IncRNA group = IDRlessthan0_2 ::: data cols = Inpa (82 / 5010) = (func/total IncRNA) ::: biotype = all_biotypes subset = 82 IncRNAs out of 5010 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 -6 -0.0 -2.55 · 0 · -2.5 false false true false true true 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 -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 false true true false true

value of facet label