lncRNA group = IDRlessthan0_1 ::: data cols = lnpa
(22 / 585) = (func/total lncRNA) ::: biotype = processed_transcript
subset =
22 lncRNAs out of 585 total lncRNAs

average features from Derrien 2012 datasheet

Facet columns: No_Exons, LncRNA_tx_size, cons_primate_intron_, ns_primate_transcrip, ns_primate_promote, ns_mammal_transcrip, cons_mammal_intron_, ns_mammal_promote, s_vertebrate_transcrip, ns_vertebrate_intron, ns_vertebrate_promot

Facet rows: false, true

y-axis: count

x-axis: value of facet label