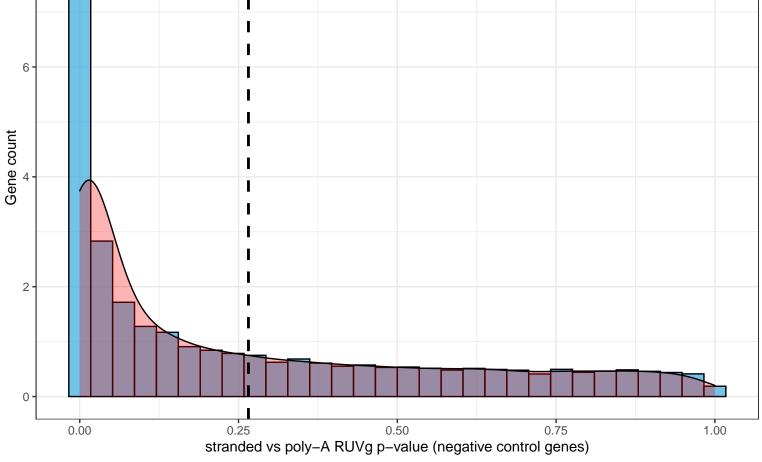
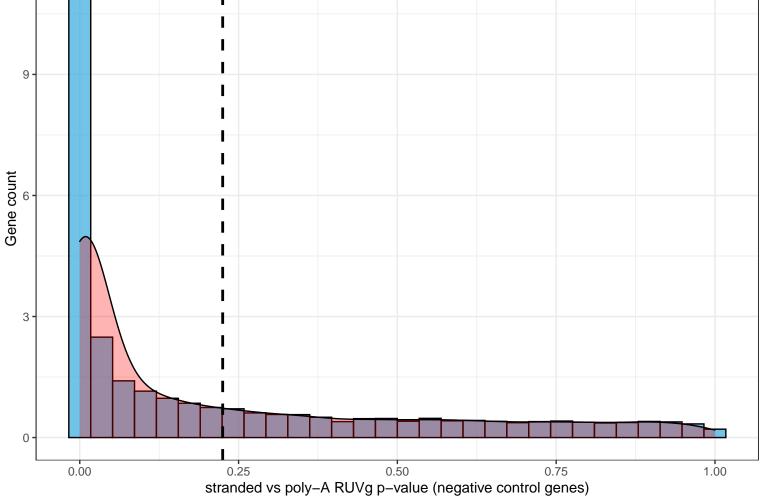
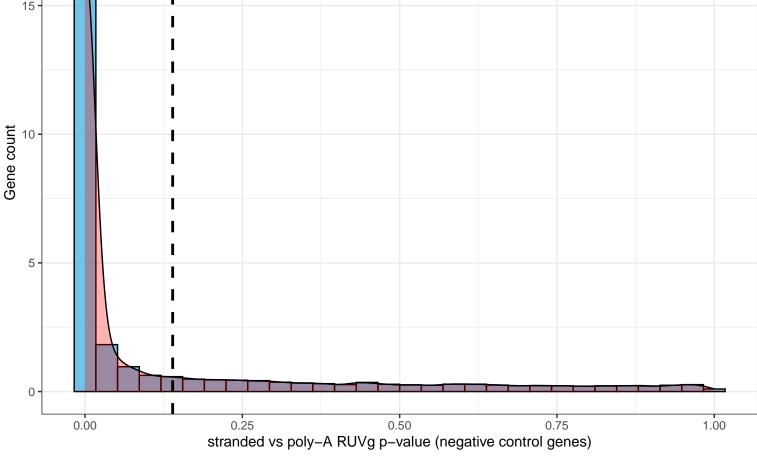
Histogram of stranded vs poly–A paired analysis (k = 1)Total number of genes: 15104 5755 genes have p-value < 0.05 9349 genes have p-value >= 0.05 4124 genes have BH FDR < 0.05 10980 genes have BH FDR >= 0.05 8 6



Histogram of stranded vs poly–A paired analysis (k = 2)Total number of genes: 15104 7158 genes have p-value < 0.05 7946 genes have p-value >= 0.05 6062 genes have BH FDR < 0.05 9042 genes have BH FDR >= 0.05 9



Histogram of stranded vs poly–A paired analysis (k = 3)Total number of genes: 15104 10191 genes have p-value < 0.05 4913 genes have p-value >= 0.05 9774 genes have BH FDR < 0.05 5330 genes have BH FDR >= 0.05 15



Histogram of stranded vs poly–A paired analysis (k = 4)Total number of genes: 15104 9357 genes have p-value < 0.05 5747 genes have p-value \geq 0.05 8765 genes have BH FDR < 0.05 6339 genes have BH FDR >= 0.05 15 -10 -Gene count 5

0.50

0

0.00

0.25

stranded vs poly–A RUVg p–value (negative control genes)

0.75

1.00

Histogram of stranded vs poly–A paired analysis (k = 5)Total number of genes: 15104 10884 genes have p-value < 0.05 4220 genes have p-value >= 0.0510575 genes have BH FDR < 0.05 4529 genes have BH FDR >= 0.05 30 -20 Gene count 10-0

0.50

0.00

0.25

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

0.75

1.00