Table S1. The overlap between identified sEV proteomes from three breast cancer cell lines studies identified i

UniProt ID	identified	Enzyme	Gene	Name	Risha et al., 2020
P49674	3	2.7.11.1	CSNK1E	casein kinase 1 epsilon	TRUE
Q14669	3	6.3.2.19	TRIP12	thyroid hormone receptor interactor 12	TRUE
O60245	3		PCDH7	protocadherin 7	TRUE
O60256	3		PRPSAP2	phosphoribosyl pyrophosphate synthetase	TRUE
O75475	3		PSIP1	PC4 and SFRS1 interacting protein 1	TRUE
P52926	3		HMGA2	high mobility group AT-hook 2	TRUE
Q16625	3		OCLN	occludin	TRUE
Q7Z4V5	3		HDGFL2	HDGF like 2	TRUE
Q96S44	3		TP53RK	TP53 regulating kinase	TRUE
Q9UGN5	2	2.4.2.30	PARP2	poly(ADP-ribose) polymerase 2	TRUE
P04183	2	2.7.1.21	TK1	thymidine kinase 1	FALSE
Q99755	2	2.7.1.68	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase	TRUE
Q6PHR2	2	2.7.11.1	ULK3	unc-51 like kinase 3	TRUE
P05771	2	2.7.11.13	PRKCB	protein kinase C beta	TRUE
P25098	2	2.7.11.15	GRK2	G protein-coupled receptor kinase 2	
P11802	2	2.7.11.22	CDK4	cyclin dependent kinase 4	TRUE
P49840	2	2.7.11.26	GSK3A	glycogen synthase kinase 3 alpha	FALSE
O14802	2	2.7.7.6	POLR3A	RNA polymerase III subunit A	TRUE
P06280	2	3.2.1.22	GLA	galactosidase alpha	TRUE
P27487	2	3.4.14.5	DPP4	dipeptidyl peptidase 4	
P13637	2	3.6.3.9	ATP1A3	ATPase Na+/K+ transporting subunit alpha	TRUE
Q13526	2	5.2.1.8	PIN1	peptidylprolyl cis/trans isomerase, NIMA-i	TRUE
Q9NR19	2	6.2.1.1	ACSS2	acyl-CoA synthetase short chain family member 2	
O00762	2	6.3.2.19	UBE2C	ubiquitin conjugating enzyme E2 C	TRUE
O00308	2	6.3.2.19	WWP2	WW domain containing E3 ubiquitin protein ligase 2	
Q9NRF8	2	6.3.4.2	CTPS2	CTP synthase 2	
P49916	2	6.5.1.1	LIG3	DNA ligase 3	TRUE
A1KXE4	2		FAM168B	family with sequence similarity 168 memb	TRUE
A1L170	2		C1orf226	chromosome 1 open reading frame 226	FALSE
O14910	2		LIN7A	lin-7 homolog A, crumbs cell polarity comp	TRUE
P05412	2		JUN	Jun proto-oncogene, AP-1 transcription fac	TRUE
P15260	2		IFNGR1	interferon gamma receptor 1	TRUE
P32856	2		STX2	syntaxin 2	TRUE
P34931	2		HSPA1L	heat shock protein family A (Hsp70) memb	TRUE
P36383	2		GJC1	gap junction protein gamma 1	TRUE
P46531	2		NOTCH1	notch receptor 1	TRUE
P51809	2		VAMP7	vesicle associated membrane protein 7	TRUE
P61254	2		RPL26	ribosomal protein L26	TRUE
P63027	2		VAMP2	vesicle associated membrane protein 2	TRUE
Q13253	2		NOG	noggin	TRUE
Q13330	2		MTA1	metastasis associated 1	FALSE
Q13480	2		GAB1	GRB2 associated binding protein 1	TRUE
Q14542	2		SLC29A2	solute carrier family 29 member 2	TRUE
Q14676	2		MDC1	mediator of DNA damage checkpoint 1	FALSE

