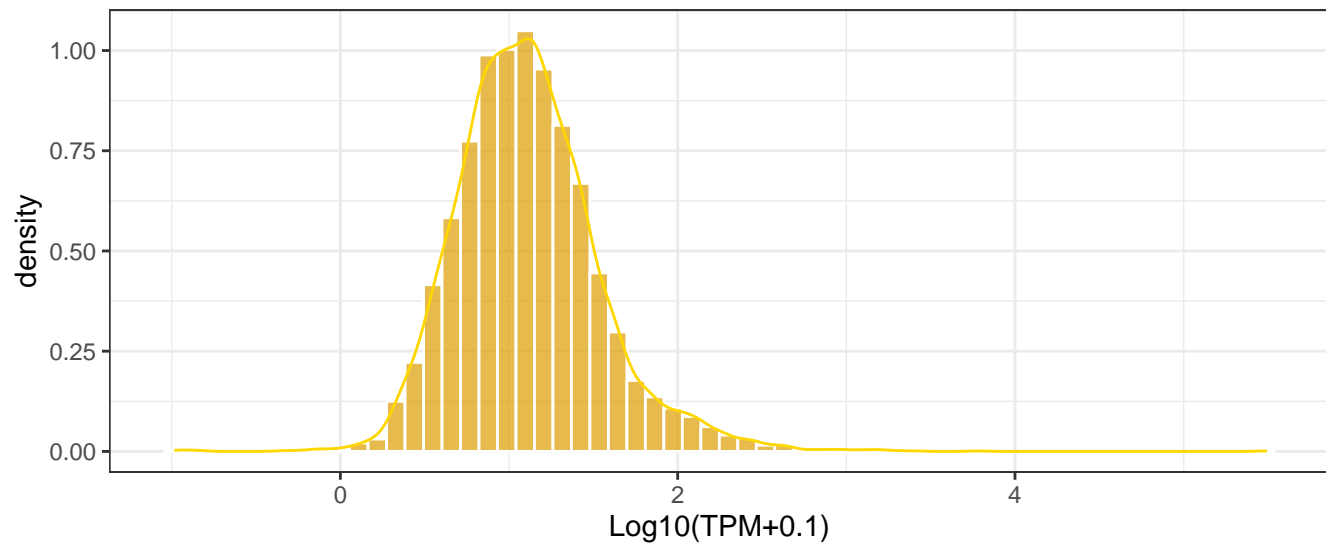
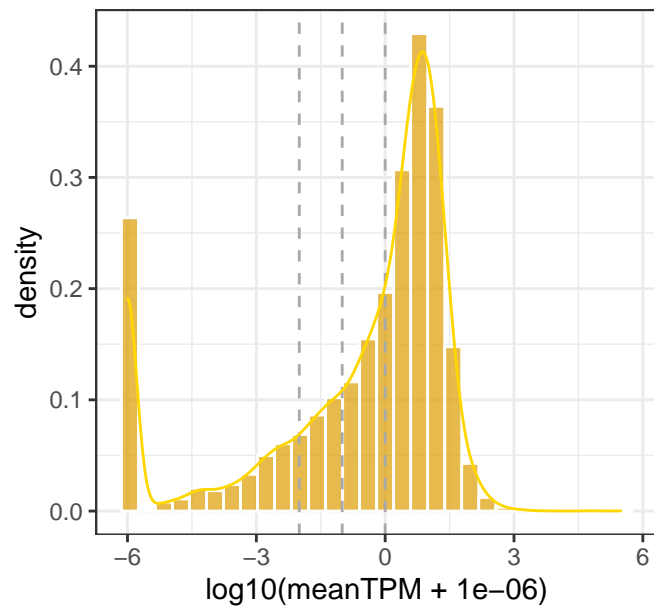


A Filtered mean TPM distribution across genes



Retaining only $\log_{10}(\text{values})$ superior to min cutoff:
`keep <- apply(LogTPM,1, function(x) sum(x > 0.1) == length(x))`

B mean TPM distribution across genes



C $\log_{10}\text{TPM}$ threshold vs genes preserved

