

Proportional Volume Distributions by Region (Left Hemisphere)

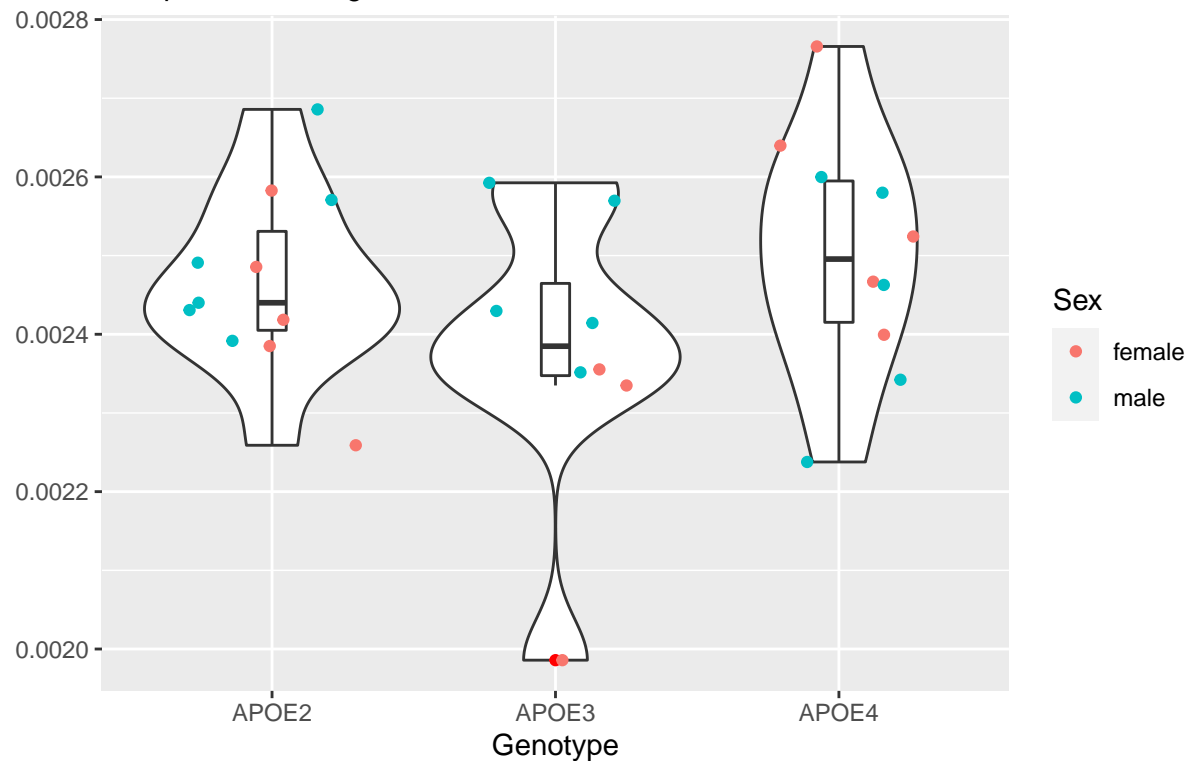
Anna MacFarlane and Jasmine King

11/14/2020

Left Hemisphere Regions

Interpeduncular Nucleus

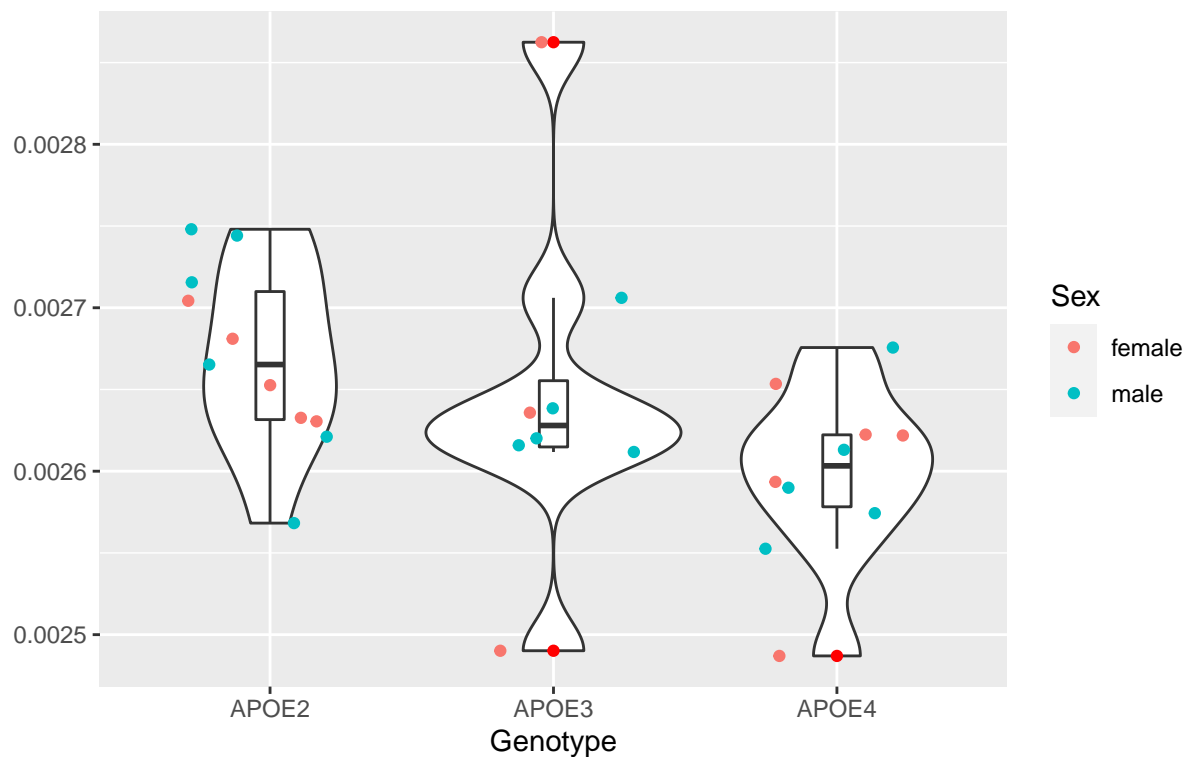
Red points denoting outliers



```
##           Df  Sum Sq  Mean Sq F value Pr(>F)
## geno       2 6.95e-08 3.477e-08   1.532  0.235
## Residuals 26 5.90e-07 2.269e-08
```

Cerebellar Cortex

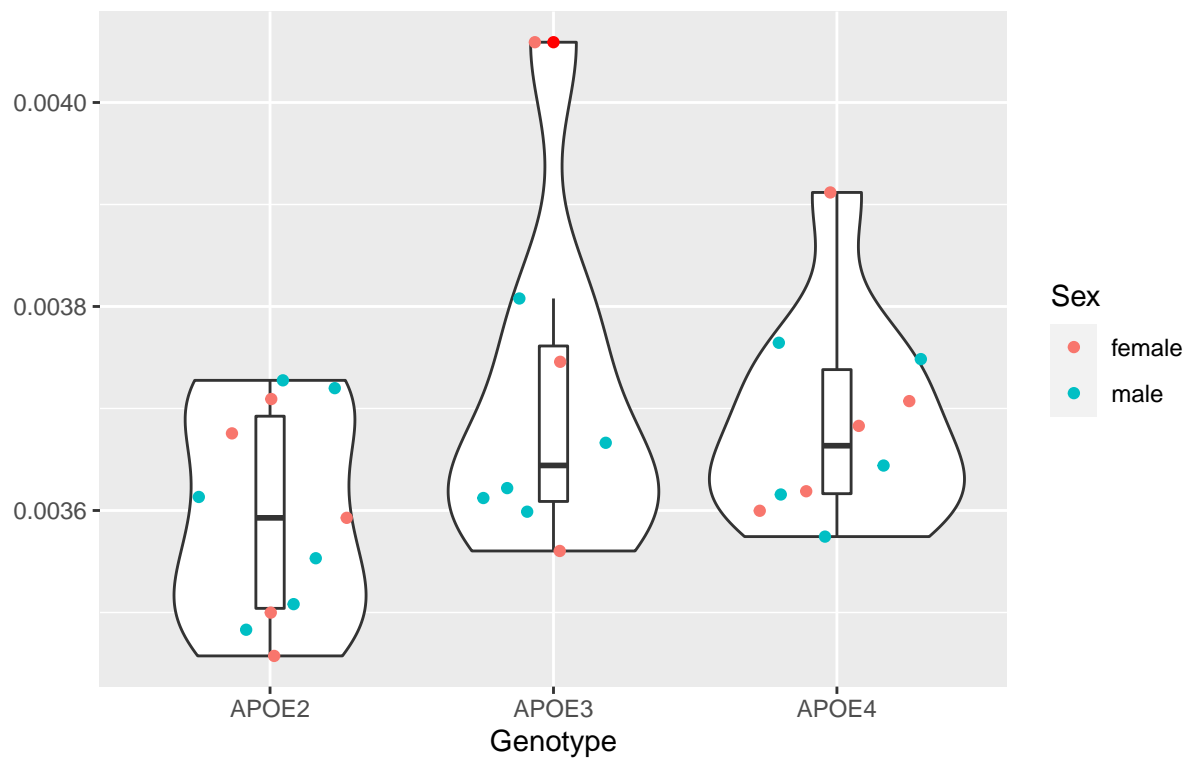
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 2.727e-08 1.364e-08   2.643 0.0902 .
## Residuals    26 1.342e-07 5.160e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Dentate (Lateral) Nucleus of Cerebellum

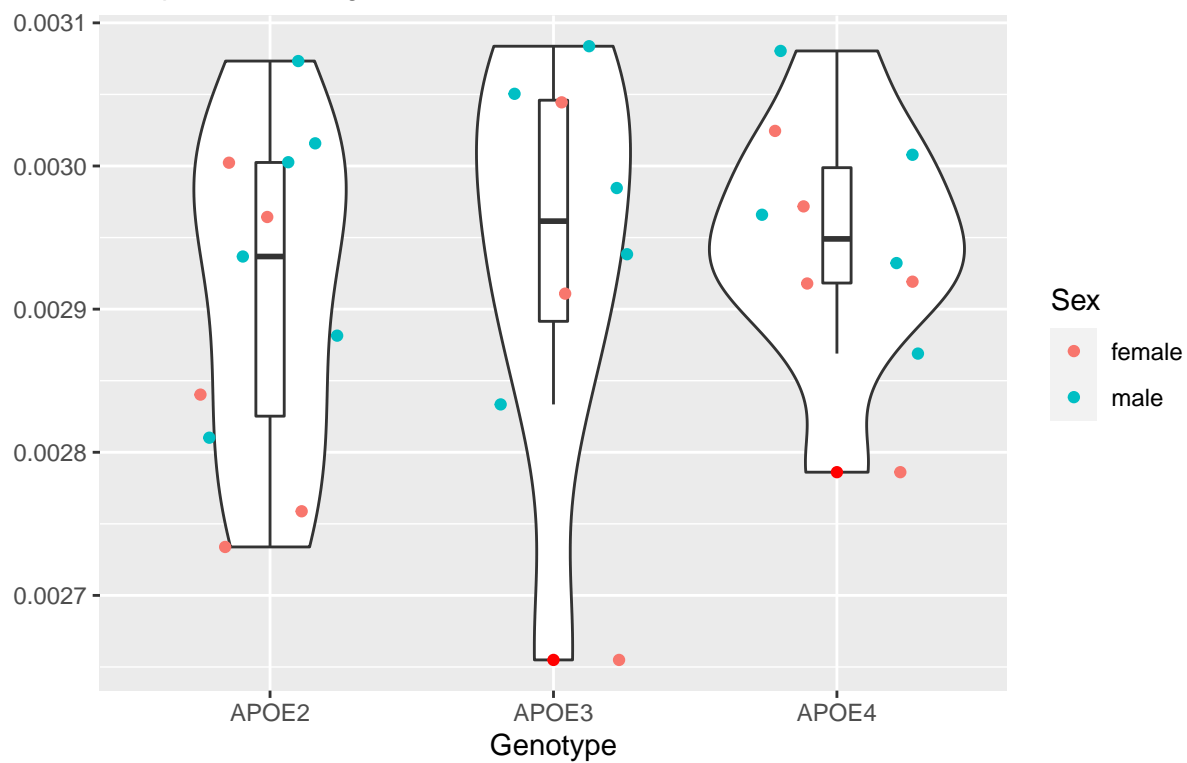
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.340e-08	3.669e-08	2.496	0.102
## Residuals	26	3.822e-07	1.470e-08		

Interposed Nucleus of Cerebellum

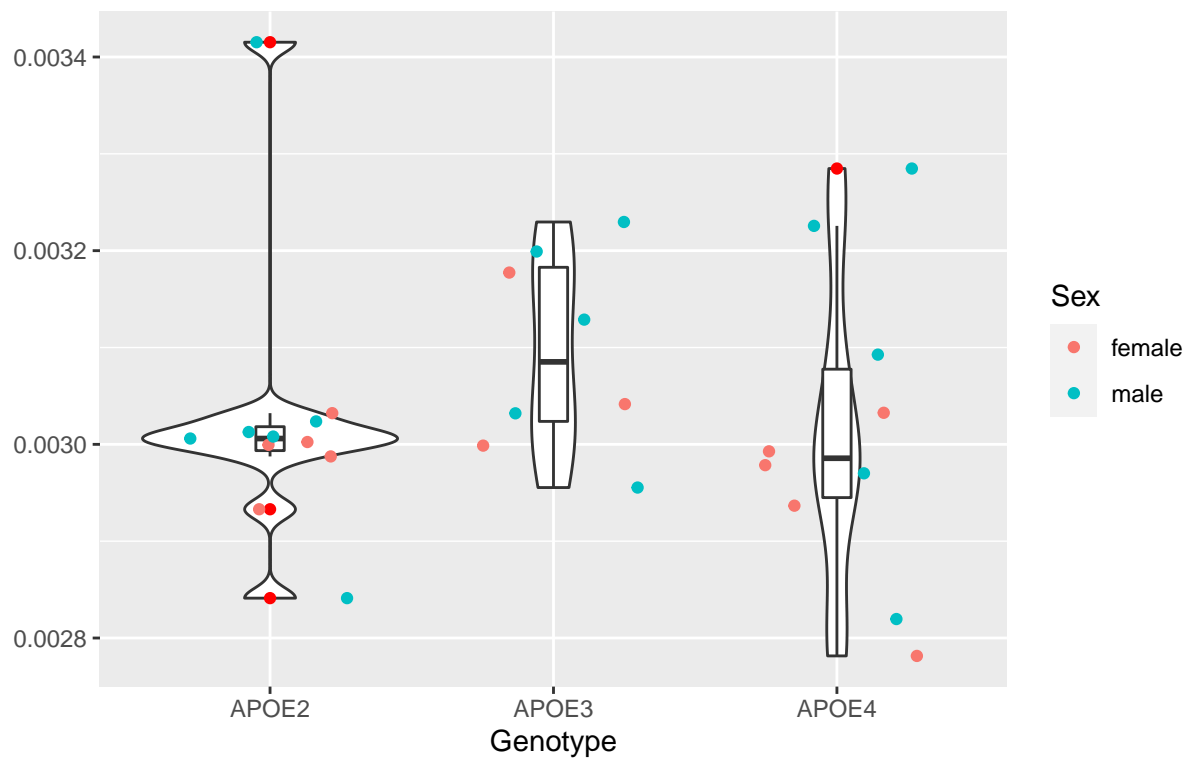
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.500e-09	3.755e-09	0.296	0.746
## Residuals	26	3.296e-07	1.268e-08		

Fastigial Medial Dorsolateral Nucleus of Cerebellum

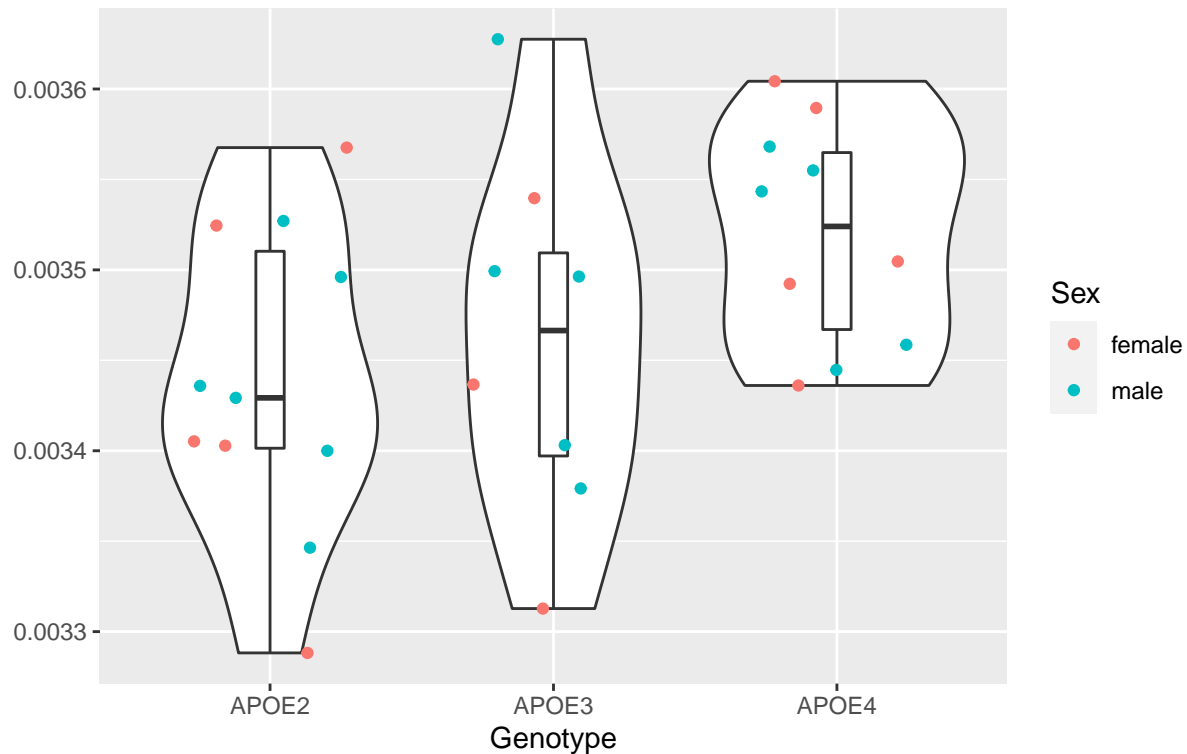
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.550e-08	1.775e-08	0.93	0.407
## Residuals	26	4.965e-07	1.909e-08		

Fastigial Medial Nucleus of Cerebellum

Red points denoting outliers



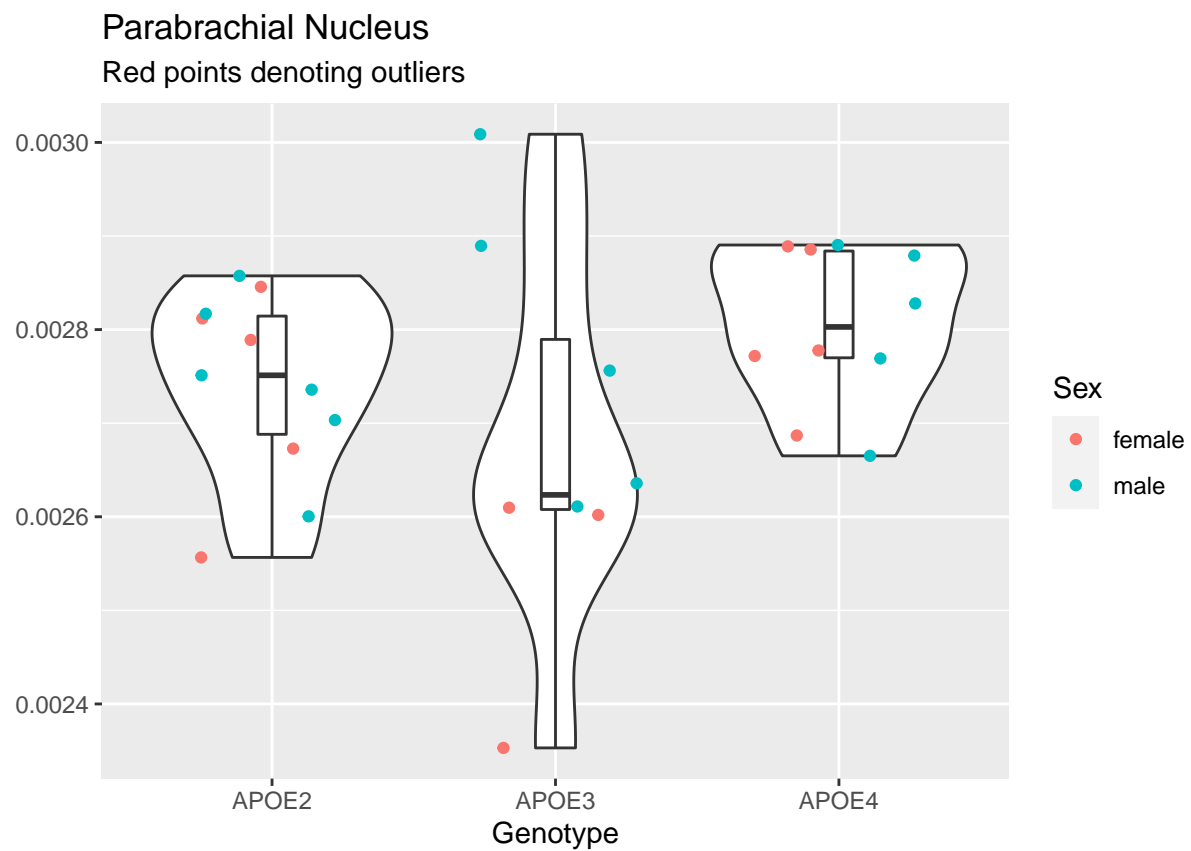
```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## geno         2 3.591e-08 1.795e-08    2.698 0.0861 .
## Residuals    26 1.730e-07 6.653e-09
```

```
## ---
```

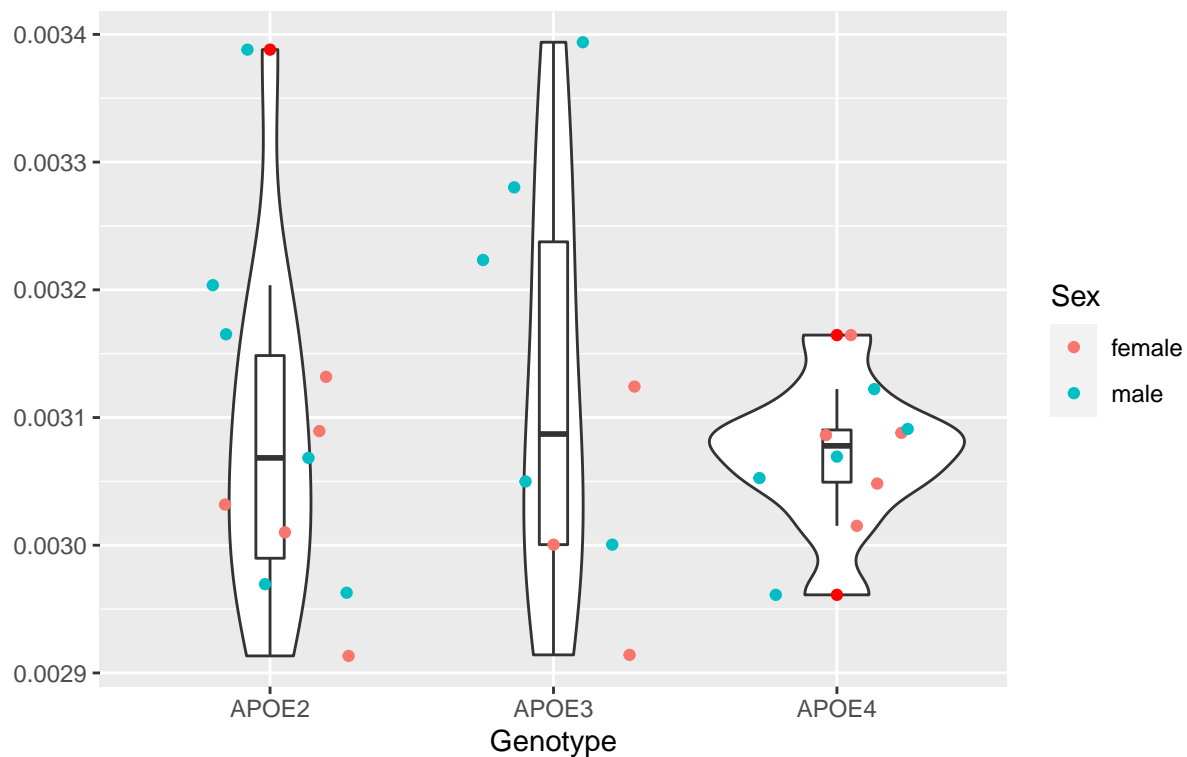
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#{r VII, echo = FALSE} #ggplot(data = new, aes(factor(geno), VII)) + #geom_violin() +
#geom_boxplot(width = 0.1, outlier.color = "red") + #geom_jitter(height = 0, width = 0.3) + #labs(x
= "Genotype", #y = "", #title = "Ventral Lateral Lemniscus Nucleus", #subtitle = "Red points denoting
outliers")
```

```
#res.aov <- aov(VII ~ geno, data = new) #summary(res.aov) #
```



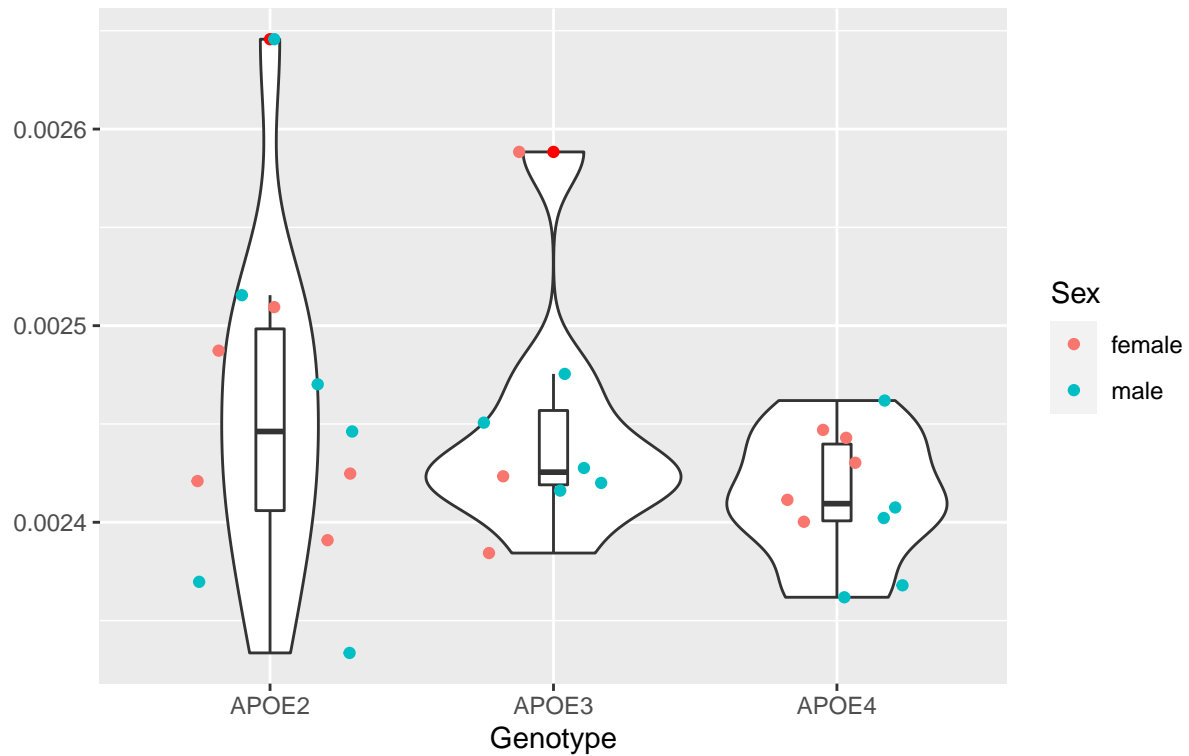
Parabrachial Medial Nucleus and Koelliker Fuse Nucleus Red points denoting outliers



```
##          Df      Sum Sq   Mean Sq F value Pr(>F)
## geno      2  1.320e-08  6.610e-09   0.433  0.653
## Residuals 26  3.965e-07  1.525e-08
```


Parvicellular Reticular Nucleus and Principal Sensory Trigeminal Nucleus

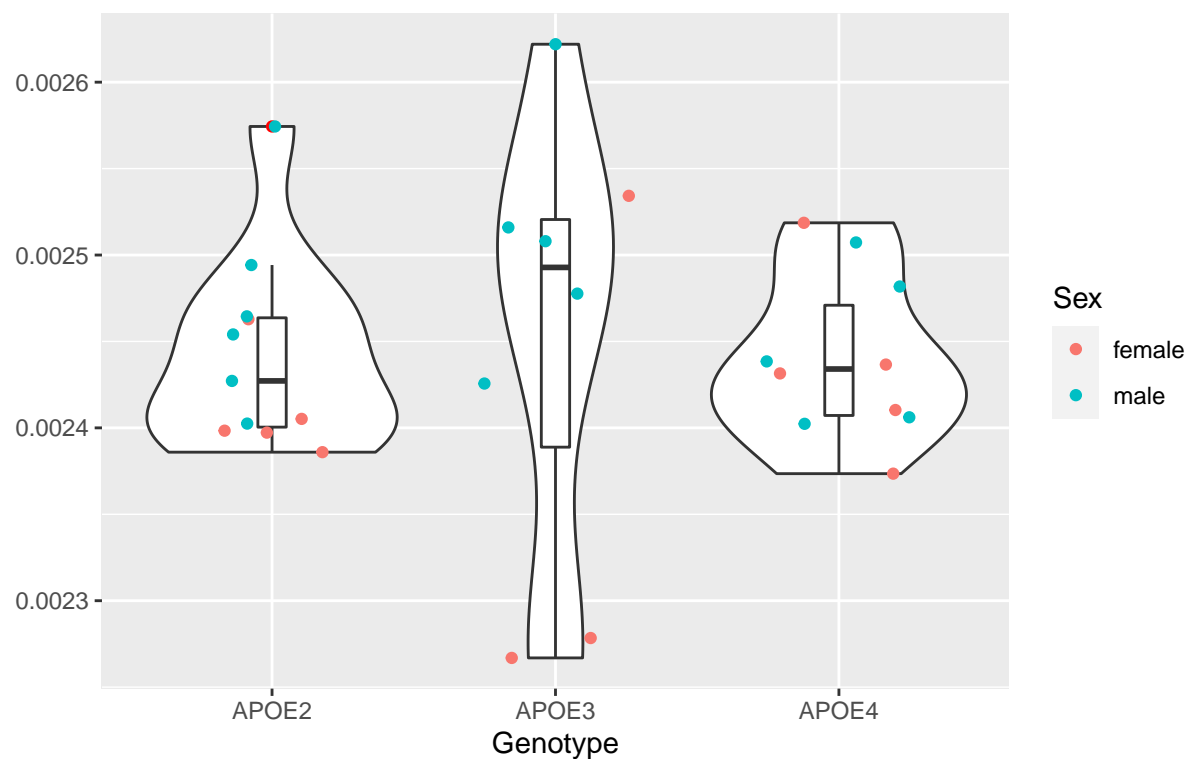
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.039e-08	5.196e-09	1.233	0.308
## Residuals	26	1.096e-07	4.215e-09		

Central Gray

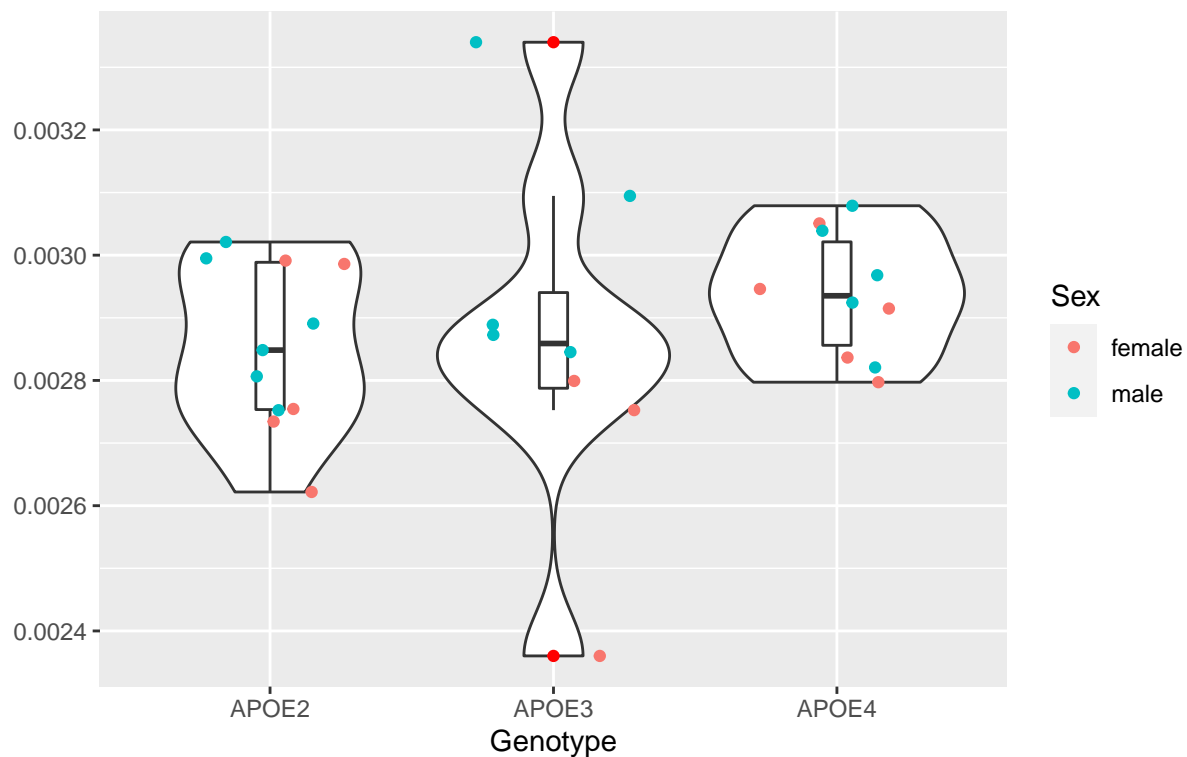
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.500e-10	4.270e-10	0.069	0.933
## Residuals	26	1.605e-07	6.174e-09		

Pedunculotegmental Medial Paralemniscial and Supratrigeminal Nuclei

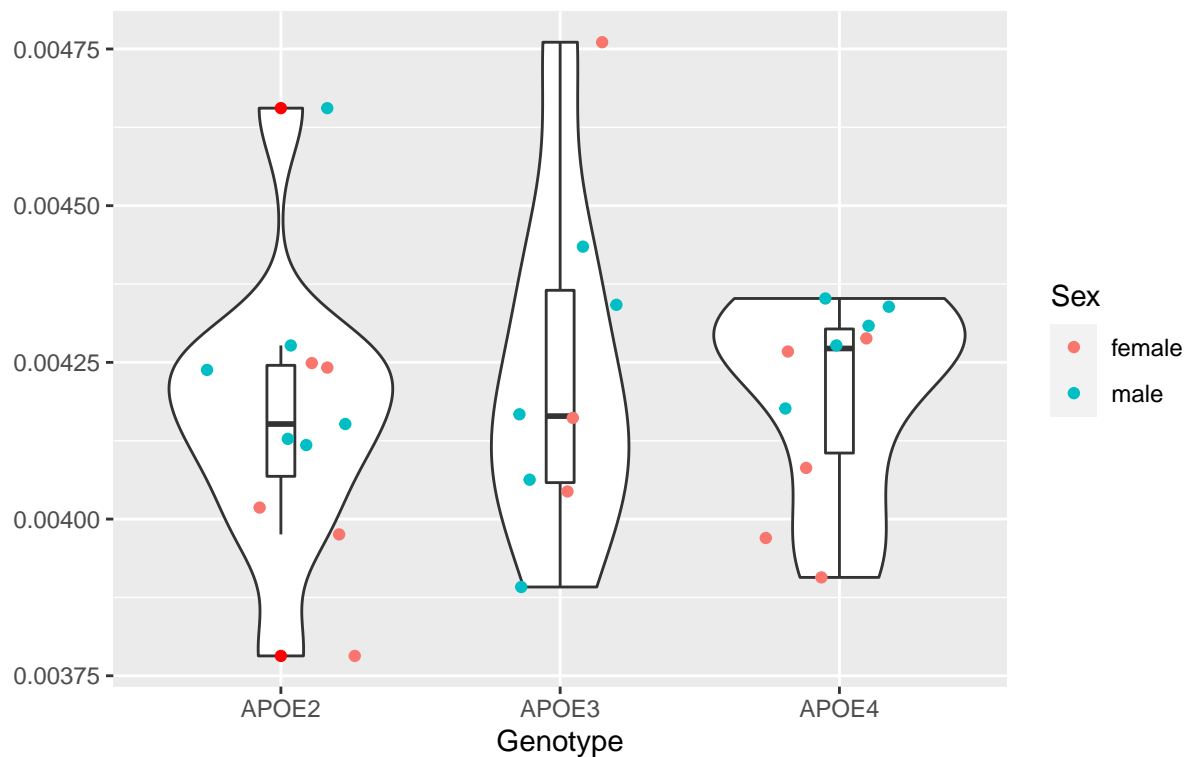
Red points denoting outliers



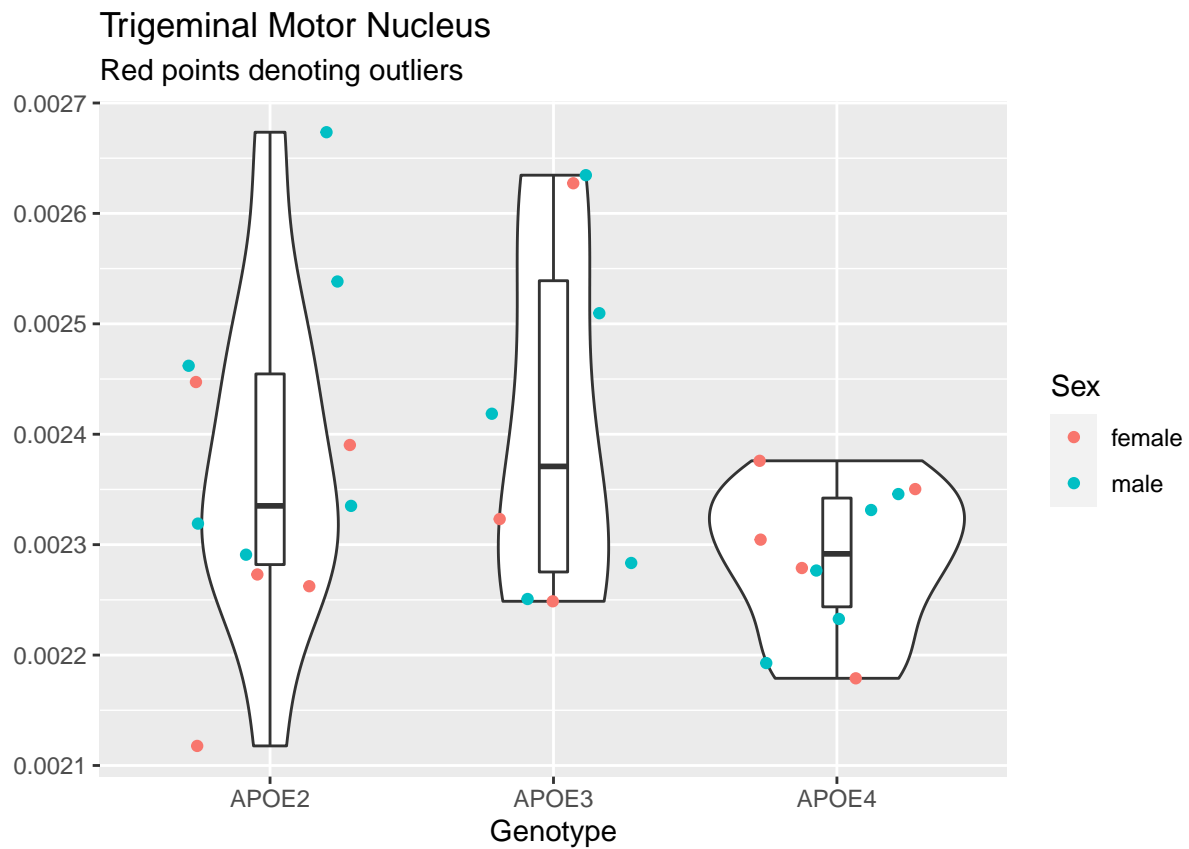
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.960e-08	1.981e-08	0.631	0.54
## Residuals	26	8.156e-07	3.137e-08		

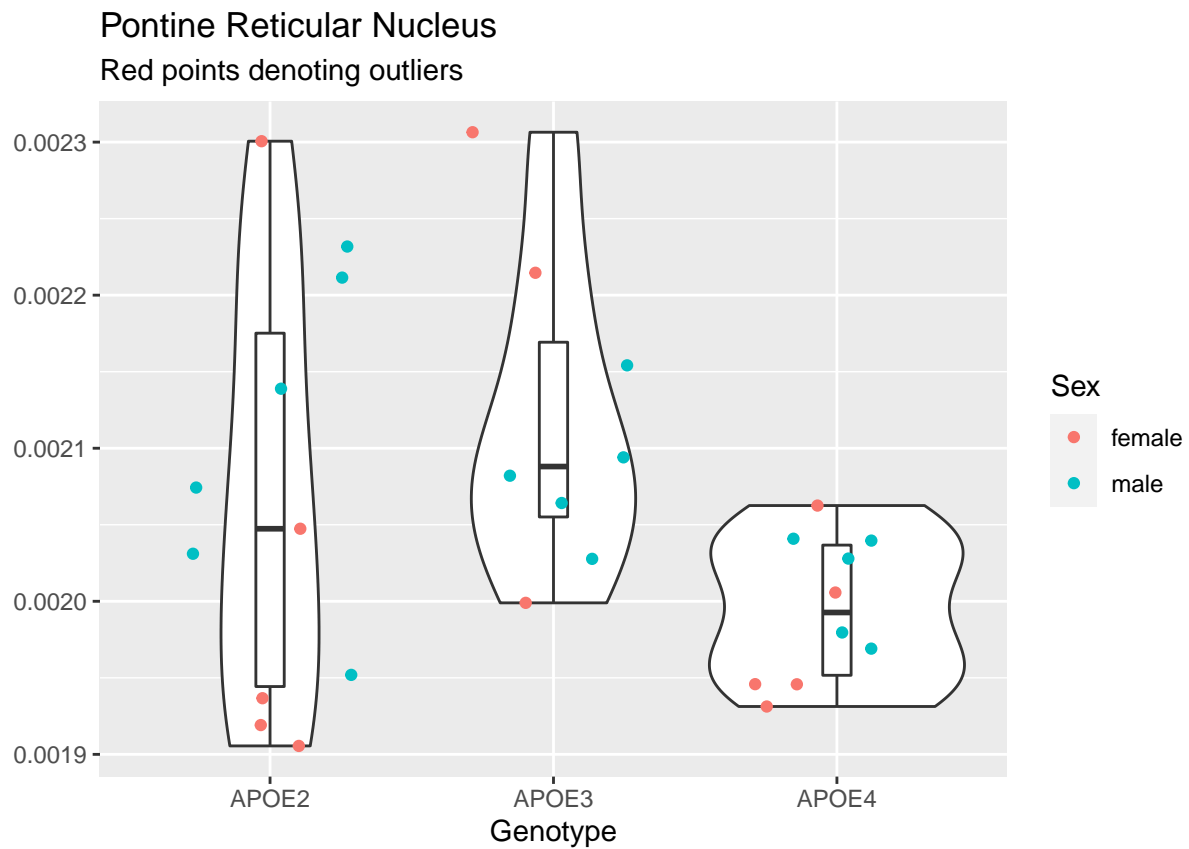
Motor Root of Trigeminal Nerve

Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.040e-08	1.018e-08	0.216	0.807
## Residuals	26	1.227e-06	4.719e-08		

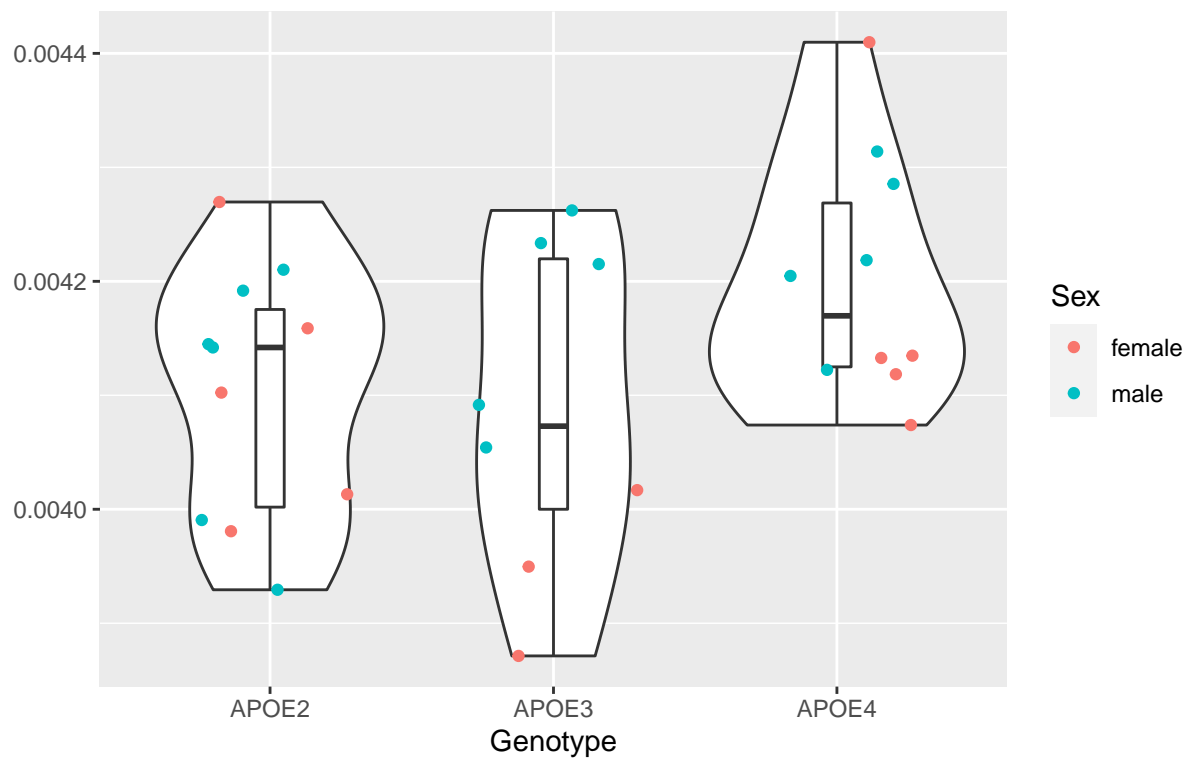




```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 6.955e-08 3.478e-08   3.223 0.0562 .
## Residuals    26 2.806e-07 1.079e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Raphe Nucleus

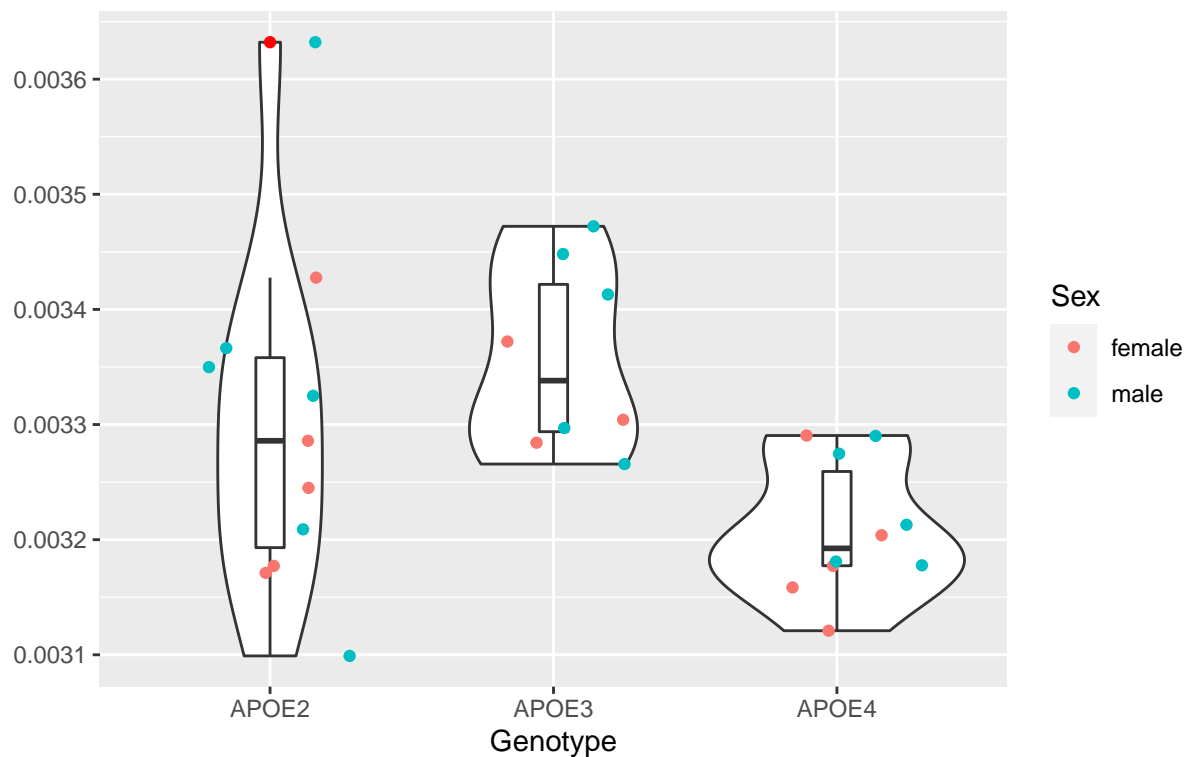
Red points denoting outliers



```
##           Df      Sum Sq  Mean Sq F value Pr(>F)
## geno         2 7.380e-08 3.69e-08   2.656 0.0892 .
## Residuals    26 3.613e-07 1.39e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Trigeminal Sensory Nucleus

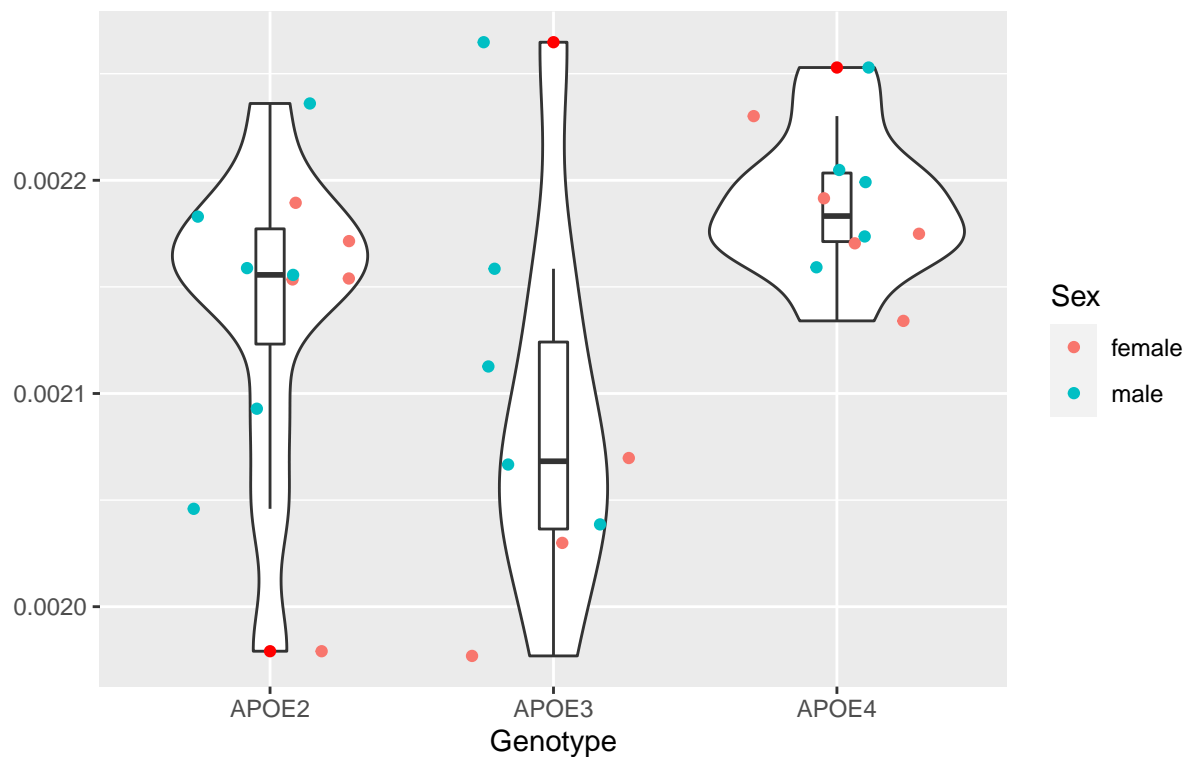
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.018e-07 5.089e-08   4.512 0.0208 *
## Residuals    26 2.933e-07 1.128e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Dorsal Tegmentum

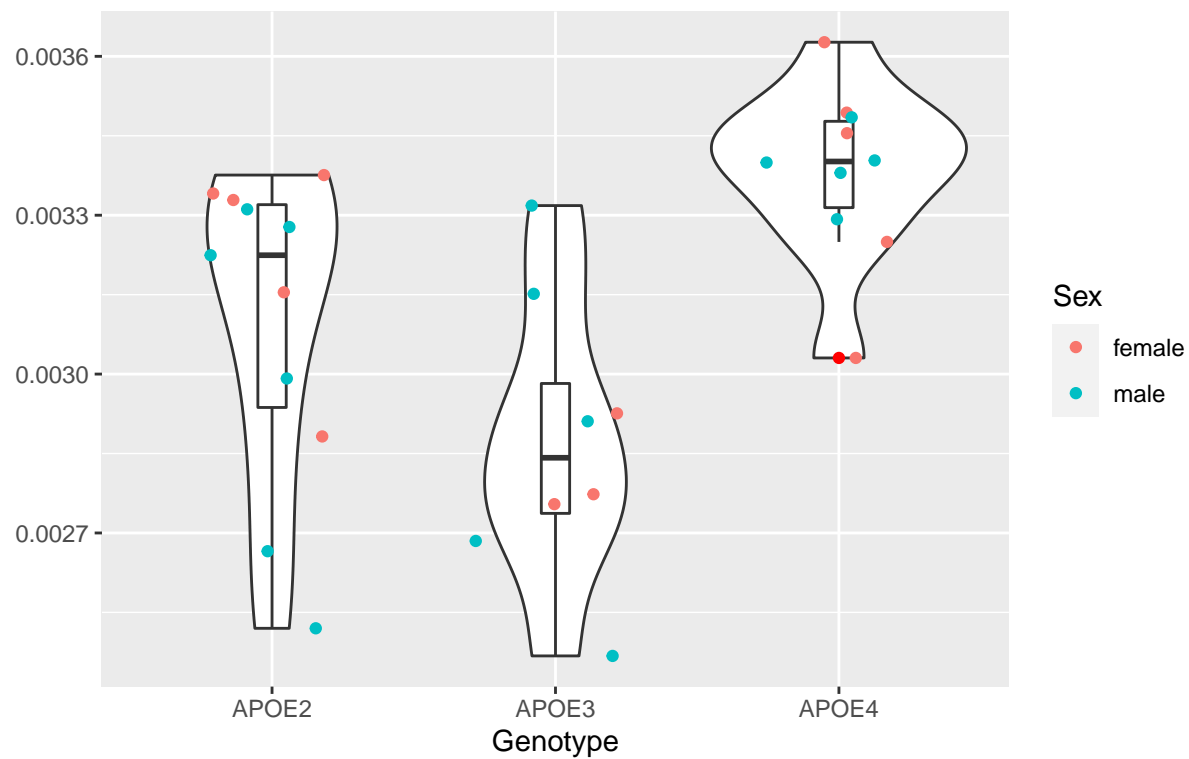
Red points denoting outliers



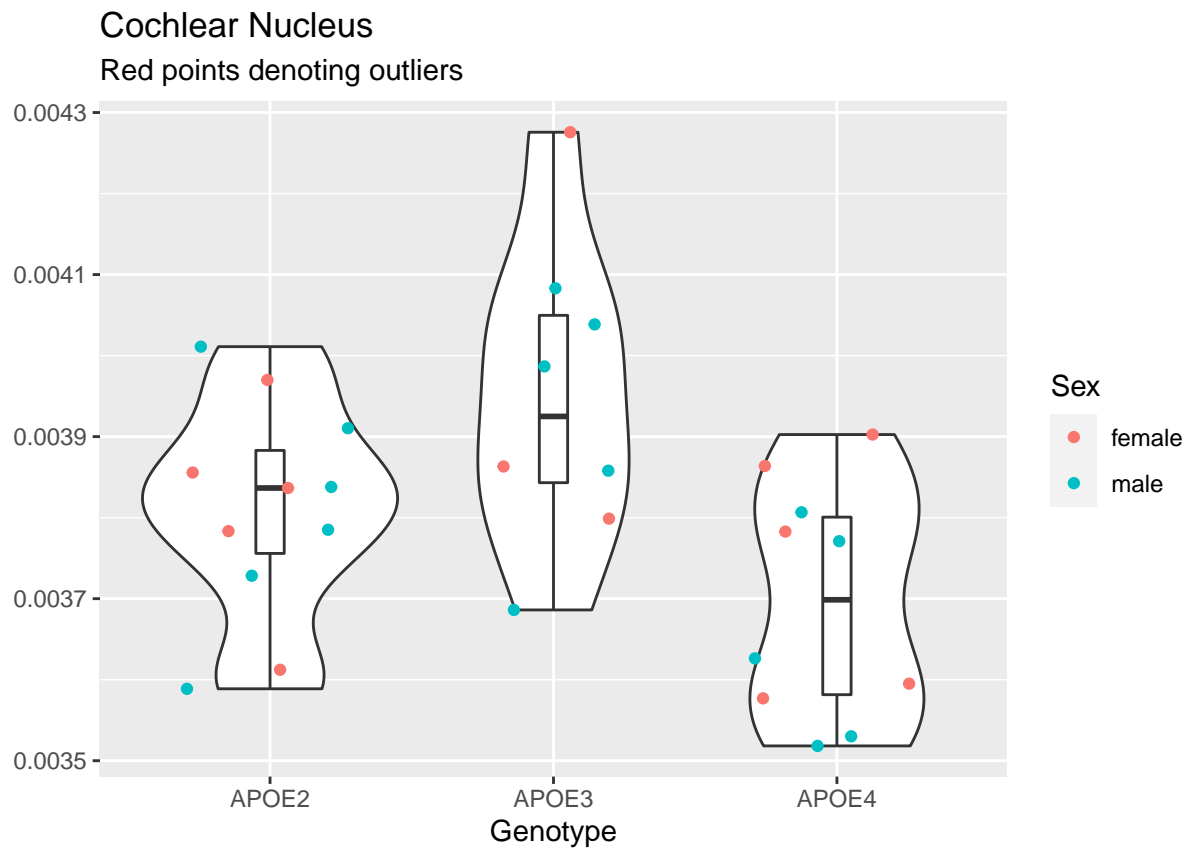
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 4.419e-08 2.209e-08   4.829 0.0165 *
## Residuals    26 1.190e-07 4.575e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Tegmental Nucleus

Red points denoting outliers



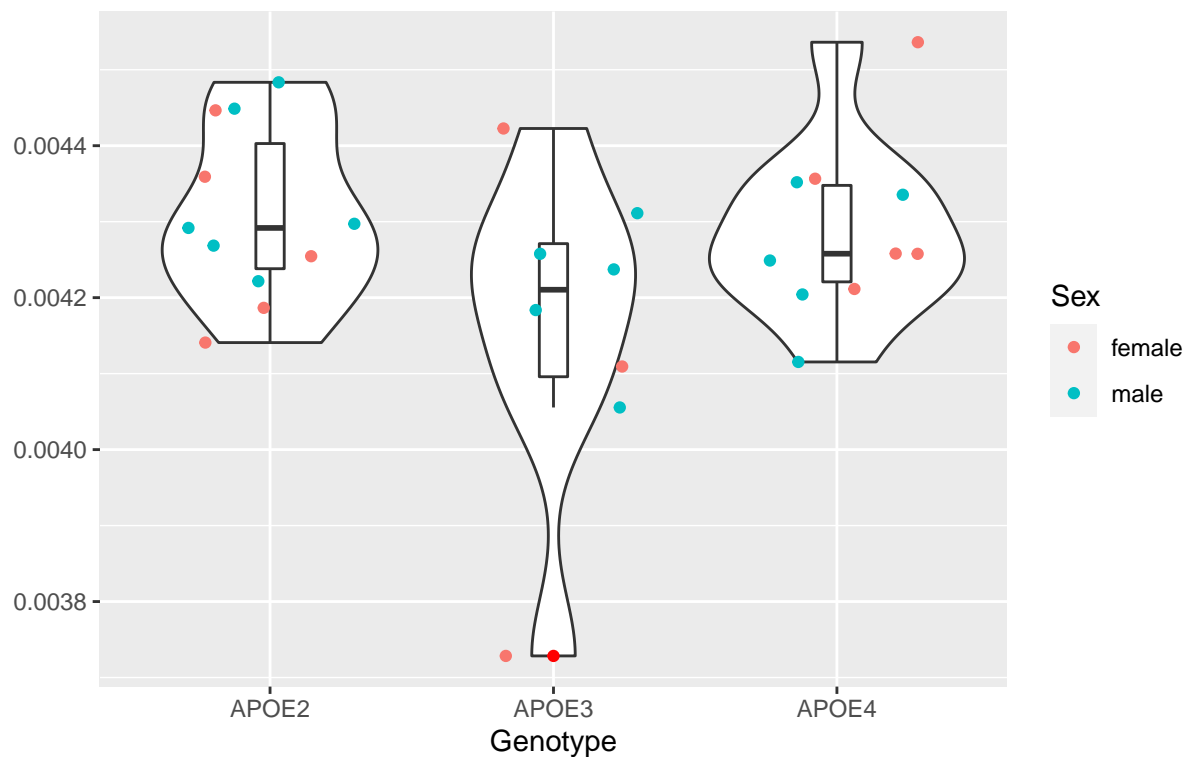
```
##          Df    Sum Sq  Mean Sq F value   Pr(>F)
## geno         2 1.171e-06 5.855e-07   9.472 0.000813 ***
## Residuals    26 1.607e-06 6.180e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##          Df    Sum Sq  Mean Sq F value   Pr(>F)
## geno         2 2.809e-07 1.404e-07    6.07 0.00687 **
## Residuals    26 6.016e-07 2.314e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pontine Nucleus

