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Supplementary Materials for

ETV7 is an essential component of a rapamycin-insensitive mTOR complex in cancer

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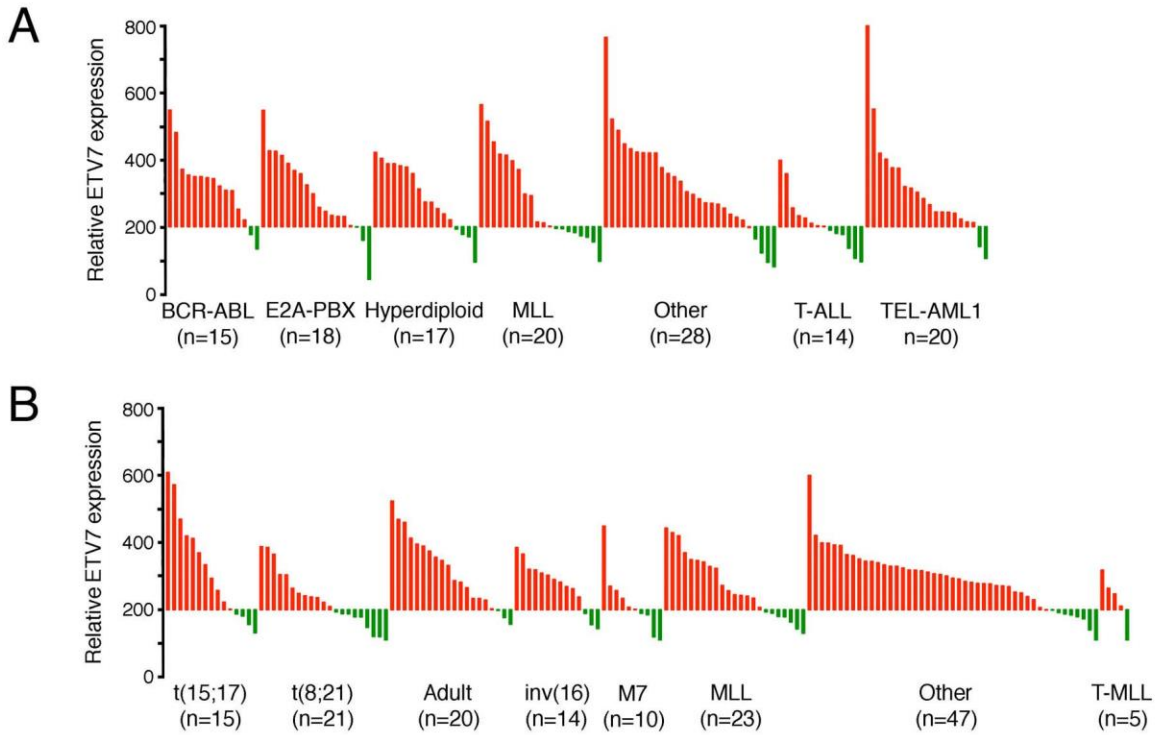
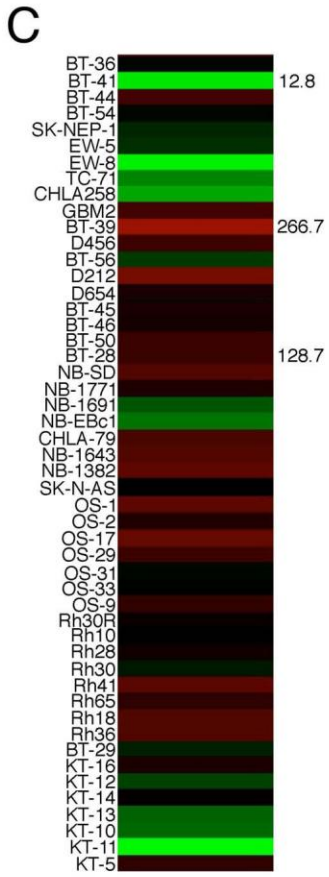

A
Relative ETV7 expression
800
600
400
200
0
BCR-ABL (n=15)
E2A-PBX (n=18)
Hyperdiploid (n=17)
MLL (n=20)
Other (n=28)
T-ALL (n=14)
TEL-AML1 n=20)
B
Relative ETV7 expression
800
600
400
200
0
t(15;17) (n=15)
t(8;21) (n=21)
Adult (n=20)
inv(16) (n=14)
M7 (n=10)
MLL (n=23)
Other (n=47)
T-MLL (n=5)


C
BT-36
BT-41
BT-44
BT-54
SK-NEP-1
EW-5
EW-8
TC-71
CHLA258
GBM2
BT-39
D456
BT-56
D212
D654
BT-45
BT-46
BT-50
BT-28
NB-SD
NB-1771
NB-1691
NB-EBc1
CHLA-79
NB-1643
NB-1382
SK-N-AS
OS-1
OS-2
OS-17
OS-29
OS-31
OS-33
OS-9
Rh30R
Rh10
Rh28
Rh30
Rh41
Rh65
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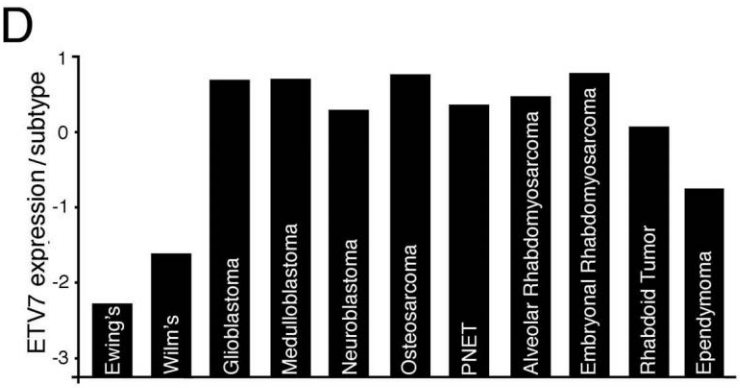
KT-10
KT-11
KT-5
12.8
266.7
128.7


D
ETV7 expression / subtype
1
0
-1
-2
-3
Ewing's
Wilm's
Glioblastoma
Medulloblastoma
Neuroblastoma
Osteosarcoma
PNET
Alveolar Rhabdomyosarcoma
Embryonal Rhabdomyosarcoma
Rhabdoid Tumor
Ependymoma

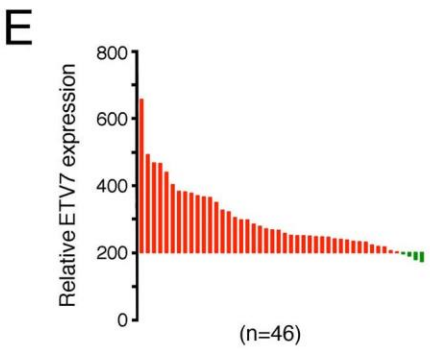

E
Relative ETV7 expression
800
600
400
200
0
(n=46)

Fig. S1. ETV7 is expressed in pediatric malignancies. Histograms of expression levels of ETV7 in (**A**) pediatric ALL (*19*) and (**B**) pediatric AML (*18*) using the Affymetrix U133Av2 array. The division of $ETV7^+$ (red) and $ETV7^-$ (green) tumors (relative expression value 200) was based on the hybridization level of ETV7 in non- ETV7 expressing T-ALL samples on the same array. (**C**) Heat map of the relative ETV7-expression levels in 50 solid tumor xenografts of the St. Jude expanded panel of pediatric preclinical tumor models using the HG-U133Plus2 GeneChip. Numbers to the right of the heat map represent the relative *ETV7* RNA hybridization signals in these xenografts, as determined by the Affymetrix HG-U133Plus2 GeneChip (20). The following tumors were included: BT-36, -41, -44, -54 (ependymoma, p, p, s, s); SK-NEP-1, EW-5, -8, TC-71, CHLA258 (Ewings sarcoma, pr, p, pr, p); GBM2, BT-39, -56, D456, D212, D645 (glioblastoma, p, r, sr, p, s, p); BT-45, -46, -50, -28 (medulloblastoma, p, p, p, p); NB-SD, -1771, -1691, -EBc1, -1643, -1382, CHLA-79, SK-N-AS (neuroblastoma, p, p, p, p, p, p, p, s); OS-1, -2, -17, -29, -31, -33, -9 (osteosarcoma, p, p, p, s, p, p, p); Rh30R, Rh10, Rh28, Rh30, Rh41, Rh65, Rh36 (ARMS, r, p, p, p, p, sr); Rh18, Rh36 (ERMS, p; sr); Bt-29, KT-16, -12, -14 (rhabdoid, p, p, s, p); KT-13, -10, -11, -5 (Wilms tumor, p, p, p, s) (p=primary, s=secondary, pr=primary relapse, sr= secondary relapse, r=relapse). (**D**) A histogram representing the average ETV7 expression per pediatric tumor type xenograft in the HG-U133Plus2 array as compared with the average ETV7 signal in all tumor xenografts. (**E**) Histogram of ETV7 expression levels using the Affymetrix U133Av2 array of 46 primary human medulloblastomas (*32*). The division of $ETV7^+$ and $ETV7^-$ tumors (relative expression value 200) was based on the hybridization level of ETV7 in non- ETV7-expressing T-ALL samples on the same U133Av2 array.

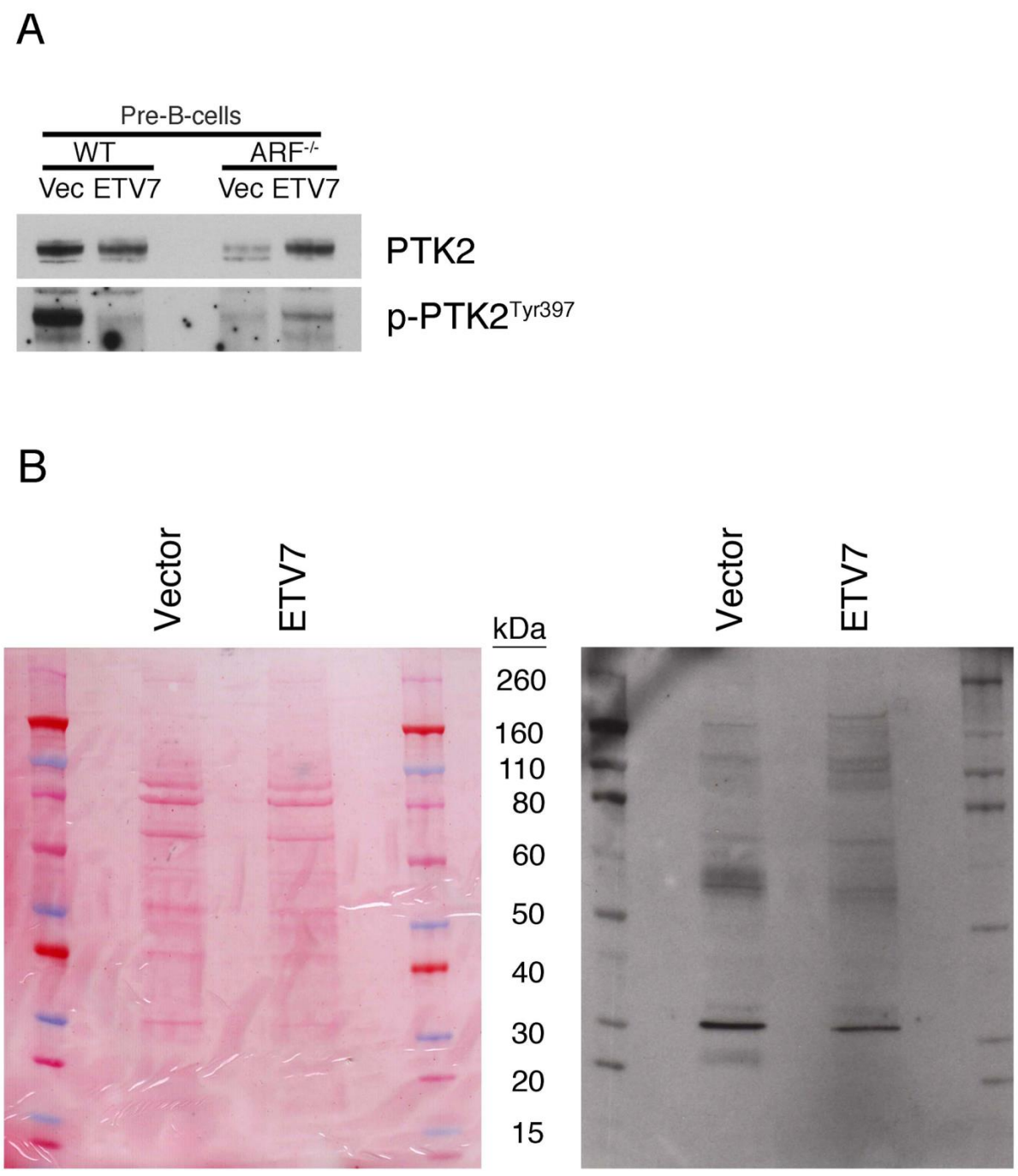


Fig. S2. PI3K and PTK2 signaling and anti–p-tyr Western blot of cell lysate of vector and ETV7 mouse pre-B cells. (**A**) Cell lysates from wild type (WT) and *Arf*$^{-/-}$mouse pre-B cells (ARF$^{-/-}$) expressing GFP (Vec) or ETV7 (ETV7) immunoblotted for p-PTK2^{Tyr397} and total PTK2. (**B**) Left panel, Ponceau-S stained nitrocellulose blot of a PAGE gel of lysates of 0.5x10^{6} vector and ETV7 transduced mouse pre-B cells. Right panel, anti-p-tyrosine immunoblot of the same gel.

