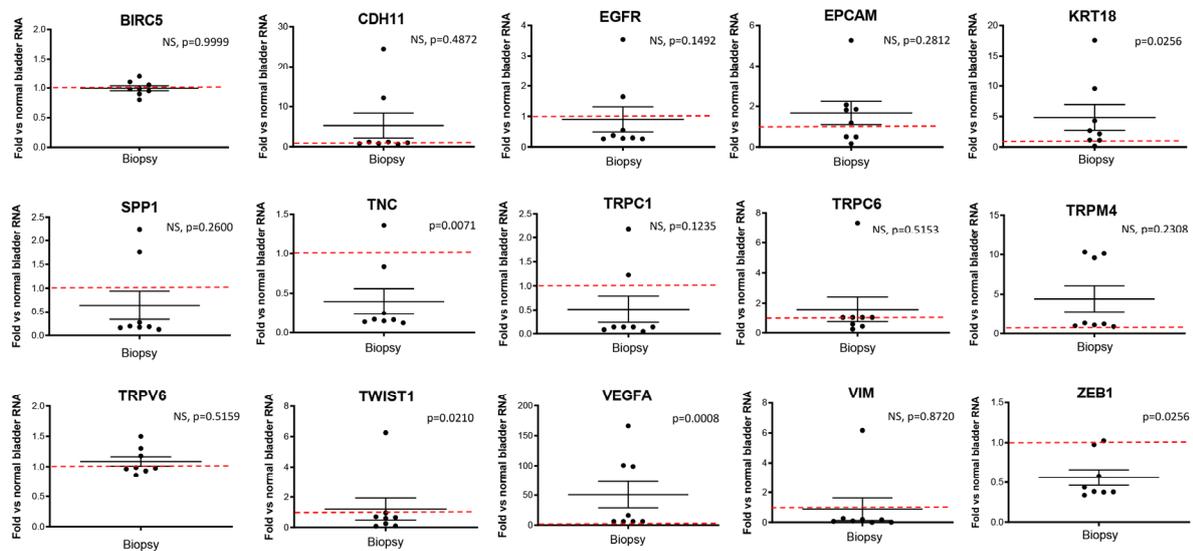
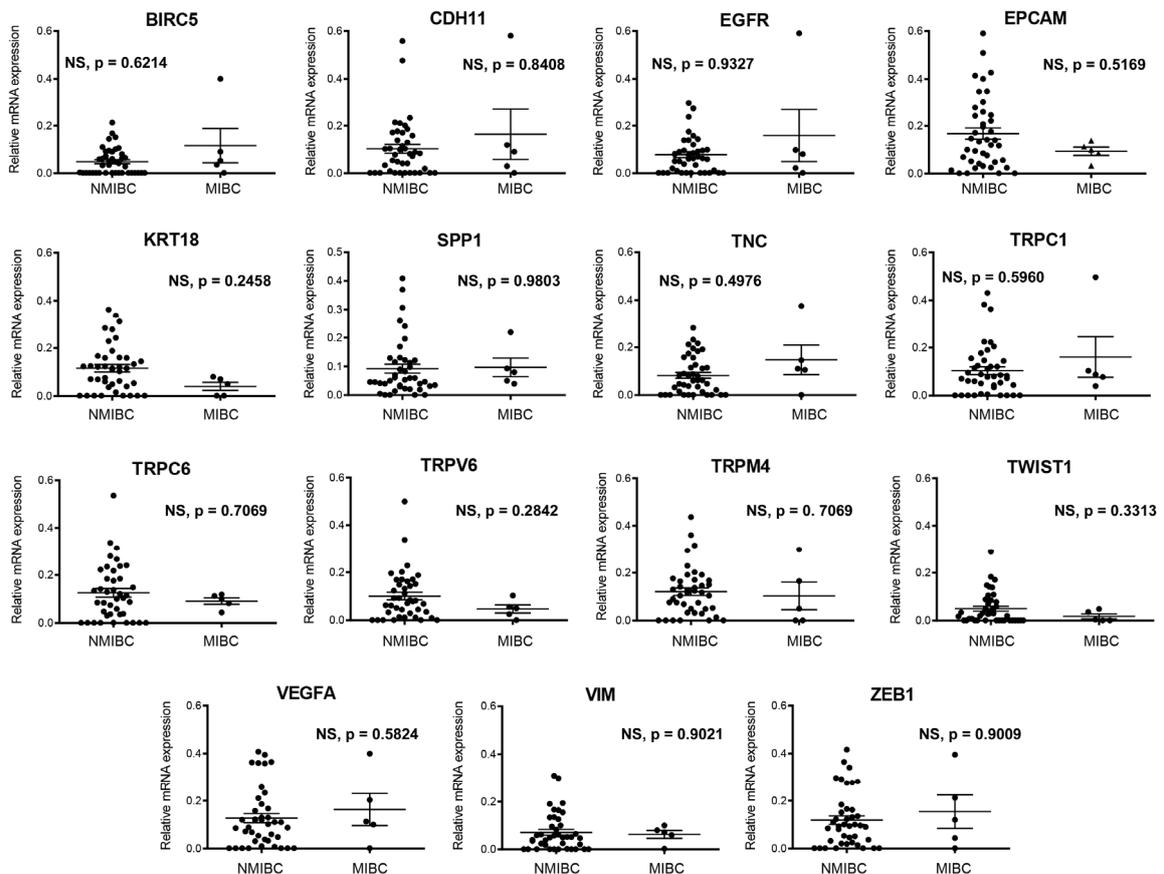


