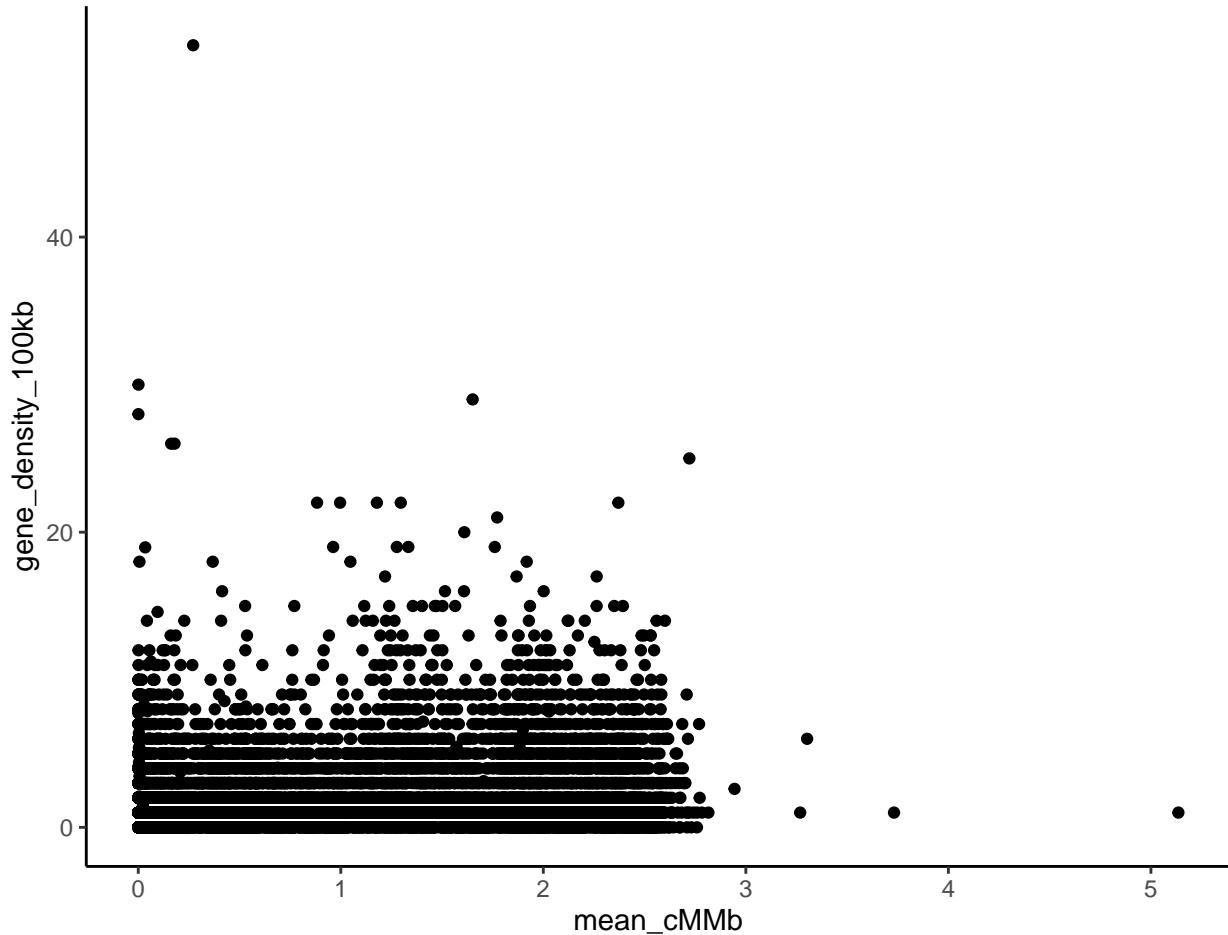


# plot fd windows

steph

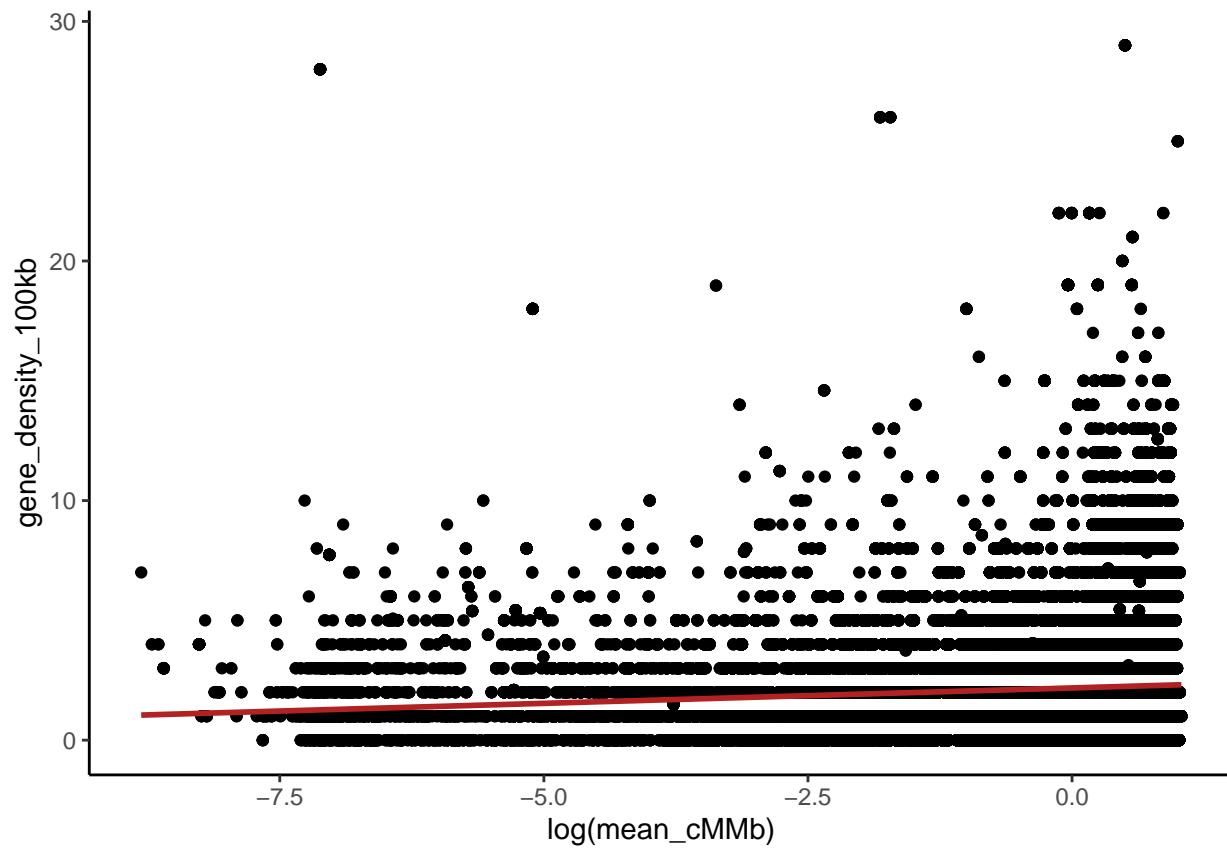
2024-04-09



```
## [1] 4.94148
```

**introgression from coastal to inland populations adjacent to hybrid zone**

Coastal (Pacific Spirit and