

winding_by_fa

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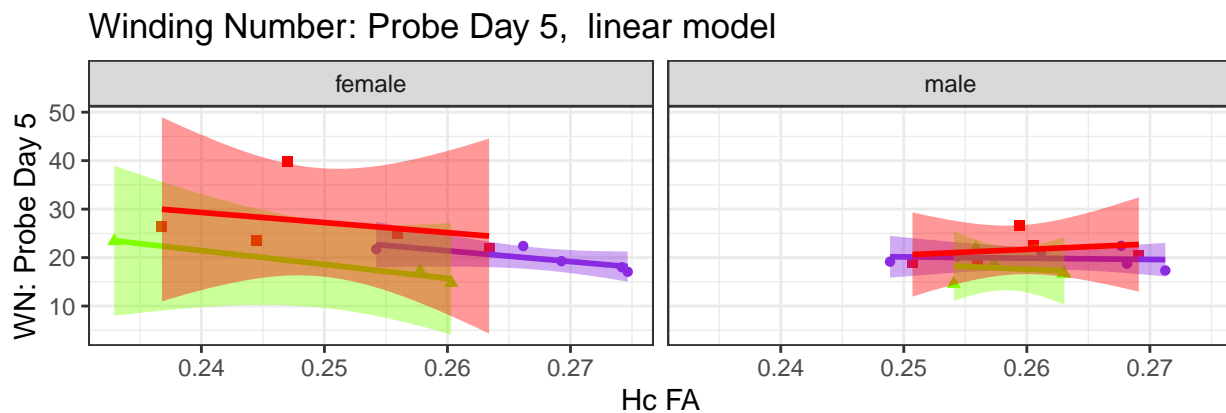
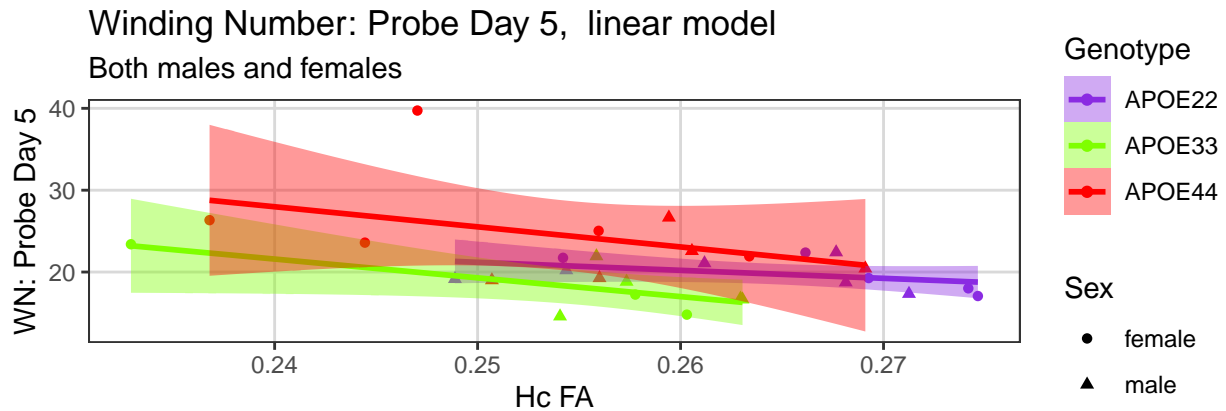
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Aim

We examine whether APOE2, APOE3, and APOE4 carriers use a hippocampal or caudate based spatial navigation strategy.

FA

Day 5 Probe By Hc FA



```
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.7884 -1.6344 -0.6007  0.9028 11.8871
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      79.1555    65.0064   1.218   0.240
## Hc             -222.1334   242.7476  -0.915   0.373
## GenotypeAPOE33    11.1811    80.4063   0.139   0.891
## GenotypeAPOE44     0.1215    81.2783   0.001   0.999
## Sexmale          -52.3686    84.4278  -0.620   0.543
## Hc:GenotypeAPOE33 -64.9119   307.5279  -0.211   0.835
## Hc:GenotypeAPOE44  13.9267   311.6158   0.045   0.965
## Hc:Sexmale        195.5625   318.1092   0.615   0.547
## GenotypeAPOE33:Sexmale  8.7780   159.1224   0.055   0.957
## GenotypeAPOE44:Sexmale -34.4001   124.5997  -0.276   0.786
## Hc:GenotypeAPOE33:Sexmale -20.6269   612.5697  -0.034   0.974
## Hc:GenotypeAPOE44:Sexmale 124.8552   478.4404   0.261   0.797
##
## Residual standard error: 4.041 on 17 degrees of freedom
## Multiple R-squared:  0.567, Adjusted R-squared:  0.2869
```

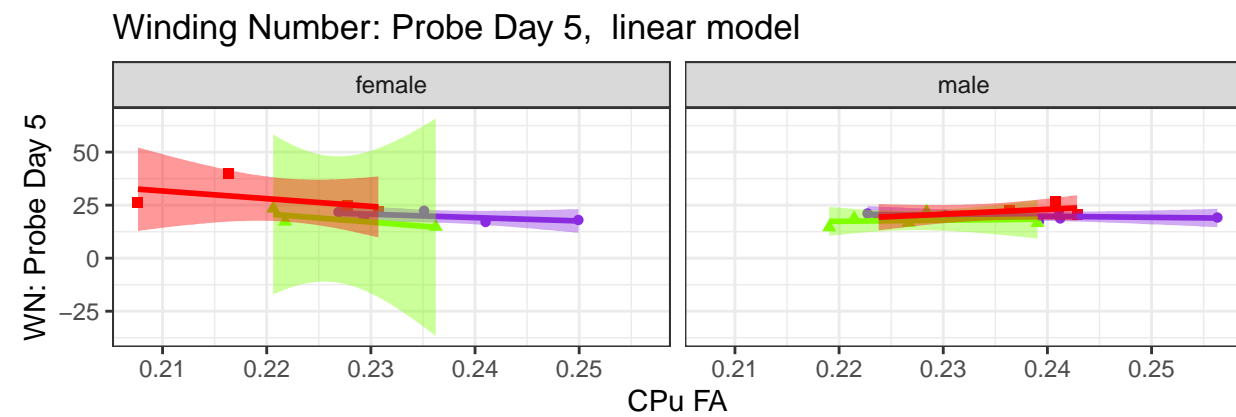
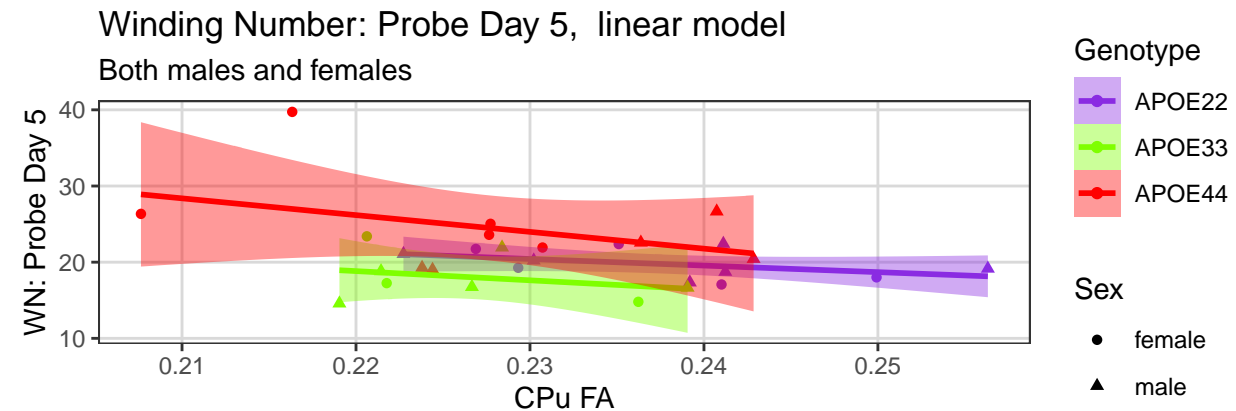
```
## F-statistic: 2.024 on 11 and 17 DF, p-value: 0.09275
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.7884 -1.0771 -0.8191 -0.0791 11.8871
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      79.1555      84.6466   0.935   0.381
## Hc             -222.1334     316.0879  -0.703   0.505
## GenotypeAPOE33    11.1811     104.6991   0.107   0.918
## GenotypeAPOE44     0.1215     105.8346   0.001   0.999
## Hc:GenotypeAPOE33 -64.9119     400.4401  -0.162   0.876
## Hc:GenotypeAPOE44  13.9267     405.7631   0.034   0.974
##
## Residual standard error: 5.262 on 7 degrees of freedom
## Multiple R-squared:  0.5857, Adjusted R-squared:  0.2897
## F-statistic: 1.979 on 5 and 7 DF, p-value: 0.1991
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.6807 -1.7185 -0.5574  1.0024  5.0419
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      26.79      38.59   0.694   0.503
## Hc             -26.57     147.27  -0.180   0.860
## GenotypeAPOE33    19.96      98.36   0.203   0.843
## GenotypeAPOE44   -34.28      67.65  -0.507   0.623
## Hc:GenotypeAPOE33 -85.54     379.50  -0.225   0.826
## Hc:GenotypeAPOE44 138.78     260.06   0.534   0.605
##
## Residual standard error: 2.895 on 10 degrees of freedom
## Multiple R-squared:  0.3253, Adjusted R-squared: -0.01205
## F-statistic: 0.9643 on 5 and 10 DF, p-value: 0.4831
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value Pr(>F)
## Hc      1 118.580  118.580   7.2625 0.01534 *
## Genotype 2 170.837   85.419   5.2315 0.01696 *
## Sex      1  16.903   16.903   1.0353 0.32319
## Hc:Genotype 2   2.652    1.326   0.0812 0.92235
## Hc:Sex      1  24.879   24.879   1.5237 0.23385
## Genotype:Sex 2  28.290   14.145   0.8663 0.43825
## Hc:Genotype:Sex 2   1.396    0.698   0.0427 0.95826
```

```
## Residuals      17 277.571  16.328
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1  132.222  132.222   4.7761 0.06512 .
## Genotype     2   140.176   70.088   2.5317 0.14883
## Hc:Genotype   2    1.527    0.763   0.0276 0.97291
## Residuals    7   193.789   27.684
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1    0.126    0.1256   0.0150 0.9050
## Genotype     2   36.850   18.4248   2.1991 0.1616
## Hc:Genotype   2    3.420    1.7099   0.2041 0.8187
## Residuals   10   83.782    8.3782
```

Day 5 Probe By CPu FA



##

```
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.1957 -1.7070 -0.0603  0.5348 10.3464
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         57.08      48.76   1.171   0.258
## CPu              -158.10     206.09  -0.767   0.454
## GenotypeAPOE33        49.39      85.75   0.576   0.572
## GenotypeAPOE44        50.74      65.52   0.774   0.449
## Sexmale             -25.14      60.56  -0.415   0.683
## CPu:GenotypeAPOE33   -230.84     373.67  -0.618   0.545
## CPu:GenotypeAPOE44   -204.44     285.07  -0.717   0.483
## CPu:Sexmale          107.34     255.17   0.421   0.679
## GenotypeAPOE33:Sexmale -75.03     108.54  -0.691   0.499
## GenotypeAPOE44:Sexmale -114.88      89.76  -1.280   0.218
## CPu:GenotypeAPOE33:Sexmale 332.10     472.37   0.703   0.492
## CPu:GenotypeAPOE44:Sexmale 485.49     386.22   1.257   0.226
##
## Residual standard error: 3.835 on 17 degrees of freedom
## Multiple R-squared:  0.61, Adjusted R-squared:  0.3576
## F-statistic: 2.417 on 11 and 17 DF, p-value: 0.04964
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.1957 -1.9014 -0.2172  0.5348 10.3464
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         57.08      64.89   0.880   0.408
## CPu              -158.10     274.27  -0.576   0.582
## GenotypeAPOE33        49.39     114.12   0.433   0.678
## GenotypeAPOE44        50.74      87.19   0.582   0.579
## CPu:GenotypeAPOE33   -230.84     497.29  -0.464   0.657
## CPu:GenotypeAPOE44   -204.44     379.37  -0.539   0.607
##
## Residual standard error: 5.104 on 7 degrees of freedom
## Multiple R-squared:  0.6101, Adjusted R-squared:  0.3317
## F-statistic: 2.191 on 5 and 7 DF, p-value: 0.1676
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.2738 -1.1642 -0.0397  0.6790  4.1098
##
```

```

## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      31.93      24.36   1.311   0.219
## CPu              -50.76     102.07  -0.497   0.630
## GenotypeAPOE33   -25.64      45.14  -0.568   0.582
## GenotypeAPOE44   -64.15      41.62  -1.541   0.154
## CPu:GenotypeAPOE33 101.26     196.04   0.517   0.617
## CPu:GenotypeAPOE44 281.05     176.78   1.590   0.143
##
## Residual standard error: 2.602 on 10 degrees of freedom
## Multiple R-squared:  0.4549, Adjusted R-squared:  0.1823
## F-statistic: 1.669 on 5 and 10 DF,  p-value: 0.2293

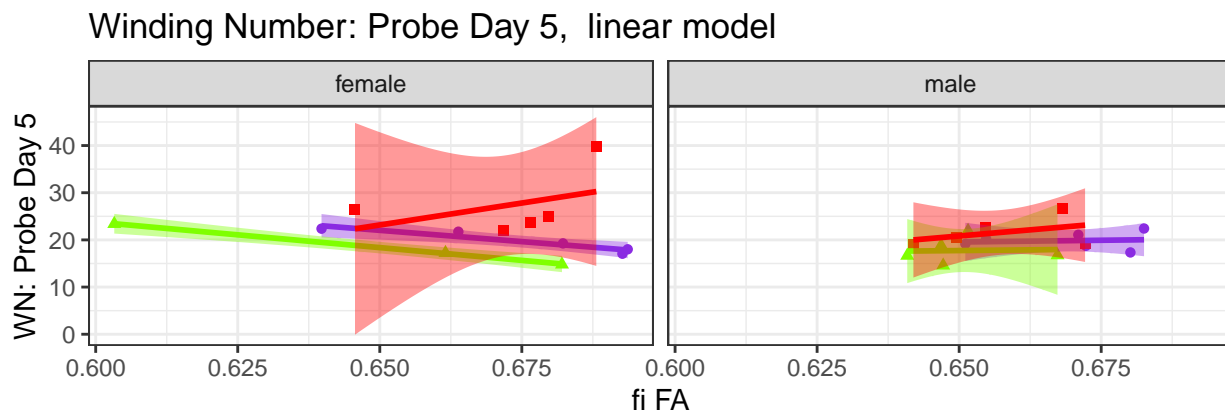
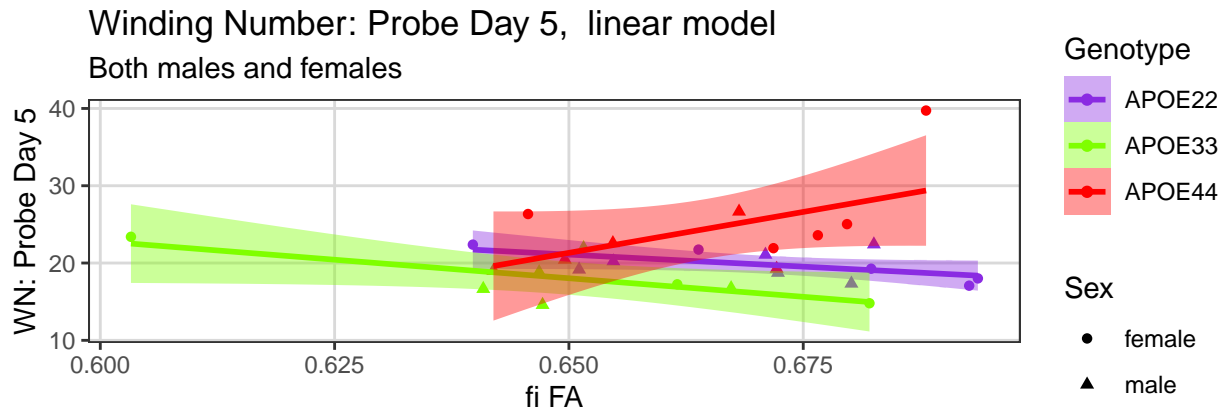
## Analysis of Variance Table
##
## Response: Probe_d5
##               Df Sum Sq Mean Sq F value    Pr(>F)
## CPu              1  66.397   66.397   4.5143 0.048576 *
## Genotype         2 194.672   97.336   6.6179 0.007488 **
## Sex              1  15.194   15.194   1.0331 0.323686
## CPu:Genotype     2   5.367    2.683   0.1824 0.834845
## CPu:Sex          1  65.748   65.748   4.4702 0.049568 *
## Genotype:Sex     2  19.363    9.681   0.6582 0.530471
## CPu:Genotype:Sex 2  24.331   12.166   0.8271 0.454148
## Residuals       17 250.037   14.708
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##               Df Sum Sq Mean Sq F value    Pr(>F)
## CPu              1 170.16  170.164   6.5323 0.03778 *
## Genotype         2 105.71   52.857   2.0291 0.20181
## CPu:Genotype     2   9.49    4.745   0.1822 0.83730
## Residuals        7 182.35   26.049
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##               Df Sum Sq Mean Sq F value    Pr(>F)
## CPu              1  9.628   9.6278   1.4223 0.2605
## Genotype         2 29.739  14.8694   2.1967 0.1619
## CPu:Genotype     2 17.120   8.5600   1.2646 0.3239
## Residuals       10 67.690   6.7690

```

Day 5 Probe By fi FA



```
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.3014 -1.1388 -0.0978  1.1190  9.4788
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      84.072     56.741   1.482  0.1567
## fi             -95.457     84.093  -1.135  0.2721
## GenotypeAPOE33    4.692     71.254   0.066  0.9483
## GenotypeAPOE44  -181.727     98.253  -1.850  0.0818 .
## Sexmale         -74.185    104.858  -0.707  0.4889
## fi:GenotypeAPOE33 -12.845    107.101  -0.120  0.9059
## fi:GenotypeAPOE44  281.339    145.937   1.928  0.0708 .
## fi:Sexmale       110.325    156.393   0.705  0.4901
## GenotypeAPOE33:Sexmale -4.620    168.504  -0.027  0.9784
## GenotypeAPOE44:Sexmale 125.266    165.350   0.758  0.4591
## fi:GenotypeAPOE33:Sexmale  9.948    256.026   0.039  0.9695
## fi:GenotypeAPOE44:Sexmale -192.506    248.231  -0.776  0.4487
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```



```

## Residual standard error: 3.834 on 17 degrees of freedom
## Multiple R-squared:  0.6101, Adjusted R-squared:  0.3579
## F-statistic: 2.419 on 11 and 17 DF,  p-value: 0.04954

##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.3014 -0.8782 -0.0344  0.3170  9.4788
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      84.072      72.898   1.153   0.287
## fi             -95.457     108.038  -0.884   0.406
## GenotypeAPOE33    4.692      91.543   0.051   0.961
## GenotypeAPOE44 -181.727     126.230  -1.440   0.193
## fi:GenotypeAPOE33 -12.845     137.597  -0.093   0.928
## fi:GenotypeAPOE44 281.339     187.492   1.501   0.177
##
## Residual standard error: 4.926 on 7 degrees of freedom
## Multiple R-squared:  0.6368, Adjusted R-squared:  0.3773
## F-statistic: 2.454 on 5 and 7 DF,  p-value: 0.1366

##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.8656 -1.1527 -0.3793  1.2293  4.1745
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9.8864     65.0737   0.152   0.882
## fi             14.8679     97.3086   0.153   0.882
## GenotypeAPOE33    0.0724    112.6861   0.001   1.000
## GenotypeAPOE44  -56.4602     98.1445  -0.575   0.578
## fi:GenotypeAPOE33  -2.8975    171.6137  -0.017   0.987
## fi:GenotypeAPOE44  88.8327    148.1848   0.599   0.562
##
## Residual standard error: 2.83 on 10 degrees of freedom
## Multiple R-squared:  0.3552, Adjusted R-squared:  0.03276
## F-statistic: 1.102 on 5 and 10 DF,  p-value: 0.4173

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fi         1   3.117   3.117    0.2120  0.651043
## Genotype   2 204.346 102.173    6.9491 0.006229 **
## Sex        1  36.344  36.344    2.4718 0.134327
## fi:Genotype 2 119.848  59.924    4.0756 0.035816 *
## fi:Sex      1   3.599   3.599    0.2448 0.627086

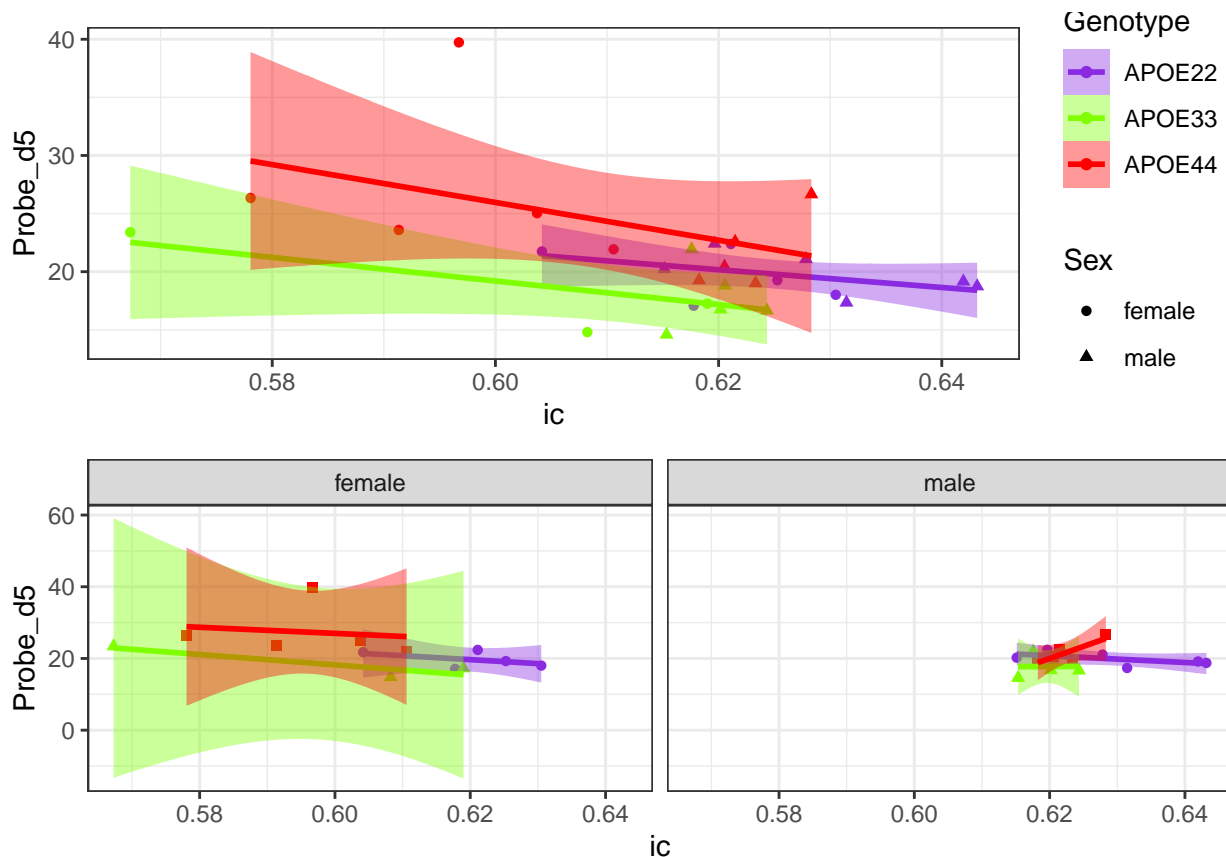
```

```
## Genotype:Sex      2  13.096    6.548  0.4453 0.647875
## fi:Genotype:Sex   2   10.806    5.403  0.3675 0.697839
## Residuals        17 249.953   14.703
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fi          1   1.972    1.972   0.0813 0.78385
## Genotype     2 223.020  111.510   4.5948 0.05315 .
## fi:Genotype   2   72.842   36.421   1.5008 0.28682
## Residuals    7  169.880   24.269
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fi          1   8.650    8.6498   1.0802 0.3231
## Genotype     2  32.041   16.0204   2.0007 0.1858
## fi:Genotype   2   3.413    1.7067   0.2131 0.8116
## Residuals   10  80.073    8.0073
```

Day 5 Probe By ic FA



```
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-4.1681	-2.2328	0.1715	1.0653	12.4600

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	88.019	126.432	0.696	0.496
ic	-110.248	203.980	-0.540	0.596
GenotypeAPOE33	16.624	141.190	0.118	0.908
GenotypeAPOE44	-9.993	159.522	-0.063	0.951
Sexmale	-8.770	161.241	-0.054	0.957
ic:GenotypeAPOE33	-33.798	229.415	-0.147	0.885
ic:GenotypeAPOE44	25.190	261.207	0.096	0.924
ic:Sexmale	15.907	258.537	0.062	0.952
GenotypeAPOE33:Sexmale	-82.443	408.838	-0.202	0.843
GenotypeAPOE44:Sexmale	-465.601	382.468	-1.217	0.240
ic:GenotypeAPOE33:Sexmale	135.107	659.725	0.205	0.840
ic:GenotypeAPOE44:Sexmale	740.661	616.076	1.202	0.246

```
##
## Residual standard error: 4.052 on 17 degrees of freedom
## Multiple R-squared: 0.5646, Adjusted R-squared: 0.2829
## F-statistic: 2.004 on 11 and 17 DF, p-value: 0.09577
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_f_FA)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-4.1681	-2.5174	-0.4982	0.4646	12.4600

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	88.019	176.341	0.499	0.633
ic	-110.248	284.501	-0.388	0.710
GenotypeAPOE33	16.624	196.925	0.084	0.935
GenotypeAPOE44	-9.993	222.493	-0.045	0.965
ic:GenotypeAPOE33	-33.798	319.976	-0.106	0.919
ic:GenotypeAPOE44	25.190	364.318	0.069	0.947

```
##
## Residual standard error: 5.652 on 7 degrees of freedom
## Multiple R-squared: 0.522, Adjusted R-squared: 0.1805
## F-statistic: 1.529 on 5 and 7 DF, p-value: 0.2938
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_m_FA)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-3.2108	-1.0320	0.3088	1.0700	4.1984

```

##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      79.25      58.20   1.362   0.2032
## ic              -94.34      92.39  -1.021   0.3313
## GenotypeAPOE33   -65.82     223.15  -0.295   0.7741
## GenotypeAPOE44  -475.59     202.18  -2.352   0.0405 *
## ic:GenotypeAPOE33 101.31     359.76   0.282   0.7840
## ic:GenotypeAPOE44  765.85     324.52   2.360   0.0400 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.357 on 10 degrees of freedom
## Multiple R-squared:  0.5527, Adjusted R-squared:  0.3291
## F-statistic: 2.472 on 5 and 10 DF,  p-value: 0.1047

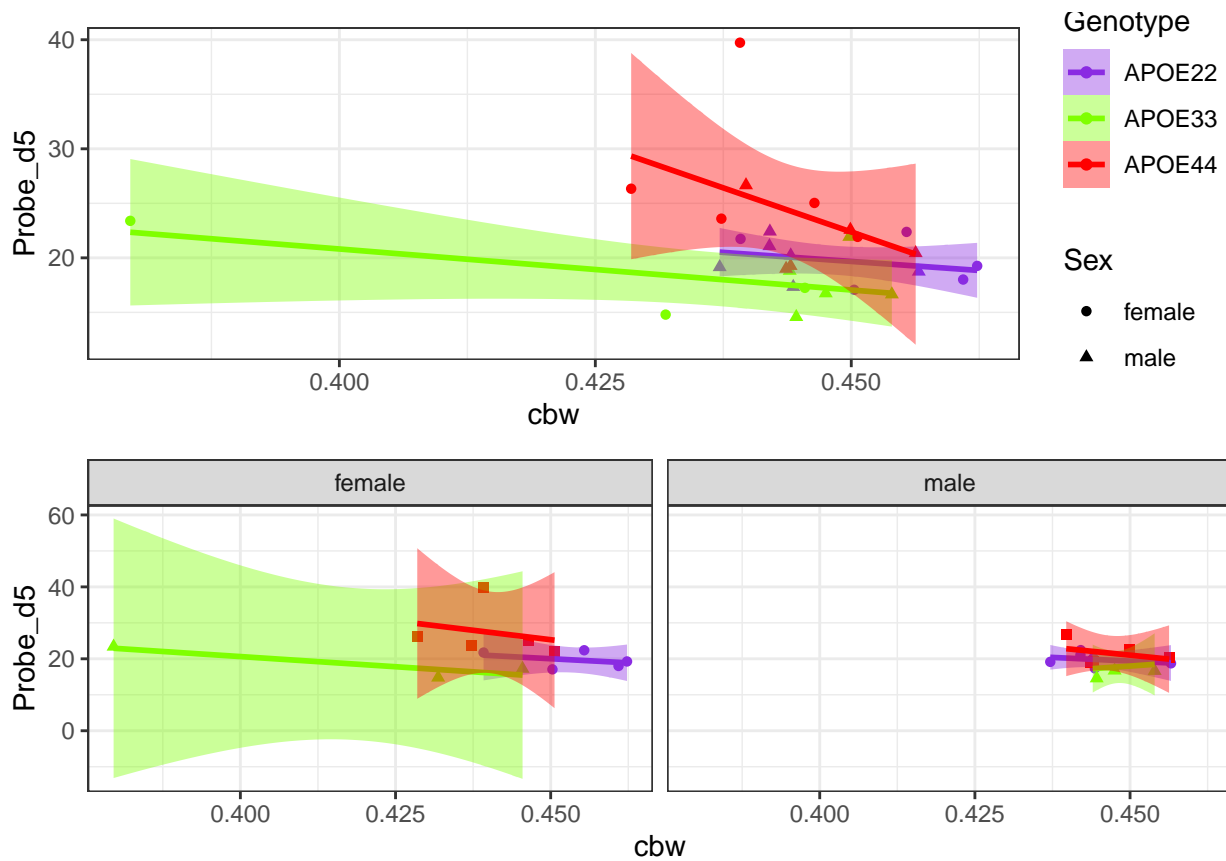
## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## ic              1 127.532 127.532   7.7675 0.01265 *
## Genotype        2 167.734  83.867   5.1080 0.01831 *
## Sex              1   0.116   0.116   0.0070 0.93409
## ic:Genotype     2   8.177   4.088   0.2490 0.78237
## ic:Sex          1   7.892   7.892   0.4807 0.49748
## Genotype:Sex    2  26.809  13.404   0.8164 0.45861
## ic:Genotype:Sex 2  23.731  11.866   0.7227 0.49977
## Residuals      17 279.117  16.419
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## ic              1 102.203 102.203   3.1999 0.1168
## Genotype        2 140.325  70.163   2.1967 0.1818
## ic:Genotype     2   1.608   0.804   0.0252 0.9752
## Residuals       7 223.578  31.940

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## ic              1   0.083   0.0833  0.0150 0.90494
## Genotype        2  37.555 18.7775   3.3809 0.07558 .
## ic:Genotype     2  30.999 15.4996   2.7907 0.10888
## Residuals      10 55.540   5.5540
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 5 Probe By cbw FA



```
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.3774 -2.4898 -0.0848  1.5434 12.1411
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      61.013    101.104   0.603   0.554
## cbw             -91.091    222.844  -0.409   0.688
## GenotypeAPOE33    4.851    107.208   0.045   0.964
## GenotypeAPOE44   58.619    147.539   0.397   0.696
## Sexmale         -4.863    162.571  -0.030   0.976
## cbw:GenotypeAPOE33 -22.008    238.476  -0.092   0.928
## cbw:GenotypeAPOE44 -118.513    330.413  -0.359   0.724
## cbw:Sexmale        9.352    362.937   0.026   0.980
## GenotypeAPOE33:Sexmale -96.613    283.407  -0.341   0.737
## GenotypeAPOE44:Sexmale -15.101    242.467  -0.062   0.951
## cbw:GenotypeAPOE33:Sexmale 222.861    633.332   0.352   0.729
## cbw:GenotypeAPOE44:Sexmale 25.470    543.619   0.047   0.963
##
## Residual standard error: 4.178 on 17 degrees of freedom
## Multiple R-squared:  0.5372, Adjusted R-squared:  0.2377
```

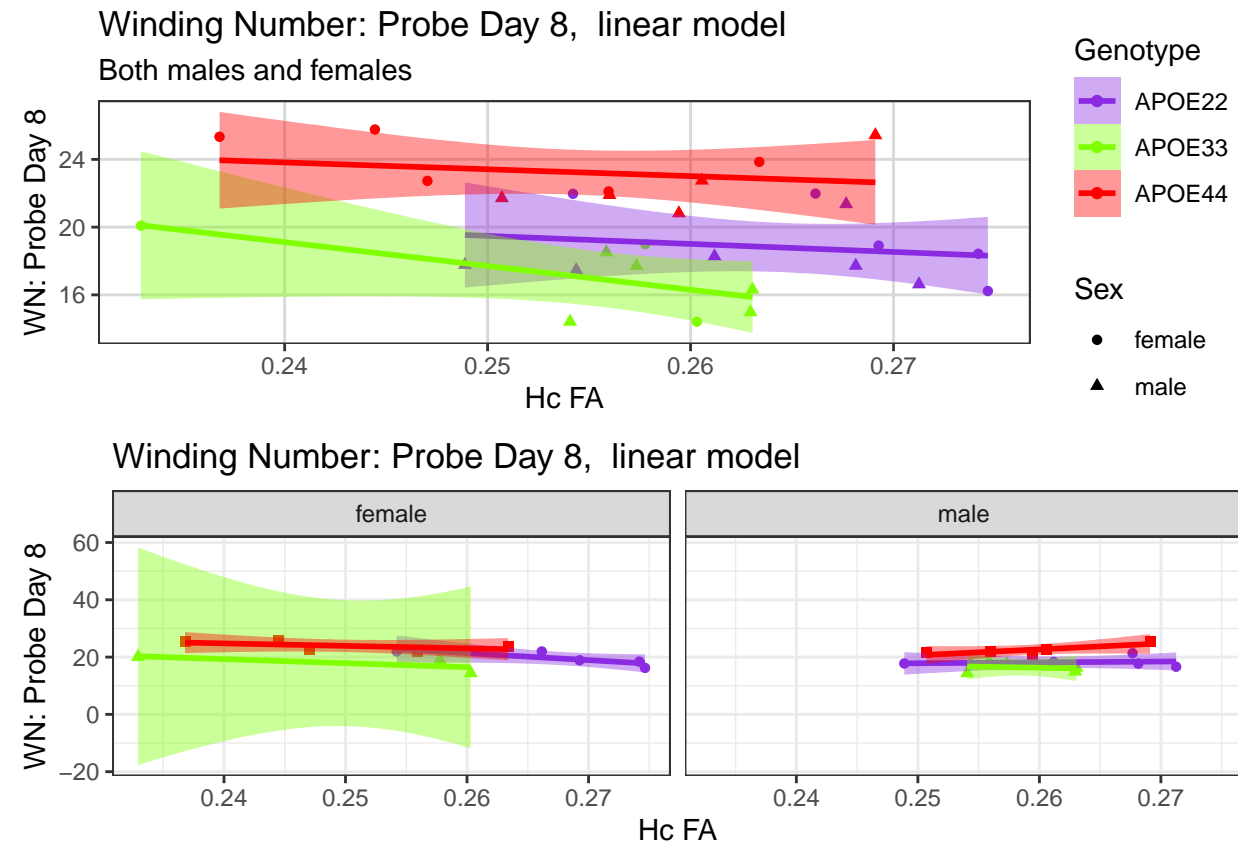
```
## F-statistic: 1.794 on 11 and 17 DF,  p-value: 0.1351
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.3774 -2.9266 -1.0160  0.7316 12.1411
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      61.013     134.736   0.453   0.664
## cbw             -91.091     296.974  -0.307   0.768
## GenotypeAPOE33    4.851     142.871   0.034   0.974
## GenotypeAPOE44   58.619     196.618   0.298   0.774
## cbw:GenotypeAPOE33 -22.008     317.805  -0.069   0.947
## cbw:GenotypeAPOE44 -118.513    440.326  -0.269   0.796
##
## Residual standard error: 5.568 on 7 degrees of freedom
## Multiple R-squared:  0.5361, Adjusted R-squared:  0.2047
## F-statistic: 1.618 on 5 and 7 DF,  p-value: 0.2713
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1235 -1.9776  0.1458  1.5444  3.9660
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      56.15      86.05   0.653   0.529
## cbw             -81.74     193.62  -0.422   0.682
## GenotypeAPOE33   -91.76     177.32  -0.518   0.616
## GenotypeAPOE44    43.52     130.05   0.335   0.745
## cbw:GenotypeAPOE33 200.85     396.56   0.506   0.623
## cbw:GenotypeAPOE44 -93.04     291.77  -0.319   0.756
##
## Residual standard error: 2.824 on 10 degrees of freedom
## Multiple R-squared:  0.3579, Adjusted R-squared:  0.03686
## F-statistic: 1.115 on 5 and 10 DF,  p-value: 0.4114
## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value    Pr(>F)
## cbw         1  34.136   34.136   1.9558 0.179939
## Genotype    2 226.481  113.240   6.4880 0.008058 **
## Sex         1  17.528   17.528   1.0043 0.330330
## cbw:Genotype 2  25.792   12.896   0.7389 0.492385
## cbw:Sex      1   4.559    4.559   0.2612 0.615873
## Genotype:Sex 2  33.581   16.790   0.9620 0.401983
## cbw:Genotype:Sex 2   2.319    1.159   0.0664 0.935975
```