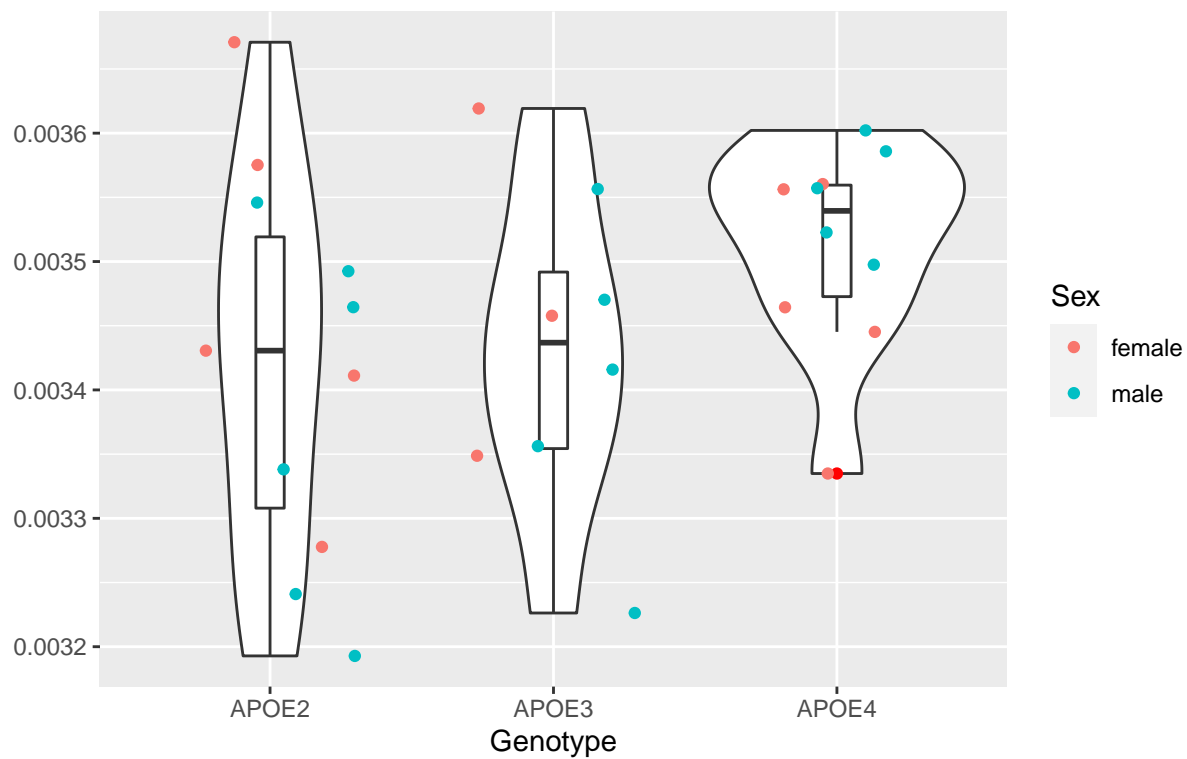
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.089e-07 5.445e-08   2.557 0.0969 .
## Residuals    26 5.536e-07 2.129e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Reticulotegmental Nucleus of Pons

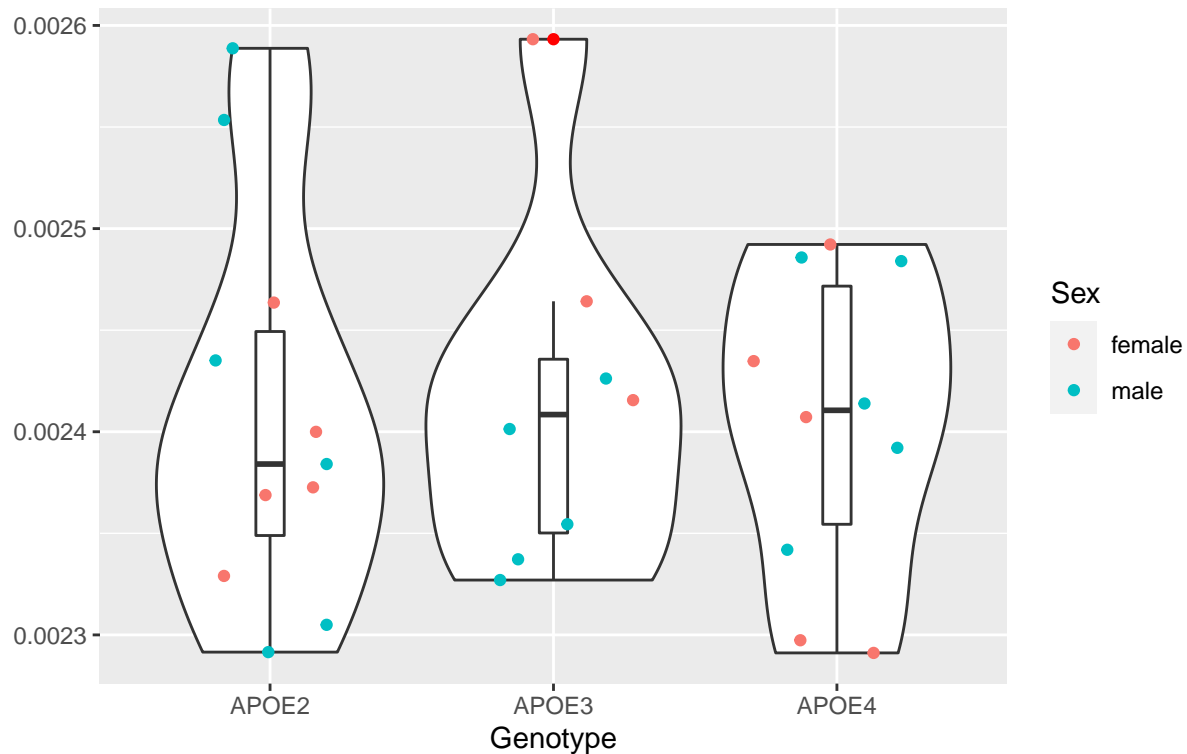
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.980e-08	2.489e-08	1.671	0.208
## Residuals	26	3.871e-07	1.489e-08		

Olivary Complex

Red points denoting outliers

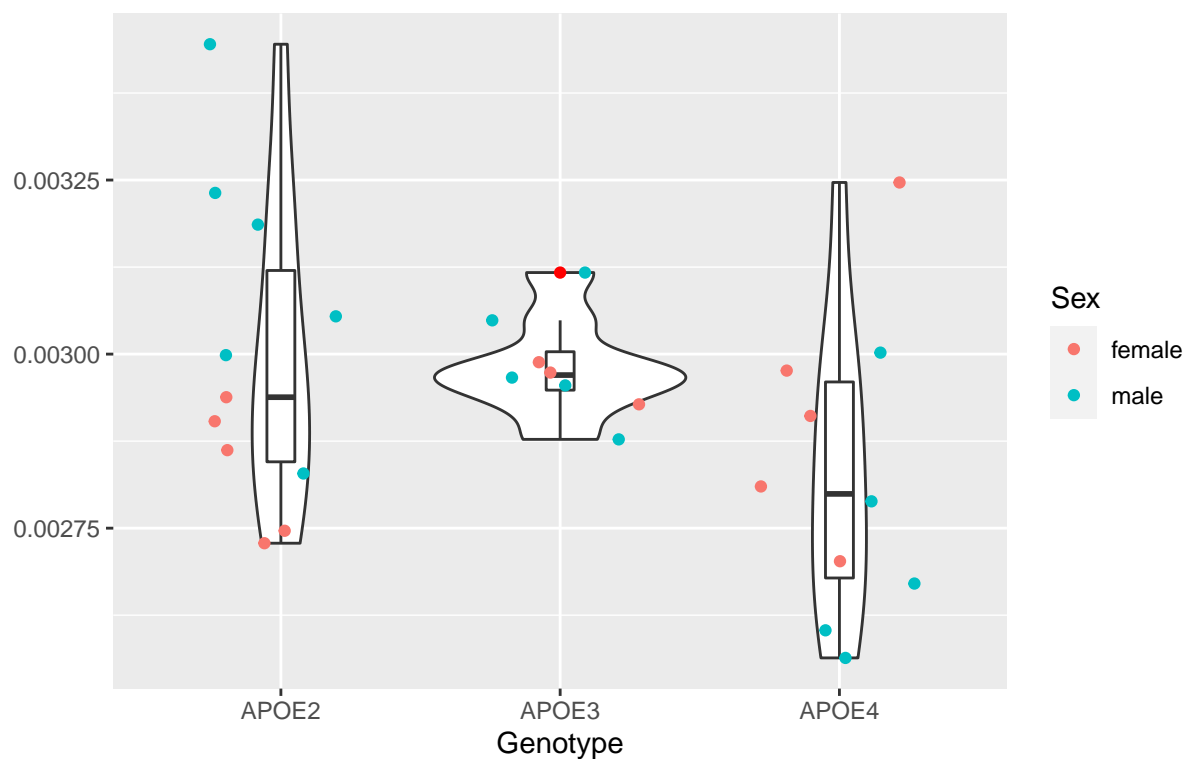


```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## geno       2 5.300e-10 2.640e-10   0.035  0.965
## Residuals 26 1.935e-07 7.441e-09
```

```
#{r PnRt, echo = FALSE} #ggplot(data = new, aes(factor(geno), PnRt)) + # geom_violin() + #
geom_boxplot(width = 0.1, outlier.color = "red") + # geom_jitter(height = 0, width = 0.3) + # labs(x =
"Genotype", # y = "", # title = "Pontine Reticular Nucleus", # subtitle = "Red points denoting outliers")
#res.aov <- aov(PnRt ~ geno, data = new) #summary(res.aov) #"
```

Spinal Trigeminal Nucleus

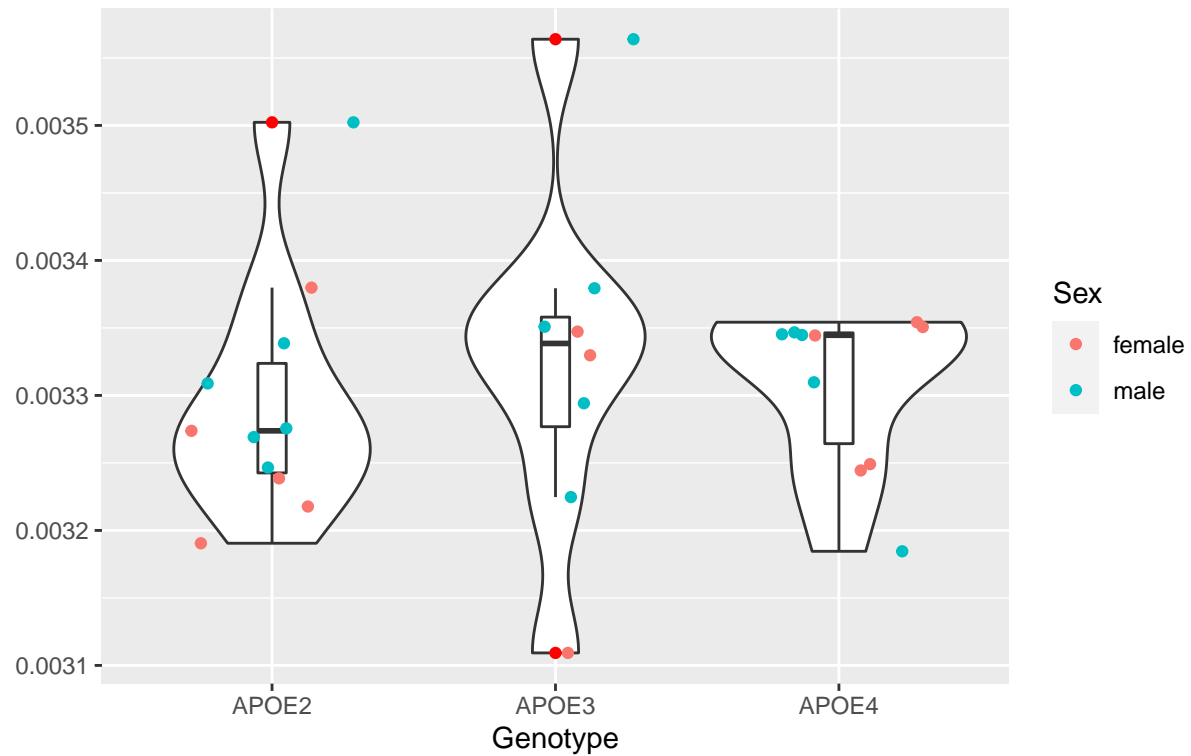
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.700e-07	8.499e-08	2.393	0.111
## Residuals	26	9.233e-07	3.551e-08		

Vestibular Nuclei

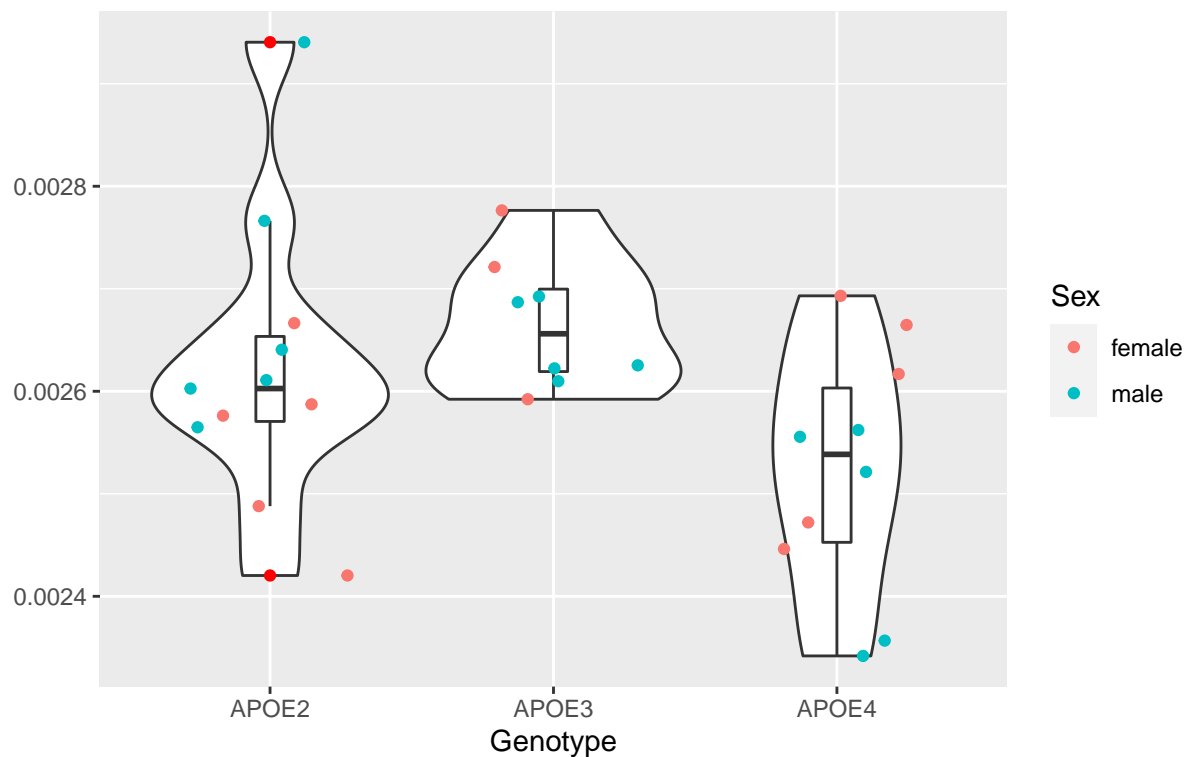
Red points denoting outliers



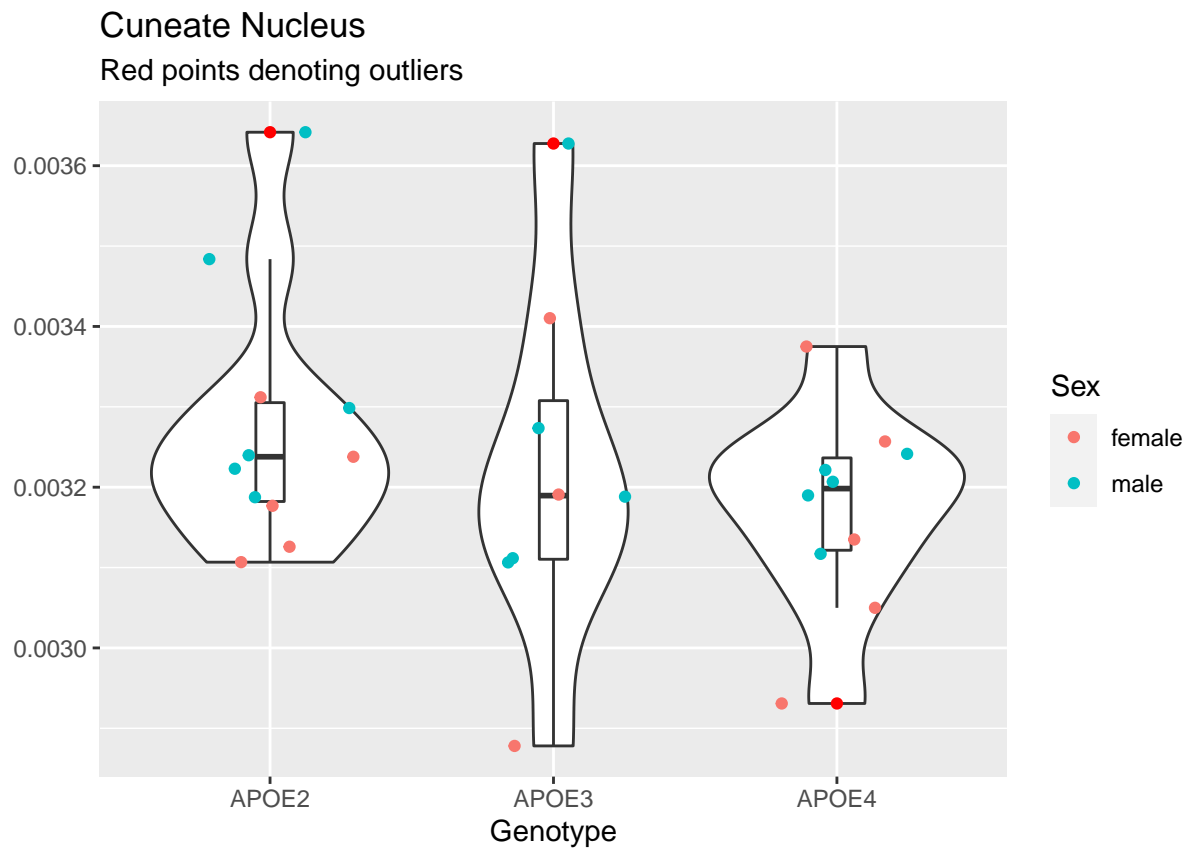
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.230e-09	2.115e-09	0.242	0.787
## Residuals	26	2.272e-07	8.739e-09		

Gigantocellular Reticular Nucleus

Red points denoting outliers



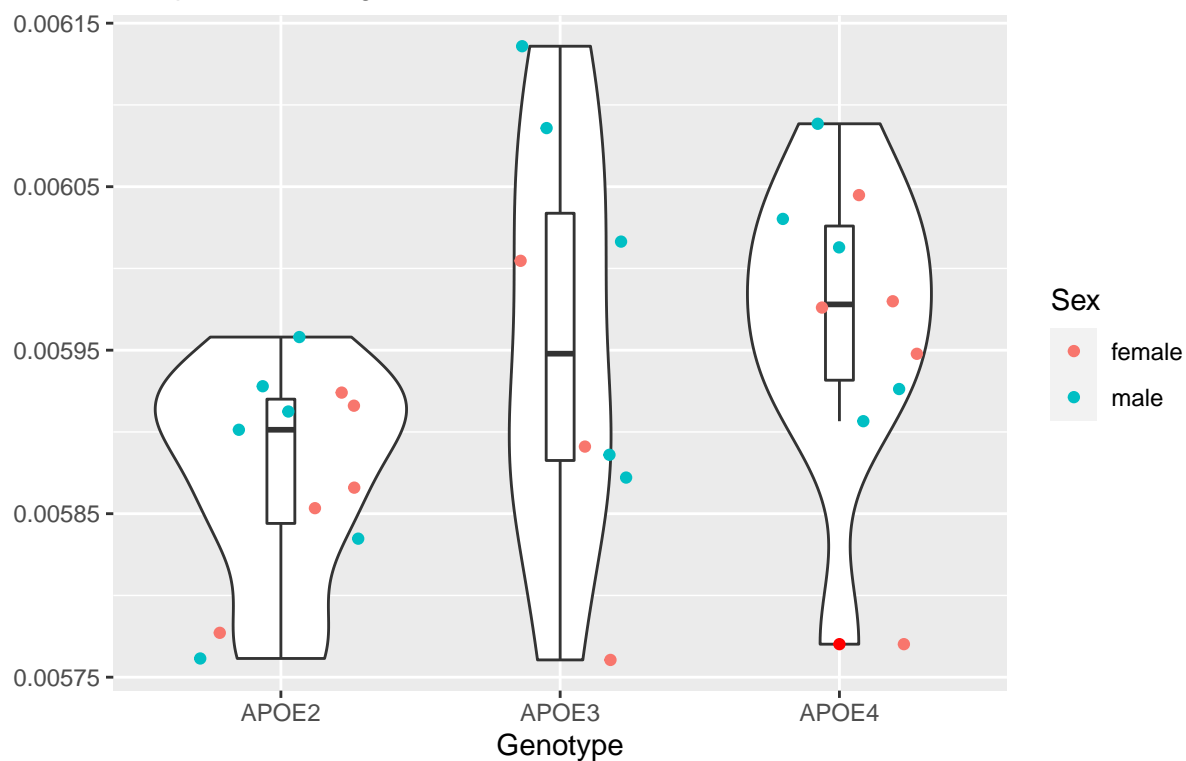
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.002e-07 5.009e-08   3.741 0.0373 *
## Residuals    26 3.482e-07 1.339e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 5.600e-08 2.800e-08   0.989  0.386
## Residuals 26 7.362e-07 2.831e-08
```

Anterior Commisure

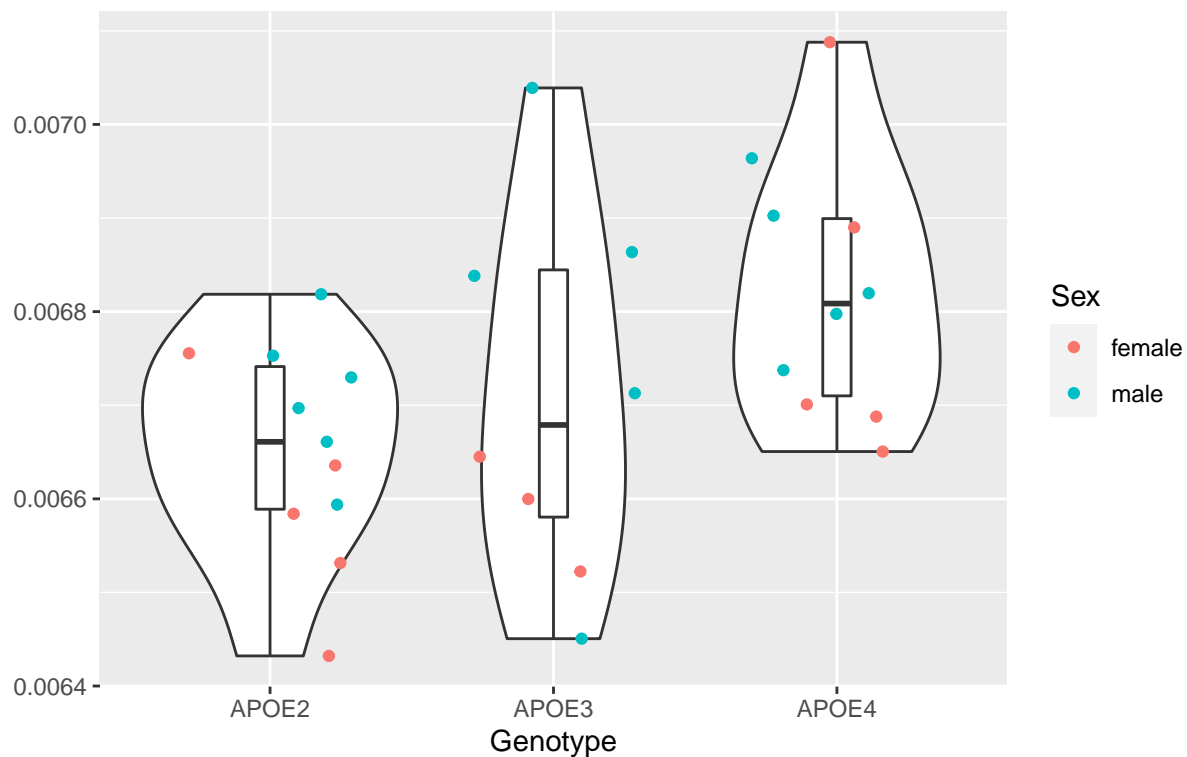
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 5.279e-08 2.639e-08   3.096 0.0622 .
## Residuals    26 2.217e-07 8.526e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Optic Tracts

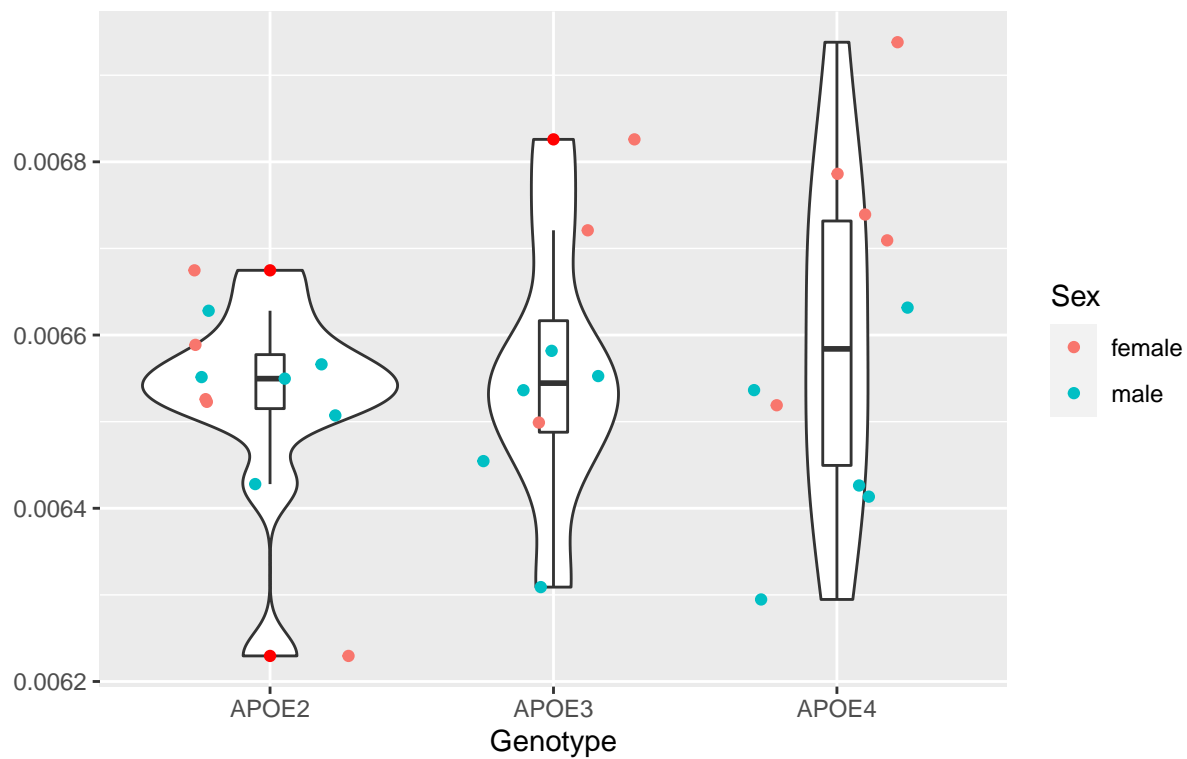
Red points denoting outliers



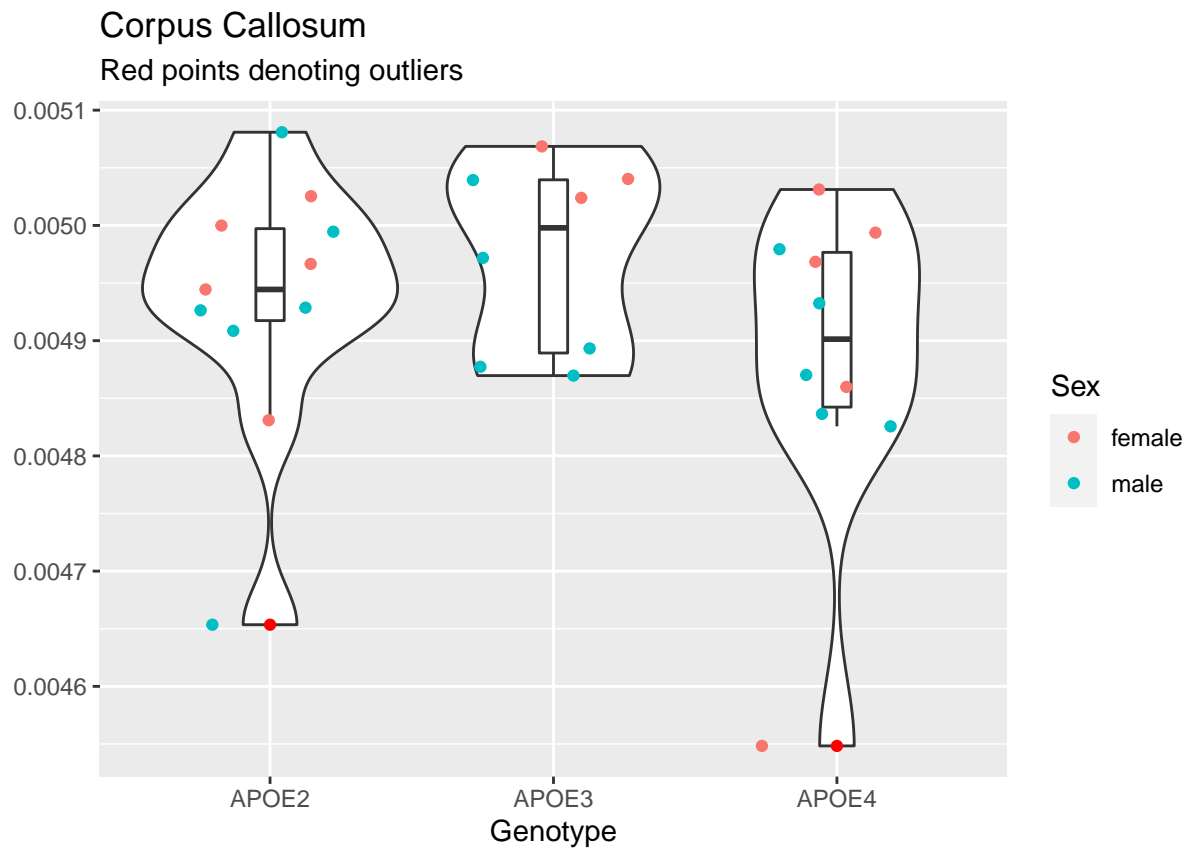
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno       2 1.553e-07 7.763e-08   3.562 0.0429 *
## Residuals 26 5.667e-07 2.179e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fimbria

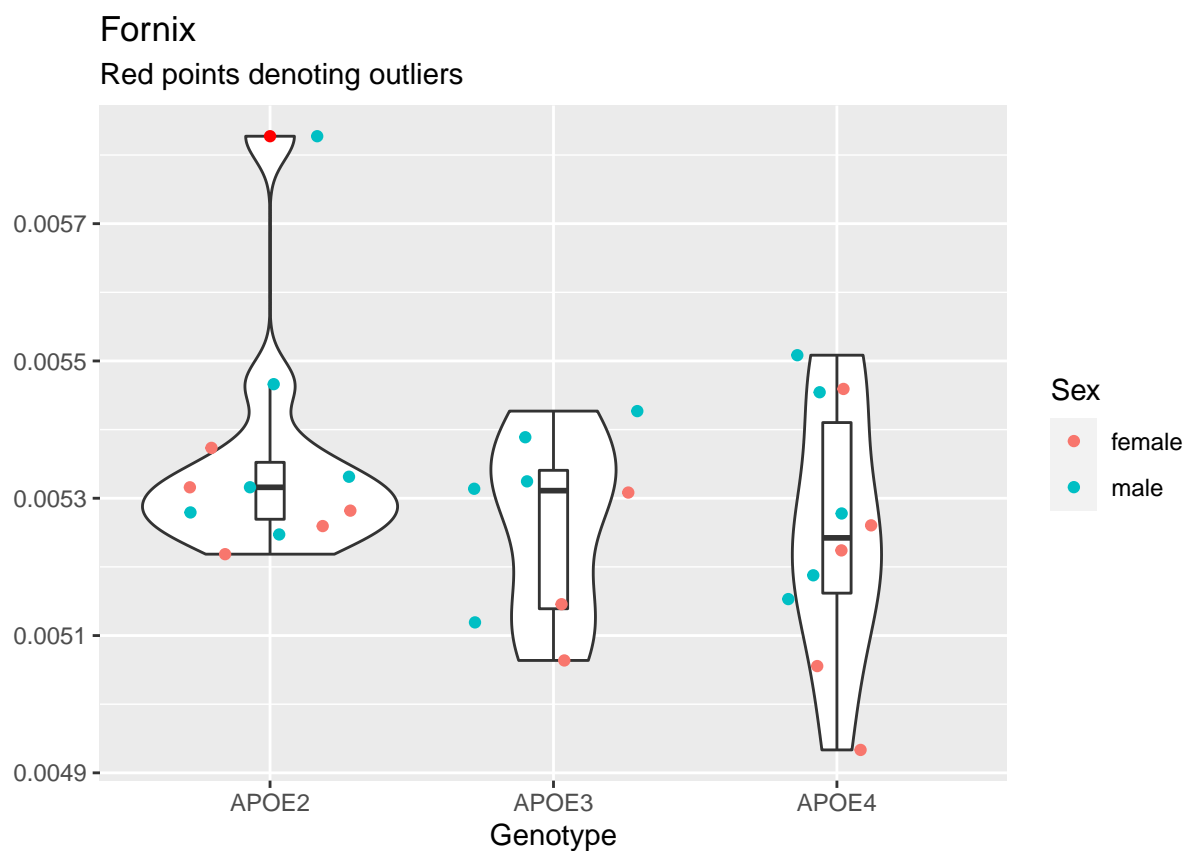
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.920e-08	1.460e-08	0.573	0.571
## Residuals	26	6.628e-07	2.549e-08		



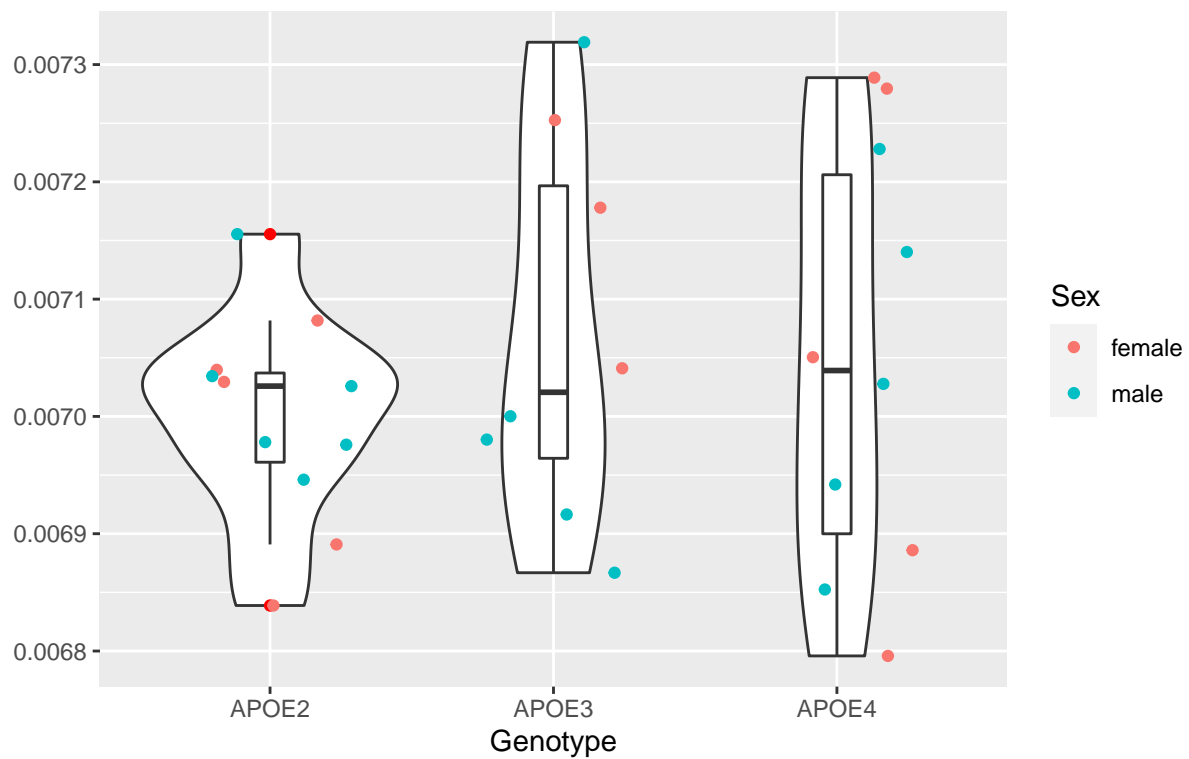
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 3.530e-08 1.766e-08   1.322  0.284
## Residuals 26 3.473e-07 1.336e-08
```



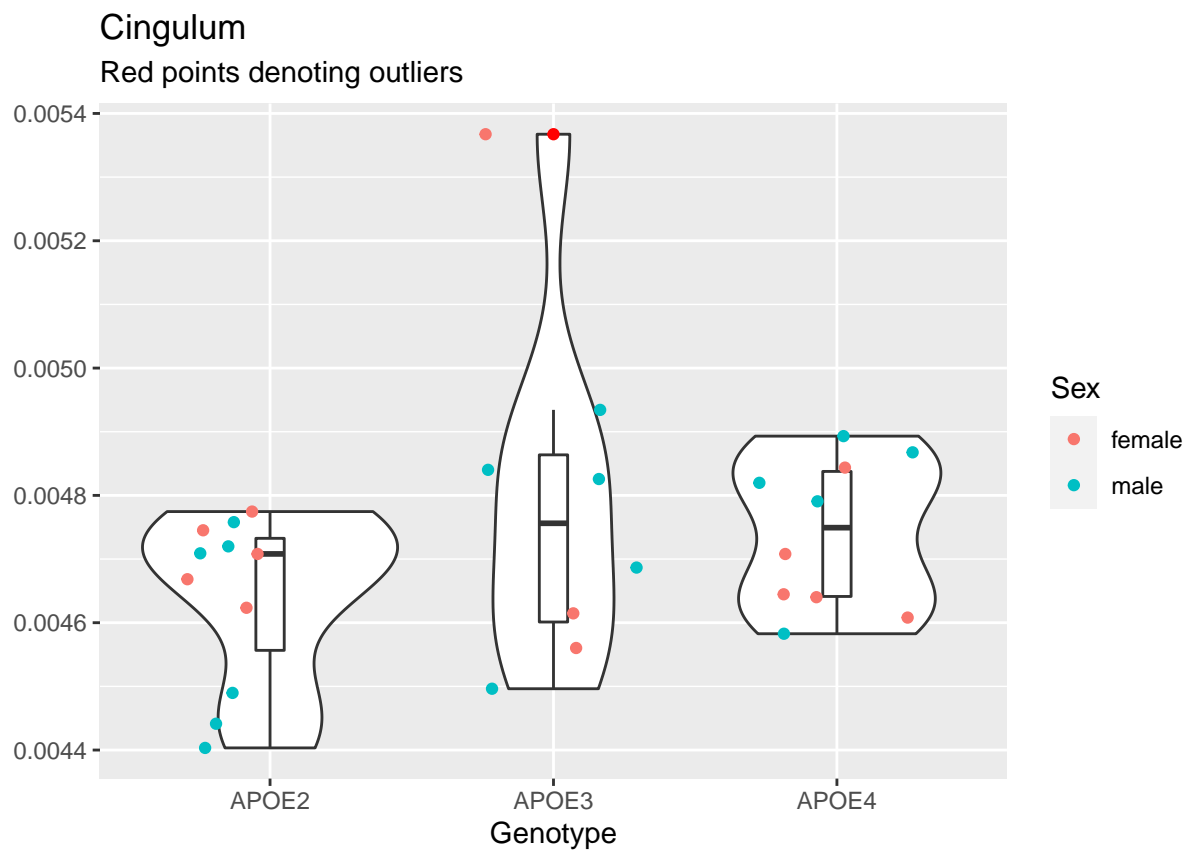
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.900e-08	3.452e-08	1.246	0.304
## Residuals	26	7.204e-07	2.771e-08		

Stria Terminalis

Red points denoting outliers

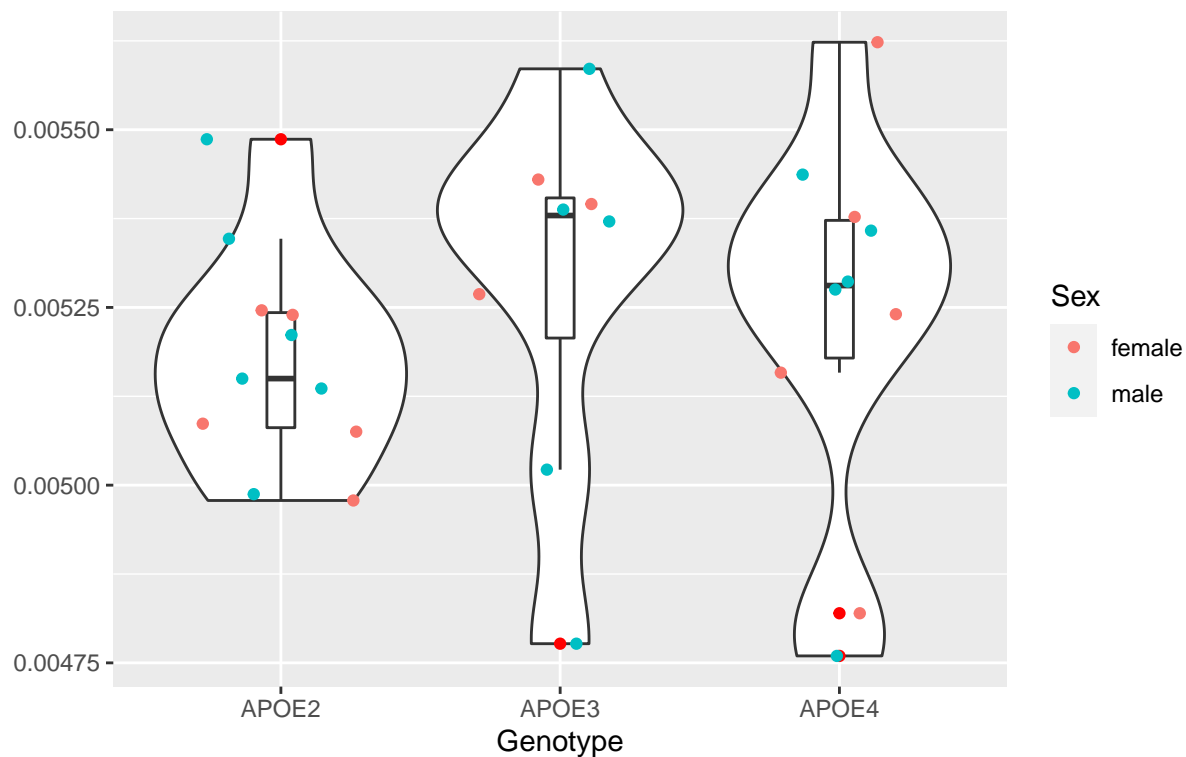


```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno      2  2.51e-08  1.255e-08   0.588  0.563
## Residuals 26  5.55e-07  2.135e-08
```

```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno       2 1.137e-07 5.686e-08   1.764  0.191
## Residuals 26 8.381e-07 3.224e-08
```

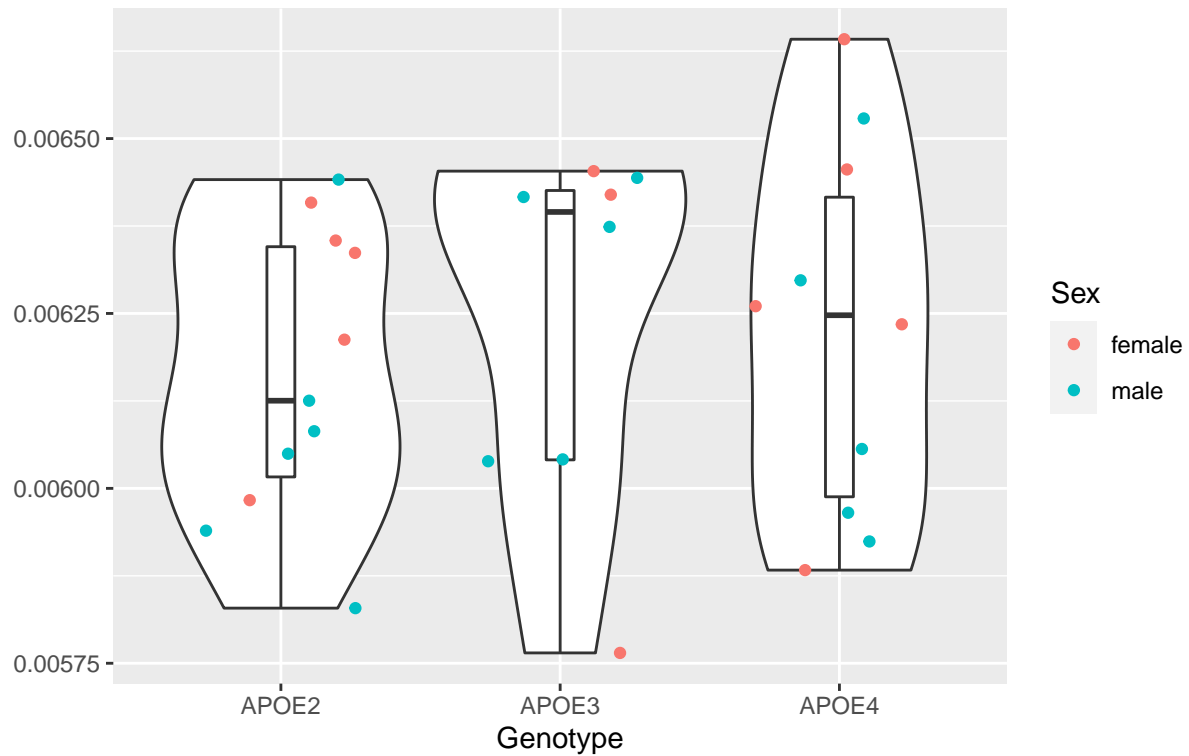
Lateral Olfactory Tract Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	5.030e-08	2.516e-08	0.49	0.618
## Residuals	26	1.335e-06	5.134e-08		

Ventral Hippocampal Commissure

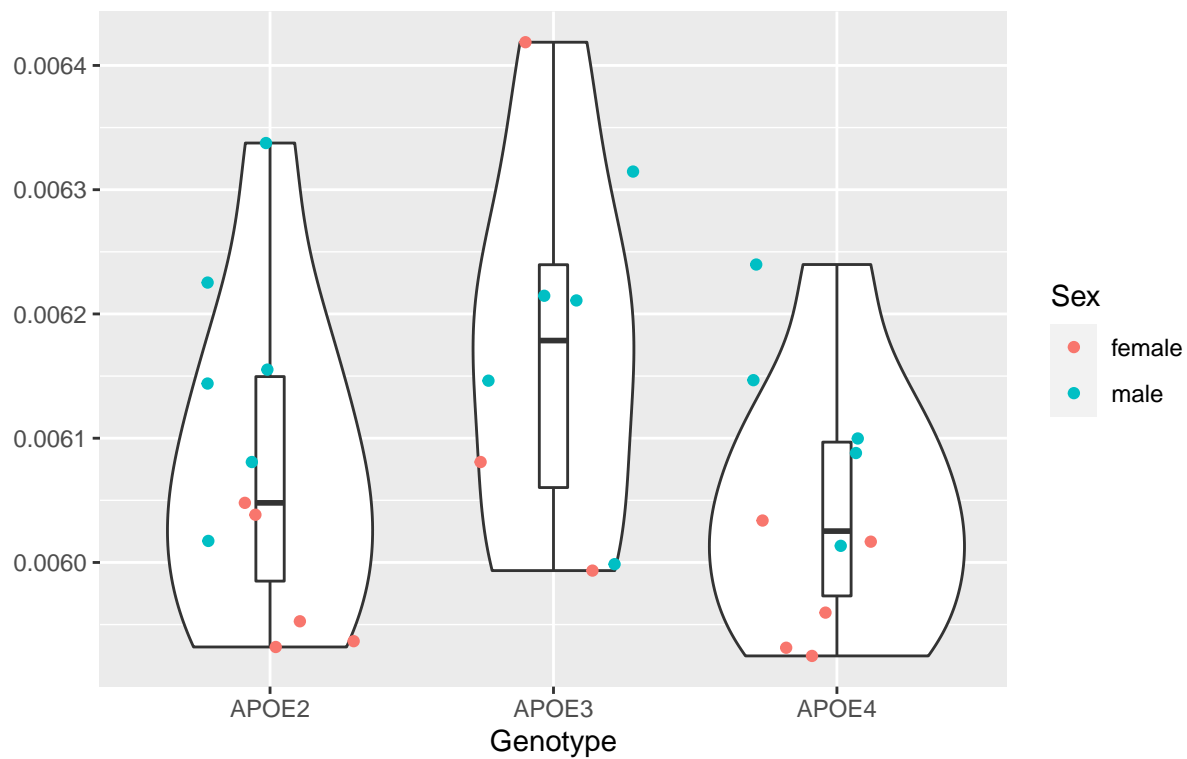
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.830e-08	1.913e-08	0.326	0.725
## Residuals	26	1.525e-06	5.866e-08		