Porpoise Bay) to BC inland (Kelowna and Kamloops) with Quebec inland as inland sister population and Hermit thrush as outgroup

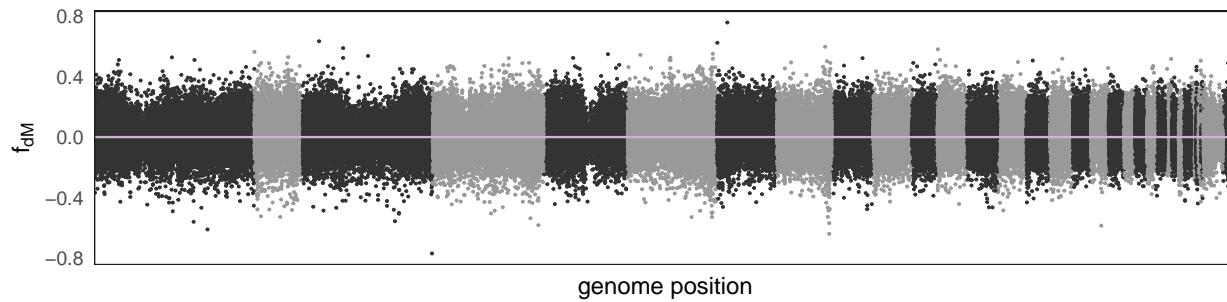


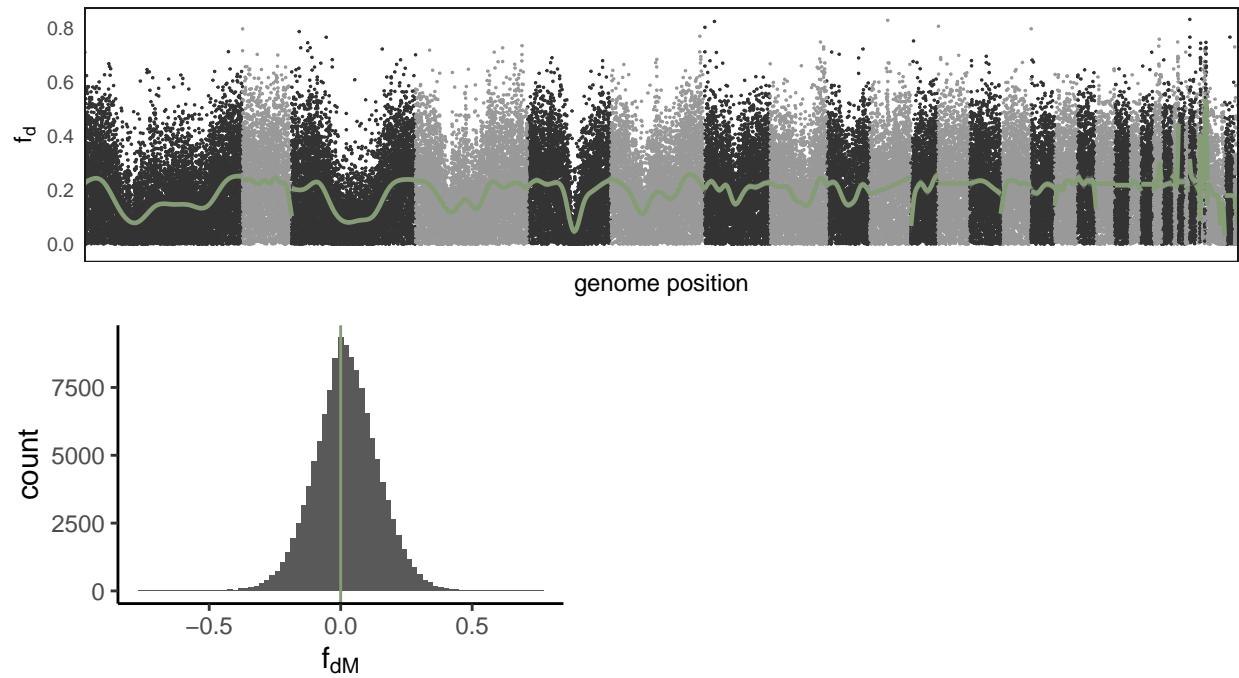
#### check overall direction of introgression

