**Supplementary Table and Figure Legends**

**Supplementary Table 1. Alphabetical list of differential abundant plasma proteins, as identified by MALDI-TOF MS after 2D-DIGE analysis, between good and poor prognosis of PAOD.** aAveraged differences between triplicate samples run on different gels show plasma protein abundance ratios for patients with PAOD with good prognosis versuspoor prognosis. Proteins are shown as 1.3-fold differences as either up- or down- regulated (*p*< 0.05). Spots in the images are listed in the table inset. Functions were assigned according to the Swiss-Prot database entries and our literature search results.

**Supplementary Figure 1. Evaluation of albumin removal efficiency from plasma samples.** Twenty-microgram quantities of crude plasma, and albumin-depleted plasma from patients with PAOD with good prognosis versuspoor prognosis were loaded and resolved by SDS-PAGE followed by staining with colloidal coomassie blue G-250.

**Supplementary Figure 2. 2D-DIGE analysis of patients with PAOD with good prognosis versuspoor prognosis-related differential abundance proteins.** (A) Plasma sample arrangement for a triplicate 2D-DIGE experiment. (B) Plasma samples (100 g) were labeled with Cy-fluorescent dyes, and were separated using 24-cm, pH 3-10 non-linear IPG strips. The figure shows 2D-DIGE images of the plasma samples from patients with PAOD with good prognosis versuspoor prognosis at the appropriate excitation and emission wavelengths (upper left and right images). Also shown is an overlaid pseudo-colored image processed with ImageQuant software (GE Healthcare) (bottom left image). Differential abundance protein features are annotated with spot numbers (bottom right image).

**Supplementary Figure 3. Percentage of plasma proteins identified from albumin-depleted plasma by 2D-DIGE/MALDI-TOF MS for patients with PAOD with good prognosis versuspoor prognosis, according to (A) biological function and (B) subcellular location.**

**Supplementary Figure 4. Representative images of the identified protein spots. (A)**Clusterin, **(B)**alpha-1-antichymotrypsin, **(C)**leucine-rich alpha-2-glycoprotein, **(D)**alpha-1B-glycoprotein, **(E)**inactive polyglycylase TTLL10, **(F)**tropomodulin-1, **(G)**haptoglobin, **(H)**apolipoprotein A-IV, **(I)**alpha-1-antitrypsin, **(J)**transthyretin, **(K)**hemopexin, and **(L)**vitamin D-binding proteindisplay changes in patients with PAOD with good prognosis versuspoor prognosis-dependent protein abundance. The levels of these proteins were visualized by fluorescence 2-DE images (top panels), three-dimensional spot images (middle panels), and protein abundance mapping (lower panels).

**Supplementary Figure 5. Protein identification by MALDI-TOF peptide mass fingerprint analysis. (A) transthyretin, (B) complement factor B were resolved by MALDI- TOF MS.**