Internal Capsule

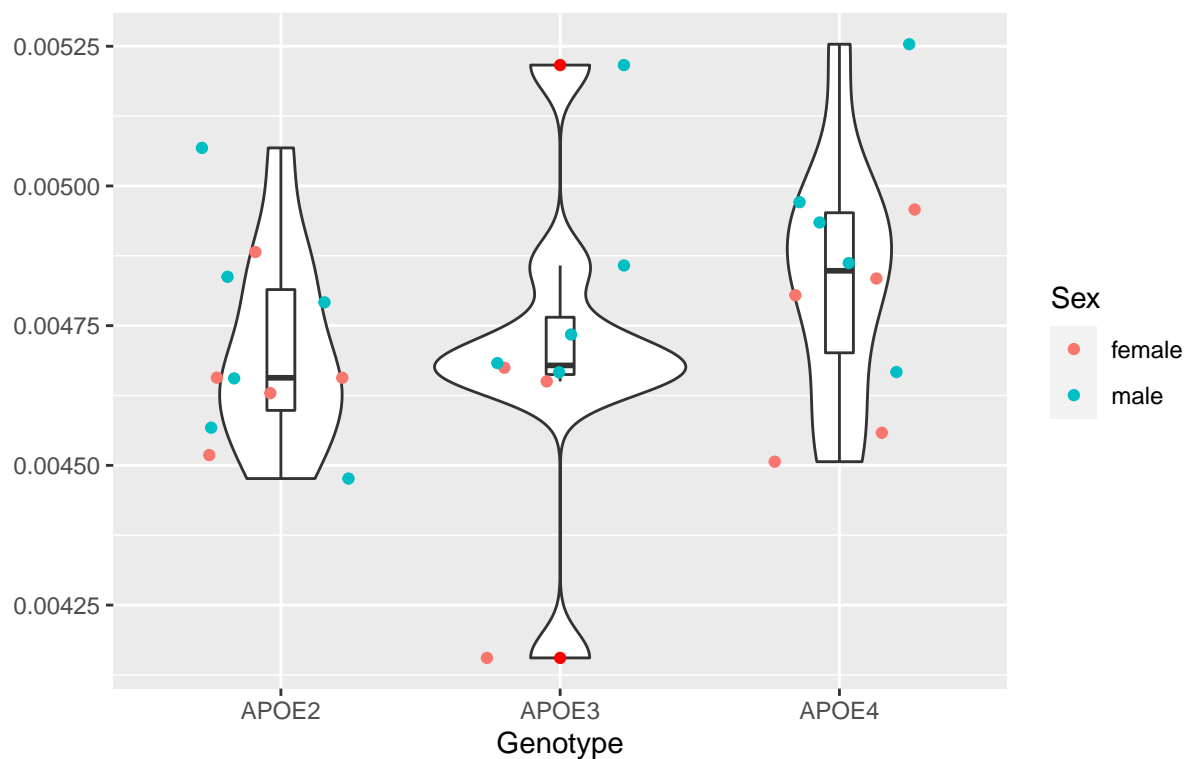
Red points denoting outliers



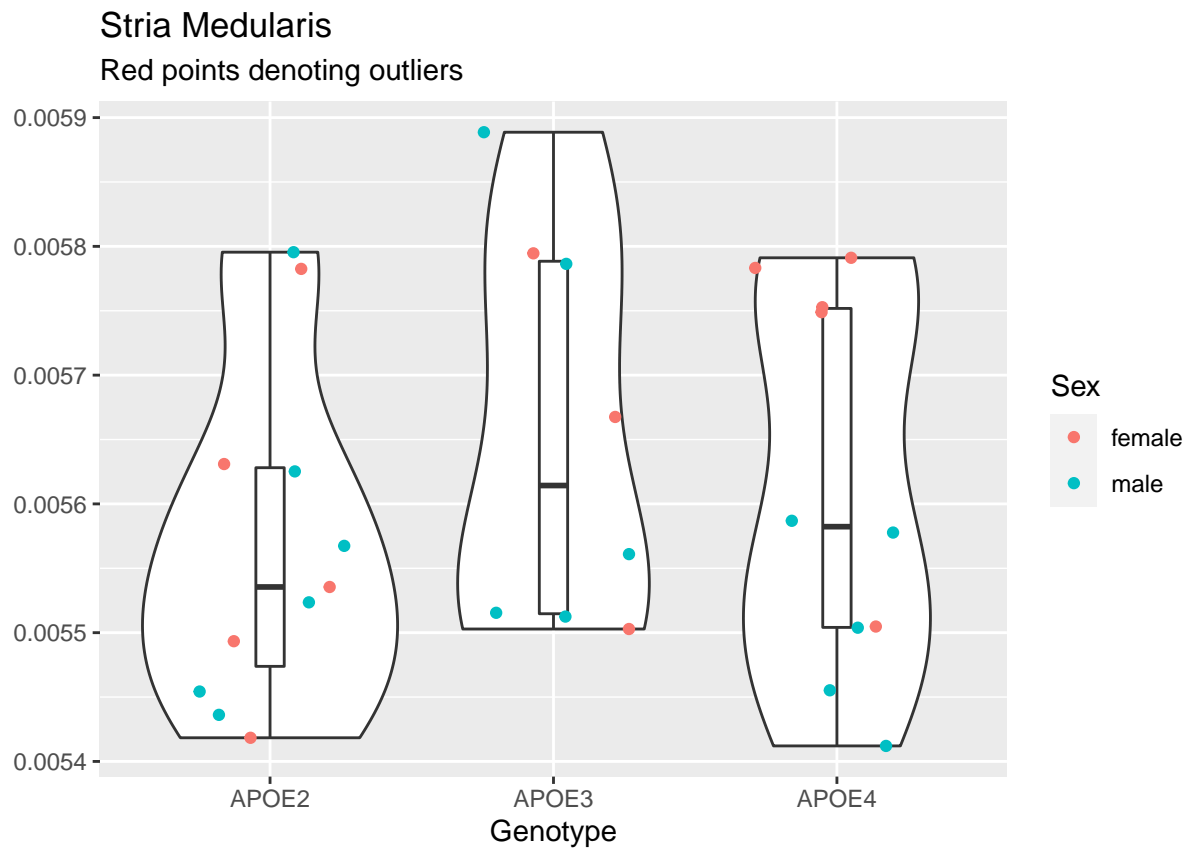
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 7.510e-08 3.755e-08   2.395  0.111
## Residuals 26 4.077e-07 1.568e-08
```

Fasciculus Retroflexus

Red points denoting outliers



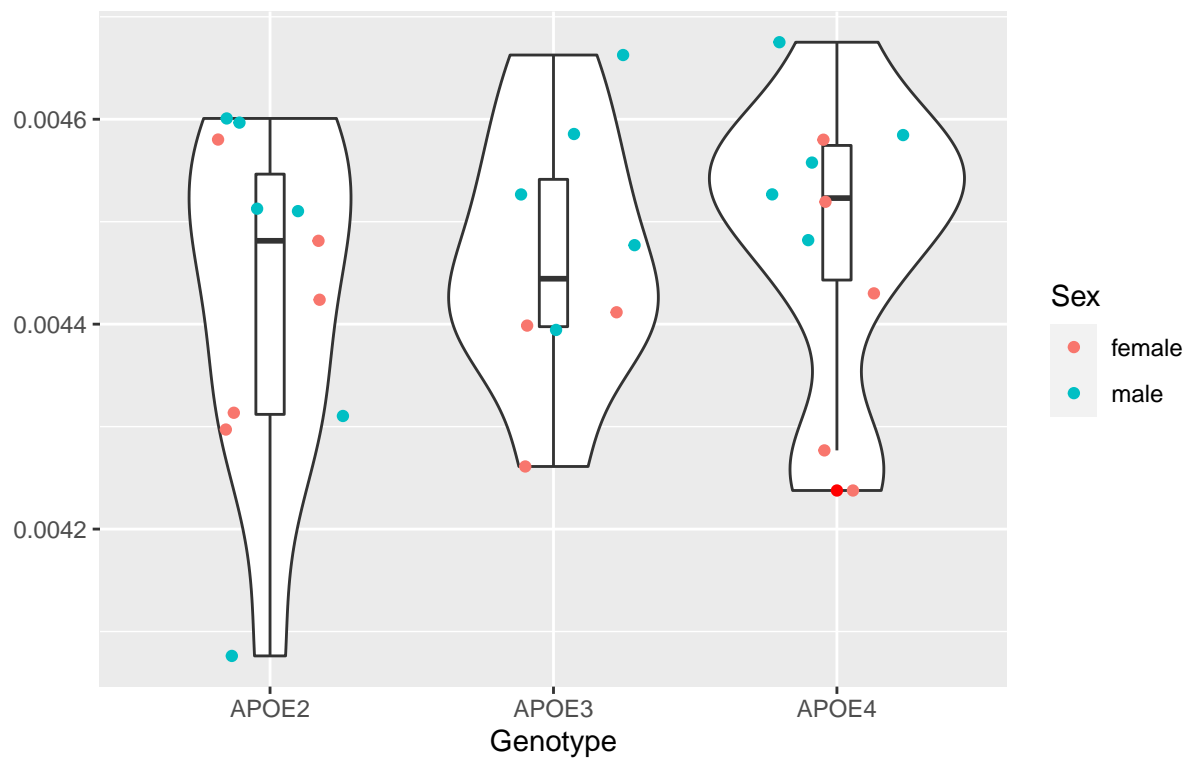
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.122e-07	5.611e-08	1.094	0.35
## Residuals	26	1.333e-06	5.128e-08		



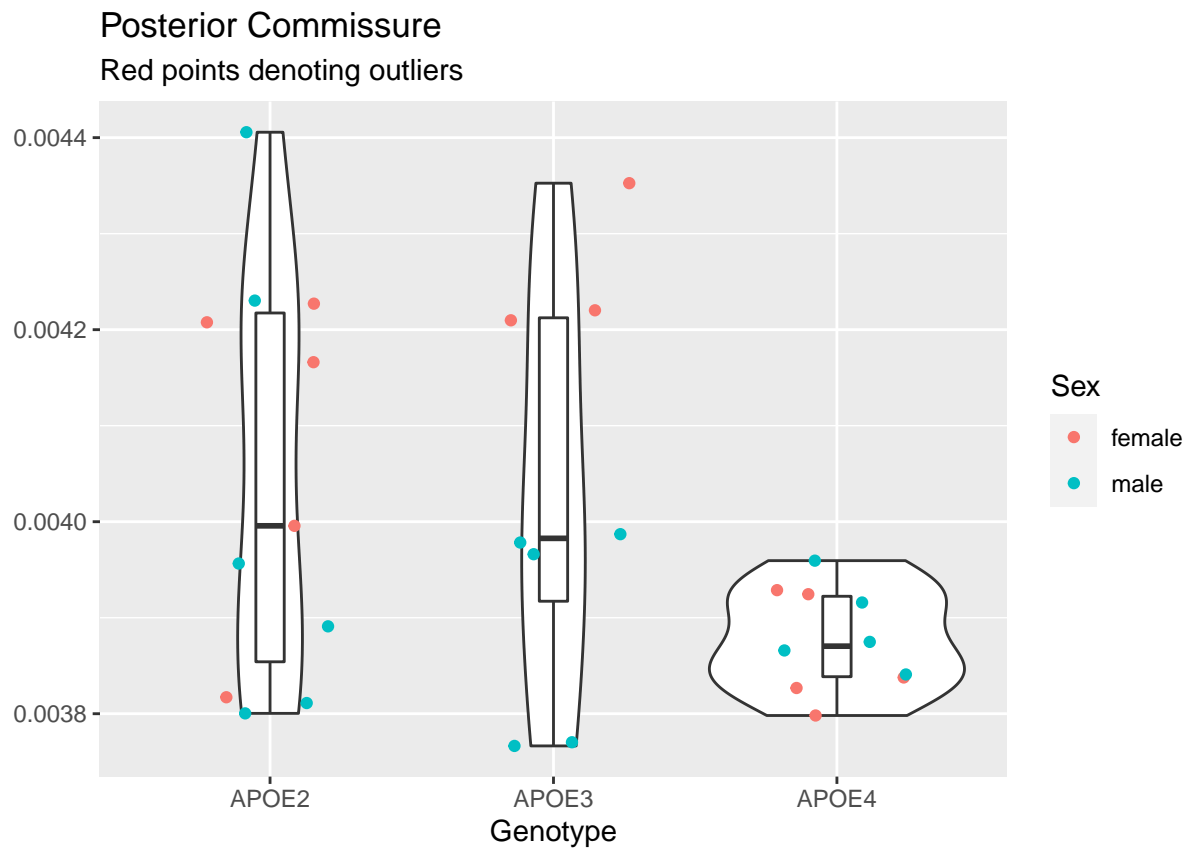
```
##           Df    Sum Sq   Mean Sq F value Pr(>F)
## geno       2 3.32e-08 1.660e-08   0.831  0.447
## Residuals 26 5.19e-07 1.996e-08
```

Mammillothalamic Tract

Red points denoting outliers



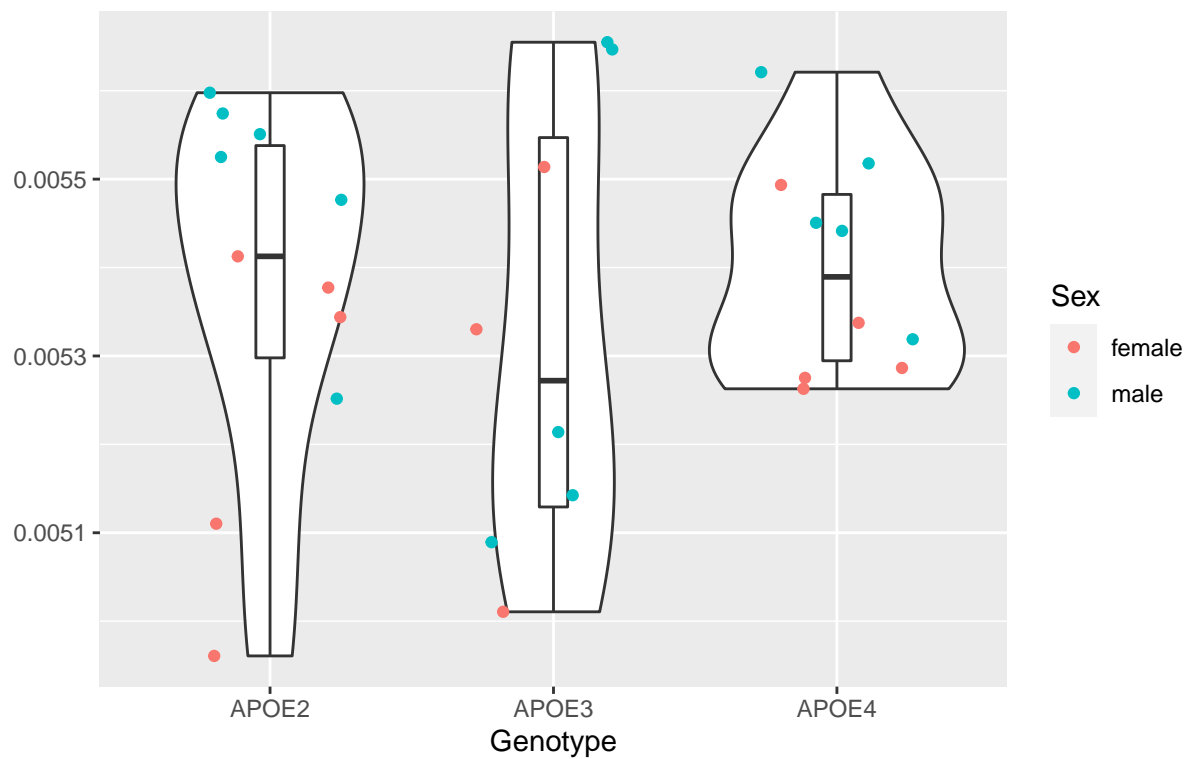
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.900e-08	9.483e-09	0.45	0.643
## Residuals	26	5.483e-07	2.109e-08		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.744e-07 8.721e-08   2.899  0.073 .
## Residuals    26 7.821e-07 3.008e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Brachium of Superior Colliculus

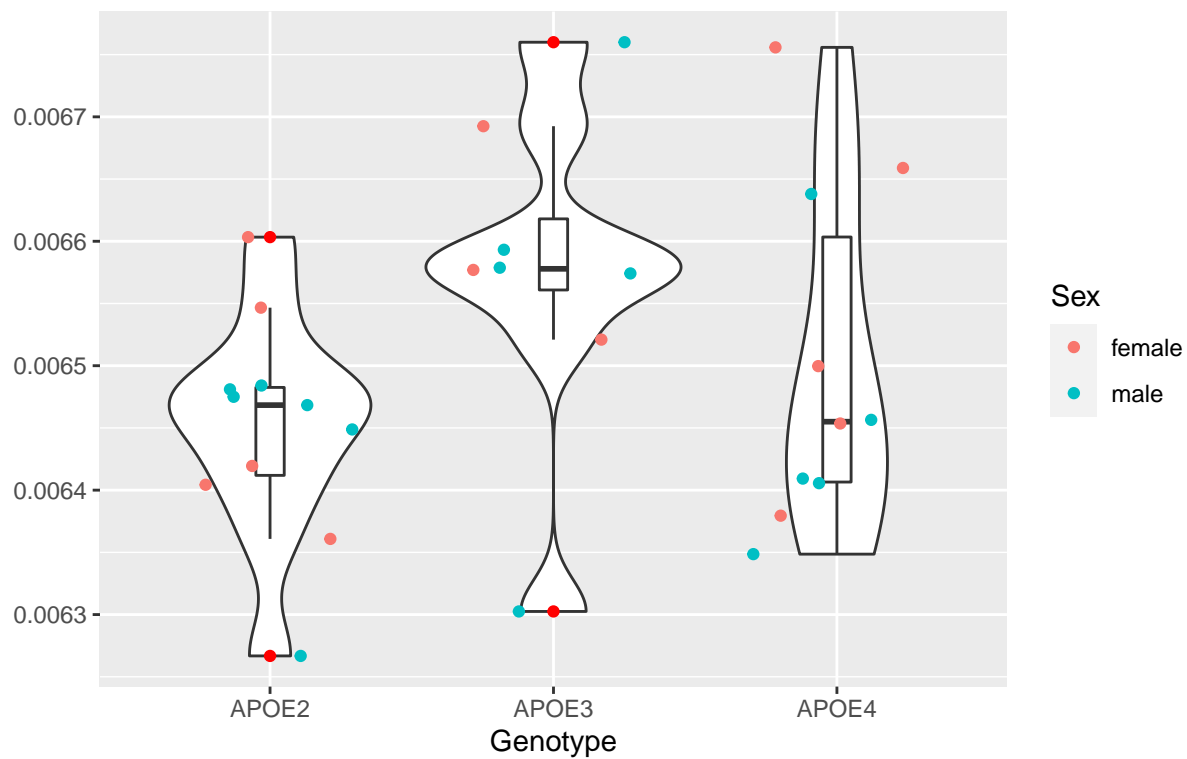
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.640e-08	1.318e-08	0.345	0.712
## Residuals	26	9.936e-07	3.822e-08		

Cerebral Peduncle

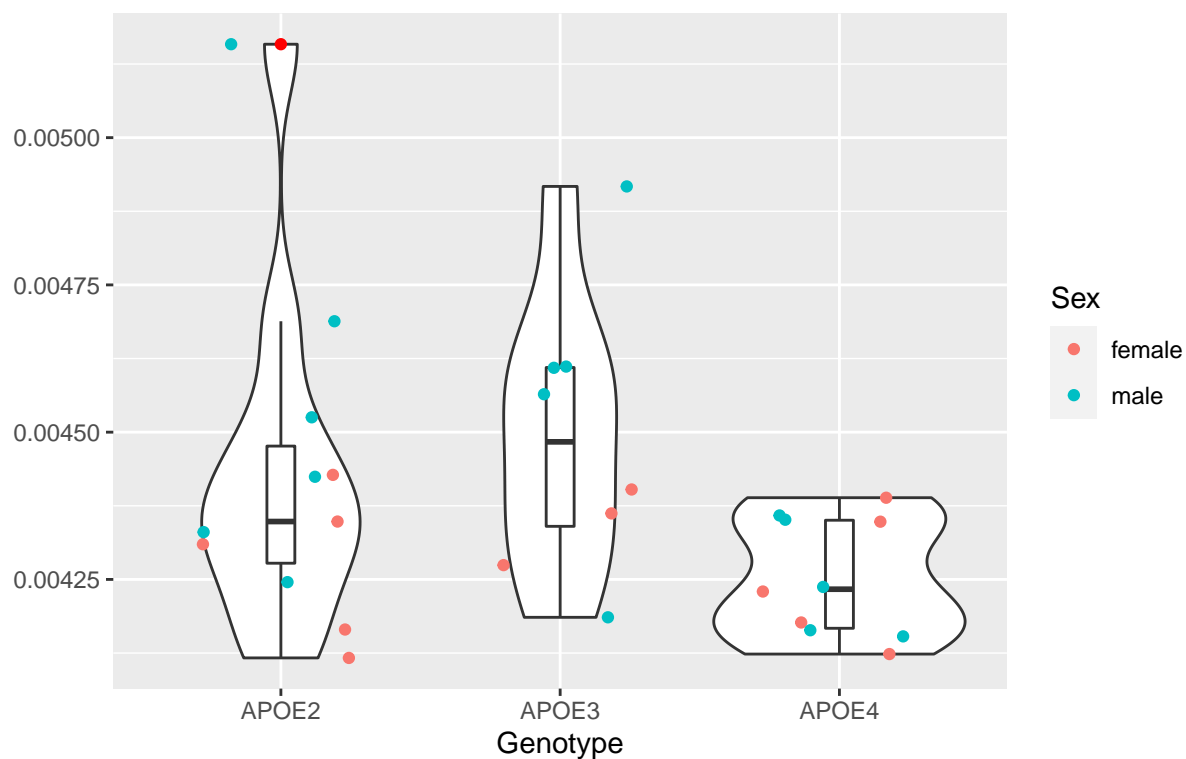
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.140e-08	3.569e-08	2.478	0.104
## Residuals	26	3.744e-07	1.440e-08		

Lateral Lemniscus

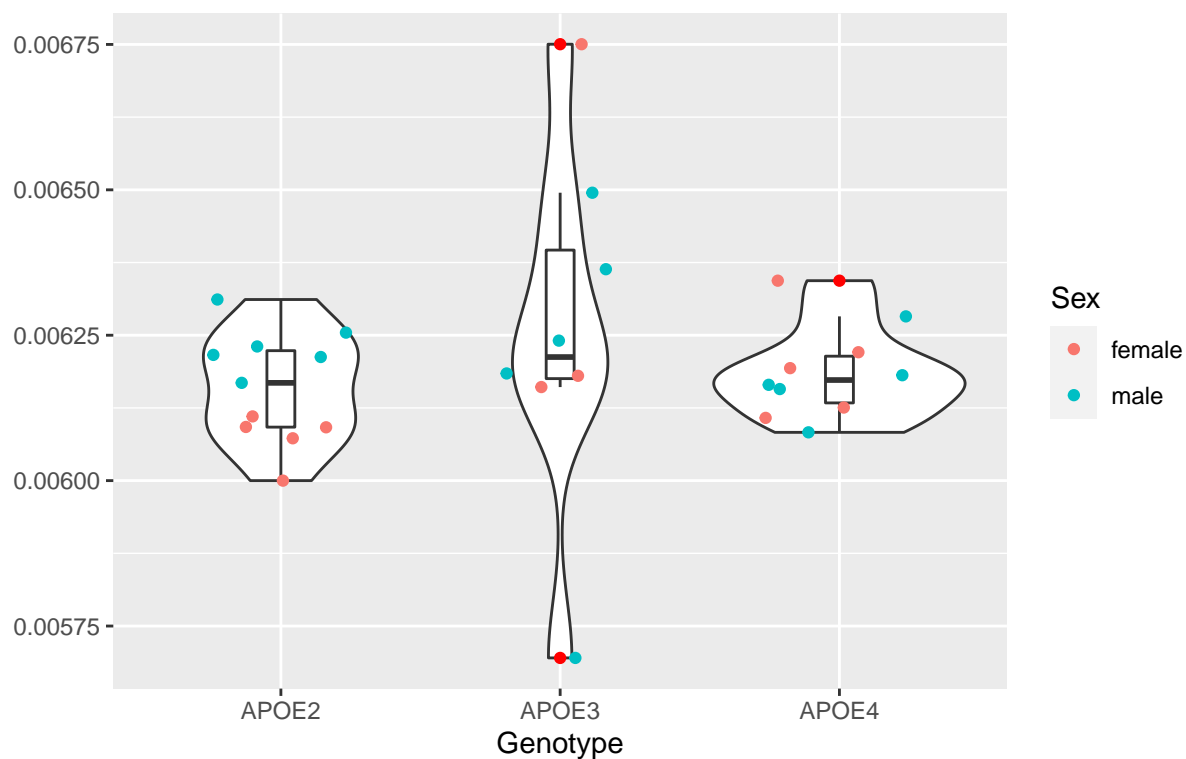
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 2.868e-07 1.434e-07    2.846 0.0762 .
## Residuals   26 1.310e-06 5.038e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Spinal Trigeminal Nerve

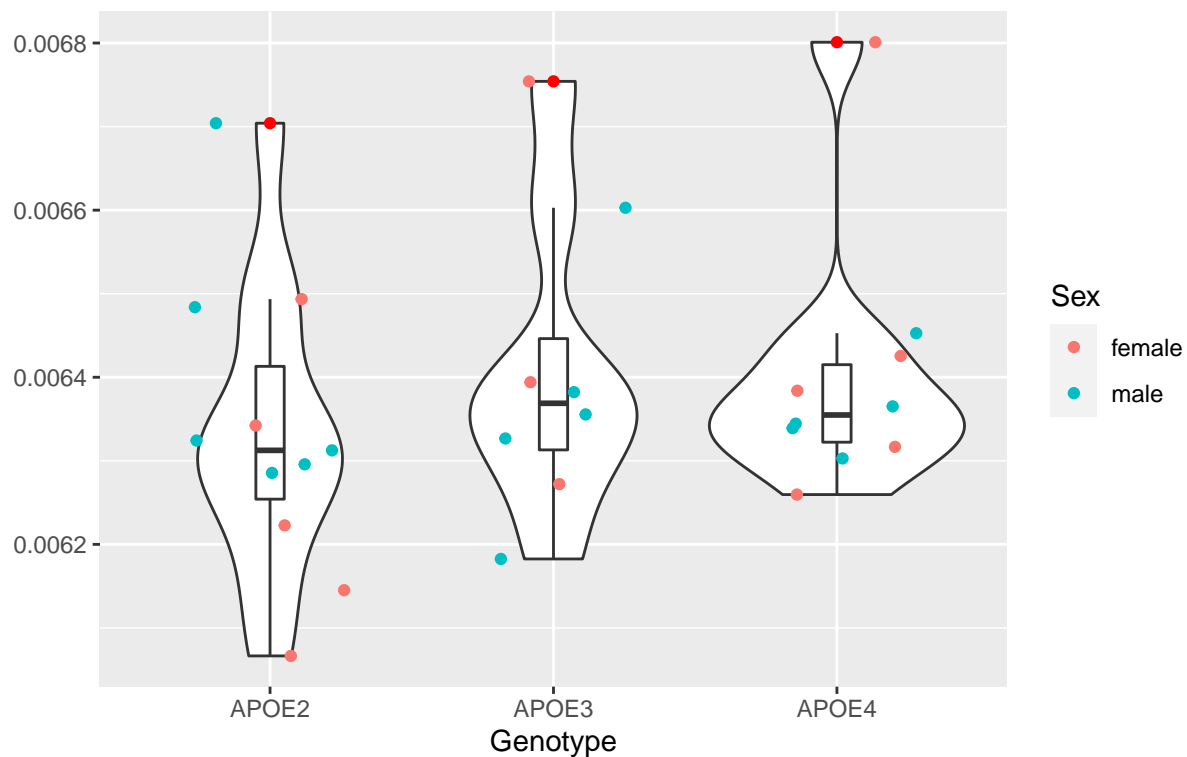
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.670e-08	2.336e-08	0.766	0.475
## Residuals	26	7.925e-07	3.048e-08		

Pyramidal Tract

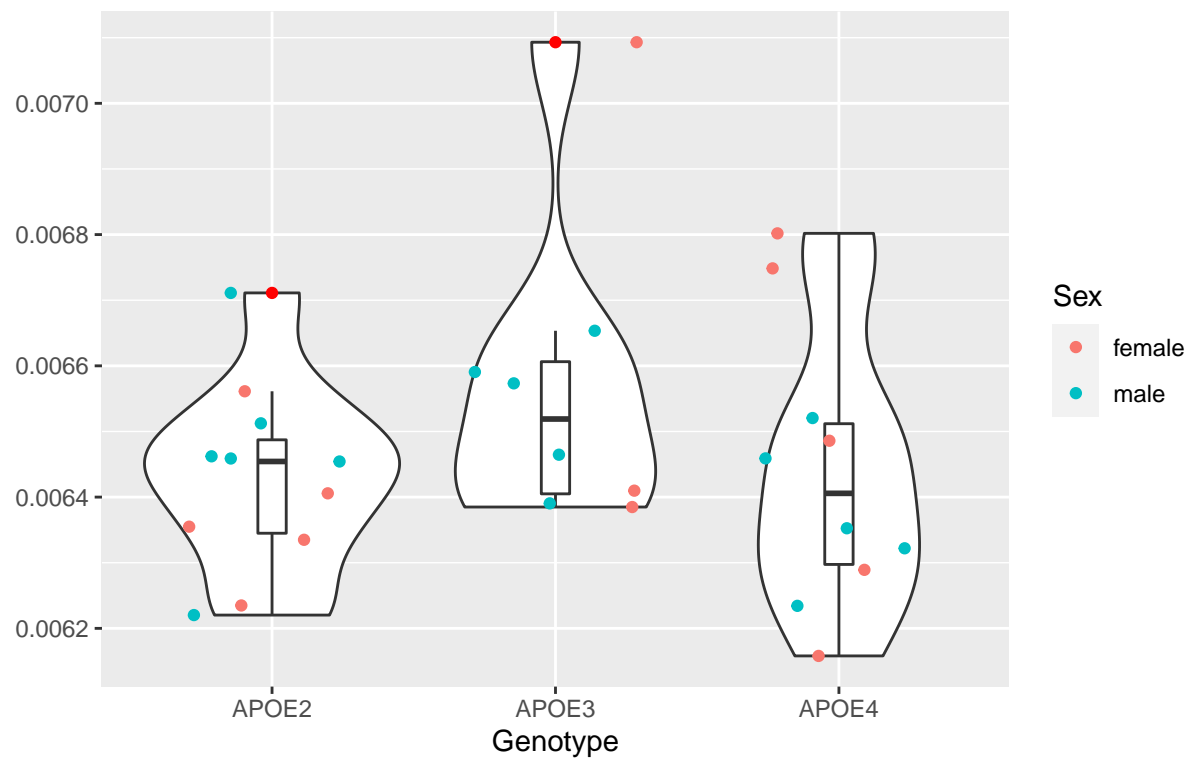
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 3.310e-08 1.655e-08    0.57  0.572
## Residuals 26 7.548e-07 2.903e-08
```

Vestibulocochlear Nerve

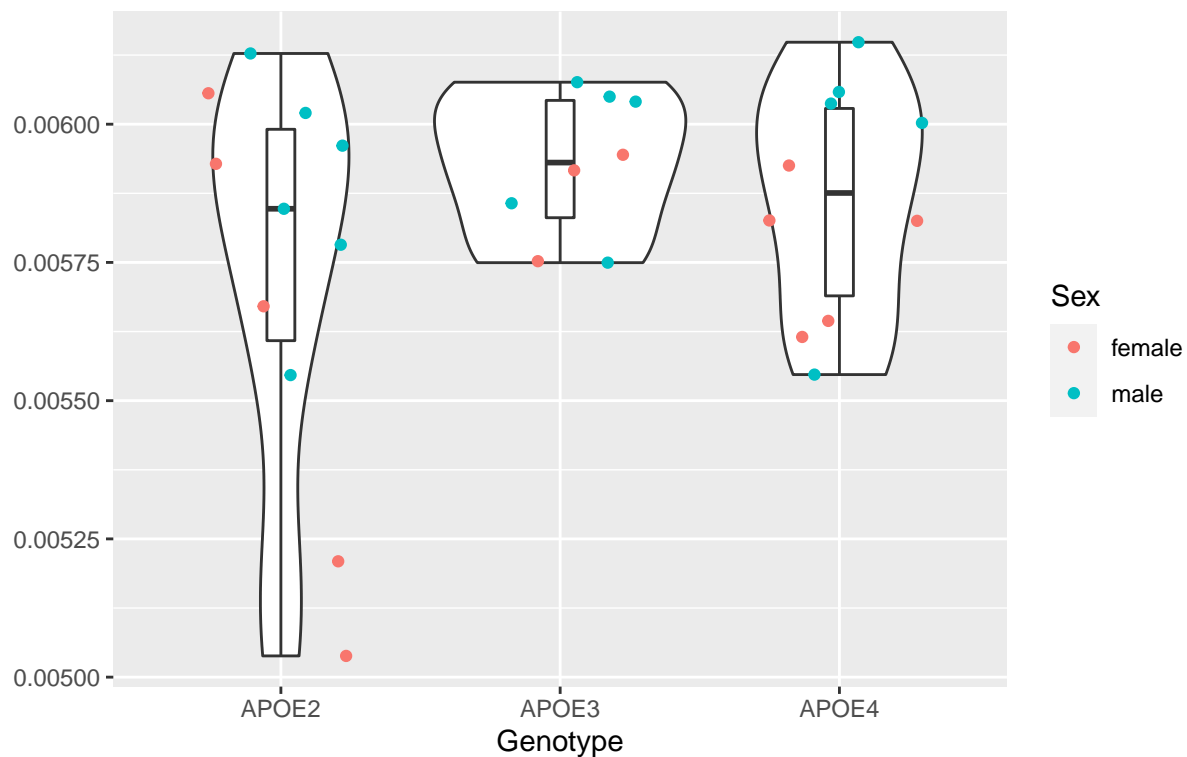
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.100e-07	5.499e-08	1.447	0.254
## Residuals	26	9.882e-07	3.801e-08		

Facial Nerve

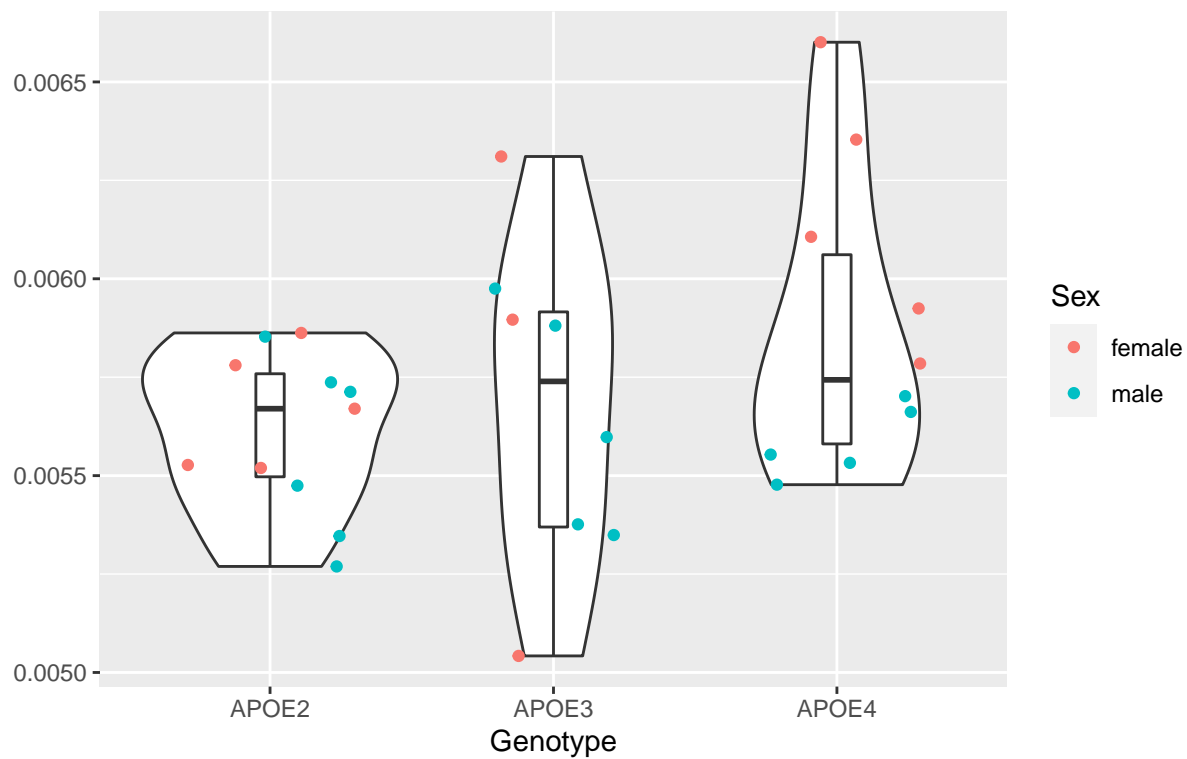
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.606e-07	8.032e-08	1.197	0.318
## Residuals	26	1.745e-06	6.711e-08		

Longitudinal Fasciculus of Pons

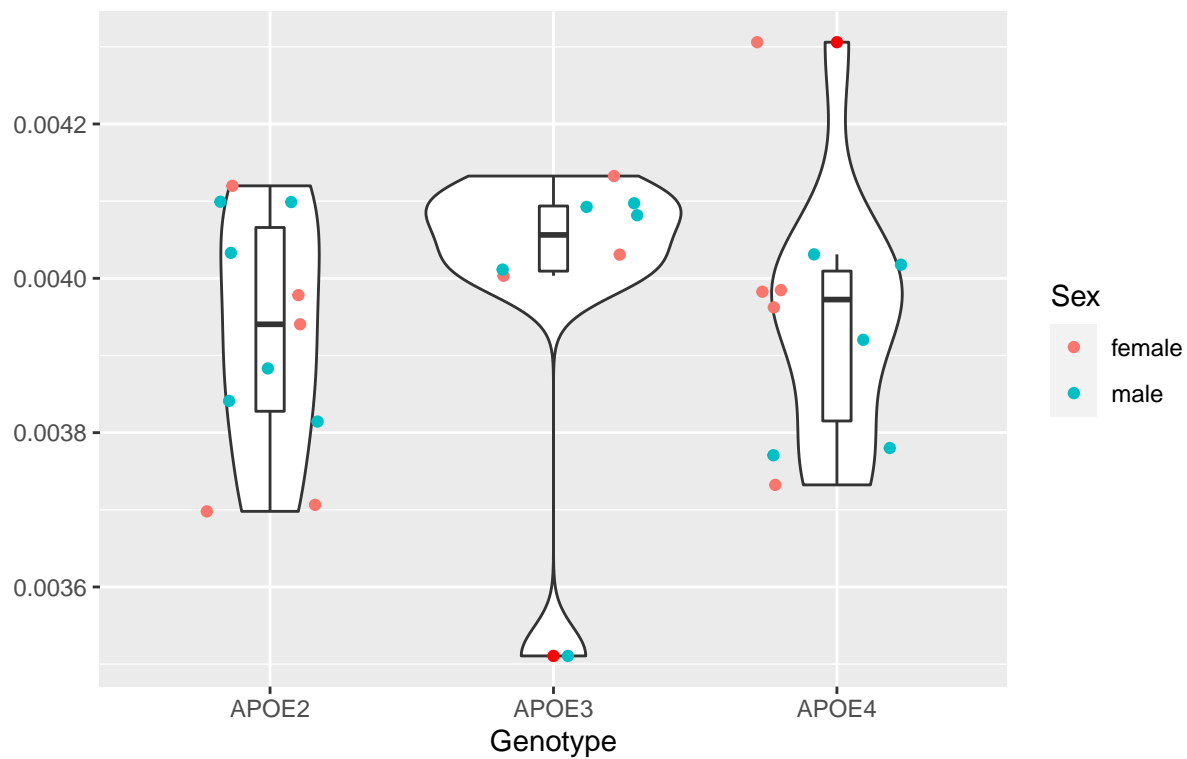
Red points denoting outliers



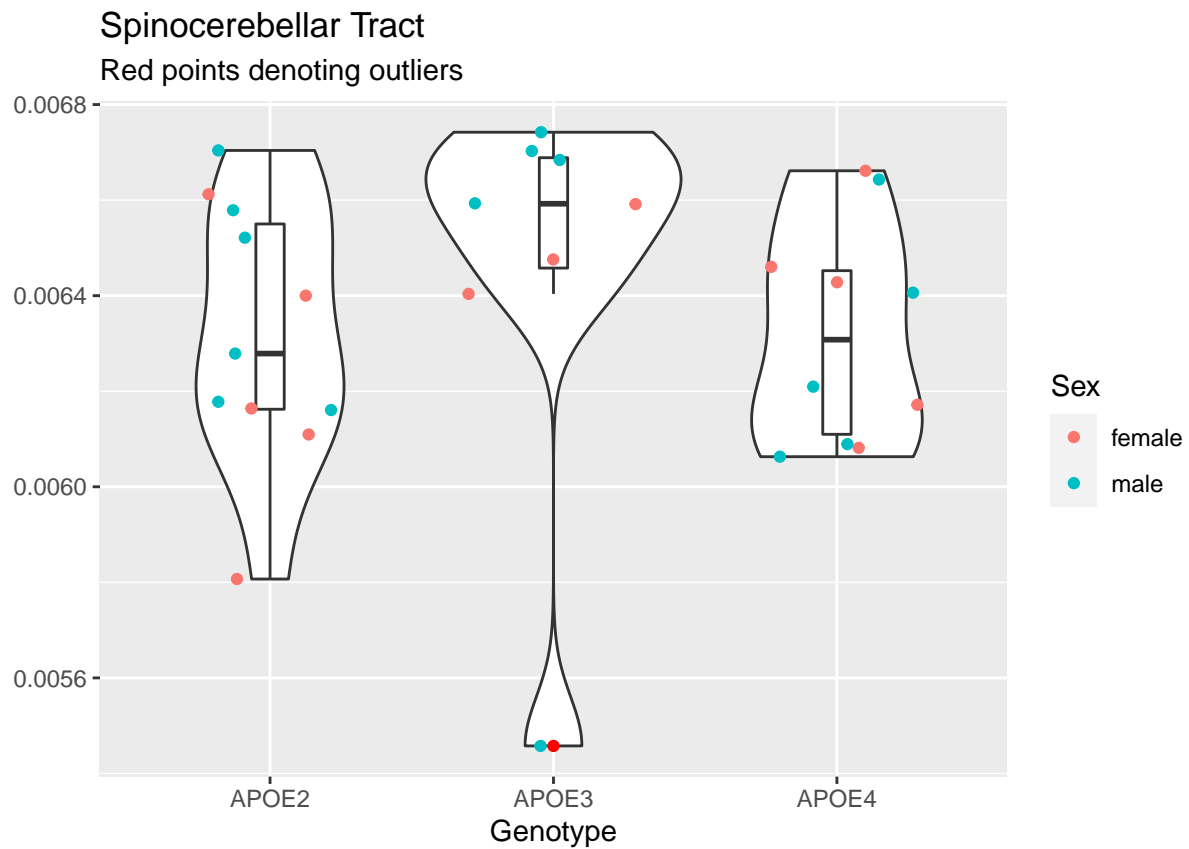
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.618e-07	1.809e-07	1.643	0.213
## Residuals	26	2.863e-06	1.101e-07		

Medial Longitudinal Fasciculus and Tectospinal Tract

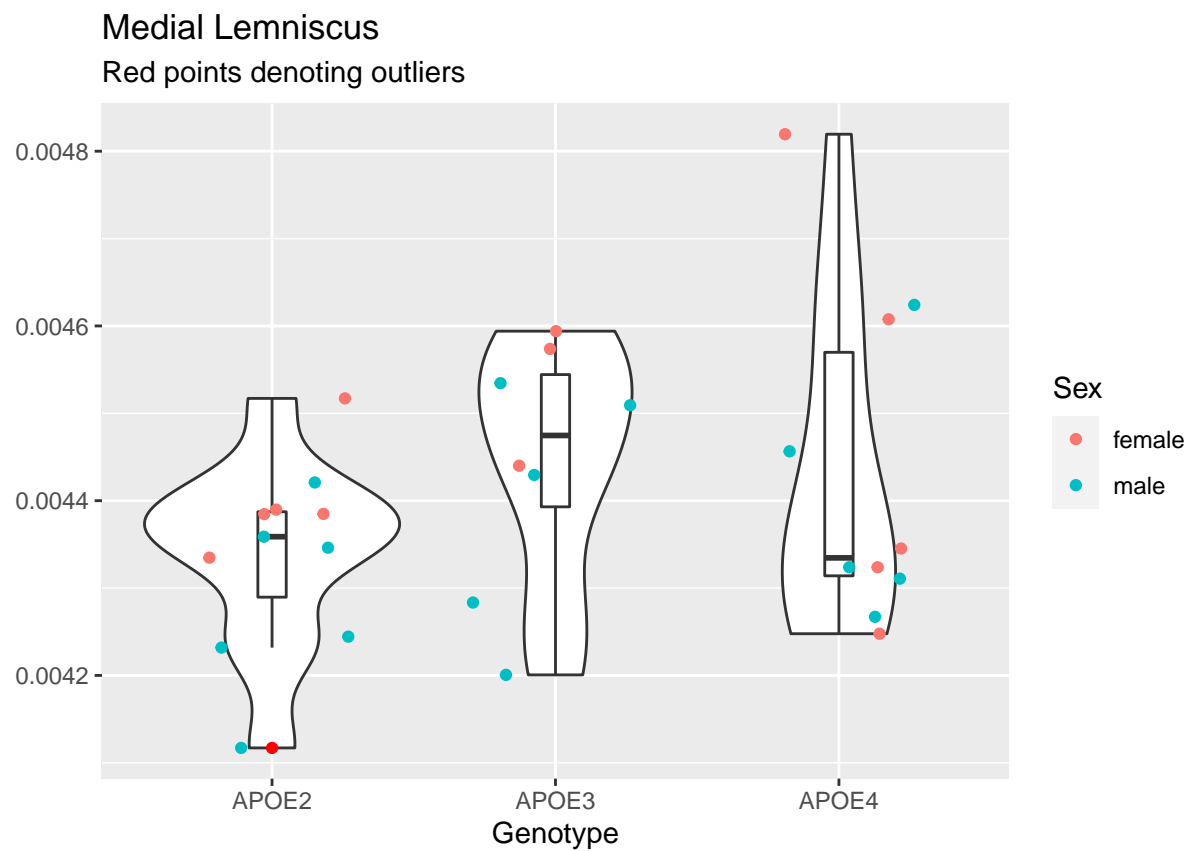
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.090e-08	1.046e-08	0.355	0.704
## Residuals	26	7.657e-07	2.945e-08		



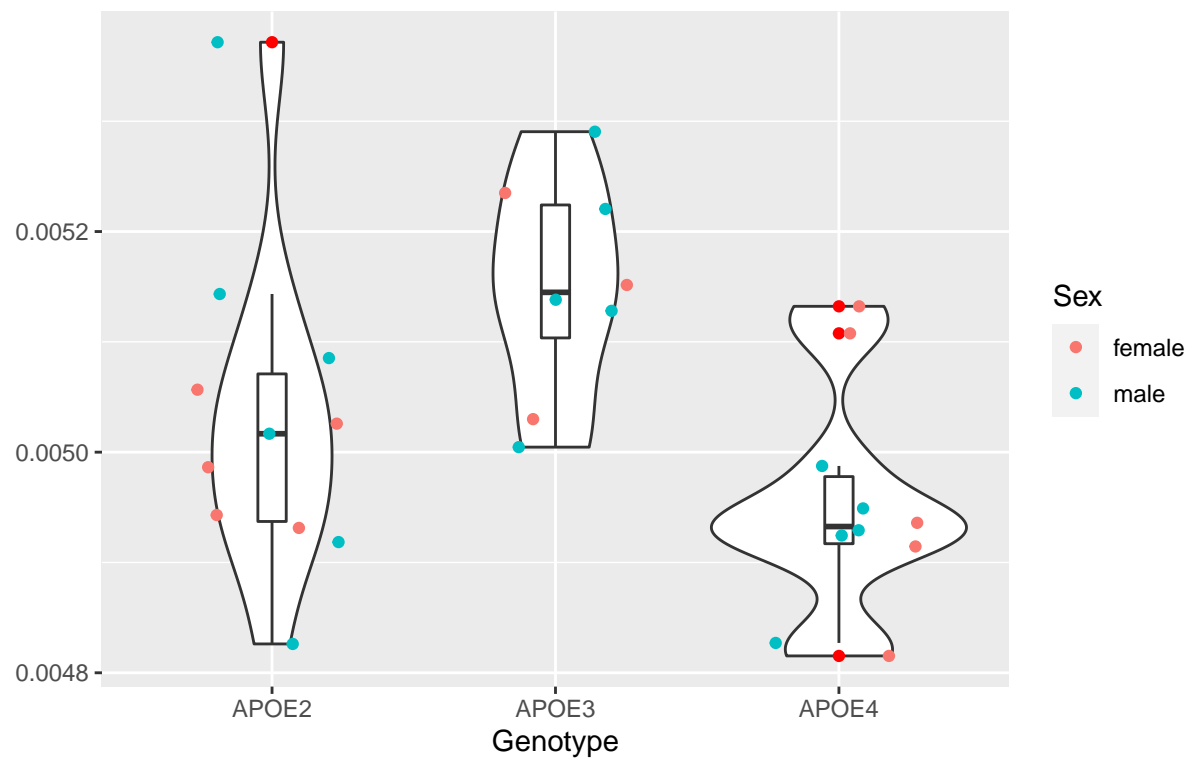
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.071e-07	5.355e-08	0.574	0.571
## Residuals	26	2.428e-06	9.338e-08		



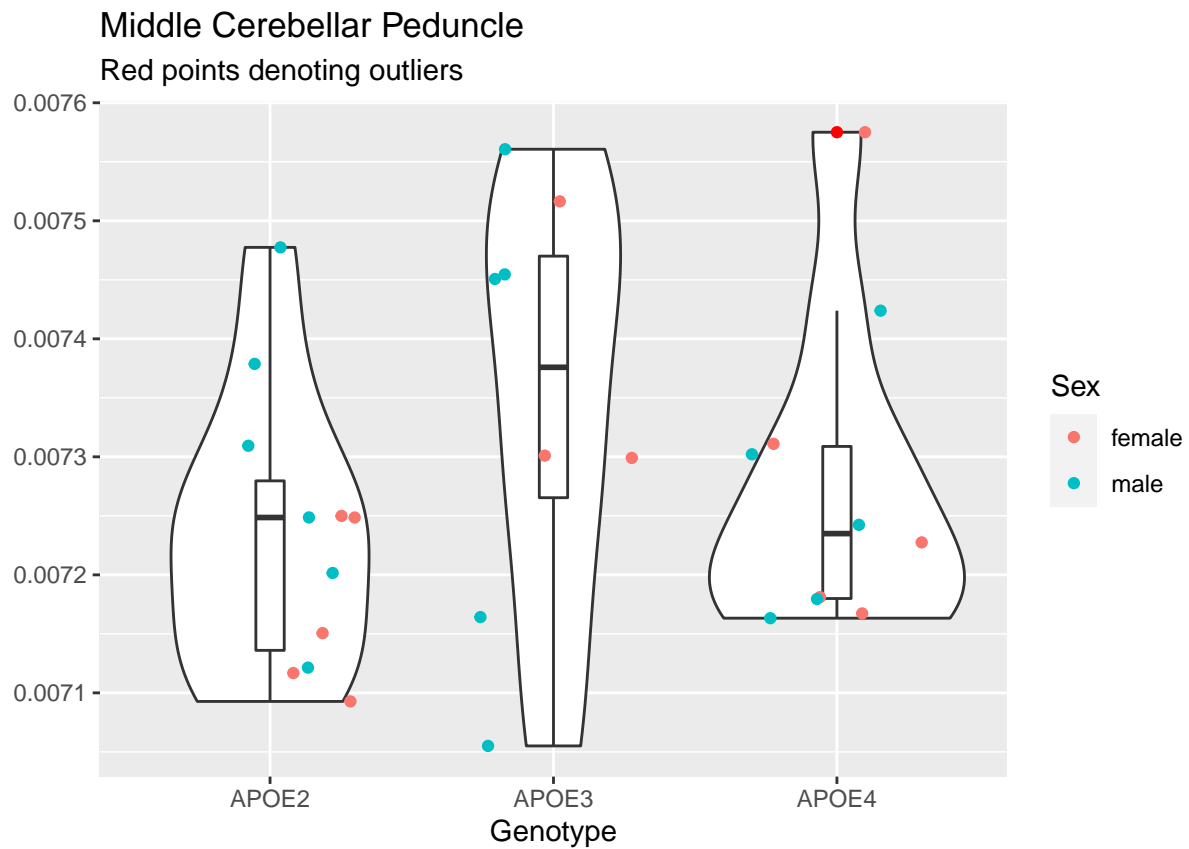
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.810e-08	3.403e-08	1.532	0.235
## Residuals	26	5.776e-07	2.221e-08		

Ventral Spinocerebellar Tract

Red points denoting outliers



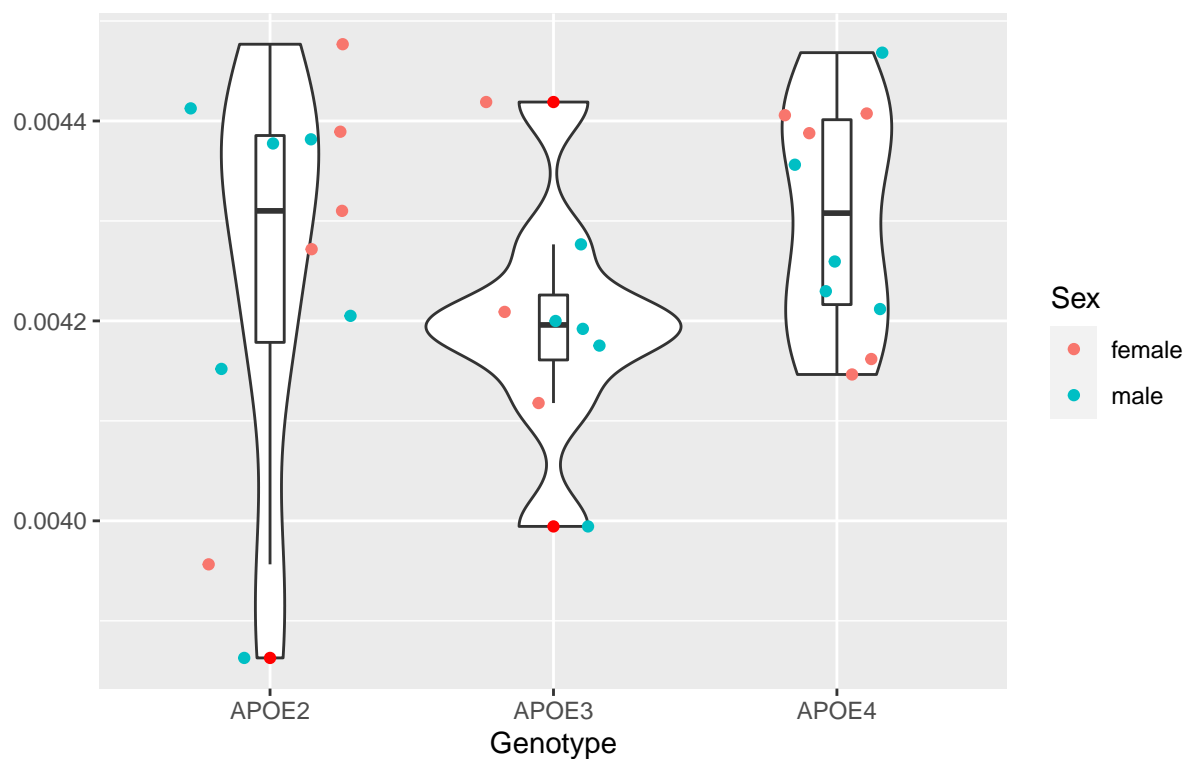
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.744e-07 8.720e-08   6.127 0.0066 **
## Residuals    26 3.700e-07 1.423e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 6.070e-08 3.037e-08   1.518  0.238
## Residuals 26 5.201e-07 2.000e-08
```

Superior Cerebellar Peduncle

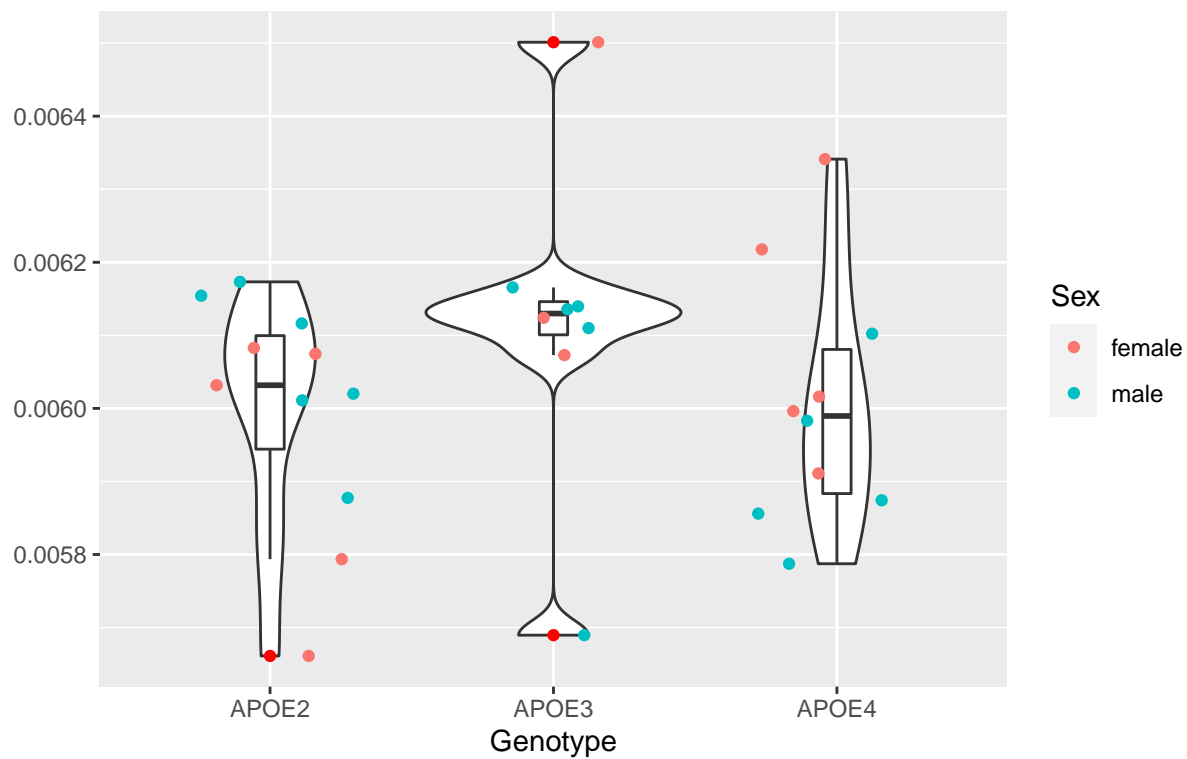
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.950e-08	2.474e-08	1.064	0.36
## Residuals	26	6.047e-07	2.326e-08		

Inferior Cerebellar Peduncle

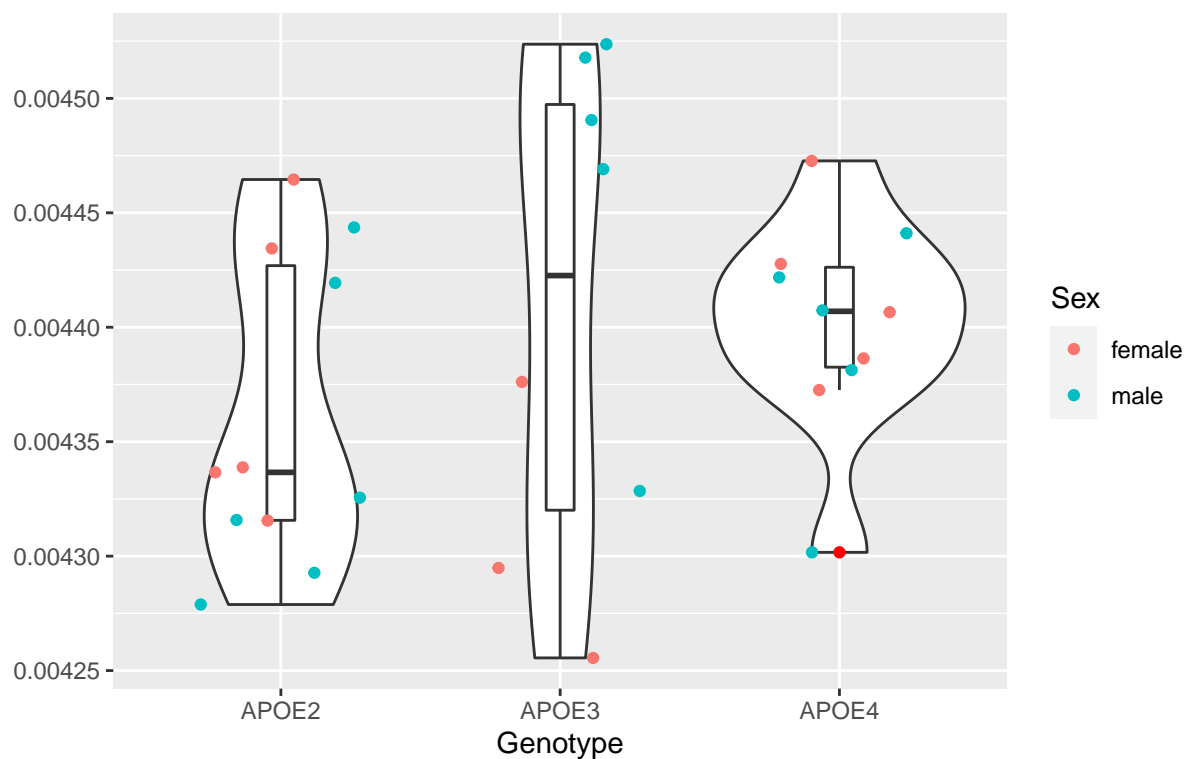
Red points denoting outliers



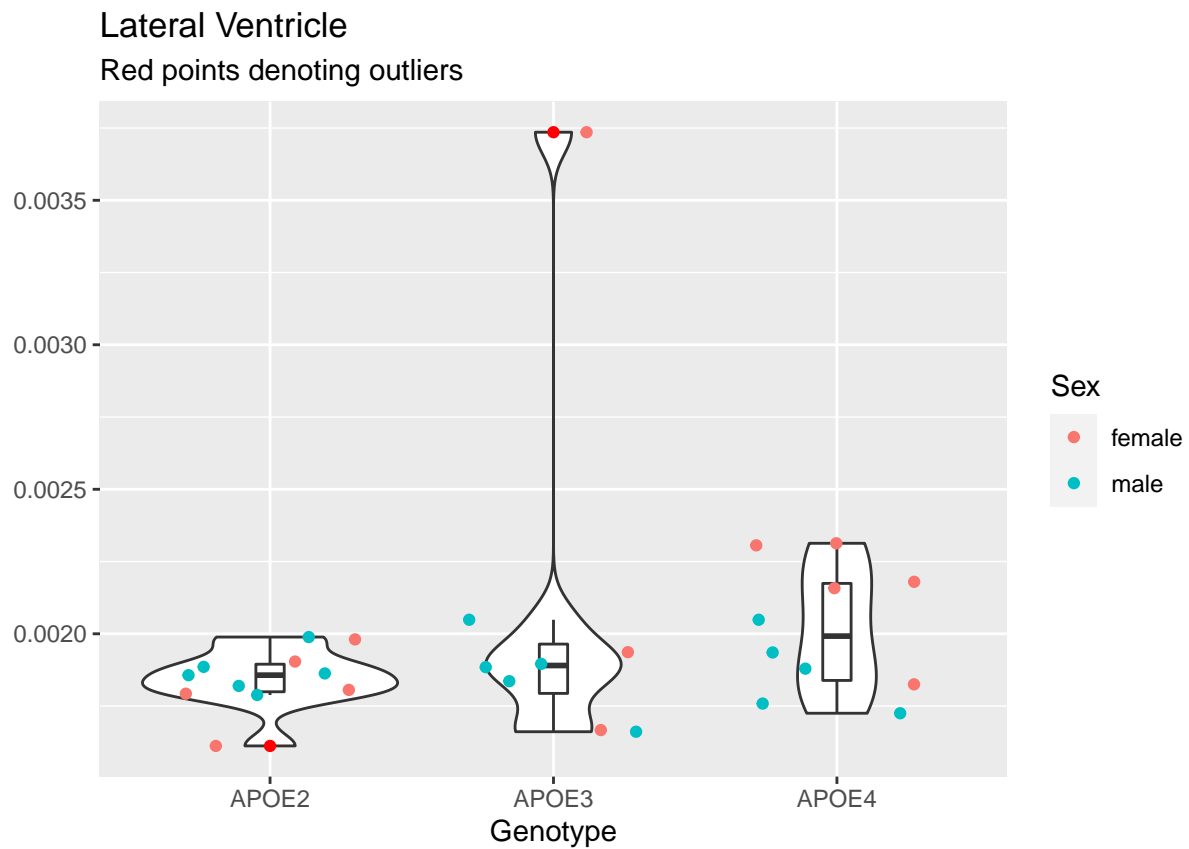
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno      2 7.50e-08 3.749e-08   1.143  0.334
## Residuals 26 8.53e-07 3.281e-08
```

Cerebellar White Matter

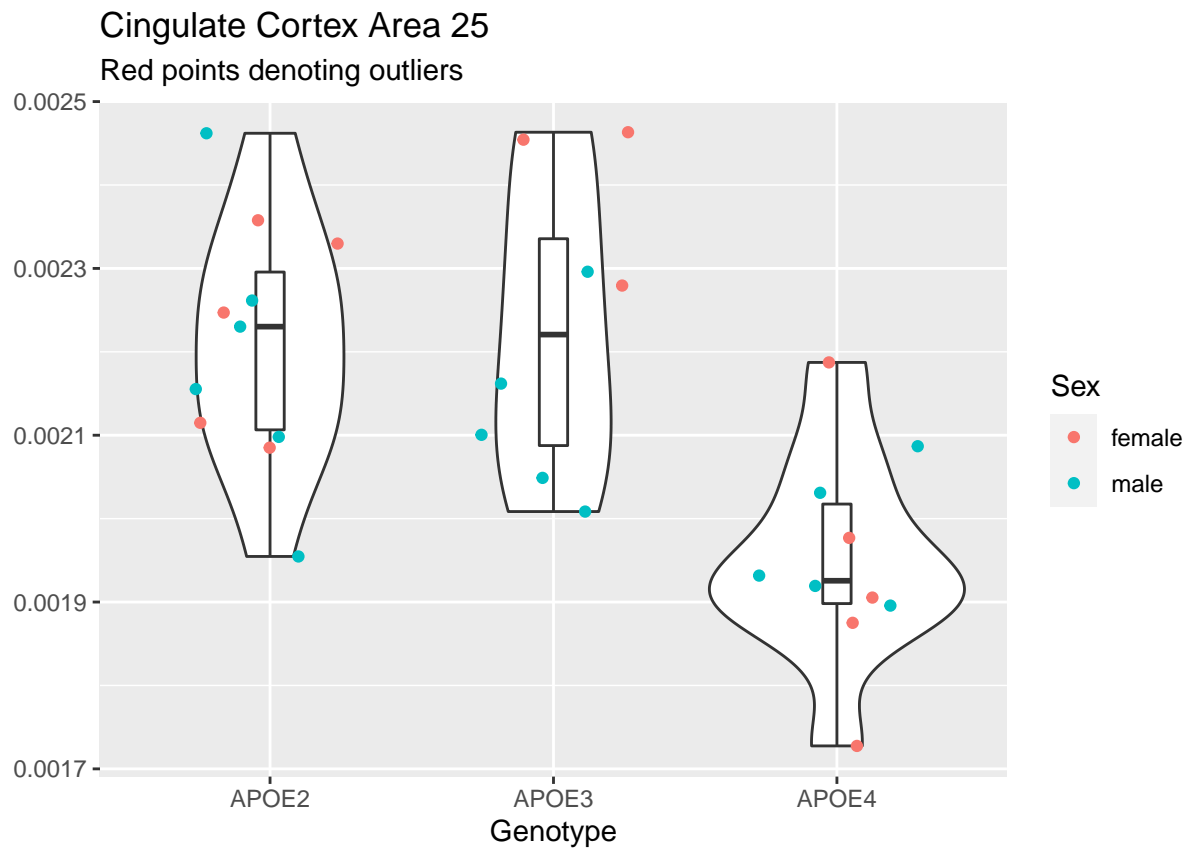
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.312e-08	6.560e-09	1.194	0.319
## Residuals	26	1.428e-07	5.493e-09		



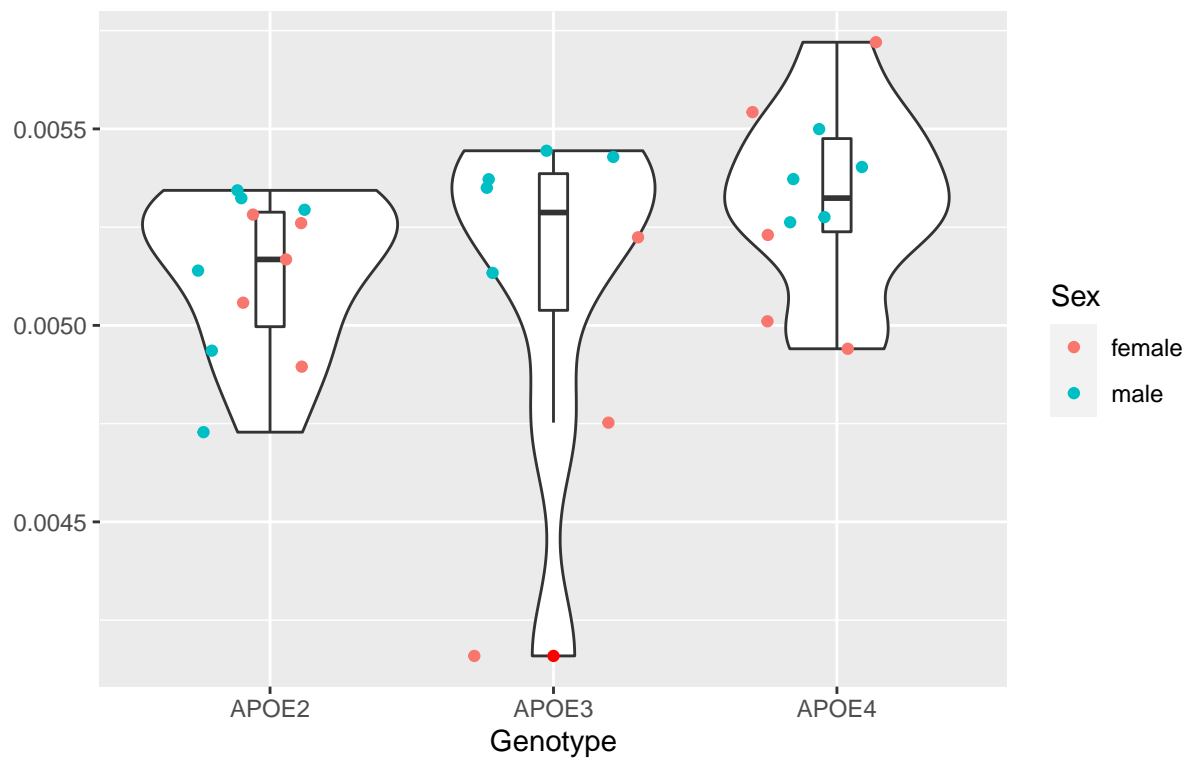
```
##          Df  Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.92e-07 1.460e-07   1.005   0.38
## Residuals 26 3.78e-06 1.454e-07
```



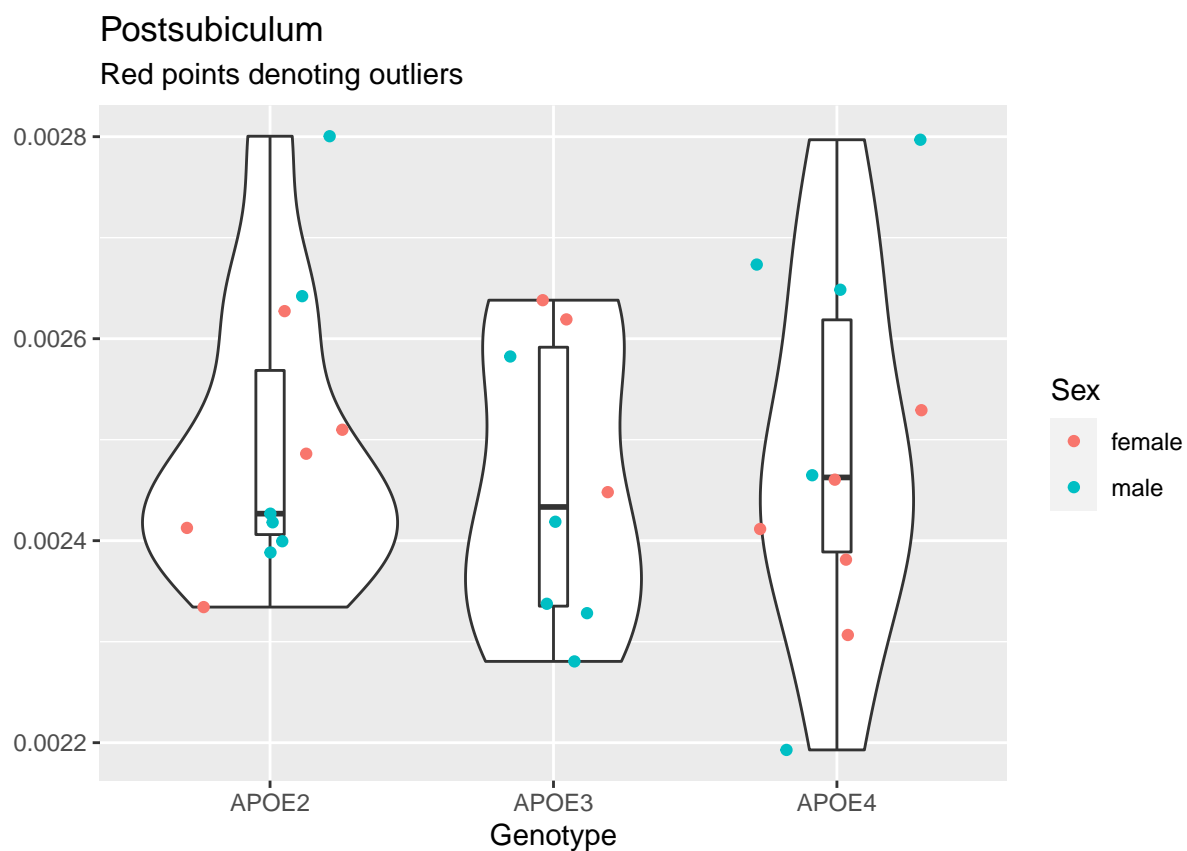
```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 4.532e-07 2.266e-07   10.38 0.000486 ***
## Residuals    26 5.677e-07 2.184e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Dorsal Acoustic Stria

Red points denoting outliers



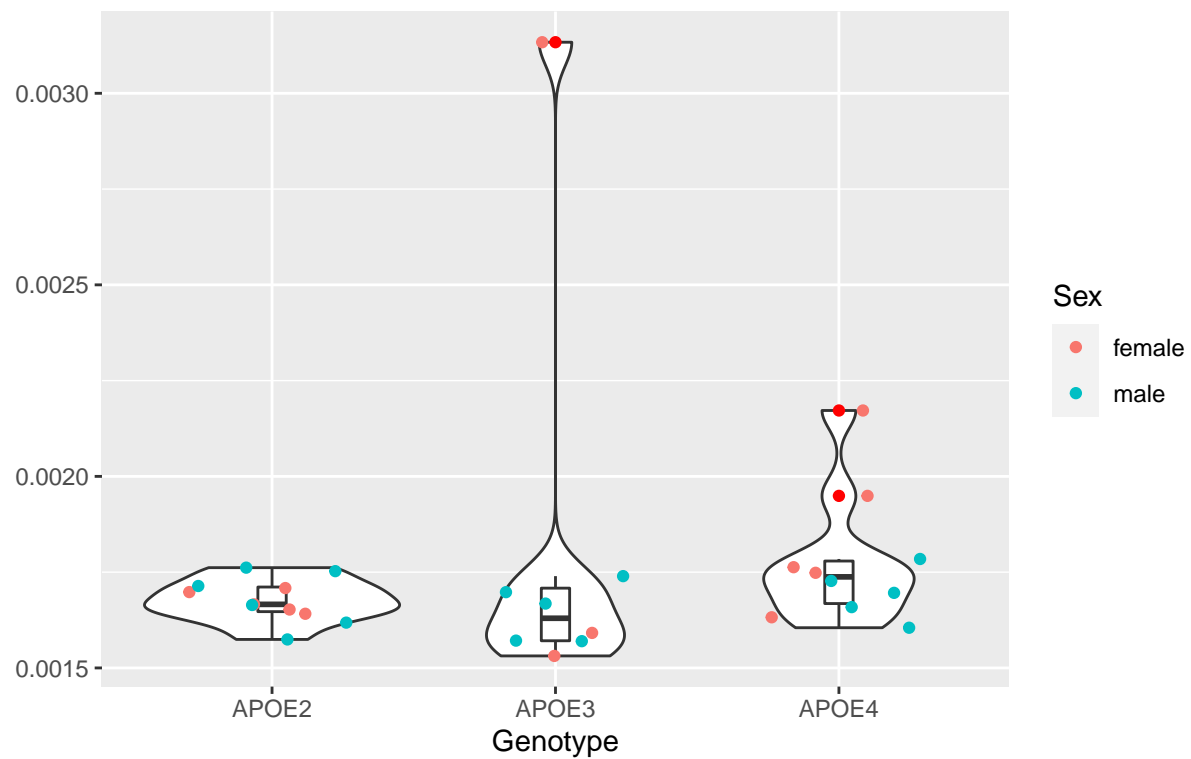
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.777e-07	1.389e-07	1.569	0.227
## Residuals	26	2.301e-06	8.852e-08		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 7.200e-09 3.620e-09   0.149  0.862
## Residuals 26 6.306e-07 2.425e-08
```