fdM allows for introgression to both subspecies

Most introgression is coastal to BC inland

Some signal in the other direction, but this could also be excess allele sharing between BC inland and Hermit thrush



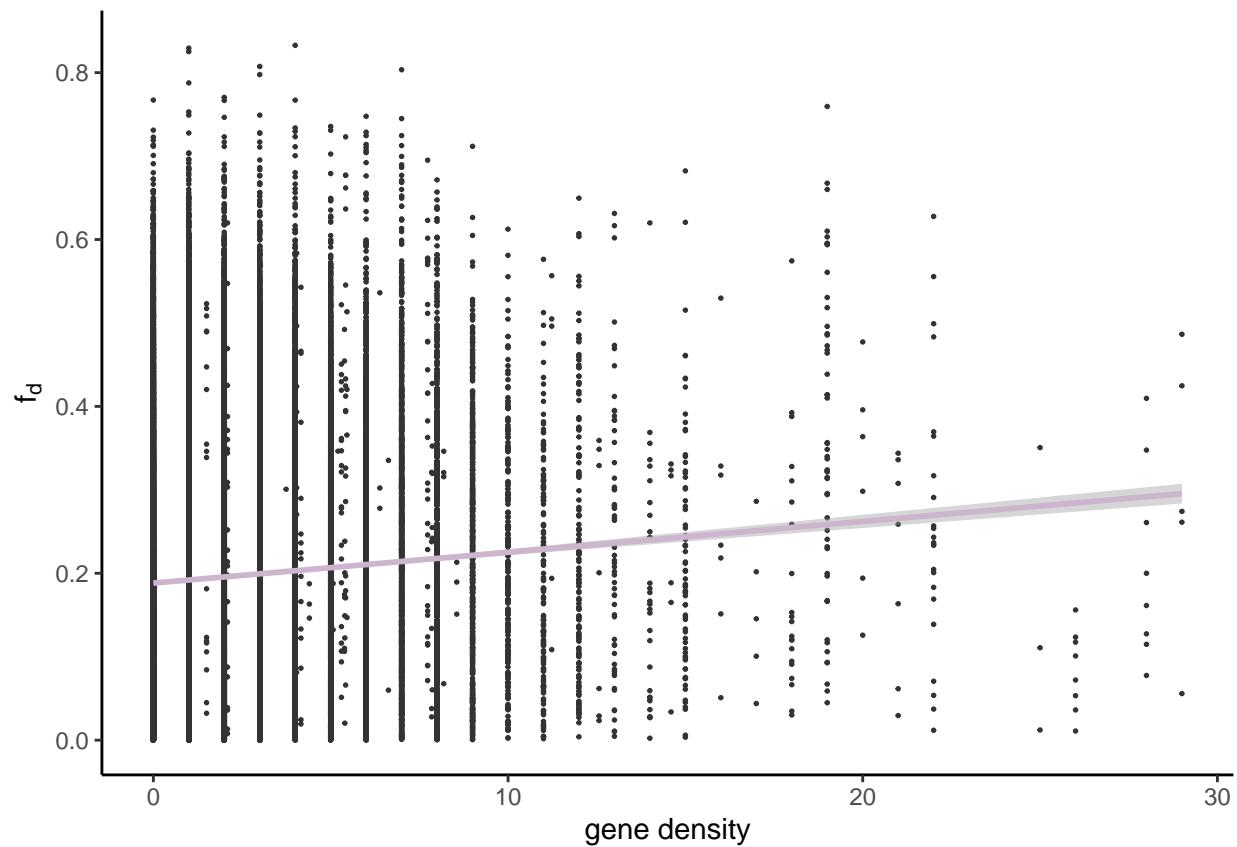


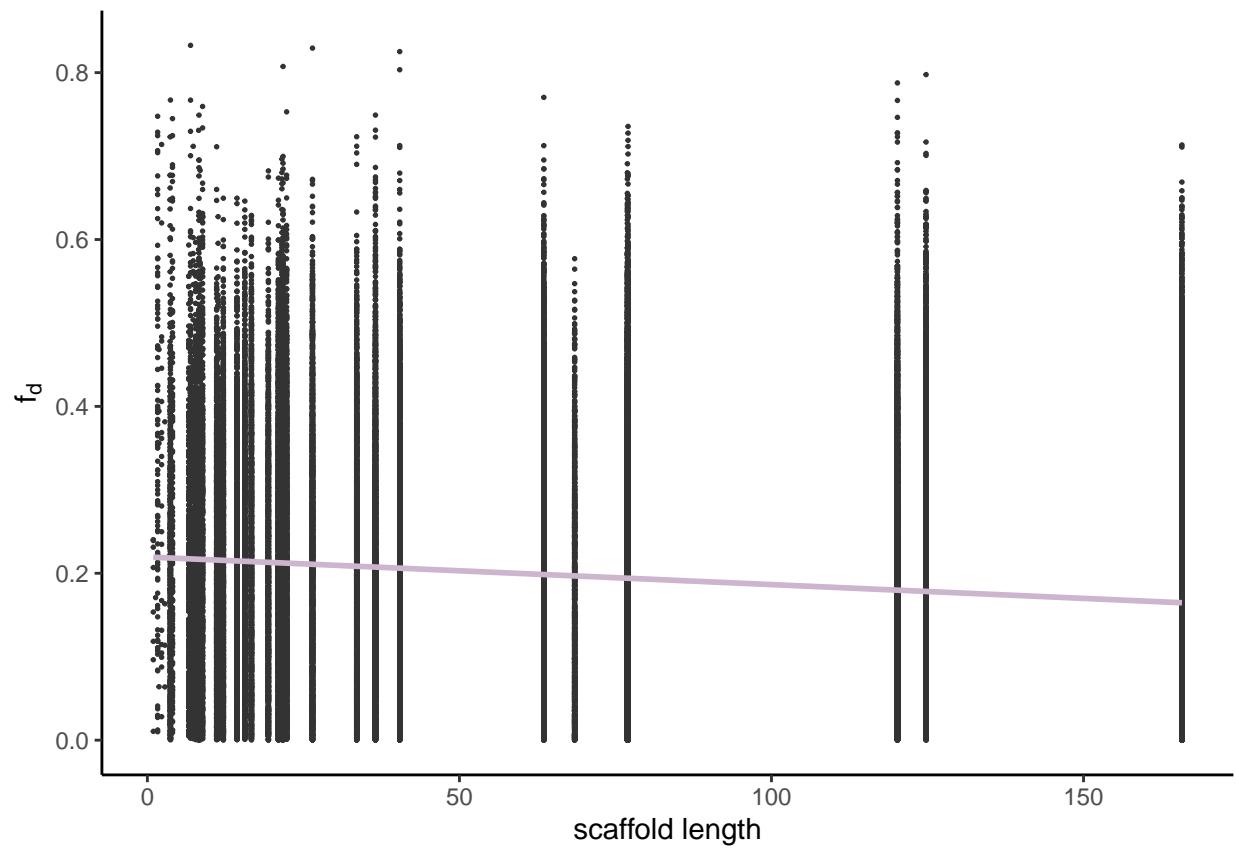
```
## # A tibble: 1 x 2
##   mean_D mean_fdm
##     <dbl>    <dbl>
## 1  0.0209   0.0215
```

