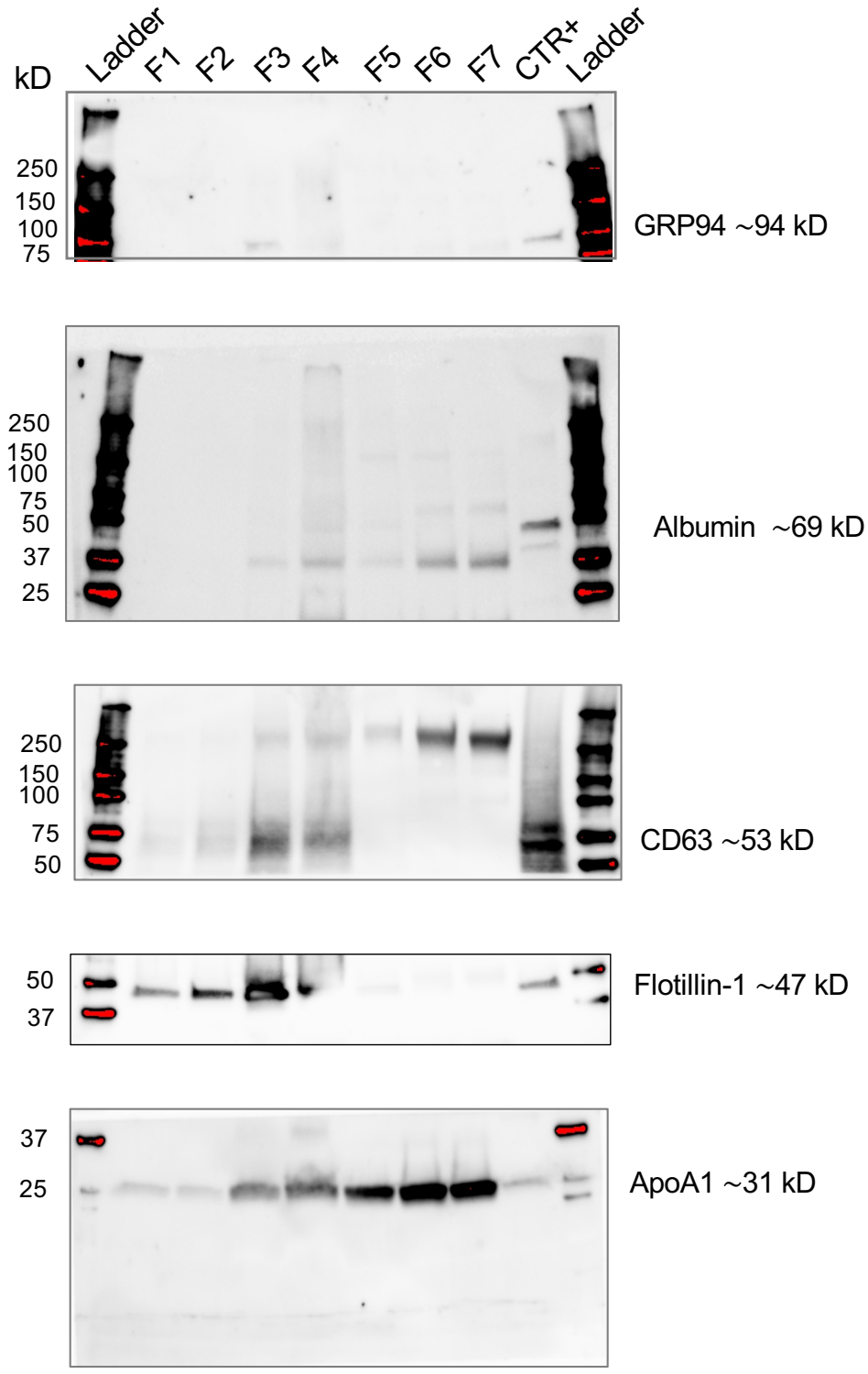
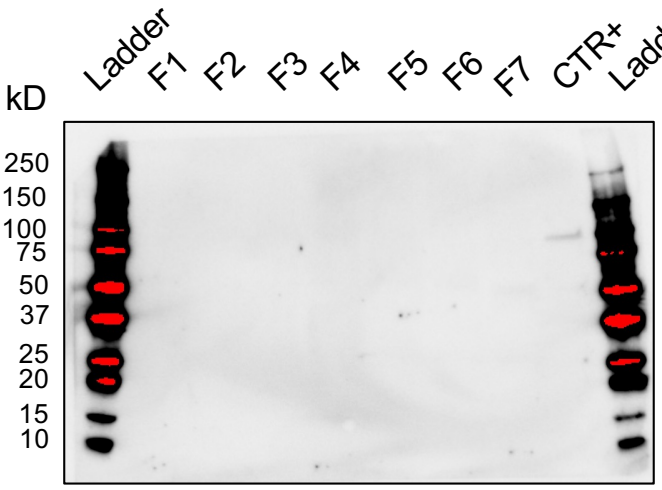
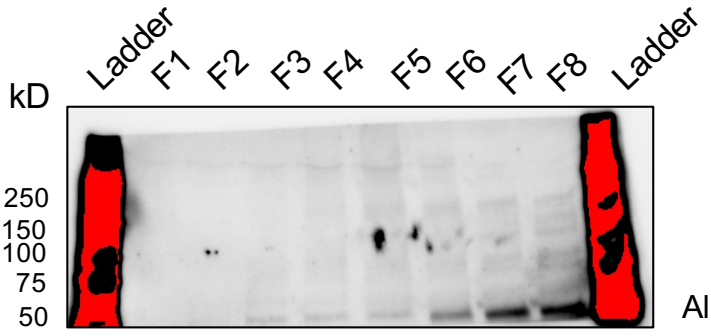
Patient 3


