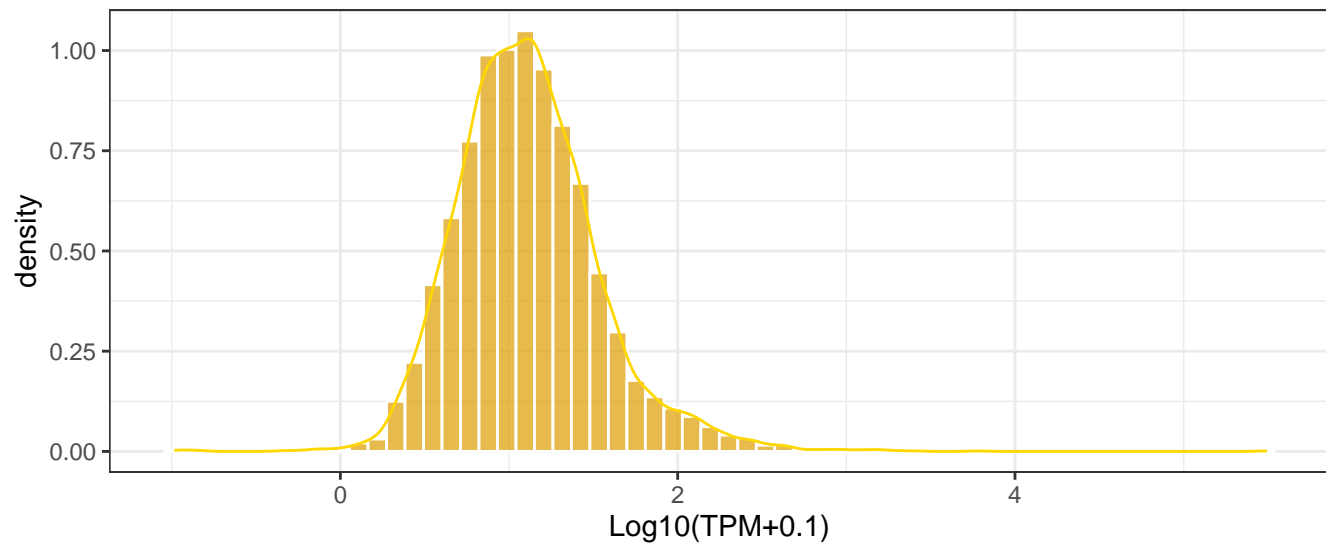
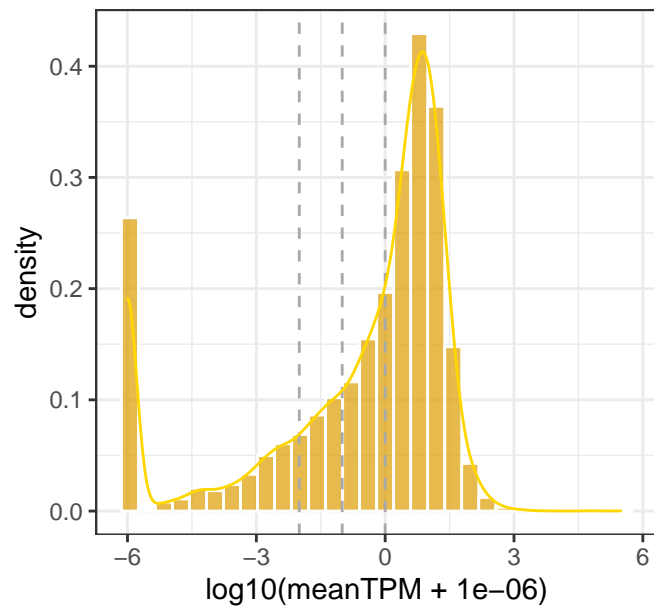


**A** After Filter: mean TPM distribution across genes



Retaining only  $\text{log}_{10}(\text{values})$  superior to min cutoff:  
`keep <- apply(LogTPM,1, function(x) sum(x > -1) == length(x))`

**B** mean TPM distribution across genes



**C**  $\text{log}_{10}\text{TPM}$  threshold vs genes preserved

