

Proportional Volume Distributions by Region (Right Hemisphere)

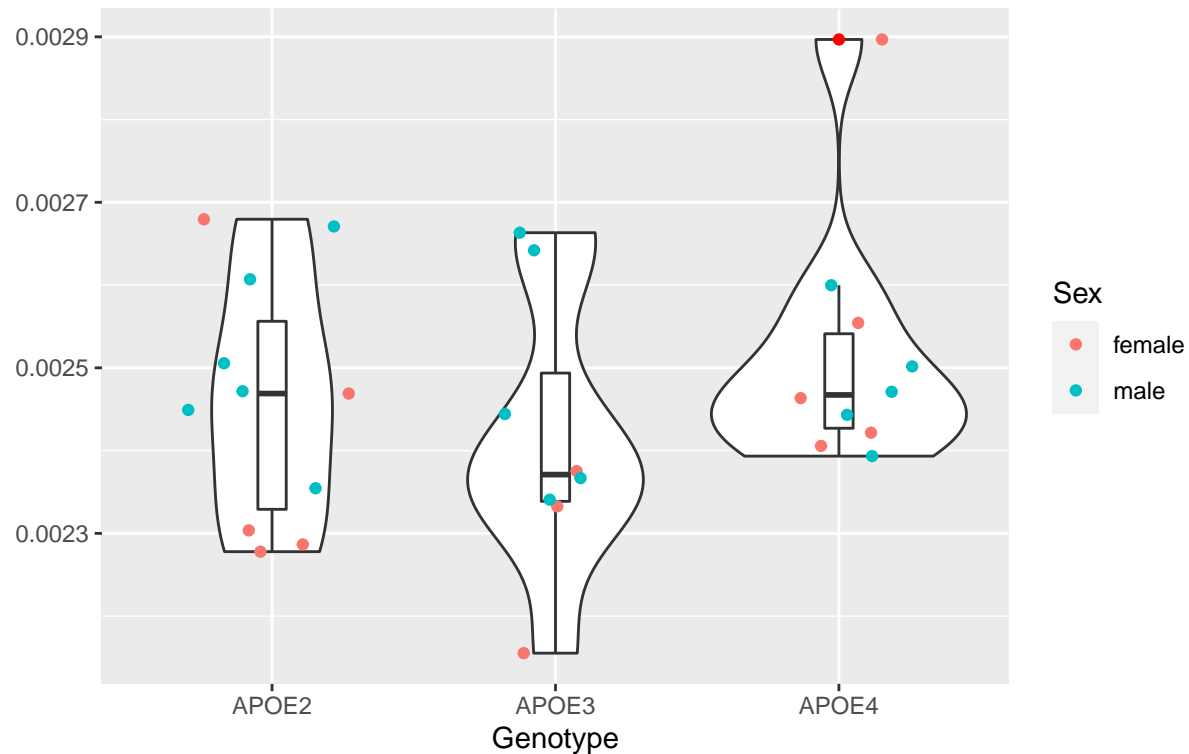
Anna MacFarlane and Jasmine King

3/2/2021

Right Hemisphere Regions

Interpeduncular Nucleus

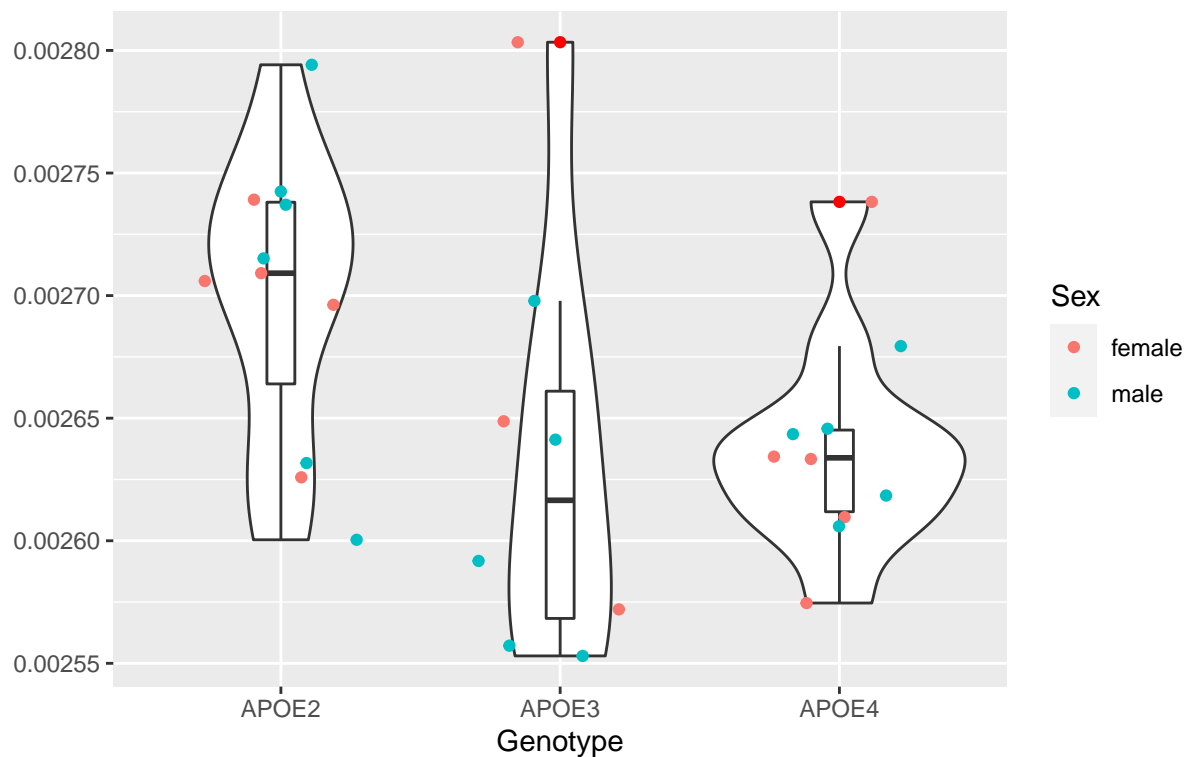
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.51e-08	2.255e-08	0.956	0.397
## Residuals	26	6.13e-07	2.358e-08		

Cerebellar Cortex

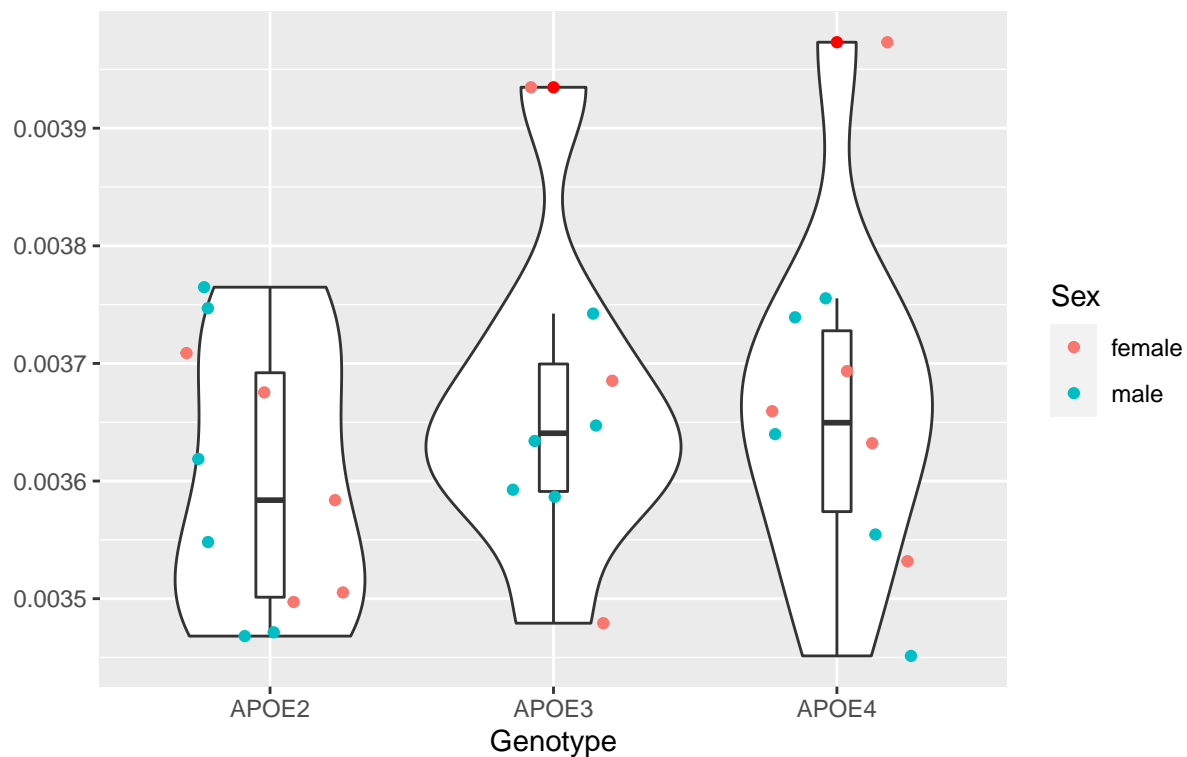
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 2.785e-08 1.393e-08   3.507 0.0448 *
## Residuals    26 1.032e-07 3.971e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Dentate (Lateral) Nucleus of Cerebellum

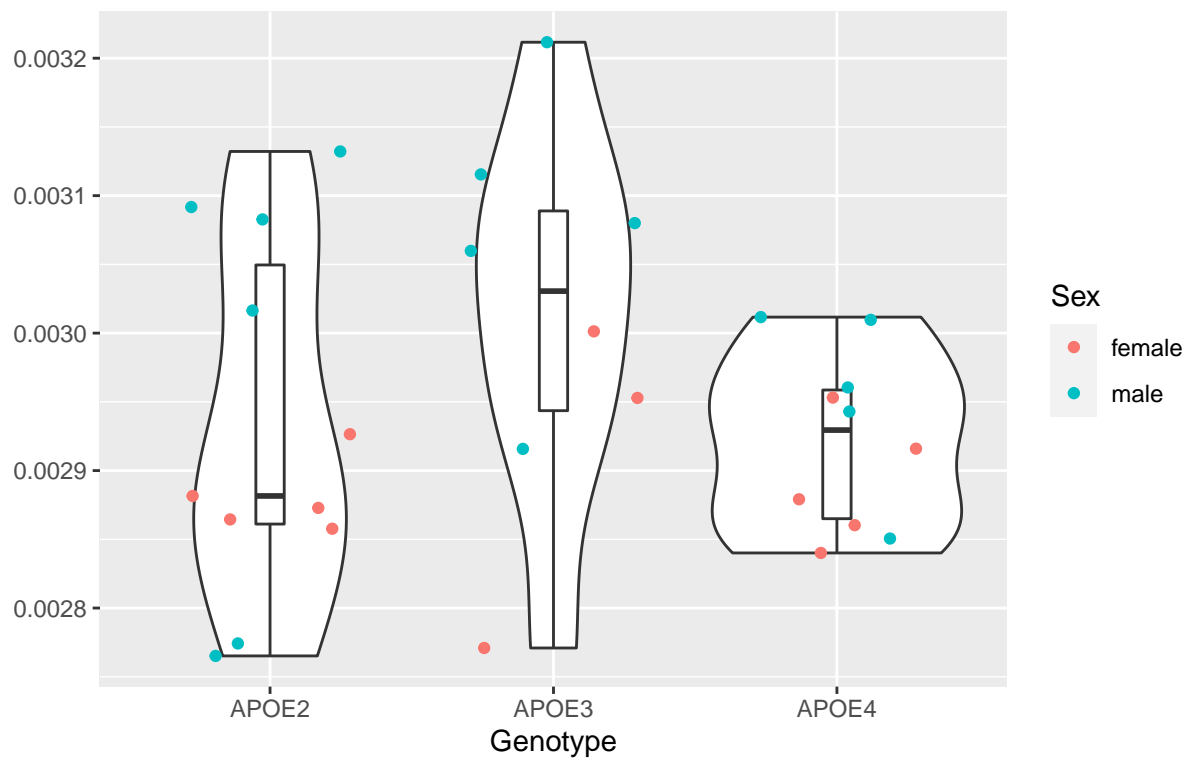
Red points denoting outliers



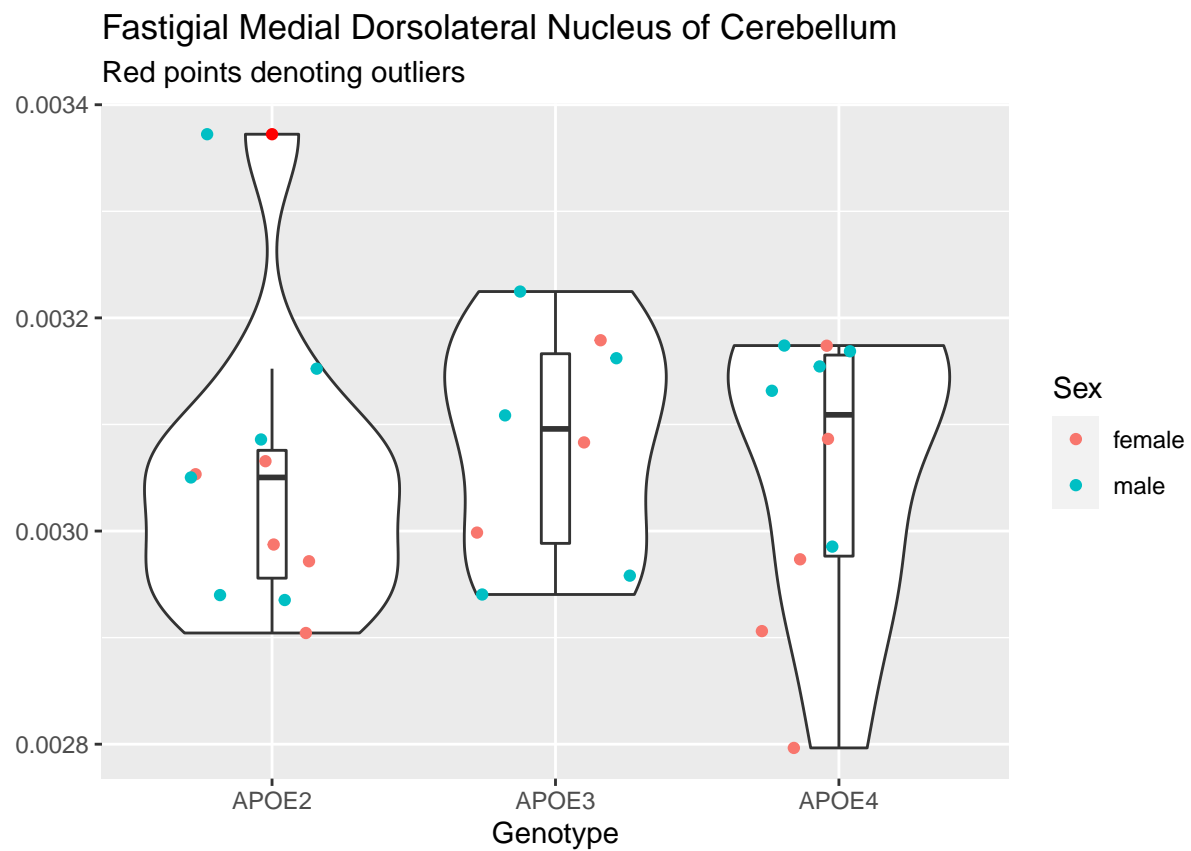
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno      2 2.79e-08 1.396e-08   0.833  0.446
## Residuals 26 4.36e-07 1.677e-08
```

Interposed Nucleus of Cerebellum

Red points denoting outliers



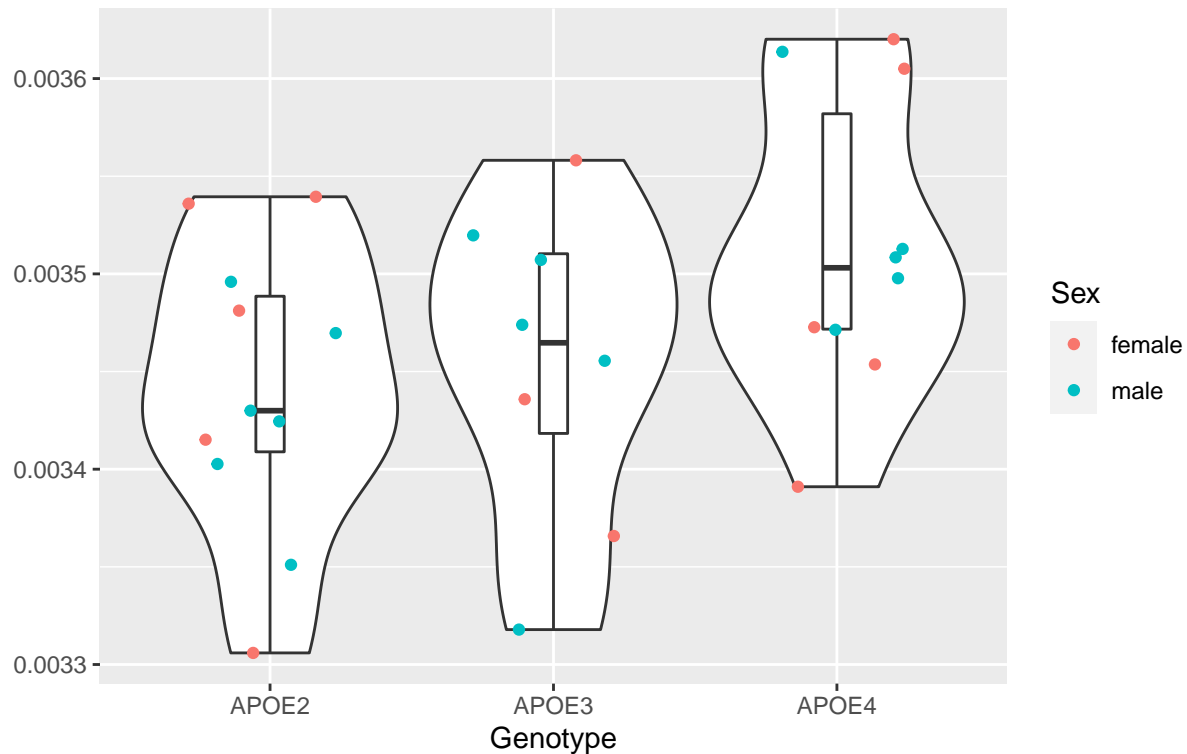
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 4.290e-08 2.144e-08   1.695  0.203
## Residuals 26 3.288e-07 1.265e-08
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 5.900e-09 2.938e-09   0.186  0.831
## Residuals 26 4.101e-07 1.577e-08
```

Fastigial Medial Nucleus of Cerebellum

Red points denoting outliers



```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## geno         2 3.116e-08 1.558e-08    2.698 0.0862 .
## Residuals    26 1.502e-07 5.775e-09
```

```
## ---
```

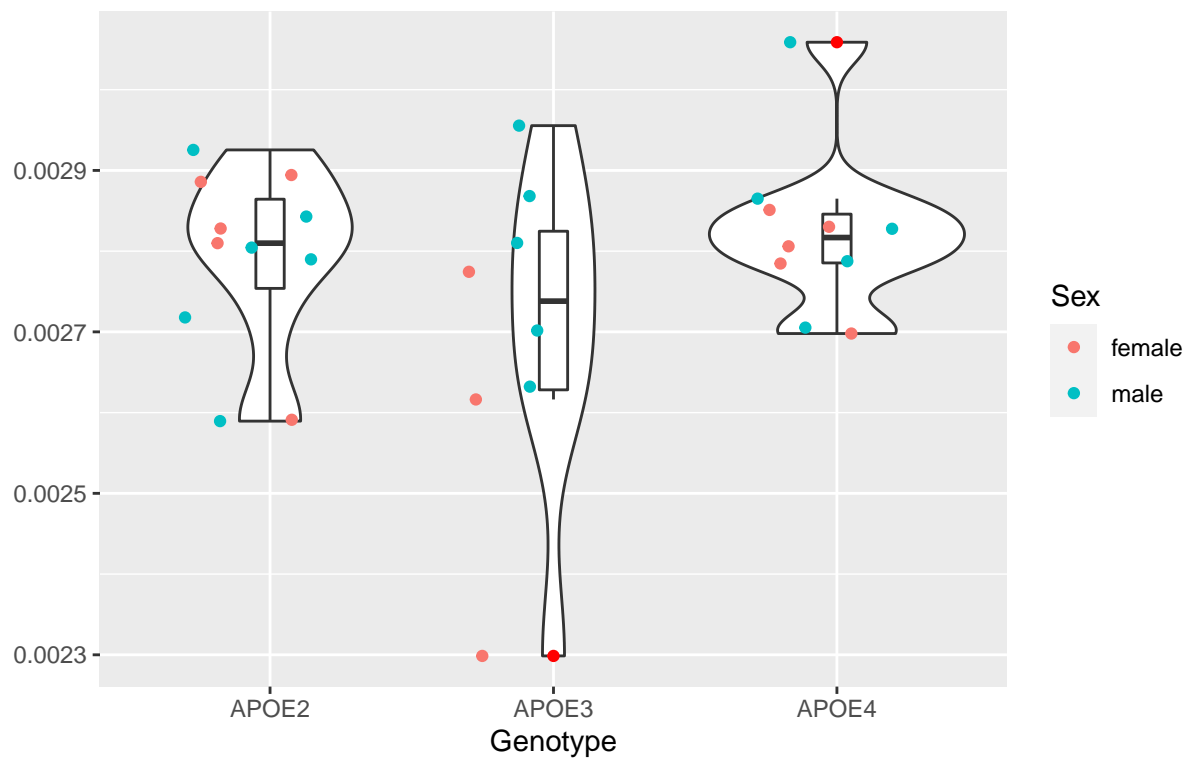
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#“{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) #“
```

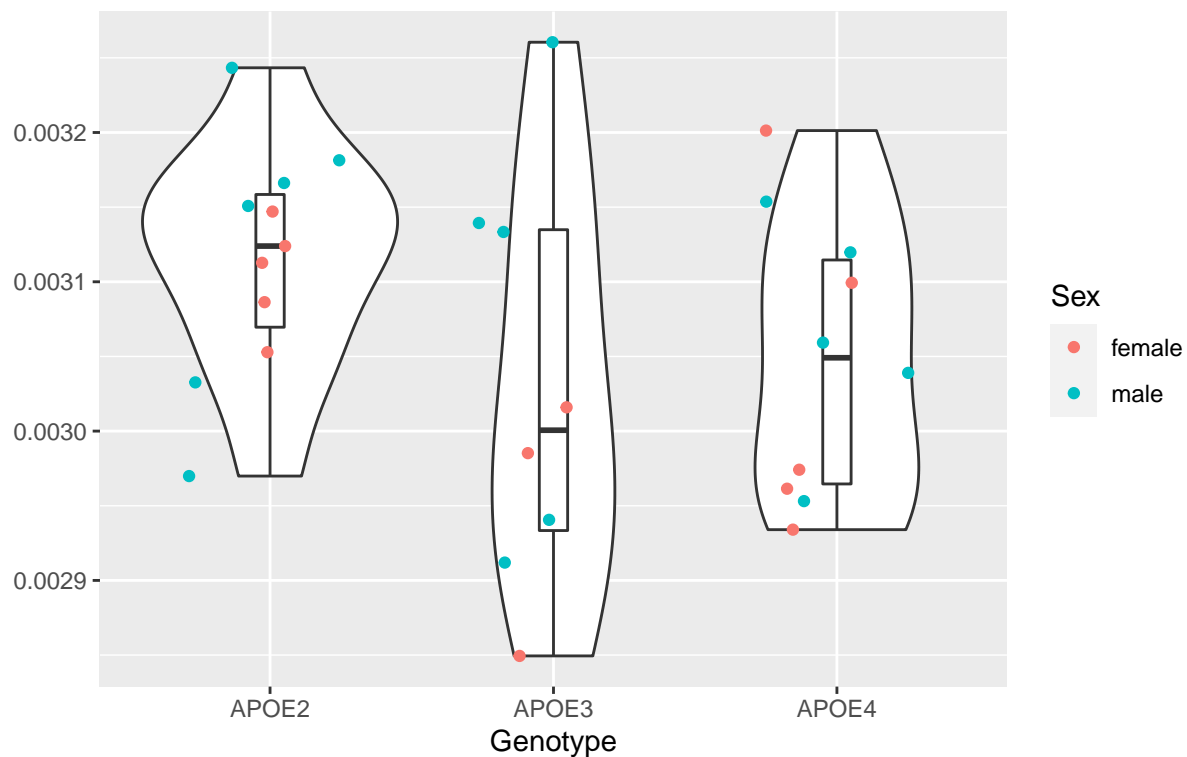
Parabrachial Nucleus

Red points denoting outliers



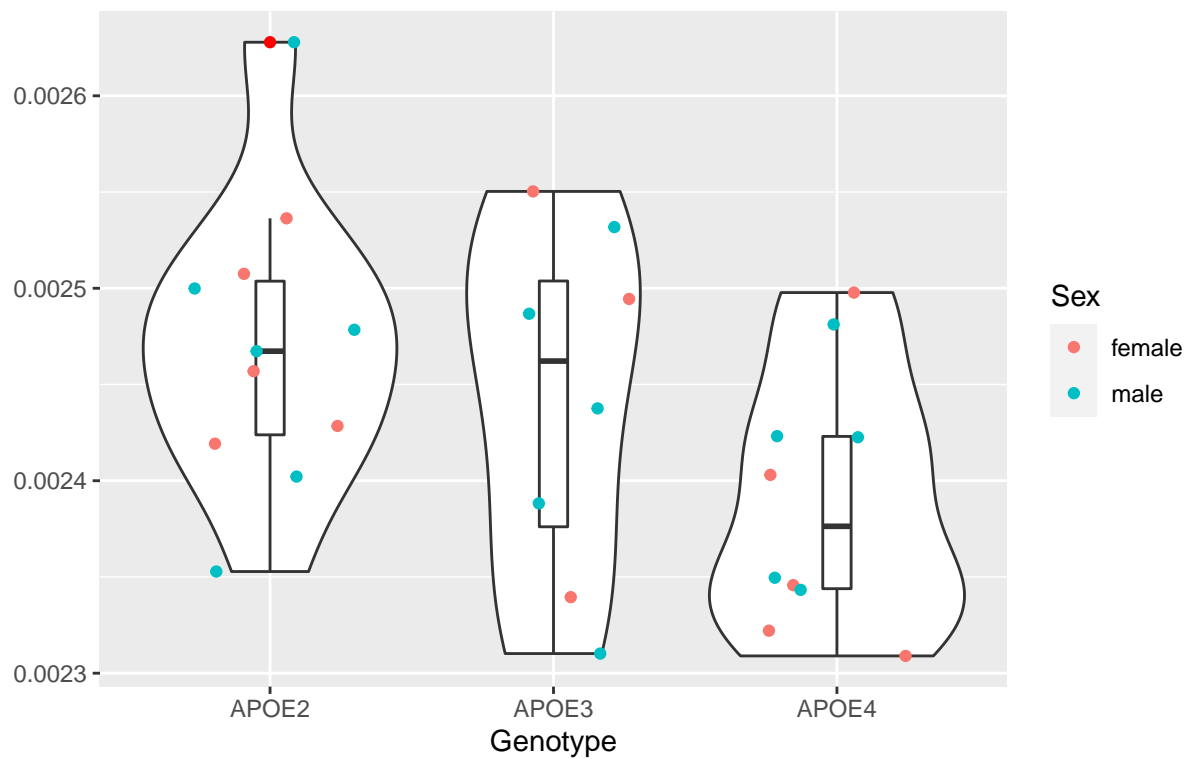
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.040e-08	3.018e-08	1.562	0.229
## Residuals	26	5.024e-07	1.932e-08		

Parabrachial Medial Nucleus and Koelliker Fuse Nucleus Red points denoting outliers

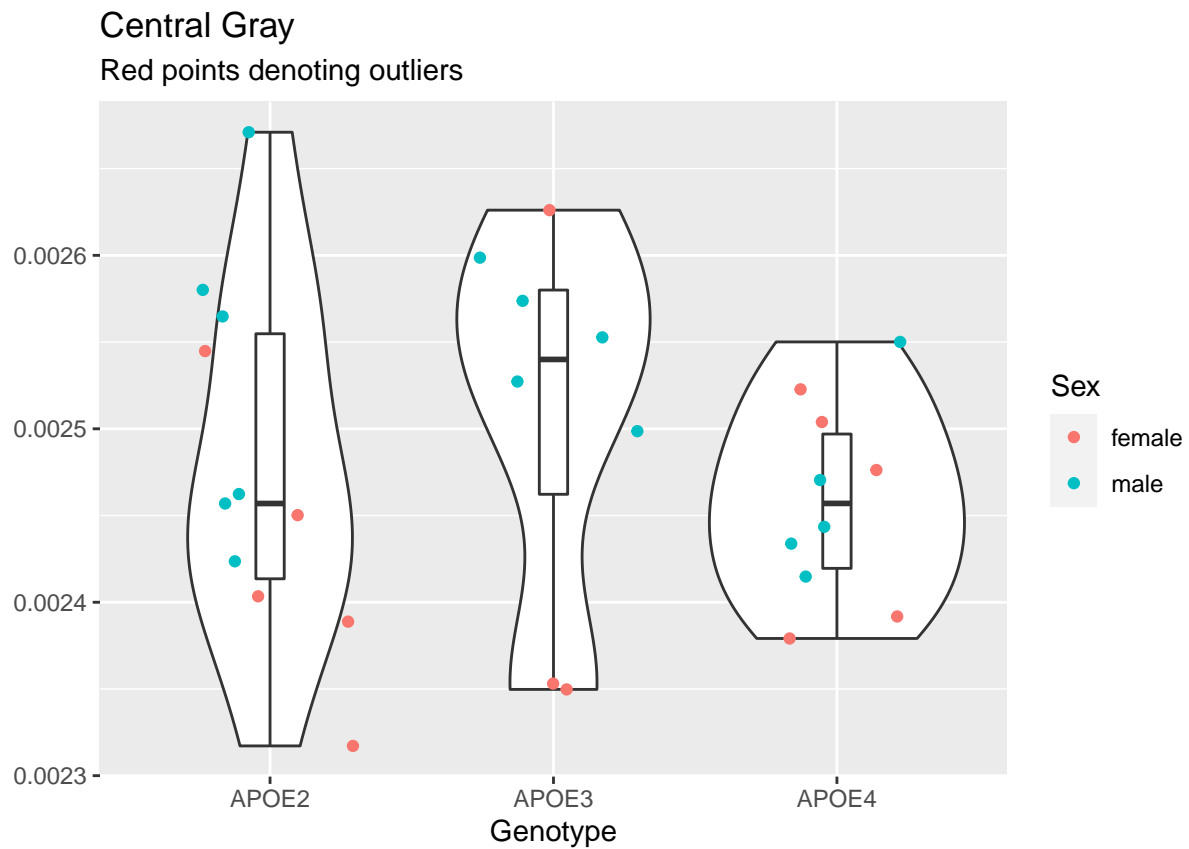


##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.973e-08	1.986e-08	1.924	0.166
## Residuals	26	2.685e-07	1.033e-08		

Parvicellular Reticular Nucleus and Principal Sensory Trigeminal Nucleus Red points denoting outliers

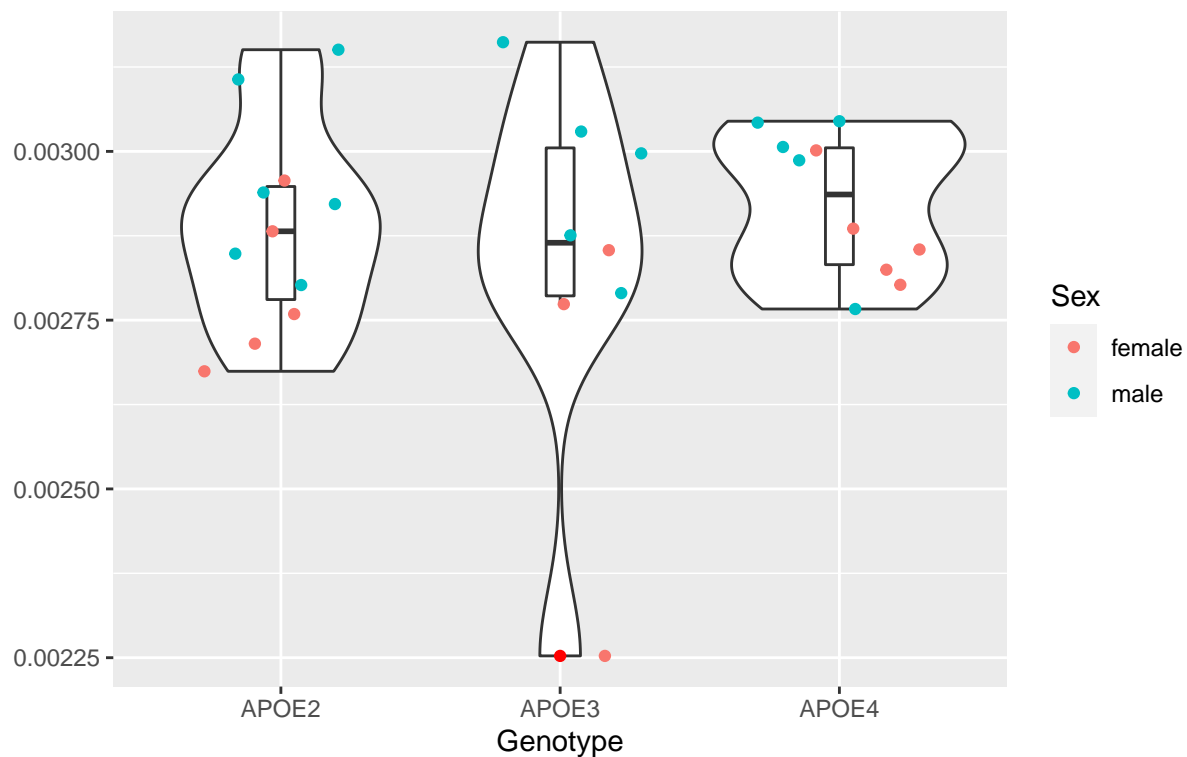


```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 3.487e-08 1.744e-08   3.042  0.065 .
## Residuals    26 1.490e-07 5.732e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 1.178e-08 5.891e-09   0.729  0.492
## Residuals 26 2.100e-07 8.076e-09
```

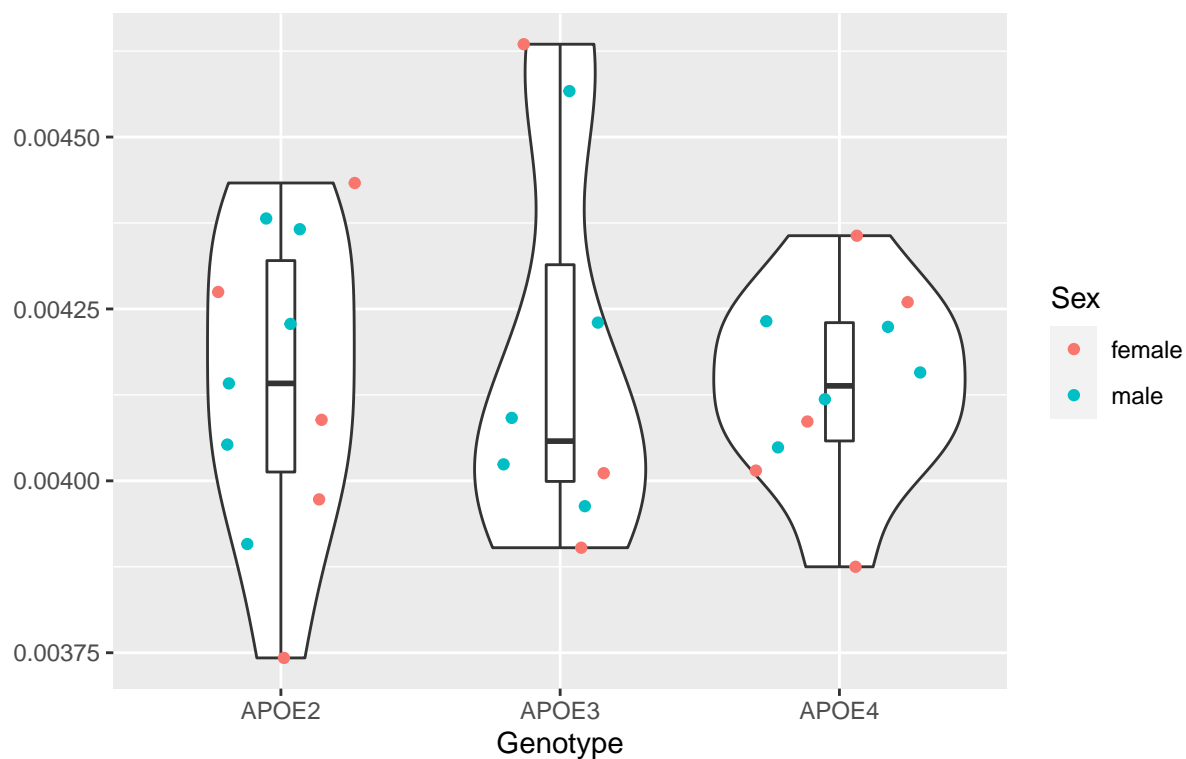
Pedunculotegmental Medial Paralemniscial and Supratrigeminal Nuclei Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.830e-08	1.417e-08	0.436	0.651
## Residuals	26	8.448e-07	3.249e-08		

Motor Root of Trigeminal Nerve

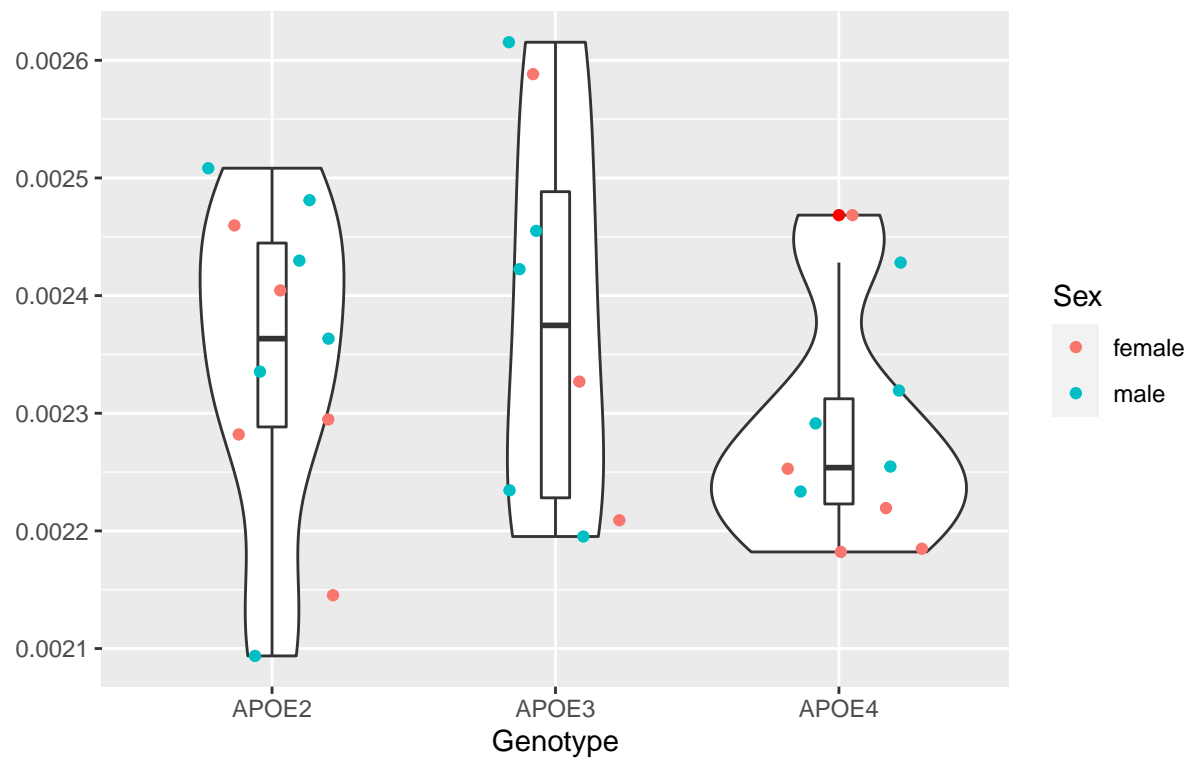
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.200e-09	4.090e-09	0.089	0.915
## Residuals	26	1.189e-06	4.574e-08		

Trigeminal Motor Nucleus

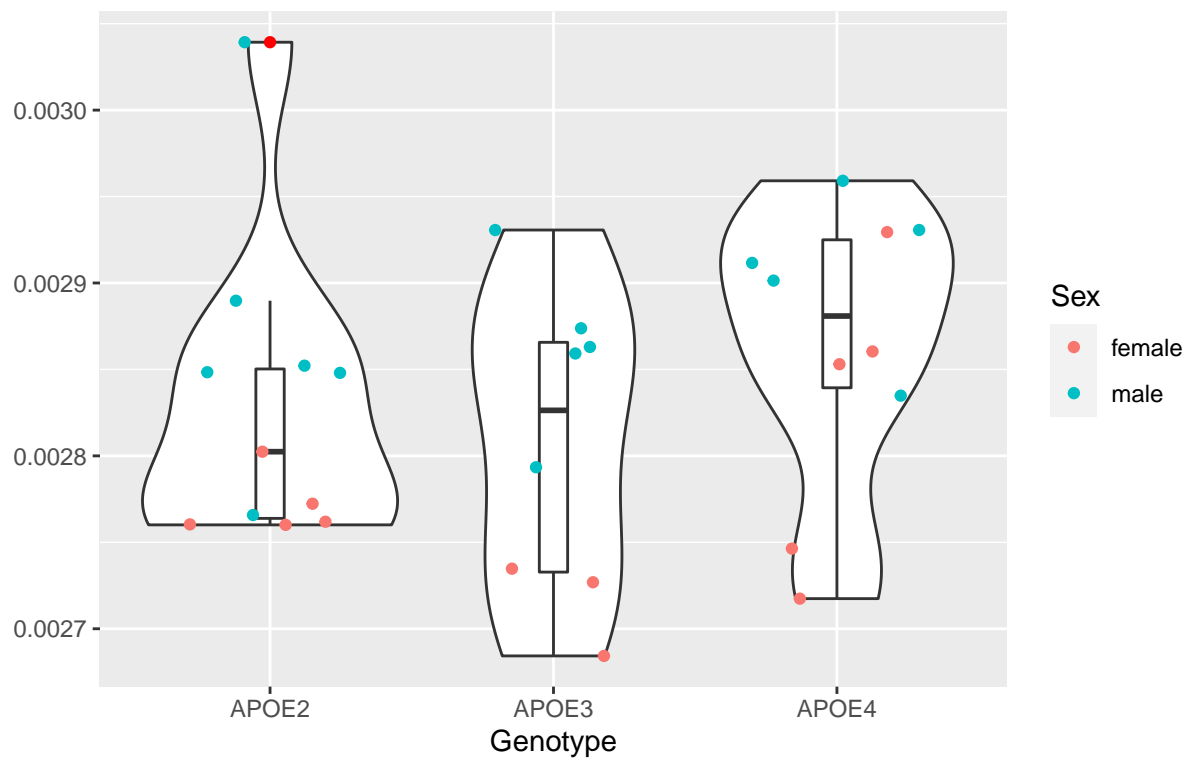
Red points denoting outliers



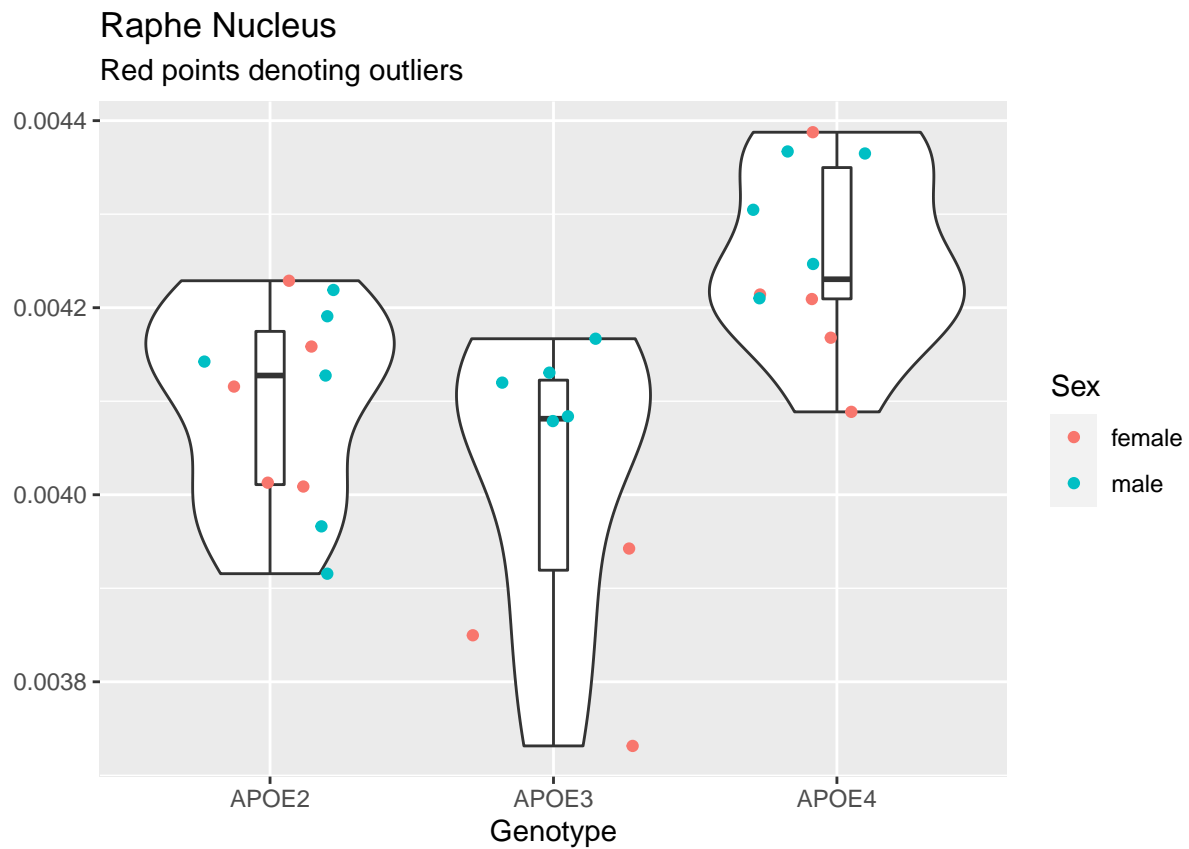
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.450e-08	2.225e-08	1.265	0.299
## Residuals	26	4.574e-07	1.759e-08		

Pontine Reticular Nucleus

Red points denoting outliers



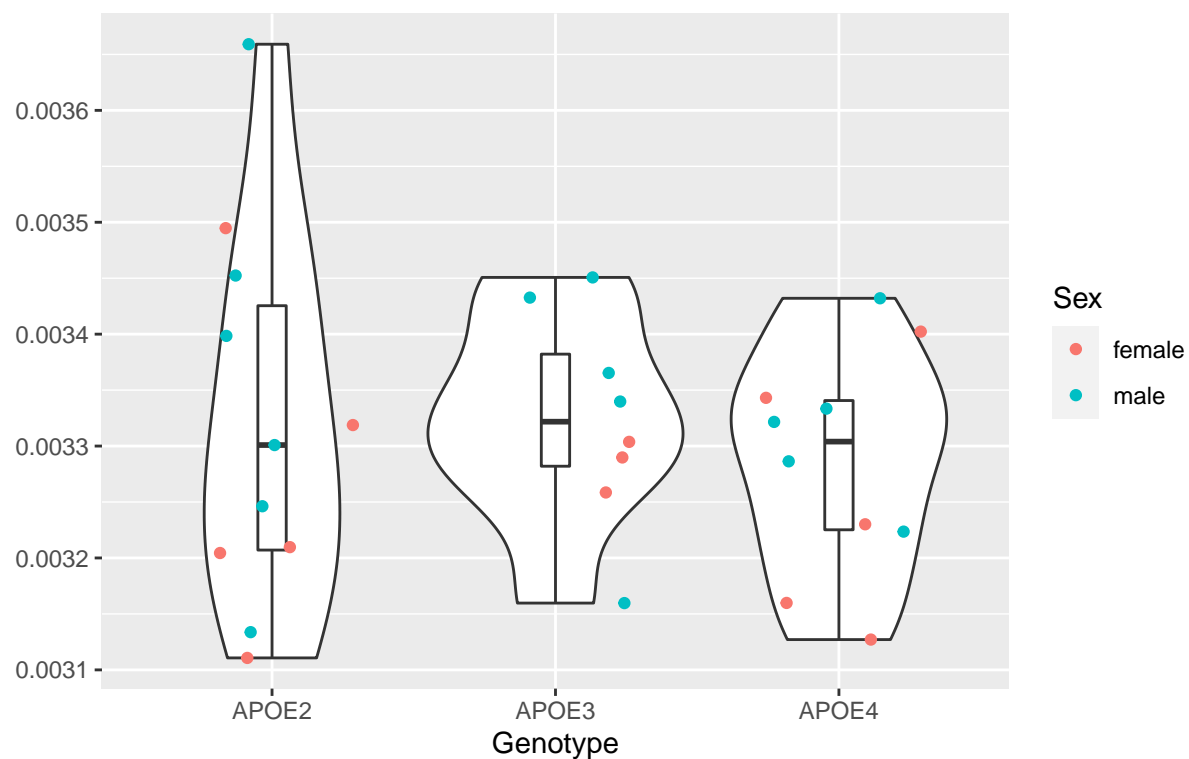
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.503e-08	7.514e-09	1.078	0.355
## Residuals	26	1.812e-07	6.970e-09		



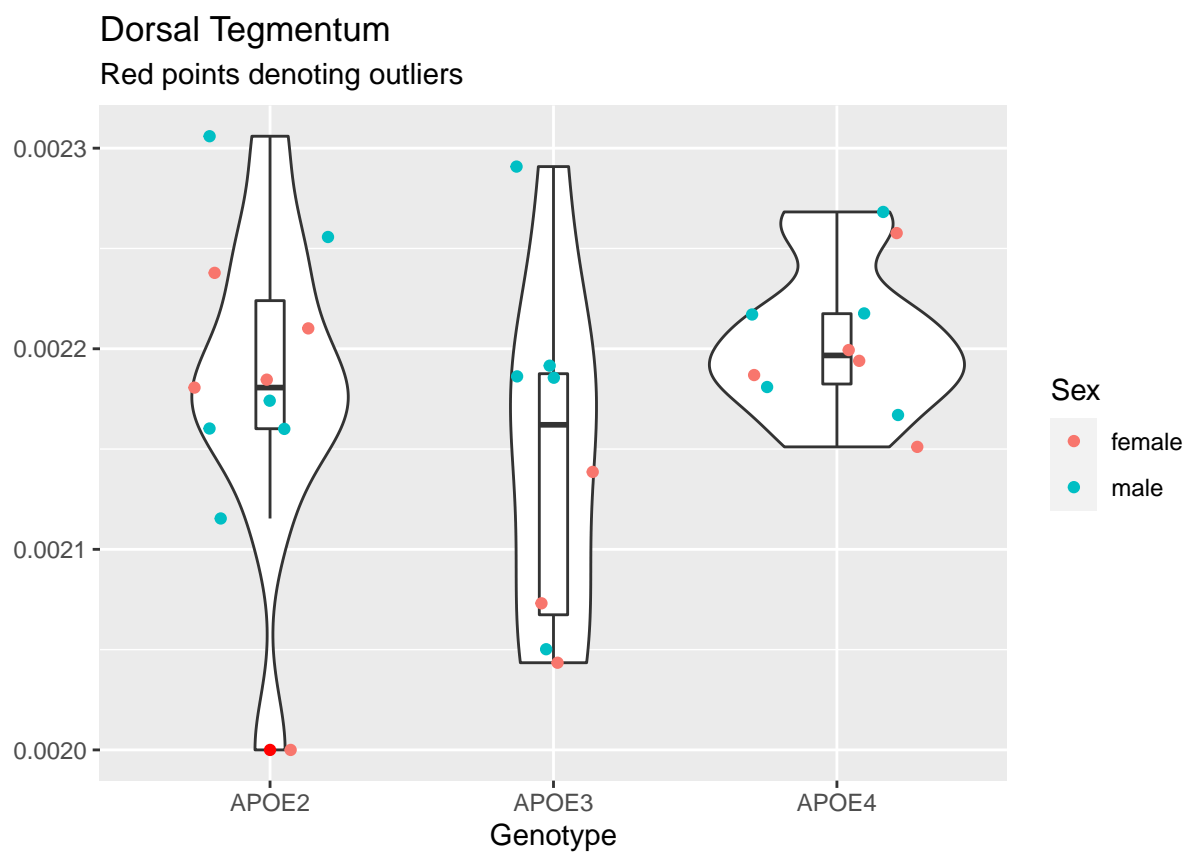
```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 2.794e-07 1.397e-07    9.87 0.000647 ***
## Residuals    26 3.680e-07 1.415e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Trigeminal Sensory Nucleus

Red points denoting outliers

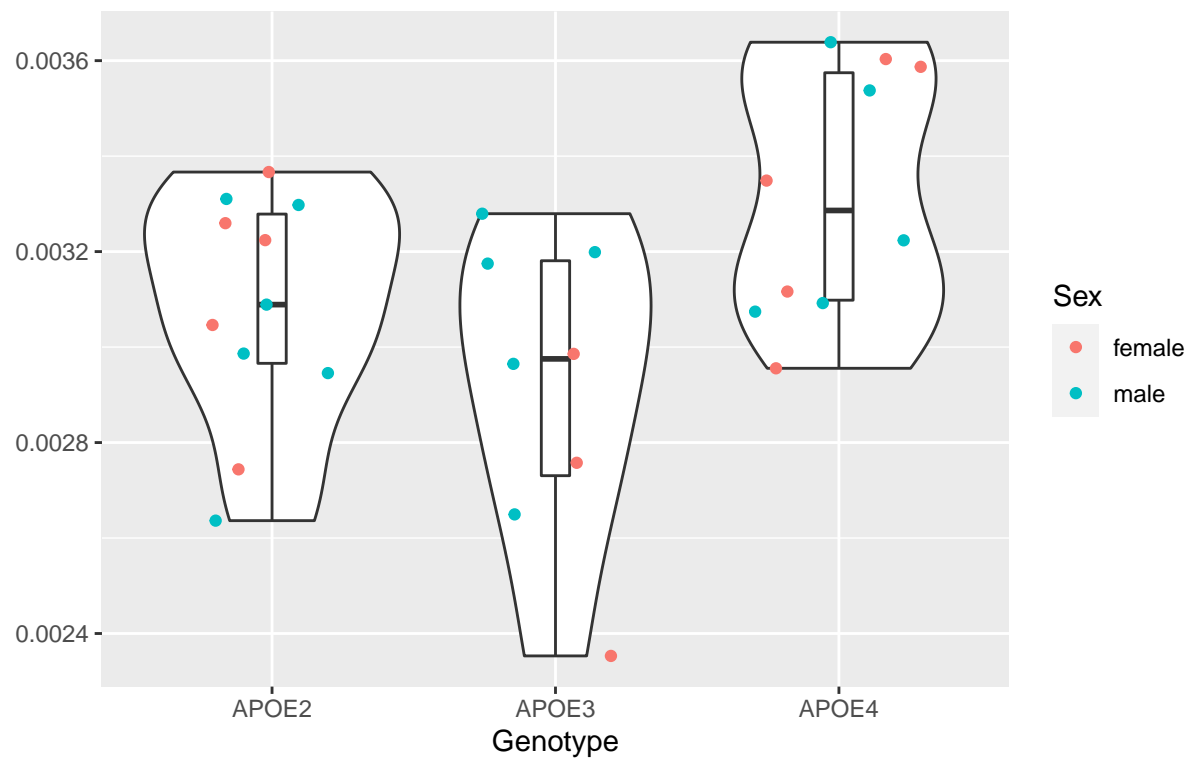


##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.900e-09	4.444e-09	0.268	0.767
## Residuals	26	4.316e-07	1.660e-08		



Tegmental Nucleus

Red points denoting outliers



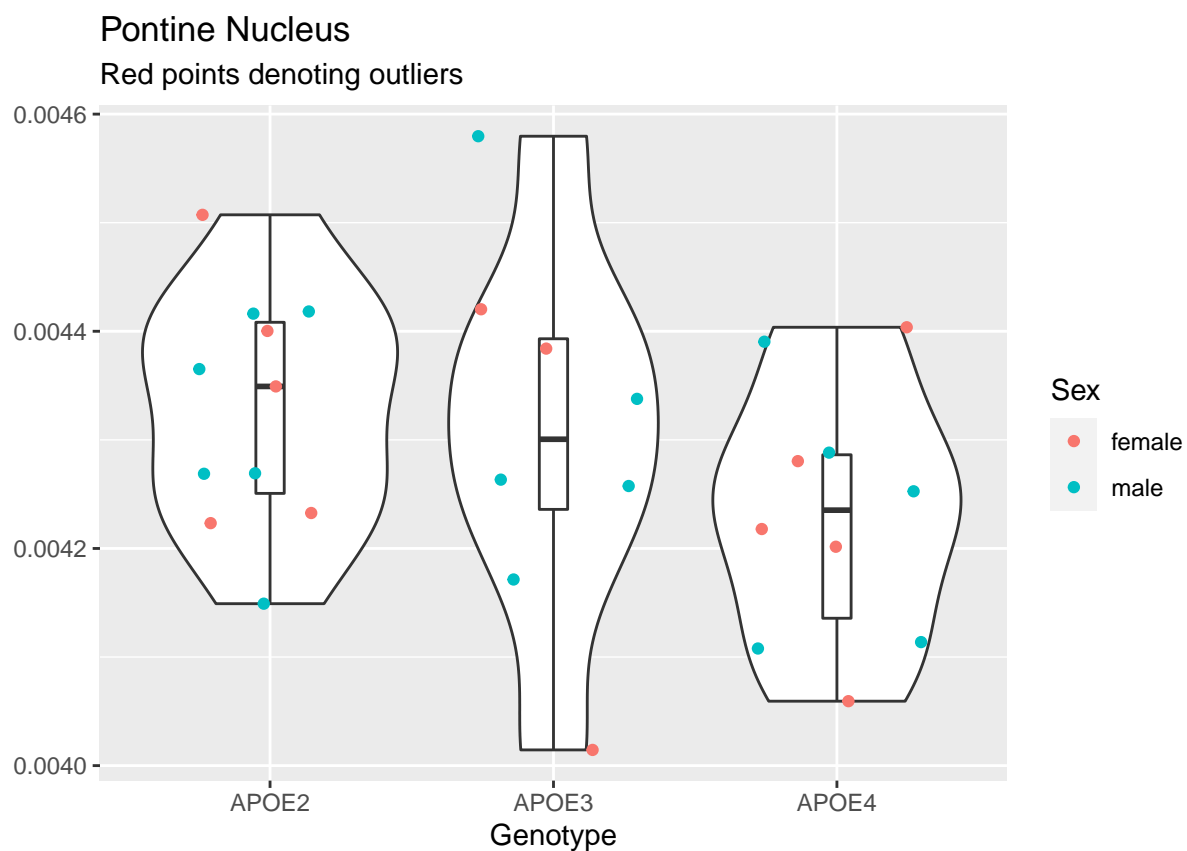
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 7.249e-07 3.625e-07   5.041 0.0141 *
## Residuals    26 1.870e-06 7.190e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cochlear Nucleus

Red points denoting outliers



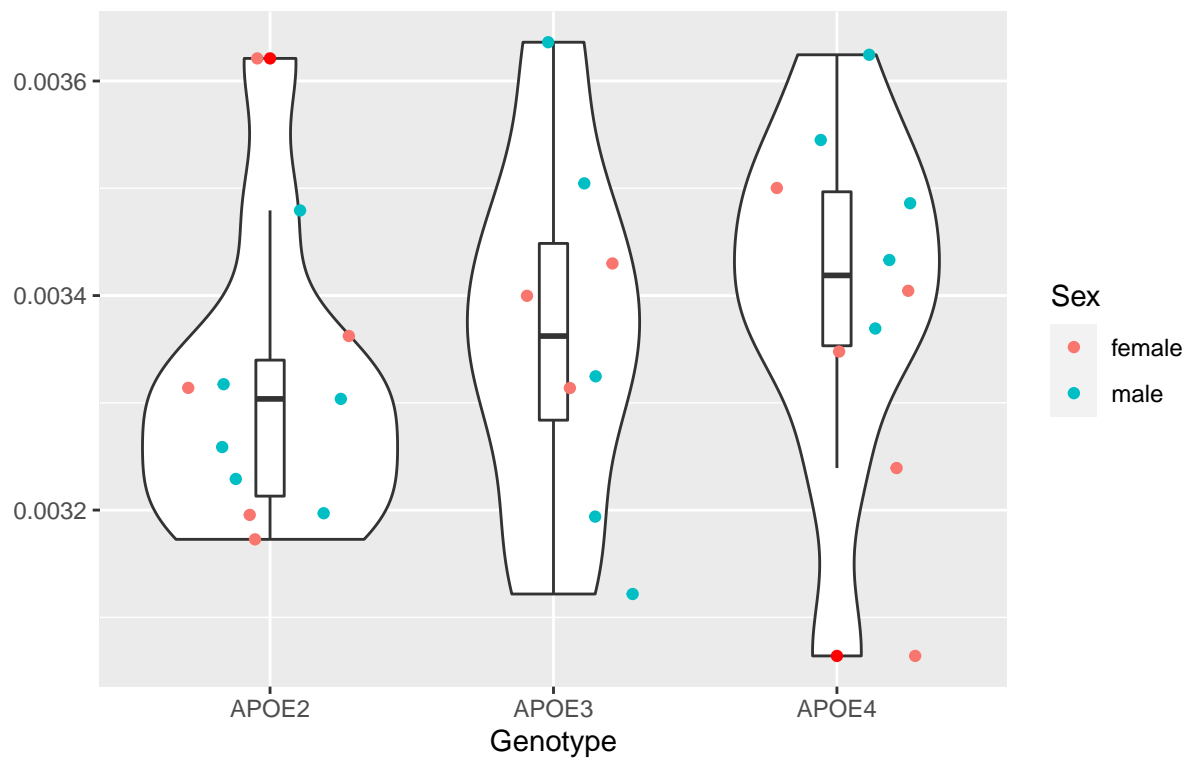
```
##           Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.205e-07 6.026e-08   2.635 0.0908 .
## Residuals    26 5.948e-07 2.288e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 5.070e-08 2.535e-08   1.507   0.24
## Residuals 26 4.372e-07 1.682e-08
```