kD
Ladder
F1
F2
F3
F4
F5
F6
F7
CTR+
Ladder
250
150
100
75
GRP94 ~94 kD
250
150
100
75
50
37
25
Albumin ~69 kD
250
150
100
75
50
CD63 ~53 kD
50
37
Flotillin-1 ~47 kD
37
25
ApoA1 ~31 kD

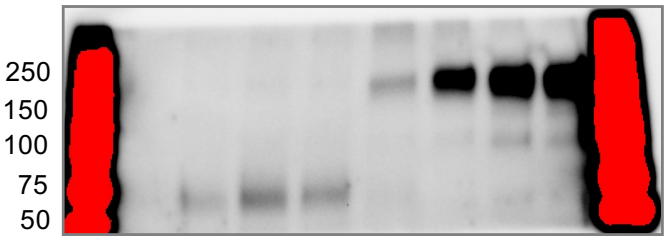
Patient 5



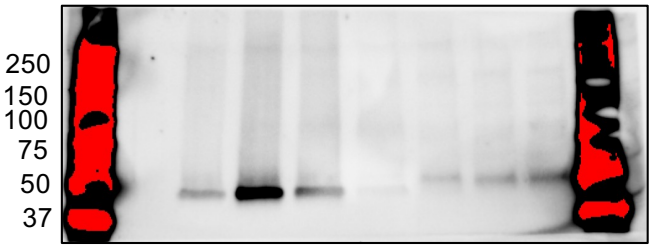
GRP94 ~94 kD



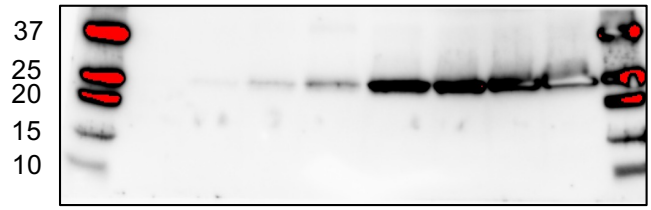
Albumin ~69 kD



CD63 ~53 kD

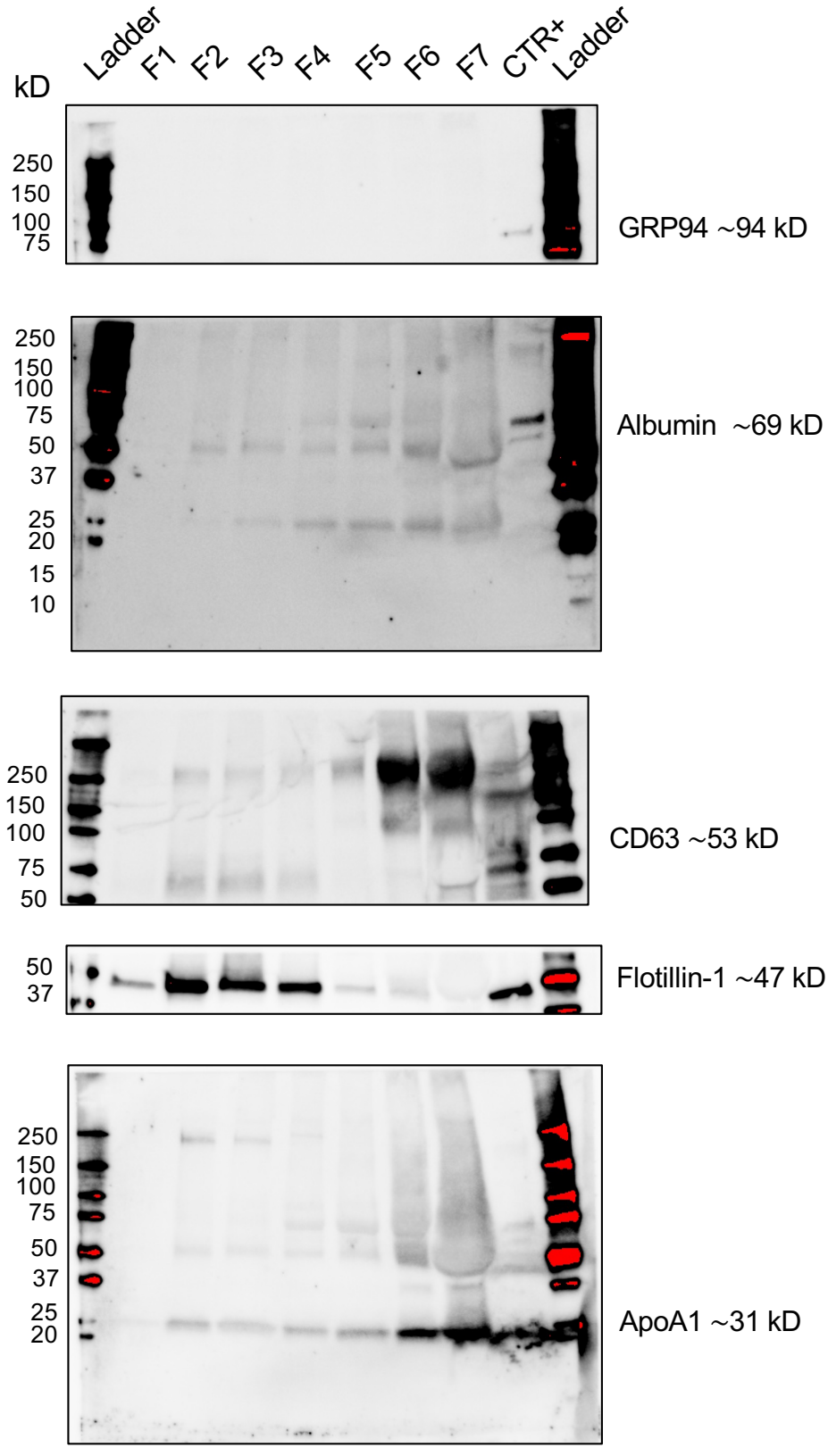


Flotillin-1 ~47 kD