Ventricular System 4th Ventricle

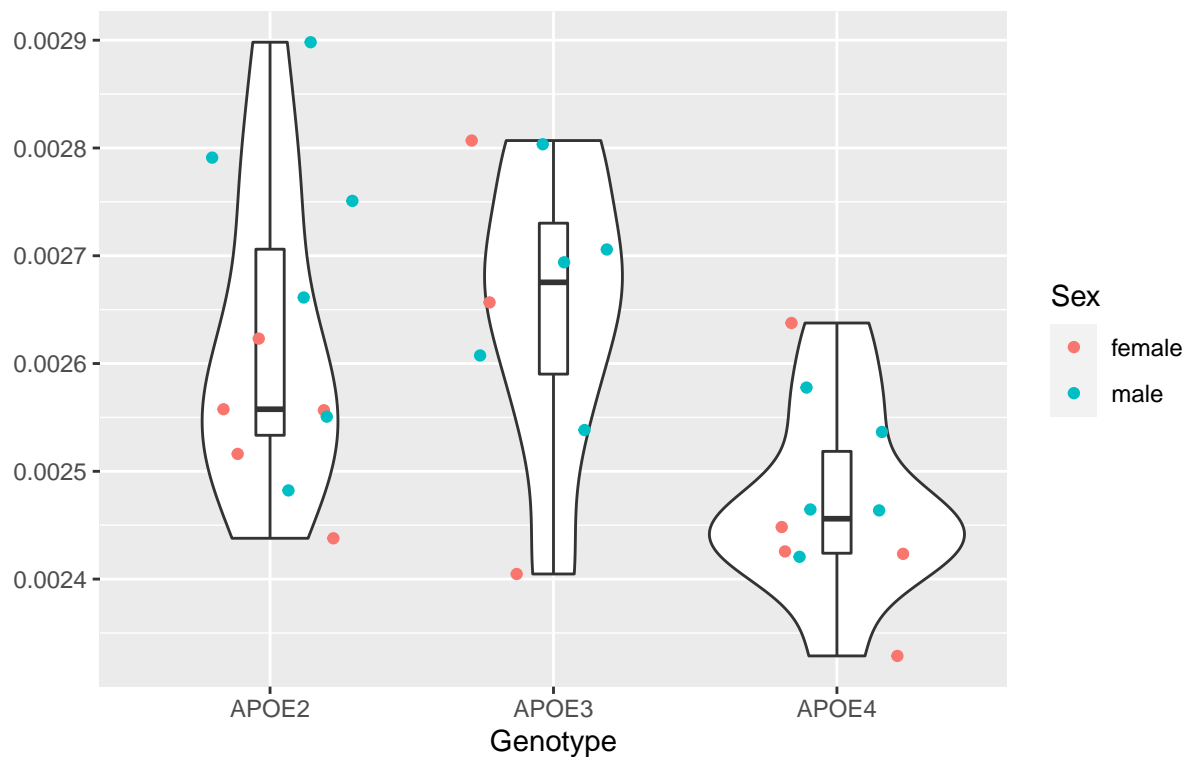
Red points denoting outliers



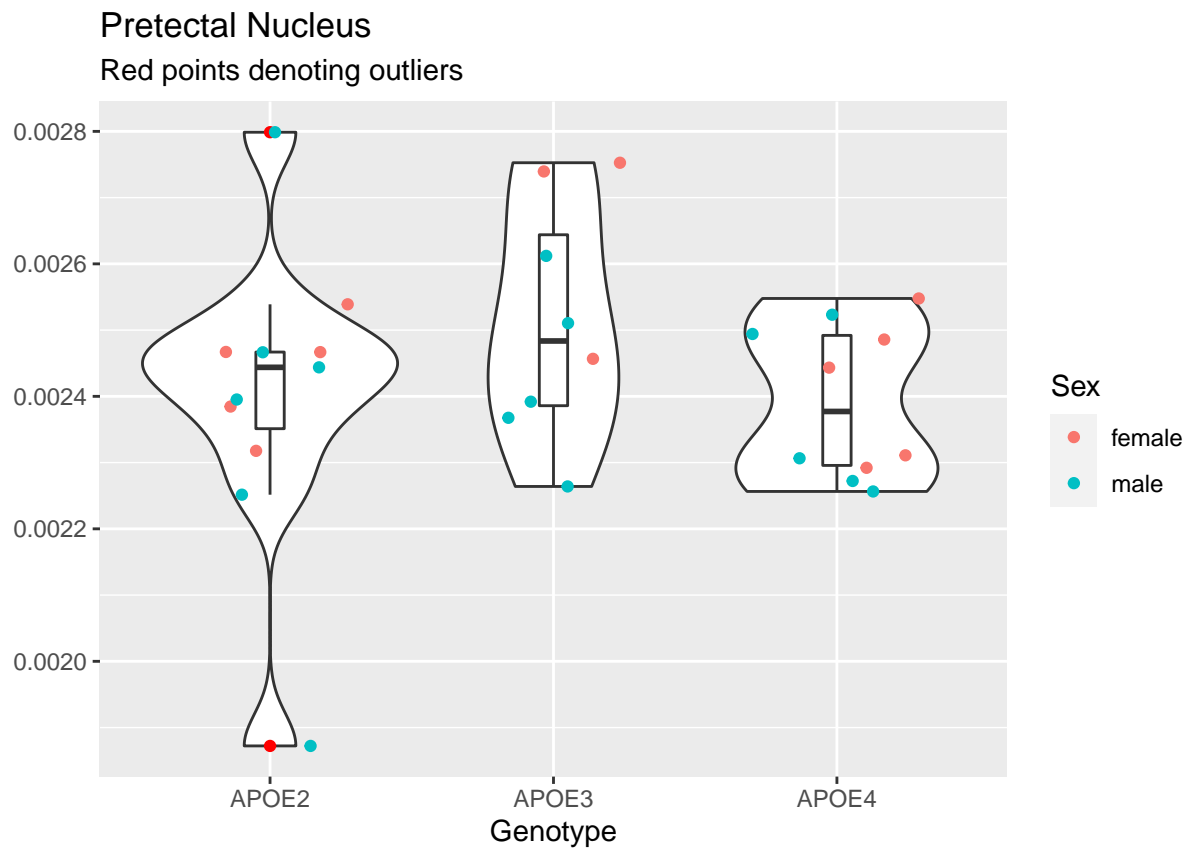
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	9.500e-08	4.749e-08	0.532	0.594
## Residuals	26	2.321e-06	8.928e-08		

Microcellular Tegmental Nucleus

Red points denoting outliers



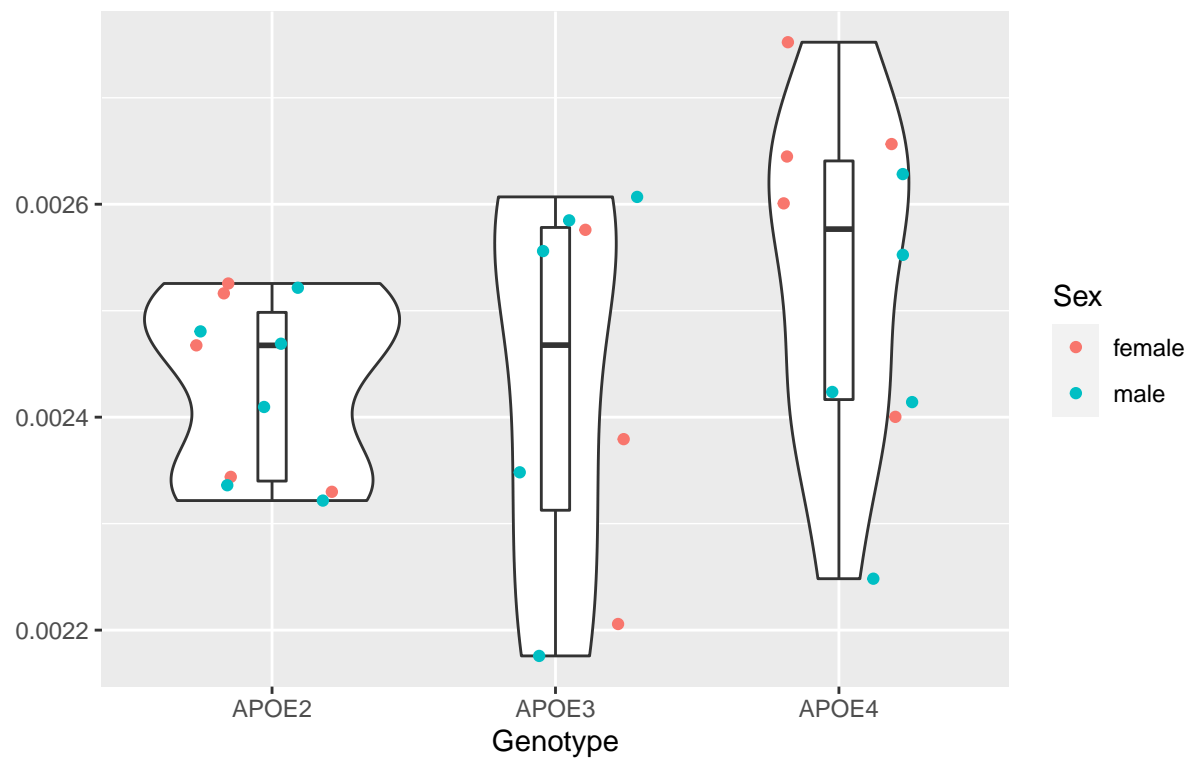
```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 1.748e-07 8.740e-08    5.682 0.00897 **
## Residuals    26 3.999e-07 1.538e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.680e-08	3.839e-08	1.187	0.321
## Residuals	26	8.405e-07	3.233e-08		

Latero Dorsal Thalamic Nucleus Ventro Lateral

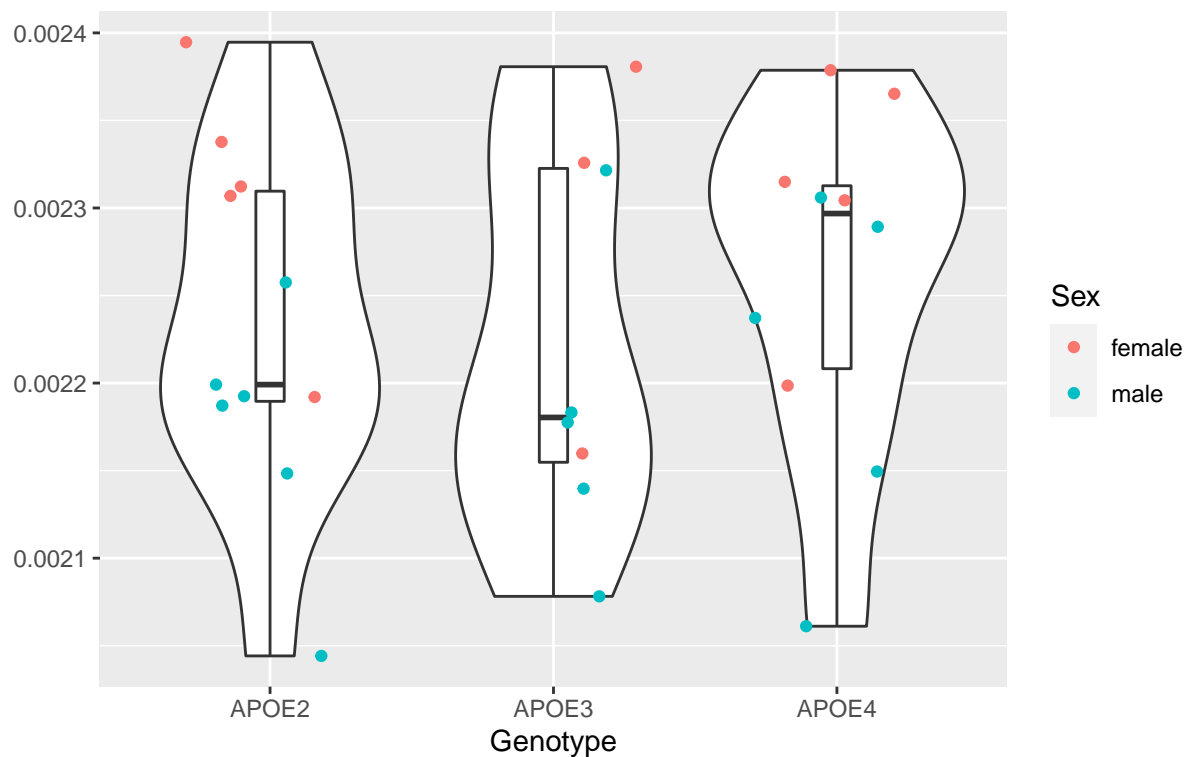
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.950e-08	3.474e-08	1.806	0.184
## Residuals	26	5.001e-07	1.923e-08		

Latero Posterior Nuclei of Thalamus

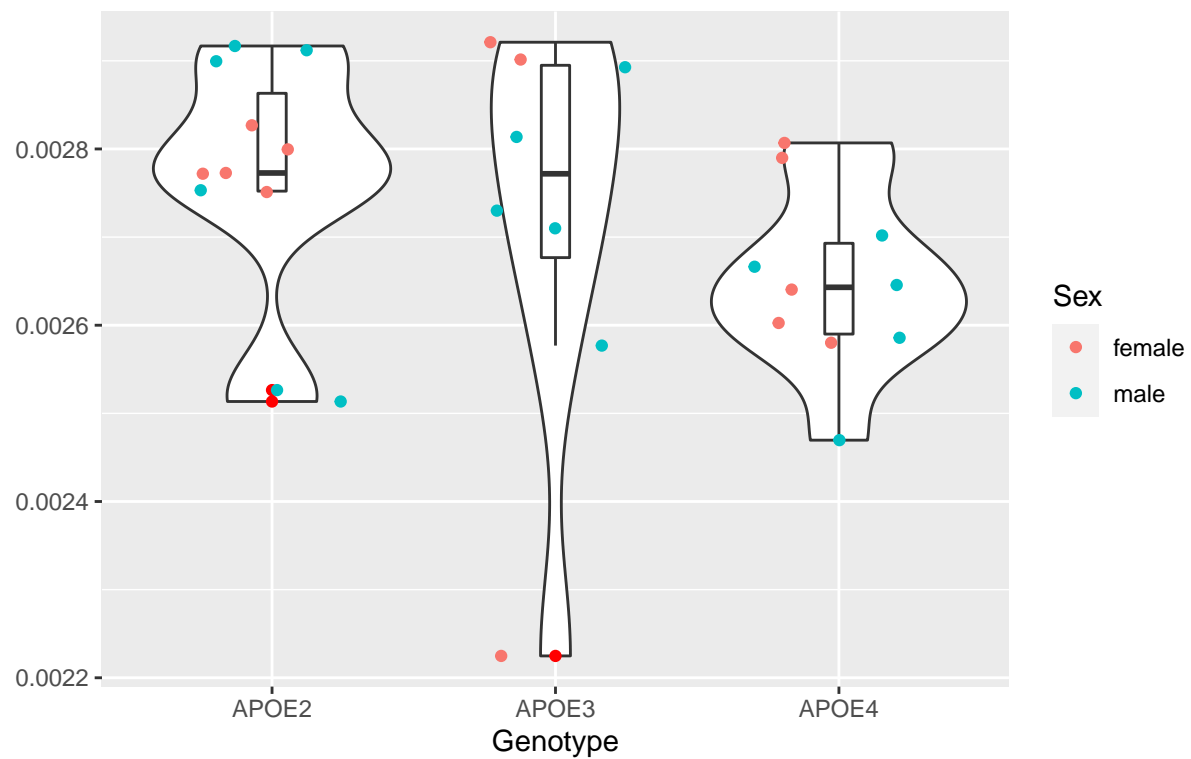
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.550e-09	3.775e-09	0.365	0.698
## Residuals	26	2.687e-07	1.033e-08		

Anterior Thalamic Nuclei

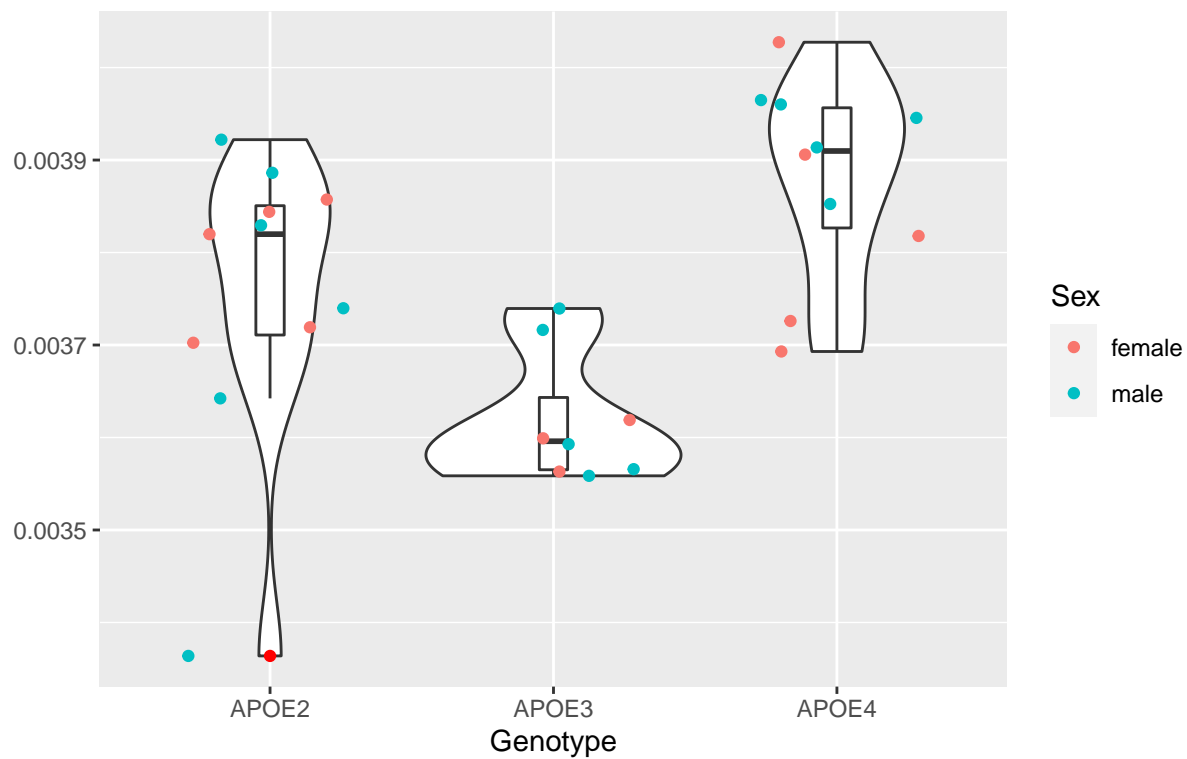
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.440e-08	3.720e-08	1.472	0.248
## Residuals	26	6.572e-07	2.528e-08		

Red Nucleus Magnocellular

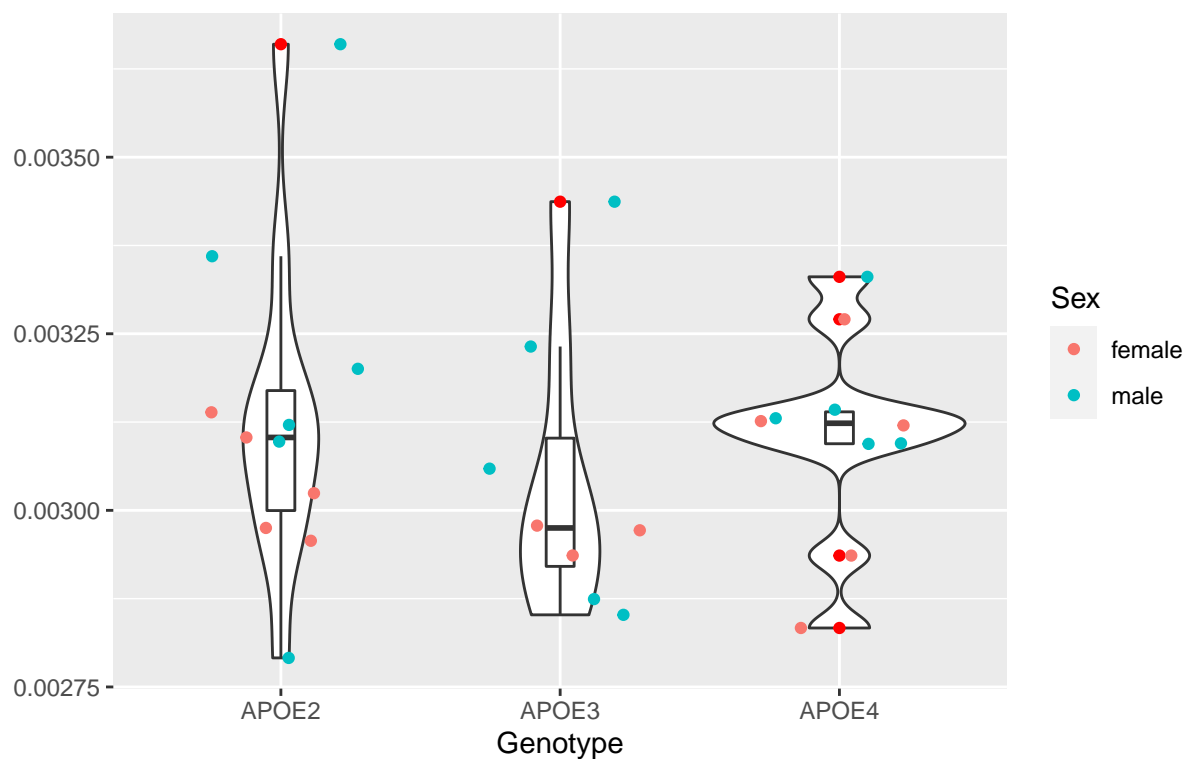
Red points denoting outliers



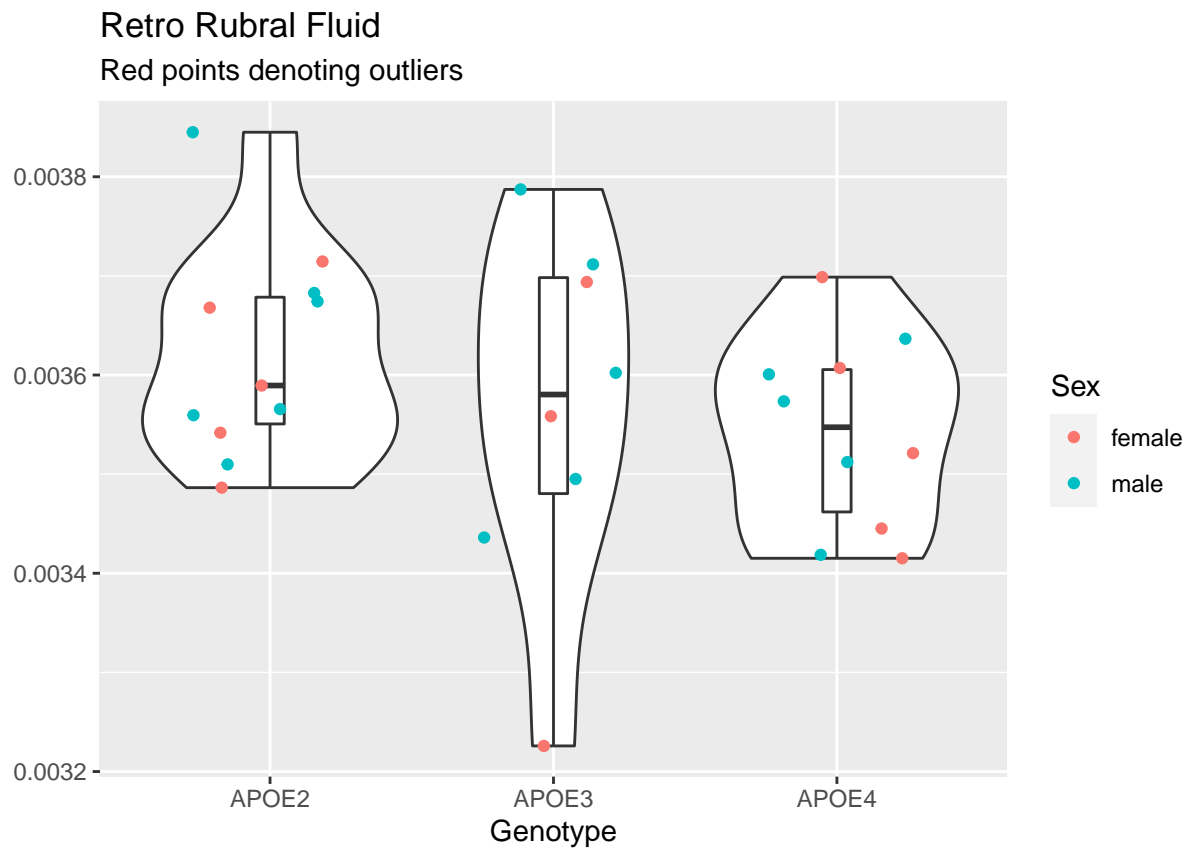
```
##           Df      Sum Sq   Mean Sq F value    Pr(>F)
## geno         2 3.041e-07 1.520e-07    10.33 0.000498 ***
## Residuals    26 3.826e-07 1.471e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pararubral Nucleus

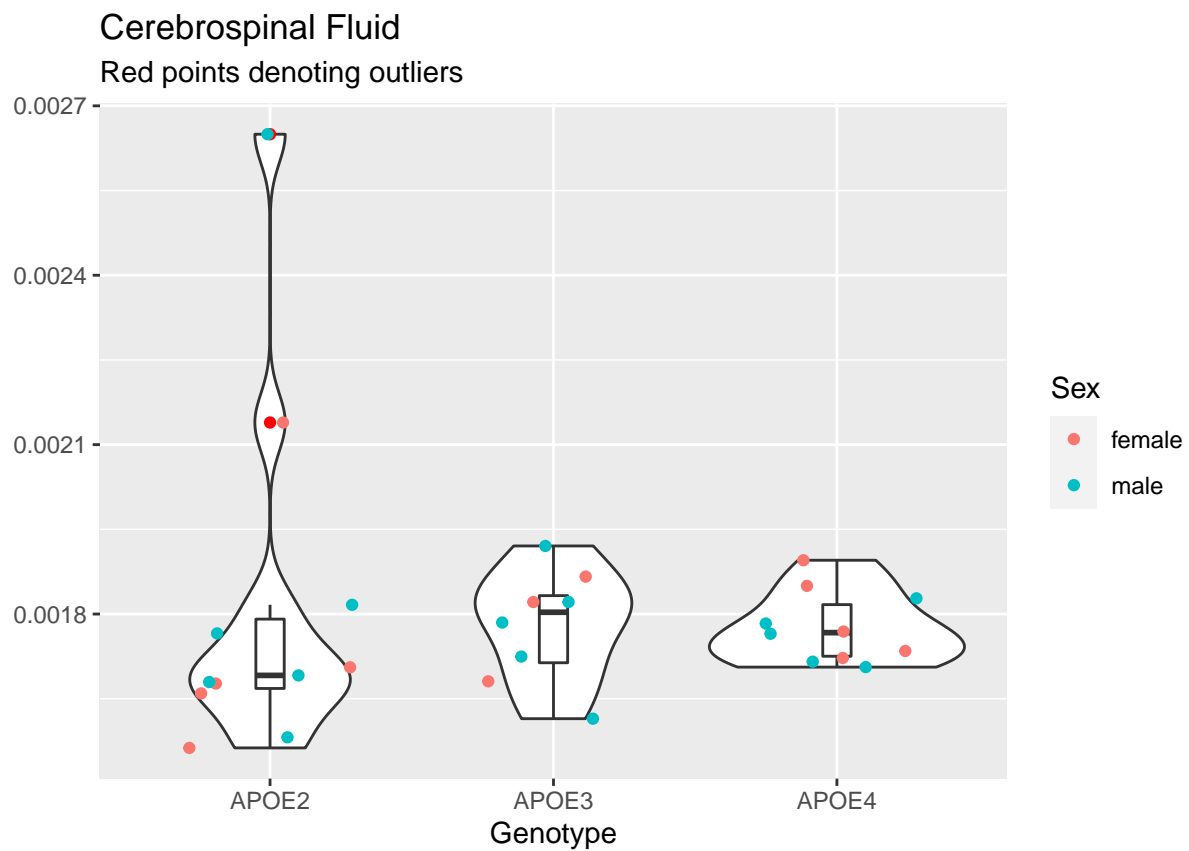
Red points denoting outliers



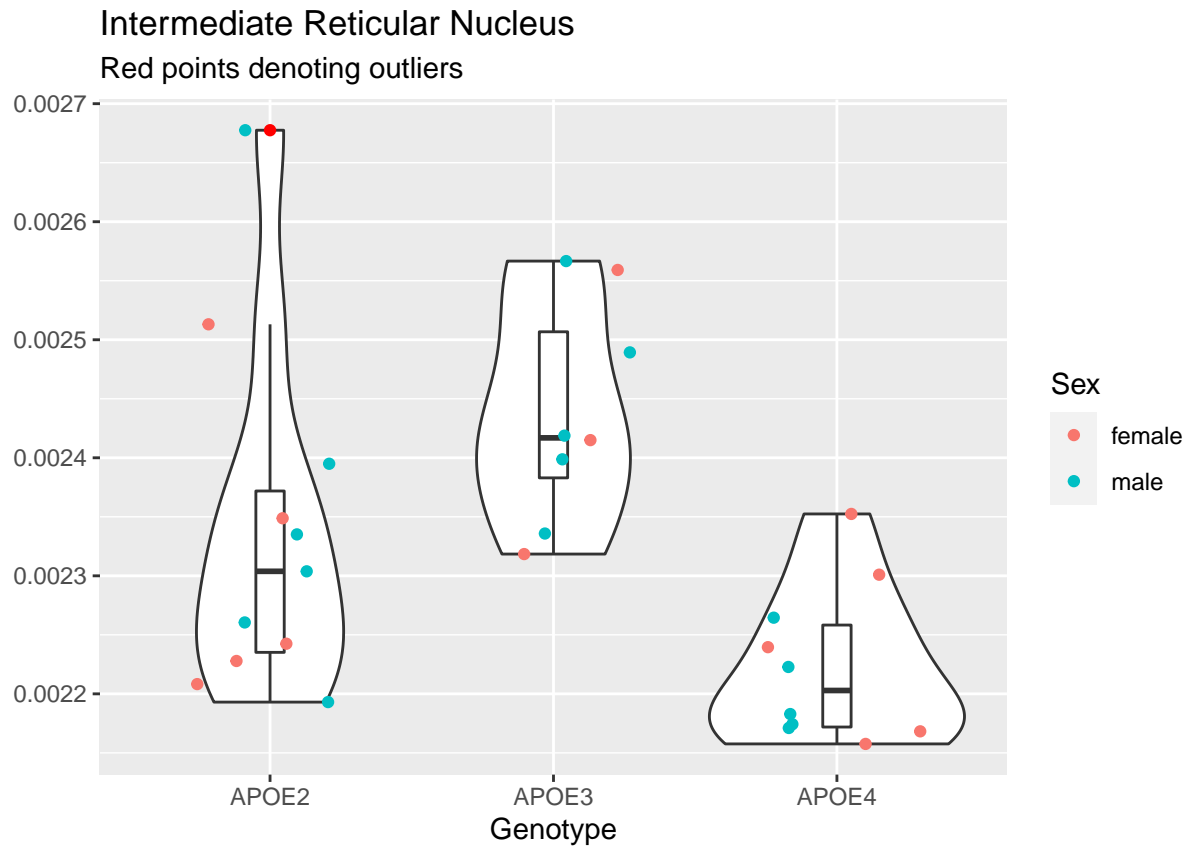
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.670e-08	1.833e-08	0.486	0.62
## Residuals	26	9.806e-07	3.772e-08		



```
##          Df  Sum Sq  Mean Sq F value Pr(>F)
## geno      2 3.48e-08 1.740e-08   1.072  0.357
## Residuals 26 4.22e-07 1.623e-08
```

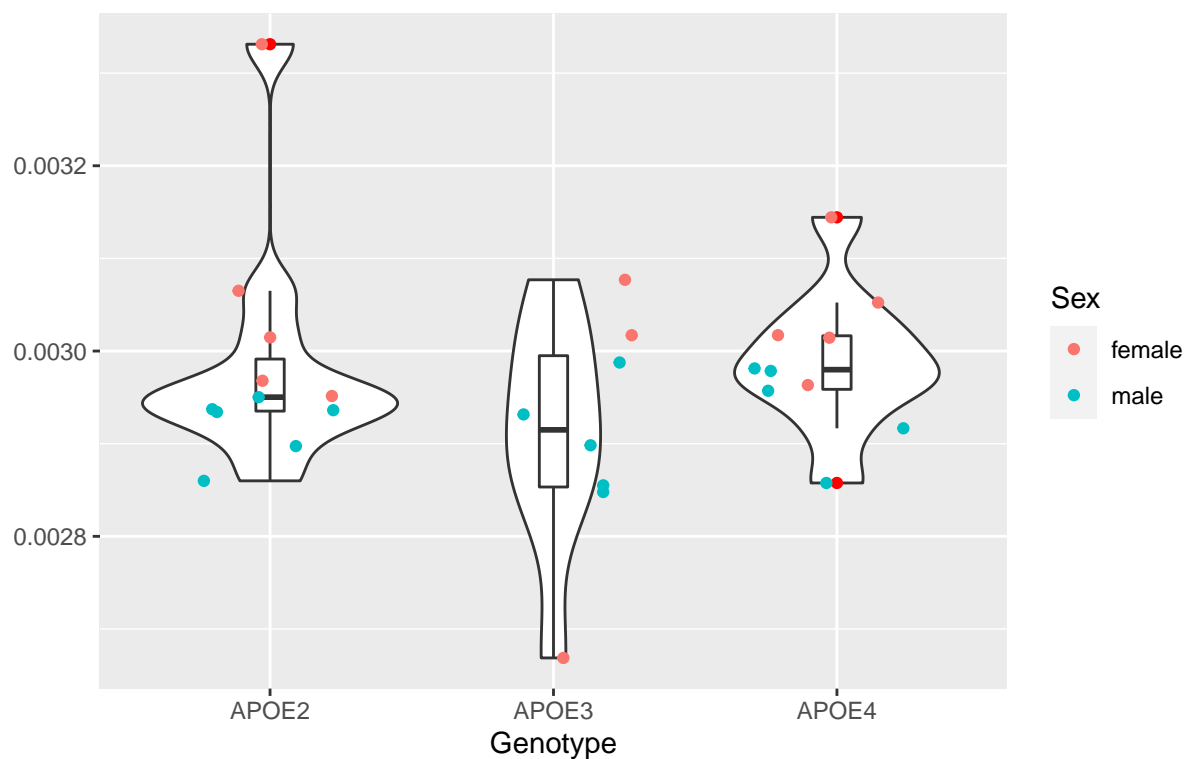


##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.800e-09	3.890e-09	0.091	0.914
## Residuals	26	1.118e-06	4.299e-08		



```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 2.063e-07 1.032e-07    8.505 0.00144 **
## Residuals    26 3.154e-07 1.213e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

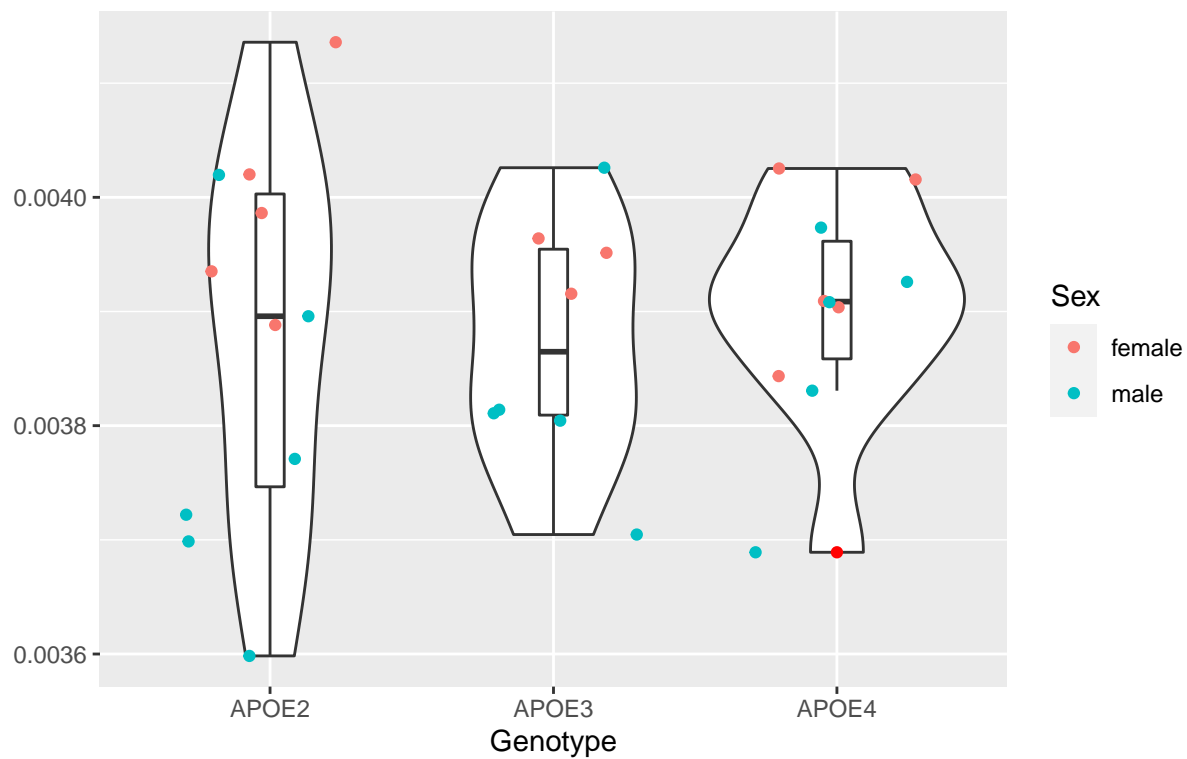
Posterior Dorsal Paraventricular Medial Parvicellular Posterior Lateral Hy
 Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.410e-08	1.704e-08	1.362	0.274
## Residuals	26	3.253e-07	1.251e-08		

Prerubral Forel

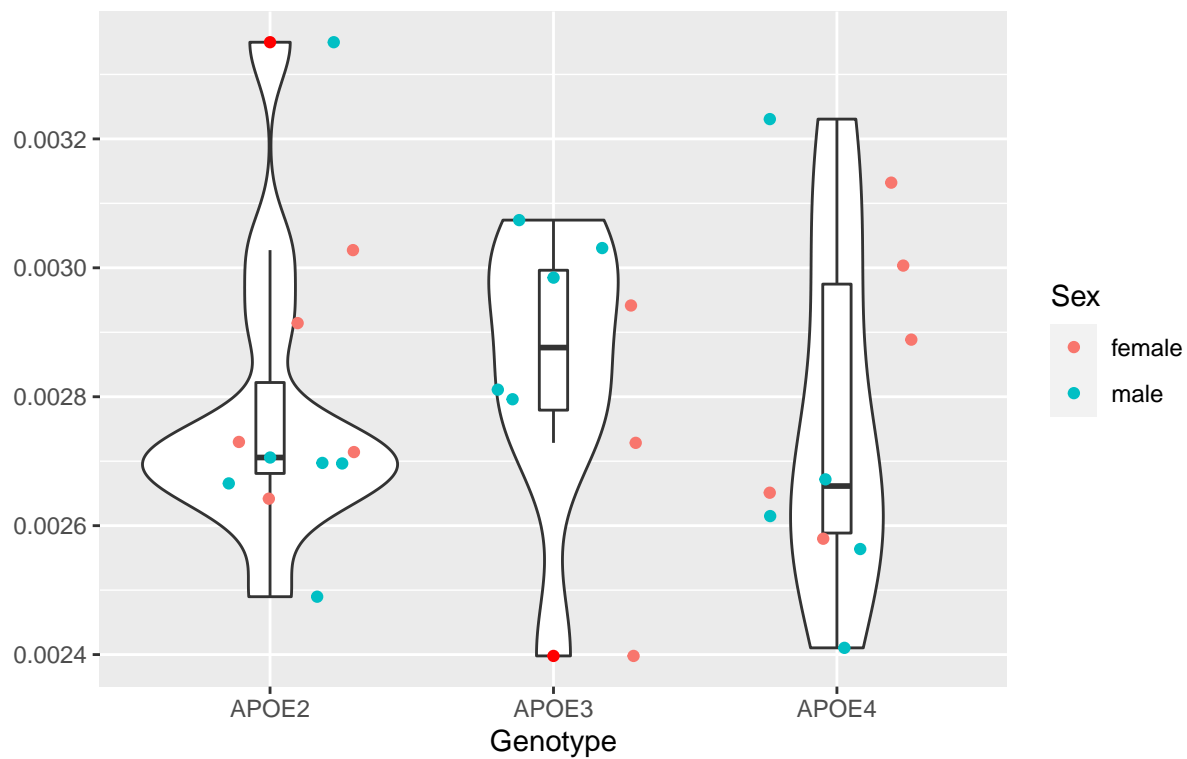
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.400e-09	2.198e-09	0.131	0.878
## Residuals	26	4.361e-07	1.677e-08		

PVG of Hypothalamus

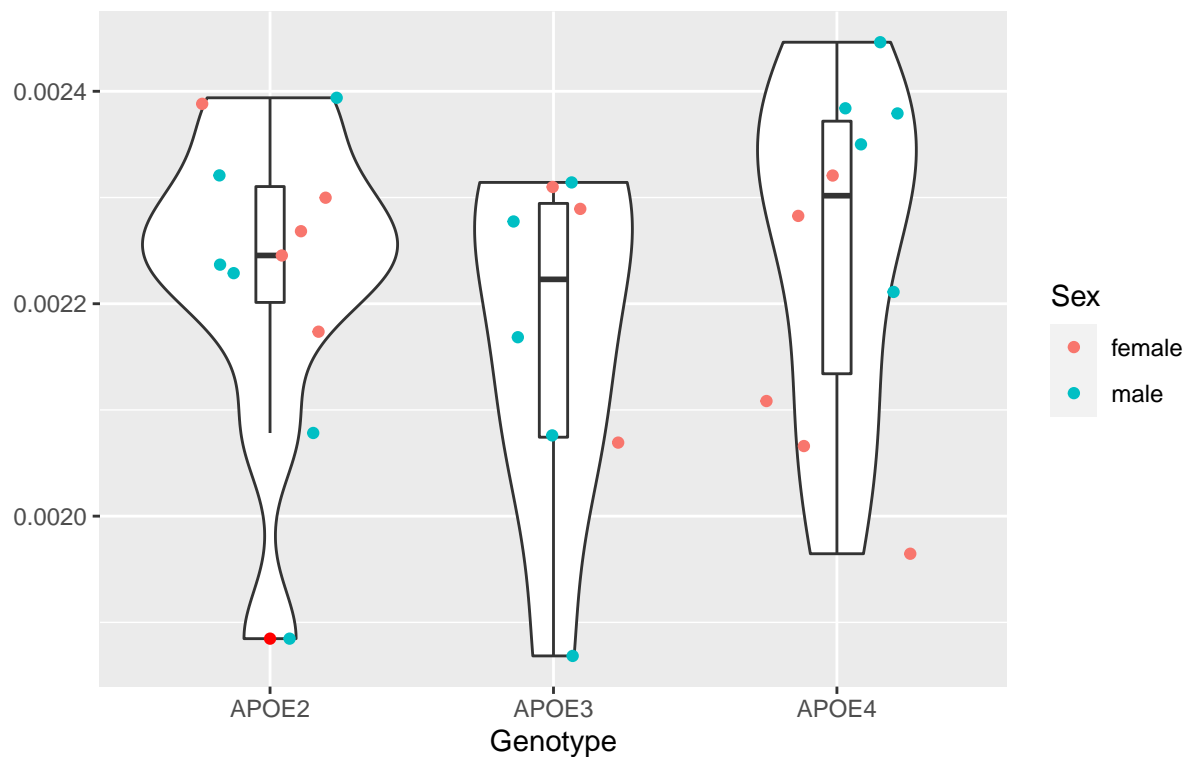
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.550e-08	1.273e-08	0.214	0.809
## Residuals	26	1.547e-06	5.950e-08		

Basal Lateral Amygdala

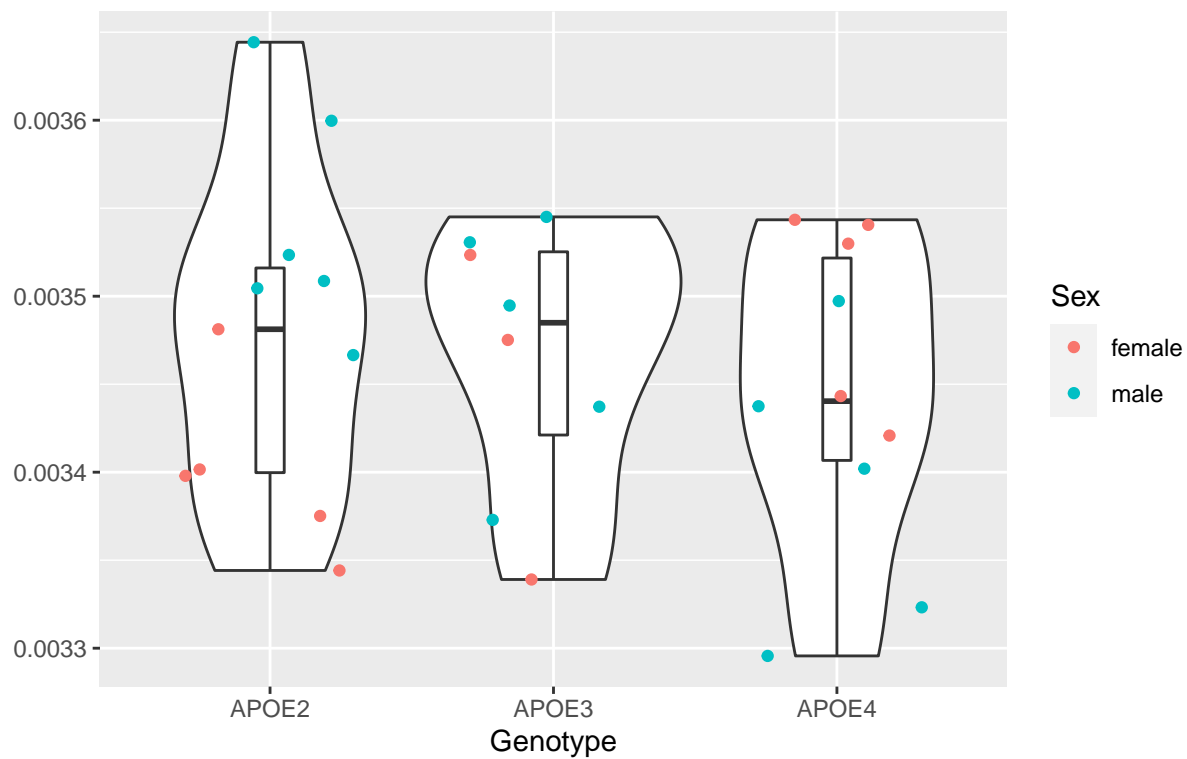
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.940e-08 1.469e-08   0.622  0.545
## Residuals 26 6.143e-07 2.363e-08
```

Brain Stem Rest

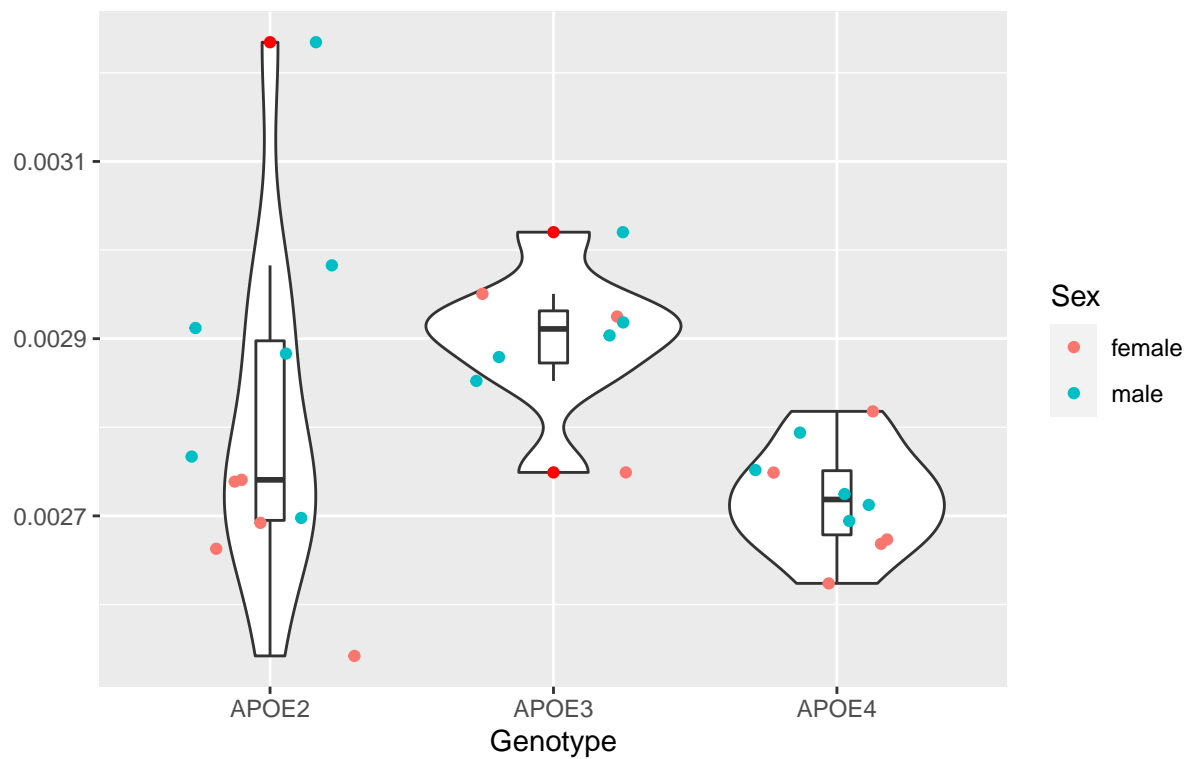
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.020e-09	3.010e-09	0.4	0.674
## Residuals	26	1.956e-07	7.523e-09		

Precuneiform Nucleus

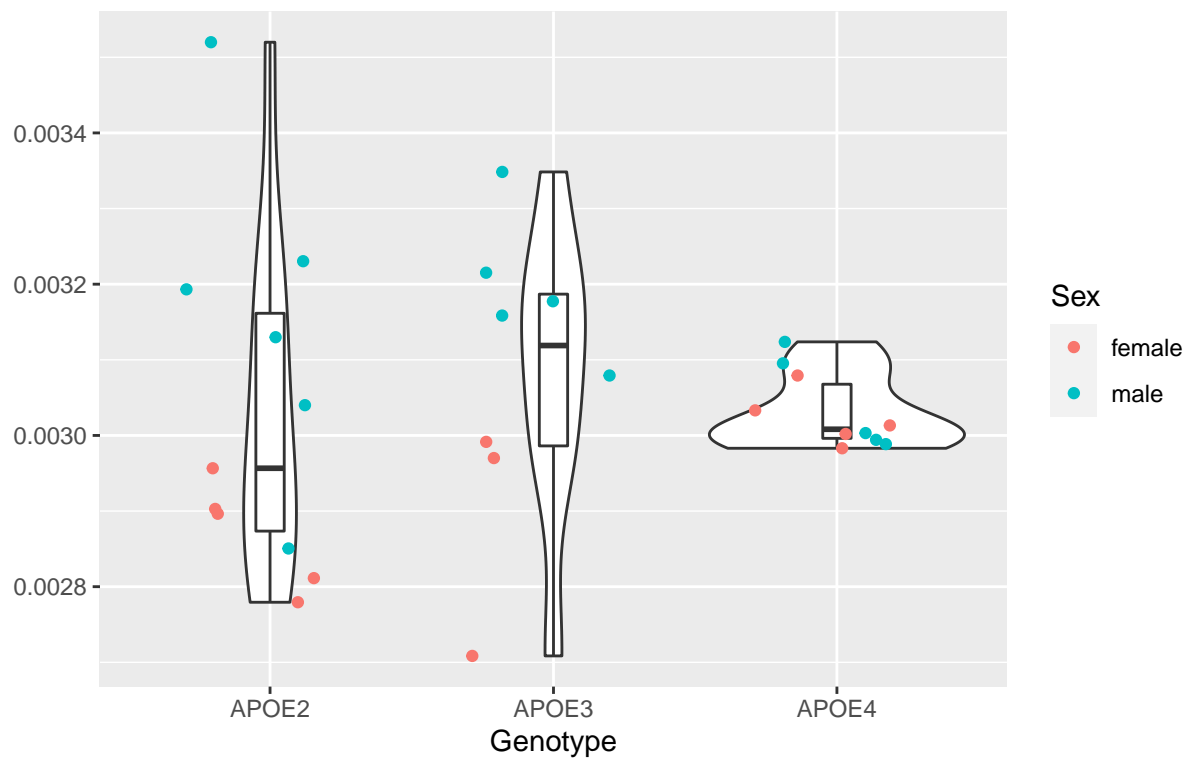
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.423e-07 7.113e-08   4.277 0.0248 *
## Residuals    26 4.324e-07 1.663e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cuneiform Nucleus

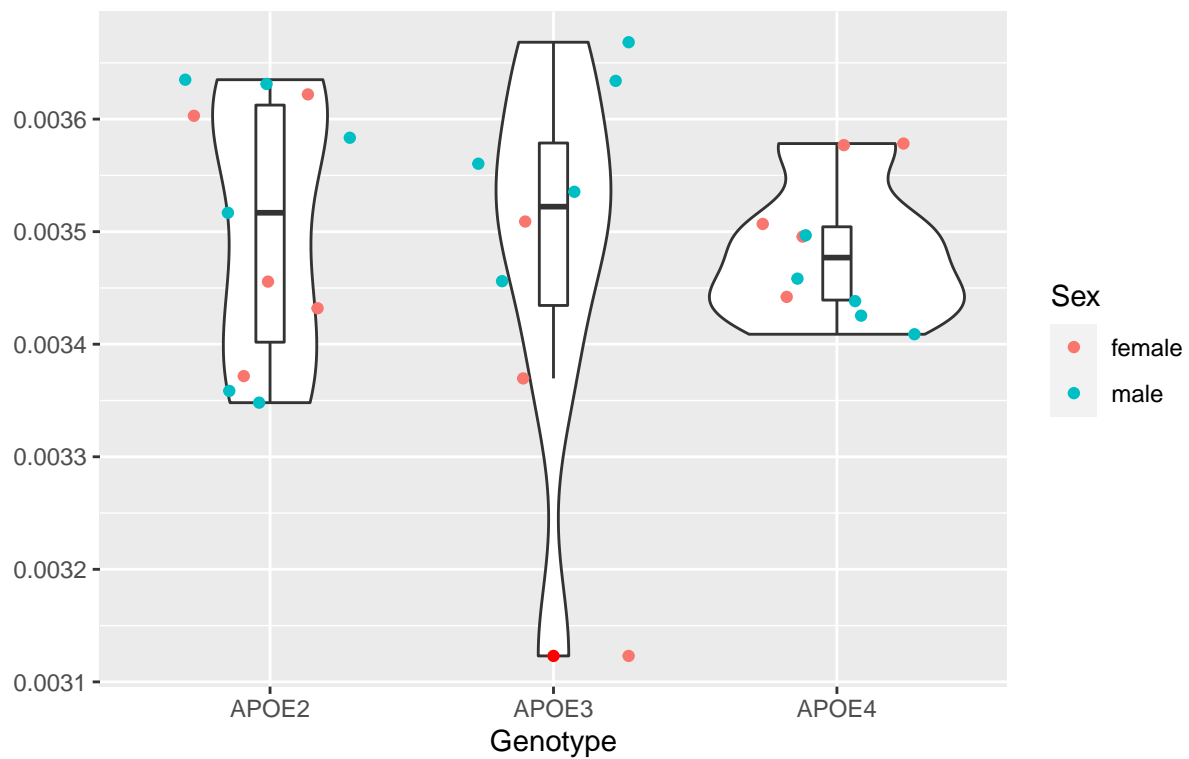
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.530e-08	7.647e-09	0.253	0.778
## Residuals	26	7.855e-07	3.021e-08		

Midbrain Linear Nucleus

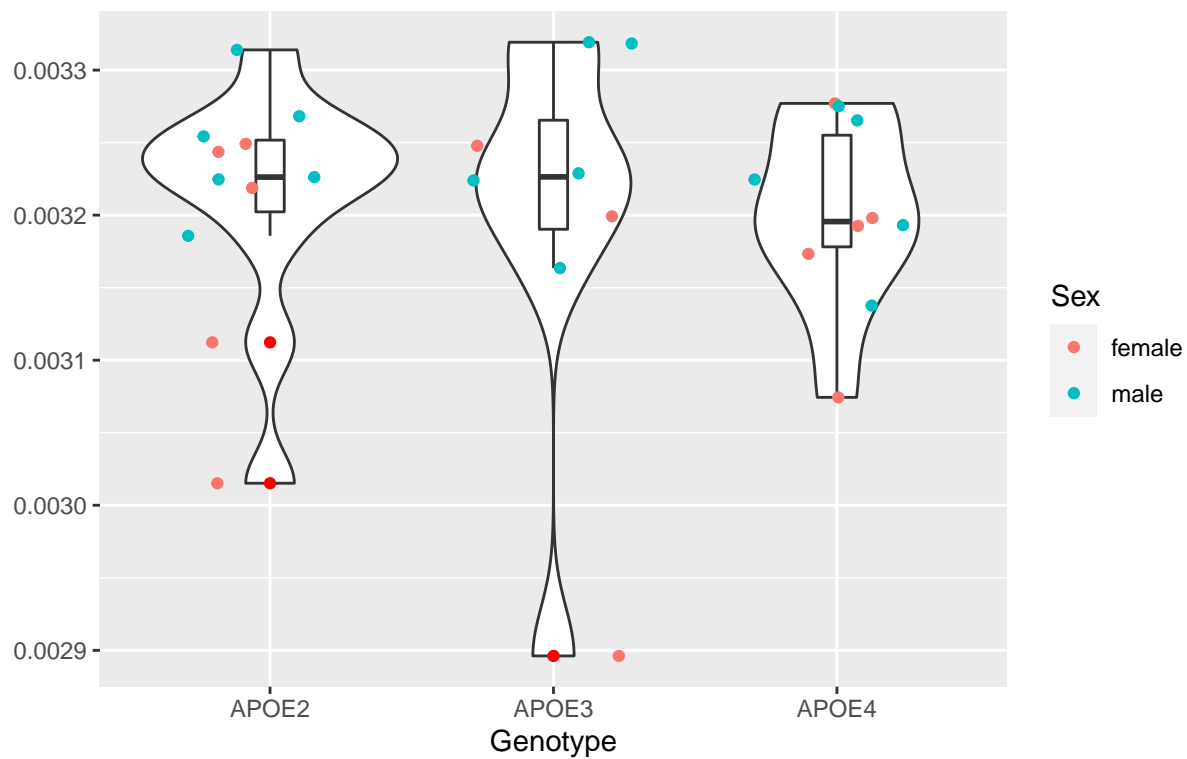
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.600e-09	1.777e-09	0.123	0.885
## Residuals	26	3.756e-07	1.445e-08		

Midbrain Reticular Nucleus

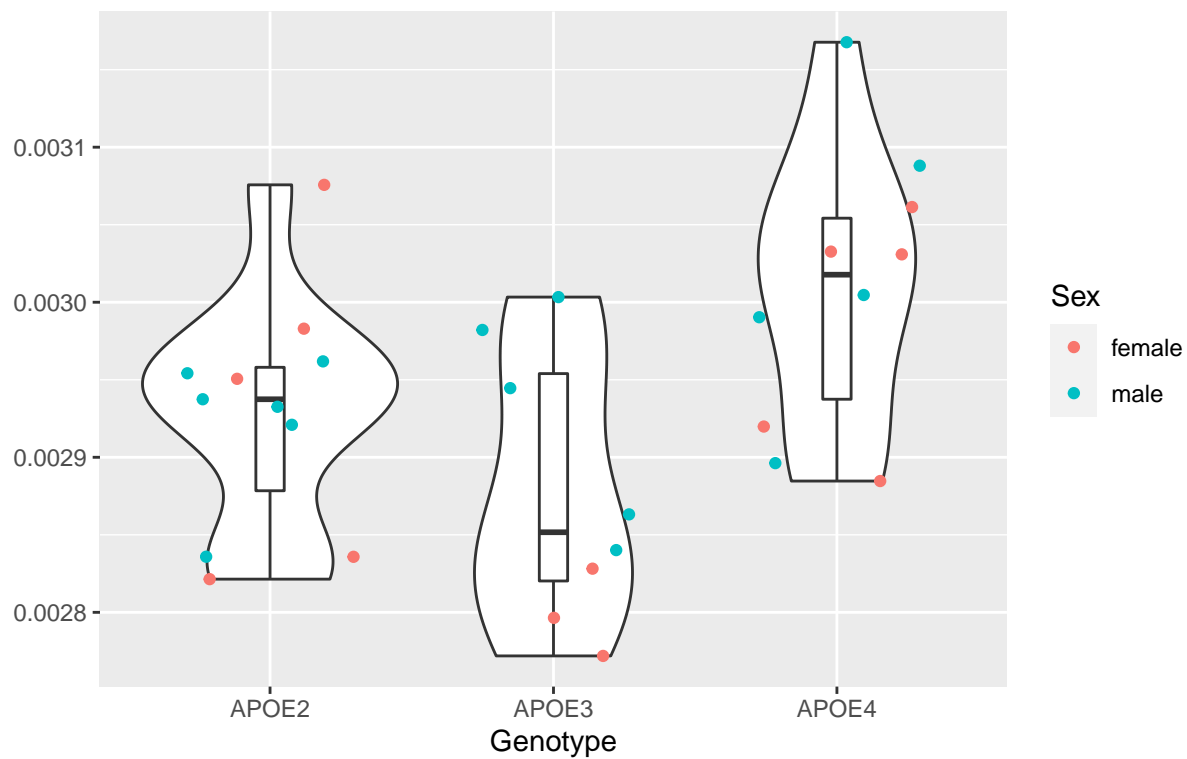
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.600e-10	3.290e-10	0.037	0.964
## Residuals	26	2.299e-07	8.844e-09		

