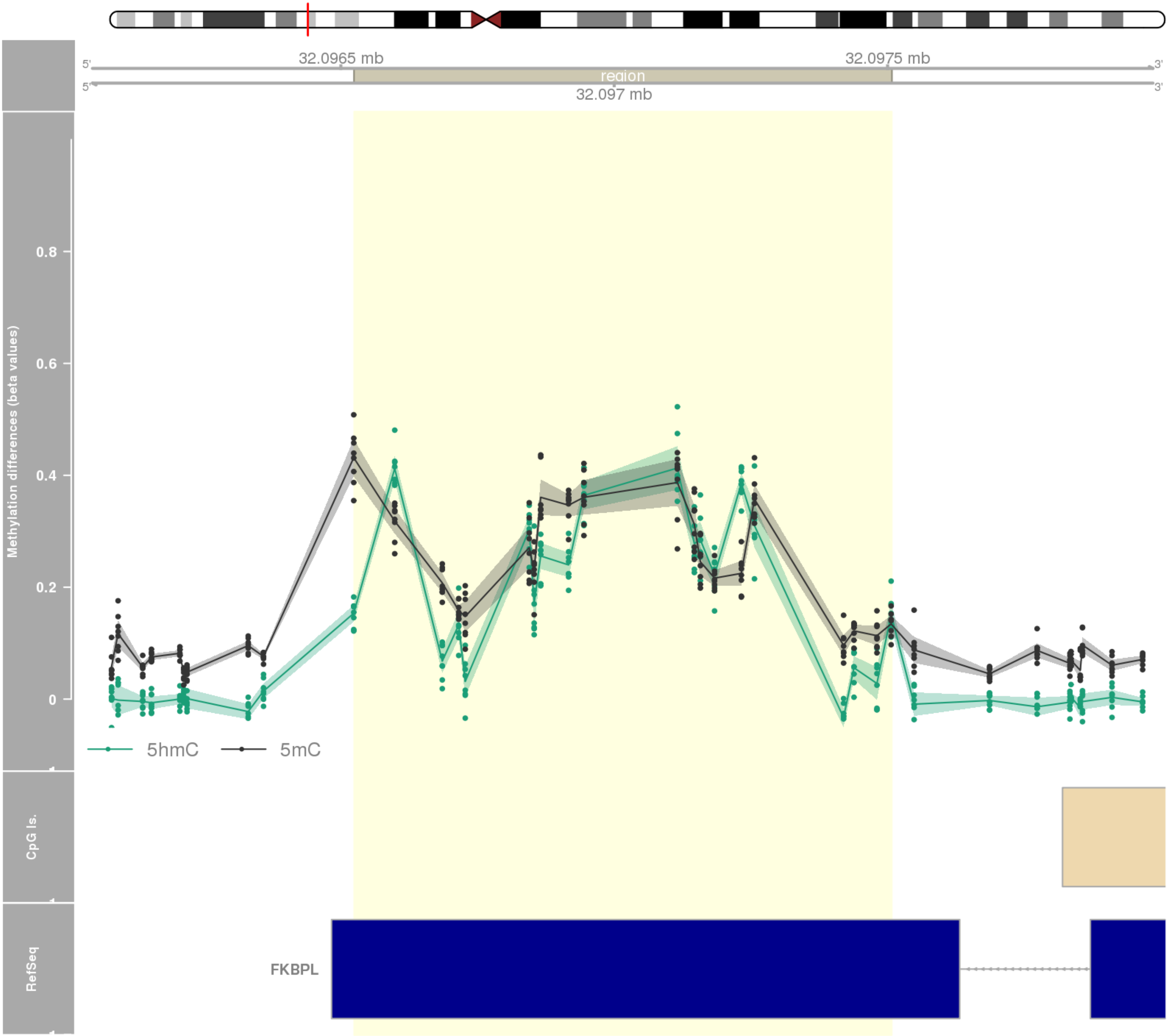
DMR 85 // chr17:76128481-76130496 // 2015 pb. (15 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: TMC6 / TMC8 -



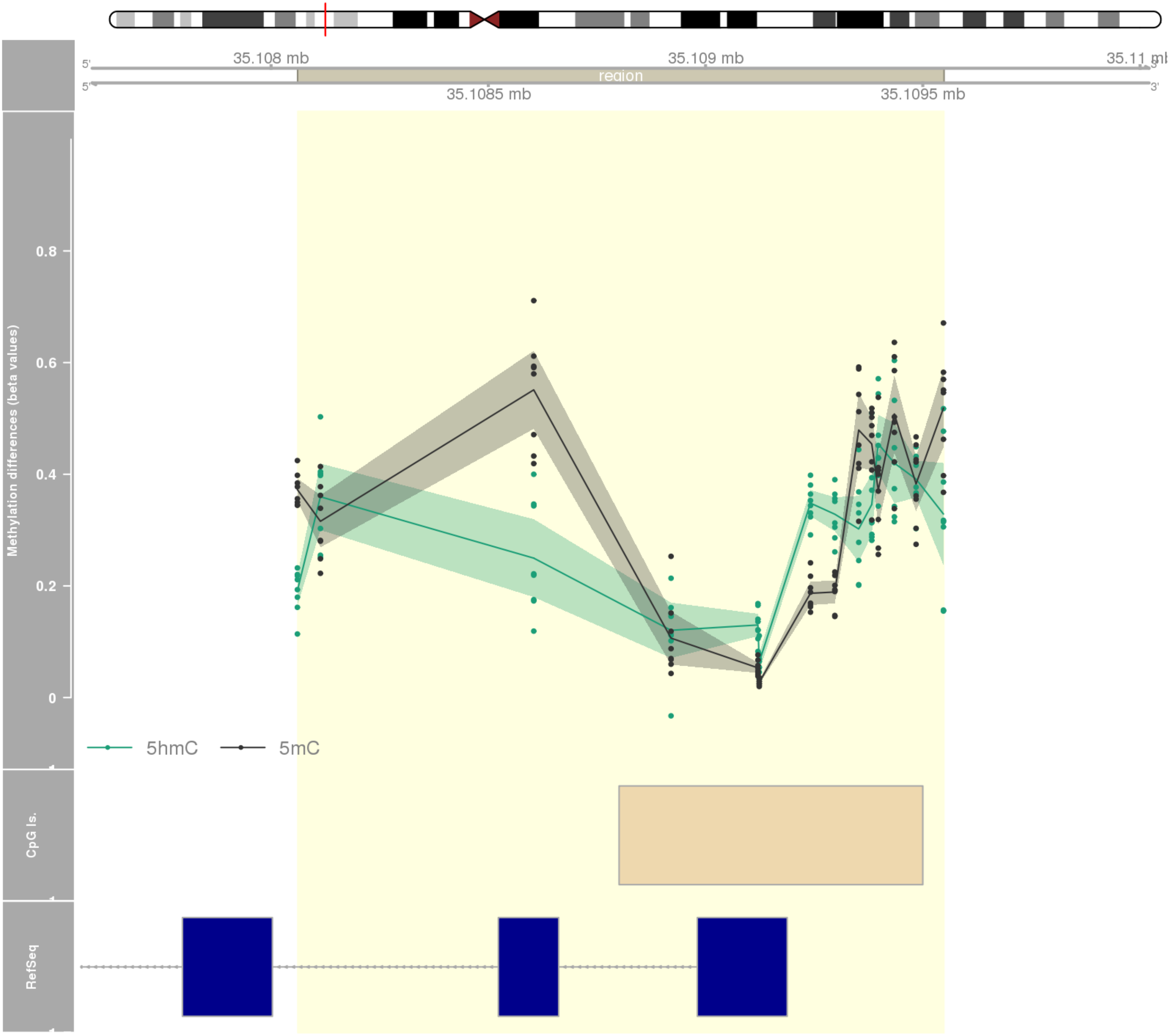
DMR 86 // chr11:1481436-1483973 // 2537 pb. (12 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.004 // fwerArea: 0.449
- genes: BRSK2 -



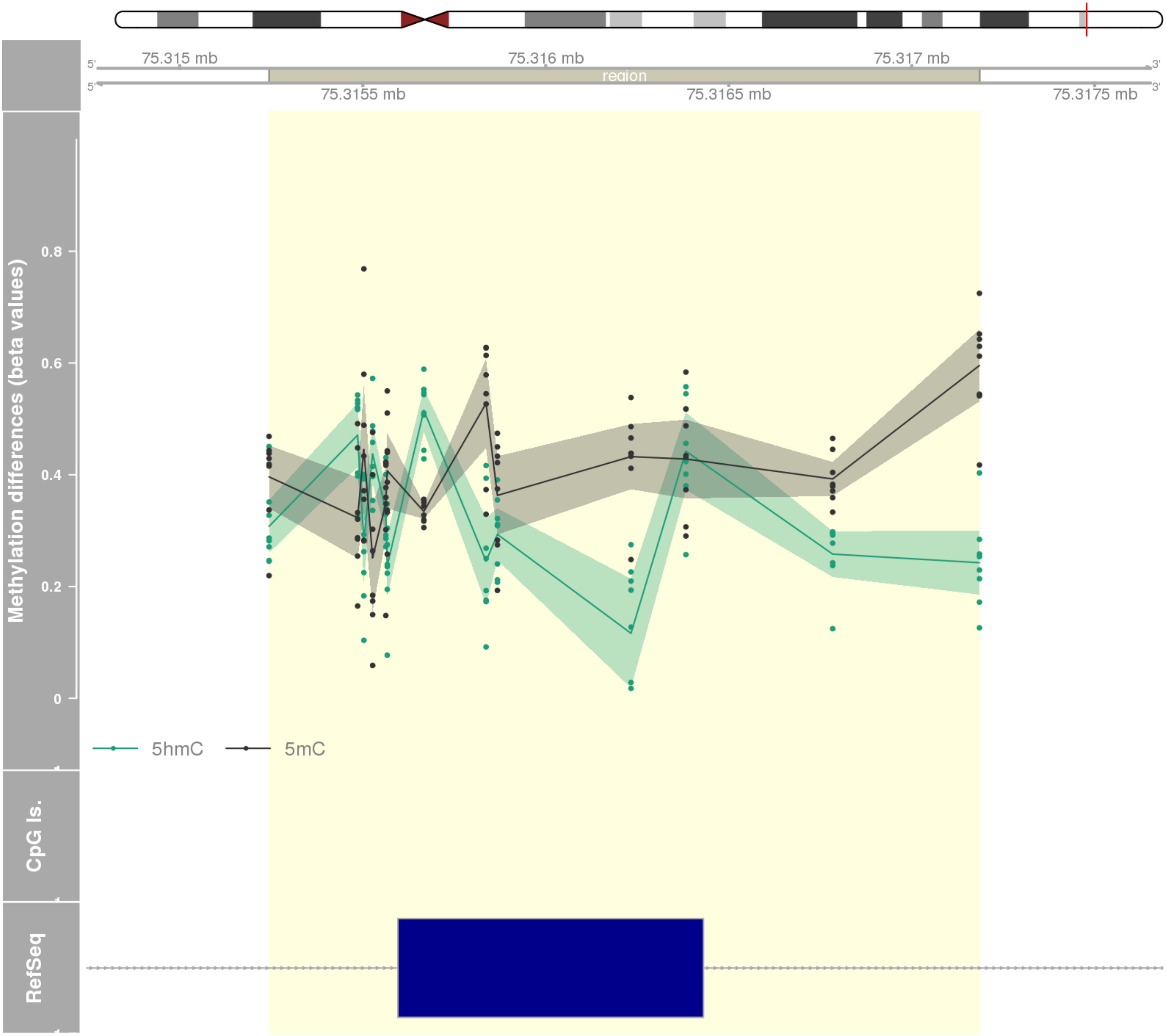
DMR 87 // chr6:32096524-32097507 // 983 pb. (20 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.449
- genes: FKBPL -



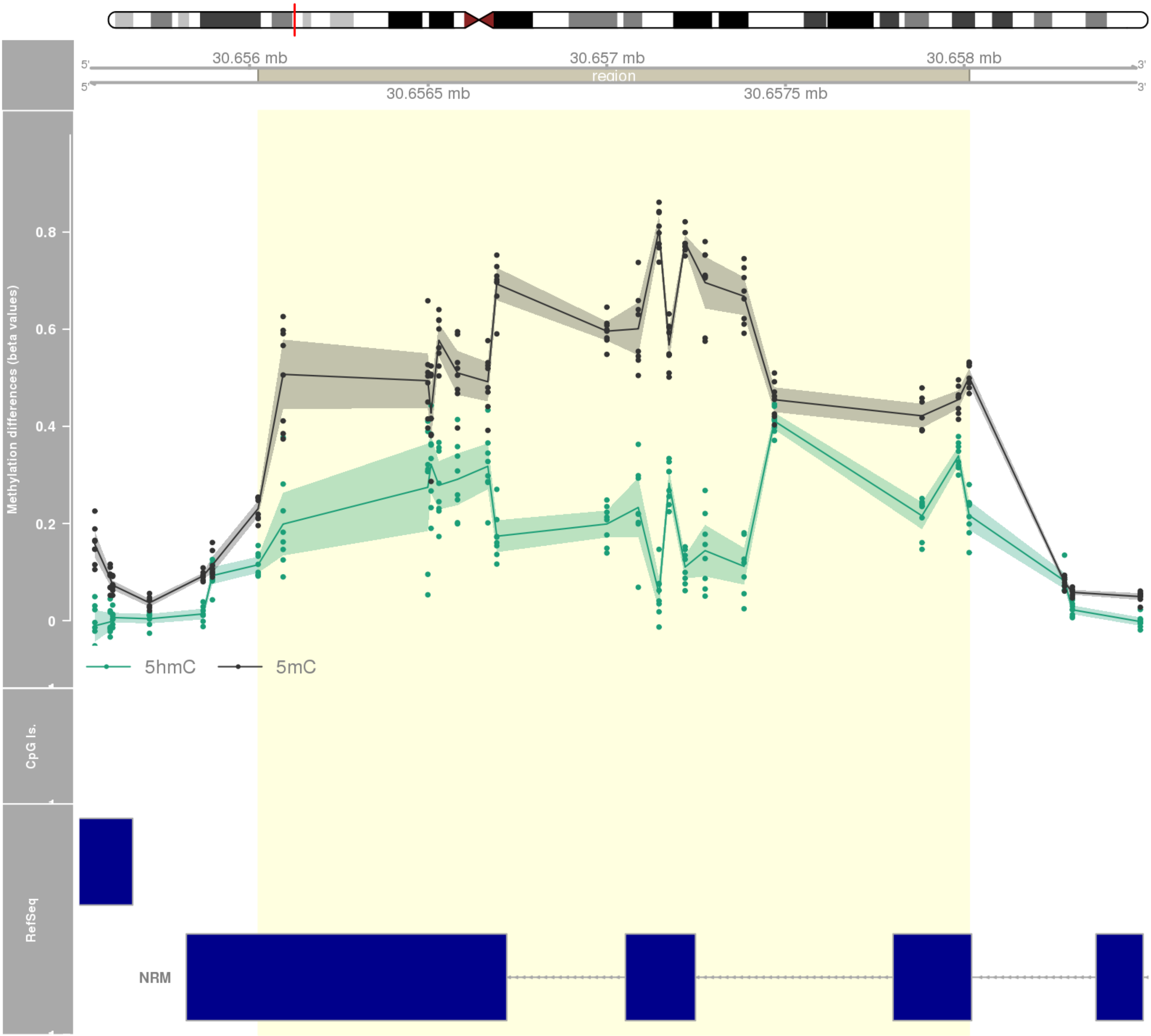
DMR 88 // chr6:35108061-35109548 // 1487 pb. (14 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.449
- genes: TCP11 -

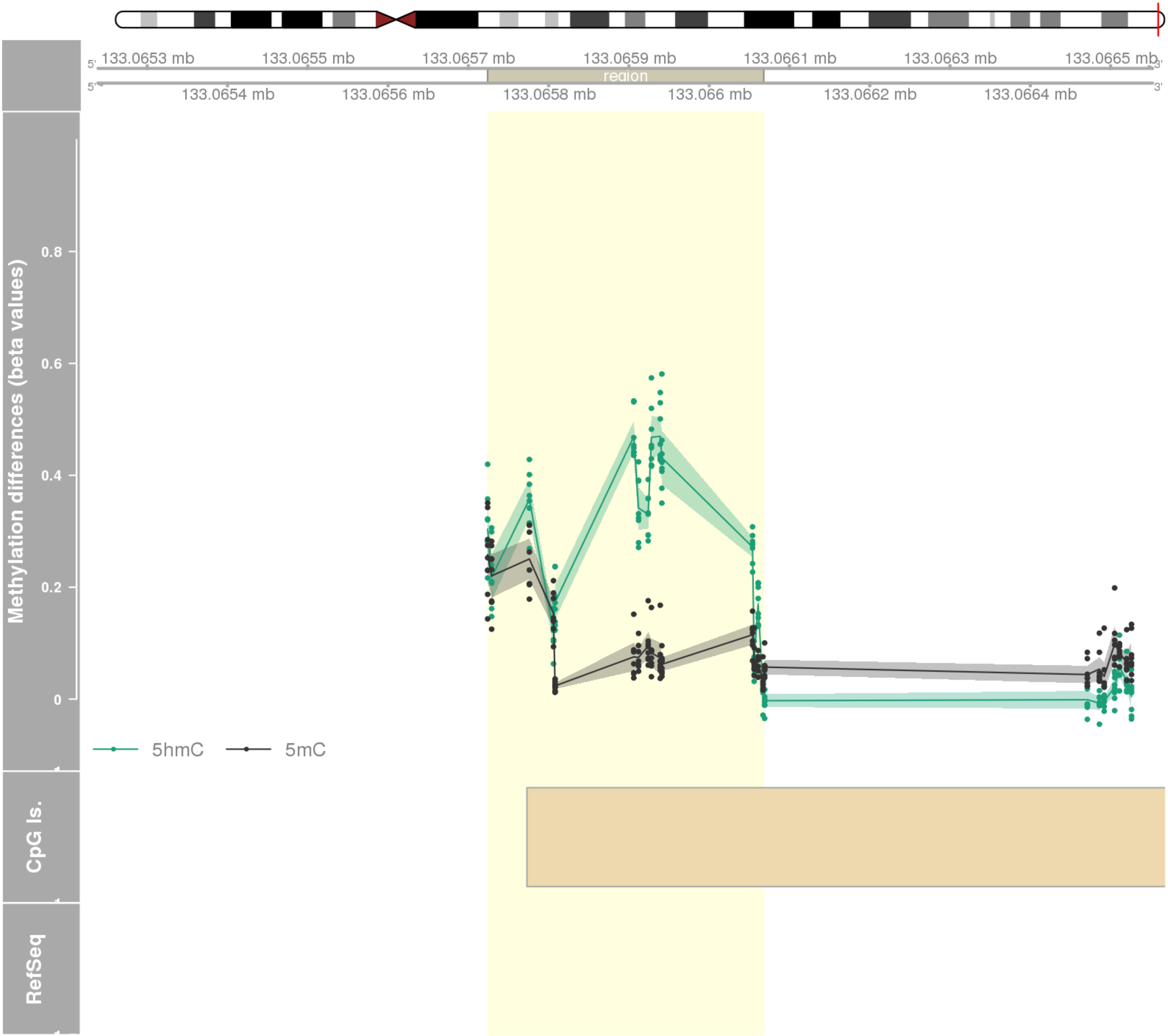


DMR 89 // chr17:75315244-75317185 // 1941 pb. (13 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.449
- genes: SEPT9 -



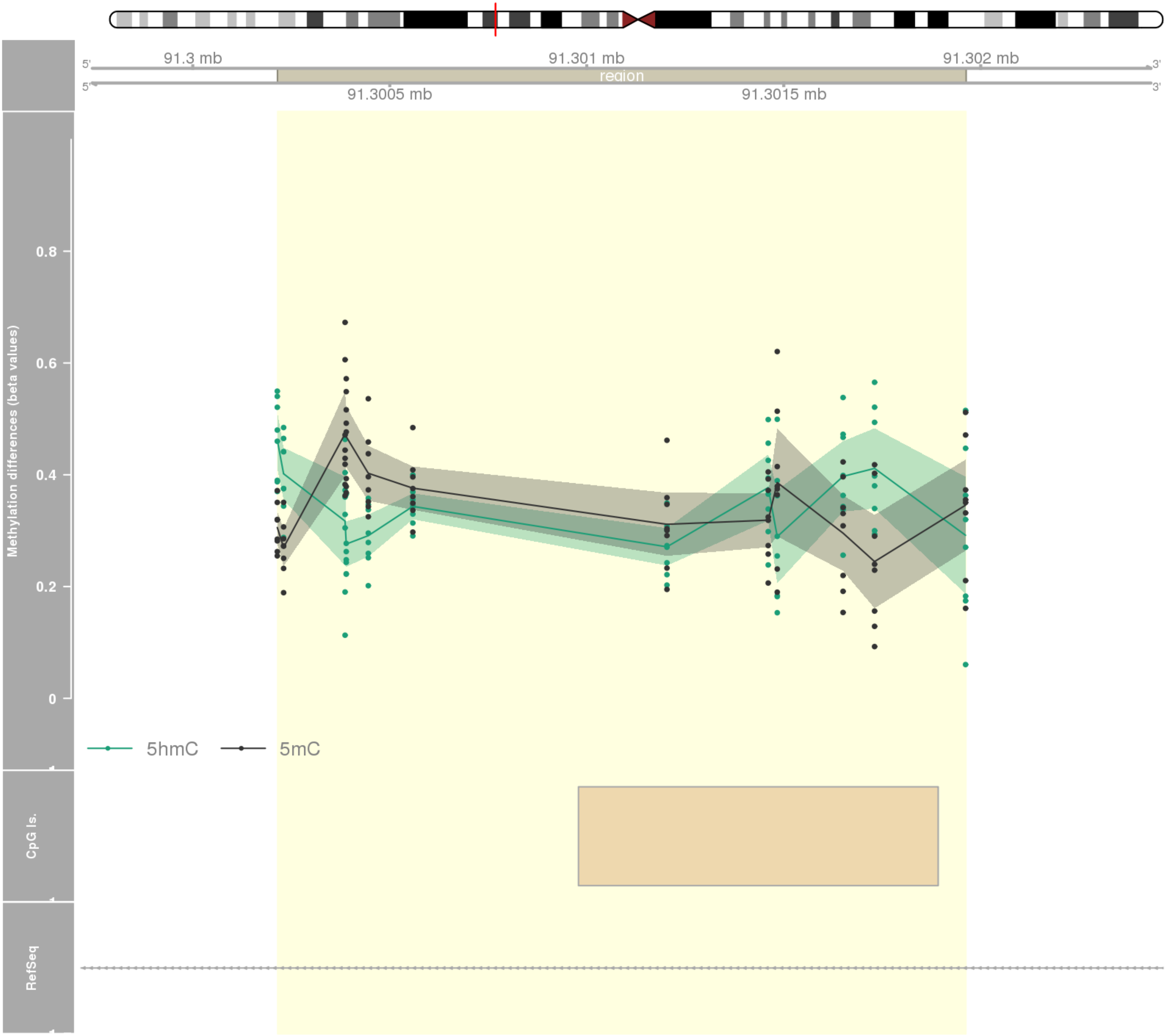
DMR 90 // chr6:30656024-30658014 // 1990 pb. (19 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.449
- genes: NRM -



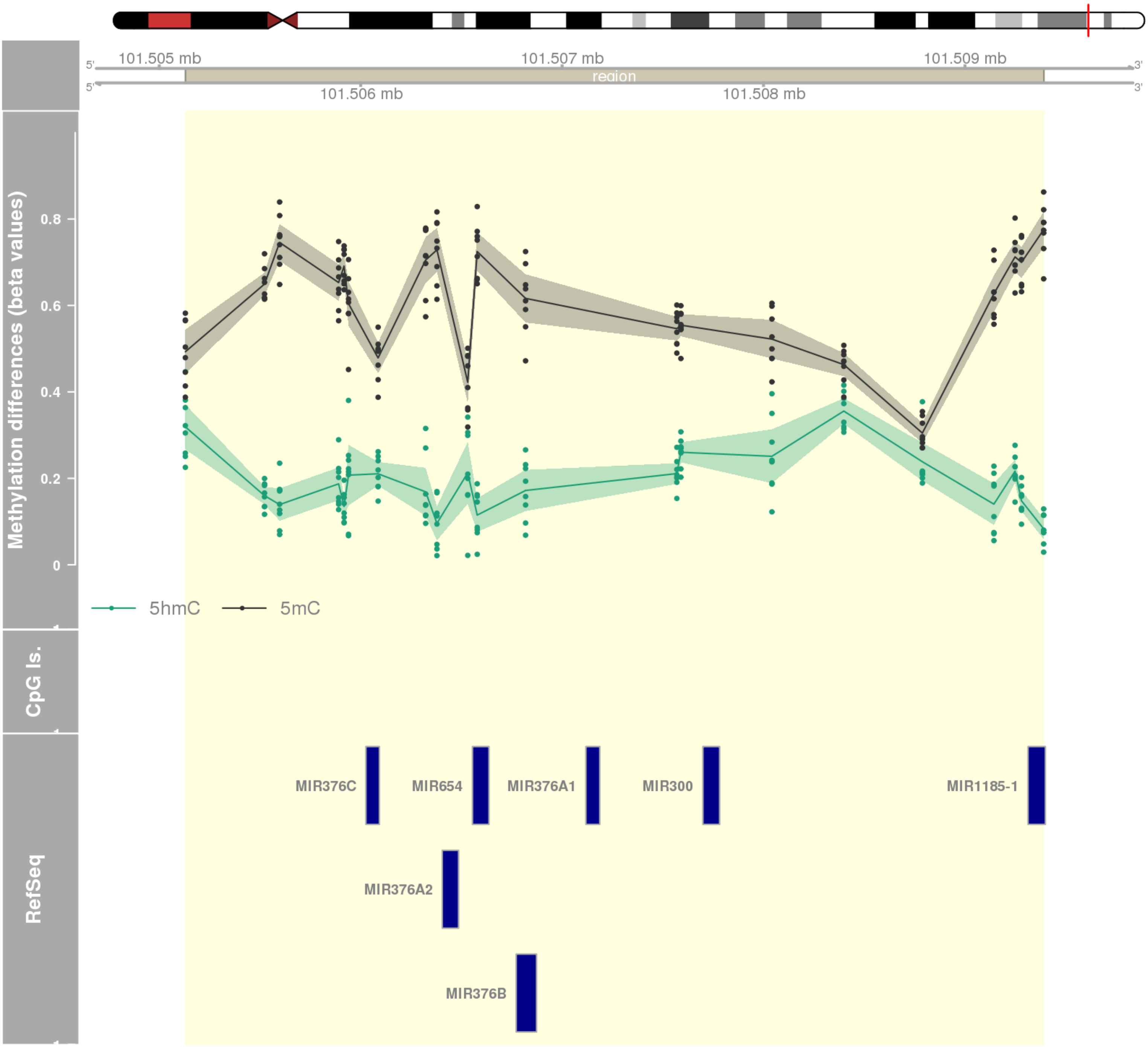


DMR 91 // chr12:133065724-133066067 // 343 pb. (15 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.449

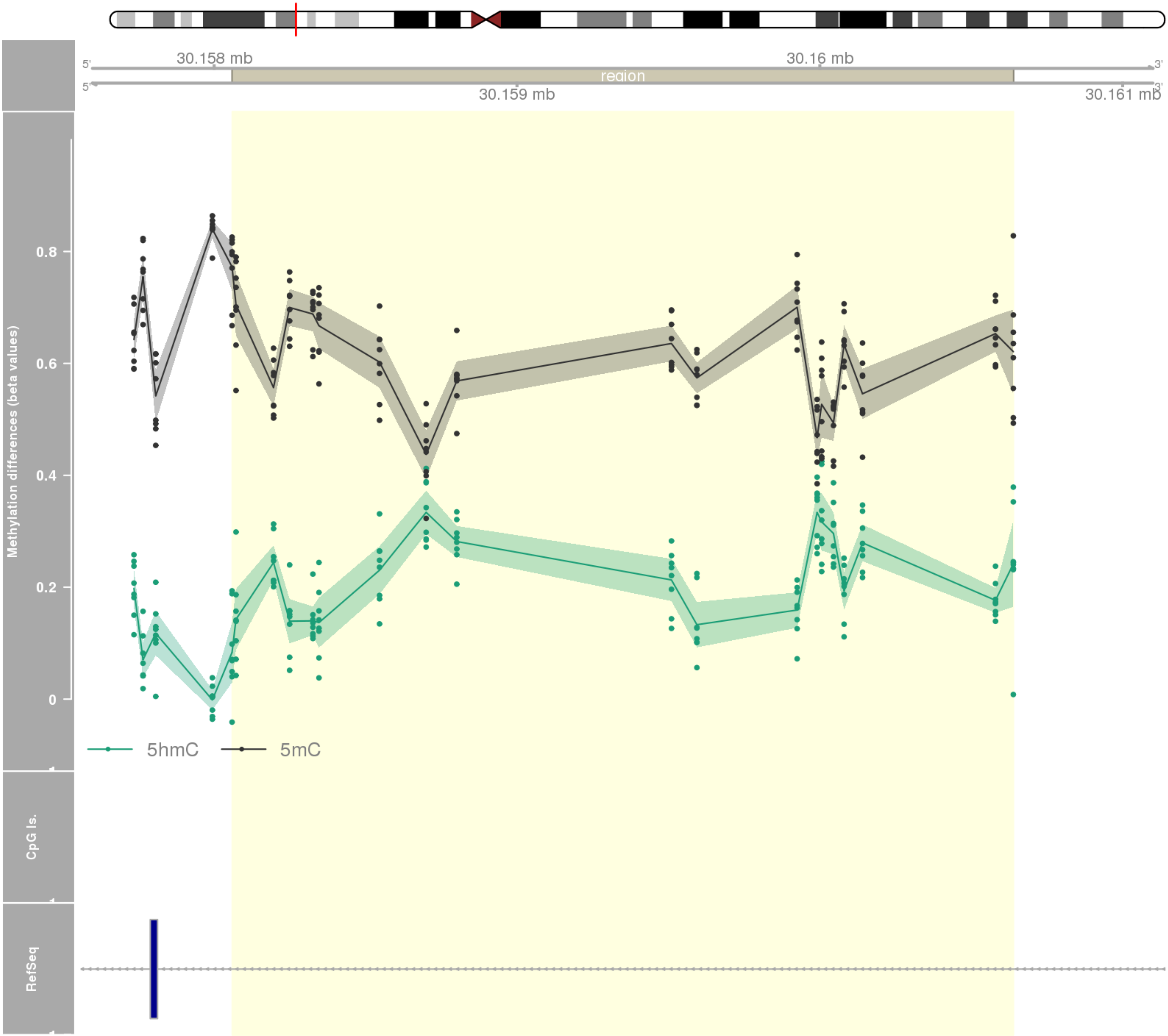
DMR 92 // chr1:91300215-91301962 // 1747 pb. (12 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.449



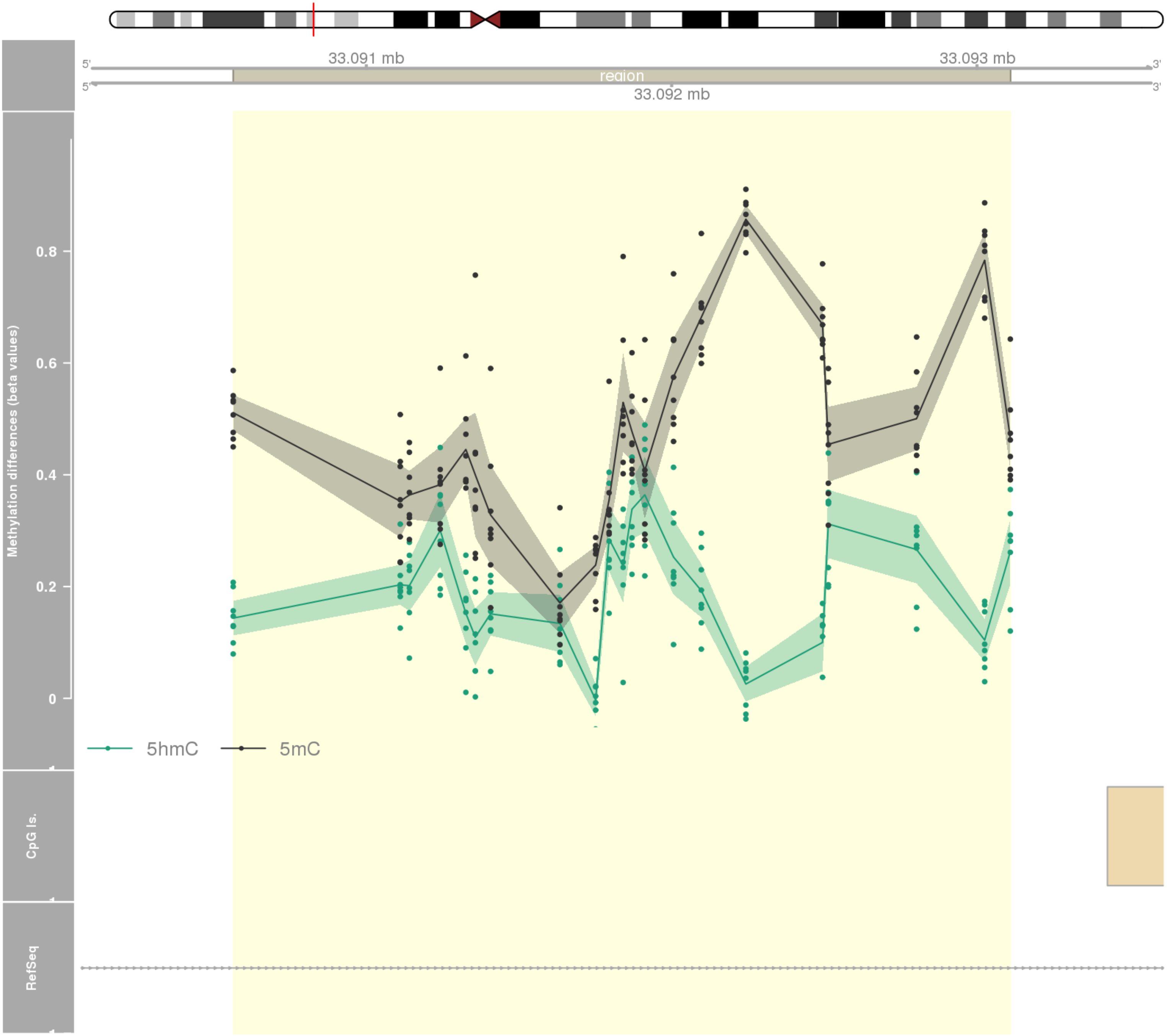
DMR 93 // chr14:101505130-101509391 // 4261 pb. (21 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.449
- genes: MIR376C / MIR654 / MIR376A1 / MIR300 / MIR1185-1 -



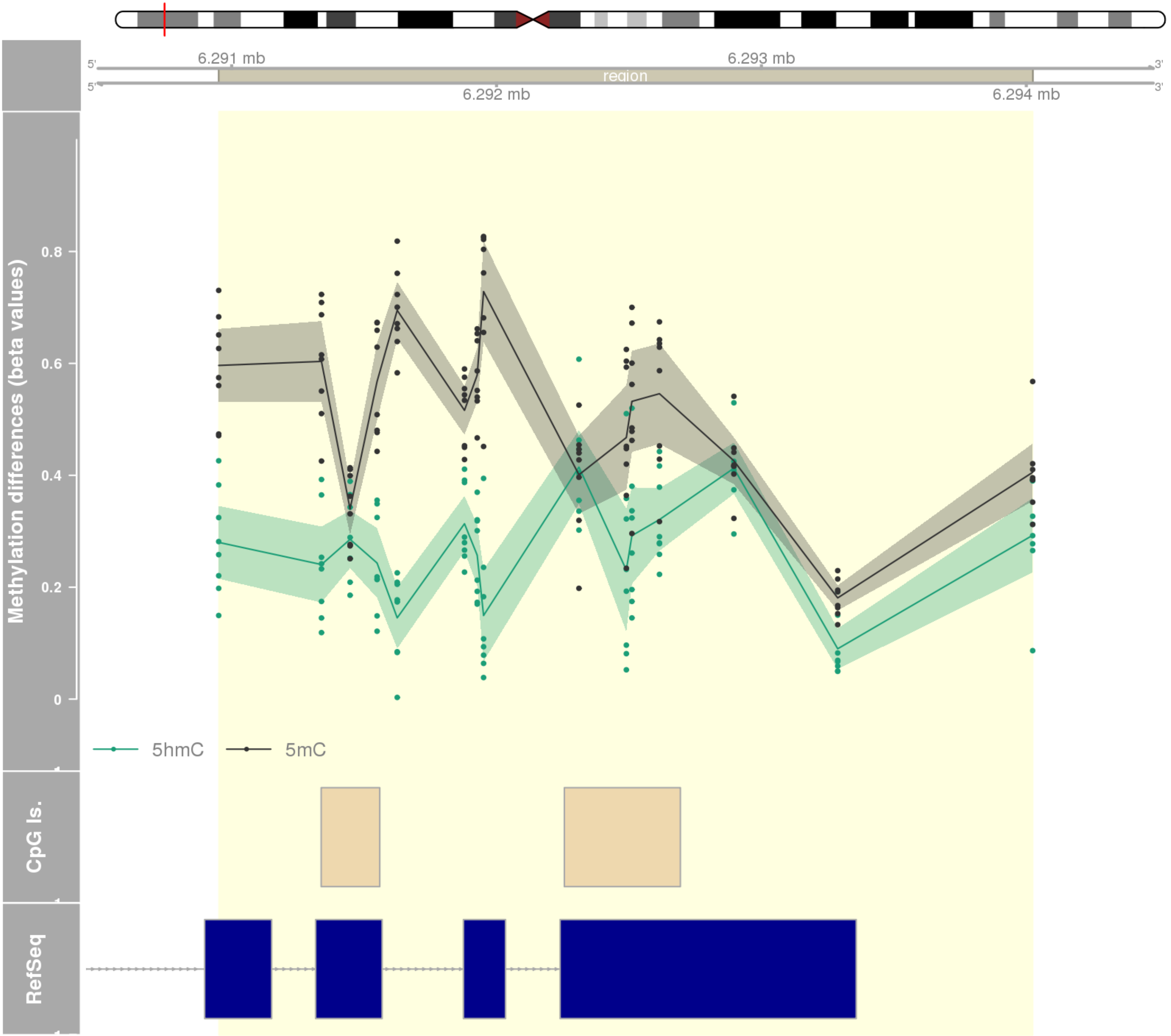
DMR 94 // chr6:30158059-30160639 // 2580 pb. (19 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: TRIM26 -



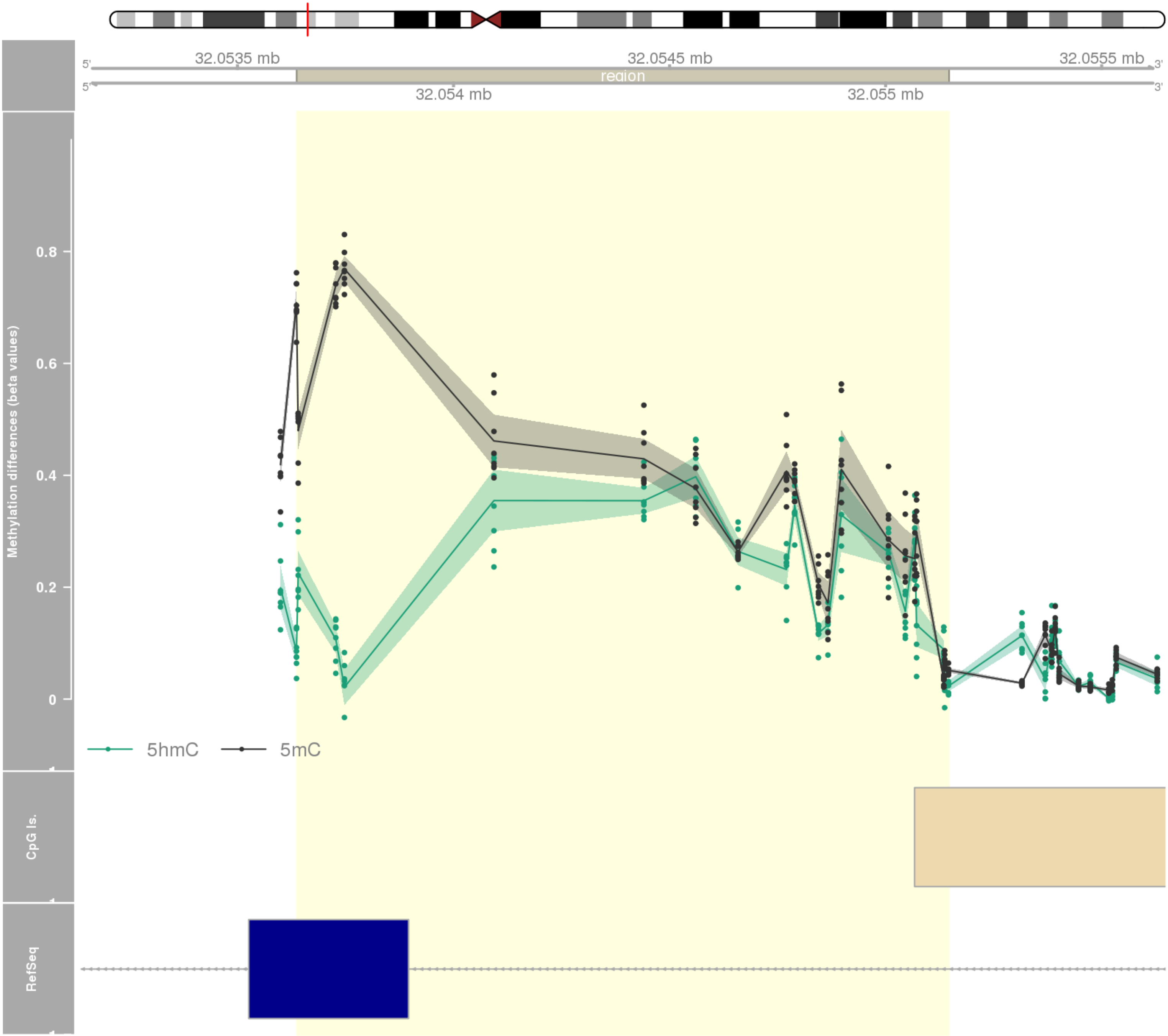
DMR 95 // chr6:33090564-33093109 // 2545 pb. (21 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: HLA-DPB2 -



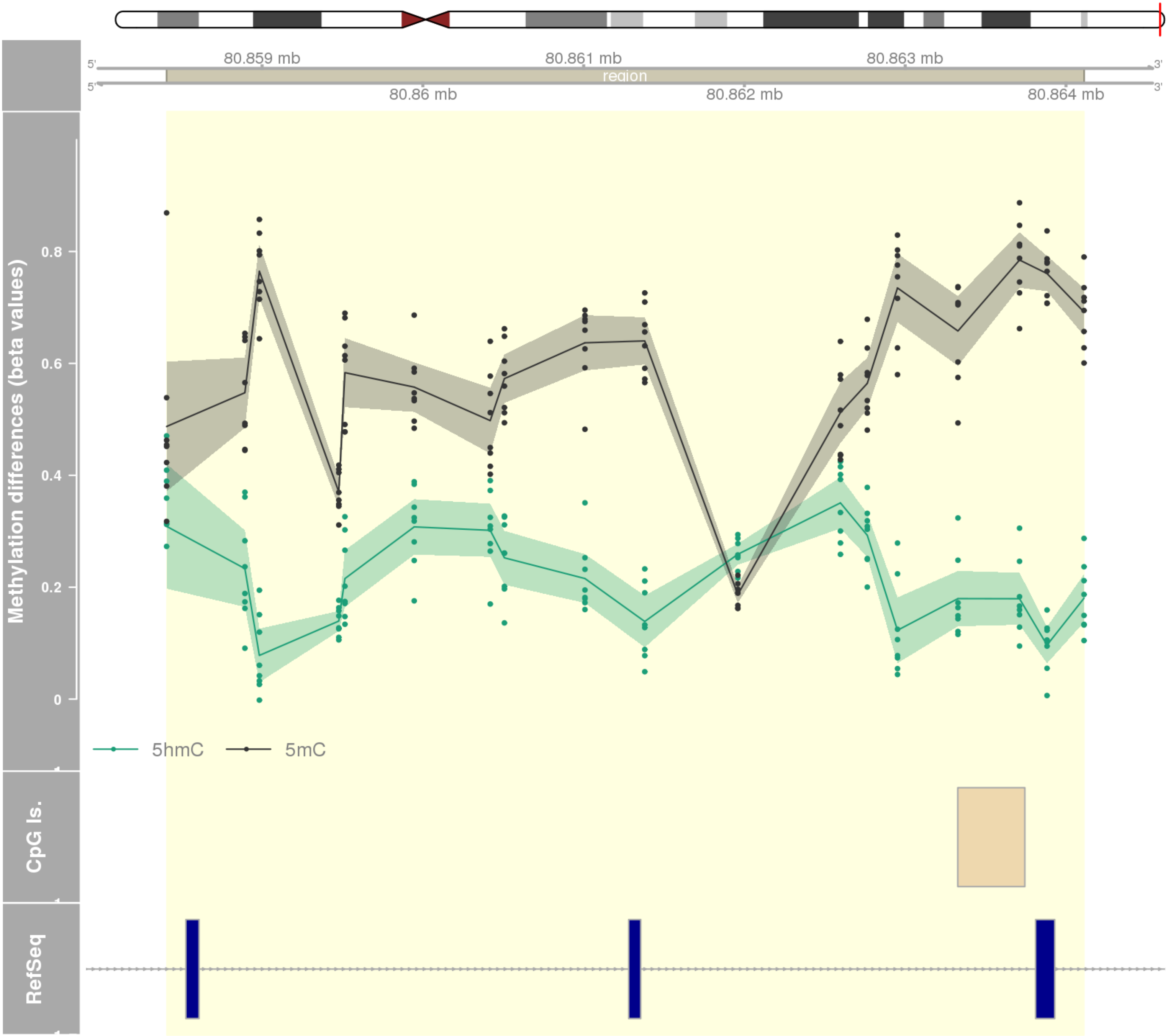
DMR 96 // chr11:6290951-6294024 // 3073 pb. (15 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: CCKBR -



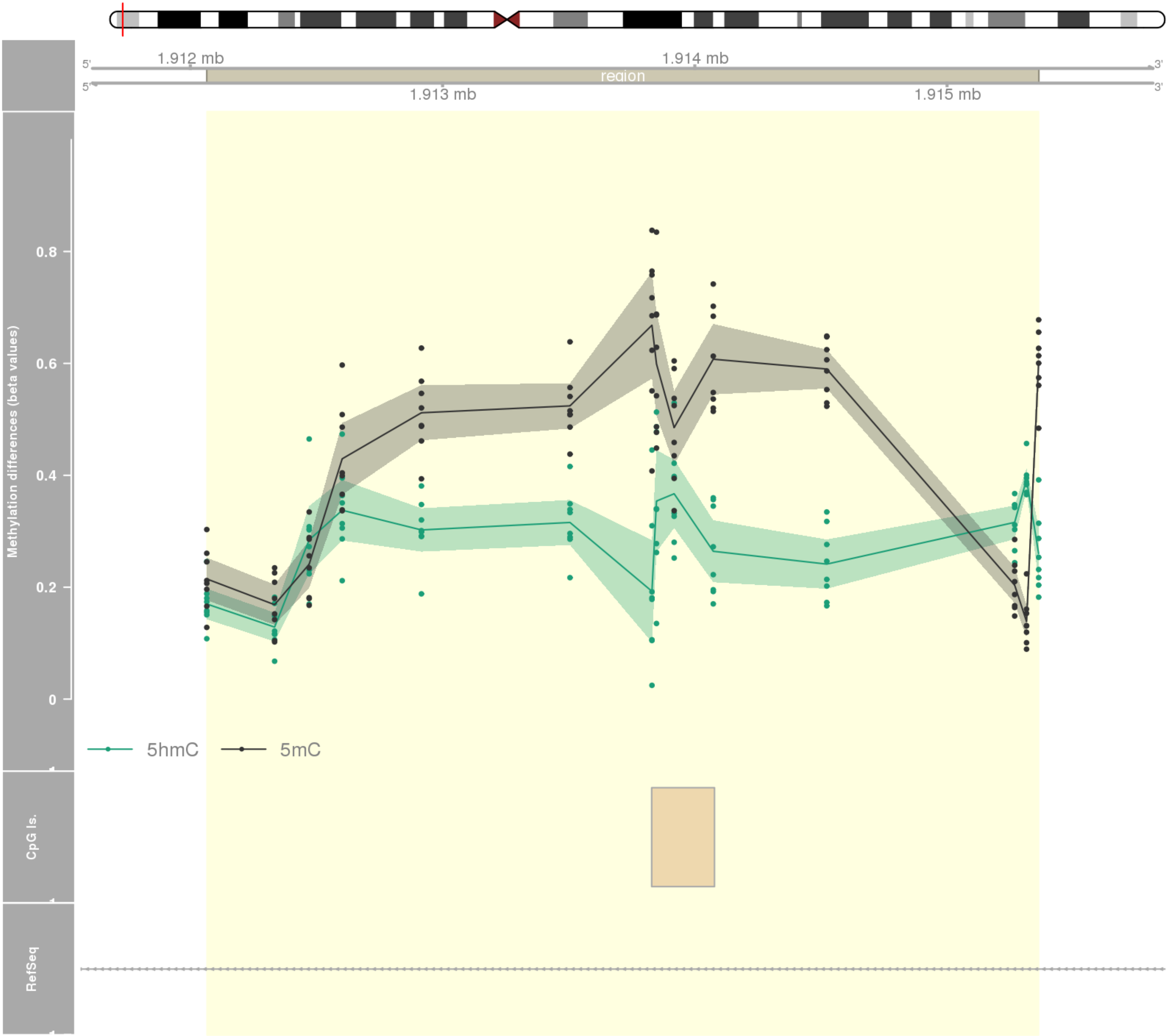
DMR 97 // chr6:32053637-32055146 // 1509 pb. (20 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: TNXB -



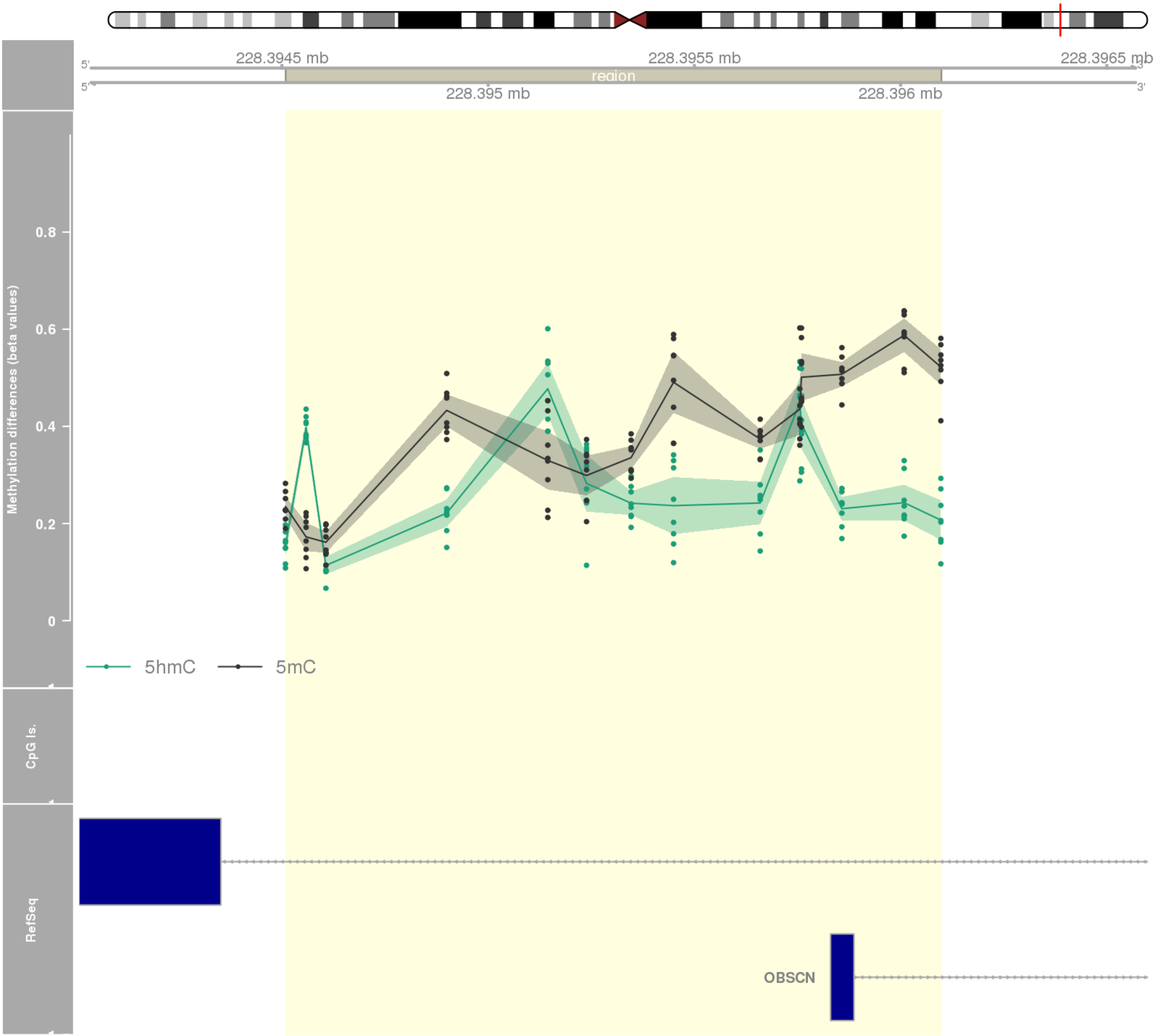
DMR 98 // chr17:80858406-80864112 // 5706 pb. (18 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: TBCD -



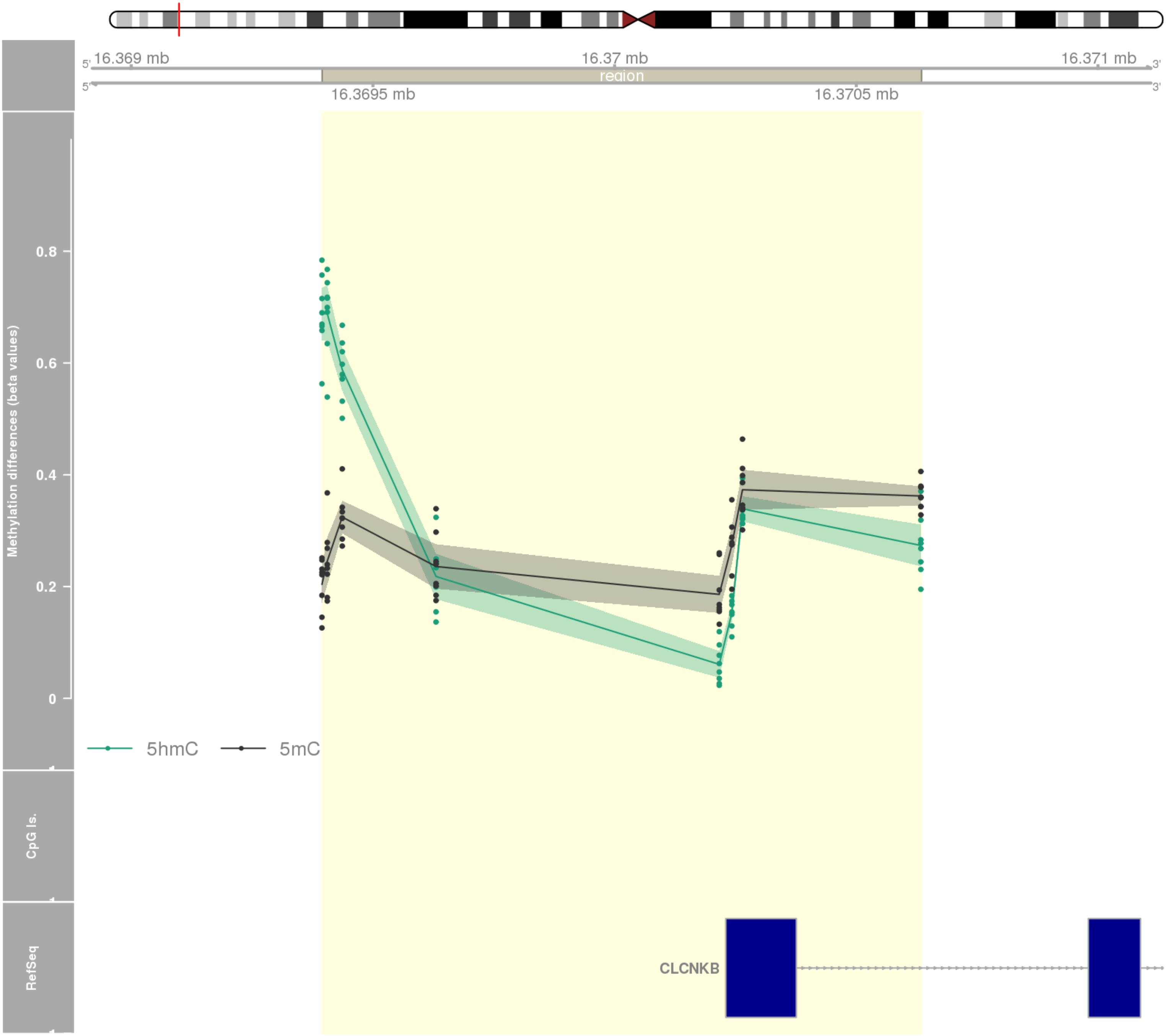
DMR 99 // chr7:1912065-1915363 // 3298 pb. (14 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: MAD1L1 -



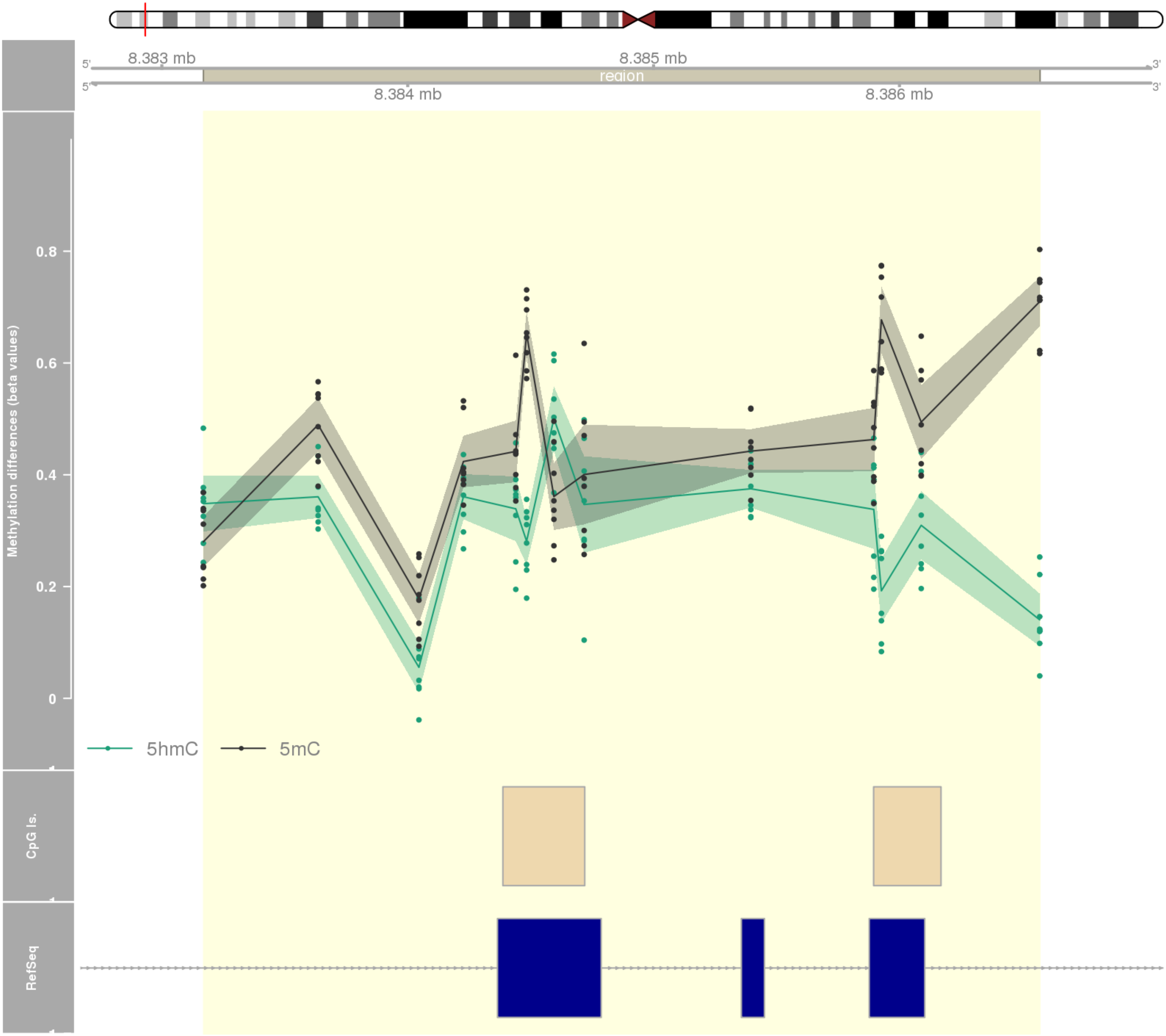
DMR 100 // chr1:228394509-228396098 // 1589 pb. (14 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: C1orf145 / OBSCN -



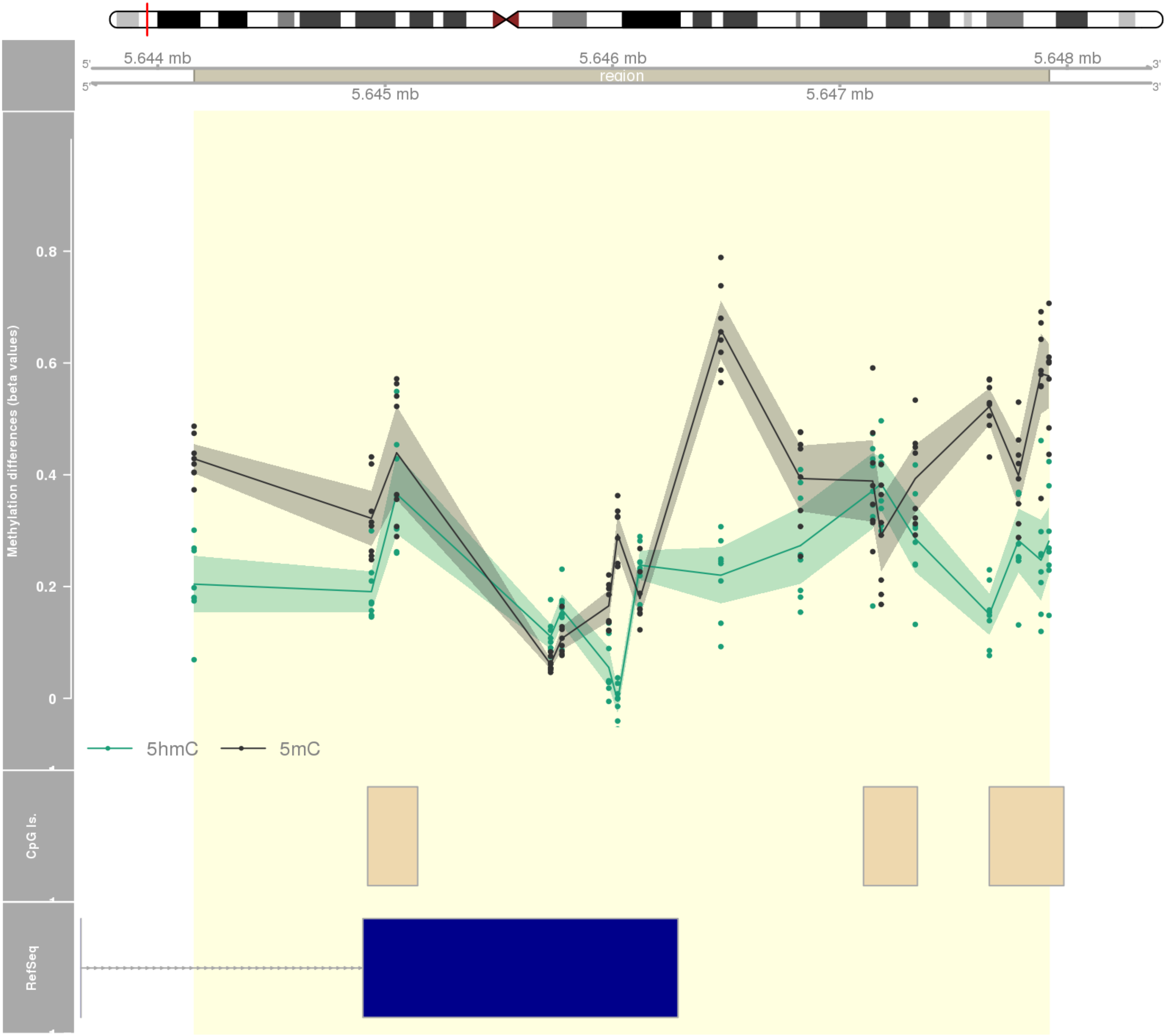
DMR 101 // chr1:16369395-16370634 // 1239 pb. (8 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: CLCNKB -



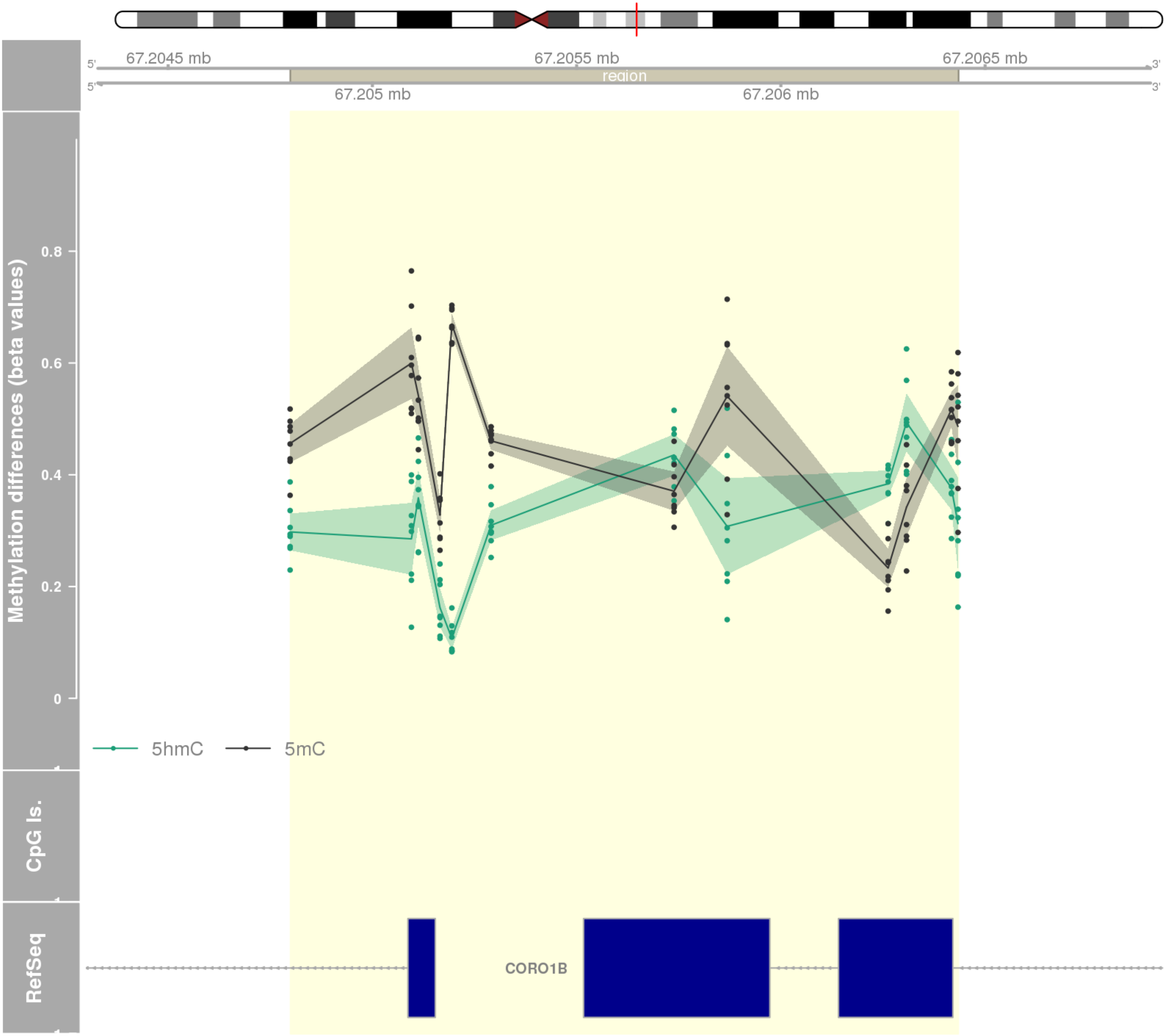
DMR 102 // chr1:8383169-8386571 // 3402 pb. (13 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: SLC45A1 -



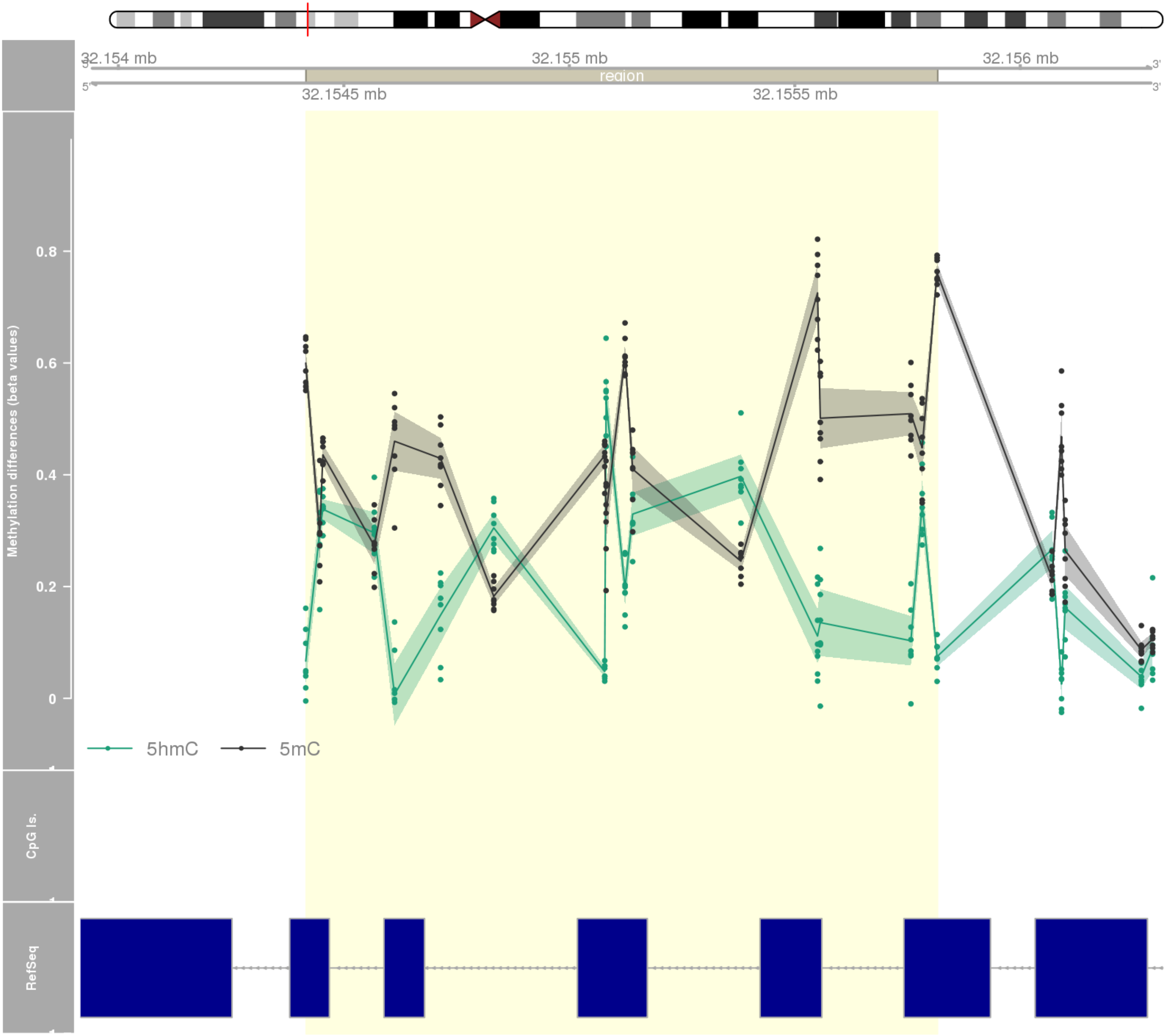
DMR 103 // chr7:5644160-5647920 // 3760 pb. (17 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.005 // fwerArea: 0.559
- genes: FSCN1 -



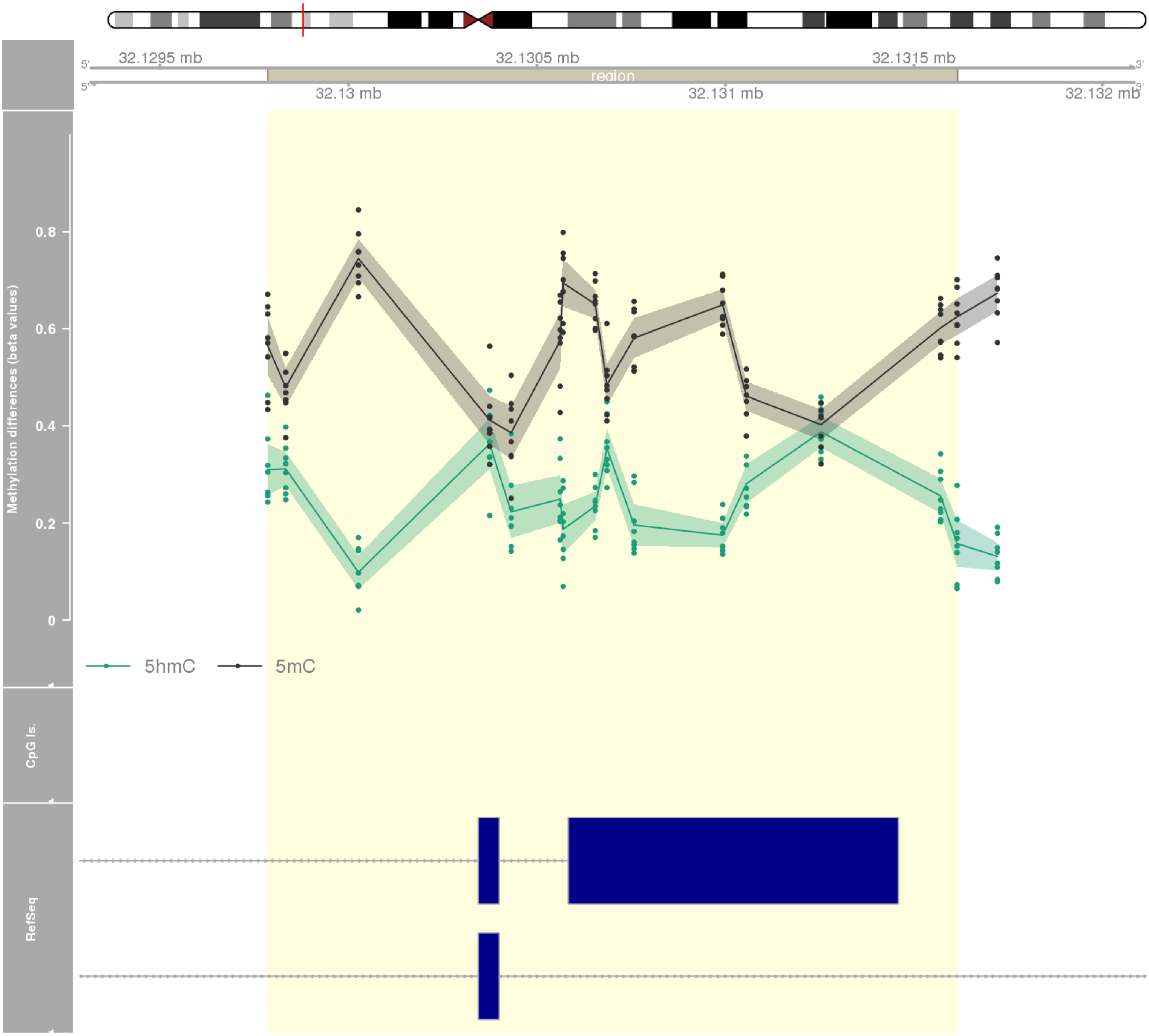
DMR 104 // chr11:67204799-67206434 // 1635 pb. (12 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: PTPRCAP / CORO1B -



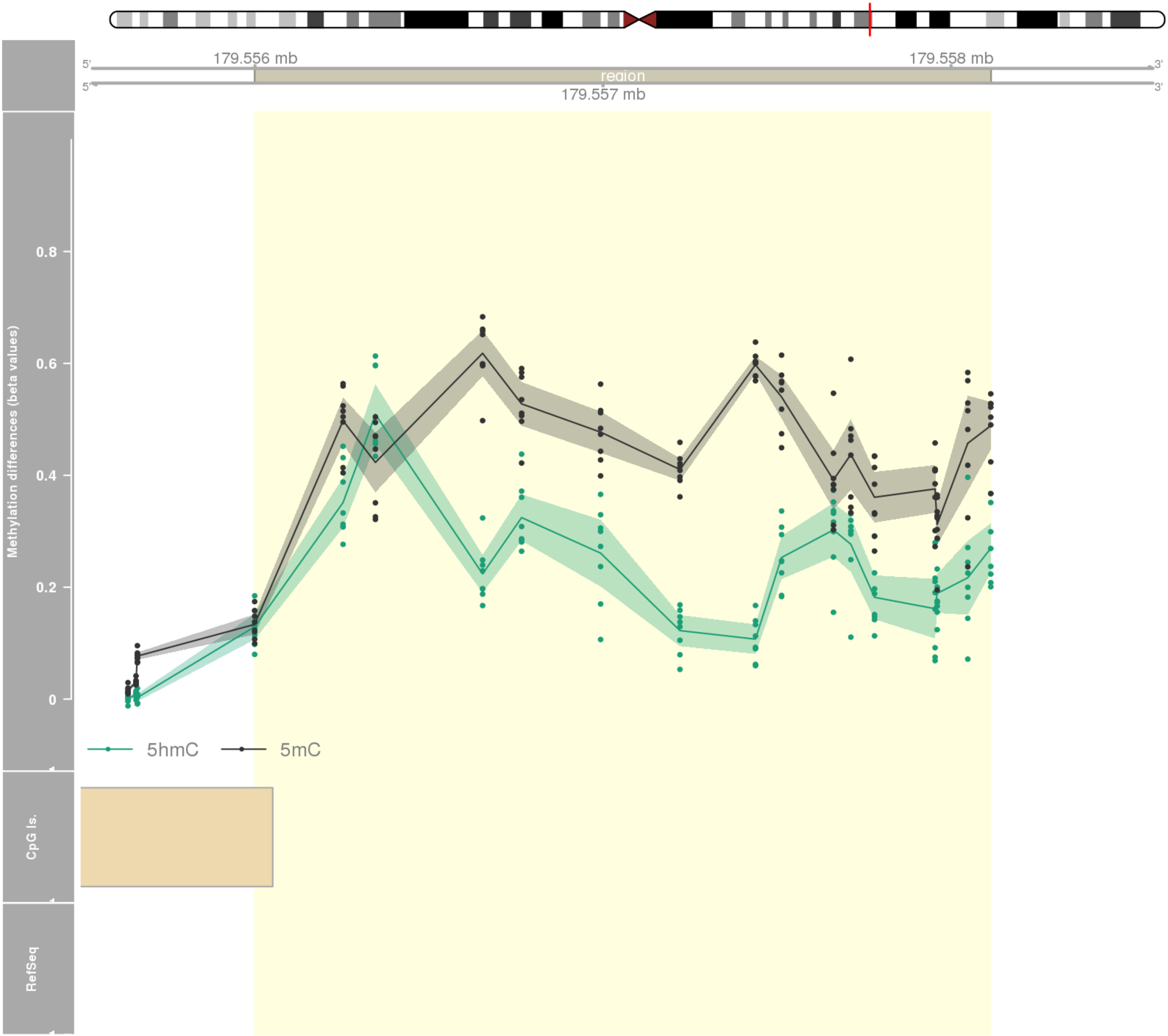
DMR 105 // chr6:32154416-32155816 // 1400 pb. (17 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: PBX2 -



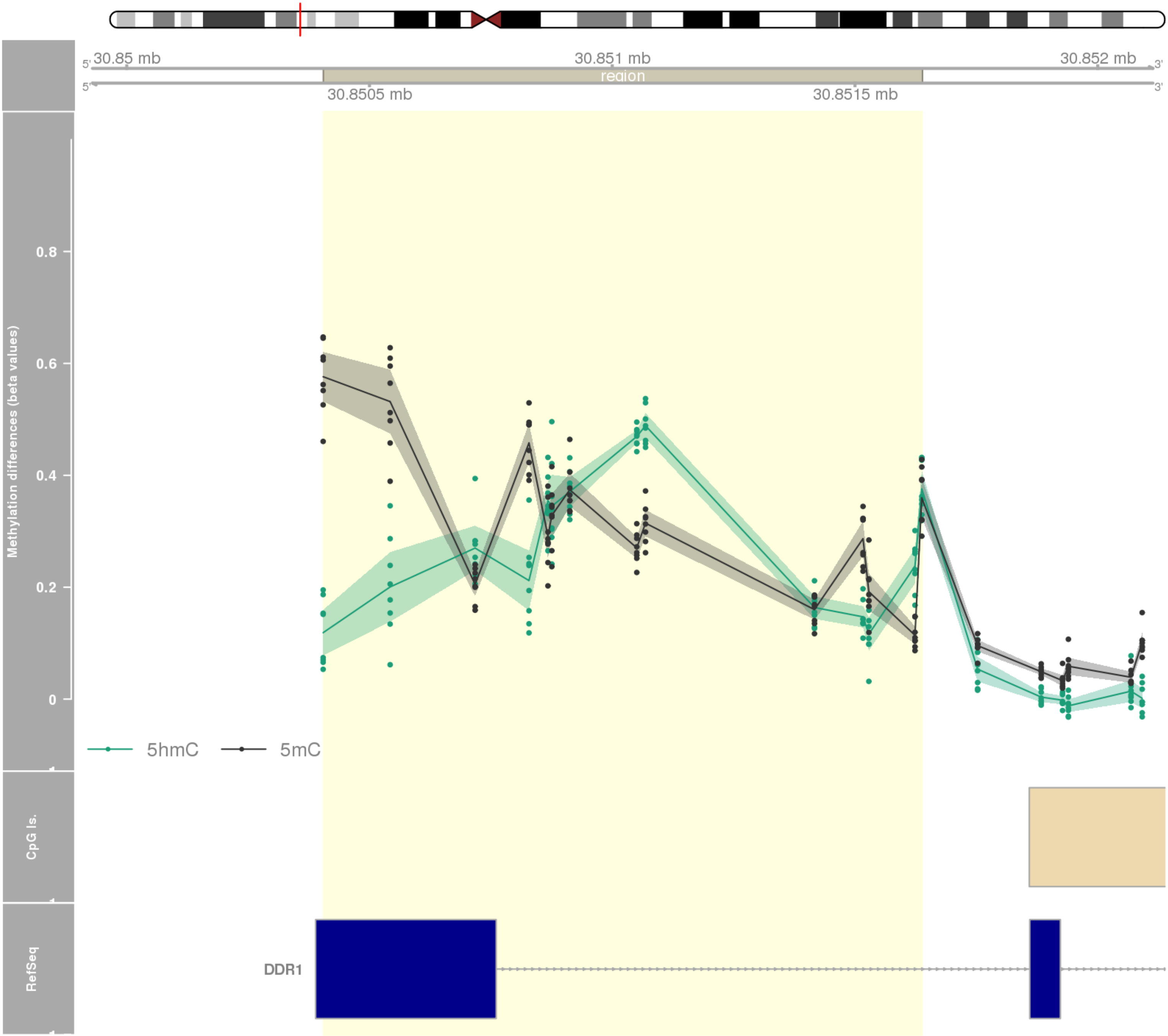
DMR 106 // chr6:32129786-32131615 // 1829 pb. (15 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: PPT2 / PPT2-EGFL8 -



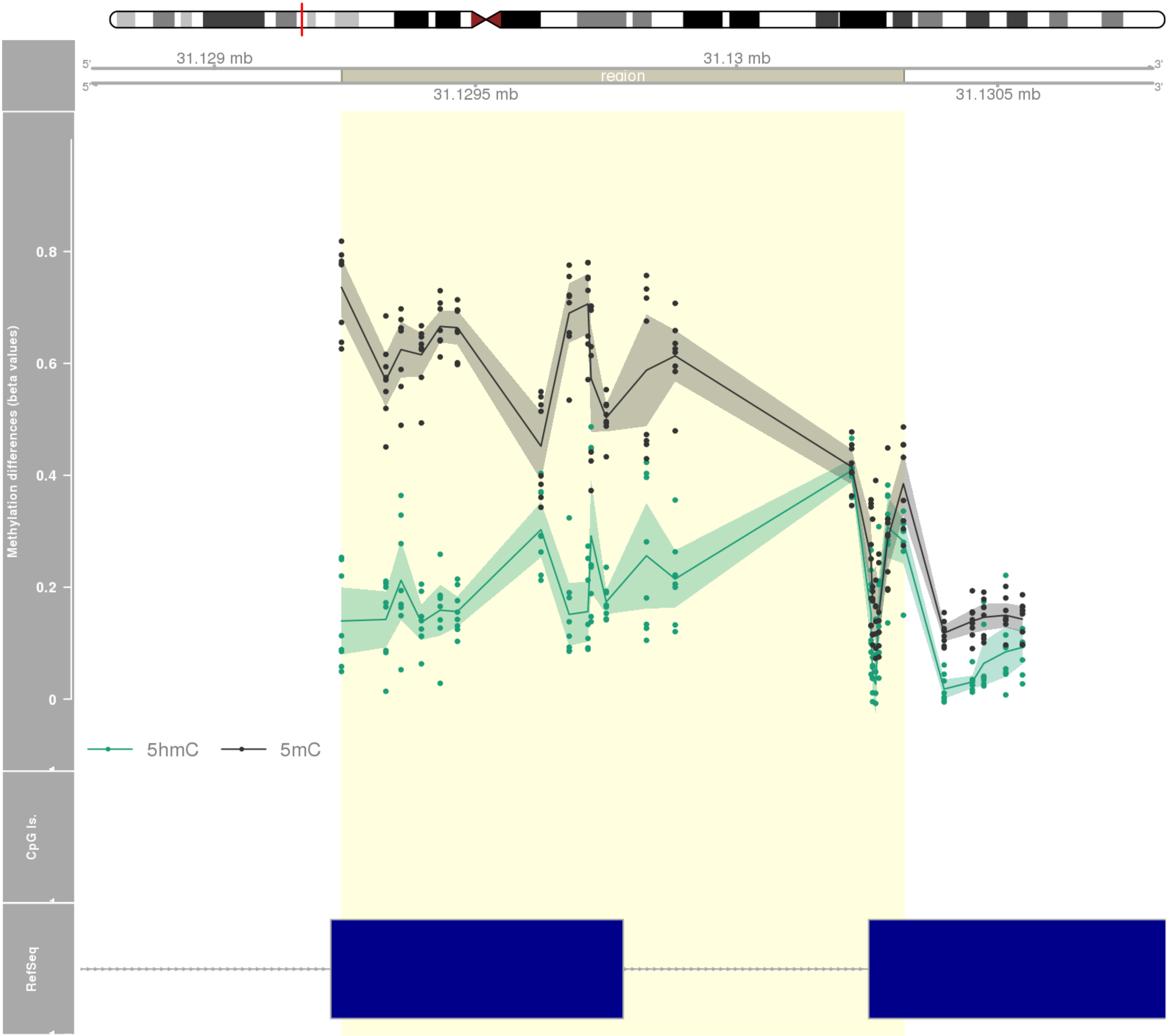
DMR 107 // chr1:179555999-179558114 // 2115 pb. (16 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559



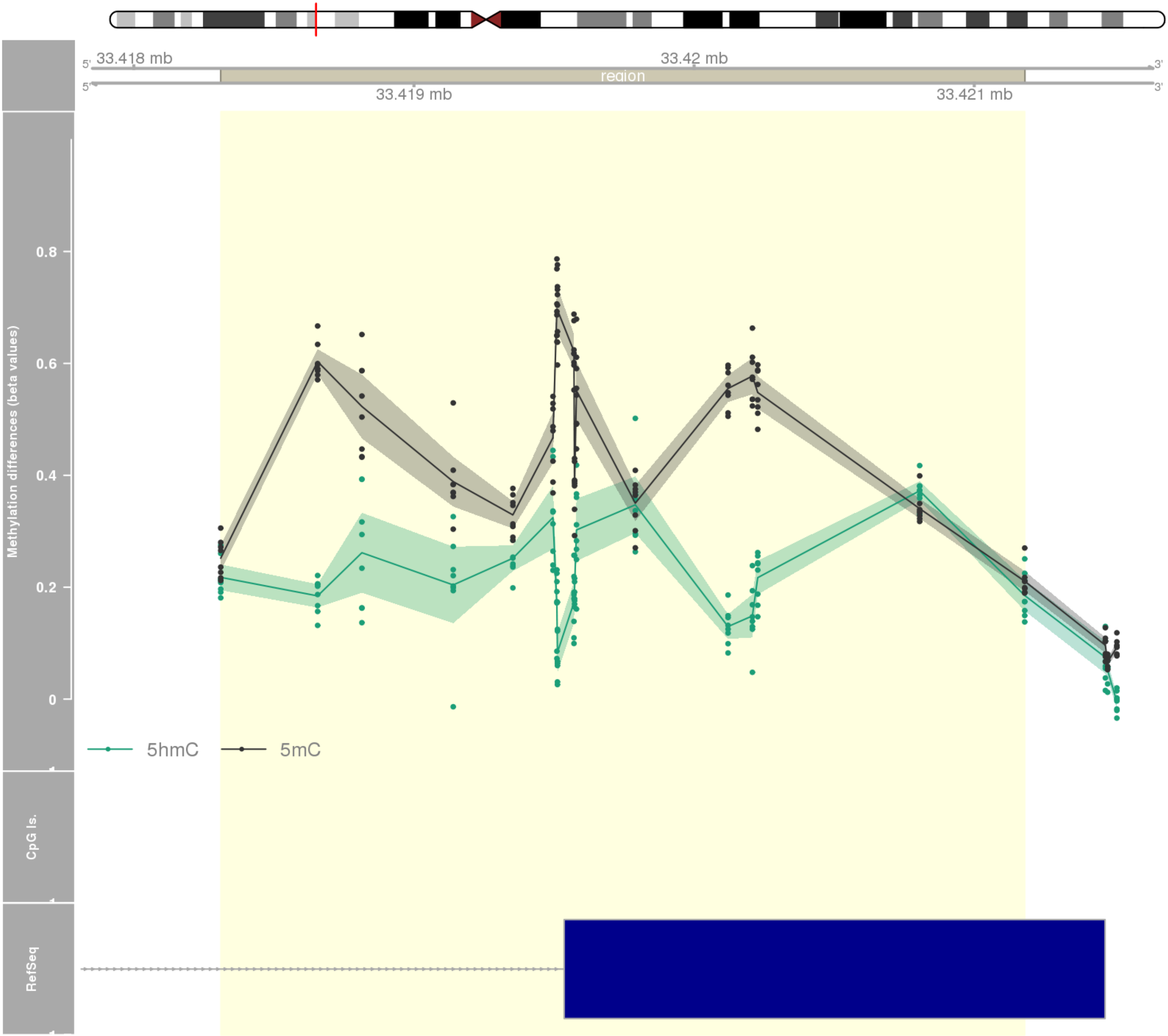
DMR 108 // chr6:30850405-30851638 // 1233 pb. (14 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: DDR1 -



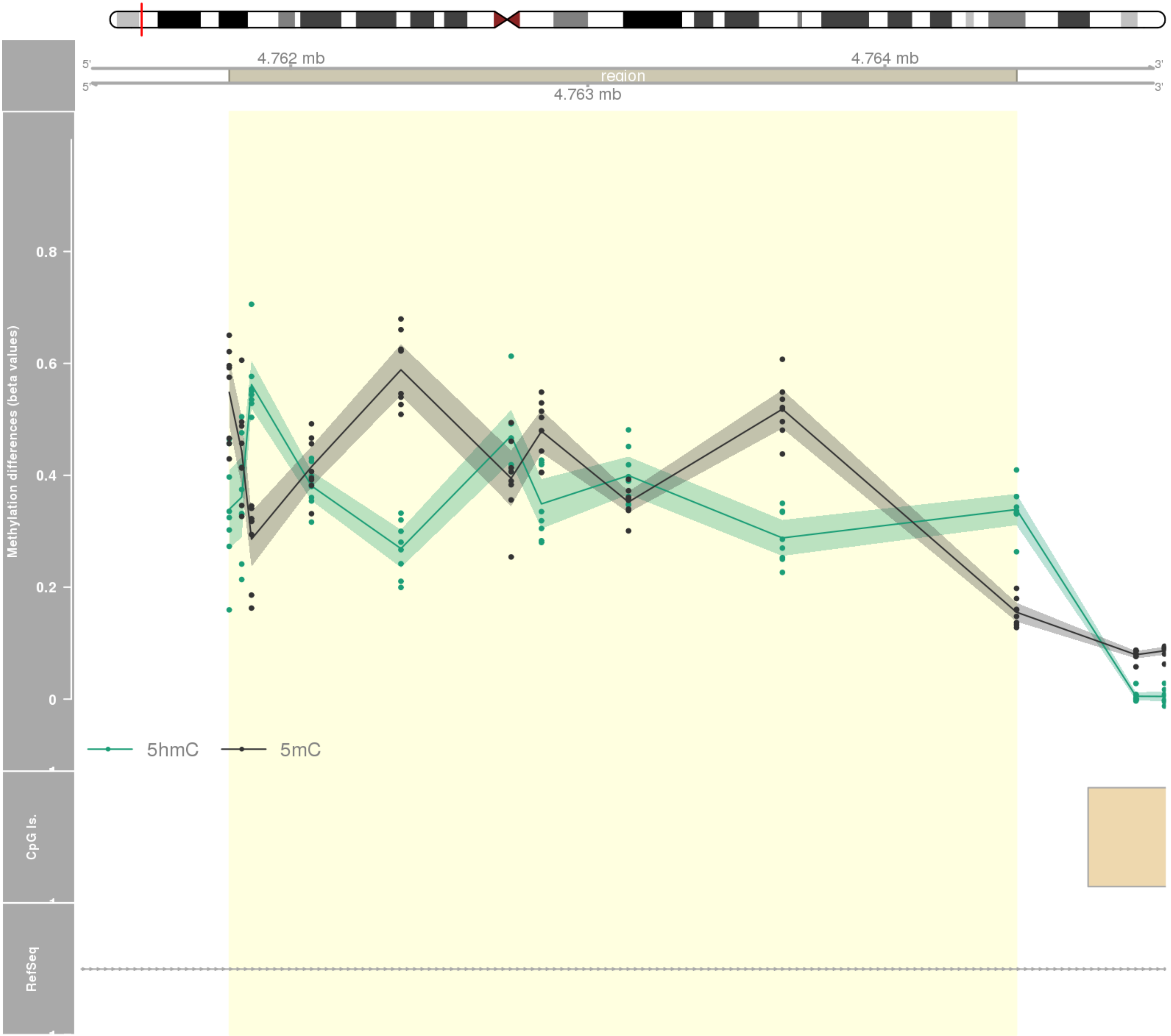
DMR 109 // chr6:31129244-31130320 // 1076 pb. (20 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: TCF19 -



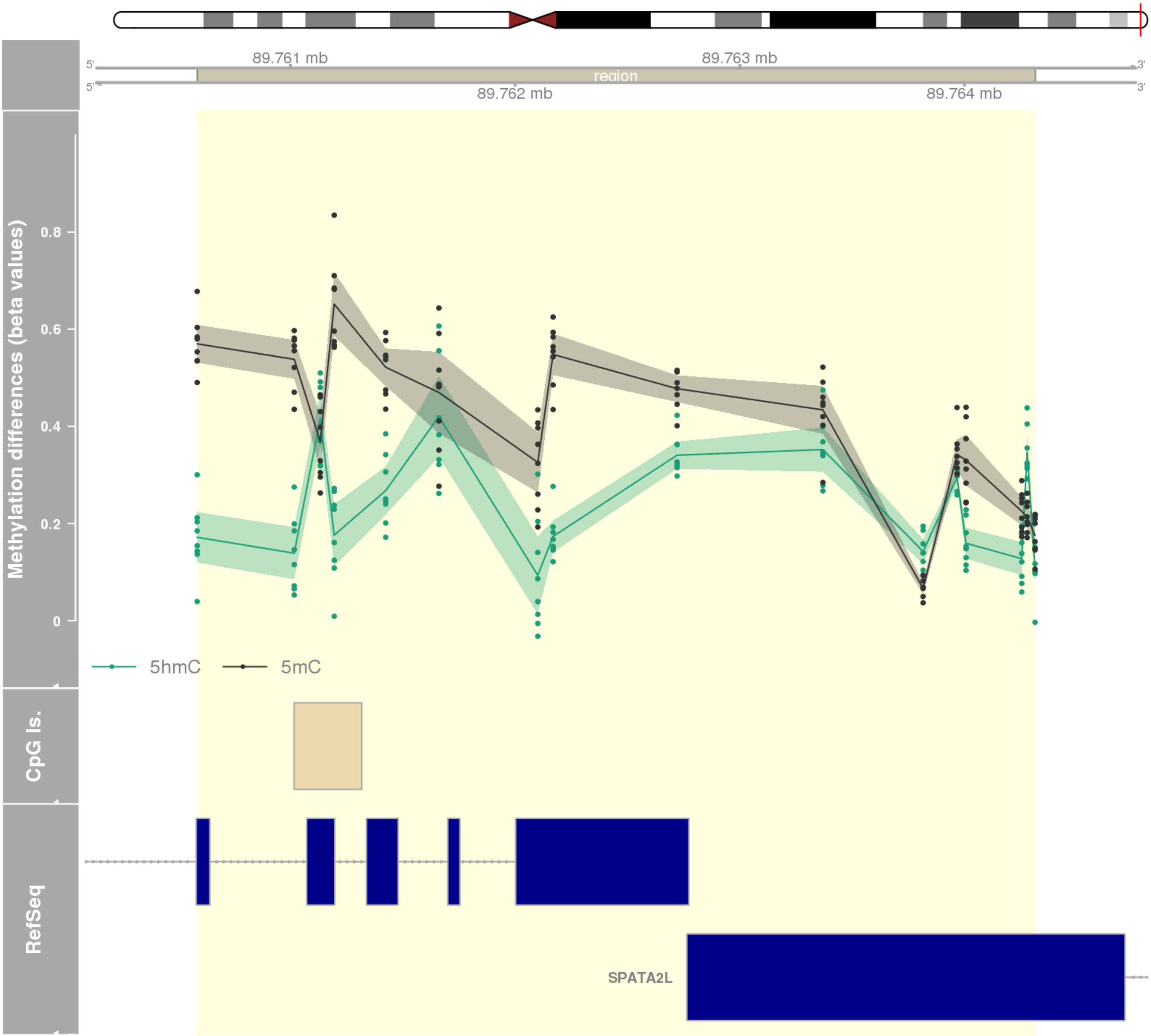
DMR 110 // chr6:33418310-33421180 // 2870 pb. (17 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: SYNGAP1 -



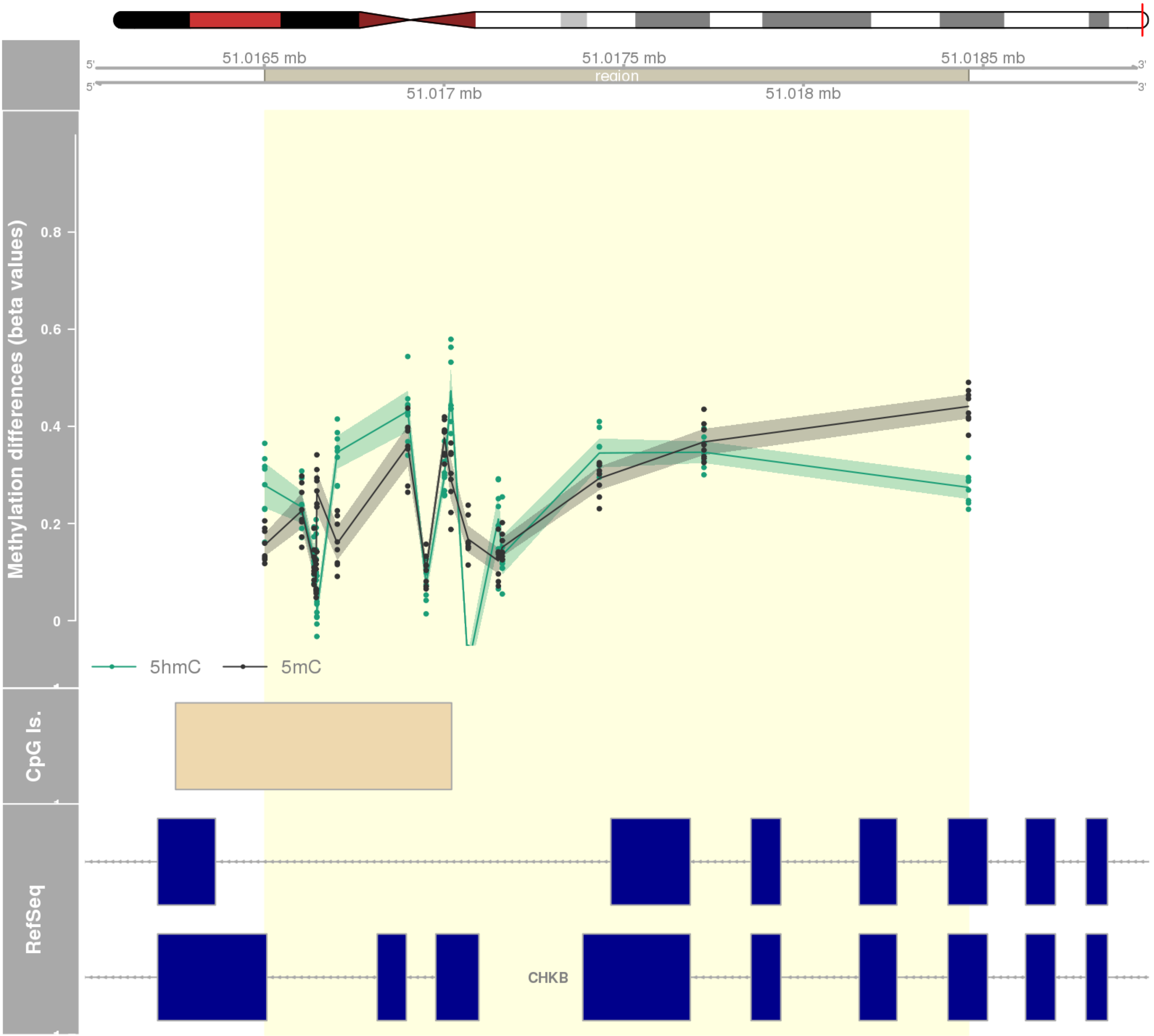
DMR 111 // chr7:4761793-4764443 // 2650 pb. (10 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: FOXK1 -



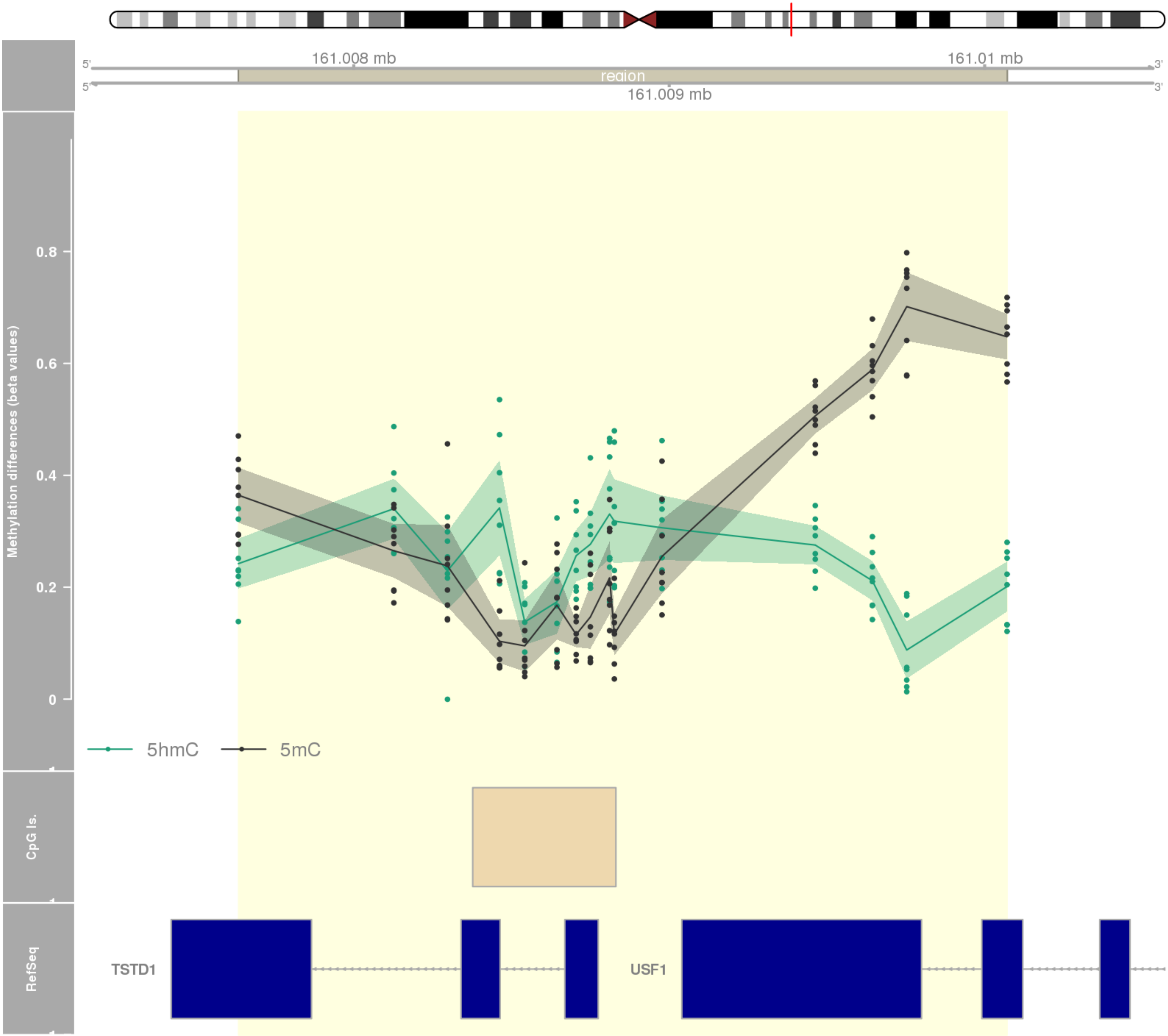
DMR 112 // chr16:89760585-89764314 // 3729 pb. (16 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: CDK10 / SPATA2L -



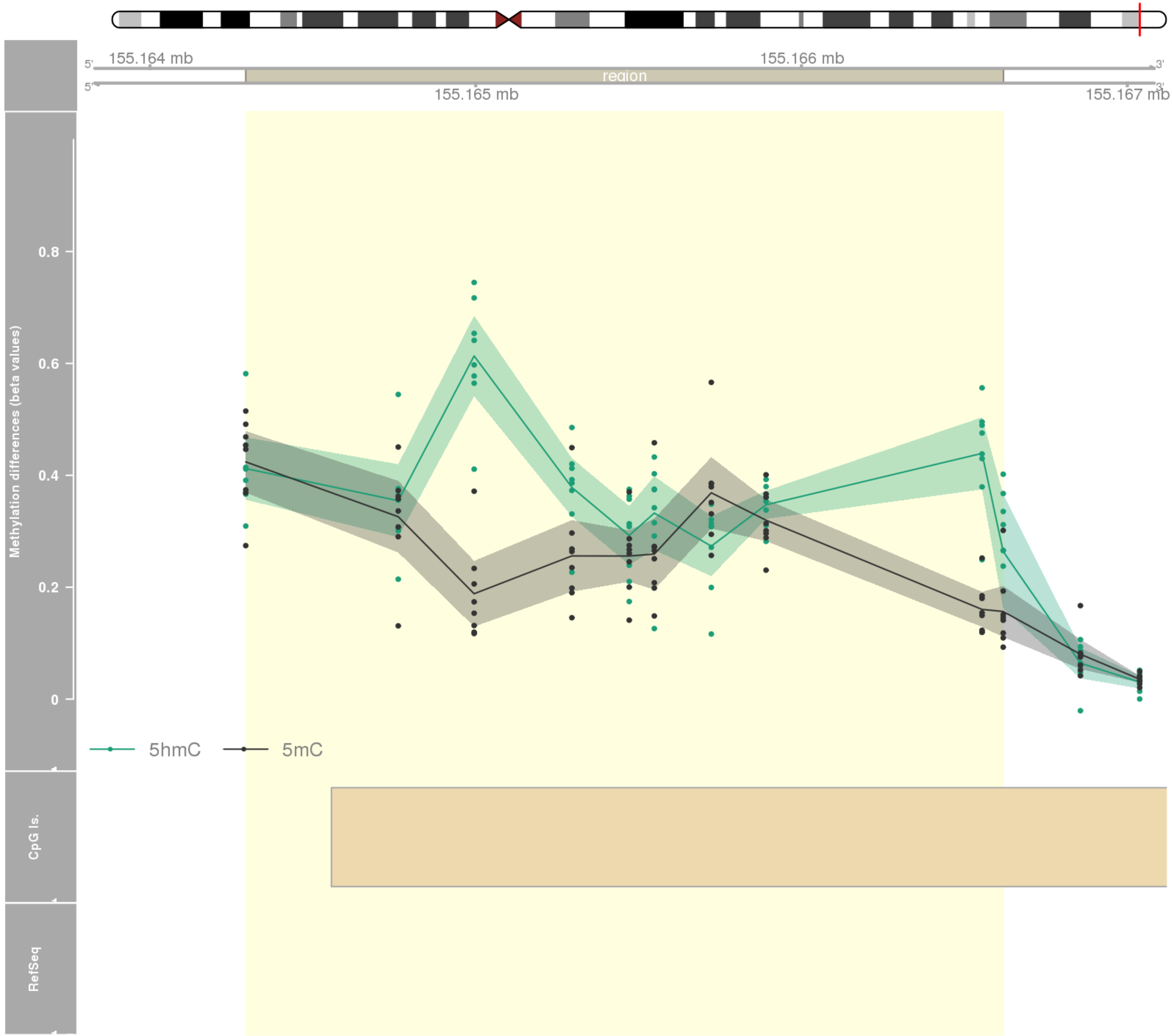
DMR 113 // chr22:51016501-51018459 // 1958 pb. (16 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: CPT1B / CHKB-CPT1B / CHKB -



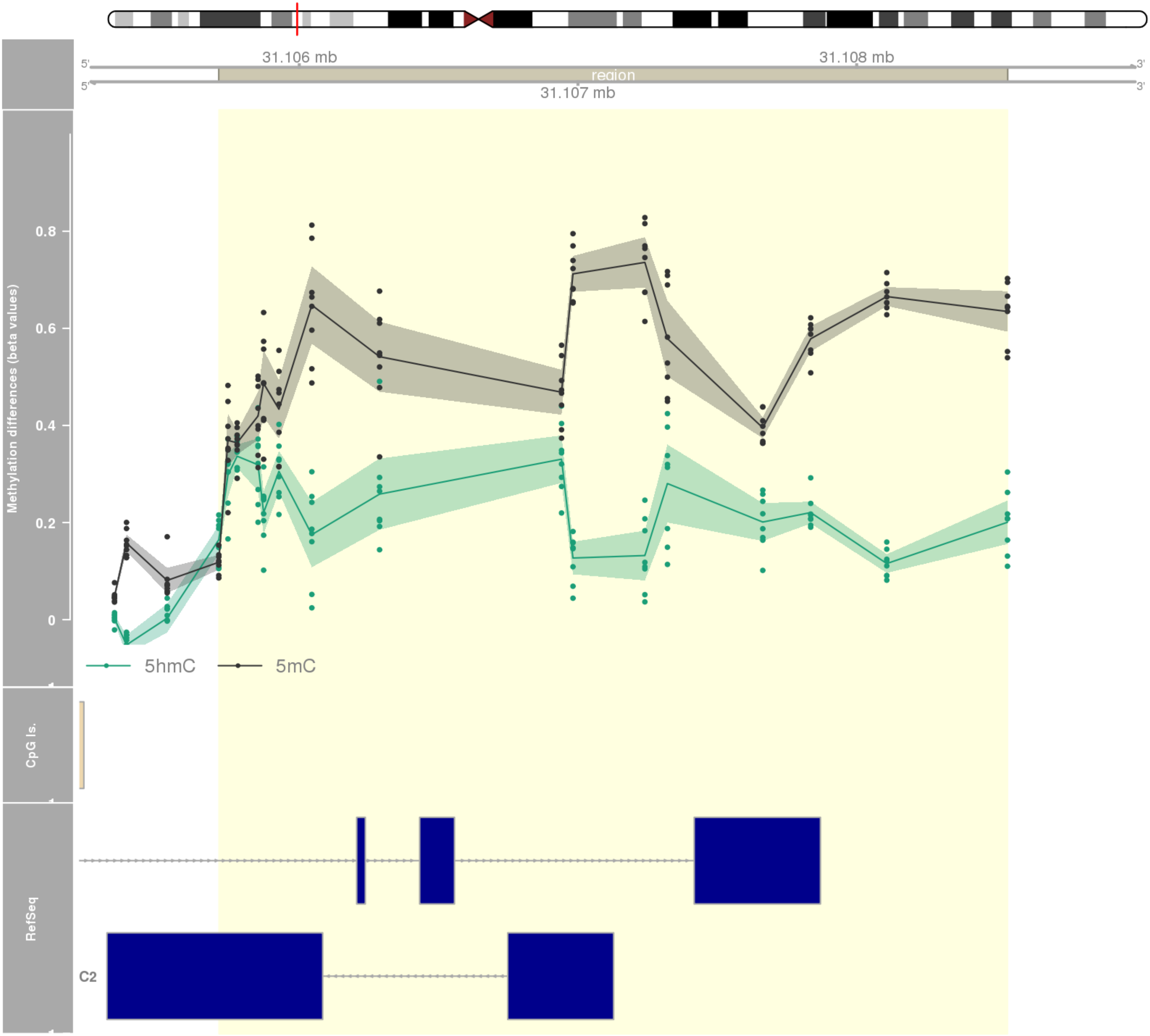
DMR 114 // chr1:161007634-161010071 // 2437 pb. (15 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: TSTD1 / USF1 -



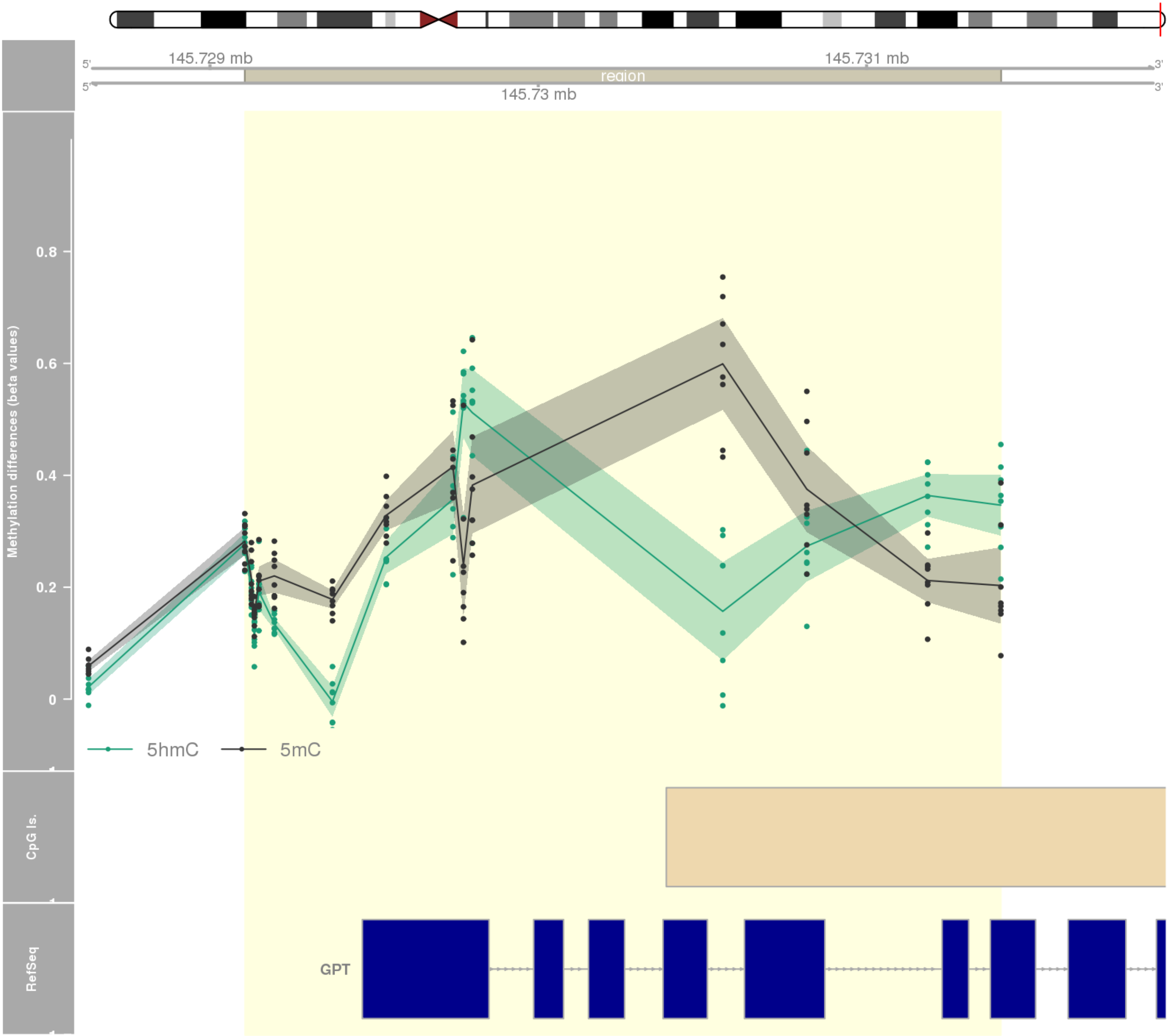
DMR 115 // chr7:155164294-155166619 // 2325 pb. (10 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559



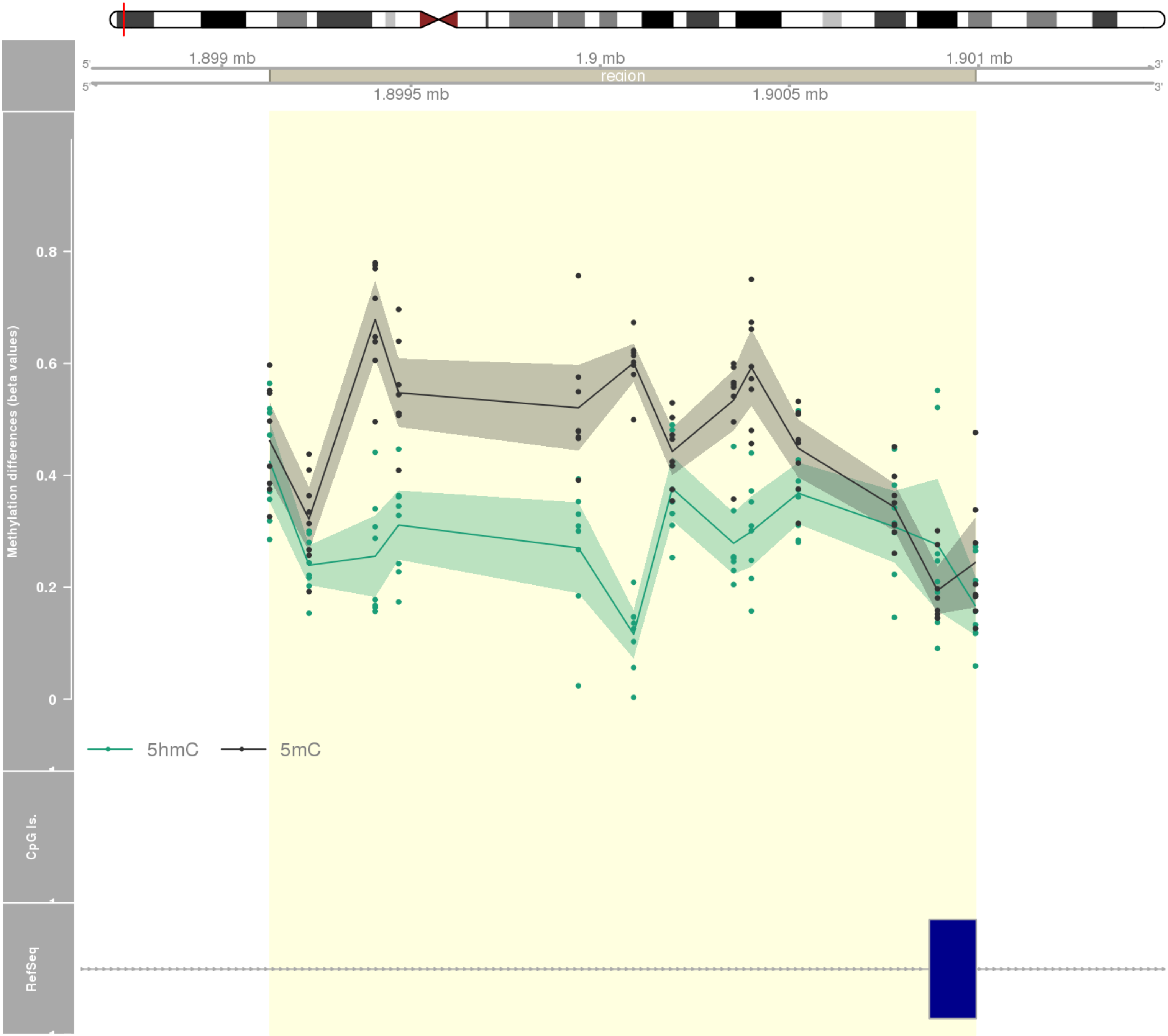
DMR 116 // chr6:31105711-31108541 // 2830 pb. (16 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: POLR2LP / PSORS1C1 / PSORS1C2 -



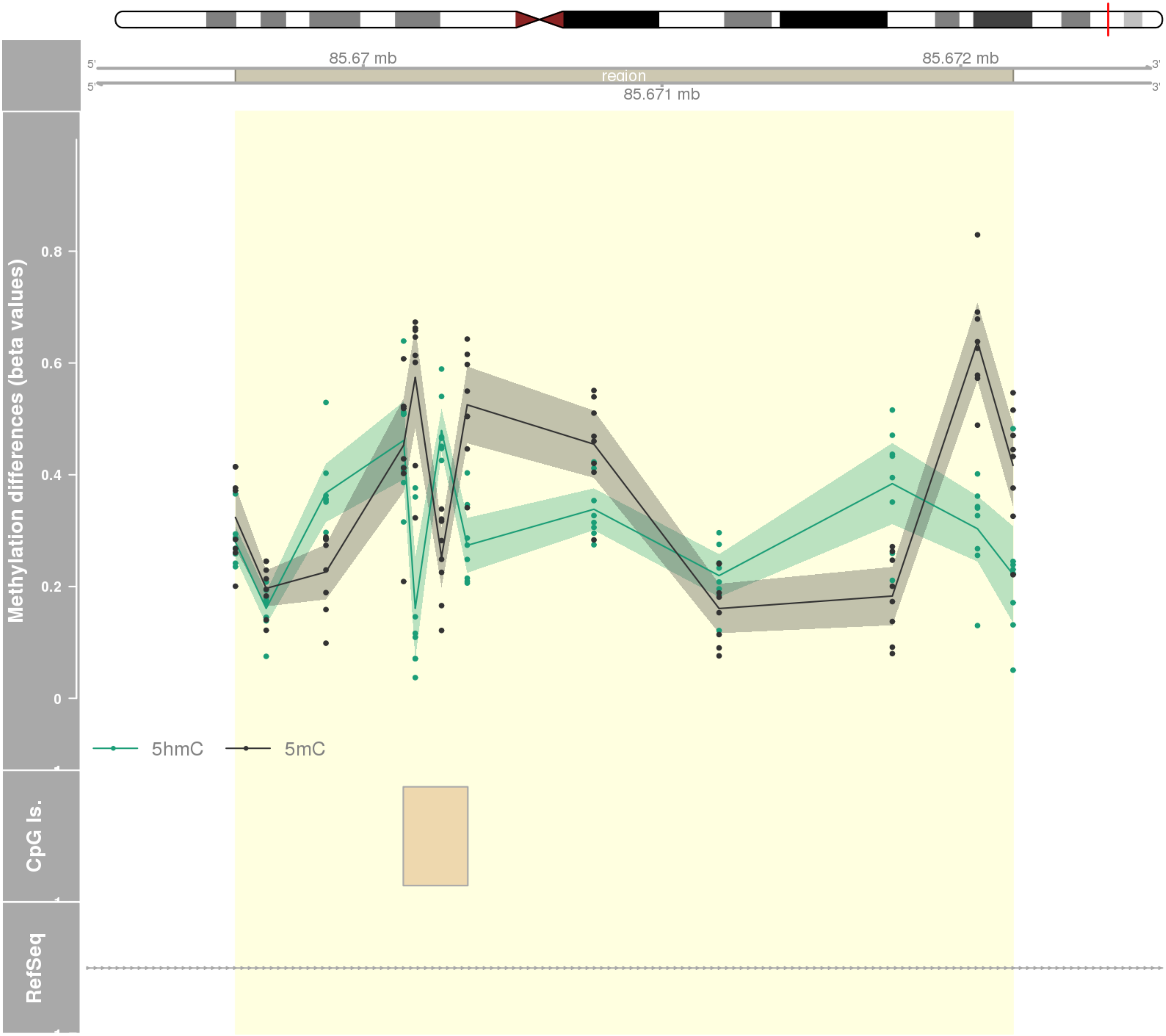
DMR 117 // chr8:145729106-145731409 // 2303 pb. (14 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: GPT -

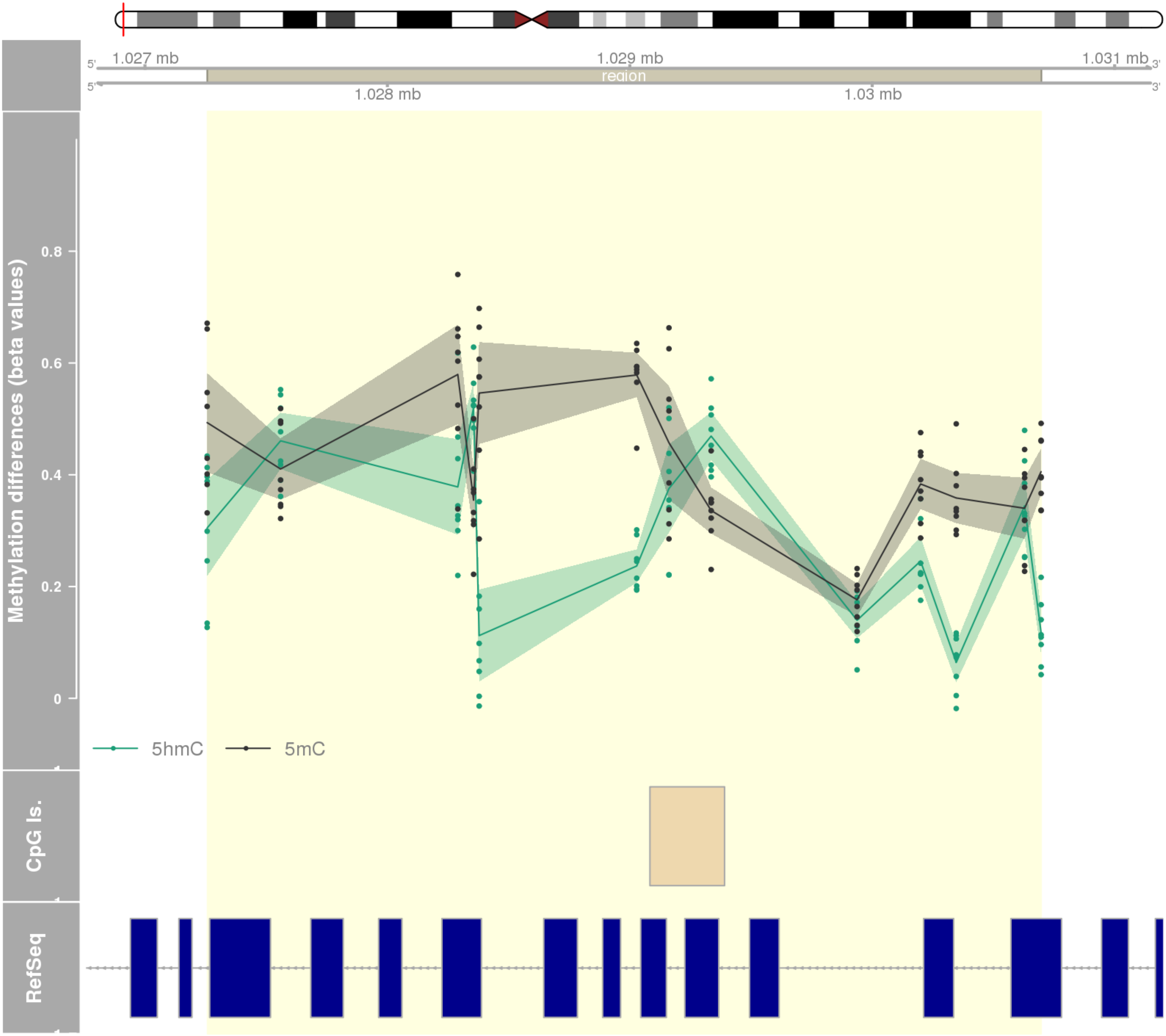


DMR 118 // chr8:1899127-1900992 // 1865 pb. (13 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: ARHGEF10 -



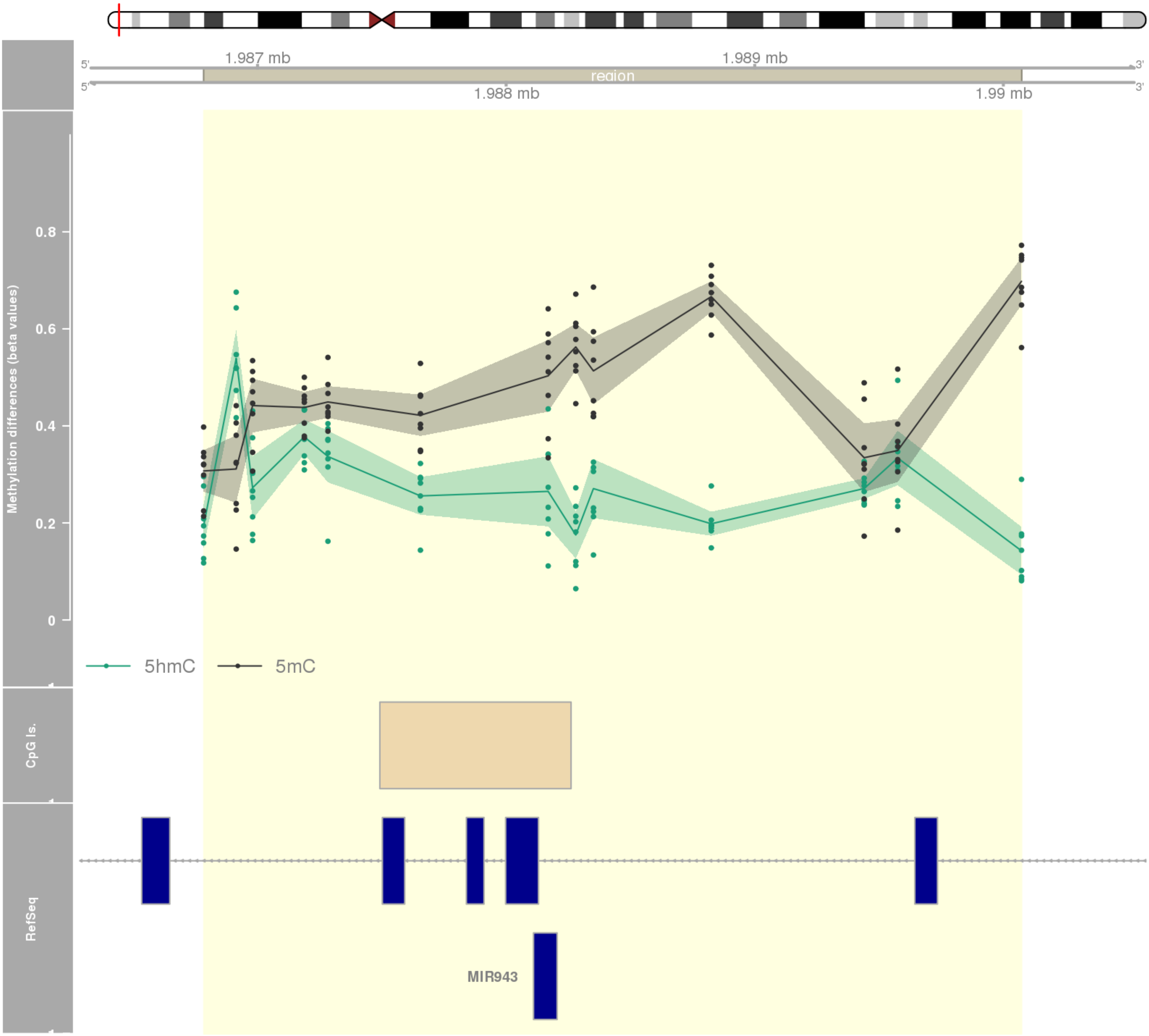
DMR 119 // chr16:85669572-85672175 // 2603 pb. (12 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: GSE1 -



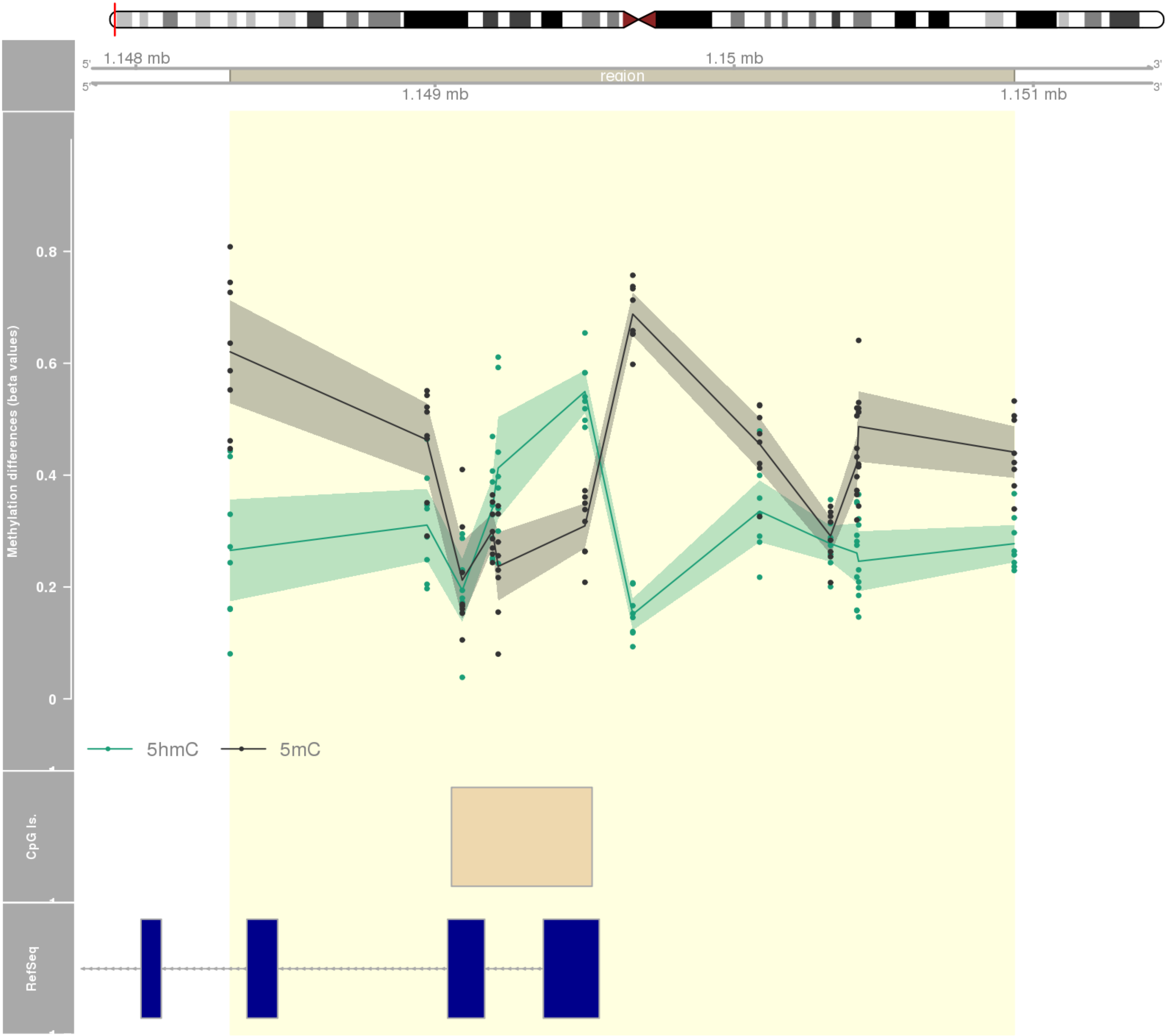


DMR 120 // chr11:1027257-1030697 // 3440 pb. (13 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: MUC6 -

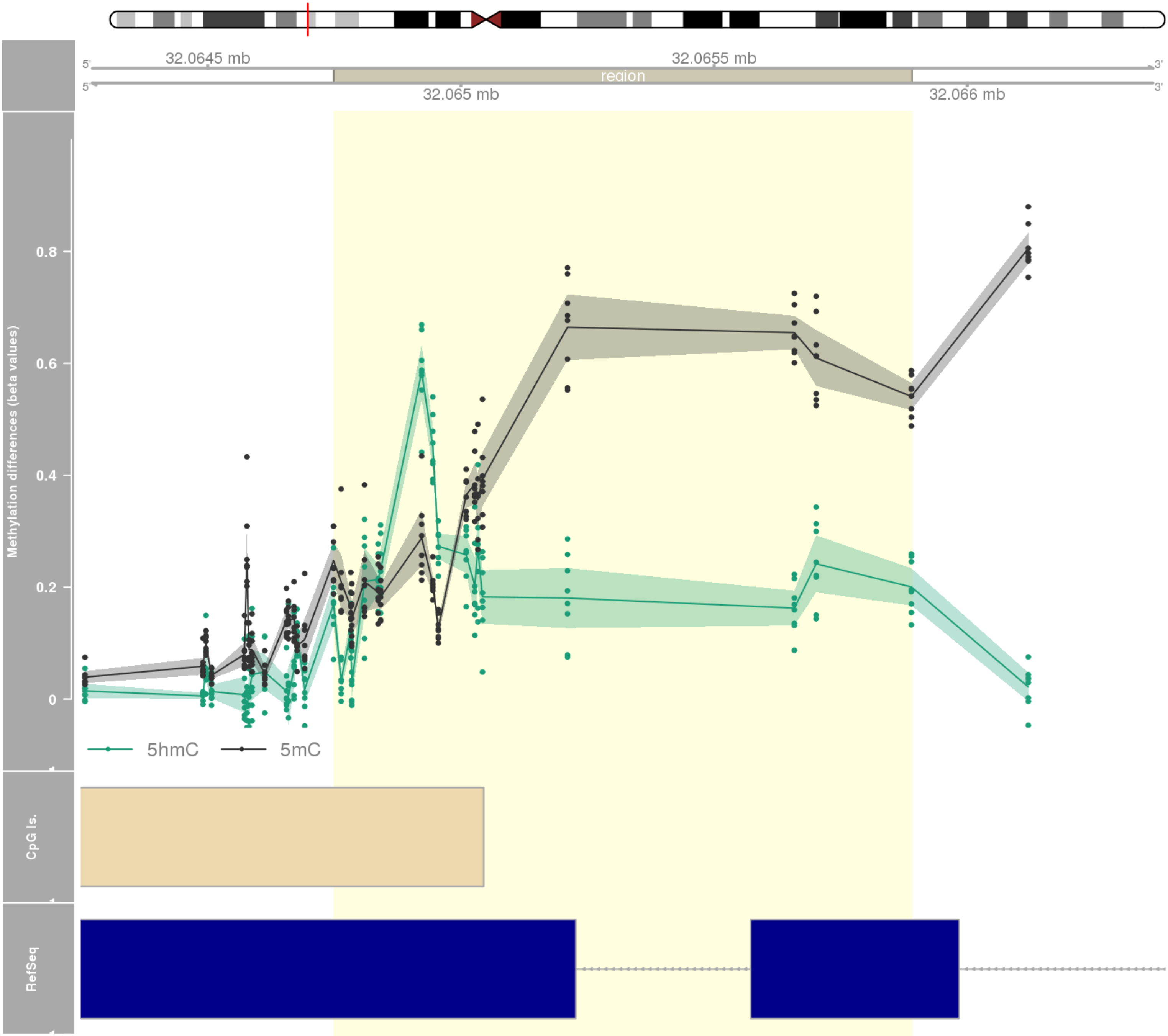
DMR 121 // chr4:1986783-1990073 // 3290 pb. (13 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: NELFA / MIR943 -



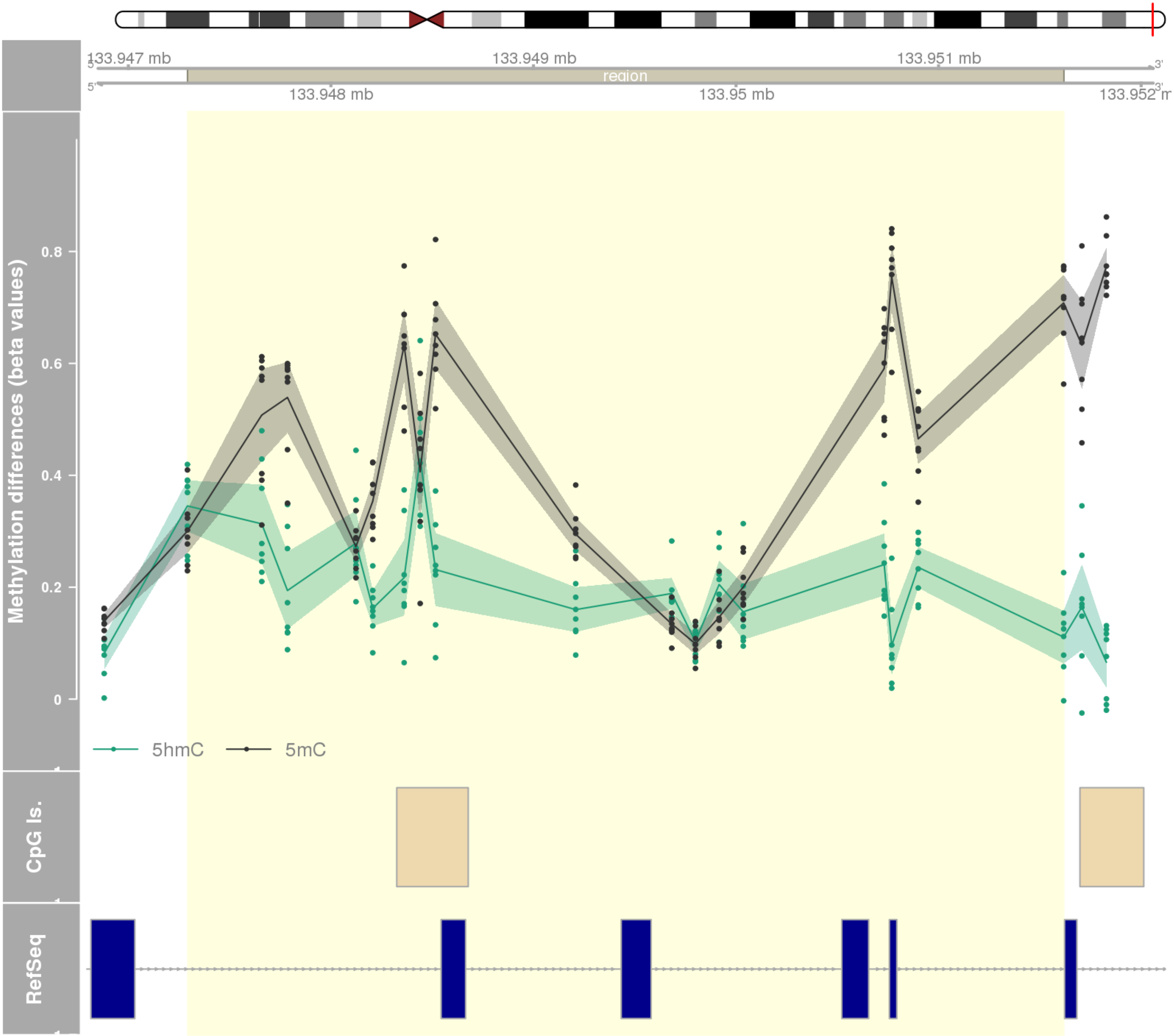
DMR 122 // chr1:1148315-1150936 // 2621 pb. (12 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: TNFRSF4 -



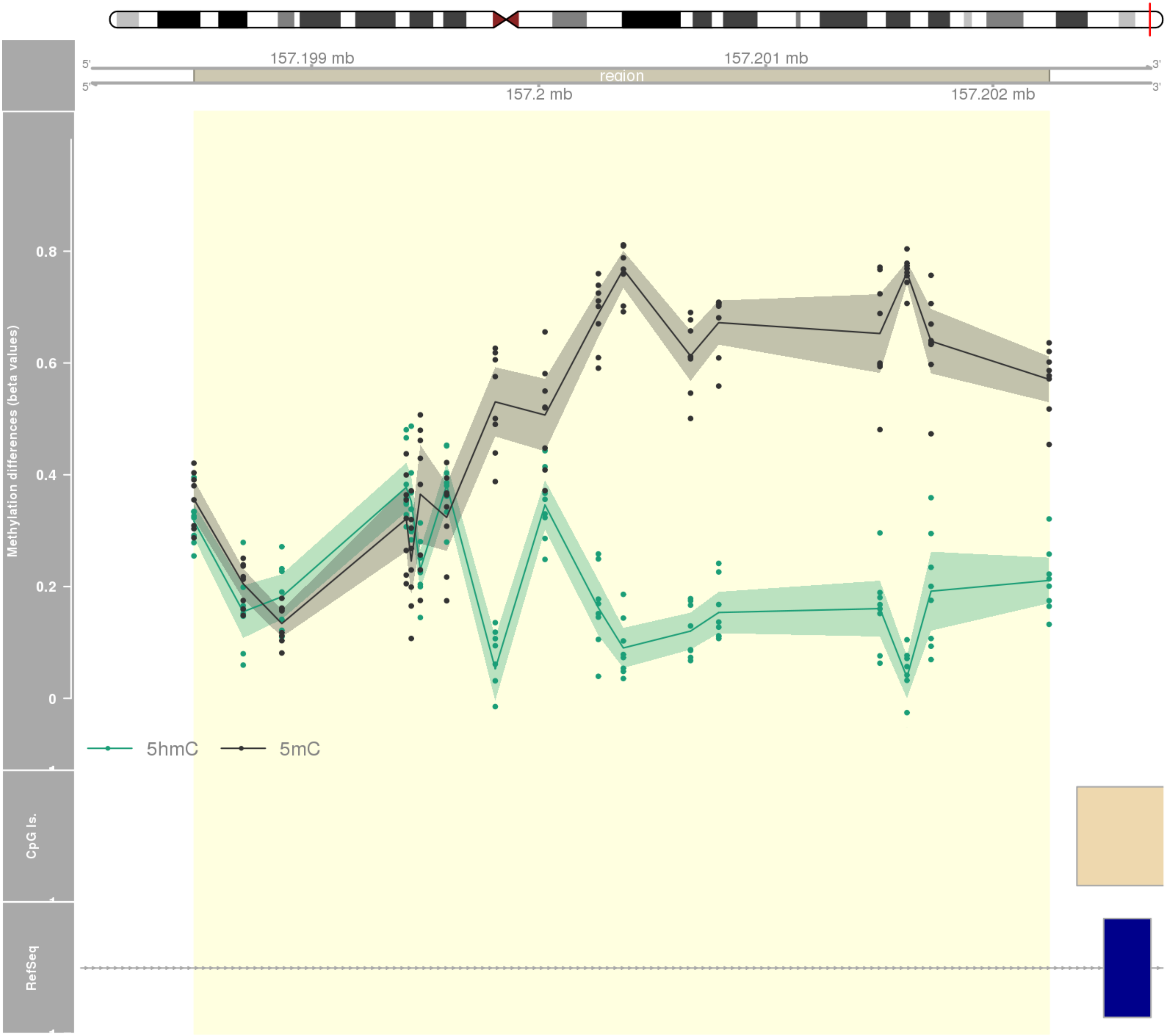
DMR 123 // chr6:32064749-32065890 // 1141 pb. (18 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.006 // fwerArea: 0.559
- genes: TNXB -



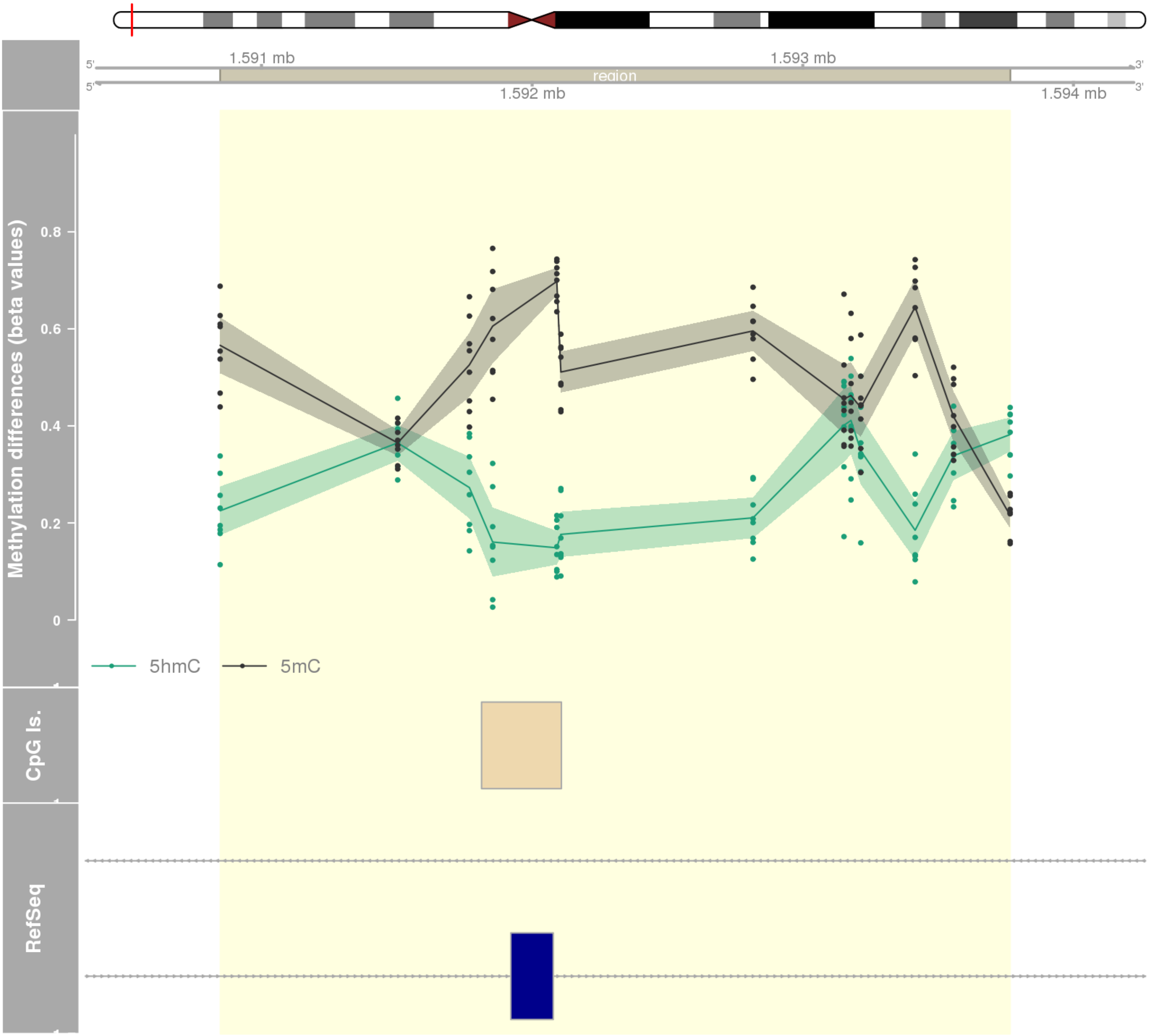
DMR 124 // chr10:133947292-133951618 // 4326 pb. (17 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: JAKMIP3 -



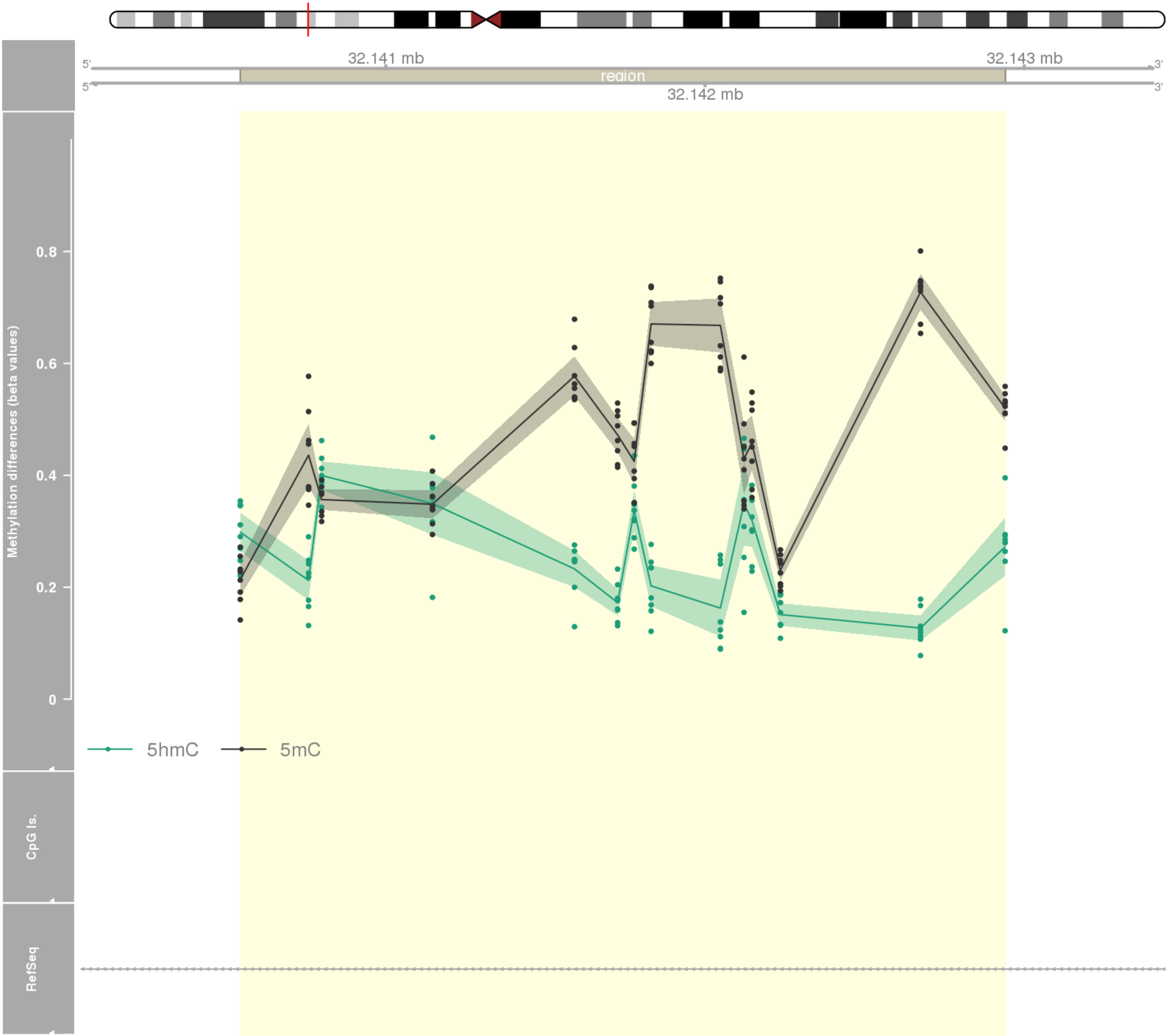
DMR 125 // chr7:157198482-157202248 // 3766 pb. (17 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: DNAJB6 -



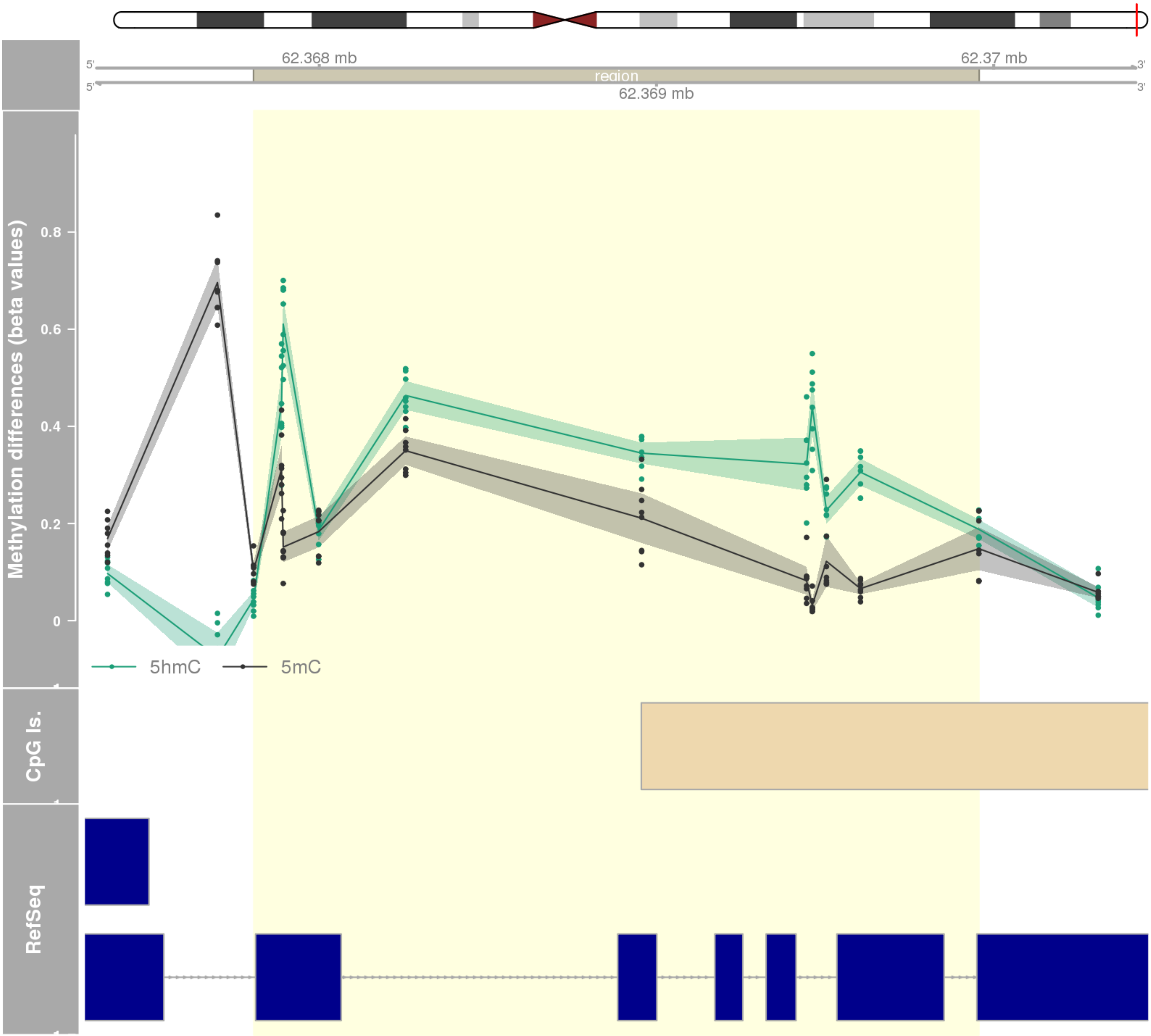
DMR 126 // chr16:1590847-1593766 // 2919 pb. (13 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: IFT140 / TMEM204 -



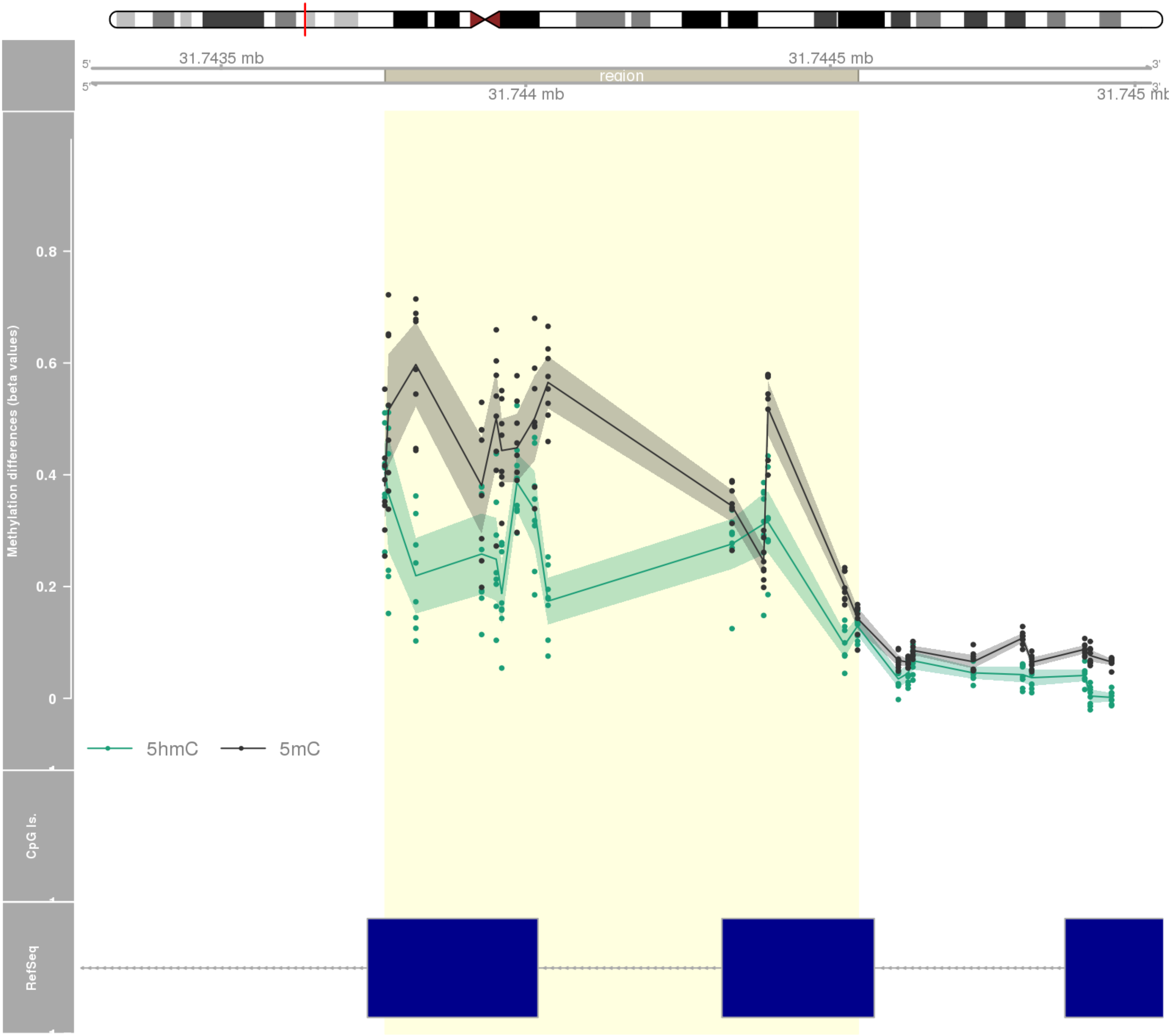
DMR 127 // chr6:32140544-32142940 // 2396 pb. (14 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: AGPAT1 -



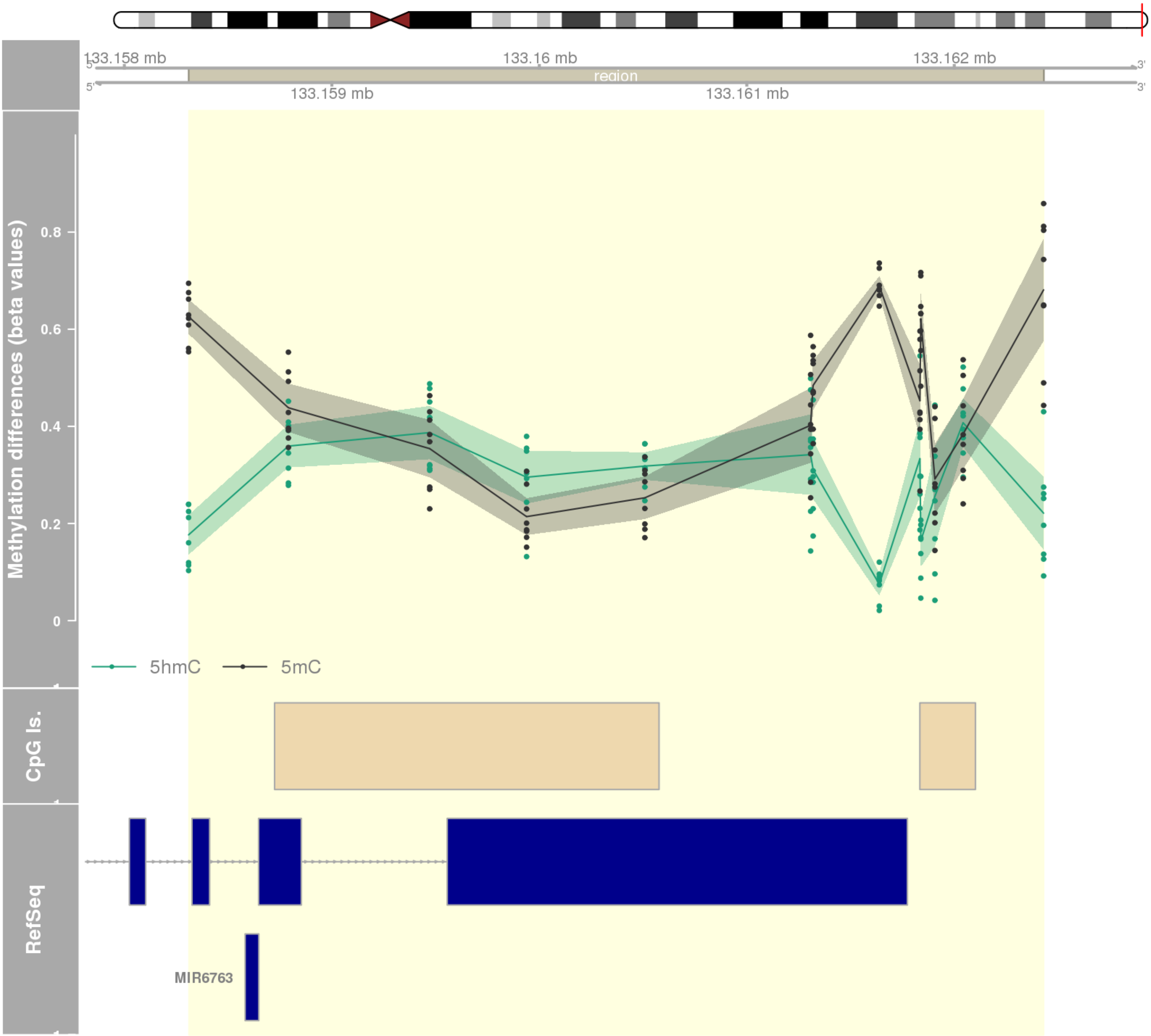
DMR 128 // chr20:62367805-62369956 // 2151 pb. (11 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: LIME1 -



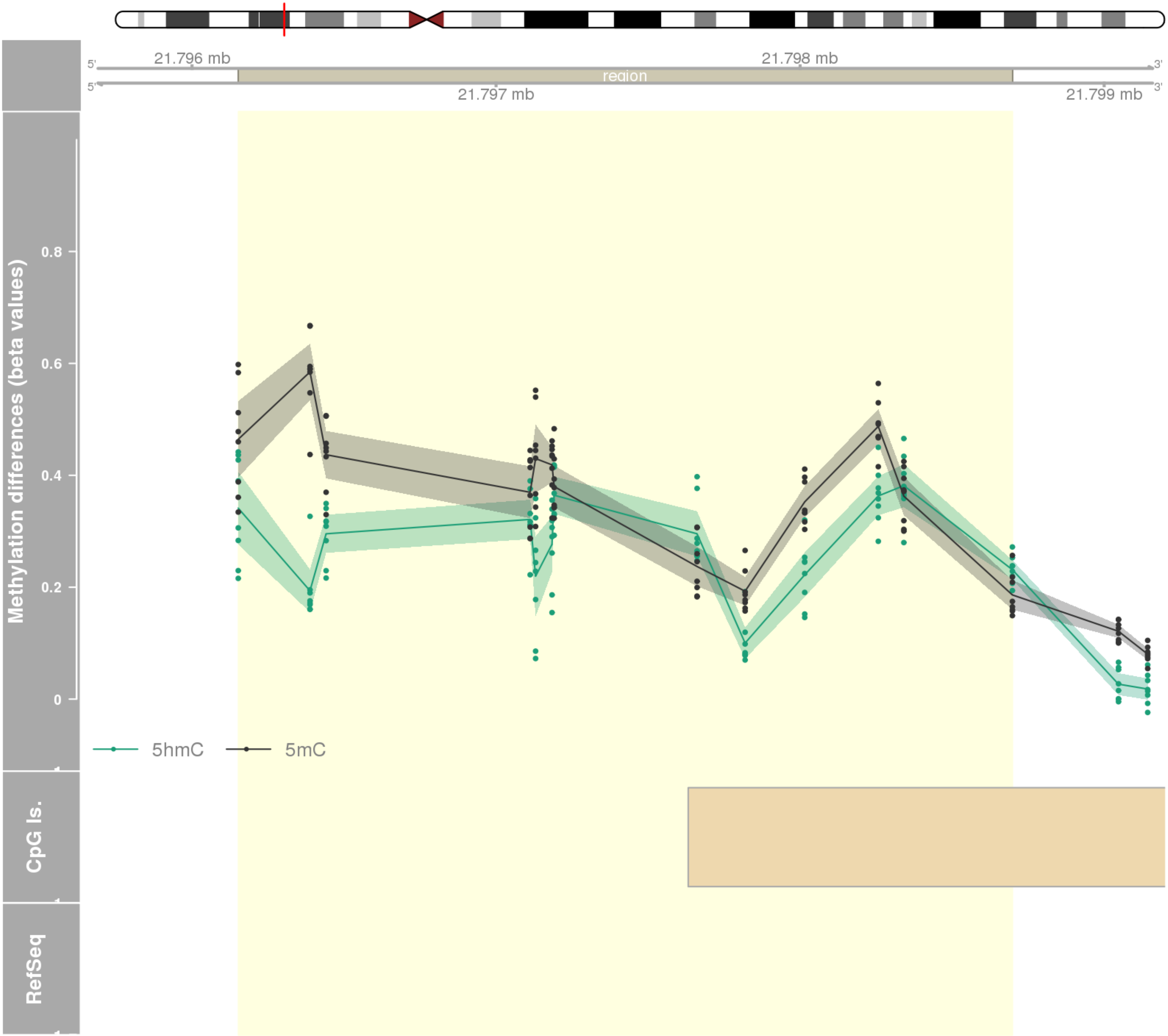
DMR 129 // chr6:31743769-31744545 // 776 pb. (14 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: VWA7 -



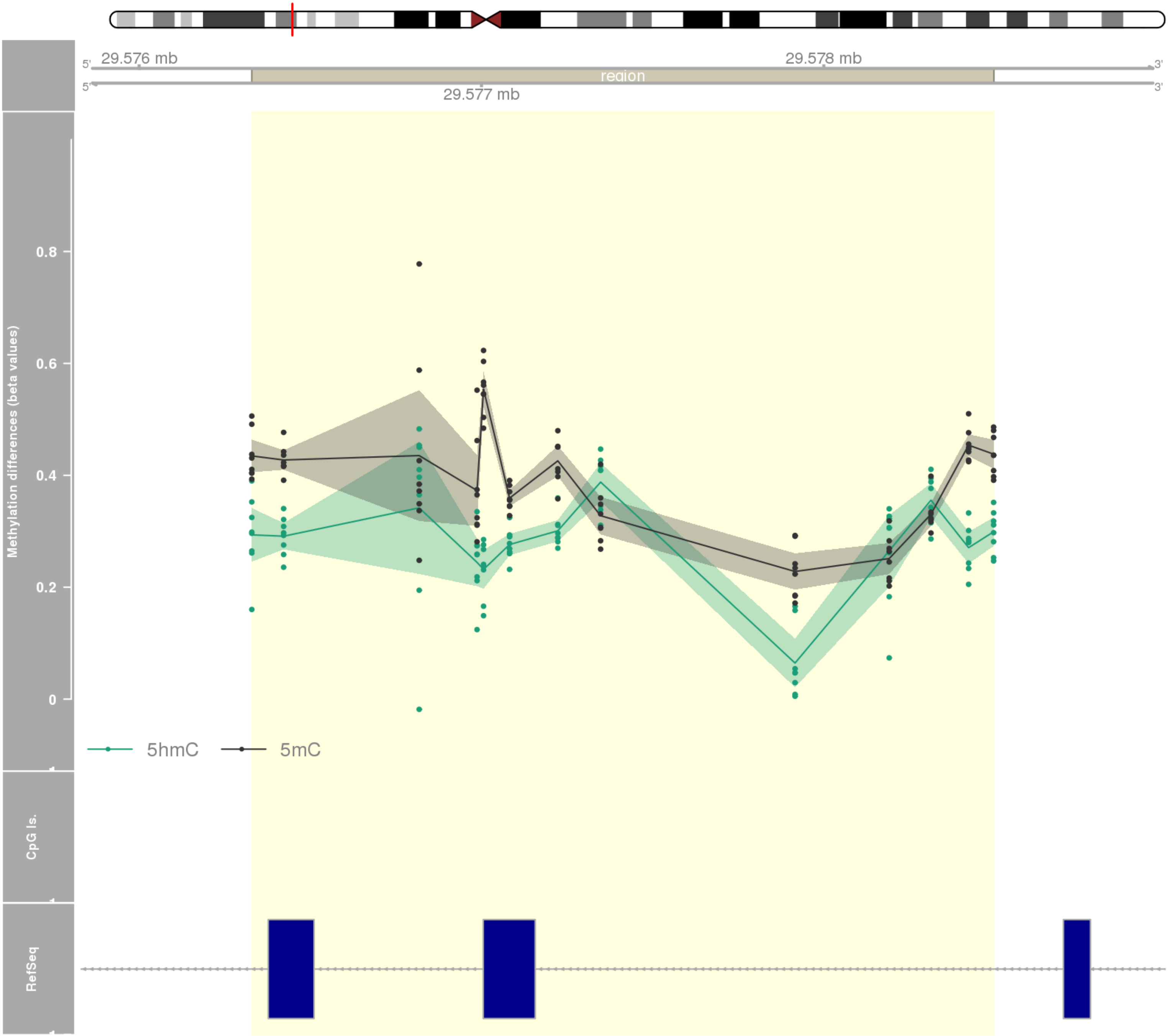
DMR 130 // chr12:133158310-133162431 // 4121 pb. (13 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: FBRSL1 -



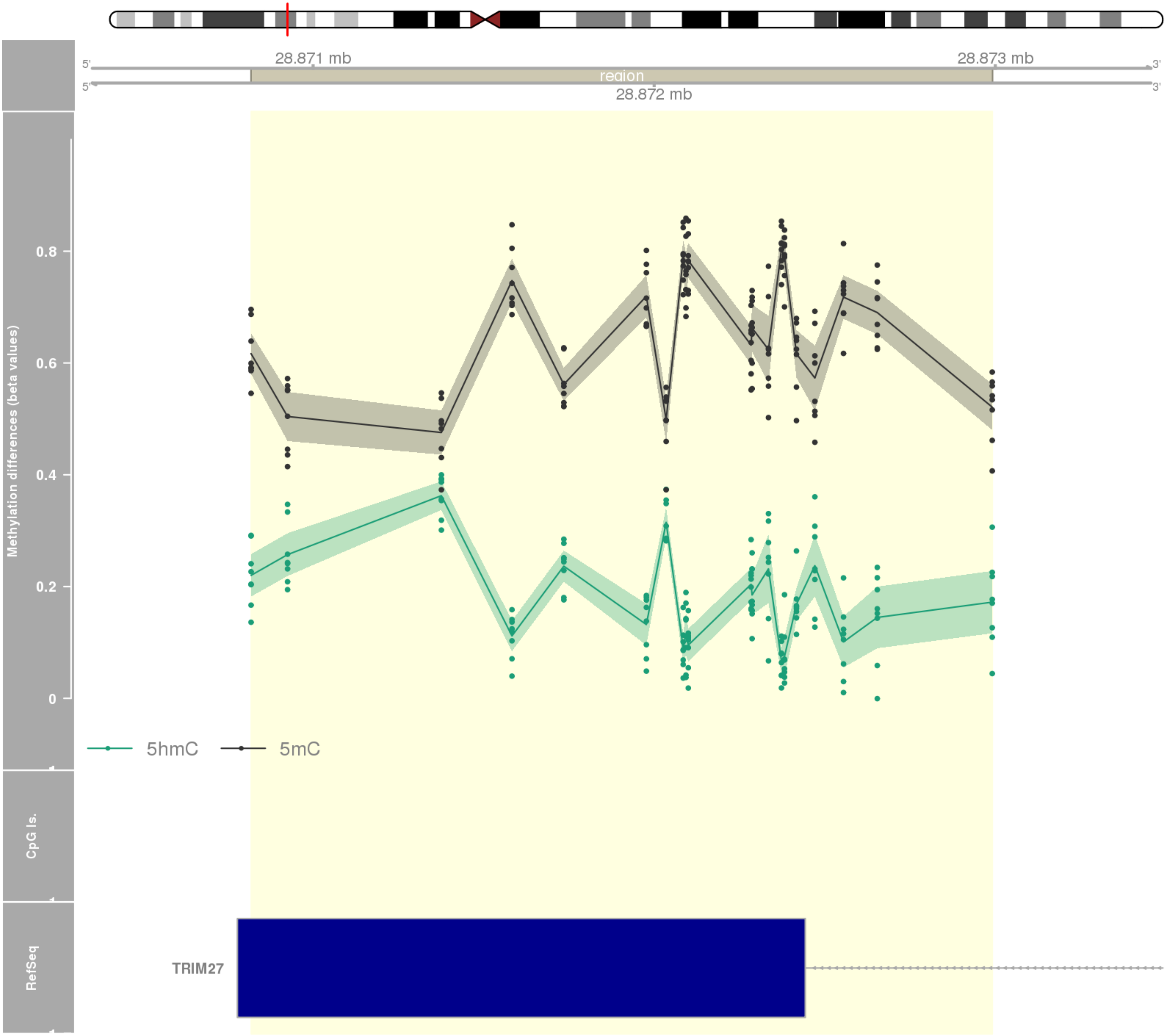
DMR 131 // chr10:21796152-21798698 // 2546 pb. (13 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559



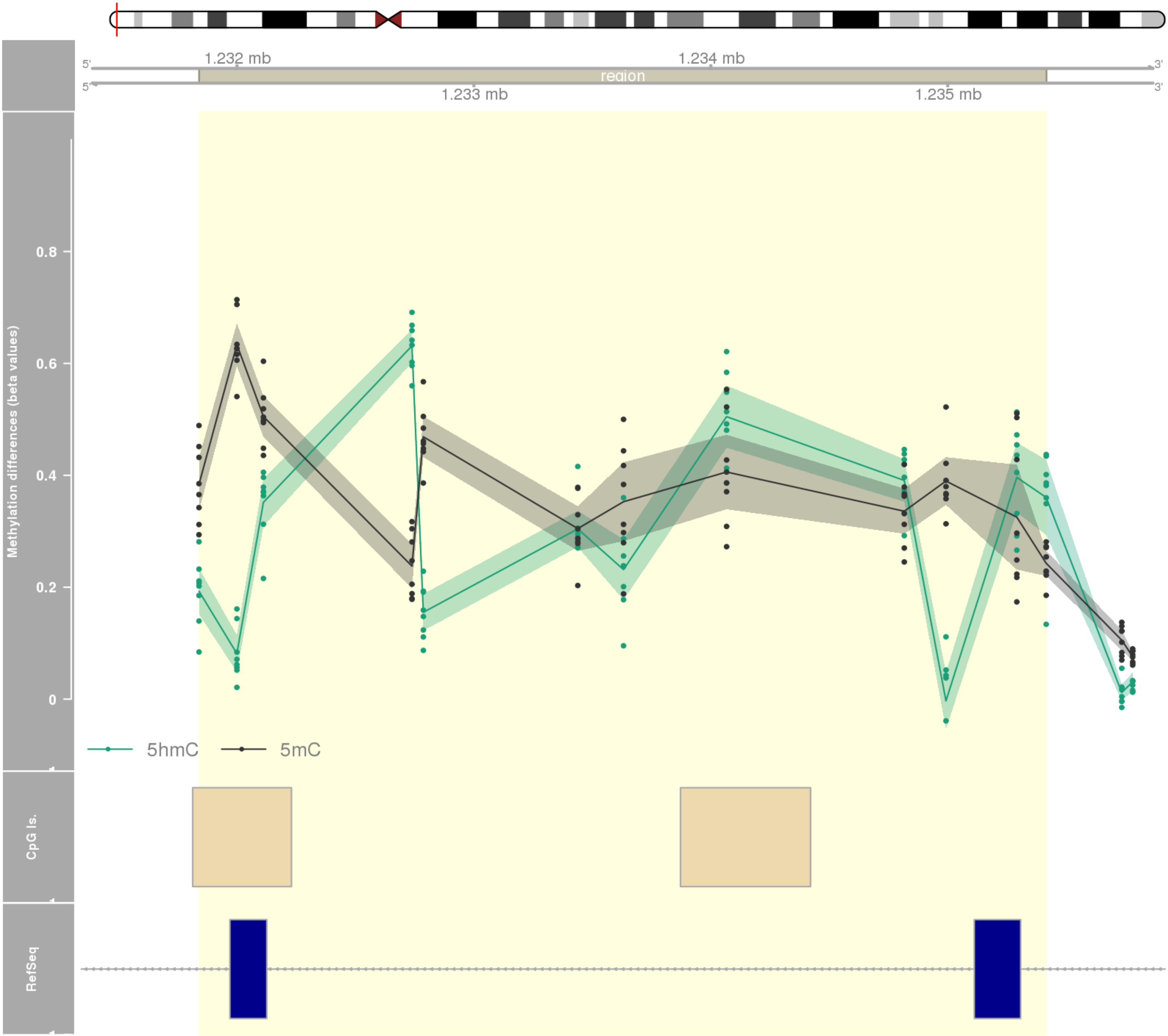
DMR 132 // chr6:29576329-29578496 // 2167 pb. (13 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: GABBR1 -



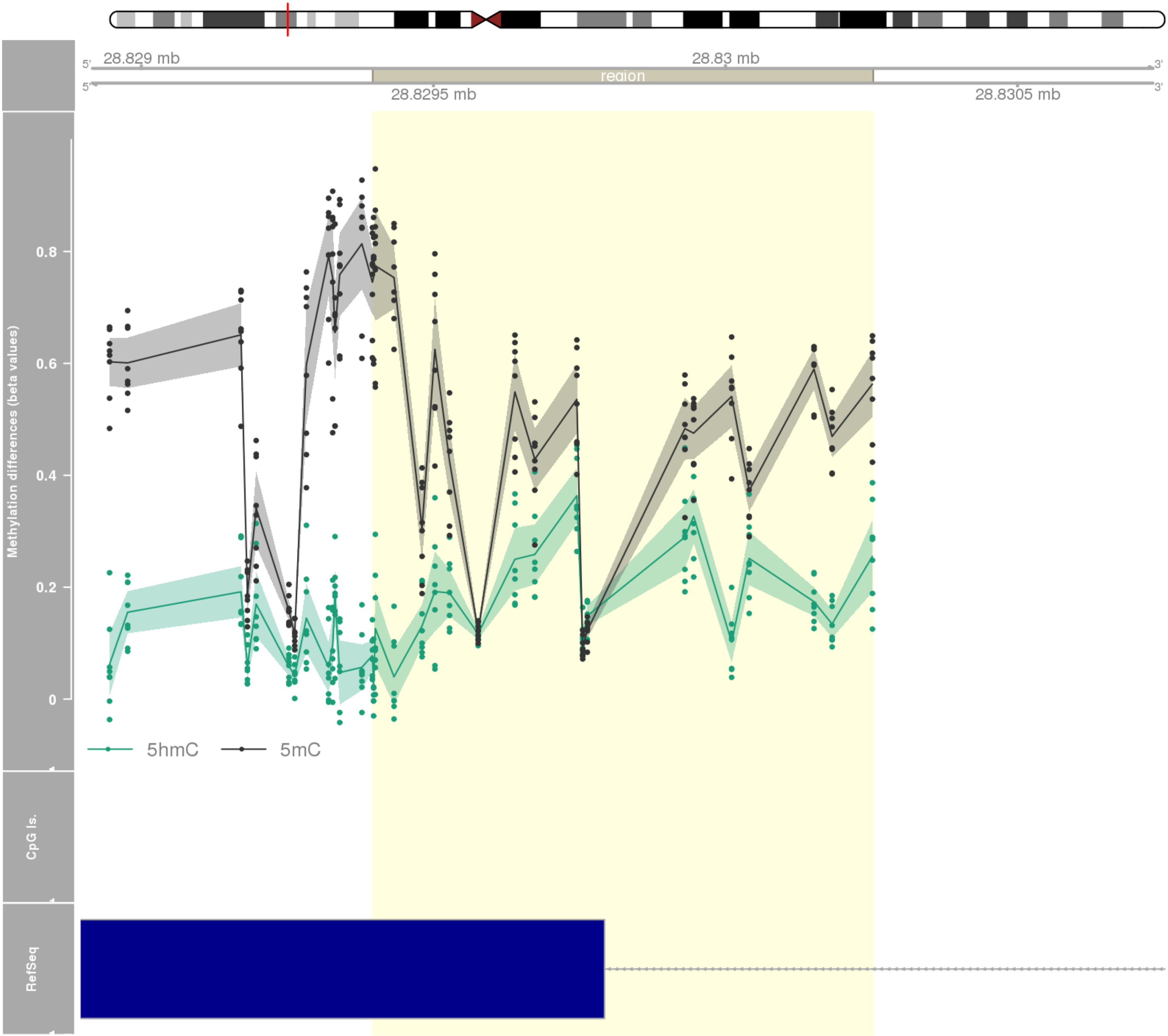
DMR 133 // chr6:28870818-28872991 // 2173 pb. (20 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: TRIM27 -



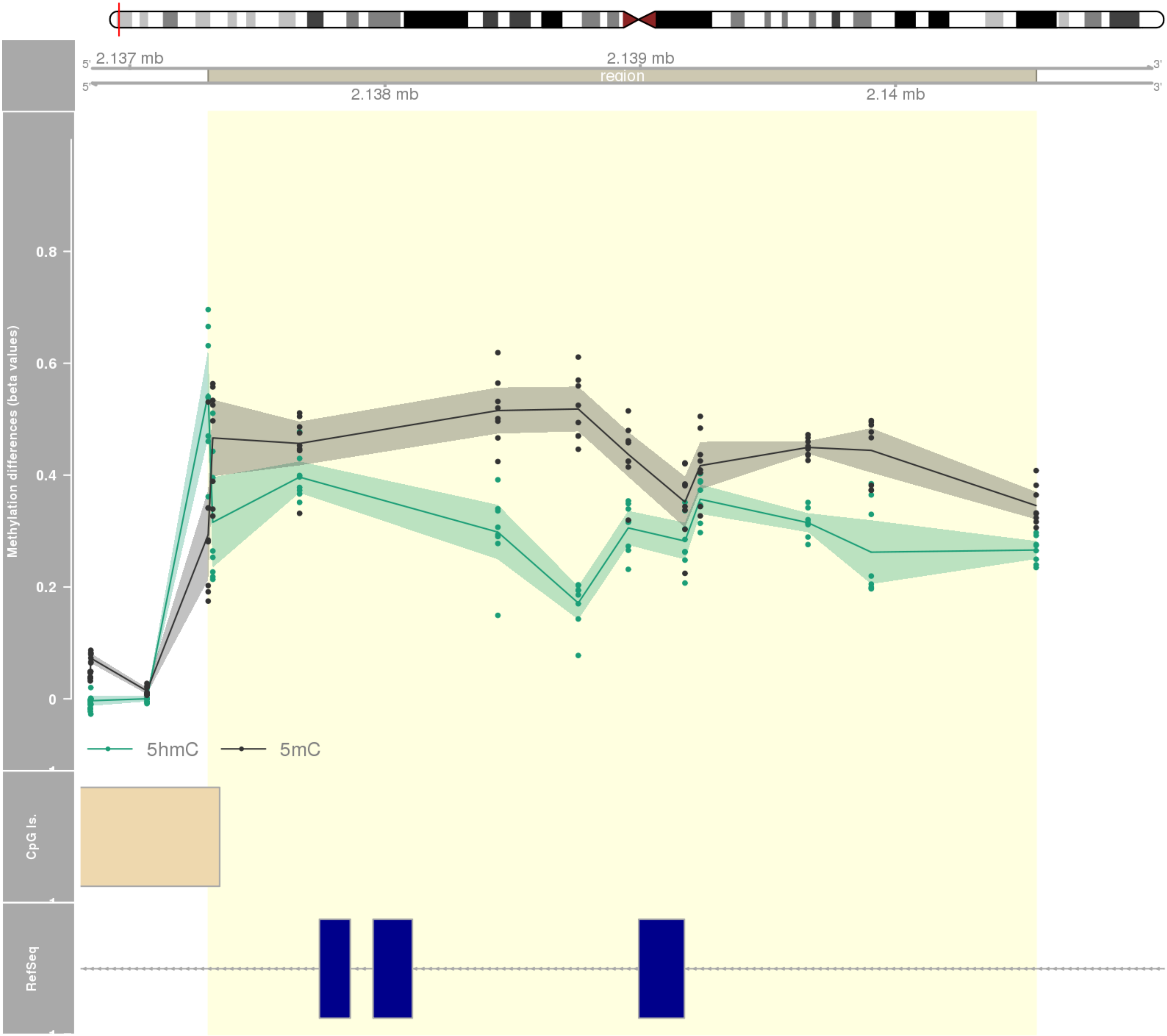
DMR 134 // chr4:1231840-1235416 // 3576 pb. (12 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: CTBP1 -



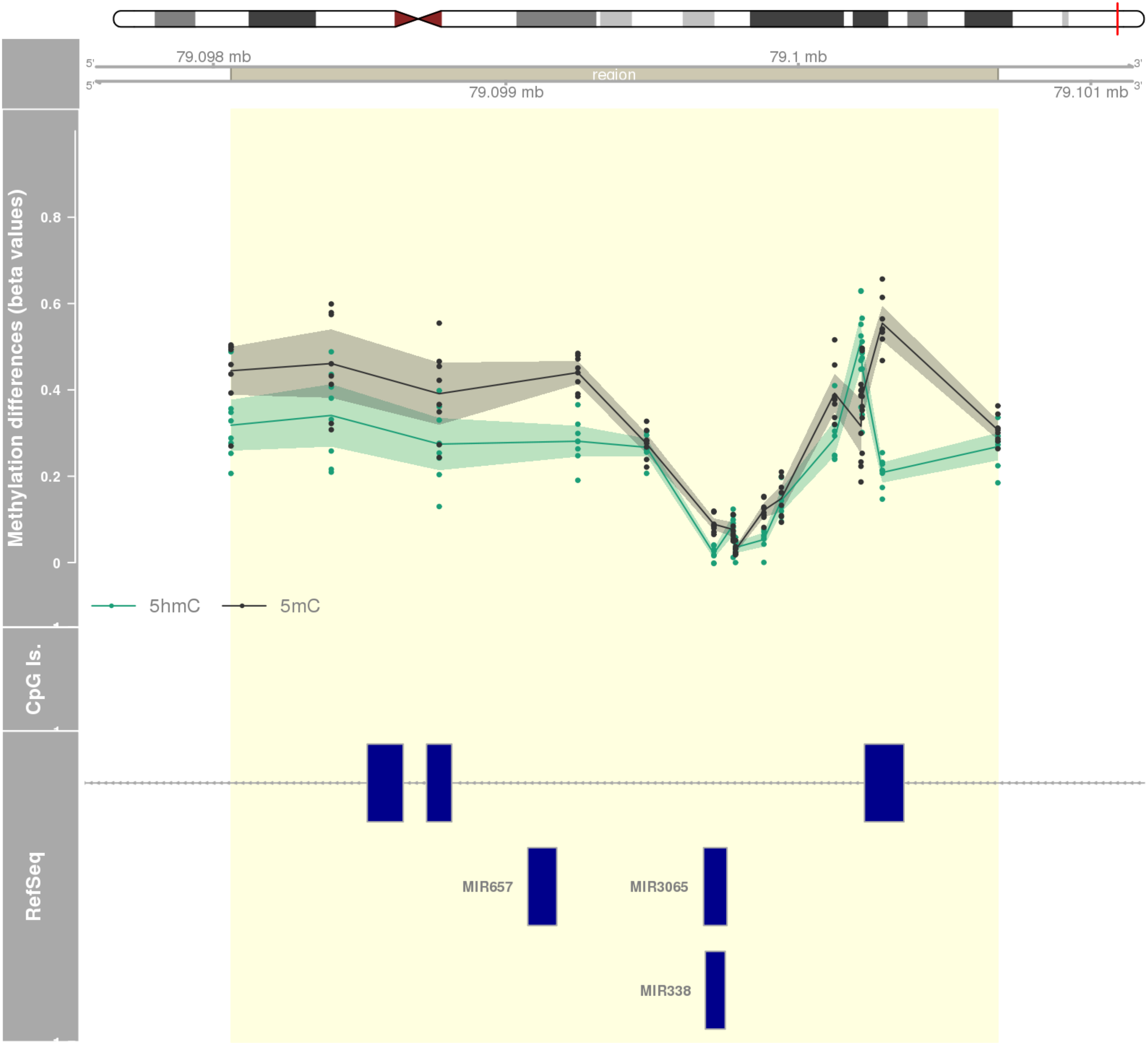
DMR 135 // chr6:28829396-28830252 // 856 pb. (20 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: RPL13P -



