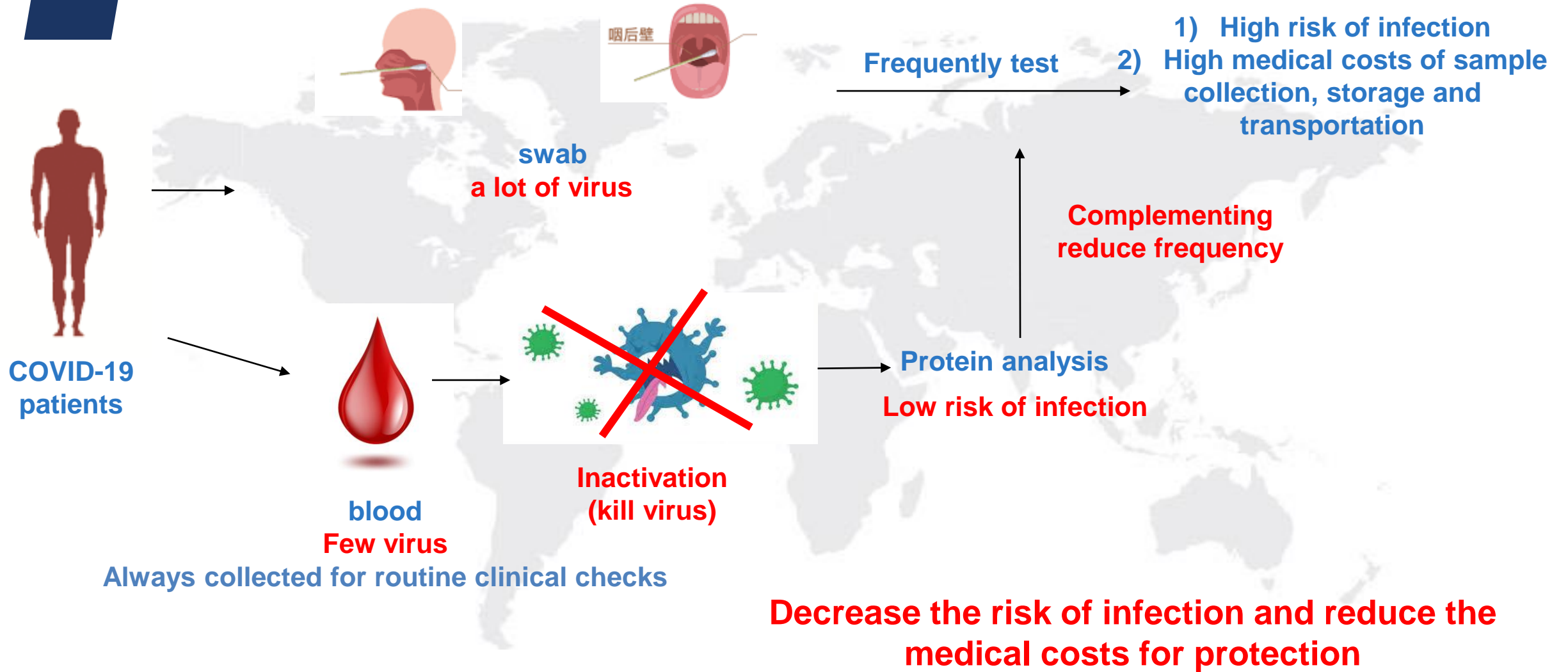


The potential use of serum proteomics for monitoring COVID-19 progression to complement RT-PCR detection