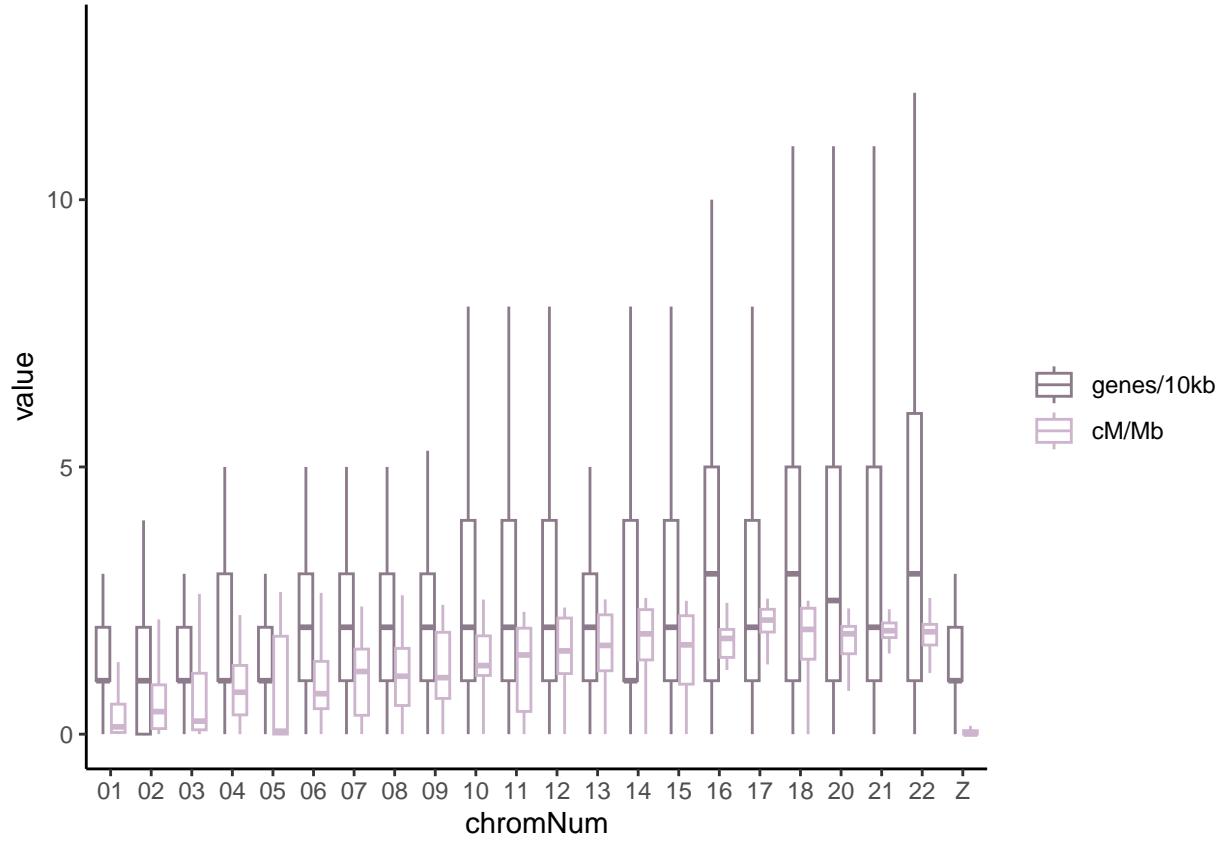
#### **test for a relationship to recombination rate**

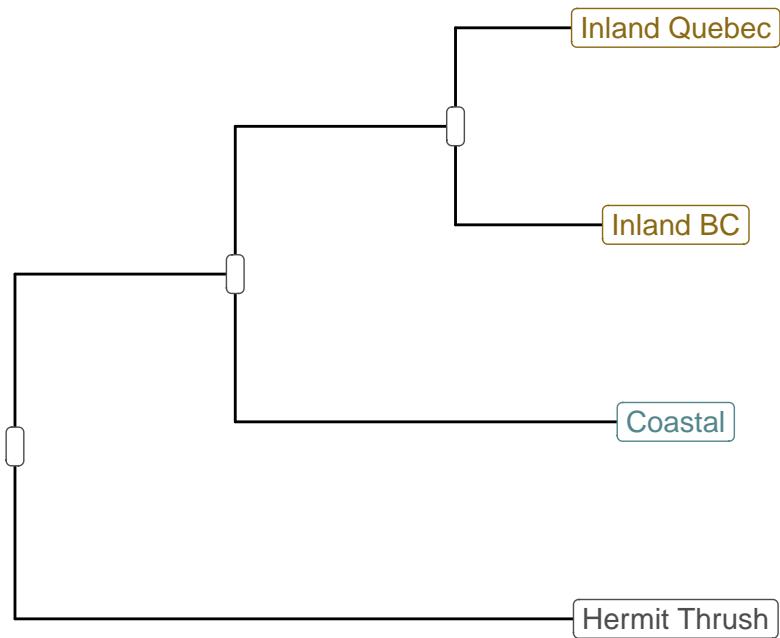
Limit to windows where  $f_{dM}$  is above zero (i.e. introgression is coastal to local inland)

Positive relationship between  $f_d$  and recombination rate - this suggests selection against introgression

