Study   Workflow

Screening cohort

ILA (n=24)   **Ctrl (n=24)**

Purification of RNA from multiples individual serum samples

x 4   x 4

Pool samples   **Pool samples**

4 RNA pools   4 RNA pools
(6 samples per pool)   (6 samples per pool)

TaqMan PCR Array (377 miRNAs)

Differentially expressed miRNAs in ILA compared to Ctrl
($p < 0.05$ and a $\log_2$ foldchange > 1.4)

7 candidate miRNAs

*Additional
5 candidate miRNAs
(associated to senescence
and IPF in literature)*

RT-qPCR
Individual serum samples

Validation cohort

ILA (n=57)   (Independent)   **Ctrl (n=88)**

Differentially expressed miRNAs in ILA compared to Ctrl
($p < 0.05$)

7 ILA-associated miRNAs

Target genes and enrichment   Receiver operator characteristic
pathway analysis   (ROC) curve analysis

Screening phase

Validation phase