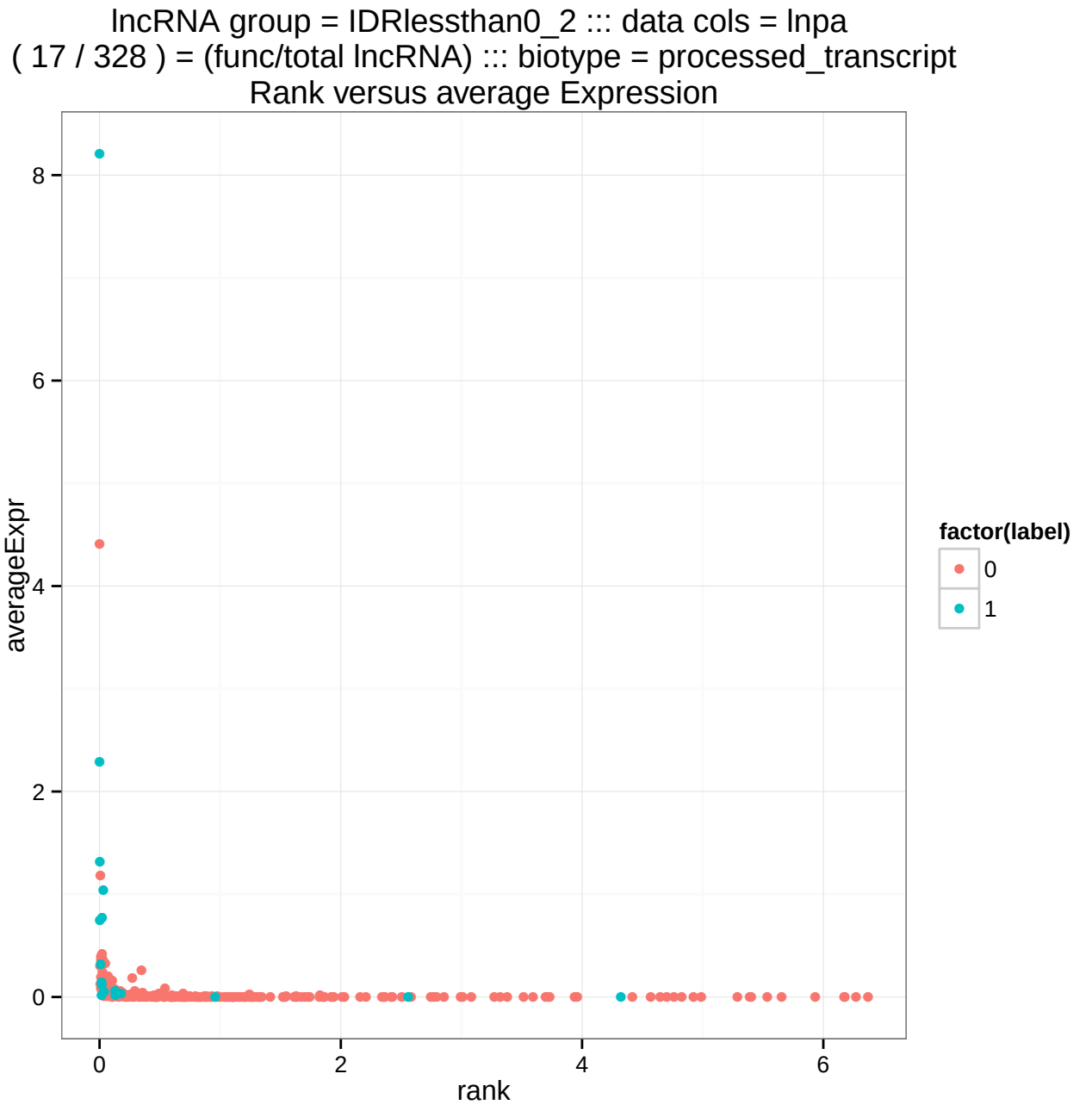
lncRNA group = IDRlessthan0_2 ::: data cols = lnpa
(17 / 328) = (func/total lncRNA) ::: biotype = processed_transcript
Rank versus average Expression
averageExpr
rank
0
2
4
6
8
factor(label)
0
1