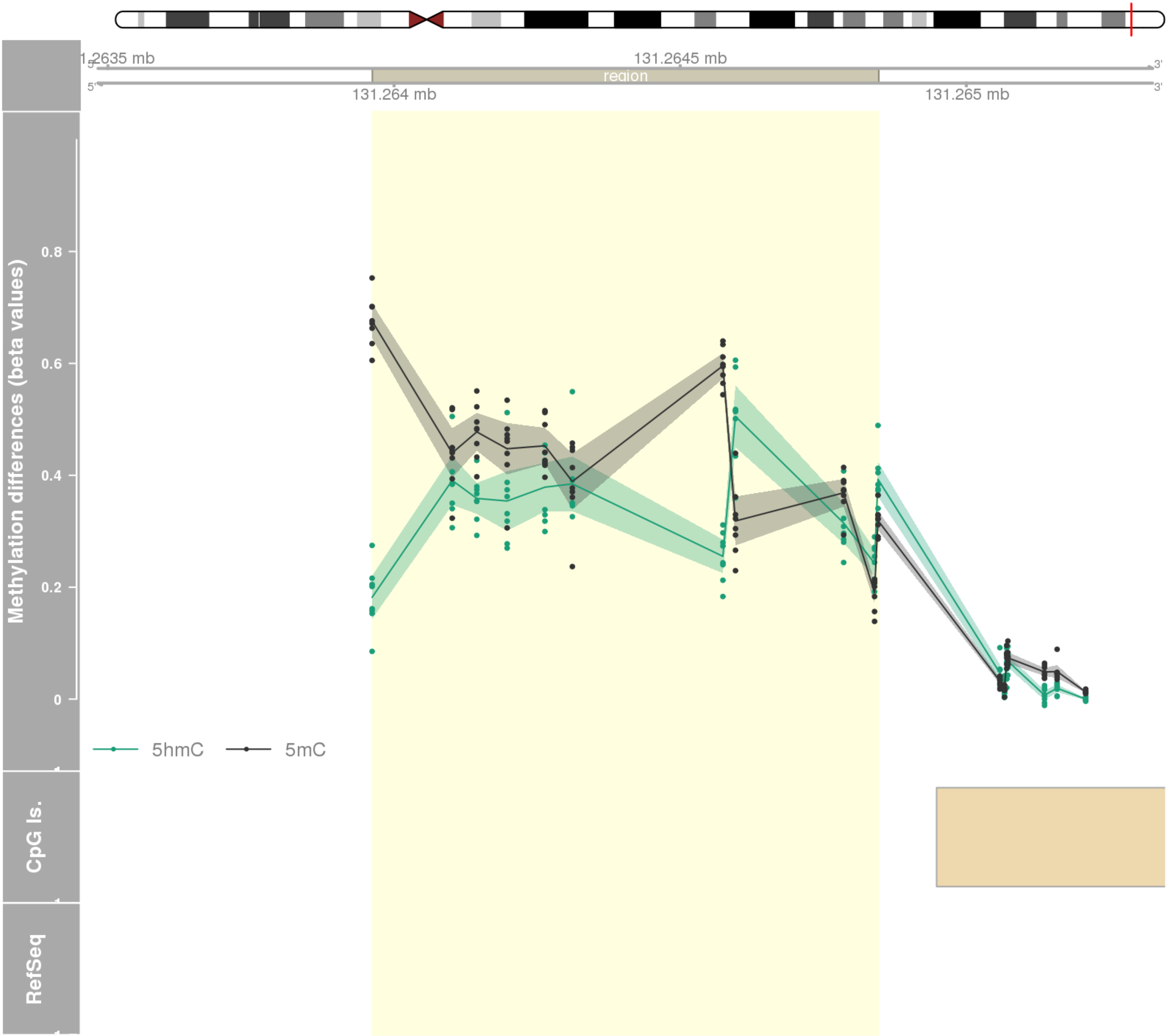
DMR 136 // chr1:2137307-2140551 // 3244 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: C1orf86 -



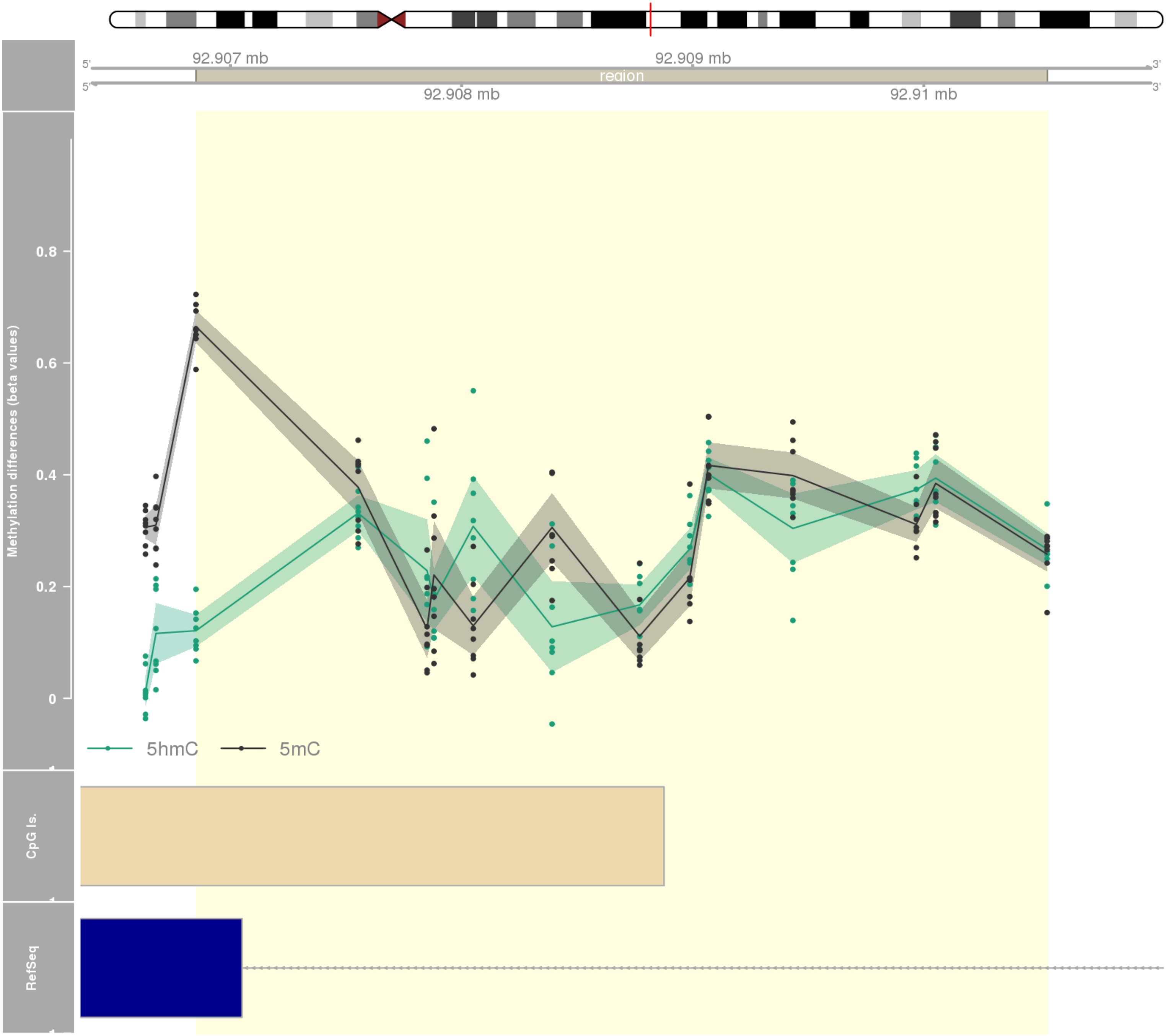
DMR 137 // chr17:79098060-79100682 // 2622 pb. (15 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: AATK / MIR657 / MIR3065 / MIR338 -



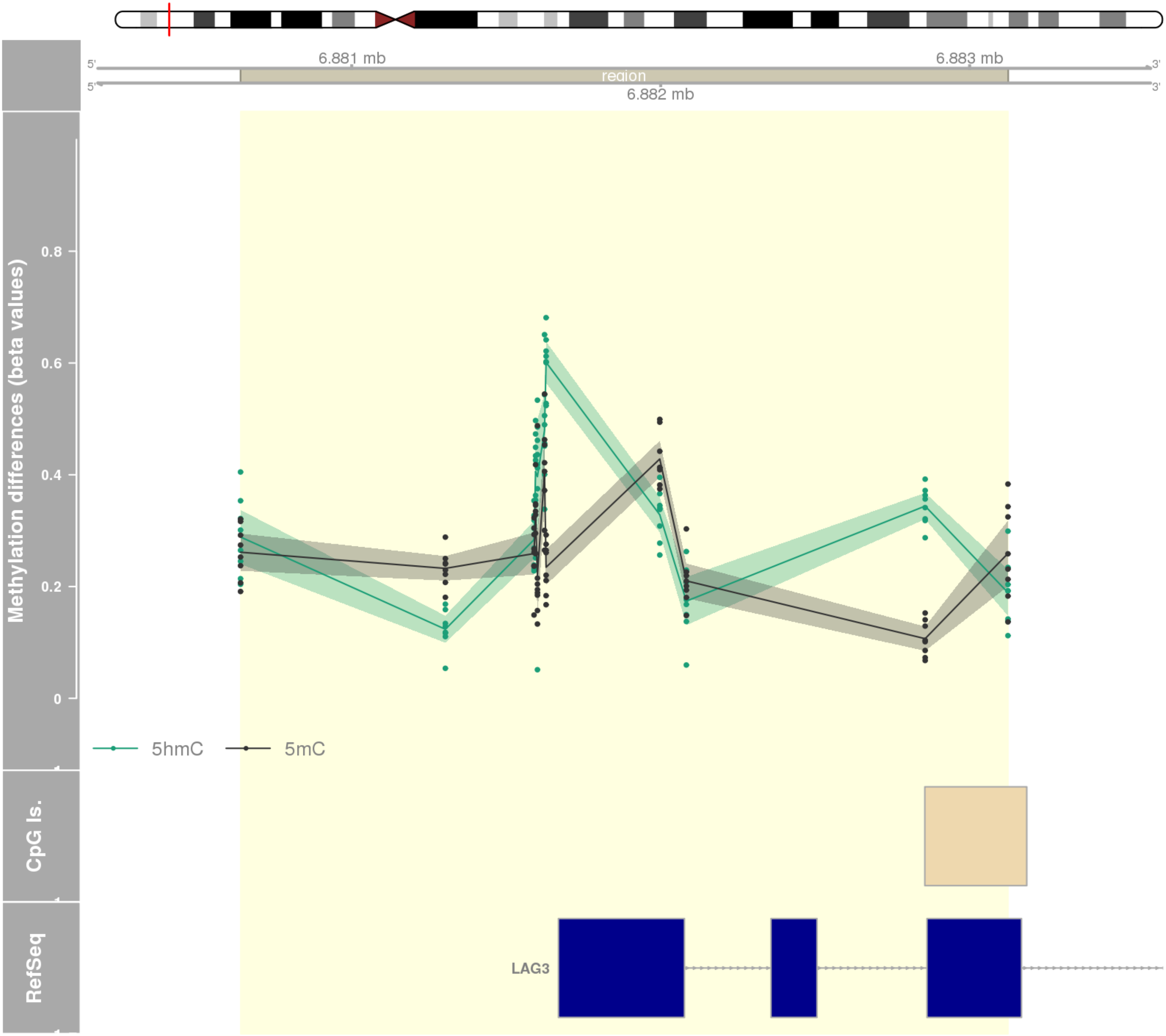
DMR 138 // chr10:131263962-131264846 // 884 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559



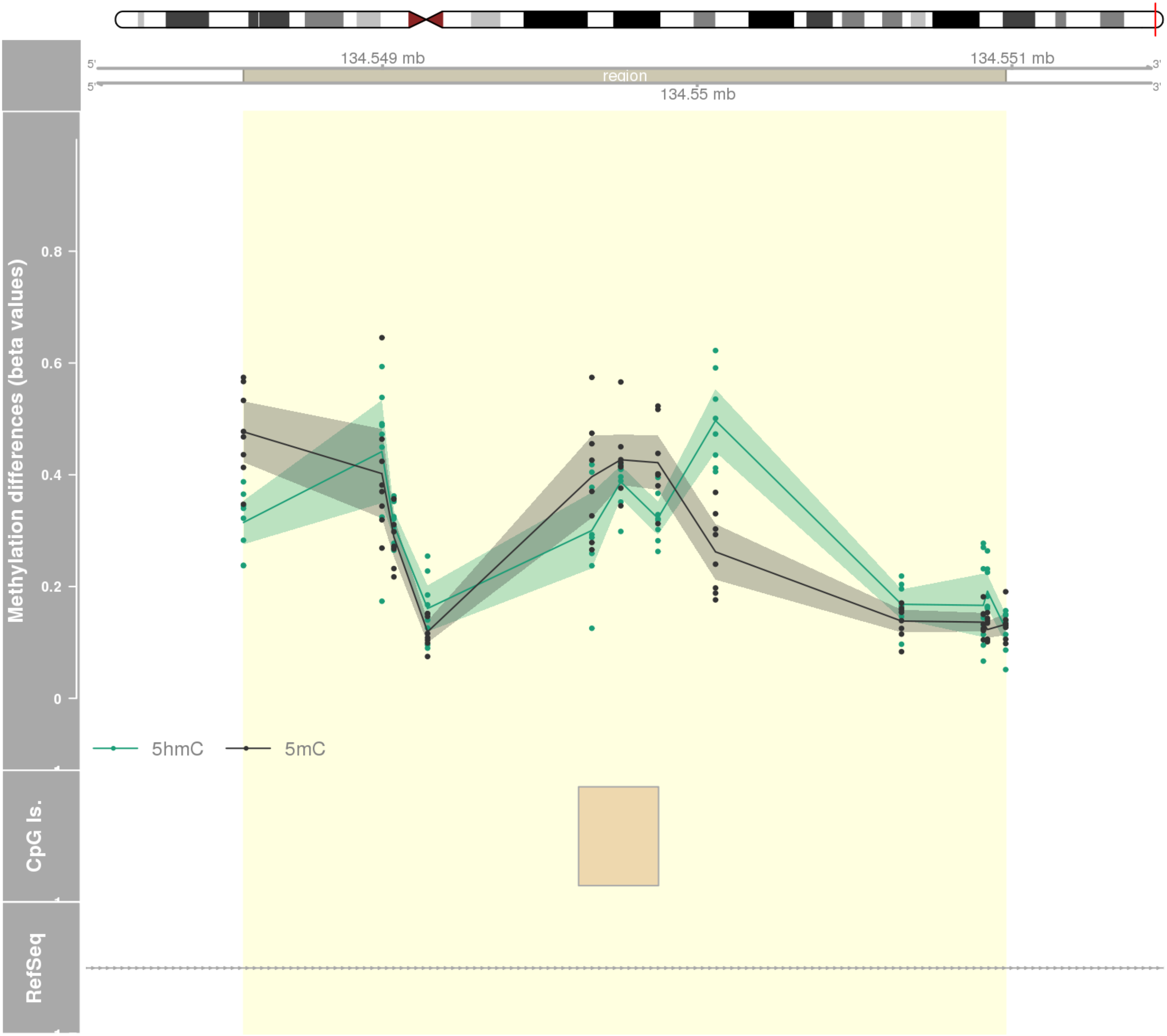
DMR 139 // chr5:92906851-92910534 // 3683 pb. (13 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: NR2F1-AS1 -



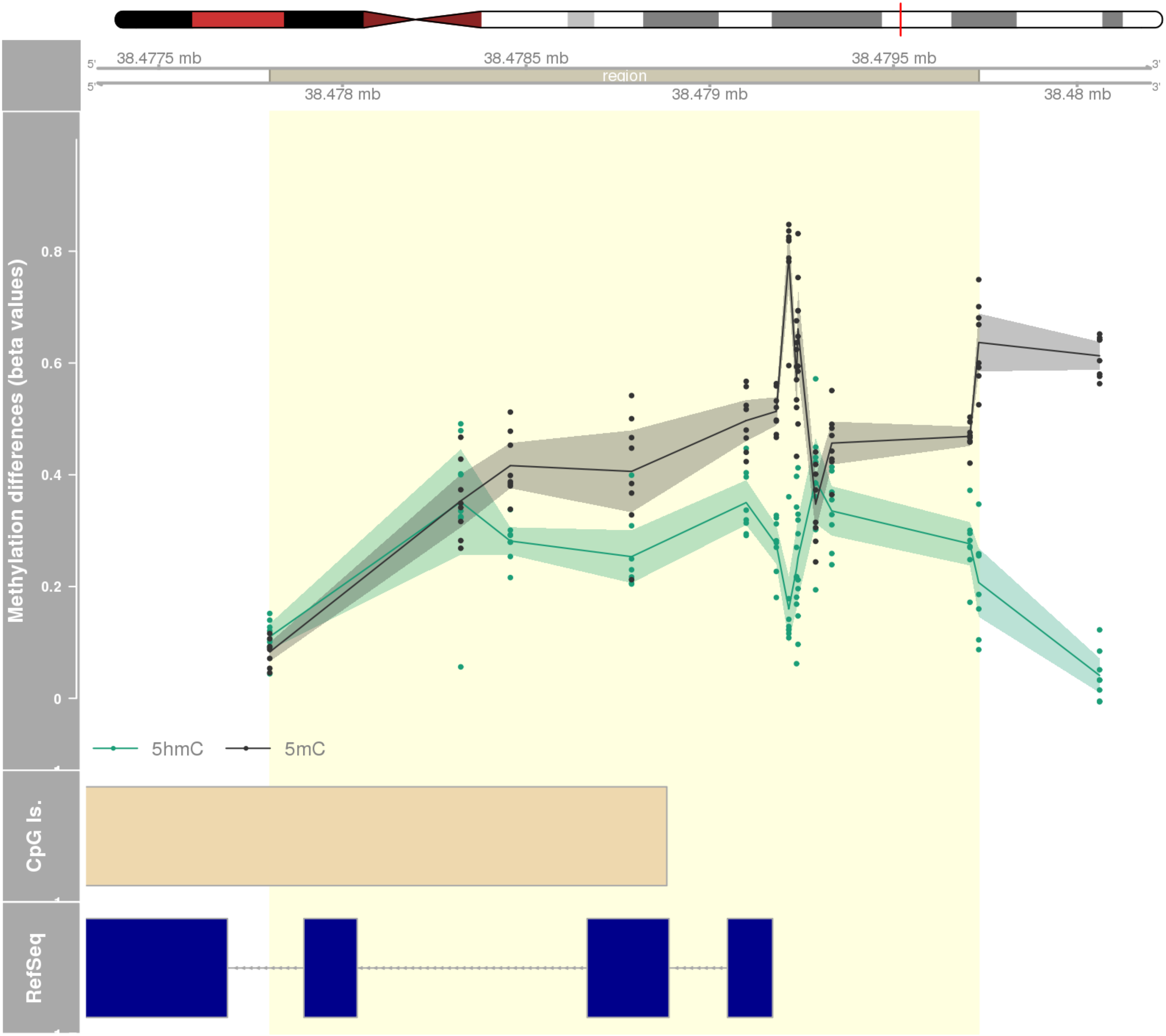
DMR 140 // chr12:6880640-6883124 // 2484 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: LAG3 -



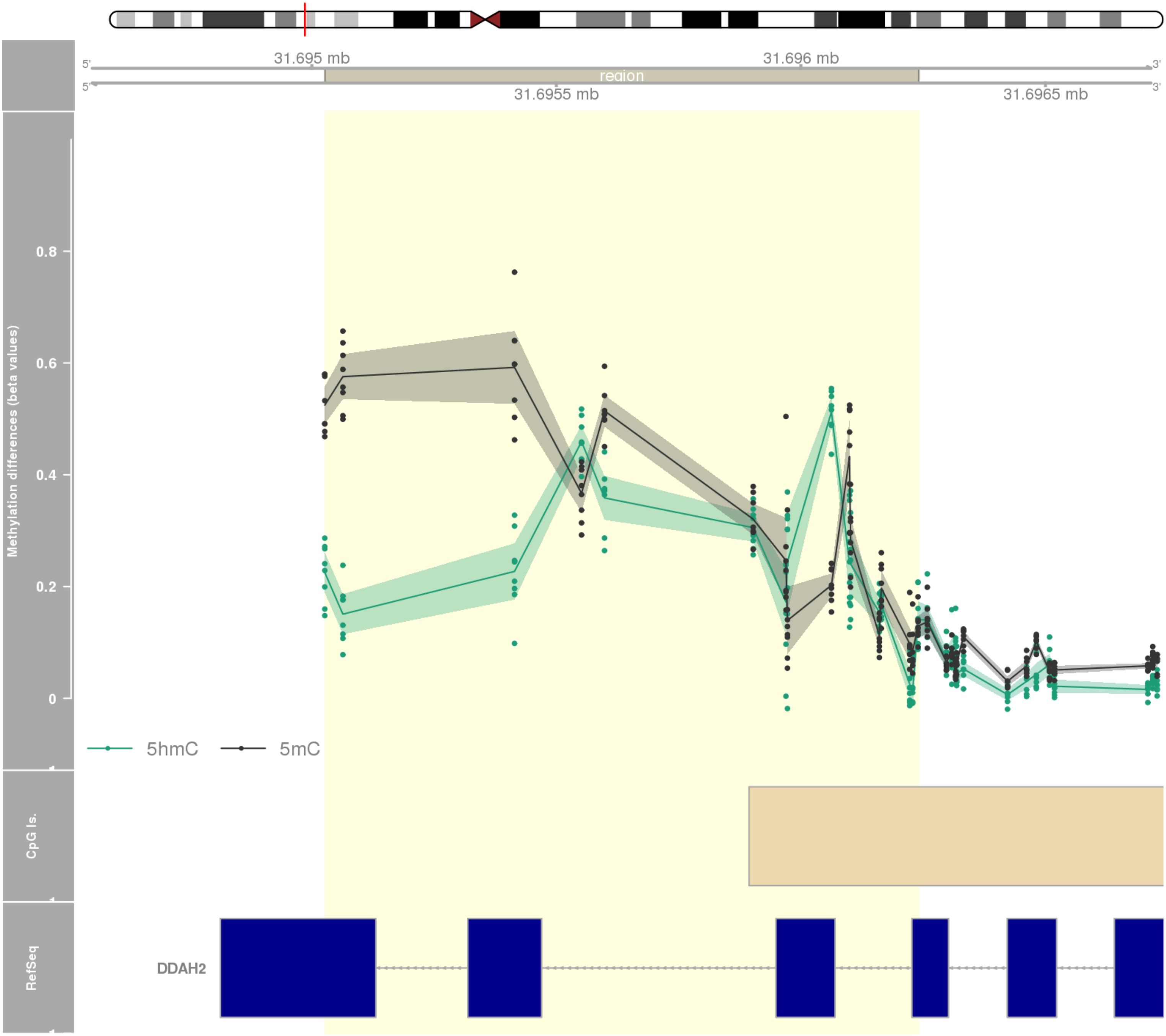
DMR 141 // chr10:134548558-134550980 // 2422 pb. (12 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: INPP5A -



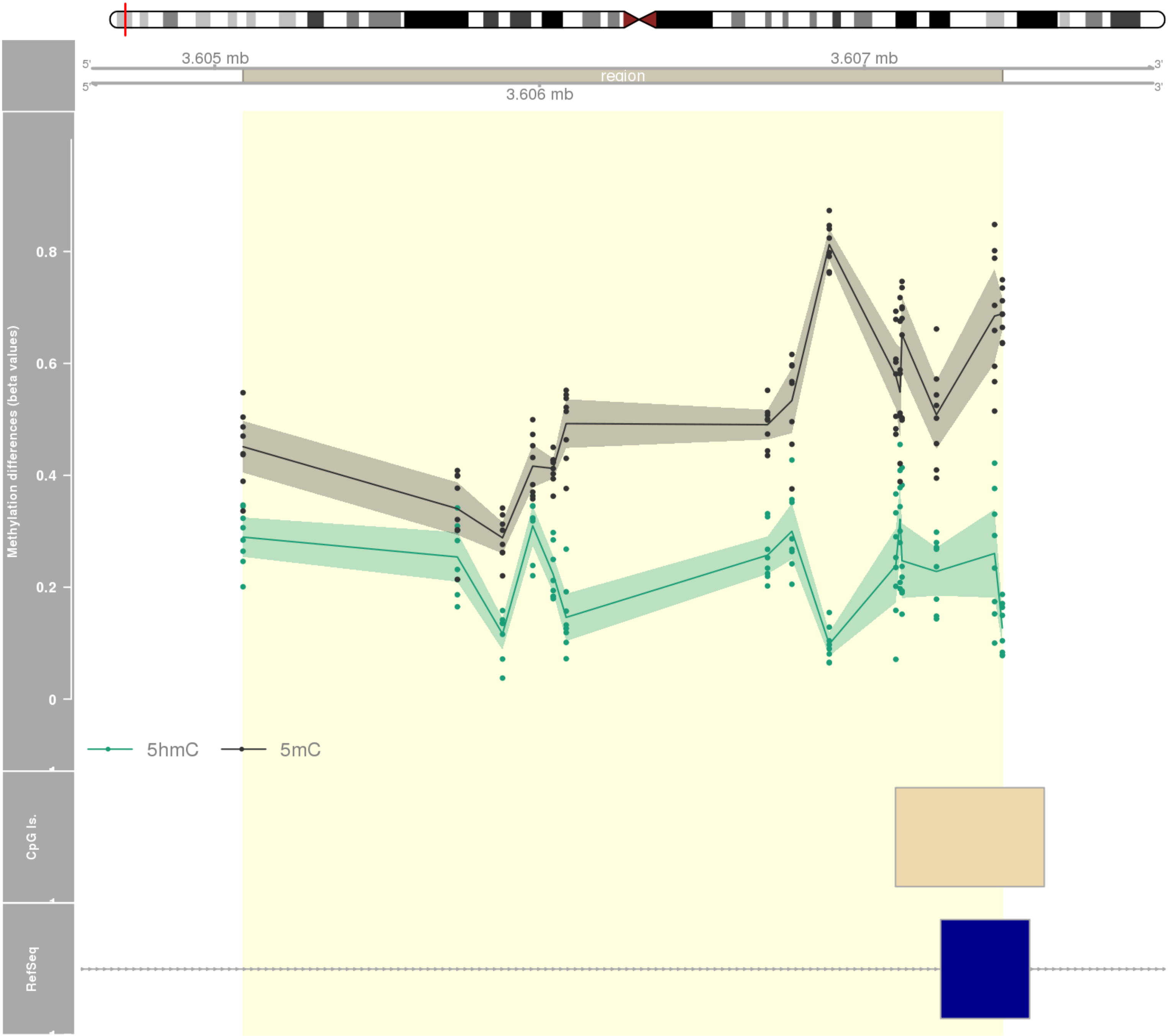
DMR 142 // chr22:38477802-38479732 // 1930 pb. (13 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: SLC16A8 -



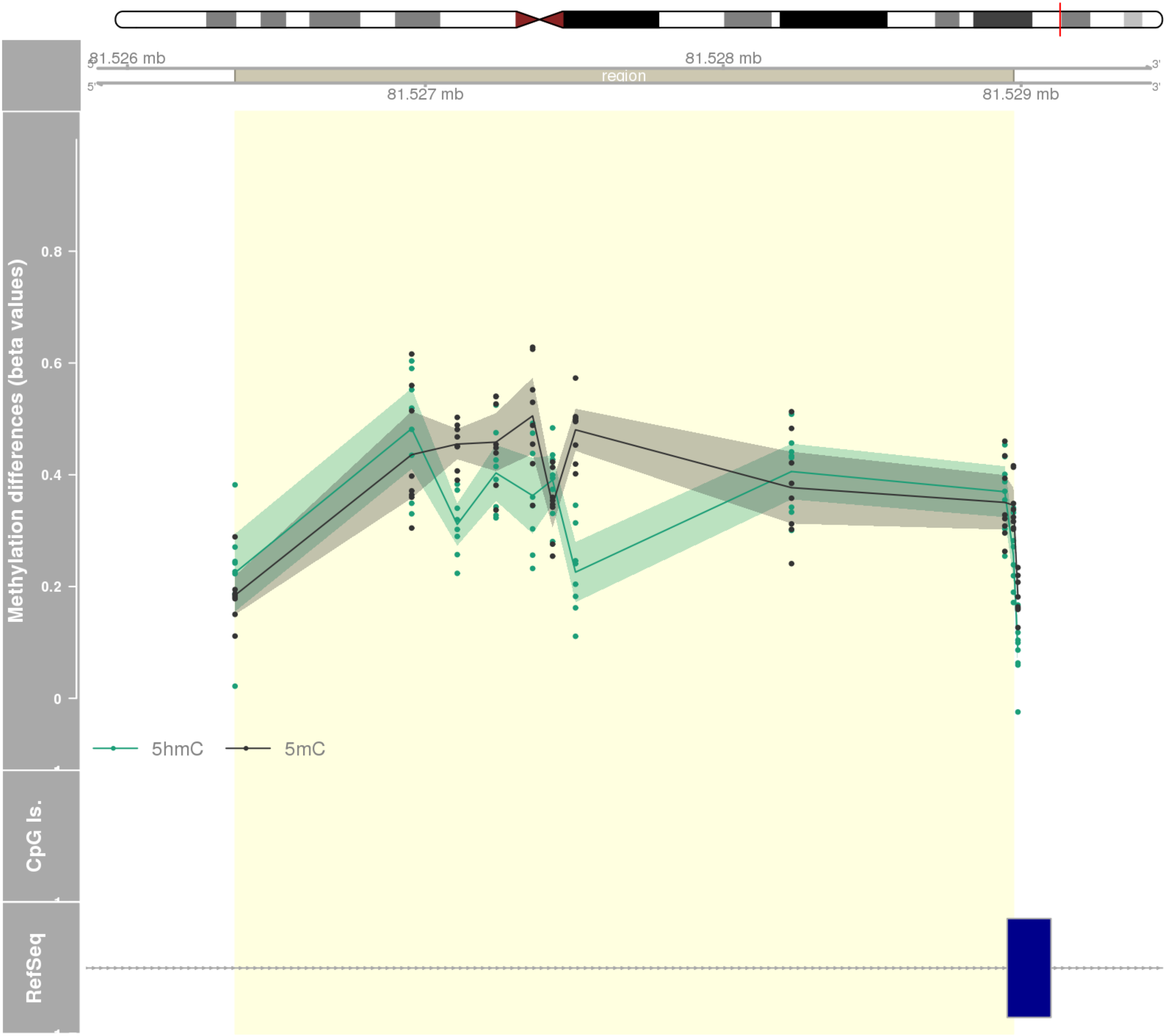
DMR 143 // chr6:31695027-31696240 // 1213 pb. (16 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.007 // fwerArea: 0.559
- genes: DDAH2 -



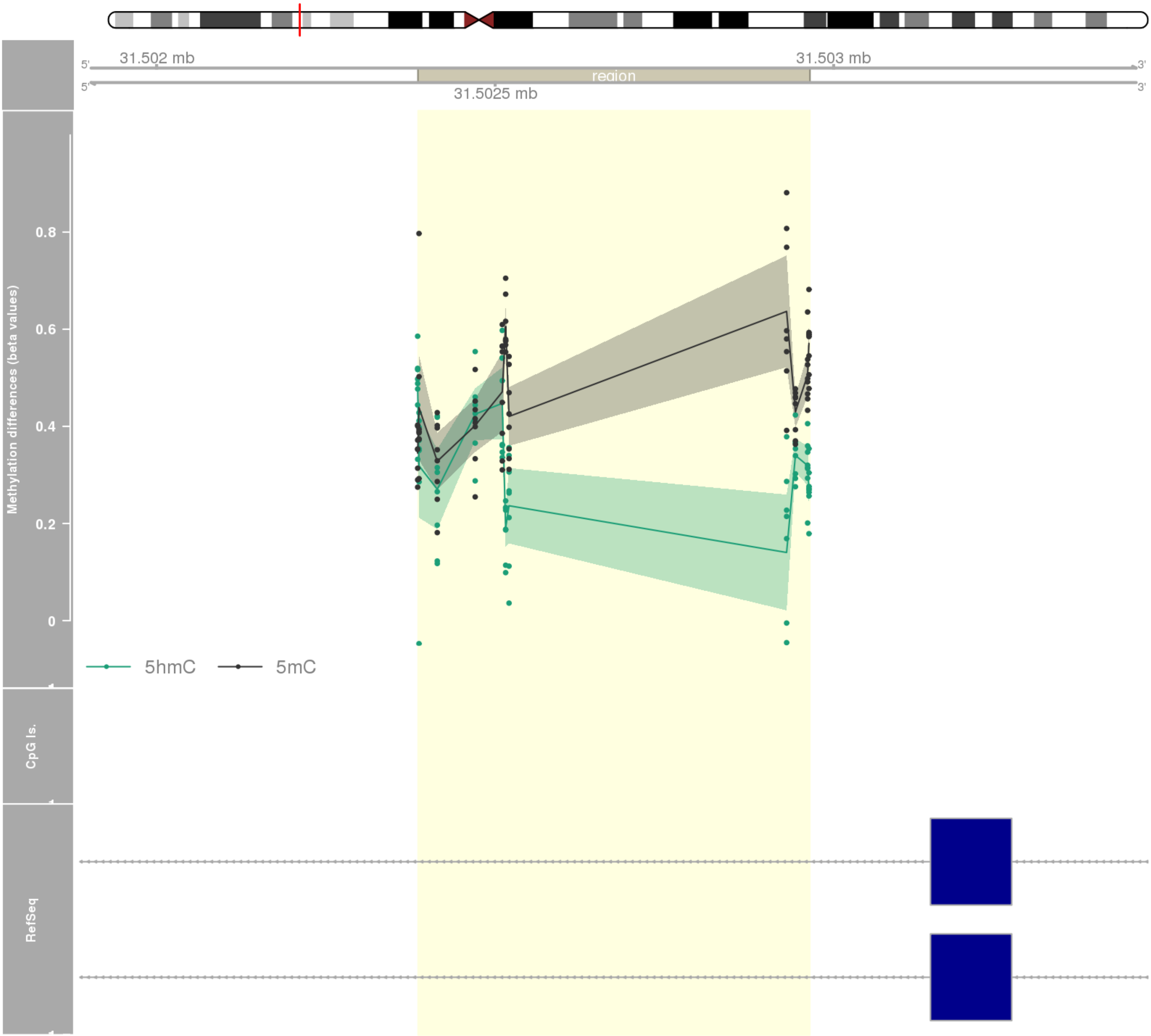
DMR 144 // chr1:3605087-3607425 // 2338 pb. (15 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: TP73 -

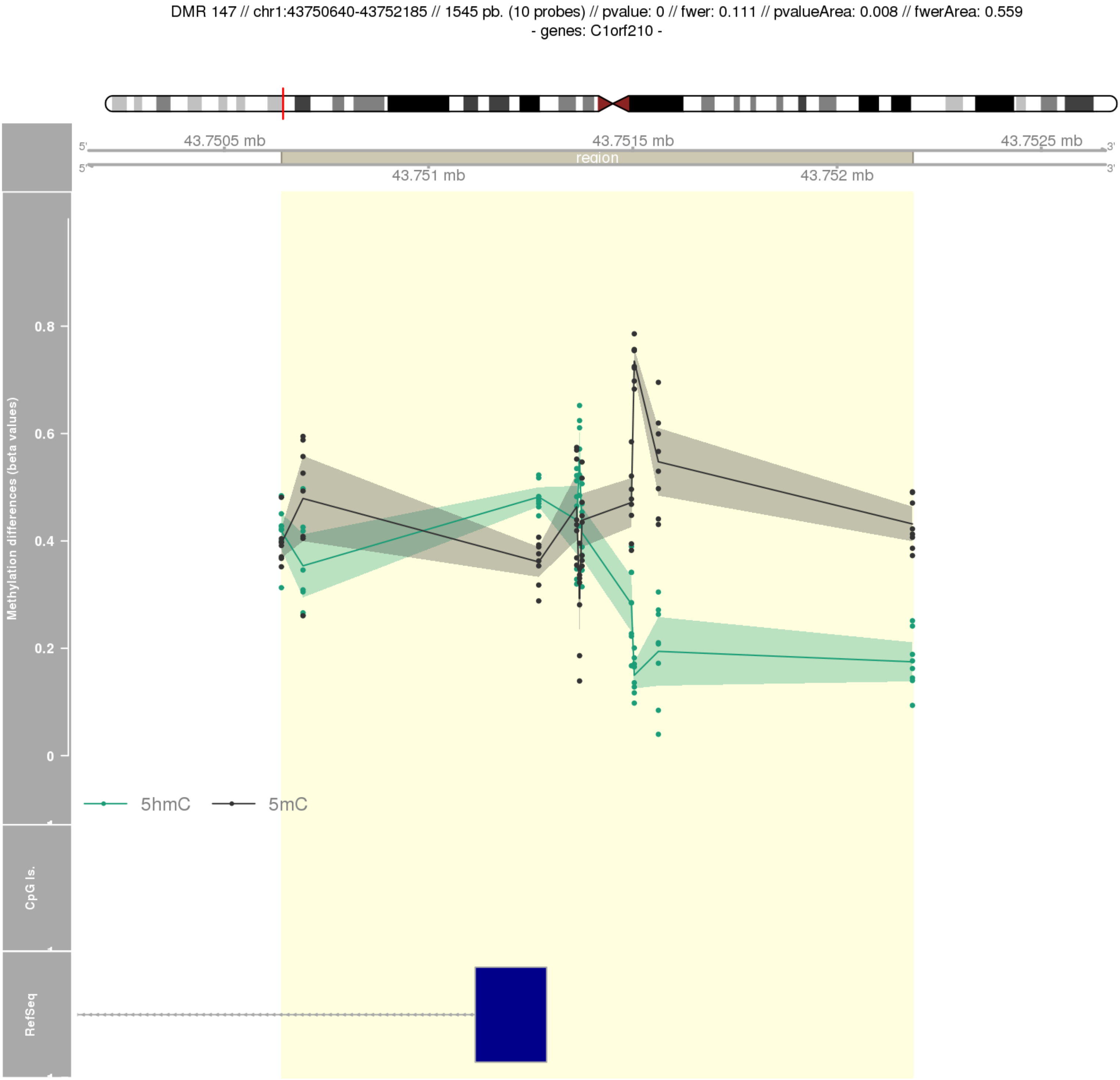


DMR 145 // chr16:81526361-81528974 // 2613 pb. (10 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: CMIP -

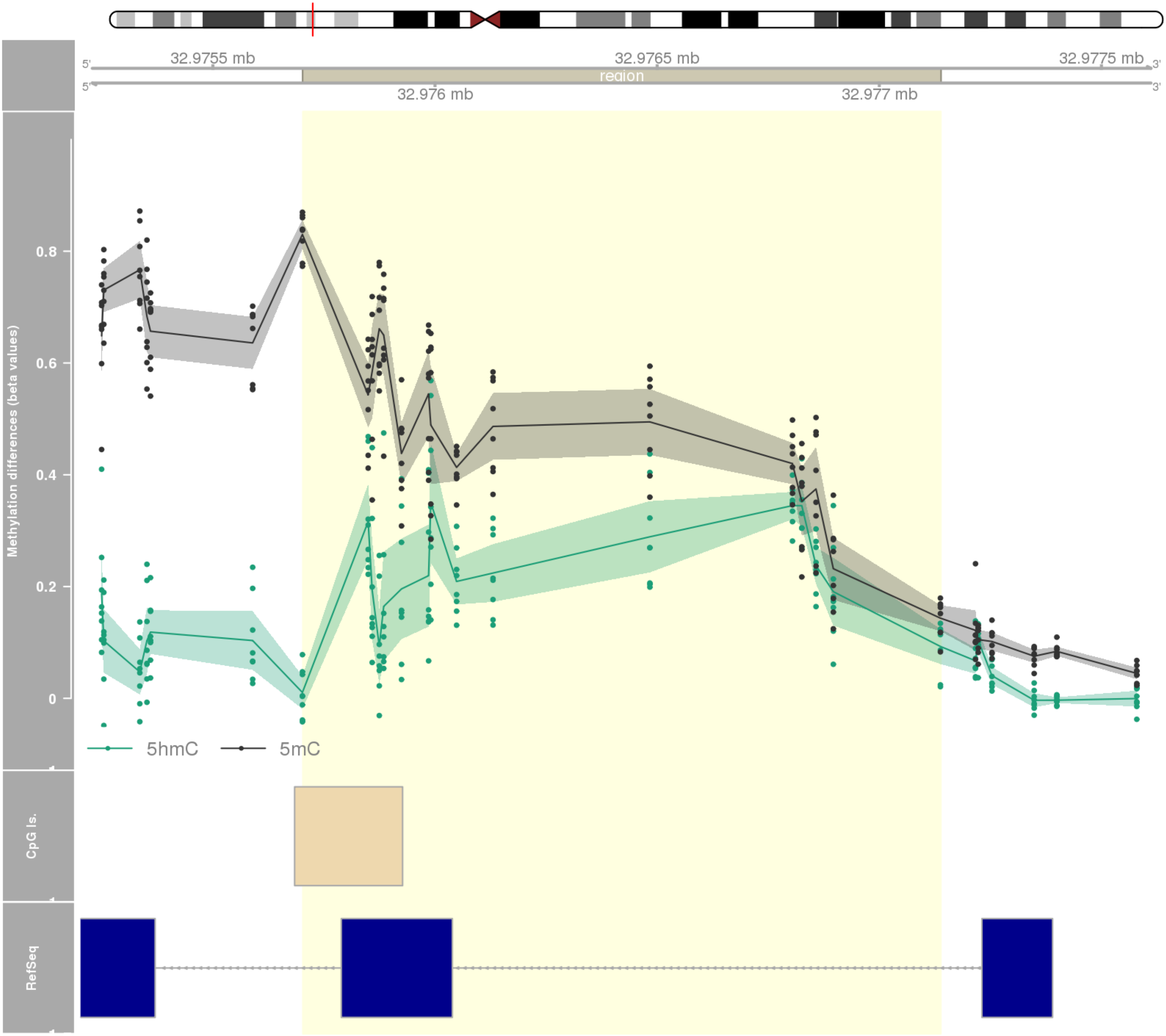


DMR 146 // chr6:31502386-31502964 // 578 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: ATP6V1G2-DDX39B / DDX39B -

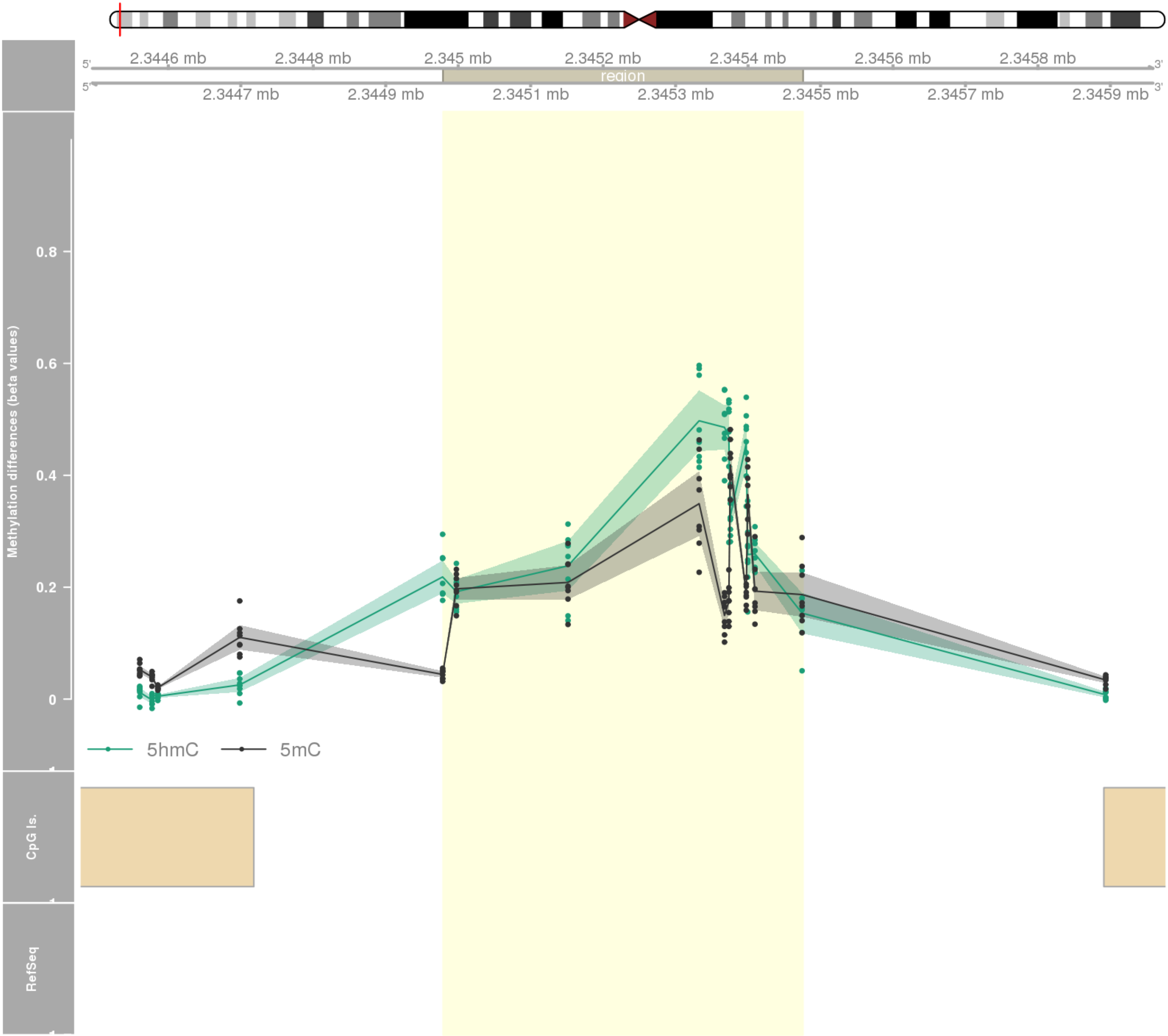



DMR 147 // chr1:43750640-43752185 // 1545 pb. (10 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: C1orf210 -
43.7505 mb
43.7515 mb
43.7525 mb
5'
3'
region
43.751 mb
43.752 mb
Methylation differences (beta values)
0.8
0.6
0.4
0.2
0
5hmC
5mC
CpG Is.
RefSeq

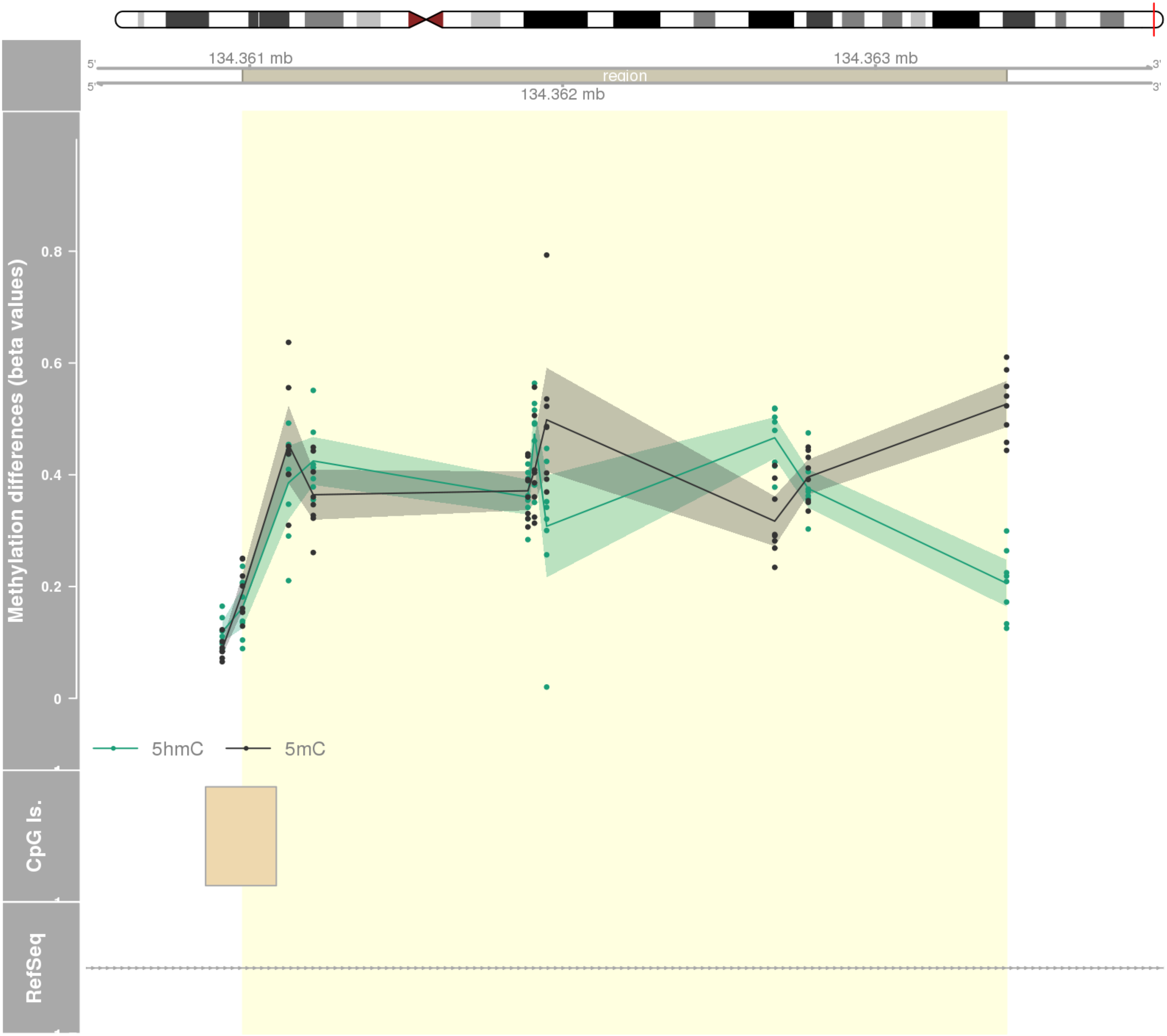
DMR 148 // chr6:32975702-32977138 // 1436 pb. (16 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: HLA-DOA -



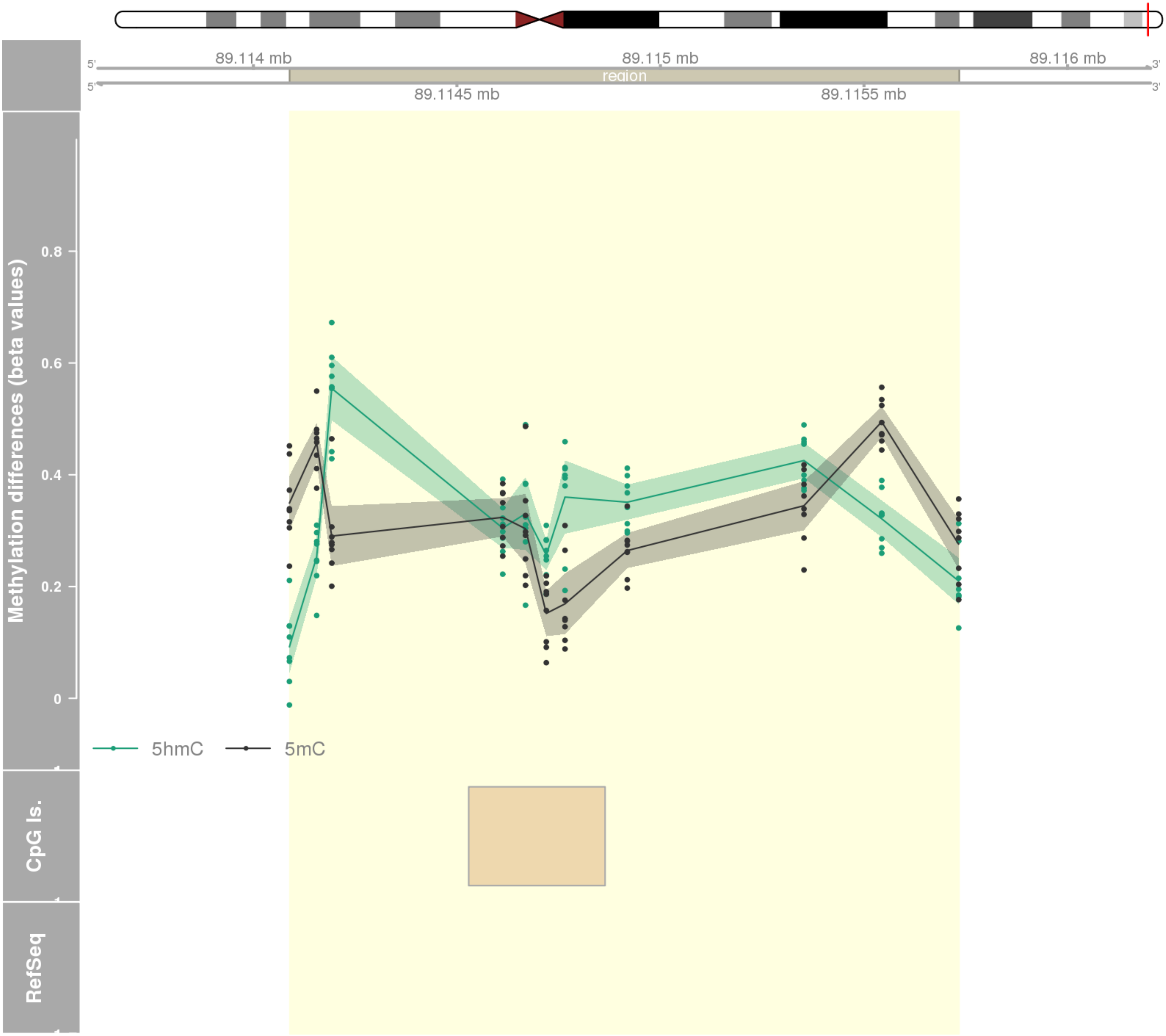
DMR 149 // chr1:2344979-2345475 // 496 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: PEX10 -



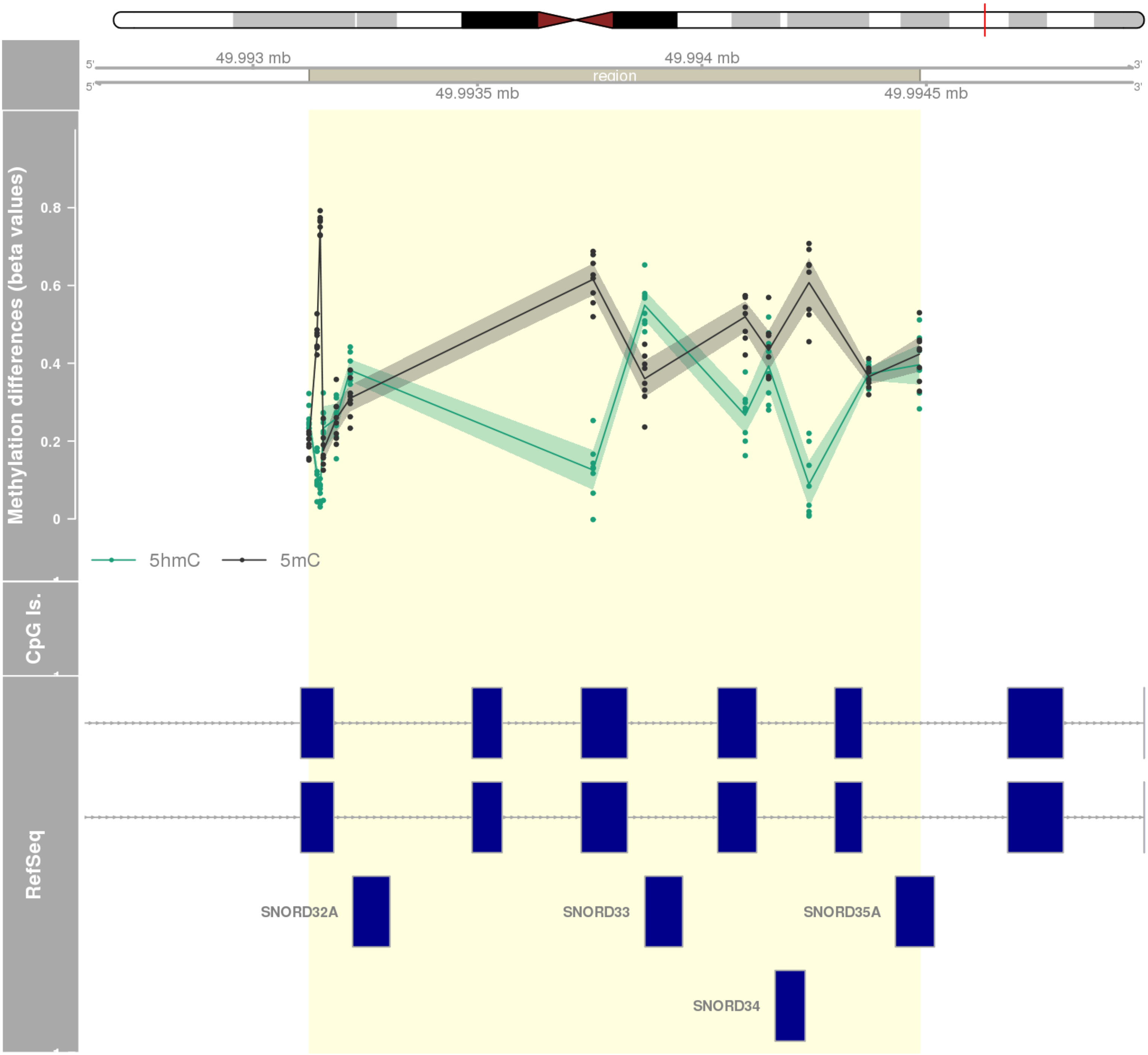
DMR 150 // chr10:134360977-134363419 // 2442 pb. (9 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: INPP5A -



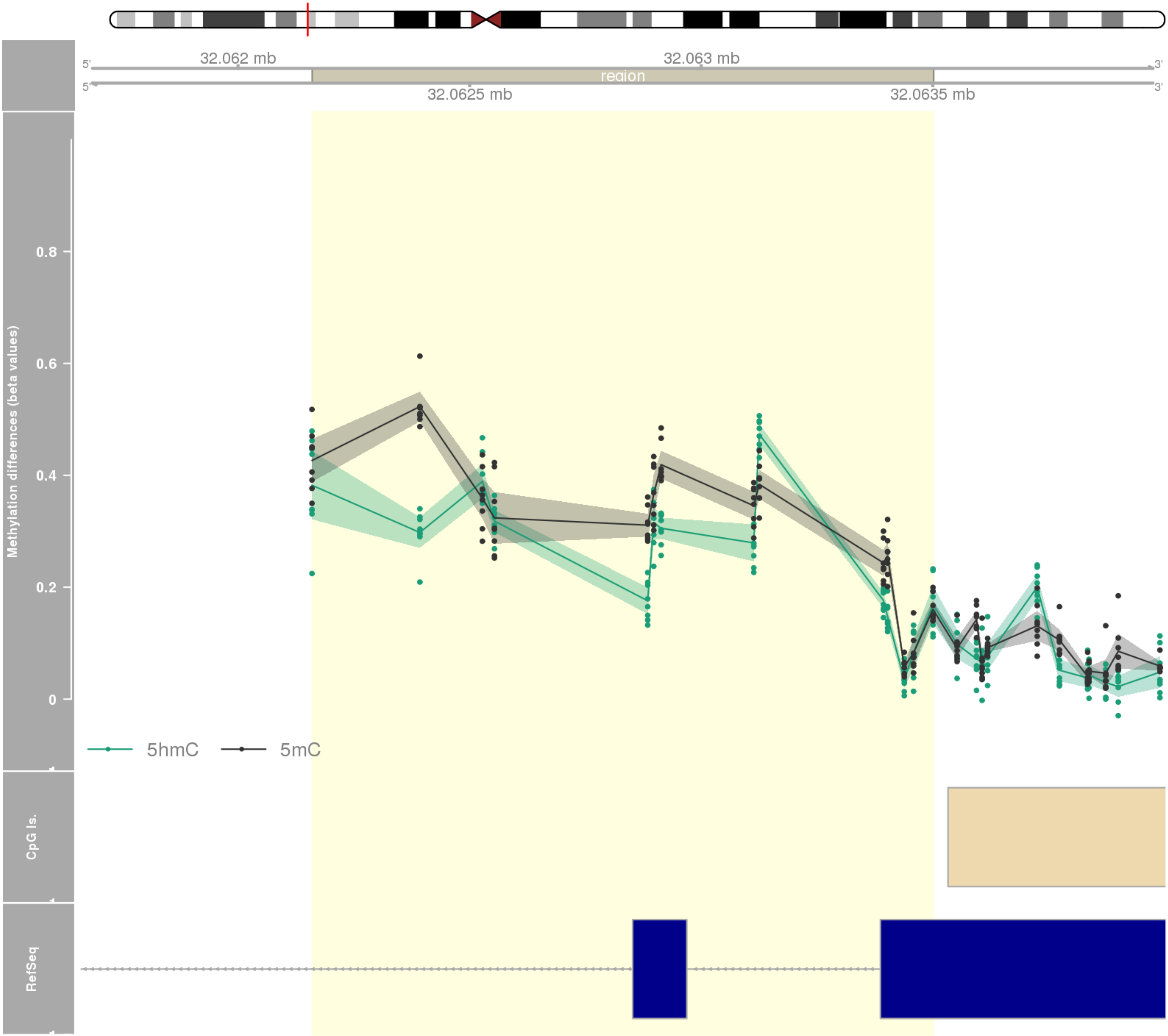
DMR 151 // chr16:89114089-89115733 // 1644 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559



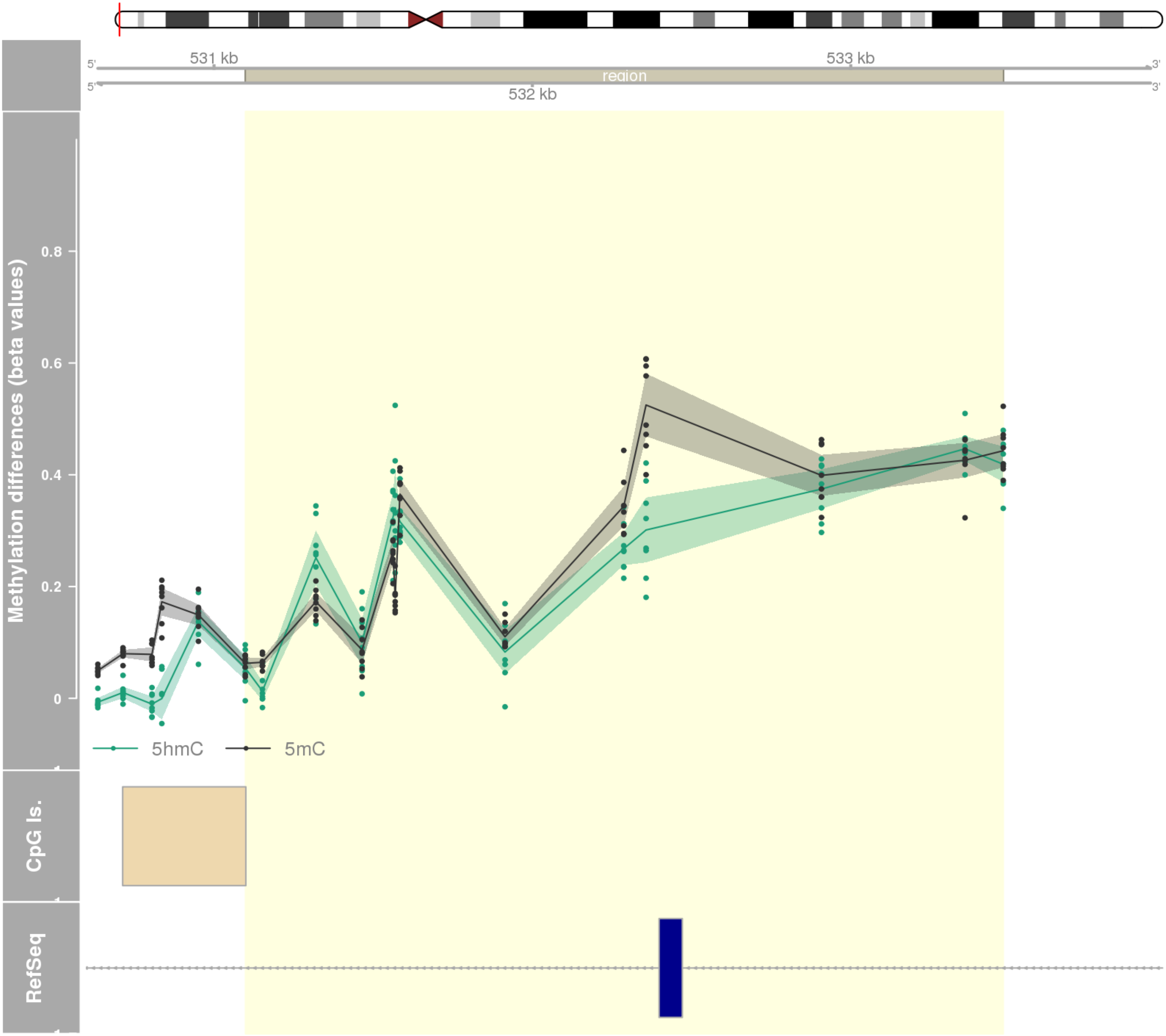
DMR 152 // chr19:49993125-49994485 // 1360 pb. (13 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: SNORD32A / SNORD33 / SNORD34 / SNORD35A / RPL13A -



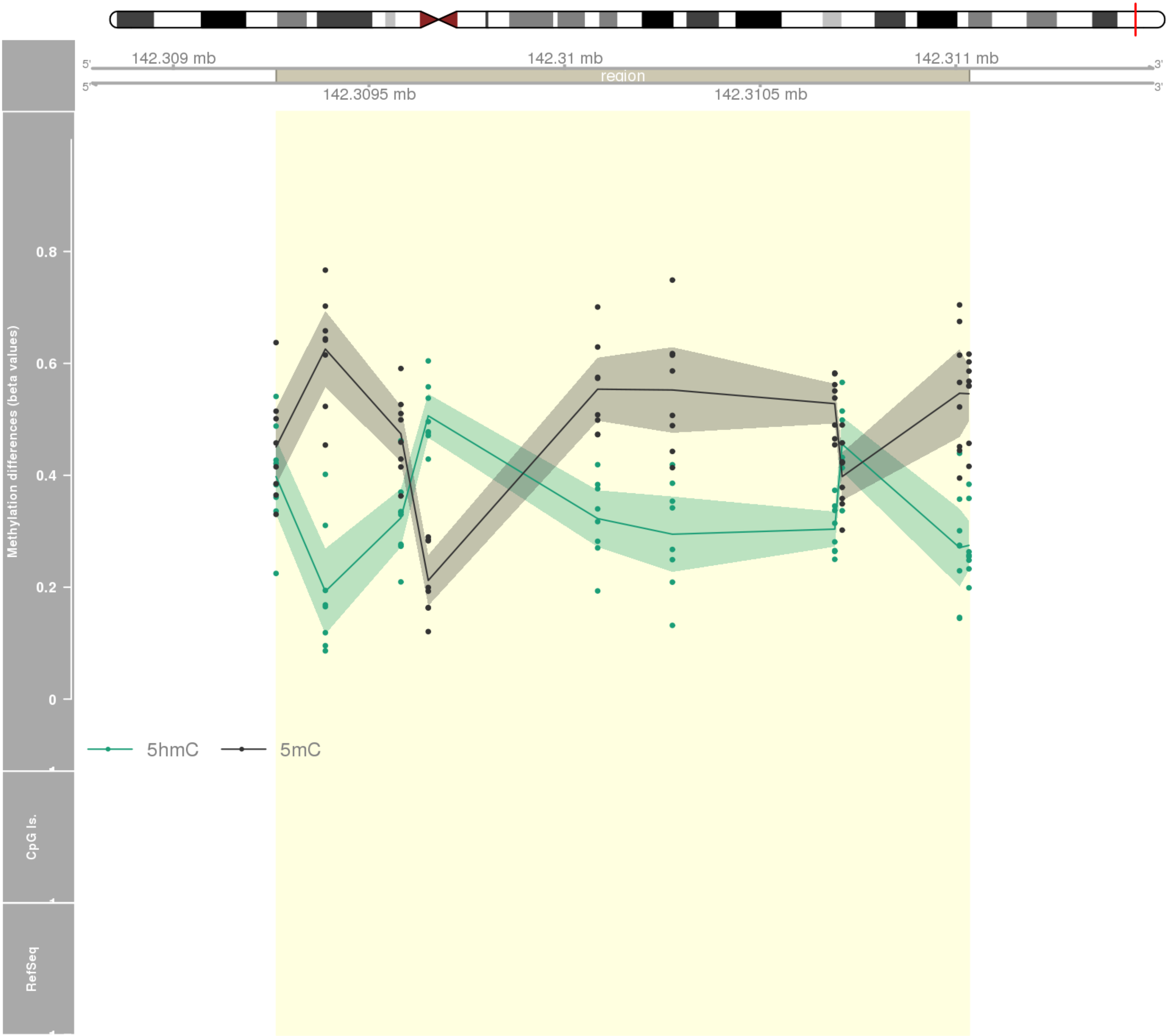
DMR 153 // chr6:32062160-32063501 // 1341 pb. (14 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: TNXB -



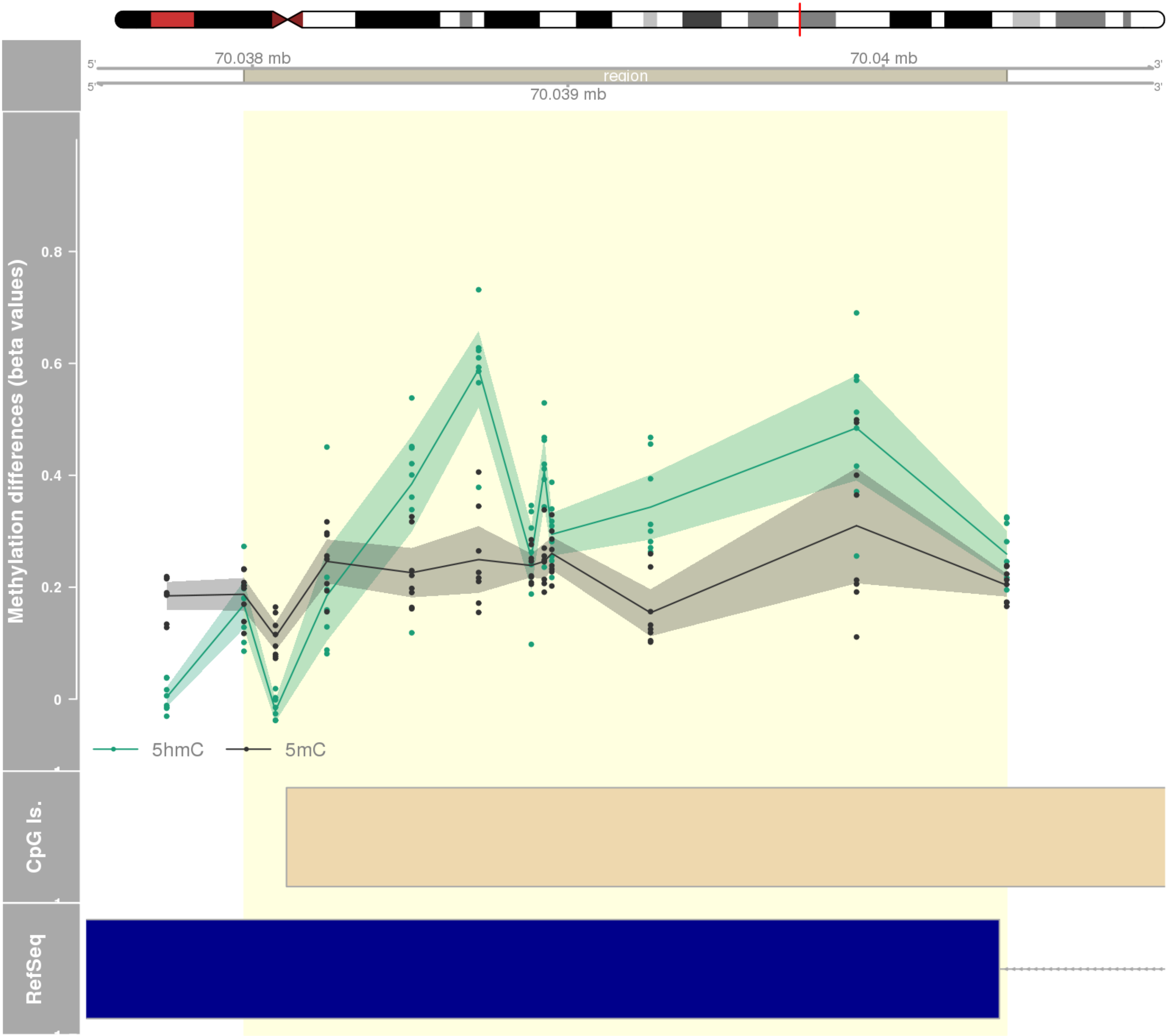
DMR 154 // chr10:531098-533479 // 2381 pb. (13 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: DIP2C -



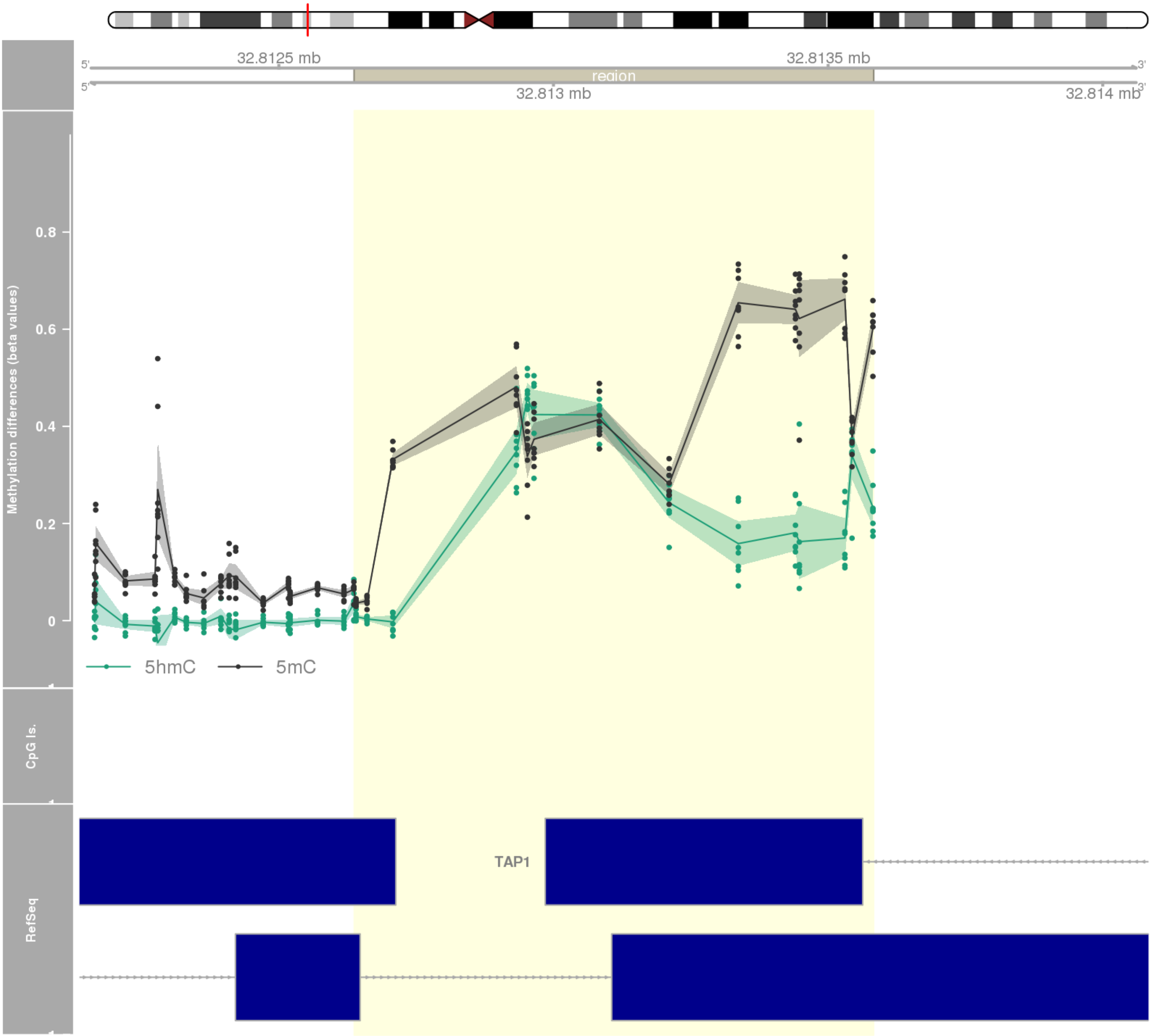
DMR 155 // chr8:142309263-142311034 // 1771 pb. (10 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: SLC45A4 -



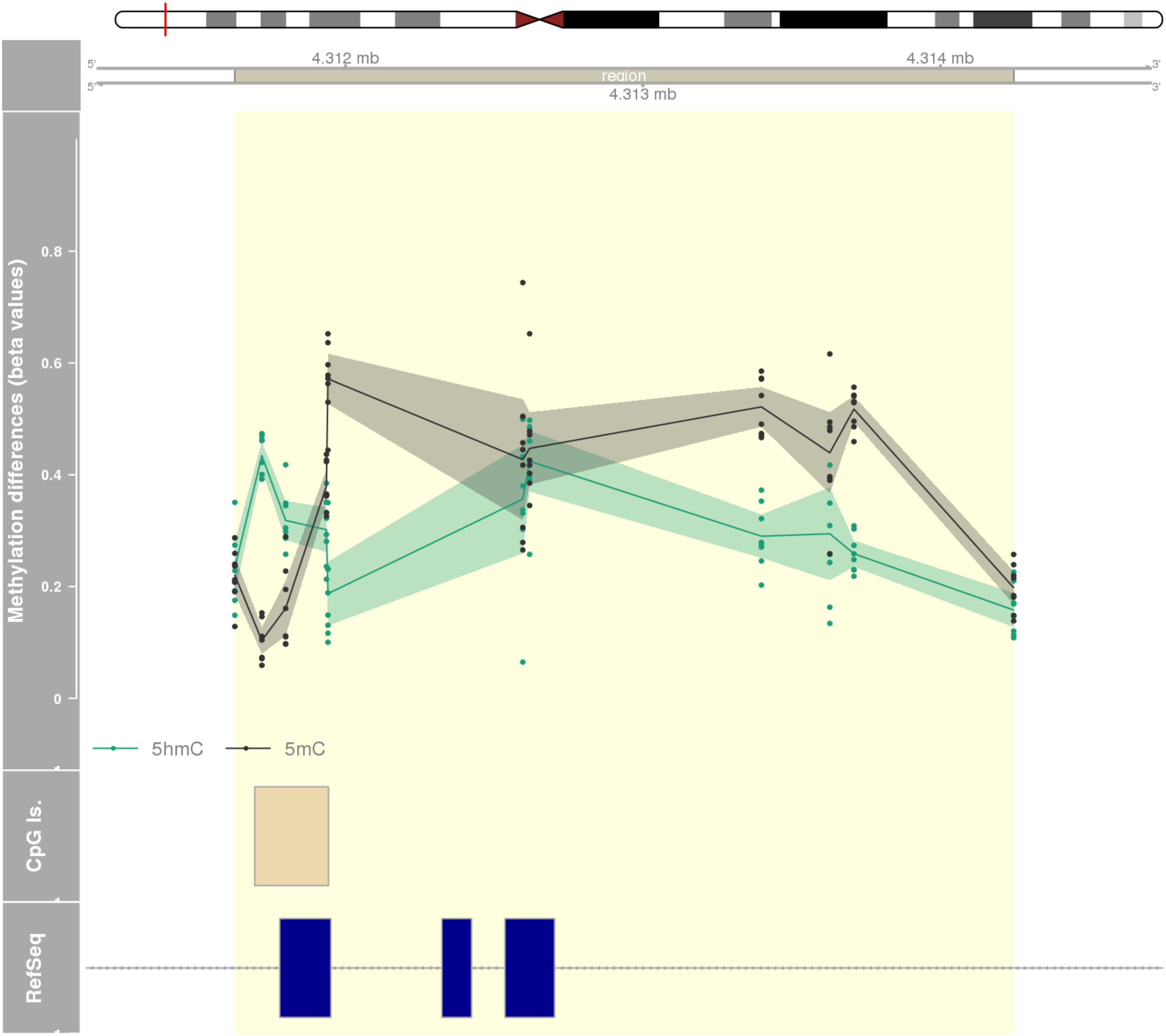
DMR 156 // chr14:70037973-70040391 // 2418 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: CCDC177 -



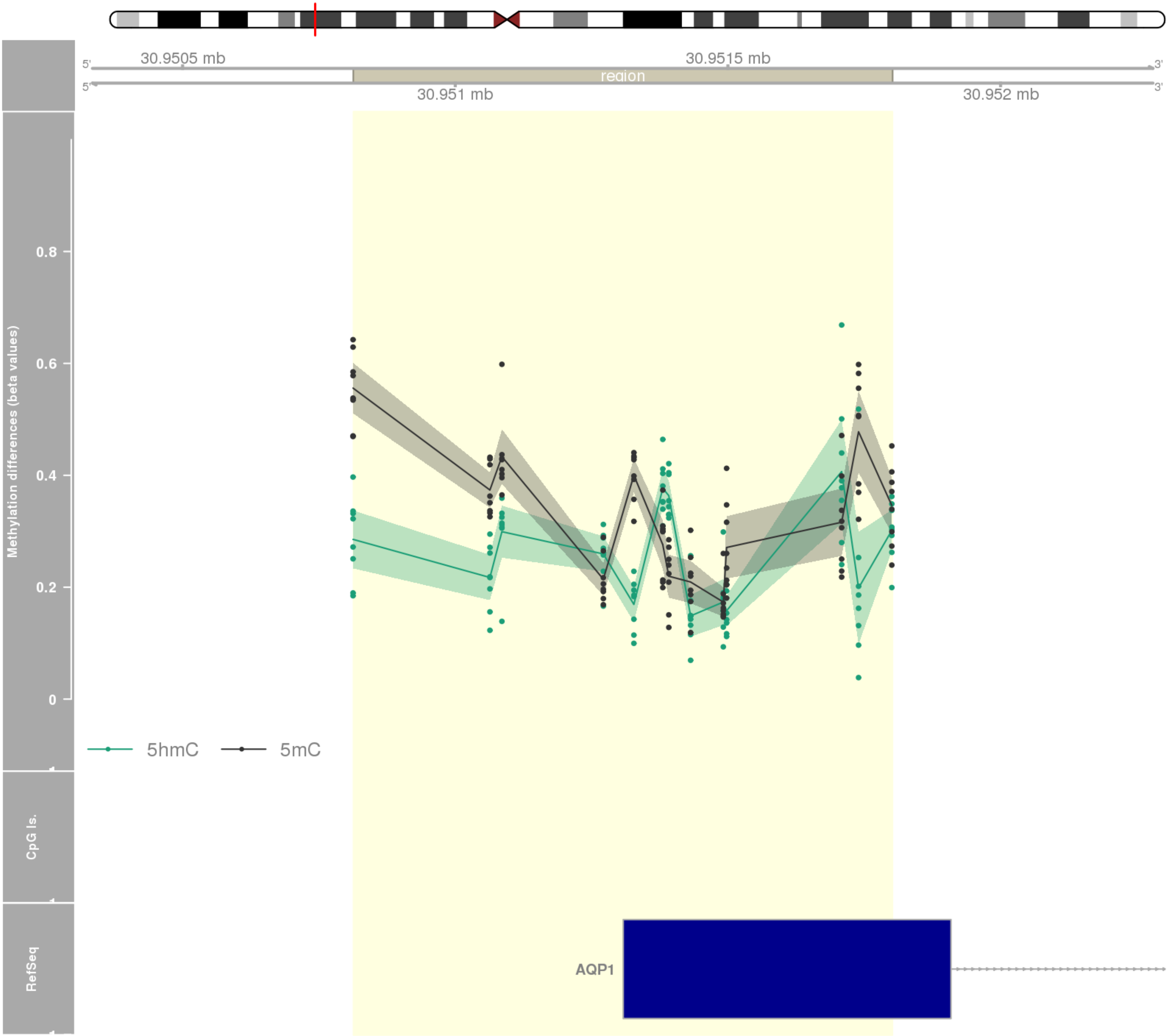
DMR 157 // chr6:32812637-32813582 // 945 pb. (15 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: TAPSAR1 / PSMB9 / TAP1 -



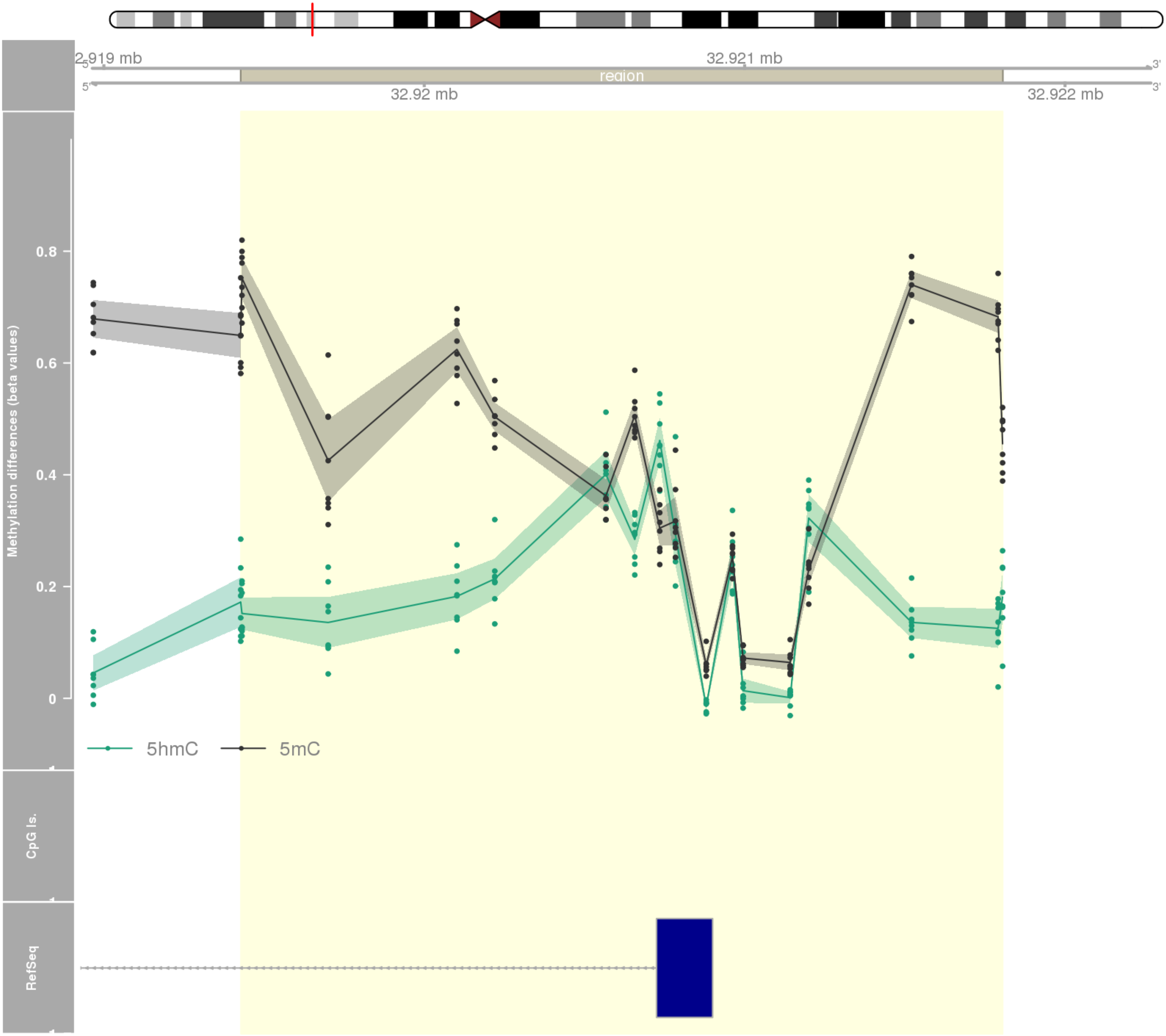
DMR 158 // chr16:4311628-4314246 // 2618 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: TFAP4 -



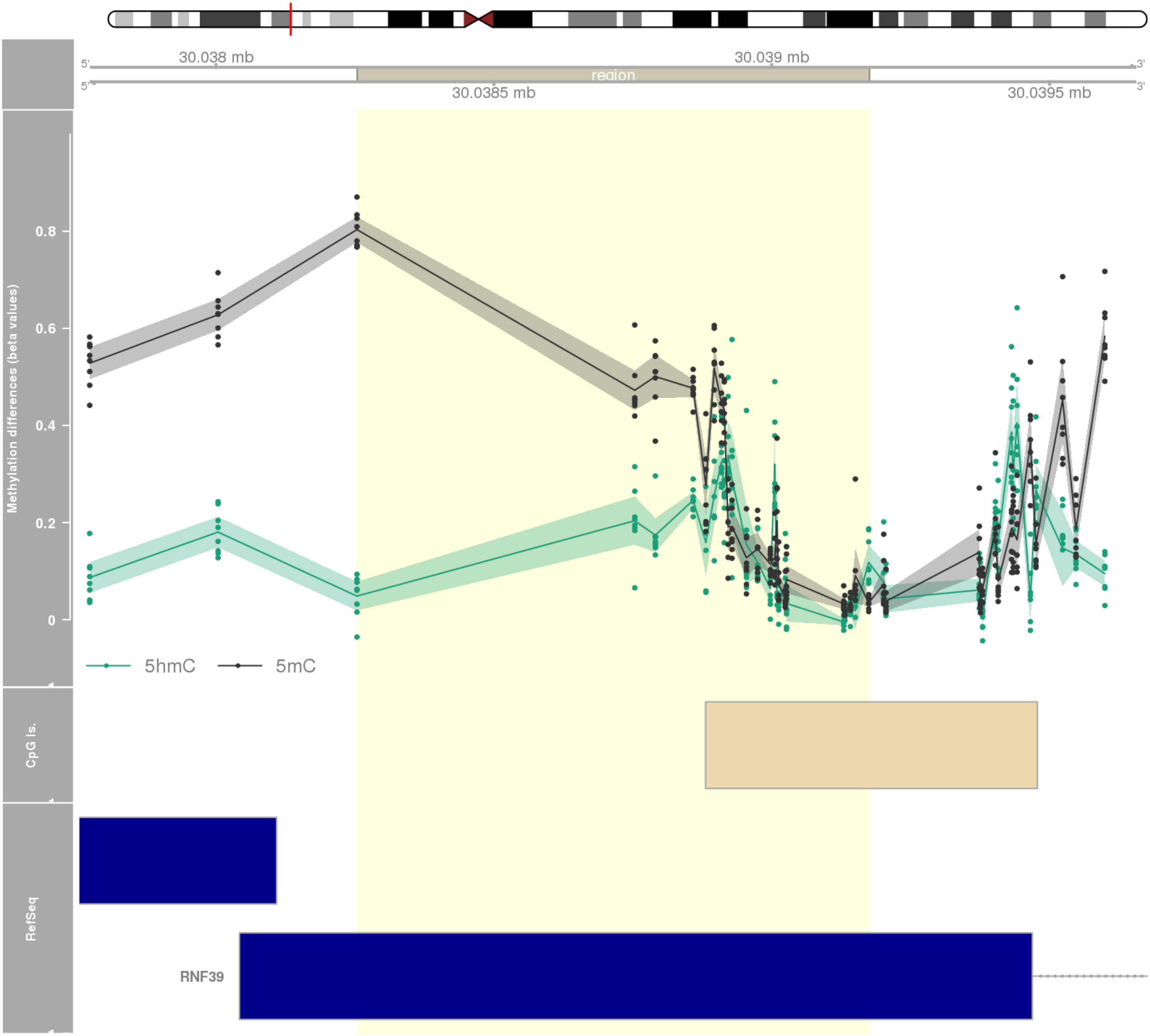
DMR 159 // chr7:30950813-30951801 // 988 pb. (13 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: AQP1 -



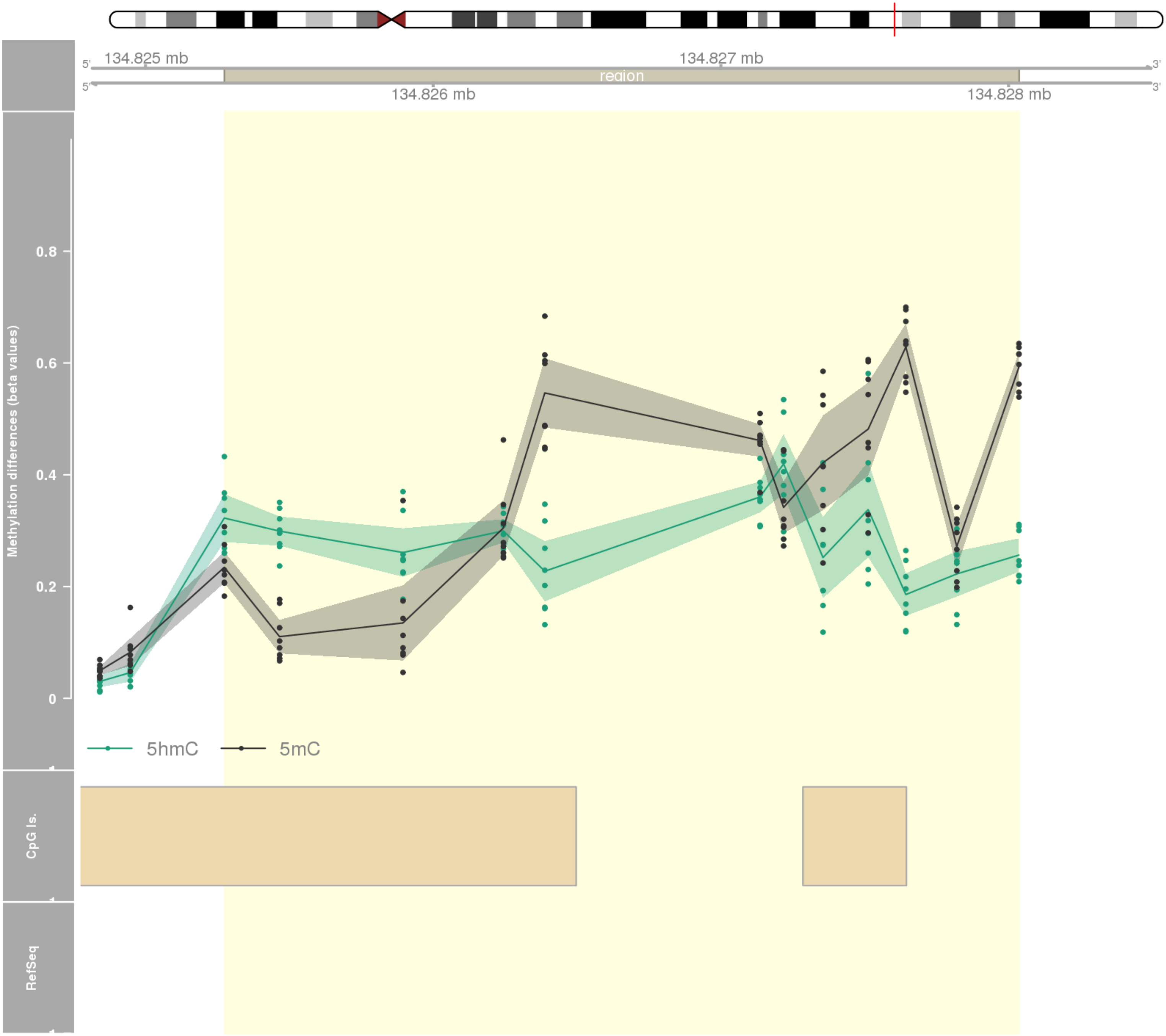
DMR 160 // chr6:32919427-32921805 // 2378 pb. (17 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: HLA-DMA -

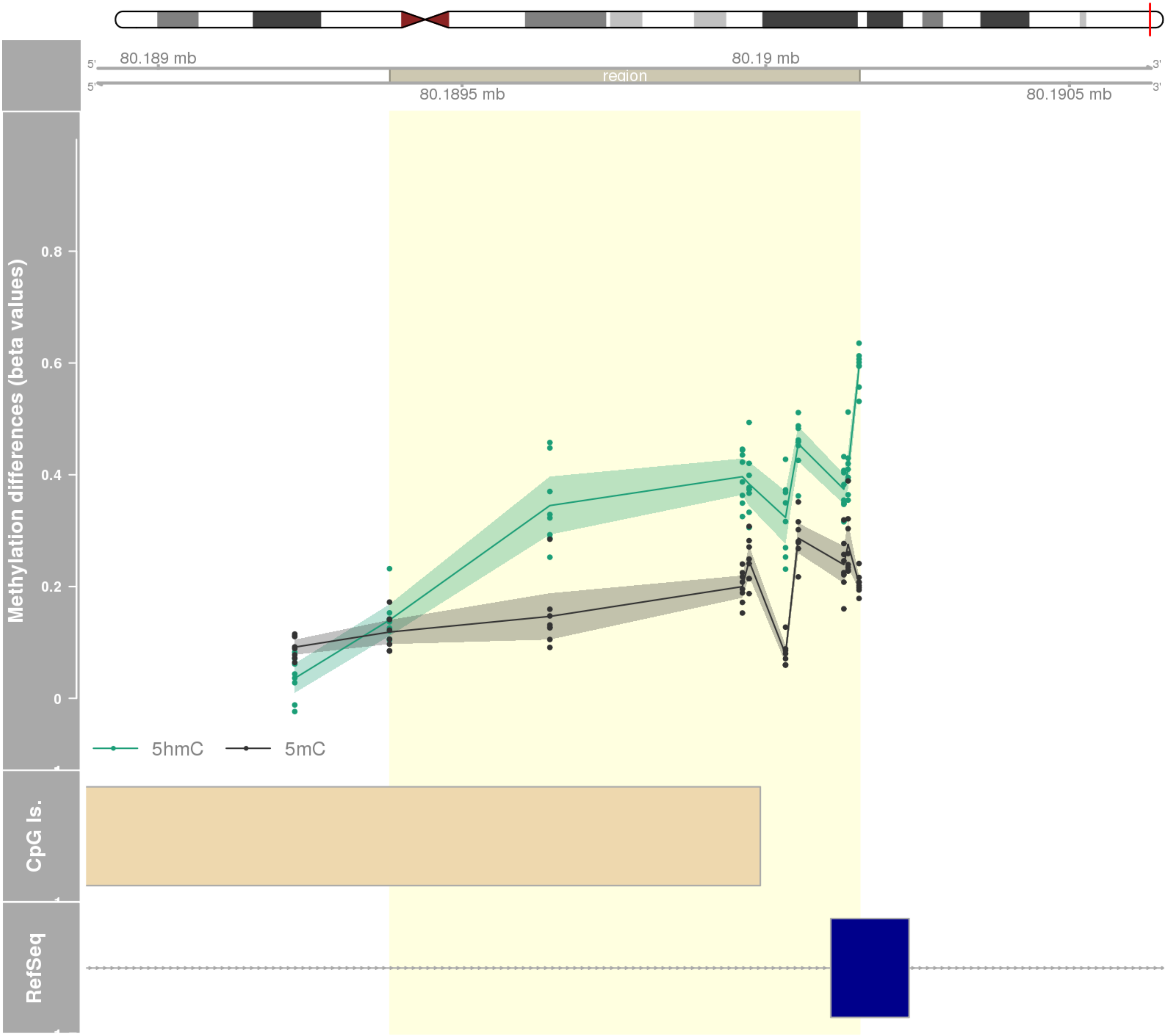


DMR 161 // chr6:30038254-30039175 // 921 pb. (23 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559
- genes: RNF39 -



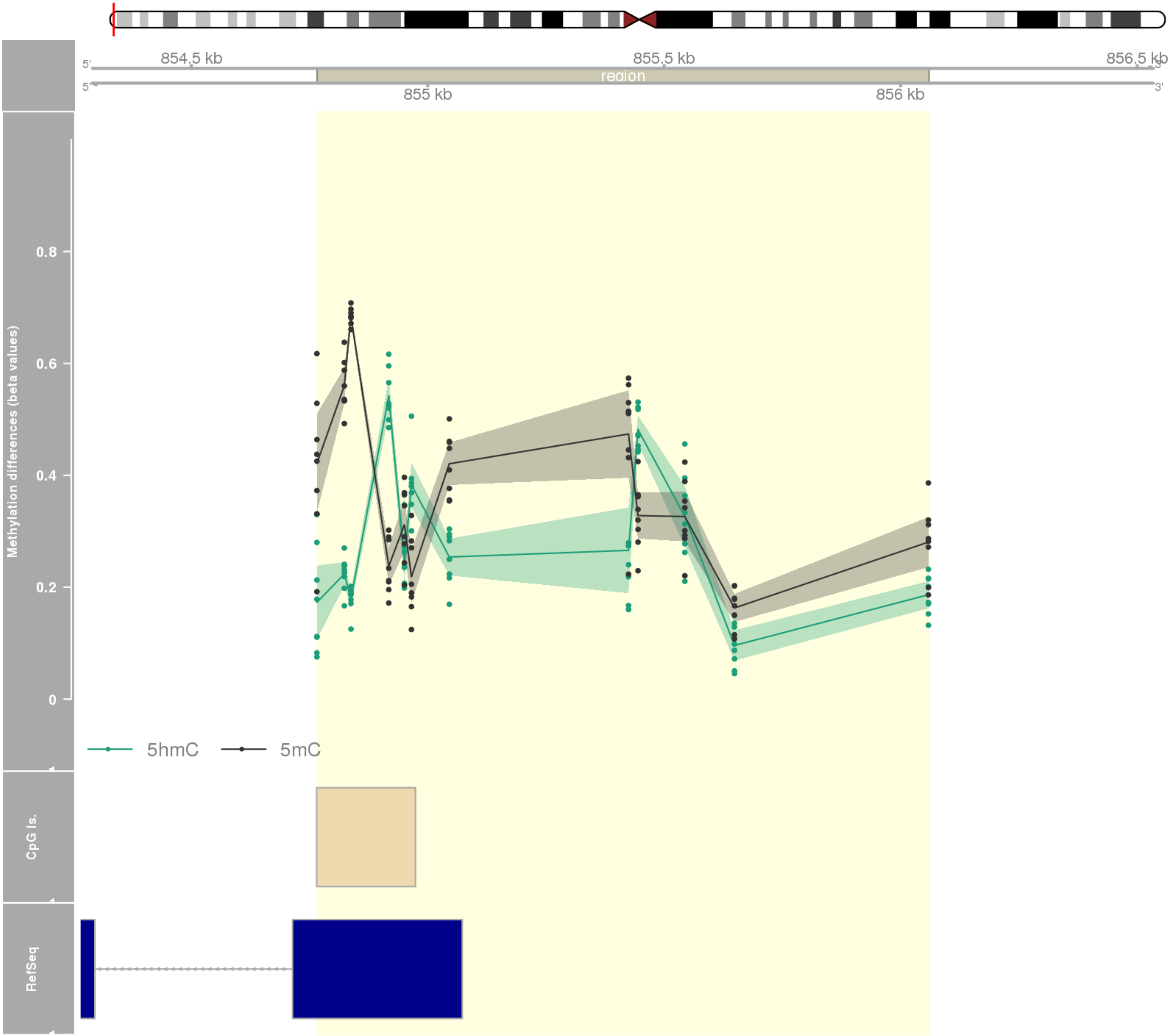
DMR 162 // chr5:134825274-134828036 // 2762 pb. (12 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.008 // fwerArea: 0.559



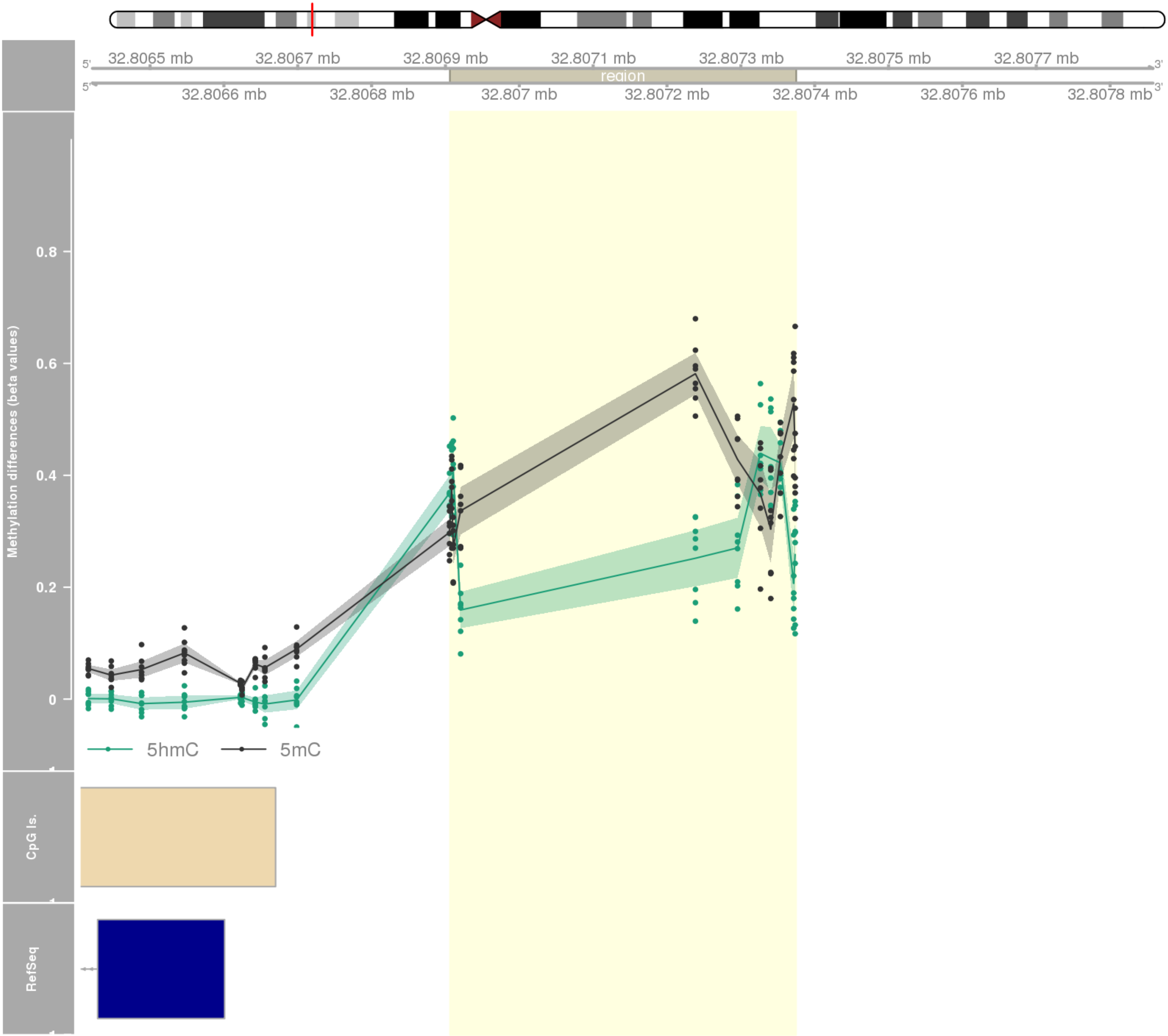


DMR 163 // chr17:80189381-80190154 // 773 pb. (9 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: SLC16A3 -

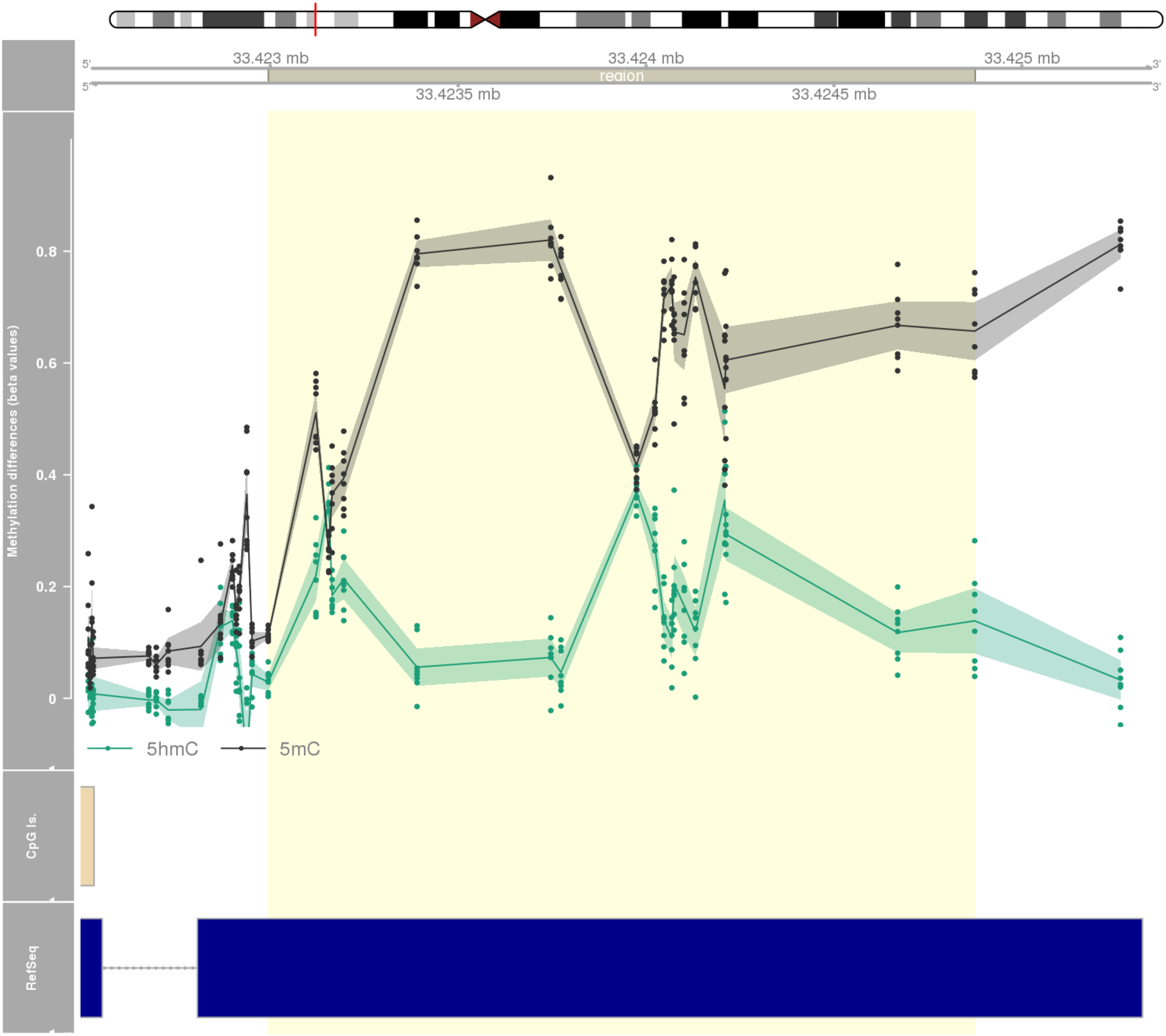
DMR 164 // chr1:854766-856059 // 1293 pb. (12 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559



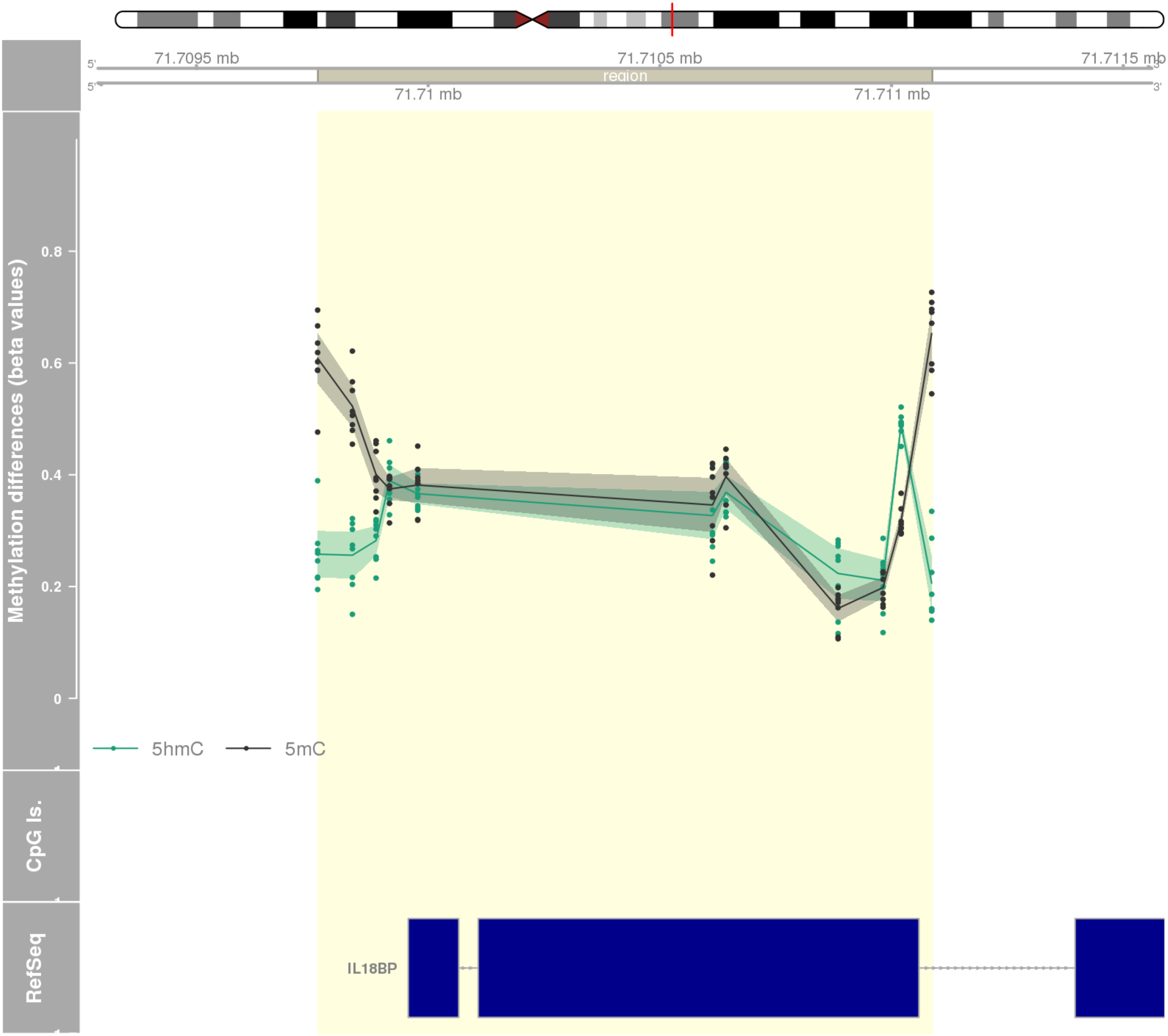
DMR 165 // chr6:32806906-32807374 // 468 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559



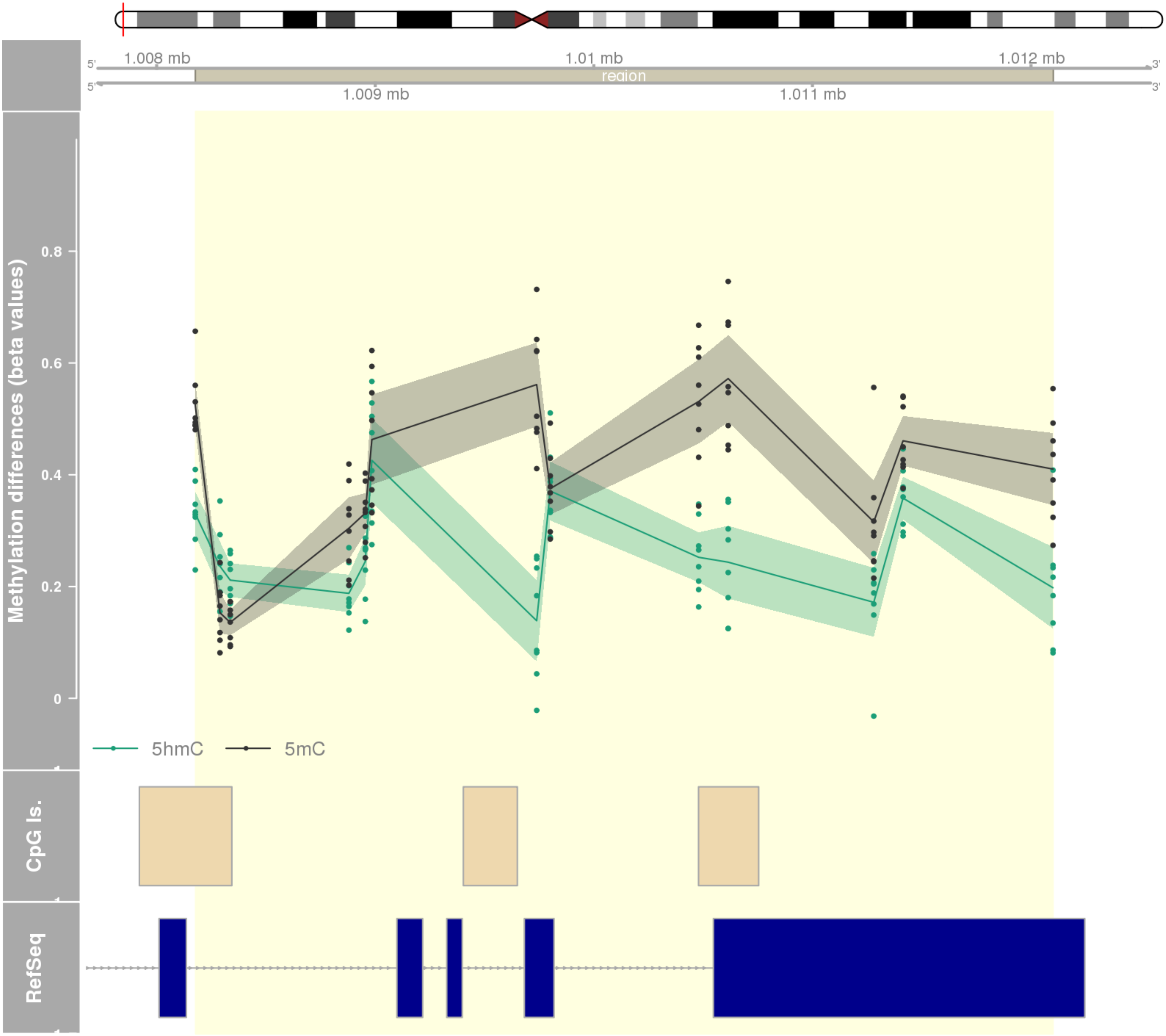
DMR 166 // chr6:33422995-33424875 // 1880 pb. (19 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: ZBTB9 -



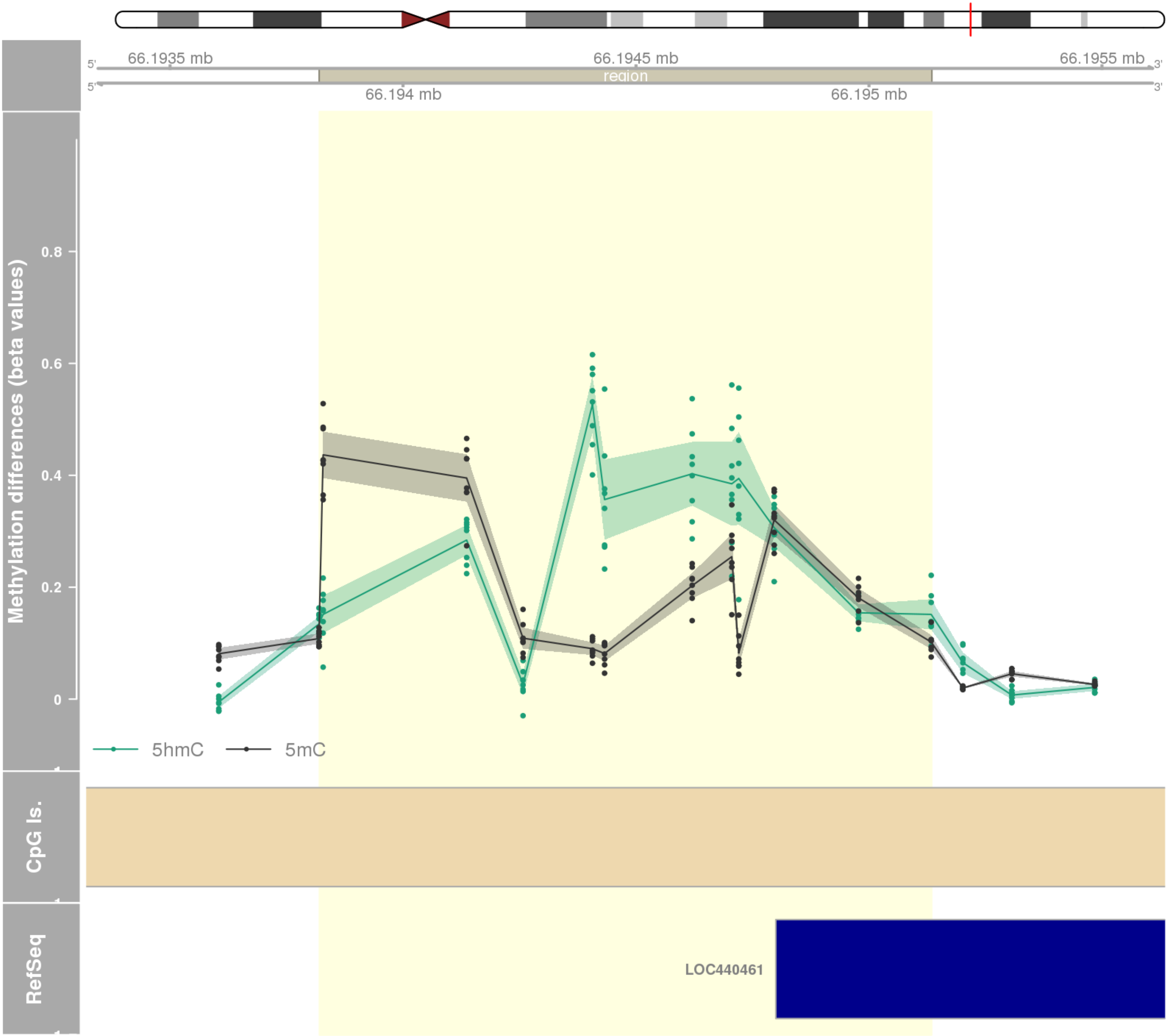
DMR 167 // chr11:71709762-71711087 // 1325 pb. (11 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: IL18BP -



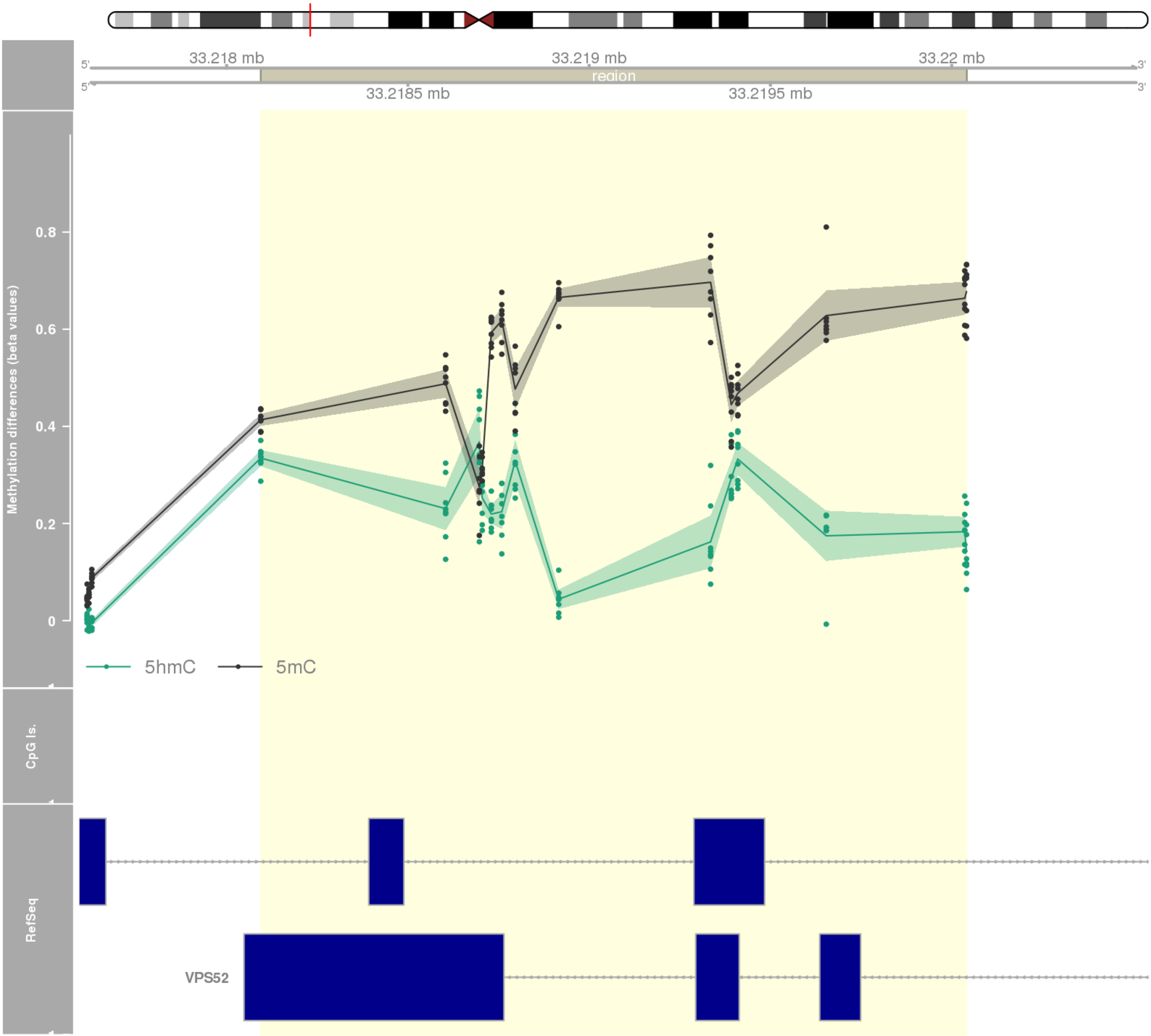
DMR 168 // chr11:1008177-1012101 // 3924 pb. (13 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: AP2A2 -



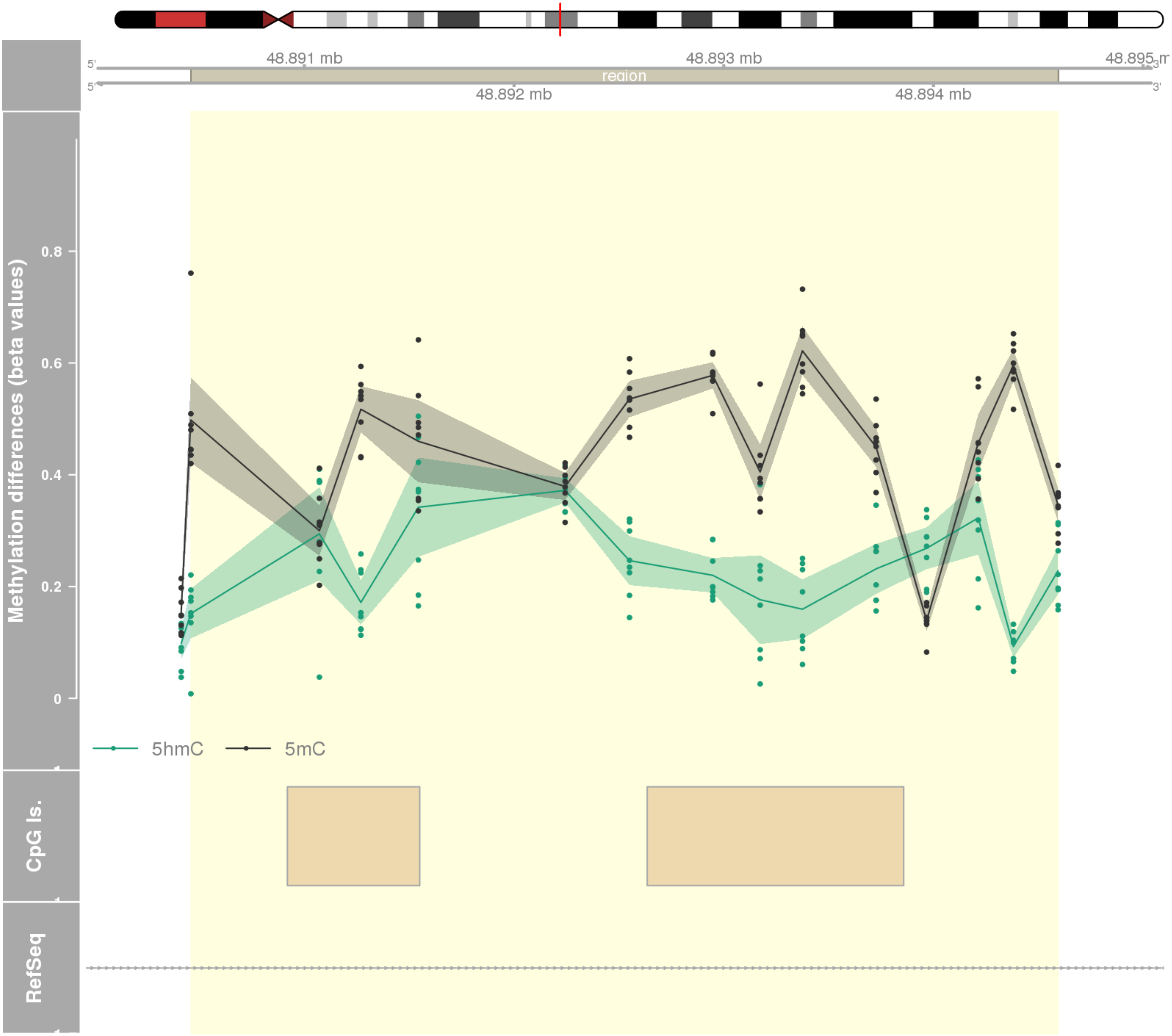
DMR 169 // chr17:66193820-66195134 // 1314 pb. (12 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559



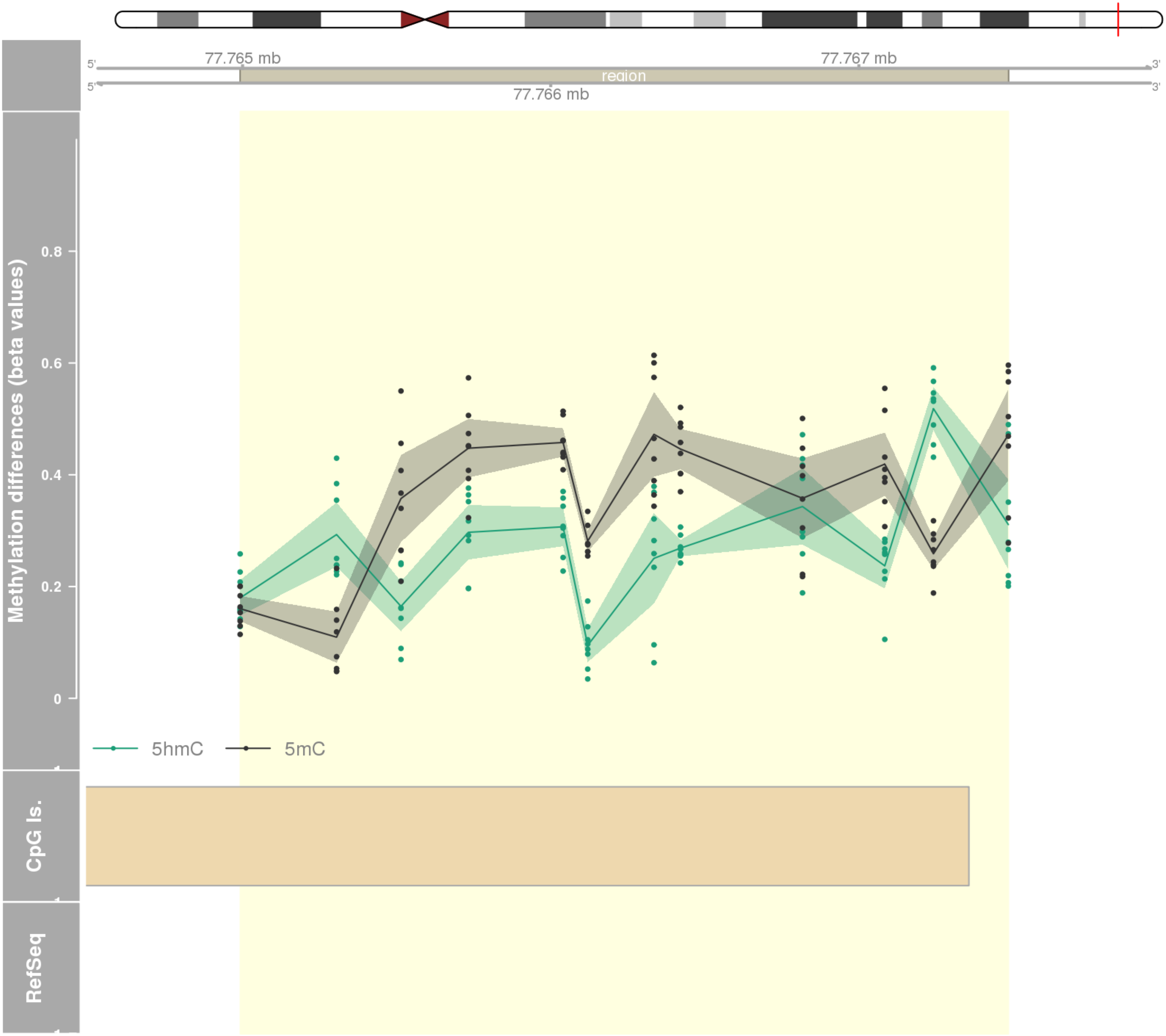
DMR 170 // chr6:33218094-33220041 // 1947 pb. (14 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: VPS52 / HCG25 -



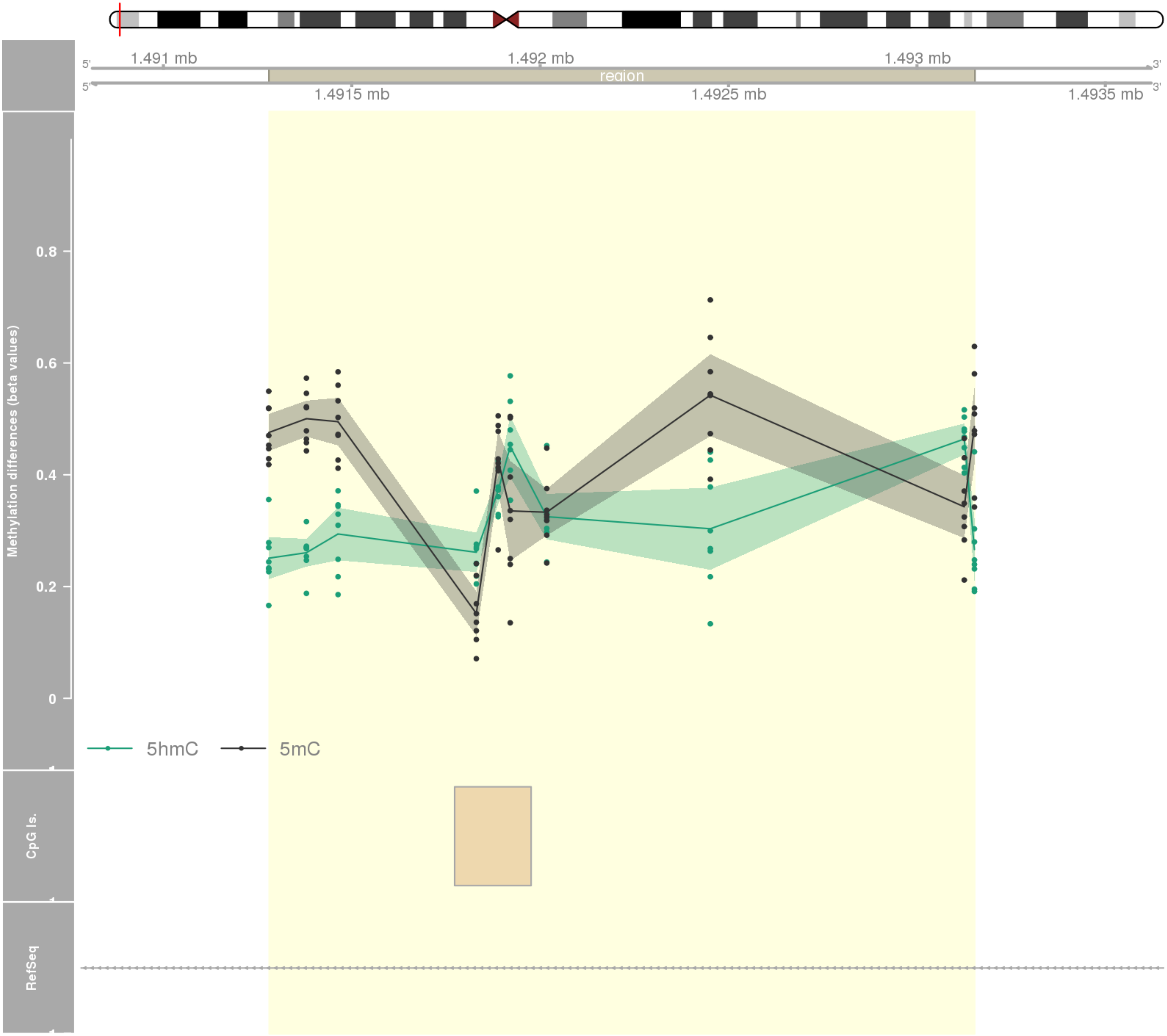
DMR 171 // chr13:48890459-48894595 // 4136 pb. (14 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: PPP1R26P1 / RB1 -

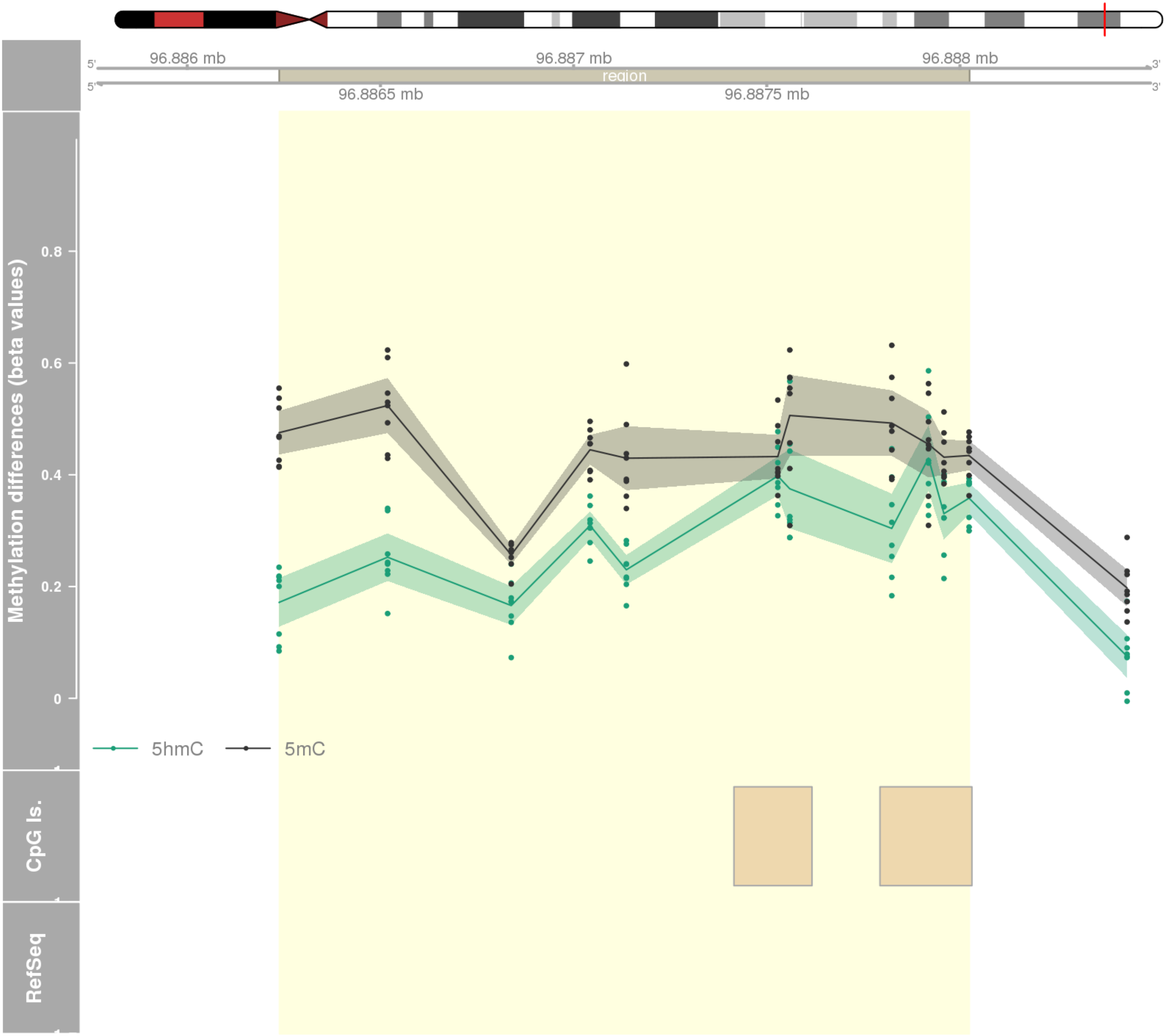


DMR 172 // chr17:77764992-77767485 // 2493 pb. (12 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: CBX8 -



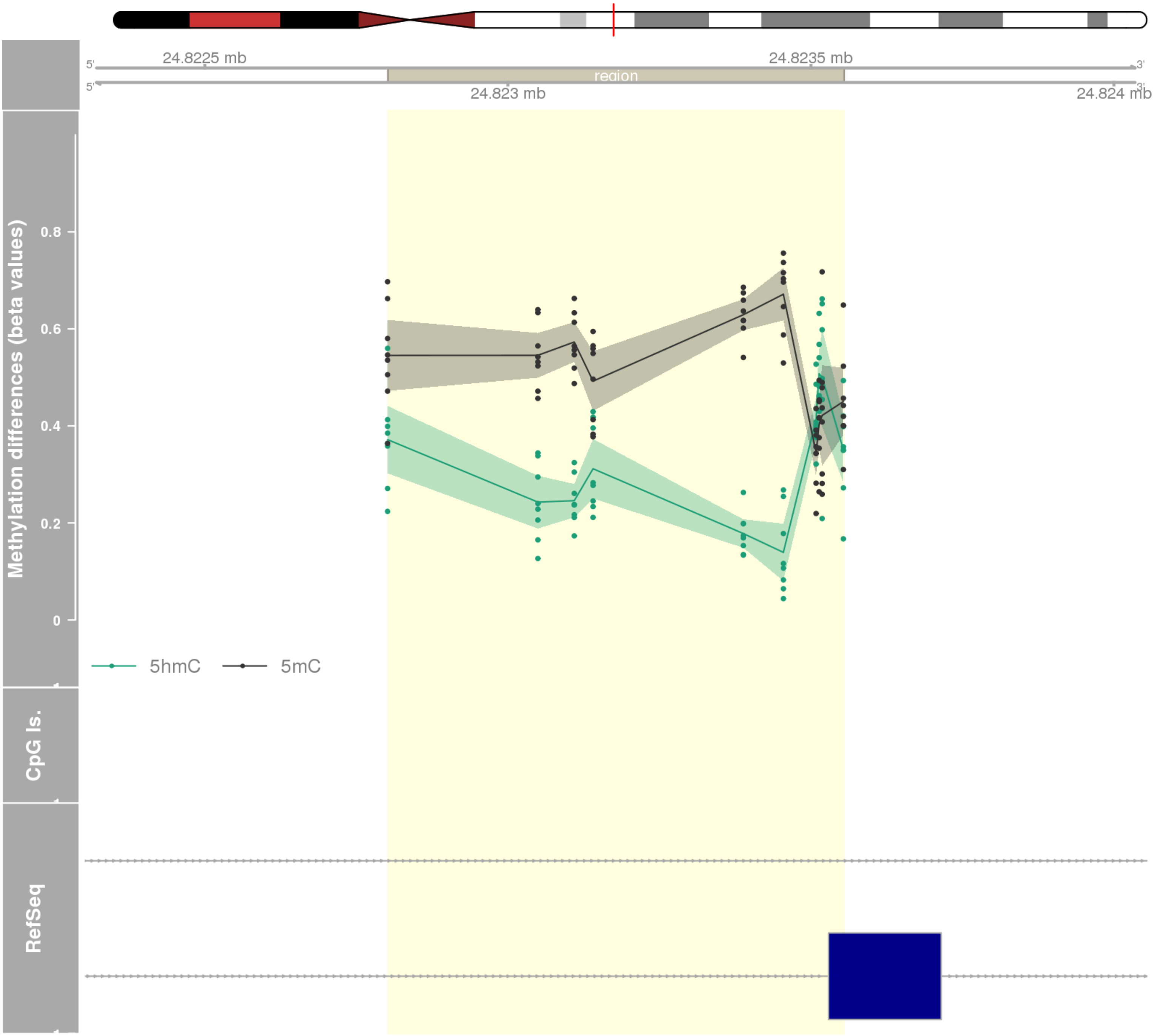
DMR 173 // chr7:1491280-1493153 // 1873 pb. (10 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: MICALL2 -



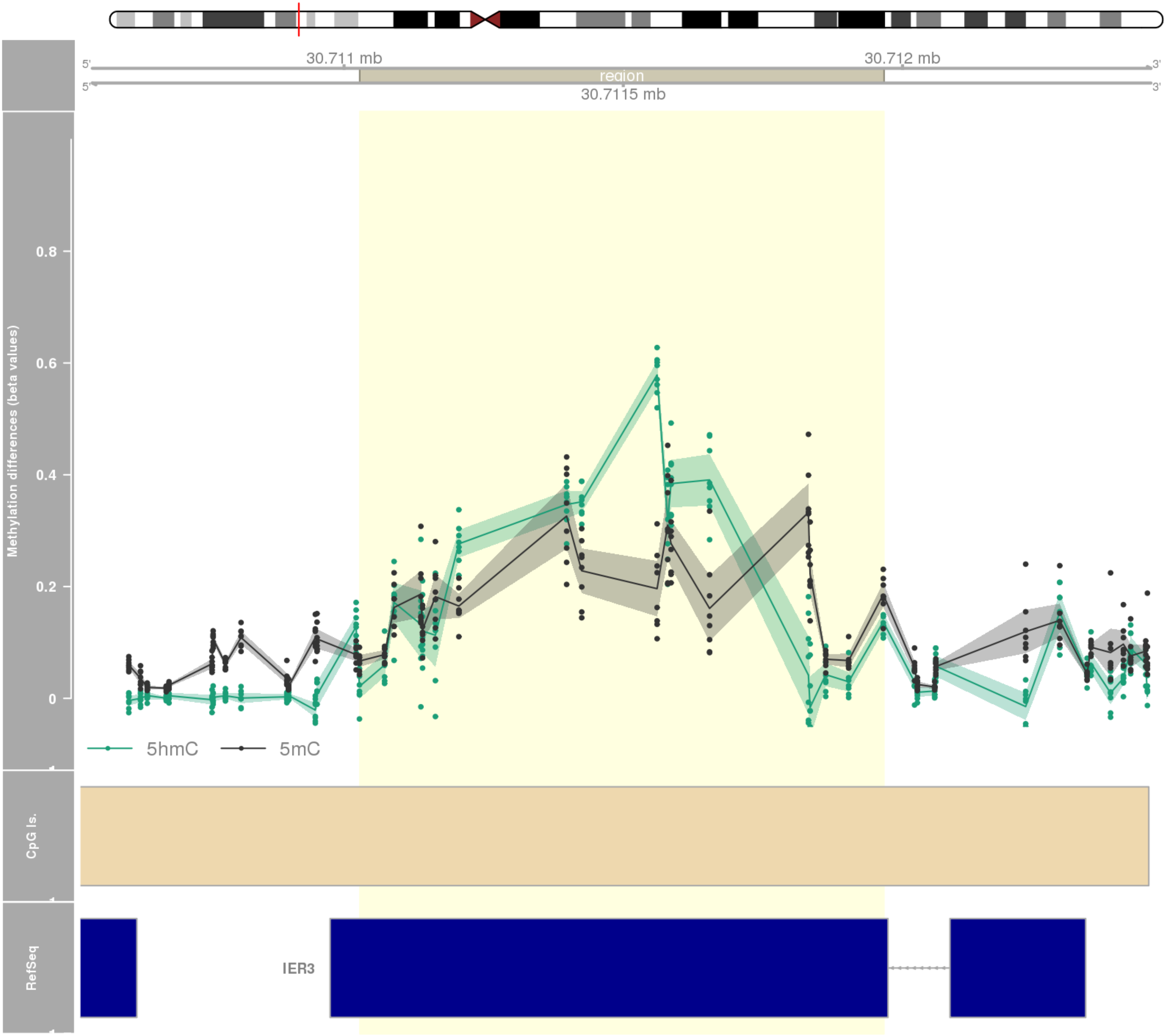


DMR 174 // chr15:96886238-96888024 // 1786 pb. (11 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559

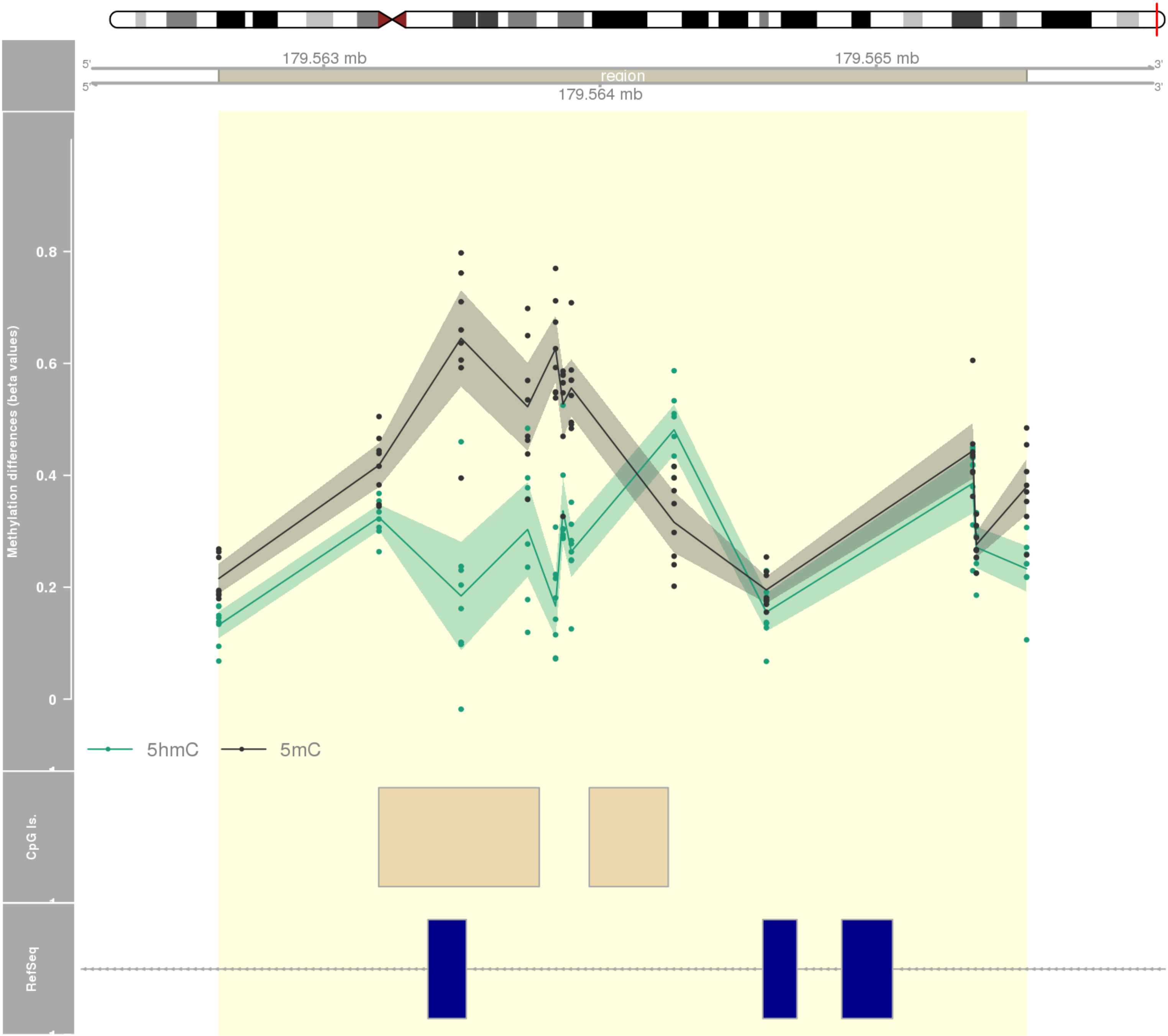
DMR 175 // chr22:24822802-24823554 // 752 pb. (10 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: SPECC1L-ADORA2A / ADORA2A -



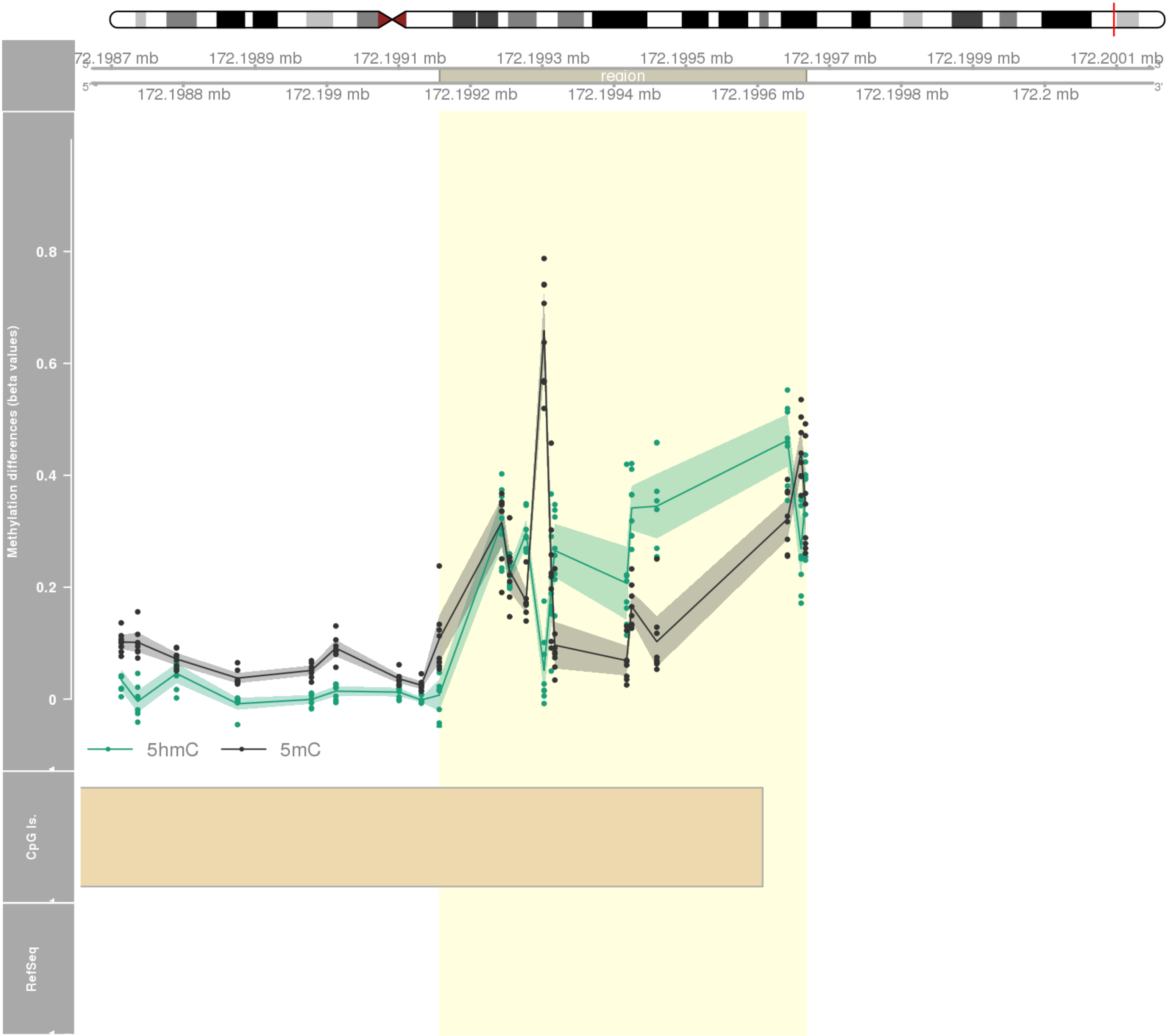
DMR 176 // chr6:30711028-30711966 // 938 pb. (18 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: IER3 -



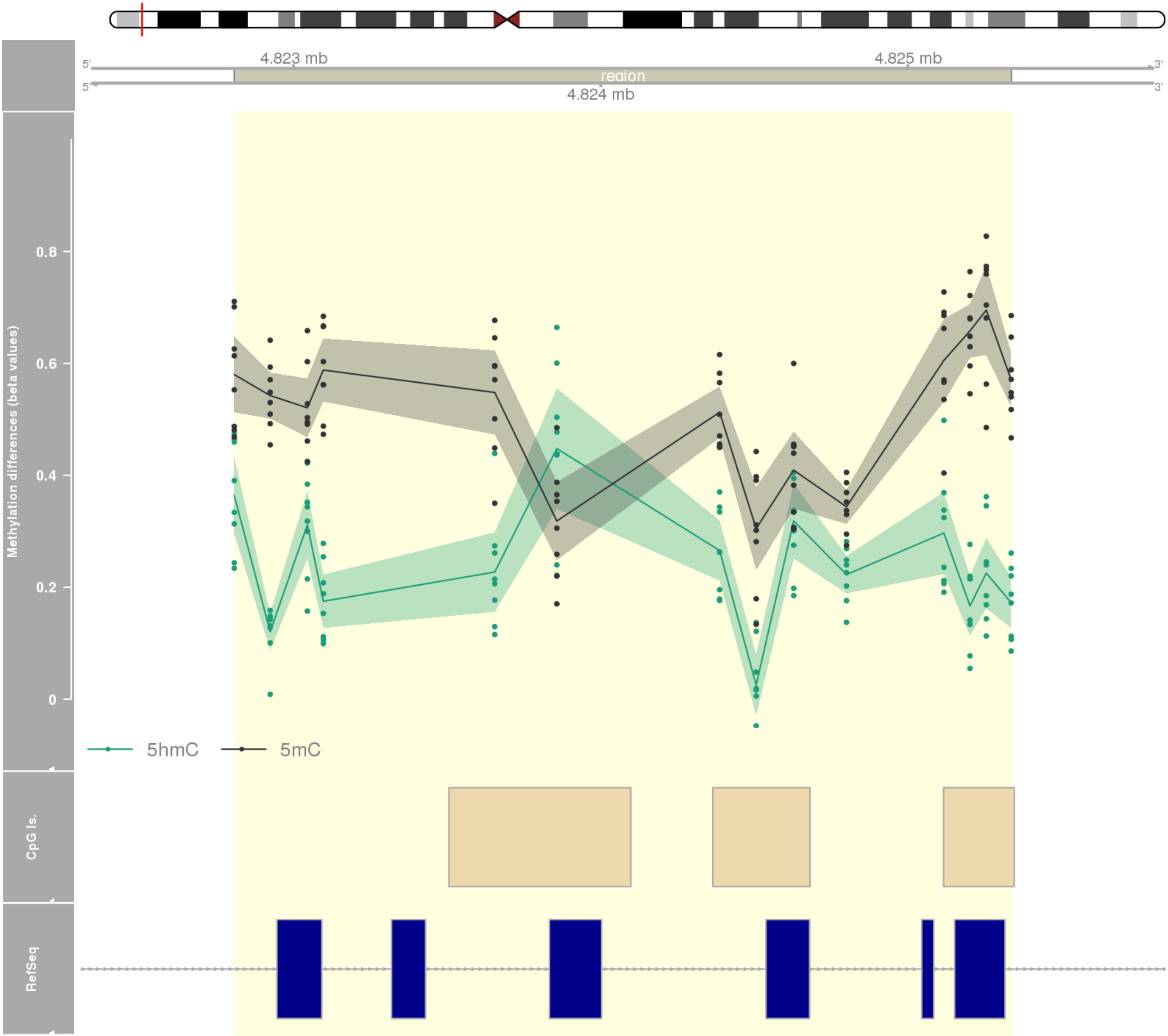
DMR 177 // chr5:179562620-179565544 // 2924 pb. (12 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: RASGEF1C -



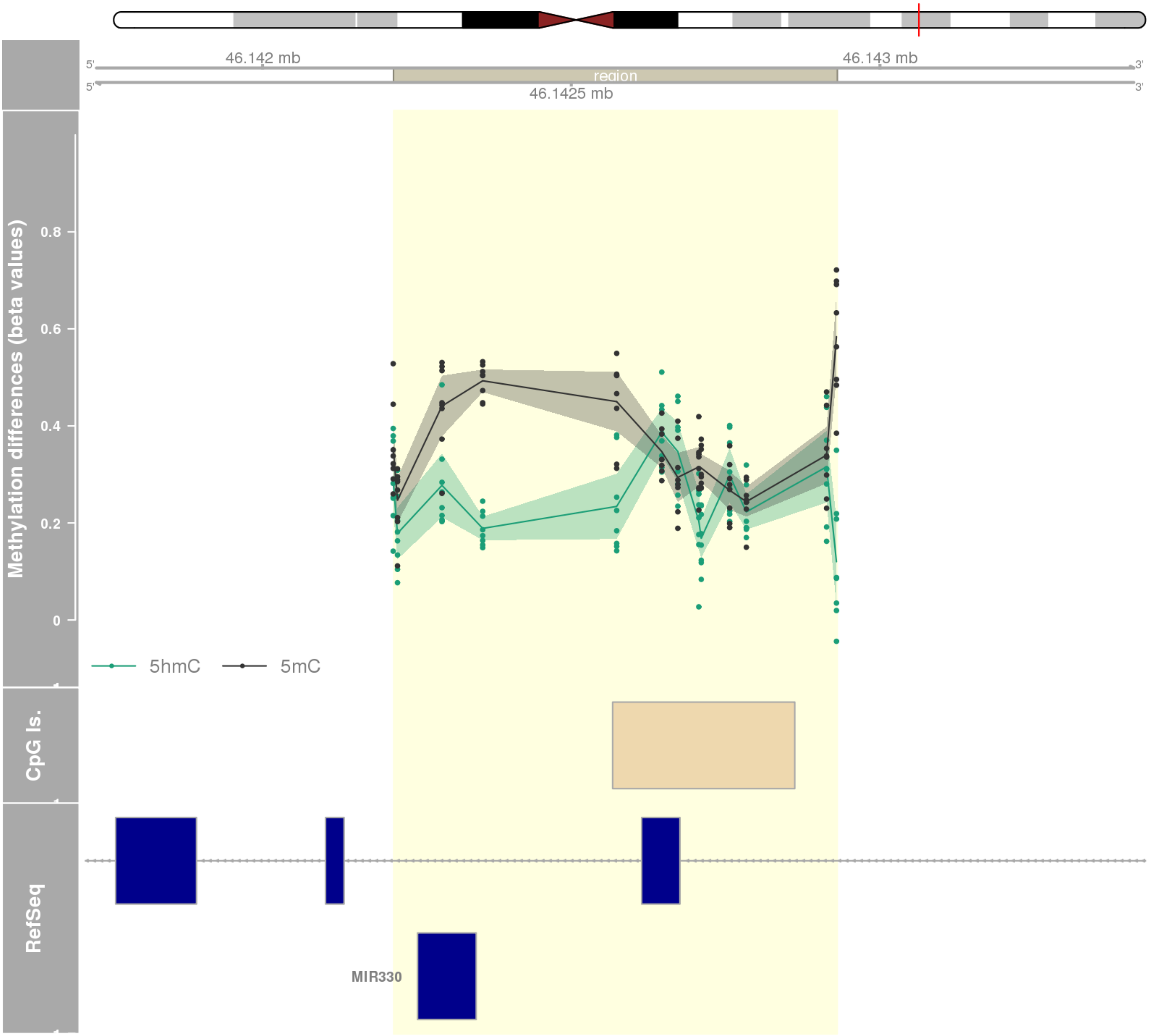
DMR 178 // chr5:172199157-172199667 // 510 pb. (13 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559



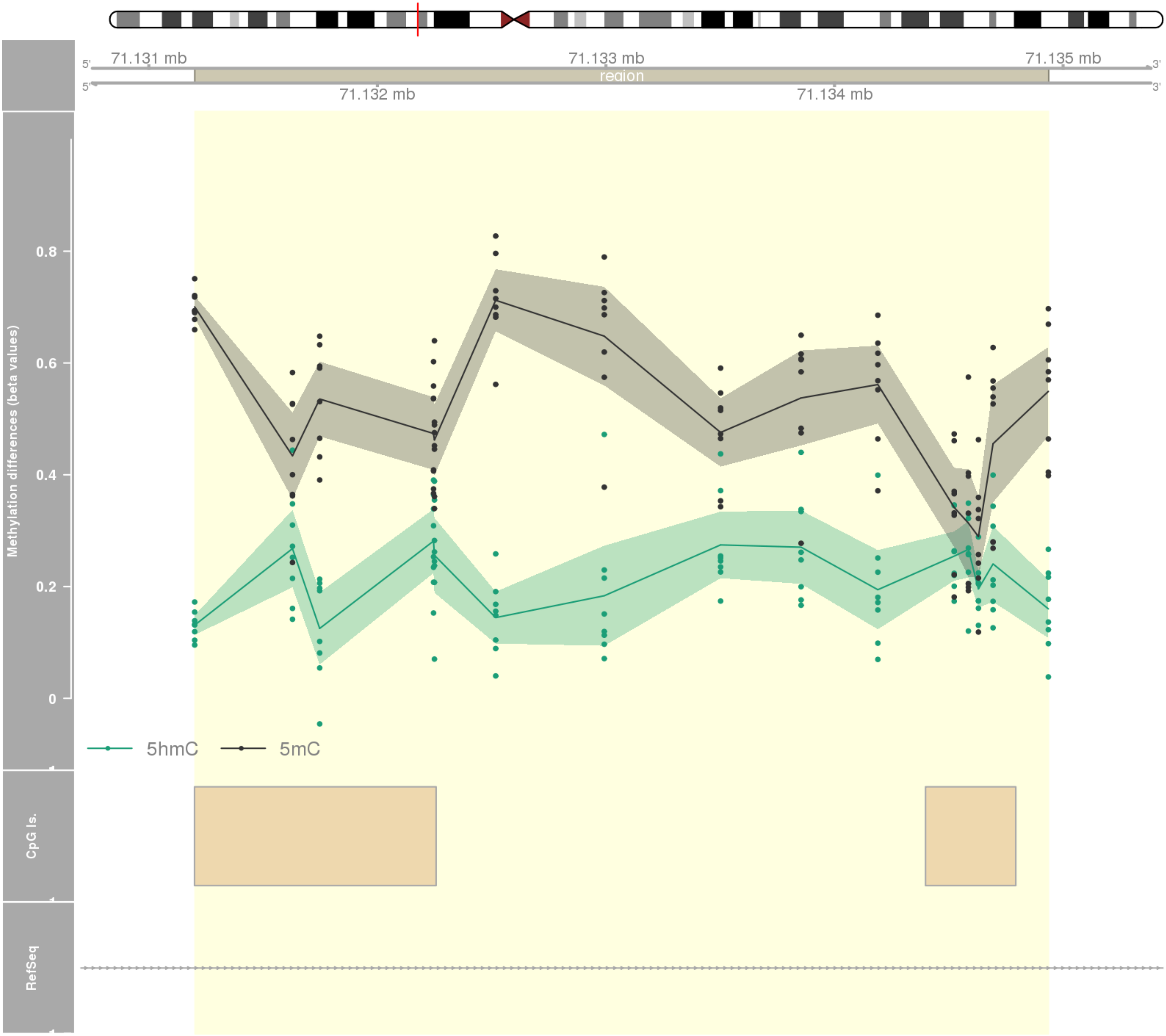
DMR 179 // chr7:4822807-4825336 // 2529 pb. (14 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: AP5Z1 -



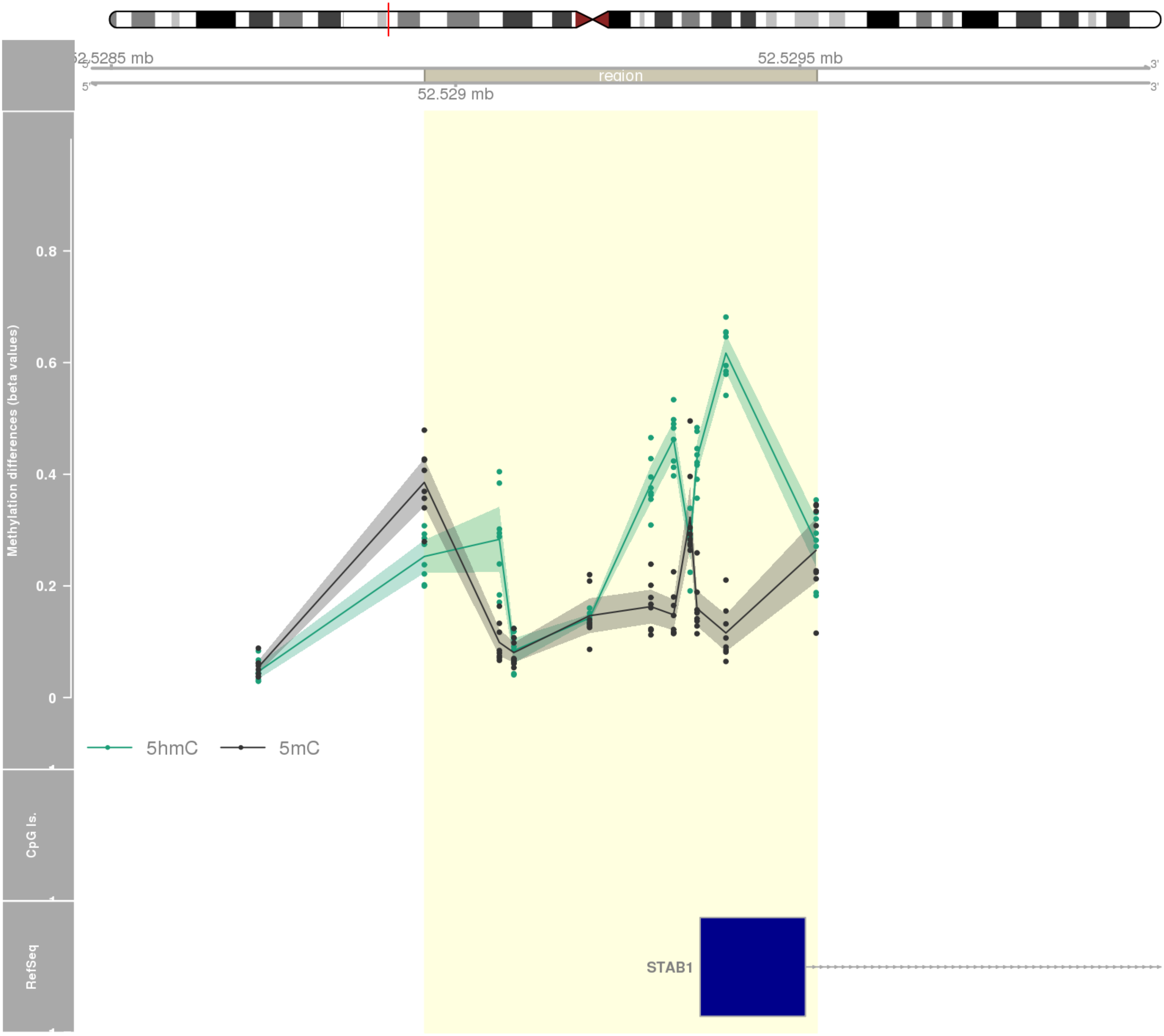
DMR 180 // chr19:46142212-46142930 // 718 pb. (13 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: MIR330 / EML2 -



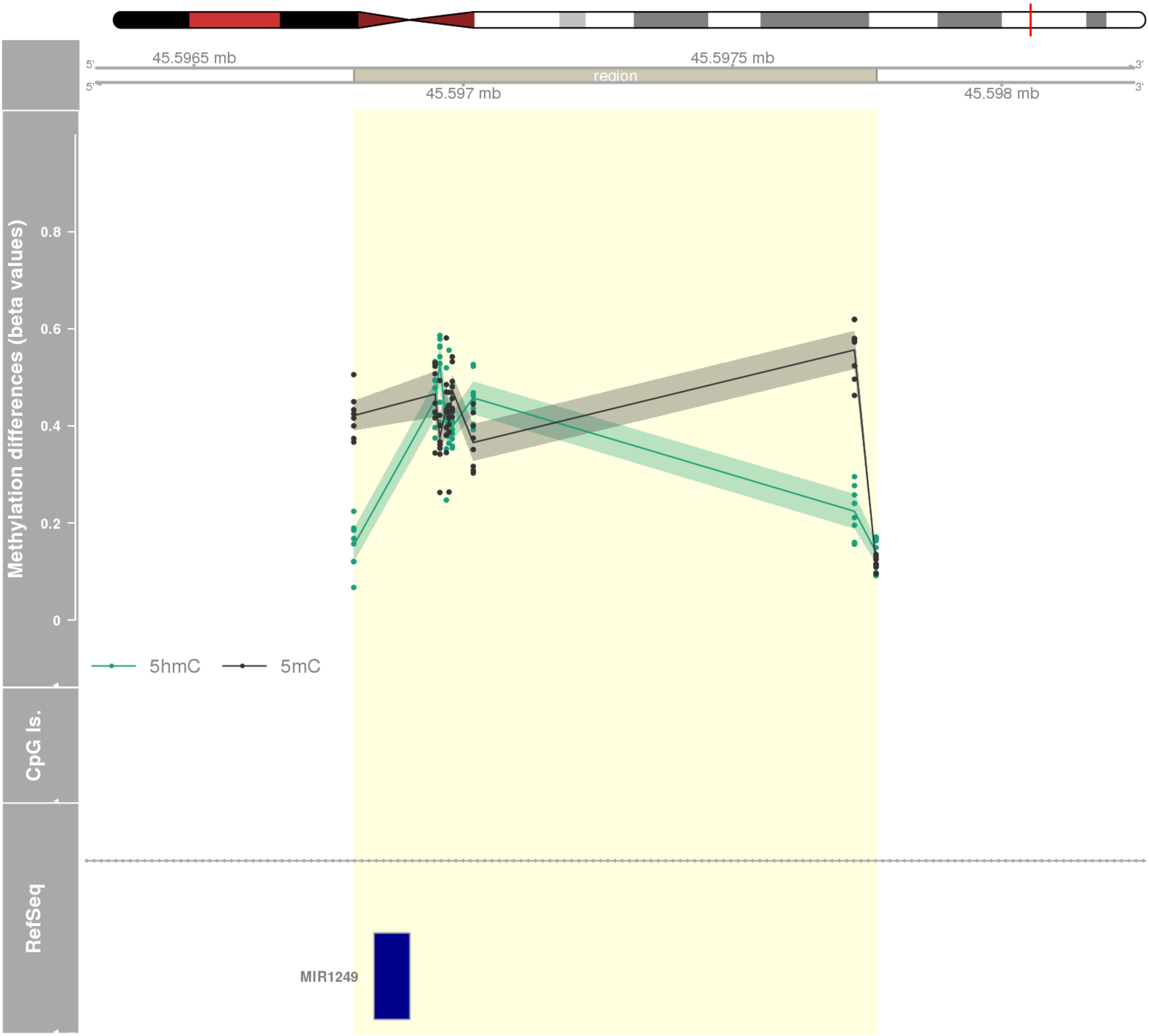
DMR 181 // chr2:71131201-71134936 // 3735 pb. (15 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: VAX2 -



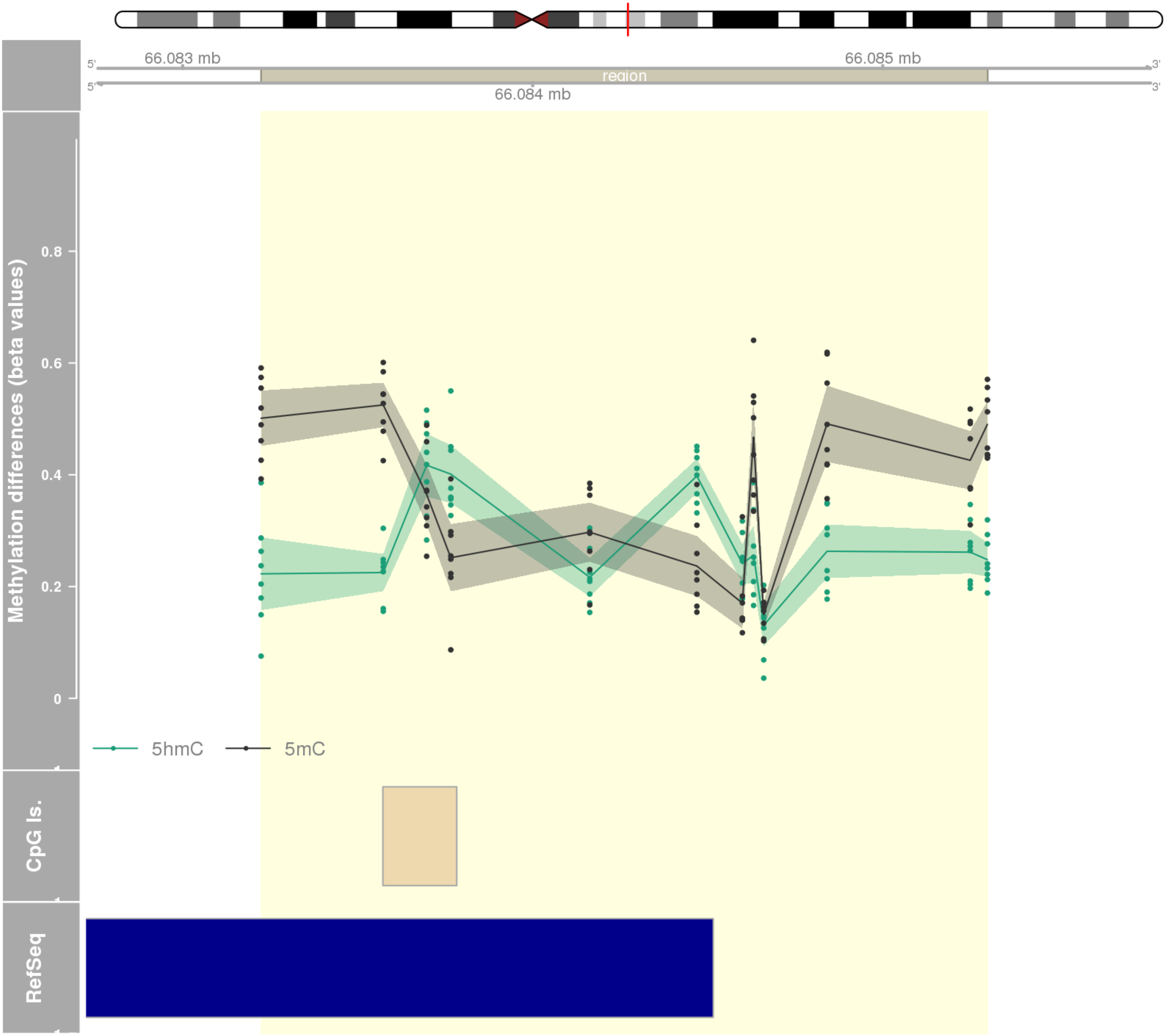
DMR 182 // chr3:52528955-52529524 // 569 pb. (10 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.009 // fwerArea: 0.559
- genes: STAB1 -



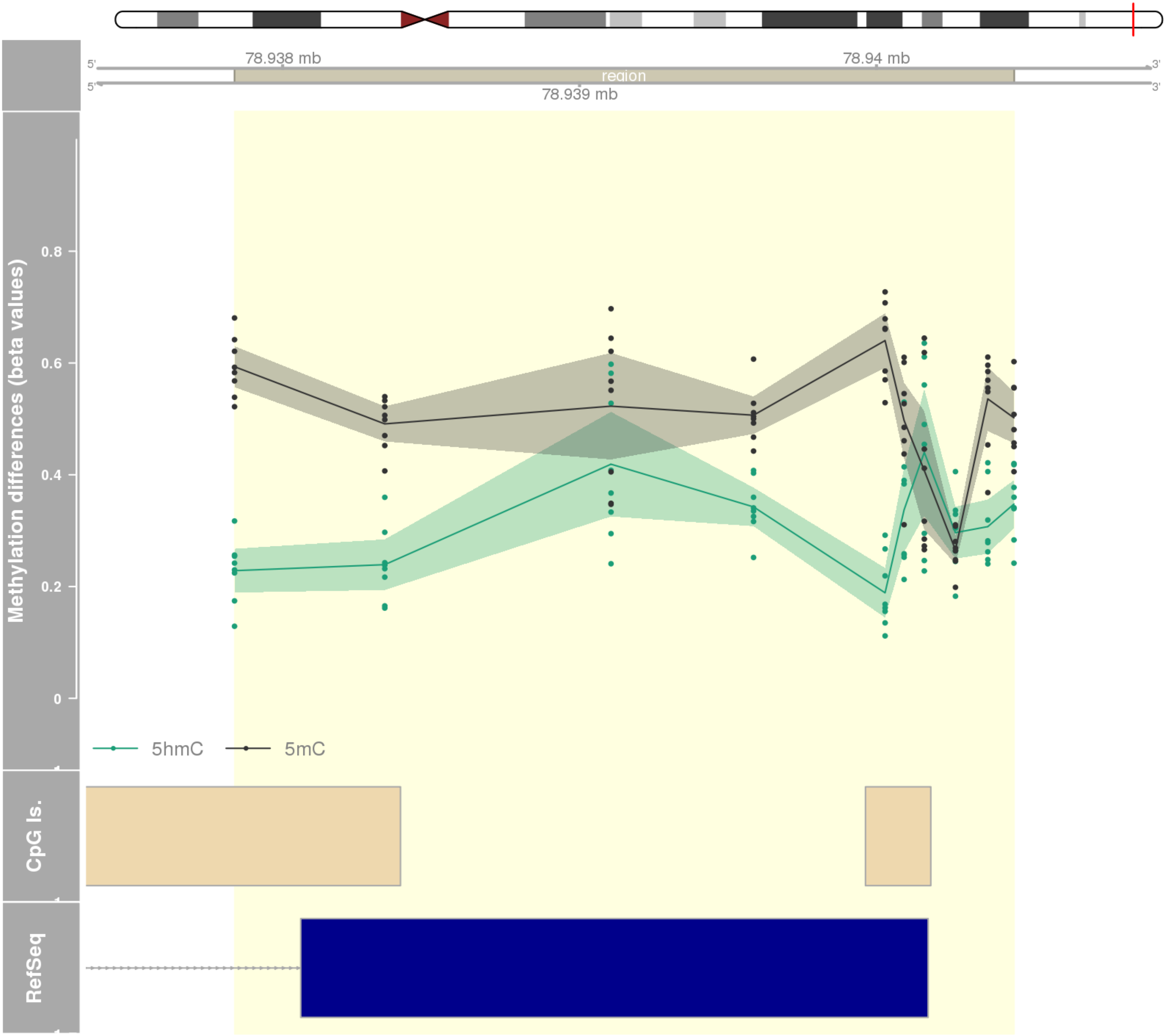
DMR 183 // chr22:45596797-45597767 // 970 pb. (9 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: MIR1249 / KIAA0930 -



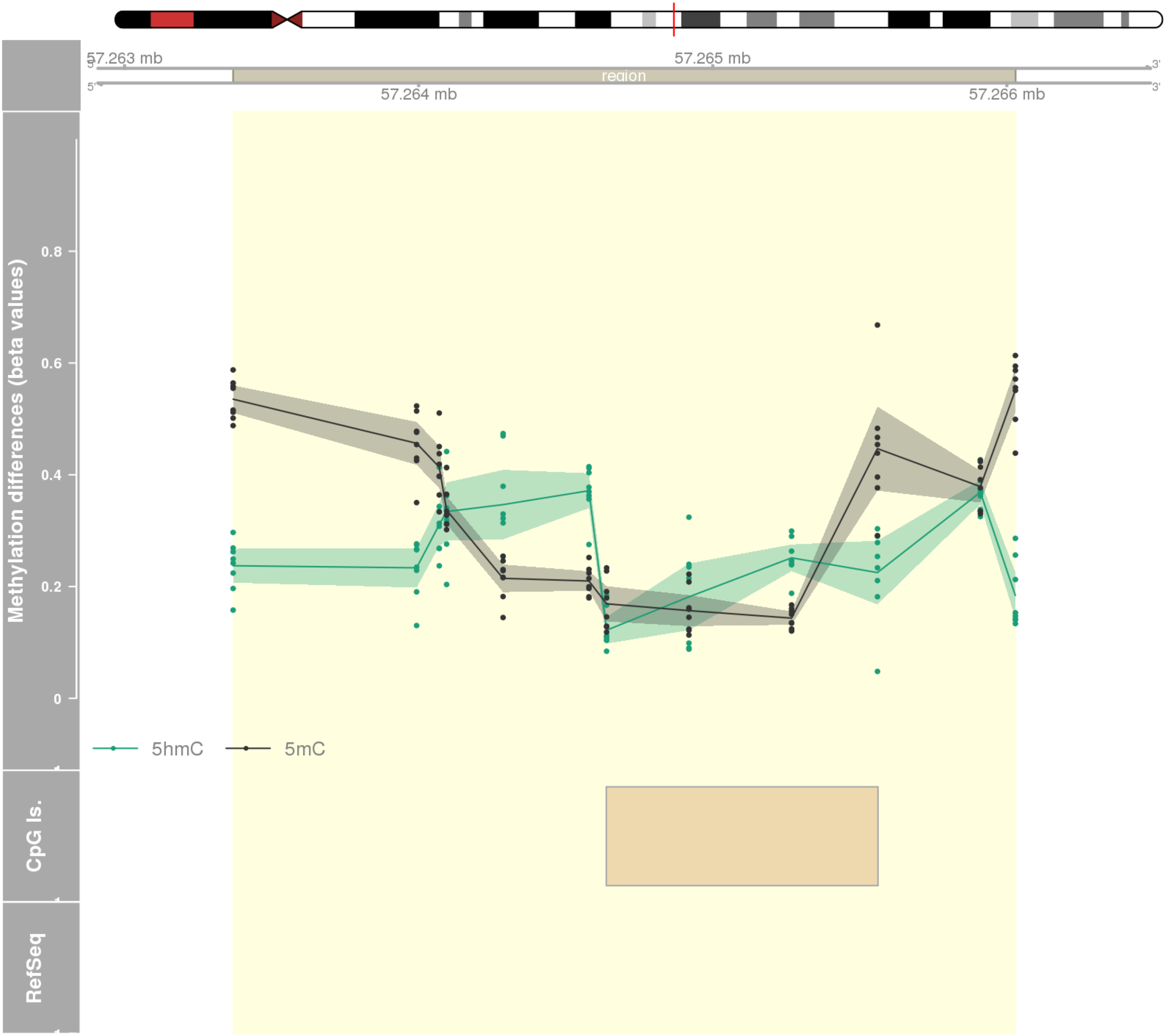
DMR 184 // chr11:66083224-66085299 // 2075 pb. (12 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: CD248 -



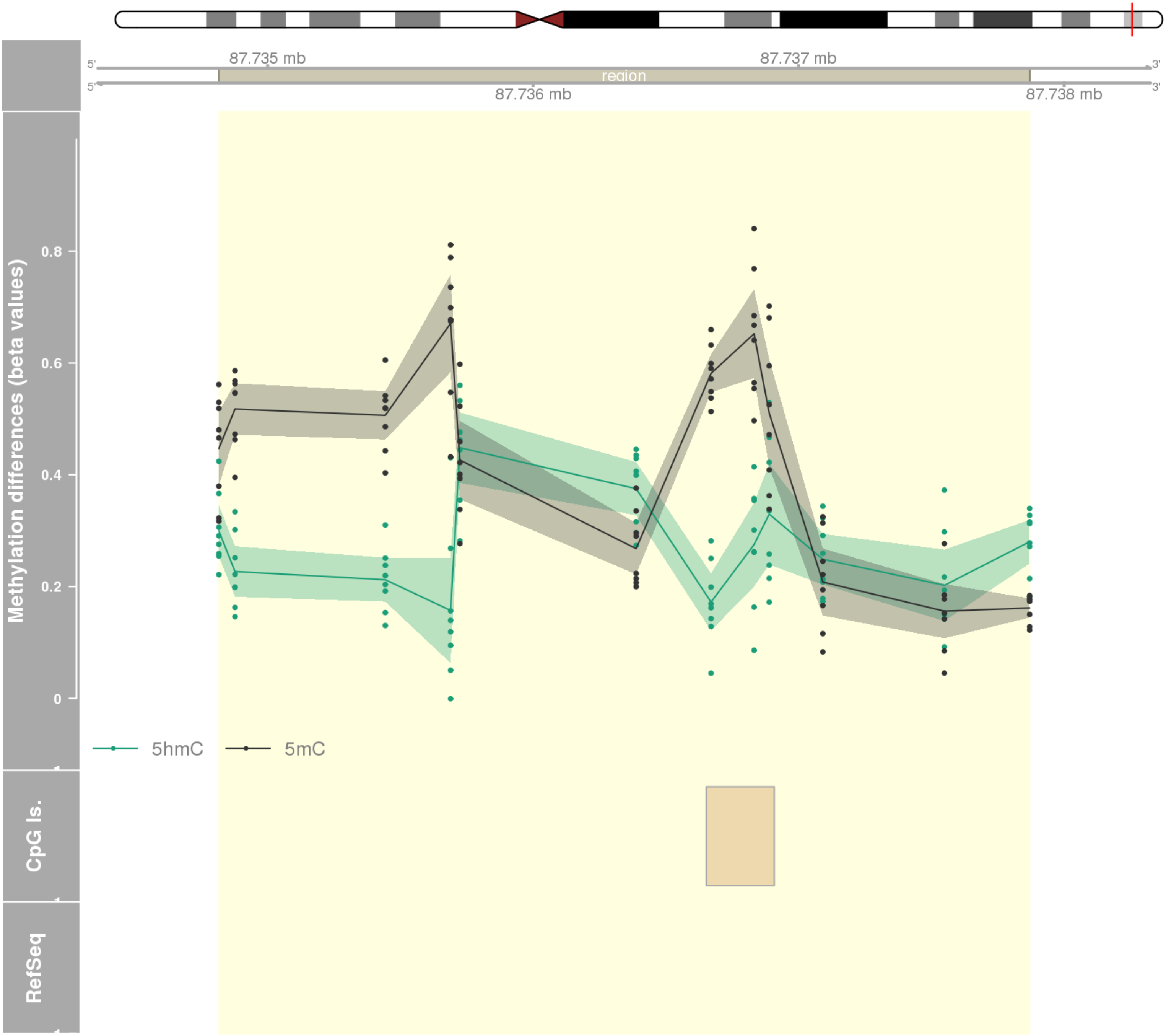
DMR 185 // chr17:78937838-78940463 // 2625 pb. (10 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: RPTOR -



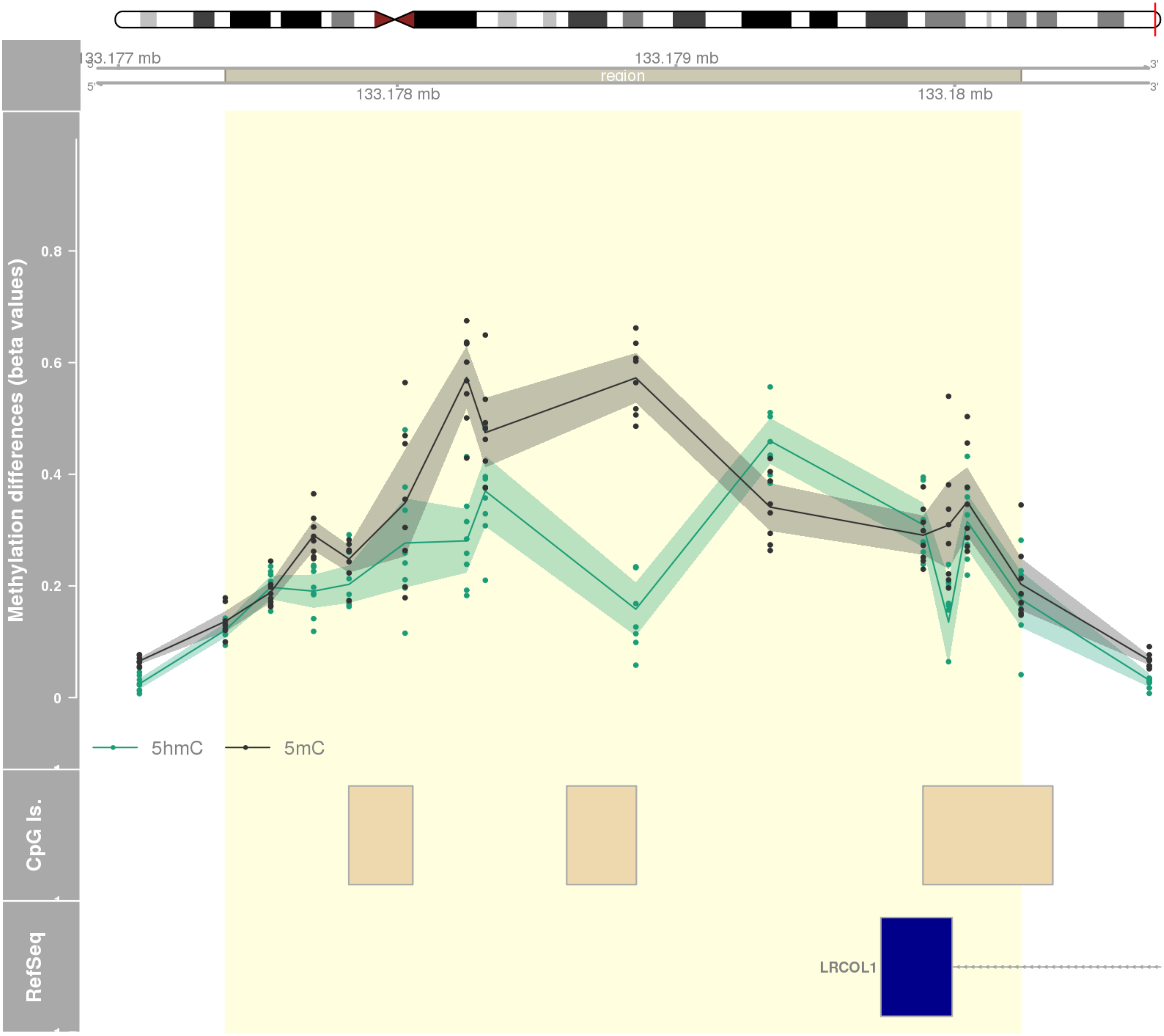
DMR 186 // chr14:57263369-57266029 // 2660 pb. (12 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559



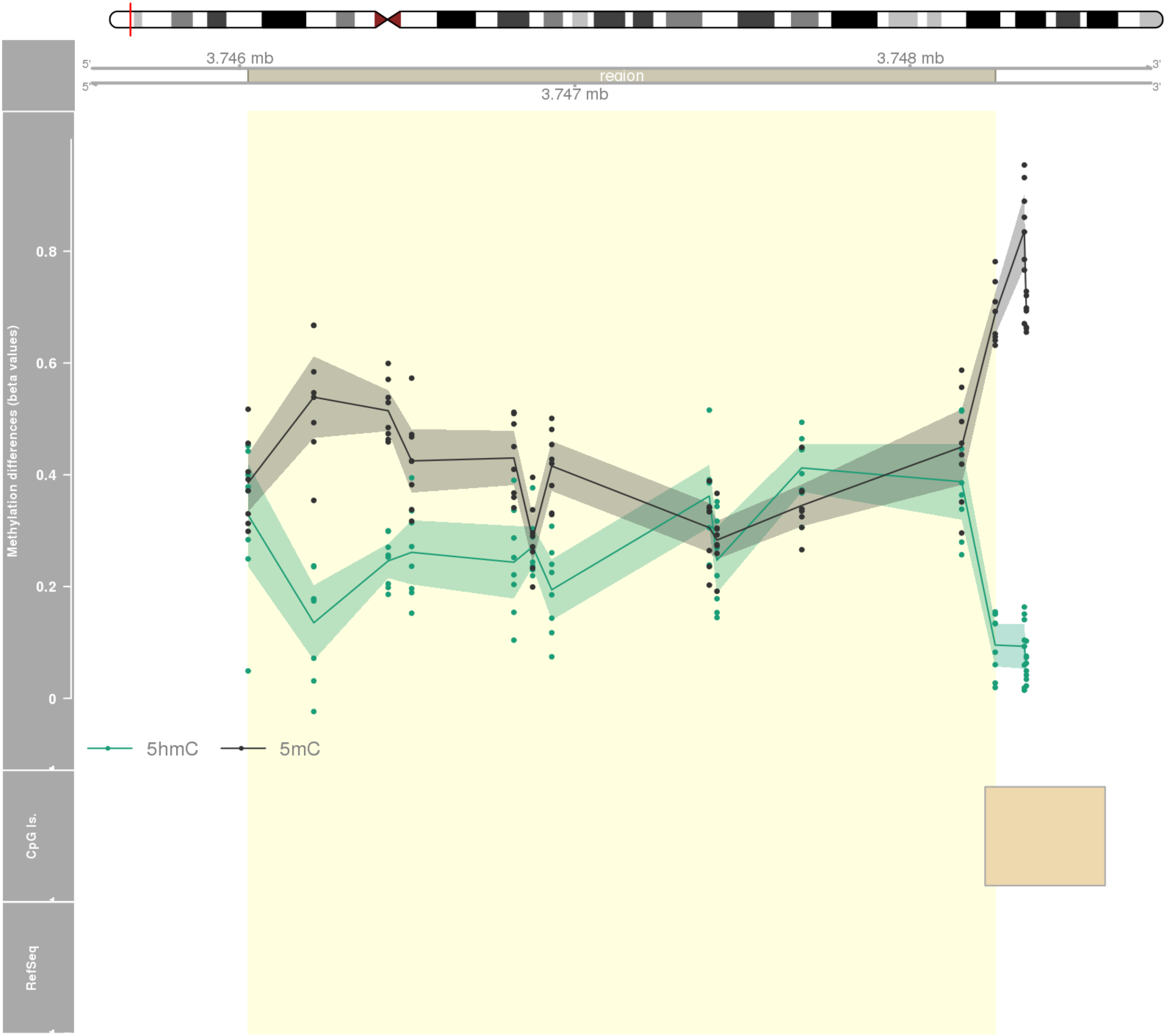
DMR 187 // chr16:87734816-87737870 // 3054 pb. (12 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: KLHDC4 -