Cai Xue

Background





Severe:
1. 36 patients
2. 251 serum samples



Non-Severe:
1. 108 patients
2. 380 serum samples



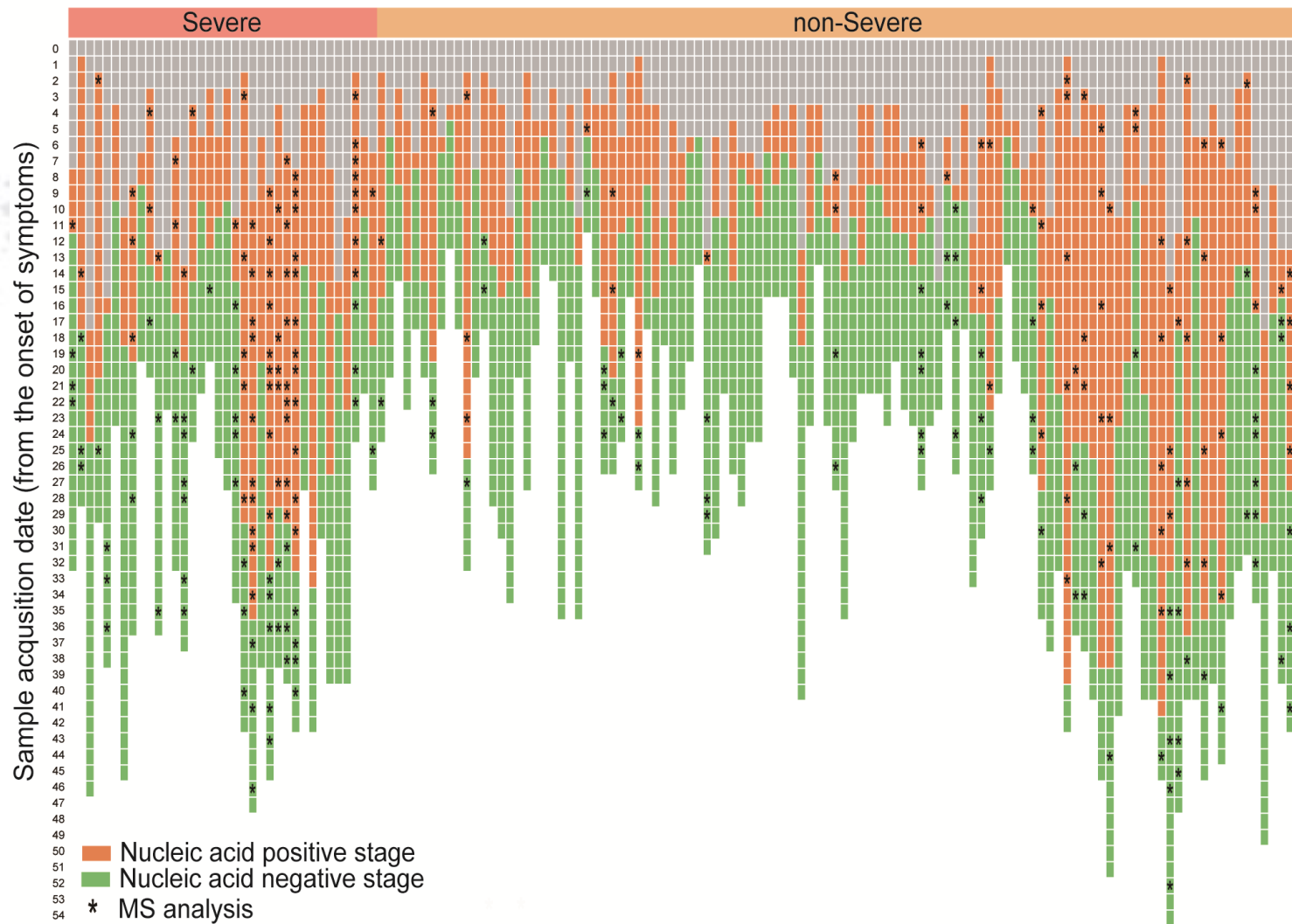
**Non-COVID:
(Ordinary flu)**
1. 24 patients
2. 24 serum samples



Healthy:
1. 21 individuals
2. 21 serum samples

Patients and samples

COVID-19 patients



Severe:

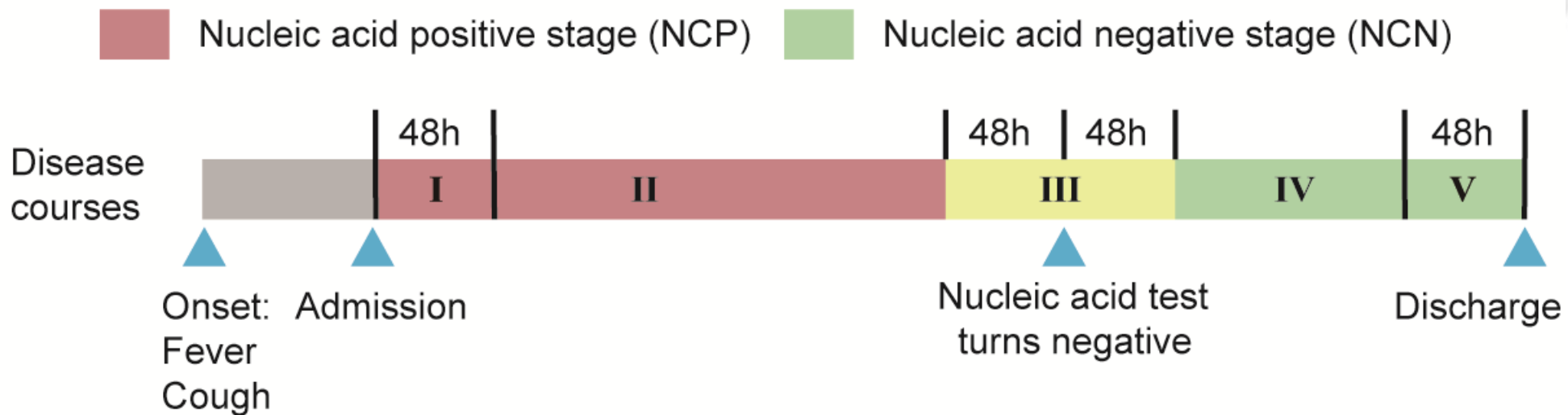
1. 36 patients
2. 251 serum samples
3. 128 serum samples for MS analysis

Non-Severe:

