IncRNA group = allLncRNA ::: data cols = bothPullDowns (28 / 2998) = (func/total IncRNA) ::: biotype = lincRNA subset = 28 IncRNAs out of 2998 total IncRNAs

average features from Derrien 2012 datasheet LncRNA_tx_size phastcons_primate_introlegations_primate_transcript_score No_Exons 9 5.0 5.0 -2 8 2.5 2.5 7 · 1 0.0 6 0.0 -5 0 -2.5 true false false true false true false true phastcons_primate_promphastscons_mammal_transcriptiastcons_mammal_inprhastscons_mammal_promoter_score 6 6 -5.0 5.0 log(value) withinSubset 4 -2.5 2.5 false 2 true 0.0 0.0 0 -0 --2.5-2.5 false true false true false true false true phastcons_vertebrate_transphattsons_vertebrate_introductstsoors_vertebrate_promoter_score 5.0 5.0 5.0 2.5 2.5 2.5 0.0 -0.0 0.0 -2.5false false true true false true

value of facet label