Reticulotegmental Nucleus of Pons

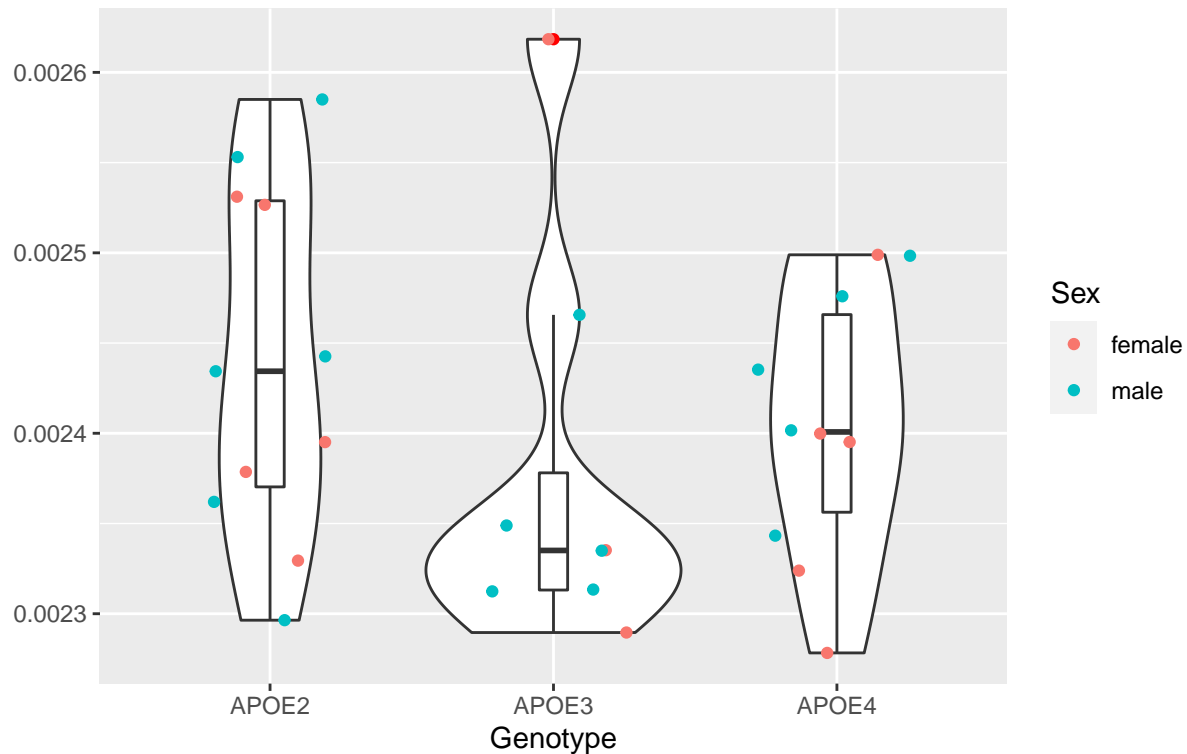
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 4.090e-08 2.043e-08   0.877  0.428
## Residuals 26 6.055e-07 2.329e-08
```

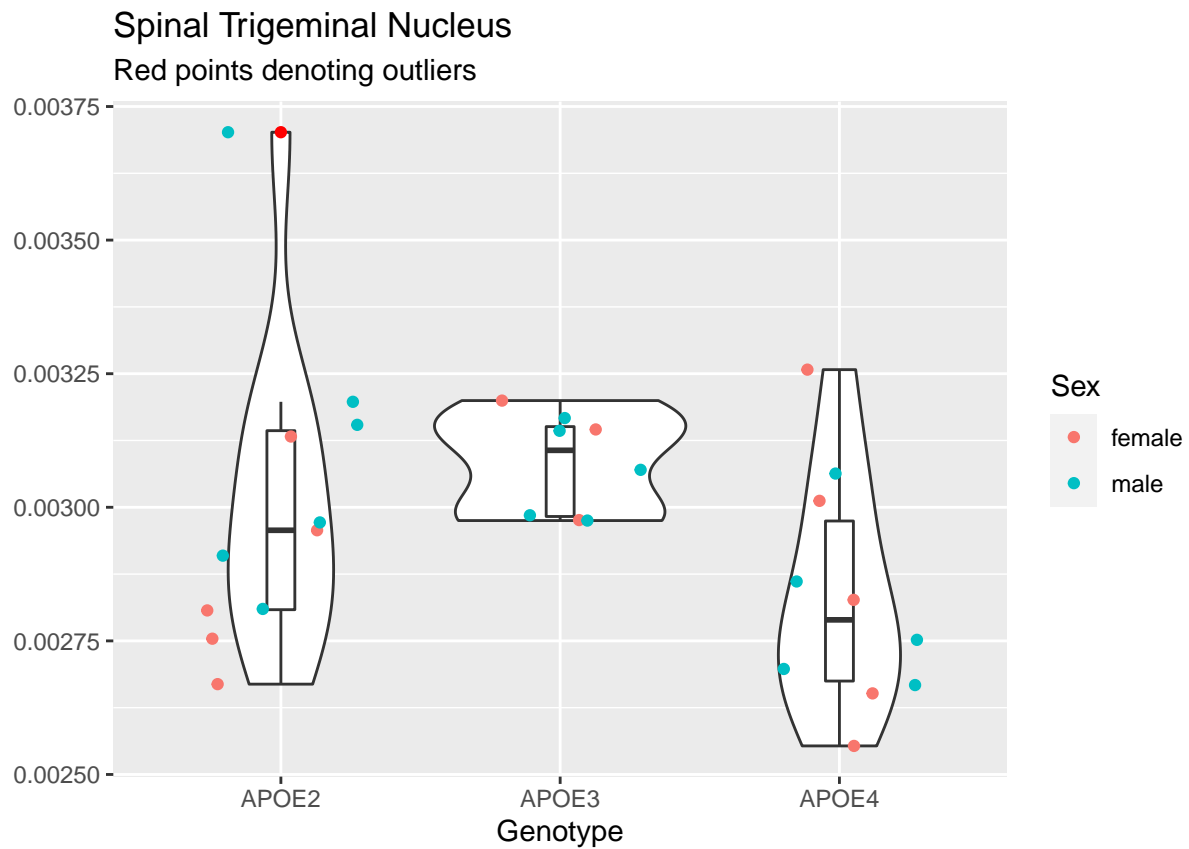
Olivary Complex

Red points denoting outliers



```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## geno       2 1.835e-08 9.176e-09   1.034   0.37
## Residuals 26 2.307e-07 8.873e-09
```

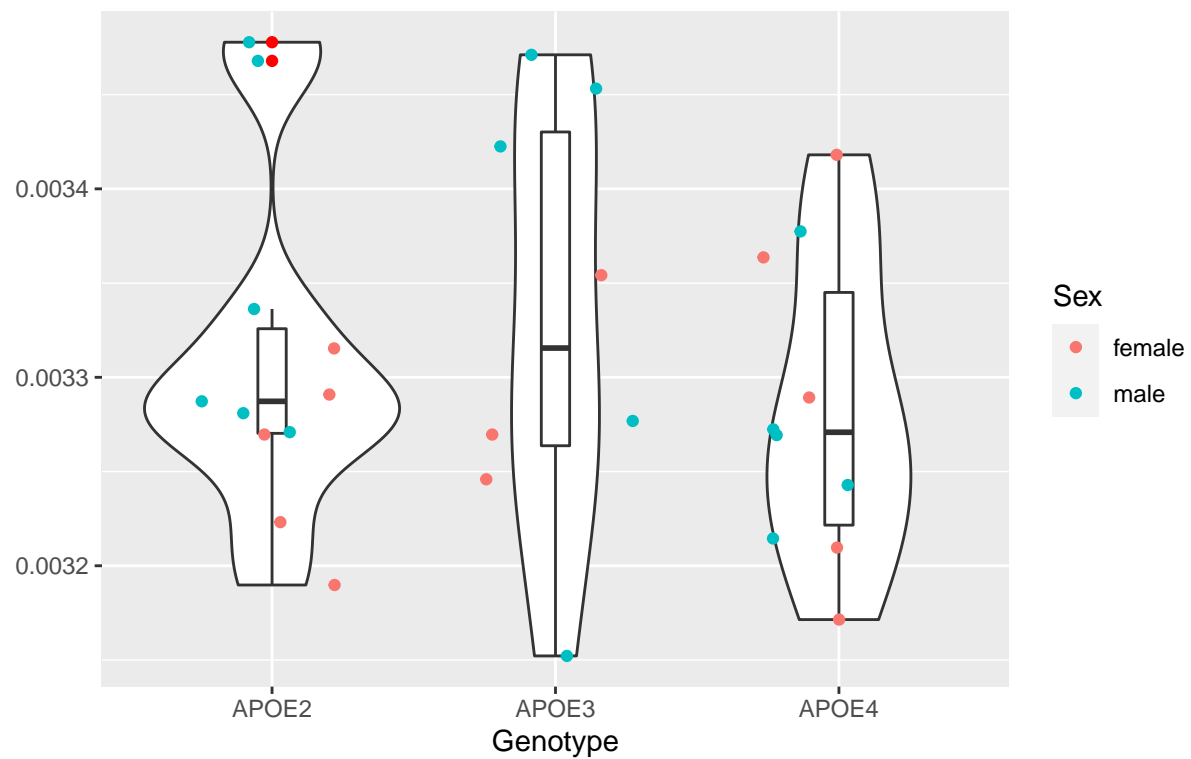
```
##“{r PnRt, echo = FALSE} #ggplot(data = new, aes(factor(geno), PnRt)) + # geom_violin() + #
geom_boxplot(width = 0.1, outlier.color = “red”) + # geom_jitter(height = 0, width = 0.3) + # labs(x =
“Genotype”, # y = “”, # title = “Pontine Reticular Nucleus“, # subtitle = “Red points denoting outliers”)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



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 2.999e-07 1.499e-07   2.959 0.0695 .
## Residuals    26 1.317e-06 5.067e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Vestibular Nuclei

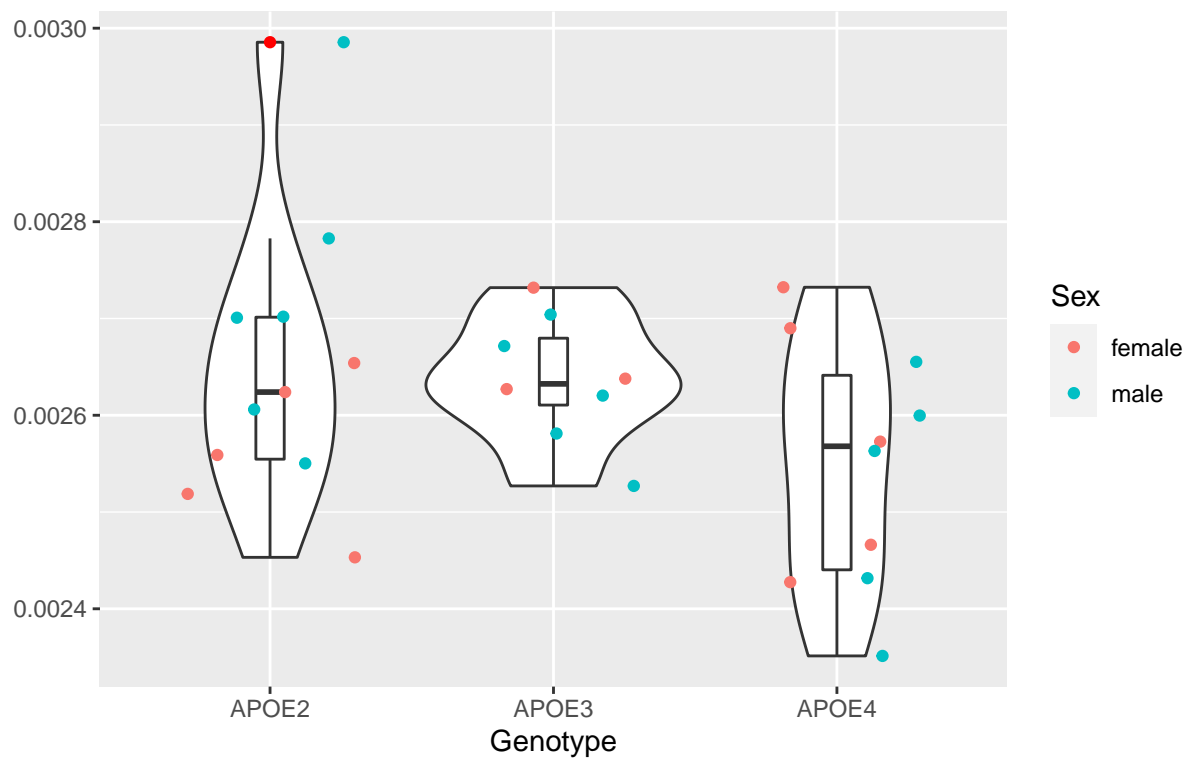
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 1.041e-08 5.204e-09   0.593   0.56
## Residuals 26 2.282e-07 8.778e-09
```


Gigantocellular Reticular Nucleus

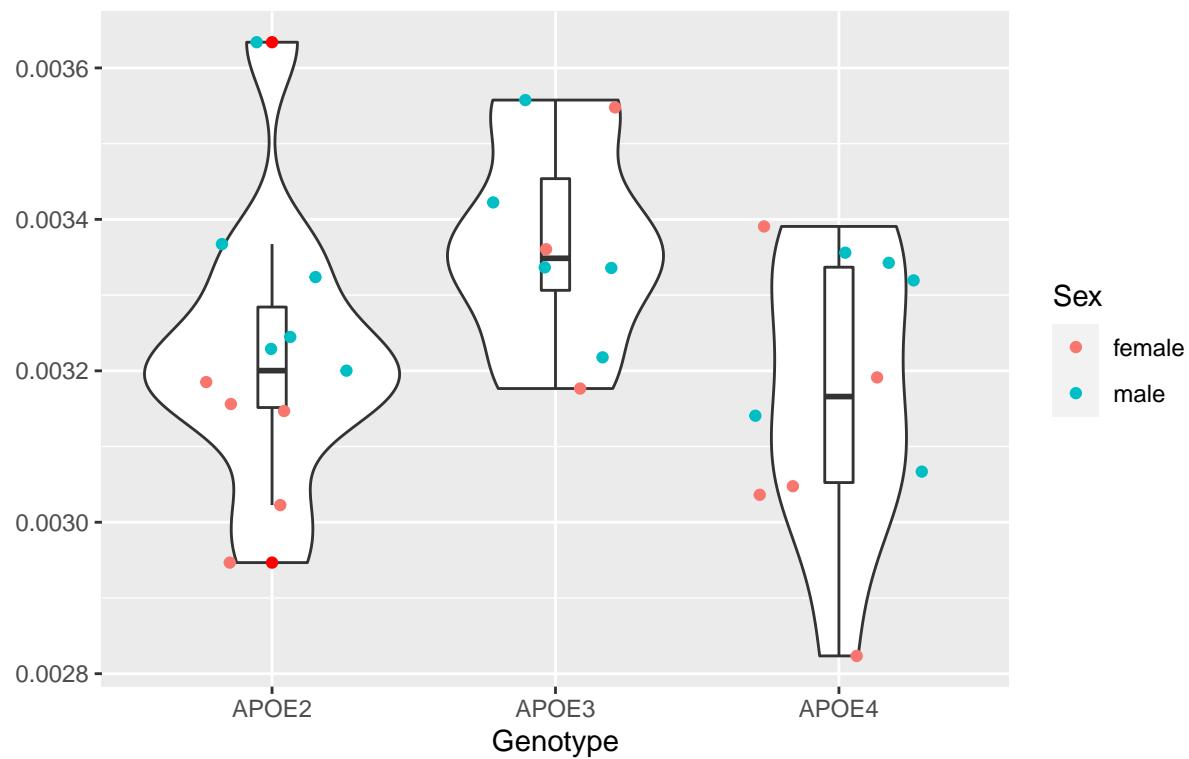
Red points denoting outliers



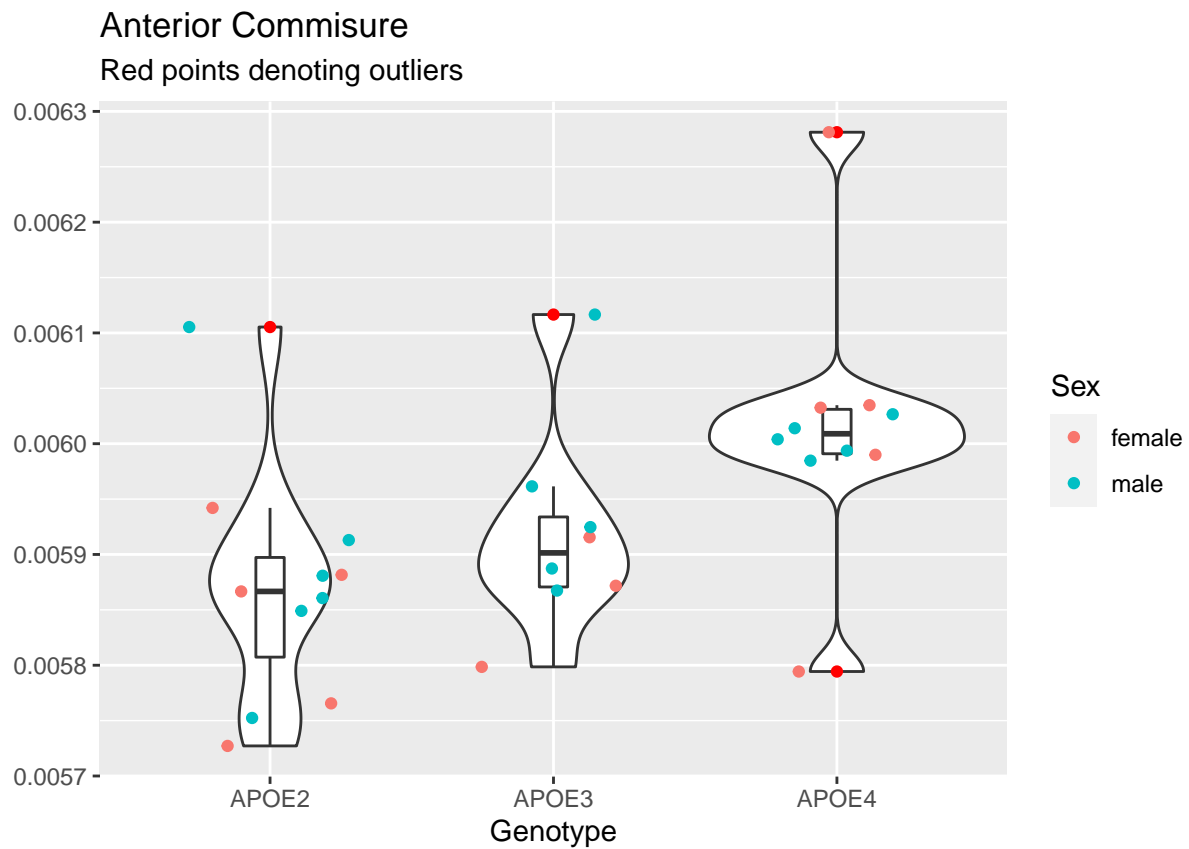
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	5.980e-08	2.990e-08	2.019	0.153
## Residuals	26	3.852e-07	1.481e-08		

Cuneate Nucleus

Red points denoting outliers



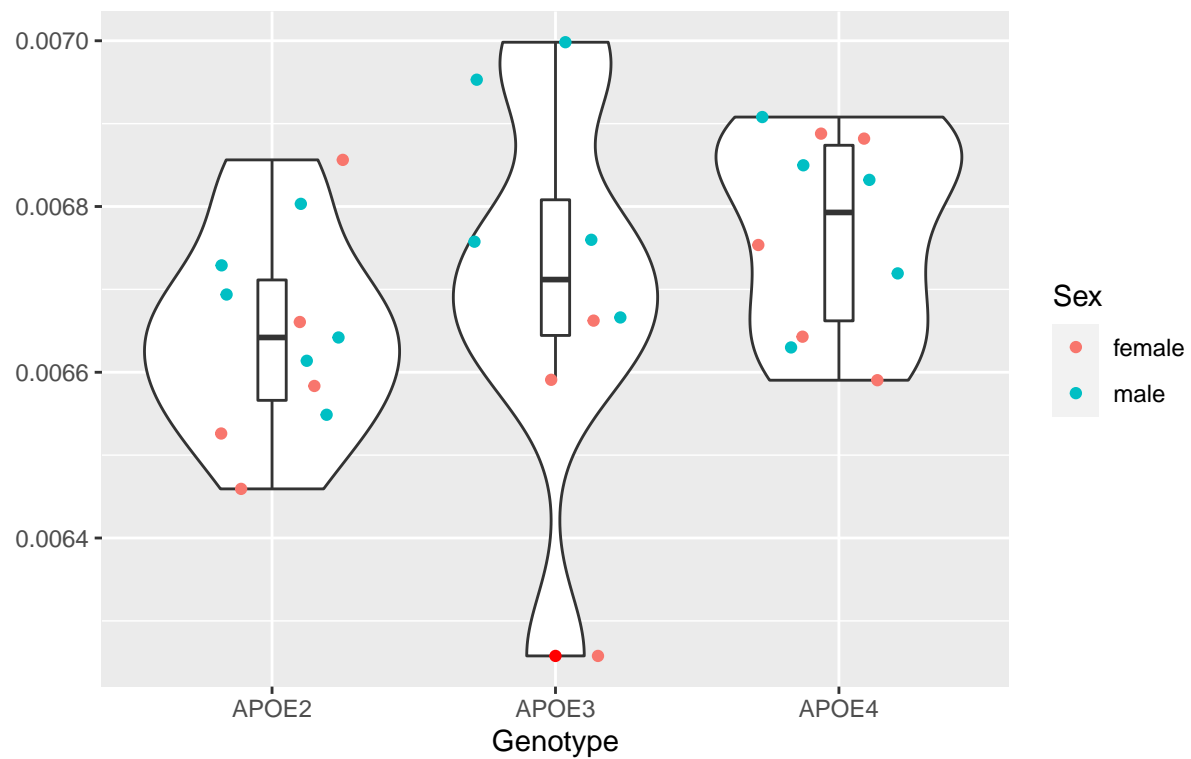
```
##          Df    Sum Sq Mean Sq F value Pr(>F)
## geno      2 1.830e-07 9.15e-08   3.123 0.0609 .
## Residuals 26 7.619e-07 2.93e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



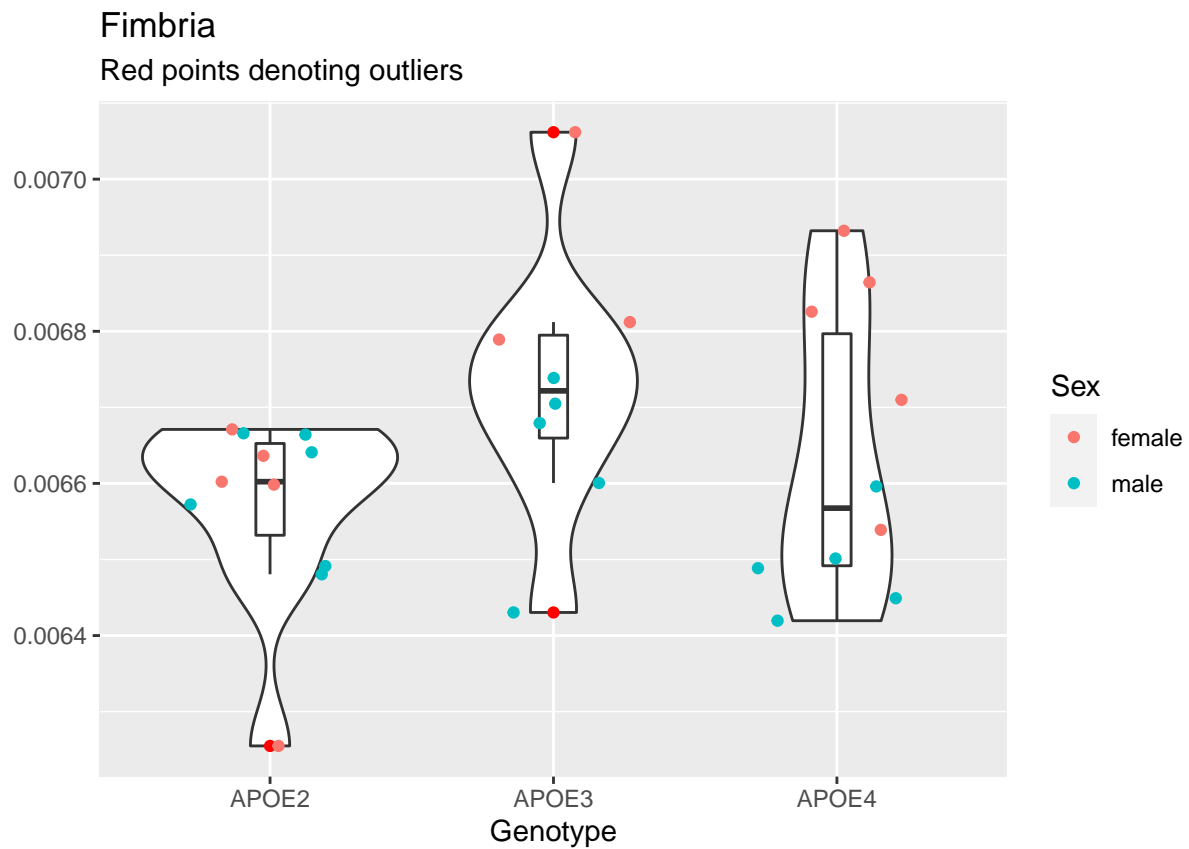
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.170e-07 5.849e-08   5.206 0.0125 *
## Residuals    26 2.921e-07 1.123e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Optic Tracts

Red points denoting outliers



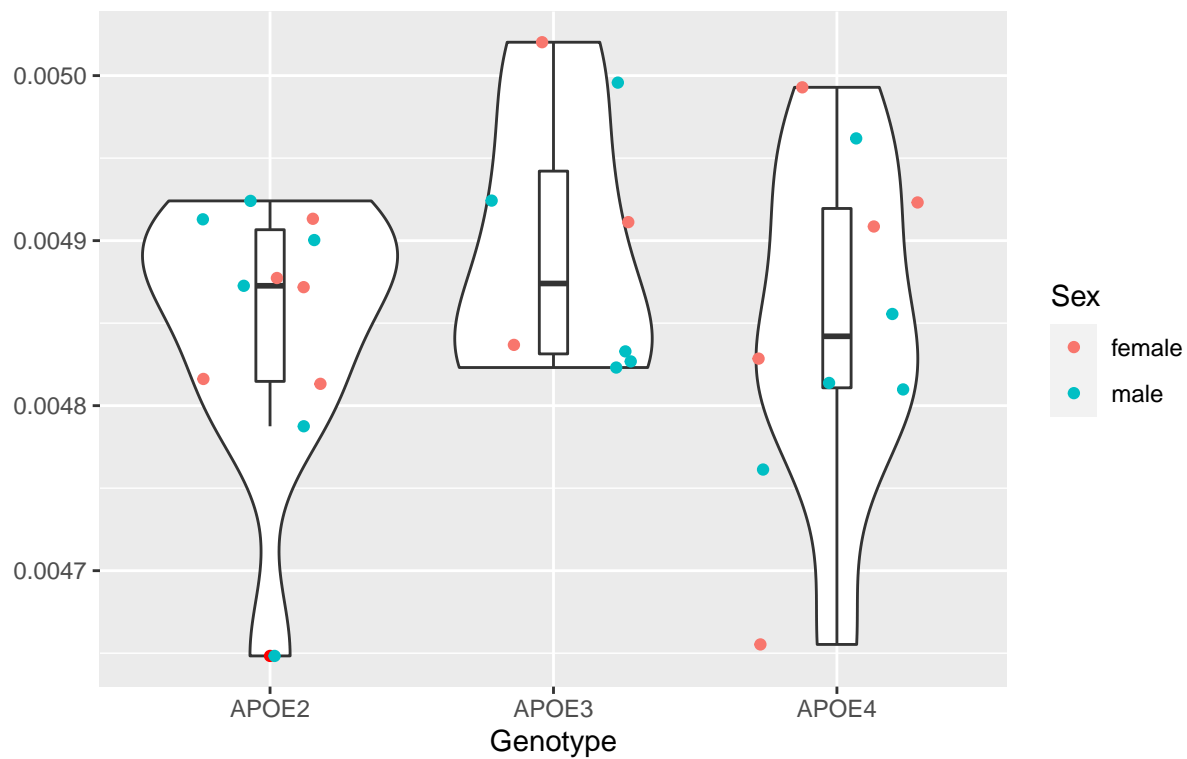
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.880e-08	3.940e-08	1.605	0.22
## Residuals	26	6.382e-07	2.455e-08		



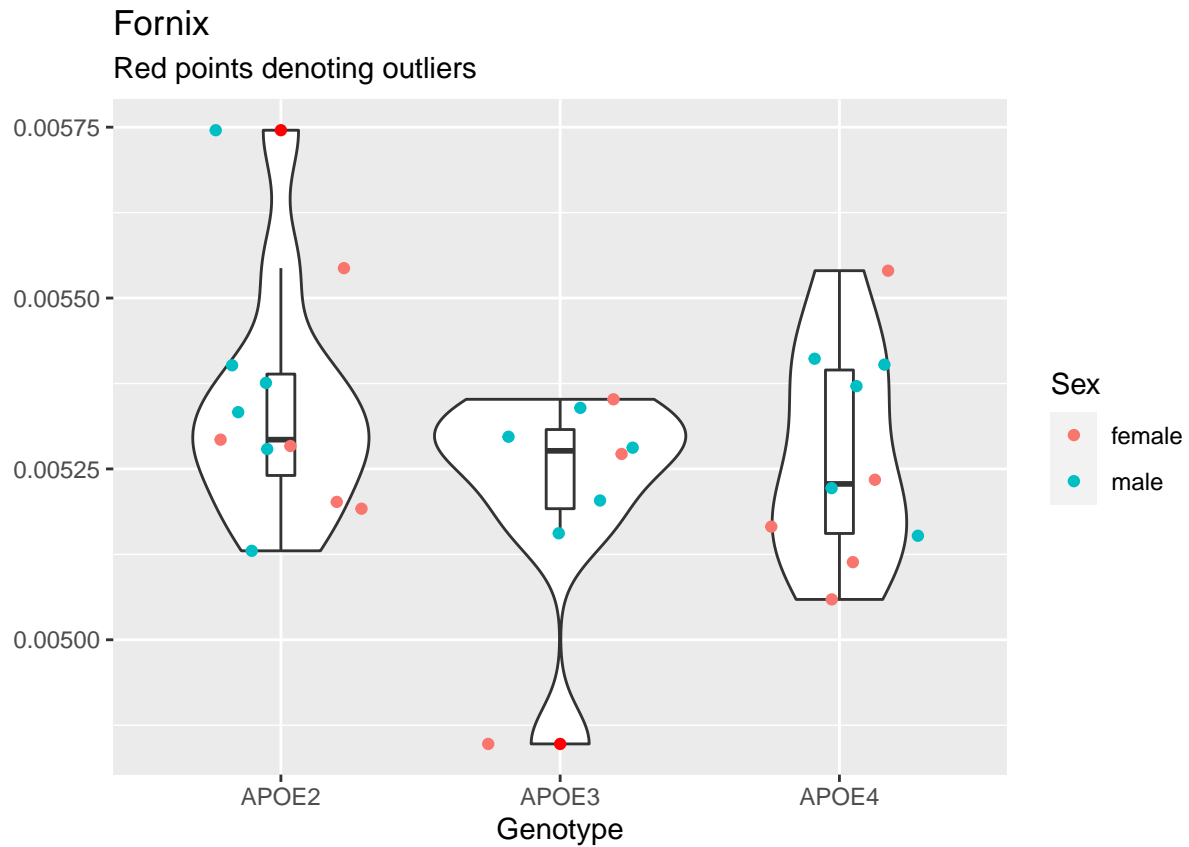
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 1.133e-07 5.666e-08    2.113  0.141
## Residuals 26 6.970e-07 2.681e-08
```

Corpus Callosum

Red points denoting outliers



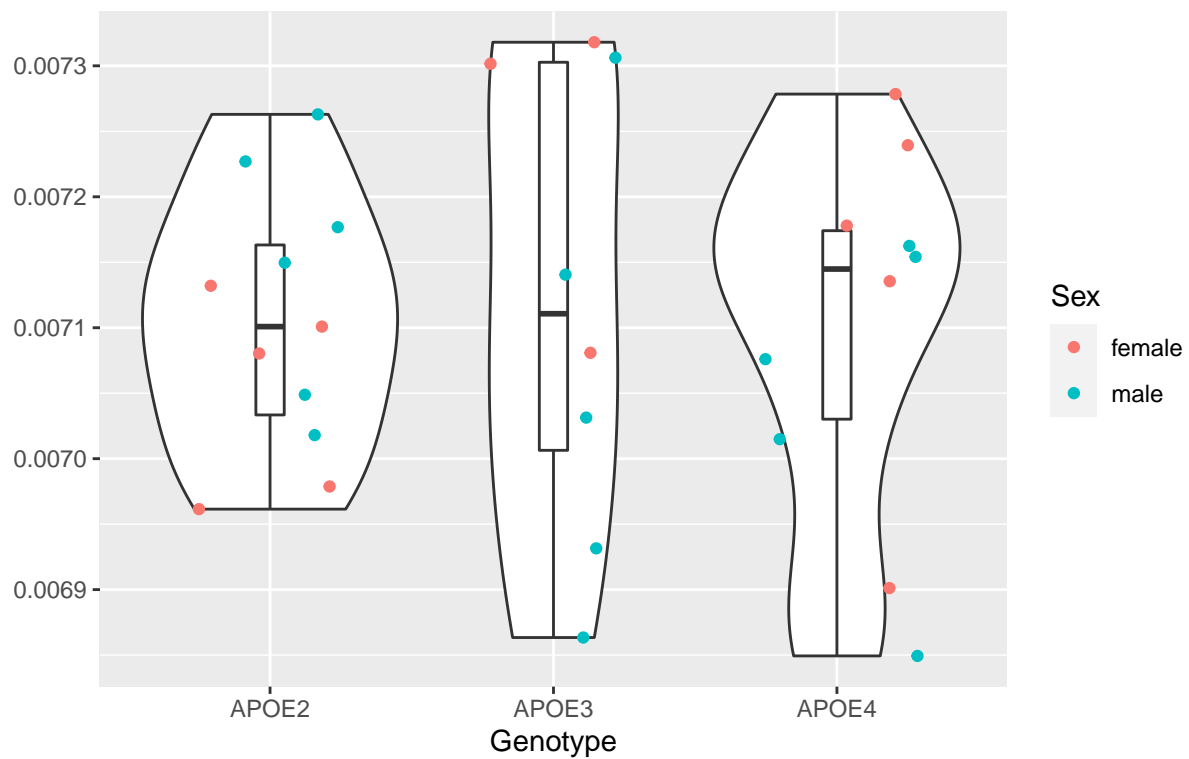
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 1.253e-08 6.265e-09   0.816  0.453
## Residuals 26 1.997e-07 7.680e-09
```



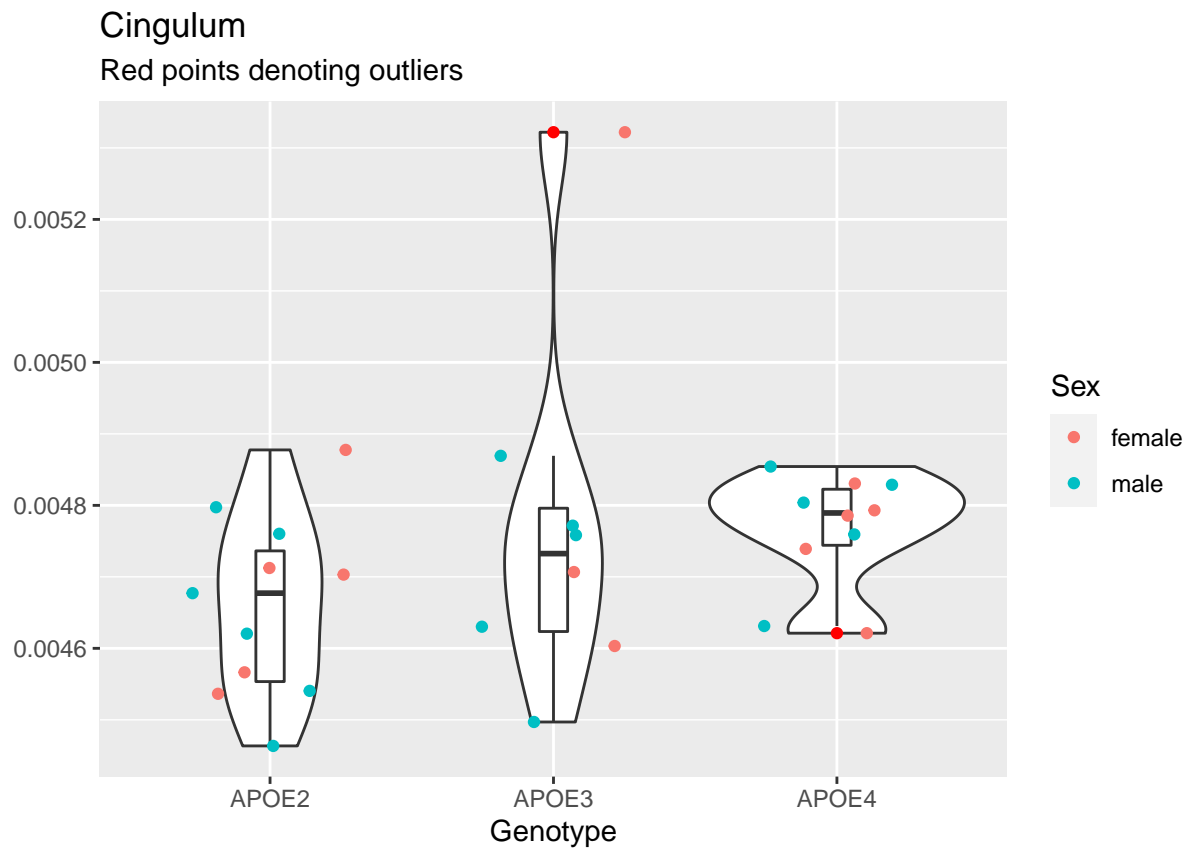
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.610e-08	3.803e-08	1.392	0.266
## Residuals	26	7.102e-07	2.732e-08		

Stria Terminalis

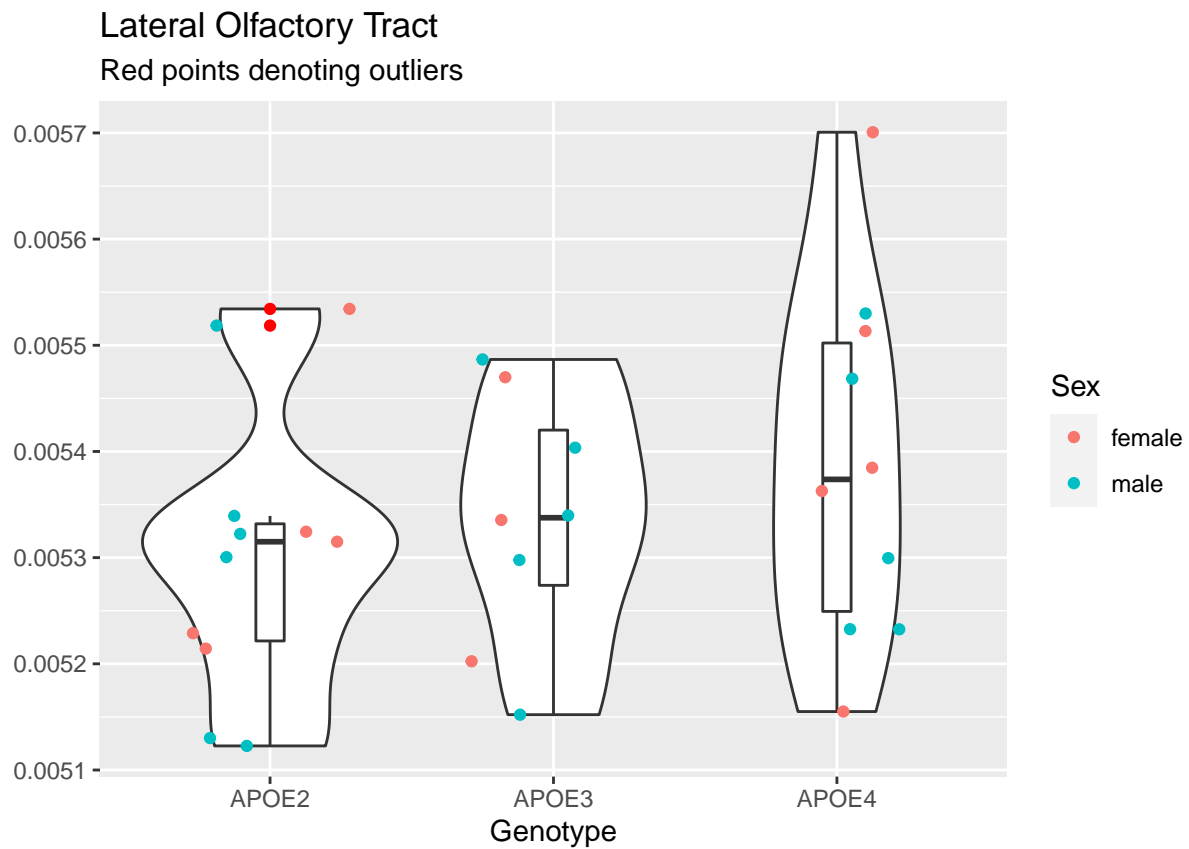
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.500e-09	1.262e-09	0.067	0.935
## Residuals	26	4.892e-07	1.882e-08		



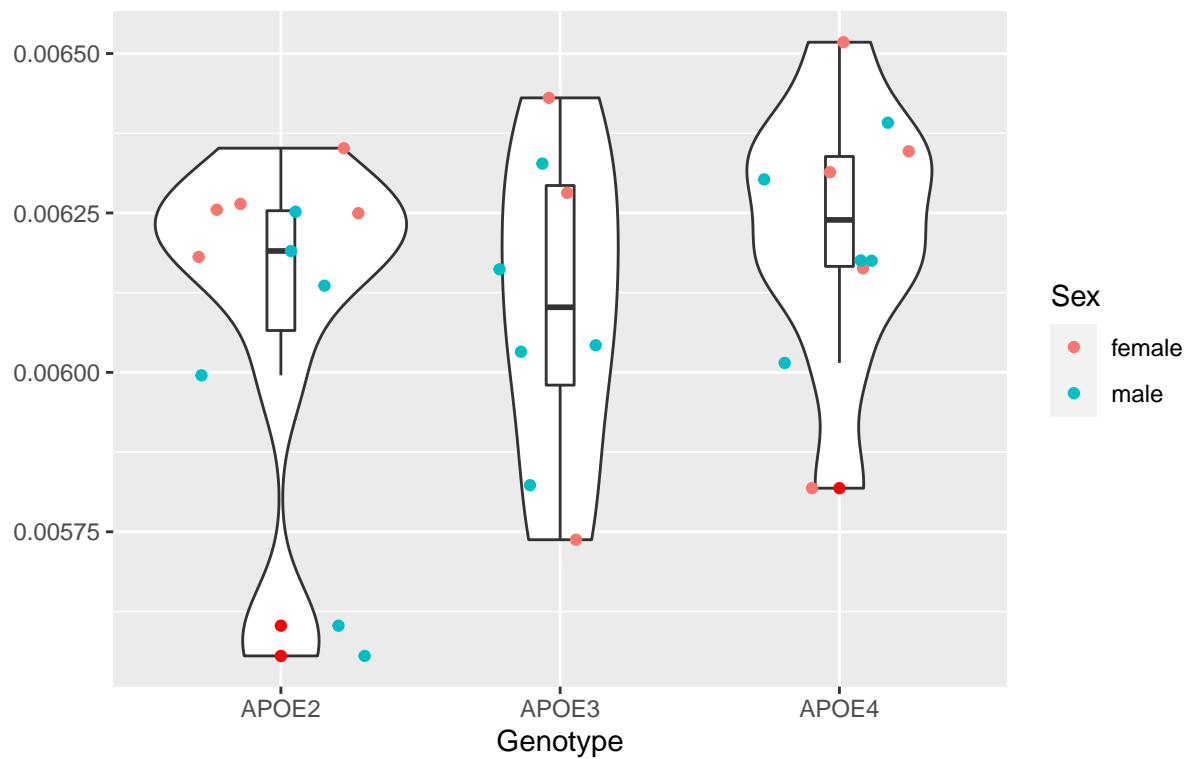
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.890e-08	3.944e-08	1.557	0.23
## Residuals	26	6.585e-07	2.533e-08		



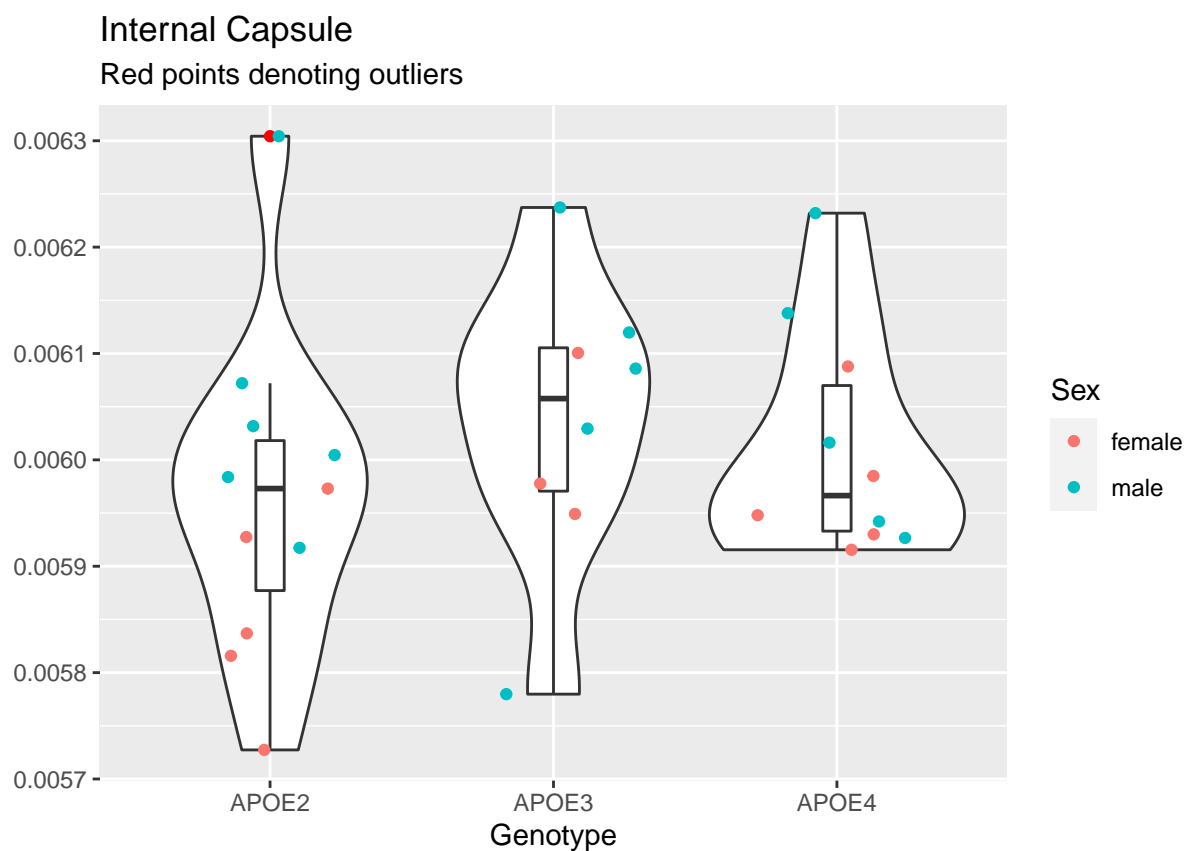
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.680e-08	1.842e-08	0.908	0.416
## Residuals	26	5.275e-07	2.029e-08		

Ventral Hippocampal Commissure

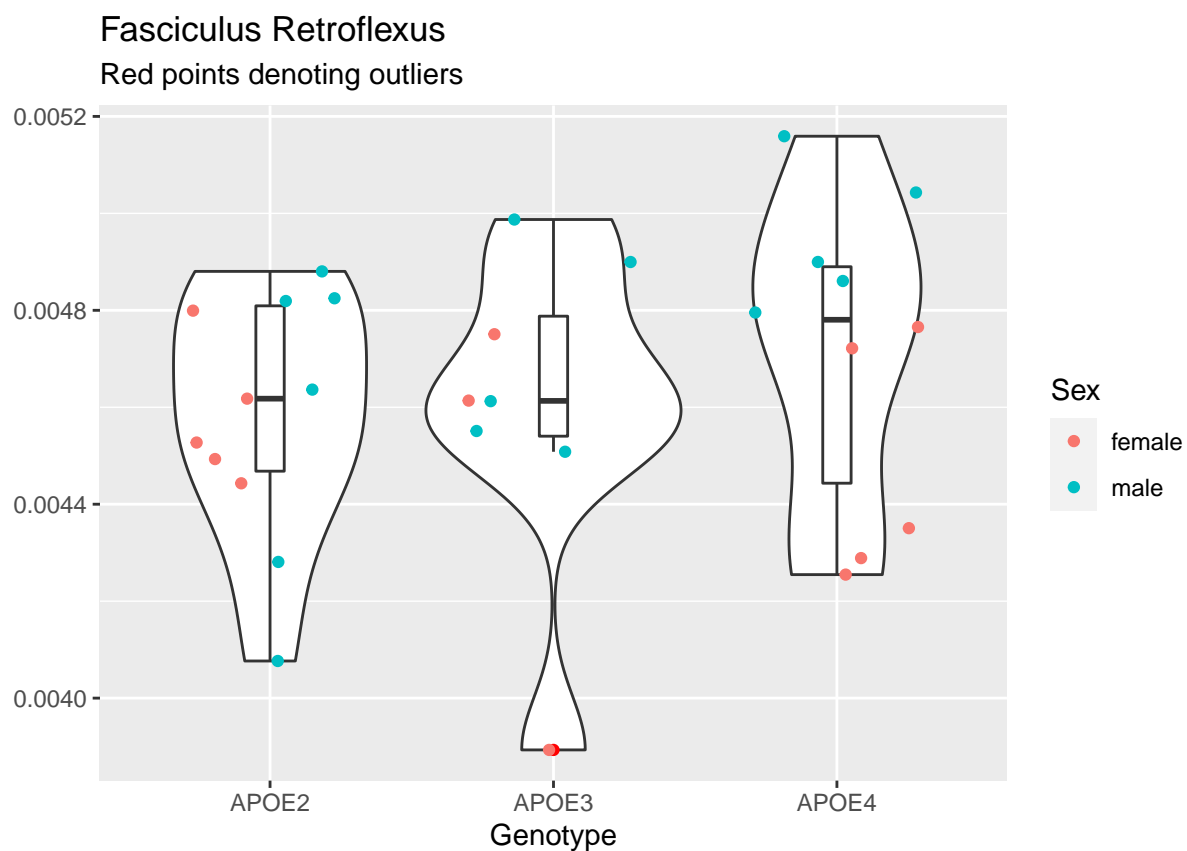
Red points denoting outliers



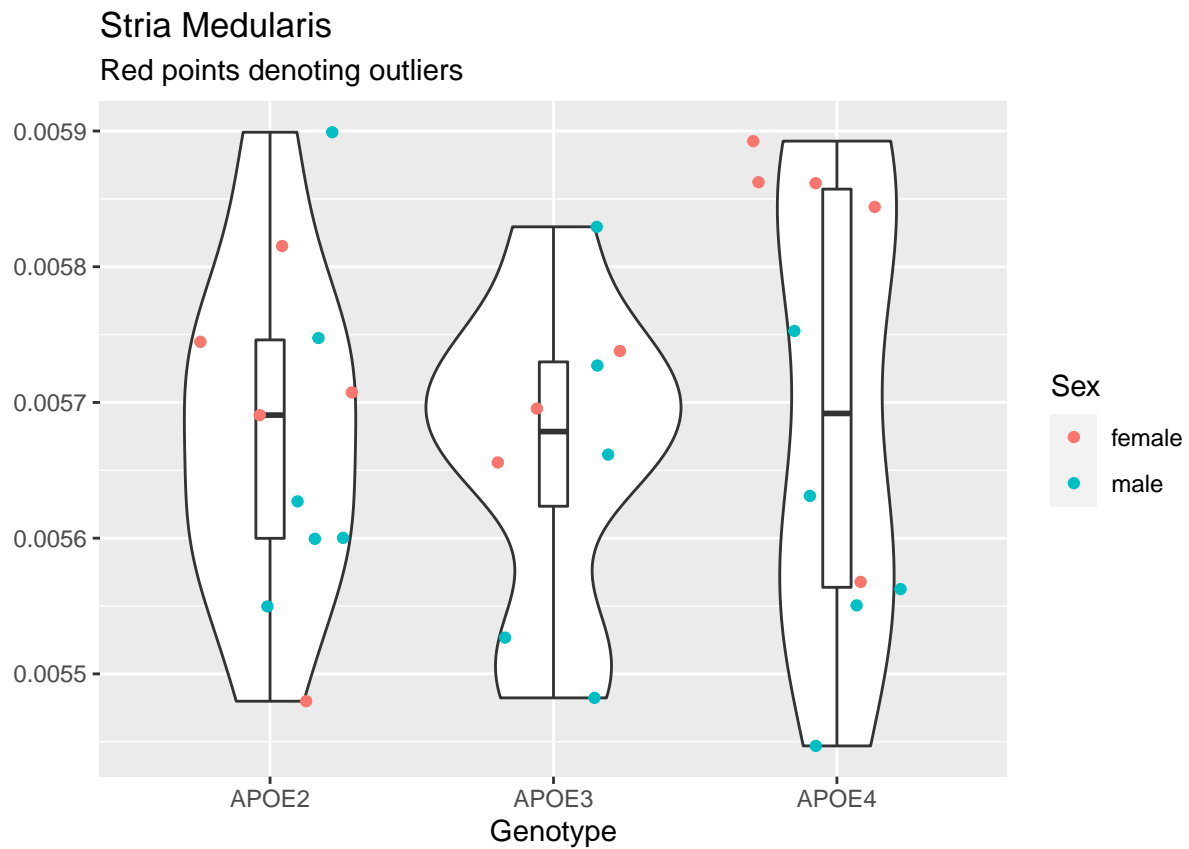
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.005e-07	5.025e-08	0.869	0.431
## Residuals	26	1.504e-06	5.784e-08		



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.620e-08	1.310e-08	0.731	0.491
## Residuals	26	4.657e-07	1.791e-08		



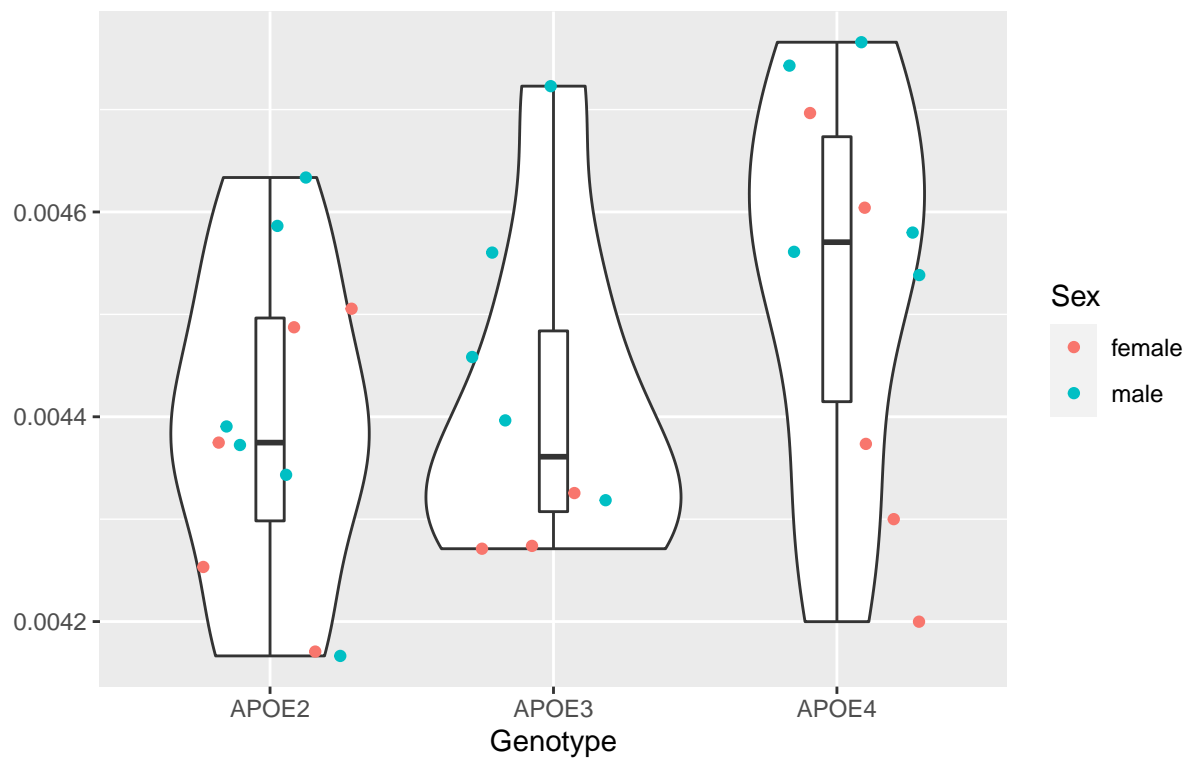
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 1.021e-07 5.104e-08   0.577  0.569
## Residuals 26 2.301e-06 8.849e-08
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 4.900e-09 2.434e-09   0.132  0.877
## Residuals 26 4.788e-07 1.842e-08
```

Mammillothalamic Tract

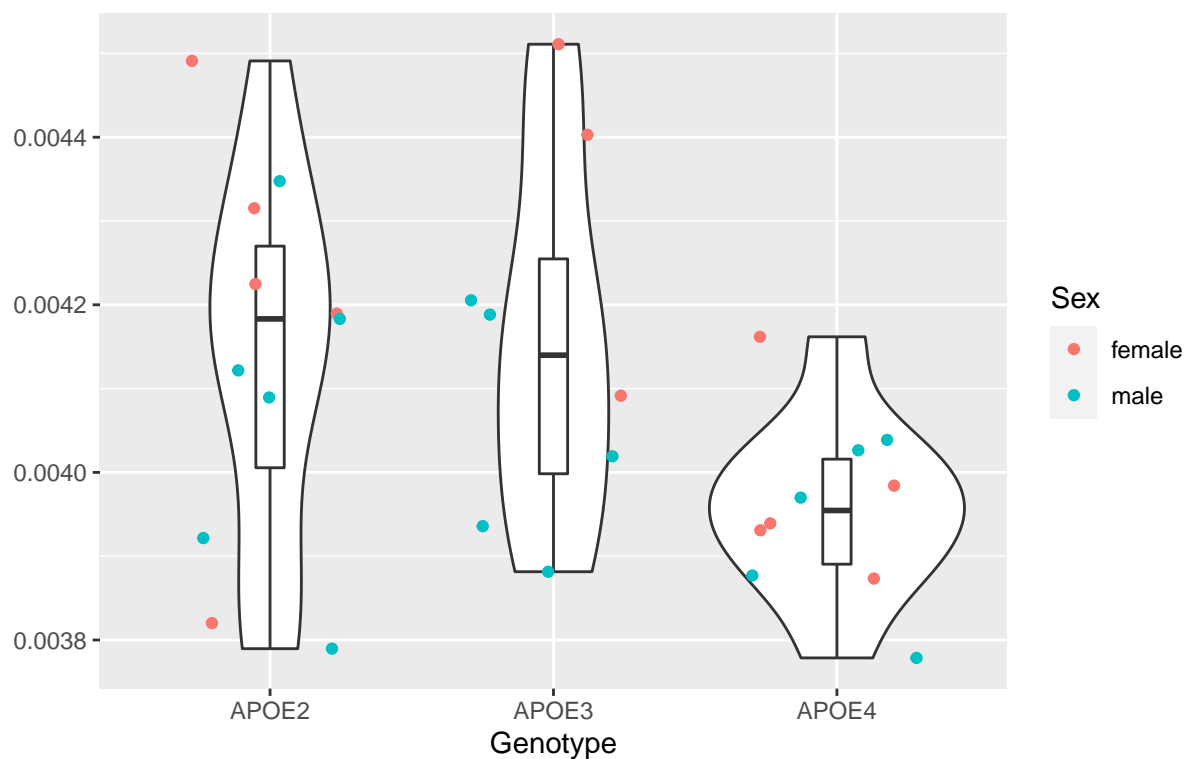
Red points denoting outliers



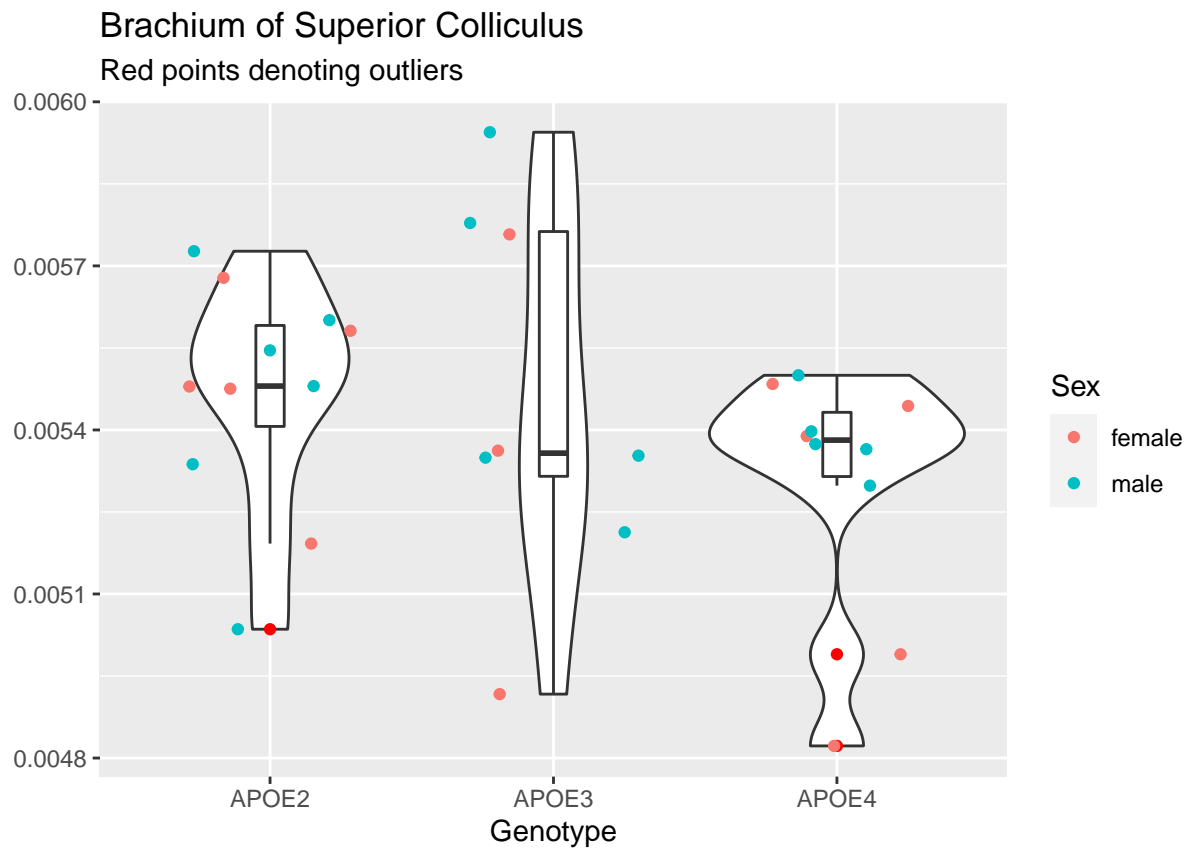
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.237e-07	6.187e-08	2.174	0.134
## Residuals	26	7.400e-07	2.846e-08		

Posterior Commissure

Red points denoting outliers

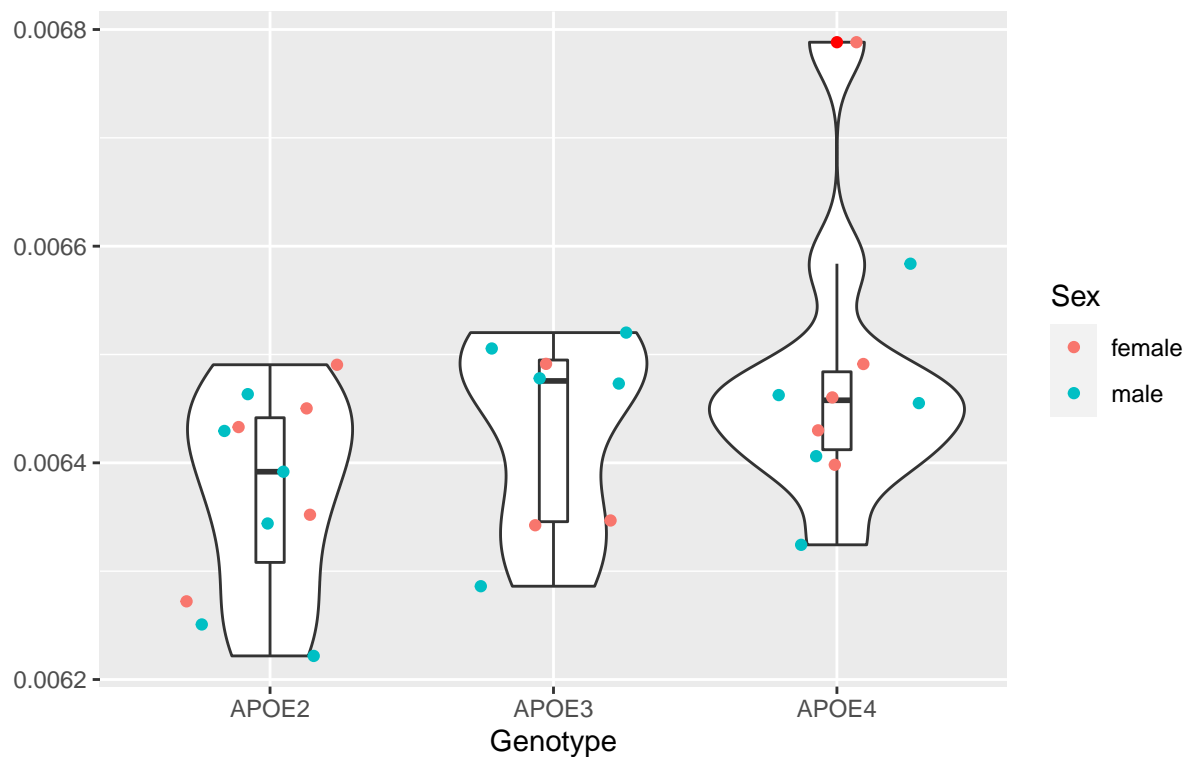


