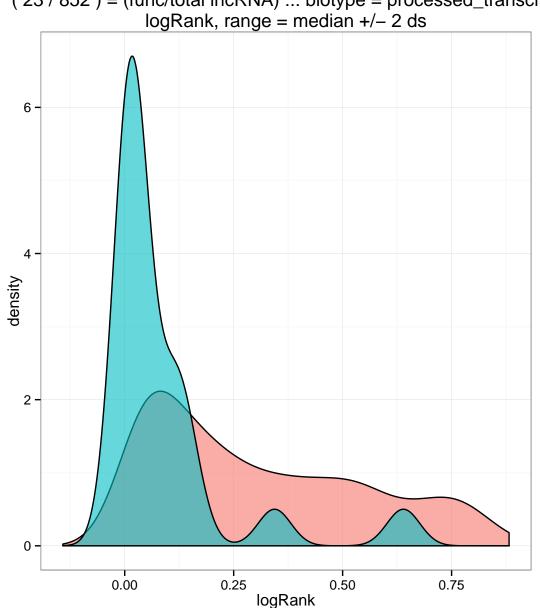
IncRNA group = IDRlessthan0_2 ::: data cols = Inpa (23 / 852) = (func/total IncRNA) ::: biotype = processed_transcript



factor(label)