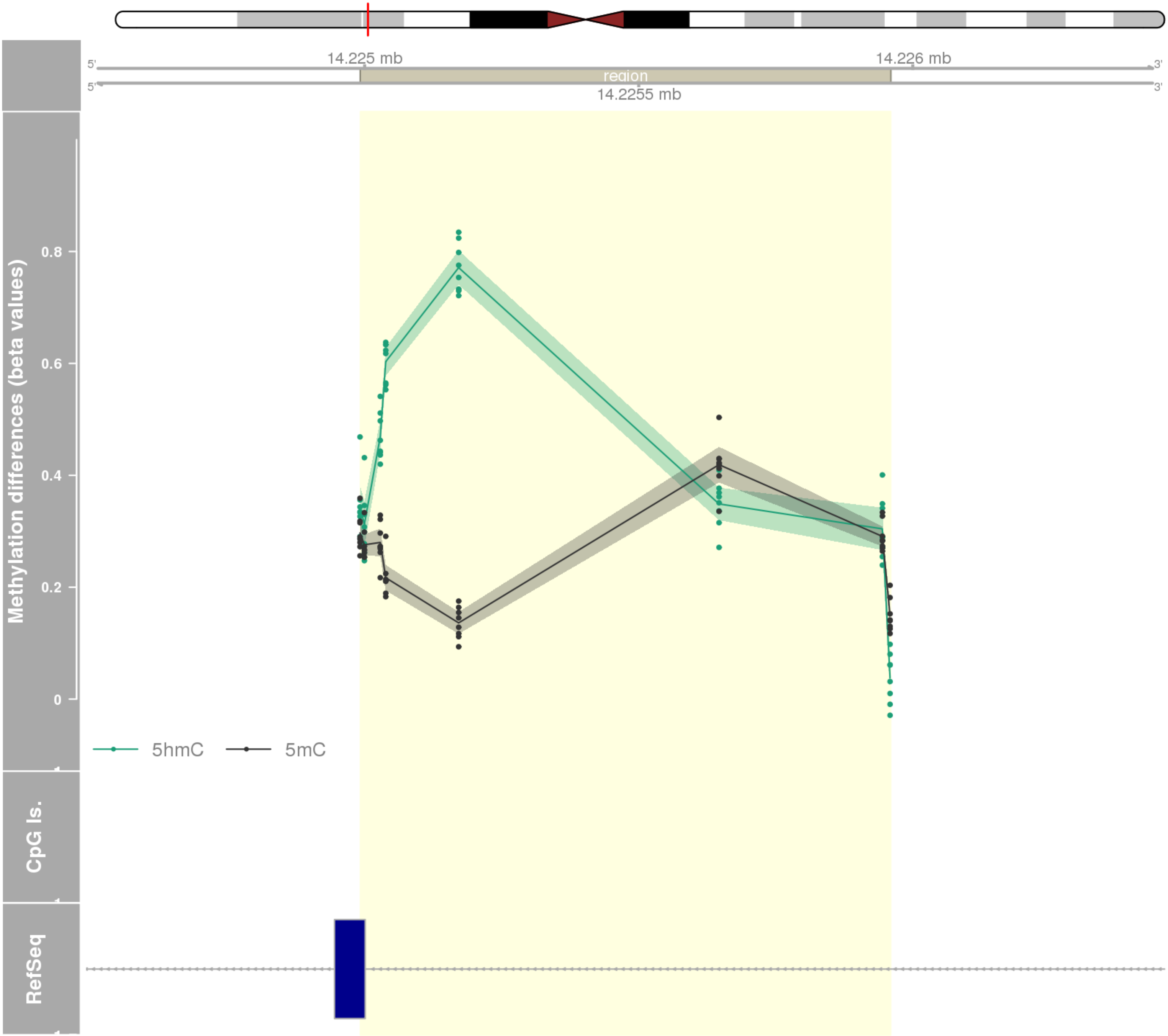
DMR 188 // chr12:133177383-133180238 // 2855 pb. (13 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: LRCOL1 -



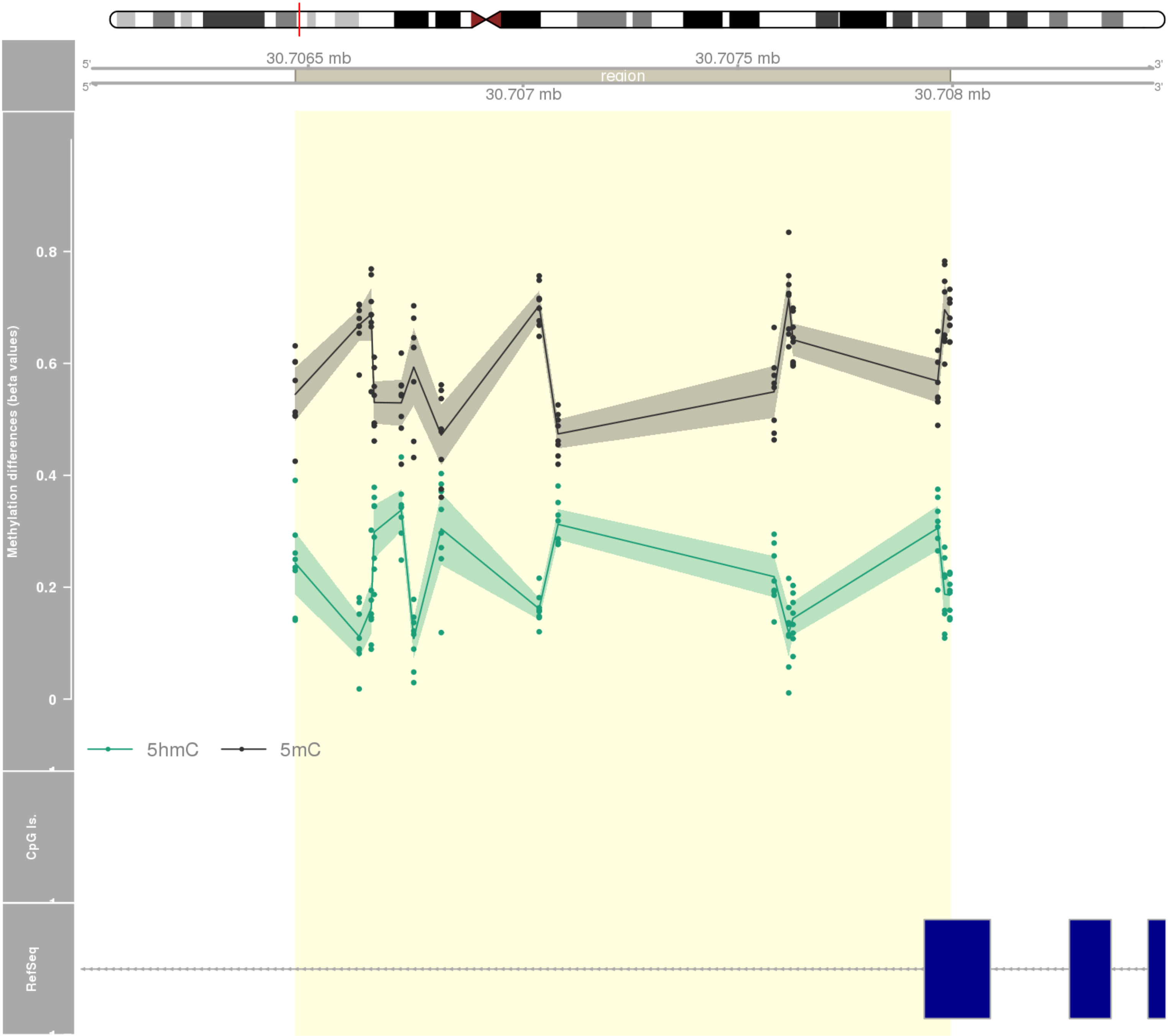
DMR 189 // chr4:3746025-3748254 // 2229 pb. (12 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559



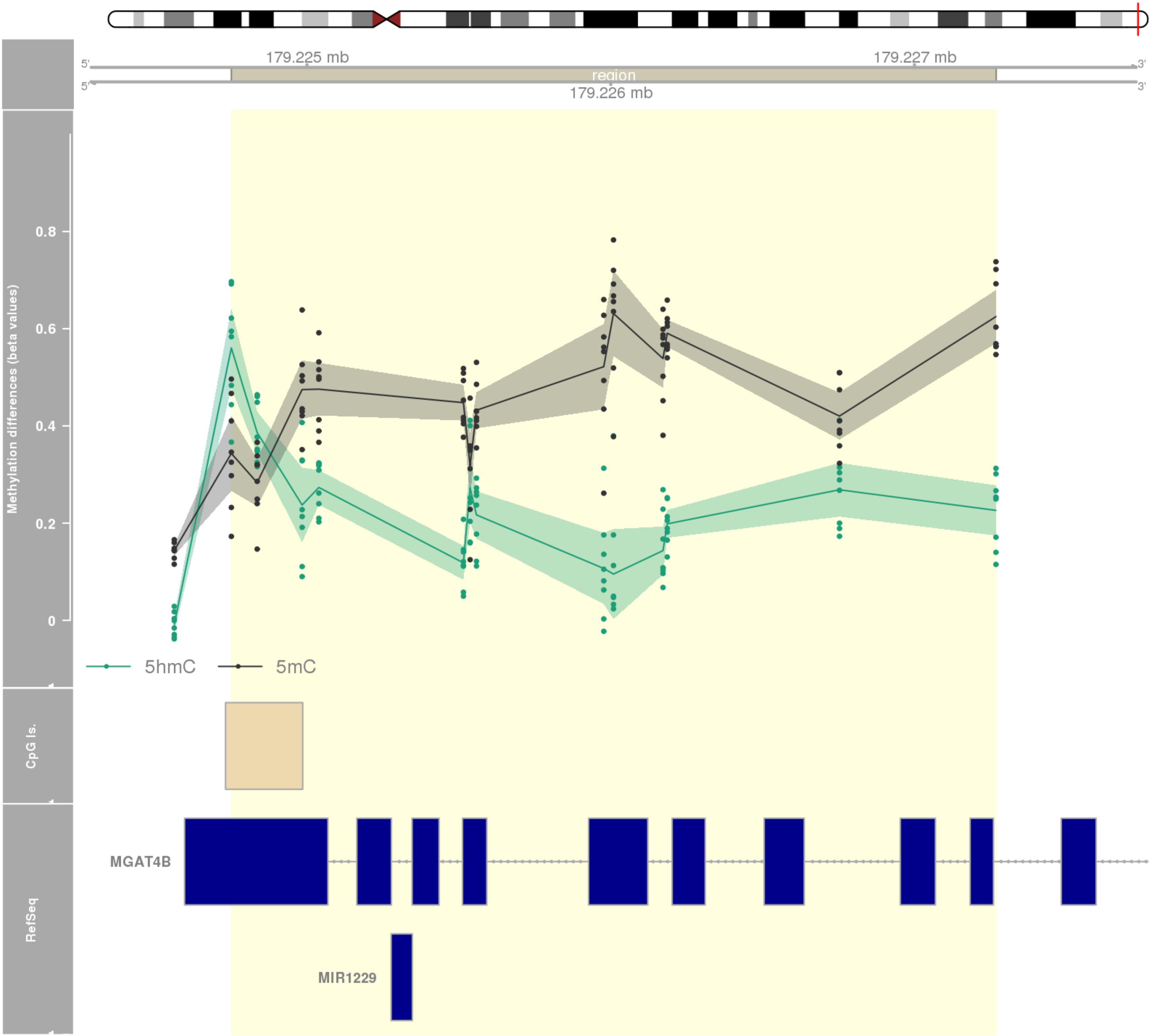
DMR 190 // chr19:14224992-14225959 // 967 pb. (8 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: PRKACA -



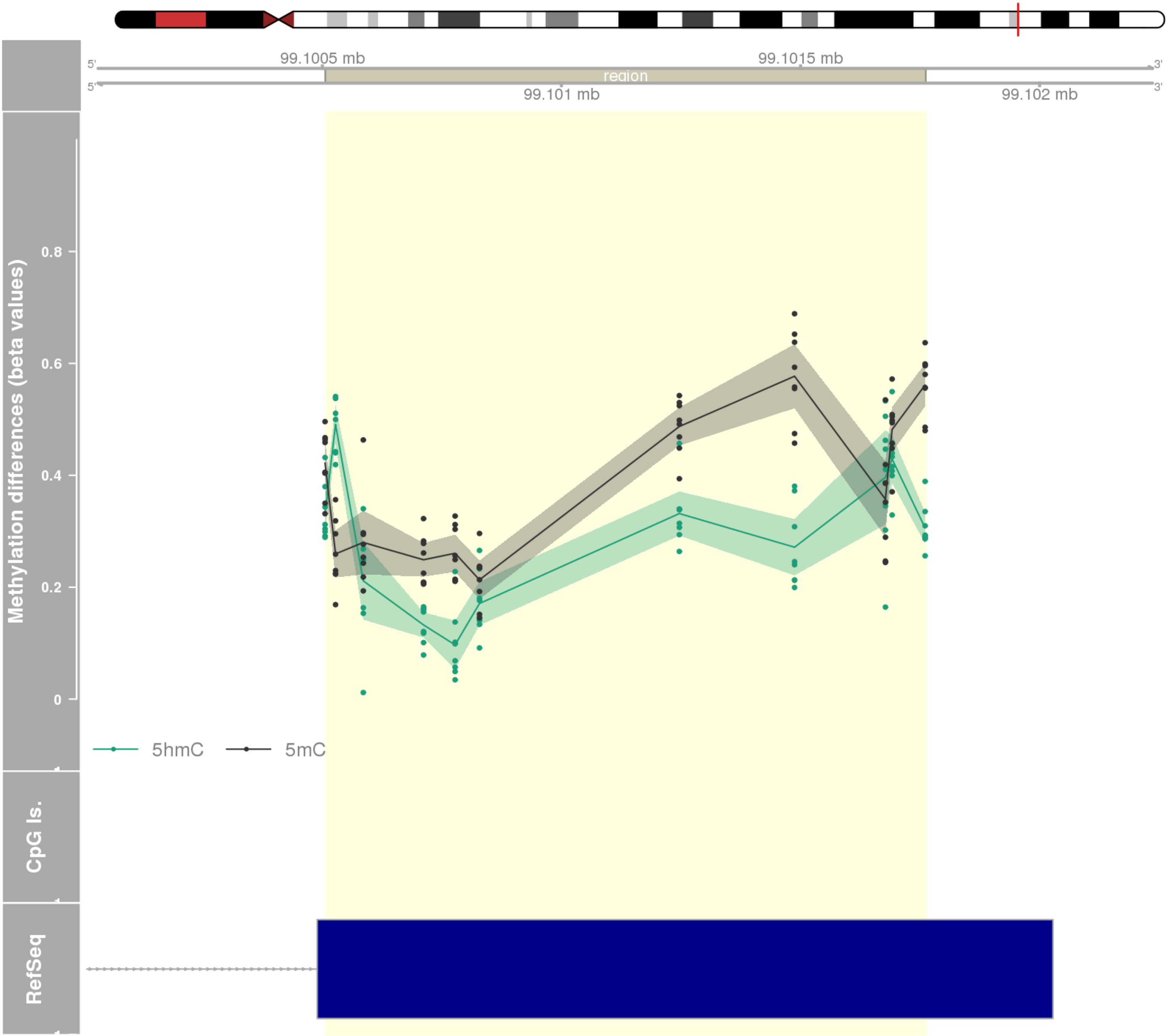
DMR 191 // chr6:30706470-30707994 // 1524 pb. (15 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: FLOT1 -



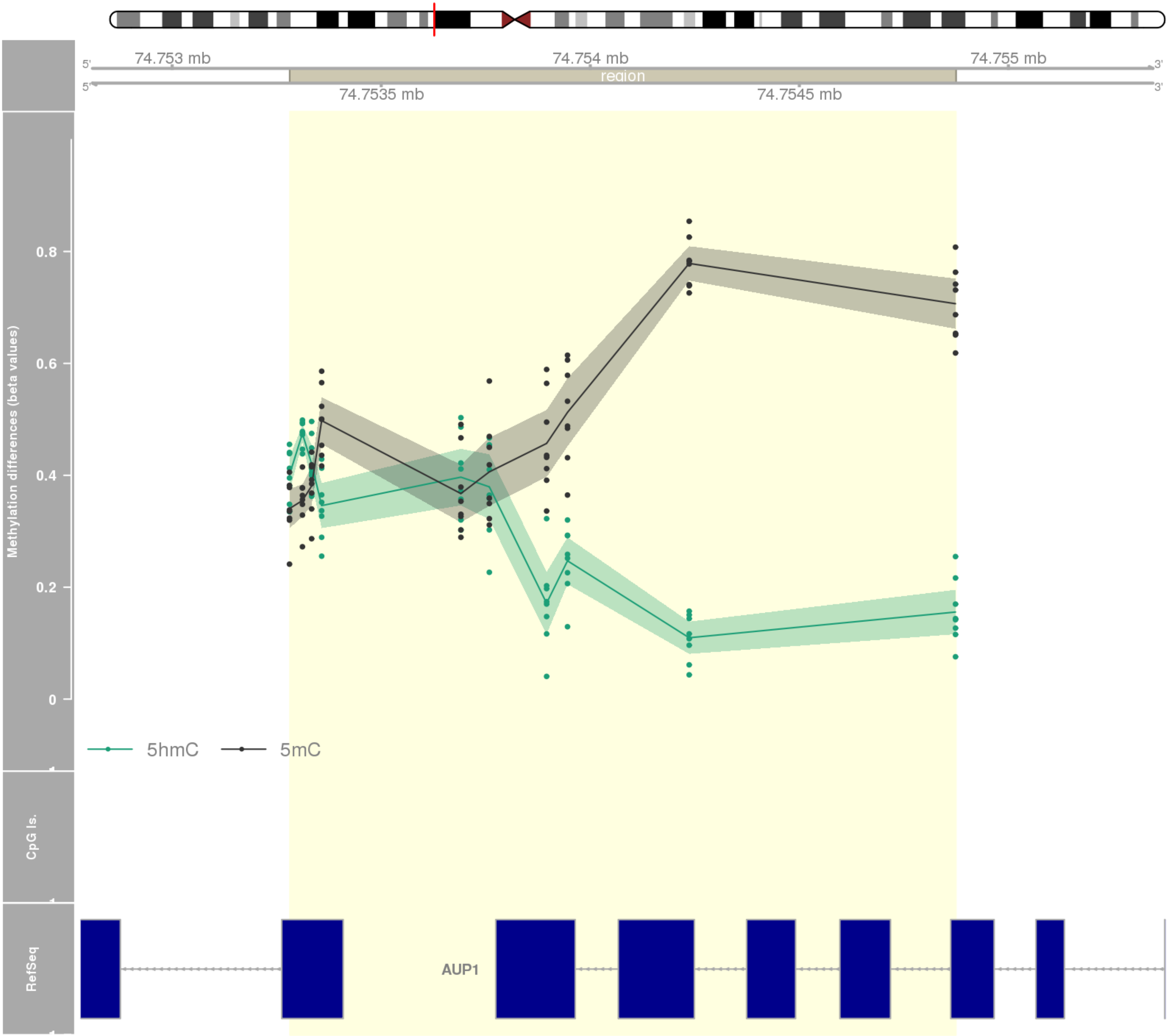
DMR 192 // chr5:179224751-179227268 // 2517 pb. (13 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: MIR1229 / MGAT4B -



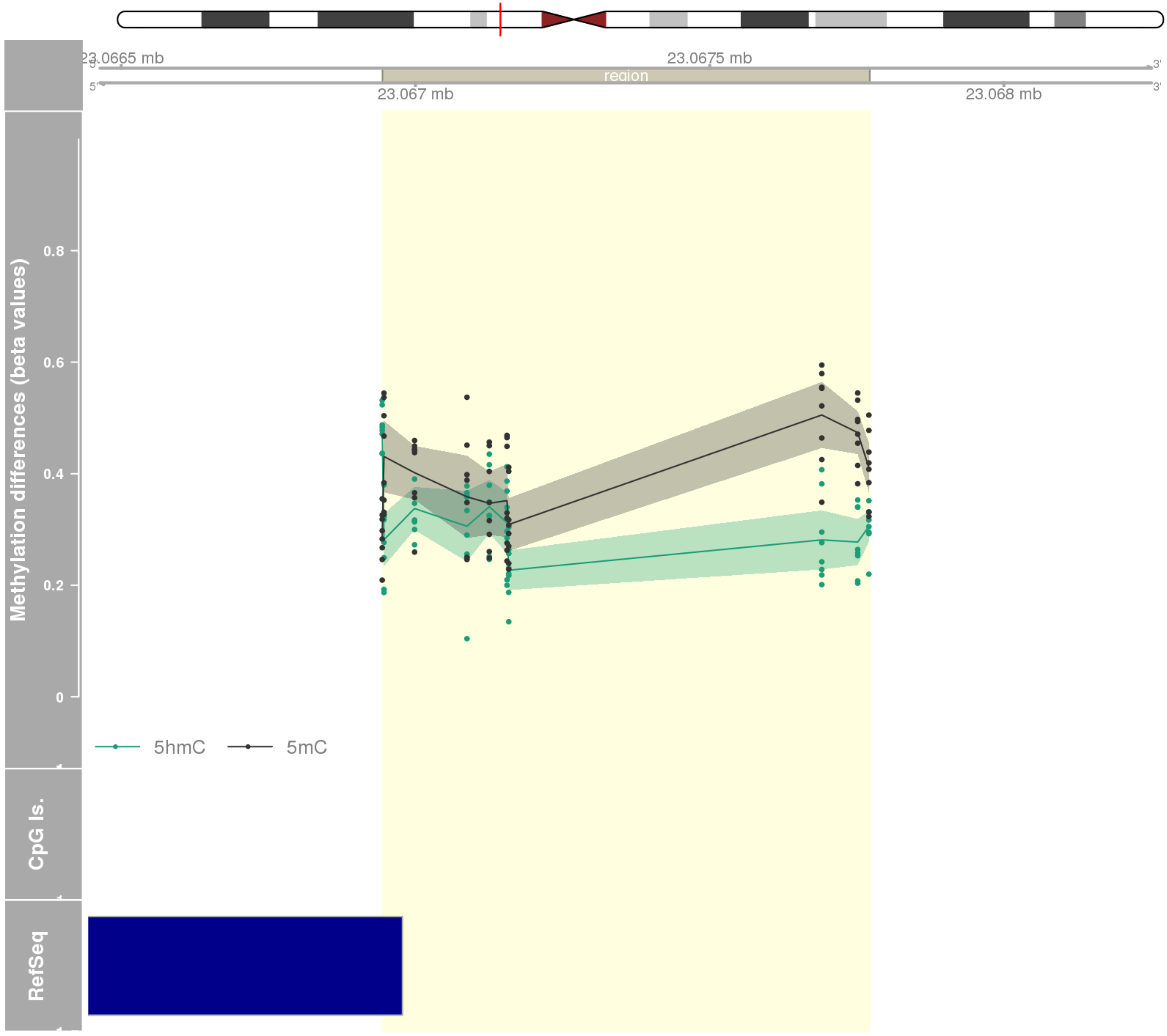
DMR 193 // chr13:99100506-99101761 // 1255 pb. (11 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: FARP1 -



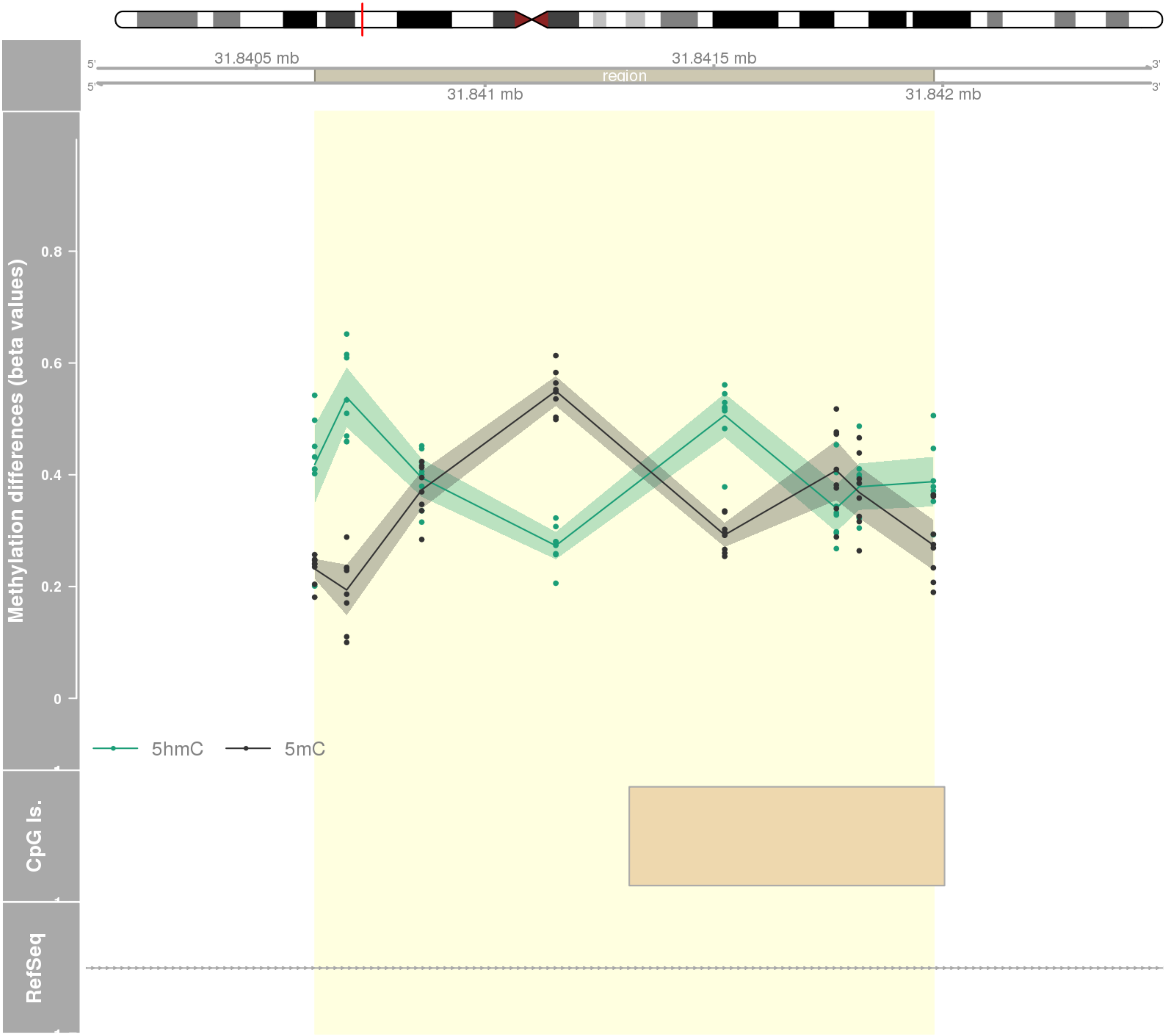
DMR 194 // chr2:74753281-74754874 // 1593 pb. (10 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: DQX1 / AUP1 -



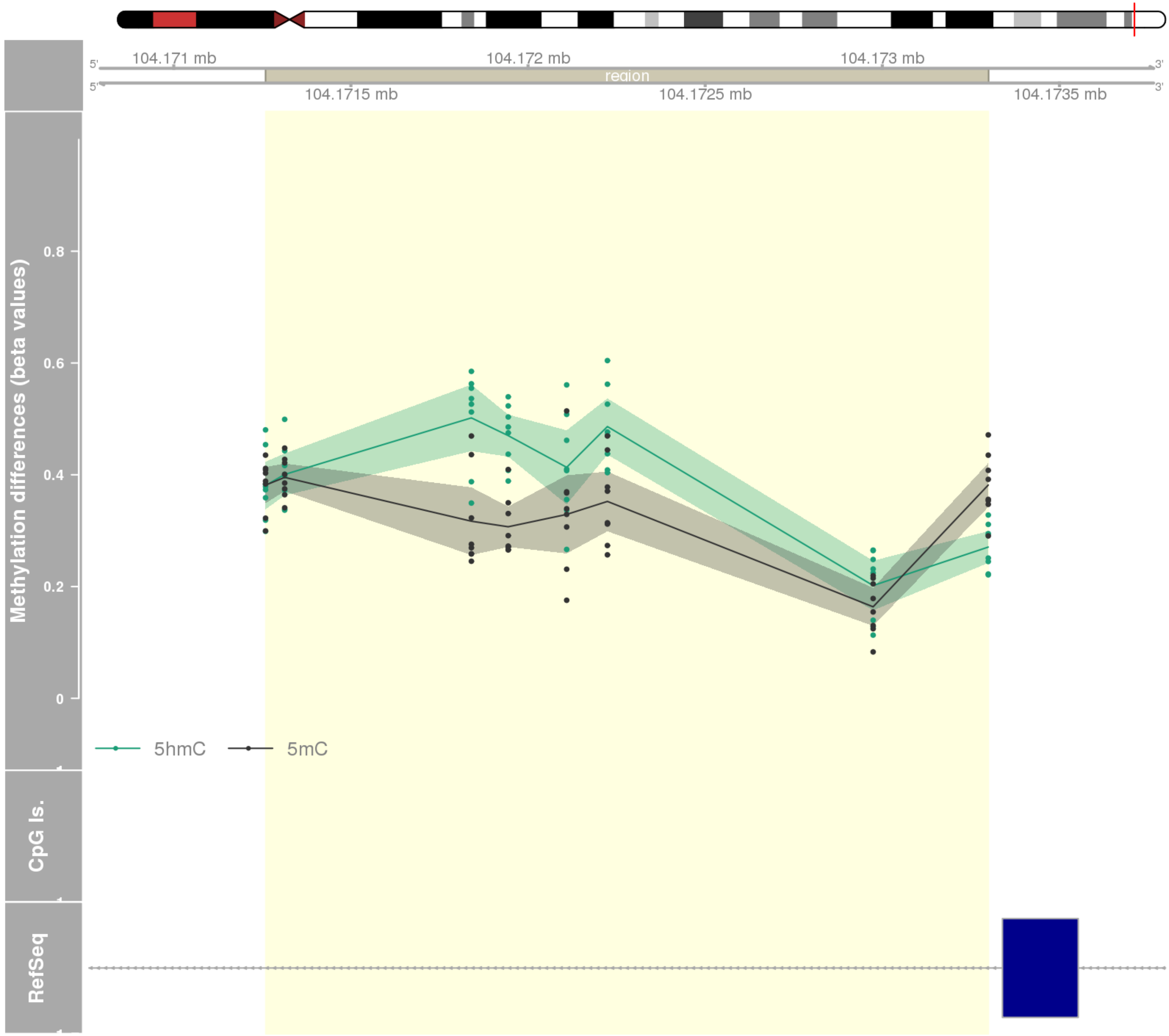
DMR 195 // chr20:23066944-23067771 // 827 pb. (10 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: CD93 -



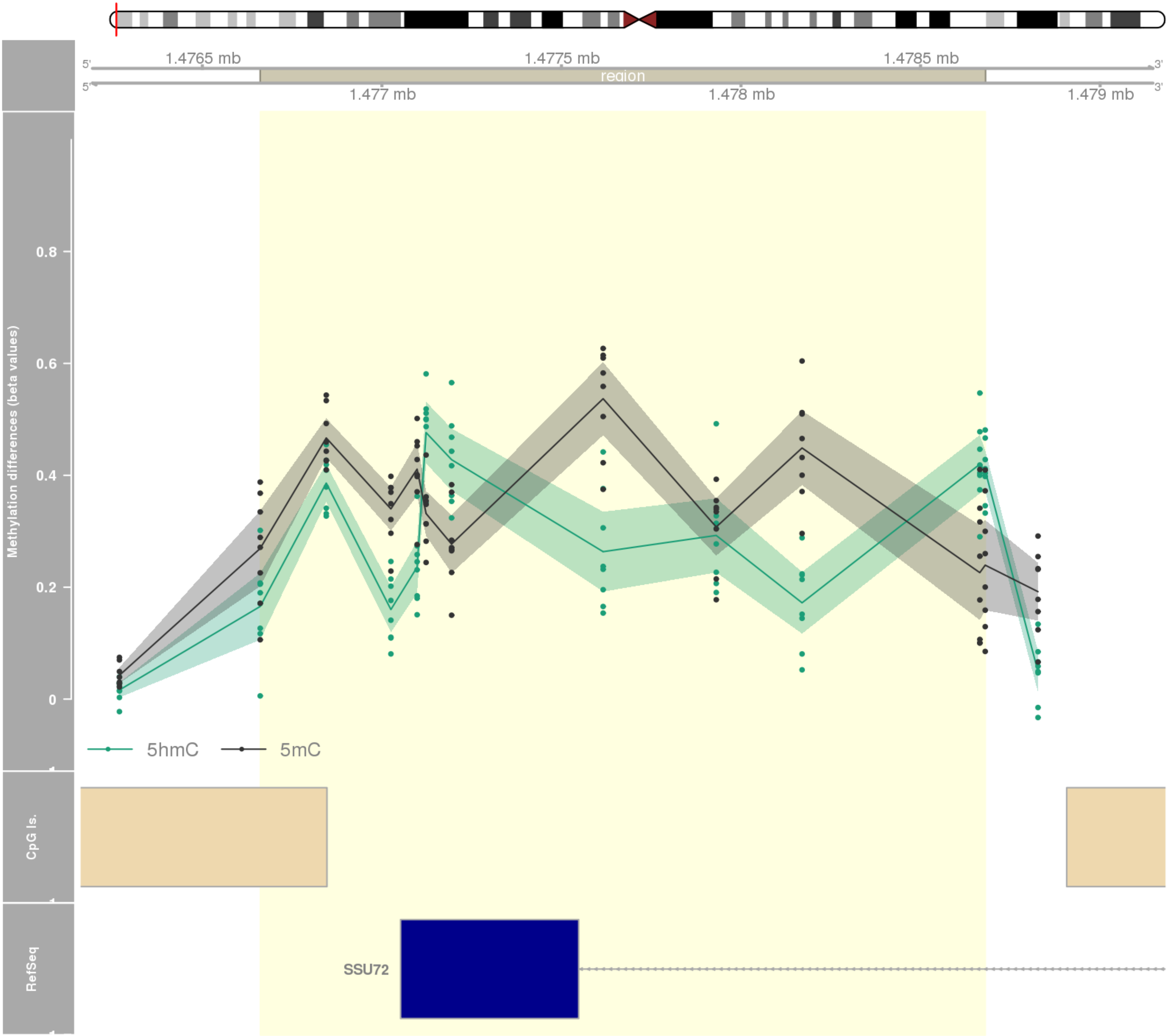
DMR 196 // chr11:31840628-31841980 // 1352 pb. (8 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: RCN1 -



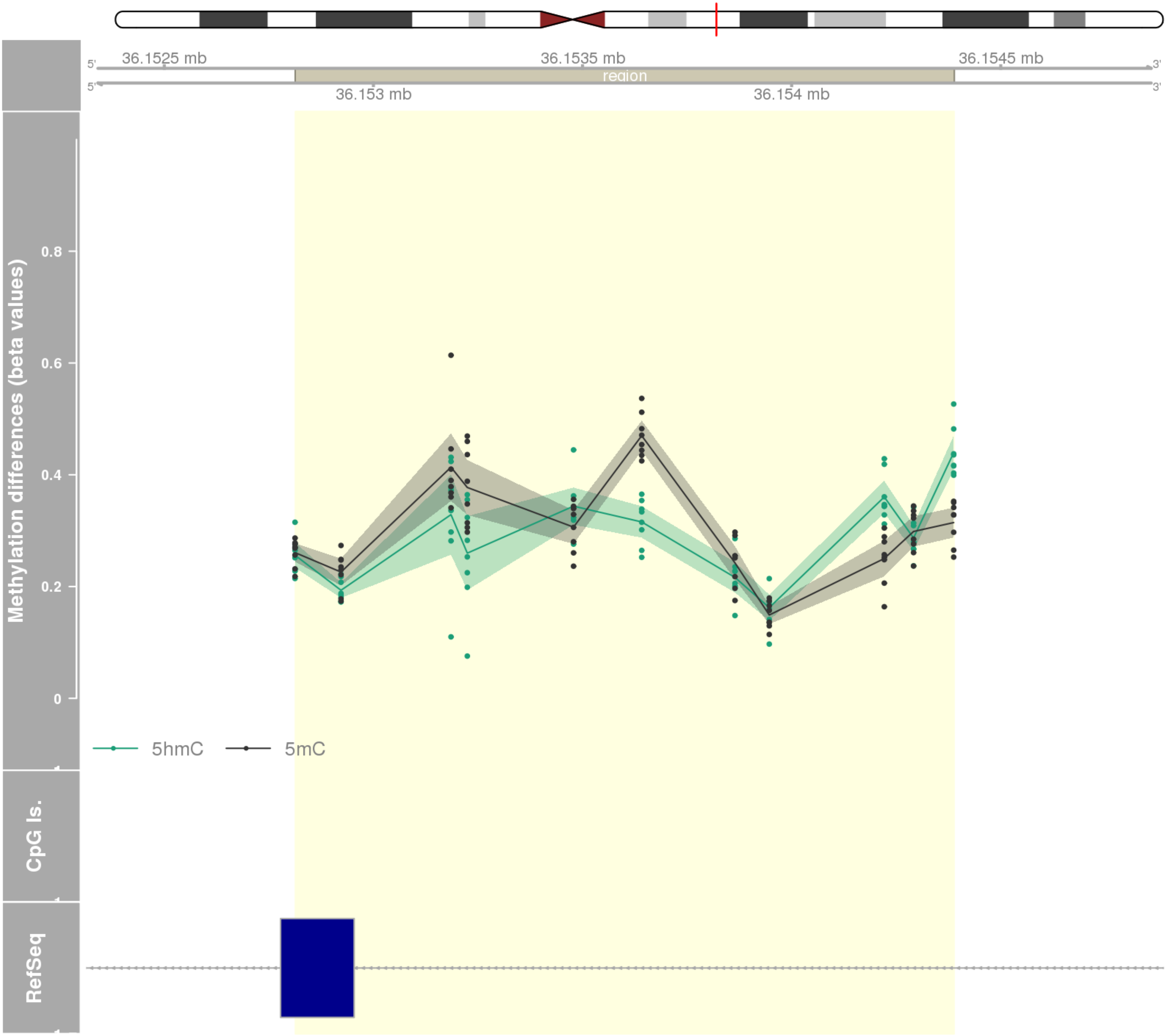
DMR 197 // chr14:104171259-104173299 // 2040 pb. (8 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: XRCC3 -



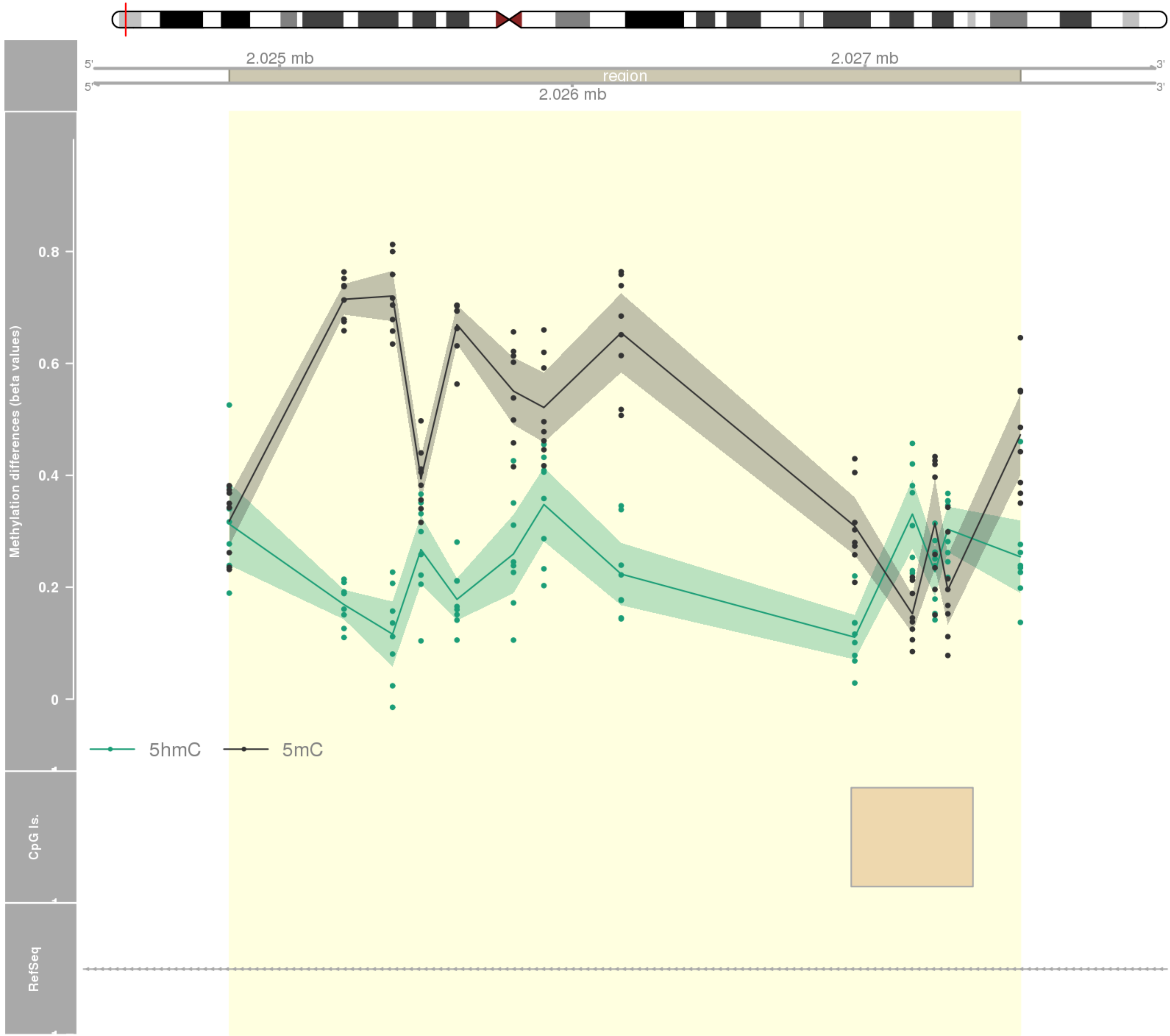
DMR 198 // chr1:1476661-1478680 // 2019 pb. (11 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: SSU72 -



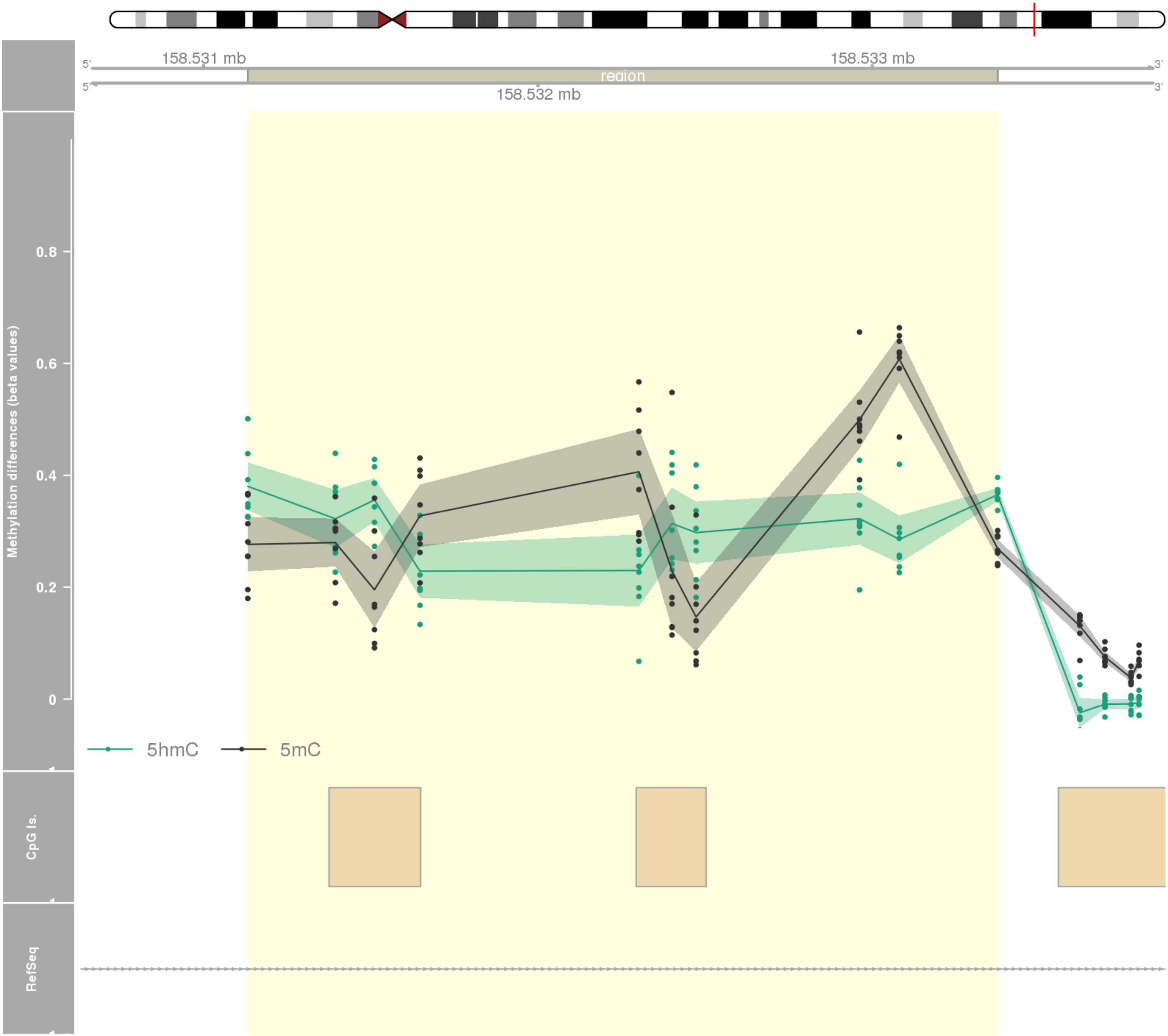
DMR 199 // chr20:36152813-36154388 // 1575 pb. (11 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: BLCAP -



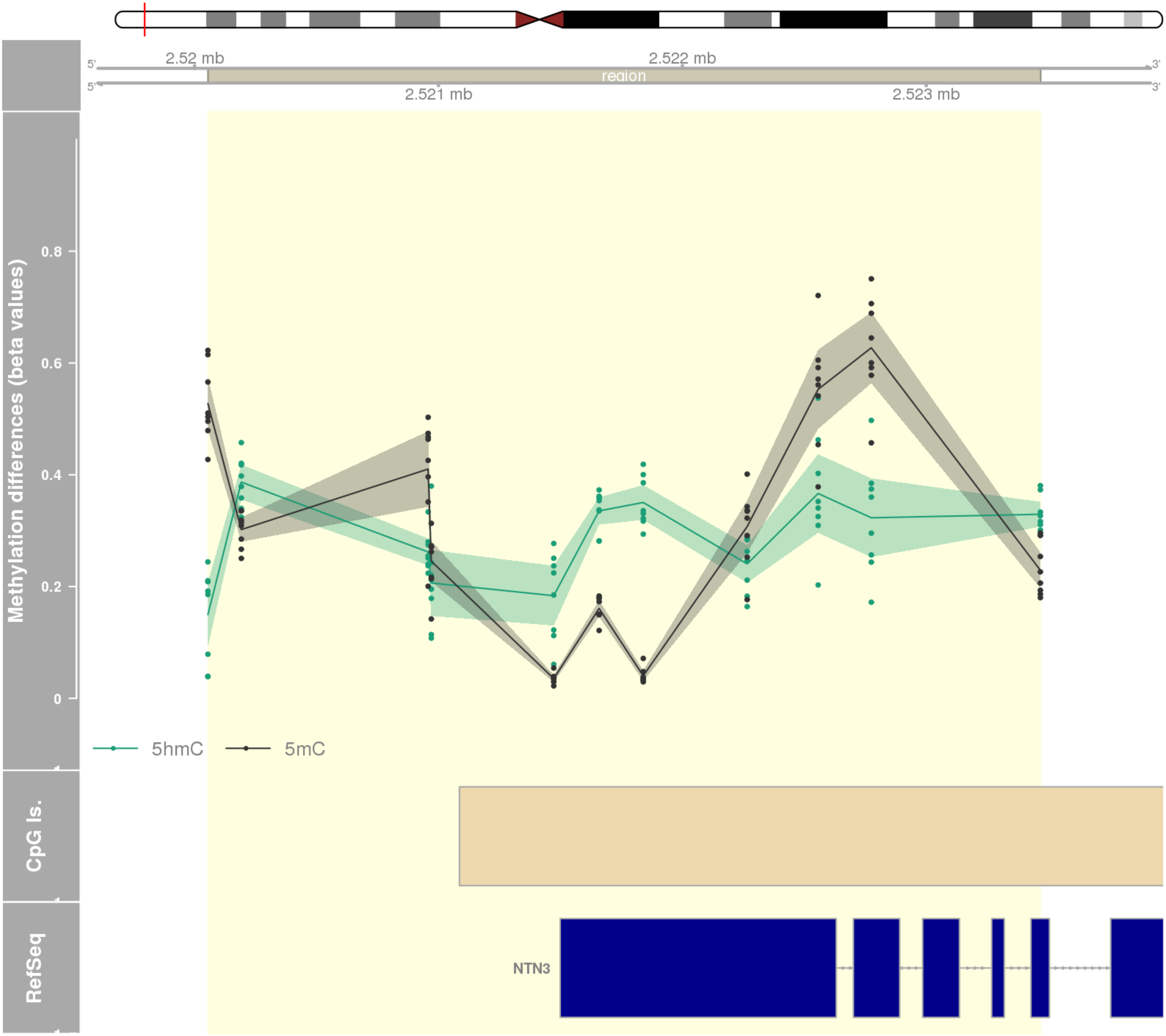
DMR 200 // chr7:2024828-2027531 // 2703 pb. (13 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.01 // fwerArea: 0.559
- genes: MAD1L1 -



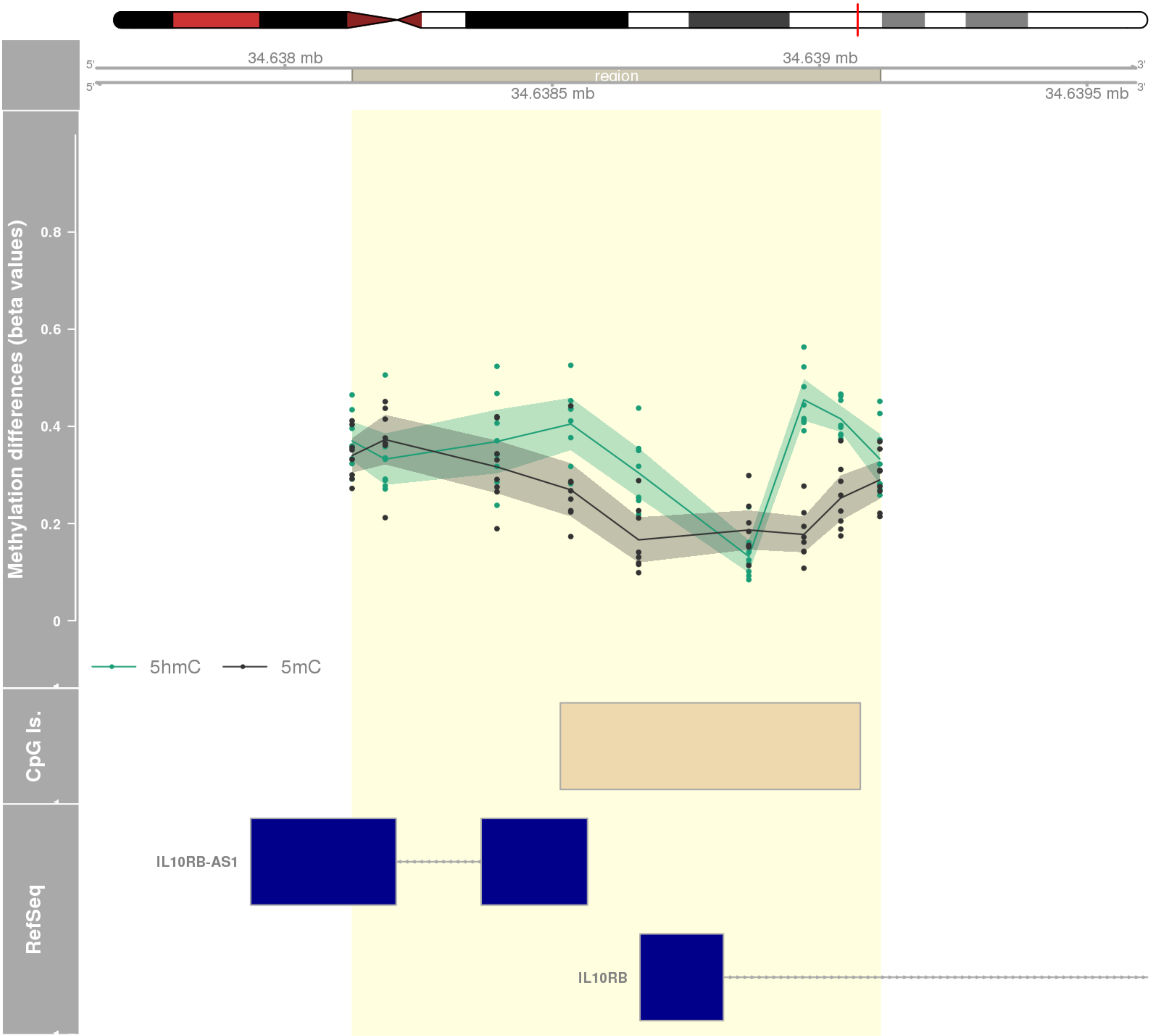
DMR 201 // chr5:158531132-158533375 // 2243 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559



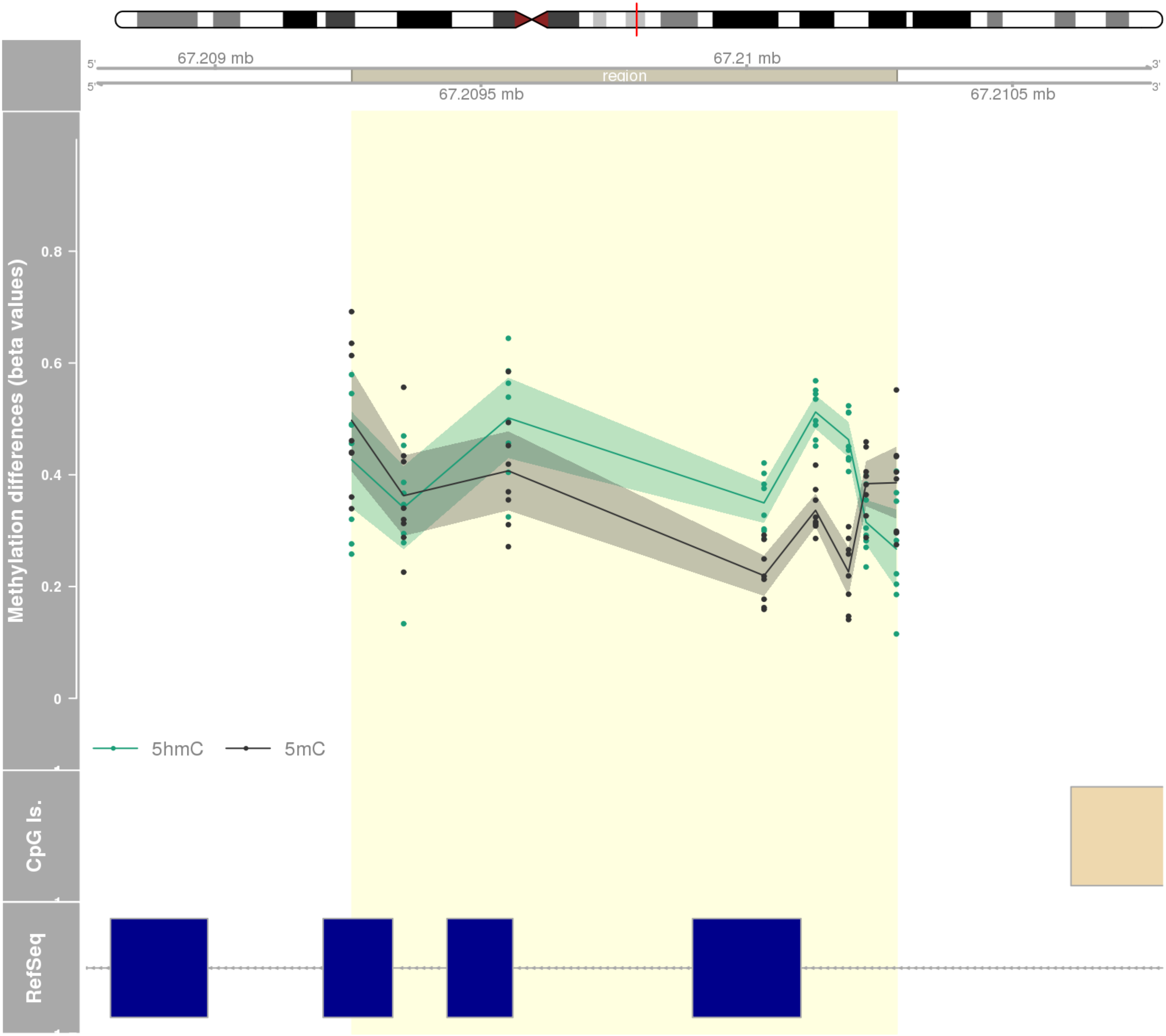
DMR 202 // chr16:2520055-2523468 // 3413 pb. (11 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: NTN3 -



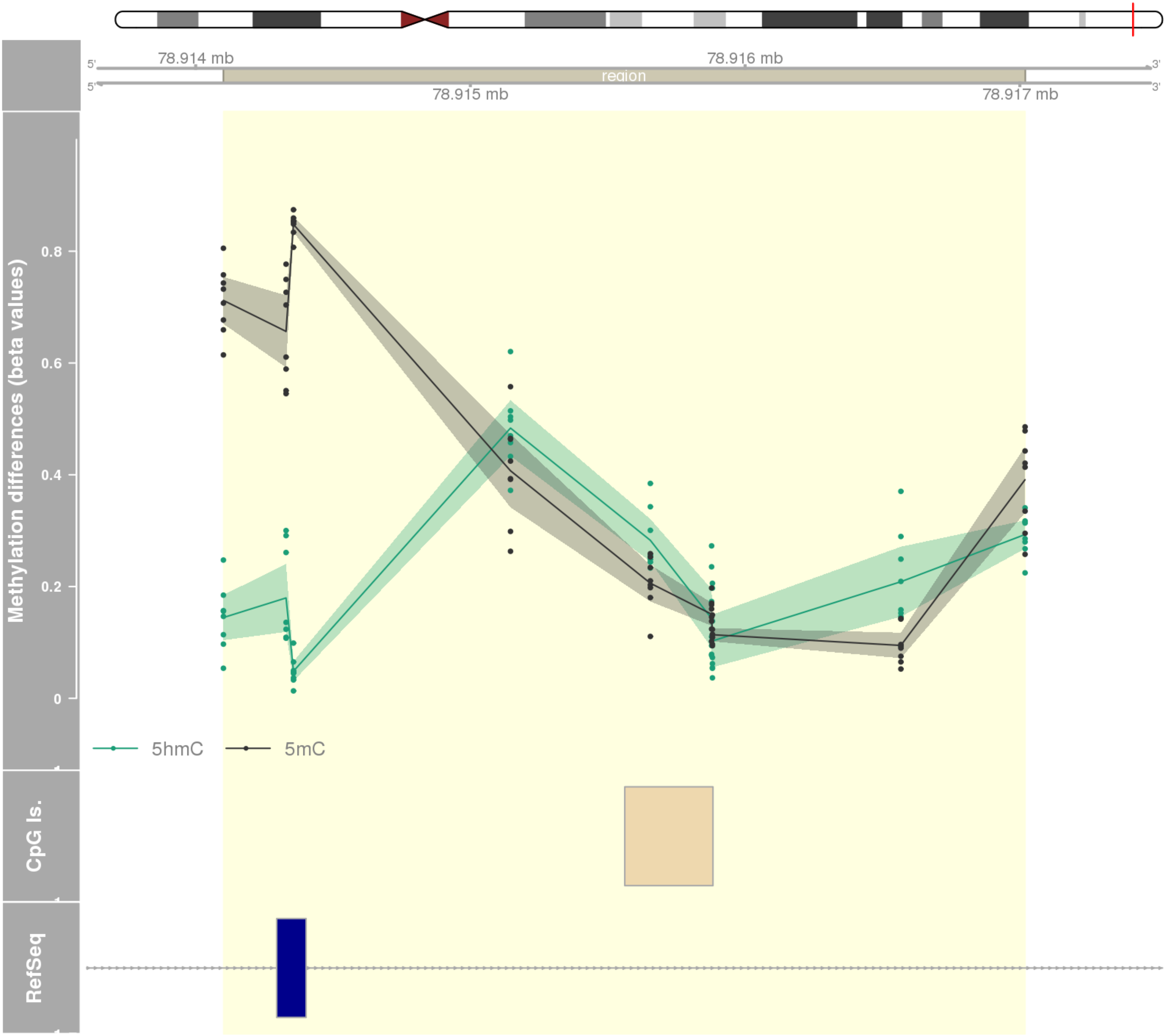
DMR 203 // chr21:34638126-34639113 // 987 pb. (9 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: IL10RB-AS1 / IL10RB -



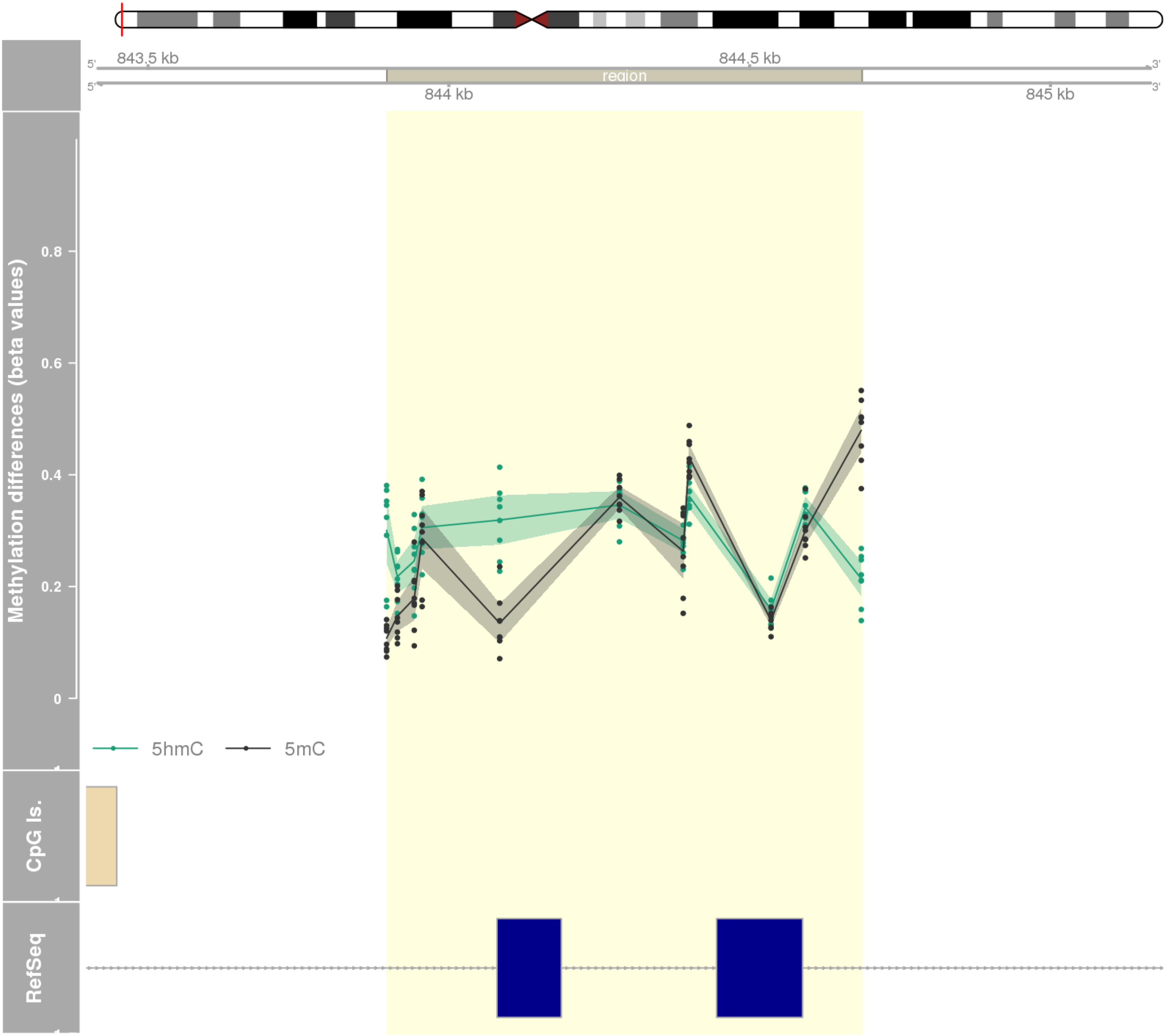
DMR 204 // chr11:67209257-67210282 // 1025 pb. (8 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: CORO1B -



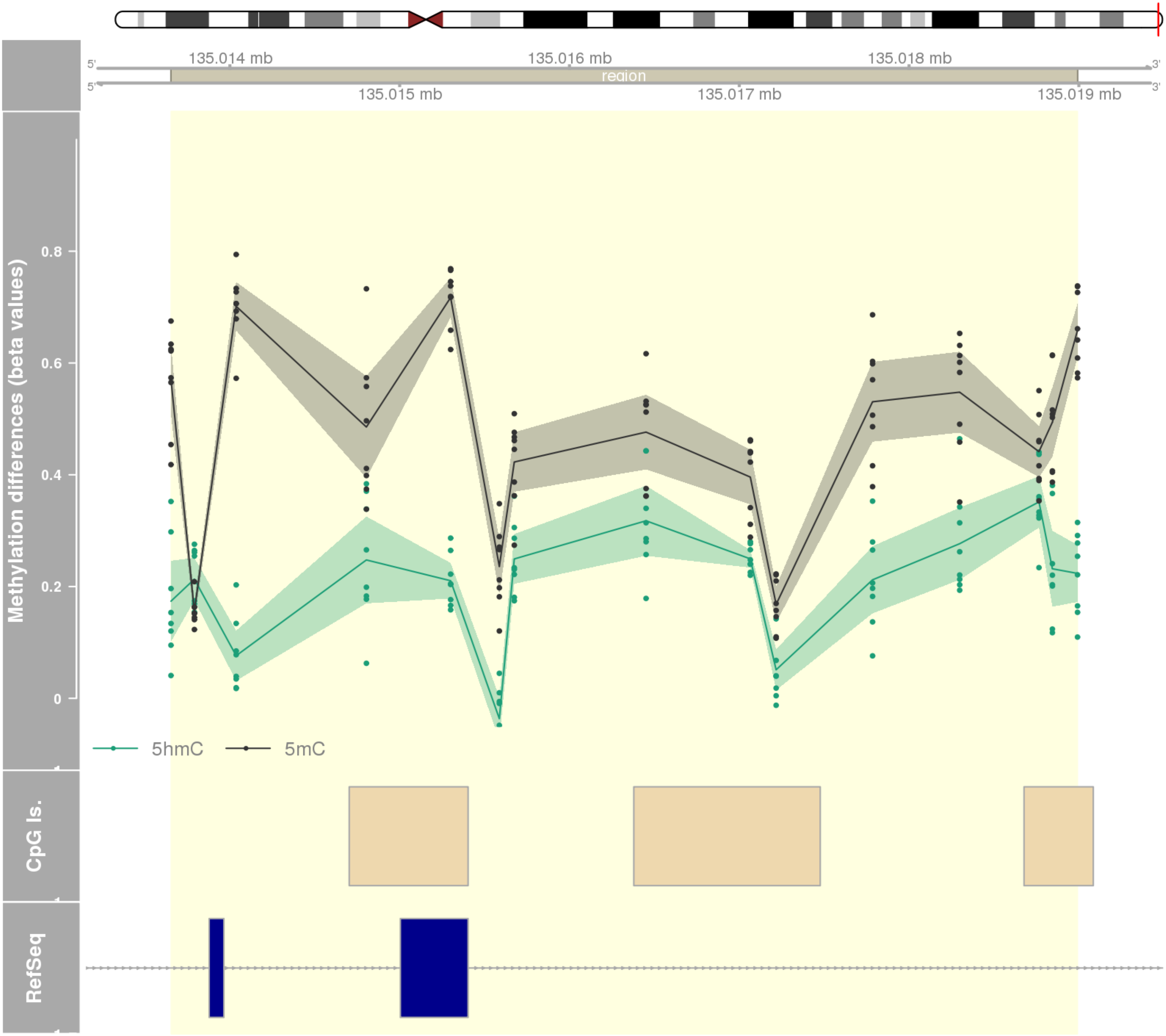
DMR 205 // chr17:78914101-78917019 // 2918 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: RPTOR -



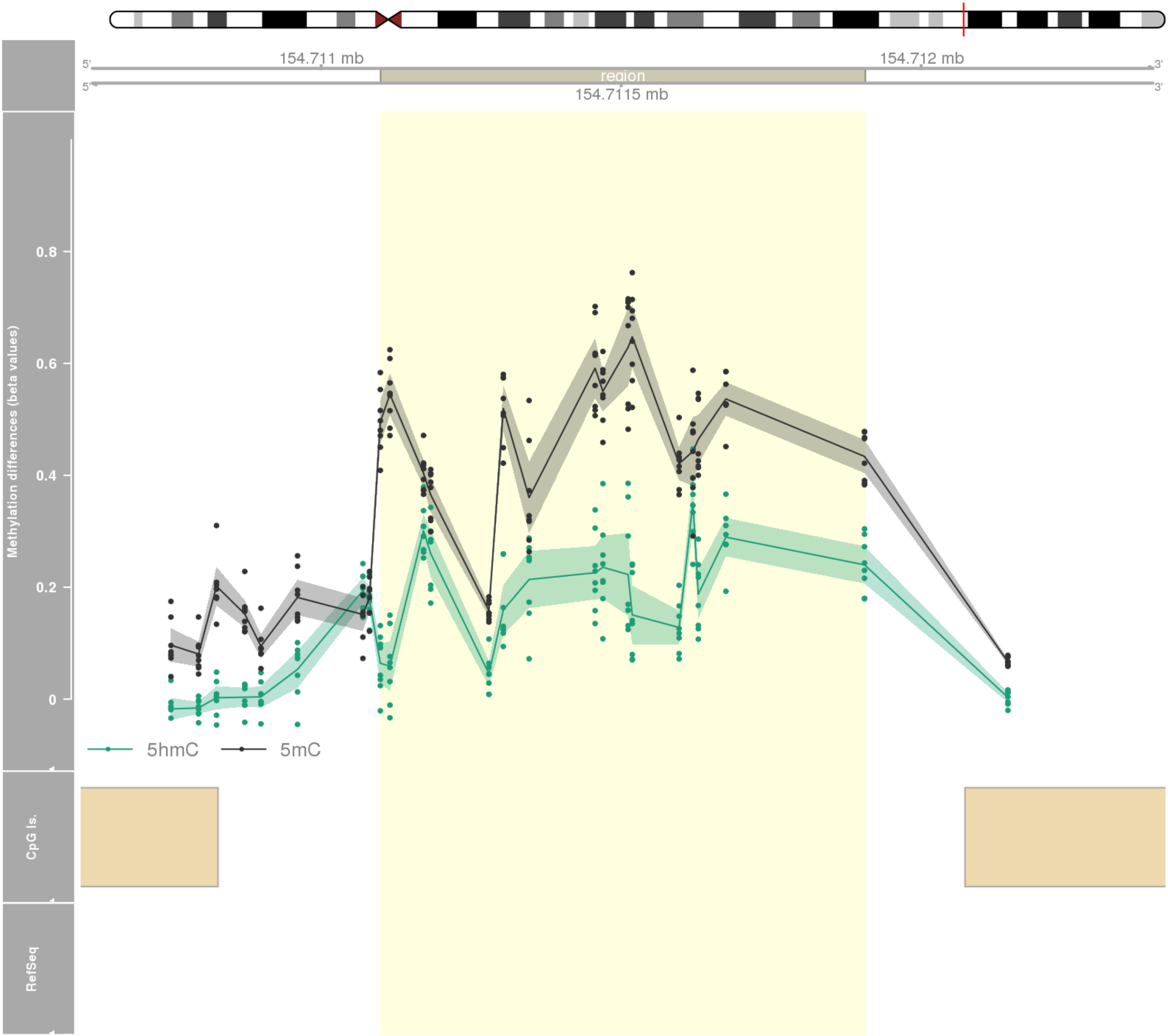
DMR 206 // chr11:843897-844686 // 789 pb. (11 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: TSPAN4 -



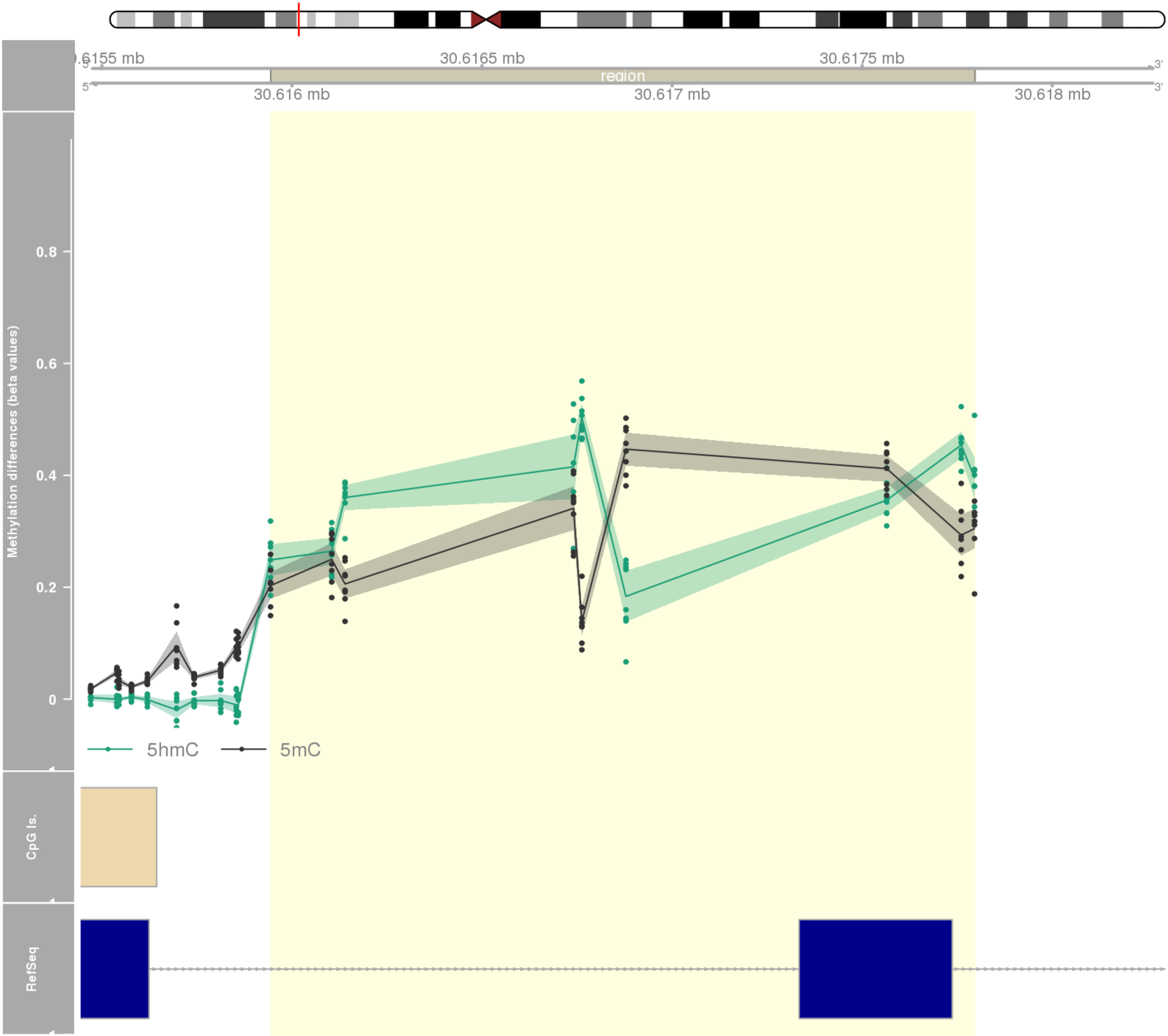
DMR 207 // chr10:135013653-135018992 // 5339 pb. (15 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: KNDC1 -



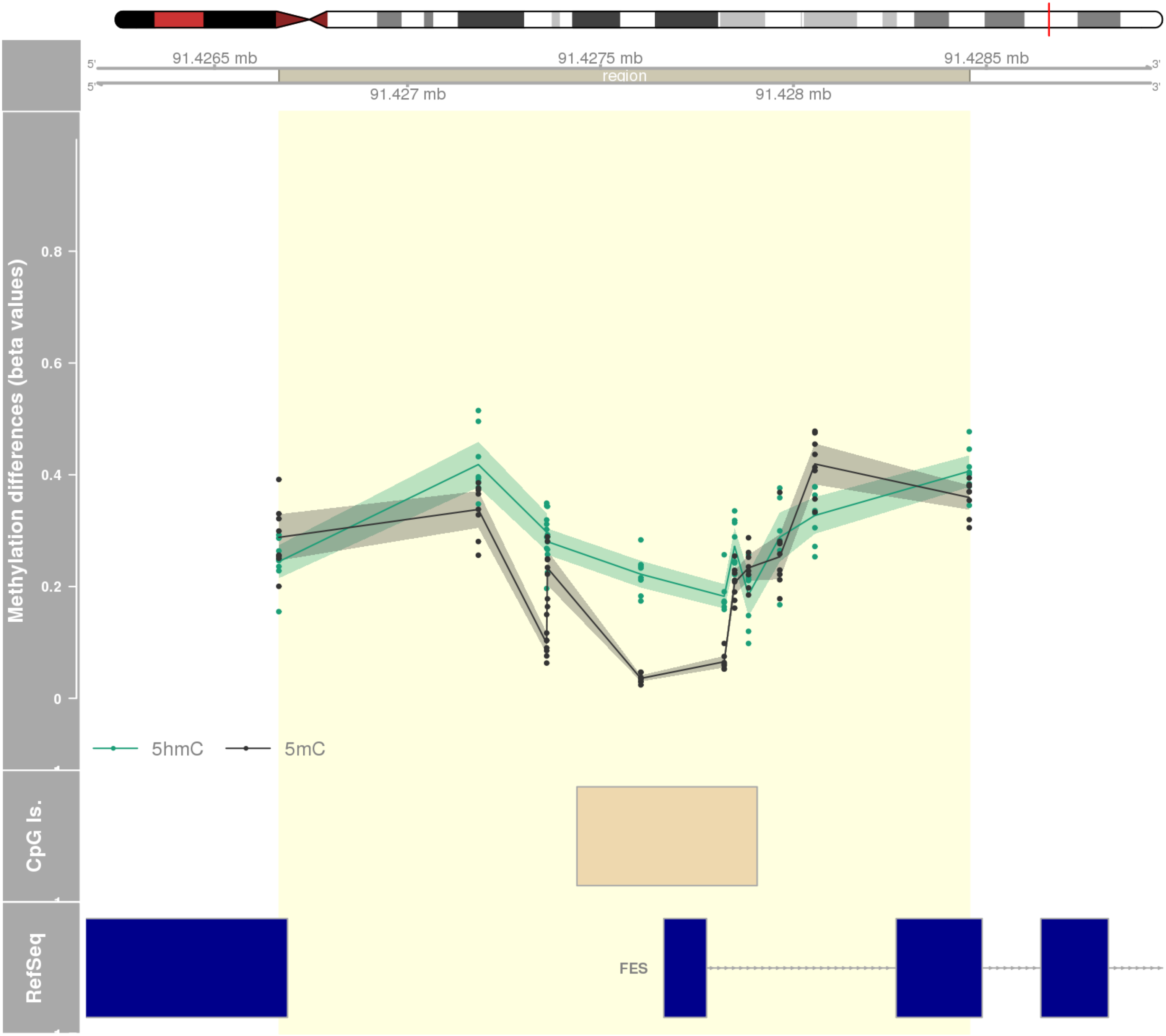
DMR 208 // chr4:154711099-154711906 // 807 pb. (16 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559



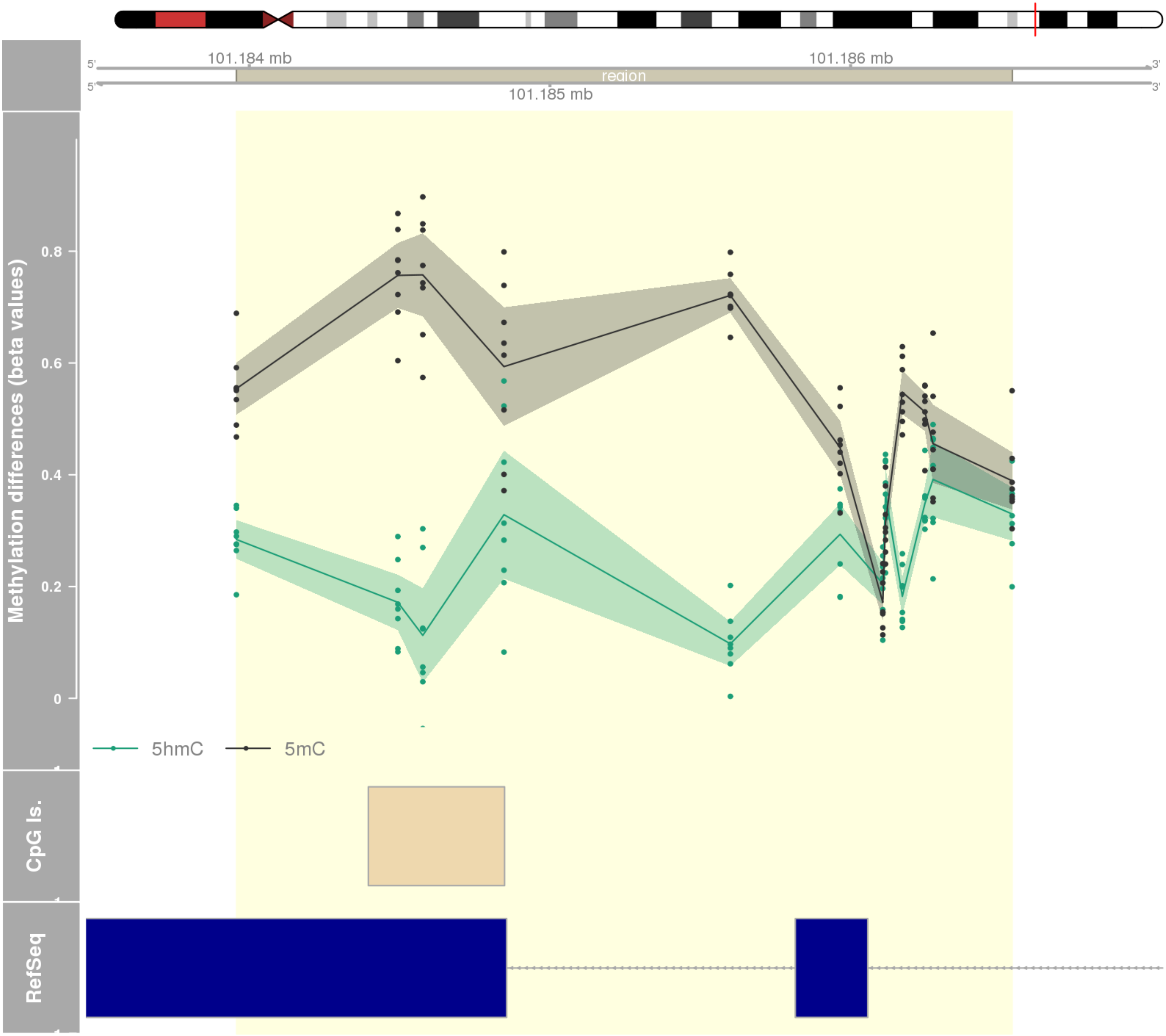
DMR 209 // chr6:30615944-30617796 // 1852 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: C6orf136 -



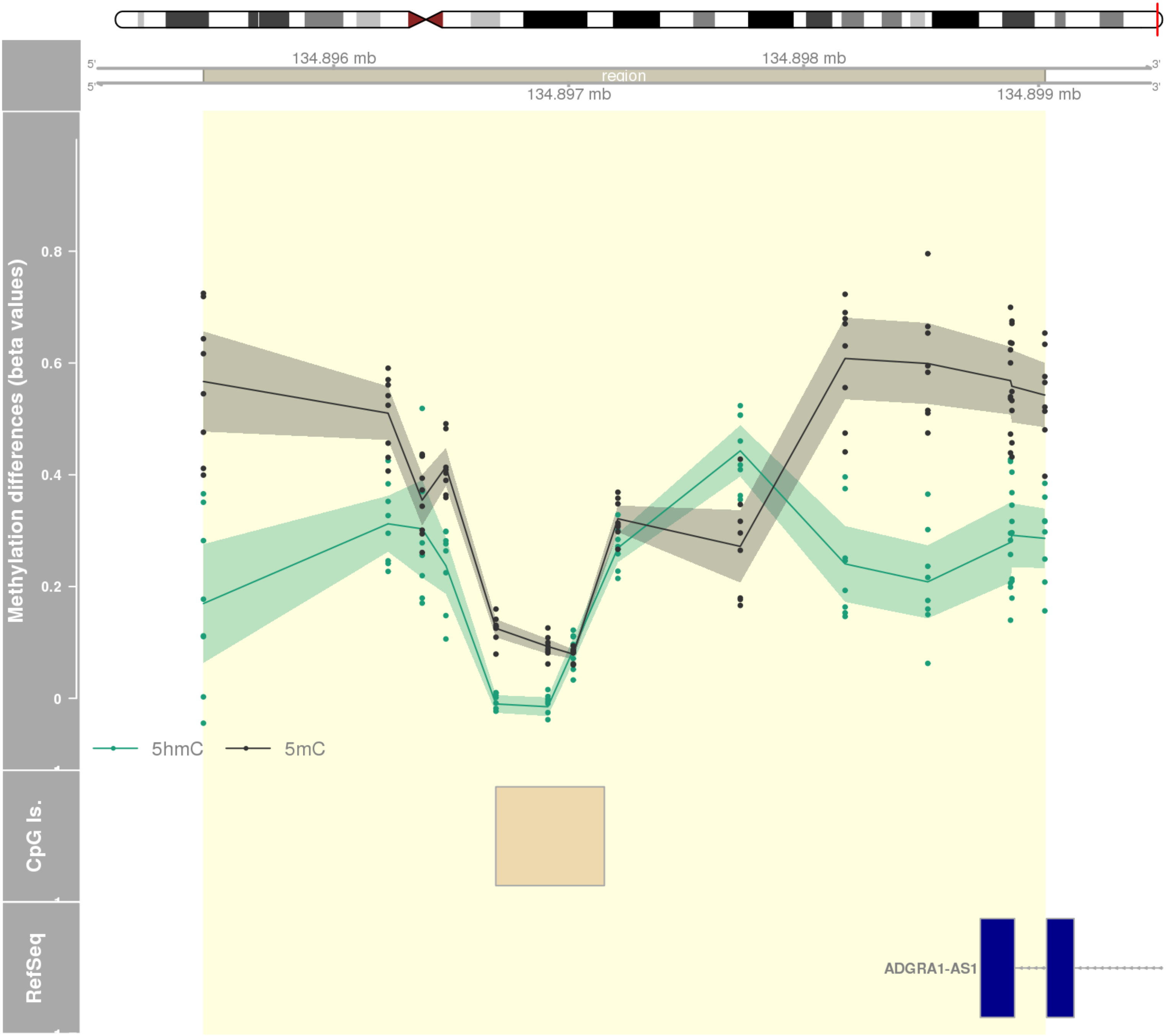
DMR 210 // chr15:91426667-91428456 // 1789 pb. (11 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: FURIN / FES -

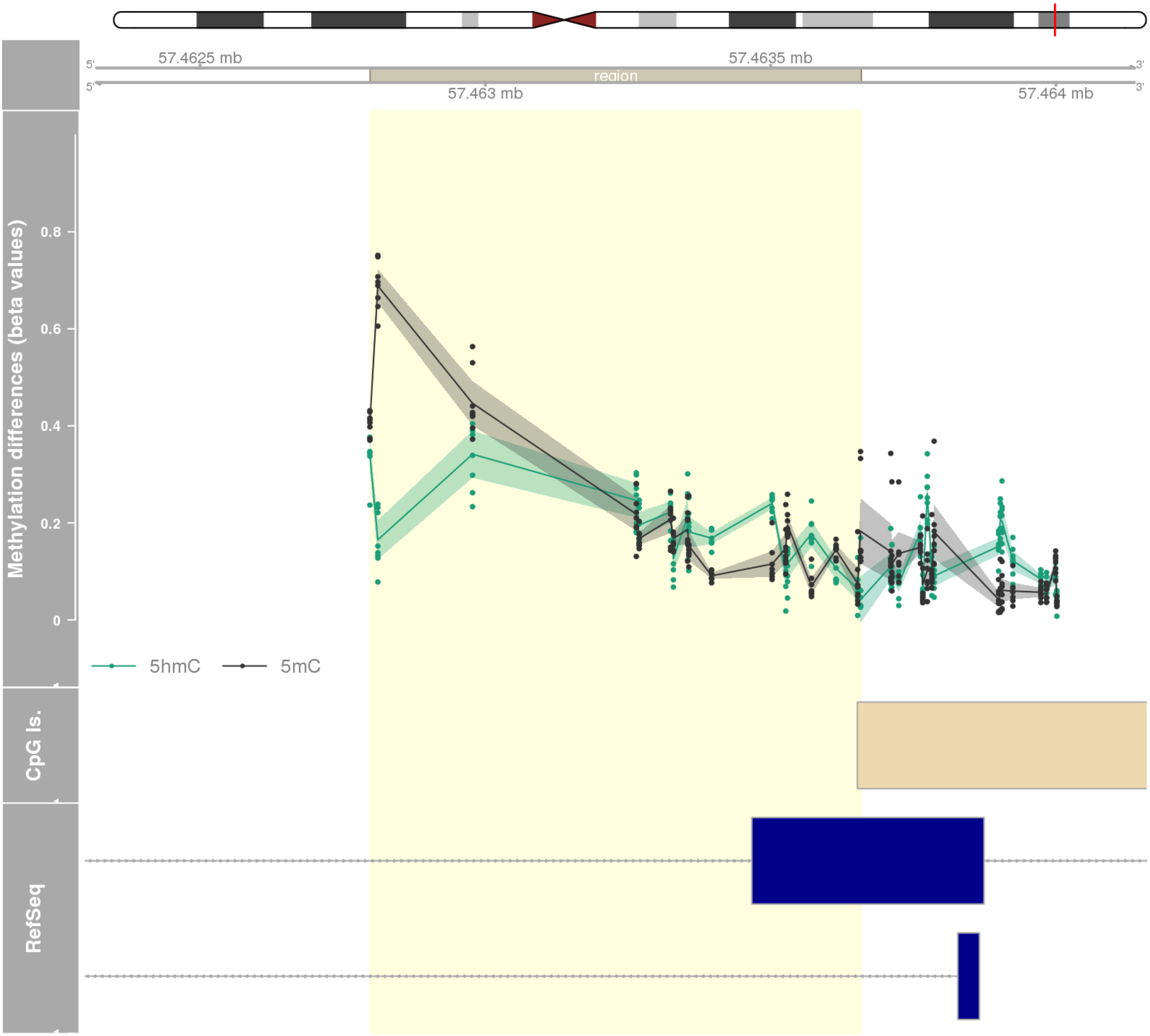


DMR 211 // chr13:101183957-101186537 // 2580 pb. (12 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: GGACT -



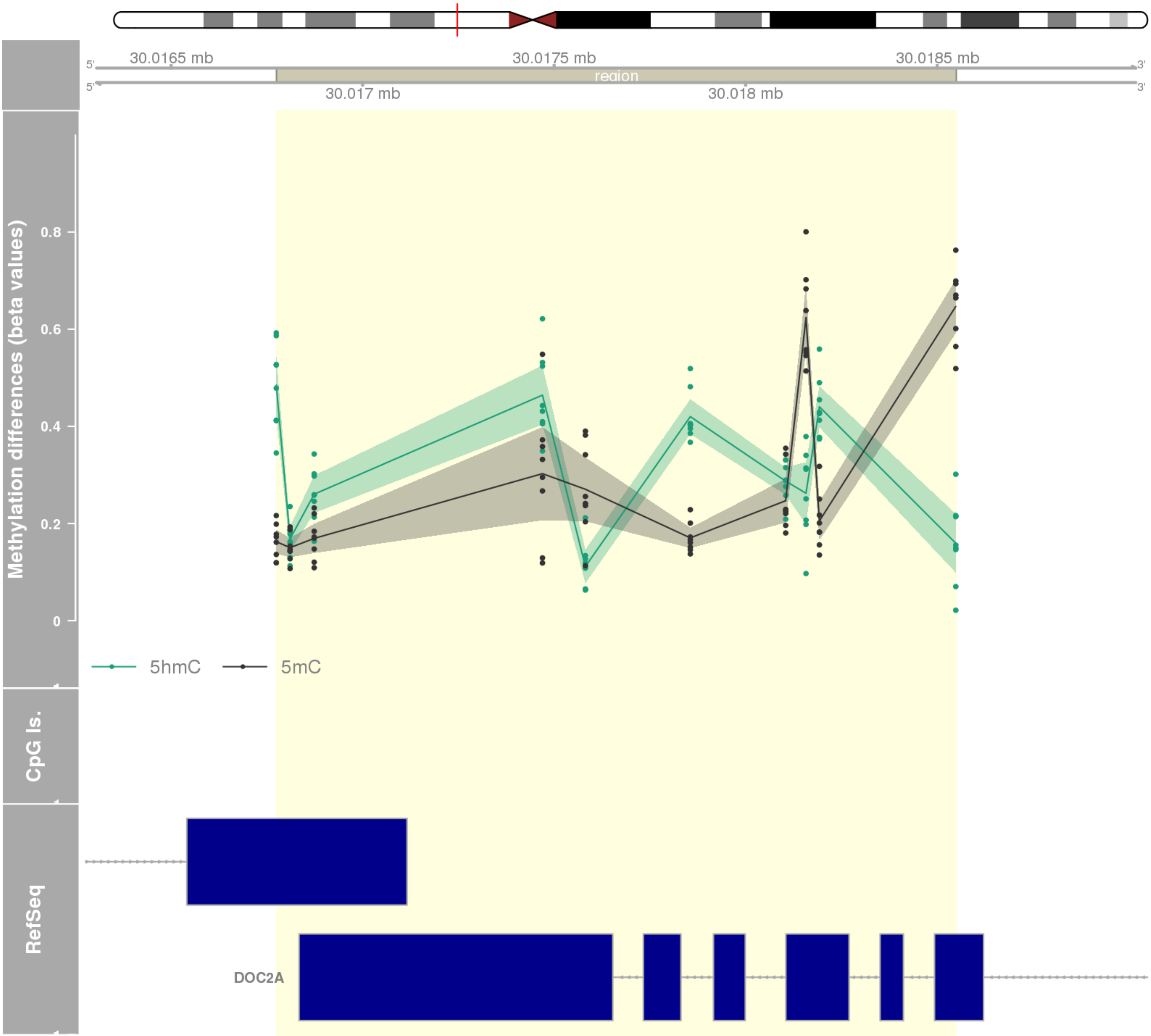
DMR 212 // chr10:134895446-134899027 // 3581 pb. (14 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: GPR123-AS1 / GPR123 -



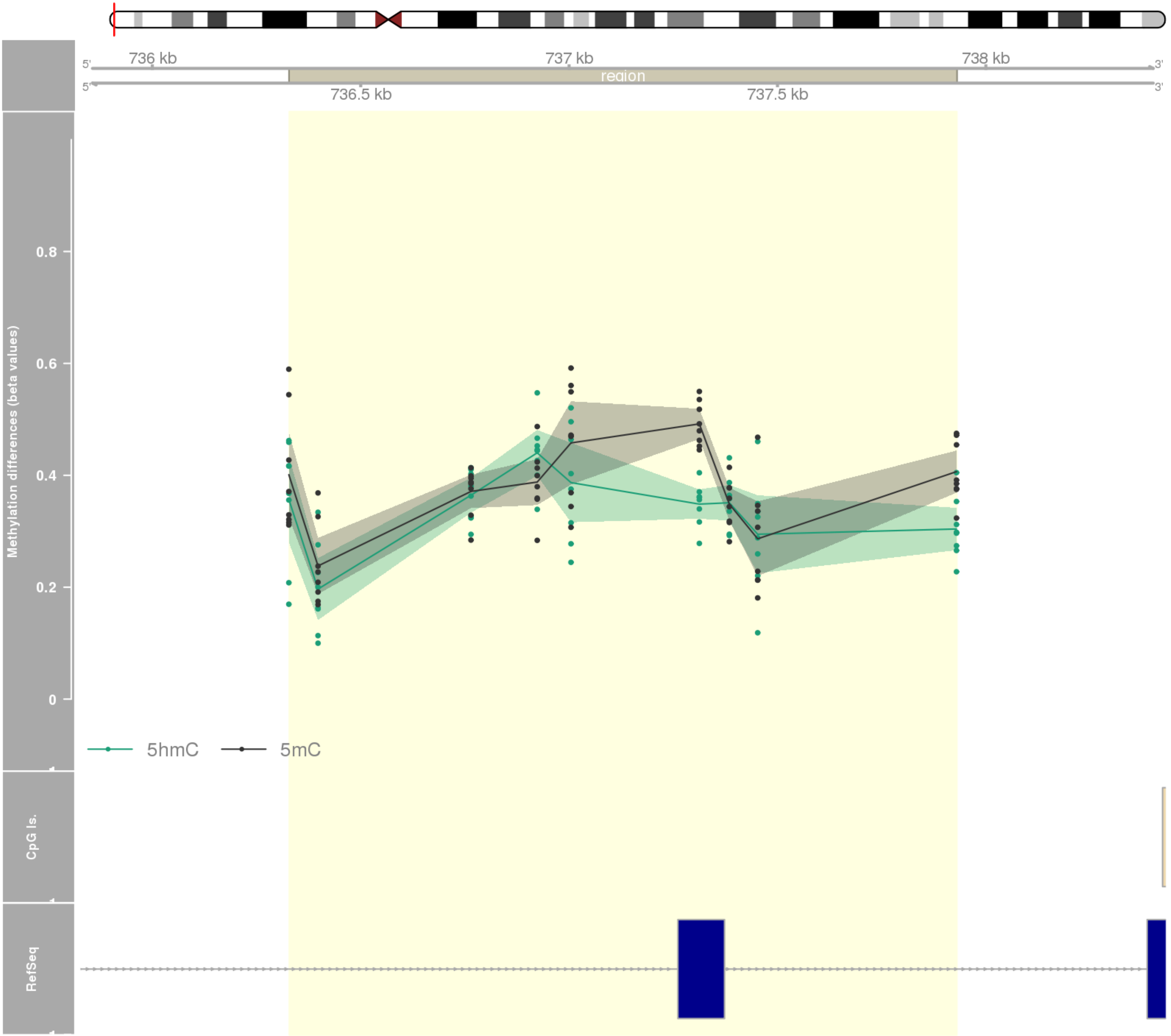


DMR 213 // chr20:57462798-57463658 // 860 pb. (17 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: GNAS -

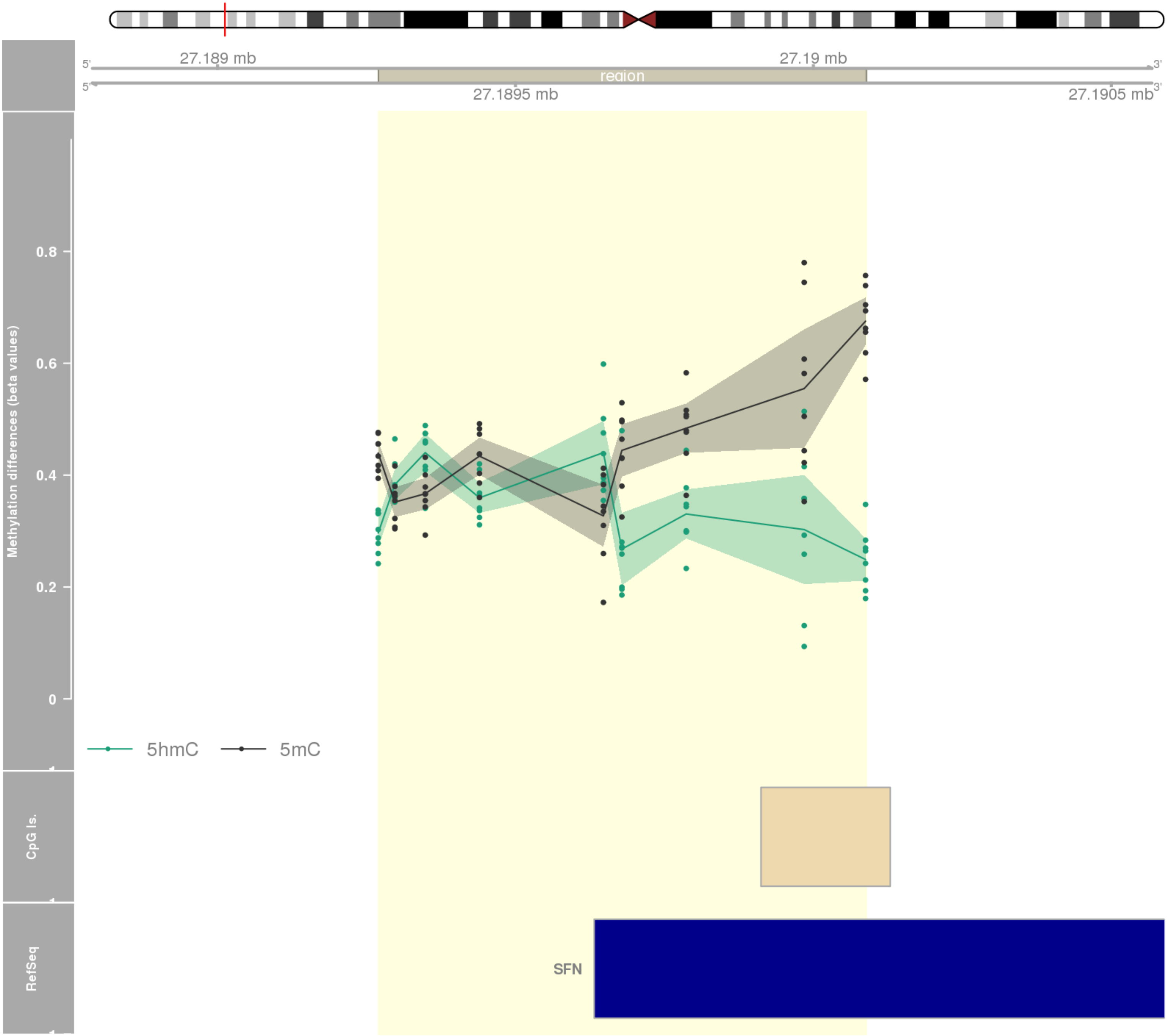
DMR 214 // chr16:30016775-30018549 // 1774 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: INO80E / DOC2A -



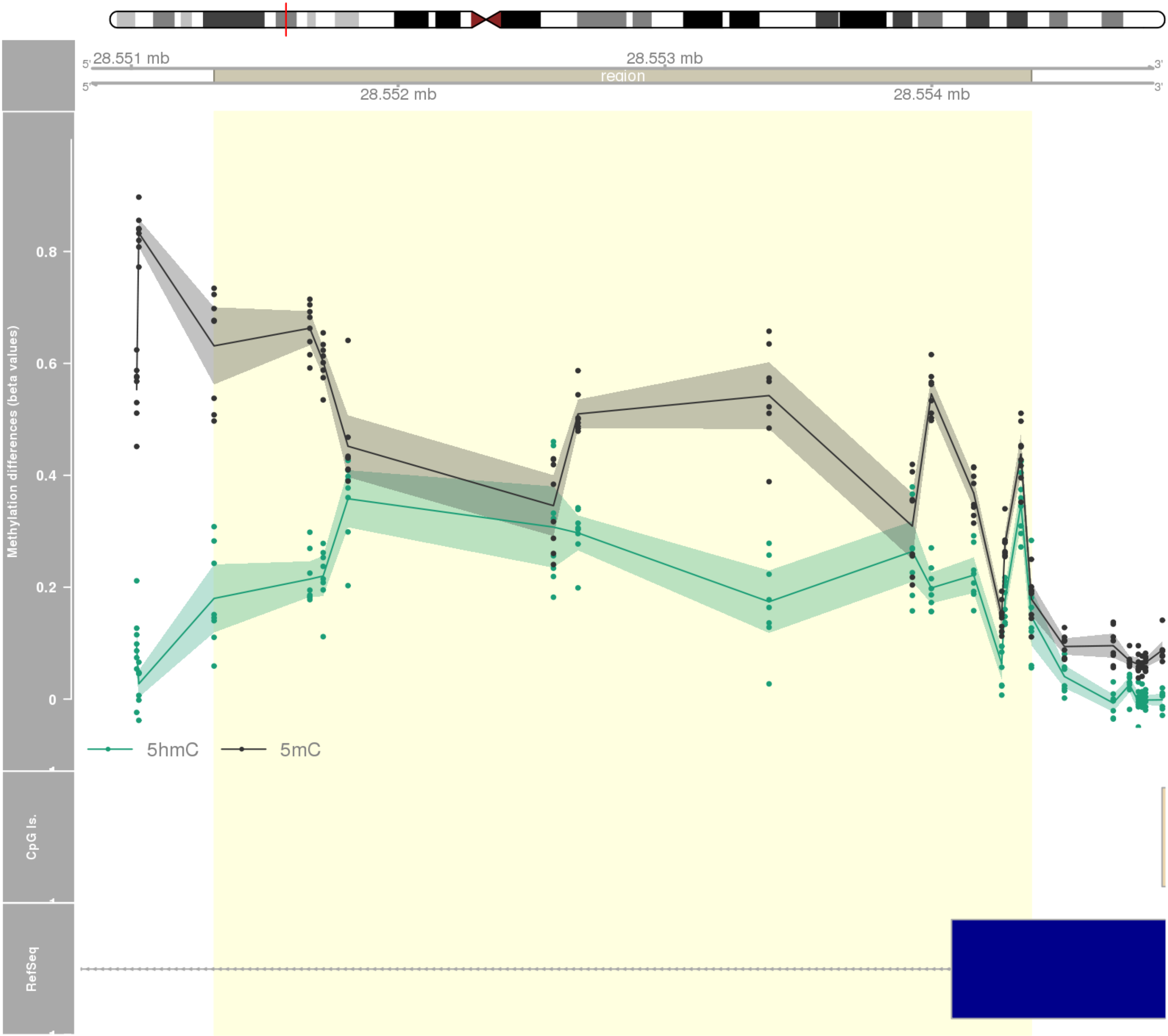
DMR 215 // chr4:736328-737930 // 1602 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: PCGF3 -



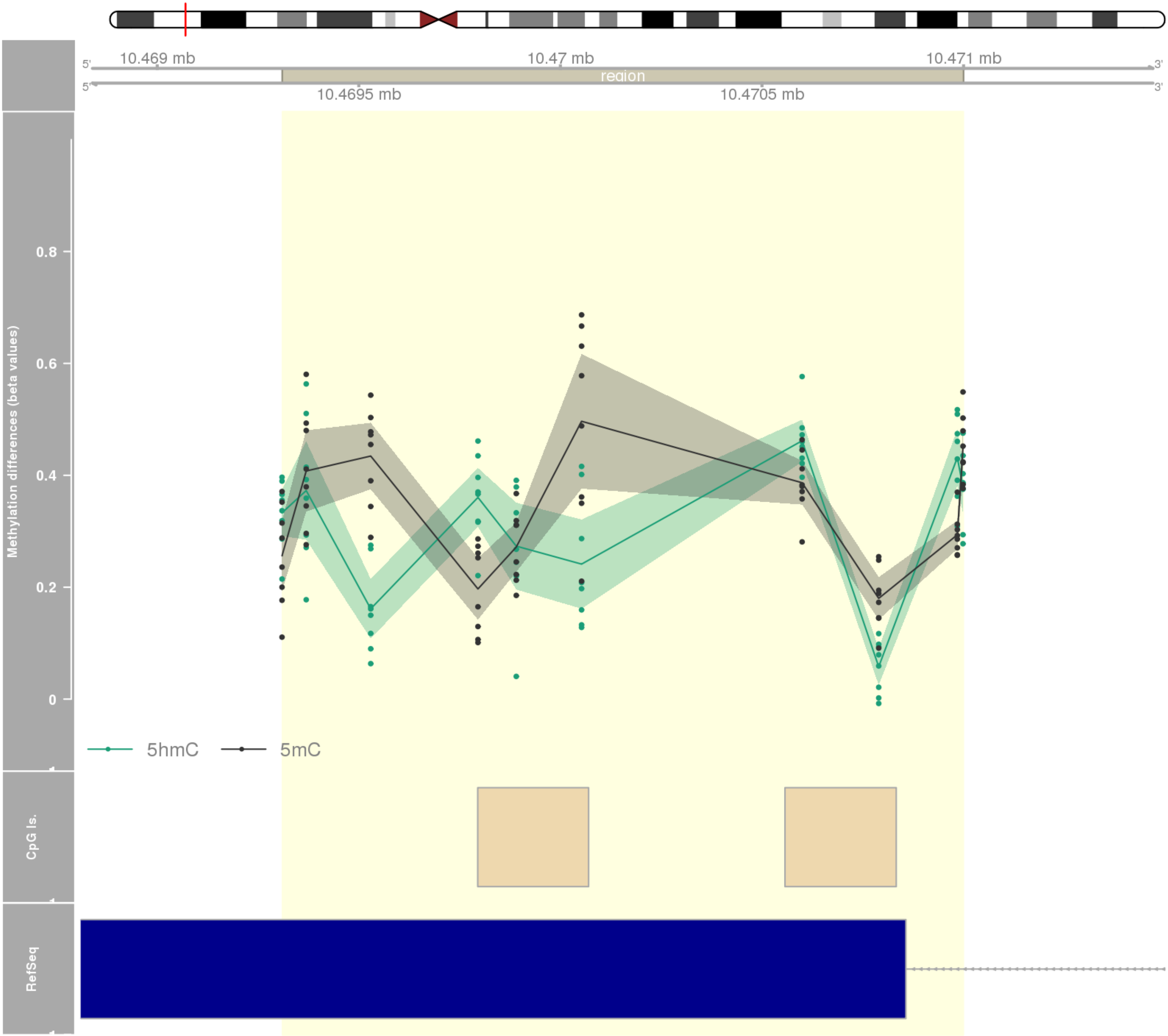
DMR 216 // chr1:27189270-27190088 // 818 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: SFN -



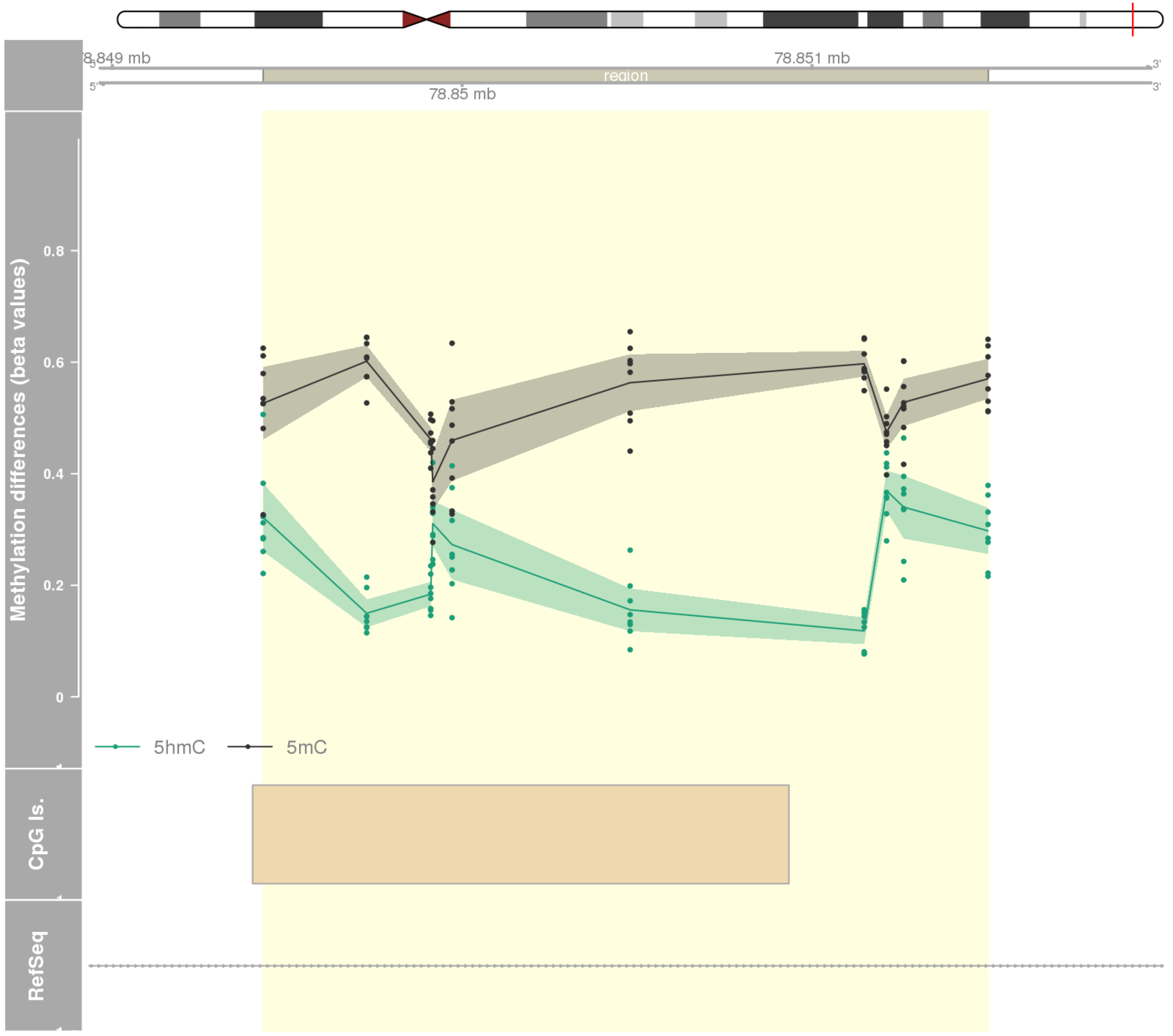
DMR 217 // chr6:28551310-28554373 // 3063 pb. (14 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: SCAND3 -



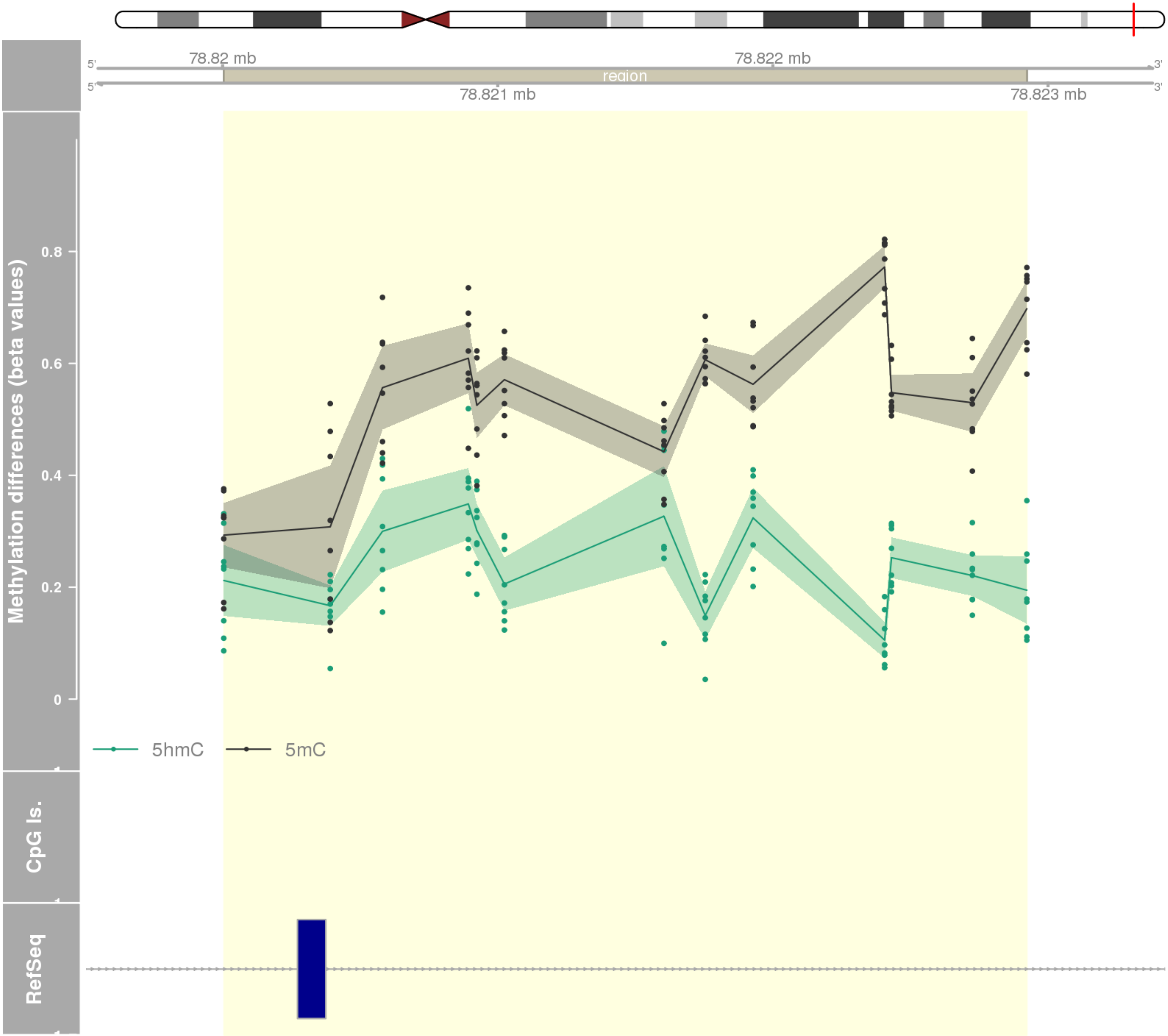
DMR 218 // chr8:10469310-10470999 // 1689 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: RP1L1 -



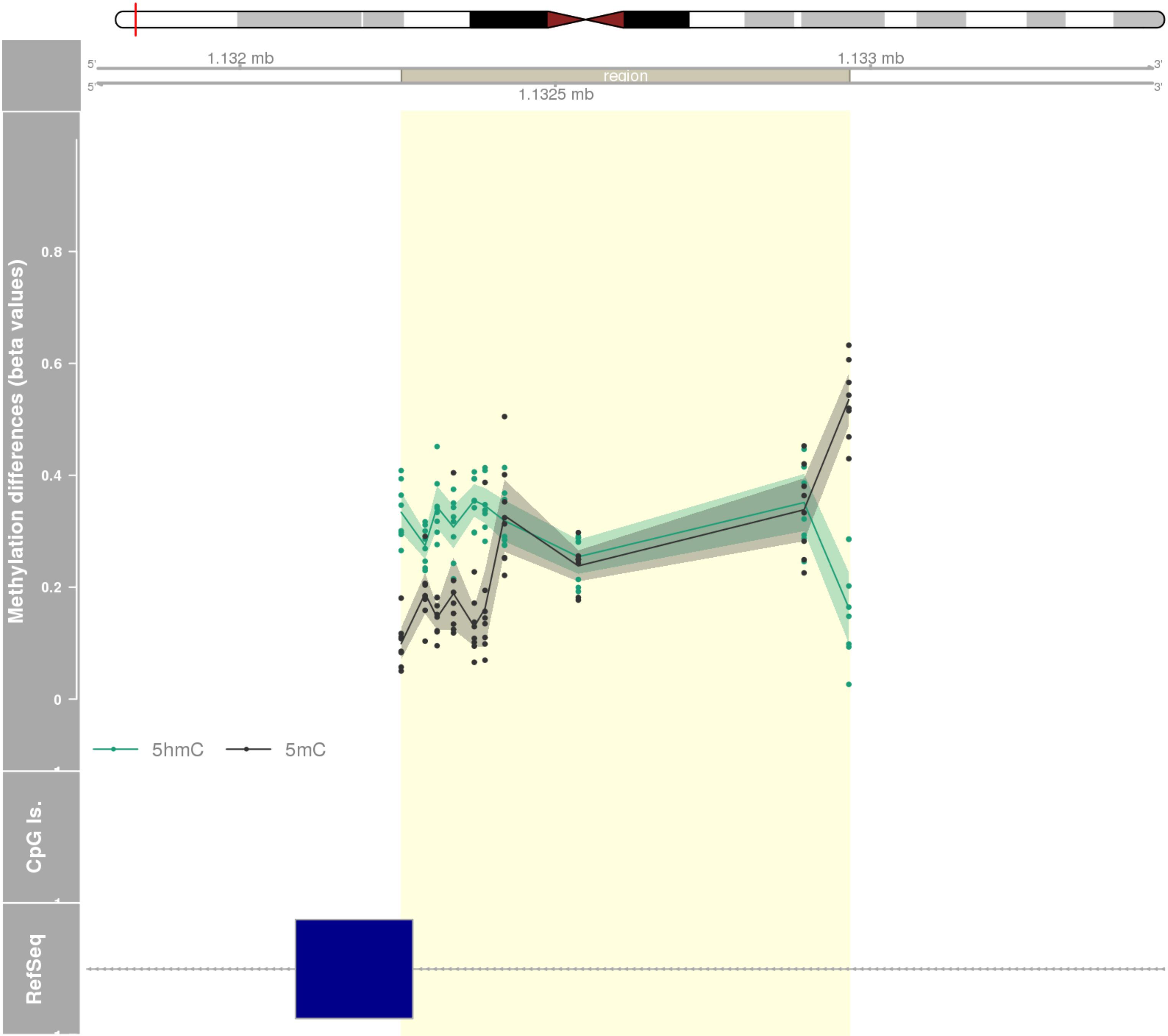
DMR 219 // chr17:78849431-78851503 // 2072 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: RPTOR -



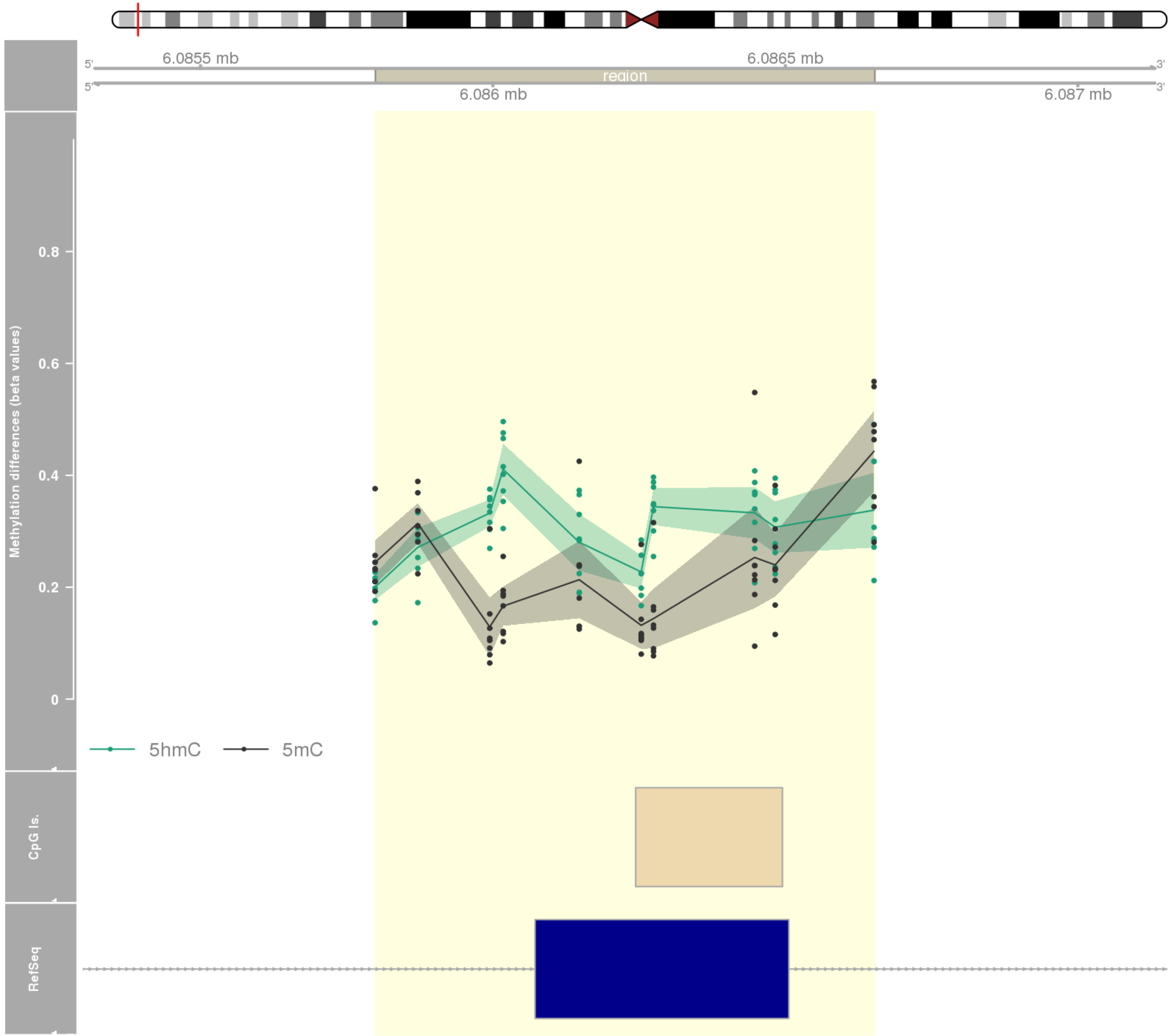
DMR 220 // chr17:78820004-78822923 // 2919 pb. (13 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.011 // fwerArea: 0.559
- genes: RPTOR -



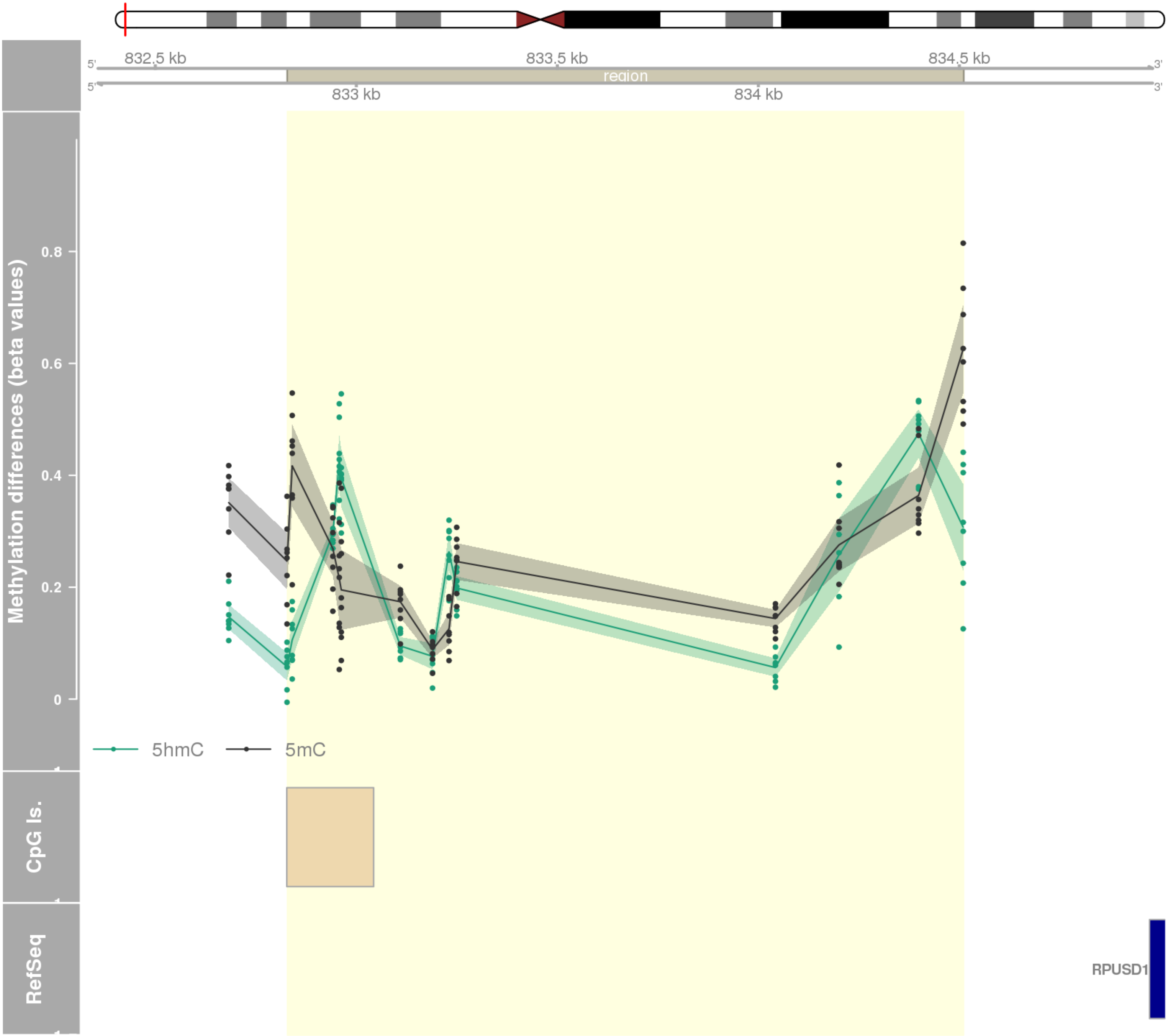
DMR 221 // chr19:1132256-1132966 // 710 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: SBNO2 -



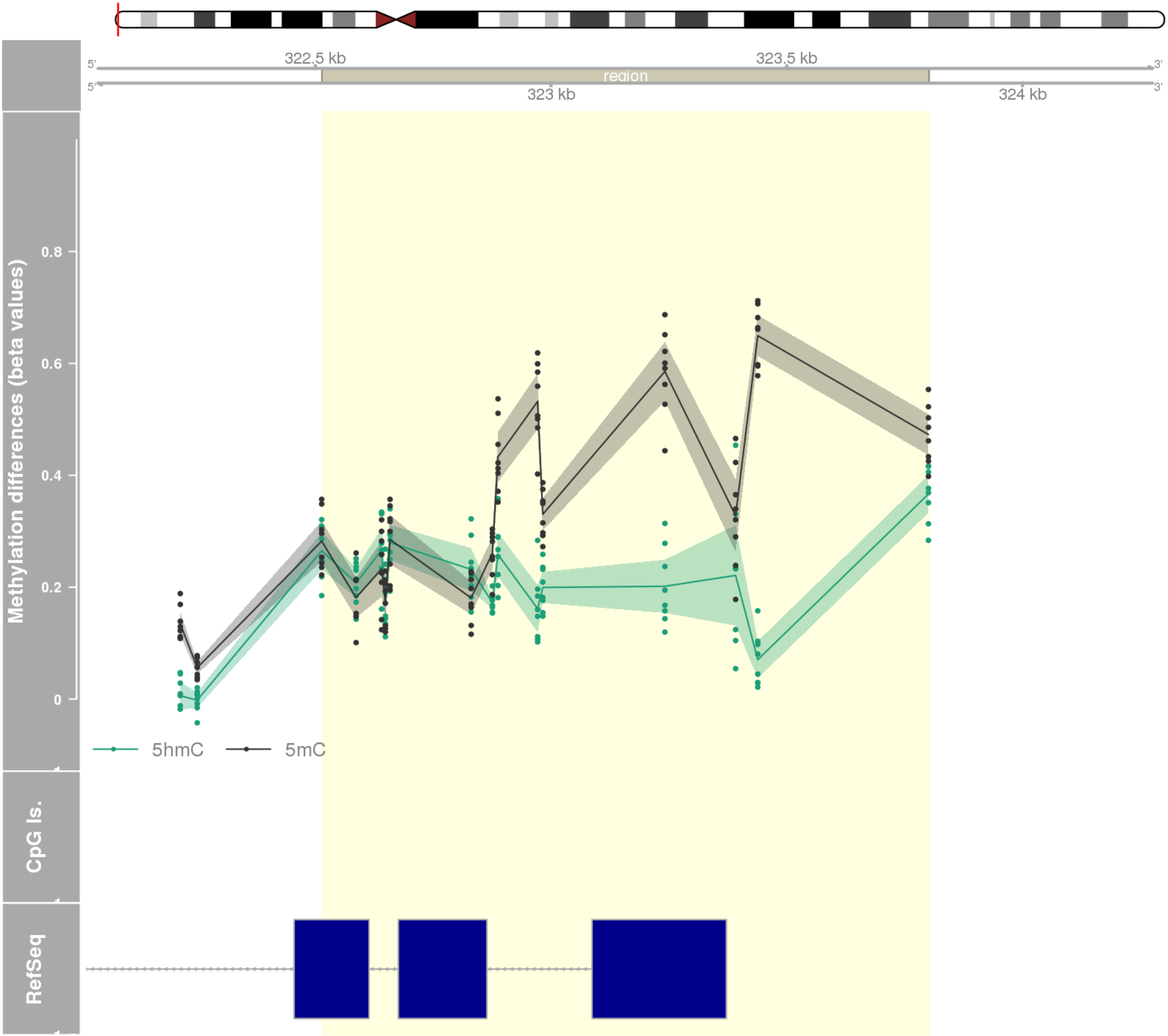
DMR 222 // chr1:6085799-6086652 // 853 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: KCNAB2 -



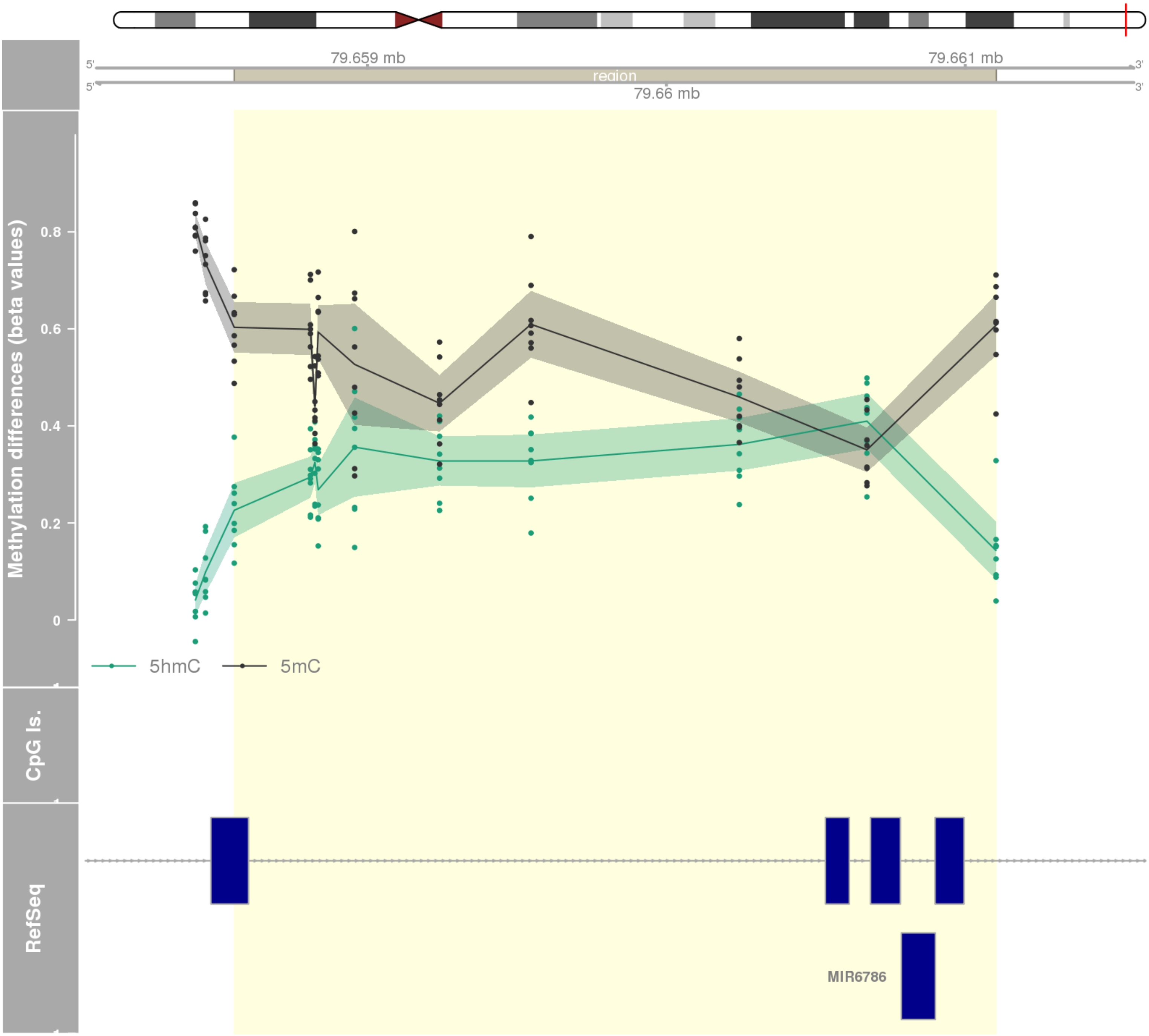
DMR 223 // chr16:832828-834510 // 1682 pb. (13 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: MSLNL -



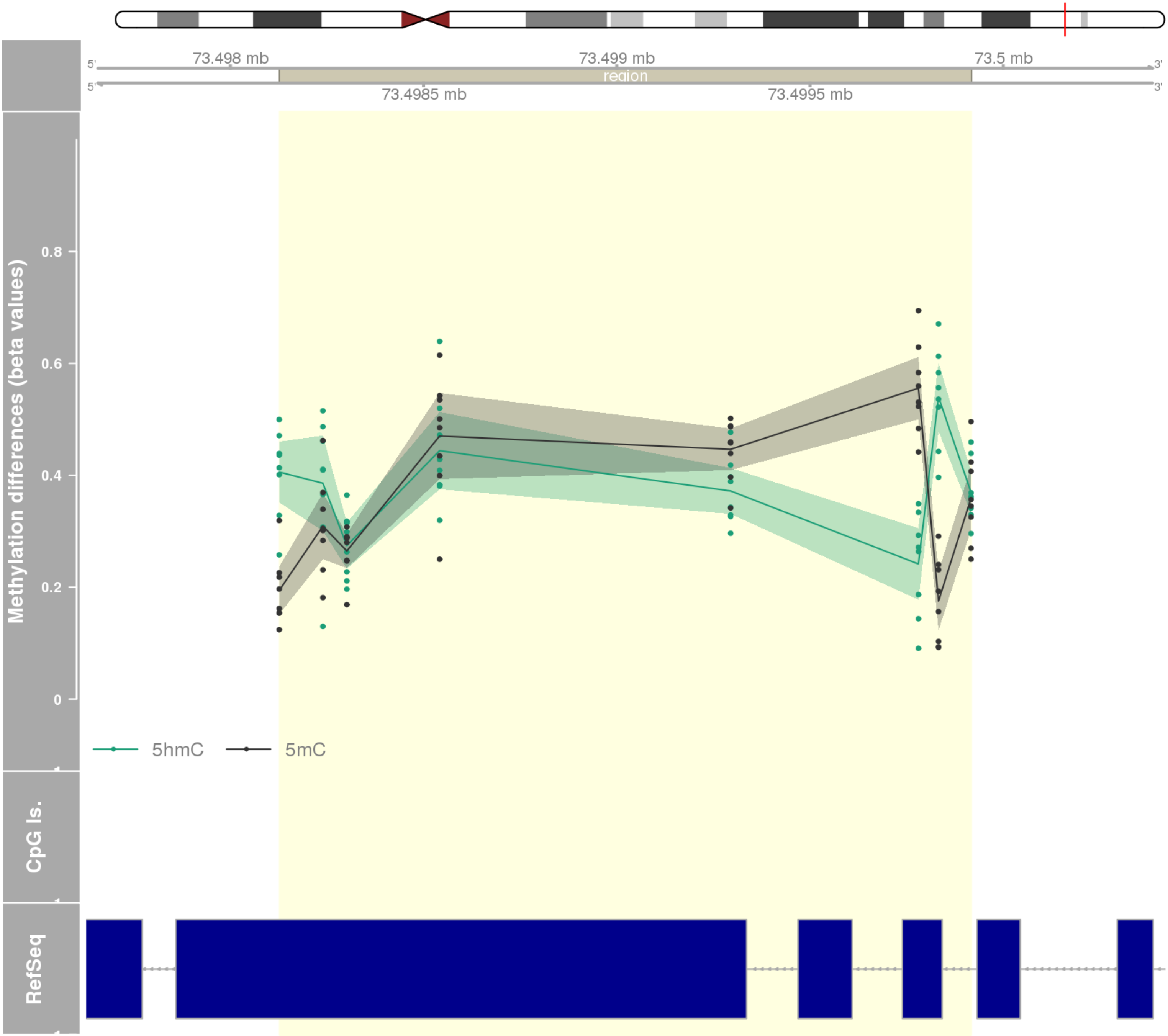
DMR 224 // chr12:322514-323801 // 1287 pb. (14 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: SLC6A12 -



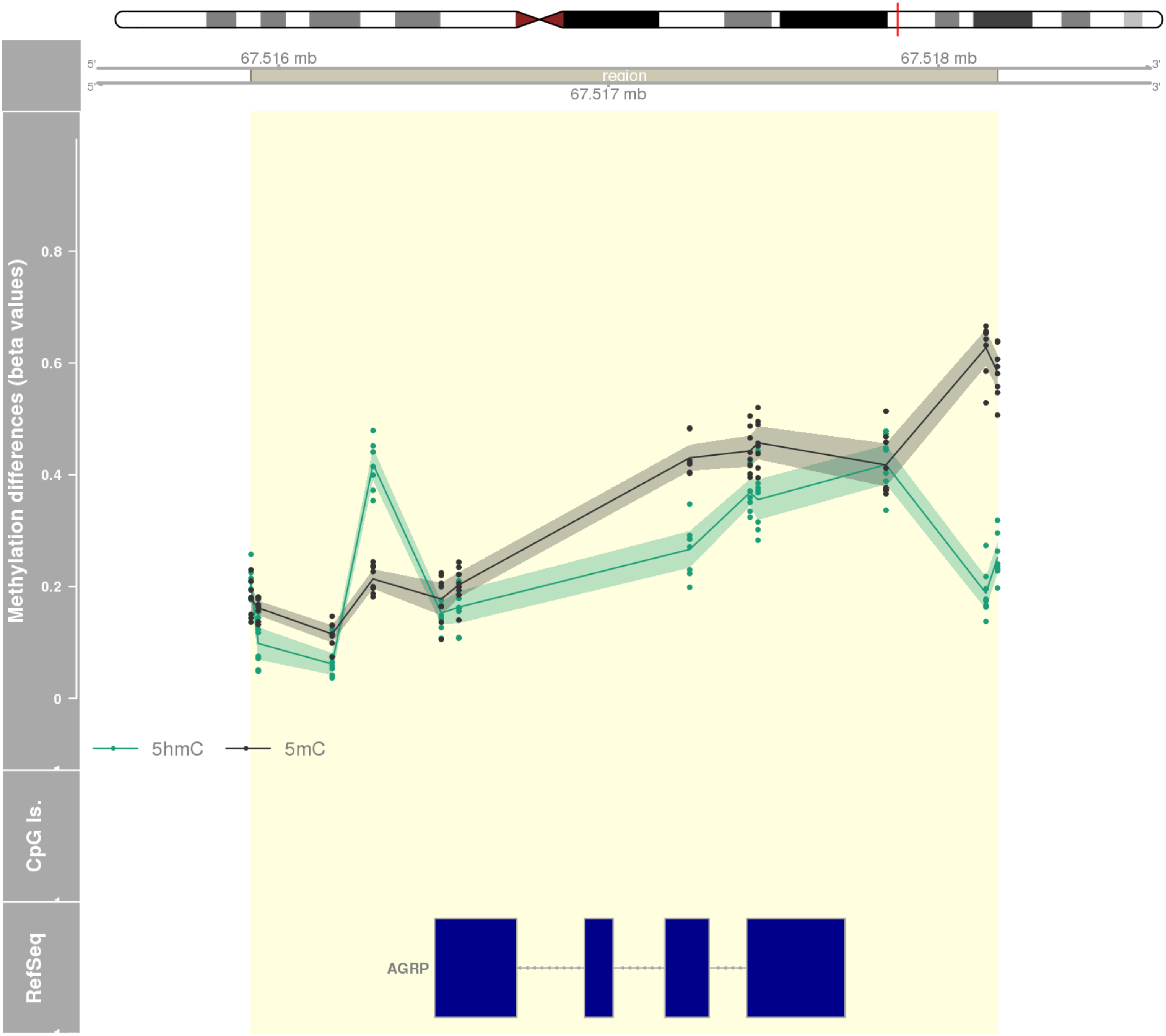
DMR 225 // chr17:79658554-79661103 // 2549 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: HGS -



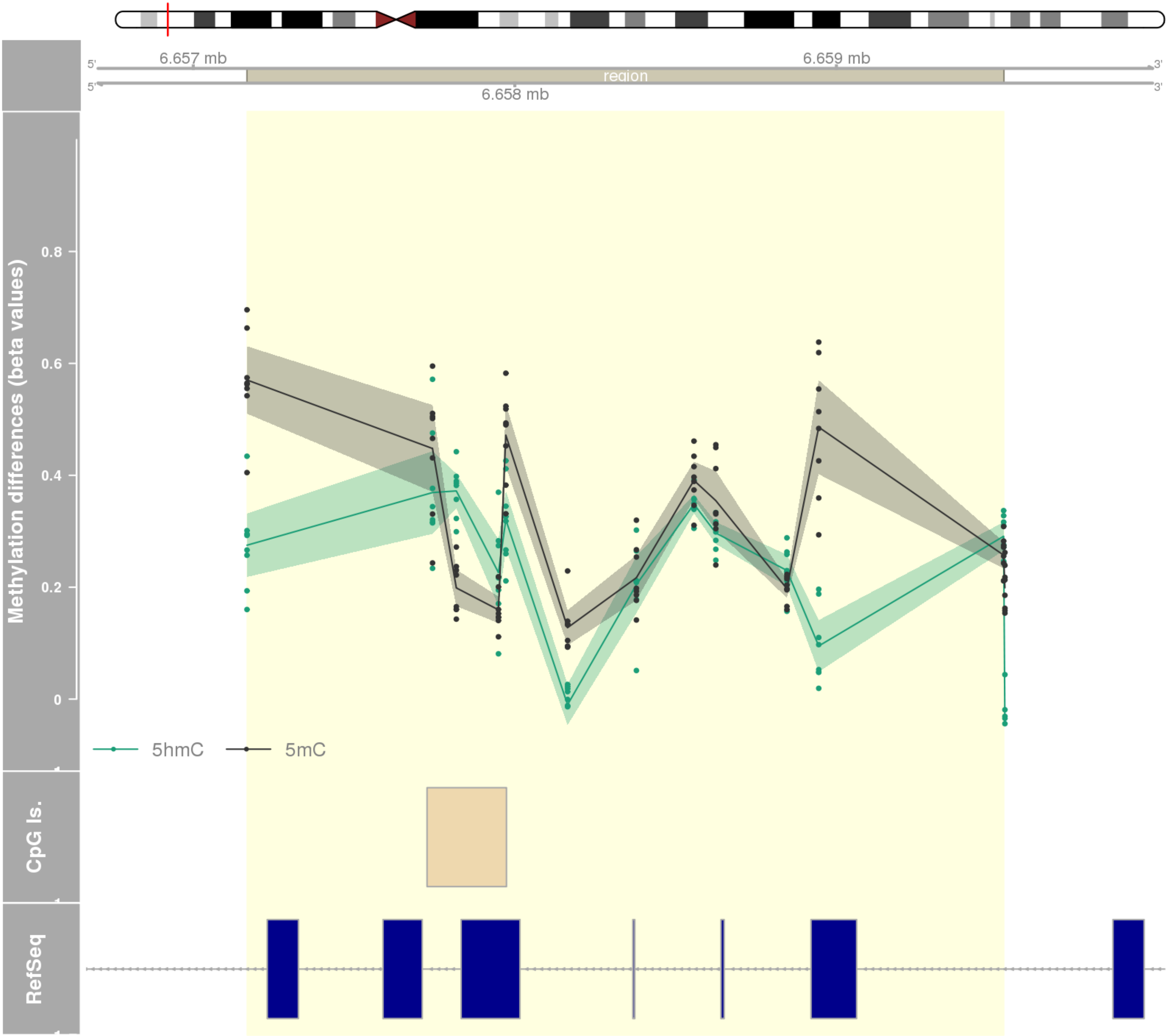
DMR 226 // chr17:73498127-73499917 // 1790 pb. (8 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: CASKIN2 -



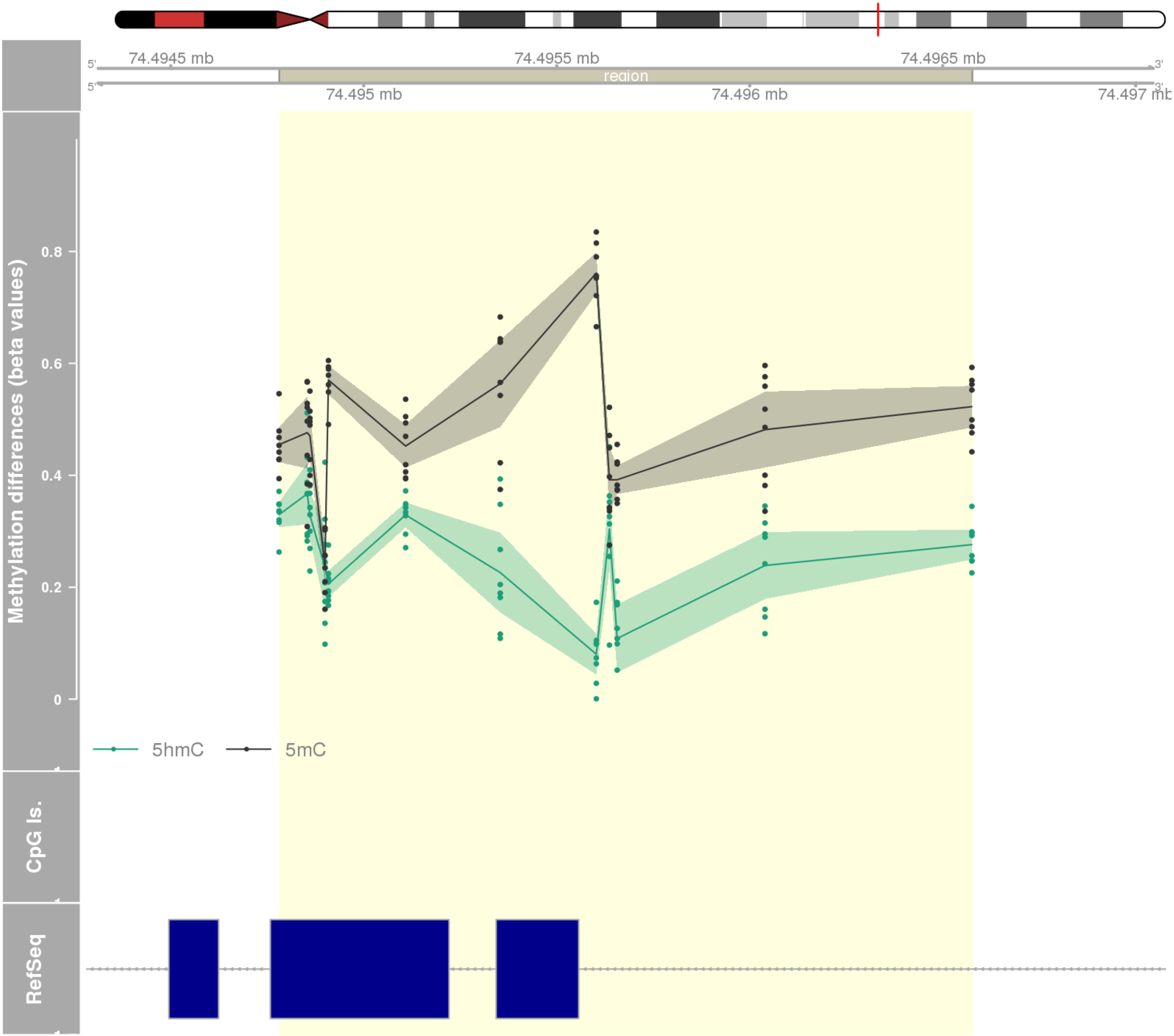
DMR 227 // chr16:67515916-67518179 // 2263 pb. (12 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: AGRP -



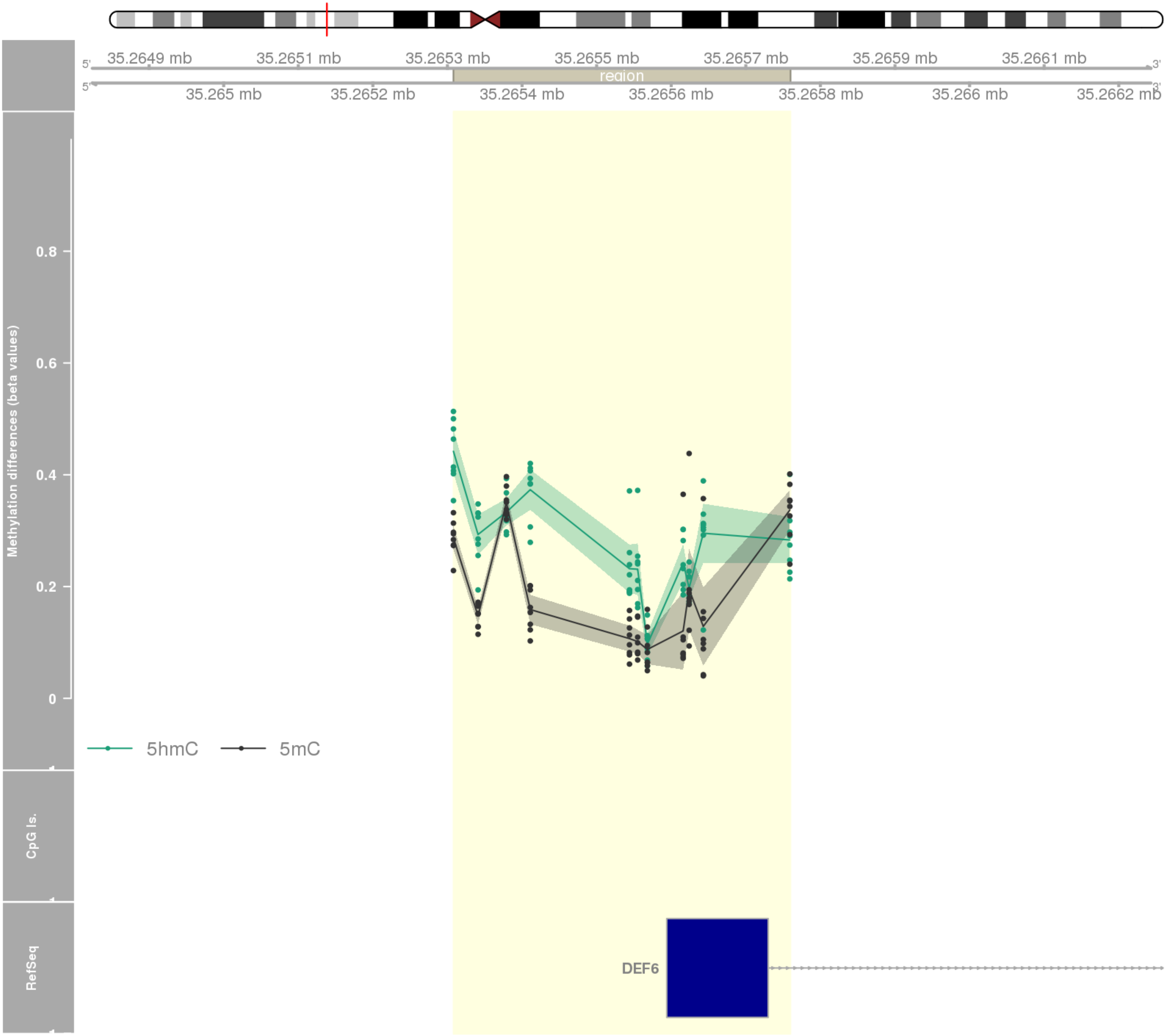
DMR 228 // chr12:6657167-6659520 // 2353 pb. (12 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: IFFO1 -



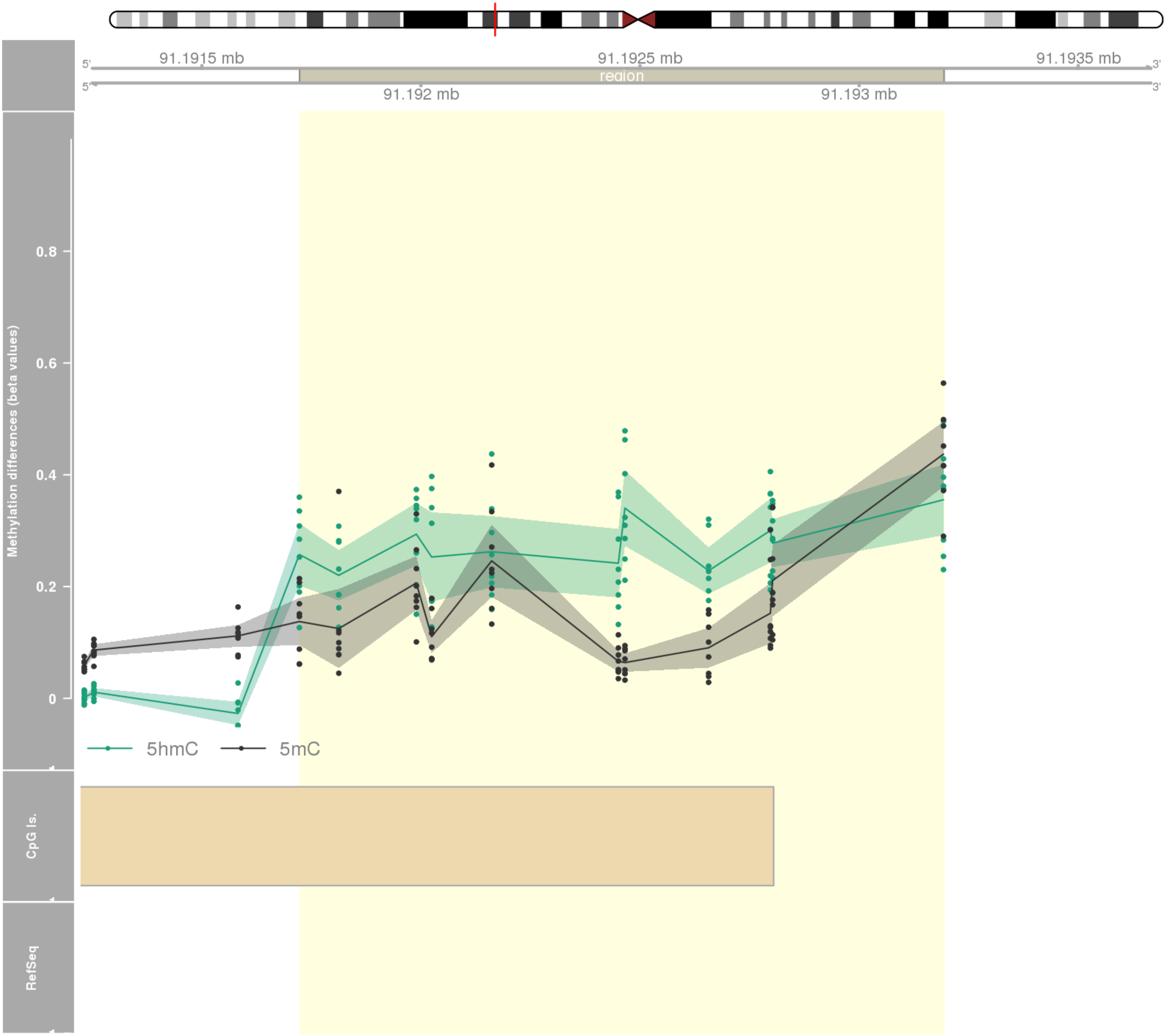
DMR 229 // chr15:74494781-74496576 // 1795 pb. (12 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: STRA6 -



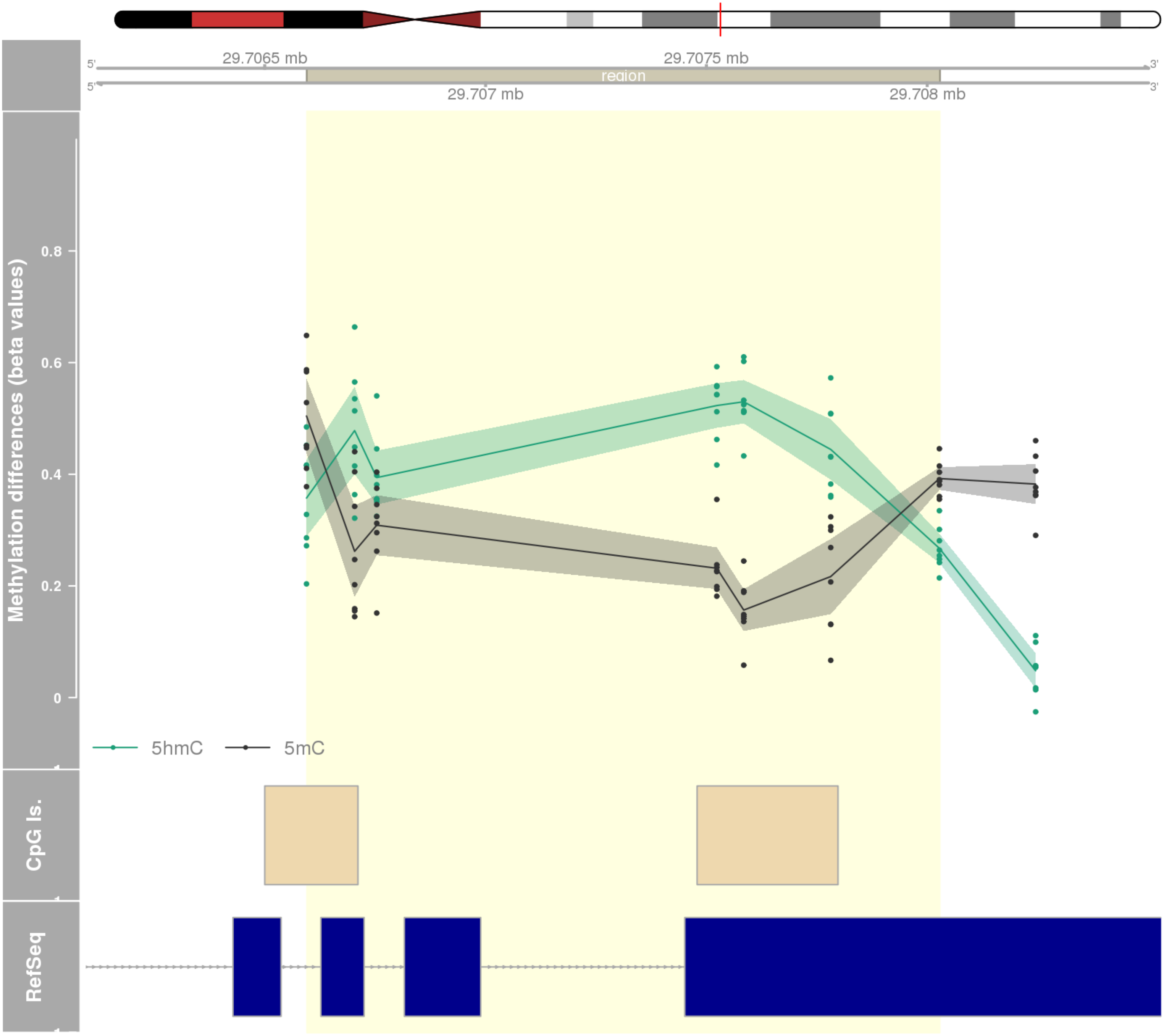
DMR 230 // chr6:35265308-35265759 // 451 pb. (11 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: DEF6 -



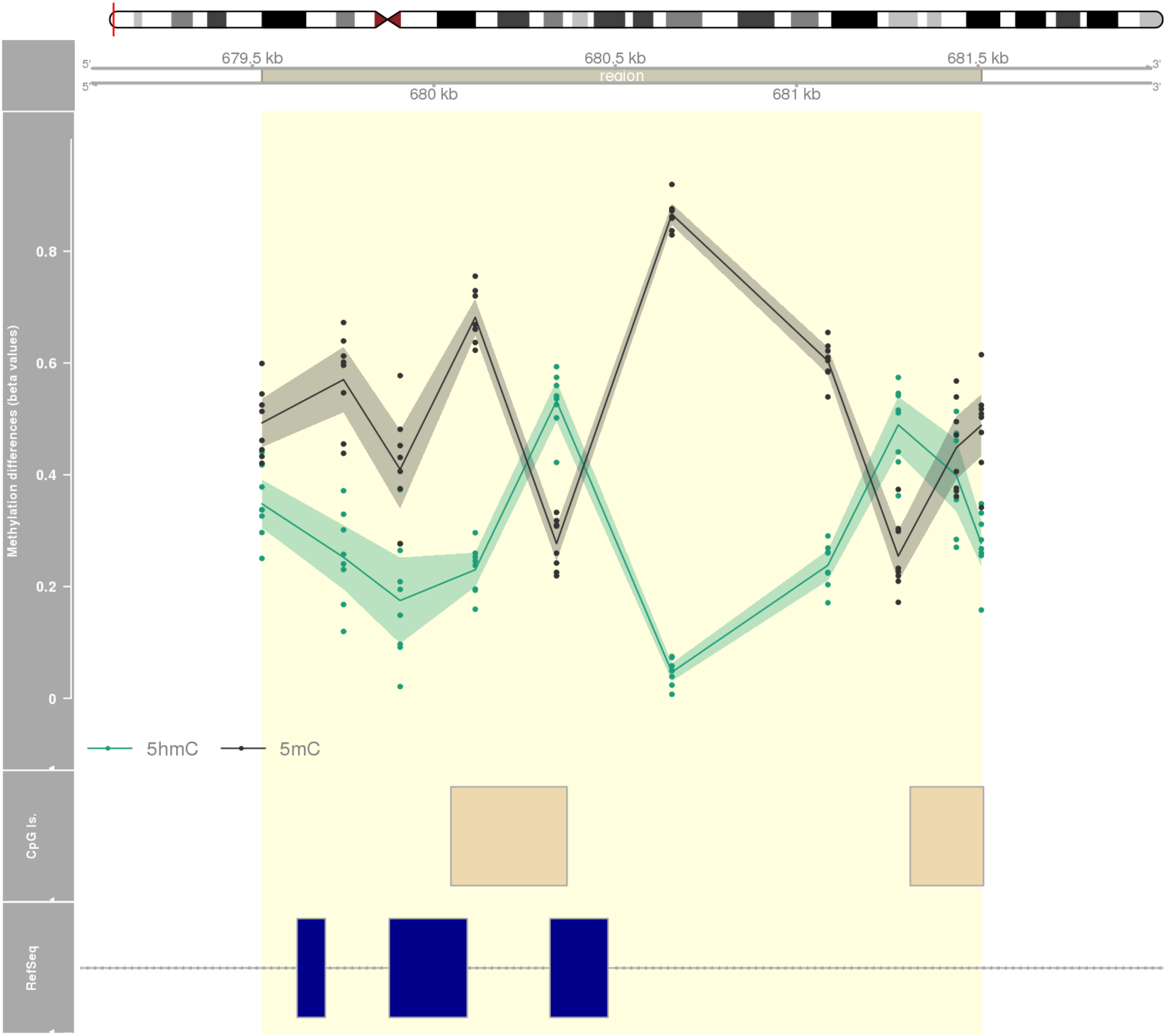
DMR 231 // chr1:91191723-91193193 // 1470 pb. (11 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559



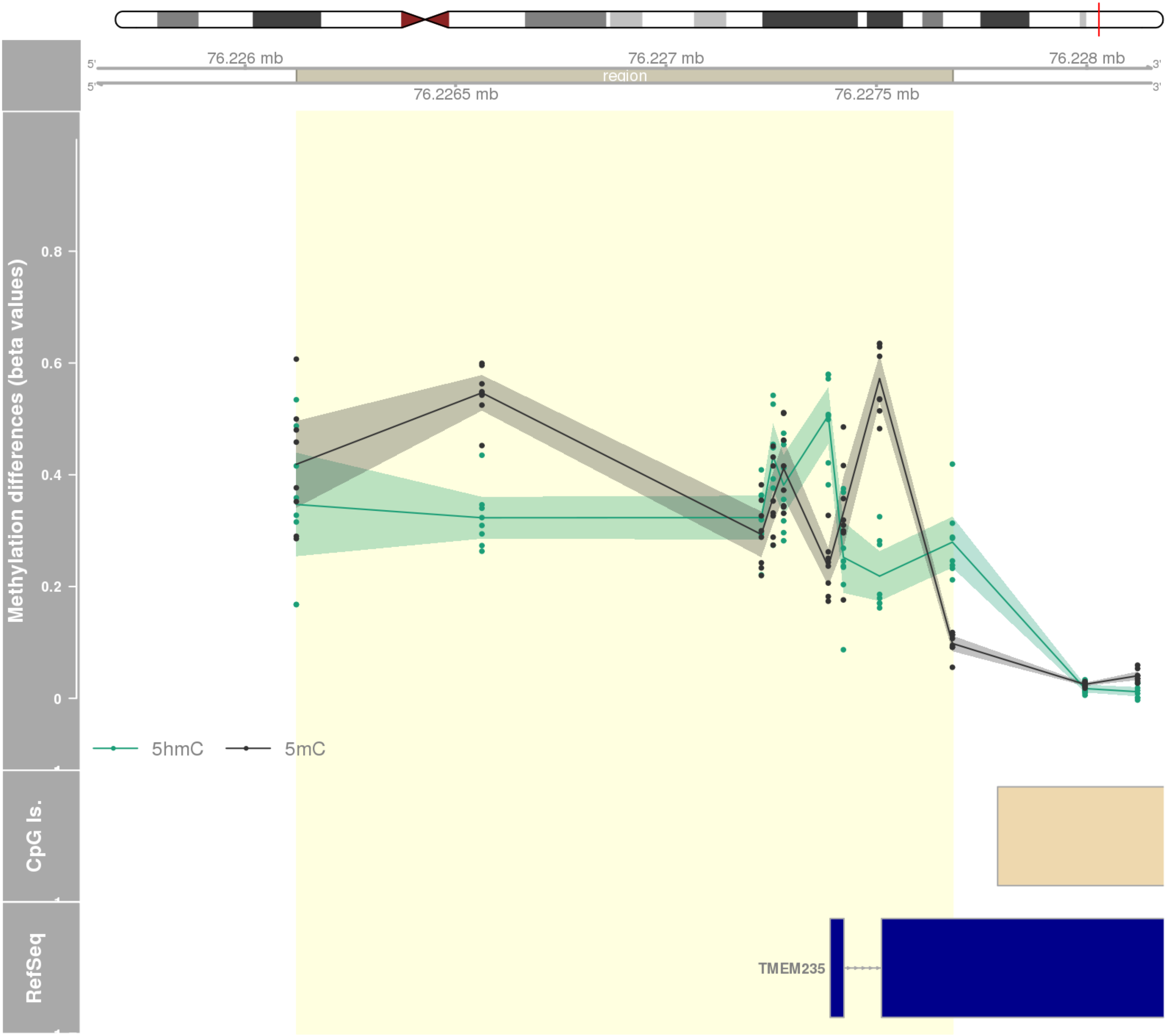
DMR 232 // chr22:29706595-29708028 // 1433 pb. (7 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: GAS2L1 -



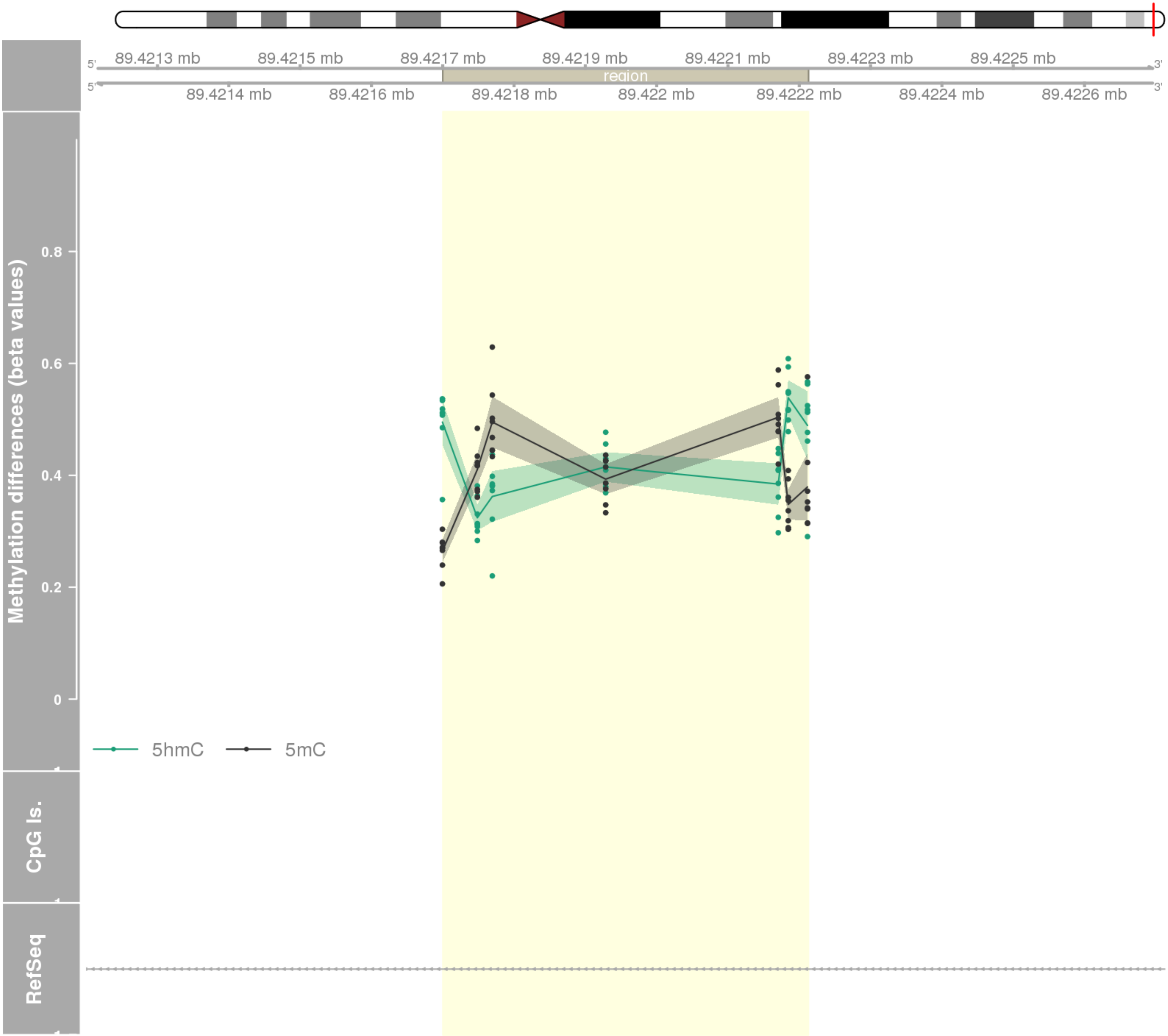
DMR 233 // chr4:679526-681509 // 1983 pb. (10 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: MFSD7 -



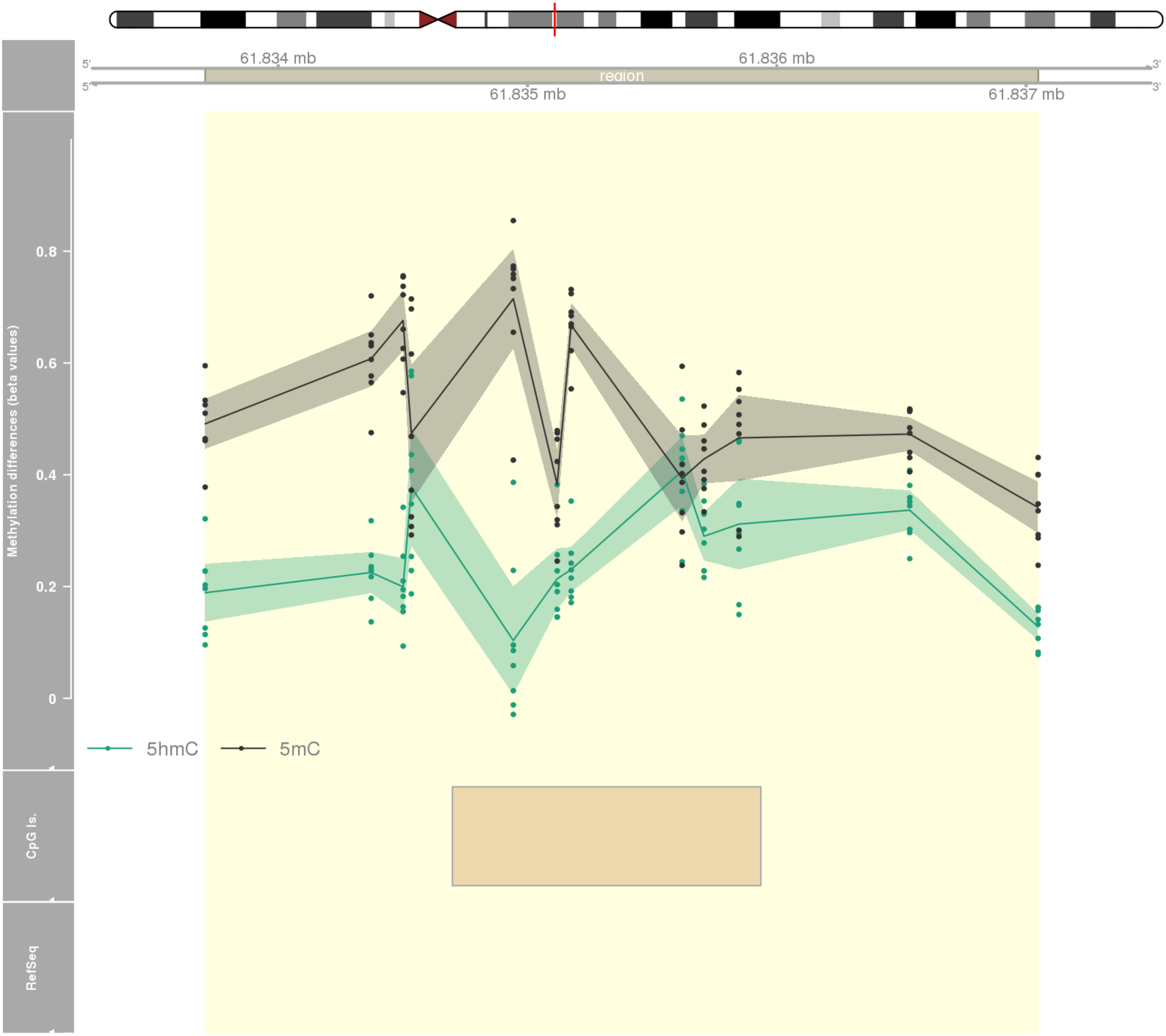
DMR 234 // chr17:76226122-76227681 // 1559 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: TMEM235 -



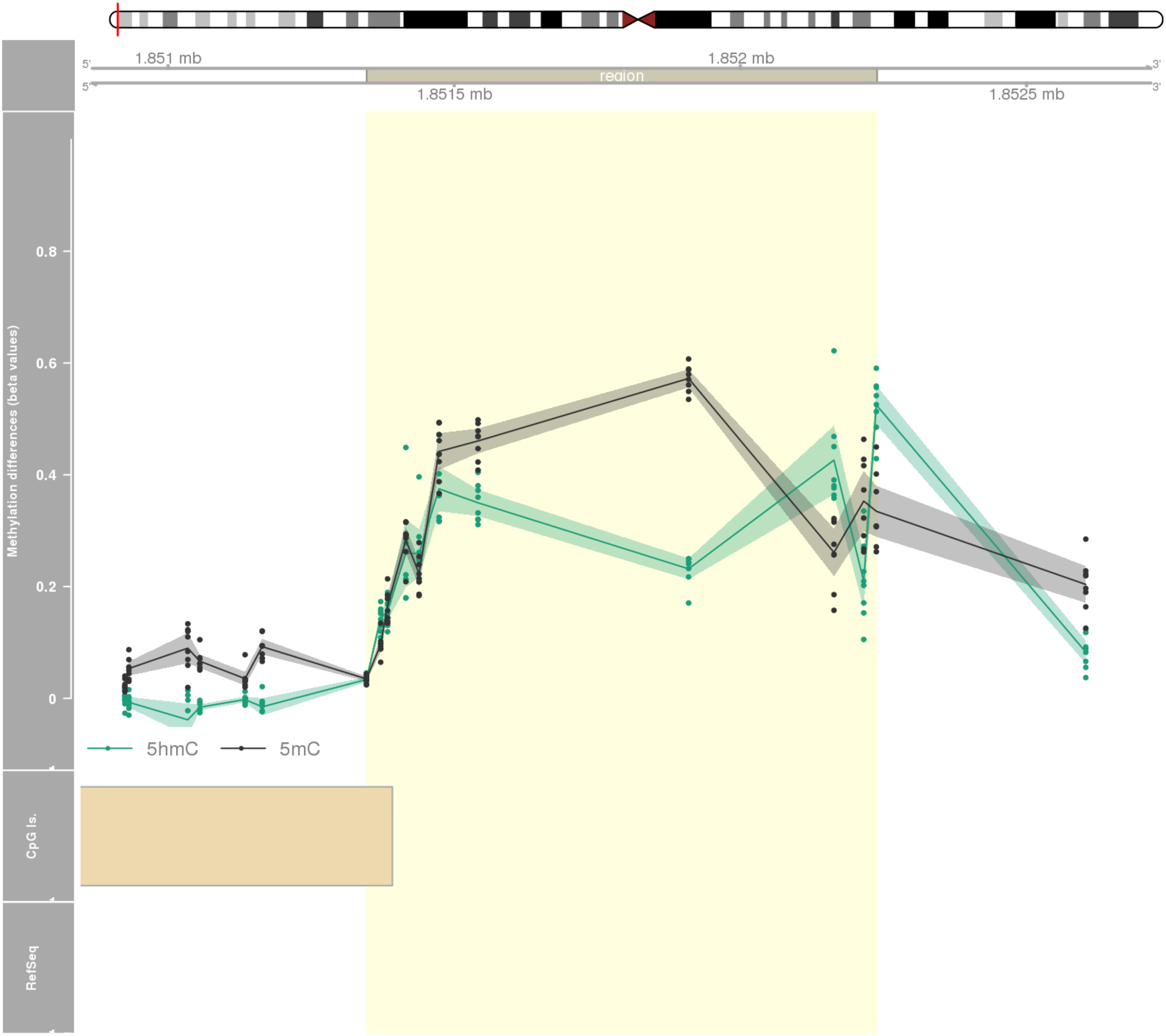
DMR 235 // chr16:89421700-89422212 // 512 pb. (7 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: ANKRD11 -



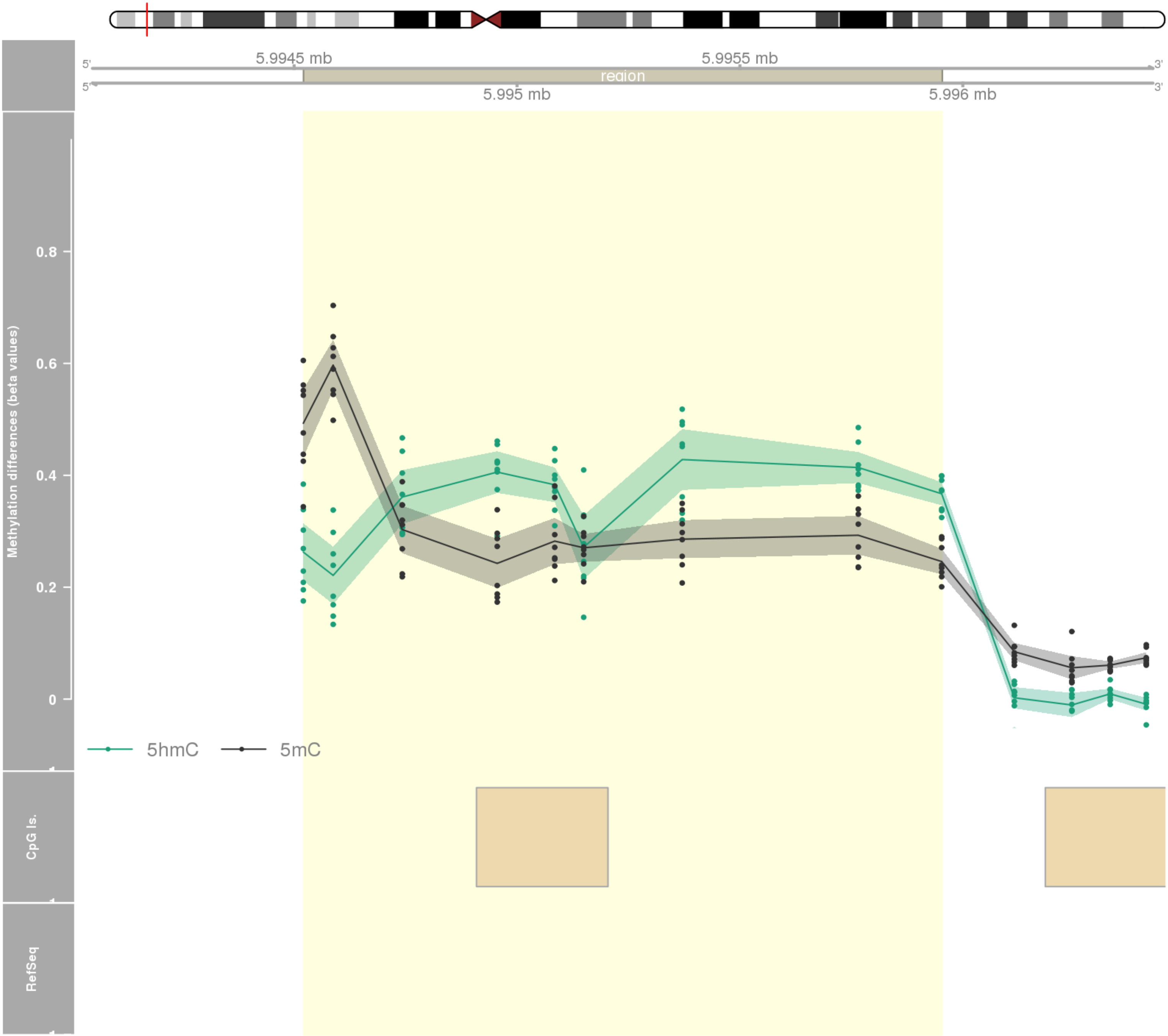
DMR 236 // chr8:61833707-61837048 // 3341 pb. (12 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559



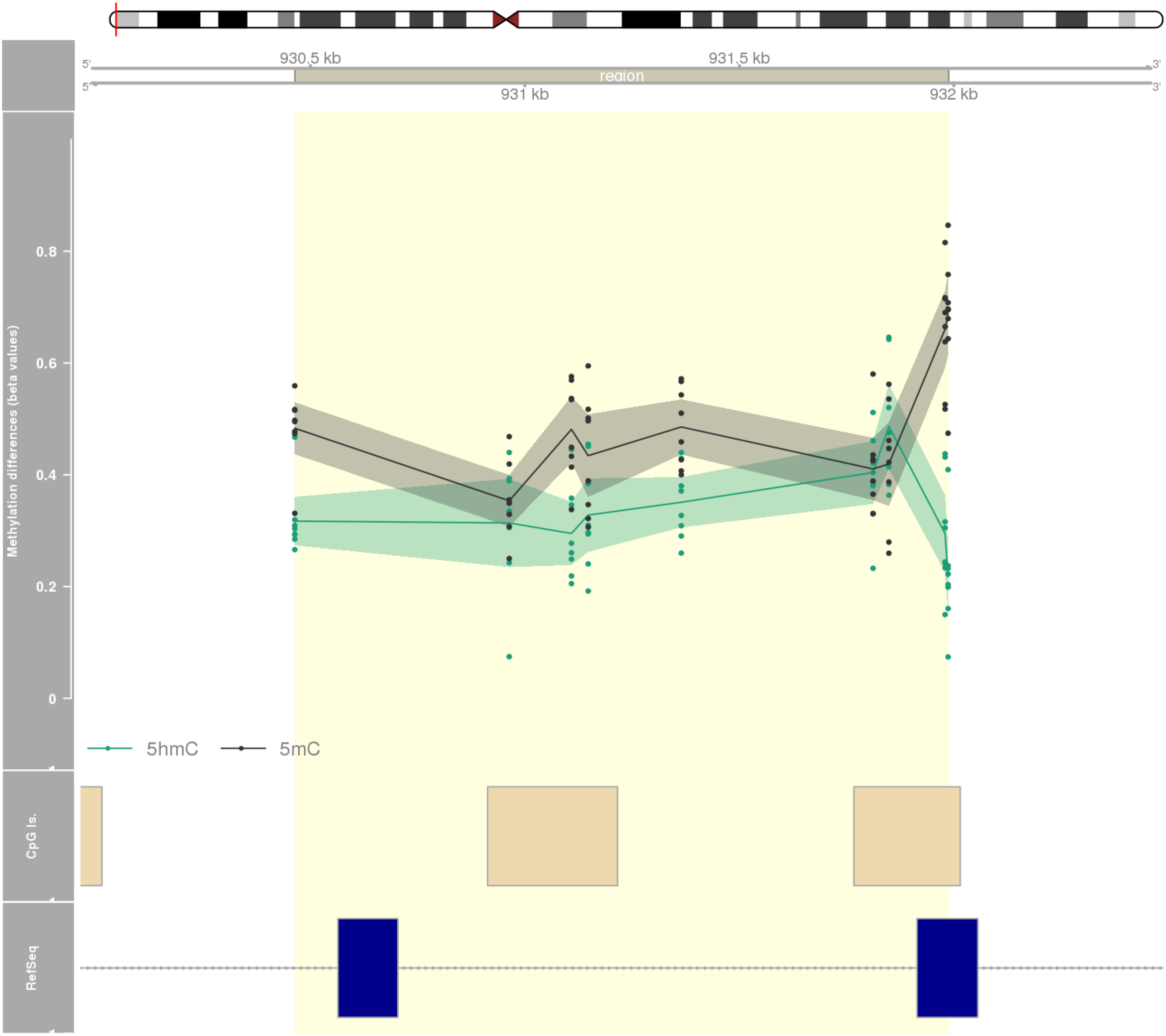
DMR 237 // chr1:1851347-1852238 // 891 pb. (11 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559

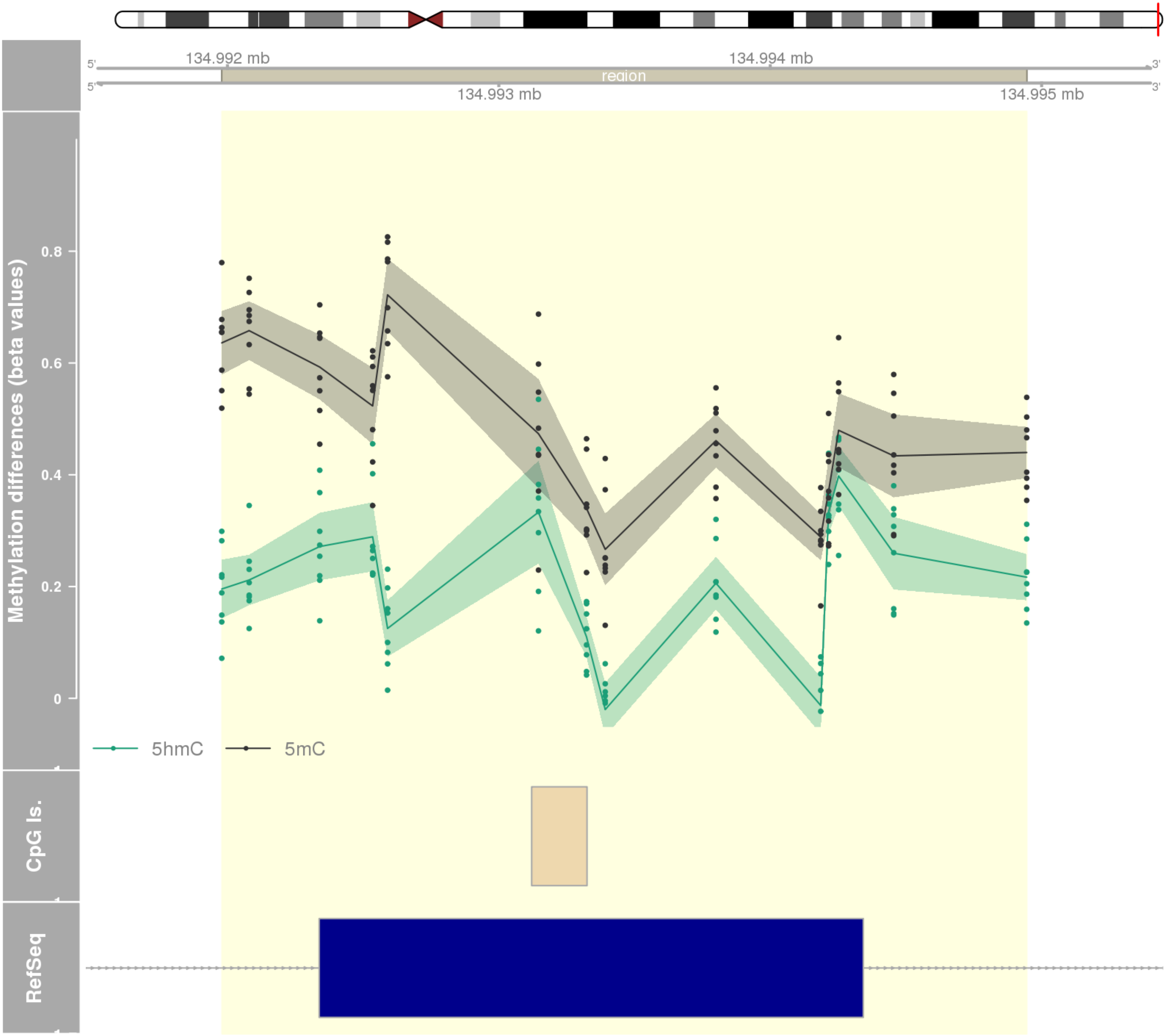


DMR 238 // chr6:5994521-5995953 // 1432 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559



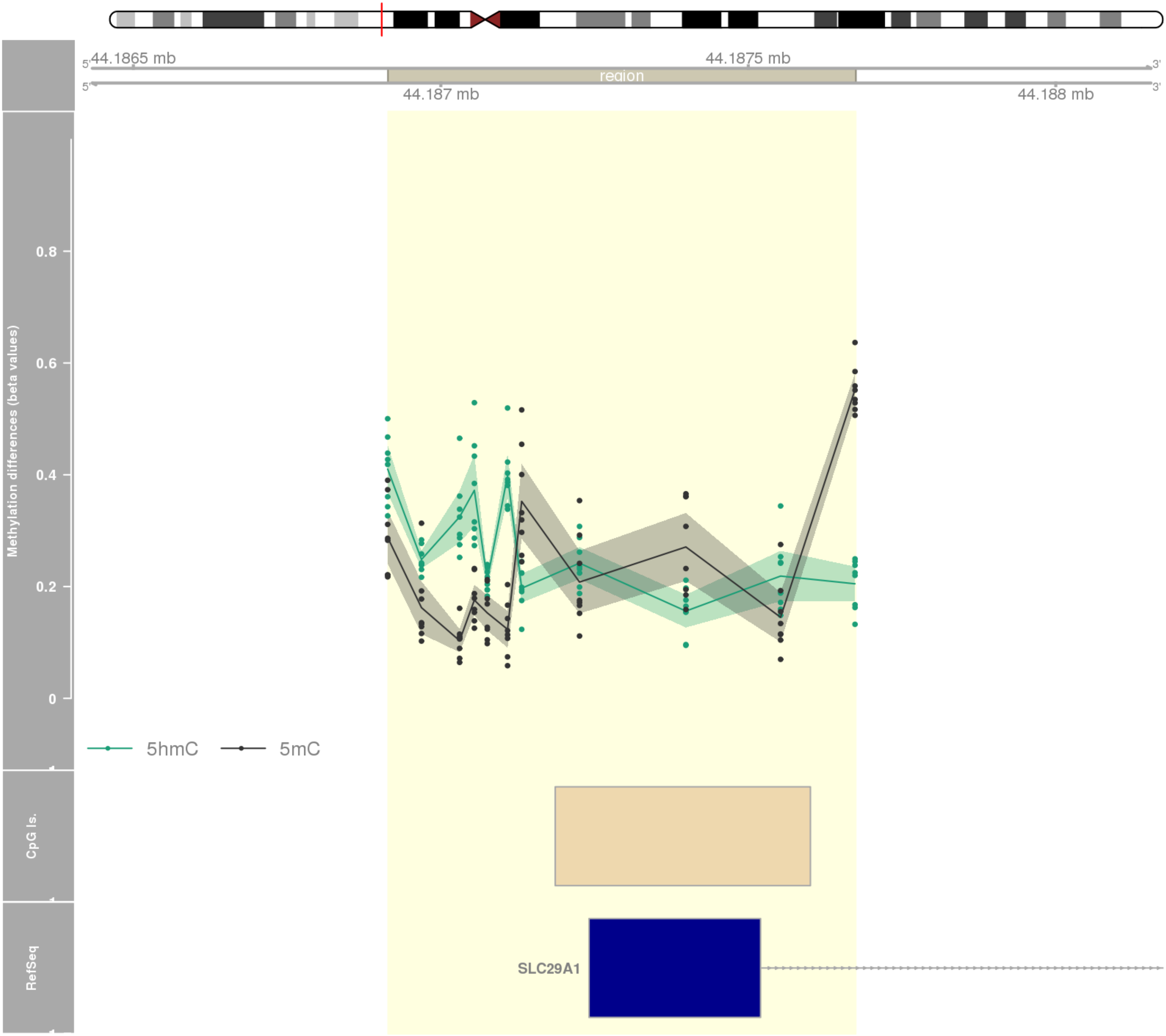
DMR 239 // chr7:930464-931987 // 1523 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: SUN1 / GET4 -