```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 2.274e-07 1.137e-07   3.207 0.0569 .
## Residuals    26 9.217e-07 3.545e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cerebral Peduncle

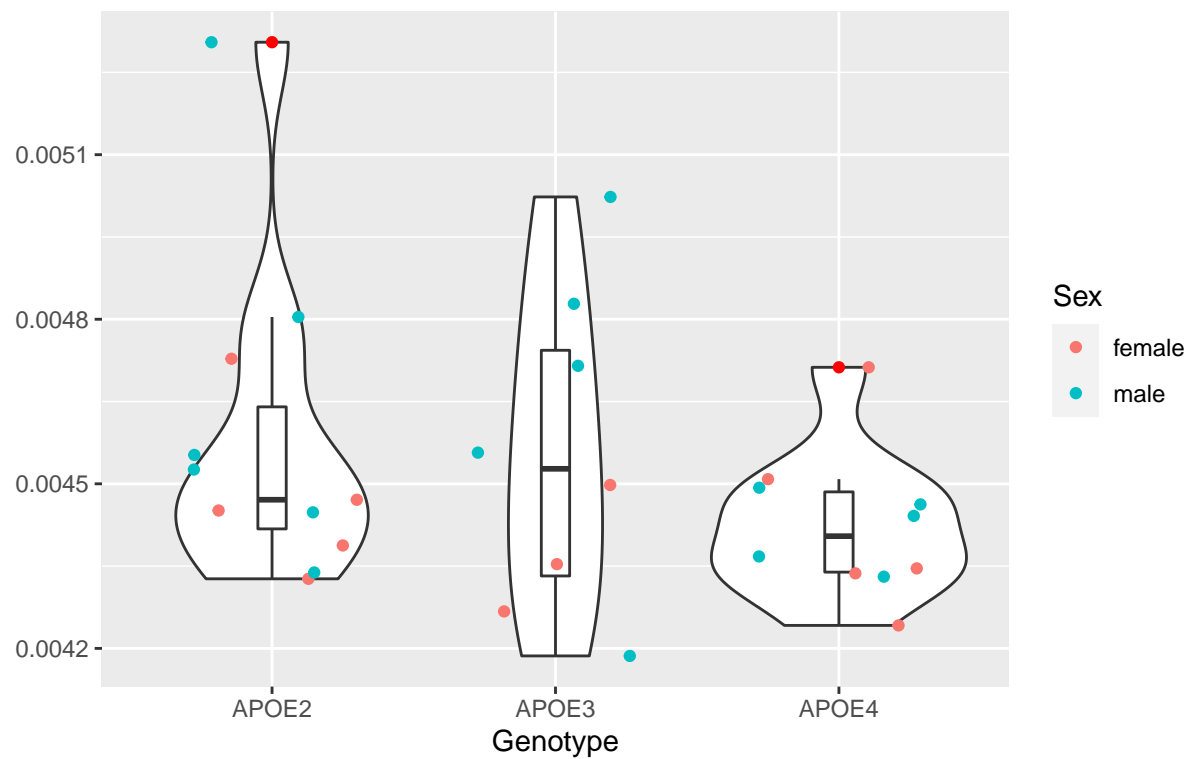
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 6.061e-08 3.030e-08   2.74 0.0832 .
## Residuals    26 2.875e-07 1.106e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Lateral Lemniscus

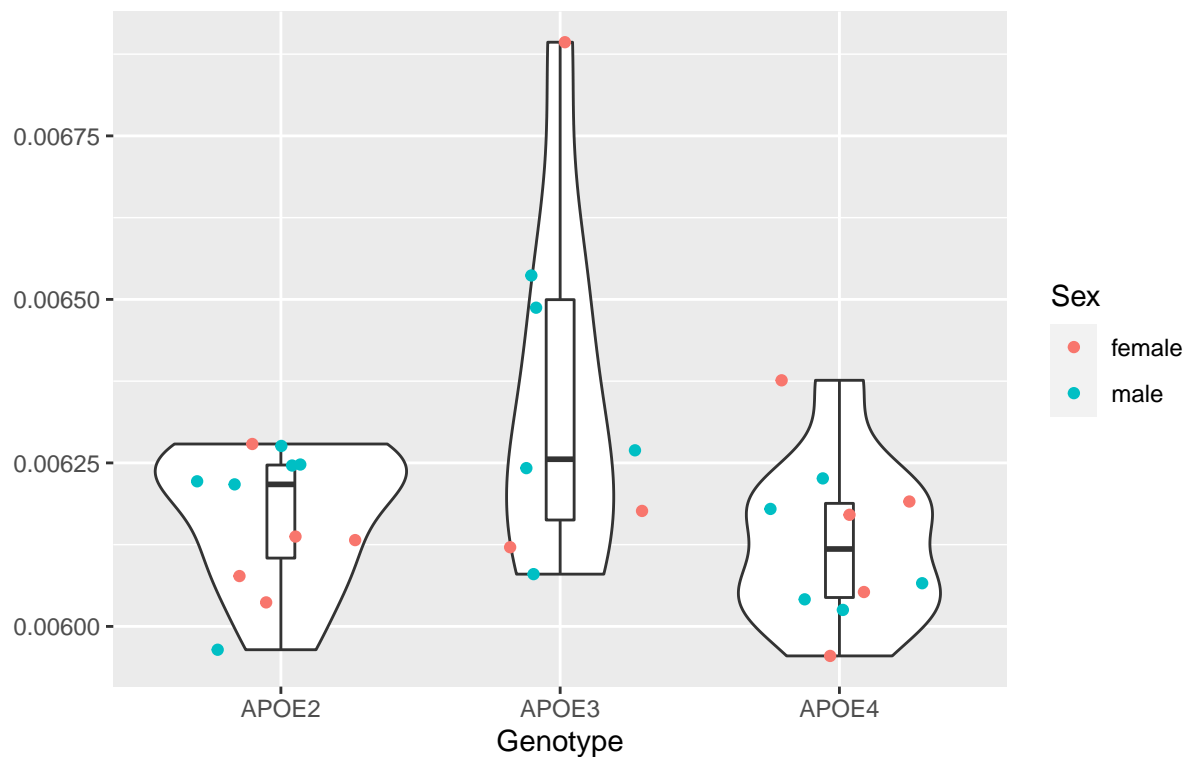
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.357e-07	6.784e-08	1.142	0.335
## Residuals	26	1.544e-06	5.939e-08		

Spinal Trigeminal Nerve

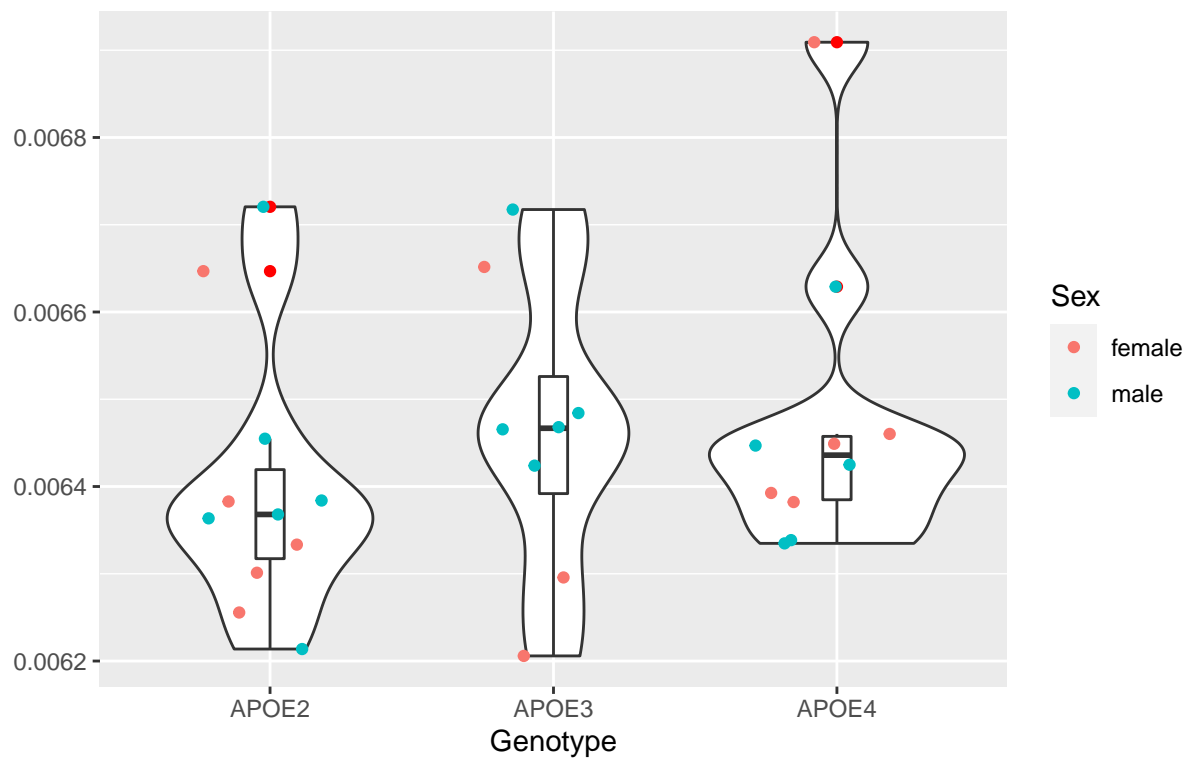
Red points denoting outliers



```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## geno         2 2.447e-07 1.223e-07   4.127 0.0278 *
## Residuals    26 7.706e-07 2.964e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pyramidal Tract

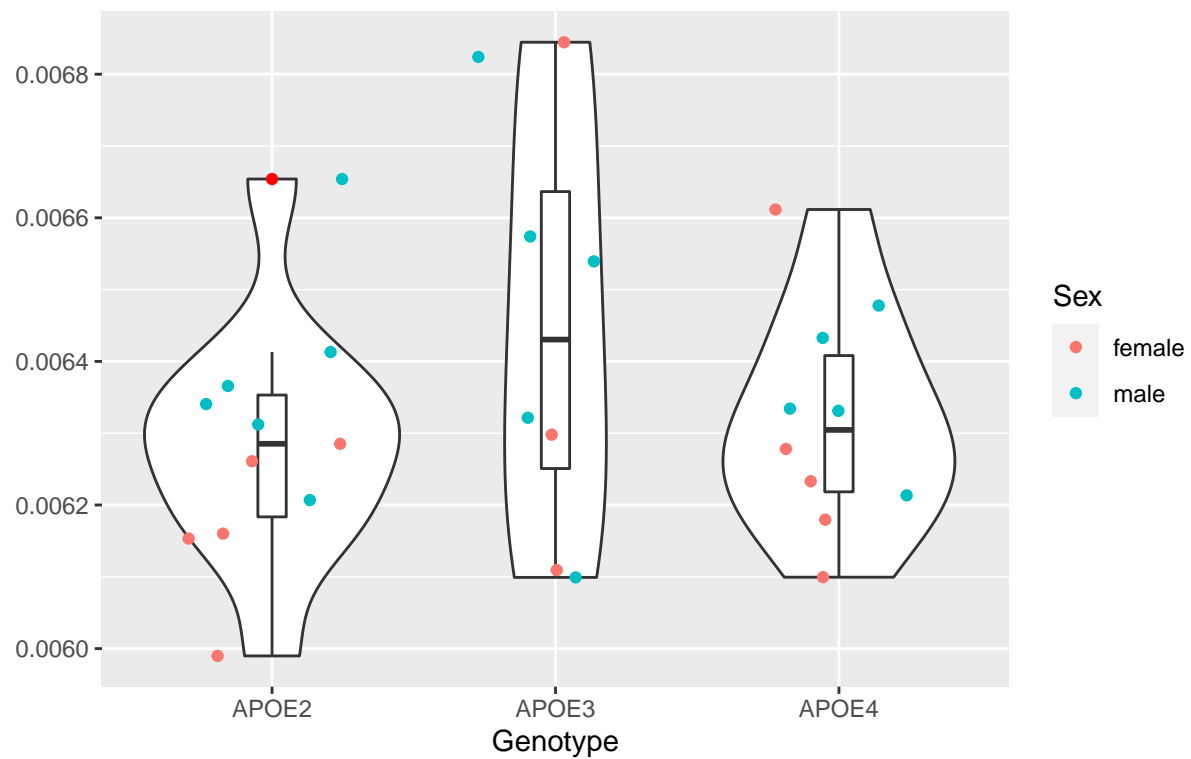
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.310e-08	1.656e-08	0.61	0.551
## Residuals	26	7.057e-07	2.714e-08		

Vestibulocochlear Nerve

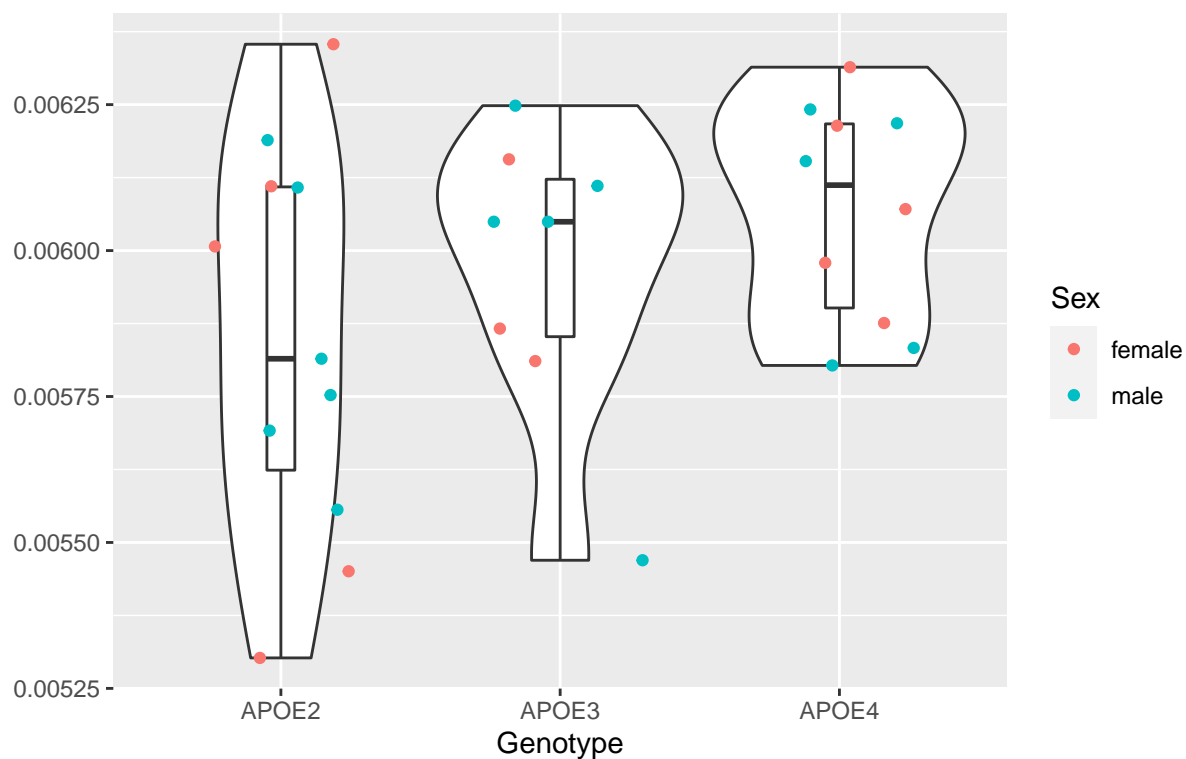
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.357e-07	6.785e-08	1.605	0.22
## Residuals	26	1.099e-06	4.228e-08		

Facial Nerve

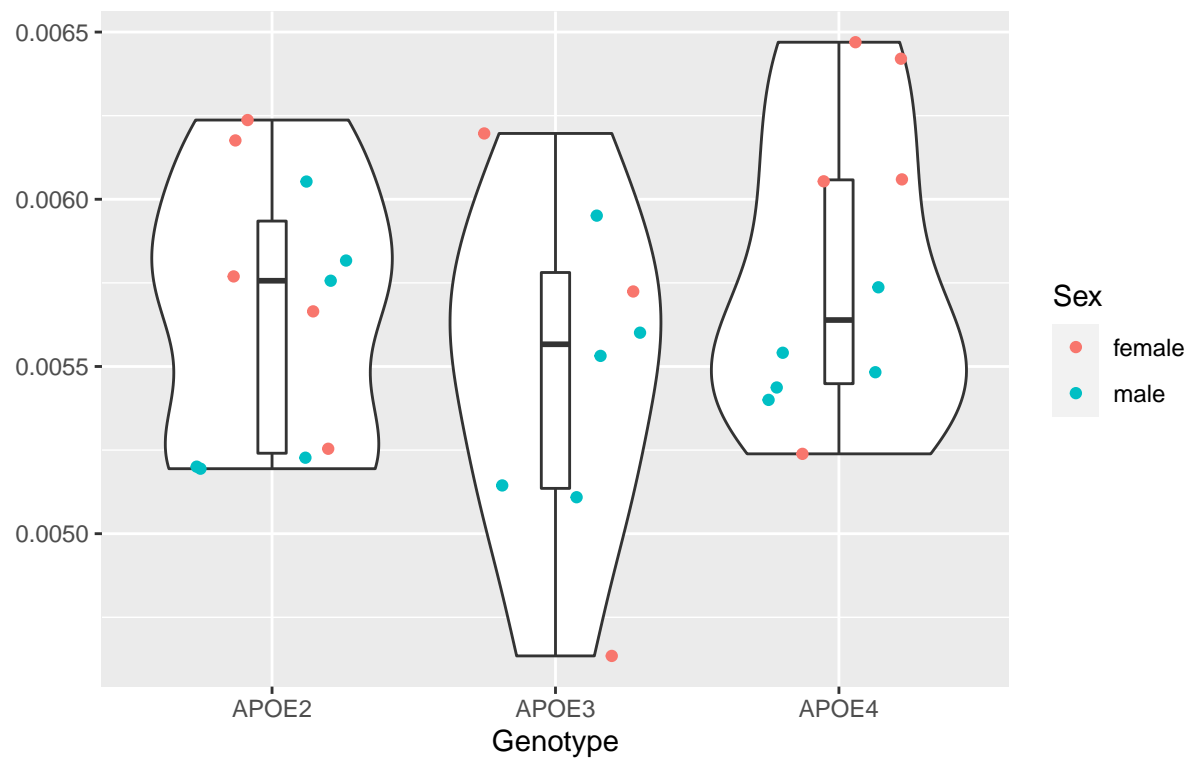
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.588e-07	1.294e-07	1.817	0.183
## Residuals	26	1.852e-06	7.124e-08		

Longitudinal Fasciculus of Pons

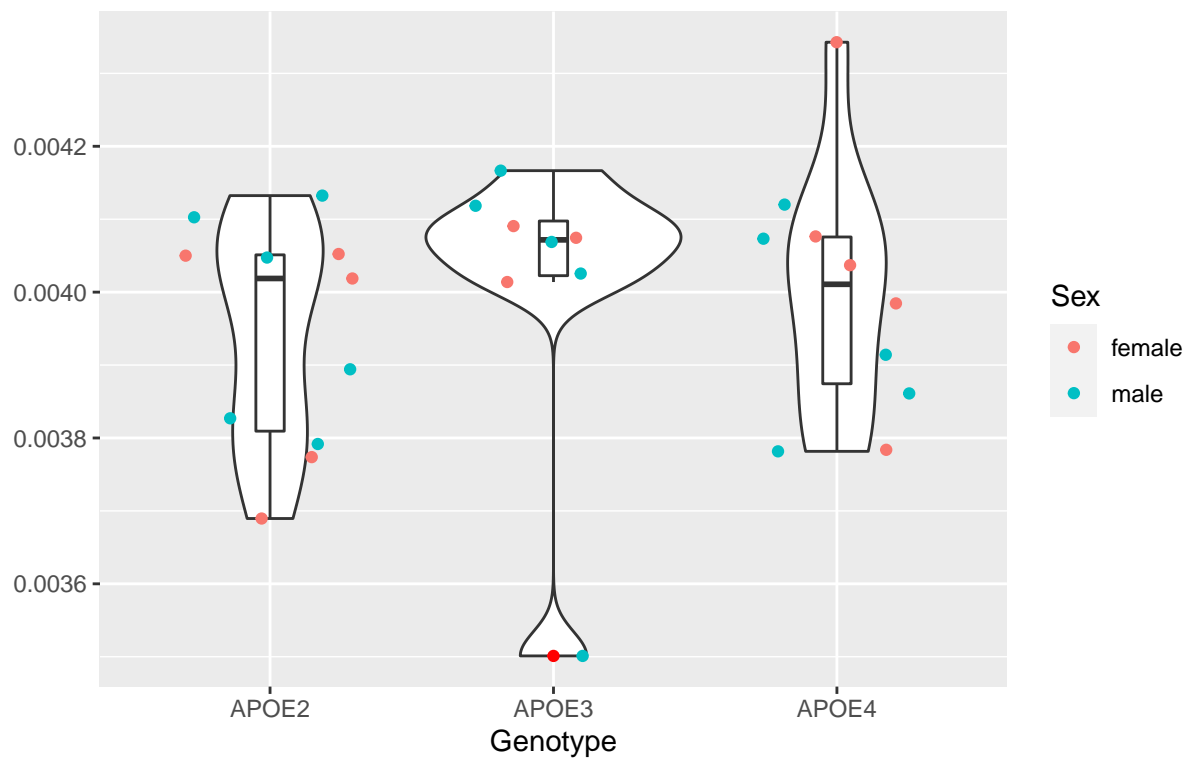
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.950e-07	1.974e-07	1.007	0.379
## Residuals	26	5.097e-06	1.960e-07		

Medial Longitudinal Fasciculus and Tectospinal Tract

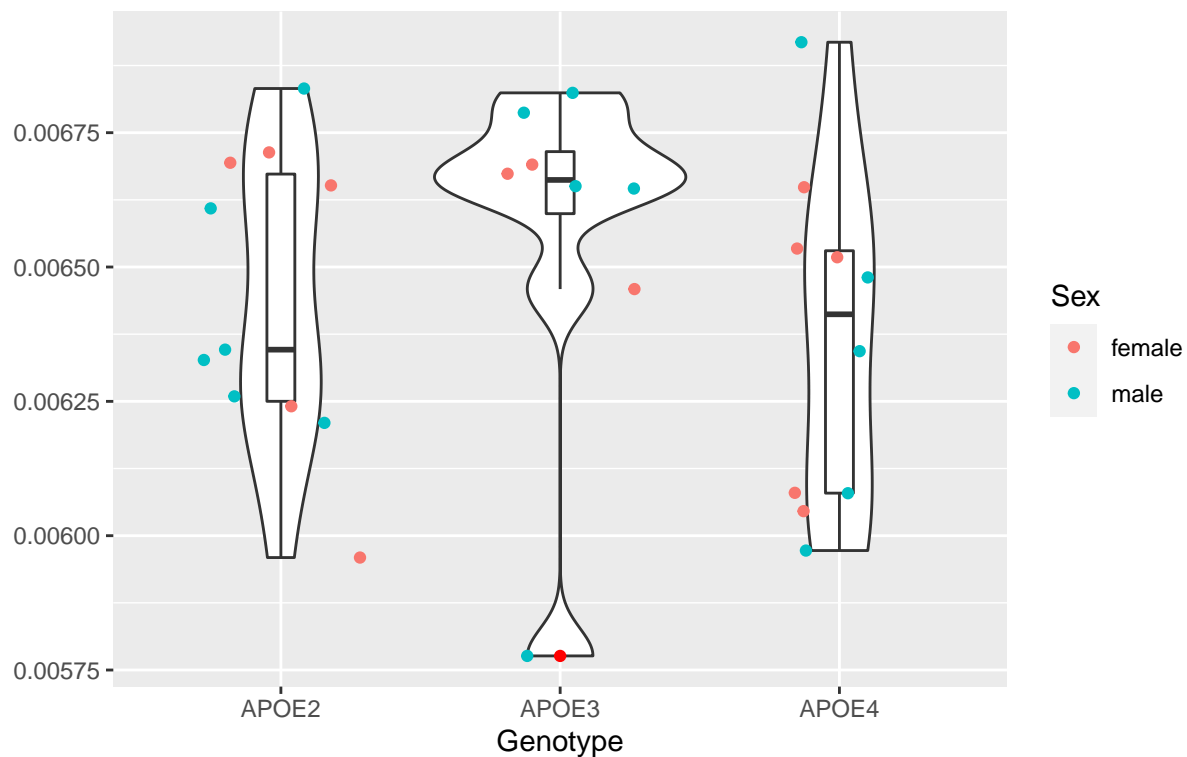
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.360e-08	1.182e-08	0.38	0.687
## Residuals	26	8.082e-07	3.108e-08		

Spinocerebellar Tract

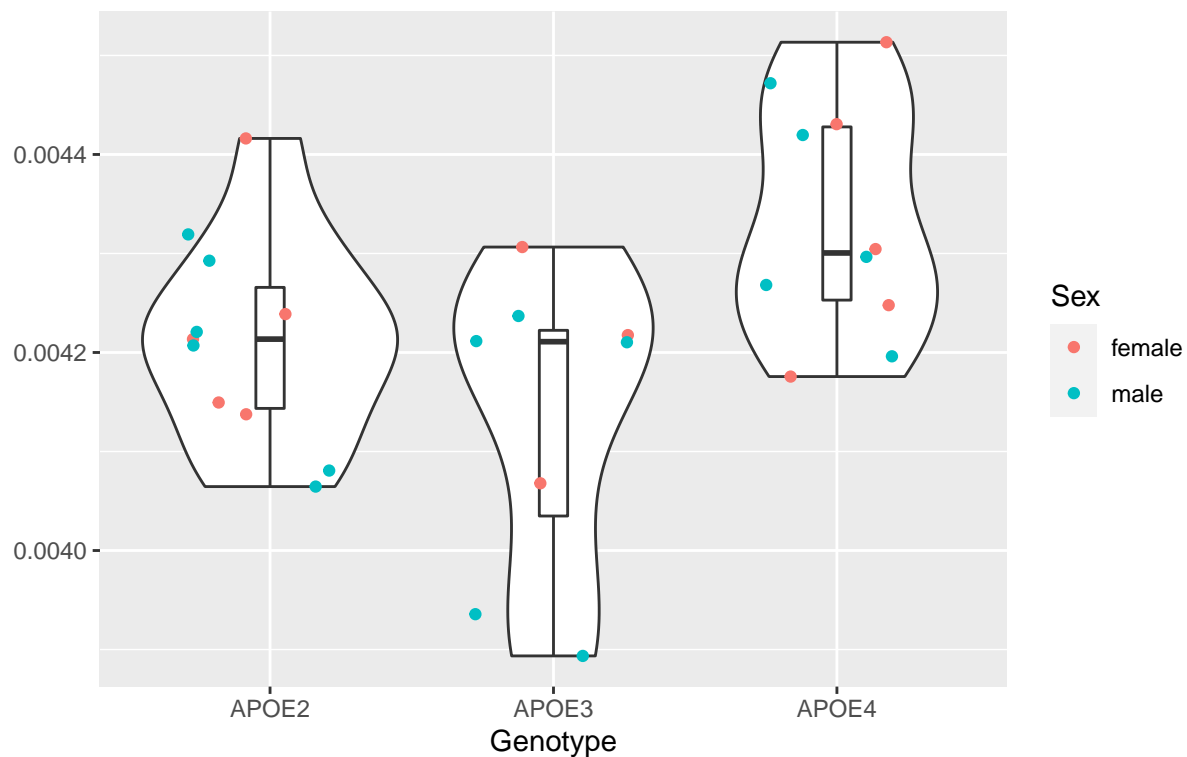
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.811e-07	9.055e-08	0.978	0.389
## Residuals	26	2.407e-06	9.260e-08		

Medial Lemniscus

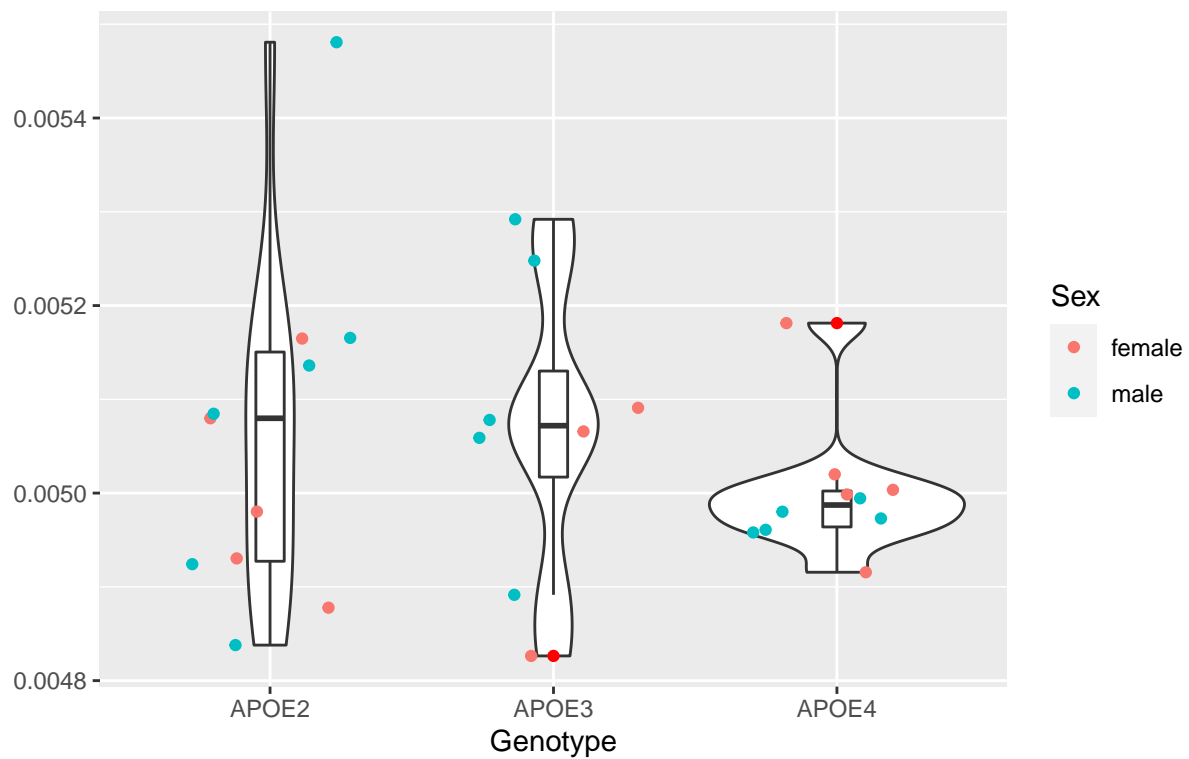
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value  Pr(>F)
## geno         2 1.802e-07 9.010e-08   5.923 0.00759 **
## Residuals    26 3.955e-07 1.521e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Ventral Spinocerebellar Tract

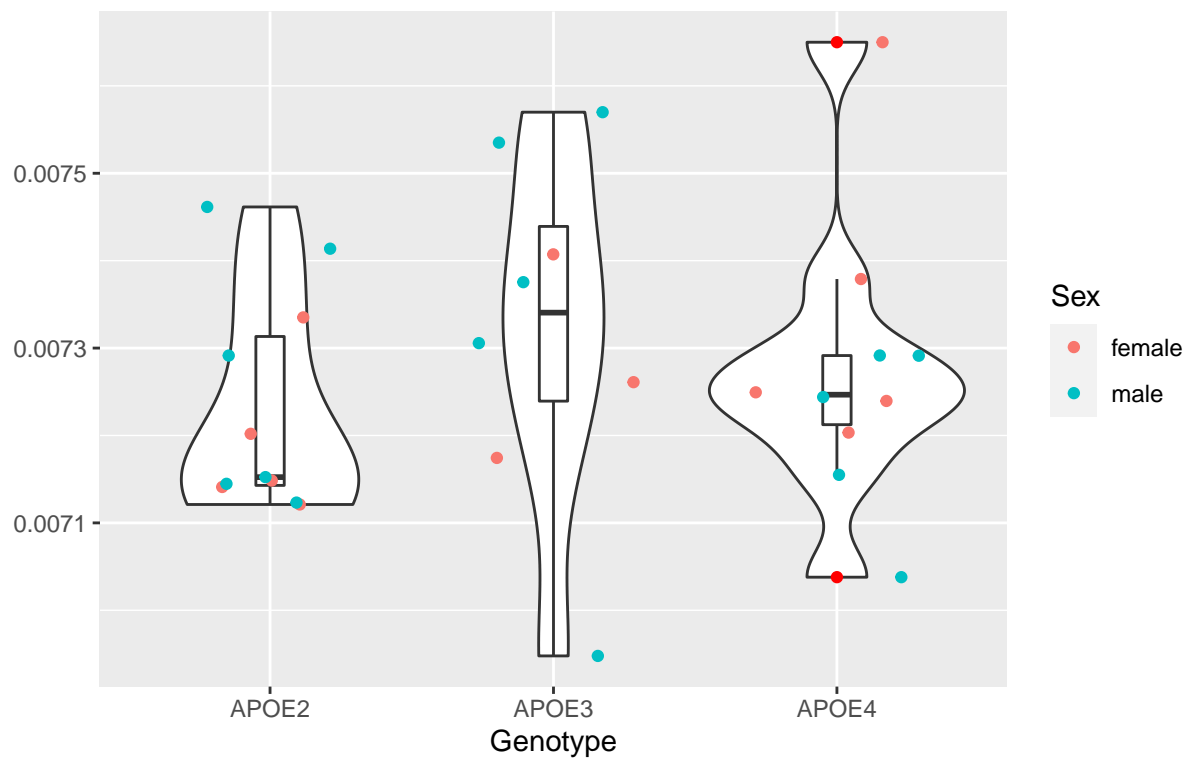
Red points denoting outliers



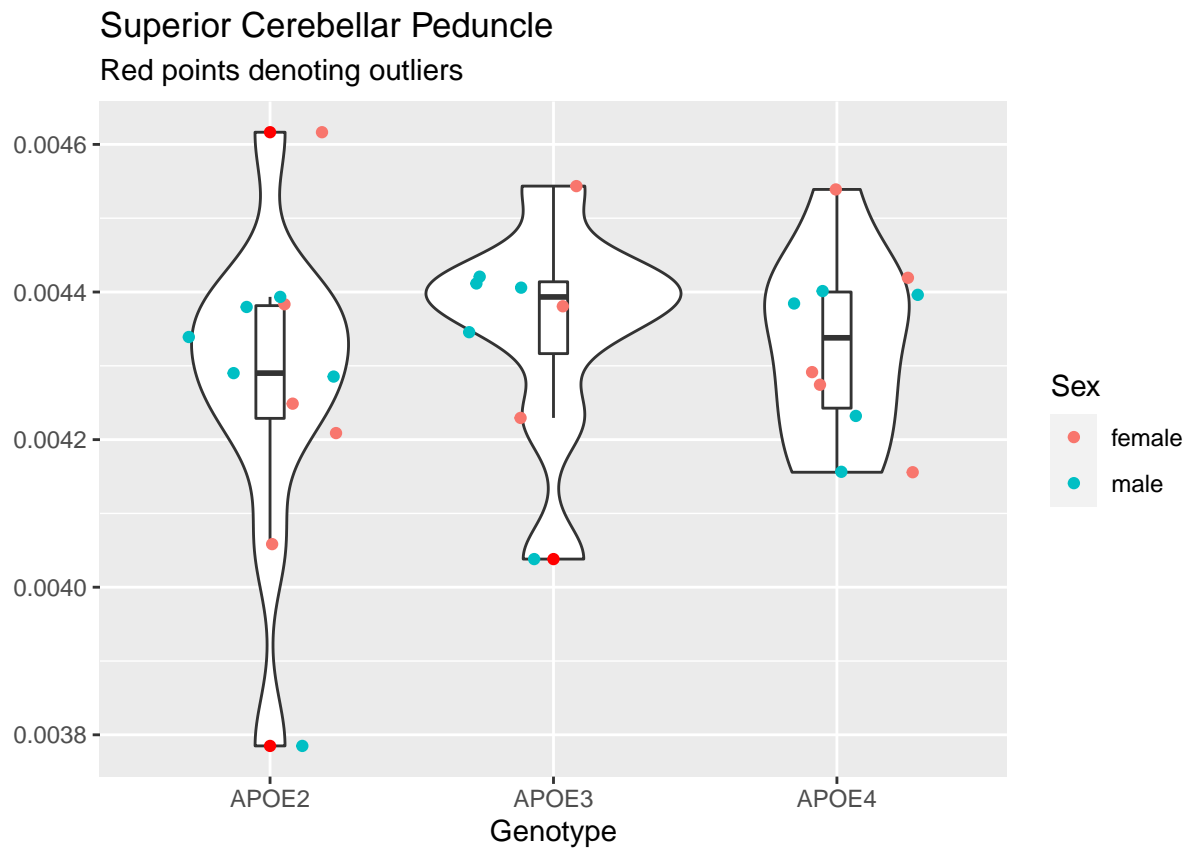
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.830e-08	1.416e-08	0.672	0.519
## Residuals	26	5.478e-07	2.107e-08		

Middle Cerebellar Peduncle

Red points denoting outliers



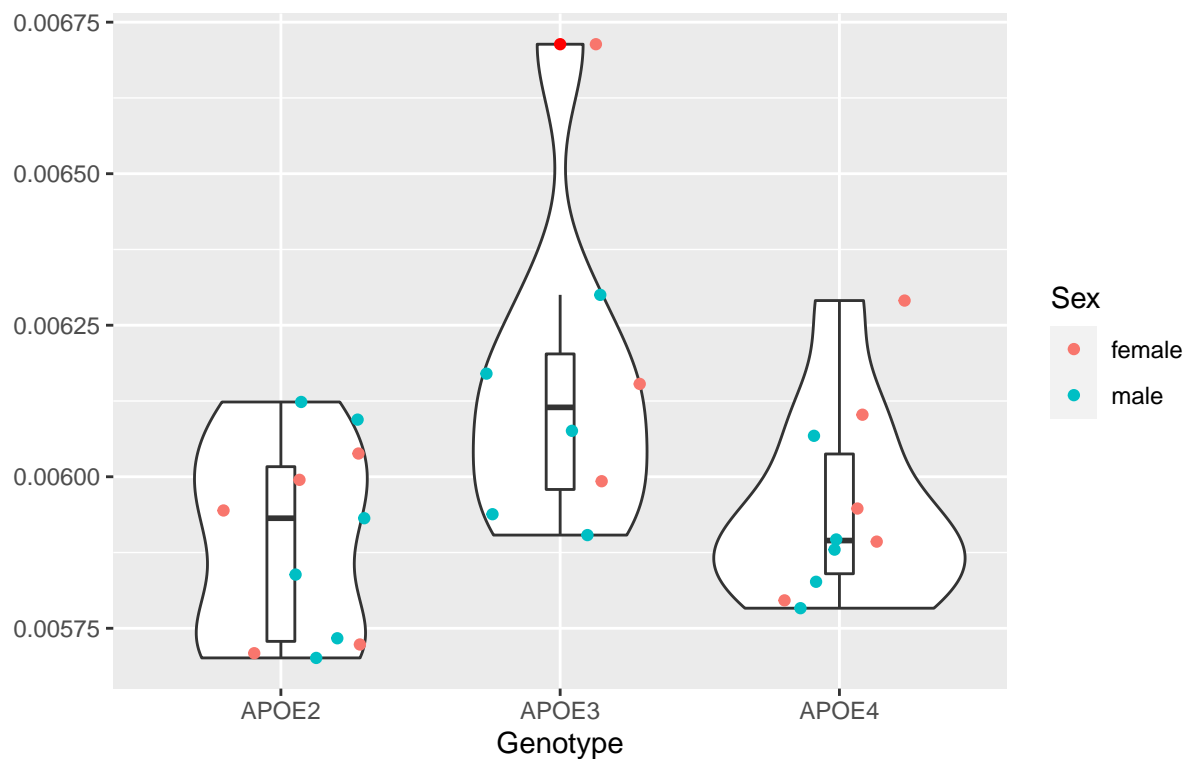
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.910e-08	1.953e-08	0.761	0.477
## Residuals	26	6.674e-07	2.567e-08		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.930e-08 1.465e-08   0.508  0.608
## Residuals 26 7.503e-07 2.886e-08
```

Inferior Cerebellar Peduncle

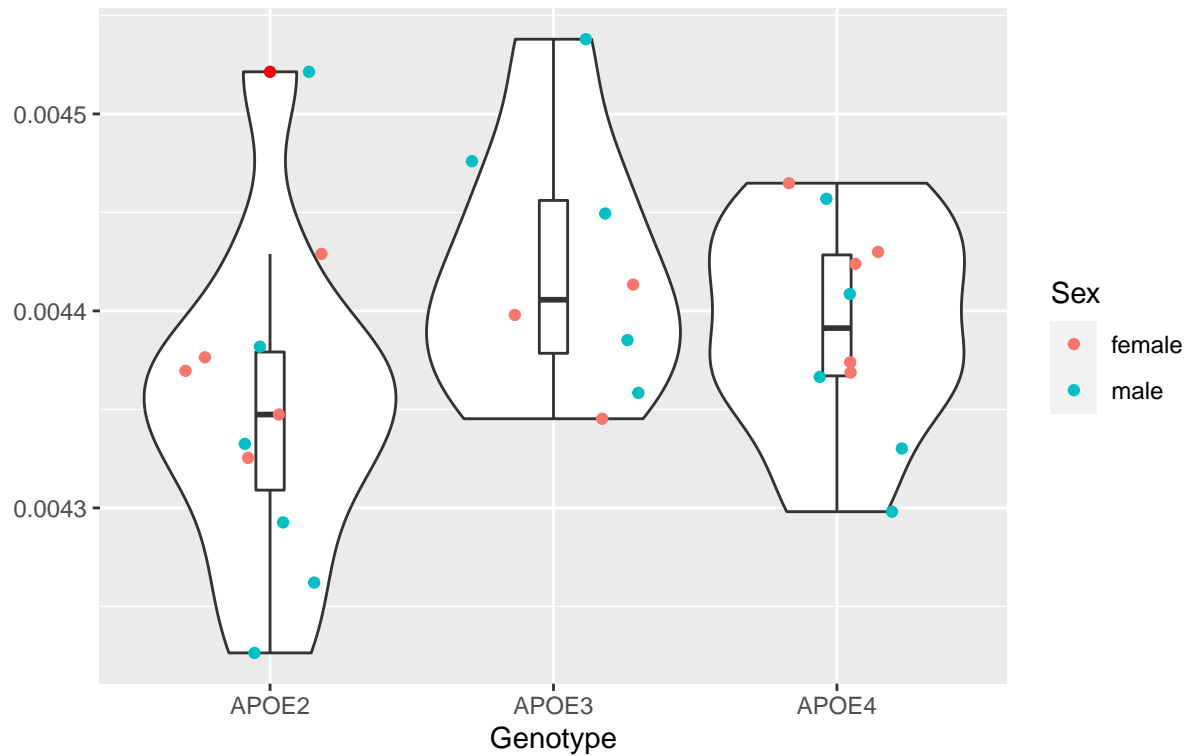
Red points denoting outliers



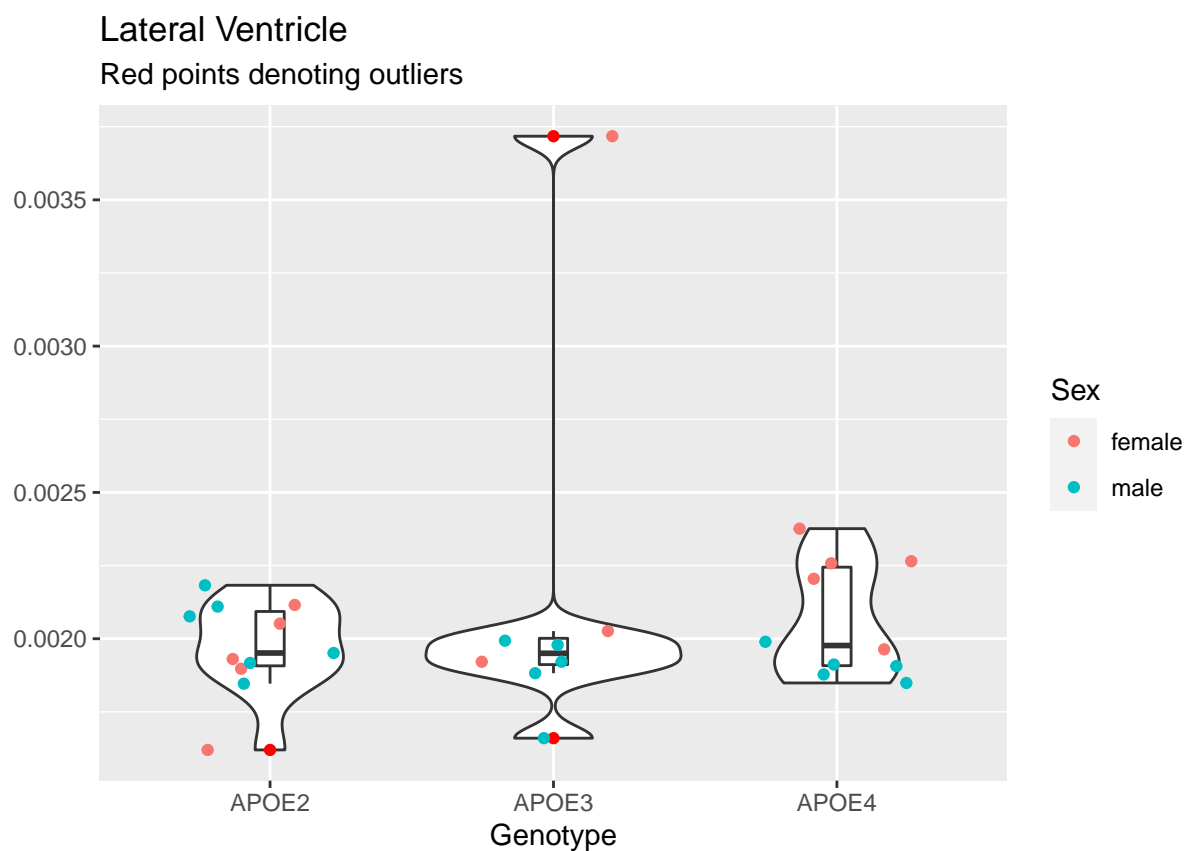
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 3.386e-07 1.693e-07   4.566   0.02 *
## Residuals    26 9.641e-07 3.708e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cerebellar White Matter

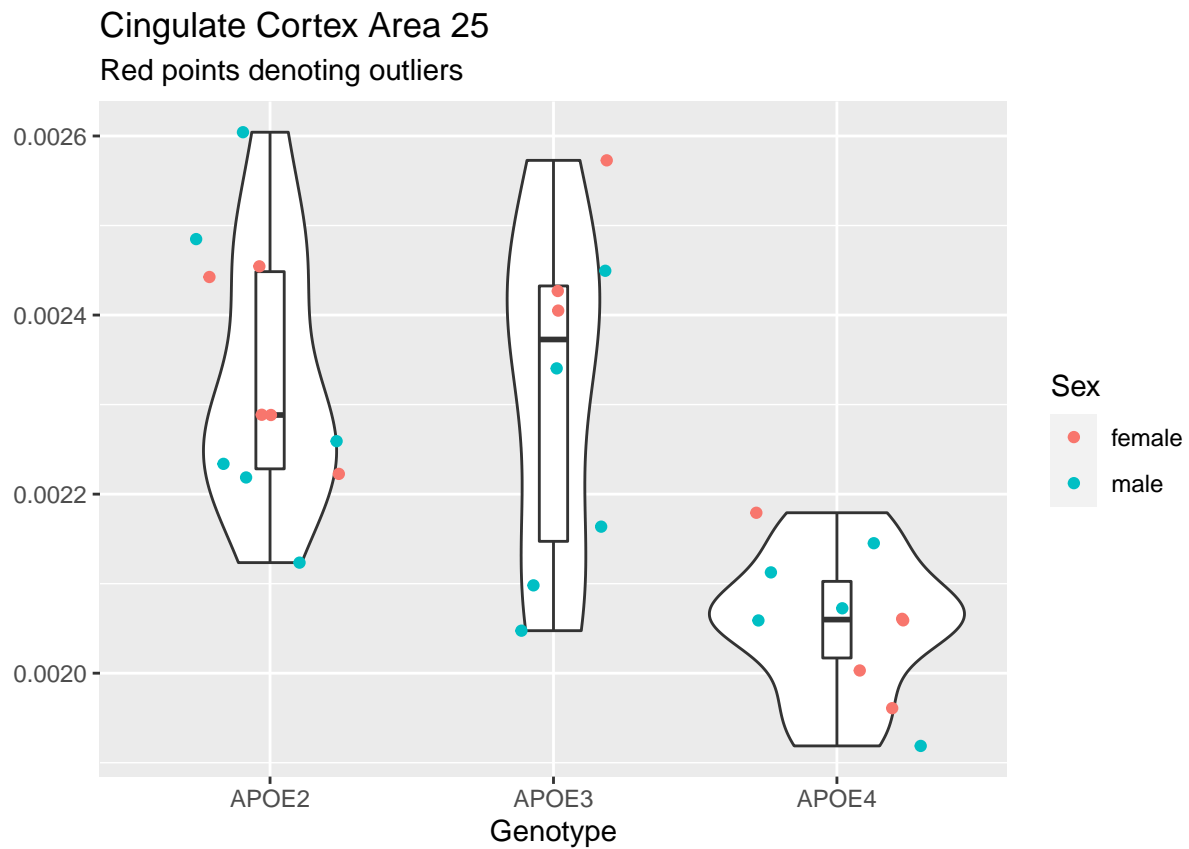
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.303e-08	1.151e-08	2.488	0.103
## Residuals	26	1.203e-07	4.628e-09		



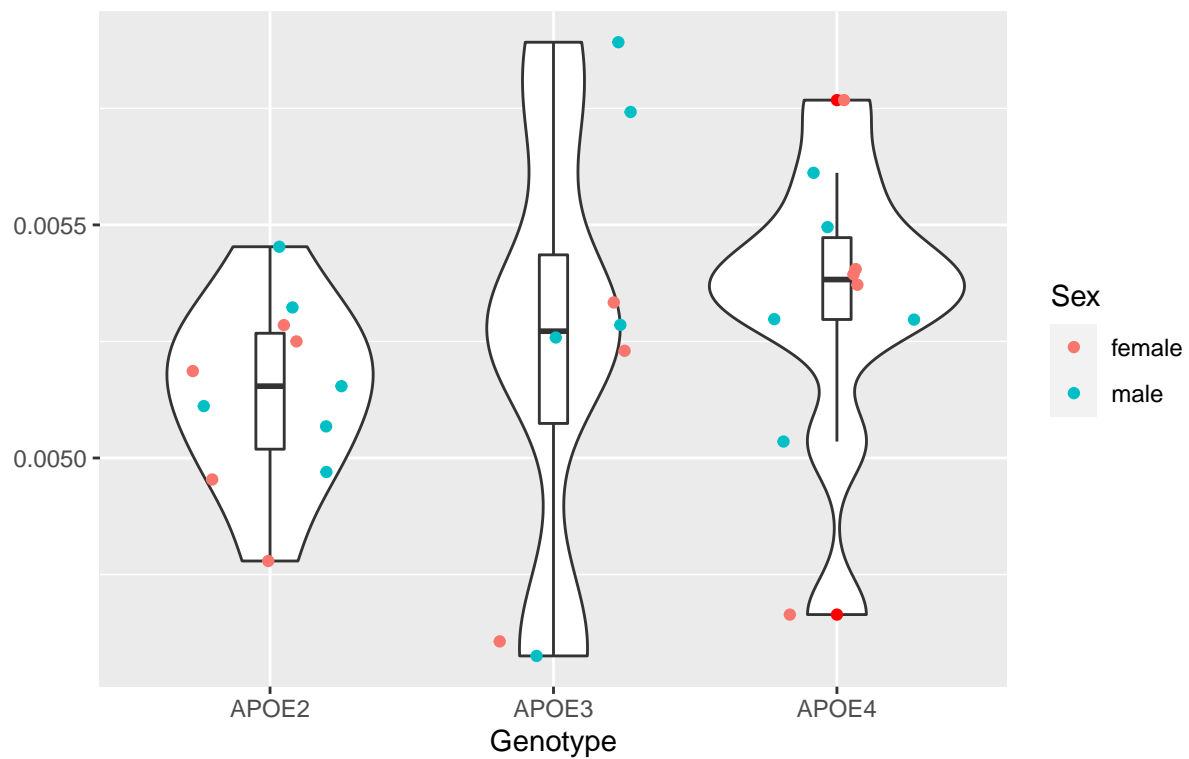
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 1.280e-07 6.413e-08   0.472  0.629
## Residuals 26 3.532e-06 1.359e-07
```



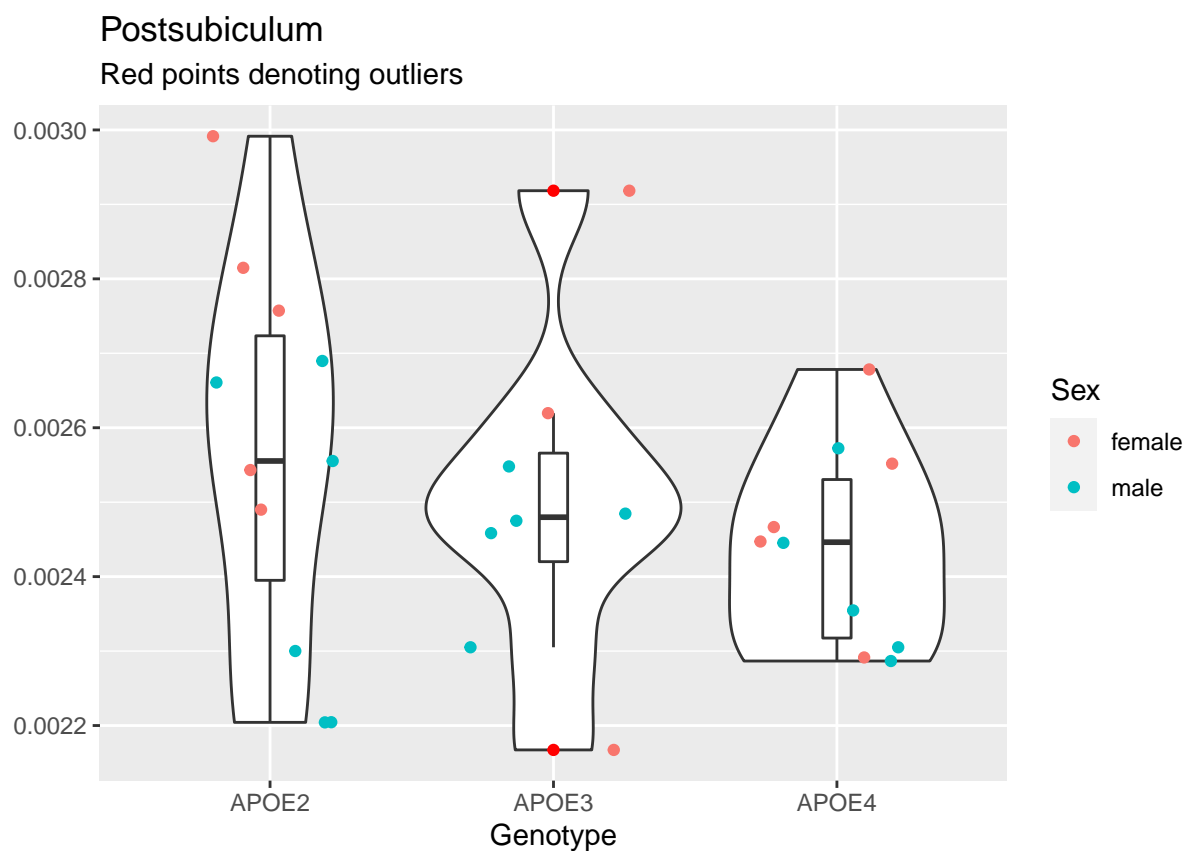
```
##          Df    Sum Sq  Mean Sq F value   Pr(>F)
## geno         2 4.622e-07 2.311e-07   11.64 0.000245 ***
## Residuals    26 5.162e-07 1.985e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Dorsal Acoustic Stria