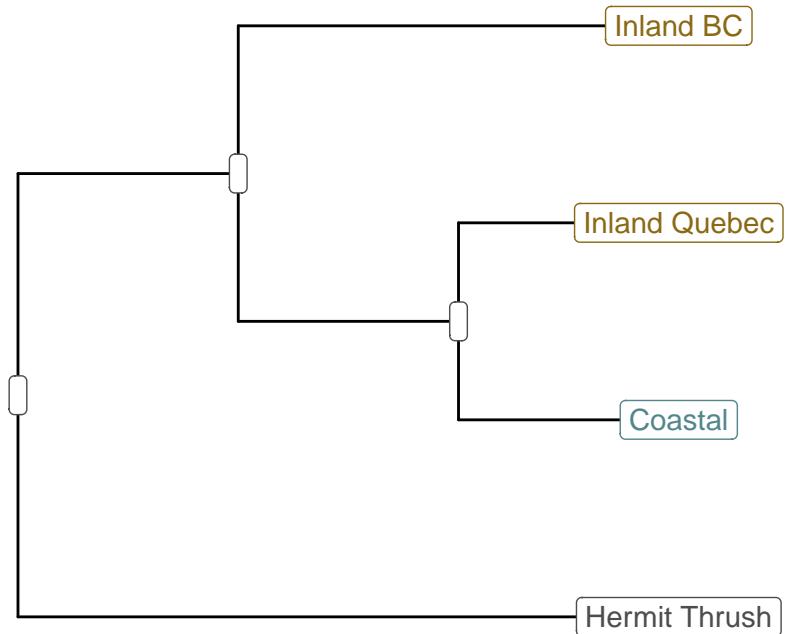


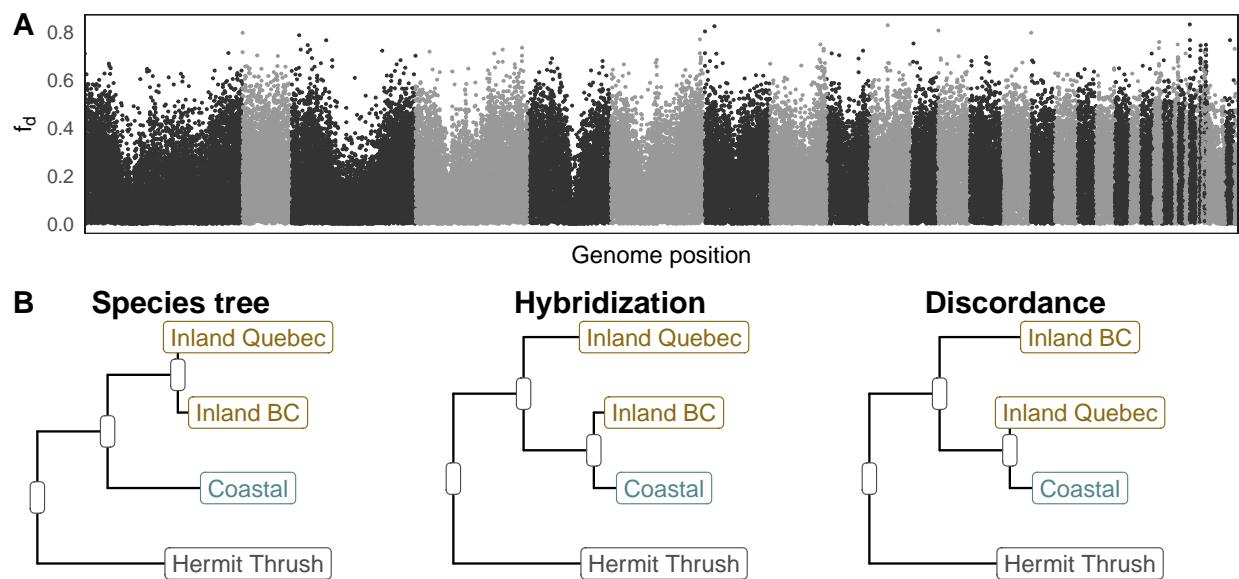