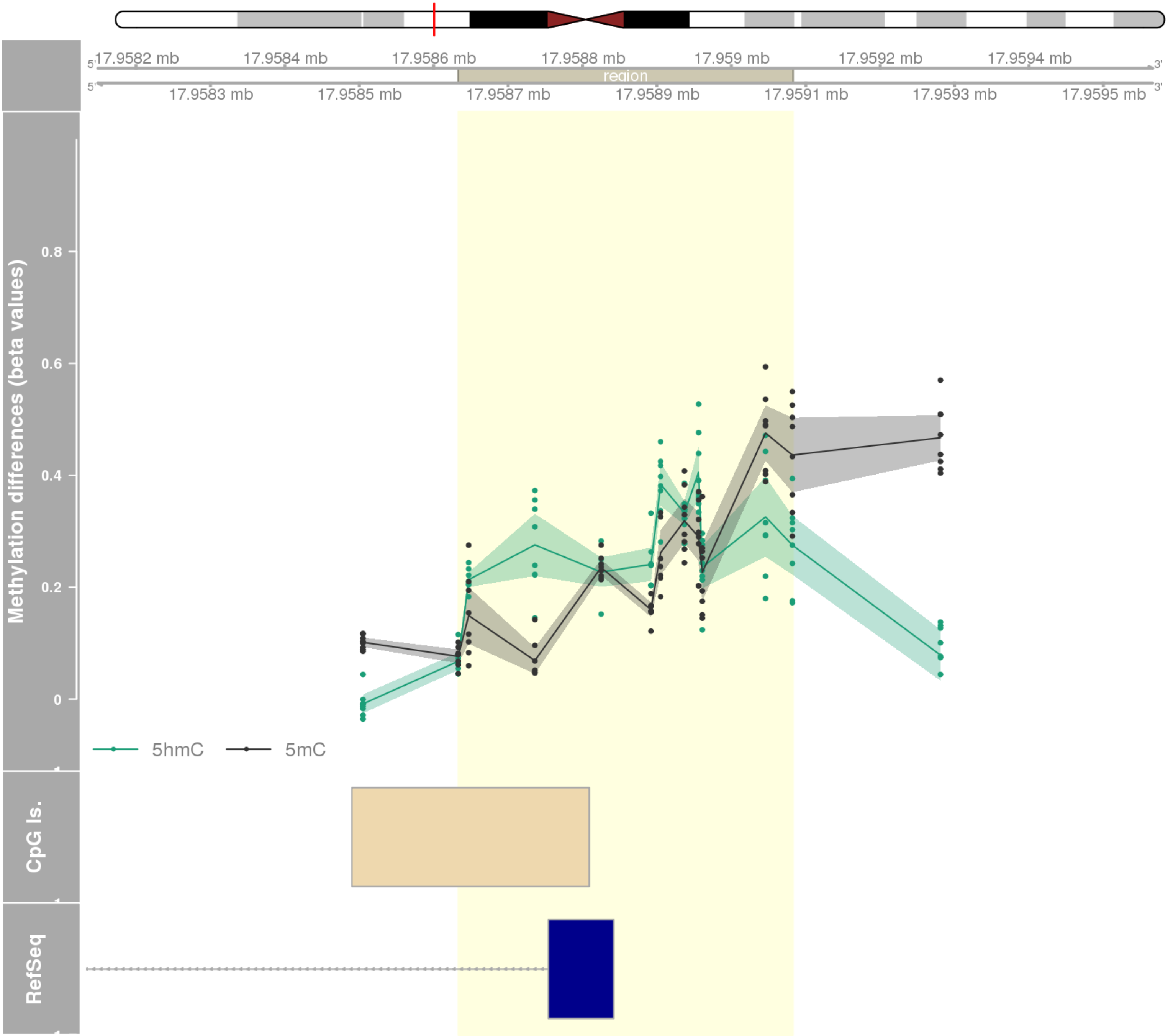


DMR 240 // chr10:134991979-134994945 // 2966 pb. (14 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.012 // fwerArea: 0.559
- genes: KNDC1 -

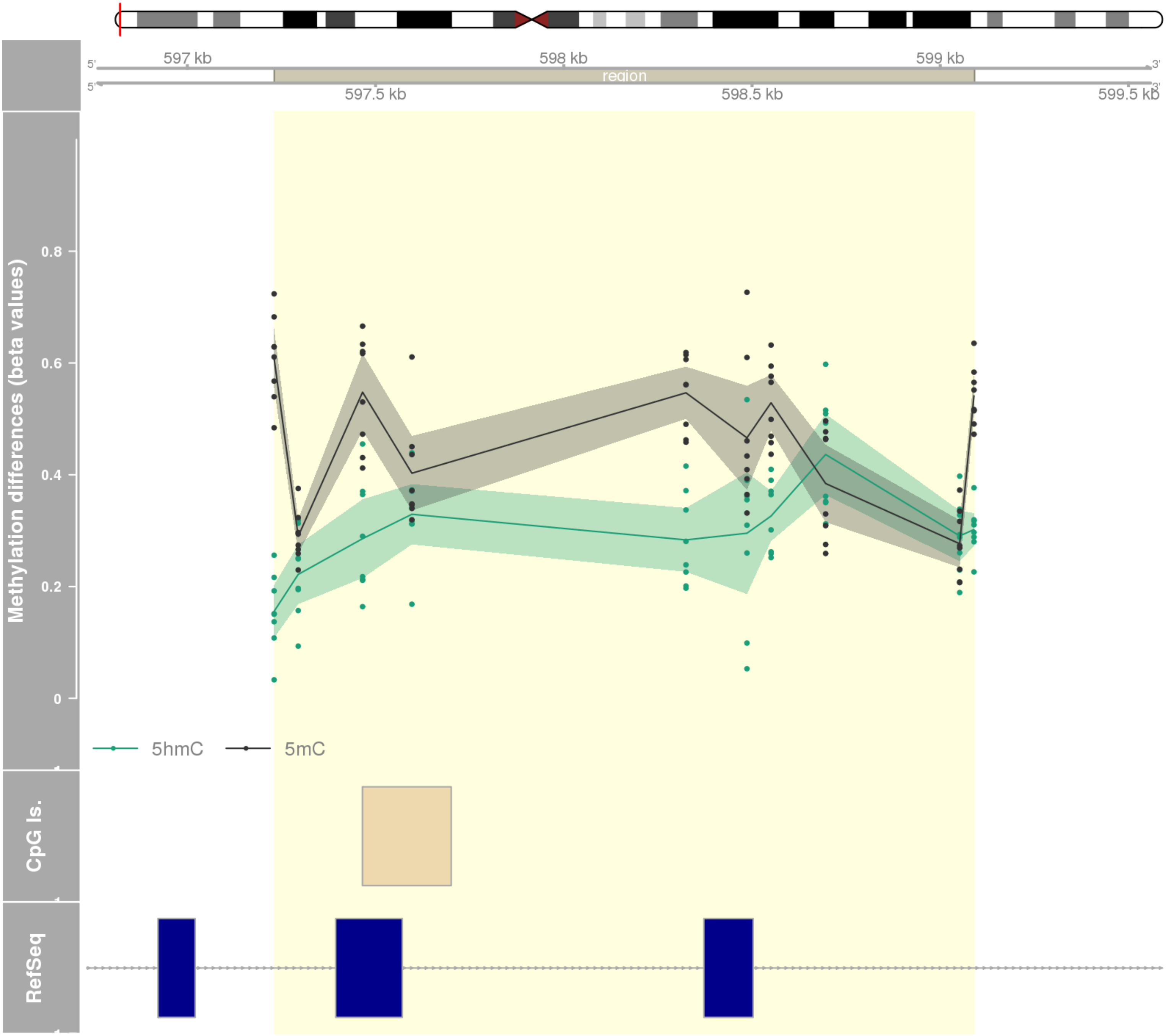
DMR 241 // chr6:44186914-44187674 // 760 pb. (11 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: SLC29A1 -



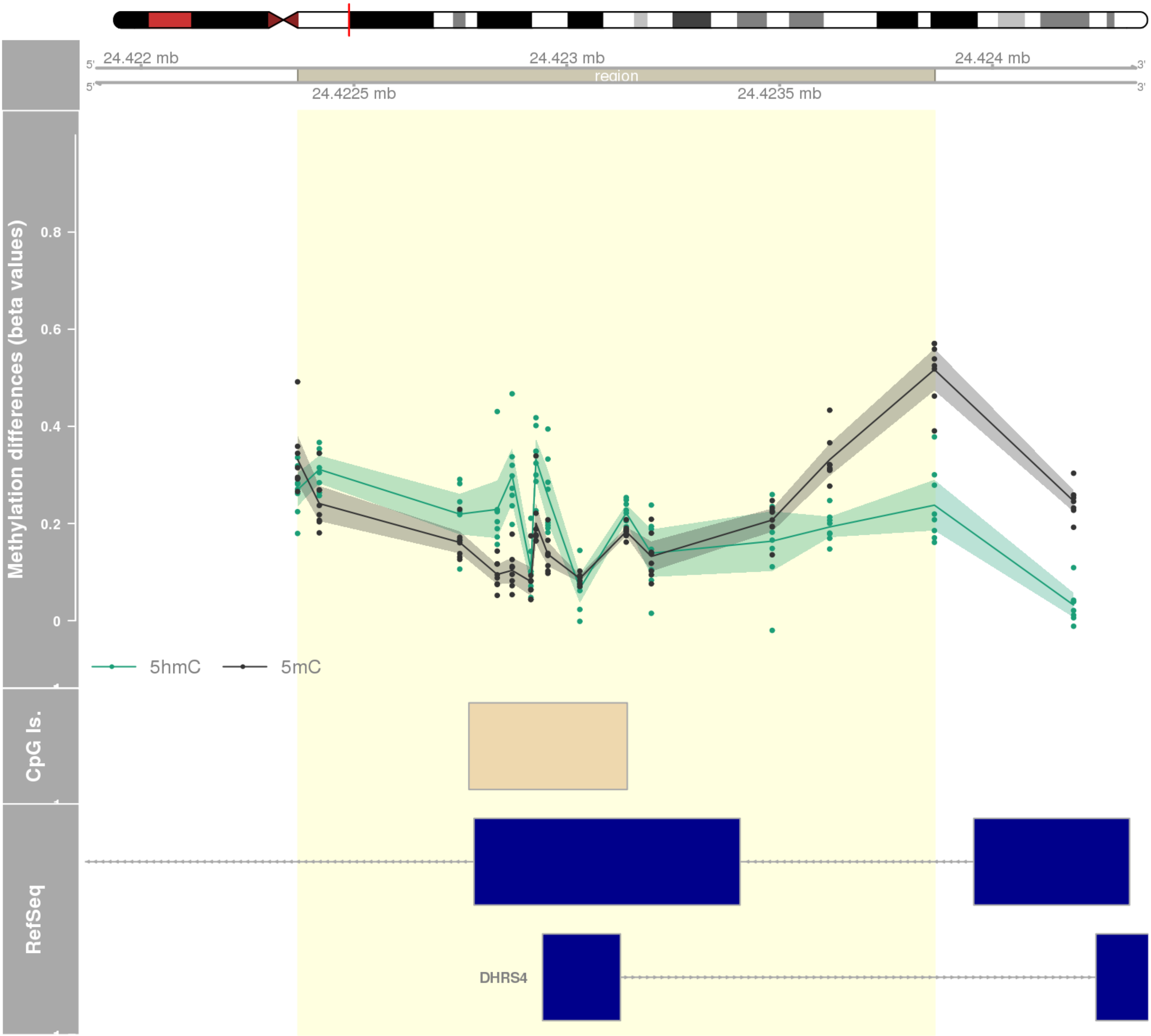
DMR 242 // chr19:17958633-17959082 // 449 pb. (11 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: JAK3 -



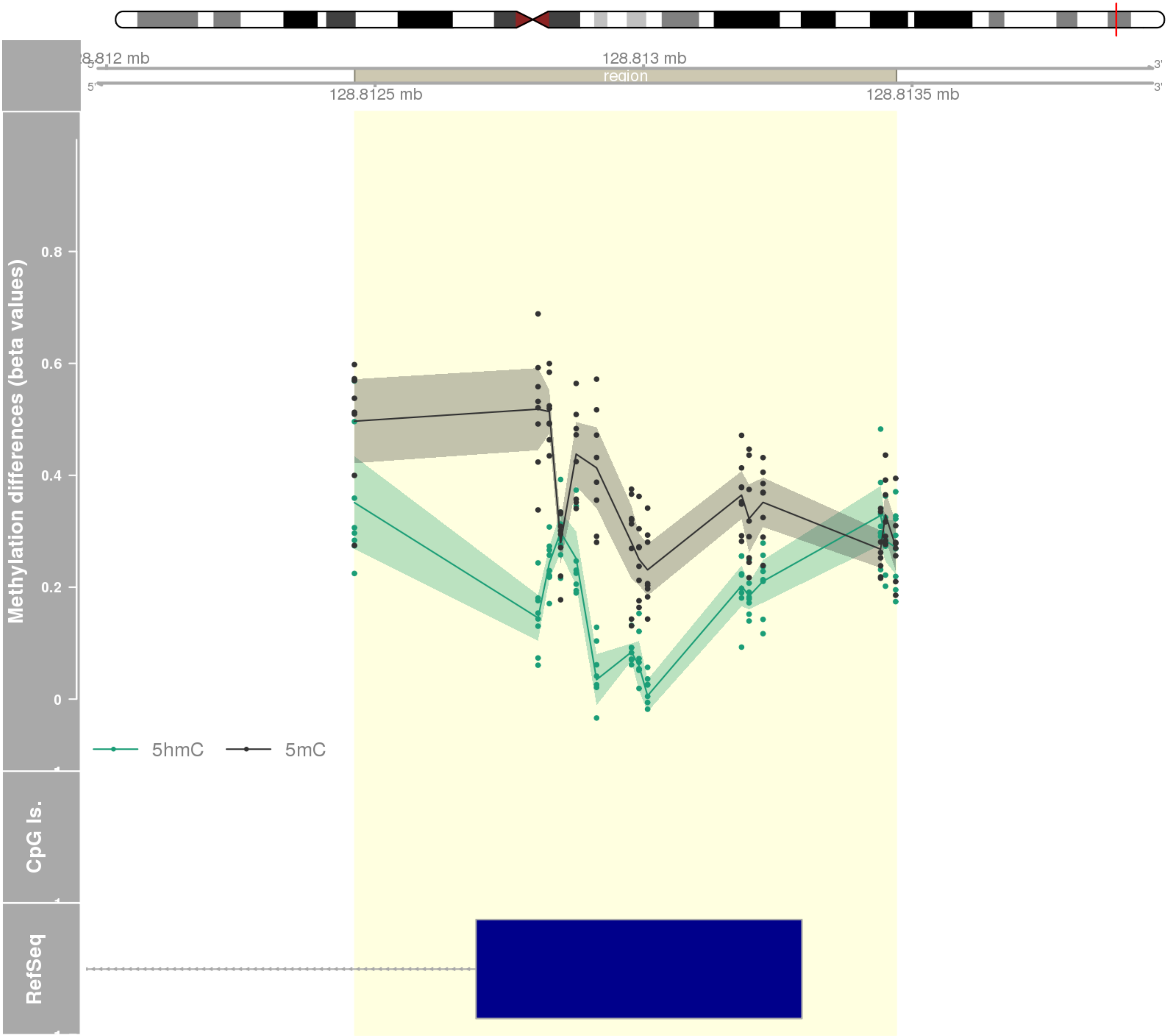
DMR 243 // chr11:597231-599090 // 1859 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: PHRF1 -



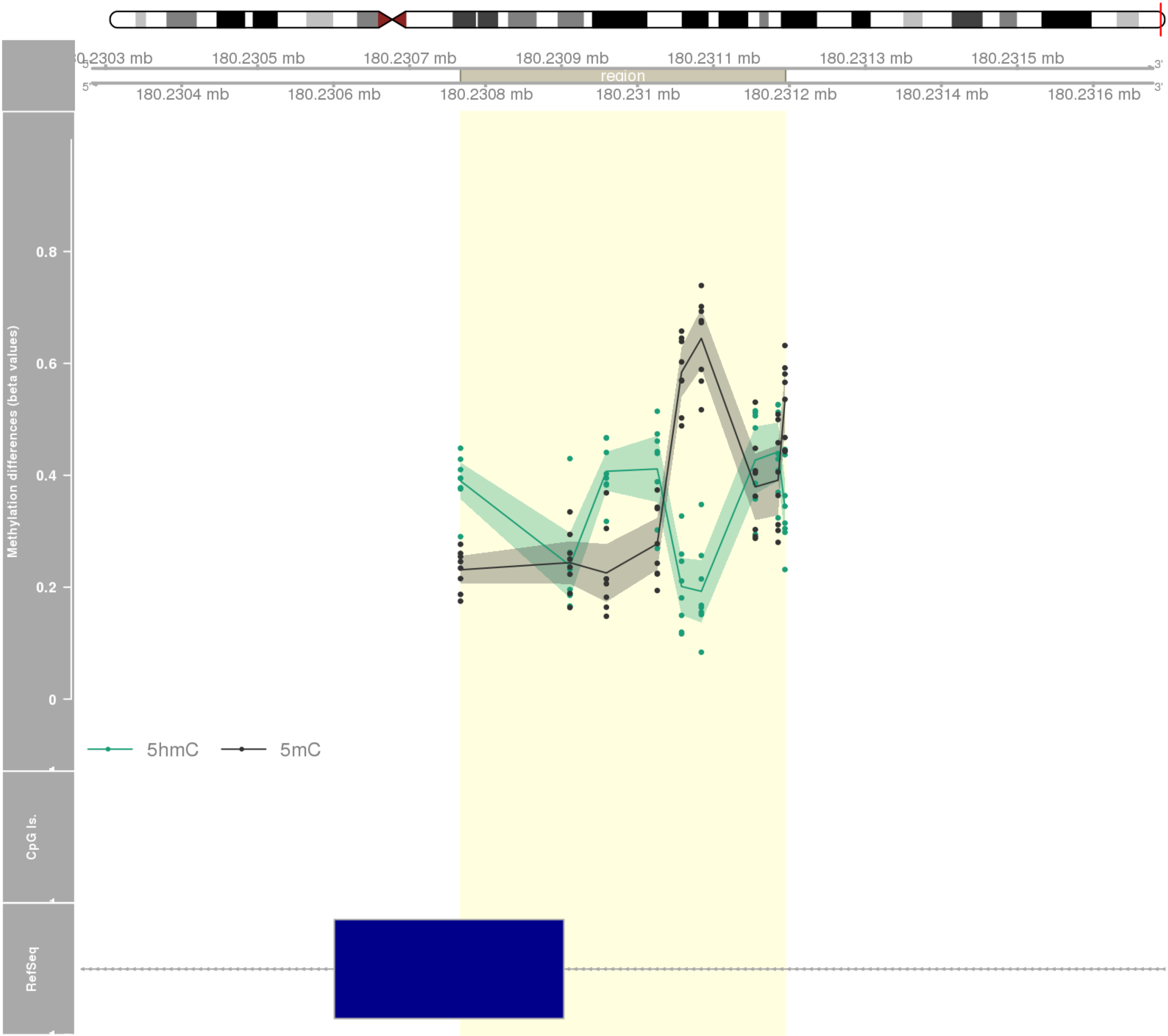
DMR 244 // chr14:24422368-24423864 // 1496 pb. (14 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: DHRS4-AS1 / DHRS4 -



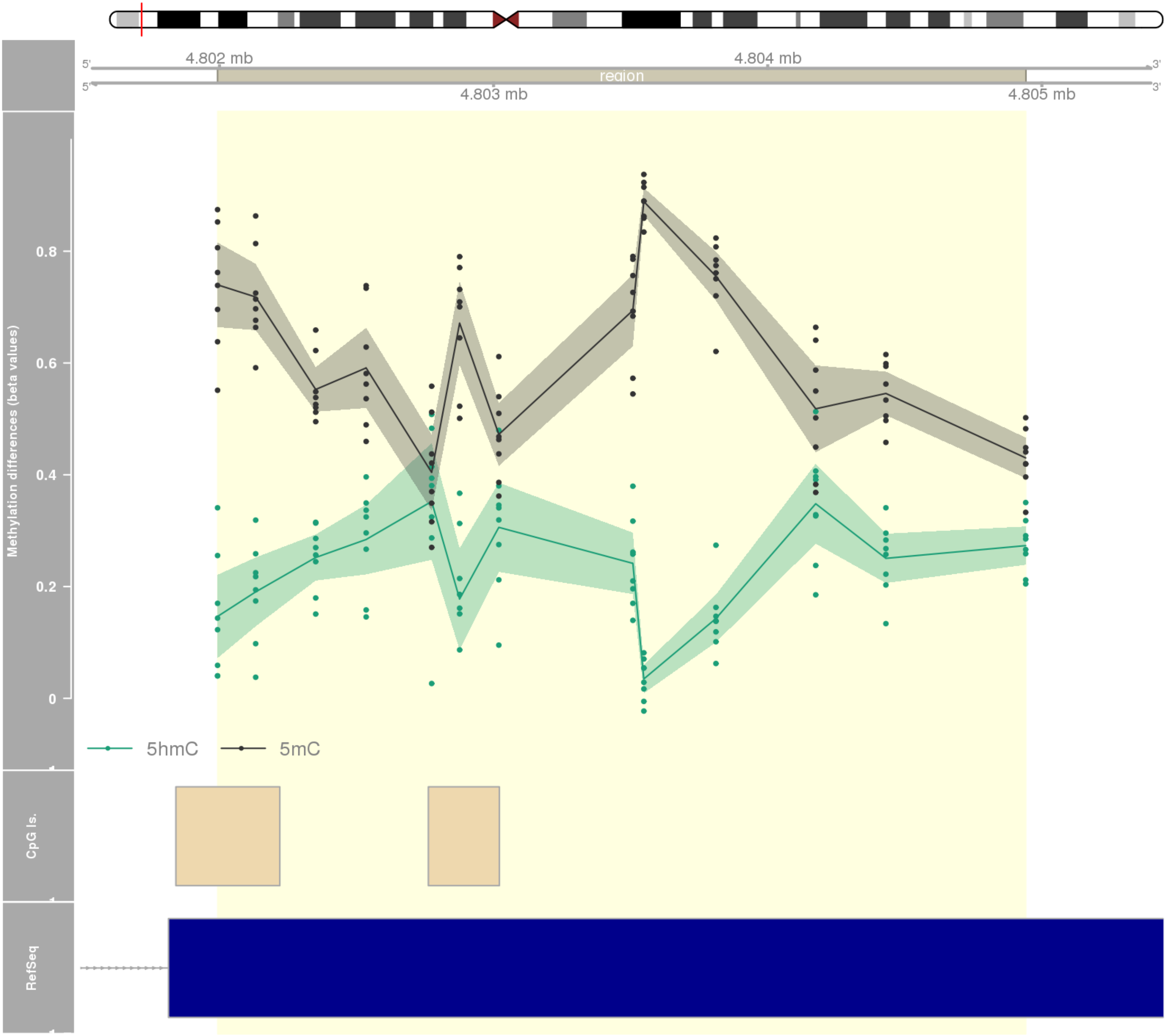
DMR 245 // chr11:128812462-128813470 // 1008 pb. (15 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: TP53AIP1 -



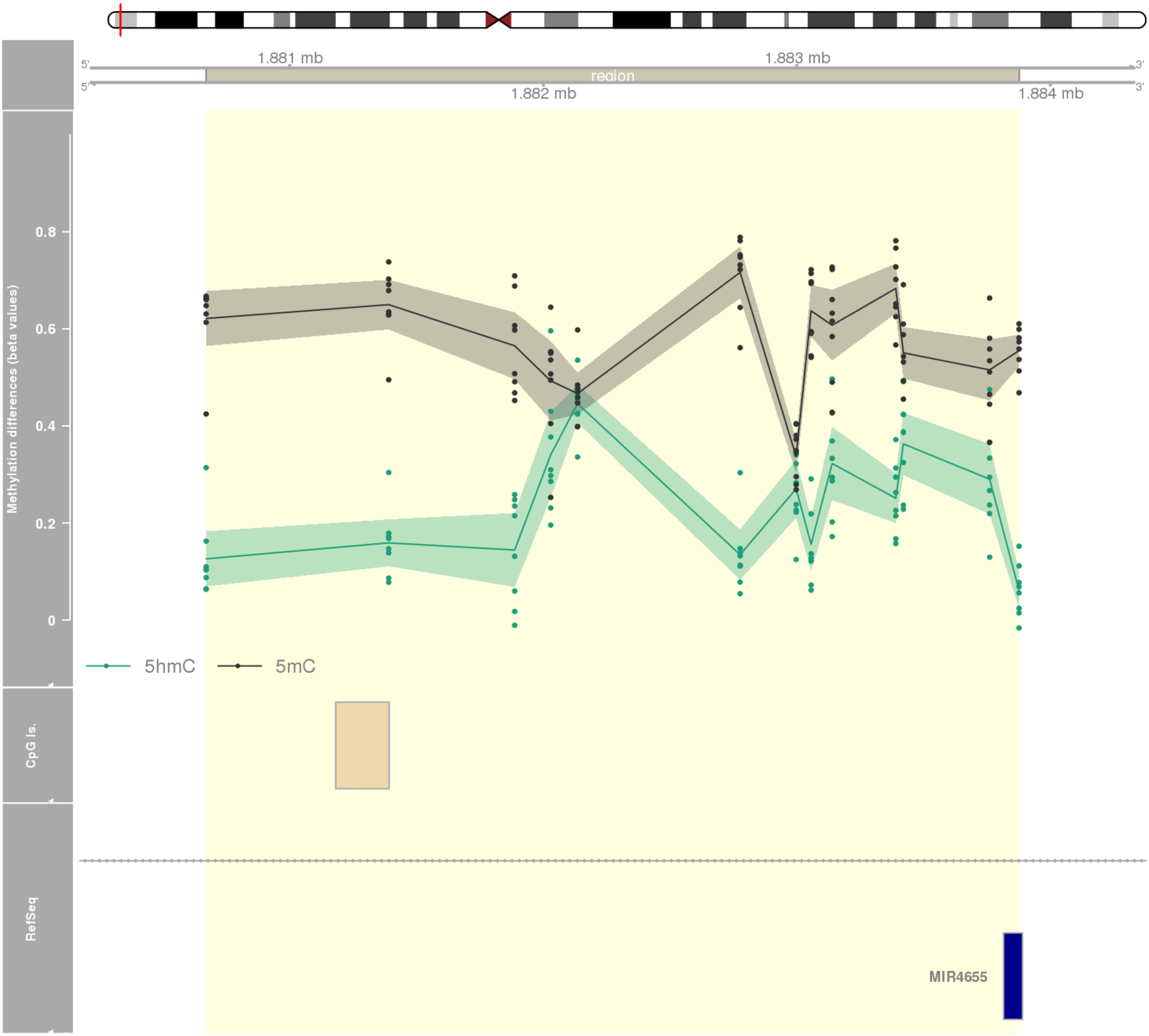
DMR 246 // chr5:180230767-180231194 // 427 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: MGAT1 -



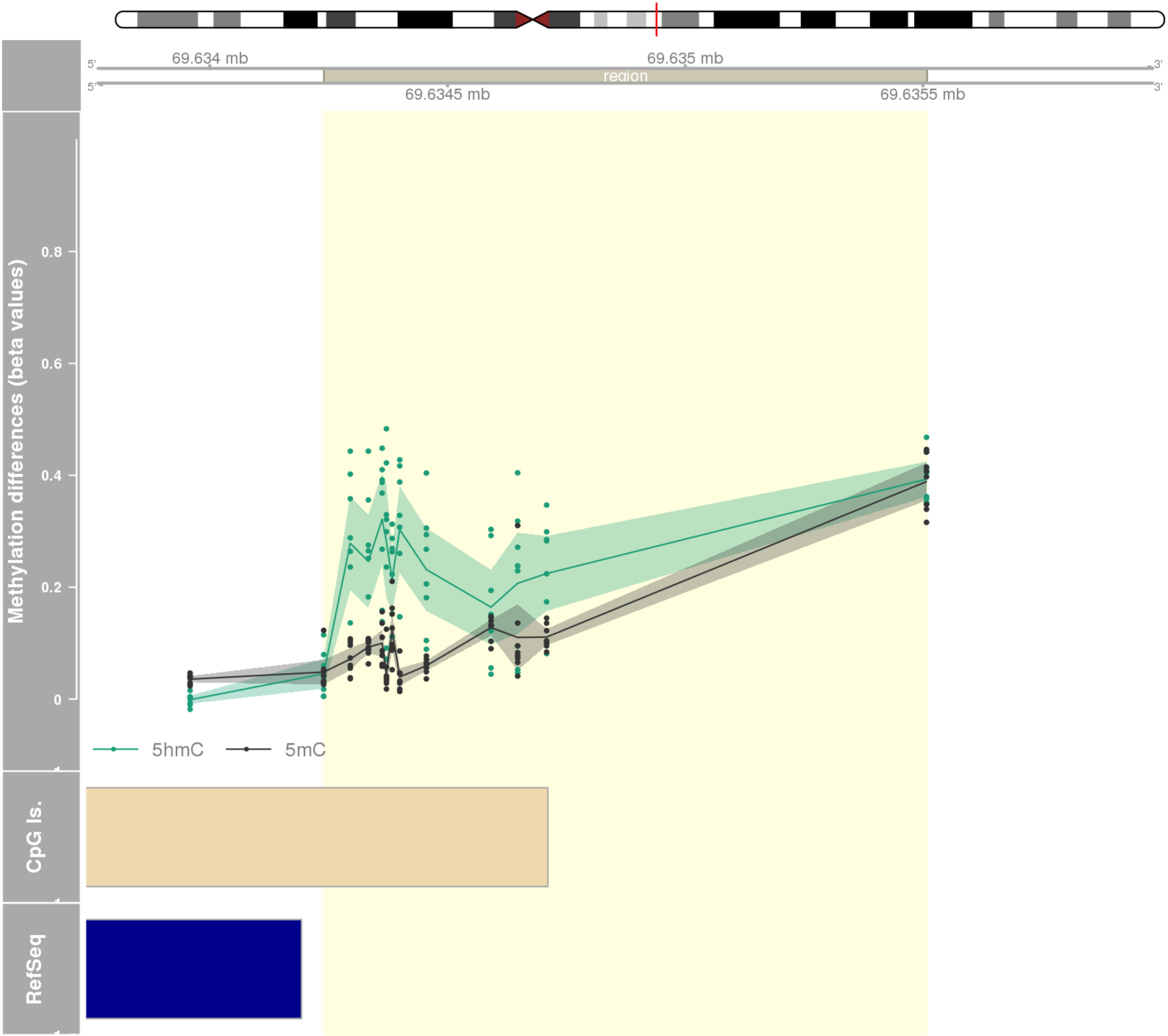
DMR 247 // chr7:4801993-4804941 // 2948 pb. (13 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: FOXK1 -



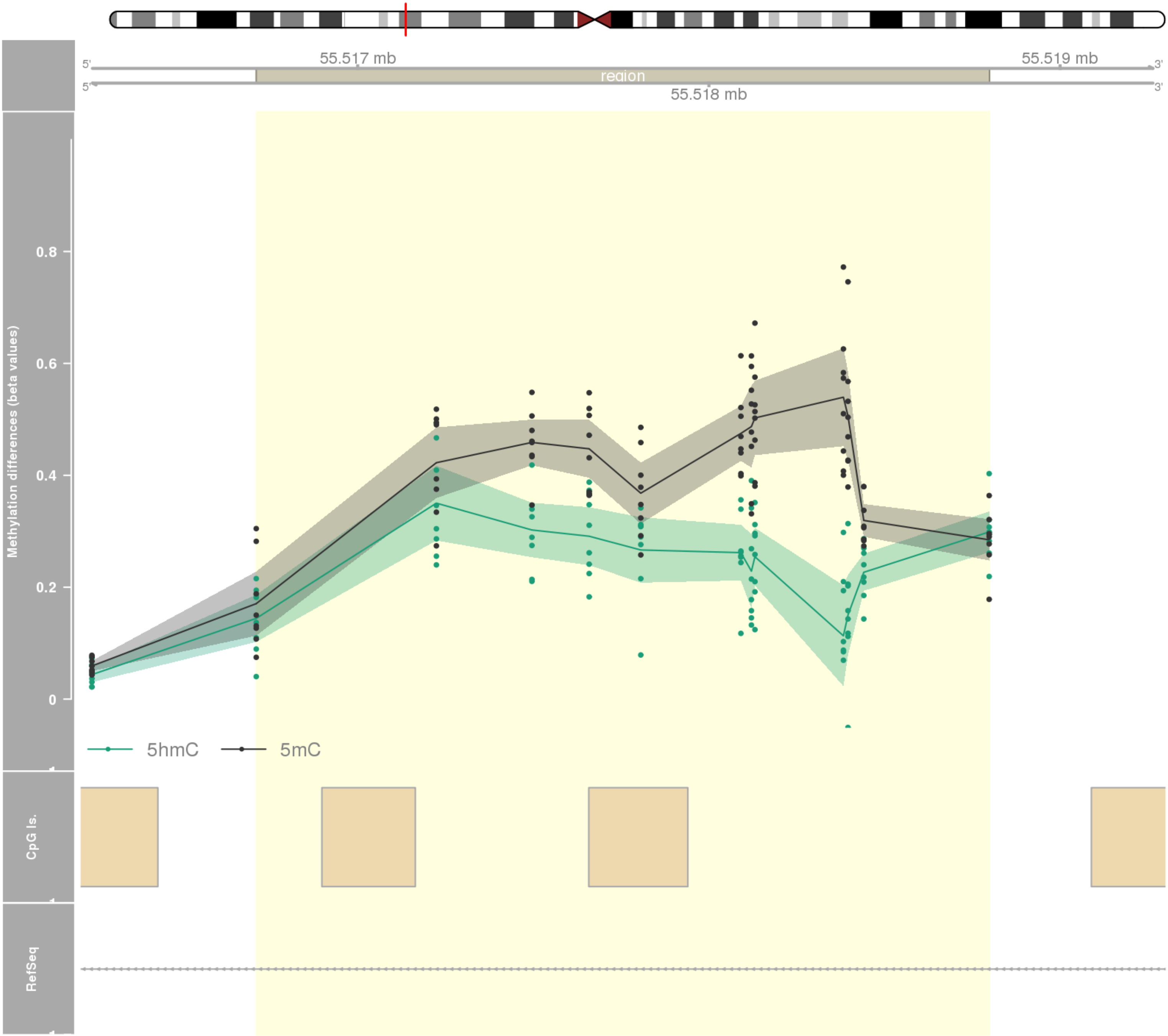
DMR 248 // chr7:1880670-1883876 // 3206 pb. (13 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: MAD1L1 / MIR4655 -



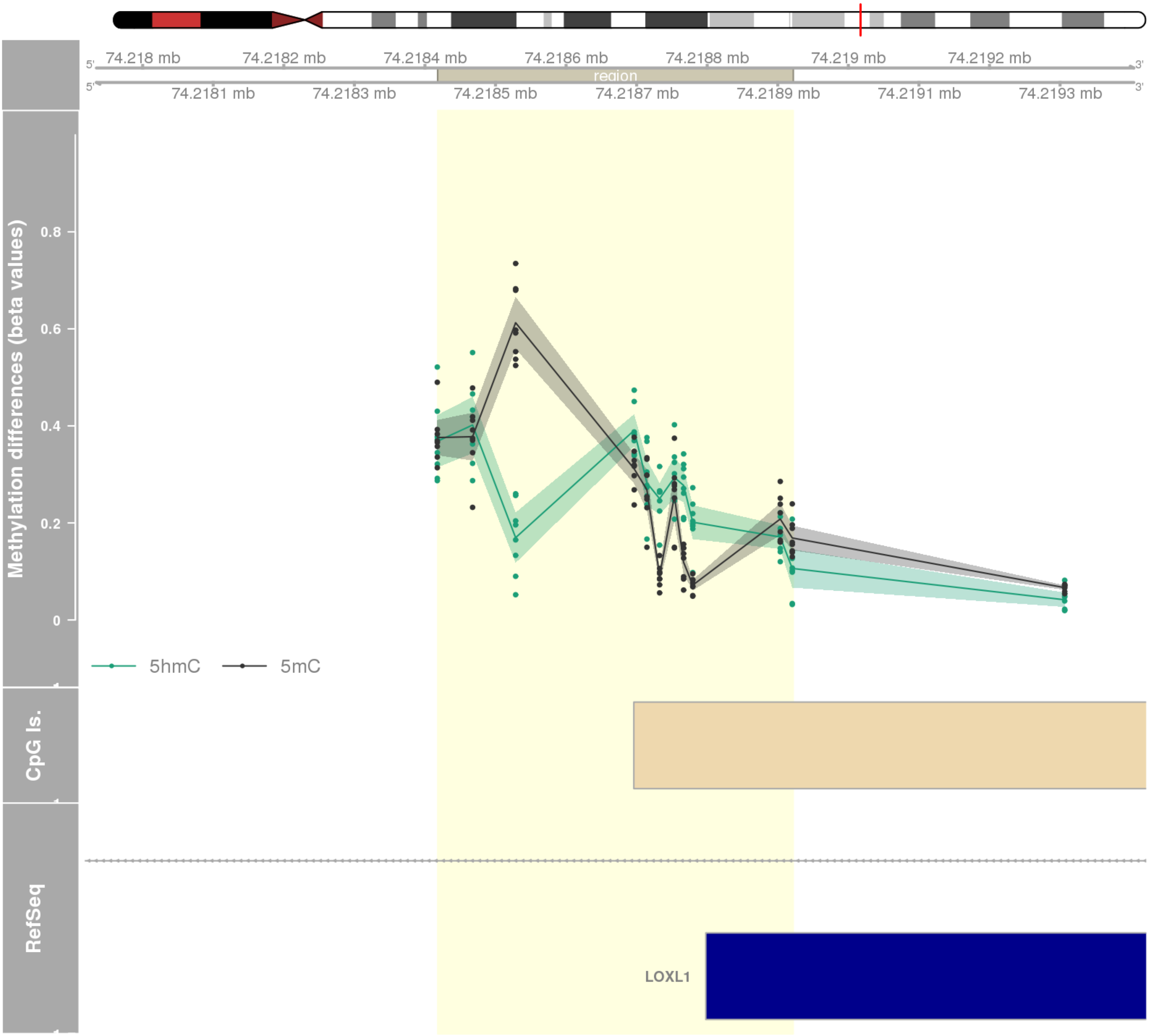
DMR 249 // chr11:69634240-69635508 // 1268 pb. (12 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559



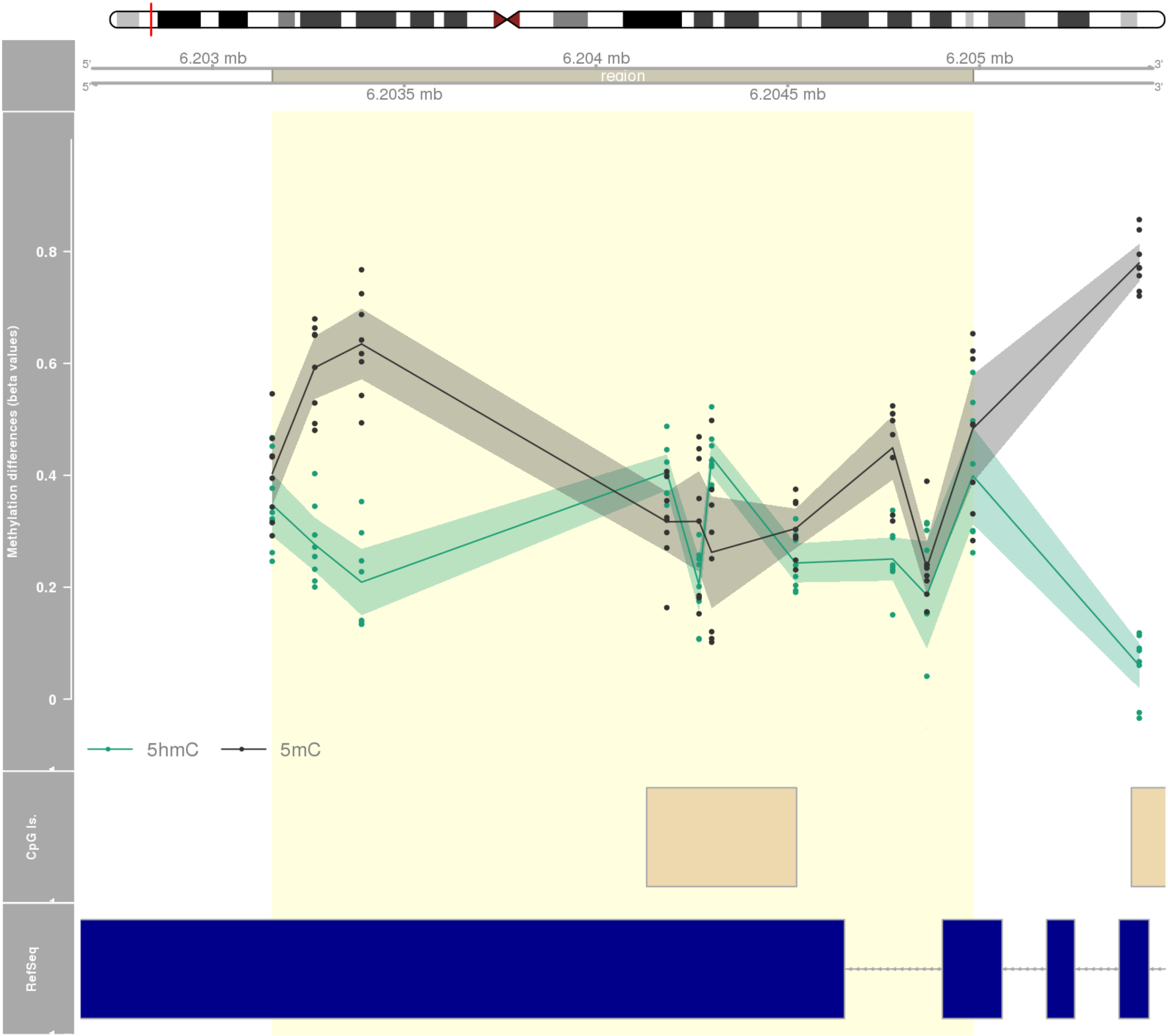
DMR 250 // chr3:55516711-55518798 // 2087 pb. (12 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: WNT5A -



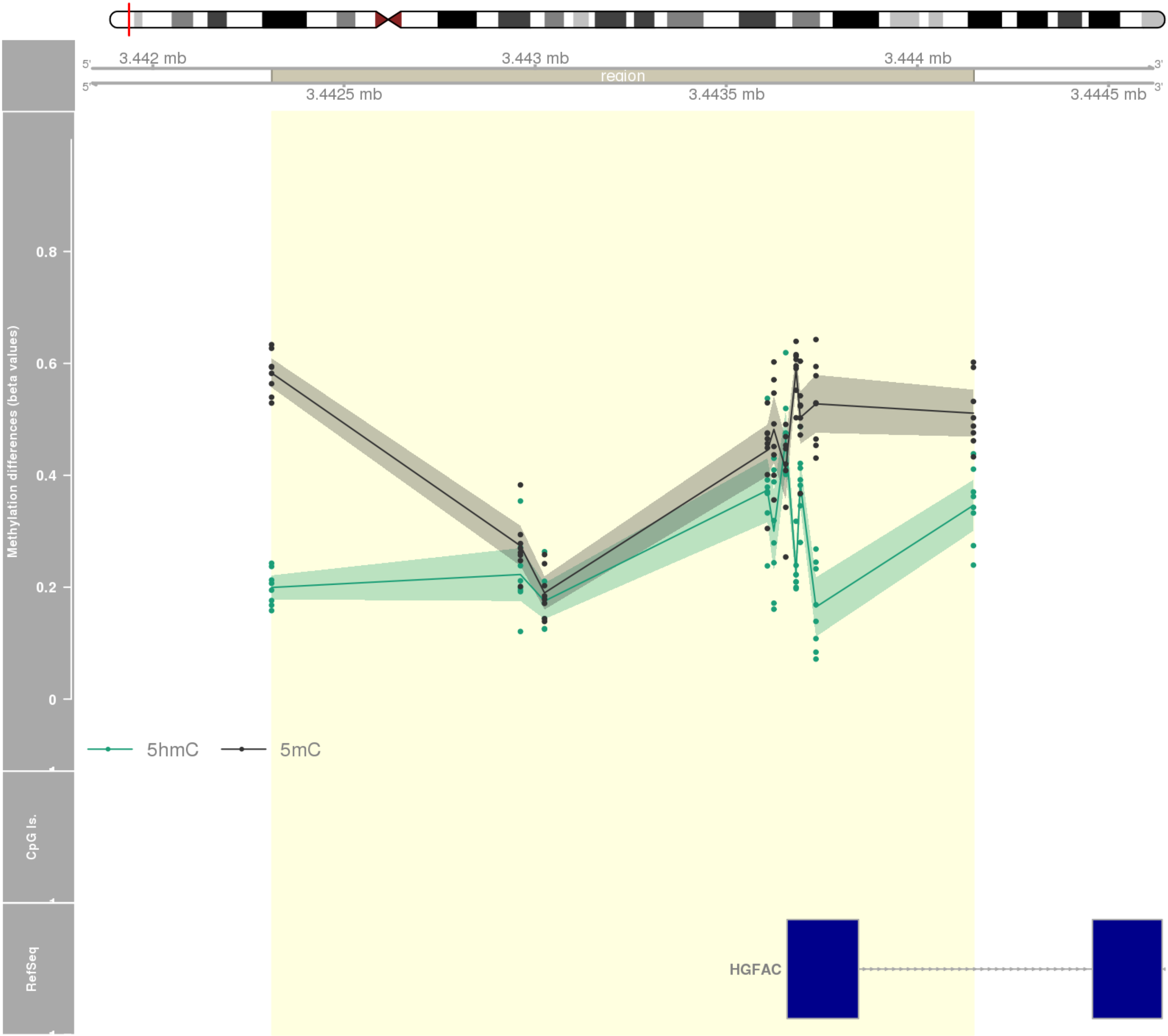
DMR 251 // chr15:74218418-74218921 // 503 pb. (11 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: LOXL1-AS1 / LOXL1 -



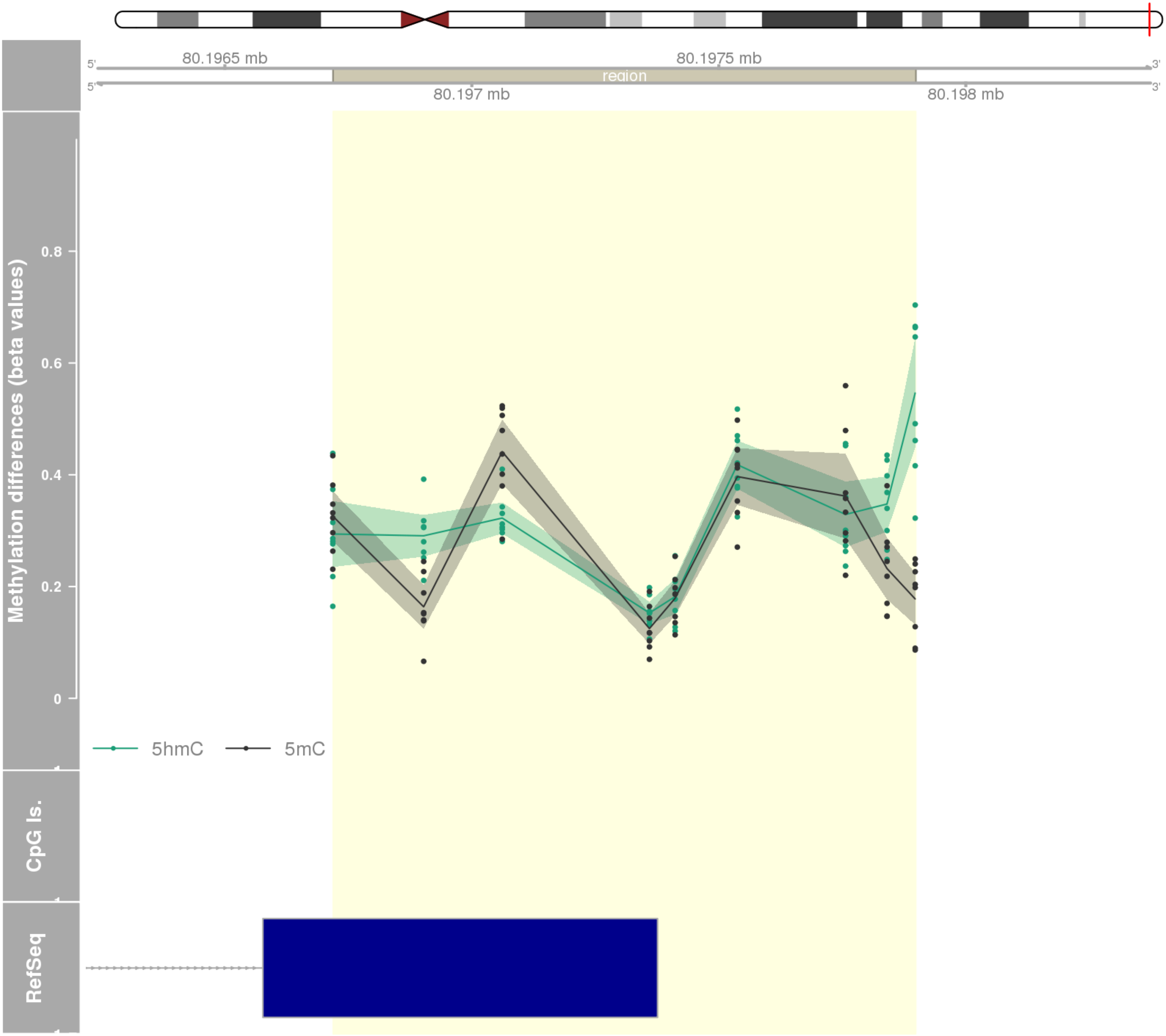
DMR 252 // chr7:6203156-6204983 // 1827 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: CYTH3 -



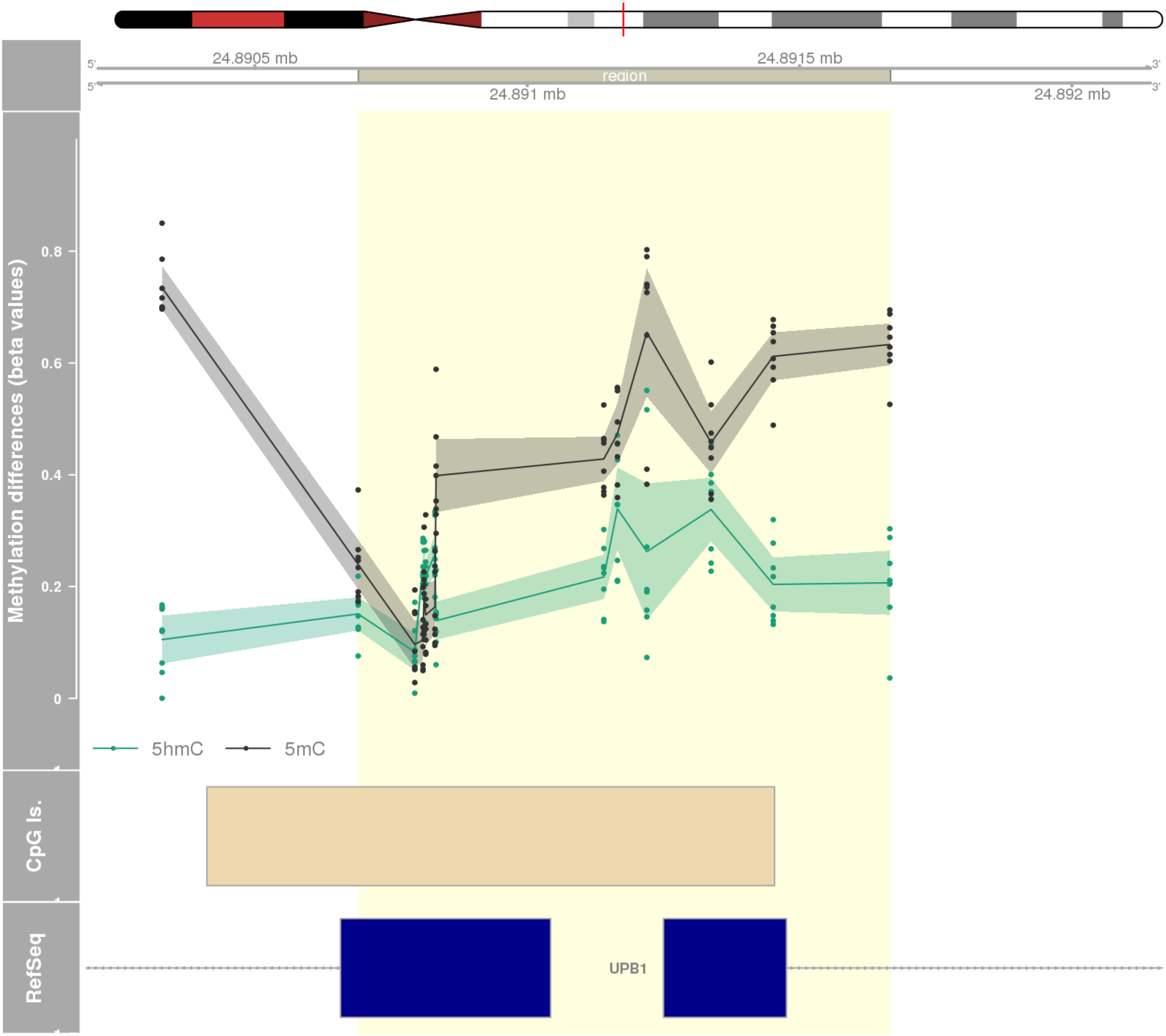
DMR 253 // chr4:3442311-3444147 // 1836 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: HGFAC -



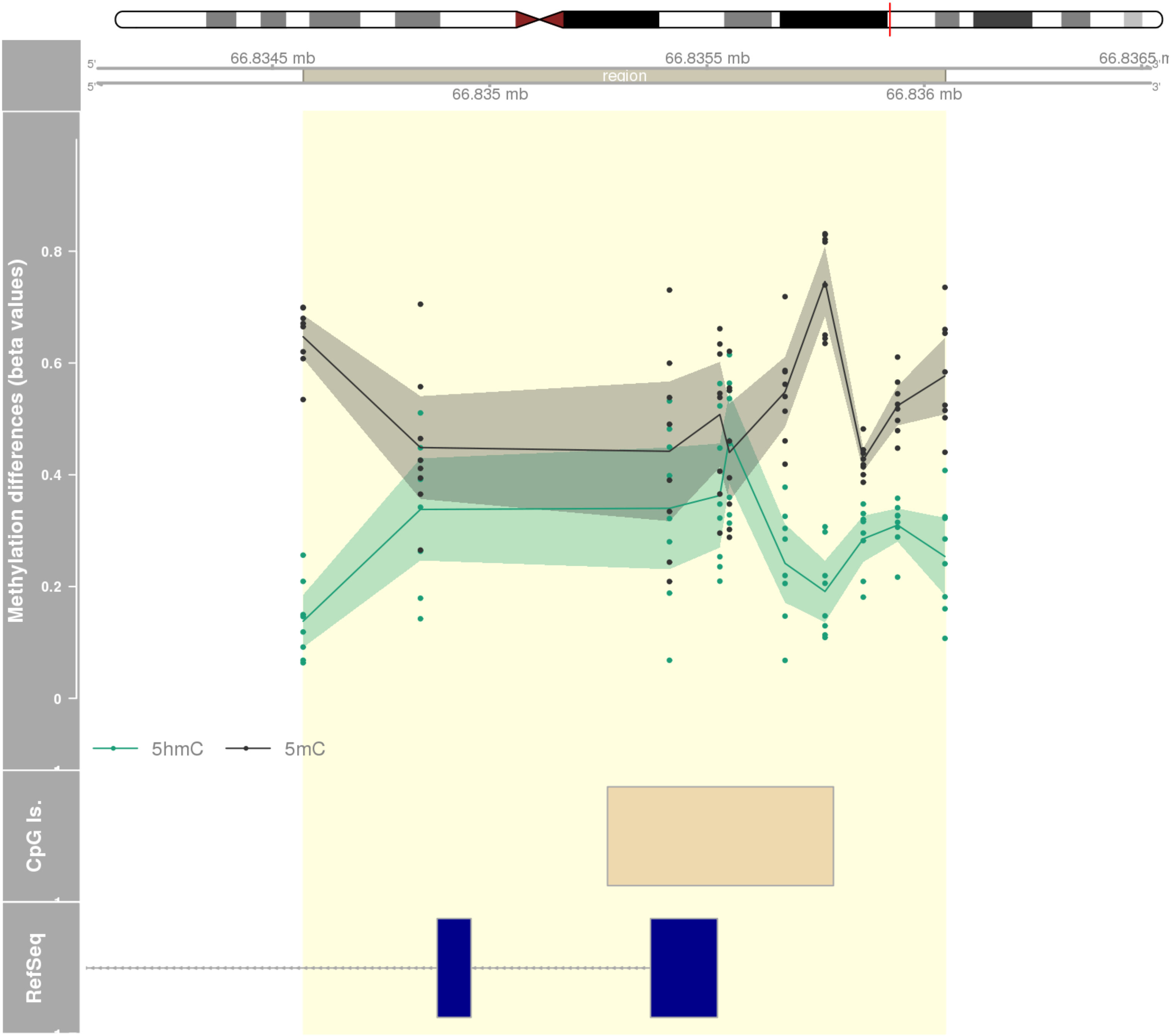
DMR 254 // chr17:80196719-80197898 // 1179 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: SLC16A3 / CSNK1D -



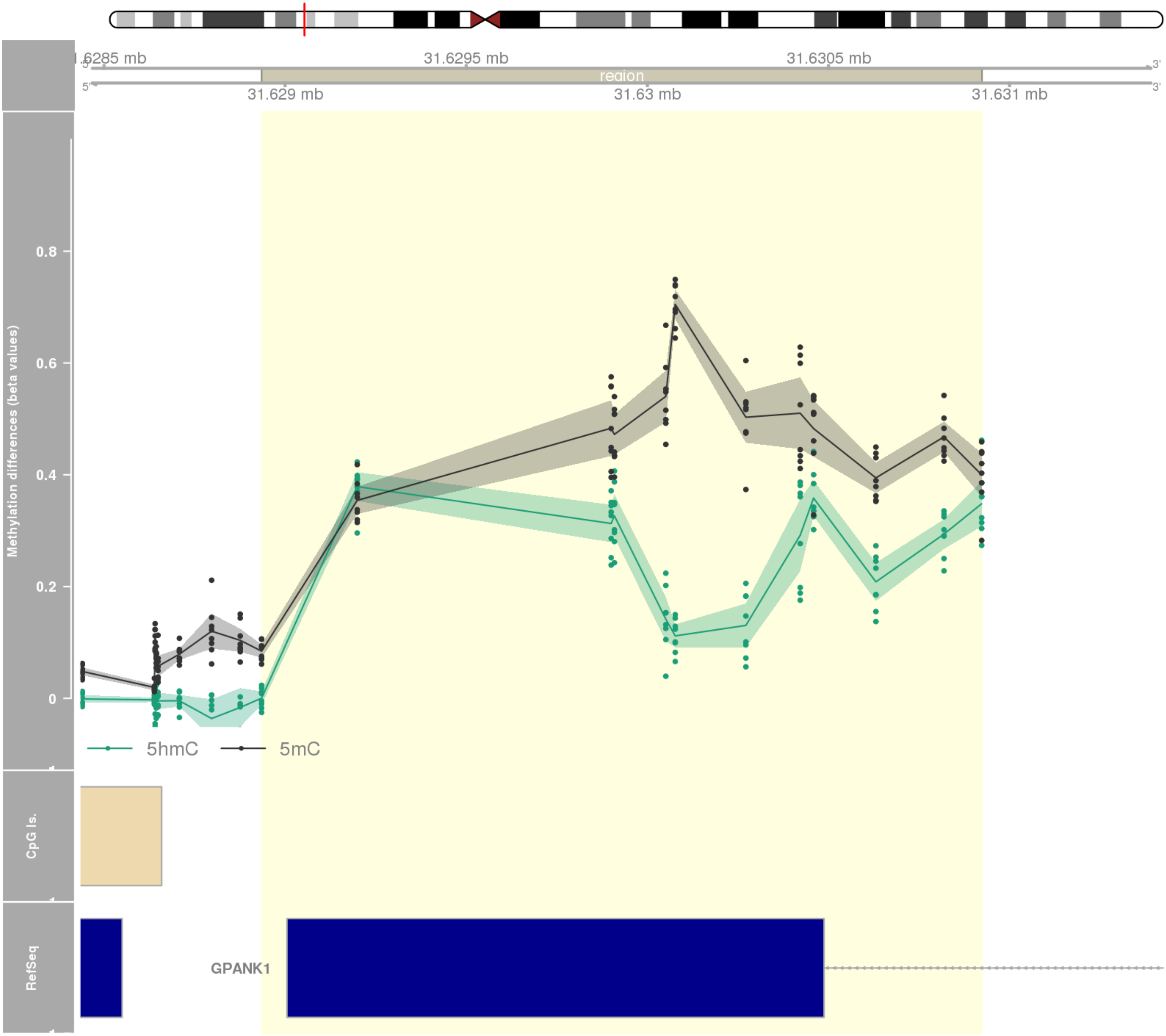
DMR 255 // chr22:24890690-24891666 // 976 pb. (13 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: UPB1 / ADORA2A-AS1 -



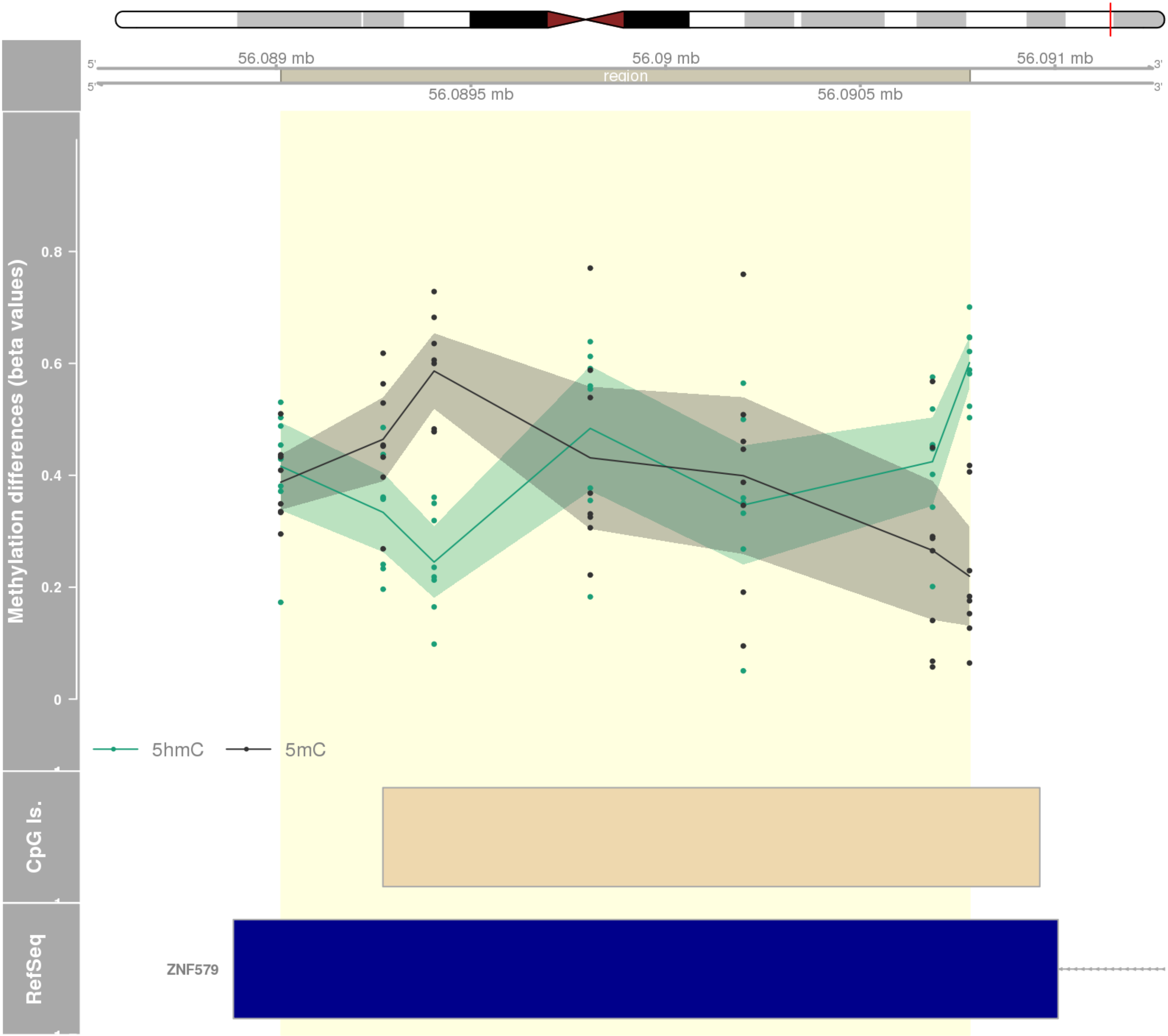
DMR 256 // chr16:66834571-66836048 // 1477 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: CCDC79 -



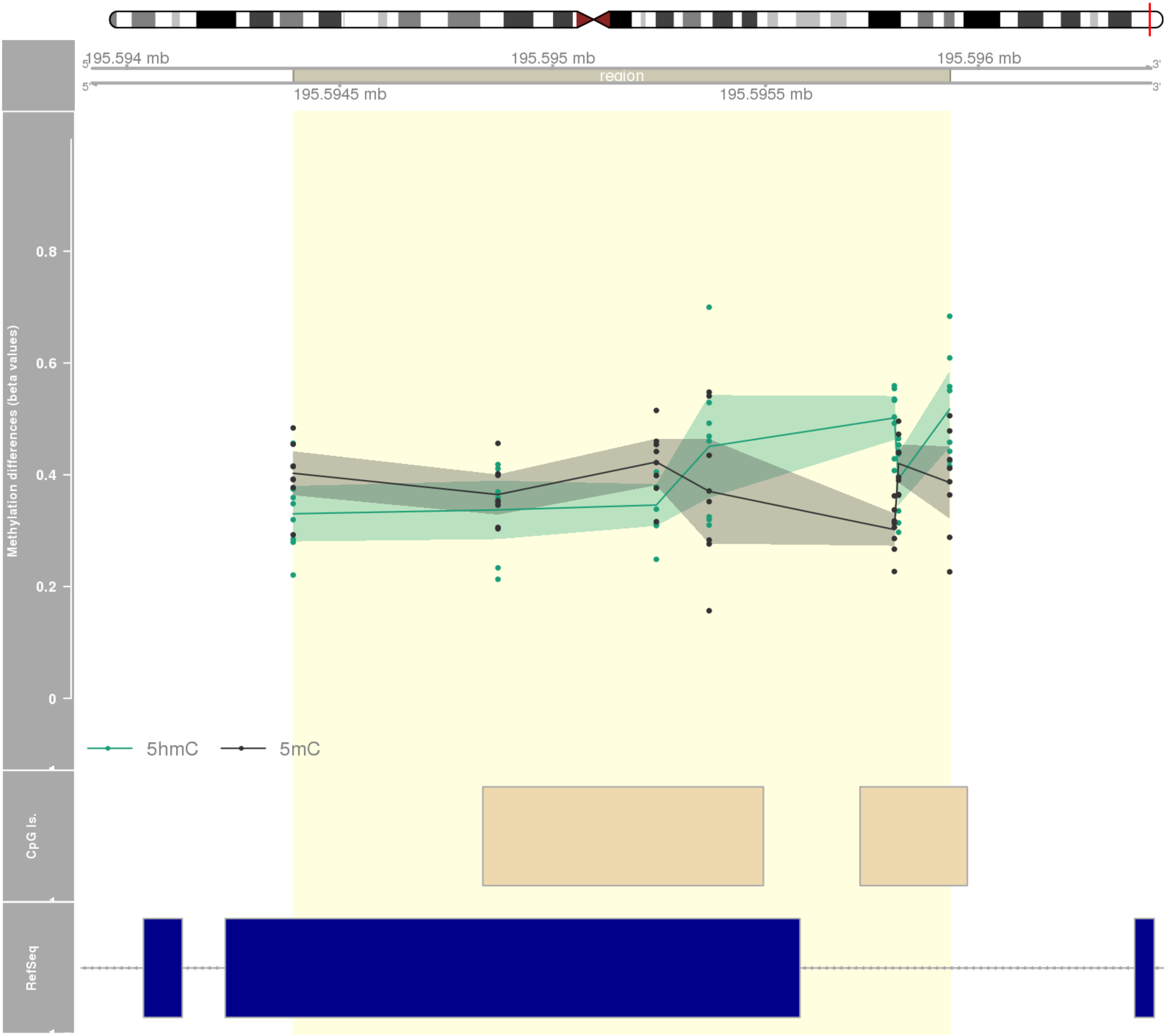
DMR 257 // chr6:31628935-31630923 // 1988 pb. (12 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: GPANK1 -



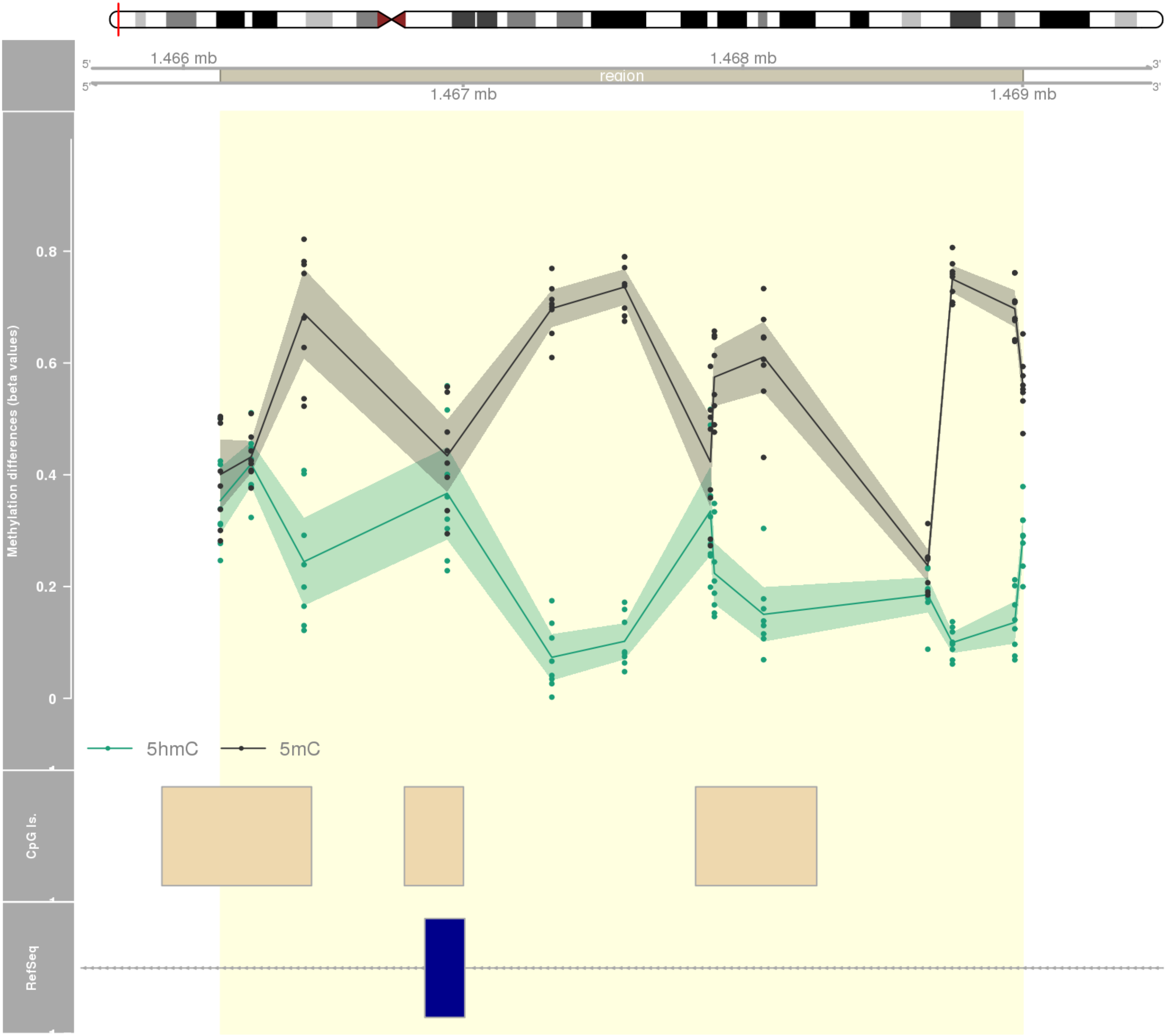
DMR 258 // chr19:56089012-56090781 // 1769 pb. (7 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: ZNF579 -



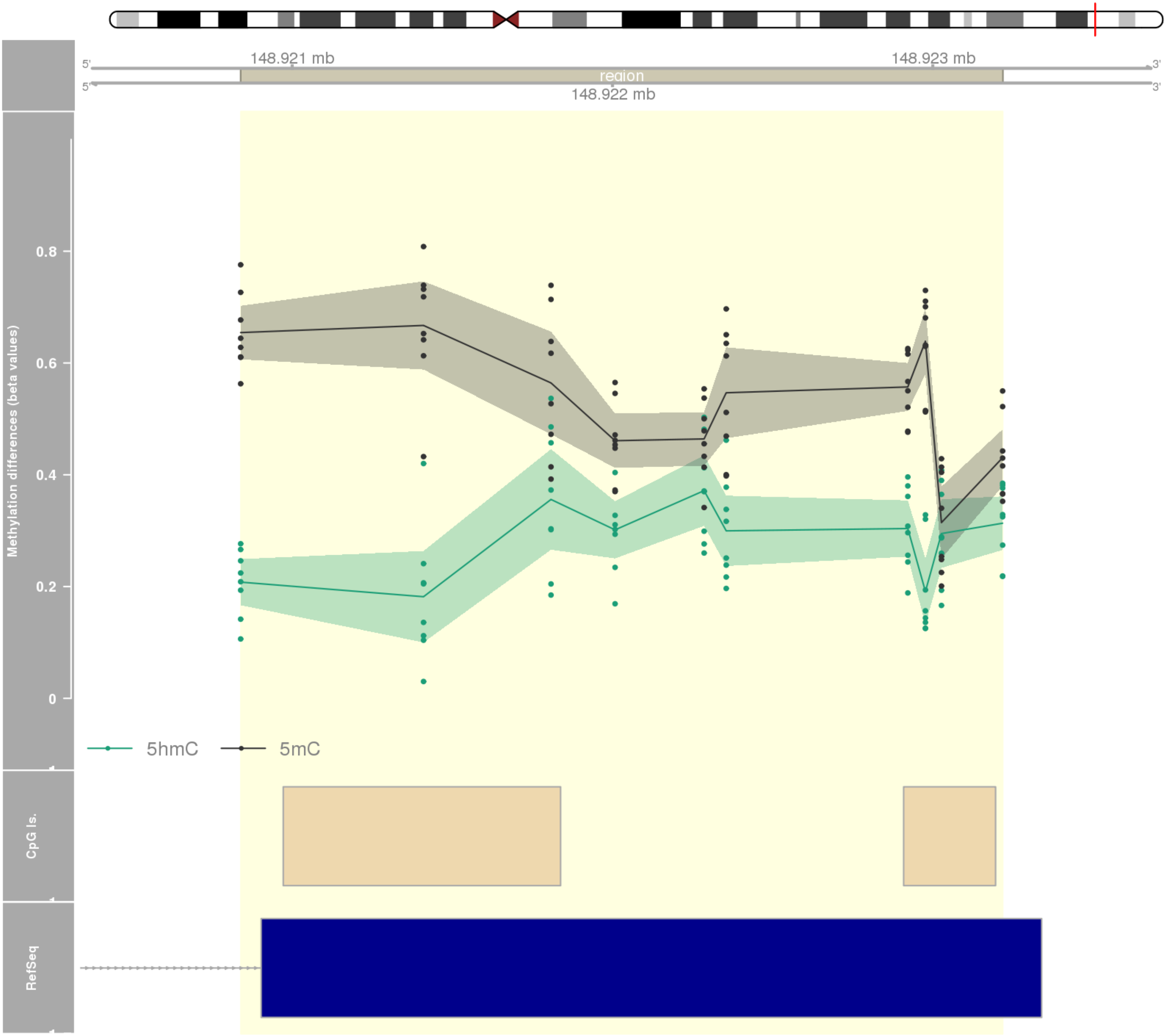
DMR 259 // chr3:195594391-195595933 // 1542 pb. (7 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.013 // fwerArea: 0.559
- genes: TNK2 -



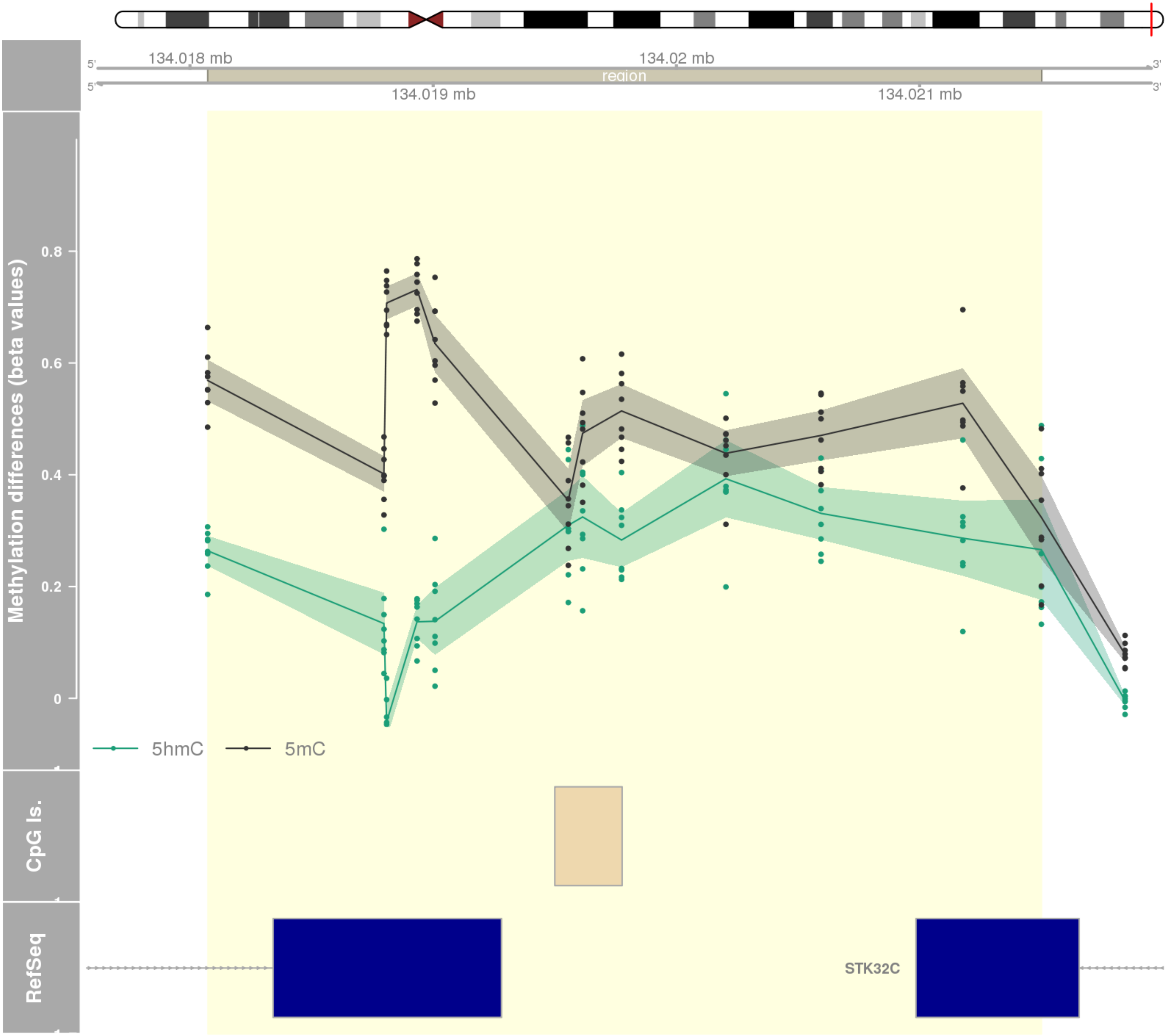
DMR 260 // chr5:1466132-1469001 // 2869 pb. (13 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: LPCAT1 -

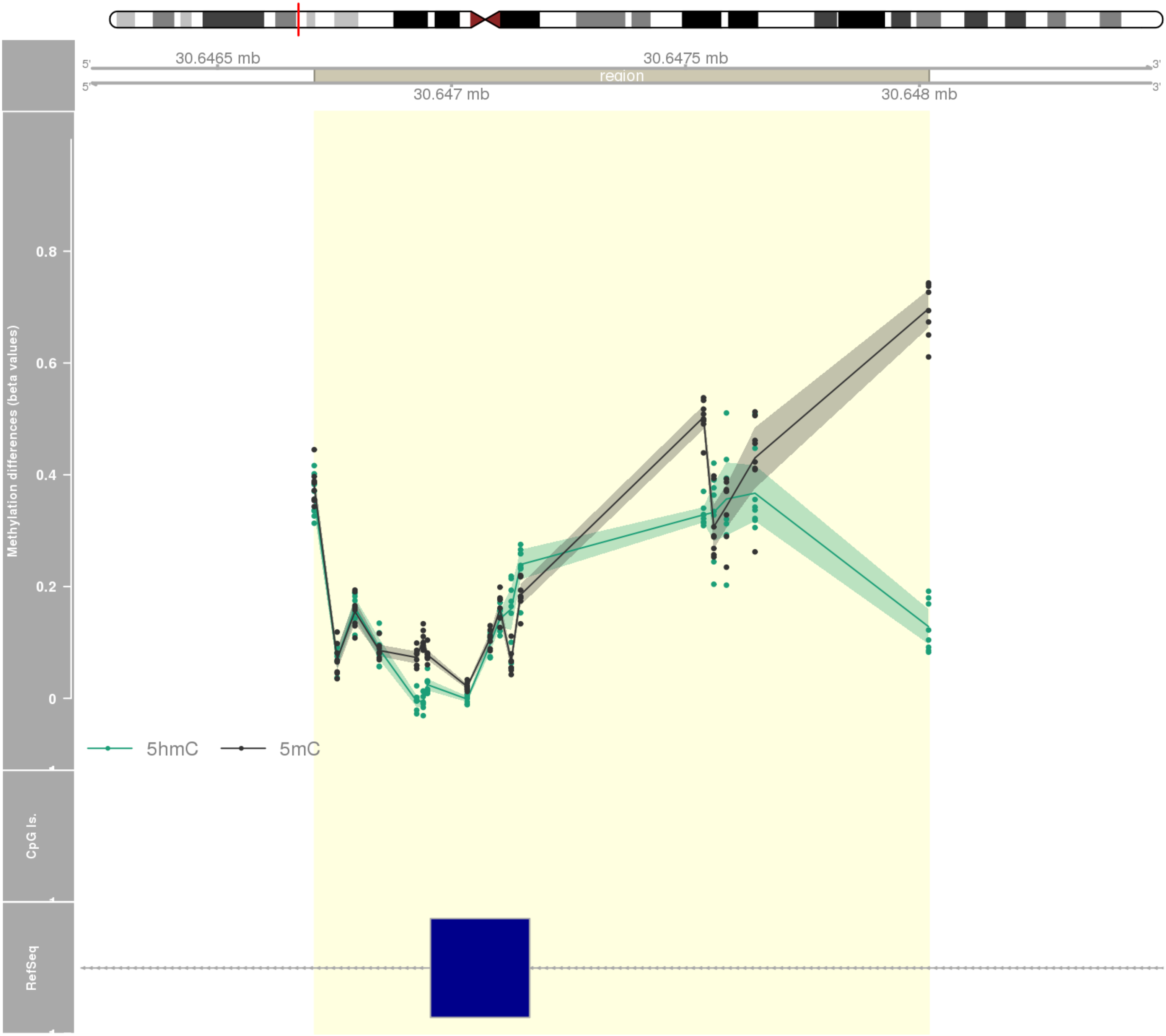


DMR 261 // chr7:148920839-148923218 // 2379 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: ZNF282 -



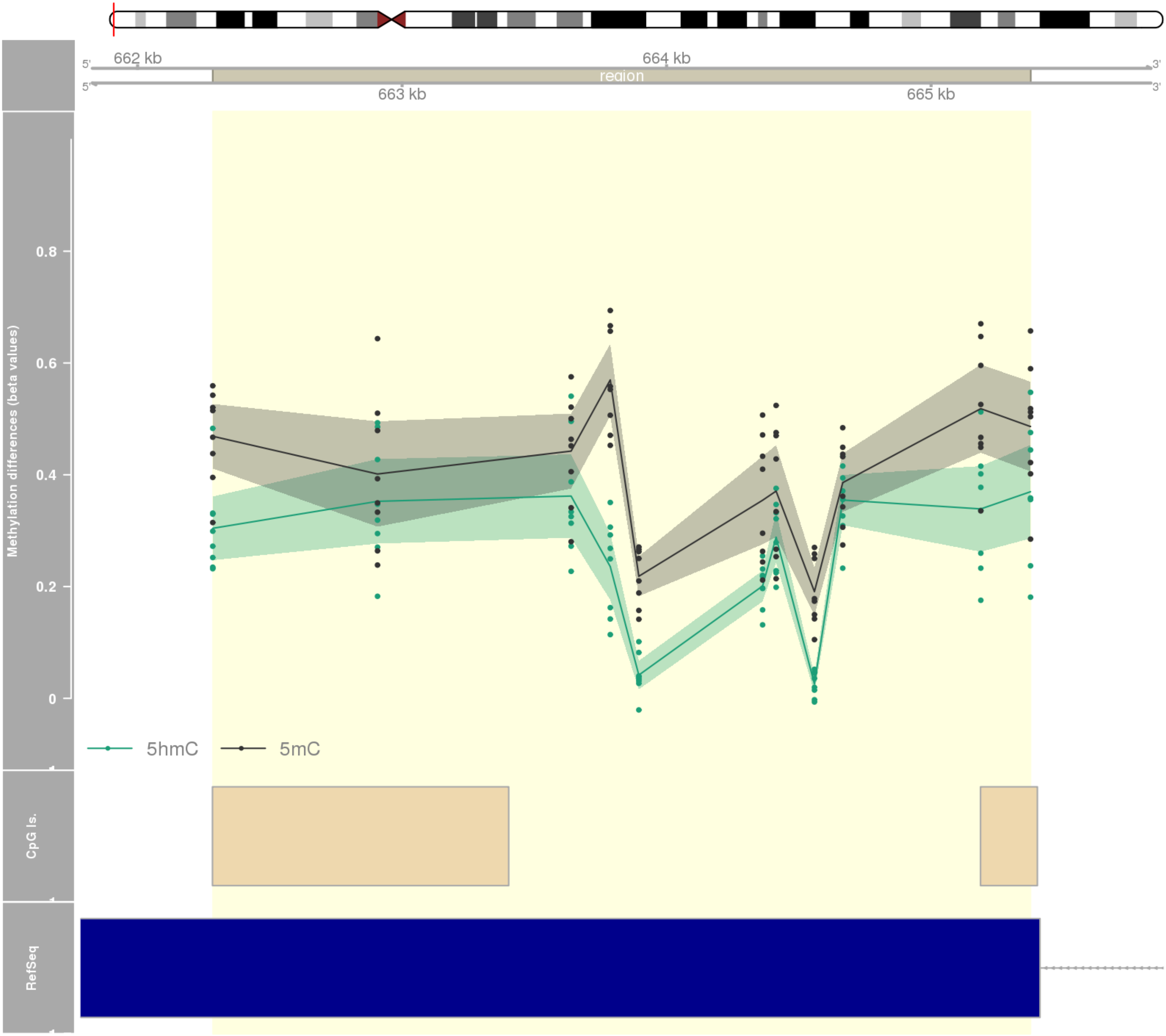
DMR 262 // chr10:134018073-134021501 // 3428 pb. (12 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: DPYSL4 / STK32C -



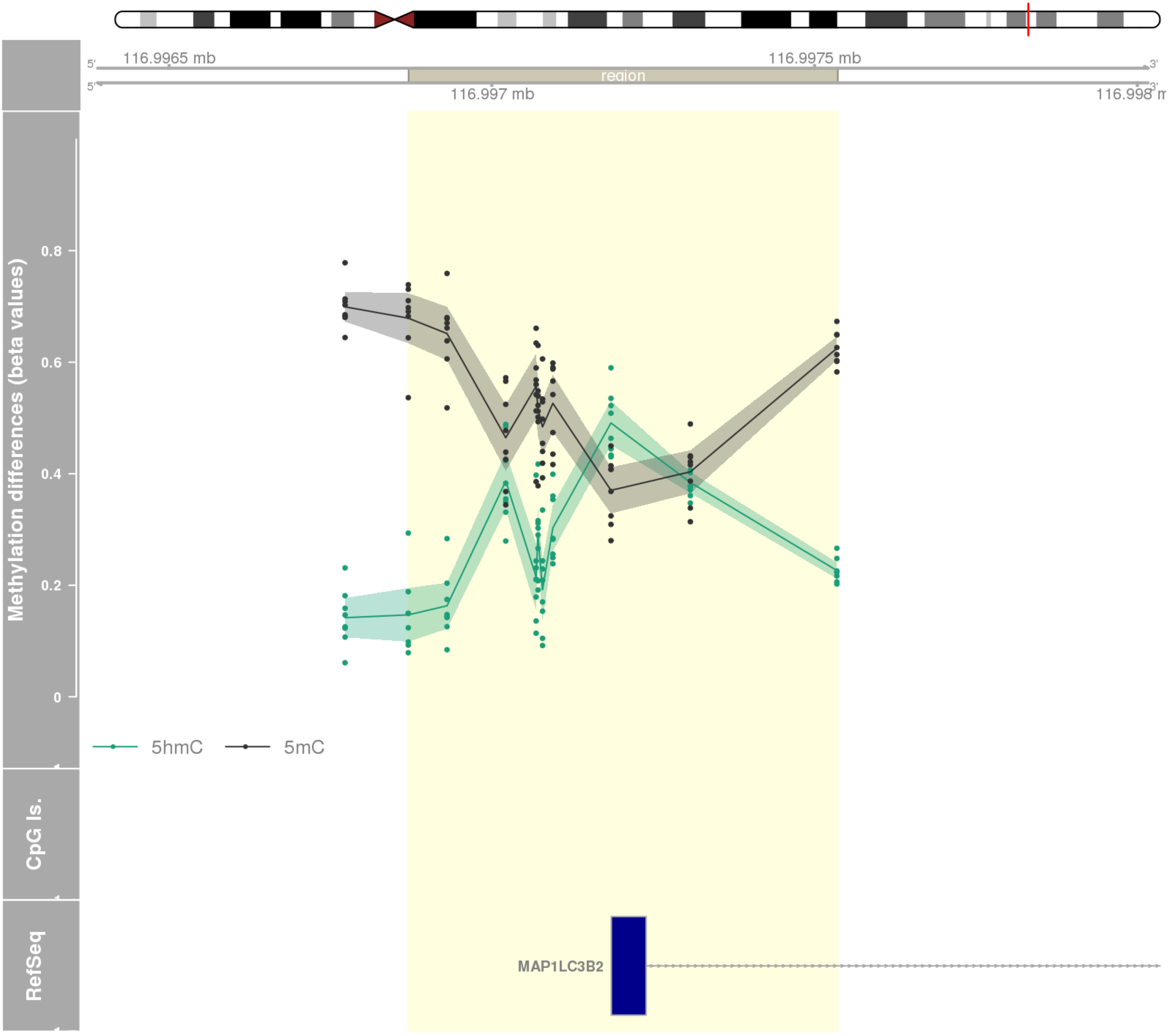


DMR 263 // chr6:30646707-30648020 // 1313 pb. (17 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: PPP1R18 -

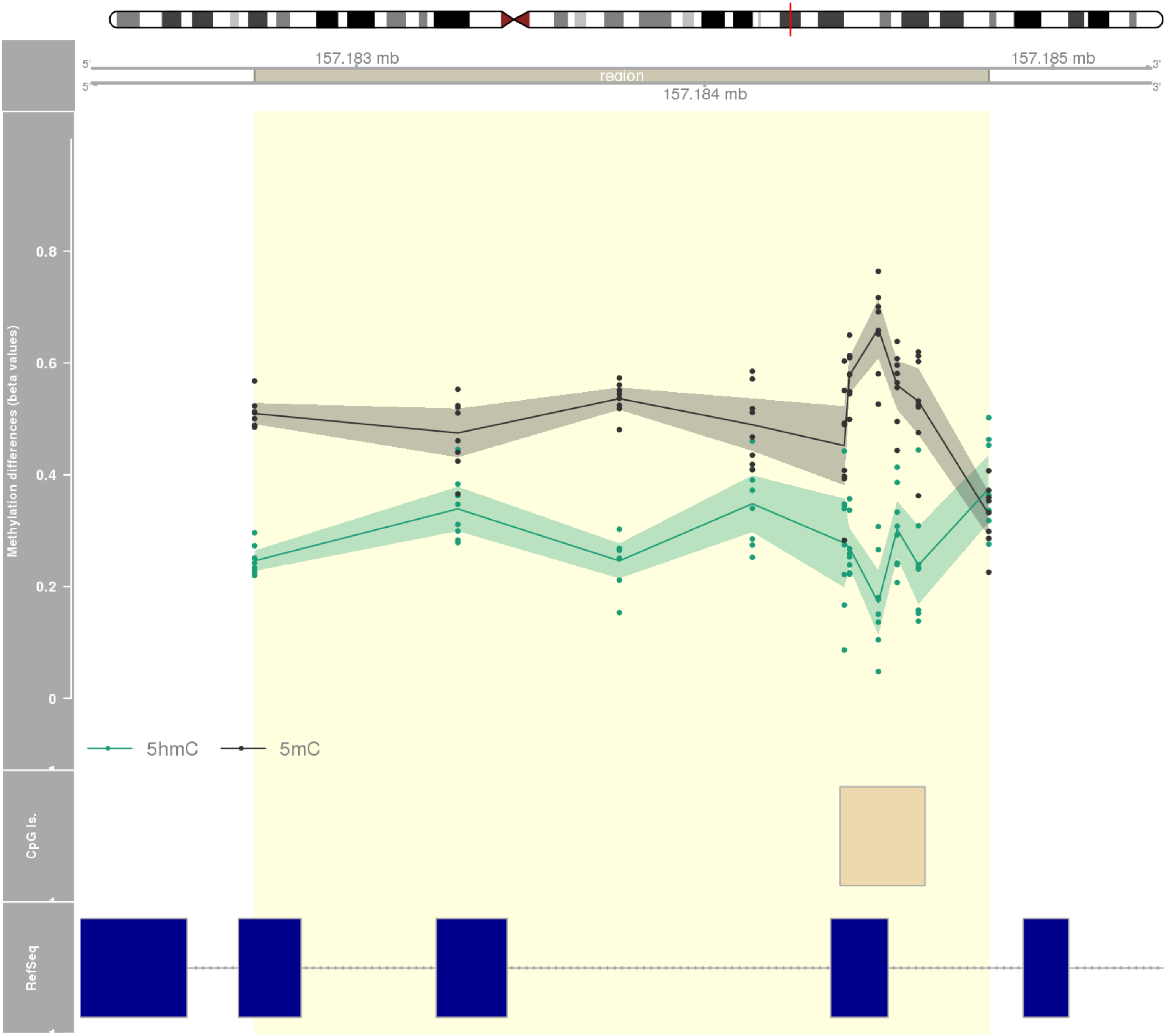
DMR 264 // chr5:662284-665376 // 3092 pb. (11 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: CEP72 / TPPP -



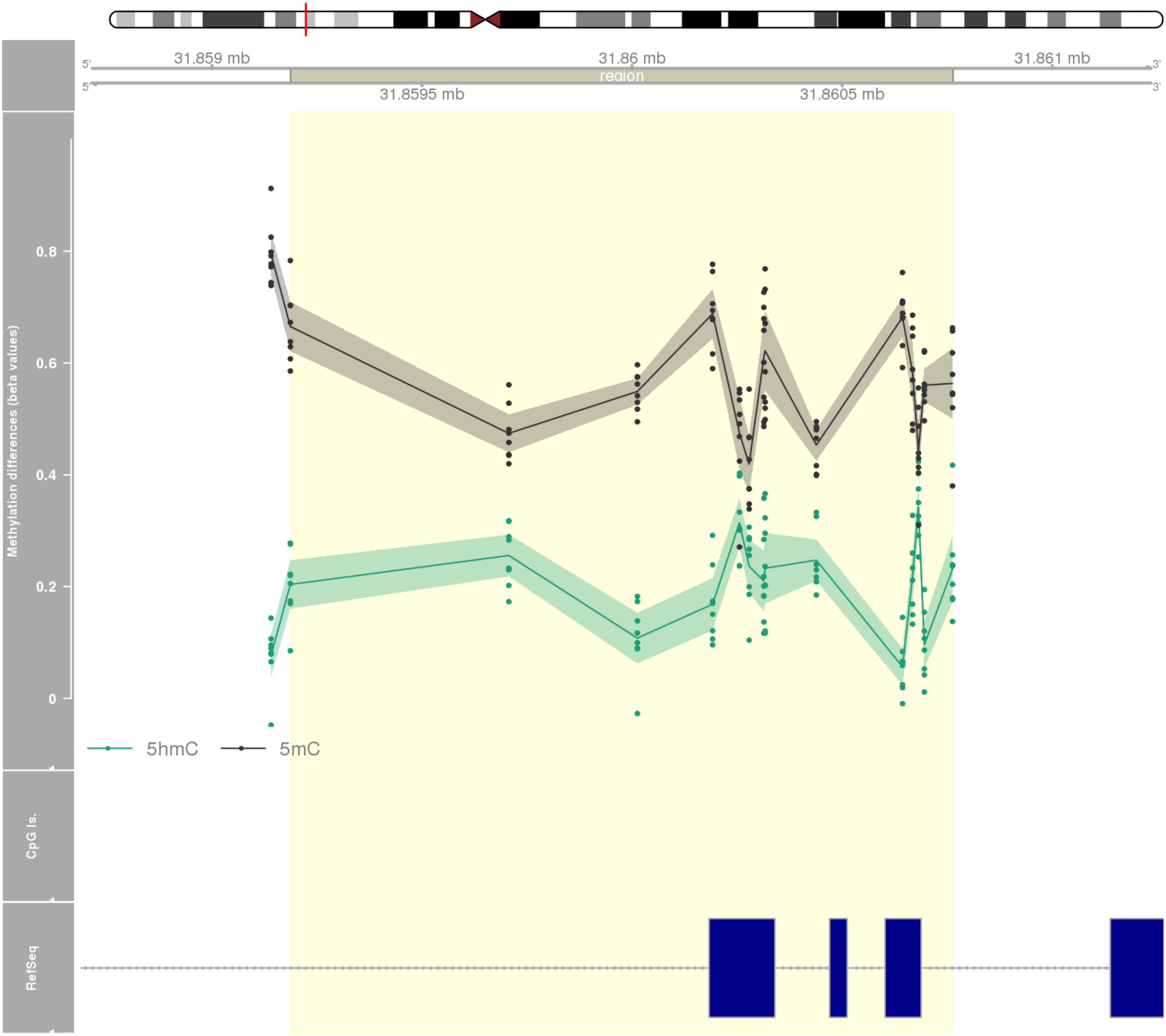
DMR 265 // chr12:116996871-116997535 // 664 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: MAP1LC3B2 -



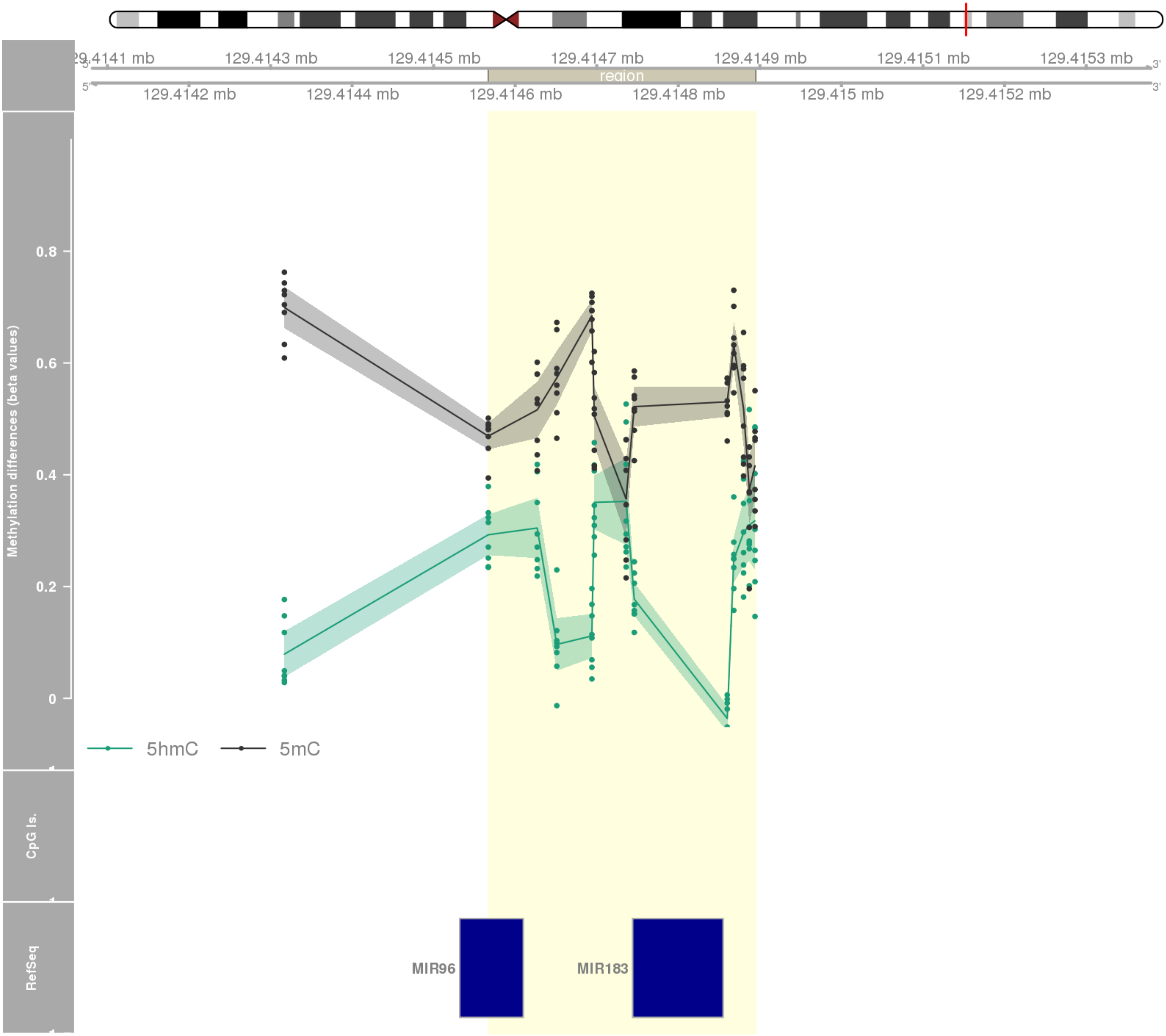
DMR 266 // chr2:157182707-157184816 // 2109 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: NR4A2 -



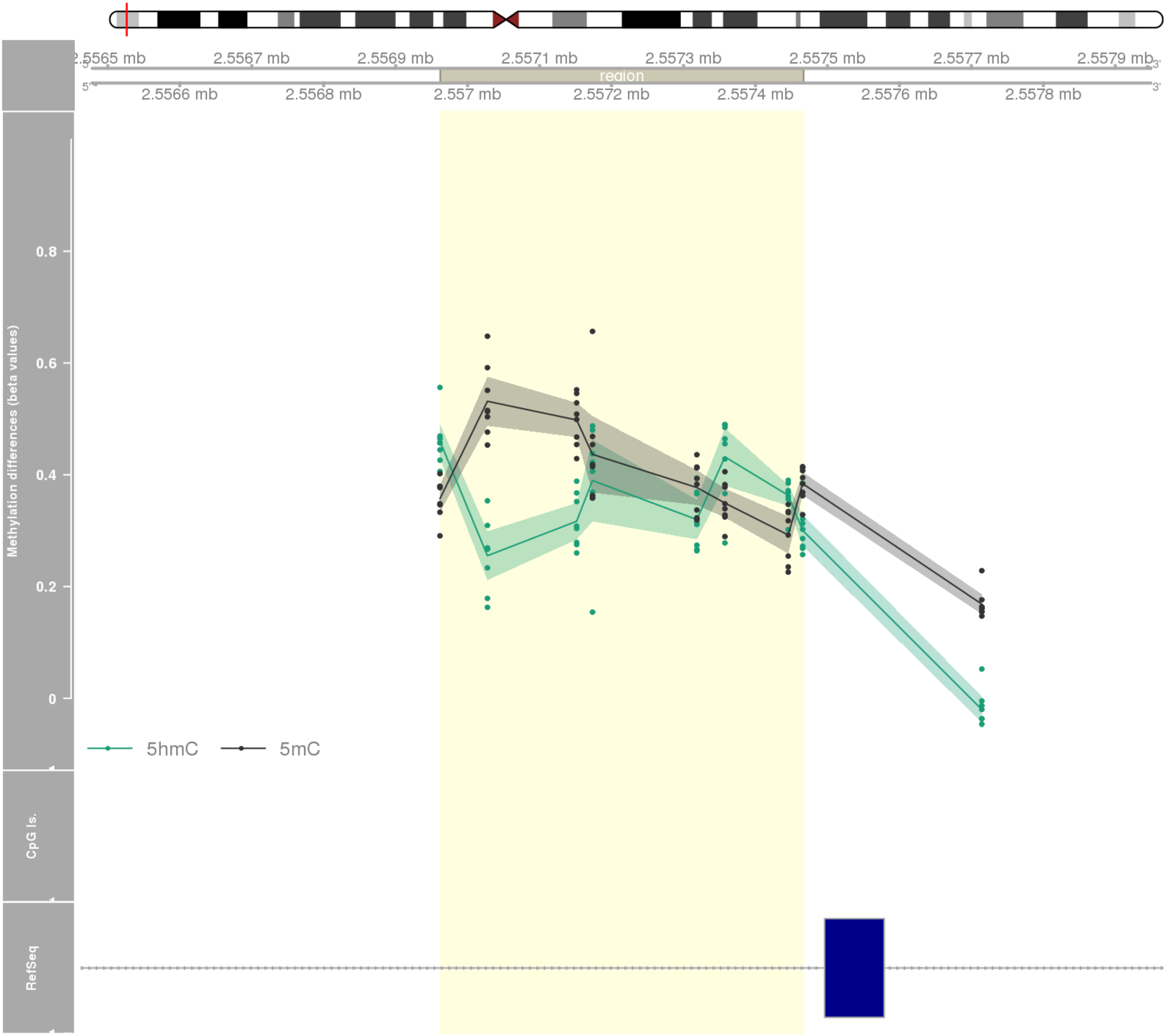
DMR 267 // chr6:31859187-31860763 // 1576 pb. (14 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: EHMT2 -



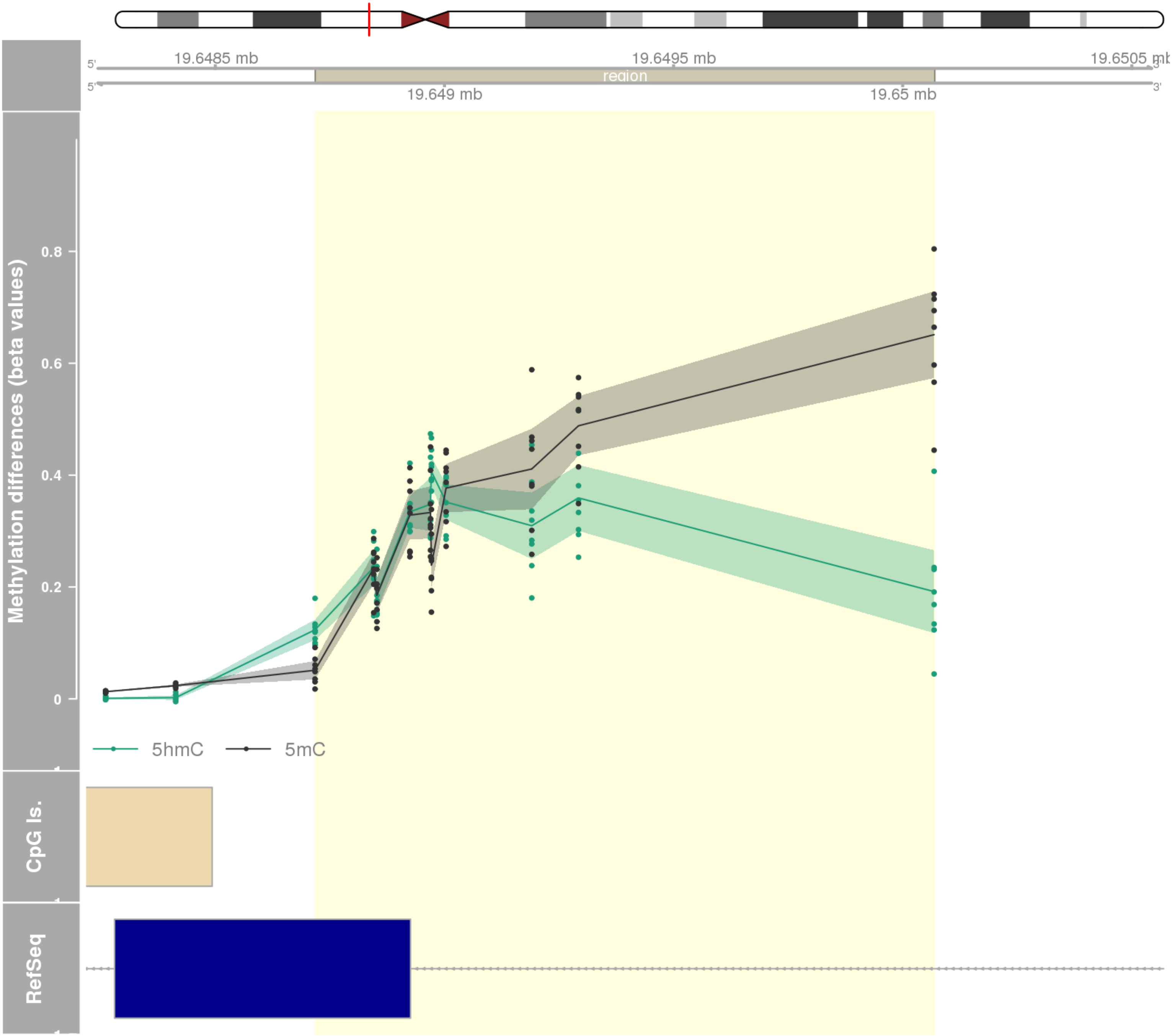
DMR 268 // chr7:129414567-129414894 // 327 pb. (12 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: MIR96 / MIR183 -



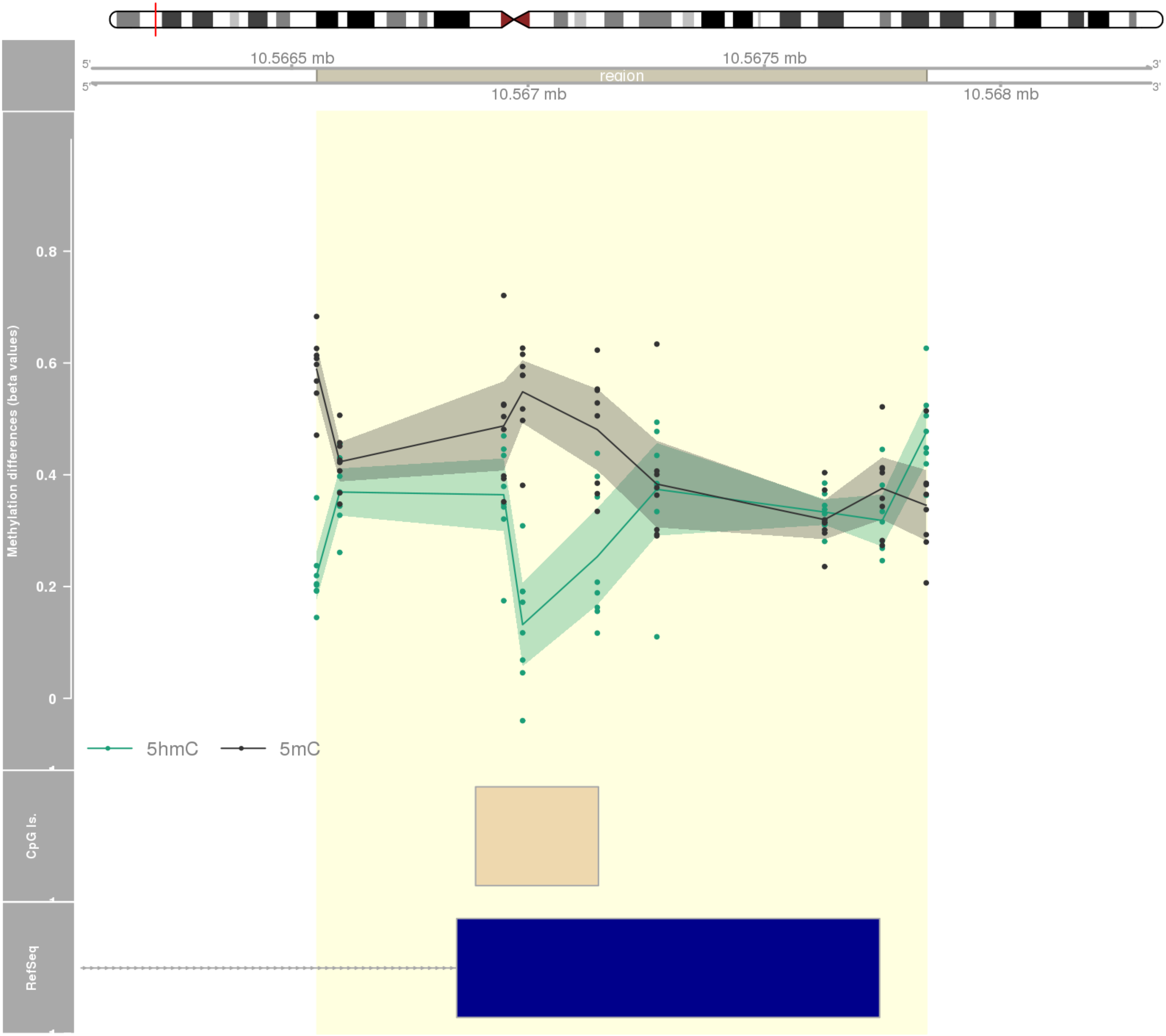
DMR 269 // chr7:2556962-2557466 // 504 pb. (8 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: LFNG -



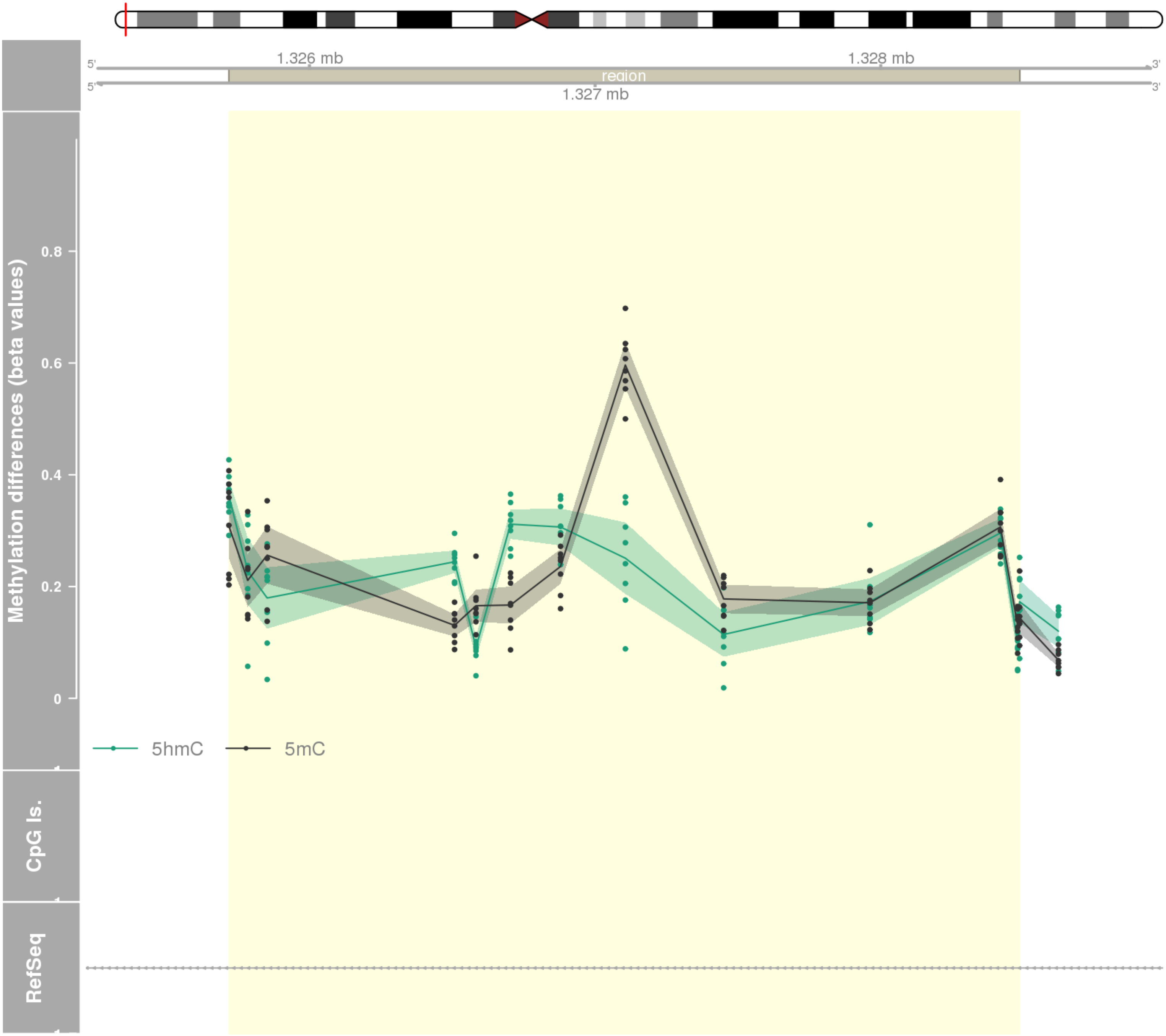
DMR 270 // chr17:19648718-19650069 // 1351 pb. (10 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: ALDH3A1 -



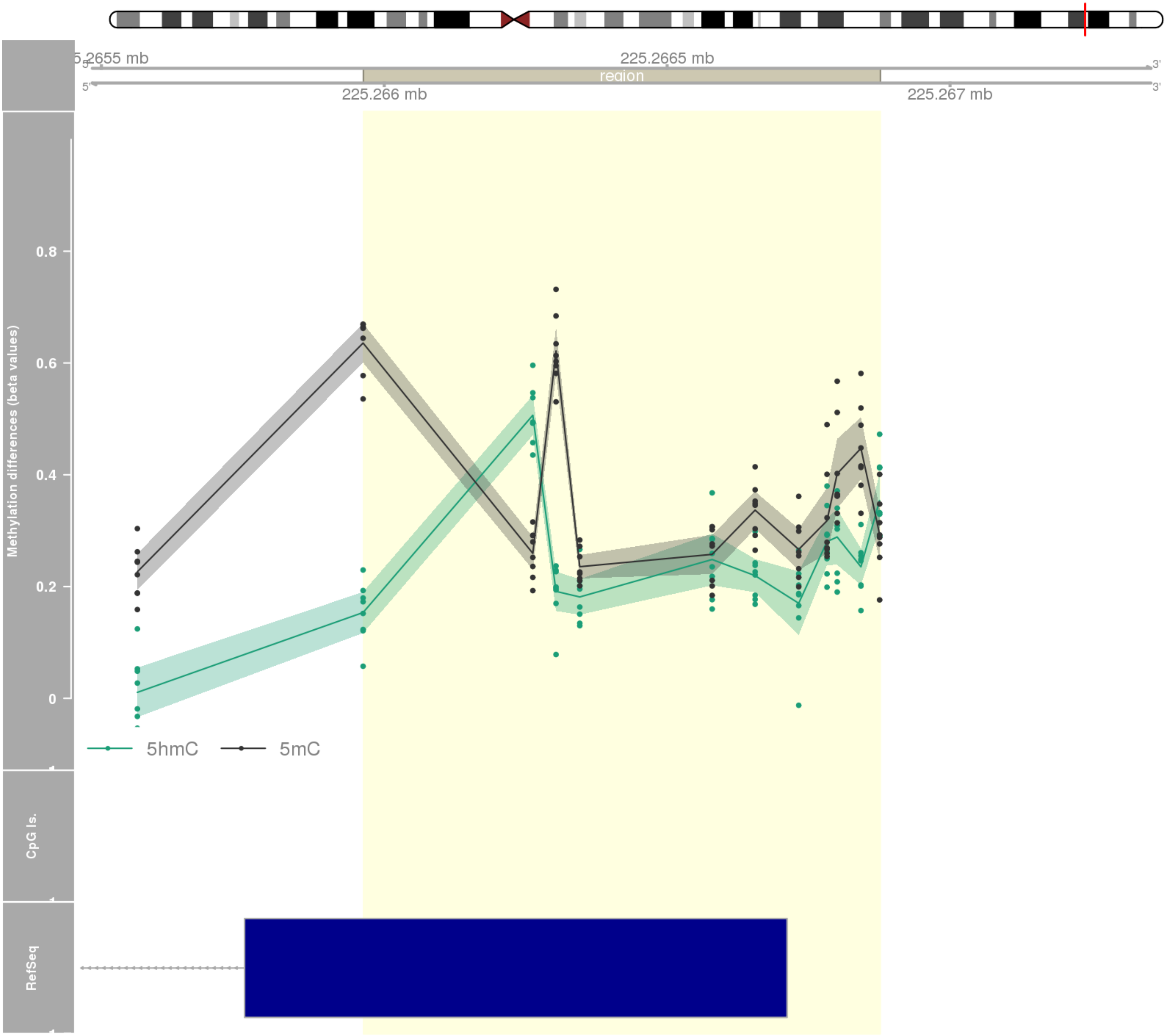
DMR 271 // chr2:10566553-10567843 // 1290 pb. (9 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: HPCAL1 -



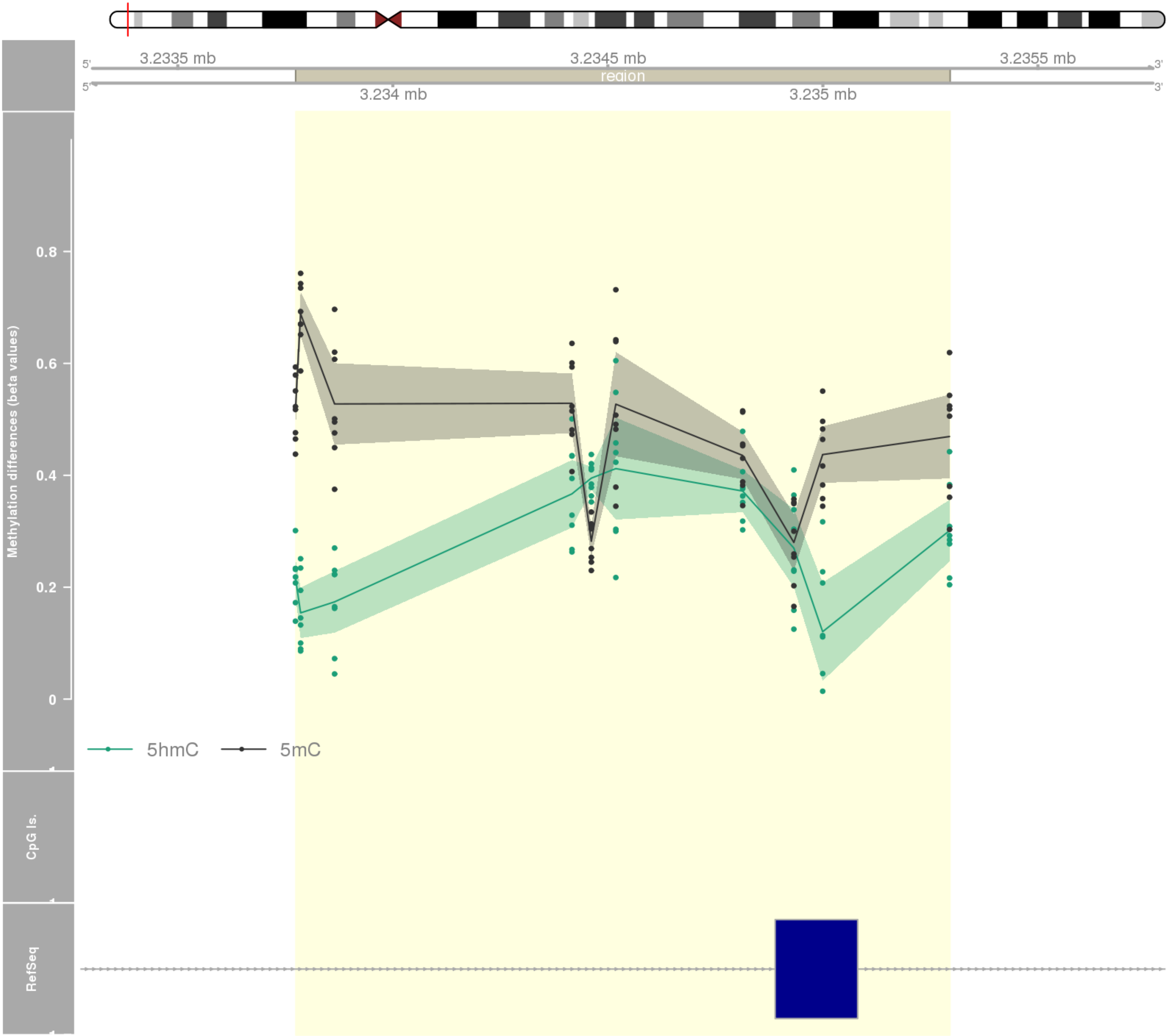
DMR 272 // chr11:1325718-1328486 // 2768 pb. (13 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: TOLLIP -



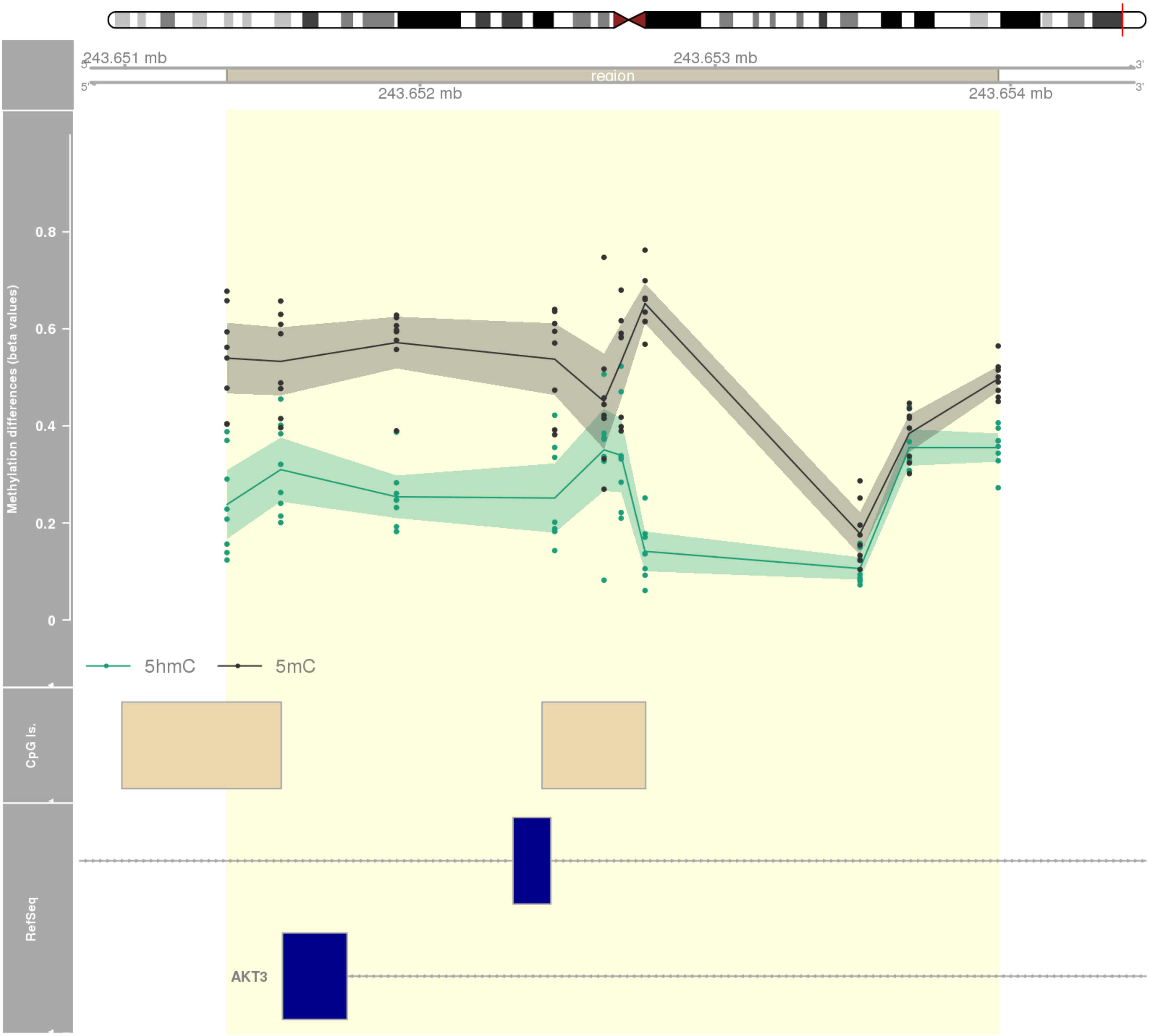
DMR 273 // chr2:225265963-225266876 // 913 pb. (11 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: FAM124B -



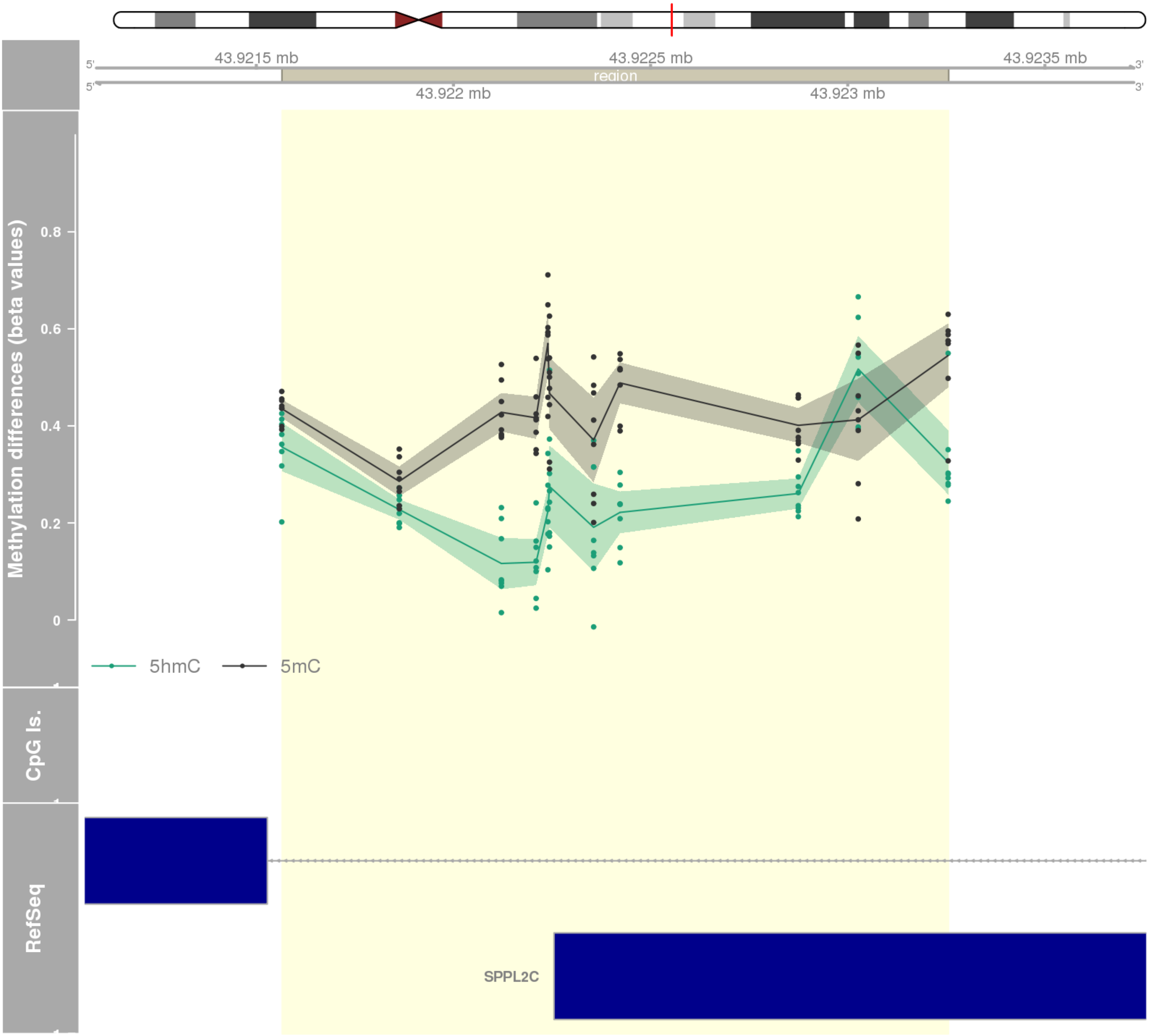
DMR 274 // chr4:3233774-3235295 // 1521 pb. (10 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: HTT -



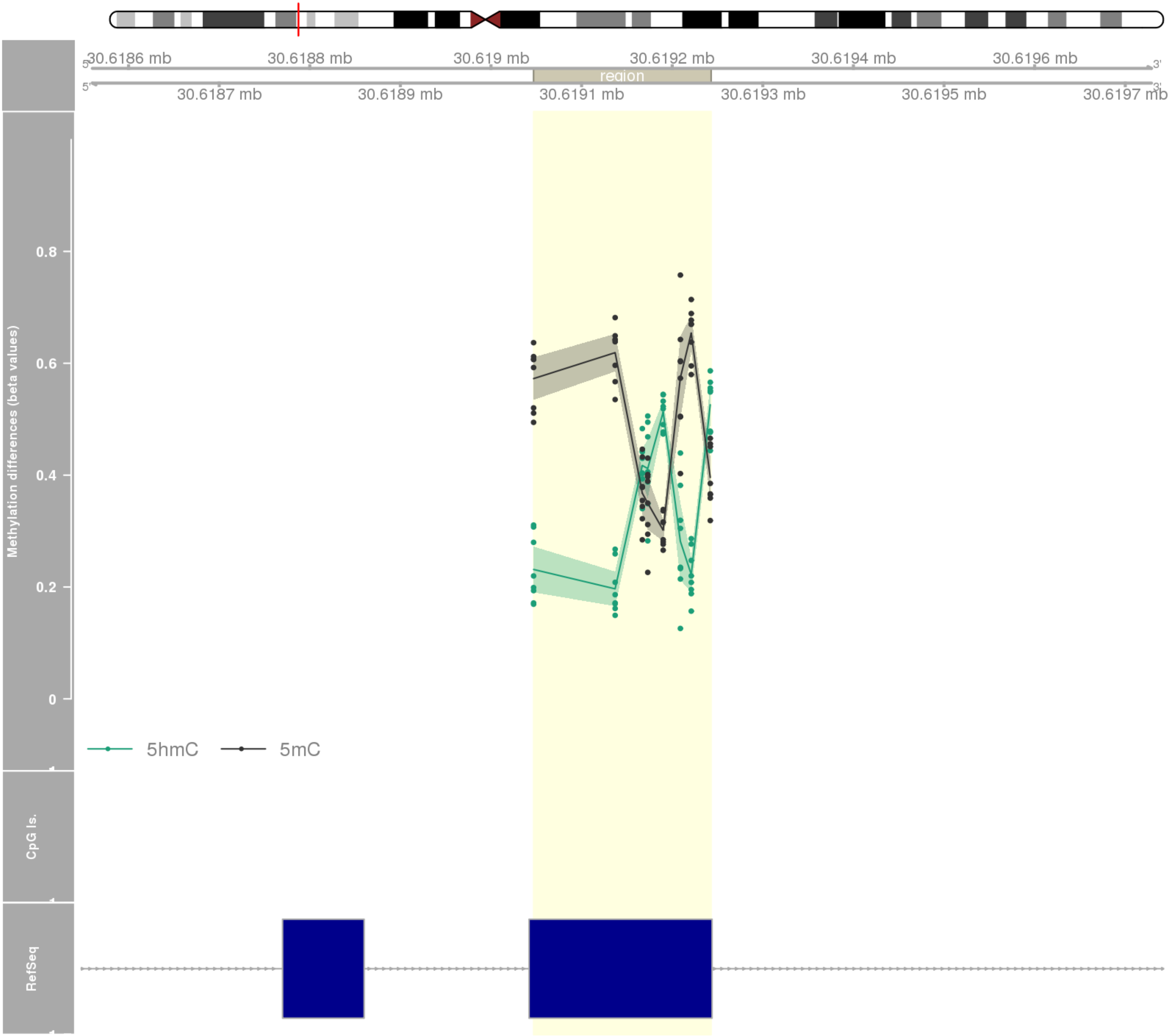
DMR 275 // chr1:243651346-243653958 // 2612 pb. (10 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: SDCCAG8 / AKT3 -



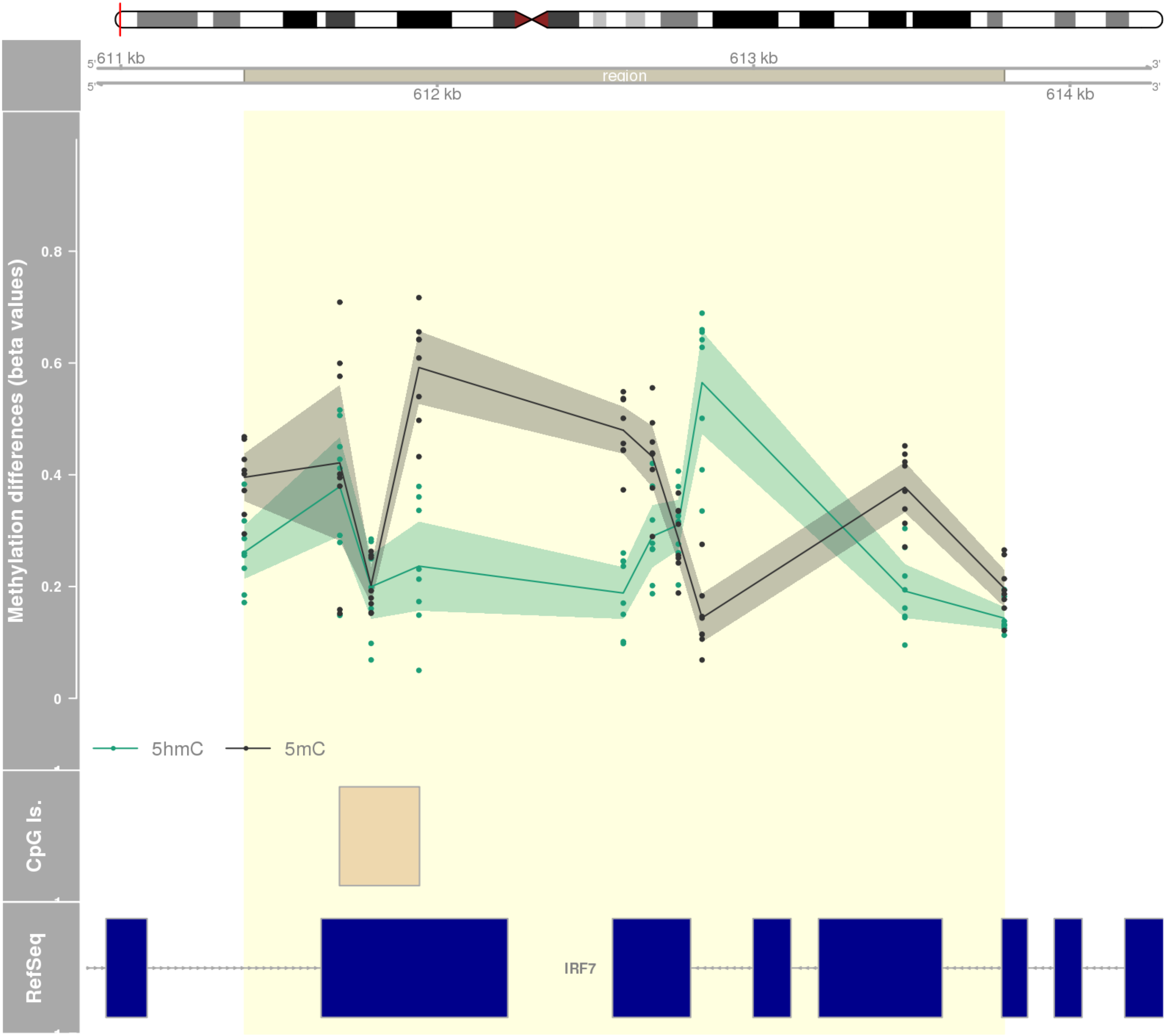
DMR 276 // chr17:43921565-43923255 // 1690 pb. (11 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: SPPL2C / MAPT-AS1 -



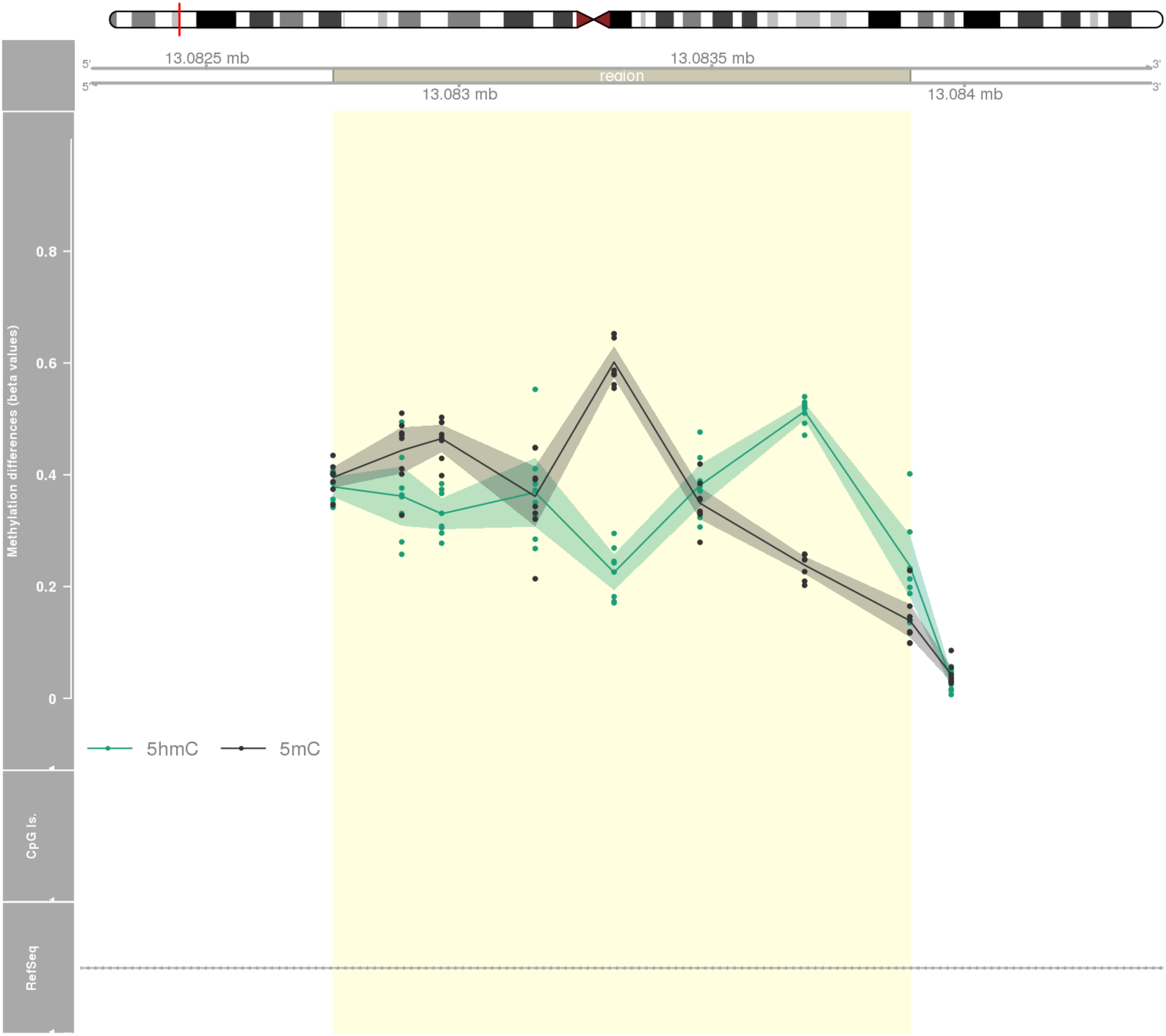
DMR 277 // chr6:30619047-30619242 // 195 pb. (8 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: C6orf136 -



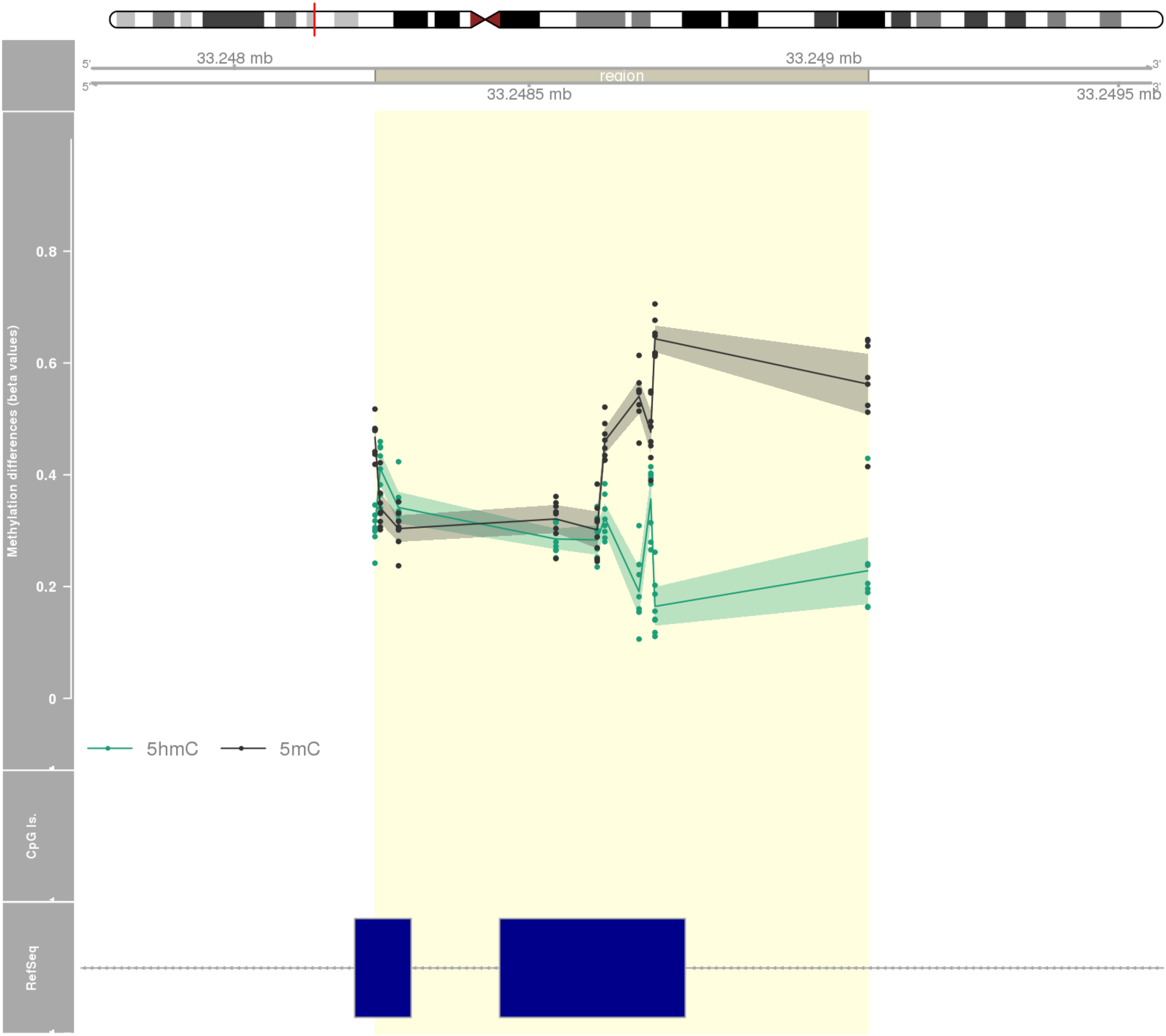
DMR 278 // chr11:611390-613792 // 2402 pb. (10 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.014 // fwerArea: 0.559
- genes: PHRF1 / IRF7 -



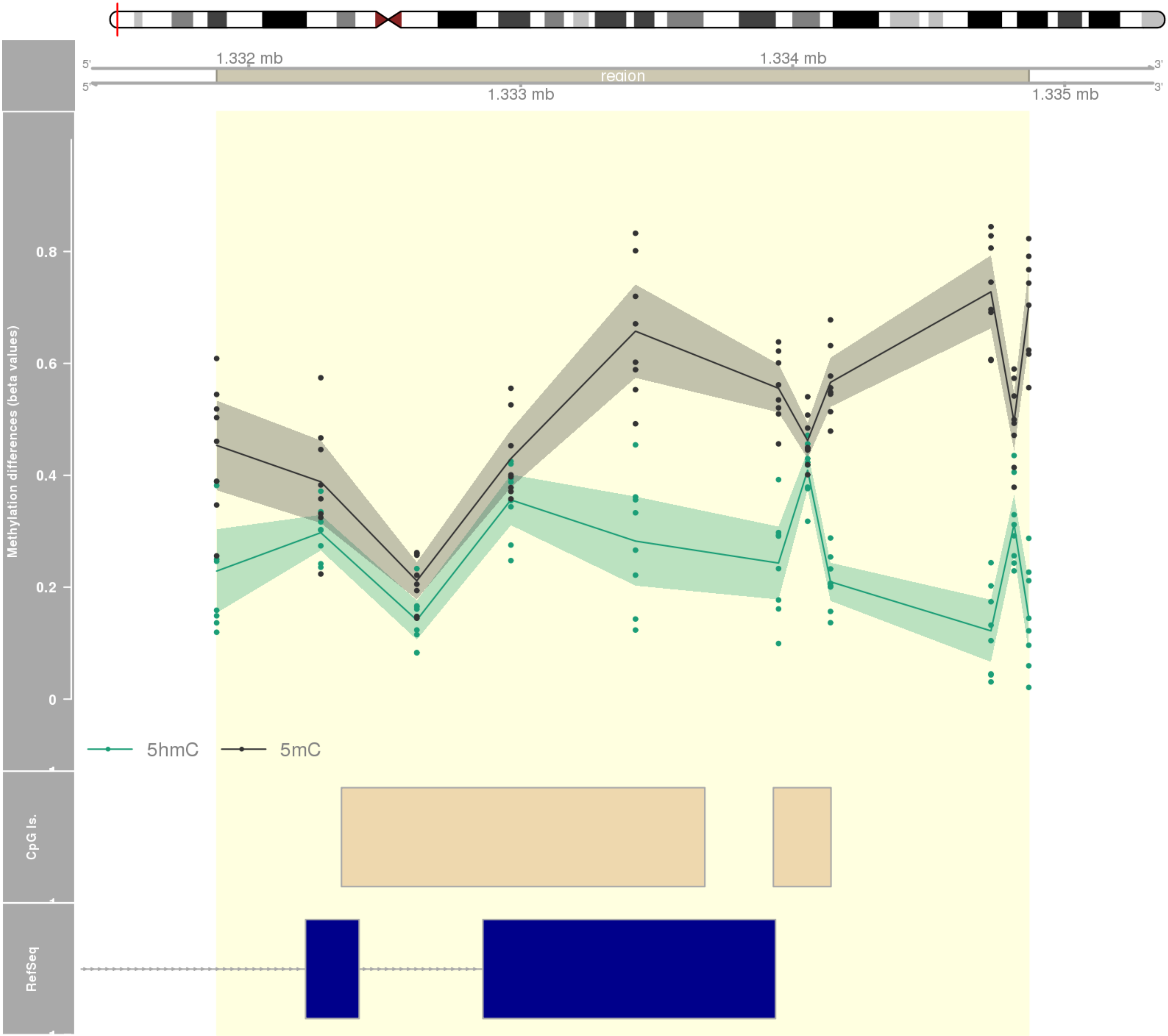
DMR 279 // chr3:13082751-13083892 // 1141 pb. (8 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: IQSEC1 -



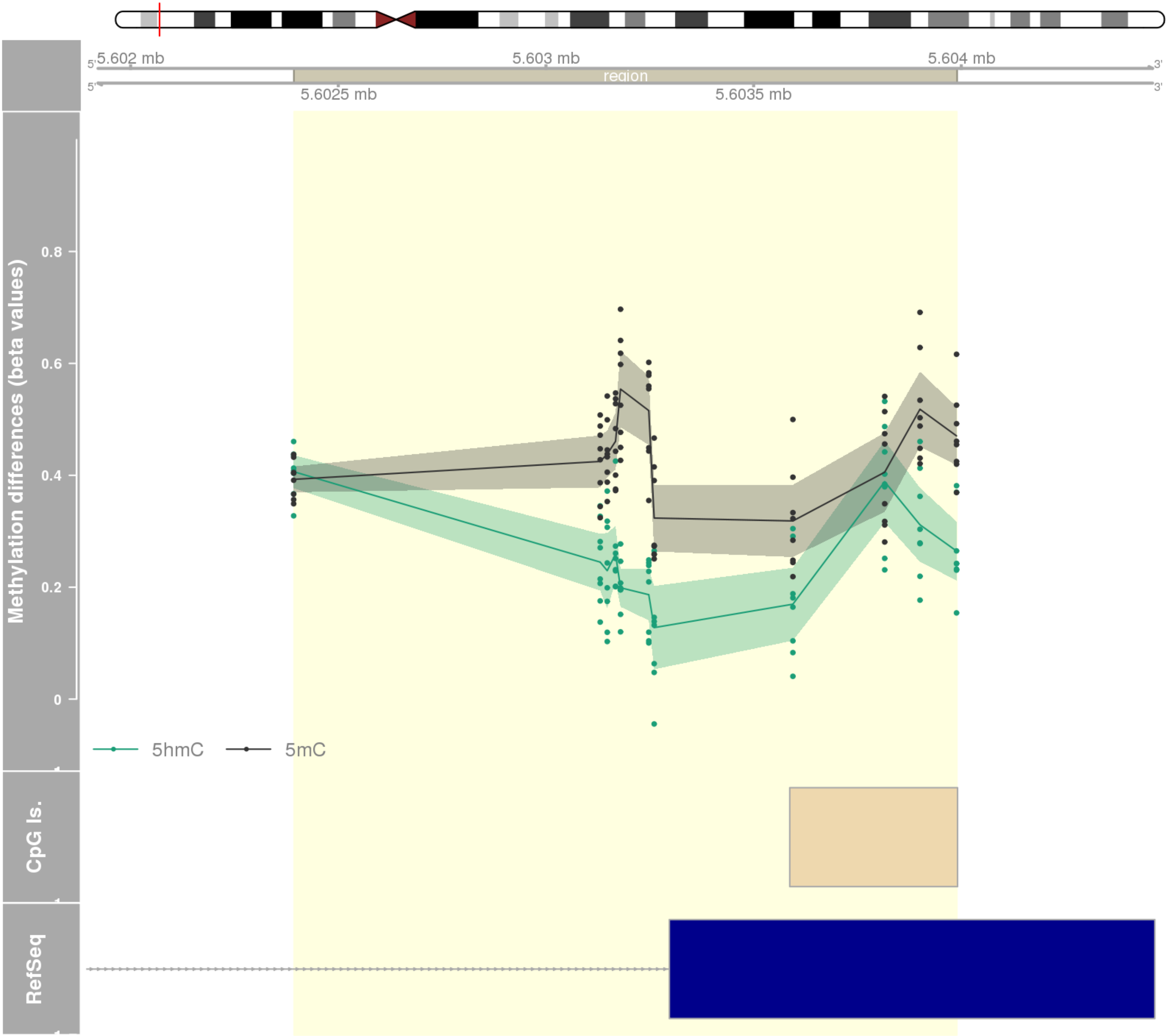
DMR 280 // chr6:33248239-33249075 // 836 pb. (10 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: B3GALT4 / WDR46 -



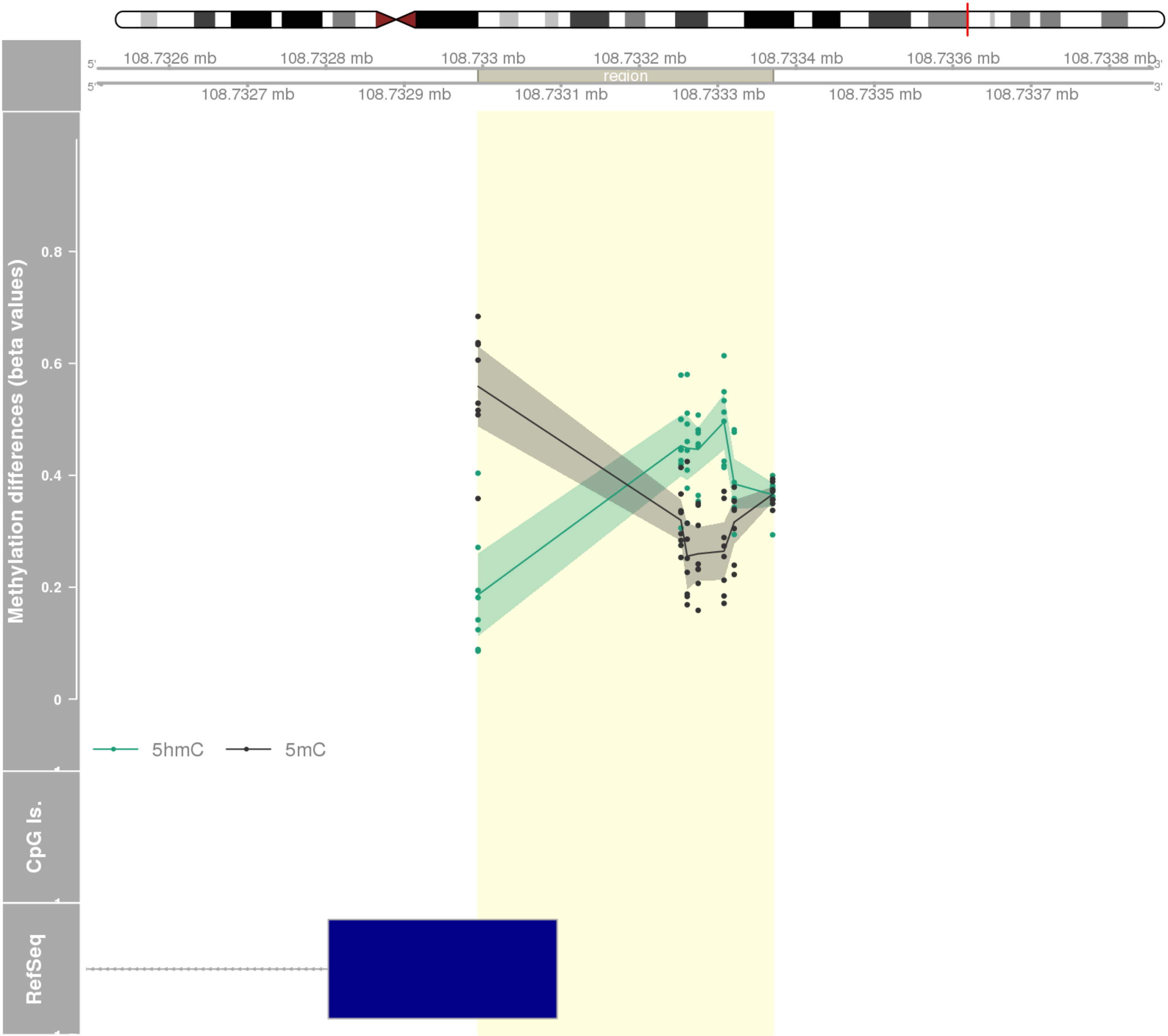
DMR 281 // chr4:1331882-1334868 // 2986 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: MAEA -



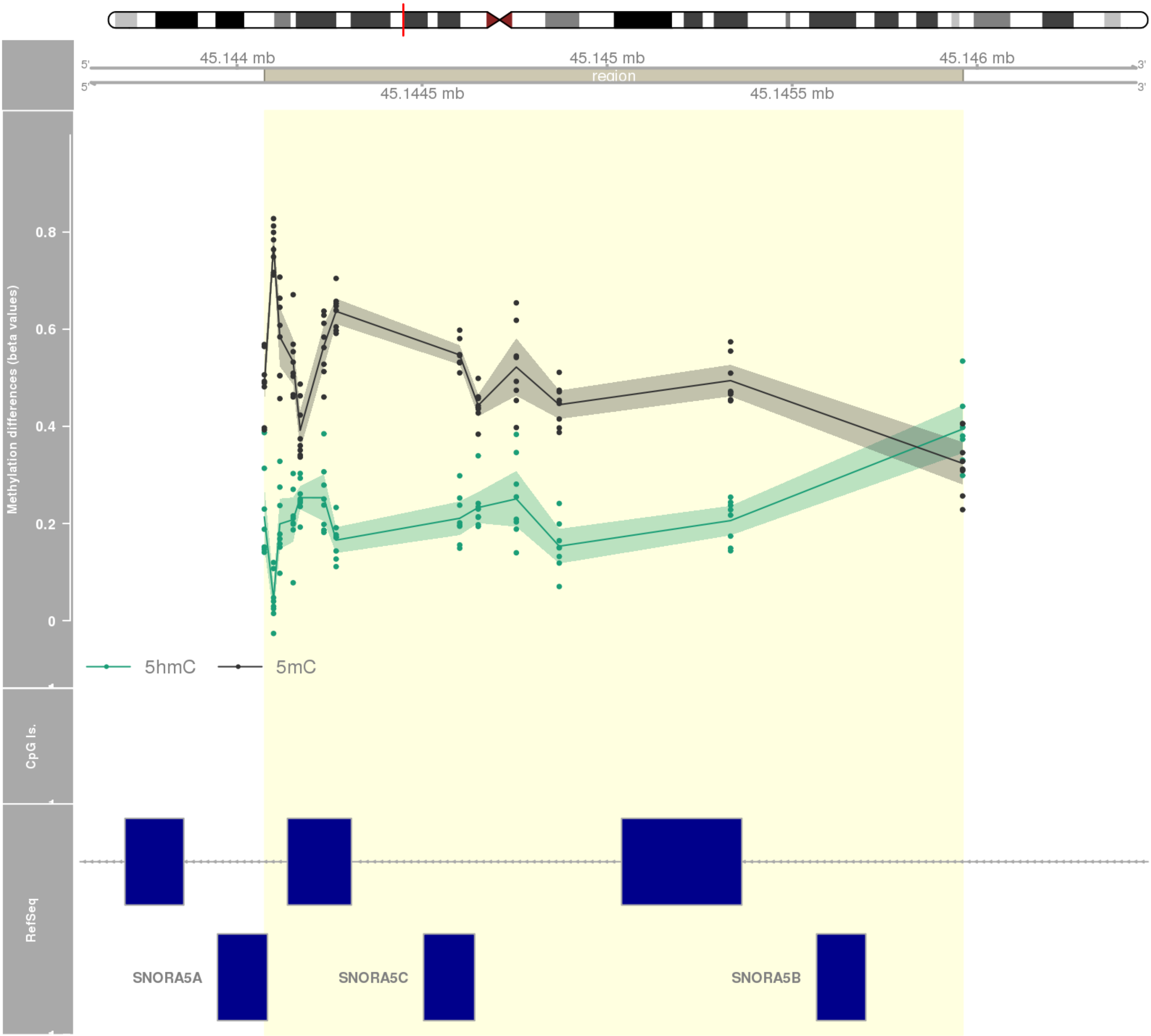
DMR 282 // chr12:5602393-5603989 // 1596 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: NTF3 -



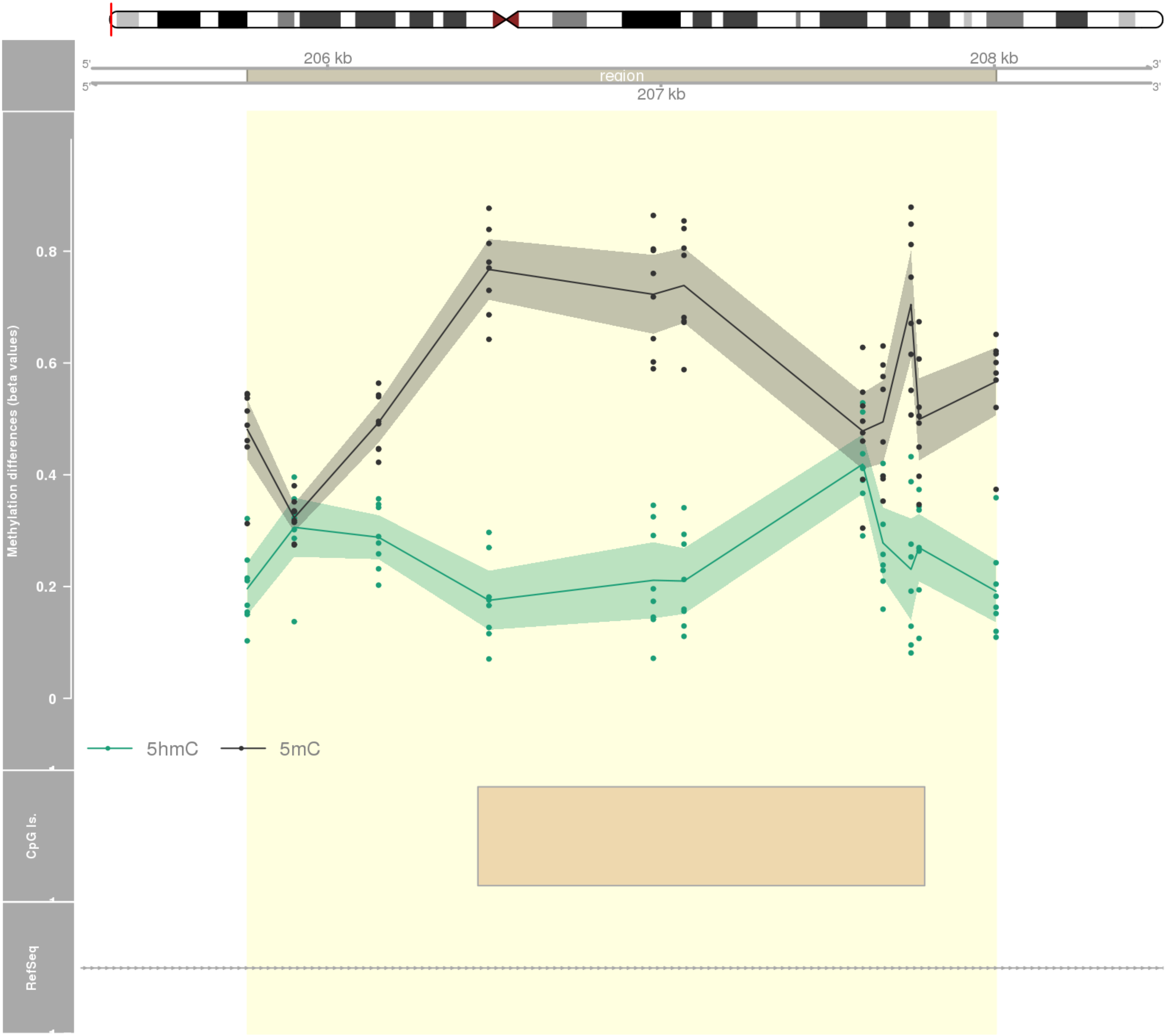
DMR 283 // chr12:108732994-108733370 // 376 pb. (7 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: CMKLR1 -



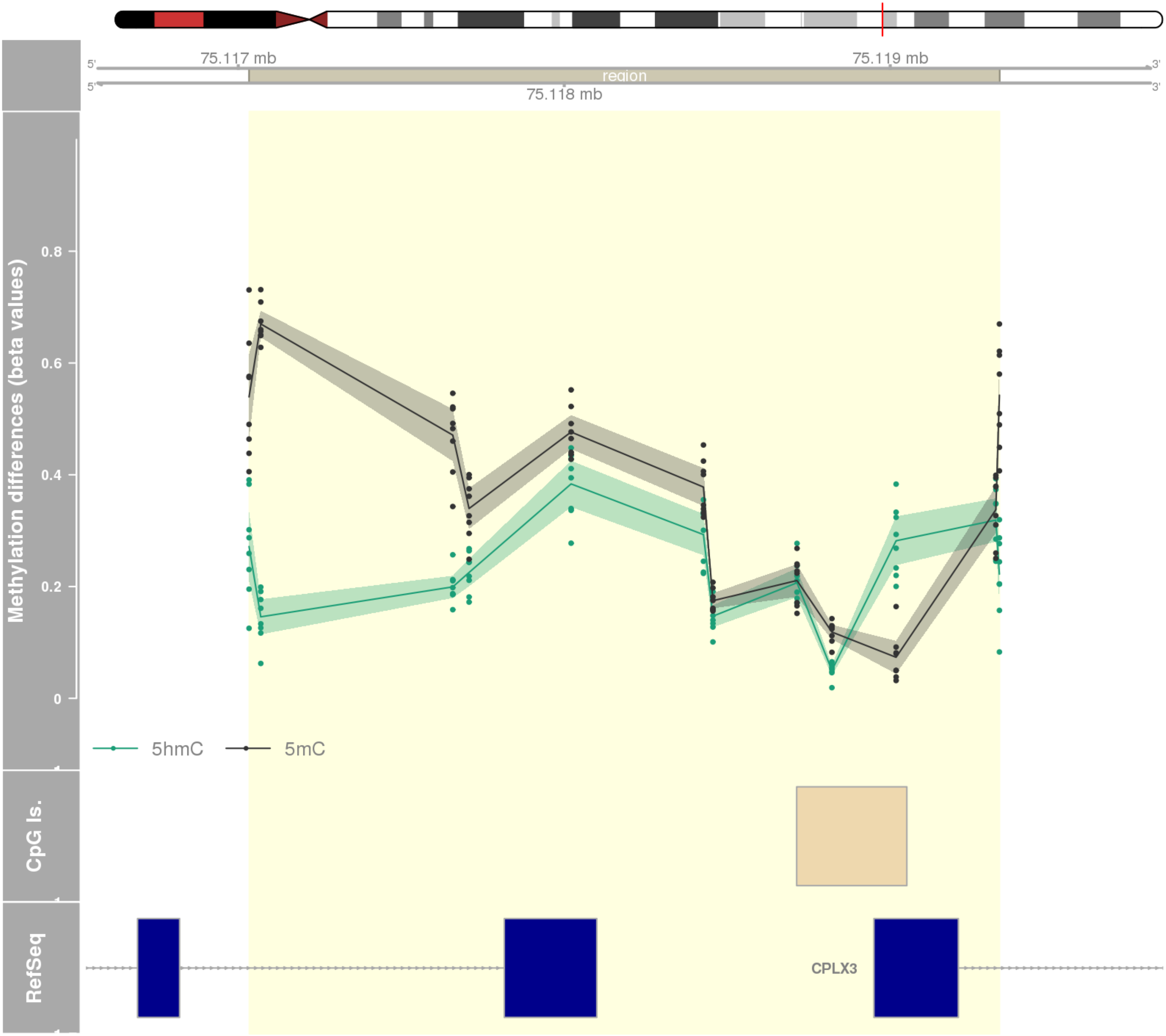
DMR 284 // chr7:45144074-45145961 // 1887 pb. (13 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: SNORA5A / SNORA5C / SNORA5B / TBRG4 -



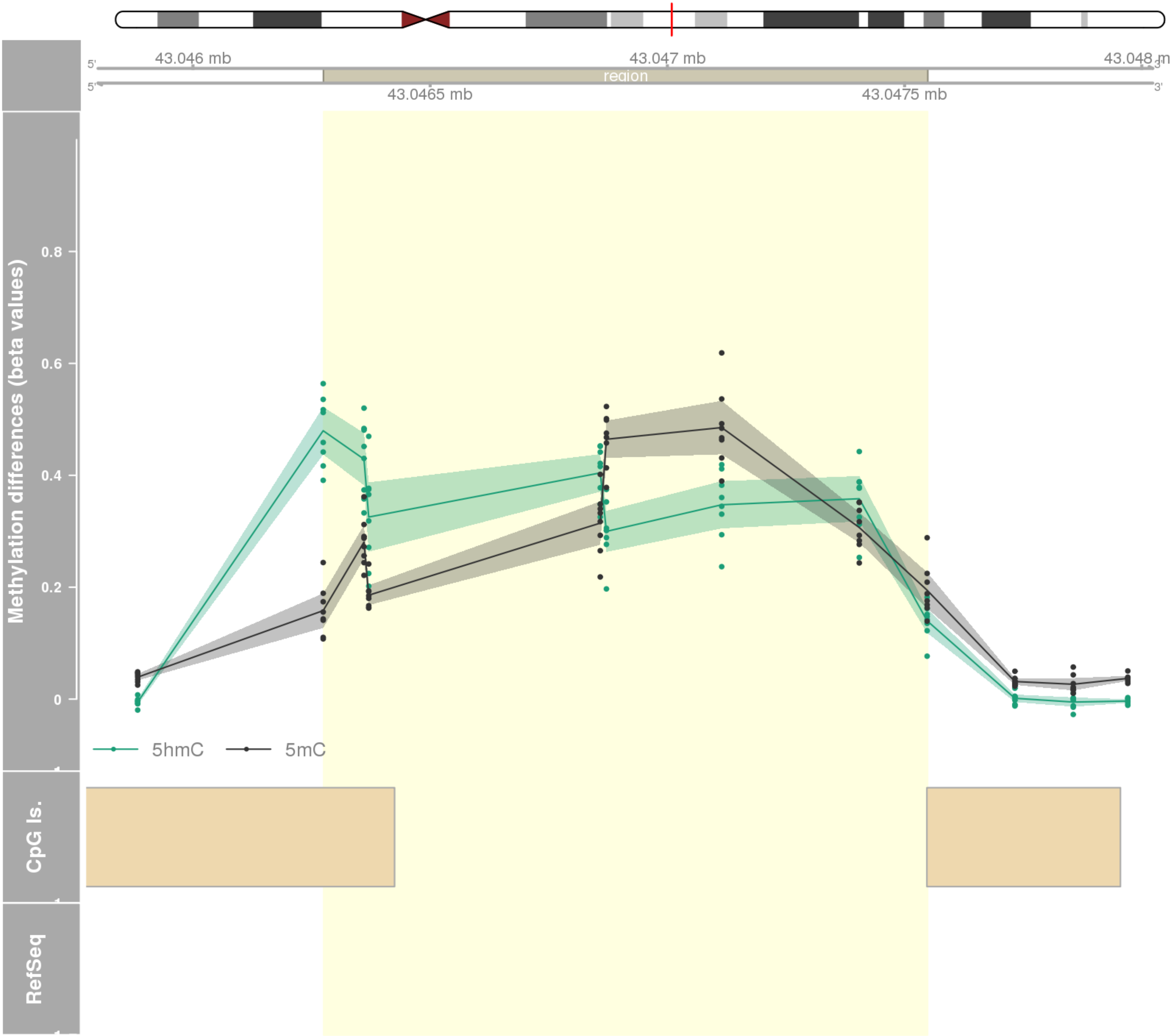
DMR 285 // chr7:205759-208005 // 2246 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: FAM20C -



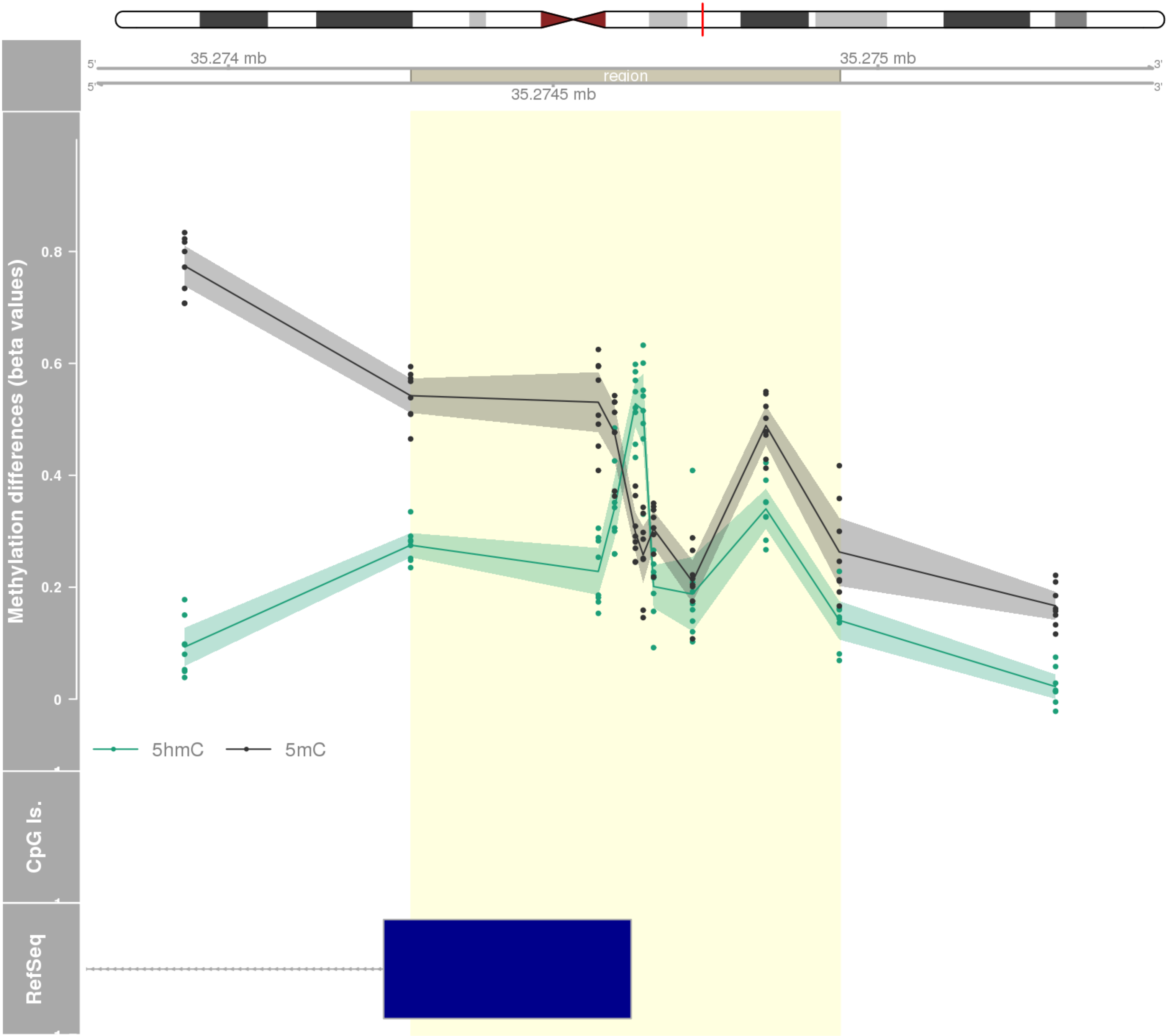
DMR 286 // chr15:75117033-75119335 // 2302 pb. (12 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: LMAN1L / CPLX3 -



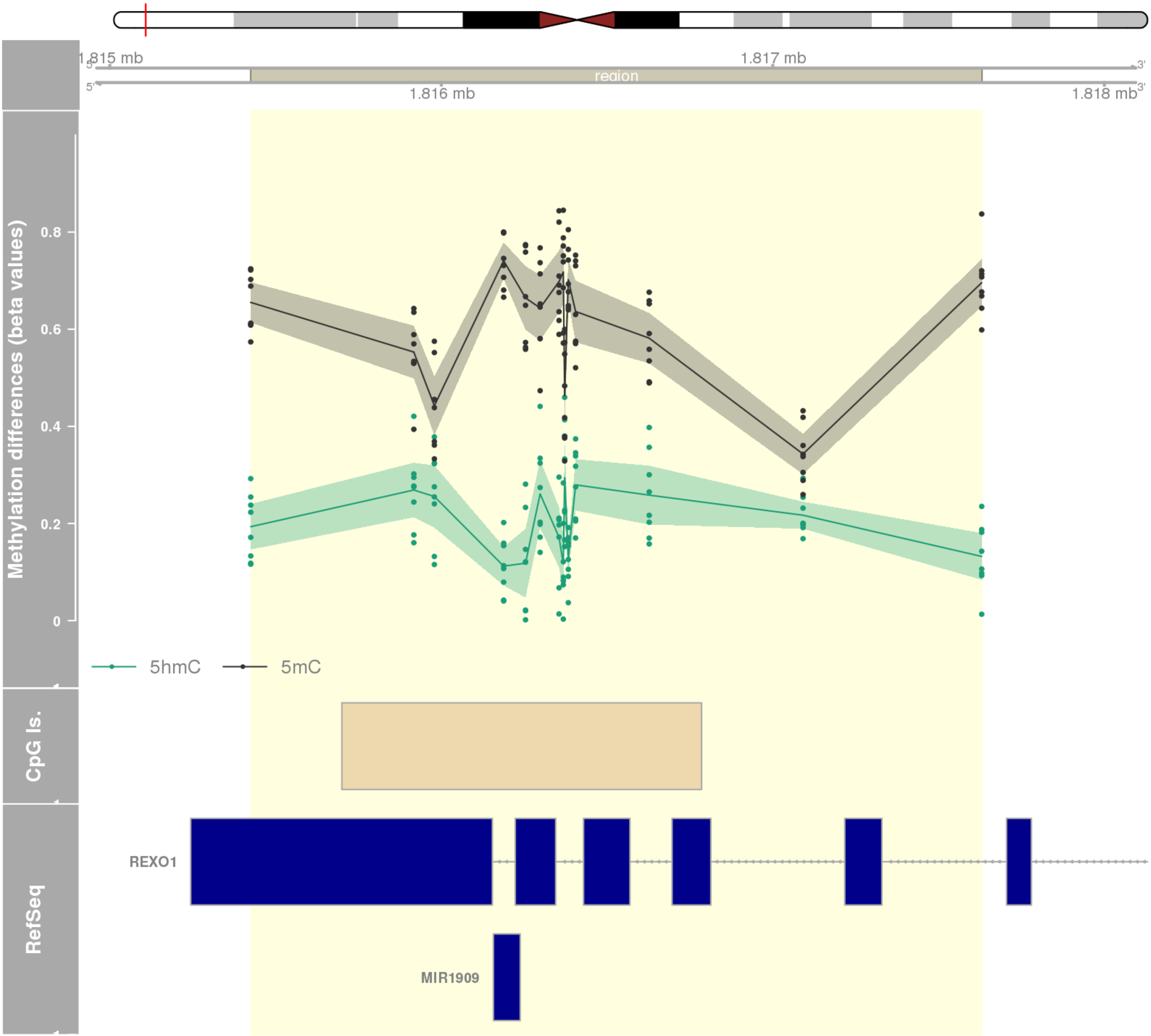
DMR 287 // chr17:43046275-43047548 // 1273 pb. (8 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559



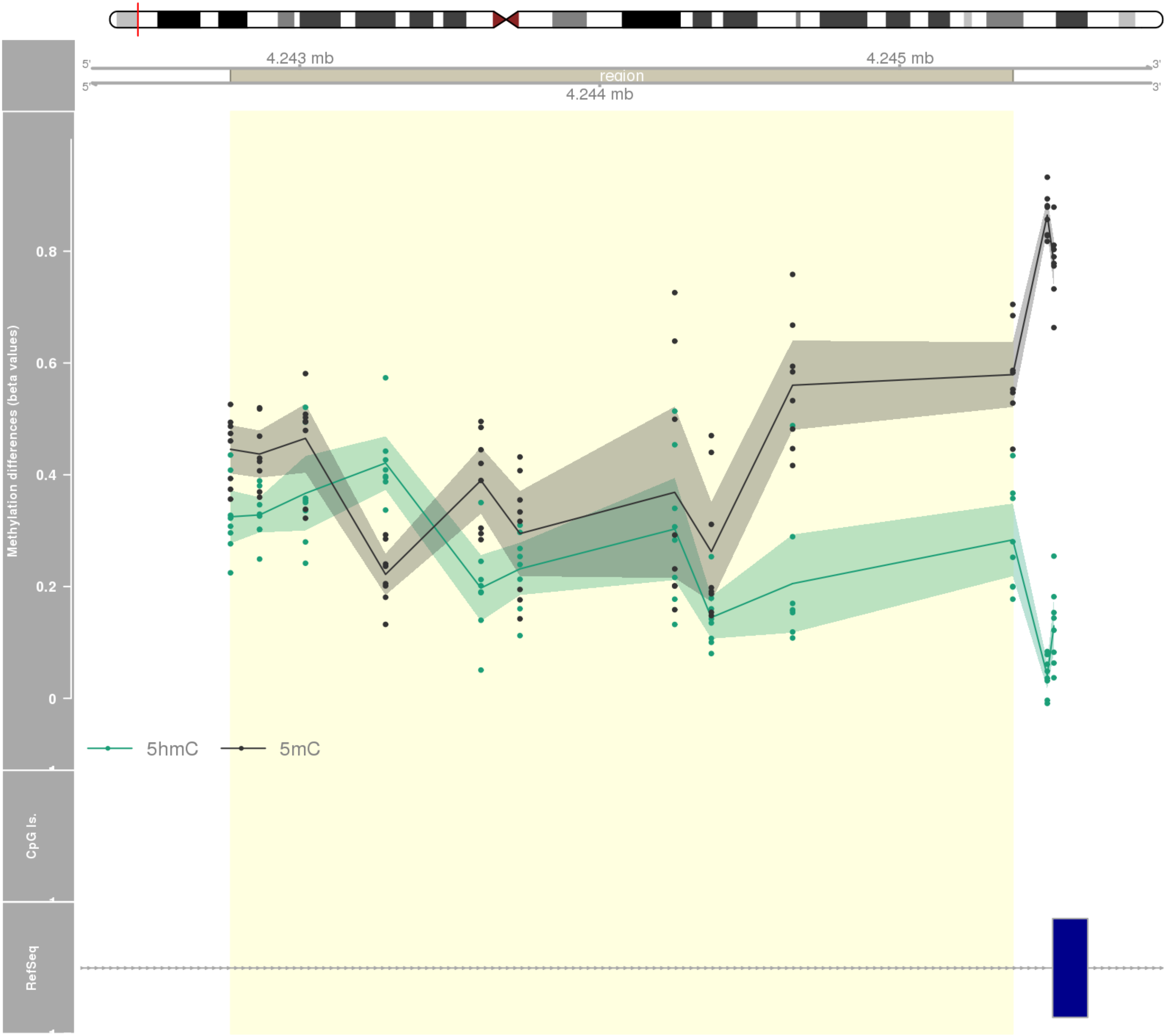
DMR 288 // chr20:35274281-35274941 // 660 pb. (9 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: SLA2 -



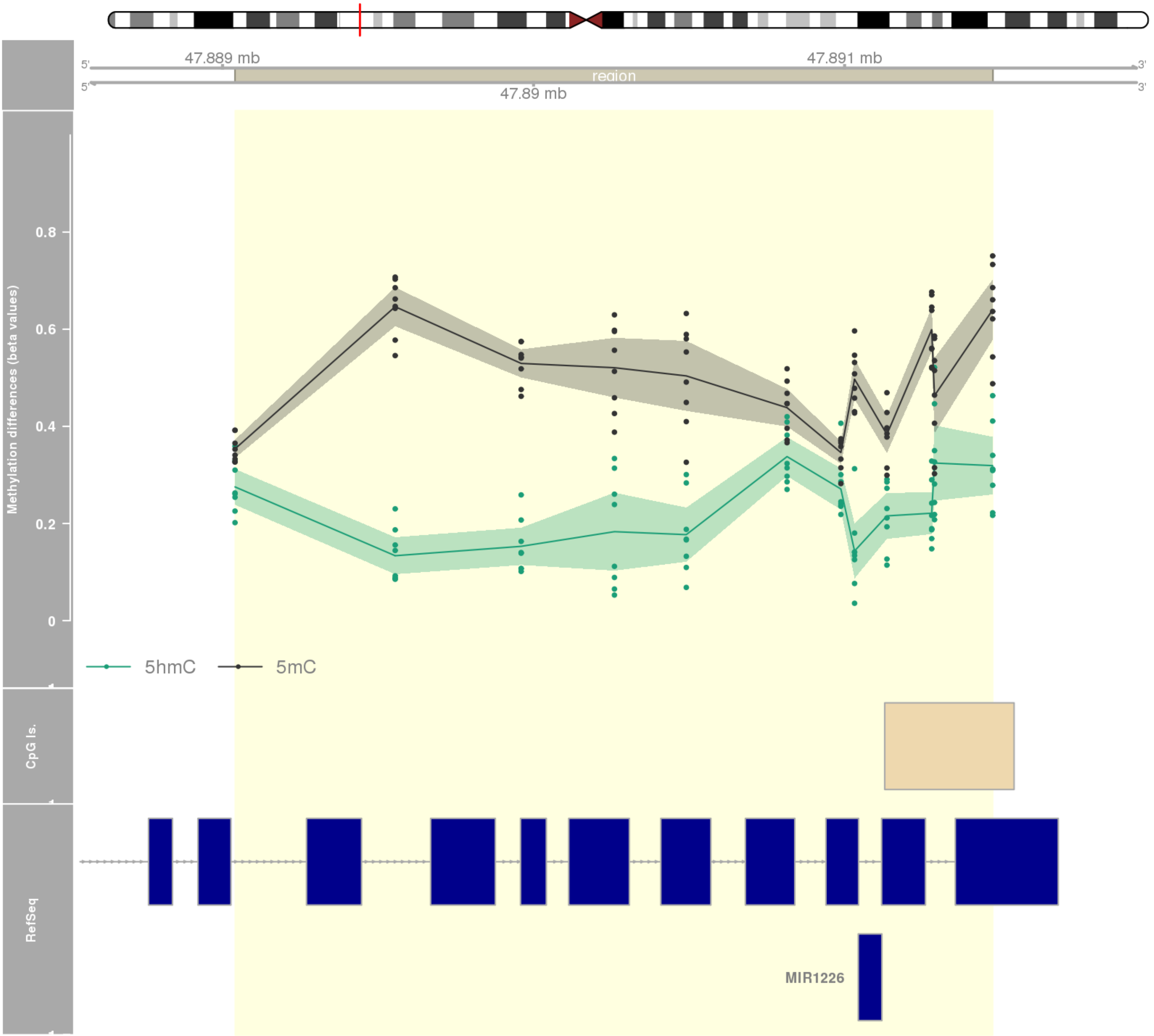
DMR 289 // chr19:1815425-1817630 // 2205 pb. (14 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: MIR1909 / REXO1 -



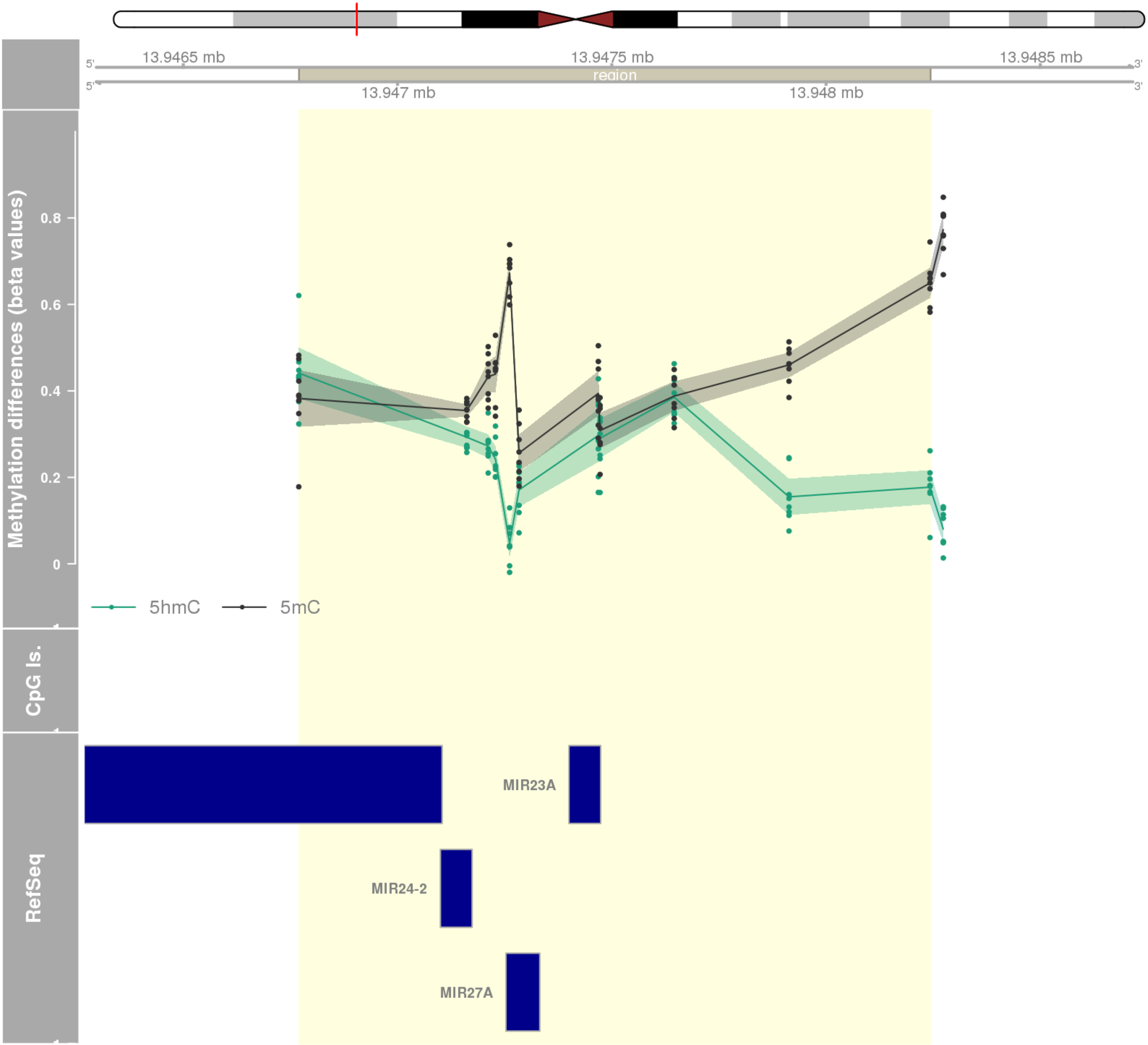
DMR 290 // chr7:4242769-4245377 // 2608 pb. (10 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: SDK1 -



