IncRNA group = IDRlessthan0_1 ::: data cols = bothPullDowns (46 / 1955) = (func/total IncRNA) ::: biotype = remove_antisense subset = 46 IncRNAs out of 1955 total IncRNAs

average features from Derrien 2012 datasheet LncRNA_tx_size phastcons_primate_intrphastcores_primate_transcript_score No Exons 3 · 9 . 5.0 5.0 -8 . 2.5 2 · 2.5 -7 0.0 -1 · 0.0 6 -2.5 0 --2.5false false true true true false false true phastcons primate promotestscons mammal transcolipassicons mammal interpressicons mammal promoter score 5.0 5.0 5.0 -5.0 log(value) withinSubset 2.5 2.5 2.5 -2.5 false true 0.0 -0.0 0.0 -0.0 -2.5 -2.5 -2.5 false true false true false true false true phastcons_vertebrate_transpriattcons_vertebrate_ipthastcons_vertebrate_promoter_score 5.0 -5.0 5.0 2.5 2.5 2.5 0.0 -0.0 0.0 -2.5

false

true

false

true

value of facet label

false

true