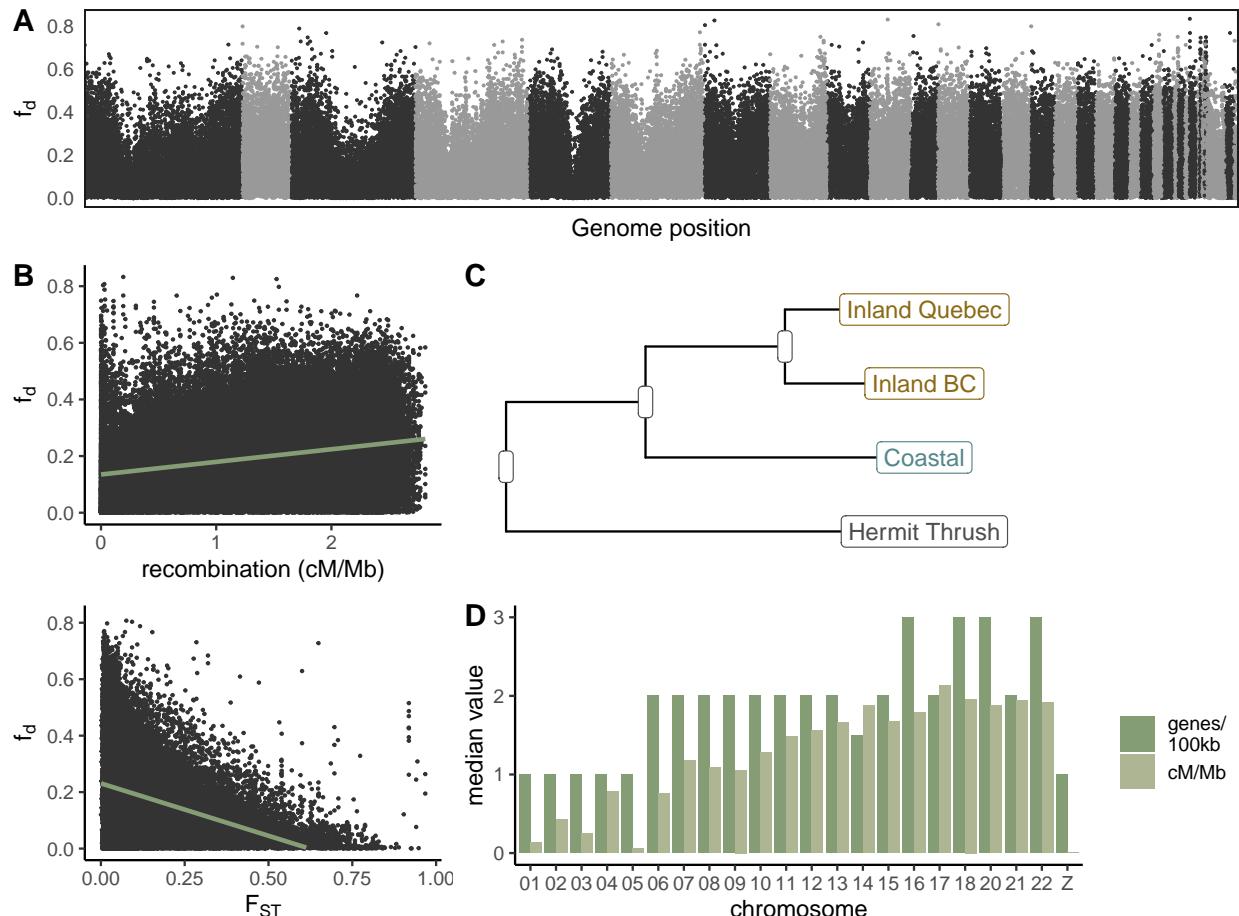






