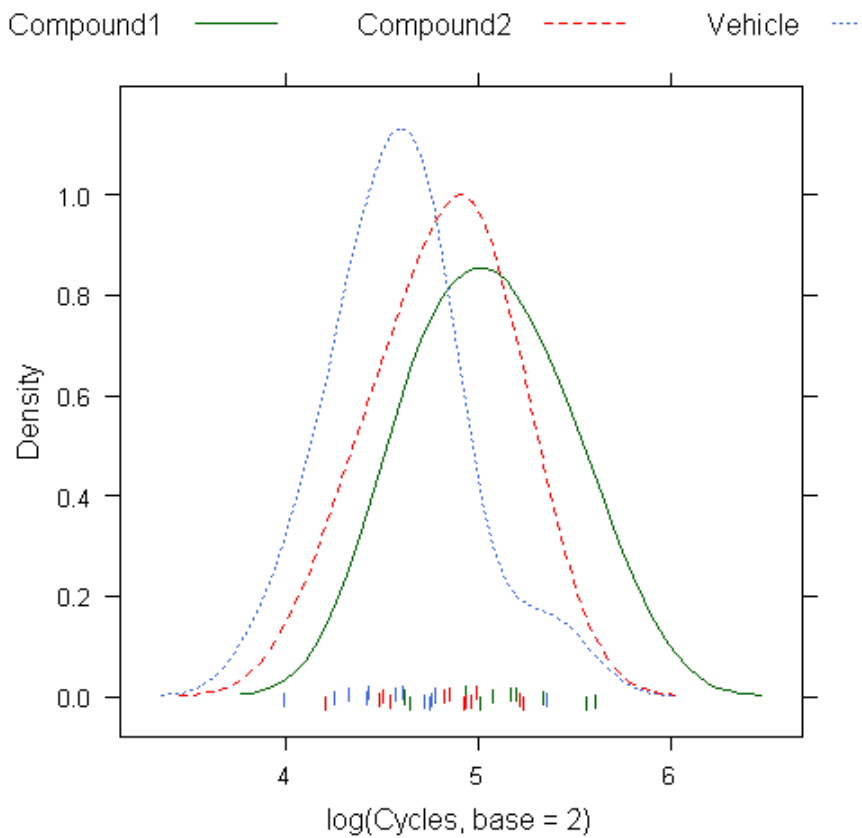There were **36** subjects measured across 3 drug groups. A density plot of the data is produced with the lattice package:

Here is a table of the mean cycles to threshold for each drug group:

Compound1	Compound2	Vehicle
5.054	4.816	4.590

Of course, we would normally look at diagnostics before going straight to the p-value

```
> linearModel <- lm(log(Cycles, base = 2) ~ Compound, data = pcrData)
> anova(linearModel)
Analysis of Variance Table

Response: log(Cycles, base = 2)
          Df Sum Sq Mean Sq F value   Pr(>F)
Compound   2 1.2947  0.6473   5.829 0.006794 **
Residuals 33 3.6648  0.1111
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```