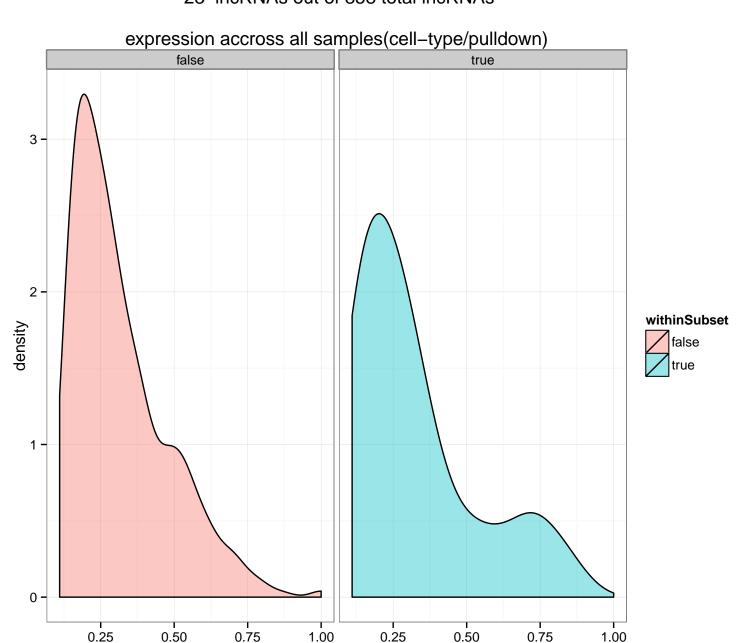
IncRNA group = IDRlessthan0_2 ::: data cols = Ipa (23 / 858) = (func/total IncRNA) ::: biotype = processed_transcript subset = 23 IncRNAs out of 858 total IncRNAs



JSD for each gene