## [1] 3





```
##  
## Call:  
## lm(formula = f_d ~ log(mean_cMMb), data = dstatsQc %>% filter(f_dM >
```

```

##      0))
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.22158 -0.10313 -0.02077  0.08537  0.71563
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.1991701 0.0004956 401.85 <2e-16 ***
## log(mean_cMMb) 0.0237196 0.0003508 67.61 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1326 on 72144 degrees of freedom
## (102 observations deleted due to missingness)
## Multiple R-squared: 0.05958, Adjusted R-squared: 0.05957
## F-statistic: 4571 on 1 and 72144 DF, p-value: < 2.2e-16

##                  2.5 %     97.5 %
## (Intercept) 0.19819867 0.20014156
## log(mean_cMMb) 0.02303192 0.02440721

##
## Call:
## lm(formula = f_d ~ gene_density_100kb, data = dstatsQc %>% filter(f_dM >
## 0))
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.27339 -0.11211 -0.02125  0.09123  0.63742
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.1882449 0.0006966 270.25 <2e-16 ***
## gene_density_100kb 0.0036956 0.0002237 16.52 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1365 on 72144 degrees of freedom
## (102 observations deleted due to missingness)
## Multiple R-squared: 0.003768, Adjusted R-squared: 0.003754
## F-statistic: 272.9 on 1 and 72144 DF, p-value: < 2.2e-16

##                  2.5 %     97.5 %
## (Intercept) 0.186879636 0.189610129
## gene_density_100kb 0.003257109 0.004134079

##
## Call:
## lm(formula = f_d ~ Fst, data = dstatsQc %>% filter(f_dM > 0))
##
## Residuals:
##      Min      1Q   Median      3Q      Max

```

```

## -0.22936 -0.09810 -0.01518  0.08232  0.73769
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.2310593  0.0006027 383.35 <2e-16 ***
## Fst         -0.3713726  0.0038802 -95.71 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1288 on 72134 degrees of freedom
##   (112 observations deleted due to missingness)
## Multiple R-squared:  0.1127, Adjusted R-squared:  0.1127
## F-statistic:  9160 on 1 and 72134 DF, p-value: < 2.2e-16

##           2.5 %    97.5 %
## (Intercept) 0.2298779 0.2322406
## Fst        -0.3789778 -0.3637674

##
## Call:
## lm(formula = f_d ~ chromosomeType, data = dstatsQc %>% filter(f_dM >
##   0))
##
## Residuals:
##      Min       1Q     Median       3Q      Max
## -0.22527 -0.11087 -0.02309  0.09028  0.64010
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.1850883  0.0006544 282.824 < 2e-16 ***
## chromosomeTypemicro 0.0401908  0.0014511 27.697 < 2e-16 ***
## chromosomeTypesex  -0.0189570  0.0031684 -5.983 2.2e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1356 on 55799 degrees of freedom
##   (16446 observations deleted due to missingness)
## Multiple R-squared:  0.01485, Adjusted R-squared:  0.01481
## F-statistic: 420.6 on 2 and 55799 DF, p-value: < 2.2e-16

##           2.5 %    97.5 %
## (Intercept) 0.18380557 0.18637094
## chromosomeTypemicro 0.03734675 0.04303494
## chromosomeTypesex  -0.02516709 -0.01274686

##   chromosomeType emmean      SE   df lower.CL upper.CL
##   macro          0.185 0.000654 55799    0.184   0.186
##   micro          0.225 0.001295 55799    0.223   0.228
##   sex            0.166 0.003100 55799    0.160   0.172
##
## Confidence level used: 0.95

##

