

Additional file

Pancreatic cancer-initiating cell exosome message transfer into noncancer-initiating cells: The importance of CD44v6 in reprogramming

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Table S1

Alphabetic list of gene symbols

Gene symbol	Gene Name
ABCA3, C3, C4, E1	ATP binding cassette subfamily A member 3, C member 3/4, E member 1
ABCG2	ATP binding cassette subfamily G member 2
ACP2	acid phosphatase 2, lysosomal
ACSS2	acyl-CoA synthetase short-chain family member 2
ADAM19	ADAM metalloproteinase with thrombospondin type 1 motif 19
ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8
ADAMTSL2	ADAMTS like 2
ADGRE2	adhesion G protein-coupled receptor E2
ADGRG6	adhesion G protein-coupled receptor G6
ADGRL1	adhesion G protein-coupled receptor L1
AGTPBP1	ATP/GTP binding protein 1
AKAP12	A-kinase anchoring protein 12
AKNA	AT-hook transcription factor
ALDH2	aldehyde dehydrogenase 2
ALDH3A1	aldehyde dehydrogenase 3 family member A1
AMIGO2	adhesion molecule with Ig like domain 2
AMOT	angiomin
ANO1	anoctamin 1
ANTXR1	anthrax toxin receptor 1
ANXA6	annexin A6
AP1AR	adaptor related protein complex 1 associated regulatory protein
APCDD1	APC down-regulated 1
APOE	apolipoprotein E
AQP3	aquaporin 3
ARGLU1	arginine and glutamate rich 1
ARHGAP1	Rho GTPase activating protein 1
ARHGAP18	Rho GTPase activating protein 18
ARHGEF40	Rho guanine nucleotide exchange factor 40
ARID5A	AT-rich interaction domain 5A
ARL15	ADP ribosylation factor like GTPase 15
ARL5B	ADP ribosylation factor like GTPase 5B
ATF3	activating transcription factor 3
ATP11A	ATPase phospholipid transporting 11A
ATP13A3	ATPase 13A3
ATP6V0D1	ATPase H ⁺ transporting V0 subunit d1
ATP6V0E2	ATPase H ⁺ transporting V0 subunit e2
ATP6V1B1	ATPase H ⁺ transporting V1 subunit B1
AXIN2	axin 2
AZGP1	alpha-2-glycoprotein 1, zinc-binding
BAMBI	BMP and activin membrane bound inhibitor
BAZ1A	bromodomain adjacent to zinc finger domain 1A
BCAS1	breast carcinoma amplified sequence 1
BCL2L15	BCL2 like 15
BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB
BHLHE40	basic helix-loop-helix family member e40
BIRC3	baculoviral IAP repeat containing 3
BMI1	BMI1 proto-oncogene, polycomb ring finger
BRWD1	bromodomain and WD repeat domain containing 1
BST2	bone marrow stromal cell antigen 2
BTAF1	B-TFIID TATA-box binding protein associated factor 1
BTBD6	BTB domain containing 6
BTG1	BTG anti-proliferation factor 1
BTG2	BTG anti-proliferation factor 2
C6orf48	chromosome 6 open reading frame 48
CACNA1D	calcium voltage-gated channel subunit alpha1D
CALHM3	calcium homeostasis modulator 3
CAPN15	calpain 15
CAPRN2	caprin family member 2
CAVIN3	caveolae associated protein 3
CCDC3	coiled-coil domain containing 3
CCDC69	coiled-coil domain containing 69
CCND2	cyclin D2
CCNL1	cyclin L1
CCNT2	cyclin T2
CD164	CD164 molecule / MUC-24
CD2AP	CD2 associated protein
CD55	CD55 molecule / DAF
CDC42EP1	CDC42 effector protein 1
CDH1	cadherin 1, E-cadherin
CDH2	cadherin 2, Ncad
CDK5	cyclin dependent kinase 5
CDK6	cyclin dependent kinase 6
CDKN1A	cyclin dependent kinase inhibitor 1A
CDKN2C	cyclin dependent kinase inhibitor 2C

Table S1 cont.

Symbol	Gene Name
CDX2	caudal type homeobox 2
CEACAM1, 5, 6	carcinoembryonic antigen related cell adhesion molecule 1, 5, 6
CEBPG	CCAAT/enhancer binding protein gamma
CEMIP	cell migration inducing hyaluronan binding protein
CEP290	centrosomal protein 290
CHAC1	ChaC glutathione specific gamma-glutamylcyclotransferase 1
CHI3L1	chitinase 3 like 1
CHML	CHM like, Rab escort protein 2
CHMP2B	charged multivesicular body protein 2B
CHORDC1	cysteine and histidine rich domain containing 1
CHRNA3, B1	cholinergic receptor nicotinic alpha 3 subunit, beta 1 subunit
CLASP2	cytoplasmic linker associated protein 2
CLDND1	claudin 1
CLEC3A	C-type lectin domain family 3 member A
CLK1	CDC like kinase 1
CLU	clusterin
COG8	component of oligomeric golgi complex 8
COL17A1	collagen type XVII alpha 1 chain
COL6A1	collagen type VI alpha 1
CPNE2	copine 2
CRAT	carnitine O-acetyltransferase
CREB3L4	cAMP responsive element binding protein 3 like 4
CREBZF	CREB/ATF bZIP transcription factor
CSNK1A1	casein kinase 1 alpha 1
CST1, 3, Z	cystatin SN, C, Z
CXCR4	C-X-C motif chemokine receptor 4
DBH	dopamine beta-hydroxylase
DBI	diazepam binding inhibitor, acyl-CoA binding protein
DCBLD2	discoidin, CUB and LCCL domain containing 2
DDAH2	dimethylarginine dimethylaminohydrolase 2
DDIT3, 4	DNA damage inducible transcript 3, 4
DDR1	discoidin domain receptor tyrosine kinase 1
DDX21,58, 60	DEAD-box helicase 21, 58, 60
DGKE, H	diacylglycerol kinase epsilon, eta
DHCR24	24-dehydrocholesterol reductase
DICER1	dicer 1, ribonuclease III
DKK1, 4	dickkopf WNT signaling pathway inhibitor 1, 4
DNAH14	dynein axonemal heavy chain 14
DNASE1	deoxyribonuclease I
DOCK6	dedicator of cytokinesis 6
DST	dystonin
DUS4L	dihydrouridine synthase 4 like
DUSP5	dual specificity phosphatase 5
DVL1	dishevelled segment polarity protein 1
DYSF	dysferlin
EBP	emopamil binding protein (sterol isomerase)
EGFR	epidermal growth factor receptor
EGR1	early growth response 1
EIF1AX	eukaryotic translation initiation factor 1A, X-linked
EIF3J, 4A2	eukaryotic translation initiation factor 3 subunit J, 4A2
EMP1	epithelial membrane protein 1
ENAH	enabled homolog
EPHA1, A4, B3	EPH receptor A1, A4, B3 [24]
EPS15	epidermal growth factor receptor pathway substrate 15
ERB2/ERB3	ERB2 estrogen receptor beta 2, HER2 / ERB-B2 receptor tyrosine kinase 3, HER3
EREG	epiregulin
ERMP1	endoplasmic reticulum metalloproteinase 1
ERRFI1	ERBB receptor feedback inhibitor 1
ESF1	ESF1 nucleolar pre-rRNA processing protein homolog
F2R	coagulation factor II thrombin receptor
FAK	protein tyrosine kinase 2, PTK2
FAM129A, 135A	family with sequence similarity 129 member A, 135 member A
FAT1	FAT atypical cadherin 1
FBXO2	F-box protein 2
FBXW4	F-box and WD repeat domain containing 4
FERMT1	fermitin family member 1
FGD3	FYVE, RhoGEF and PH domain containing 3
FGFR1,2,3,4	fibroblast growth factor receptor 1, 2, 3, 4
FHL1	four and a half LIM domains 1
FLNA	filamin A, B
FLT3	fms related tyrosine kinase 3
FMNL2	formin like 2
FOXP2	forkhead box N2
FRMD5	FERM domain containing 5
FSTL3	follicle-stimulating hormone-like 3
FUCA1	fucosidase, alpha-L- 1, tissue
FXYD6	FXYD domain containing ion transport regulator 6

Table S1 cont.

