Exon Ontology: Functional Genomics At Exon Level Resolution

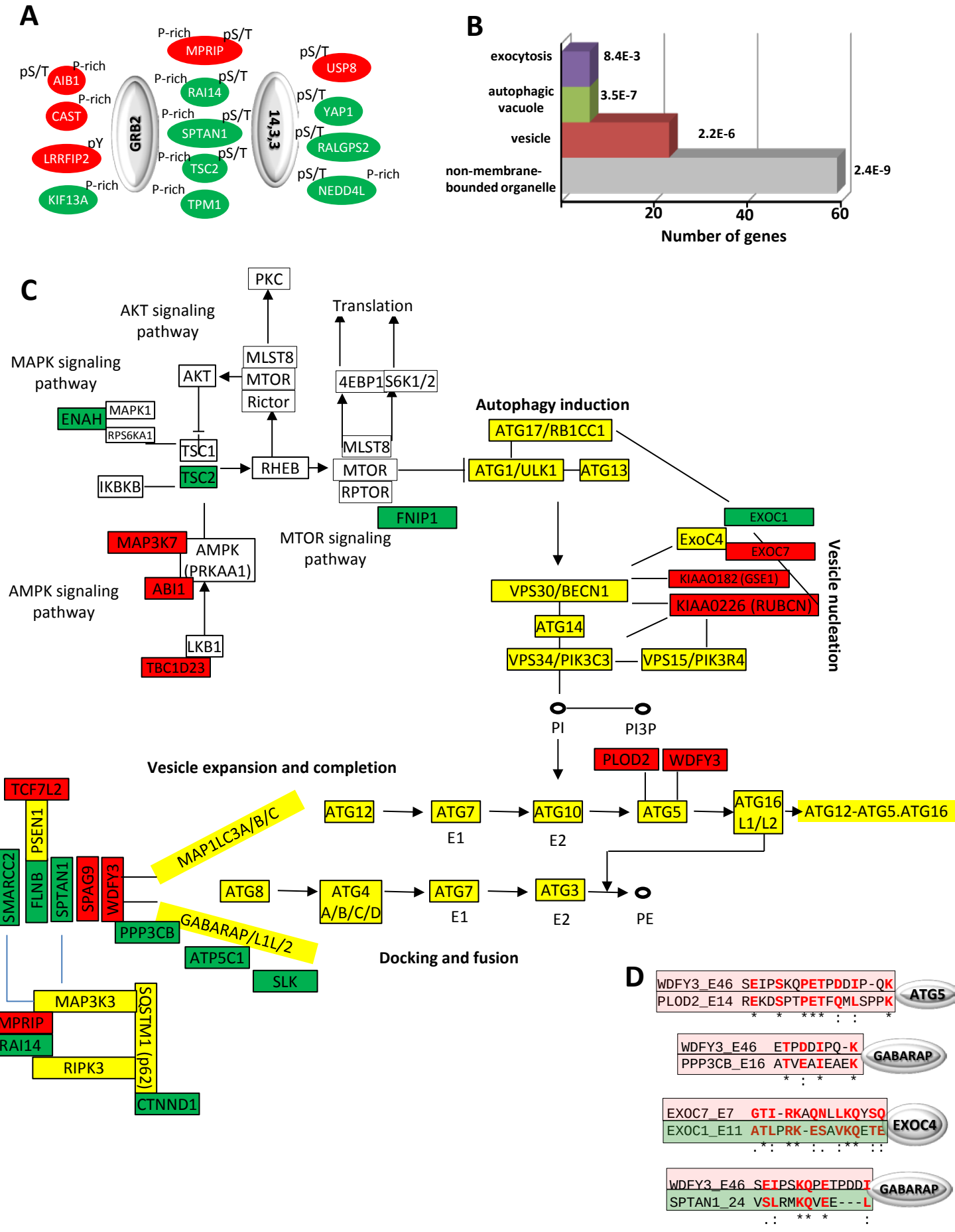
Supplemental Figure S6

A. Several genes differentially spliced between mesenchymal and epithelial cells produce proteins interacting with GRB2 and/or 14.3.3 proteins. pS/T means exons encoding phosphorylated peptides; “P-rich” means exons encoding peptides with proline-rich regions. The GRB2 protein interacts with P-rich regions or phospho-tyrosines (pY). The 14.3.3 proteins interact with phospho-serine or –threonine (pS/T). Red and green proteins correspond to genes with alternative exons more and less included, respectively in mesenchymal- than epithelial-like cells.

B. Proteins coded by genes containing the alternative exons that are differentially spliced when comparing mesenchymal- and epithelial-like cells interact with proteins involved in biological processes relying on “non-membrane bound organelle”, “vesicle”, “autophagic vacuole” and “exocytosis”. The analysis of GO term enrichment was performed with “DAVID Ontology” (https://david.ncifcrf.gov/).

C. Autophagy process derived from KEGG pathway (yellow proteins are autophagic factors) where genes with alternative exons differentially spliced when comparing mesenchymal- and epithelial-like cells are represented by a color code: red and green proteins correspond to genes with alternative exons more and less included, respectively in mesenchymal- than epithelial-like cells.

