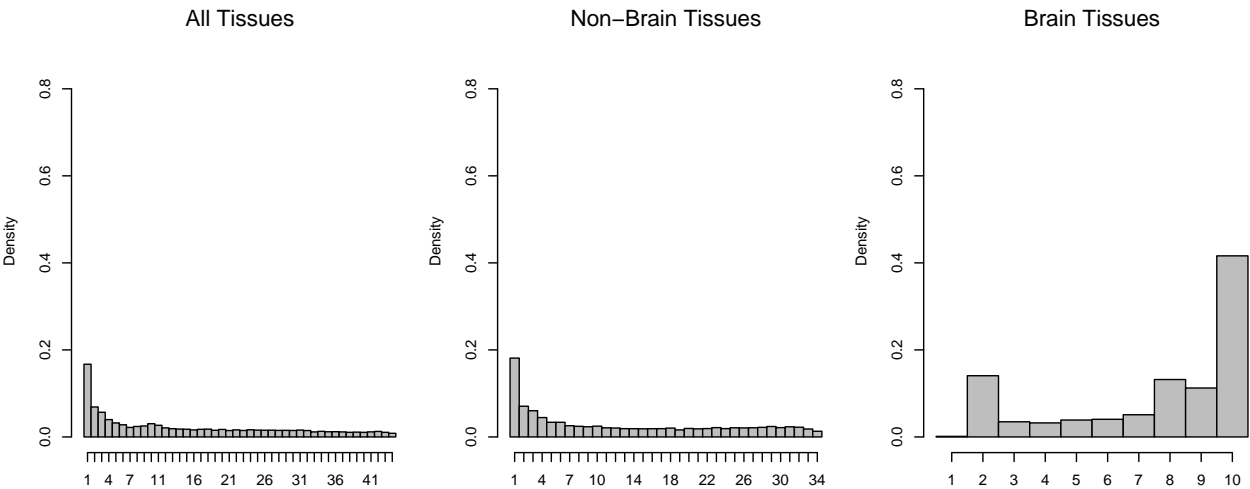# NumberofTissuesSharedbyMagnitudeandSign

In this document, we generate plots for Heterogeneity Distributions

```
## Warning: package 'knitr' was built under R version 3.2.5
```

Let's plot heterogneity by magnitude from the global analysis.

Now, let's make the same plot with all tissue effects measuring the number of tissues which have a sign equivalent to max effect:

""