Red points denoting outliers



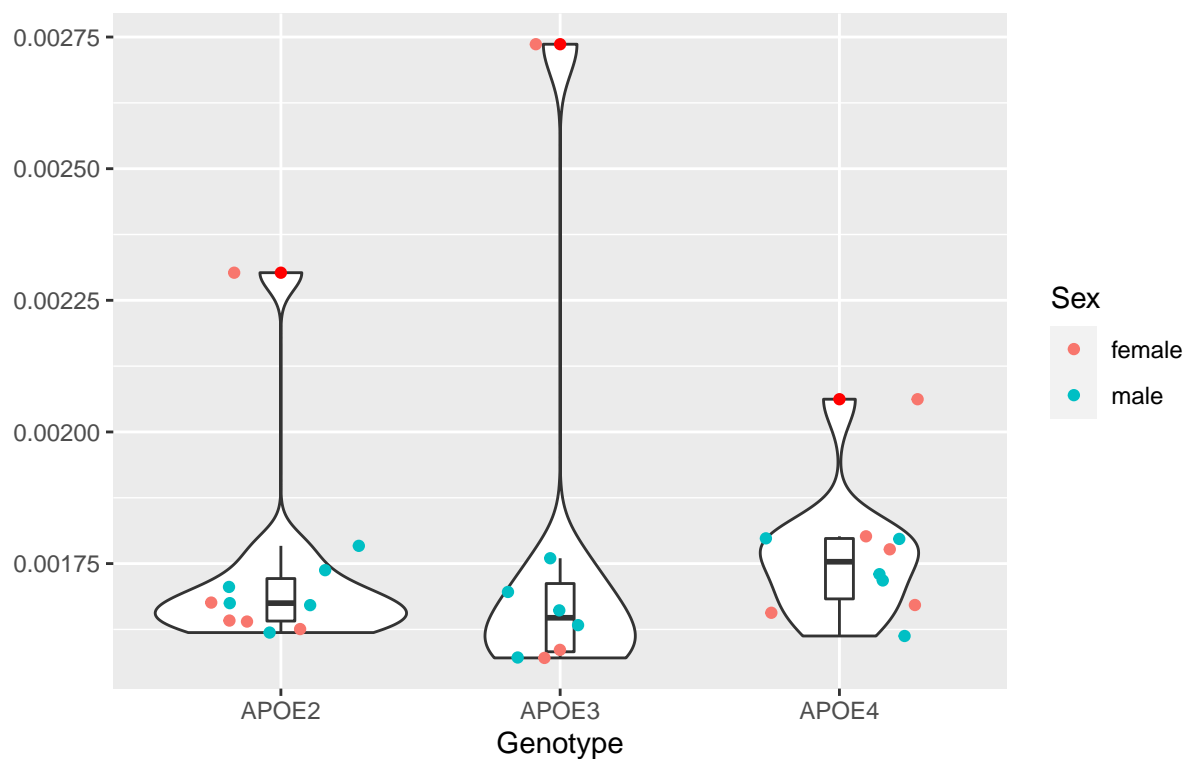
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.986e-07	9.930e-08	0.942	0.403
## Residuals	26	2.740e-06	1.054e-07		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 8.190e-08 4.094e-08   0.931  0.407
## Residuals 26 1.144e-06 4.400e-08
```

Ventricular System 4th Ventricle

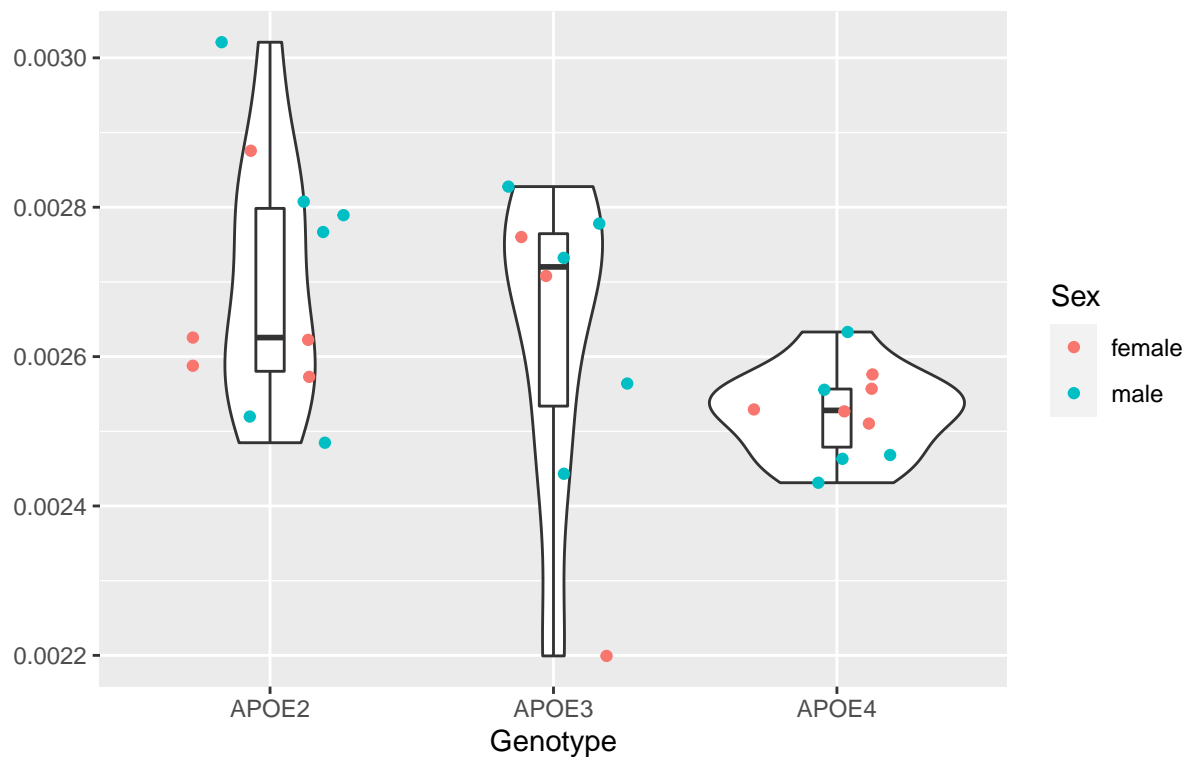
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	9.100e-09	4.540e-09	0.074	0.929
## Residuals	26	1.601e-06	6.158e-08		

Microcellular Tegmental Nucleus

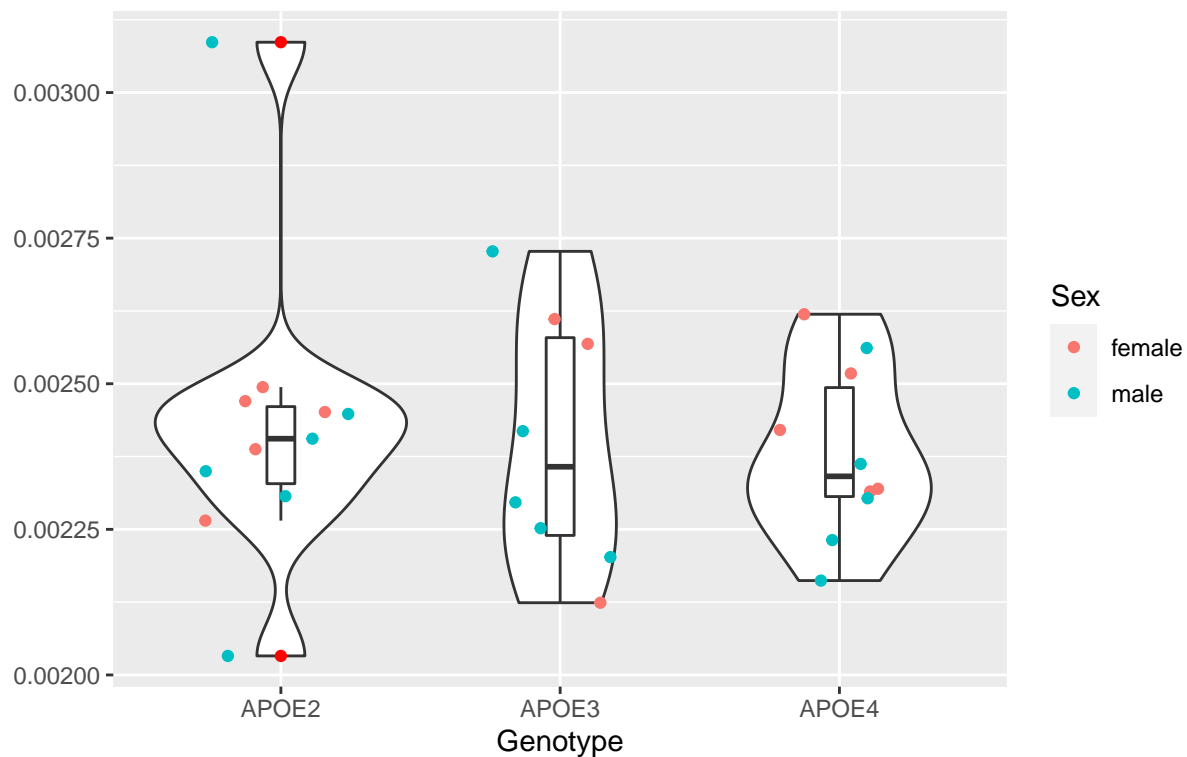
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 1.566e-07 7.831e-08    3.24 0.0554 .
## Residuals    26 6.284e-07 2.417e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pretectal Nucleus

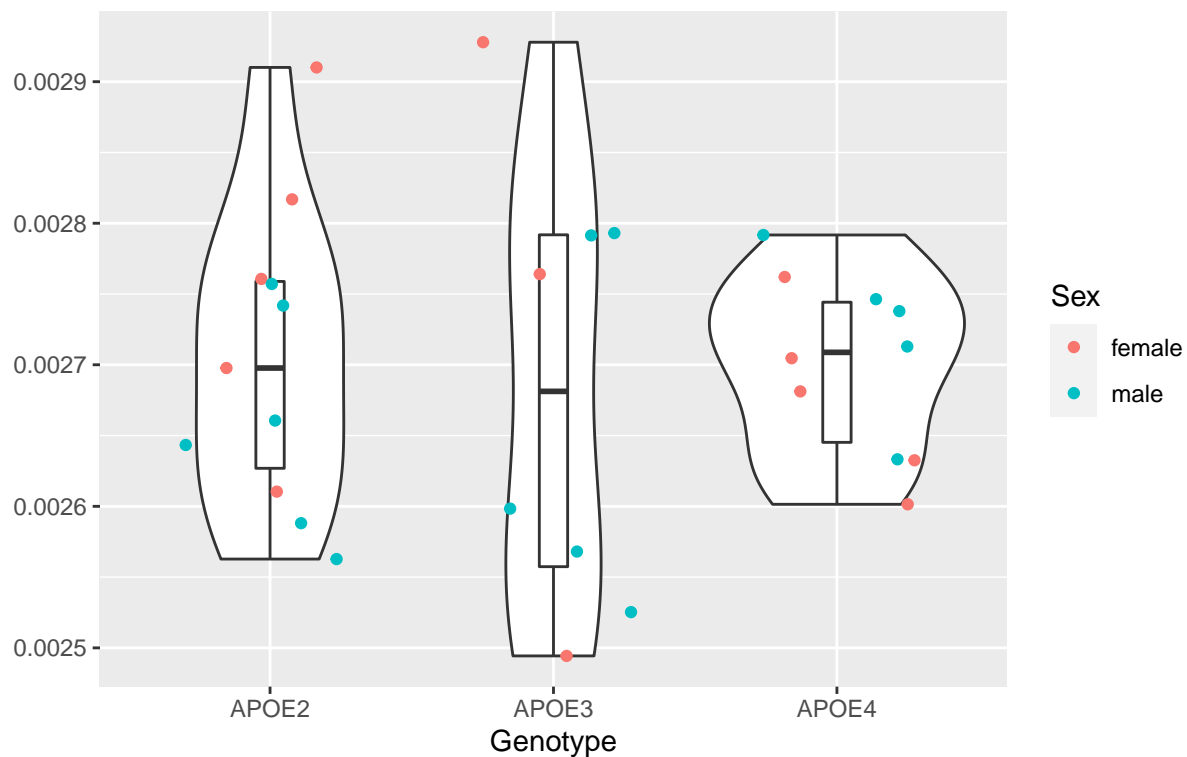
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.110e-08	5.570e-09	0.124	0.884
## Residuals	26	1.169e-06	4.497e-08		

Latero Dorsal Thalamic Nucleus Ventro Lateral

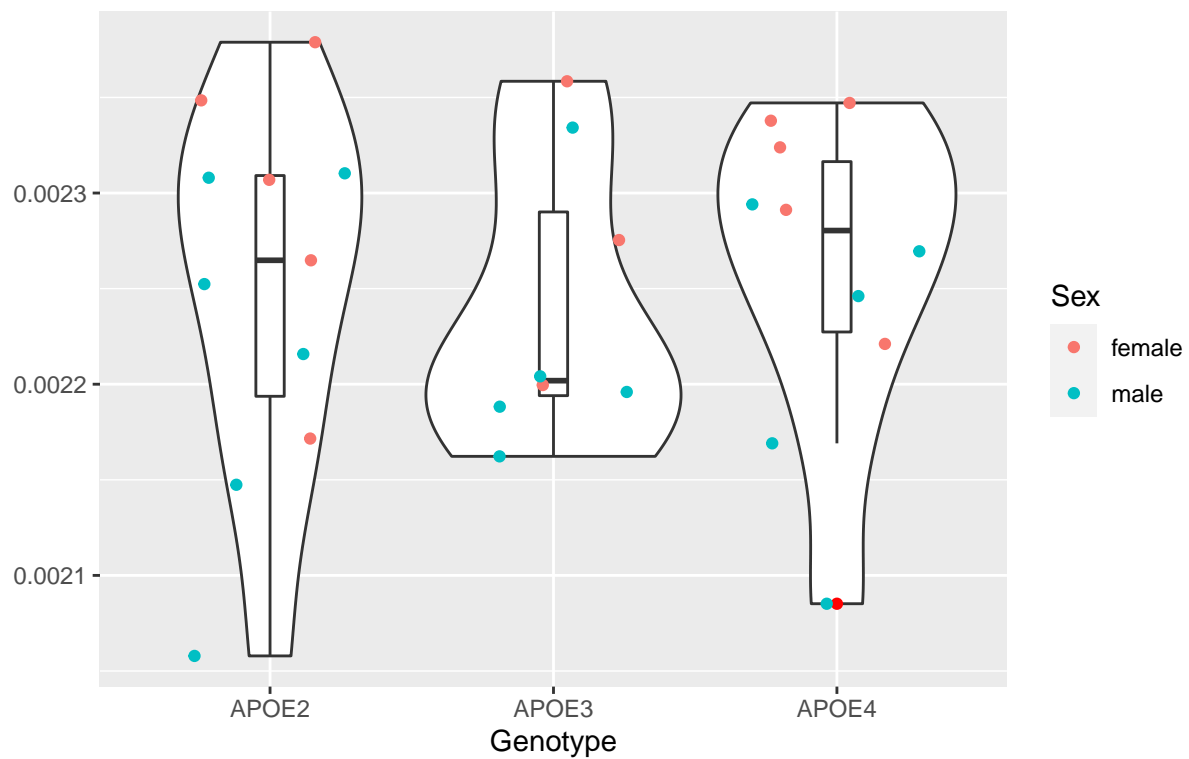
Red points denoting outliers



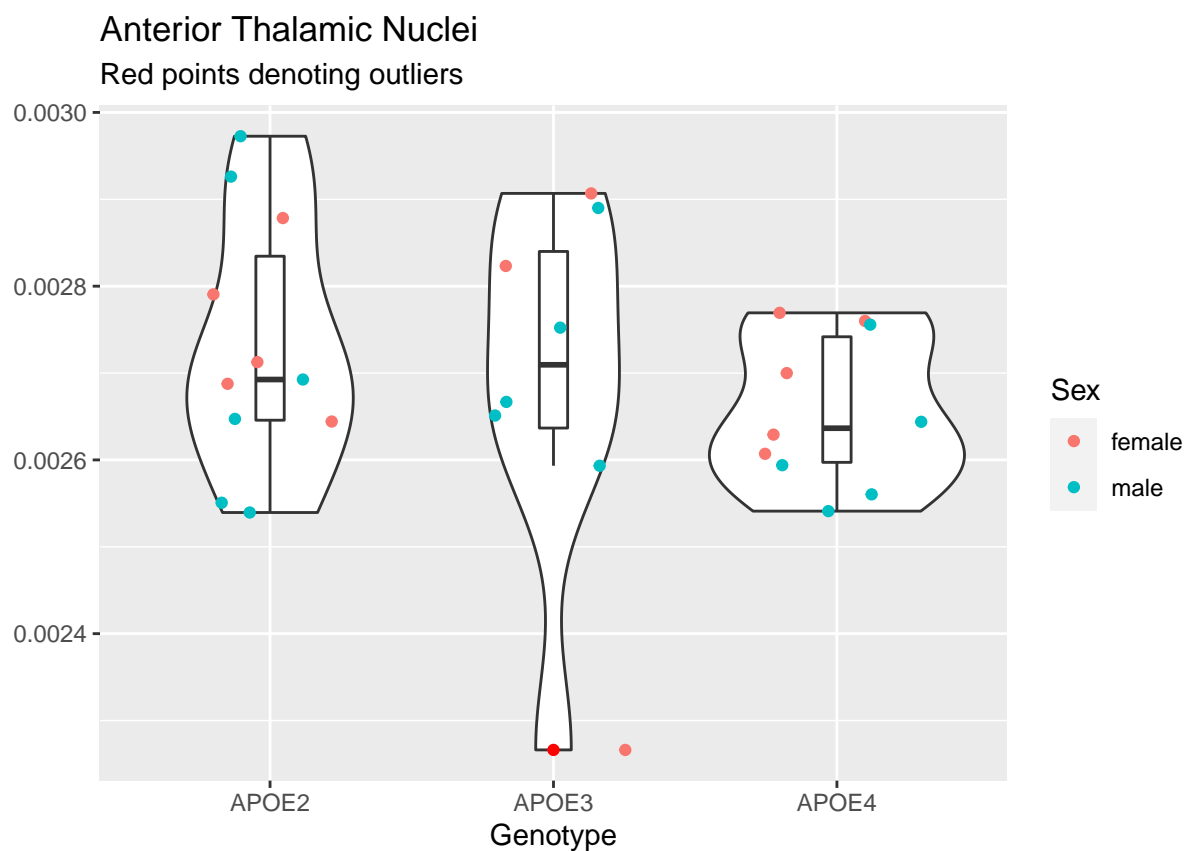
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.300e-09	1.173e-09	0.096	0.909
## Residuals	26	3.168e-07	1.218e-08		

Latero Posterior Nuclei of Thalamus

Red points denoting outliers



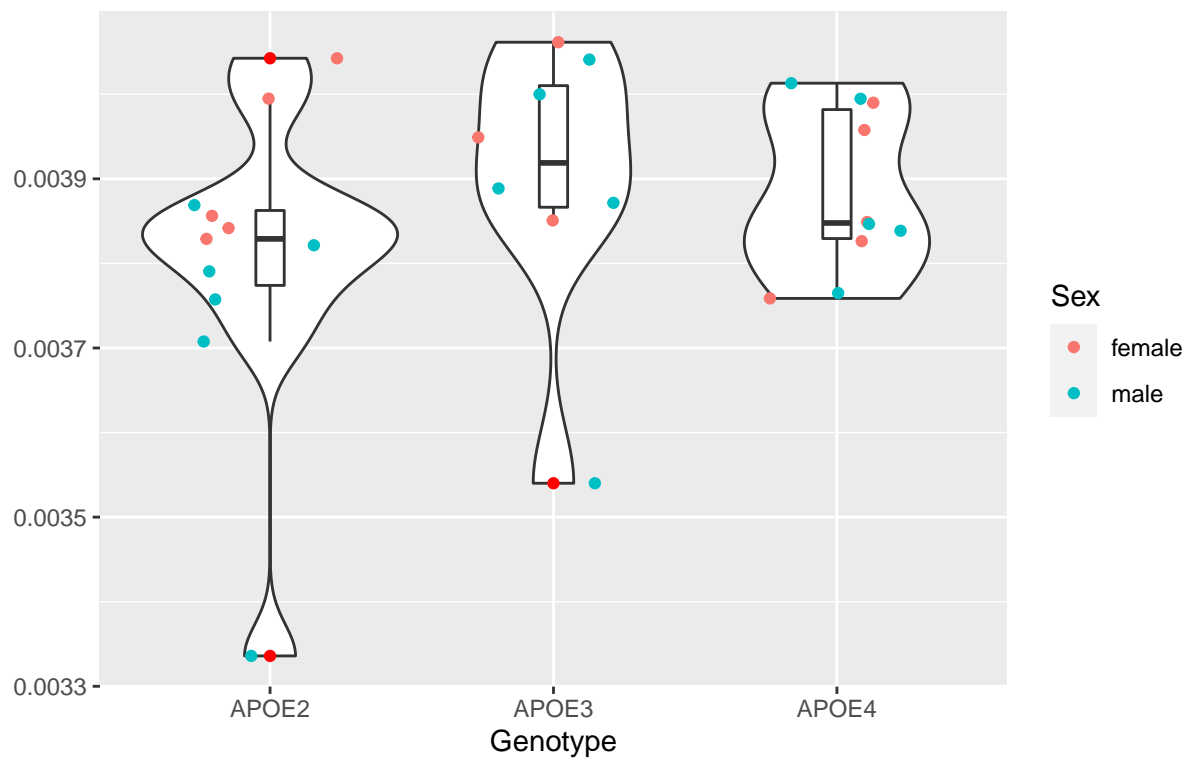
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.560e-09	7.820e-10	0.107	0.899
## Residuals	26	1.897e-07	7.297e-09		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.950e-08 1.477e-08   0.669  0.521
## Residuals 26 5.737e-07 2.207e-08
```

Red Nucleus Magnocellular

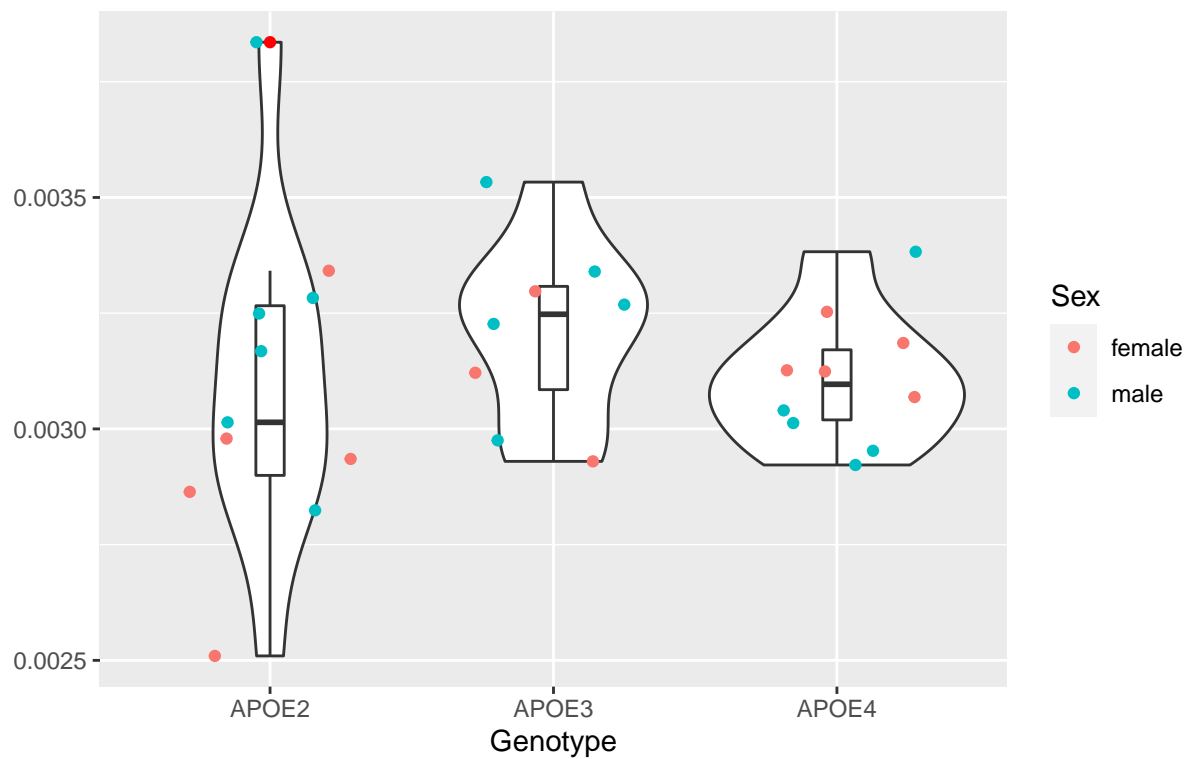
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	5.290e-08	2.644e-08	1.131	0.338
## Residuals	26	6.081e-07	2.339e-08		

Pararubral Nucleus

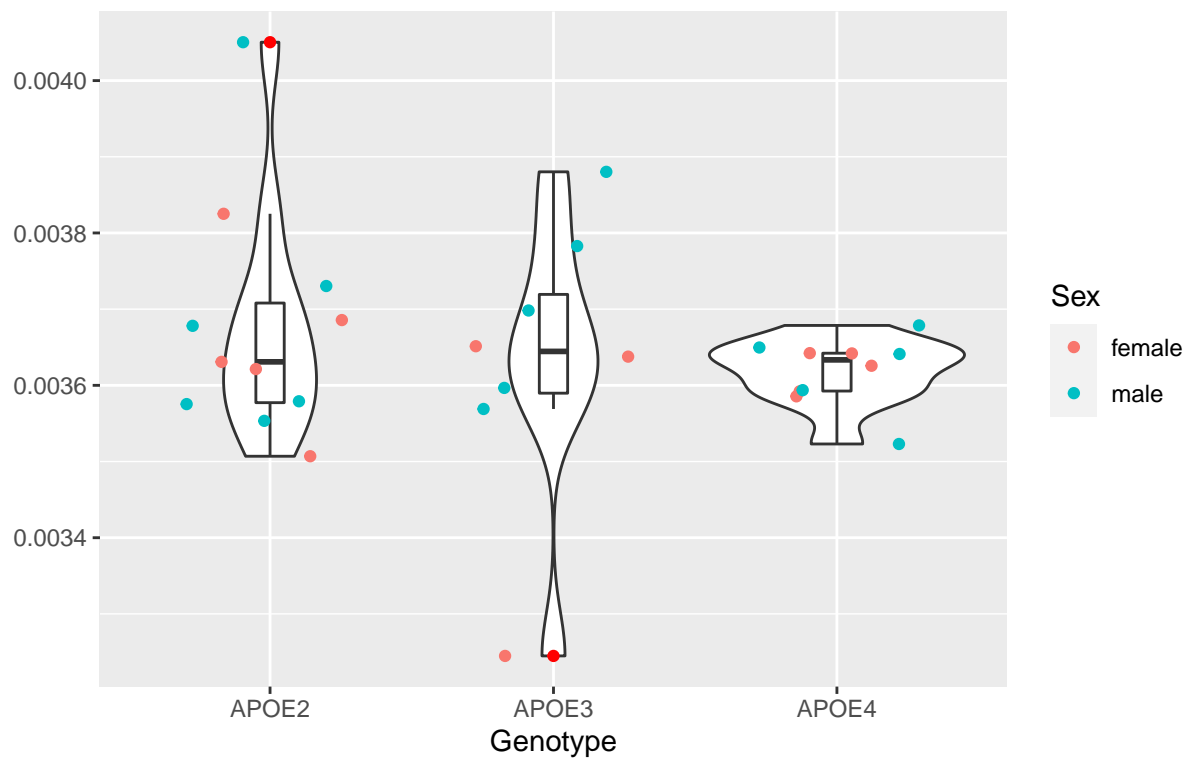
Red points denoting outliers



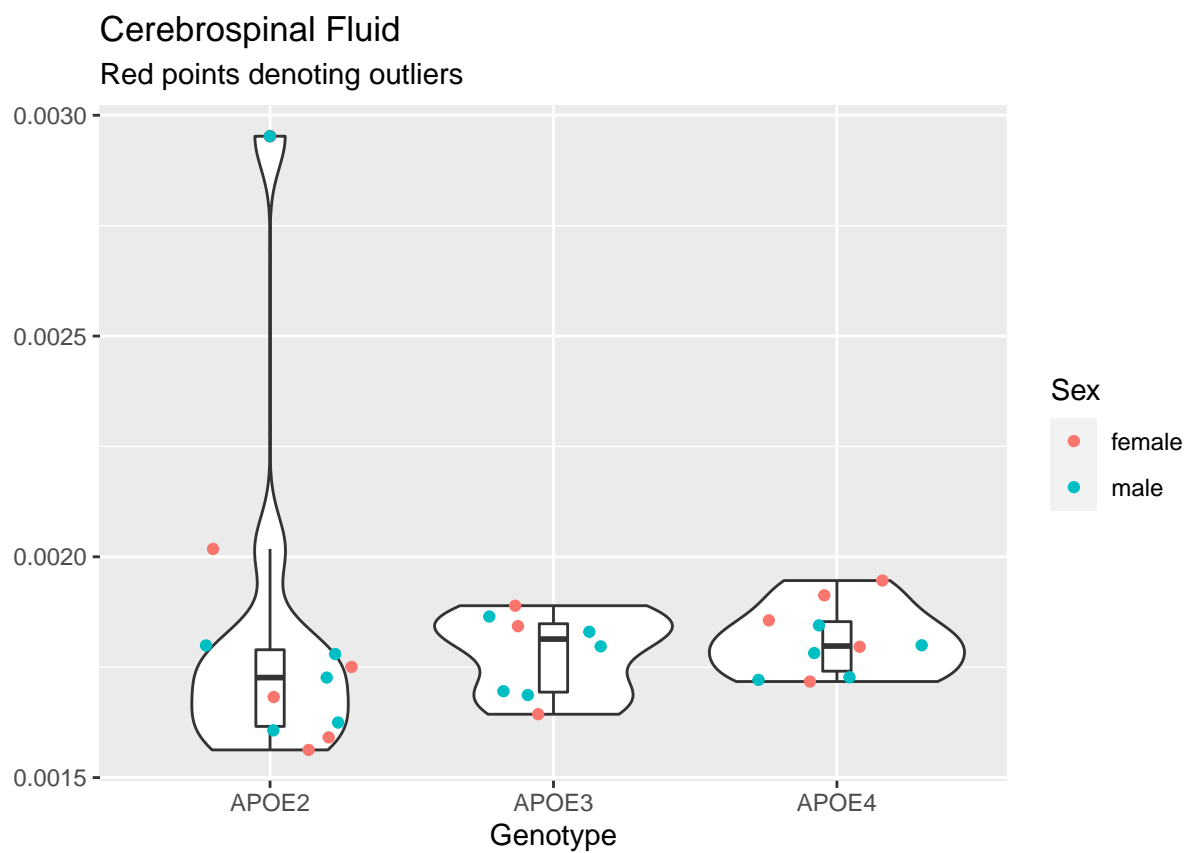
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.510e-08	3.754e-08	0.595	0.559
## Residuals	26	1.639e-06	6.305e-08		

Retro Rubral Fluid

Red points denoting outliers



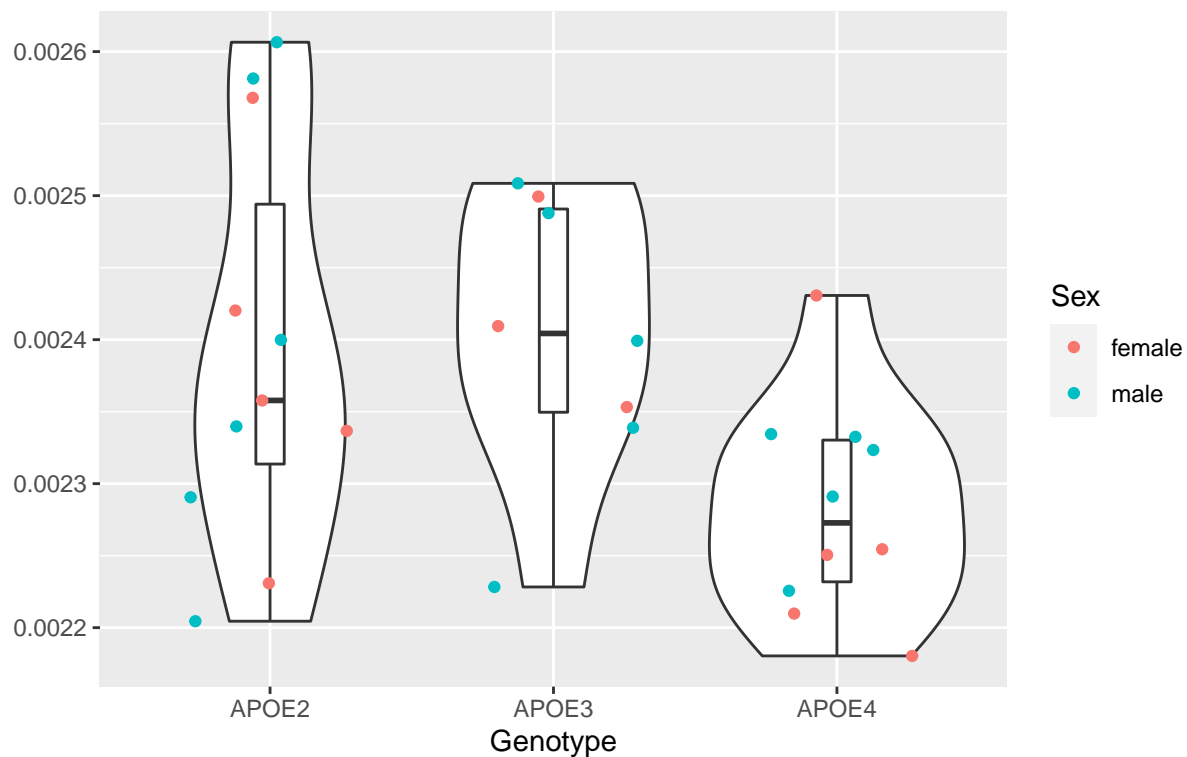
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.940e-08	9.721e-09	0.51	0.606
## Residuals	26	4.956e-07	1.906e-08		



```
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## geno       2 9.600e-09 4.810e-09   0.075  0.928
## Residuals 26 1.675e-06 6.442e-08
```

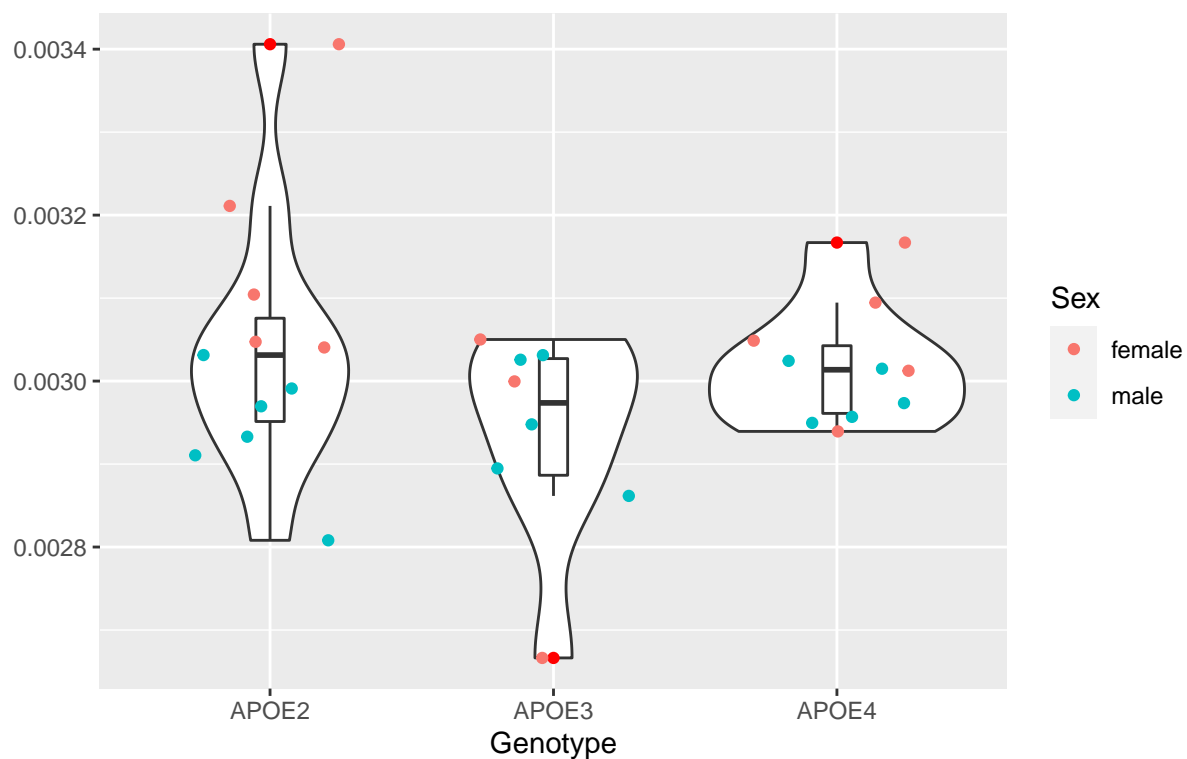
Intermediate Reticular Nucleus

Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 8.648e-08 4.324e-08   3.668 0.0395 *
## Residuals    26 3.065e-07 1.179e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

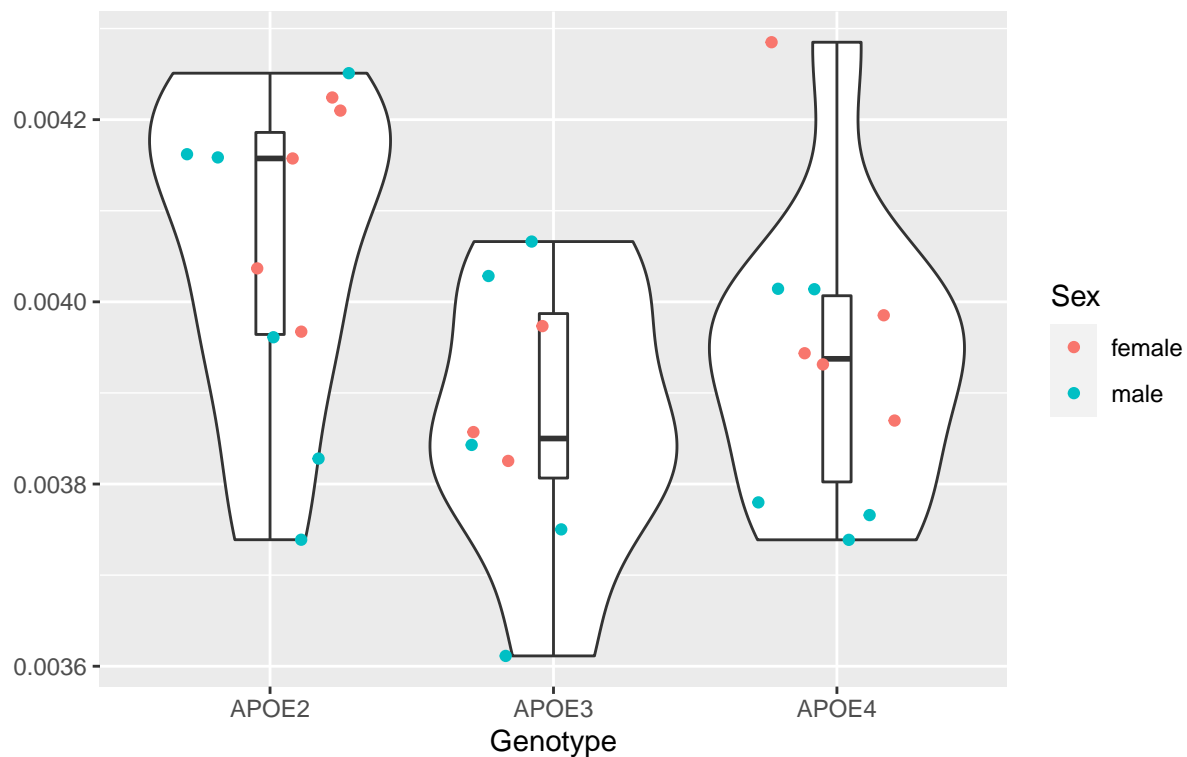
Posterior Dorsal Paraventricular Medial Parvicellular Posterior Lateral Hy
 Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 5.560e-08 2.782e-08   1.736  0.196
## Residuals 26 4.167e-07 1.602e-08
```


Prerubral Forel

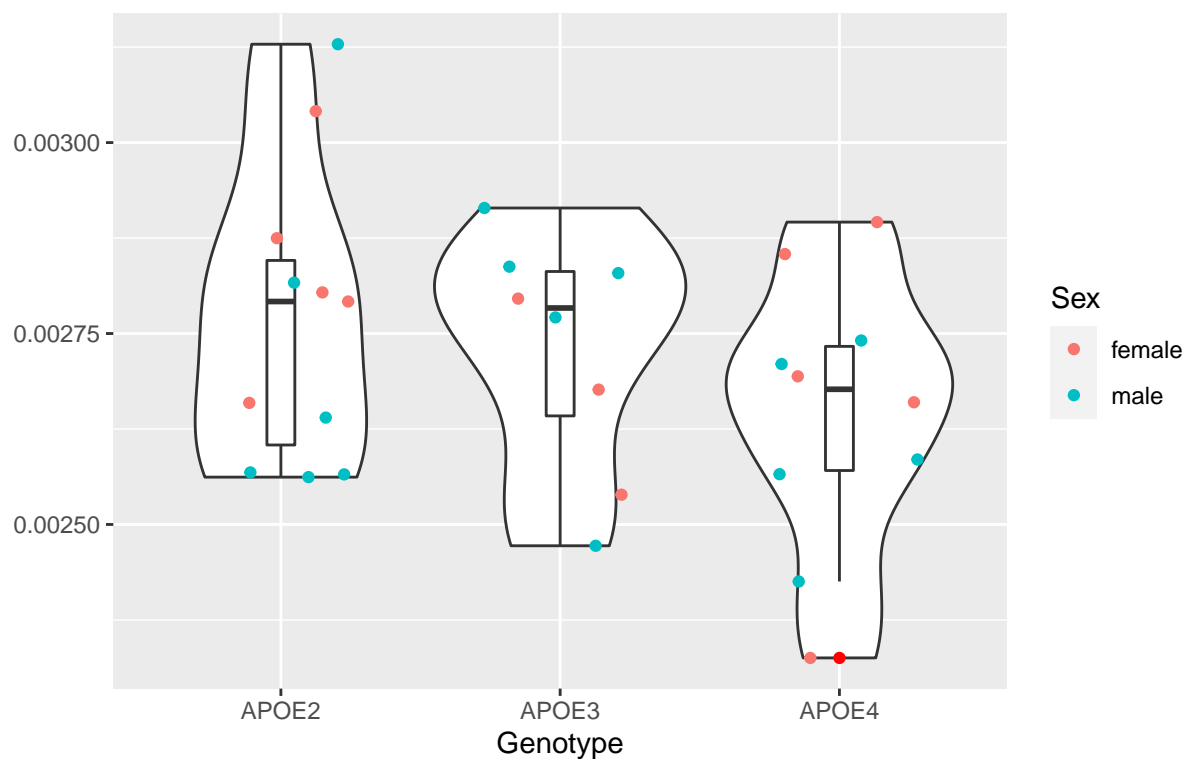
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.897e-07 9.484e-08   3.611 0.0413 *
## Residuals    26 6.828e-07 2.626e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

PVG of Hypothalamus

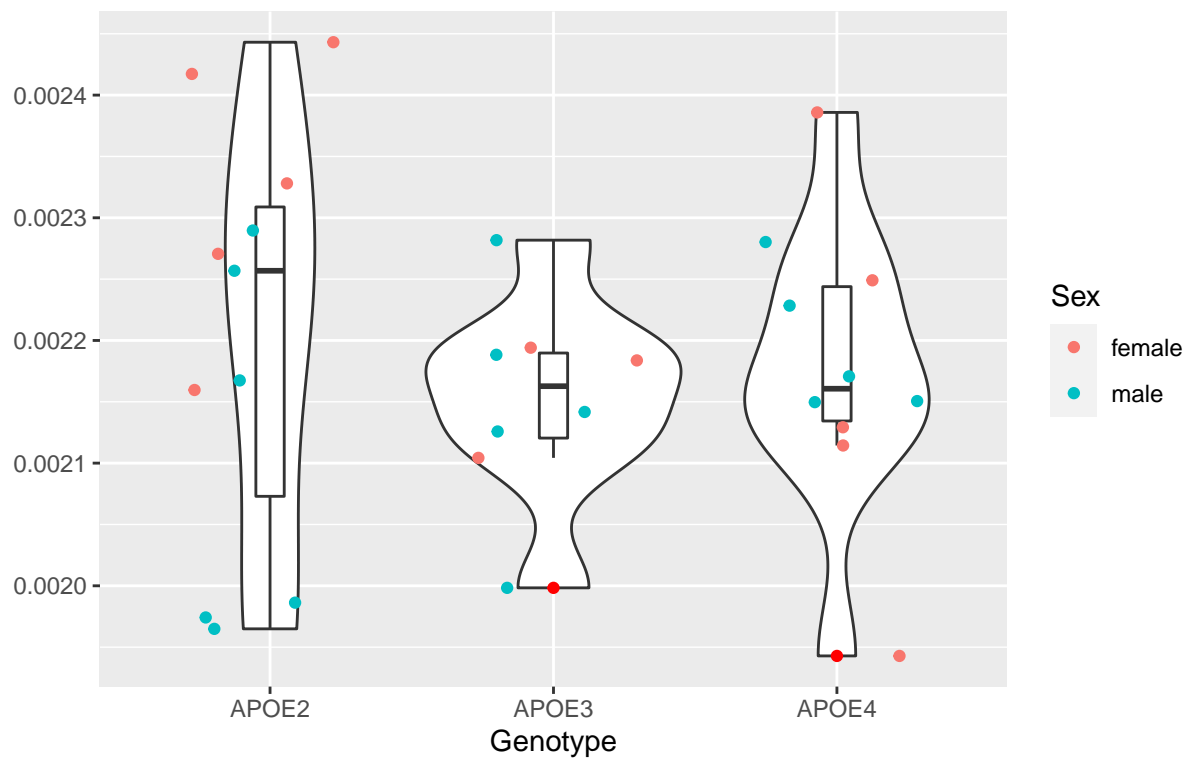
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 8.110e-08 4.055e-08   1.282  0.294
## Residuals 26 8.223e-07 3.163e-08
```

Basal Lateral Amygdala

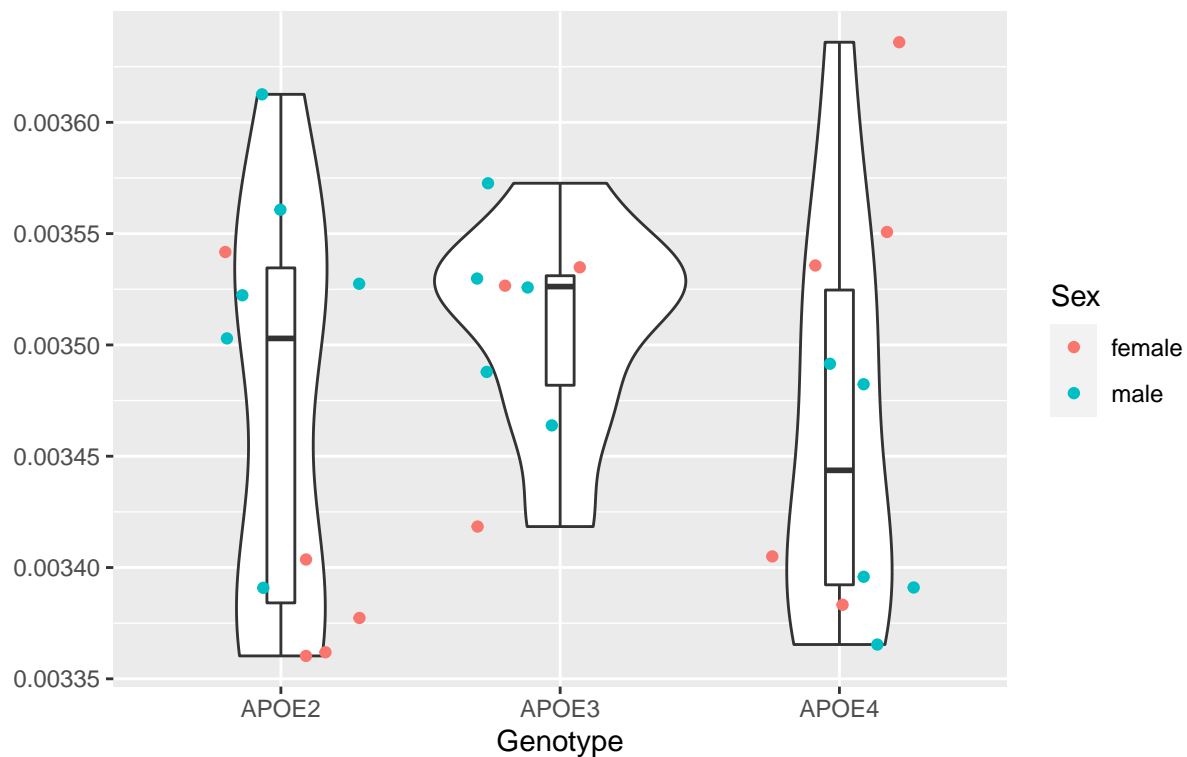
Red points denoting outliers



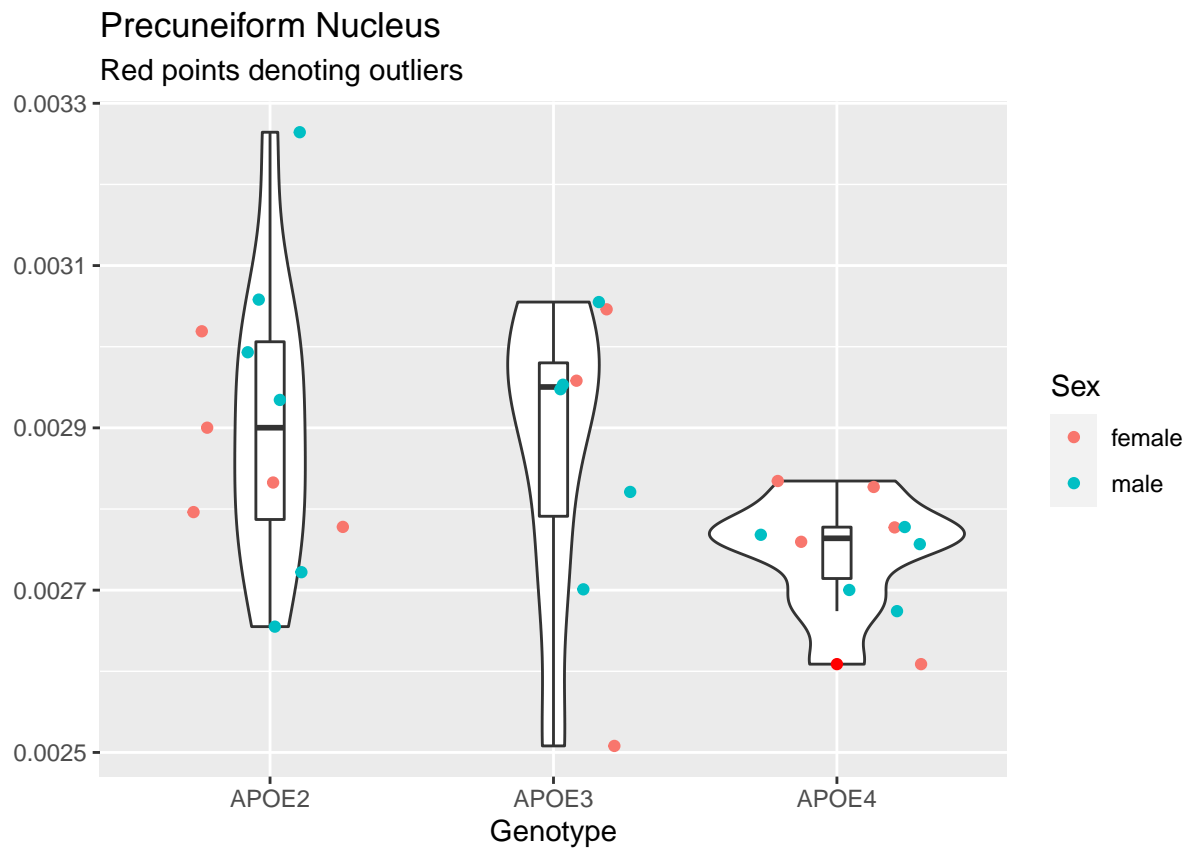
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.310e-08	6.532e-09	0.365	0.698
## Residuals	26	4.654e-07	1.790e-08		

Brain Stem Rest

Red points denoting outliers



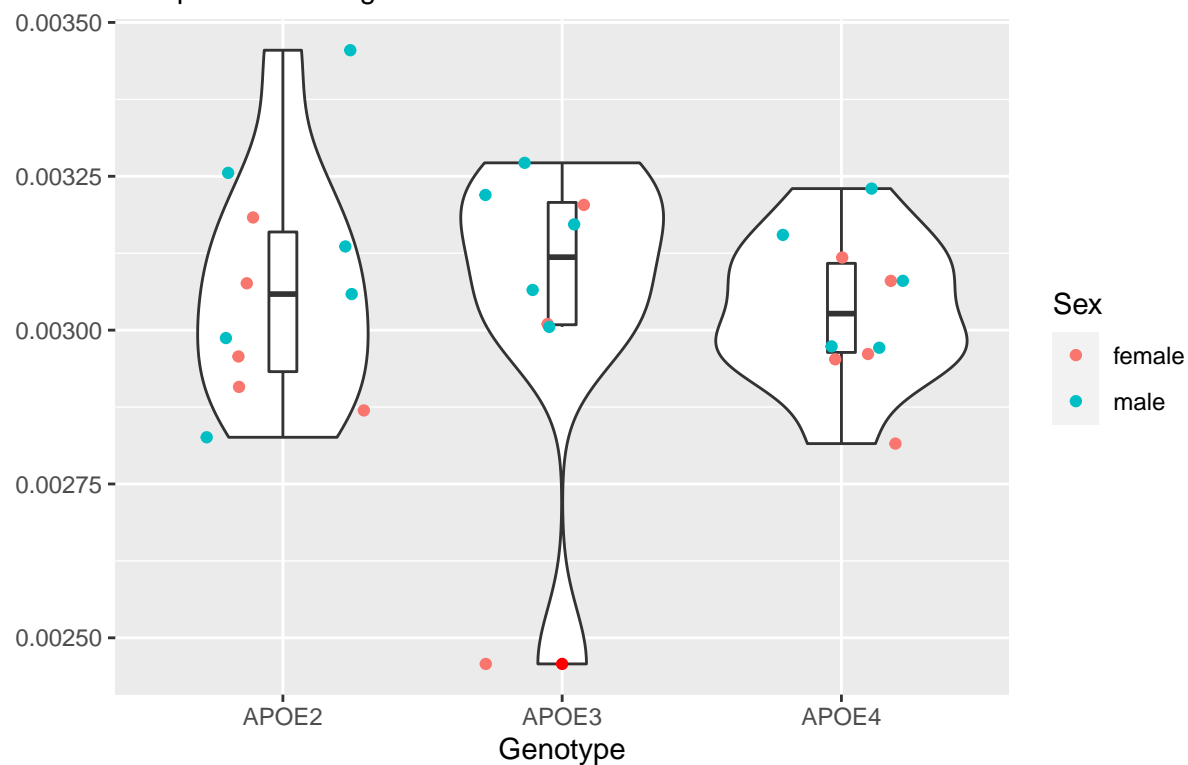
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	9.850e-09	4.923e-09	0.739	0.487
## Residuals	26	1.732e-07	6.663e-09		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.390e-07 6.950e-08    3.04 0.0651 .
## Residuals    26 5.944e-07 2.286e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cuneiform Nucleus

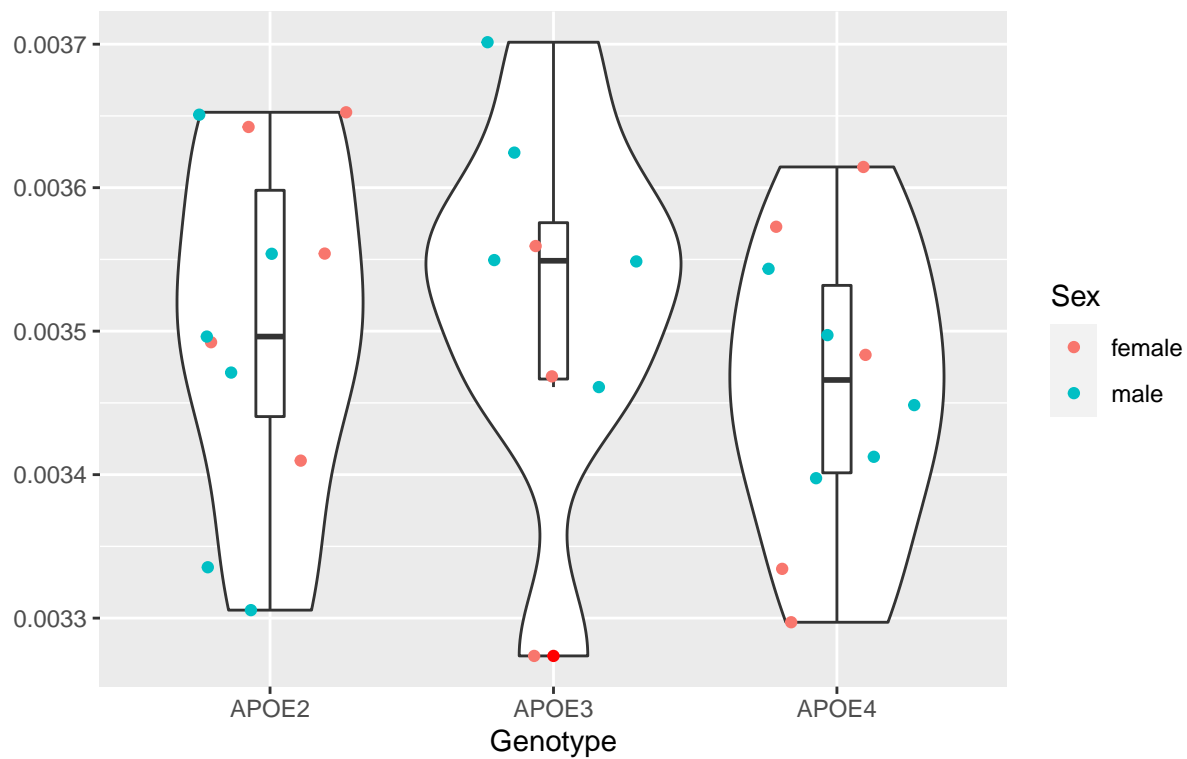
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	5.000e-09	2.510e-09	0.069	0.934
## Residuals	26	9.478e-07	3.645e-08		

Midbrain Linear Nucleus

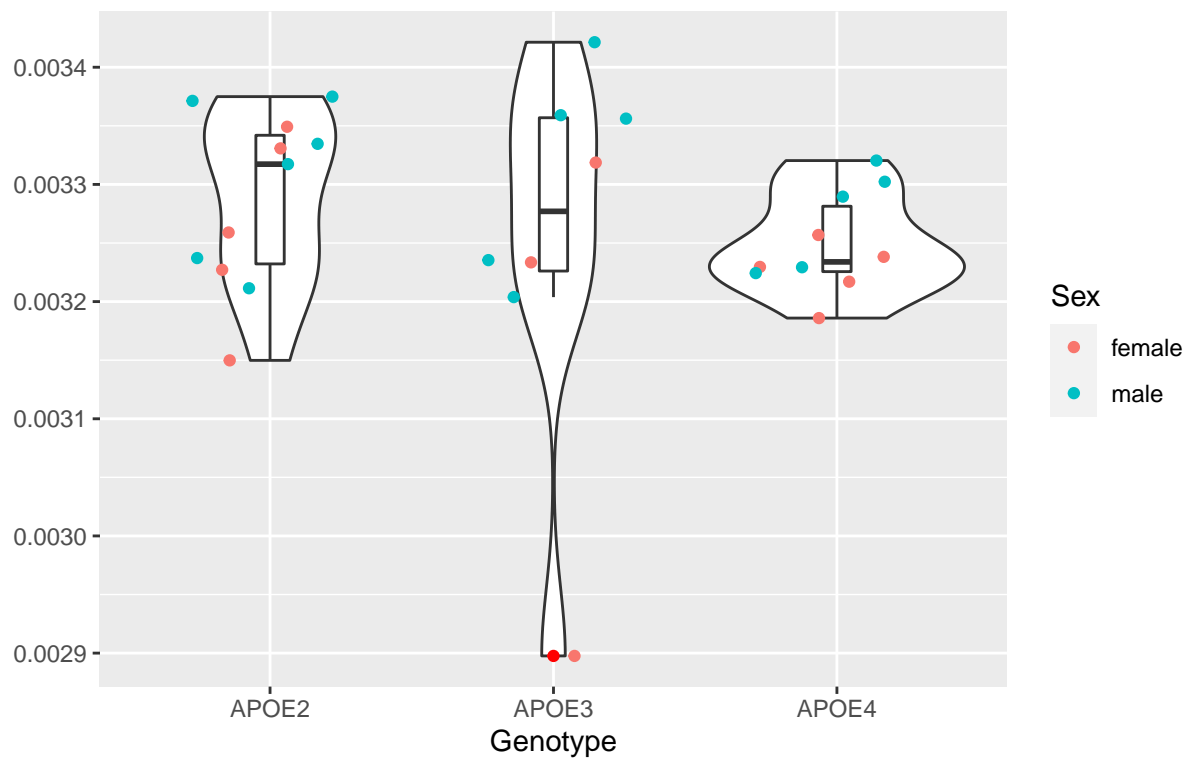
Red points denoting outliers



```
##          Df    Sum Sq Mean Sq F value Pr(>F)
## geno      2 1.990e-08 9.93e-09    0.73  0.491
## Residuals 26 3.535e-07 1.36e-08
```

Midbrain Reticular Nucleus

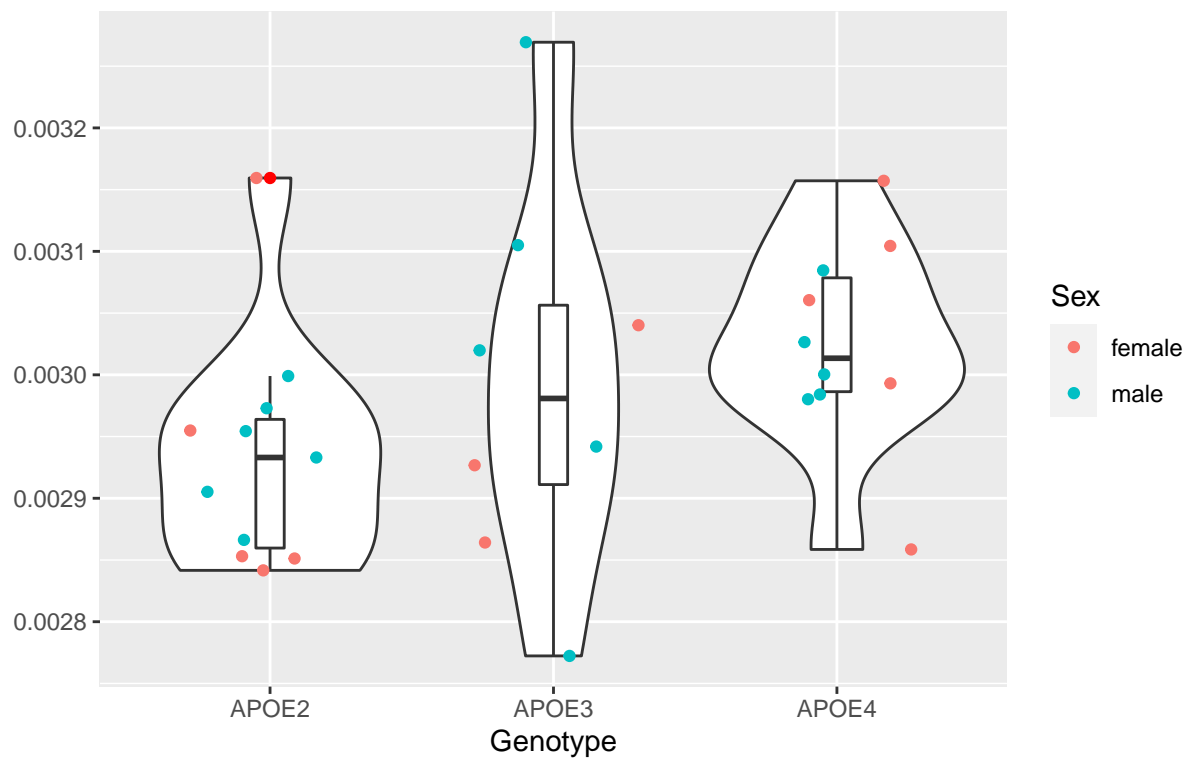
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	9.140e-09	4.572e-09	0.466	0.633
## Residuals	26	2.553e-07	9.819e-09		