Red Nucleus Parvicellular

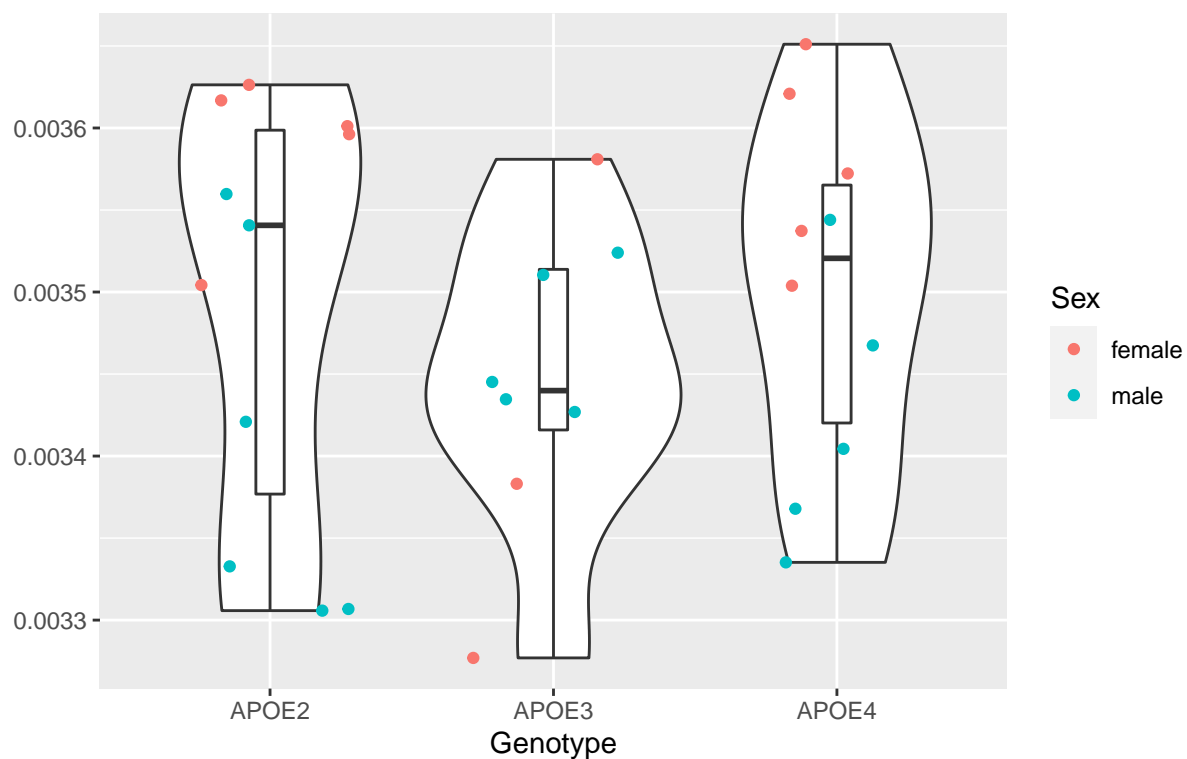
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 7.724e-08 3.862e-08    5.565 0.00973 **
## Residuals    26 1.804e-07 6.940e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Substantia Nigra

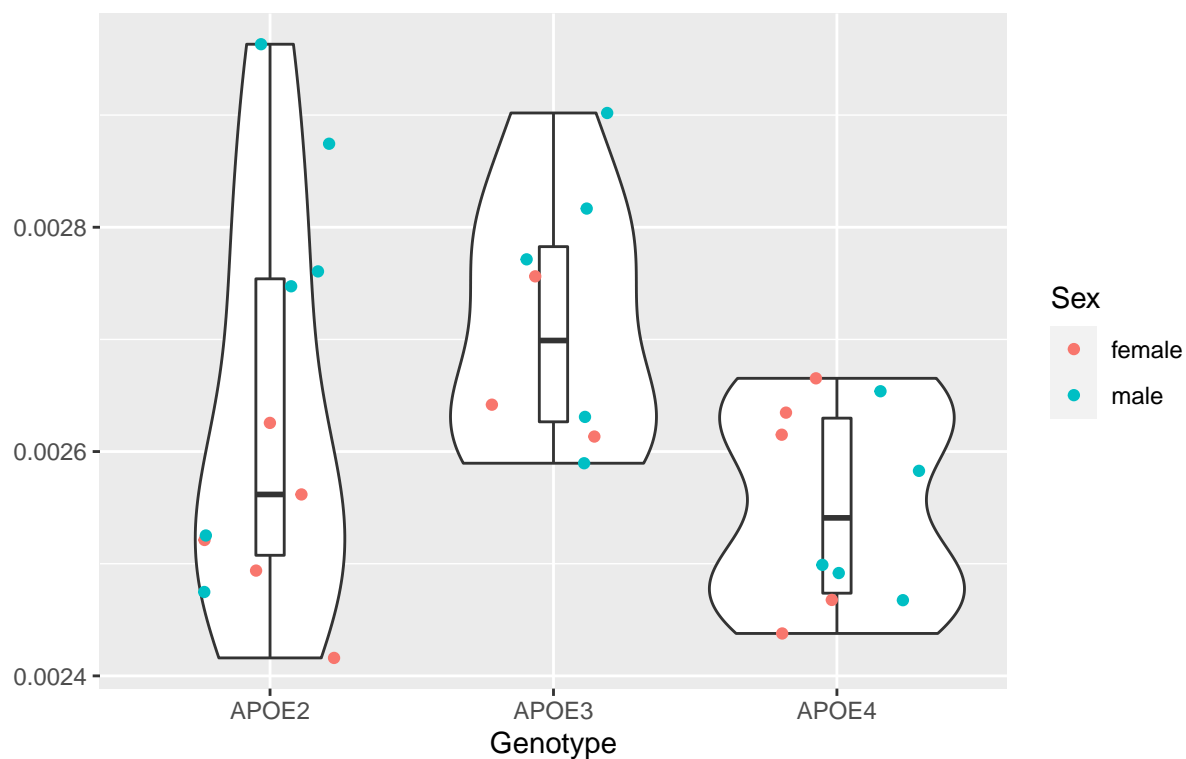
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.380e-08	6.924e-09	0.554	0.581
## Residuals	26	3.251e-07	1.251e-08		

Inferior Colliculus

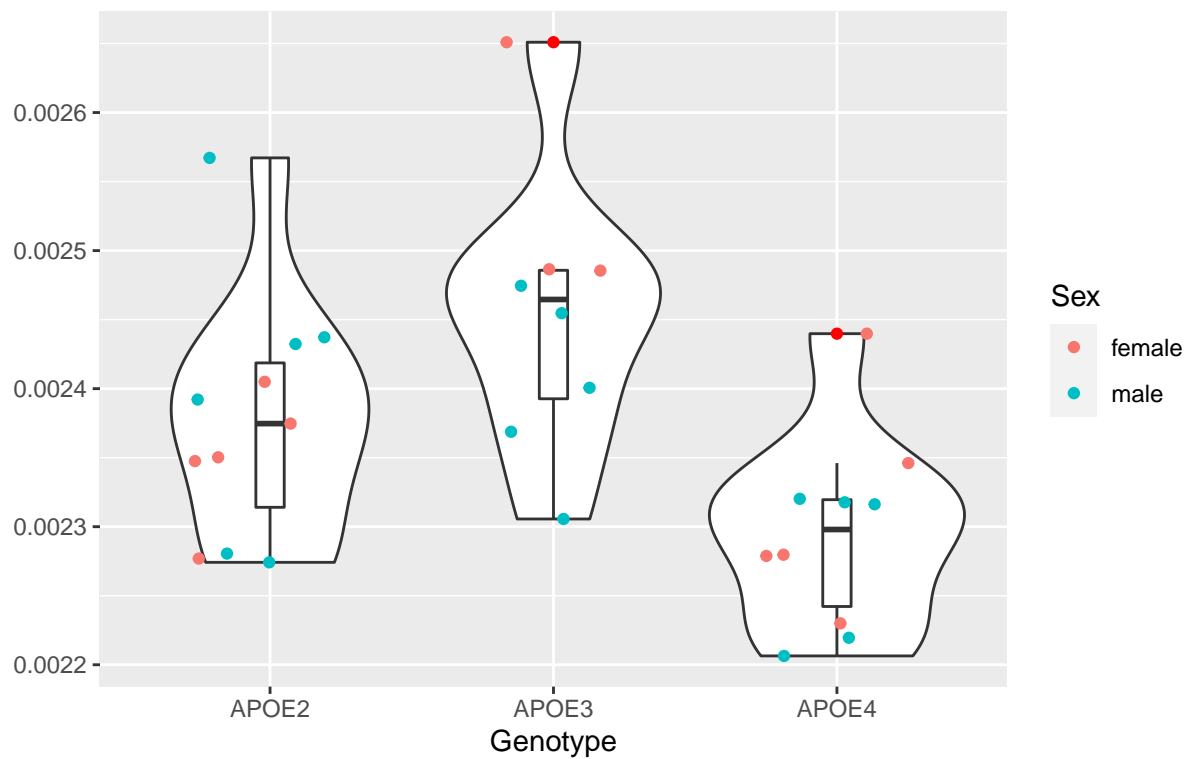
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.196e-07 5.981e-08   3.276 0.0539 .
## Residuals    26 4.747e-07 1.826e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Superior Colliculus

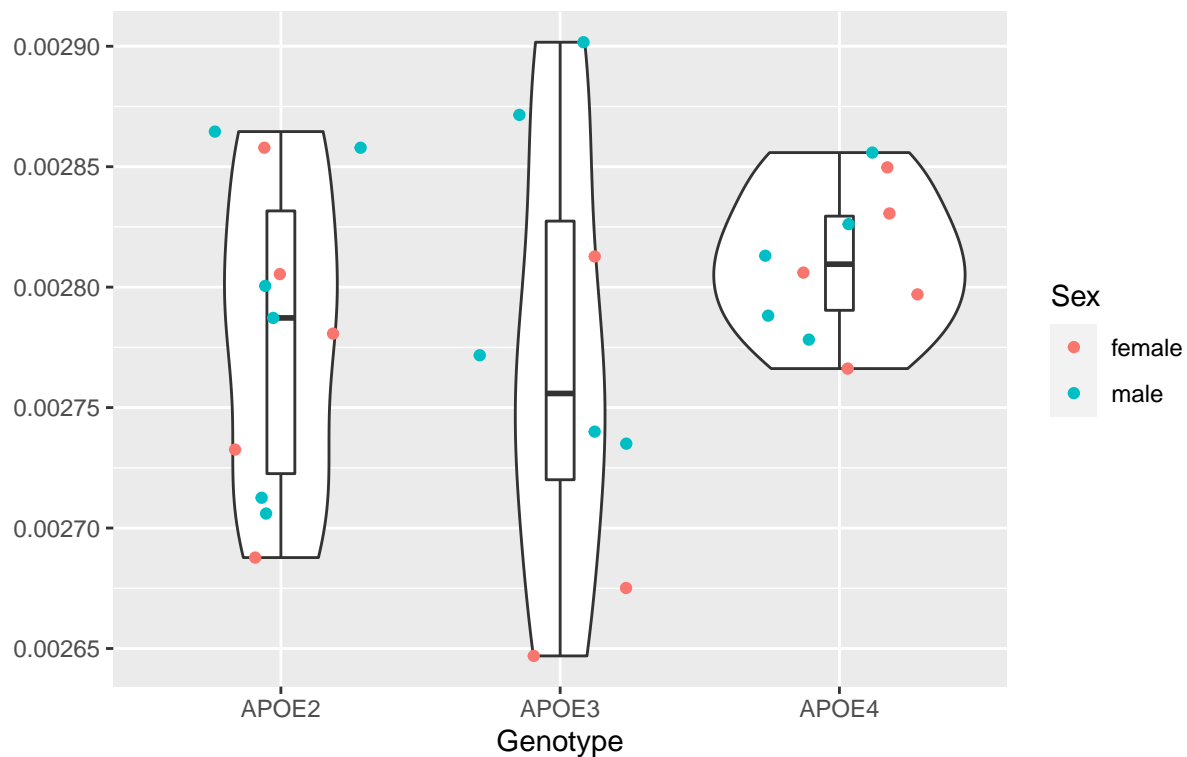
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.116e-07 5.581e-08   7.552 0.0026 **
## Residuals    26 1.921e-07 7.390e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Deep Mesencephalic Nuclei

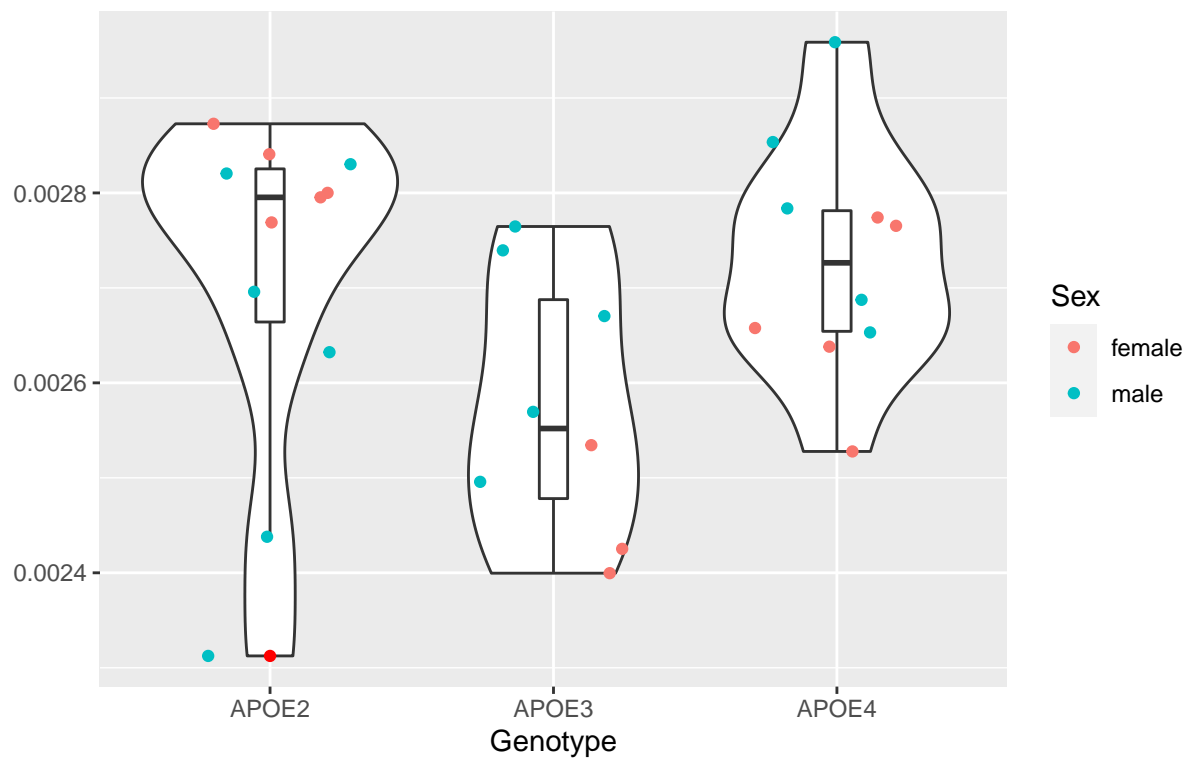
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 8.630e-09 4.315e-09    1.07  0.358
## Residuals 26 1.049e-07 4.033e-09
```

Subbrachial Nucleus and Peripeduncular Nucleus

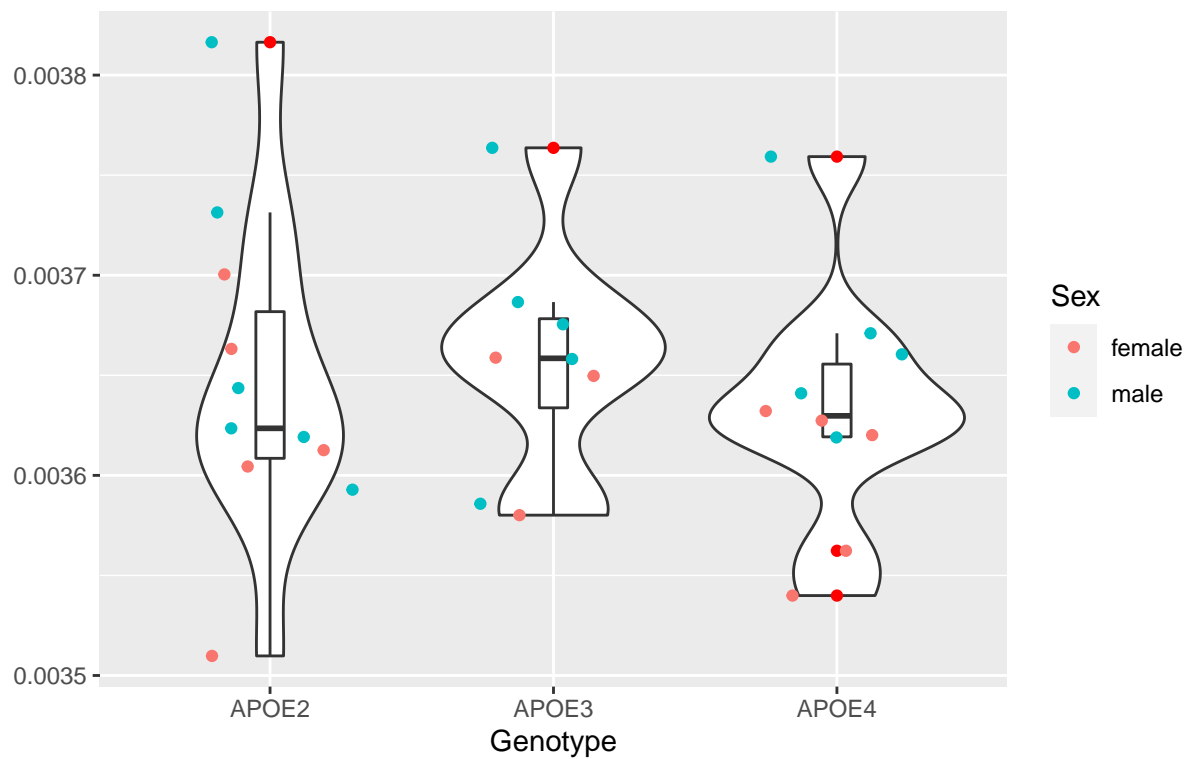
Red points denoting outliers



```
##           Df    Sum Sq   Mean Sq F value Pr(>F)
## geno       2 1.231e-07 6.155e-08   2.682 0.0873 .
## Residuals 26 5.966e-07 2.294e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Reticular Nucleus of Thalamus

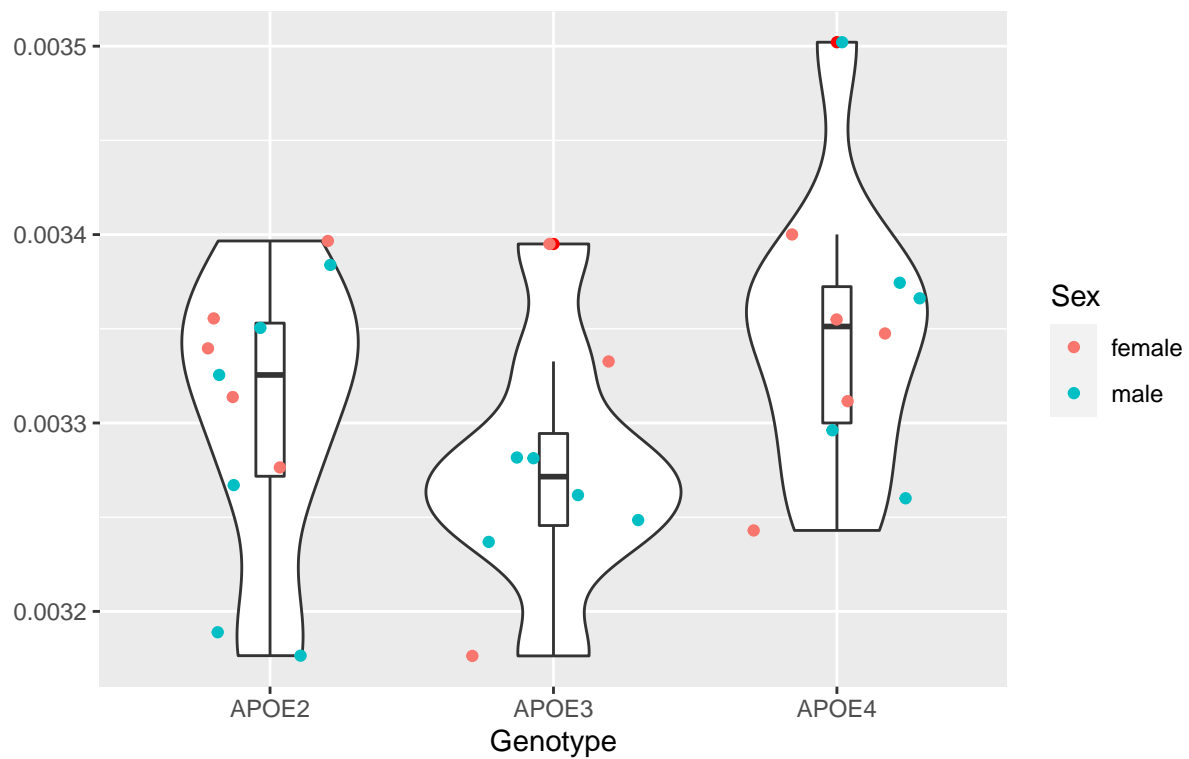
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.630e-09	1.317e-09	0.283	0.756
## Residuals	26	1.209e-07	4.651e-09		

Zona Incerta

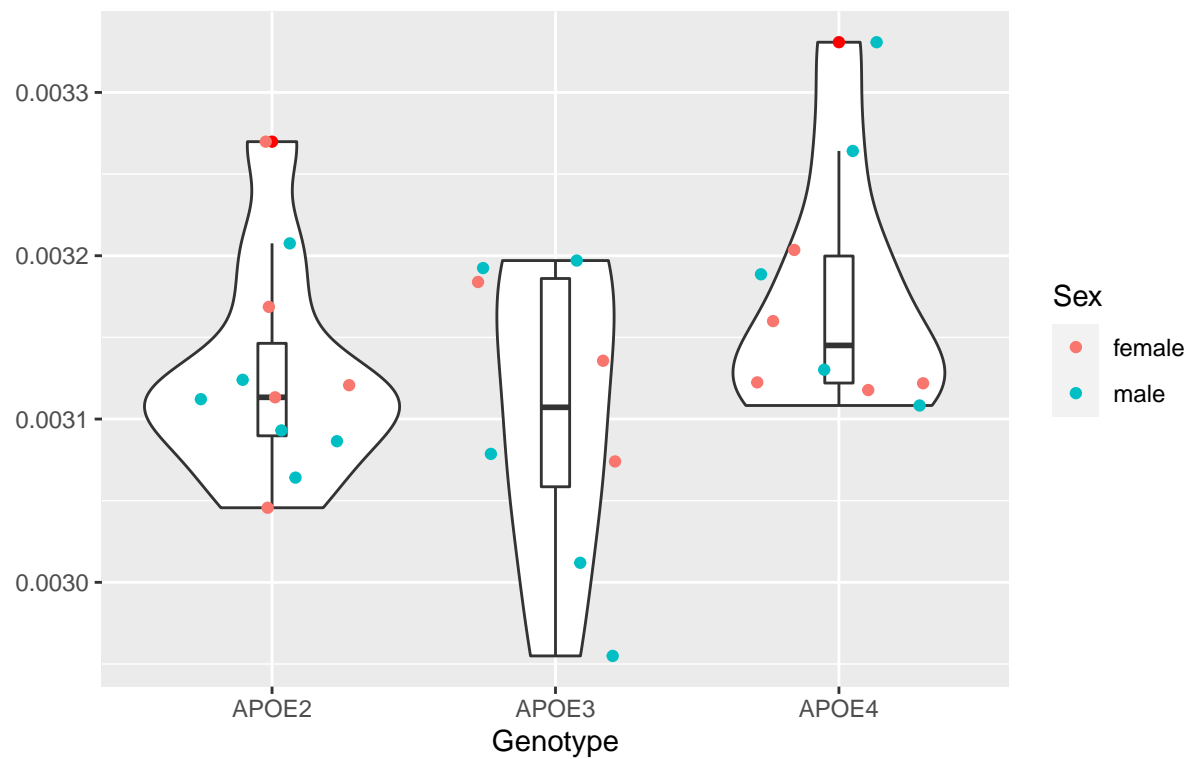
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.152e-08 1.076e-08    2.1  0.143
## Residuals 26 1.333e-07 5.125e-09
```


Lateral Geniculate Nucleus

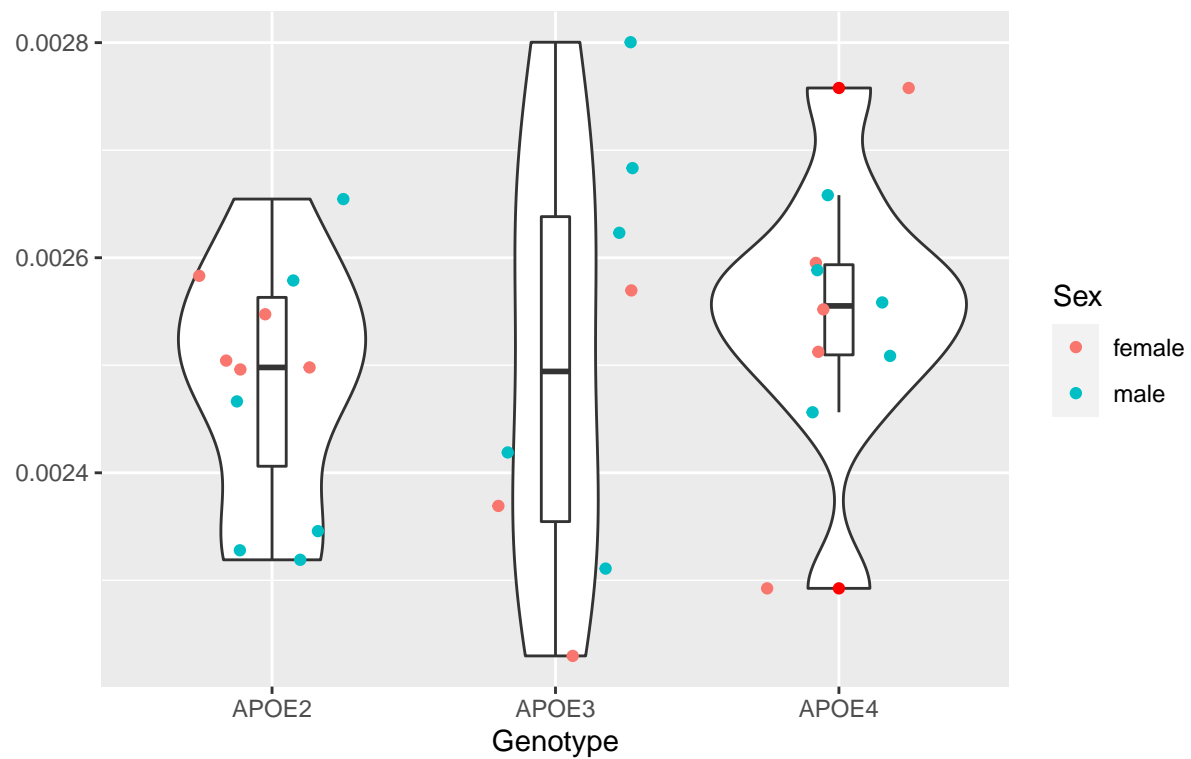
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.412e-08	1.206e-08	2.129	0.139
## Residuals	26	1.473e-07	5.666e-09		

Medial Geniculate Nucleus

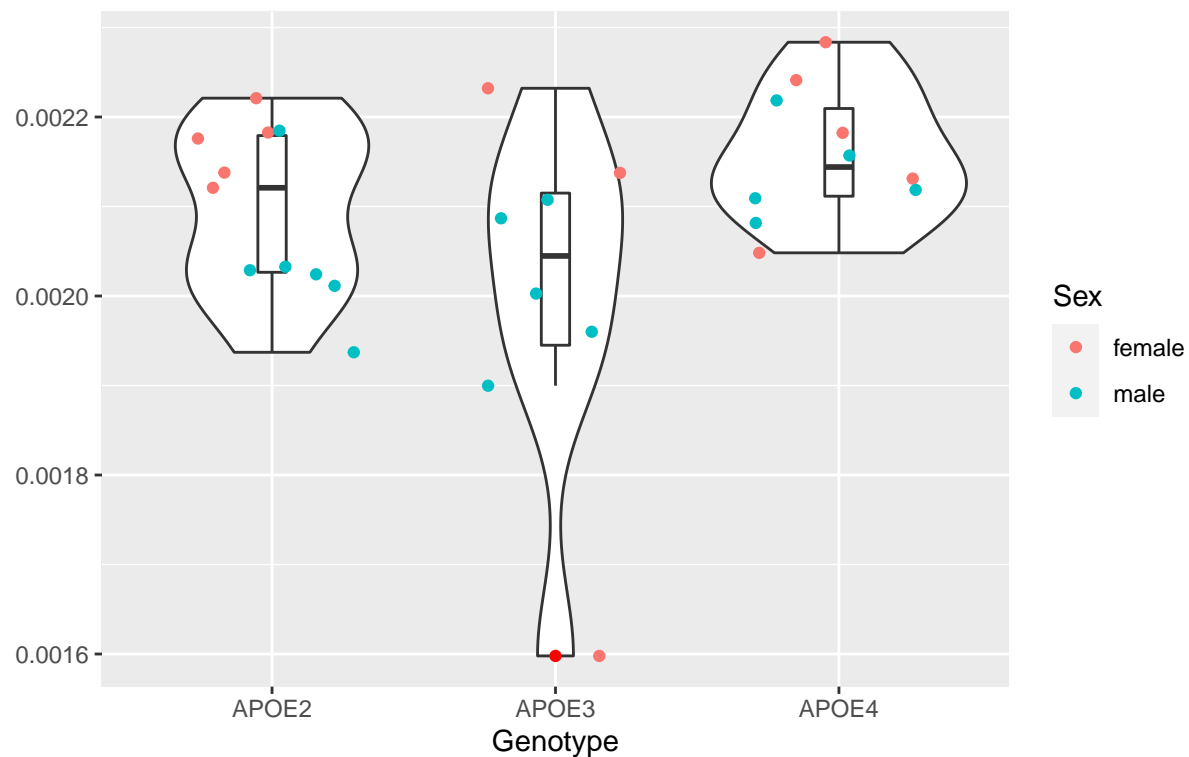
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno       2 2.270e-08 1.135e-08    0.55  0.584
## Residuals 26 5.367e-07 2.064e-08
```

Latero Dorsal Nucleus of Thalamus

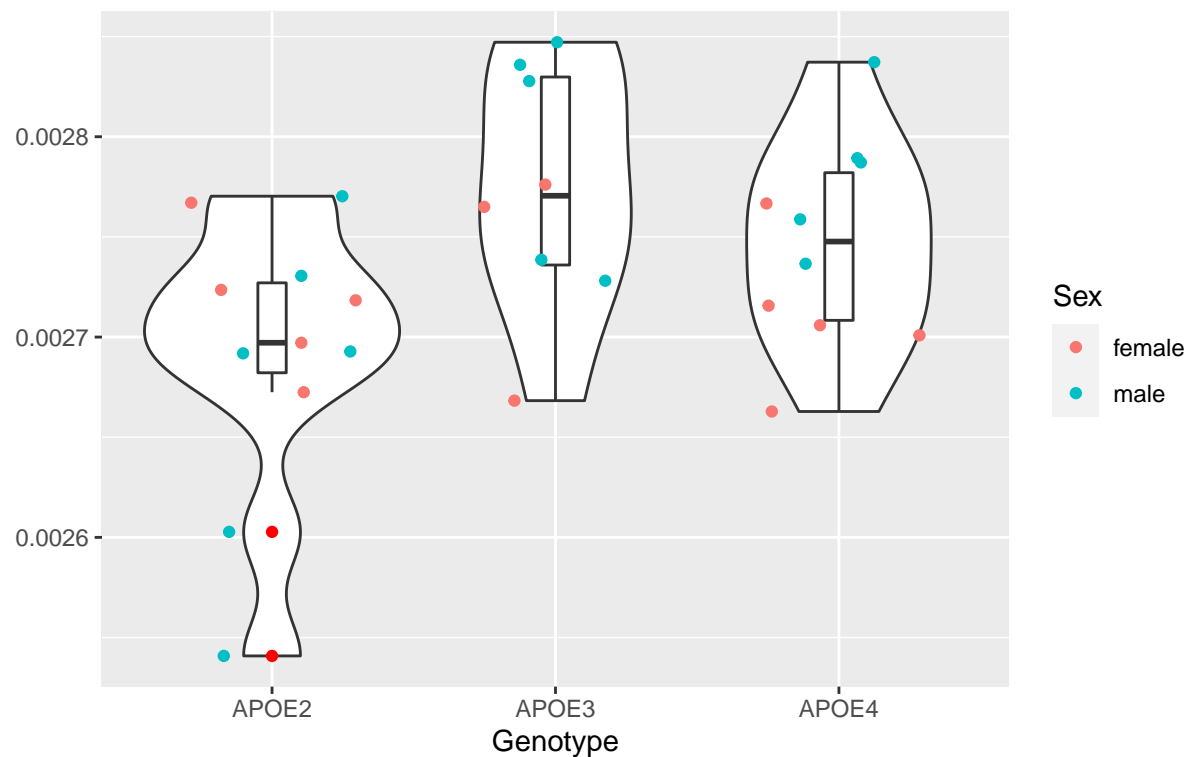
Red points denoting outliers



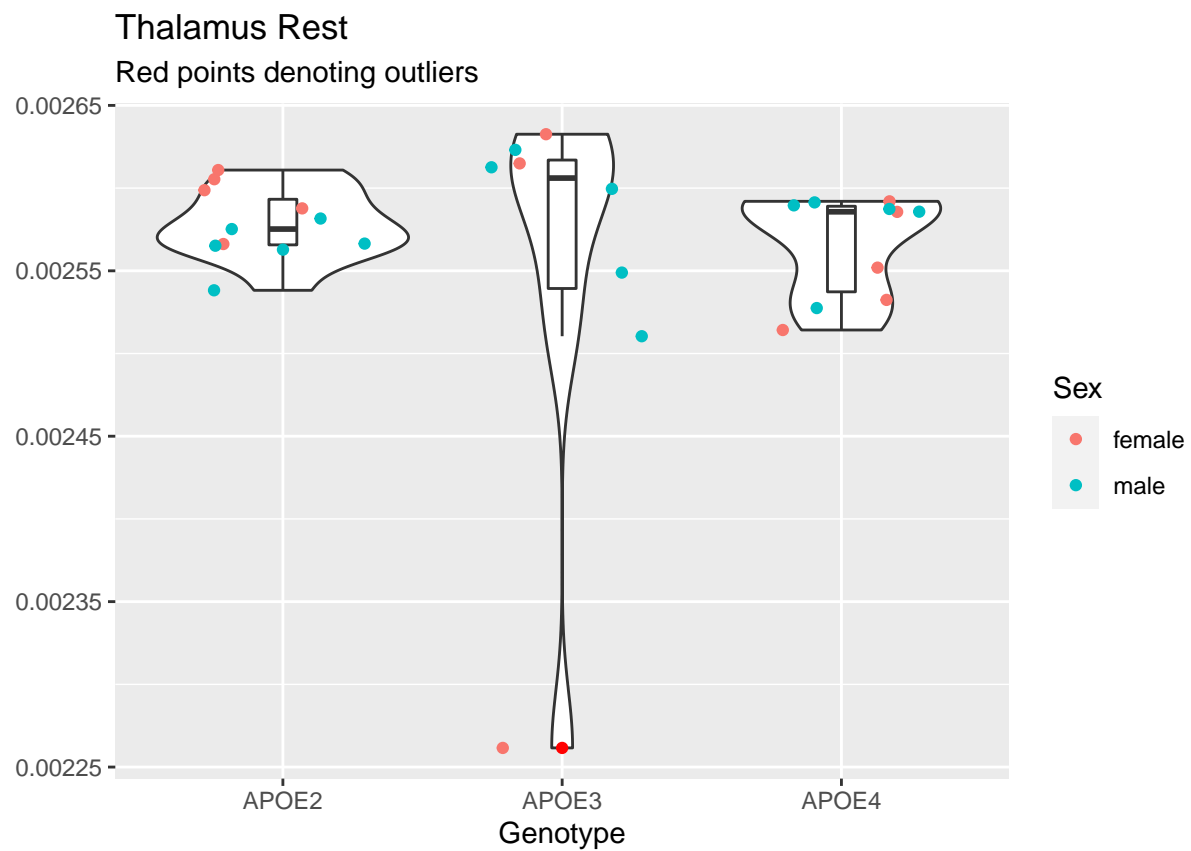
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.059e-07 5.296e-08   3.438 0.0473 *
## Residuals    26 4.005e-07 1.540e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Ventral Thalamic Nuclei

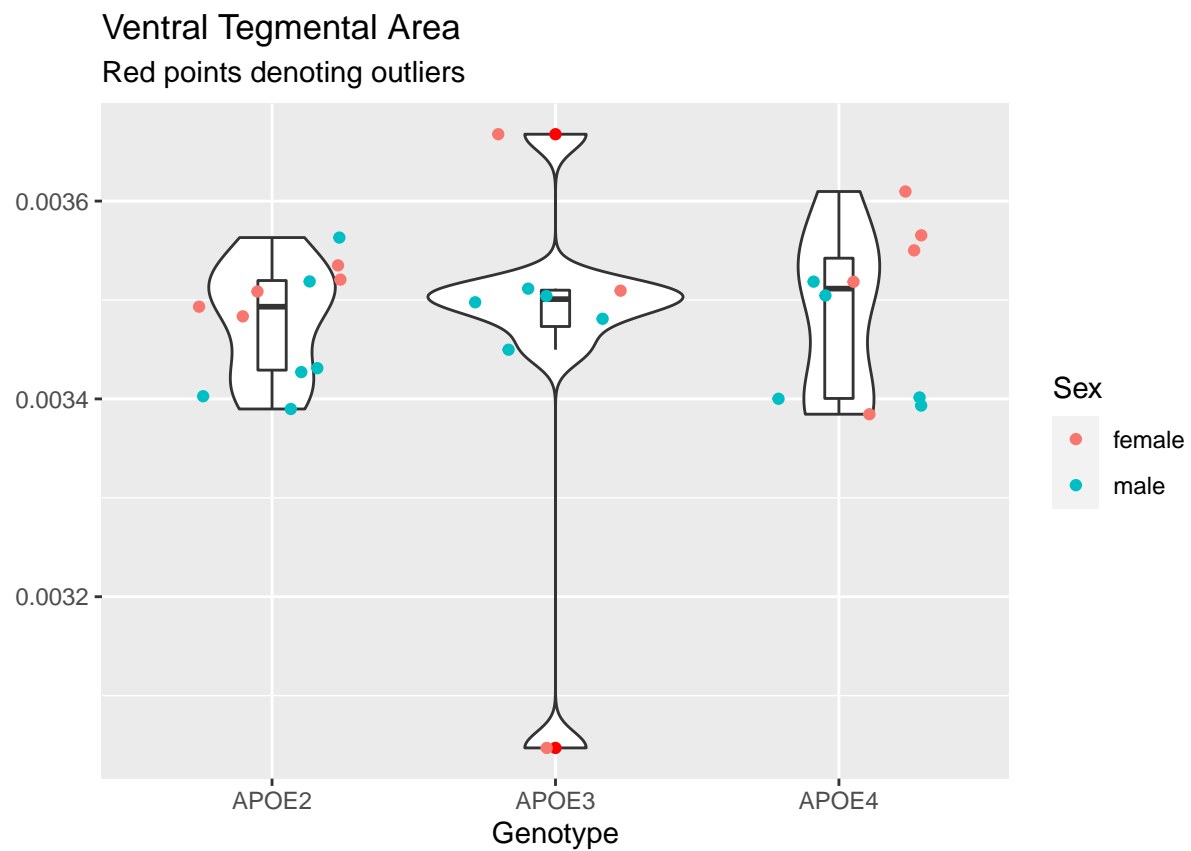
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno       2 3.360e-08 1.680e-08   4.507 0.0209 *
## Residuals 26 9.693e-08 3.728e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



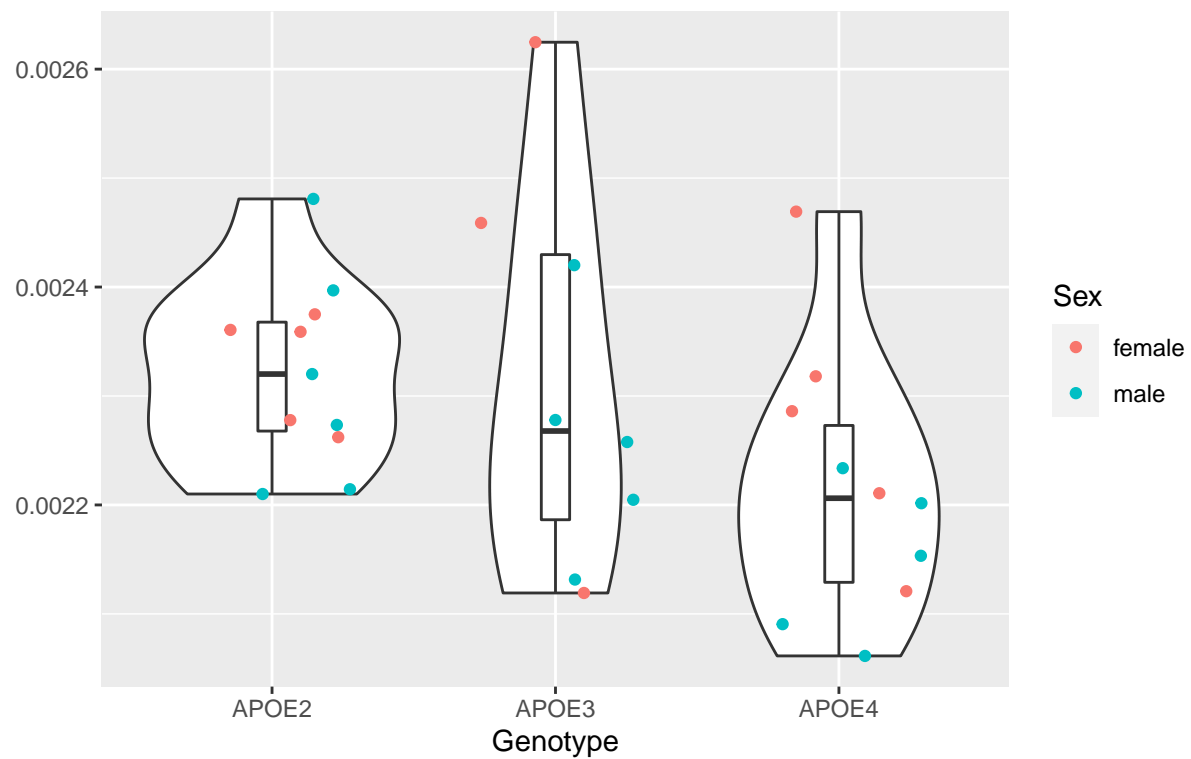
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.520e-09	1.762e-09	0.379	0.688
## Residuals	26	1.207e-07	4.644e-09		



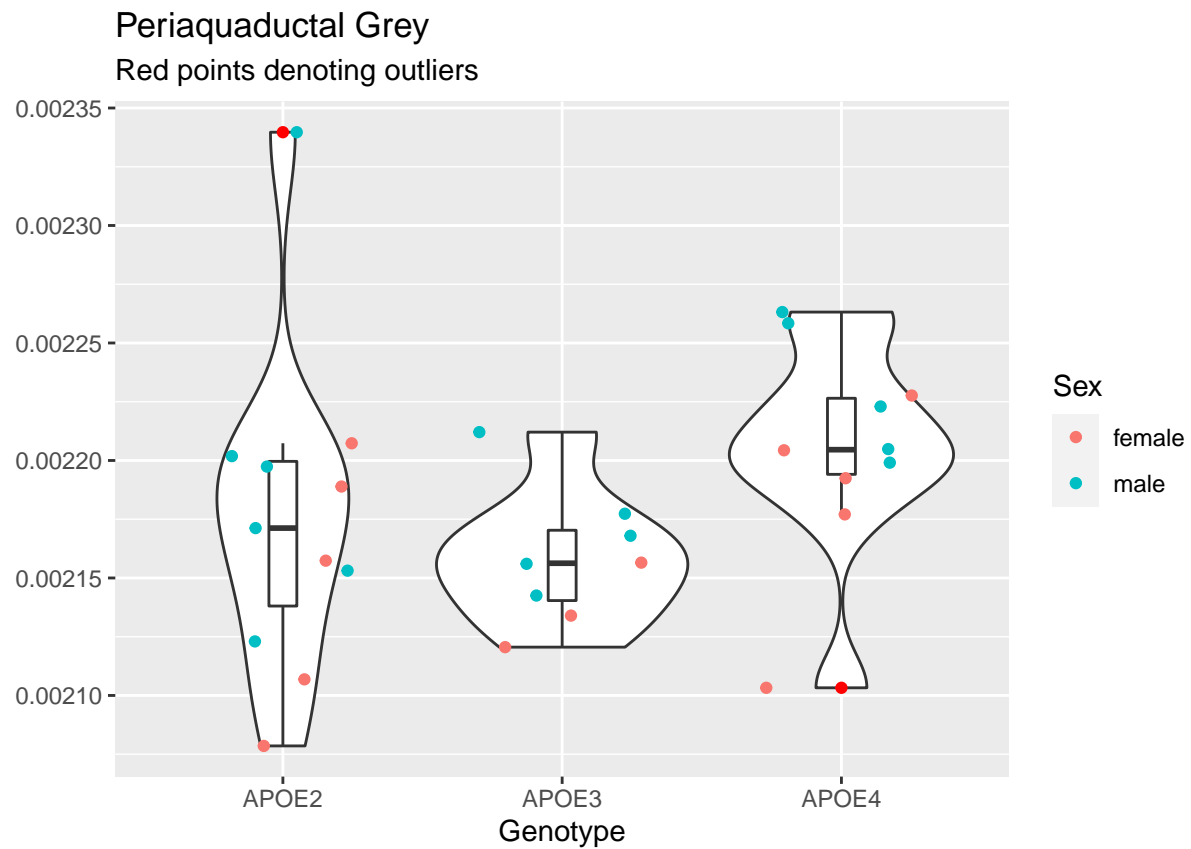
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.300e-09	1.654e-09	0.135	0.874
## Residuals	26	3.175e-07	1.221e-08		

Anterior Pretectal Nucleus

Red points denoting outliers



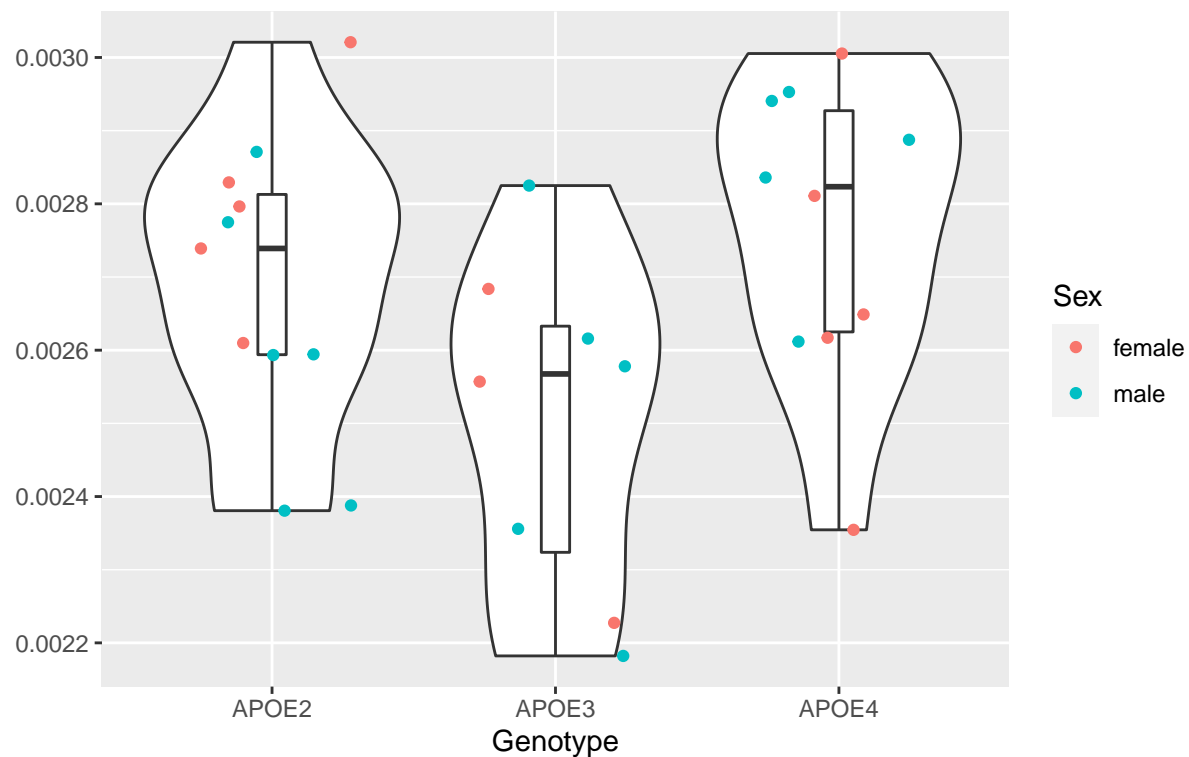
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.930e-08	3.464e-08	2.158	0.136
## Residuals	26	4.174e-07	1.606e-08		



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.040e-08	5.201e-09	1.903	0.169
## Residuals	26	7.105e-08	2.733e-09		

Ventral Pallidum

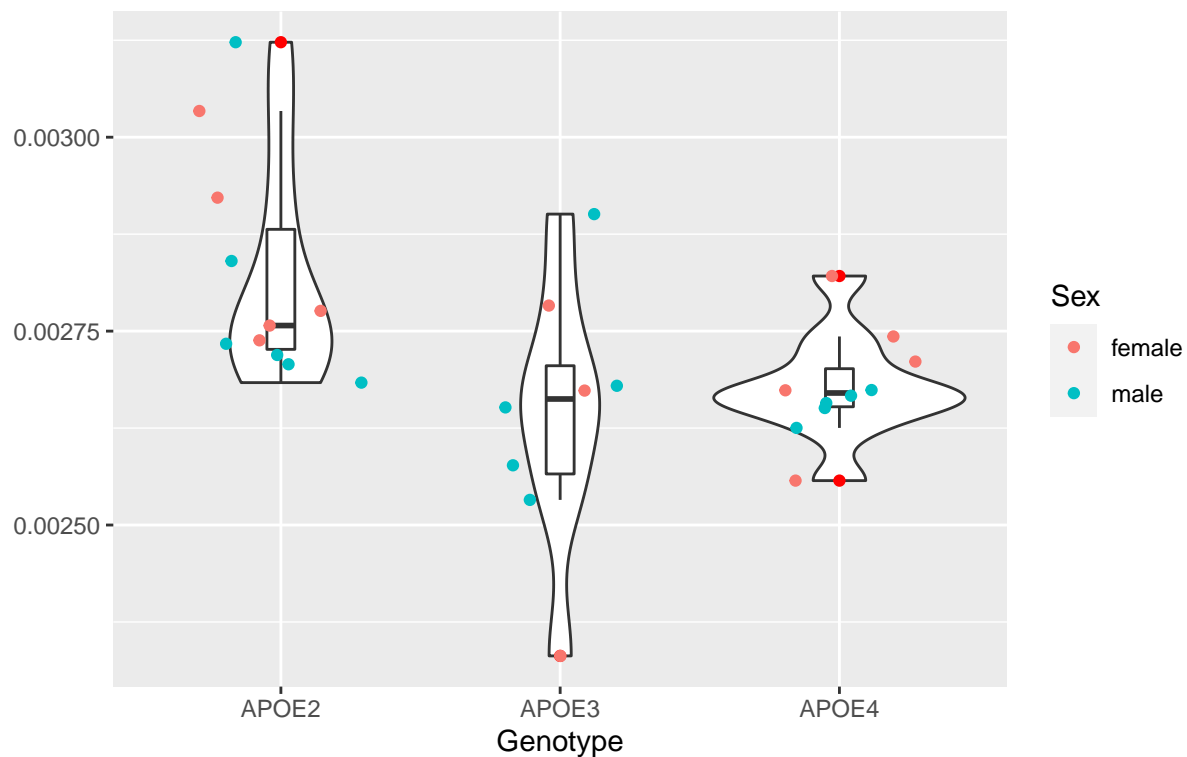
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 3.199e-07 1.600e-07   3.694 0.0387 *
## Residuals    26 1.126e-06 4.331e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Bed Nucleus of the Stria Terminalis

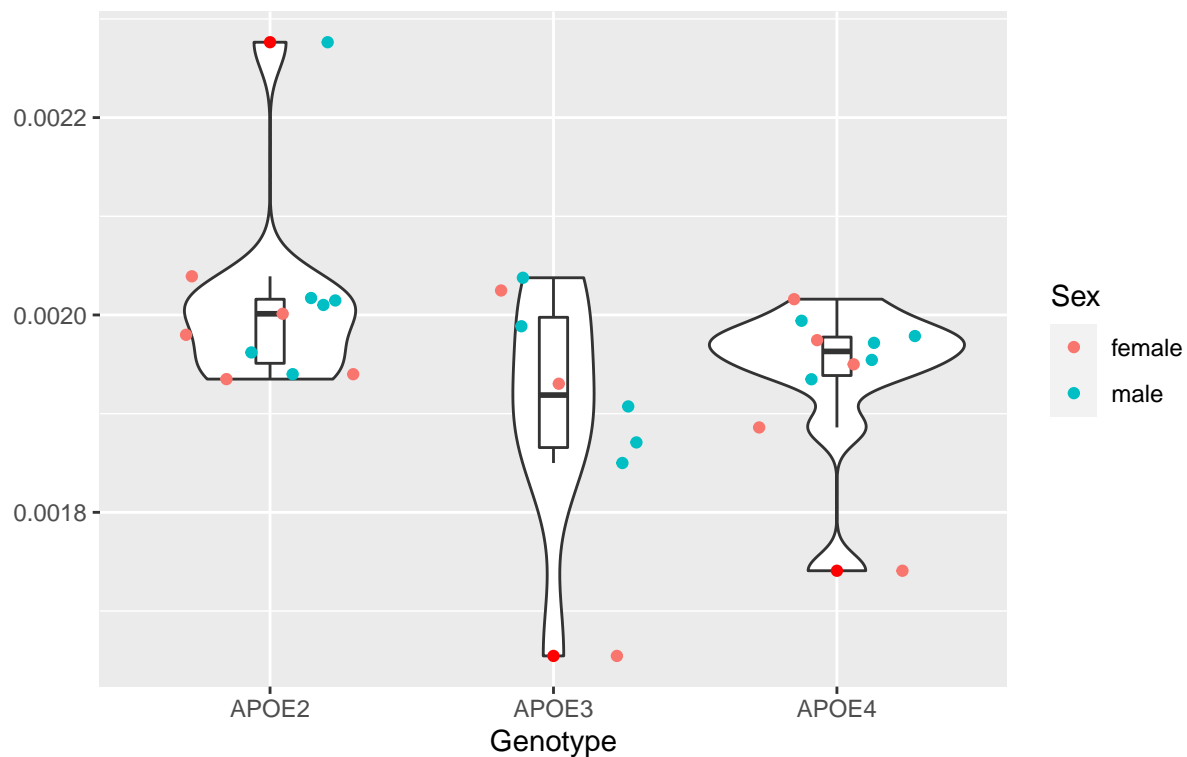
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.801e-07 9.003e-08   5.132 0.0132 *
## Residuals    26 4.561e-07 1.754e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Acumbens

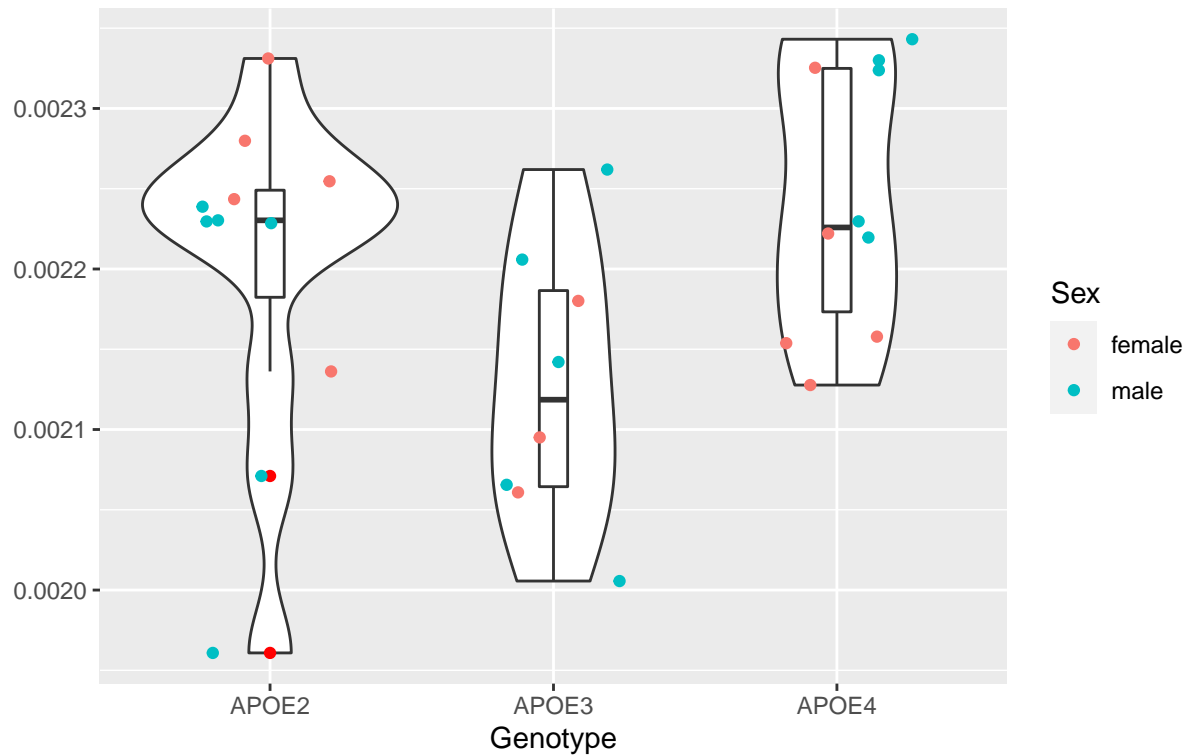
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 5.354e-08 2.677e-08   2.758  0.082 .
## Residuals    26 2.524e-07 9.707e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Amygdala

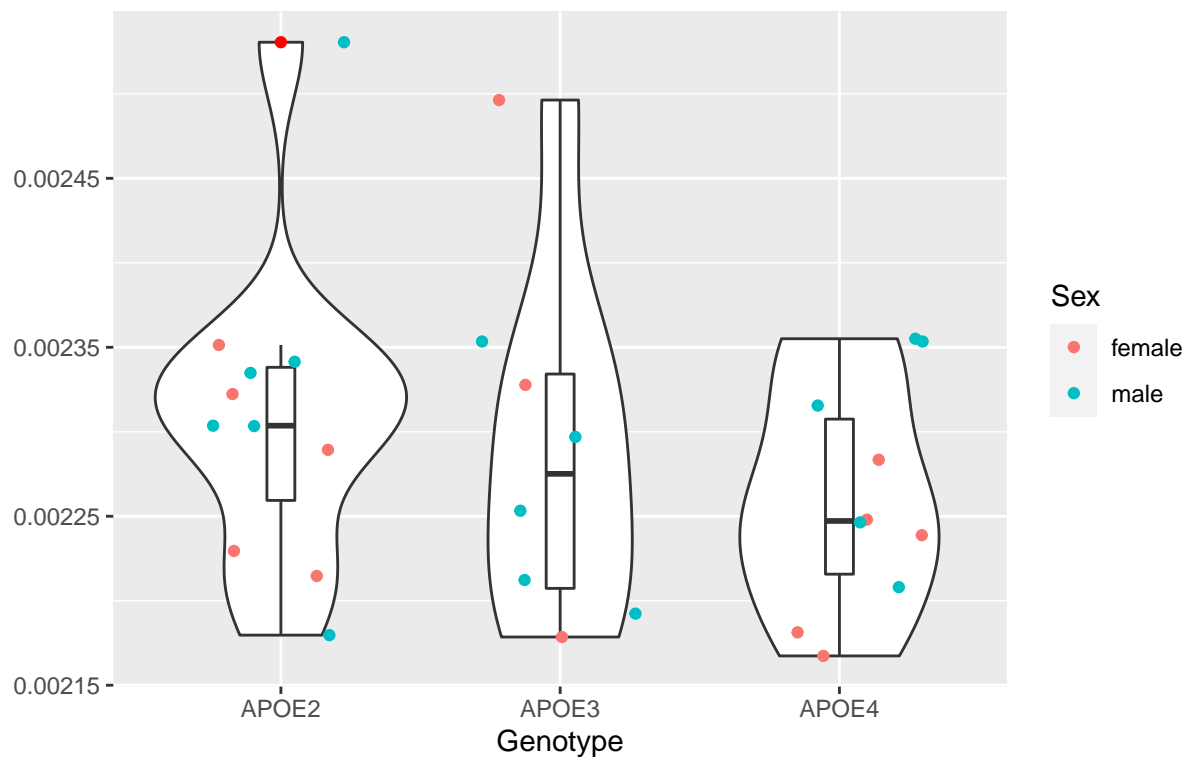
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno       2 6.050e-08 3.025e-08   3.536 0.0438 *
## Residuals 26 2.224e-07 8.554e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Striatum

