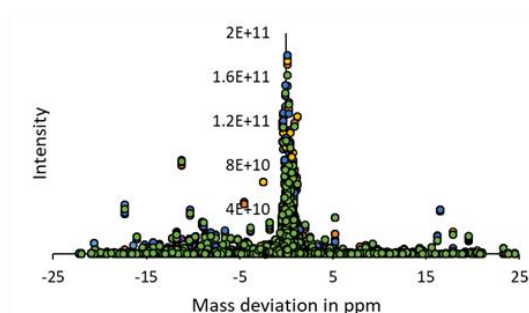


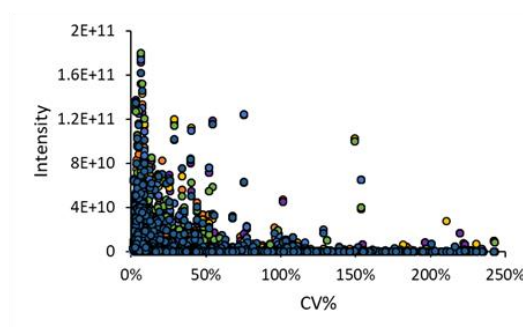
# Systemic Proteome Alterations Linked to Early Stage Pancreatic Cancer in Diabetic Patients

Hong Peng, Sheng Pan, Yuanqing Yan, Randall E. Brand, Gloria M. Petersen, Suresh T. Chari, Lisa A. Lai, Jimmy K. Eng, Teresa A. Brentnall and Ru Chen

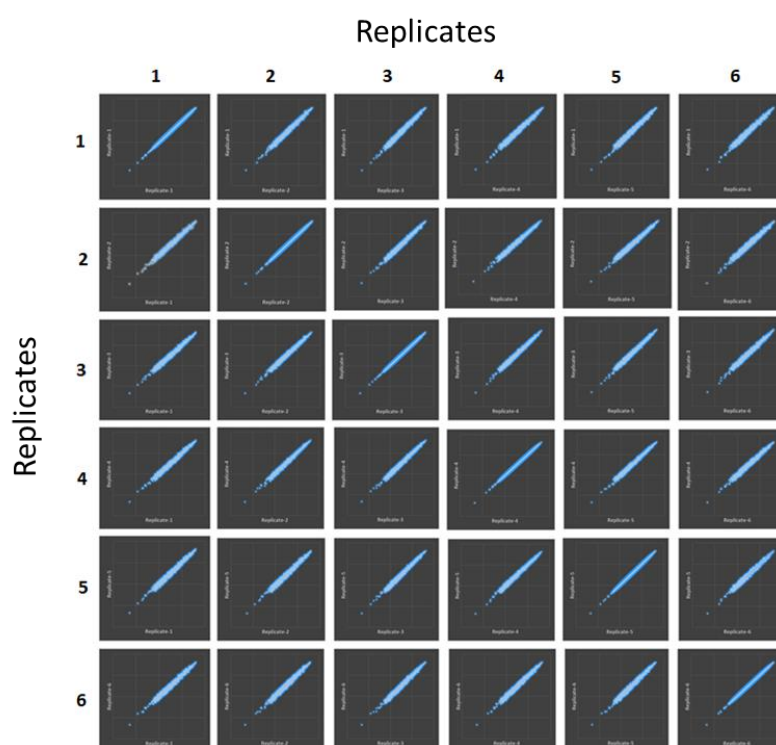
**A.** Distribution - peptide intensity vs mass deviation  
85% of peptides has a mass deviation  $\leq 5$  ppm