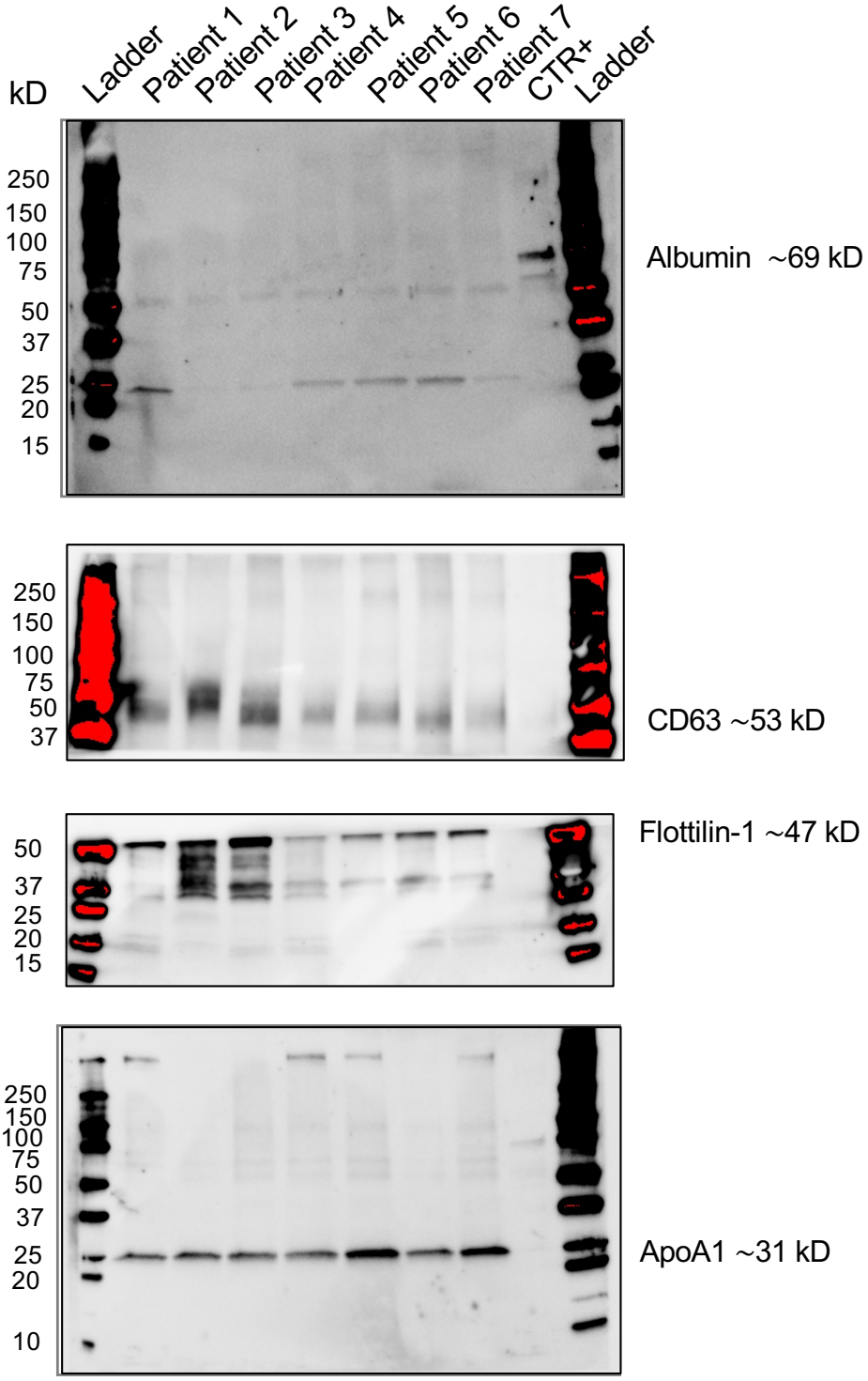


ApoA1 ~31 kD

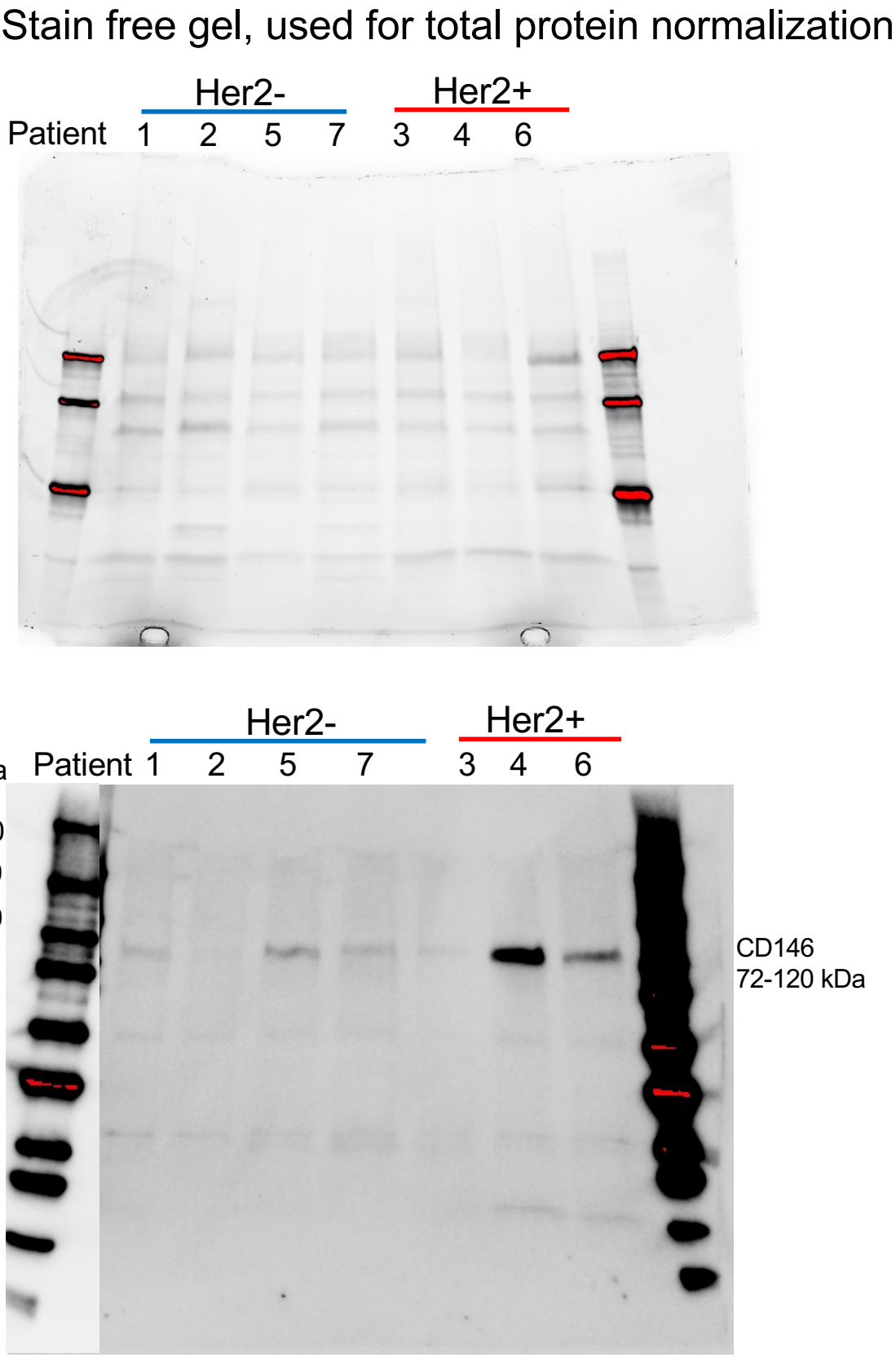
Patient 6


Ladder
F1
F2
F3
F4
F5
F6
F7
CTR+
Ladder
kD
250
150
100
75
GRP94 ~94 kD
250
150
100
75
50
37
25
20
15
10
Albumin ~69 kD
250
150
100
75
50
CD63 ~53 kD
50
37
Flotillin-1 ~47 kD
250
150
100
75
50
37
25
20
ApoA1 ~31 kD

All patients – fractions 2 - 4 combined



All patients – fractions 2 - 4 combined



Additional file 7 . Uncropped images of all western blots included in the manuscript are shown in the figure. For patient 3, 5 and 6, proteins extracted from individual SEC fractions (F1-7 or 8) were separated on the gel and blotted for GRP94, albumin, CD63, Flotillin-1 and ApoA1. Proteins extracted from patient 1-7 was analyzed for albumin, CD63, Flotillin-1, ApoA1 and CD146. In each lane, 10 µg of proteins (9 for patient 2) was loaded for pooled EV fraction 2-4 and 20 µg for individual fractions except for F1 in patient 4 and 6 where the maximum volume was loaded (2.5 and 3.4 µg respectively) due to low protein concentration in those samples. The positive control (CTR+) used was proteins extracted from MSC cell lysate (Grp94 and Flotillin-1), EVs from MSCs (CD63), human melanoma metastatic tissue (albumin and ApoA1). For CD146, the unstained gel is shown which was used for total protein normalization step.