Symbol	Gene Name
GABRP	gamma-aminobutyric acid type A receptor pi subunit
GAL	galanin and GMAP prepropeptide
GAS5	growth arrest specific 5 (non-protein coding)
GATA2	GATA binding protein 2
GATA2-AS1	GATA2 antisense RNA1
GBP2	guanylate binding protein 2
GCLC, M	glutamate-cysteine ligase catalytic subunit, modifier subunit
GCSAM	germinal center associated signaling and motility
GDF15	growth differentiation factor 15
GEMIN5	gem nuclear organelle associated protein 5
GFPT1	glutamine--fructose-6-phosphate transaminase 1
GJB1	gap junction protein beta 1
GLUL	glutamate-ammonia ligase
GMFG	glia maturation factor gamma
GOLT1B	golgi transport 1B
GPD1L	glycerol-3-phosphate dehydrogenase 1-like
GPR155	G protein-coupled receptor 155
GPRC5A	G protein-coupled receptor class C group 5 member A
GRB10	growth factor receptor bound protein 10
GRM8	glutamate metabotropic receptor 8
GTF2F2	general transcription factor IIF subunit 2
GYP A	glycophorin A
H1F0	H1 histone family member 0
HELZ2	helicase with zinc finger 2
HES7	hes family bHLH transcription factor 7
HMGA1	high mobility group AT-hook 1
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase
HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1
HOXA11, B7, B8	homeobox A11, B7, B8
HPGD	15-hydroxyprostaglandin dehydrogenase
HSPA1A, 1B	heat shock protein family A (Hsp70) member 1A, 1B
HUNK	hormonally up-regulated Neu-associated kinase
HYAL2	hyaluronoglucosaminidase 2
ID1	inhibitor of DNA binding 1, HLH protein
IFI27	interferon alpha inducible protein 27 like 2
IFI5	interferon alpha inducible protein 6
IFI6	interferon induced with helicase C domain 1
IFIH1	interferon induced with helicase C domain 1
IFIT1, 2, 3	interferon induced protein with tetratricopeptide repeats 1, 2, 3
IFITM3	interferon induced transmembrane protein 3
IGFBP6	insulin like growth factor binding protein 6
IGF1R	insulin like growth factor 1 receptor
IL17RD	interleukin 17 receptor D
IKBKB	inhibitor of nuclear factor kappa B kinase, IKK β
INHBE	inhibin beta E subunit
INSIG1	insulin induced gene 1
INSR	insulin receptor
INTS5	integrator complex subunit 5
IPMK	inositol polyphosphate multikinase
ISG15	ISG15 ubiquitin-like modifier
ITGA6, B1, B4	integrin subunit alpha 6, beta 1, beta 4
ITK	IL2 inducible T cell kinase
JAG1, 2	jagged 1, 2
JMY	junction mediating and regulatory protein, p53 cofactor
JPH1	junctionophilin 1
JUN	Jun proto-oncogene, AP-1 transcription factor subunit
KAZALD1	Kazal type serine peptidase inhibitor domain 1
KCNJ5	potassium voltage-gated channel subfamily J member 5
KCNQ1OT1	KCNQ1 opposite strand/antisense transcript 1 (non-protein coding)
KIAA1804	mixed lineage kinase 4
KLHL17	kelch like family member 17
KLK1	kallikrein 1
KLK10	kallikrein related peptidase 10
L1CAM	L1 cell adhesion molecule
LAMA3, A5, B3, C2	laminin subunit alpha 3, alpha 5, beta 3, gamma 2
LCN2	lipocalin 2
LCOR	ligand dependent nuclear receptor corepressor
LDHA	lactate dehydrogenase A
LGALS1	galectin 1
LIN7C	lin-7 homolog C, crumbs cell polarity complex component
LMO4	LIM domain only 4
LONP1	lon peptidase 1, mitochondrial
LPR6	LDL receptor related protein 6
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
LUC7L3	LUC7 like 3 pre-mRNA splicing factor
LYPLA1	lysophospholipase I
MAFK	MAF bZIP transcription factor K

Table S1 cont.

Symbol	Gene Name
MAK16	MAK16 homolog
MAL2	mal, T-cell differentiation protein 2 (gene/pseudogene)
MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
MAPK	mitogen-activated protein kinase
MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3
MBNL2	muscleblind like splicing regulator 2
MBP	myelin basic protein
MBTPS2	membrane bound transcription factor peptidase, site 2
MCOLN3	mucolipin 3
MCSFR	colony stimulating factor 1 receptor, CSF1R
MCTP1	multiple C2 and transmembrane domain containing 1
MDN1	midasin AAA ATPase 1
MEIS2	Meis homeobox 2
MET	MET proto-oncogene receptor tyrosine kinase
MIB1	mindbomb E3 ubiquitin protein ligase 1
MRPL12	mitochondrial ribosomal protein L12
MSMO1	methylsterol monooxygenase 1
MT-ND5	NADH dehydrogenase, subunit 5 (complex I)
MTSS1	metastasis suppressor 1
MVK	mevalonate kinase
MX1, 2	MX dynamin like GTPase 1, 2
MXD1	MAX dimerization protein 1
MXI1	MAX interactor 1, dimerization protein
MYC	v-myc avian myelocytomatosis viral oncogene homolog
MYCL	v-myc avian myelocytomatosis viral oncogene lung carc homolog, bHLH transcription factor
MYHB7	myosin heavy chain 7B
MYL6	myosin light chain 6
MYO10, 1D	myosin X, 1D
MYSM1	Myb like, SWIRM and MPN domains 1
NAE1	NEDD8 activating enzyme E1 subunit 1
NAMPT	nicotinamide phosphoribosyltransferase
NANOG	Nanog homeobox
NCS1	neuronal calcium sensor 1
NDRG1	N-myc downstream regulated 1
NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)
NEBL	nebullette
NEDD9	neural precursor cell expressed, developmentally down-regulated 9
NEK6	NIMA related kinase 6
NEURL1B	neuralized E3 ubiquitin protein ligase 1B
NFATC4	nuclear factor of activated T-cells 4
NFE2	nuclear factor, erythroid 2
NFXL1	nuclear transcription factor, X-box binding like 1
NGFR	nerve growth factor receptor
NKD1	naked cuticle homolog 1
NLN	neurolysin
NMD3	NMD3 ribosome export adaptor
NOP58	NOP58 ribonucleoprotein
NOTCH1	neurogenic locus notch homolog protein 1
NOTUM	NOTUM, palmitoleoyl-protein carboxylesterase
NOX1	NADPH oxidase 1
NPC2	NPC intracellular cholesterol transporter 2
NR1D1	nuclear receptor subfamily 1 group D member 1
NRP1	neuropilin 1
NTN1	netrin 1
NTSR1	neurotensin receptor 1 (high affinity)
OAS1, 2, 3	2'-5'-oligoadenylate synthetase 1, 2, 3
OASL	2'-5'-oligoadenylate synthetase like
OBSL1	obscurin like 1
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase
ORAI3	ORAI calcium release-activated calcium modulator 3
OTUD3	OTU deubiquitinase 3
PABPC1L	poly(A) binding protein cytoplasmic 1 like
PAPD5	PAP associated domain containing 5
PAQR3	progesterin and adipoQ receptor family member 3
PARD6B	par-6 family cell polarity regulator beta
PARM1	prostate androgen-regulated mucin-like protein 1
PARP10	poly(ADP-ribose) polymerase family member 10
PARP9	poly(ADP-ribose) polymerase family member 9
PAWR	pro-apoptotic WT1 regulator
PAXB1	PAX3 and PAX7 binding protein 1
PBXIP1	PAX interacting protein 1
PCOLCE2	procollagen C-endopeptidase enhancer 2
PCSK5	proprotein convertase subtilisin/kexin type 5
PCSK9	proprotein convertase subtilisin/kexin type 9
PDGFRB	platelet derived growth factor receptor beta
PER1	period circadian clock 1
PHLDA2, B2	pleckstrin homology like domain family A member 2, B member 2

Table S1 cont.

Symbol	Gene Name
PIK3R3	phosphoinositide-3-kinase regulatory subunit 3
PIM1, 3	Pim-1, 3 proto-oncogene, serine/threonine kinase
PKD1	polycystin 1, transient receptor potential channel interacting
PKN2	protein kinase N2
PLAUR	plasminogen activator, urokinase receptor
PLIN3	perilipin 3
PLSCR1	phospholipid scramblase 1
PM20D2	peptidase M20 domain containing 2
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1
PMEPA1	prostate transmembrane protein, androgen induced 1
PNN	pinin, desmosome associated protein
POLR1D	RNA polymerase I subunit D
POLR3E, 3G	RNA polymerase III subunit E, G
PPARD	peroxisome proliferator activated receptor delta
PPP3CA	protein phosphatase 3 catalytic subunit alpha
PRDX2	peroxiredoxin 2
PRICKLE4	prickle planar cell polarity protein 4
PRKCBDBP	protein kinase C delta binding protein
PRPF39	pre-mRNA processing factor 39
PRR5L	proline rich 5 like
PRSS23, 3	serine protease 23, 3
PSD3	pleckstrin and Sec7 domain containing 3
PSMB9	proteasome subunit beta 9
PTPN11, 2	protein tyrosine phosphatase, non-receptor type 11, 2
PUM3	pumilio RNA binding family member 3
PUS7	pseudouridylate synthase 7 (putative)
PVR	poliovirus receptor
RAB12, 15, 42	RAB12,15, 42 member RAS oncogene family
RABGGTB	Rab geranylgeranyltransferase beta subunit
RARRS1, 3	retinoic acid receptor responder 1, 3
RASL11A, 11B	RAS like family 11 member A, B
RBM26, 39	RNA binding motif protein 26, 39
REEP2	receptor accessory protein 2
RET	ret proto-oncogene
RGS2	regulator of G-protein signaling 2
RHBDL2	rhomboid like 2
RHPN1	rhopilin Rho GTPase binding protein 1
RICTOR	RPTOR independent companion of MTOR complex 2
RIDA	reactive intermediate imine deaminase A homolog
RIF1	replication timing regulatory factor 1
RON	macrophage stimulating 1 receptor, MST1R, CD136
RPL32P3	ribosomal protein L32 pseudogene 3
S100A13	S100 calcium binding protein A13
SAMHD1	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1
SASS6	SAS-6 centriolar assembly protein
SAT1	spermidine/spermine N1-acetyltransferase 1
SCAMP1	secretory carrier membrane protein 1
SCD	stearoyl-CoA desaturase
SCEL	sciellin
SCML1	sex comb on midleg-like 1 (Drosophila)
SCNN1A	sodium channel epithelial 1 alpha subunit
SDC4	syndecan 4
SEC14L2	SEC14 like lipid binding 2
SERPINA2, E1, E2	serpin family A member 2, E member 1, 2
SFN	stratifin
SHROOM1	shroom family member 1
SHTN1	shootin 1
SIK1	siah E3 ubiquitin protein ligase 2
SLC12A4	solute carrier family 12 member 4
SLC19A2	solute carrier family 19 member 2
SLC1A4	solute carrier family 1 member 4
SLC20A1	solute carrier family 20 member 1
SLC22A3	solute carrier family 22 member A3
SLC25A1	solute carrier family 25 member 1
SLC25A36	solute carrier family 25 member 36
SLC25A37	solute carrier family 25 member 37
SLC2A6	solute carrier family 2 member 6
SLC35A3	solute carrier family 35 member A3
SLC35D1	solute carrier family 35 member D1
SLC35F2	solute carrier family 35 member F2
SLC38A11	solute carrier family 38 member 11
SLC3A2	solute carrier family 3 member 2
SLC40A1	solute carrier family 40 member 1
SLC4A4	solute carrier family 4 member 4
SLC4A7	solute carrier family 4 member 7
SLC4A8	solute carrier family 4 member 8
SLC5A1	solute carrier family 5 member 1

Table S1 cont.