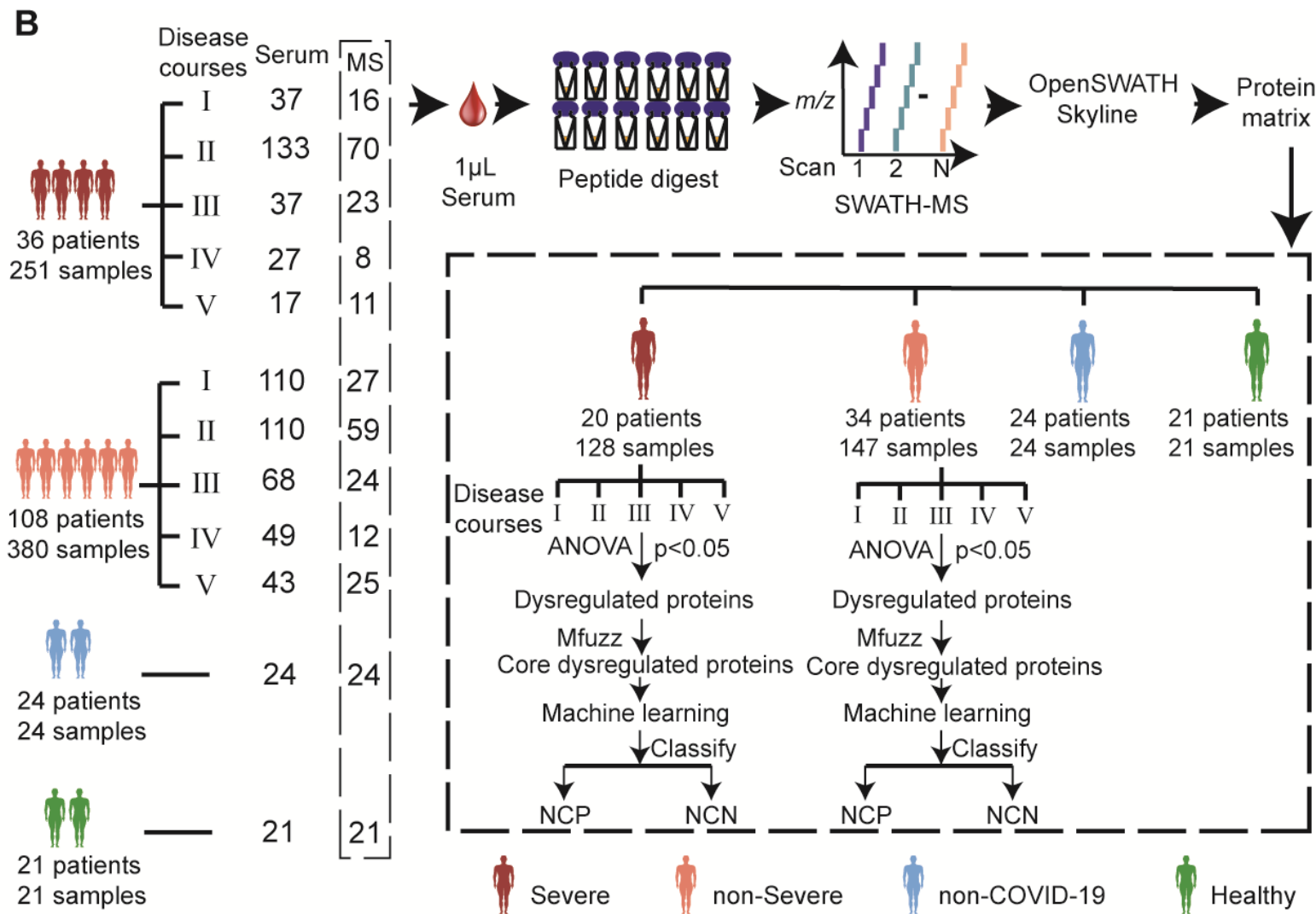
1. 108 patients
2. 380 serum samples
3. 147 serum samples for MS analysis