```
## Residuals      17 296.713  17.454
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## cbw         1  16.283   16.283   0.5253 0.49209
## Genotype     2 231.688  115.844   3.7373 0.07866 .
## cbw:Genotype  2   2.764    1.382   0.0446 0.95667
## Residuals    7 216.980   30.997
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## cbw         1   5.703    5.7026   0.7152 0.4175
## Genotype     2 34.617   17.3087   2.1708 0.1648
## cbw:Genotype  2   4.124    2.0618   0.2586 0.7771
## Residuals   10 79.733    7.9733
```

Day 8 Probe By Hc FA



##

```
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.30619 -1.09248 -0.04203  0.93254  2.98467
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      84.949      28.493   2.981  0.00838 **
## Hc             -244.489     106.401  -2.298  0.03454 *
## GenotypeAPOE33   -31.763      35.244  -0.901  0.38005
## GenotypeAPOE44   -39.387      35.626  -1.106  0.28431
## Sexmale         -74.578      37.006  -2.015  0.05997 .
## Hc:GenotypeAPOE33 103.264     134.795   0.766  0.45413
## Hc:GenotypeAPOE44 157.908     136.587   1.156  0.26363
## Hc:Sexmale       274.396     139.433   1.968  0.06561 .
## GenotypeAPOE33:Sexmale 56.762      69.746   0.814  0.42699
## GenotypeAPOE44:Sexmale -1.879      54.614  -0.034  0.97296
## Hc:GenotypeAPOE33:Sexmale -206.565     268.500  -0.769  0.45226
## Hc:GenotypeAPOE44:Sexmale 18.307      209.709   0.087  0.93146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.771 on 17 degrees of freedom
## Multiple R-squared:  0.8221, Adjusted R-squared:  0.707
## F-statistic: 7.143 on 11 and 17 DF, p-value: 0.0001939
##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.0078 -1.2948 -0.2052  1.0960  2.2130
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      84.95      29.64   2.866  0.0241 *
## Hc             -244.49     110.70  -2.209  0.0629 .
## GenotypeAPOE33   -31.76      36.67  -0.866  0.4151
## GenotypeAPOE44   -39.39      37.06  -1.063  0.3232
## Hc:GenotypeAPOE33 103.26     140.24   0.736  0.4855
## Hc:GenotypeAPOE44 157.91     142.10   1.111  0.3032
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.843 on 7 degrees of freedom
## Multiple R-squared:  0.827, Adjusted R-squared:  0.7034
## F-statistic: 6.691 on 5 and 7 DF, p-value: 0.01347
##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_m_FA)
##
```



```

## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.30619 -0.77520 -0.00646  0.87628  2.98467
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      10.37      22.92   0.452   0.661
## Hc                29.91      87.48   0.342   0.740
## GenotypeAPOE33     25.00      58.42   0.428   0.678
## GenotypeAPOE44    -41.27      40.18  -1.027   0.329
## Hc:GenotypeAPOE33 -103.30     225.41  -0.458   0.657
## Hc:GenotypeAPOE44  176.21     154.47   1.141   0.281
##
## Residual standard error: 1.719 on 10 degrees of freedom
## Multiple R-squared:  0.7859, Adjusted R-squared:  0.6788
## F-statistic:  7.34 on 5 and 10 DF,  p-value: 0.003936

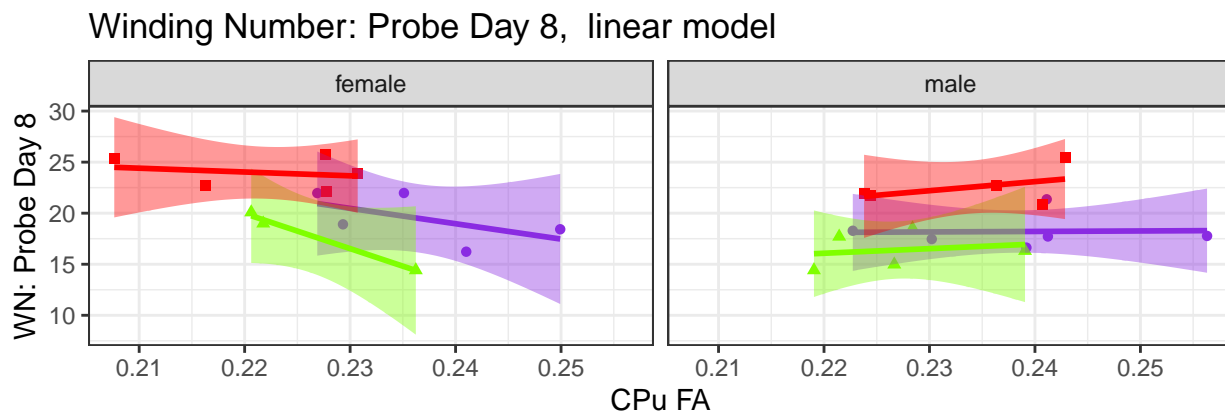
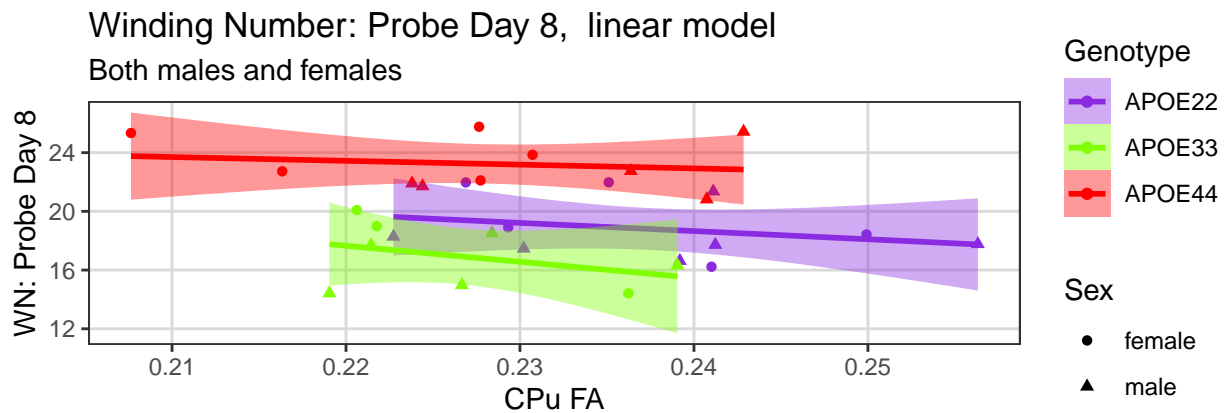
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Hc              1  31.852   31.852  10.1539 0.005402 **
## Genotype        2 175.243   87.622  27.9323 4.241e-06 ***
## Sex              1   9.619    9.619   3.0664 0.097948 .
## Hc:Genotype      2   4.401    2.200   0.7015 0.509661
## Hc:Sex           1  13.229   13.229   4.2172 0.055729 .
## Genotype:Sex     2   9.826    4.913   1.5661 0.237536
## Hc:Genotype:Sex  2   2.300    1.150   0.3666 0.698405
## Residuals       17  53.328    3.137
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Hc              1  41.228   41.228  12.1421 0.010203 *
## Genotype        2  68.153   34.076  10.0359 0.008791 **
## Hc:Genotype      2   4.208    2.104   0.6197 0.565226
## Residuals       7  23.768    3.395
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Hc              1   2.125    2.125   0.7190 0.4163150
## Genotype        2 100.943   50.472  17.0746 0.0005962 ***
## Hc:Genotype      2   5.408    2.704   0.9147 0.4316884
## Residuals       10  29.560    2.956
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By CPu FA



```
##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5879 -1.3965  0.0113  0.9516  3.1440
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      55.087     24.160   2.280  0.0358 *
## CPu             -150.499    102.115  -1.474  0.1588
## GenotypeAPOE33     40.442     42.489   0.952  0.3545
## GenotypeAPOE44    -22.848     32.462  -0.704  0.4911
## Sexmale          -38.019     30.006  -1.267  0.2222
## CPu:GenotypeAPOE33 -192.979    185.145  -1.042  0.3119
## CPu:GenotypeAPOE44  113.201    141.245   0.801  0.4339
## CPu:Sexmale       155.261    126.432   1.228  0.2362
## GenotypeAPOE33:Sexmale -51.341     53.779  -0.955  0.3531
## GenotypeAPOE44:Sexmale   7.511     44.472   0.169  0.8679
## CPu:GenotypeAPOE33:Sexmale 233.244    234.051   0.997  0.3330
## CPu:GenotypeAPOE44:Sexmale -28.966    191.366  -0.151  0.8815
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.9 on 17 degrees of freedom
## Multiple R-squared:  0.7952, Adjusted R-squared:  0.6628
## F-statistic: 6.002 on 11 and 17 DF,  p-value: 0.0005633

##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5879 -1.4406  0.2206  0.9516  2.2750
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      55.09      24.71   2.229   0.061 .
## CPu             -150.50     104.44  -1.441   0.193
## GenotypeAPOE33     40.44     43.46   0.931   0.383
## GenotypeAPOE44    -22.85     33.20  -0.688   0.514
## CPu:GenotypeAPOE33 -192.98     189.36  -1.019   0.342
## CPu:GenotypeAPOE44  113.20     144.46   0.784   0.459
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 1.944 on 7 degrees of freedom
## Multiple R-squared:  0.8075, Adjusted R-squared:  0.67
## F-statistic: 5.873 on 5 and 7 DF,  p-value: 0.01905

##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.3370 -0.8735 -0.2557  0.5827  3.1440
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      17.068      17.505   0.975   0.353
## CPu               4.762      73.337   0.065   0.950
## GenotypeAPOE33    -10.899     32.431  -0.336   0.744
## GenotypeAPOE44    -15.337     29.902  -0.513   0.619
## CPu:GenotypeAPOE33  40.266     140.854   0.286   0.781
## CPu:GenotypeAPOE44  84.235     127.016   0.663   0.522
##
## Residual standard error: 1.869 on 10 degrees of freedom
## Multiple R-squared:  0.7469, Adjusted R-squared:  0.6203
## F-statistic: 5.9 on 5 and 10 DF,  p-value: 0.008554

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## CPu         1  13.682   13.682   3.7891  0.06831 .
## Genotype    2 188.273   94.136  26.0704 6.623e-06 ***
## Sex         1   9.697    9.697   2.6854  0.11964

```

```

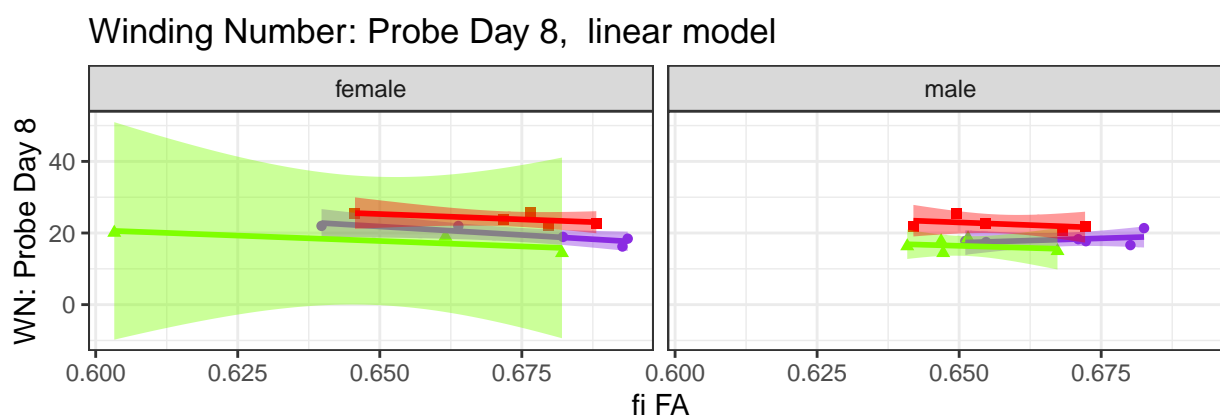
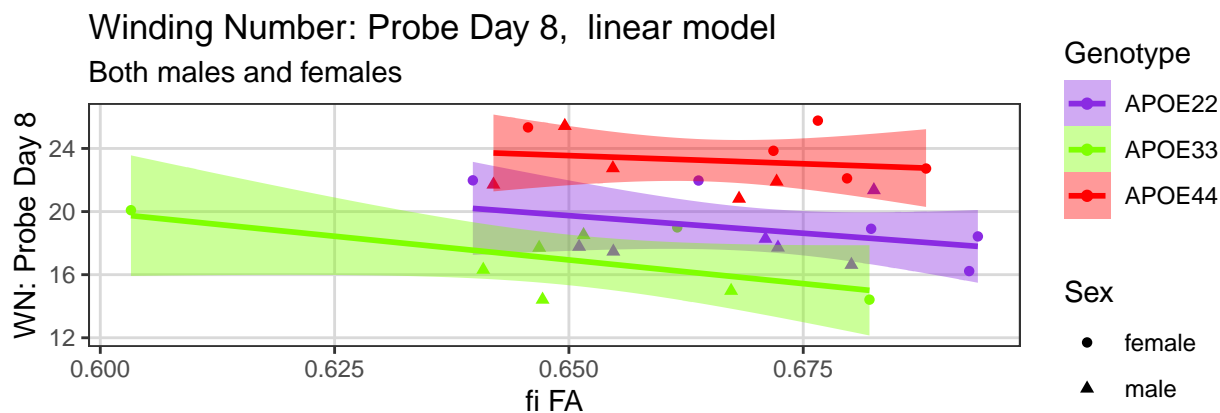
## CPu:Genotype      2   4.238   2.119  0.5868   0.56696
## CPu:Sex           1  14.786  14.786  4.0949   0.05903 .
## Genotype:Sex      2   3.088   1.544  0.4276   0.65888
## CPu:Genotype:Sex  2   4.650   2.325  0.6439   0.53760
## Residuals        17  61.385   3.611
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1  44.699   44.699  11.8338 0.01084 *
## Genotype      2  55.934   27.967   7.4041 0.01874 *
## CPu:Genotype  2  10.283    5.141   1.3611 0.31671
## Residuals     7  26.441    3.777
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1   7.300    7.300   2.0892 0.178947
## Genotype      2  94.226   47.113  13.4825 0.001449 **
## CPu:Genotype  2   1.566    0.783   0.2240 0.803204
## Residuals    10  34.944    3.494
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By fi FA



```
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.1491 -0.8123 -0.1364  0.7454  2.4662
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      83.47      25.59   3.262  0.00459 **
## fi             -94.85      37.92  -2.501  0.02289 *
## GenotypeAPOE33  -26.53      32.13  -0.826  0.42047
## GenotypeAPOE44  -19.13      44.31  -0.432  0.67133
## Sexmale        -98.46      47.29  -2.082  0.05274 .
## fi:GenotypeAPOE33  34.58      48.30   0.716  0.48368
## fi:GenotypeAPOE44  34.79      65.81   0.529  0.60390
## fi:Sexmale       144.49      70.53   2.049  0.05625 .
## GenotypeAPOE33:Sexmale  88.82      75.99   1.169  0.25859
## GenotypeAPOE44:Sexmale  96.00      74.57   1.287  0.21518
## fi:GenotypeAPOE33:Sexmale -131.73     115.46  -1.141  0.26969
## fi:GenotypeAPOE44:Sexmale -144.31     111.94  -1.289  0.21461
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.729 on 17 degrees of freedom
## Multiple R-squared:  0.8305, Adjusted R-squared:  0.7207
## F-statistic: 7.57 on 11 and 17 DF, p-value: 0.0001341

##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5411 -0.8123 -0.2271  0.7454  2.0594
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      83.47      23.79   3.508  0.00988 **
## fi             -94.85      35.26  -2.690  0.03108 *
## GenotypeAPOE33   -26.53      29.88  -0.888  0.40407
## GenotypeAPOE44   -19.13      41.20  -0.464  0.65648
## fi:GenotypeAPOE33  34.58      44.91   0.770  0.46643
## fi:GenotypeAPOE44  34.79      61.19   0.569  0.58745
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 1.608 on 7 degrees of freedom
## Multiple R-squared:  0.8683, Adjusted R-squared:  0.7742
## F-statistic: 9.227 on 5 and 7 DF, p-value: 0.005478

##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.14911 -0.76307 -0.04523  0.61308  2.46620
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -14.99      41.61  -0.360   0.726
## fi              49.64      62.22   0.798   0.444
## GenotypeAPOE33    62.29      72.05   0.865   0.408
## GenotypeAPOE44    76.87      62.75   1.225   0.249
## fi:GenotypeAPOE33 -97.15     109.73  -0.885   0.397
## fi:GenotypeAPOE44 -109.52     94.75  -1.156   0.275
##
## Residual standard error: 1.809 on 10 degrees of freedom
## Multiple R-squared:  0.7629, Adjusted R-squared:  0.6443
## F-statistic: 6.434 on 5 and 10 DF, p-value: 0.006328

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fi         1  1.720   1.720   0.5752  0.45857
## Genotype   2 212.070 106.035 35.4629 8.587e-07 ***
## Sex        1  21.455   21.455   7.1756  0.01586 *

```

```

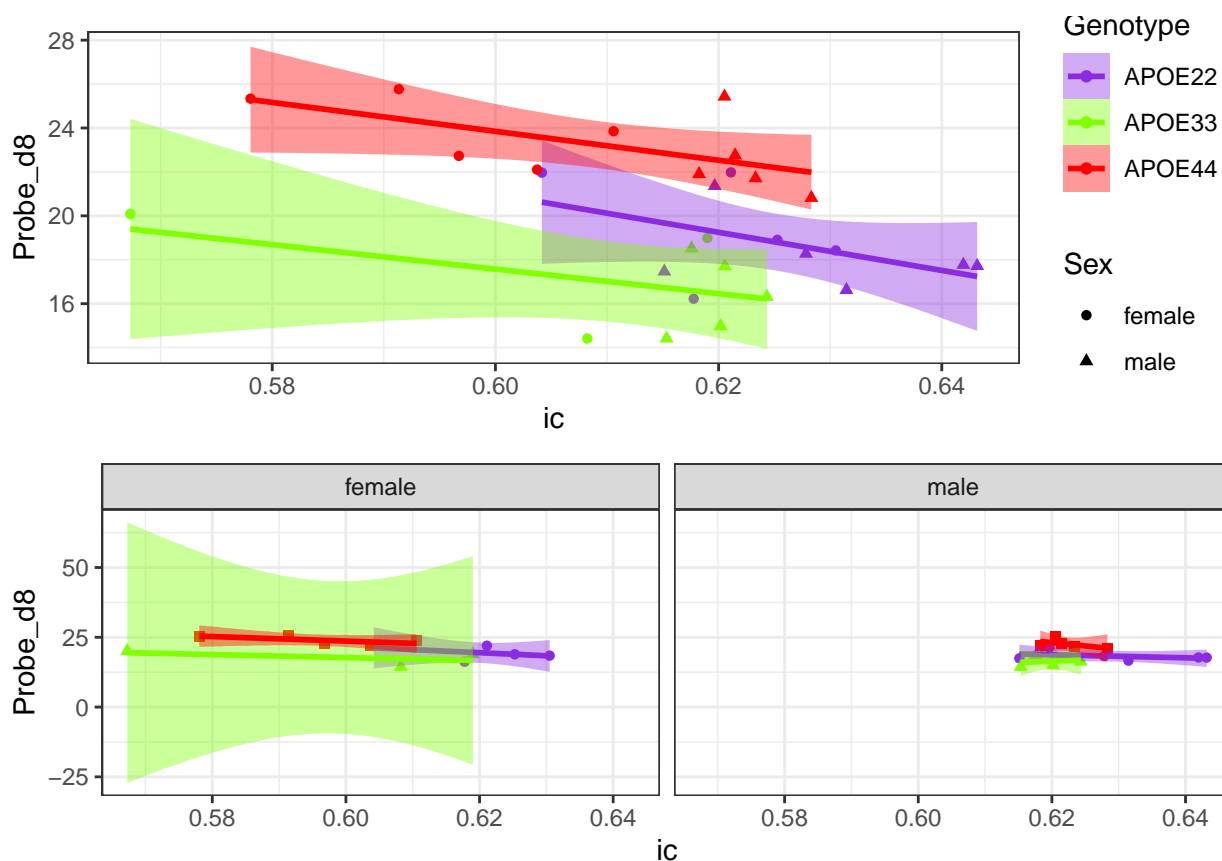
## fi:Genotype      2   0.101   0.050   0.0169   0.98328
## fi:Sex           1   4.024   4.024   1.3459   0.26203
## Genotype:Sex     2   3.169   1.584   0.5299   0.59808
## fi:Genotype:Sex  2   6.429   3.214   1.0750   0.36339
## Residuals       17  50.830   2.990
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## fi          1    8.895    8.895    3.441 0.105987
## Genotype    2  108.675   54.338   21.020 0.001099 **
## fi:Genotype  2    1.691    0.845    0.327 0.731544
## Residuals   7   18.096    2.585
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## fi          1    0.098    0.098    0.0300 0.8659567
## Genotype    2  100.042   50.021  15.2807 0.0009108 ***
## fi:Genotype  2    5.161    2.580    0.7882 0.4809680
## Residuals  10   32.735    3.273
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By ic FA



```
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4936 -1.2343  0.0117  1.0684  2.6254
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      87.70      64.17   1.367   0.190
## ic             -110.04     103.53  -1.063   0.303
## GenotypeAPOE33   -37.82      71.66  -0.528   0.604
## GenotypeAPOE44   -15.54      80.96  -0.192   0.850
## Sexmale         -34.96      81.83  -0.427   0.675
## ic:GenotypeAPOE33  56.46     116.43   0.485   0.634
## ic:GenotypeAPOE44  29.18     132.57   0.220   0.828
## ic:Sexmale        55.21     131.22   0.421   0.679
## GenotypeAPOE33:Sexmale -55.31    207.50  -0.267   0.793
## GenotypeAPOE44:Sexmale 136.09    194.11   0.701   0.493
## ic:GenotypeAPOE33:Sexmale  90.00    334.83   0.269   0.791
## ic:GenotypeAPOE44:Sexmale -216.58    312.68  -0.693   0.498
##
## Residual standard error: 2.057 on 17 degrees of freedom
## Multiple R-squared:  0.7602, Adjusted R-squared:  0.605
```



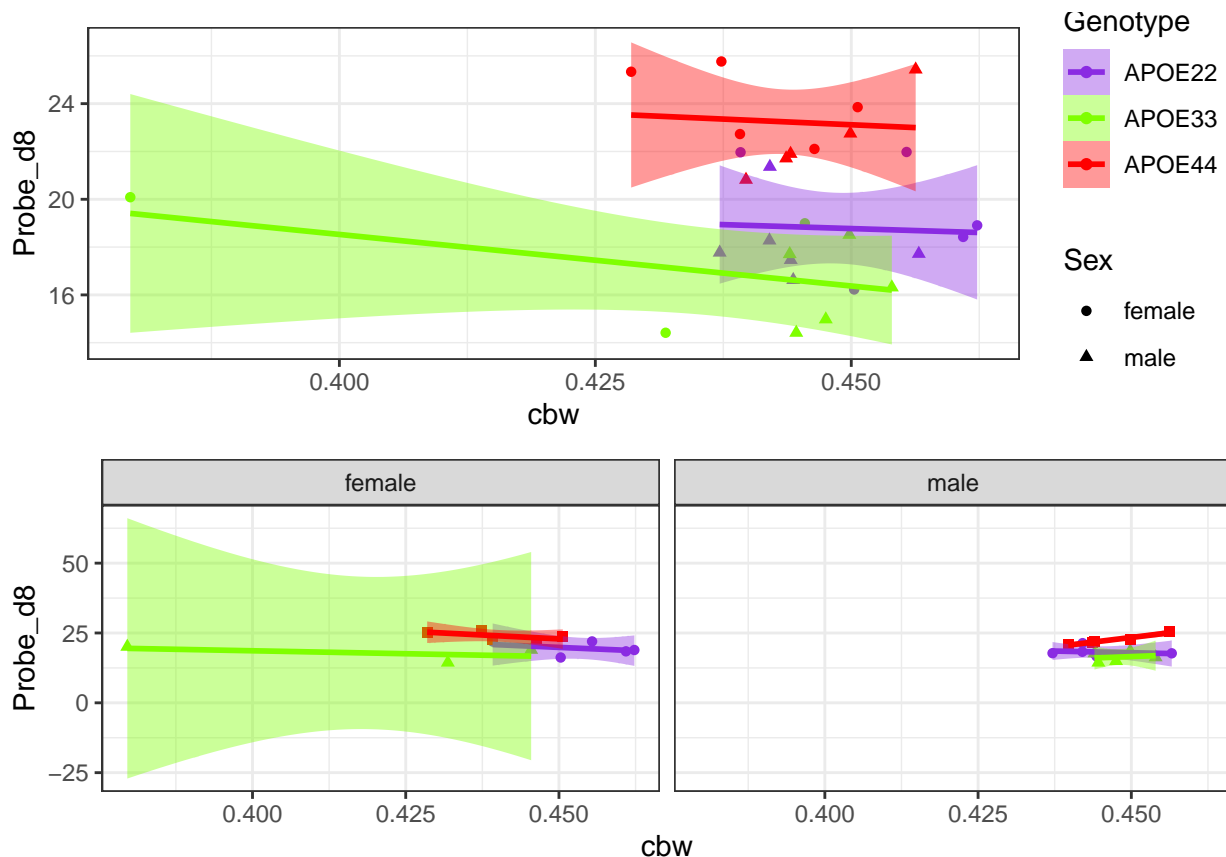
```
## F-statistic: 4.899 on 11 and 17 DF,  p-value: 0.001814
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4936 -1.1772  0.1056  1.0684  2.6254
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      87.70      74.20   1.182   0.276
## ic             -110.04     119.71  -0.919   0.389
## GenotypeAPOE33    -37.82      82.86  -0.456   0.662
## GenotypeAPOE44   -15.54      93.62  -0.166   0.873
## ic:GenotypeAPOE33   56.46     134.64   0.419   0.688
## ic:GenotypeAPOE44   29.18     153.30   0.190   0.854
##
## Residual standard error: 2.378 on 7 degrees of freedom
## Multiple R-squared:  0.7118, Adjusted R-squared:  0.506
## F-statistic: 3.458 on 5 and 7 DF,  p-value: 0.06826
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.6205 -1.4686 -0.1517  0.4931  2.5965
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      52.74      44.39   1.188   0.262
## ic             -54.84      70.47  -0.778   0.454
## GenotypeAPOE33   -93.13     170.21  -0.547   0.596
## GenotypeAPOE44   120.55     154.21   0.782   0.452
## ic:GenotypeAPOE33  146.46     274.40   0.534   0.605
## ic:GenotypeAPOE44 -187.41     247.52  -0.757   0.466
##
## Residual standard error: 1.798 on 10 degrees of freedom
## Multiple R-squared:  0.7659, Adjusted R-squared:  0.6489
## F-statistic: 6.544 on 5 and 10 DF,  p-value: 0.005958
## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic         1  53.343   53.343  12.6130  0.002454 **
## Genotype   2 169.108   84.554  19.9929 3.426e-05 ***
## Sex        1   0.226    0.226   0.0534  0.819975
## ic:Genotype 2   0.785    0.393   0.0928  0.911806
## ic:Sex      1   0.248    0.248   0.0587  0.811448
## Genotype:Sex 2   1.525    0.762   0.1803  0.836616
## ic:Genotype:Sex 2   2.666    1.333   0.3152  0.733838
```

```
## Residuals      17  71.897   4.229
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1  29.576   29.576   5.2301 0.05606 .
## Genotype      2  67.090   33.545   5.9320 0.03113 *
## ic:Genotype   2   1.106    0.553   0.0978 0.90808
## Residuals     7  39.585    5.655
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1   1.844    1.844   0.5706 0.4674520
## Genotype      2 100.901   50.450  15.6136 0.0008396 ***
## ic:Genotype   2   2.980    1.490   0.4611 0.6433621
## Residuals    10  32.312    3.231
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Day 8 Probe By cbw FA



```
##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5903 -0.7719  0.0559  1.0330  3.0475
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         62.43      47.97   1.301   0.210
## cbw                -94.63     105.73  -0.895   0.383
## GenotypeAPOE33     -26.93      50.87  -0.529   0.603
## GenotypeAPOE44      10.49      70.00   0.150   0.883
## Sexmale            -23.30      77.13  -0.302   0.766
## cbw:GenotypeAPOE33   52.47     113.15   0.464   0.649
## cbw:GenotypeAPOE44  -16.54     156.77  -0.106   0.917
## cbw:Sexmale         47.54     172.20   0.276   0.786
## GenotypeAPOE33:Sexmale -32.53     134.47  -0.242   0.812
## GenotypeAPOE44:Sexmale -146.25     115.04  -1.271   0.221
## cbw:GenotypeAPOE33:Sexmale  76.59     300.49   0.255   0.802
## cbw:GenotypeAPOE44:Sexmale 330.35     257.93   1.281   0.217
##
## Residual standard error: 1.982 on 17 degrees of freedom
## Multiple R-squared:  0.7772, Adjusted R-squared:  0.633
## F-statistic: 5.391 on 11 and 17 DF, p-value: 0.001057
##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5903 -1.1842  0.2283  1.0998  2.6463
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         62.43      58.99   1.058   0.325
## cbw                -94.63     130.03  -0.728   0.490
## GenotypeAPOE33     -26.93      62.56  -0.431   0.680
## GenotypeAPOE44      10.49      86.09   0.122   0.906
## cbw:GenotypeAPOE33   52.47     139.15   0.377   0.717
## cbw:GenotypeAPOE44  -16.54     192.80  -0.086   0.934
##
## Residual standard error: 2.438 on 7 degrees of freedom
## Multiple R-squared:  0.6972, Adjusted R-squared:  0.4808
## F-statistic: 3.223 on 5 and 7 DF, p-value: 0.07943
##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.69432 -0.75688 -0.01126  0.21228  3.04748
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      39.13      48.37   0.809   0.4374
## cbw              -47.09     108.84  -0.433   0.6745
## GenotypeAPOE33   -59.46      99.68  -0.597   0.5641
## GenotypeAPOE44  -135.76      73.11  -1.857   0.0930 .
## cbw:GenotypeAPOE33 129.05     222.92   0.579   0.5755
## cbw:GenotypeAPOE44 313.81     164.02   1.913   0.0847 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.587 on 10 degrees of freedom
## Multiple R-squared:  0.8175, Adjusted R-squared:  0.7262
## F-statistic: 8.957 on 5 and 10 DF,  p-value: 0.001857

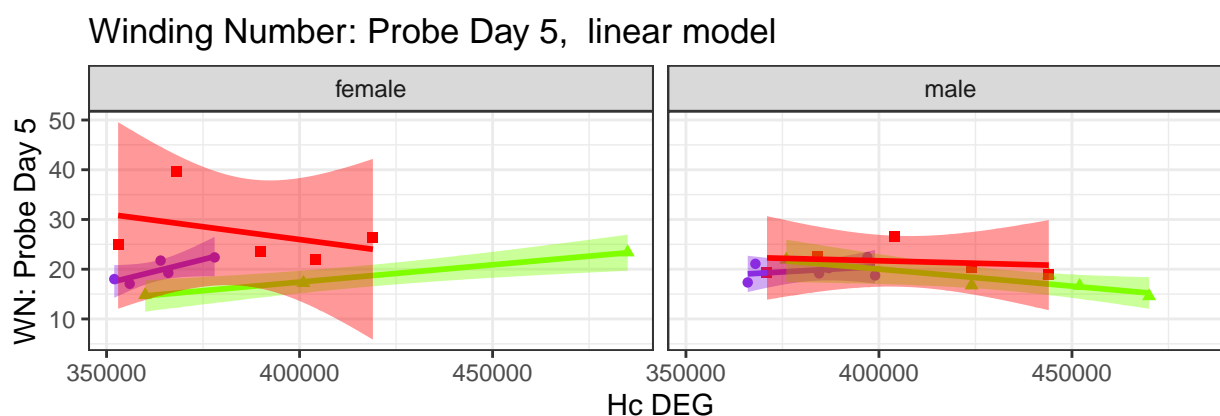
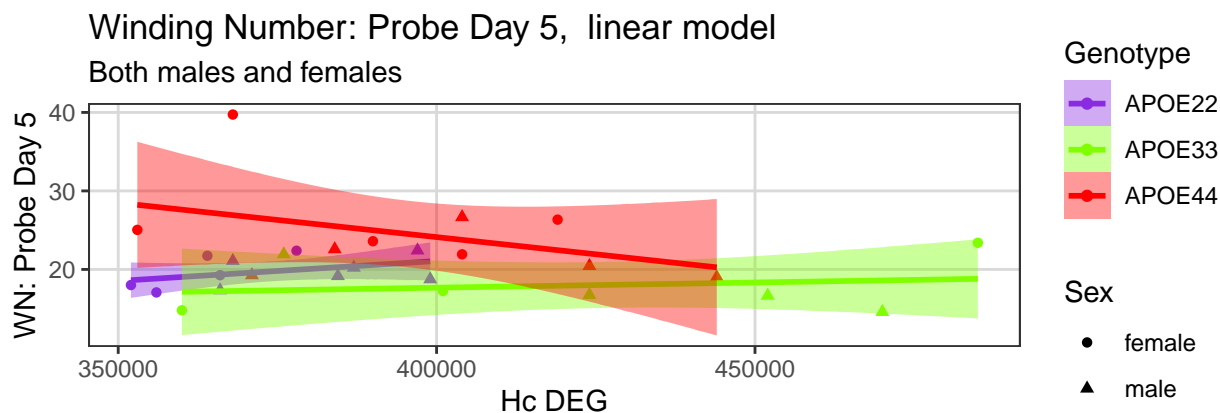
## Analysis of Variance Table
##
## Response: Probe_d8
##               Df Sum Sq Mean Sq F value    Pr(>F)
## cbw             1   1.783    1.783   0.4537    0.5096
## Genotype        2 200.779  100.389  25.5505 7.534e-06 ***
## Sex             1  10.010    10.010   2.5477    0.1289
## cbw:Genotype    2   1.807     0.904   0.2300    0.7970
## cbw:Sex         1   9.444     9.444   2.4036    0.1395
## Genotype:Sex    2   2.481     1.241   0.3157    0.7334
## cbw:Genotype:Sex 2   6.700     3.350   0.8526    0.4437
## Residuals      17  66.794     3.929
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##               Df Sum Sq Mean Sq F value    Pr(>F)
## cbw             1   0.750     0.750   0.1262   0.73286
## Genotype        2  93.133   46.567   7.8362 0.01635 *
## cbw:Genotype    2   1.876     0.938   0.1579 0.85692
## Residuals       7 41.598     5.943
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##               Df Sum Sq Mean Sq F value    Pr(>F)
## cbw             1   2.506     2.506   0.9947 0.342114
## Genotype        2 101.105   50.552  20.0633 0.000316 ***
## cbw:Genotype    2   9.228     4.614   1.8313 0.210059
## Residuals      10  25.196     2.520
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Degree of Connectivity