Red Nucleus Parvicellular

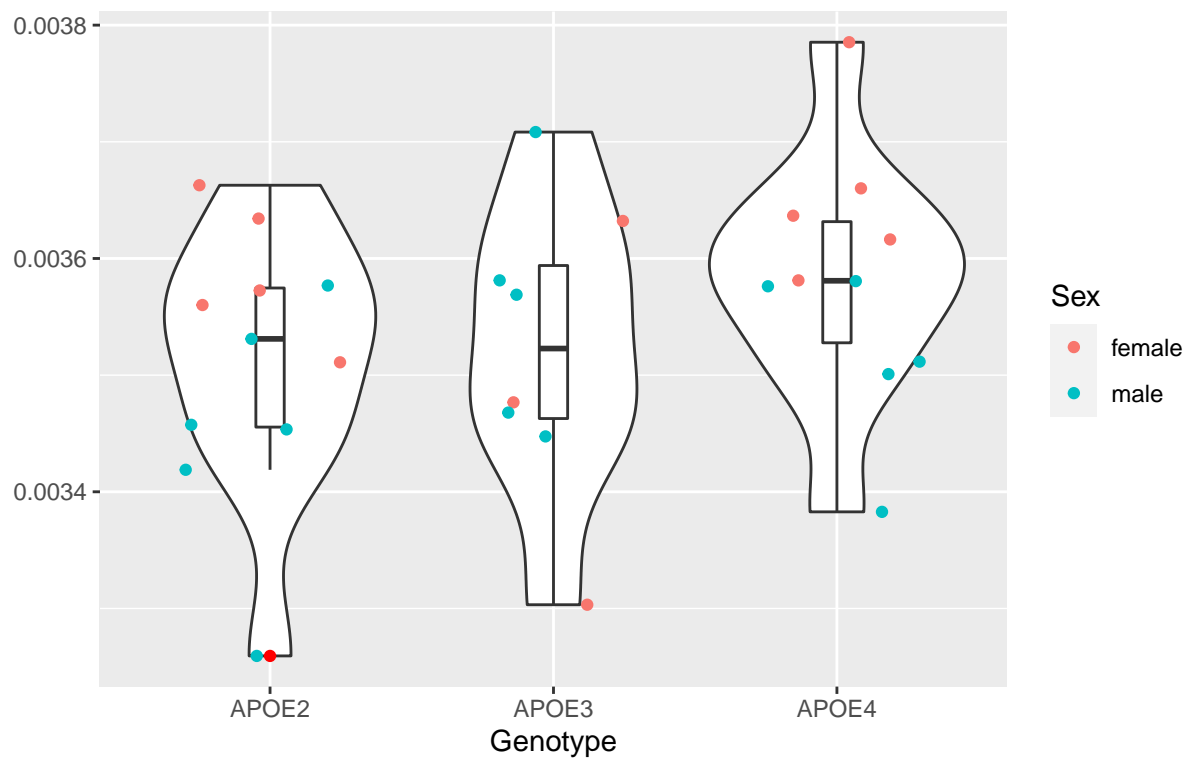
Red points denoting outliers



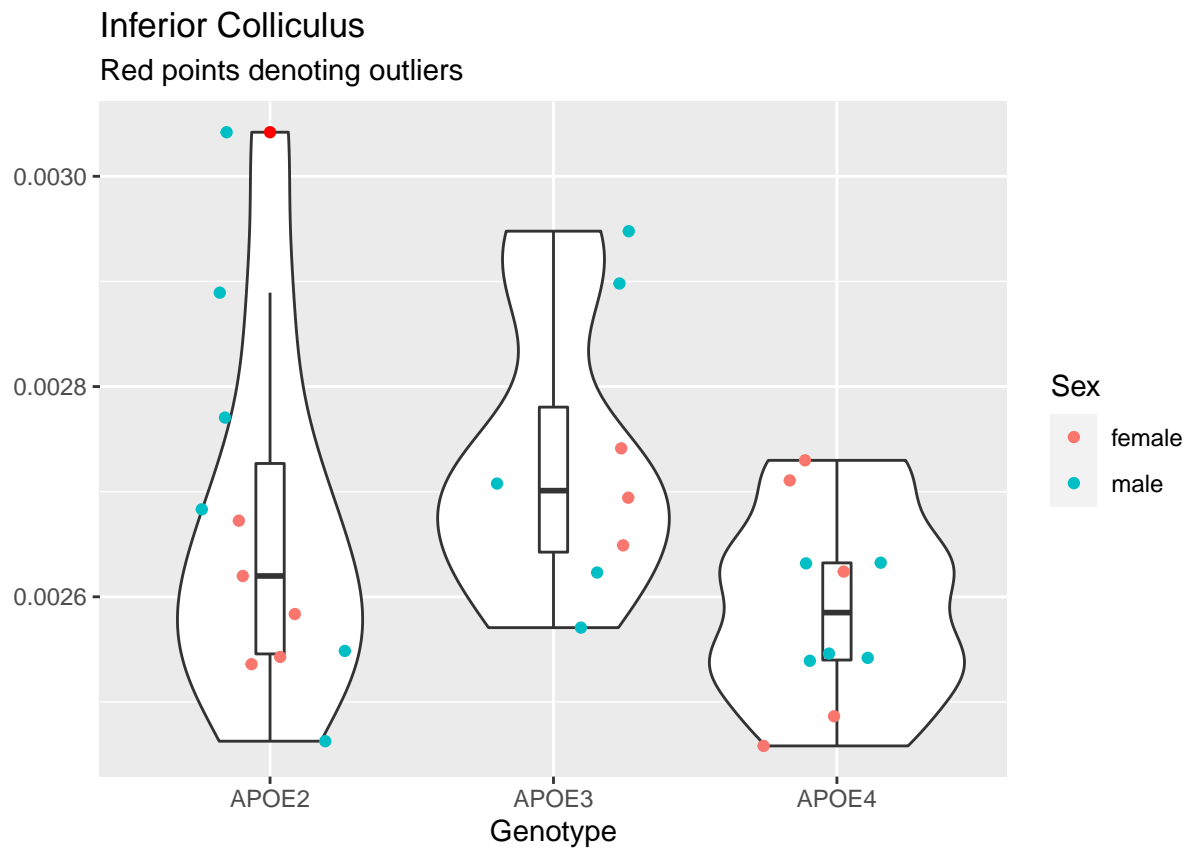
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.305e-08	2.152e-08	1.802	0.185
## Residuals	26	3.105e-07	1.194e-08		

Substantia Nigra

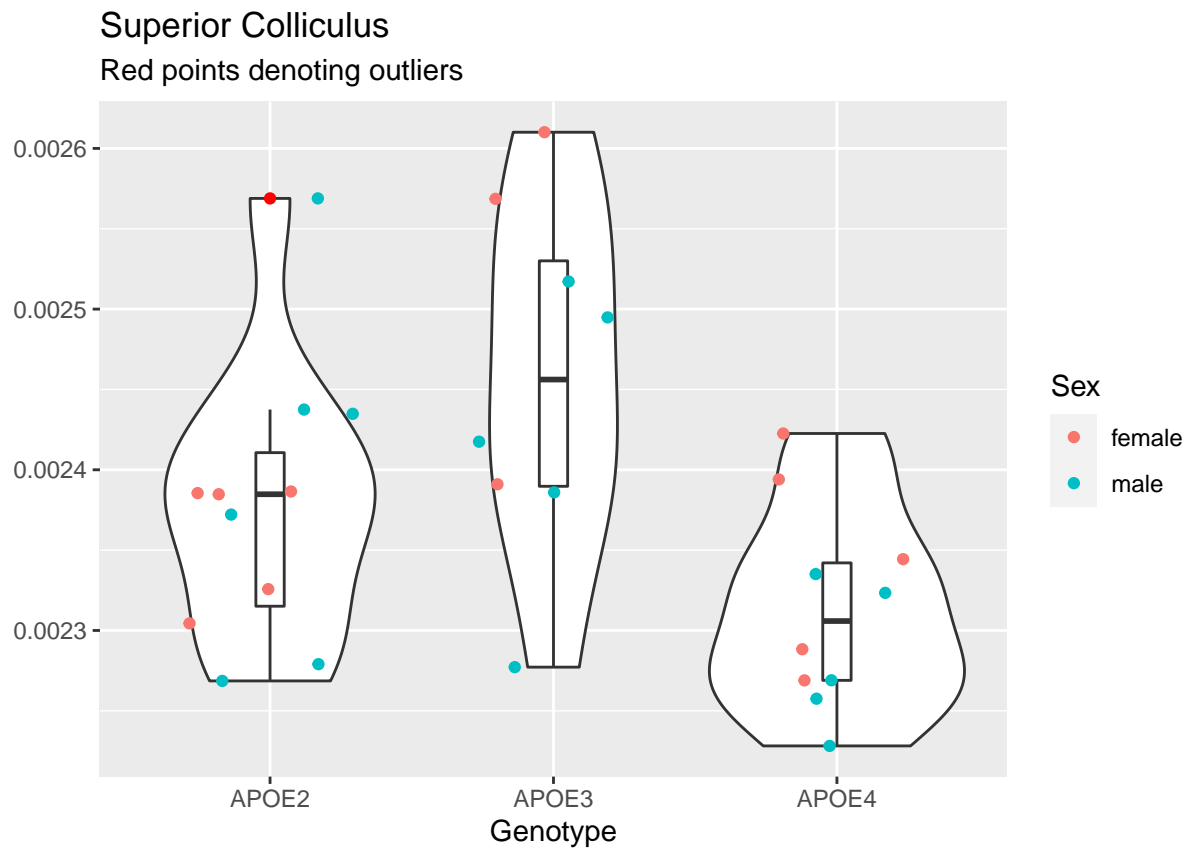
Red points denoting outliers



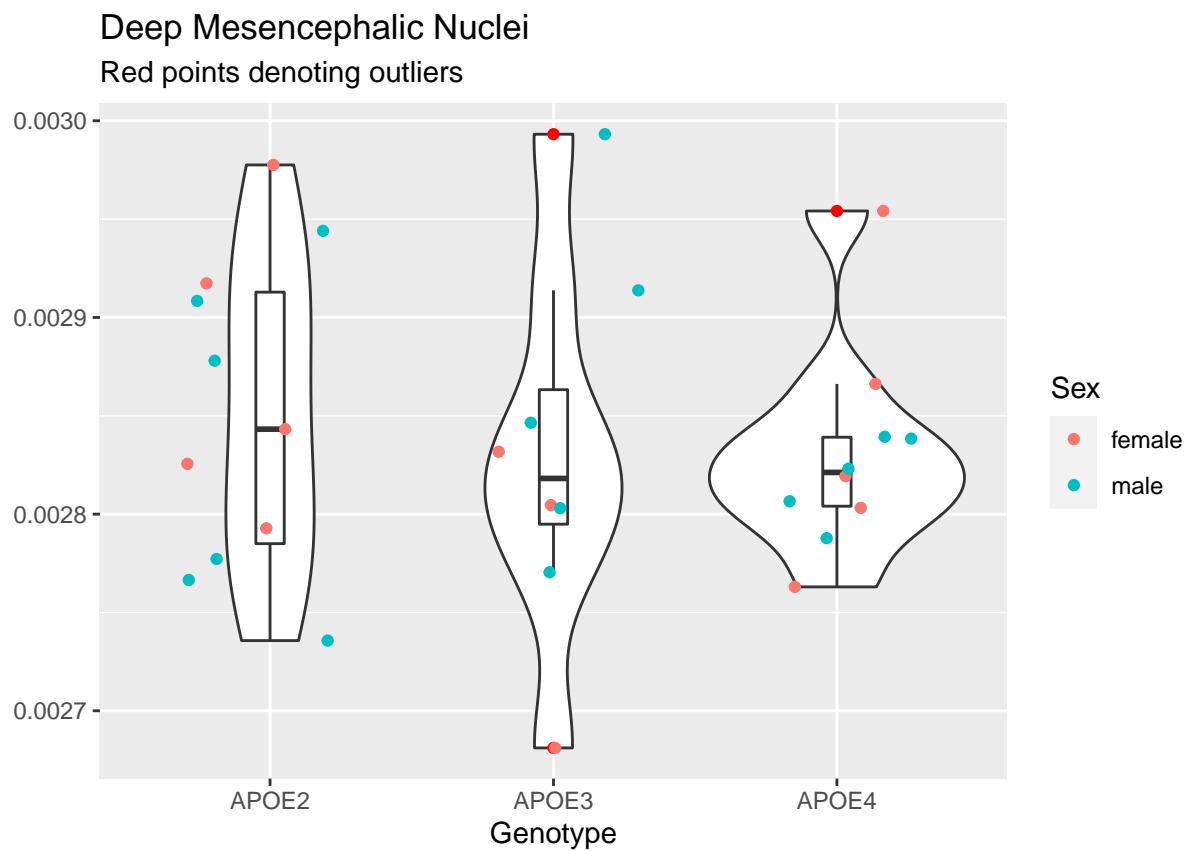
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.920e-08	1.459e-08	1.113	0.344
## Residuals	26	3.409e-07	1.311e-08		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 8.770e-08 4.383e-08    2.31  0.119
## Residuals 26 4.933e-07 1.897e-08
```



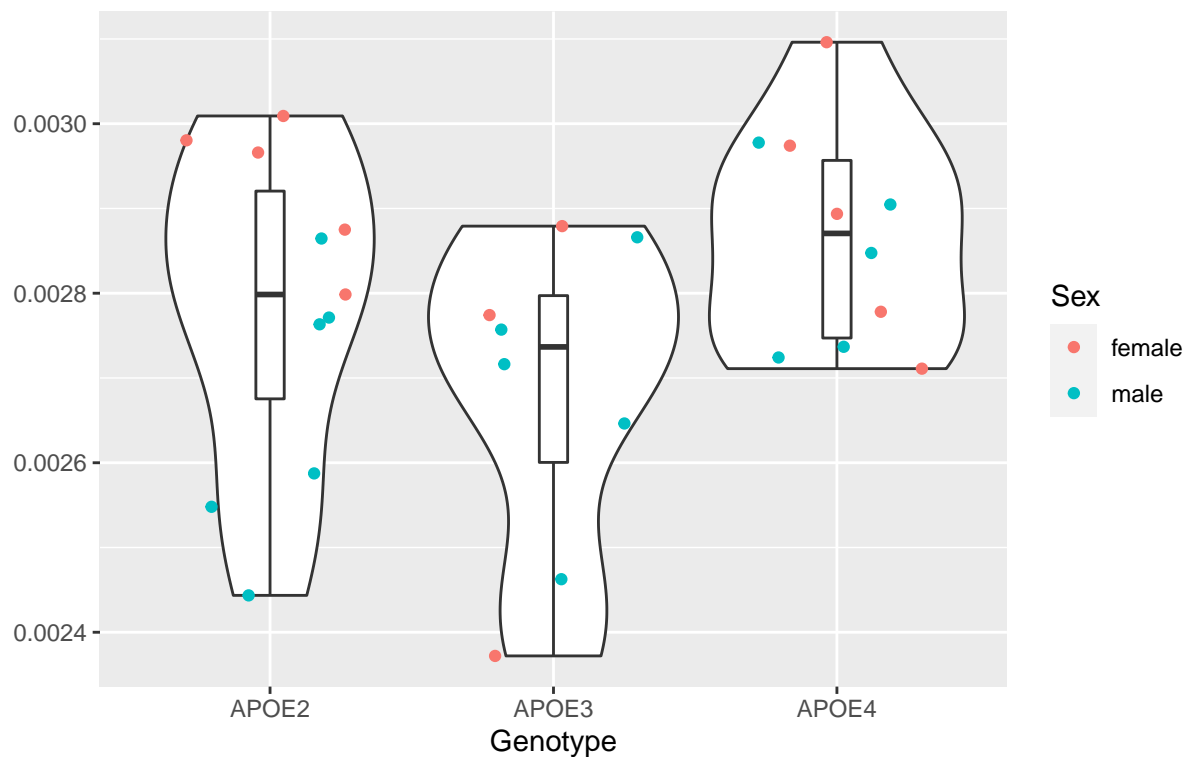
```
##          Df    Sum Sq Mean Sq F value    Pr(>F)
## geno         2 9.299e-08 4.65e-08    6.281 0.00595 **
## Residuals    26 1.925e-07 7.40e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.070e-09	1.533e-09	0.268	0.767
## Residuals	26	1.486e-07	5.717e-09		

Subbrachial Nucleus and Peripeduncular Nucleus

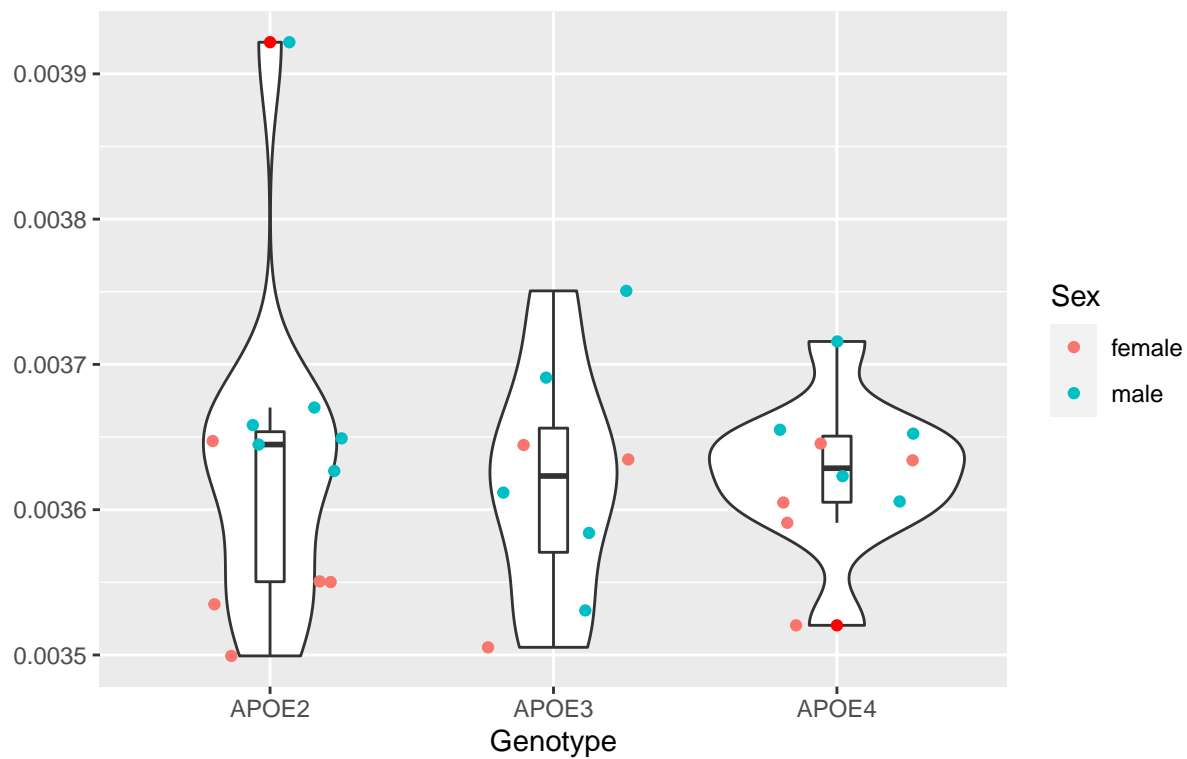
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.443e-07 7.215e-08   2.57 0.0958 .
## Residuals    26 7.299e-07 2.807e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Reticular Nucleus of Thalamus

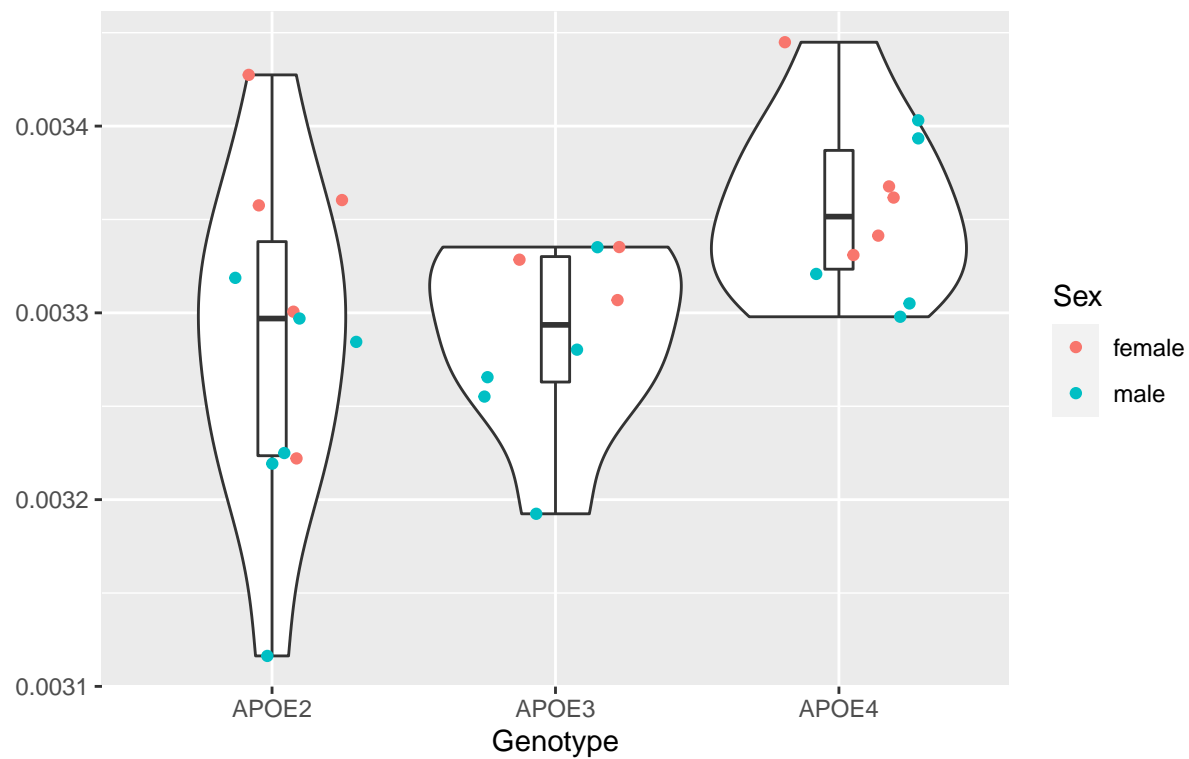
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.100e-10	4.070e-10	0.054	0.948
## Residuals	26	1.959e-07	7.533e-09		

Zona Incerta

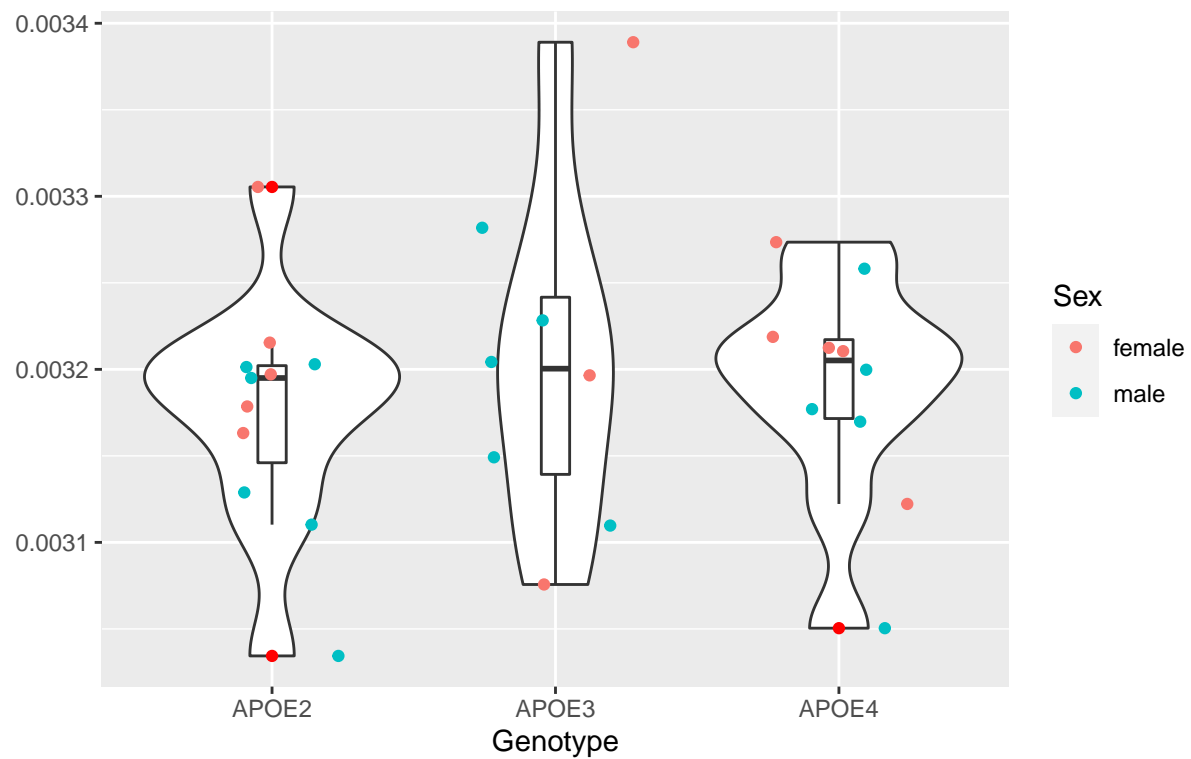
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno       2 3.308e-08 1.654e-08   3.908 0.0328 *
## Residuals 26 1.100e-07 4.233e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Lateral Geniculate Nucleus

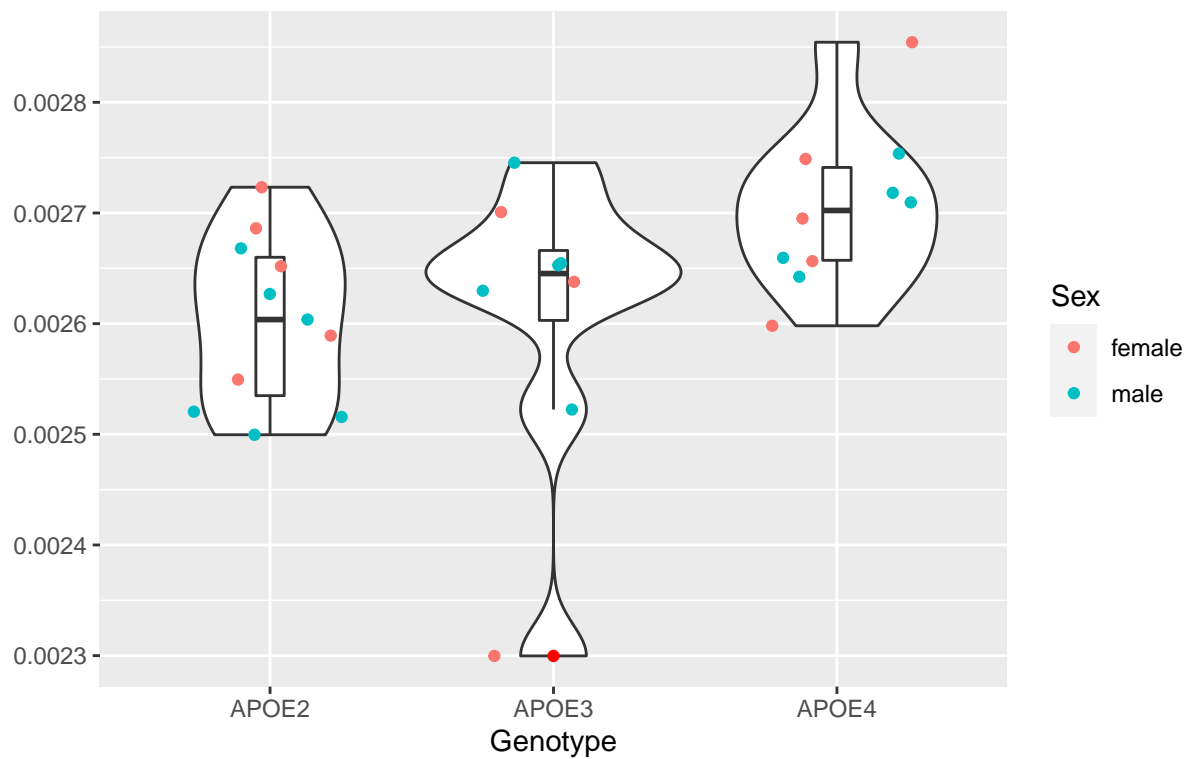
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 3.810e-09 1.906e-09   0.32  0.729
## Residuals 26 1.547e-07 5.949e-09
```

Medial Geniculate Nucleus

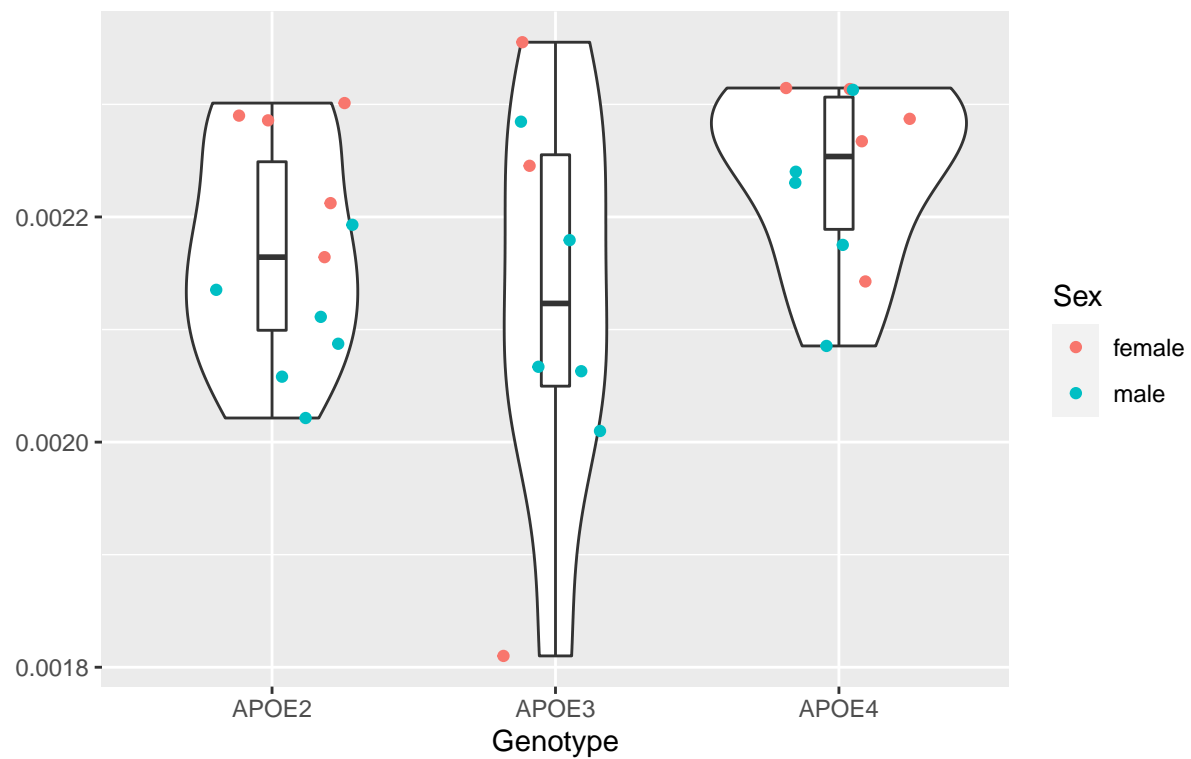
Red points denoting outliers



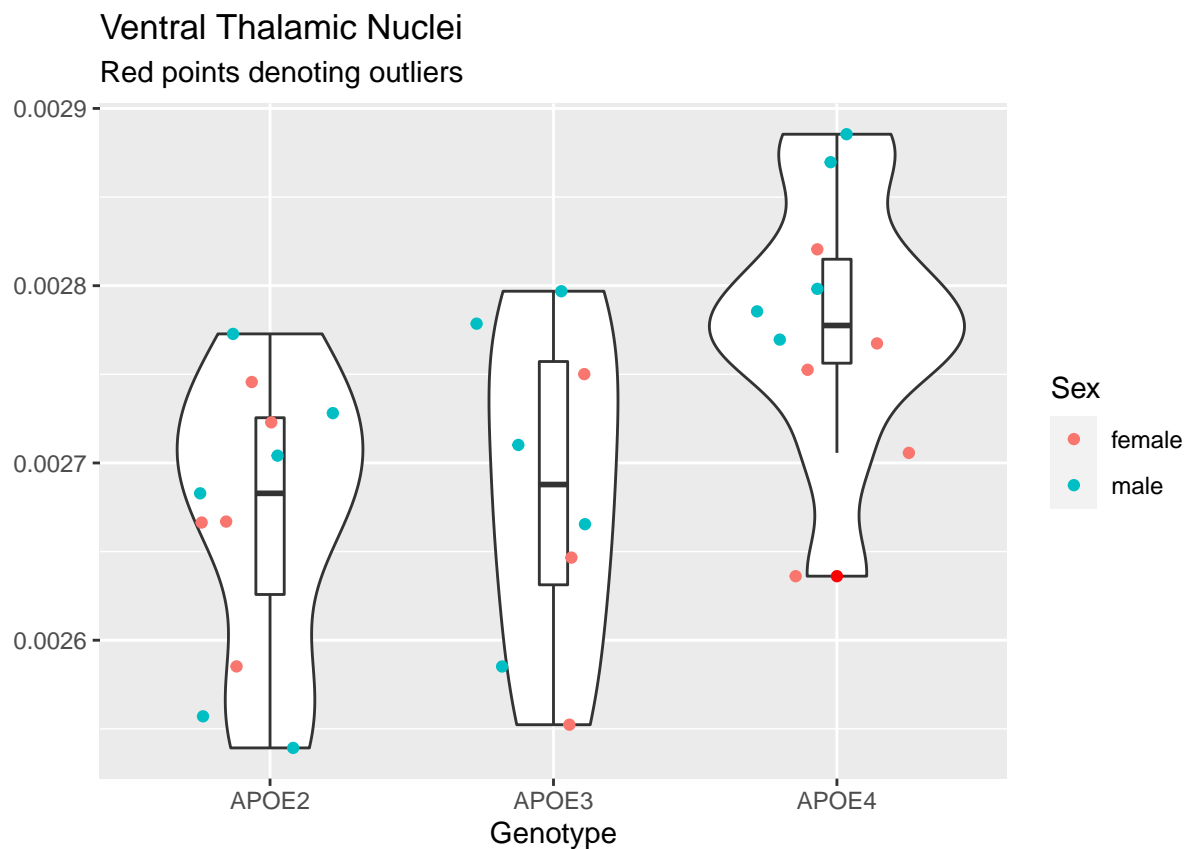
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 6.491e-08 3.246e-08   3.535 0.0439 *
## Residuals    26 2.387e-07 9.180e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Latero Dorsal Nucleus of Thalamus

Red points denoting outliers



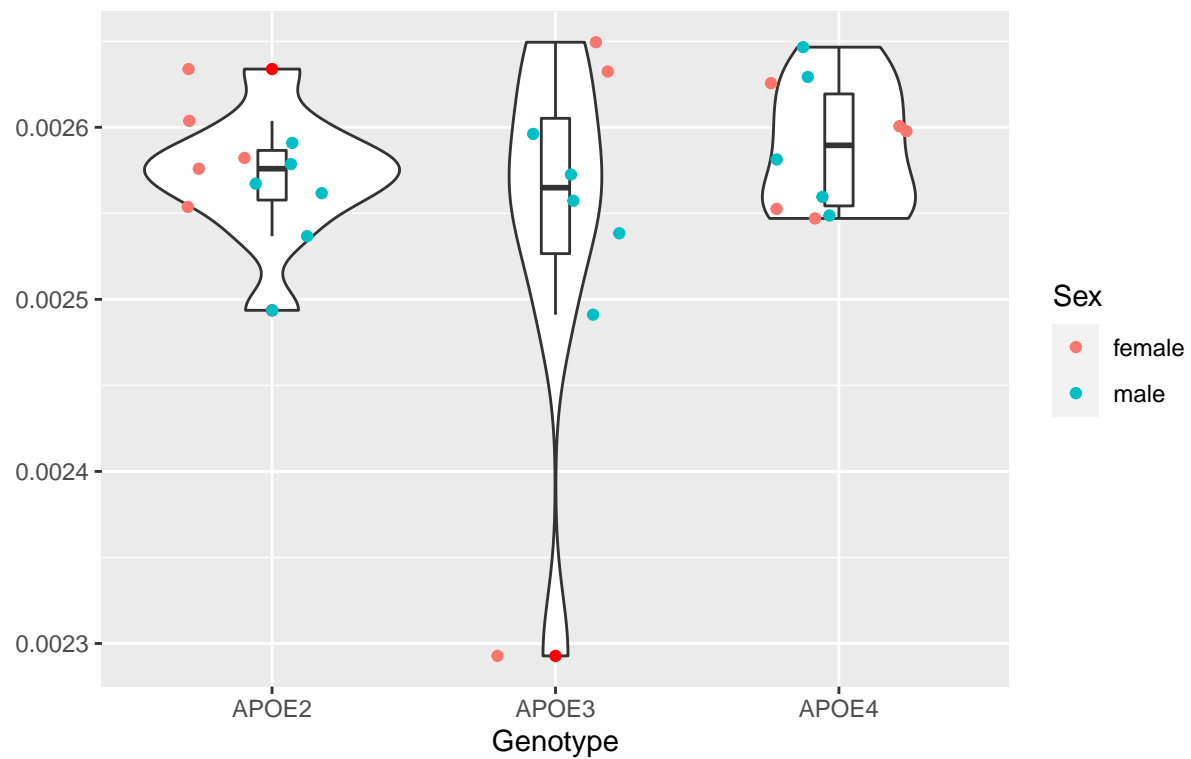
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	5.630e-08	2.817e-08	2.002	0.155
## Residuals	26	3.659e-07	1.407e-08		



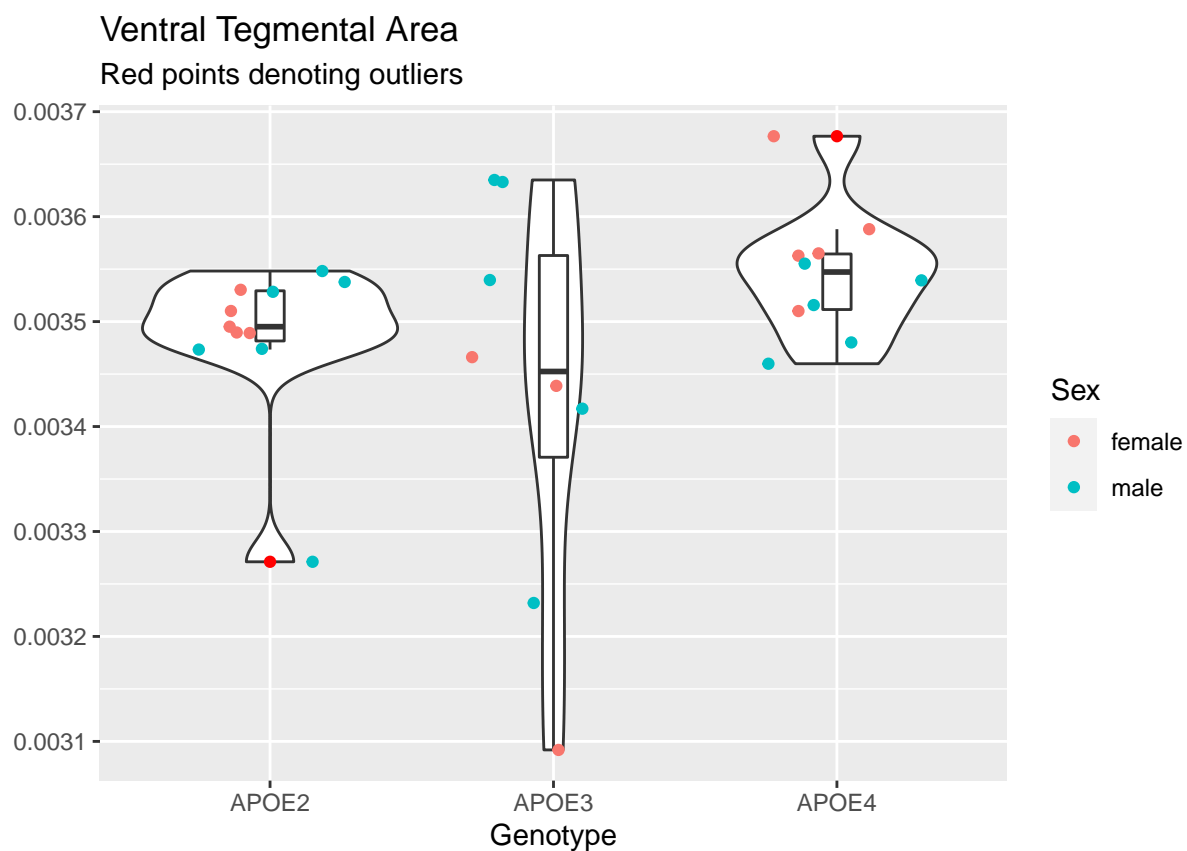
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 6.983e-08 3.492e-08   5.508 0.0101 *
## Residuals    26 1.648e-07 6.340e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

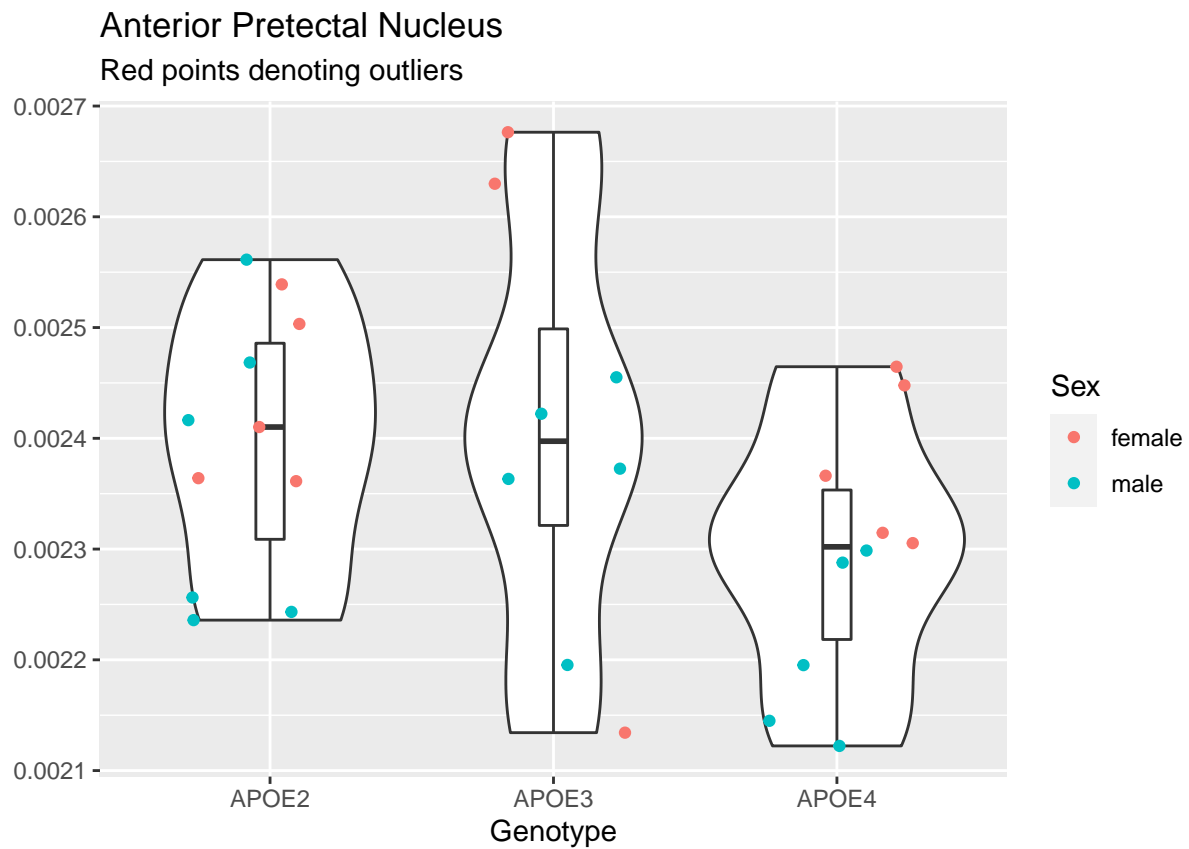
Thalamus Rest

Red points denoting outliers



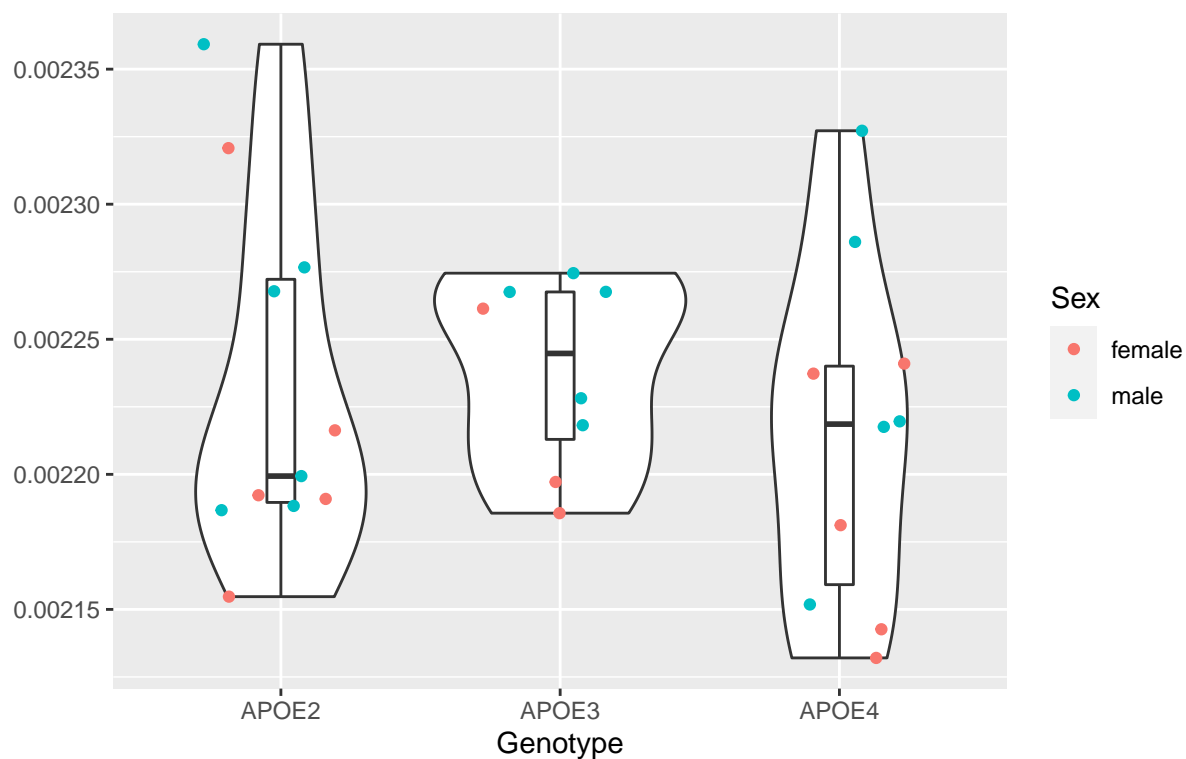
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.015e-08	5.076e-09	1.159	0.329
## Residuals	26	1.139e-07	4.379e-09		



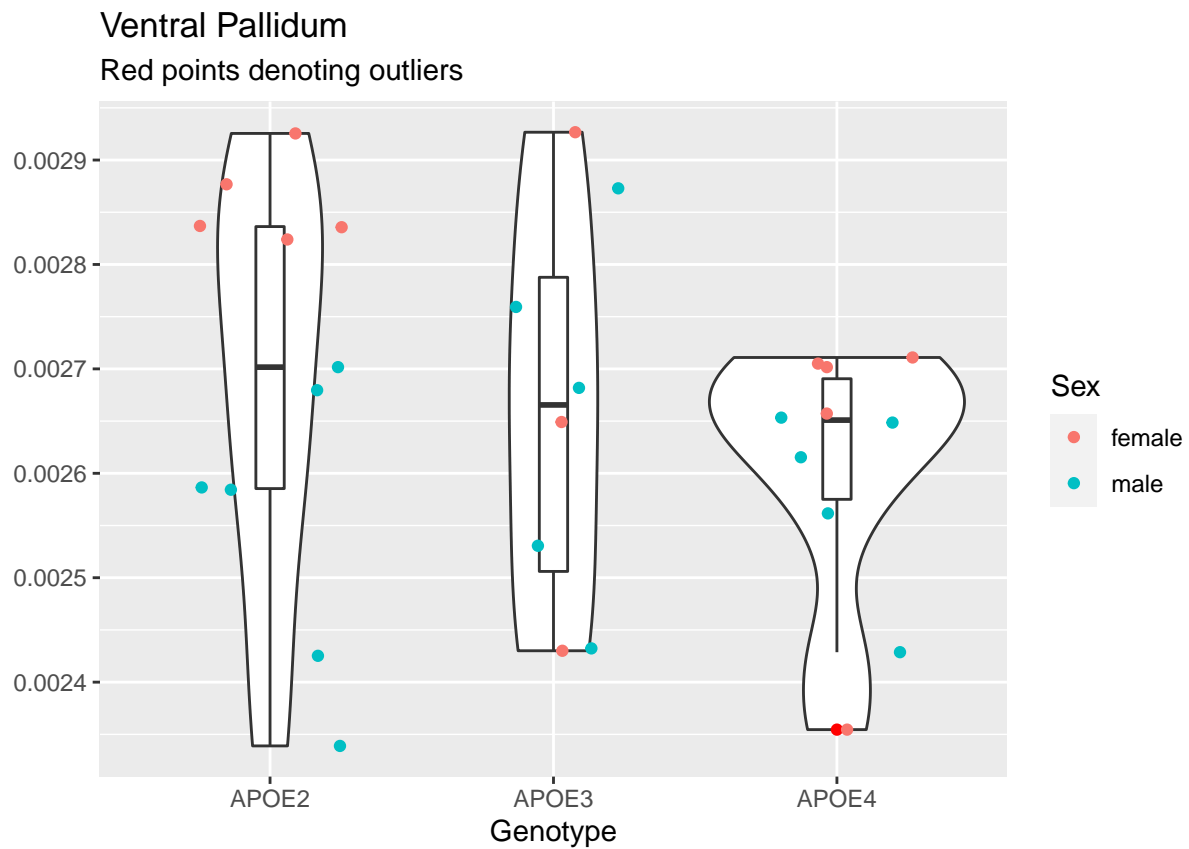


```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 7.360e-08 3.681e-08   1.903  0.169
## Residuals 26 5.029e-07 1.934e-08
```

Periaqueductal Grey Red points denoting outliers



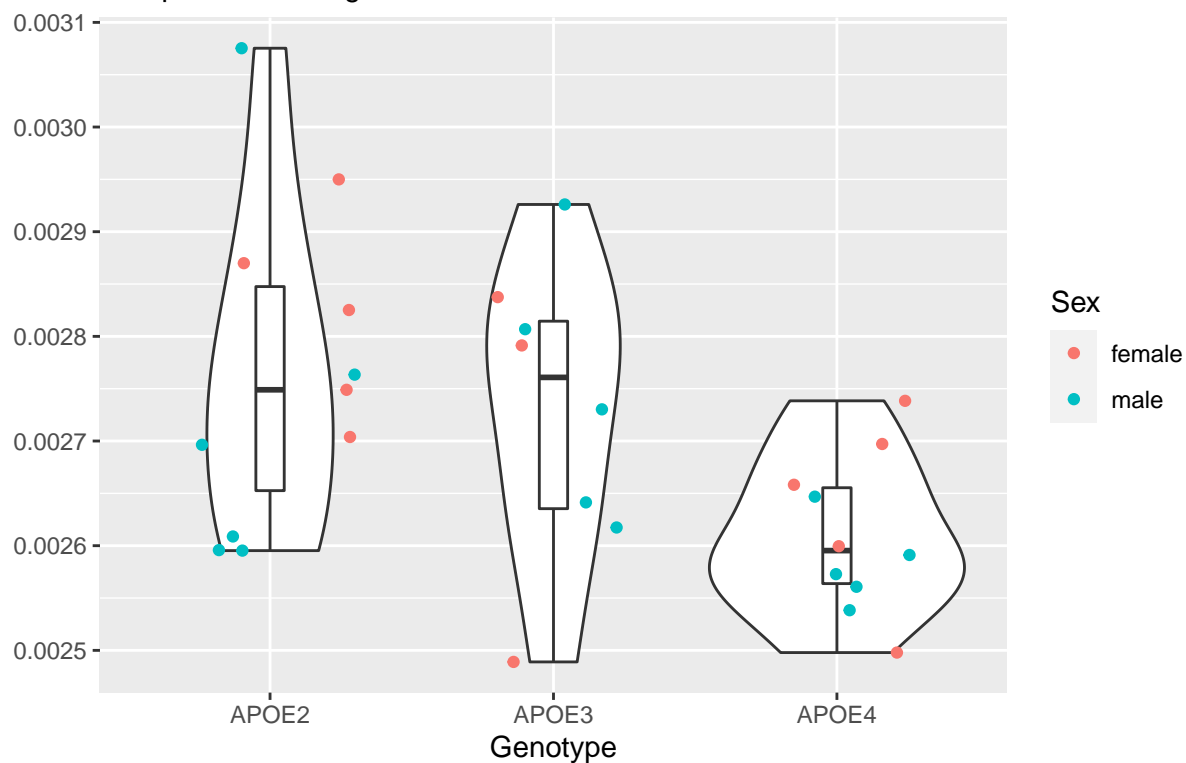
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.950e-09	1.476e-09	0.444	0.646
## Residuals	26	8.643e-08	3.324e-09		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 4.170e-08 2.085e-08   0.725  0.494
## Residuals 26 7.482e-07 2.878e-08
```

Bed Nucleus of the Stria Terminalis

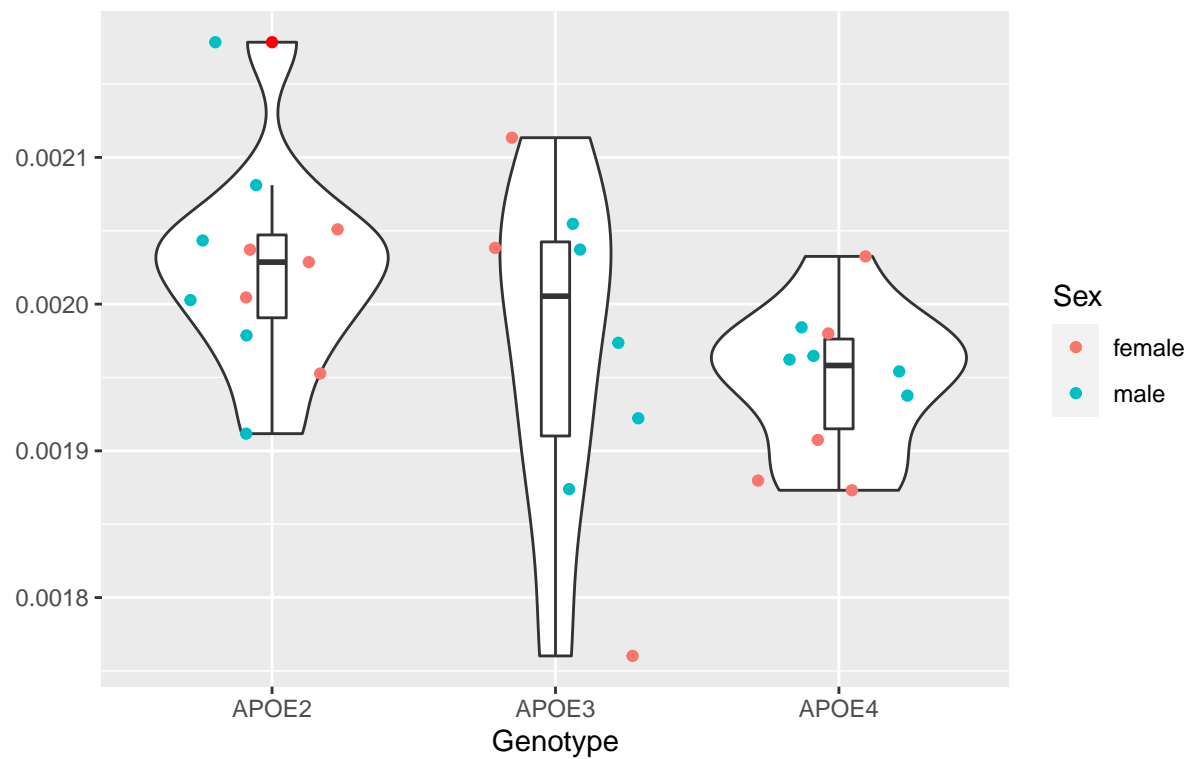
Red points denoting outliers



```
##           Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.366e-07 6.832e-08   4.193 0.0264 *
## Residuals    26 4.237e-07 1.630e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Acumbens

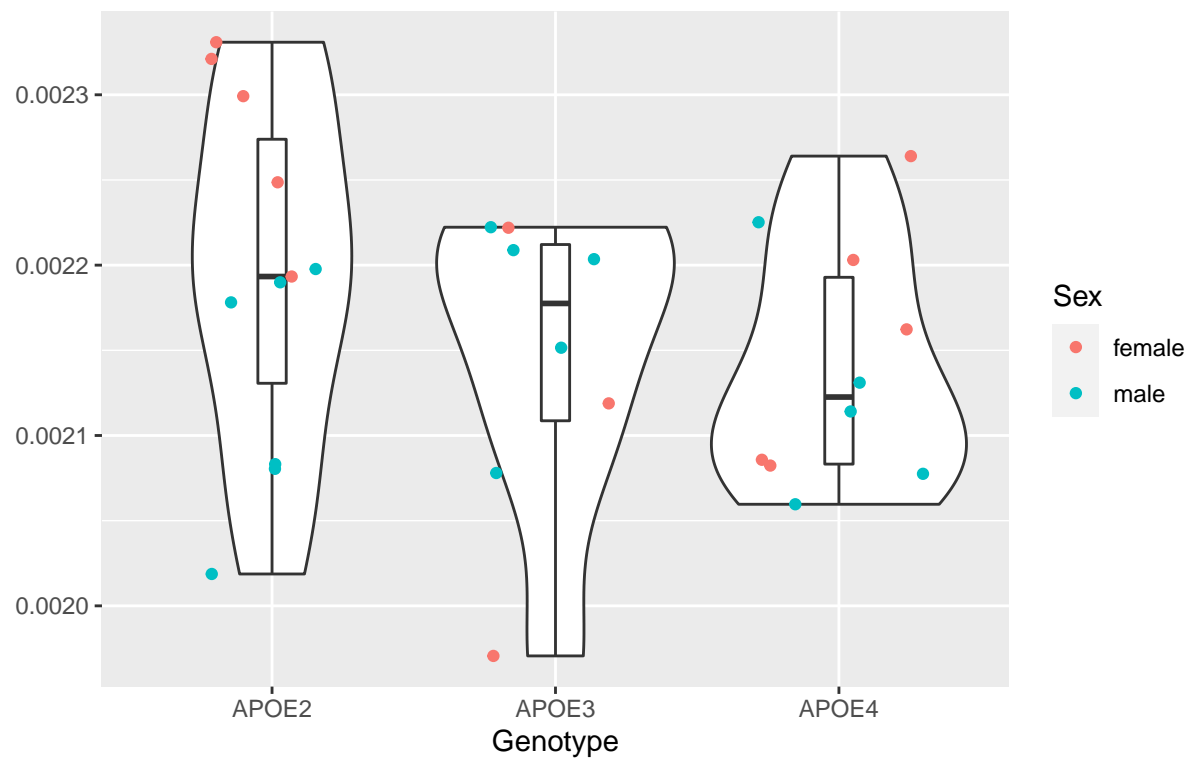
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 3.256e-08 1.628e-08   2.589 0.0943 .
## Residuals    26 1.635e-07 6.288e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Amygdala

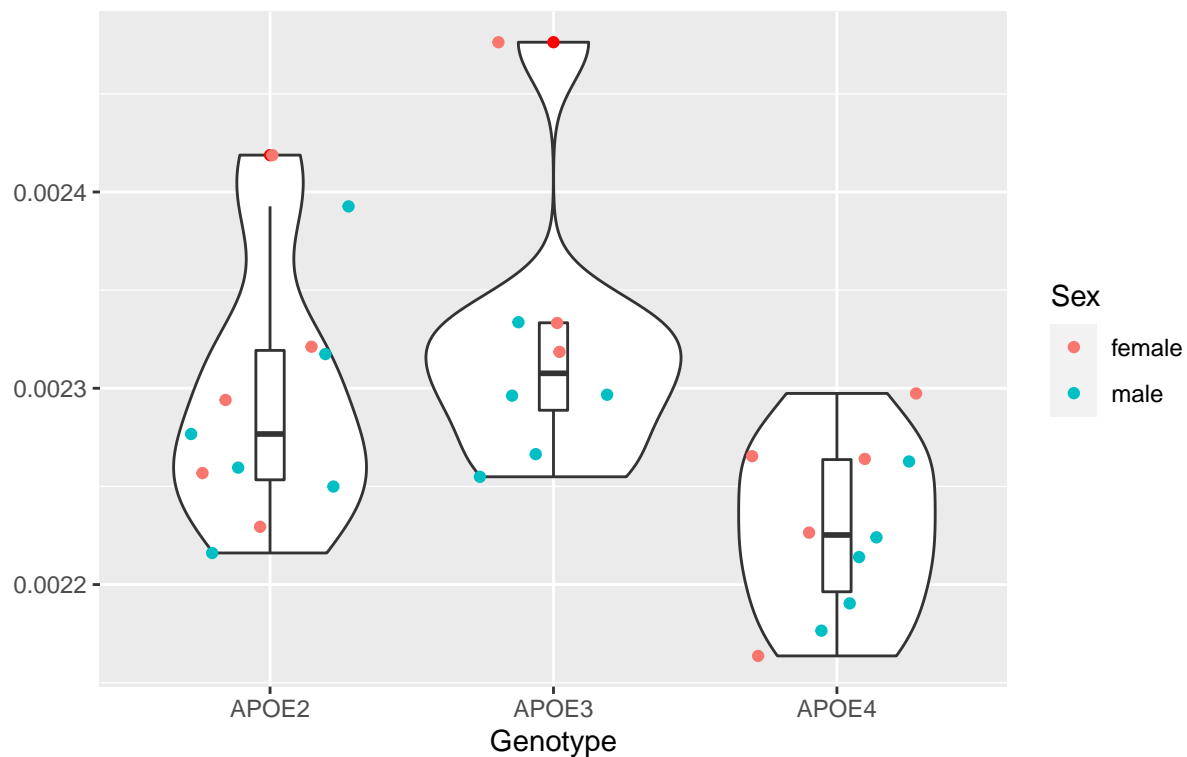
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.815e-08	9.074e-09	1.153	0.331
## Residuals	26	2.046e-07	7.868e-09		

Striatum

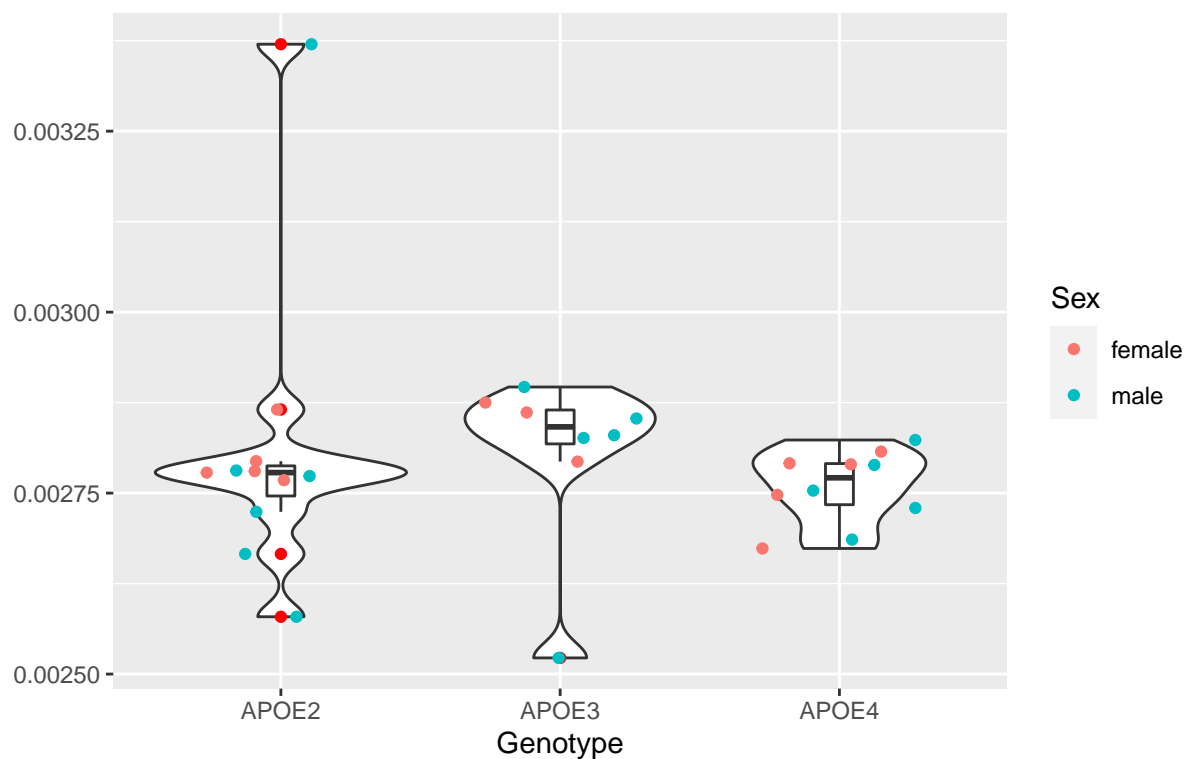
Red points denoting outliers



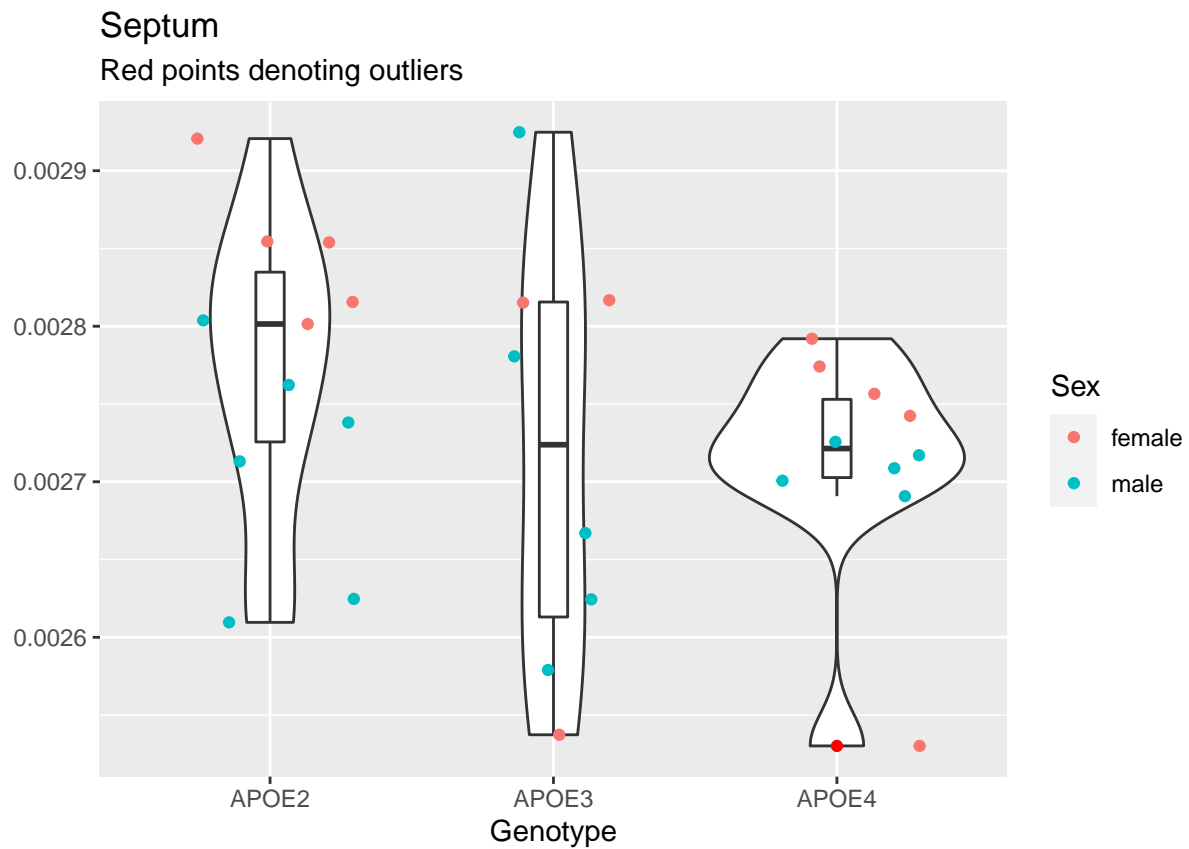
```
##           Df      Sum Sq   Mean Sq F value    Pr(>F)
## geno         2 4.278e-08 2.139e-08    6.061 0.00691 **
## Residuals    26 9.175e-08 3.529e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Globus Pallidus