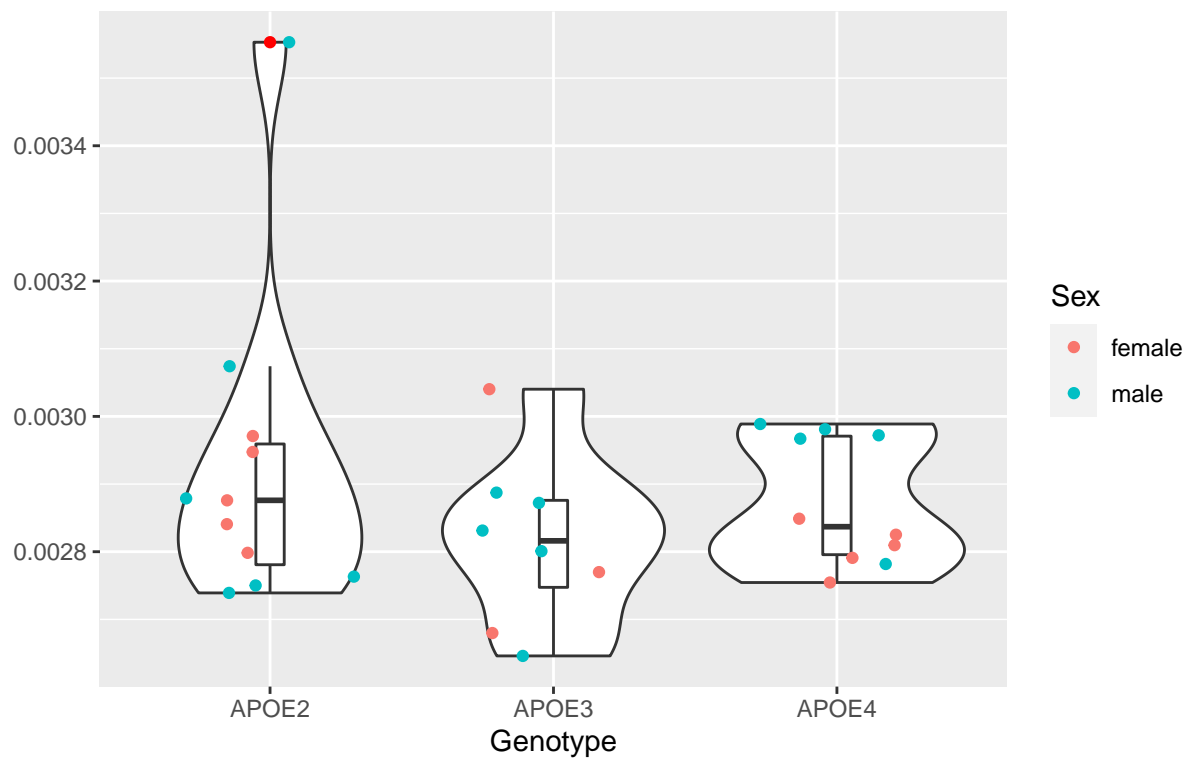
Red points denoting outliers



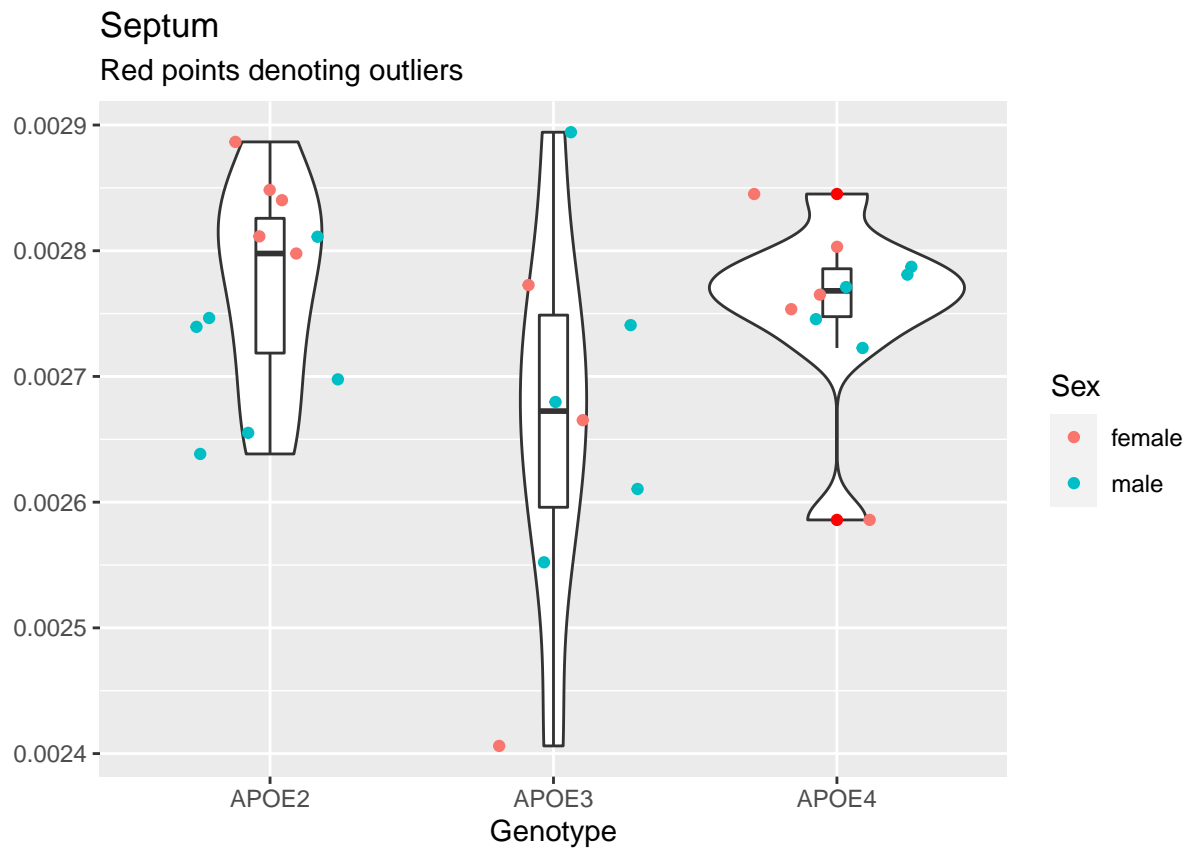
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.285e-08	6.425e-09	0.826	0.449
## Residuals	26	2.023e-07	7.779e-09		

Globus Pallidus

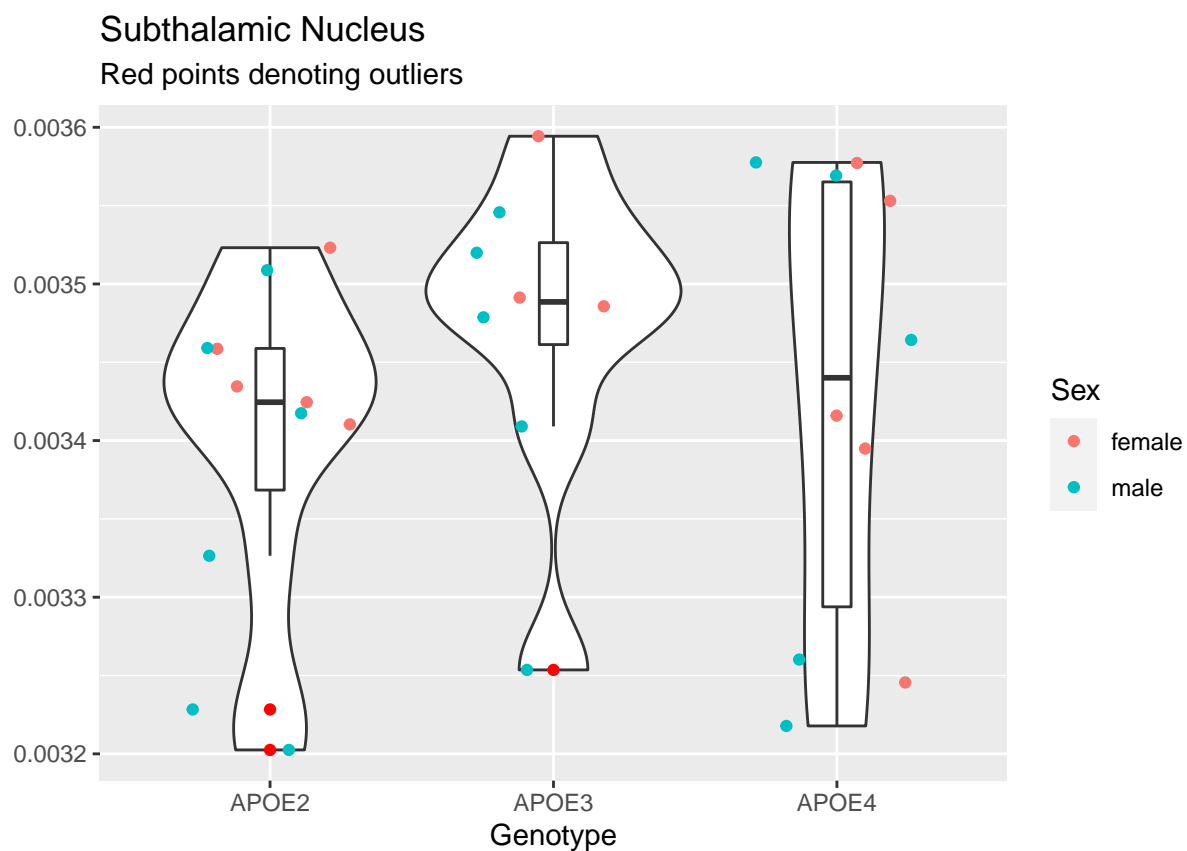
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	5.710e-08	2.853e-08	1.021	0.374
## Residuals	26	7.264e-07	2.794e-08		

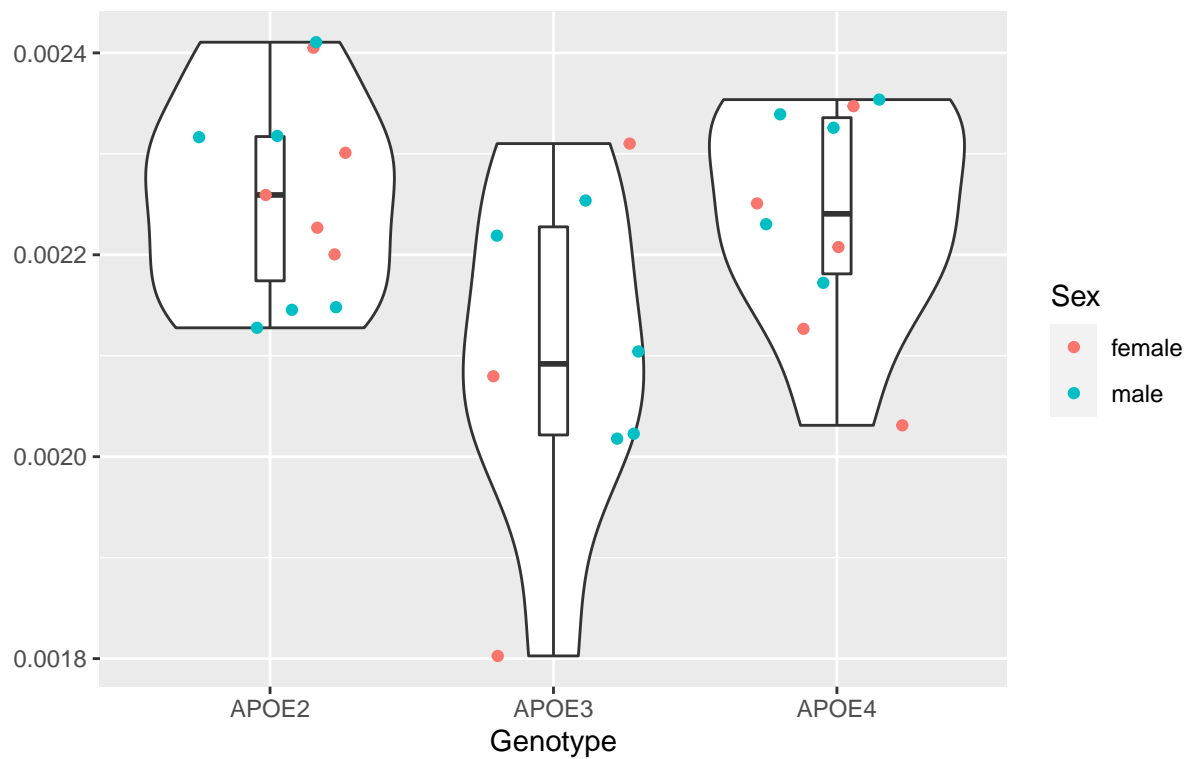


```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 5.702e-08 2.851e-08   2.838 0.0768 .
## Residuals    26 2.612e-07 1.004e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Preoptic Telencephalon

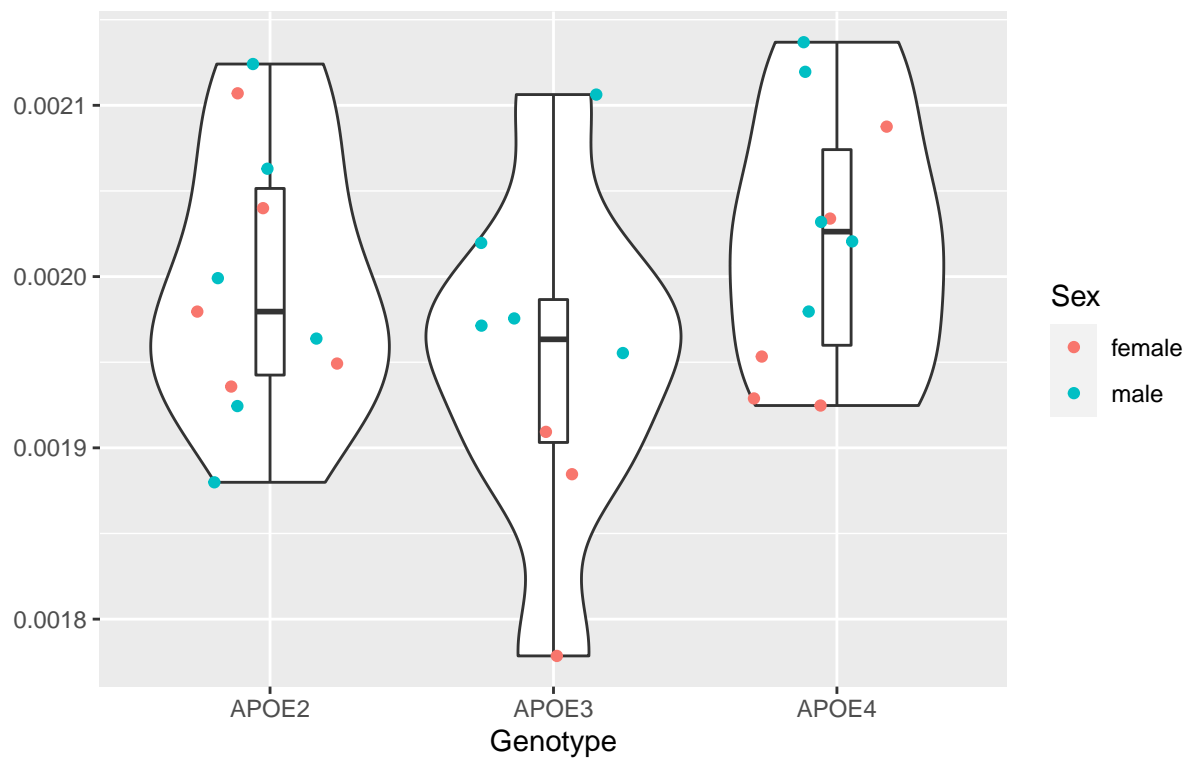
Red points denoting outliers



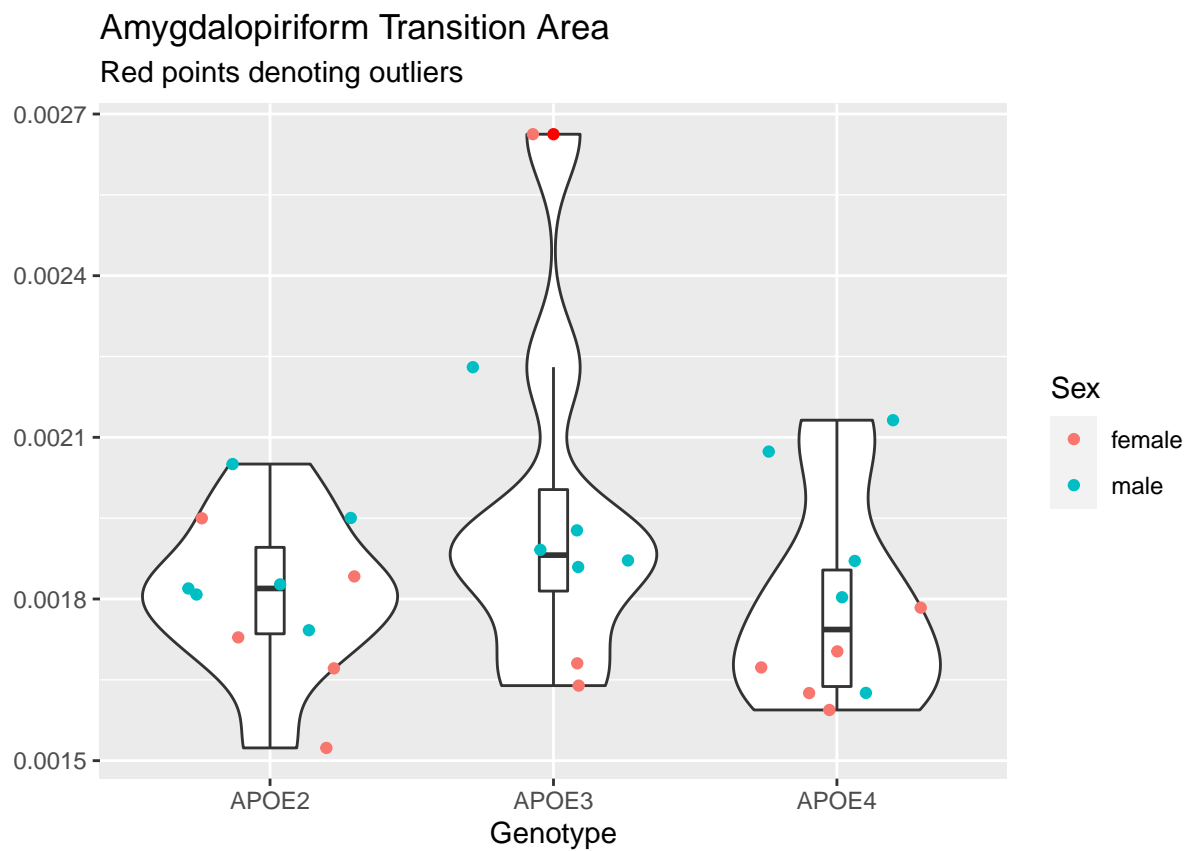
```
##           Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.300e-07 6.502e-08   4.365 0.0232 *
## Residuals    26 3.872e-07 1.489e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hypothalamus

Red points denoting outliers



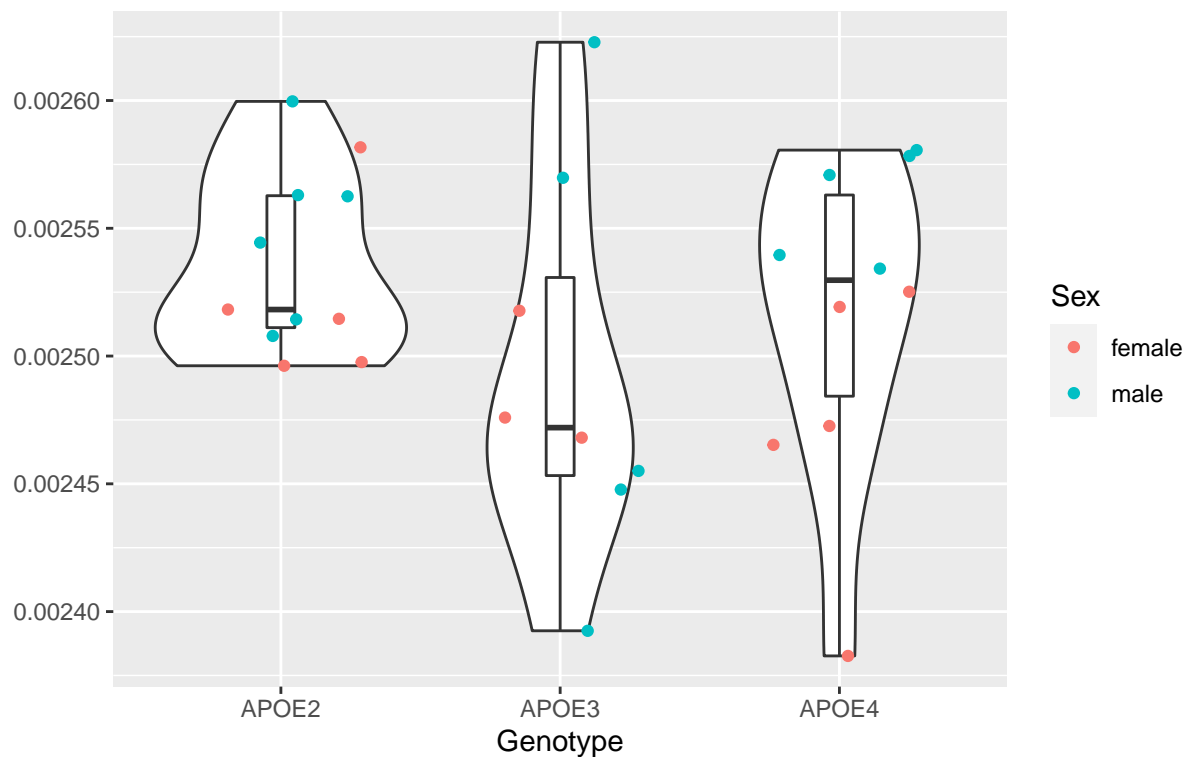
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.312e-08	1.156e-08	1.683	0.205
## Residuals	26	1.785e-07	6.867e-09		



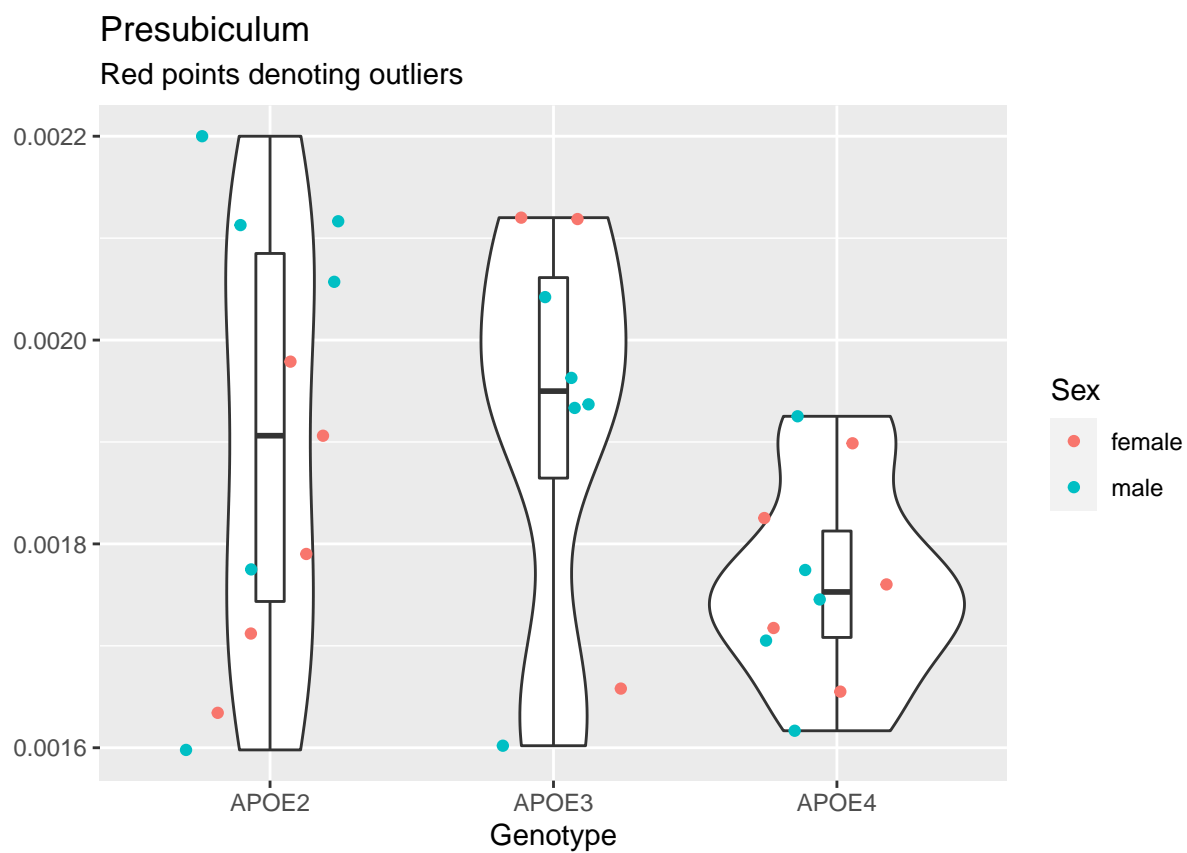
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 1.707e-07 8.535e-08   1.708  0.201
## Residuals 26 1.299e-06 4.996e-08
```

Periform Cortex

Red points denoting outliers

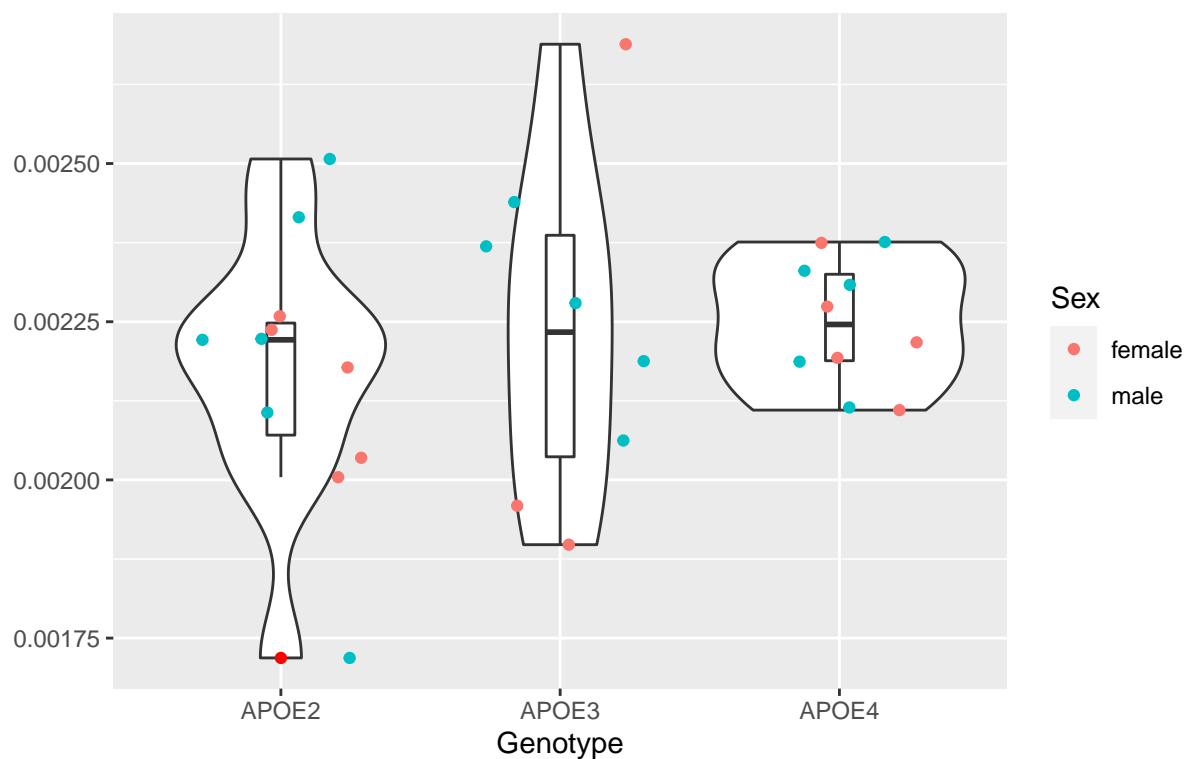


##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.450e-09	4.226e-09	1.295	0.291
## Residuals	26	8.487e-08	3.264e-09		

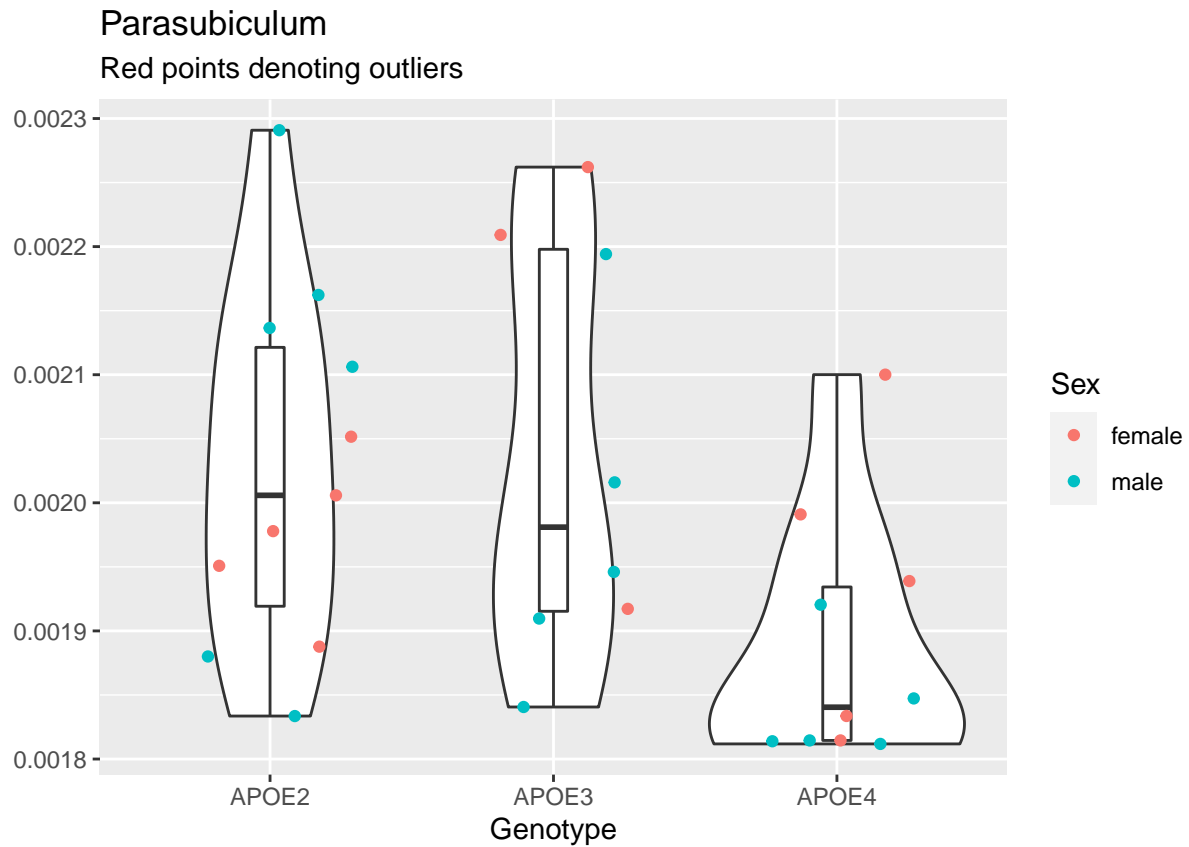


```
##          Df      Sum Sq   Mean Sq F value Pr(>F)
## geno       2 1.418e-07 7.090e-08    2.327  0.118
## Residuals 26 7.921e-07 3.046e-08
```

Perirhinal Cortex Red points denoting outliers



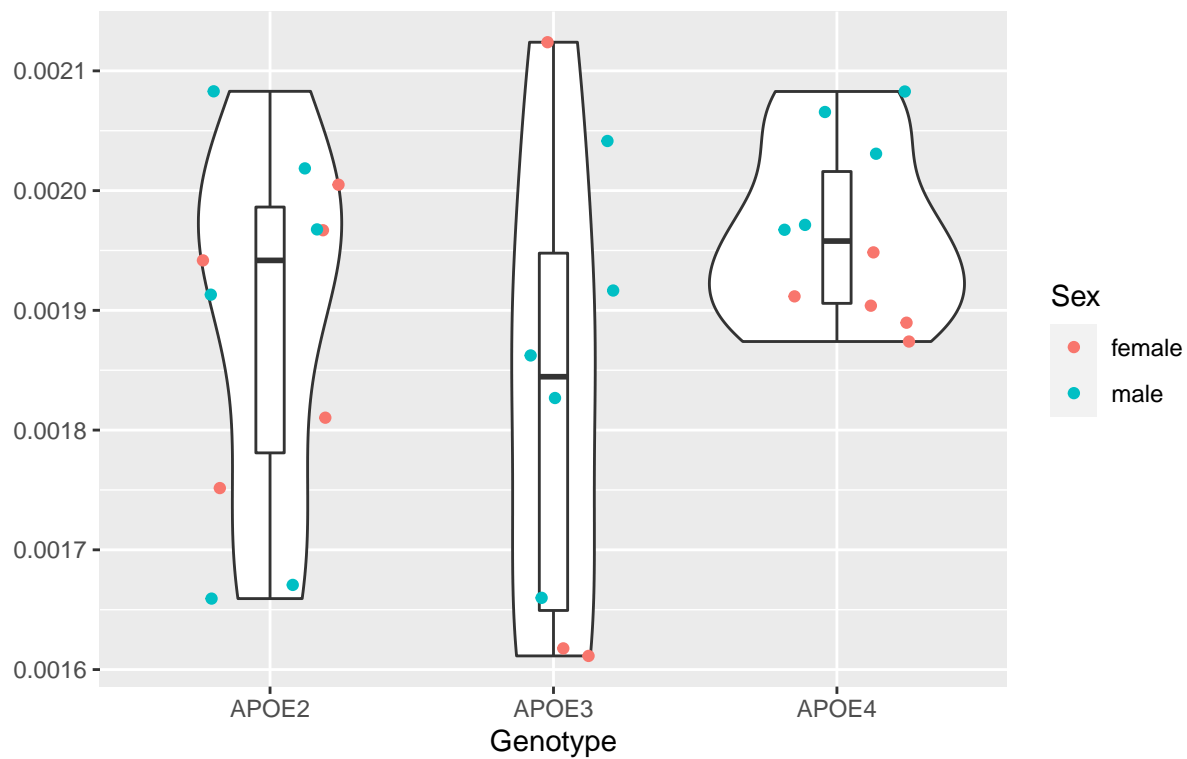
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.380e-08	1.689e-08	0.43	0.655
## Residuals	26	1.022e-06	3.932e-08		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.324e-07 6.618e-08   3.72  0.038 *
## Residuals    26 4.626e-07 1.779e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Ectorhinal Cortex

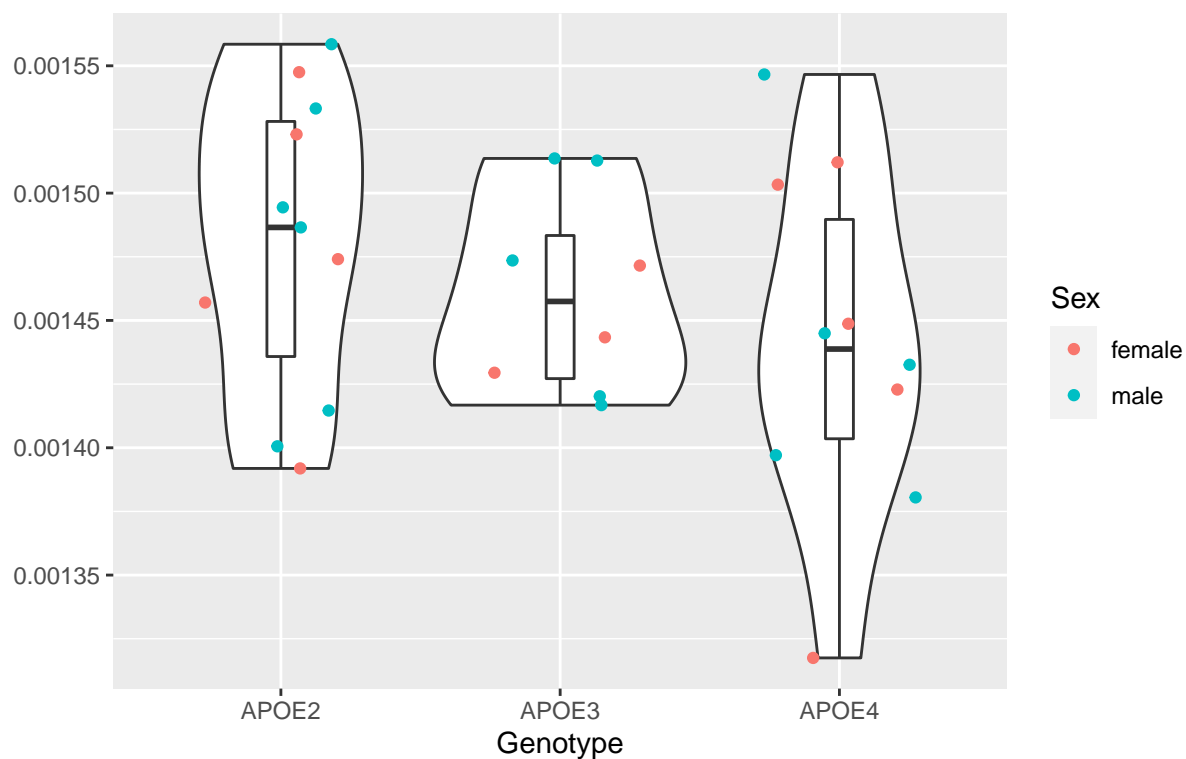
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.930e-08	3.963e-08	1.983	0.158
## Residuals	26	5.195e-07	1.998e-08		

Dorsal Tenia Tecta

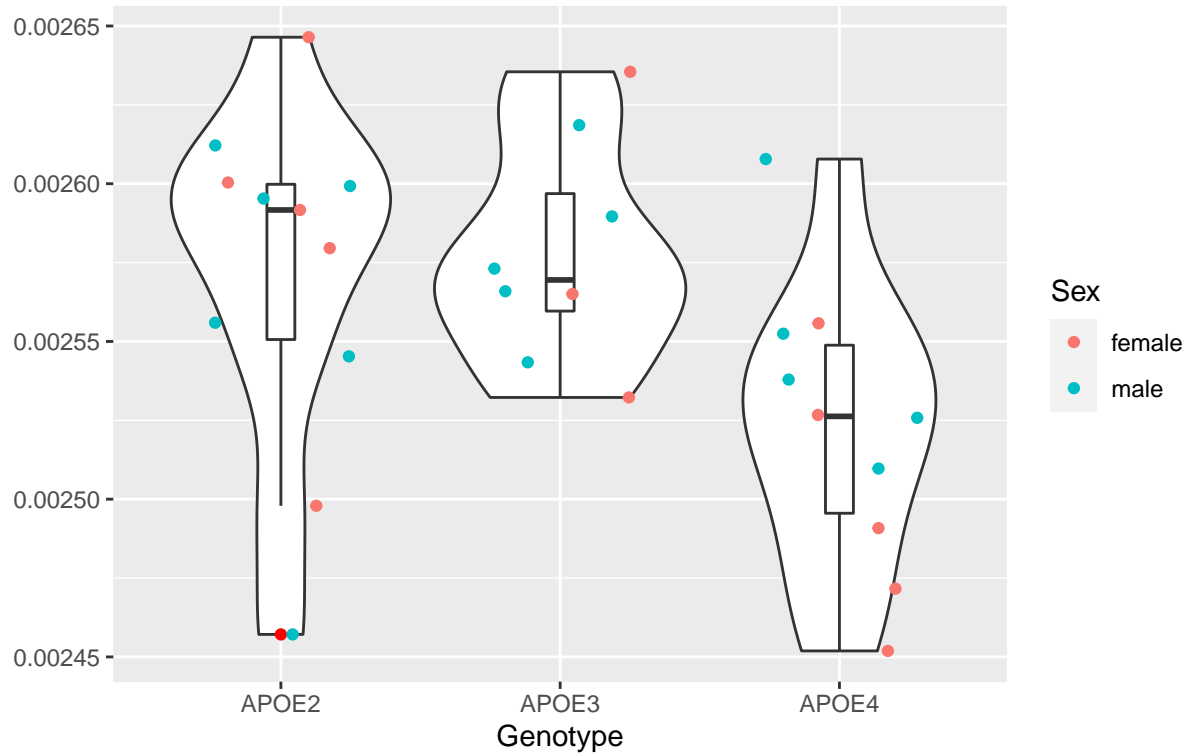
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.180e-09	4.092e-09	1.228	0.309
## Residuals	26	8.661e-08	3.331e-09		

Hippocampus

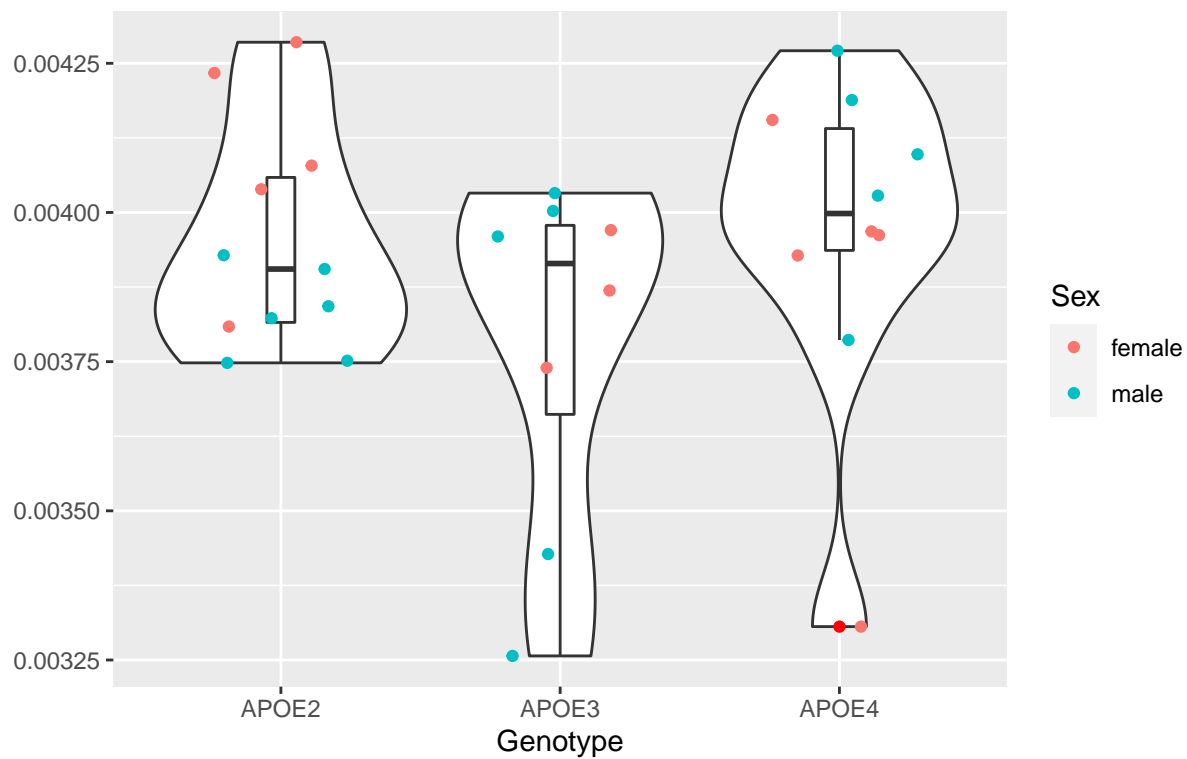
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.717e-08 8.586e-09   3.963 0.0315 *
## Residuals    26 5.633e-08 2.167e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Ventral Claustrum

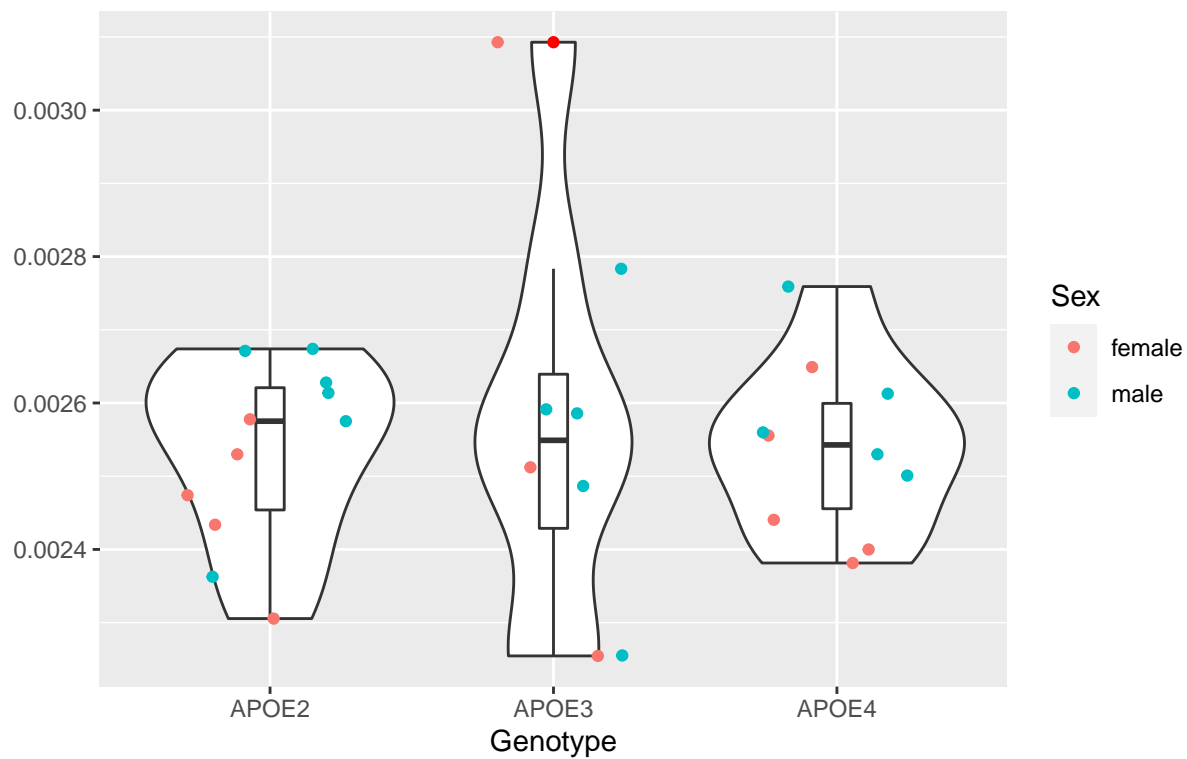
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.825e-07	9.124e-08	1.477	0.247
## Residuals	26	1.606e-06	6.176e-08		

Posterolateral Cortical Amygdaloid Area

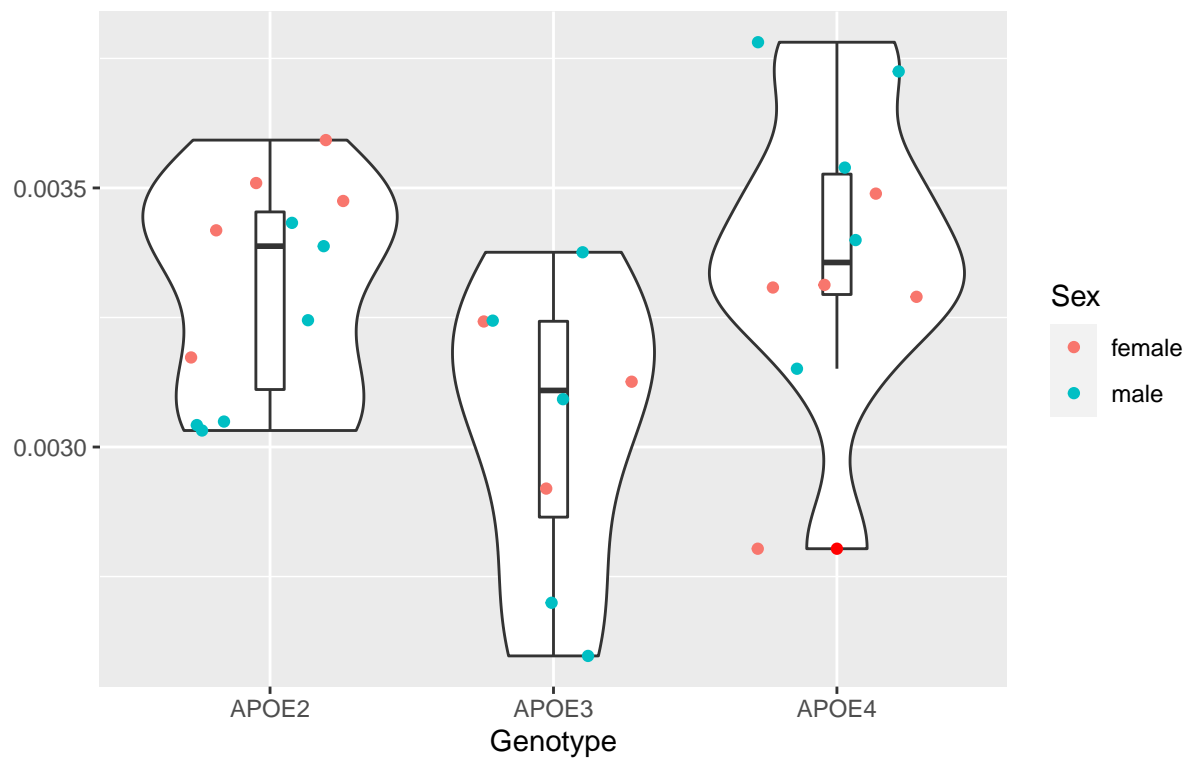
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 7.500e-09 3.744e-09   0.121  0.886
## Residuals 26 8.029e-07 3.088e-08
```

Dorsal Claustrum

Red points denoting outliers



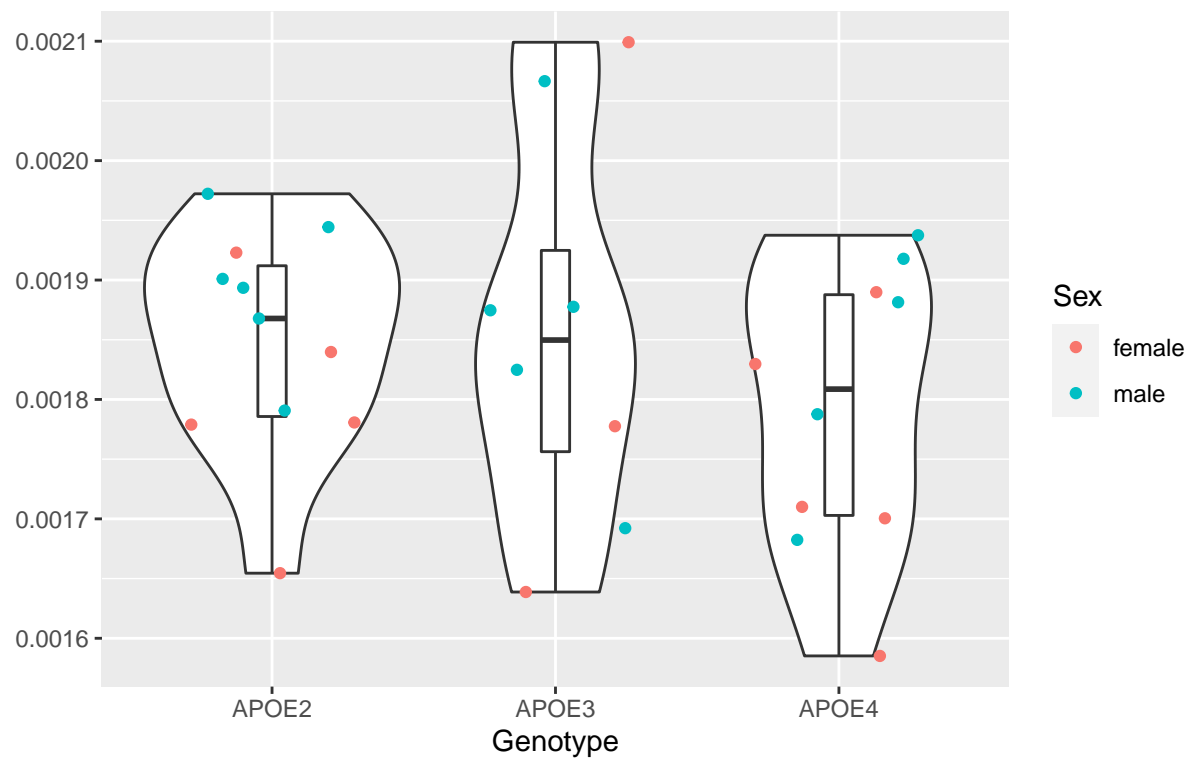
```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## geno         2 5.636e-07 2.818e-07   4.383 0.0229 *
## Residuals    26 1.672e-06 6.429e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.001e-07	5.007e-08	0.738	0.488
## Residuals	26	1.763e-06	6.781e-08		

Ventral Intermediate Entorhinal Cortex

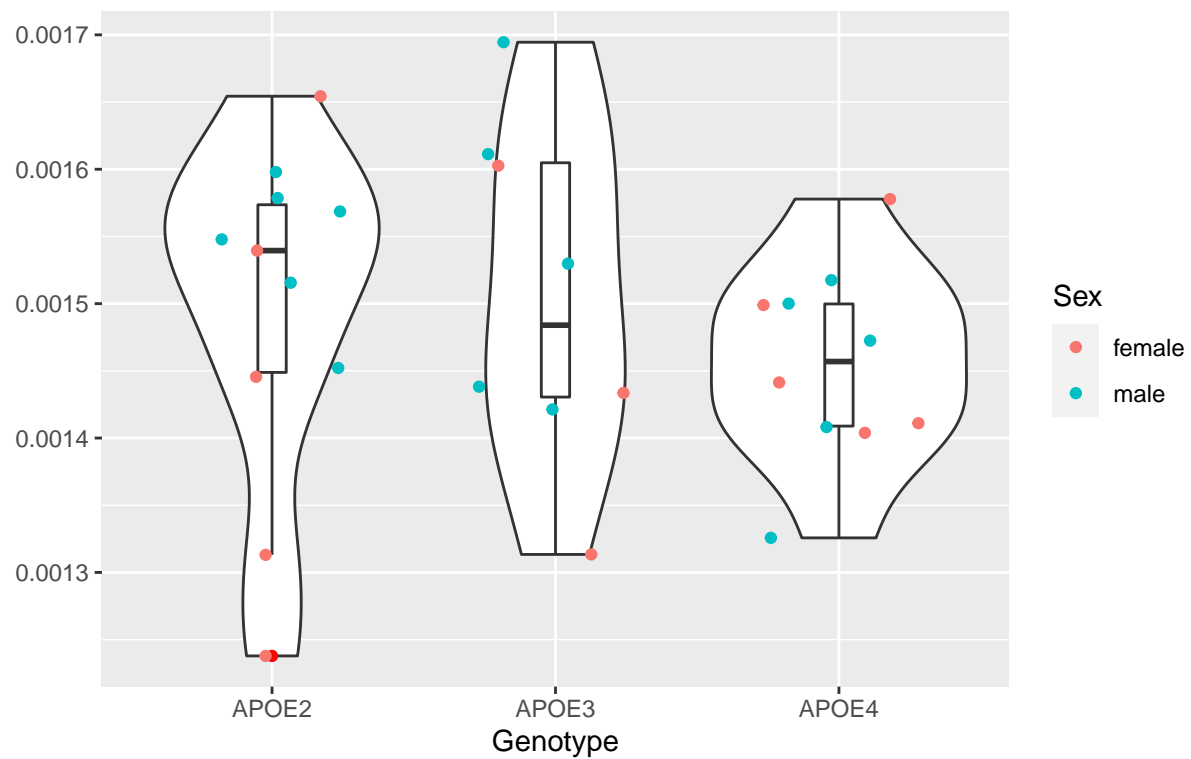
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.400e-08 1.202e-08   0.787  0.466
## Residuals 26 3.969e-07 1.526e-08
```

Left Caudomedial Entorhinal Cortex

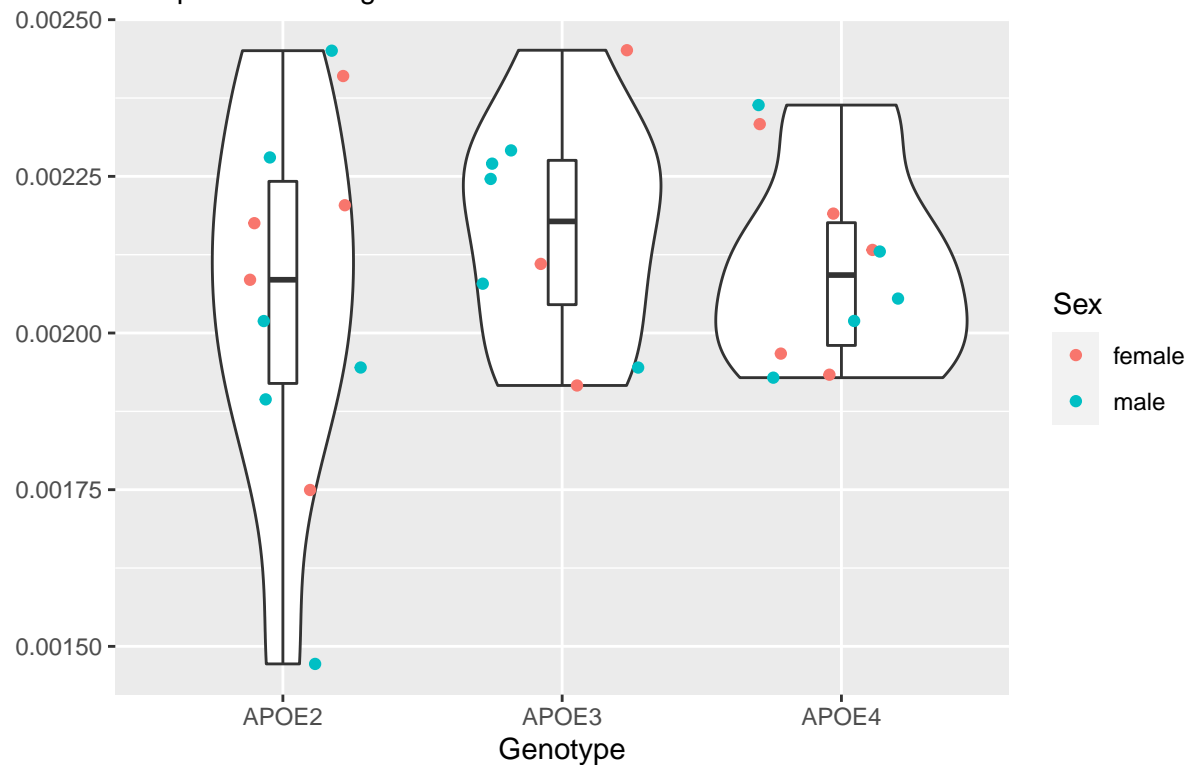
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.319e-08	6.597e-09	0.545	0.586
## Residuals	26	3.145e-07	1.210e-08		

Left Dorsolateral Entorhinal Cortex

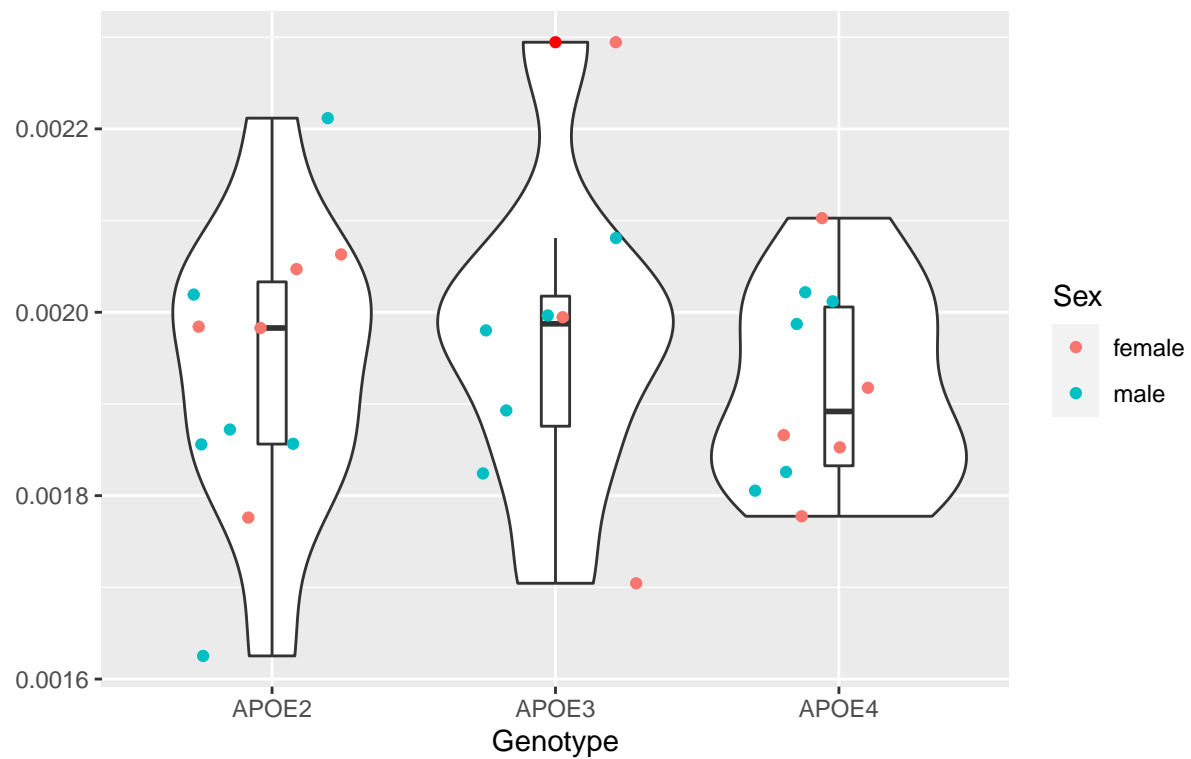
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.760e-08	2.381e-08	0.478	0.626
## Residuals	26	1.296e-06	4.985e-08		

Left Dorsal Intermediate Entorhinal Cortex

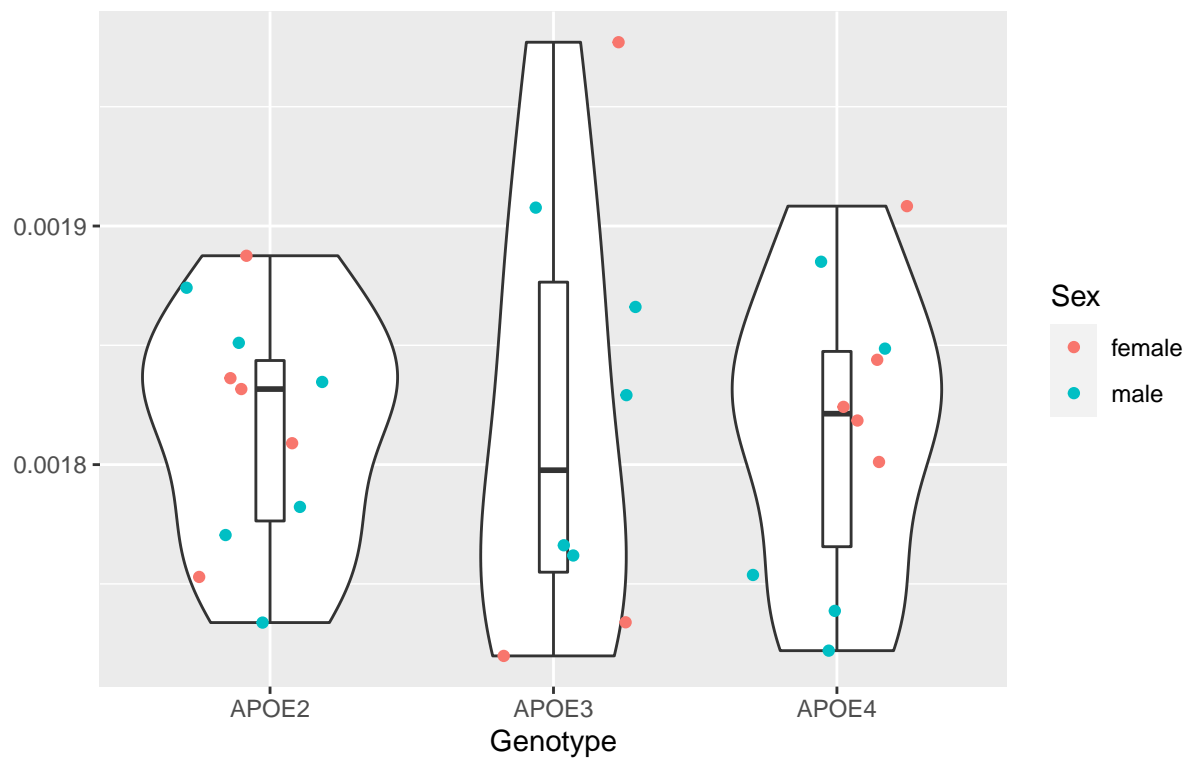
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.320e-08	6.611e-09	0.297	0.745
## Residuals	26	5.779e-07	2.223e-08		