Five stages of the COVID-19 course

A

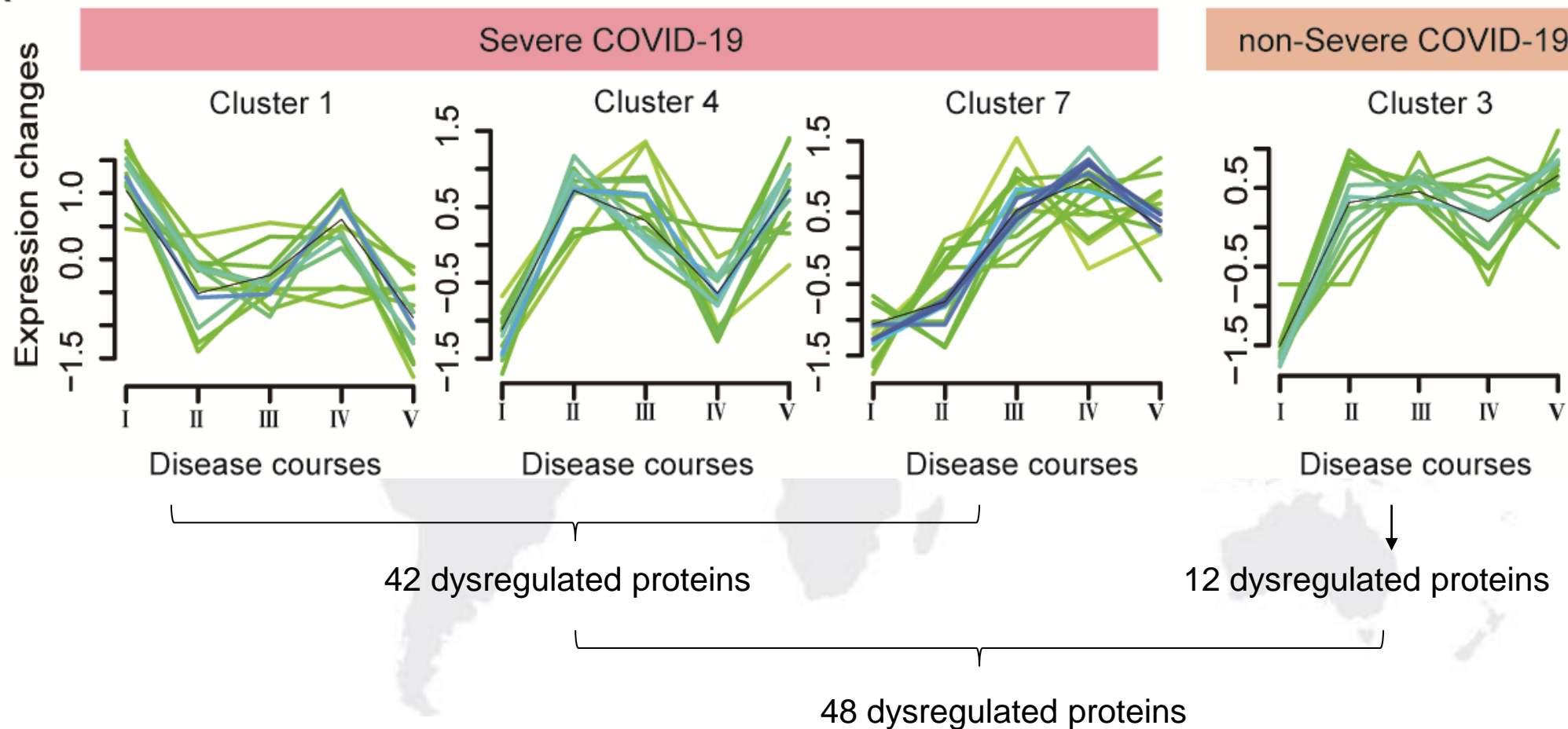


Optimization of PulseDIA

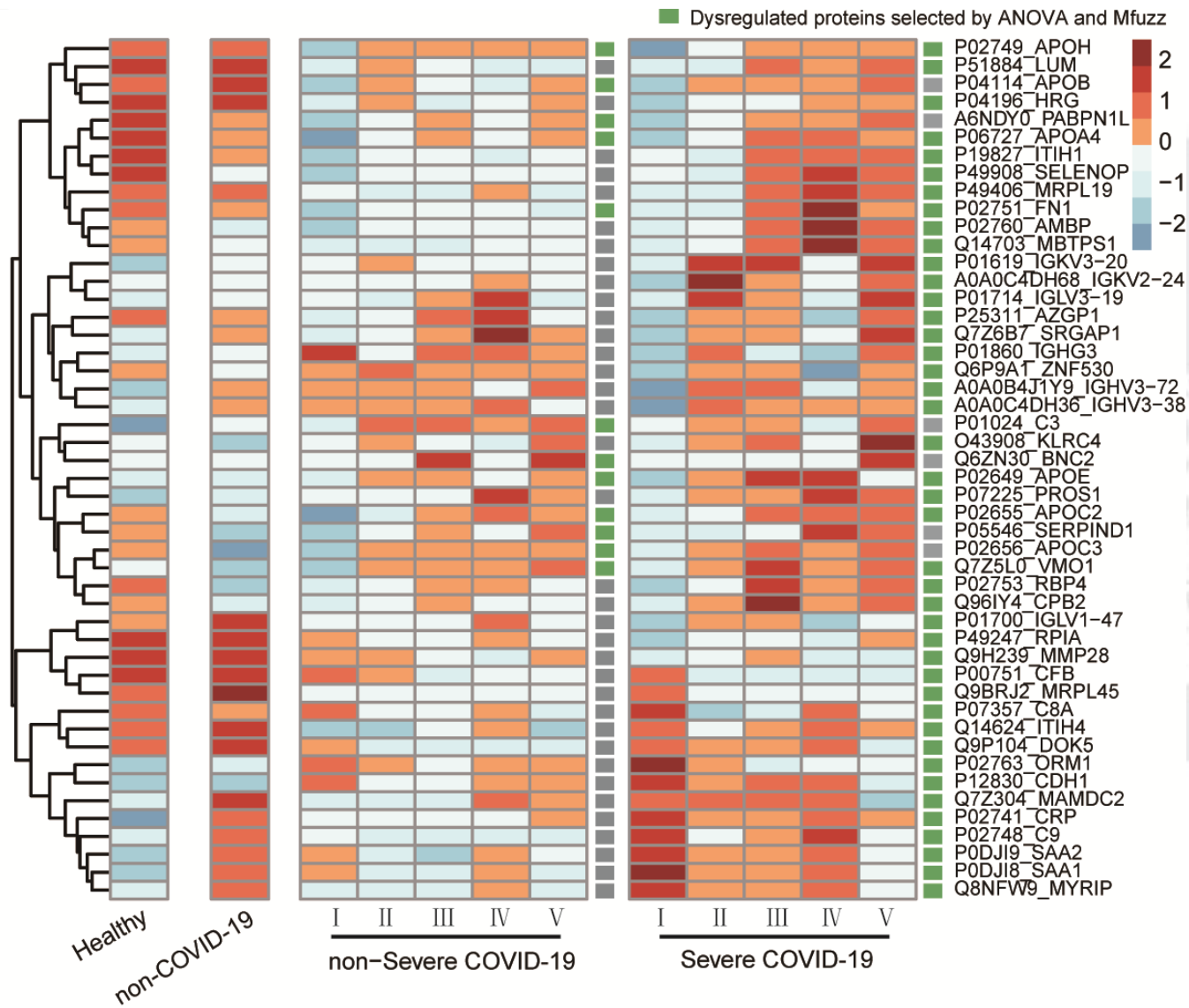


Proteins dysregulated during different stages

A

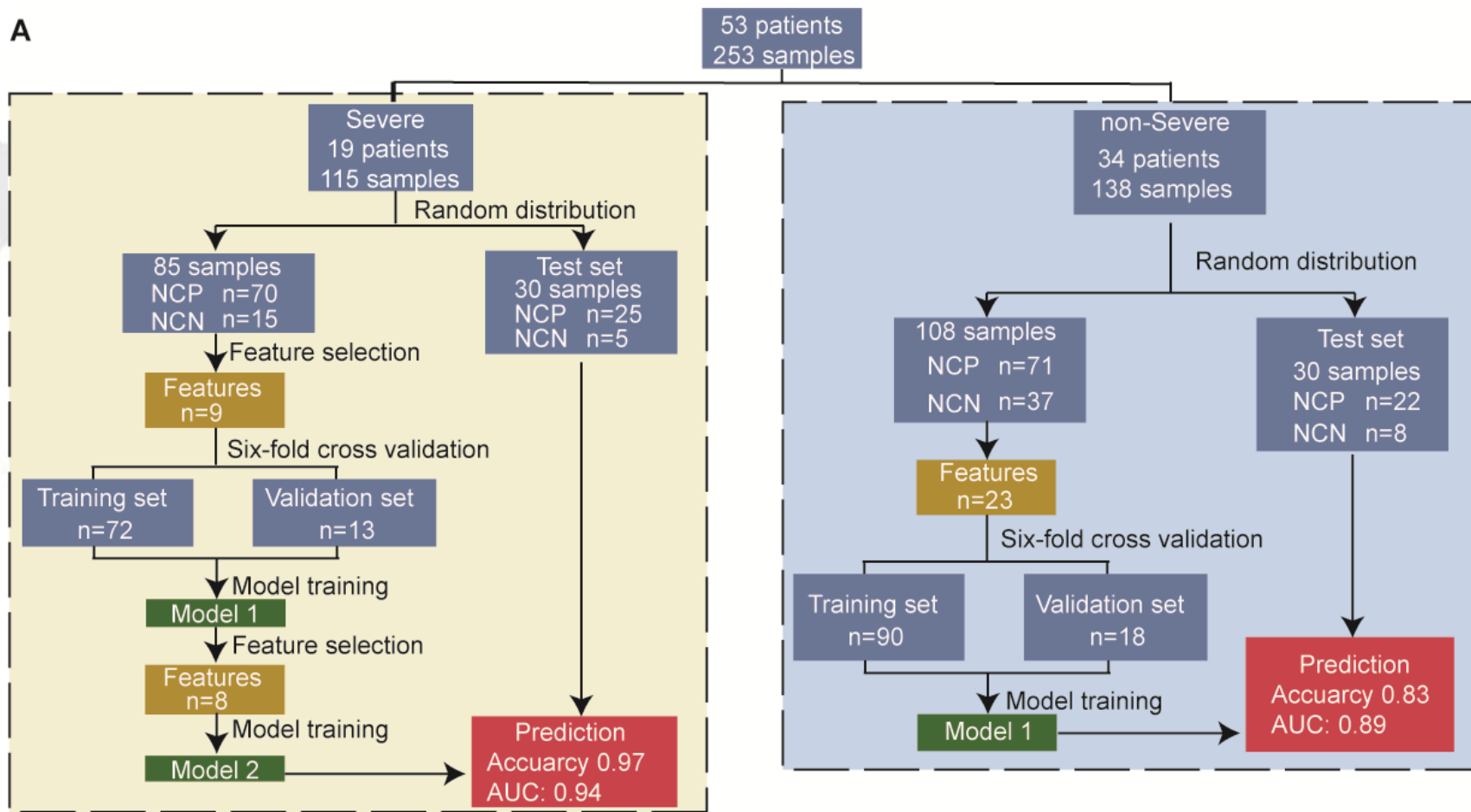


Performance of 48 dysregulated proteins



