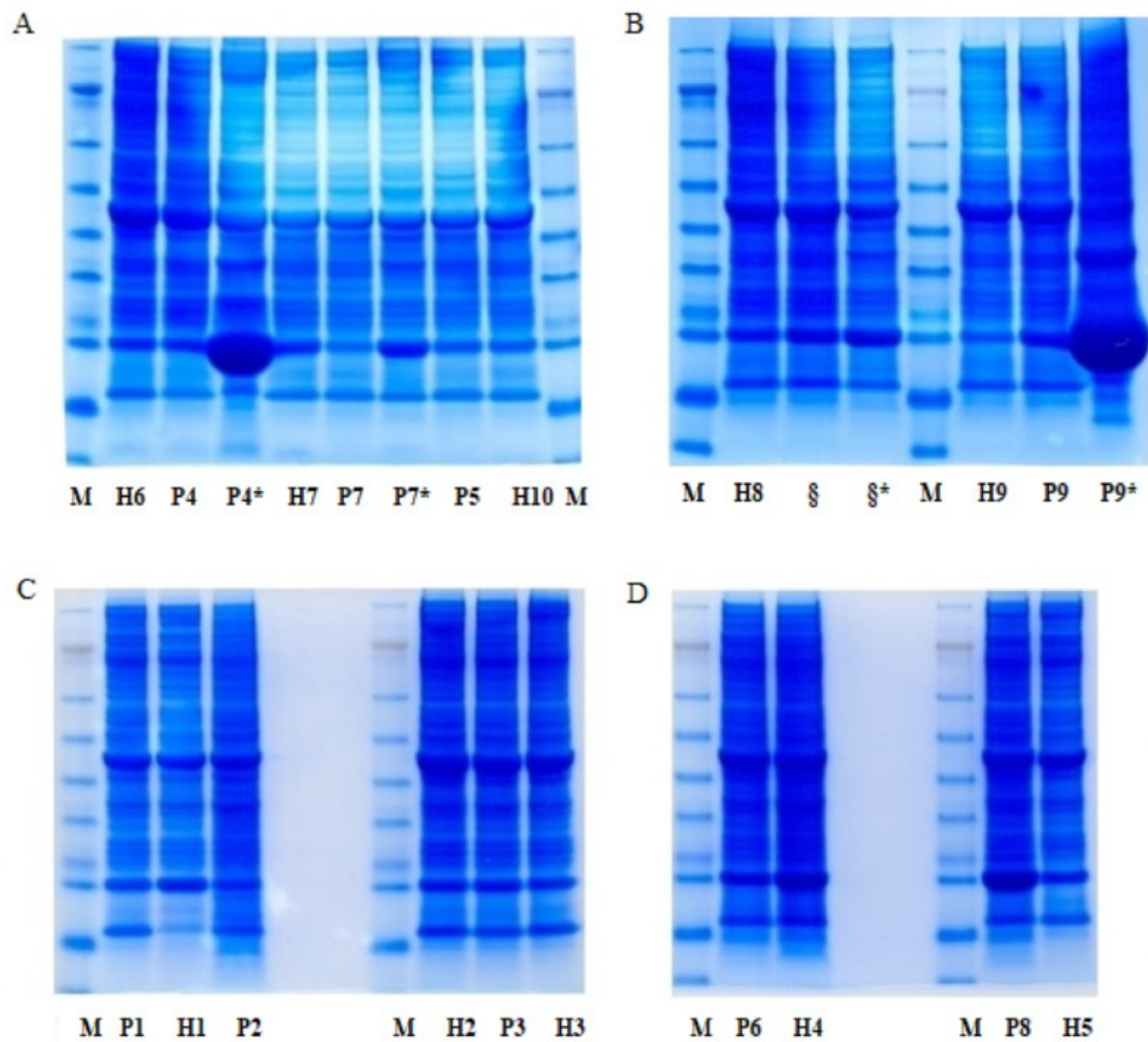
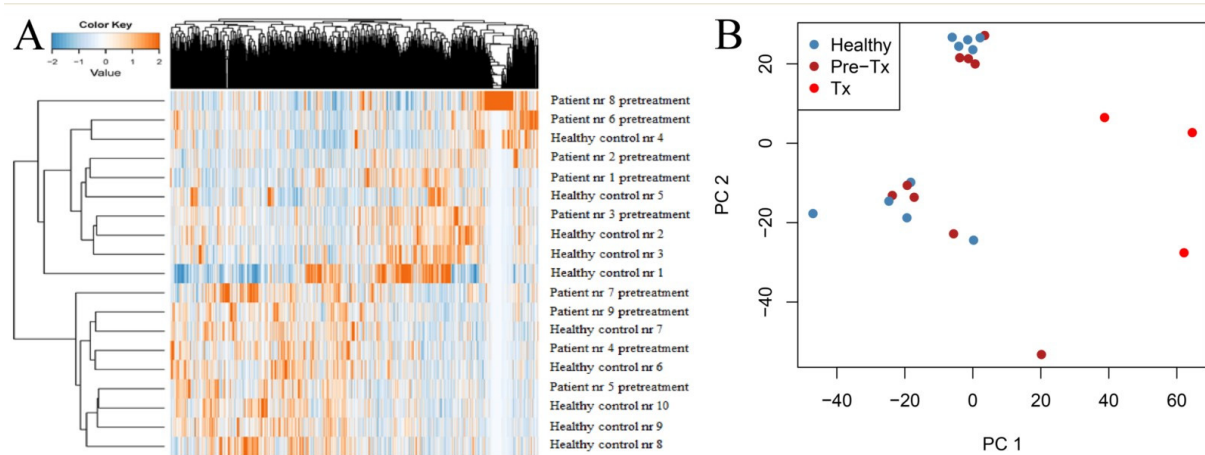


**Figure S1.** Gel electrophoresis and Coomassie staining of platelet samples from patients with cancer (n=9) and healthy controls (n=10).



M=marker, H=Healthy, P=patient, \*=after start of treatment, §Patient was excluded from further analysis due to meeting of exclusion criteria.

**Figure S2.** Heat map and unsupervised cluster analysis and principal component analysis using protein expression data from platelets of patients with cancer (n=9) and healthy controls (n=10).



A) Heat map and unsupervised cluster analysis using protein expression data from platelets of patients with cancer (n=9) before treatment and healthy controls (n=10). The unsupervised cluster analysis does not show a clear separation of samples.

B) Principal component analysis using protein expression data from platelets of patients with cancer (n=9) before treatment and after start of treatment (n=3) and healthy controls (n=10). This analysis does not show a clear separation of the samples of patients before treatment and of the healthy volunteers.

**Figure S3.** Protein-protein networks of platelet proteins, in paired patient samples, with a higher abundance before compared to after initiation of antitumor treatment. ( $p < 0.05$ , fold change  $\geq 5$ ). The networks were generated using default settings in String and visualized using Cytoscape.