D. Protein sequence comparison between sequences encoded by alternative exons from genes involved in autophagy and sharing common partners. Red and green rectangles correspond to alternative exons that are more or less included, respectively, in mesenchymal- compared to epithelial-like cells.


A
GRB2
14,3,3
MPRIP
AIB1
CAST
LRRFIP2
KIF13A
RAI14
SPTAN1
TSC2
TPM1
USP8
YAP1
RALGPS2
NEDD4L
P-rich
pS/T
pY
B
exocytosis
autophagic vacuole
vesicle
non-membrane-bounded organelle
8.4E-3
3.5E-7
2.2E-6
2.4E-9
20
40
60
Number of genes
C
PKC
AKT signaling pathway
Translation
MAPK signaling pathway
MLST8
MTOR
Rictor
AKT
4EBP1
S6K1/2
ENAH
MAPK1
RPS6KA1
TSC1
TSC2
IKBKB
RHEB
MLST8
MTOR
RPTOR
FNIP1
Autophagy induction
ATG17/RB1CC1
ATG1/ULK1
ATG13
MTOR signaling pathway
MAP3K7
AMPK (PRKAA1)
ABI1
LKB1
TBC1D23
AMPK signaling pathway
EXOC1
ExoC4
EXOC7
KIAA0182 (GSE1)
VPS30/BECN1
KIAA0226 (RUBCN)
ATG14
VPS34/PIK3C3
VPS15/PIK3R4
Vesicle nucleation
PI
PI3P
Vesicle expansion and completion
PLOD2
WDFY3
TCF7L2
PSEN1
SMARCC2
FLNB
SPTAN1
SPAG9
WDFY3
MAP1LC3A/B/C
ATG12
ATG7
E1
ATG10
E2
ATG5
ATG16 L1/L2
ATG12-ATG5.ATG16
ATG8
ATG4 A/B/C/D
ATG7
E1
ATG3
E2
PE
PPP3CB
GABARAP/L1L2
ATP5C1
SLK
Docking and fusion
MAP3K3
SQSTM1 (p62)
MPRIP
RAI14
RIPK3
CTNND1
D
WDFY3_E46 SEIPSKQPETPDDIP-QK
PLOD2_E14 REKDSPTPETFQMLSPPK
ATG5
WDFY3_E46 ETPDDIPQ-K
PPP3CB_E16 ATVEAIEAEK
GABARAP
EXOC7_E7 GTI-RKAQNLLKQYSQ
EXOC1_E11 ATLPRK-ESAVKQETE
EXOC4
WDFY3_E46 SEIPSKQPETPDDI
SPTAN1_24 VSLRMKQVEE---L
GABARAP