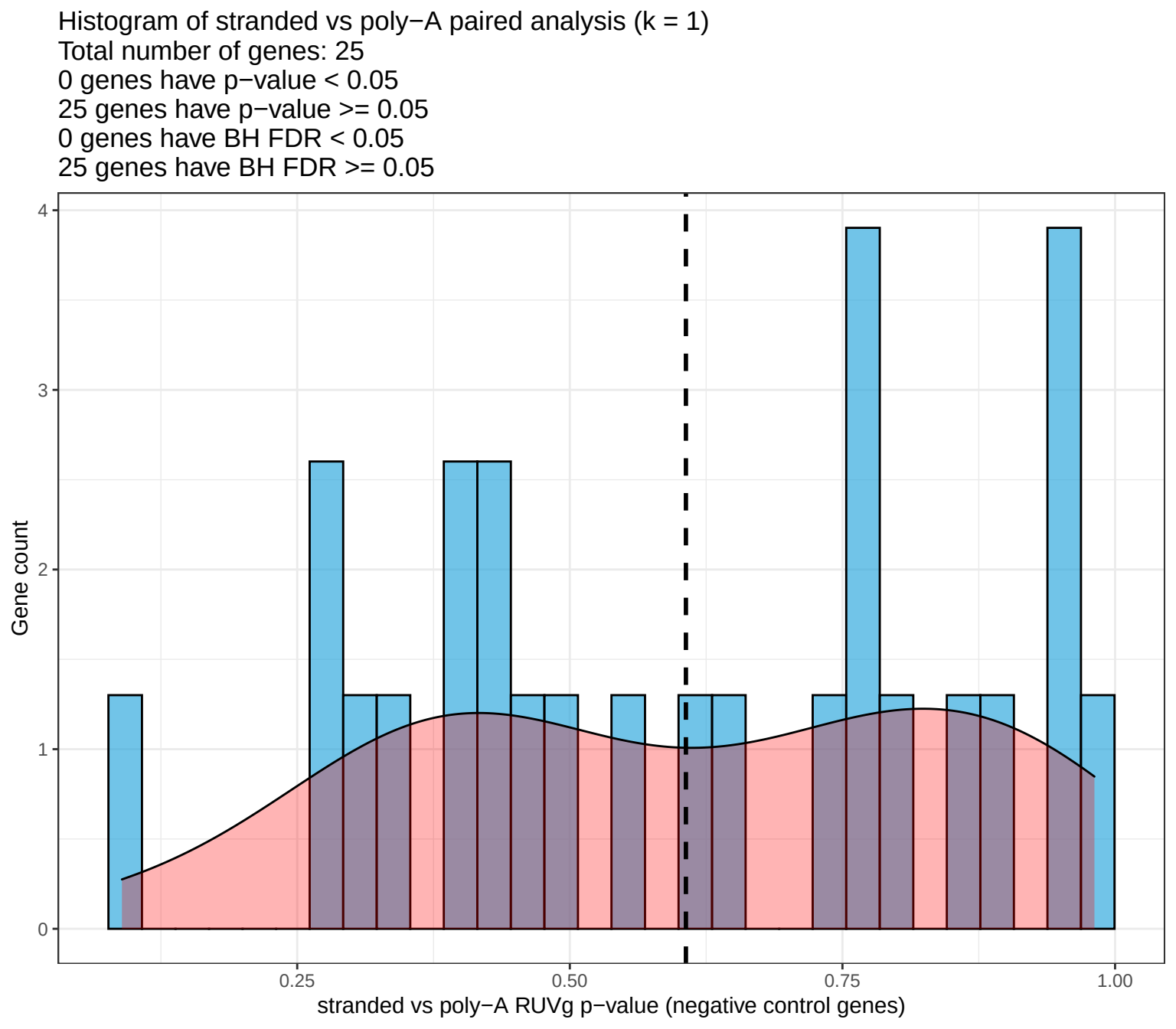
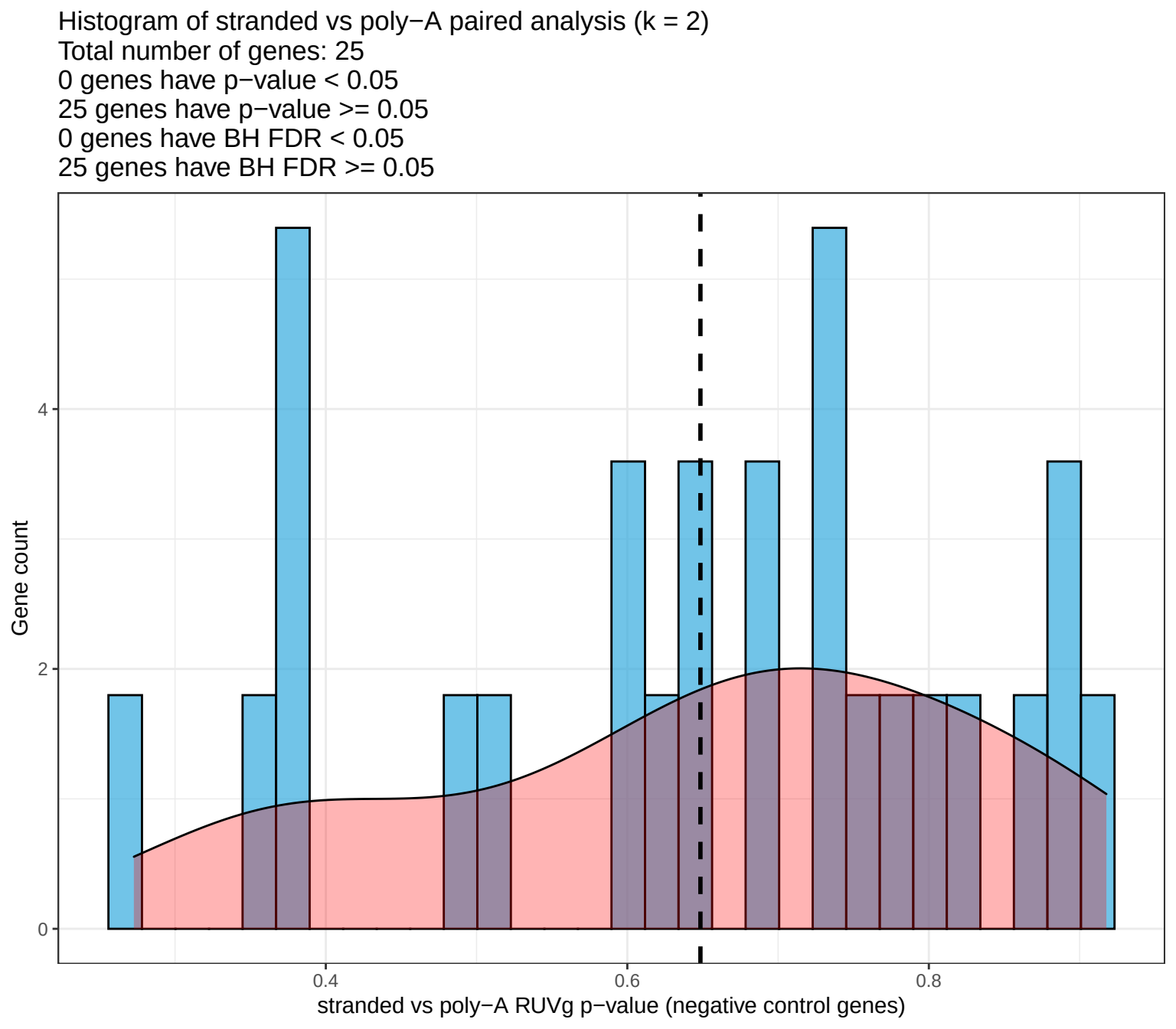
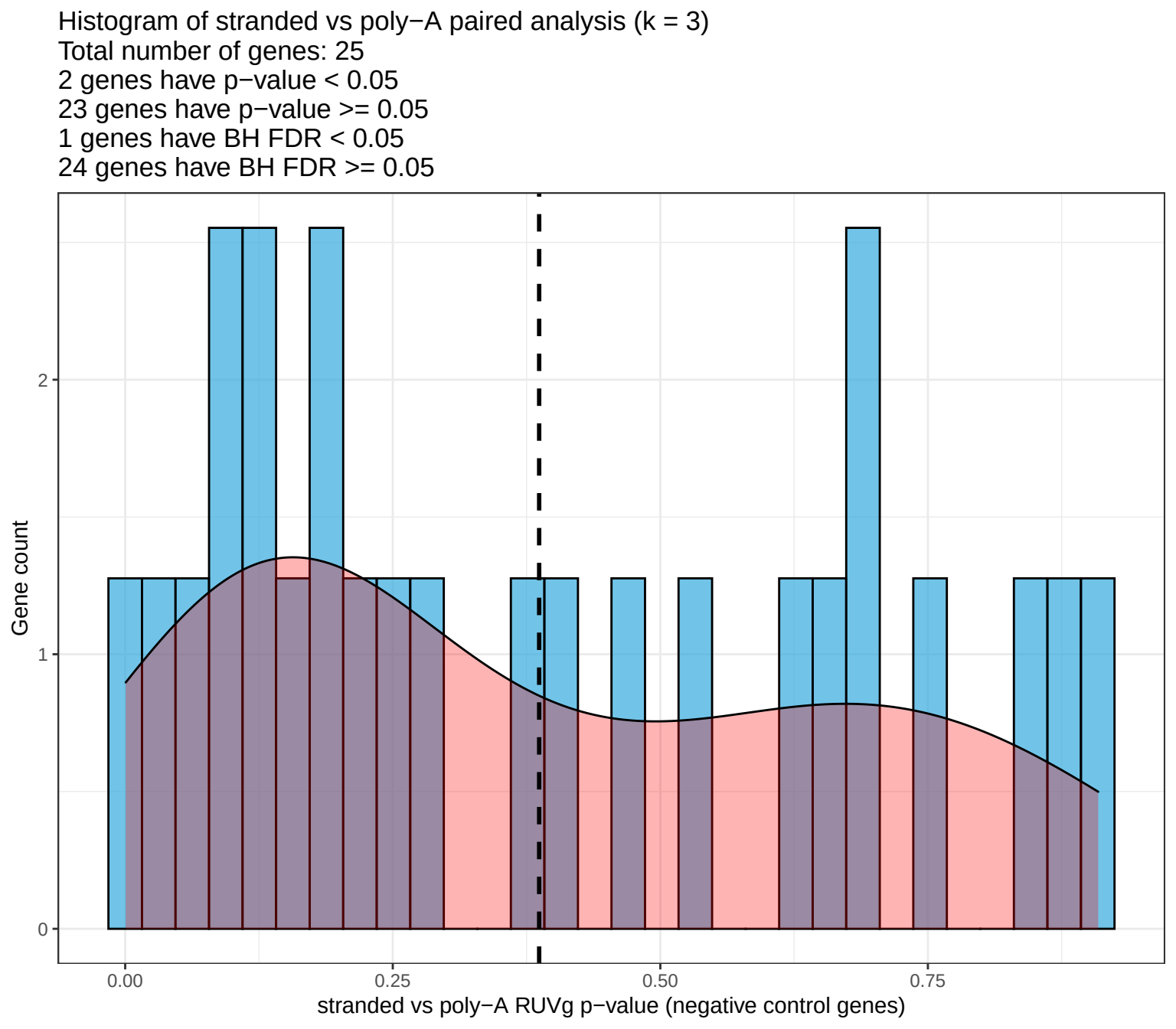
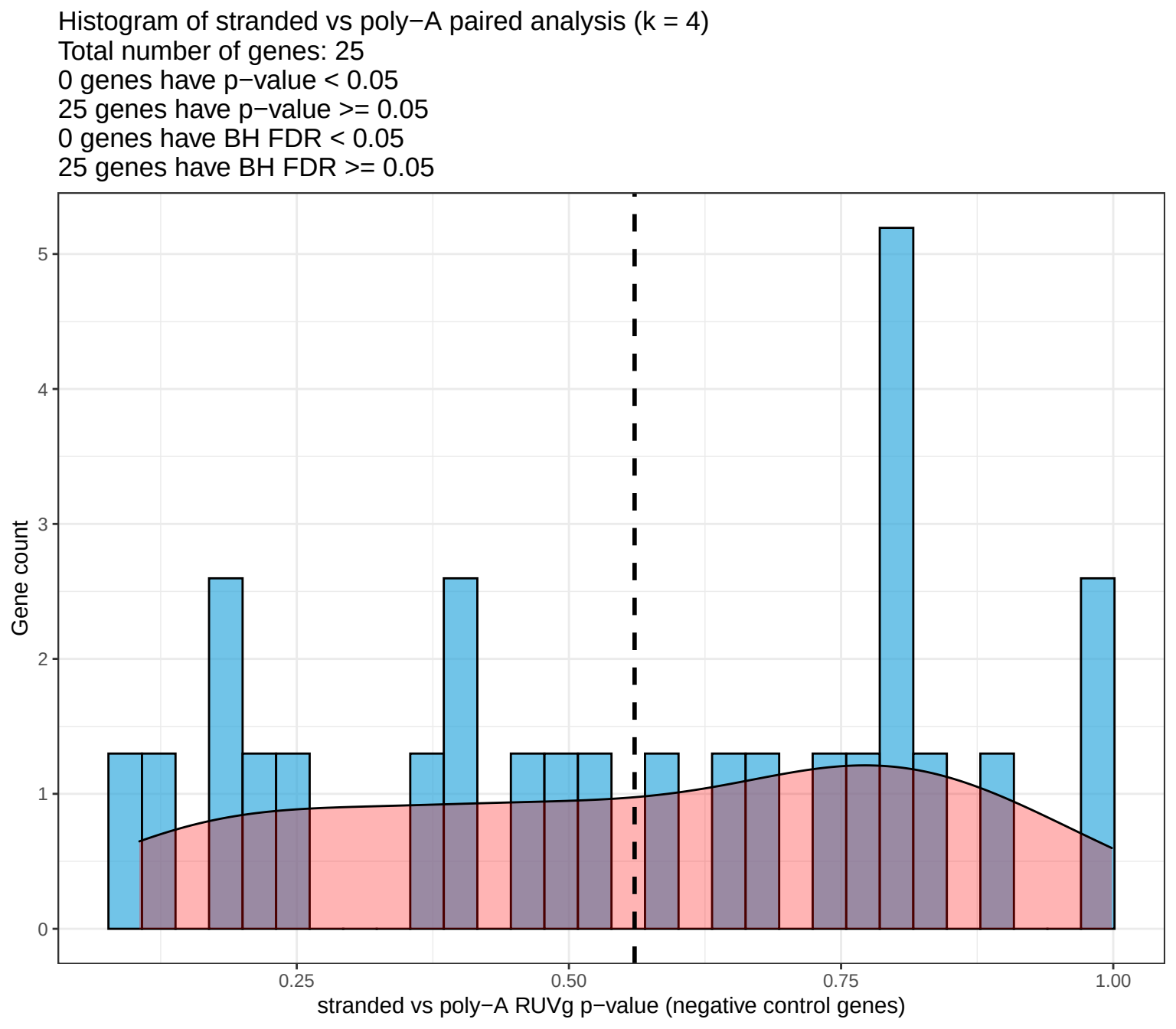
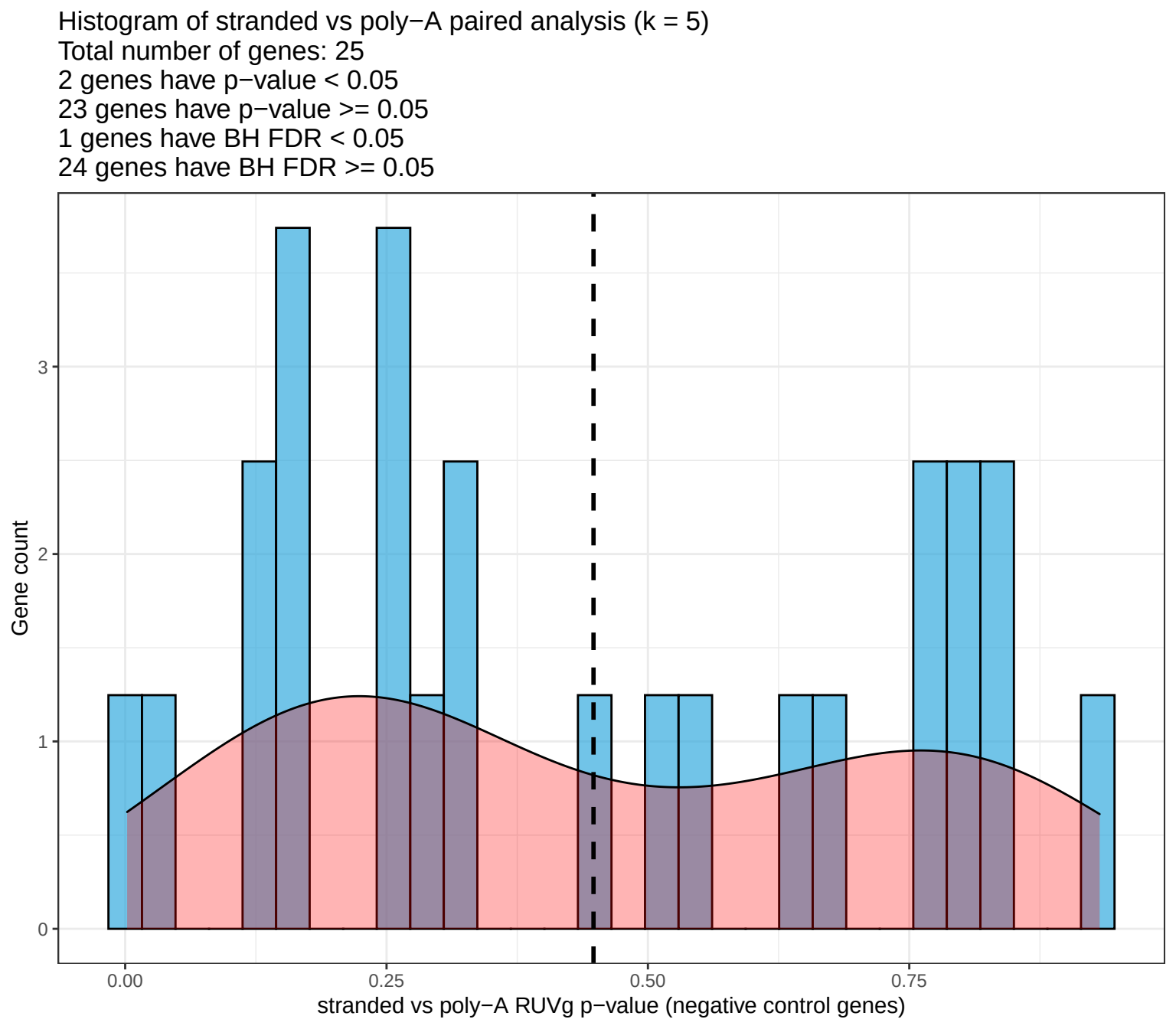

Histogram of stranded vs poly−A paired analysis (k = 1)
Total number of genes: 25
0 genes have p−value < 0.05
25 genes have p−value >= 0.05
0 genes have BH FDR < 0.05
25 genes have BH FDR >= 0.05
Gene count
0
1
2
3
4
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 2)
Total number of genes: 25
0 genes have p−value < 0.05
25 genes have p−value >= 0.05
0 genes have BH FDR < 0.05
25 genes have BH FDR >= 0.05
Gene count
0
2
4
0.4
0.6
0.8
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 3)
Total number of genes: 25
2 genes have p−value < 0.05
23 genes have p−value >= 0.05
1 genes have BH FDR < 0.05
24 genes have BH FDR >= 0.05
Gene count
0
1
2
0.00
0.25
0.50
0.75
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 4)
Total number of genes: 25
0 genes have p−value < 0.05
25 genes have p−value >= 0.05
0 genes have BH FDR < 0.05
25 genes have BH FDR >= 0.05
Gene count
0
1
2
3
4
5
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: 25
2 genes have p−value < 0.05
23 genes have p−value >= 0.05
1 genes have BH FDR < 0.05
24 genes have BH FDR >= 0.05
Gene count
0
1
2
3
0.00
0.25
0.50
0.75
stranded vs poly−A RUVg p−value (negative control genes)