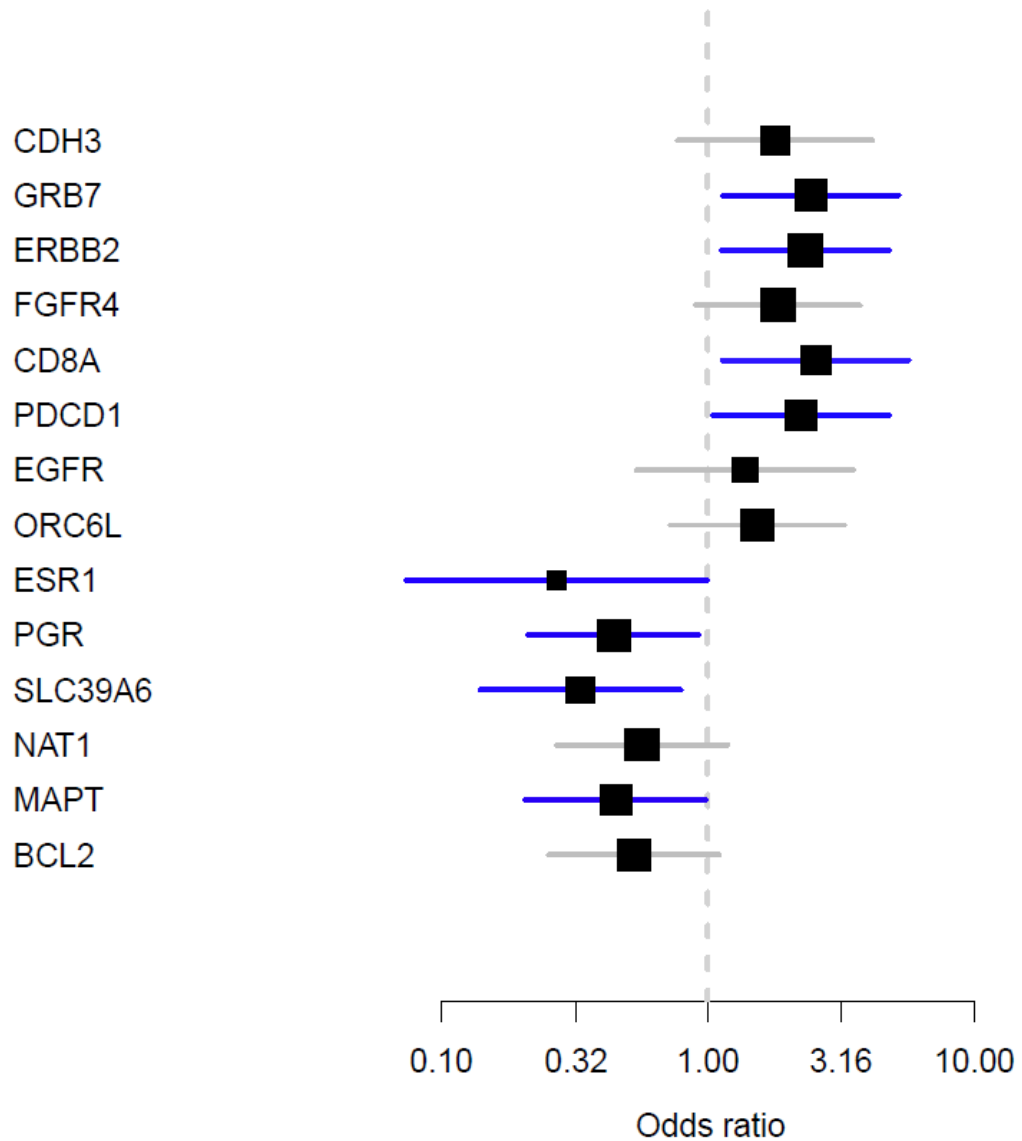**Figure S3 - Effect of 14 single genes on pCR adjusting for clinicopathological parameters.**

A false discovery rate < 0.01 is considered significant. Each gene has been standardized to have a mean of 0 and a standard deviation of 1. Square indicate odds ratio (OR), and error bars, 95% confidence interval (CI). Square size is inversely proportional to the size of the CI.