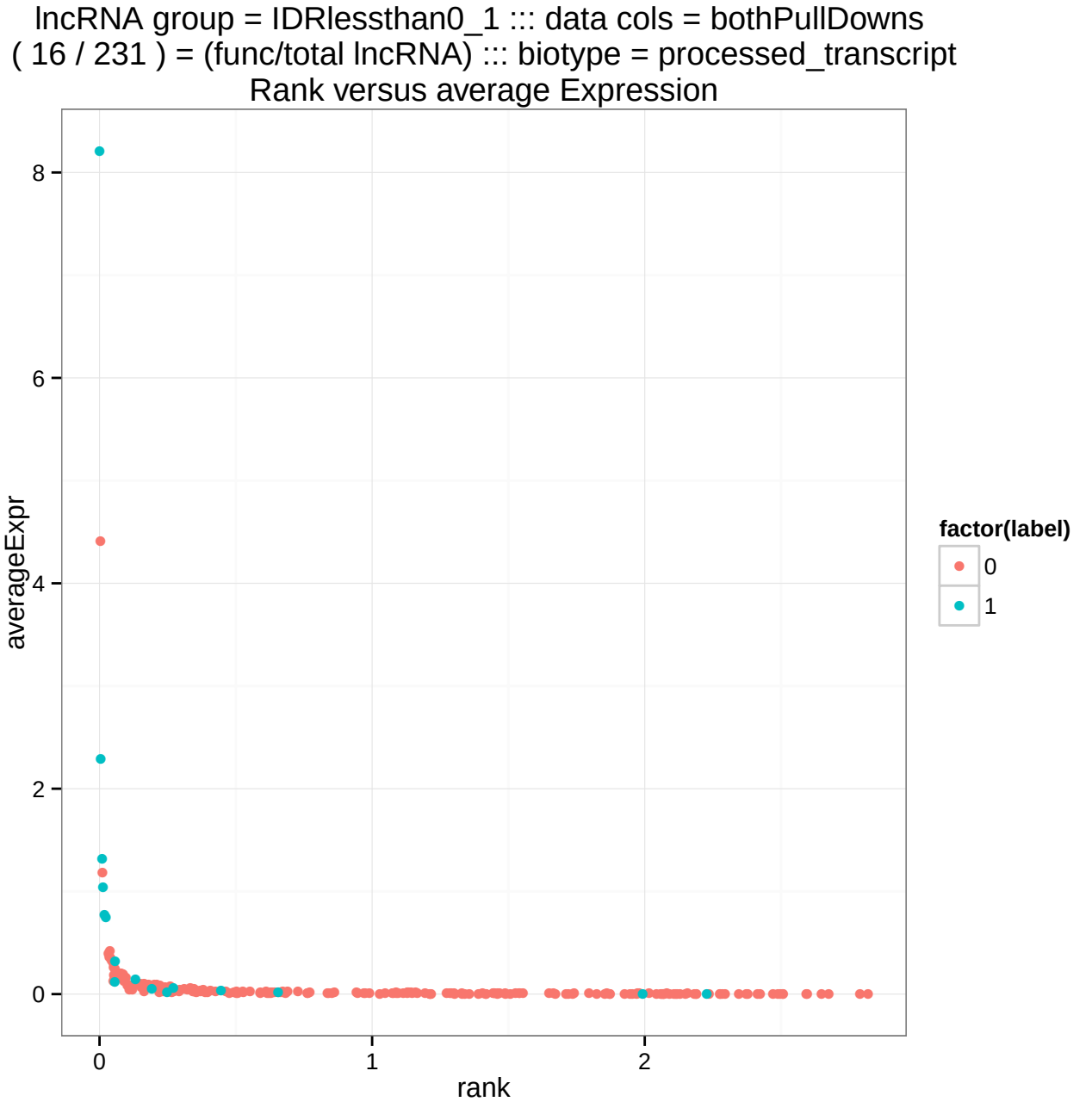
lncRNA group = IDRlessthan0_1 ::: data cols = bothPullDowns
( 16 / 231 ) = (func/total lncRNA) ::: biotype = processed_transcript
Rank versus average Expression
averageExpr
rank
0
2
4
6
8
0
1
2
factor(label)
0
1