Symbol	Gene Name
SLC7A11	solute carrier family 7 member 11
SLC7A2	solute carrier family 7 member 2
SLC7A8	solute carrier family 7 member 8
SLCO4A1	solute carrier organic anion transporter family member 4A1
SLMAP	sarcolemma associated protein
SNHG1, 15, 17	small nucleolar RNA host gene 1, 15, 17
SORT1	sortilin 1
SP5	Sp5 transcription factor
SPCS3	signal peptidase complex subunit 3
SPINK1	serine peptidase inhibitor, Kazal type 1
SPIRE1	spire type actin nucleation factor 1
SPNS2	sphingolipid transporter 2
SPRY1,2,3,4	sprouty RTK signaling antagonist 1, 2, 3, 4
SPTB	spectrin beta, erythrocytic
SPTBN2	spectrin beta, non-erythrocytic 2
SREBF1, B2	sterol regulatory element binding transcription factor 1, 2
ST5	suppression of tumorigenicity 5
STARD13, 3, 4	STAR related lipid transfer domain containing 13, 3, 4
STAT1, 2	signal transducer and activator of transcription 1, 2
STEAP2	STEAP2 metalloreductase
STK26	serine/threonine protein kinase 26
SV2A	synaptic vesicle glycoprotein 2A
SVIL	supervillin
SYK	spleen associated tyrosine kinase
SYNE1	spectrin repeat containing nuclear envelope protein 1
TAF1D	TATA-box binding protein associated factor, RNA polymerase I subunit D
TAP1	transporter 1, ATP binding cassette subfamily B member
TAS1R3	taste 1 receptor member 3
TBC1D17, 4	TBC1 domain family member 17, 4
TCEA1	transcription elongation factor A1
TDGF1	teratocarcinoma-derived growth factor 1
TEF	TEF, PAR bZIP transcription factor
TEK	TEK receptor tyrosine kinase, Tie2
TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)
TFRC	transferrin receptor
TGFB1/1	transforming growth factor beta 1 induced transcript 1
TGM2	transglutaminase 2
THBS1	thrombospondin 1
TIA1	TIA1 cytotoxic granule-associated RNA binding protein
TIMP1	Metallopeptidase inhibitor 1
TINAGL1	tubulointerstitial nephritis antigen like 1
TMED7	transmembrane p24 trafficking protein 7
TNC	tenascin C
TNFRSF11B, 19, 1B	TNF receptor superfamily member 11B, 19, 1B
TP53INP2	tumor protein p53 inducible nuclear protein 2
TRABD2A	TraB domain containing 2A
TRAF5	TNF receptor associated factor 5
TRDC	T cell receptor delta constant
TRIM21, 29, 69	tripartite motif containing 21, 29, 69
TRMT11	tRNA methyltransferase 11 homolog
TRNT1	tRNA nucleotidyl transferase 1
TRUB1	TruB pseudouridine synthase family member 1
TUBA1A1	tubulin alpha 1a
TWF1	twinfilin actin binding protein 1
TXNRD1	thioredoxin reductase 1
TYRO3	TYRO3 protein tyrosine kinase, Sky
U2SURP	U2 snRNP associated SURP domain containing
UBE2L6	ubiquitin conjugating enzyme E2 L6
VAMP8	vesicle associated membrane protein 8
VDAC3	voltage dependent anion channel 3
VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor
VEGFA, B	vascular endothelial growth factor A, B
VEGFR	vascular endothelial growth factor receptor
VMP1	vacuole membrane protein 1
VPS13A	vacuolar protein sorting 13 homolog A
VPS18	VPS18, CORVET/HOPS core subunit
WASL	Wiskott-Aldrich syndrome like
WBP2	WW domain binding protein 2
WDR19, 35, 36, 43	WD repeat domain 19, 35, 36, 43
WNK2	WNK lysine deficient protein kinase 2
WNT	proto-oncogene Wnt, wingless-type MMTV integration site family
WWOX	WW domain containing oxidoreductase
XPOT	exportin for tRNA
YRDC	yrDC N6-threonylcarbamoyltransferase domain containing
ZBTB10, 21,7C	zinc finger and BTB domain containing 10, 21, 7C
ZFAS1	ZNF1 antisense RNA 1
ZMYM1	zinc finger MYM-type containing 1

Table S1 cont.

Symbol	Gene Name
ZNF121, 146, 267	zinc finger protein 121, 146, 267
ZNF280C, 518A	zinc finger protein 280C, 518A
ZNF697, 704	zinc finger protein 697, 704
ZNF770, 831, 92	zinc finger protein 770, 831, 92
ZRANB2	zinc finger RANBP2-type containing 2

TableS2
Antibodies and Reagents
Table S2A
Antibodies

Antibody	origin	supplier
Actin	mouse	Becton Dickinson, HD, G
AIF	rabbit	Santa Cruz, HD, G
AKT	mouse	Becton Dickinson, HD, G
p-AKT	mouse	Becton Dickinson, HD, G
APC	mouse	Cell Signaling, Frankfurt, G
Axin1	rabbit	Santa Cruz, HD, G
Axin2	rabbit	Santa Cruz, HD, G
BAD	hamster	Becton Dickinson, HD, G
p-BAD	rabbit	Cell Signaling, Frankfurt, G
BAK	rabbit	Becton Dickinson, HD, G
BAX	rabbit	Becton Dickinson, HD, G
BCL2	rabbit	Becton Dickinson, HD, G
BCLXL	rabbit	Cell Signaling, Frankfurt, G
BID	mouse	Becton Dickinson, HD, G
Caspase1	mouse	Becton Dickinson, HD, G
Caspase3	mouse	Becton Dickinson, HD, G
Casp3-activ.	rabbit	Becton Dickinson, HD, G
Caspase9	mouse	Becton Dickinson, HD, G
Casp9-cleaved	rabbit	Cell Signaling, Frankfurt, G
CD9	mouse	ImmunoTools, Friesoythe, G
CD11b (m)	rat	Becton Dickinson, HD, G
CD31 (m)	rat	Becton Dickinson, HD, G
CD44v6 (vFF18)	mouse	[1]
CD49c	mouse	Becton Dickinson, HD, G
CD49e	mouse	Becton Dickinson, HD, G
CD49f	mouse	Becton Dickinson, HD, G
CD54	mouse	Becton Dickinson, HD, G
CD56	mouse	Becton Dickinson, HD, G
CD63	mouse	Becton Dickinson, HD, G
CD81	mouse	Becton Dickinson, HD, G
CD95	hamster	Becton Dickinson, HD, G
CD95L	hamster	Becton Dickinson, HD, G
CD104	rabbit	Becton Dickinson, HD, G
CD106	mouse	Becton Dickinson, HD, G
CD133	rabbit	Becton Dickinson, HD, G
CD166	mouse	Becton Dickinson, HD, G
CD184 (CXCR4)	mouse	Becton Dickinson, HD, G
CytochromC	mouse	Becton Dickinson, HD, G
E-cadherin	mouse	Becton Dickinson, HD, G
EGFR (p)	mouse	BioTrend, Cologne, G
p-EGFR	mouse	Cell Signaling, Frankfurt, G
EpCAM (HEA125)	mouse	[2]
EphA1	rabbit	SantaCruz, HD, G
EphA4	rabbit	Santa Cruz, HD, G
ERK1/2	mouse	Becton Dickinson, HD, G
p-ERK1/2	mouse	Becton Dickinson, HD, G
Ezrin	rabbit	Sigma, Munich, G
p-Ezrin	rabbit	Santa Cruz, HD, G
FAK	rabbit	Cell Signaling, Frankfurt, G
p-FAK	rabbit	Cell Signaling, Frankfurt, G
Fos	rabbit	Cell Signaling, Frankfurt, G
FN	mouse	Becton Dickinson, HD, G
Gr1 (m)	rat	Becton Dickinson, HD, G
HER2 (p)	mouse	Becton Dickinson, HD, G
IGFR1	mouse	Becton Dickinson, HD, G
IGFR2	mouse	Becton Dickinson, HD, G
I κ B α	rabbit	Santa Cruz, HD, G
p-I κ B α	mouse	Becton Dickinson, HD, G
InsR	rabbit	SantaCruz, HD, G
JNK	rabbit	G Santa Cruz, HD, G
p-JNK	mouse	Becton Dickinson, HD, G
Jun	rabbit	Santa Cruz, HD, G
p-Jun	mouse	Becton Dickinson, HD, G
MDR1	mouse	Becton Dickinson, HD, G
MET	mouse	Cell Signaling, Frankfurt, G
MMP2	rabbit	Dianova, Hamburg, G
MMP9	rabbit	Dianova, Hamburg, G
MTOR	rabbit	Cell Signaling, Frankfurt, G
NANOG	rabbit	Santa Cruz, HD, G
N-Cadherin	mouse	Becton Dickinson, HD, G
NFAT	mouse	Becton Dickinson, HD, G
NGFR	mouse	Becton Dickinson, HD, G
NOTCH	mouse	Biolegend, San Diego, Ca, US

Table S2A contin.

