

## SUPPLEMENTARY MATERIAL

### Title:

Integrated bioinformatics analysis identifies crucial biochemical processes shared between pancreatitis and pancreatic ductal adenocarcinoma

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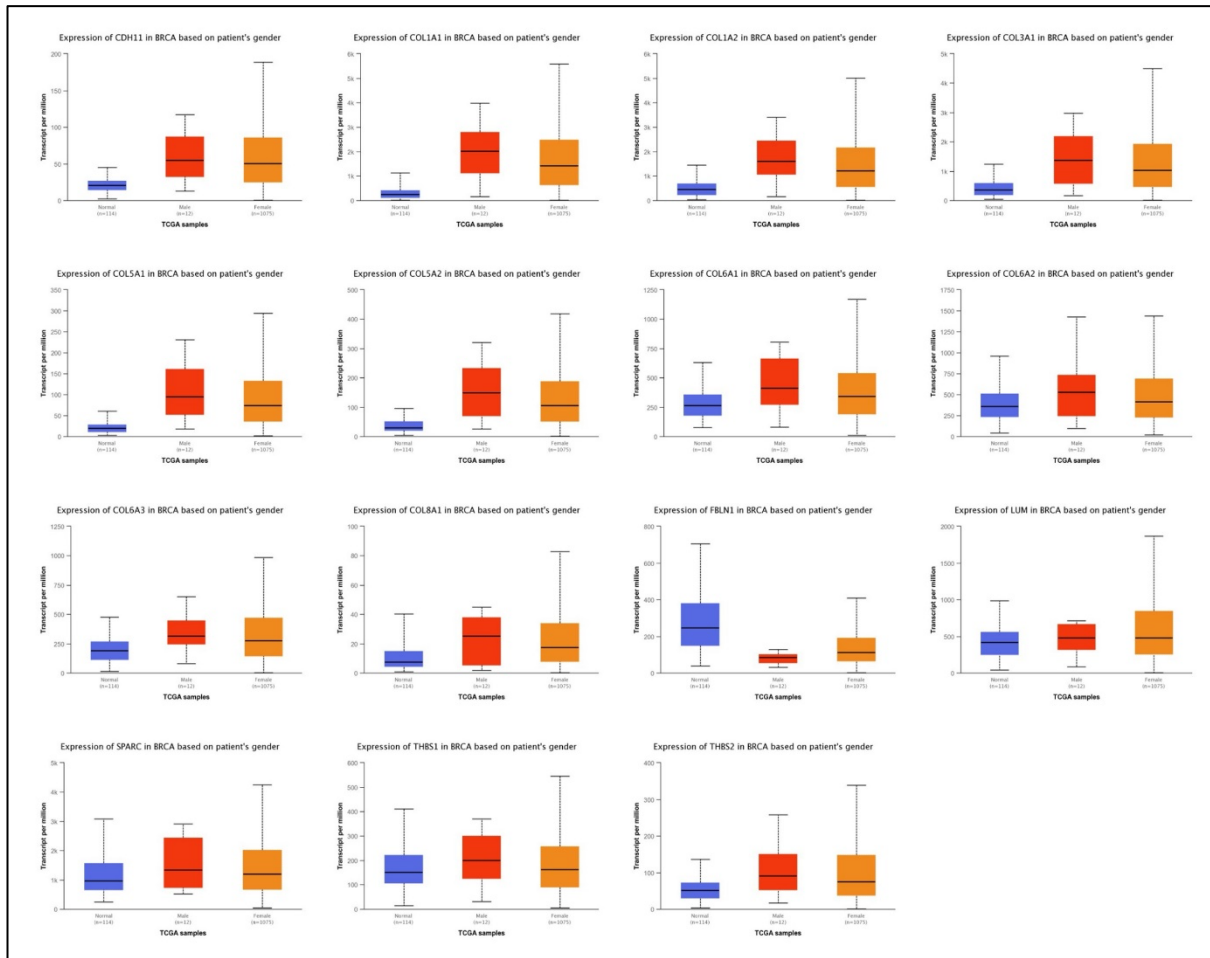
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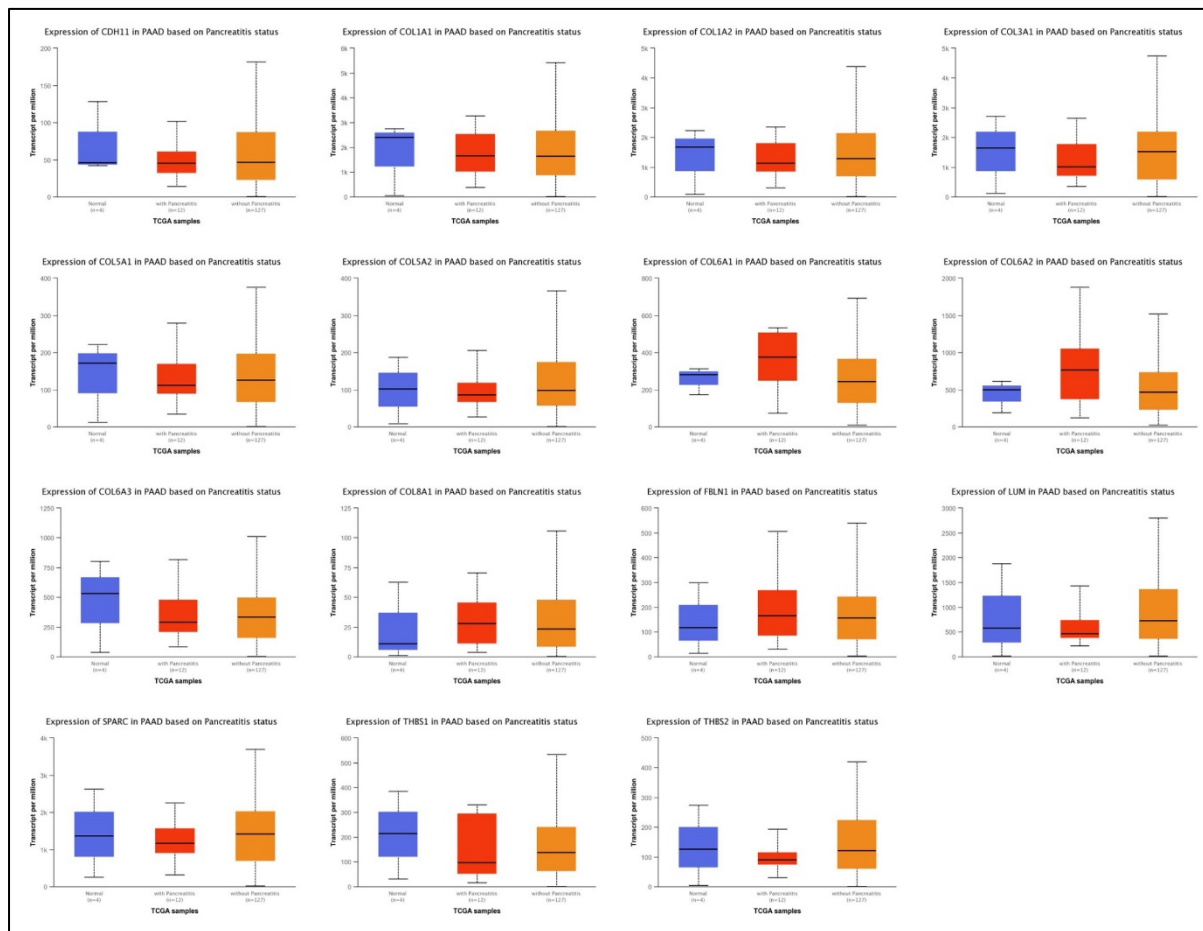
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