```

```

## Call:
## lm(formula = f_d ~ abs(logRatioMu), data = dstatsQc %>% filter(f_dM >
##      0))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.21686 -0.10902 -0.02060  0.08946  0.63244
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            0.2169276  0.0007304 297.00  <2e-16 ***
## abs(logRatioMu) -0.0467999  0.0012023 -38.92  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1347 on 70344 degrees of freedom
## (1902 observations deleted due to missingness)
## Multiple R-squared:  0.02108, Adjusted R-squared:  0.02107
## F-statistic:  1515 on 1 and 70344 DF, p-value: < 2.2e-16

##                               2.5 %      97.5 %
## (Intercept)            0.21549604  0.21835924
## abs(logRatioMu) -0.04915642 -0.04444331

##
## Call:
## lm(formula = f_d ~ scaffoldLength_Mb + gene_density_100kb + mean_cMMb +
##      Fst, data = dstatsQc %>% filter(f_dM > 0) %>% filter(!scaffold %in%
##      sexScafs))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.26159 -0.09769 -0.01446  0.08230  0.73170
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            2.199e-01  1.981e-03 110.963  < 2e-16 ***
## scaffoldLength_Mb -3.066e-05  1.022e-05 -3.000  0.0027 **
## gene_density_100kb  1.685e-03  2.197e-04   7.667 1.78e-14 ***
## mean_cMMb             5.721e-03  8.960e-04   6.385 1.73e-10 ***
## Fst                  -3.473e-01  5.979e-03 -58.084  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1287 on 70218 degrees of freedom
## (96 observations deleted due to missingness)
## Multiple R-squared:  0.1159, Adjusted R-squared:  0.1158
## F-statistic:  2301 on 4 and 70218 DF, p-value: < 2.2e-16

##                               2.5 %      97.5 %
## (Intercept)            2.159726e-01  2.237395e-01
## scaffoldLength_Mb -5.068582e-05 -1.062591e-05
## gene_density_100kb  1.253956e-03  2.115210e-03

```

```

## mean_cMMb      3.964750e-03  7.477086e-03
## Fst          -3.589803e-01 -3.355440e-01

##
## Call:
## lm(formula = f_d ~ gene_density_100kb + mean_cMMb + Fst, data = dstatsQc %>%
##     filter(f_dM > 0) %>% filter(scaffold == "super_scaffold_1"))
##
## Residuals:
##       Min     1Q   Median     3Q    Max
## -0.23961 -0.08214 -0.01605  0.06580  0.50341
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            0.1840928  0.0040030 45.989 <2e-16 ***
## gene_density_100kb    0.0006808  0.0006732  1.011   0.312
## mean_cMMb              0.0226774  0.0019286 11.759 <2e-16 ***
## Fst                  -0.2610845  0.0120774 -21.618 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.116 on 9875 degrees of freedom
## (5 observations deleted due to missingness)
## Multiple R-squared:  0.1935, Adjusted R-squared:  0.1933
## F-statistic: 789.8 on 3 and 9875 DF,  p-value: < 2.2e-16

##                               2.5 %      97.5 %
## (Intercept)            0.1762461407  0.191939515
## gene_density_100kb    -0.0006388818  0.002000458
## mean_cMMb              0.0188970215  0.026457773
## Fst                  -0.2847587065 -0.237410305

##
## Call:
## lm(formula = f_d ~ gene_density_100kb + mean_cMMb + Fst, data = dstatsQc %>%
##     filter(f_dM > 0) %>% filter(scaffold == "super_scaffold_3"))
##
## Residuals:
##       Min     1Q   Median     3Q    Max
## -0.24589 -0.07826 -0.01629  0.06499  0.71213
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            0.1745665  0.0049219 35.467 <2e-16 ***
## gene_density_100kb    -0.0003757  0.0007341 -0.512   0.609
## mean_cMMb              0.0307826  0.0026116 11.787 <2e-16 ***
## Fst                  -0.2446510  0.0140575 -17.404 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1175 on 7749 degrees of freedom
## (5 observations deleted due to missingness)
## Multiple R-squared:  0.2189, Adjusted R-squared:  0.2186
## F-statistic: 724.1 on 3 and 7749 DF,  p-value: < 2.2e-16

```

```

##          2.5 %      97.5 %
## (Intercept) 0.164918199 0.184214888
## gene_density_100kb -0.001814867 0.001063373
## mean_cMMb     0.025663125 0.035902156
## Fst           -0.272207377 -0.217094533

## 
## Call:
## lm(formula = f_d ~ gene_density_100kb + mean_cMMb + Fst, data = dstatsQc %>%
##     filter(f_dM > 0) %>% filter(scaffold == "scaffold_4_arrow_ctg1"))
##
## Residuals:
##    Min     1Q   Median     3Q    Max
## -0.22806 -0.09394 -0.00954  0.08004  0.47416
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.1747622  0.0072442 24.124 < 2e-16 ***
## gene_density_100kb 0.0013504  0.0009393  1.438  0.151
## mean_cMMb     0.0228016  0.0032492  7.018 2.54e-12 ***
## Fst           -0.2467971  0.0172330 -14.321 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1254 on 5237 degrees of freedom
## Multiple R-squared:  0.1688, Adjusted R-squared:  0.1684
## F-statistic: 354.6 on 3 and 5237 DF,  p-value: < 2.2e-16

##          2.5 %      97.5 %
## (Intercept) 0.1605605738 0.188963882
## gene_density_100kb -0.0004910708 0.003191825
## mean_cMMb     0.0164318575 0.029171338
## Fst           -0.2805810159 -0.213013211

```

### variation across the genome

Note, as always, chromosome 5