Day 5 Probe By Hc DEG



```
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.7704  -1.6278  -0.1620   0.5598  10.4695
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.022e+01  6.771e+01  -0.742   0.468
## Hc              1.925e-04  1.864e-04   1.033   0.316
## GenotypeAPOE33  3.987e+01  6.991e+01   0.570   0.576
## GenotypeAPOE44  1.174e+02  7.300e+01   1.608   0.126
## Sexmale         5.328e+01  8.181e+01   0.651   0.524
## Hc:GenotypeAPOE33 -1.231e-04  1.910e-04  -0.644   0.528
## Hc:GenotypeAPOE44 -2.955e-04  1.992e-04  -1.483   0.156
## Hc:Sexmale       -1.488e-04  2.215e-04  -0.672   0.511
## GenotypeAPOE33:Sexmale  4.565e+00  8.665e+01   0.053   0.959
## GenotypeAPOE44:Sexmale -9.077e+01  9.002e+01  -1.008   0.327
## Hc:GenotypeAPOE33:Sexmale 1.070e-05  2.313e-04   0.046   0.964
## Hc:GenotypeAPOE44:Sexmale 2.318e-04  2.409e-04   0.962   0.349
##
## Residual standard error: 3.75 on 17 degrees of freedom
## Multiple R-squared:  0.6272, Adjusted R-squared:  0.3859
```

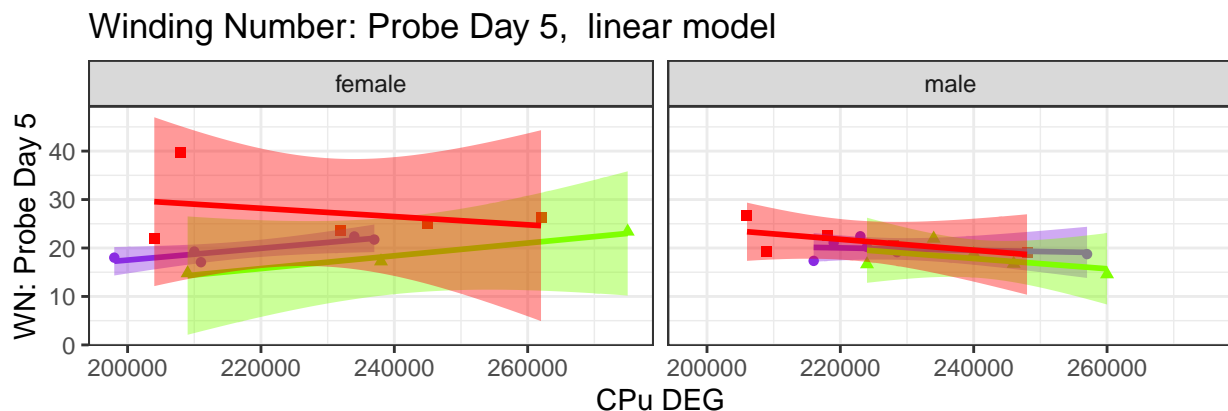
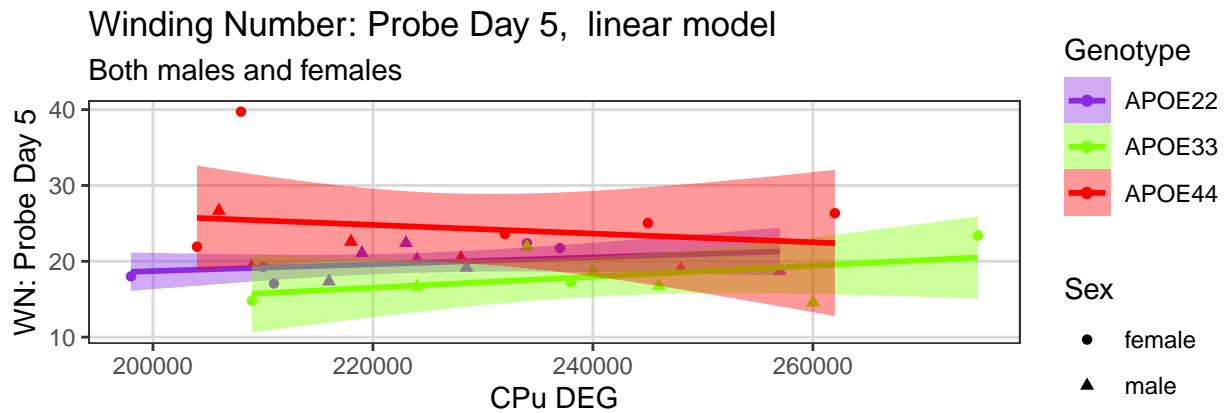
```
## F-statistic: 2.6 on 11 and 17 DF, p-value: 0.03746
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.7704 -1.2366 -0.1620  0.4741 10.4695
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5.022e+01  9.144e+01  -0.549    0.600
## Hc              1.925e-04  2.517e-04   0.765    0.469
## GenotypeAPOE33  3.987e+01  9.441e+01   0.422    0.686
## GenotypeAPOE44  1.174e+02  9.858e+01   1.191    0.273
## Hc:GenotypeAPOE33 -1.231e-04  2.579e-04  -0.477    0.648
## Hc:GenotypeAPOE44 -2.955e-04  2.690e-04  -1.098    0.308
##
## Residual standard error: 5.064 on 7 degrees of freedom
## Multiple R-squared: 0.6163, Adjusted R-squared: 0.3421
## F-statistic: 2.248 on 5 and 7 DF, p-value: 0.1602
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.0103 -1.6504 -0.2215  0.8732  5.0438
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.059e+00  2.988e+01   0.102    0.920
## Hc              4.371e-05  7.785e-05   0.561    0.587
## GenotypeAPOE33  4.443e+01  3.331e+01   1.334    0.212
## GenotypeAPOE44  2.661e+01  3.428e+01   0.776    0.456
## Hc:GenotypeAPOE33 -1.124e-04  8.491e-05  -1.323    0.215
## Hc:GenotypeAPOE44 -6.365e-05  8.816e-05  -0.722    0.487
##
## Residual standard error: 2.44 on 10 degrees of freedom
## Multiple R-squared: 0.5206, Adjusted R-squared: 0.2809
## F-statistic: 2.172 on 5 and 10 DF, p-value: 0.1389
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value Pr(>F)
## Hc      1  15.305   15.305   1.0885 0.31141
## Genotype 2 195.804   97.902   6.9632 0.00618 **
## Sex      1  28.919   28.919   2.0569 0.16966
## Hc:Genotype 2  69.296   34.648   2.4643 0.11487
## Hc:Sex     1  11.482   11.482   0.8166 0.37880
## Genotype:Sex 2  28.221   14.111   1.0036 0.38727
## Hc:Genotype:Sex 2  53.062   26.531   1.8870 0.18193
```

```
## Residuals      17 239.020  14.060
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1   6.659    6.659   0.2597 0.62599
## Genotype     2 208.055  104.027   4.0571 0.06761 .
## Hc:Genotype   2  73.515   36.758   1.4336 0.30073
## Residuals    7 179.485   25.641
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1 27.464  27.4636   4.6131 0.05728 .
## Genotype     2 24.642  12.3212   2.0696 0.17696
## Hc:Genotype   2 12.537   6.2683   1.0529 0.38462
## Residuals   10 59.534   5.9534
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Day 5 Probe By CPu DEG



```
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.6358 -1.0272  0.3014  0.7483 10.5125
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -6.796e+00  2.520e+01  -0.270    0.791
## CPu              1.215e-04  1.153e-04   1.054    0.307
## GenotypeAPOE33   -6.463e+00  3.221e+01  -0.201    0.843
## GenotypeAPOE44    5.375e+01  3.111e+01   1.728    0.102
## Sexmale          3.234e+01  3.663e+01   0.883    0.390
## CPu:GenotypeAPOE33  1.037e-05  1.420e-04   0.073    0.943
## CPu:GenotypeAPOE44  -2.068e-04  1.397e-04  -1.480    0.157
## CPu:Sexmale       -1.466e-04  1.639e-04  -0.894    0.384
## GenotypeAPOE33:Sexmale  2.422e+01  5.431e+01   0.446    0.661
## GenotypeAPOE44:Sexmale -3.290e+01  4.816e+01  -0.683    0.504
## CPu:GenotypeAPOE33:Sexmale -9.139e-05  2.334e-04  -0.392    0.700
## CPu:GenotypeAPOE44:Sexmale  1.200e-04  2.147e-04   0.559    0.584
##
## Residual standard error: 3.876 on 17 degrees of freedom
## Multiple R-squared:  0.6017, Adjusted R-squared:  0.3439
## F-statistic: 2.334 on 11 and 17 DF,  p-value: 0.05652
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.6358 -1.0272  0.3867  0.7429 10.5125
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -6.796e+00  3.400e+01  -0.200    0.847
## CPu              1.215e-04  1.556e-04   0.781    0.460
## GenotypeAPOE33   -6.463e+00  4.346e+01  -0.149    0.886
## GenotypeAPOE44    5.375e+01  4.197e+01   1.281    0.241
## CPu:GenotypeAPOE33  1.037e-05  1.916e-04   0.054    0.958
## CPu:GenotypeAPOE44  -2.068e-04  1.885e-04  -1.097    0.309
##
## Residual standard error: 5.23 on 7 degrees of freedom
## Multiple R-squared:  0.5907, Adjusted R-squared:  0.2983
## F-statistic:  2.02 on 5 and 7 DF,  p-value: 0.1924
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.7563 -0.7754 -0.0267  0.9981  3.4628
```



```

##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.554e+01  1.735e+01   1.472   0.172
## CPu            -2.508e-05  7.599e-05  -0.330   0.748
## GenotypeAPOE33  1.775e+01  2.853e+01   0.622   0.548
## GenotypeAPOE44  2.085e+01  2.398e+01   0.870   0.405
## CPu:GenotypeAPOE33 -8.102e-05  1.208e-04  -0.671   0.518
## CPu:GenotypeAPOE44 -8.677e-05  1.064e-04  -0.815   0.434
##
## Residual standard error: 2.529 on 10 degrees of freedom
## Multiple R-squared:  0.4851, Adjusted R-squared:  0.2277
## F-statistic: 1.884 on 5 and 10 DF,  p-value: 0.1842

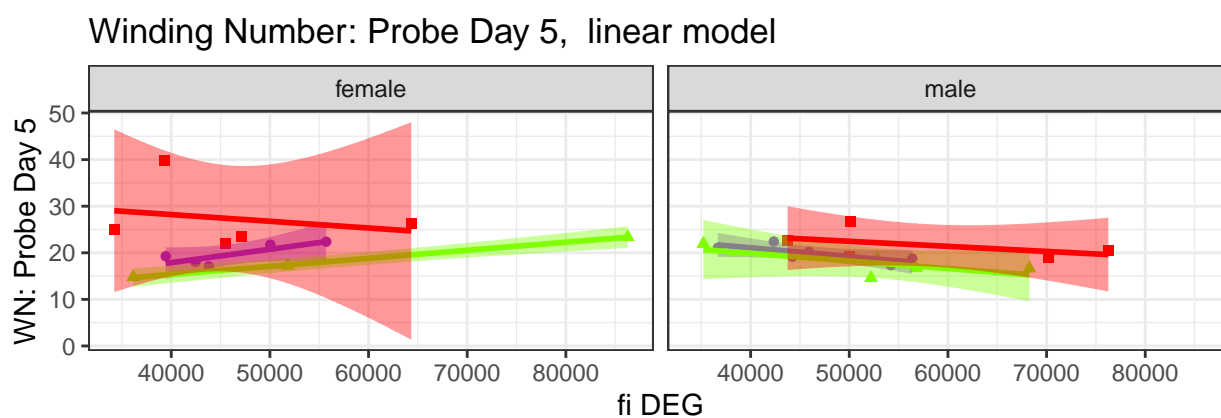
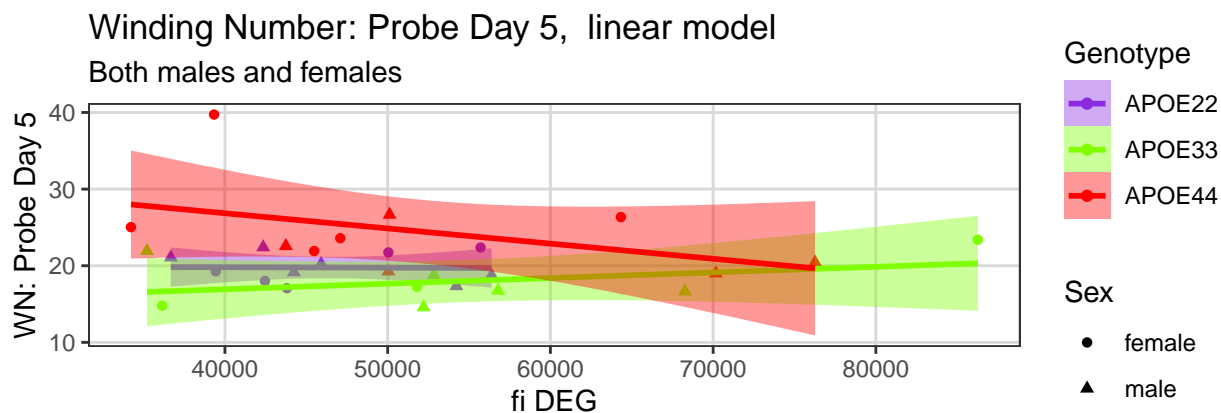
## Analysis of Variance Table
##
## Response: Probe_d5
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## CPu            1   3.626   3.626   0.2414 0.62951
## Genotype       2 204.575 102.287   6.8090 0.00673 **
## Sex            1  33.483  33.483   2.2289 0.15378
## CPu:Genotype   2  45.179  22.590   1.5037 0.25043
## CPu:Sex        1  14.601  14.601   0.9720 0.33801
## Genotype:Sex   2  69.502  34.751   2.3133 0.12925
## CPu:Genotype:Sex 2  14.763   7.382   0.4914 0.62021
## Residuals     17 255.380  15.022
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## CPu            1  10.088  10.088   0.3688 0.56281
## Genotype       2 202.344 101.172   3.6993 0.08012 .
## CPu:Genotype   2  63.839  31.919   1.1671 0.36524
## Residuals     7 191.445  27.349
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value  Pr(>F)
## CPu            1 44.465  44.465   6.9547 0.02485 *
## Genotype       2 10.784   5.392   0.8434 0.45871
## CPu:Genotype   2  4.993   2.497   0.3905 0.68660
## Residuals     10 63.935   6.394
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 5 Probe By fi DEG



```
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4892 -1.1194 -0.0115  1.0358 11.4312
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    6.428e+00  1.377e+01   0.467   0.646
## fi             2.865e-04  2.951e-04   0.971   0.345
## GenotypeAPOE33  2.025e+00  1.525e+01   0.133   0.896
## GenotypeAPOE44  2.754e+01  1.591e+01   1.731   0.102
## Sexmale        2.212e+01  1.757e+01   1.259   0.225
## fi:GenotypeAPOE33 -1.139e-04  3.136e-04  -0.363   0.721
## fi:GenotypeAPOE44 -4.307e-04  3.400e-04  -1.267   0.222
## fi:Sexmale       -4.735e-04  3.752e-04  -1.262   0.224
## GenotypeAPOE33:Sexmale -4.124e+00  2.071e+01  -0.199   0.845
## GenotypeAPOE44:Sexmale -2.819e+01  2.091e+01  -1.348   0.195
## fi:GenotypeAPOE33:Sexmale 1.369e-04  4.224e-04   0.324   0.750
## fi:GenotypeAPOE44:Sexmale 5.091e-04  4.332e-04   1.175   0.256
##
## Residual standard error: 3.854 on 17 degrees of freedom
## Multiple R-squared:  0.6061, Adjusted R-squared:  0.3512
```

```
## F-statistic: 2.378 on 11 and 17 DF, p-value: 0.05276
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4892 -1.9108 -0.0115  0.9715 11.4312
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    6.4284753  19.0807515   0.337   0.746
## fi              0.0002865   0.0004089   0.701   0.506
## GenotypeAPOE33    2.0254031  21.1363520   0.096   0.926
## GenotypeAPOE44   27.5414513  22.0503731   1.249   0.252
## fi:GenotypeAPOE33 -0.0001139   0.0004347  -0.262   0.801
## fi:GenotypeAPOE44 -0.0004307   0.0004712  -0.914   0.391
##
## Residual standard error: 5.341 on 7 degrees of freedom
## Multiple R-squared:  0.573, Adjusted R-squared:  0.268
## F-statistic: 1.879 on 5 and 7 DF, p-value: 0.2165
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.306 -1.080 -0.060  1.091  4.208
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.855e+01  6.512e+00  4.384 0.00137 **
## fi             -1.870e-04  1.382e-04  -1.353 0.20579
## GenotypeAPOE33  -2.098e+00  8.355e+00  -0.251 0.80679
## GenotypeAPOE44  -6.535e-01  8.089e+00  -0.081 0.93721
## fi:GenotypeAPOE33  2.302e-05  1.687e-04   0.136 0.89414
## fi:GenotypeAPOE44  7.842e-05  1.600e-04   0.490 0.63474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.298 on 10 degrees of freedom
## Multiple R-squared:  0.5747, Adjusted R-squared:  0.3621
## F-statistic: 2.703 on 5 and 10 DF, p-value: 0.0849
##
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value Pr(>F)
## fi      1    8.333    8.333   0.5610 0.464102
## Genotype 2 207.999 103.999   7.0013 0.006052 **
## Sex      1   29.277   29.277   1.9709 0.178355
## fi:Genotype 2  49.614   24.807   1.6700 0.217686
## fi:Sex     1  37.329   37.329   2.5130 0.131336
```

```

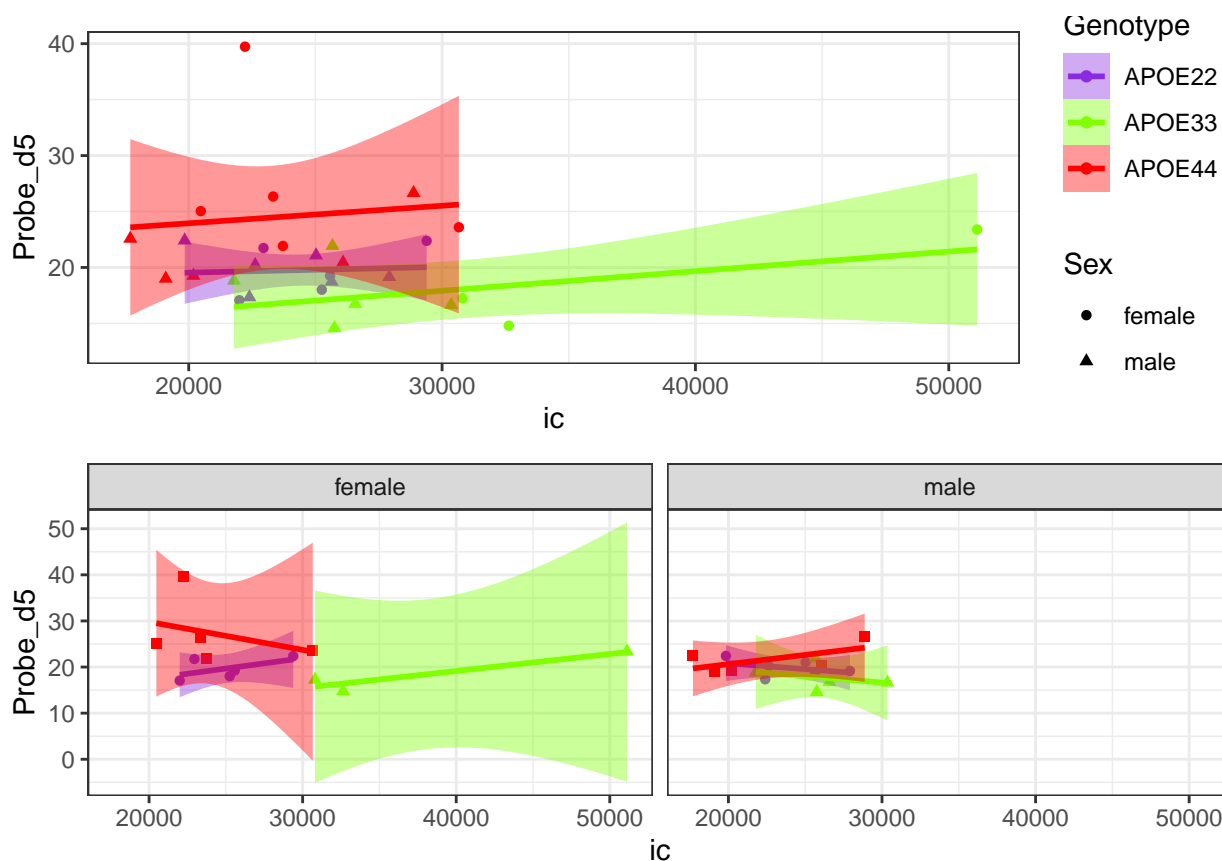
## Genotype:Sex      2  23.258  11.629  0.7829 0.472893
## fi:Genotype:Sex   2  32.777  16.389  1.1033 0.354399
## Residuals        17 252.523  14.854
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fi          1   1.503    1.503   0.0527 0.82502
## Genotype     2 222.582  111.291   3.9007 0.07274 .
## fi:Genotype   2  43.914   21.957   0.7696 0.49875
## Residuals    7 199.715   28.531
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fi          1 17.843  17.8430   3.3789 0.09589 .
## Genotype     2 51.792  25.8960   4.9038 0.03280 *
## fi:Genotype   2  1.734   0.8672   0.1642 0.85080
## Residuals   10 52.808   5.2808
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 5 Probe By ic DEG



```
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.6224 -1.4387 -0.1177  1.4889 11.2766
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.418e+00  1.739e+01   0.484   0.634
## ic              4.504e-04  6.909e-04   0.652   0.523
## GenotypeAPOE33  -4.011e+00  1.995e+01  -0.201   0.843
## GenotypeAPOE44   3.352e+01  2.136e+01   1.569   0.135
## Sexmale          1.754e+01  2.291e+01   0.765   0.455
## ic:GenotypeAPOE33 -8.184e-05  7.346e-04  -0.111   0.913
## ic:GenotypeAPOE44 -1.057e-03  8.586e-04  -1.231   0.235
## ic:Sexmale        -7.066e-04  9.286e-04  -0.761   0.457
## GenotypeAPOE33:Sexmale  3.104e+00  3.016e+01   0.103   0.919
## GenotypeAPOE44:Sexmale -4.689e+01  2.768e+01  -1.694   0.108
## ic:GenotypeAPOE33:Sexmale 5.770e-05  1.160e-03   0.050   0.961
## ic:GenotypeAPOE44:Sexmale 1.716e-03  1.136e-03   1.511   0.149
##
## Residual standard error: 3.963 on 17 degrees of freedom
## Multiple R-squared:  0.5836, Adjusted R-squared:  0.3142
```

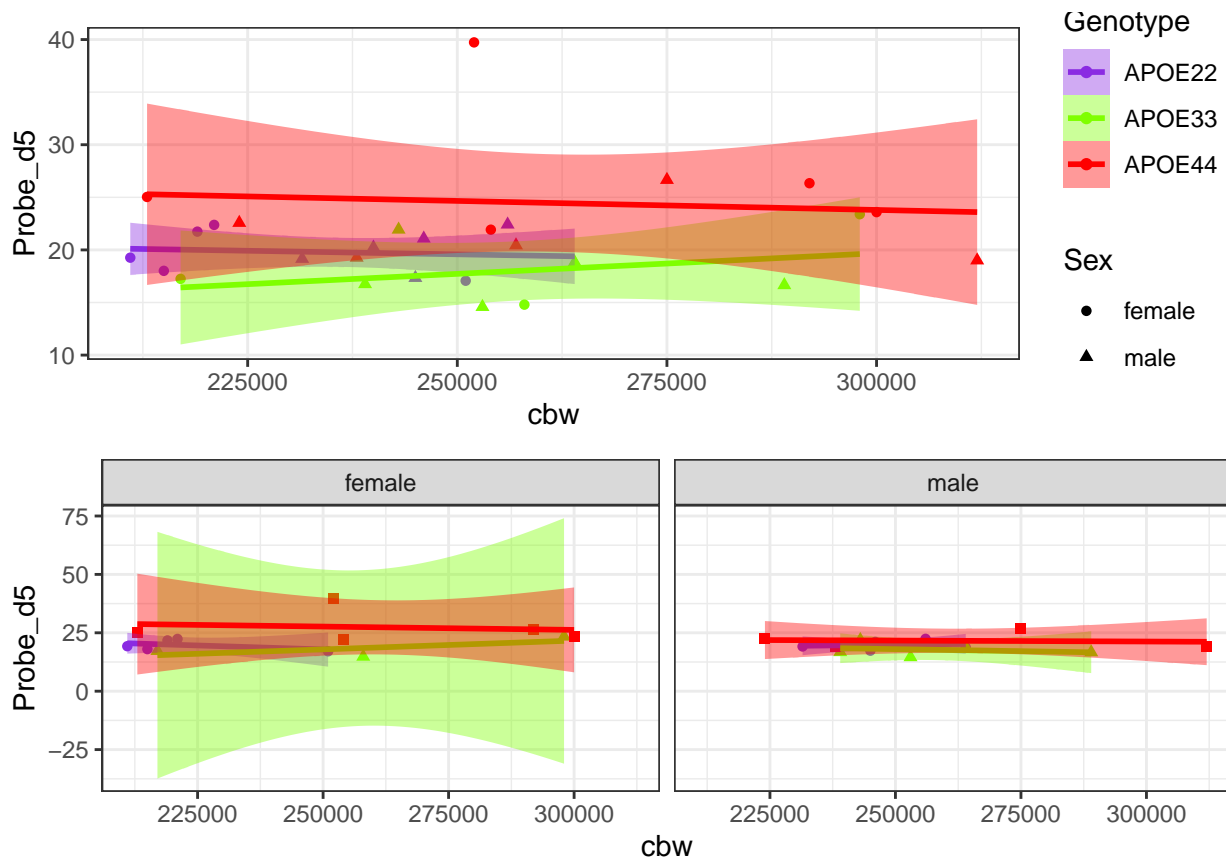
```
## F-statistic: 2.166 on 11 and 17 DF, p-value: 0.0738
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.6224 -1.6362 -0.6745  0.7248 11.2766
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    8.418e+00  2.348e+01   0.358   0.731
## ic             4.504e-04  9.332e-04   0.483   0.644
## GenotypeAPOE33 -4.011e+00  2.695e+01  -0.149   0.886
## GenotypeAPOE44  3.352e+01  2.884e+01   1.162   0.283
## ic:GenotypeAPOE33 -8.184e-05  9.920e-04  -0.082   0.937
## ic:GenotypeAPOE44 -1.057e-03  1.160e-03  -0.912   0.392
##
## Residual standard error: 5.352 on 7 degrees of freedom
## Multiple R-squared:  0.5713, Adjusted R-squared:  0.2651
## F-statistic: 1.866 on 5 and 7 DF, p-value: 0.2189
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.2435 -1.3028 -0.0235  1.5427  4.0844
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.595e+01  9.706e+00   2.674   0.0233 *
## ic             -2.563e-04  4.036e-04  -0.635   0.5398
## GenotypeAPOE33 -9.071e-01  1.471e+01  -0.062   0.9520
## GenotypeAPOE44 -1.337e+01  1.145e+01  -1.168   0.2700
## ic:GenotypeAPOE33 -2.414e-05  5.842e-04  -0.041   0.9678
## ic:GenotypeAPOE44  6.586e-04  4.837e-04   1.362   0.2032
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.578 on 10 degrees of freedom
## Multiple R-squared:  0.4648, Adjusted R-squared:  0.1972
## F-statistic: 1.737 on 5 and 10 DF, p-value: 0.2138
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value    Pr(>F)
## ic      1   2.882    2.882    0.1835 0.673738
## Genotype 2 224.497 112.249    7.1481 0.005586 **
## Sex      1  18.572   18.572    1.1827 0.291988
## ic:Genotype 2   1.091    0.546    0.0348 0.965914
## ic:Sex     1   7.267    7.267    0.4628 0.505499
```

```
## Genotype:Sex      2  59.797  29.899  1.9040 0.179418
## ic:Genotype:Sex  2  60.047  30.023  1.9119 0.178257
## Residuals        17 266.955  15.703
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic          1  14.213   14.213   0.4962 0.50392
## Genotype     2 204.431  102.215   3.5687 0.08542 .
## ic:Genotype  2  48.574   24.287   0.8479 0.46800
## Residuals    7 200.497   28.642
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic          1   1.648    1.6479   0.2480 0.6293
## Genotype     2 36.951  18.4757   2.7801 0.1096
## ic:Genotype  2 19.120   9.5599   1.4385 0.2824
## Residuals   10 66.458    6.6458
```

Day 5 Probe By cbw DEG



```
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.6353 -2.2500 -0.2919  1.7489 12.1149
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.480e+01  3.059e+01   1.138   0.271
## cbw             -6.763e-05  1.367e-04  -0.495   0.627
## GenotypeAPOE33   -3.573e+01  3.639e+01  -0.982   0.340
## GenotypeAPOE44   -5.649e-04  3.470e+01   0.000   1.000
## Sexmale         -2.100e+01  5.172e+01  -0.406   0.690
## cbw:GenotypeAPOE33  1.430e-04  1.563e-04   0.914   0.373
## cbw:GenotypeAPOE44  3.912e-05  1.501e-04   0.261   0.798
## cbw:Sexmale        9.203e-05  2.171e-04   0.424   0.677
## GenotypeAPOE33:Sexmale  4.857e+01  6.203e+01   0.783   0.444
## GenotypeAPOE44:Sexmale  9.962e+00  5.675e+01   0.176   0.863
## cbw:GenotypeAPOE33:Sexmale -2.019e-04  2.542e-04  -0.794   0.438
## cbw:GenotypeAPOE44:Sexmale -7.183e-05  2.345e-04  -0.306   0.763
##
## Residual standard error: 4.346 on 17 degrees of freedom
## Multiple R-squared:  0.4992, Adjusted R-squared:  0.1751
## F-statistic:  1.54 on 11 and 17 DF,  p-value: 0.2051
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.6353 -2.6535 -0.7559  1.8311 12.1149
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.480e+01  4.092e+01   0.850   0.423
## cbw             -6.763e-05  1.828e-04  -0.370   0.722
## GenotypeAPOE33   -3.573e+01  4.868e+01  -0.734   0.487
## GenotypeAPOE44   -5.649e-04  4.641e+01   0.000   1.000
## cbw:GenotypeAPOE33  1.430e-04  2.091e-04   0.684   0.516
## cbw:GenotypeAPOE44  3.912e-05  2.007e-04   0.195   0.851
##
## Residual standard error: 5.813 on 7 degrees of freedom
## Multiple R-squared:  0.4943, Adjusted R-squared:  0.1331
## F-statistic: 1.369 on 5 and 7 DF,  p-value: 0.3399
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3248 -1.7690 -0.1509  1.2841  5.1865
```



```

##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.380e+01  2.791e+01   0.494   0.632
## cbw            2.440e-05  1.128e-04   0.216   0.833
## GenotypeAPOE33  1.284e+01  3.361e+01   0.382   0.710
## GenotypeAPOE44  9.962e+00  3.005e+01   0.332   0.747
## cbw:GenotypeAPOE33 -5.892e-05  1.342e-04  -0.439   0.670
## cbw:GenotypeAPOE44 -3.271e-05  1.205e-04  -0.271   0.792
##
## Residual standard error: 2.908 on 10 degrees of freedom
## Multiple R-squared:  0.3189, Adjusted R-squared:  -0.02163
## F-statistic: 0.9365 on 5 and 10 DF,  p-value: 0.4976

