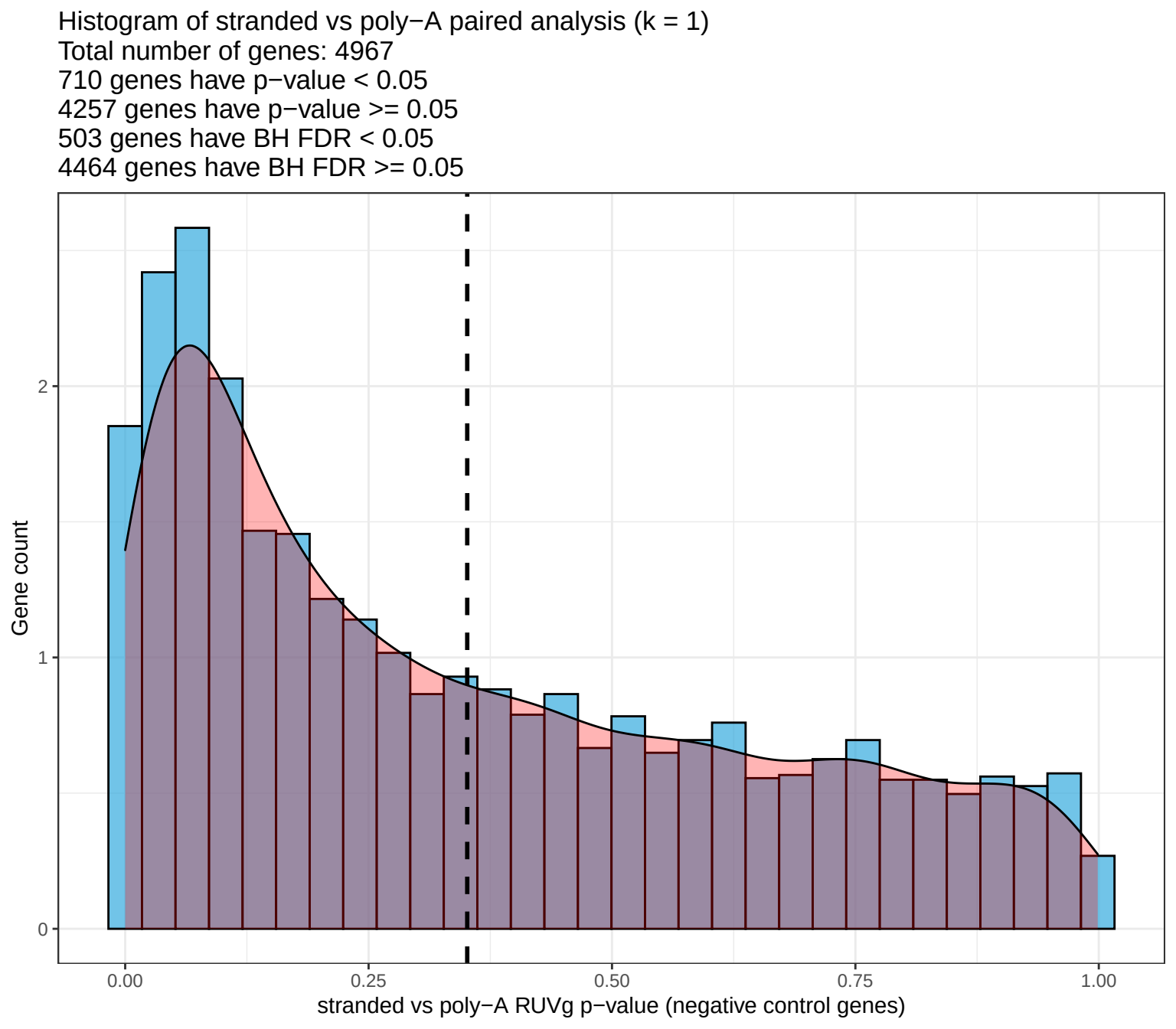
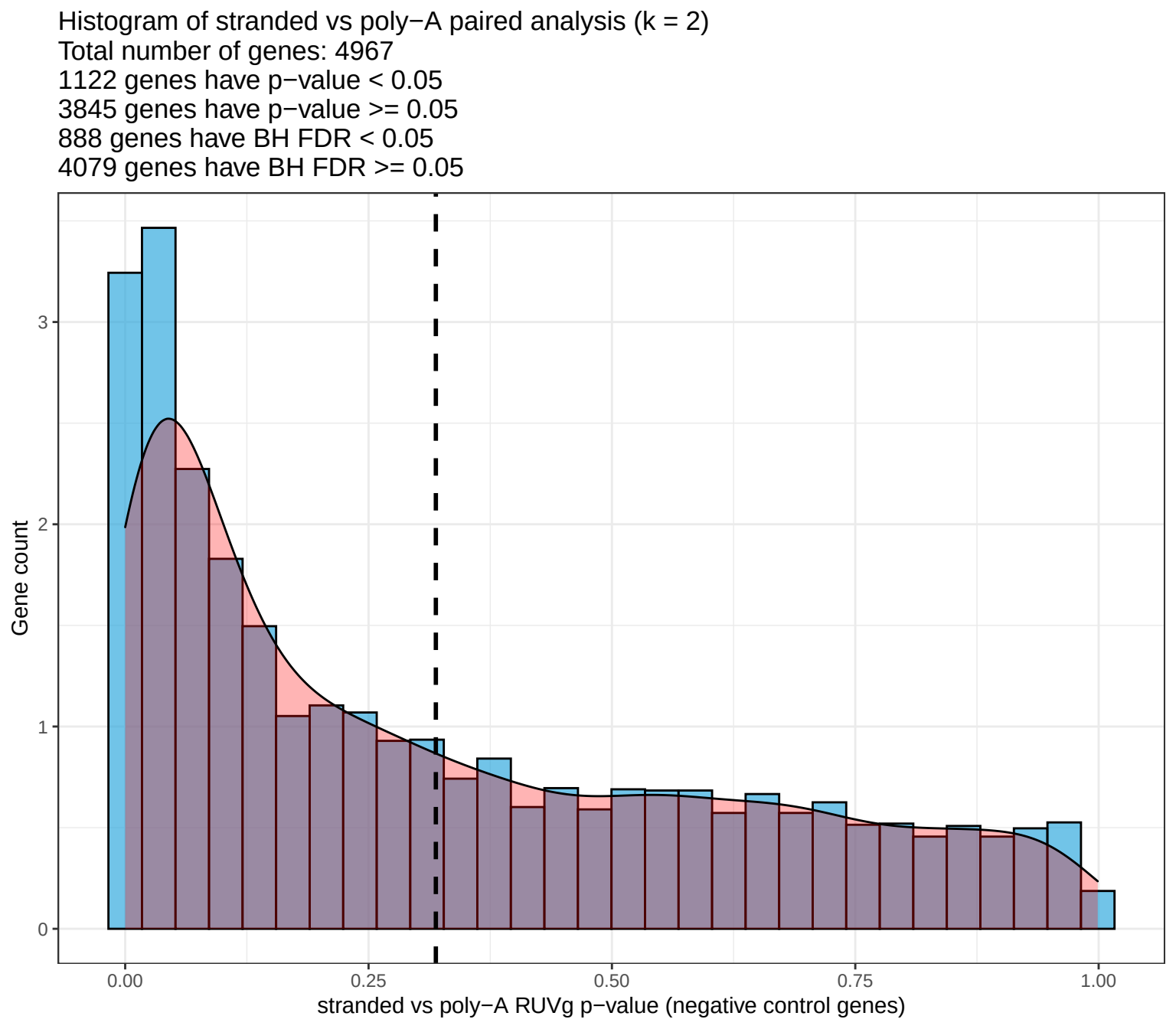
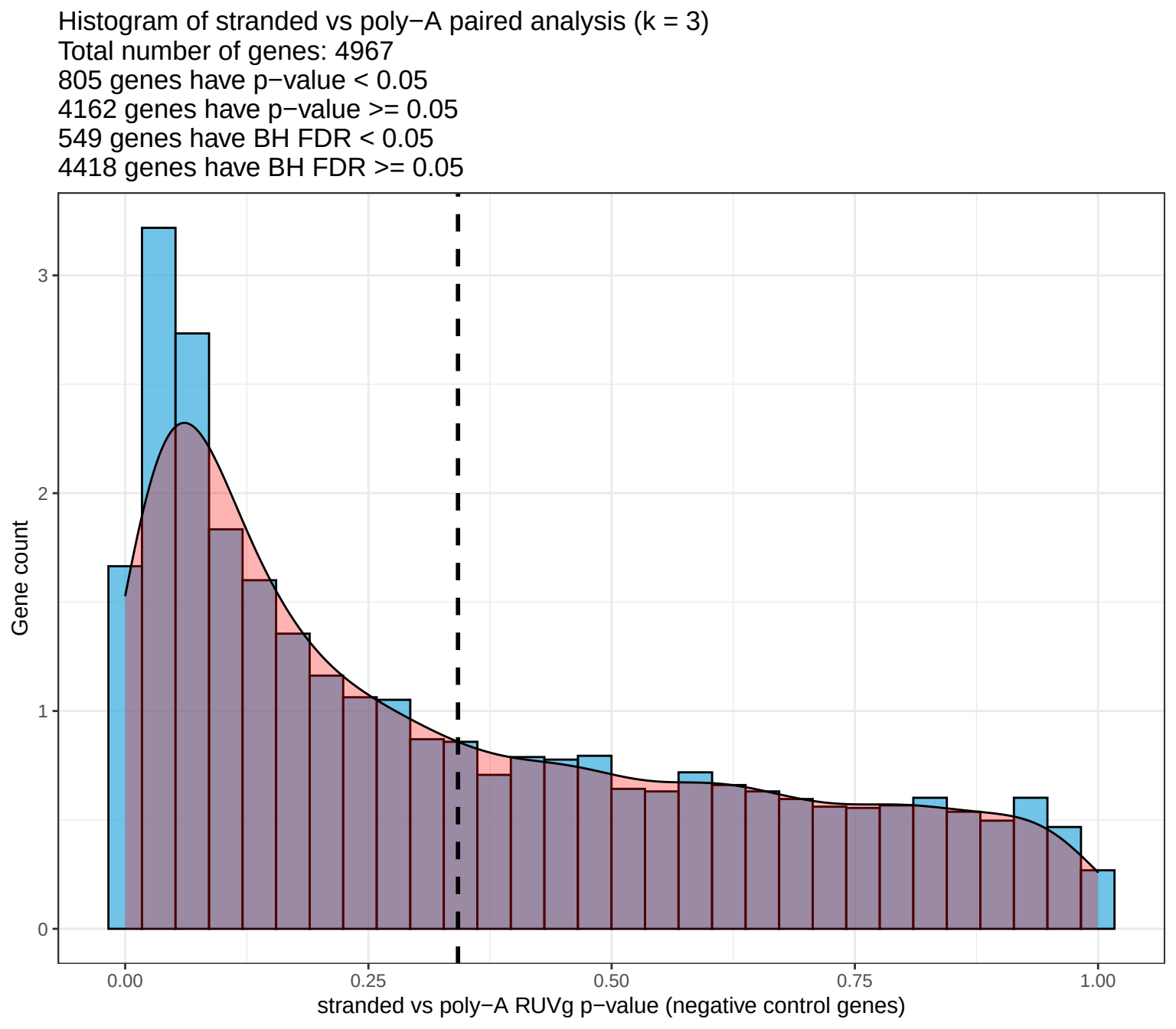
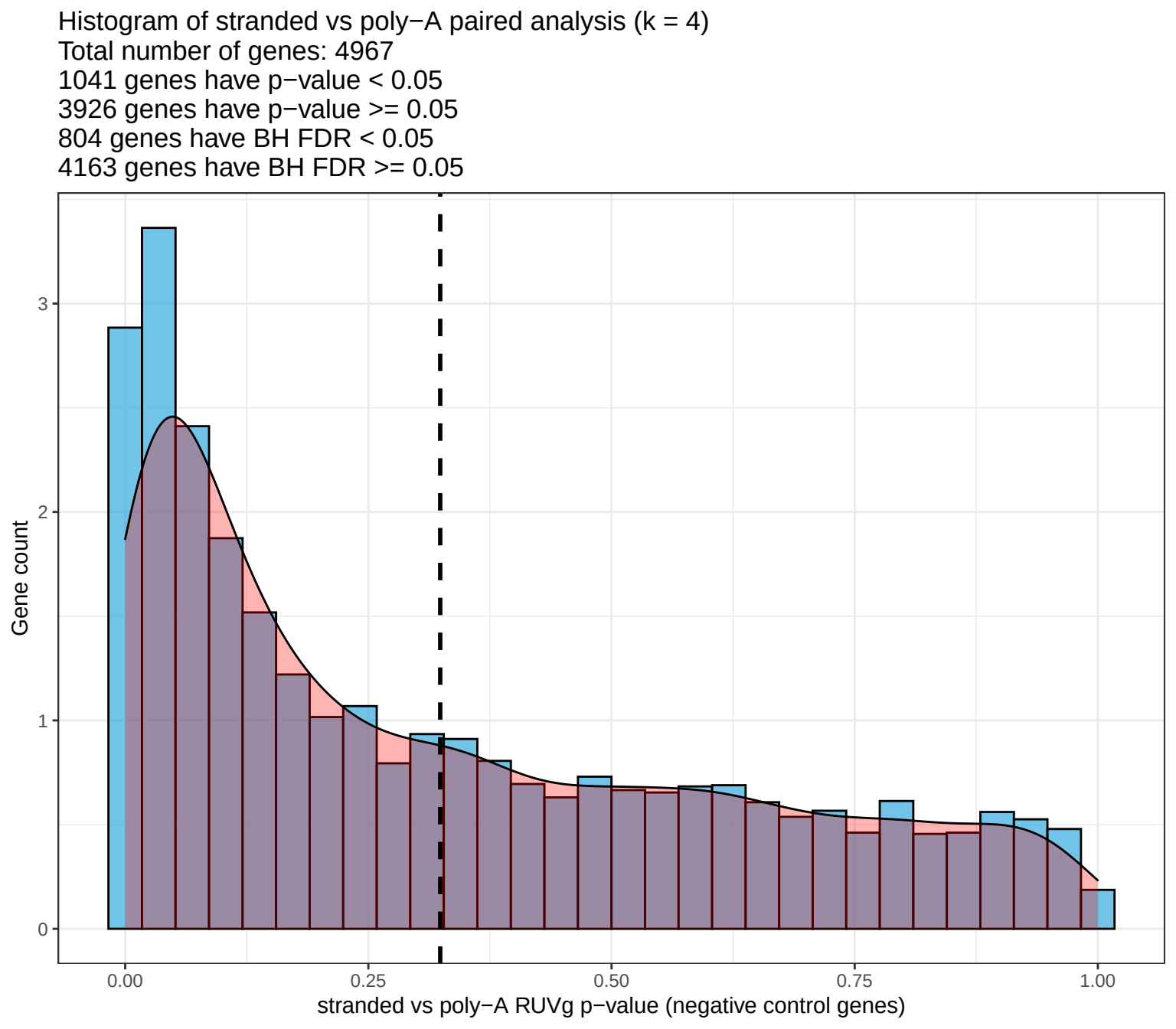
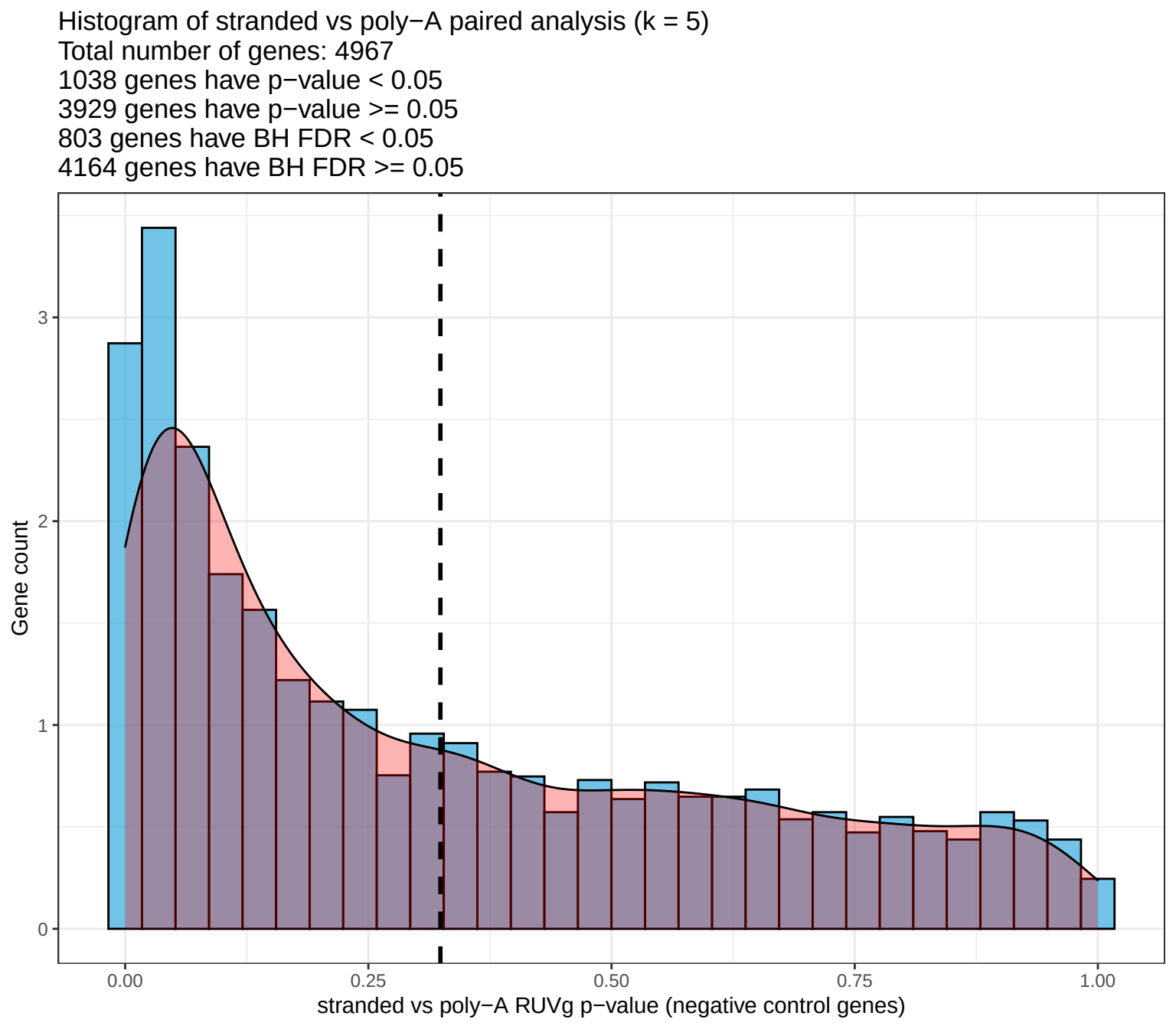

Histogram of stranded vs poly−A paired analysis (k = 1)
Total number of genes: 4967
710 genes have p−value < 0.05
4257 genes have p−value >= 0.05
503 genes have BH FDR < 0.05
4464 genes have BH FDR >= 0.05
Gene count
2
1
0
0.00
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)


Histogram of stranded vs poly−A paired analysis (k = 2)
Total number of genes: 4967
1122 genes have p−value < 0.05
3845 genes have p−value >= 0.05
888 genes have BH FDR < 0.05
4079 genes have BH FDR >= 0.05
Gene count
0
1
2
3
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: 4967
805 genes have p−value < 0.05
4162 genes have p−value >= 0.05
549 genes have BH FDR < 0.05
4418 genes have BH FDR >= 0.05
Gene count
0
1
2
3
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: 4967
1041 genes have p−value < 0.05
3926 genes have p−value >= 0.05
804 genes have BH FDR < 0.05
4163 genes have BH FDR >= 0.05
Gene count
0
1
2
3
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: 4967
1038 genes have p−value < 0.05
3929 genes have p−value >= 0.05
803 genes have BH FDR < 0.05
4164 genes have BH FDR >= 0.05
Gene count
0
1
2
3
0.00
0.25
0.50
0.75
1.00
stranded vs poly−A RUVg p−value (negative control genes)