<u>Antibody</u>	<u>origin</u>	<u>supplier</u>
p-P38	rabbit	Santa Cruz, HD, G Santa Cruz, HD, G
Parp	mouse	Biolegend, San Diego, Ca, US
Parp-cleaved	mouse	Biolegend, San Diego, Ca, US
PDGFRA	mouse	Becton Dickinson, HD, G
PDGFRB	mouse	Becton Dickinson, HD, G
PI3K	rabbit	Cell Signaling, Frankfurt, G
p-PI3K	rabbit	Cell Signaling, Frankfurt, G
p-PKC	rabbit	Cell Signaling, Frankfurt, G
p-PLC	rabbit	Cell Signaling, Frankfurt, G
Pten	rabbit	Cell Signaling, Frankfurt, G
p-Pten	rabbit	Cell Signaling, Frankfurt, G
p-Rac	rabbit	Cell Signaling, Frankfurt, G
p-Ras	mouse	Santa Cruz, HD, G
RhoGDI	rabbit	Abcam, Cambridge, GB
SLUG	rabbit	Santa Cruz, HD, G
SMAC/DIABLO	mouse	Becton Dickinson, HD, G
SNAIL	rabbit	Santa Cruz, HD, G
SOX2	rabbit	Santa Cruz, HD, G
Src	rabbit	Santa Cruz, HD, G
p-src	rabbit	Cell Signaling, Frankfurt, G
Syndecan	rabbit	Santa Cruz, HD, G
TIMP1	mouse	Santa Cruz, HD, G
TNFR1	mouse	Becton Dickinson, HD, G
TNFR2	rat	Santa Cruz, HD, G
TRAIL	rabbit	Santa Cruz, HD, G
Tspan8 (CO029)	mouse	[3]
TWIST	rabbit	Becton Dickinson, HD, G
UPAR	mouse	Calbiochem, Darmstadt, G
VEGFR1	mouse	Becton Dickinson, HD, G
VEGFR2	mouse	Becton Dickinson, HD, G
VEGFR3	rabbit	Santa Cruz, HD, G
VIMENTIN	mouse	Becton Dickinson, HD, G
Wnt1	rabbit	Santa Cruz, HD, G
Wnt5a/b	rabbit	Santa Cruz, HD, G
XIAP	mouse	Becton Dickinson, HD, G
ZEB1	rabbit	Santa Cruz, HD, G
dye or biotin labeled secondary antibodies / Streptavidin		Dianova, Becton Dickinson, Amersham

Table S2B

Reagents

<u>Reagent</u>	<u>Dose</u>	<u>Supplier</u>
AnnexinV-FITC / -APC	variable	Becton Dickinson, HD, G
CFSE (carboxyfluoresc.-succinimidylester)	5µM	Invitrogen, Darmstadt, G
Cisplatin	5-30µg/ml	Sigma, Munich, G
DAPI	1µg/ml	Invitrogen, Darmstadt, G
PI	variable	Becton Dickinson, HD, G

Table S2C

qRT-PCR miRNA primers**Primers**

miR-1246 SL	GTTGGCTCTGGTGCAGGTCCAGGTATTCGCACCAGAGCCAACCCTGCT
miR-1246 fw	GGGCTAATGGATTTTTGGAGC
miR-3196 SL	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAAC GAGGCC
miR-3196 fw	TTTTTTCGGGGCGGCAGG
miR-6087 SL	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAAC GCTCGC
miR-6087 fw	TTGTTTTGAGGCGGGGG
miR-7704 SL	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAAC GCCGGG
miR-7704 fw	TTTTTTCGGGGTCCGCGG
Univ.reverse	GTGCAGGGTCCGAGGT

References

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- Momburg F, Moldenhauer G, Hämmerling GJ, Möller P. Immunohistochemical study of the expression of a Mr 34,000 human epithelium-specific surface glycoprotein in normal and malignant tissues. *Cancer Res.* 1987;47:2883-91.
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Table S3

The impact of CIC-TEX treatment on mRNA recovery in CD44v6kd and Tspan8k cells

Table S3A

Increased mRNA recovery in CIC-TEX-treated Tspan8kd cells

Symbol	Tsp8kd	Tsp8kd+TEX	Tsp8kd+TEX:		Gene Name
			Tsp8kd	Tsp8kd	
ADAM19	2957	7989	2.702		ADAM metallopeptidase domain 19
AHNAK2	734	1928	2.625		AHNAK nucleoprotein 2
AKAP12	1433	4331	3.023		A-kinase anchoring protein 12
AKR1B10	1393	2848	2.044		aldo-keto reductase family 1 member B10
ANXA10	1679	3758	2.238		annexin A10
CALB2	2954	5968	2.02		calbindin 2
CAPRIN2	2225	6480	2.912		caprin family member 2
CCAT1	624	1253	2.007		colon cancer associated transcript 1 (non-protein coding)
CEACAM5	321	4033	12.578		carcinoembryonic antigen related cell adhesion molecule 5
CEACAM6	1230	8612	7.003		carcinoembryonic antigen related cell adhesion molecule 6
CEMIP	4256	9726	2.285		cell migration inducing hyaluronan binding protein
CHAC1	710	1713	2.414		ChaC glutathione specific gamma-glutamylcyclotransferase 1
COL17A1	3337	8869	2.658		collagen type XVII alpha 1
DCBLD2	3135	7757	2.474		discoïdin, CUB and LCCL domain containing 2
DDIT3	612	1646	2.69		DNA damage inducible transcript 3
DDIT4	1828	4879	2.668		DNA damage inducible transcript 4
DKK1	2518	6444	2.559		dickkopf WNT signaling pathway inhibitor 1
DUSP5	568	1135	1.997		dual specificity phosphatase 5
EGR1	1742	3700	2.124		early growth response 1
EMP1	1981	5526	2.79		epithelial membrane protein 1
EREG	8012	16798	2.097		Epiregulin
ERRFI1	4536	13557	2.989		ERBB receptor feedback inhibitor 1
FAM129A	1730	3450	1.994		family with sequence similarity 129 member A
FAM135A	930	1894	2.036		family with sequence similarity 135 member A
FRMD5	621	1236	1.991		FERM domain containing 5
H1F0	11089	33900	3.057		H1 histone family member 0
HMGA1	32429	66203	2.041		high mobility group AT-hook 1
ID1	1280	3276	2.559		inhibitor of DNA binding 1, HLH protein
IFI27	1863	6985	3.749		interferon alpha inducible protein 27
IFI6	1105	2514	2.275		interferon alpha inducible protein 6
IGFBP6	3224	6619	2.053		insulin like growth factor binding protein 6
JAG1	1956	6030	3.083		jagged 1
KLK10	1770	3634	2.053		kallikrein related peptidase 10
LAMA3	1699	3660	2.154		laminin subunit alpha 3
LAMC2	1850	4027	2.177		laminin subunit gamma 2
LCN2	8428	17538	2.081		lipocalin 2
LINC00941	374	1534	4.097		long intergenic non-protein coding RNA 941
MAOB	543	1190	2.193		monoamine oxidase B
NDRG1	2303	6502	2.824		N-myc downstream regulated 1
NEBL	827	1797	2.173		Nebulette
NR1D1	723	2202	3.045		nuclear receptor subfamily 1 group D member 1
NR1D2	1248	2932	2.35		nuclear receptor subfamily 1 group D member 2
NRP1	933	2345	2.514		neuropilin 1
NTSR1	3605	8527	2.365		neurotensin receptor 1 (high affinity)
PER1	667	1406	2.109		period circadian clock 1
PMEPA1	4418	9628	2.179		prostate transmembrane protein, androgen induced 1
PSD3	1879	3824	2.035		pleckstrin and Sec7 domain containing 3
SCEL	714	2590	3.627		Sciellin
SERPINE2	612	1315	2.148		serpin family E member 2
SLCO4A1	1270	3104	2.444		solute carrier organic anion transporter family member 4A1
SMOX	1392	3598	2.584		spermine oxidase
UPP1	697	2110	3.027		uridine phosphorylase 1

Table S3B

Increased mRNA recovery in CIC-TEX-treated CD44v6kd cells

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd+TEX: v6kd	Gene Name
ABCA3	1475	3161	2.143	ATP binding cassette subfamily A member 3
ABCC3	1023	2101	2.054	ATP binding cassette subfamily C member 3
ABCC4	1081	2576	2.383	ATP binding cassette subfamily C member 4
ABCE1	2367	5887	2.487	ATP binding cassette subfamily E member 1
ADGRL1	1235	2472	2.002	adhesion G protein-coupled receptor L1
AGTPBP1	736	1697	2.305	ATP/GTP binding protein 1
AHNAK2	1124	2857	2.542	AHNAK nucleoprotein 2
AHSA2	753	1670	2.218	AHA1, activator of heat shock 90kDa protein
AKAP12	2129	5899	2.771	A-kinase anchoring protein 12
AKNA	330	1118	3.389	AT-hook transcription factor
ANO1	4644	9998	2.153	anoctamin 1
AP1AR	610	1304	2.138	adaptor related protein complex 1 associated regulatory protein
ARGLU1	1471	4483	3.047	arginine and glutamate rich 1
ARL5B	1318	2787	2.115	ADP ribosylation factor like GTPase 5B
ASNS	5813	26338	4.531	asparagine synthetase (glutamine-hydrolyzing)
ASS1	2767	5833	2.108	argininosuccinate synthase 1
ATF3	508	1149	2.262	activating transcription factor 3
ATP11A	3036	6499	2.141	ATPase phospholipid transporting 11A
ATP13A3	5803	11534	1.988	ATPase 13A3
B3GNT5	562	1152	2.049	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransf 5
B4GALNT4	418	1097	2.624	beta-1,4-N-acetyl-galactosaminyltransferase 4
BAG2	1348	2773	2.057	BCL2 associated athanogene 2
BAZ1A	2091	4375	2.092	bromodomain adjacent to zinc finger domain 1A
BDP1	1603	3594	2.242	B double prime 1, subunit polymerase IIIB
BMI1	511	1331	2.604	BMI1 proto-oncogene, polycomb ring finger
BRWD1	2618	5939	2.269	bromodomain and WD repeat domain containing 1
BTAFL1	2307	5829	2.527	B-TFIID TATA-box binding protein associated factor 1
C6orf48	2450	4933	2.013	chromosome 6 open reading frame 48
CAPRIN2	631	1650	2.615	caprin family member 2
CARNMT1	680	1647	2.422	carosine N-methyltransferase 1
CBS/CBSL	1946	4273	2.196	cystathionine-beta-synthase
CCDC112	528	1534	2.905	coiled-coil domain containing 112
CCDC14	1242	2739	2.205	coiled-coil domain containing 14
CCND2	1747	5230	2.994	cyclin D2
CCNL1	1820	4429	2.434	cyclin L1
CCNT2	1194	2501	2.095	cyclin T2
CD55	283	1411	4.985	CD55 molecule (Cromer blood group)
CDC42EP1	178	1171	6.576	CDC42 effector protein 1
CDK6	3158	9488	3.004	cyclin dependent kinase 6
CEBPG	1899	4959	2.612	CCAAT/enhancer binding protein gamma
CENPJ	1438	3038	2.112	centromere protein J
CEP290	633	1907	3.012	centrosomal protein 290
CFAP97	3123	6474	2.073	cilia and flagella associated protein 97
CHML	919	2395	2.606	CHM like, Rab escort protein 2
CHORDC1	864	2489	2.88	cysteine and histidine rich domain containing 1
CLDND1	548	1111	2.027	claudin domain containing 1
CLK1	1589	4123	2.595	CDC like kinase 1
CMTM4	2831	5835	2.061	CKLF like MARVEL transmembrane domain containing 4
CNTRL	496	1120	2.258	Centriolin
CREBZF	1230	3739	3.04	CREB/ATF bZIP transcription factor
CSNK1A1	443	1087	2.453	casein kinase 1 alpha 1
DCAF17	574	1201	2.093	DDB1 and CUL4 associated factor 17
DCBLD2	3053	11916	3.903	discoidin, CUB and LCCL domain containing 2
DCUN1D4	722	1771	2.452	defective in cullin neddylation 1 domain containing 4