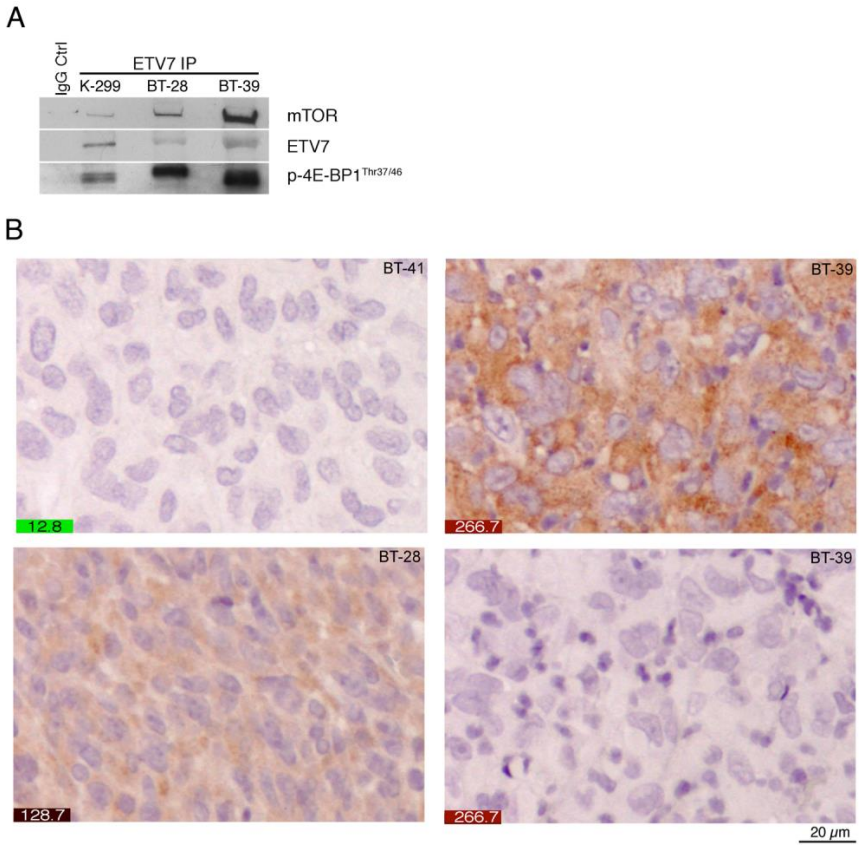


Fig. S3. ETV7 expression in human pediatric tumor xenografts. (**A**) IPs (ETV7 IP, IgG Ctrl) of lysates from Karpas-299 cells (K-299), and xenograft tumors (BT-28, medulloblastoma; BT-39, glioblastoma) immunoblotted for mTOR, ETV7 or p-4E-BP1$^{Thr37/46}$. (**B**) ETV7 immunostaining of a BT41 ependymoma xenograft section (no ETV7 expression), a BT28 medulloblastoma xenograft (intermediate ETV7 expression), a BT39 glioblastoma xenograft section (high ETV7 expression) and a BT39 section competed with the peptide against which the anti-ETV7 antibody was raised. Numbers in the lower left corner of the micrographs represent the relative ETV7 RNA hybridization signals in these xenografts, as determined by the Affymetrix HG-U133Plus2 GeneChip, shown in fig. S1C.

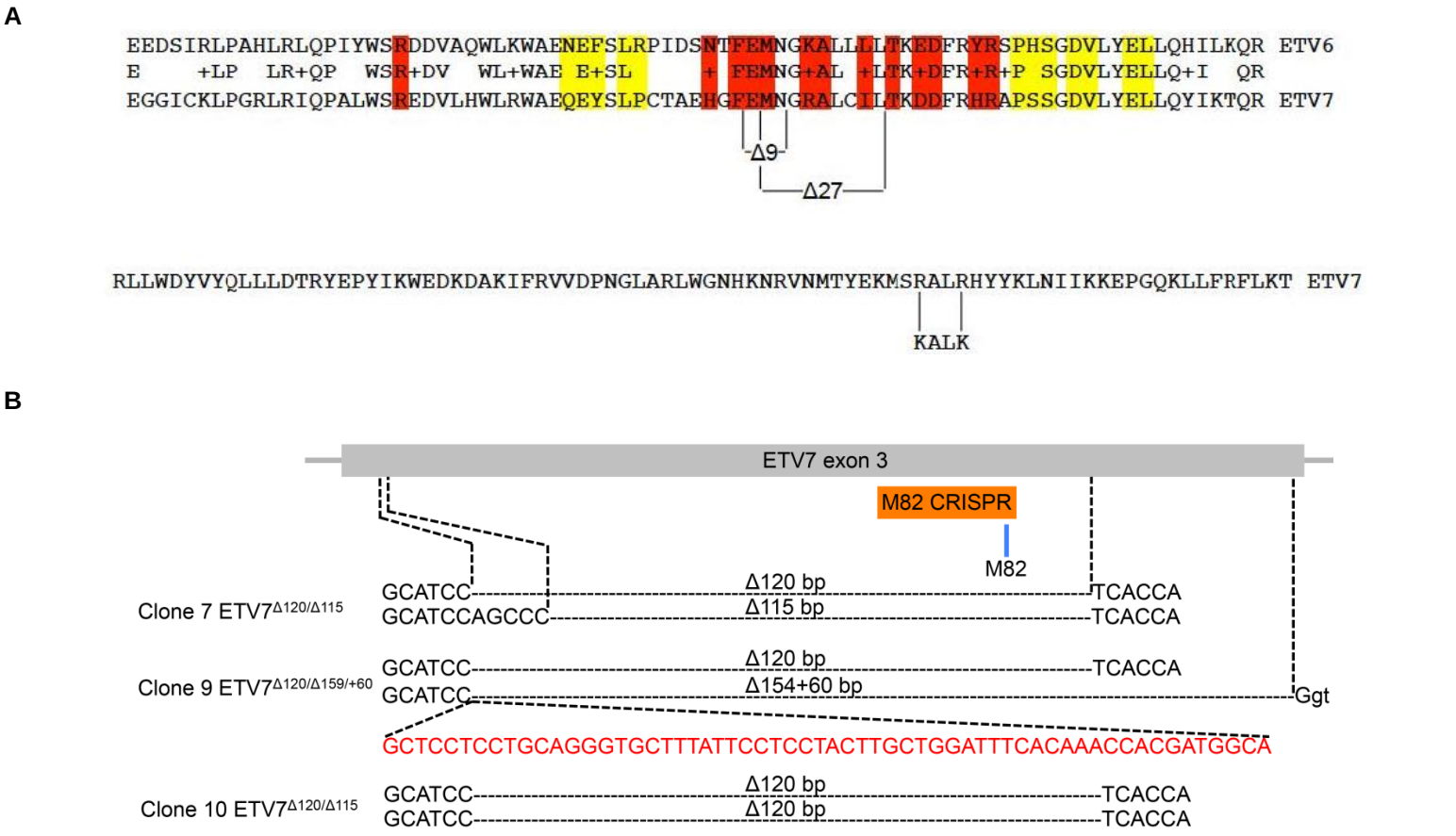


Fig. S4. Sequence comparison of ETV6 and ETV7 PNT domains and the position of Δ9, Δ27, Δ120/Δ115, Δ120/Δ159/+60 mutations in the ETV7 PNT domain, and the KALK mutation in the ETV7 ETS domain. (**A**) The upper part shows the protein sequence comparison of the ETV6 PNT domain (amino acid 44 to 124) with that of the ETV7 PNT domain (amino acid 37 to 117). The line in the middle shows the homology between the two PNT domains. The red and yellow highlights in the ETV6 PNT sequence indicate residues forming the ML and EH interaction surfaces (65), respectively. The sequences in the ETV7 PNT domain coinciding with the ETV6 ML and EH surfaces are also highlighted in red and yellow. Δ9 (Δ$E^{81}MN^{83}$) and Δ27 (Δ$M^{82}NGRALCIL^{90}$) indicate the ETV7 PNT domain deletion mutants used in Fig. 2E and 2F. The sequence underneath shows the position of the $R^{281}ALR^{284}$ to $K^{281}ALK^{284}$ mutation in the ETV7 ETS domain (amino acids 224 to 307), which prevents DNA binding. (**B**) Top bar depicts exon 3 of ETV7 (165 bp) with underneath the relative positions of the M82 CRISPR (not to scale) and the methionine 82 codon (M82). Underneath are the partial sequences of Karpas-299-EBNA-Cas9 clones 7, 9 and 10. Clone 9 (K-$E^{Δ120/Δ159+60}$) was used for experiments shown in Fig. 5A, 5B, and fig. S7B. Dashed vertical lines demarcate the deletions in the different alleles with the juxtaposed 5' and 3' nucleotide sequences indicated. The 120bp deletion (Δ120) encodes a highly unstable ETV7 protein with a 40-amino acid (aa) deletion in the PNT domain, including M82, which is undetectable in ETV7 IP/western blots (Fig. 5A, insert). The 115bp deletion encodes an out of frame protein of 63 aa containing the 49 aa ETV7 N-terminus followed by 14 aa from the -1-reading frame. The 154 bp deletion/60 bp insertion (red lettering) encodes a 50-aa protein containing the 49 aa ETV7 N-terminus followed by one non-ETV7 aa.

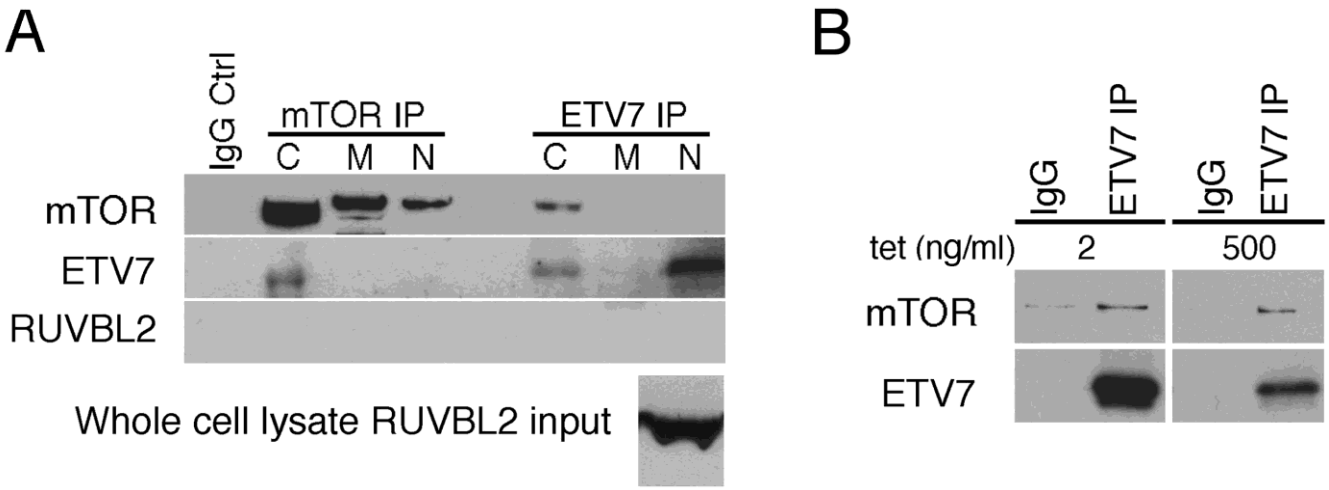


Fig. S5. mTOR localization and assembly. (**A**) mTOR (mTOR IP) or ETV7 (ETV7 IP) IP of subcellular fractions (C=cytoplasm, M=membrane, N=nucleus) of Karpas-299 cells immunoblotted for mTOR, ETV7 or RUVBL2. (**B**) IgG or ETV7 IP of lysate from tetracycline-treated (tet) Tet-off U937T cells carrying a $tet^{operator}$CMV minimal promoter-driven ETV7 construct, immunoblotted for mTOR and ETV7. Higher ETV7 expression (2 ng/mL tetracycline) does not result in more mTOR coprecipitation.