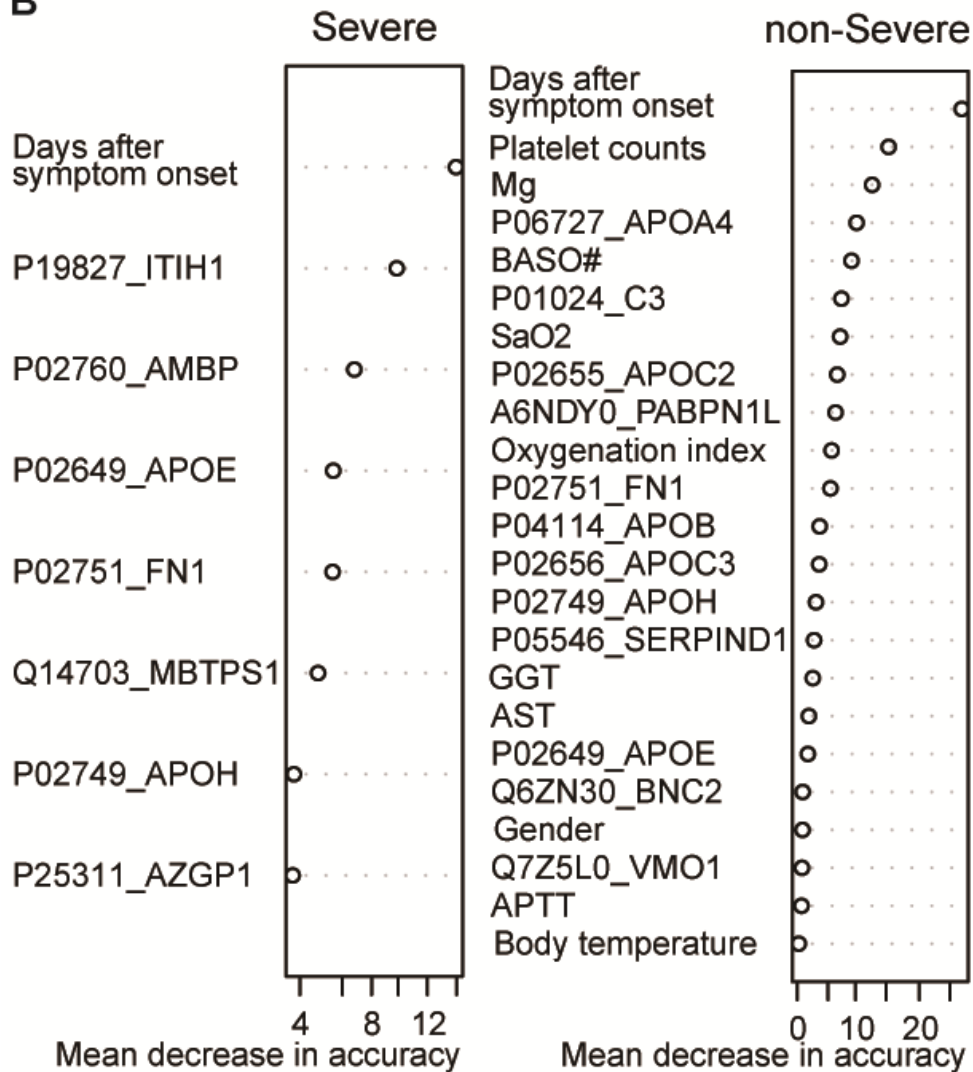
Machine learning models

A

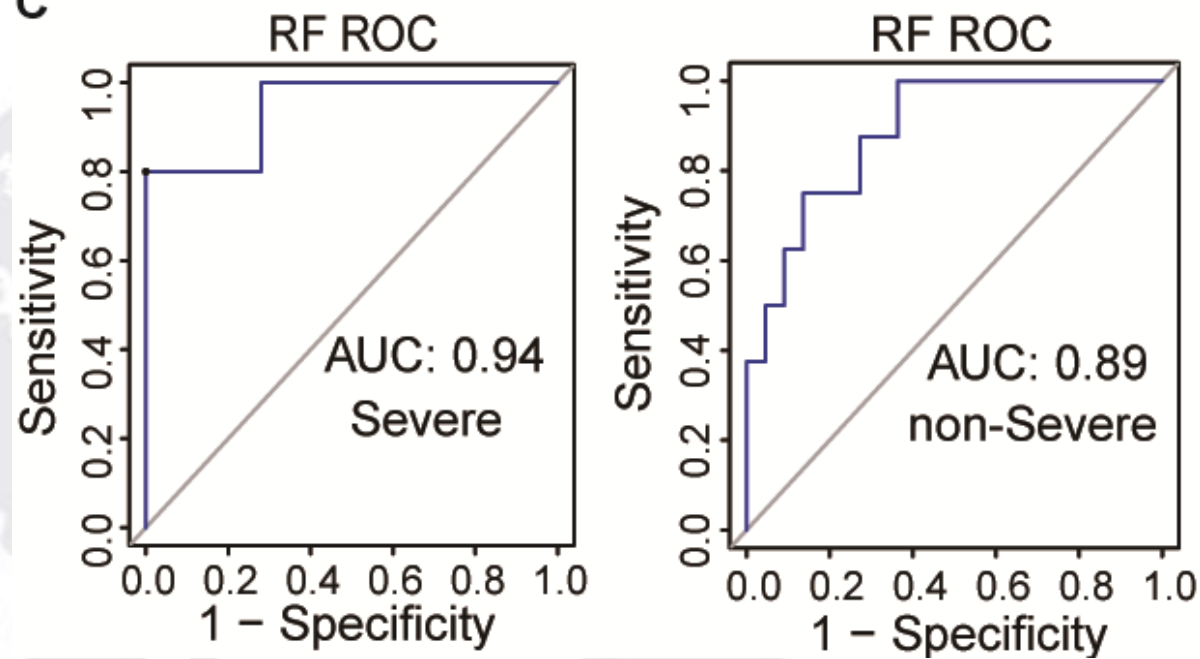


Machine learning models

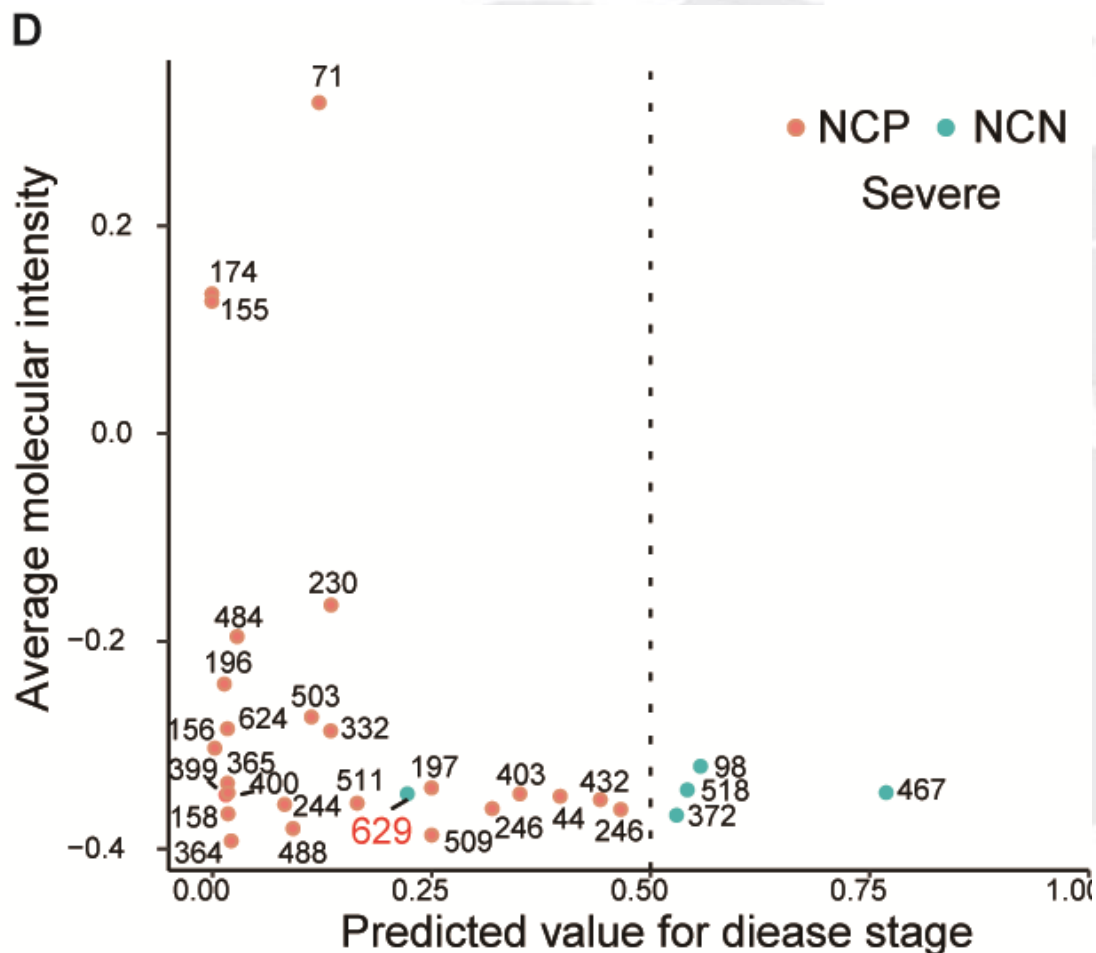
B



C



Machine learning models

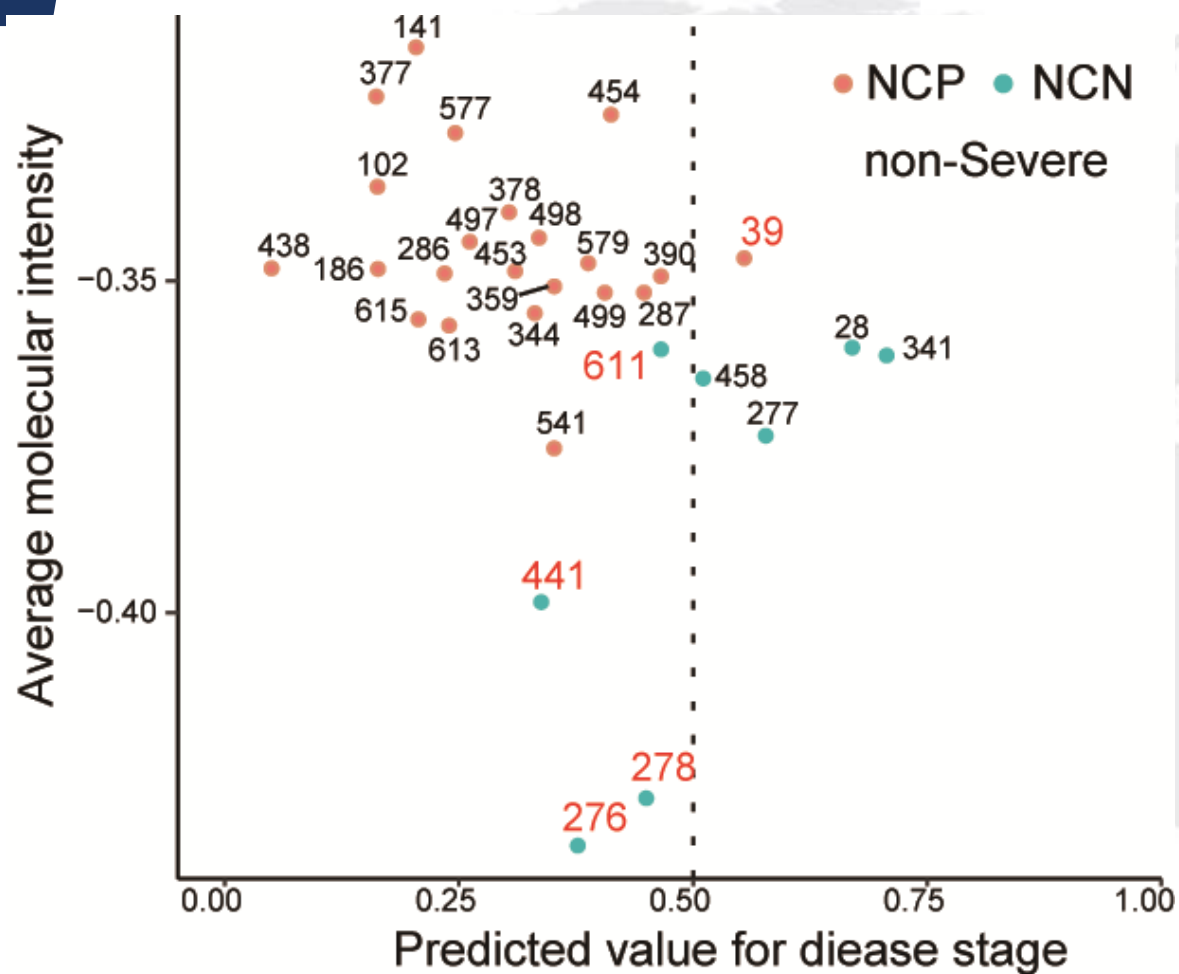