Table S3B continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd+TEX: v6kd	Gene Name
DDIT3	634	1294	2.041	DNA damage inducible transcript 3
DDX21	8676	18053	2.081	DEAD-box helicase 21
DGKE	615	1333	2.168	diacylglycerol kinase epsilon
DGKH	2233	4493	2.012	diacylglycerol kinase eta
DICER1	2766	5784	2.091	dicer 1, ribonuclease III
DLGAP1-AS2	2430	4851	1.996	DLGAP1 antisense RNA 2
DNAH14	513	1291	2.517	dynein axonemal heavy chain 14
DNAJB14	784	1682	2.145	DnaJ heat shock protein family (Hsp40) member B14
DNAJC2	2044	4155	2.033	DnaJ heat shock protein family (Hsp40) member C2
DOCK6	435	1257	2.89	dedicator of cytokinesis 6
DPY19L3	577	1562	2.707	dpy-19 like 3 (C. elegans)
DST	1300	5515	4.242	Dystonin
DUS4L	593	1271	2.143	dihydrouridine synthase 4 like
DVL1	4848	10235	2.111	dishevelled segment polarity protein 1
EDEM3	1139	2445	2.147	ER degradation enhancing alpha-mannosidase like protein 3
EFHC1	680	1387	2.039	EF-hand domain containing 1
EIF1AX	1185	2421	2.043	eukaryotic translation initiation factor 1A, X-linked
EIF3J	2929	6047	2.065	eukaryotic translation initiation factor 3 subunit J
EIF4A2	7489	15815	2.112	eukaryotic translation initiation factor 4A2
EMP1	1511	4992	3.304	epithelial membrane protein 1
ENAH	3202	6730	2.102	enabled homolog (Drosophila)
ESF1	813	1660	2.042	ESF1 nucleolar pre-rRNA processing protein homolog
FAM107B	972	2397	2.466	family with sequence similarity 107 member B
FAM129A	122	1052	8.626	family with sequence similarity 129 member A
FAM135A	394	1018	2.584	family with sequence similarity 135 member A
FAM171A1	594	1207	2.033	family with sequence similarity 171 member A1
FAM60A	2818	5934	2.106	family with sequence similarity 60 member A
FBRSL1	1094	2294	2.097	fibrosin like 1
FHL1	411	2053	4.994	four and a half LIM domains 1
FMNL2	2008	4287	2.135	formin like 2
FOXN2	922	2261	2.452	forkhead box N2
FSTL3	203	1136	5.597	follicle-stimulating-like 3
GAL	950	2326	2.448	galanin and GMAP prepropeptide
GALNT18	617	1526	2.474	polypeptide N-acetylgalactosaminyltransferase 18
GAS5	5263	12864	2.444	growth arrest specific 5 (non-protein coding)
GCLC	1541	3889	2.524	glutamate-cysteine ligase catalytic subunit
GCLM	1261	3361	2.665	glutamate-cysteine ligase modifier subunit
GDF15	1592	4419	2.776	growth differentiation factor 15
GEMIN5	2369	5416	2.286	gem nuclear organelle associated protein 5
GNL3	2381	6260	2.629	G protein nucleolar 3
GOLT1B	1204	2428	2.016	golgi transport 1B
GPD1L	888	2152	2.423	glycerol-3-phosphate dehydrogenase 1-like
GPRC5A	623	2166	3.476	G protein-coupled receptor class C group 5 member A
GRB10	179	1641	9.167	growth factor receptor bound protein 10
GSTP1	959	2078	2.167	glutathione S-transferase pi 1
GTF2F2	2414	4904	2.031	general transcription factor IIF subunit 2
HAUS6	1403	2903	2.069	HAUS augmin like complex subunit 6
HES7	524	1240	2.367	hes family bHLH transcription factor 7
HK2	1711	3530	2.063	hexokinase 2
HMGA1	23082	46601	2.019	high mobility group AT-hook 1
HSPA1A/1B	765	2131	2.786	heat shock protein family A (Hsp70) member 1A
INHBE	662	1365	2.062	inhibin beta E subunit
IPMK	418	1009	2.414	inositol polyphosphate multikinase
JPH1	506	1472	2.909	junctionophilin 1

Table S3B continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd+TEX: v6kd	Gene Name
KCNQ1OT1	695	1420	2.043	KCNQ1 opposite strand/antisense transcript 1
KIAA1551	556	1193	2.147	KIAA1551
KIAA1804	1032	2597	2.516	mixed lineage kinase 4
KIF21A	913	1965	2.152	kinesin family member 21A
KLHL17	625	1608	2.573	kelch like family member 17
L1CAM	465	2035	4.376	L1 cell adhesion molecule
LAMB3	1517	3353	2.21	laminin subunit beta 3
LCOR	1174	2434	2.073	ligand dependent nuclear receptor corepressor
LENG8	2506	5624	2.244	leukocyte receptor cluster member 8
LIN7C	806	1676	2.08	lin-7 homolog C, crumbs cell polarity complex component
SIK1	662	1537	2.321	salt inducible kinase 1
LUC7L3	2366	8118	3.431	LUC7 like 3 pre-mRNA splicing factor
LYPLA1	2020	4184	2.071	lysophospholipase I
MAFK	469	1009	2.152	MAF bZIP transcription factor K
MAK16	689	1432	2.079	MAK16 homolog
MAL2	4146	8340	2.012	mal, T-cell differentiation protein 2 (gene/pseudogene)
MALAT1	4201	17347	4.129	metastasis associated lung adenocarcinoma transcript 1
MAPK8IP3	1111	2363	2.127	mitogen-activated protein kinase 8 interacting protein 3
MAT2A	5655	13086	2.314	methionine adenosyltransferase 2A
MBNL2	766	1694	2.212	muscleblind like splicing regulator 2
MBP	613	1237	2.017	myelin basic protein
MCOLN3	767	1605	2.093	mucolipin 3
MDN1	2213	4399	1.988	midasin AAA ATPase 1
MIB1	2744	5700	2.077	mindbomb E3 ubiquitin protein ligase 1
MRPL12	535	1096	2.048	mitochondrial ribosomal protein L12
MTHFD2	6552	15060	2.299	methylenetetrahydrofolate dehydrogenase 2
MT-ND5	66592	137906	2.071	NADH dehydrogenase, subunit 5 (complex I)
MTURN	449	2034	4.529	maturin, neural progenitor differentiation regulator
MXD1	1571	3245	2.065	MAX dimerization protein 1
MXI1	1235	2684	2.174	MAX interactor 1, dimerization protein
MYC	6589	23296	3.536	v-myc avian myelocytomatosis viral oncogene homolog
MYSM1	902	2067	2.291	Myb like, SWIRM and MPN domains 1
NAA16	740	1552	2.097	N(alpha)-acetyltransferase 16, NatA auxiliary subunit
NAA25	1298	3020	2.327	N(alpha)-acetyltransferase 25, NatB auxiliary subunit
NAE1	2976	5981	2.01	NEDD8 activating enzyme E1 subunit 1
NAMPT	2289	4992	2.181	nicotinamide phosphoribosyltransferase
NCS1	509	2295	4.51	neuronal calcium sensor 1
NEAT1	3531	9058	2.565	nuclear paraspeckle assembly transcript 1 (non-protein coding)
NEK6	462	1199	2.594	NIMA related kinase 6
NFXL1	782	1687	2.157	nuclear transcription factor, X-box binding like 1
NKTR	1244	3169	2.547	natural killer cell triggering receptor
NMD3	3667	7479	2.039	NMD3 ribosome export adaptor
NOLC1	12943	27160	2.098	nucleolar and coiled-body phosphoprotein 1
NOP58	4169	8455	2.028	NOP58 ribonucleoprotein
NR1D1	2341	5135	2.193	nuclear receptor subfamily 1 group D member 1
NRP1	1308	3005	2.297	neuropilin 1
ODC1	6478	15478	2.389	ornithine decarboxylase 1
OGT	4423	16037	3.626	O-linked N-acetylglucosamine (GlcNAc) transferase
OTUD3	505	1031	2.041	OTU deubiquitinase 3
OTUD6B	679	1613	2.375	OTU domain containing 6B
PABPC1L	684	2698	3.945	poly(A) binding protein cytoplasmic 1 like
PAPD5	487	1385	2.845	PAP associated domain containing 5
PAQR3	599	1792	2.992	progesterone and adiponectin receptor family member 3
PARD6B	486	1079	2.22	par-6 family cell polarity regulator beta

