Table S1. Clinicopathological features of melanoma patients

Gender	
Male	22
Female	16
Median Age	55.5 (23-89)
Cutaneous Sites	
Periphereal	12
Axial	26
Breslow	1.1 (*in situ*-3.5)
Ulceration	
Presence	12
Absence	26
SLN[*]	
Positive	8
Negative	30
Stages	
0	6
I [∞]	10
II [∞∞]	10
III [∞∞∞]	4
IV	8

Table S1. Clinicopathological features of melanoma patients. Axial site, for anatomic sites of primary tumor, included head, neck, and trunk, while peripheral site included upper and lower limbs; SNL indicates Sentinel Lymph Node; ∞ out of which 7 stages IA and 2 stages IB; ∞∞ out of which 5 stages IIA, 4 stage IIB and 1 stage IIC; ∞∞∞ 3 stage IIIA and 1 stage IIIB.

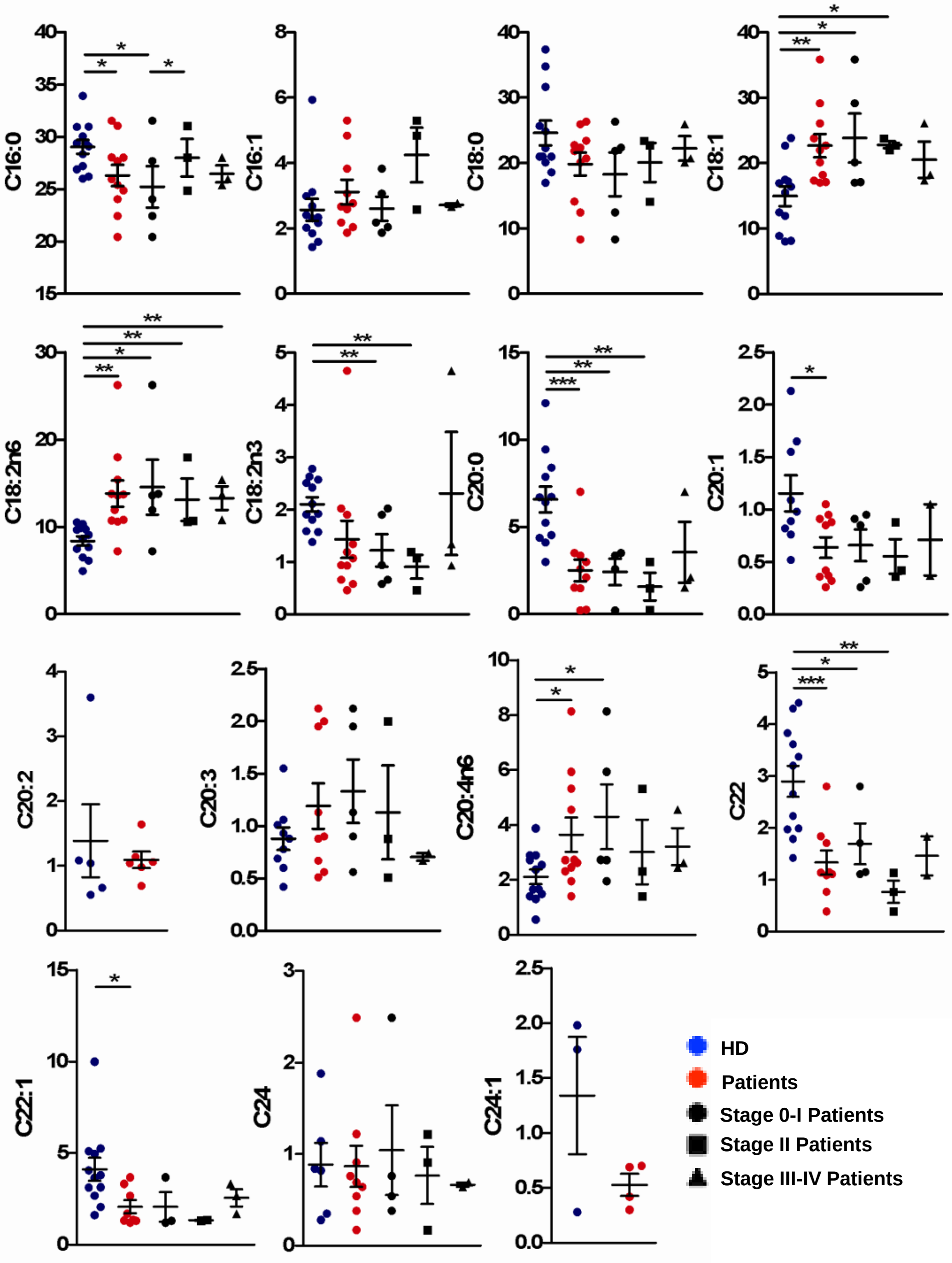

Figure S1. Fatty acids in total sEV. Single fatty acids of HD, patients, stage 0-I, stage II, and stage III-IV in total sEV. Statistical significance was achieved with unpaired t-test. * p<0.05, ** p<0.001, *** p<0.0001.