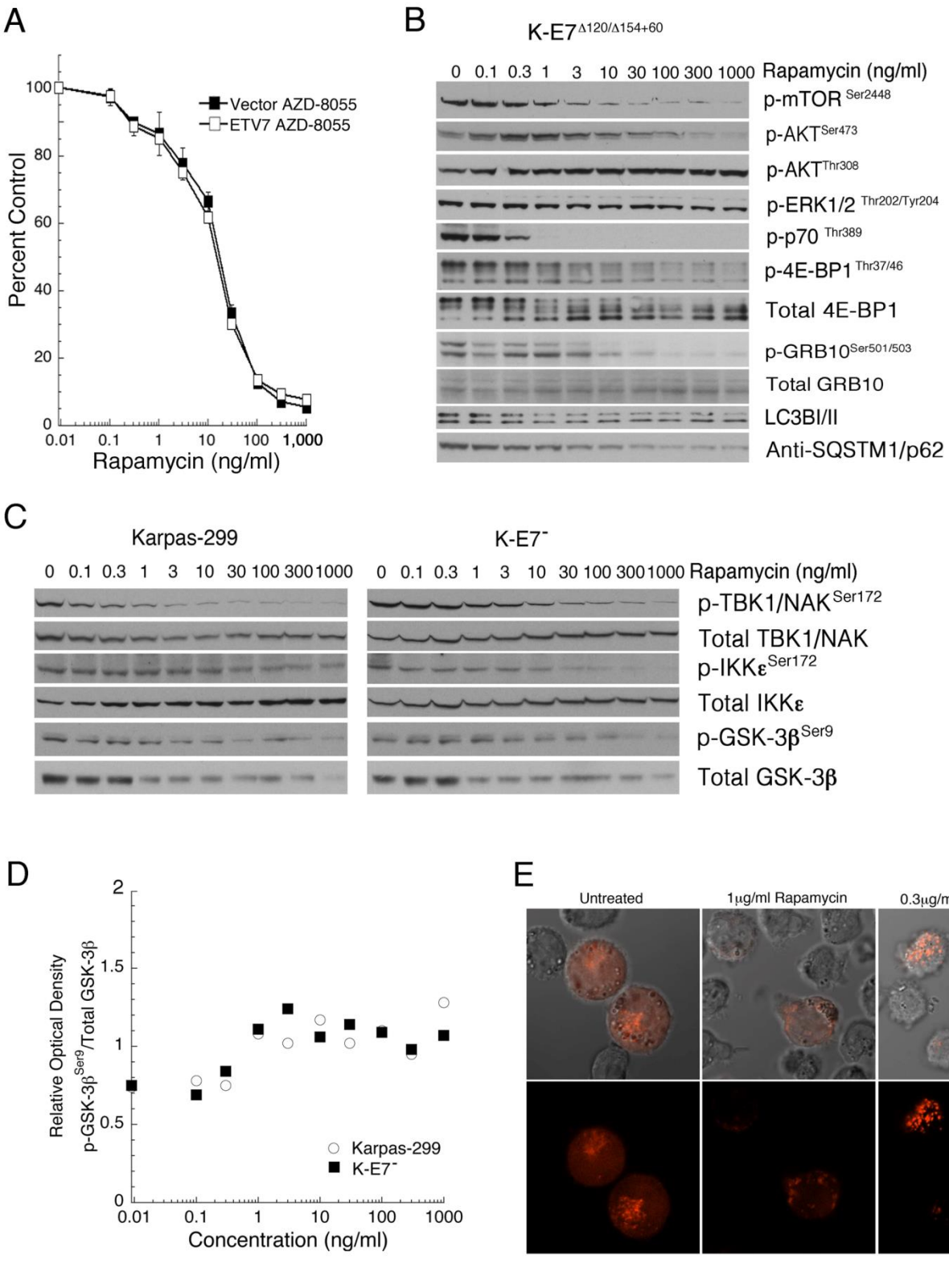

A
Vector AZD-8055
ETV7 AZD-8055
Percent Control
Rapamycin (ng/ml)
B
K-E7Δ120/Δ154+60
0 0.1 0.3 1 3 10 30 100 300 1000 Rapamycin (ng/ml)
p-mTOR Ser2448
p-AKTSer473
p-AKTThr308
p-ERK1/2 Thr202/Tyr204
p-p70 Thr389
p-4E-BP1 Thr37/46
Total 4E-BP1
p-GRB10Ser501/503
Total GRB10
LC3BI/II
Anti-SQSTM1/p62
C
Karpas-299
K-E7-
0 0.1 0.3 1 3 10 30 100 300 1000 Rapamycin (ng/ml)
p-TBK1/NAKSer172
Total TBK1/NAK
p-IKKεSer172
Total IKKε
p-GSK-3βSer9
Total GSK-3β
D
Relative Optical Density
p-GSK-3βSer9/Total GSK-3β
Karpas-299
K-E7-
Concentration (ng/ml)
E
Untreated
1μg/ml Rapamycin
0.3μg/ml AZD-8055
10μm

Fig. S6. Effects of mTOR inhibitors and mTORC3 loss on mTOR signaling. (**A**) Proliferating Ew-8 Ewing's sarcoma cells transduced with MSCV-IRES-GFP (vector) or MSCV-ETV7-IRES-GFP (ETV7) were treated with increasing amounts (0.1, 0.3, 1.3, 10, 30, 100, 300, 1,000 ng/mL) of AZD-8055 for 3 population doublings. Cell densities (Percent Control) were plotted as the percentage of cells treated with vehicle. Data are represented as mean +/- SEM from 3 independent experiments. 30% control or less means no proliferation. (**B**) Immunoblots of K-E7$^{\Delta 120/\Delta 154+60}$ cell lysates treated with increasing amounts of rapamycin (0.1, 0.3, 1.3, 10, 30, 100, 300, 1,000 ng/mL) probed for p-mTOR^{Ser2448} p-AKT^{Ser473}, p-AKT^{Thr308}, p-ERK1/2$^{Thr202/Tyr204}$, p-p70S6K^{Thr389}, p-4E-BP1$^{Thr37/46}$, total 4E-BP1, LC3BI/II and SQSTM1/p62. (**C**) Immunoblots of lysates of equal numbers of Karpas-299, and K-E7^{-} cells were treated with increasing amounts of rapamycin (0.1, 0.3, 1.3, 10, 30, 100, 300, 1,000 ng/mL) and probed for, phospho-IKKε^{Ser172}, total IKKε, phospho-TBK1^{Ser172}, total TBK1, p-GSK3-β^{Ser9} and total GSK3-β. (**D**) p-GSK3-β^{Ser9} and total GSK3-β band intensities at each rapamycin concentration of the western blot in C were determined using a densitometer and plotted as the p-GSK3-β^{Ser9}/GSK3-β relative intensities to show that loss of p-GSK3-β^{Ser9} signal follows the loss of total GSK3-β. (**E**) Karpas-299 cells transduced with LC3B-mCherry retrovirus were treated or not (untreated) with rapamycin (1,000ng/ml rapamycin) or AZD-8055 (300 ng/ml AZD-8055) for 72 hours. Cells were visualized using phase contrast/fluorescence microscopy (top row) or fluorescence microscopy alone (bottom row). Only cells treated with AZD-8055 show active autophagy as indicated by punctate staining. mTORC2 signaling in Karpas-299 cells either.

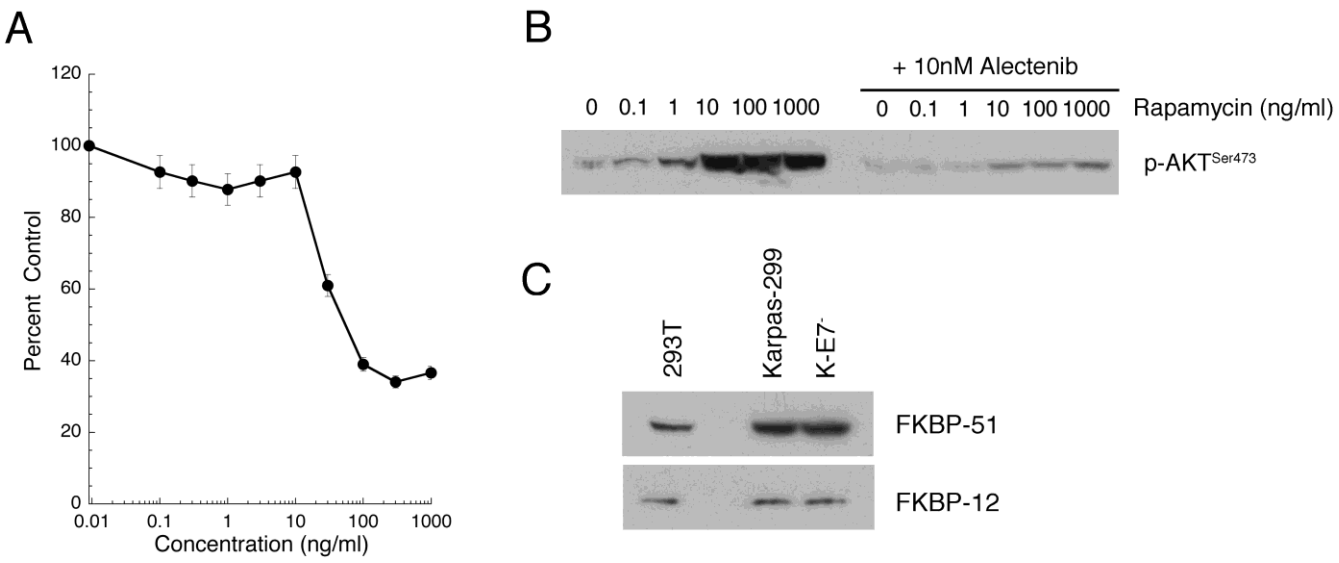


Fig. S7. Effect of ALK inhibition on p-AKT^{Ser473} and relative FK506-binding protein expression in Karpas-299 cells. (**A**) Proliferating Karpas-299 cells were treated with increasing amounts (0.1, 0.3, 1, 3, 10, 30, 100, 300, 1,000 nM) of the ALK inhibitor alectinib for 3 population doublings. Cell densities (percent control) were plotted as the percentage of cells treated with vehicle. Data are represented as mean +/- SEM from 3 independent experiments. (**B**) Proliferating Karpas-299 cells were treated with increasing amounts (0.1, 1, 10, 100, 1,000 ng/mL) of rapamycin in the absence or presence of 10ng/ml alectinib for 72 hours. Cell lysates were immunoblotted for p-AKT^{Ser473}. Compared to cells treated with rapamycin alone, NPM-ALK inhibition with 10nM alectinib greatly reduced the p-AKT^{Ser473} feedback phosphorylation with increasing rapamycin concentration. (**C**) Lysates of 293T, Karpas-299 and K-E7$^-$ cells were immunoblotted for FKBP-12 and FKBP-51. The levels of these two proteins in Karpas-299 and K-E7$^-$ cells are similar to that in 293T cells. The relative amounts of FKBP-12 and FKBP-51 in 293T cells are such that they cannot fully inhibit mTORC2 signaling upon long-term rapamycin treatment (*40*), predicting that they cannot inhibit mTORC2 signaling in Karpas-299 cells either.