Table S3B continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd+TEX: v6kd	Gene Name
PAWR	2382	5064	2.126	pro-apoptotic WT1 regulator
PAXBP1	1829	4754	2.599	PAX3 and PAX7 binding protein 1
PFDN2	2354	4812	2.044	prefoldin subunit 2
PHLDA2	585	1310	2.24	pleckstrin homology like domain family A member 2
PIM1	759	1540	2.03	Pim-1 proto-oncogene, serine/threonine kinase
PIM3	1732	3455	1.995	Pim-3 proto-oncogene, serine/threonine kinase
PKD1	1136	3108	2.736	polycystin 1, transient receptor potential channel interacting
PLAUR	729	1697	2.328	plasminogen activator, urokinase receptor
PMAIP1	1309	3451	2.636	phorbol-12-myristate-13-acetate-induced protein 1
PMEPA1	1371	3316	2.419	prostate transmembrane protein, androgen induced 1
PMS1	799	1811	2.267	PMS1 homolog 1, mismatch repair system component
PNISR	1610	3277	2.035	PNN interacting serine and arginine rich protein
PNN	4326	9989	2.309	pinin, desmosome associated protein
PODXL	1310	2606	1.989	podocalyxin like
POLQ	1073	2139	1.994	DNA polymerase theta
POLR3E	1519	3062	2.016	RNA polymerase III subunit E
POLR3G	332	1847	5.563	RNA polymerase III subunit G
PPP3CA	1433	2847	1.987	protein phosphatase 3 catalytic subunit alpha
PPTC7	1068	2509	2.349	PTC7 protein phosphatase homolog
PRMT3	1555	3549	2.282	protein arginine methyltransferase 3
PRPF39	799	1749	2.189	pre-mRNA processing factor 39
PRPS2	1332	3245	2.436	phosphoribosyl pyrophosphate synthetase 2
PSAT1	6706	14446	2.154	phosphoserine aminotransferase 1
PSD3	182	1610	8.848	pleckstrin and Sec7 domain containing 3
PTER	1185	2373	2.002	phosphotriesterase related
PUM3	1473	3011	2.044	pumilio RNA binding family member 3
PUS7	1950	4000	2.051	pseudouridylate synthase 7 (putative)
PVR	2873	6405	2.229	poliovirus receptor
RAB12	869	2233	2.57	RAB12, member RAS oncogene family
RABGGTB	2625	5779	2.202	Rab geranylgeranyltransferase beta subunit
RAD18	715	1561	2.183	RAD18, E3 ubiquitin protein ligase
RBM26	1832	3781	2.064	RNA binding motif protein 26
RBM39	6346	13679	2.155	RNA binding motif protein 39
RHPN1	654	1443	2.206	rhopilin Rho GTPase binding protein 1
RICTOR	1044	2243	2.149	RPTOR independent companion of MTOR complex 2
RIDA	552	1176	2.13	reactive intermediate imine deaminase A homolog
RIF1	4250	9166	2.157	replication timing regulatory factor 1
RIMKLB	376	1056	2.809	ribosomal modification protein rimK like family member B
RPF2	1161	2327	2.004	ribosome production factor 2 homolog
RPIA	1027	2062	2.007	ribose 5-phosphate isomerase A
RPL32P3	374	1057	2.827	ribosomal protein L32 pseudogene 3
RSRC2	2127	4227	1.987	arginine and serine rich coiled-coil 2
RSRP1	1096	2498	2.279	arginine and serine rich protein 1
S100A2	639	2325	3.638	S100 calcium binding protein A2
SACS	3533	8228	2.329	sacsin molecular chaperone
SASS6	569	1340	2.354	SAS-6 centriolar assembly protein
SAT1	4870	11578	2.377	spermidine/spermine N1-acetyltransferase 1
SCAMP1	1253	2627	2.097	secretory carrier membrane protein 1
SCML1	834	1748	2.095	sex comb on midleg-like 1 (Drosophila)
SLC19A2	540	1118	2.071	solute carrier family 19 member 2
SLC20A1	7097	15458	2.178	solute carrier family 20 member 1
SLC25A36	2683	7144	2.663	solute carrier family 25 member 36
SLC25A37	715	1609	2.25	solute carrier family 25 member 37
SLC35A3	563	1225	2.176	solute carrier family 35 member A3

Table S3B continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd+TEX: v6kd	Gene Name
SLC35F2	1219	3143	2.578	solute carrier family 35 member F2
SLC4A7	510	3123	6.123	solute carrier family 4 member 7
SLC7A11	274	1229	4.486	solute carrier family 7 member 11
SLC7A2	117	1021	8.723	solute carrier family 7 member 2
SLFN5	691	1932	2.796	schlafen family member 5
SMC5	1620	3359	2.074	structural maintenance of chromosomes 5
SNHG1	1852	5187	2.801	small nucleolar RNA host gene 1
SNHG15	1003	2076	2.069	small nucleolar RNA host gene 15
SNHG17	701	1399	1.996	small nucleolar RNA host gene 17
SOWAHC	1207	3208	2.658	sosondowah ankyrin repeat domain family member C
SPNS2	1566	3172	2.026	sphingolipid transporter 2
STEAP1	839	2326	2.772	six transmembrane epithelial antigen of the prostate 1
STEAP2	1014	2529	2.494	STEAP2 metalloredutase
STK26	2998	5970	1.991	serine/threonine protein kinase 26
SVIL	282	1342	4.759	Supervillin
TAF1D	2204	5678	2.576	TATA-box binding protein associated factor, polymerase ID
TBC1D4	1825	3960	2.17	TBC1 domain family member 4
TCEA1	1634	3757	2.299	transcription elongation factor A1
TEX19	534	1139	2.133	testis expressed 19
TFAP4	692	1424	2.057	transcription factor AP-4 (activating enhancer binding protein 4)
THAP9-AS1	694	1849	2.665	THAP9 antisense RNA 1
TIA1	1389	2898	2.086	TIA1 cytotoxic granule-associated RNA binding protein
TMED7	2066	4326	2.094	transmembrane p24 trafficking protein 7
TMEM168	506	1154	2.281	transmembrane protein 168
TPD52	3004	6154	2.049	tumor protein D52
TRAF5	507	1093	2.156	TNF receptor associated factor 5
TRMT11	572	1193	2.086	tRNA methyltransferase 11 homolog
TRNT1	550	1302	2.366	tRNA nucleotidyl transferase 1
TRUB1	902	1931	2.14	TruB pseudouridine synthase family member 1
TTC14	396	1256	3.171	tetratricopeptide repeat domain 14
TXNRD1	4802	14924	3.108	thioredoxin reductase 1
U2SURP	7106	15134	2.13	U2 snRNP associated SURP domain containing
UHRF2	1131	2481	2.194	ubiquitin like with PHD and ring finger domains 2
UPP1	596	3968	6.658	uridine phosphorylase 1
USPL1	929	1915	2.062	ubiquitin specific peptidase like 1
VMP1	3127	8174	2.614	vacuole membrane protein 1
VPS13A	2970	6025	2.028	vacuolar protein sorting 13 homolog A
WDR19	405	1063	2.624	WD repeat domain 19
WDR35	1189	3069	2.582	WD repeat domain 35
WDR36	2300	5636	2.45	WD repeat domain 36
WDR43	3775	7576	2.007	WD repeat domain 43
WNK2	578	1492	2.582	WNK lysine deficient protein kinase 2
XPOT	5223	10933	2.093	exportin for tRNA
XRCC2	929	2002	2.155	X-ray repair cross complementing 2
YOD1	919	2620	2.85	YOD1 deubiquitinase
YRDC	900	1790	1.988	yrdc N6-threonylcarbamoyltransferase domain containing
ZBTB10	618	1233	1.995	zinc finger and BTB domain containing 10
ZBTB21	1123	2438	2.171	zinc finger and BTB domain containing 21
ZCCHC7	1114	2224	1.997	zinc finger CCHC-type containing 7
ZFAND1	1422	3499	2.461	zinc finger AN1-type containing 1
ZFAS1	4764	10723	2.251	ZNF1 antisense RNA 1
ZMYM1	729	1627	2.232	zinc finger MYM-type containing 1
ZNF121	394	1218	3.09	zinc finger protein 121
ZNF146	3692	7551	2.045	zinc finger protein 146

Table S3B continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd+TEX: v6kd	Gene Name
ZNF267	521	1313	2.52	zinc finger protein 267
ZNF280C	444	1030	2.319	zinc finger protein 280C
ZNF518A	604	1328	2.199	zinc finger protein 518A
ZNF697	1113	2328	2.092	zinc finger protein 697
ZNF770	1128	2459	2.18	zinc finger protein 770
ZNF92	491	1031	2.099	zinc finger protein 92
ZRANB2	2235	5606	2.508	zinc finger RANBP2-type containing 2

