

## Supplementary File

**Figure S1:** Pathways and canonical pathways identified in the IPA functional analysis.

| Top Canonical Pathways         |          |             |
|--------------------------------|----------|-------------|
| Name                           | p-value  | Overlap     |
| Acute Phase Response Signaling | 9.94E-14 | 4.7 % 8/169 |
| LXR/RXR Activation             | 1.65E-10 | 5.0 % 6/121 |
| FXR/RXR Activation             | 2.11E-10 | 4.8 % 6/126 |
| Coagulation System             | 9.08E-09 | 11.4 % 4/35 |
| Atherosclerosis Signaling      | 1.62E-06 | 3.2 % 4/125 |

  

| Top Networks   |       |
|--|-------|
| ID Associated Network Functions  | Score |
| 1 Infectious Diseases, Inflammatory Disease, Organismal Injury and Abnormalities                 | 31    |
| 2 Cell-To-Cell Signaling and Interaction, Cellular Compromise, Cellular Function and Maintenance | 3     |

**Table S2:** Dye-switching strategy applied during labeling to avoid dye-specific bias. A total of 20 patient samples were run on 10 2D-PAGE gels. Samples were labeled randomly with Cy3 and Cy5, and a pooled sample was used as an internal standard and was stained with Cy2.

| Gel | Cy3                  | Cy5                  | Cy2           |
|-----|----------------------|----------------------|---------------|
| 1   | 1<br>(Euthyroid)     | 11<br>(Hyperthyroid) | Pooled sample |
| 2   | 12<br>(Hyperthyroid) | 2<br>(Euthyroid)     | Pooled sample |
| 3   | 5<br>(Euthyroid)     | 13<br>(Hyperthyroid) | Pooled sample |
| 4   | 14<br>(Hyperthyroid) | 3<br>(Euthyroid)     | Pooled sample |
| 5   | 15<br>(Hyperthyroid) | 6<br>(Euthyroid)     | Pooled sample |
| 6   | 16<br>(Hyperthyroid) | 4<br>(Euthyroid)     | Pooled sample |
| 7   | 7<br>(Euthyroid)     | 17<br>(Hyperthyroid) | Pooled sample |
| 8   | 18<br>(Hyperthyroid) | 8<br>(Euthyroid)     | Pooled sample |
| 9   | 9<br>(Euthyroid)     | 19<br>(Hyperthyroid) | Pooled sample |
| 10  | 20<br>(Hyperthyroid) | 10<br>(Euthyroid)    | Pooled sample |