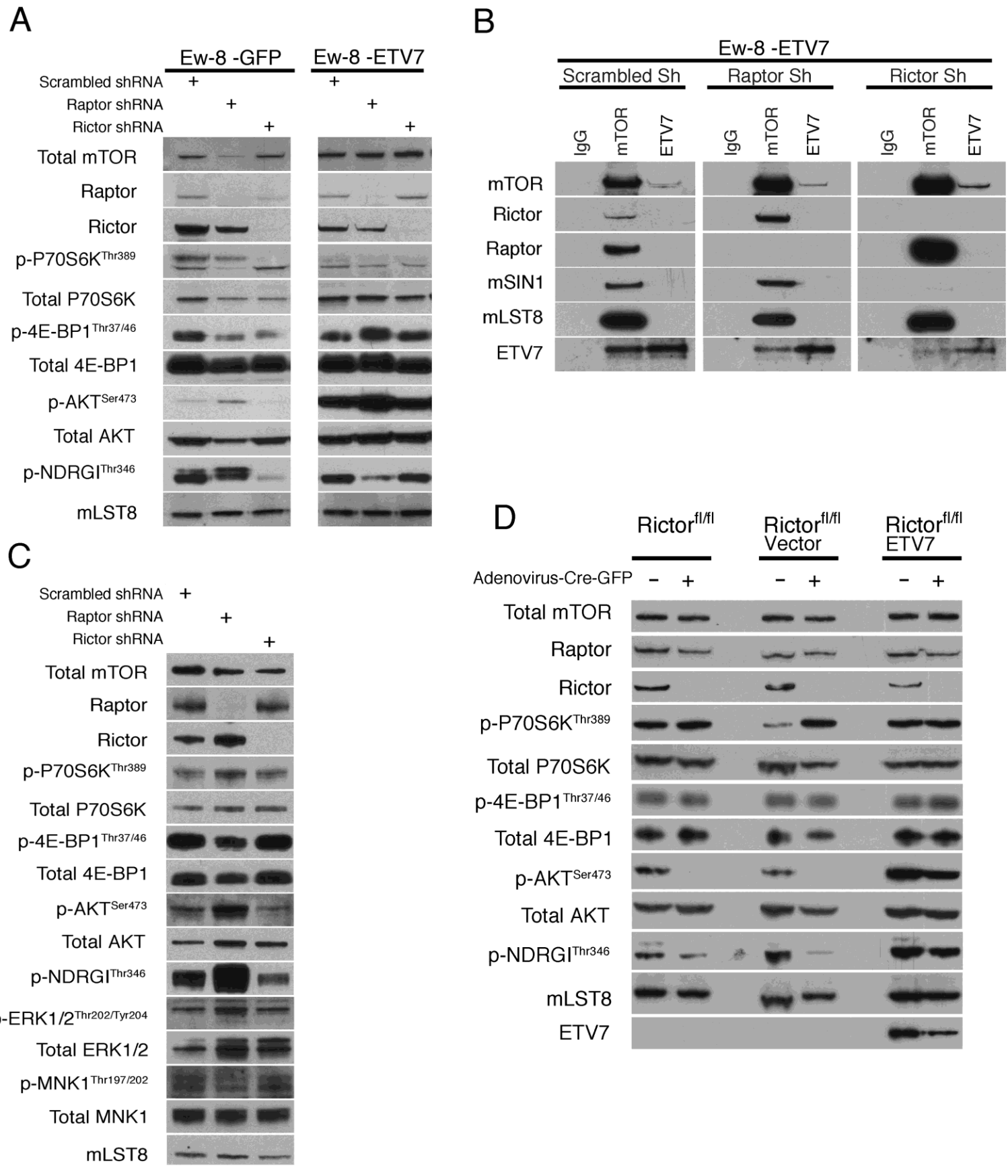

A
Ew-8 -GFP
Ew-8 -ETV7
Scrambled shRNA
Raptor shRNA
Rictor shRNA
Total mTOR
Raptor
Rictor
p-P70S6K Thr389
Total P70S6K
p-4E-BP1 Thr37/46
Total 4E-BP1
p-AKT Ser473
Total AKT
p-NDRGI Thr346
mLST8
B
Ew-8 -ETV7
Scrambled Sh
Raptor Sh
Rictor Sh
IgG
mTOR
ETV7
mTOR
Rictor
Raptor
mSIN1
mLST8
ETV7
C
Scrambled shRNA
Raptor shRNA
Rictor shRNA
Total mTOR
Raptor
Rictor
p-P70S6K Thr389
Total P70S6K
p-4E-BP1 Thr37/46
Total 4E-BP1
p-AKT Ser473
Total AKT
p-NDRGI Thr346
p-ERK1/2 Thr202/Tyr204
Total ERK1/2
p-MNK1 Thr197/202
Total MNK1
mLST8
D
Rictor fl/fl
Rictor fl/fl Vector
Rictor fl/fl ETV7
Adenovirus-Cre-GFP
Total mTOR
Raptor
Rictor
p-P70S6K Thr389
Total P70S6K
p-4E-BP1 Thr37/46
Total 4E-BP1
p-AKT Ser473
Total AKT
p-NDRGI Thr346
mLST8
ETV7

Fig. S8. mTORC3 kinase is insensitive to Raptor or Rictor knockdown or Rictor knockout. (**A**) Immunoblots of lysates of EW-8 Ewing's sarcoma cells transduced with GFP or ETV7 lentivirus and super transduced with scrambled-shRNA, Raptor-shRNA or Rictor-shRNA lentivirus were probed for mTOR, Raptor, Rictor, p-P70S6K^{Thr389}, total P70S6K, p-4E-BP1$^{Thr37/46}$, total 4E-BP1, p-AKT^{Ser473}, total AKT, p-NDRG1^{Thr346} and mLST8. **(B)** mTOR and ETV7 IPs of the same EW-8 lysates as in A were immunoblotted for mTOR, Rictor, Raptor, mSIN1, mLST8 and ETV7. (**C**) Lysates of scrambled, Raptor, or Rictor Karpas-299 knockdown cells immunoblotted for mTOR, Rictor, Raptor, p-P70S6K^{Thr389}, total P70S6K, p-AKT^{Ser473}, total AKT, p-NDRG1^{Thr346}, p-4E-BP1$^{Thr37/46}$, total 4E-BP1, p-ERK1/2$^{Thr202/Tyr204}$, total ERK1/2, p-MNK1$^{Thr197/202}$, total MNK1 and mLST8. mLST8 serves as the loading control. (**D**) Ninety hours after infection with Adenovirus-GFP-iCre (+) or not (-), lysates of *Rictor*$^{fl/f}$ (*Rictor*$^{fl/f}$)*, Rictor*$^{fl/fl}$-vector (*Rictor*$^{fl/fl}$-vector) or *Rictor*$^{fl/fl}$-ETV7 (*Rictor*$^{fl/fl}$-ETV7) MEFs were immunoblotted for Rictor, ETV7, p-AKT^{Ser473}, total AKT, p-NDRG1^{Thr346}, Raptor, p-p70S6K^{Thr389}, total p70S6K, p-4E-BP1$^{36/47}$, total 4E-BP1 and mLST8 as a loading control.

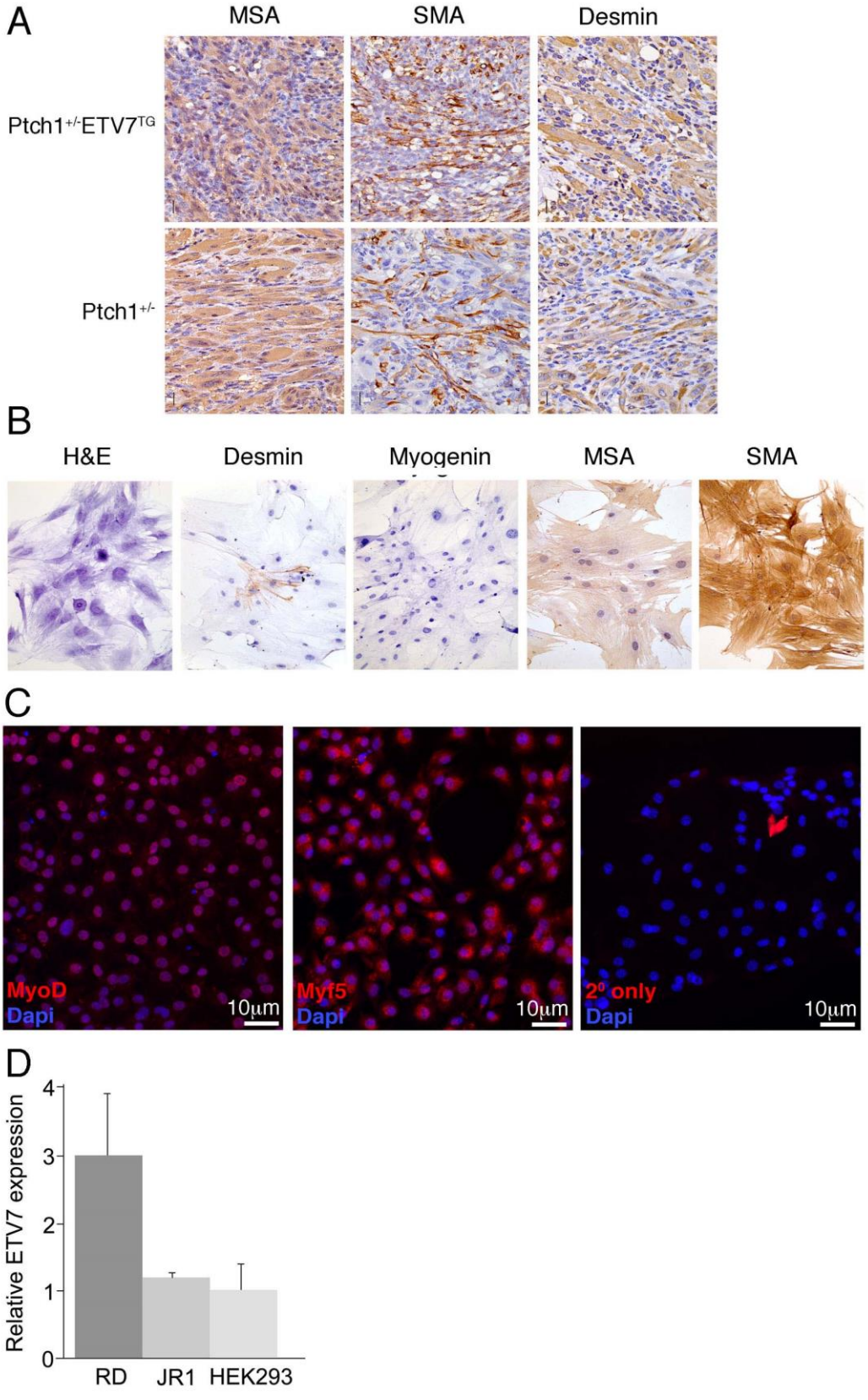

A
MSA
SMA
Desmin
Ptch1+/-ETV7TG
Ptch1+/-
B
H&E
Desmin
Myogenin
MSA
SMA
C
MyoD
Dapi
10μm
Myf5
Dapi
10μm
2º only
Dapi
10μm
D
Relative ETV7 expression
0
1
2
3
4
RD
JR1
HEK293

Fig. S9. ERMS-specific markers in Ptch$^{+/-}$/ETV$^{TG+/-}$ tumors are preserved in Ptch$^{+/-}$/ETV$^{TG+/-}$ cell lines. (**A**) Representative example of formalin fixed paraffin embedded sections of a Ptch1$^{+/-}$/ETV7^{TG} (upper panel) and Ptch1$^{+/-}$ (lower panel) primary tumor stained with MSA antibody, SMA antibody, or desmin antibody. Scale bar represents 20µm. (**B**) Representative example of formalin fixed cell line of a Ptch1$^{+/-}$/ETV7^{TG} tumor stained with: H&E, anti-Desmin, -Myogenin, -MSA, -SMA antibody. (**C**) Representative example of formaldehyde fixed cell line of a Ptch1$^{+/-}$/ETV7^{TG} tumor stained with: MyoD antibody and Dapi, Myf5 antibody and Dapi, Secondary antibody alone and Dapi. Scale bar represents 10µm. (**D**) ETV7 Q-RT-PCR of RNA from ERMS cell lines RD and JR and HEK 293T cells. Q-RT PCR results were normalized to endogenous HPRT expression. Data are the mean +/- SEM from two independent experiments.

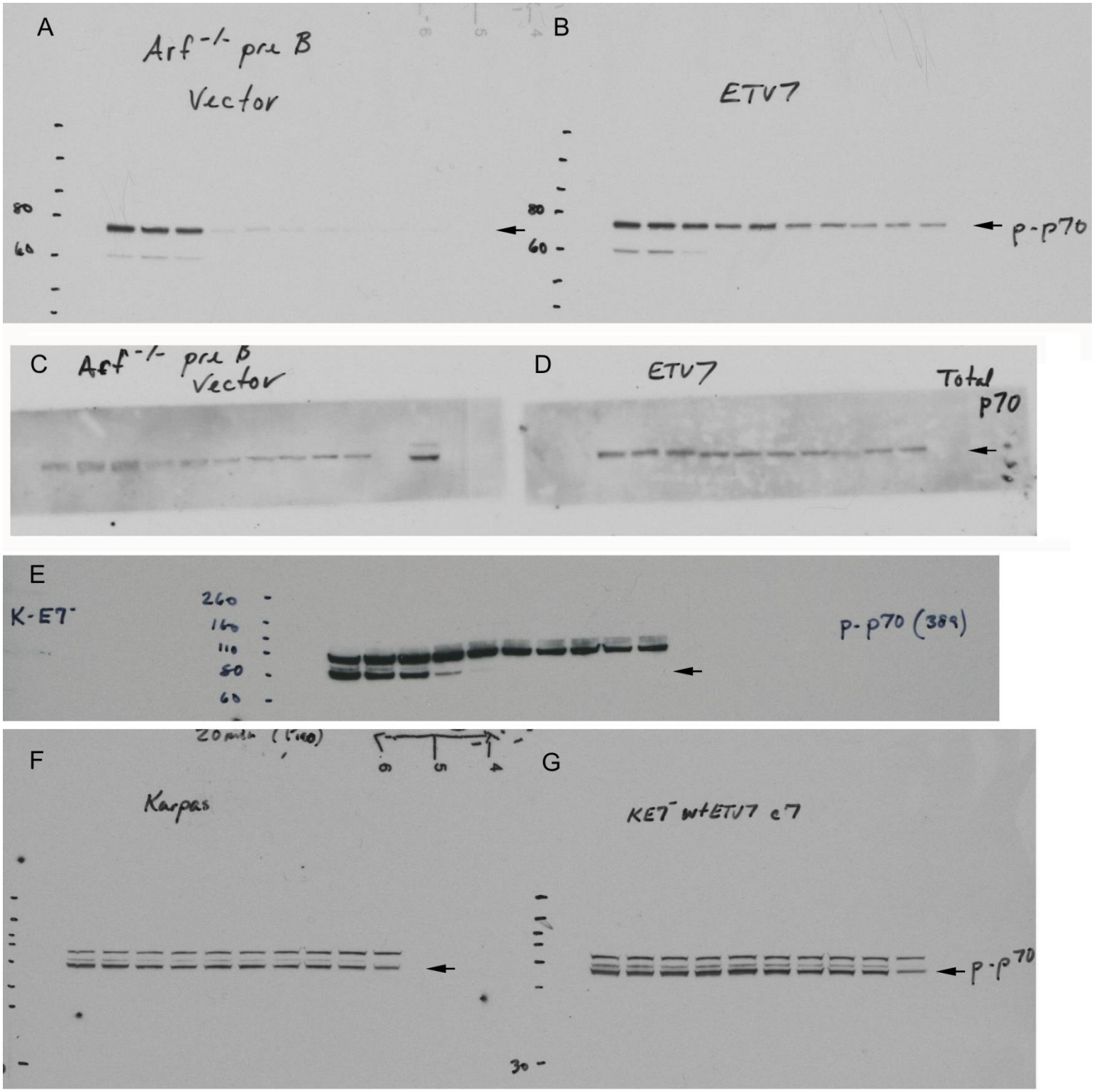

A
Arf-/- pre B
Vector
80
60
B
ETV7
80
60
p-p70
C
Arf-/- pre B
Vector
D
ETV7
Total
p70
E
K-ET-
260
160
110
80
60
p-p70 (389)
F
Karpas
30
G
KET- wtETV7 e7
p-p70