Table S3C

Decreased mRNA recovery in CIC-TEX-treated Tspan8kd cells

Symbol	Tsp8-kd	Tsp8kd+TEX	Tsp8kd: Tsp8kd+TEX	Gene Name
ABCG2	4644	2235	2.078	ATP binding cassette subfamily G member 2
ACSS2	1661	683	2.431	acyl-CoA synthetase short-chain family member 2
ADAMTS6	1352	265	5.098	ADAM metalloproteinase with thrombospondin type 1 motif 6
ALDH1L1	1791	390	4.593	aldehyde dehydrogenase 1 family member L1
ALDH6A1	1766	810	2.18	aldehyde dehydrogenase 6 family member A1
ALDOC	1146	424	2.705	aldolase, fructose-bisphosphate C
AQP3	1316	534	2.465	aquaporin 3 (Gill blood group)
ARL15	1386	610	2.272	ADP ribosylation factor like GTPase 15
ATP6V1B1	1263	483	2.614	ATPase H ⁺ transporting V1 subunit B1
AZGP1	3600	1592	2.261	alpha-2-glycoprotein 1, zinc-binding
BCAS1	5945	3009	1.976	breast carcinoma amplified sequence 1
BTG2	1721	728	2.365	BTG anti-proliferation factor 2
CACNA1D	1587	705	2.252	calcium voltage-gated channel subunit alpha1 D
CEACAM1	9303	4720	1.971	carcinoembryonic antigen related cell adhesion molecule 1
CFH	1315	447	2.941	complement factor H
CLEC3A	9588	1484	6.46	C-type lectin domain family 3 member A
DDX60	4491	1740	2.58	DEXD/H-box helicase 60
ERMP1	11078	5048	2.194	endoplasmic reticulum metalloproteinase 1
F2R	8165	3005	2.718	coagulation factor II thrombin receptor
FGD3	1148	569	2.017	FYVE, RhoGEF and PH domain containing 3
FUCA1	2131	966	2.207	fucosidase, alpha-L- 1, tissue
GAA	2069	1003	2.064	glucosidase alpha, acid
GABRP	4490	2111	2.126	gamma-aminobutyric acid type A receptor pi subunit
GATA2	8199	3244	2.527	GATA binding protein 2
GATA2AS1	1911	863	2.214	GATA2 antisense RNA 1
GBP2	1040	443	2.351	guanylate binding protein 2
HMGCS1	7189	2852	2.521	3-hydroxy-3-methylglutaryl-CoA synthase 1
HOTTIP	3111	1180	2.636	HOXA distal transcript antisense RNA
HOXB8	2106	996	2.114	homeobox B8
HPGD	1037	496	2.091	hydroxyprostaglandin dehydrogenase 15-(NAD)
IDI1	3957	1773	2.232	isopentenyl-diphosphate delta isomerase 1
IFIT2	2916	933	3.125	interferon induced protein with tetratricopeptide repeats 2
IFIT3	2839	1081	2.628	interferon induced protein with tetratricopeptide repeats 3
INSIG1	3274	1013	3.233	insulin induced gene 1
KLHDC7A	1266	548	2.312	kelch domain containing 7A
LMO4	10229	3767	2.716	LIM domain only 4
MBOAT2	1359	591	2.299	membrane bound O-acyltransferase domain containing 2
MEIS2	9415	4140	2.274	Meis homeobox 2
MGAM2	2484	906	2.742	maltase-glucoamylase 2 (putative)
MSMO1	2912	977	2.98	methylsterol monooxygenase 1
NCMAP	1023	519	1.974	non-compact myelin associated protein
NOX1	1677	563	2.979	NADPH oxidase 1
OASL	6539	2820	2.319	2'-5'-oligoadenylate synthetase like
OLMALINC	1692	731	2.313	oligodendrocyte maturation-associated long intergenic ncRNA
PRICKLE4	2683	1145	2.343	prickle planar cell polarity protein 4
PRSS23	6053	2498	2.423	protease, serine 23
QPRT	1796	776	2.315	quinolinate phosphoribosyltransferase
RARRES1	1380	409	3.373	retinoic acid receptor responder 1
RARRES3	1546	263	5.87	retinoic acid receptor responder 3
RASL11A	1178	235	5.007	RAS like family 11 member A
RGS2	10876	4429	2.456	regulator of G-protein signaling 2
RHBDL2	1725	842	2.05	rhomboid like 2
RNF141	3863	1790	2.158	ring finger protein 141
SARDH	1328	458	2.901	sarcosine dehydrogenase

Table S3C continued

Symbol	Tsp8-kd	Tsp8kd+TEX	Tsp8kd: Tsp8kd+TEX	Gene Name
SCD	34887	17273	2.02	stearoyl-CoA desaturase
SHROOM1	4997	899	5.561	shroom family member 1
SLC35D1	1330	556	2.393	solute carrier family 35 member D1
SLC38A11	1551	553	2.806	solute carrier family 38 member 11
SLC40A1	4517	2230	2.025	solute carrier family 40 member 1
SLC4A4	2337	1167	2.004	solute carrier family 4 member 4
TACSTD2	5802	2923	1.985	tumor-associated calcium signal transducer 2
TGM2	10533	1108	9.509	transglutaminase 2
THBS1	2225	1089	2.044	thrombospondin 1
VSIG2	2214	967	2.288	V-set and immunoglobulin domain containing 2
WWOX	1337	653	2.05	WW domain containing oxidoreductase
ZNF704	5987	2226	2.689	zinc finger protein 704

Table S3D

Decreased mRNA recovery in CIC-TEX-treated CD44v6kd cells

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd: v6kd+TEX	Gene Name
ABHD12B	2244	1043	2.15	abhydrolase domain containing 12B
ACAT2	2936	876	3.353	acetyl-CoA acetyltransferase 2
ACP2	1264	578	2.186	acid phosphatase 2, lysosomal
ACSS2	8557	2313	3.699	acyl-CoA synthetase short-chain family member 2
ADAMTS8	2118	627	3.38	ADAM metalloproteinase with thrombospondin type 1 motif 8
ADAMTSL2	3112	1144	2.721	ADAMTS like 2
ADI1	4928	2506	1.966	acireductone dioxygenase 1
ALDH2	1411	580	2.435	aldehyde dehydrogenase 2 family (mitochondrial)
ALDH3A1	3034	755	4.019	aldehyde dehydrogenase 3 family member A1
ALDH4A1	2693	845	3.186	aldehyde dehydrogenase 4 family member A1
AMOT	8365	3113	2.687	Angiomotin
ANXA6	39236	19594	2.002	annexin A6
ANXA9	1002	422	2.375	annexin A9
APCDD1	37708	9437	3.996	APC down-regulated 1
APOBEC3G	2836	1406	2.017	apolipoprotein B mRNA editing enzyme catalytic subunit 3G
APOE	1179	314	3.756	apolipoprotein E
ARHGAP1	6621	2883	2.297	Rho GTPase activating protein 1
ARHGAP18	3013	1491	2.021	Rho GTPase activating protein 18
ARHGEF40	1592	582	2.735	Rho guanine nucleotide exchange factor 40
ARID5A	2026	1037	1.953	AT-rich interaction domain 5A
ARMC7	1081	494	2.186	armadillo repeat containing 7
ASPSCR1	13039	3911	3.334	ASPSCR1, UBX domain containing tether for SLC2A4
ATP6V0D1	4912	1901	2.583	ATPase H ⁺ transporting V0 subunit d1
ATP6V0E2	3560	1238	2.876	ATPase H ⁺ transporting V0 subunit e2
AXIN2	8545	4220	2.025	axin 2
BAMBI	9476	4385	2.161	BMP and activin membrane bound inhibitor
BCL2L15	1939	805	2.41	BCL2 like 15
BHLHE40	8945	4339	2.061	basic helix-loop-helix family member e40
BST2	9193	3602	2.552	bone marrow stromal cell antigen 2
BTBD6	2275	985	2.31	BTB domain containing 6
C12orf57	1782	796	2.24	chromosome 12 open reading frame 57
C14orf1	3625	1504	2.411	chromosome 14 open reading frame 1
C6orf223	3193	407	7.851	chromosome 6 open reading frame 223
CA6	1725	412	4.189	carbonic anhydrase 6
CALHM3	1289	470	2.741	calcium homeostasis modulator 3
CASS4	1178	421	2.8	Cas scaffolding protein family member 4
CCDC3	3544	826	4.29	coiled-coil domain containing 3
CCDC69	1069	469	2.279	coiled-coil domain containing 69
CD82	3368	1511	2.229	CD82 molecule
CD8BP	1654	583	2.835	CD8b molecule pseudogene
CDK5	1913	871	2.197	cyclin dependent kinase 5
CDKN1A	4082	1872	2.18	cyclin dependent kinase inhibitor 1A
CDKN2C	1584	511	3.1	cyclin dependent kinase inhibitor 2C
CDX2	7338	2543	2.885	caudal type homeobox 2
CEACAM1	1523	521	2.923	carcinoembryonic antigen related cell adhesion molecule 1
CEMIP	31231	15002	2.082	cell migration inducing hyaluronan binding protein
CHI3L1	4814	1654	2.911	chitinase 3 like 1
CHRNA3	5538	1712	3.235	cholinergic receptor nicotinic alpha 3 subunit
CHRNB1	1835	877	2.092	cholinergic receptor nicotinic beta 1 subunit
CHST14	1387	534	2.598	carbohydrate sulfotransferase 14
CLU	20601	10515	1.959	Clusterin
CPNE2	2742	1139	2.408	copine 2
CRAT	10391	3479	2.987	carnitine O-acetyltransferase
CREB3L4	2488	965	2.579	cAMP responsive element binding protein 3 like 4

Table S3D continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd: v6kd+TEX	Gene Name
CST1	6792	623	10.906	cystatin SN
CST3	9482	4840	1.959	cystatin C
CTSZ	32292	11012	2.932	cathepsin Z
CXCR4	2985	710	4.201	C-X-C motif chemokine receptor 4
DBH	4592	1191	3.856	dopamine beta-hydroxylase
DBH-AS1	7913	2711	2.919	DBH antisense RNA 1
DBI	6889	3523	1.955	diazepam binding inhibitor, acyl-CoA binding protein
DCAF11	5547	2372	2.339	DDB1 and CUL4 associated factor 11
DDAH2	1887	858	2.199	dimethylarginine dimethylaminohydrolase 2
DDX58	2559	602	4.248	DEXD/H-box helicase 58
DDX60	4267	830	5.141	DEXD/H-box helicase 60
DHCR24	23681	8809	2.688	24-dehydrocholesterol reductase
DHCR7	7942	2520	3.151	7-dehydrocholesterol reductase
DHRS1	1573	766	2.052	dehydrogenase/reductase 1
DKK4	135196	53360	2.534	dickkopf WNT signaling pathway inhibitor 4
DNASE1	2915	1401	2.081	deoxyribonuclease I
DYSF	7152	2500	2.861	Dysferlin
EBP	4309	1406	3.065	emopamil binding protein (sterol isomerase)
ENTPD8	13017	4268	3.05	ectonucleoside triphosphate diphosphohydrolase 8
FADS2	2244	798	2.811	fatty acid desaturase 2
FAM178B	1088	456	2.384	family with sequence similarity 178 member B
FAM210B	4509	1983	2.274	family with sequence similarity 210 member B
FAM46C	1996	571	3.498	family with sequence similarity 46 member C
FAM63A	2766	1364	2.028	family with sequence similarity 63 member A
FBXO2	2108	616	3.42	F-box protein 2
FBXW4	1680	855	1.964	F-box and WD repeat domain containing 4
FDFT1	4327	1655	2.615	farnesyl-diphosphate farnesyltransferase 1
FDPS	8391	3325	2.524	farnesyl diphosphate synthase
FUCA1	7863	2500	3.145	fucosidase, alpha-L- 1, tissue
FXYP6	1515	562	2.697	FXYP domain containing ion transport regulator 6
GALNT6	10950	5477	1.999	polypeptide N-acetylgalactosaminyltransferase 6
GBA	1834	799	2.294	glucosylceramidase beta
GJB1	9511	4635	2.052	gap junction protein beta 1
GLUL	20455	7662	2.67	glutamate-ammonia ligase
GMFG	1159	436	2.659	glia maturation factor gamma
GPR155	8955	4578	1.956	G protein-coupled receptor 155
GPX2	18065	8085	2.234	glutathione peroxidase 2
GRM8	1514	561	2.701	glutamate metabotropic receptor 8
GUSB	5110	2621	1.95	glucuronidase beta
HCP5	1188	520	2.285	HLA complex P5 (non-protein coding)
HELZ2	4314	2170	1.988	helicase with zinc finger 2
HMGCR	6319	2458	2.571	3-hydroxy-3-methylglutaryl-CoA reductase
HMGCS1	4377	1082	4.047	3-hydroxy-3-methylglutaryl-CoA synthase 1
HOXA11	1040	484	2.148	homeobox A11
HOXB7	1527	775	1.97	homeobox B7
HOXB8	3111	1213	2.566	homeobox B8
HUNK	13717	5027	2.729	hormonally up-regulated Neu-associated kinase
HYAL2	4505	2204	2.044	hyaluronoglucosaminidase 2
IDI1	2827	962	2.938	isopentenyl-diphosphate delta isomerase 1
IFI27L2	1310	643	2.037	interferon alpha inducible protein 27 like 2
IFI6	5172	412	12.559	interferon alpha inducible protein 6
IFIH1	3120	774	4.031	interferon induced with helicase C domain 1
IFIT1	1751	296	5.913	interferon induced protein with tetratricopeptide repeats 1
IFIT3	1526	313	4.881	interferon induced protein with tetratricopeptide repeats 3