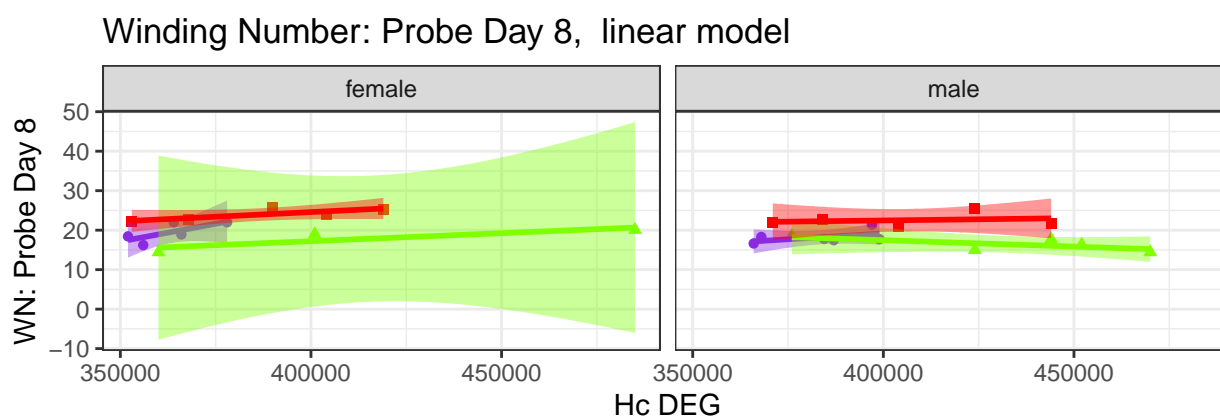
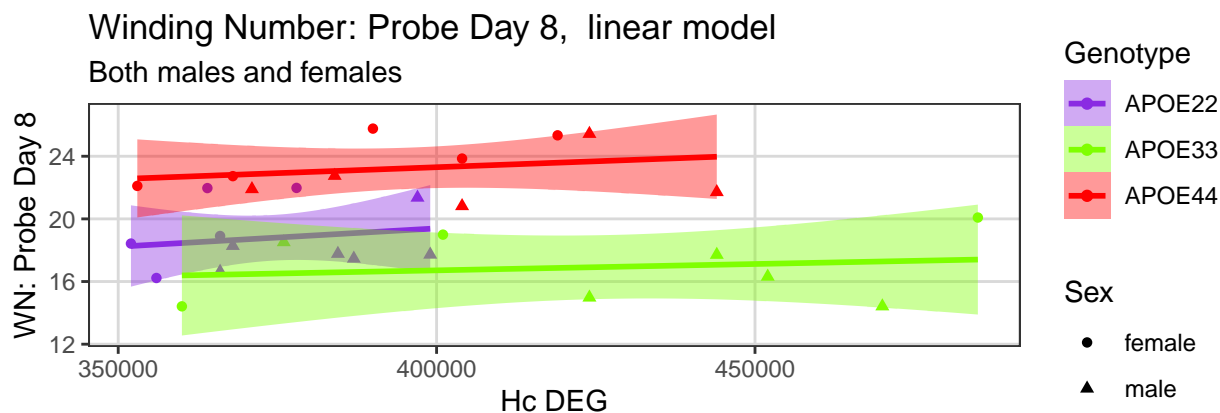
## Analysis of Variance Table
##
## Response: Probe_d5
##               Df Sum Sq Mean Sq F value Pr(>F)
## cbw            1   7.22    7.215   0.3820 0.5447
## Genotype       2 199.67   99.834   5.2857 0.0164 *
## Sex            1  33.92   33.919   1.7958 0.1979
## cbw:Genotype   2  13.26    6.629   0.3510 0.7090
## cbw:Sex        1   5.92    5.916   0.3132 0.5830
## Genotype:Sex   2  42.93   21.466   1.1365 0.3441
## cbw:Genotype:Sex 2  17.11    8.555   0.4529 0.6432
## Residuals     17 321.09   18.888
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##               Df Sum Sq Mean Sq F value Pr(>F)
## cbw            1  27.299   27.299   0.8079 0.3986
## Genotype       2 176.837   88.419   2.6169 0.1417
## cbw:Genotype   2  27.062   13.531   0.4005 0.6844
## Residuals      7 236.516   33.788

## Analysis of Variance Table
##
## Response: Probe_d5
##               Df Sum Sq Mean Sq F value Pr(>F)
## cbw            1   0.346   0.3460   0.0409 0.8438
## Genotype       2  37.501  18.7504   2.2170 0.1596
## cbw:Genotype   2   1.755   0.8777   0.1038 0.9024
## Residuals     10  84.575    8.4575

```

Day 8 Probe By Hc DEG



```
##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9830 -0.9422 -0.2559  0.9330  2.6846
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -4.564e+01  3.051e+01  -1.496  0.1529
## Hc             1.794e-04  8.396e-05   2.136  0.0475 *
## GenotypeAPOE33  4.663e+01  3.150e+01   1.480  0.1571
## GenotypeAPOE44  5.133e+01  3.289e+01   1.561  0.1370
## Sexmale        4.098e+01  3.686e+01   1.112  0.2817
## Hc:GenotypeAPOE33 -1.388e-04  8.603e-05  -1.613  0.1251
## Hc:GenotypeAPOE44 -1.321e-04  8.975e-05  -1.472  0.1592
## Hc:Sexmale       -1.197e-04  9.978e-05  -1.200  0.2466
## GenotypeAPOE33:Sexmale -1.150e+01  3.904e+01  -0.295  0.7719
## GenotypeAPOE44:Sexmale -2.900e+01  4.056e+01  -0.715  0.4843
## Hc:GenotypeAPOE33:Sexmale  4.668e-05  1.042e-04   0.448  0.6598
## Hc:GenotypeAPOE44:Sexmale  8.448e-05  1.085e-04   0.778  0.4471
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.689 on 17 degrees of freedom
## Multiple R-squared:  0.8382, Adjusted R-squared:  0.7335
## F-statistic: 8.005 on 11 and 17 DF,  p-value: 9.358e-05

##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9830 -0.9165 -0.2559  0.9330  2.3223
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -4.564e+01  3.049e+01  -1.497   0.1780
## Hc             1.794e-04  8.392e-05   2.137   0.0699 .
## GenotypeAPOE33  4.663e+01  3.148e+01   1.481   0.1821
## GenotypeAPOE44  5.133e+01  3.287e+01   1.562   0.1623
## Hc:GenotypeAPOE33 -1.388e-04  8.598e-05  -1.614   0.1505
## Hc:GenotypeAPOE44 -1.321e-04  8.970e-05  -1.473   0.1842
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 1.688 on 7 degrees of freedom
## Multiple R-squared:  0.8547, Adjusted R-squared:  0.751
## F-statistic: 8.237 on 5 and 7 DF,  p-value: 0.007579

##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7071 -1.0247 -0.3478  0.6545  2.6846
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -4.666e+00  2.070e+01  -0.225   0.826
## Hc             5.962e-05  5.392e-05   1.106   0.295
## GenotypeAPOE33  3.513e+01  2.307e+01   1.523   0.159
## GenotypeAPOE44  2.234e+01  2.374e+01   0.941   0.369
## Hc:GenotypeAPOE33 -9.212e-05  5.881e-05  -1.566   0.148
## Hc:GenotypeAPOE44 -4.765e-05  6.106e-05  -0.780   0.453
##
## Residual standard error: 1.69 on 10 degrees of freedom
## Multiple R-squared:  0.7931, Adjusted R-squared:  0.6896
## F-statistic: 7.666 on 5 and 10 DF,  p-value: 0.003351

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Hc           1   0.860    0.860   0.3014   0.59016
## Genotype     2 197.921   98.961  34.6762 1.001e-06 ***
## Sex           1  20.731   20.731   7.2642   0.01533 *

```

```

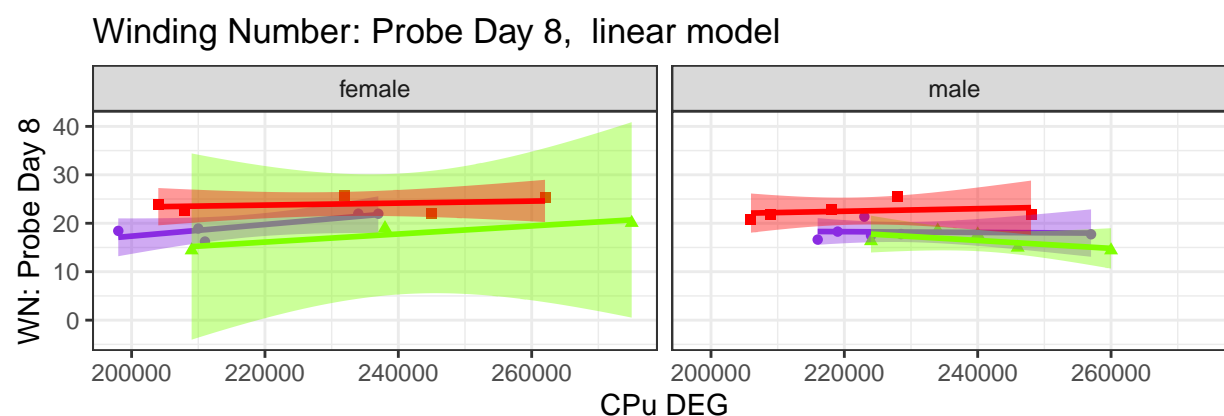
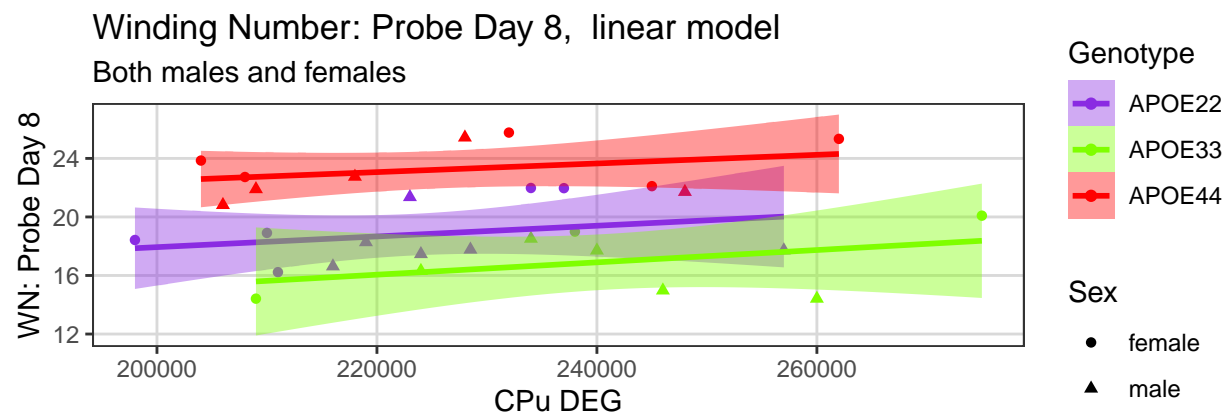
## Hc:Genotype      2   6.600   3.300   1.1564   0.33817
## Hc:Sex            1   8.134   8.134   2.8500   0.10963
## Genotype:Sex      2  14.595   7.297   2.5570   0.10694
## Hc:Genotype:Sex    2   2.442   1.221   0.4278   0.65877
## Residuals         17  48.515   2.854
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Hc              1  11.530   11.530   4.0446 0.084226 .
## Genotype         2  98.444   49.222  17.2669 0.001965 **
## Hc:Genotype      2   7.428    3.714   1.3029 0.330347
## Residuals        7  19.955    2.851
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Hc              1   6.538    6.538   2.2893 0.1612140
## Genotype         2  93.957   46.979  16.4486 0.0006884 ***
## Hc:Genotype      2   8.979    4.490   1.5720 0.2549045
## Residuals       10  28.561    2.856
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By CPu DEG



```
##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.4339 -0.7765 -0.2521  0.7235  3.1176
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -6.673e+00  1.141e+01  -0.585   0.5664
## CPu             1.201e-04  5.223e-05   2.299   0.0345 *
## GenotypeAPOE33  4.441e+00  1.459e+01   0.304   0.7645
## GenotypeAPOE44  2.589e+01  1.409e+01   1.837   0.0837 .
## Sexmale        2.669e+01  1.659e+01   1.608   0.1262
## CPu:GenotypeAPOE33 -3.669e-05  6.431e-05  -0.571   0.5758
## CPu:GenotypeAPOE44 -9.948e-05  6.329e-05  -1.572   0.1344
## CPu:Sexmale      -1.280e-04  7.424e-05  -1.724   0.1028
## GenotypeAPOE33:Sexmale  1.168e+01  2.460e+01   0.475   0.6410
## GenotypeAPOE44:Sexmale -2.931e+01  2.181e+01  -1.344   0.1967
## CPu:GenotypeAPOE33:Sexmale -3.737e-05  1.057e-04  -0.354   0.7280
## CPu:GenotypeAPOE44:Sexmale  1.342e-04  9.728e-05   1.379   0.1857
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.756 on 17 degrees of freedom
## Multiple R-squared:  0.8252, Adjusted R-squared:  0.7121
## F-statistic: 7.297 on 11 and 17 DF,  p-value: 0.0001695

##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.4339 -0.7718  0.3674  0.7235  1.7700
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -6.673e+00  1.103e+01  -0.605   0.5642
## CPu             1.201e-04  5.047e-05   2.379   0.0489 *
## GenotypeAPOE33  4.441e+00  1.410e+01   0.315   0.7619
## GenotypeAPOE44  2.589e+01  1.362e+01   1.902   0.0990 .
## CPu:GenotypeAPOE33 -3.669e-05  6.214e-05  -0.590   0.5734
## CPu:GenotypeAPOE44 -9.948e-05  6.115e-05  -1.627   0.1478
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 1.696 on 7 degrees of freedom
## Multiple R-squared:  0.8533, Adjusted R-squared:  0.7486
## F-statistic: 8.146 on 5 and 7 DF,  p-value: 0.007821

##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.6724 -1.0569 -0.3368  0.5619  3.1176
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.001e+01  1.232e+01   1.624   0.135
## CPu           -7.948e-06  5.397e-05  -0.147   0.886
## GenotypeAPOE33  1.612e+01  2.026e+01   0.796   0.445
## GenotypeAPOE44 -3.420e+00  1.703e+01  -0.201   0.845
## CPu:GenotypeAPOE33 -7.406e-05  8.581e-05  -0.863   0.408
## CPu:GenotypeAPOE44  3.467e-05  7.557e-05   0.459   0.656
##
## Residual standard error: 1.796 on 10 degrees of freedom
## Multiple R-squared:  0.7663, Adjusted R-squared:  0.6495
## F-statistic: 6.559 on 5 and 10 DF,  p-value: 0.005908

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## CPu         1  0.018    0.018  0.0058  0.94018
## Genotype    2 206.960   103.480  33.5721 1.248e-06 ***
## Sex         1  14.260    14.260   4.6264  0.04616 *

```

```

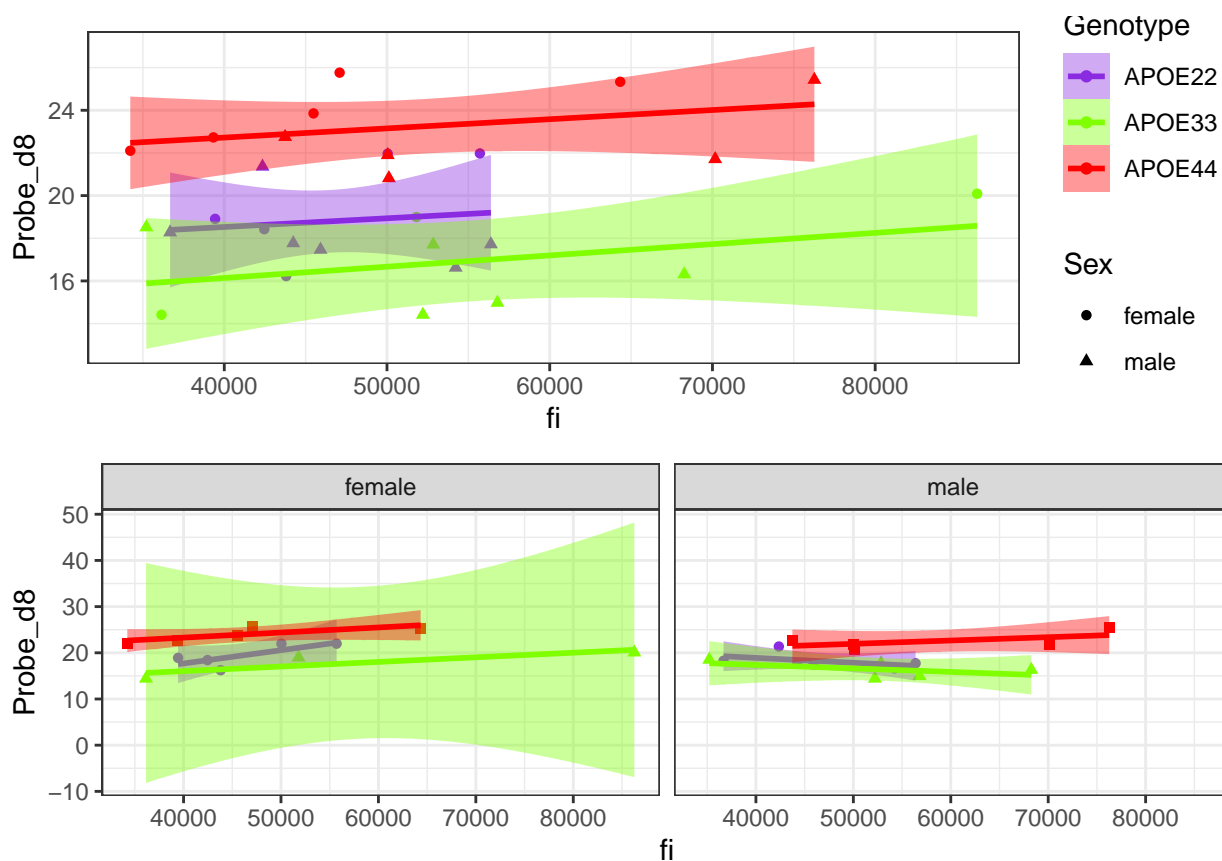
## CPu:Genotype      2    1.603    0.801    0.2600    0.77408
## CPu:Sex           1   10.326   10.326    3.3500    0.08480 .
## Genotype:Sex      2    3.205    1.602    0.5199    0.60375
## CPu:Genotype:Sex  2   11.027    5.514    1.7888    0.19723
## Residuals        17   52.399    3.082
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1  18.681   18.681   6.4913 0.038226 *
## Genotype      2  89.609   44.804  15.5682 0.002649 **
## CPu:Genotype  2   8.921    4.461   1.5499 0.277165
## Residuals     7  20.146    2.878
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1  24.933   24.933   7.7303 0.019440 *
## Genotype      2  75.550   37.775  11.7118 0.002397 **
## CPu:Genotype  2   5.299    2.649   0.8214 0.467429
## Residuals    10  32.254    3.225
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By fi DEG



```
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5622 -0.8146 -0.2222  1.2606  2.7017
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    6.231e+00  5.920e+00   1.052  0.3073
## fi             2.867e-04  1.269e-04   2.259  0.0373 *
## GenotypeAPOE33  5.809e+00  6.558e+00   0.886  0.3881
## GenotypeAPOE44  1.265e+01  6.841e+00   1.850  0.0818 .
## Sexmale        1.693e+01  7.557e+00   2.240  0.0387 *
## fi:GenotypeAPOE33 -1.869e-04  1.349e-04  -1.386  0.1836
## fi:GenotypeAPOE44 -1.766e-04  1.462e-04  -1.208  0.2435
## fi:Sexmale       -3.929e-04  1.613e-04  -2.435  0.0262 *
## GenotypeAPOE33:Sexmale -8.544e+00  8.906e+00  -0.959  0.3508
## GenotypeAPOE44:Sexmale -1.747e+01  8.991e+00  -1.943  0.0687 .
## fi:GenotypeAPOE33:Sexmale 2.171e-04  1.816e-04   1.195  0.2484
## fi:GenotypeAPOE44:Sexmale 3.549e-04  1.863e-04   1.905  0.0738 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```



```

## Residual standard error: 1.657 on 17 degrees of freedom
## Multiple R-squared:  0.8443, Adjusted R-squared:  0.7435
## F-statistic: 8.378 on 11 and 17 DF,  p-value: 6.95e-05

##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5622 -0.5587 -0.2222  1.3718  1.7879
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    6.2307542   5.9256536   1.051   0.3280
## fi              0.0002867   0.0001270   2.257   0.0586 .
## GenotypeAPOE33    5.8090575   6.5640340   0.885   0.4055
## GenotypeAPOE44   12.6545130   6.8478893   1.848   0.1071
## fi:GenotypeAPOE33 -0.0001869   0.0001350  -1.385   0.2087
## fi:GenotypeAPOE44 -0.0001766   0.0001463  -1.207   0.2666
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.659 on 7 degrees of freedom
## Multiple R-squared:  0.8598, Adjusted R-squared:  0.7596
## F-statistic: 8.584 on 5 and 7 DF,  p-value: 0.006741

##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.0344 -1.0189 -0.3647  1.1283  2.7017
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.316e+01  4.693e+00   4.934 0.000592 ***
## fi             -1.063e-04  9.960e-05  -1.067 0.311039
## GenotypeAPOE33   -2.735e+00  6.021e+00  -0.454 0.659386
## GenotypeAPOE44   -4.817e+00  5.830e+00  -0.826 0.427921
## fi:GenotypeAPOE33  3.018e-05  1.216e-04   0.248 0.808964
## fi:GenotypeAPOE44  1.783e-04  1.153e-04   1.546 0.153236
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.656 on 10 degrees of freedom
## Multiple R-squared:  0.8013, Adjusted R-squared:  0.7019
## F-statistic: 8.065 on 5 and 10 DF,  p-value: 0.002771

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value Pr(>F)
## fi              1   8.131   8.131   2.9606 0.10346

```

```

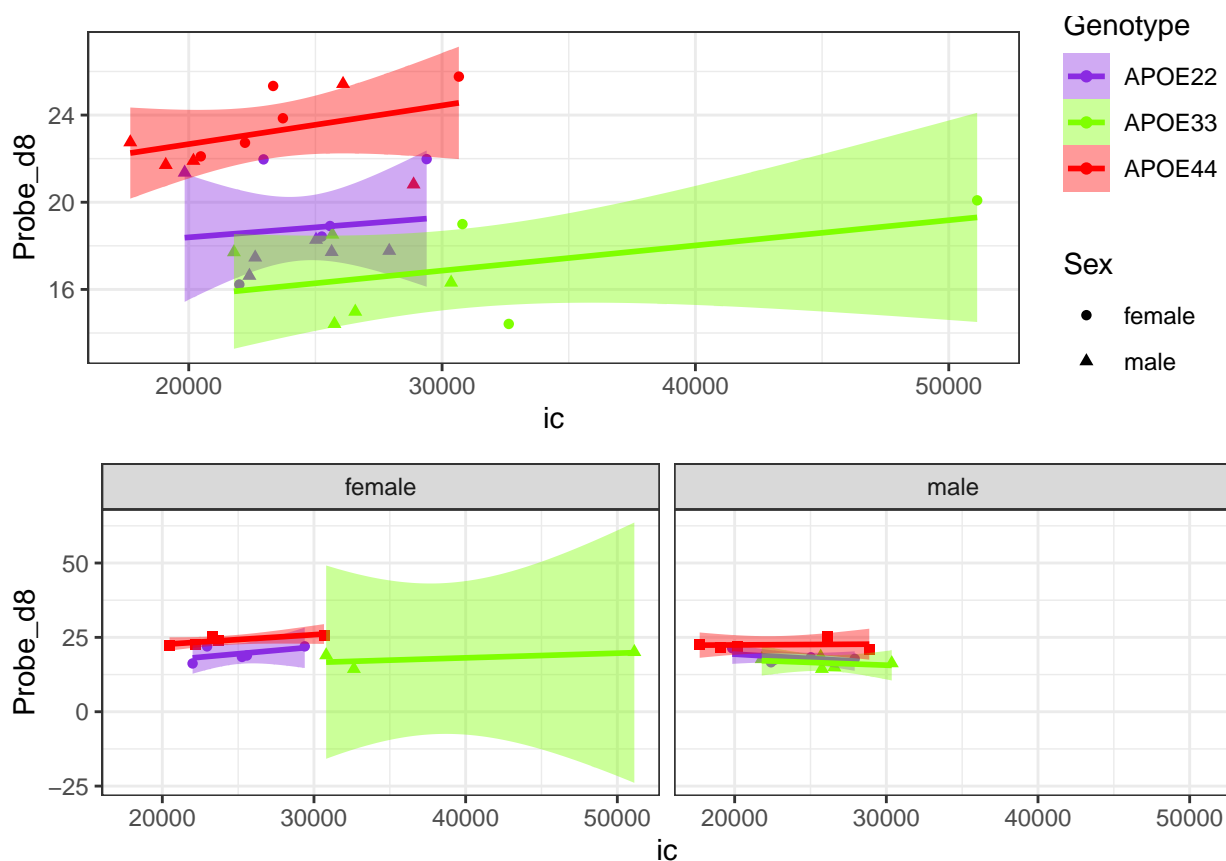
## Genotype          2 196.463  98.231 35.7660 8.1e-07 ***
## Sex               1  16.863  16.863  6.1400 0.02401 *
## fi:Genotype       2   0.685   0.343  0.1248 0.88350
## fi:Sex            1  17.204  17.204  6.2638 0.02282 *
## Genotype:Sex      2   3.296   1.648  0.6001 0.55998
## fi:Genotype:Sex   2  10.464   5.232  1.9050 0.17927
## Residuals        17  46.691   2.747
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fi              1   7.062    7.062   2.5663 0.153194
## Genotype        2 105.709   52.855  19.2082 0.001437 **
## fi:Genotype     2   5.324    2.662   0.9675 0.425611
## Residuals       7  19.262    2.752
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fi              1   5.447    5.447   1.9858 0.1891140
## Genotype        2  94.686   47.343  17.2602 0.0005717 ***
## fi:Genotype     2  10.474    5.237   1.9094 0.1984551
## Residuals      10  27.429    2.743
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By ic DEG



```
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5476 -1.1157  0.0155  0.7299  3.4185
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.046e+00  8.659e+00   0.929   0.366
## ic              4.576e-04  3.441e-04   1.330   0.201
## GenotypeAPOE33   3.811e+00  9.938e+00   0.383   0.706
## GenotypeAPOE44   8.001e+00  1.064e+01   0.752   0.462
## Sexmale         1.718e+01  1.141e+01   1.506   0.150
## ic:GenotypeAPOE33 -3.011e-04  3.658e-04  -0.823   0.422
## ic:GenotypeAPOE44 -1.291e-04  4.276e-04  -0.302   0.766
## ic:Sexmale       -7.515e-04  4.625e-04  -1.625   0.123
## GenotypeAPOE33:Sexmale -7.830e+00  1.502e+01  -0.521   0.609
## GenotypeAPOE44:Sexmale -1.135e+01  1.378e+01  -0.823   0.422
## ic:GenotypeAPOE33:Sexmale 4.097e-04  5.778e-04   0.709   0.488
## ic:GenotypeAPOE44:Sexmale 4.516e-04  5.656e-04   0.798   0.436
##
## Residual standard error: 1.974 on 17 degrees of freedom
## Multiple R-squared:  0.7791, Adjusted R-squared:  0.6362
```

```
## F-statistic: 5.452 on 11 and 17 DF, p-value: 0.0009904
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5476 -0.8425 -0.3547  0.4839  3.4185
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    8.0458838   9.5372019   0.844   0.427
## ic              0.0004576   0.0003790   1.207   0.266
## GenotypeAPOE33    3.8106153  10.9450443   0.348   0.738
## GenotypeAPOE44    8.0009047  11.7136382   0.683   0.517
## ic:GenotypeAPOE33 -0.0003011  0.0004029  -0.747   0.479
## ic:GenotypeAPOE44 -0.0001291  0.0004709  -0.274   0.792
##
## Residual standard error: 2.174 on 7 degrees of freedom
## Multiple R-squared:  0.7592, Adjusted R-squared:  0.5873
## F-statistic: 4.415 on 5 and 7 DF, p-value: 0.03898
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.0219 -1.1635  0.1948  0.7340  2.8016
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    25.2306699   6.8540445   3.681 0.00424 **
## ic             -0.0002940   0.0002850  -1.031 0.32667
## GenotypeAPOE33  -4.0191120  10.3876712  -0.387 0.70693
## GenotypeAPOE44  -3.3463598   8.0865744  -0.414 0.68774
## ic:GenotypeAPOE33  0.0001086  0.0004125   0.263 0.79777
## ic:GenotypeAPOE44  0.0003225  0.0003415   0.944 0.36733
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.82 on 10 degrees of freedom
## Multiple R-squared:  0.7599, Adjusted R-squared:  0.6399
## F-statistic: 6.33 on 5 and 10 DF, p-value: 0.006699
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1   6.196    6.196   1.5907    0.2243
## Genotype        2 201.981  100.990  25.9300 6.856e-06 ***
## Sex              1   6.128    6.128   1.5734    0.2267
## ic:Genotype      2   0.842    0.421   0.1081    0.8982
## ic:Sex           1  10.694   10.694   2.7457    0.1159
```

```

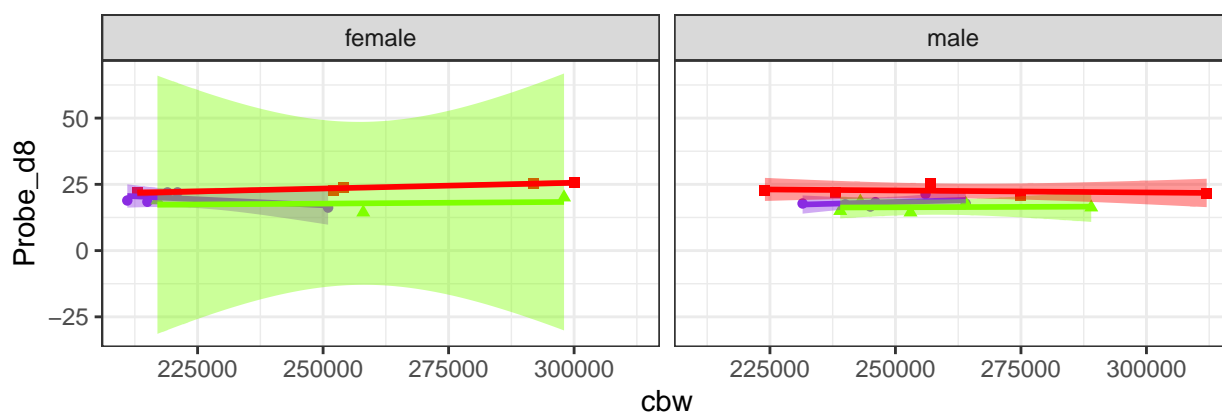
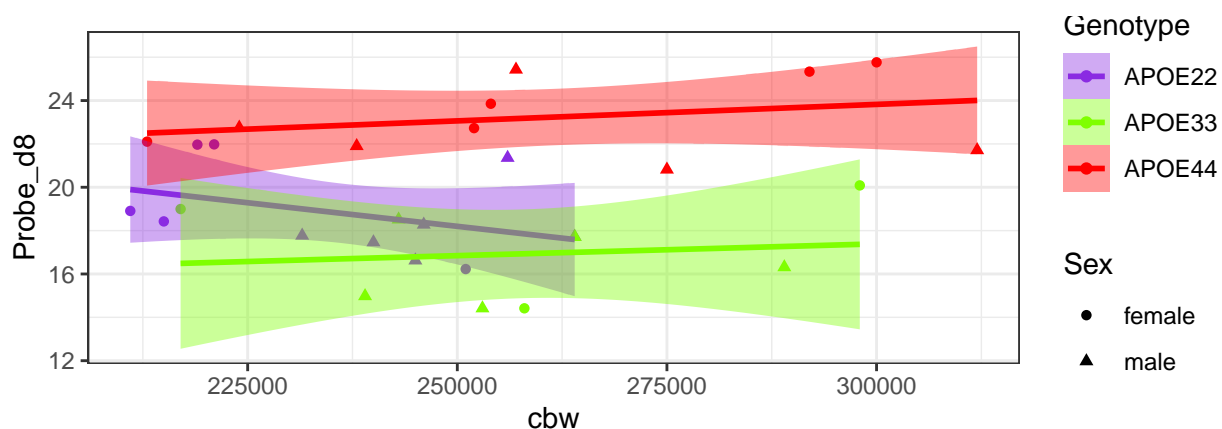
## Genotype:Sex      2    5.028    2.514    0.6454    0.5368
## ic:Genotype:Sex   2    2.720    1.360    0.3491    0.7102
## Residuals        17   66.211    3.895
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1  4.435    4.435   0.9388 0.364862
## Genotype        2 96.272   48.136  10.1890 0.008452 **
## ic:Genotype     2  3.579    1.790   0.3788 0.697888
## Residuals       7 33.070    4.724
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1 24.347   24.347   7.3468 0.021915 *
## Genotype        2 77.201   38.601  11.6476 0.002444 **
## ic:Genotype     2  3.347    1.673   0.5049 0.618135
## Residuals      10 33.140    3.314
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By cbw DEG



```
##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4210 -1.2884 -0.0445  1.2805  2.8440
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.956e+01  1.425e+01  2.776  0.0130 *
## cbw          -8.977e-05  6.367e-05 -1.410  0.1766
## GenotypeAPOE33 -2.506e+01  1.695e+01 -1.478  0.1577
## GenotypeAPOE44 -2.702e+01  1.617e+01 -1.672  0.1129
## Sexmale       -3.442e+01  2.409e+01 -1.429  0.1712
## cbw:GenotypeAPOE33  1.027e-04  7.282e-05  1.411  0.1764
## cbw:GenotypeAPOE44  1.333e-04  6.992e-05  1.907  0.0735 .
## cbw:Sexmale       1.427e-04  1.011e-04  1.411  0.1763
## GenotypeAPOE33:Sexmale  3.466e+01  2.889e+01  1.199  0.2468
## GenotypeAPOE44:Sexmale  4.835e+01  2.644e+01  1.829  0.0850 .
## cbw:GenotypeAPOE33:Sexmale -1.492e-04  1.184e-04 -1.260  0.2248
## cbw:GenotypeAPOE44:Sexmale -2.013e-04  1.092e-04 -1.843  0.0828 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 2.025 on 17 degrees of freedom
## Multiple R-squared:  0.7676, Adjusted R-squared:  0.6172
## F-statistic: 5.104 on 11 and 17 DF,  p-value: 0.001443

##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4210 -0.7967  0.1600  1.6894  2.2622
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.956e+01  1.566e+01   2.526  0.0395 *
## cbw           -8.977e-05  6.997e-05  -1.283  0.2403
## GenotypeAPOE33 -2.506e+01  1.863e+01  -1.345  0.2206
## GenotypeAPOE44 -2.702e+01  1.777e+01  -1.521  0.1721
## cbw:GenotypeAPOE33  1.027e-04  8.003e-05   1.284  0.2402
## cbw:GenotypeAPOE44  1.333e-04  7.684e-05   1.735  0.1263
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 2.225 on 7 degrees of freedom
## Multiple R-squared:  0.7477, Adjusted R-squared:  0.5675
## F-statistic: 4.149 on 5 and 7 DF,  p-value: 0.04516

##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9396 -1.3109 -0.3034  0.6146  2.8439
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.133e+00  1.796e+01   0.286  0.781
## cbw           5.290e-05  7.262e-05   0.728  0.483
## GenotypeAPOE33  9.595e+00  2.163e+01   0.444  0.667
## GenotypeAPOE44  2.133e+01  1.934e+01   1.103  0.296
## cbw:GenotypeAPOE33 -4.646e-05  8.633e-05  -0.538  0.602
## cbw:GenotypeAPOE44 -6.797e-05  7.757e-05  -0.876  0.401
##
## Residual standard error: 1.872 on 10 degrees of freedom
## Multiple R-squared:  0.7463, Adjusted R-squared:  0.6194
## F-statistic: 5.882 on 5 and 10 DF,  p-value: 0.008647

## Analysis of Variance Table
##
## Response: Probe_d8
##      Df Sum Sq Mean Sq F value    Pr(>F)
## cbw    1   8.910    8.910  2.1739  0.15865
## Genotype 2 186.737   93.369 22.7797 1.55e-05 ***
## Sex     1  14.660   14.660  3.5768  0.07576 .