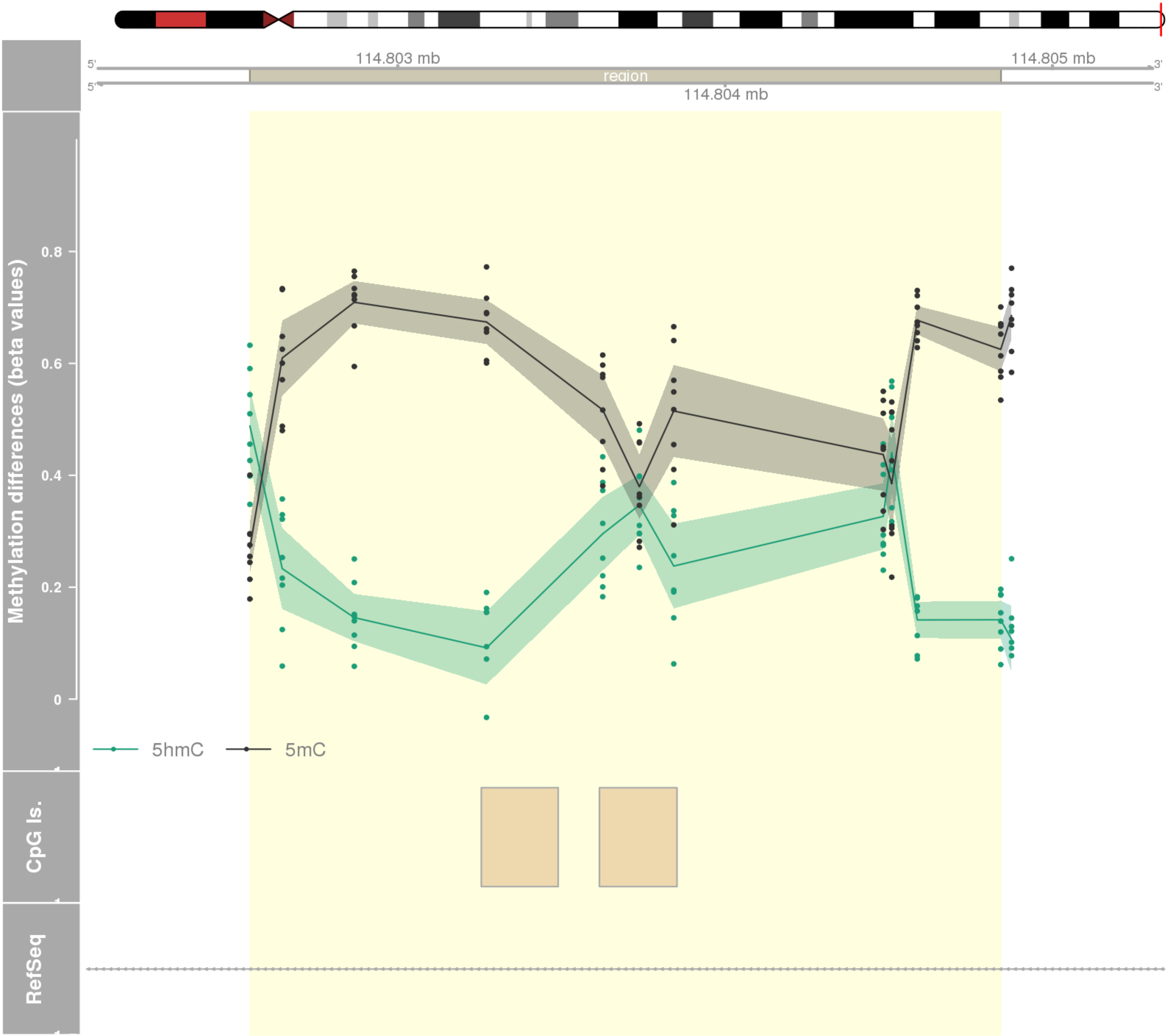
DMR 291 // chr3:47889040-47891476 // 2436 pb. (12 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: MIR1226 / DHX30 -



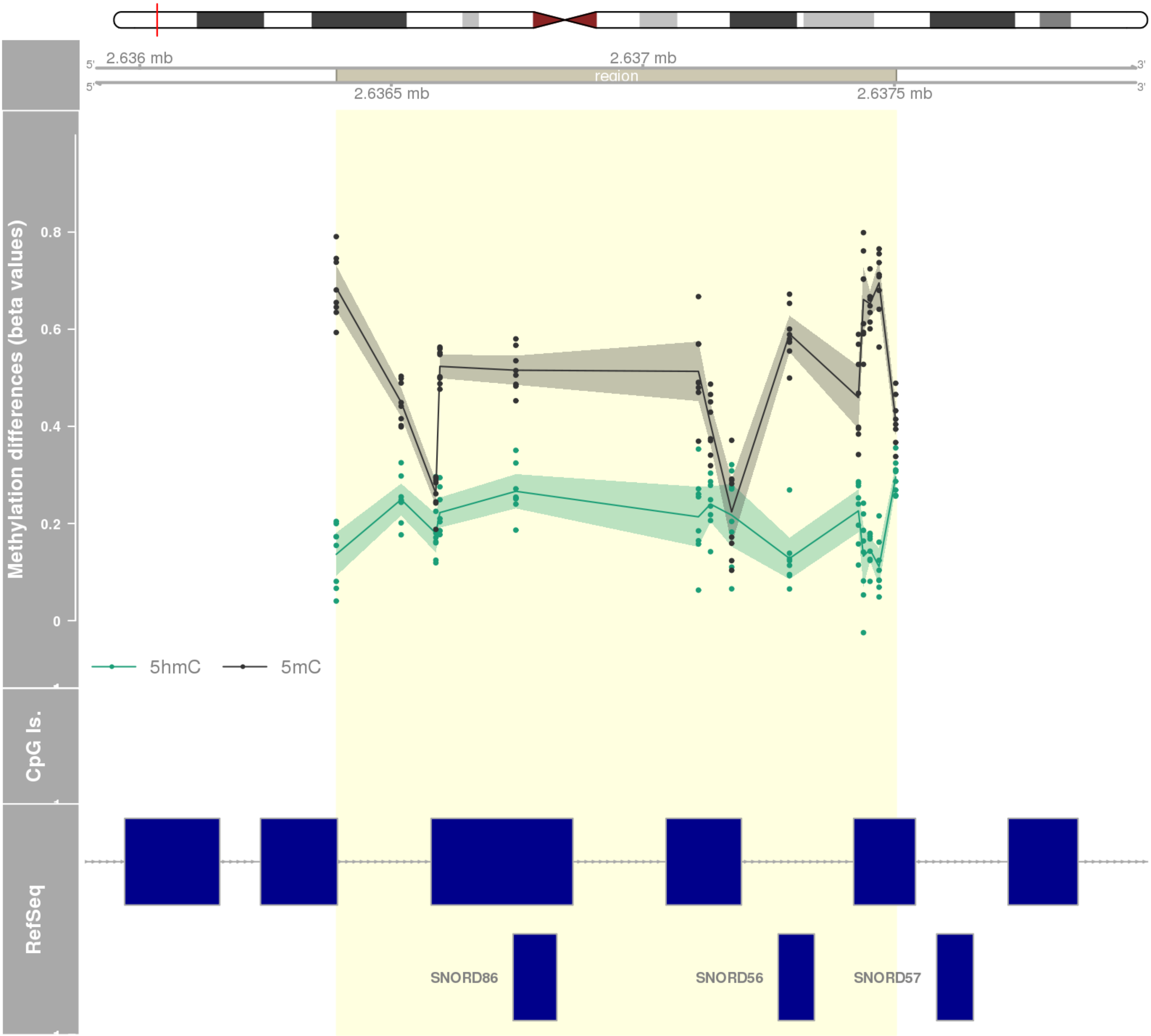
DMR 292 // chr19:13946770-13948243 // 1473 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: MIR24-2 / MIR27A / MIR23A -



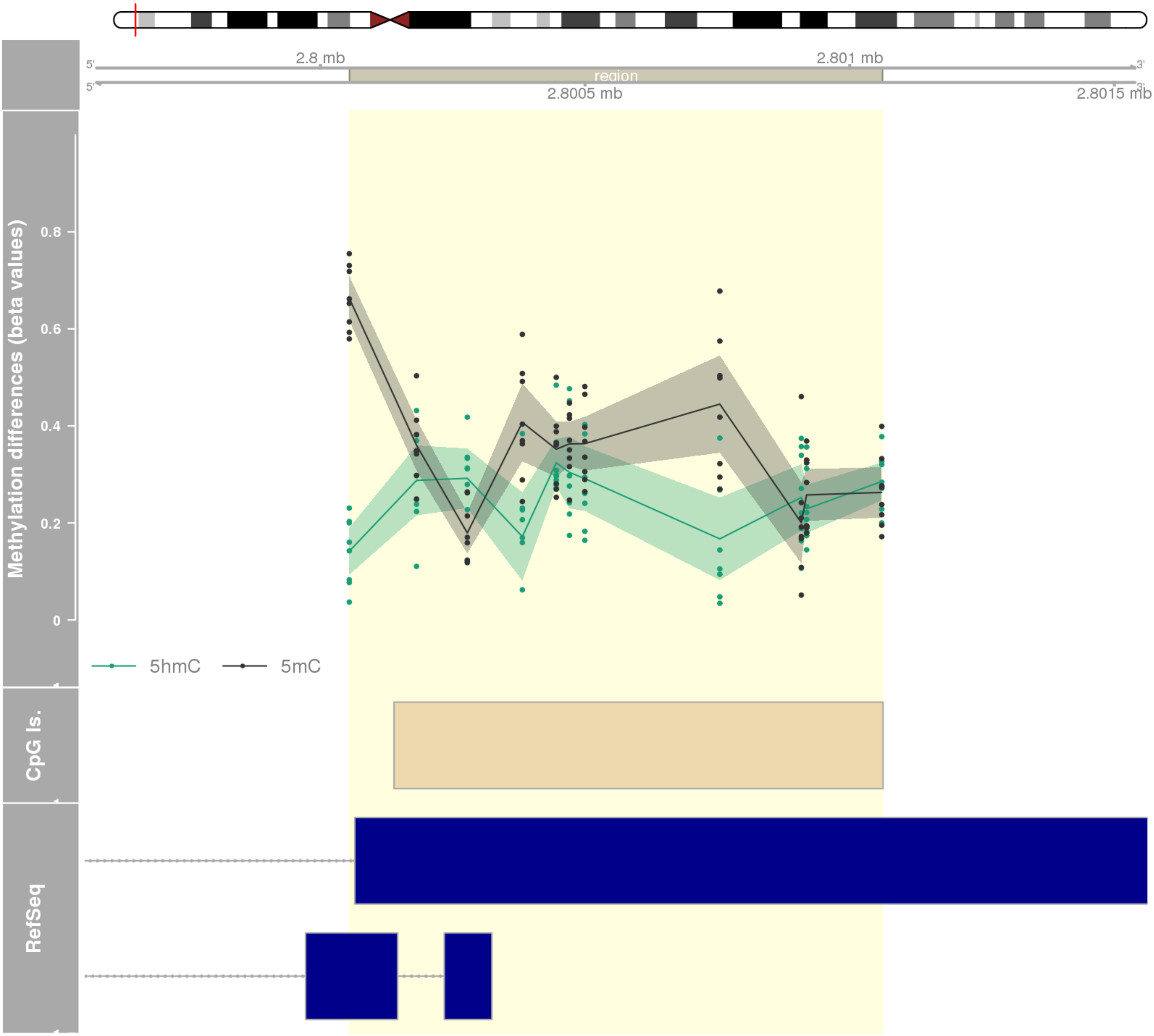
DMR 293 // chr13:114802548-114804842 // 2294 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: RASA3 -



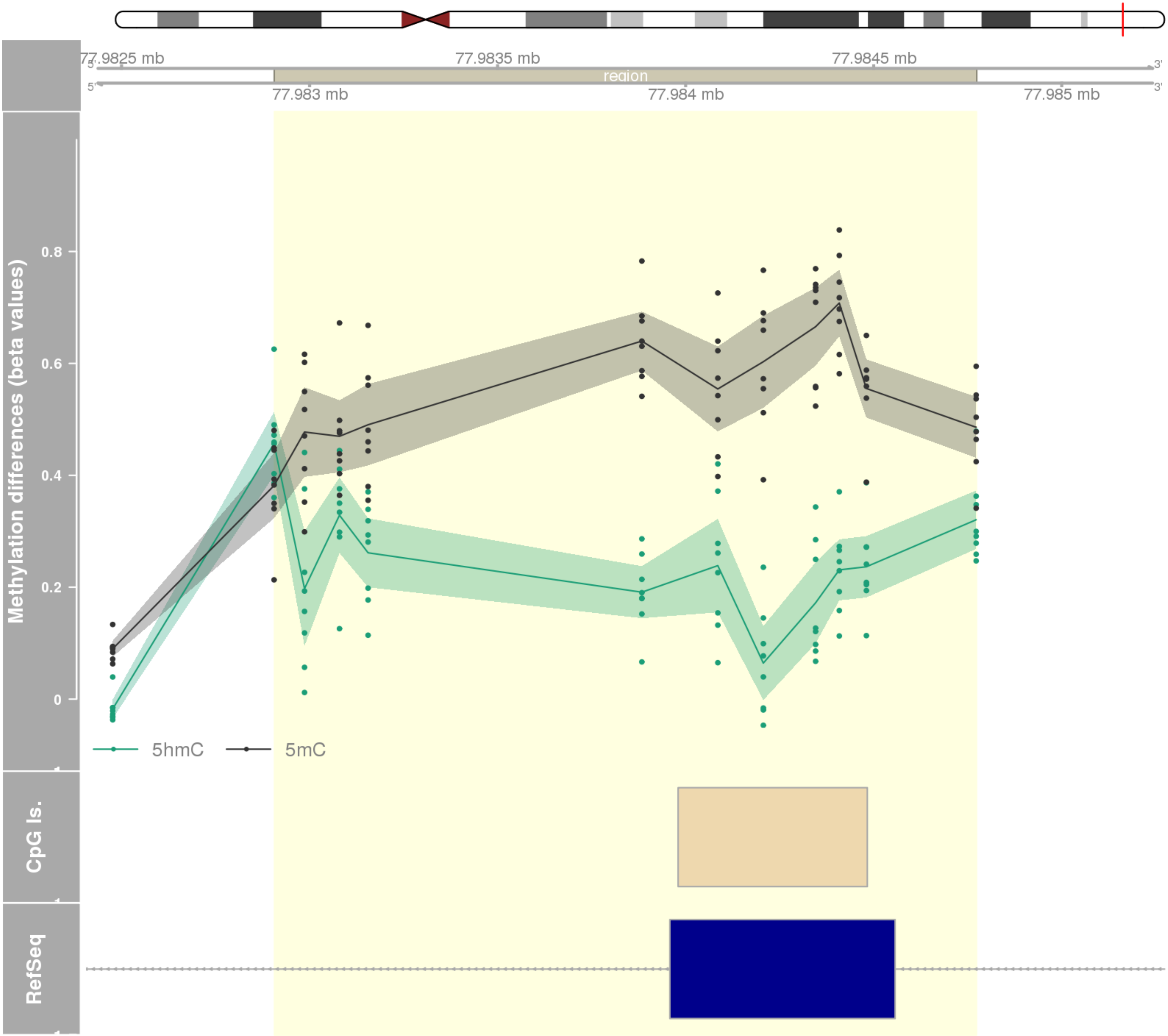
DMR 294 // chr20:2636391-2637503 // 1112 pb. (14 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: SNORD86 / SNORD56 / NOP56 -



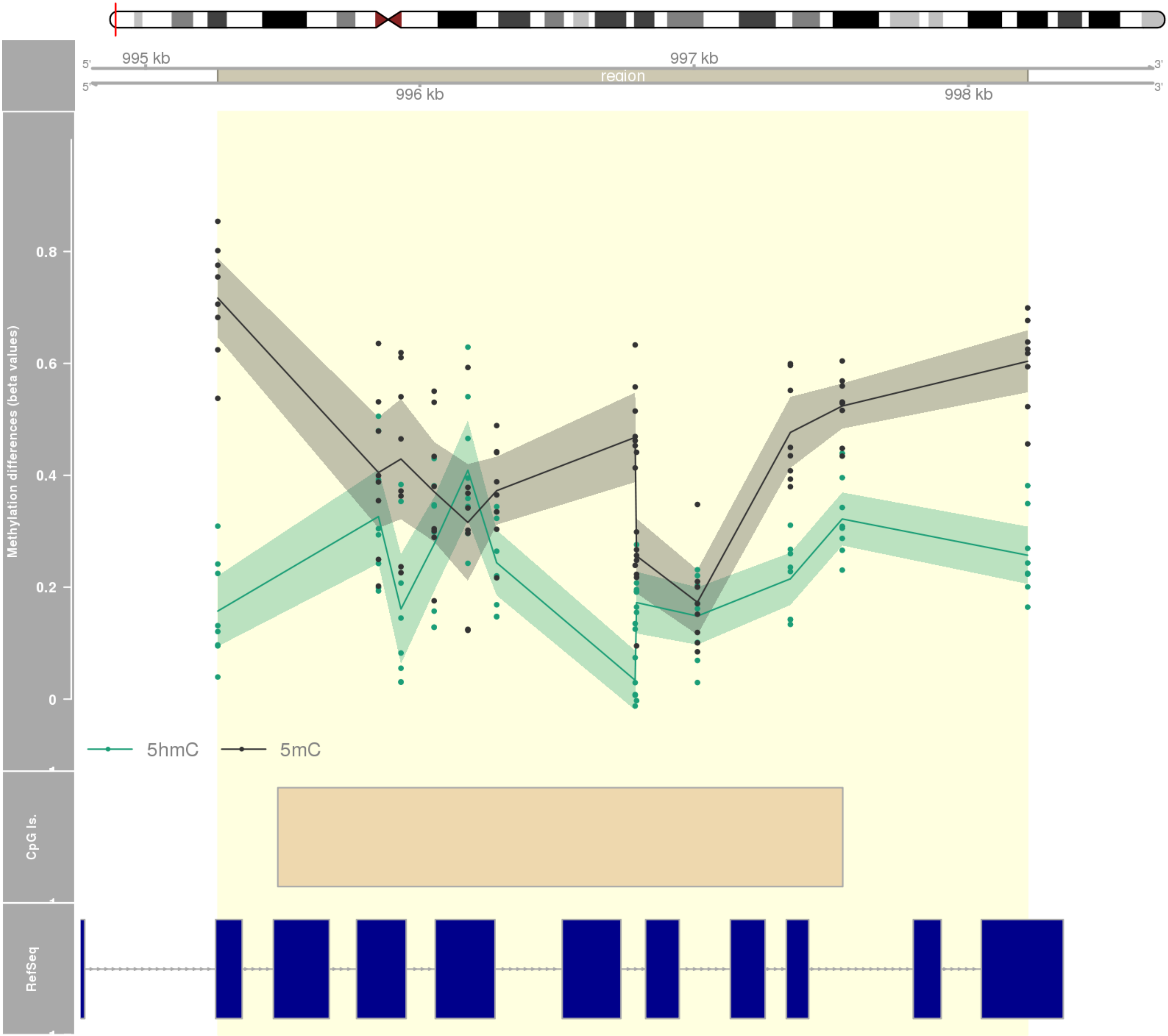
DMR 295 // chr12:2800055-2801061 // 1006 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: CACNA1C-AS1 / CACNA1C -



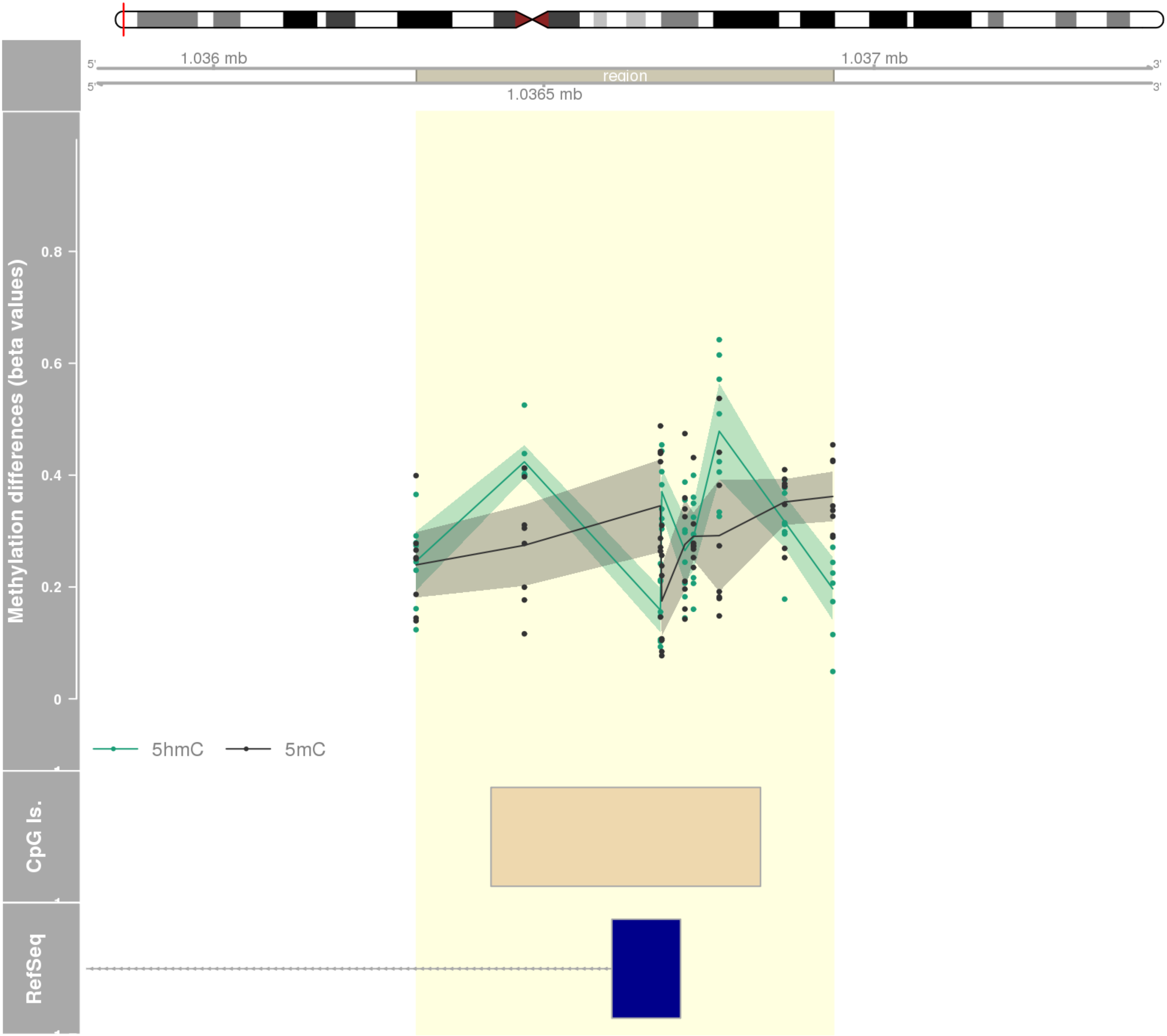
DMR 296 // chr17:77982906-77984773 // 1867 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: TBC1D16 -



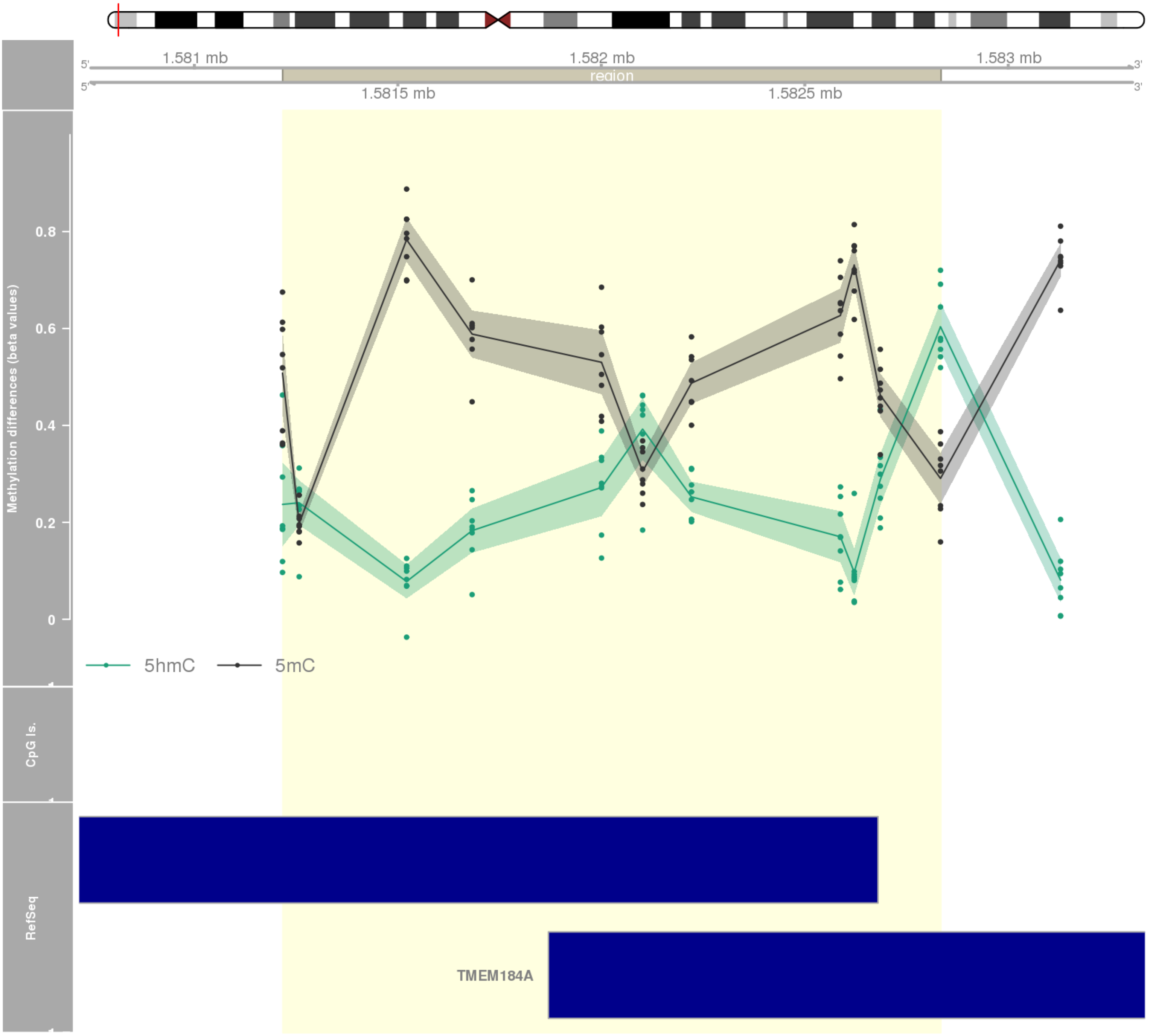
DMR 297 // chr4:995263-998216 // 2953 pb. (12 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: IDUA -

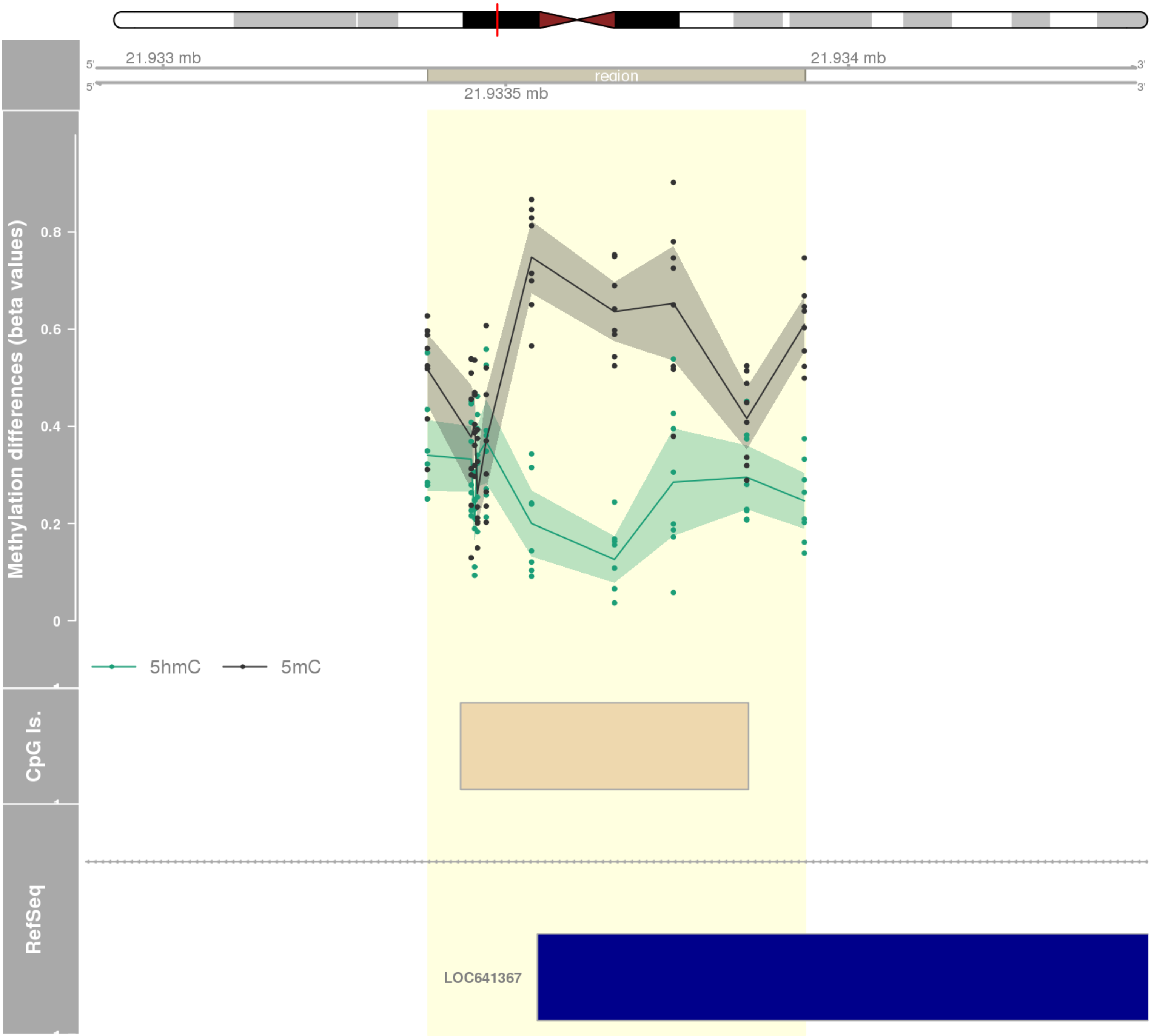


DMR 298 // chr11:1036307-1036938 // 631 pb. (9 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.015 // fwerArea: 0.559
- genes: MUC6 -

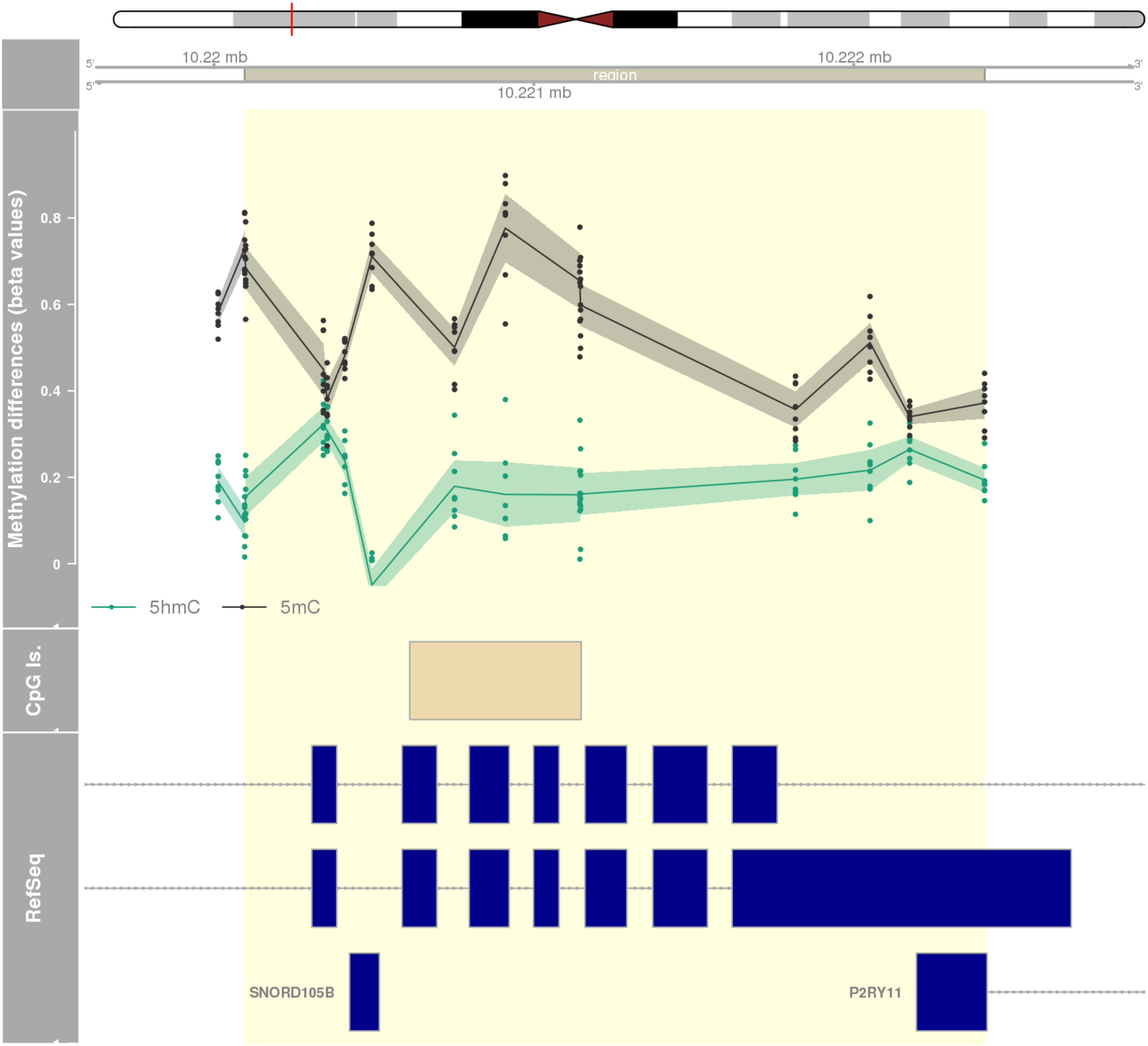


DMR 299 // chr7:1581217-1582834 // 1617 pb. (11 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: MAFK / TMEM184A -

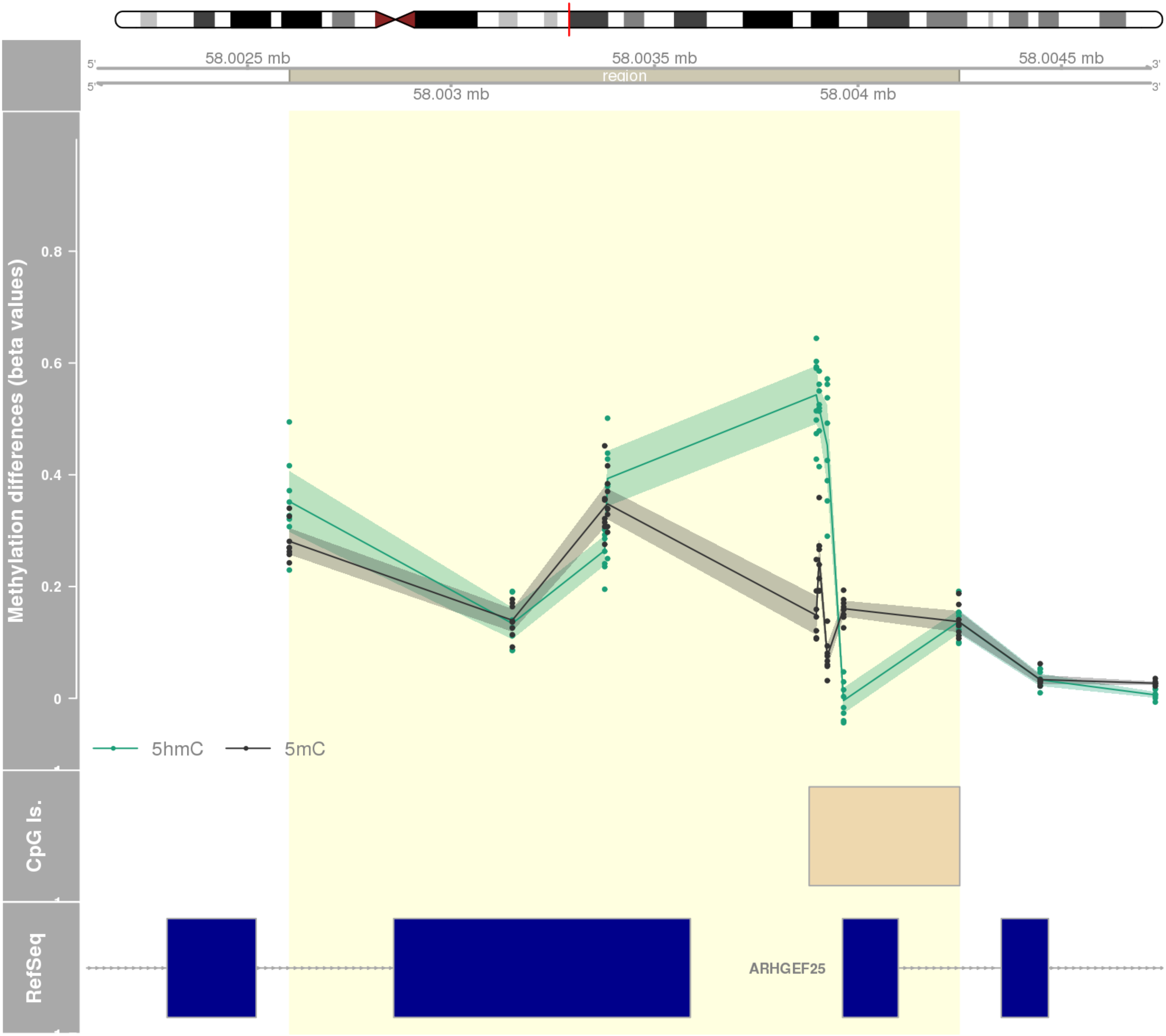



DMR 300 // chr19:21933386-21933936 // 550 pb. (10 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: ZNF100 -

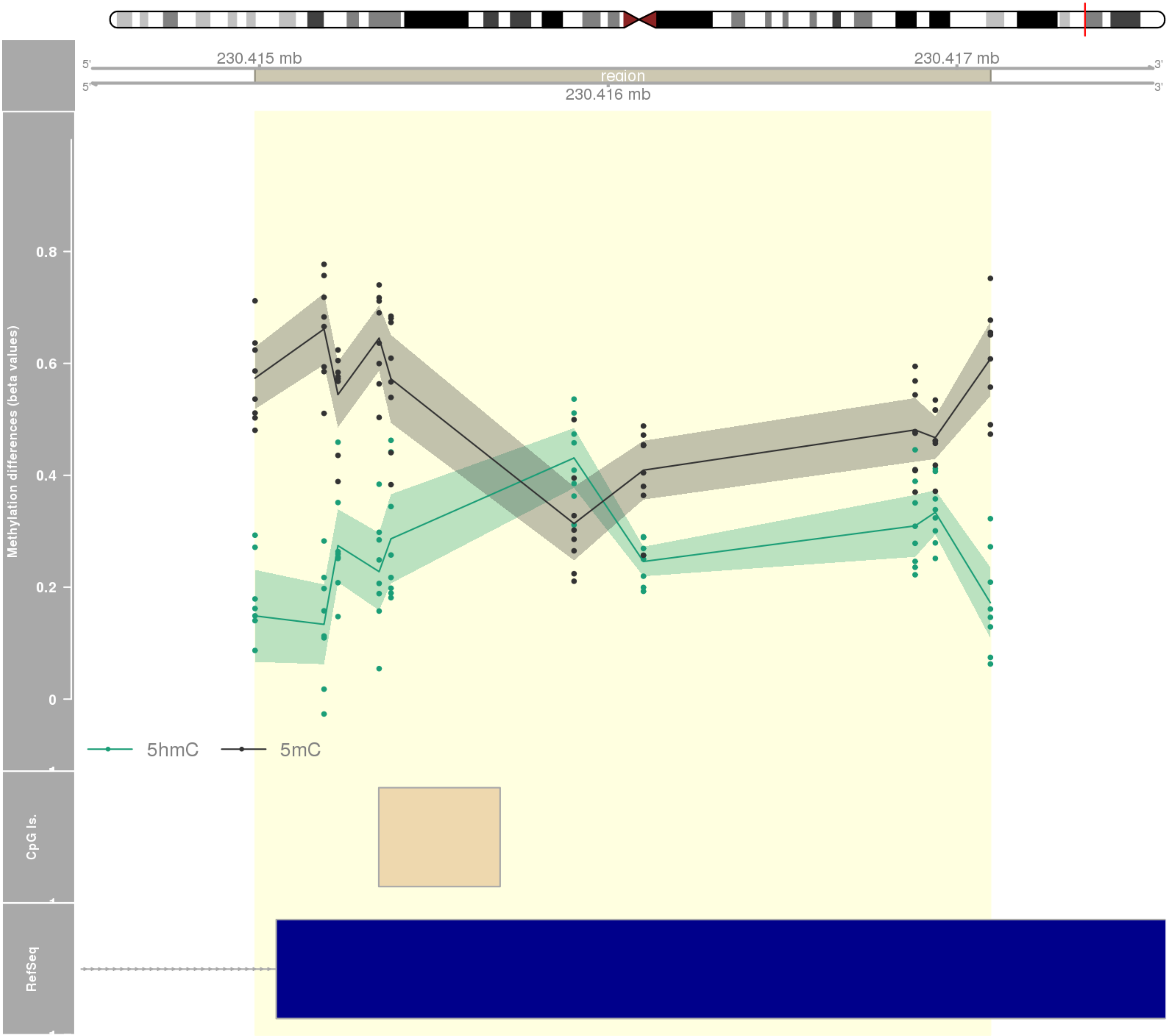
DMR 301 // chr19:10220096-10222409 // 2313 pb. (14 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: PPAN-P2RY11 / PPAN / P2RY11 / SNORD105B -



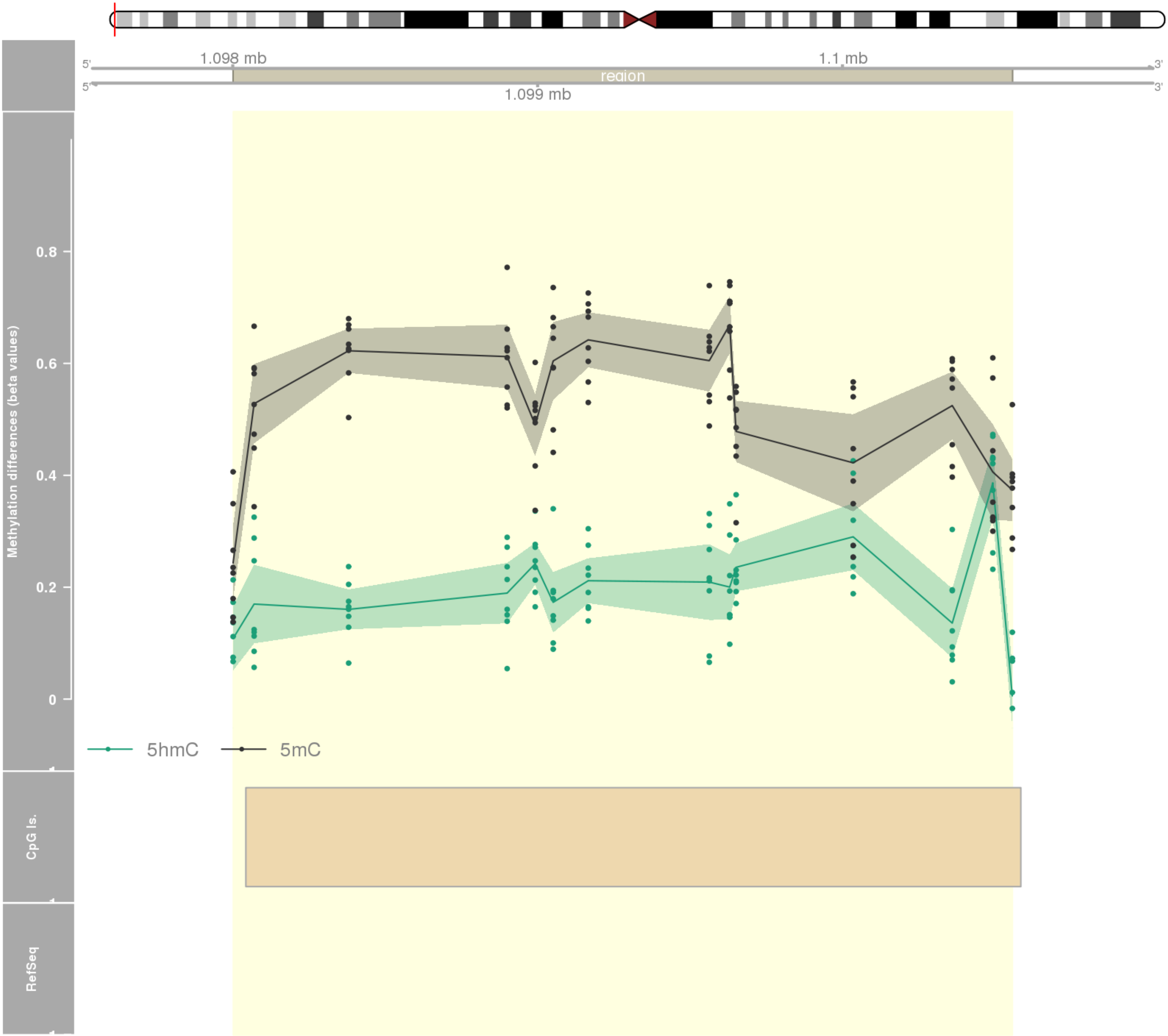
DMR 302 // chr12:58002603-58004248 // 1645 pb. (9 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: DTX3 / ARHGEF25 -



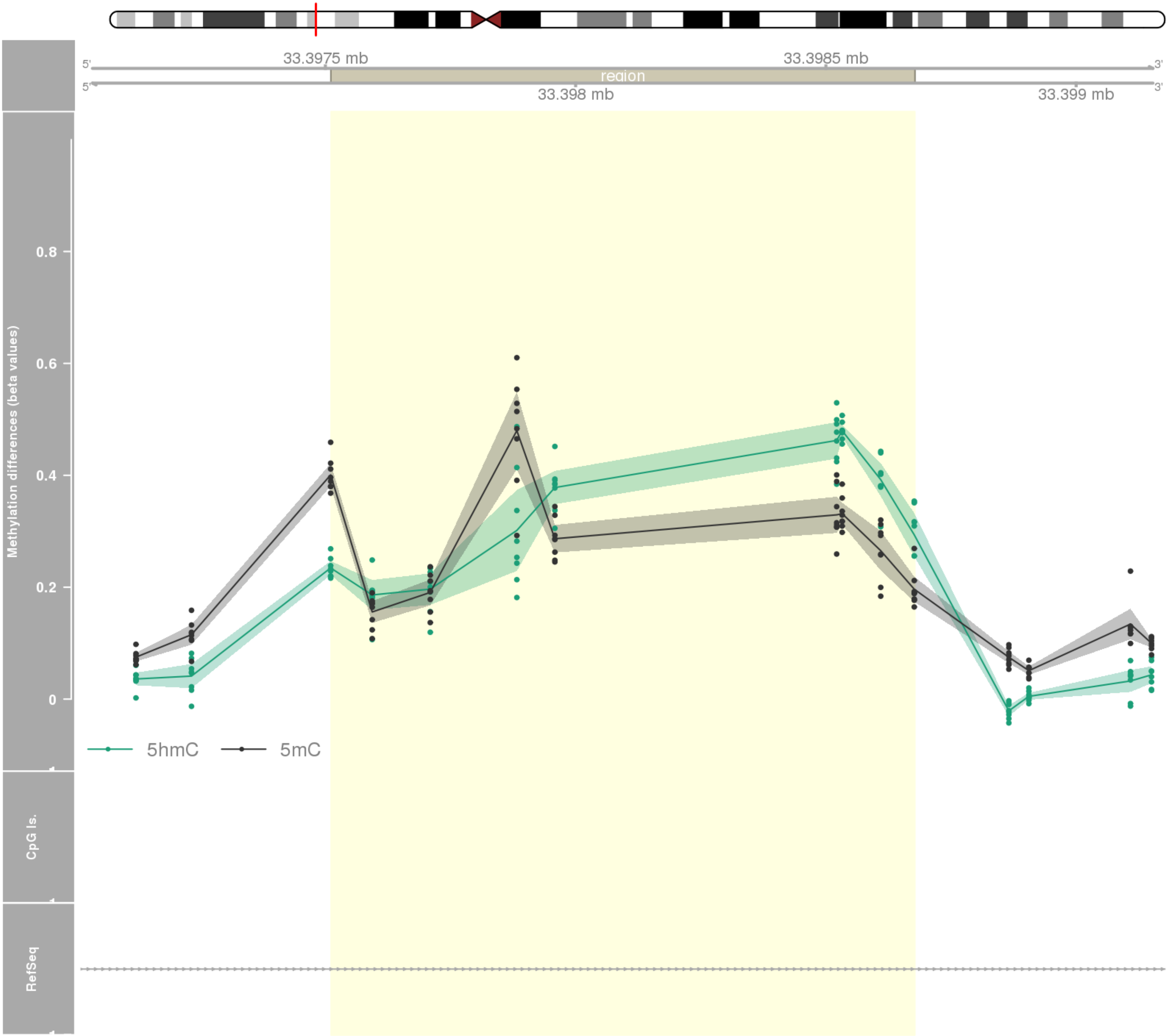
DMR 303 // chr1:230414987-230417096 // 2109 pb. (10 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: GALNT2 -



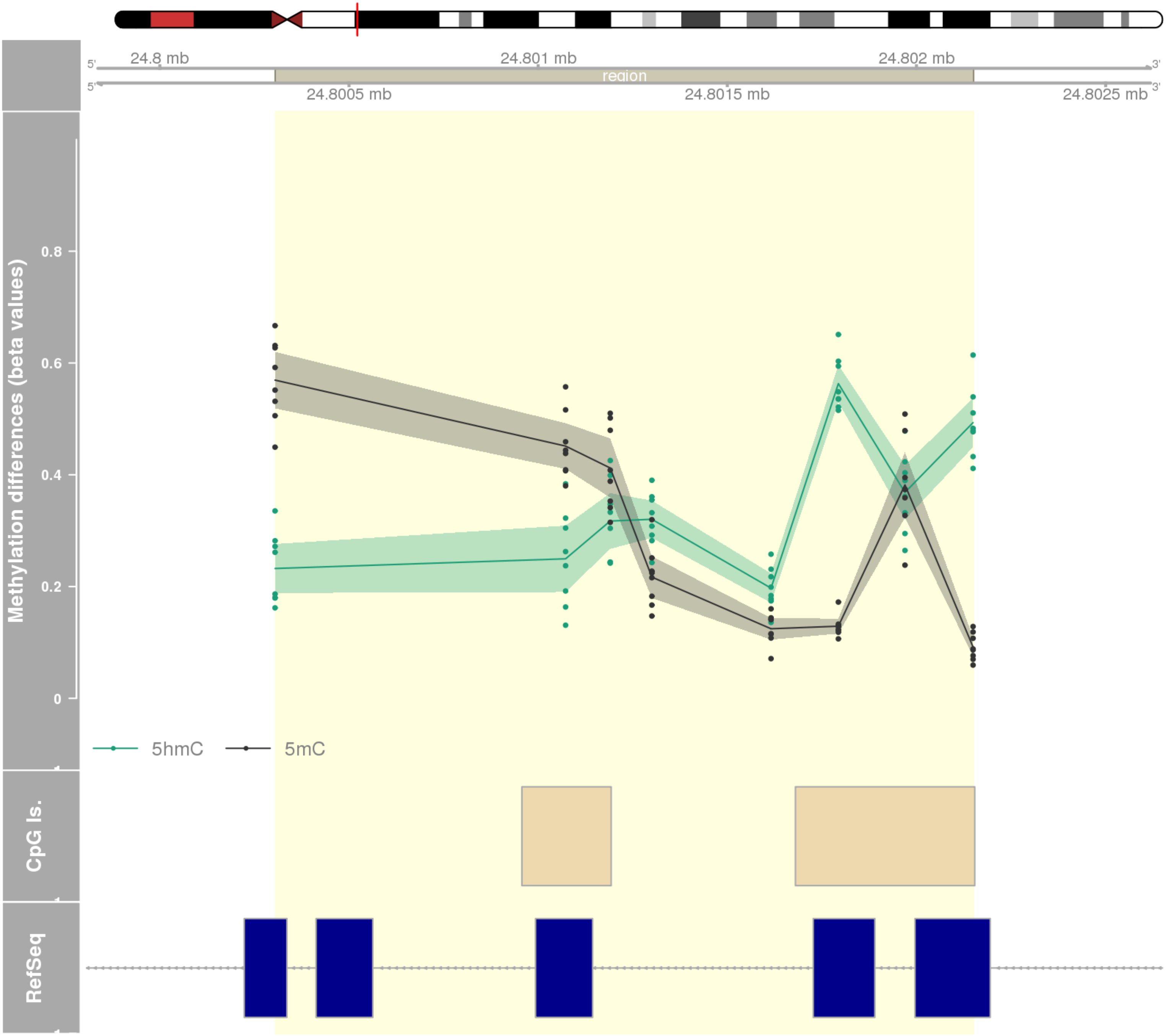
DMR 304 // chr1:1098001-1100557 // 2556 pb. (14 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559



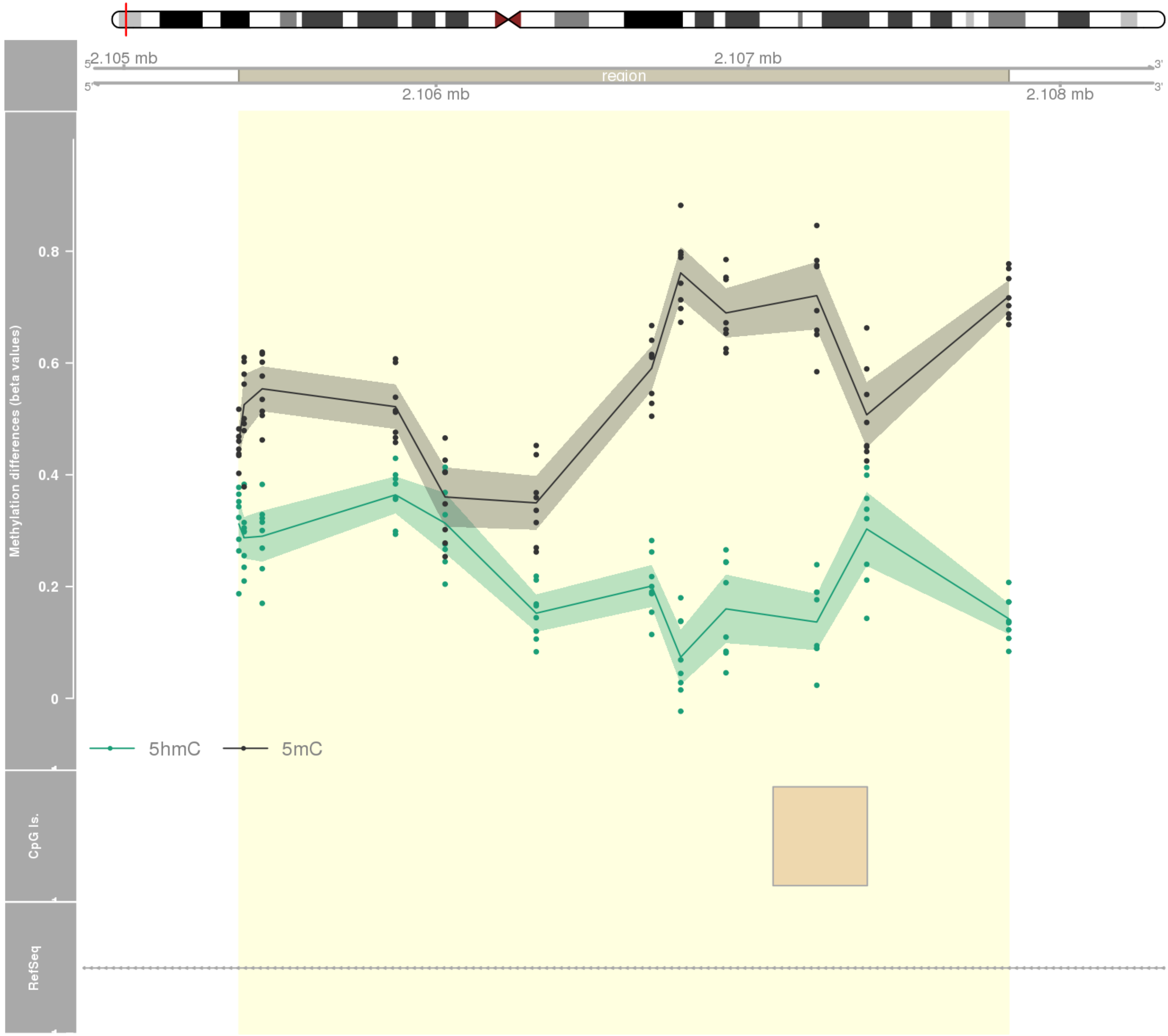
DMR 305 // chr6:33397511-33398677 // 1166 pb. (9 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: SYNGAP1 -



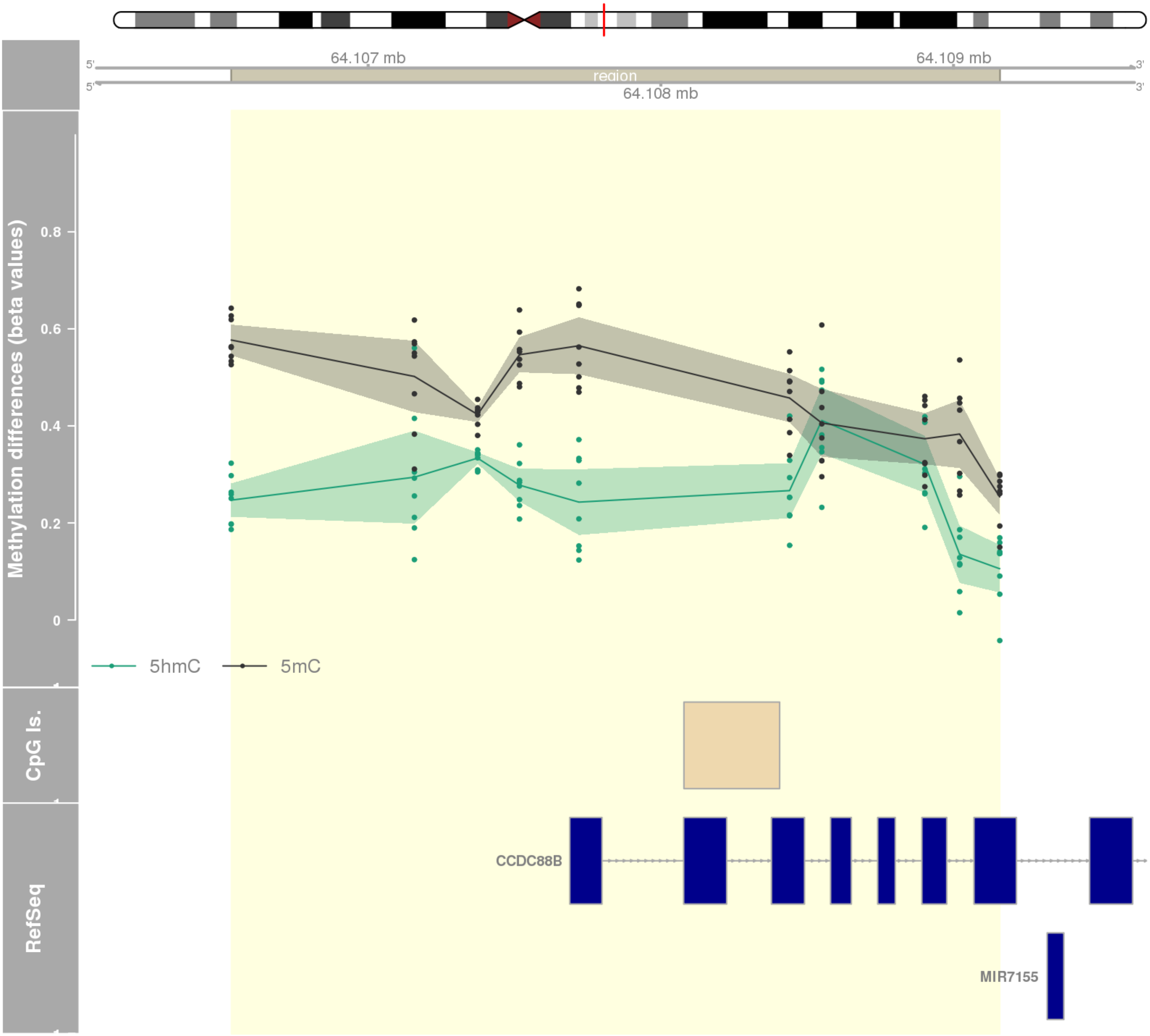
DMR 306 // chr14:24800305-24802150 // 1845 pb. (8 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: ADCY4 -



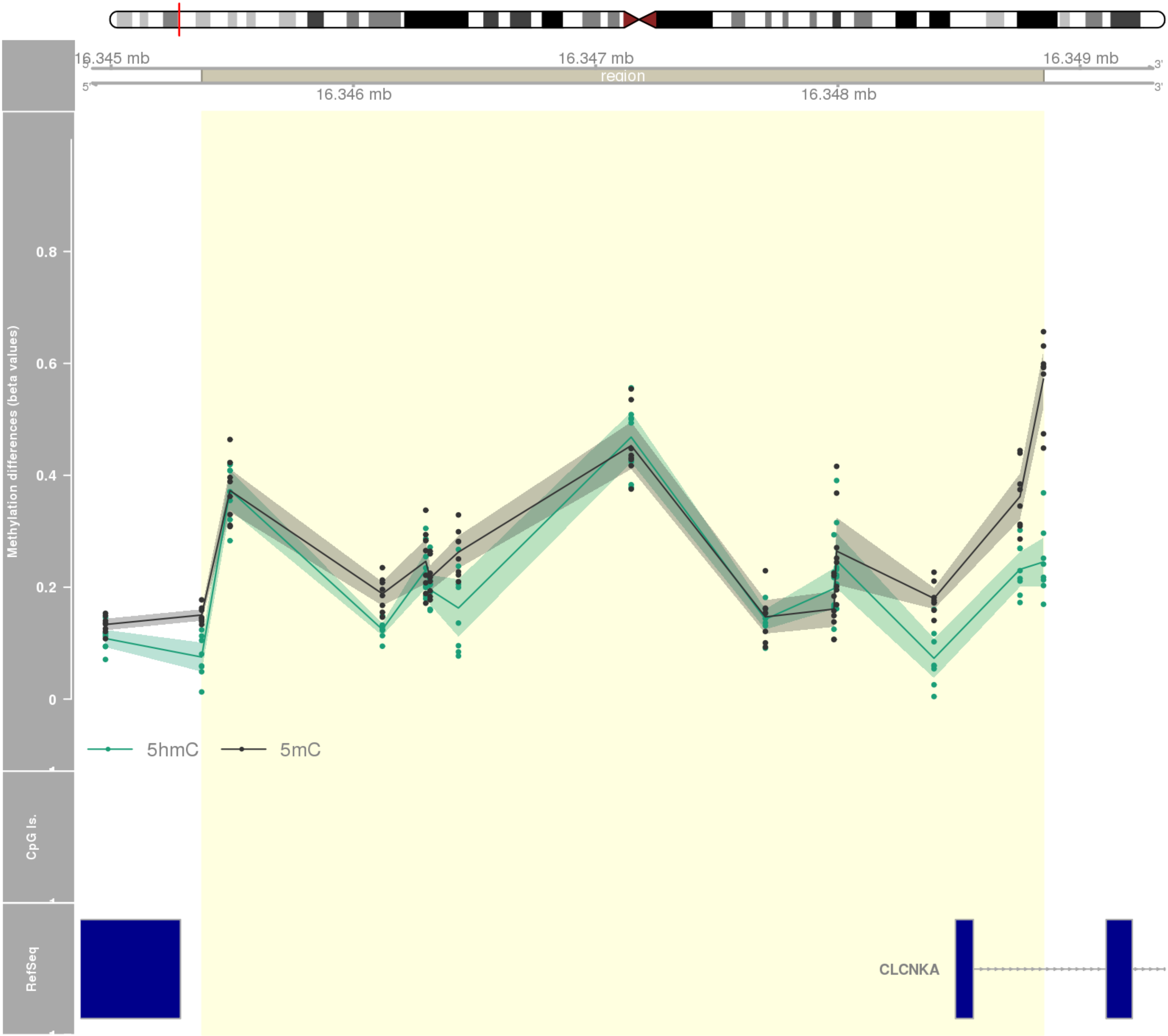
DMR 307 // chr7:2105368-2107835 // 2467 pb. (12 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: MAD1L1 -



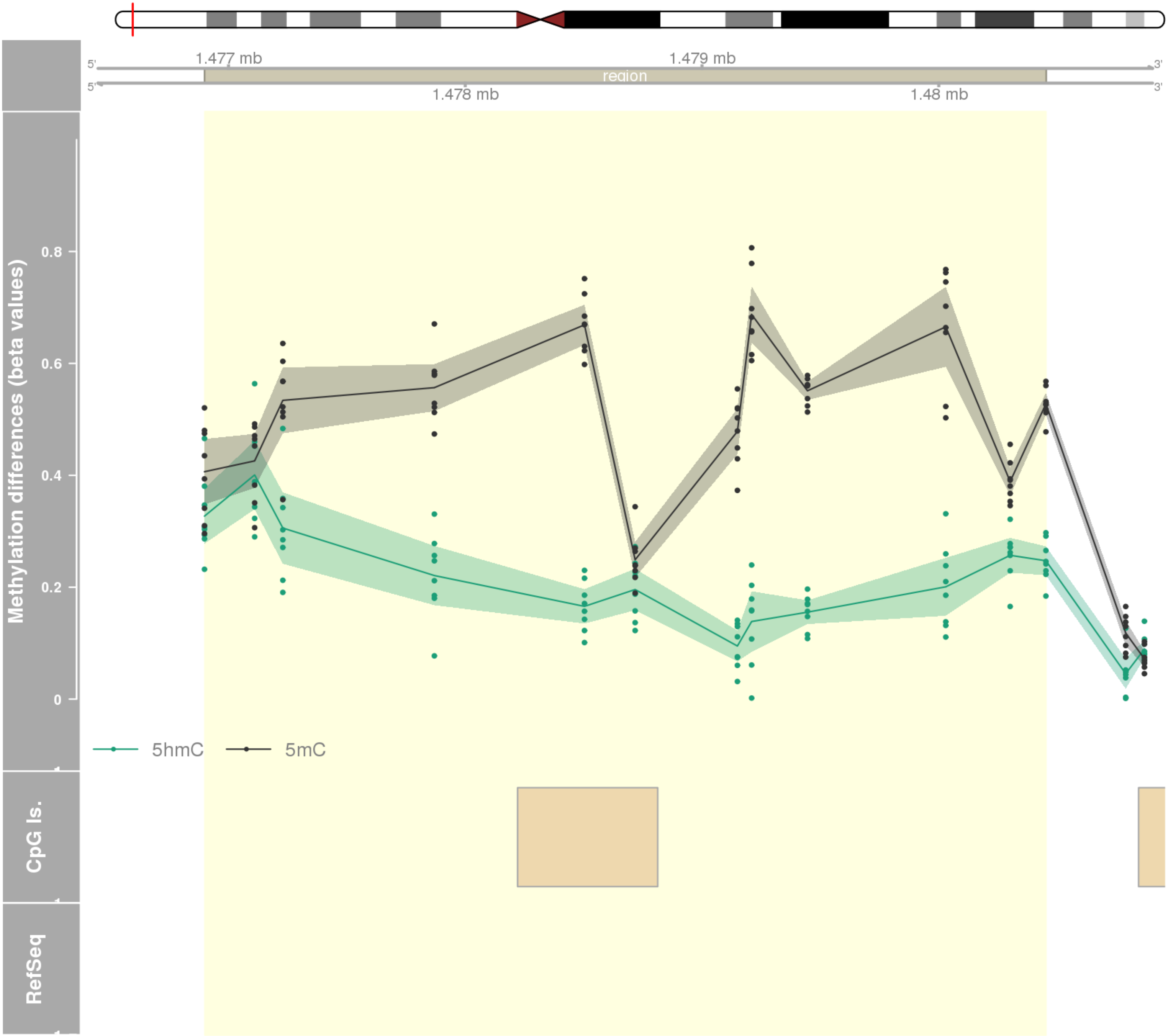
DMR 308 // chr11:64106532-64109158 // 2626 pb. (10 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: CCDC88B -



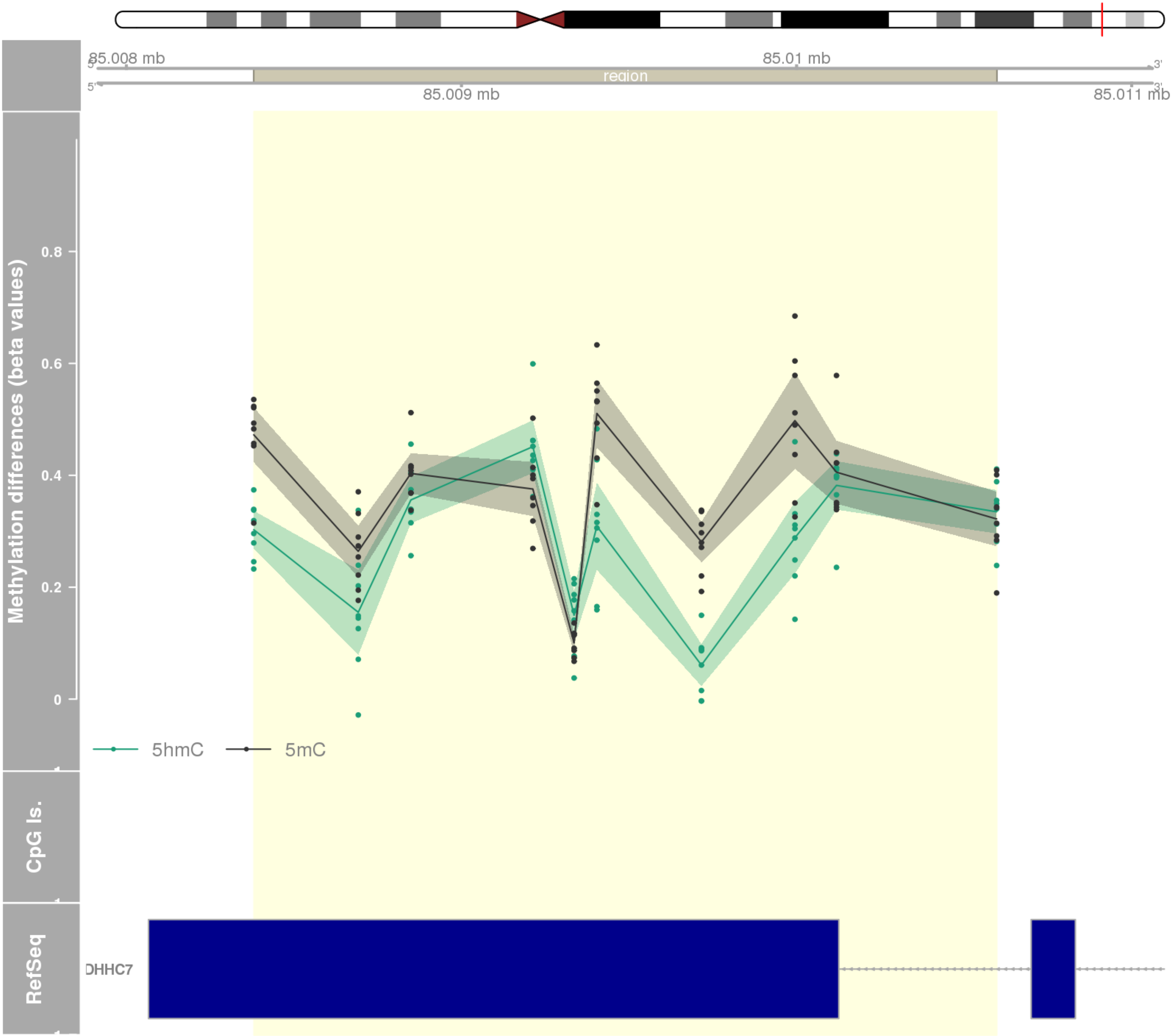
DMR 309 // chr1:16345374-16348849 // 3475 pb. (13 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: HSPB7 / CLCNKA -



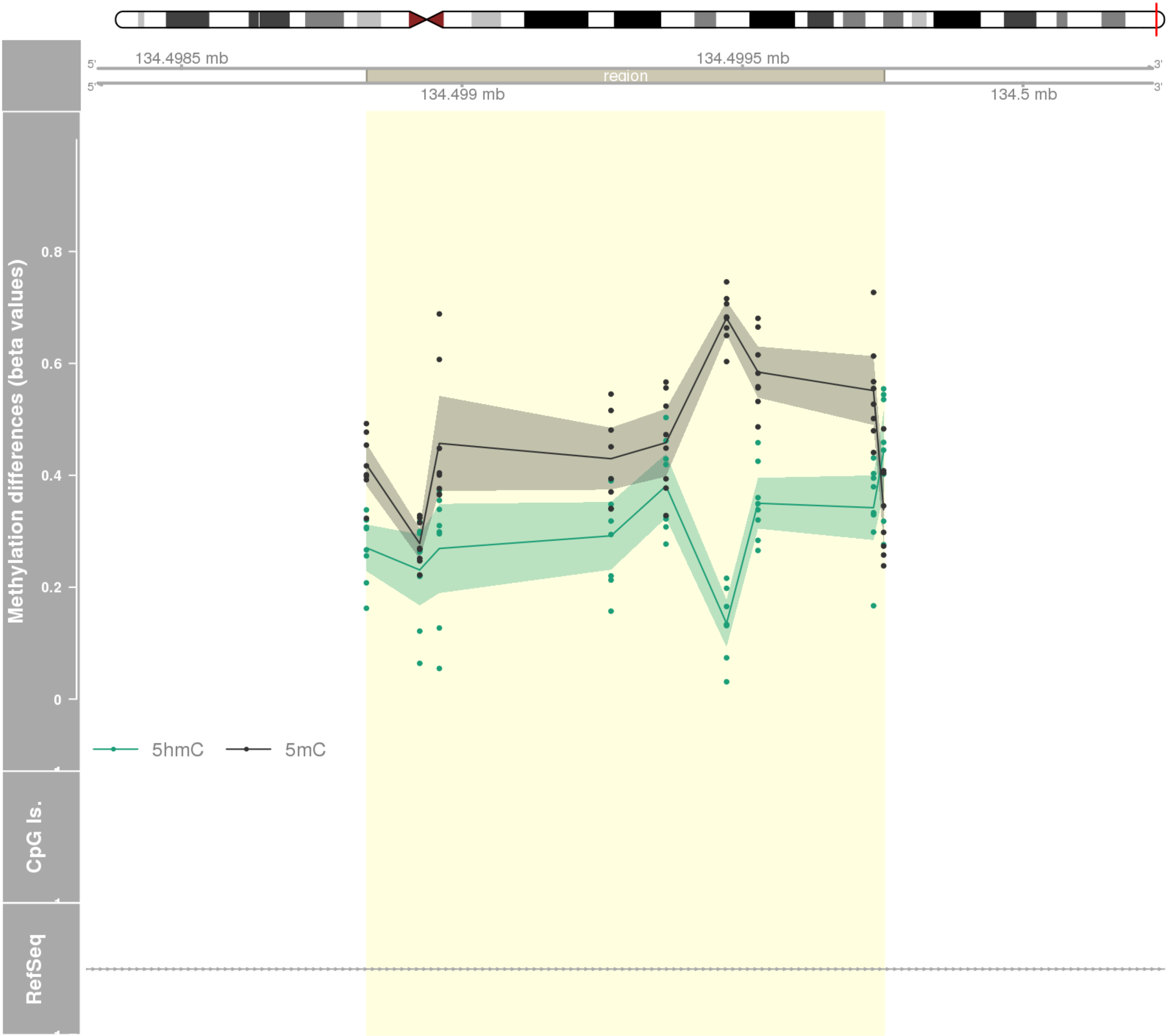
DMR 310 // chr16:1476899-1480453 // 3554 pb. (12 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: C16orf91 -



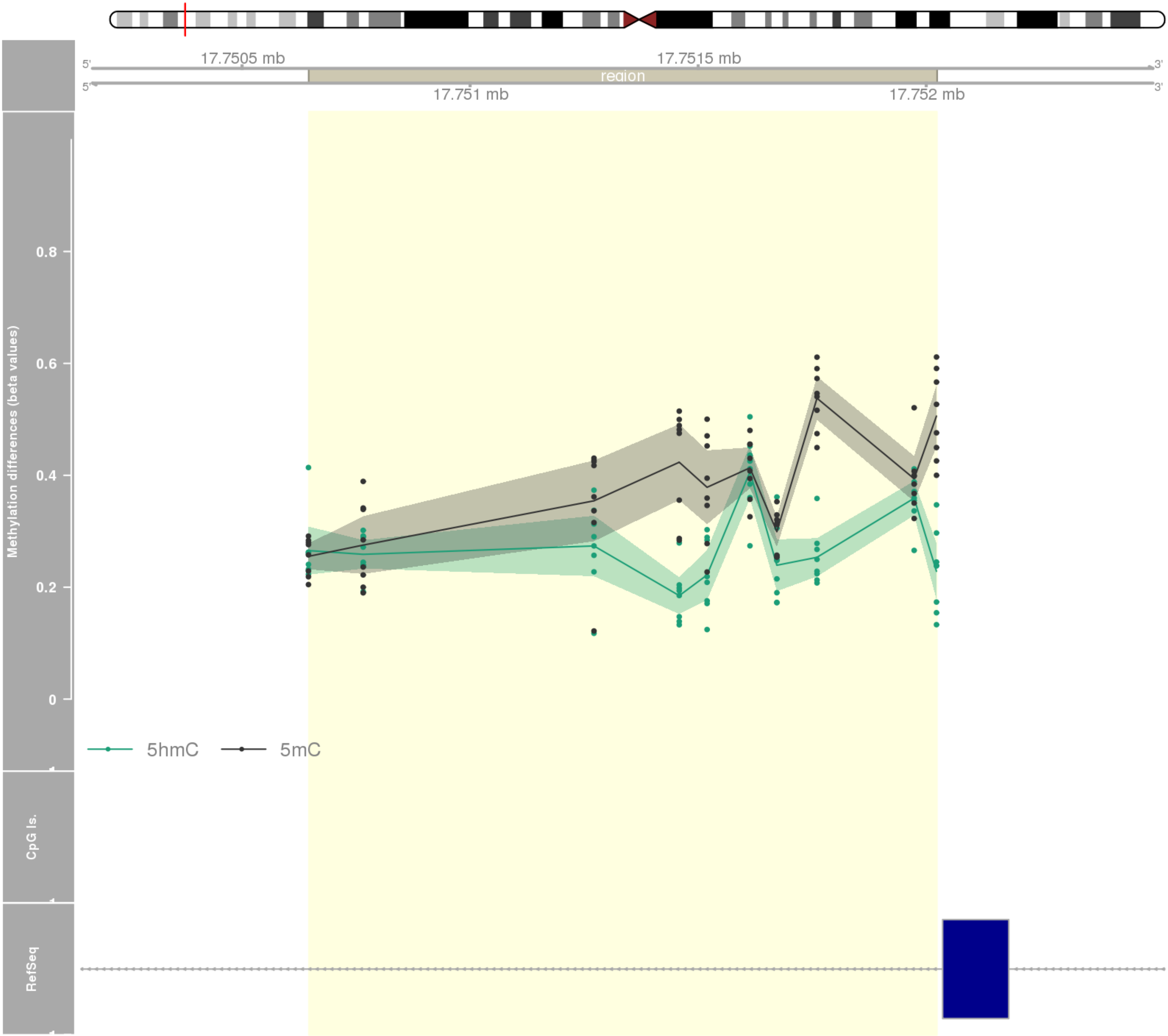
DMR 311 // chr16:85008380-85010597 // 2217 pb. (10 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: ZDHHC7 -



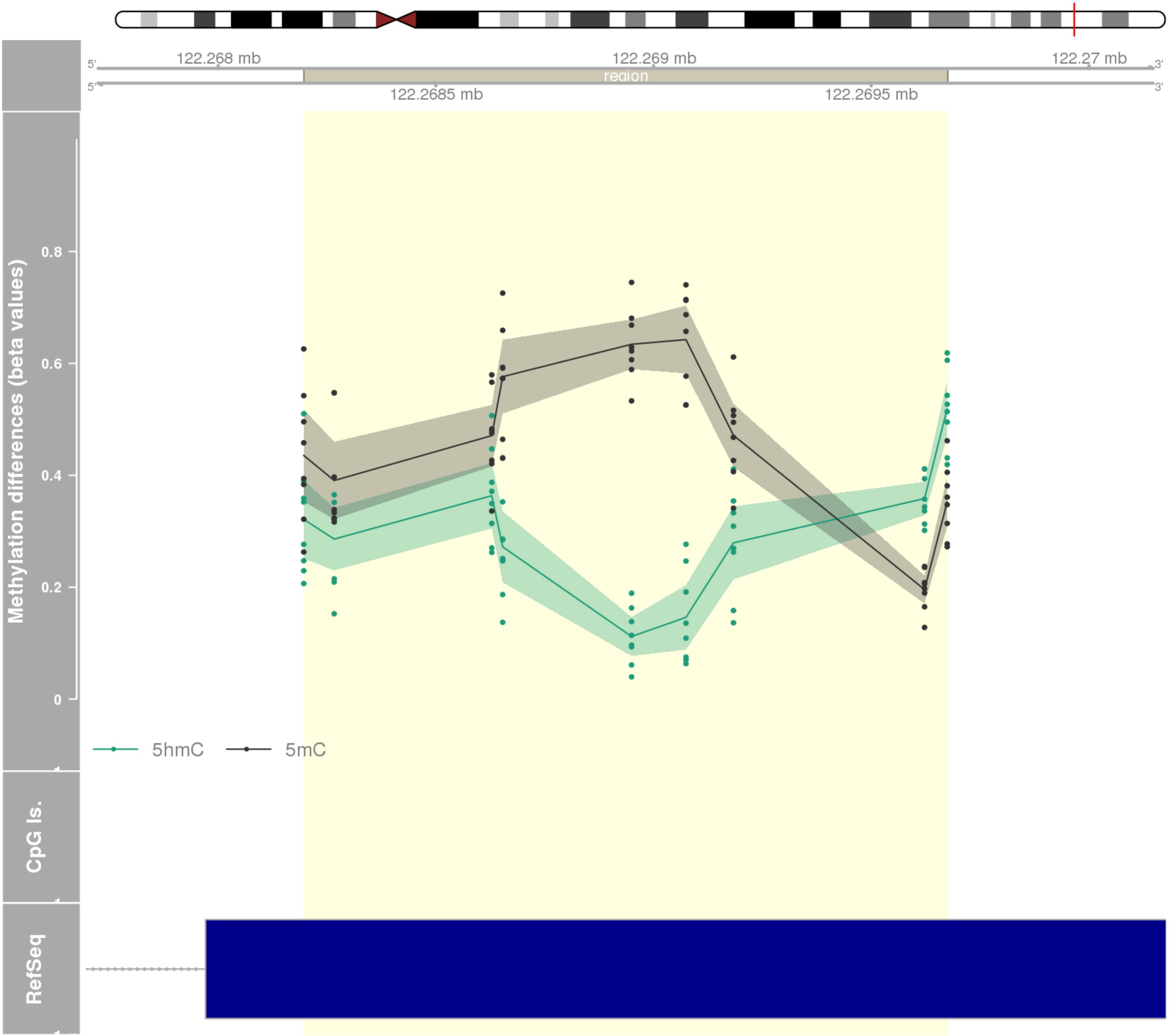
DMR 312 // chr10:134498830-134499752 // 922 pb. (9 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: INPP5A -



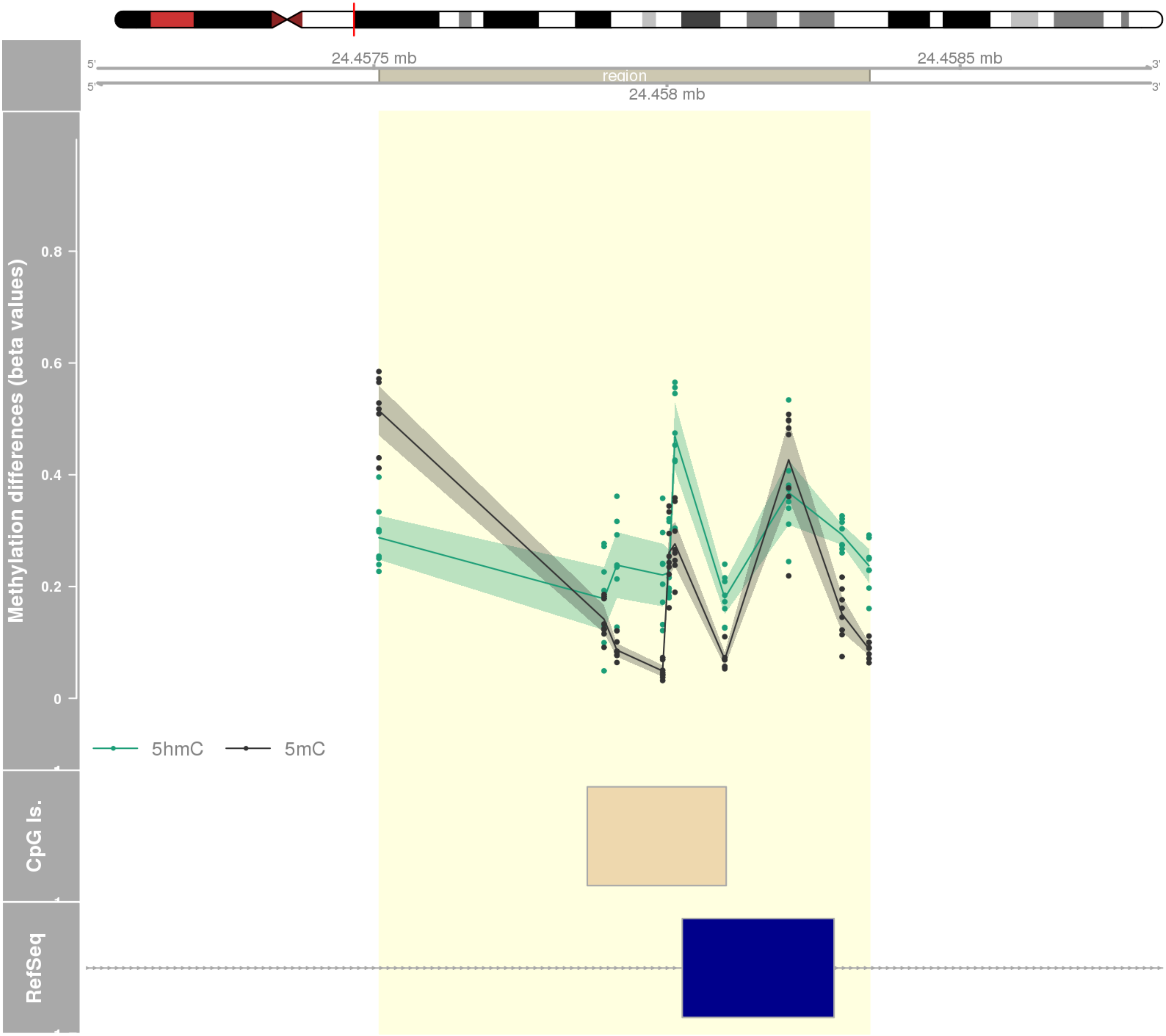
DMR 313 // chr1:17750646-17752023 // 1377 pb. (10 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: RCC2 -



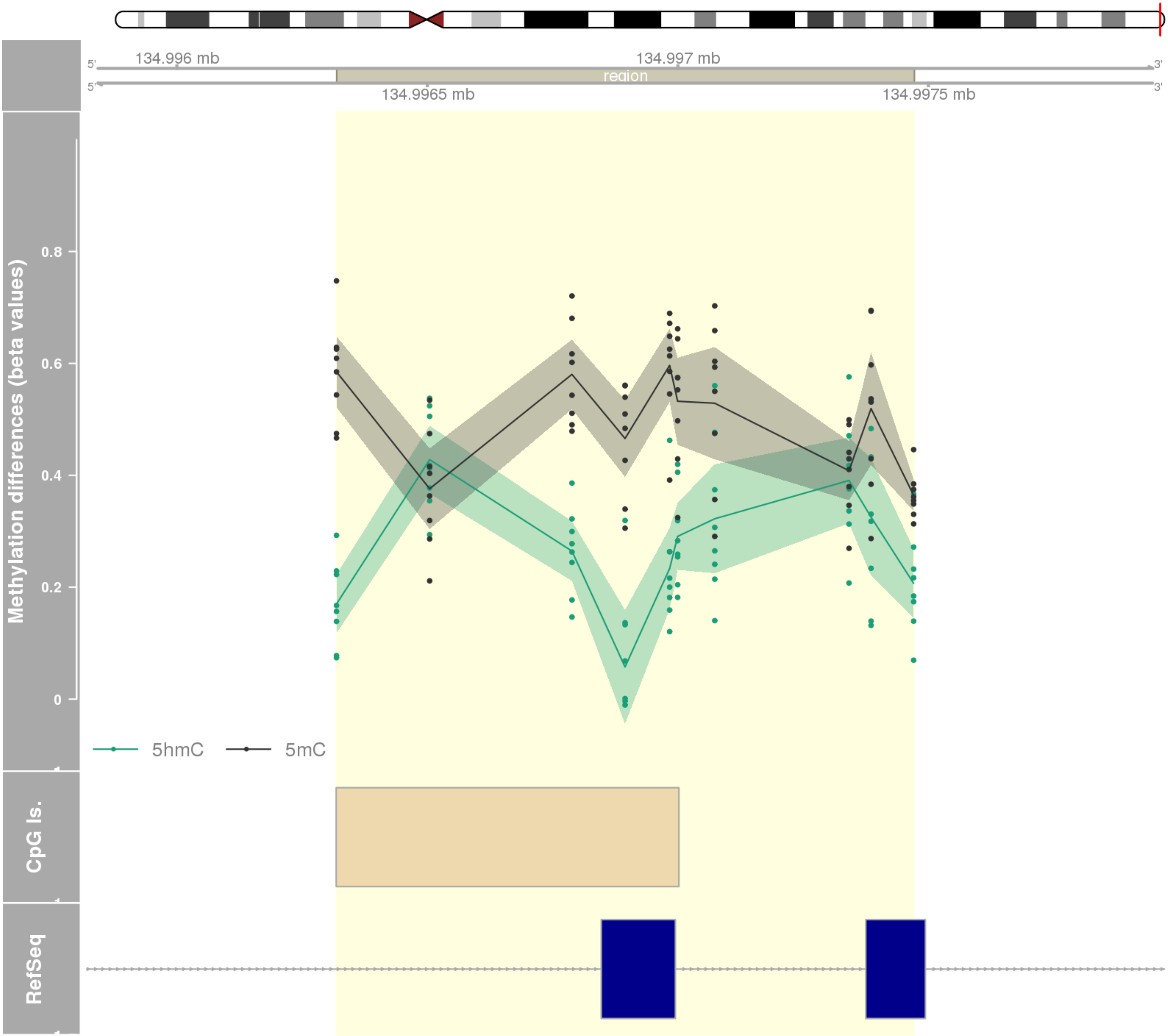
DMR 314 // chr12:122268197-122269675 // 1478 pb. (9 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: SETD1B -



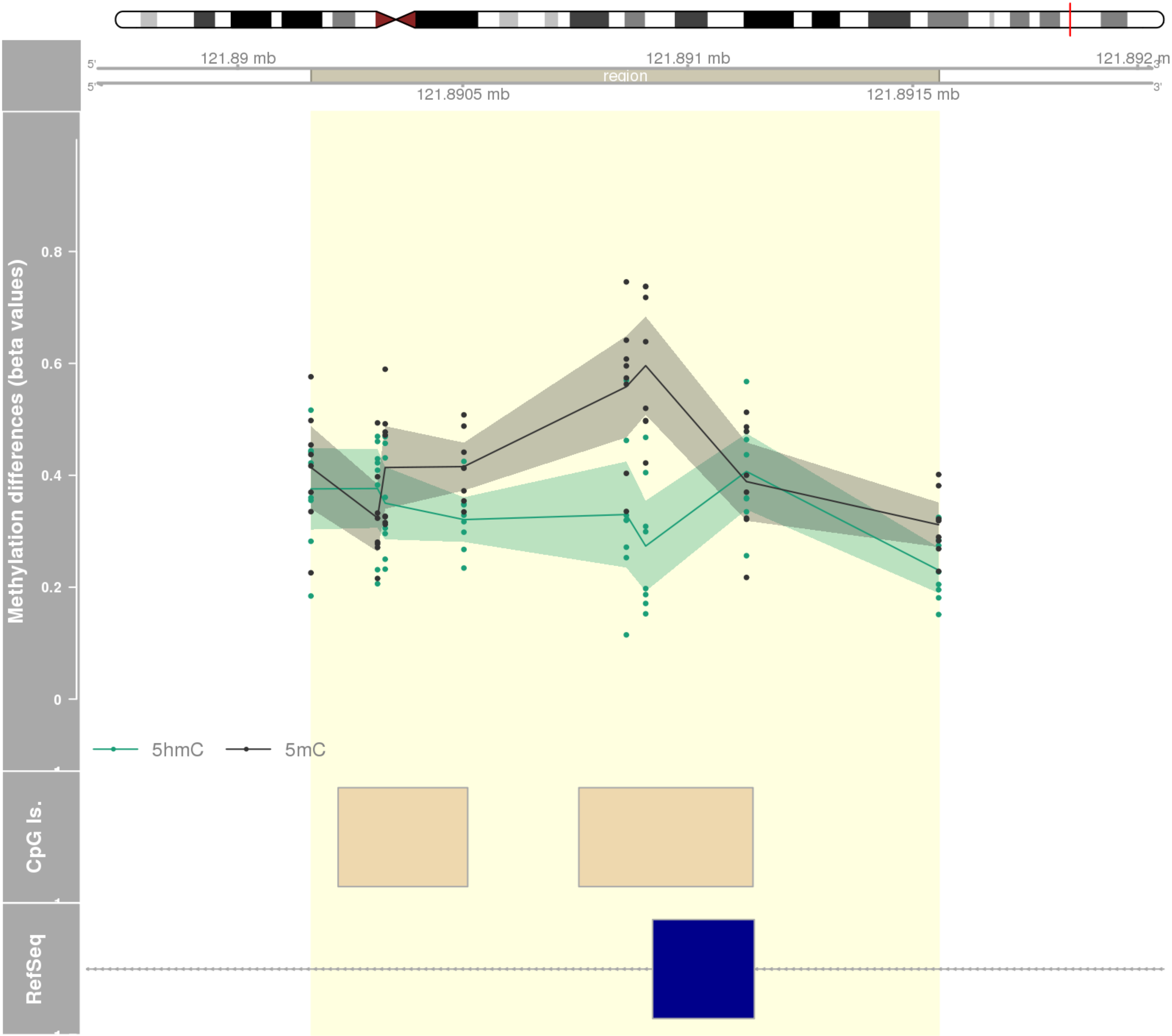
DMR 315 // chr14:24457509-24458345 // 836 pb. (10 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: DHRS4-AS1 / DHRS4L2 -



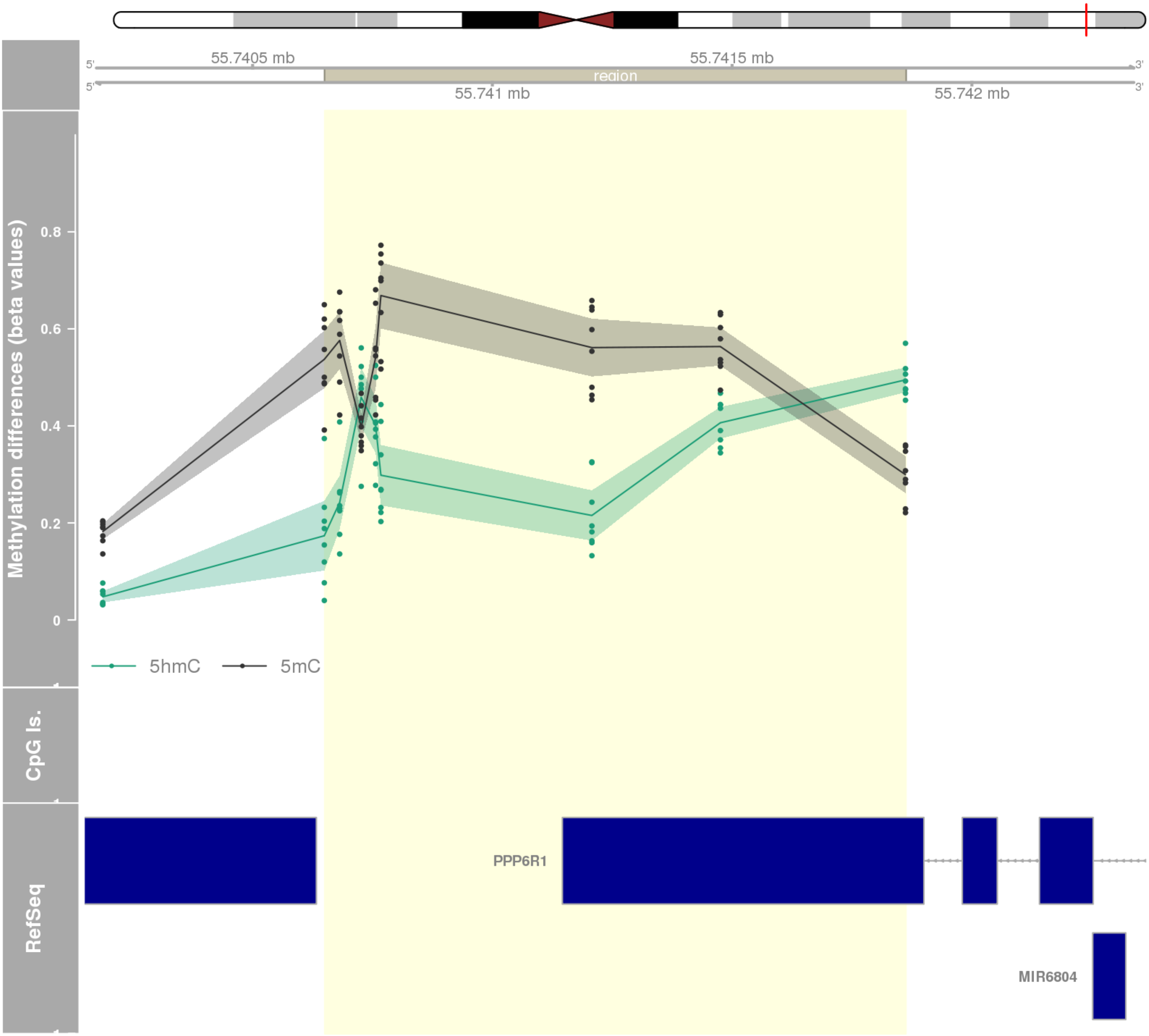
DMR 316 // chr10:134996319-134997471 // 1152 pb. (10 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: KNDC1 -



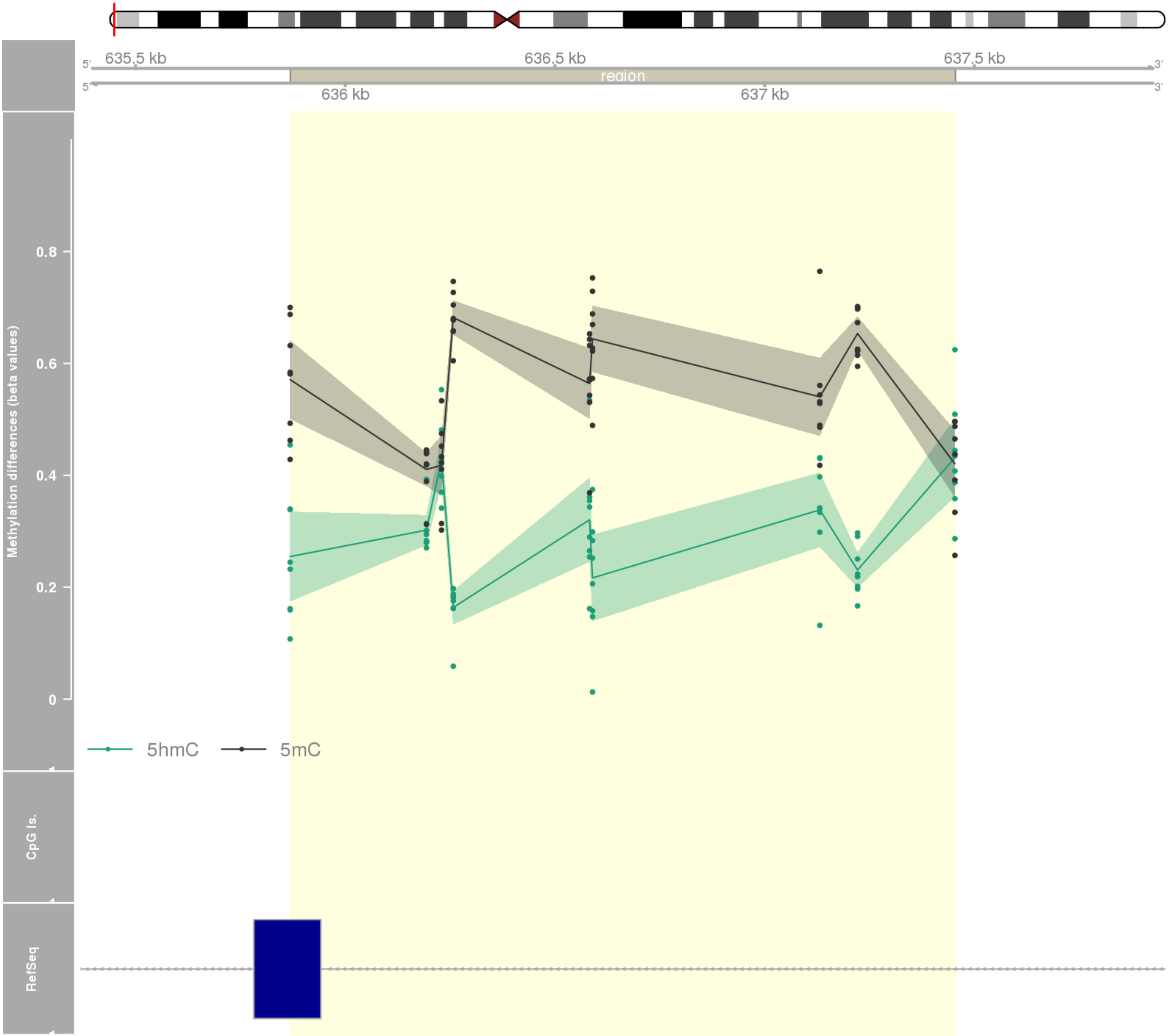
DMR 317 // chr12:121890163-121891558 // 1395 pb. (8 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: KDM2B -



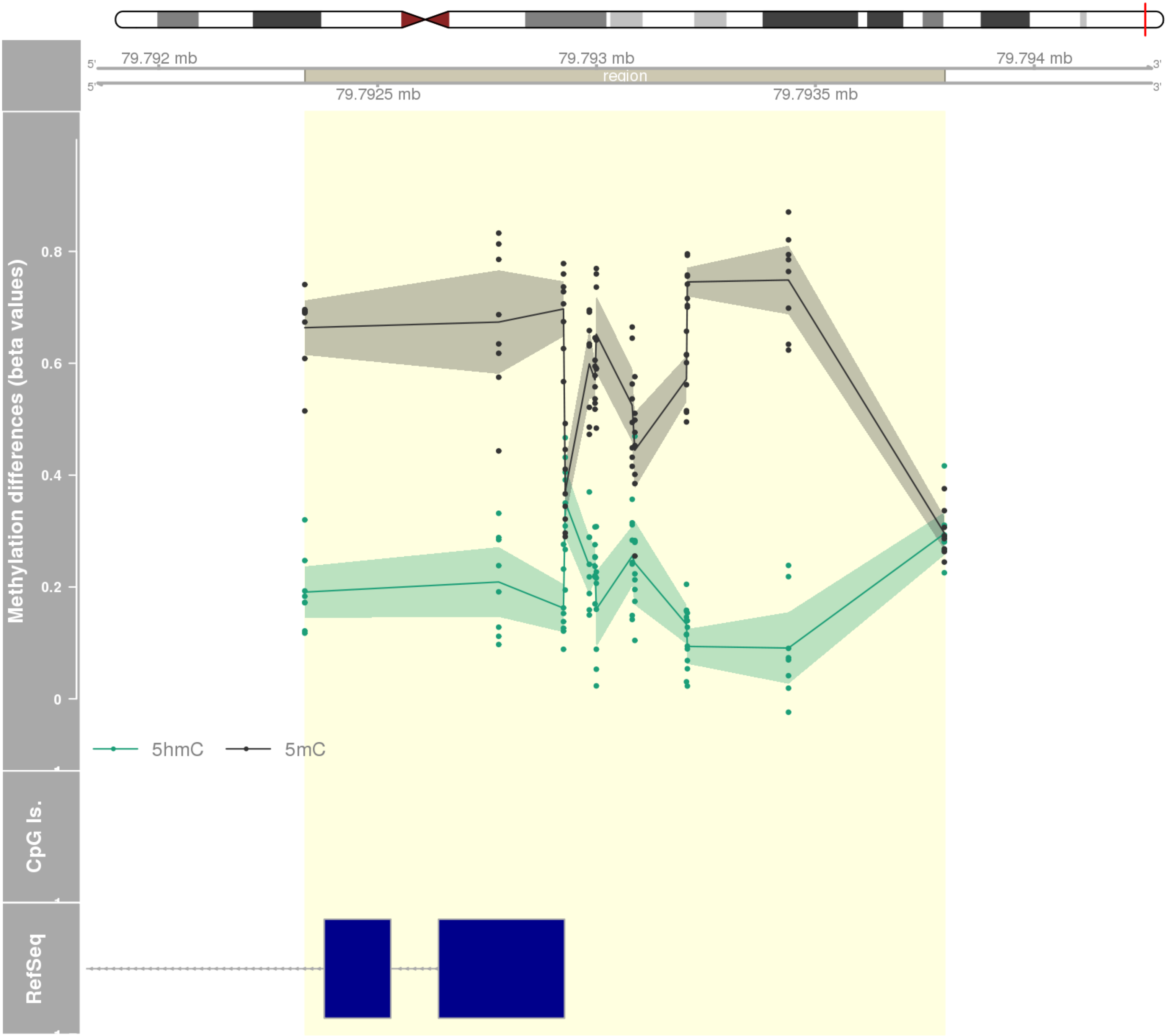
DMR 318 // chr19:55740650-55741862 // 1212 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.016 // fwerArea: 0.559
- genes: TMEM86B / PPP6R1 -



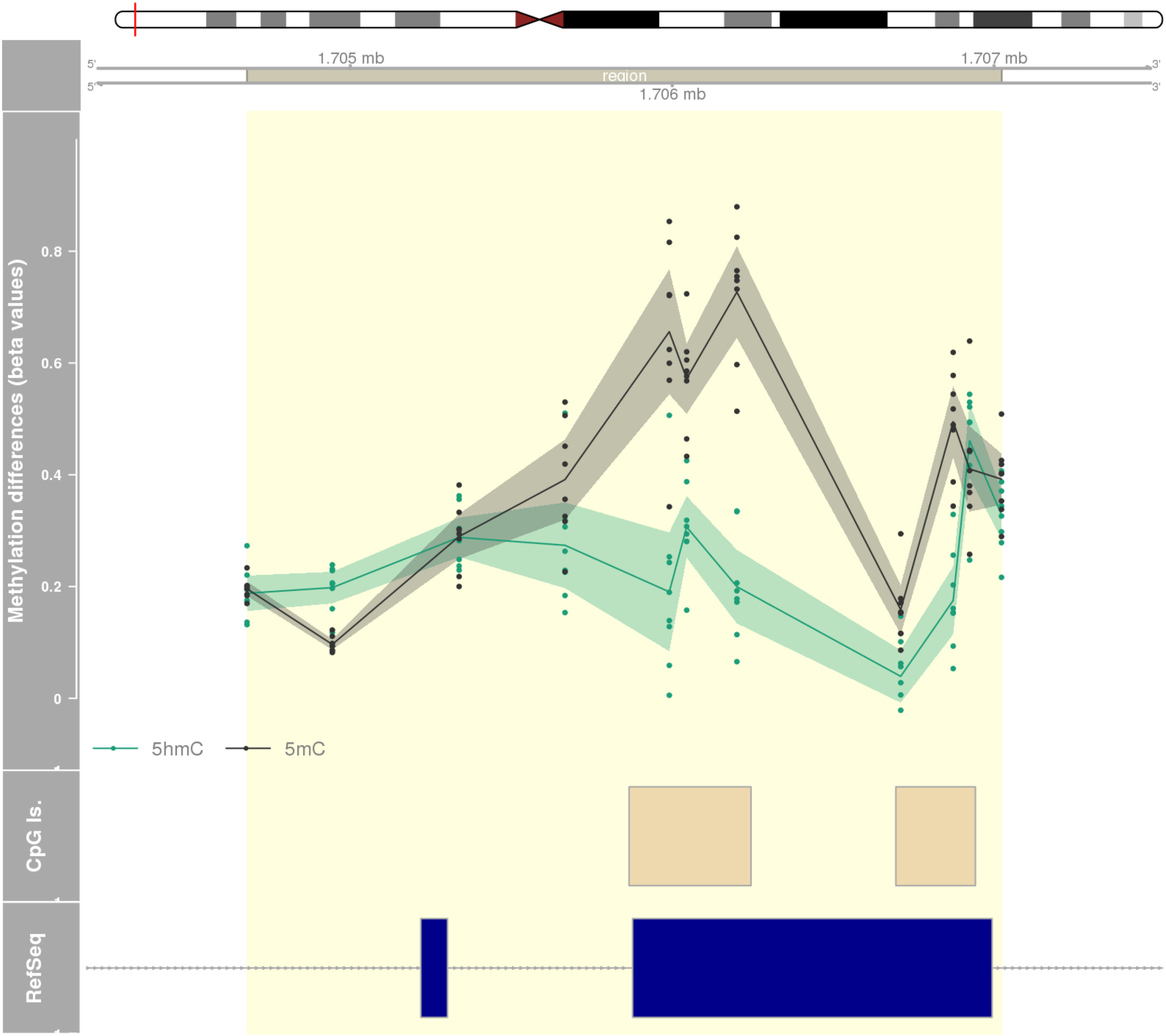
DMR 319 // chr7:635869-637454 // 1585 pb. (9 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: PRKAR1B -



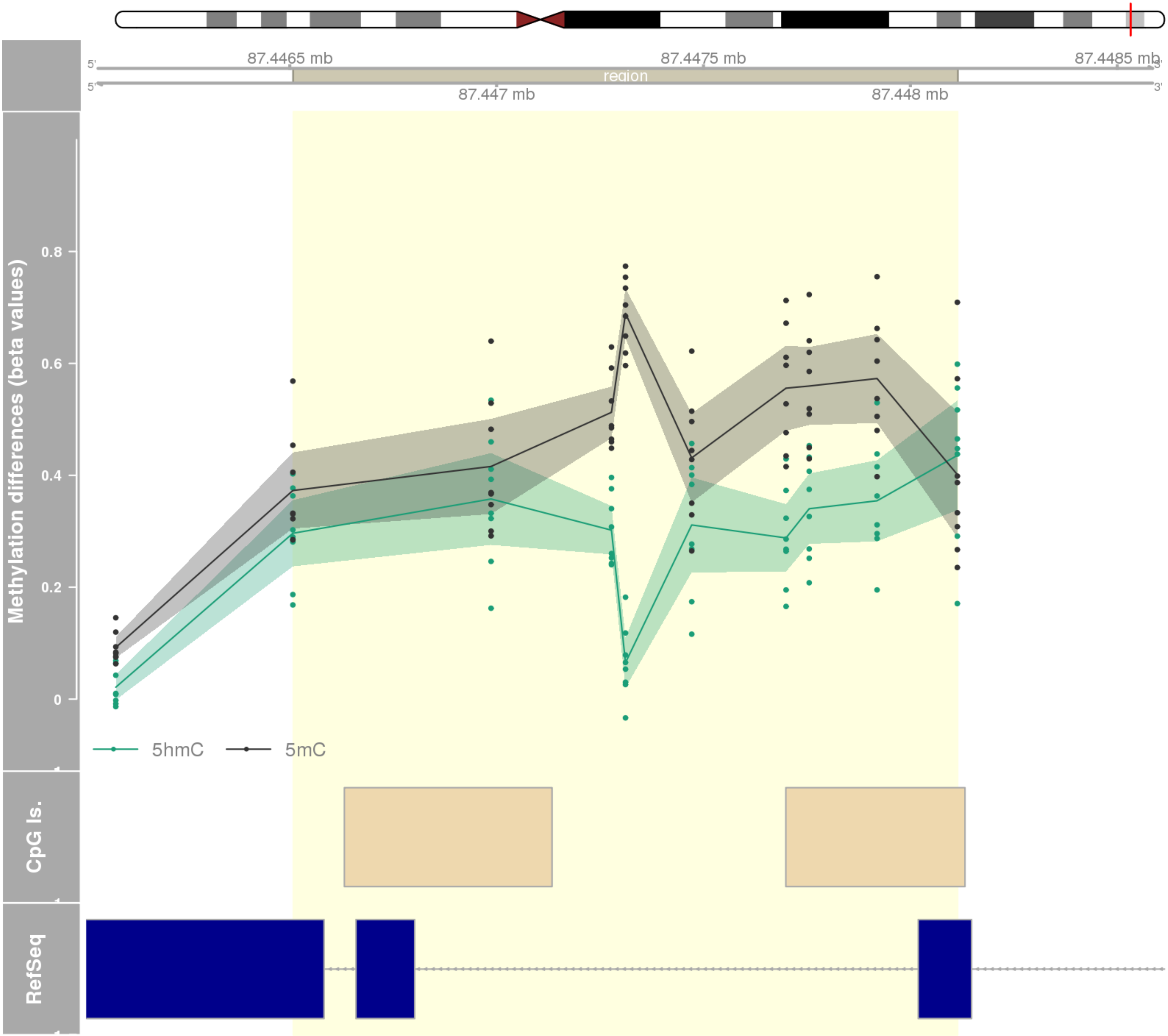
DMR 320 // chr17:79792334-79793795 // 1461 pb. (13 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: PPP1R27 -



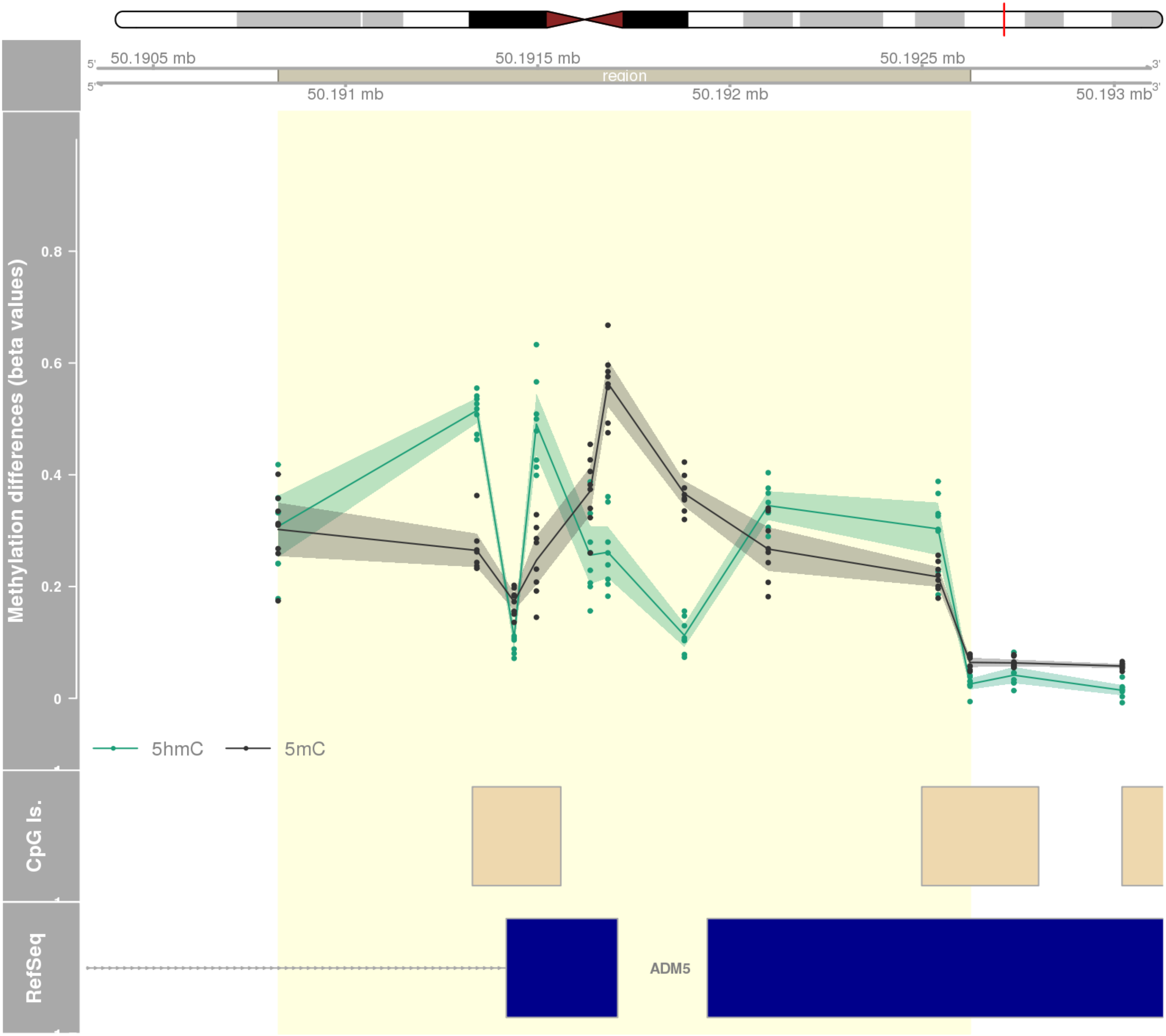
DMR 321 // chr16:1704679-1707023 // 2344 pb. (11 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: CRAMP1L -



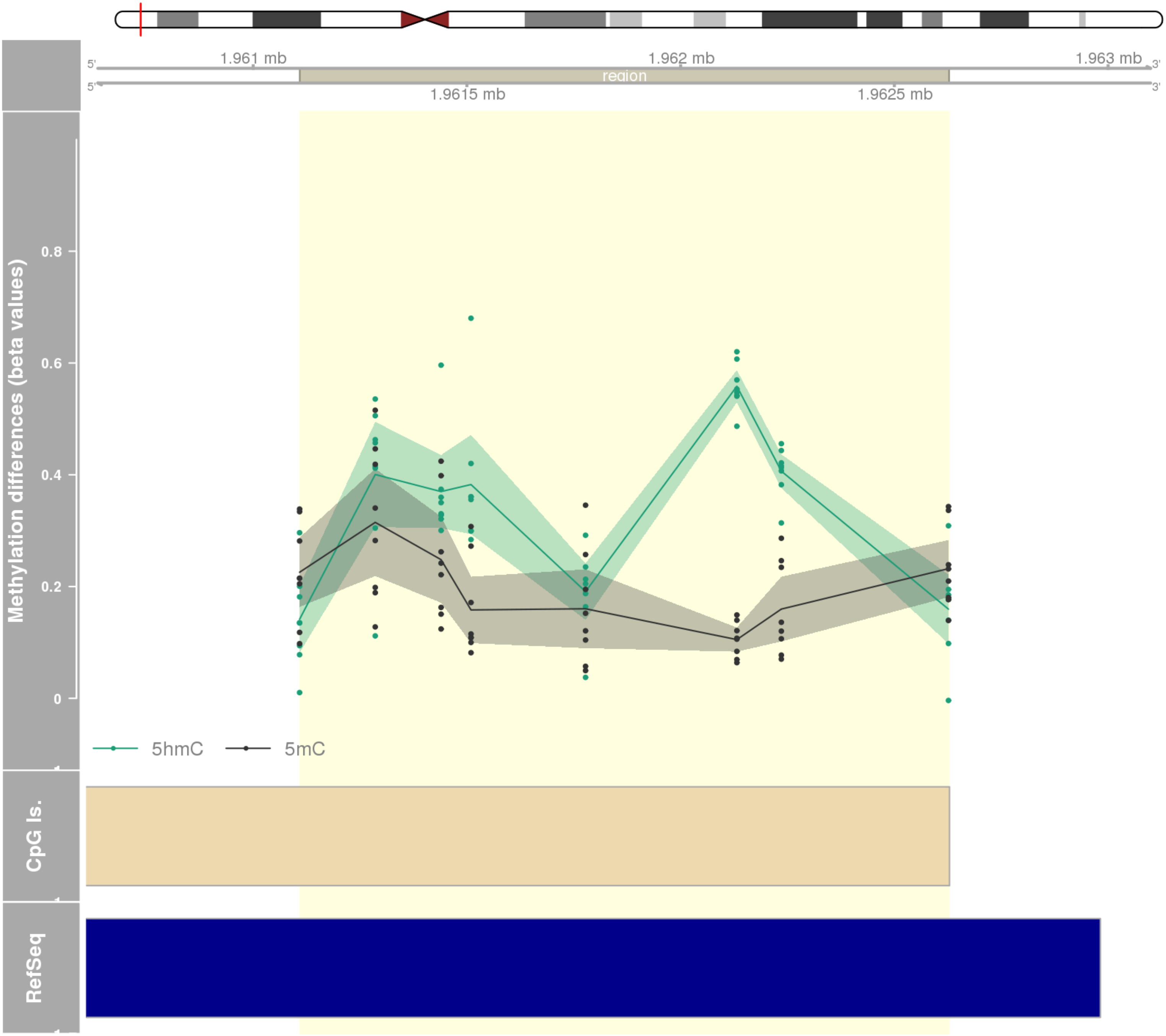
DMR 322 // chr16:87446508-87448114 // 1606 pb. (9 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: ZCCHC14 -



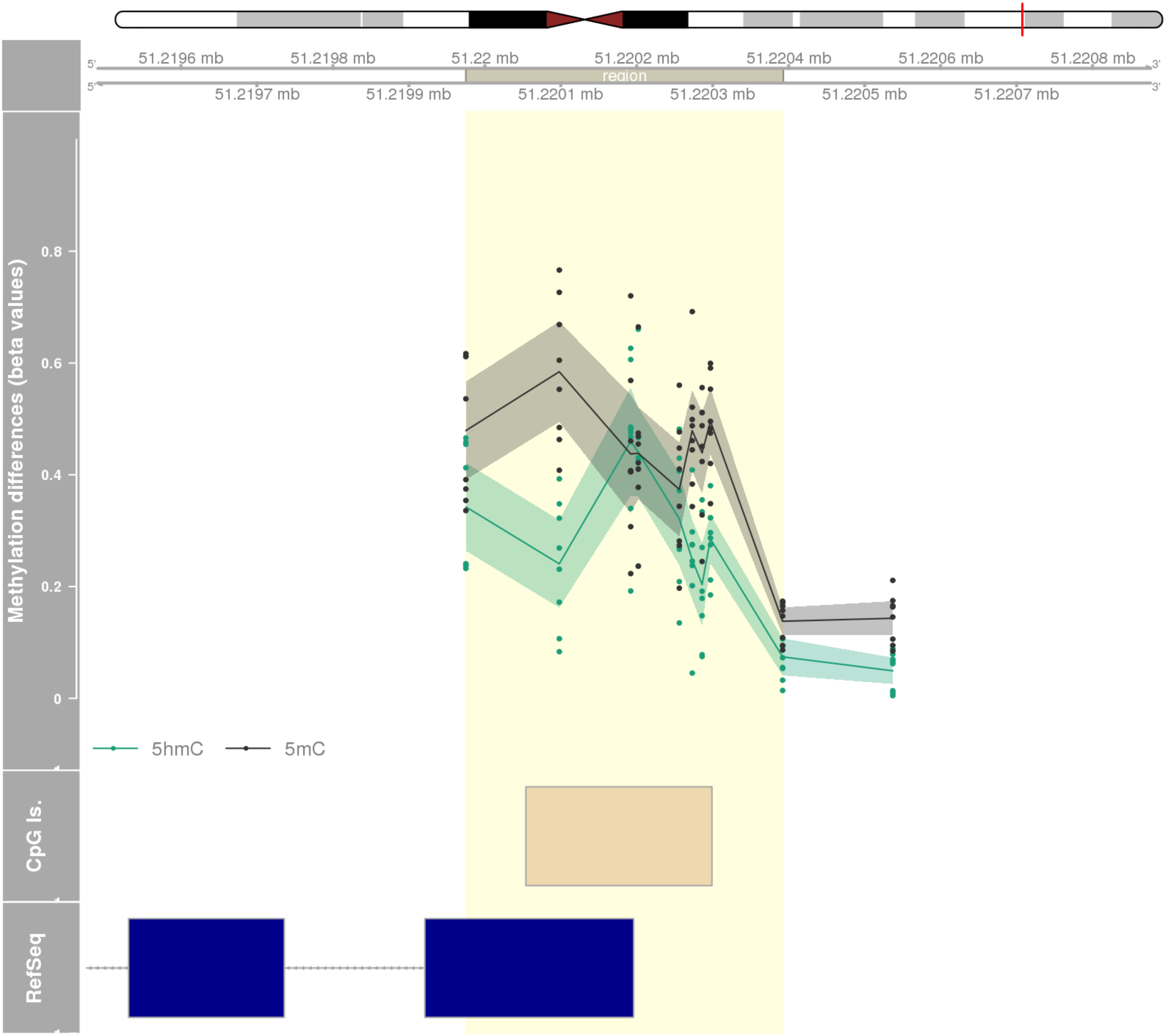
DMR 323 // chr19:50190825-50192625 // 1800 pb. (10 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: PRMT1 / ADM5 -



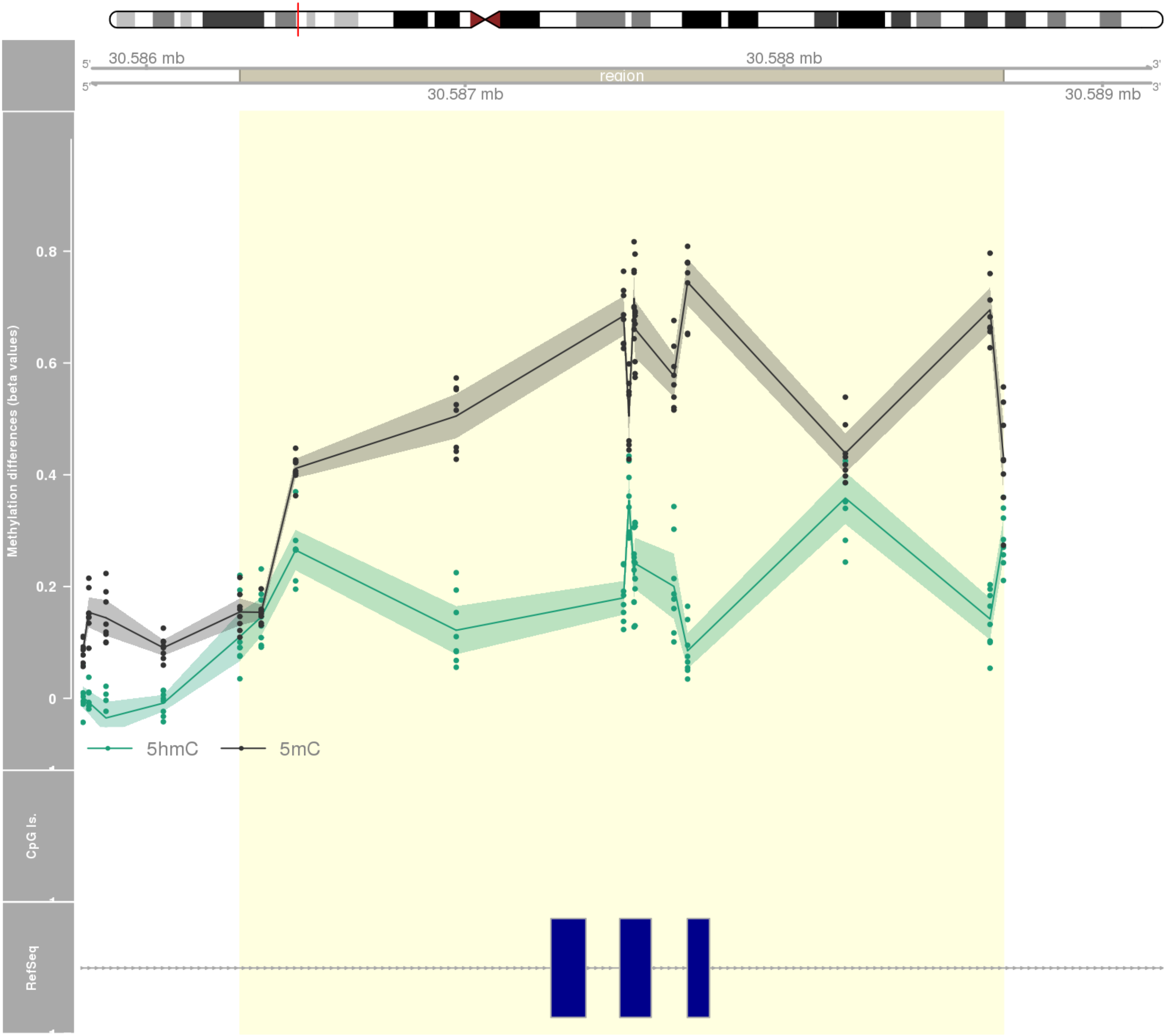
DMR 324 // chr17:1961109-1962627 // 1518 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: HIC1 -

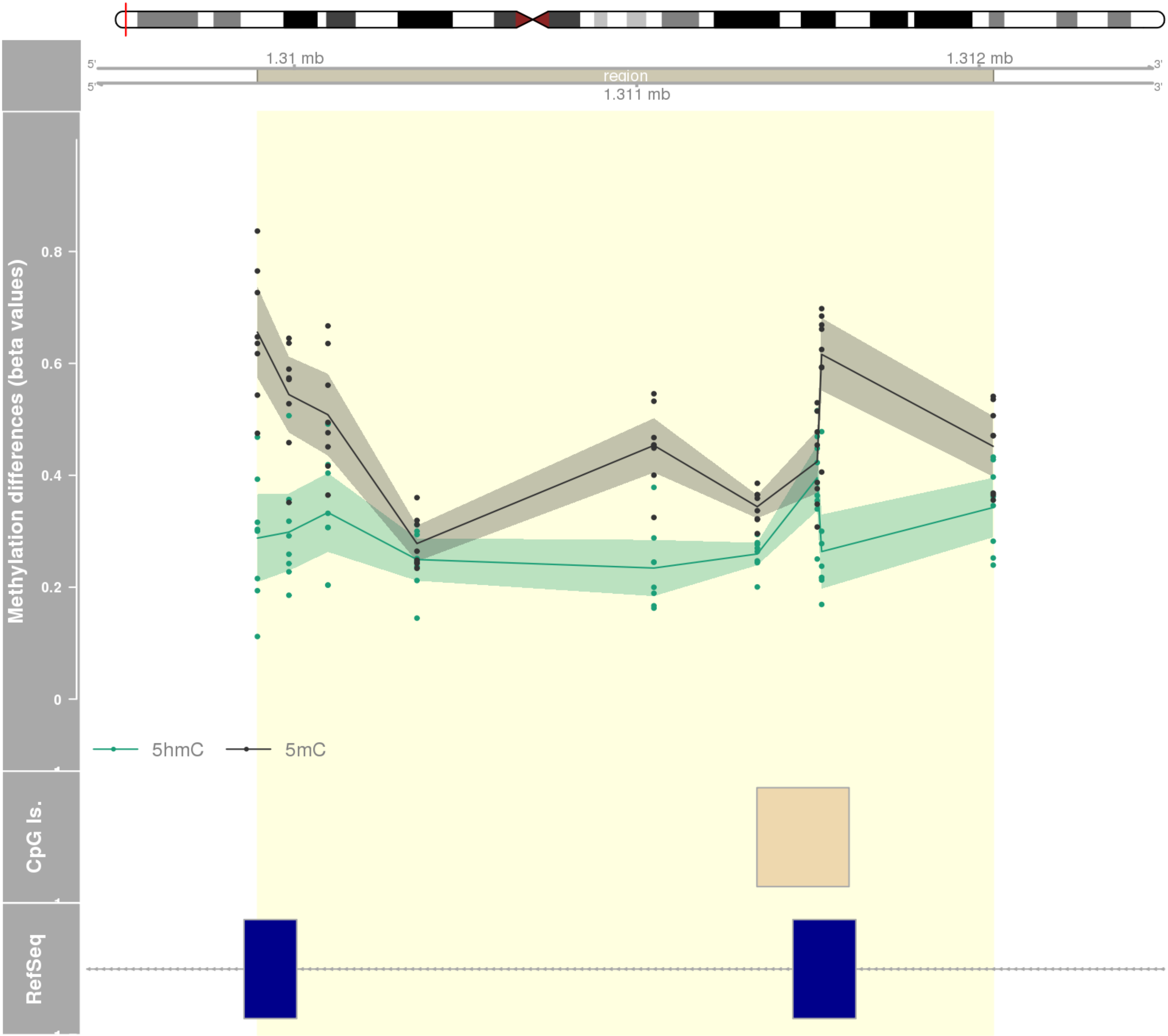


DMR 325 // chr19:51219975-51220392 // 417 pb. (9 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: SHANK1 -



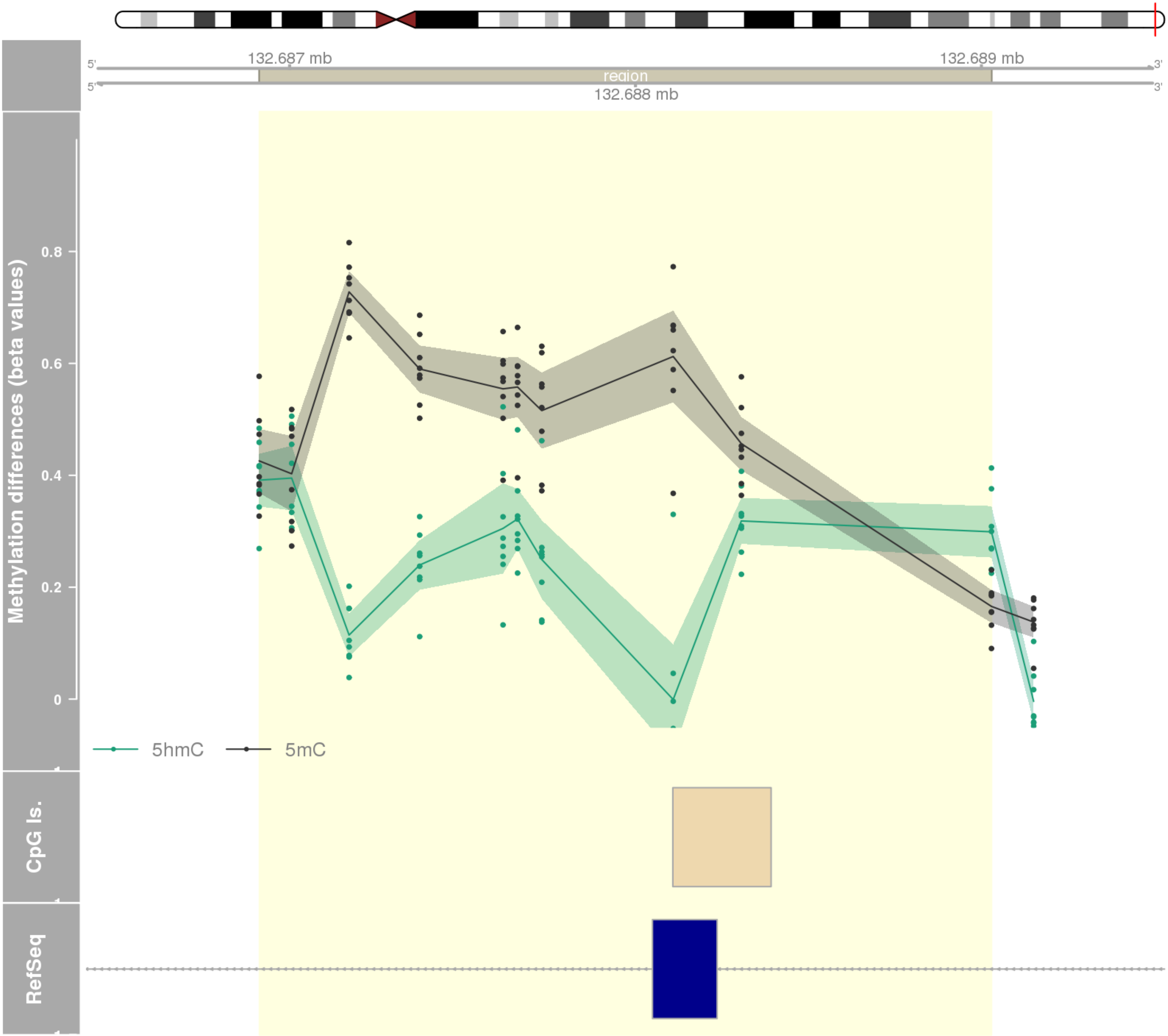
DMR 326 // chr6:30586293-30588689 // 2396 pb. (13 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: PPP1R10 / MRPS18B -



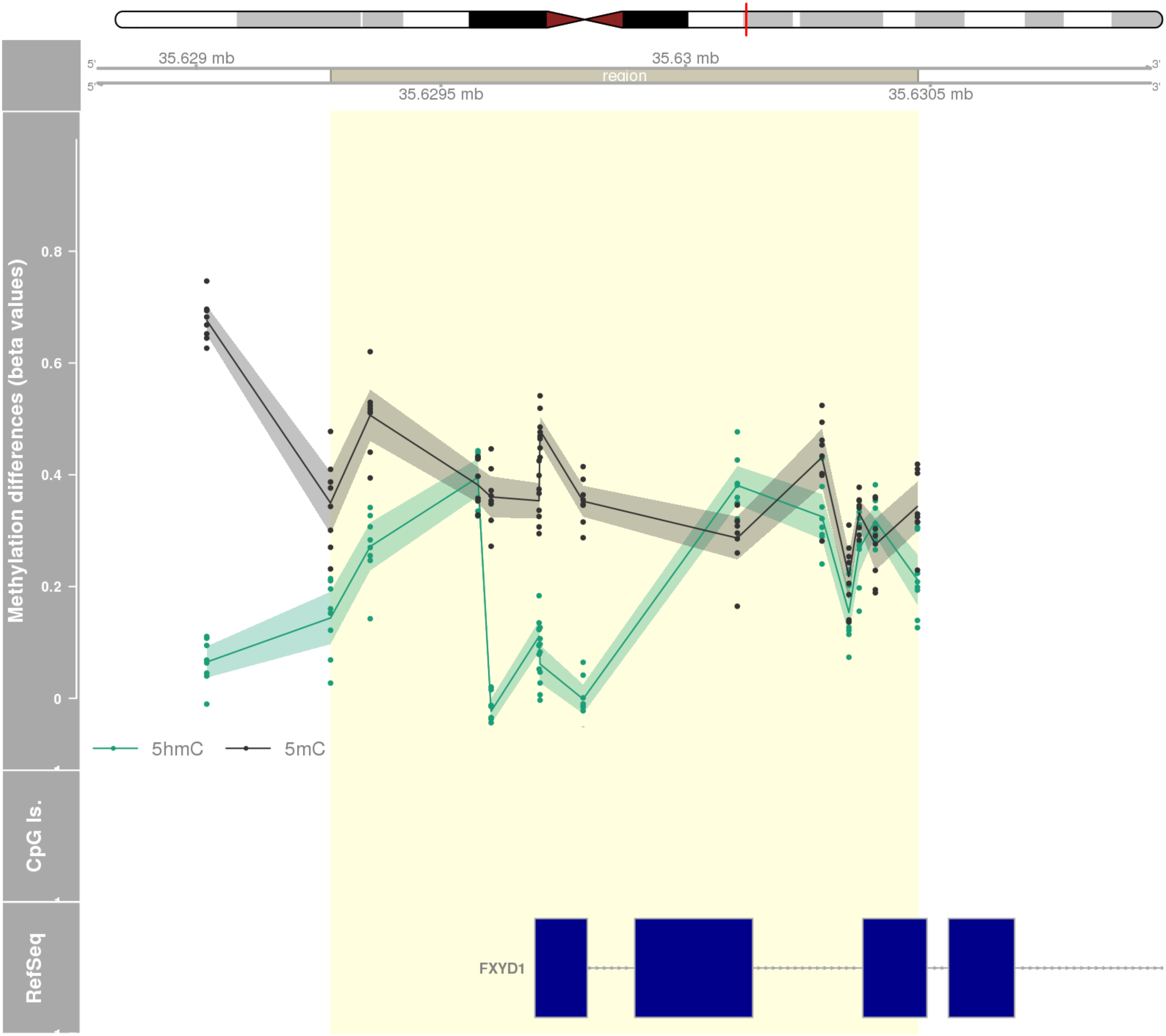


DMR 327 // chr11:1309892-1312041 // 2149 pb. (9 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: TOLLIP -

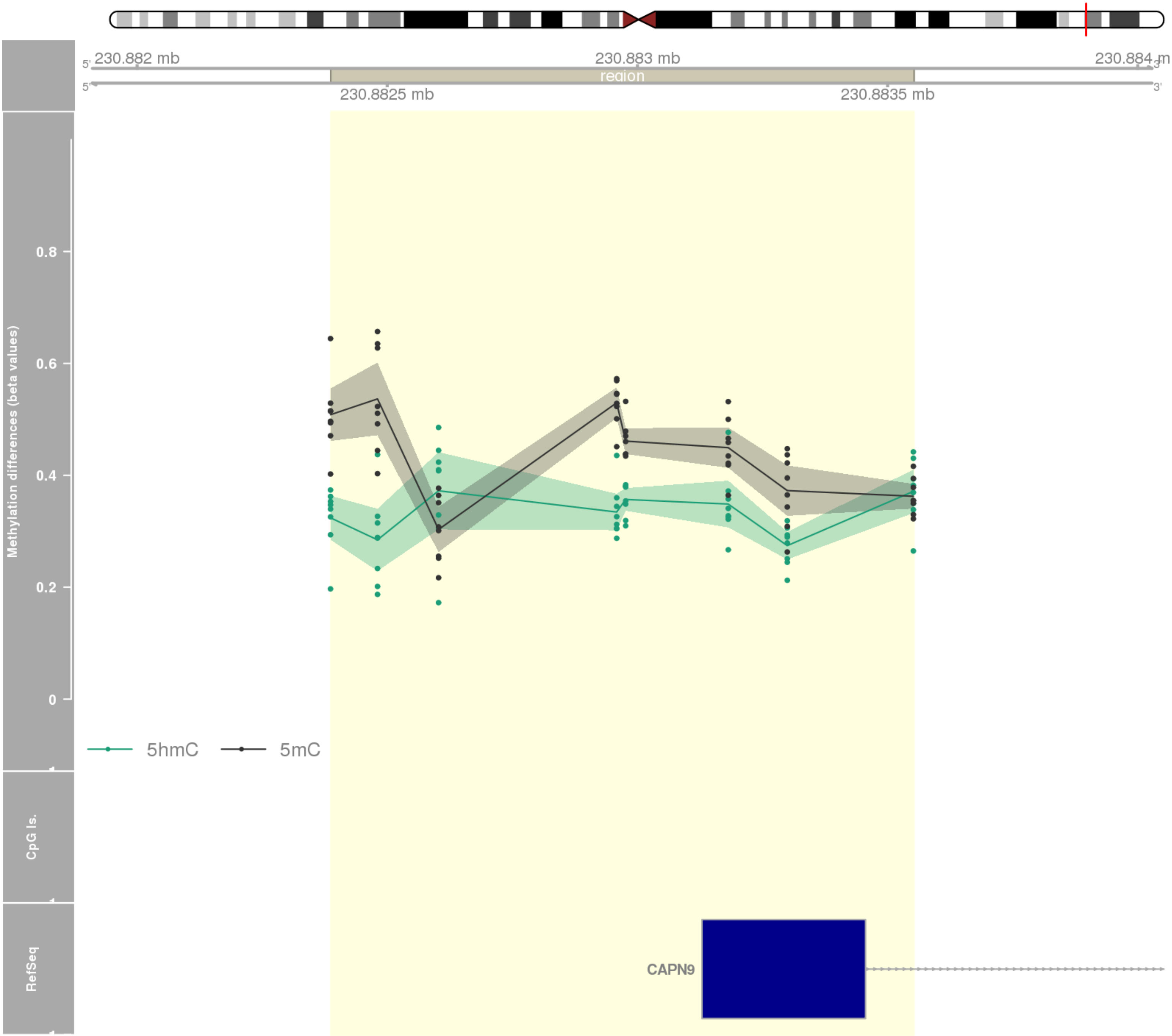
DMR 328 // chr12:132686912-132689029 // 2117 pb. (10 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: GALNT9 -



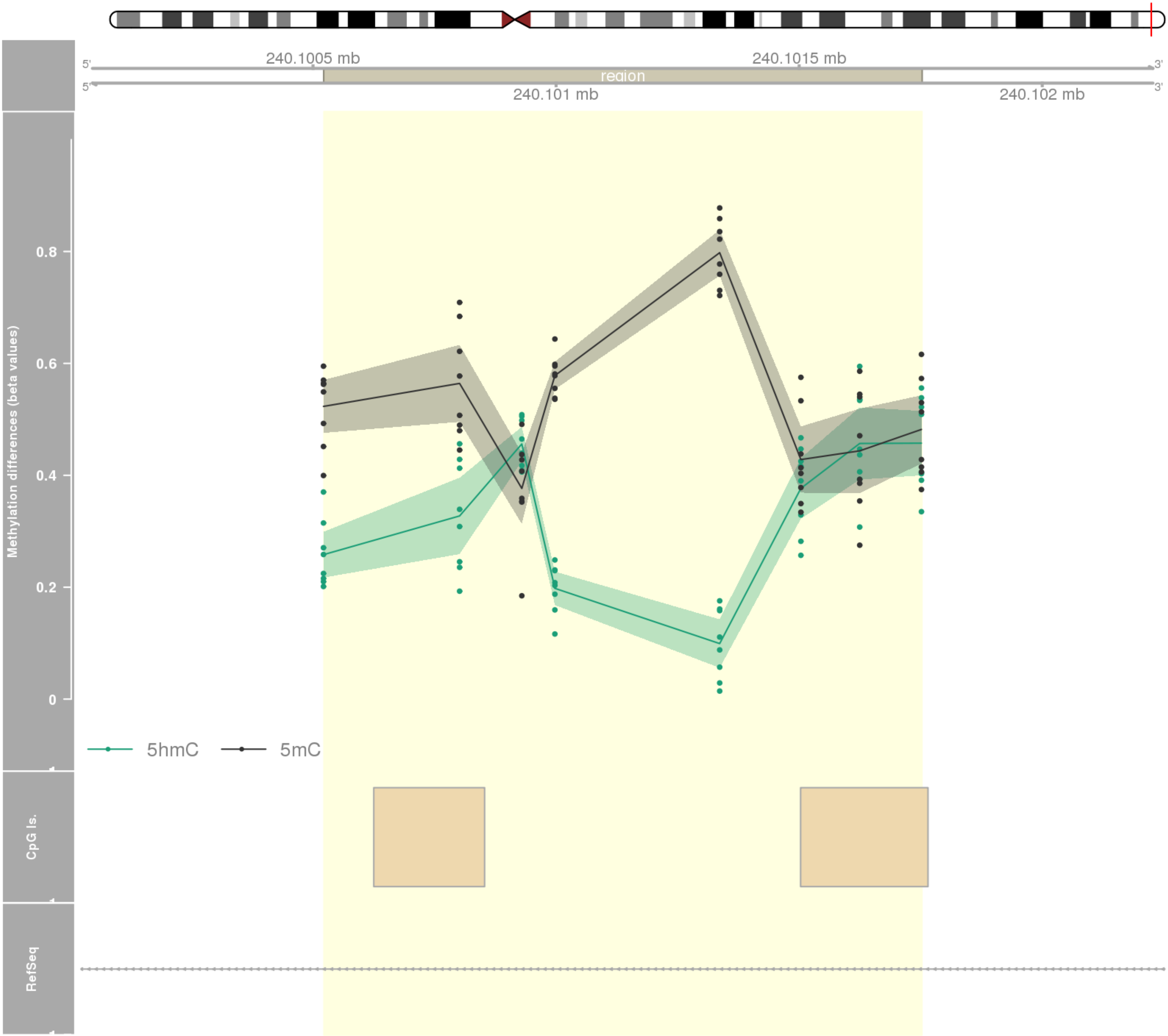
DMR 329 // chr19:35629275-35630474 // 1199 pb. (13 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: LGI4 / FXYD1 -



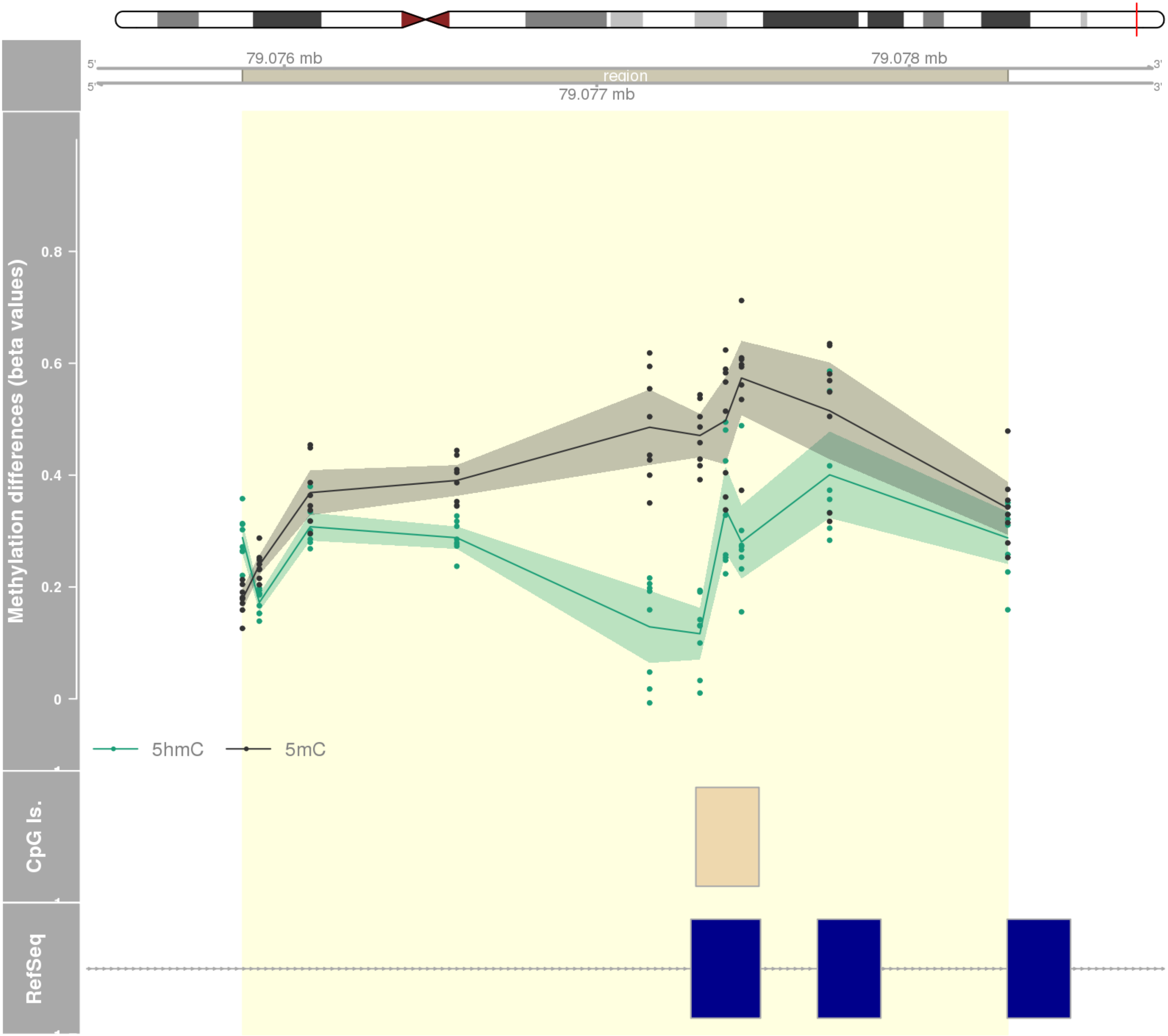
DMR 330 // chr1:230882387-230883552 // 1165 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: CAPN9 -



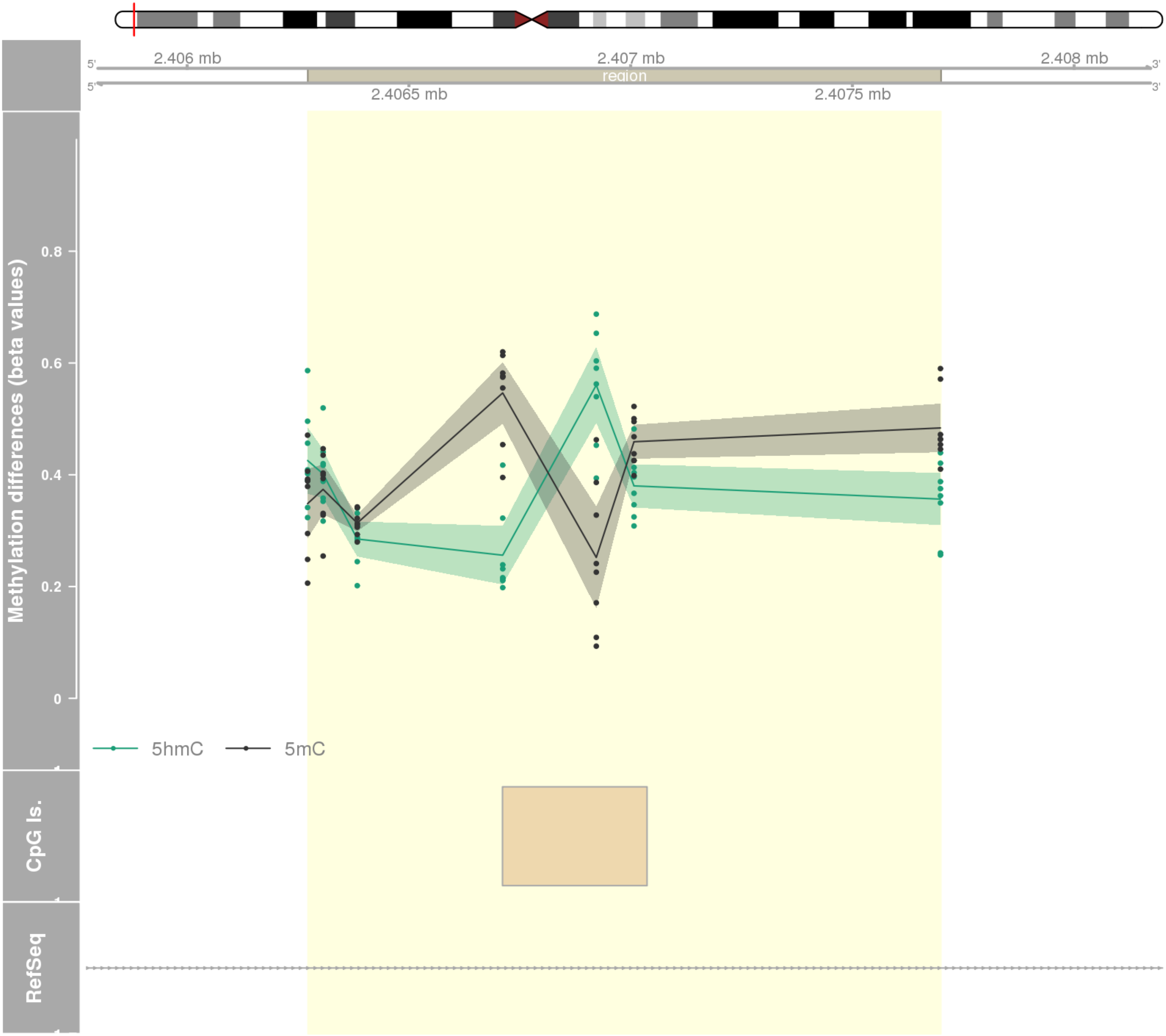
DMR 331 // chr2:240100522-240101752 // 1230 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: HDAC4 -



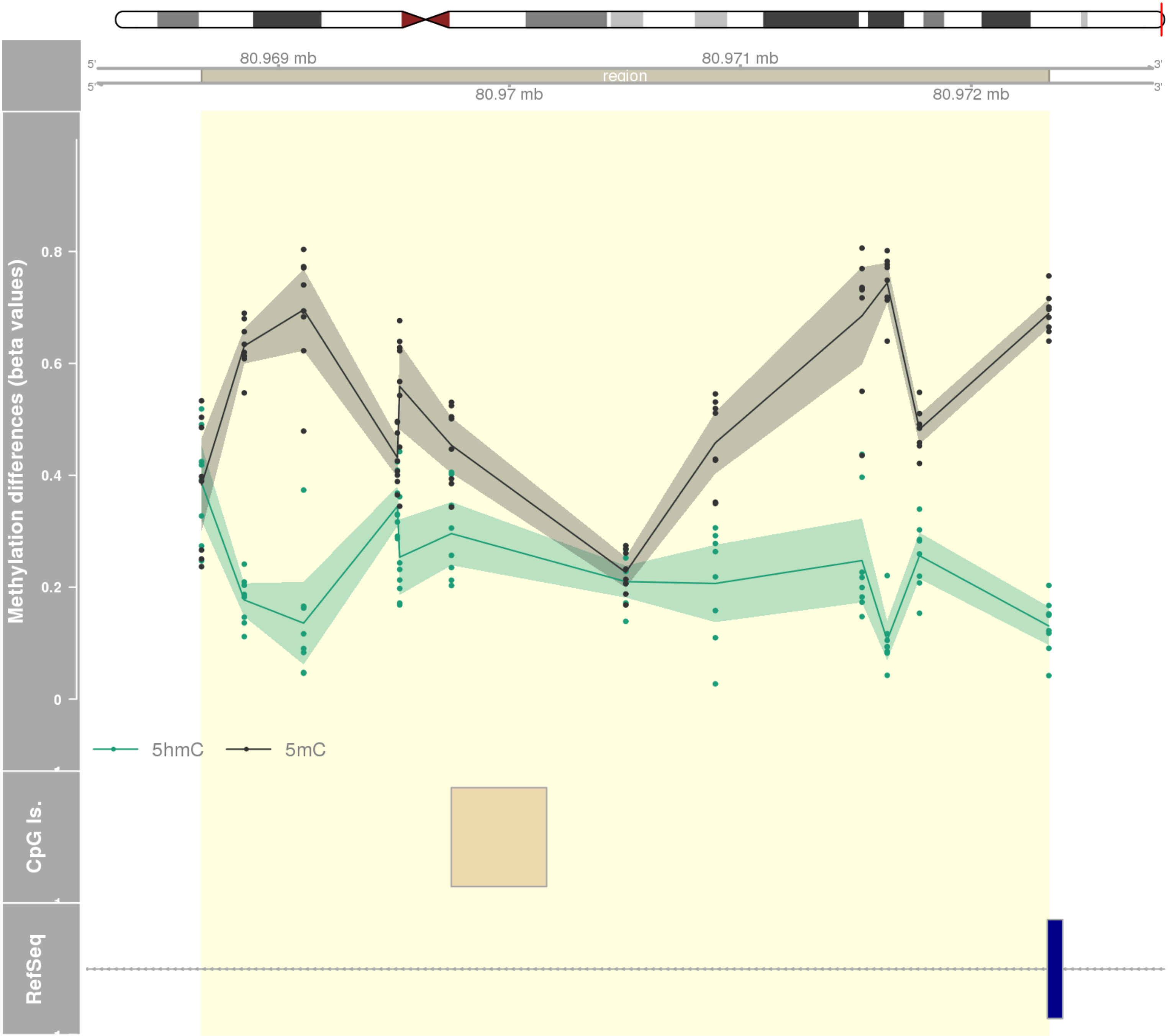
DMR 332 // chr17:79075866-79078315 // 2449 pb. (10 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: BAIAP2 -



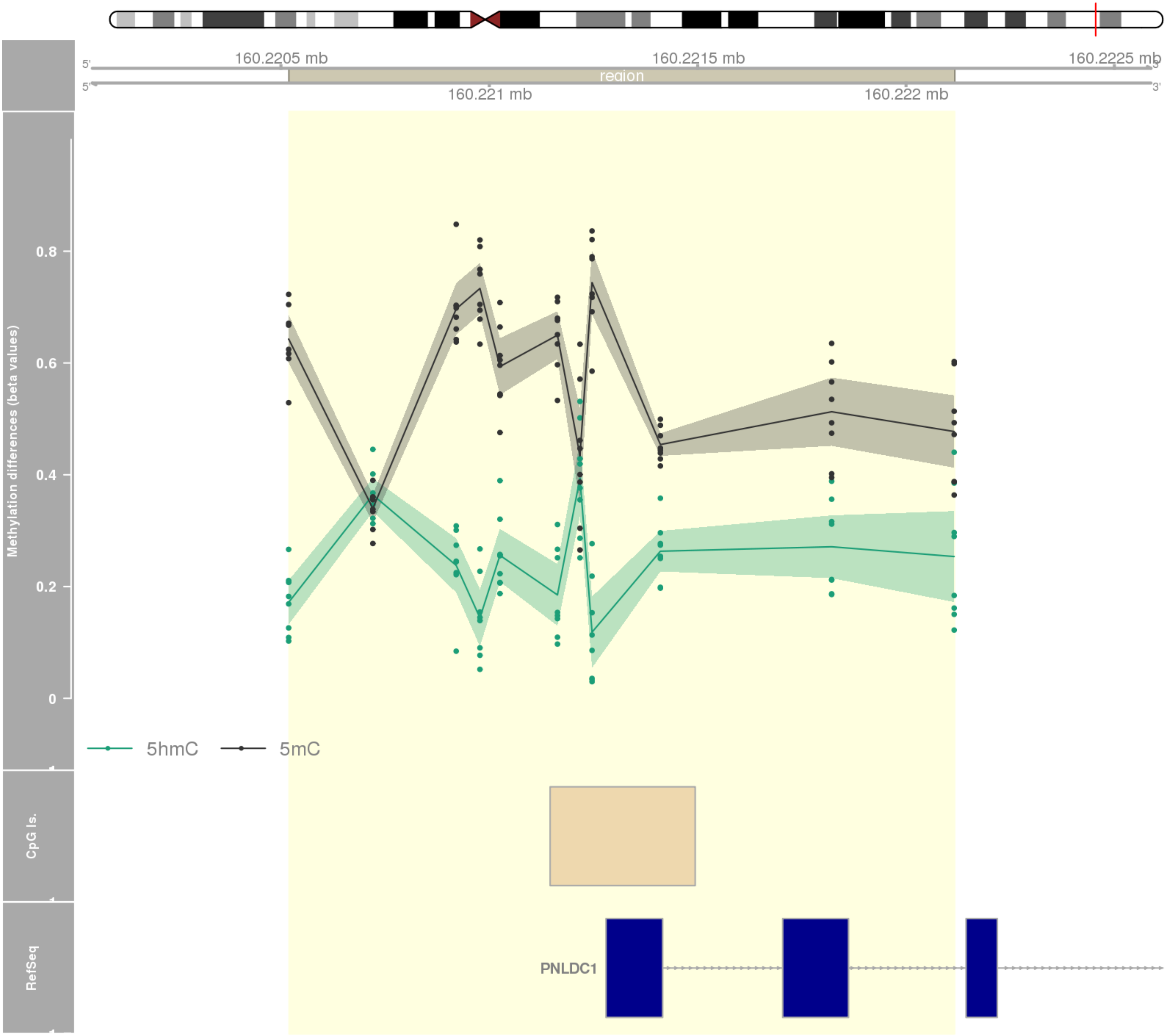
DMR 333 // chr11:2406272-2407699 // 1427 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: CD81 -



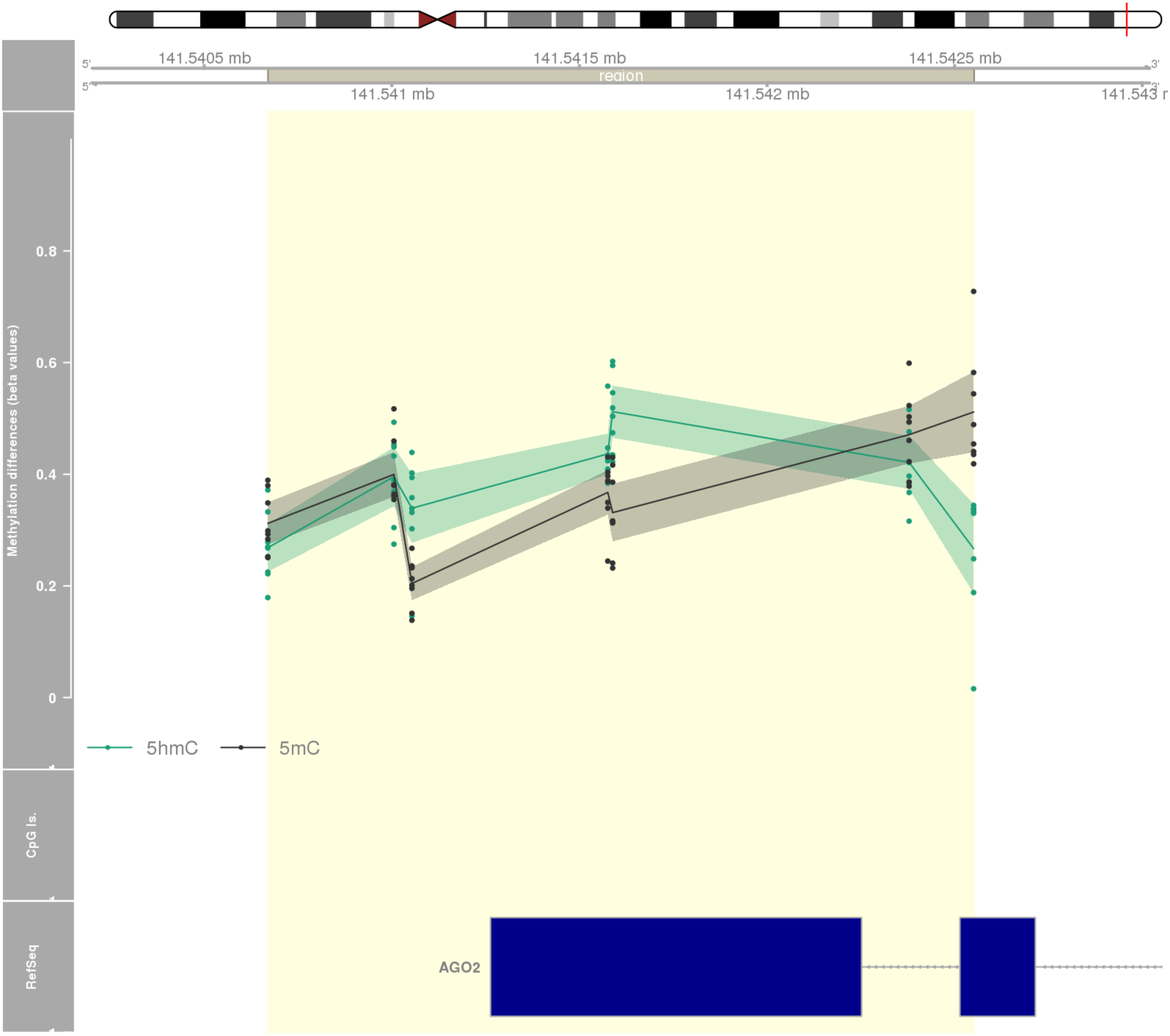
DMR 334 // chr17:80968667-80972336 // 3669 pb. (12 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: B3GNTL1 -



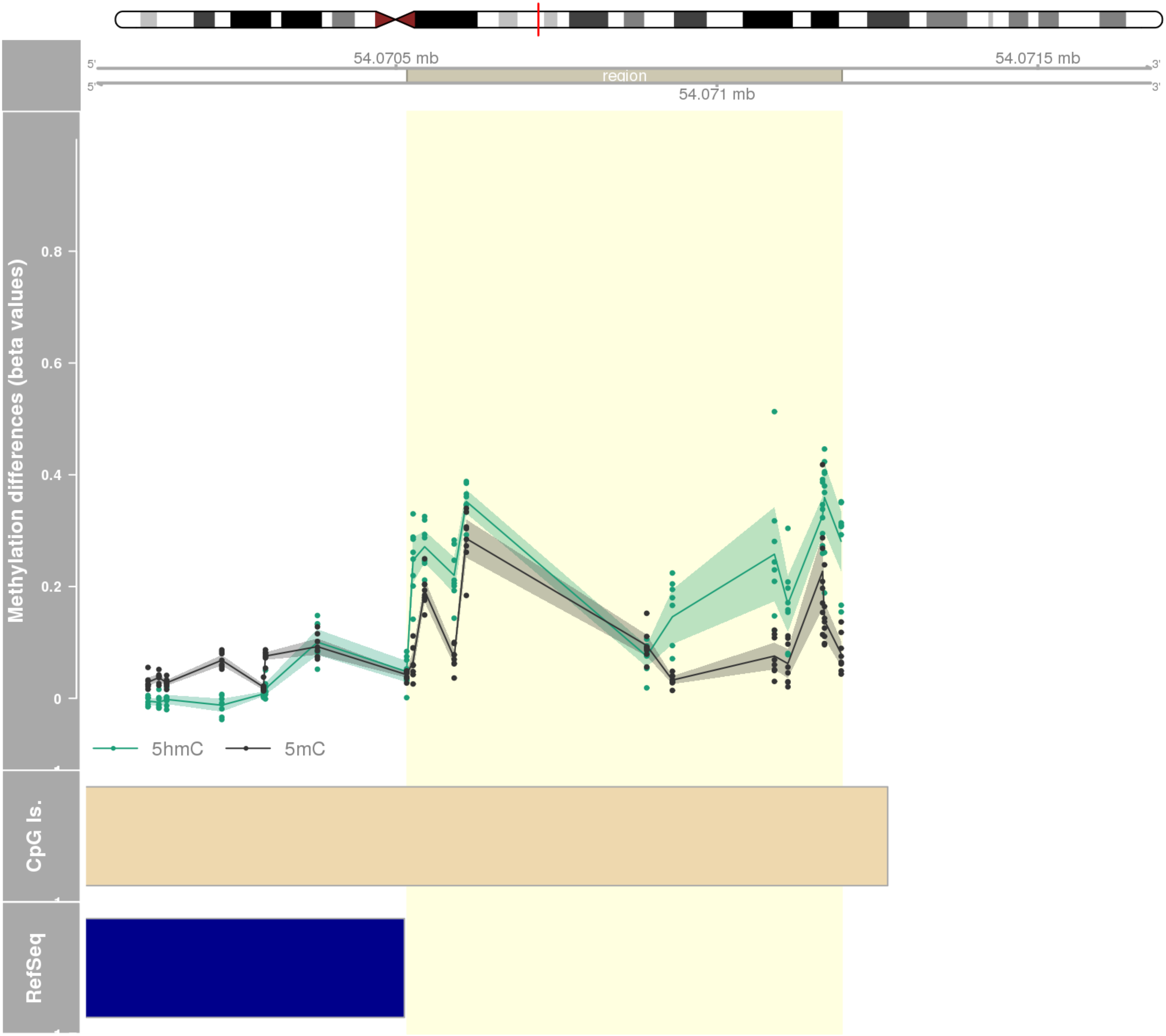
DMR 335 // chr6:160220519-160222116 // 1597 pb. (11 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: PNLDC1 -



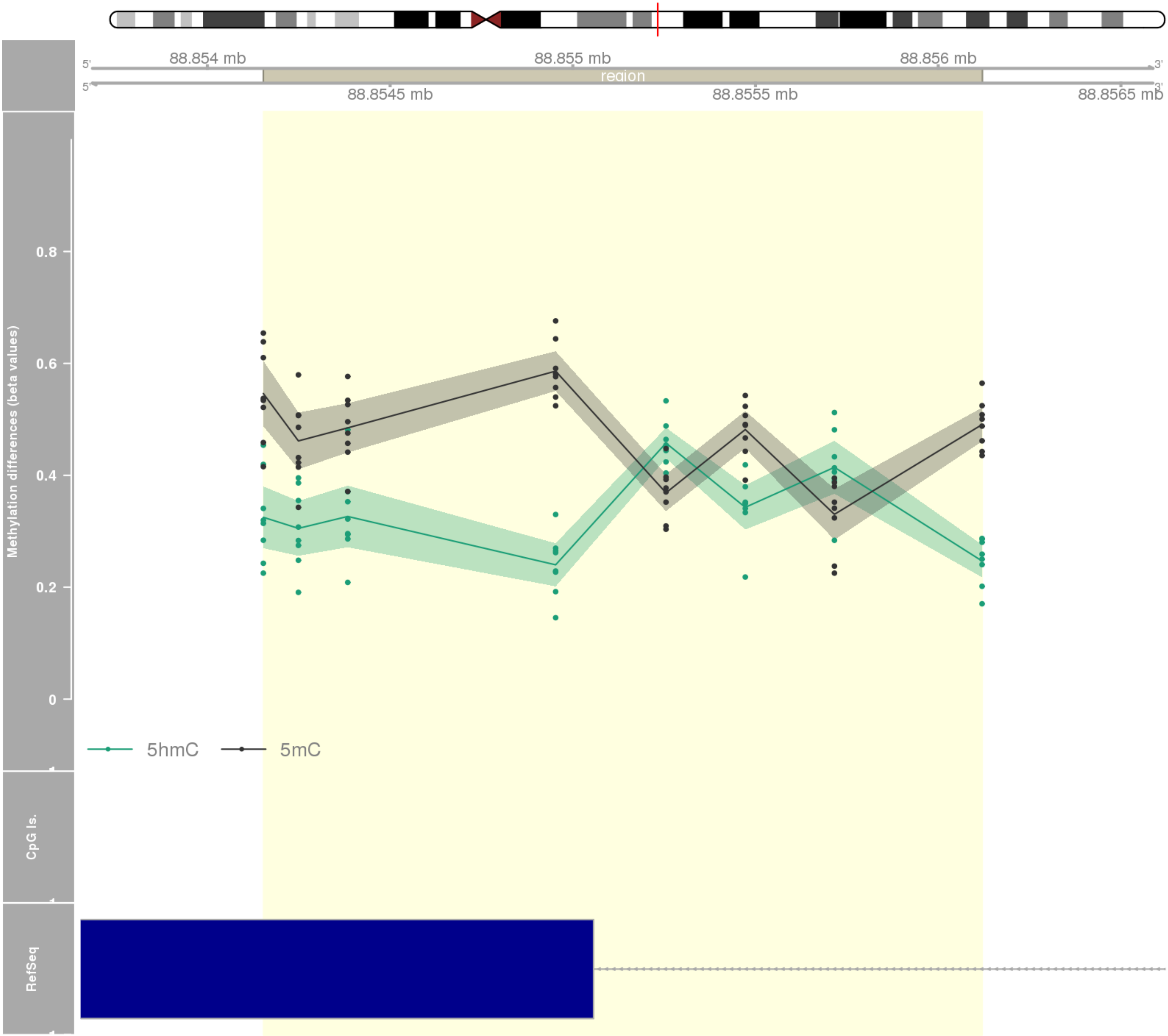
DMR 336 // chr8:141540670-141542551 // 1881 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: AGO2 -



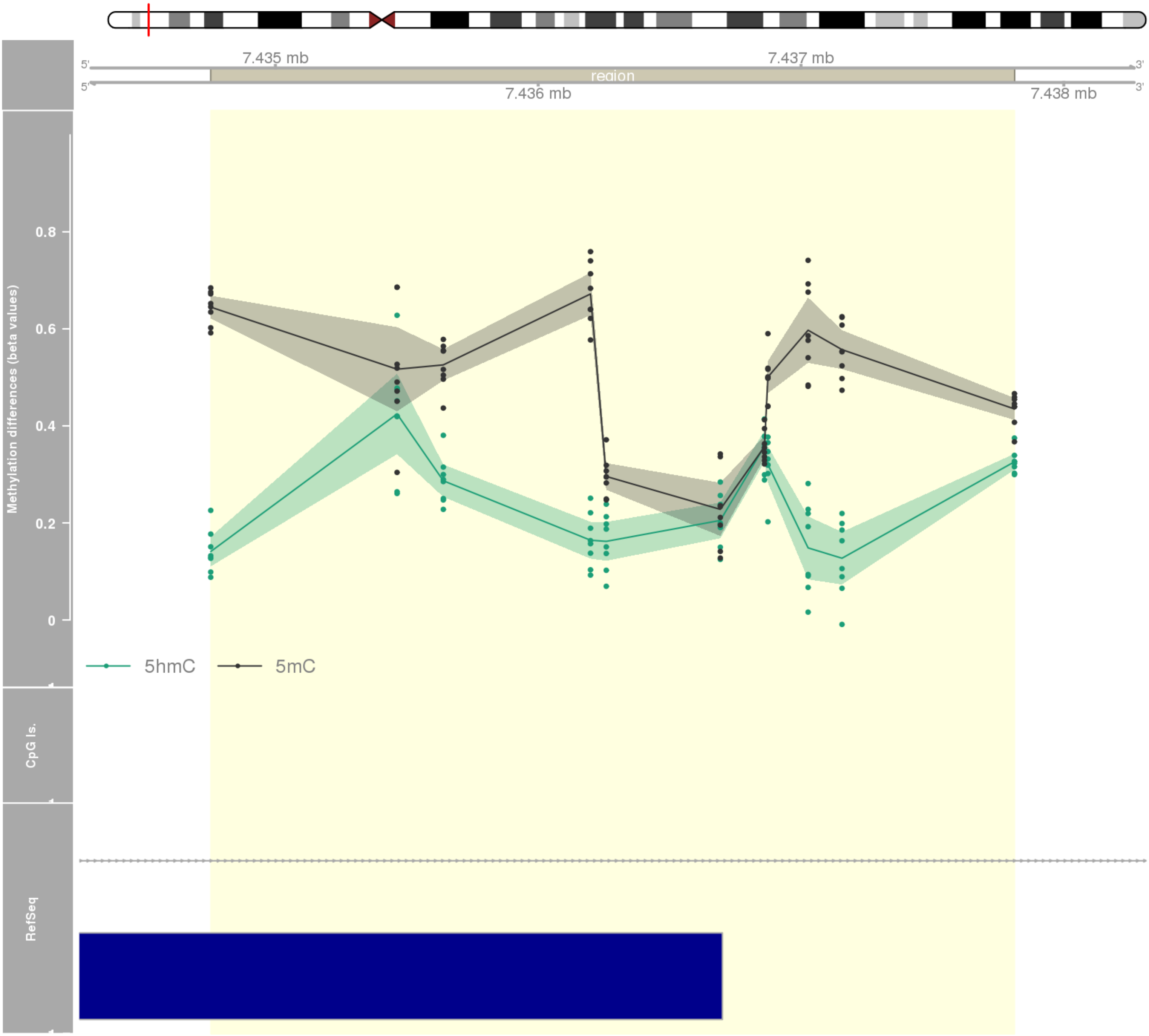
DMR 337 // chr12:54070517-54071194 // 677 pb. (12 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.017 // fwerArea: 0.559
- genes: ATP5G2 -



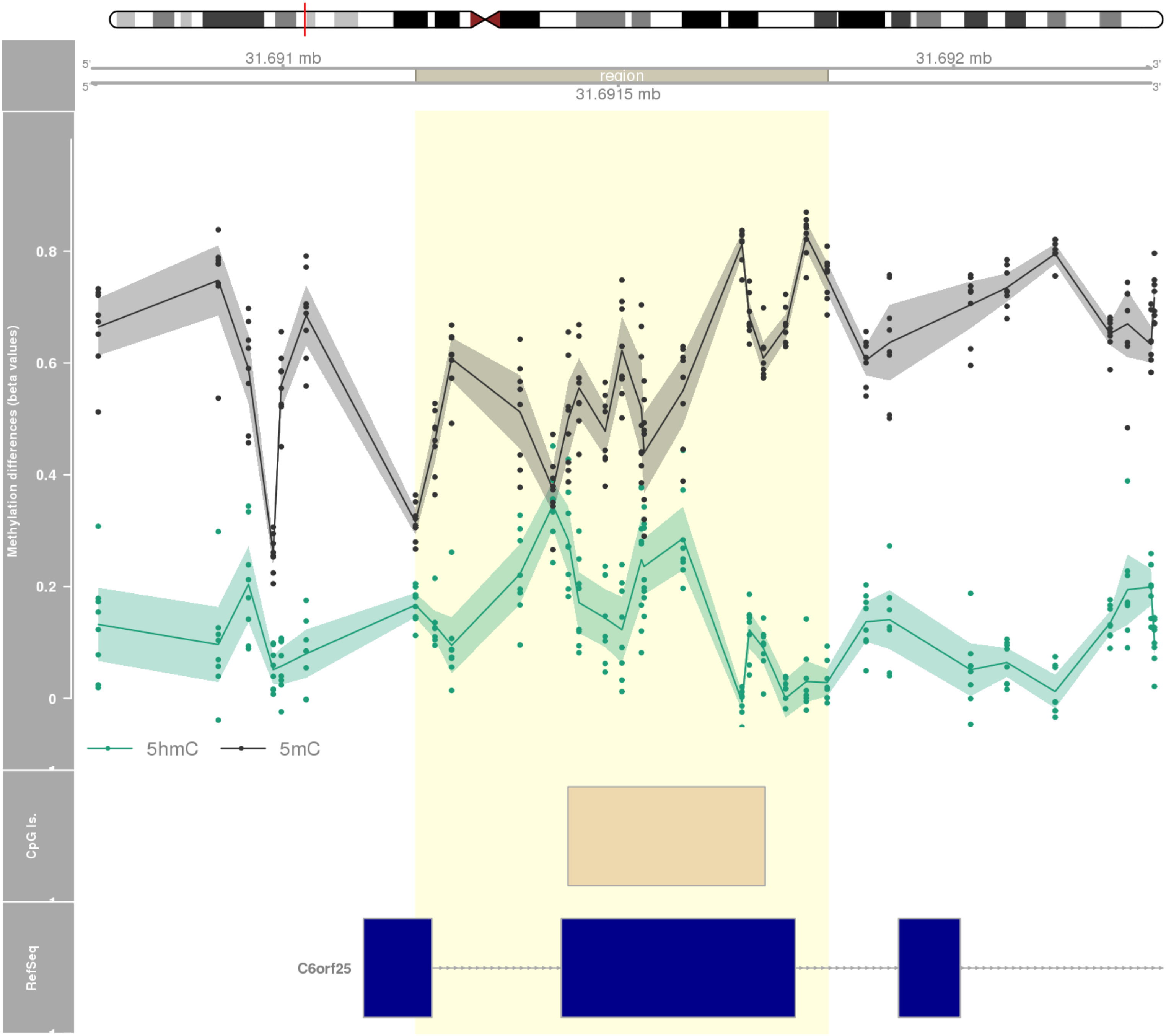
DMR 338 // chr6:88854153-88856120 // 1967 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: CNR1 -



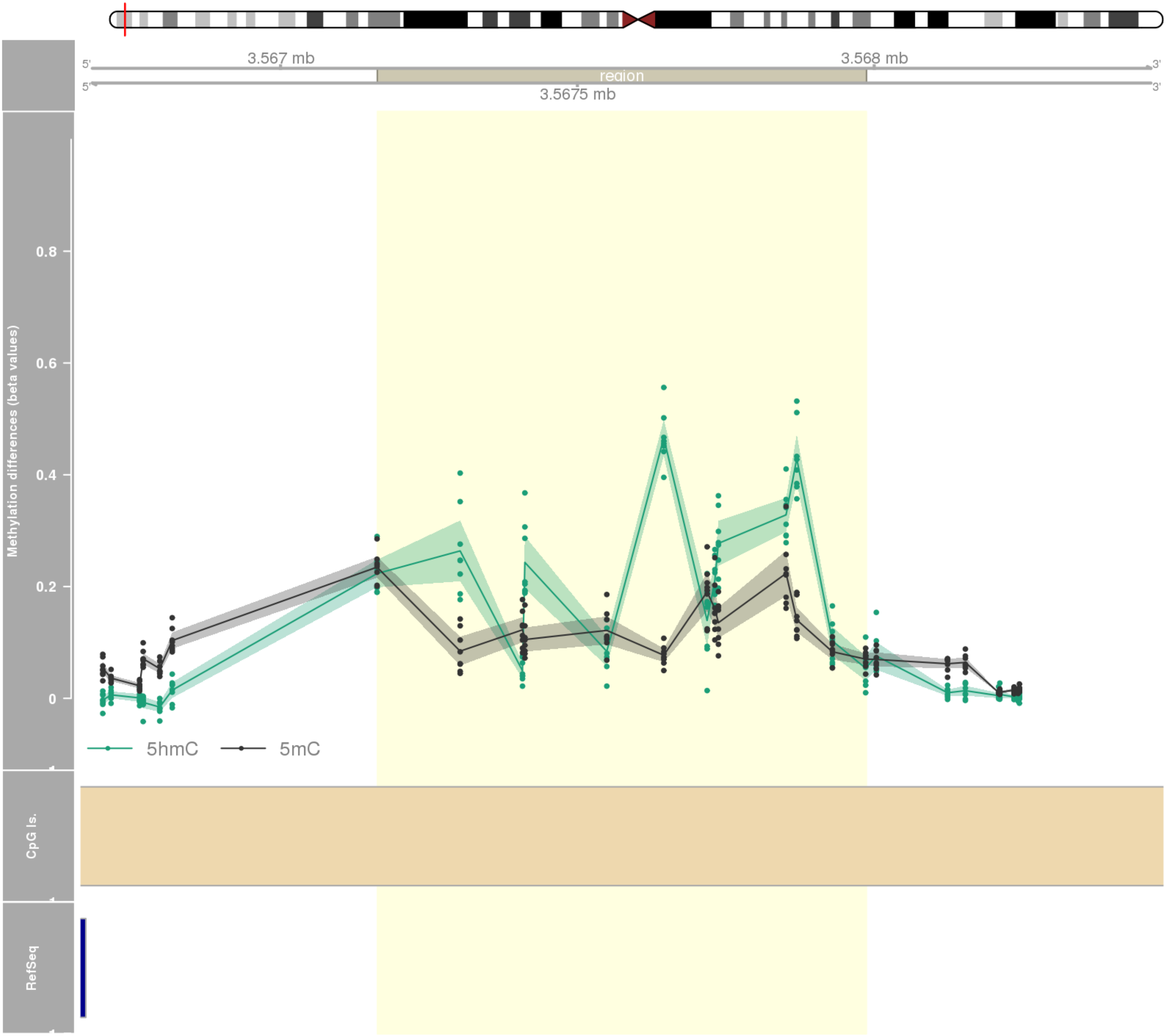
DMR 339 // chr4:7434754-7437812 // 3058 pb. (11 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: SORCS2 / PSAPL1 -



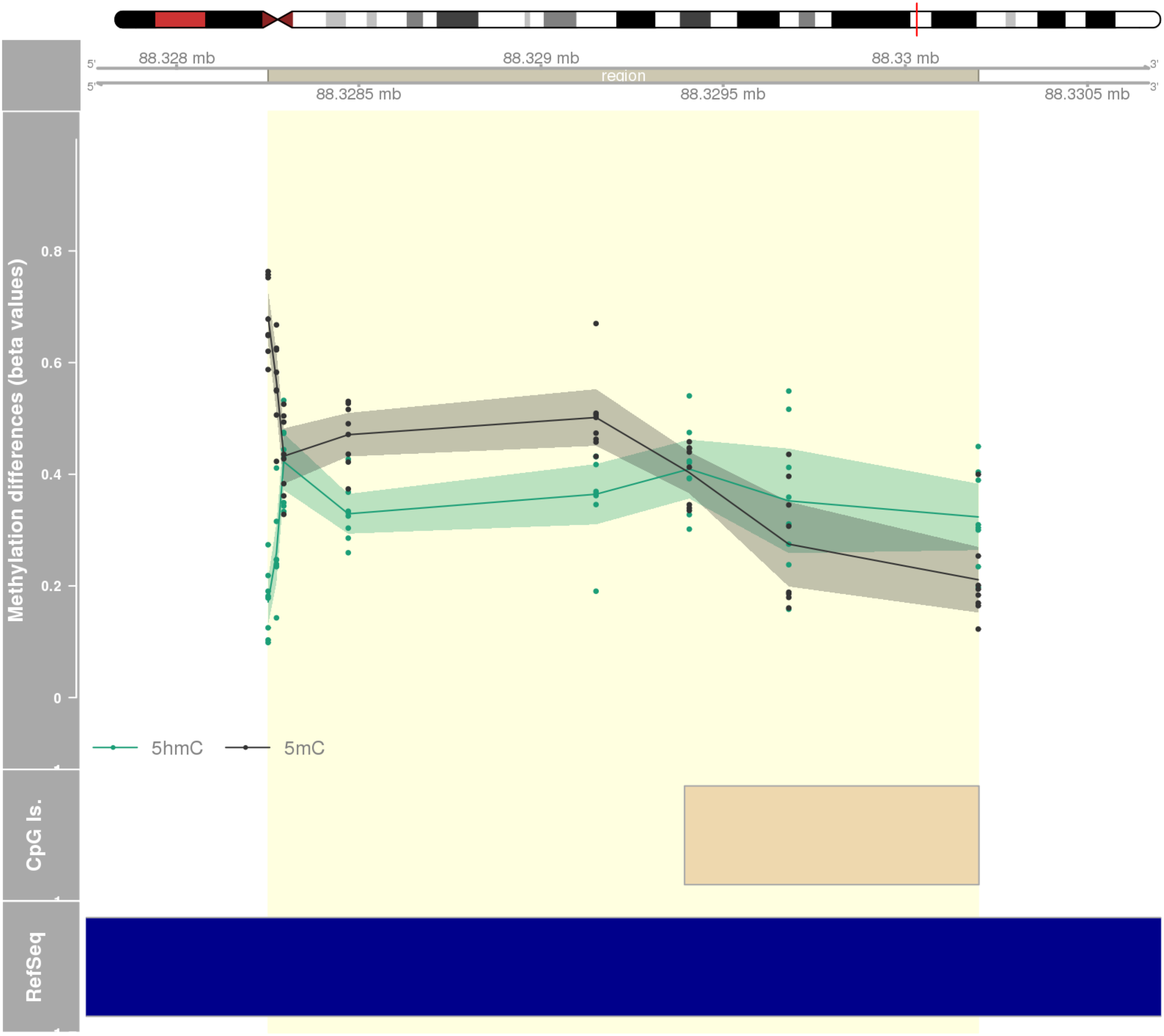
DMR 340 // chr6:31691198-31691812 // 614 pb. (18 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: C6orf25 -



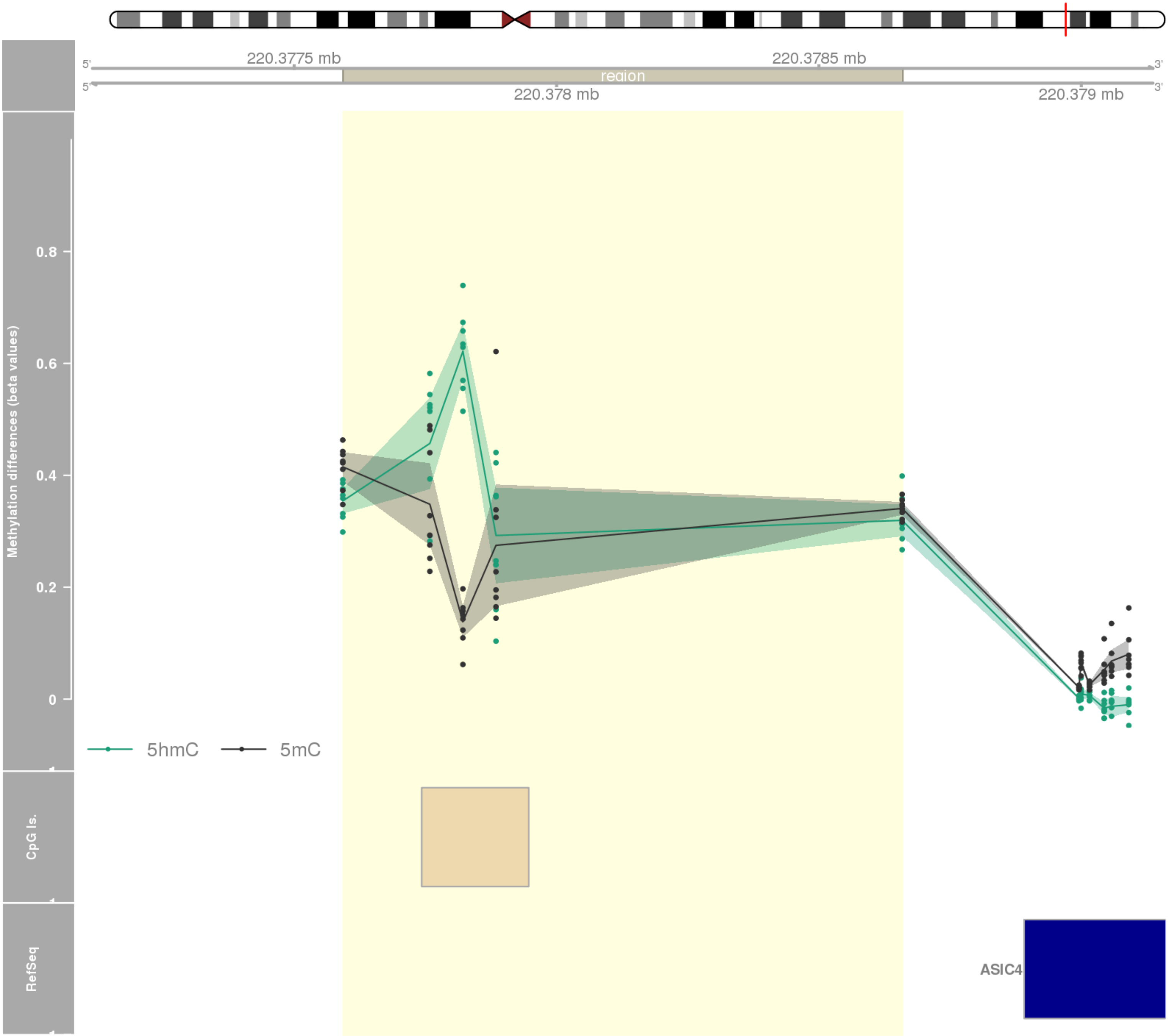
DMR 341 // chr1:3567163-3567986 // 823 pb. (13 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: WRAP73 -



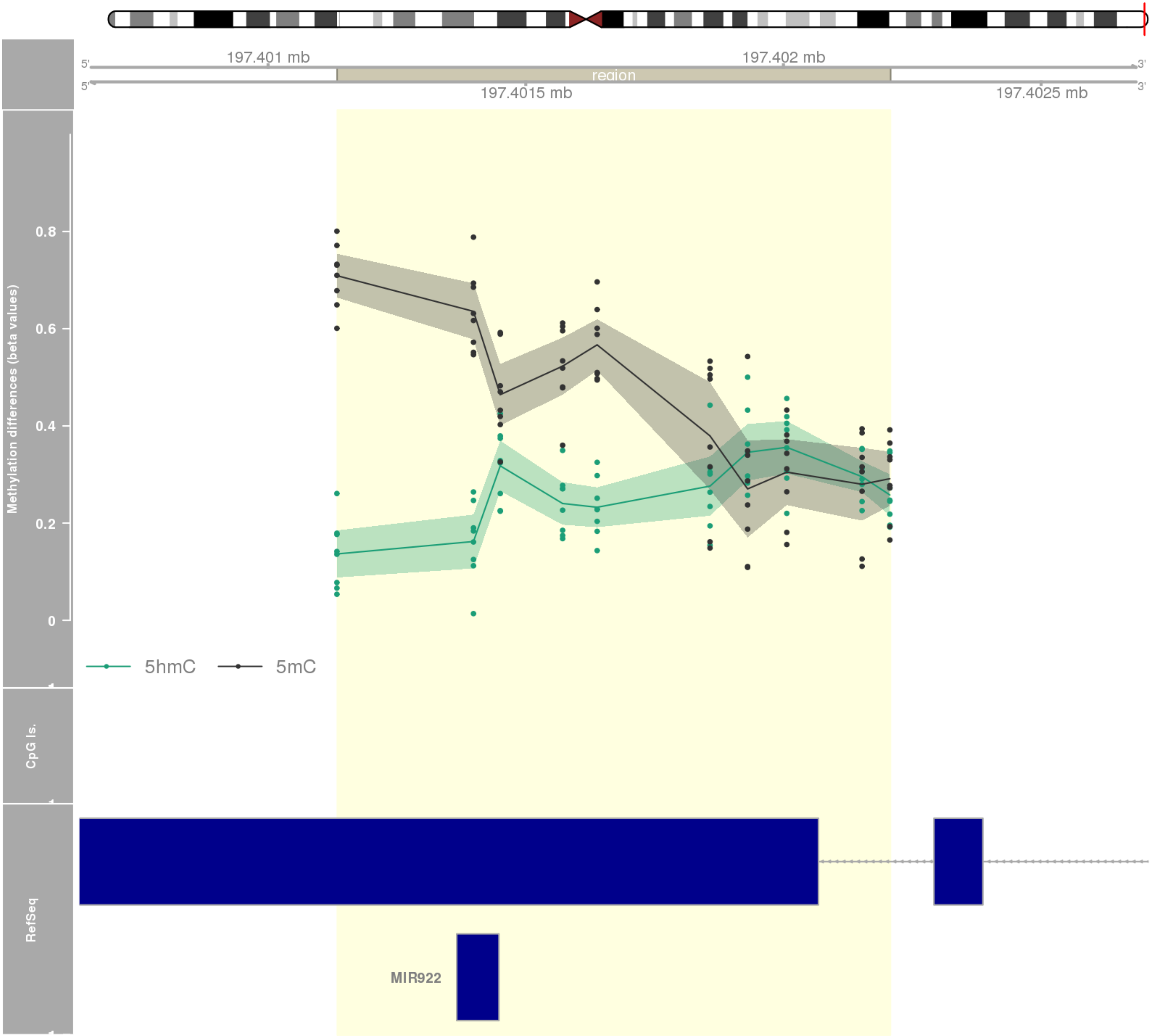
DMR 342 // chr13:88328251-88330200 // 1949 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: SLITRK5 -



