IncRNA group = IDRIessthan0_2 ::: data cols = bothPullDowns (23 / 866) = (func/total IncRNA) ::: biotype = processed_transcript subset = 23 IncRNAs out of 866 total IncRNAs

average features from Derrien 2012 datasheet No Exons LncRNA_tx_size phastcons_primate_intrphastcores_primate_transcript_score 0.06 0.04 -6e - 040.3 0.03 0.04 4e-04 0.2 0.02 0.02 -2e-04 0.1 $0.01 \cdot$ 0.00 0.0 0e+00 0.00 10 20 2000 4000 6000 0 100200300400 100200300400 phastcons primate promphastscons mammal transcriptisticons mammal introduces come mammal promoter score 0.025 0.0250.015 0.04 0.020 0.020 withinSubset density 0.015 0.03 0.010 0.015 false 0.02 0.010 true 0.005 0.01 0.005 -0.005 0.000 0.000 0.00 0.000 0 100200300400 0 200400600800 0 100200300400 250 500 750 phastcons_vertebrate_transphiattoons_vertebrate_iptrantcorror vertebrate_promoter_score 0.012 0.015 -0.009 0.02 0.010 0.006 -0.01 0.005 0.003 0.000 0.00 0.000

0 200400600800

value of facet label

0 200 400 600

200 400 600