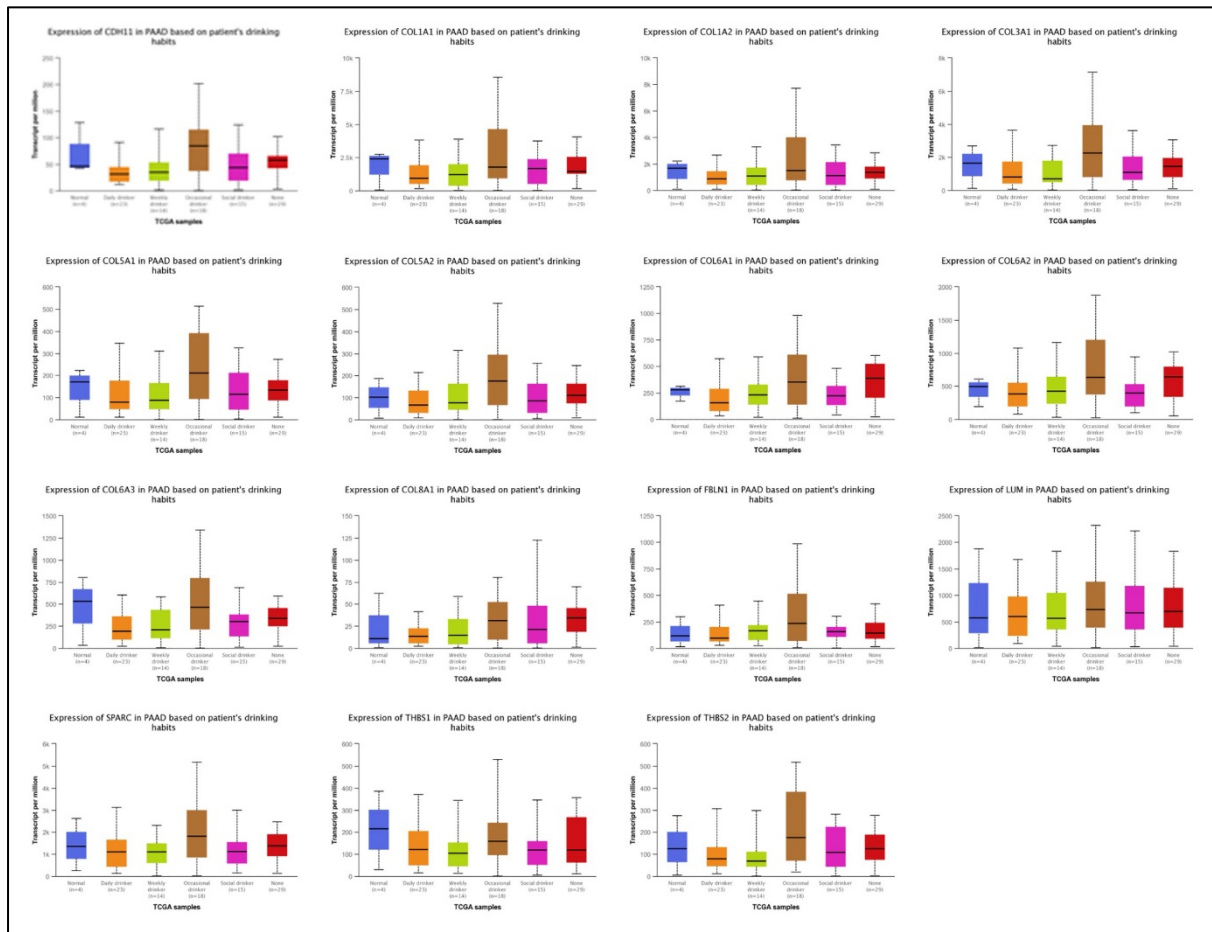
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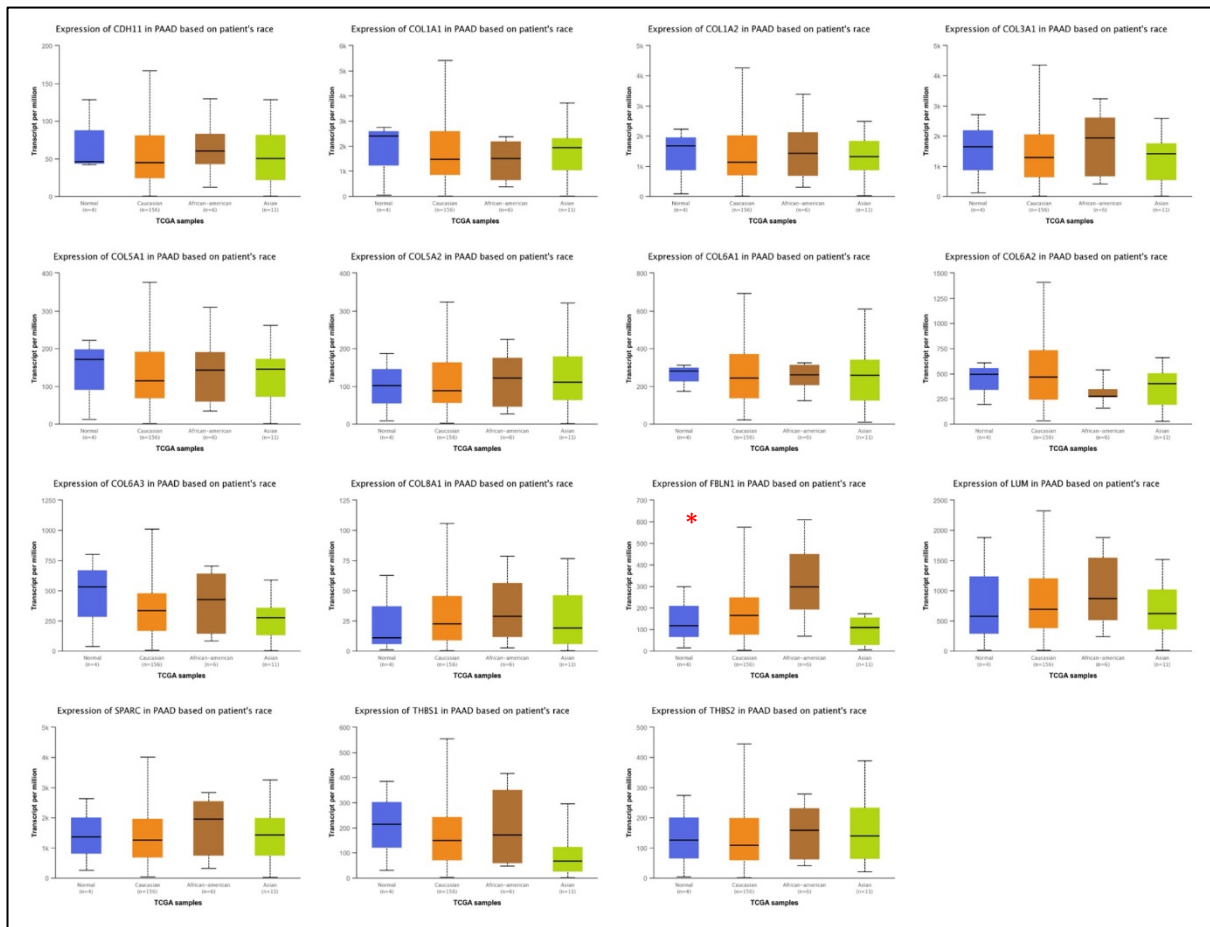
**Supplementary Fig. 1:** Box plots comparing the expression profiles of 15 hub genes between male (red) and female (orange) PDAC samples. Samples from normal tissues are represented in blue. The expression values observed do not differ significantly between samples from male and female PDAC tissues.