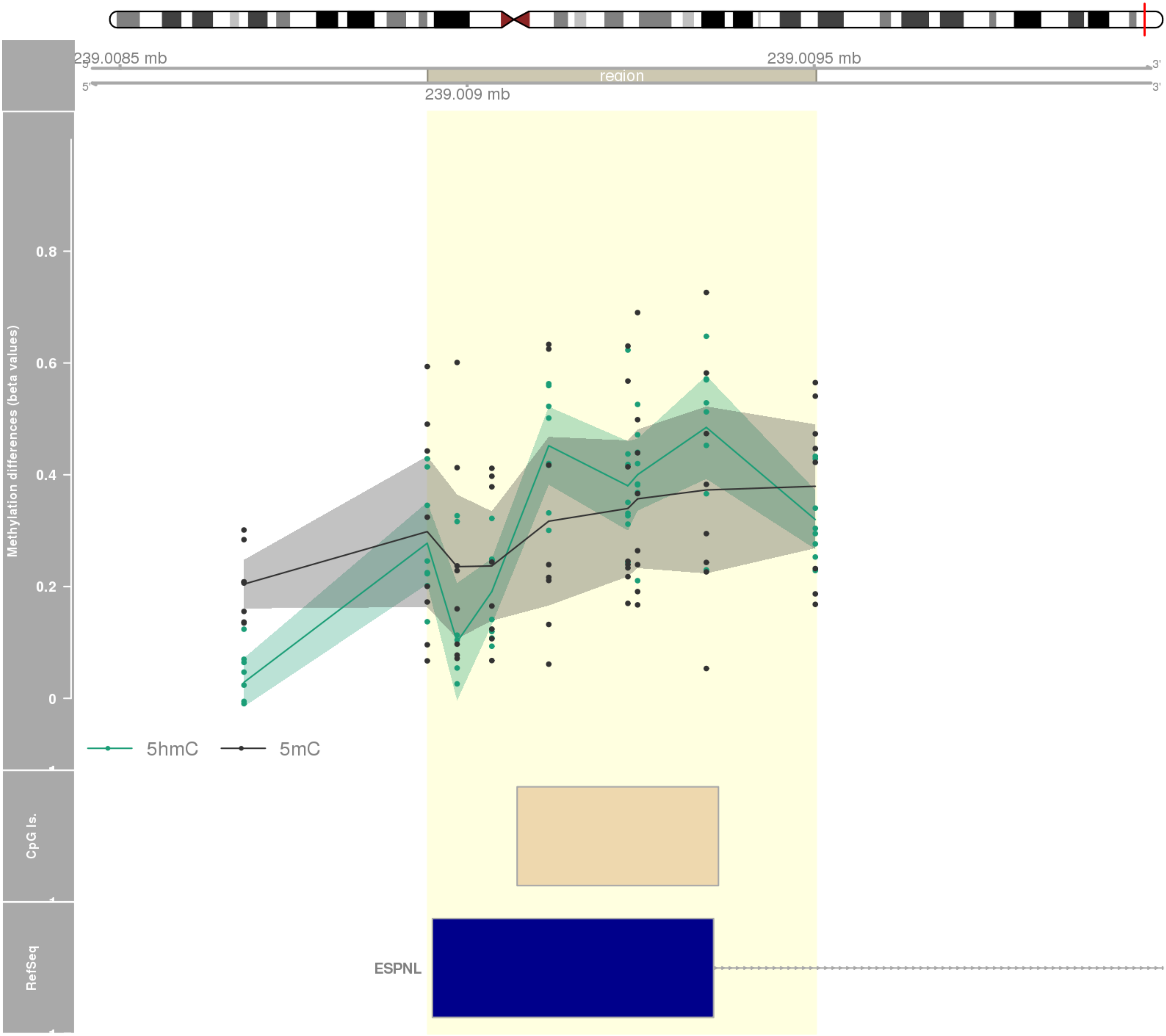
DMR 343 // chr2:220377593-220378659 // 1066 pb. (5 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559



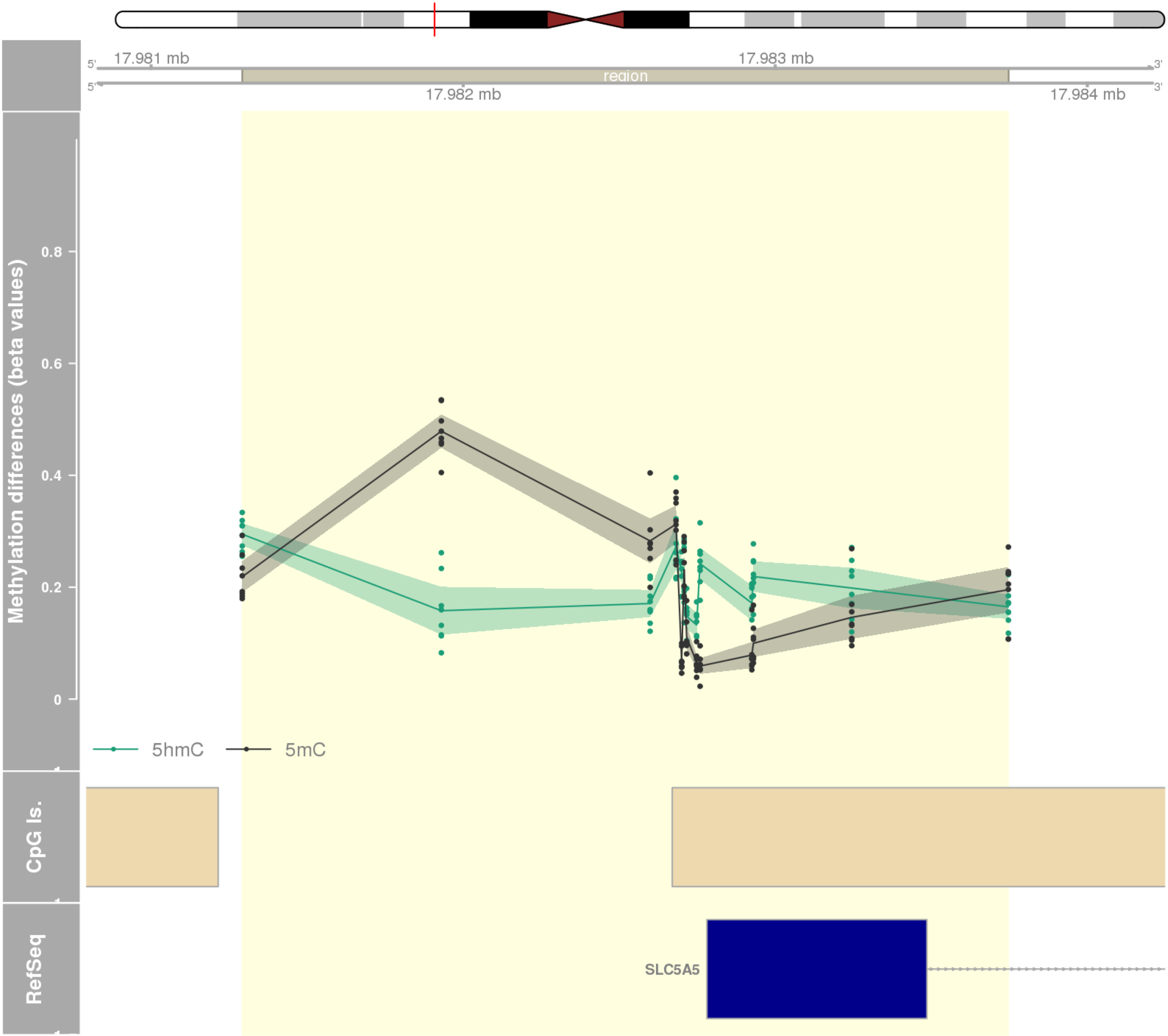
DMR 344 // chr3:197401134-197402207 // 1073 pb. (10 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: MIR922 / KIAA0226 -



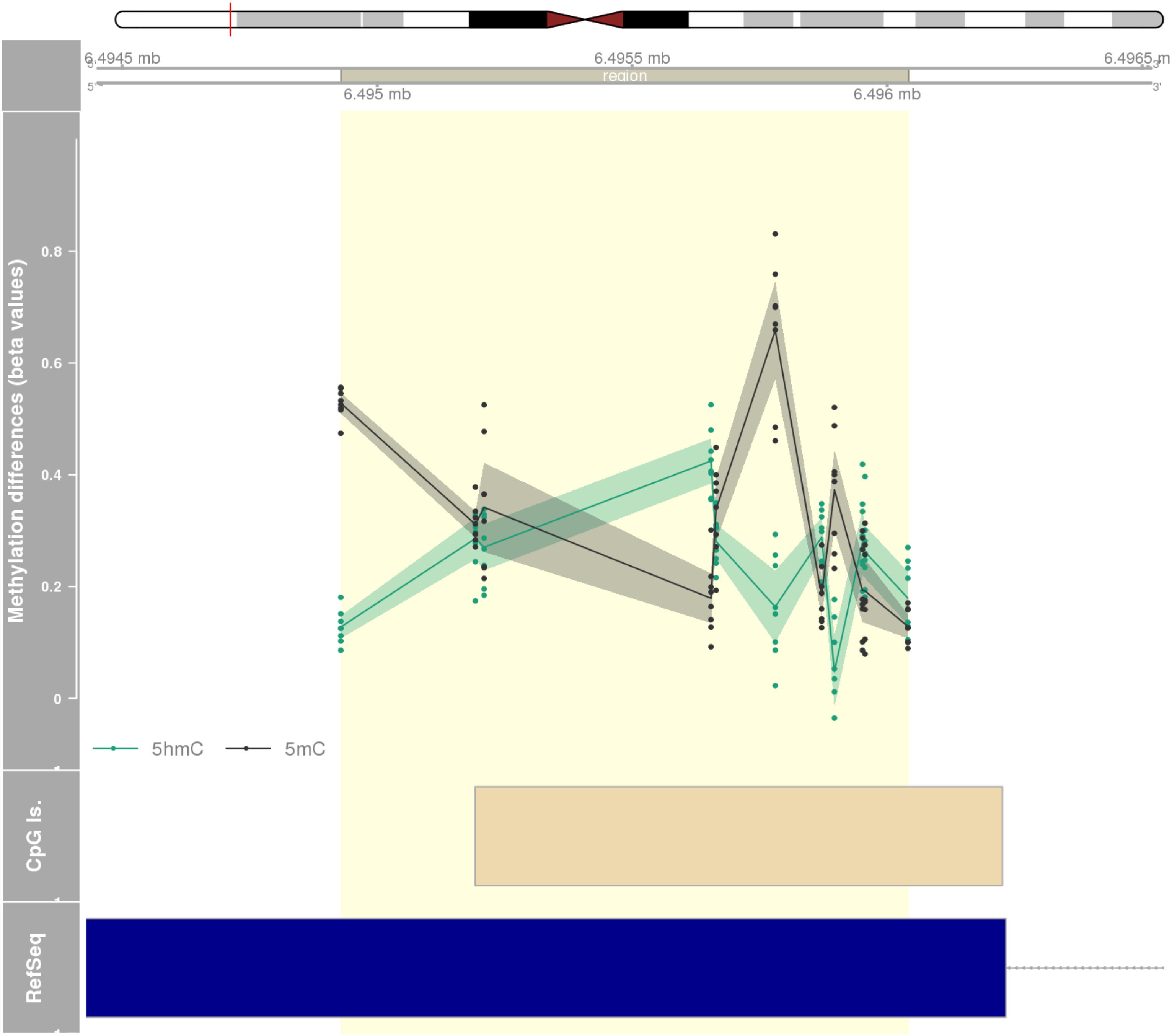
DMR 345 // chr2:239008943-239009502 // 559 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: ESPNL -



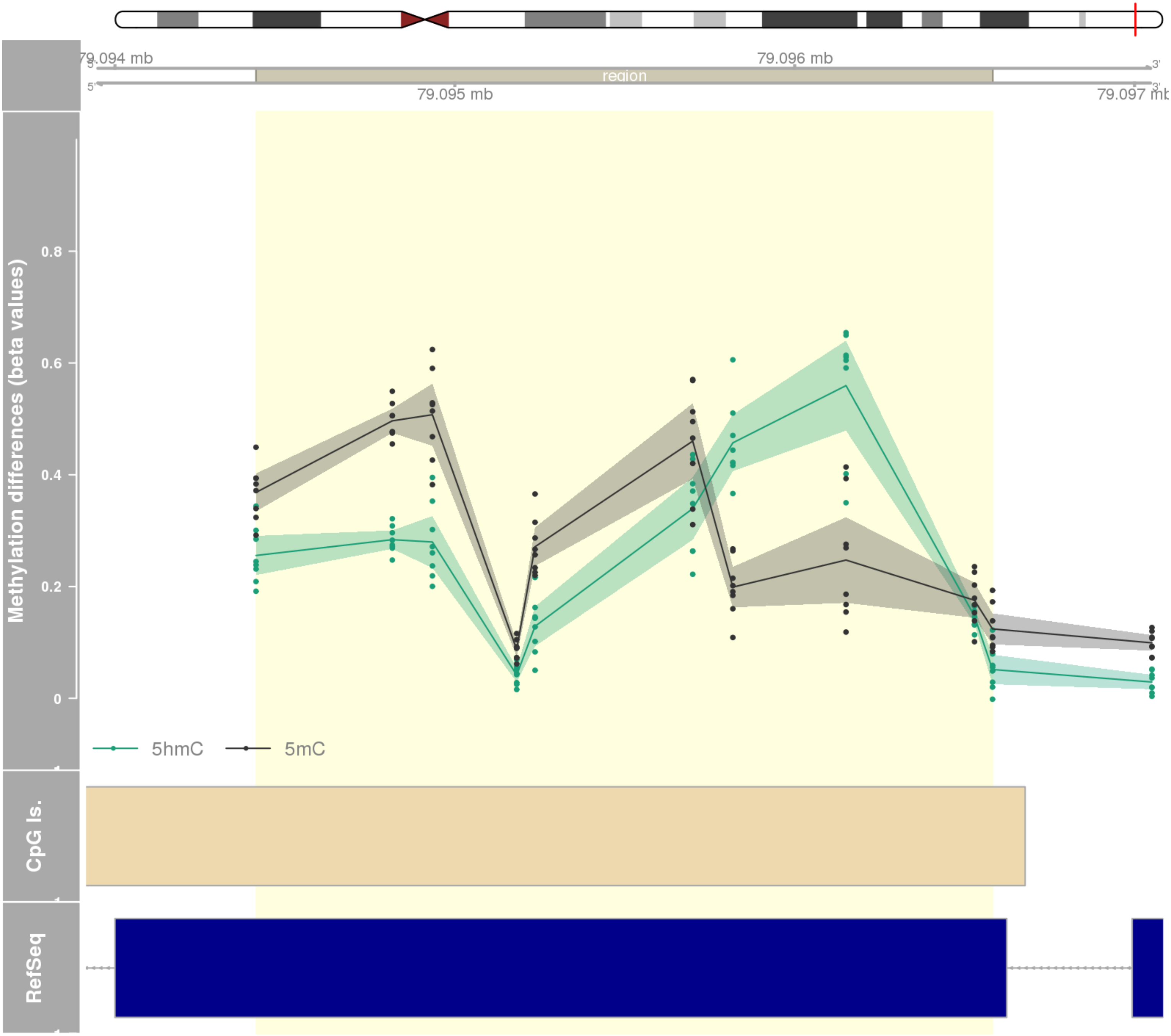
DMR 346 // chr19:17981292-17983747 // 2455 pb. (13 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: SLC5A5 -



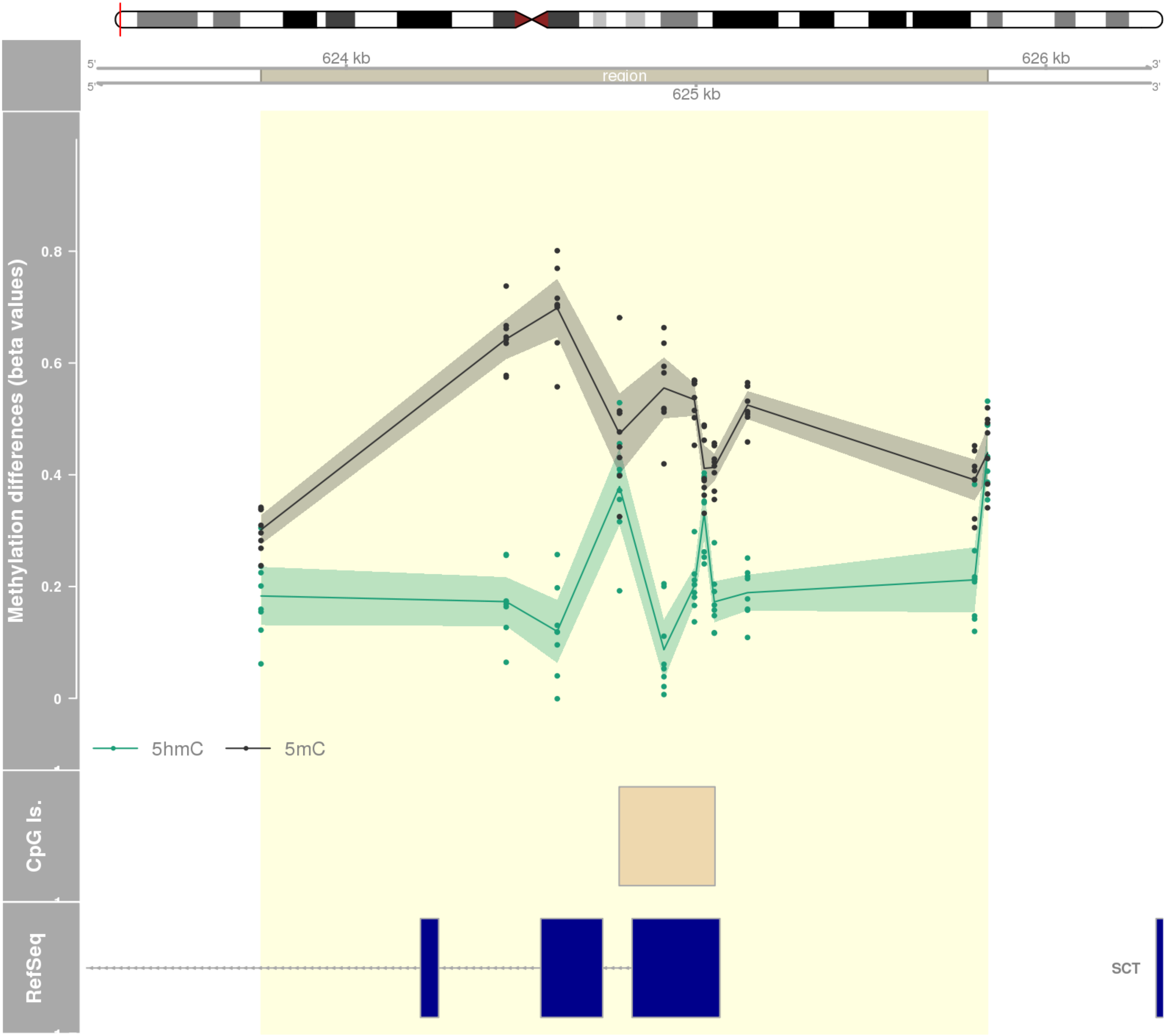
DMR 347 // chr19:6494929-6496041 // 1112 pb. (11 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: TUBB4A -



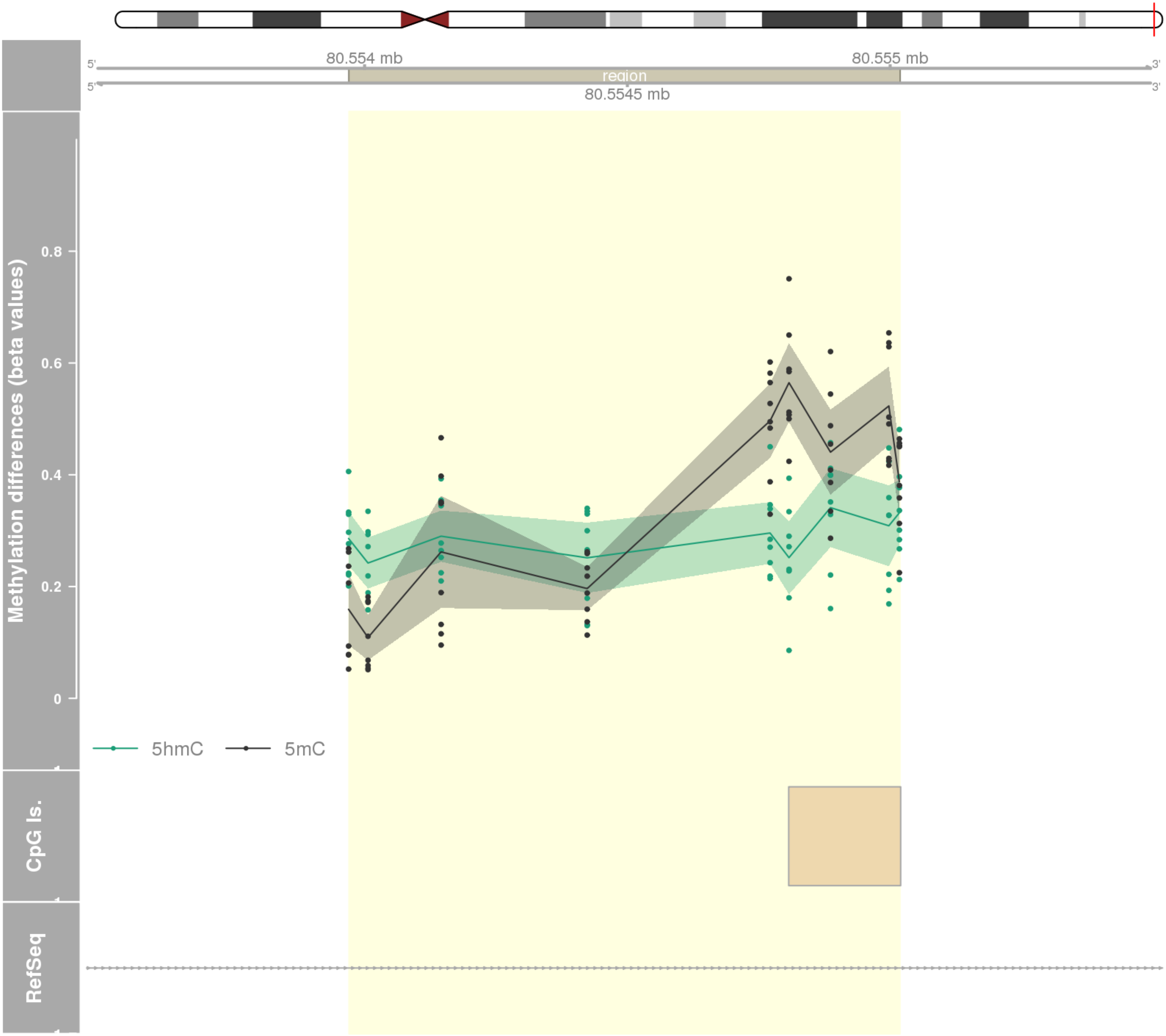
DMR 348 // chr17:79094415-79096582 // 2167 pb. (10 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: AATK -



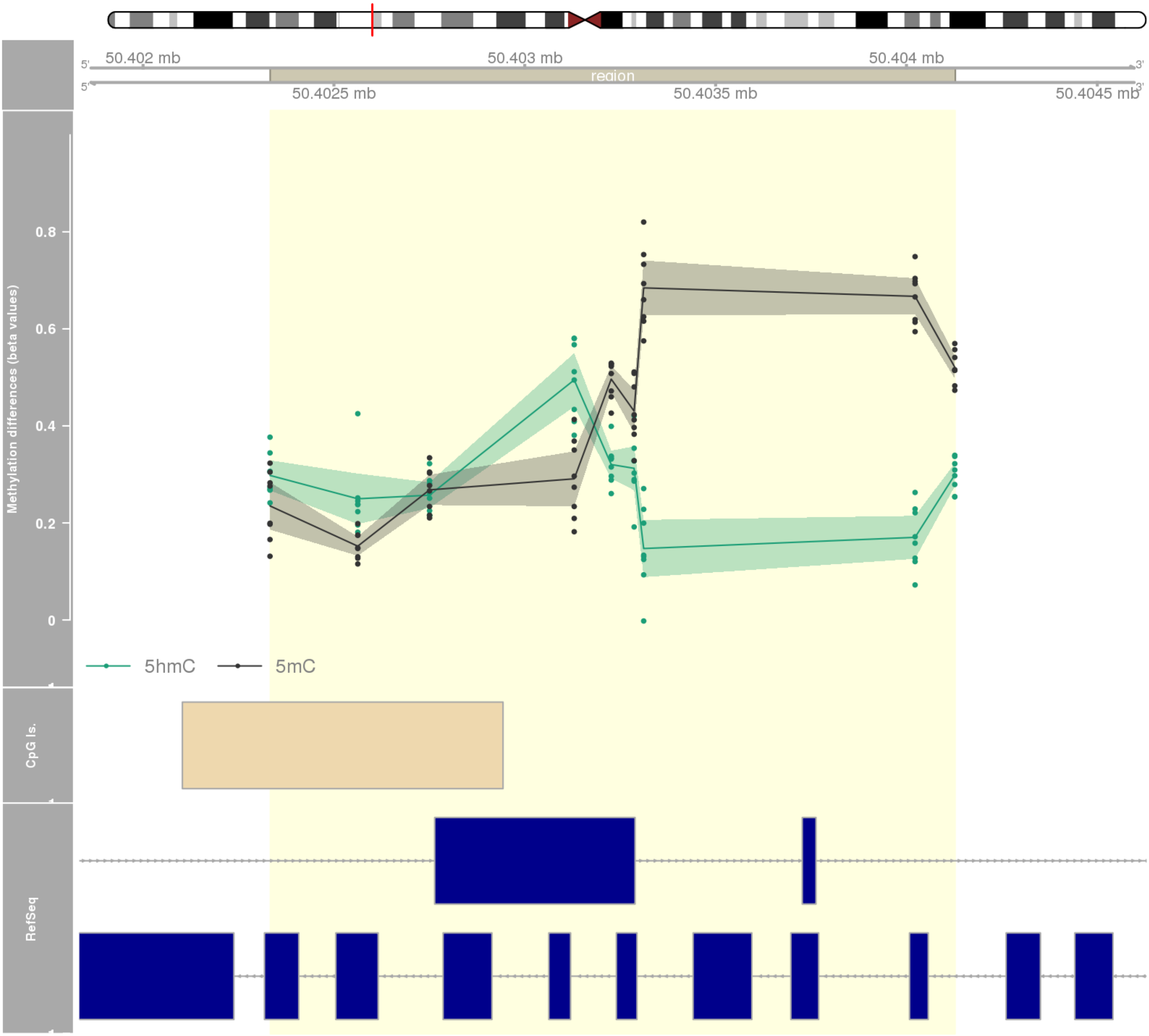
DMR 349 // chr11:623756-625833 // 2077 pb. (11 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: CDHR5 -



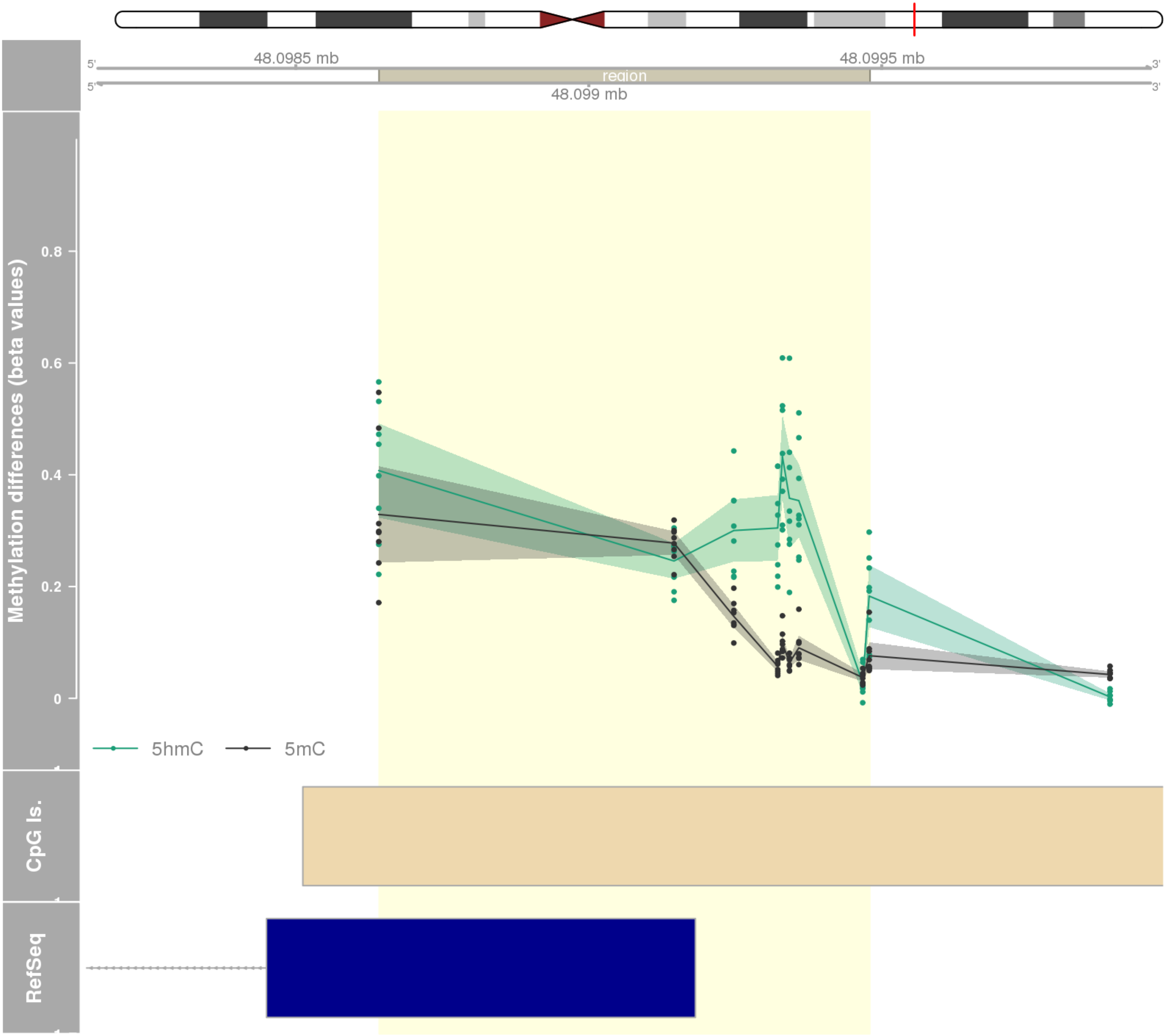
DMR 350 // chr17:80553970-80555018 // 1048 pb. (9 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: FOXK2 -



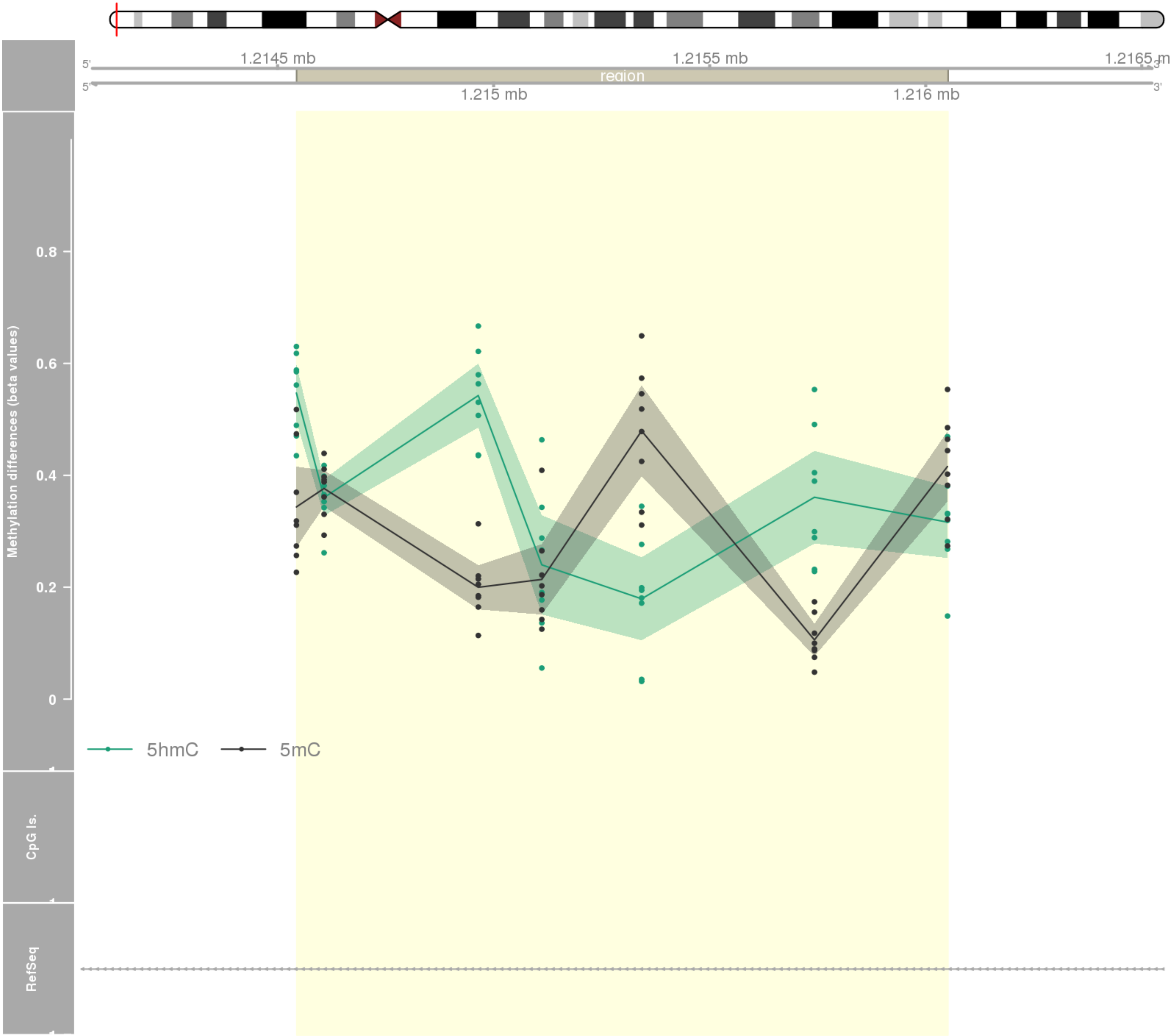
DMR 351 // chr3:50402333-50404127 // 1794 pb. (9 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: CACNA2D2 -



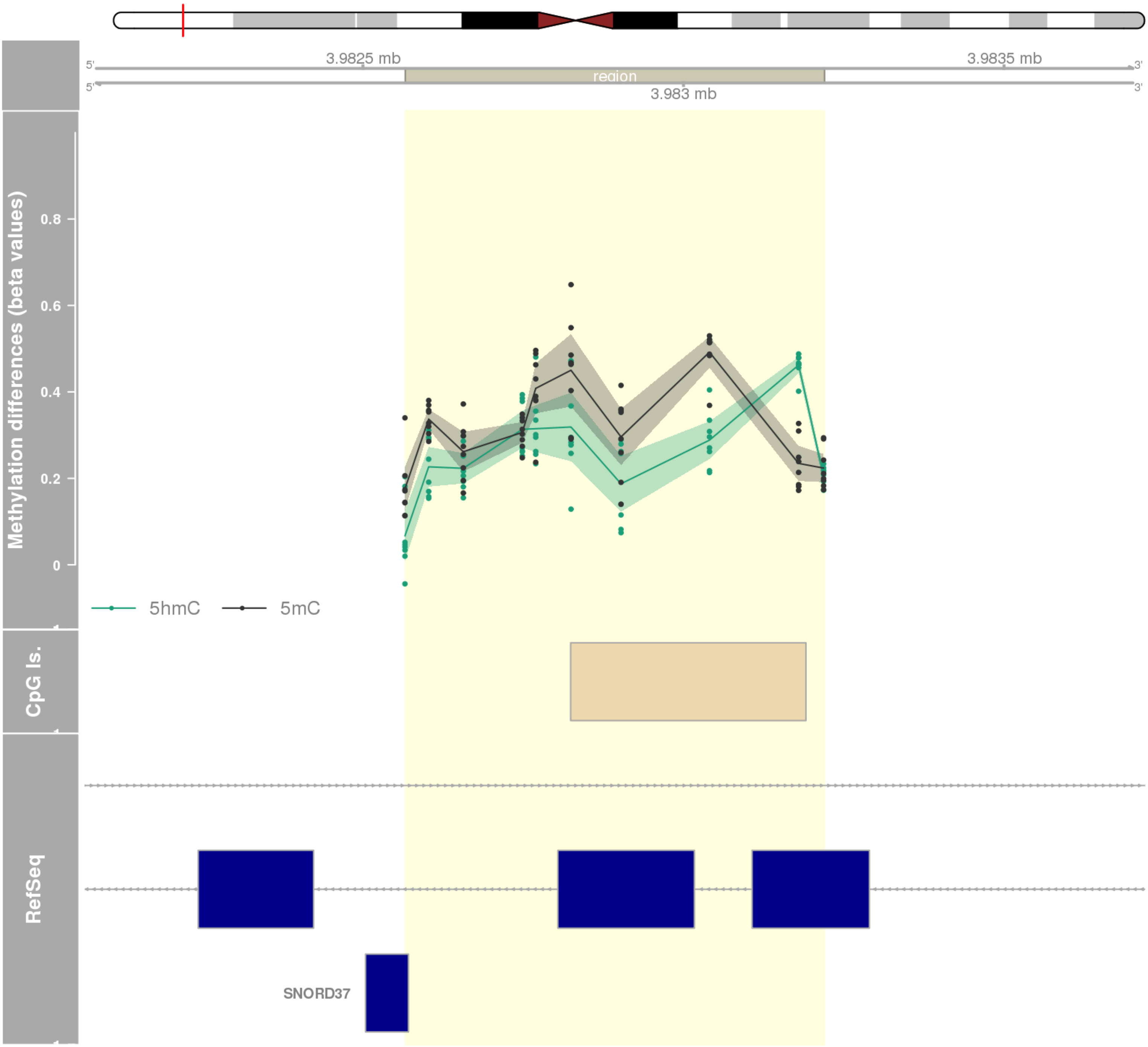
DMR 352 // chr20:48098642-48099479 // 837 pb. (9 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: KCNB1 -



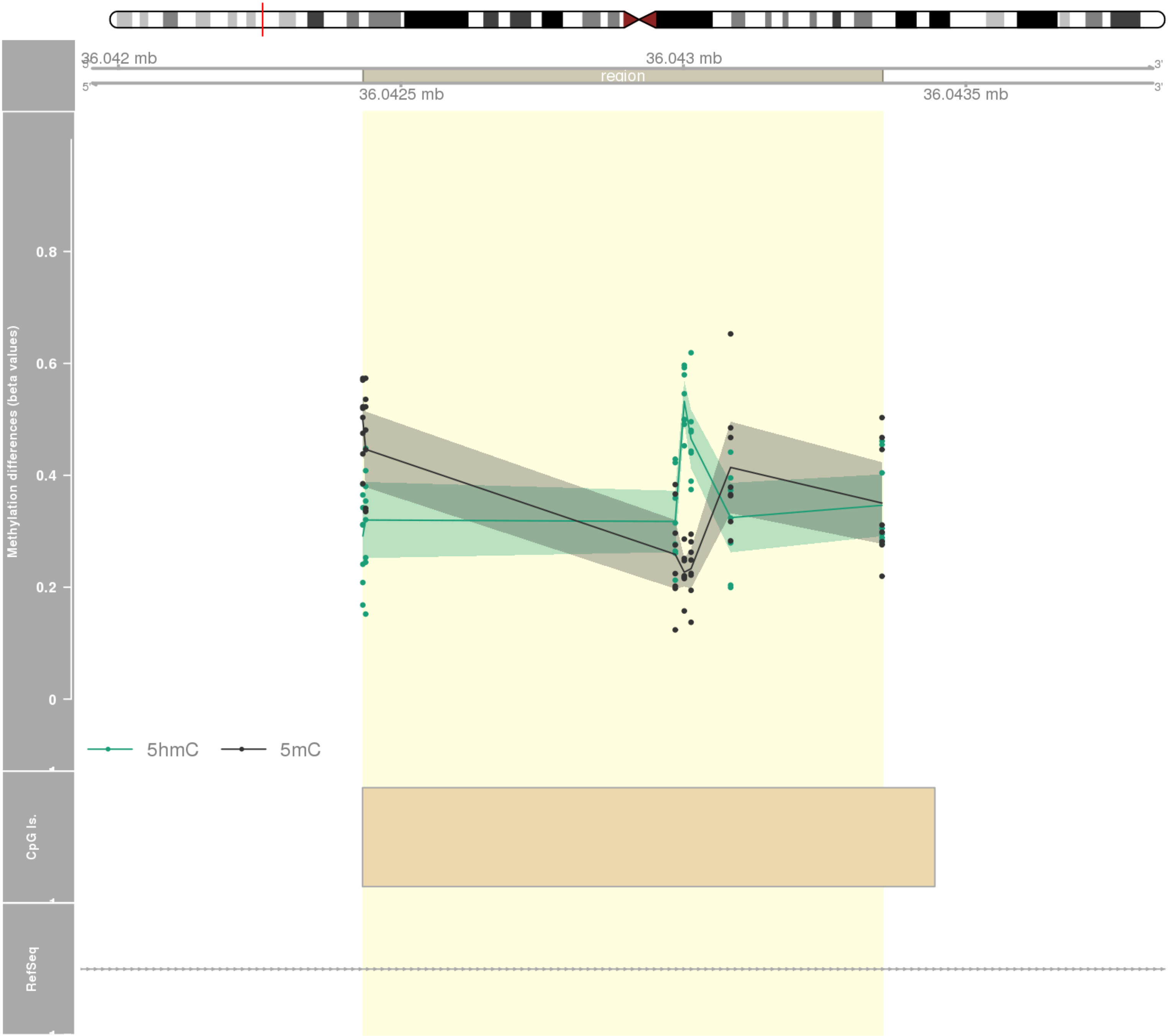
DMR 353 // chr4:1214544-1216051 // 1507 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: CTBP1 -



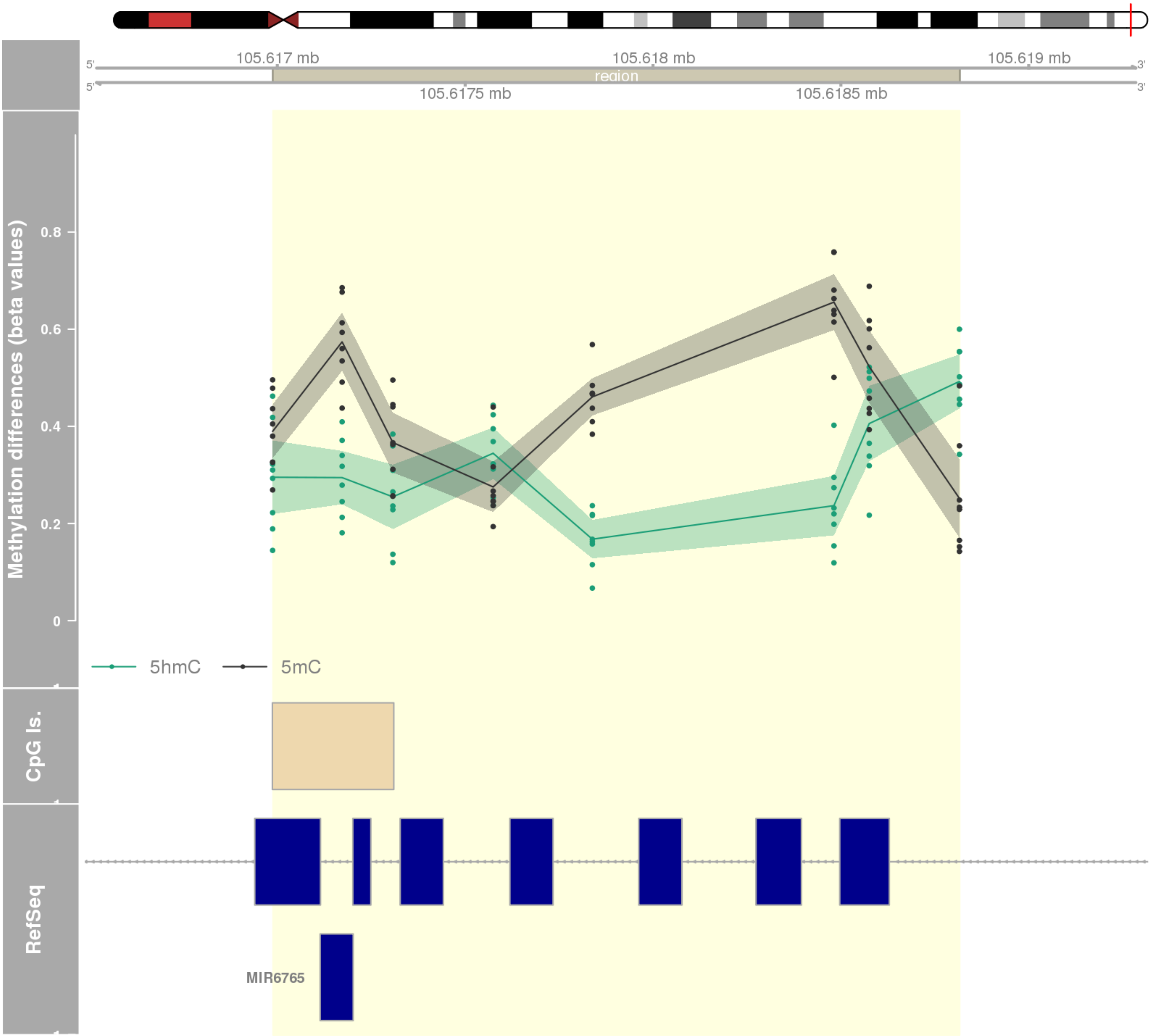
DMR 354 // chr19:3982566-3983219 // 653 pb. (10 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: SNORD37 / EEF2 -



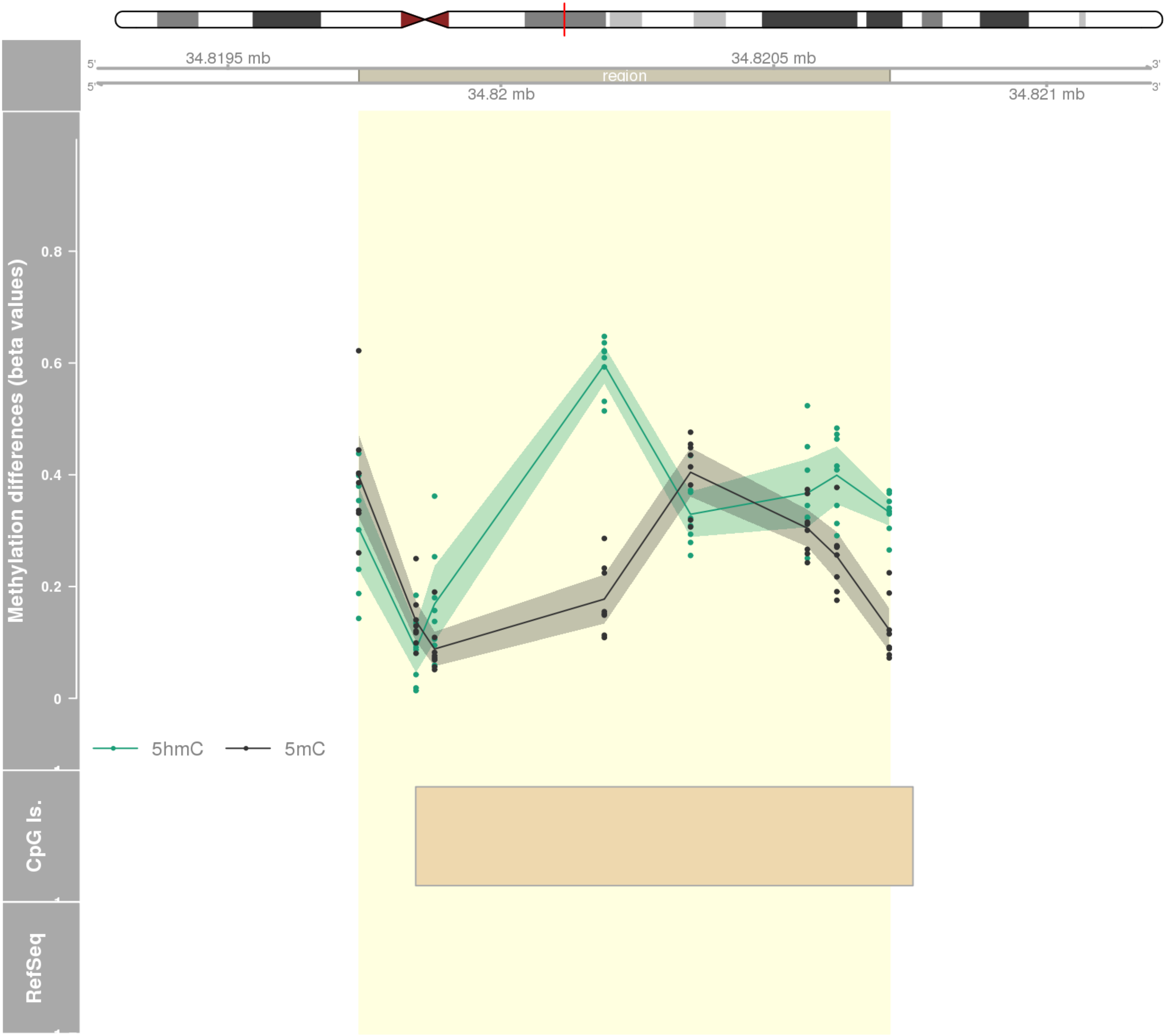
DMR 355 // chr1:36042433-36043352 // 919 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: TFAP2E -



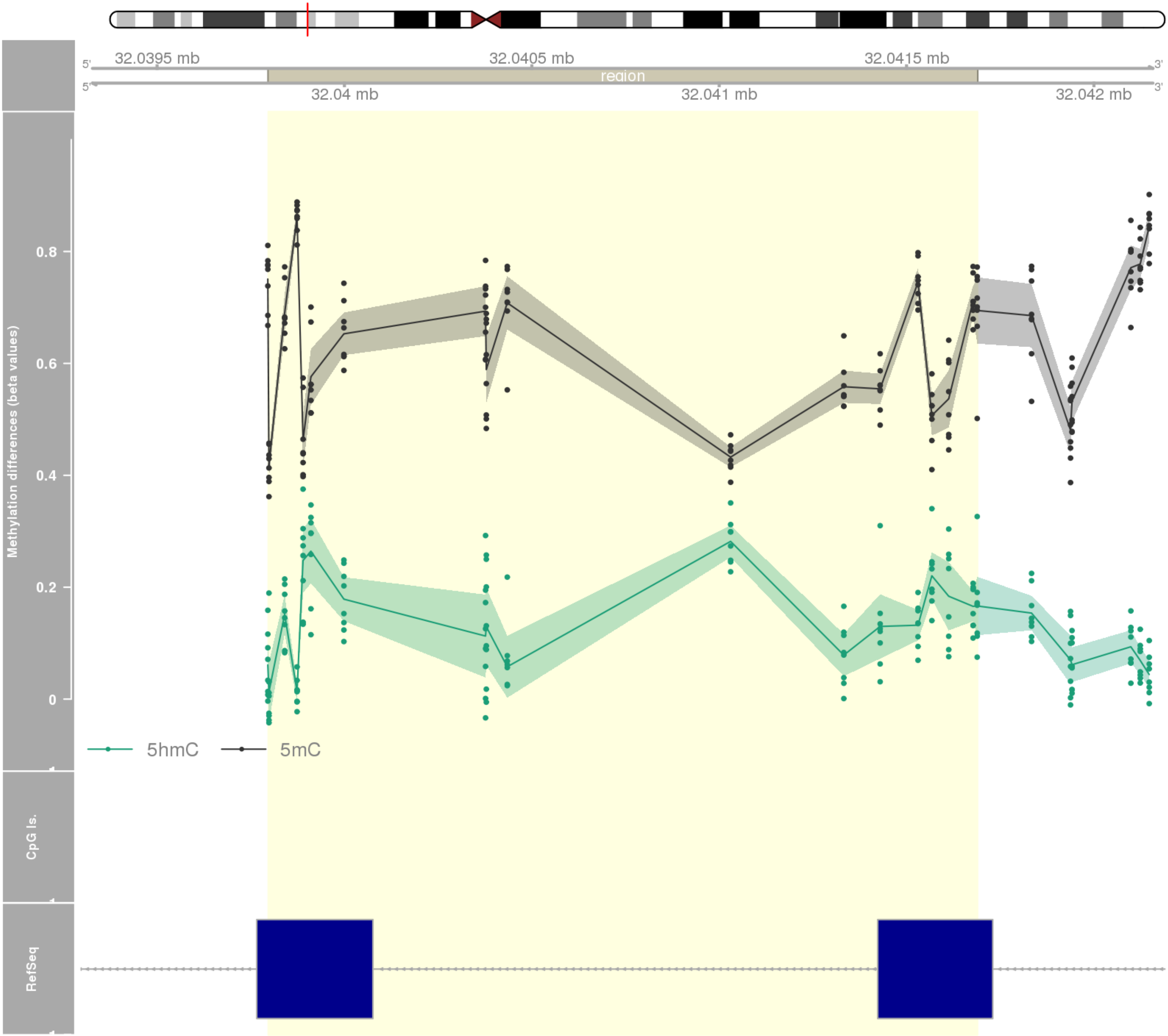
DMR 356 // chr14:105616988-105618816 // 1828 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559
- genes: JAG2 -



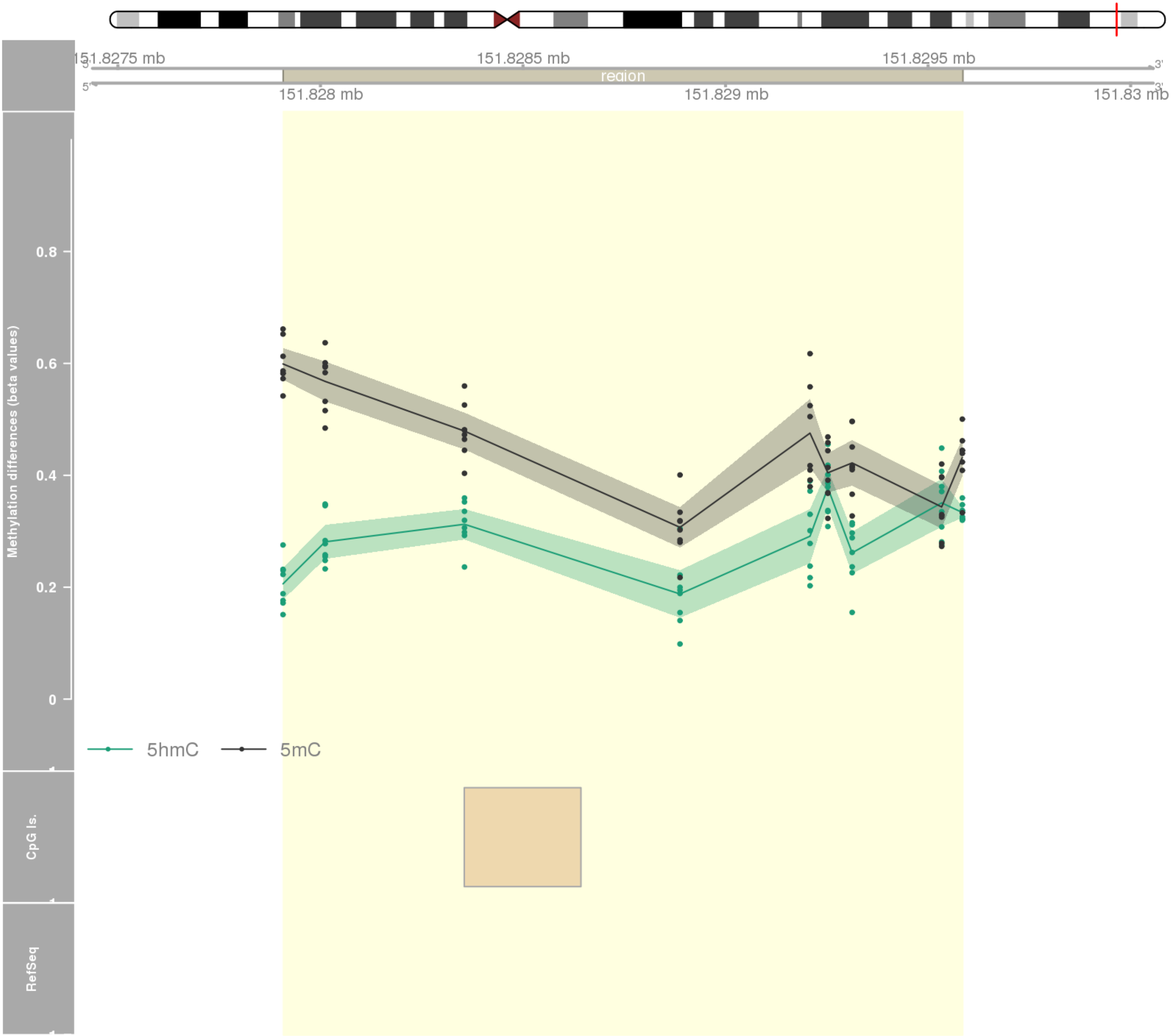
DMR 357 // chr17:34819740-34820712 // 972 pb. (8 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.018 // fwerArea: 0.559



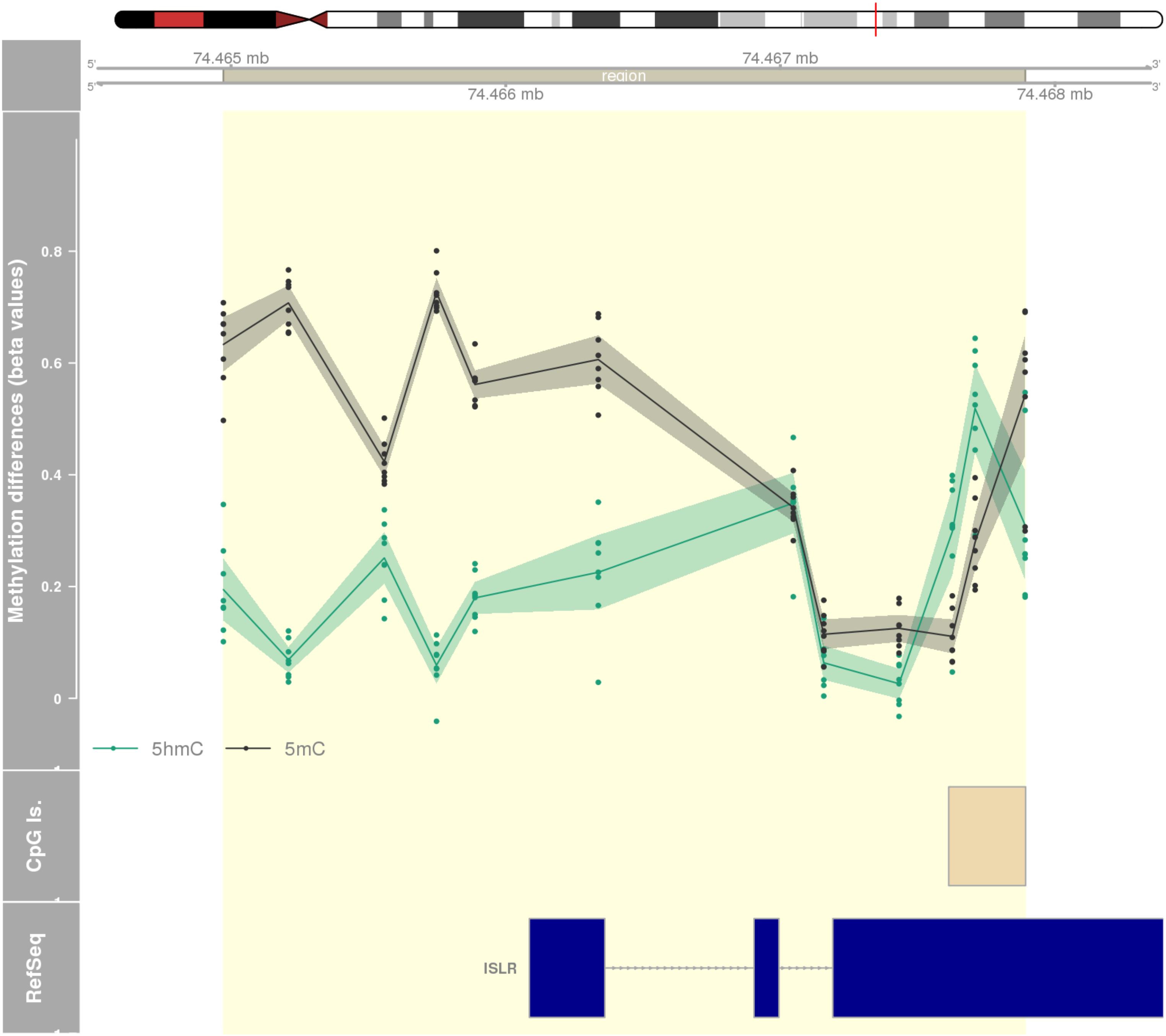
DMR 358 // chr6:32039796-32041689 // 1893 pb. (18 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: TNXB -



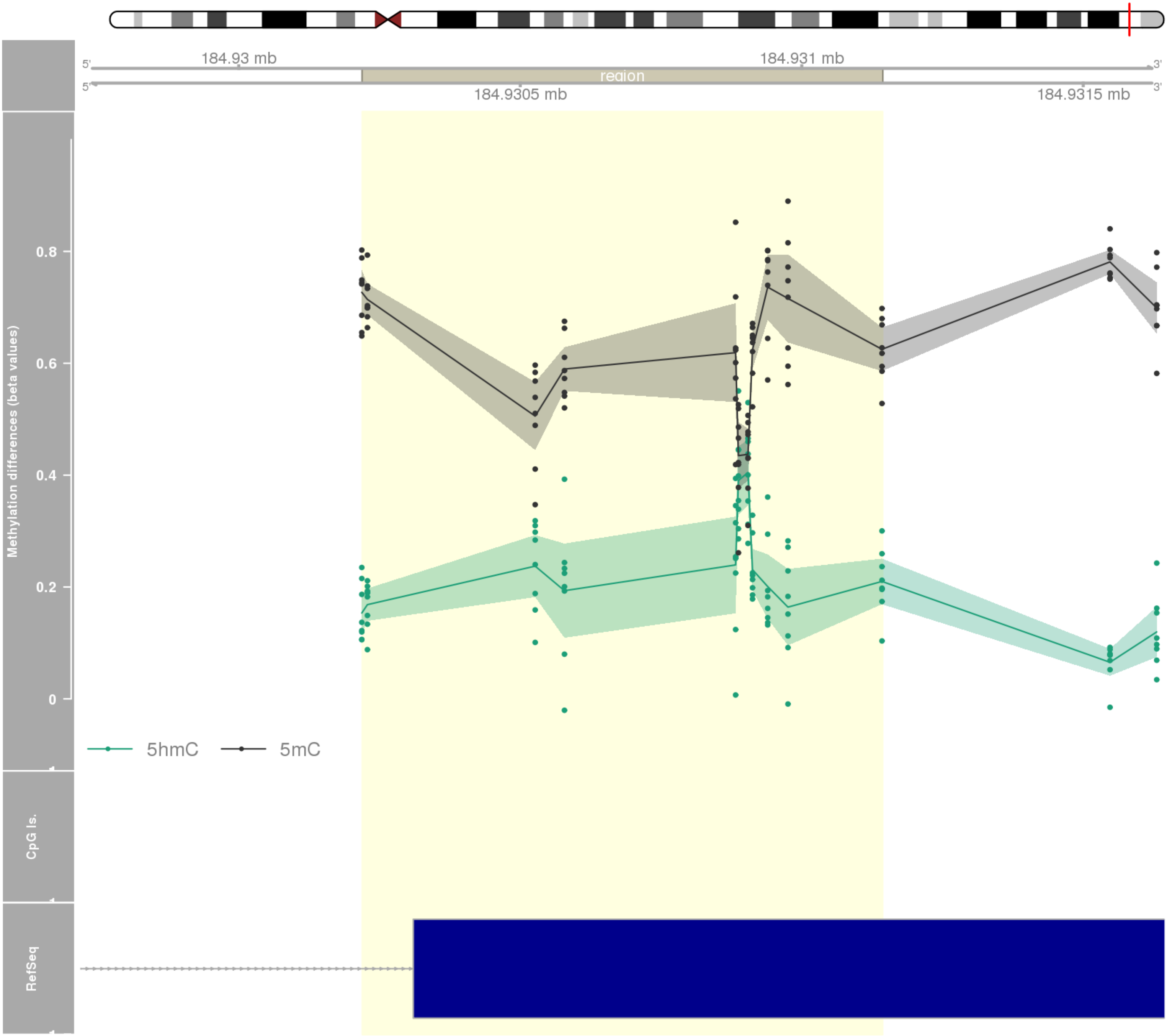
DMR 359 // chr7:151827908-151829585 // 1677 pb. (9 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559



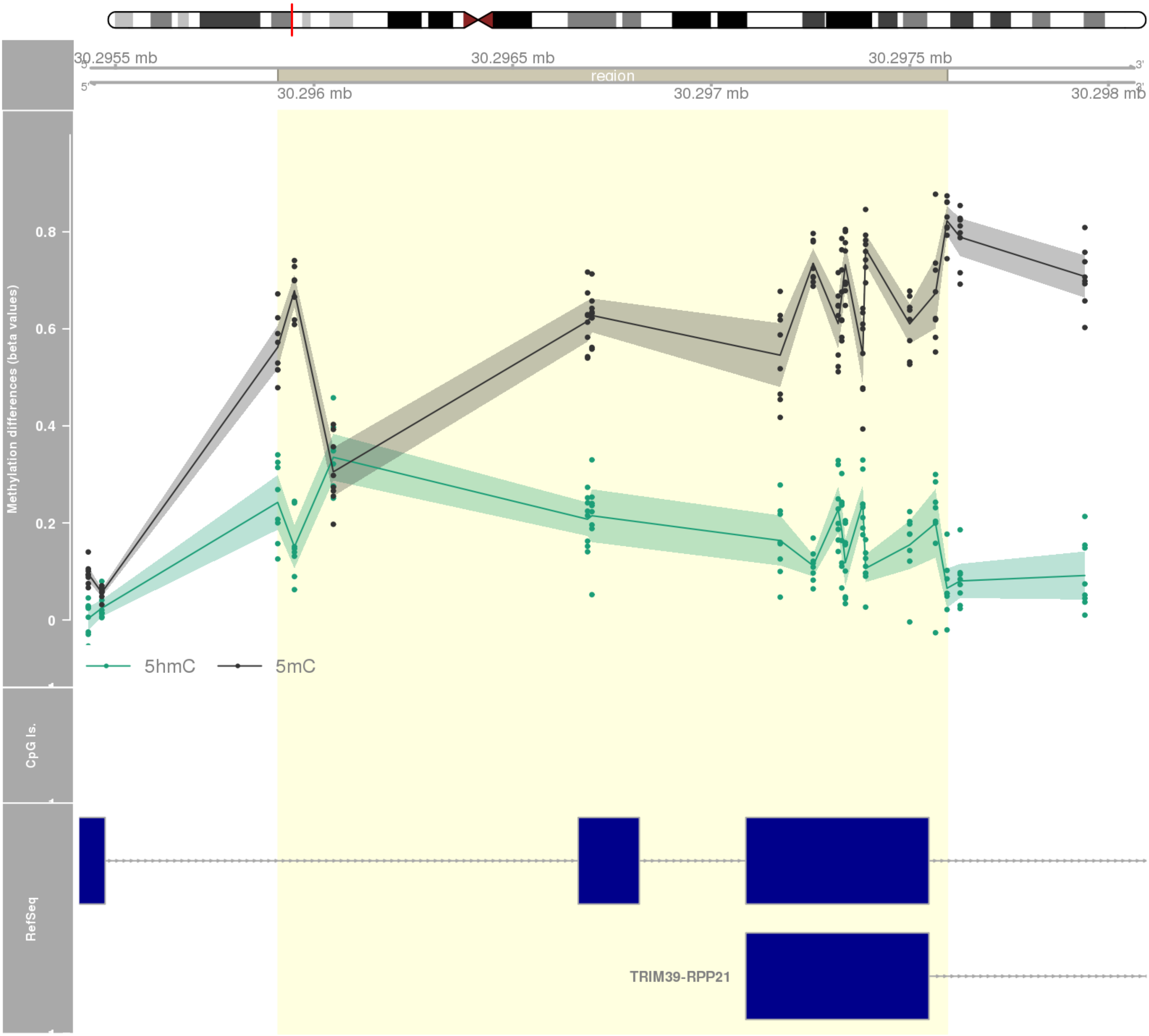
DMR 360 // chr15:74464972-74467891 // 2919 pb. (12 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: ISLR -



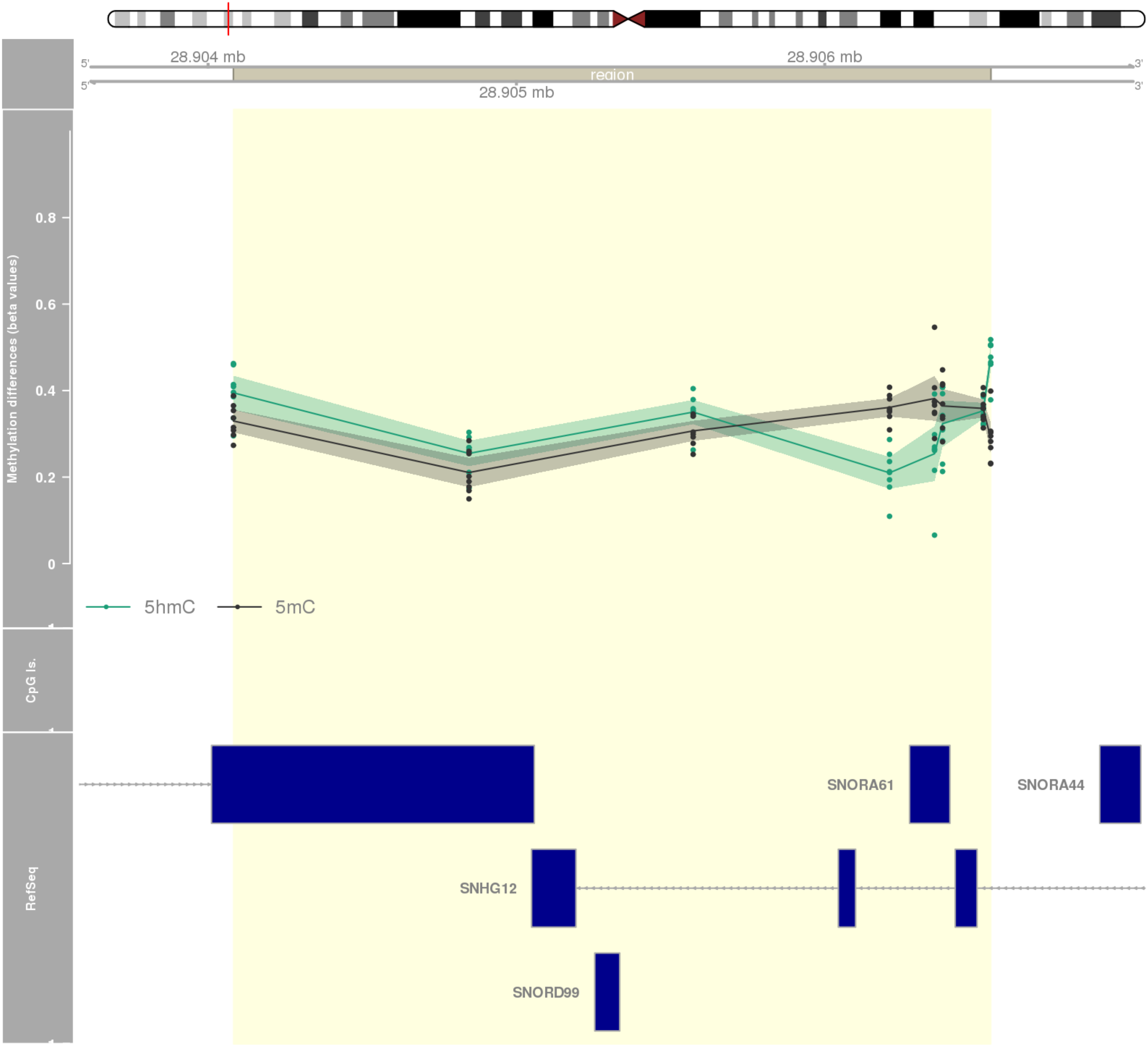
DMR 361 // chr4:184930219-184931143 // 924 pb. (11 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: STOX2 -



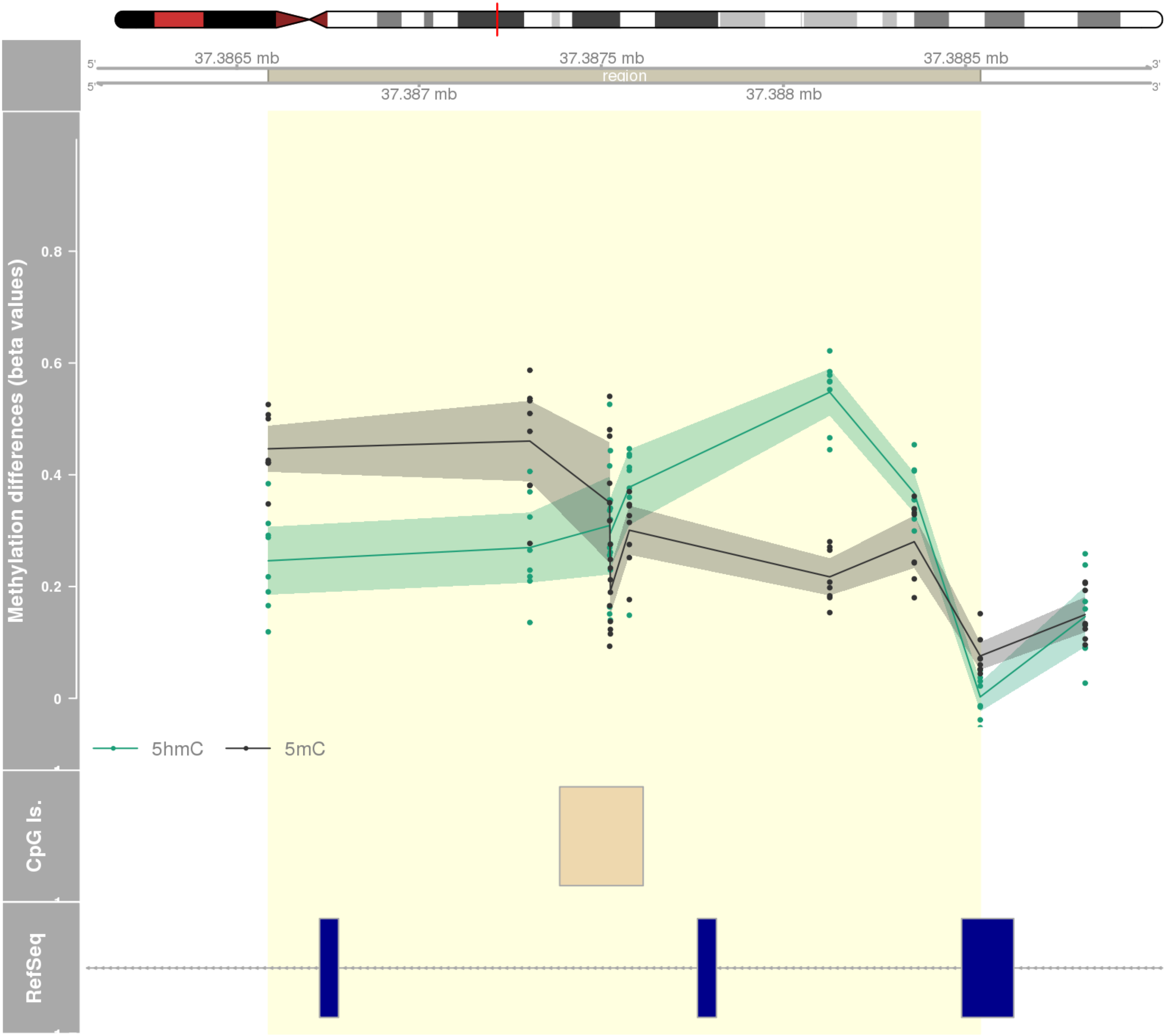
DMR 362 // chr6:30295909-30297594 // 1685 pb. (15 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: TRIM39 / TRIM39-RPP21 -



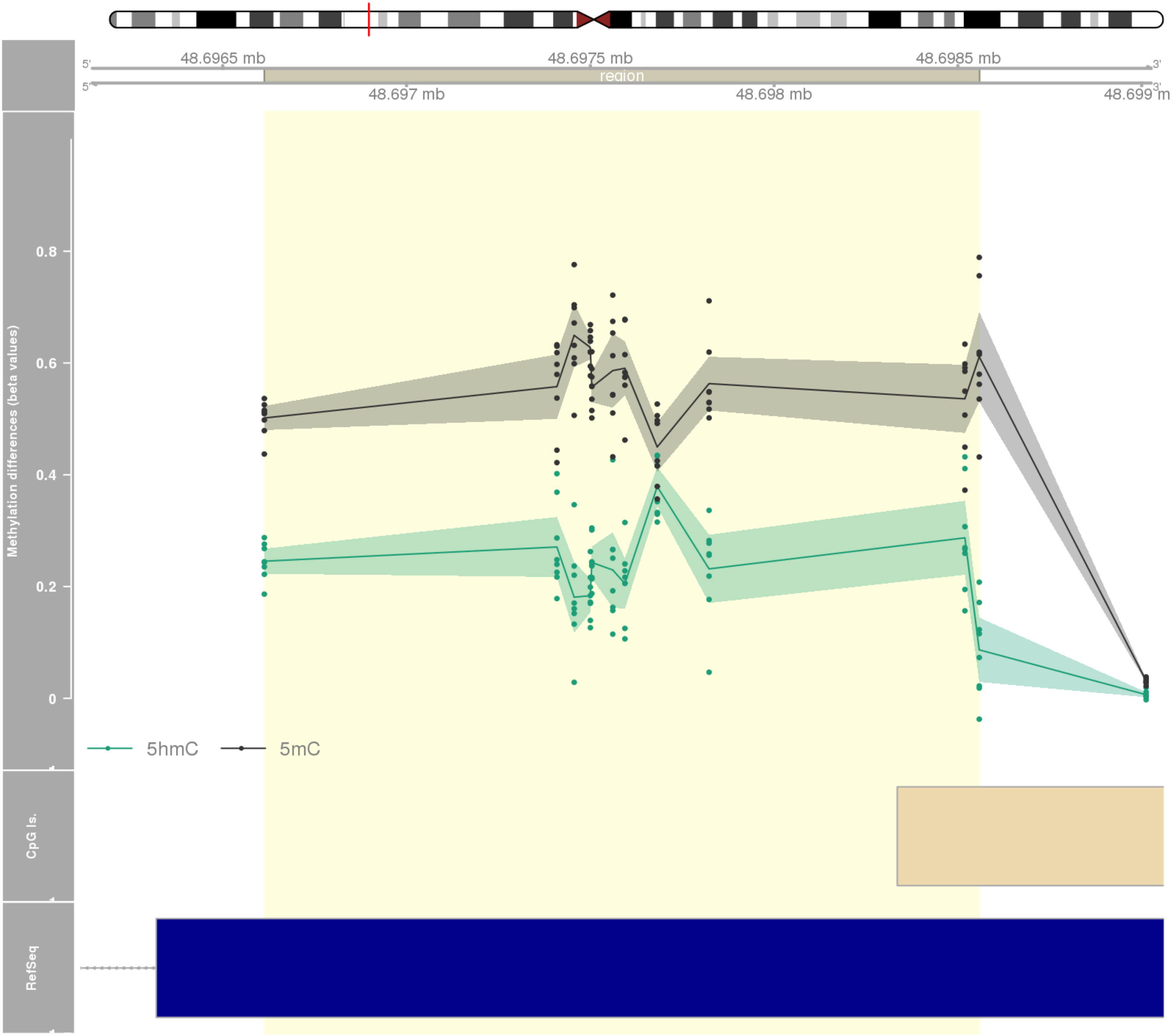
DMR 363 // chr1:28904082-28906538 // 2456 pb. (8 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: SNHG12 / SNORD99 / TRNAU1AP -



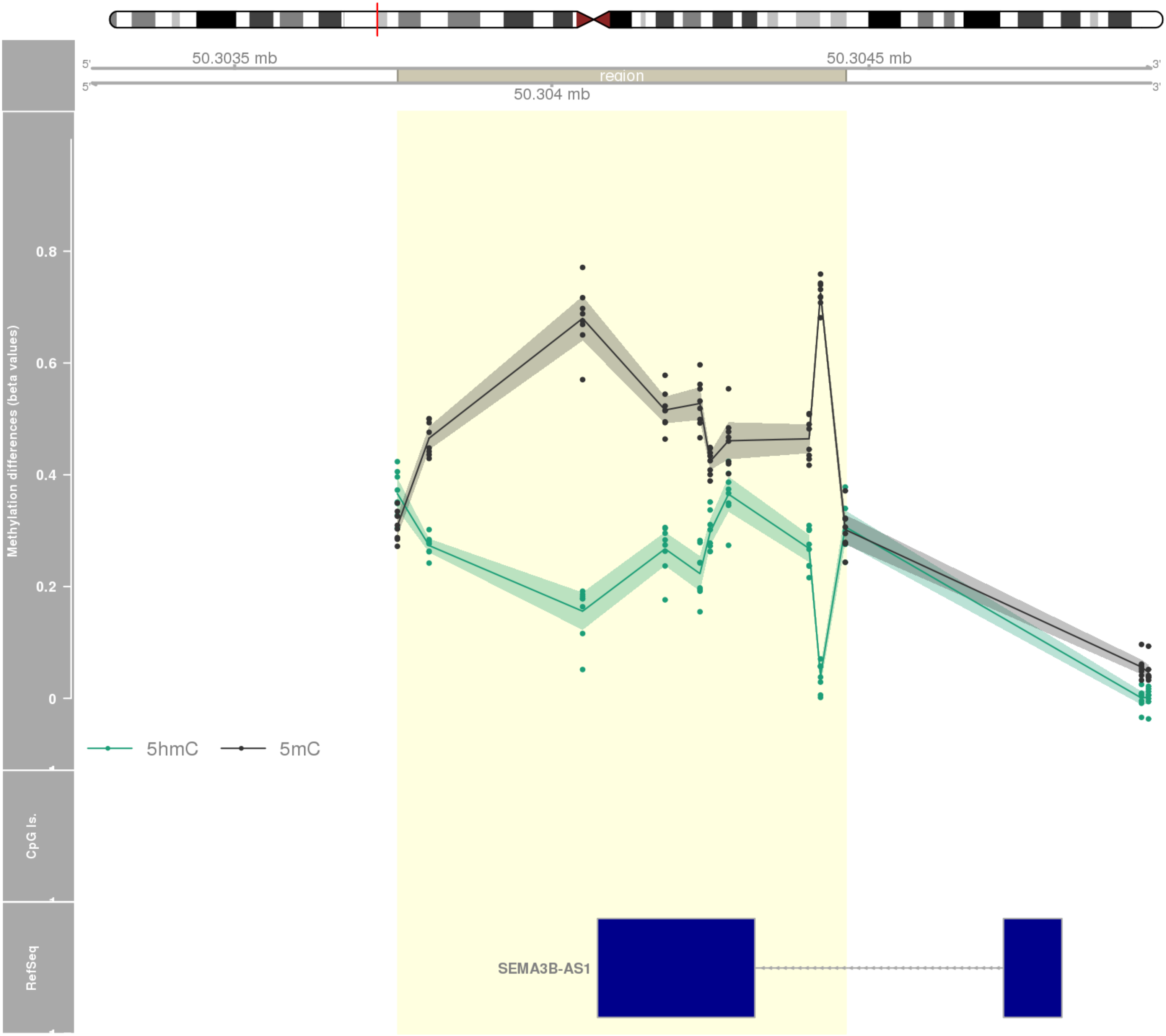
DMR 364 // chr15:37386586-37388540 // 1954 pb. (8 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: MEIS2 -



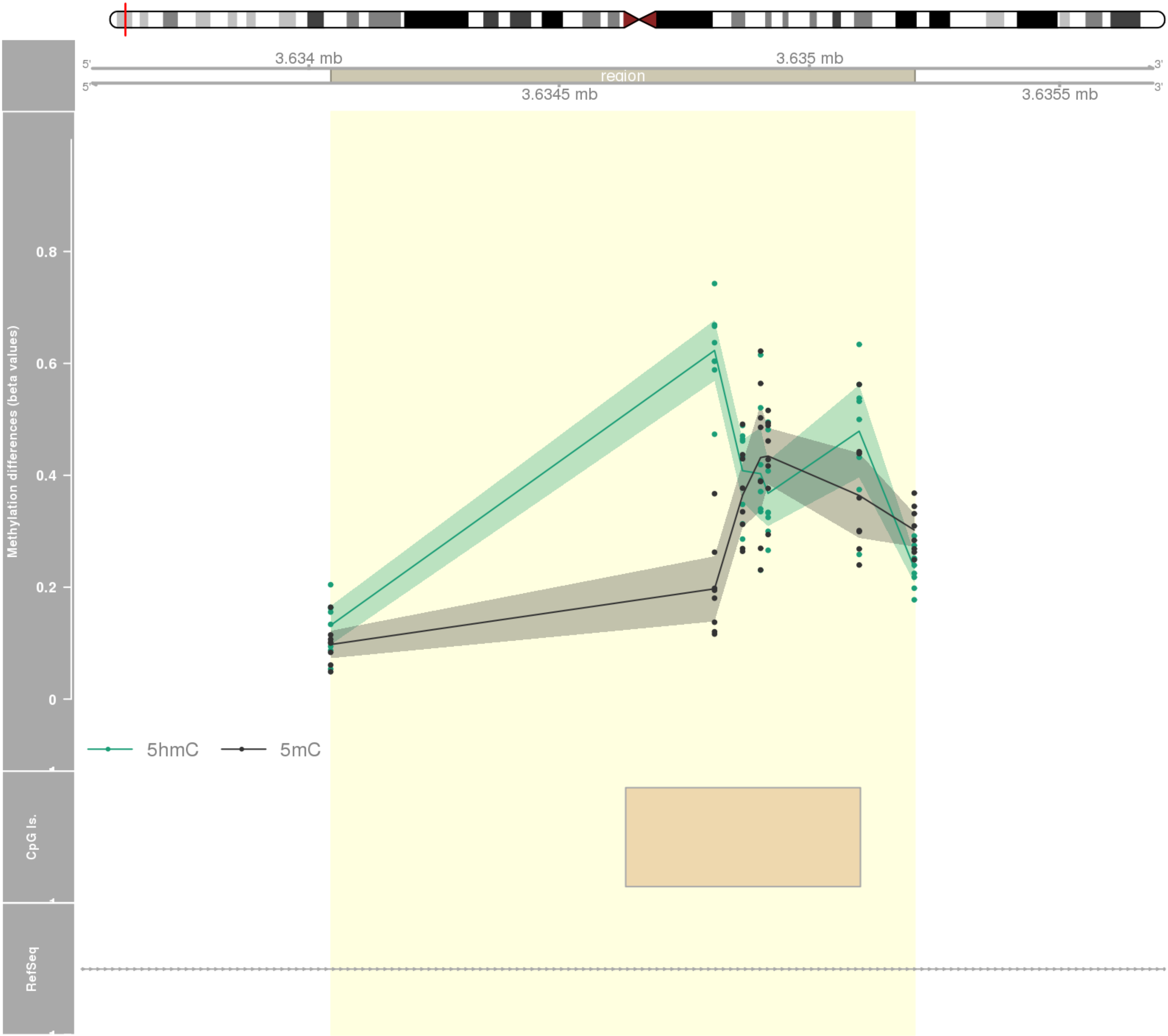
DMR 365 // chr3:48696613-48698558 // 1945 pb. (11 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: CELSR3 -



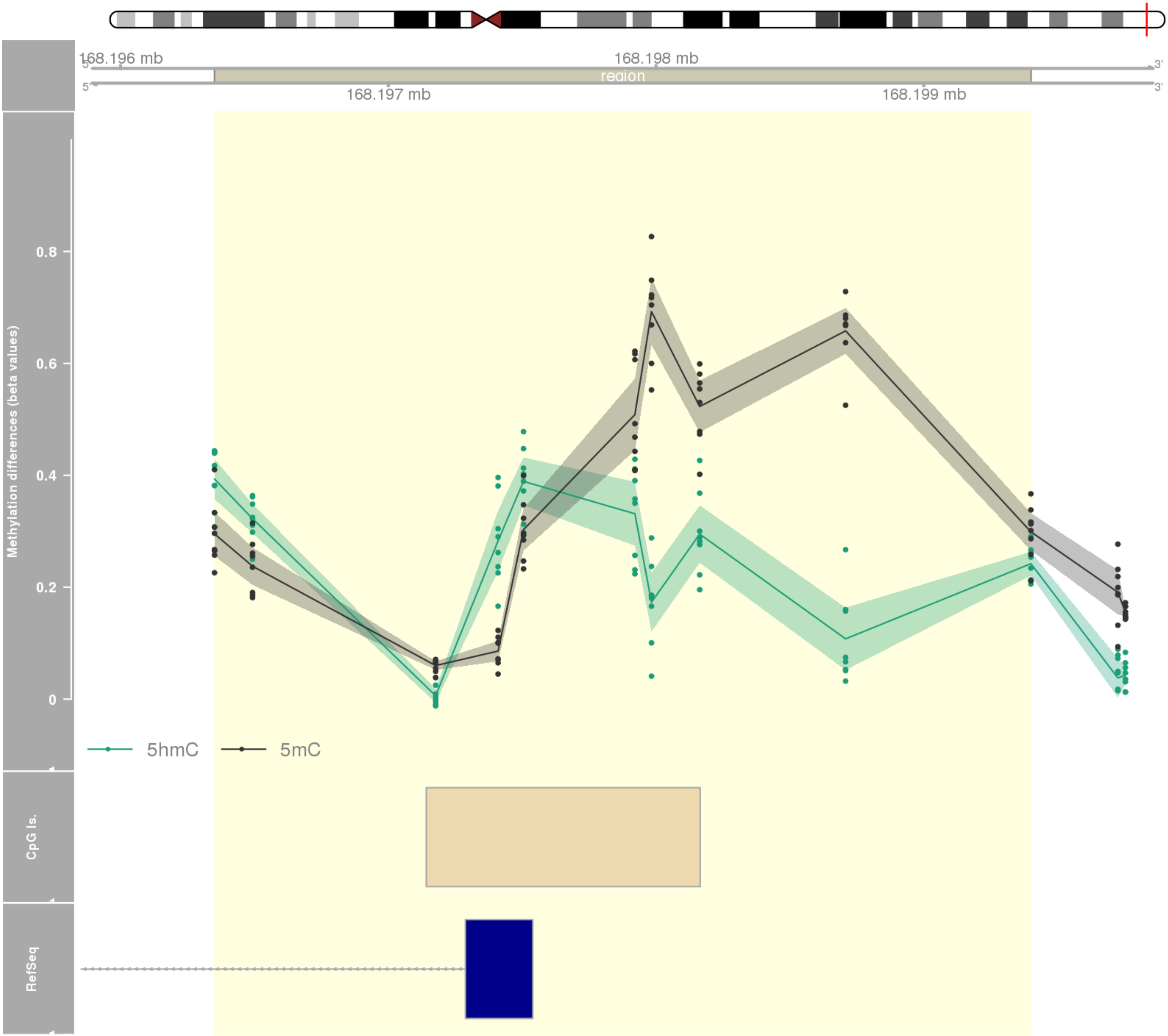
DMR 366 // chr3:50303757-50304463 // 706 pb. (10 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: SEMA3B-AS1 -



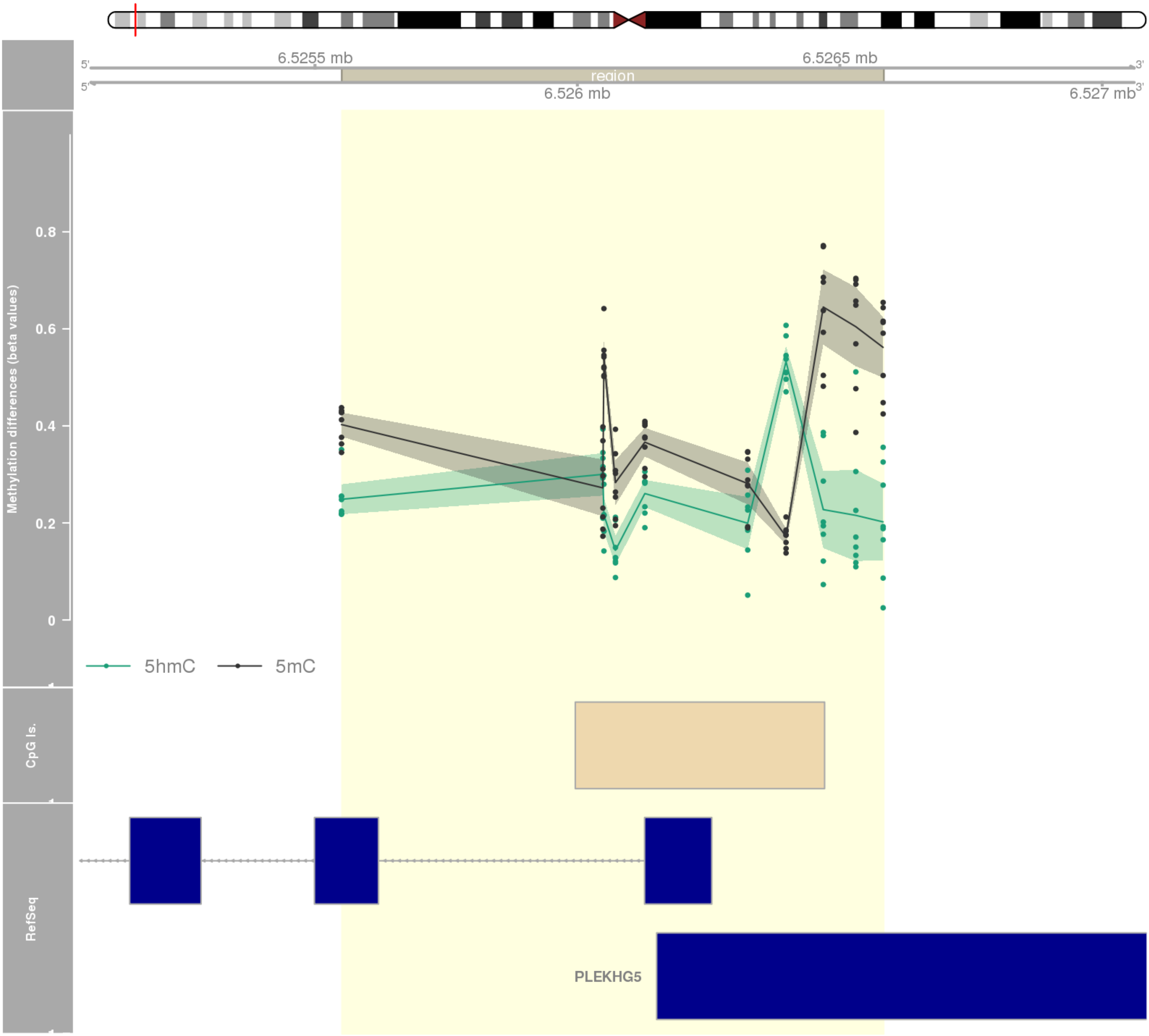
DMR 367 // chr1:3634044-3635210 // 1166 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: TP73 -



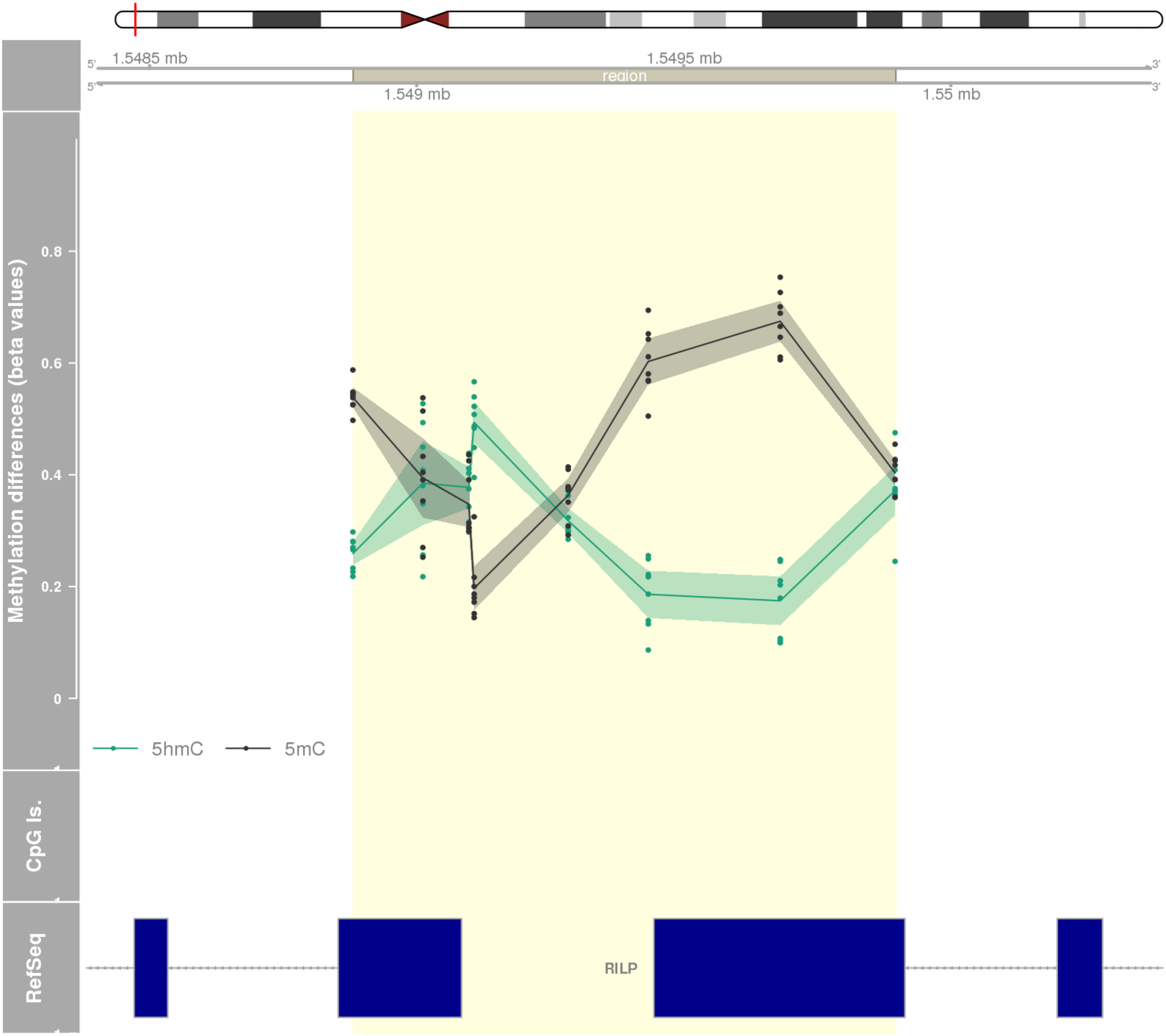
DMR 368 // chr6:168196351-168199400 // 3049 pb. (10 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: C6orf123 -



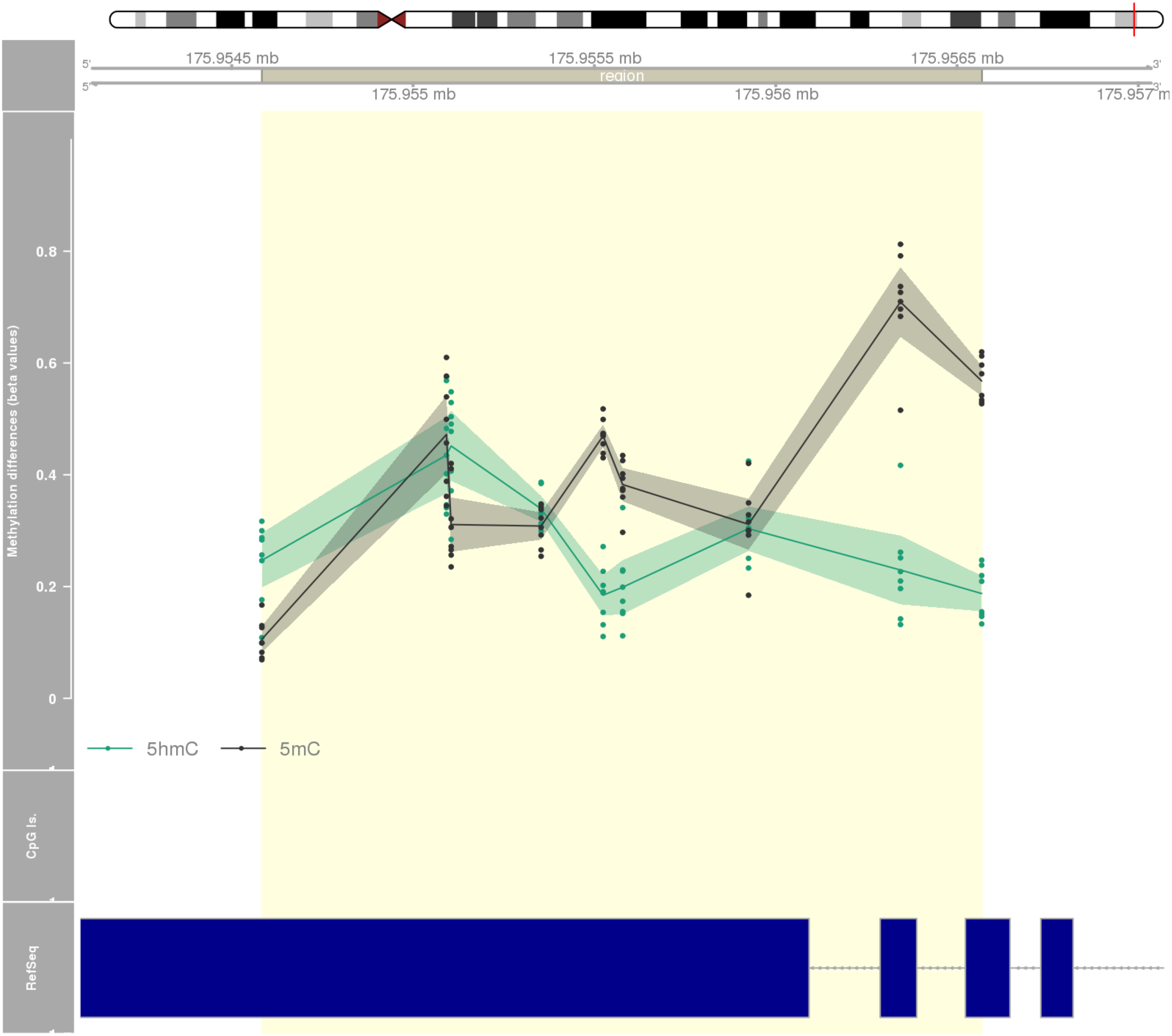
DMR 369 // chr1:6525551-6526583 // 1032 pb. (10 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: TNFRSF25 / PLEKHG5 -



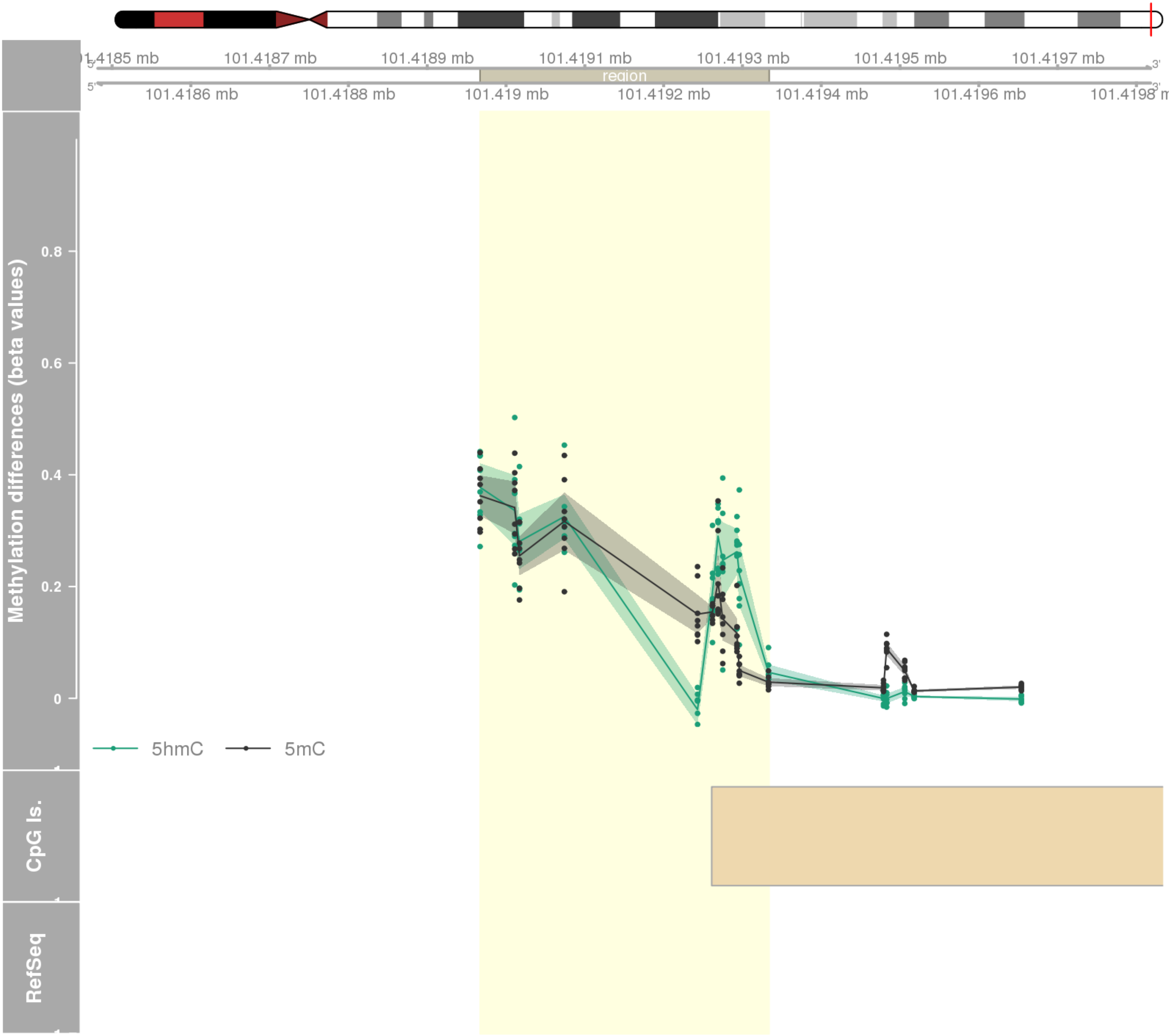
DMR 370 // chr17:1548881-1549896 // 1015 pb. (8 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: SCARF1 / RILP -



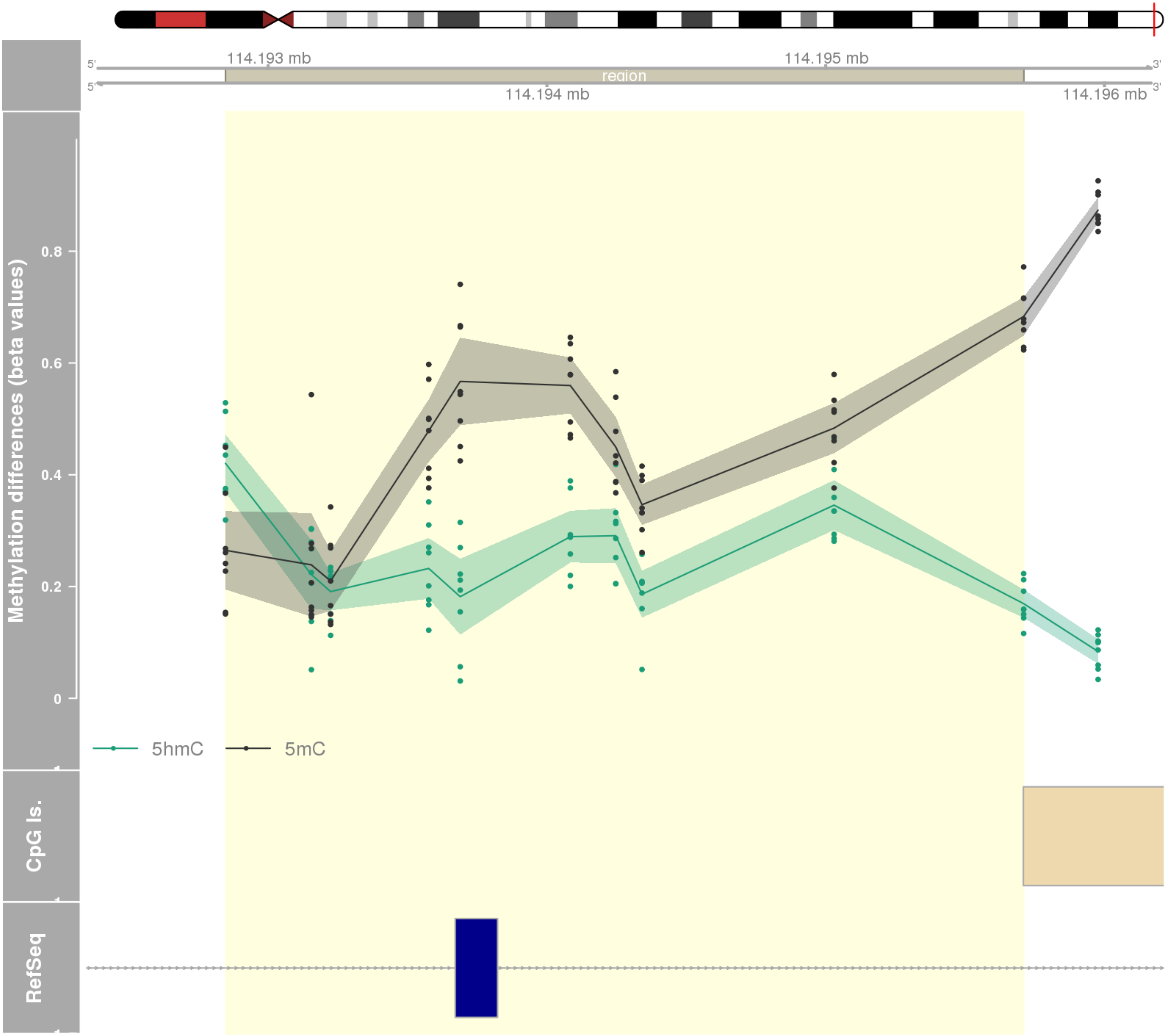
DMR 371 // chr5:175954583-175956568 // 1985 pb. (9 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: RNF44 -



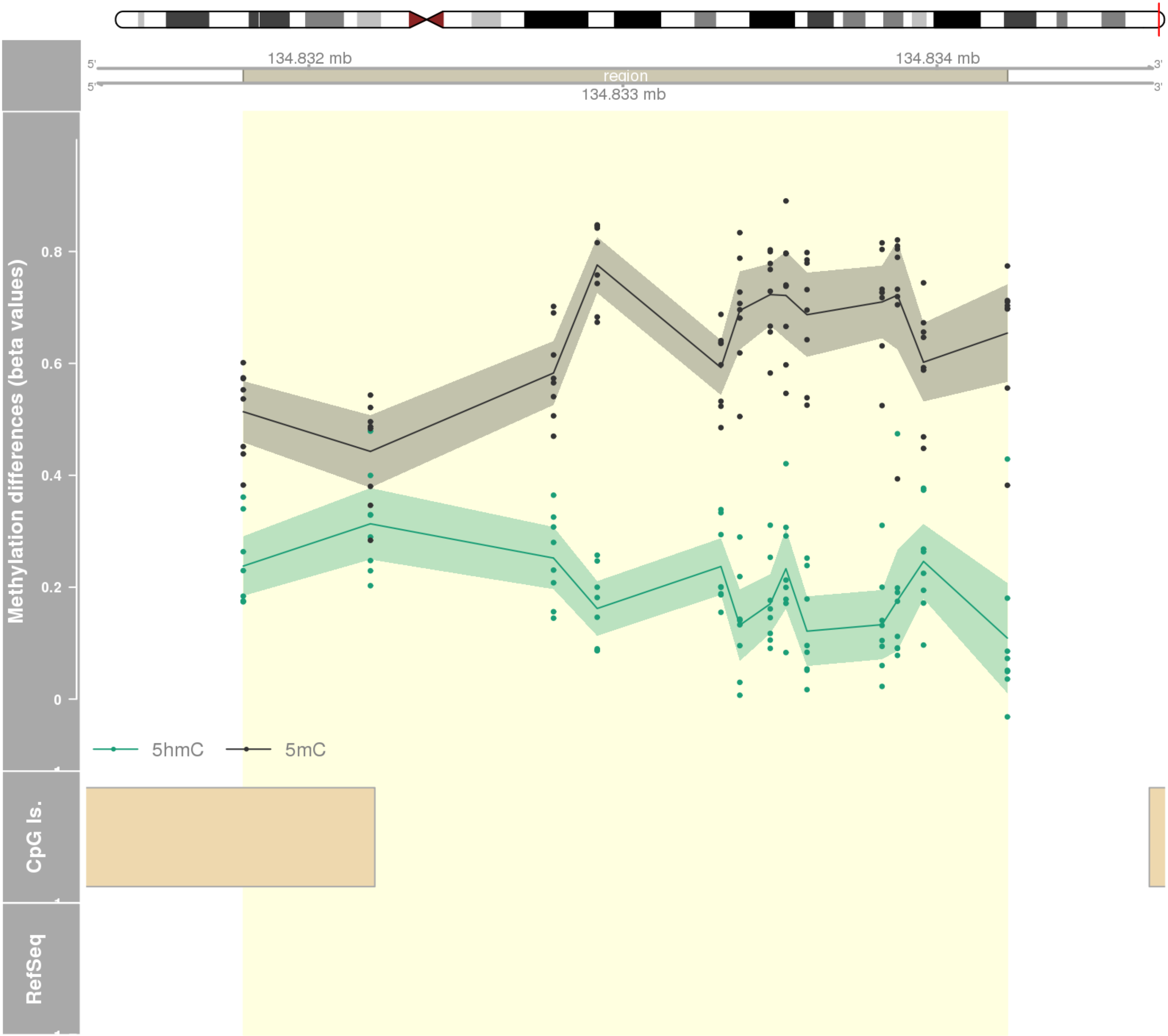
DMR 372 // chr15:101418967-101419333 // 366 pb. (11 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: ALDH1A3 -



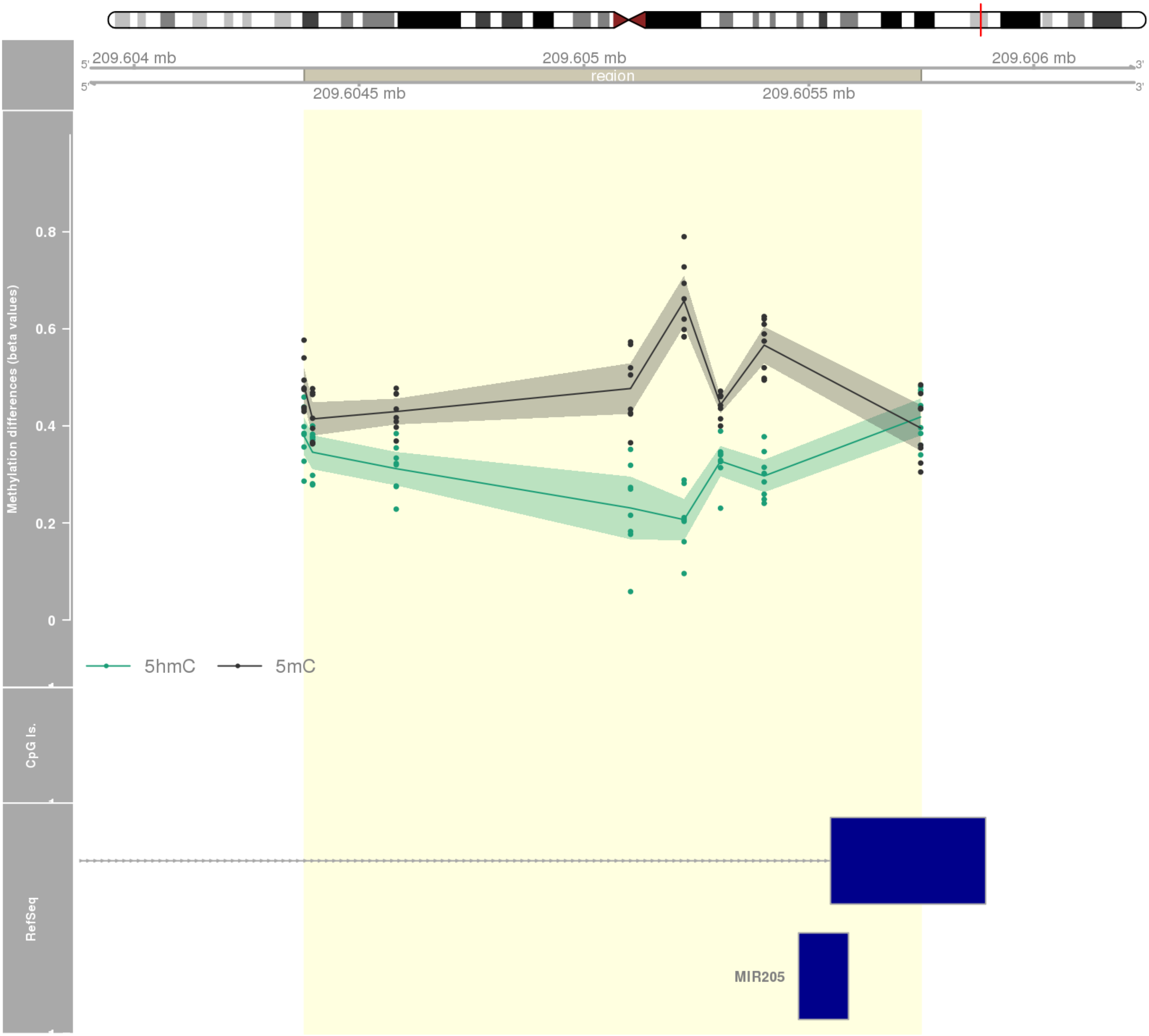
DMR 373 // chr13:114192847-114195710 // 2863 pb. (10 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: TMCO3 -



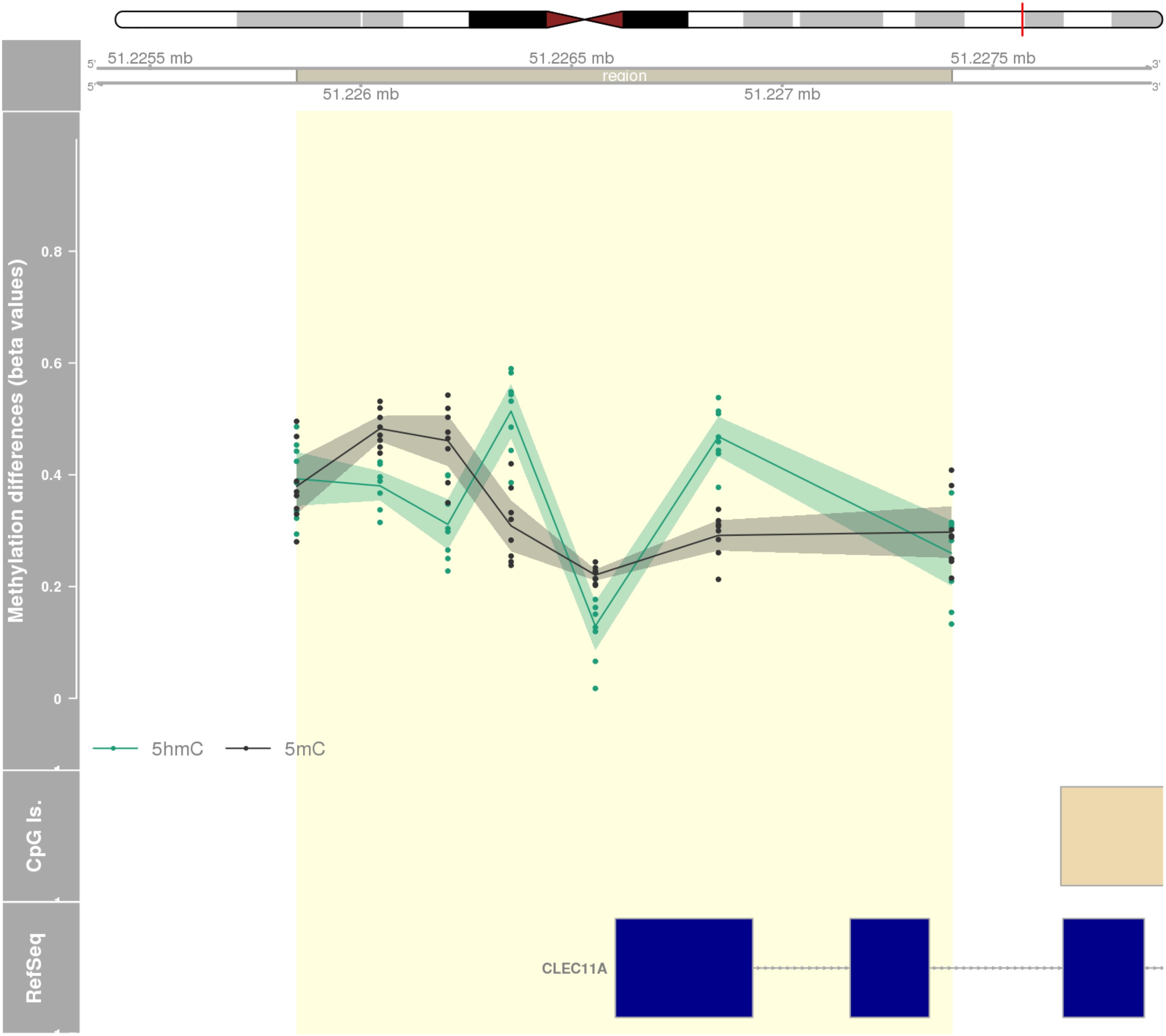
DMR 374 // chr10:134831791-134834224 // 2433 pb. (13 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559



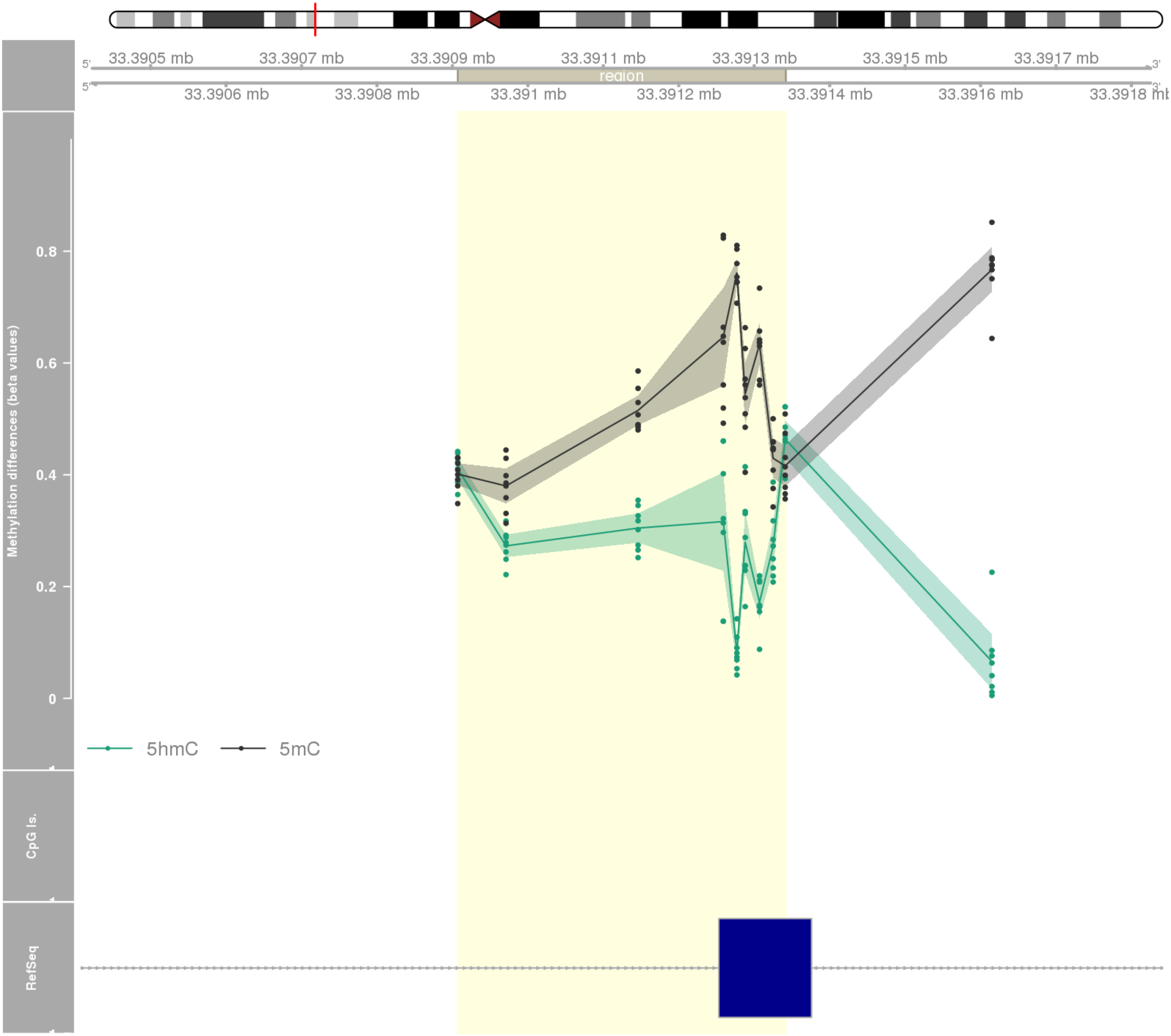
DMR 375 // chr1:209604378-209605749 // 1371 pb. (8 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.019 // fwerArea: 0.559
- genes: MIR205HG -



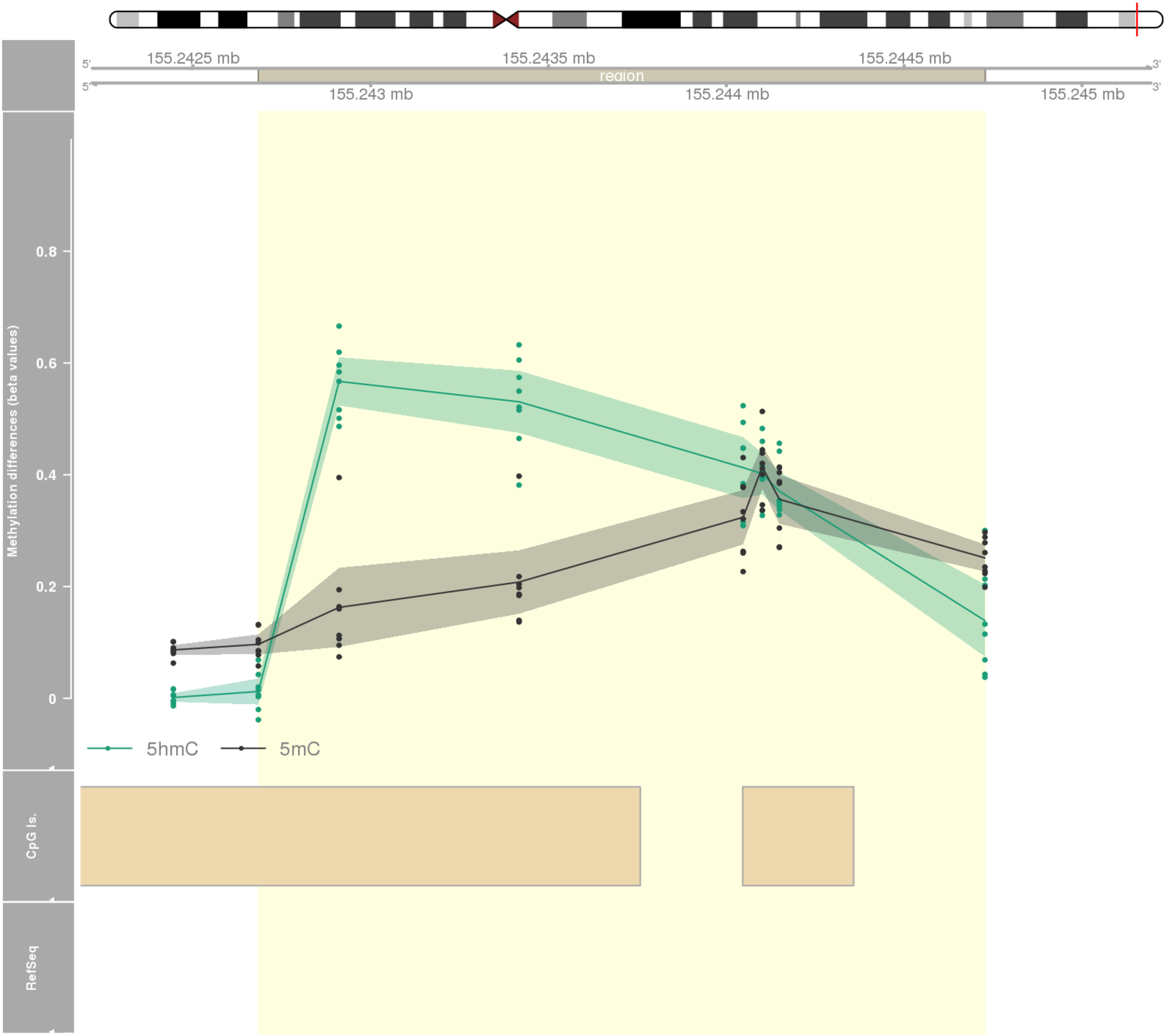
DMR 376 // chr19:51225848-51227402 // 1554 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: CLEC11A -



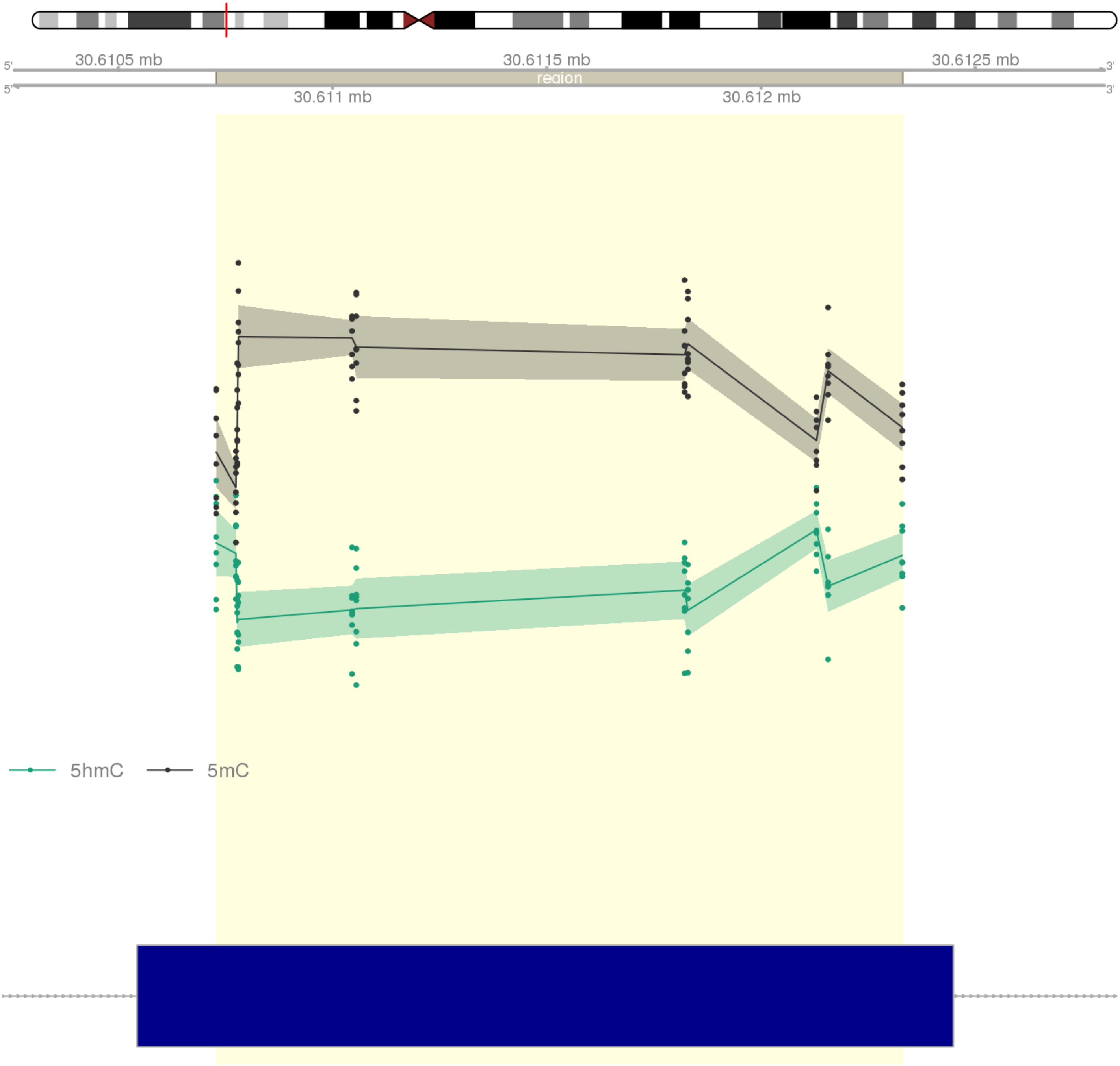
DMR 377 // chr6:33390907-33391341 // 434 pb. (9 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: SYNGAP1 -



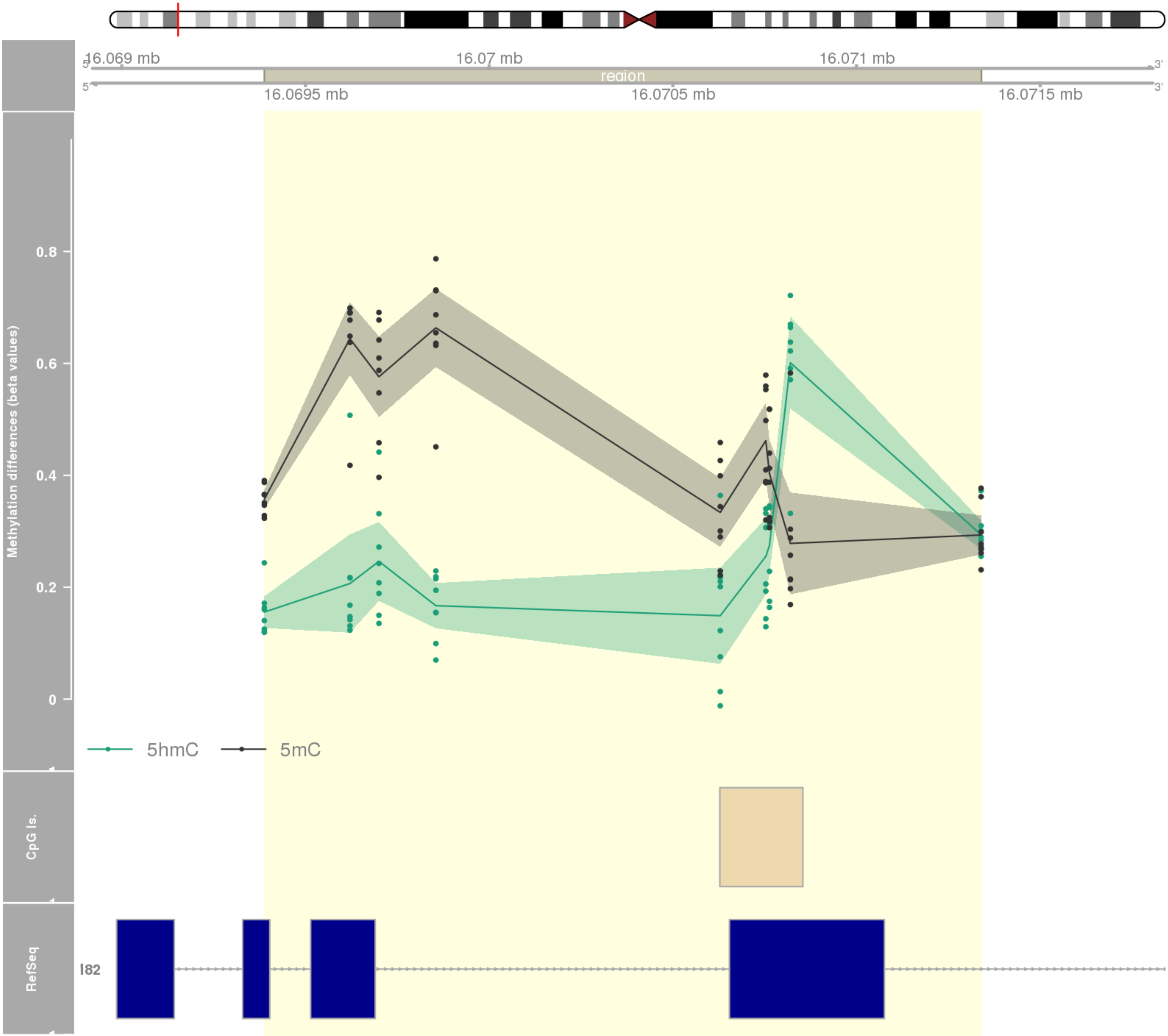
DMR 378 // chr7:155242684-155244727 // 2043 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559



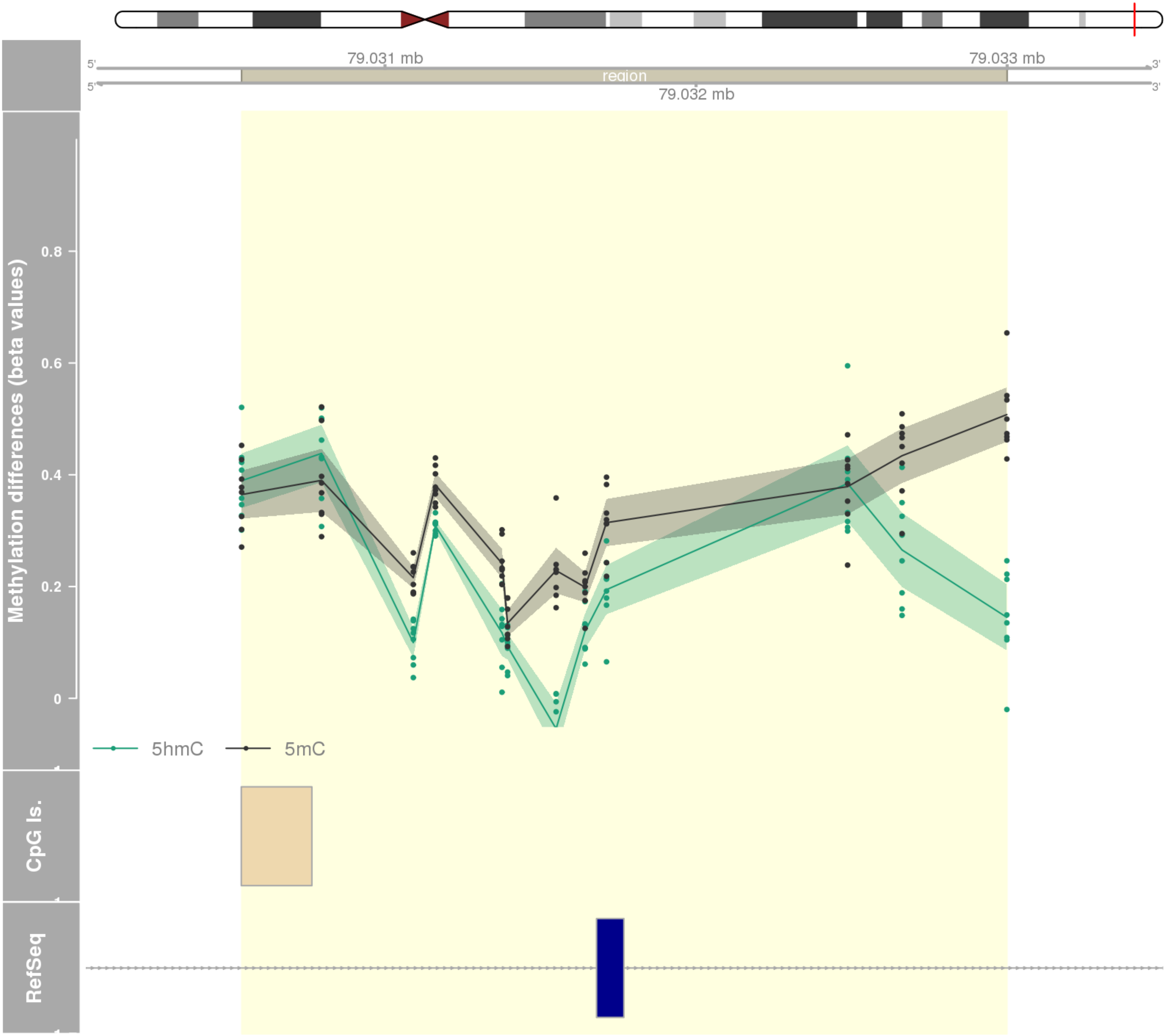
DMR 379 // chr6:30610729-30612330 // 1601 pb. (11 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: ATAT1 -



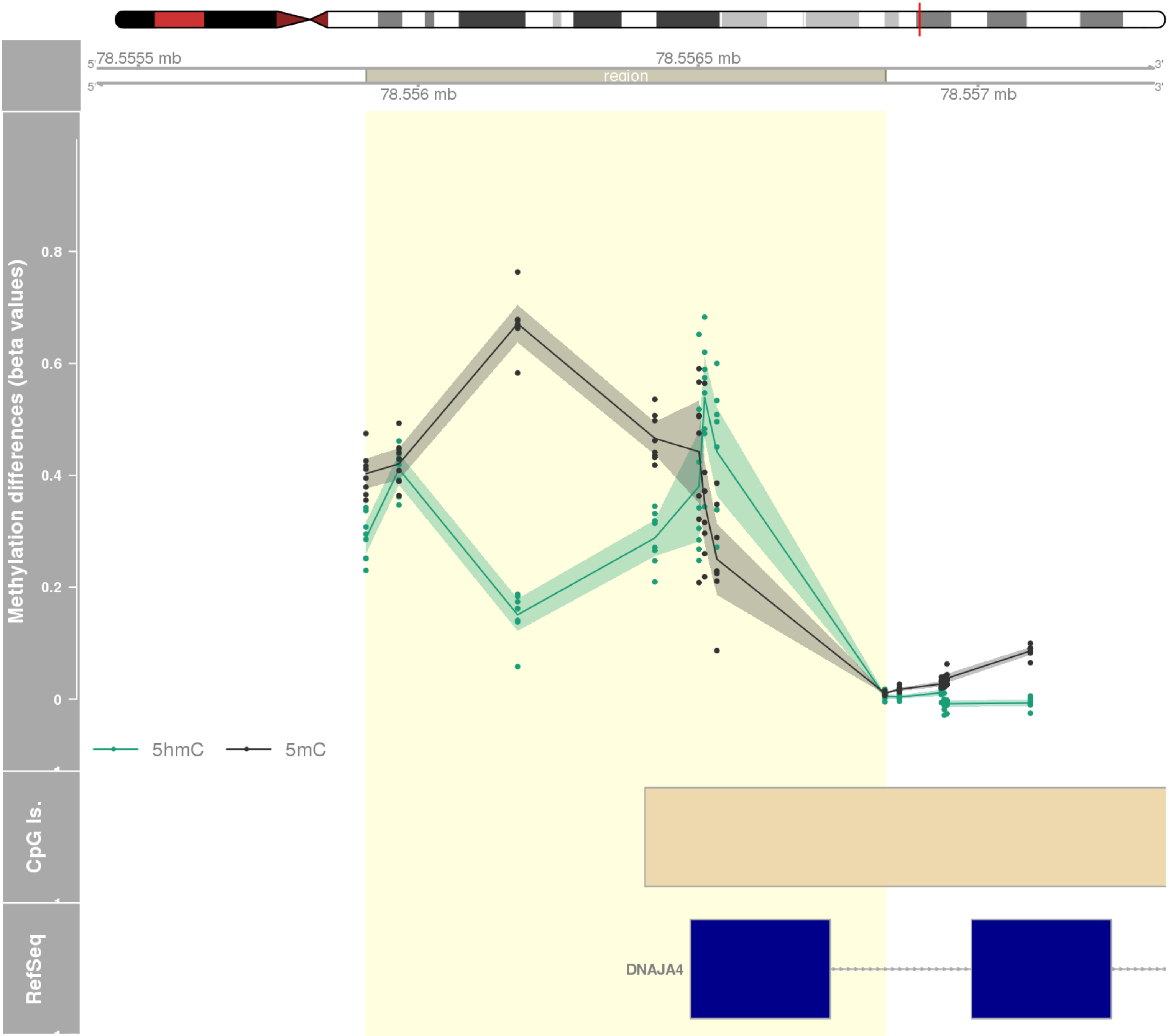
DMR 380 // chr1:16069388-16071339 // 1951 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: TMEM82 -



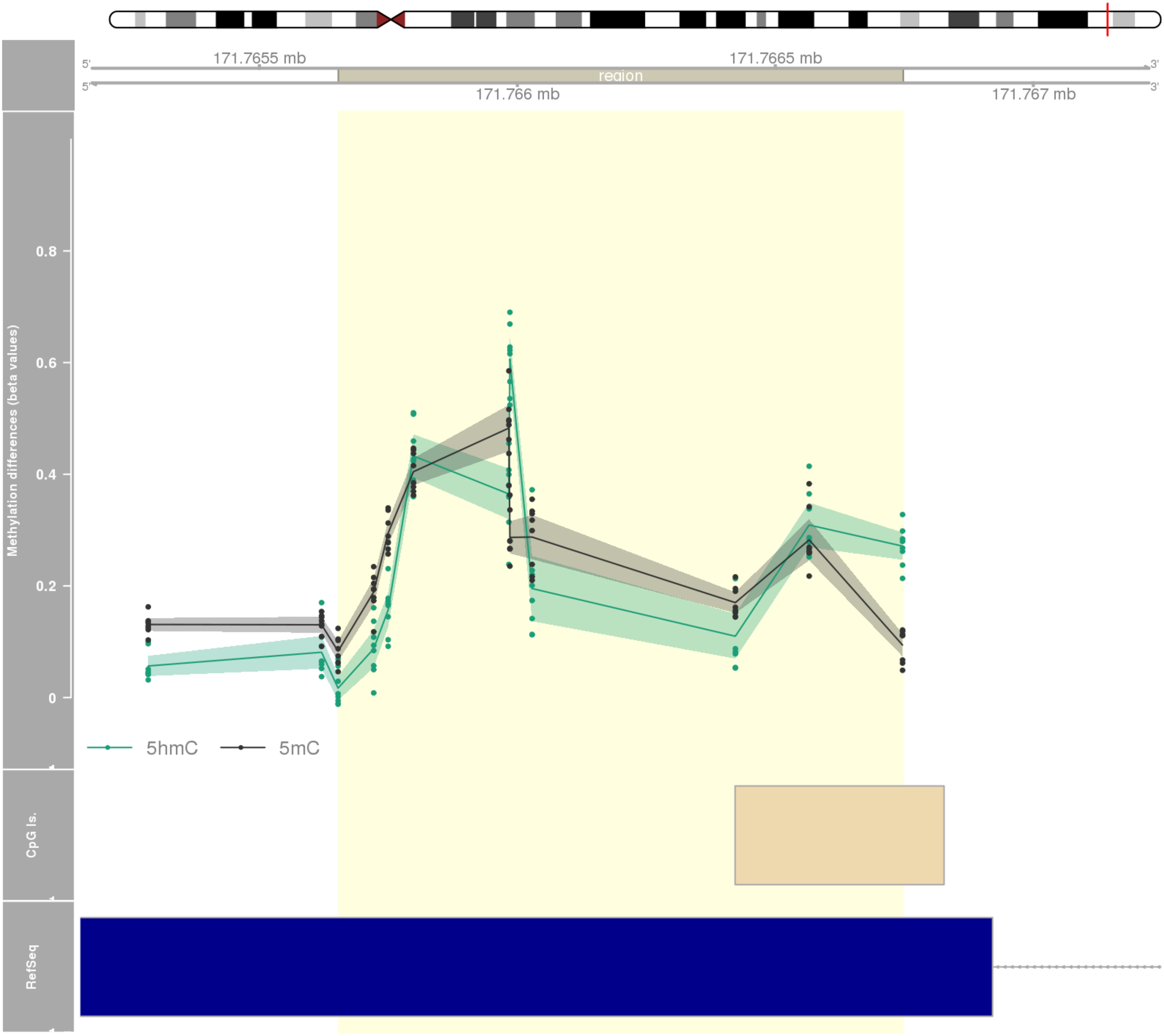
DMR 381 // chr17:79030539-79032999 // 2460 pb. (12 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: BAIAP2 -



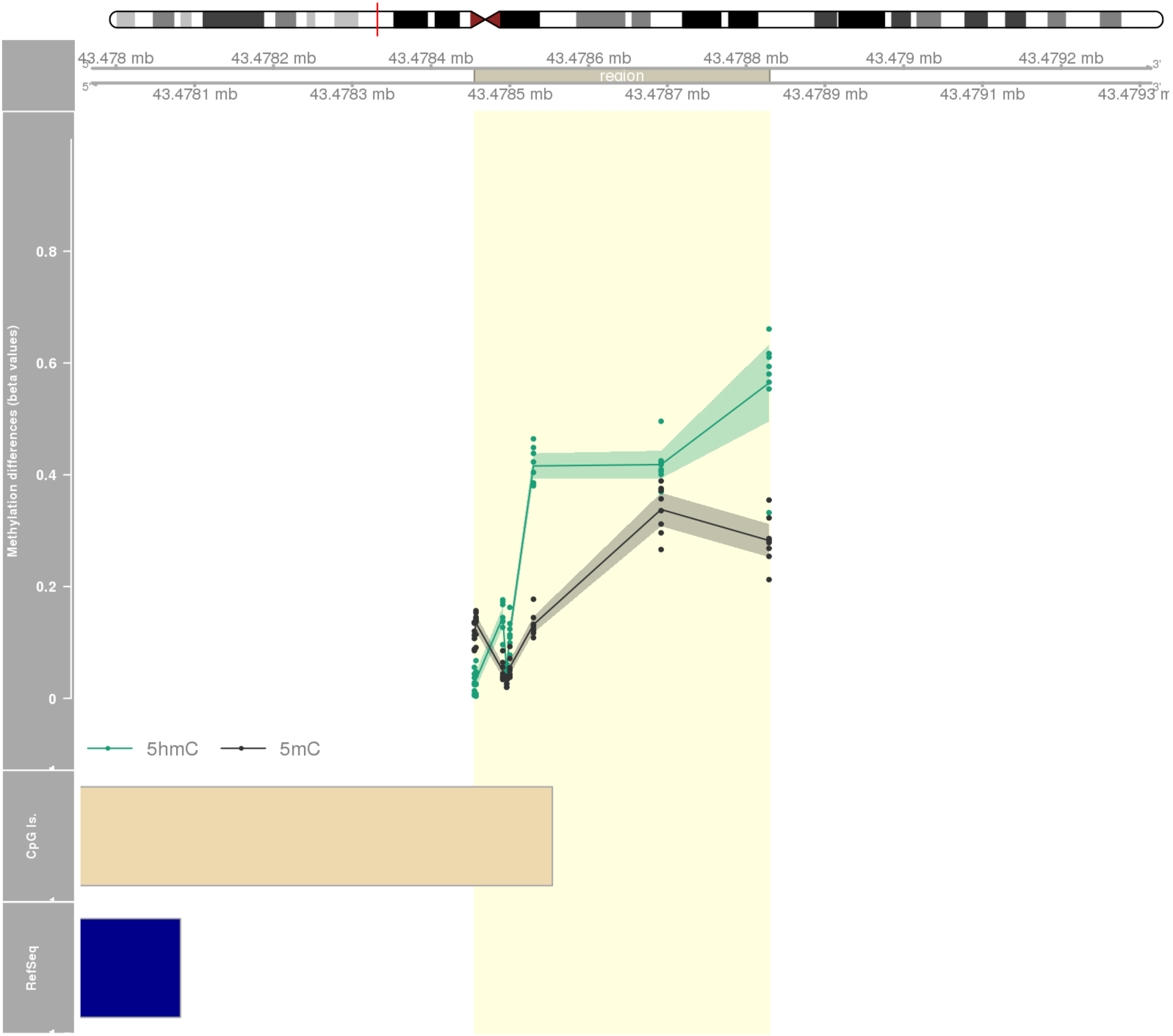
DMR 382 // chr15:78555907-78556834 // 927 pb. (8 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: DNAJA4 -



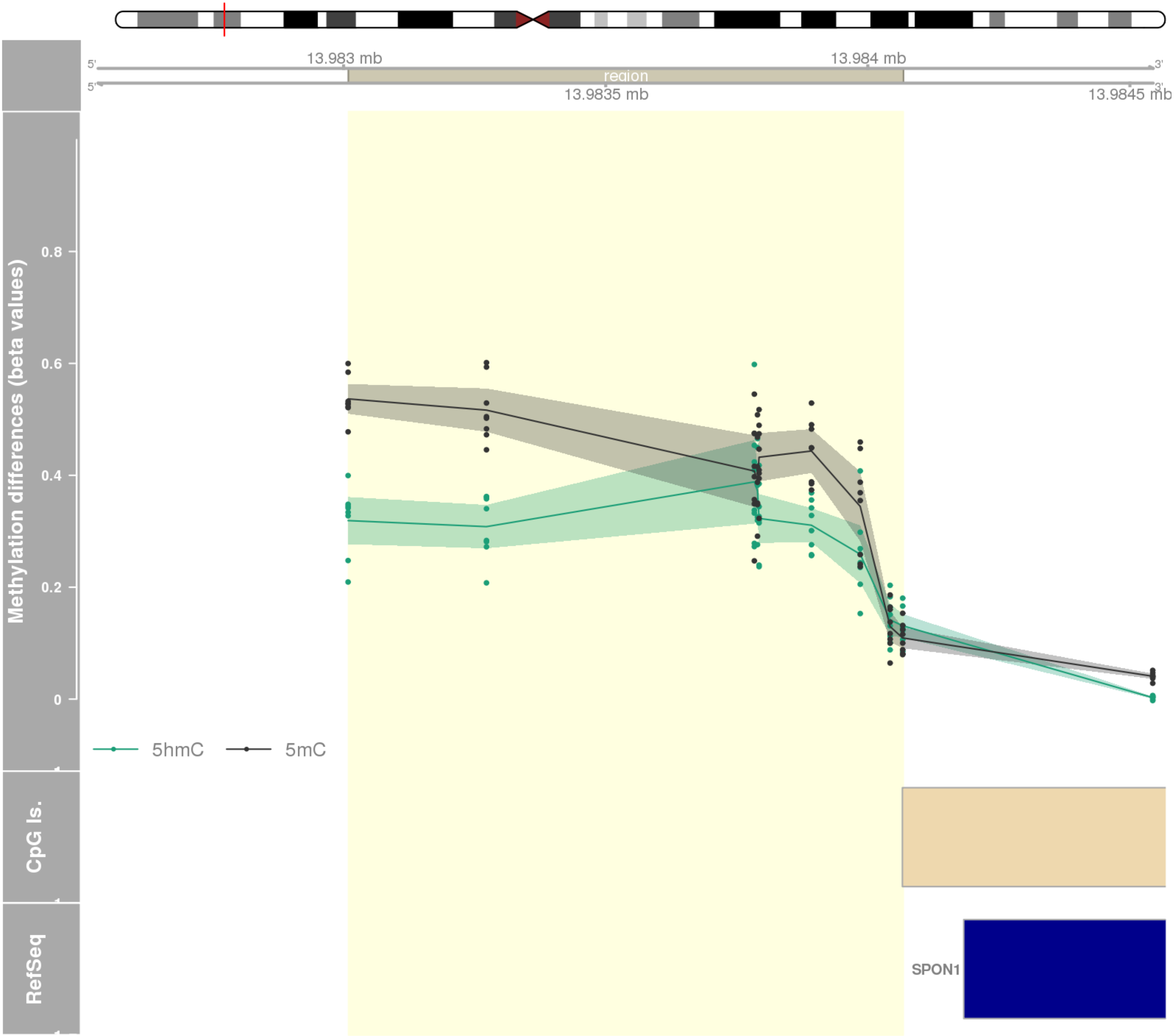
DMR 383 // chr5:171765653-171766747 // 1094 pb. (10 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: SH3PXD2B -



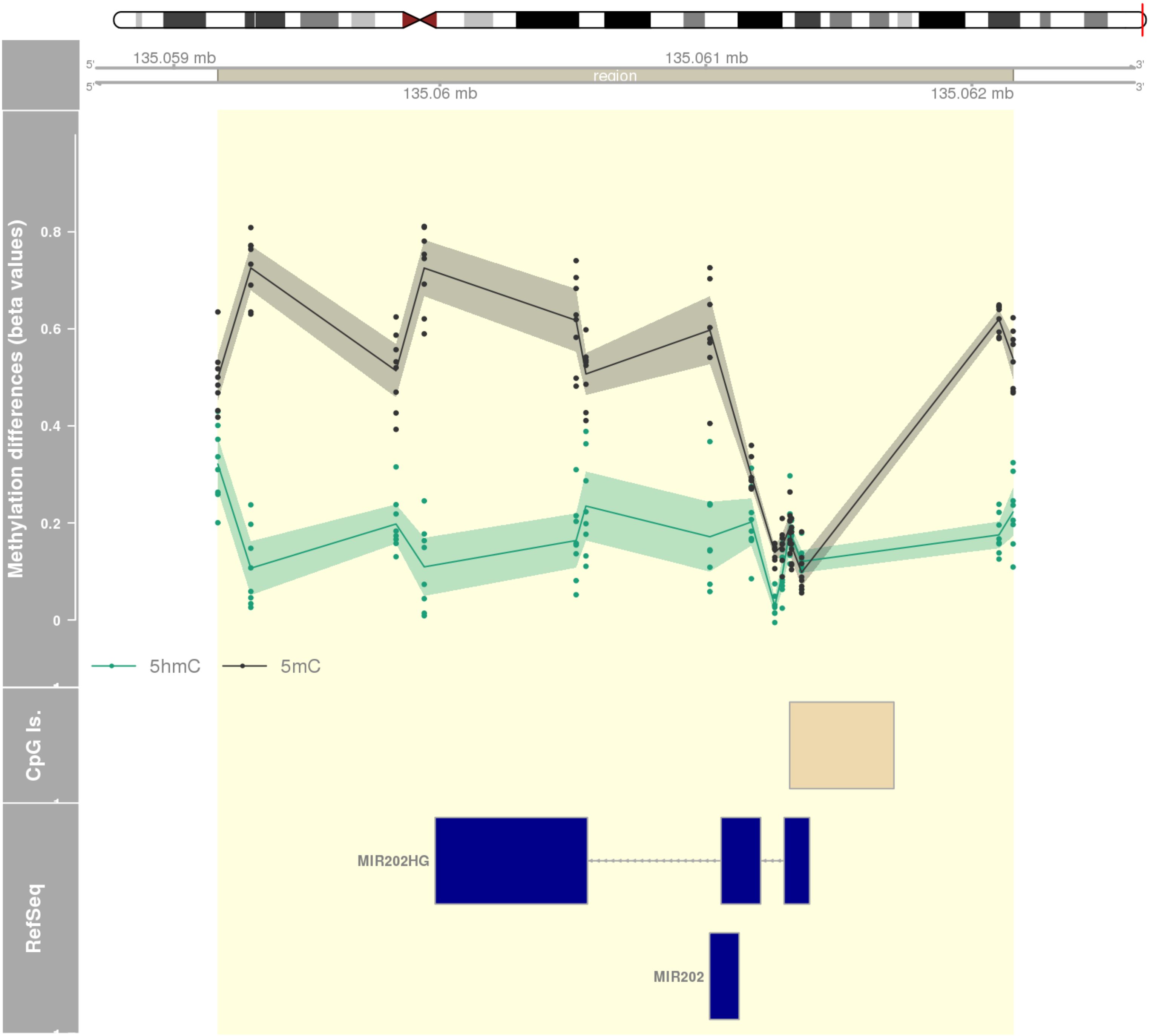
DMR 384 // chr6:43478455-43478829 // 374 pb. (8 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: POLR1C -



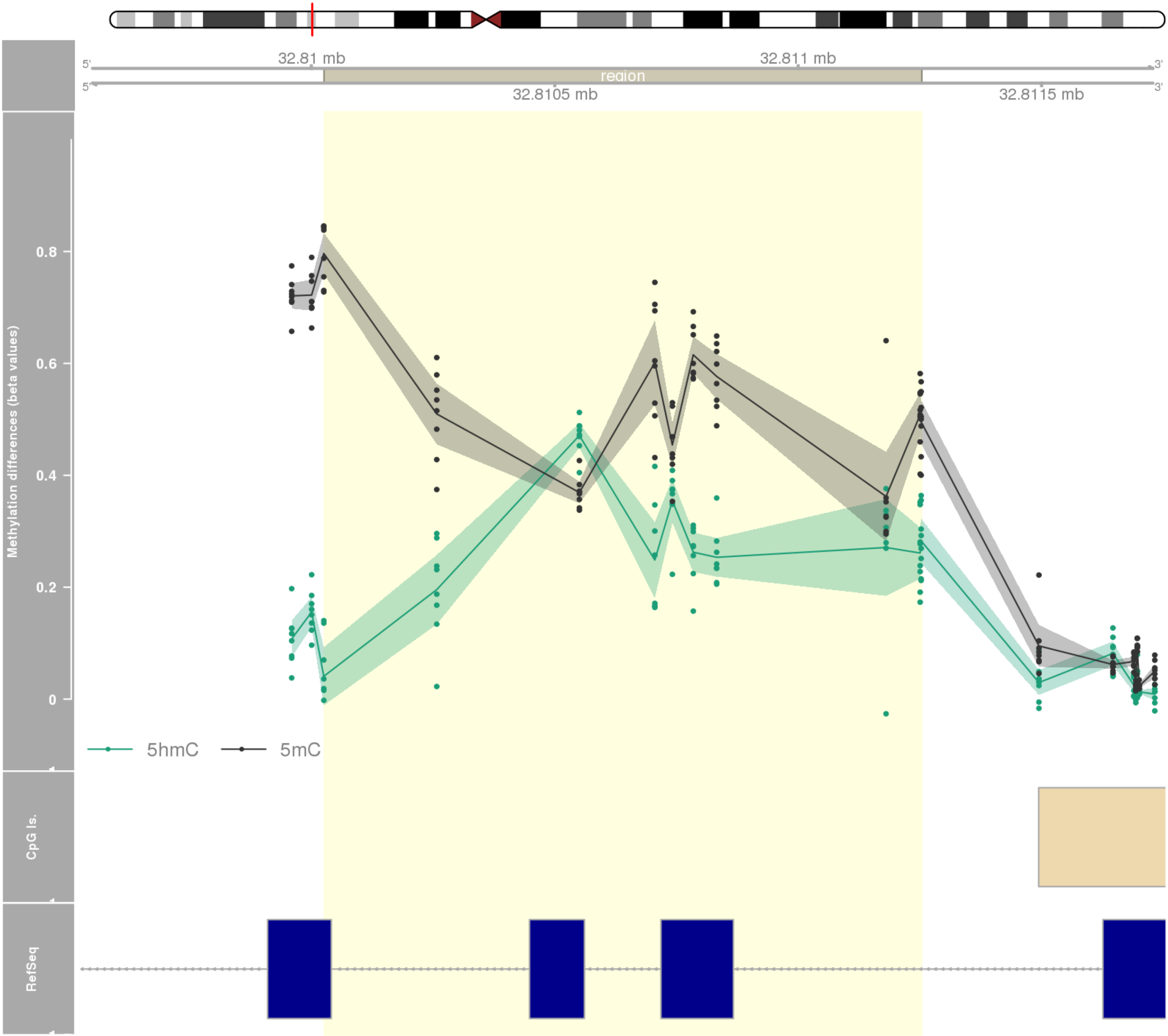
DMR 385 // chr11:13983009-13984067 // 1058 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: SPON1 -



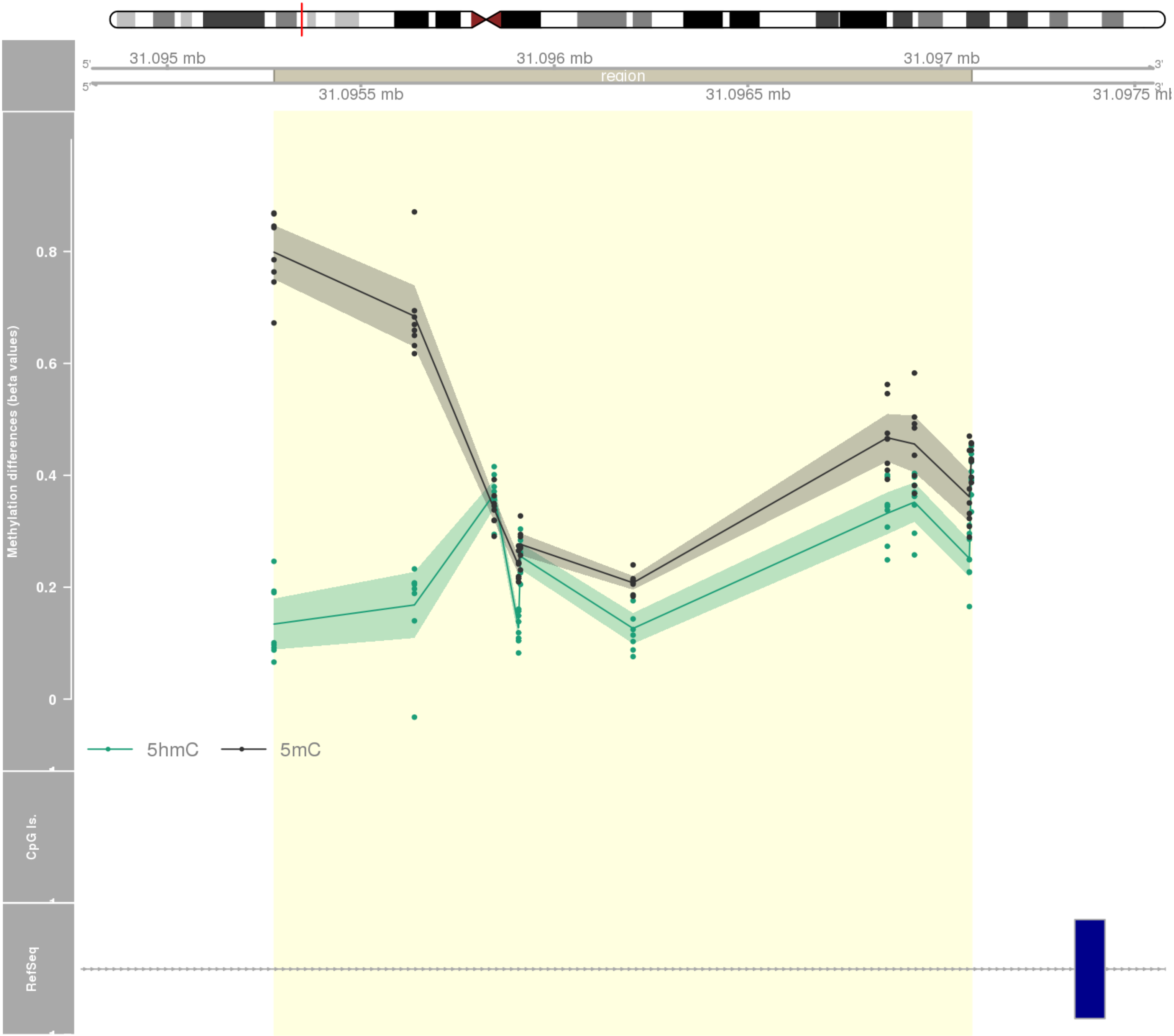
DMR 386 // chr10:135059165-135062155 // 2990 pb. (15 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: MIR202HG -



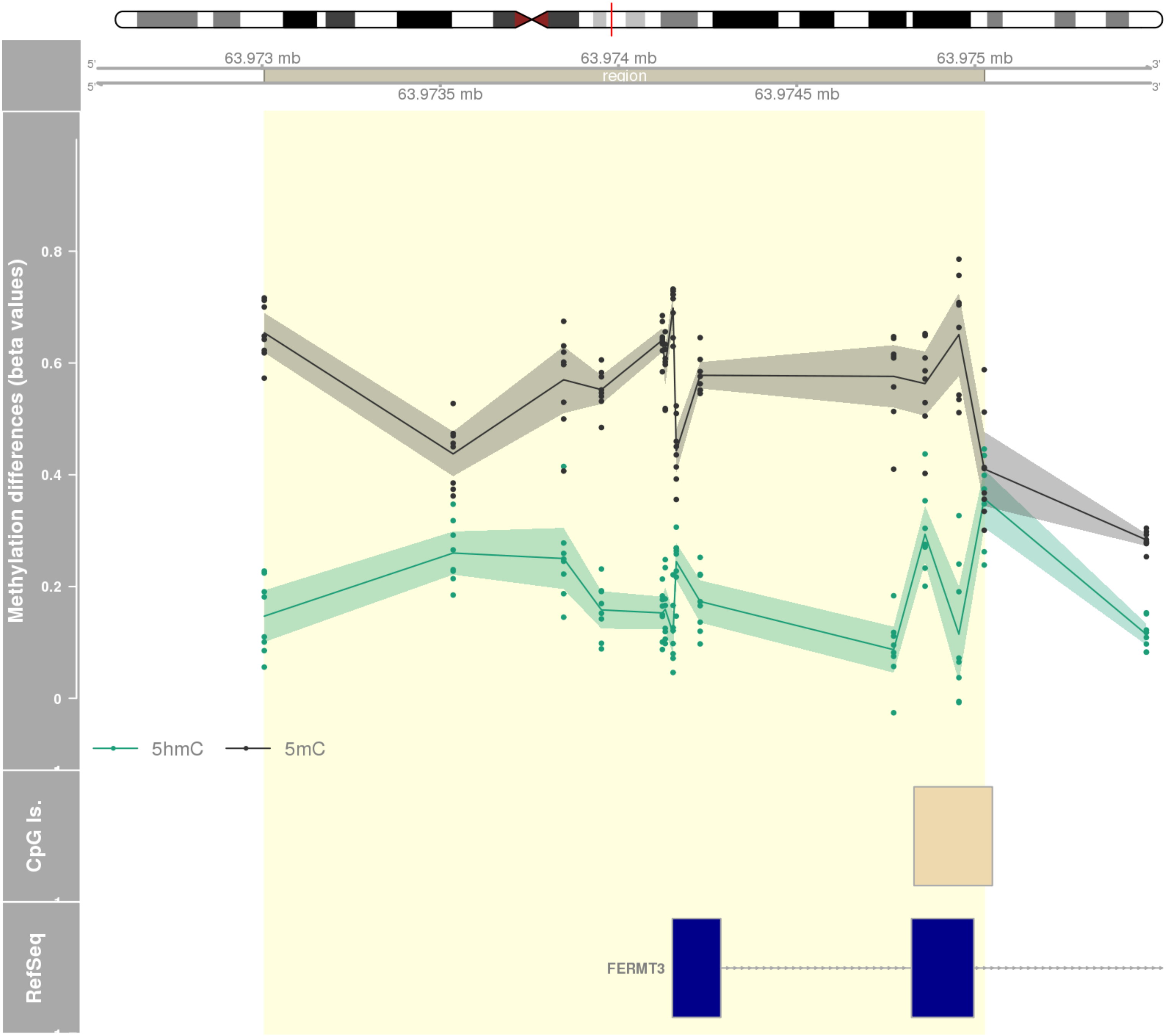
DMR 387 // chr6:32810026-32811253 // 1227 pb. (10 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: PSMB8 -



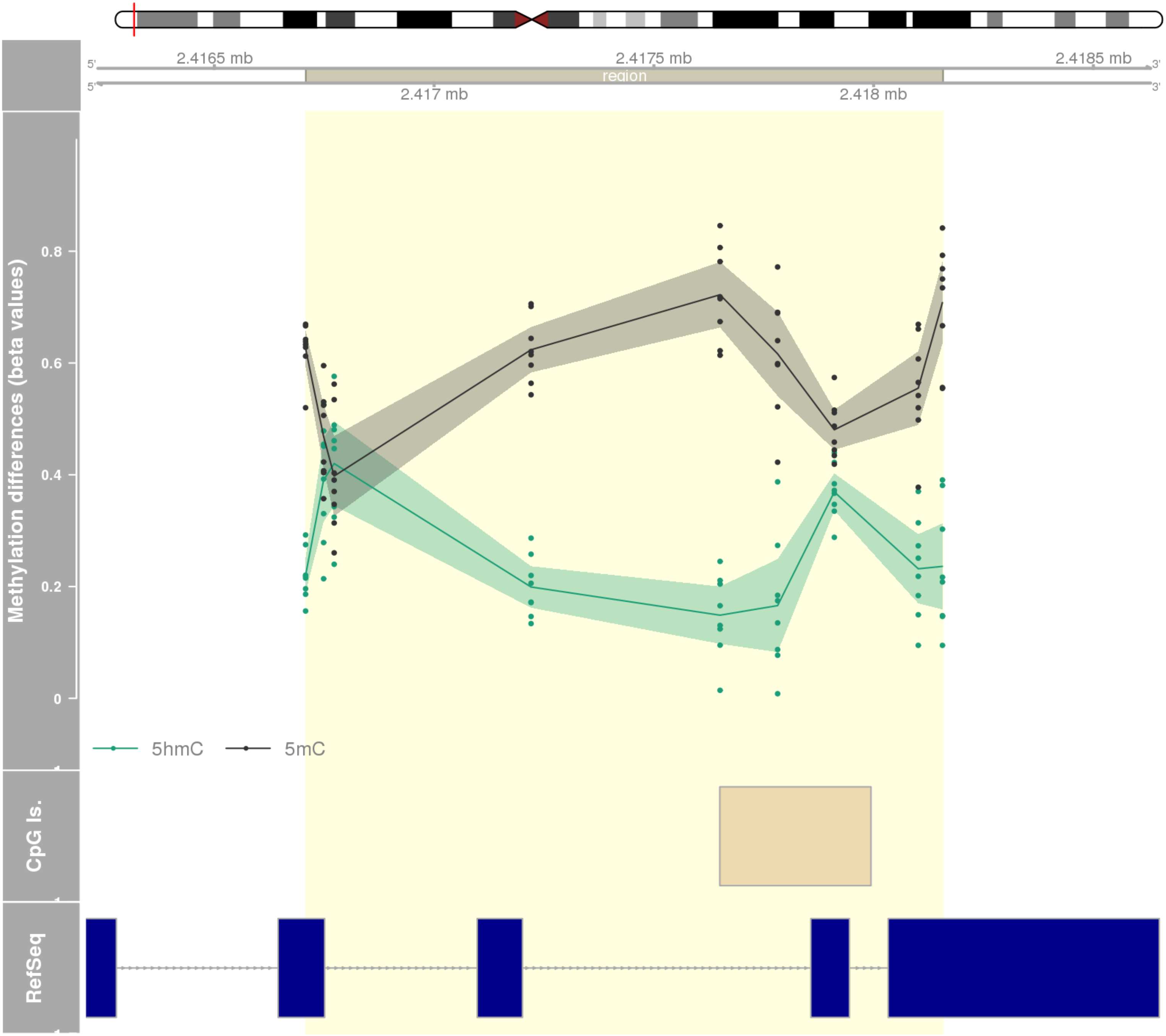
DMR 388 // chr6:31095276-31097078 // 1802 pb. (10 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: PSORS1C1 -



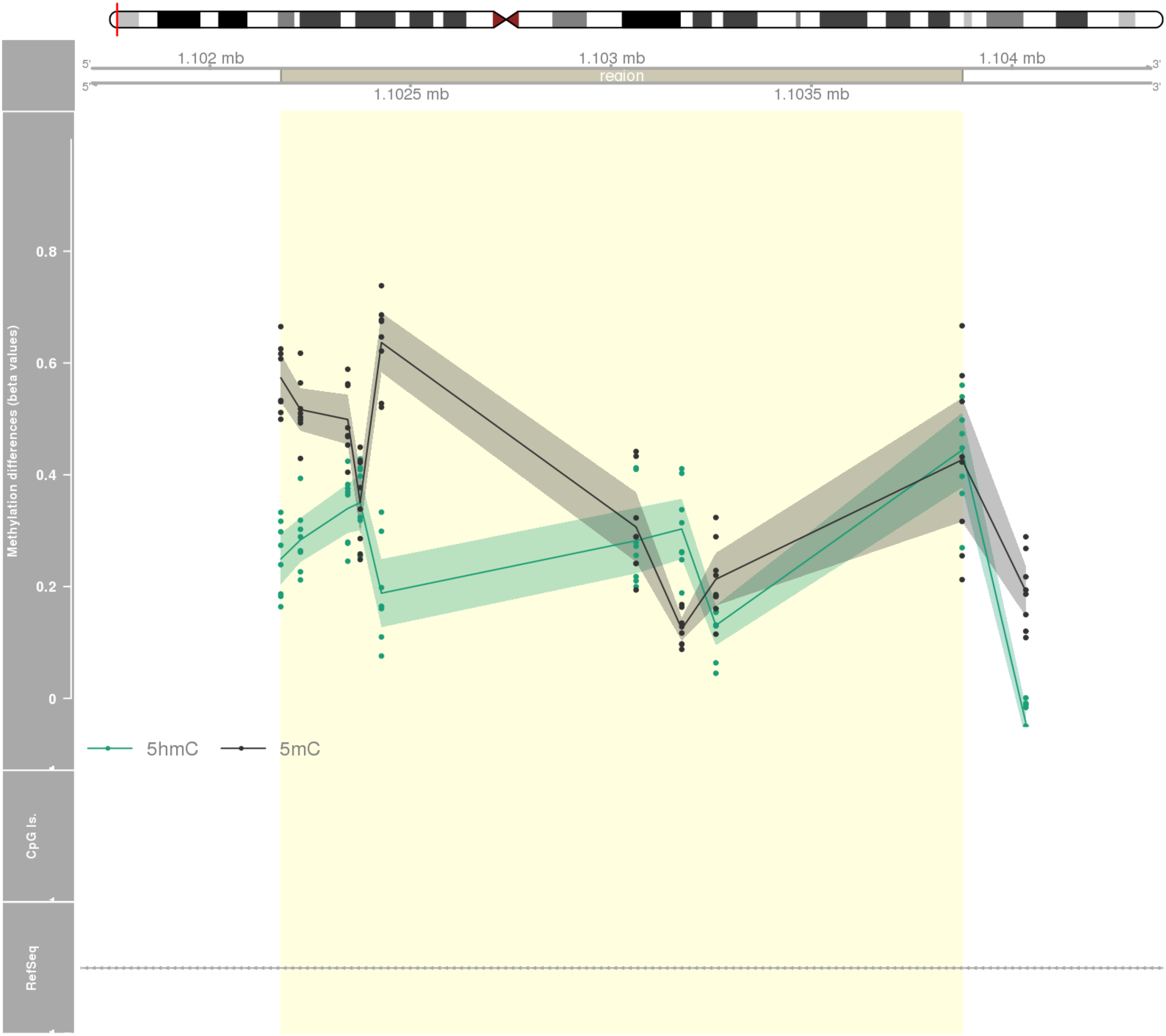
DMR 389 // chr11:63973006-63975026 // 2020 pb. (13 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: FERMT3 -



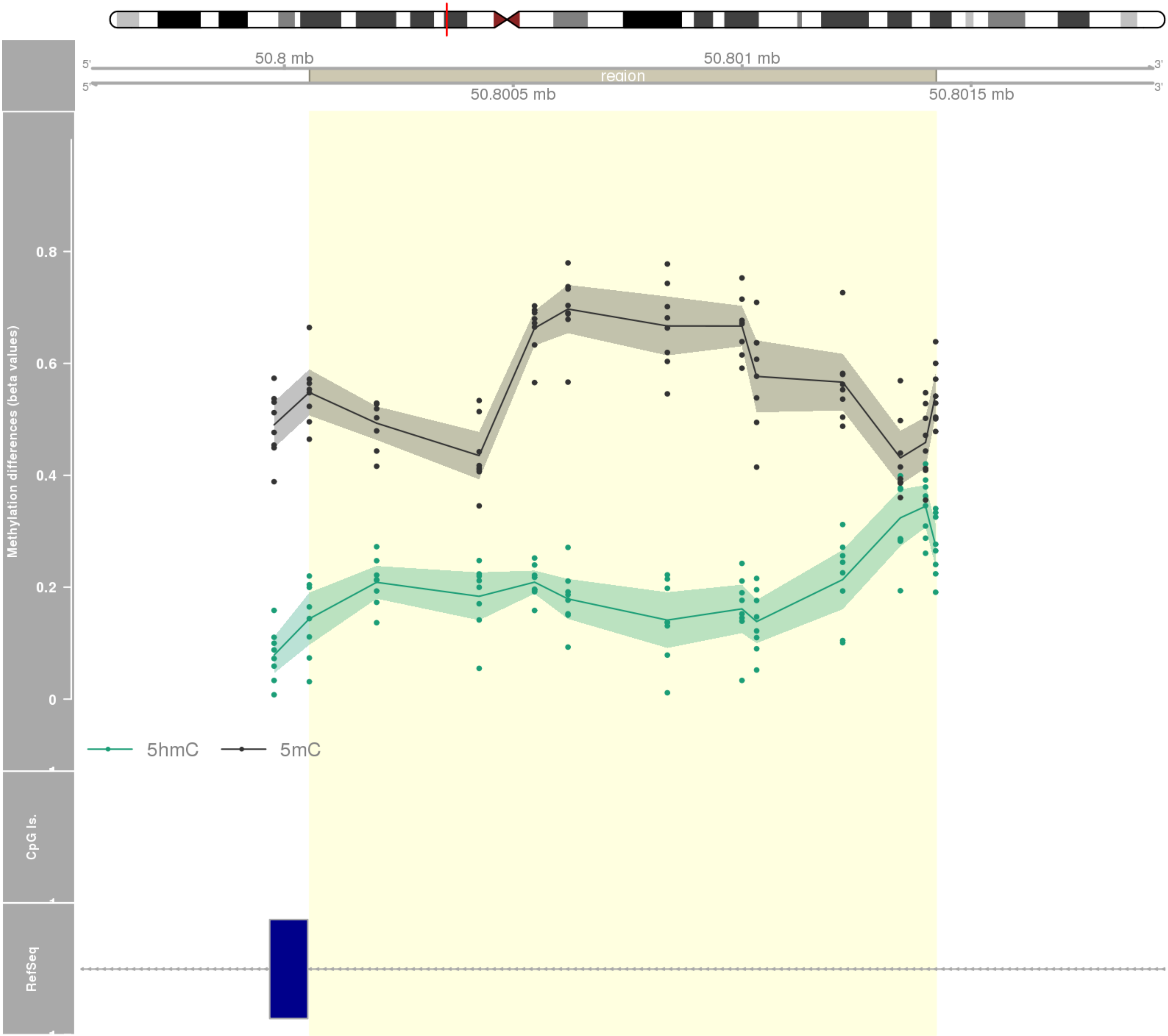
DMR 390 // chr11:2416708-2418157 // 1449 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: CD81 -



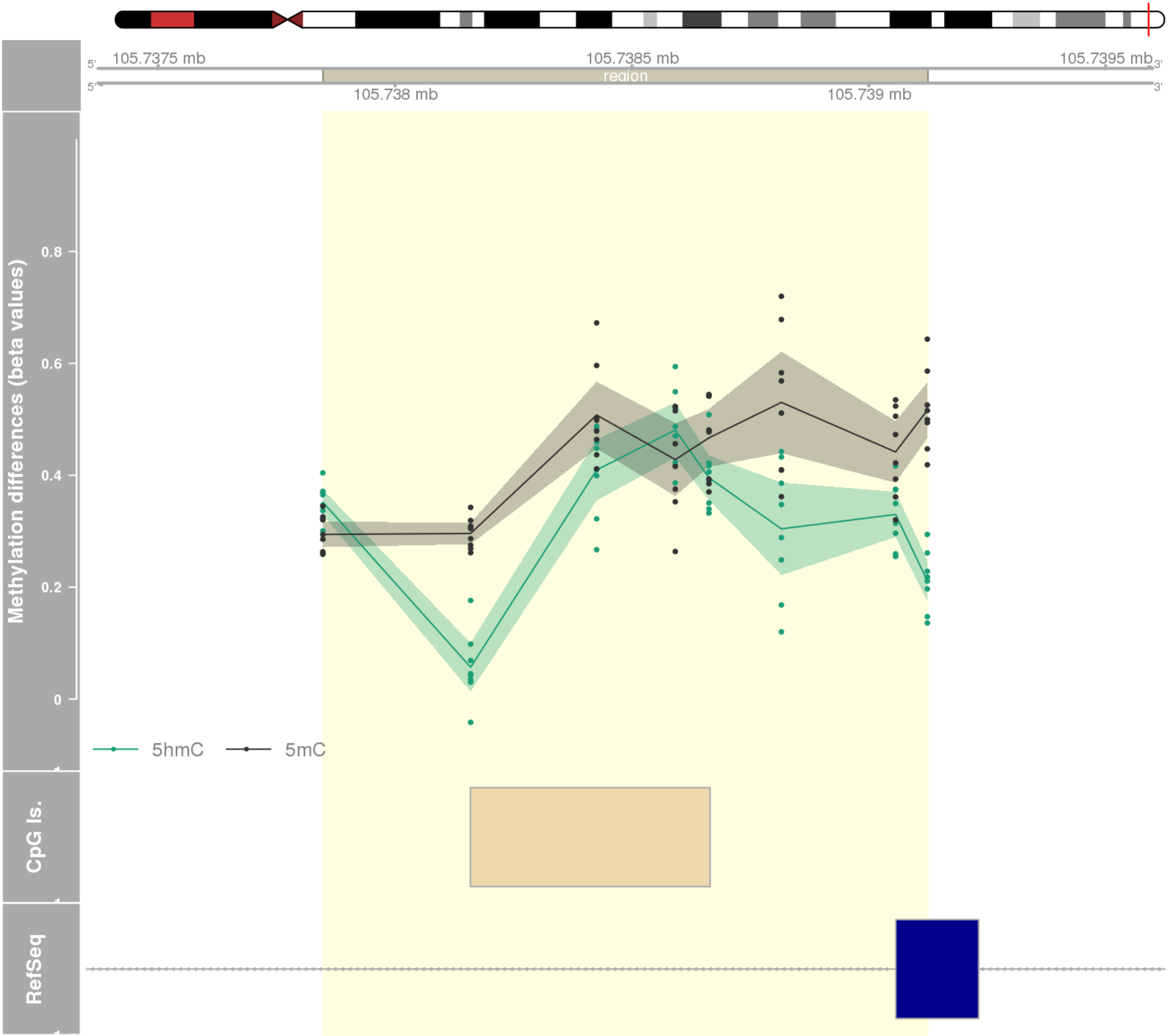
DMR 391 // chr7:1102177-1103876 // 1699 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: C7orf50 -



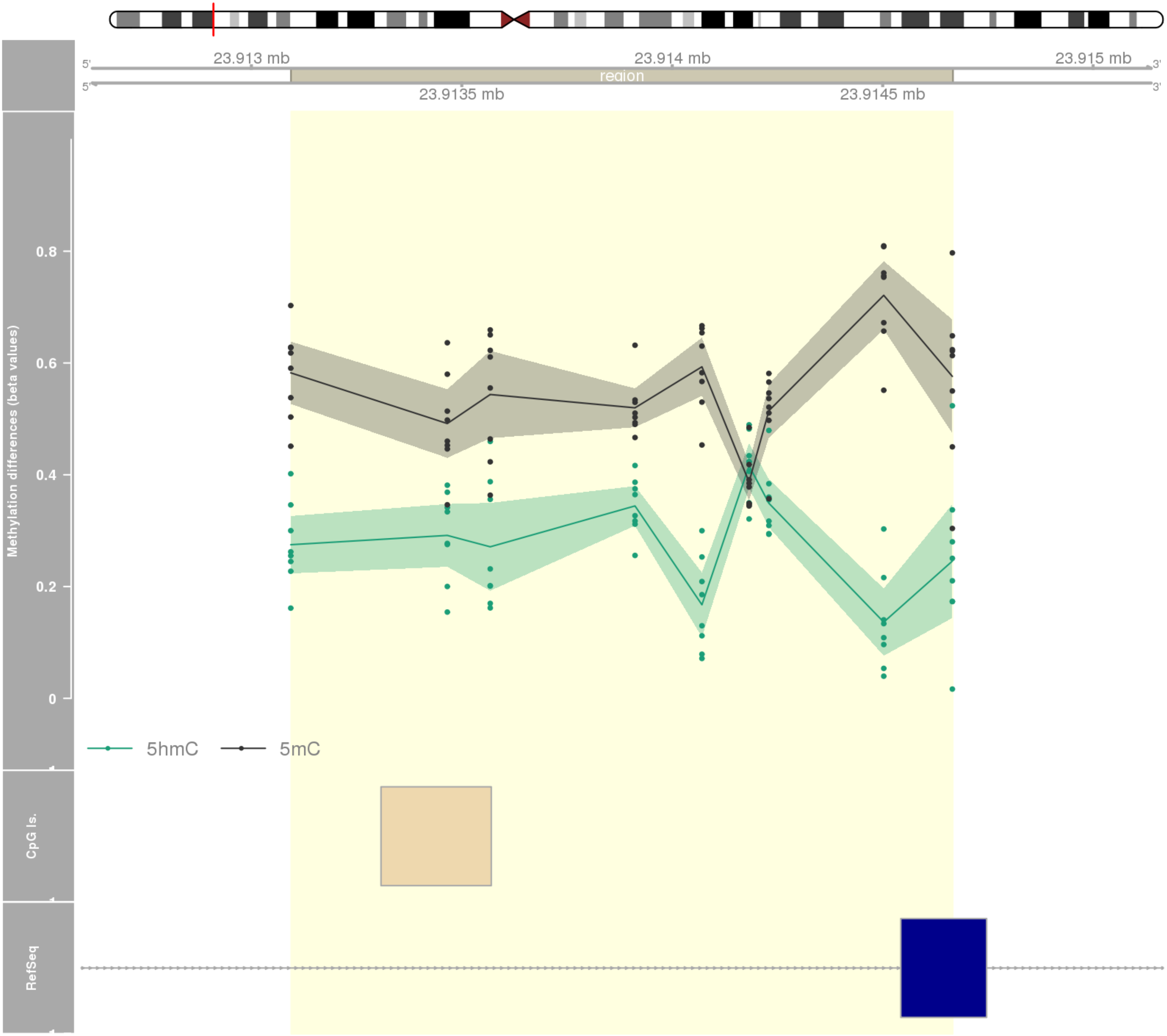
DMR 392 // chr7:50800055-50801423 // 1368 pb. (12 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: GRB10 -



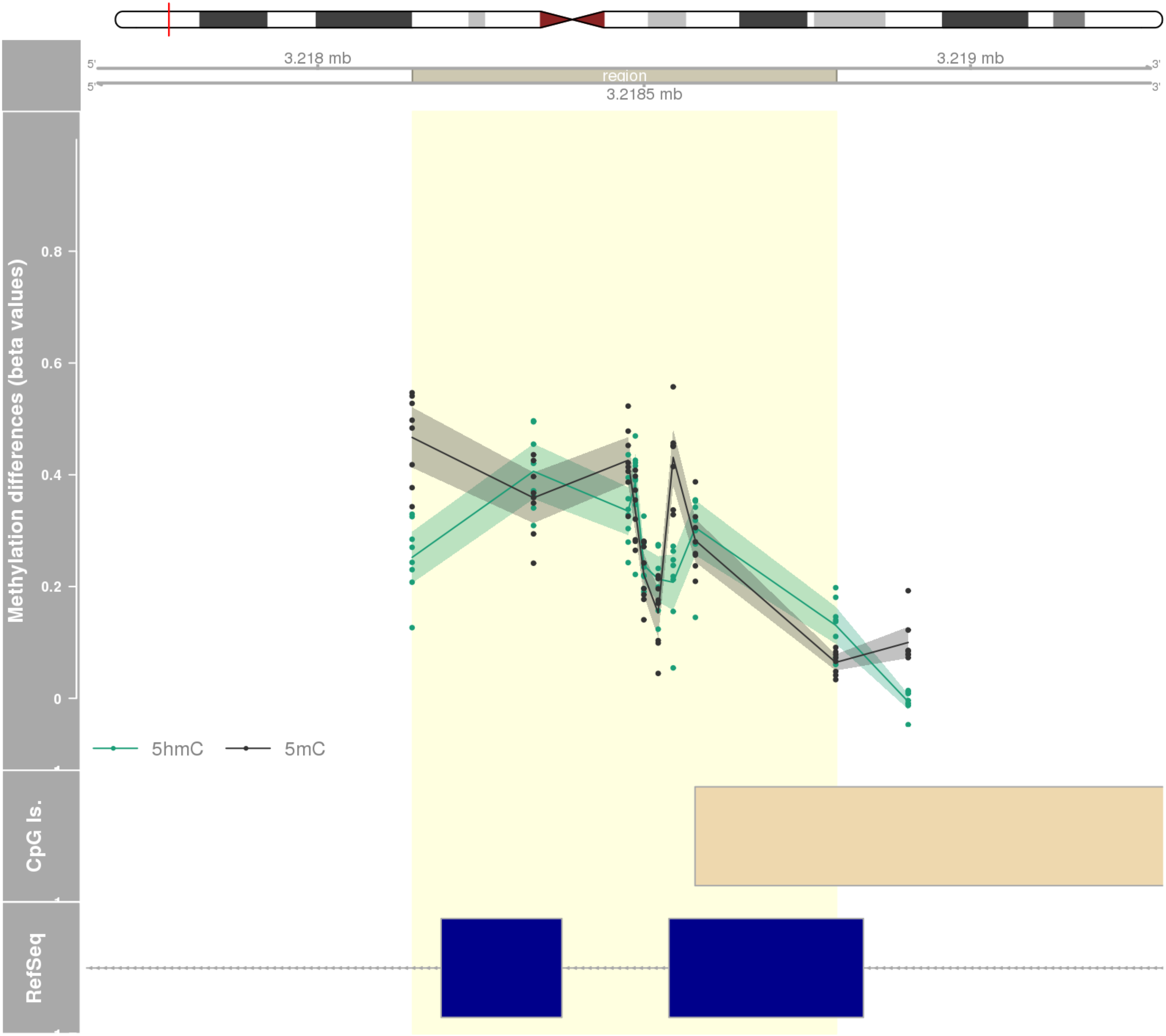
DMR 393 // chr14:105737848-105739124 // 1276 pb. (8 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: BRF1 -