Q15651	2	HMGN3	high mobility group nucleosomal binding d	TRUE
Q15768	2	EFNB3	ephrin B3	TRUE
Q4G0J3	2	LARP7	La ribonucleoprotein 7, transcriptional reg	FALSE
Q5VUB5	2	FAM171A1	family with sequence similarity 171 memb	TRUE
Q7Z2K8	2	GPRIN1	G protein regulated inducer of neurite out	TRUE
Q86UY6	2	NAA40	N-alpha-acetyltransferase 40, NatD catalyt	TRUE
Q8N0X7	2	SPART	spartin	TRUE
Q8NBA8	2	DTWD2	DTW domain containing 2	TRUE
Q96KN1	2	LRATD2	LRAT domain containing 2	FALSE
Q96Q45	2	TMEM237	transmembrane protein 237	TRUE
Q99614	2	TTC1	tetratricopeptide repeat domain 1	TRUE
Q99986	2	VRK1	VRK serine/threonine kinase 1	TRUE
Q9BRG1	2	VPS25	vacuolar protein sorting 25 homolog	TRUE
Q9BRP1	2	PDCD2L	programmed cell death 2 like	TRUE
Q9BSA4	2	TTYH2	tweety family member 2	TRUE
Q9BWQ6	2	YIPF2	Yip1 domain family member 2	TRUE
Q9BX67	2	JAM3	junctional adhesion molecule 3	TRUE
Q9BYG3	2	NIFK	nucleolar protein interacting with the FHA	TRUE
Q9H6S0	2	YTHDC2	YTH domain containing 2	TRUE
Q9H8Y8	2	GORASP2	golgi reassembly stacking protein 2	TRUE
Q9H910	2	JPT2	Jupiter microtubule associated homolog 2	TRUE
Q9HAT8	2	PELI2	pellino E3 ubiquitin protein ligase family m	TRUE
Q9NRN7	2	AASDHPPT	aminoadipate-semialdehyde dehydrogena	TRUE
Q9NV92	2	NDFIP2	Nedd4 family interacting protein 2	TRUE
Q9NWV8	2	BABAM1	BRISC and BRCA1 A complex member 1	FALSE
Q9NXU5	2	ARL15	ADP ribosylation factor like GTPase 15	TRUE
Q9Y666	2	SLC12A7	solute carrier family 12 member 7	TRUE
O00479	2	HMGN4	high mobility group nucleosomal binding domain 4	
O15551	2	CLDN3	claudin 3	
O43314	2	PPIP5K2	diphosphoinositol pentakisphosphate kinase 2	
O43581	2	SYT7	synaptotagmin 7	
O94964	2	SOGA1	suppressor of glucose, autophagy associated 1	
O95049	2	TJP3	tight junction protein 3	
P05204	2	HMGN2	high mobility group nucleosomal binding domain 2	
P42858	2	HTT	huntingtin	
P46019	2	PHKA2	phosphorylase kinase regulatory subunit alpha 2	
P48634	2	PRRC2A	proline rich coiled-coil 2A	
P49447	2	CYB561	cytochrome b561	
P52569	2	SLC7A2	solute carrier family 7 member 2	
Q13523	2	PRPF4B	pre-mRNA processing factor 4B	
Q14694	2	USP10	ubiquitin specific peptidase 10	
Q15059	2	BRD3	bromodomain containing 3	
Q15773	2	MLF2	myeloid leukemia factor 2	
Q5VT52	2	RPRD2	regulation of nuclear pre-mRNA domain containing 2	
Q86X27	2	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	
Q8IY67	2	RAVER1	ribonucleoprotein, PTB binding 1	
Q8N1G2	2	CMTR1	cap methyltransferase 1	

Q8TAB3	2	PCDH19	protocadherin 19
Q8TD19	2	NEK9	NIMA related kinase 9
Q8TE59	2	ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif 19
Q92625	2	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A
Q96FV9	2	THOC1	THO complex 1
Q96JB3	2	HIC2	HIC ZBTB transcriptional repressor 2
Q96Q15	2	SMG1	SMG1 nonsense mediated mRNA decay associated PI3K related kin
Q9C0J8	2	WDR33	WD repeat domain 33
Q9H4A3	2	WNK1	WNK lysine deficient protein kinase 1
Q9HCG8	2	CWC22	CWC22 spliceosome associated protein homolog
Q9NQ55	2	PPAN	peter pan homolog
Q9NZT2	2	OGFR	opioid growth factor receptor
Q9UKL0	2	RCOR1	REST corepressor 1
Q9Y2I8	2	WDR37	WD repeat domain 37
Q9Y5J1	2	UTP18	UTP18 small subunit processome component