```

```

## cbw:Genotype      2    2.427    1.214    0.2961    0.74749
## cbw:Sex           1    2.865    2.865    0.6989    0.41475
## Genotype:Sex      2    0.168    0.084    0.0205    0.97968
## cbw:Genotype:Sex  2   14.351    7.175    1.7506    0.20356
## Residuals        17   69.679    4.099
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

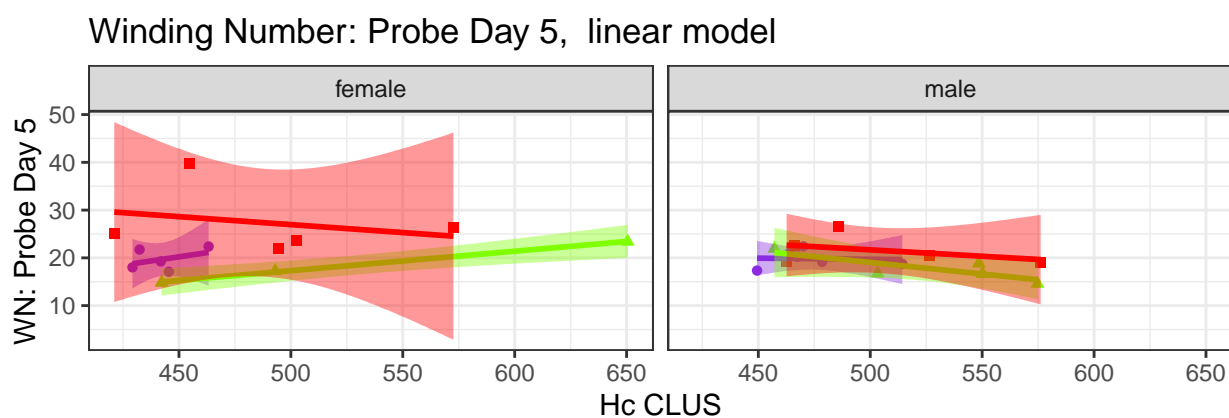
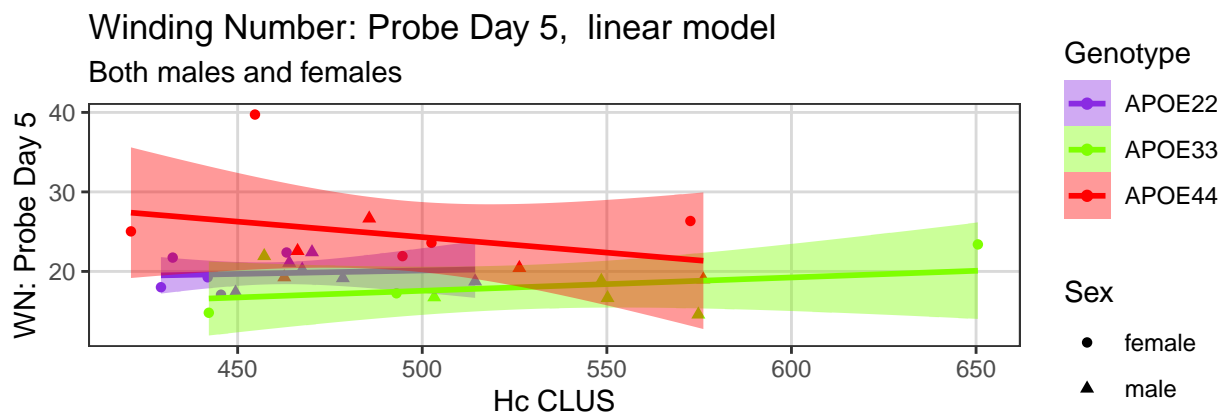
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw           1  15.989   15.989   3.2298 0.11536
## Genotype      2  71.676   35.838   7.2394 0.01976 *
## cbw:Genotype  2  15.039    7.519   1.5189 0.28320
## Residuals     7  34.653    4.950
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw           1   1.009    1.009   0.2882 0.603127
## Genotype      2  99.098   49.549  14.1463 0.001215 **
## cbw:Genotype  2   2.902    1.451   0.4143 0.671622
## Residuals    10  35.026    3.503
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Clustering Coefficient

Day 5 Probe By Hc CLUS



```
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.2171  -0.9027  -0.1636   1.2098  11.2582
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -11.03523    65.44982   -0.169   0.868
## Hc              0.06945     0.14787    0.470   0.645
## GenotypeAPOE33    7.97996    66.89387    0.119   0.906
## GenotypeAPOE44   54.66612    67.64423    0.808   0.430
## Sexmale         32.99401    75.83057    0.435   0.669
## Hc:GenotypeAPOE33 -0.02871     0.15010   -0.191   0.851
## Hc:GenotypeAPOE44 -0.10279     0.15190   -0.677   0.508
## Hc:Sexmale       -0.07395     0.16847   -0.439   0.666
## GenotypeAPOE33:Sexmale 13.30470    80.27475    0.166   0.870
## GenotypeAPOE44:Sexmale -41.52758    80.49196   -0.516   0.613
## Hc:GenotypeAPOE33:Sexmale -0.01519     0.17564   -0.087   0.932
## Hc:GenotypeAPOE44:Sexmale 0.08045     0.17692    0.455   0.655
##
## Residual standard error: 3.962 on 17 degrees of freedom
## Multiple R-squared:  0.5838, Adjusted R-squared:  0.3145
```

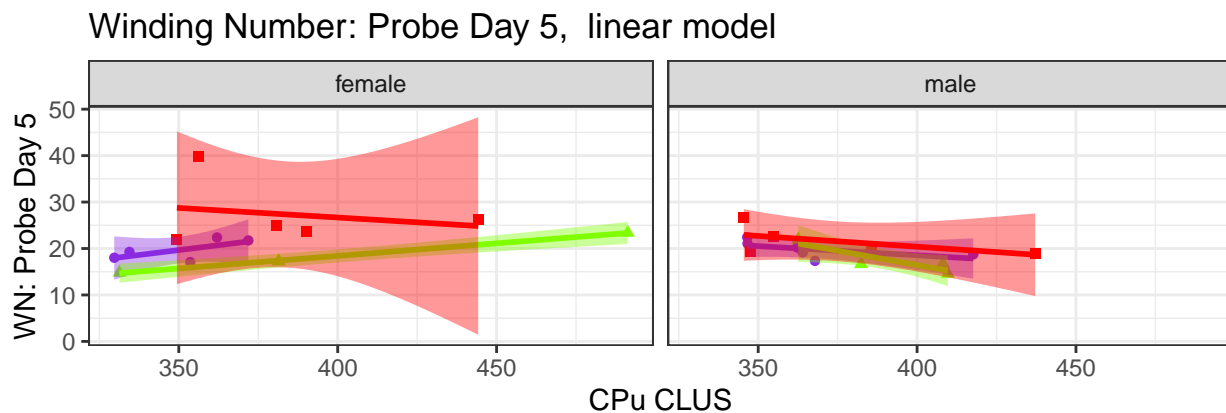
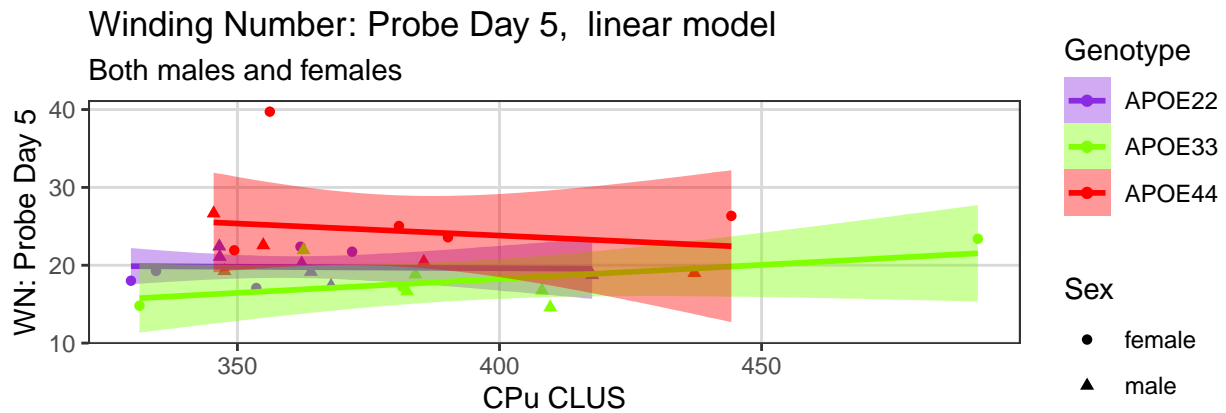
```
## F-statistic: 2.168 on 11 and 17 DF, p-value: 0.07357
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.2171 -2.8335 -0.1636  1.2426 11.2582
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -11.03523    89.76956  -0.123   0.906
## Hc              0.06945     0.20282   0.342   0.742
## GenotypeAPOE33    7.97996    91.75018   0.087   0.933
## GenotypeAPOE44   54.66612    92.77936   0.589   0.574
## Hc:GenotypeAPOE33 -0.02871     0.20588  -0.139   0.893
## Hc:GenotypeAPOE44 -0.10279     0.20834  -0.493   0.637
##
## Residual standard error: 5.434 on 7 degrees of freedom
## Multiple R-squared:  0.5581, Adjusted R-squared:  0.2425
## F-statistic: 1.768 on 5 and 7 DF, p-value: 0.2379
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4184 -0.8581 -0.2731  0.9148  4.5954
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   21.958776   23.704708   0.926   0.376
## Hc            -0.004497    0.049968  -0.090   0.930
## GenotypeAPOE33  21.284657   27.468140   0.775   0.456
## GenotypeAPOE44  13.138544   27.003690   0.487   0.637
## Hc:GenotypeAPOE33 -0.043901    0.056449  -0.778   0.455
## Hc:GenotypeAPOE44 -0.022339    0.056145  -0.398   0.699
##
## Residual standard error: 2.452 on 10 degrees of freedom
## Multiple R-squared:  0.5157, Adjusted R-squared:  0.2736
## F-statistic: 2.13 on 5 and 10 DF, p-value: 0.1446
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value Pr(>F)
## Hc      1   3.709   3.709   0.2363 0.633066
## Genotype 2 204.560 102.280   6.5168 0.007928 **
## Sex      1  31.755  31.755   2.0233 0.172995
## Hc:Genotype 2  47.908  23.954   1.5262 0.245692
## Hc:Sex      1  22.984  22.984   1.4645 0.242780
## Genotype:Sex 2  36.281  18.141   1.1558 0.338336
## Hc:Genotype:Sex 2  27.100  13.550   0.8633 0.439444
```

```
## Residuals      17 266.811  15.695
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1  10.542   10.542   0.3571 0.56897
## Genotype     2 202.377  101.189   3.4272 0.09168 .
## Hc:Genotype   2  48.117   24.058   0.8148 0.48069
## Residuals    7 206.678   29.525
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1  30.756  30.7559   5.1146 0.04724 *
## Genotype     2  28.919   14.4597   2.4046 0.14039
## Hc:Genotype   2   4.368    2.1842   0.3632 0.70423
## Residuals   10  60.133    6.0133
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Day 5 Probe By CPu CLUS



```
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.8371 -0.8096  0.1058  0.8967 11.2501
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -9.77929    37.51142   -0.261    0.797
## CPu              0.08412     0.10696    0.786    0.442
## GenotypeAPOE33    6.54299    39.86883    0.164    0.872
## GenotypeAPOE44   52.97002    42.37485    1.250    0.228
## Sexmale         44.11518    44.61083    0.989    0.337
## CPu:GenotypeAPOE33 -0.03001     0.11199   -0.268    0.792
## CPu:GenotypeAPOE44 -0.12543     0.11855   -1.058    0.305
## CPu:Sexmale      -0.12360     0.12546   -0.985    0.338
## GenotypeAPOE33:Sexmale 25.12820    60.09257    0.418    0.681
## GenotypeAPOE44:Sexmale -48.36573    52.20672   -0.926    0.367
## CPu:GenotypeAPOE33:Sexmale -0.05446     0.16221   -0.336    0.741
## CPu:GenotypeAPOE44:Sexmale  0.11853     0.14425    0.822    0.423
##
## Residual standard error: 3.841 on 17 degrees of freedom
## Multiple R-squared:  0.6088, Adjusted R-squared:  0.3557
## F-statistic: 2.405 on 11 and 17 DF, p-value: 0.05059
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.8371 -2.4273  0.0548  0.9055 11.2501
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -9.77929    52.95190   -0.185    0.859
## CPu              0.08412     0.15099    0.557    0.595
## GenotypeAPOE33    6.54299    56.27967    0.116    0.911
## GenotypeAPOE44   52.97002    59.81722    0.886    0.405
## CPu:GenotypeAPOE33 -0.03001     0.15809   -0.190    0.855
## CPu:GenotypeAPOE44 -0.12543     0.16734   -0.750    0.478
##
## Residual standard error: 5.422 on 7 degrees of freedom
## Multiple R-squared:  0.56, Adjusted R-squared:  0.2457
## F-statistic: 1.782 on 5 and 7 DF, p-value: 0.2351
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5588 -0.6863  0.2669  0.8773  3.7424
```

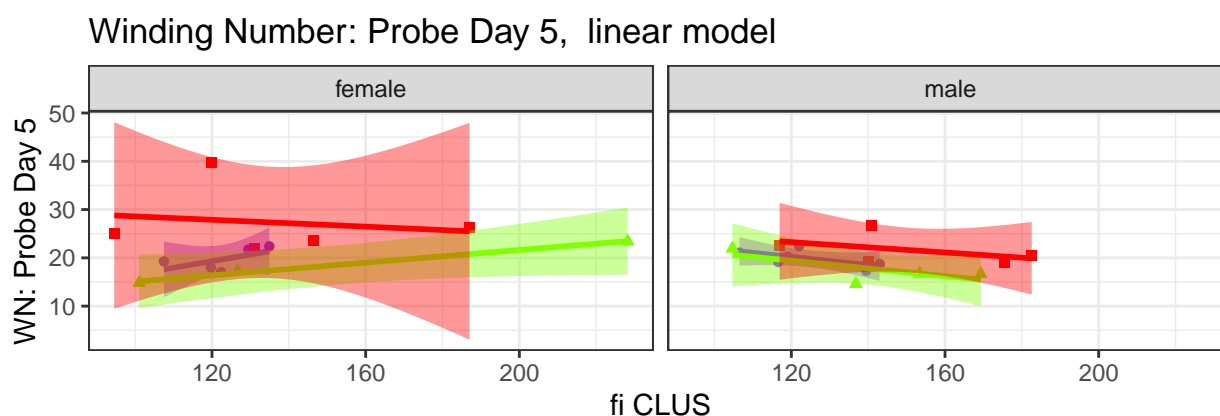
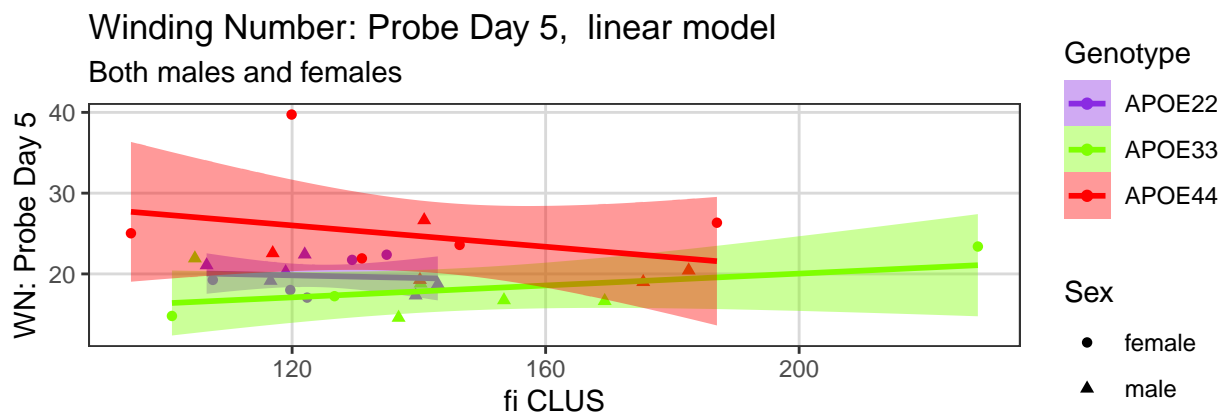
```
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   34.335885  13.337767   2.574   0.0277 *
## CPu           -0.039478   0.036216  -1.090   0.3013
## GenotypeAPOE33 31.671196  24.836392   1.275   0.2311
## GenotypeAPOE44  4.604288  16.844688   0.273   0.7902
## CPu:GenotypeAPOE33 -0.084471  0.064818  -1.303   0.2217
## CPu:GenotypeAPOE44 -0.006899  0.045402  -0.152   0.8822
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.122 on 10 degrees of freedom
## Multiple R-squared:  0.6375, Adjusted R-squared:  0.4562
## F-statistic: 3.517 on 5 and 10 DF,  p-value: 0.0429

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1  0.106   0.106   0.0072 0.933285
## Genotype      2 207.537 103.769   7.0337 0.005946 **
## Sex           1  33.119  33.119   2.2449 0.152397
## CPu:Genotype  2  31.859  15.929   1.0797 0.361876
## CPu:Sex       1  34.668  34.668   2.3499 0.143693
## Genotype:Sex  2  51.791  25.896   1.7553 0.202773
## CPu:Genotype:Sex 2  31.225  15.613   1.0583 0.368844
## Residuals    17 250.803  14.753
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1  27.903  27.903   0.9491 0.36239
## Genotype      2 193.762  96.881   3.2955 0.09805 .
## CPu:Genotype  2  40.262  20.131   0.6848 0.53504
## Residuals     7 205.787  29.398
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1 47.027  47.027 10.4468 0.008988 **
## Genotype      2 23.455  11.728   2.6052 0.122825
## CPu:Genotype  2  8.678   4.339   0.9639 0.414181
## Residuals    10 45.016   4.502
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Day 5 Probe By fi CLUS



```
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.5707 -1.2855 -0.0589  1.0409 11.8439
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.02664    23.42854   0.129   0.899
## fi              0.13572     0.19025   0.713   0.485
## GenotypeAPOE33    5.48222    24.38049   0.225   0.825
## GenotypeAPOE44   29.10415    24.77361   1.175   0.256
## Sexmale          27.27563    28.25234   0.965   0.348
## fi:GenotypeAPOE33 -0.07012     0.19478  -0.360   0.723
## fi:GenotypeAPOE44 -0.17112     0.19885  -0.861   0.401
## fi:Sexmale        -0.21991     0.22832  -0.963   0.349
## GenotypeAPOE33:Sexmale -6.80837    31.35605  -0.217   0.831
## GenotypeAPOE44:Sexmale -29.71573    31.42283  -0.946   0.358
## fi:GenotypeAPOE33:Sexmale  0.07462     0.24645   0.303   0.766
## fi:GenotypeAPOE44:Sexmale  0.20171     0.24653   0.818   0.425
##
## Residual standard error: 3.97 on 17 degrees of freedom
## Multiple R-squared:  0.582, Adjusted R-squared:  0.3115
```

```

## F-statistic: 2.152 on 11 and 17 DF, p-value: 0.07549
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.5707 -2.5653 -0.0862  1.0409 11.8439
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.02664    32.38900   0.093   0.928
## fi              0.13572     0.26301   0.516   0.622
## GenotypeAPOE33  5.48222    33.70503   0.163   0.875
## GenotypeAPOE44 29.10415    34.24849   0.850   0.424
## fi:GenotypeAPOE33 -0.07012     0.26927  -0.260   0.802
## fi:GenotypeAPOE44 -0.17112     0.27490  -0.622   0.553
##
## Residual standard error: 5.489 on 7 degrees of freedom
## Multiple R-squared:  0.5491, Adjusted R-squared:  0.227
## F-statistic: 1.705 on 5 and 7 DF, p-value: 0.2513
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4926 -1.2354 -0.0283  1.0598  4.5174
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    30.302275    9.501954   3.189 0.00967 **
## fi             -0.084184    0.075962  -1.108 0.29370
## GenotypeAPOE33 -1.326149   11.866238  -0.112 0.91323
## GenotypeAPOE44 -0.611576   11.633044  -0.053 0.95911
## fi:GenotypeAPOE33  0.004498    0.090871   0.049 0.96150
## fi:GenotypeAPOE44  0.030595    0.087698   0.349 0.73442
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.389 on 10 degrees of freedom
## Multiple R-squared:  0.5403, Adjusted R-squared:  0.3104
## F-statistic: 2.35 on 5 and 10 DF, p-value: 0.1172
##
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value Pr(>F)
## fi      1    0.185    0.185    0.0117 0.91507
## Genotype 2 207.668 103.834    6.5870 0.00762 **
## Sex      1   32.592   32.592    2.0676 0.16862
## fi:Genotype 2   39.408   19.704    1.2500 0.31155
## fi:Sex     1   50.071   50.071    3.1764 0.09258 .

```

```

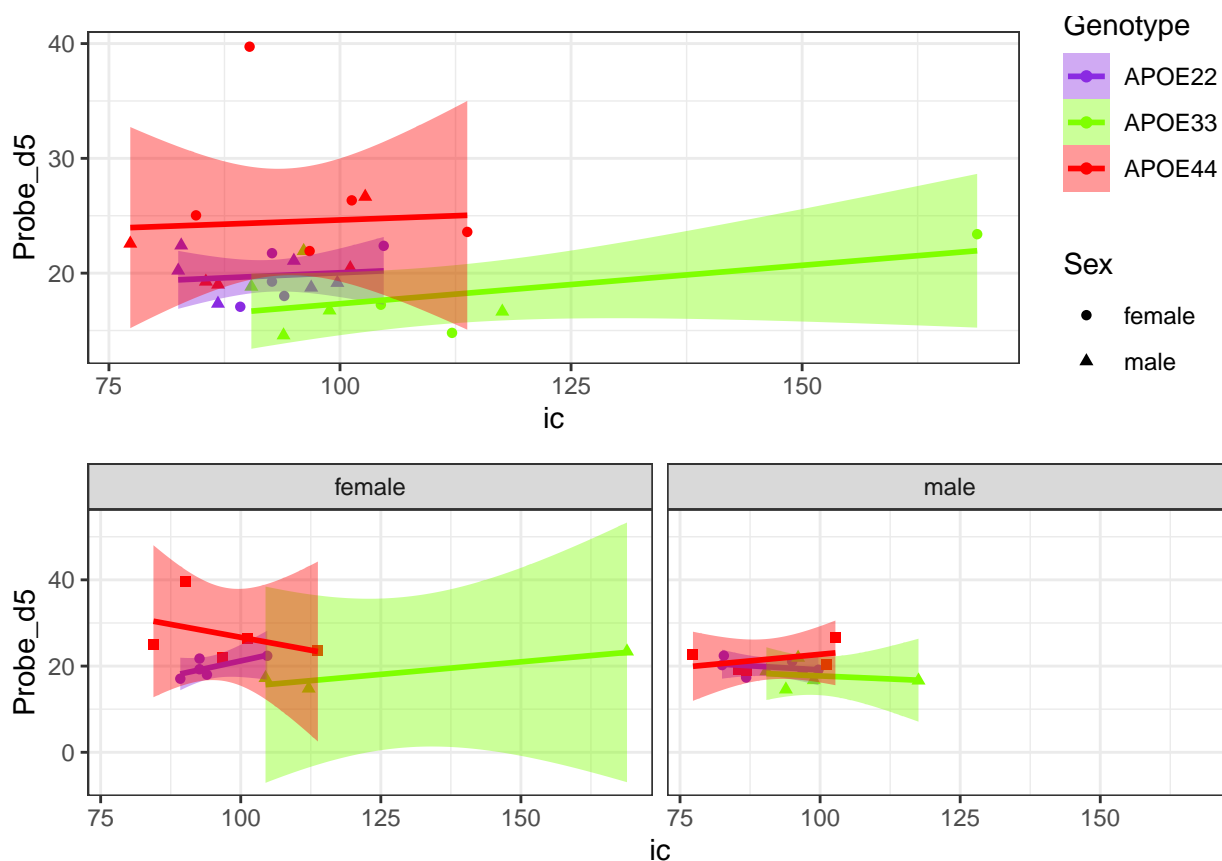
## Genotype:Sex      2  23.133  11.567  0.7338 0.49470
## fi:Genotype:Sex   2  20.075  10.037  0.6368 0.54116
## Residuals        17 267.977  15.763
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fi          1  14.005   14.005   0.4649 0.51727
## Genotype     2 206.587  103.293   3.4286 0.09162 .
## fi:Genotype   2  36.234   18.117   0.6014 0.57410
## Residuals     7 210.888   30.127
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fi          1  13.939   13.939   2.4416 0.14922
## Genotype     2  51.958   25.979   4.5506 0.03933 *
## fi:Genotype   2   1.190    0.5949 0.1042 0.90200
## Residuals    10  57.089    5.7089
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```


Day 5 Probe By ic CLUS



```
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.5368 -1.6892 -0.0694  1.5669 10.7149
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -6.8933    31.7997  -0.217   0.831
## ic              0.2809     0.3355   0.837   0.414
## GenotypeAPOE33  10.4346    33.4816   0.312   0.759
## GenotypeAPOE44  57.5143    36.1939   1.589   0.130
## Sexmale        33.5593    38.3513   0.875   0.394
## ic:GenotypeAPOE33 -0.1647     0.3448  -0.478   0.639
## ic:GenotypeAPOE44 -0.5204     0.3792  -1.372   0.188
## ic:Sexmale      -0.3564     0.4101  -0.869   0.397
## GenotypeAPOE33:Sexmale -13.7586    43.8976  -0.313   0.758
## GenotypeAPOE44:Sexmale -73.6708    45.2243  -1.629   0.122
## ic:GenotypeAPOE33:Sexmale  0.1838     0.4575   0.402   0.693
## ic:GenotypeAPOE44:Sexmale  0.7180     0.4823   1.489   0.155
##
## Residual standard error: 3.966 on 17 degrees of freedom
## Multiple R-squared:  0.583, Adjusted R-squared:  0.3131
```

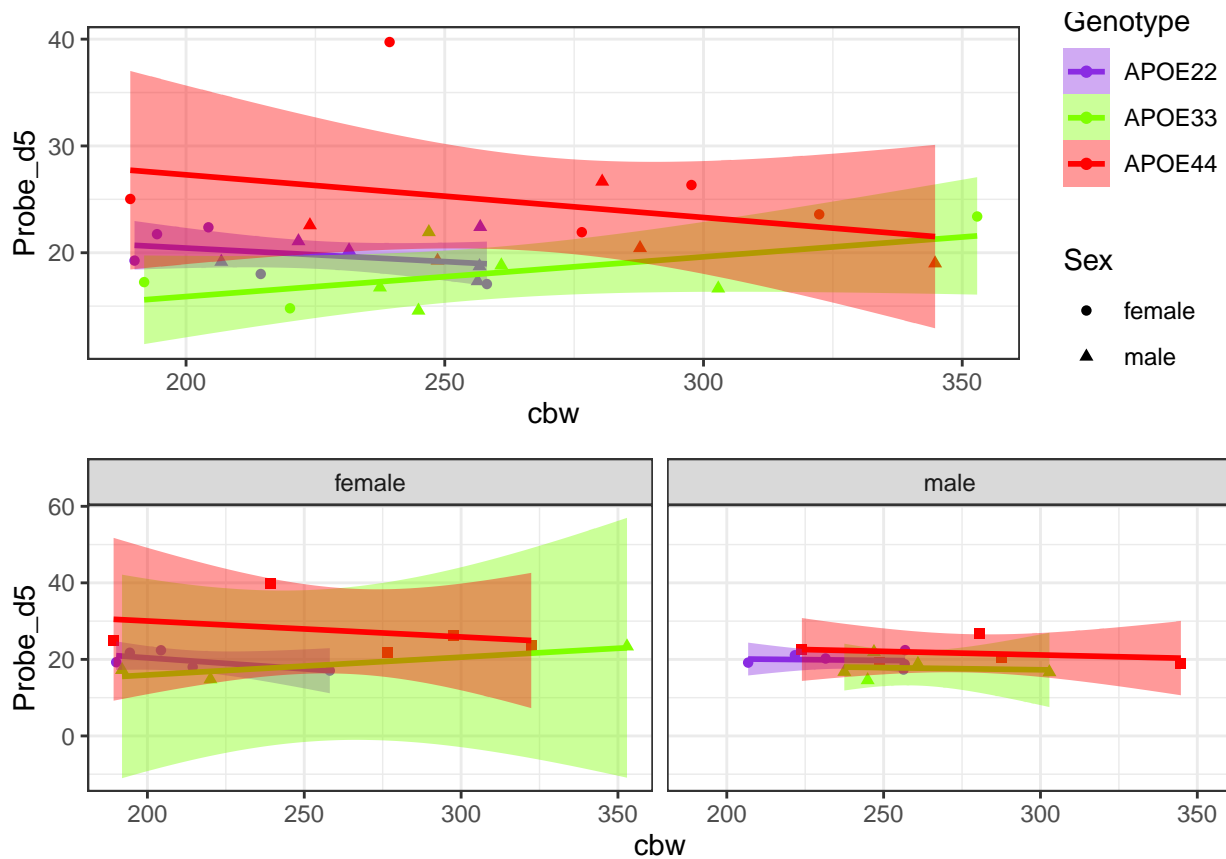
```
## F-statistic: 2.16 on 11 and 17 DF, p-value: 0.07447
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.5368 -1.4939 -0.0276  0.2182 10.7149
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -6.8933     41.8064  -0.165   0.874
## ic              0.2809      0.4411   0.637   0.544
## GenotypeAPOE33  10.4346     44.0175   0.237   0.819
## GenotypeAPOE44  57.5143     47.5833   1.209   0.266
## ic:GenotypeAPOE33 -0.1647      0.4533  -0.363   0.727
## ic:GenotypeAPOE44 -0.5204      0.4985  -1.044   0.331
##
## Residual standard error: 5.214 on 7 degrees of freedom
## Multiple R-squared: 0.5932, Adjusted R-squared: 0.3026
## F-statistic: 2.041 on 5 and 7 DF, p-value: 0.1891
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4739 -1.7942 -0.1414  1.6894  3.9992
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    26.66596    15.00892   1.777   0.106
## ic             -0.07546     0.16515  -0.457   0.657
## GenotypeAPOE33  -3.32399    19.87567  -0.167   0.871
## GenotypeAPOE44 -16.15645    18.98329  -0.851   0.415
## ic:GenotypeAPOE33  0.01917     0.21051   0.091   0.929
## ic:GenotypeAPOE44  0.19763     0.20860   0.947   0.366
##
## Residual standard error: 2.776 on 10 degrees of freedom
## Multiple R-squared: 0.3792, Adjusted R-squared: 0.06886
## F-statistic: 1.222 on 5 and 10 DF, p-value: 0.3669
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value Pr(>F)
## ic      1  0.003   0.003   0.0002 0.989219
## Genotype 2 227.190 113.595   7.2229 0.005364 **
## Sex      1 18.729  18.729   1.1909 0.290376
## ic:Genotype 2  2.461   1.231   0.0782 0.925068
## ic:Sex      1  1.155   1.155   0.0734 0.789698
## Genotype:Sex 2 69.156  34.578   2.1987 0.141502
## ic:Genotype:Sex 2 55.056  27.528   1.7504 0.203600
```

```
## Residuals      17 267.359  15.727
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic          1   2.568    2.568   0.0945 0.76751
## Genotype     2 215.165  107.583   3.9578 0.07081 .
## ic:Genotype  2   59.706   29.853   1.0983 0.38474
## Residuals    7  190.275   27.182
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic          1   3.791    3.7912  0.4918 0.4991
## Genotype     2  33.278   16.6389  2.1585 0.1662
## ic:Genotype  2  10.024    5.0120  0.6502 0.5427
## Residuals   10  77.084    7.7084
```

Day 5 Probe By cbw CLUS



##

```

## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4429 -1.5568 -0.6023  1.0977 11.3372
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      31.94460    16.05984   1.989   0.063 .
## cbw              -0.05772     0.07516  -0.768   0.453
## GenotypeAPOE33   -25.32038    18.37707  -1.378   0.186
## GenotypeAPOE44     6.40618    19.23721   0.333   0.743
## Sexmale          -10.14705    25.94911  -0.391   0.701
## cbw:GenotypeAPOE33  0.10422     0.08241   1.265   0.223
## cbw:GenotypeAPOE44  0.01611     0.08484   0.190   0.852
## cbw:Sexmale        0.04946     0.11364   0.435   0.669
## GenotypeAPOE33:Sexmale 24.14641    34.19370   0.706   0.490
## GenotypeAPOE44:Sexmale -1.42026    30.72735  -0.046   0.964
## cbw:GenotypeAPOE33:Sexmale -0.10707    0.14222  -0.753   0.462
## cbw:GenotypeAPOE44:Sexmale -0.02659    0.12840  -0.207   0.838
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.107 on 17 degrees of freedom
## Multiple R-squared:  0.5527, Adjusted R-squared:  0.2633
## F-statistic:  1.91 on 11 and 17 DF, p-value: 0.1117
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4429 -1.7118  0.0255  1.0148 11.3372
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      31.94460    21.05620   1.517   0.173
## cbw              -0.05772     0.09855  -0.586   0.576
## GenotypeAPOE33   -25.32038    24.09434  -1.051   0.328
## GenotypeAPOE44     6.40618    25.22207   0.254   0.807
## cbw:GenotypeAPOE33  0.10422     0.10804   0.965   0.367
## cbw:GenotypeAPOE44  0.01611     0.11124   0.145   0.889
##
## Residual standard error: 5.385 on 7 degrees of freedom
## Multiple R-squared:  0.566, Adjusted R-squared:  0.256
## F-statistic: 1.826 on 5 and 7 DF, p-value: 0.2264
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max