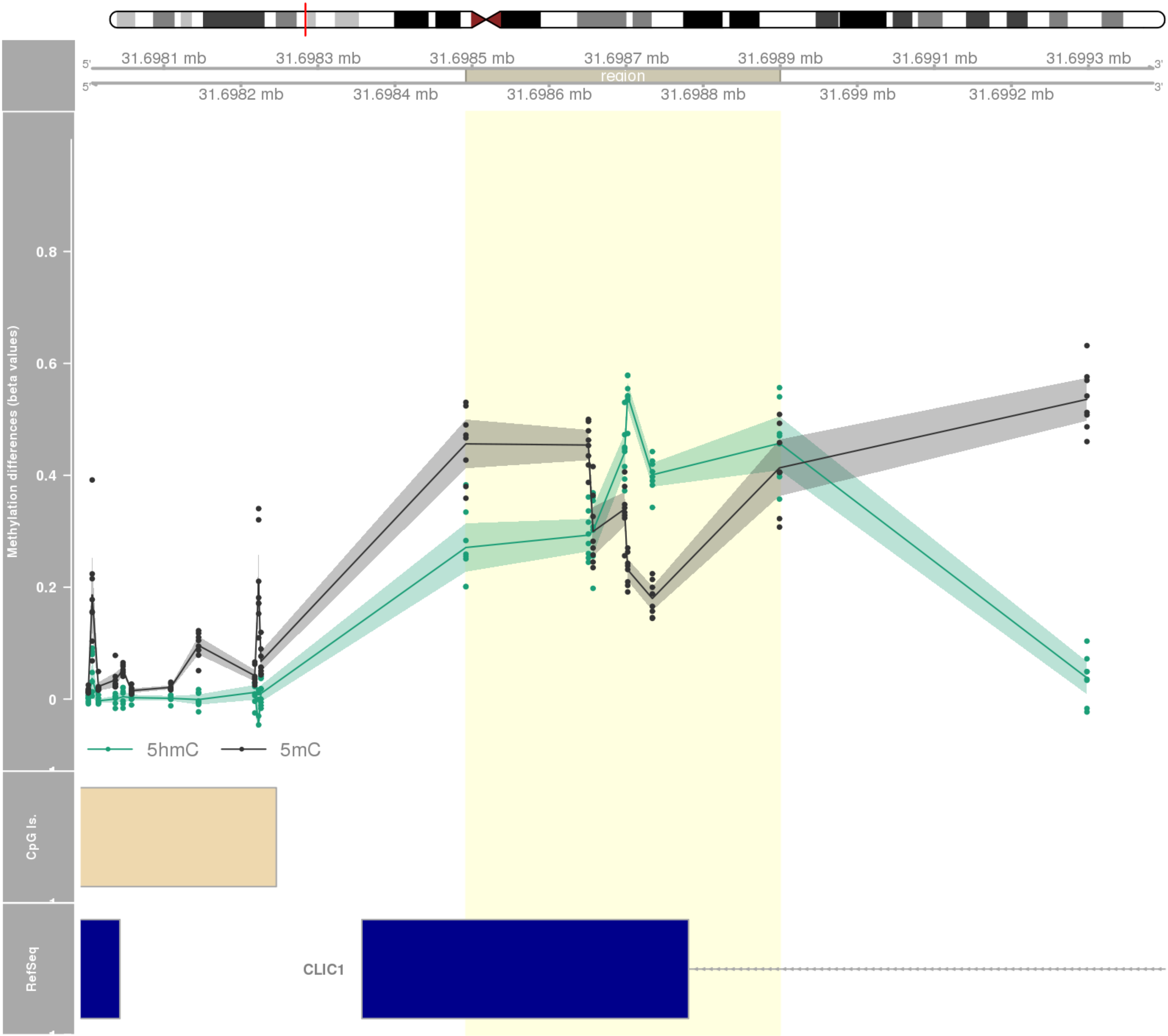
DMR 394 // chr2:23913094-23914666 // 1572 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: KLHL29 -



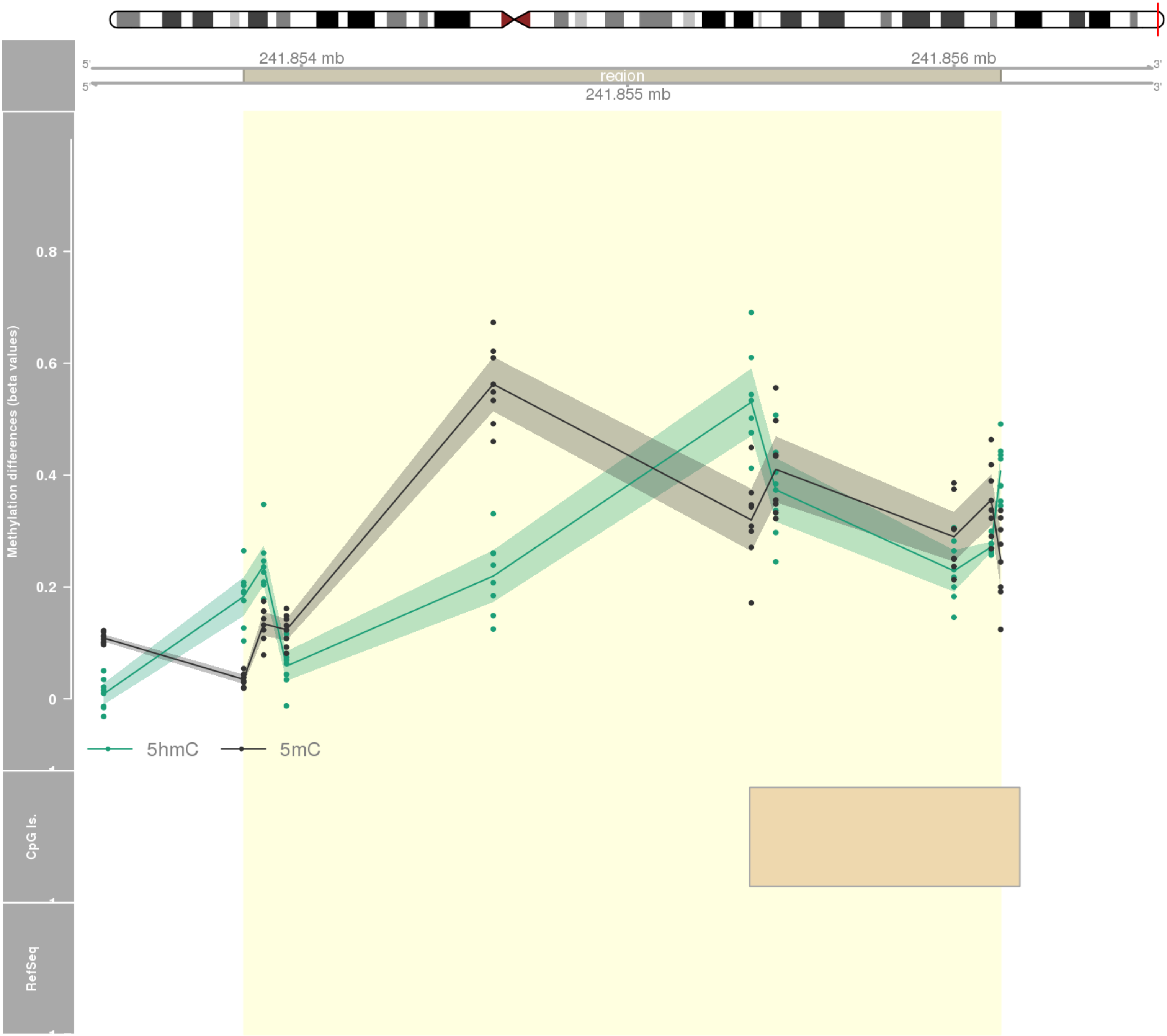
DMR 395 // chr20:3218145-3218794 // 649 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.02 // fwerArea: 0.559
- genes: SLC4A11 -



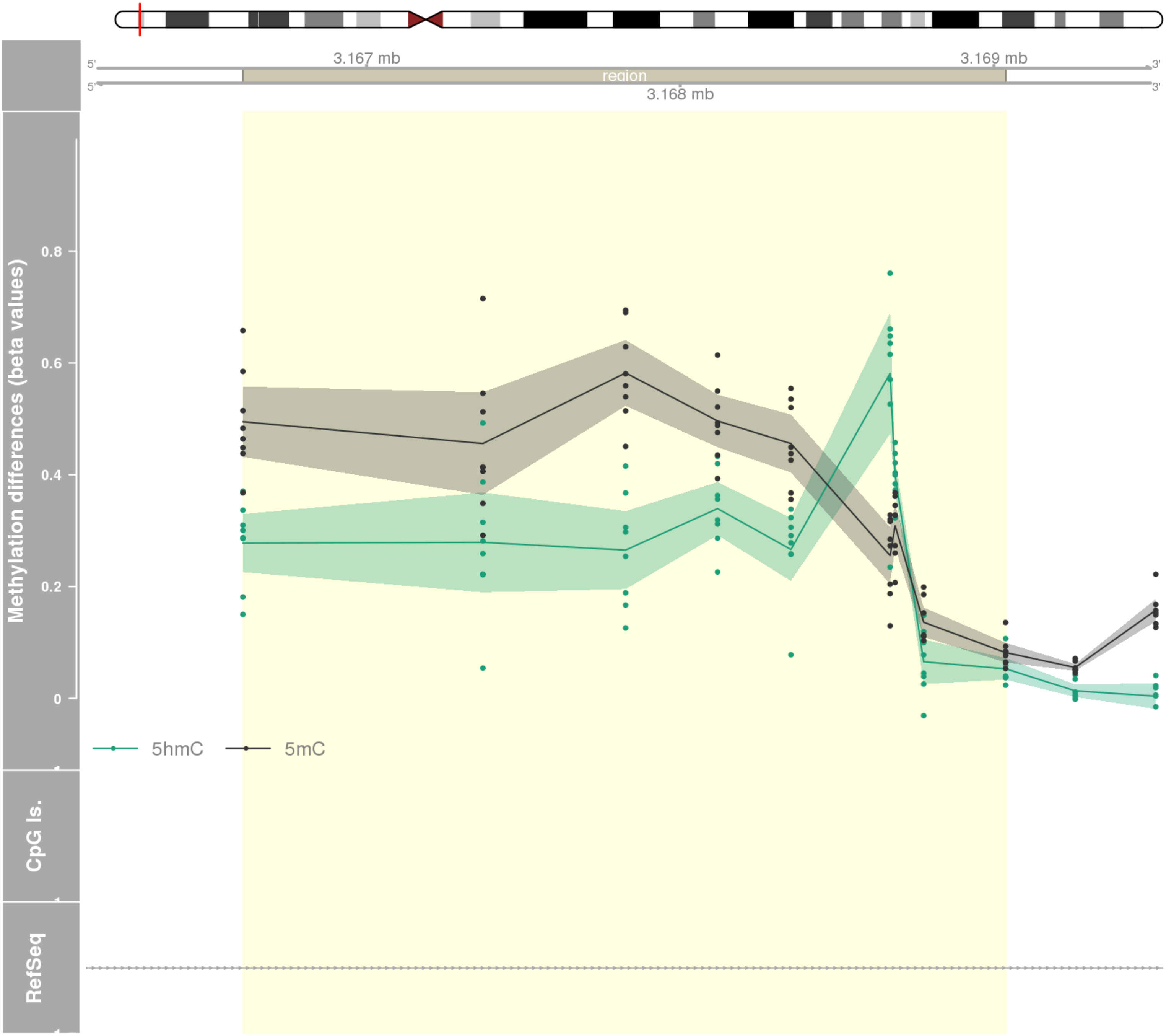
DMR 396 // chr6:31698492-31698899 // 407 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: CLIC1 -



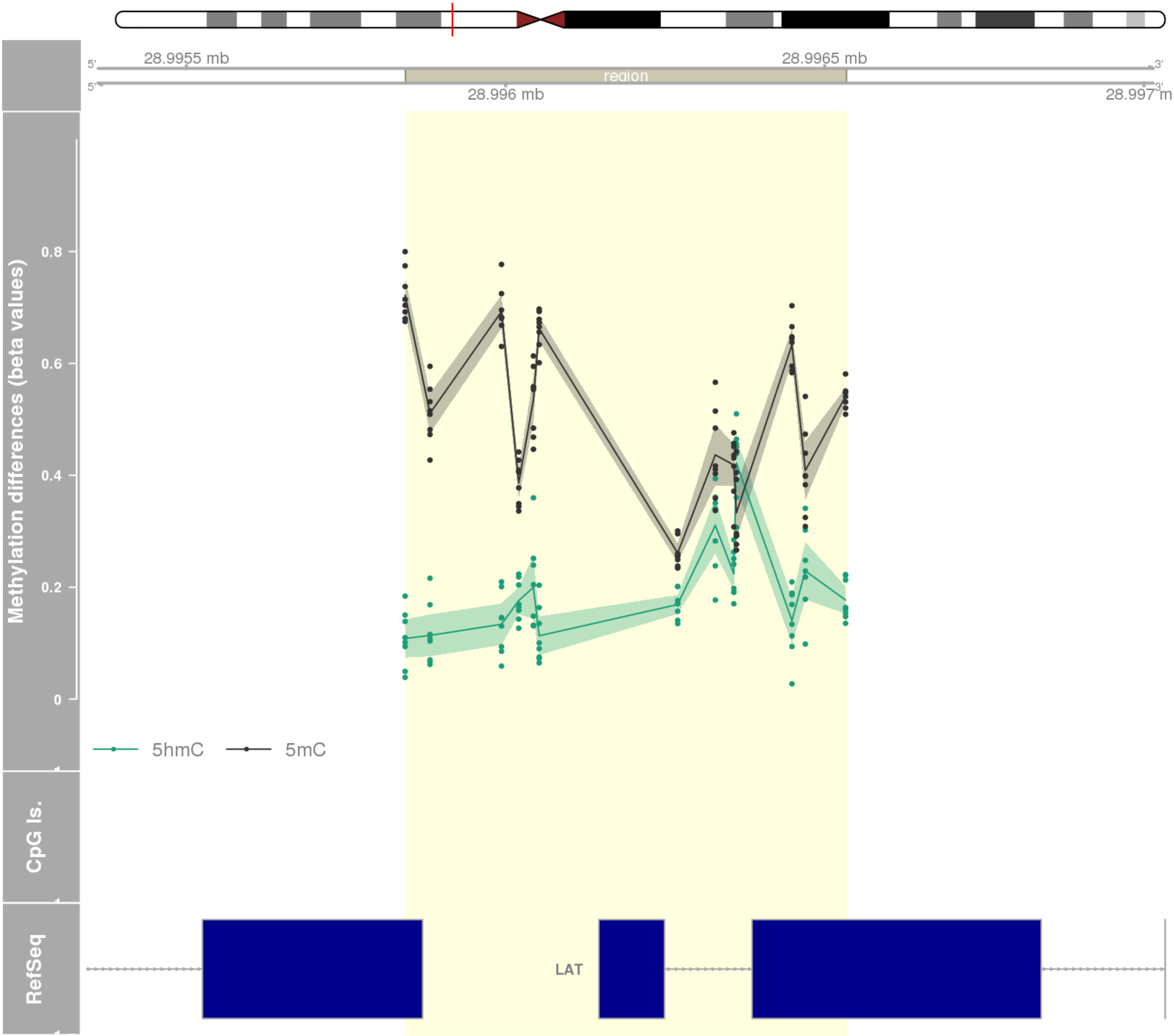
DMR 397 // chr2:241853823-241856143 // 2320 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559



DMR 398 // chr10:3166606-3169037 // 2431 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: PFKP -

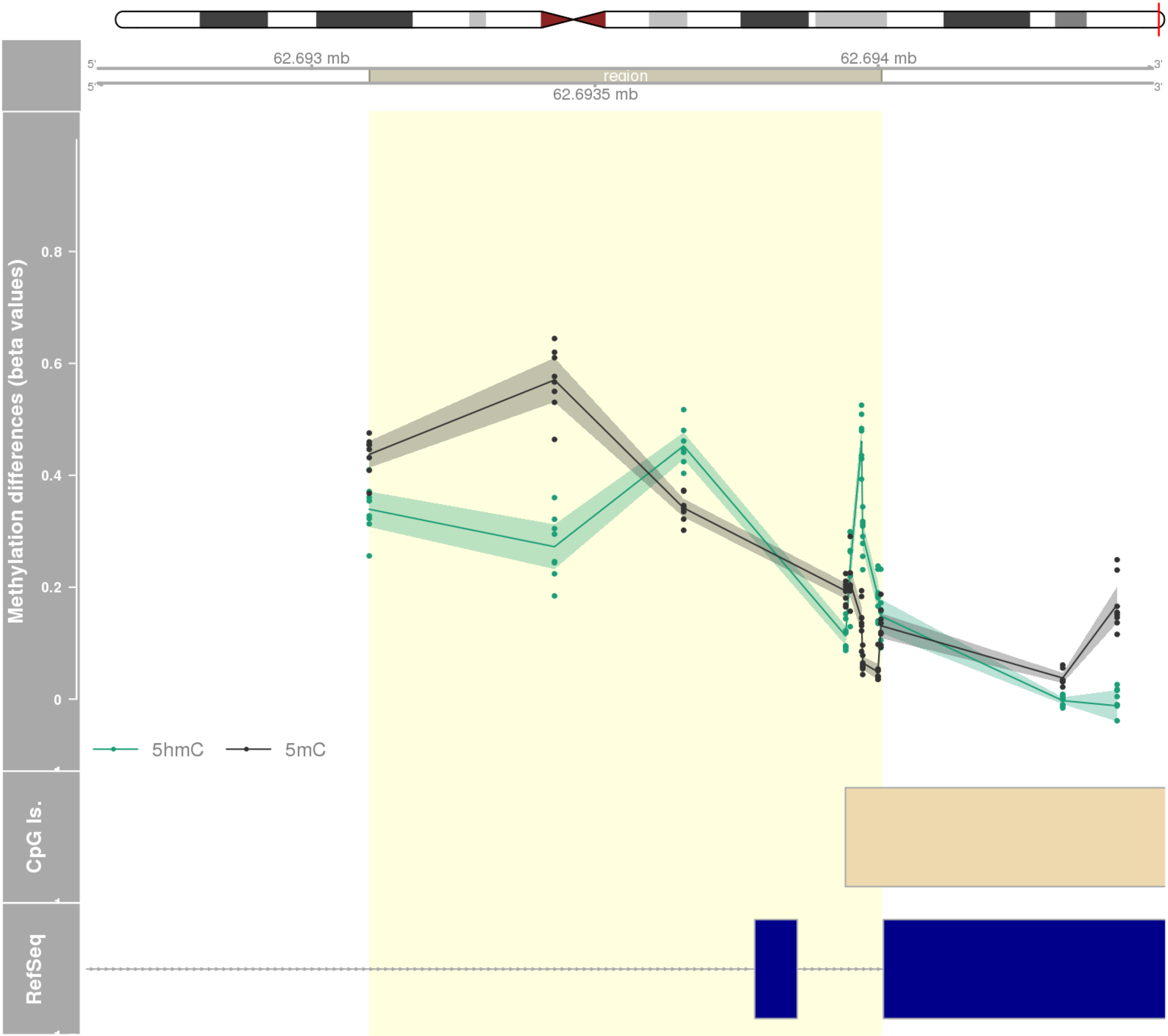


DMR 399 // chr16:28995843-28996533 // 690 pb. (13 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: SPNS1 / LAT -

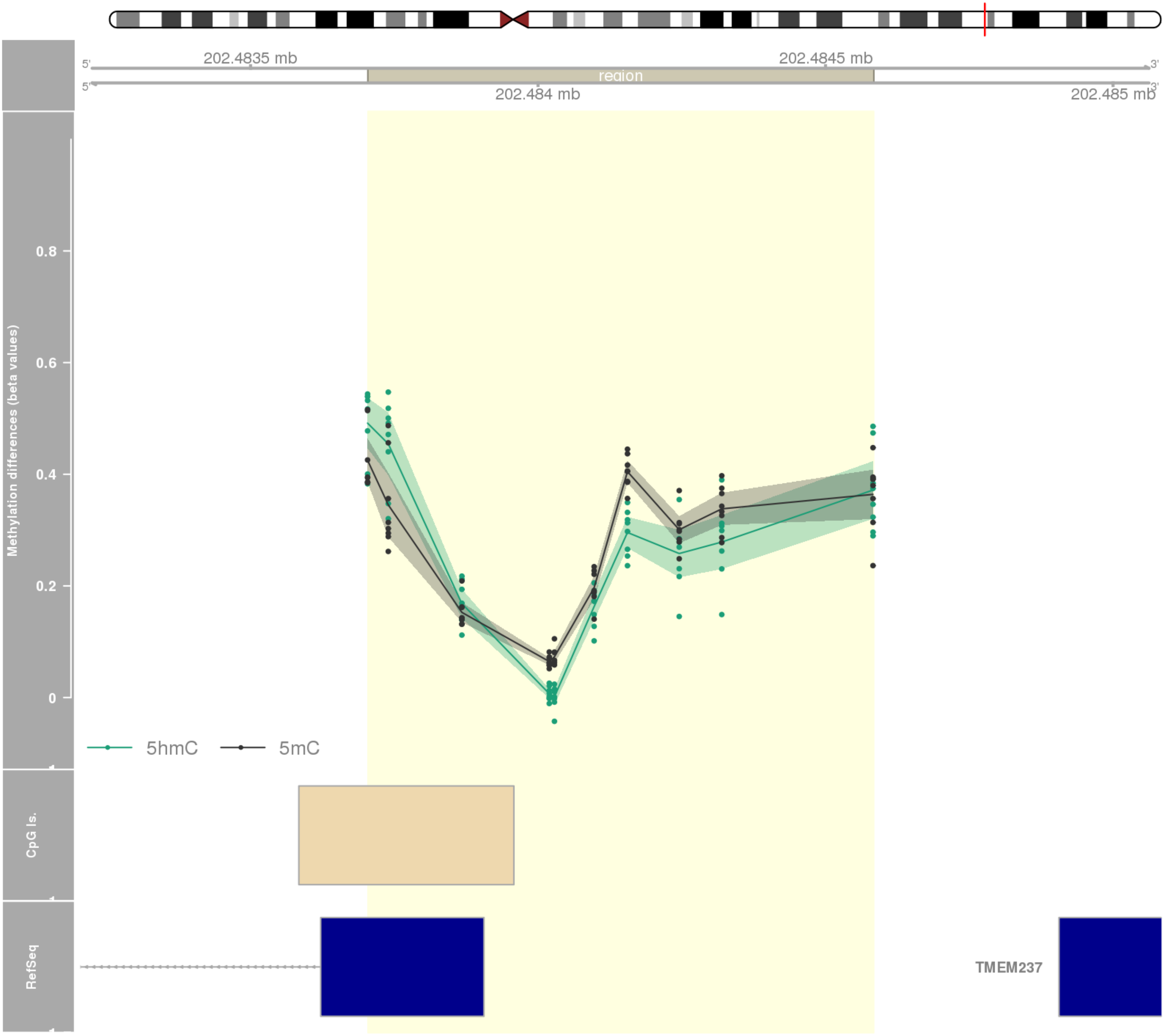


DMR 400 // chr22:19118165-19120047 // 1882 pb. (10 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: DGCR14 / TSSK2 -

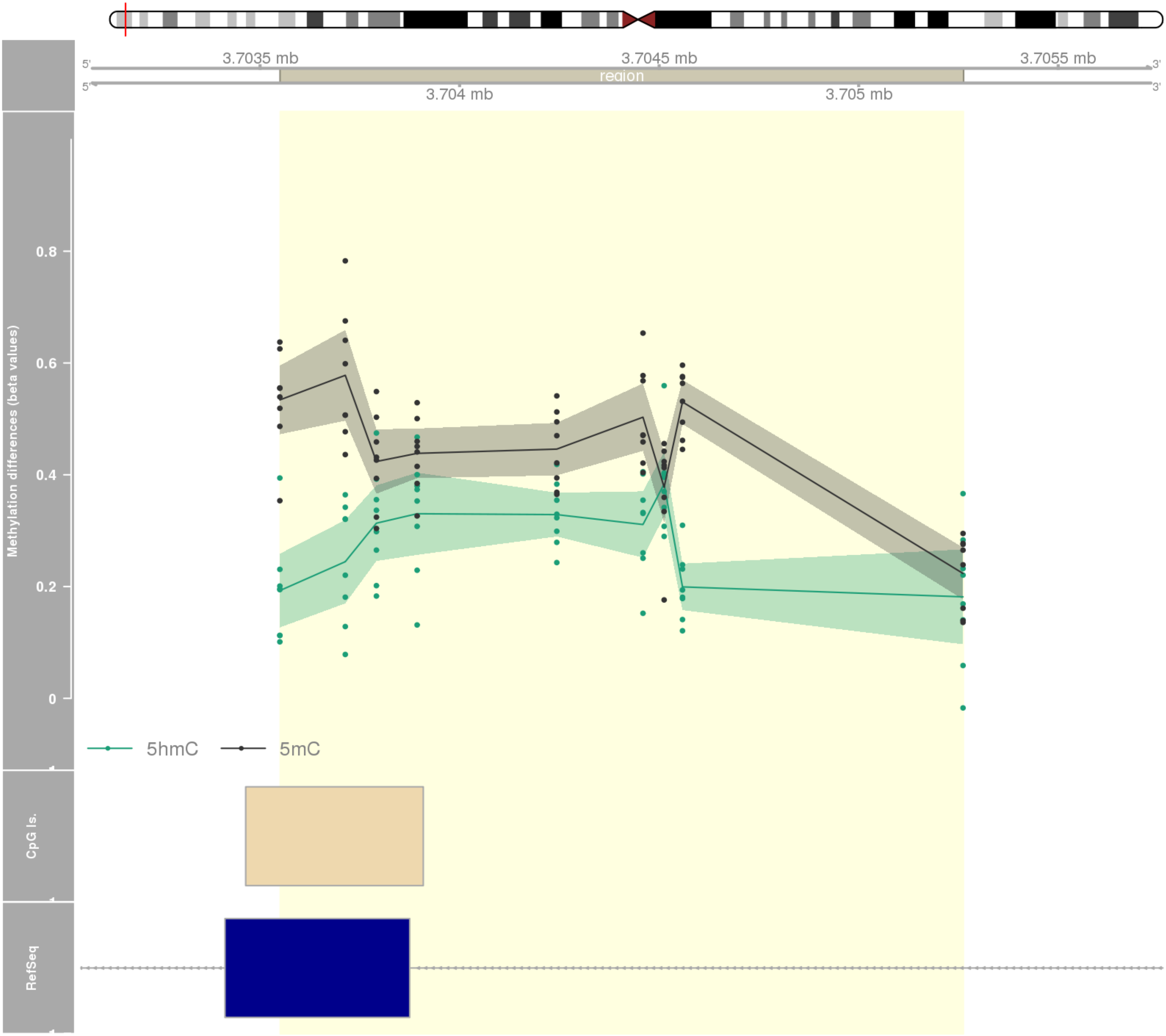
DMR 401 // chr20:62693102-62694005 // 903 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: TCEA2 -



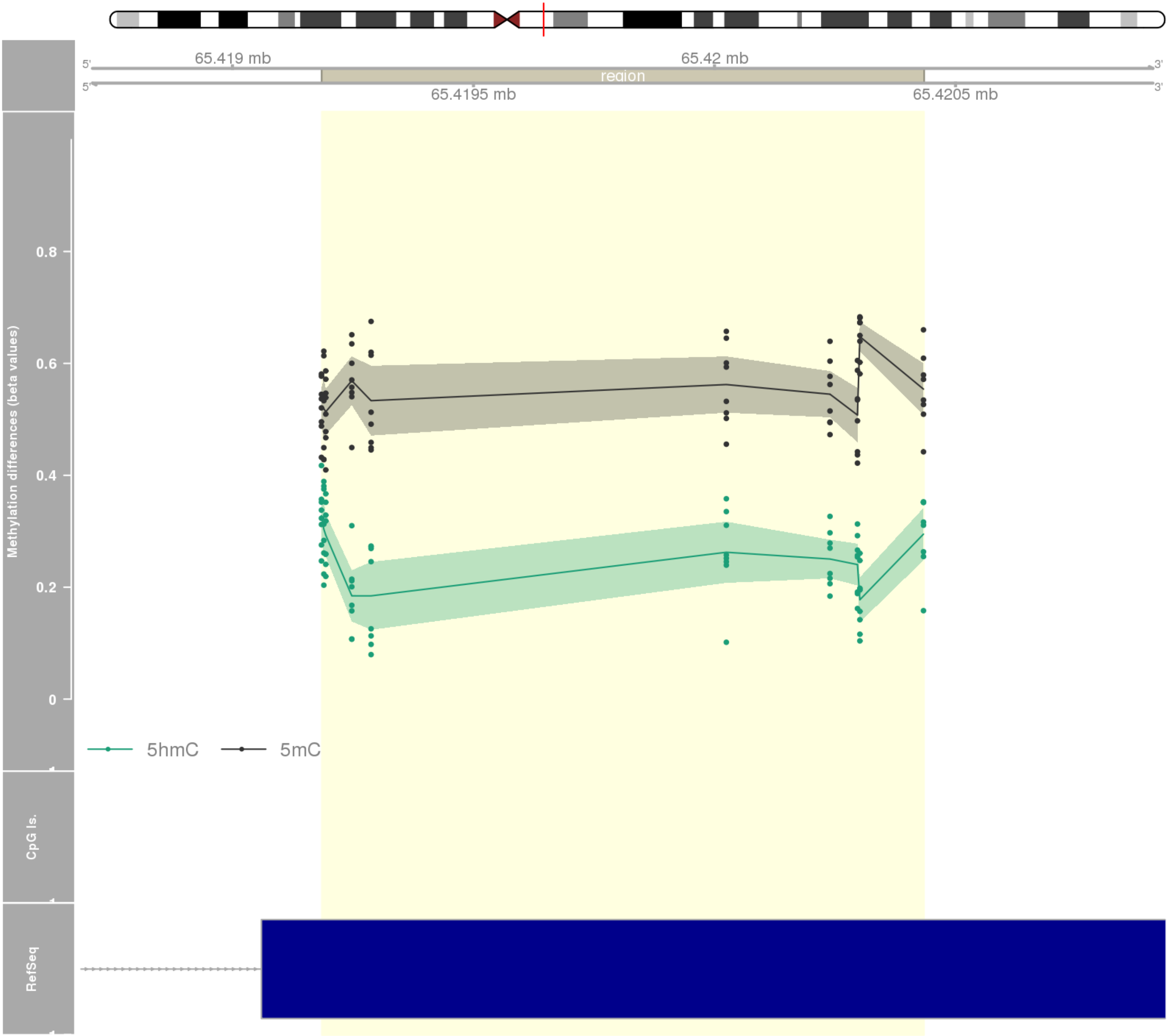
DMR 402 // chr2:202483704-202484583 // 879 pb. (10 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: ALS2CR11 -



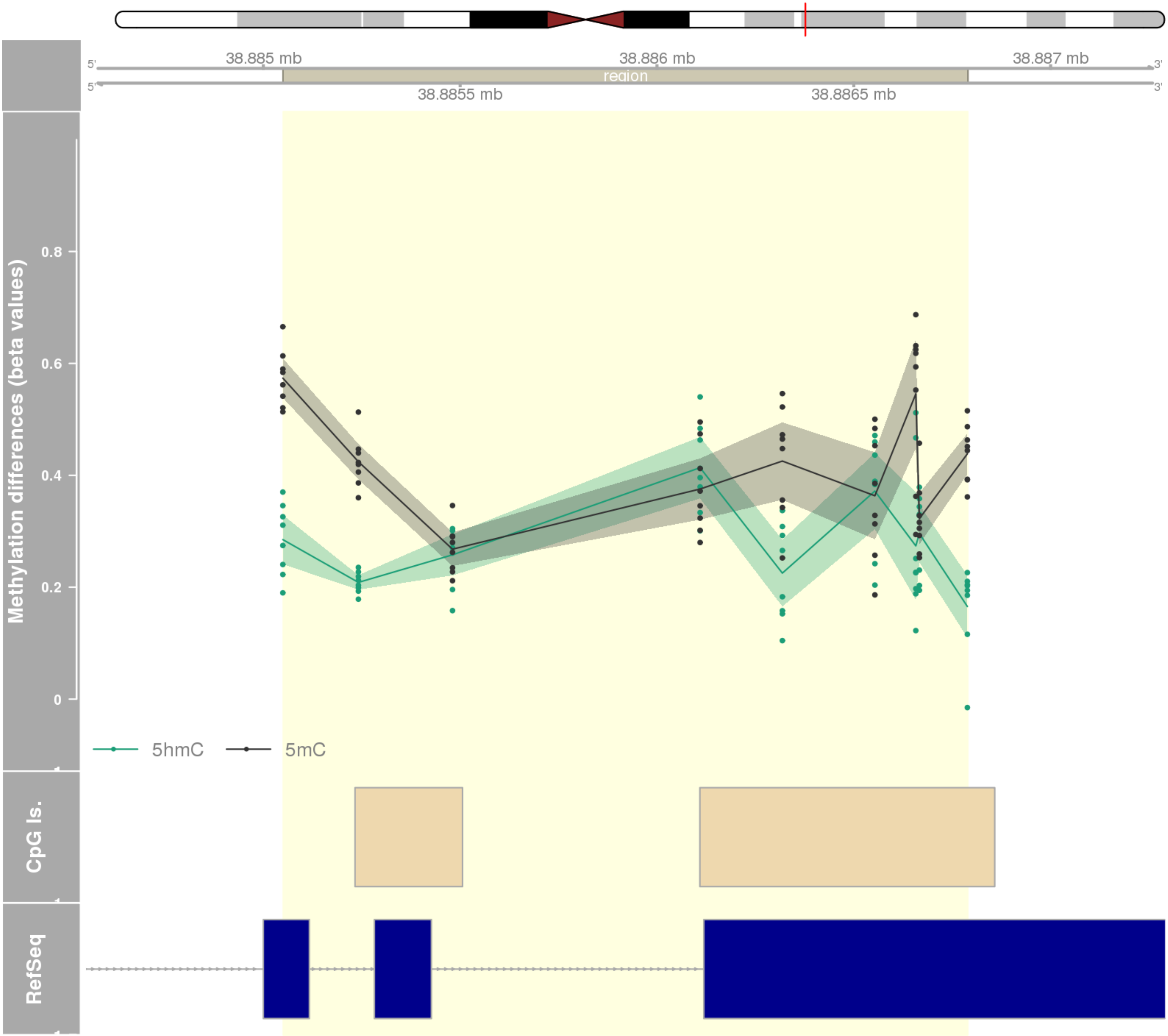
DMR 403 // chr1:3703550-3705262 // 1712 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: LRRC47 -



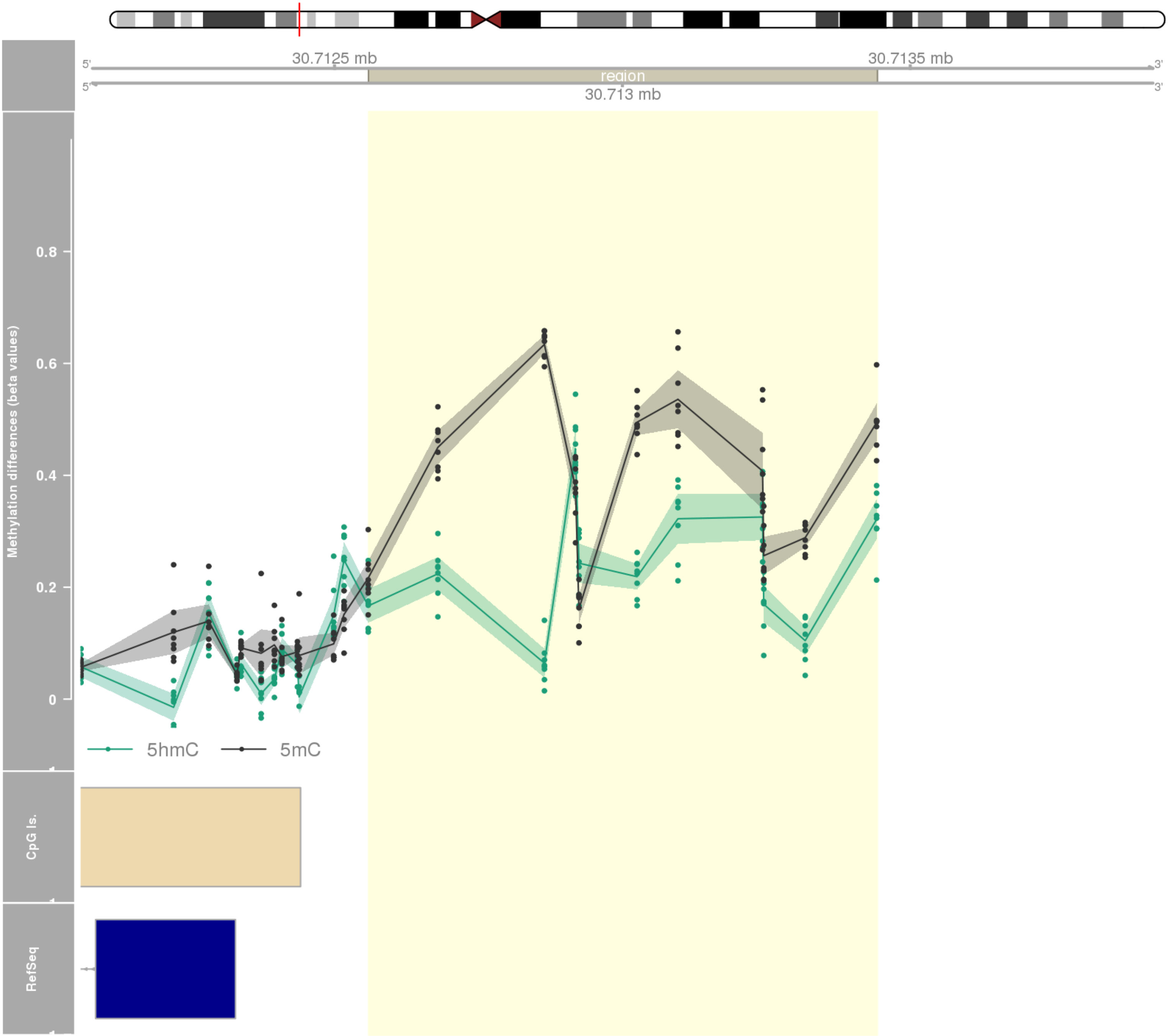
DMR 404 // chr7:65419185-65420434 // 1249 pb. (10 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: VKORC1L1 -



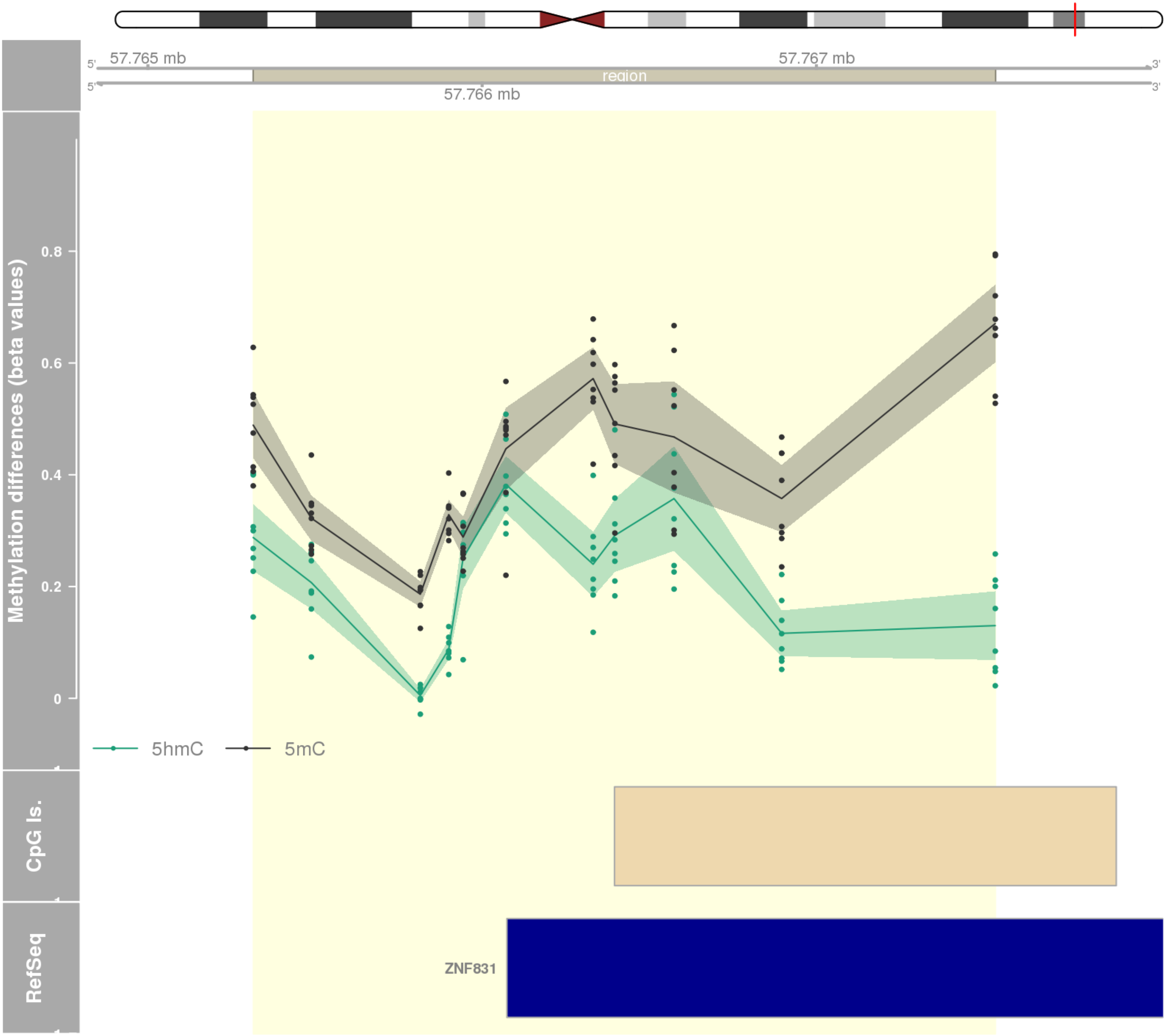
DMR 405 // chr19:38885050-38886789 // 1739 pb. (9 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: SPRED3 -



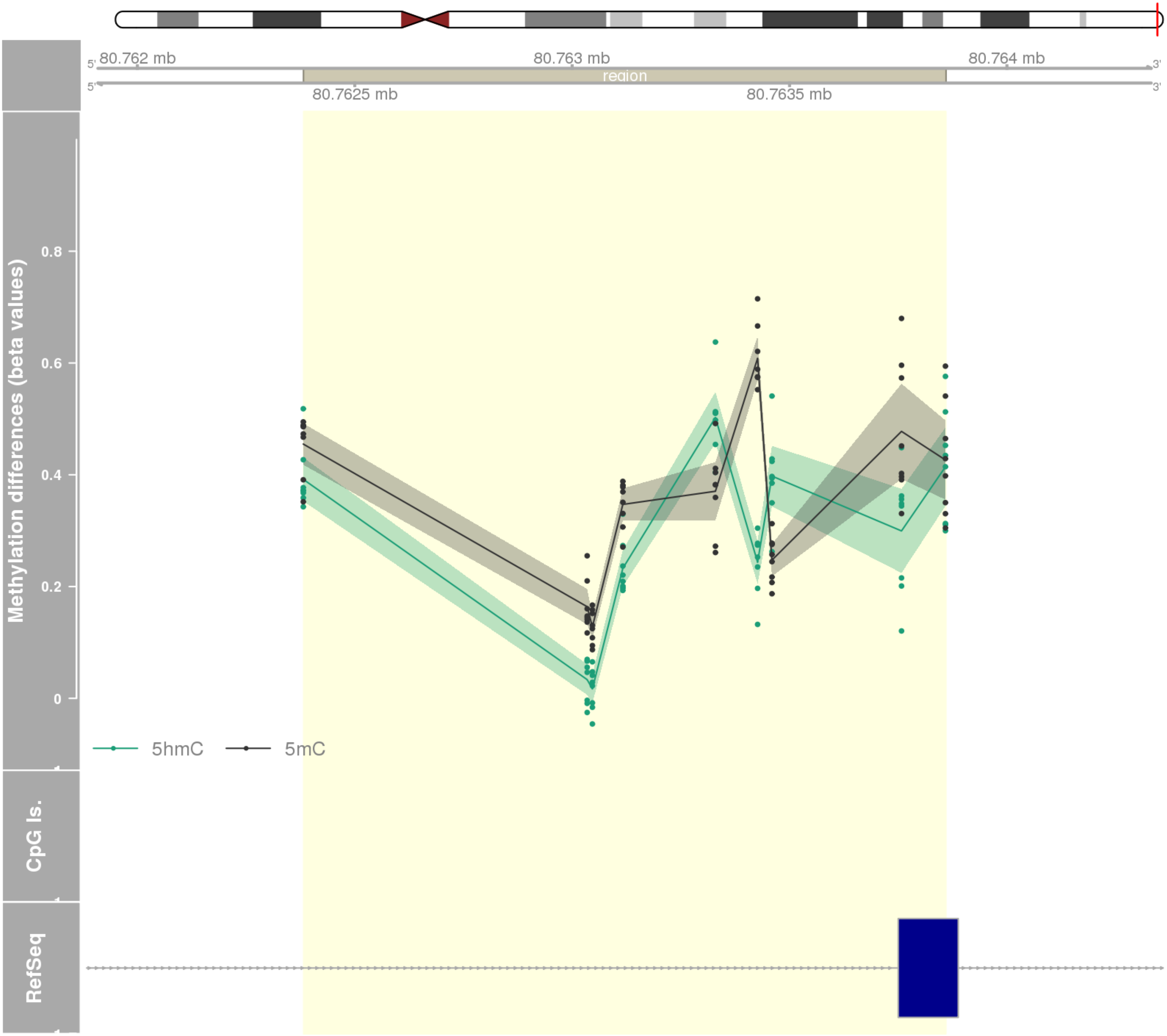
DMR 406 // chr6:30712559-30713442 // 883 pb. (11 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559



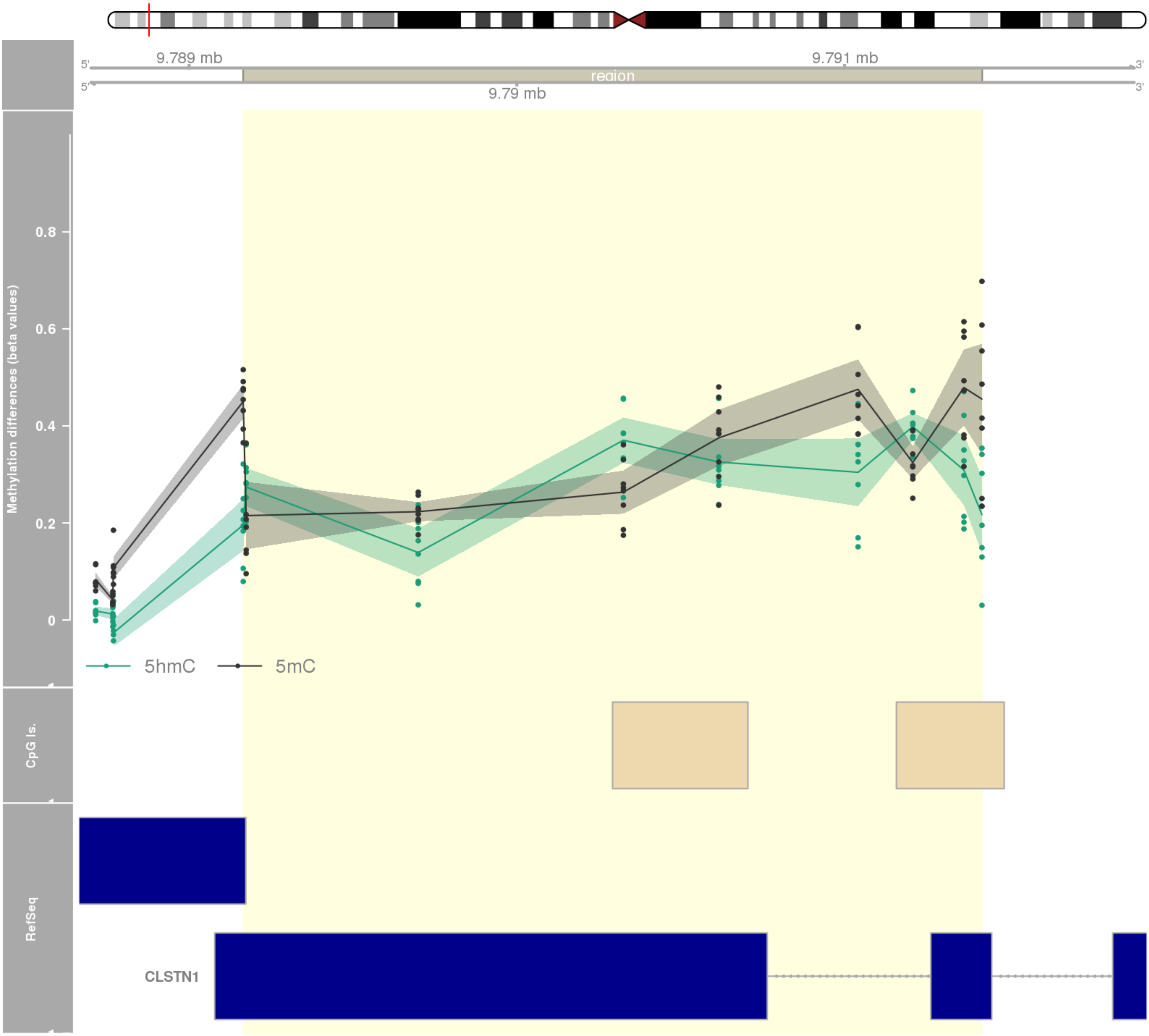
DMR 407 // chr20:57765315-57767535 // 2220 pb. (11 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: ZNF831 -



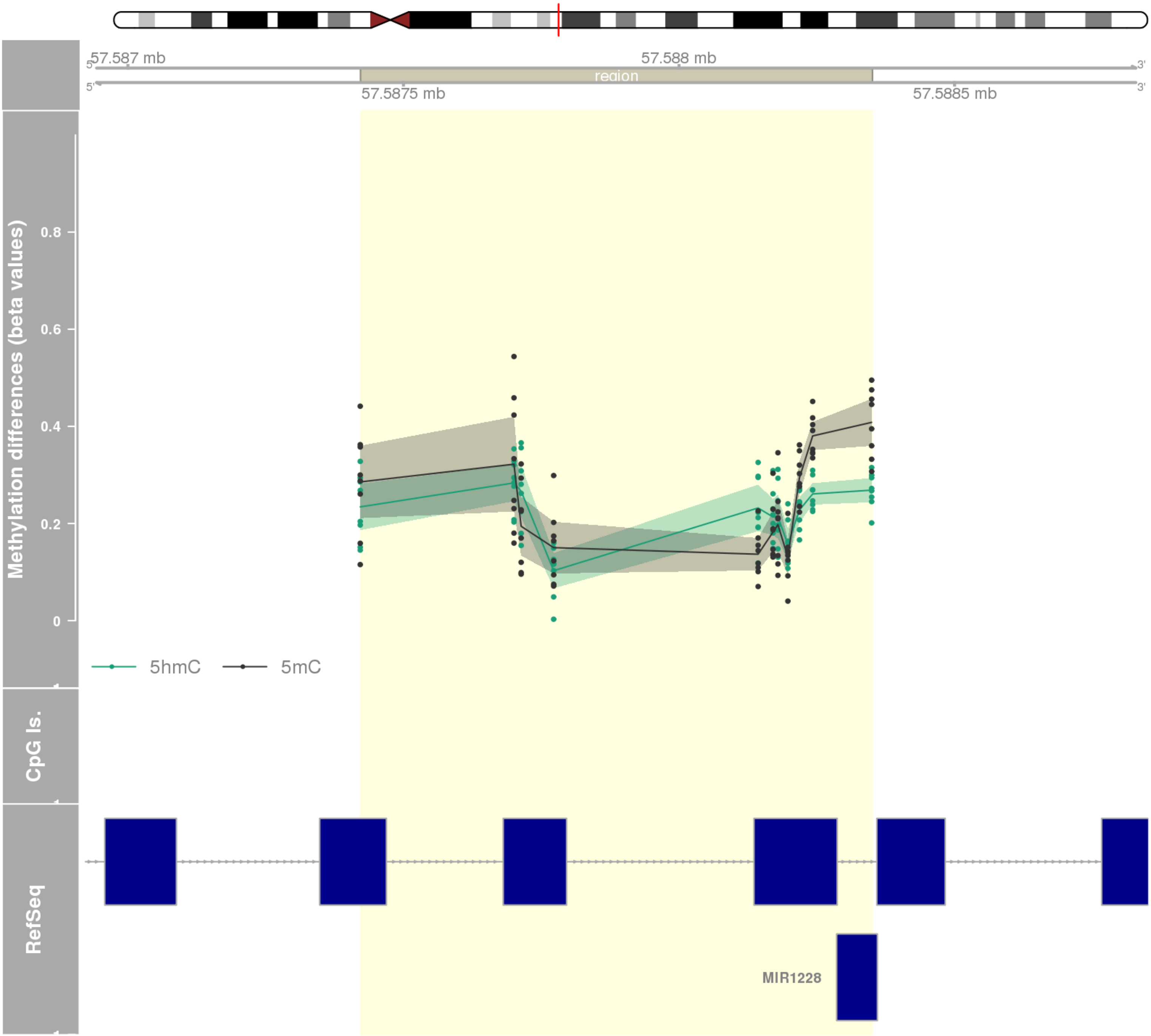
DMR 408 // chr17:80762382-80763859 // 1477 pb. (9 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: TBCD -



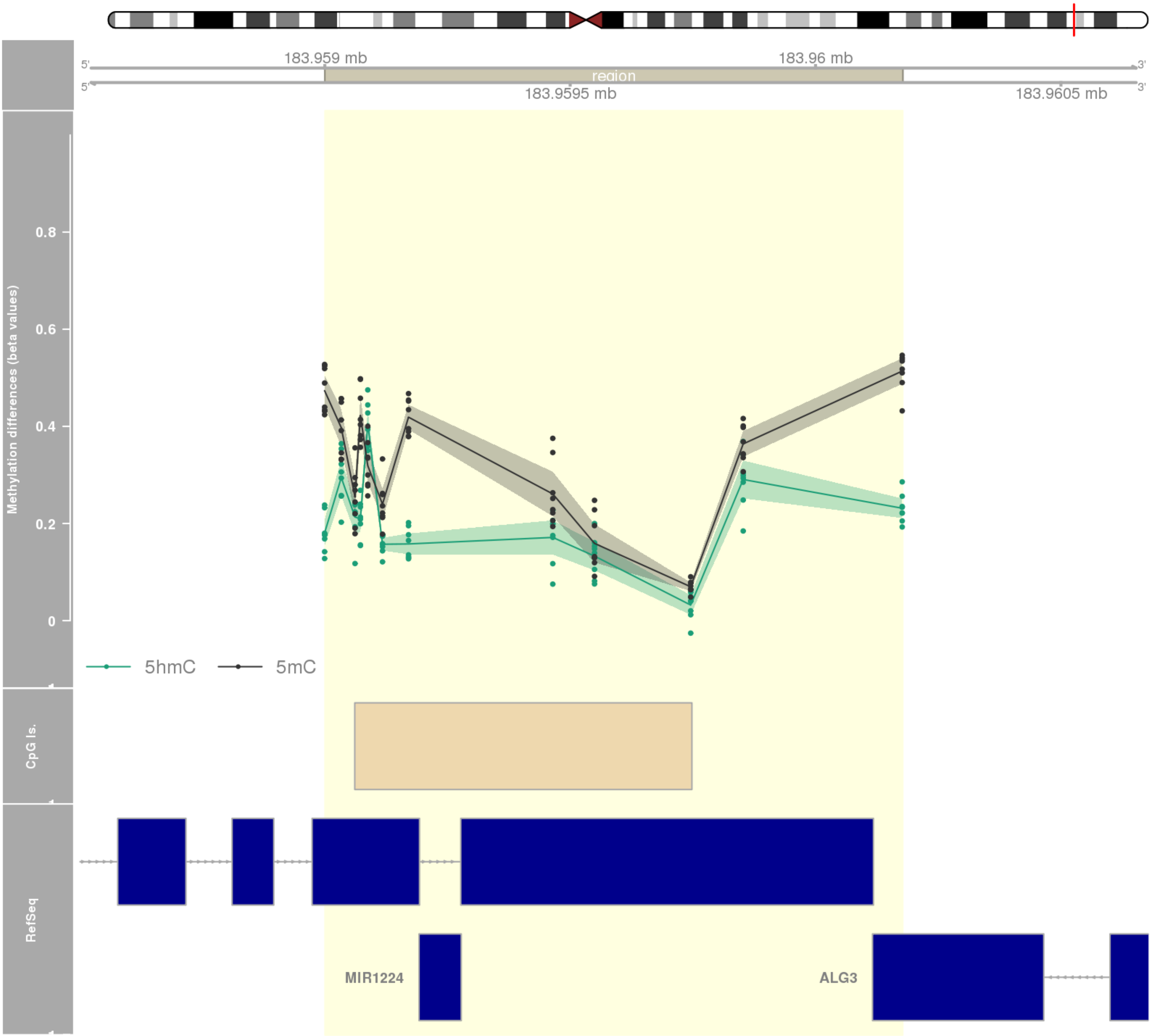
DMR 409 // chr1:9789165-9791419 // 2254 pb. (9 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: PIK3CD / CLSTN1 -



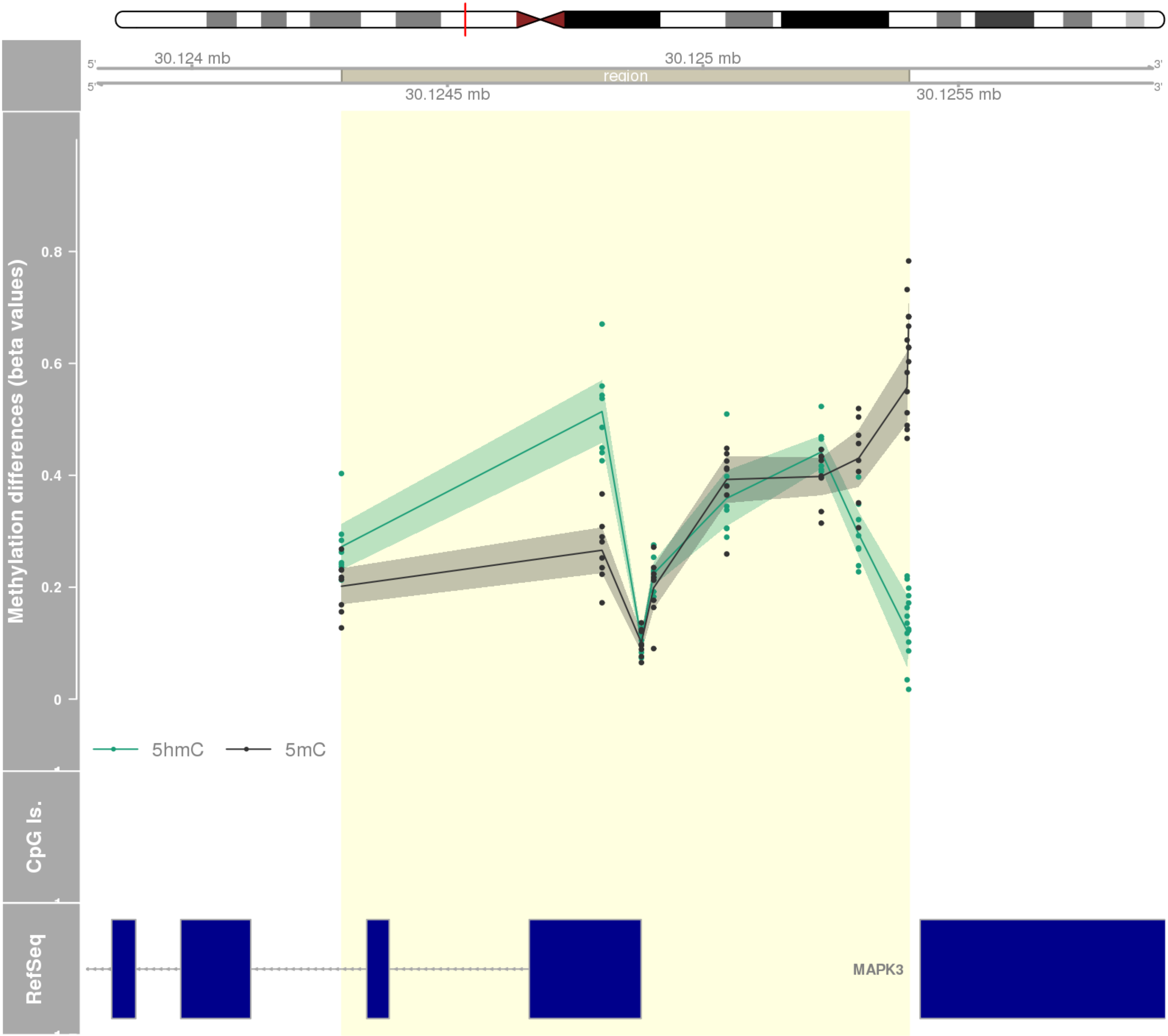
DMR 410 // chr12:57587422-57588350 // 928 pb. (11 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: MIR1228 / LRP1 -



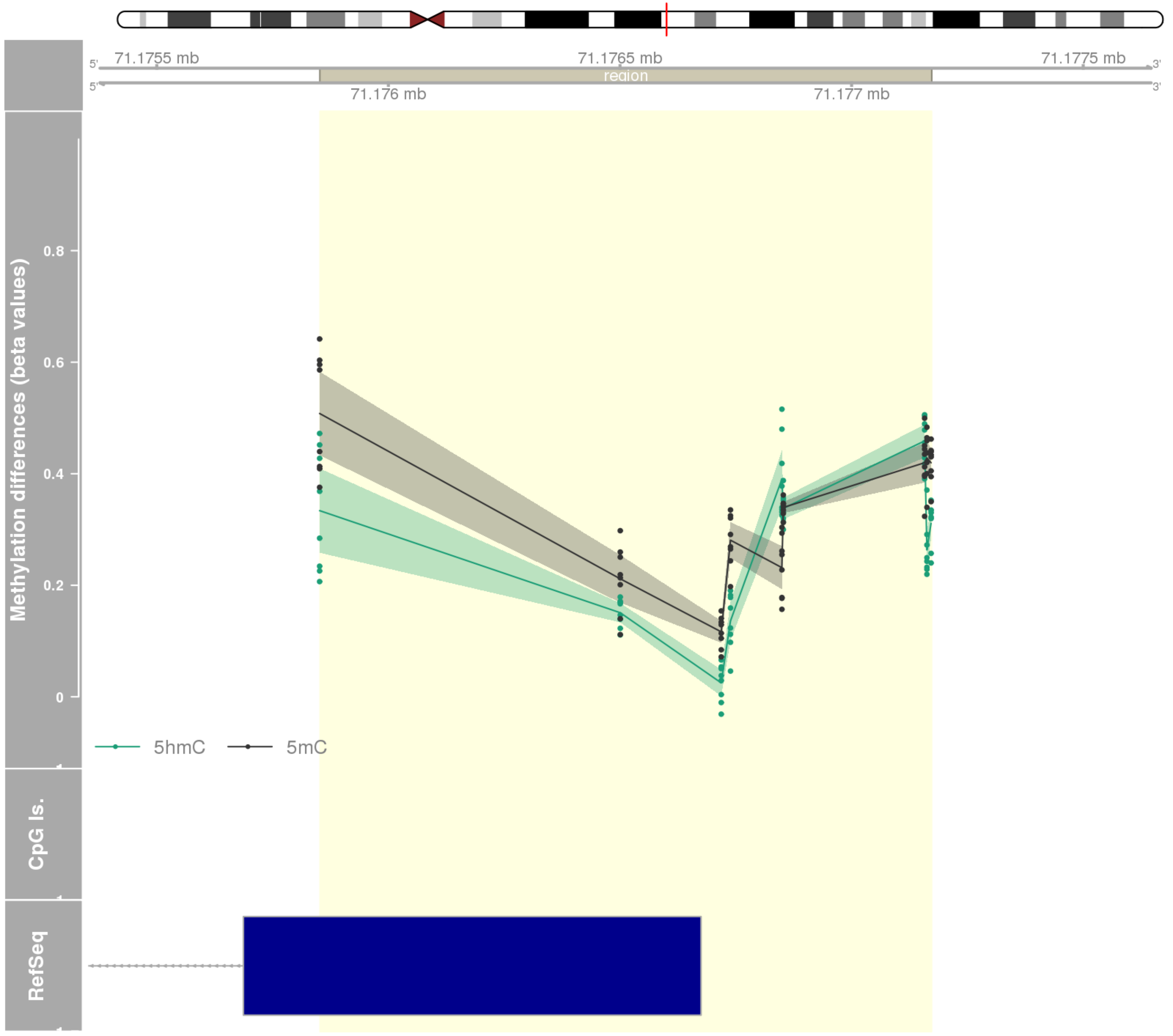
DMR 411 // chr3:183959000-183960177 // 1177 pb. (12 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: MIR1224 / EIF2B5 / VWA5B2 / ALG3 -



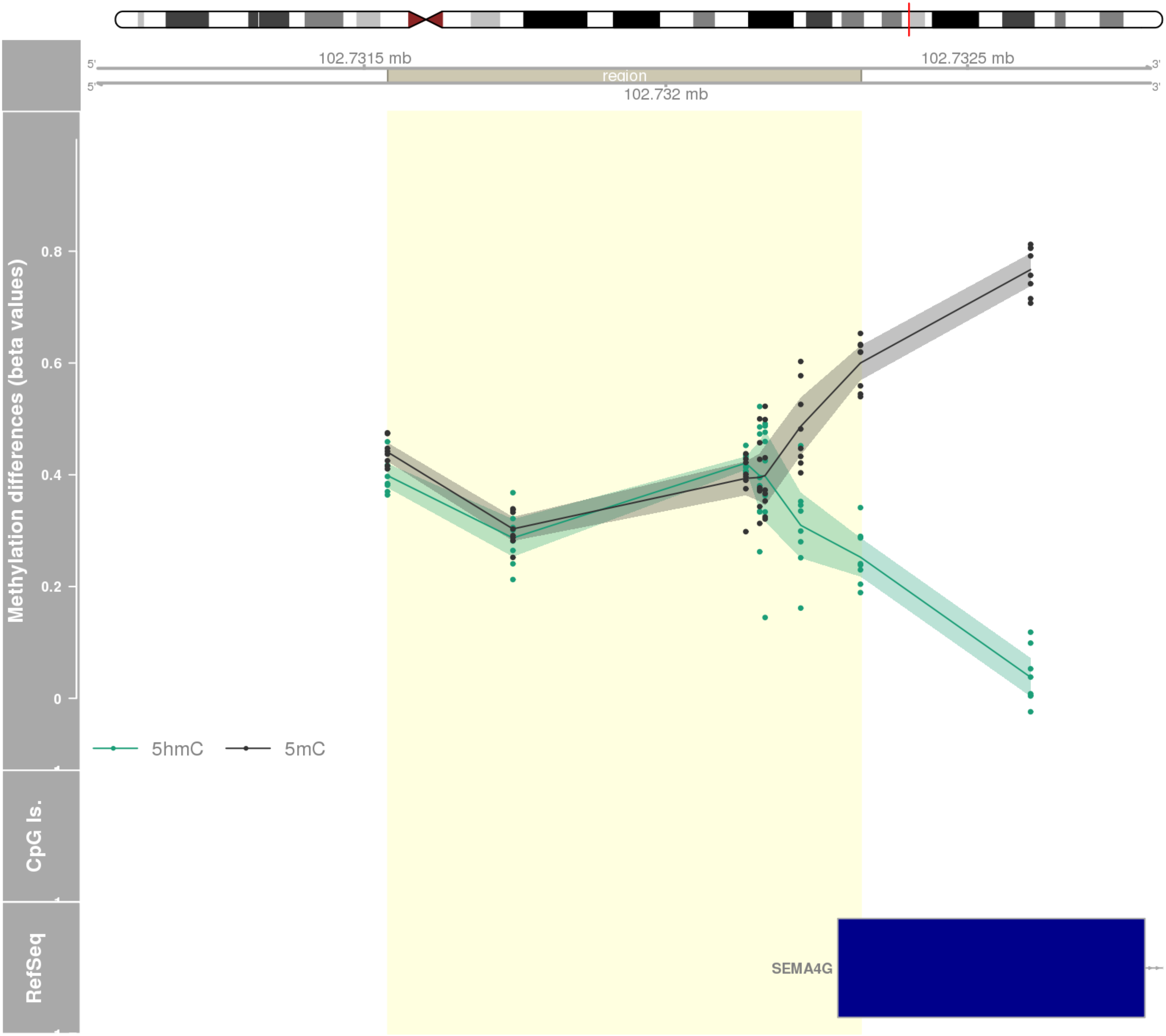
DMR 412 // chr16:30124293-30125403 // 1110 pb. (9 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: GDPD3 -



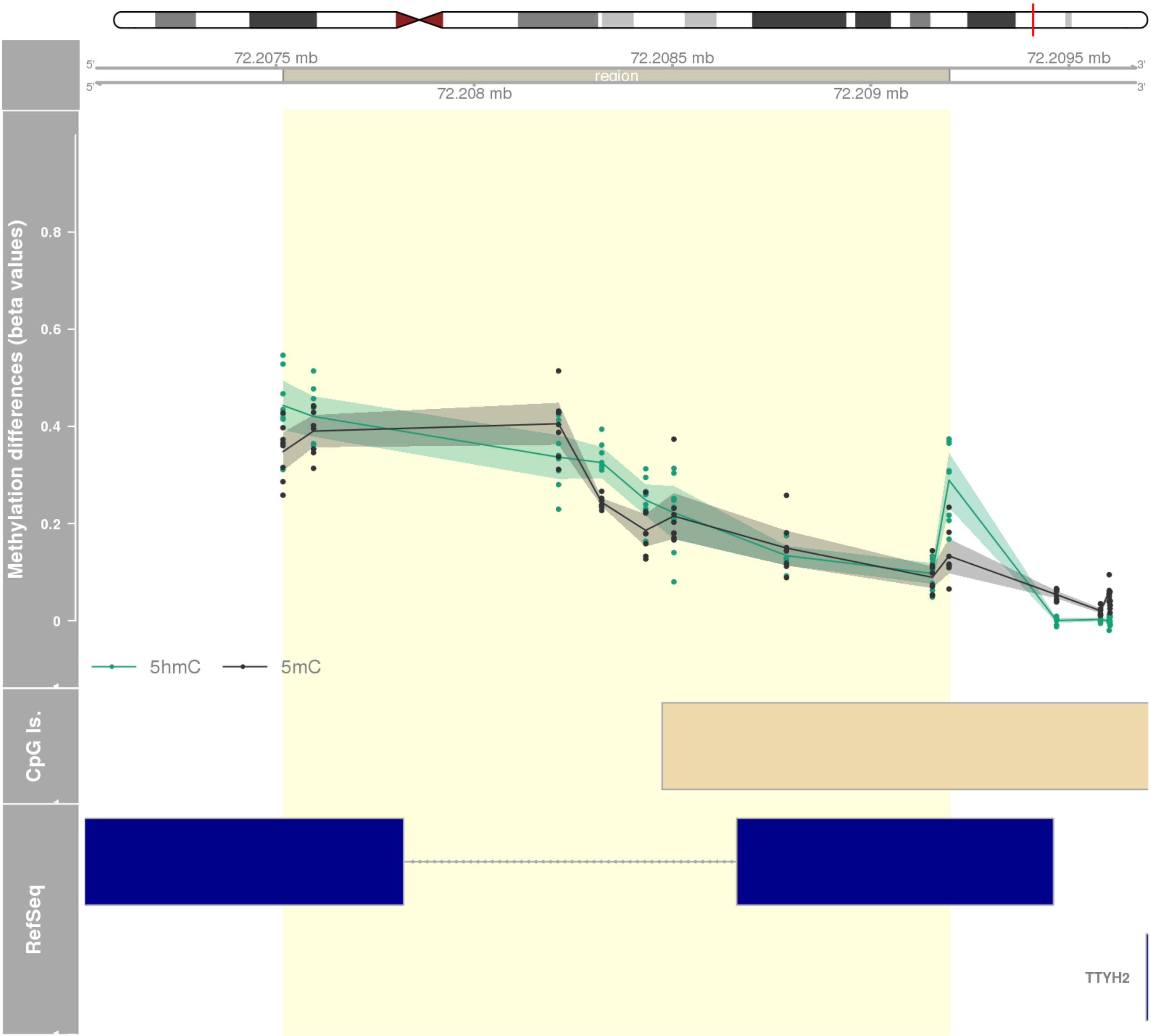
DMR 413 // chr10:71175852-71177172 // 1320 pb. (9 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: TACR2 -



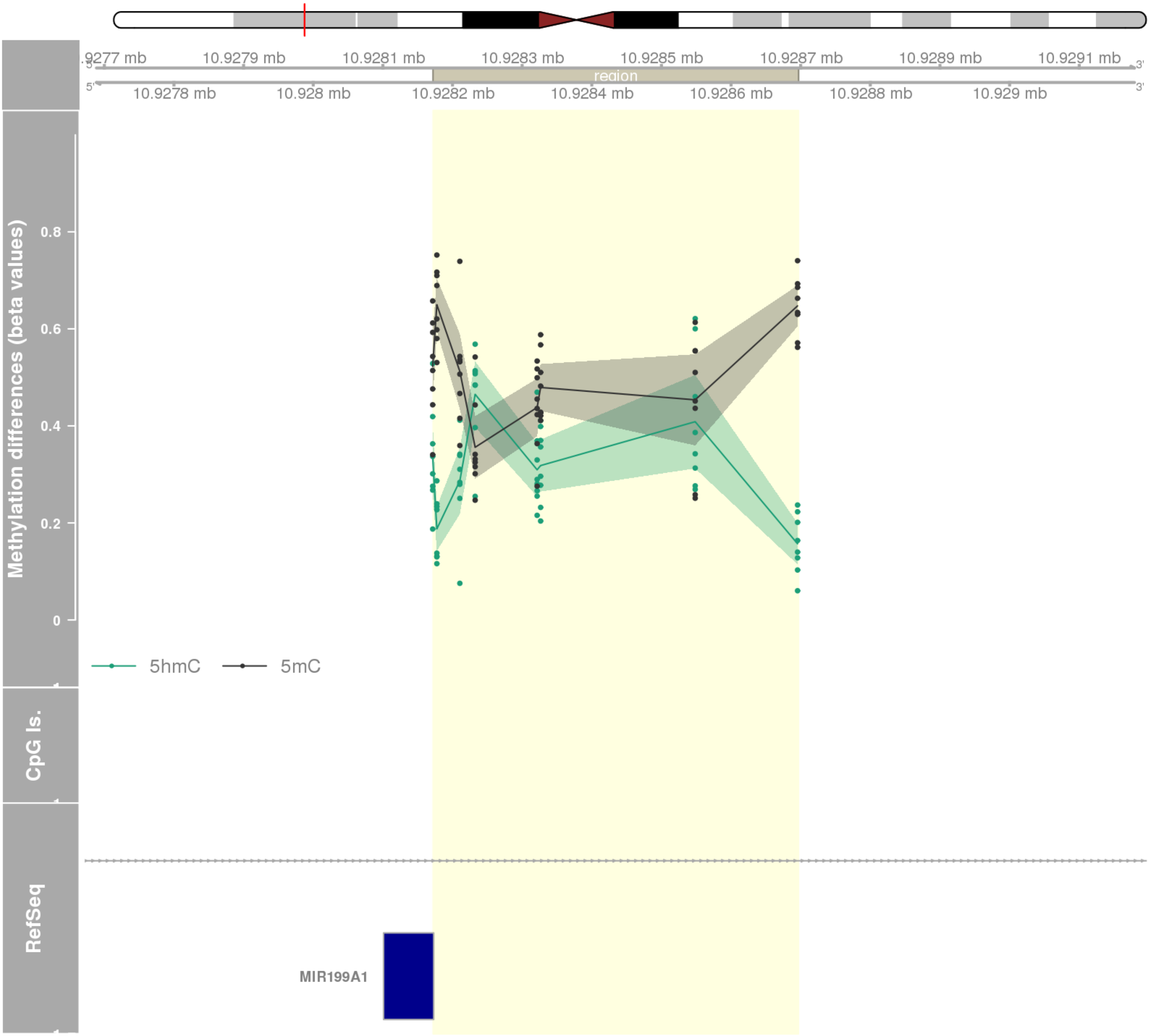
DMR 414 // chr10:102731539-102732323 // 784 pb. (7 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559
- genes: MRPL43 / SEMA4G -



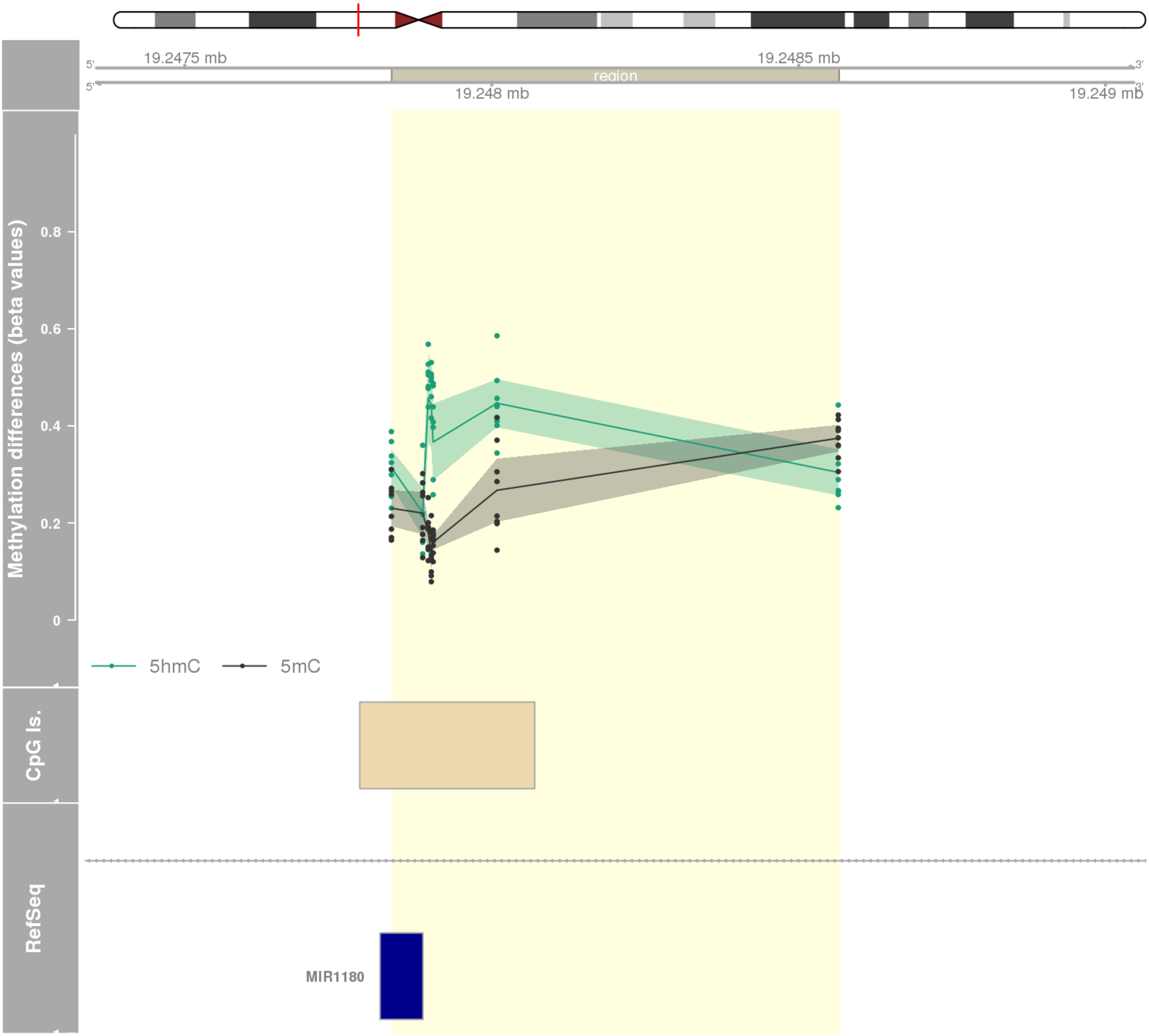
DMR 415 // chr17:72207518-72209198 // 1680 pb. (9 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.021 // fwerArea: 0.559



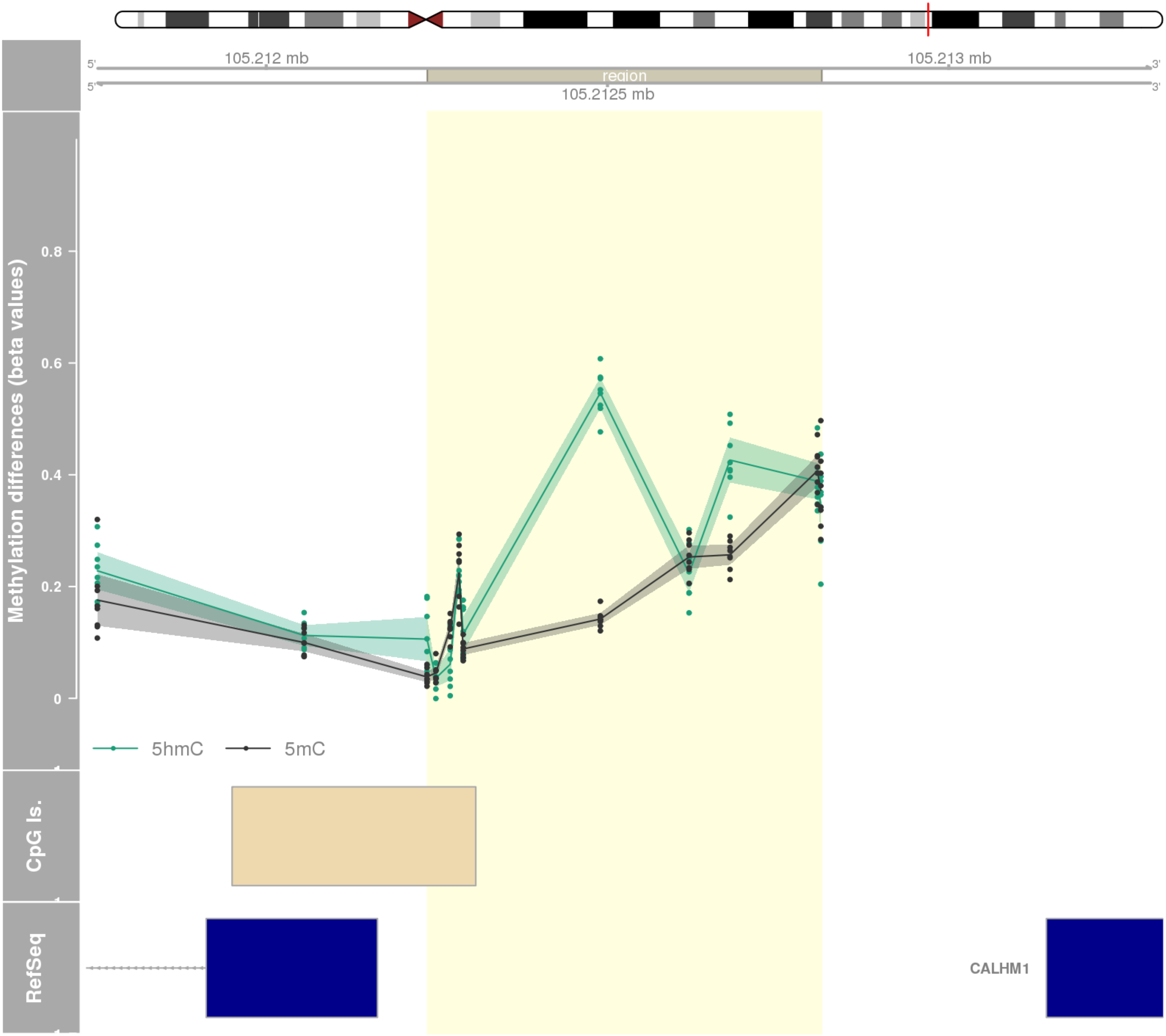
DMR 416 // chr19:10928172-10928696 // 524 pb. (8 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: DNM2 / MIR199A1 -



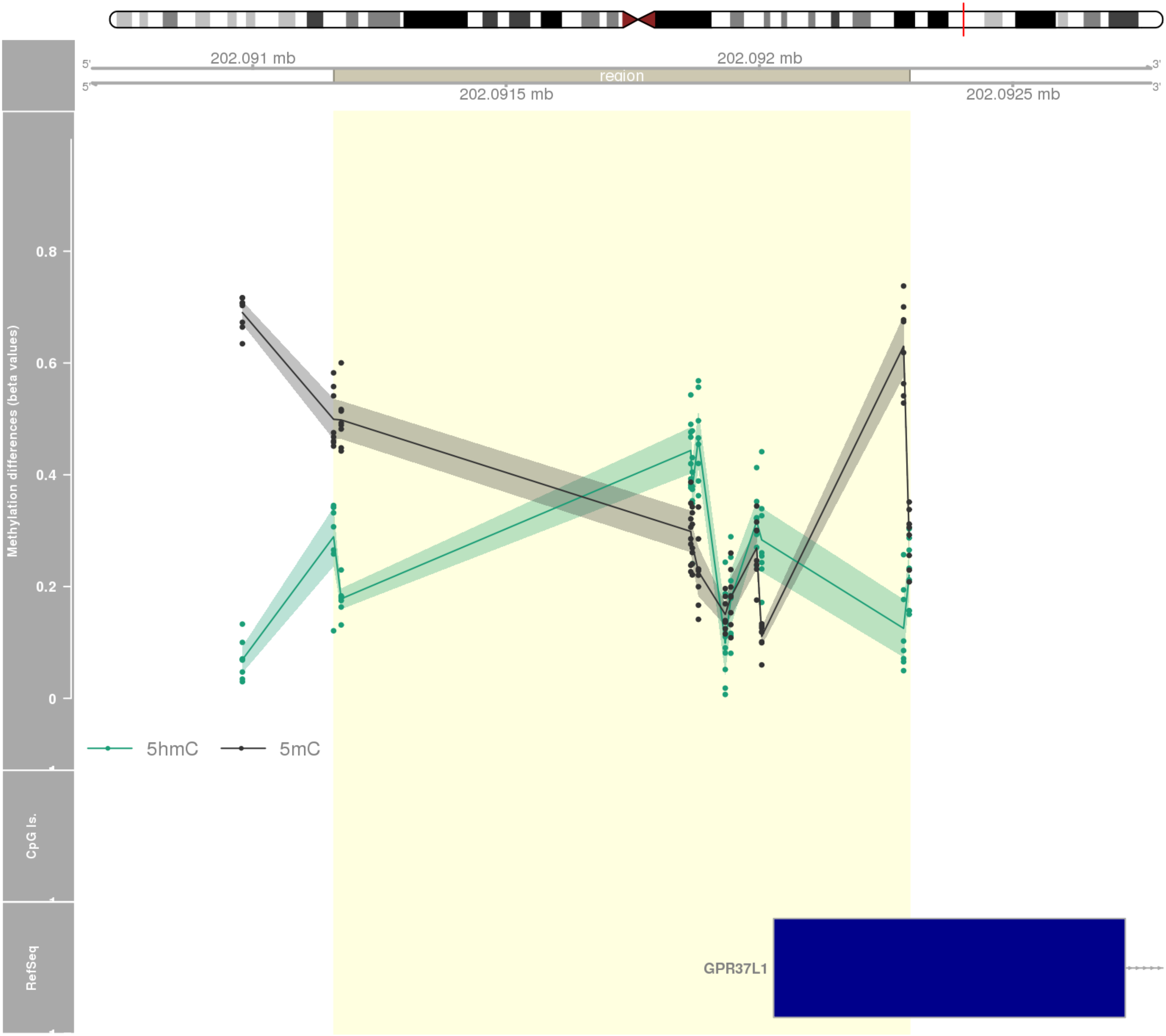
DMR 417 // chr17:19247837-19248565 // 728 pb. (7 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: MIR1180 / B9D1 -



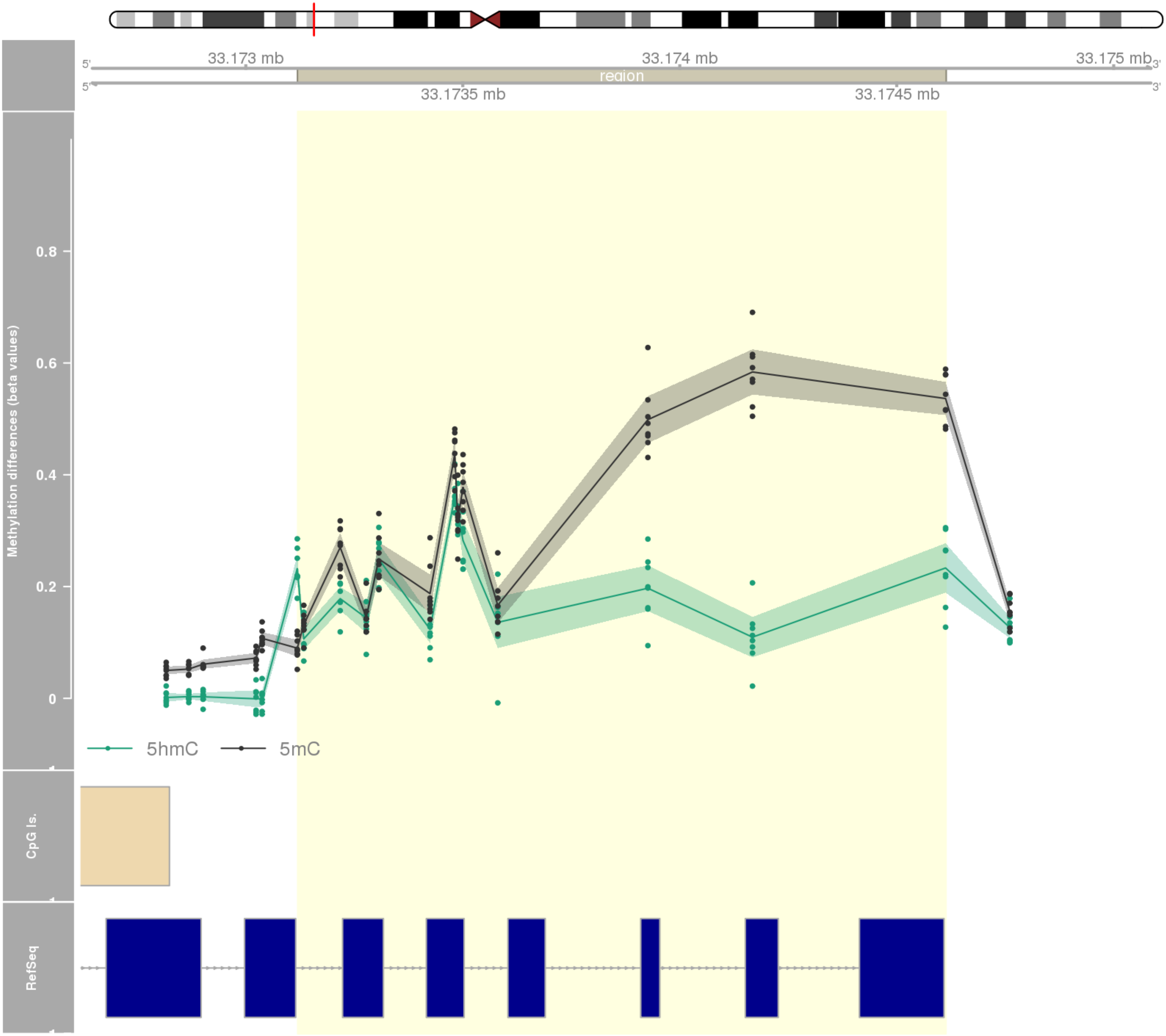
DMR 418 // chr10:105212236-105212813 // 577 pb. (10 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: CALHM2 -



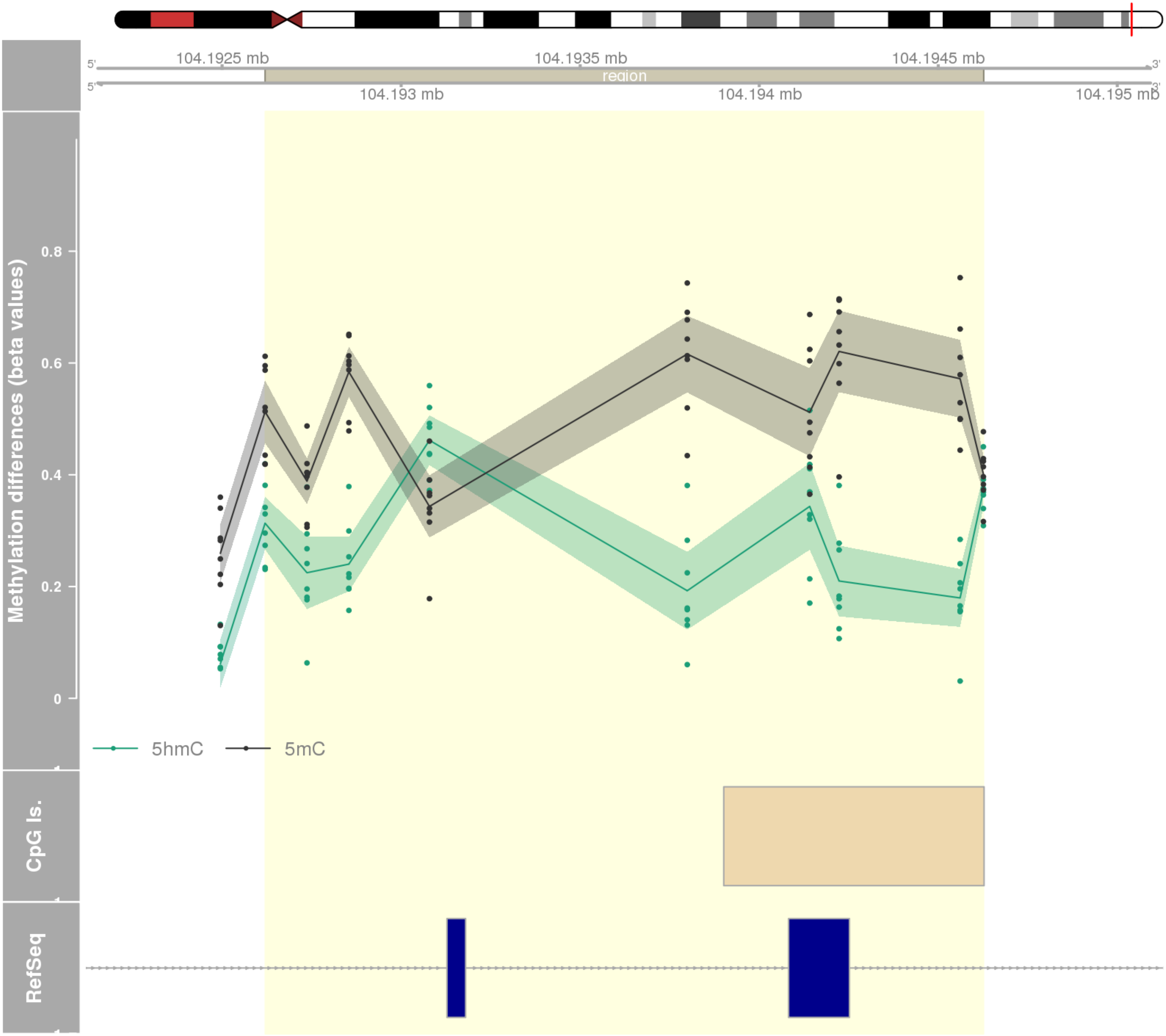
DMR 419 // chr1:202091160-202092296 // 1136 pb. (11 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: GPR37L1 -



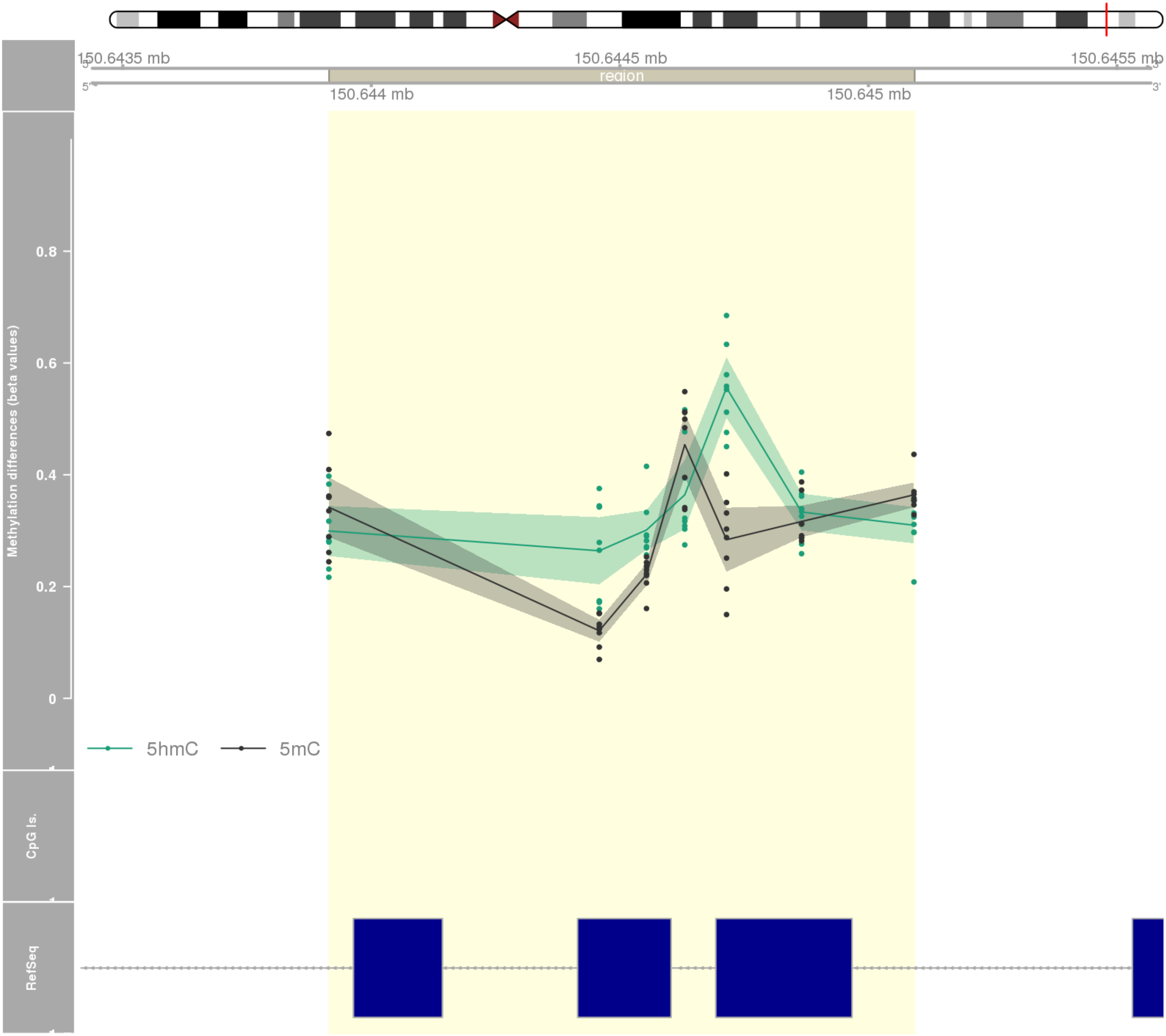
DMR 420 // chr6:33173119-33174613 // 1494 pb. (13 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: HSD17B8 -



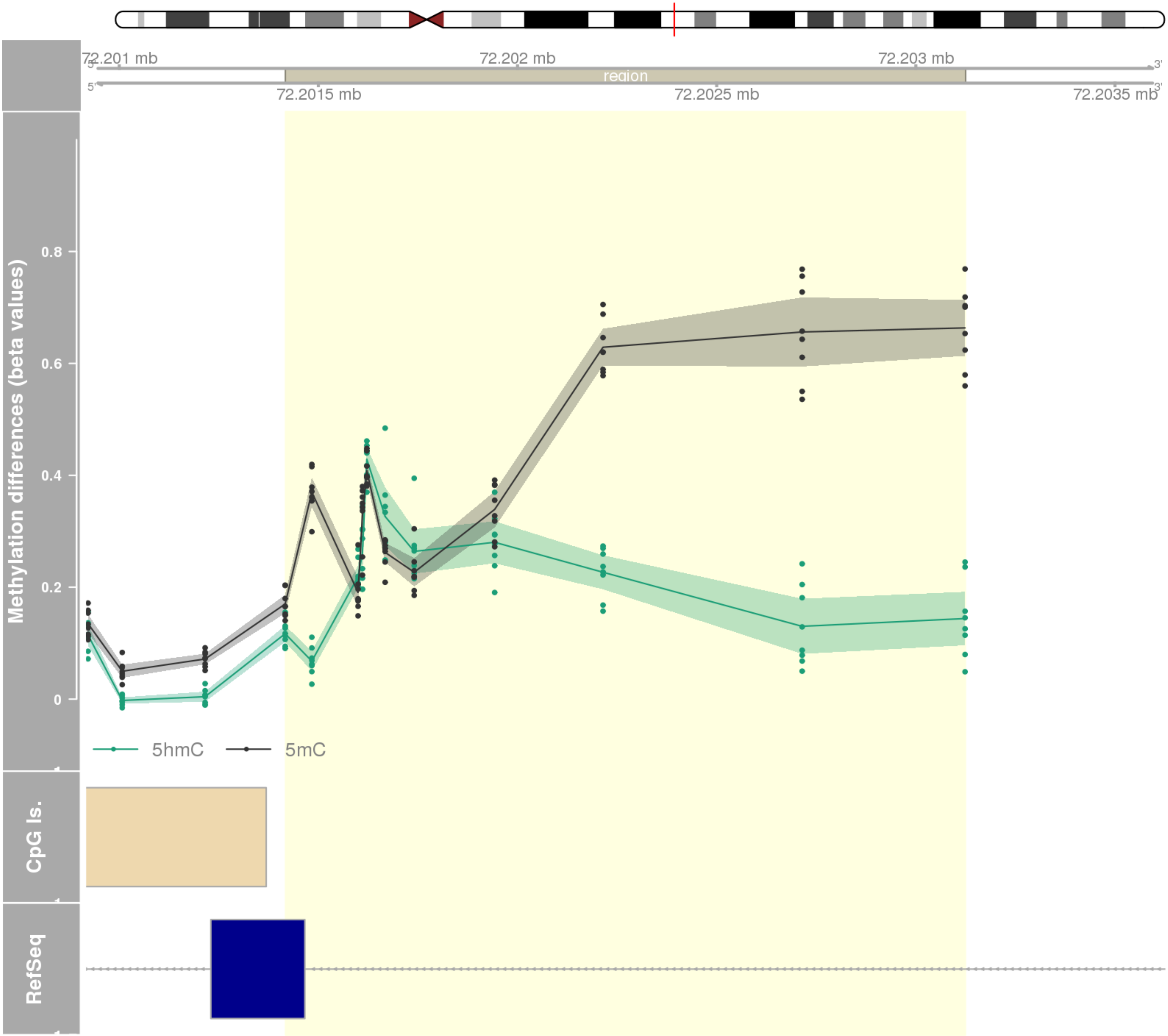
DMR 421 // chr14:104192620-104194626 // 2006 pb. (9 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: ZFYVE21 -



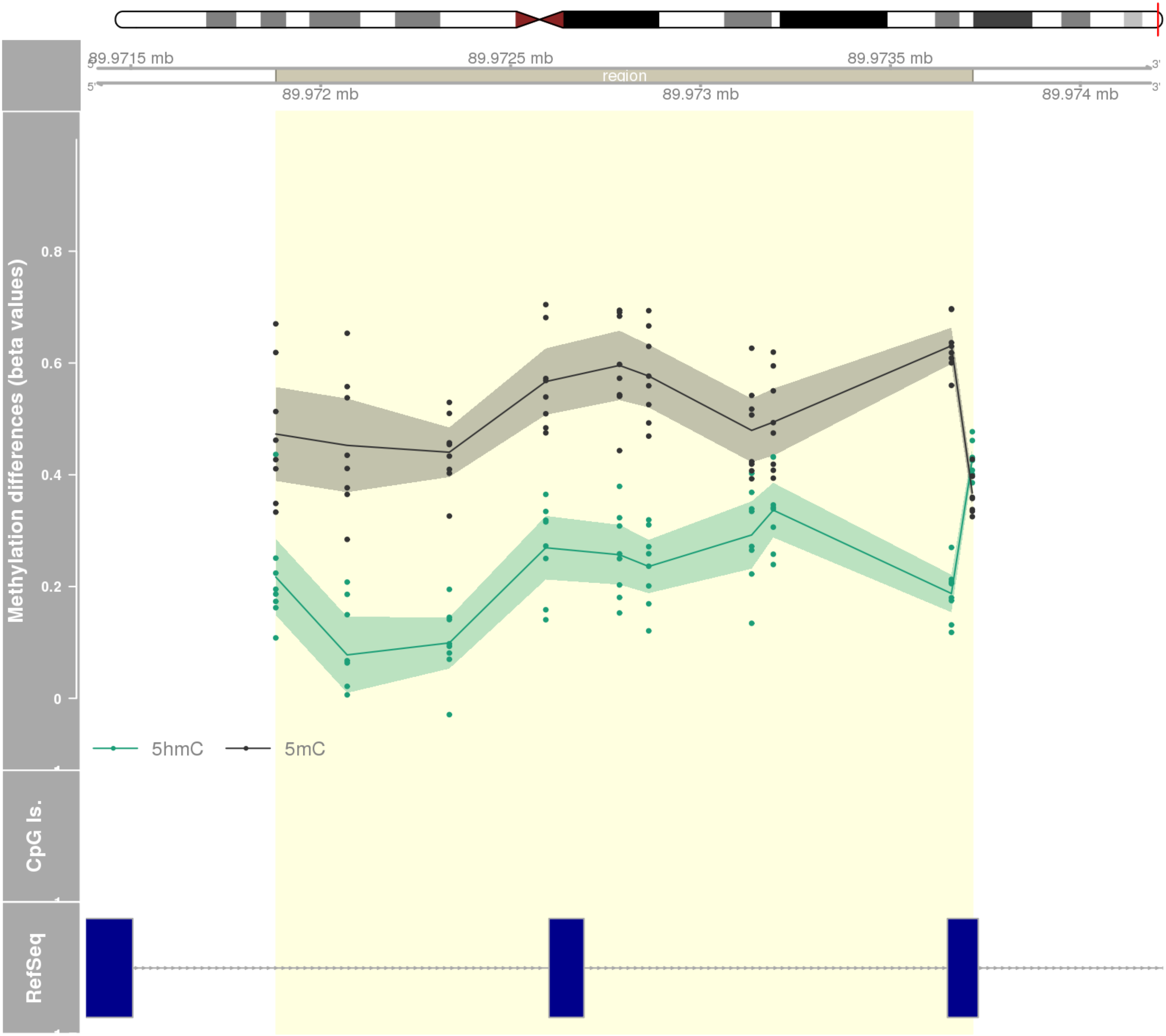
DMR 422 // chr7:150643915-150645092 // 1177 pb. (7 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: KCNH2 -



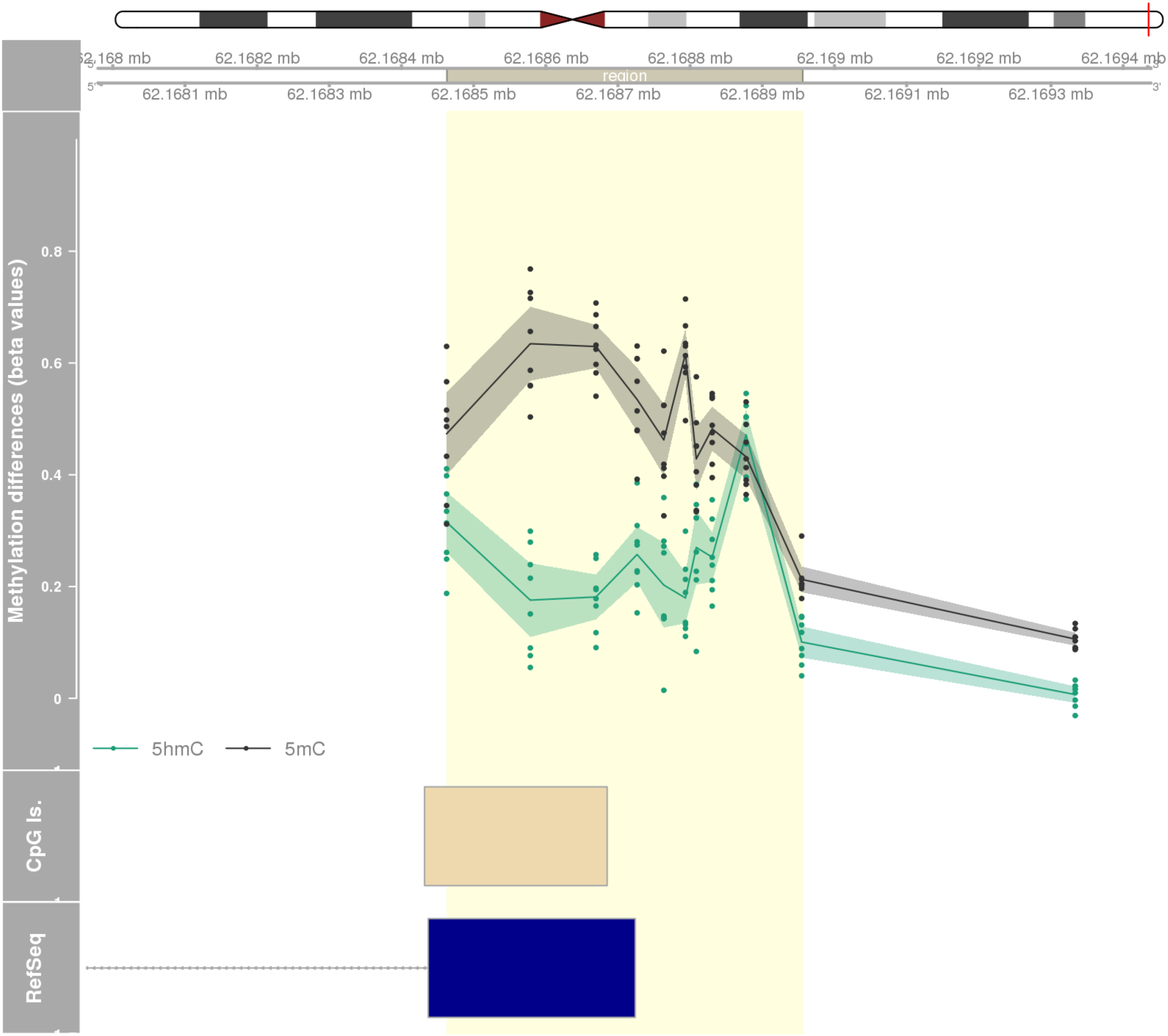
DMR 423 // chr10:72201417-72203124 // 1707 pb. (11 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: NODAL -



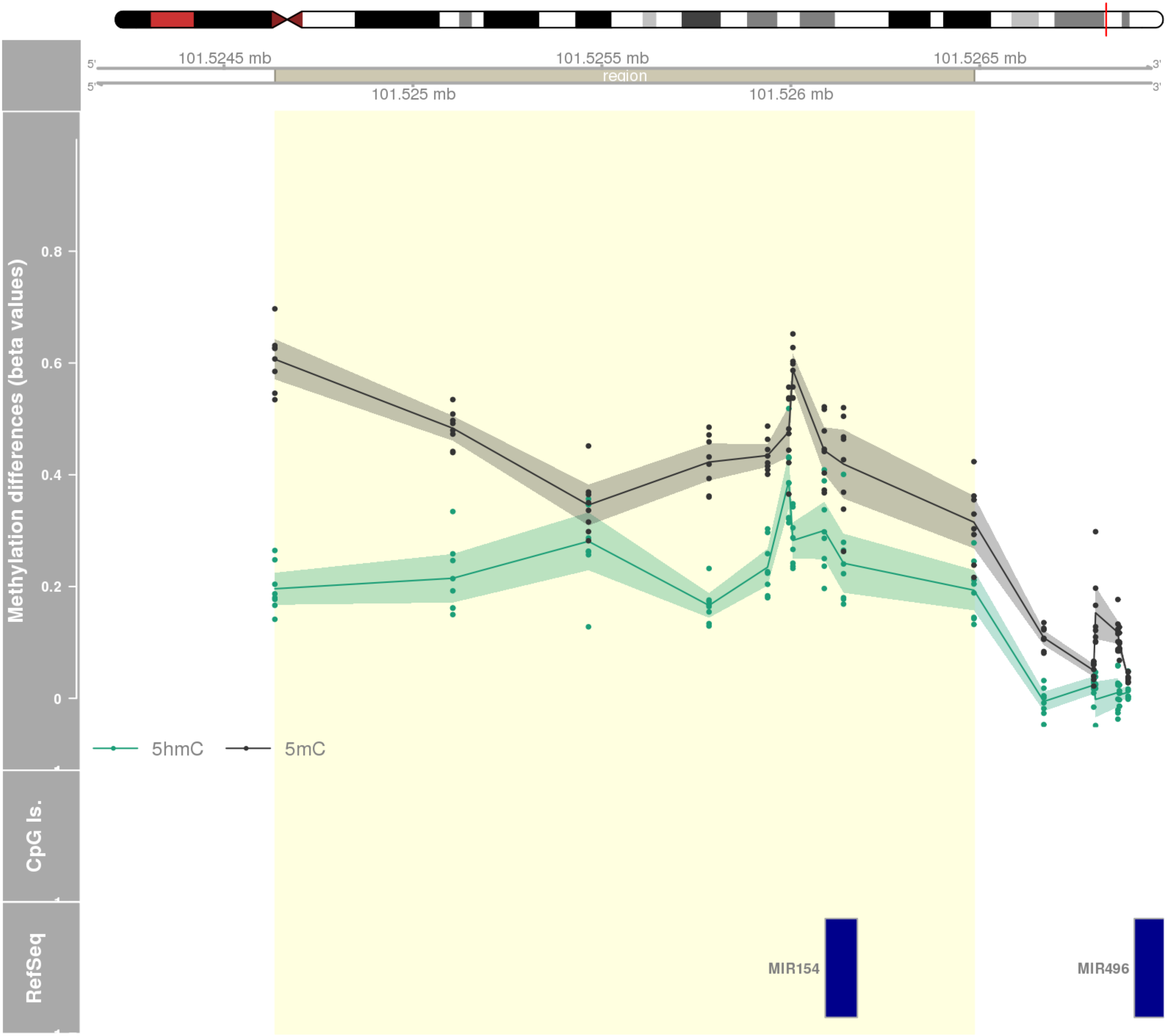
DMR 424 // chr16:89971882-89973716 // 1834 pb. (10 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: TCF25 -



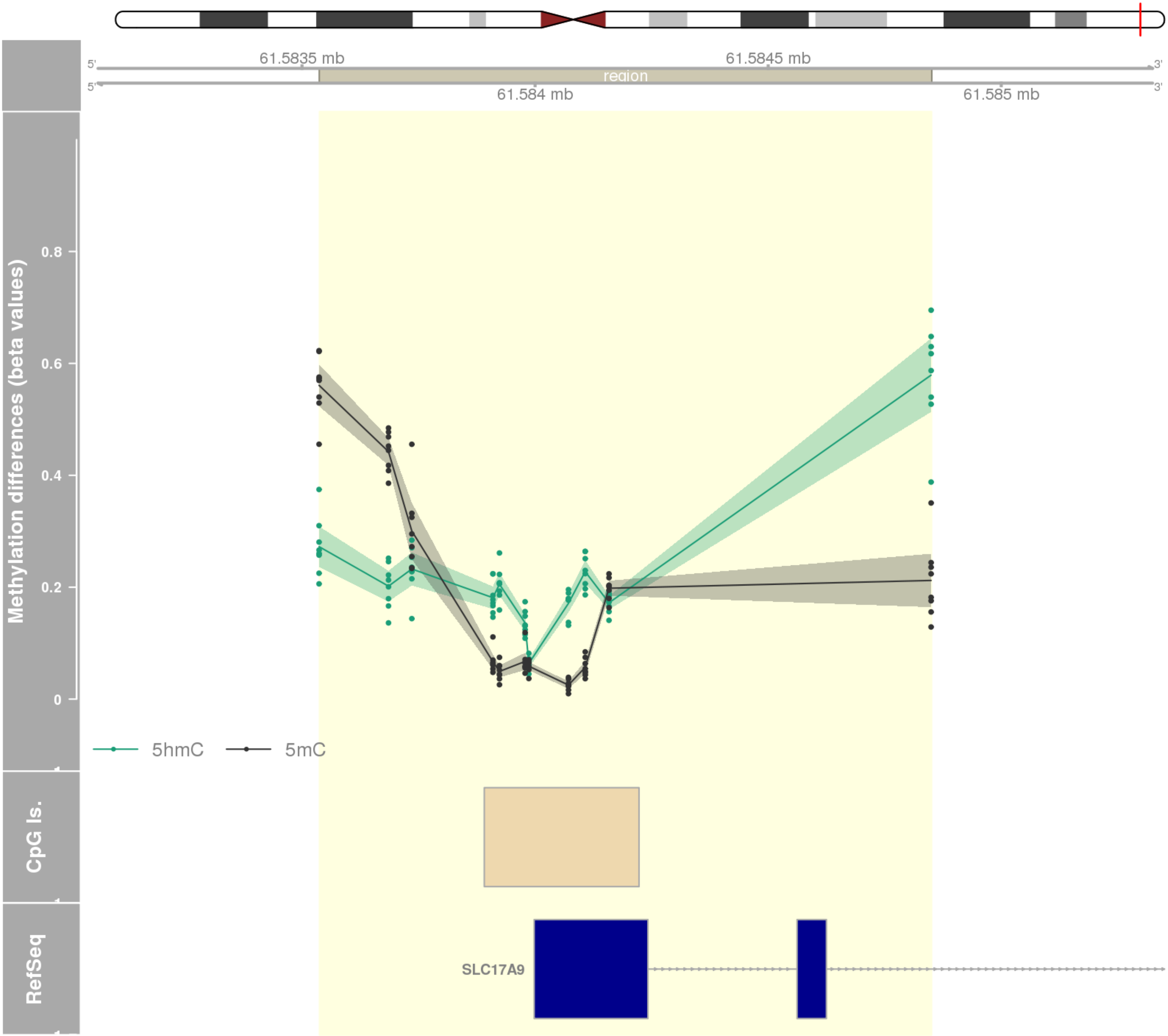
DMR 425 // chr20:62168463-62168955 // 492 pb. (10 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: PTK6 -



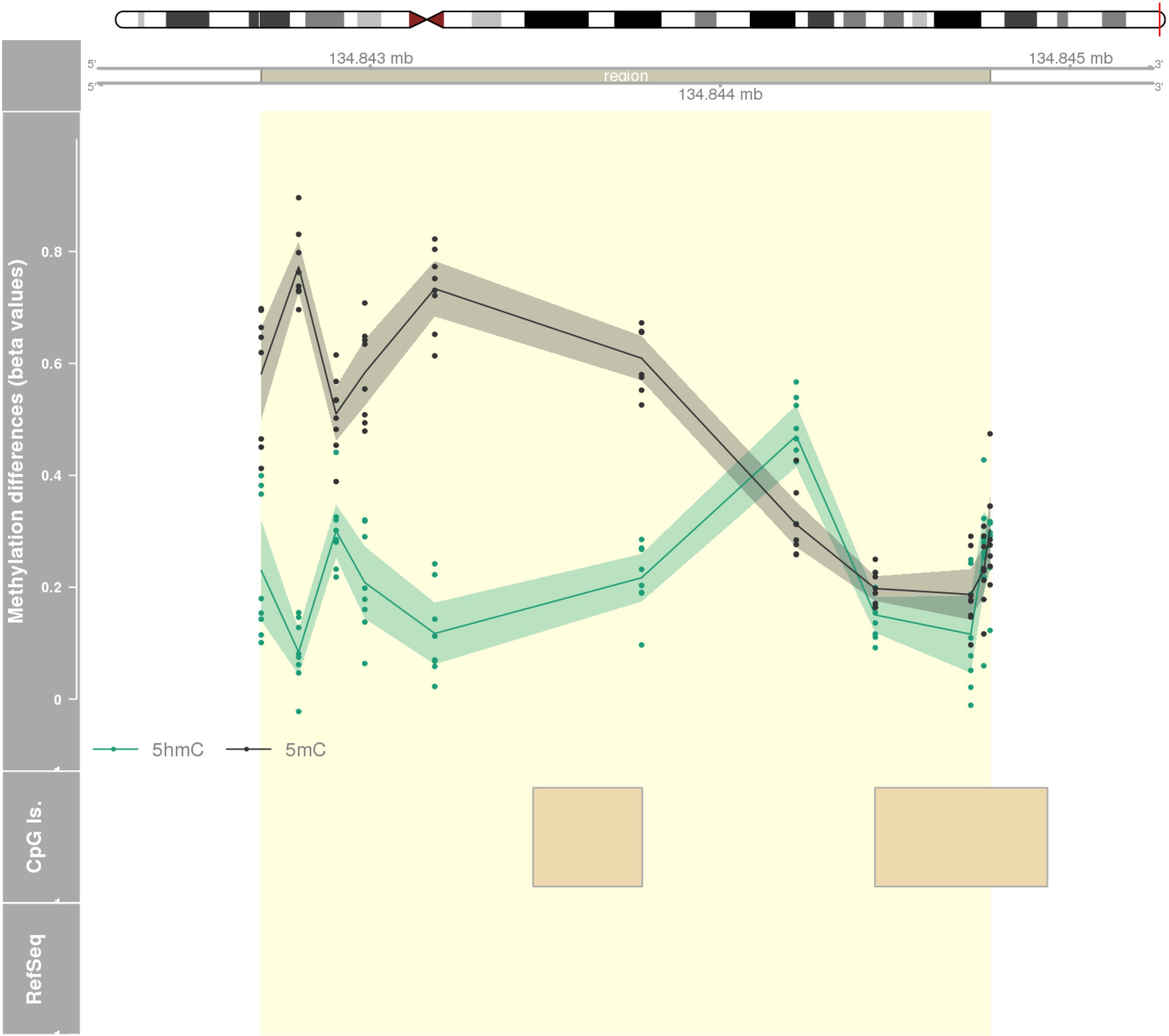
DMR 426 // chr14:101524635-101526485 // 1850 pb. (10 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: MIR154 -



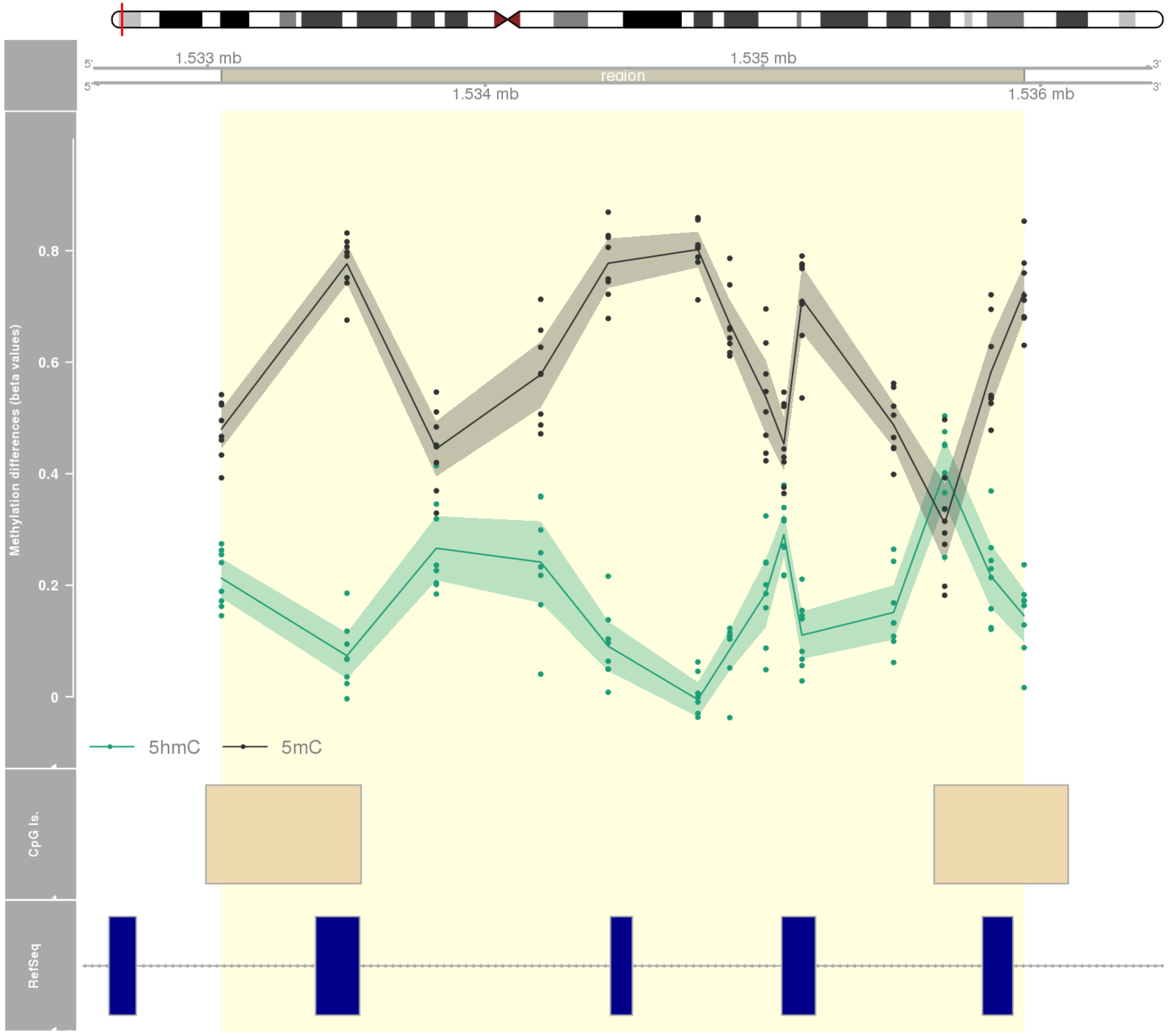
DMR 427 // chr20:61583537-61584850 // 1313 pb. (11 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: SLC17A9 -



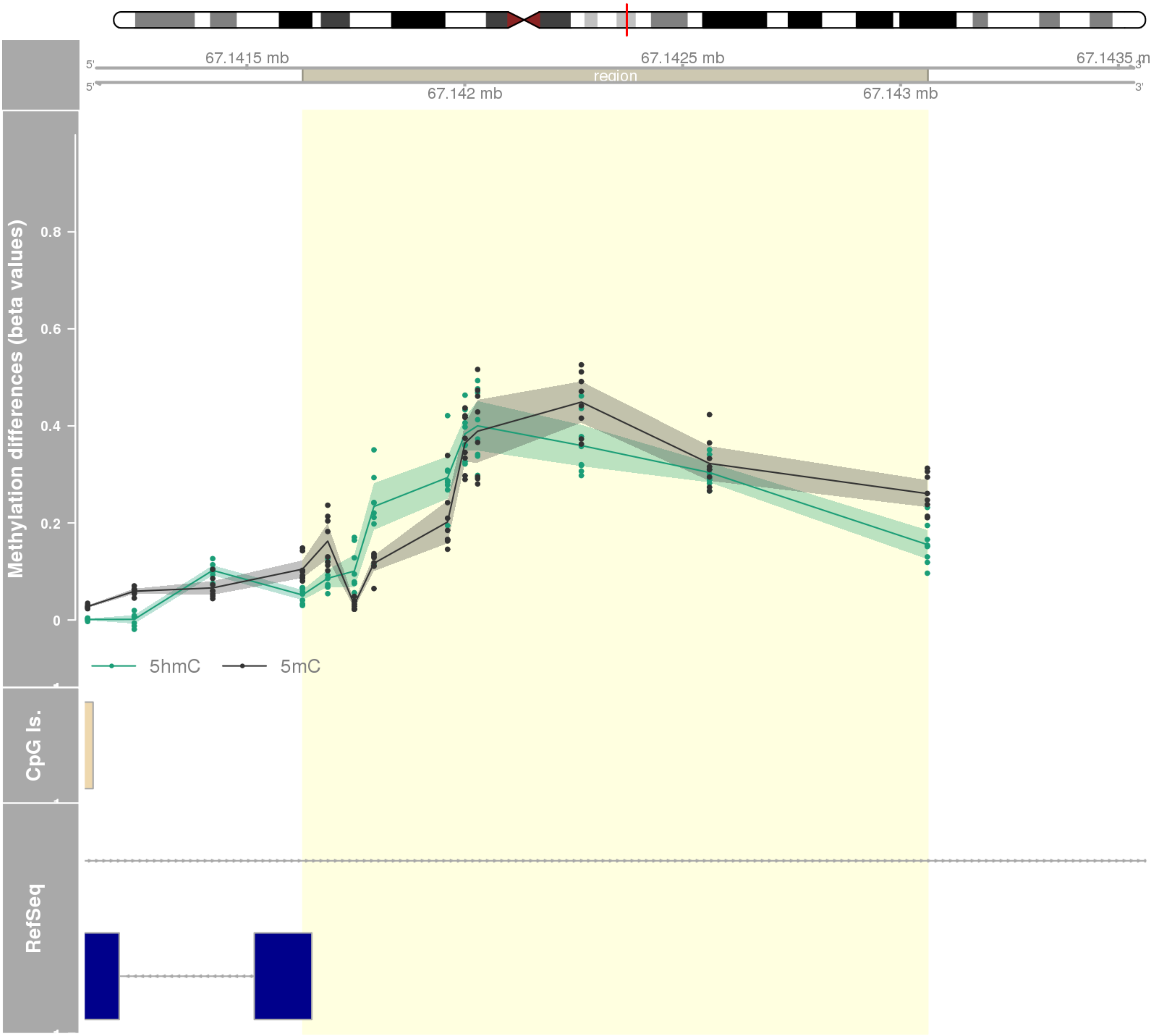
DMR 428 // chr10:134842688-134844771 // 2083 pb. (11 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559



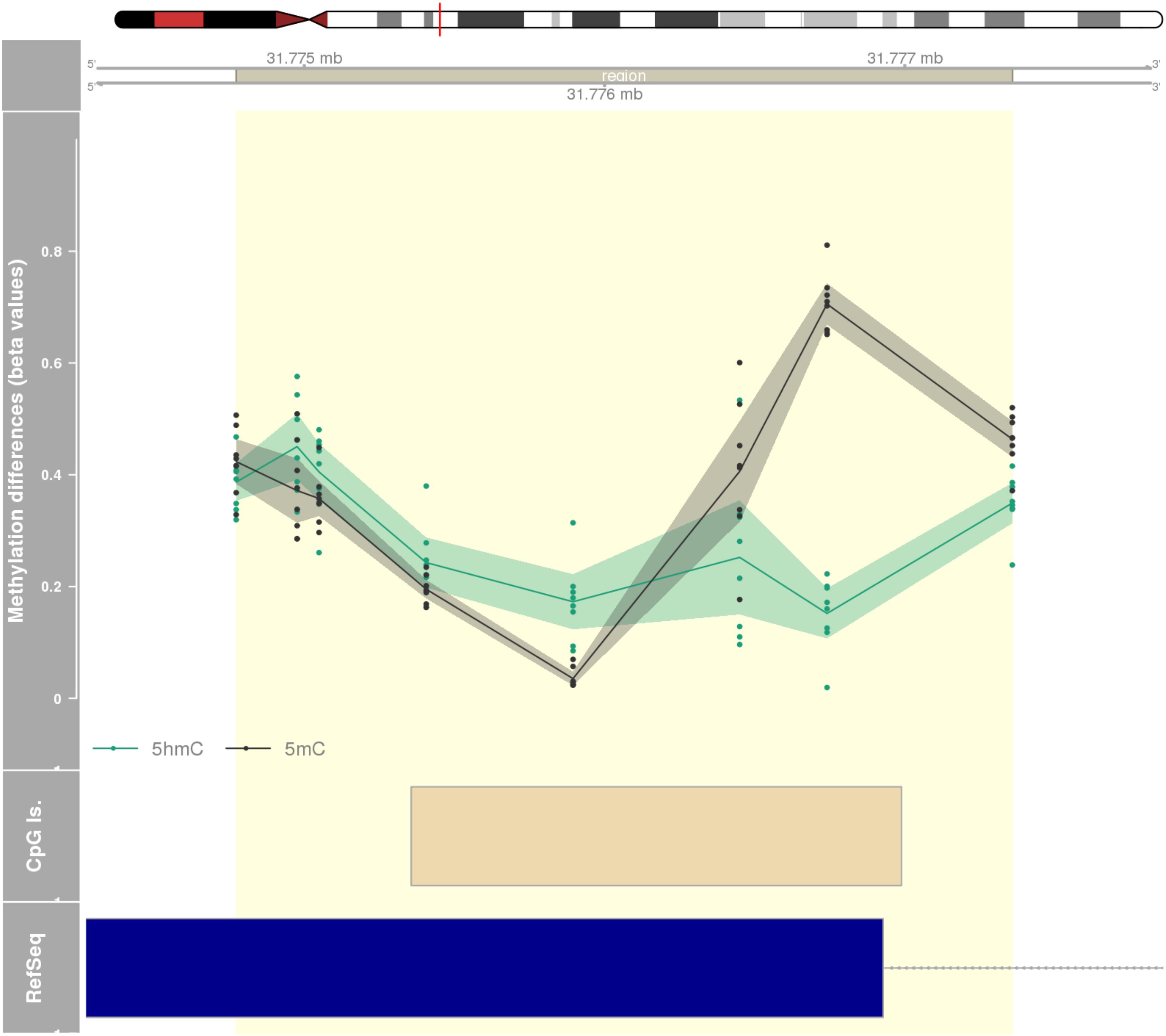
DMR 429 // chr7:1533050-1535941 // 2891 pb. (14 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: INTS1 -



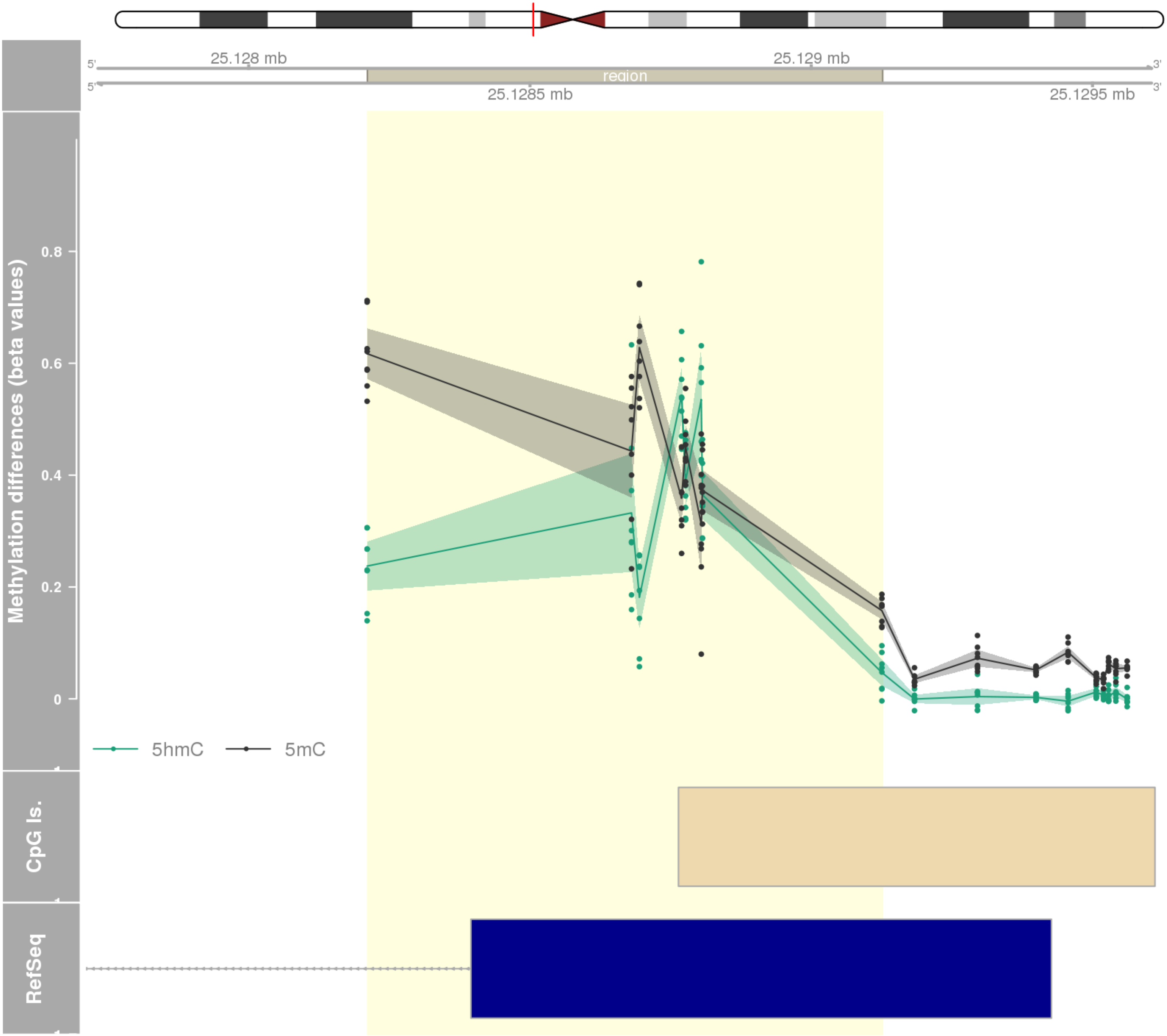
DMR 430 // chr11:67141628-67143062 // 1434 pb. (10 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: CLCF1 -



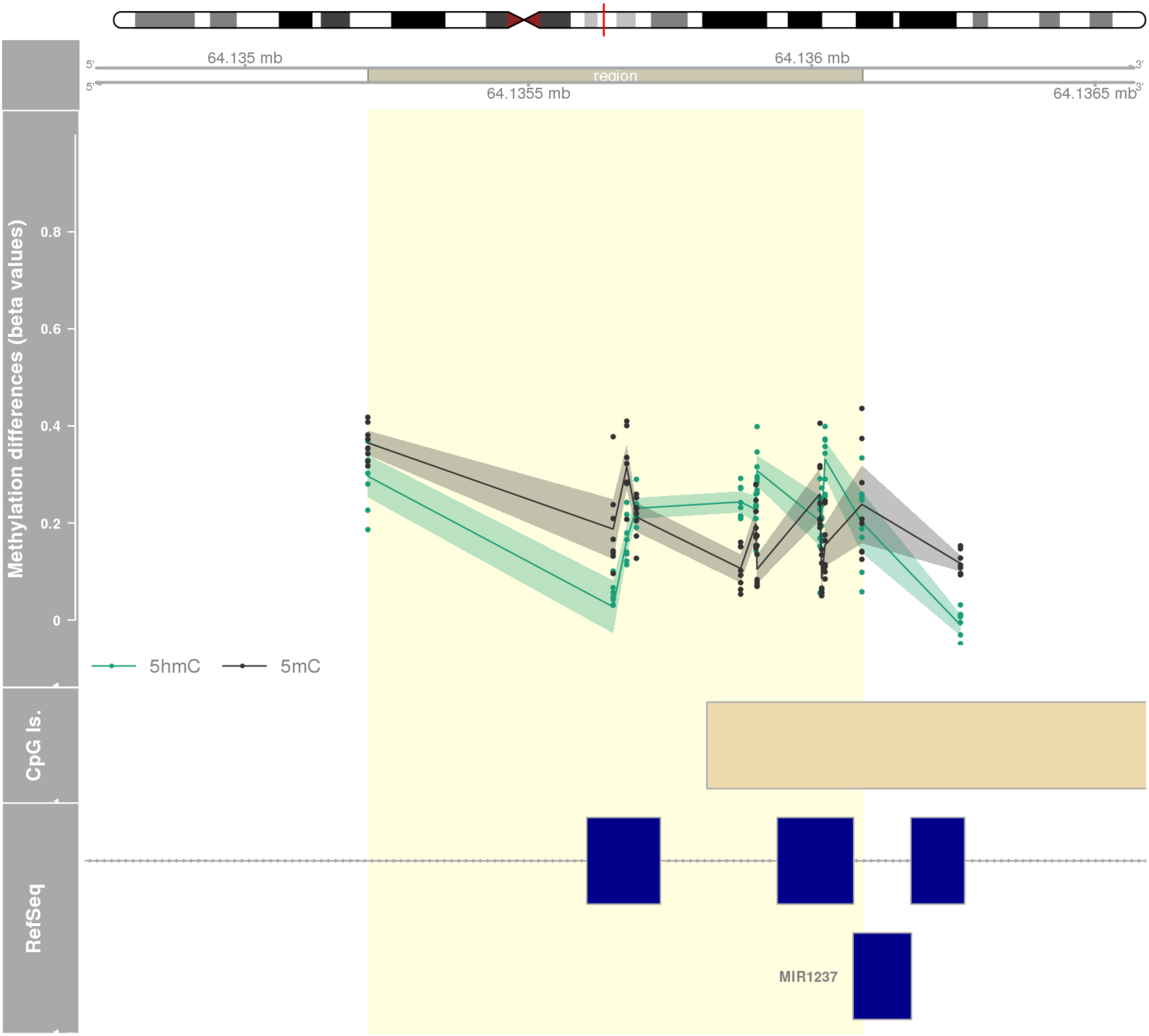
DMR 431 // chr15:31774773-31777358 // 2585 pb. (8 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: OTUD7A -



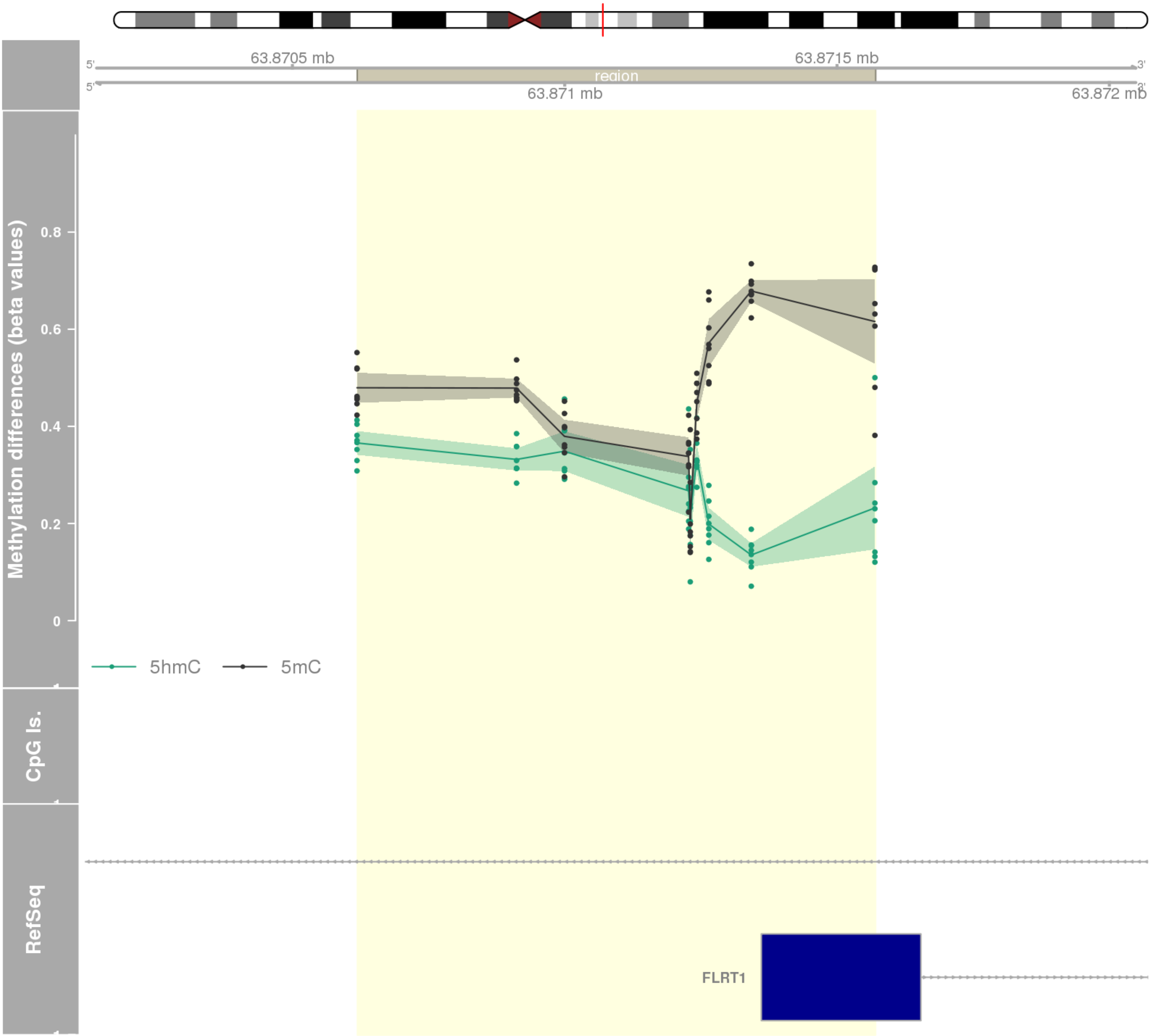
DMR 432 // chr20:25128211-25129126 // 915 pb. (8 probes) // pvalue: 0.004 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559



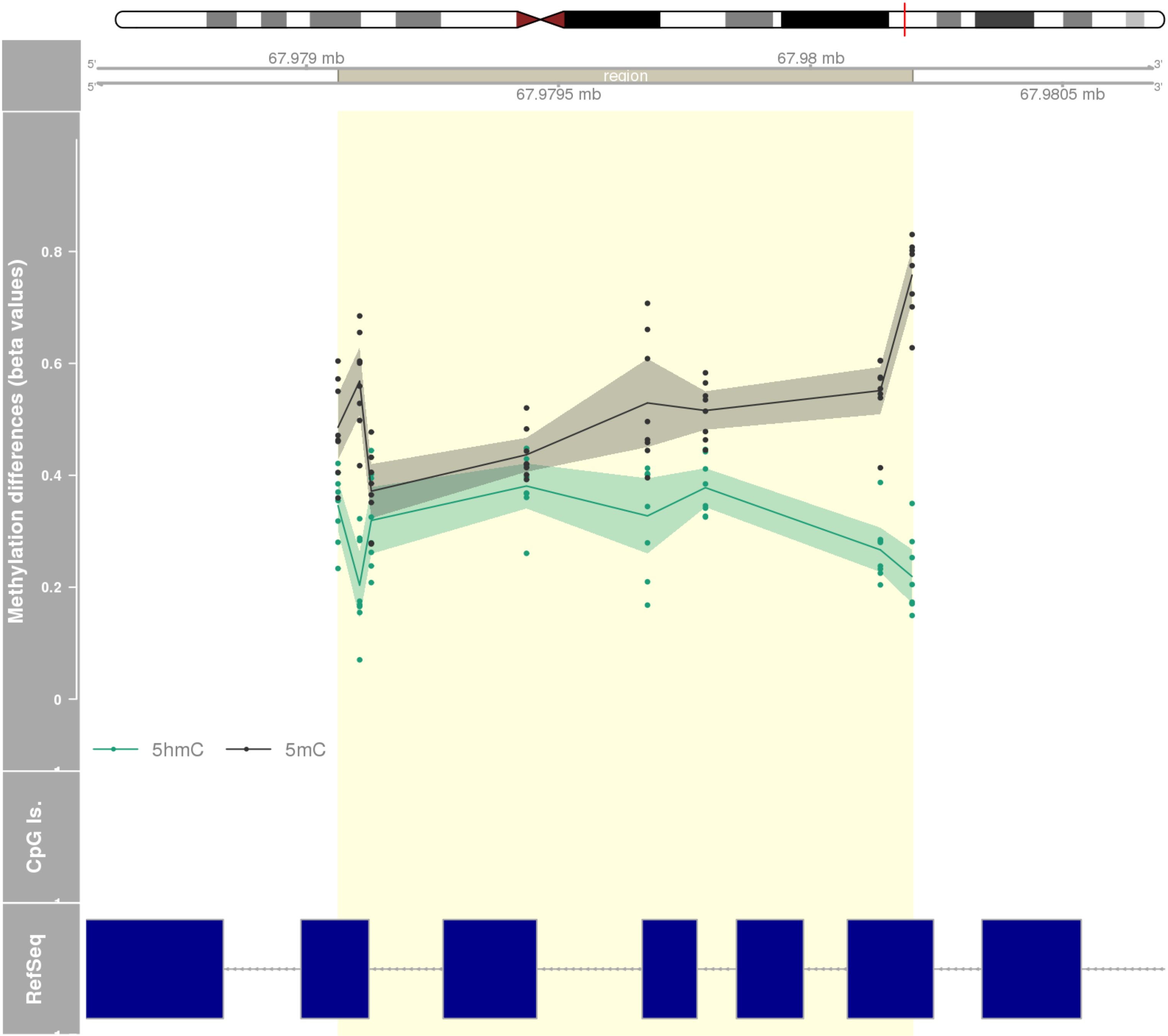
DMR 433 // chr11:64135217-64136089 // 872 pb. (11 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: MIR1237 / RPS6KA4 -



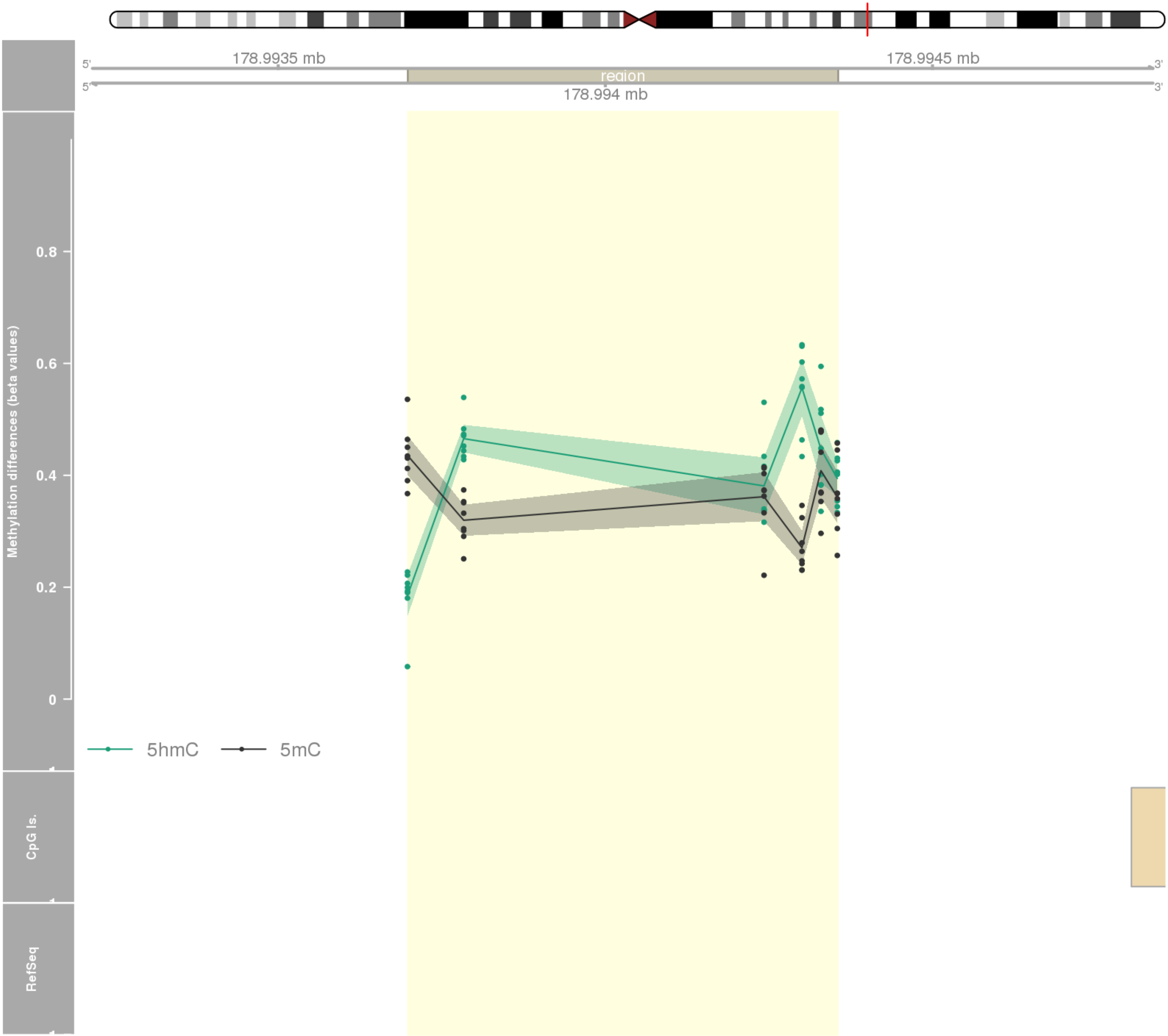
DMR 434 // chr11:63870619-63871570 // 951 pb. (9 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: MACROD1 / FLRT1 -



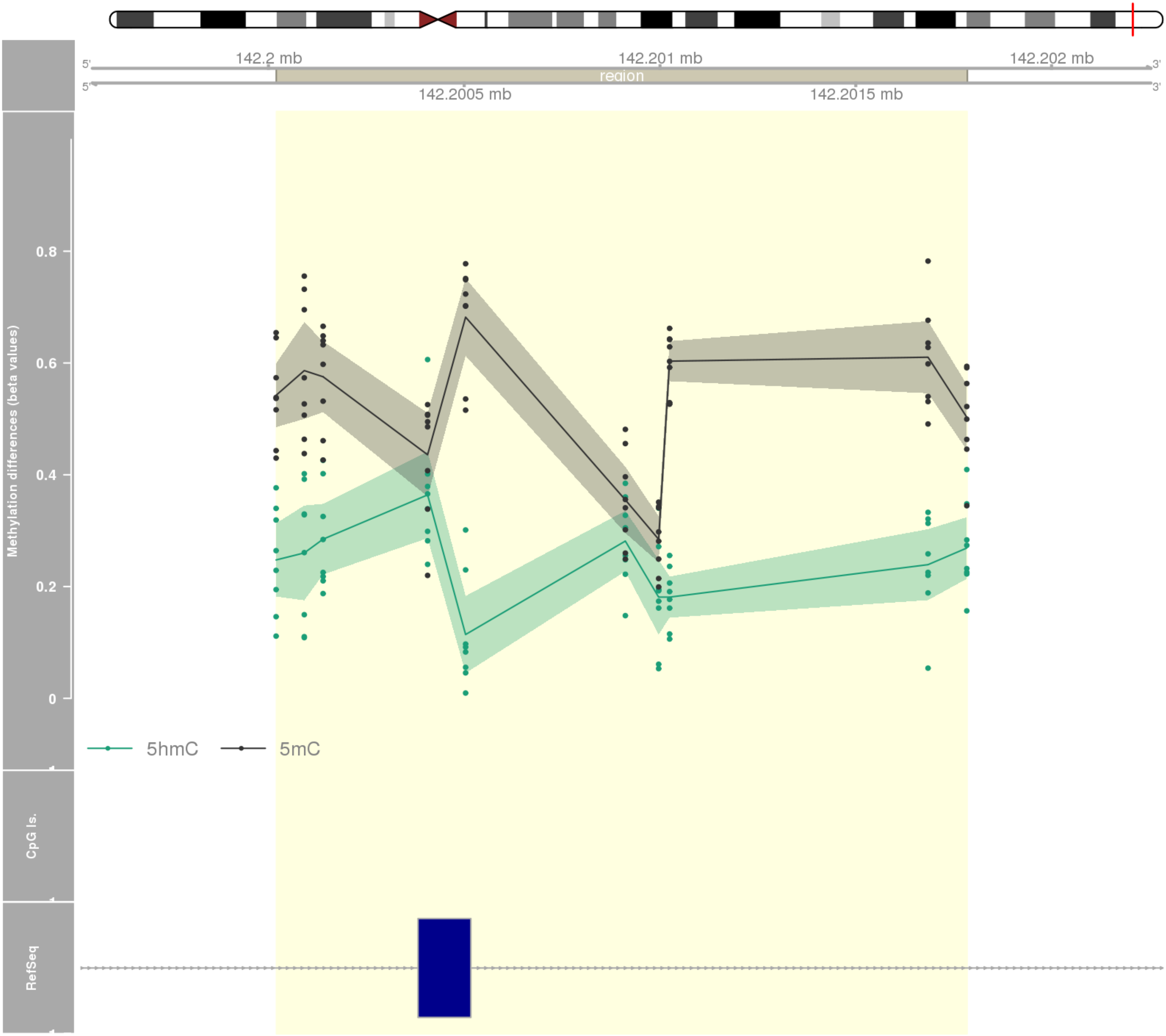
DMR 435 // chr16:67979063-67980202 // 1139 pb. (8 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.022 // fwerArea: 0.559
- genes: SLC12A4 -



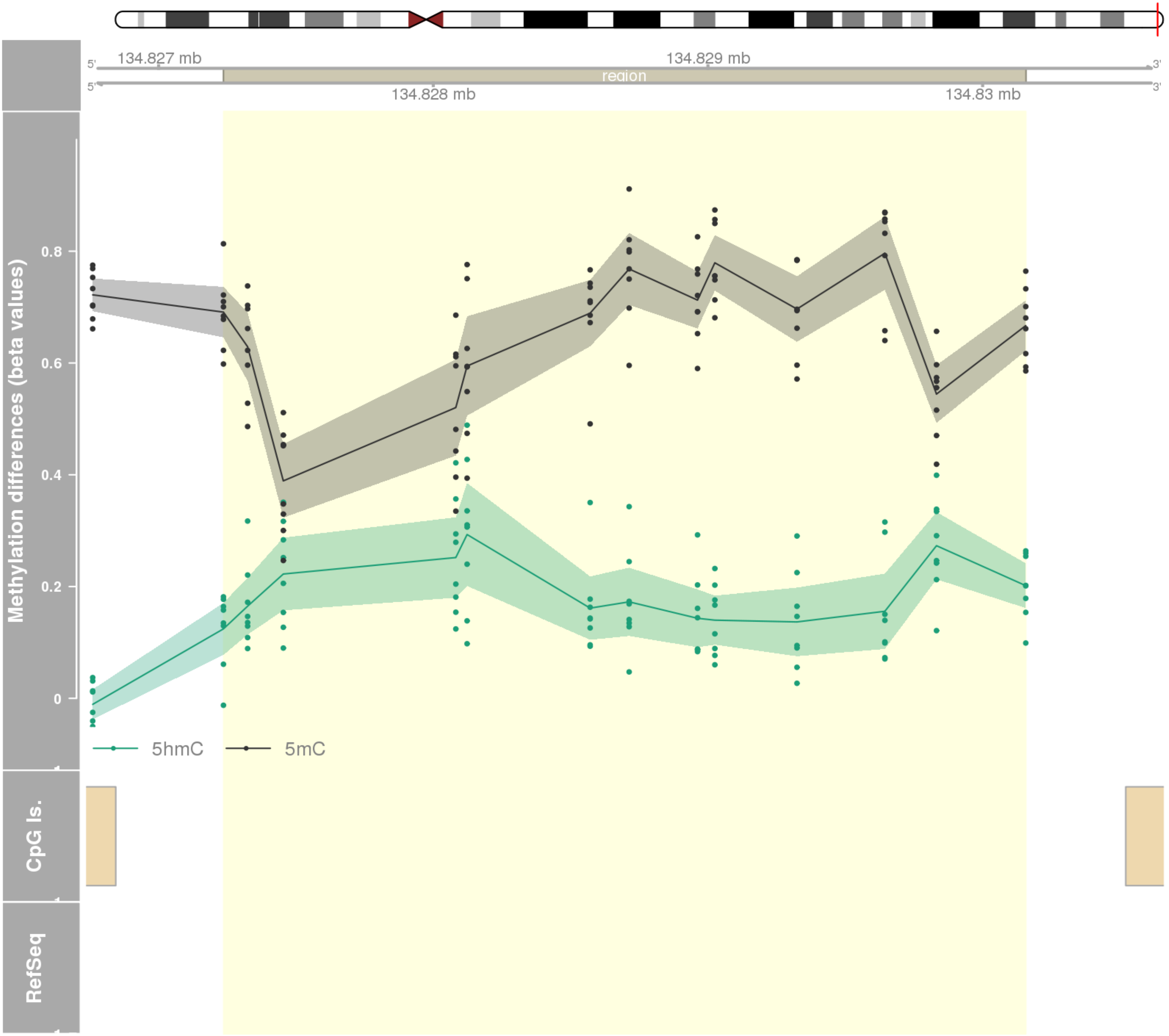
DMR 436 // chr1:178993698-178994355 // 657 pb. (6 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559



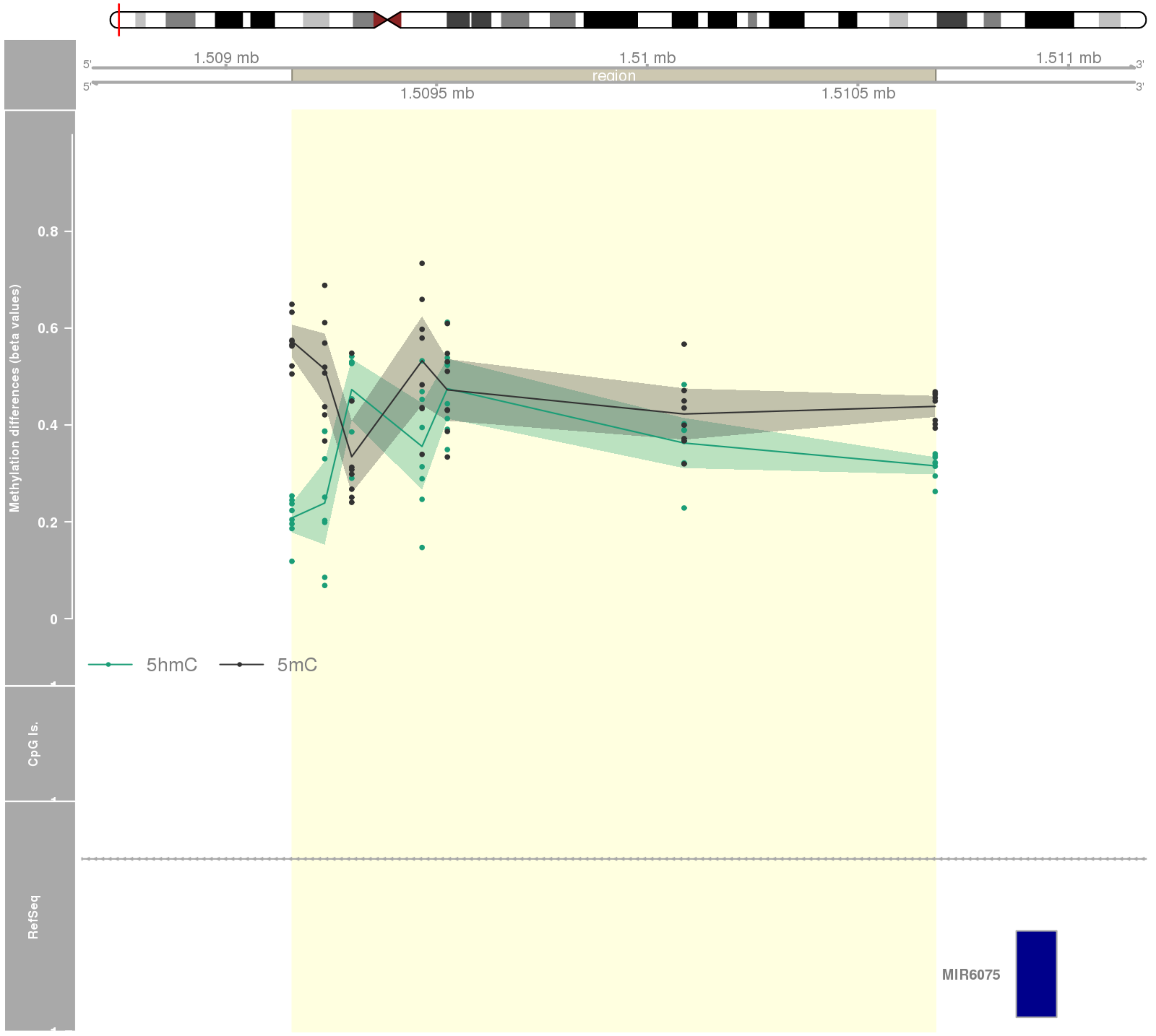
DMR 437 // chr8:142200020-142201784 // 1764 pb. (10 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559
- genes: DENND3 -



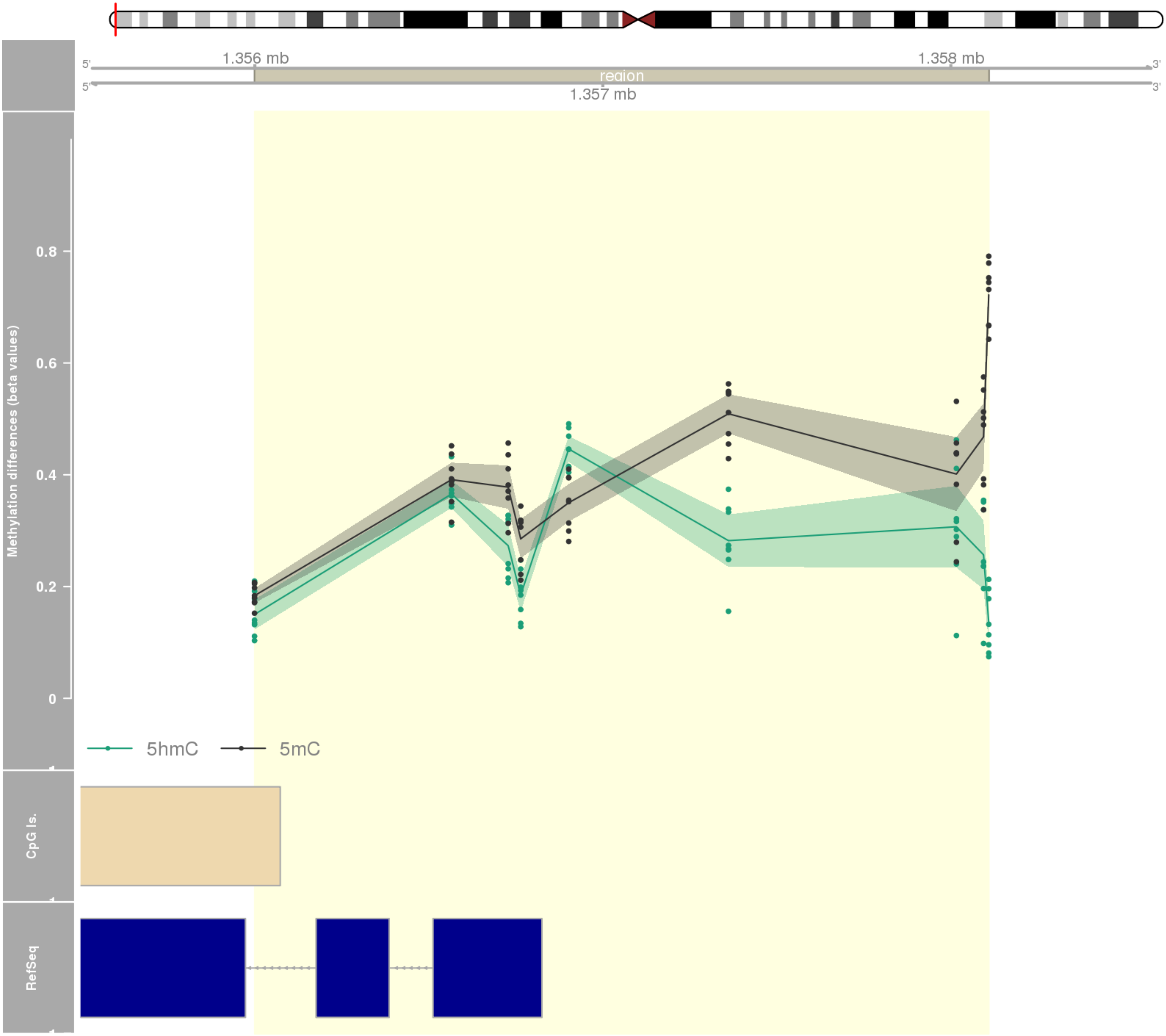
DMR 438 // chr10:134827236-134830157 // 2921 pb. (13 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559



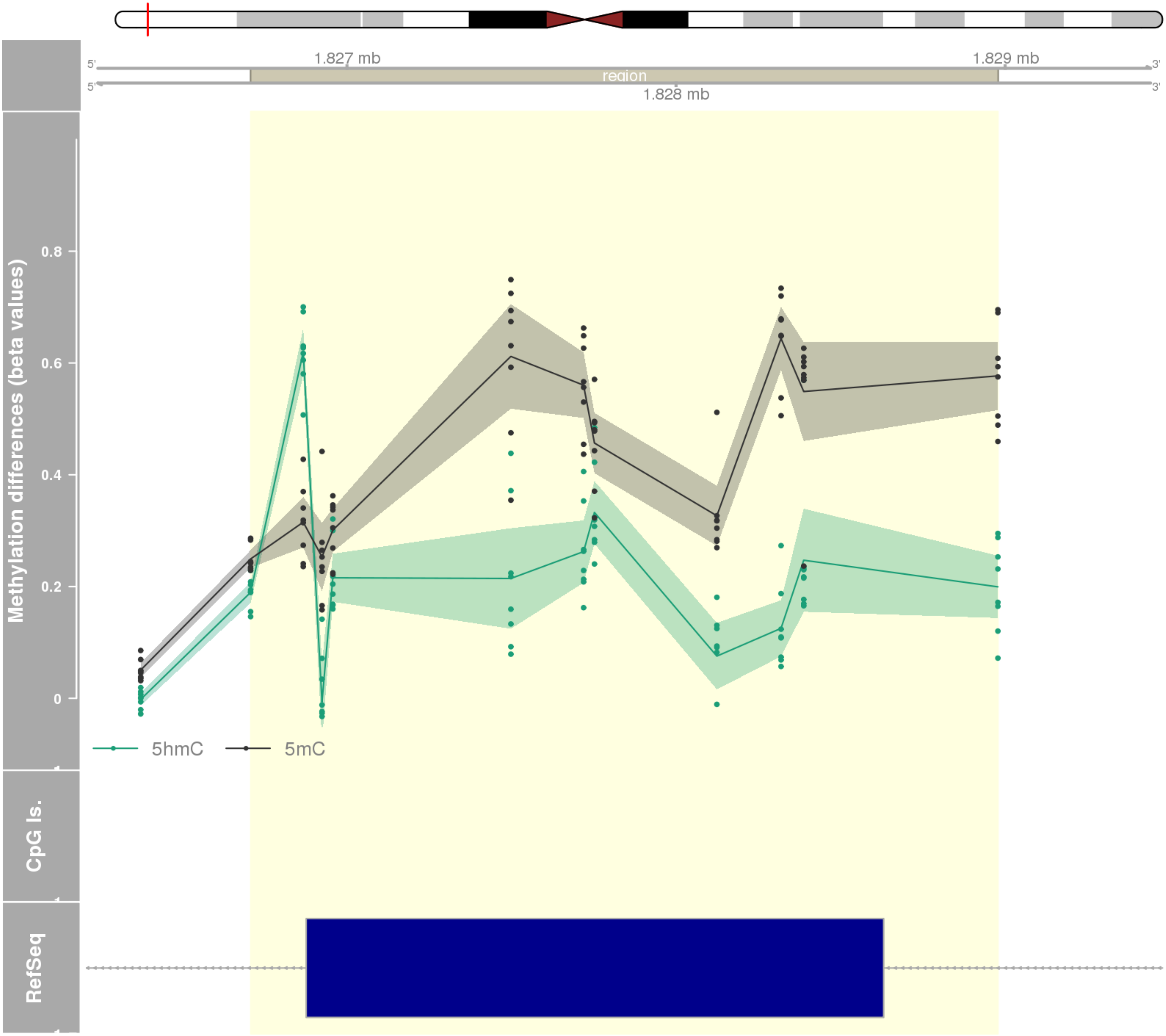
DMR 439 // chr5:1509157-1510684 // 1527 pb. (7 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559
- genes: LPCAT1 -



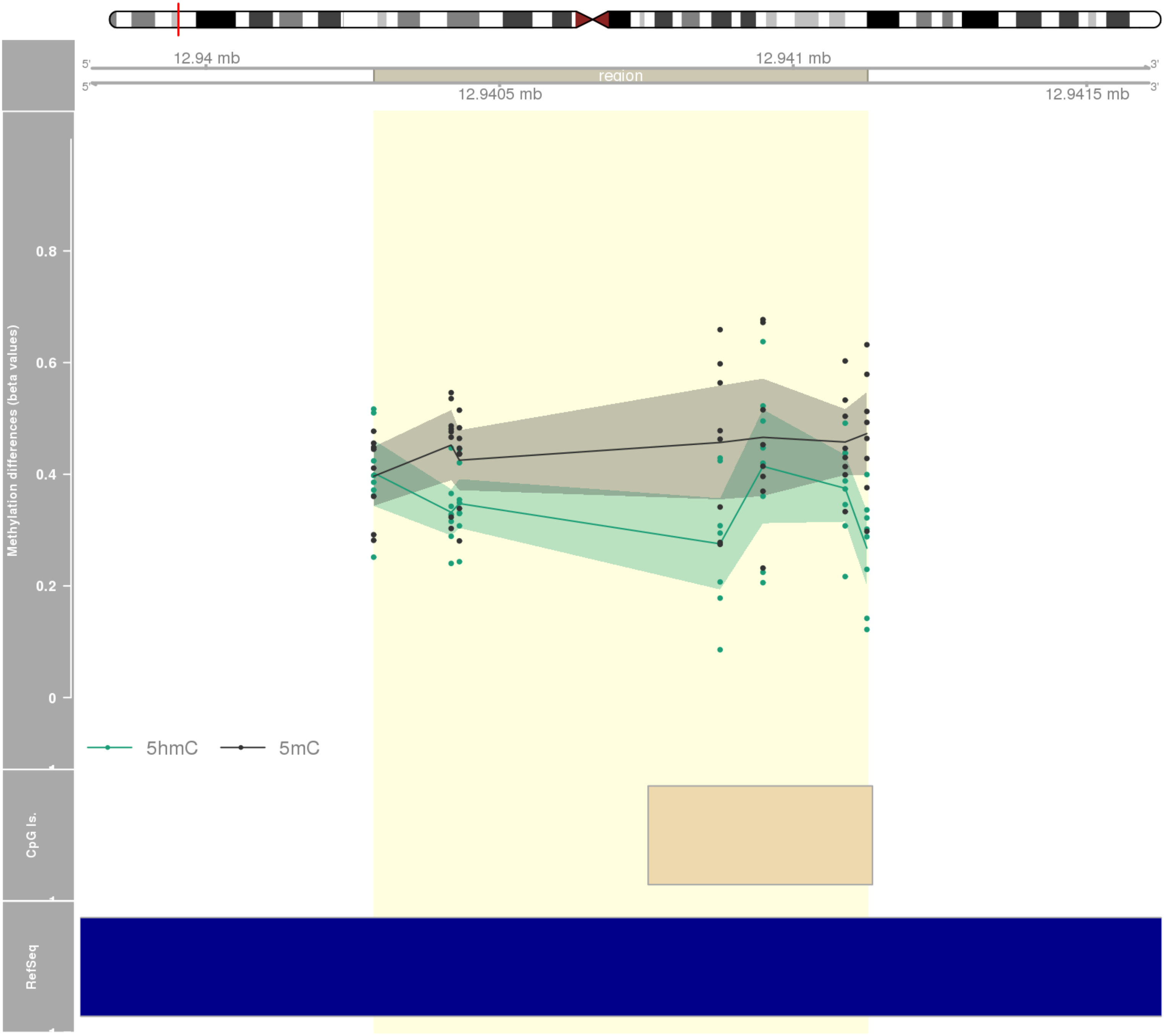
DMR 440 // chr1:1355999-1358109 // 2110 pb. (9 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559
- genes: ANKRD65 -



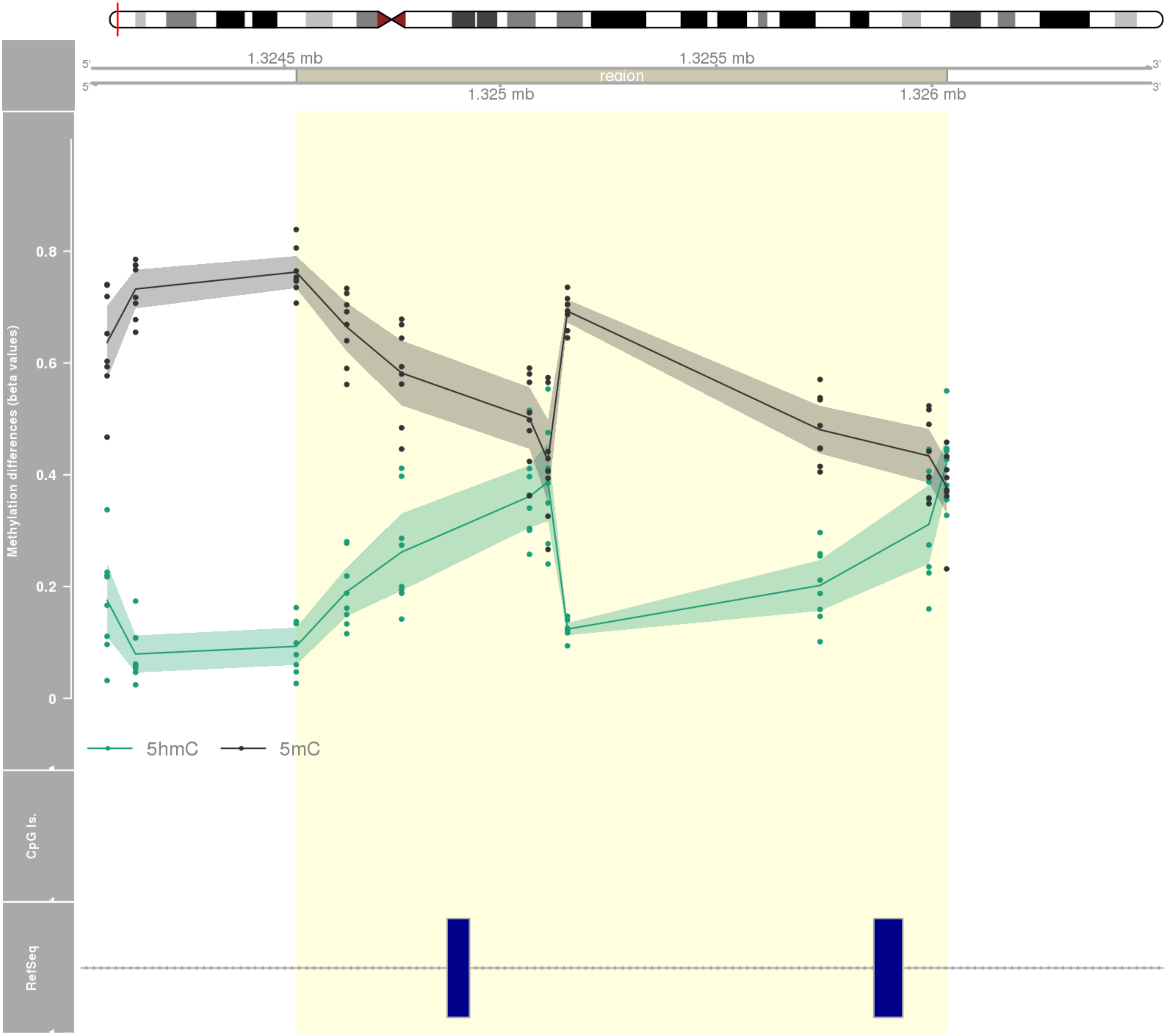
DMR 441 // chr19:1826707-1828978 // 2271 pb. (11 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559
- genes: REXO1 -



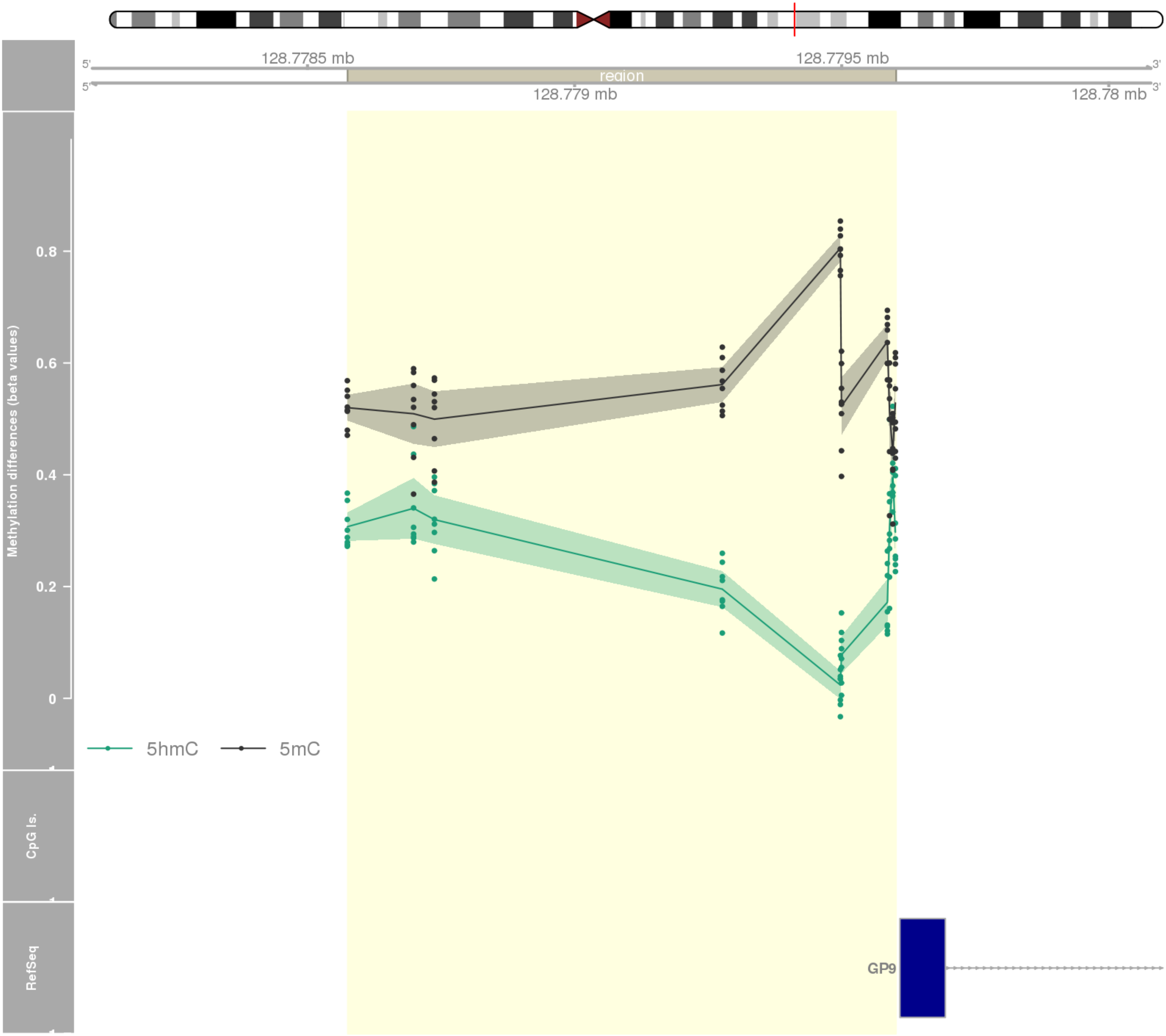
DMR 442 // chr3:12940286-12941126 // 840 pb. (7 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559
- genes: IQSEC1 -



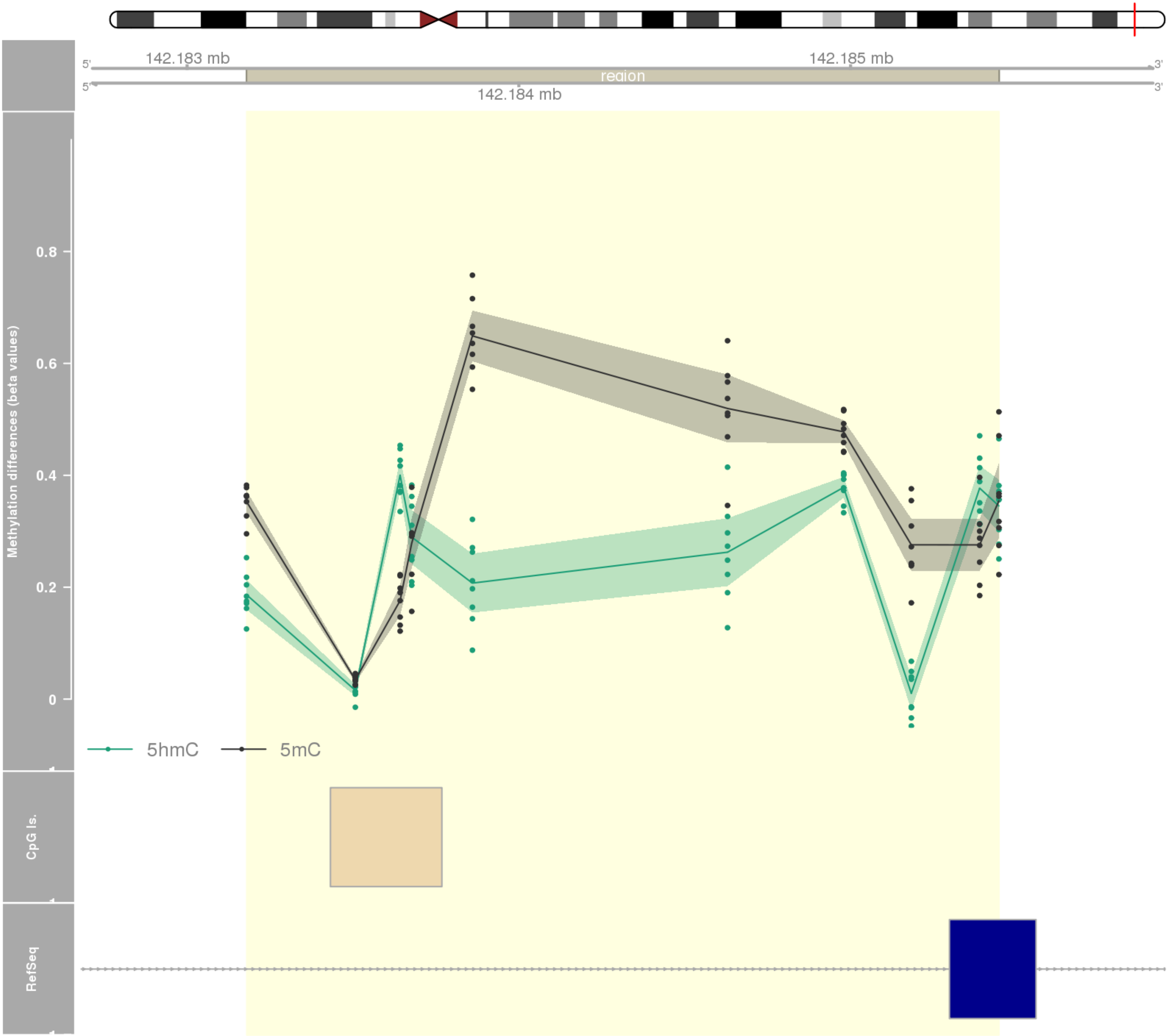
DMR 443 // chr5:1324528-1326034 // 1506 pb. (9 probes) // pvalue: 0.008 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.559
- genes: CLPTM1L -



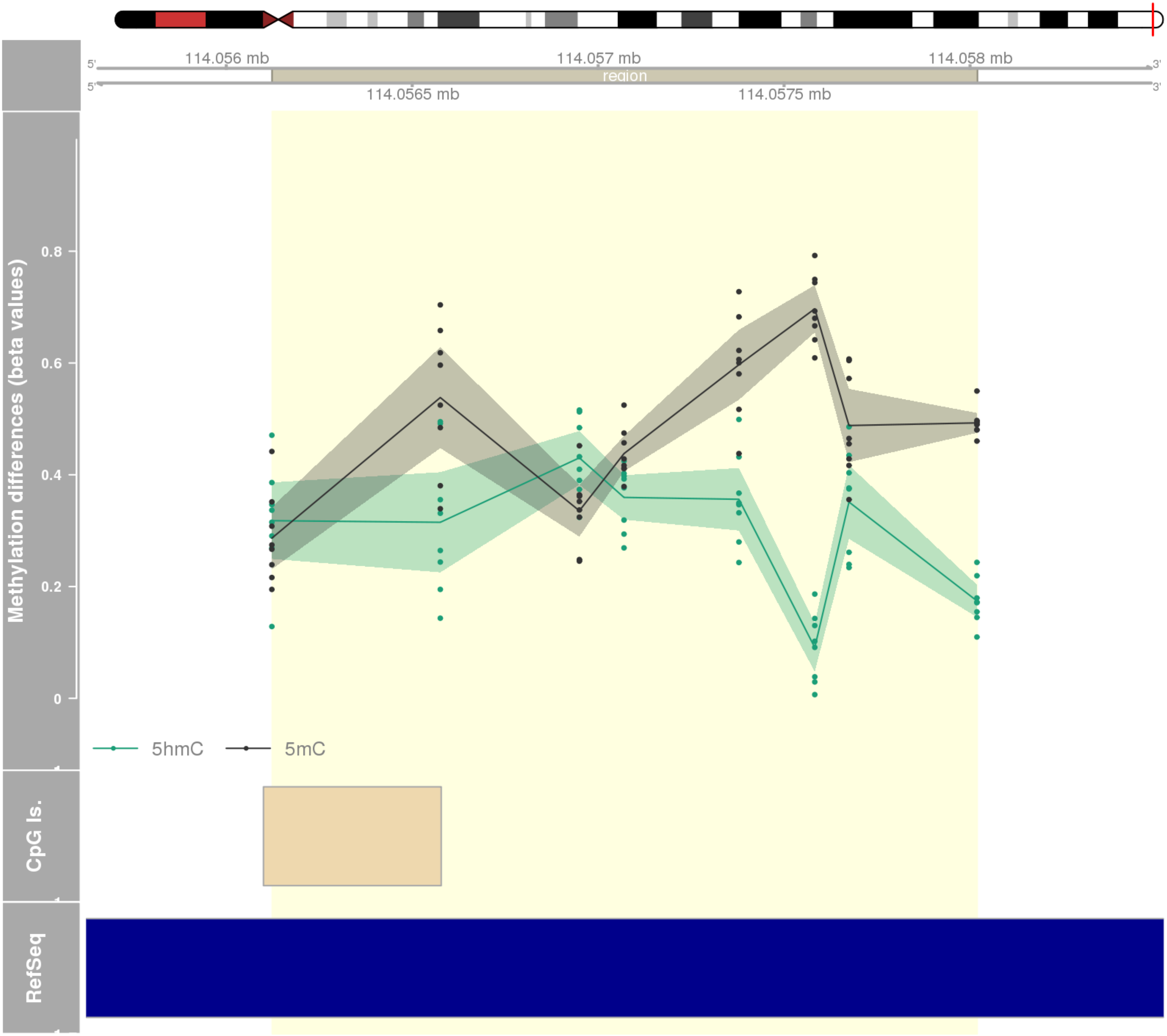
DMR 444 // chr3:128778575-128779601 // 1026 pb. (10 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679



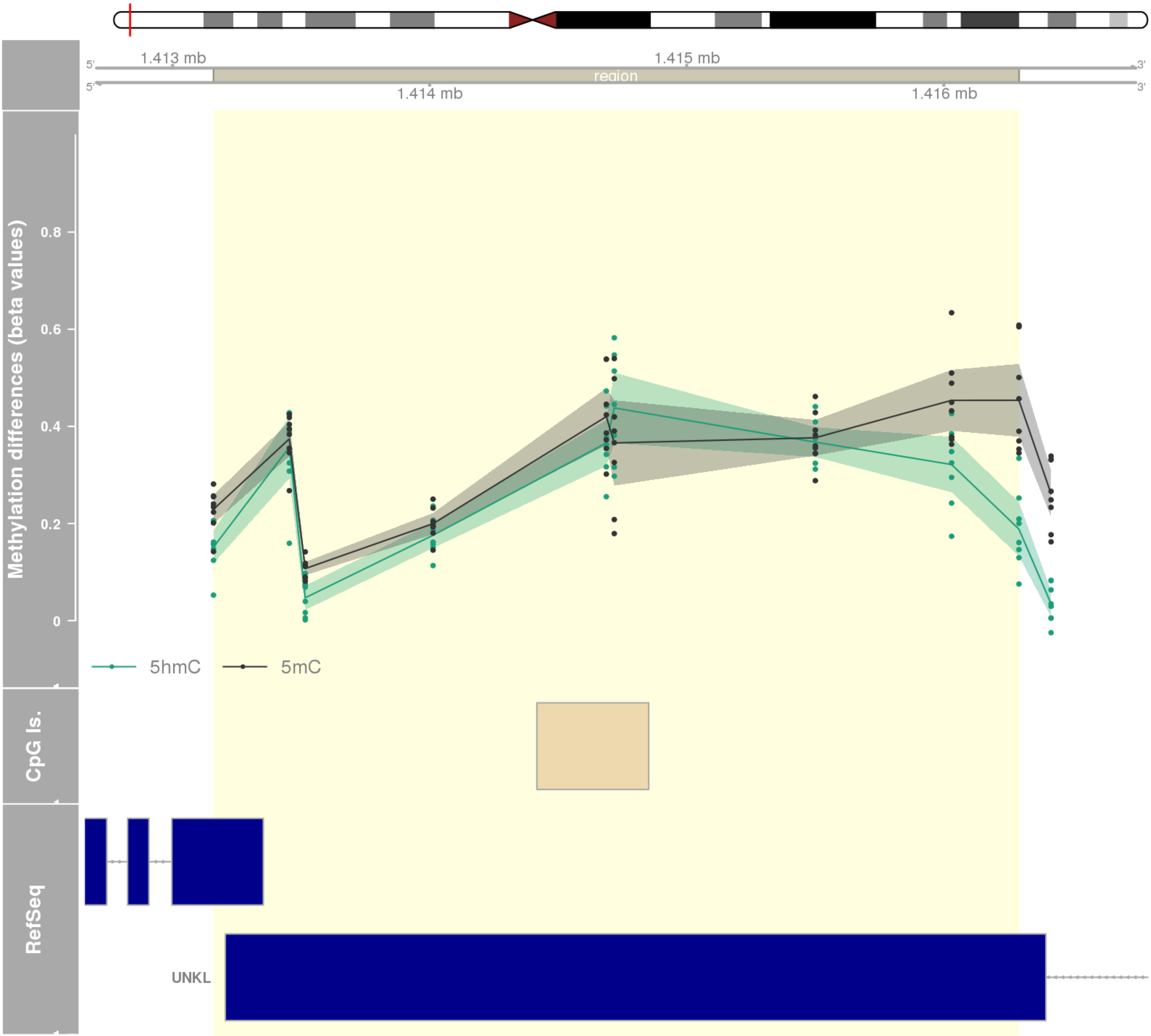
DMR 445 // chr8:142183179-142185447 // 2268 pb. (10 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: DENND3 -



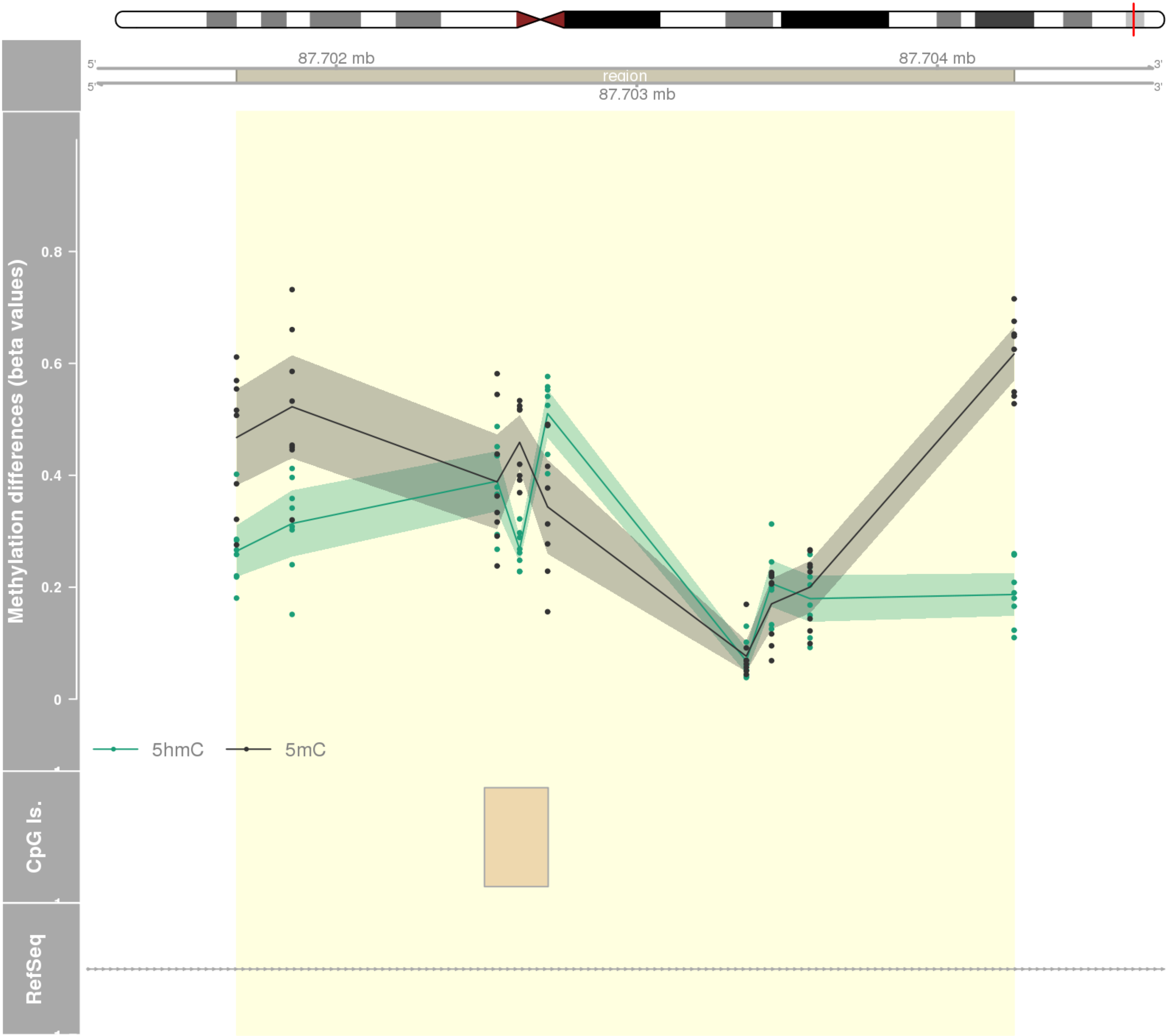
DMR 446 // chr13:114056123-114058019 // 1896 pb. (8 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679



