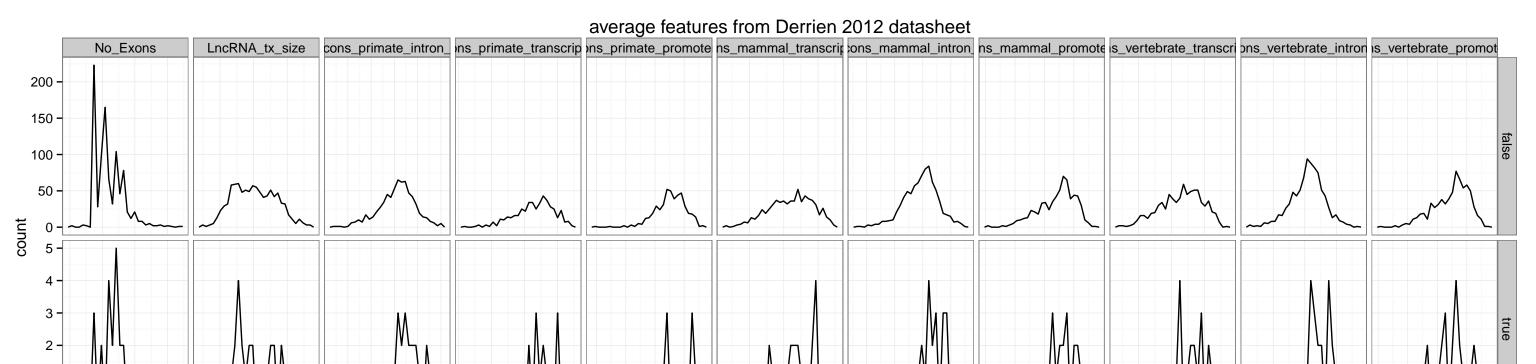
IncRNA group = allLncRNA ::: data cols = Inpa ( 23 / 962 ) = (func/total IncRNA) ::: biotype = processed\_transcript subset = 23 IncRNAs out of 962 total IncRNAs



0.0 2.5

value of facet label

5.0

-2.5 0.0 2.5 5.0 -2.5 0.0 2.5 5.0

7.5

0.0 2.5

5.0

-2.5 0.0 2.5

5.0

6-2.5 0.0

2.5

5.0

-2.5 0.0 2.5 5.0