Fig. S10. Whole phospho-p70S6K^{Thr389} and p70S6K Western blots relating to Figs. 1C and 5D. This figure shows images of the whole western blots of lysates of mouse *Arf*$^{-/-}$ pre-B cells expressing (**A**) vector or (**B**) ETV7, treated with increasing amounts of rapamycin (from left to right: 0, 0.1, 0.3, 1, 3, 10, 30, 100, 300, 1000 ng/ml rapamycin), probed with the anti-phospho-p70S6K^{Thr389} antibody or the same blots probed with a total anti-p70S6K antibody (**C**, **D**). These whole images represent the phospho-p70S6K^{Thr389} and total p70S6K cutouts shown in Fig. 1C. (**E**, **F** and **G**) show KE7^{-}(no ETV7), Karpas-299, and KE7^{-}-ETV7 lysates of cells treated with the same increasing amounts of rapamycin, probed with the anti-phospho-p70S6K^{Thr389} antibody. These whole images represent the phospho-p70S6K^{Thr389} cutouts shown in Fig. 5D. The arrows indicate the position of the phospho-p70S6K^{Thr389} or p70S6K bands. The horizontal lines at the left of each blot indicate the position of the molecular weight markers (260, 160, 110, 80, 60, 40, and 30 kDa. respectively).

Table S1. Expression effects of ETV7.

A. Upregulated ETV7 expression in adult tumor samples.

Tumor Type	Over-expression	Platform
Well Differentiated Liposarcoma (Henderson et al, Genome biol 6, R76, 2005; Nakayama et al, Modern Pathology, Inc 20,749-59, 2007)	Top 1%	U133A 2.0, U133A
B-cell Acute Lymphoblastic Leukemia (Raetz et al, Pediatric Blood Cancer 47, 130-40, 2006).	Top 1%	U133A
Easophageal Carcinoma (Kimchi et al, Cancer Research 65, 3146-54, 2005)	Top 1%	U133A
Invasive Ductal Breast Carcinoma (Turashvili et al, BMC Cancer 7, 55, 2007)	Top 1%	U133 Plus 2.0
Liver Cell Dysplasia vs. Normal (Wurmbach, Hepatology 45, 938-47, 2007)	Top 1%	U133 Plus 2.0
B-cell Acute Lymphoblastic Leukemia (Maia et al, Cancer Res 65, 10050-58, 2005; Bhojwani et al, Blood 108, 711-17, 2006)	Top 5%	U133A
Superficial Bladder Cancer (Modlich et al, Cin Cancer Res 10, 3410-21, 2004)	Top 5%	U133A
Gastric mixed Adenocarcinoma (Ooi et al, PLoS Genet 5, e1000676, 2010)	Top 5%	U133A
Pleomorphic Myxofibrosarcoma vs. Normal (Barretina et al, Nat Genet 42, 715-21, 2010)	Top 5%	U133A
Ovarian Clear Cell Adenocarcinoma (Lu et al, Clin Cancer Res 10, 3291-00, 2004)	Top 5%	U95D
Ductal breast carcinoma (Turashvili et al, BMC Cancer 7, 55, 2007)	Top 5%	U133 Plus 2.0
Gastric Cancer (Bittner et al, GCEPO, 2005)	Top 5%	U133 Plus 2.0
Liver Cirrhosis vs. Normal (Wurmbach, Hepatology 45, 938-47, 2007)	Top 5%	U133 Plus 2.0
Acute Myeloid Leukemia FAB subtype M5 (Metzeler et al, Blood 112, 4193-01, 2008)	Top 5%	U133 Plus 2.0
Gastric Intestinal Type Adenocarcinoma (Ooi et al, PLoS Genet 5, e1000676 2010)	Top 5%	U133 Plus 2.0
Gastrointestinal Part: Descencing Colon (Sabates-Bellver et al, Mol Cancer Res 5, 1263-75, 2007)	Top 5%	U133 Plus 2.0
Renal Carcinoma (Yusenko et al, BMC Cancer 9, 152, 2009)	Top 5%	U133 Plus 2.0
Leukemia Precursor (Wouters et al, Bloo 113, 3088-91, 2009)	Top 5%	U133 Plus 2.0
Clear Cell Renal Cell Carcinoma (Bittner et al, GCEPO, 2005, Yusenko et al, BMC Cancer 9, 152, 2009)	Top 5%	U133 Plus 2.0
Brain Part: Brain Nucleus (Su et al, Proc Natl Acad Sci USA, 101, 6062-67, 2004)	Top 10%	U133A
Malignant Fibrous Histiocytoma (Detwiller et al, Cancer Res 65, 5881-89, 2005)	Top 10%	U133A
Ovarian Clear Cell Carcinoma vs. Normal (Hendrix et al, Cancer Res 66, 1354-62, 2006)	Top 10%	U133A
Invasive Ductal Breast Carcinoma (Radvanyi et al, Proc Natl Acad Sci USA, 102, 11005-10, 2005)	Top 10%	Hu03 Custom

Brain Part: Putamen (Roth et al, Neurogenetics 7, 67-80, 2006)	Top 10%	U133 Plus 2.0
Ductal Breast Carcinoma (Kimchi et al, Cancer Research 65, 3146-54, 2005, Roth et al, Neurogenetics 7, 67-80, 2006, Richardson et al, Cancer Cell 9, 121-32, 2006)	Top 10%	U133 Plus 2.0
Medullary Breast Cancer (Ginestier et al, Clin Cancer Res 12, 4533-44, 2006)	Top 10%	U133 Plus 2.0
Bladder Cancer (Bittner et al, GCEPO, 2005)	Top 10%	U133 Plus 2.0
Cecum Adenocarcinoma (Kaiser et al, Genome Biol 8, R131, 2007)	Top 10%	U133 Plus 2.0
Germinal Center B-Cell-Like Diffuse Large B-cell Lymphoma (Lentz et al, N Eng J Med 359, 2313-23, 2006)	Top 10%	U133 Plus 2.0
Type 3 Diffuse Large B-Cell Lymphoma (Lentz et al, N Eng J Med 359, 2313-23, 2006)	Top 10%	U133 Plus 2.0
Type II Endometrial Carcinoma (Bittner et al, GCEPO, 2005)	Top 10%	U133 Plus 2.0
Liver Cirrhosis vs. Normal (Wurmbach, Hepatology 45, 938-47, 2007)	Top 10%	U133 Plus 2.0
Acute Myeloid Leukemia FAB subtype M5 (Kool et al, PLoS One 3, e3088, 2008)	Top 10%	U133 Plus 2.0

B: Differential expression (log2 ratio) of mTOR-related genes in vector versus ETV7 ARF$^{-/-}$ mouse pre-B cells as determined by Affymetrix array analysis.

C: Differential expression (log2 ratio>0.5) of kinase genes in vector versus ETV7 ARF$^{-/-}$ mouse pre-B cells as determined by Affymetrix array analysis.

D: Differential expression (log2 ratio>0.5) of cytokine, growth factor and growth factor receptor genes in vector versus ETV7 ARF$^{-/-}$ mouse pre-B cells as determined by Affymetrix array analysis.

B

Gene Symbol	ETV7 vs Vector
Prkaa2	0.90428
Grb10	0.56929
Deptor	0.3964
Prkar2b	0.32123
Mtor	0.2073
Lamtor3	0.20379
Lamtor5	0.2028
Lamtor3	0.1998
Prkab2	0.18871
Lamtor1	0.16293
Prkab1	0.1521
Prkag1	0.1283
Prkar1b	0.1213
Lamtor2	0.10599
Mlst8	0.05355
Prkar1a	0.04963
Pten	-0.0131
Prkag3	-0.02545
Prkaa1	-0.0395
Tsc2	-0.04166
Prkacb	-0.0426
Rptor	-0.09697
Rictor	-0.09717
Prkag2	-0.10246
Tsc1	-0.10304
Lamtor4	-0.24397
Prkaca	-0.25174
Prkar2a	-0.43749

C

Gene Symbol	ETV7 vs Vector
Ptk2	1.61
Irak3	0.97
Prkaa2	0.90
Camk4	0.80
Ak4	0.80
Cdk14	0.73
Mapk11	0.71
Plk2	0.62
Rps6kl1	0.59
Pfkp	0.56
Nim1k	0.56
Lck	0.53
Pkmyt1	0.53
Tnk2	0.51
Itpkb	-0.51
Camk1d	-0.52
Pik3r3	-0.52
Ak5	-0.54
Sik1	-0.56
Ret	-0.56
Eif2ak2	-0.57
Pik3cg	-0.59
Map3k8	-0.61
Pik3r5	-0.62
Ryk	-0.69
Bmpr2	-0.71
Prkcq	-0.84
Dgka	-1.04
Hck	-1.09
Adck1	-1.12

D

Gene Symbol	ETV7 vs Vector	Gene Symbol	ETV7 vs Vector
Gpr12	1.37	Klrb1a	-0.55
Ccl9	1.37	Milr1	-0.56
Olfr820	1.04	Csf2rb	-0.56
Il12rb2	0.97	Vmn2r41	-0.60
Trav9d-1	0.90	Olfr1205	-0.61
Trav9d-4	0.89	Chrnb1	-0.63
Trav16n	0.88	Igf2bp3	-0.64
Mc1r	0.82	Gria2	-0.68
Igf2r	0.67	Ryk	-0.69
Lrp4	0.67	Gpr84	-0.71
Ccl6	0.66	Il5ra	-0.71
Vmn2r51	0.64	Olfr372	-0.72
Gpr125	0.64	Tnfrsf13c	-0.72
Bmpr1a	0.64	Igfbp4	-0.72
Bmp4	0.64	Gprc5b	-0.76
Trav9-2	0.61	Fcrl6	-0.77
Trav6-3	0.61	Nr2c1	-0.81
Tnfrsf22	0.58	Ephb2	-0.83
Tnfrsf22	0.58	Gpr174	-0.87
Olfr1437	0.56	Gpr128	-0.90
Olfr1238	0.56	Tlr9	-0.96
Olfr687	0.53	Klrb1f	-0.97
Nr1d1	0.53	Il2ra	-0.99
Tnk2	0.51	Tnfsf8	-0.99
Fcgr3	0.51	Bmpr2	-1.10
Ifnab	0.51	P2ry13	-1.10
Olfr988	0.50	Igf1	-1.13
Olfr205	-0.52	Sorl1	-1.33
Igf1r	-0.52	Csf2rb2	-1.40
Tgfbr2	-0.52	Gpr18	-1.41
Tgfbr3	-0.52	Il18	-1.42
Angptl2	-0.52	Il10ra	-1.46
Tnf	-0.52	Igf2	-1.97
Fcrla	-0.53		
Lpar6	-0.53		
Cysltr1	-0.54		
Il4ra	-0.54		

E: Gene Set Enrichment Analysis using Hallmark and canonical databases identifying ETV7 up and down regulated pathways in ETV7 versus vector ARF$^{-/-}$ mouse pre-B cells.