```

```

## -3.3184 -1.2521 -0.7672  1.1027  5.1341
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    21.797551  14.364747   1.517   0.160
## cbw            -0.008266   0.060069  -0.138   0.893
## GenotypeAPOE33 -1.173970  20.322361  -0.058   0.955
## GenotypeAPOE44  4.985917  16.886470   0.295   0.774
## cbw:GenotypeAPOE33 -0.002851   0.081689  -0.035   0.973
## cbw:GenotypeAPOE44 -0.010481   0.067919  -0.154   0.880
##
## Residual standard error: 2.895 on 10 degrees of freedom
## Multiple R-squared:  0.3253, Adjusted R-squared:  -0.01207
## F-statistic: 0.9642 on 5 and 10 DF,  p-value: 0.4832

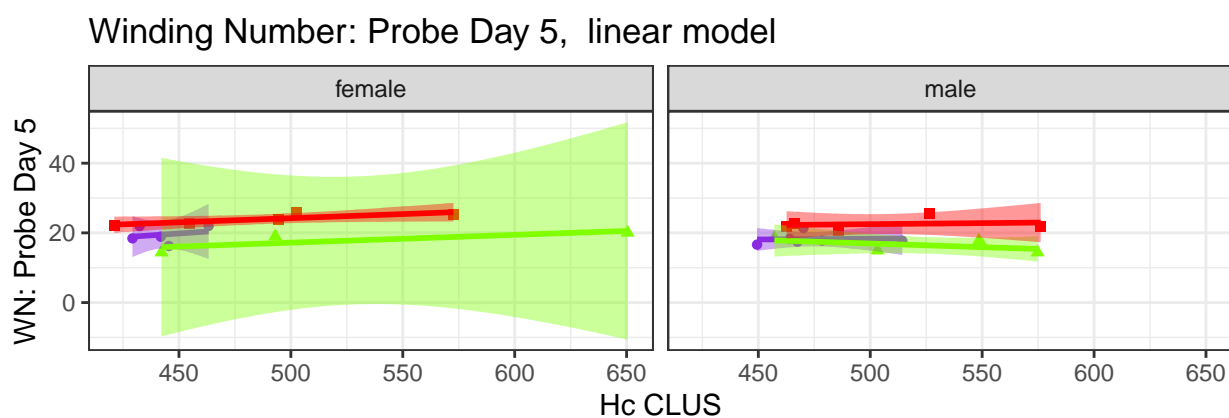
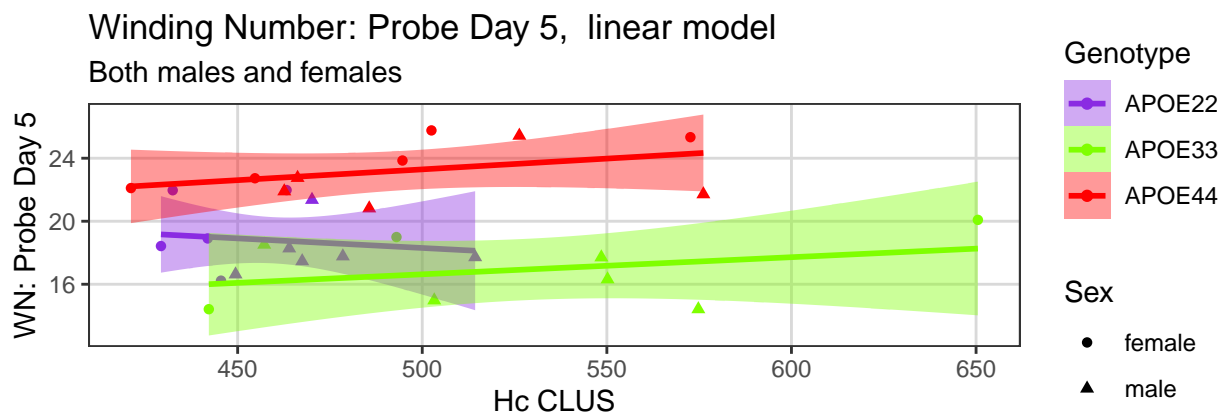
## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## cbw            1  5.732   5.732   0.3398 0.56761
## Genotype       2 203.343 101.671   6.0274 0.01051 *
## Sex            1  31.074  31.074   1.8422 0.19245
## cbw:Genotype   2  51.780  25.890   1.5348 0.24391
## cbw:Sex        1   6.703   6.703   0.3974 0.53684
## Genotype:Sex   2  42.583  21.292   1.2622 0.30824
## cbw:Genotype:Sex 2  13.133   6.567   0.3893 0.68343
## Residuals     17 286.761  16.868
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## cbw            1  21.32   21.320   0.7353 0.4196
## Genotype       2 182.79   91.393   3.1518 0.1057
## cbw:Genotype   2  60.63   30.315   1.0455 0.4006
## Residuals      7 202.98   28.997

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## cbw            1  0.122   0.1216   0.0145 0.9065
## Genotype       2 40.010  20.0048   2.3877 0.1420
## cbw:Genotype   2  0.262   0.1309   0.0156 0.9845
## Residuals     10 83.784   8.3784

```

Day 8 Probe By Hc CLUS



```
##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4072 -0.7136 -0.4157  0.6722  3.1713
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.154247   32.563320   0.005   0.996
## Hc              0.043727    0.073570   0.594   0.560
## GenotypeAPOE33    5.834486   33.281779   0.175   0.863
## GenotypeAPOE44   12.249771   33.655104   0.364   0.720
## Sexmale         16.235909   37.728063   0.430   0.672
## Hc:GenotypeAPOE33 -0.021319    0.074681  -0.285   0.779
## Hc:GenotypeAPOE44 -0.020105    0.075575  -0.266   0.793
## Hc:Sexmale       -0.039901    0.083820  -0.476   0.640
## GenotypeAPOE33:Sexmale  5.186597   39.939181   0.130   0.898
## GenotypeAPOE44:Sexmale -9.118977   40.047248  -0.228   0.823
## Hc:GenotypeAPOE33:Sexmale -0.003435    0.087384  -0.039   0.969
## Hc:GenotypeAPOE44:Sexmale  0.022244    0.088023   0.253   0.804
##
## Residual standard error: 1.971 on 17 degrees of freedom
## Multiple R-squared:  0.7797, Adjusted R-squared:  0.6372
```

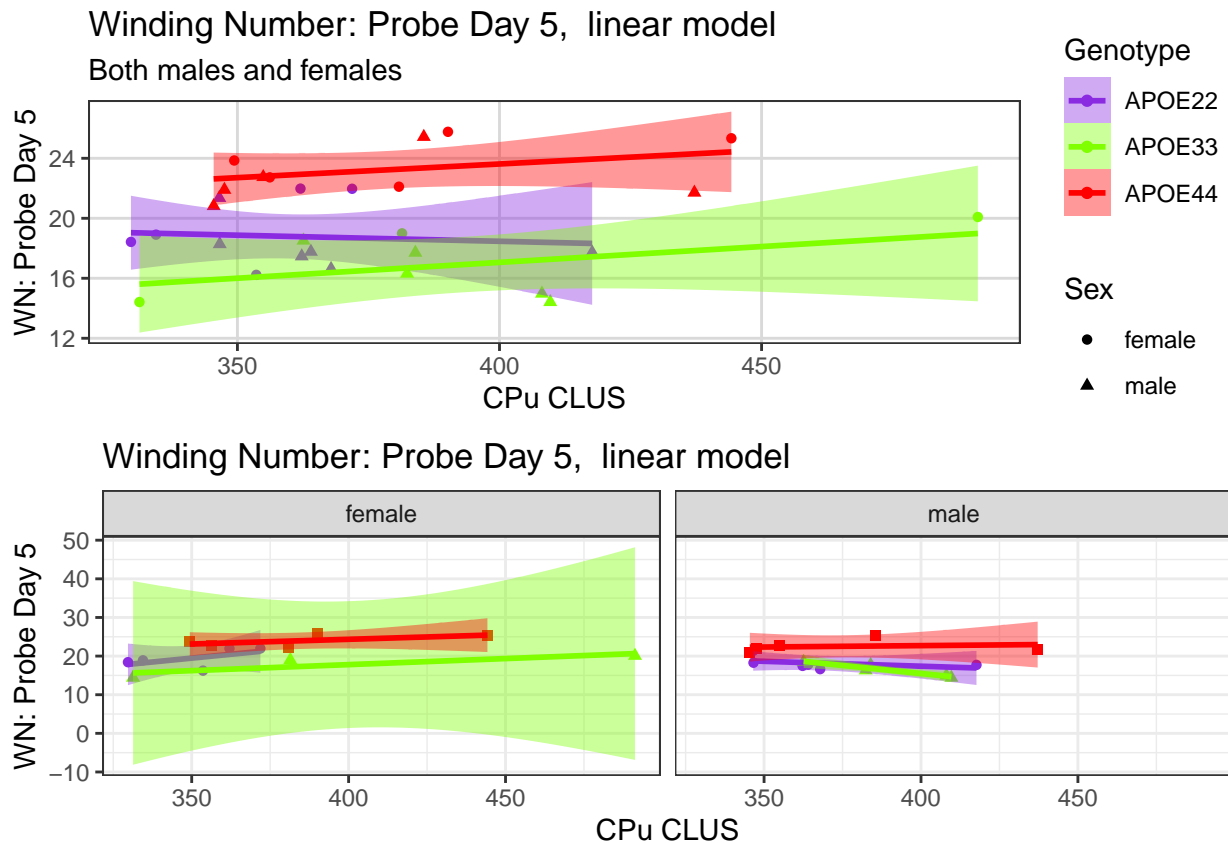
```
## F-statistic: 5.47 on 11 and 17 DF, p-value: 0.0009722
##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4072 -0.5681 -0.4157  1.4910  2.9049
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.15425   35.43554   0.004   0.997
## Hc              0.04373    0.08006   0.546   0.602
## GenotypeAPOE33  5.83449   36.21737   0.161   0.877
## GenotypeAPOE44 12.24977   36.62362   0.334   0.748
## Hc:GenotypeAPOE33 -0.02132    0.08127  -0.262   0.801
## Hc:GenotypeAPOE44 -0.02011    0.08224  -0.244   0.814
##
## Residual standard error: 2.145 on 7 degrees of freedom
## Multiple R-squared: 0.7655, Adjusted R-squared: 0.5981
## F-statistic: 4.571 on 5 and 7 DF, p-value: 0.03584
##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9007 -1.0347 -0.4135  0.5060  3.1713
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  16.390156  17.782857   0.922   0.378
## Hc            0.003826   0.037485   0.102   0.921
## GenotypeAPOE33 11.021083  20.606118   0.535   0.604
## GenotypeAPOE44  3.130794  20.257696   0.155   0.880
## Hc:GenotypeAPOE33 -0.024754   0.042347  -0.585   0.572
## Hc:GenotypeAPOE44  0.002138   0.042119   0.051   0.961
##
## Residual standard error: 1.84 on 10 degrees of freedom
## Multiple R-squared: 0.7548, Adjusted R-squared: 0.6323
## F-statistic: 6.158 on 5 and 10 DF, p-value: 0.007379
## Analysis of Variance Table
##
## Response: Probe_d8
##      Df Sum Sq Mean Sq F value    Pr(>F)
## Hc      1  0.956    0.956    0.2460  0.62624
## Genotype 2 200.220 100.110 25.7680 7.137e-06 ***
## Sex      1 17.562   17.562   4.5204  0.04844 *
## Hc:Genotype 2  0.418    0.209   0.0538  0.94779
## Hc:Sex      1  8.179    8.179   2.1052  0.16500
## Genotype:Sex 2  4.459    2.230   0.5739  0.57388
## Hc:Genotype:Sex 2  1.959    0.979   0.2521  0.78002
```

```
## Residuals      17  66.046   3.885
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Hc          1  13.038   13.038   2.8339  0.136169
## Genotype     2  91.795   45.898   9.9764  0.008928 **
## Hc:Genotype  2   0.319    0.160   0.0347  0.966038
## Residuals    7  32.204    4.601
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Hc          1   2.891    2.891   0.8544  0.377084
## Genotype     2  97.815   48.907  14.4520  0.001122 **
## Hc:Genotype  2   3.488    1.744   0.5154  0.612307
## Residuals   10  33.841    3.384
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Day 8 Probe By CPu CLUS




```
##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5353 -0.6546 -0.1020  0.7443  2.8252
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -8.489937   17.183388  -0.494   0.6276
## CPu              0.079899    0.048997   1.631   0.1213
## GenotypeAPOE33   13.768454   18.263279   0.754   0.4612
## GenotypeAPOE44   23.070760   19.411249   1.189   0.2510
## Sexmale         36.026354   20.435513   1.763   0.0959 .
## CPu:GenotypeAPOE33 -0.048617    0.051303  -0.948   0.3566
## CPu:GenotypeAPOE44 -0.055490    0.054304  -1.022   0.3212
## CPu:Sexmale      -0.105294    0.057469  -1.832   0.0845 .
## GenotypeAPOE33:Sexmale  7.569013   27.527452   0.275   0.7867
## GenotypeAPOE44:Sexmale -30.771575   23.915072  -1.287   0.2154
## CPu:GenotypeAPOE33:Sexmale -0.009429    0.074306  -0.127   0.9005
## CPu:GenotypeAPOE44:Sexmale  0.088069    0.066080   1.333   0.2002
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.759 on 17 degrees of freedom
## Multiple R-squared:  0.8245, Adjusted R-squared:  0.7109
## F-statistic: 7.258 on 11 and 17 DF, p-value: 0.0001752
##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5353 -0.5594  0.5735  0.7443  1.7859
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -8.48994   19.52393  -0.435   0.677
## CPu              0.07990    0.05567   1.435   0.194
## GenotypeAPOE33   13.76845   20.75092   0.664   0.528
## GenotypeAPOE44   23.07076   22.05525   1.046   0.330
## CPu:GenotypeAPOE33 -0.04862    0.05829  -0.834   0.432
## CPu:GenotypeAPOE44 -0.05549    0.06170  -0.899   0.398
##
## Residual standard error: 1.999 on 7 degrees of freedom
## Multiple R-squared:  0.7963, Adjusted R-squared:  0.6508
## F-statistic: 5.474 on 5 and 7 DF, p-value: 0.02286
##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_m_CLUS)
##
## Residuals:
```

```

##      Min      1Q  Median      3Q      Max
## -1.5684 -0.7088 -0.3510  0.4729  2.8252
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    27.53642    9.87030   2.790  0.0191 *
## CPu            -0.02540    0.02680  -0.948  0.3657
## GenotypeAPOE33  21.33747   18.37958   1.161  0.2726
## GenotypeAPOE44  -7.70082   12.46551  -0.618  0.5505
## CPu:GenotypeAPOE33 -0.05805    0.04797  -1.210  0.2541
## CPu:GenotypeAPOE44  0.03258    0.03360   0.970  0.3551
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.57 on 10 degrees of freedom
## Multiple R-squared:  0.8214, Adjusted R-squared:  0.7321
## F-statistic: 9.199 on 5 and 10 DF,  p-value: 0.001674

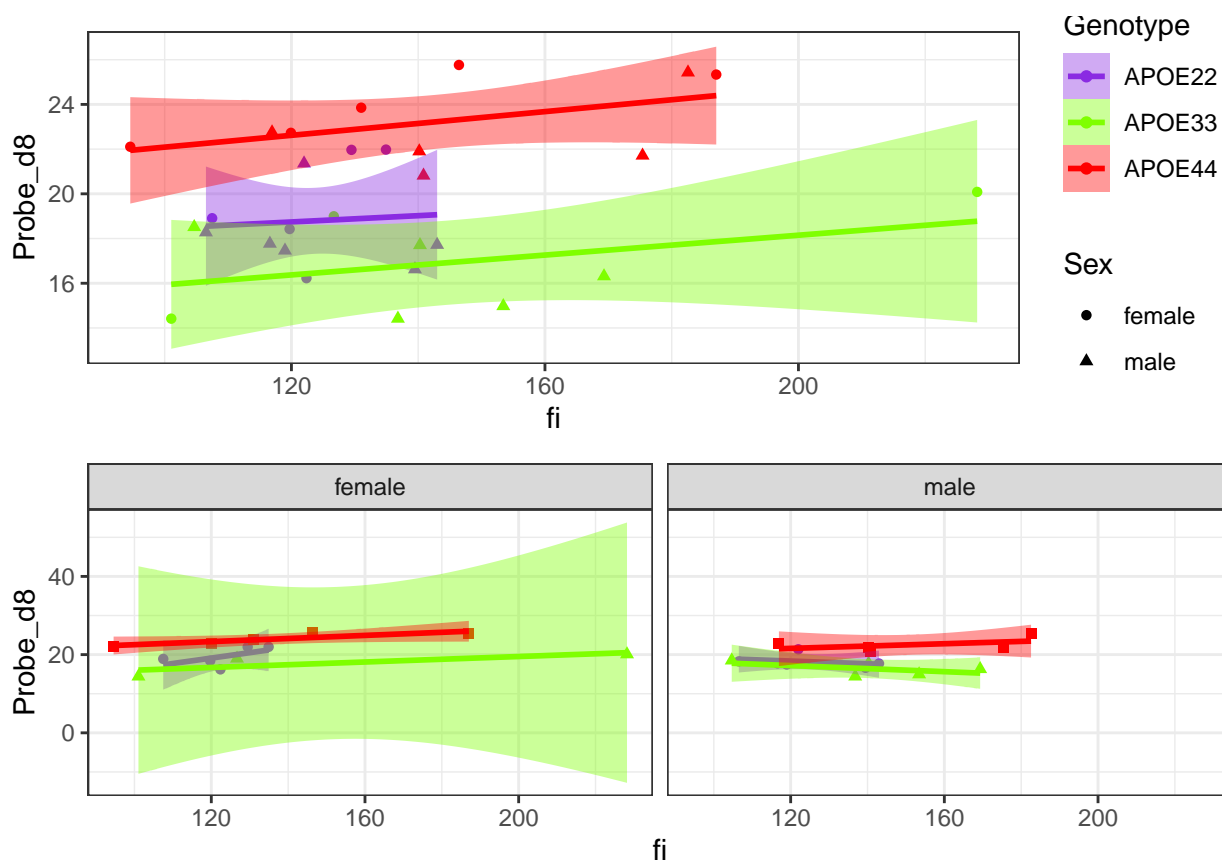
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu            1   3.630    3.630   1.1724  0.29402
## Genotype       2 199.270   99.635  32.1837 1.66e-06 ***
## Sex            1  13.596   13.596   4.3916  0.05139 .
## CPu:Genotype   2   1.032    0.516   0.1667  0.84780
## CPu:Sex        1  13.840   13.840   4.4707  0.04956 *
## Genotype:Sex   2   4.382    2.191   0.7077  0.50675
## CPu:Genotype:Sex 2  11.420    5.710   1.8444  0.18839
## Residuals     17  52.629    3.096
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu            1  20.604   20.604   5.1554 0.057431 .
## Genotype       2  85.490   42.745  10.6953 0.007443 **
## CPu:Genotype   2   3.287    1.643   0.4112 0.677890
## Residuals      7  27.976    3.997
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu            1   9.405    9.405   3.8151 0.0793237 .
## Genotype       2  93.363   46.682  18.9359 0.0003977 ***
## CPu:Genotype   2  10.615    5.307   2.1529 0.1668916
## Residuals     10  24.653    2.465
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By fi CLUS



```
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.2160 -0.9189 -0.2939  1.2458  3.0720
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.50281    10.76810   0.232   0.819
## fi              0.13843     0.08744   1.583   0.132
## GenotypeAPOE33    10.01245    11.20563   0.894   0.384
## GenotypeAPOE44    16.08950    11.38631   1.413   0.176
## Sexmale          20.02242    12.98519   1.542   0.141
## fi:GenotypeAPOE33 -0.10344     0.08952  -1.156   0.264
## fi:GenotypeAPOE44 -0.09892     0.09139  -1.082   0.294
## fi:Sexmale        -0.17317     0.10494  -1.650   0.117
## GenotypeAPOE33:Sexmale -10.65106    14.41170  -0.739   0.470
## GenotypeAPOE44:Sexmale -20.58066    14.44239  -1.425   0.172
## fi:GenotypeAPOE33:Sexmale  0.09914     0.11327   0.875   0.394
## fi:GenotypeAPOE44:Sexmale  0.16335     0.11331   1.442   0.168
##
## Residual standard error: 1.825 on 17 degrees of freedom
## Multiple R-squared:  0.8112, Adjusted R-squared:  0.689
```

```
## F-statistic: 6.639 on 11 and 17 DF, p-value: 0.0003057
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.2160 -0.6463 -0.2237  1.3868  2.0476
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.50281    11.35041   0.221   0.832
## fi              0.13843     0.09217   1.502   0.177
## GenotypeAPOE33    10.01245    11.81160   0.848   0.425
## GenotypeAPOE44    16.08950    12.00205   1.341   0.222
## fi:GenotypeAPOE33 -0.10344     0.09436  -1.096   0.309
## fi:GenotypeAPOE44 -0.09892     0.09634  -1.027   0.339
##
## Residual standard error: 1.923 on 7 degrees of freedom
## Multiple R-squared:  0.8114, Adjusted R-squared:  0.6768
## F-statistic: 6.025 on 5 and 7 DF, p-value: 0.01782
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.1292 -0.9594 -0.4208  1.0890  3.0720
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    22.525236     6.969095   3.232 0.00899 **
## fi             -0.034734     0.055714  -0.623 0.54695
## GenotypeAPOE33 -0.638608     8.703150  -0.073 0.94295
## GenotypeAPOE44 -4.491163     8.532117  -0.526 0.61010
## fi:GenotypeAPOE33 -0.004302     0.066649  -0.065 0.94981
## fi:GenotypeAPOE44  0.064426     0.064321   1.002 0.34014
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.752 on 10 degrees of freedom
## Multiple R-squared:  0.7775, Adjusted R-squared:  0.6663
## F-statistic: 6.99 on 5 and 10 DF, p-value: 0.004704
##
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fi              1  19.263   19.263   5.7847  0.02784 *
## Genotype        2 187.755   93.878  28.1920 3.992e-06 ***
## Sex              1  15.144   15.144   4.5479  0.04784 *
## fi:Genotype      2   0.991    0.495   0.1488  0.86288
## fi:Sex           1  10.187   10.187   3.0592  0.09831 .
```

```

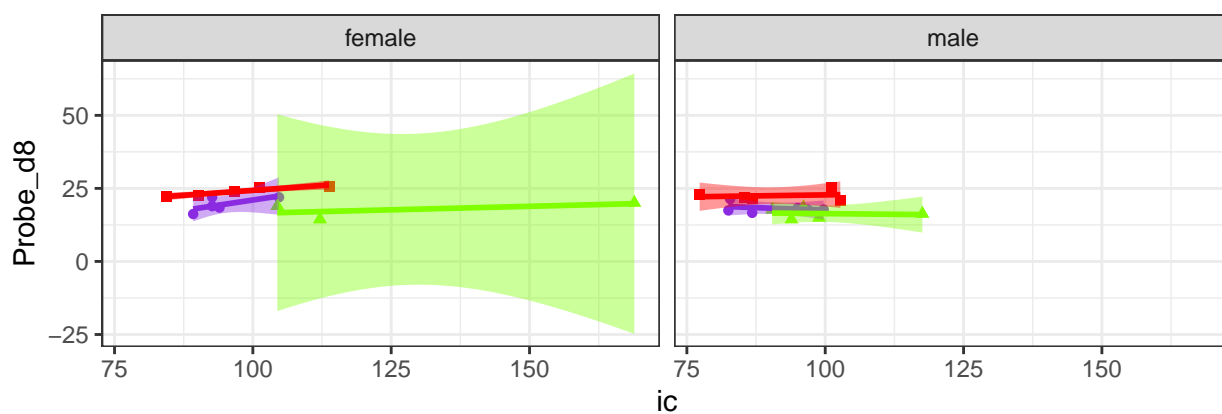
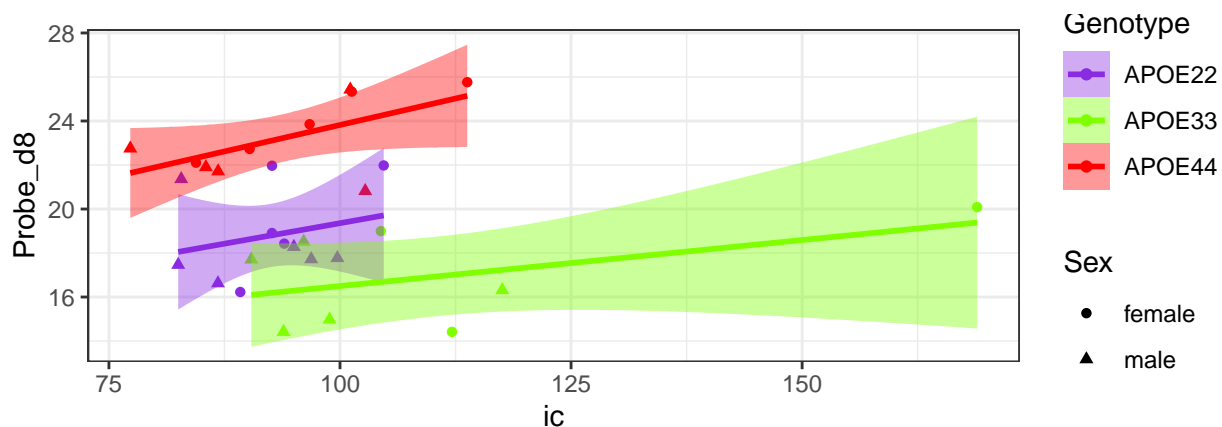
## Genotype:Sex      2   1.278   0.639   0.1919   0.82717
## fi:Genotype:Sex   2   8.571   4.285   1.2869   0.30169
## Residuals        17  56.609   3.330
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fi           1  16.059   16.059   4.3404 0.075708 .
## Genotype     2  90.953   45.476  12.2915 0.005126 **
## fi:Genotype   2   4.446    2.223   0.6009 0.574333
## Residuals    7  25.899    3.700
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fi           1   6.039    6.039   1.9664 0.1911001
## Genotype     2  94.179   47.089  15.3335 0.0008991 ***
## fi:Genotype   2   7.108    3.554   1.1573 0.3531108
## Residuals   10  30.710    3.071
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By ic CLUS



```
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.63145 -0.88545 -0.05743  0.59757  3.03328
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -7.4313    15.3978  -0.483   0.6355
## ic              0.2846     0.1624   1.752   0.0978 .
## GenotypeAPOE33  19.1013    16.2122   1.178   0.2549
## GenotypeAPOE44  18.2768    17.5256   1.043   0.3116
## Sexmale        31.7955    18.5702   1.712   0.1050
## ic:GenotypeAPOE33 -0.2366     0.1670  -1.417   0.1745
## ic:GenotypeAPOE44 -0.1498     0.1836  -0.816   0.4259
## ic:Sexmale      -0.3526     0.1986  -1.775   0.0937 .
## GenotypeAPOE33:Sexmale -25.1692    21.2558  -1.184   0.2527
## GenotypeAPOE44:Sexmale -22.6161    21.8982  -1.033   0.3162
## ic:GenotypeAPOE33:Sexmale  0.2854     0.2215   1.288   0.2149
## ic:GenotypeAPOE44:Sexmale  0.2453     0.2335   1.051   0.3082
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.92 on 17 degrees of freedom
## Multiple R-squared:  0.7909, Adjusted R-squared:  0.6556
## F-statistic: 5.846 on 11 and 17 DF,  p-value: 0.0006592

##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6315 -0.4158 -0.1191  0.3140  3.0333
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -7.4313     15.6010  -0.476   0.648
## ic              0.2846      0.1646   1.729   0.127
## GenotypeAPOE33  19.1013     16.4261   1.163   0.283
## GenotypeAPOE44  18.2768     17.7568   1.029   0.338
## ic:GenotypeAPOE33 -0.2366      0.1692  -1.399   0.205
## ic:GenotypeAPOE44 -0.1498      0.1860  -0.805   0.447
##
## Residual standard error: 1.946 on 7 degrees of freedom
## Multiple R-squared:  0.8071, Adjusted R-squared:  0.6693
## F-statistic: 5.857 on 5 and 7 DF,  p-value: 0.01919

##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.07437 -1.32249  0.06453  0.73558  2.62643
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    24.36424    10.28376   2.369   0.0393 *
## ic             -0.06799     0.11316  -0.601   0.5613
## GenotypeAPOE33  -6.06792    13.61835  -0.446   0.6654
## GenotypeAPOE44  -4.33934    13.00691  -0.334   0.7456
## ic:GenotypeAPOE33  0.04876     0.14424   0.338   0.7423
## ic:GenotypeAPOE44  0.09553     0.14293   0.668   0.5190
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.902 on 10 degrees of freedom
## Multiple R-squared:  0.7378, Adjusted R-squared:  0.6068
## F-statistic: 5.629 on 5 and 10 DF,  p-value: 0.01005

## Analysis of Variance Table
##
## Response: Probe_d8
##      Df Sum Sq Mean Sq F value    Pr(>F)
## ic      1  0.116    0.116   0.0315   0.8613
## Genotype 2 213.103 106.551 28.8961 3.397e-06 ***
## Sex      1  4.865    4.865   1.3195   0.2666

```

```

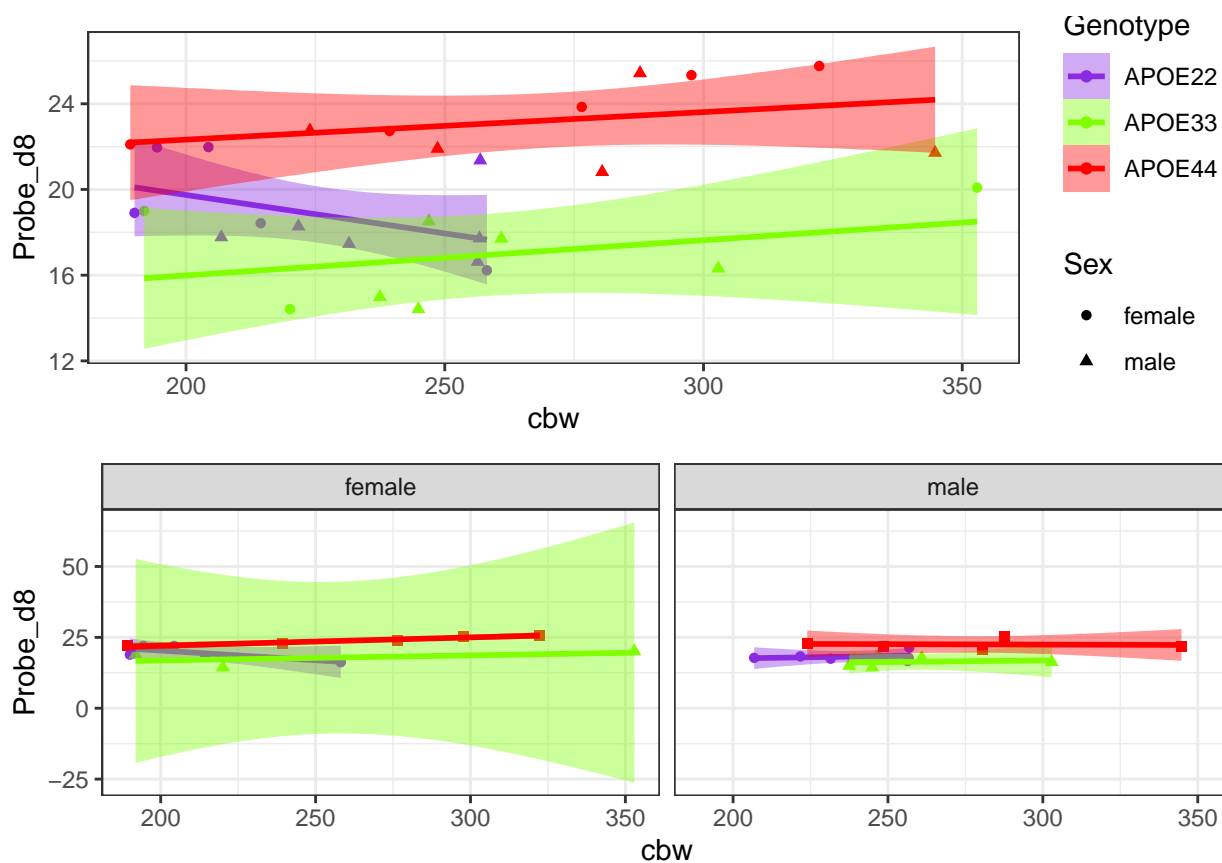
## ic:Genotype      2   2.406   1.203   0.3263   0.7260
## ic:Sex            1   7.447   7.447   2.0197   0.1734
## Genotype:Sex      2   3.014   1.507   0.4086   0.6709
## ic:Genotype:Sex   2   6.161   3.081   0.8354   0.4507
## Residuals        17  62.686   3.687
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1   0.238    0.238    0.0628  0.809392
## Genotype        2 100.888   50.444   13.3263  0.004105 **
## ic:Genotype     2   9.734    4.867    1.2857  0.334522
## Residuals       7  26.497    3.785
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1 10.999   10.999    3.0394  0.111870
## Genotype        2  89.197   44.598   12.3240  0.002003 **
## ic:Genotype     2   1.652    0.826    0.2282  0.799992
## Residuals      10 36.188    3.619
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```


Day 8 Probe By cbw CLUS



```
##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7880 -0.7888 -0.1535  0.4882  2.9380
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    33.94133     7.44500   4.559 0.000278 ***
## cbw            -0.06803     0.03484  -1.952 0.067562 .
## GenotypeAPOE33 -20.70565     8.51922  -2.430 0.026443 *
## GenotypeAPOE44 -17.75571     8.91796  -1.991 0.062803 .
## Sexmale        -19.69532    12.02946  -1.637 0.119953
## cbw:GenotypeAPOE33  0.08606     0.03820   2.253 0.037775 *
## cbw:GenotypeAPOE44  0.09736     0.03933   2.475 0.024139 *
## cbw:Sexmale        0.08463     0.05268   1.607 0.126574
## GenotypeAPOE33:Sexmale 19.84642    15.85148   1.252 0.227514
## GenotypeAPOE44:Sexmale 26.83209    14.24455   1.884 0.076831 .
## cbw:GenotypeAPOE33:Sexmale -0.09106     0.06593  -1.381 0.185086
## cbw:GenotypeAPOE44:Sexmale -0.11684     0.05952  -1.963 0.066215 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.904 on 17 degrees of freedom
## Multiple R-squared:  0.7944, Adjusted R-squared:  0.6614
## F-statistic: 5.973 on 11 and 17 DF,  p-value: 0.0005802

##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7880 -0.4756  0.1253  0.4882  2.2998
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    33.94133     7.34255   4.623  0.00242 **
## cbw             -0.06803     0.03436  -1.980  0.08823 .
## GenotypeAPOE33  -20.70565     8.40198  -2.464  0.04319 *
## GenotypeAPOE44  -17.75571     8.79524  -2.019  0.08328 .
## cbw:GenotypeAPOE33  0.08606     0.03768   2.284  0.05629 .
## cbw:GenotypeAPOE44  0.09736     0.03879   2.510  0.04041 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 1.878 on 7 degrees of freedom
## Multiple R-squared:  0.8203, Adjusted R-squared:  0.692
## F-statistic: 6.391 on 5 and 7 DF,  p-value: 0.01524

##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8770 -0.8823 -0.6005  0.5865  2.9380
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    14.246011     9.538765   1.493   0.166
## cbw             0.016605     0.039889   0.416   0.686
## GenotypeAPOE33  -0.859229    13.494858  -0.064   0.950
## GenotypeAPOE44   9.076385    11.213289   0.809   0.437
## cbw:GenotypeAPOE33 -0.005006     0.054245  -0.092   0.928
## cbw:GenotypeAPOE44 -0.019490     0.045101  -0.432   0.675
##
## Residual standard error: 1.922 on 10 degrees of freedom
## Multiple R-squared:  0.7324, Adjusted R-squared:  0.5985
## F-statistic: 5.473 on 5 and 10 DF,  p-value: 0.01104

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## cbw         1  21.974   21.974    6.0616  0.02480 *
## Genotype    2 175.285   87.643   24.1767 1.069e-05 ***
## Sex         1  16.213   16.213    4.4723  0.04952 *

