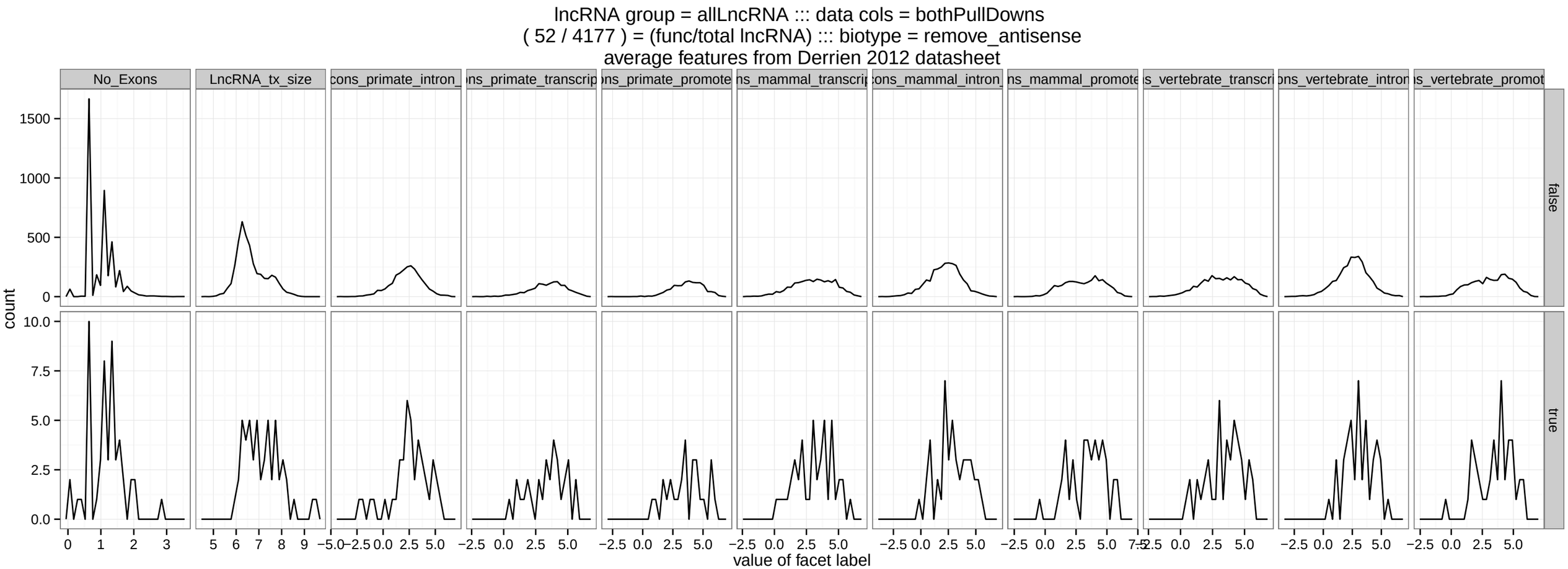
lncRNA group = allLncRNA ::: data cols = bothPullDowns
(52 / 4177) = (func/total lncRNA) ::: biotype = remove_antisense
average features from Derrien 2012 datasheet
No_Exons
LncRNA_tx_size
cons_primate_intron_
ns_primate_transcrip
ns_primate_promote
ns_mammal_transcrip
cons_mammal_intron_
ns_mammal_promote
s_vertebrate_transcri
ons_vertebrate_intron
s_vertebrate_promot
false
true
count
value of facet label