E

Up regulated Hallmark pathways

NAME	SIZE	NES	NOM p-val	FDR q-val
HALLMARK_MYC_TARGETS_V2	57	1.849533	0	0.005558
HALLMARK_MYC_TARGETS_V1	195	1.839917	0	0.00335
HALLMARK_E2F_TARGETS	194	1.807984	0	0.002945
HALLMARK_MTORC1_SIGNALING	189	1.737239	0	0.007111
HALLMARK_APICAL_SURFACE	44	1.632676	0.010504	0.014033
HALLMARK_HEDGEHOG_SIGNALING	36	1.543138	0.025341	0.027647
HALLMARK_FATTY_ACID_METABOLISM	145	1.505772	0.004695	0.035686
HALLMARK_OXIDATIVE_PHOSPHORYLATION	190	1.504944	0.002217	0.031484
HALLMARK_SPERMATOGENESIS	132	1.497038	0.00432	0.030267
HALLMARK_ANGIOGENESIS	35	1.419507	0.057971	0.053691
HALLMARK_CHOLESTEROL_HOMEOSTASIS	68	1.399752	0.044118	0.058805
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	111	1.286486	0.069869	0.132809
HALLMARK_GLYCOLYSIS	191	1.164008	0.141256	0.306158
HALLMARK_ADIPOGENESIS	194	1.161185	0.143498	0.289727
HALLMARK_G2M_CHECKPOINT	193	1.033894	0.366667	0.598651
HALLMARK_XENOBIOTIC_METABOLISM	187	1.029852	0.375556	0.574139
HALLMARK_BILE_ACID_METABOLISM	110	0.971861	0.519427	0.727518
HALLMARK_PEROXISOME	99	0.929117	0.636364	0.826374
HALLMARK_PI3K_AKT_MTOR_SIGNALING	104	0.893945	0.703872	0.898499
HALLMARK_DNA_REPAIR	136	0.884729	0.745614	0.88112
HALLMARK_MYOGENESIS	197	0.859496	0.842105	0.903522
HALLMARK_HEME_METABOLISM	179	0.784741	0.96083	0.999151
HALLMARK_WNT_BETA_CATENIN_SIGNALING	41	0.772495	0.836032	0.970219
HALLMARK_PROTEIN_SECRETION	94	0.768796	0.909457	0.933819

Down regulated Hallmark pathways

NAME	SIZE	NES	NOM p-val	FDR q-val
HALLMARK_INTERFERON_ALPHA_RESPONSE	86	-2.31227	0	0
HALLMARK_INTERFERON_GAMMA_RESPONSE	183	-2.22526	0	0
HALLMARK_INFLAMMATORY_RESPONSE	194	-1.70631	0.001739	0.014258
HALLMARK_TNFA_SIGNALING_VIA_NFKB	195	-1.68275	0	0.013594
HALLMARK_ALLOGRAFT_REJECTION	182	-1.51006	0.005386	0.062058
HALLMARK_IL6_JAK_STAT3_SIGNALING	85	-1.4678	0.016227	0.07681
HALLMARK_UV_RESPONSE_DN	142	-1.34444	0.037801	0.177414
HALLMARK_APOPTOSIS	156	-1.34156	0.044405	0.159596
HALLMARK_COMPLEMENT	181	-1.33302	0.031308	0.151301
HALLMARK_TGF_BETA_SIGNALING	54	-1.3122	0.109959	0.162122
HALLMARK_ANDROGEN_RESPONSE	94	-1.30829	0.078755	0.151324
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	194	-1.28012	0.063636	0.17192
HALLMARK_KRAS_SIGNALING_UP	190	-1.23218	0.082437	0.226756
HALLMARK_COAGULATION	130	-1.20748	0.13594	0.24977
HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY	44	-1.18368	0.215606	0.272473
HALLMARK_IL2_STAT5_SIGNALING	194	-1.13565	0.186257	0.347795
HALLMARK_NOTCH_SIGNALING	31	-1.0307	0.380567	0.59108
HALLMARK_ESTROGEN_RESPONSE_EARLY	197	-1.0261	0.375235	0.571045
HALLMARK_HYPOXIA	192	-0.94878	0.591228	0.770025
HALLMARK_P53_PATHWAY	195	-0.93745	0.589161	0.764326
HALLMARK_UV_RESPONSE_UP	145	-0.91001	0.625229	0.803595
HALLMARK_KRAS_SIGNALING_DN	189	-0.89046	0.747715	0.8224
HALLMARK_PANCREAS_BETA_CELLS	39	-0.8738	0.67086	0.830947
HALLMARK_ESTROGEN_RESPONSE_LATE	191	-0.86581	0.777972	0.816015
HALLMARK_MITOTIC_SPINDLE	195	-0.84197	0.853933	0.838576
HALLMARK_APICAL_JUNCTION	194	-0.76891	0.960303	0.923438

F: Differential expression of genes in ETV7^{KALK} versus ETV7 expressing EW8 cells as determined by Affymetrix analysis.

Transcript ID	Gene Symbol	KALK vs ETV7	Transcript ID	Gene Symbol	KALK vs ETV7	Transcript ID	Gene Symbol	KALK vs ETV7
16987001	---	4.56	16745637	OR8D1	0.94	16905108	DLX2	0.71
17113549	KIAA1210	3.58	16905464	LOC105373760	0.94	16722299	PDE3B	0.71
17053917	EN2	2.44	16975592	GABRG1	0.93	16696811	ANGPTL1	0.71
16917373	FLRT3	2.27	17029847	---	0.93	17053850	PAXIP1-AS2	0.71
17103626	GAGE2D	2.21	16798496	GABRG3	0.92	16991418	MIR378H	0.71
17103647	GAGE2C	2.21	16883194	LOC100506123	0.91	16725041	FAM111B	0.70
17103679	GAGE12F	2.17	16978976	CFI	0.91	16873495	NOVA2	0.70
17103653	GAGE13	2.13	17105082	GPR174	0.91	16981444	AADAT	0.70
17113362	CAPN6	1.99	16886491	TNFAIP6	0.91	16974925	LGI2	0.70
16997816	EDIL3	1.89	16716063	MAT1A	0.90	16924149	LOC105379278	0.70
17103620	GAGE13	1.83	17110071	SRPX	0.90	16707120	STAMBPL1	0.70
17103673	GAGE12F	1.74	16669781	NBPF19	0.90	16698421	TMEM81	0.70
16854540	B4GALT6	1.74	17063394	KIAA1549	0.89	17057016	LOC105375249	0.70
16990284	PCDHB8	1.71	16914972	DOK5	0.89	16891603	KCNE4	0.69
17103655	GAGE12C	1.65	16659343	AADACL4	0.89	16770177	LOC105369980	0.69
17103661	GAGE12C	1.65	17042548	---	0.88	16894883	MATN3	0.69
17103667	GAGE12C	1.65	16714381	CSTF2T	0.88	16971382	DCLK2	0.69
17103690	GAGE12H	1.64	17112560	NAP1L3	0.87	16743890	CASP1	0.69
16748817	---	1.61	16900724	LOC100506123	0.87	16692834	CTSS	0.69
16986943	LOC105379057	1.56	16980160	INPP4B	0.86	17077004	SNAI2	0.69
17117110	CD24	1.54	16908926	---	0.86	16860667	KCTD15	0.69
17054201	LOC105379753	1.53	17050134	PIK3CG	0.86	16990264	PCDHB4	0.69
16677057	SYT14	1.48	16987773	---	0.85	16876731	SOX11	0.68
17091877	TUBBP5	1.47	16723318	PRRG4	0.85	16673652	LOC100127910	0.68
16708572	ELOVL3	1.46	17040662	---	0.84	16860152	ZNF430	0.68
16754895	NTS	1.46	16743721	MMP1	0.84	16830284	BCL6B	0.68
16950131	---	1.45	16804106	ADAMTSL3	0.84	16662664	MANEAL	0.68
16721011	TSSC2	1.45	16981099	NPY1R	0.84	16748227	KLRF1	0.68
16946280	CLSTN2	1.44	16798252	---	0.83	16930811	SEPT3	0.68
17100771	---	1.41	16900286	LINC00342	0.83	16847686	CSH1	0.68
16738657	GLYATL2	1.38	16679301	FMN2	0.83	16802771	BBS4	0.68
16734877	HBE1	1.37	17025989	DLL1	0.83	16782893	---	0.68
16854594	GAREM1	1.34	16889966	ADAM23	0.82	16716365	FAS-AS1	0.68
17105903	MUM1L1	1.34	16965798	PCDH7	0.82	17067729	NRG1-IT1	0.68
17049408	PCOLCE	1.30	16682098	EPHA2	0.82	16732807	VWA5A	0.68
16853879	PIEZO2	1.27	16999475	FBN2	0.82	16980744	RNF175	0.68
16985229	RGS7BP	1.26	16728141	GAL	0.82	17113335	SNORD96B	0.67
16767983	LOC101928395	1.25	16806467	TJP1	0.81	16677556	TGFB2	0.67
16972993	TLR3	1.25	16787790	OTUB2	0.81	16762941	DENND5B	0.67
16978896	COL25A1	1.23	17087413	GALNT12	0.81	16973247	FRG1	0.67
16998162	MCTP1	1.23	16753663	---	0.81	16999041	CDO1	0.67
16707149	FAS	1.22	16701106	CHML	0.81	16972480	CEP44	0.67
16997802	HAPLN1	1.20	16980051	CLGN	0.81	16714747	RTKN2	0.67
16676988	HSD11B1	1.20	16980126	RNF150	0.81	16994521	ANKH	0.67
16901986	IL1B	1.20	17074896	SGCZ	0.81	16900737	ANKRD36B	0.66
17063254	PTN	1.18	16805623	LOC400464	0.80	16812738	HDGFRP3	0.66
16786058	SNORD56B	1.18	16696348	LOC105371611	0.80	16932117	---	0.66
17007257	HLA-DRA	1.17	16962689	GMNC	0.80	16676965	CAMK1G	0.66
16692614	HIST2H3D	1.16	16979800	LOC101927359	0.80	16982477	---	0.66
17035880	---	1.16	16922920	BACE2	0.80	17061879	---	0.66
17038596	---	1.16	16972198	TLL1	0.80	16847711	GH1	0.66
17041225	---	1.16	17043095	SDK1	0.80	17020846	COL12A1	0.66
16857110	ANKRD24	1.16	16678851	KIAA1804	0.80	---	---	0.66
17103614	GAGE12J	1.16	17015324	NRN1	0.79	16891922	SP100	0.66
16903537	NMI	1.15	16982483	PLEKHG4B	0.79	16901591	MIR4266	0.66
16843417	SLFN12	1.15	16819161	GNAO1	0.79	16703251	KIAA1217	0.66
16979985	MGARP	1.15	16677071	SERTAD4	0.79	16805422	NR2F2	0.66
17033604	---	1.15	16981582	---	0.79	16705641	C10orf35	0.66
17096958	FRRS1L	1.14	16877297	TRIB2	0.79	16679142	RYR2	0.66
16770848	NOS1	1.14	16684391	NKAIN1	0.78	16982161	PDLIM3	0.65
16963113	APOD	1.13	16864907	ERVV-2	0.78	17103263	SSX1	0.65
16758440	---	1.12	17001506	PDE6A	0.78	17084413	---	0.65
16807172	---	1.12	16921475	---	0.78	16850410	---	0.65
16888912	MYO1B	1.10	16924066	---	0.77	16864565	SNAR-F	0.65
17114272	GPC4	1.10	16942866	CADM2	0.77	16761858	RERG	0.65
16898804	ADD2	1.10	17072125	MAL2	0.77	17105862	NRK	0.65
16734886	OR51B5	1.09	16722455	NCR3LG1	0.77	16734883	OR51B4	0.65
17031139	---	1.09	16730429	ARHGAP42	0.77	16956532	VGLL3	0.65
17028313	---	1.09	17071144	SDC2	0.77	17103756	CCNB3	0.65
17112060	PHKA1	1.06	16791580	PRKD1	0.77	16701238	AKT3	0.65
16904514	SCN3A	1.06	16821541	CRISPLD2	0.76	16701957	AKR1E2	0.65
16719025	FGFR2	1.06	17103789	---	0.76	16669501	LOC105379521	0.64
16978500	---	1.05	16693142	POGZ	0.76	16750154	CNTN1	0.64
16990321	PCDHB14	1.05	17105719	LL0XNC01-250H12.3	0.76	16764724	SMAGP	0.64
16893143	TWIST2	1.05	16910728	SIRPA	0.76	16798479	GABRA5	0.64
16807931	---	1.04	16902353	---	0.75	16966645	---	0.64
16991816	GABRG2	1.04	16700554	PCNXL2	0.75	17100991	---	0.64
17056825	TRGJP1	1.04	16970080	CEP170P1	0.75	16990280	PCDHB7	0.64
16969646	---	1.03	16924602	ADAMTS1	0.75	16852389	DCC	0.64
16833204	CCL2	1.02	16993335	ZNF354C	0.74	16979432	NDNF	0.64
17106518	LINC01285	1.02	16701119	PLD5	0.74	16753426	SRGAP1	0.64
17113463	LRCH2	1.01	16967602	MOB1B	0.74	16730104	SCARNA9	0.64
16754134	LGR5	1.00	16666326	ST6GALNAC3	0.74	16984049	---	0.64
16769419	GLT8D2	1.00	16738646	GLYAT	0.73	16853613	---	0.64
16709713	SLC18A2	1.00	16691969	LOC105371220	0.73	16972835	STOX2	0.64
16886382	KIF5C	1.00	16696373	VAMP4	0.73	16743091	FZD4	0.64
17102566	SYTL5	1.00	16901974	IL1A	0.73	17067739	NRG1	0.64
17027187	---	1.00	16705959	---	0.73	17113378	DCX	0.64
17034851	---	1.00	16996953	---	0.73	17026034	---	0.64
17037331	---	1.00	16981523	SCRG1	0.73	16787135	FLRT2	0.64
16878731	EHD3	1.00	16761139	LOC728715	0.73	16971443	FAM160A1	0.63
17040037	---	0.99	16697004	RNASEL	0.72	16662755	MACF1	0.63
17095111	GNAQ	0.99	16865153	CACNG7	0.72	17010703	PRSS35	0.63
16753222	LOC105369783	0.98	16944665	DTX3L	0.72	16928422	LOC105372966	0.63
17094494	---	0.98	17010278	---	0.72	16924061	DIP2A-IT1	0.63
17106552	LOC101928336	0.97	16837324	---	0.72	16977251	ANTXR2	0.63
16854360	ZNF521	0.97	16922940	---	0.72	16883201	---	0.63
17070110	PI15	0.97	16750254	---	0.72	16699174	PTPN14	0.63
16705507	SRGN	0.97	16737056	PAX6	0.72	16695216	IGSF9	0.63
16995177	PRLR	0.96	16667258	FNBP1L	0.72	16949467	LPP	0.63
17094175	---	0.96	17094863	---	0.72	17109714	SCARNA9L	0.63
16863534	---	0.96	16938527	RBMS3	0.72	16972824	STOX2	0.63
16840442	ALOX12-AS1	0.96	16765622	---	0.72	17113710	TMEM255A	0.62
17105727	LL0XNC01-250H12.3	0.96	16722445	NCR3LG1	0.71	16944982	---	0.62
16972076	NPY5R	0.96	16863209	---	0.71	16677407	SMYD2	0.62
17018039	HLA-DPA1	0.95	17085558	LOC105379826	0.71	16807763	EHD4	0.62
17032533	---	0.95	16980096	TBC1D9	0.71	16880478	C2orf74	0.62
16746341	MIR4697HG	0.95	16883853	POU3F3	0.71	17097731	PAPPA-AS1	0.62
			16816386	TMC7	0.71	16861438	LOC105372391	0.62
						16988359	---	0.62