Left Caudomedial Entorhinal Cortex

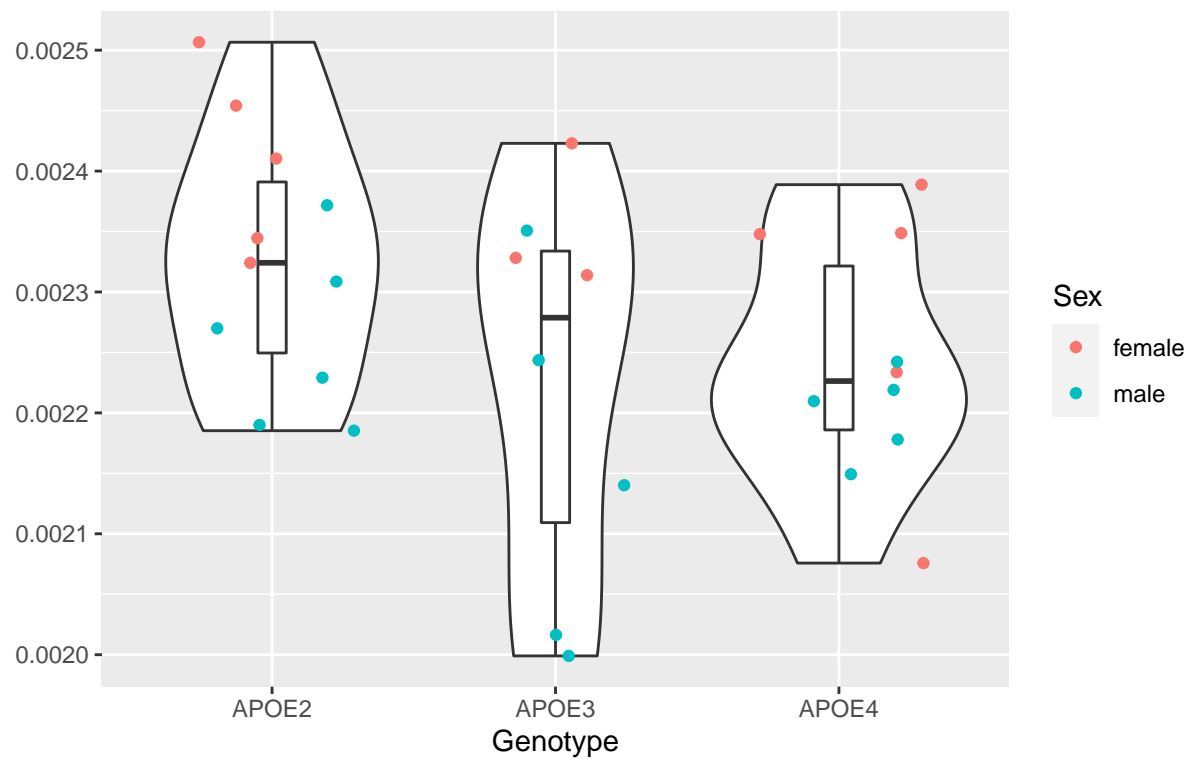
Red points denoting outliers



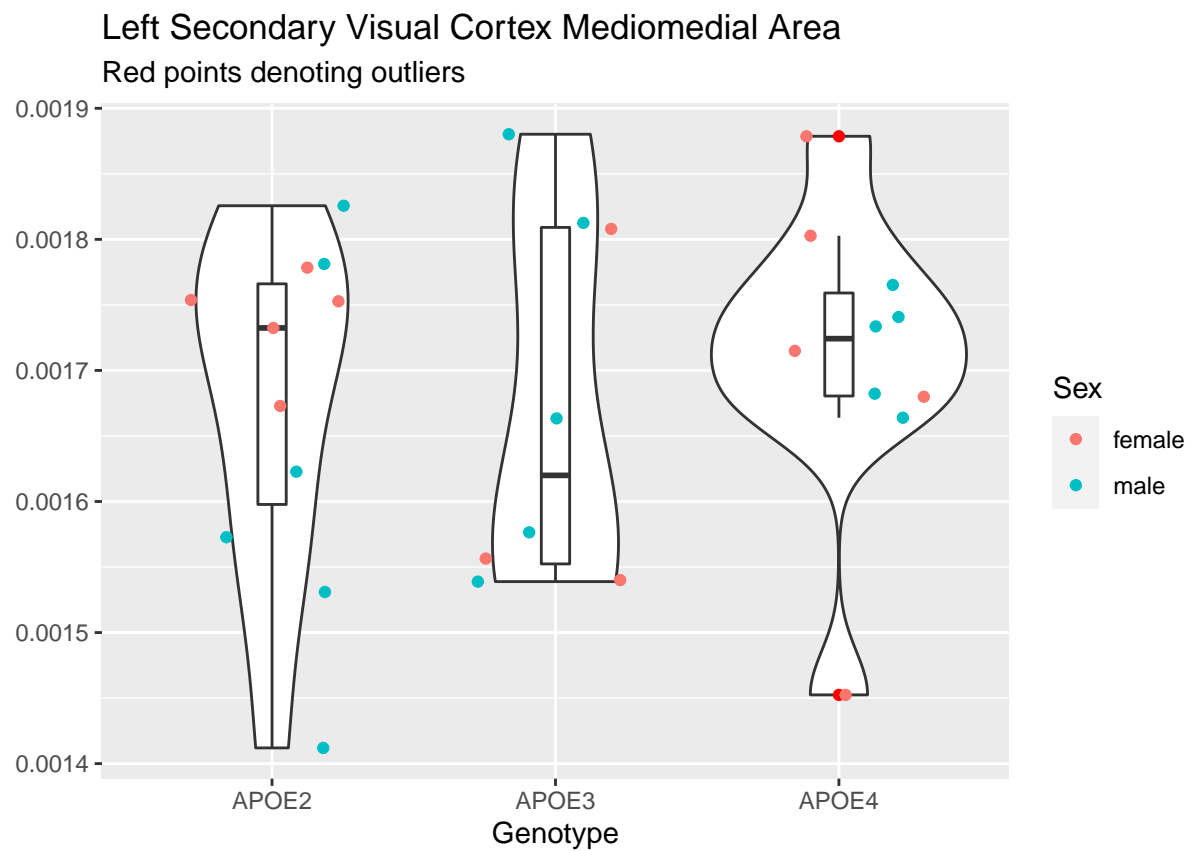
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.800e-10	9.000e-11	0.02	0.98
## Residuals	26	1.171e-07	4.503e-09		

Left Ventral Orbital Cortex

Red points denoting outliers

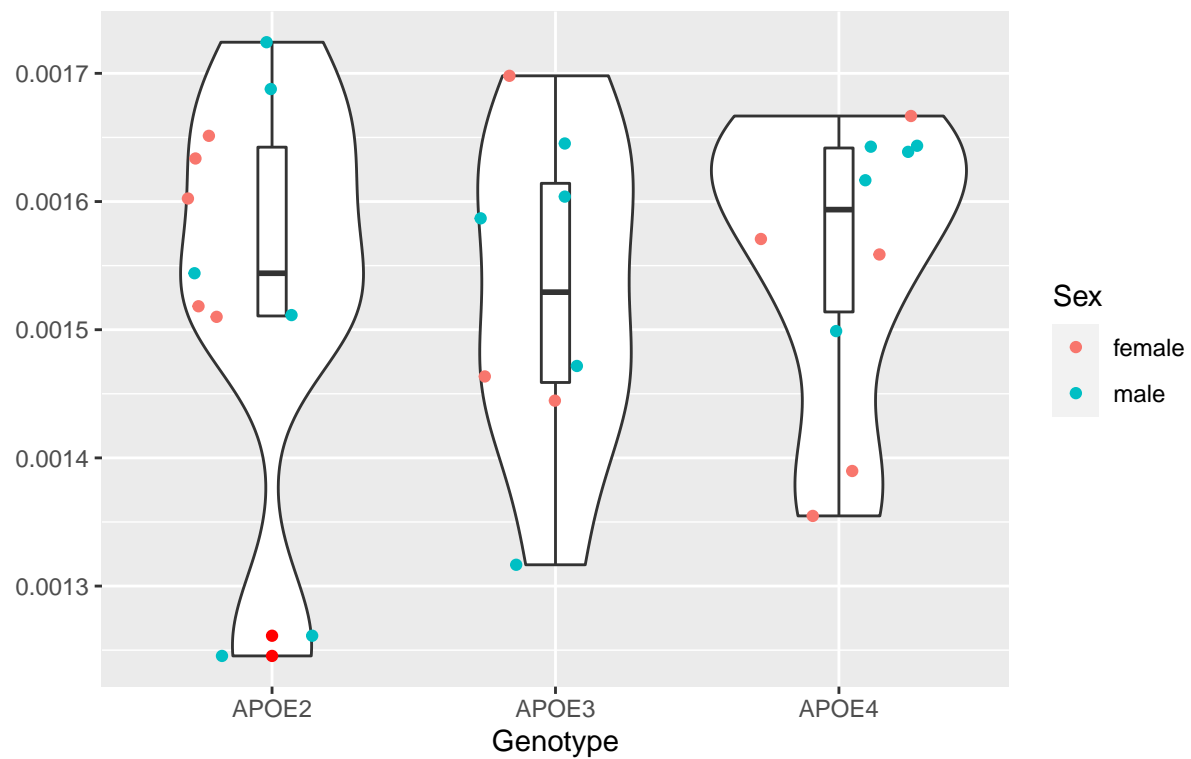


##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	5.970e-08	2.987e-08	2.091	0.144
## Residuals	26	3.714e-07	1.428e-08		



Left Secondary Visual Cortex Mediolateral Area

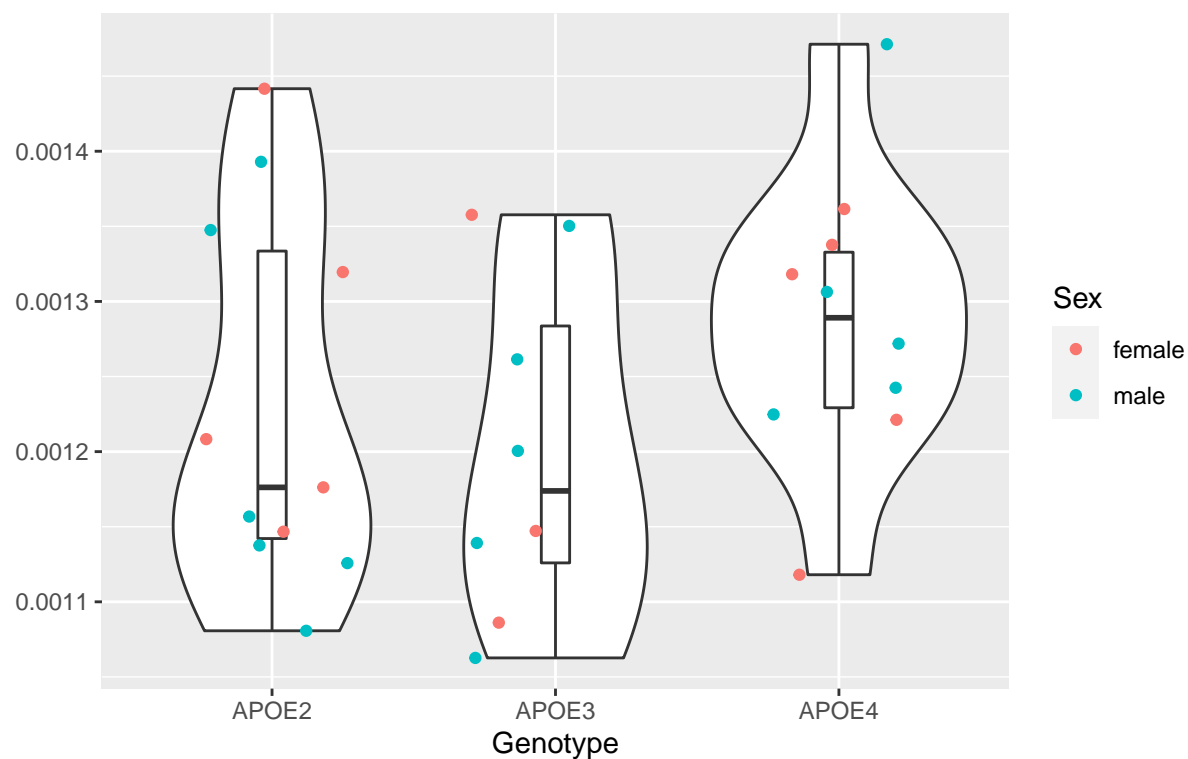
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.500e-09	2.227e-09	0.124	0.884
## Residuals	26	4.676e-07	1.798e-08		

Left Secondary Visual Cortex Lateral Area

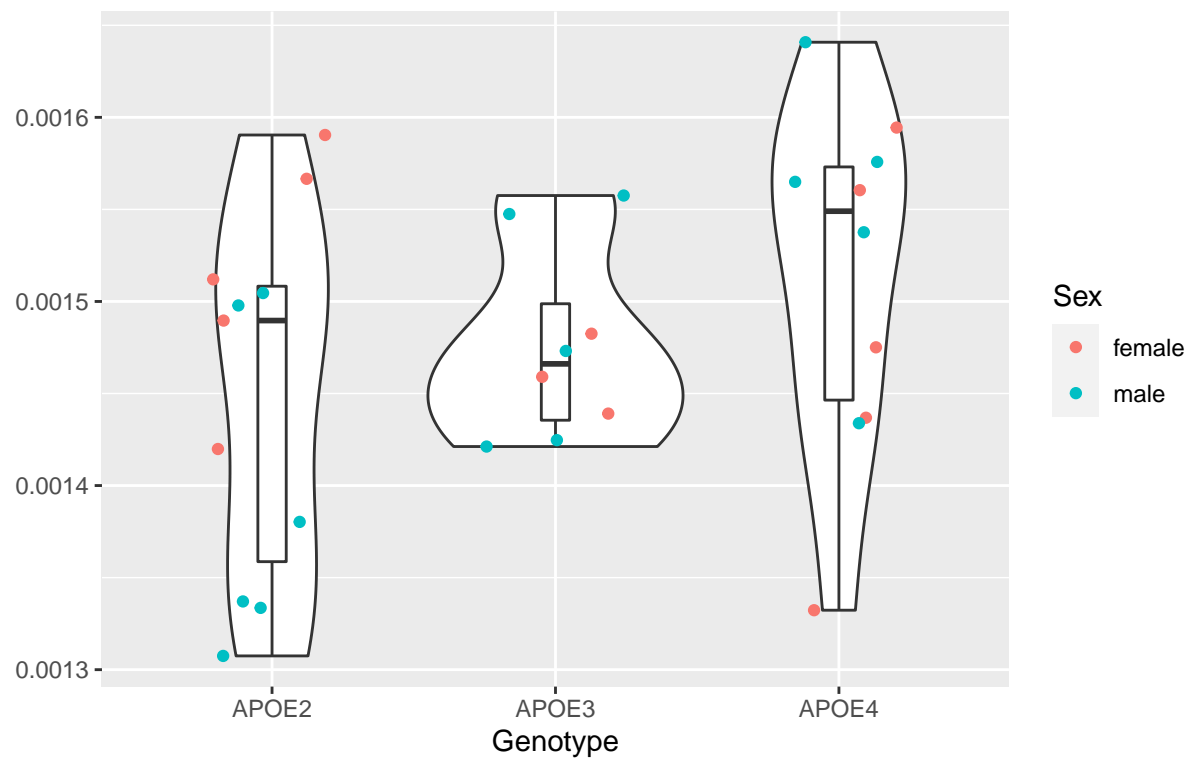
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.570e-08	1.787e-08	1.441	0.255
## Residuals	26	3.224e-07	1.240e-08		

Left Primary Visual Cortex Monocular Area

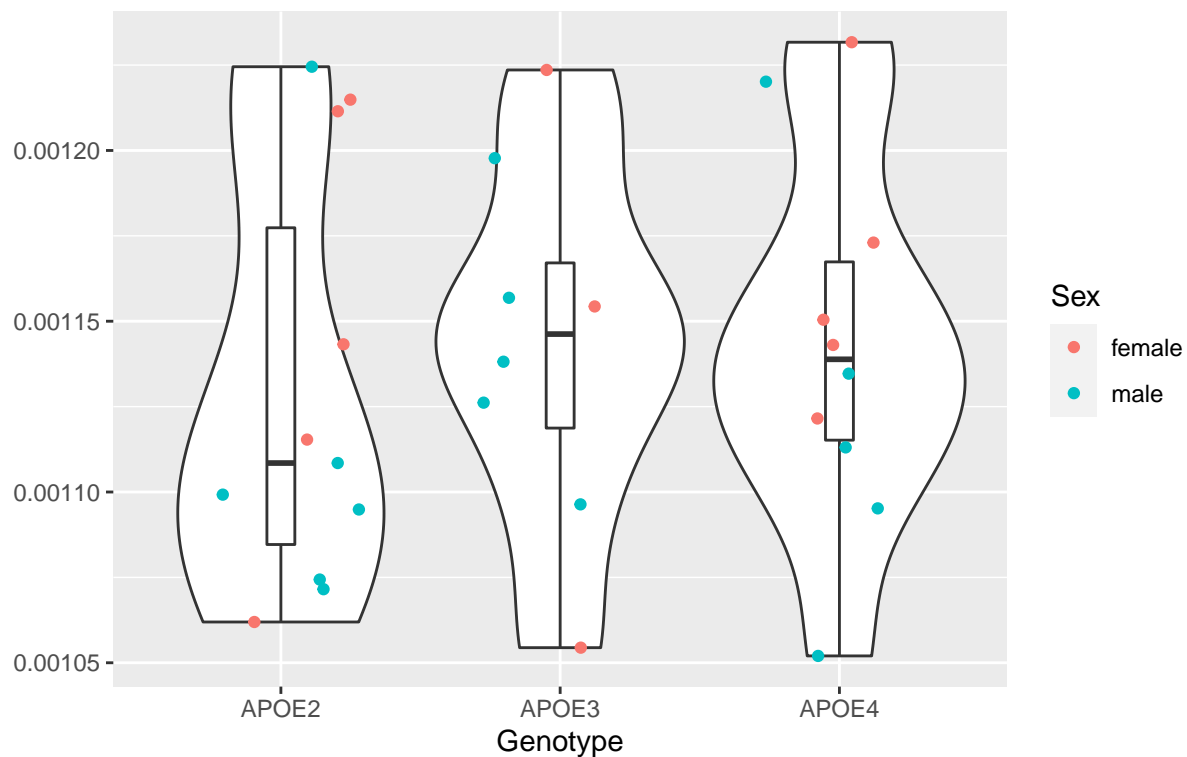
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.309e-08	1.155e-08	1.547	0.232
## Residuals	26	1.940e-07	7.463e-09		

Left Primary Visual Cortex Binocular Area

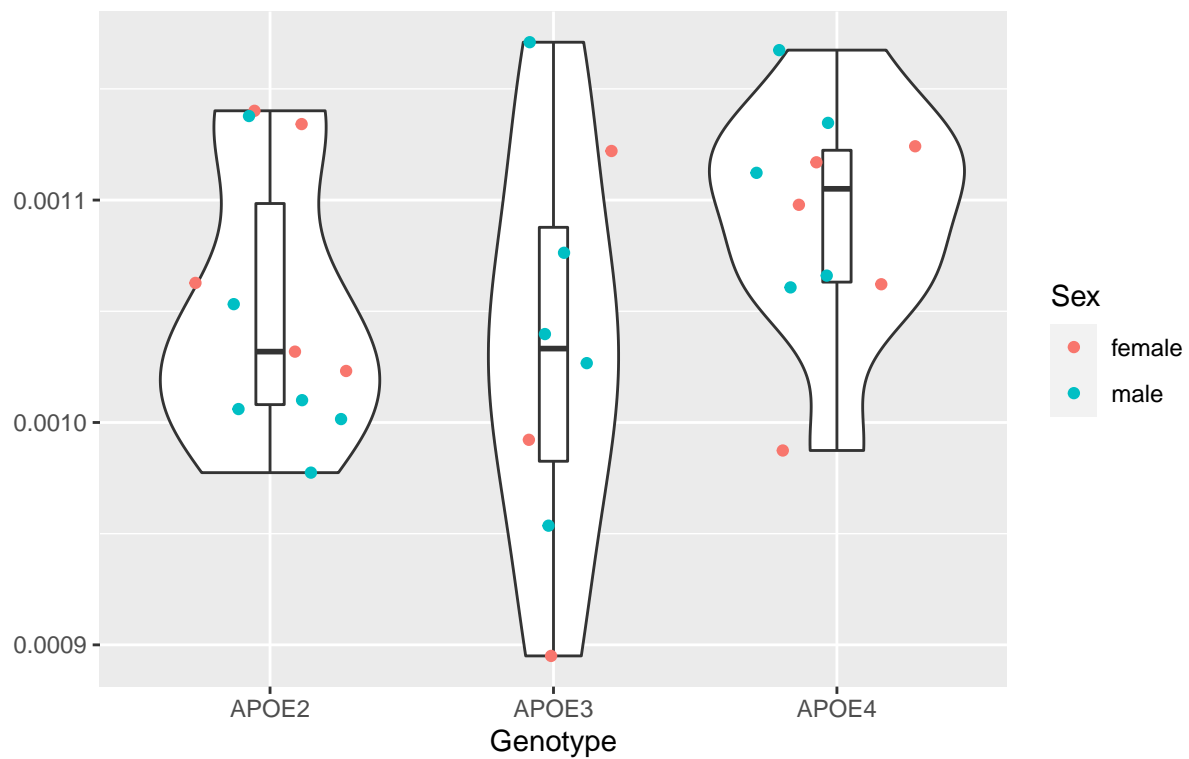
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.410e-09	7.070e-10	0.219	0.805
## Residuals	26	8.384e-08	3.225e-09		

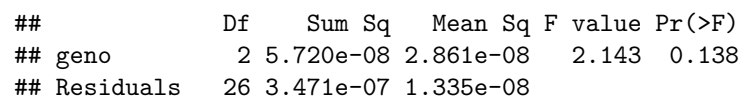
Left Primary Visual Cortex

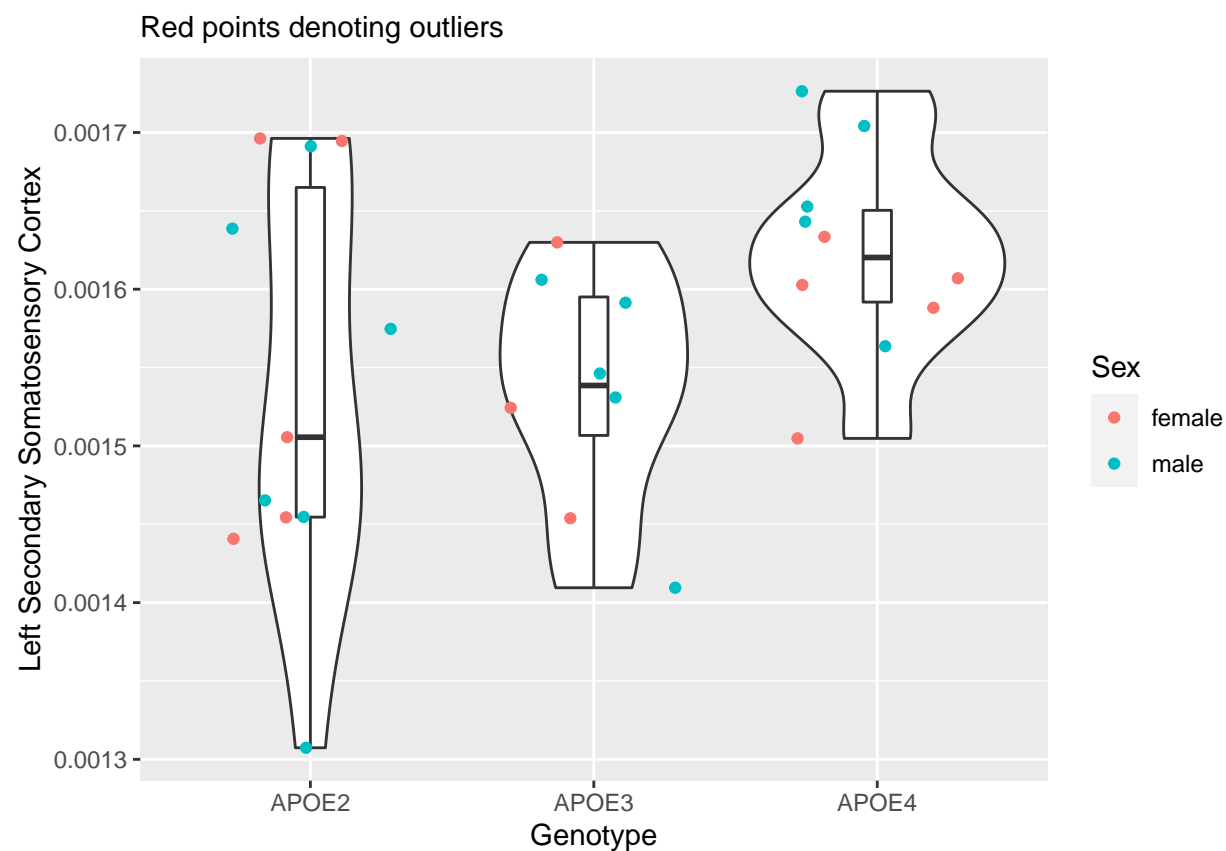
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.659e-08	8.293e-09	1.888	0.172
## Residuals	26	1.142e-07	4.393e-09		

Red points denoting outliers

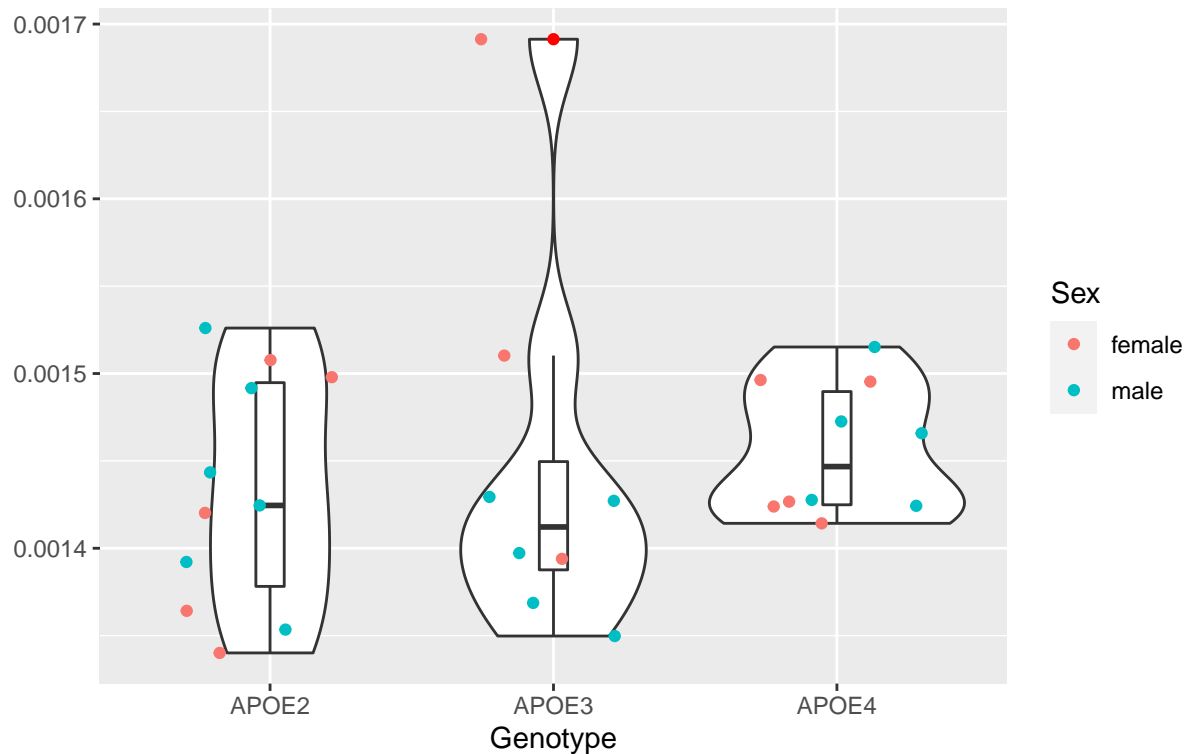




##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.730e-08	2.365e-08	2.507	0.101
## Residuals	26	2.453e-07	9.434e-09		

Left Primary Somatosensory Cortex Upper Lip Region

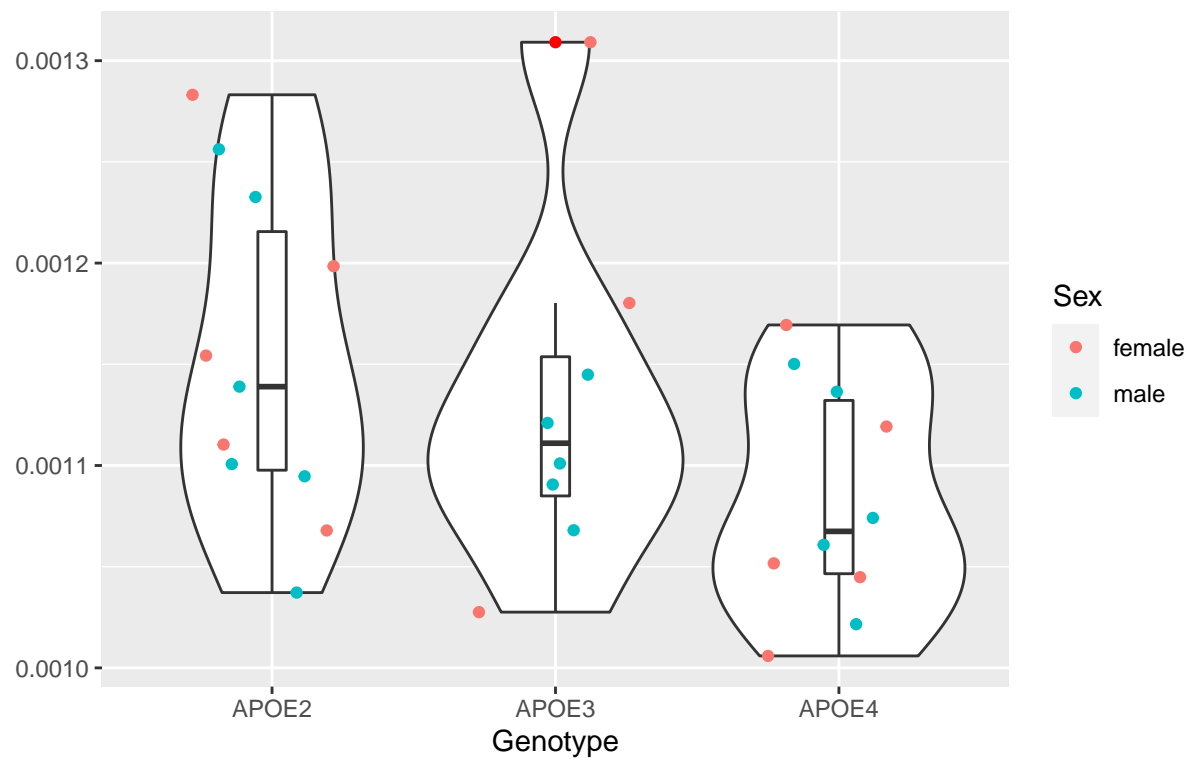
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.880e-09	1.441e-09	0.265	0.769
## Residuals	26	1.414e-07	5.437e-09		

Left Primary Somatosensory Cortex Trunk Region

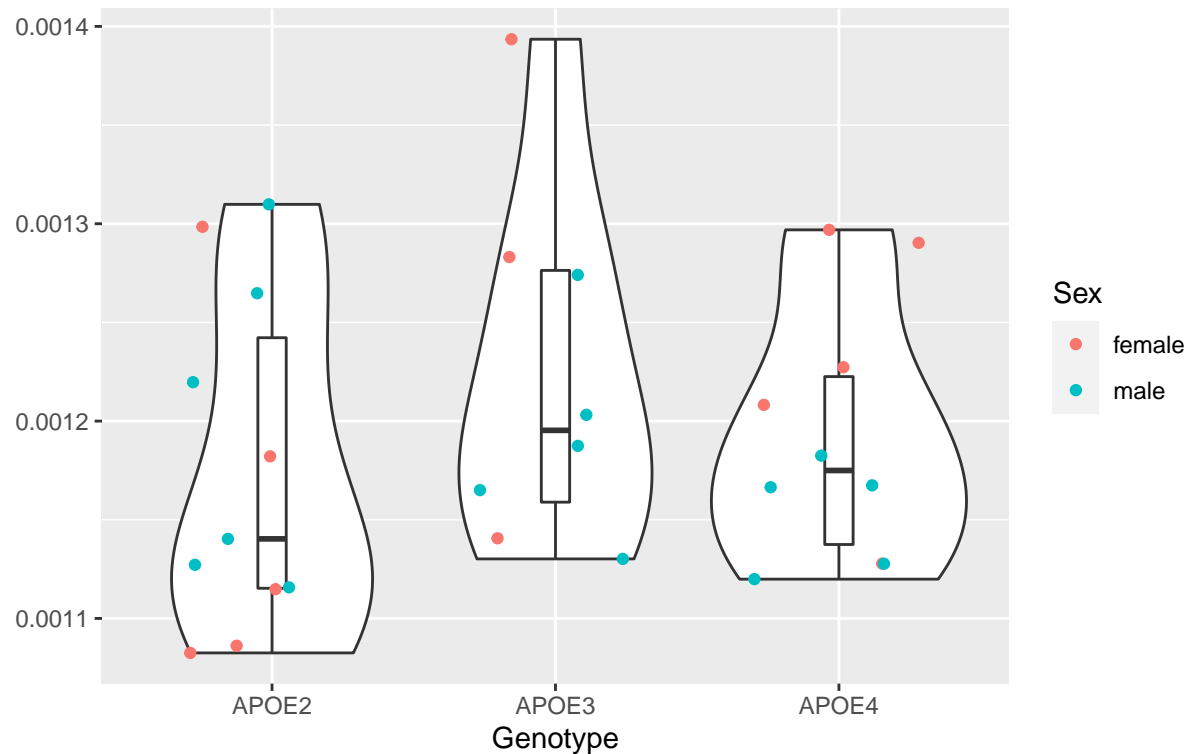
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.549e-08	1.274e-08	2.28	0.122
## Residuals	26	1.453e-07	5.589e-09		

Left Primary Somatosensory Cortex Shoulder Region

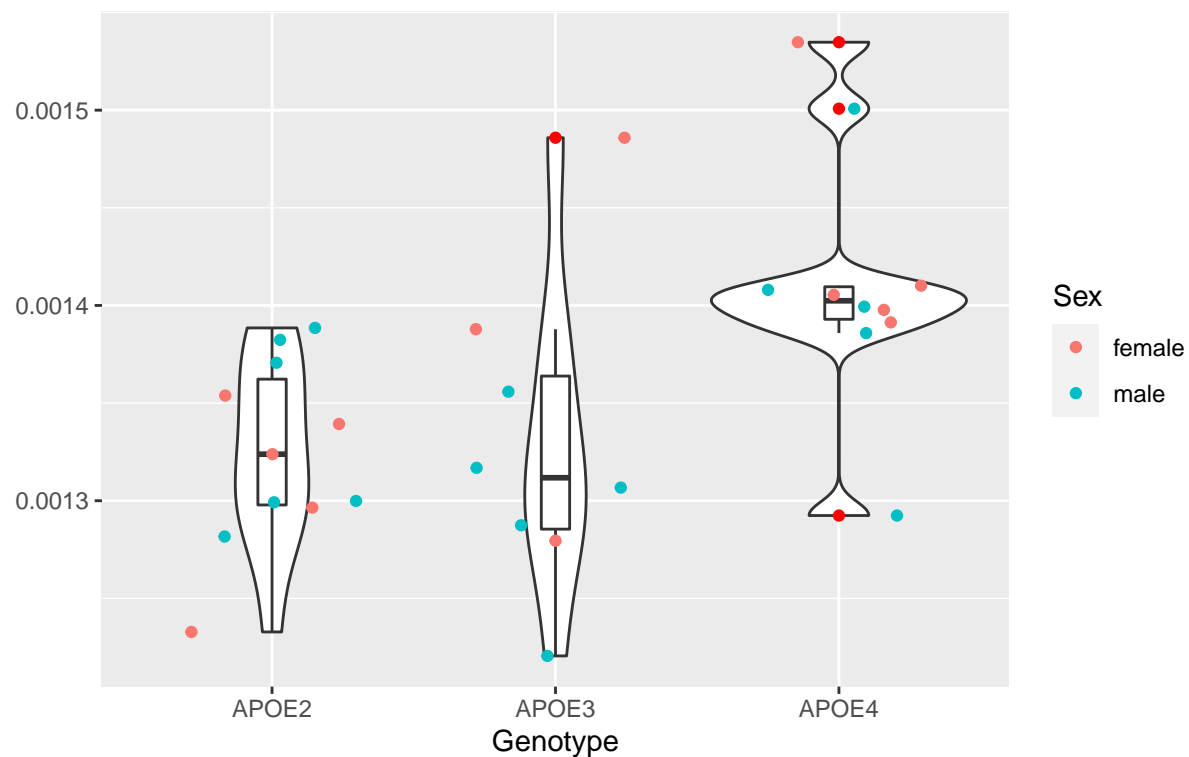
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 9.760e-09 4.882e-09   0.777   0.47
## Residuals 26 1.633e-07 6.279e-09
```

Left Primary Somatosensory Cortex Jaw Region

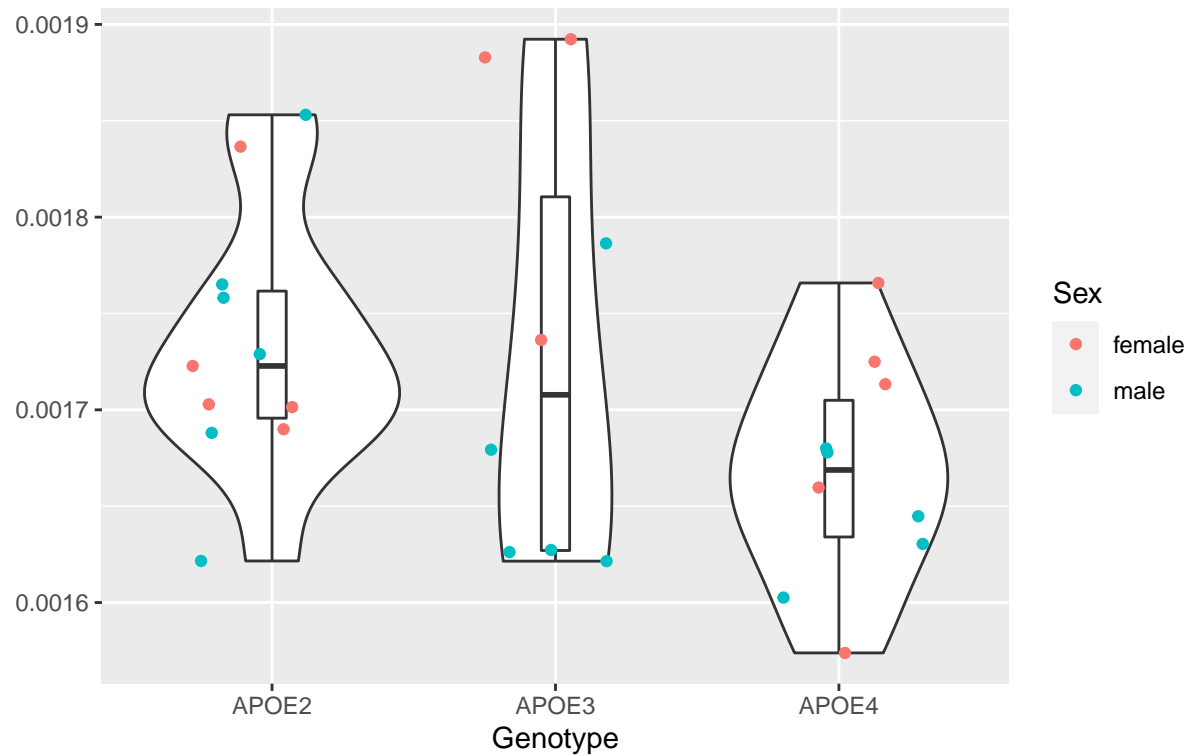
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 4.835e-08 2.418e-08    5.869 0.00788 **
## Residuals    26 1.071e-07 4.119e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Left Primary Somatosensory Cortex Hindlimb Region

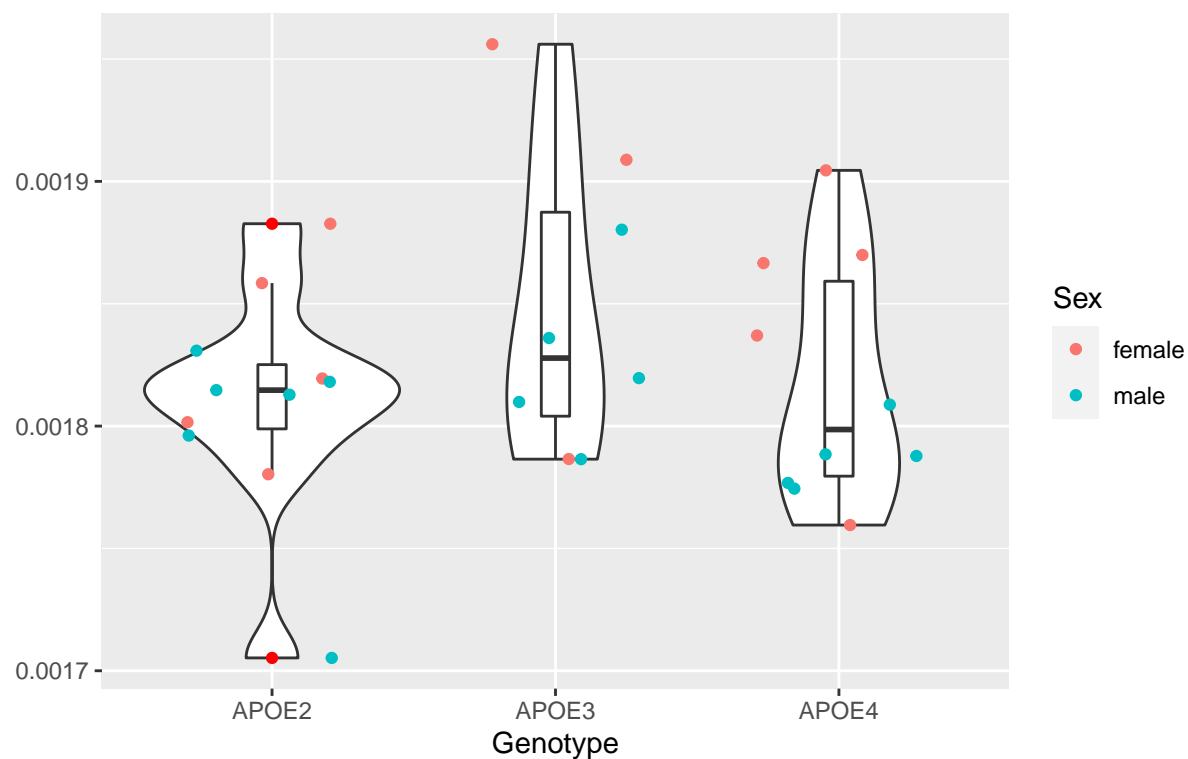
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.799e-08	1.399e-08	2.218	0.129
## Residuals	26	1.640e-07	6.308e-09		

Left Primary Somatosensory Cortex Forelimb Region

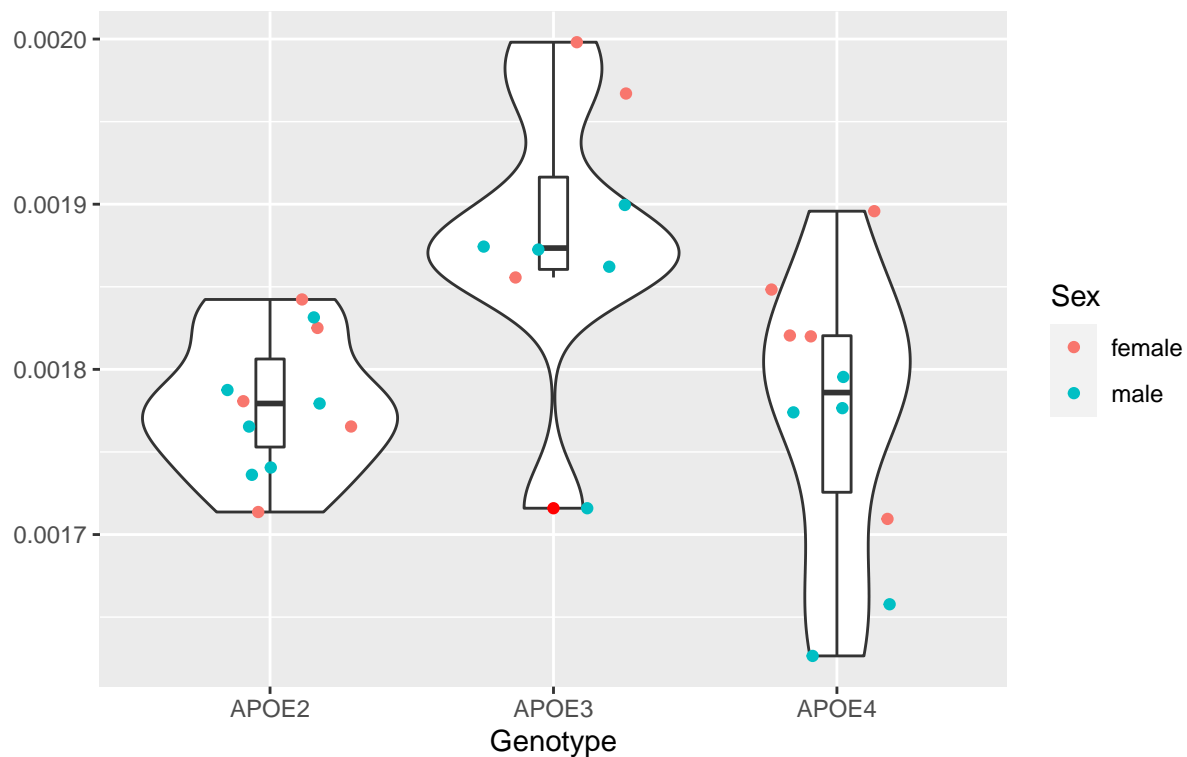
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.890e-09	3.447e-09	1.308	0.288
## Residuals	26	6.852e-08	2.635e-09		

Left Primary Somatosensory Cortex Dysgranular Zone

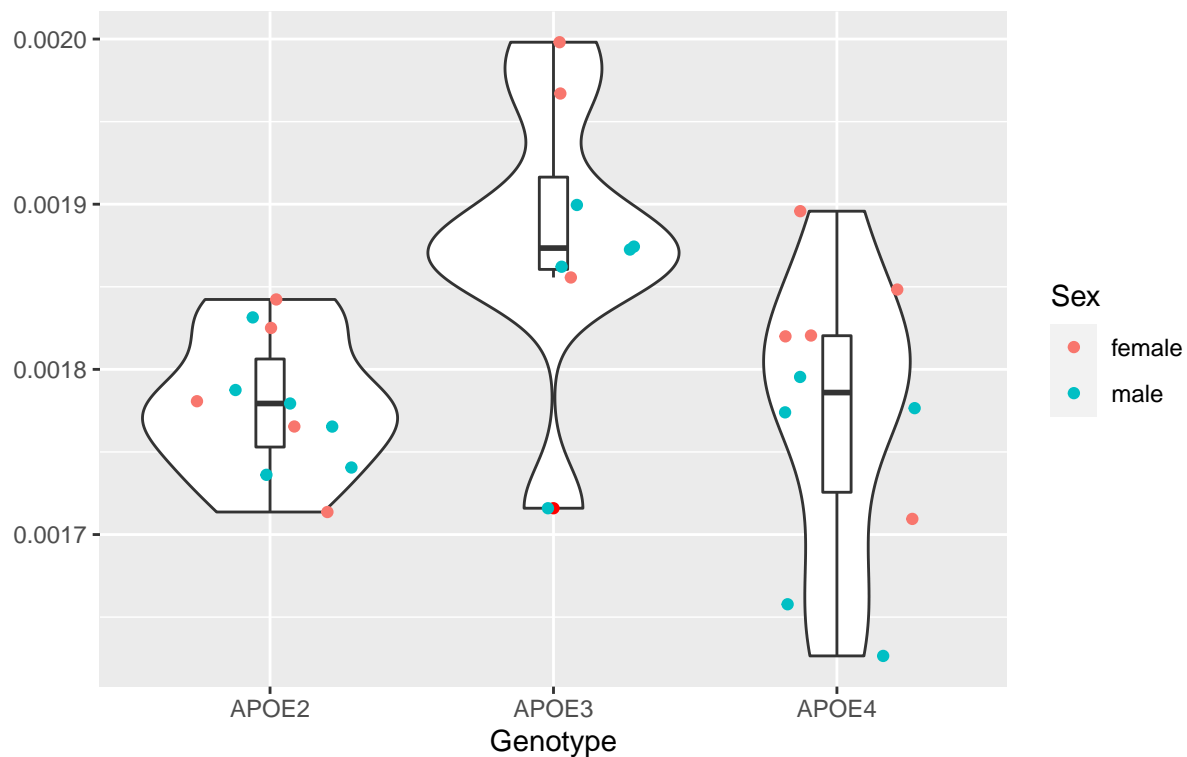
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.821e-08 9.103e-09   2.722 0.0845 .
## Residuals    26 8.696e-08 3.345e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Somatosensory Cortex Barrel Field

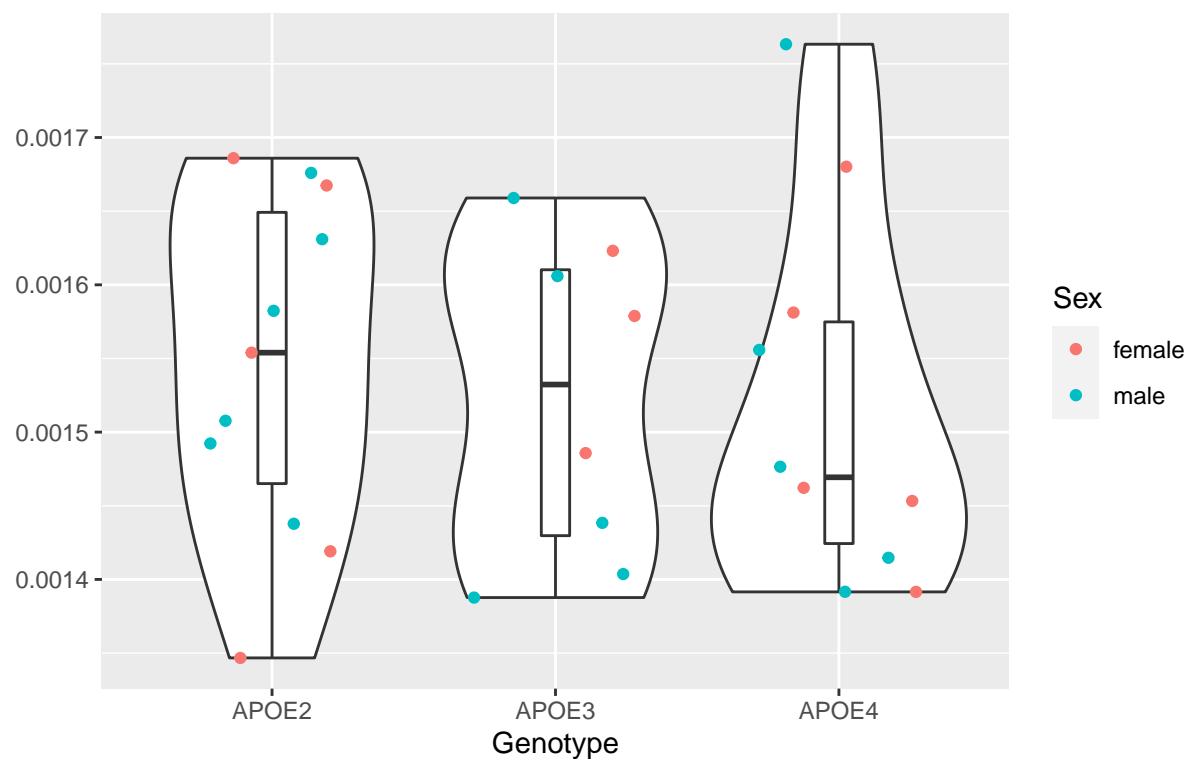
Red points denoting outliers



```
##           Df    Sum Sq   Mean Sq F value    Pr(>F)
## geno         2 6.391e-08 3.196e-08    6.331 0.00575 **
## Residuals   26 1.312e-07 5.050e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Somatosensory Cortex

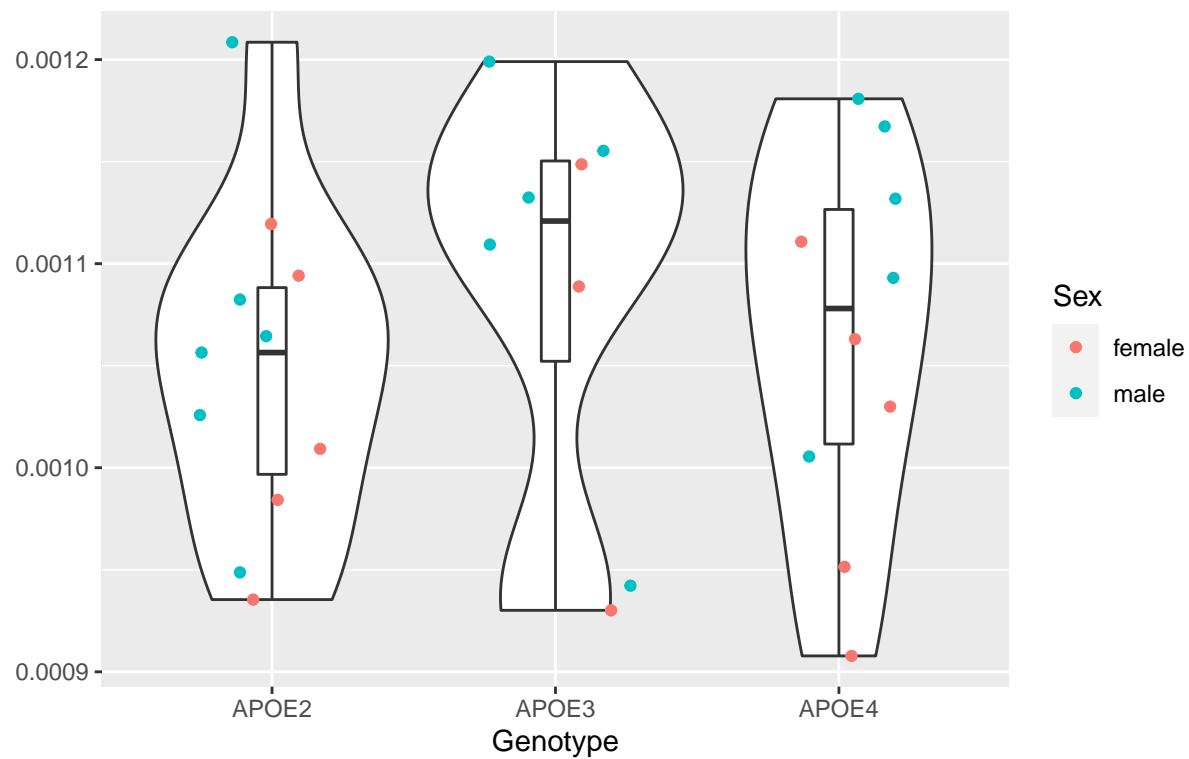
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.700e-09	2.361e-09	0.173	0.842
## Residuals	26	3.549e-07	1.365e-08		

Left Parietal Cortex Posterial Area Rostral Part

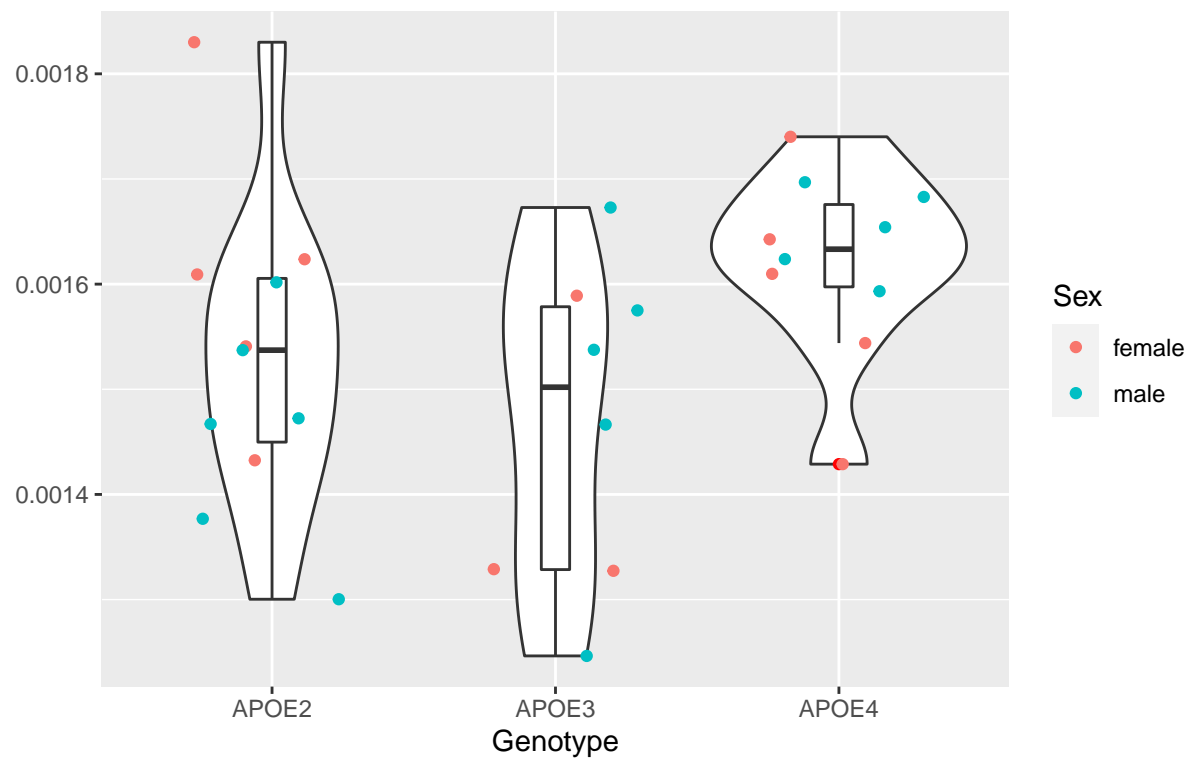
Red points denoting outliers



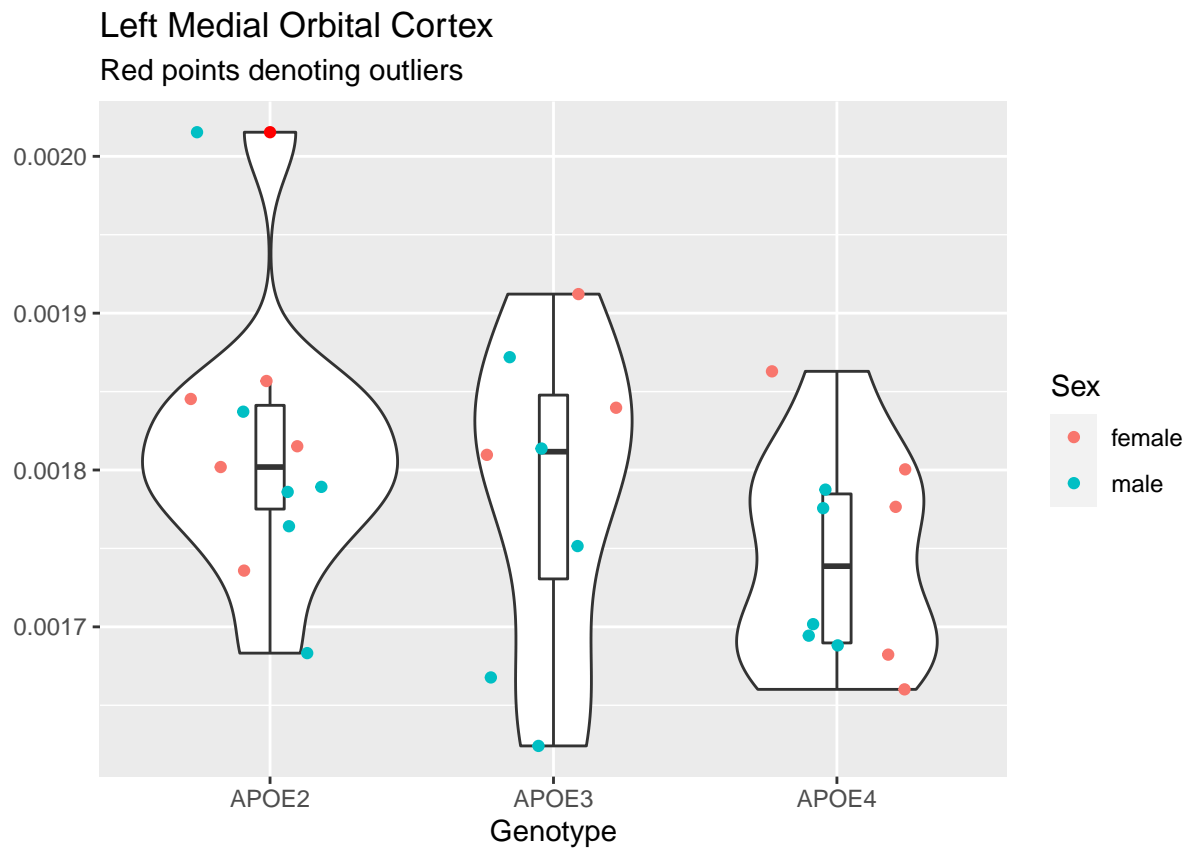
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.480e-09	3.738e-09	0.472	0.629
## Residuals	26	2.058e-07	7.917e-09		