Red points denoting outliers



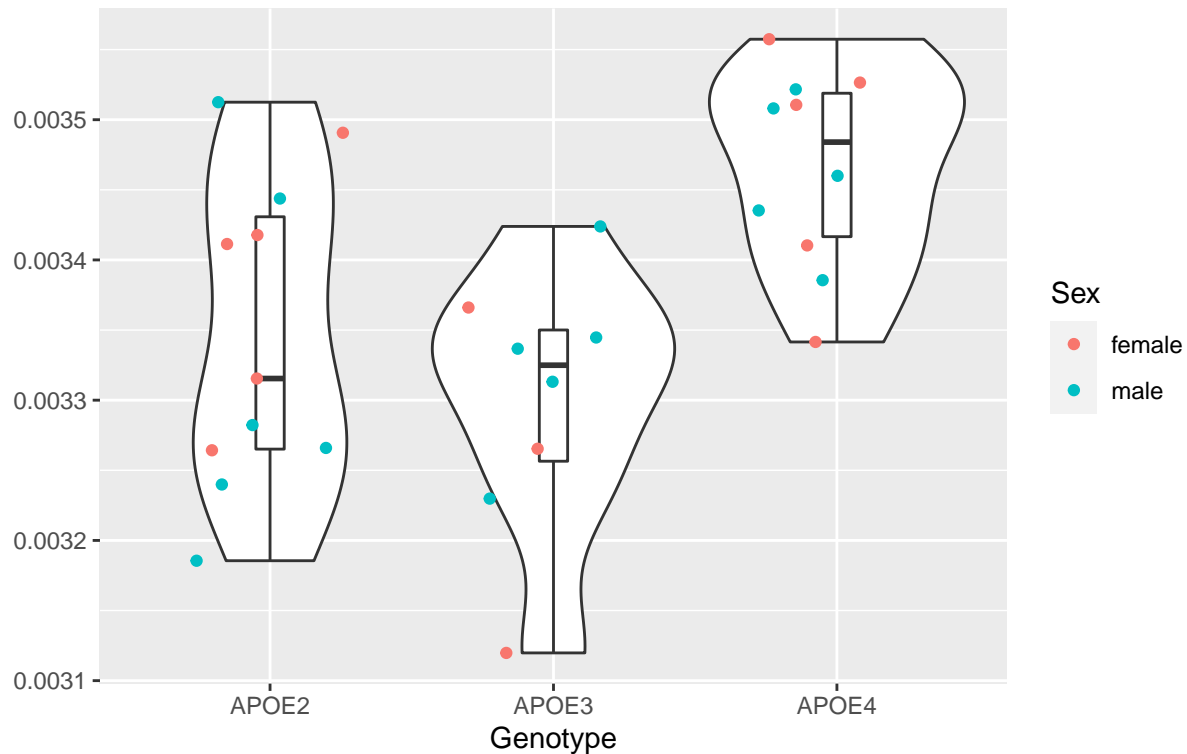
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.520e-08	7.623e-09	0.376	0.69
## Residuals	26	5.271e-07	2.027e-08		



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 2.210e-08 1.105e-08   1.071  0.357
## Residuals 26 2.683e-07 1.032e-08
```

Subthalamic Nucleus

Red points denoting outliers



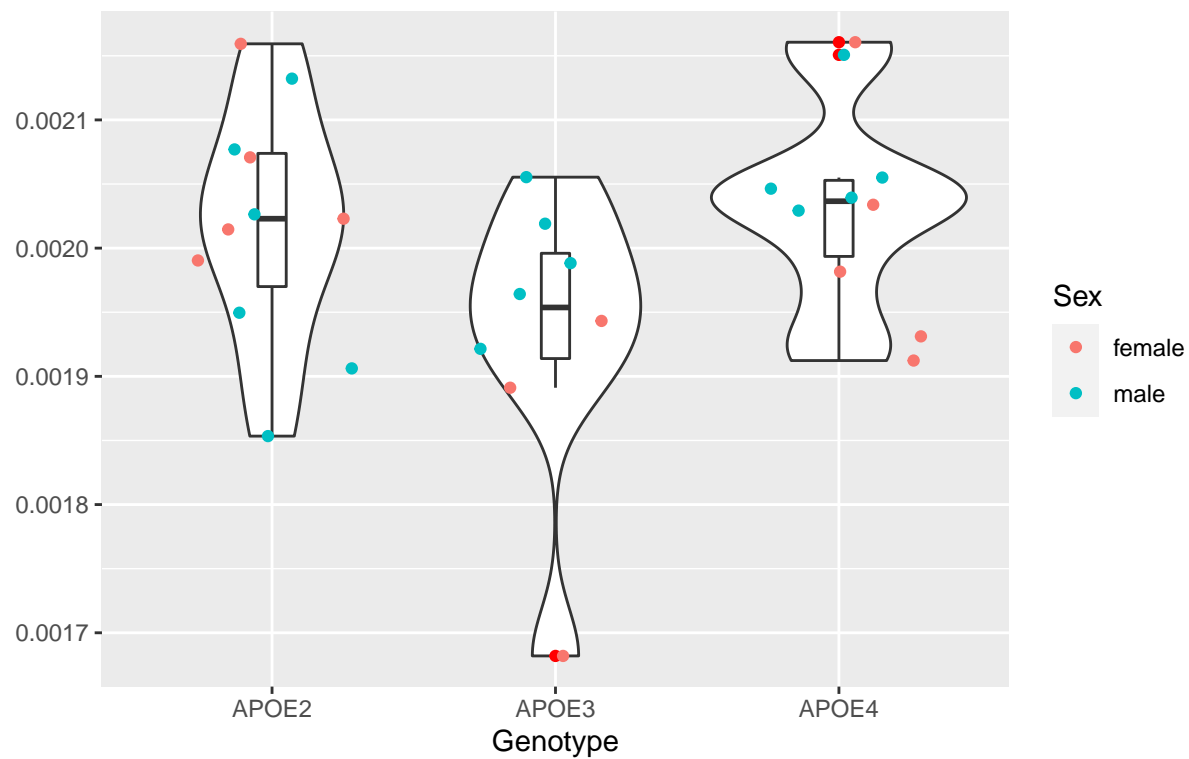
```
##           Df      Sum Sq   Mean Sq F value    Pr(>F)
## geno         2 1.353e-07 6.763e-08    7.664 0.00242 **
## Residuals    26 2.294e-07 8.820e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#“{r Preopt, echo = FALSE} #ggplot(data = new, aes(factor(geno), Preopt)) + #geom_violin() +
#geom_boxplot(width = 0.1, outlier.color = “red”) + #geom_jitter(height = 0, width = 0.3, aes(color
= Sex)) + #labs(x = “Genotype”, #y = “”, #title =”Preoptic Telencephalon“, #subtitle =”Red points
denoting outliers”)

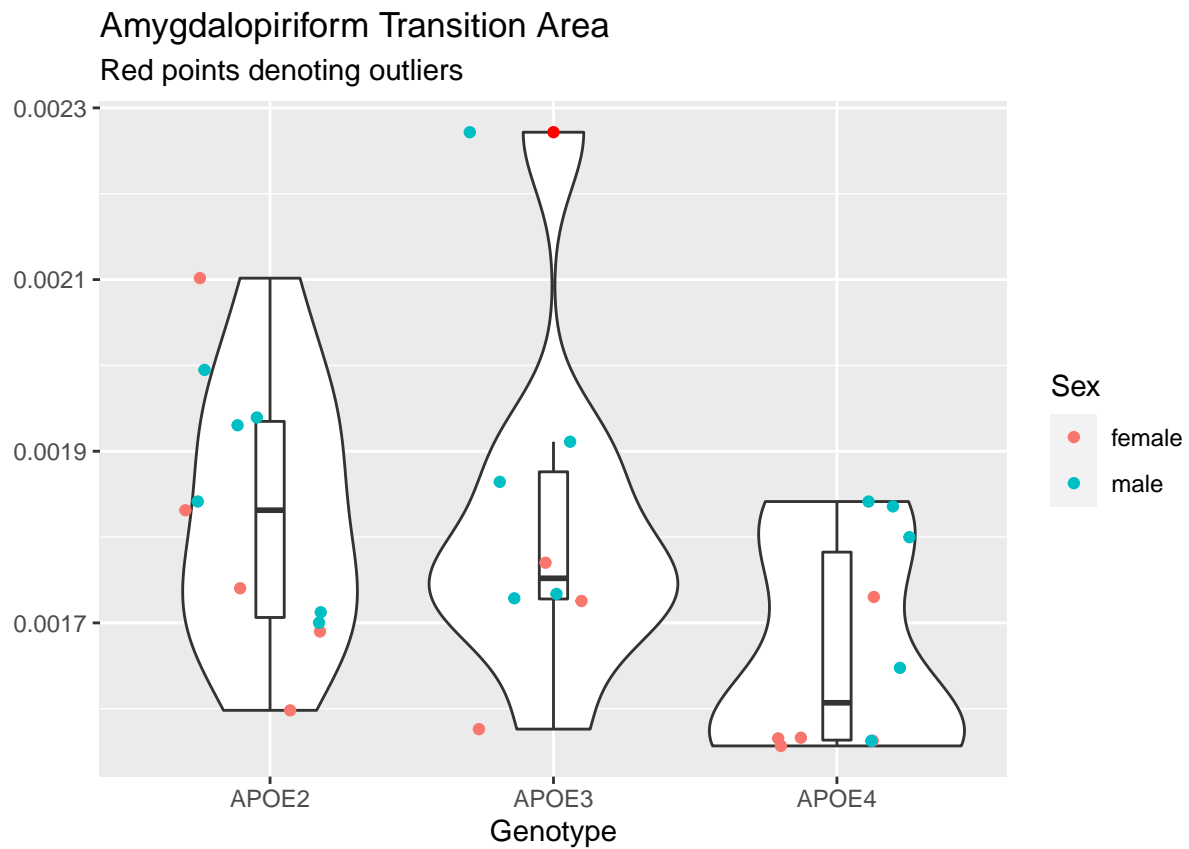
#res.aov <- aov(Preopt ~ geno, data = new) #summary(res.aov) #““
```


Hypothalamus

Red points denoting outliers

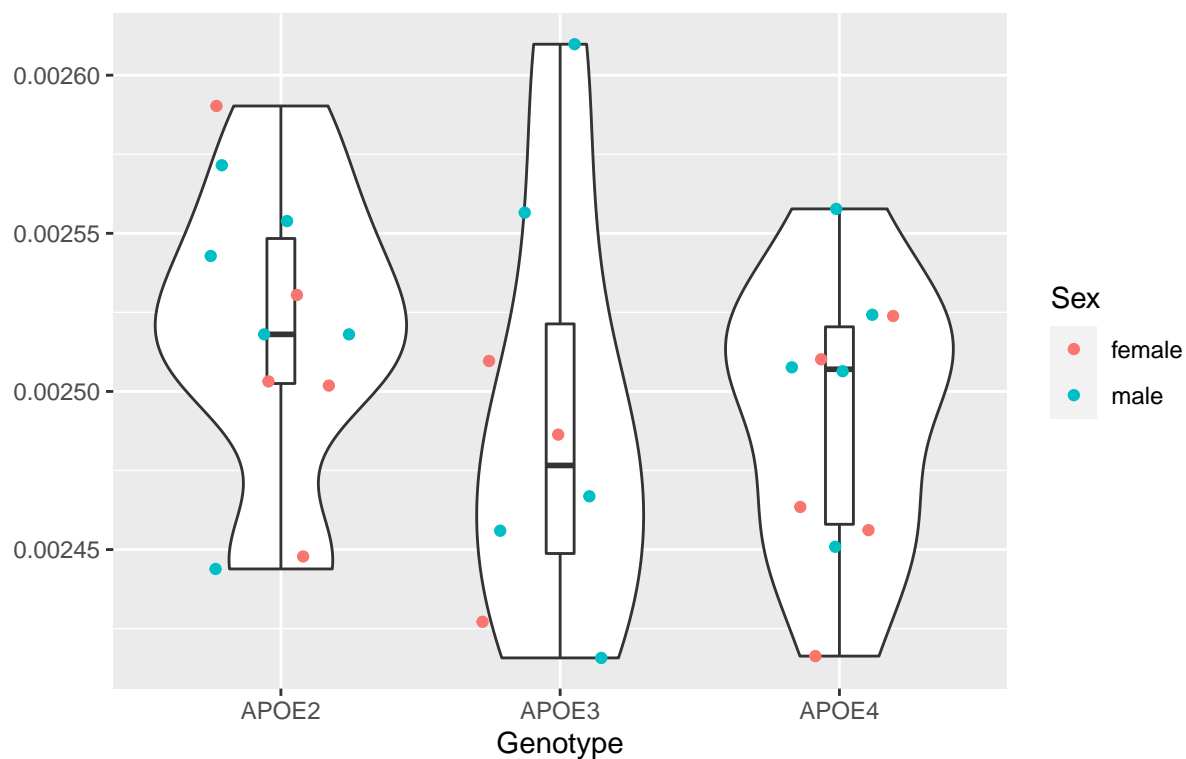


```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 5.114e-08 2.557e-08   2.838 0.0768 .
## Residuals    26 2.342e-07 9.009e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 1.624e-07 8.120e-08   3.146 0.0597 .
## Residuals    26 6.710e-07 2.581e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

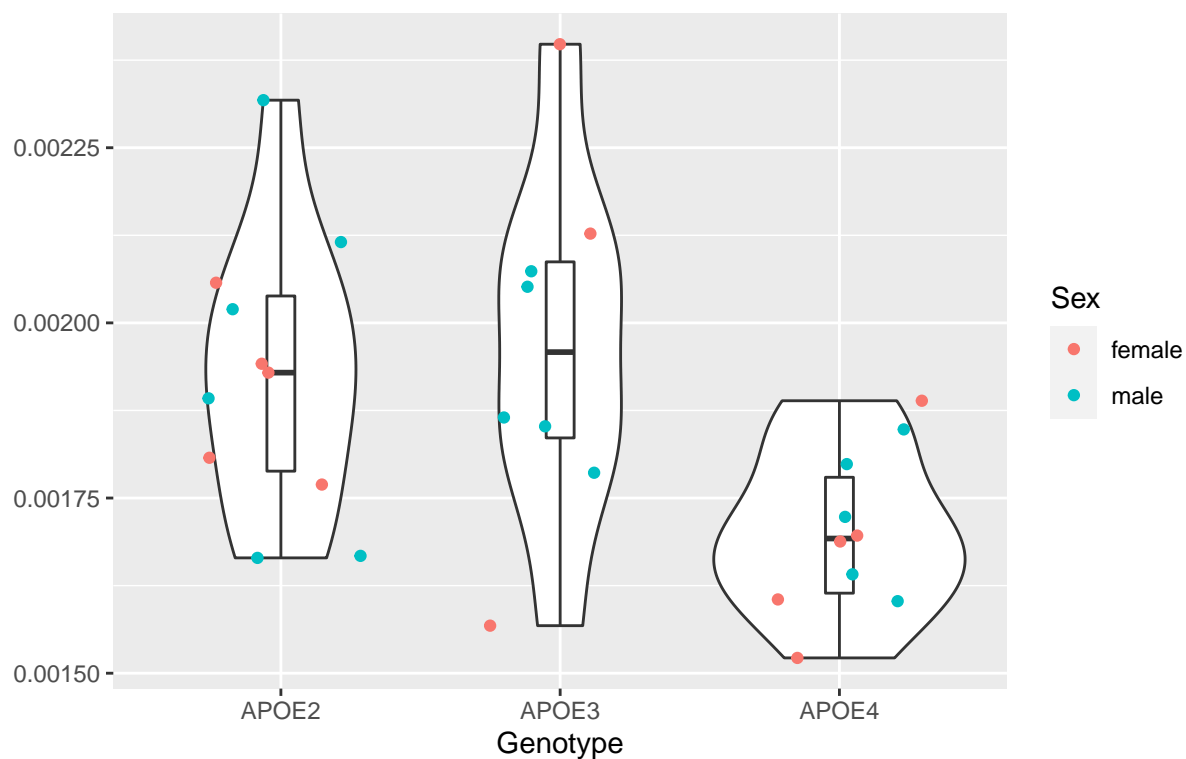
Periform Cortex Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 5.660e-09 2.830e-09   1.082  0.354
## Residuals 26 6.801e-08 2.616e-09
```

Presubiculum

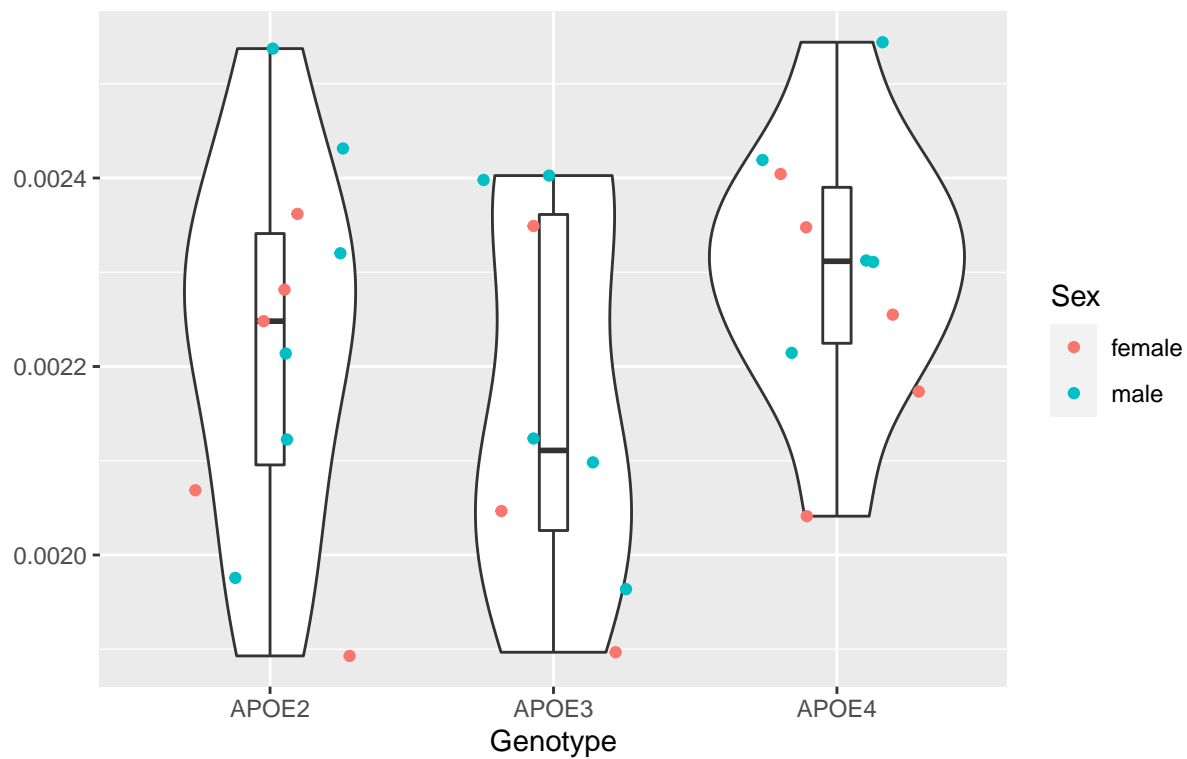
Red points denoting outliers



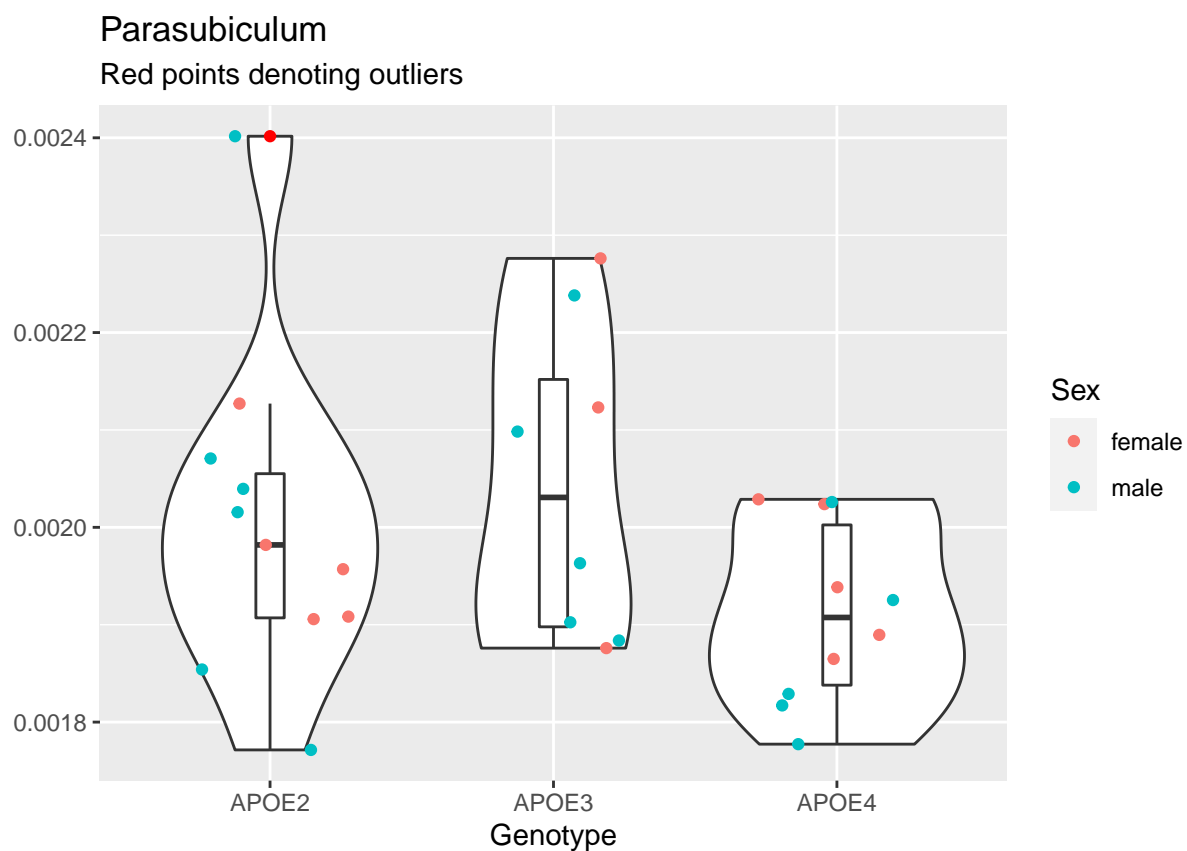
```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 3.874e-07 1.937e-07   5.261 0.0121 *
## Residuals    26 9.574e-07 3.682e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Perirhinal Cortex

Red points denoting outliers



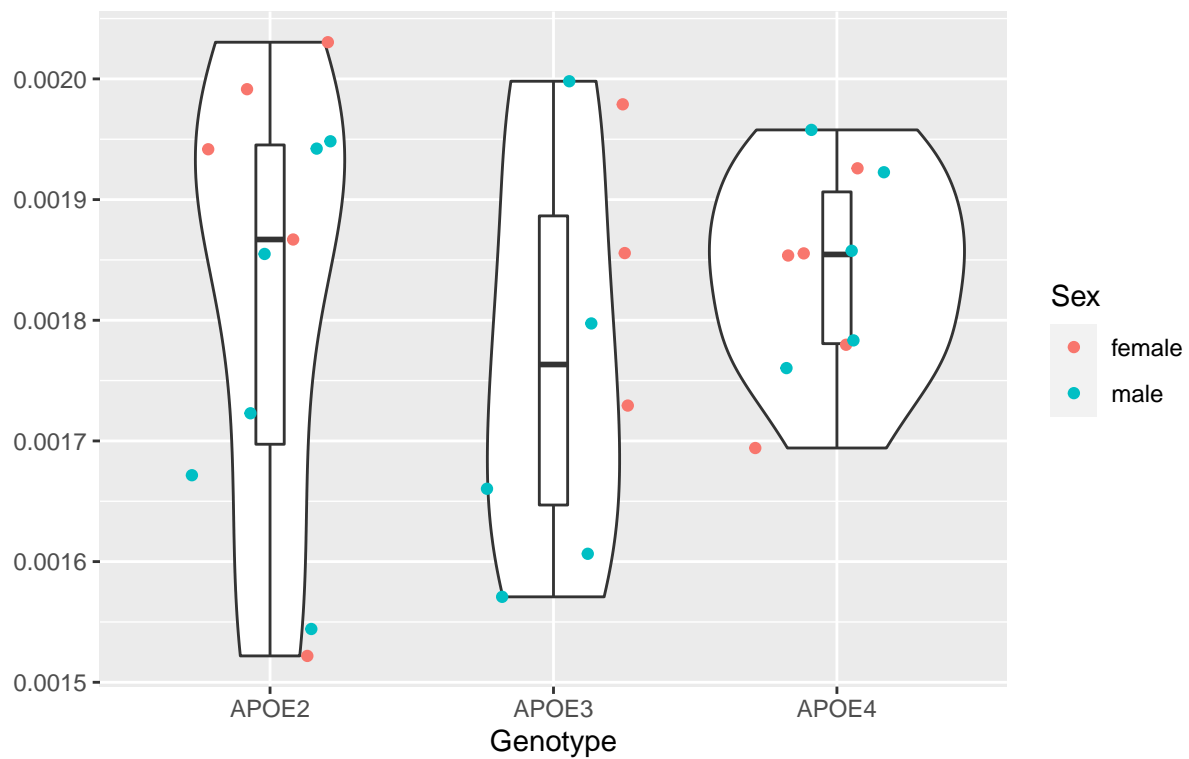
```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 9.190e-08 4.593e-08   1.429  0.258
## Residuals 26 8.355e-07 3.214e-08
```



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 8.570e-08 4.283e-08   2.081  0.145
## Residuals 26 5.351e-07 2.058e-08
```

Ectorhinal Cortex

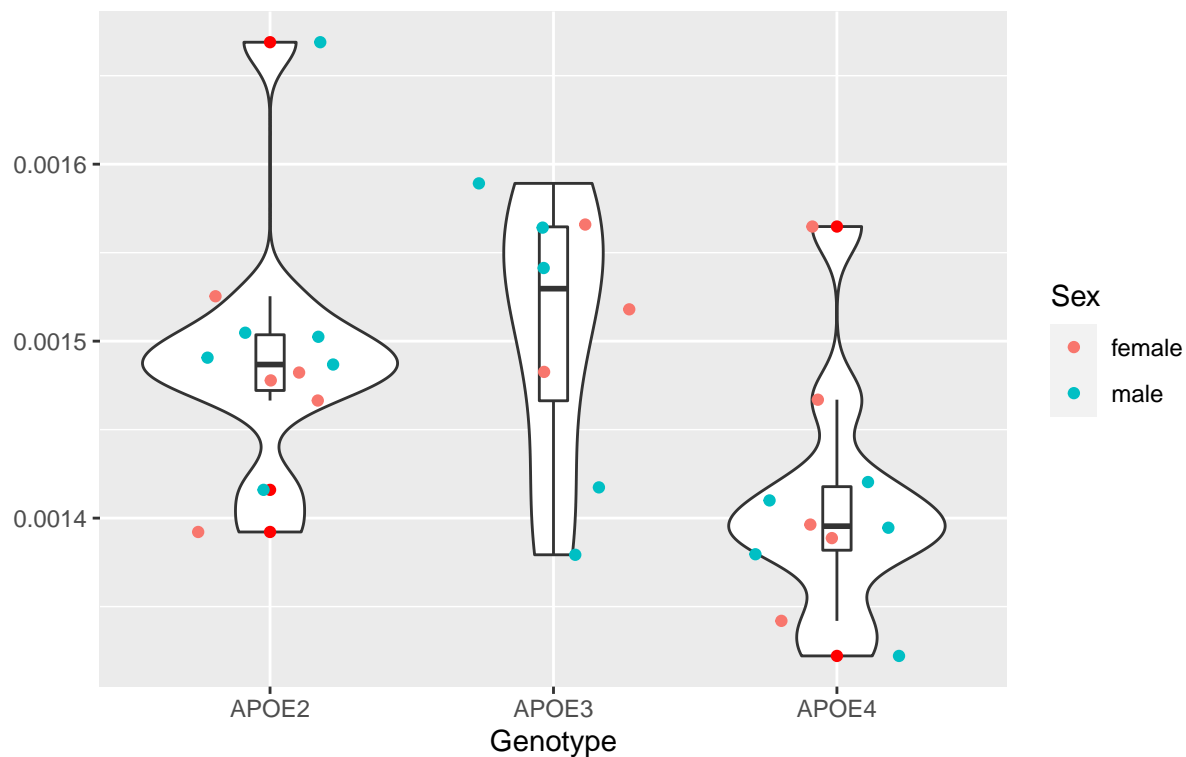
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.930e-08	9.642e-09	0.442	0.647
## Residuals	26	5.667e-07	2.179e-08		

Dorsal Tenia Tecta

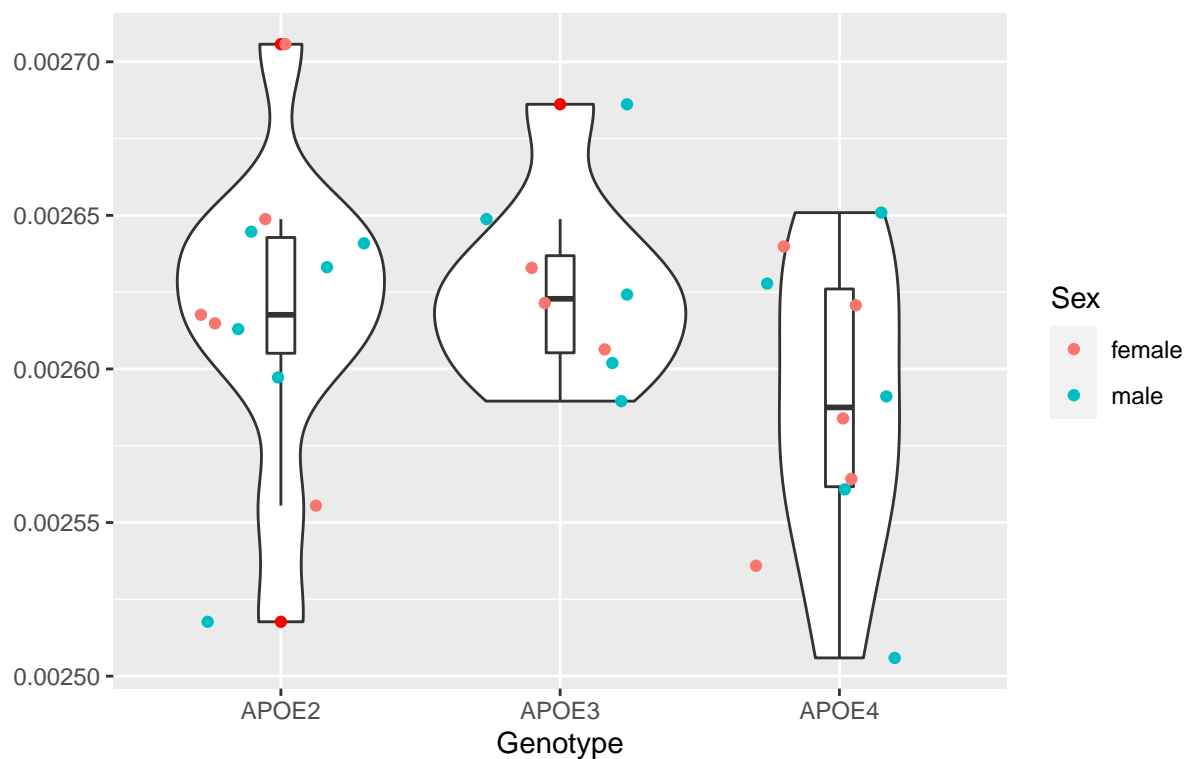
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 5.407e-08 2.704e-08   5.384 0.0111 *
## Residuals    26 1.306e-07 5.022e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Hippocampus

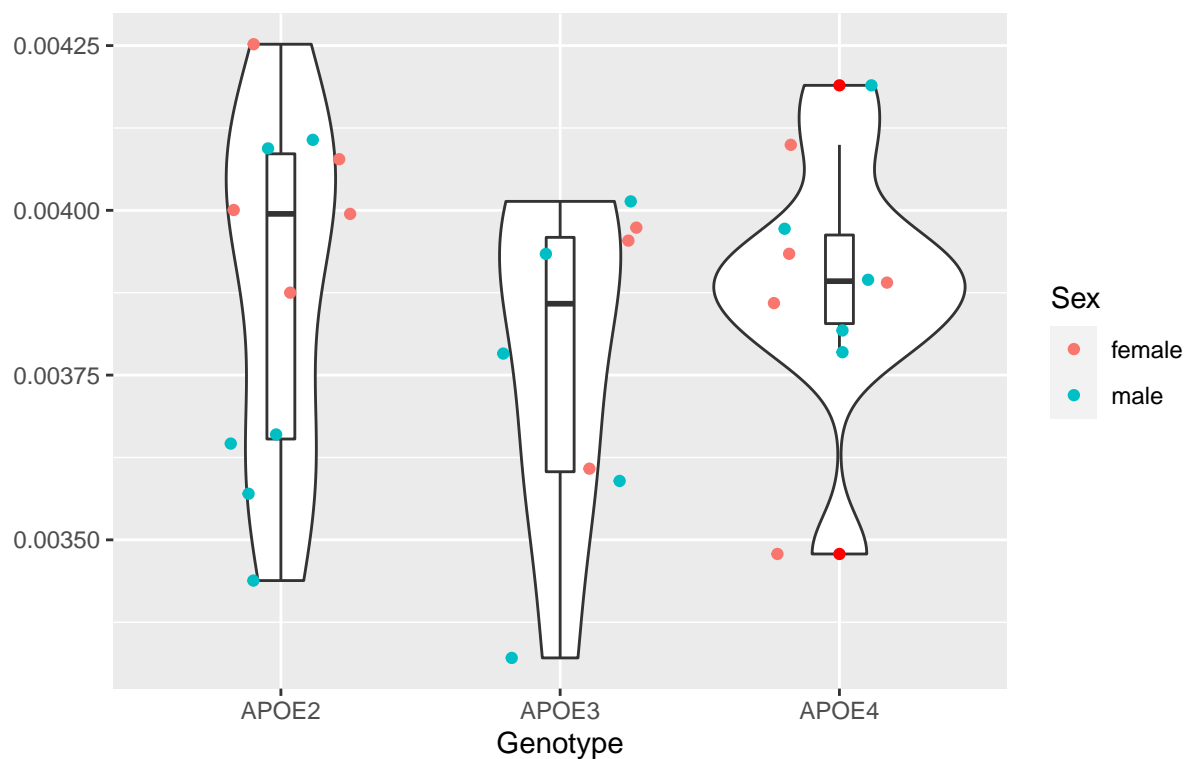
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.510e-09	3.756e-09	1.91	0.168
## Residuals	26	5.112e-08	1.966e-09		

Ventral Claustrum

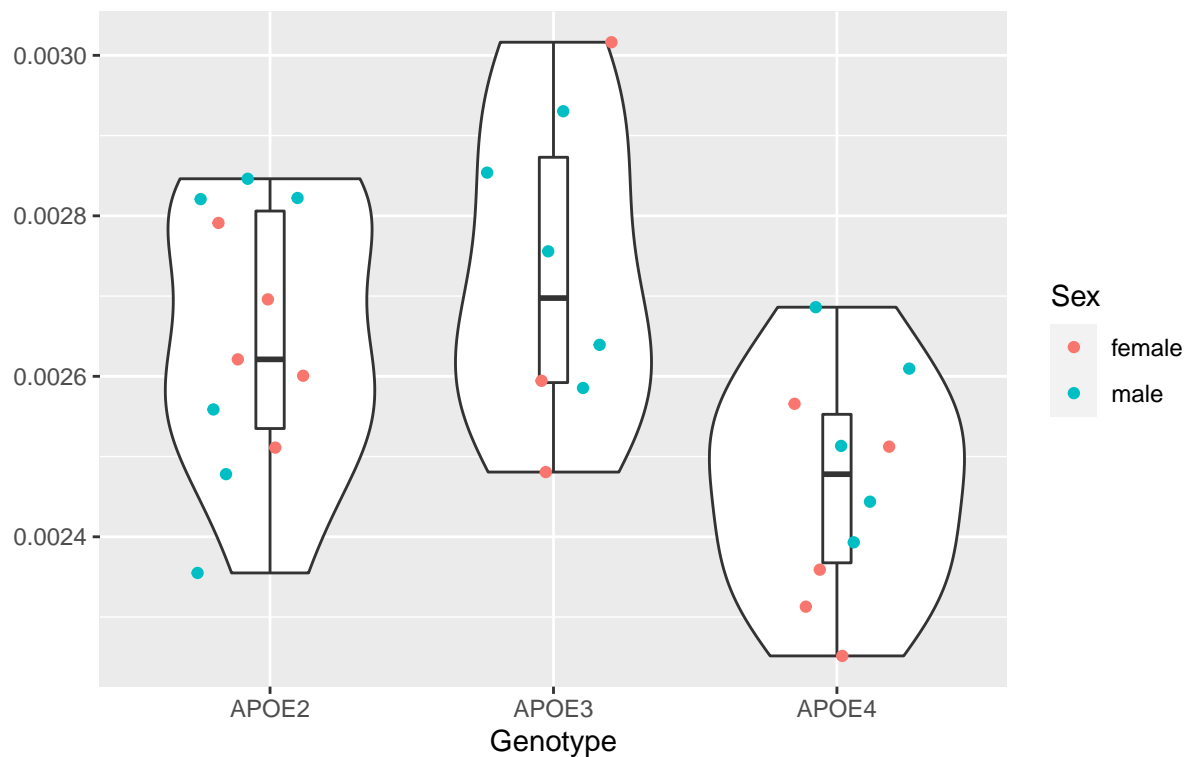
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.750e-08	3.876e-08	0.696	0.508
## Residuals	26	1.448e-06	5.569e-08		

Posterolateral Cortical Amygdaloid Area

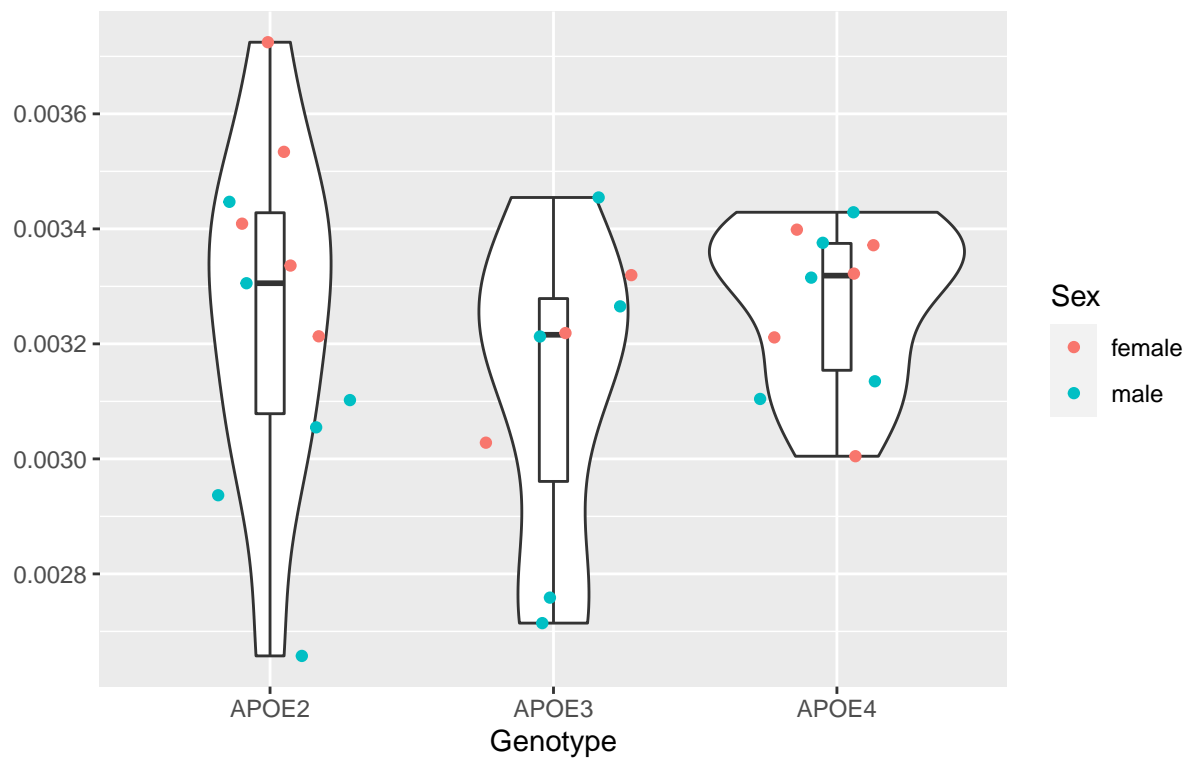
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value    Pr(>F)
## geno         2 3.437e-07 1.719e-07    6.529 0.00504 **
## Residuals    26 6.844e-07 2.632e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Dorsal Claustrum

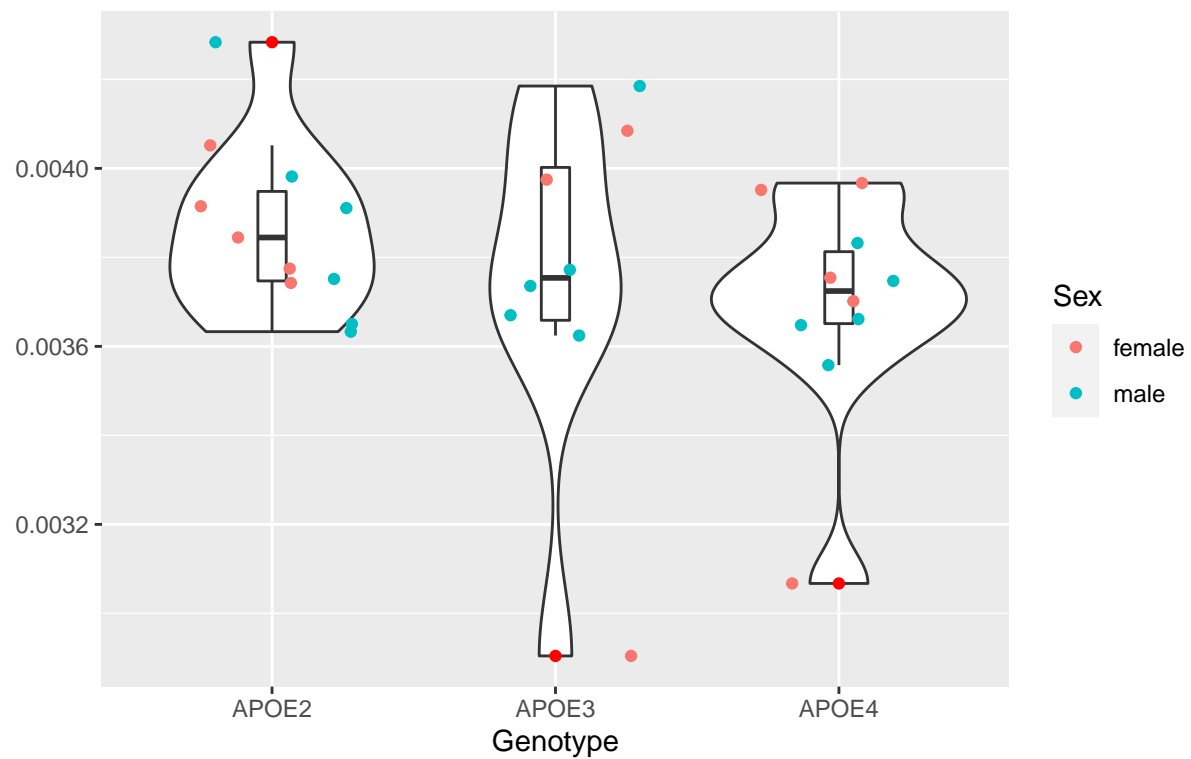
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.076e-07	5.38e-08	0.889	0.423
## Residuals	26	1.573e-06	6.05e-08		

Claustrum

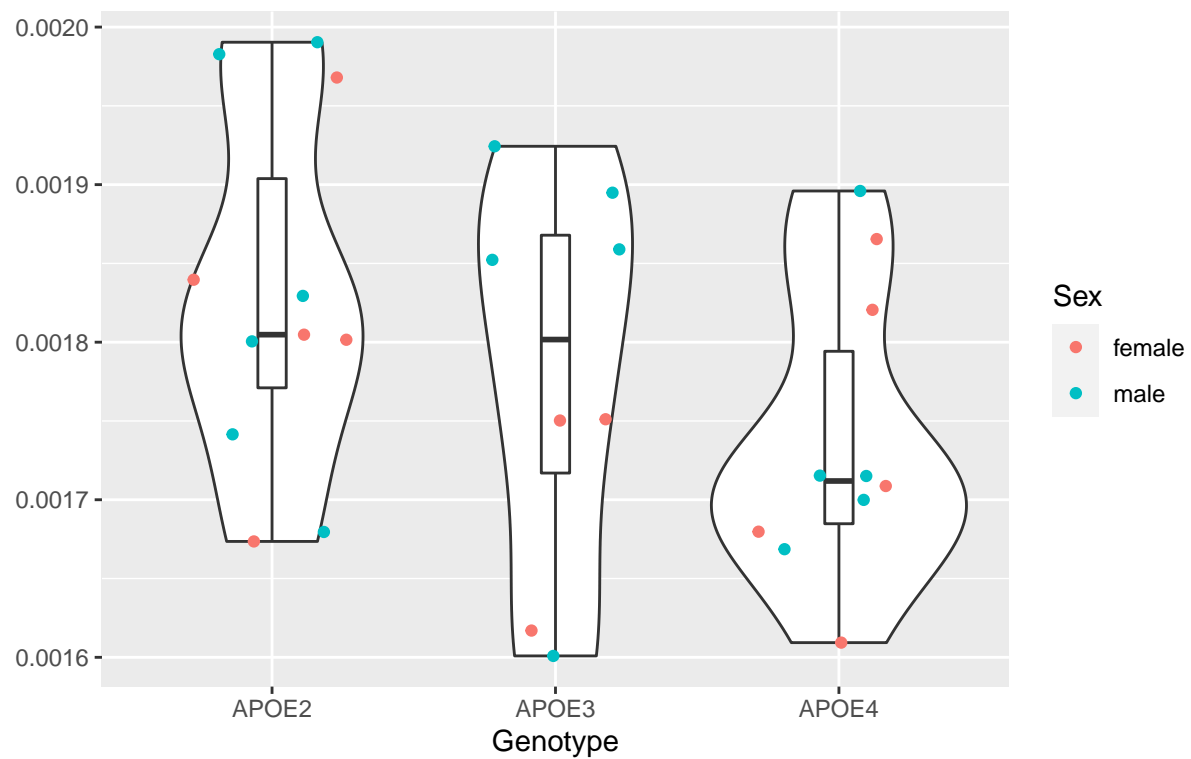
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.753e-07	8.764e-08	1.12	0.341
## Residuals	26	2.034e-06	7.824e-08		

Ventral Intermediate Entorhinal Cortex

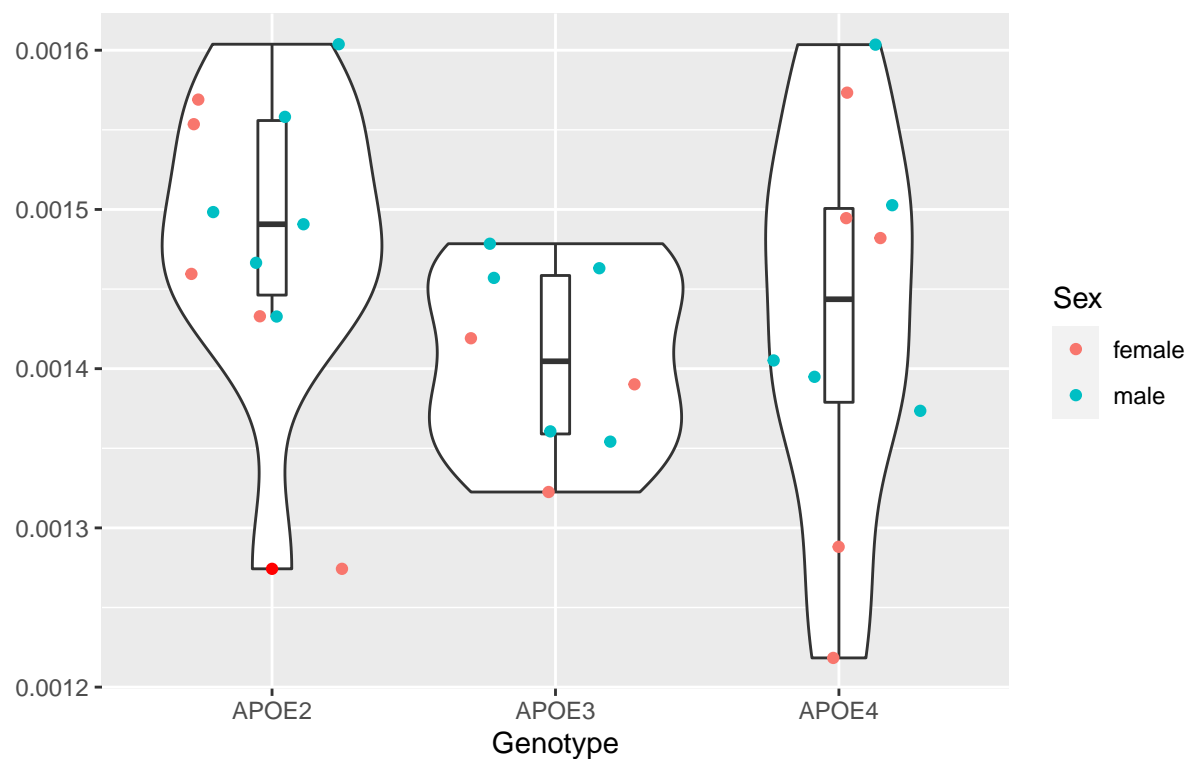
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	4.296e-08	2.148e-08	1.817	0.183
## Residuals	26	3.074e-07	1.182e-08		

Left Caudomedial Entorhinal Cortex

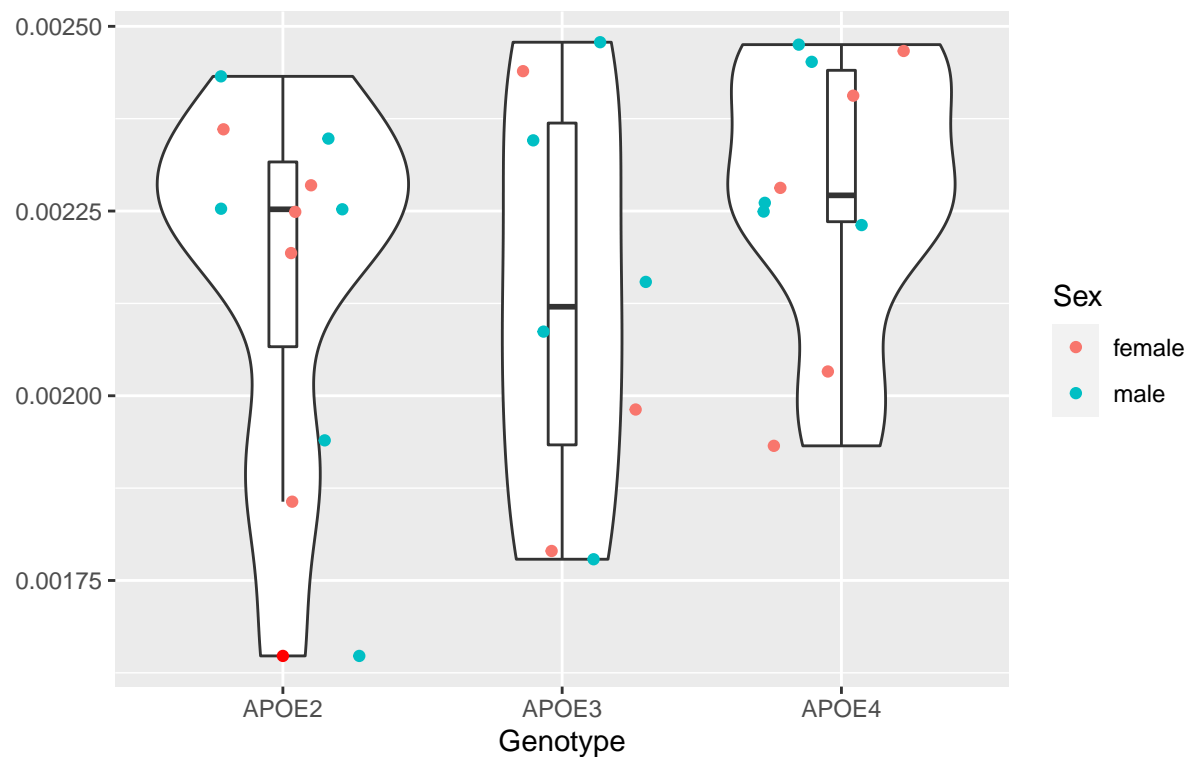
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.164e-08	1.582e-08	1.727	0.198
## Residuals	26	2.381e-07	9.159e-09		

Left Dorsolateral Entorhinal Cortex

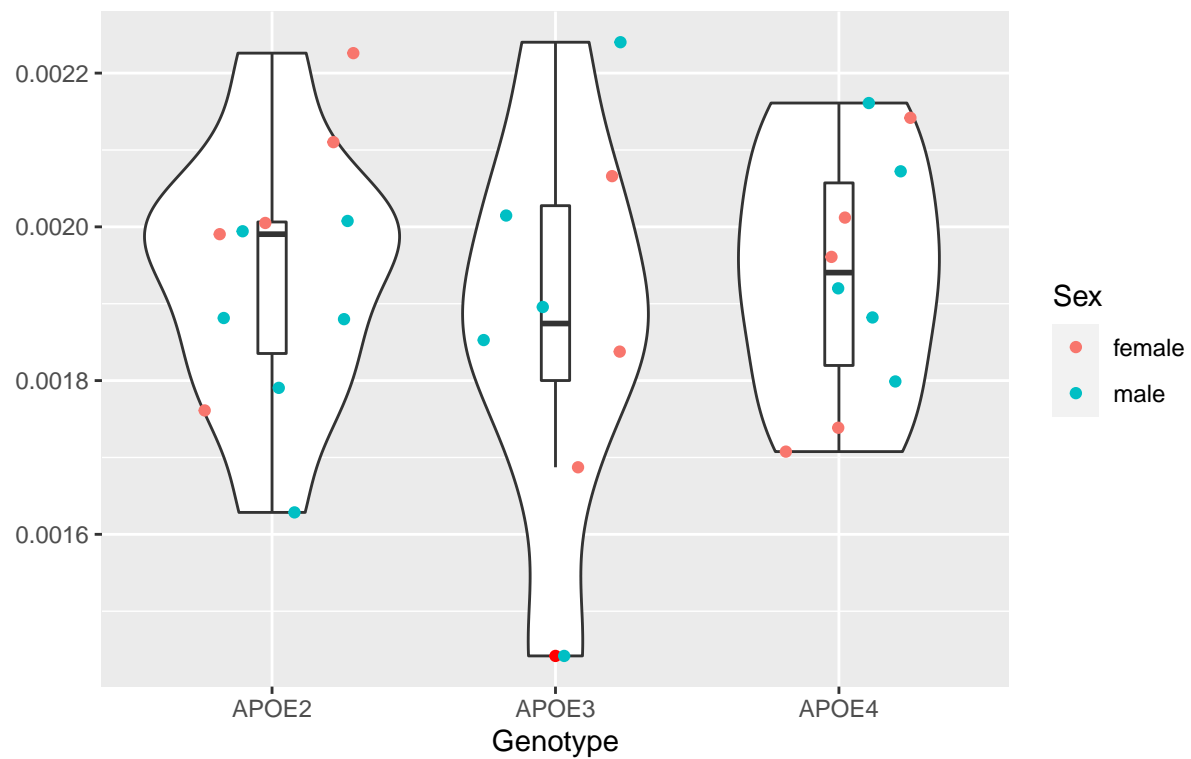
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.119e-07	5.595e-08	1.02	0.374
## Residuals	26	1.425e-06	5.483e-08		

Left Dorsal Intermediate Entorhinal Cortex

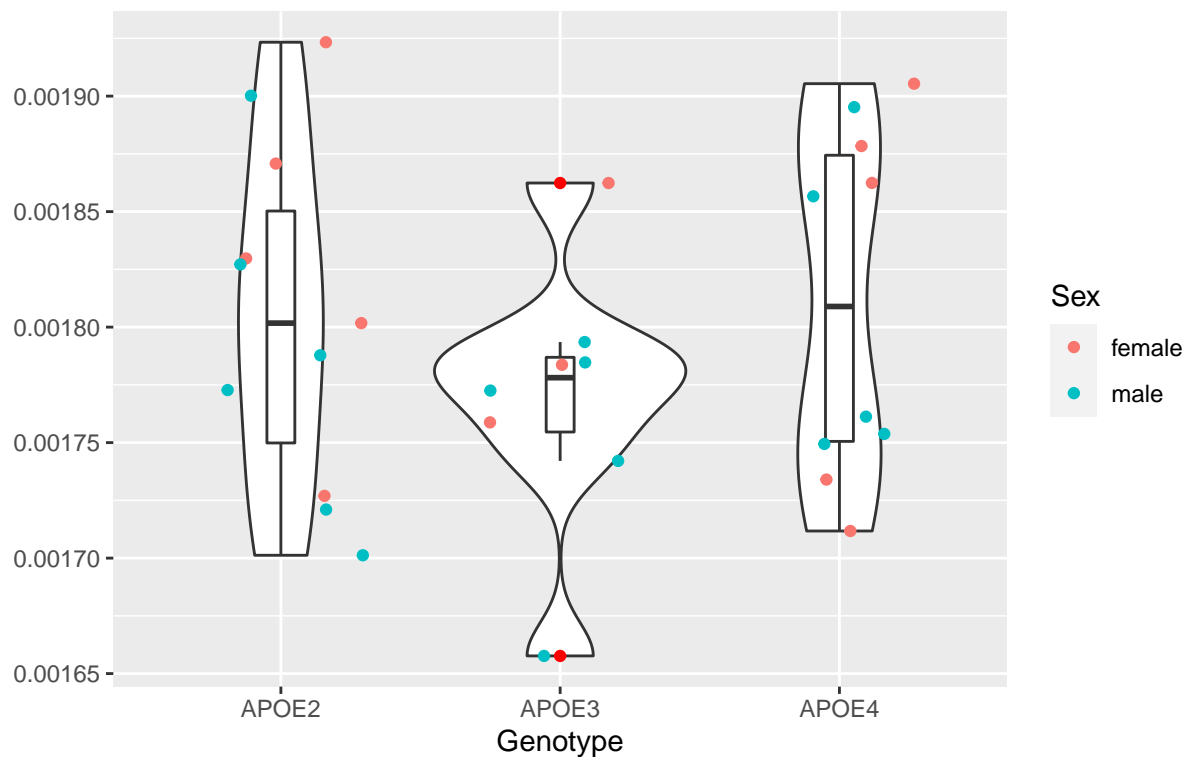
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.910e-08	9.550e-09	0.267	0.767
## Residuals	26	9.283e-07	3.571e-08		

Left Caudomedial Entorhinal Cortex

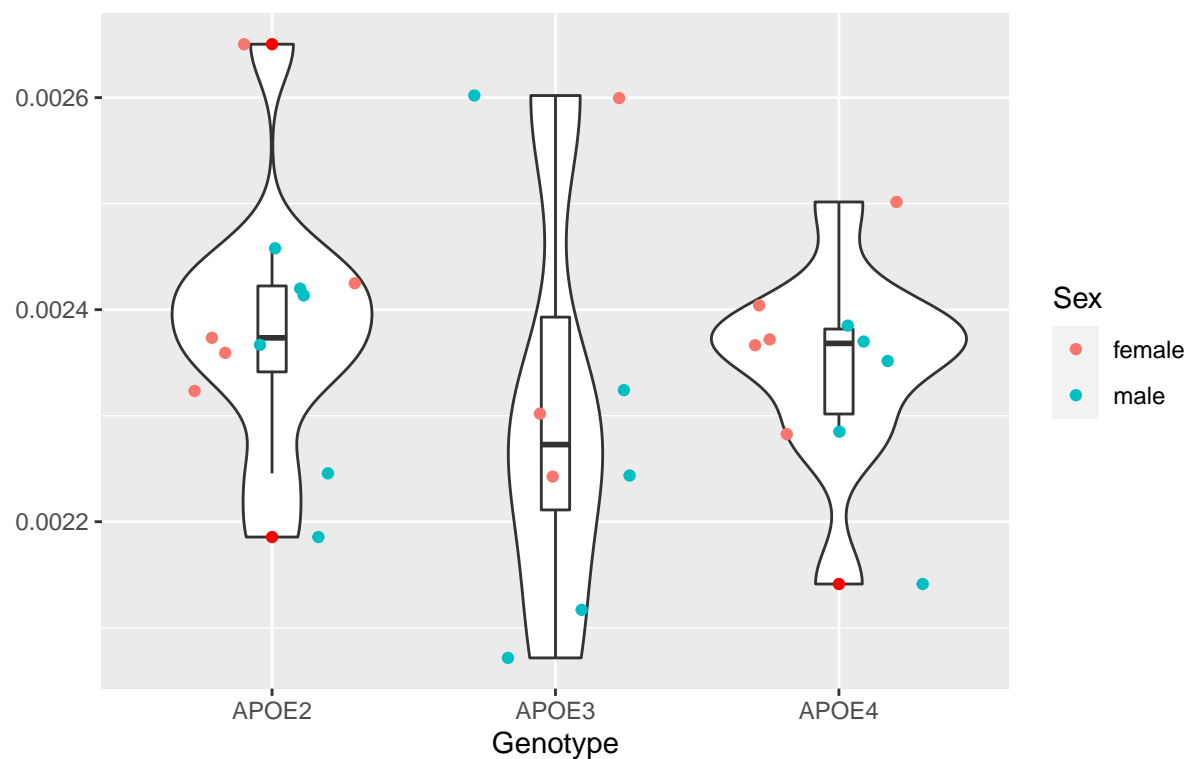
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.820e-09	4.412e-09	0.901	0.419
## Residuals	26	1.274e-07	4.899e-09		

Left Ventral Orbital Cortex

Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.370e-08	1.185e-08	0.621	0.545
## Residuals	26	4.963e-07	1.909e-08		

Left Secondary Visual Cortex Mediomedial Area

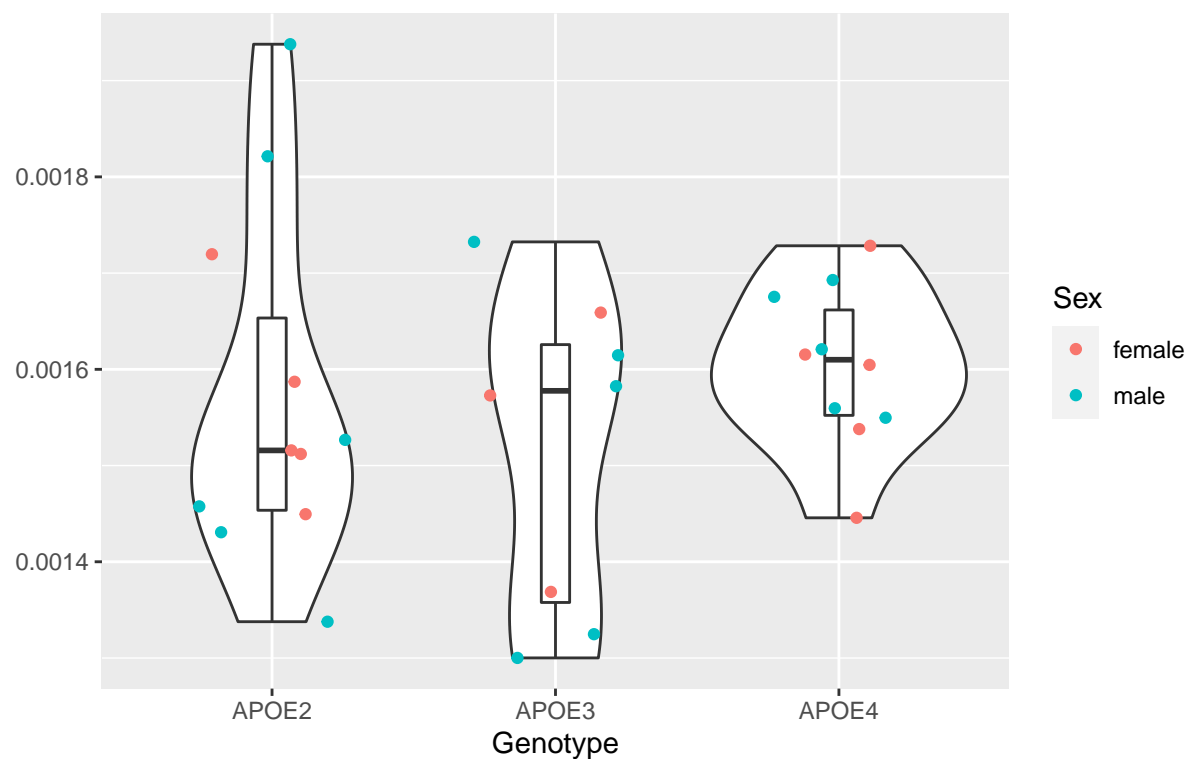
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 1.337e-07 6.683e-08    5.574 0.00967 **
## Residuals    26 3.117e-07 1.199e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Secondary Visual Cortex Mediolateral Area

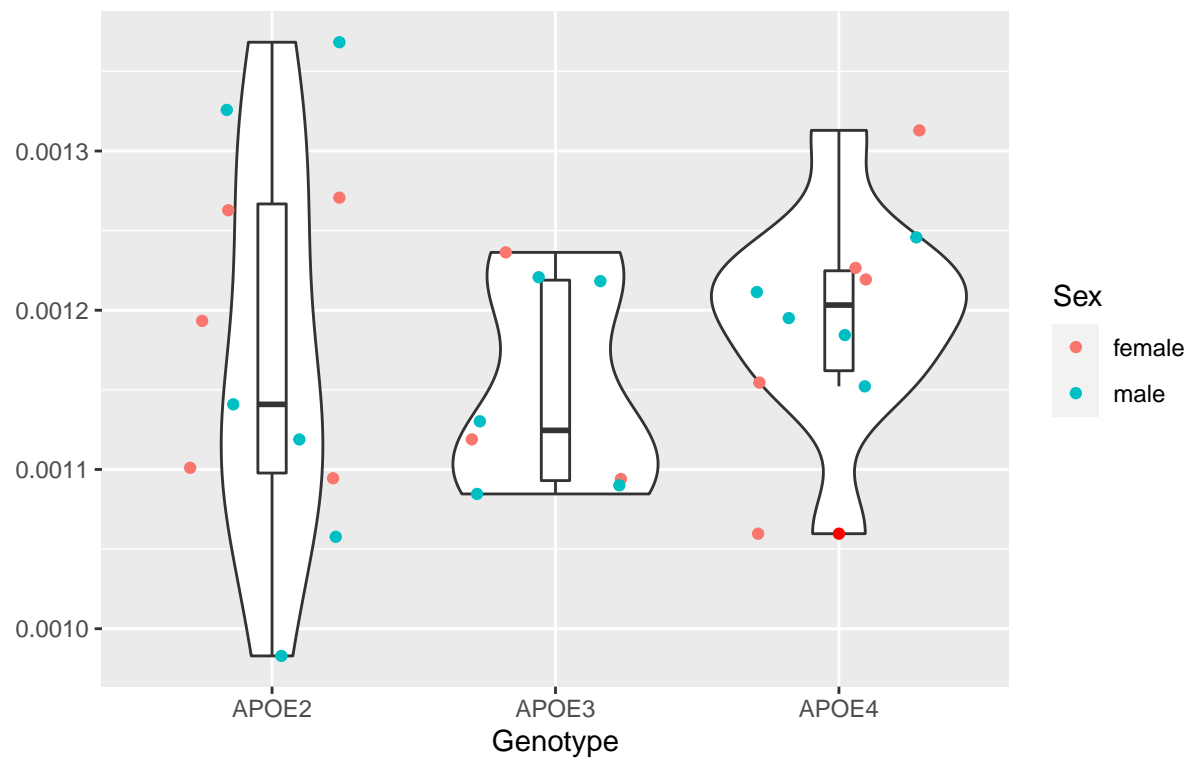
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.140e-08	1.57e-08	0.701	0.505
## Residuals	26	5.825e-07	2.24e-08		

Left Secondary Visual Cortex Lateral Area

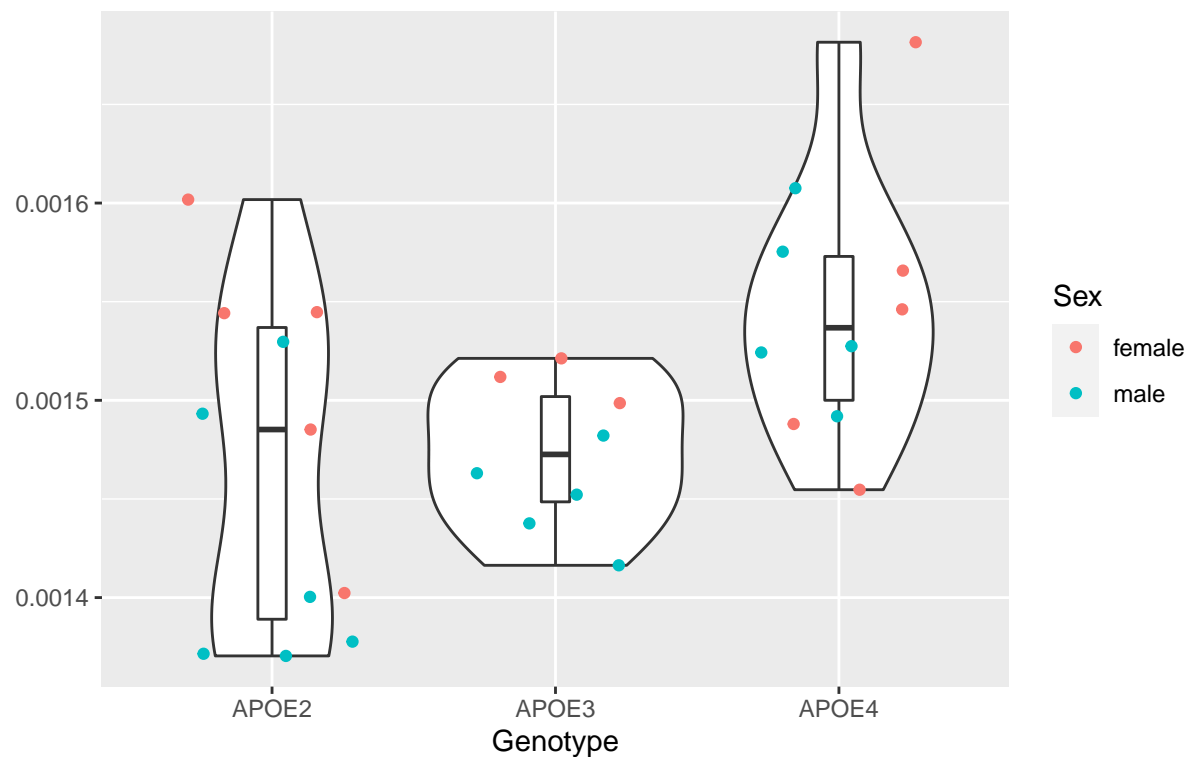
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	9.85e-09	4.924e-09	0.598	0.557
## Residuals	26	2.14e-07	8.229e-09		

Left Primary Visual Cortex Monocular Area

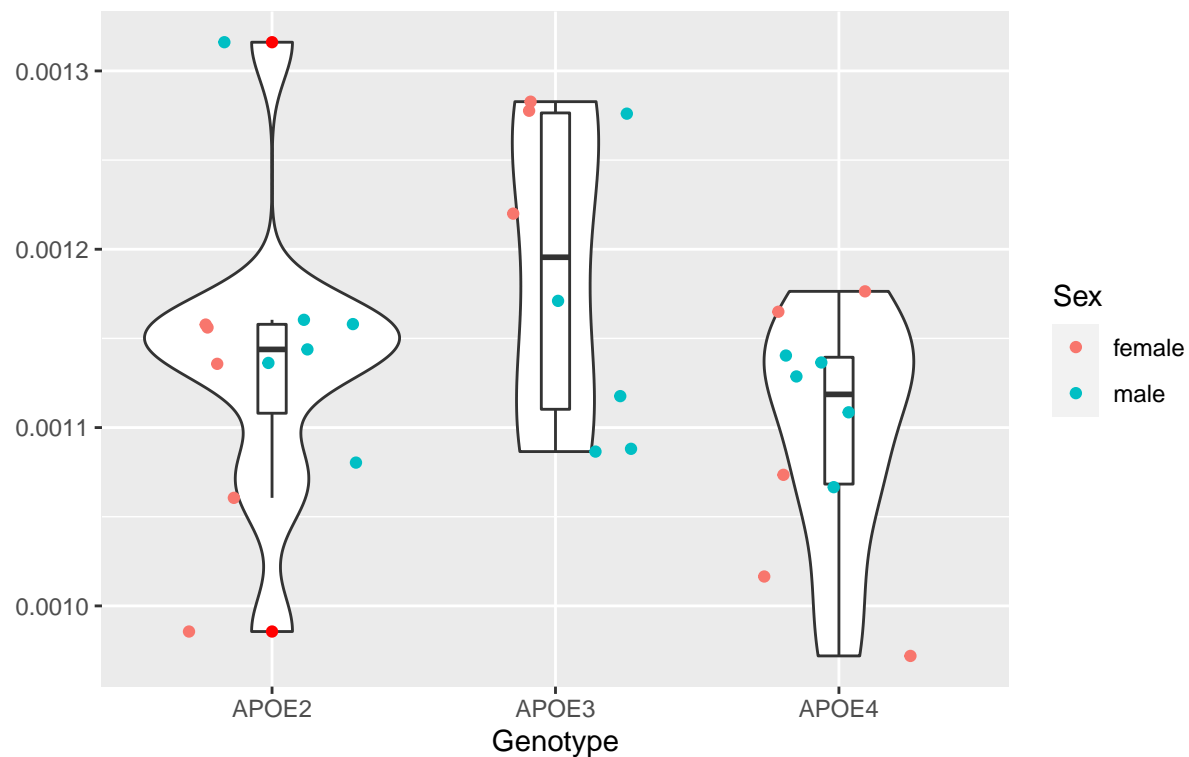
Red points denoting outliers



