

Supplementary Figure

A

Proteins quantified in the pSILAC dataset that matches the top 25 proteins in Exocarta

ACTB	ACTG1	ALB	ALDOA	ANXA2
ANXA5	CD63	CD81	CD9	CFL1
EEF1A1	EEF2	ENO1	GAPDH	HSP90AA1
HSP90AB1	HSPA8	LDHA	MSN	PDCD6IP
PGK1	SDCBP	YWHAE	YWHAZ	

B

Proteins quantified in the pSILAC dataset that matches the top 100 EV protein in Vesiclepedia

A2M	ACLY	ACTB	ACTN1	ACTN4
AHCY	ALB	ALDOA	ANXA1	ANXA2
ANXA5	C3	CCT2	CCT3	CCT4
CCT6A	CD63	CD81	CD9	CDC42
CFL1	CLIC1	CLTC	EEF1A1	EEF2
EIF4A1	ENO1	FASN	FLNA	FLOT1
FN1	GAPDH	GNAI2	GNAS	GNB1
GNB2	GSN	HIST1H4A	HSP90AA1	HSP90AB1
HSPA8	ITGB1	KPNB1	KRT1	KRT10
LDHA	LDHB	LGALS3BP	MYH9	PDCD6IP
PFN1	PGK1	PKM	PRDX1	RAB5C
RAB7A	RAC1	RALA	RAN	RAP1B
SDCBP	TCP1	TFRC	TLN1	TPI1
TSG101	TUBB4B	UBA1	VCP	YWHAE
YWHAG	YWHAQ	YWHAZ		

Figure S1: Number of proteins identified in Exocarta and Vesiclepedia

(A)

	Identified Proteins	Quantified Proteins
Cell Lysate	7327	6062
Lysosome	1545	1125
EVs	545	392

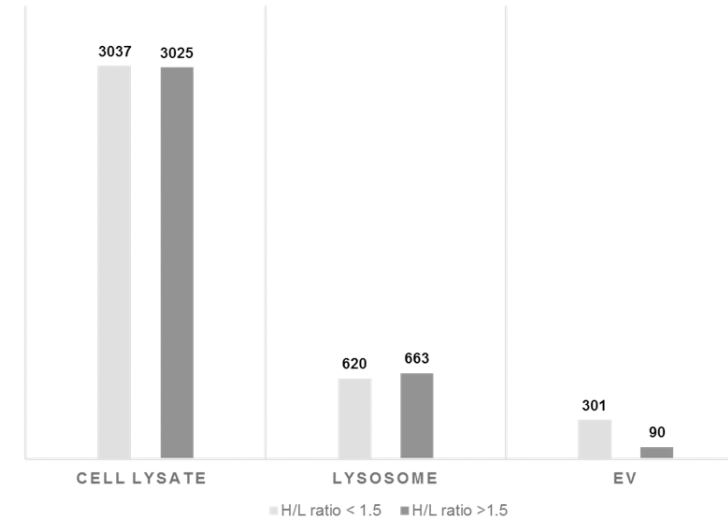
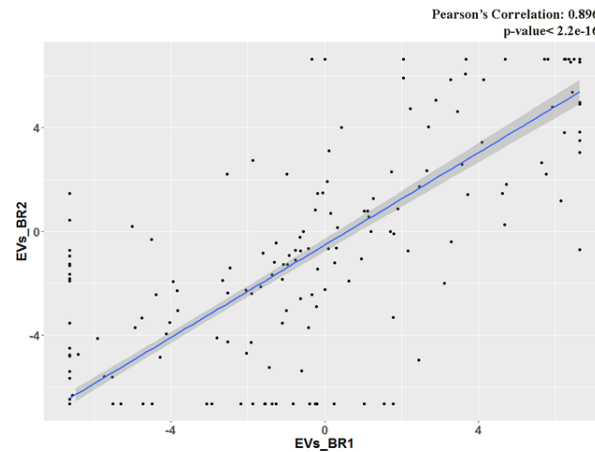
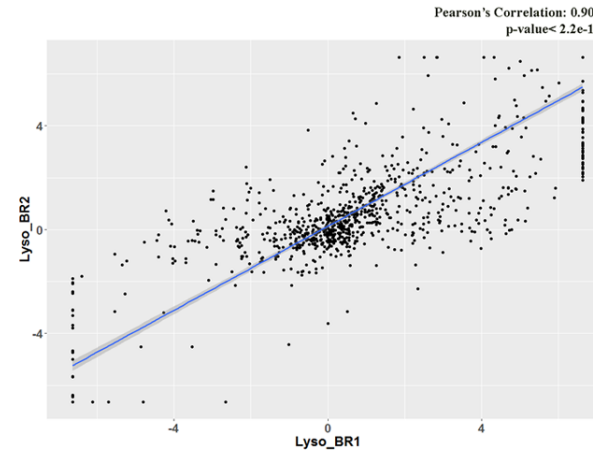
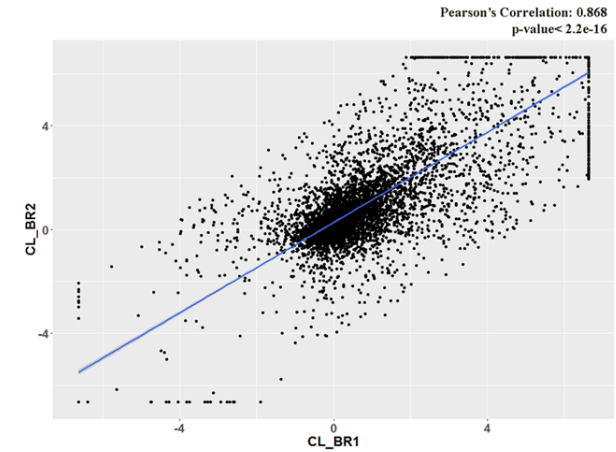
(B)**(C)****(D)****(E)**

Figure S2: pSILAC-based quantitative proteomics analysis of mHypoA 2/28 cell lysate, lysosome and EVs. (A) Summary of proteins identified in the mHypoA cell lysate, lysosome and EV proteome respectively. Proteins were considered as quantified if they were identified in both biological replicates and proteins with large variation were omitted. (B) The quantified proteins were further subcategorized to newly synthesized protein (H/L ratio > 1.5) or pre-existing protein (H/L ratio < 1.5). (C-E) Pearson's correlation coefficients between two biological replicates from the EV, lysosome and cell lysate proteomes.