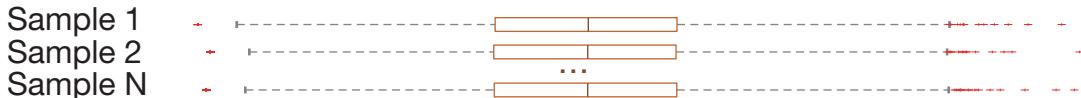


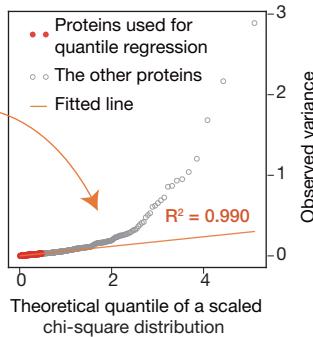
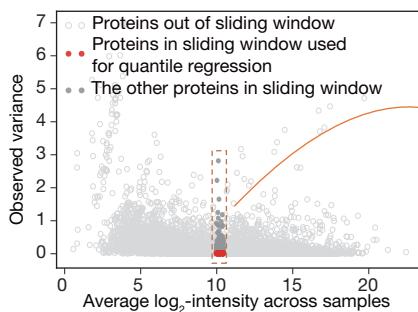
## Step 1: input data

Proteins	Sample 1	Sample 2	...	Sample N
AAAS	6900	7350	...	6515
AACS	7823	5427	...	4878
...	...	...	...	...

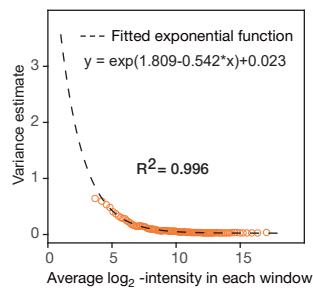
## Step 2: normalization



## Step 3: sliding-window process



## Step 4: MVC fitting



## Step 5: hypervariable analysis and z-transformation

Proteins	$\chi^2$ -statistic	P-value	Sample 1	Sample 2	...	Sample N
HBG2	748.63	6e-162	-13.40	-1.01	...	22.44
HBA1	600.67	3e-126	-12.50	8.31	...	15.64
...	...	...	...	...	...	...

$\downarrow$  z-transformed  $\log_2$ -intensities (z-statistic)