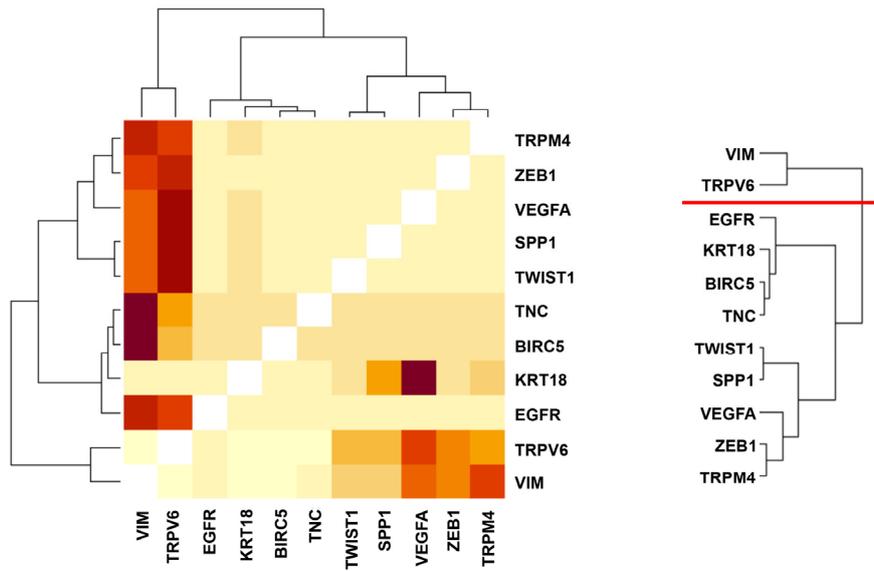
## Supplementary Materials



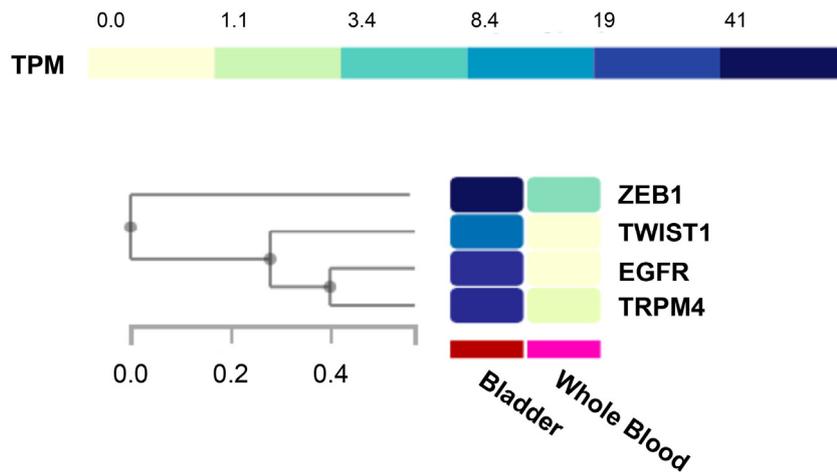
**Figure S1.** Gene expression of selected biomarker candidates in biopsies respect to NHB. Gene expression levels, evaluated by ddPCR, are expressed as fold changes with respect to NHB, used as calibrators=1. NS= not statistically significant, \*  $p \leq 0.05$  was considered as statistically significant. Red dotted line represents NHB used as calibrator= 1.



**Figure S2.** Gene expression analysis of selected biomarkers. The analysis was performed in CTCs by stratifying patients according to clinico-pathological subgroups in NMIBC and MIBC. Unpaired, non-parametric, Mann-Whitney test was used to analyze the significant level of the selected biomarkers between NMIBC and MIBC.



**Figure S3.** Correlation matrix analysis. Heat map and hierarchical tree of selected biomarker candidates based on correlation matrix values.



**Figure S4.** Profiles retrieved from the GTEx to support and validate our selection. Heatmap showing the expression level of the selected markers in bladder and whole blood.