Figure S1

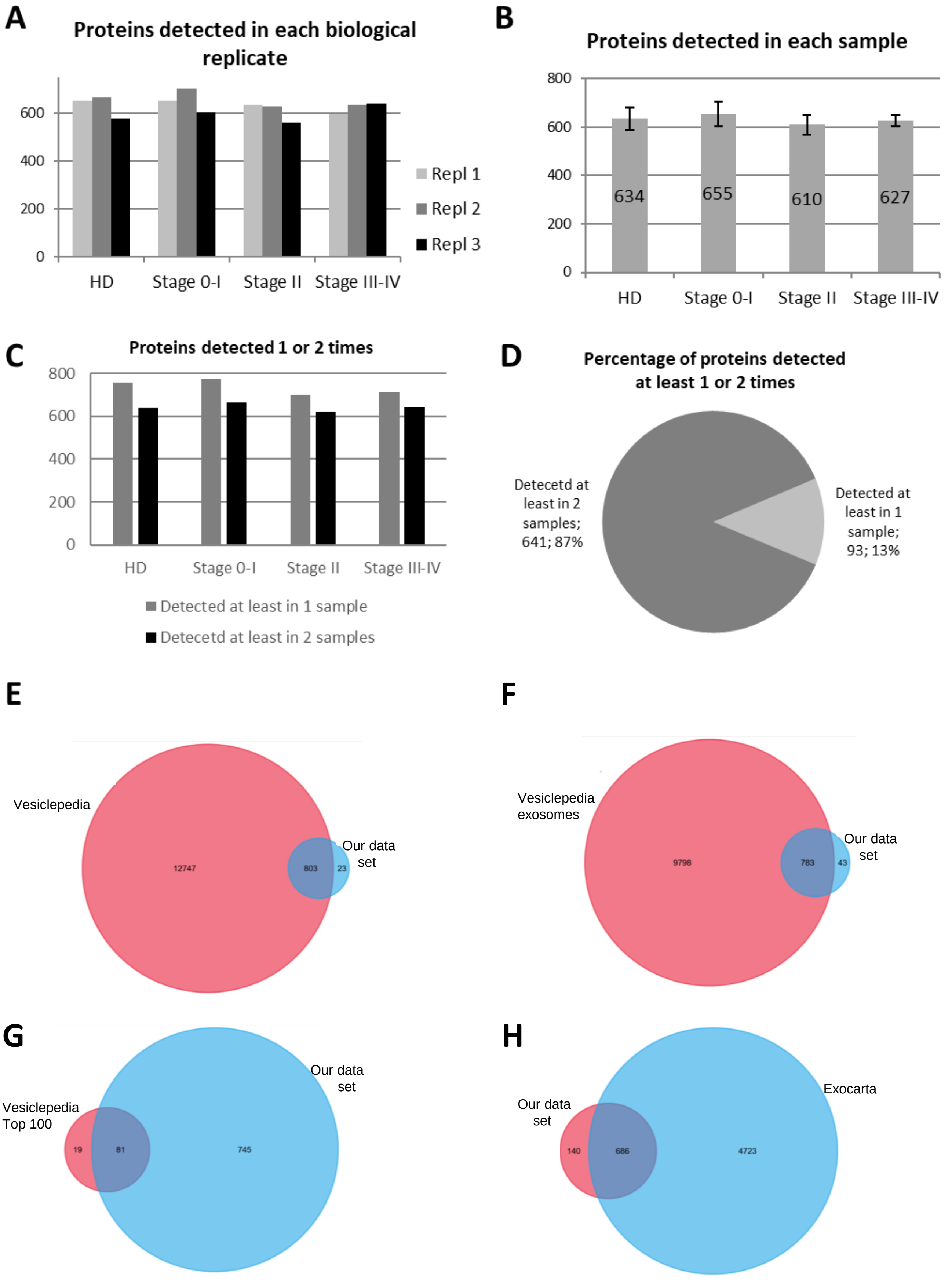
A
Proteins detected in each biological replicate
0
200
400
600
HD
Stage 0-I
Stage II
Stage III-IV
Repl 1
Repl 2
Repl 3
B
Proteins detected in each sample
0
200
400
600
800
634
655
610
627
HD
Stage 0-I
Stage II
Stage III-IV
C
Proteins detected 1 or 2 times
0
200
400
600
800
HD
Stage 0-I
Stage II
Stage III-IV
Detected at least in 1 sample
Detecetd at least in 2 samples
D
Percentage of proteins detected at least 1 or 2 times
Detecetd at least in 2 samples; 641; 87%
Detected at least in 1 sample; 93; 13%
E
Vesiclepedia
12747
803
23
Our data set
F
Vesiclepedia exosomes
9798
783
43
Our data set
G
Vesiclepedia Top 100
19
81
745
Our data set
H
Our data set
140
686
4723
Exocarta

Figure S2

Figure S2. Proteomic analysis of CD81sEV. A. Histograms representing the number of proteins detected in each biological replicate (HD, stage 0-I, stage II, stage III-IV). B. Histograms representing the average number of proteins detected for each stage group, vertical bars represent standard deviation. C. Number of proteins detected in at least one sample and in two samples for each sample group. D. Percentage of proteins detected in at least two samples (87%) or in one sample (13%). E. Comparison of experimental data with Vesiclepedia database comprehensive of all vesicle types using FunRich tool. F. Comparison of experimental data with Vesiclepedia-exosome specific database, using FunRich tool. G. Comparison of experimental data with the top 100 Vesiclepedia proteins. H. Comparison with Exocarta database.