```

```

## cbw:Genotype      2    8.722    4.361    1.2030    0.32461
## cbw:Sex           1    1.269    1.269    0.3499    0.56193
## Genotype:Sex      2    0.739    0.369    0.1019    0.90365
## cbw:Genotype:Sex  2   13.970    6.985    1.9269    0.17610
## Residuals        17   61.626    3.625
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

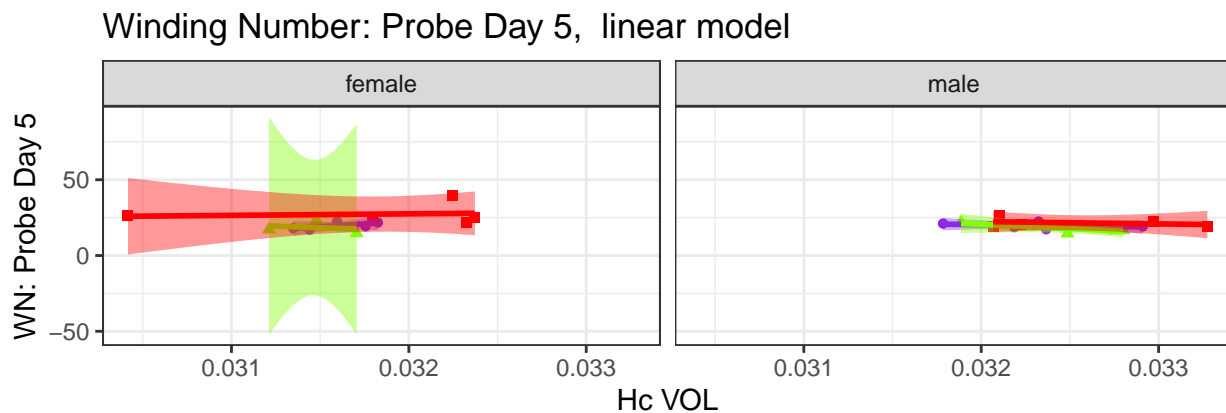
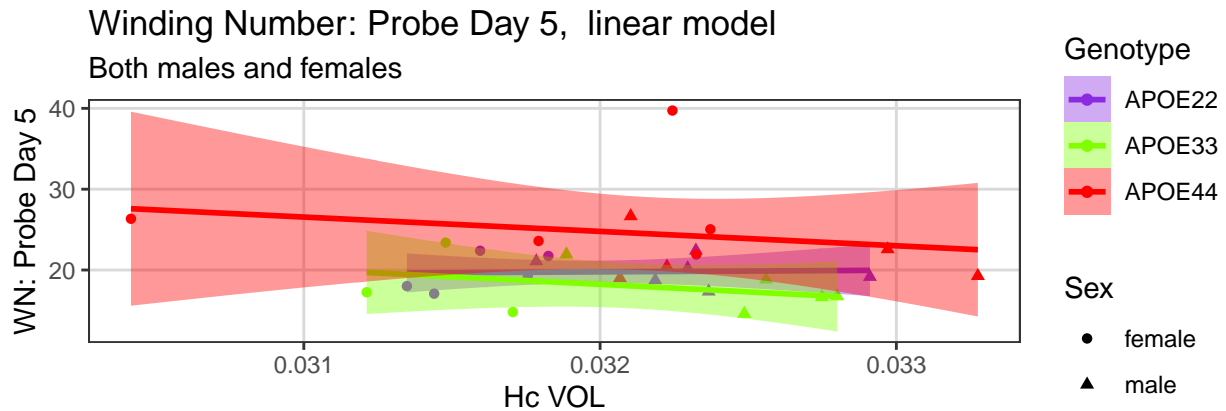
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw           1  18.725   18.725   5.3107 0.054629 .
## Genotype      2  71.072   35.536  10.0783 0.008695 **
## cbw:Genotype  2  22.877   11.439   3.2440 0.100697
## Residuals     7  24.682    3.526
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw           1  12.512   12.512   3.3867 0.095551 .
## Genotype      2  87.661   43.831  11.8639 0.002291 **
## cbw:Genotype  2   0.918    0.459   0.1242 0.884502
## Residuals    10  36.944    3.694
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Volume

Day 5 Probe By Hc VOL



```
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.9045 -2.2851  0.2789  0.7352 11.9846
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -216.2     335.8   -0.644   0.528
## Hc             7466.1    10627.7    0.703   0.492
## GenotypeAPOE33    365.5     513.0    0.713   0.486
## GenotypeAPOE44    211.1     345.9    0.610   0.550
## Sexmale         287.3     377.1    0.762   0.457
## Hc:GenotypeAPOE33 -11624.7  16274.5  -0.714   0.485
## Hc:GenotypeAPOE44 -6449.3   10944.7  -0.589   0.563
## Hc:Sexmale       -9052.3   11882.8  -0.762   0.457
## GenotypeAPOE33:Sexmale -233.7    573.9  -0.407   0.689
## GenotypeAPOE44:Sexmale -210.3    406.2  -0.518   0.611
## Hc:GenotypeAPOE33:Sexmale 7513.3  18108.7   0.415   0.683
## Hc:GenotypeAPOE44:Sexmale 6488.5  12767.3   0.508   0.618
##
## Residual standard error: 4.305 on 17 degrees of freedom
## Multiple R-squared:  0.5087, Adjusted R-squared:  0.1907
```

```
## F-statistic: 1.6 on 11 and 17 DF, p-value: 0.1859
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_VOL)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-5.9045	-2.6844	-1.4808	0.4536	11.9846

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-216.2	465.9	-0.464	0.657
Hc	7466.1	14745.2	0.506	0.628
GenotypeAPOE33	365.5	711.7	0.514	0.623
GenotypeAPOE44	211.1	480.0	0.440	0.673
Hc:GenotypeAPOE33	-11624.7	22579.8	-0.515	0.623
Hc:GenotypeAPOE44	-6449.3	15185.1	-0.425	0.684

```
##
## Residual standard error: 5.972 on 7 degrees of freedom
## Multiple R-squared: 0.4662, Adjusted R-squared: 0.08484
## F-statistic: 1.223 on 5 and 7 DF, p-value: 0.3895
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_VOL)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-3.2968	-1.3665	0.3588	0.9100	4.4142

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	71.0777	101.9763	0.697	0.502
Hc	-1586.1443	3155.9047	-0.503	0.626
GenotypeAPOE33	131.8214	152.8389	0.862	0.409
GenotypeAPOE44	0.8303	126.4182	0.007	0.995
Hc:GenotypeAPOE33	-4111.4365	4715.0413	-0.872	0.404
Hc:GenotypeAPOE44	39.2137	3903.1279	0.010	0.992

```
##
## Residual standard error: 2.556 on 10 degrees of freedom
## Multiple R-squared: 0.474, Adjusted R-squared: 0.211
## F-statistic: 1.802 on 5 and 10 DF, p-value: 0.2001
## Analysis of Variance Table
##
## Response: Probe_d5
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Hc	1	9.084	9.084	0.4902	0.49329
Genotype	2	216.414	108.207	5.8397	0.01173 *
Sex	1	14.908	14.908	0.8046	0.38226
Hc:Genotype	2	16.190	8.095	0.4369	0.65311
Hc:Sex	1	38.755	38.755	2.0915	0.16630
Genotype:Sex	2	25.643	12.822	0.6919	0.51416
Hc:Genotype:Sex	2	5.109	2.554	0.1379	0.87219

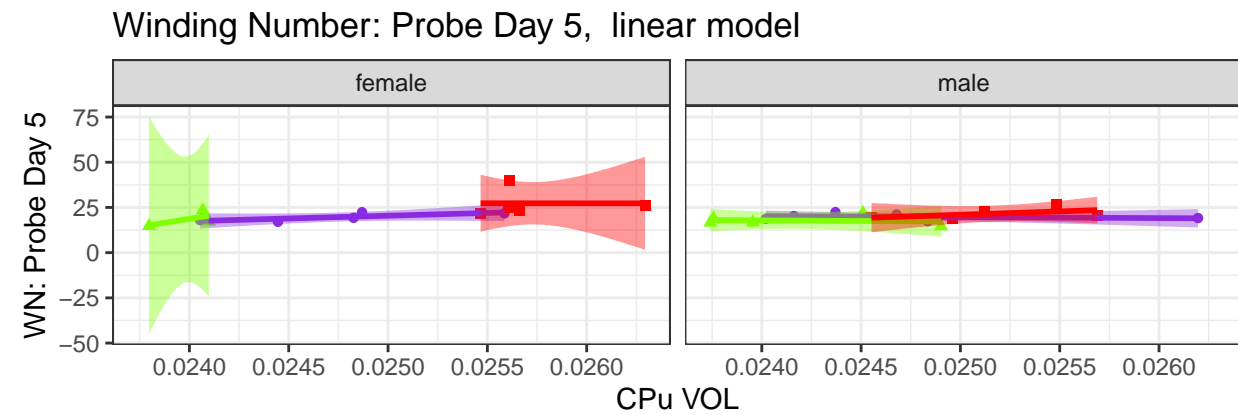
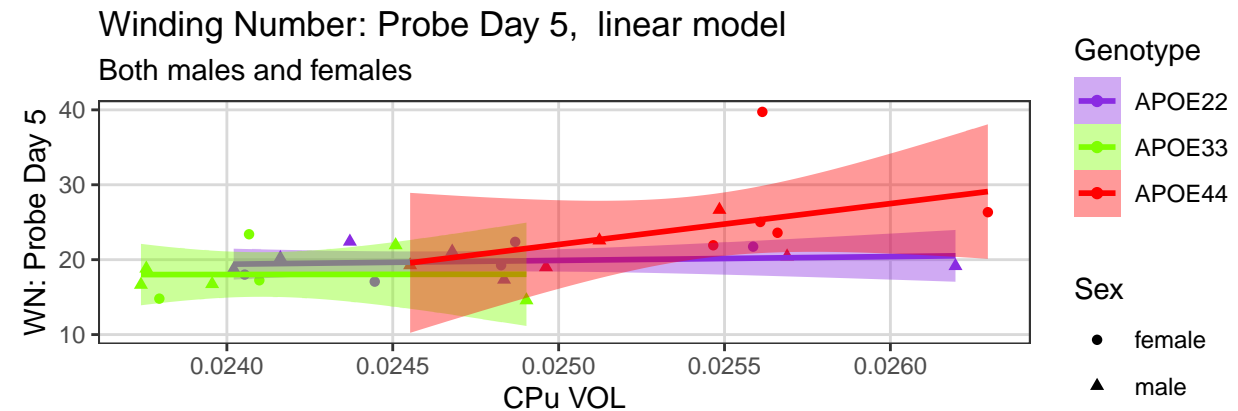
```
## Residuals      17 315.005  18.530
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1  35.942   35.942   1.0077 0.3489
## Genotype     2 172.057   86.028   2.4118 0.1597
## Hc:Genotype   2  10.030    5.015   0.1406 0.8712
## Residuals    7 249.685   35.669

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hc          1  13.040   13.040   1.9964 0.18804
## Genotype     2  38.705   19.352   2.9627 0.09762 .
## Hc:Genotype   2   7.112    3.556   0.5444 0.59644
## Residuals   10  65.320    6.5320

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Day 5 Probe By CPu VOL



##

```
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4172 -1.8458 -0.4934  1.1308 12.3989
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -56.06      92.86  -0.604   0.554
## CPu             3059.99    3750.13   0.816   0.426
## GenotypeAPOE33   -343.55     446.72  -0.769   0.452
## GenotypeAPOE44     84.93     193.15   0.440   0.666
## Sexmale          89.36     110.44   0.809   0.430
## CPu:GenotypeAPOE33 14369.76   18598.19   0.773   0.450
## CPu:GenotypeAPOE44 -3120.15    7575.66  -0.412   0.686
## CPu:Sexmale       -3605.28    4462.45  -0.808   0.430
## GenotypeAPOE33:Sexmale 343.23     461.80   0.743   0.467
## GenotypeAPOE44:Sexmale -189.30     235.40  -0.804   0.432
## CPu:GenotypeAPOE33:Sexmale -14454.81   19211.14  -0.752   0.462
## CPu:GenotypeAPOE44:Sexmale 7347.52     9283.56   0.791   0.440
##
## Residual standard error: 4.27 on 17 degrees of freedom
## Multiple R-squared:  0.5165, Adjusted R-squared:  0.2036
## F-statistic: 1.651 on 11 and 17 DF,  p-value: 0.1709
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4172 -2.2966 -0.6442  0.4679 12.3989
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -56.06     125.97  -0.445   0.670
## CPu             3059.99    5087.33   0.601   0.566
## GenotypeAPOE33   -343.55     606.00  -0.567   0.588
## GenotypeAPOE44     84.93     262.02   0.324   0.755
## CPu:GenotypeAPOE33 14369.76   25229.79   0.570   0.587
## CPu:GenotypeAPOE44 -3120.15    10276.94  -0.304   0.770
##
## Residual standard error: 5.793 on 7 degrees of freedom
## Multiple R-squared:  0.4978, Adjusted R-squared:  0.139
## F-statistic: 1.388 on 5 and 7 DF,  p-value: 0.334
##
## Call:
## lm(formula = Probe_d5 ~ CPu * Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.0892 -1.5568  0.0102  1.1575  4.3958
##
```

```

## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      33.302      38.369   0.868   0.406
## CPu              -545.288    1552.093  -0.351   0.733
## GenotypeAPOE33    -0.316      75.118  -0.004   0.997
## GenotypeAPOE44   -104.362      86.346  -1.209   0.255
## CPu:GenotypeAPOE33 -85.057    3089.267  -0.028   0.979
## CPu:GenotypeAPOE44 4227.368    3443.425   1.228   0.248
##
## Residual standard error: 2.74 on 10 degrees of freedom
## Multiple R-squared:  0.3953, Adjusted R-squared:  0.09293
## F-statistic: 1.307 on 5 and 10 DF,  p-value: 0.335

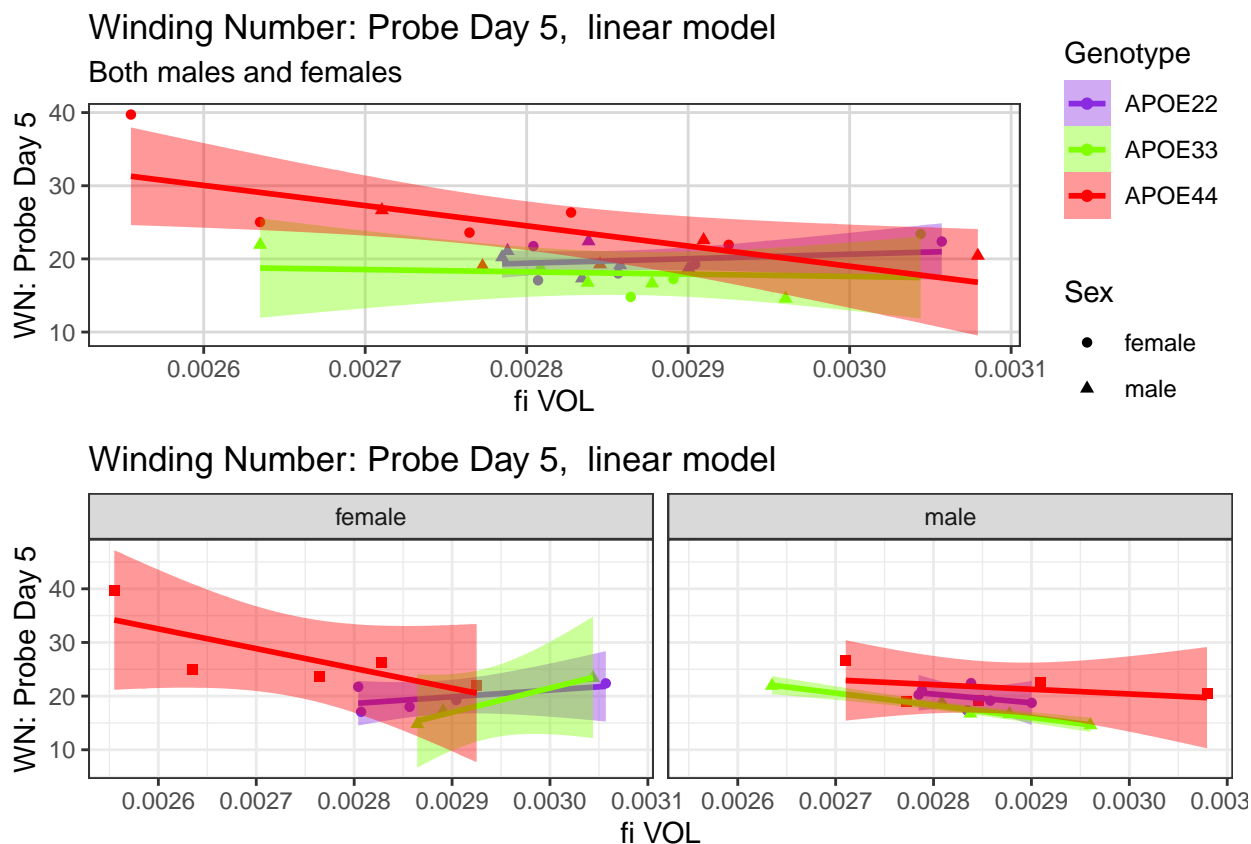
## Analysis of Variance Table
##
## Response: Probe_d5
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## CPu              1 179.863  179.863   9.8636 0.005962 **
## Genotype         2  50.289   25.145   1.3789 0.278632
## Sex              1  25.410   25.410   1.3935 0.254072
## CPu:Genotype     2  22.167   11.084   0.6078 0.555955
## CPu:Sex          1  18.073   18.073   0.9911 0.333430
## Genotype:Sex     2  10.835    5.417   0.2971 0.746756
## CPu:Genotype:Sex 2   24.476   12.238   0.6711 0.524166
## Residuals       17 309.995   18.235
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## CPu              1 185.959  185.959   5.5415 0.05079 .
## Genotype         2  31.561   15.781   0.4703 0.64324
## CPu:Genotype     2  15.290    7.645   0.2278 0.80195
## Residuals        7 234.904   33.558
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##               Df Sum Sq Mean Sq F value Pr(>F)
## CPu              1 13.711  13.7110   1.8259 0.2064
## Genotype         2 23.318  11.6591   1.5527 0.2587
## CPu:Genotype     2 12.056   6.0282   0.8028 0.4750
## Residuals       10 75.091   7.5091

```


Day 5 Probe By fi VOL



```
##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.2107  -0.6788  -0.0603   0.7291   5.5410
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -16.27     40.94  -0.397  0.69602
## fi           12461.14    14178.44   0.879  0.39172
## GenotypeAPOE33    -97.90      75.32  -1.300  0.21099
## GenotypeAPOE44    144.52      49.24   2.935  0.00924 **
## Sexmale           82.16      95.11   0.864  0.39966
## fi:GenotypeAPOE33  32764.74    25793.11   1.270  0.22109
## fi:GenotypeAPOE44 -49277.81    17331.06  -2.843  0.01123 *
## fi:Sexmale       -28716.96    33442.80  -0.859  0.40246
## GenotypeAPOE33:Sexmale  114.03     119.38   0.955  0.35285
## GenotypeAPOE44:Sexmale -163.91     103.35  -1.586  0.13117
## fi:GenotypeAPOE33:Sexmale -39270.41    41641.97  -0.943  0.35887
## fi:GenotypeAPOE44:Sexmale  56829.68    36410.75   1.561  0.13699
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 2.953 on 17 degrees of freedom
## Multiple R-squared:  0.7687, Adjusted R-squared:  0.6191
## F-statistic: 5.136 on 11 and 17 DF,  p-value: 0.001392

##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.2107 -1.3180 -0.0998  1.3618  5.5410
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -16.27      52.27  -0.311  0.7647
## fi             12461.14    18104.71   0.688  0.5134
## GenotypeAPOE33     -97.90      96.18  -1.018  0.3426
## GenotypeAPOE44     144.52      62.87   2.299  0.0551 .
## fi:GenotypeAPOE33  32764.74   32935.72   0.995  0.3530
## fi:GenotypeAPOE44 -49277.81   22130.36  -2.227  0.0613 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 3.771 on 7 degrees of freedom
## Multiple R-squared:  0.7871, Adjusted R-squared:  0.6351
## F-statistic: 5.177 on 5 and 7 DF,  p-value: 0.02634

##
## Call:
## lm(formula = Probe_d5 ~ fi * Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3737 -0.4697 -0.0331  0.7247  3.7386
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)       65.90      64.16   1.027  0.329
## fi             -16255.82   22638.18  -0.718  0.489
## GenotypeAPOE33     16.13      69.22   0.233  0.820
## GenotypeAPOE44    -19.38      67.91  -0.285  0.781
## fi:GenotypeAPOE33 -6505.67   24434.64  -0.266  0.795
## fi:GenotypeAPOE44  7551.87   23933.47   0.316  0.759
##
## Residual standard error: 2.207 on 10 degrees of freedom
## Multiple R-squared:  0.6076, Adjusted R-squared:  0.4114
## F-statistic: 3.097 on 5 and 10 DF,  p-value: 0.0604

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fi         1 155.368  155.368  17.8124 0.0005756 ***
## Genotype   2 138.410   69.205   7.9341 0.0036832 **
## Sex        1  35.961   35.961   4.1227 0.0582560 .

```

```

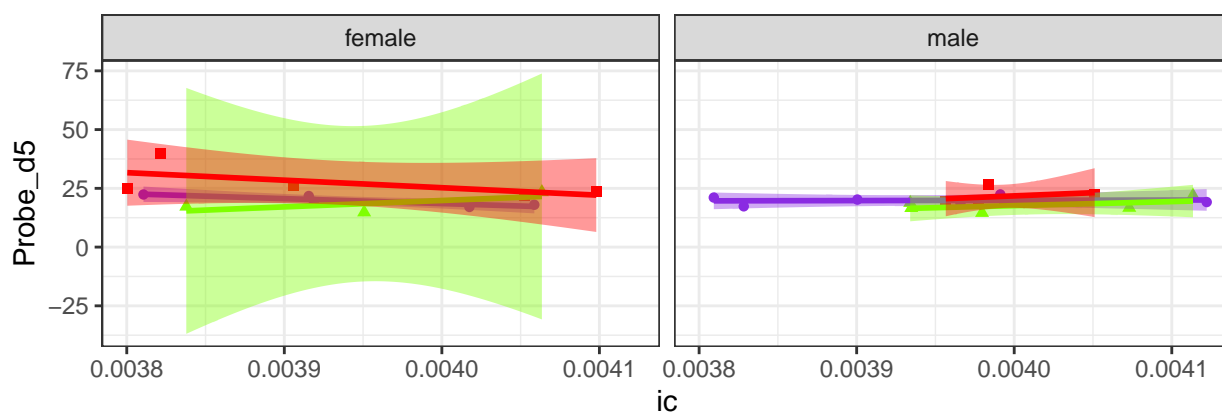
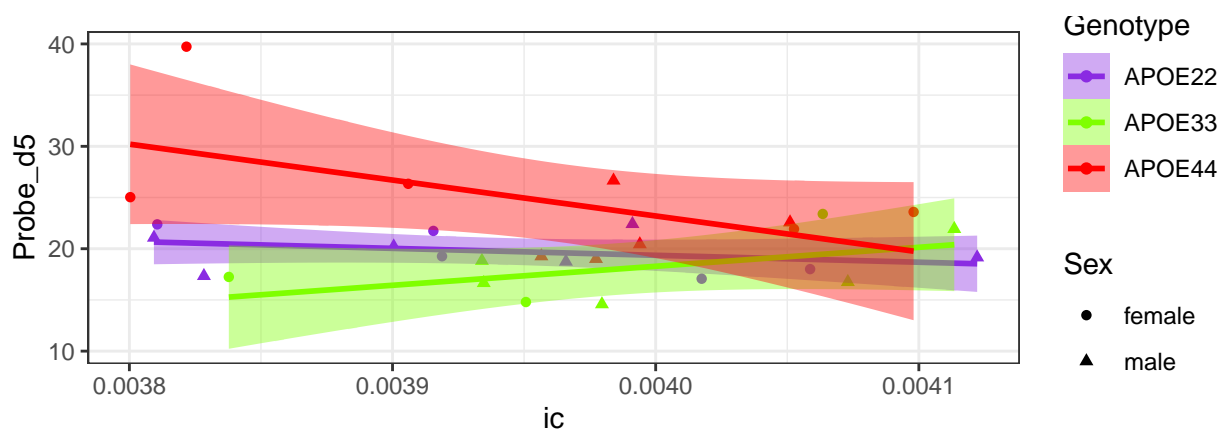
## fi:Genotype      2  45.035  22.517  2.5815 0.1049454
## fi:Sex           1   0.164   0.164  0.0188 0.8924384
## Genotype:Sex     2  12.716   6.358  0.7289 0.4969182
## fi:Genotype:Sex  2 105.172  52.586  6.0288 0.0104982 *
## Residuals       17 148.283   8.723
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## fi              1 152.355  152.355  10.7125 0.01362 *
## Genotype        2   74.249   37.124   2.6103 0.14224
## fi:Genotype     2 141.555   70.777   4.9765 0.04524 *
## Residuals       7   99.556   14.222
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## fi              1  21.158   21.1579   4.3421 0.06379 .
## Genotype        2  47.621   23.8103   4.8865 0.03309 *
## fi:Genotype     2   6.672    3.3358   0.6846 0.52645
## Residuals      10  48.727    4.8727
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 5 Probe By ic VOL



```
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.6240 -1.6598 -0.5915  1.4659  8.7543
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      102.30      74.58   1.372   0.188
## ic             -20943.17 18905.07  -1.108   0.283
## GenotypeAPOE33    -191.38    117.66  -1.627   0.122
## GenotypeAPOE44     51.06     91.99   0.555   0.586
## Sexmale          -87.13     93.09  -0.936   0.362
## ic:GenotypeAPOE33  48169.33 29794.37   1.617   0.124
## ic:GenotypeAPOE44 -11079.30 23333.81  -0.475   0.641
## ic:Sexmale        22126.56 23611.64   0.937   0.362
## GenotypeAPOE33:Sexmale 124.62   158.04   0.789   0.441
## GenotypeAPOE44:Sexmale -152.37   233.27  -0.653   0.522
## ic:GenotypeAPOE33:Sexmale -32049.57 39847.88  -0.804   0.432
## ic:GenotypeAPOE44:Sexmale 36879.32 58585.94   0.629   0.537
##
## Residual standard error: 3.675 on 17 degrees of freedom
## Multiple R-squared:  0.6418, Adjusted R-squared:  0.4101
```

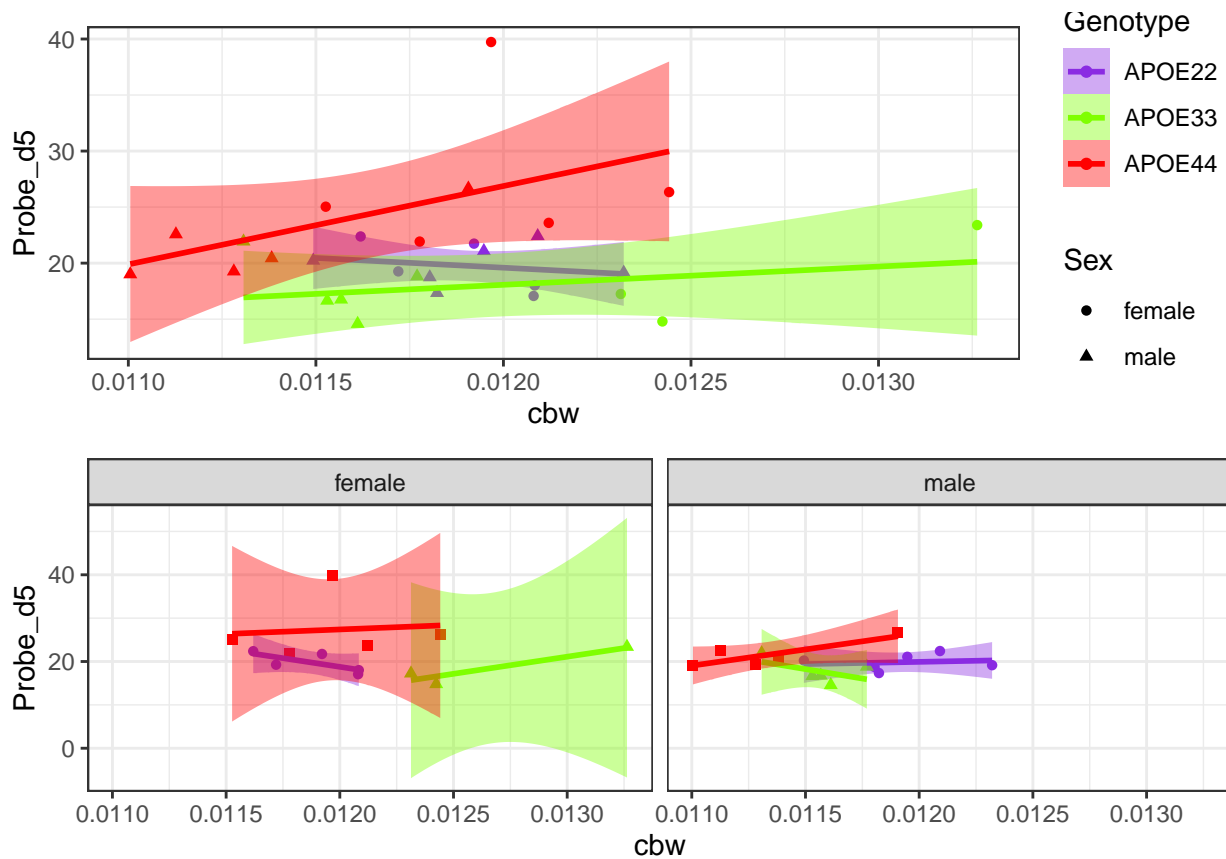
```
## F-statistic: 2.77 on 11 and 17 DF, p-value: 0.029
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.6240 -1.6598 -0.1114  1.4659  8.7543
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      102.30      95.26   1.074   0.319
## ic           -20943.17    24146.71  -0.867   0.415
## GenotypeAPOE33    -191.38     150.28  -1.273   0.244
## GenotypeAPOE44     51.06     117.50   0.435   0.677
## ic:GenotypeAPOE33  48169.33    38055.19   1.266   0.246
## ic:GenotypeAPOE44 -11079.30    29803.38  -0.372   0.721
##
## Residual standard error: 4.694 on 7 degrees of freedom
## Multiple R-squared: 0.6702, Adjusted R-squared: 0.4347
## F-statistic: 2.845 on 5 and 7 DF, p-value: 0.1027
##
## Call:
## lm(formula = Probe_d5 ~ ic * Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6926 -1.5495 -0.7418  1.6374  5.3037
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      15.17      41.61   0.365   0.723
## ic           1183.40    10567.15   0.112   0.913
## GenotypeAPOE33    -66.75     78.82  -0.847   0.417
## GenotypeAPOE44   -101.31     160.13  -0.633   0.541
## ic:GenotypeAPOE33 16119.76    19766.11   0.816   0.434
## ic:GenotypeAPOE44 25800.02    40143.28   0.643   0.535
##
## Residual standard error: 2.745 on 10 degrees of freedom
## Multiple R-squared: 0.393, Adjusted R-squared: 0.08955
## F-statistic: 1.295 on 5 and 10 DF, p-value: 0.3394
## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic         1  30.663  30.663   2.2702 0.150242
## Genotype   2 203.811 101.905   7.5447 0.004516 **
## Sex        1  24.361  24.361   1.8036 0.196934
## ic:Genotype 2 101.179  50.589   3.7455 0.044902 *
## ic:Sex      1   4.155   4.155   0.3076 0.586361
## Genotype:Sex 2  28.919  14.460   1.0705 0.364837
## ic:Genotype:Sex 2  18.406   9.203   0.6813 0.519227
```

```
## Residuals      17 229.616  13.507
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic          1  53.502   53.502   2.4281 0.16314
## Genotype     2 193.352   96.676   4.3874 0.05821 .
## ic:Genotype   2  66.615   33.308   1.5116 0.28466
## Residuals    7 154.245   22.035
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic          1   2.233    2.2329   0.2963 0.5982
## Genotype     2 39.417   19.7086   2.6149 0.1220
## ic:Genotype   2   7.156    3.5780   0.4747 0.6354
## Residuals   10 75.371    7.5371
```

Day 5 Probe By cbw VOL



##

```
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.0066 -1.7503 -0.9083  1.2193 12.4045
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      114.75     112.23   1.022   0.321
## cbw             -7997.92    9441.77  -0.847   0.409
## GenotypeAPOE33    -196.26     131.48  -1.493   0.154
## GenotypeAPOE44    -112.32     131.56  -0.854   0.405
## Sexmale          -107.14     135.10  -0.793   0.439
## cbw:GenotypeAPOE33 15892.16   10879.32   1.461   0.162
## cbw:GenotypeAPOE44 10078.76   11046.76   0.912   0.374
## cbw:Sexmale        9023.53   11357.05   0.795   0.438
## GenotypeAPOE33:Sexmale 306.97    204.54   1.501   0.152
## GenotypeAPOE44:Sexmale  41.53    164.80   0.252   0.804
## cbw:GenotypeAPOE33:Sexmale -25619.35 17309.58  -1.480   0.157
## cbw:GenotypeAPOE44:Sexmale -3629.01 13944.88  -0.260   0.798
##
## Residual standard error: 3.971 on 17 degrees of freedom
## Multiple R-squared:  0.5819, Adjusted R-squared:  0.3114
## F-statistic: 2.151 on 11 and 17 DF, p-value: 0.07559
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.0066 -1.7665 -1.0584  0.5625 12.4045
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      114.7       157.3   0.730   0.489
## cbw             -7997.9    13230.5  -0.605   0.565
## GenotypeAPOE33    -196.3      184.2  -1.065   0.322
## GenotypeAPOE44    -112.3      184.3  -0.609   0.562
## cbw:GenotypeAPOE33 15892.2    15244.9   1.042   0.332
## cbw:GenotypeAPOE44 10078.8    15479.5   0.651   0.536
##
## Residual standard error: 5.564 on 7 degrees of freedom
## Multiple R-squared:  0.5366, Adjusted R-squared:  0.2057
## F-statistic: 1.621 on 5 and 7 DF, p-value: 0.2705
##
## Call:
## lm(formula = Probe_d5 ~ cbw * Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6945 -1.3622 -0.4928  1.4167  2.9226
##
```

```

## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      7.609    42.909   0.177   0.863
## cbw             1025.607   3600.913   0.285   0.782
## GenotypeAPOE33    110.705    89.392   1.238   0.244
## GenotypeAPOE44   -70.794    56.626  -1.250   0.240
## cbw:GenotypeAPOE33 -9727.191  7681.221  -1.266   0.234
## cbw:GenotypeAPOE44  6449.744  4855.488   1.328   0.214
##
## Residual standard error: 2.265 on 10 degrees of freedom
## Multiple R-squared:  0.5867, Adjusted R-squared:  0.3801
## F-statistic: 2.839 on 5 and 10 DF,  p-value: 0.07531

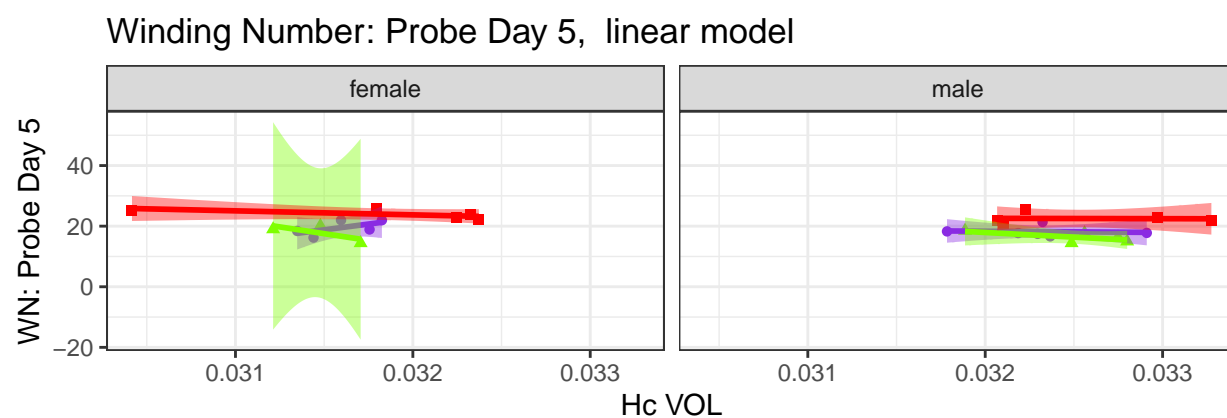
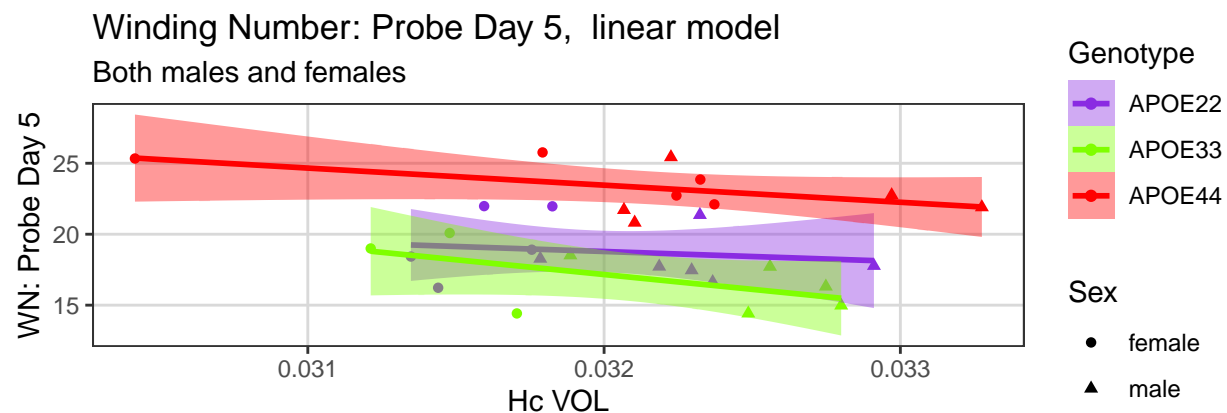
## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value    Pr(>F)
## cbw      1   8.048    8.048   0.5104 0.484654
## Genotype  2 254.126 127.063   8.0588 0.003454 **
## Sex       1   3.352    3.352   0.2126 0.650593
## cbw:Genotype  2  46.134   23.067   1.4630 0.259263
## cbw:Sex      1   3.402    3.402   0.2158 0.648185
## Genotype:Sex  2  17.256    8.628   0.5472 0.588413
## cbw:Genotype:Sex  2  40.753   20.377   1.2924 0.300275
## Residuals   17 268.038   15.767
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value    Pr(>F)
## cbw      1   4.120    4.120   0.1331 0.72603
## Genotype  2 212.207 106.103   3.4272 0.09168 .
## cbw:Genotype  2  34.671   17.336   0.5599 0.59486
## Residuals    7 216.716   30.959
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d5
##      Df Sum Sq Mean Sq F value    Pr(>F)
## cbw      1   0.812    0.8120   0.1582 0.69916
## Genotype  2  45.552  22.7762   4.4379 0.04173 *
## cbw:Genotype  2  26.491  13.2454   2.5809 0.12481
## Residuals   10  51.322    5.1322
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```


Day 8 Probe By Hc VOL



