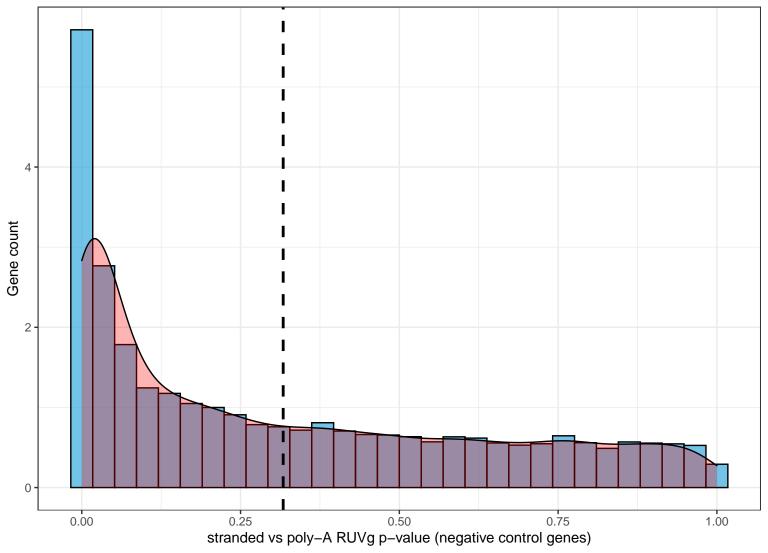
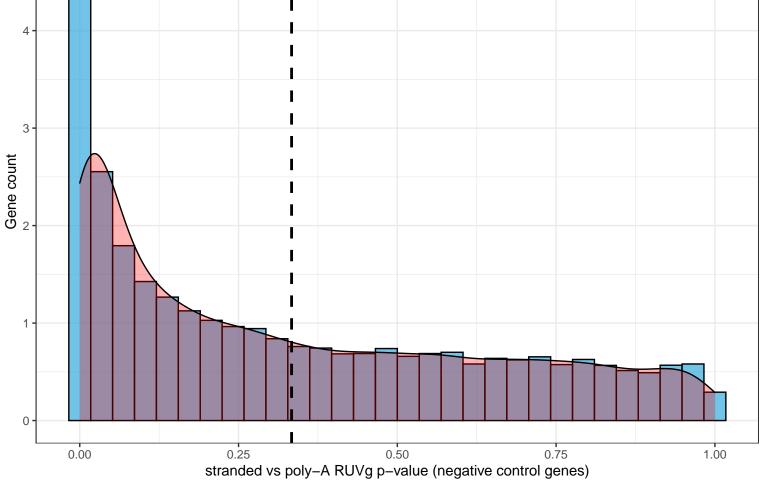
Histogram of stranded vs poly–A paired analysis (k = 1) Total number of genes: 18138 5239 genes have p-value < 0.05 12899 genes have p-value >= 0.05 2591 genes have BH FDR < 0.05 15547 genes have BH FDR >= 0.05

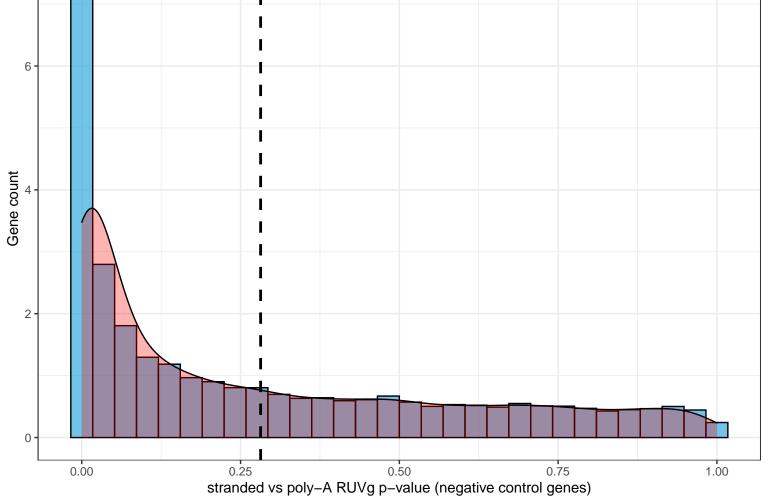


Histogram of stranded vs poly–A paired analysis (k = 2)Total number of genes: 18138 4477 genes have p-value < 0.05 13661 genes have p-value >= 0.05 1782 genes have BH FDR < 0.05 16356 genes have BH FDR >= 0.05 3 -



Histogram of stranded vs poly–A paired analysis (k = 3)

Total number of genes: 18138
6315 genes have p-value < 0.05
11823 genes have p-value >= 0.05
4084 genes have BH FDR < 0.05
14054 genes have BH FDR >= 0.05



Histogram of stranded vs poly–A paired analysis (k = 4)Total number of genes: 18138 6360 genes have p-value < 0.05 11778 genes have p-value >= 0.05 4379 genes have BH FDR < 0.05 13759 genes have BH FDR >= 0.05 8 6 Gene count 2

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: 18138 4702 genes have p-value < 0.05 13436 genes have p-value >= 0.05 2723 genes have BH FDR < 0.05 15415 genes have BH FDR >= 0.05