```
##          Df    Sum Sq   Mean Sq F value Pr(>F)
## geno         2 3.972e-08 1.986e-08   4.357 0.0233 *
## Residuals    26 1.185e-07 4.559e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Visual Cortex Binocular Area

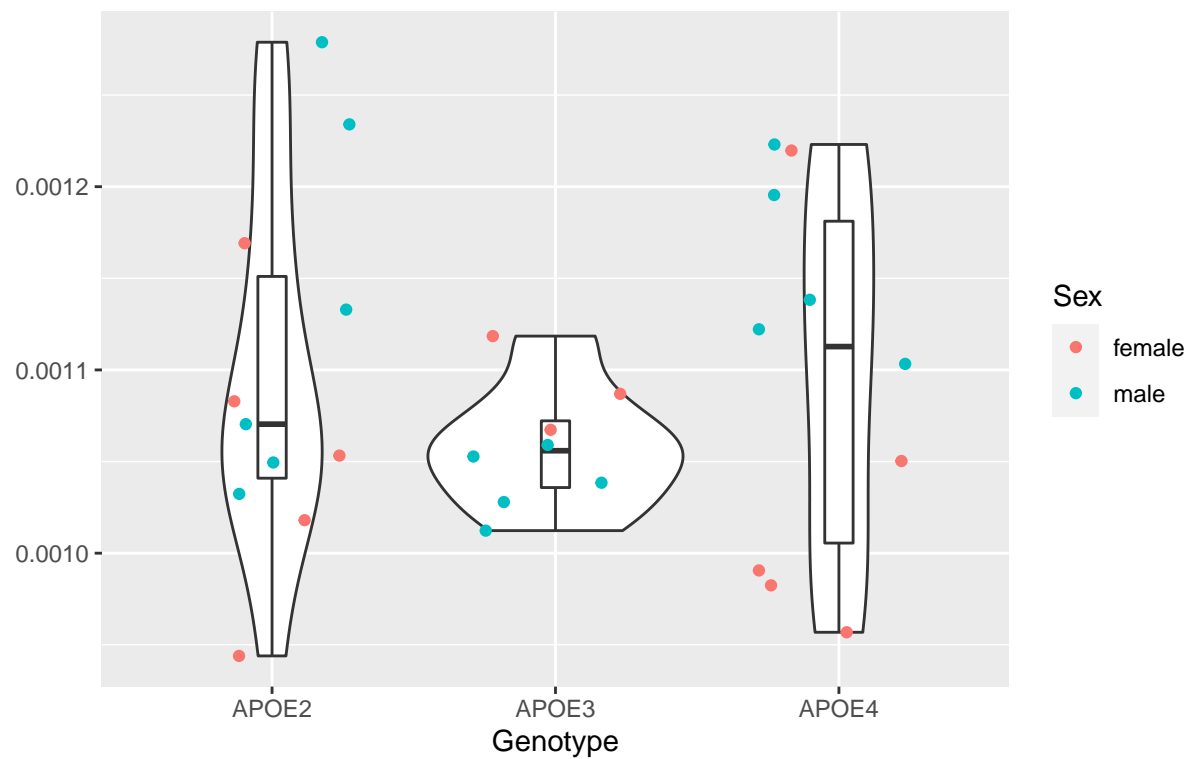
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 3.735e-08 1.868e-08   3.109 0.0616 .
## Residuals    26 1.562e-07 6.008e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Left Primary Visual Cortex

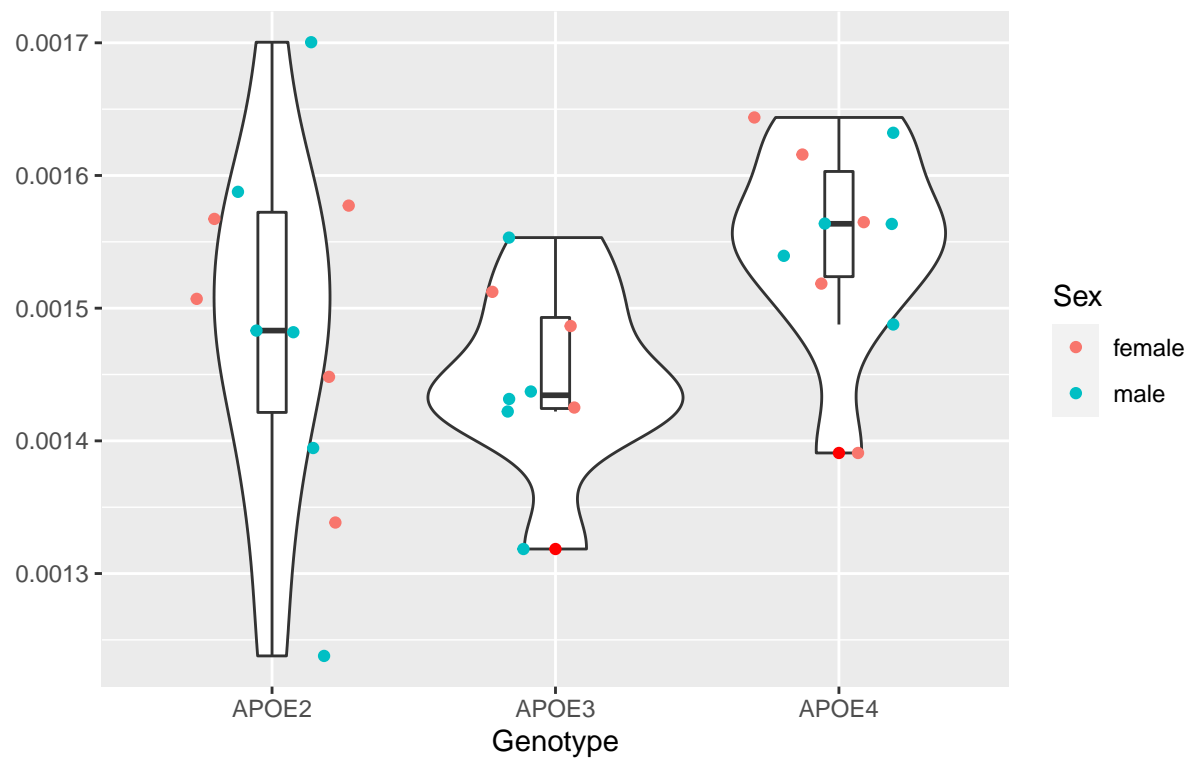
Red points denoting outliers



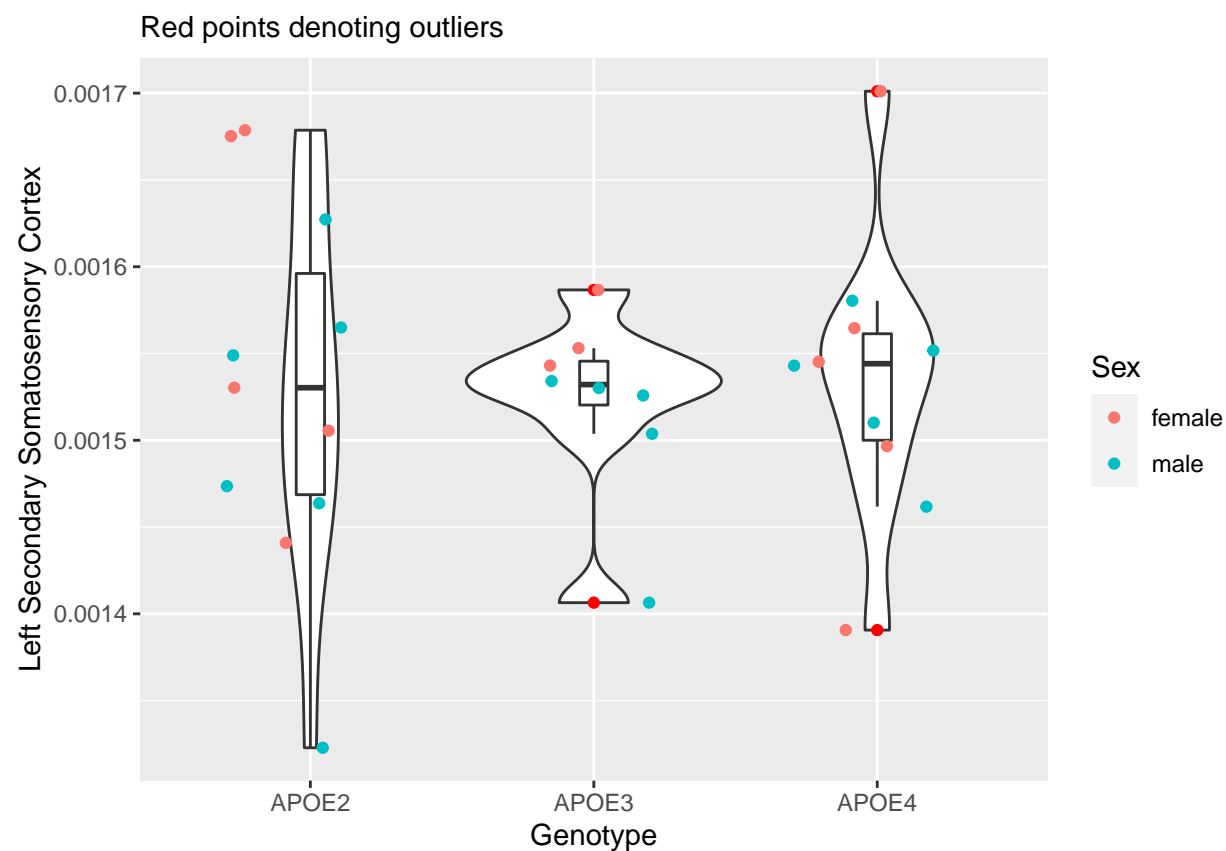
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	9.090e-09	4.546e-09	0.608	0.552
## Residuals	26	1.945e-07	7.481e-09		

Left Temporal Association Cortex

Red points denoting outliers

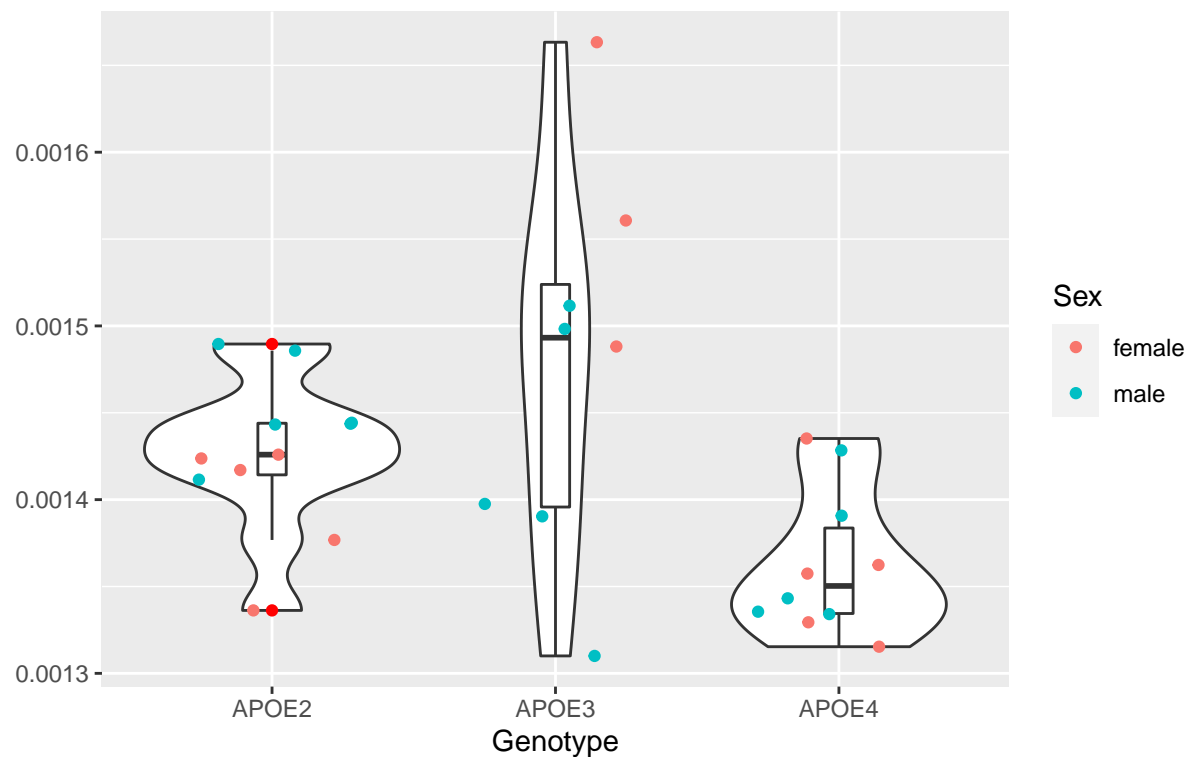


```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 5.110e-08 2.555e-08   2.651 0.0896 .
## Residuals    26 2.506e-07 9.637e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.100e-10	3.040e-10	0.041	0.96
## Residuals	26	1.921e-07	7.387e-09		

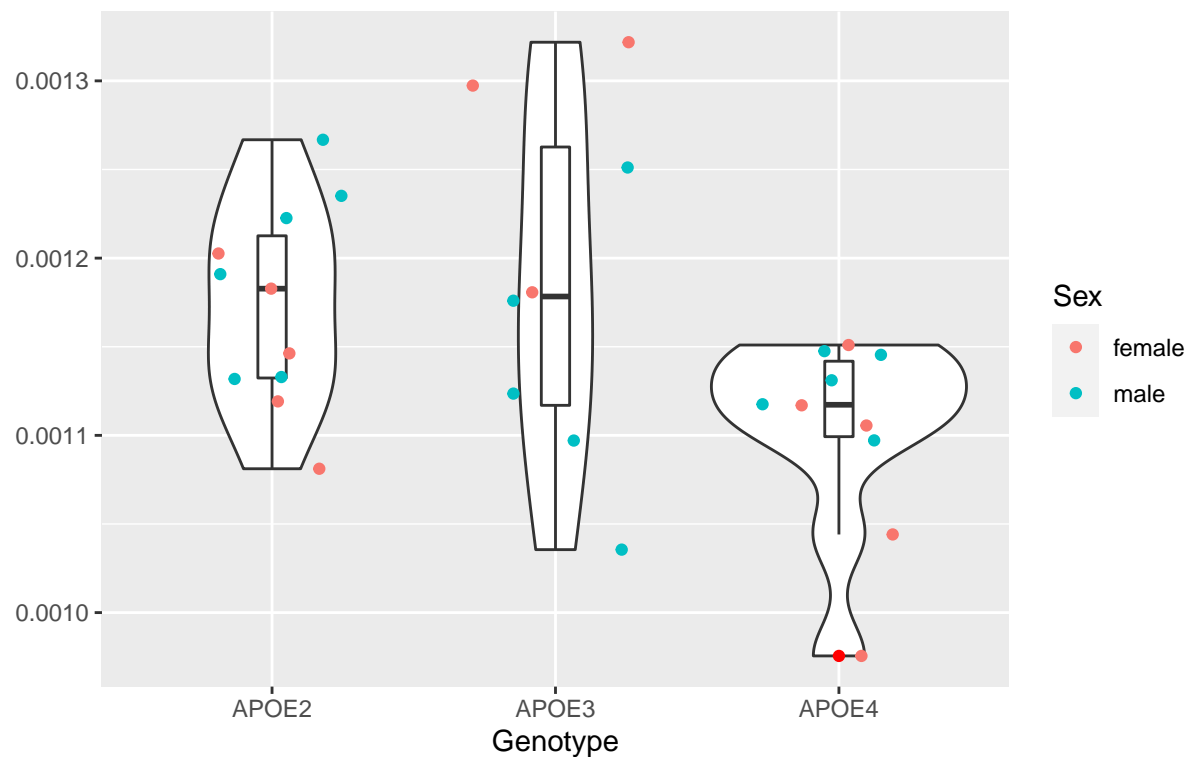
Left Primary Somatosensory Cortex Upper Lip Region Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 5.927e-08 2.964e-08    6.412 0.00545 **
## Residuals   26 1.202e-07 4.622e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Somatosensory Cortex Trunk Region

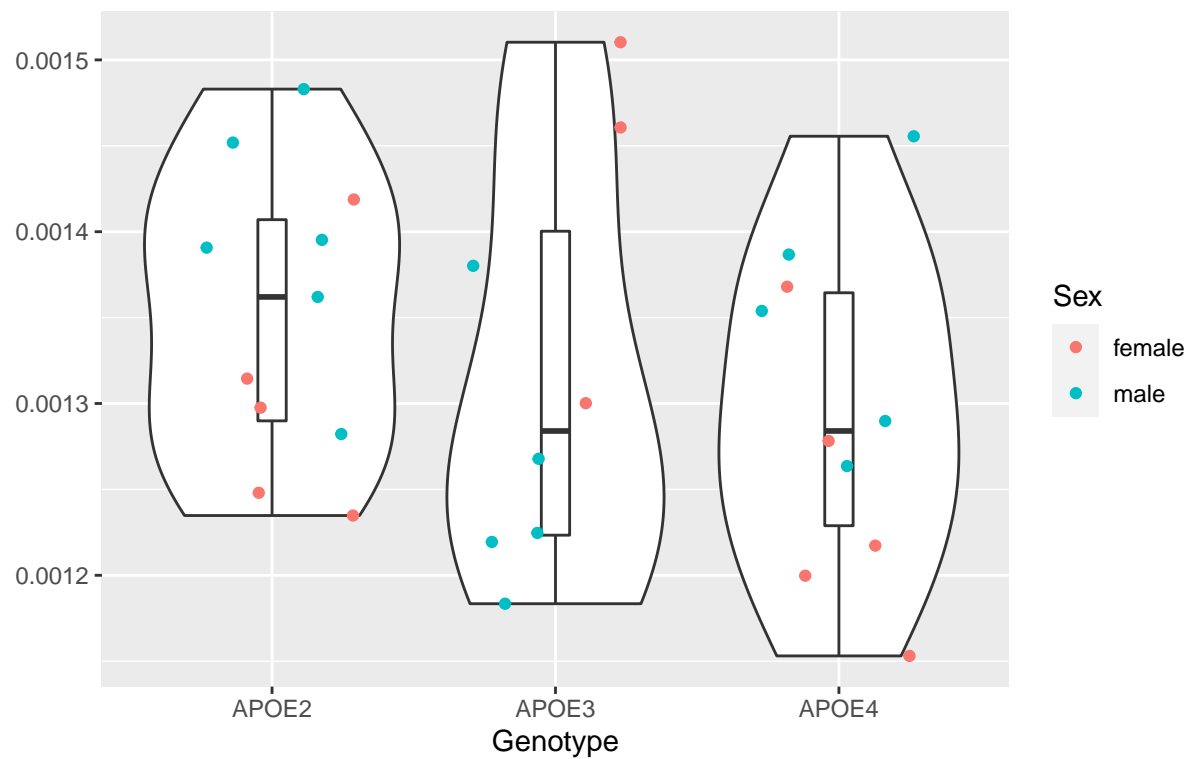
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno      2 3.797e-08 1.899e-08   3.844 0.0345 *
## Residuals 26 1.284e-07 4.940e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Somatosensory Cortex Shoulder Region

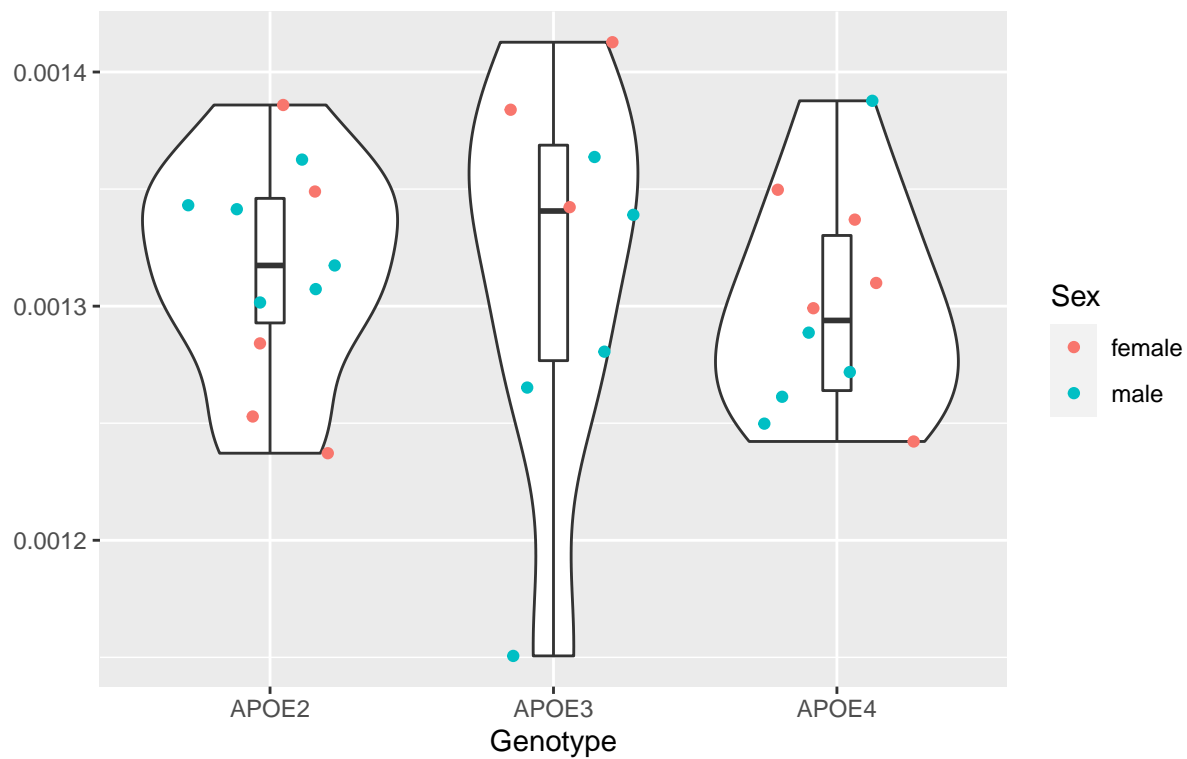
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.677e-08	8.387e-09	0.876	0.428
## Residuals	26	2.489e-07	9.573e-09		

Left Primary Somatosensory Cortex Jaw Region

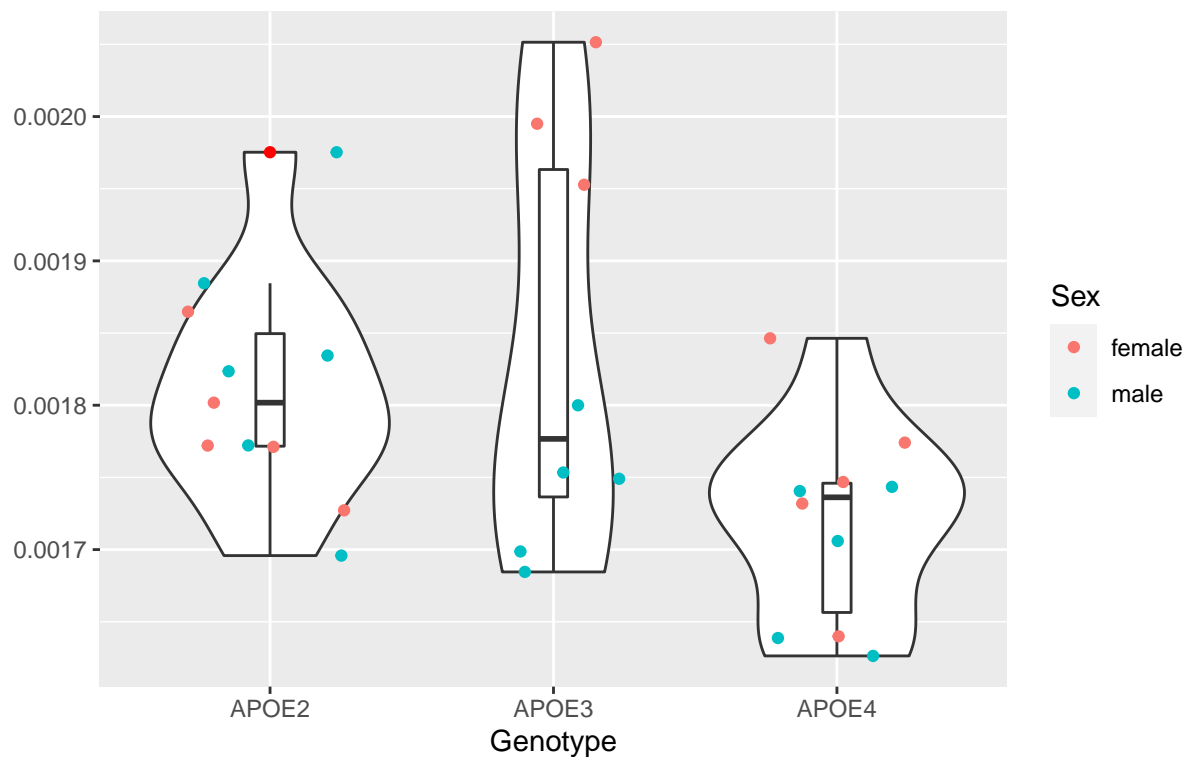
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.930e-09	9.630e-10	0.28	0.758
## Residuals	26	8.956e-08	3.445e-09		

Left Primary Somatosensory Cortex Hindlimb Region

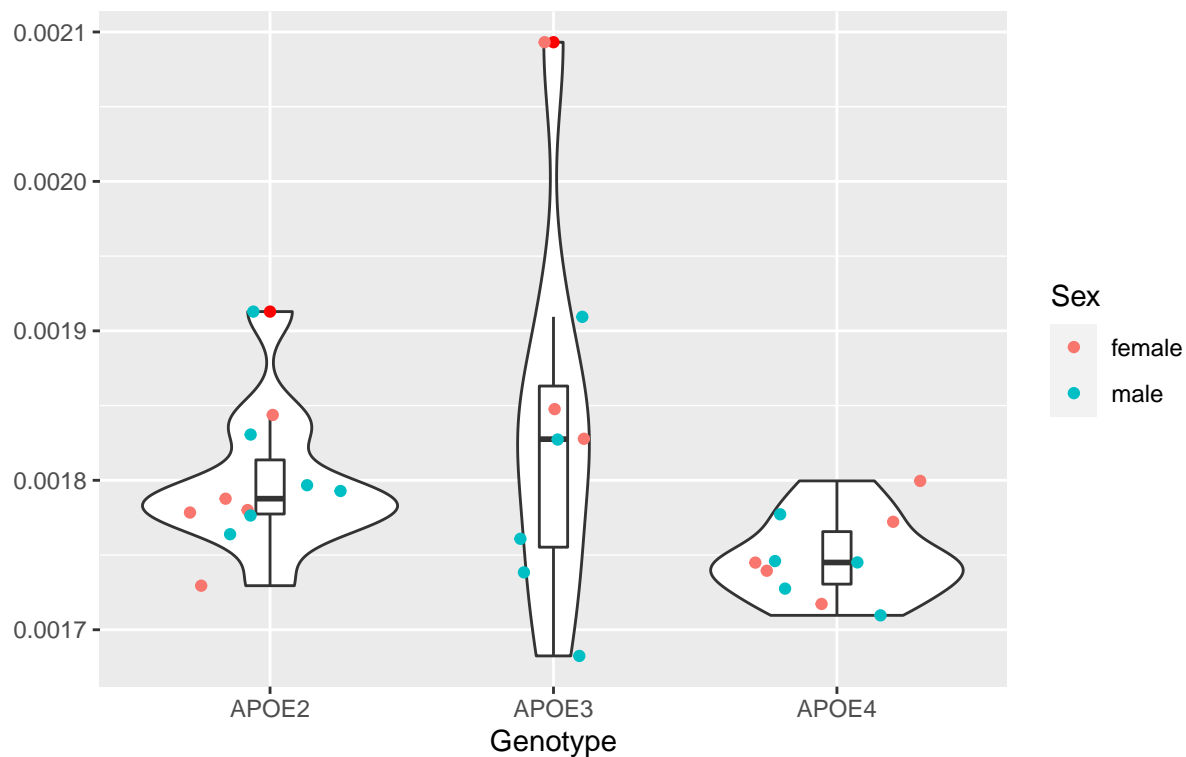
Red points denoting outliers



```
##          Df    Sum Sq Mean Sq F value Pr(>F)
## geno         2 7.099e-08 3.55e-08   3.744 0.0372 *
## Residuals    26 2.465e-07 9.48e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Left Primary Somatosensory Cortex Forelimb Region

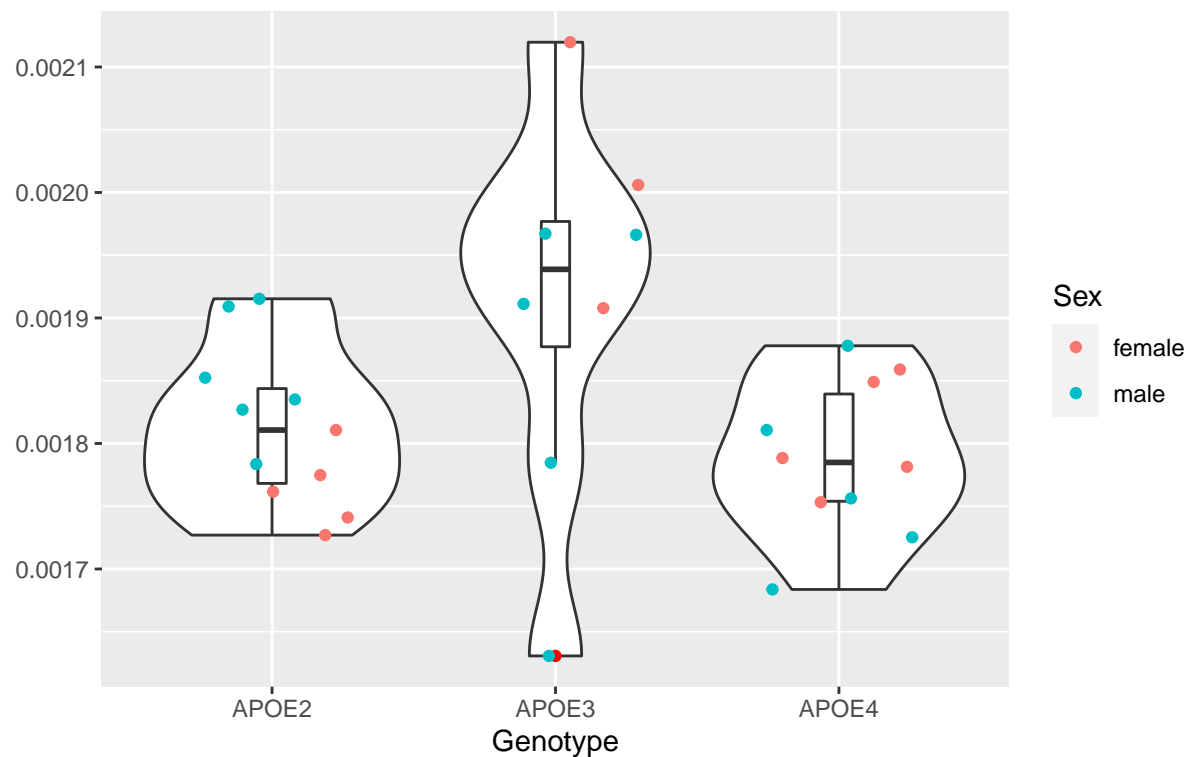
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno       2 3.544e-08 1.772e-08   3.266 0.0543 .
## Residuals 26 1.411e-07 5.425e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Somatosensory Cortex Dysgranular Zone

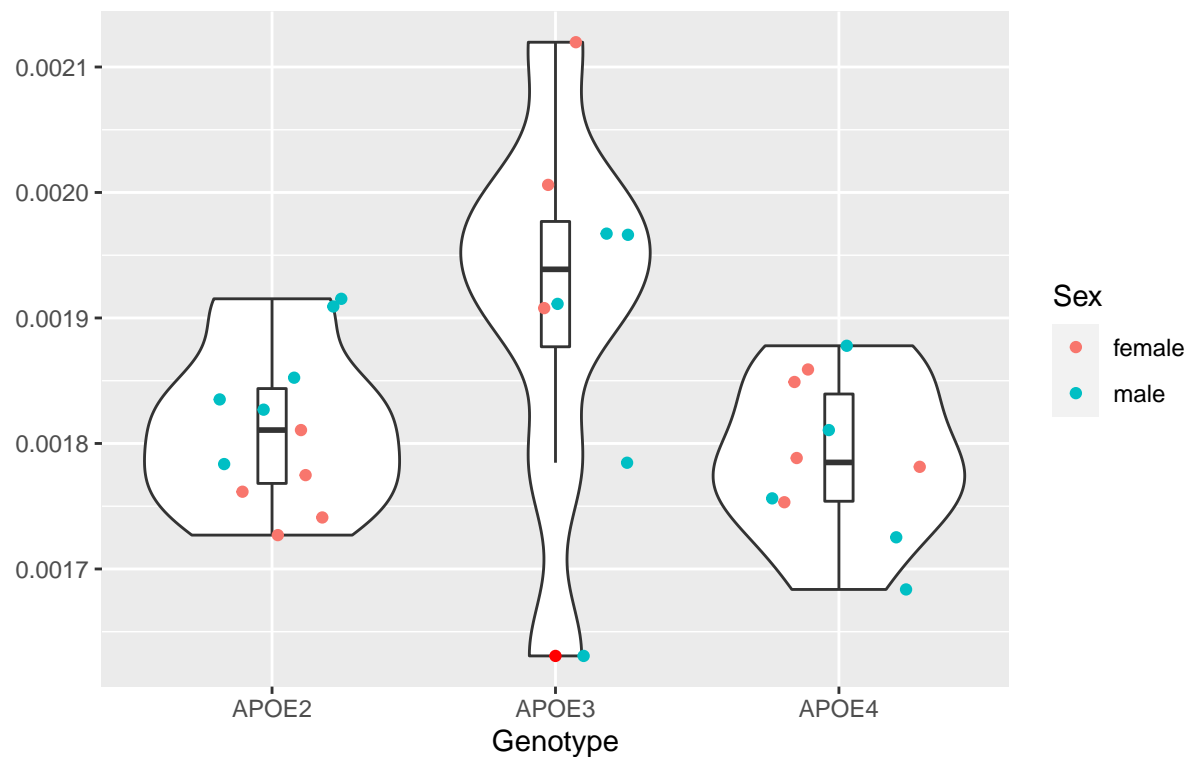
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 4.792e-08 2.396e-08   3.396 0.0489 *
## Residuals    26 1.834e-07 7.055e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Somatosensory Cortex Barrel Field

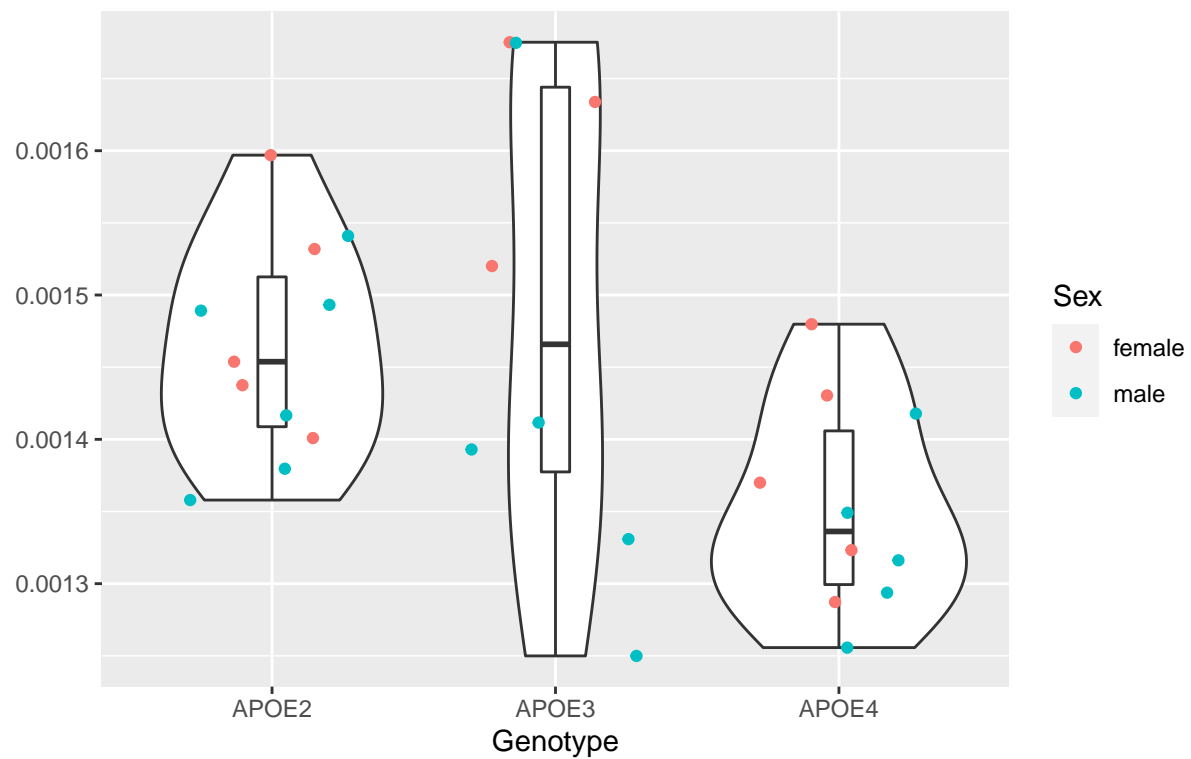
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 7.397e-08 3.699e-08   4.231 0.0257 *
## Residuals    26 2.273e-07 8.740e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Primary Somatosensory Cortex

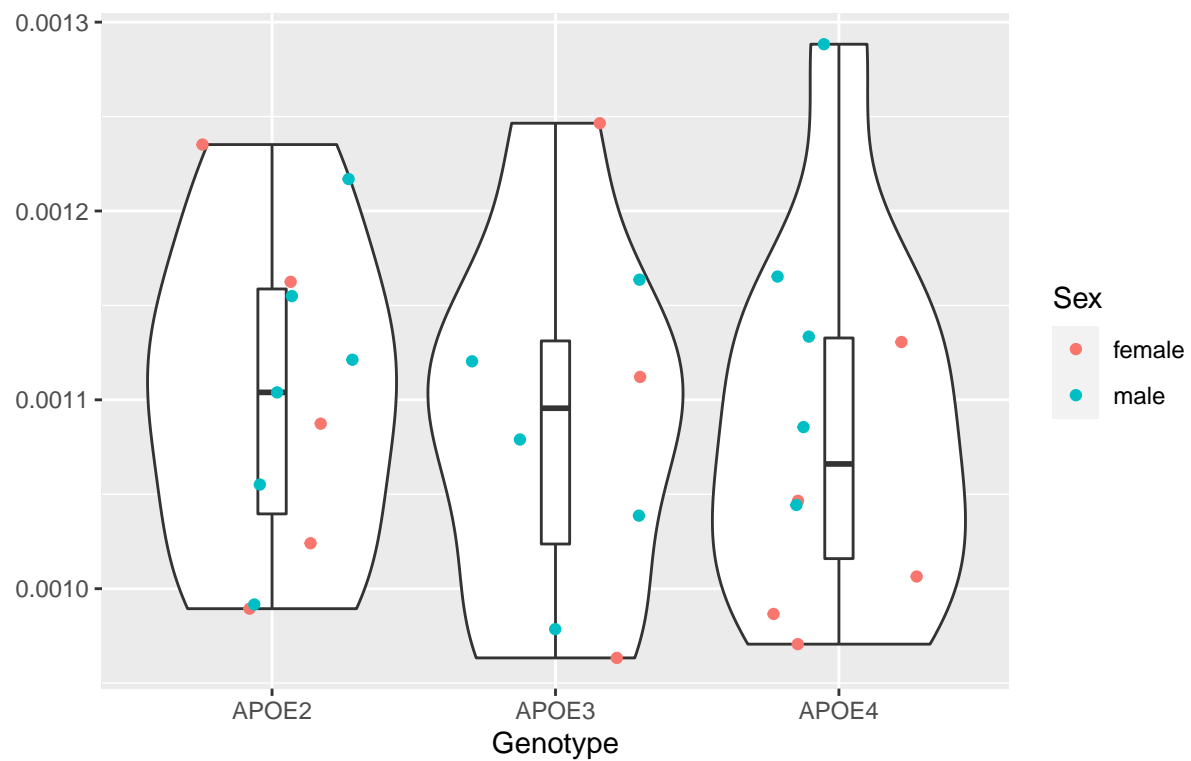
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 9.783e-08 4.892e-08   4.392 0.0227 *
## Residuals    26 2.896e-07 1.114e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Parietal Cortex Posterial Area Rostral Part

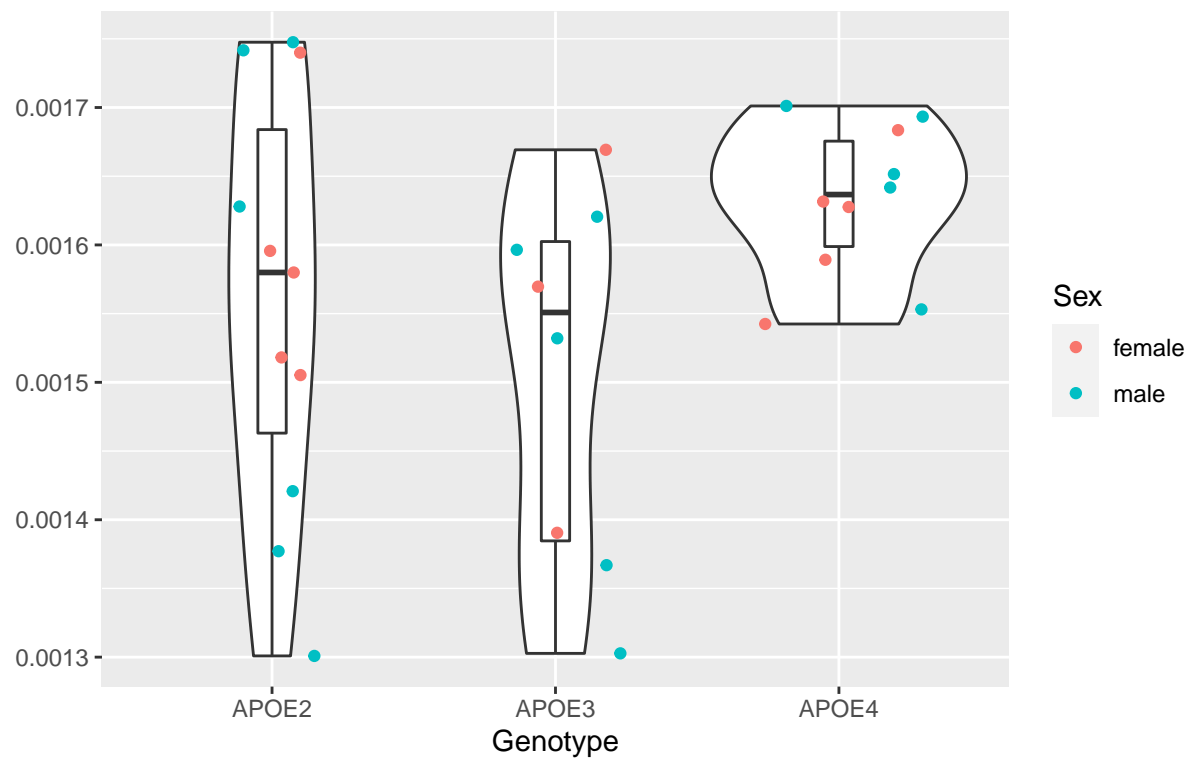
Red points denoting outliers



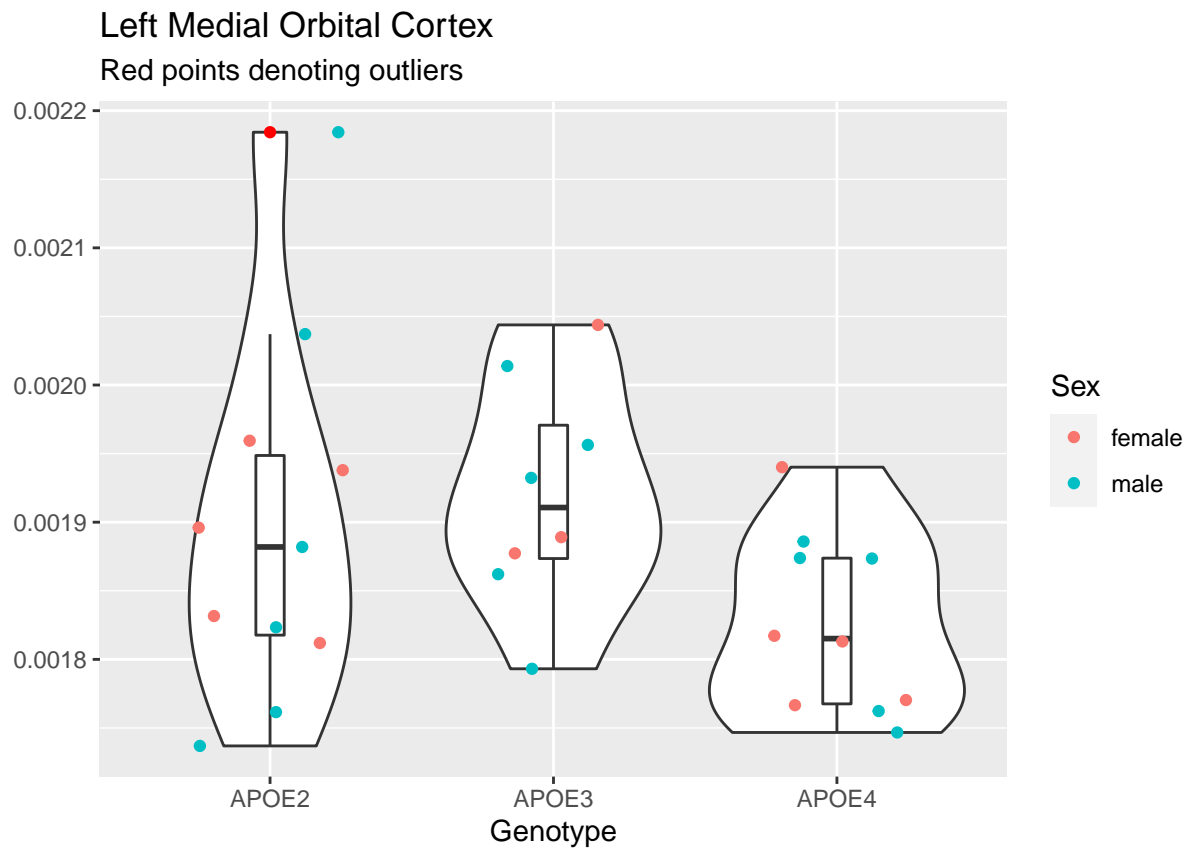
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.030e-09	1.017e-09	0.121	0.886
## Residuals	26	2.179e-07	8.379e-09		

