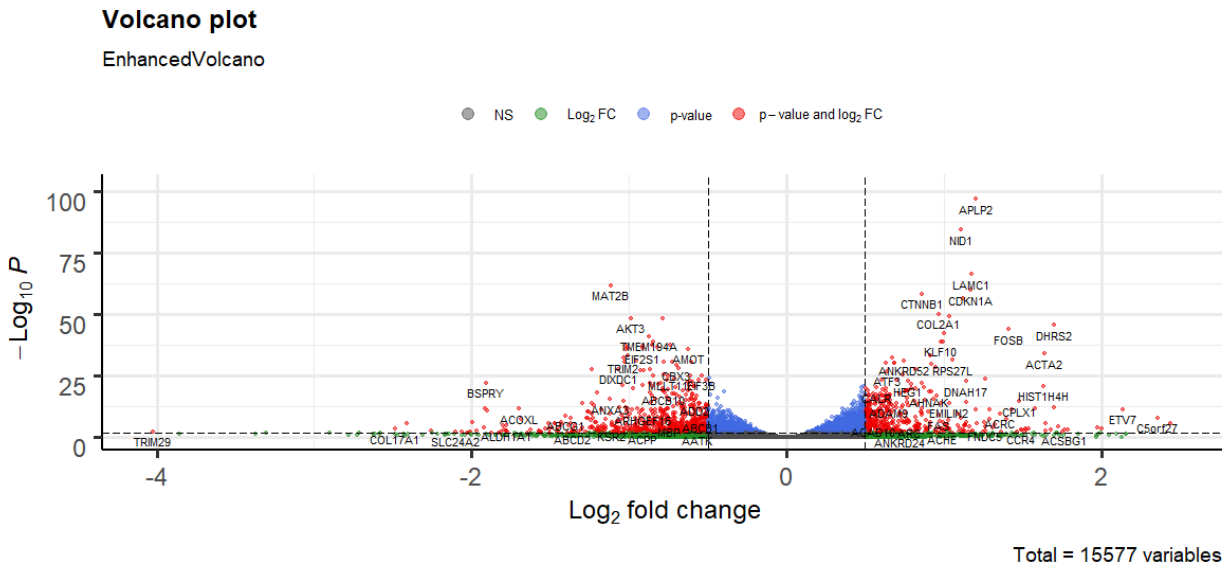
How many adjusted p-values were less than 0.1?
7429

out of 19748 with nonzero total read count
adjusted p-value < 0.1
LFC > 0 (up)   : 3582, 18%
LFC < 0 (down)   : 3847, 19%
outliers [1]   : 0, 0%
low counts [2]   : 3413, 17%
(mean count < 3)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results

Explore the results table summary for the Mov10_knockdown comparison to control. How many genes are differentially expressed at FDR < 0.1? How many fewer genes do we find at FDR < 0.05?

out of 19748 with nonzero total read count
adjusted p-value < 0.1
LFC > 0 (up)   : 3112, 16%
LFC < 0 (down)   : 2727, 14%
outliers [1]   : 0, 0%
low counts [2]   : 4171, 21%
(mean count < 5)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results

out of 19748 with nonzero total read count
adjusted p-value < 0.05
LFC > 0 (up)   : 2668, 14%
LFC < 0 (down)   : 2241, 11%
outliers [1]   : 0, 0%
low counts [2]   : 4171, 21%
(mean count < 5)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results



Total = 15577 variables

The x -axis represents the log fold change (representation of upregulation and downregulation) while the y axis represents significance.