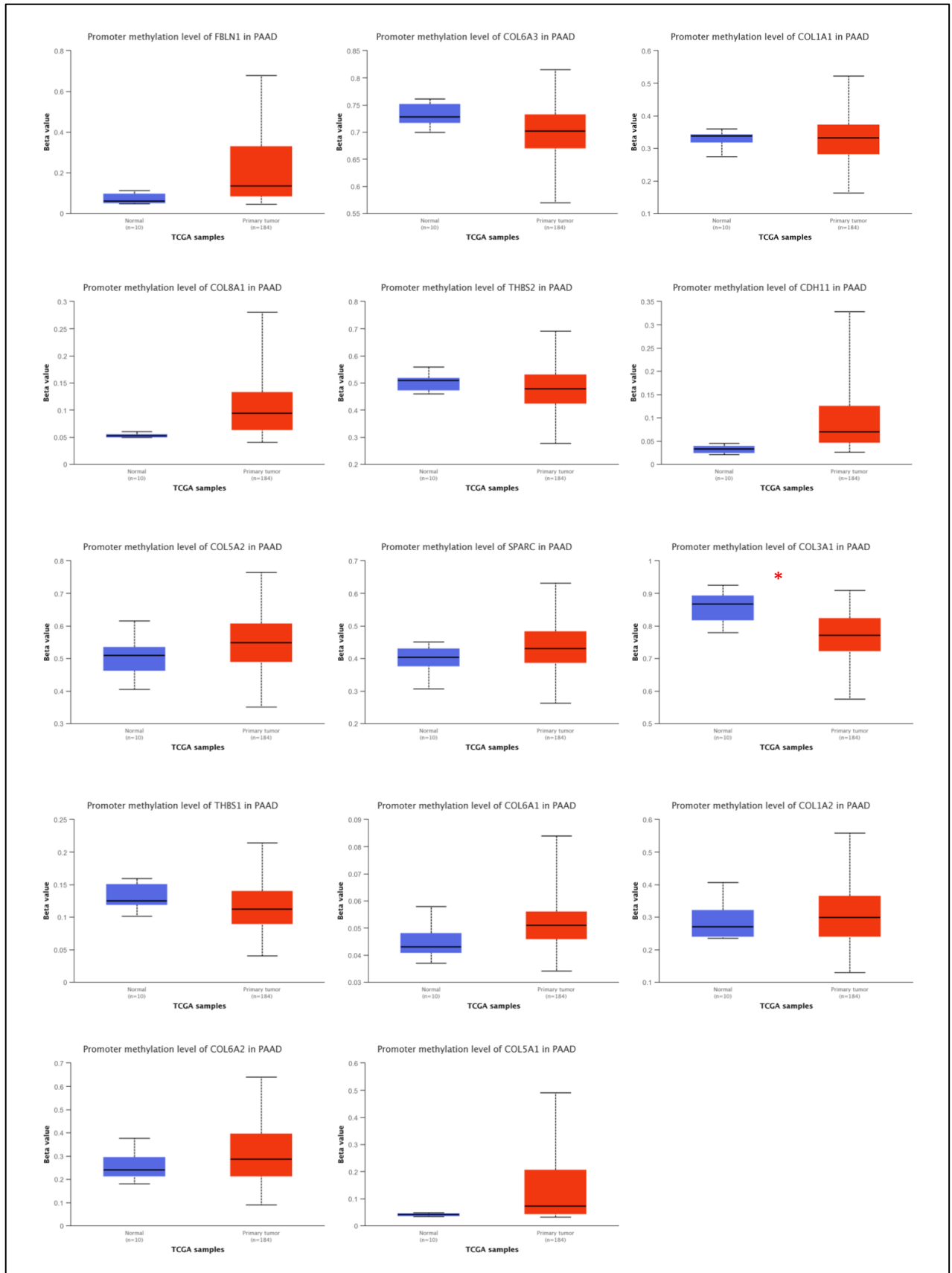
**Supplementary Fig. 2:** Box plots comparing the expression profiles of 15 hub genes based of chronic pancreatitis status. Most of the genes did not show any significant change in expression in both cancer sample sets with (red) and without (orange) pre-existing pancreatitis when compared to samples from normal tissues (blue). Higher transcript per million values observed for gene - COL6A1.



**Supplementary Fig. 3:** Box plots comparing the expression profiles of 15 hub genes based on patient's drinking habits. The expression is shown for PDAC samples from daily drinkers (orange), weekly drinkers (green), occasional drinkers (brown), social drinkers (pink) and patients who did not engage in drinking activities (red). Samples from occasional drinkers show higher transcript per million values (but highly probable values make it less reliable).



**Supplementary Fig. 4:** Box plots comparing expression profiles for 15 hub genes based on the patient's race. The hub gene - FBLN1 (marked with an \*) displays an increased expression in samples from African American patients (brown) when compared to Caucasians (orange), Asians (green) and normal samples (blue).



**Supplementary Fig. 5:** Box plots comparing promoter methylation profiles for 14 hub genes between normal and PDAC samples. The gene - COL3A1 (marked with an \*) shows a deviation when compared to normal samples.