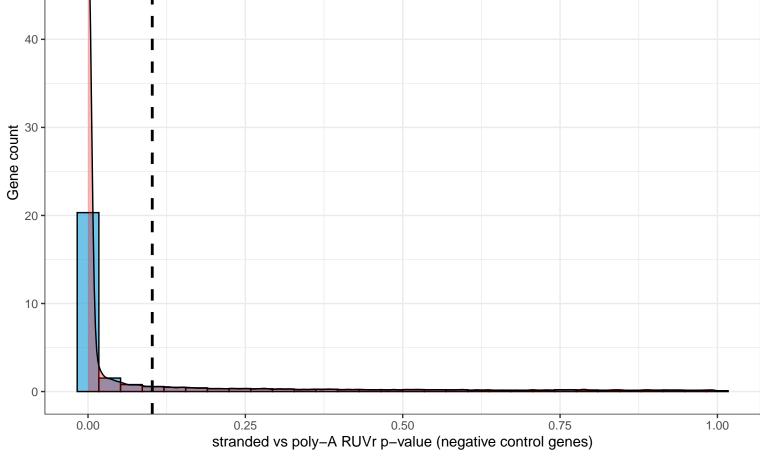
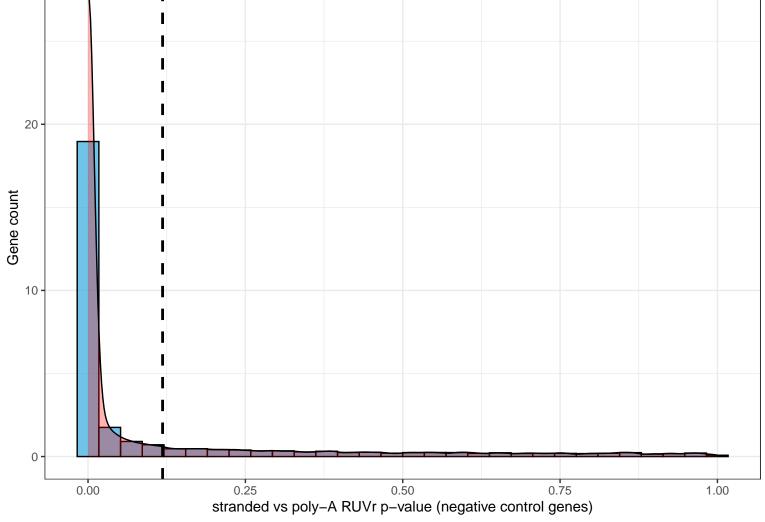
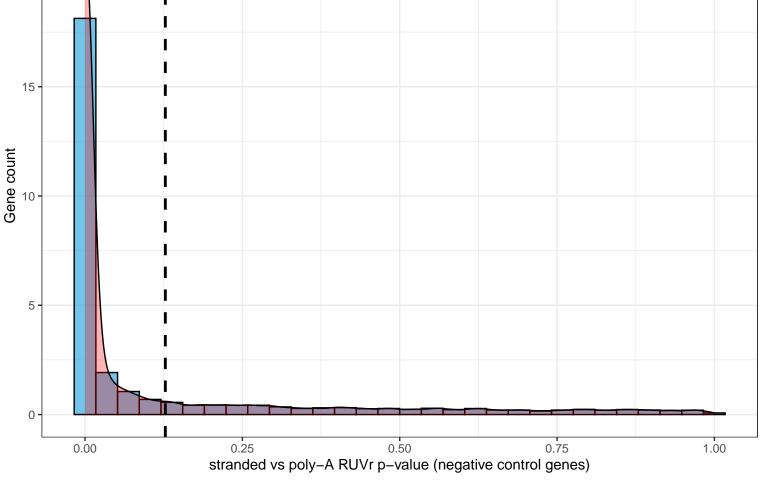
Histogram of stranded vs poly–A paired analysis (k = 1)Total number of genes: 15104 11344 genes have p-value < 0.05 3760 genes have p-value >= 0.05 11097 genes have BH FDR < 0.05 4007 genes have BH FDR >= 0.05 50 40 30 20



Histogram of stranded vs poly–A paired analysis (k = 2)Total number of genes: 15104 10753 genes have p-value < 0.05 4351 genes have p-value \geq 0.05 10438 genes have BH FDR < 0.05 4666 genes have BH FDR >= 0.05 20



Histogram of stranded vs poly–A paired analysis (k = 3)Total number of genes: 15104 10408 genes have p-value < 0.05 4696 genes have p-value >= 0.05 10026 genes have BH FDR < 0.05 5078 genes have BH FDR >= 0.05 20 15 10



Histogram of stranded vs poly–A paired analysis (k = 4)Total number of genes: 15104 10370 genes have p-value < 0.05 4734 genes have p-value >= 0.05 9945 genes have BH FDR < 0.05 5159 genes have BH FDR >= 0.05 20 15 -Gene count 5 ·

0.50

stranded vs poly-A RUVr p-value (negative control genes)

0.75

1.00

0

0.00

0.25

Histogram of stranded vs poly–A paired analysis (k = 5)Total number of genes: 15104 10301 genes have p-value < 0.05 4803 genes have p-value >= 0.05 9910 genes have BH FDR < 0.05 5194 genes have BH FDR >= 0.05 20 15 -Gene count 10 -5

