Supplemental Figure 1. Optimized pooling strategy to achieve increased number of protein identifications. By pooling strong cation exchange chromatography fractions in 1,2, 3 and 5 min pools (pooling method 2), an increase of ~50-60% was achievable in the number of total proteins identified through mass spectrometry, in comparison to analysis of 5 min pools (pooling method 1). The resulting increase in MS analysis time was kept to a minimum through reduction of reverse-phase gradient times (pooling method 2).

Supplemental Figure 2. KEGG pancreatic secretion pathway (hsa04972) (58,59). This figure was obtained through Protein Center software and is one of the pathways depicted as overrepresented in the pancreatic juice proteome in comparison to the combined cell line proteome. Proteins shown in red font are unique to the pancreatic juice proteome. Proteins shown in green font are unique to the cell line proteome and proteins shown in yellow-orange font are common to both proteomes.

Supplemental Figure 3. Percentage of total pancreatic juice (light grey) and cell line (dark grey) proteins and their molecular functions (a) and biological processes (b) annotated from the genome ontology consortium. Proteins can contain multiple GO annotations resulting in a sum of percentages >100%. Data was obtained through Protein Center software.

Supplemental Figure 4. Top network associated with the proteins in Table 3 (63 extracellular and cell surface proteins showing >5-fold expression in at least 3 cancer cell lines in comparison to HPDE). The top network (depicted here) associated with these proteins is ‘cellular movement, cancer and cell-to-cell signaling and interaction’ based on Ingenuity Pathway Analysis. Filled in shapes represent proteins from the dataset; unfilled shapes represent
relevant nodes/proteins added by Ingenuity. Solid lines connecting proteins indicated direct interactions while dotted lines indicate indirect interactions. Among the four canonical pathways (CP) annotated are components of two core pathways shown to be deregulated in most pancreatic cancers: integrin signaling and TGF-β signaling (73).
Supplemental Figure 1.

**Pooling Method 1**

- Absorbance (mAU)
- Time (min)
- Reverse-phase gradient times: 2 hours

**Pooling Method 2**

- Absorbance (mAU)
- Time (min)
- 54 min. 94 min.
Supplemental Figure 2.
Supplemental Figure 3a.
Supplemental Figure 3b.
Supplemental Figure 4.