No. 629

77-year old severe female patient

- 1) Hypertension
- 2) Diabetes
- 3) renal insufficiency
- 4) type 1 respiratory failure
- 5) cardiac insufficiency
- 6) hypoproteinemia
- 7) fungal infection
- 8) aortic wall calcification
- 9) cystic lesions of the pancreas
- 10) small stones in the left kidney

Machine learning models



No. 611

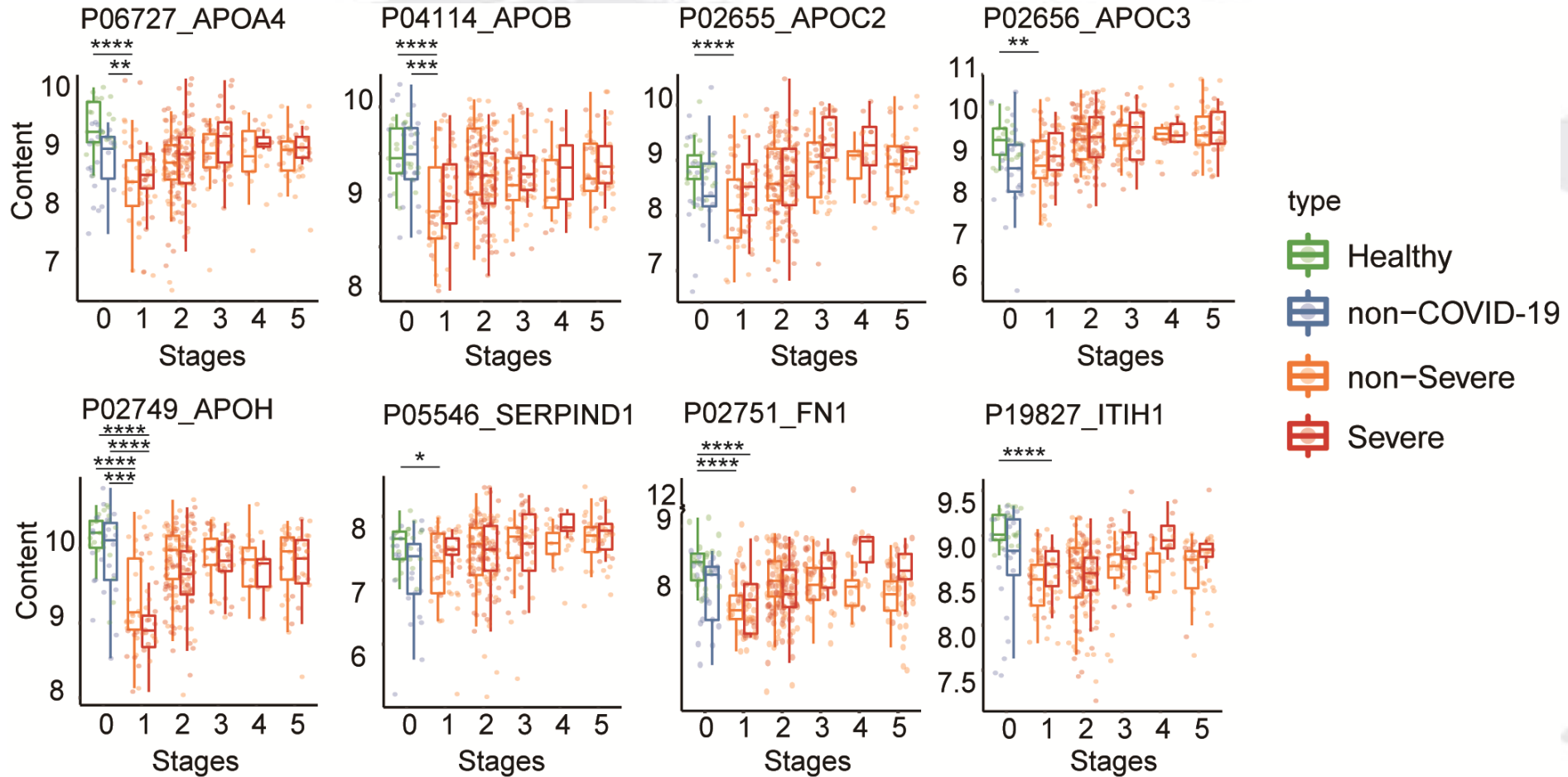
54-year old non-severe male patient positive in his stool sample collected 14 days after discharge. So this complexity of the COVID-19 viral infection may thus provide several confounding factors

No. 276,278

53-year old non-severe female patient

- 1) Uterus was removed by operation
- 2) the only patient affected by anemia.

Performance of eight significantly dysregulated proteins





THANK YOU

西湖大學
WESTLAKE UNIVERSITY