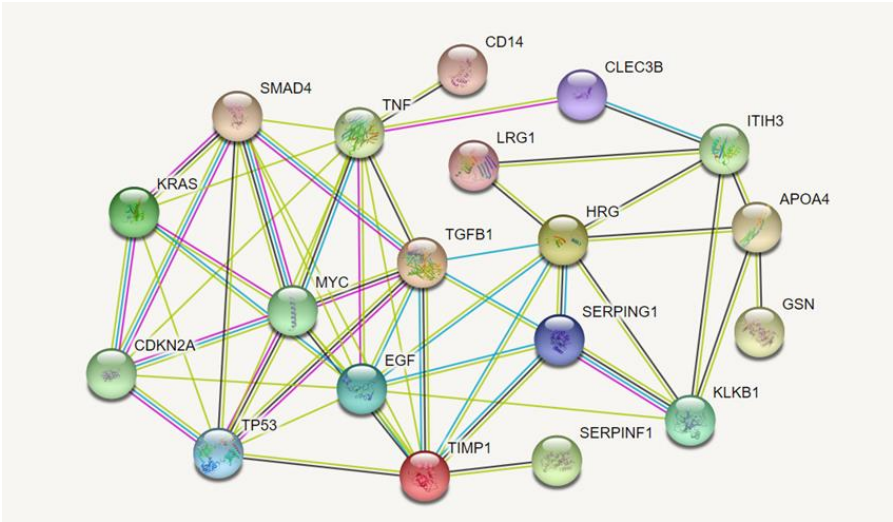
**B.** Distribution - peptide intensity vs CV%  
62% of peptides has a CV%  $\leq 25\%$



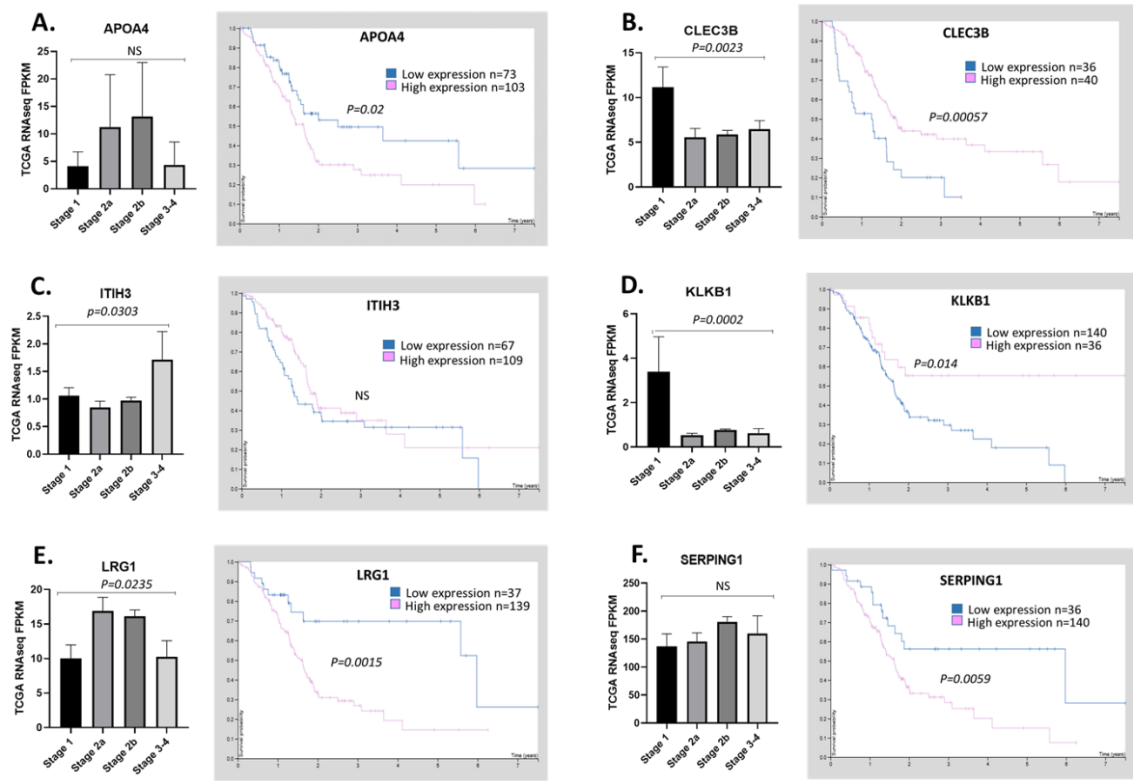
**Figure S1.** Replicate evaluation of proteomic plasma data. A) Distribution of peptide intensity versus mass deviation; B) Distribution of peptide intensity versus CV%.



