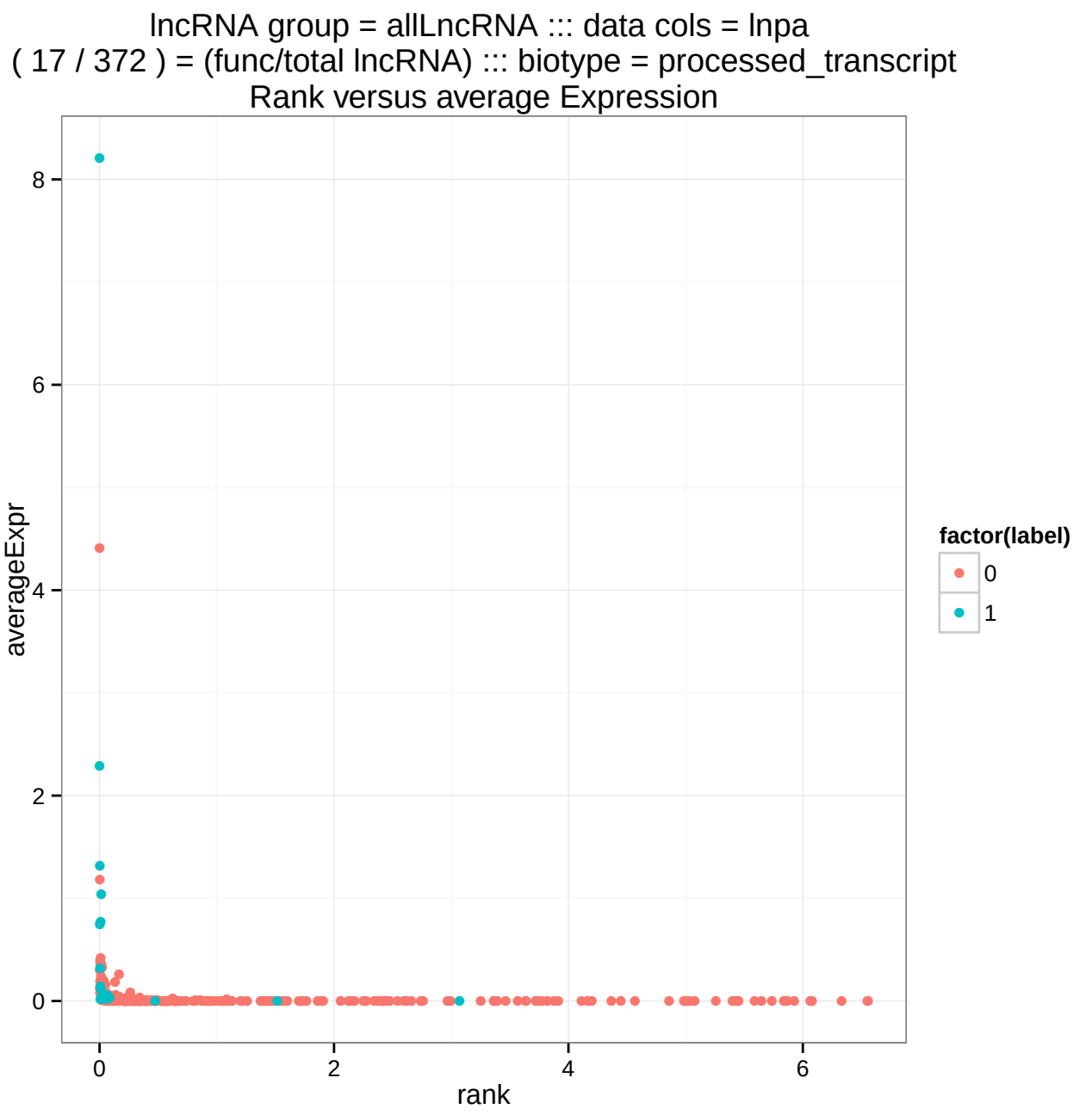
lncRNA group = allLncRNA ::: data cols = lnpa
( 17 / 372 ) = (func/total lncRNA) ::: biotype = processed_transcript
Rank versus average Expression
averageExpr
rank
0
2
4
6
8
factor(label)
0
1