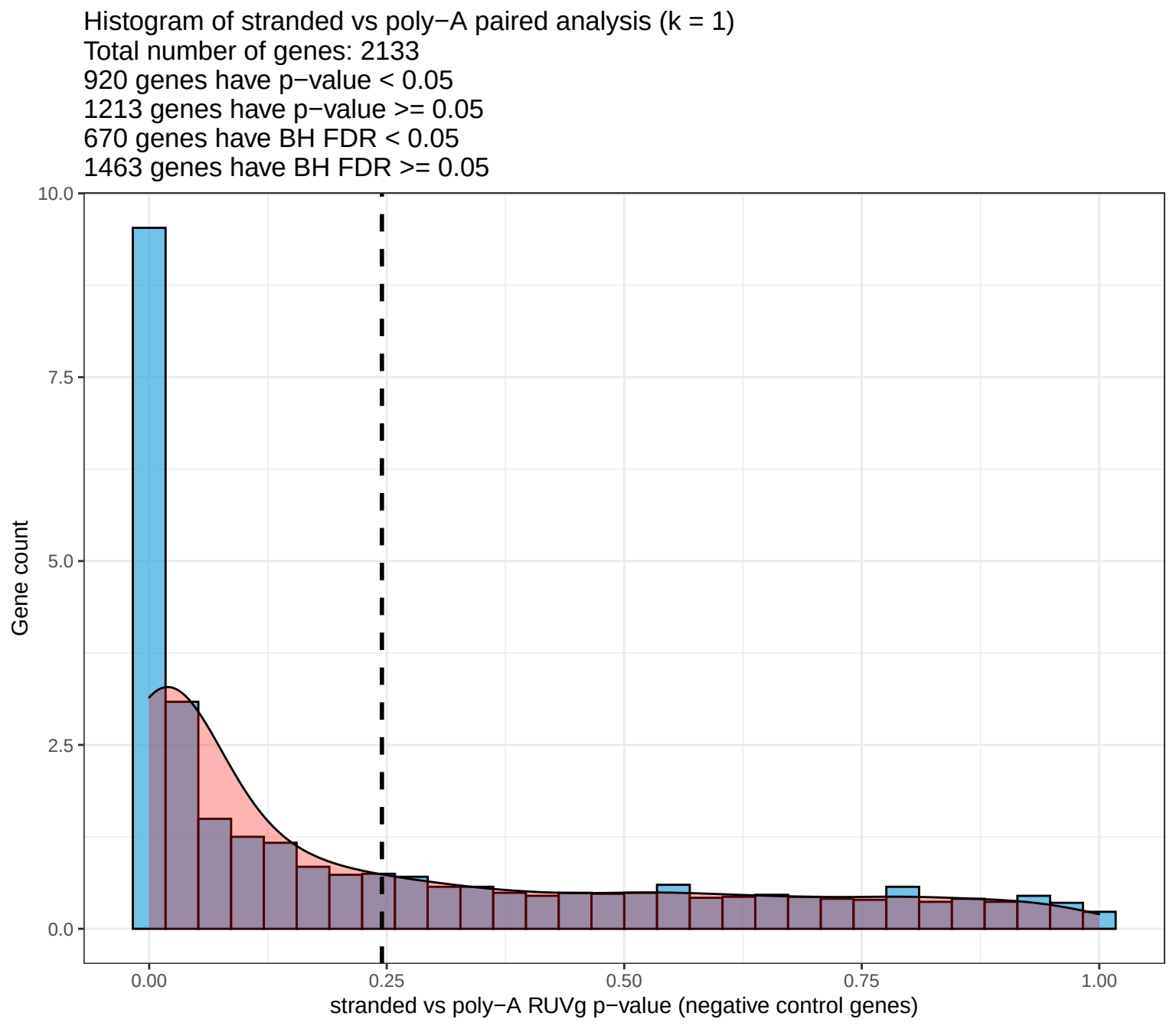
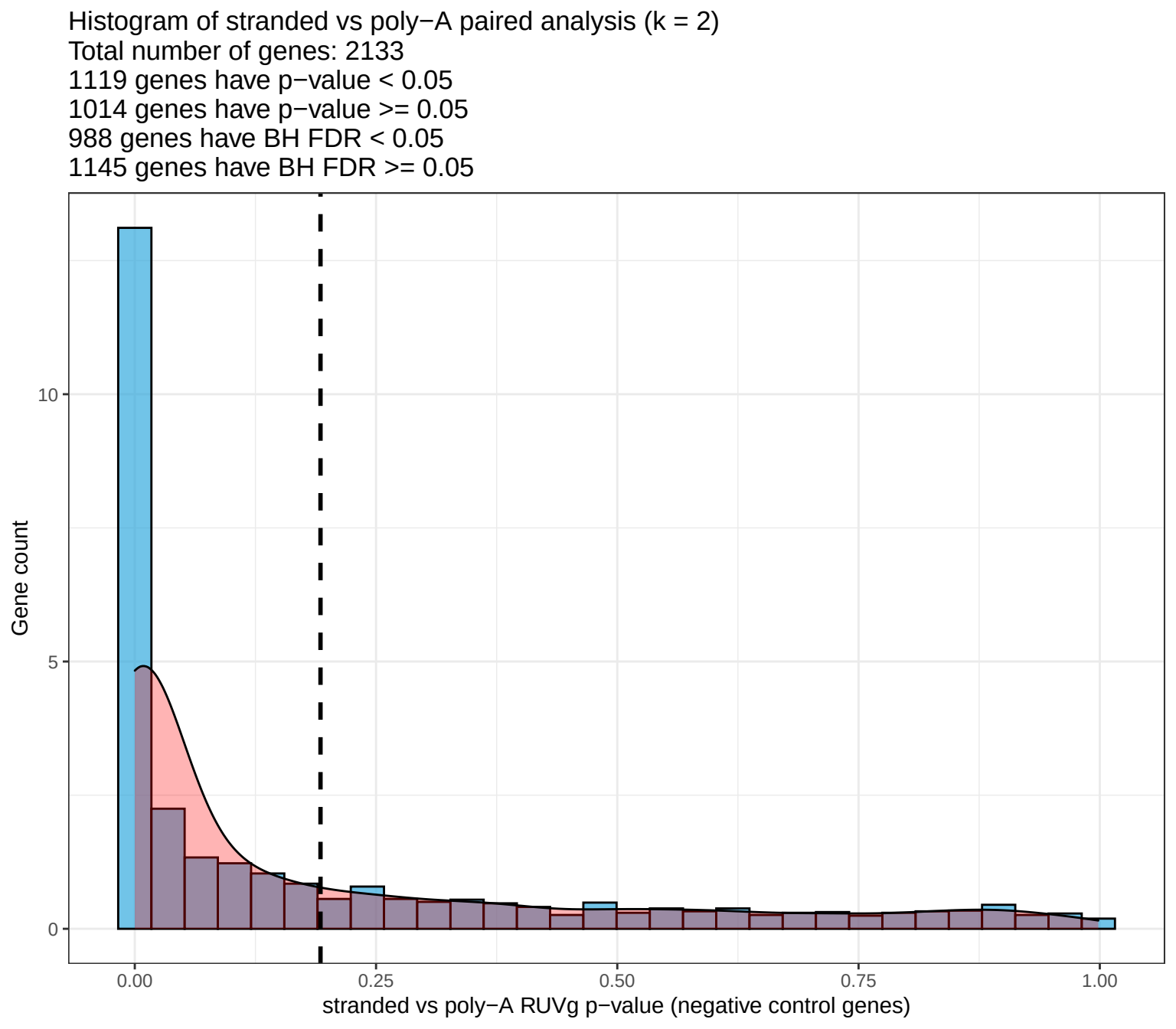
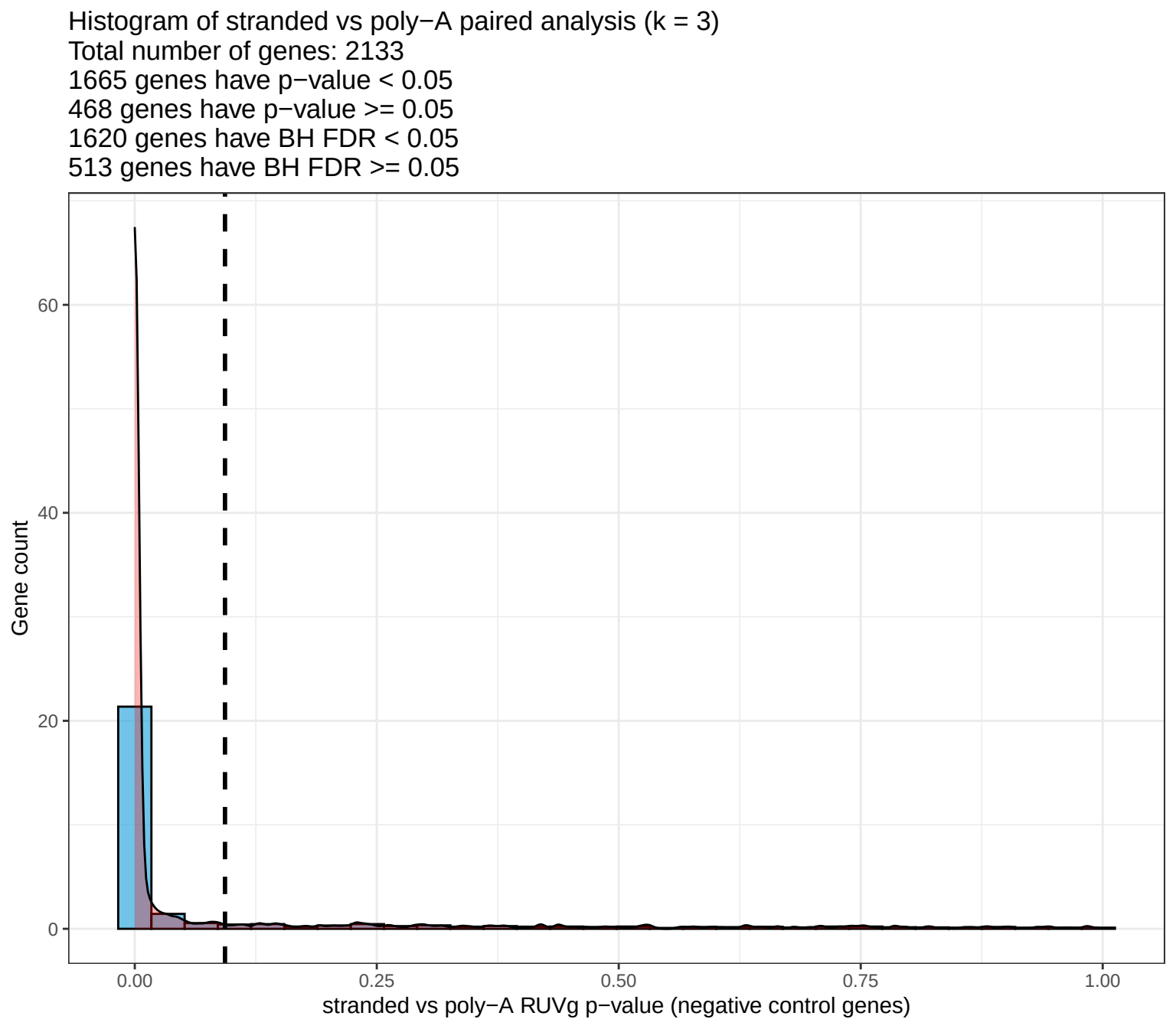
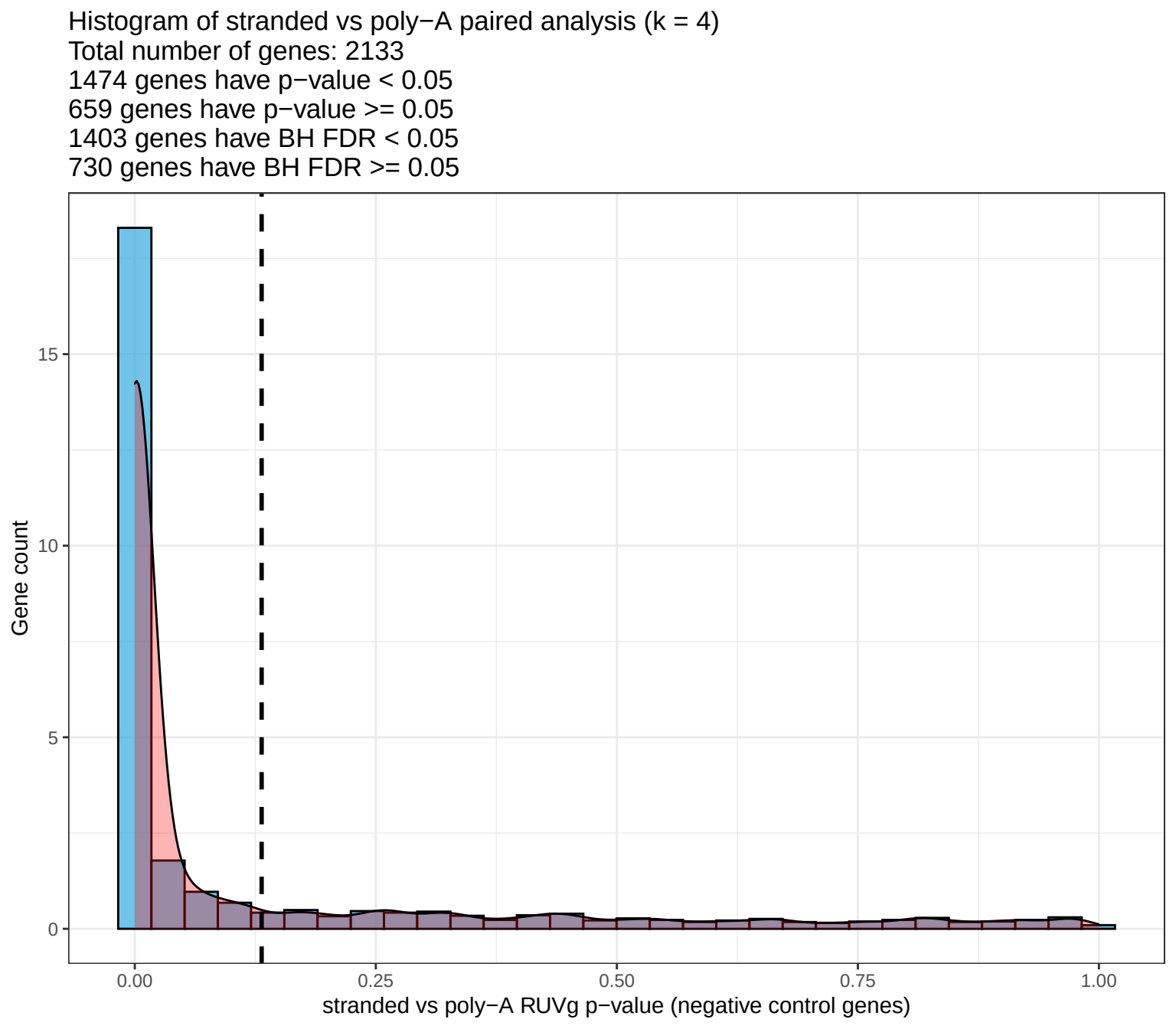
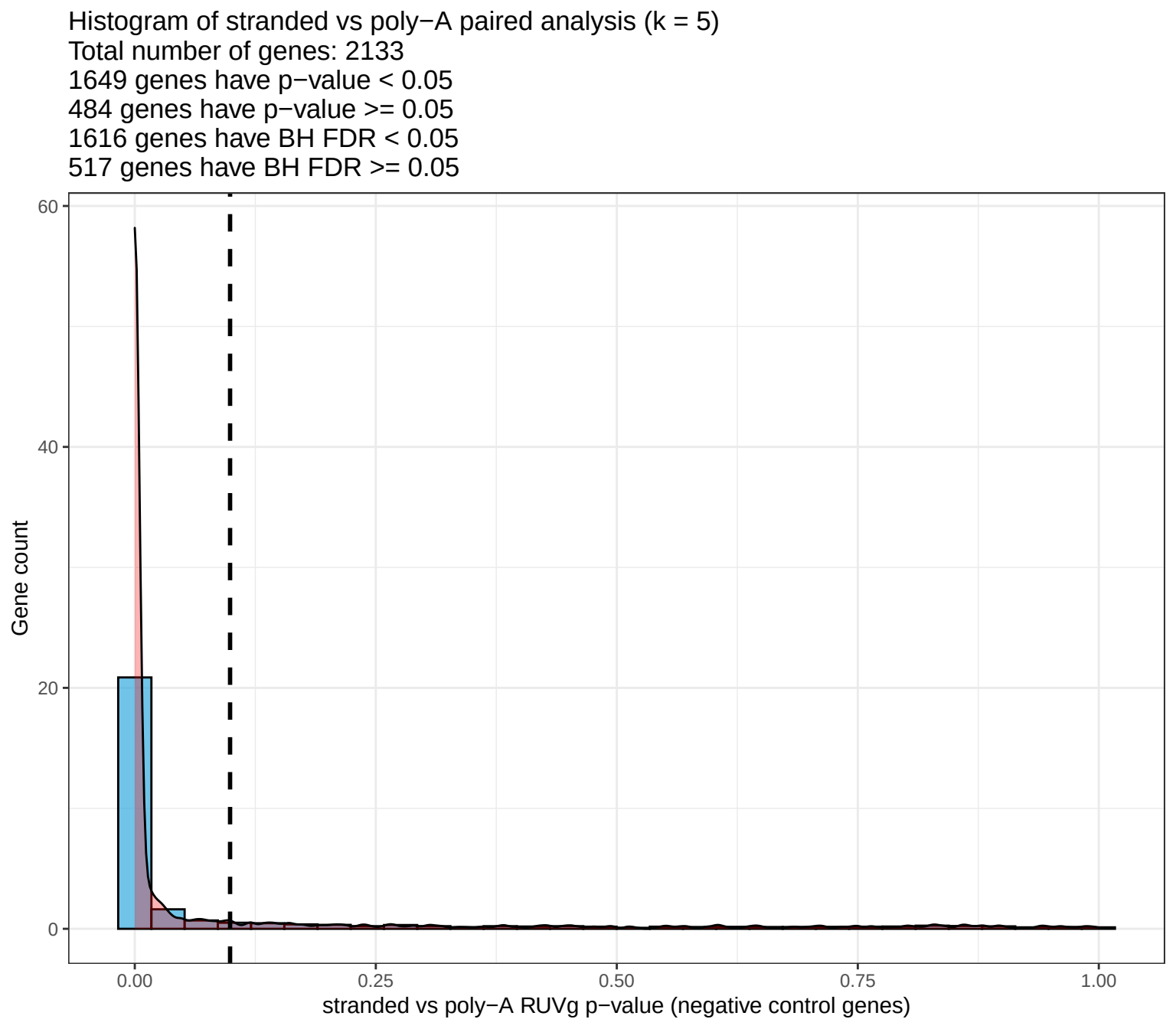

Histogram of stranded vs poly−A paired analysis (k = 1)
Total number of genes: 2133
920 genes have p−value < 0.05
1213 genes have p−value >= 0.05
670 genes have BH FDR < 0.05
1463 genes have BH FDR >= 0.05
10.0
7.5
5.0
2.5
0.0
Gene count
0.00
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 2)
Total number of genes: 2133
1119 genes have p−value < 0.05
1014 genes have p−value >= 0.05
988 genes have BH FDR < 0.05
1145 genes have BH FDR >= 0.05
Gene count
10
5
0
0.00
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 3)
Total number of genes: 2133
1665 genes have p−value < 0.05
468 genes have p−value >= 0.05
1620 genes have BH FDR < 0.05
513 genes have BH FDR >= 0.05
Gene count
60
40
20
0
0.00
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 4)
Total number of genes: 2133
1474 genes have p−value < 0.05
659 genes have p−value >= 0.05
1403 genes have BH FDR < 0.05
730 genes have BH FDR >= 0.05
Gene count
15
10
5
0
0.00
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 5)
Total number of genes: 2133
1649 genes have p−value < 0.05
484 genes have p−value >= 0.05
1616 genes have BH FDR < 0.05
517 genes have BH FDR >= 0.05
60
40
20
0
Gene count
0.00
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)