Table S2. Gene ontology enrichment result using Biological Process terms for 106 overlapping BC p

ID	Description	GeneRatio	BgRatio	pvalue
GO:0055021	regulation of cardiac muscle tissue growth	4/101	14/5040	0.000130353
GO:0060420	regulation of heart growth	4/101	16/5040	0.000229796
GO:0006281	DNA repair	12/101	190/5040	0.000365174
GO:0055017	cardiac muscle tissue growth	4/101	21/5040	0.000699607
GO:0017156	calcium-ion regulated exocytosis	4/101	22/5040	0.000842013
GO:0046620	regulation of organ growth	4/101	22/5040	0.000842013
GO:0035633	maintenance of blood-brain barrier	4/101	23/5040	0.001003717
GO:0060419	heart growth	4/101	23/5040	0.001003717
GO:0007267	cell-cell signaling	19/101	452/5040	0.001350768
GO:1990573	potassium ion import across plasma membrane	3/101	12/5040	0.001506902
GO:0018209	peptidyl-serine modification	9/101	137/5040	0.001560456
GO:0006974	cellular response to DNA damage stimulus	14/101	288/5040	0.001630197
GO:0071805	potassium ion transmembrane transport	5/101	44/5040	0.00170945
GO:0000077	DNA damage checkpoint signaling	5/101	45/5040	0.001892966
GO:0006836	neurotransmitter transport	6/101	67/5040	0.002072909
GO:0042770	signal transduction in response to DNA damage	6/101	67/5040	0.002072909
GO:0031570	DNA integrity checkpoint signaling	5/101	47/5040	0.002302719
GO:0001505	regulation of neurotransmitter levels	6/101	71/5040	0.002789448
GO:0019083	viral transcription	3/101	15/5040	0.00298322
GO:0006302	double-strand break repair	7/101	97/5040	0.0030966
GO:0044773	mitotic DNA damage checkpoint signaling	4/101	31/5040	0.003154492
GO:0018105	peptidyl-serine phosphorylation	8/101	124/5040	0.003192987
GO:0006813	potassium ion transport	5/101	51/5040	0.003310622
GO:0007269	neurotransmitter secretion	5/101	51/5040	0.003310622
GO:0031398	positive regulation of protein ubiquitination	5/101	51/5040	0.003310622
GO:0099643	signal release from synapse	5/101	51/5040	0.003310622
GO:0044774	mitotic DNA integrity checkpoint signaling	4/101	32/5040	0.003550366
GO:0032869	cellular response to insulin stimulus	7/101	100/5040	0.00367479
GO:2001020	regulation of response to DNA damage stimulus	7/101	101/5040	0.003884737

roteins vs. all identified cell li

p.adjust	qvalue
0.000130353	0.230763136
0.000229796	0.230763136
0.000365174	0.244474197
0.000699607	0.251985755
0.000842013	0.251985755
0.000842013	0.251985755
0.001003717	0.251985755
0.001003717	0.251985755
0.001350768	0.255735473
0.001506902	0.255735473
0.001560456	0.255735473
0.001630197	0.255735473
0.00170945	0.255735473
0.001892966	0.255735473
0.002072909	0.255735473
0.002072909	0.255735473
0.002302719	0.255735473
0.002789448	0.255735473
0.00298322	0.255735473
0.0030966	0.255735473
0.003154492	0.255735473
0.003192987	0.255735473
0.003310622	0.255735473
0.003310622	0.255735473
0.003310622	0.255735473
0.003310622	0.255735473
0.003550366	0.263590221
0.00367479	0.263590221
0.003884737	0.26904094

ine proteins.

