IncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns (28 / 1813) = (func/total IncRNA) ::: biotype = lincRNA subset = 28 IncRNAs out of 1813 total IncRNAs

average features from Derrien 2012 datasheet LncRNA_tx_sizephastcons_primate_introdrastcons_primate_transcript_score No_Exons 15 -600 10000 -400 10 400 5000 200 200 -5 0 false false true false true false true true phastcons primate promoderastcones mammal transplinations mammal inploastscons mammal promoder score 800 800 600 600 600 600 withinSubset 400 value value 400 false 400 true 200 200 200 200 0 0 true false true false false true false true phastcons_vertebrate_transcriptastcons_vertebrate_iphastcons_vertebrate_promoter_score 800 600 -600 600 400 -400 400 200 -200 200 0 0 false false false true true true

value of facet label