Left Medial Parietal Association Cortex

Red points denoting outliers



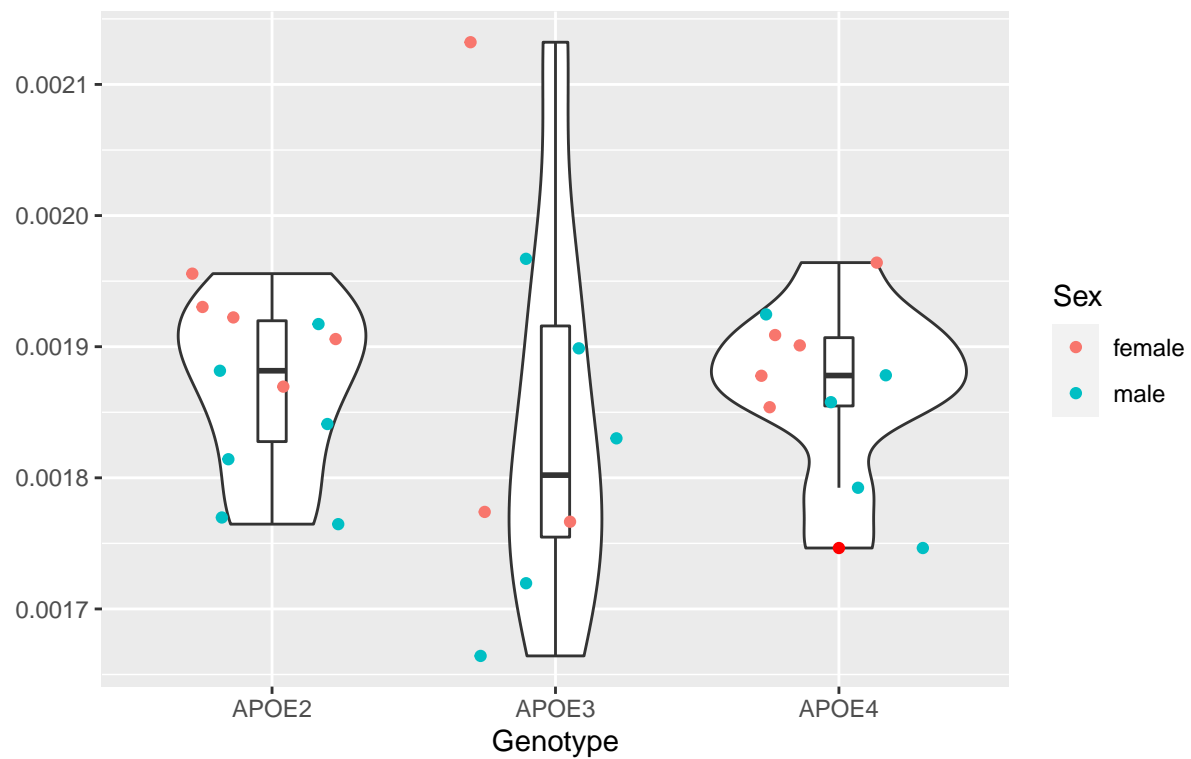
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.099e-07 5.494e-08   3.295  0.053 .
## Residuals    26 4.335e-07 1.667e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.515e-08 1.257e-08   1.822  0.182
## Residuals 26 1.794e-07 6.902e-09
```


Left Secondary Motor Cortex

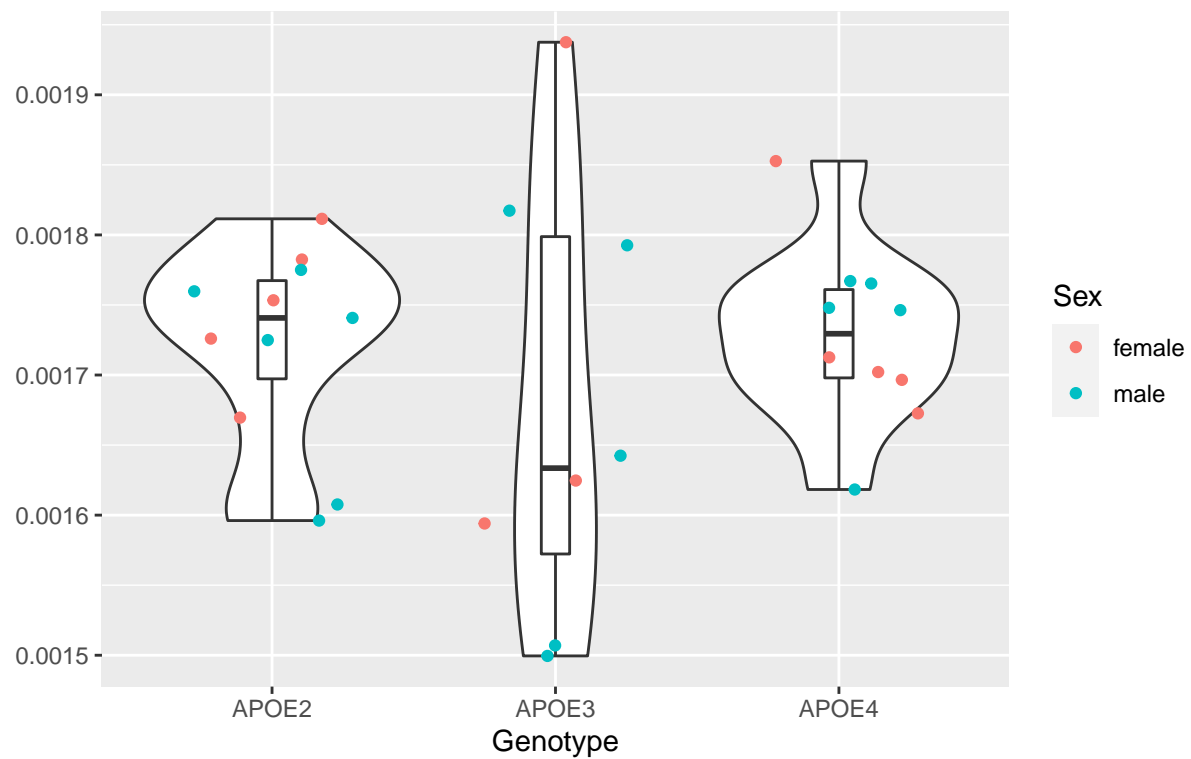
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.010e-09	2.004e-09	0.218	0.805
## Residuals	26	2.387e-07	9.181e-09		

Left Primary Motor Cortex

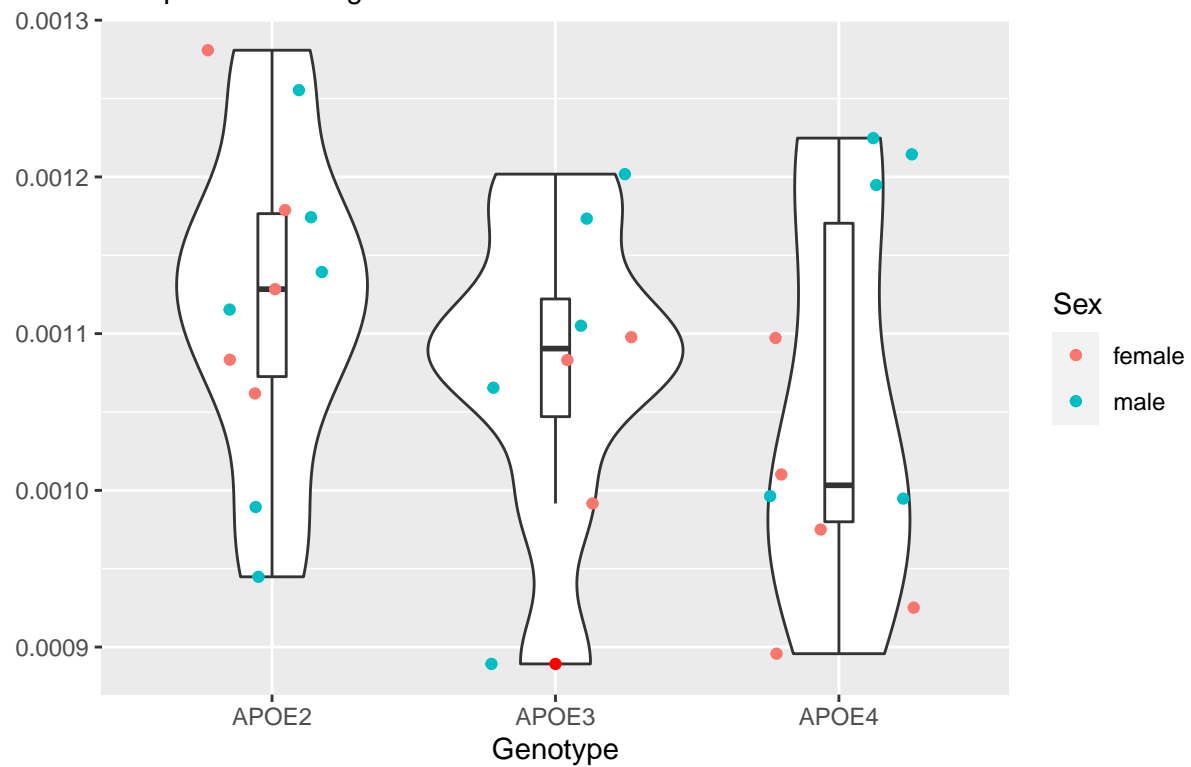
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.368e-08	6.839e-09	0.691	0.51
## Residuals	26	2.573e-07	9.895e-09		

Left Lateral Parietal Association Cortex

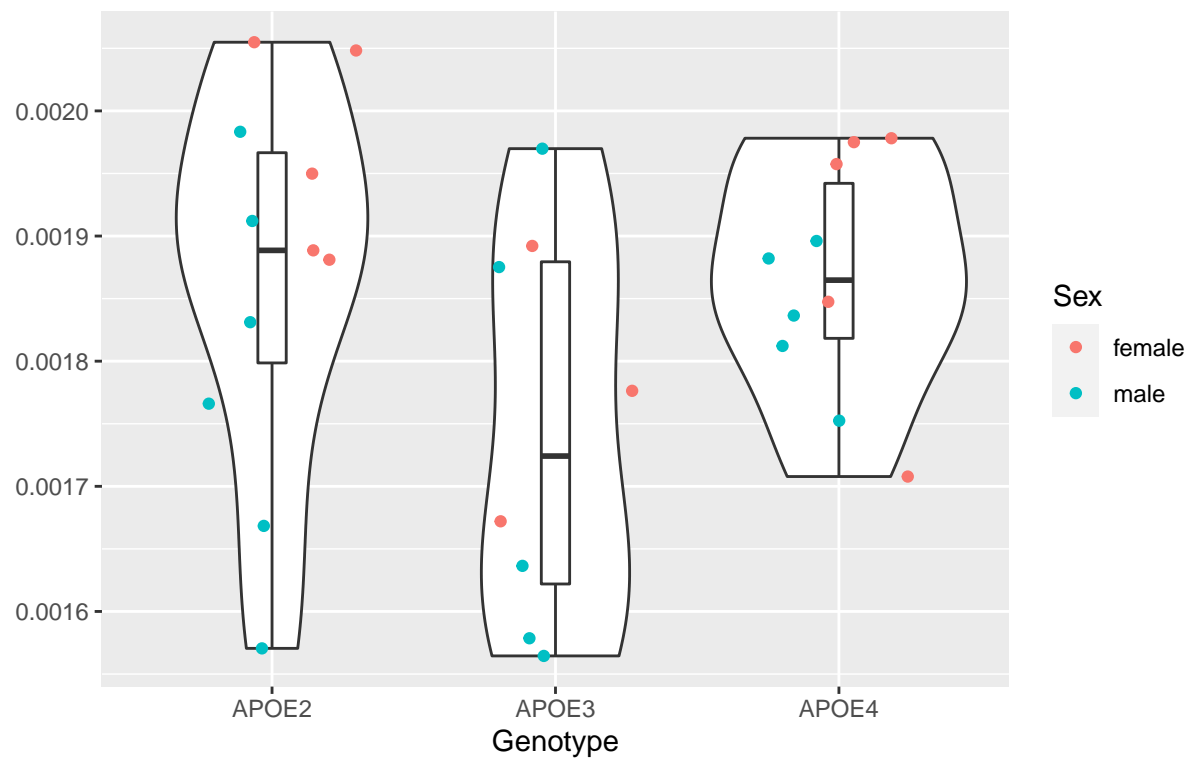
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.678e-08	1.339e-08	1.14	0.335
## Residuals	26	3.055e-07	1.175e-08		

Left Lateral Orbital Cortex

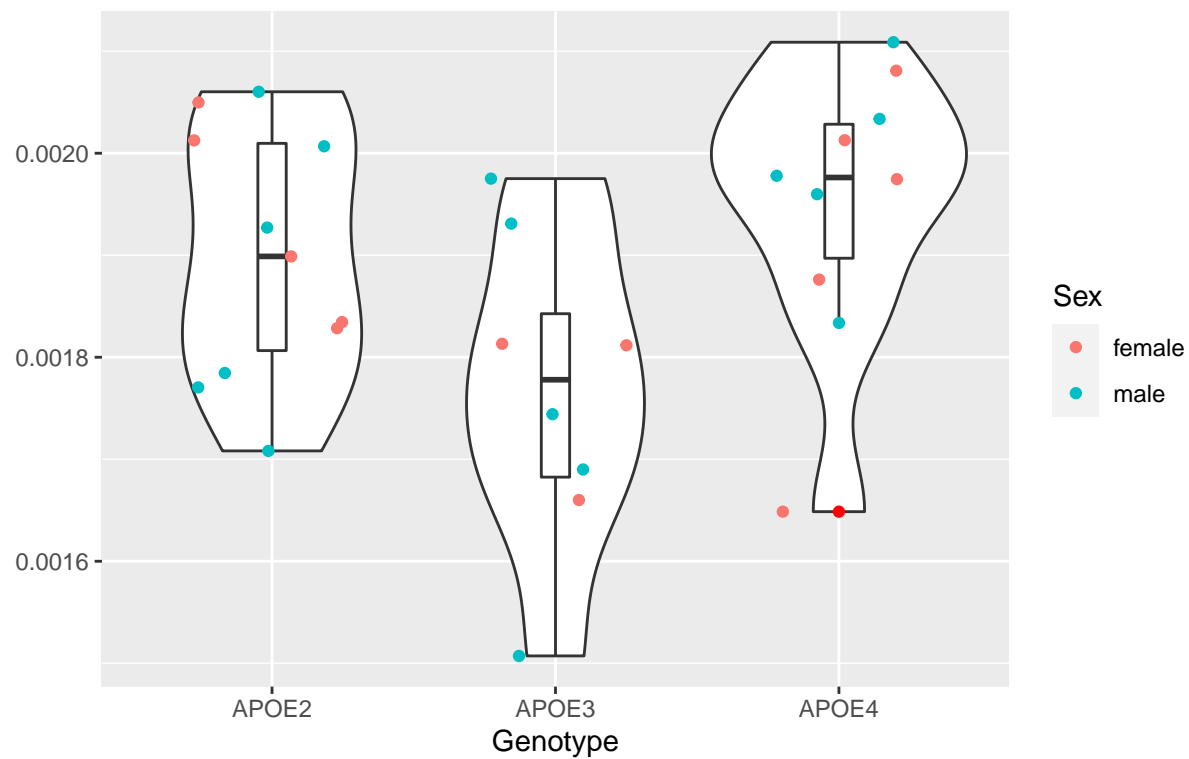
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.490e-08	4.246e-08	2.331	0.117
## Residuals	26	4.736e-07	1.821e-08		

Left Insular Cortex

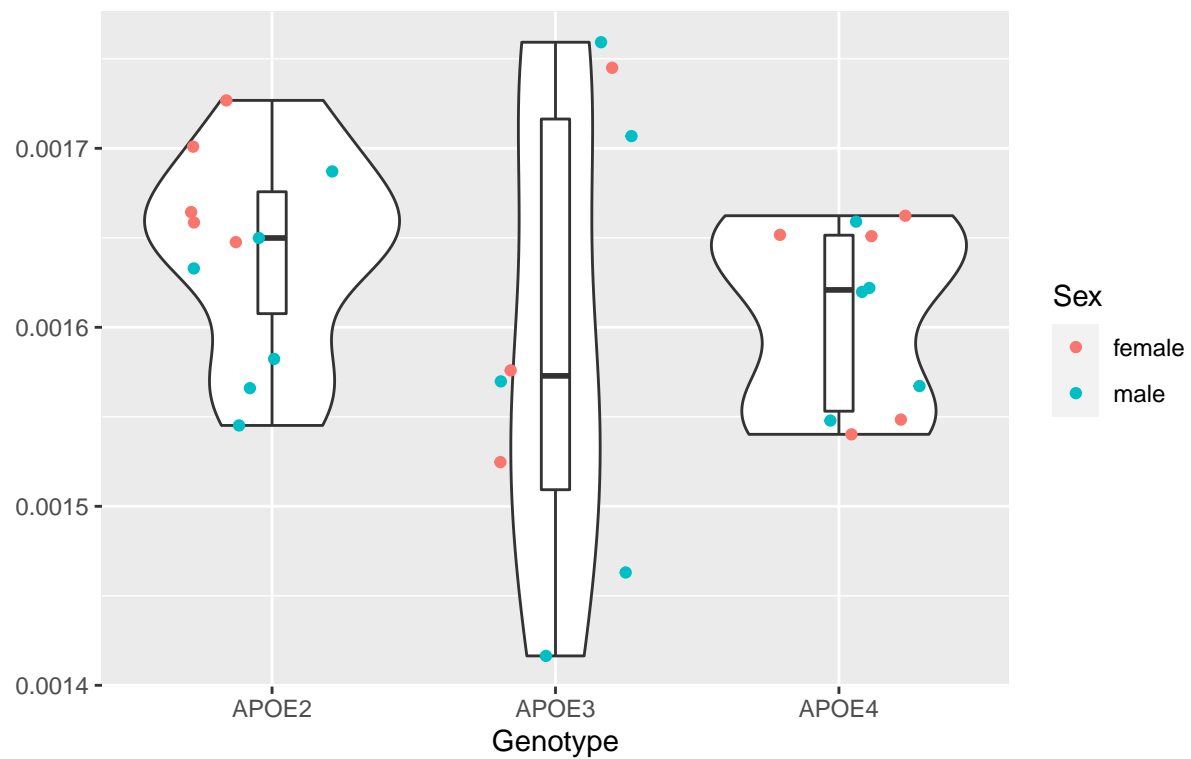
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.566e-07 7.831e-08   4.299 0.0244 *
## Residuals    26 4.736e-07 1.822e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Frontal Association Cortex

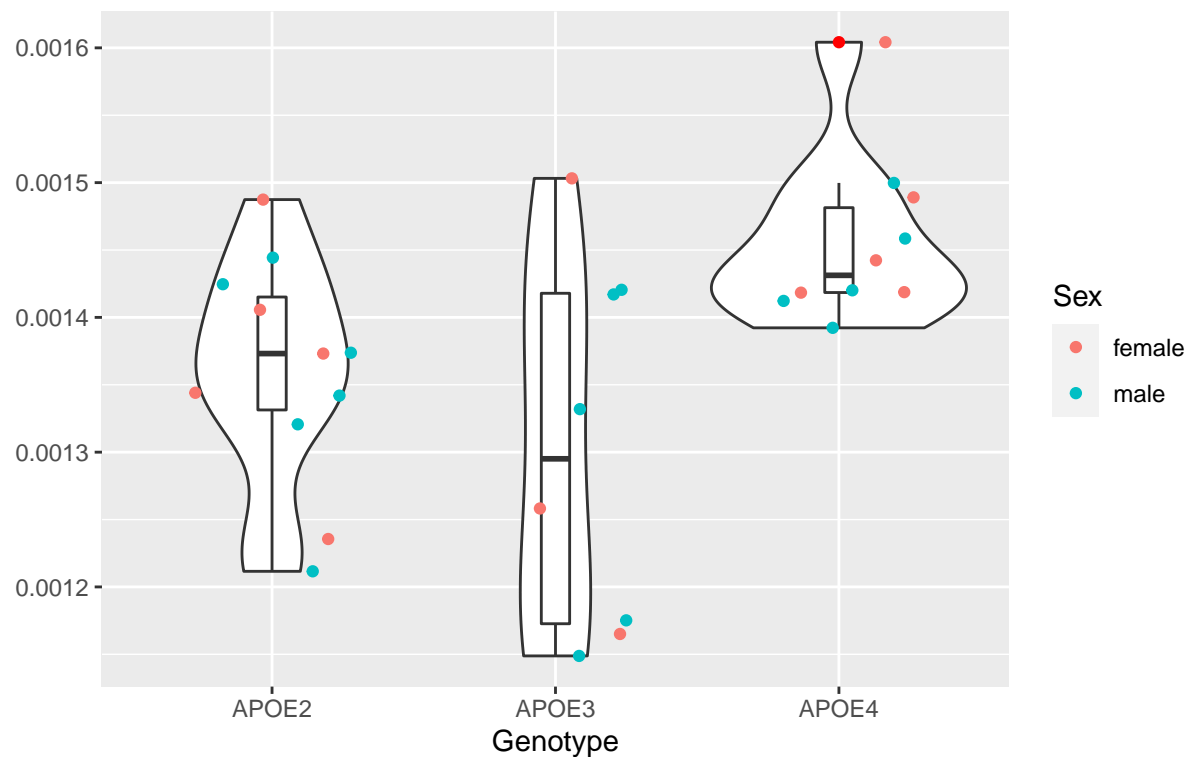
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.170e-08	5.85e-09	0.881	0.426
## Residuals	26	1.726e-07	6.64e-09		

Left Frontal Cortex Area 3

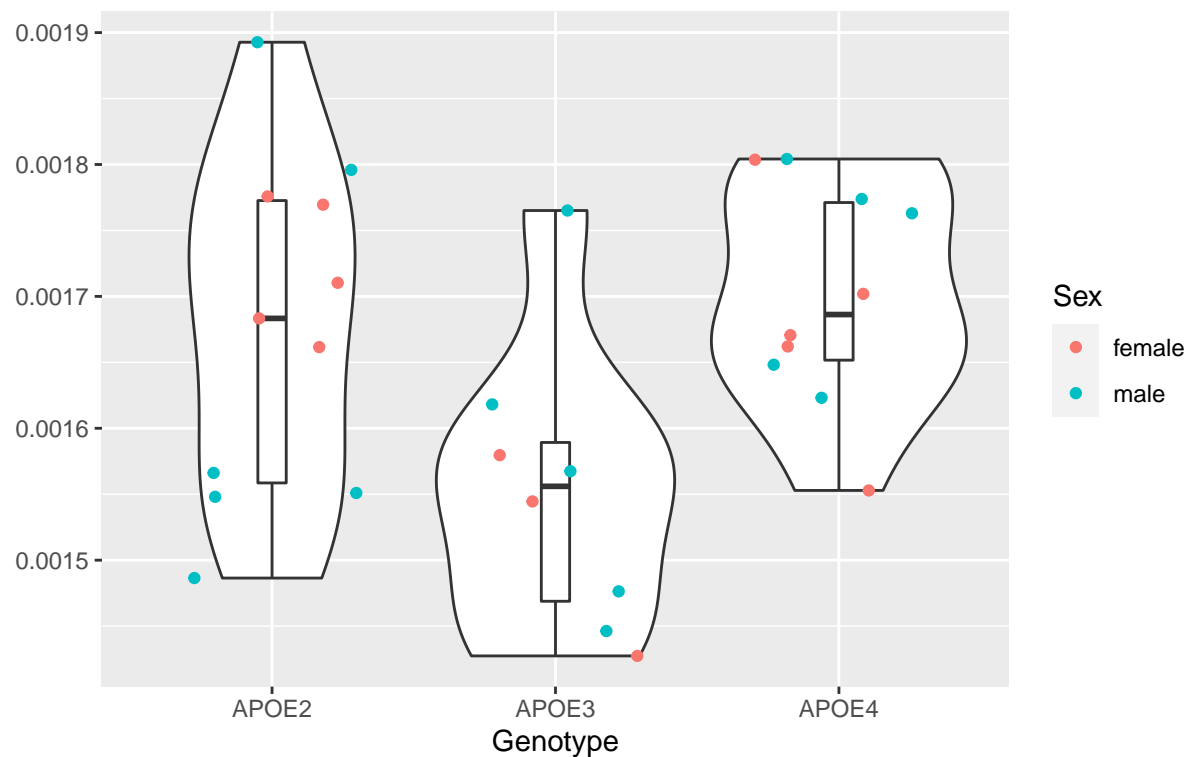
Red points denoting outliers



```
##          Df    Sum Sq Mean Sq F value    Pr(>F)
## geno         2 1.092e-07 5.46e-08    6.076 0.00684 **
## Residuals    26 2.337e-07 8.99e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Dorsolateral Orbital Cortex

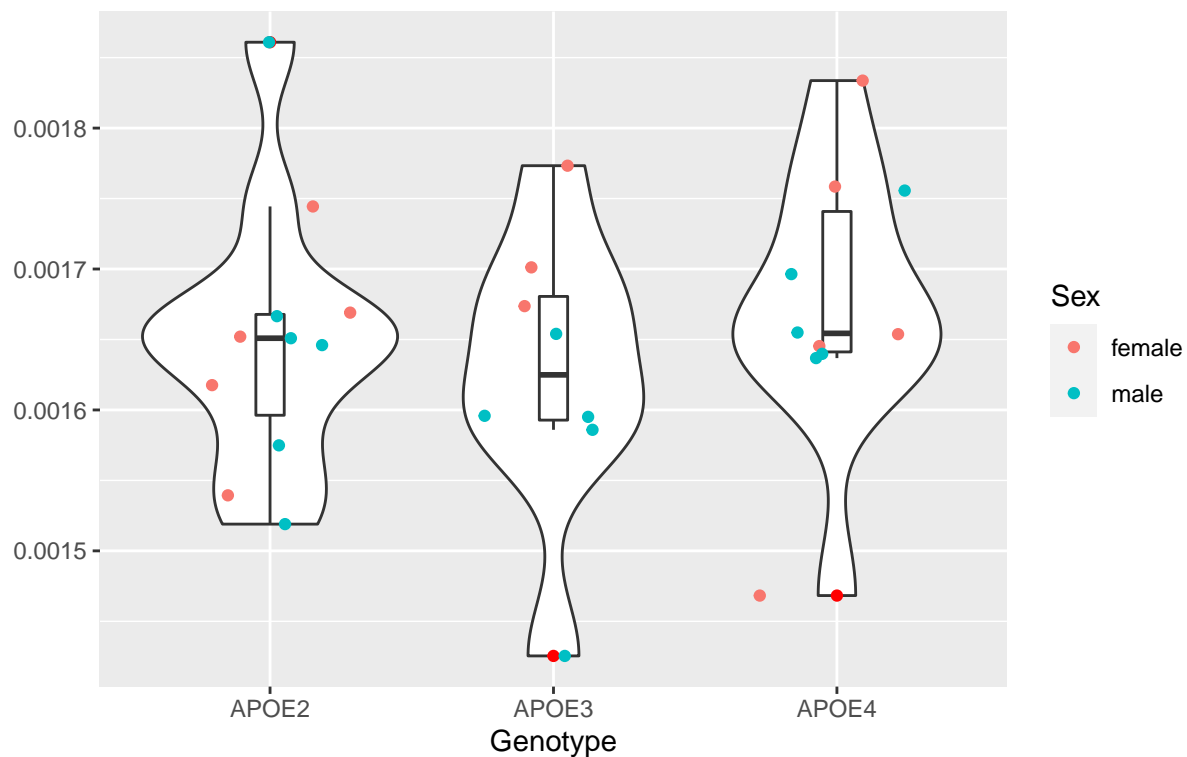
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.081e-07 5.405e-08   4.558 0.0201 *
## Residuals    26 3.083e-07 1.186e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Left Secondary Auditory Cortex Ventral Part

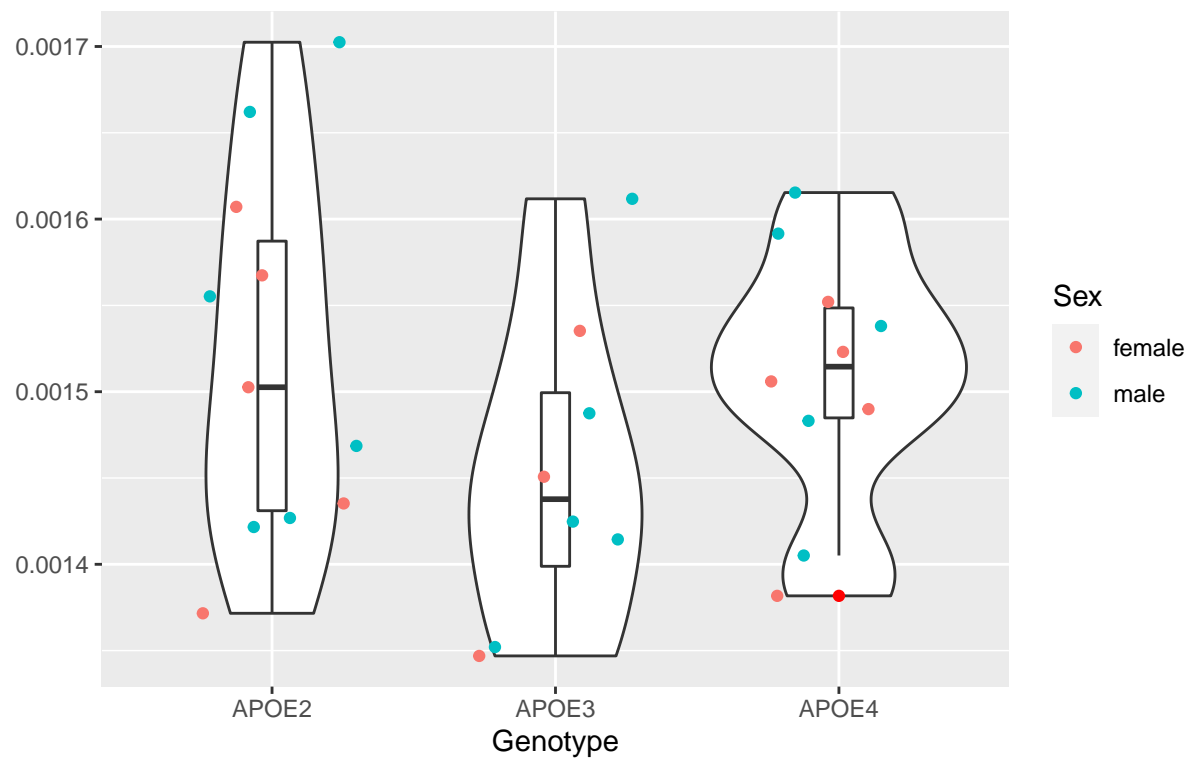
Red points denoting outliers



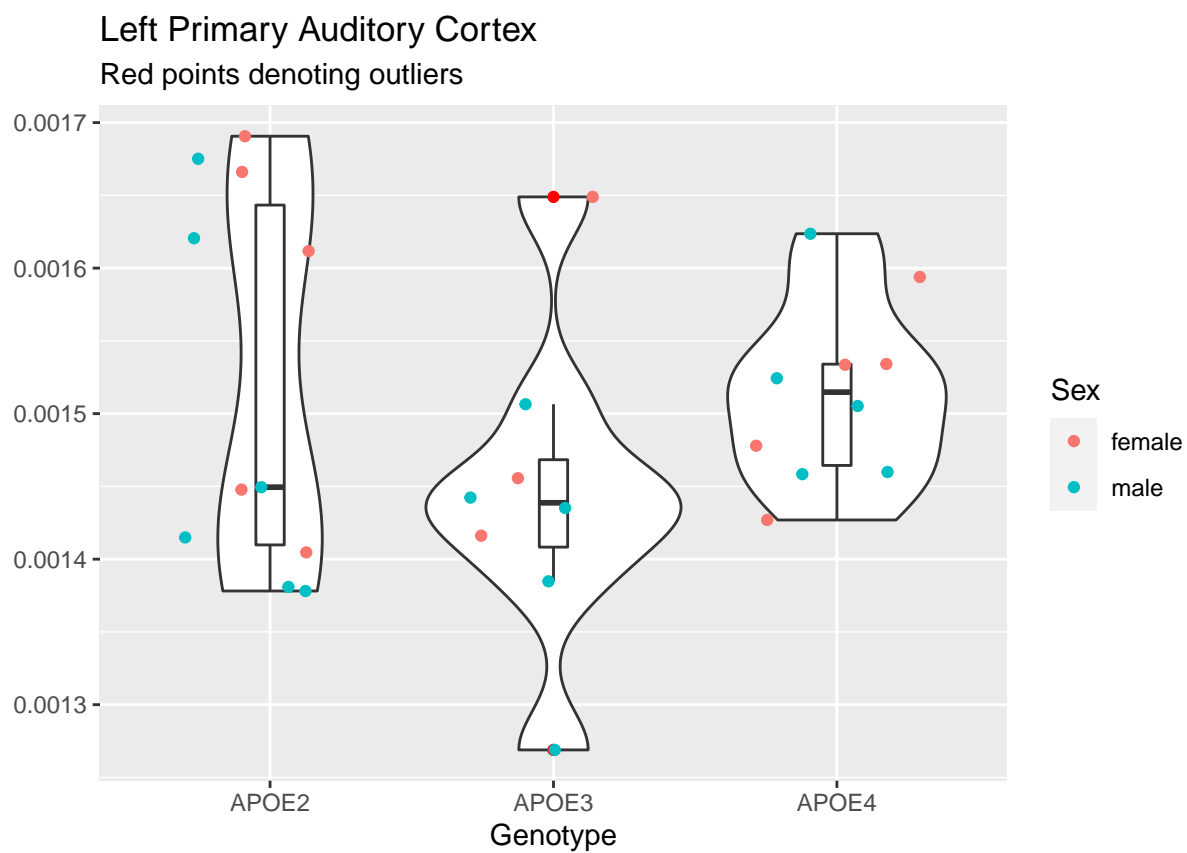
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.065e-08	5.325e-09	0.553	0.582
## Residuals	26	2.505e-07	9.636e-09		

Left Secondary Auditory Cortex Dorsal Part

Red points denoting outliers



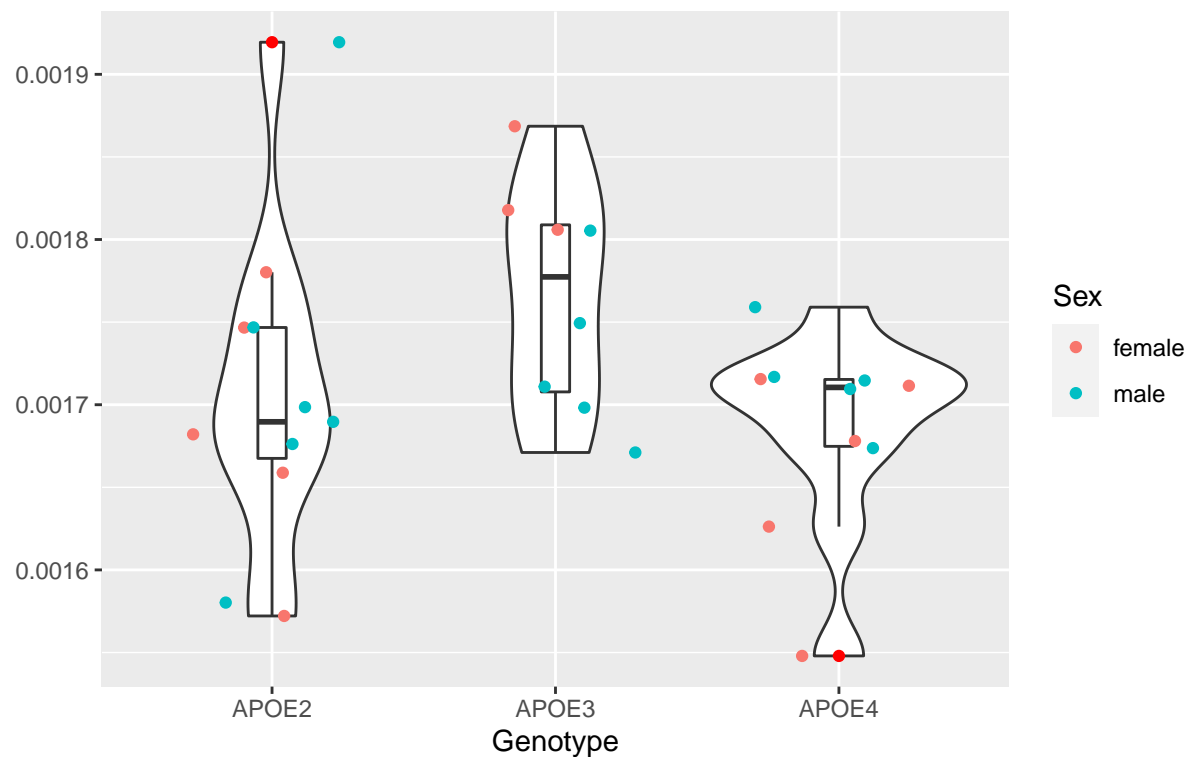
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.273e-08	1.137e-08	1.337	0.28
## Residuals	26	2.210e-07	8.501e-09		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 3.139e-08 1.569e-08   1.445  0.254
## Residuals 26 2.823e-07 1.086e-08
```

Left Cingulate Cortex Area 32

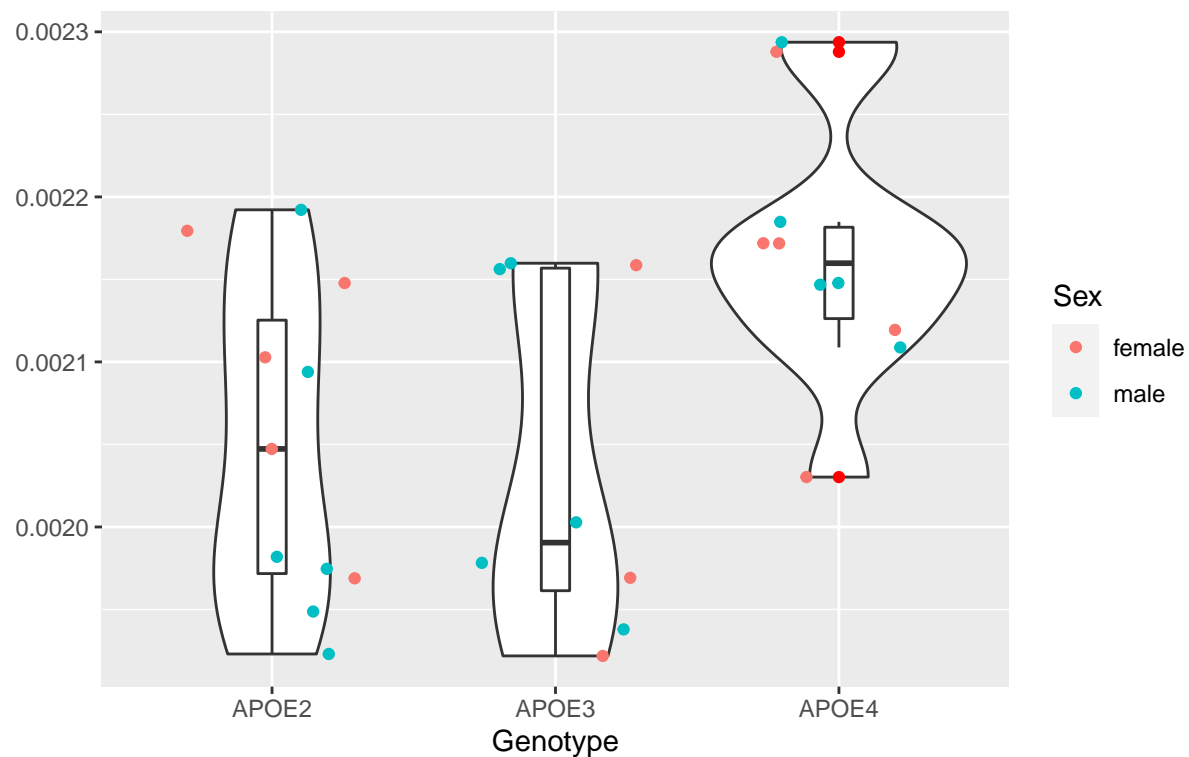
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 3.075e-08 1.537e-08   2.539 0.0983 .
## Residuals    26 1.574e-07 6.054e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Cingulate Cortex Area 30

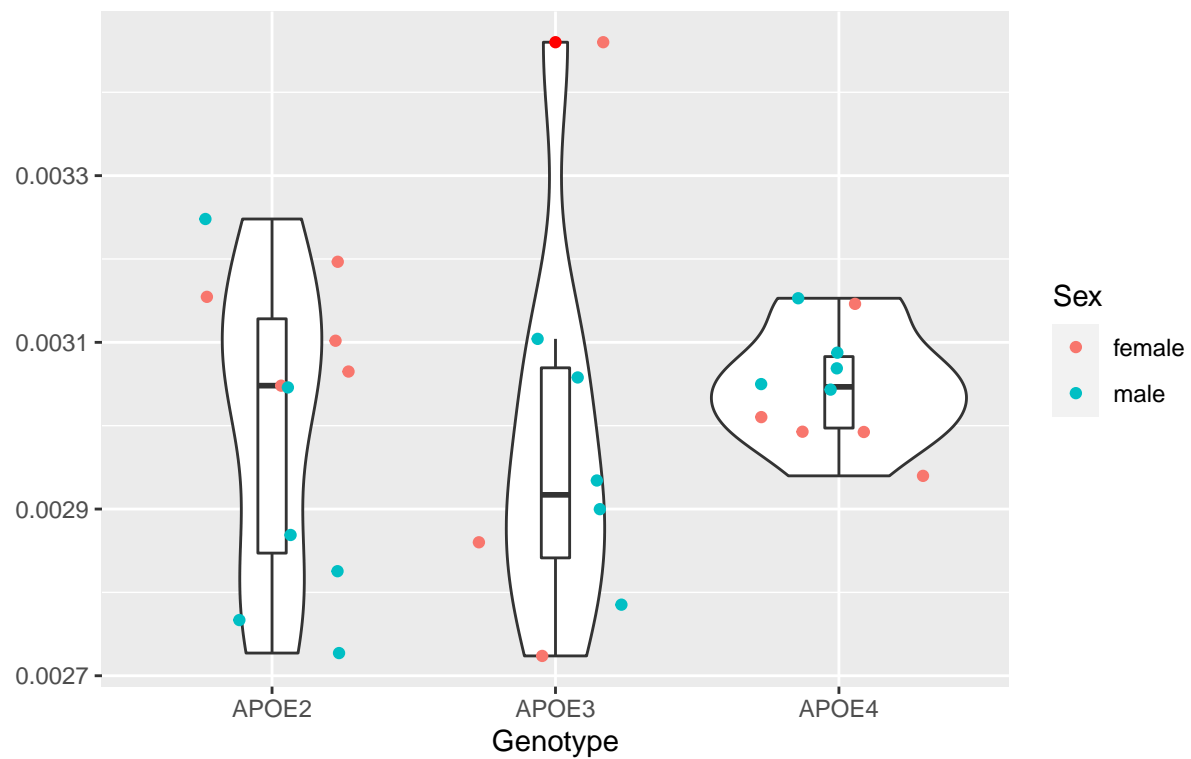
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 9.835e-08 4.918e-08   5.631 0.0093 **
## Residuals    26 2.271e-07 8.730e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Cingulate Cortex Area 29c

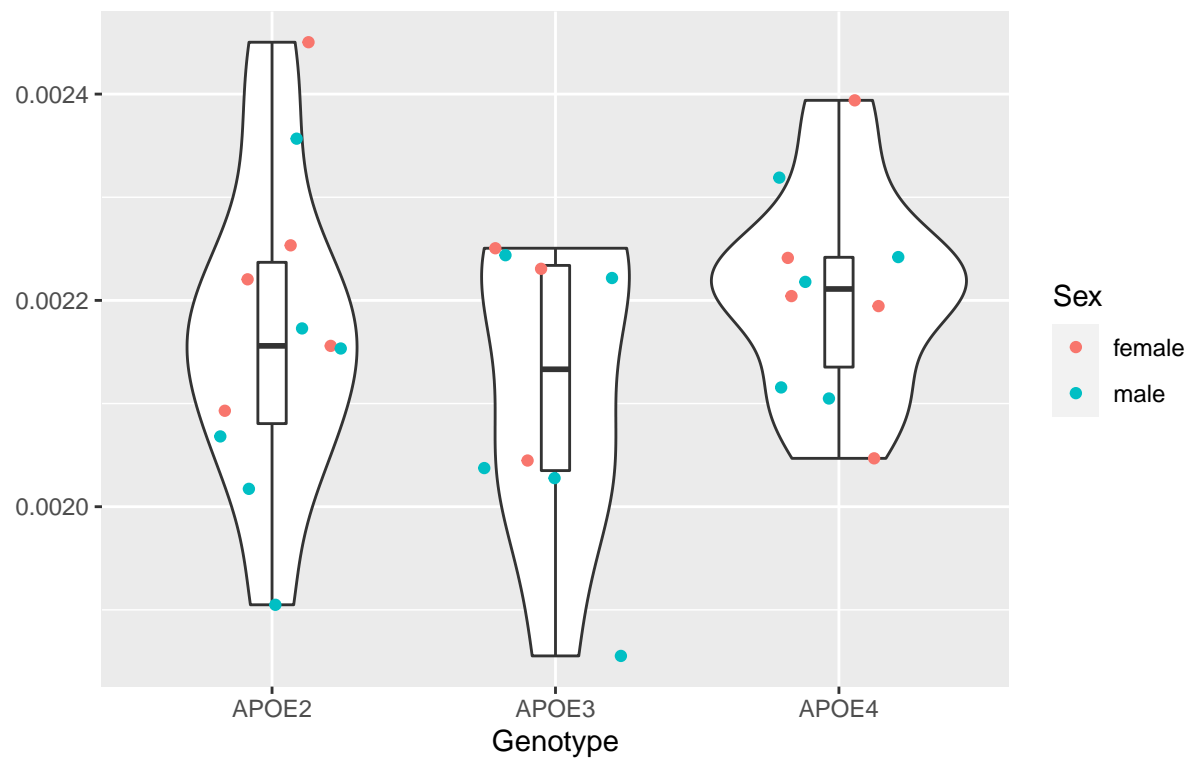
Red points denoting outliers



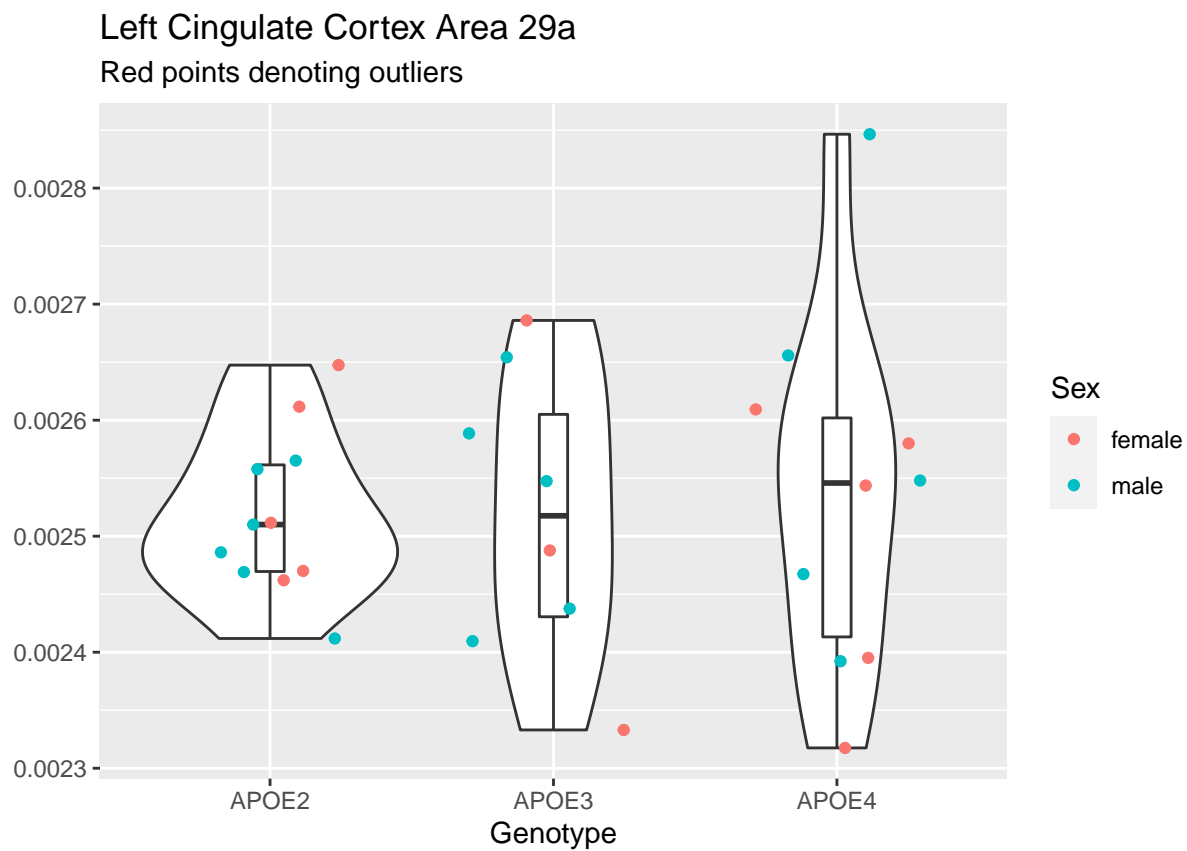
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.300e-08	1.152e-08	0.405	0.671
## Residuals	26	7.396e-07	2.845e-08		

Left Cingulate Cortex Area 29b

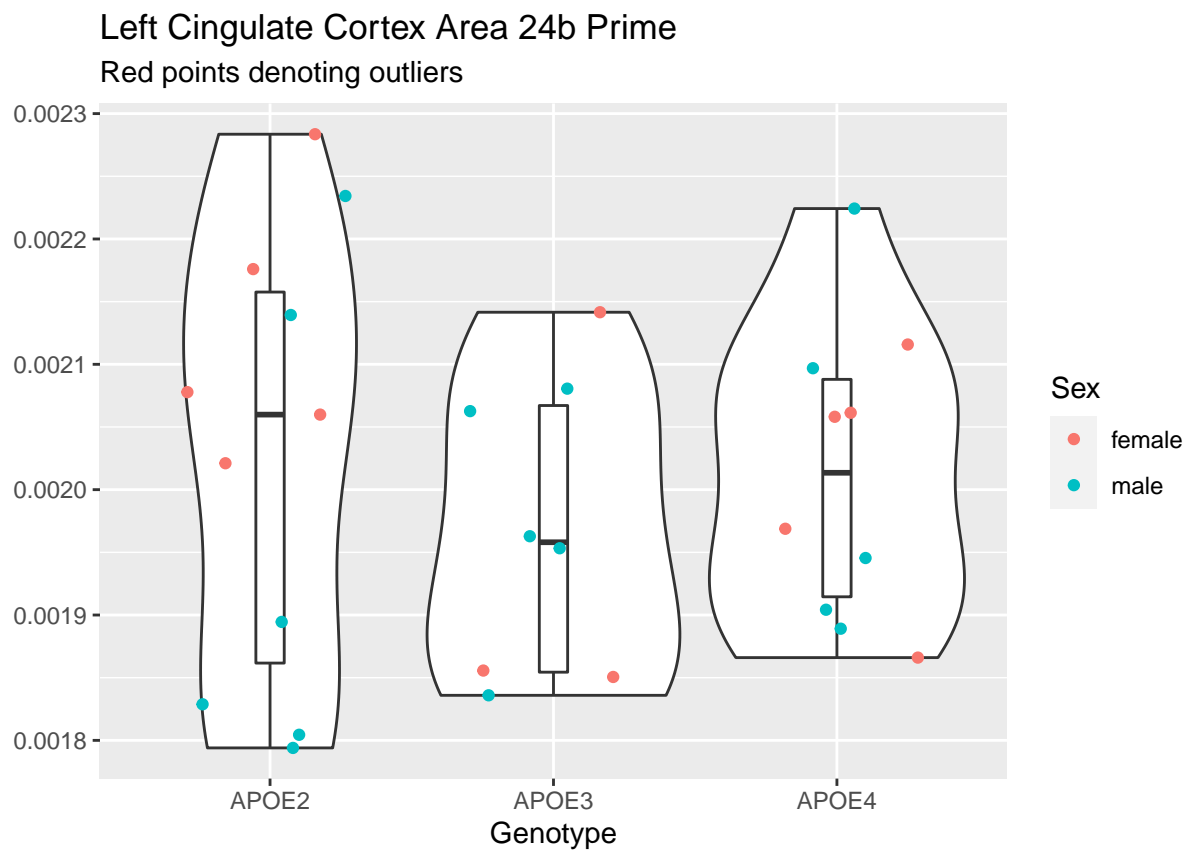
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.930e-08	1.965e-08	1.079	0.355
## Residuals	26	4.736e-07	1.821e-08		



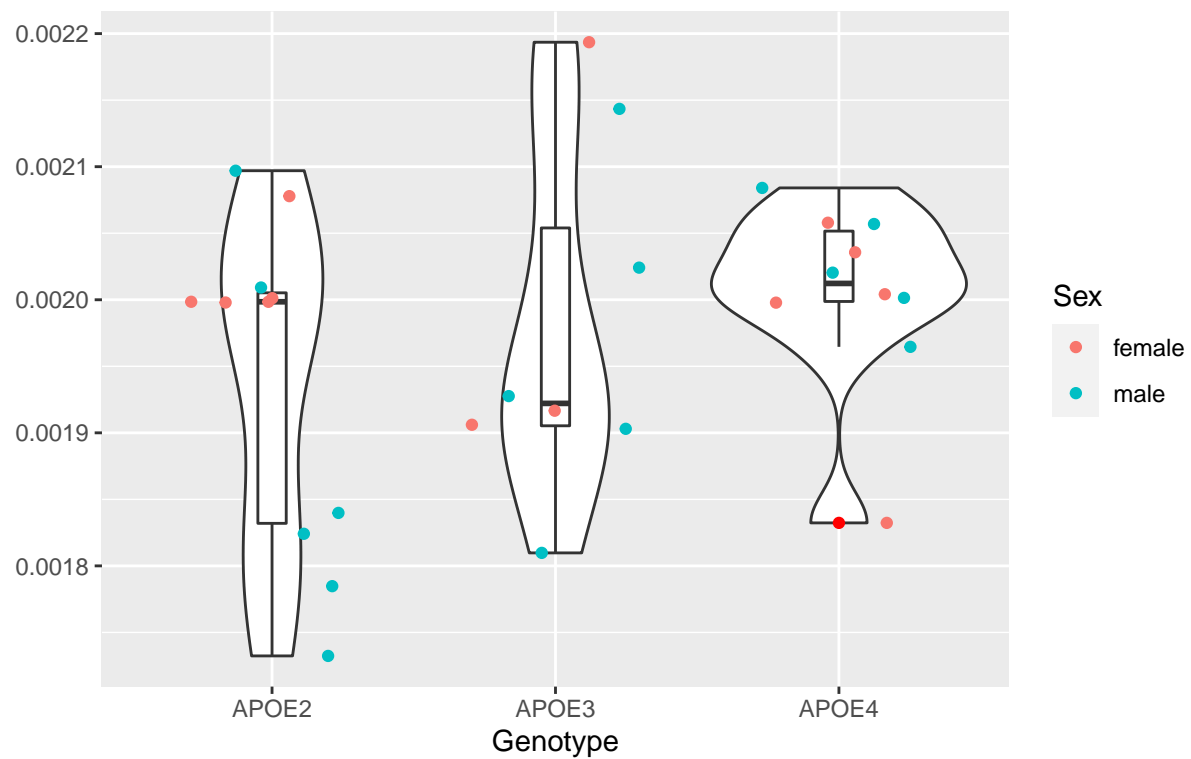
```
##          Df    Sum Sq Mean Sq F value Pr(>F)
## geno      2 2.000e-09 9.79e-10  0.069  0.933
## Residuals 26 3.667e-07 1.41e-08
```

##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.770e-08	8.841e-09	0.437	0.65
## Residuals	26	5.257e-07	2.022e-08		

Left Cingulate Cortex Area 24b

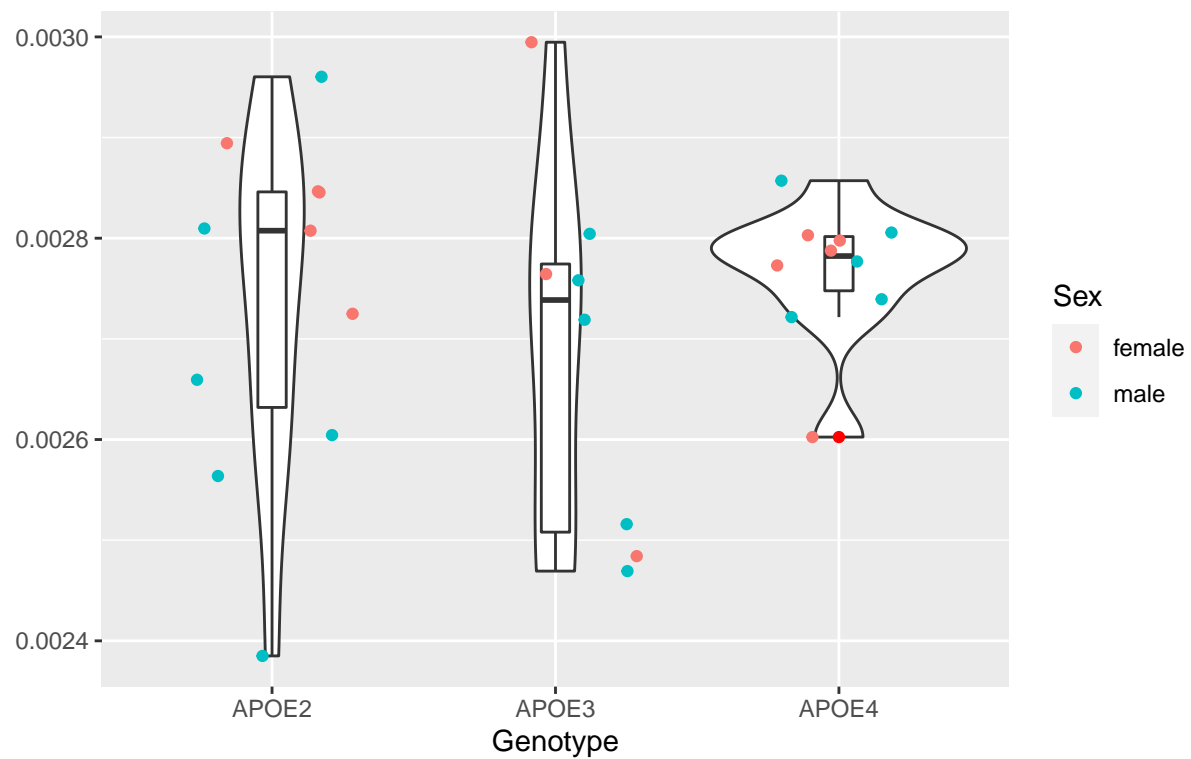
Red points denoting outliers



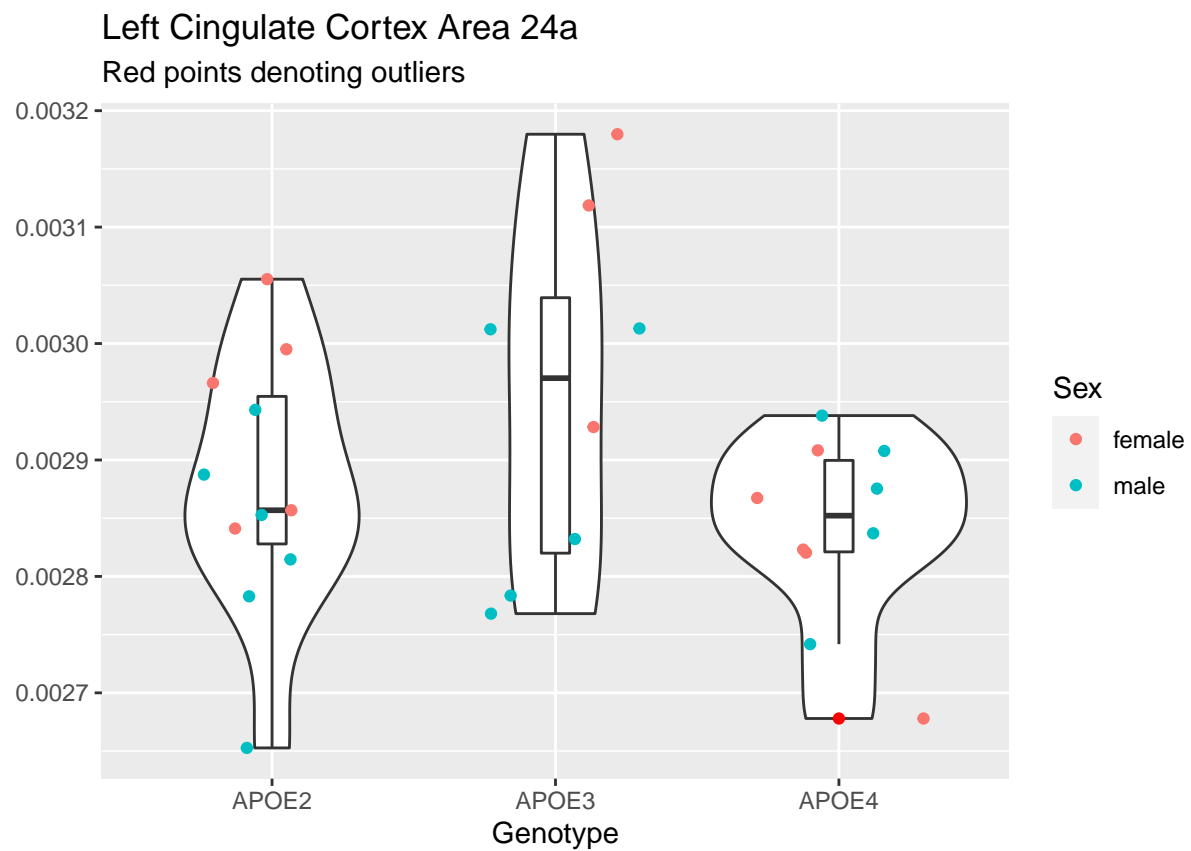
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.140e-08	1.069e-08	0.872	0.43
## Residuals	26	3.188e-07	1.226e-08		

Left Cingulate Cortex Area 24a Prime

Red points denoting outliers



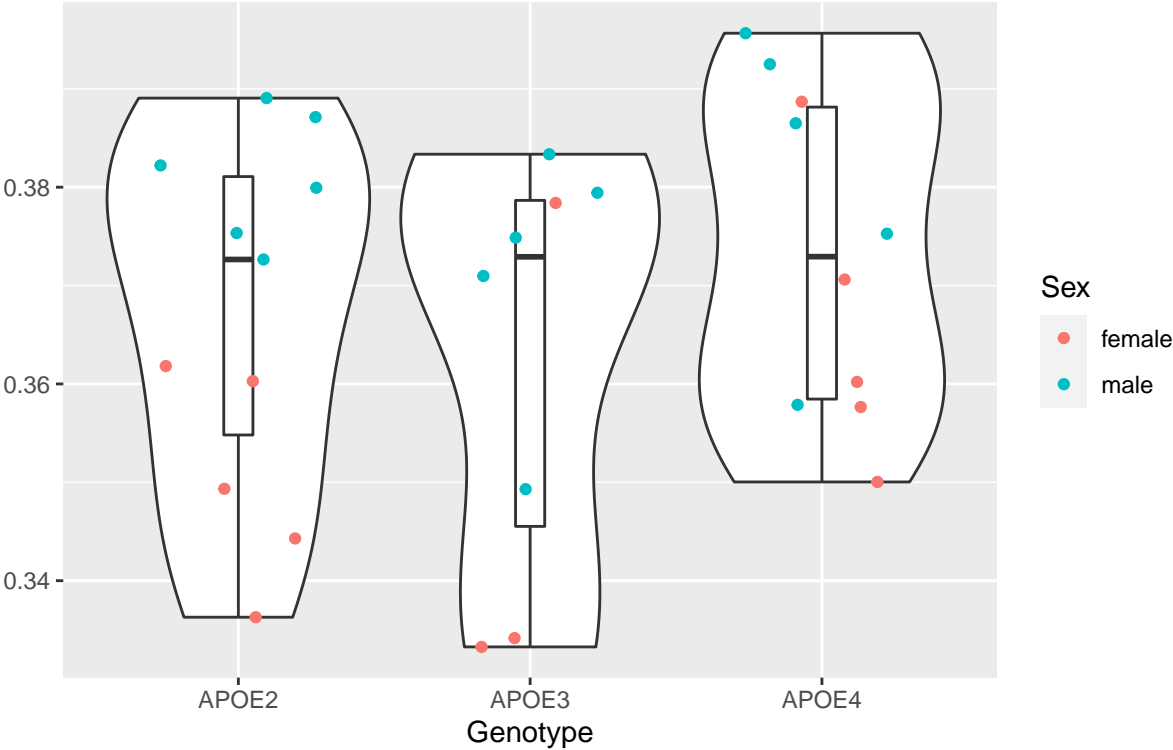
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.70e-08	1.348e-08	0.618	0.547
## Residuals	26	5.67e-07	2.181e-08		



```
##           Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 5.98e-08 2.988e-08   2.252  0.125
## Residuals    26 3.45e-07 1.327e-08
```

Exterior

Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	0.000512	0.0002562	0.761	0.477
## Residuals	26	0.008750	0.0003365		