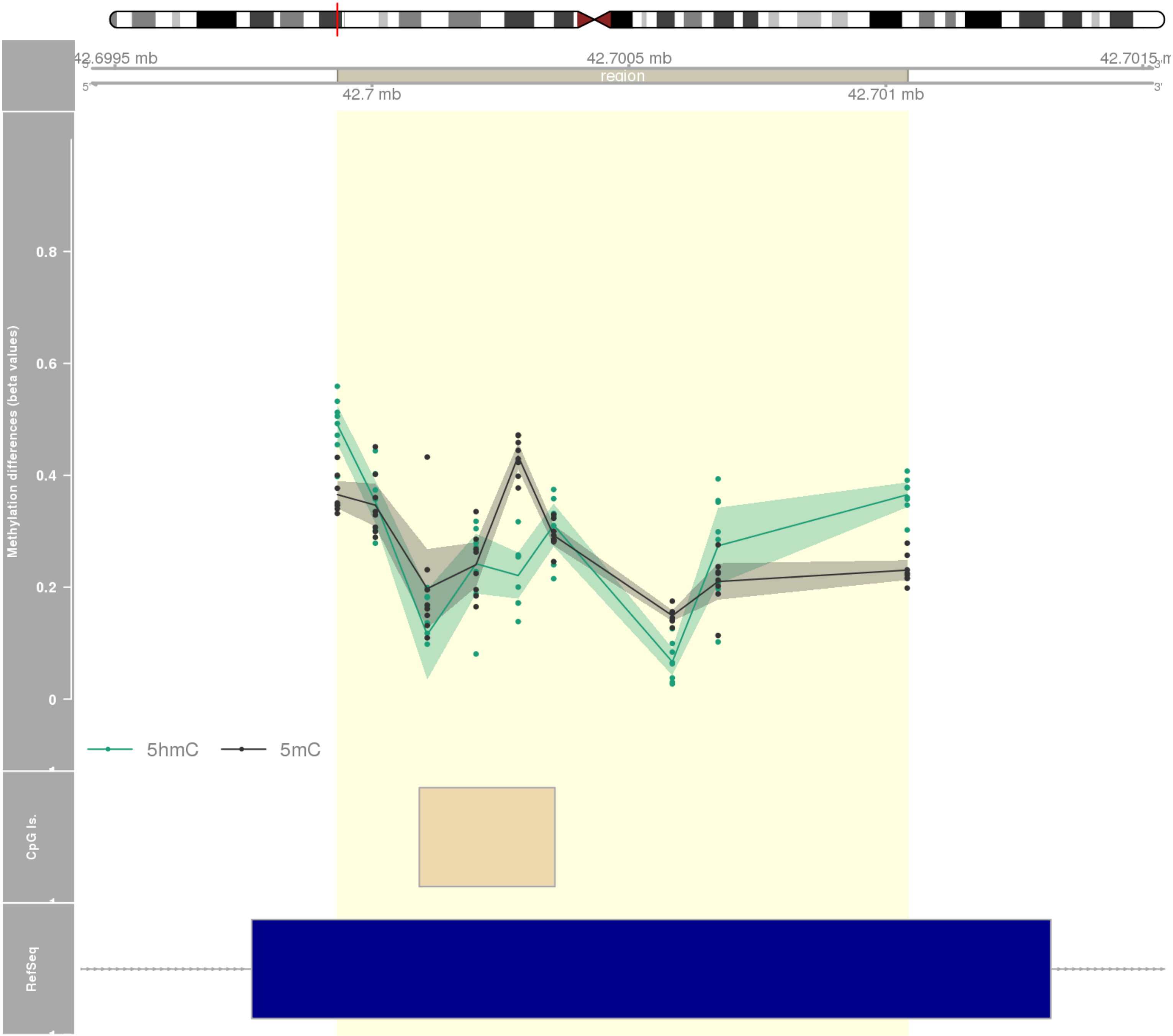
DMR 447 // chr16:1413159-1416292 // 3133 pb. (9 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: GNPTG / UNKL -



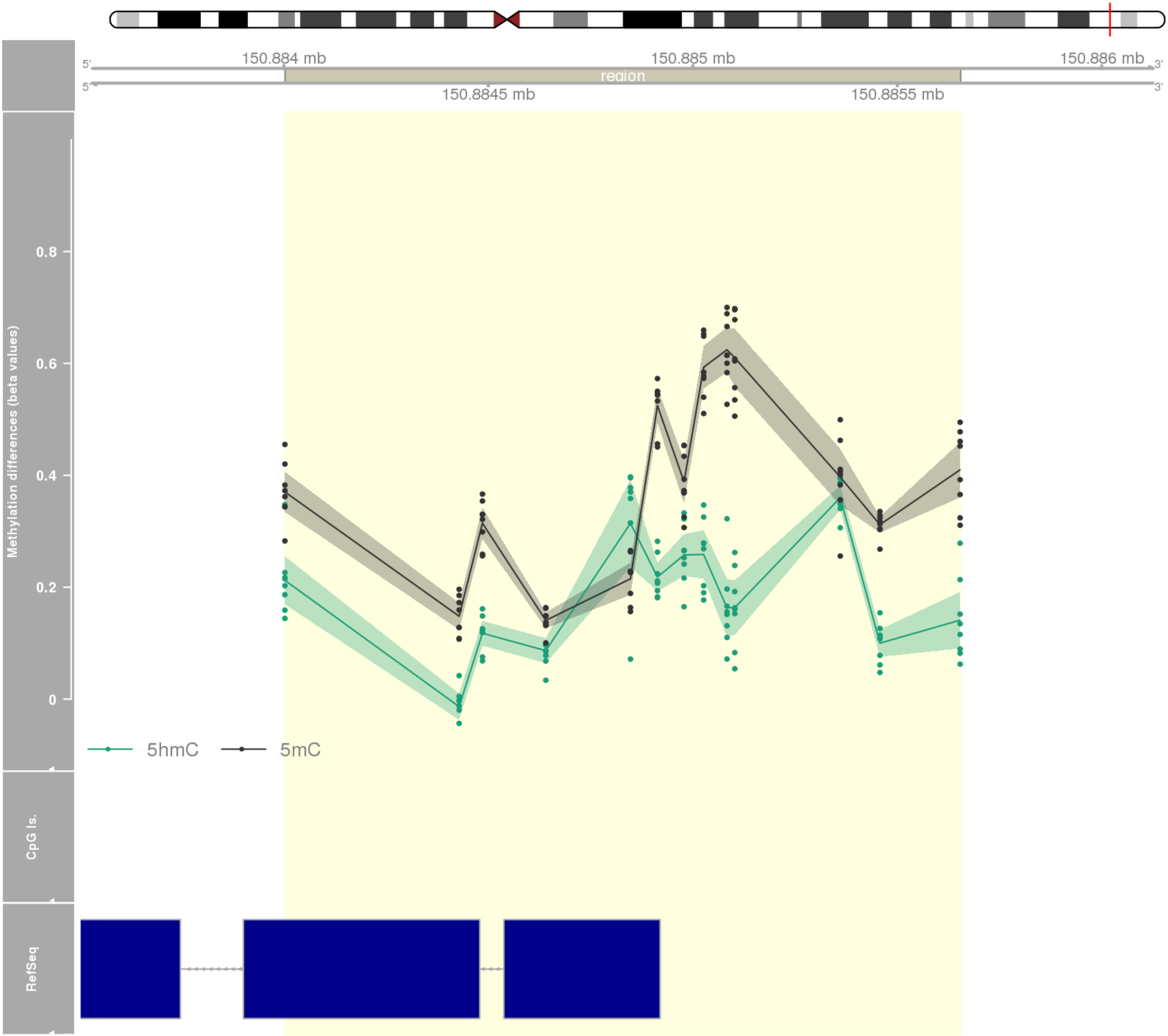
DMR 448 // chr16:87701668-87704255 // 2587 pb. (9 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: JPH3 -



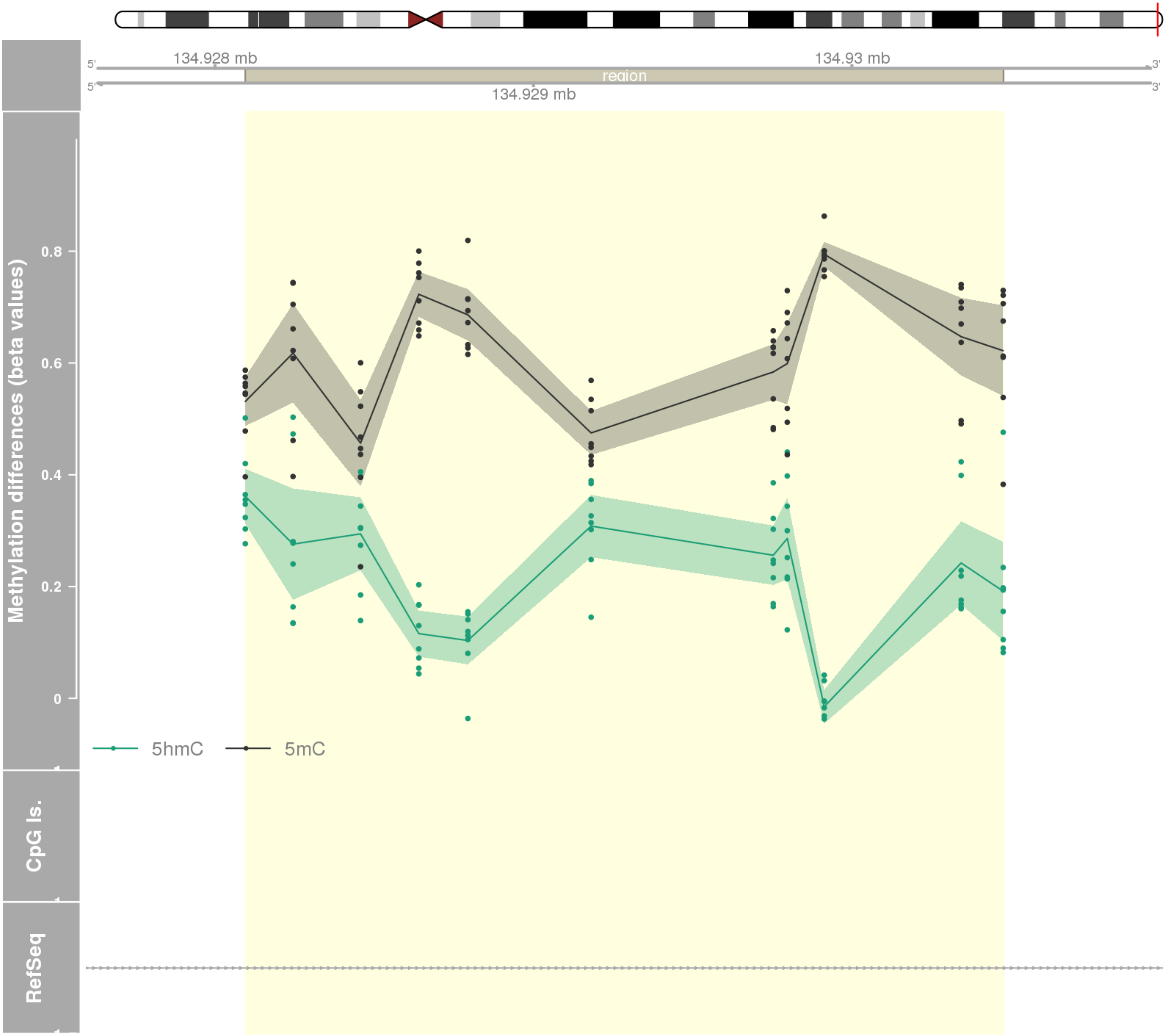
DMR 449 // chr3:42699933-42701042 // 1109 pb. (9 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: ZBTB47 -



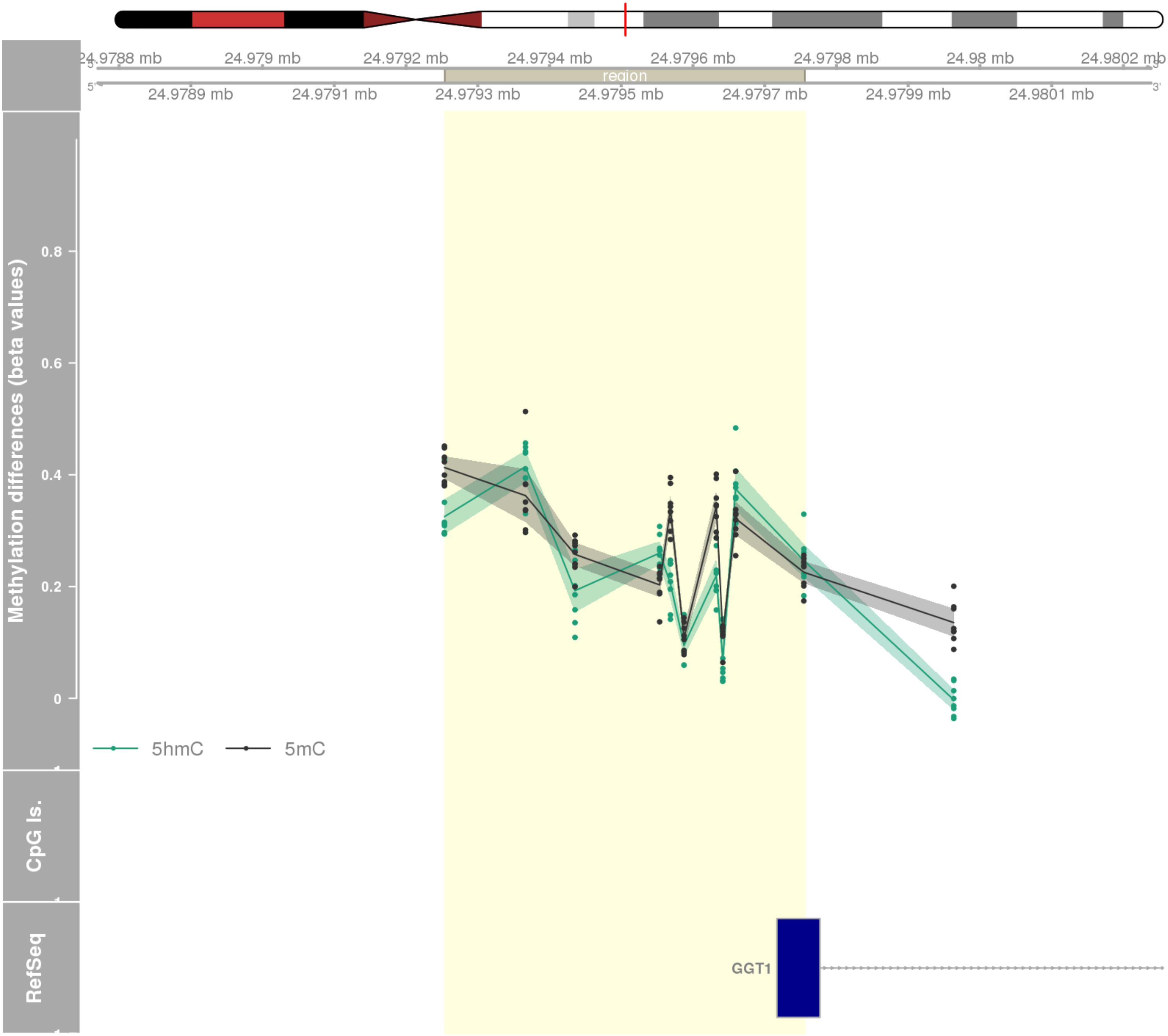
DMR 450 // chr7:150884003-150885654 // 1651 pb. (13 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: ASB10 -



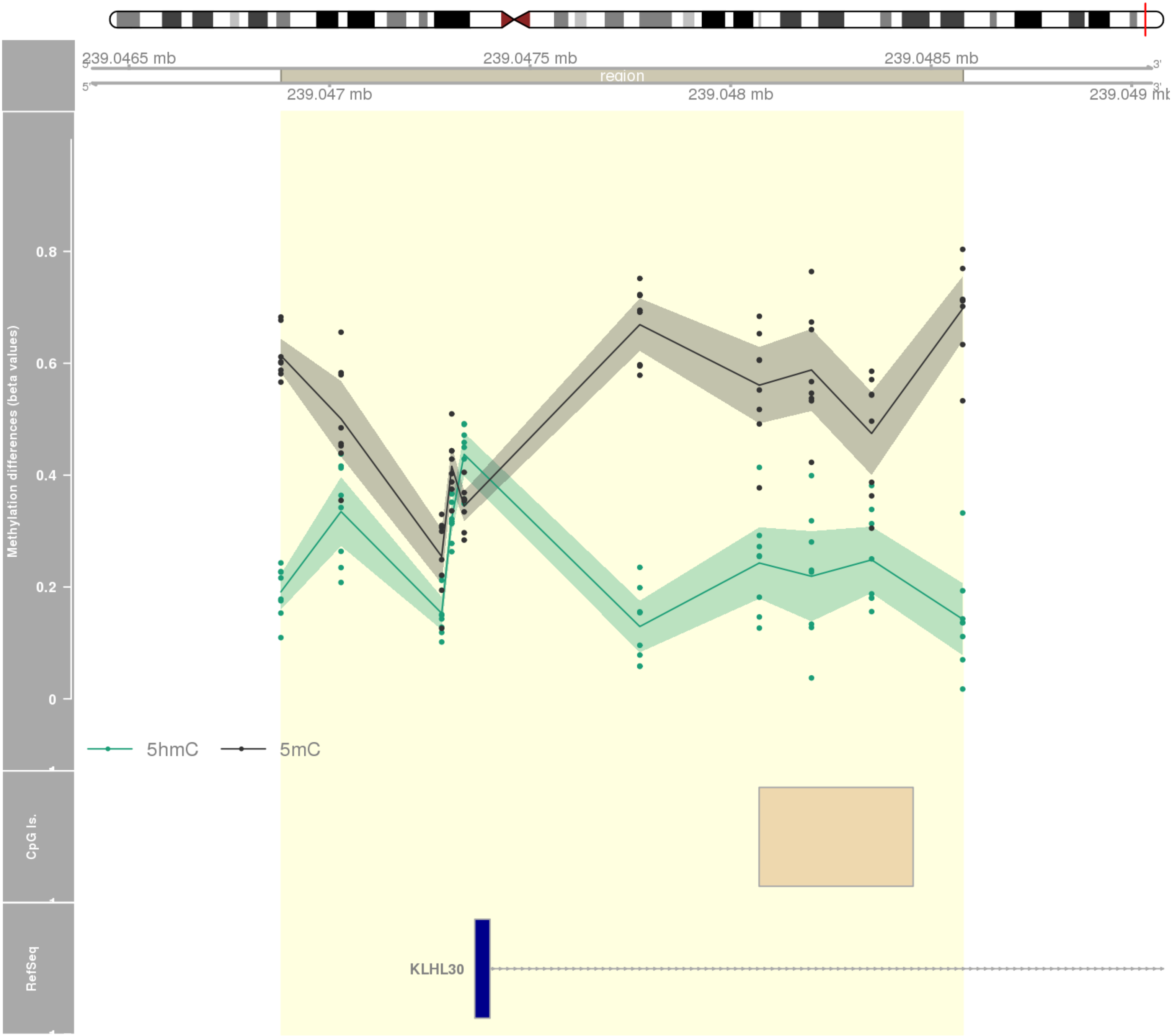
DMR 451 // chr10:134928095-134930475 // 2380 pb. (11 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: GPR123 -



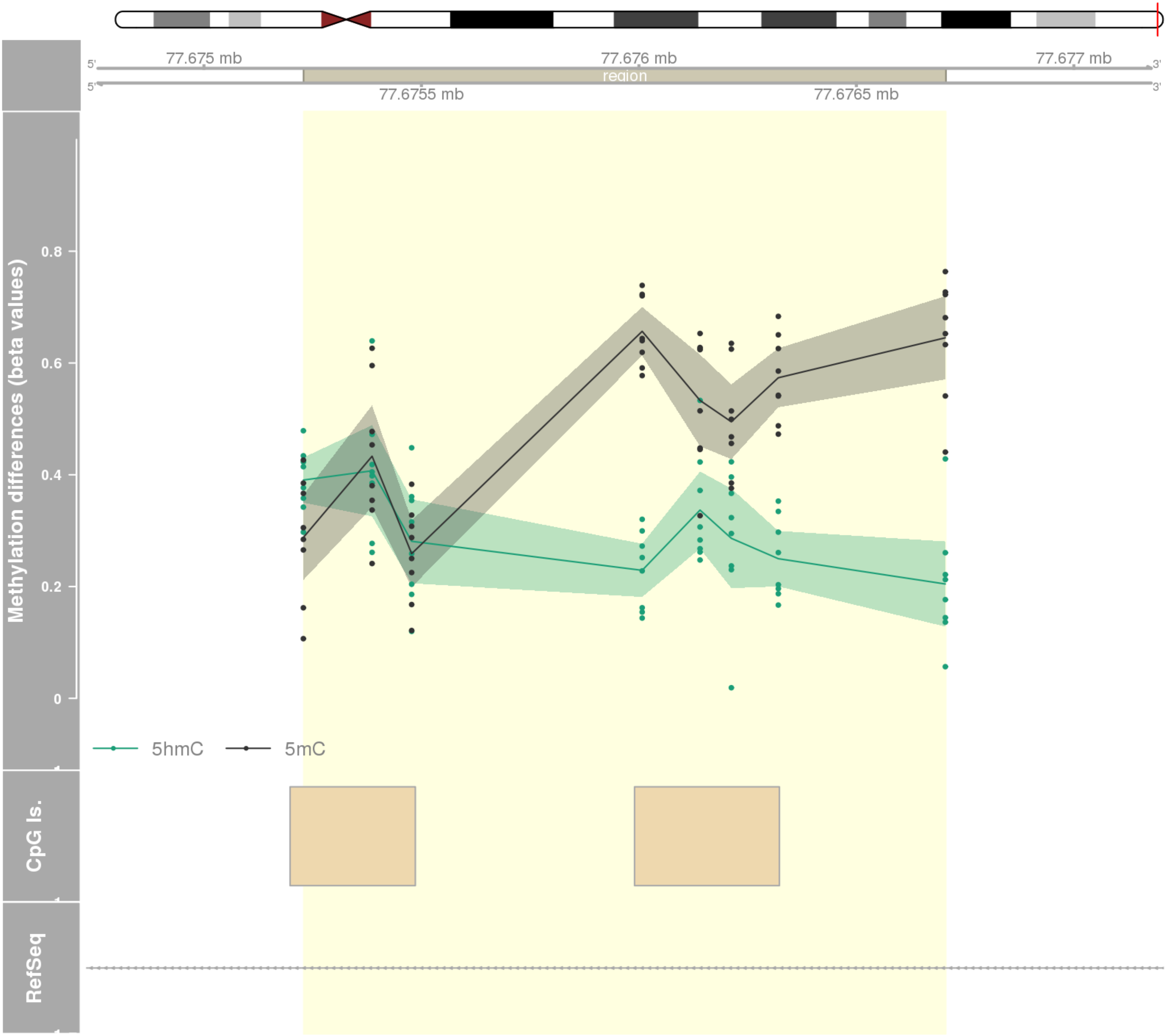
DMR 452 // chr22:24979254-24979755 // 501 pb. (10 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: SNRPD3 / GGT1 -



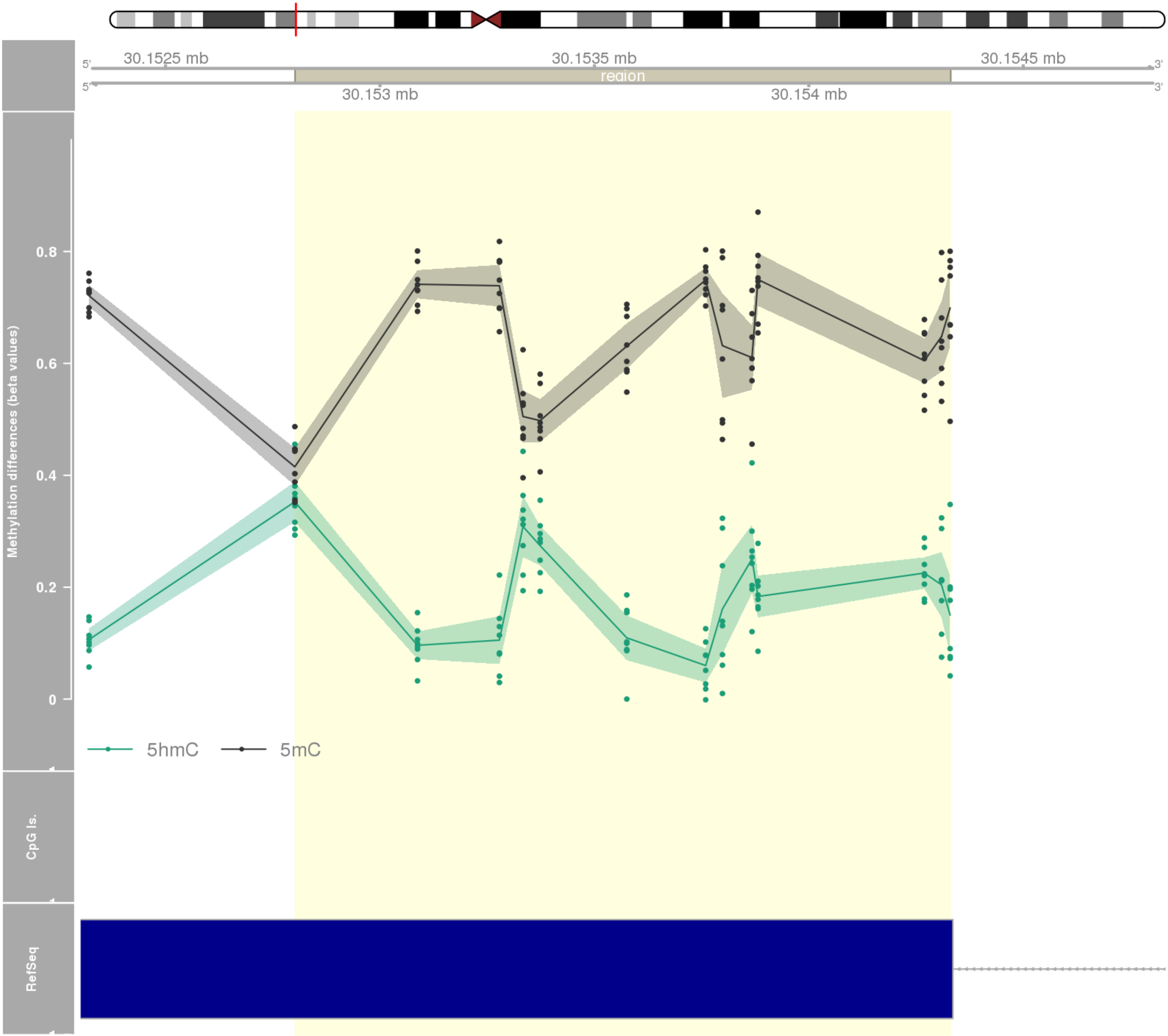
DMR 453 // chr2:239046879-239048579 // 1700 pb. (10 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.023 // fwerArea: 0.679
- genes: KLHL30 -



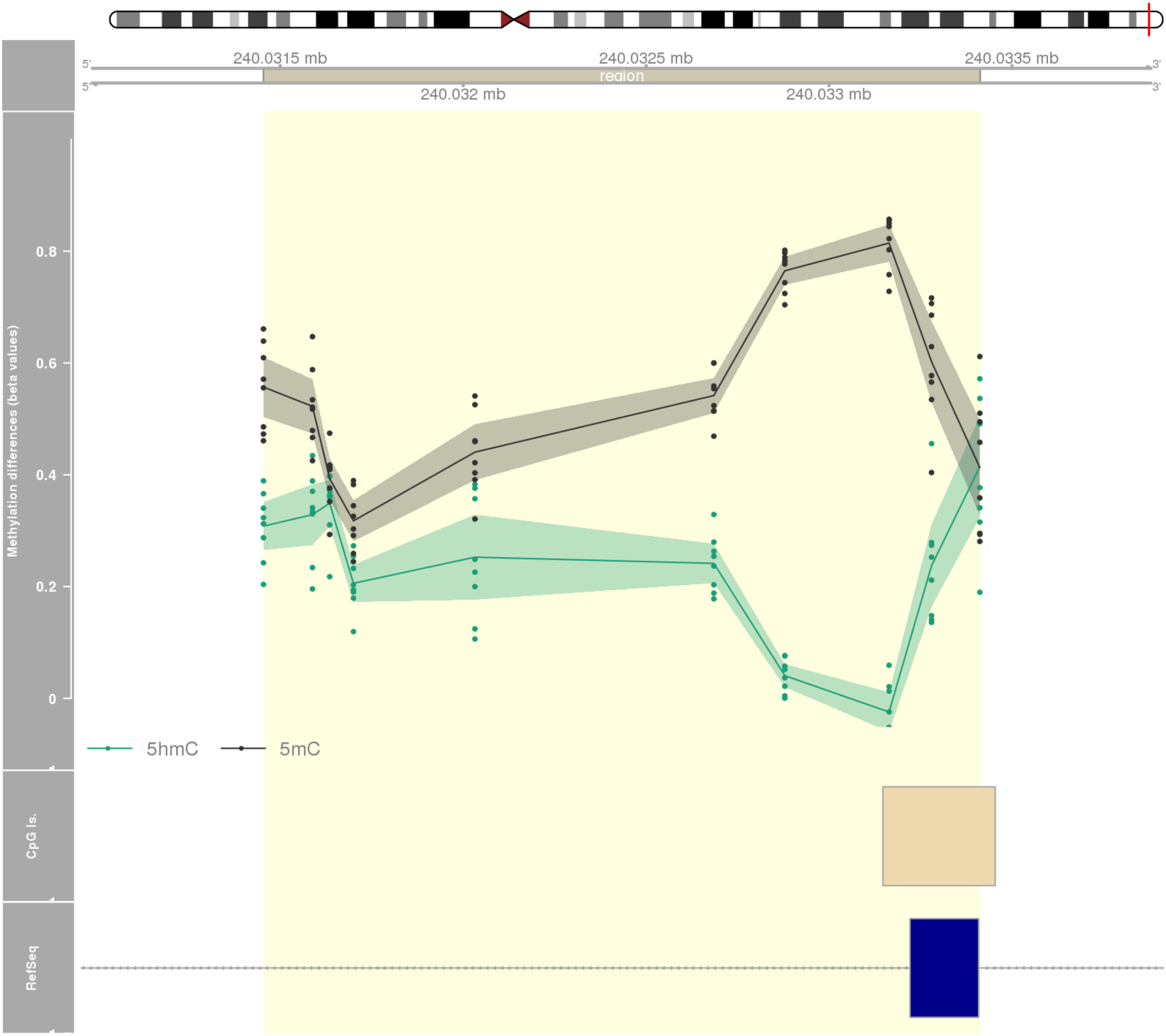
DMR 454 // chr18:77675229-77676705 // 1476 pb. (8 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: PQLC1 -



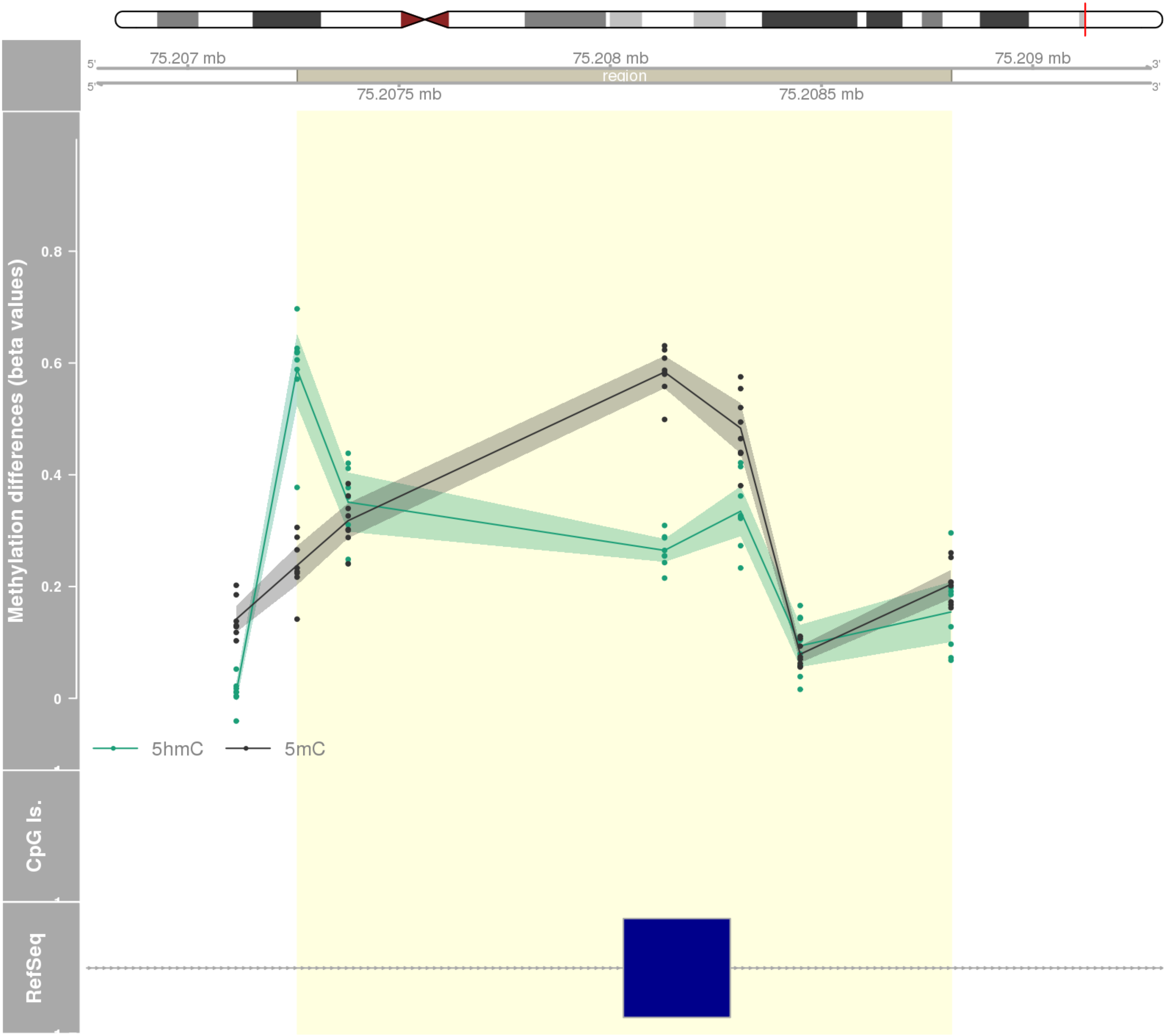
DMR 455 // chr6:30152802-30154330 // 1528 pb. (13 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: TRIM26 -



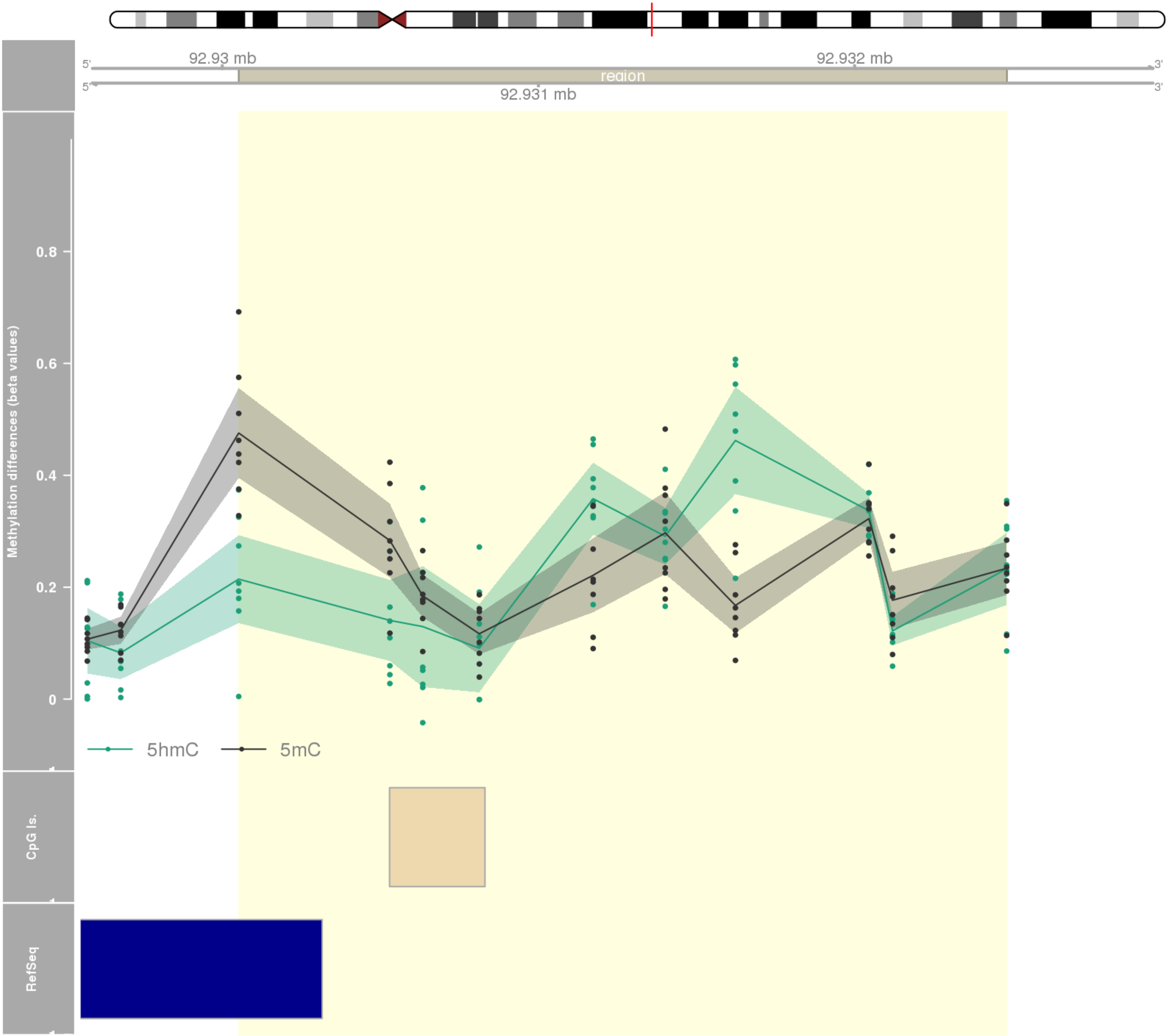
DMR 456 // chr2:240031454-240033412 // 1958 pb. (10 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: HDAC4 -



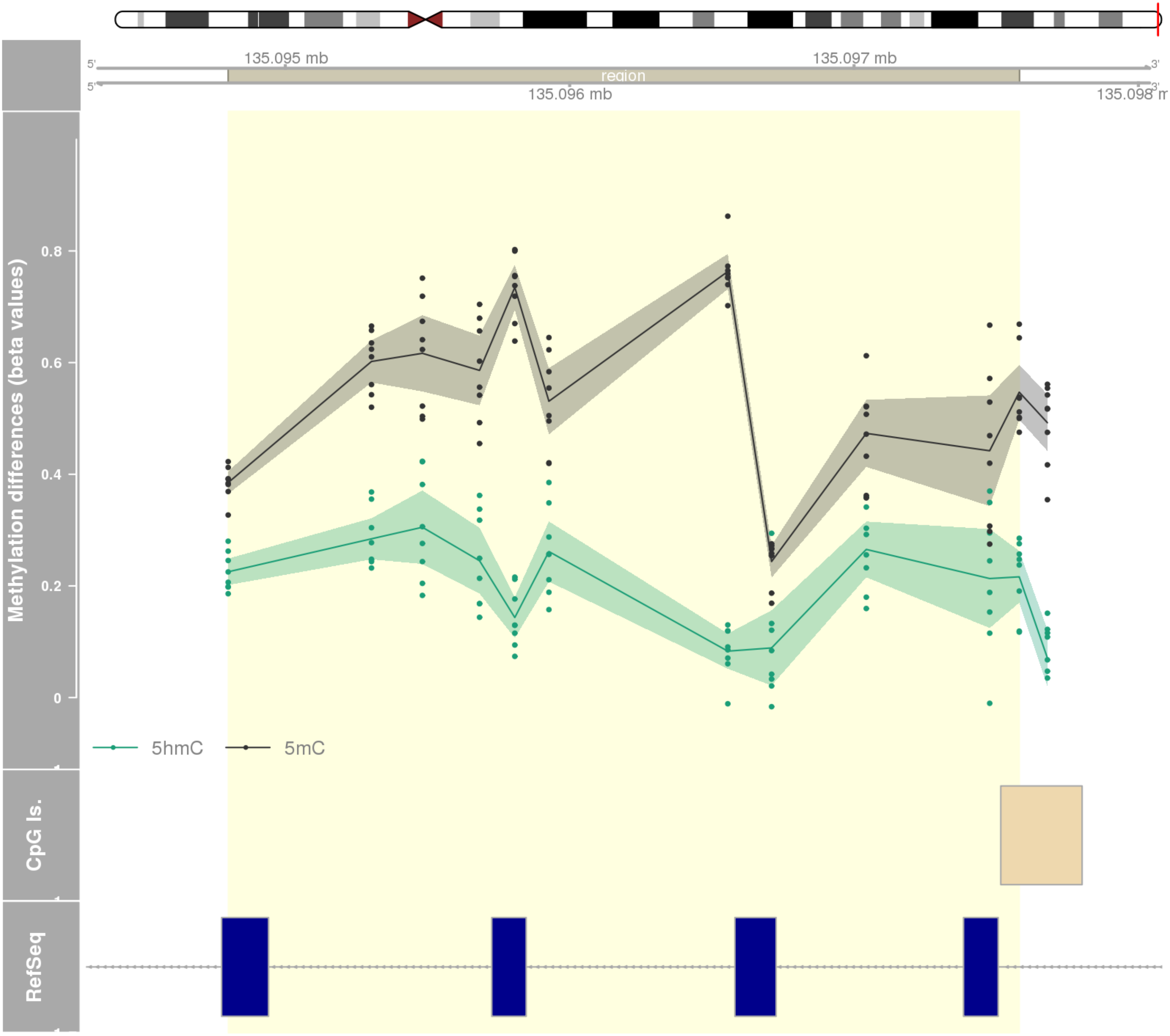
DMR 457 // chr17:75207259-75208807 // 1548 pb. (6 probes) // pvalue: 0 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: SEC14L1 -



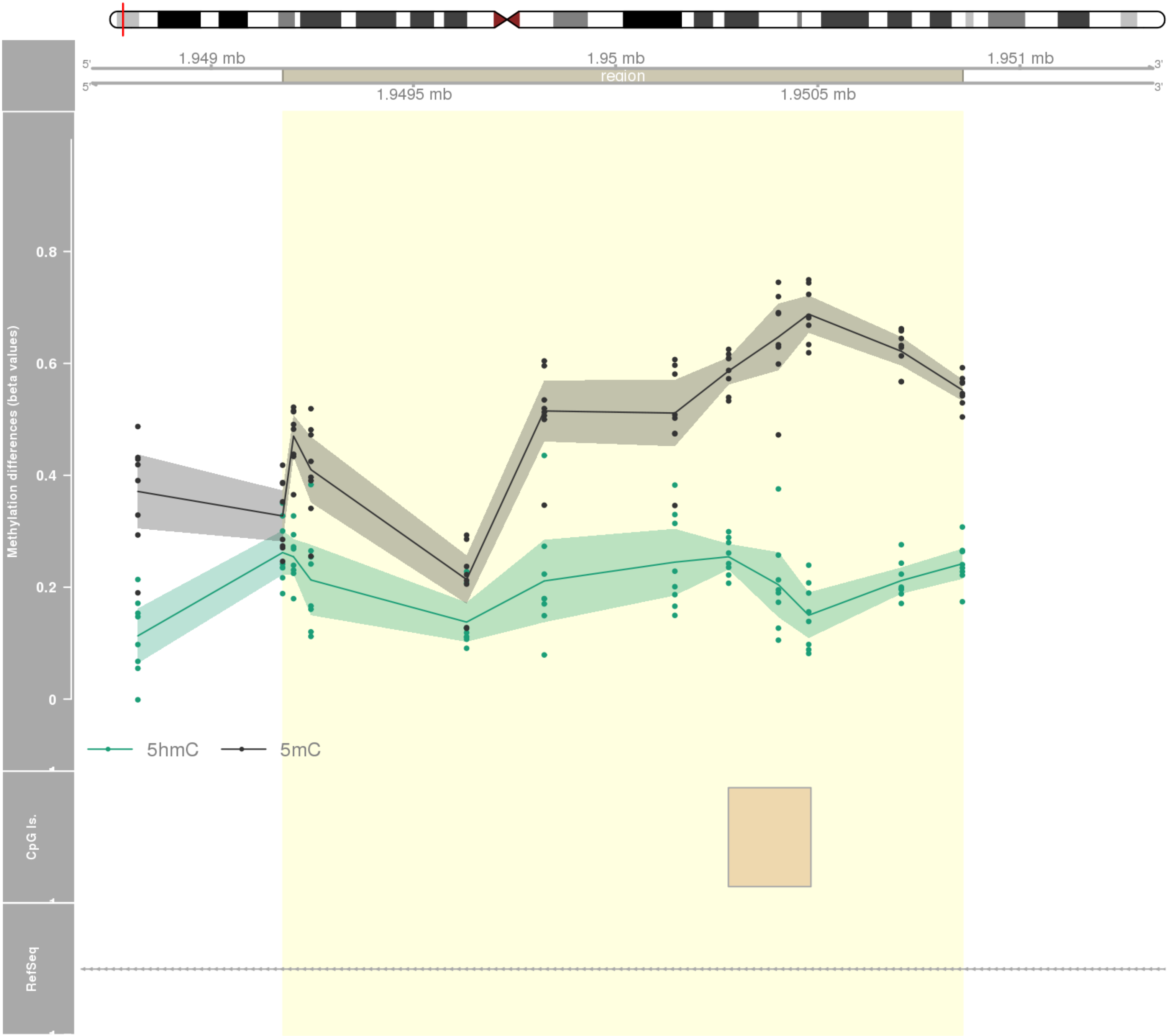
DMR 458 // chr5:92930052-92932481 // 2429 pb. (10 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: NR2F1 -



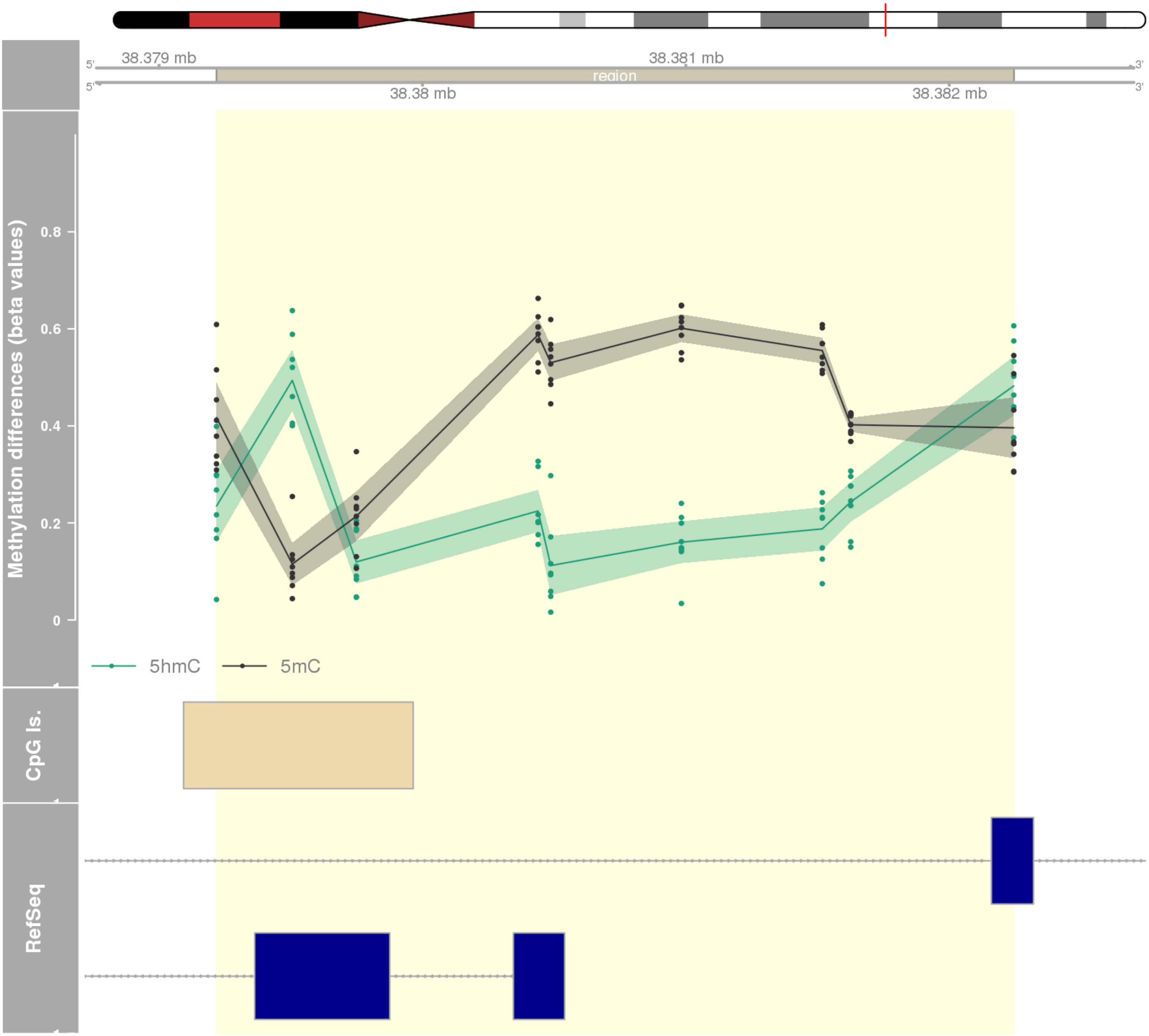
DMR 459 // chr10:135094799-135097581 // 2782 pb. (11 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: TUBGCP2 -



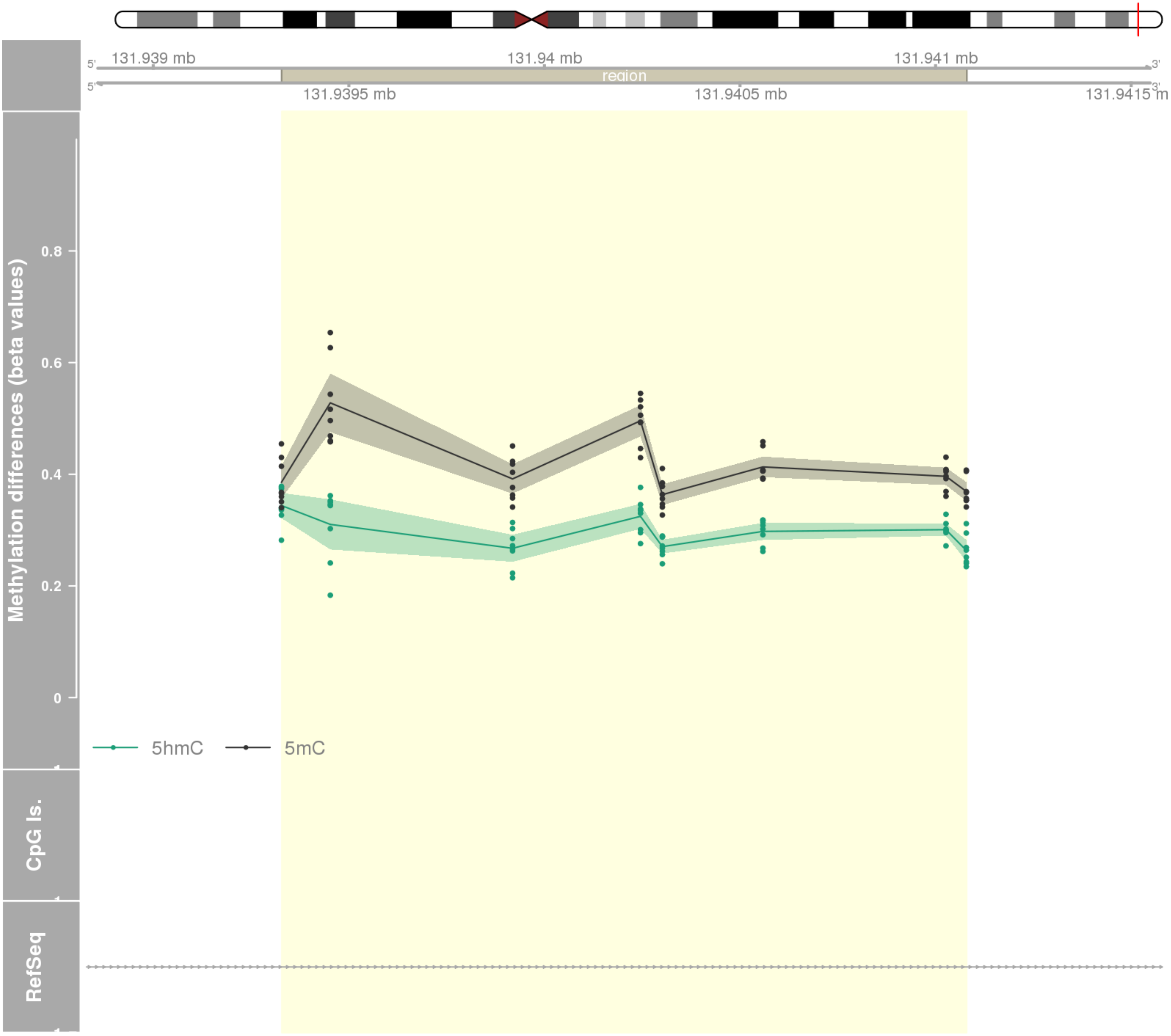
DMR 460 // chr7:1949177-1950858 // 1681 pb. (11 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: MAD1L1 -



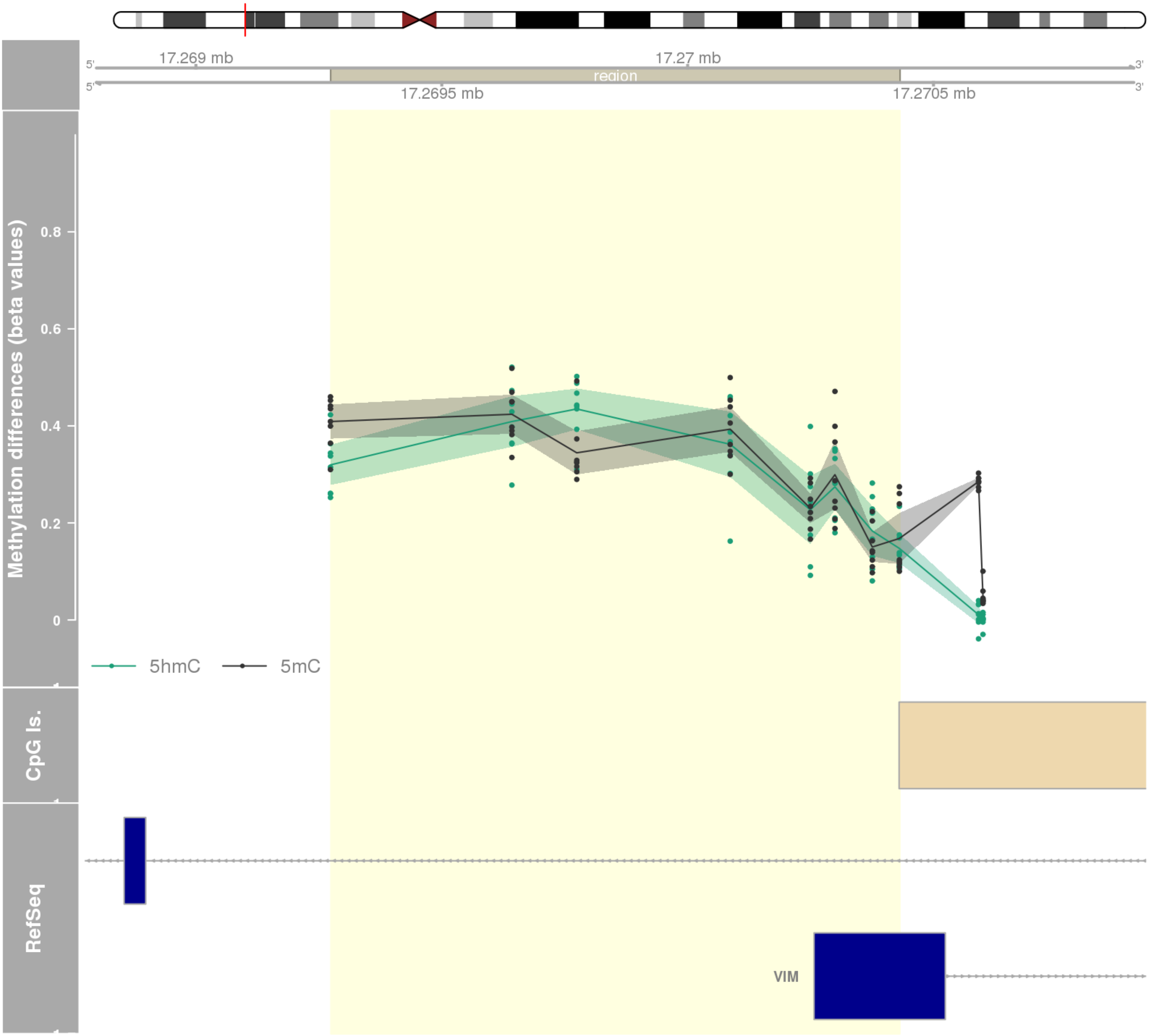
DMR 461 // chr22:38379218-38382245 // 3027 pb. (9 probes) // pvalue: 0.009 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: POLR2F / SOX10 -



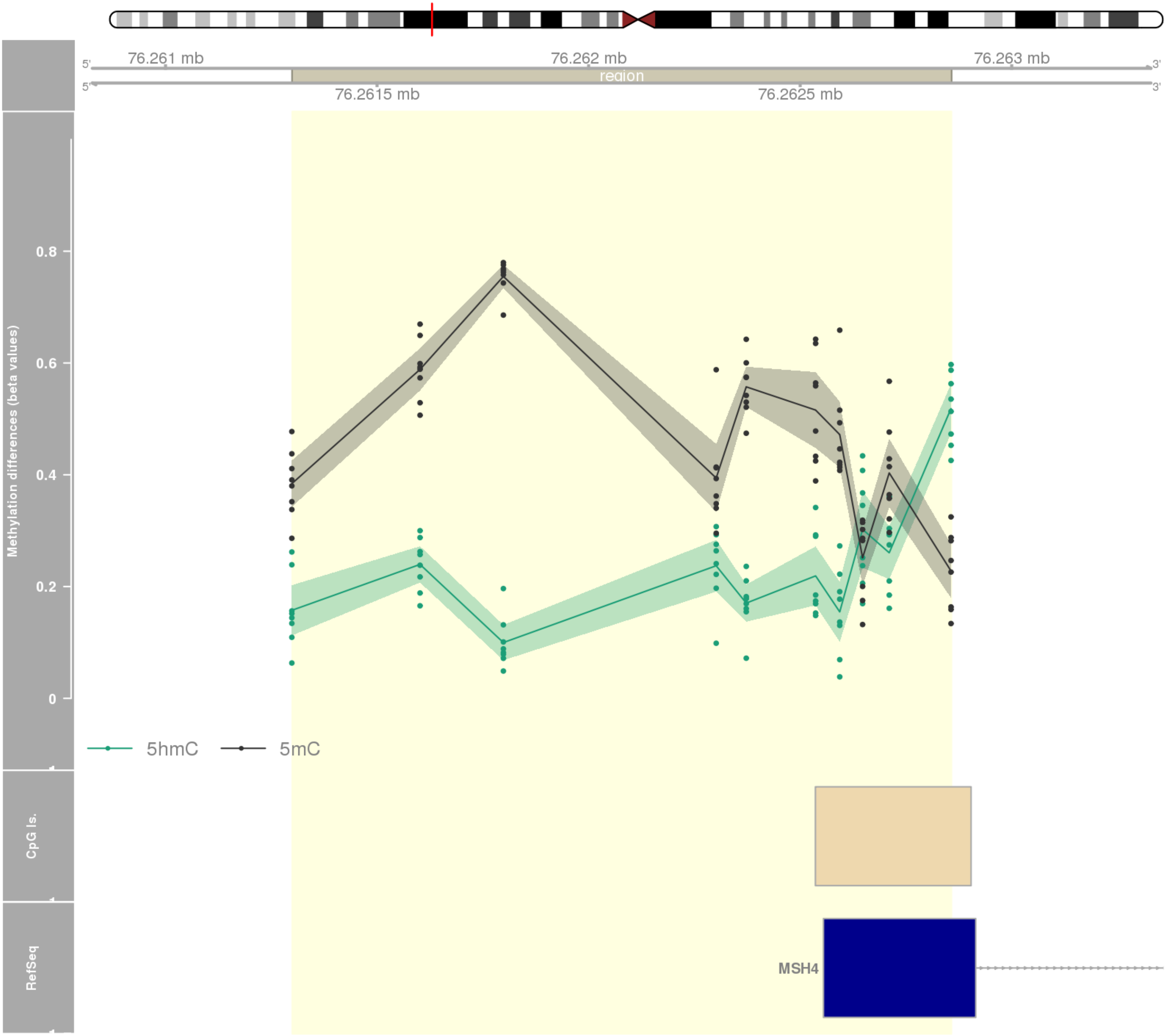
DMR 462 // chr11:131939328-131941079 // 1751 pb. (8 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: NTM -



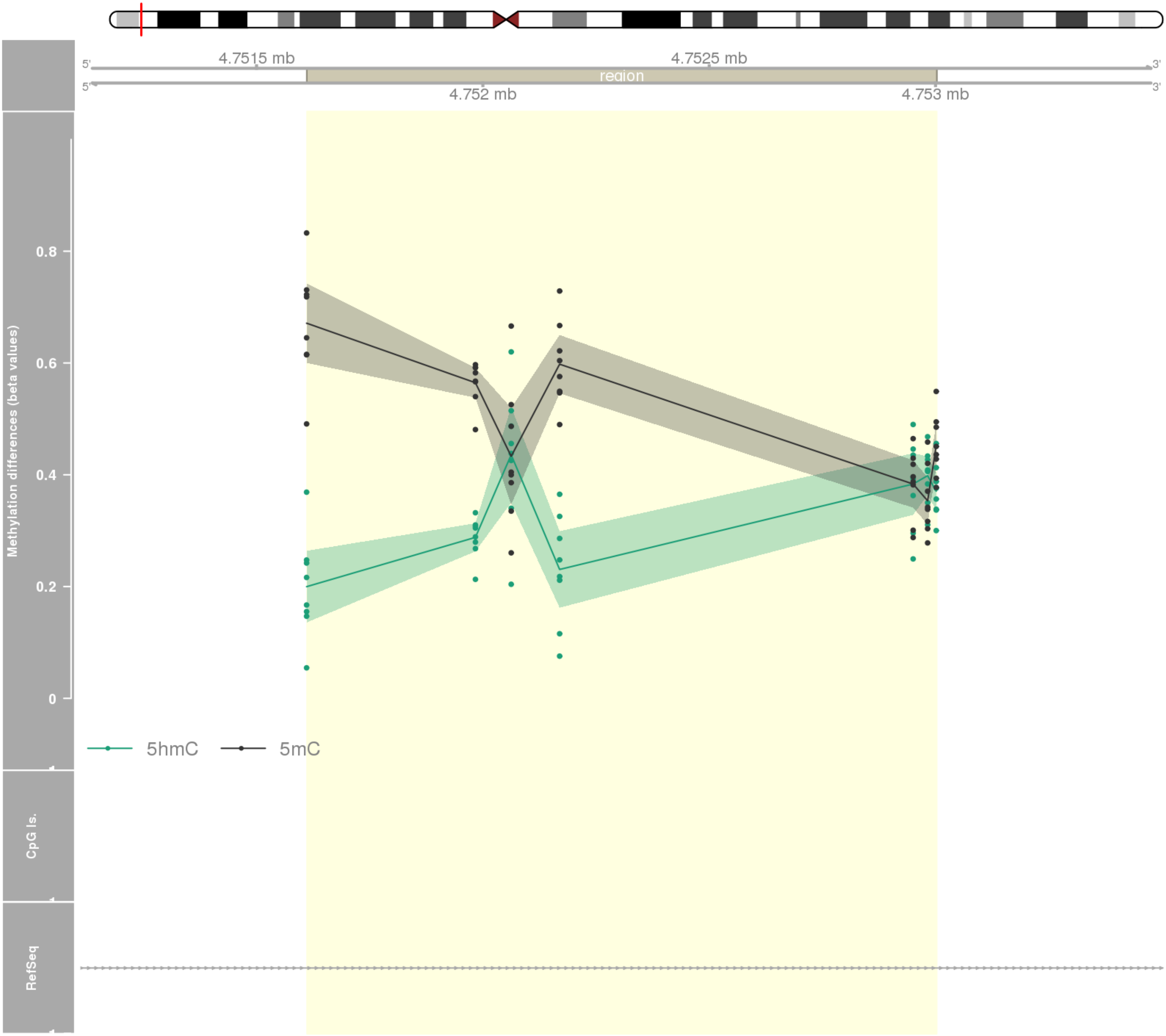
DMR 463 // chr10:17269274-17270431 // 1157 pb. (8 probes) // pvalue: 0.005 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: VIM-AS1 / VIM -



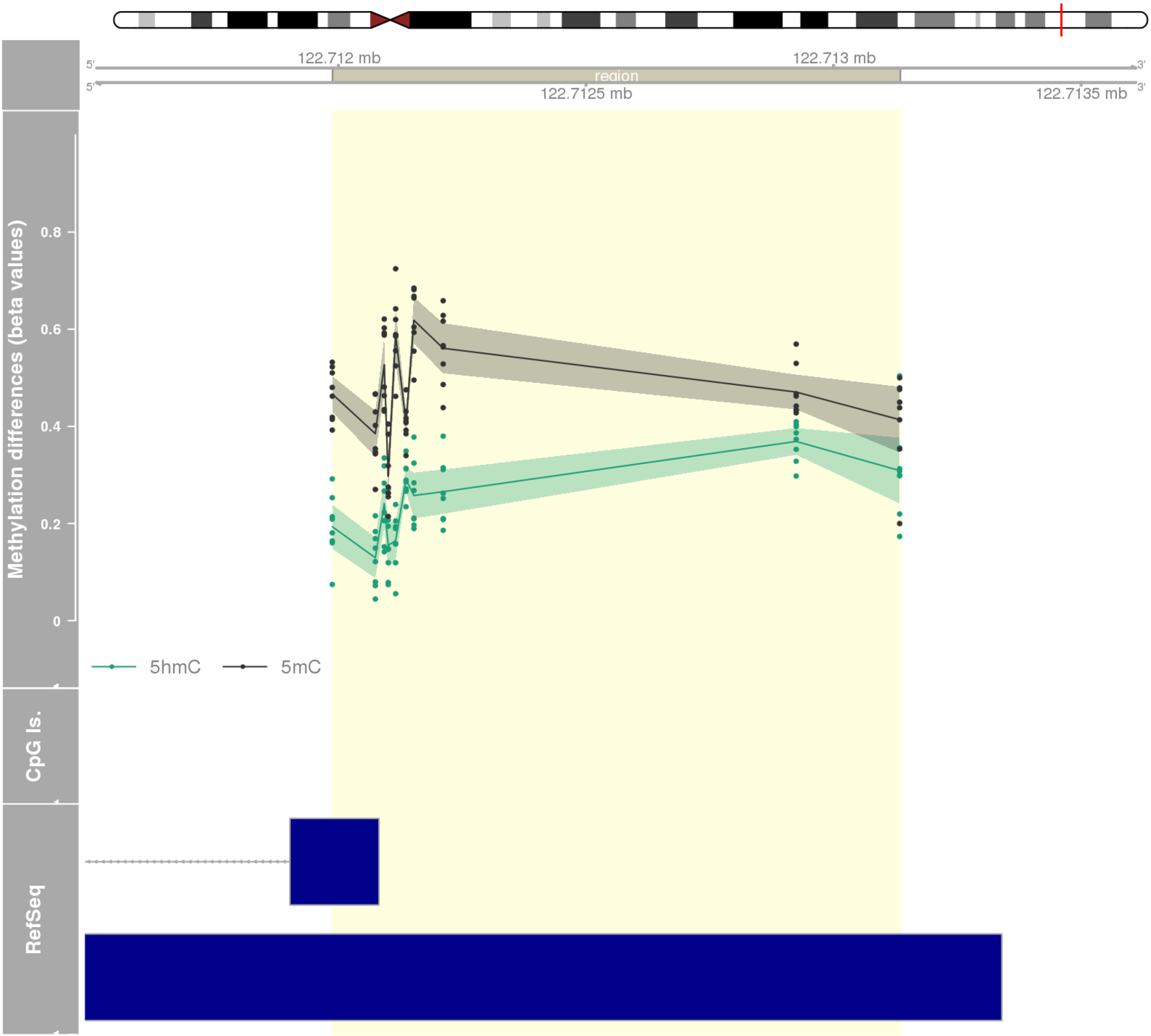
DMR 464 // chr1:76261299-76262857 // 1558 pb. (10 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: MSH4 -



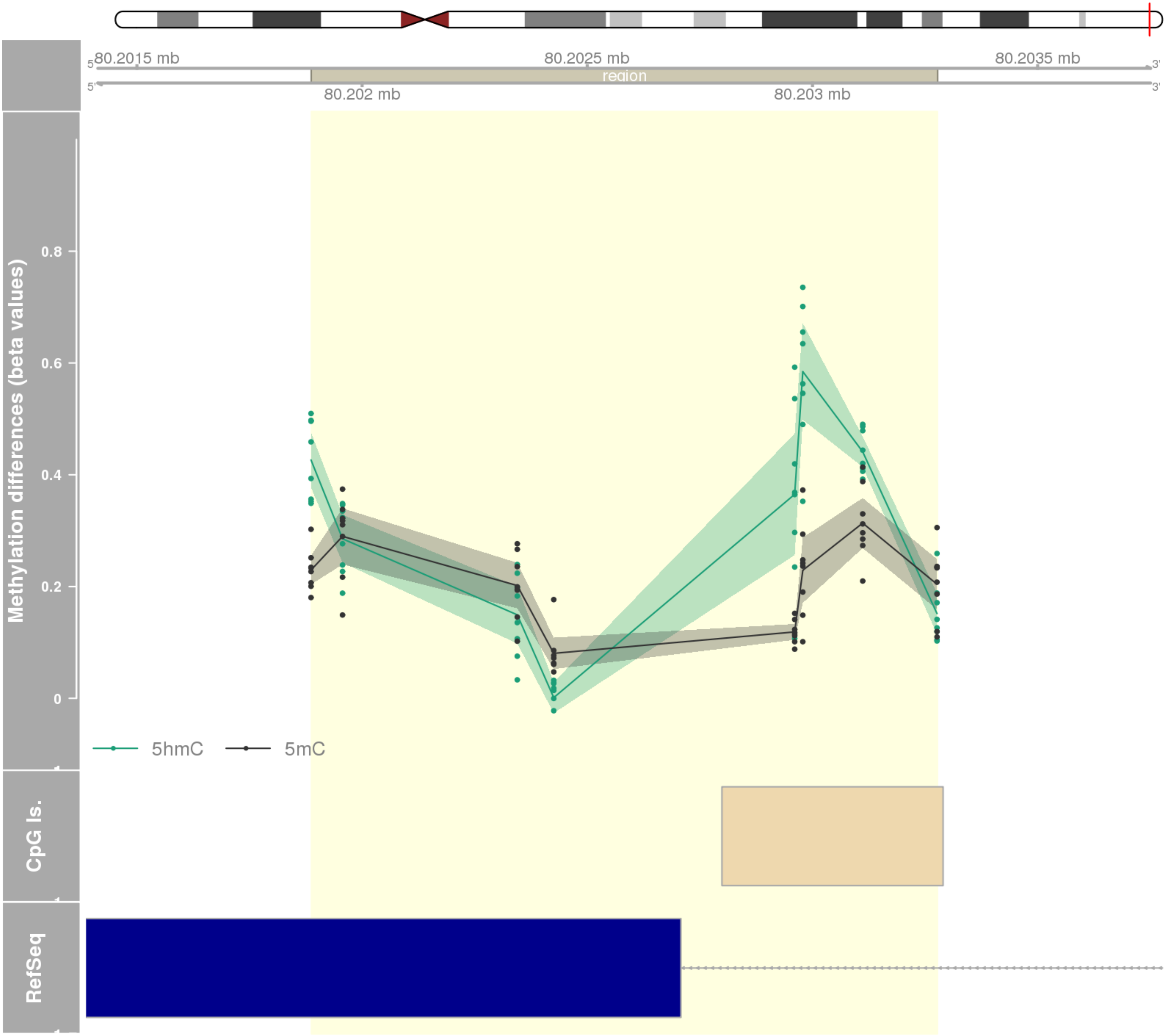
DMR 465 // chr7:4751611-4753002 // 1391 pb. (7 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: FOXK1 -



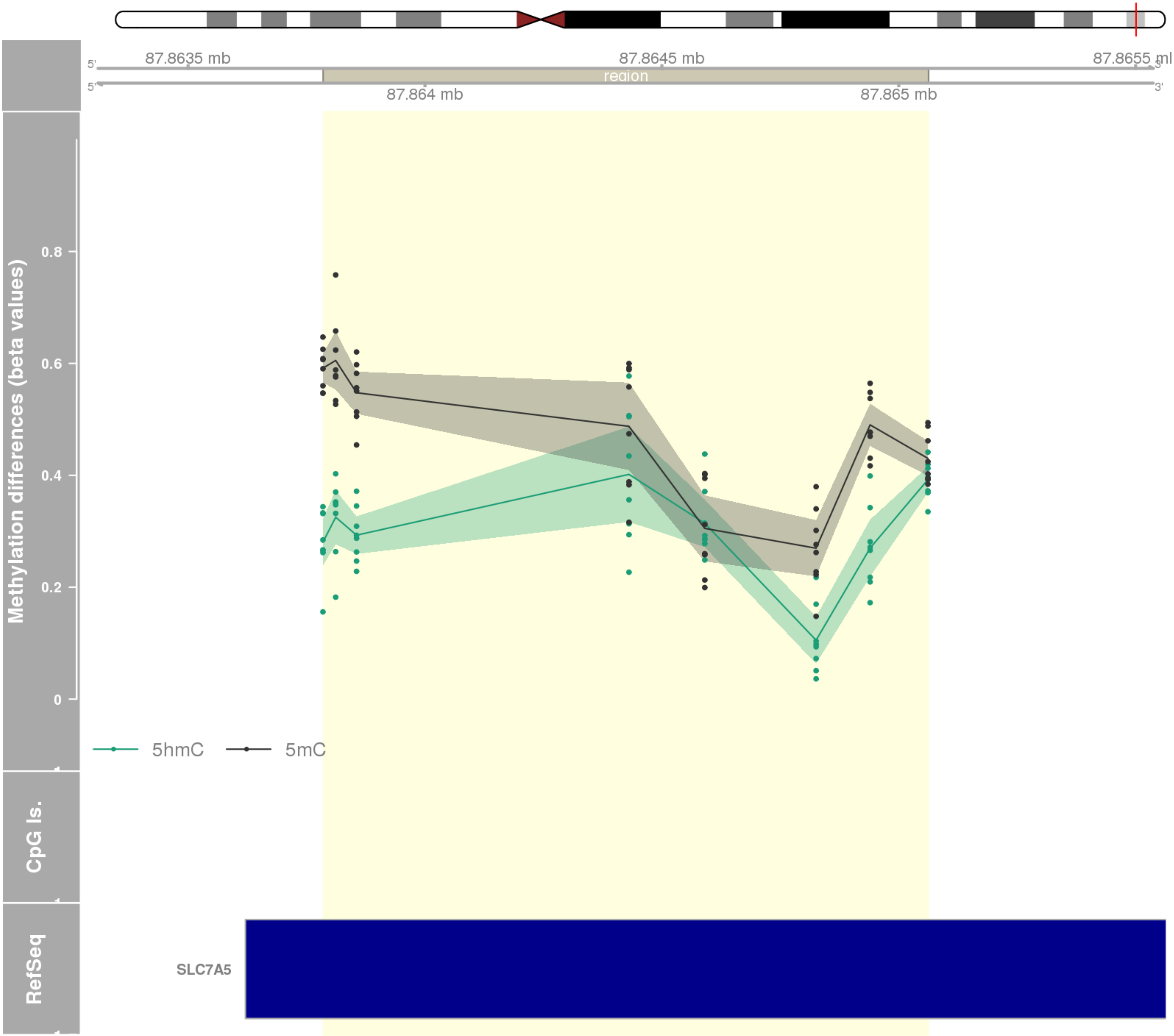
DMR 466 // chr12:122711988-122713134 // 1146 pb. (10 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: DIABLO -



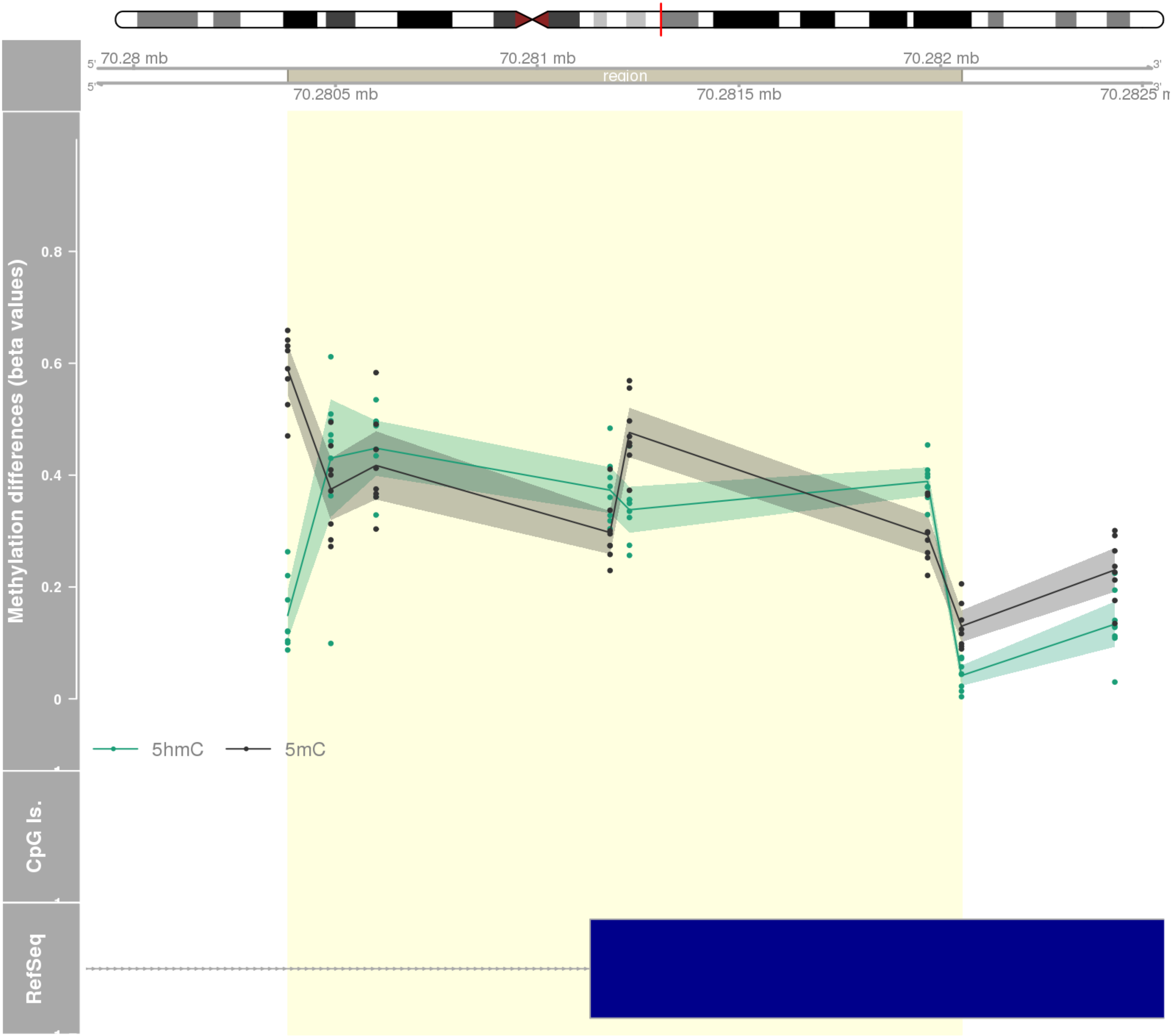
DMR 467 // chr17:80201887-80203277 // 1390 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: SLC16A3 / CSNK1D -



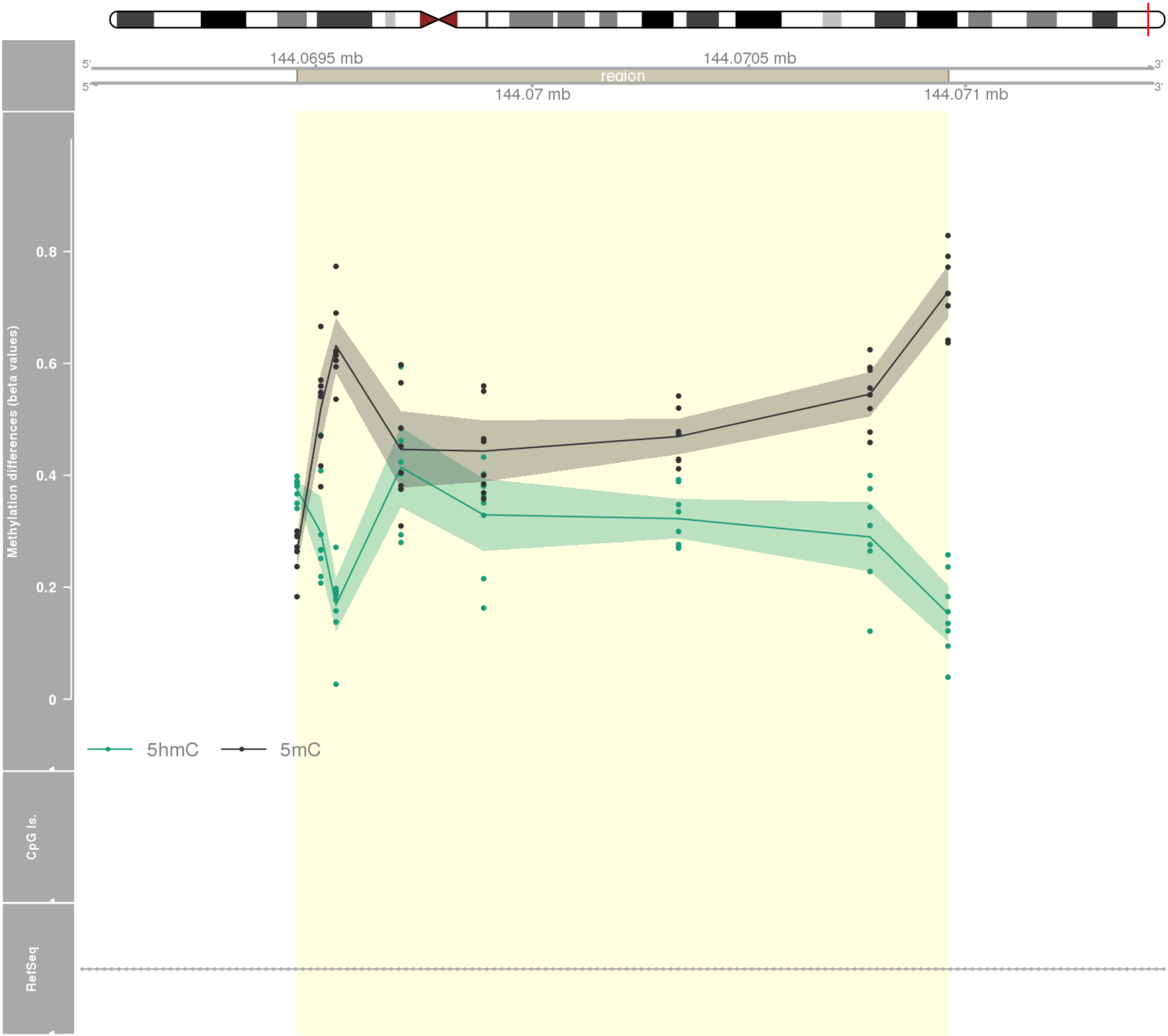
DMR 468 // chr16:87863785-87865062 // 1277 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: SLC7A5 -

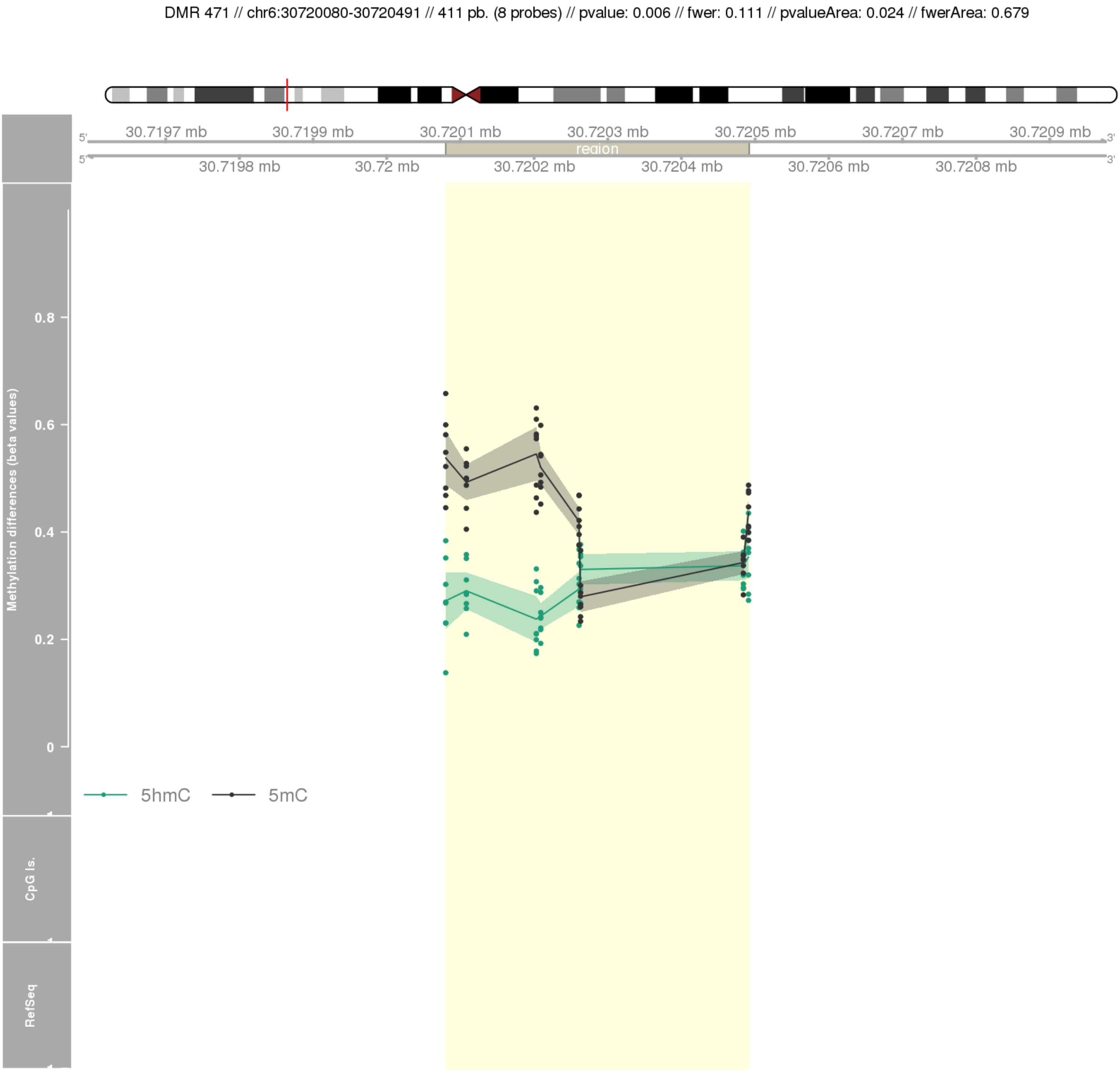


DMR 469 // chr11:70280382-70282052 // 1670 pb. (7 probes) // pvalue: 0.002 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: CTTN -



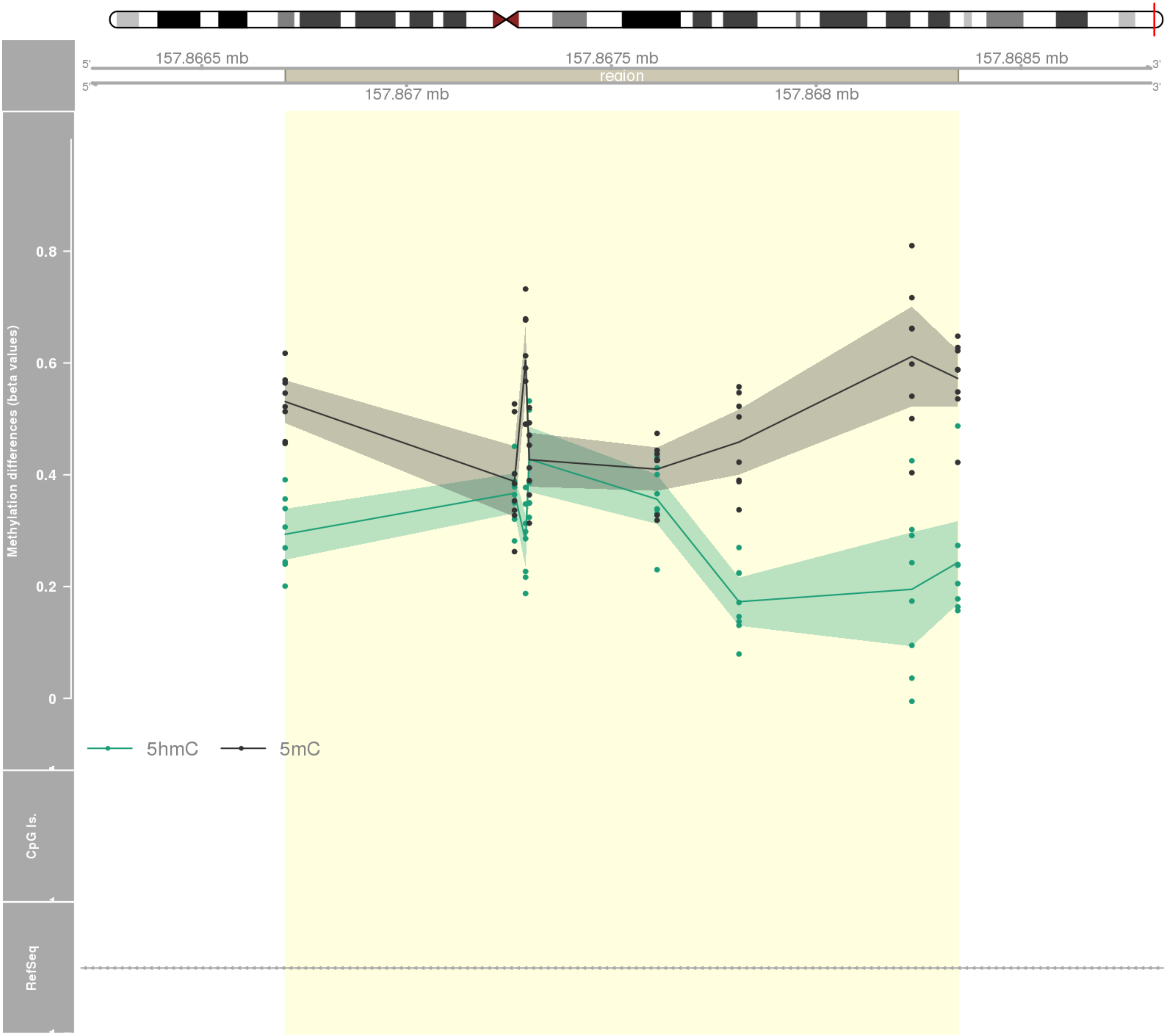
DMR 470 // chr8:144069457-144070960 // 1503 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679



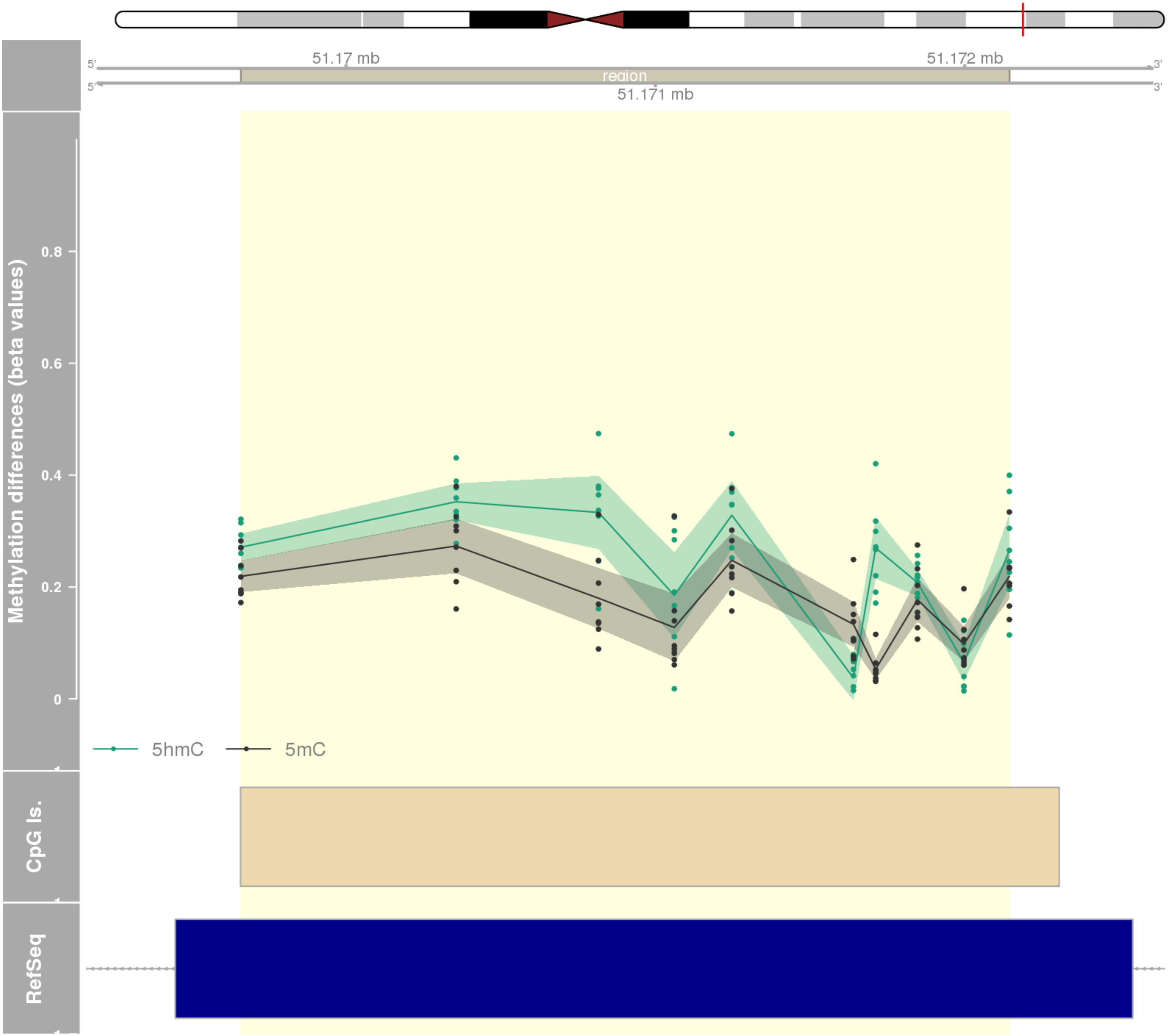


DMR 471 // chr6:30720080-30720491 // 411 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679

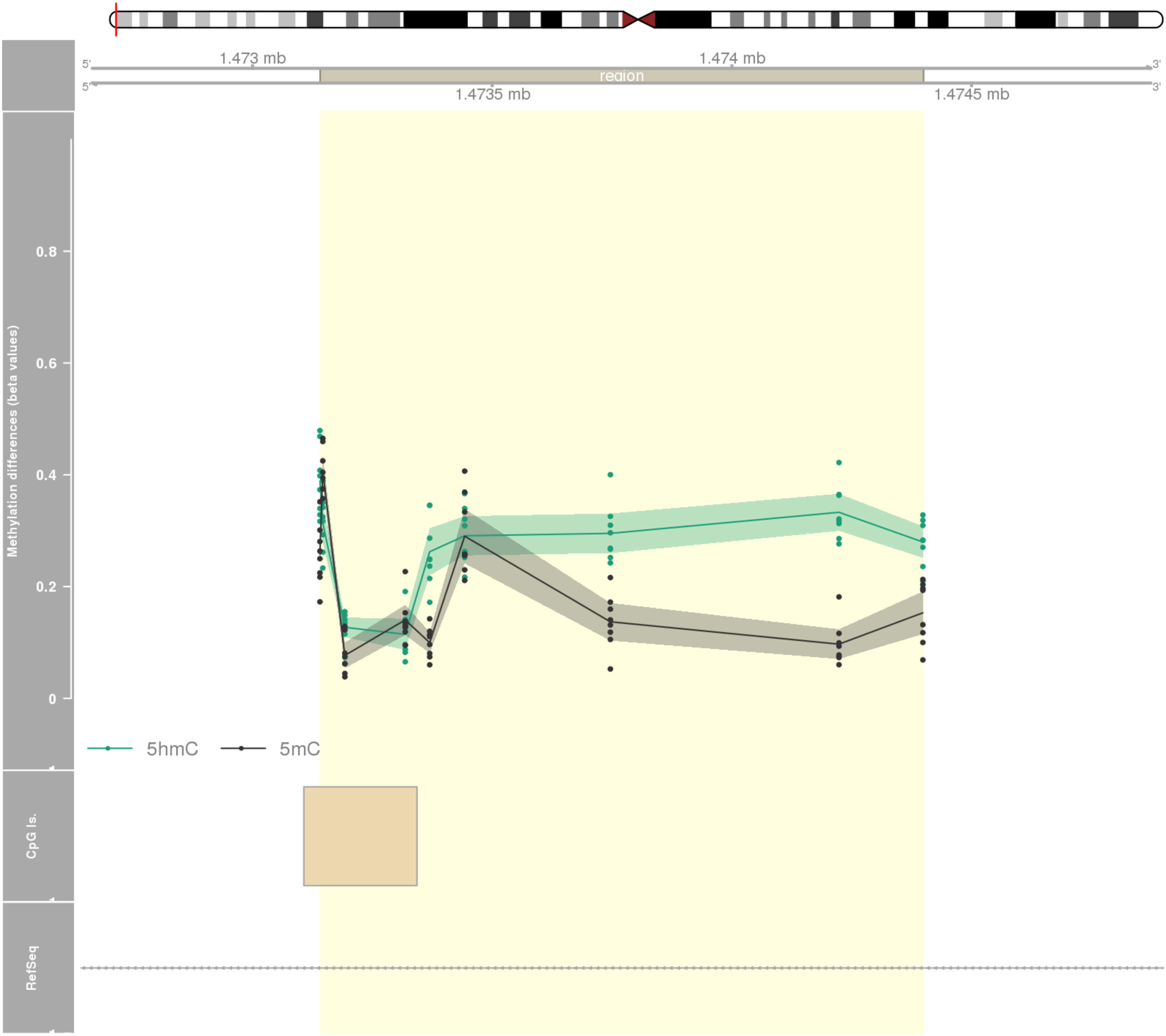
DMR 472 // chr7:157866704-157868346 // 1642 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.024 // fwerArea: 0.679
- genes: PTPRN2 -



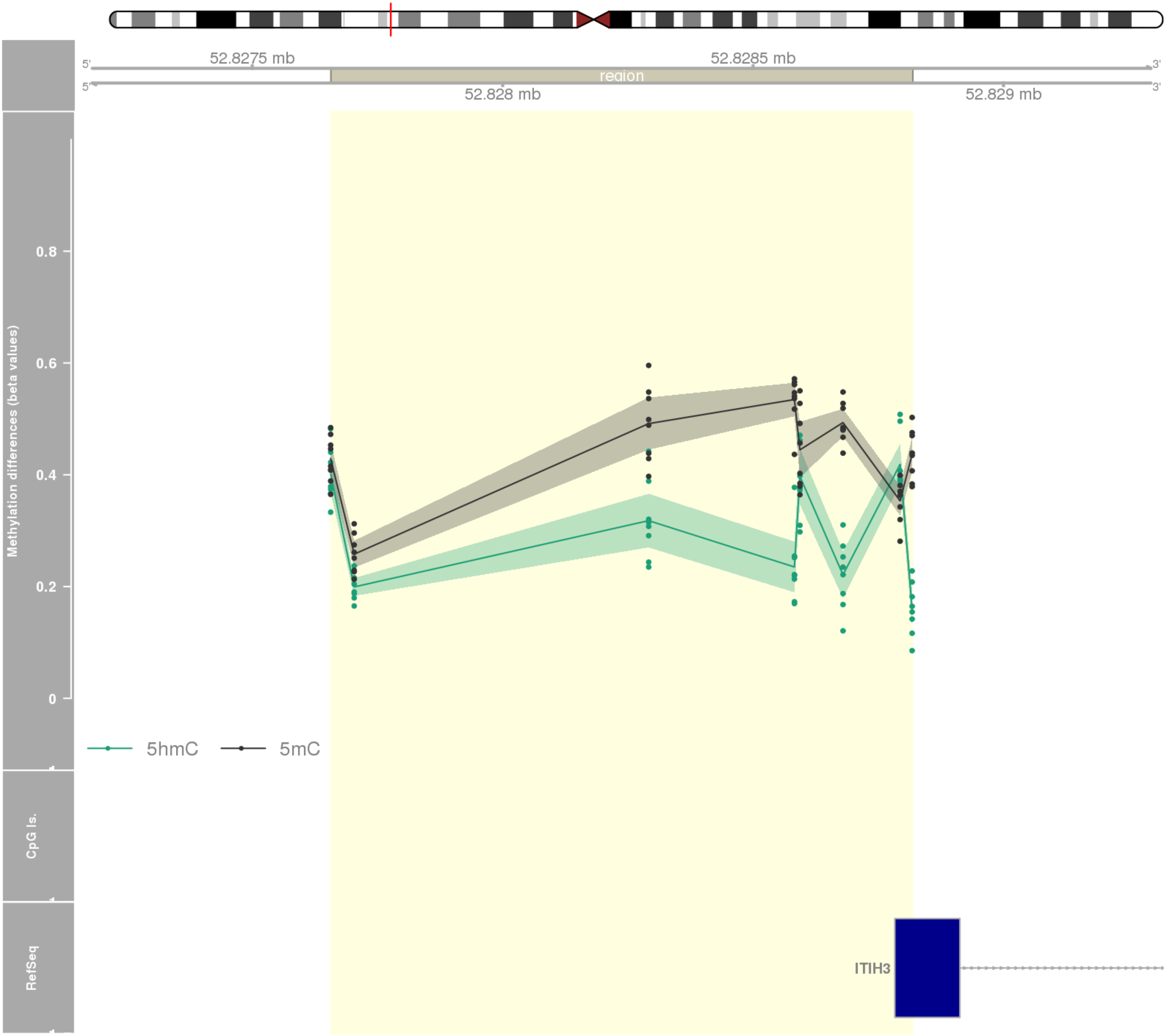
DMR 473 // chr19:51169660-51172144 // 2484 pb. (10 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: SYT3 / SHANK1 -



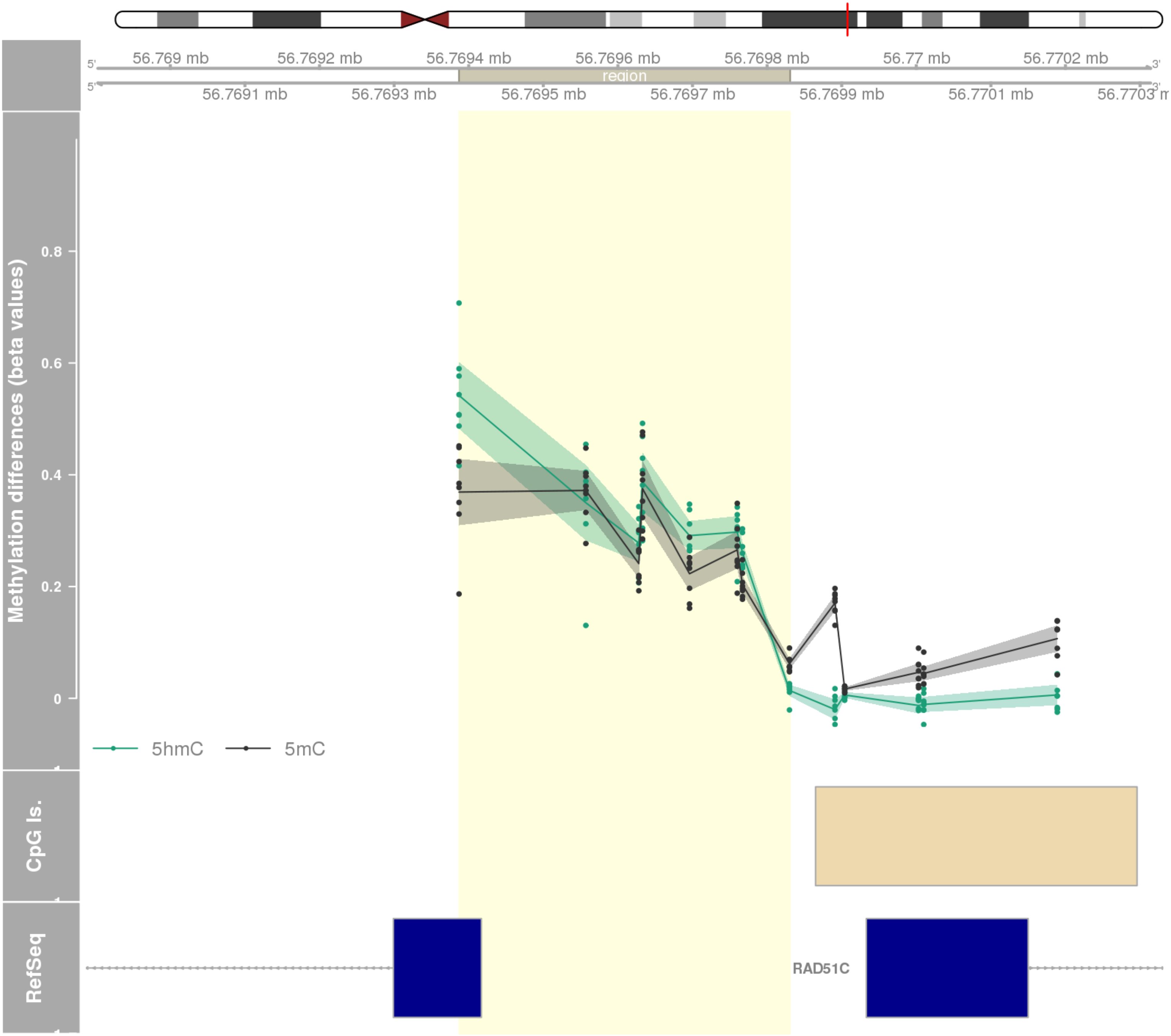
DMR 474 // chr1:1473141-1474399 // 1258 pb. (9 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: TMEM240 -



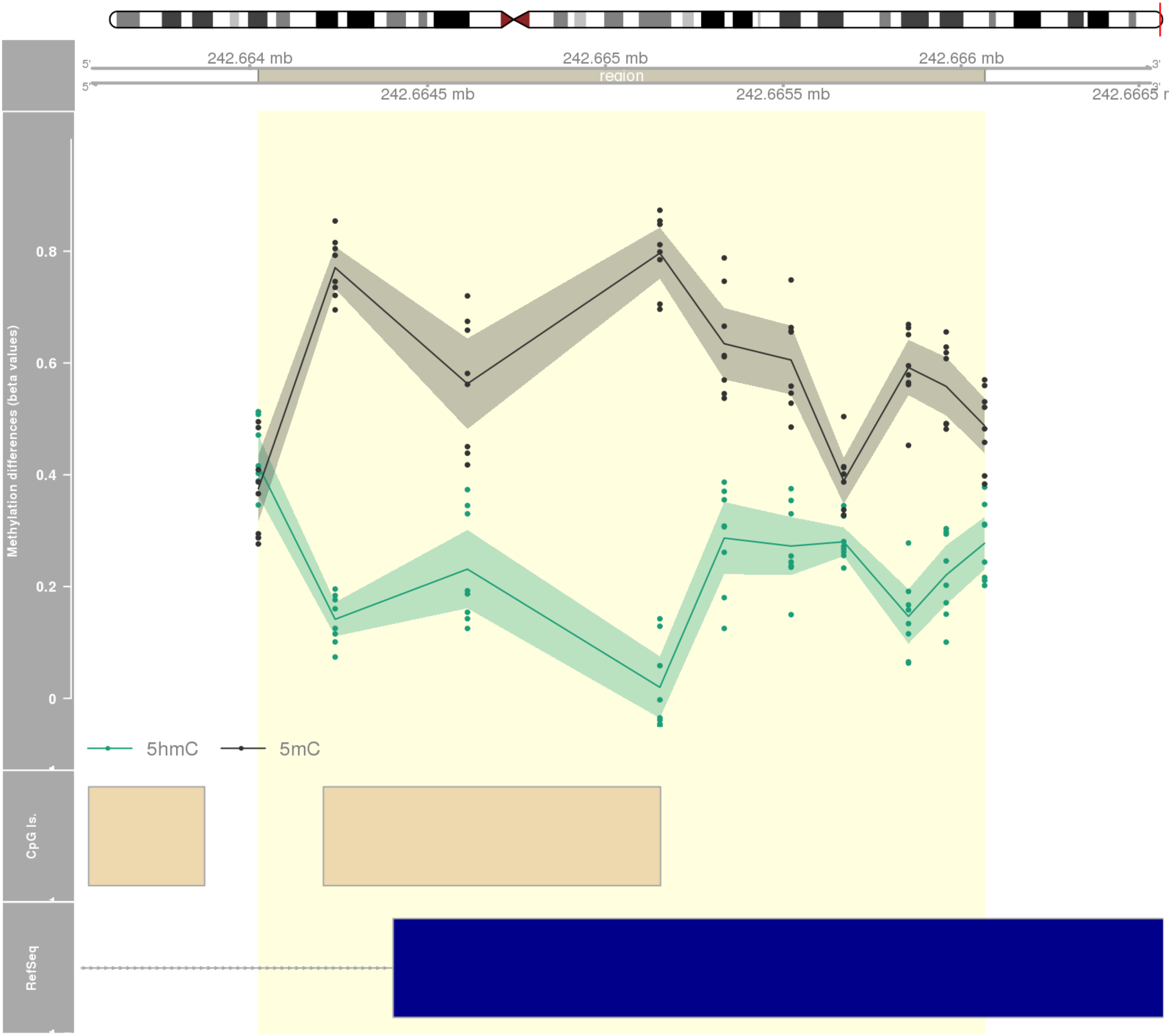
DMR 475 // chr3:52827657-52828818 // 1161 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: ITIH3 -



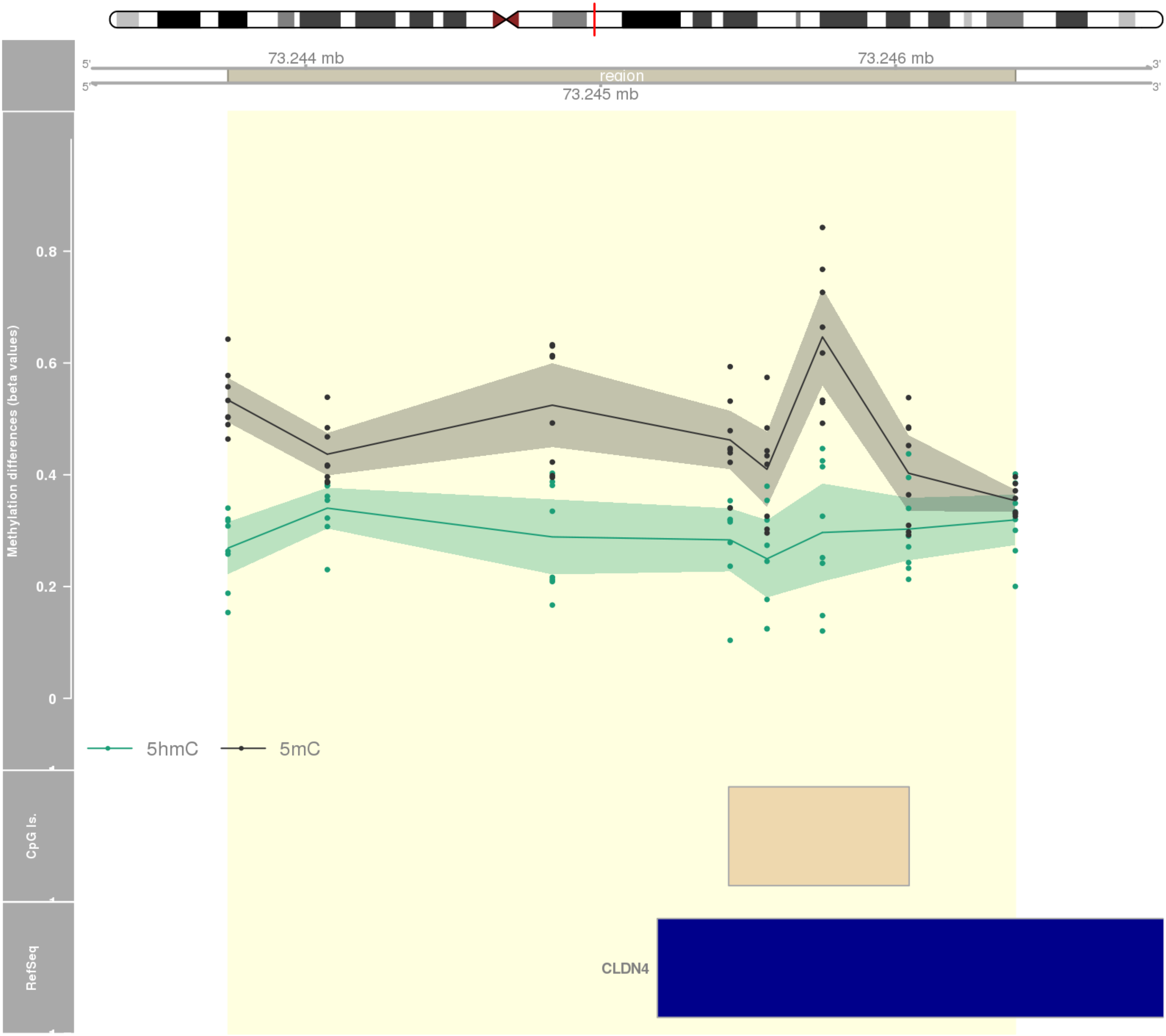
DMR 476 // chr17:56769387-56769830 // 443 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: TEX14 -



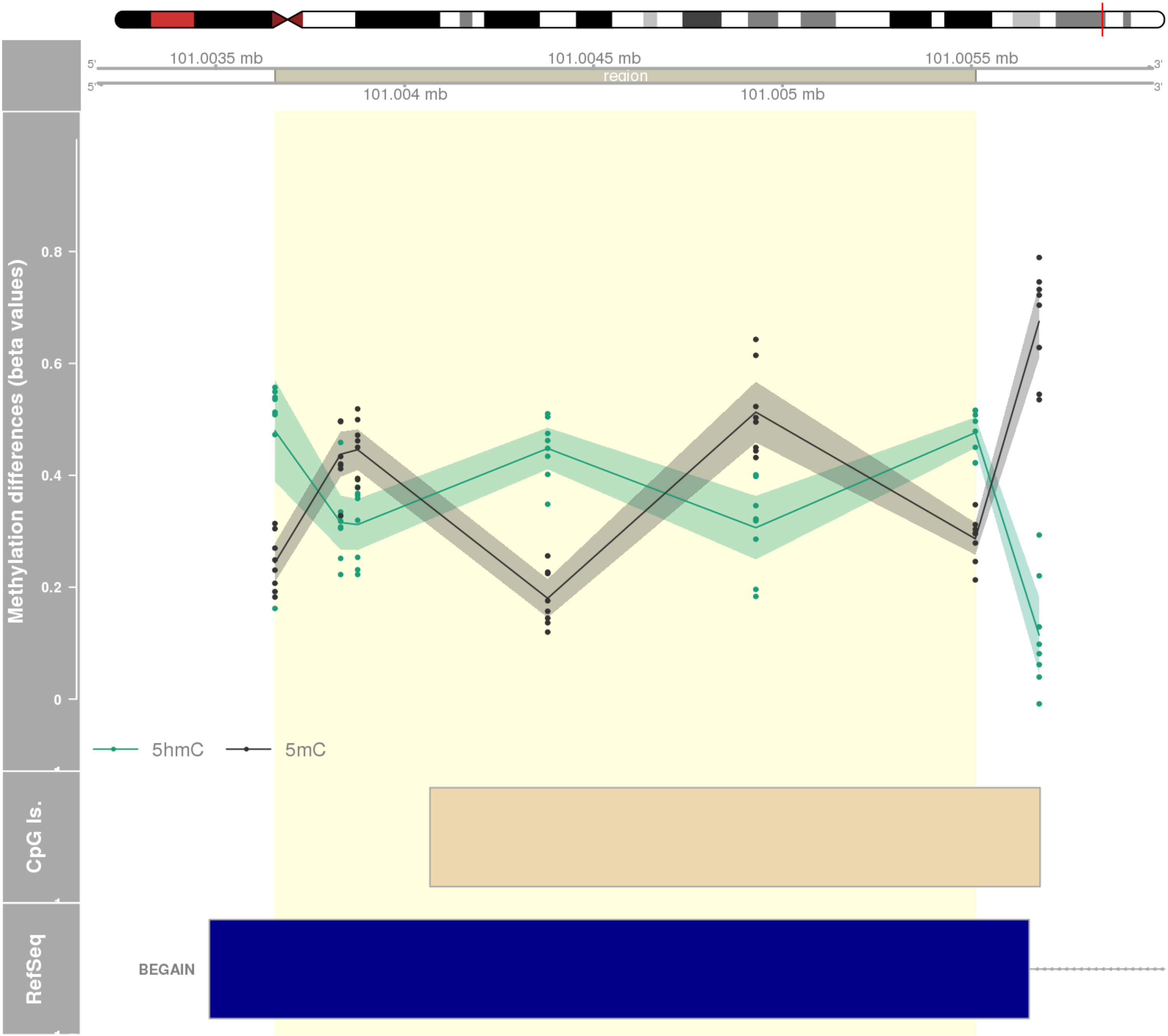
DMR 477 // chr2:242664024-242666066 // 2042 pb. (10 probes) // pvalue: 0.012 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: ING5 -



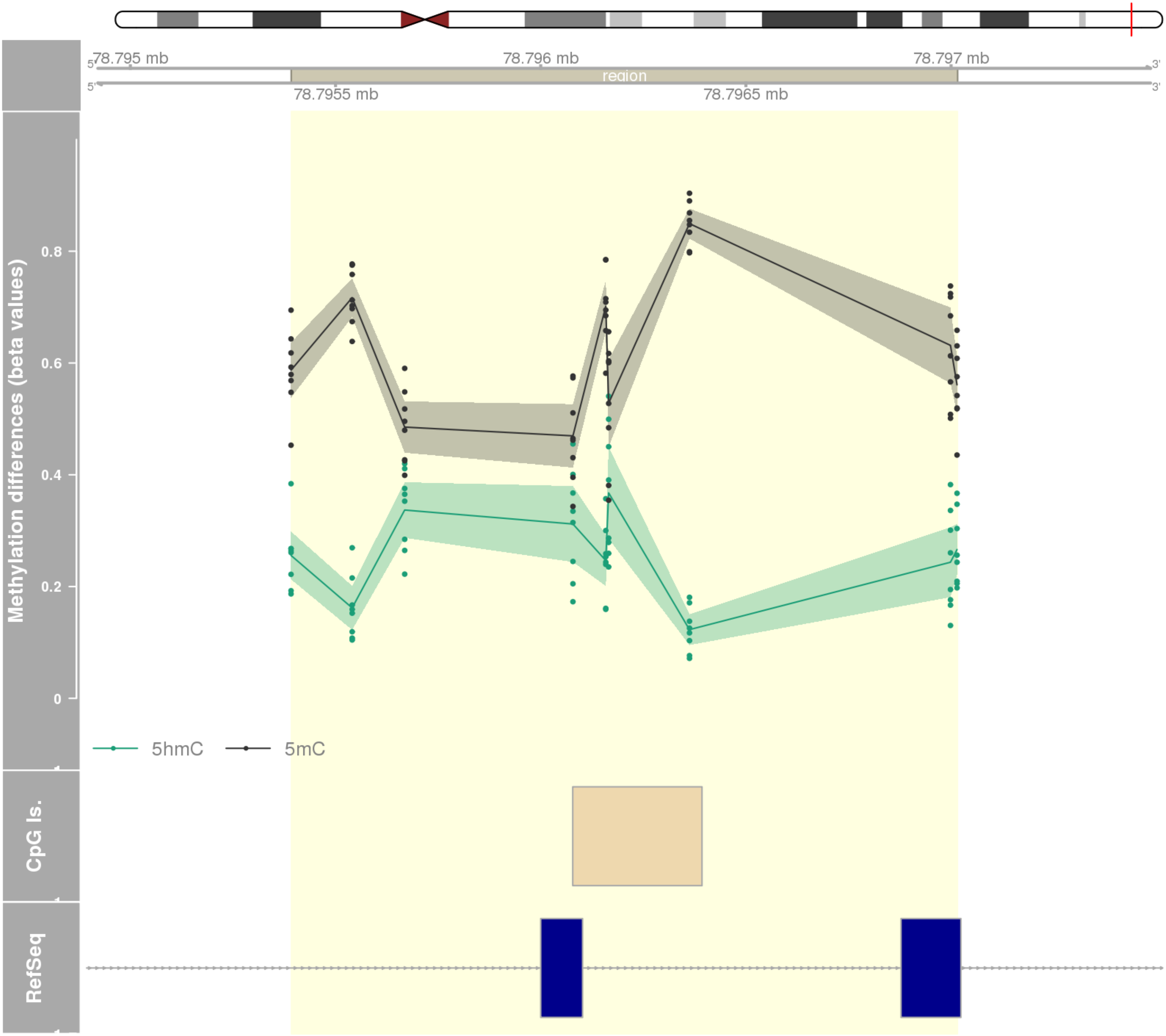
DMR 478 // chr7:73243736-73246406 // 2670 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: CLDN4 -



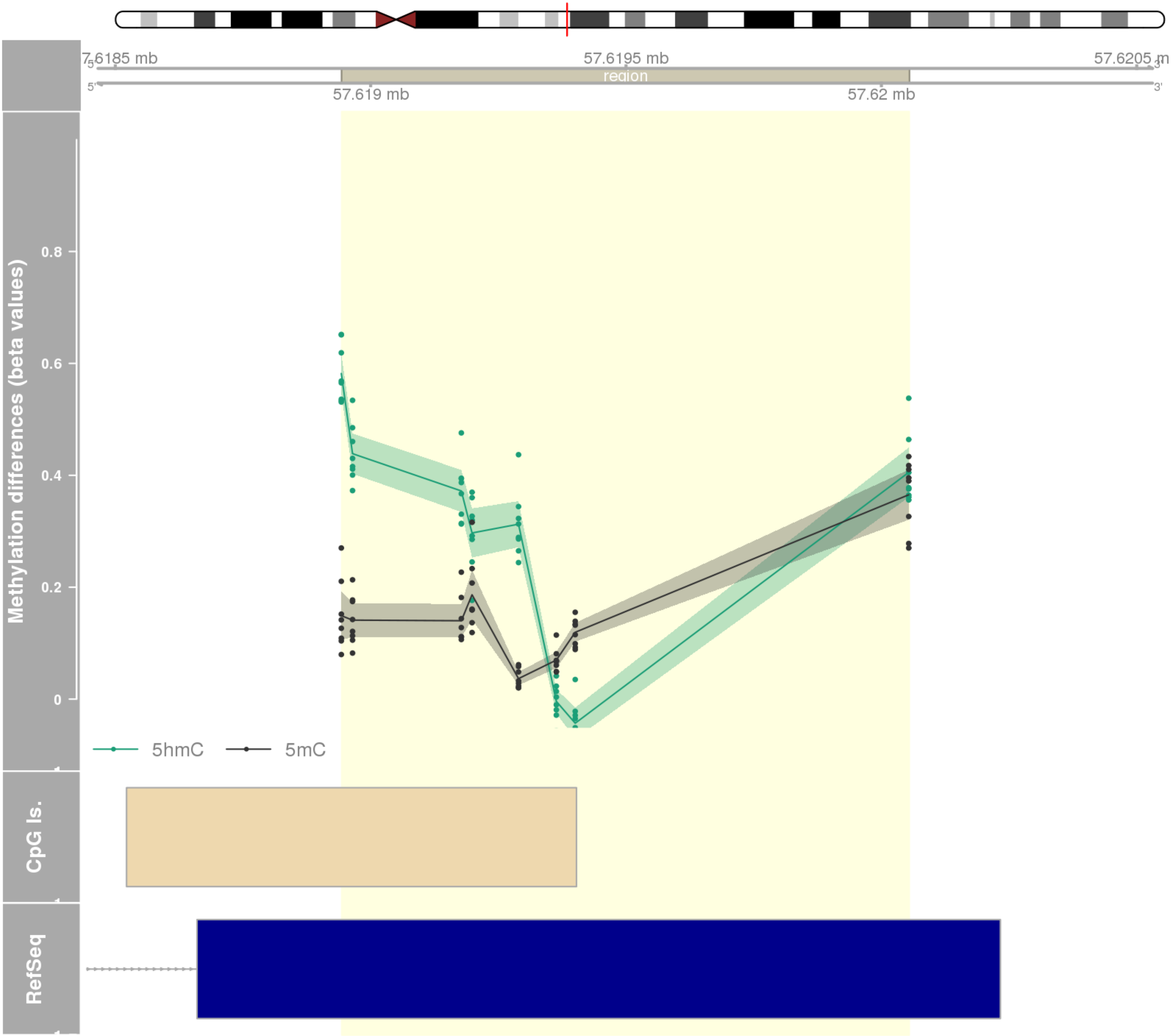
DMR 479 // chr14:101003657-101005511 // 1854 pb. (6 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: BEGAIN -



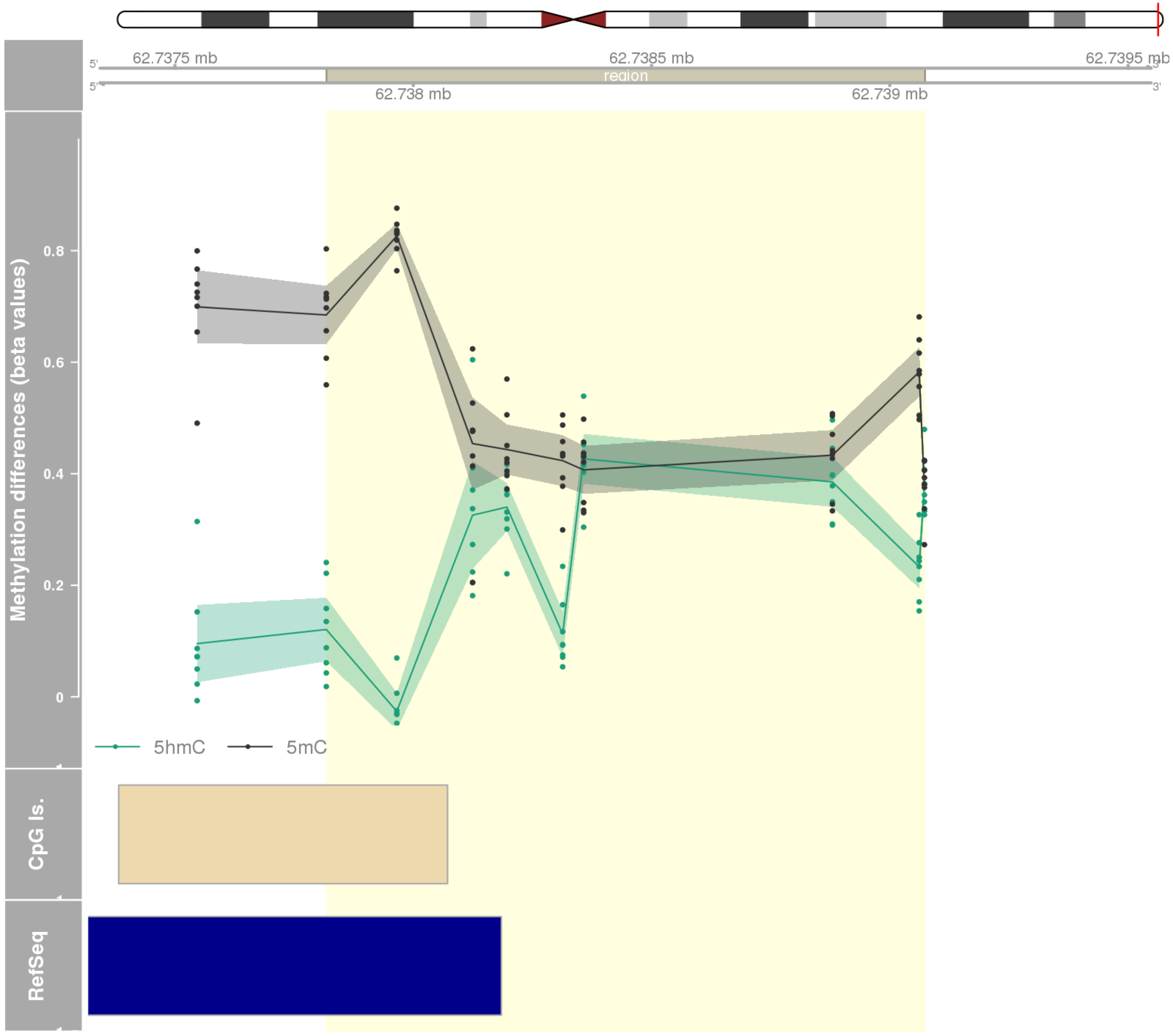
DMR 480 // chr17:78795392-78797015 // 1623 pb. (9 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: RPTOR -



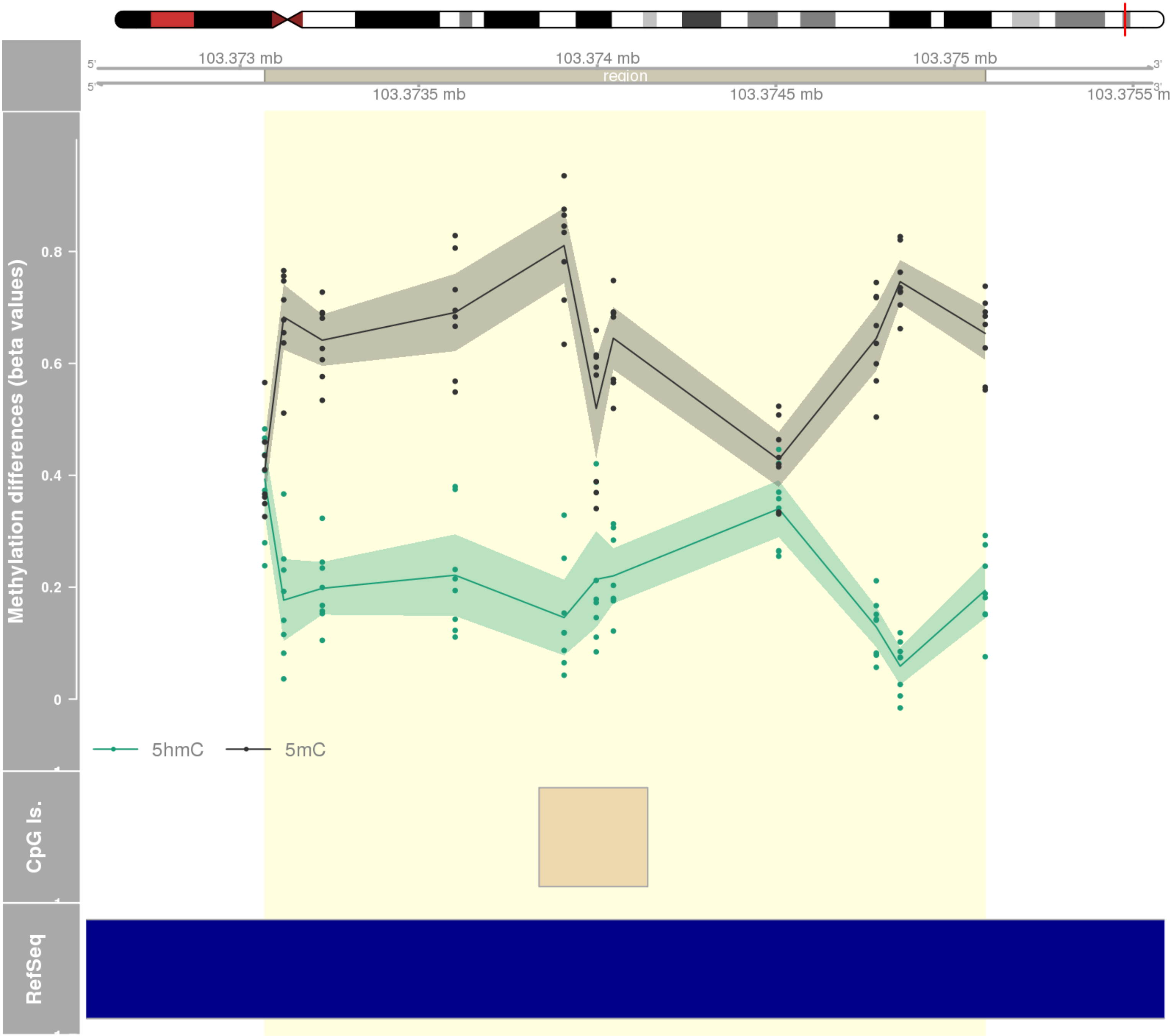
DMR 481 // chr12:57618943-57620054 // 1111 pb. (8 probes) // pvalue: 0.001 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: NXPH4 -



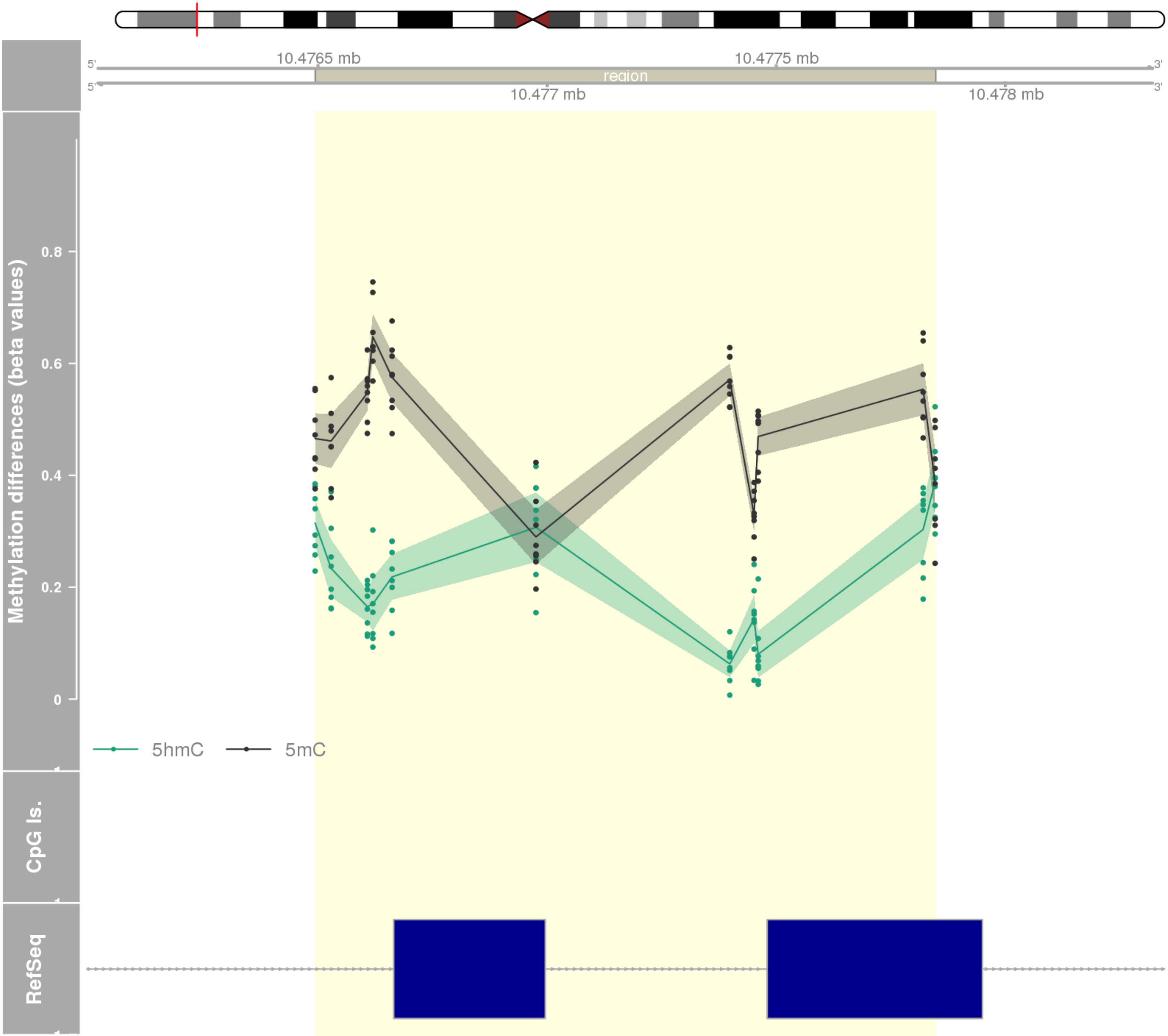
DMR 482 // chr20:62737818-62739073 // 1255 pb. (9 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: NPBWR2 -



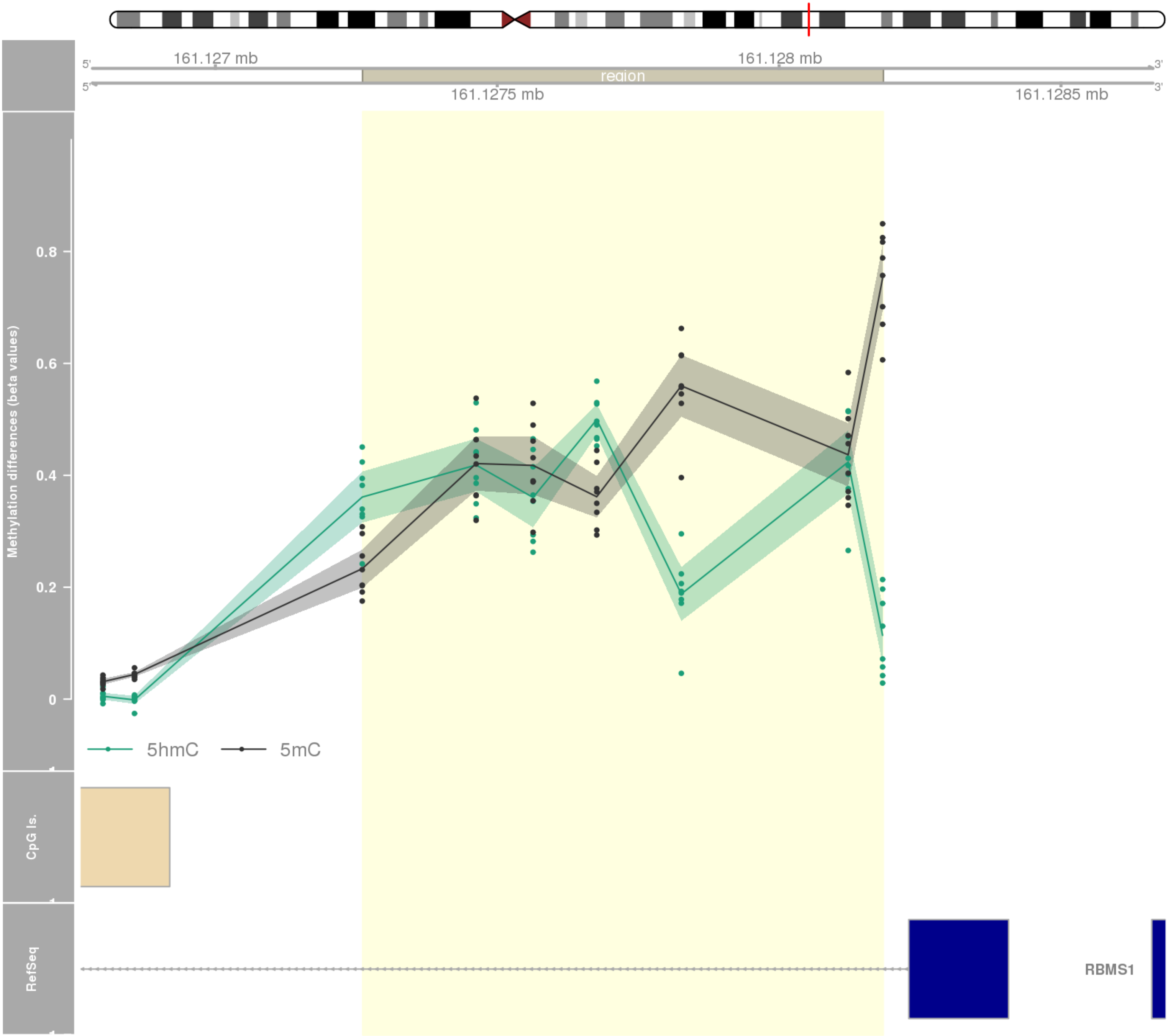
DMR 483 // chr14:103373069-103375086 // 2017 pb. (11 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: TRAF3 -



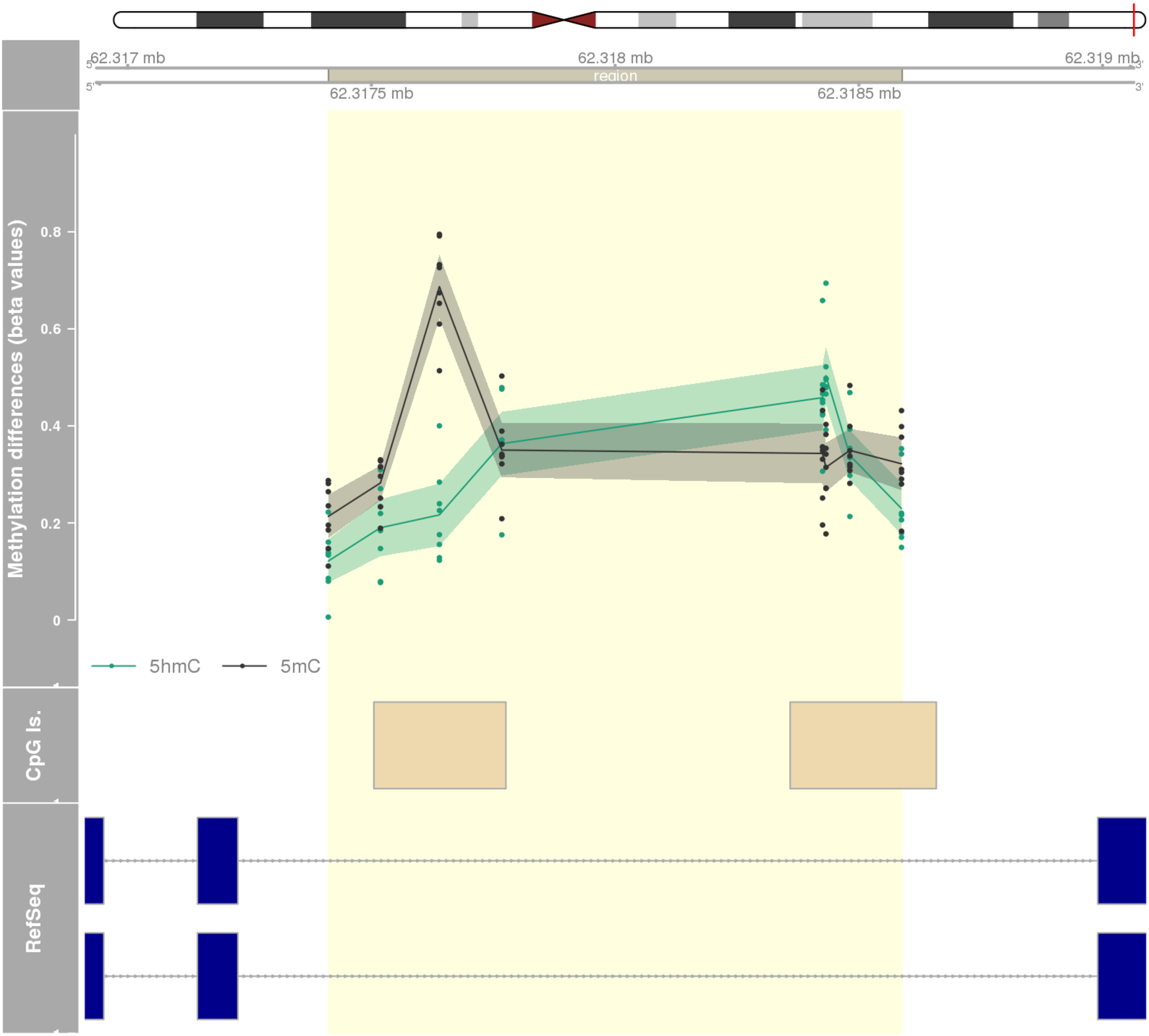
DMR 484 // chr11:10476494-10477847 // 1353 pb. (11 probes) // pvalue: 0.011 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: AMPD3 -



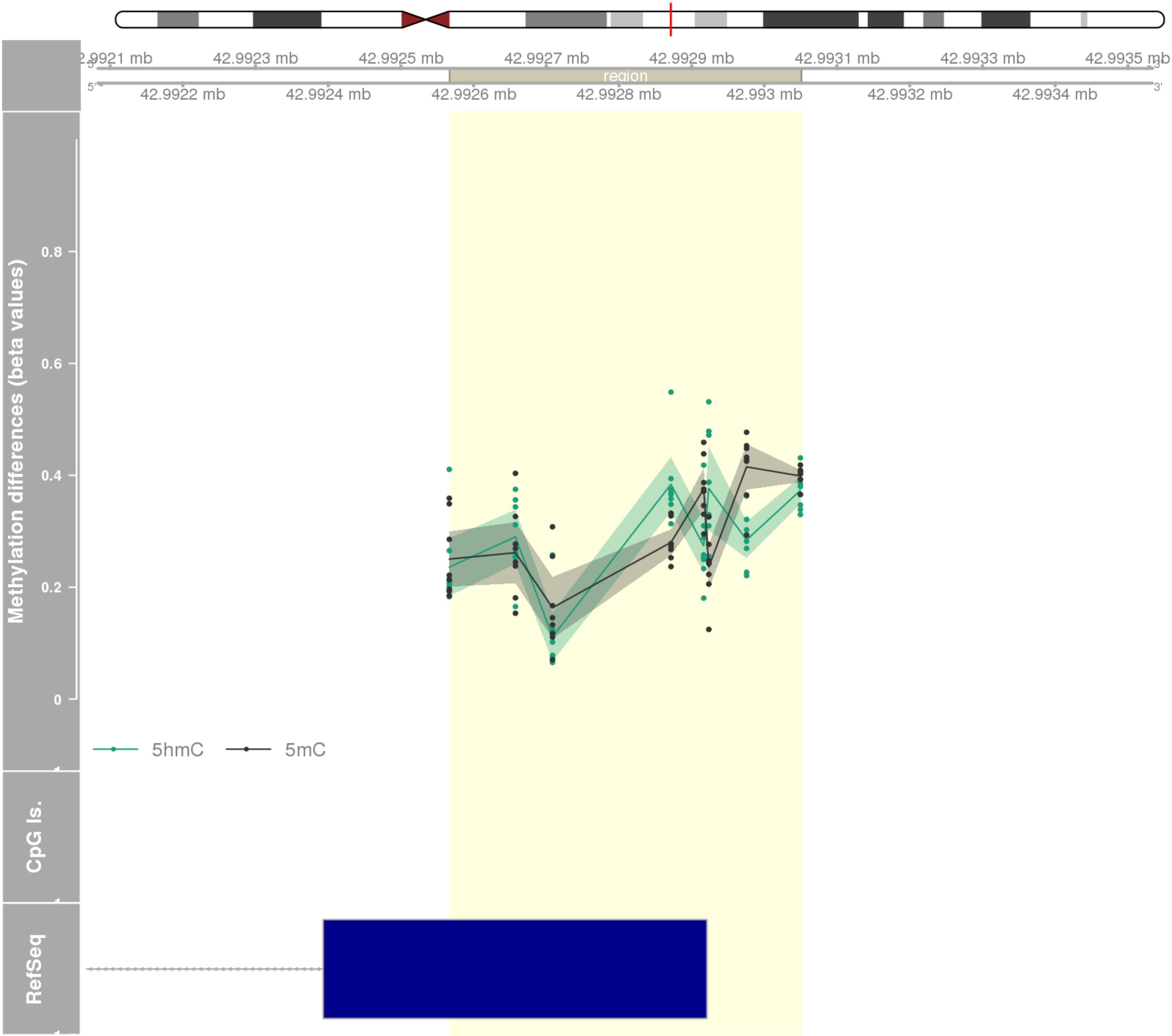
DMR 485 // chr2:161127261-161128184 // 923 pb. (7 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: ITGB6 -



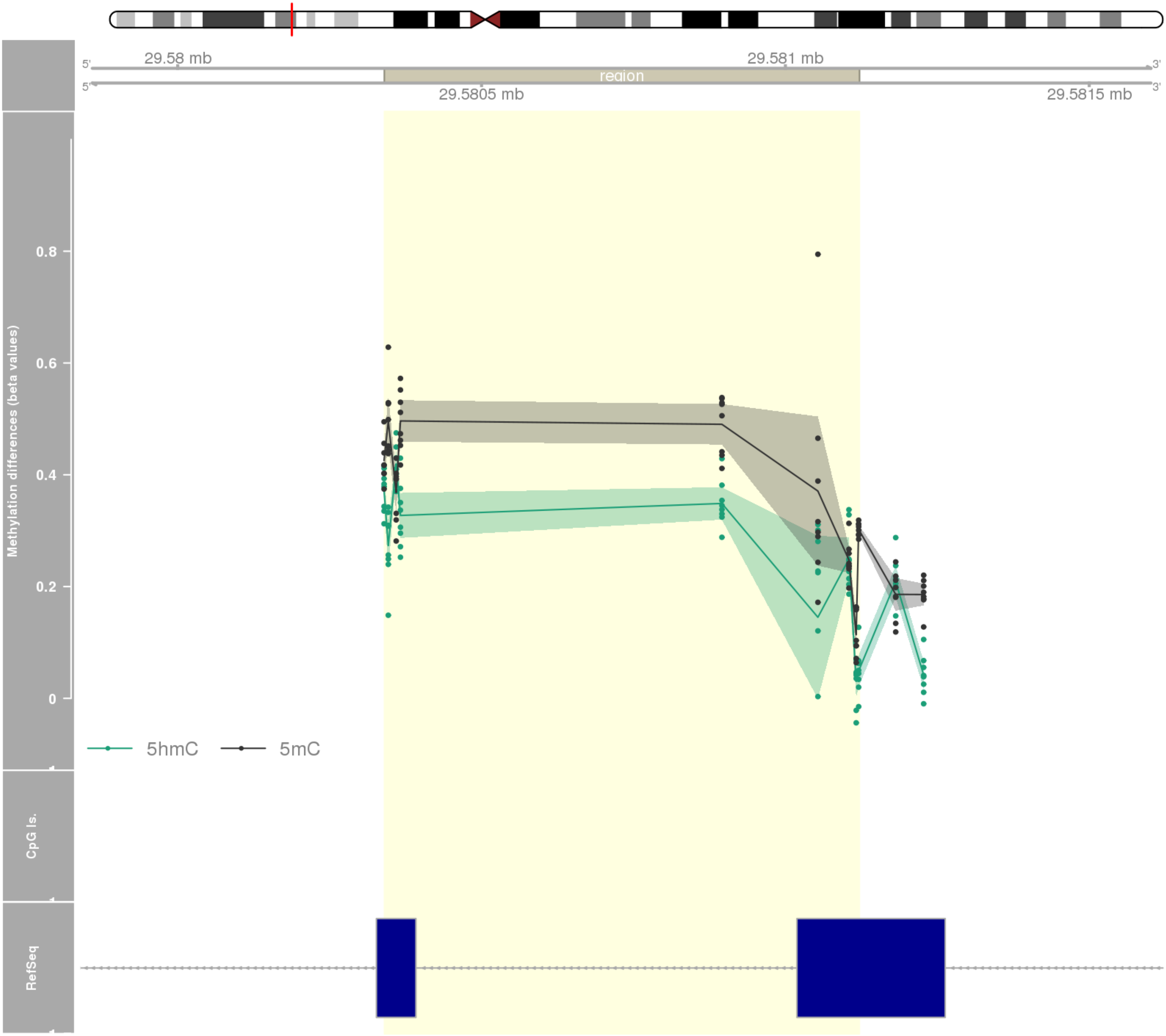
DMR 486 // chr20:62317412-62318588 // 1176 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: RTEL1 / RTEL1-TNFRSF6B -



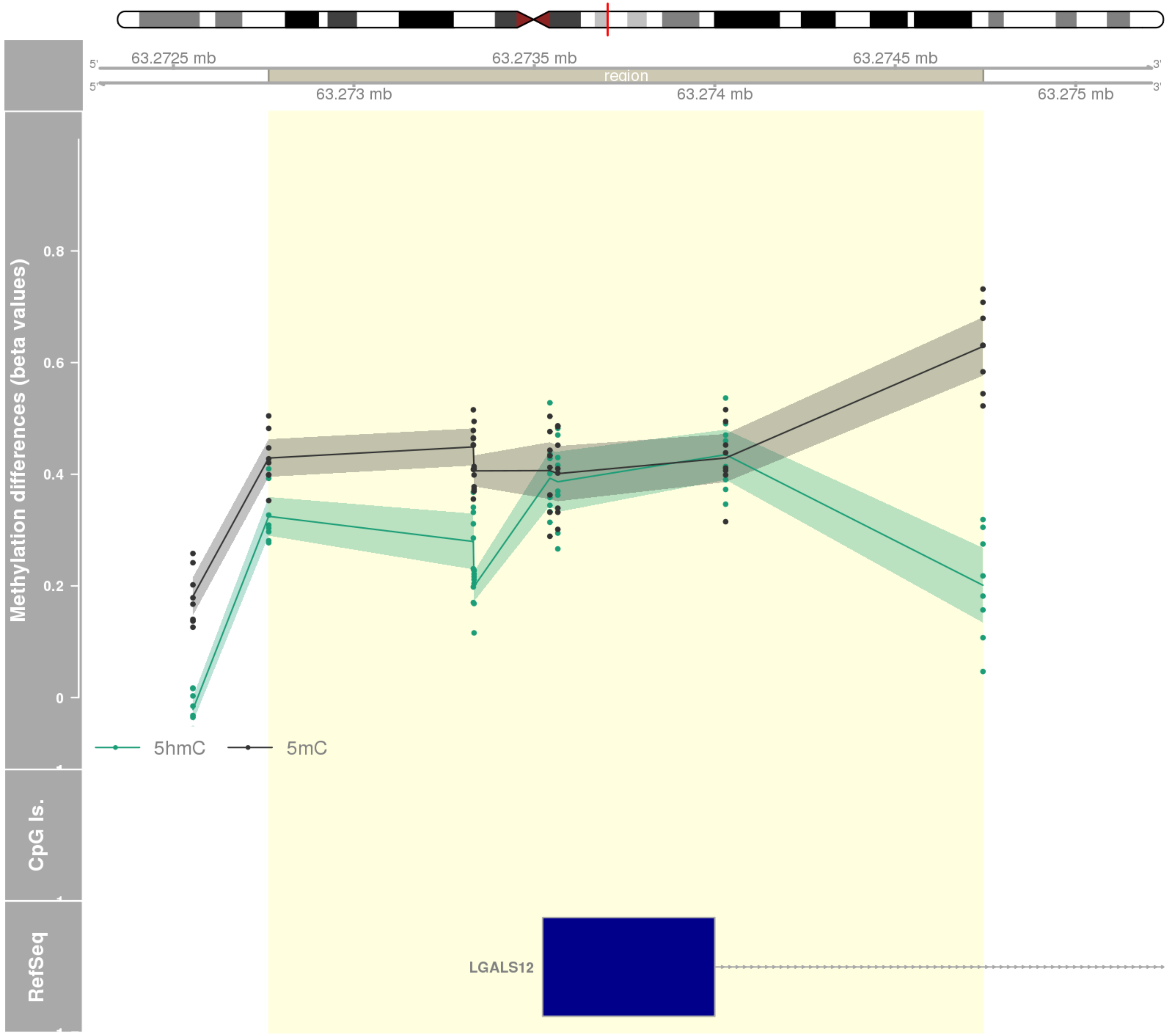
DMR 487 // chr17:42992567-42993050 // 483 pb. (8 probes) // pvalue: 0.006 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: GFAP -



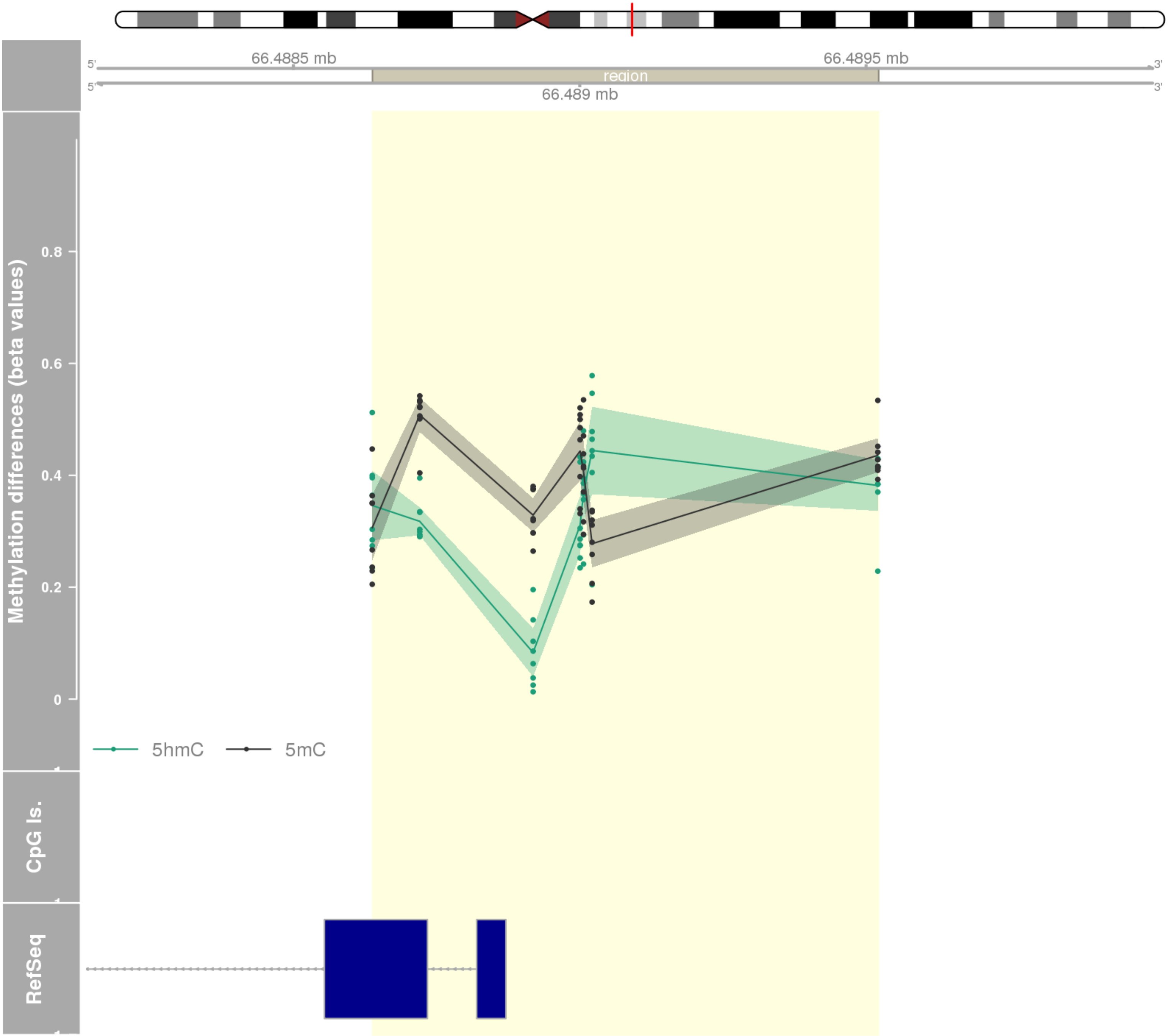
DMR 488 // chr6:29580340-29581121 // 781 pb. (9 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: GABBR1 -



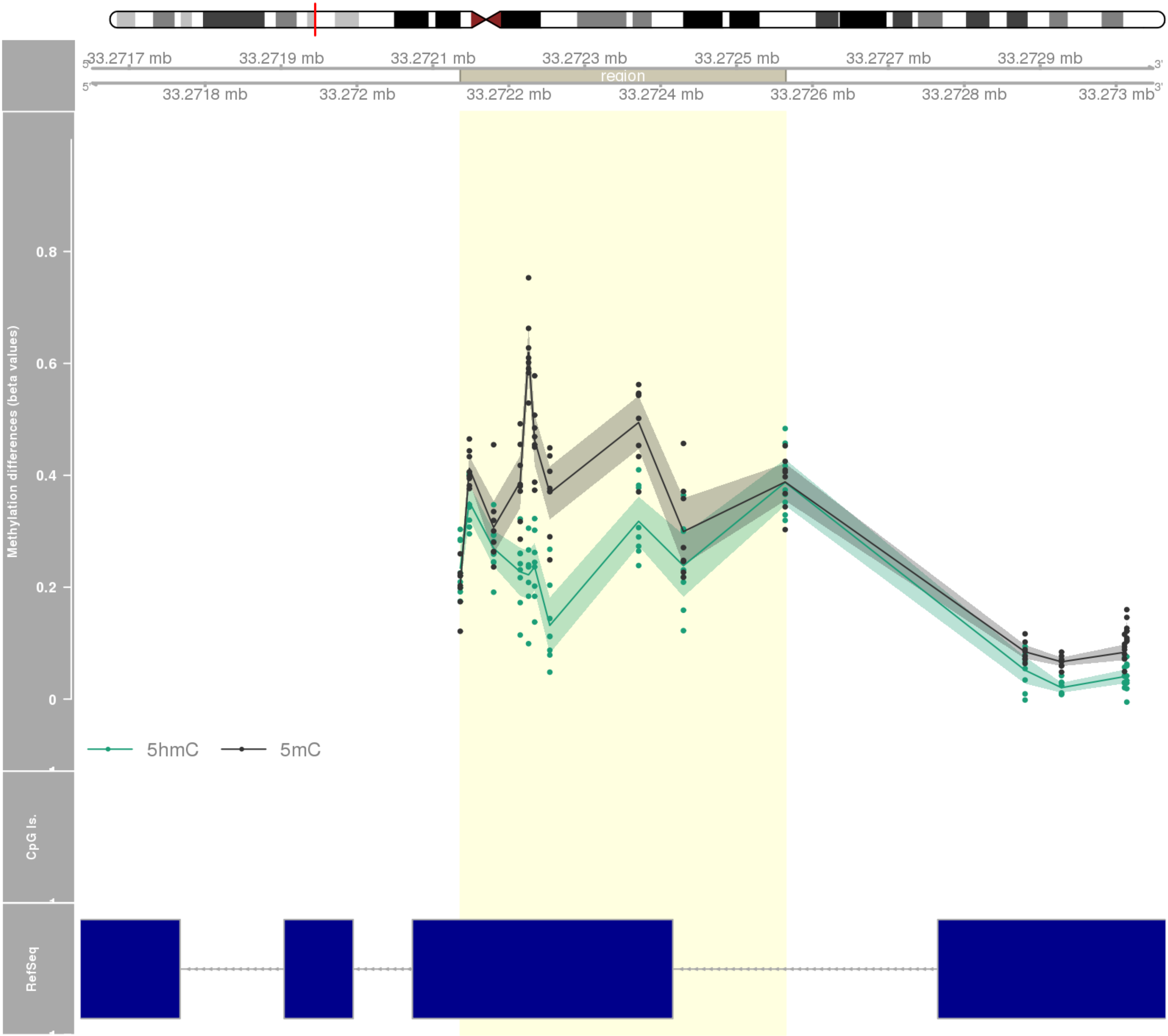
DMR 489 // chr11:63272764-63274743 // 1979 pb. (7 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: LGALS12 -



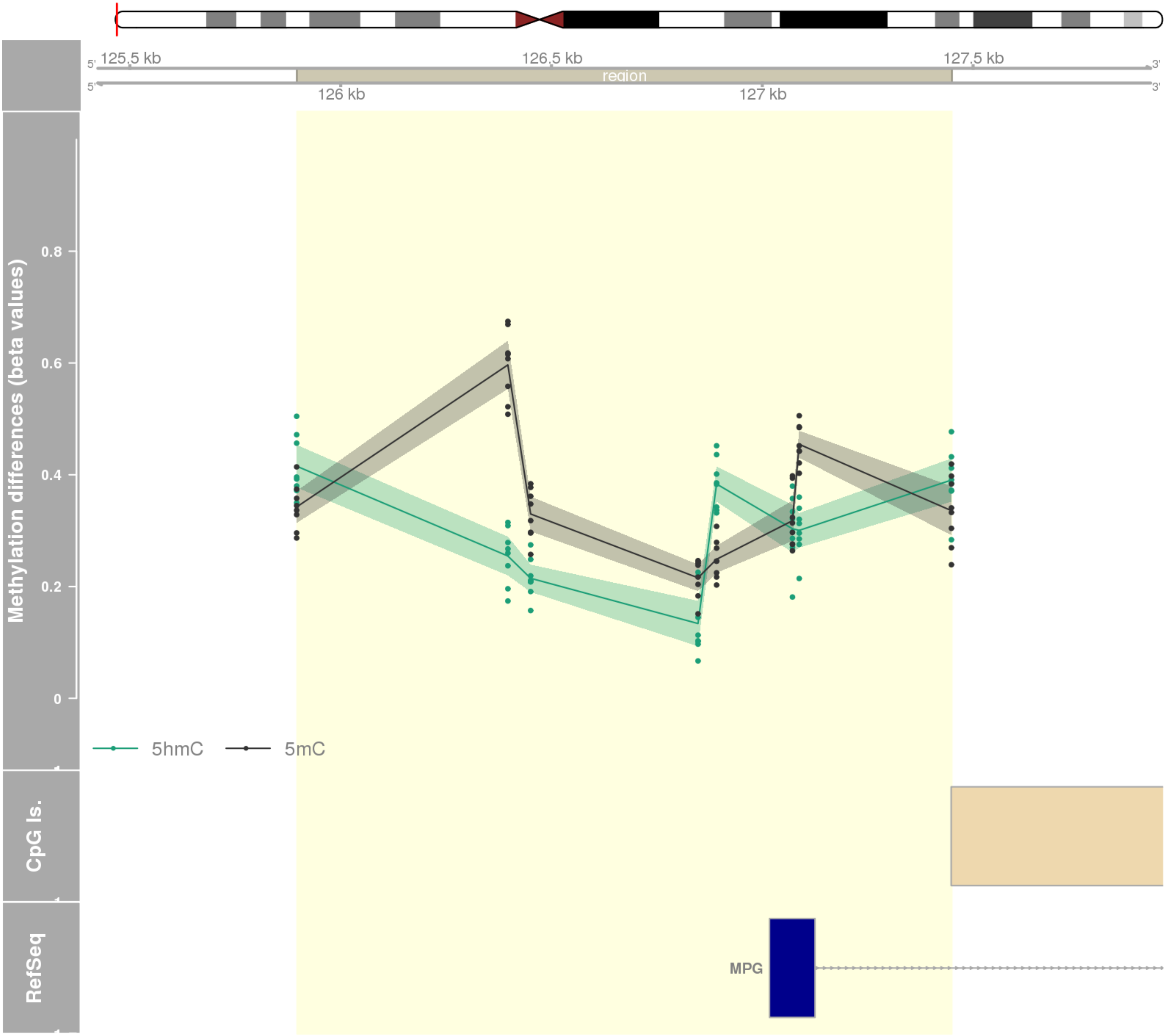
DMR 490 // chr11:66488638-66489521 // 883 pb. (7 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: SPTBN2 -



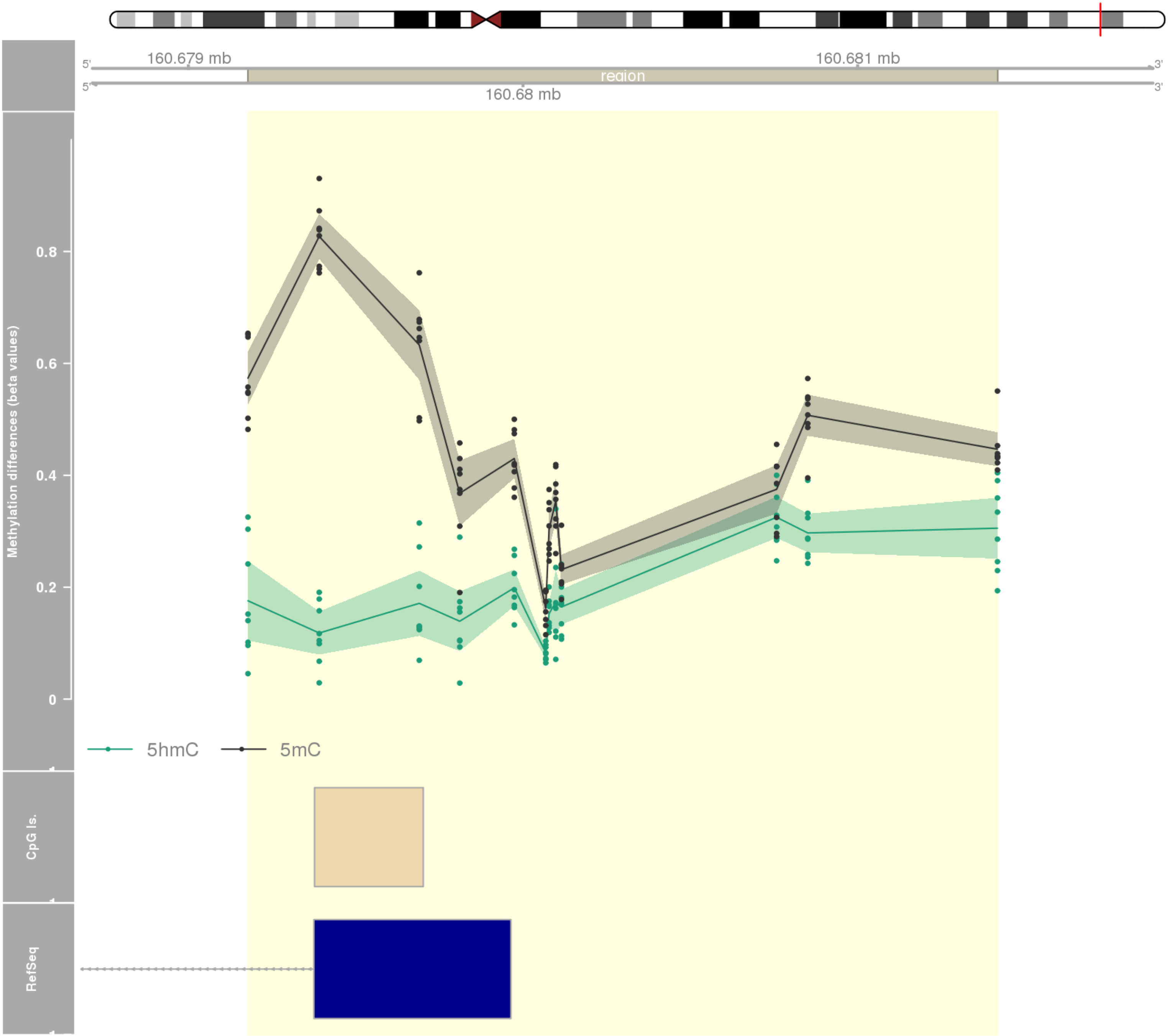
DMR 491 // chr6:33272136-33272564 // 428 pb. (10 probes) // pvalue: 0.012 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: TAPBP -



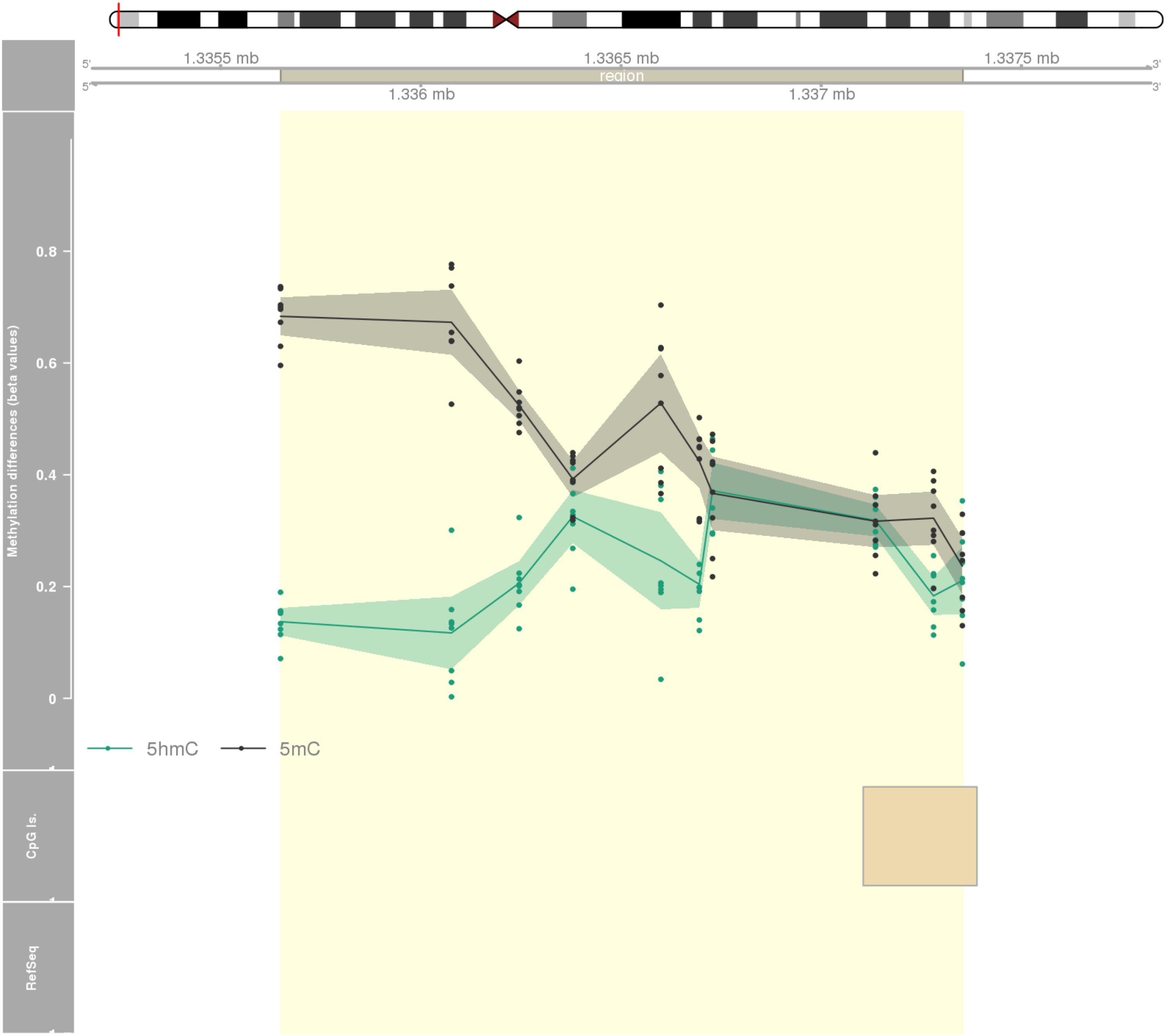
DMR 492 // chr16:125896-127449 // 1553 pb. (8 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.025 // fwerArea: 0.679
- genes: RHBDF1 / MPG -



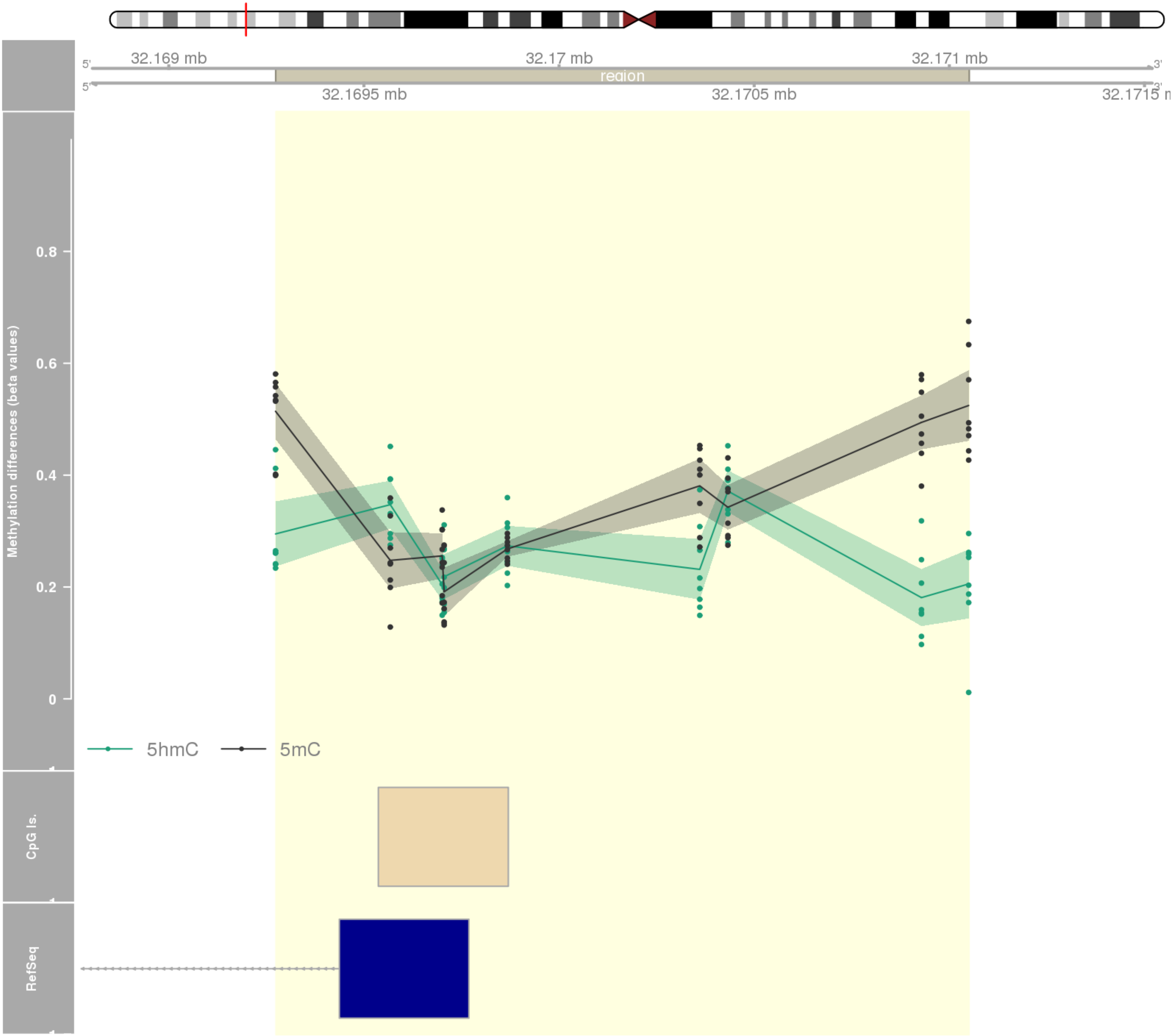
DMR 493 // chr6:160679178-160681418 // 2240 pb. (12 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679
- genes: SLC22A2 -

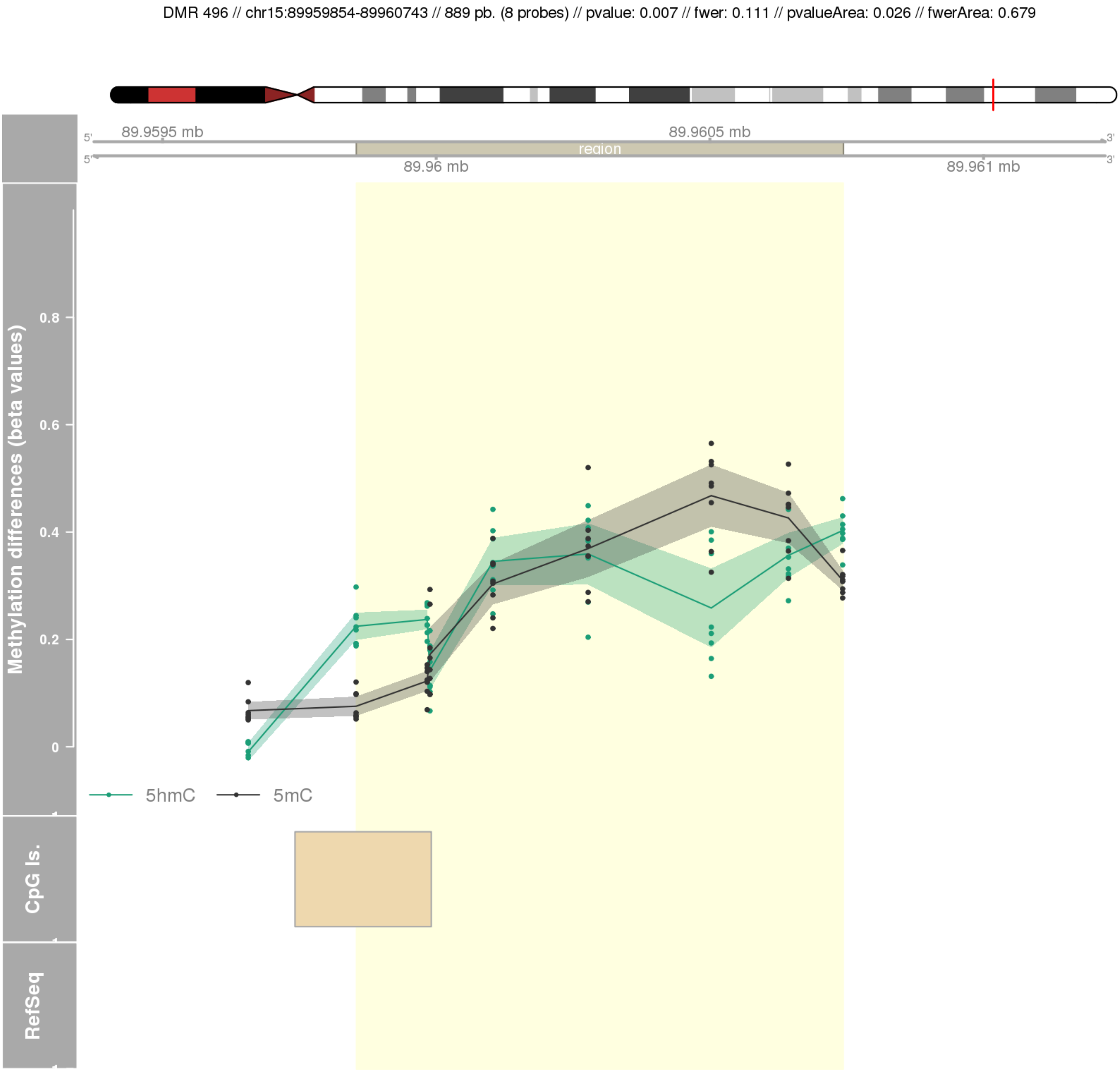


DMR 494 // chr7:1335650-1337353 // 1703 pb. (10 probes) // pvalue: 0.012 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679

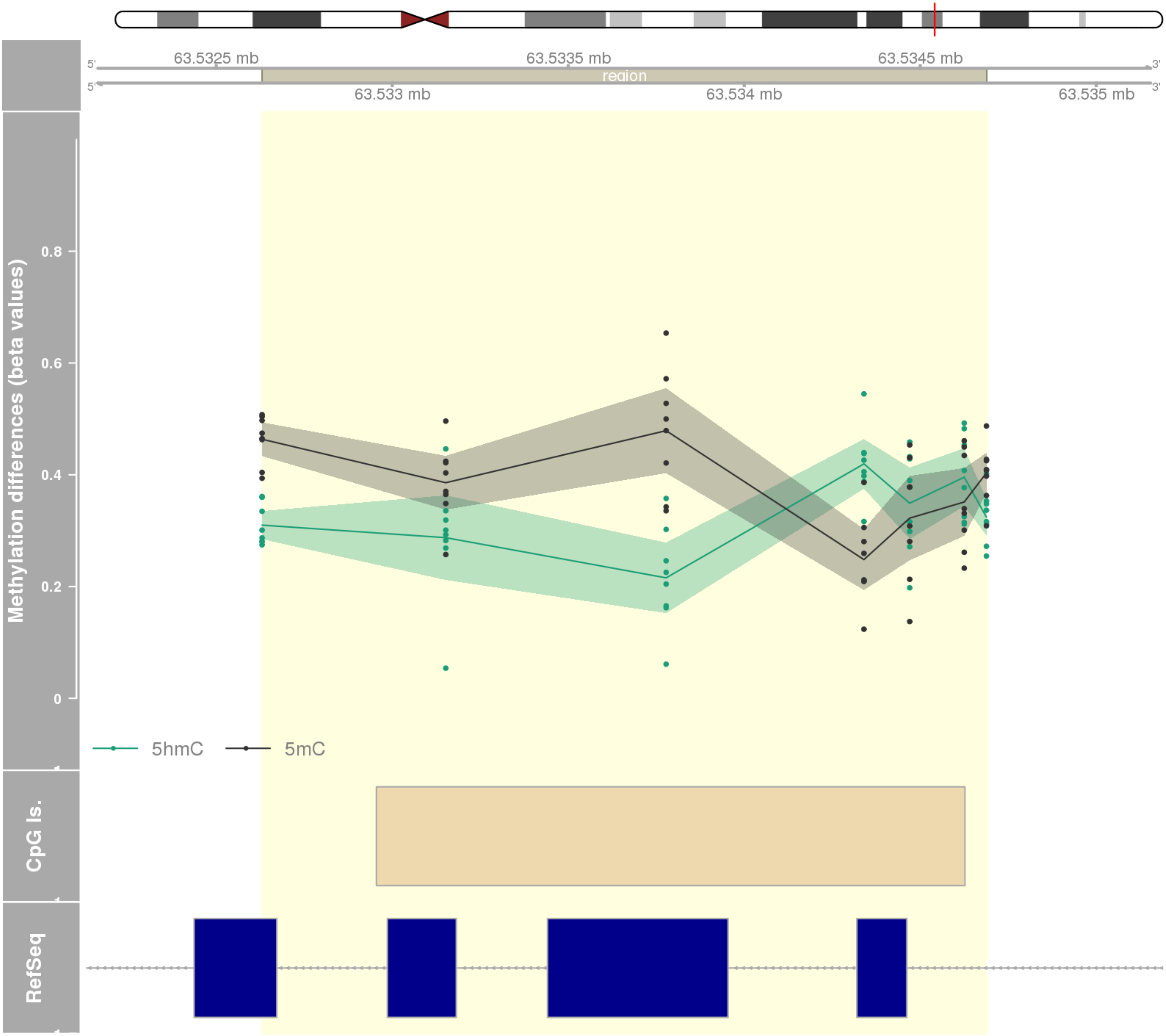


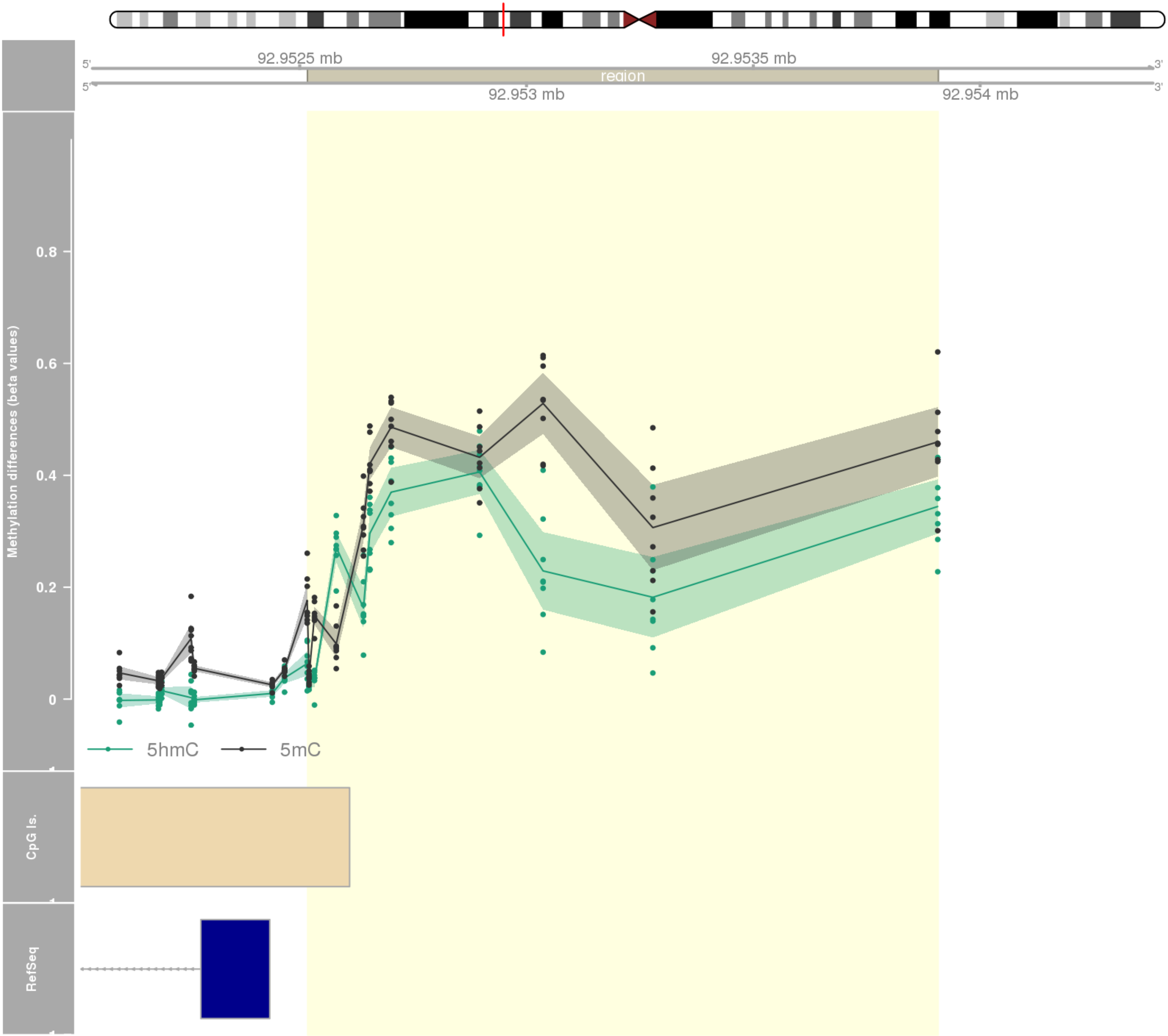
DMR 495 // chr1:32169274-32171050 // 1776 pb. (9 probes) // pvalue: 0.01 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679
- genes: COL16A1 -




DMR 496 // chr15:89959854-89960743 // 889 pb. (8 probes) // pvalue: 0.007 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679
89.9595 mb
89.9605 mb
region
89.96 mb
89.961 mb
5'
3'
5'
3'
Methylation differences (beta values)
0.8
0.6
0.4
0.2
0
5hmC
5mC
CpG Is.
RefSeq

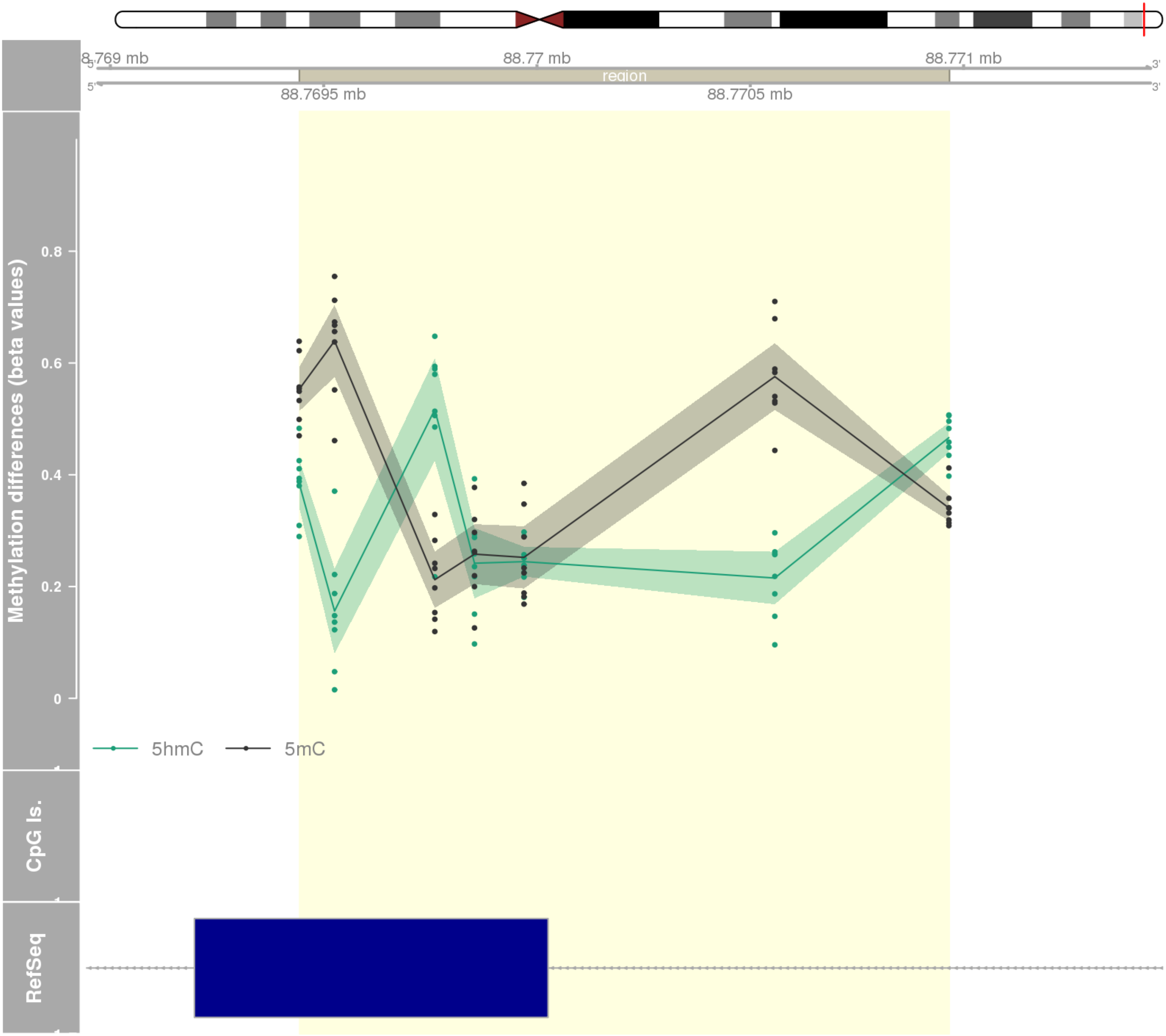
DMR 497 // chr17:63532630-63534688 // 2058 pb. (7 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679
- genes: AXIN2 -





DMR 498 // chr1:92952517-92953907 // 1390 pb. (11 probes) // pvalue: 0.012 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679

DMR 499 // chr16:88769443-88770966 // 1523 pb. (7 probes) // pvalue: 0.003 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679
- genes: RNF166 -



DMR 500 // chr10:463561-465584 // 2023 pb. (10 probes) // pvalue: 0.012 // fwer: 0.111 // pvalueArea: 0.026 // fwerArea: 0.679
- genes: DIP2C -