F continued

Transcript ID	Gene Symbol	KALK vs ETV7	Transcript ID	Gene Symbol	KALK vs ETV7	Transcript ID	Gene Symbol	KALK vs ETV7
16911804	SLC24A3	0.61	16849148	RNF157	0.55	16900098	IGKV3D-15	0.50
17096956	MIR32	0.61	17018960	---	0.55	16798812	ARHGAP11B	0.50
16985950	MAP1B	0.61	16746638	---	0.55	16854301	ANKRD29	0.50
16798782	GOLGA8H	0.61	17051626	MEST	0.54	17097955	C5	0.50
16763577	SLC38A4	0.61	16972961	C4orf47	0.54	17025292	---	0.50
16798134	---	0.61	16884736	---	0.54	16838791	BAHCC1	0.50
17113606	SEPT6	0.61	16899533	LRRTM1	0.54	16816171	---	-0.50
17080516	ENPP2	0.61	17102559	SYTL5	0.54	16955440	---	-0.50
16994779	CDH10	0.61	17117888	ZEB2	0.54	17065117	---	-0.50
16943350	ADGRG7	0.61	16988537	---	0.54	17046249	MRPS17	-0.50
16991729	FABP6	0.61	16700074	CDC42BPA	0.54	17088819	OR1L4	-0.50
17117973	---	0.61	16872323	ZNF780A	0.54	16900016	---	-0.50
16958251	MYLK	0.61	16708122	CNNM1	0.54	17074342	LINC00965	-0.47
16904588	TTC21B	0.61	16932914	ZNF280B	0.54	17101029	PLCXD1	-0.50
16753710	HELB	0.61	16968583	AFF1	0.54	17070075	---	-0.50
16921724	NCAM2	0.61	16890675	IGFBP2	0.54	17005001	CD83	-0.51
16820386	---	0.61	17107287	BRS3	0.54	16973271	DBET	-0.51
16917877	LOC105372571	0.60	17087032	---	0.54	17067773	---	-0.51
17094893	ALDH1A1	0.60	16714890	HERC4	0.54	16847839	MIR5047	-0.51
17047459	SNORA14A	0.60	17037192	---	0.54	16734469	KCNQ1-AS1	-0.51
16701396	---	0.60	16881136	---	0.54	17118054	---	-0.51
16971660	LRAT	0.60	16686557	PIK3R3	0.54	17046094	---	-0.51
17092936	IZUMO3	0.60	17003401	LOC202181	0.54	16829469	---	-0.51
17054846	---	0.60	16970188	LOC645513	0.54	16911261	BMP2	-0.51
16916352	SRXN1	0.60	16677221	MIR3122	0.54	16789723	CRIP2	-0.51
16681827	DHRS3	0.60	16912224	LOC105372582	0.54	16788395	---	-0.51
16797599	IGHV3-72	0.60	17080849	LOC101927588	0.54	16863753	EMP3	-0.51
16749639	TSPAN11	0.60	17110551	SSX9	0.54	16693459	S100A3	-0.51
17010544	SH3BGRL2	0.59	17093031	MOB3B	0.54	16837126	---	-0.51
17023646	CTGF	0.59	17063194	SLC13A4	0.54	17046393	LOC102724777	-0.51
16979043	---	0.59	16679003	GPR137B	0.53	16949572	CLDN16	-0.51
16730471	CEP126	0.59	16807174	LOC105370772	0.53	16773032	---	-0.51
16904425	GRB14	0.59	16997650	ANKRD34B	0.53	16788653	SNORD114-9	-0.51
16686255	---	0.59	16696425	TNFSF4	0.53	16777198	CRYL1	-0.51
16798665	GOLGA8J	0.59	16692846	CTSK	0.53	16748500	APOLD1	-0.51
17093463	CNTFR	0.59	16675197	PLA2G4A	0.53	17019338	DNPH1	-0.52
16906308	TFPI	0.59	17105163	ZNF711	0.53	16954608	---	-0.52
16758730	DNAH10	0.59	17070381	LRRCC1	0.53	16835604	NXPH3	-0.52
16877463	VSNL1	0.59	16838249	LOC100507351	0.53	16798763	---	-0.52
16706174	---	0.59	16698049	KDM5B	0.53	16806536	---	-0.52
16678231	---	0.59	16701185	CEP170	0.53	16696612	---	-0.52
16701317	HNRNPU	0.59	17111435	WNK3	0.53	16974224	---	-0.52
16854639	NOL4	0.59	16880168	RPL23AP32	0.53	16840756	---	-0.52
16736595	PTPN5	0.59	16930144	APOBEC3A_B	0.53	16864737	MIR99B	-0.52
17028407	---	0.59	17012598	ENPP3	0.53	16844046	SNORA21	-0.52
16721809	ZNF143	0.59	16808306	PPIP5K1	0.53	16847203	---	-0.52
16944695	PARP14	0.59	17020727	MIR30A	0.53	17051573	---	-0.52
16743293	---	0.58	16748474	---	0.53	16871067	---	-0.52
16705329	MYPN	0.58	16931532	FAM19A5	0.53	16837391	KCNJ2	-0.52
16874604	SHANK1	0.58	16806461	NDNL2	0.53	17116050	PRKY	-0.52
16696478	ANKRD45	0.58	16996004	BRCAT54	0.53	17060235	---	-0.52
16761518	TAS2R31	0.58	16939283	WDR48	0.52	16774071	RFXAP	-0.52
16783887	LINC00871	0.58	16730180	PANX1	0.52	16814910	NPW	-0.52
16794980	TGFB3	0.58	16980882	MAP9	0.52	16849298	MXRA7	-0.53
16718696	HSPA12A	0.58	16905495	---	0.52	16773942	---	-0.53
16810473	DAPK2	0.58	16705976	MCU	0.52	17074521	---	-0.53
16920806	SYCP2	0.58	16678496	HIST3H2BB	0.52	16693449	S100A4	-0.53
16761583	LRP6	0.58	17085500	LOC102725126	0.52	16813029	HAPLN3	-0.53
16716350	ACTA2	0.58	16922959	MX2	0.52	16721375	SMPD1	-0.53
17092526	CER1	0.57	16983456	---	0.52	17114970	GABRE	-0.53
16686980	---	0.57	17090512	---	0.52	17115271	L1CAM	-0.53
16872803	CEACAM1	0.57	16990294	PCDHB10	0.52	17013694	PLEKHG1	-0.53
17103141	ZNF157	0.57	17105816	H2BFXP	0.52	16869291	SNORD41	-0.53
16691619	LINC00622	0.57	16861543	ZNF527	0.52	16898432	---	-0.53
16667662	CDC14A	0.57	16792154	SLC25A21	0.52	17090320	---	-0.53
16851383	GATA6	0.57	16675192	OCLM	0.52	16983742	---	-0.54
16677514	SPATA17	0.57	16761938	LMO3	0.52	17085520	---	-0.54
16723246	RCN1	0.57	16692080	LOC101928979	0.52	16737102	---	-0.54
16851933	GALNT1	0.57	16922613	SIM2	0.52	16858148	ICAM4	-0.54
17039907	---	0.57	17098477	ANGPTL2	0.52	17076586	ZMAT4	-0.54
16869427	CACNA1A	0.57	16990288	PCDHB16	0.52	17049003	GS1-259H13.2	-0.54
16703242	OTUD1	0.57	16826273	ITFG1	0.52	16839019	SLC16A3	-0.54
16906991	RFTN2	0.57	16782003	TRDC	0.52	17060012	SHFM1	-0.54
16684331	SDC3	0.57	17113928	TENM1	0.52	17100695	---	-0.54
16719233	OAT	0.57	16669997	NBPF12	0.51	17014798	SMOC2	-0.54
17106526	LONRF3	0.57	16978834	LEF1	0.51	16675227	ERVMER61-1	-0.54
16704107	LINC00839	0.57	16979944	---	0.51	16965834	LOC102723846	-0.54
16688323	GNG12	0.57	16966721	SNORA26	0.51	16788760	MIR539	-0.54
16982479	PLEKHG4B	0.57	17036177	---	0.51	16961372	TERC	-0.55
16744991	MPZL3	0.57	16665439	L1TD1	0.51	16732836	OR10D3	-0.55
16921664	CXADR	0.57	16692452	NBPF26	0.51	16787112	---	-0.55
16941871	IL17RB	0.56	16949909	MIR570	0.51	17065903	---	-0.55
16744205	ARHGAP20	0.56	16757347	OAS3	0.51	16973278	DUX4L25	-0.55
16673227	---	0.56	16978568	CENPE	0.51	16973287	DUX4L25	-0.55
16685729	BMP8B	0.56	16971019	GAB1	0.51	17012721	EYA4	-0.55
16860097	ZNF253	0.56	16797152	MIR4710	0.51	16960111	---	-0.55
16692724	ANP32E	0.56	16980834	---	0.51	16872682	GRIK5	-0.55
16789859	---	0.56	16984562	PARP8	0.51	16788614	SNORD113-9	-0.55
16850672	DLGAP1-AS5	0.56	16922899	PCP4	0.51	17059388	KIAA1324L	-0.55
16937793	---	0.56	16861510	ZNF383	0.51	17048576	PPP1R9A	-0.55
17056105	HOXA2	0.56	17012546	TMEM200A	0.51	16994340	CMBL	-0.55
16706662	TSPAN14	0.56	17075731	CLU	0.51	17072617	---	-0.55
16712442	SKIDA1	0.56	16705130	PHYHIPL	0.51	16904095	---	-0.56
16696918	---	0.55	16728991	---	0.51	17118088	---	-0.56
17010273	KCNQ5-IT1	0.55	16885976	---	0.51	17001944	---	-0.56
16868986	ELAVL3	0.55	16666416	NEXN	0.51	16982717	SLC6A18	-0.56
16681013	CHD5	0.55	17106511	ZCCHC12	0.50	16958161	SEMA5B	-0.56
17094224	ZNF658B	0.55	16709760	CASC2	0.50	17052910	OR2A2	-0.56
16889631	SNORD11	0.55	16984287	PTGER4	0.50	16994743	CDH12	-0.56
16990261	PCDHB3	0.55	16709317	MIR4295	0.51	16768543	SOCS2-AS1	-0.56
16662636	DNALI1	0.55	16981574	LOC101928509	0.50	16880291	---	-0.56
16798744	GOLGA8Q	0.55	16929920	H1F0	0.50	16688302	---	-0.56
17094656	LOC105379251	0.55	16854792	MIR924HG	0.50	17104098	PAGE2	-0.56
16677904	FBXO28	0.55	16973038	CYP4V2	0.50	17116061	---	-0.56
17100784	---	0.55	16966932	---	0.50	16863760	SYNGR4	-0.56
16906140	PDE1A	0.55	17105249	PCDH11X	0.50	17099697	MIR3689D1	-0.56
16708757	BORCS7	0.55	16717150	RRP12	0.50	16876507	LOC105373354	-0.56
16666485	IFI44L	0.55	16674737	LOC284648	0.50	16734284	KRTAP5-2	-0.57
			16854954	LOXHD1	0.50	17012699	RPS12	-0.57
						16676217	LAX1	-0.57

