## IncRNA group = IDRlessthan0\_2 ::: data cols = Ipa ( 83 / 5087 ) = (func/total IncRNA) ::: biotype = all\_biotypes subset = 83 IncRNAs out of 5087 total IncRNAs

average features from Derrien 2012 datasheet No Exons LncRNA\_tx\_sizephastcons\_primate\_introph\_asstocens\_primate\_transcript\_score 0.3 0.3 -0.8 -0.6 2 0.2 -0.2 0.4 -1 · 0.1 0.1 -0.2 -0.0 0 2 6 7 8 9 -2.50.0 2.5 5.0 -2.5 0.0 2.5 5.0 phastcons primate prompters to mammal transcultations mammal introductions mammal promoter score 0.3 -0.25 -0.20 0.20 -0.2 withinSubset density 0.2 0.15 -0.15 false 0.10 0.10 -0.1 true 0.05 -0.05 -0.0 0.00 0.00 0.0 -2.5 0.0 2.5 5.0 -2.5 0.0 2.5 5.0 -2.5 0.0 2.5 5.0 -2.5 0.0 2.5 5.0 phastcons\_vertebrate\_transpliateons\_vertebrate\_iphastcons\_vertebrate\_promoter\_score 0.3 0.3 0.2 0.2 0.2 -0.1 -0.1 0.1 -0.0 0.0 0.0

0.0 2.5

value of facet label

5.0

0.0 2.5 5.0

-2.5 0.0 2.5 5.0