A)

B)

Figure S.1 Boxplot for miR ratios on small-RNA sequencing (panel A) and q-RT-PCR (panel B) data in cases (red) and controls (green). As ratios on sequencing data originally were not $\log_2$-transformed, to enable direct comparability of the results, RT-qPCR expression values were reported as 2^{Ct}
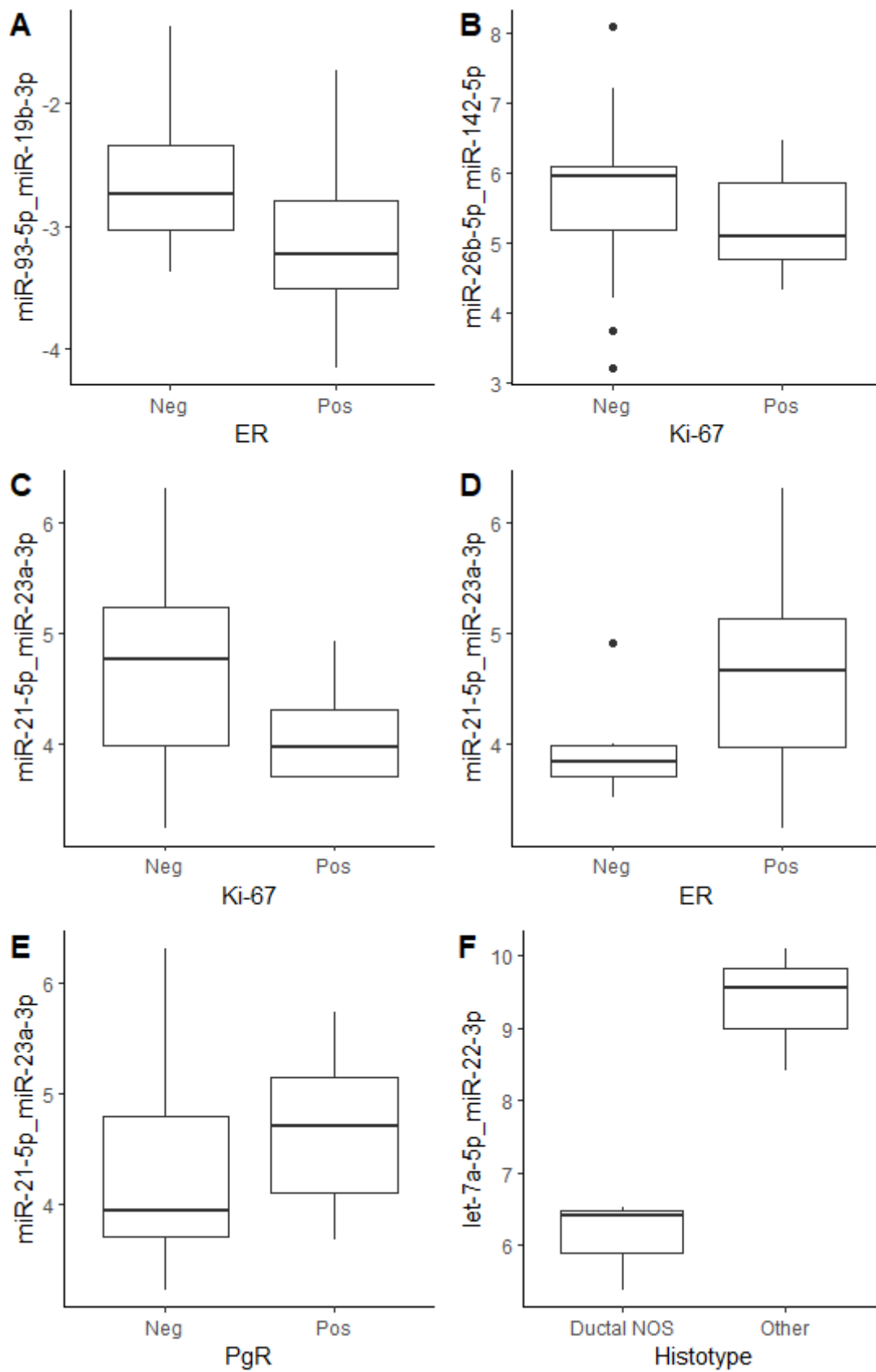
Figure S.2 Expression values for ratio associated with clinico-pathological BC cases characteristics. Panels A-E refer to invasive tumors whereas panel F to *in situ* ones
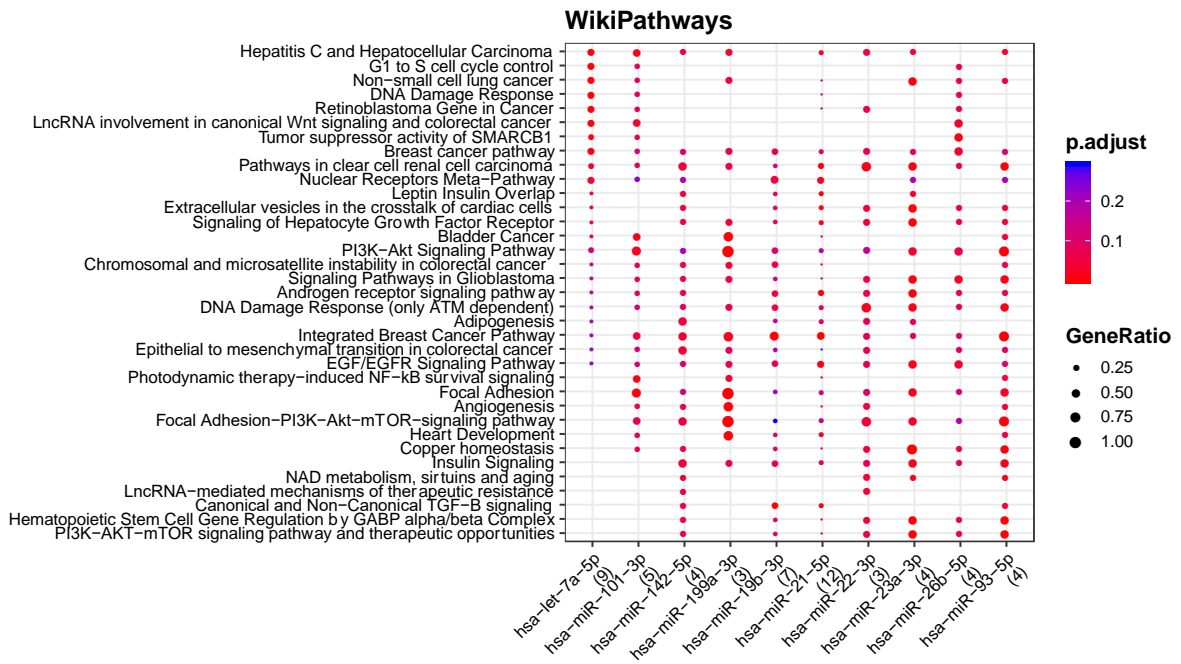
Figure S.3 Functional target enrichment results (Wikipathways database) on miRs making up the ratios within the model including non-molecular variables