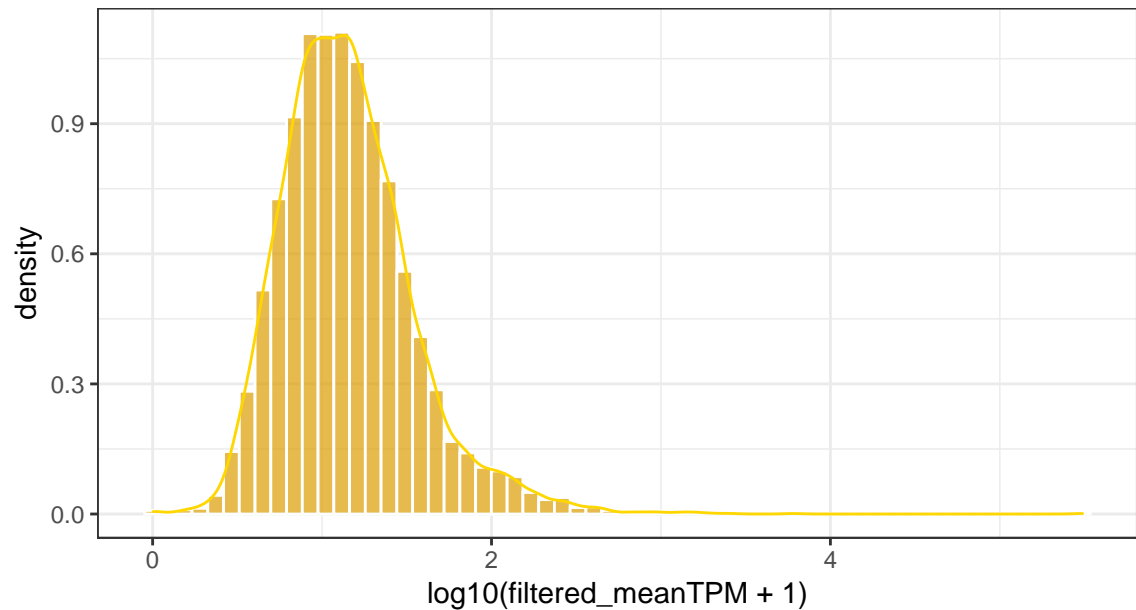


# Filtered mean TPM distribution across genes



Retaining only  $\log_{10}(\text{values})$  superior to zero:

```
keep <- apply(LprotcodTPM, 1, function(row) sum(row > 0) == length(row))
```