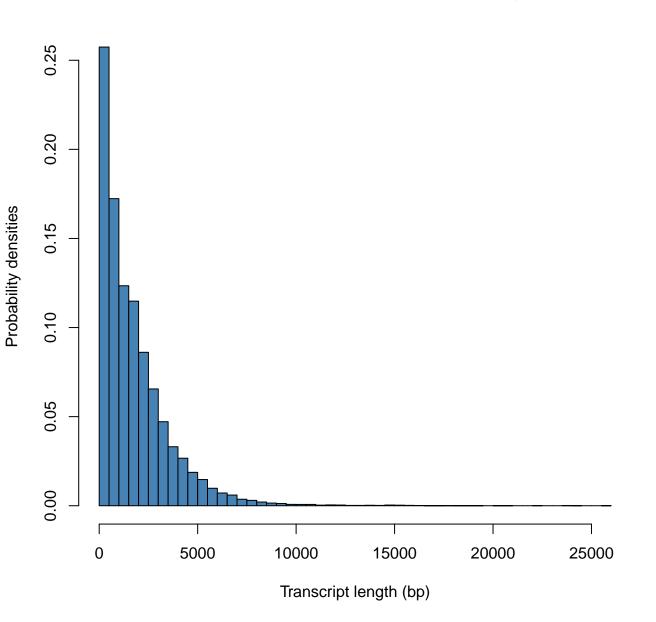
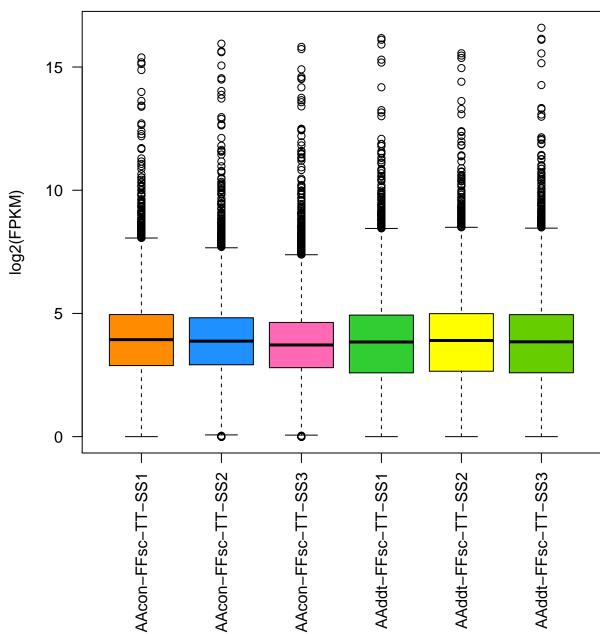
con vs ddt Distribution of transcript lengths



Distribution of FPKMs for all 6 libraries

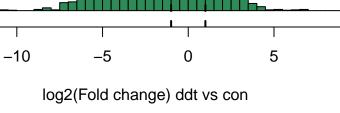


Distribution of differential expression values Fold-change = 2 0.20 0.15 0.10 0.05

Probability densities

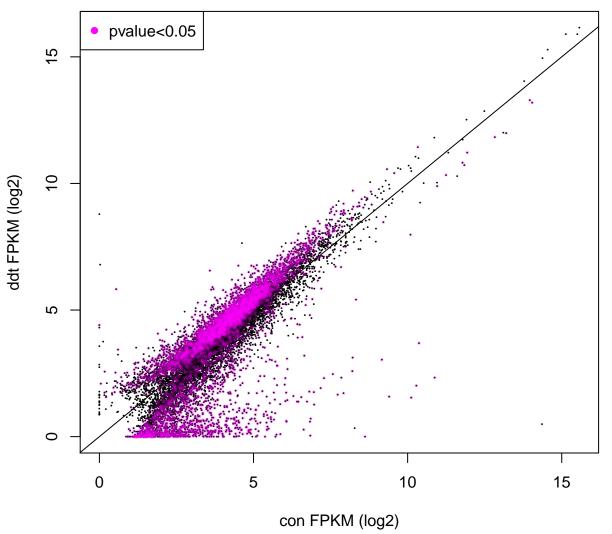
0.00

-15



10

con vs ddt FPKMs



con vs ddt Transcript P values P_value = 0.05 0.10 0.08 Probability densities 90.0 0.04 0.02 0.00

0.4

0.6

P value

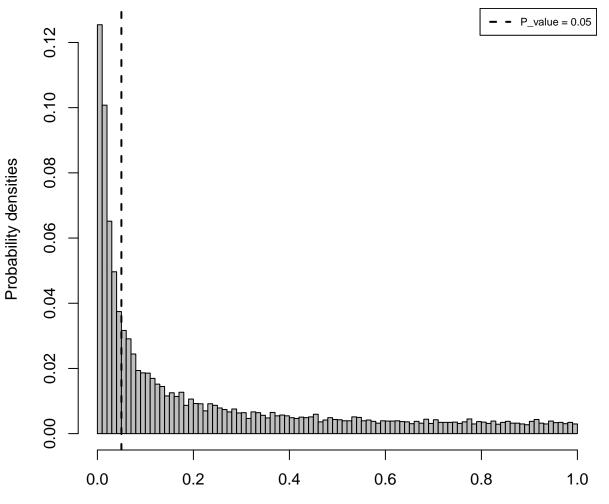
8.0

1.0

0.0

0.2

con vs ddt Gene P values



P value