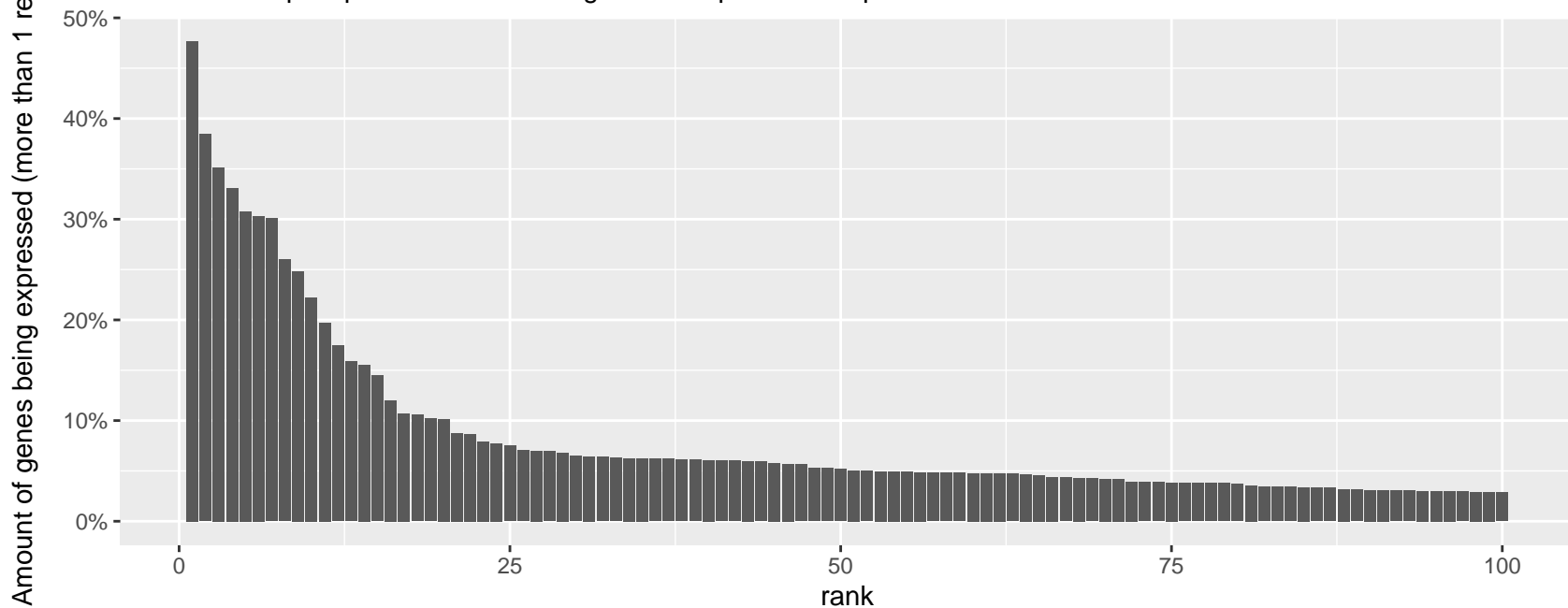


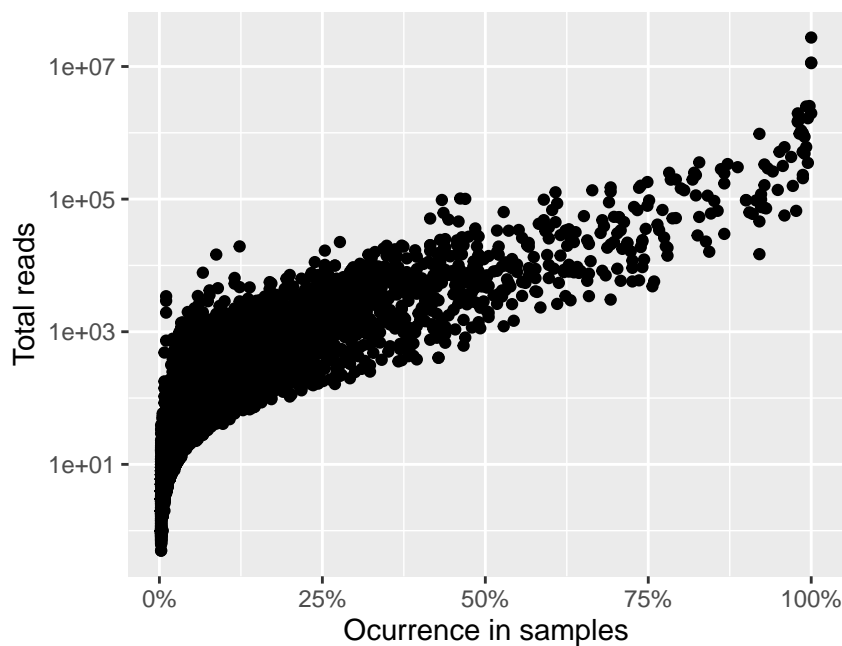
The metaT do not present the whole *Florenciella* genome

51 of the samples present >5% of the genome expressed. Expected?



Some genes are present in all the samples

Around 200 of them present 100 reads in all Tara metaT:



Sourmash vs salmon quantification stats

In all these samples there is 'something'