**Figure S2.** Correlation of replicate analysis in peptide intensity.



**Figure S3.** Protein interaction of APOA4, CD14, CLEC3B, GSN, HRG, ITIH3, KLKB1, LRG1, SERPING1, SERPINF1 and TIMP1 with known oncogenes associated with PDAC.



**Figure S4.** Tissue RNA expression analysis using TCGA database. **A)** APOA4, **B)** CLEC3B, **C)** ITIH3, **D)** KLKB1, **E)** LRG1, **F)** SERPING1.

**Table S1.** The demographic information for the pilot cohort.

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| Disease group DM |     | Age | Sex | DM duration (year) | PDAC stage |
|------------------|-----|-----|-----|--------------------|------------|
| Ctrl DM          | Yes | 79  | M   | 6                  |            |
| Ctrl DM          | Yes | 65  | F   | 2                  |            |
| Ctrl DM          | Yes | 63  | M   | 4                  |            |
| Ctrl DM          | Yes | 74  | M   | 21                 |            |
| Ctrl DM          | Yes | 63  | M   | 9                  |            |
| Ctrl DM          | Yes | 80  | M   | 15                 |            |
| Ctrl DM          | Yes | 74  | M   | 4                  |            |
| Ctrl DM          | Yes | 76  | F   | 41                 |            |
| Ctrl DM          | Yes | 76  | M   | 3                  |            |
| Ctrl DM          | Yes | 74  | M   | 14                 |            |
| PDAC DM          | Yes | 70  | M   | 12                 | 2A         |
| PDAC DM          | Yes | 62  | M   | 8                  | 2          |
| PDAC DM          | Yes | 75  | M   | 6                  | 2B         |
| PDAC DM          | Yes | 81  | M   | 7                  | 2B         |
| PDAC DM          | Yes | 65  | M   | 22                 | 2          |
| PDAC DM          | Yes | 74  | M   | 3                  | 2B         |
| PDAC DM          | Yes | 65  | F   | 5                  | 2          |
| PDAC DM          | Yes | 77  | M   | 10                 | 1          |
| PDAC DM          | Yes | 75  | F   | 4                  | 2          |
| PDAC DM          | Yes | 77  | M   | 2                  | 2B         |

**Table S2.** Selected protein candidates in pilot cohort.**Table S2.** Selected protein candidates in pilot cohort

| Gene name | Protein name                                 | Plasma conc. range (ng/ml)<br>Ref: Mol Cell Proteomics.<br>2011 10(9):M110.006353 | Fitting AUC |
|-----------|--|---|-------------|
| APOA4     | Apolipoprotein A-IV                          | 240000  | 0.89        |
| CD14      | Monocyte differentiation antigen CD14        | 420   | 0.72        |
| CLEC3B    | Tetranectin                                  | 8200  | 0.72        |
| GSN       | Gelsolin                                     | 300000  | 0.72        |
| HRG       | Histidine-rich glycoprotein                  | 100000  | 0.75        |
| ITIH3     | Inter-alpha-trypsin inhibitor heavy chain H3 | 150000  | 0.78        |
| KLKB1     | Plasma kallikrein                            | 2600  | 0.74        |
| LRG1      | Leucine-rich alpha-2-glycoprotein            | 20000   | 0.67        |
| SERPING1  | Plasma protease C1 inhibitor                 | 280000  | 0.82        |
| SERPINF1  | Pigment epithelium-derived factor            | 5000  | 0.80        |
| TIMP1     | metalloproteinase inhibitor 1                | 14  | 0.60        |