F continued

Transcript ID	Gene Symbol	KALK vs ETV7
16784098	FRMD6	-0.57
17092817	---	-0.57
16908817	---	-0.57
16772583	---	-0.57
16926754	S100B	-0.57
16722890	ANO5	-0.58
17078558	PAG1	-0.58
16685330	GRIK3	-0.58
16835592	NGFR	-0.58
16877667	FKBP1B	-0.58
17116497	---	-0.59
17099701	MIR3689D2	-0.59
17093083	---	-0.59
16870200	BST2	-0.59
16845518	TMEM101	-0.59
16885842	GPR39	-0.59
16959805	RBP1	-0.59
16833476	DHRS11	-0.59
16844356	TNS4	-0.60
17093059	---	-0.60
16918683	MMP24-AS1	-0.60
17019935	PKHD1	-0.60
16997141	---	-0.60
16948136	---	-0.60
16945187	---	-0.60
16748529	GPRC5A	-0.60
16913486	VSTM2L	-0.60
16947873	---	-0.60
16947018	---	-0.60
16698980	SLC30A1	-0.60
16752870	INHBC	-0.60
17116894	FAM197Y9	-0.60
16819207	MT2A	-0.60
17055447	MEOX2	-0.60
16995914	CCL28	-0.60
16981791	---	-0.60
16726880	NEAT1	-0.61
16777882	LOC105370145	-0.61
16866081	ZIK1	-0.61
17094191	---	-0.61
17117829	LOC105372488	-0.61
16676167	PRELP	-0.62
16912900	ASIP	-0.62
16906175	FRZB	-0.62
17077723	CYP7B1	-0.62
16788616	SNORD114-1	-0.62
17070094	---	-0.62
17085073	---	-0.62
17004208	FOXC1	-0.63
16691016	LINC01356	-0.63
16757090	---	-0.63
16788683	SNORD114-21	-0.63
16931514	---	-0.63
16746217	---	-0.63
17048879	ARPC1B	-0.63
17096457	CORO2A	-0.63
16850892	---	-0.64
17024079	MAP3K5	-0.64
16982699	SLC6A19	-0.64
17079407	TSPYL5	-0.64
16862491	TMEM91	-0.64
17100655	---	-0.65
16915564	---	-0.65
16744104	---	-0.65
16947148	ARHGEF26	-0.65
17099699	MIR3689B	-0.65
17099695	MIR3689A	-0.65
16683624	RUNX3	-0.65
16767324	SNORA70G	-0.65
16853325	HSBP1L1	-0.65
16846532	DLX3	-0.65
16788691	SNORD114-25	-0.65
16951557	---	-0.65
16853472	---	-0.66
16782010	TRAJ59	-0.66
16817624	SPN	-0.66
17087133	---	-0.66
16885502	RAB6C	-0.66
16942560	ARL6IP5	-0.67
16762992	LOC105369724	-0.67
16737422	---	-0.67
16780640	LOC105370333	-0.68
16835556	ABI3	-0.69
16840318	NLRP1	-0.69
16972987	---	-0.70
17044193	LOC101927841	-0.70
17077267	---	-0.70
16834196	FKBP10	-0.70
16967273	---	-0.70
16670164	---	-0.71
17059119	SEMA3C	-0.71
16973934	CYTL1	-0.71
16900189	---	-0.72
17090296	ASS1	-0.72
16718252	LOC102724418	-0.72
16695508	TSTD1	-0.73
16912362	ID1	-0.73
17019543	LOC101929705	-0.73
17070482	---	-0.73
17020787	MB21D1	-0.74
17005858	HIST1H2AI	-0.74
16965606	SLC34A2	-0.74
16971272	EDNRA	-0.75
16957263	DPPA4	-0.75
16815310	TNFRSF12A	-0.75
16778829	CPB2	-0.75
16704237	---	-0.76
16983159	---	-0.76
17002874	---	-0.76
17048742	NPTX2	-0.76
16961094	---	-0.77
16929396	---	-0.77
17095150	TLE1	-0.78
16858118	SNORD105	-0.78
17078751	REXO1L1P	-0.79
16995848	SEPP1	-0.79
16760889	C3AR1	-0.79
17104253	MSN	-0.79
16680258	MXRA8	-0.79
17116344	XKRY2	-0.80
17117044	XKRY2	-0.80
17010175	OGFRL1	-0.80
16934300	---	-0.80
16879250	GALM	-0.81
16853855	---	-0.83
16979163	ARSJ	-0.84
16681924	PRAMEF14	-0.84
16762154	ABCC9	-0.85
17004198	FOXF2	-0.85
16677254	SNORA16B	-0.86
16917183	JAG1	-0.86
16850428	ROCK1P1	-0.87
16887900	---	-0.88
16882821	---	-0.88
16770664	TBX5	-0.89
17116028	TBL1Y	-0.90
17092794	HACD4	-0.90
16873174	ZNF229	-0.91
16833426	CCL4L2	-0.91
16774405	DNAJC15	-0.92
16860123	ZNF486	-0.92
17110920	PAGE1	-0.92
16833420	CCL4	-0.93
16870776	ZNF826P	-0.93
16788657	SNORD114-11	-0.95
16691090	PTPN22	-0.96
16735938	LINC00958	-0.98
16870782	ZNF737	-0.98
16819264	MT1X	-0.98
16924878	TIAM1	-0.99
16919242	MAFB	-1.00
16979825	PABPC4L	-1.00
17058863	CCL26	-1.01
16709405	PLEKHS1	-1.02
16855906	NETO1	-1.03
16854660	---	-1.03
16748590	EMP1	-1.04
16719638	LOC102725247	-1.04
17057868	LINC01446	-1.05
16838017	GALR2	-1.06
16829505	---	-1.07
17094358	---	-1.09
17092268	GLDC	-1.09
16816018	MIR365A	-1.10
16998551	SLCO4C1	-1.11
16753914	LYZ	-1.13
17099703	MIR3689E	-1.13
16870984	ZNF681	-1.18
16657746	---	-1.20
17024305	---	-1.23
17018615	ETV7	-1.24
17046407	ZNF727	-1.24
16862563	CEACAM6	-1.28
16941230	GRM2	-1.28
17046817	WBSCR17	-1.30
16716782	PDLIM1	-1.30
16698234	FMOD	-1.31
16966240	CHRNA9	-1.32
17107867	MAGEA6	-1.36
16754118	LOC105369827	-1.41
17097211	PTGR1	-1.44
16783729	LOC644919	-1.61
16691755	---	-1.61
16944618	CD86	-1.62
16911432	SLX4IP	-1.66
16781897	TRAV8-6	-1.67
16942958	EPHA3	-1.72
16713395	---	-1.77
16990267	PCDHB5	-1.98
16885244	CNTNAP5	-2.13
16659371	PRAMEF1	-2.13
17020497	---	-2.15
16681907	PRAMEF14	-2.19
17116675	---	-2.26
17114520	ARHGEF6	-2.97
16736773	SLC5A12	-3.83
16977052	CXCL10	-3.84

G: Mass spectrometry analysis of purified Origene human ETV7 protein.

H: Mass spectrometry analysis of purified Origene human mTOR protein.

G

Description	Spectral Count	Total Peptides
Transcription factor ETV7	716	20
Tubulin beta chain	29	12
Tubulin beta-4A chain	29	11
Heat shock 70 kDa protein 1A/1B	21	12
Tubulin beta-2A chain	20	8
Pyruvate kinase PKM	17	11
Heat shock protein HSP 90-beta	14	11
L-lactate dehydrogenase B chain	14	7
Elongation factor 2	14	7
Heat shock cognate 71 kDa protein	11	8
Histone H2B type 1-O	11	2
Histone H2B type 1-H	11	2
Heat shock 70 kDa protein 6	10	5
Histone H4	9	4
Guanine nucleotide-binding protein subunit beta-2-like 1	9	7
Heat shock protein HSP 90-alpha	7	5
Heat shock cognate 71 kDa protein (Fragment)	6	4
ATP-dependent RNA helicase A	6	6
Actin, gamma-enteric smooth muscle	5	1
ATP synthase subunit beta, mitochondrial	5	5
Glyceraldehyde-3-phosphate dehydrogenase	4	3
40S ribosomal protein S14	4	2
Rab GDP dissociation inhibitor alpha	4	3
ATP synthase subunit alpha, mitochondrial	4	4
Histone H2A type 1-D	4	2
Histone H1.2	4	3
Elongation factor 1-alpha 1	4	3
Ubiquitin (Fragment)	4	2
Nuclease-sensitive element-binding protein 1	4	4
L-lactate dehydrogenase A chain 2	4	3
60S ribosomal protein L8	4	3
Heterogeneous nuclear ribonucleoproteins C1/C2	4	2
Fatty acid synthase	4	3
Rab GDP dissociation inhibitor beta	3	2
40S ribosomal protein S3	3	2
Histone H3.2	3	2
40S ribosomal protein S8	3	2
Histone H3.1	3	2
60S ribosomal protein L19	3	2
T-complex protein 1 subunit epsilon	3	2
T-complex protein 1 subunit alpha	3	3
D-3-phosphoglycerate dehydrogenase	3	3
60S ribosomal protein L10	3	2
Poly [ADP-ribose] polymerase 1	3	2
Dolichyl-diphosphooligosaccharide-protein	3	2
glycosyltransferase subunit	3	3
60S ribosomal protein L23	3	2
Proliferating cell nuclear antigen	3	3
Cofilin-1	2	2
Eukaryotic initiation factor 4A-II	2	2
ADP/ATP translocase 1	2	2
40S ribosomal protein S11	2	2
78 kDa glucose-regulated protein	2	2
60S ribosomal protein L13	2	2
Neutral alpha-glucosidase AB	2	2
40S ribosomal protein S4, X isoform	2	2
Ubiquitin-40S ribosomal protein S27a	2	1
Prohibitin-2	2	2
Heterogeneous nuclear ribonucleoprotein U	2	2
60S ribosomal protein L14	2	2

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Description	Spectral Count	Total Peptides
Serine/threonine-protein kinase mTOR	1341	187
Heat shock 70 kDa protein 1A/1B	215	38
Heat shock cognate 71 kDa protein	162	34
Heat shock 70 kDa protein 1-like	104	13
Protein arginine N-methyltransferase 5	85	26
Heat shock cognate 71 kDa protein (Fragment)	80	12
Tubulin beta-4B chain	61	18
Tubulin beta chain	56	16
Tubulin beta-4A chain	49	14
Heat shock 70 kDa protein 6	46	8
Kinesin-like protein KIF11	44	25
Tubulin beta-2A chain	42	12
Tubulin beta-2B chain	42	12
Methylosome protein 50	42	11
Protein phosphatase 1B	41	18
Heat shock 70 kDa protein 4	38	23
60 kDa heat shock protein, mitochondrial	36	23
Stress-70 protein, mitochondrial	33	17
Tubulin beta-3 chain	26	7
Heat shock protein 105 kDa	23	18
BAG family molecular chaperone regulator 2	18	10
Ubiquitin (Fragment)	16	4
Tubulin beta-8 chain	14	4
40S ribosomal protein S3	11	9
ADP/ATP translocase 2	11	7
Heat shock protein HSP 90-beta	9	9
78 kDa glucose-regulated protein	9	4
Ubiquitin-40S ribosomal protein S27a	9	3
Heat shock 70 kDa protein 4L	9	9
Protein phosphatase 1A	8	3
40S ribosomal protein S27	8	4
E3 ubiquitin-protein ligase CHIP	8	5
60S ribosomal protein L23	8	2
Serine/threonine-protein kinase 38	8	6
Heat shock protein HSP 90-alpha	7	6
Phosphate carrier protein, mitochondrial	7	4
Elongation factor Tu, mitochondrial	6	4
Sodium/potassium-transporting ATPase subunit alpha-1	5	5
ADP/ATP translocase 1	5	4
40S ribosomal protein S2	5	5
RNA-binding protein 10	5	4
ATP synthase subunit alpha, mitochondrial	4	4
Elongation factor 1-alpha 1	4	3
DnaJ homolog subfamily A member 1	4	4
40S ribosomal protein S18	3	3
Eukaryotic translation initiation factor 4B	3	3
60S ribosomal protein L10	3	2
26S proteasome non-ATPase regulatory subunit 1	3	3
BAG family molecular chaperone regulator 5	3	3
Sodium/potassium-transporting ATPase subunit alpha-3	2	2
ATP synthase subunit alpha, mitochondrial	2	2
40S ribosomal protein S16	2	1
Methylosome subunit pICln	2	1
60S ribosomal protein L11	2	1
OTU domain-containing protein 4	2	2
Serine/threonine-protein kinase RIO1	2	1