

# PROTEOMICS

## Supporting Information for Proteomics

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**Plasma profiles in active systemic juvenile idiopathic arthritis: Biomarkers and  
biological implications**

## Supporting Information Figure legends

**Supporting Information Figure 1.** Data analysis process and sample allocation in each analysis step.

**Supporting Information Figure 2.** DIGE analysis. A. Two SJIA patient plasma samples were compared through DIGE analysis before and after the protocol of Agilent column protein depletion, demonstrating the effectiveness of depleting the plasma top 6 most abundant proteins and enriching for less abundant proteins. B. Composite gray scale image view of the 2-D Difference Gel Electrophoresis (DIGE), including all protein species from SJIA flare, SJIA quiescent, Poly JIA flare, Poly JIA quiescent, Kawasaki Disease and febrile illness control samples. Total of 89 spots (labeled by arrows) from 26 different protein precursors (right panel) were identified by mass spectrometric analysis. Different species of the same protein with different molecular weights (MW) and isoelectric points (pI) were labeled with the same index number but different alphabetical labels.

**Supporting Information Figure 3.** Quantification of the protein abundance of SJIA marker proteins through DIGE and ELISA assays. The box-whisker graphs illustrate the spread of the protein abundance of each biomarker from SJIA F/Q, KD and FI samples using either DIGE or ELISA assays. Boxes contain the 50% of values falling between the 25<sup>th</sup> and 75<sup>th</sup> percentiles; the horizontal line within the box represents the median value and the “whisker” lines extend to the highest and lowest values.