Left Medial Parietal Association Cortex

Red points denoting outliers



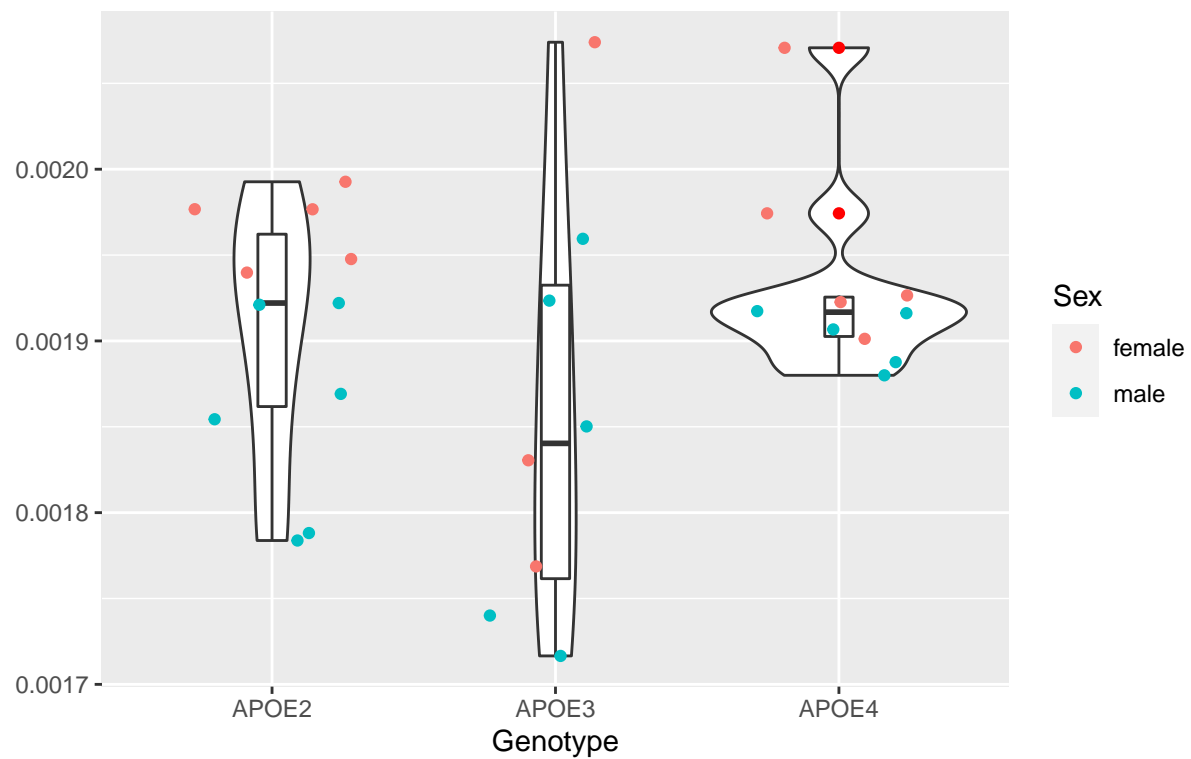
##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	7.18e-08	3.591e-08	2.419	0.109
## Residuals	26	3.86e-07	1.484e-08		



```
##          Df      Sum Sq   Mean Sq F value Pr(>F)
## geno       2 4.669e-08 2.334e-08    2.379  0.112
## Residuals 26 2.551e-07 9.810e-09
```

Left Secondary Motor Cortex

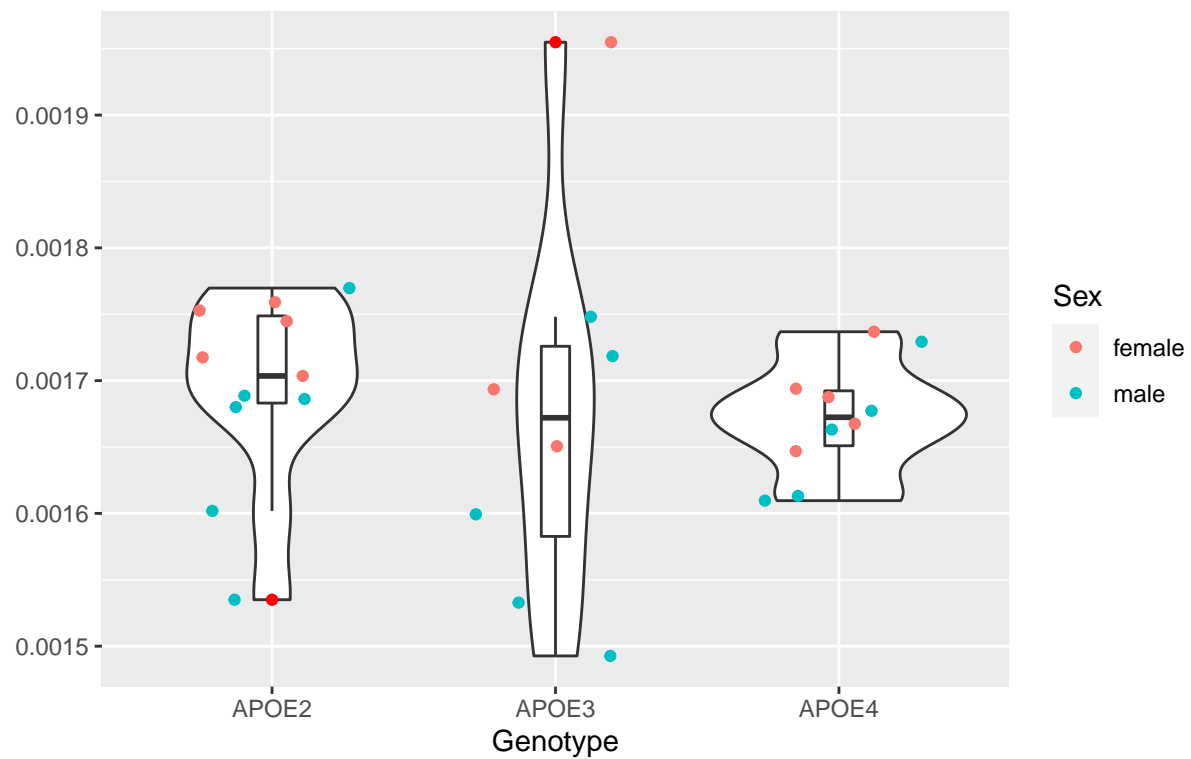
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.381e-08	1.191e-08	1.669	0.208
## Residuals	26	1.855e-07	7.134e-09		

Left Primary Motor Cortex

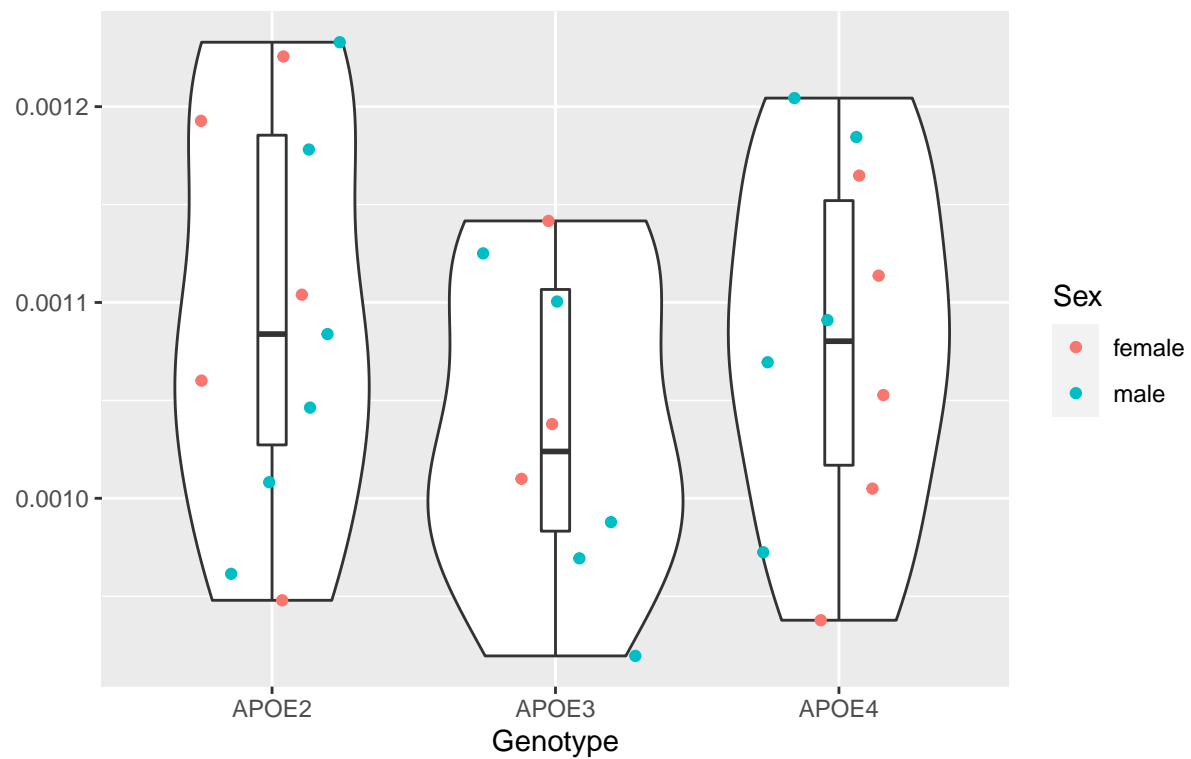
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.130e-09	1.564e-09	0.191	0.827
## Residuals	26	2.127e-07	8.181e-09		

Left Lateral Parietal Association Cortex

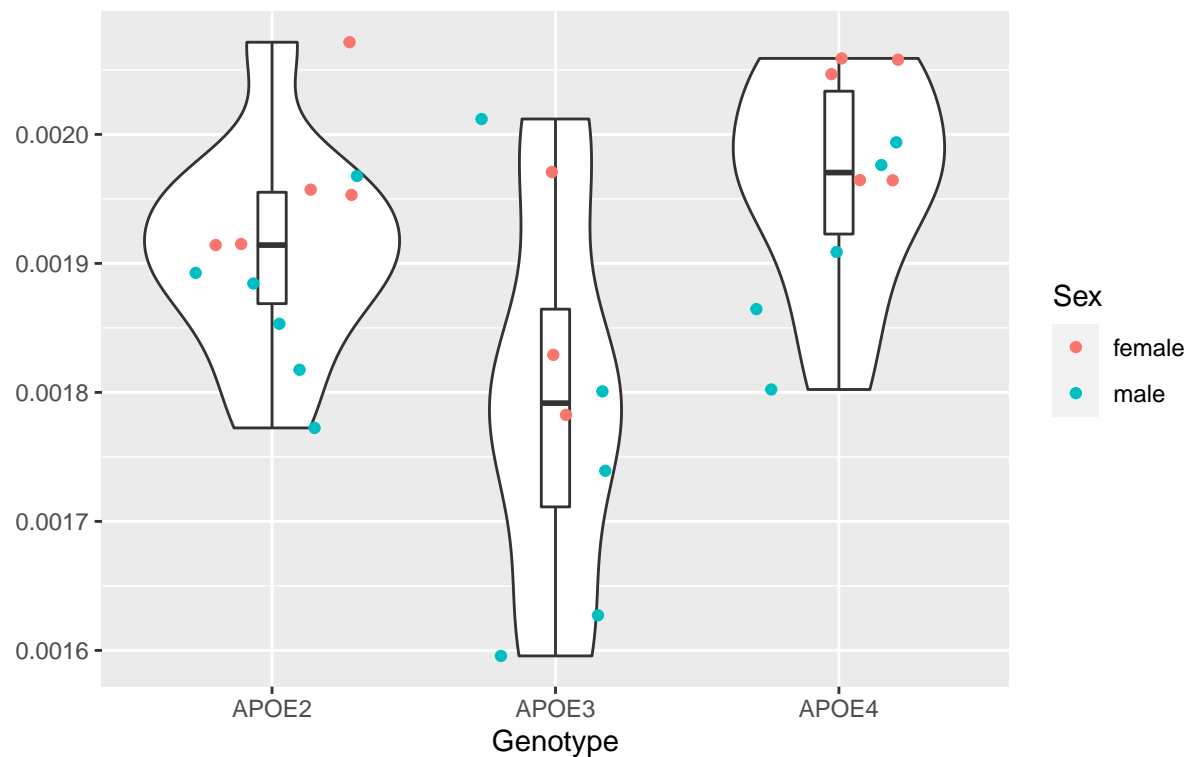
Red points denoting outliers



```
##          Df    Sum Sq Mean Sq F value Pr(>F)
## geno      2 1.626e-08 8.13e-09   0.958  0.397
## Residuals 26 2.207e-07 8.49e-09
```

Left Lateral Orbital Cortex

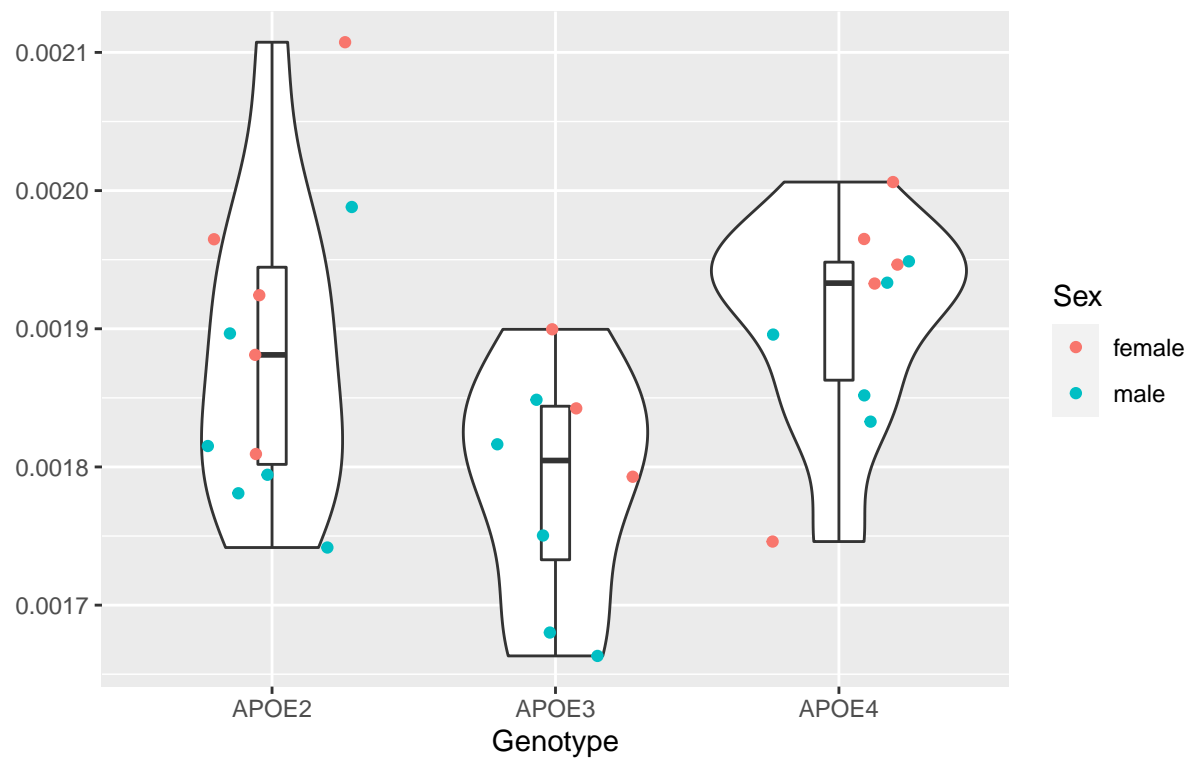
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 1.300e-07 6.500e-08     6.03 0.00706 **
## Residuals    26 2.803e-07 1.078e-08
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Insular Cortex

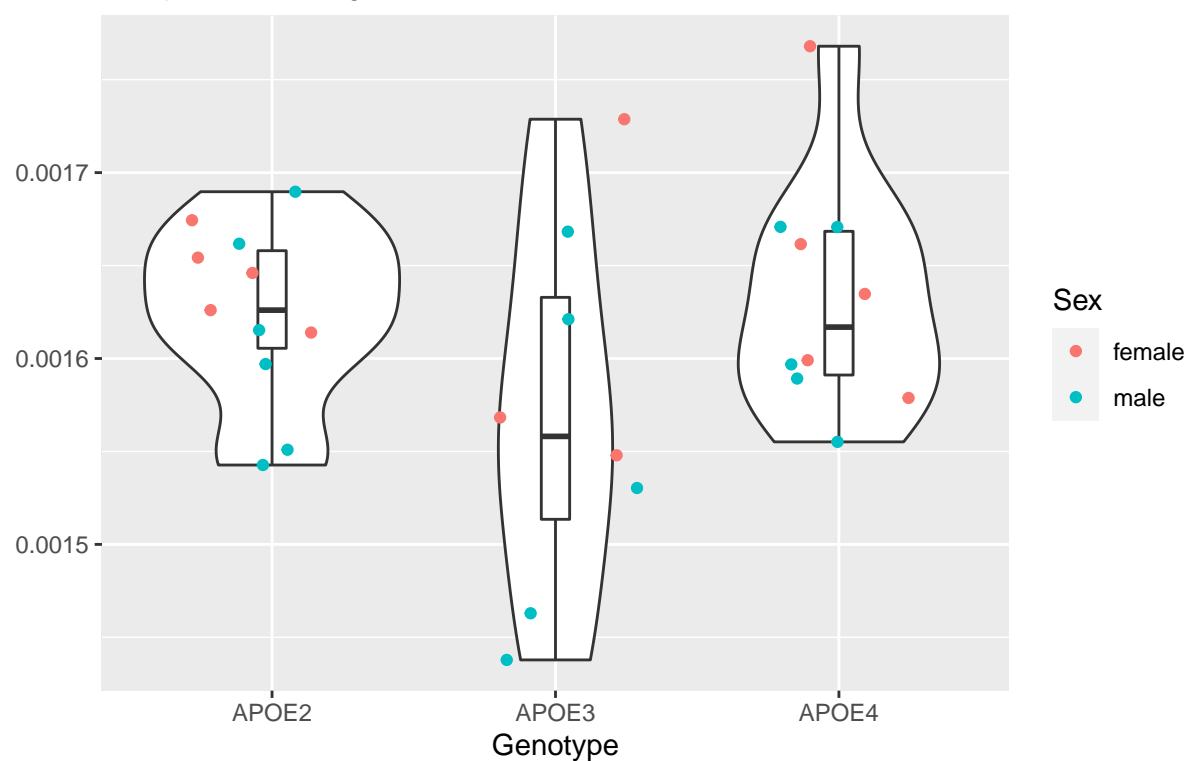
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 6.896e-08 3.448e-08   4.089 0.0286 *
## Residuals    26 2.192e-07 8.430e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Frontal Association Cortex

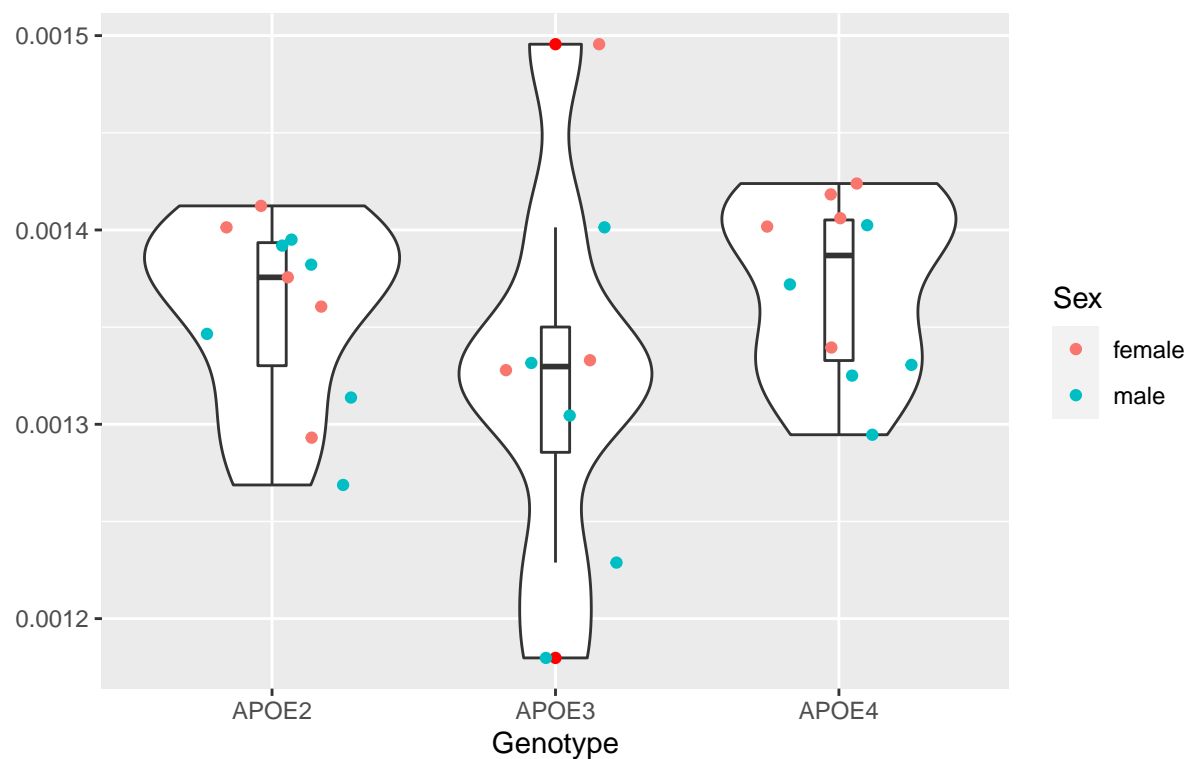
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.963e-08	9.817e-09	2.021	0.153
## Residuals	26	1.263e-07	4.856e-09		

Left Frontal Cortex Area 3

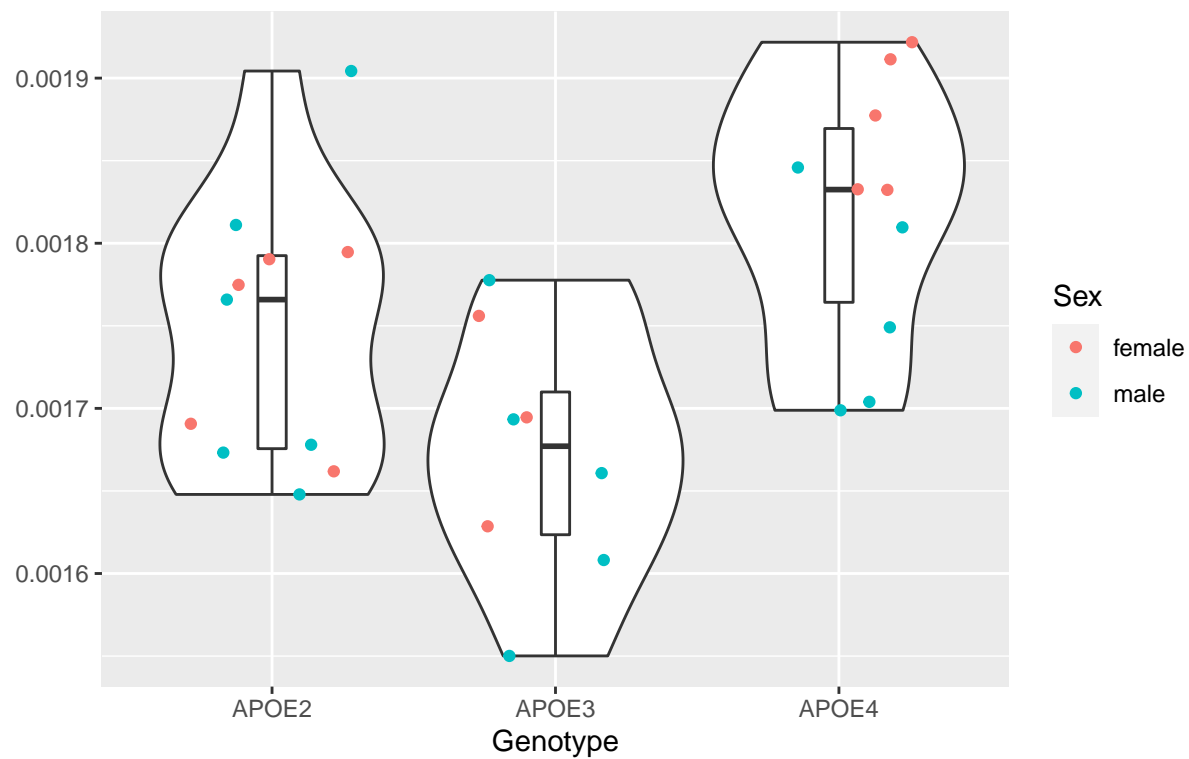
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	9.820e-09	4.912e-09	1.193	0.319
## Residuals	26	1.071e-07	4.119e-09		

Left Dorsolateral Orbital Cortex

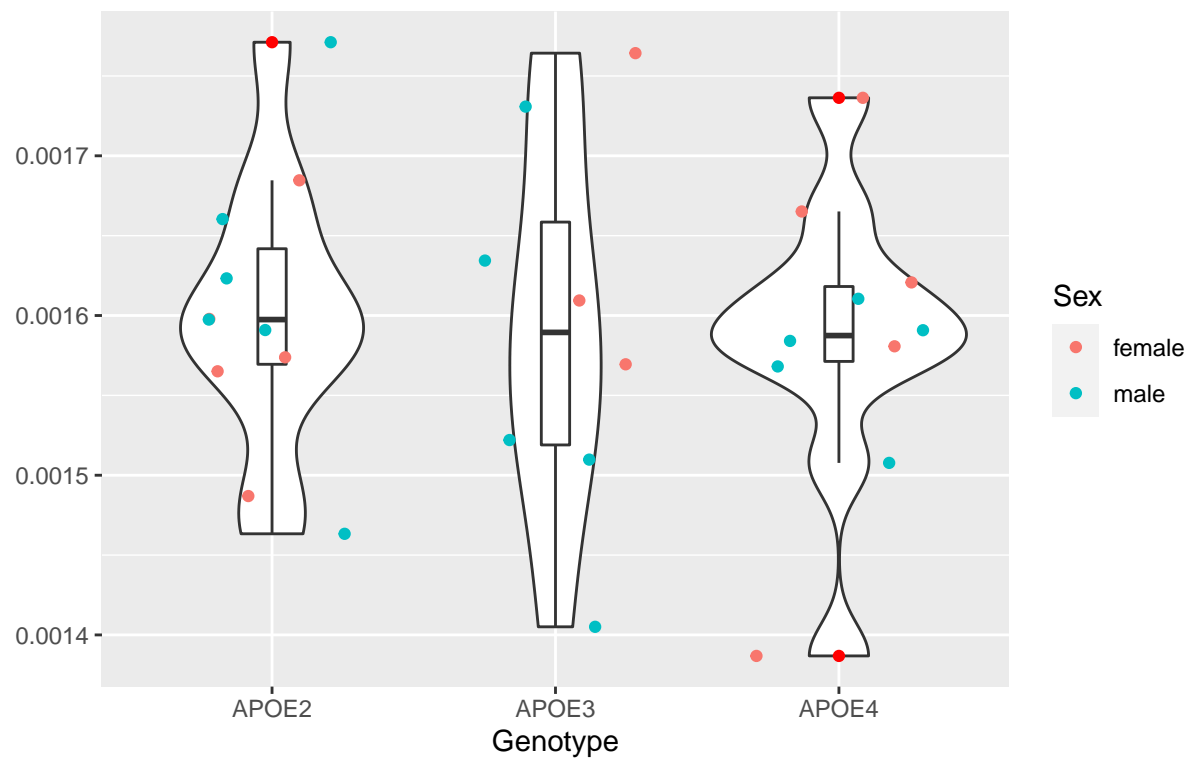
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 9.667e-08 4.834e-08   7.812 0.0022 **
## Residuals    26 1.609e-07 6.190e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Secondary Auditory Cortex Ventral Part

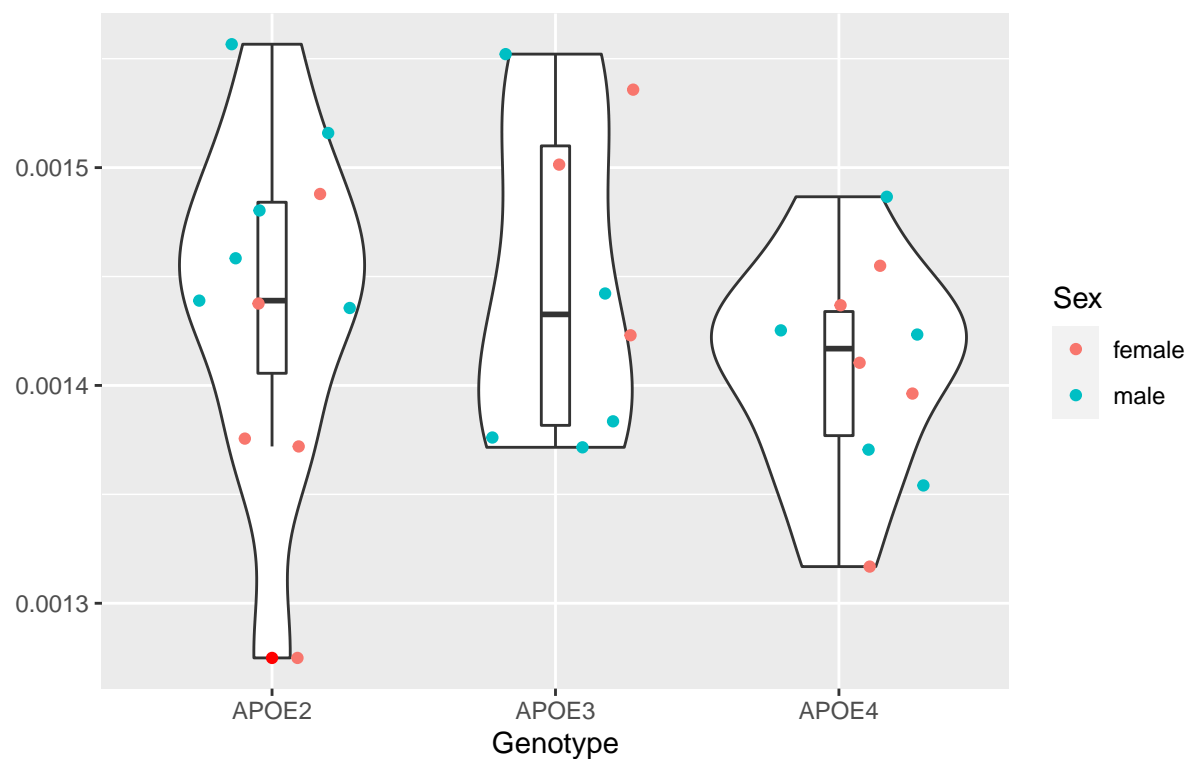
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.38e-09	6.920e-10	0.072	0.93
## Residuals	26	2.49e-07	9.578e-09		

Left Secondary Auditory Cortex Dorsal Part

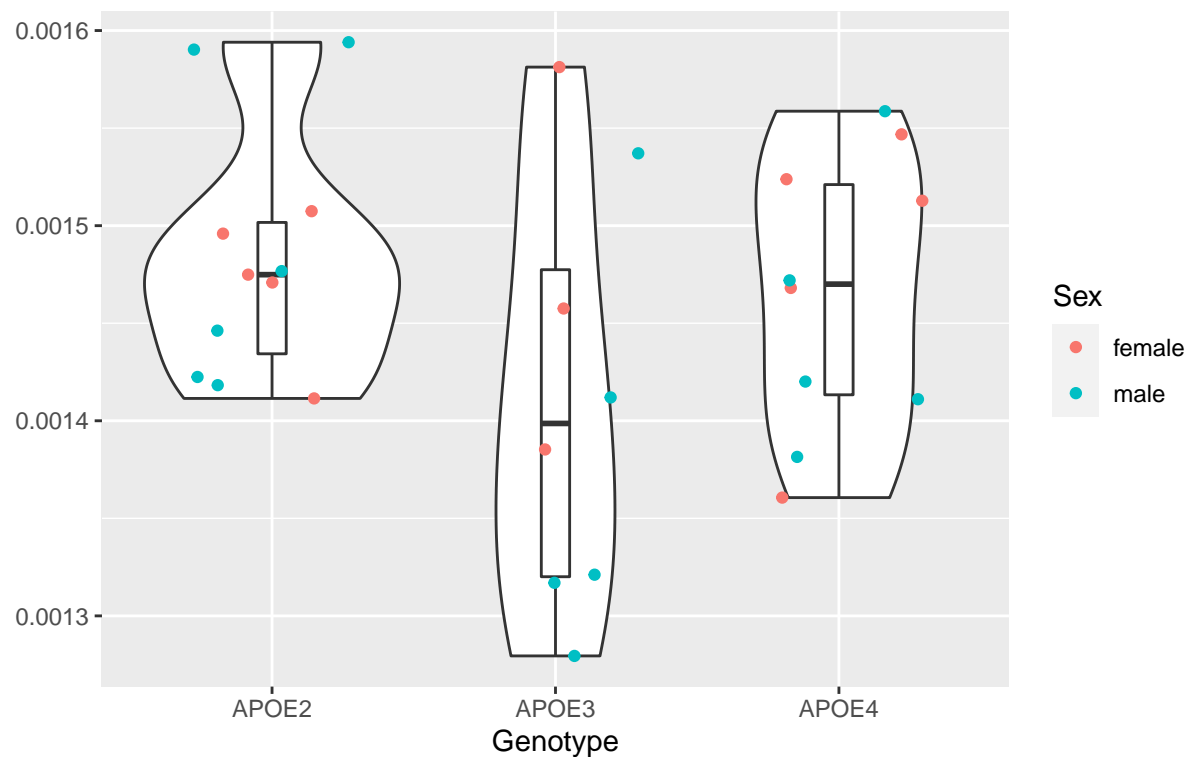
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	8.670e-09	4.333e-09	0.944	0.402
## Residuals	26	1.194e-07	4.592e-09		

Left Primary Auditory Cortex

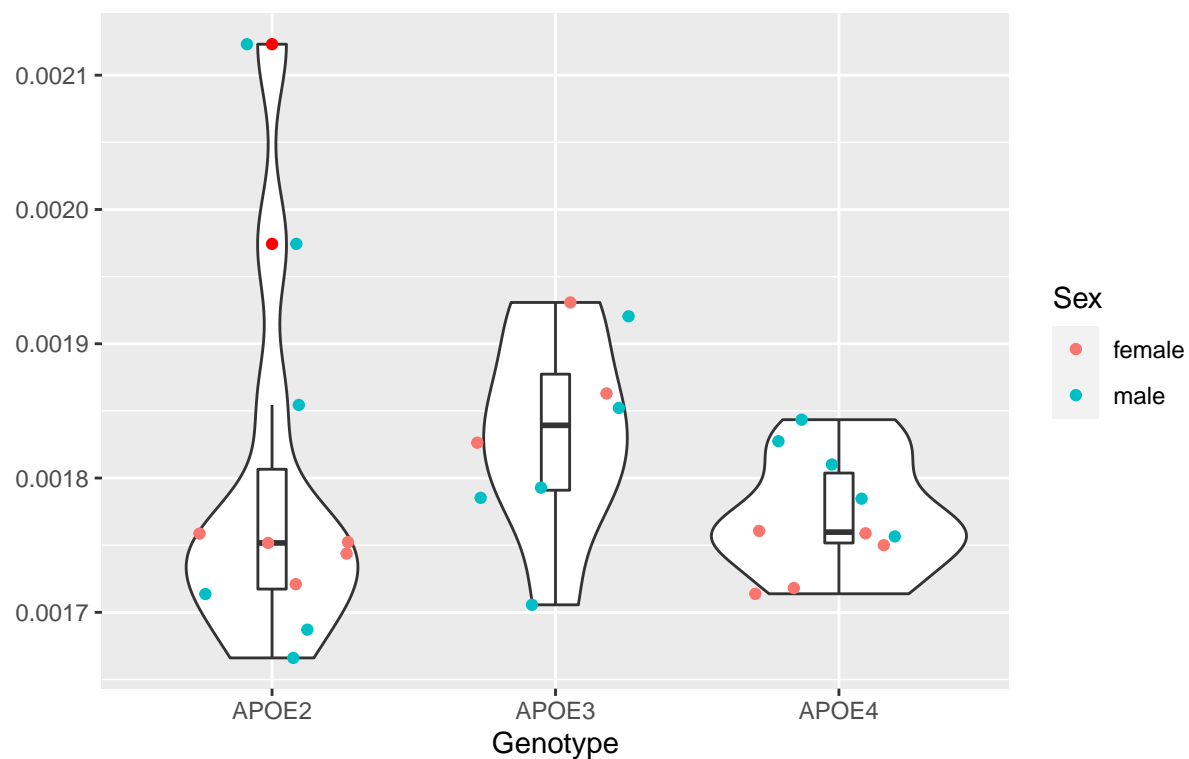
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.461e-08	1.230e-08	1.937	0.164
## Residuals	26	1.652e-07	6.352e-09		

Left Cingulate Cortex Area 32

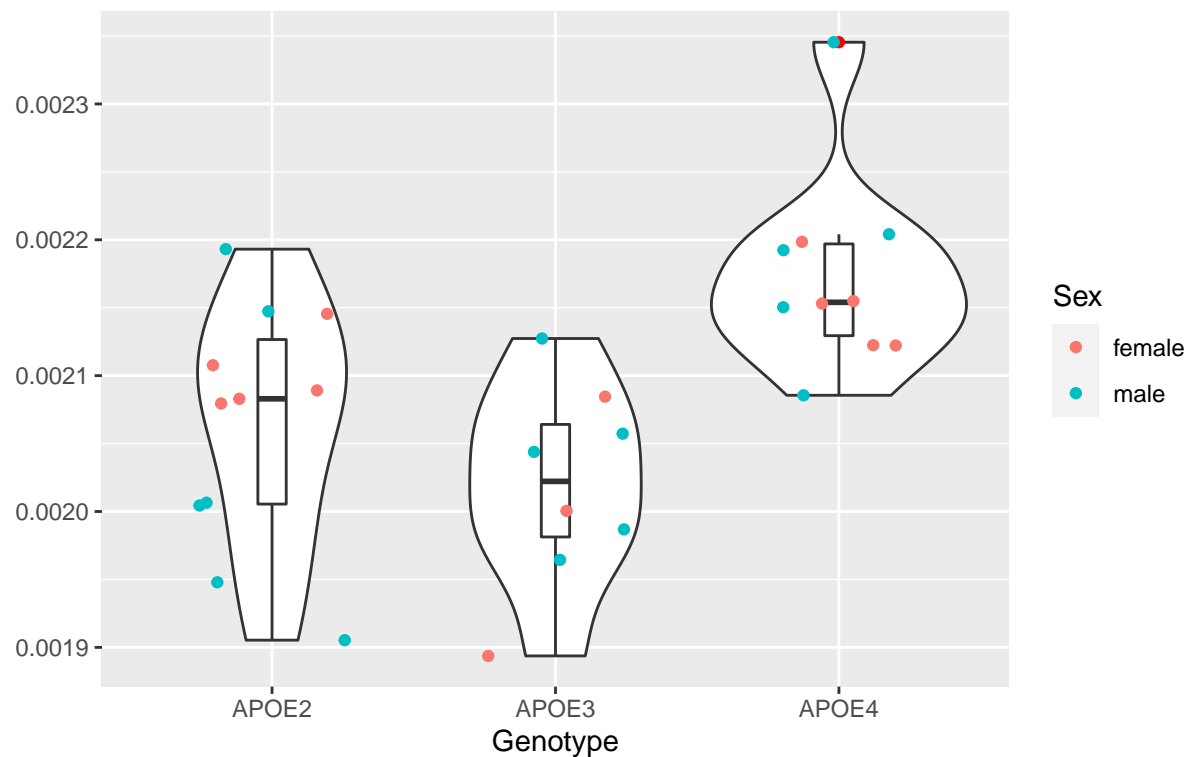
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	1.736e-08	8.680e-09	0.913	0.414
## Residuals	26	2.471e-07	9.504e-09		

Left Cingulate Cortex Area 30

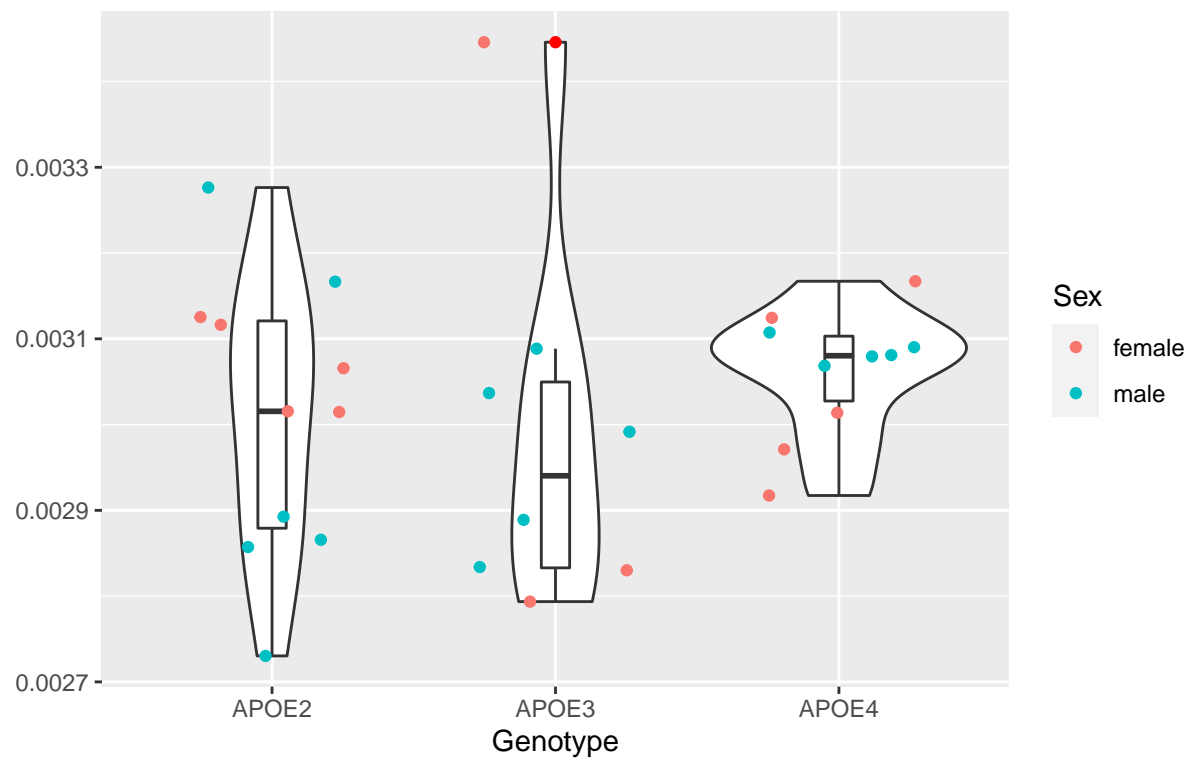
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value    Pr(>F)
## geno         2 1.153e-07 5.764e-08    9.203 0.000951 ***
## Residuals    26 1.629e-07 6.260e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Cingulate Cortex Area 29c

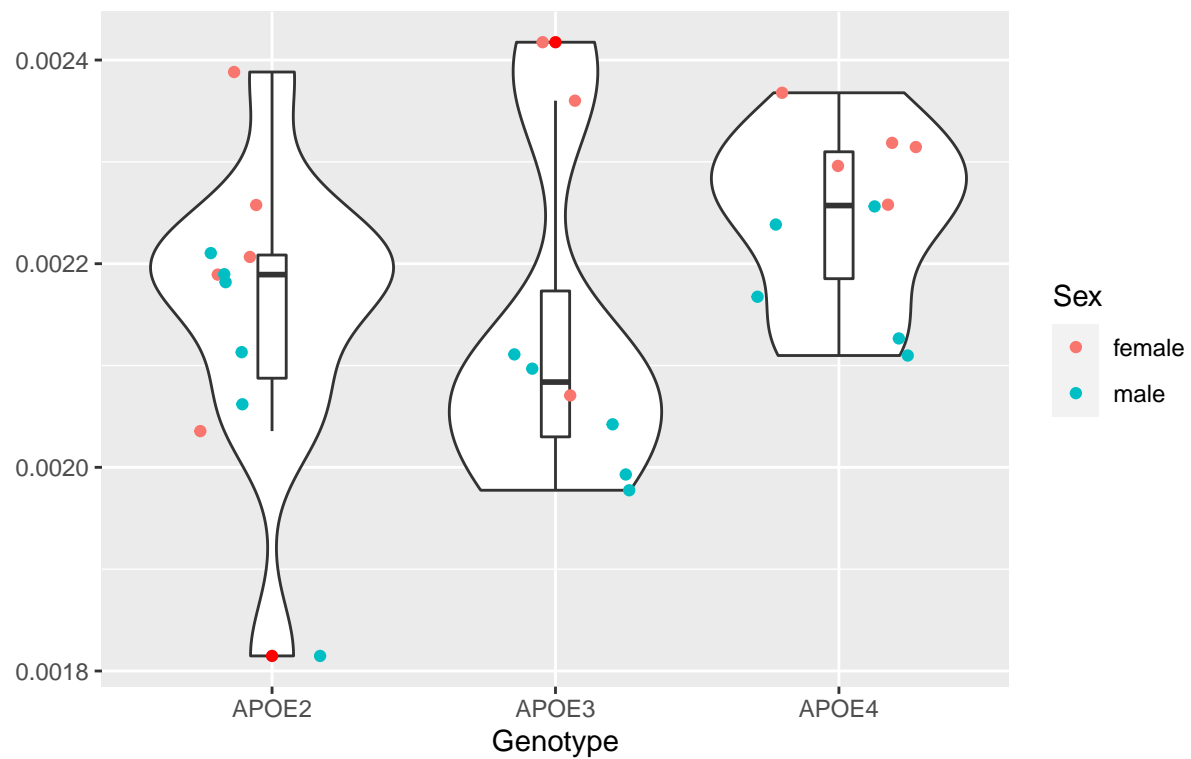
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.610e-08	1.307e-08	0.541	0.588
## Residuals	26	6.278e-07	2.415e-08		

Left Cingulate Cortex Area 29b

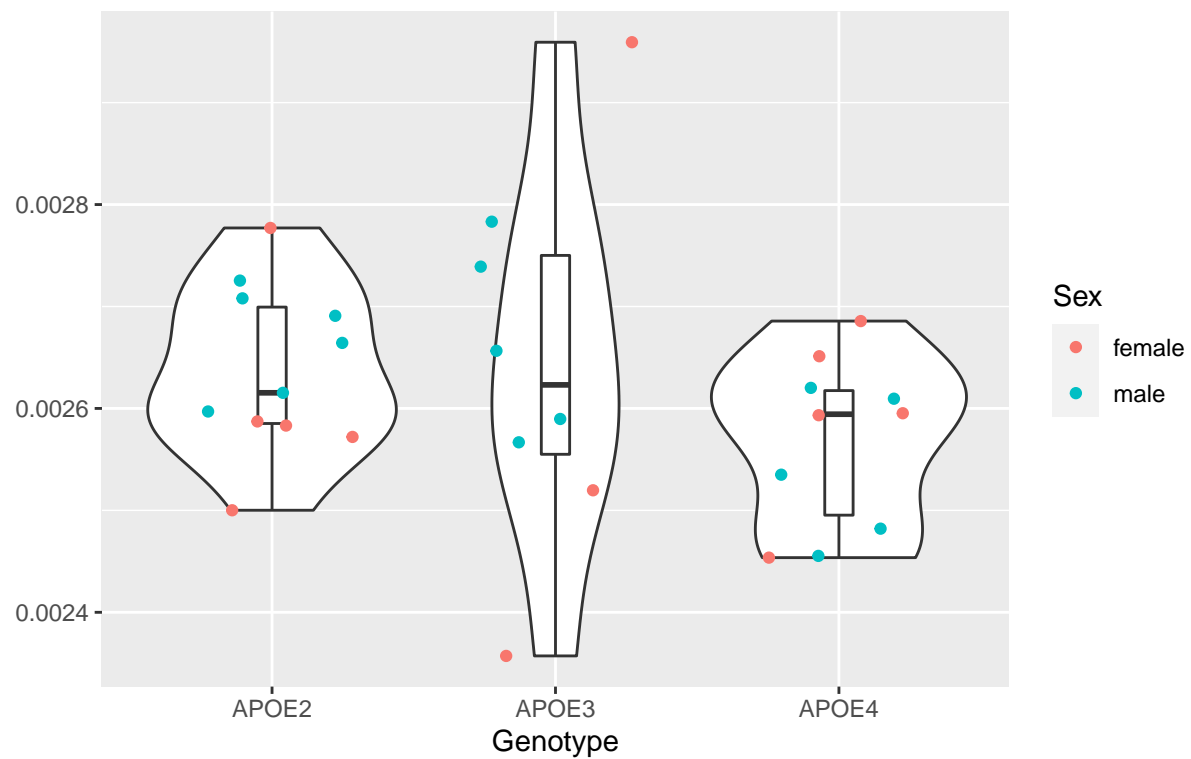
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	6.980e-08	3.491e-08	1.928	0.166
## Residuals	26	4.707e-07	1.810e-08		

Left Cingulate Cortex Area 29a

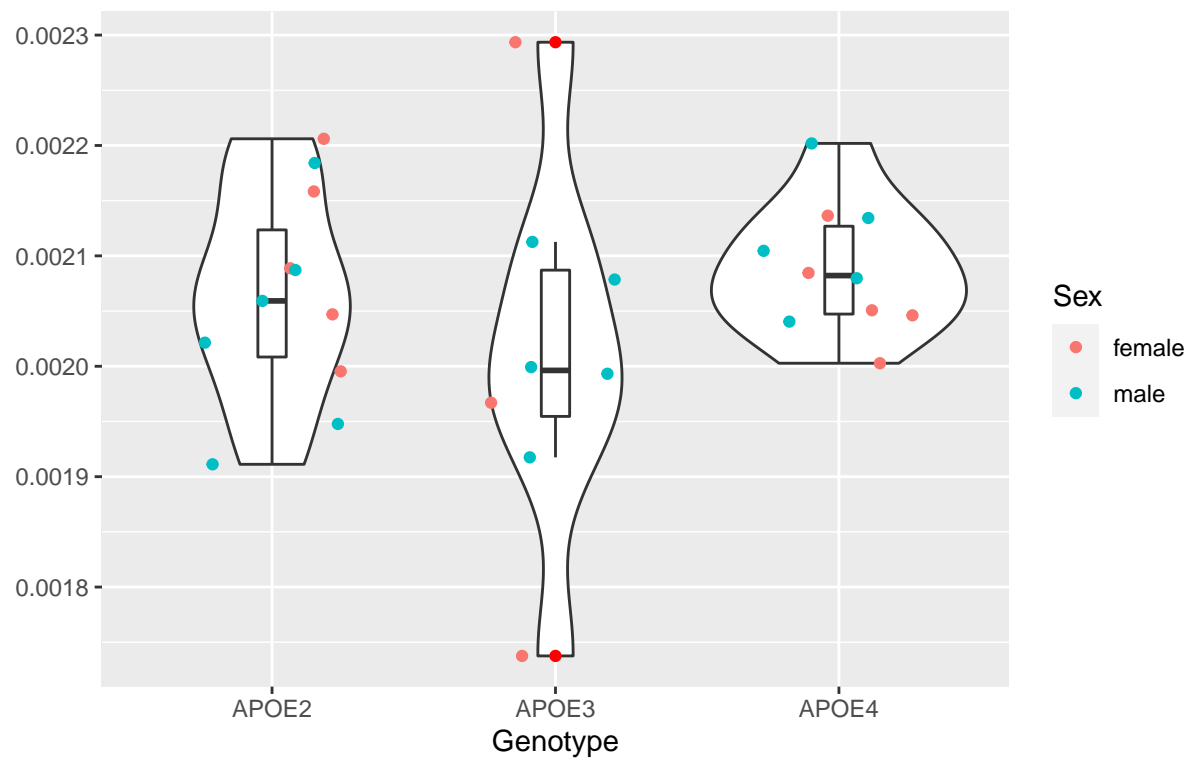
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.580e-08	1.788e-08	1.285	0.294
## Residuals	26	3.619e-07	1.392e-08		

Left Cingulate Cortex Area 24b Prime

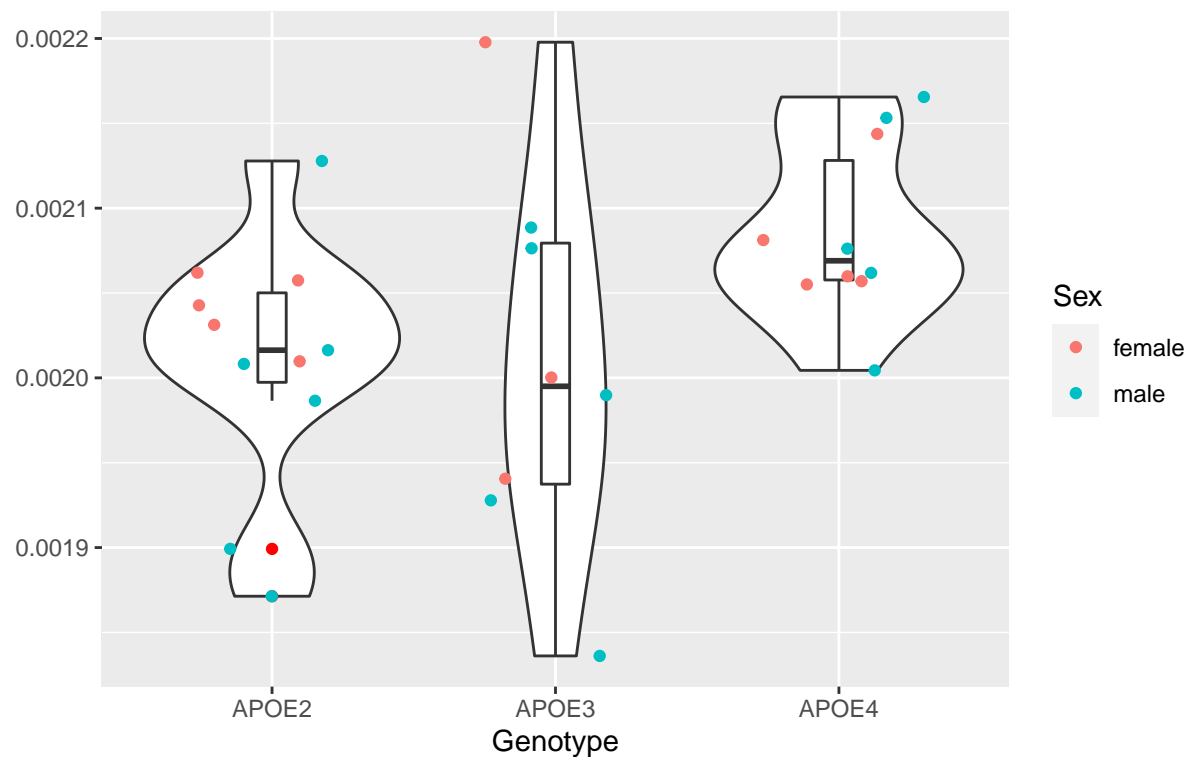
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.614e-08	1.307e-08	1.135	0.337
## Residuals	26	2.994e-07	1.152e-08		

Left Cingulate Cortex Area 24b

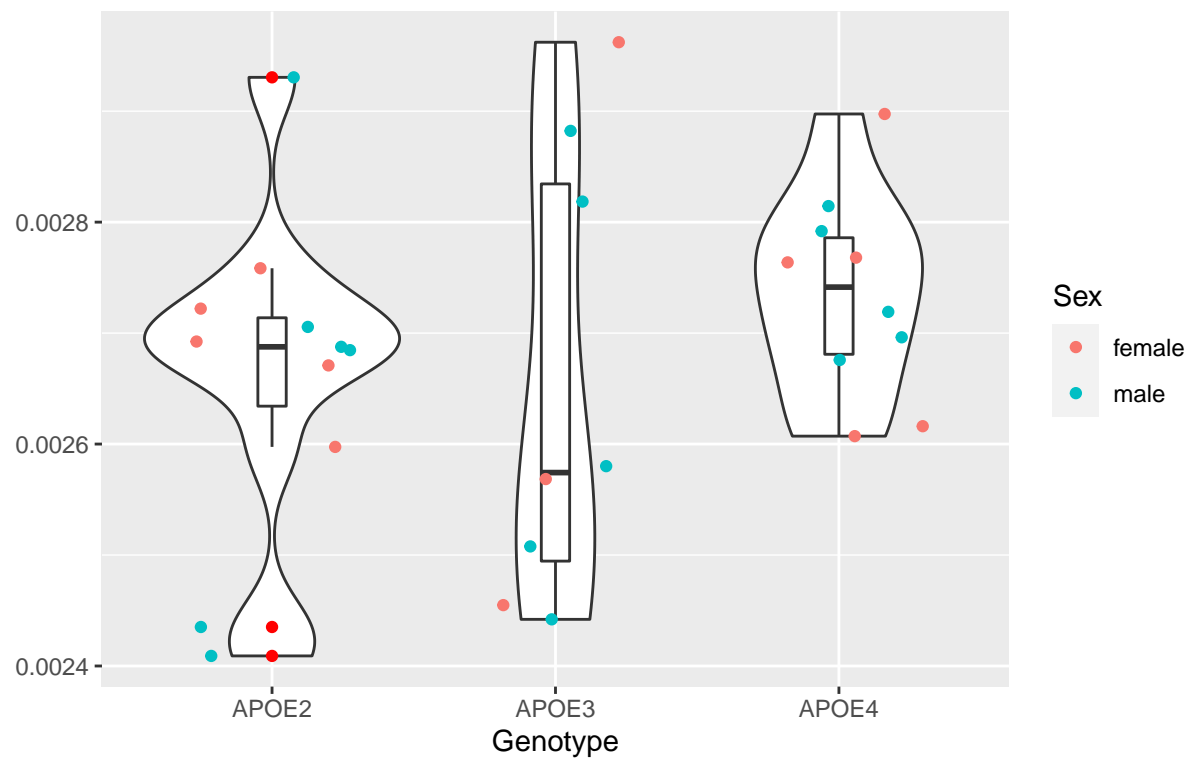
Red points denoting outliers



```
##          Df    Sum Sq  Mean Sq F value Pr(>F)
## geno         2 3.875e-08 1.937e-08   3.061  0.064 .
## Residuals    26 1.646e-07 6.330e-09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Left Cingulate Cortex Area 24a Prime

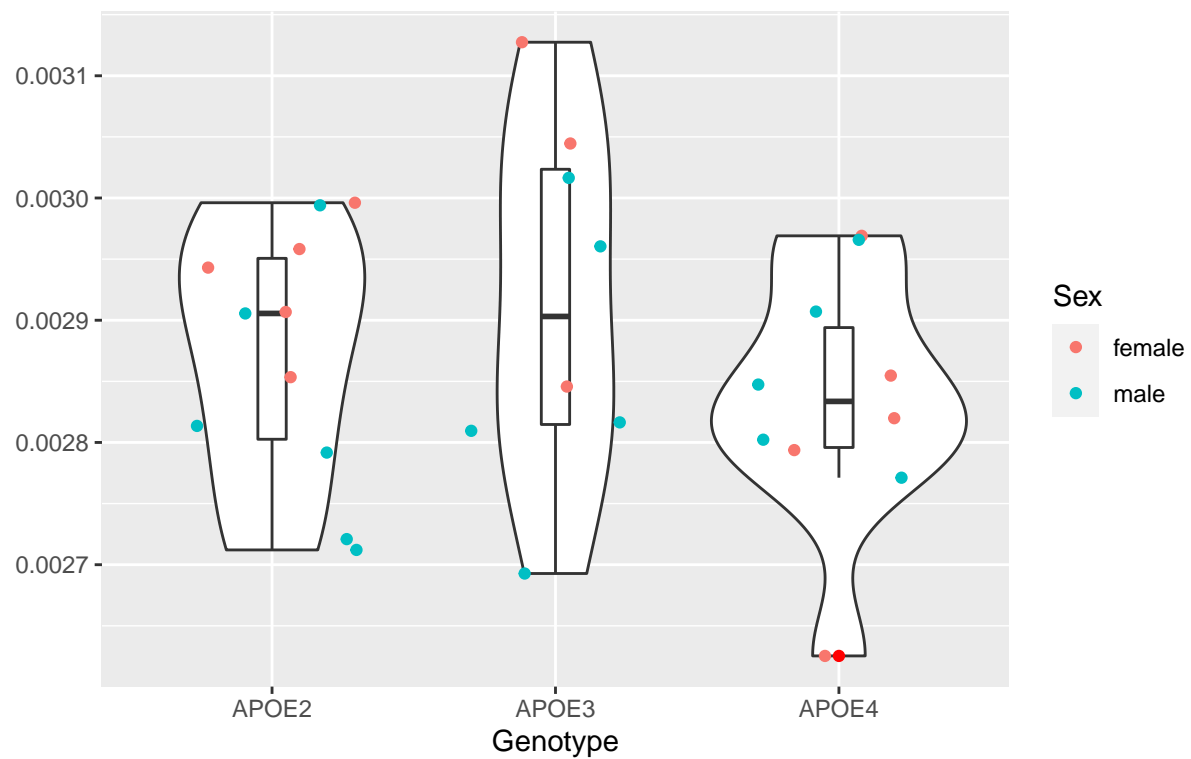
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	3.900e-08	1.950e-08	0.881	0.426
## Residuals	26	5.751e-07	2.212e-08		

Left Cingulate Cortex Area 24a

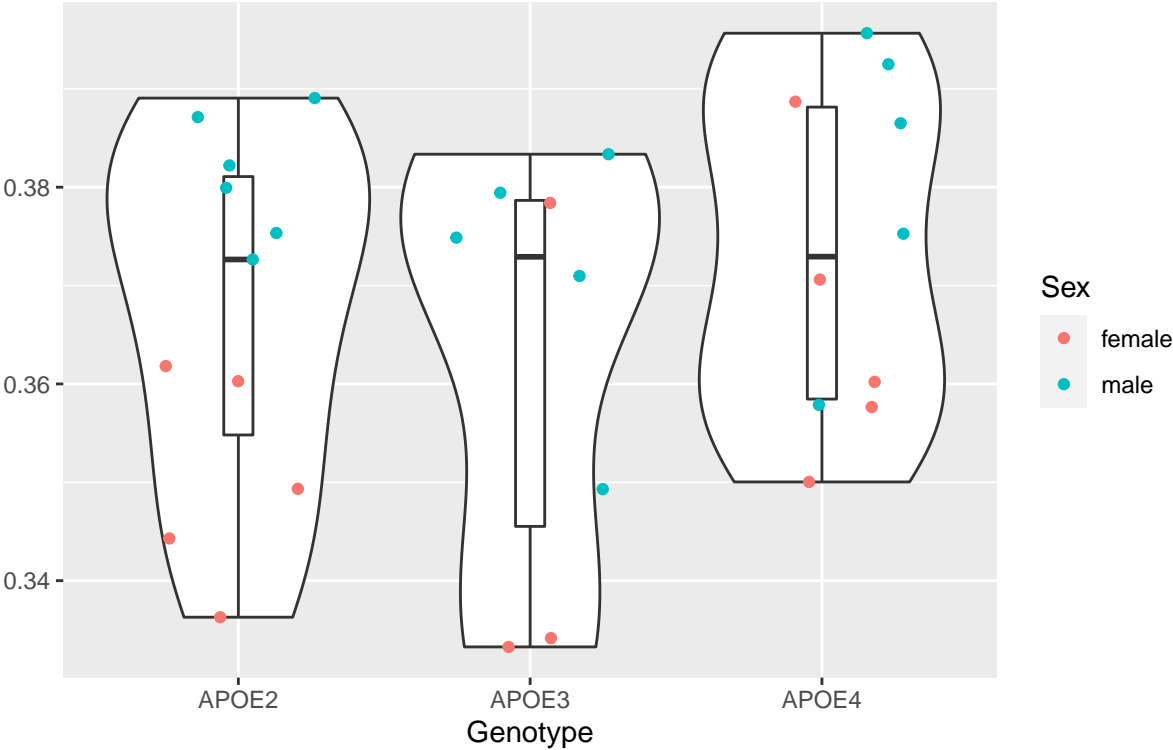
Red points denoting outliers



##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## geno	2	2.740e-08	1.372e-08	1.034	0.37
## Residuals	26	3.448e-07	1.326e-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		