geneID	Count
NOTCH1/GSK3A/NOG/PARP2	4
NOTCH1/GSK3A/NOG/PARP2	4
CSNK1E/LIG3/HMGA2/MTA1/TRIP12/MDC1/HDGFL2/BABAM1/PARP2/USP10/SMG1/WDR33	12
NOTCH1/GSK3A/NOG/PARP2	4
NOTCH1/VAMP7/VAMP2/SYT7	4
NOTCH1/GSK3A/NOG/PARP2	4
OCLN/JAM3/CLDN3/TJP3	4
NOTCH1/GSK3A/NOG/PARP2	4
LIN7A/PRKCB/STX2/GJC1/NOTCH1/CSNK1E/GSK3A/VAMP7/HMGA2/VAMP2/NOG/PIN1/HM	19
ATP1A3/SLC12A7/WNK1	3
PRKCB/CSNK1E/HMGA2/ULK3/VRK1/PARP2/GRK2/SMG1/WNK1	9
CSNK1E/LIG3/HMGA2/RPL26/MTA1/TRIP12/MDC1/HDGFL2/BABAM1/PARP2/USP10/THOC1/	14
ATP1A3/VAMP2/SLC12A7/WWP2/WNK1	5
HMGA2/RPL26/MDC1/BABAM1/THOC1	5
LIN7A/PRKCB/STX2/VAMP2/SLC29A2/SYT7	6
HMGA2/RPL26/MDC1/BABAM1/USP10/THOC1	6
HMGA2/RPL26/MDC1/BABAM1/THOC1	5
LIN7A/PRKCB/STX2/VAMP2/SLC29A2/SYT7	6
JUN/HMGA2/LARP7	3
LIG3/HMGA2/MTA1/TRIP12/HDGFL2/BABAM1/PARP2	7
HMGA2/RPL26/MDC1/BABAM1	4
PRKCB/CSNK1E/HMGA2/ULK3/VRK1/GRK2/SMG1/WNK1	8
ATP1A3/VAMP2/SLC12A7/WWP2/WNK1	5
LIN7A/PRKCB/STX2/VAMP2/SYT7	5
UBE2C/GSK3A/MTA1/PIN1/NDFIP2	5
LIN7A/PRKCB/STX2/VAMP2/SYT7	5
HMGA2/RPL26/MDC1/BABAM1	4
PRKCB/CDK4/GSK3A/VAMP2/GAB1/SLC29A2/SOGA1	7
HMGA2/RPL26/TRIP12/HDGFL2/BABAM1/THOC1/SMG1	7

Table 3. Proteins that are related to cell-cell signaling function in Gene Ontology anal

UniProt ID	Gene	Protein Name
O14910	LIN7A	lin-7 homolog A, crumbs cell polarity complex component
P05771	PRKCB*	protein kinase C beta
P32856	STX2	syntaxin 2
P36383	GJC1	gap junction protein gamma 1
P46531	NOTCH1	notch receptor 1
P49674	CSNK1E*	casein kinase 1 epsilon
P49840	GSK3A*	glycogen synthase kinase 3 alpha
P51809	VAMP7	vesicle associated membrane protein 7
P52926	HMGA2	high mobility group AT-hook 2
P63027	VAMP2	vesicle associated membrane protein 2
Q13253	NOG	noggin
Q13526	PIN1*	peptidylprolyl cis/trans isomerase, NIMA-interacting 1
Q15651	HMGN3	high mobility group nucleosomal binding domain 3
Q15768	EFNB3	ephrin B3
Q96Q45	TMEM237	transmembrane protein 237
Q9Y666	SLC12A7	solute carrier family 12 member 7
O43581	SYT7	synaptotagmin 7
P25098	GRK2*	G protein-coupled receptor kinase 2
Q9H4A3	WNK1	WNK lysine deficient protein kinase 1

ysis. * indicates that the protein is an enzyme. T indicates the enzymes are identified in the p

Risha *et al.*	**Minic *et al.***	**Rontogianni *et al.***	**Muraoka *et al.***
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roteomic data from the published BC cell lines studies.

n at least two out of the three studies.

Minic et al., 2022	Rontogianni et al., 2(	Muraoka et al., 2022
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