```
##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.1125 -1.0904 -0.4708  0.7050  3.1618
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -220.5      148.5   -1.485  0.1559
## Hc             7597.6     4701.4    1.616  0.1245
## GenotypeAPOE33    518.3      226.9    2.284  0.0355 *
## GenotypeAPOE44    286.5      153.0    1.872  0.0784 .
## Sexmale         252.3      166.8    1.512  0.1489
## Hc:GenotypeAPOE33 -16493.4    7199.3   -2.291  0.0350 *
## Hc:GenotypeAPOE44  -8919.1    4841.6   -1.842  0.0830 .
## Hc:Sexmale       -8016.9    5256.6   -1.525  0.1456
## GenotypeAPOE33:Sexmale -433.4      253.9   -1.707  0.1060
## GenotypeAPOE44:Sexmale -292.0      179.7   -1.625  0.1226
## Hc:GenotypeAPOE33:Sexmale 13828.1    8010.7    1.726  0.1024
## Hc:GenotypeAPOE44:Sexmale  9222.1    5647.9    1.633  0.1209
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.904 on 17 degrees of freedom
## Multiple R-squared:  0.7944, Adjusted R-squared:  0.6613
## F-statistic: 5.971 on 11 and 17 DF,  p-value: 0.0005814

##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.1125 -1.1358 -0.4898  0.7848  2.4610
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -220.5      158.3   -1.393   0.2061
## Hc             7597.6     5009.4    1.517   0.1731
## GenotypeAPOE33    518.3      241.8    2.143   0.0693 .
## GenotypeAPOE44    286.5      163.1    1.757   0.1223
## Hc:GenotypeAPOE33 -16493.4   7671.0   -2.150   0.0686 .
## Hc:GenotypeAPOE44 -8919.1    5158.8   -1.729   0.1275
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 2.029 on 7 degrees of freedom
## Multiple R-squared:  0.7902, Adjusted R-squared:  0.6403
## F-statistic: 5.273 on 5 and 7 DF,  p-value: 0.02515

##
## Call:
## lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9989 -0.7748 -0.3256  0.3866  3.1618
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    31.750      72.291    0.439   0.670
## Hc            -419.242    2237.228   -0.187   0.855
## GenotypeAPOE33    84.872    108.348    0.783   0.452
## GenotypeAPOE44   -5.446     89.618   -0.061   0.953
## Hc:GenotypeAPOE33 -2665.255   3342.503   -0.797   0.444
## Hc:GenotypeAPOE44  303.005    2766.936    0.110   0.915
##
## Residual standard error: 1.812 on 10 degrees of freedom
## Multiple R-squared:  0.7622, Adjusted R-squared:  0.6433
## F-statistic:  6.41 on 5 and 10 DF,  p-value: 0.00641

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Hc          1   8.886    8.886   2.4504   0.1359
## Genotype    2 204.234  102.117  28.1617 4.02e-06 ***
## Sex         1   1.412    1.412   0.3893   0.5409

```

```

## Hc:Genotype      2   2.642   1.321   0.3644   0.6999
## Hc:Sex            1   0.075   0.075   0.0207   0.8872
## Genotype:Sex      2   8.164   4.082   1.1258   0.3474
## Hc:Genotype:Sex   2  12.741   6.370   1.7568   0.2025
## Residuals        17  61.644   3.626
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Hc              1   0.627    0.627   0.1524 0.707860
## Genotype        2  87.960   43.980  10.6830 0.007465 **
## Hc:Genotype     2  19.951    9.976   2.4231 0.158600
## Residuals       7  28.818    4.117
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

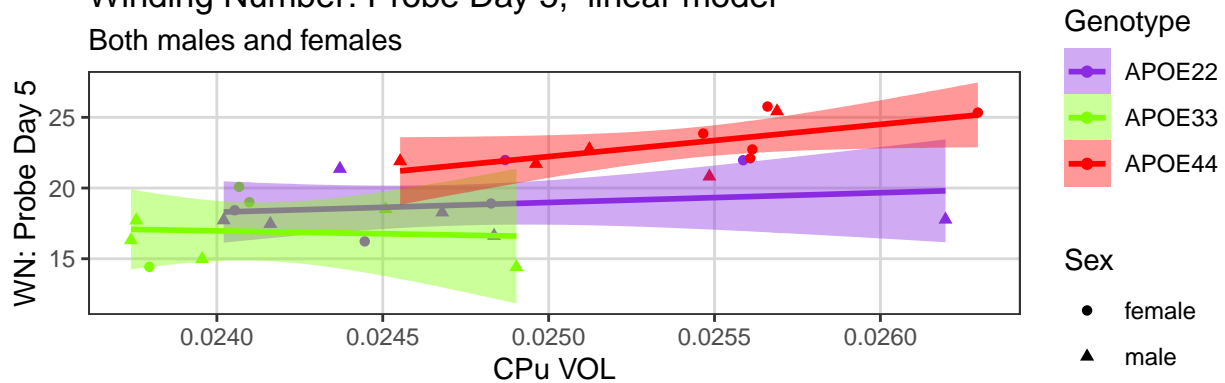
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Hc              1   0.152    0.152   0.0462 0.8340898
## Genotype        2 101.612   50.806  15.4775 0.0008679 ***
## Hc:Genotype     2   3.446    1.723   0.5249 0.6070557
## Residuals      10  32.826    3.283
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

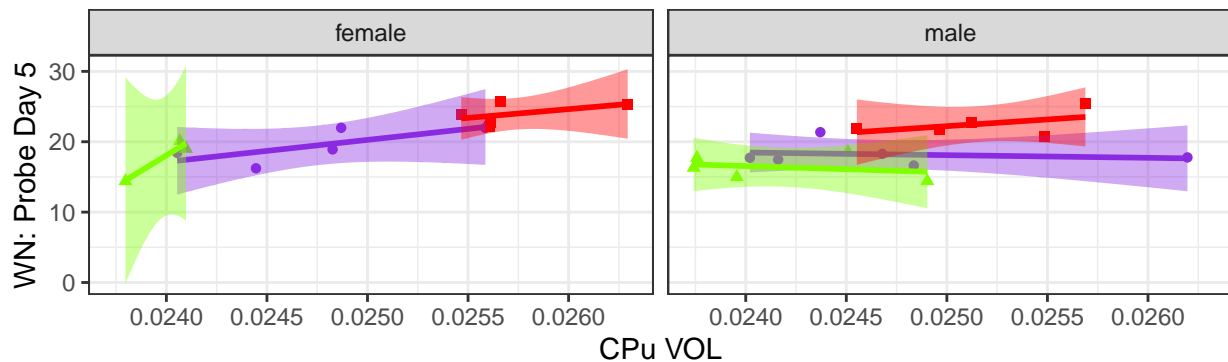
Day 8 Probe By CPu VOL

Winding Number: Probe Day 5, linear model

Both males and females



Winding Number: Probe Day 5, linear model



```
##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.3190 -0.9447 -0.0881  0.8593  3.0286
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -57.96      38.93  -1.489  0.1548
## CPu             3129.08    1572.12   1.990  0.0629 .
## GenotypeAPOE33   -343.18     187.27  -1.833  0.0845 .
## GenotypeAPOE44    17.96      80.97   0.222  0.8271
## Sexmale          85.48      46.30   1.846  0.0824 .
## CPu:GenotypeAPOE33 14337.48   7796.67   1.839  0.0835 .
## CPu:GenotypeAPOE44  -643.18   3175.84  -0.203  0.8419
## CPu:Sexmale      -3505.81   1870.73  -1.874  0.0782 .
## GenotypeAPOE33:Sexmale 353.53    193.59   1.826  0.0854 .
## GenotypeAPOE44:Sexmale  -70.85     98.68  -0.718  0.4825
## CPu:GenotypeAPOE33:Sexmale -14849.27  8053.63  -1.844  0.0827 .
## CPu:GenotypeAPOE44:Sexmale 2923.46   3891.82   0.751  0.4628
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.79 on 17 degrees of freedom
## Multiple R-squared:  0.8183, Adjusted R-squared:  0.7007
## F-statistic: 6.959 on 11 and 17 DF,  p-value: 0.0002283

##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.3026 -0.8131 -0.0881  0.8593  2.1247
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -57.96      37.31  -1.553  0.1643
## CPu             3129.08     1506.92   2.076  0.0765 .
## GenotypeAPOE33   -343.18      179.50  -1.912  0.0975 .
## GenotypeAPOE44     17.96       77.61   0.231  0.8236
## CPu:GenotypeAPOE33 14337.48     7473.33   1.918  0.0965 .
## CPu:GenotypeAPOE44  -643.18     3044.14  -0.211  0.8387
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 1.716 on 7 degrees of freedom
## Multiple R-squared:  0.8499, Adjusted R-squared:  0.7428
## F-statistic:  7.93 on 5 and 7 DF,  p-value: 0.008434

##
## Call:
## lm(formula = Probe_d8 ~ CPu * Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.3190 -1.0393 -0.1832  0.6428  3.0286
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      27.51      25.77   1.068  0.311
## CPu             -376.73     1042.37  -0.361  0.725
## GenotypeAPOE33     10.35      50.45   0.205  0.842
## GenotypeAPOE44    -52.89      57.99  -0.912  0.383
## CPu:GenotypeAPOE33 -511.79     2074.72  -0.247  0.810
## CPu:GenotypeAPOE44 2280.28     2312.57   0.986  0.347
##
## Residual standard error: 1.84 on 10 degrees of freedom
## Multiple R-squared:  0.7546, Adjusted R-squared:  0.632
## F-statistic: 6.151 on 5 and 10 DF,  p-value: 0.007407

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## CPu         1 135.382  135.382  42.2452 5.448e-06 ***
## Genotype     2  66.790   33.395  10.4207 0.001112 **
## Sex          1  10.988   10.988   3.4286 0.081525 .

```

```

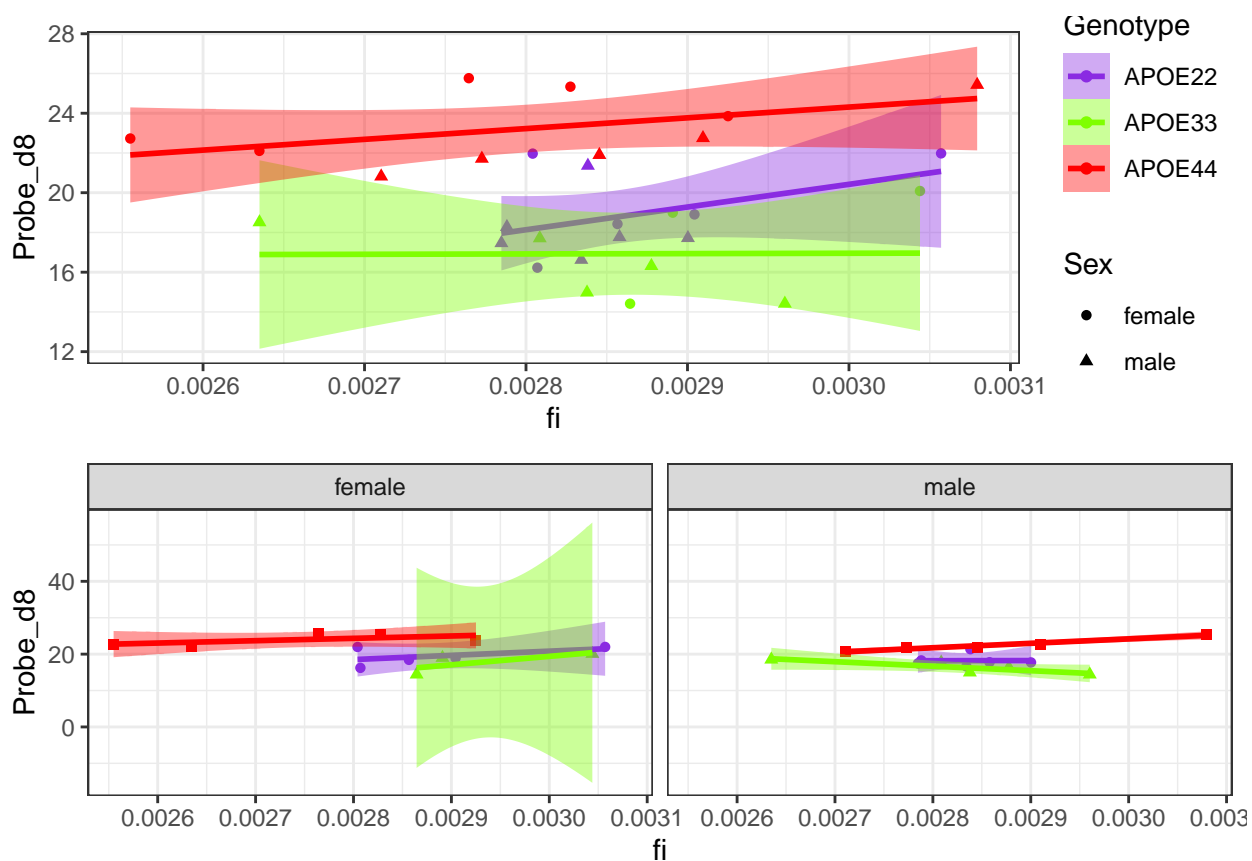
## CPu:Genotype      2   1.821   0.910   0.2841   0.756206
## CPu:Sex           1   2.550   2.550   0.7956   0.384860
## Genotype:Sex      2  13.922   6.961   2.1721   0.144526
## CPu:Genotype:Sex  2  13.867   6.933   2.1635   0.145511
## Residuals        17  54.479   3.205
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1 102.193 102.193 34.7079 0.0006047 ***
## Genotype      2   3.233   1.617   0.5491 0.6004717
## CPu:Genotype  2  11.320   5.660   1.9222 0.2160810
## Residuals     7  20.611   2.944
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1  27.858   27.858   8.2254 0.016726 *
## Genotype      2  72.227   36.114  10.6628 0.003315 **
## CPu:Genotype  2   4.081    2.041   0.6025 0.566141
## Residuals    10  33.869    3.387
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By fi VOL



```
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.3641 -0.7386 -0.2772  0.4998  3.4095
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -13.84      23.84  -0.580   0.569
## fi             11551.93    8257.09   1.399   0.180
## GenotypeAPOE33    -36.29     43.86  -0.827   0.419
## GenotypeAPOE44     20.07     28.67   0.700   0.494
## Sexmale           30.90     55.39   0.558   0.584
## fi:GenotypeAPOE33  11618.43   15021.12   0.773   0.450
## fi:GenotypeAPOE44 -5085.53   10093.08  -0.504   0.621
## fi:Sexmale       -11148.95   19476.07  -0.572   0.575
## GenotypeAPOE33:Sexmale    70.64     69.52   1.016   0.324
## GenotypeAPOE44:Sexmale   -49.49     60.19  -0.822   0.422
## fi:GenotypeAPOE33:Sexmale -24422.46  24251.01  -1.007   0.328
## fi:GenotypeAPOE44:Sexmale  16866.95  21204.51   0.795   0.437
##
## Residual standard error: 1.72 on 17 degrees of freedom
## Multiple R-squared:  0.8323, Adjusted R-squared:  0.7237
```

```
## F-statistic: 7.667 on 11 and 17 DF, p-value: 0.0001235
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_f_VOL)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-2.3641	-1.1635	-0.3151	0.8214	3.4095

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-13.84	30.15	-0.459	0.660
fi	11551.93	10443.05	1.106	0.305
GenotypeAPOE33	-36.29	55.48	-0.654	0.534
GenotypeAPOE44	20.07	36.26	0.553	0.597
fi:GenotypeAPOE33	11618.43	18997.78	0.612	0.560
fi:GenotypeAPOE44	-5085.53	12765.10	-0.398	0.702

```
##
## Residual standard error: 2.175 on 7 degrees of freedom
## Multiple R-squared: 0.7588, Adjusted R-squared: 0.5866
## F-statistic: 4.406 on 5 and 7 DF, p-value: 0.03918
##
## Call:
## lm(formula = Probe_d8 ~ fi * Genotype, data = combo_m_VOL)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-1.5778	-0.4586	-0.2455	0.2814	3.1549

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	17.06	38.08	0.448	0.664
fi	402.98	13437.09	0.030	0.977
GenotypeAPOE33	34.34	41.09	0.836	0.423
GenotypeAPOE44	-29.43	40.31	-0.730	0.482
fi:GenotypeAPOE33	-12804.03	14503.39	-0.883	0.398
fi:GenotypeAPOE44	11781.42	14205.92	0.829	0.426

```
##
## Residual standard error: 1.31 on 10 degrees of freedom
## Multiple R-squared: 0.8756, Adjusted R-squared: 0.8134
## F-statistic: 14.08 on 5 and 10 DF, p-value: 0.0002962
## Analysis of Variance Table
##
## Response: Probe_d8
```

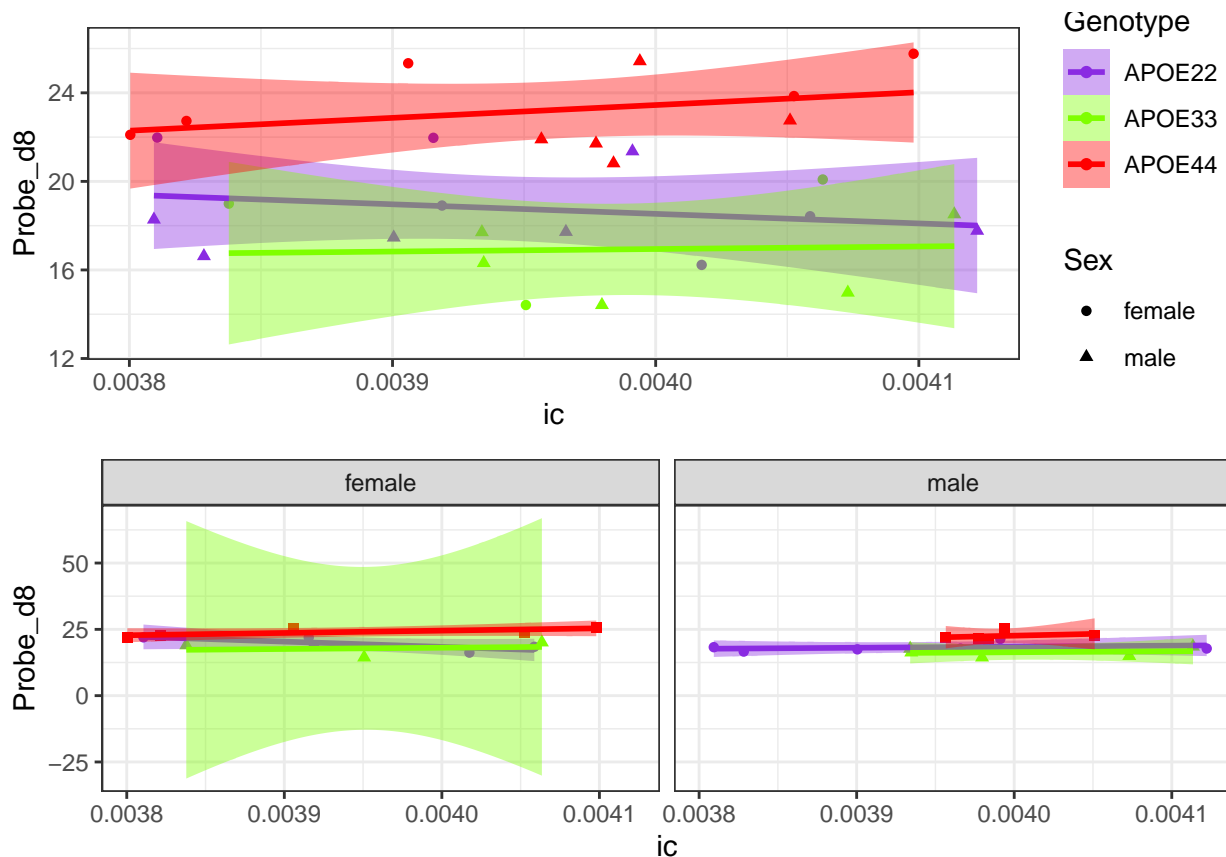
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
fi	1	0.144	0.144	0.0488	0.82781
Genotype	2	204.378	102.189	34.5435	1.028e-06 ***
Sex	1	13.071	13.071	4.4184	0.05076 .
fi:Genotype	2	8.179	4.089	1.3823	0.27782
fi:Sex	1	1.210	1.210	0.4092	0.53092
Genotype:Sex	2	4.169	2.085	0.7046	0.50816
fi:Genotype:Sex	2	18.356	9.178	3.1024	0.07102 .


```
## Residuals      17  50.291   2.958
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fi           1   5.914    5.914   1.2498 0.300482
## Genotype      2  93.859   46.930   9.9176 0.009065 **
## fi:Genotype   2   4.460    2.230   0.4712 0.642686
## Residuals     7  33.124    4.732
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fi           1   5.648    5.648   3.2901 0.09977 .
## Genotype      2  94.872   47.436  27.6318 8.446e-05 ***
## fi:Genotype   2  20.349   10.175   5.9268 0.02006 *
## Residuals    10  17.167    1.717
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Day 8 Probe By ic VOL



```
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4169 -1.1252 -0.2323  1.5821  2.9401
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         97.75      40.42   2.419  0.0271 *
## ic             -19839.16    10244.87  -1.936  0.0696 .
## GenotypeAPOE33      -98.99       63.76  -1.553  0.1389
## GenotypeAPOE44     -108.19       49.85  -2.170  0.0445 *
## Sexmale           -95.06       50.45  -1.884  0.0767 .
## ic:GenotypeAPOE33   24667.36    16145.89   1.528  0.1450
## ic:GenotypeAPOE44   28577.71    12644.85   2.260  0.0372 *
## ic:Sexmale         23779.79    12795.41   1.858  0.0805 .
## GenotypeAPOE33:Sexmale    98.39       85.65   1.149  0.2666
## GenotypeAPOE44:Sexmale    74.91      126.41   0.593  0.5613
## ic:GenotypeAPOE33:Sexmale -25039.09    21594.00  -1.160  0.2623
## ic:GenotypeAPOE44:Sexmale -19215.80    31748.36  -0.605  0.5530
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.992 on 17 degrees of freedom
## Multiple R-squared:  0.7751, Adjusted R-squared:  0.6295
## F-statistic: 5.326 on 11 and 17 DF, p-value: 0.001134
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4169 -1.0972 -0.1732  1.6381  1.8965
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         97.75      43.18   2.264  0.0580 .
## ic             -19839.16    10944.99  -1.813  0.1128
## GenotypeAPOE33      -98.99       68.12  -1.453  0.1895
## GenotypeAPOE44     -108.19       53.26  -2.031  0.0818 .
## ic:GenotypeAPOE33   24667.36    17249.29   1.430  0.1958
## ic:GenotypeAPOE44   28577.71    13508.99   2.115  0.0722 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.128 on 7 degrees of freedom
## Multiple R-squared:  0.7693, Adjusted R-squared:  0.6045
## F-statistic: 4.668 on 5 and 7 DF, p-value: 0.03406
##
## Call:
## lm(formula = Probe_d8 ~ ic * Genotype, data = combo_m_VOL)
```

```

##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8716 -1.1555 -0.5732  0.8266  2.9401
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.692      28.653   0.094   0.927
## ic             3940.638    7276.725   0.542   0.600
## GenotypeAPOE33    -0.606     54.278  -0.011   0.991
## GenotypeAPOE44   -33.281    110.267  -0.302   0.769
## ic:GenotypeAPOE33 -371.731   13611.282  -0.027   0.979
## ic:GenotypeAPOE44 9361.910    27643.354   0.339   0.742
##
## Residual standard error: 1.891 on 10 degrees of freedom
## Multiple R-squared:  0.7411, Adjusted R-squared:  0.6116
## F-statistic: 5.724 on 5 and 10 DF,  p-value: 0.009488

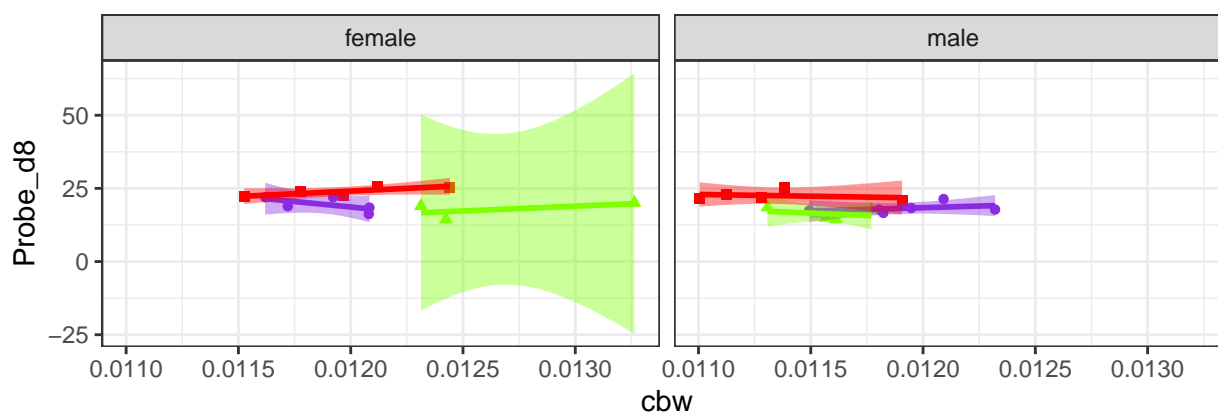
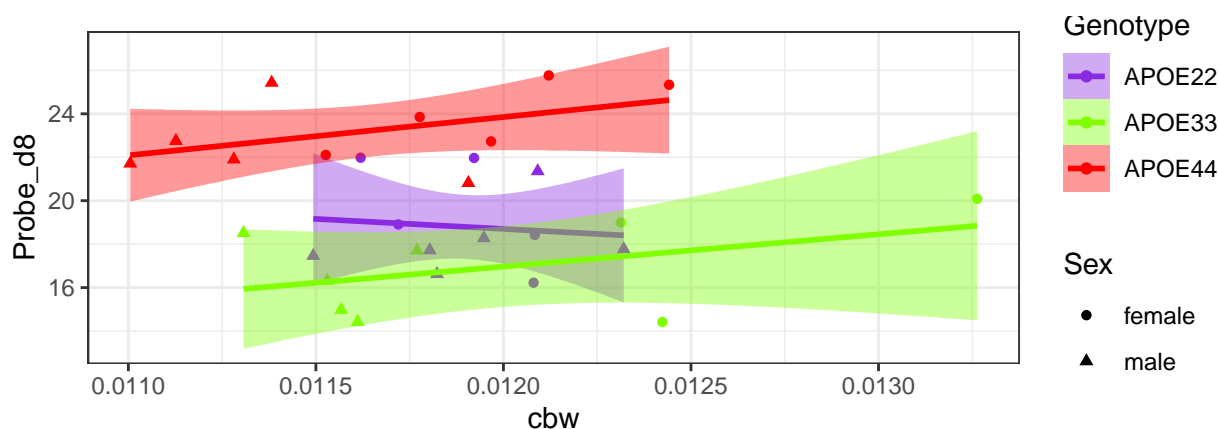
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1  0.058   0.058   0.0147   0.90491
## Genotype        2 195.431  97.715  24.6351 9.498e-06 ***
## Sex              1  14.303  14.303   3.6060   0.07468 .
## ic:Genotype     2   8.285   4.143   1.0444   0.37342
## ic:Sex           1   6.553   6.553   1.6521   0.21591
## Genotype:Sex    2   1.950   0.975   0.2458   0.78478
## ic:Genotype:Sex 2   5.787   2.893   0.7294   0.49668
## Residuals      17  67.431   3.967
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1  0.257   0.257   0.0567  0.81864
## Genotype        2  84.428  42.214   9.3246 0.01062 *
## ic:Genotype     2  20.982  10.491   2.3173 0.16893
## Residuals       7  31.690   4.527
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ic              1  2.232   2.232   0.6246 0.447684
## Genotype        2  99.633  49.816  13.9384 0.001283 **
## ic:Genotype     2   0.430   0.215   0.0602 0.941901
## Residuals      10  35.740   3.574
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Day 8 Probe By cbw VOL



```
##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6241 -1.2310 -0.1624  0.5957  2.9577
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      108.44      55.08   1.969  0.0655 .
## cbw             -7483.73    4633.70  -1.615  0.1247
## GenotypeAPOE33   -131.97      64.53  -2.045  0.0566 .
## GenotypeAPOE44   -128.61      64.56  -1.992  0.0627 .
## Sexmale         -117.17      66.30  -1.767  0.0951 .
## cbw:GenotypeAPOE33 10749.02    5339.20   2.013  0.0602 .
## cbw:GenotypeAPOE44 11171.30    5421.37   2.061  0.0550 .
## cbw:Sexmale        9744.23    5573.65   1.748  0.0985 .
## GenotypeAPOE33:Sexmale 195.44     100.38   1.947  0.0683 .
## GenotypeAPOE44:Sexmale 173.57      80.88   2.146  0.0466 *
## cbw:GenotypeAPOE33:Sexmale -16328.27  8494.95  -1.922  0.0715 .
## cbw:GenotypeAPOE44:Sexmale -14640.09  6843.67  -2.139  0.0472 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 1.949 on 17 degrees of freedom
## Multiple R-squared:  0.7847, Adjusted R-squared:  0.6453
## F-statistic: 5.631 on 11 and 17 DF,  p-value: 0.0008209

##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6241 -1.2310  0.3064  0.5957  2.7405
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      108.44      58.99   1.838  0.1086
## cbw             -7483.73    4962.76  -1.508  0.1753
## GenotypeAPOE33    -131.97      69.11  -1.910  0.0978 .
## GenotypeAPOE44    -128.61      69.15  -1.860  0.1052
## cbw:GenotypeAPOE33 10749.02    5718.36   1.880  0.1022
## cbw:GenotypeAPOE44 11171.30    5806.37   1.924  0.0958 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 2.087 on 7 degrees of freedom
## Multiple R-squared:  0.778, Adjusted R-squared:  0.6194
## F-statistic: 4.907 on 5 and 7 DF,  p-value: 0.03013

##
## Call:
## lm(formula = Probe_d8 ~ cbw * Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7894 -1.2498 -0.1989  0.4835  2.9577
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -8.727      34.958  -0.250  0.808
## cbw             2260.507    2933.716   0.771  0.459
## GenotypeAPOE33     63.468      72.829   0.871  0.404
## GenotypeAPOE44     44.952      46.134   0.974  0.353
## cbw:GenotypeAPOE33 -5579.249    6258.002  -0.892  0.394
## cbw:GenotypeAPOE44 -3468.786    3955.836  -0.877  0.401
##
## Residual standard error: 1.846 on 10 degrees of freedom
## Multiple R-squared:  0.7532, Adjusted R-squared:  0.6298
## F-statistic: 6.104 on 5 and 10 DF,  p-value: 0.007607

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## cbw         1   1.345    1.345   0.3542  0.55960
## Genotype    2 203.830  101.915  26.8375 5.496e-06 ***
## Sex         1   5.404    5.404   1.4231  0.24928

```

```

## cbw:Genotype      2   1.448   0.724  0.1906   0.82818
## cbw:Sex           1   1.185   1.185  0.3121   0.58365
## Genotype:Sex      2   1.425   0.712  0.1876   0.83066
## cbw:Genotype:Sex  2  20.604  10.302  2.7128   0.09495 .
## Residuals        17  64.557   3.797
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw           1  5.071    5.071   1.1641  0.316385
## Genotype      2 83.686   41.843   9.6058 0.009843 **
## cbw:Genotype  2 18.108    9.054   2.0785 0.195620
## Residuals     7 30.492    4.356
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw           1 16.147   16.147   4.7402 0.054504 .
## Genotype      2 83.870   41.935  12.3102 0.002011 **
## cbw:Genotype  2  3.953    1.977   0.5802 0.577558
## Residuals    10 34.065    3.407
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```