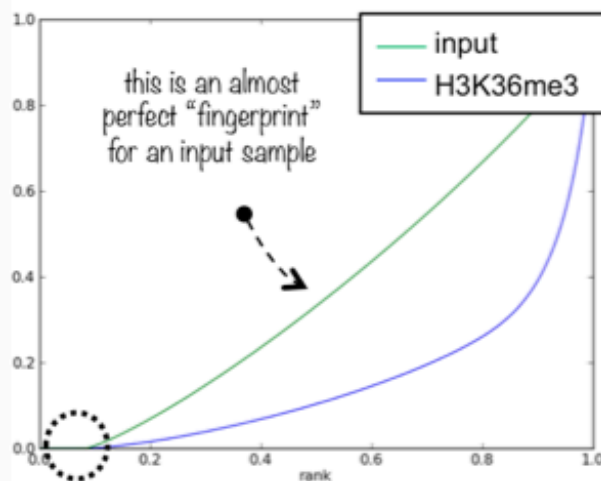
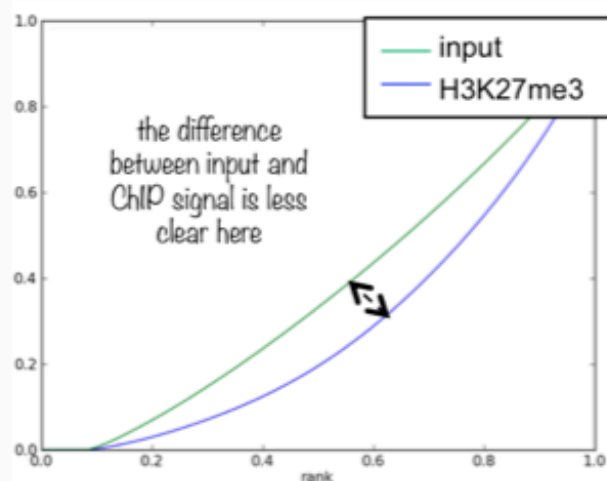


when counting the reads contained in 97% of all genomic bins, only ca. 55% of the maximum number of reads are reached, i.e. 3% of the genome contain a very large fraction of reads!

→ this indicates very localized, very strong enrichments!
(as every biologist hopes for in a ChIP for H3K4me3)



pay attention to where the curves start to rise – this already gives you an assessment of how much of the genome you have not sequenced at all (i.e. bins containing zero reads – for this example, ca. 10% of the entire genome do not have any read)



H3K27me3 is a mark that yields broad domains instead of narrow peaks

→ it is more difficult to distinguish input and ChIP, it does not mean, however, that this particular ChIP experiment failed