

Electronic Supplementary Material

Proteomic Profiling of Purified Rabies Virus Particles

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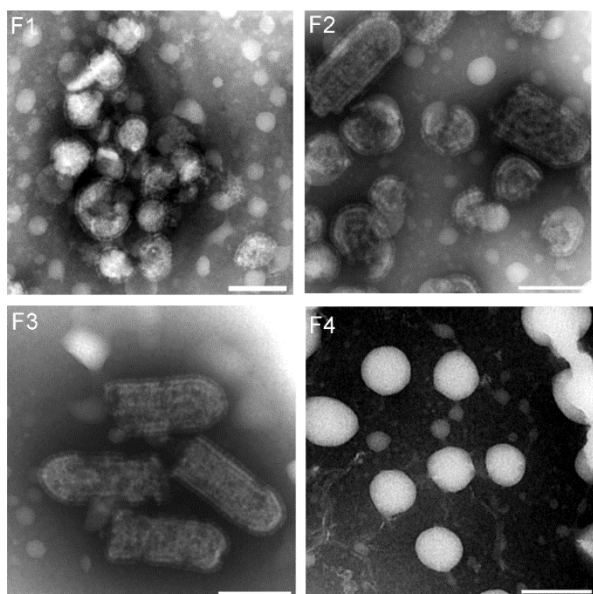


Fig. S1 EM examination of four fraction bands (F1, F2, F3 and F4) in iodixanol density gradient in Fig. 1A (Scale bar = 100 nm)

Table S1 Function classification of host proteins according to their GO annotation.

Function classification	GO_ID	Term	Proein name
Endocytosis	GO:0006897	endocytosis	RAC1, CDC42, SNX, nWASP
	GO:0045807	positive regulation of endocytosis	CD151, CD63
Cell adhesion	GO:0007155	cell adhesion	CD9, RAC1
	GO:0045785	positive regulation of cell adhesion	CD63
	GO:0098609	cell-cell adhesion	CDC42, Ezrin
	GO:0007157	heterophilic cell-cell adhesion via plasmamembrane cell adhesion molecules	Galectin-1
Cytoskeleton organization	GO:0030036	actin cytoskeleton organization	RAC1, Syntenin-1, PACSIN2, CDC42, HSJ-2, nWASP
	GO:0007010	cytoskeleton organization	Cofilin-1
	GO:0000226	microtubule cytoskeleton organization	GAPDH, Tubulin β -5
	GO:0030866	cortical actin	ARF6, β -actin
	GO:0030836	cytoskeletonorganization positive regulation of actin filament depolymerization	Destrin
Regulation of gene expression	GO:0010628	positive regulation of gene expression	HSC70, DDX3X, Ezrin
	GO:0010629	negative regulation of gene expression	RACK1
Transcription	GO:0006357	regulation of transcription by RNA polymerase II	RhoA
	GO:0045892	negative regulation of transcription, DNA-templated	HSJ-2
	GO:0045944	positive regulation of transcription by RNA polymerase II	DDX3X, PCBP1, nWASP
	GO:0045892	negative regulation of transcription, DNA-templated	TSG101
	GO:0000122	negative regulation of transcription by RNA polymerase II	Ezrin
Translation	GO:0017148	negative regulation of translation	GAPDH, RACK1
	GO:0045901	positive regulation of translational elongation	EIF5a
	GO:0045727	positive regulation of translation	RhoA
	GO:0045948	positive regulation of translational initiation	DDX3X
Transport	GO:0015031	protein transport	ARF3, CD63, Alix, SNX, TSG101, CHMP2A, ARF6, VPS37B, VPS4B
	GO:0006886	intracellular protein transport	Rab-5C, Rab-7A
	GO:0035721	intraciliary retrograde transport	DL8
	GO:0015804	neutral amino acid transport	SLC3, SLC1
	GO:0051223	regulation of protein transport	HSP40
	GO:0042147	retrograde transport, endosome to Golgi	VAMP3
Protein localization	GO:0072659	protein localization to plasma membrane	RAC1, Ezrin
	GO:1905873	positive regulation of protein localization to cell leading edge	Cofilin-1
	GO:0008104	protein localization	CD81, RACK1
	GO:0036010	protein localization to endosome	PACSIN2, ARF6
	GO:0034613	cellular protein localization	CD63, CDC42
	GO:0034504	protein localization to nucleus	HSJ-2
GO:2000010	positive regulation of protein localization to cell surface	HSP90 β	

Protein ubiquitination	GO:0051683	establishment of Golgi localization	14-3-3 ζ/θ
	GO:0016567	protein ubiquitination	Ubc, Ube2, RACK1
	GO:0031397	negative regulation of protein ubiquitination	HSP40, VPS28
Morphogenesis	GO:0031396	regulation of protein ubiquitination	HSP90β
	GO:0022604	regulation of cell morphogenesis	RAC1, Cofilin-1
	GO:0048858	cell projection morphogenesis	PACSIN2
Exosomal secretion	GO:0048812	neuron projection morphogenesis	RhoA, GAP43
	GO:1903543	positive regulation of exosomal secretion	Syntenin-1, Alix, TSG101, CHMP2A, Rab-7A, VPS4B
Viral process	GO:0046598	positive regulation of viral entry	Galectin-1, CD9, CD81, CD151, CD63
	GO:0046597	negative regulation of viral entry	IFITM2
	GO:0039694	viral RNA genome replication	PCBP1
	GO:0044829	positive regulation of viral genome replication	HSC70, ARF3
	GO:0045070	positive regulation of viral genome replication	CyPA, DDX3X, ENO1, Rack1
	GO:0045071	negative regulation of viral genome replication	IFITM2, DDX3X
	^a PMID:23711381	Viral capsid assembly	HSP90β
	GO:0039702	viral budding via host ESCRT complex	ALIX, CHMP4B, CHMP2A, VPS4B
	GO:1903774	positive regulation of viral budding via host ESCRT complex	TSG101, VPS37B, VPS28
	GO:0019076	viral release	Rab-7A, Cofilin-1
	^a PMID:29891700	viral spread	PACSIN2

^a The function annotations of HSP90β and PACSIN2 were not available from GO database, which, therefore, were from published papers.

Table S2 Protein-protein interaction of RABV virion-packaged cellular proteins.

Color	MCODE	GO ^a	Description	Log10 (p-value) ^b
●	MCODE_1	CORUM:725	P2X7 receptor signaling complex	-7.6
●	MCODE_1	R-HSA-8856828	Clathrin-mediated endocytosis	-6.1
●	MCODE_1	GO: 0070201	Regulation of establishment of protein localization	-6.0
●	MCODE_2	GO:0039702	Viral budding via host ESCRT complex	-21.7
●	MCODE_2	GO:0046755	Viral budding	-21.3
●	MCODE_2	R-HSA-162588	Budding and maturation of HIV virion	-20.8
●	MCODE_3	R-HSA-5625970	RHO GTPases activate KTN1	-9.6
●	MCODE_3	GO: 0050870	Positive regulation of T cell activation	-8.3
●	MCODE_3	GO: 0010810	Regulation of cell-substrate adhesion	-8.3

^a The data resources of Metascape referred to biological processes are as follows: Gene Ontology, Reactome Pathway Database and CORUM. The top three related GO terms are retained in each MOCDE.

^b P-values were calculated based on the cumulative hypergeometric distribution.