Identification of differentialy expressed genes in colorrectal cancer using RNA-seq data

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1 Introduction

In this report, we analyse genes expressed differentialy in colorrectal cancer (CR). For this purpose, we made use of the R software for statistical analysis and data visualisation.
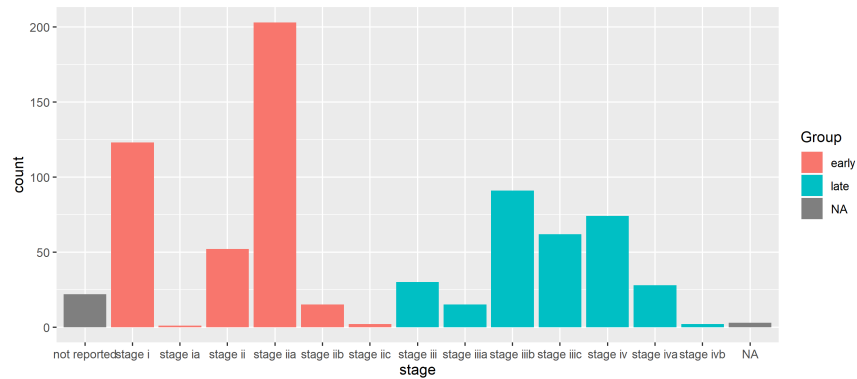

Figure 1: CR tumor stage count

2 Results

In figure 2 it is shown that some genes are differentialy expressed in CR cells. Nonetheless, since these genes do not appear in the corresponding gene ontology, results are hard to explain.
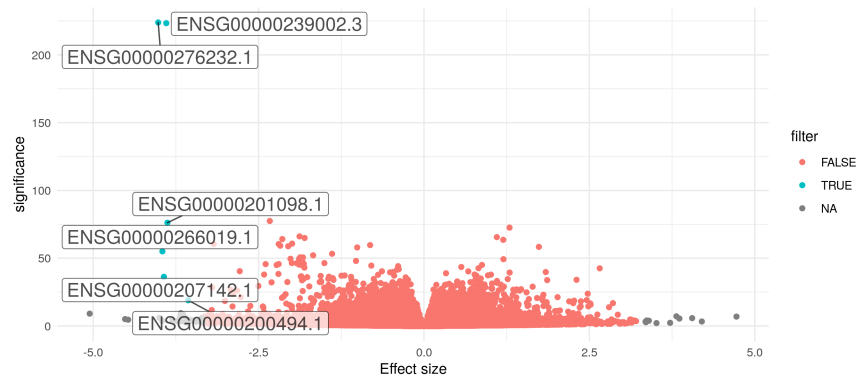
Figure 2: Volcano plot showing statistically significant differentialy expressed genes in CR cells.