Table S3D continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd: v6kd+TEX	Gene Name
IFITM3	12775	4876	2.62	interferon induced transmembrane protein 3
IL17RD	6464	2986	2.165	interleukin 17 receptor D
INSIG1	8277	1642	5.04	insulin induced gene 1
INTS5	3627	1453	2.497	integrator complex subunit 5
ISG15	11508	2532	4.545	ISG15 ubiquitin-like modifier
JHDM1D-AS1	4286	2095	2.046	JHDM1D antisense RNA 1 (head to head)
KAZALD1	4430	2212	2.003	Kazal type serine peptidase inhibitor domain 1
KCNJ5	13520	4235	3.192	potassium voltage-gated channel subfamily J member 5
KLHL25	1143	576	1.985	kelch like family member 25
KLK1	2772	1317	2.105	kallikrein 1
LINC00868	1466	423	3.464	long intergenic non-protein coding RNA 868
LINC01124	2595	731	3.551	long intergenic non-protein coding RNA 1124
LRRC37A16P	3146	1417	2.22	leucine rich repeat containing 37 member A16, pseudogene
LRRC75A	1289	449	2.873	leucine rich repeat containing 75A
LSS	6536	1946	3.359	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
MCTP1	1604	822	1.951	multiple C2 and transmembrane domain containing 1
MMAB	1867	652	2.863	methylmalonic aciduria (cobalamin deficiency) cblB type
MSMO1	3820	1501	2.545	methylsterol monooxygenase 1
MSRB2	3793	1496	2.535	methionine sulfoxide reductase B2
MSRB3	1579	760	2.077	methionine sulfoxide reductase B3
MTHFR	1285	399	3.22	methylenetetrahydrofolate reductase (NAD(P)H)
MVD	3607	1205	2.994	mevalonate diphosphate decarboxylase
MVK	1990	417	4.773	mevalonate kinase
MX1	1550	117	13.256	MX dynamin like GTPase 1
MX2	2187	519	4.217	MX dynamin like GTPase 2
MYCL	2108	929	2.269	v-myc myelocytomatosis viral oncogene lung carc. homolog
MYH7B	7607	2159	3.523	myosin heavy chain 7B
MYL6	18417	8288	2.222	myosin light chain 6
MYO1D	23131	10295	2.247	myosin ID
NAT16	1437	583	2.463	N-acetyltransferase 16 (putative)
Nd	1556	771	2.017	ENSG00000184674
NEDD9	2997	666	4.5	neural precursor cell expressed, developm. down-regulated 9
NEU1	1662	655	2.539	neuraminidase 1 (lysosomal sialidase)
NEURL1B	2029	381	5.321	neuralized E3 ubiquitin protein ligase 1B
NFATC4	1357	684	1.985	nuclear factor of activated T-cells 4
NFE2	1886	397	4.756	nuclear factor, erythroid 2
NGFR	4891	2491	1.963	nerve growth factor receptor
NKD1	34355	16133	2.13	naked cuticle homolog 1
NOTUM	10550	3935	2.681	NOTUM, palmitoleoyl-protein carboxylesterase
NPC2	4468	1709	2.614	NPC intracellular cholesterol transporter 2
NSDHL	3208	1289	2.489	NAD(P) dependent steroid dehydrogenase-like
NUCB1	4164	2044	2.037	nucleobindin 1
NUDT19	1863	904	2.062	nudix hydrolase 19
OAS1	3875	323	12.003	2'-5'-oligoadenylate synthetase 1
OAS2	2316	519	4.466	2'-5'-oligoadenylate synthetase 2
OAS3	12947	2559	5.06	2'-5'-oligoadenylate synthetase 3
OBSL1	7008	3455	2.029	obscurin like 1
OGDHL	1087	530	2.051	oxoglutarate dehydrogenase-like
ORAI3	1703	527	3.229	ORAI calcium release-activated calcium modulator 3
PARM1	2457	1093	2.248	prostate androgen-regulated mucin-like protein 1
PARP10	1436	624	2.301	poly(ADP-ribose) polymerase family member 10
PARP9	3223	731	4.41	poly(ADP-ribose) polymerase family member 9
PBXIP1	3670	1404	2.613	PBX homeobox interacting protein 1
PCCA	8956	3785	2.366	propionyl-CoA carboxylase alpha subunit

Table S3D continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd: v6kd+TEX	Gene Name
PCSK9	7031	919	7.651	proprotein convertase subtilisin/kexin type 9
PCYT2	2751	996	2.761	phosphate cytidyltransferase 2, ethanolamine
PDE6D	1592	707	2.253	phosphodiesterase 6D
PHLDB2	1509	425	3.555	pleckstrin homology like domain family B member 2
PIK3R3	1108	380	2.916	phosphoinositide-3-kinase regulatory subunit 3
PLEKHA4	2805	1408	1.992	pleckstrin homology domain containing A4
PLIN3	4356	2128	2.047	perilipin 3
PLSCR1	1790	671	2.667	phospholipid scramblase 1
POLR1D	22521	10703	2.104	RNA polymerase I subunit D
PPARD	6848	3124	2.192	peroxisome proliferator activated receptor delta
PPP2R2C	7648	3561	2.148	protein phosphatase 2 regulatory subunit Bgamma
PRDX2	10652	4637	2.297	peroxiredoxin 2
PRKCDBP	1709	679	2.518	Protein kinase C delta binding protein
PRR5L	1063	472	2.254	Proline rich 5 like
PRSS56	6034	2872	2.101	protease, serine 56
PSG1	1272	159	8.006	pregnancy specific beta-1-glycoprotein 1
PSMB9	1344	464	2.897	proteasome subunit beta 9
QSOX1	21136	10172	2.078	quiescin sulfhydryl oxidase 1
RAB15	4242	1102	3.85	RAB15, member RAS oncogene family
RAB42	1313	500	2.629	RAB42, member RAS oncogene family
RASL11B	1087	524	2.076	RAS like family 11 member B
RDH11	6646	3030	2.193	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)
REEP2	2235	971	2.302	receptor accessory protein 2
S100A13	3685	1685	2.186	S100 calcium binding protein A13
S100A3	4092	1351	3.029	S100 calcium binding protein A3
SAMHD1	6940	2391	2.903	SAM and HD domain contain triphosphohydrolase 1
SCARA3	1509	572	2.638	scavenger receptor class A member 3
SCD	28071	7636	3.676	stearoyl-CoA desaturase
SCNN1A	7678	3692	2.079	sodium channel epithelial 1 alpha subunit
SEC14L2	1308	522	2.504	SEC14 like lipid binding 2
SFN	27841	7711	3.61	Stratifin
SLC12A4	2948	1393	2.116	solute carrier family 12 member 4
SLC1A4	7280	3180	2.289	solute carrier family 1 member 4
SLC25A1	2442	1240	1.969	solute carrier family 25 member 1
SLC2A6	1236	377	3.274	solute carrier family 2 member 6
SLC4A8	1994	662	3.011	solute carrier family 4 member 8
SLC5A1	1302	524	2.486	solute carrier family 5 member 1
SLC7A8	28073	9675	2.902	solute carrier family 7 member 8
SORT1	8271	3663	2.258	sortilin 1
SP5	4517	2087	2.164	Sp5 transcription factor
SPRY4	1991	925	2.152	SPRY domain containing 4
SPTB	3058	1059	2.888	spectrin beta, erythrocytic
SQLE	6213	2594	2.395	squalene epoxidase
SREBF1	5429	2538	2.139	sterol regulatory element binding transcription factor 1
SREBF2	8646	3796	2.277	sterol regulatory element binding transcription factor 2
ST5	1712	833	2.056	suppression of tumorigenicity 5
STARD13	1892	910	2.079	StAR related lipid transfer domain containing 13
STARD3	2942	1393	2.112	StAR related lipid transfer domain containing 3
STARD4	5260	2673	1.968	StAR related lipid transfer domain containing 4
STAT1	12986	4635	2.802	signal transducer and activator of transcription 1
STAT2	4200	1994	2.106	signal transducer and activator of transcription 2
SUOX	1410	477	2.958	sulfite oxidase
SV2A	1857	671	2.767	synaptic vesicle glycoprotein 2A
SYK	31970	11806	2.708	spleen associated tyrosine kinase

Table S3D continued

Symbol	CD44v6kd	CD44v6kd +TEX	v6kd: v6kd+TEX	Gene Name
SYNE1	1139	438	2.598	spectrin repeat containing nuclear envelope protein 1
TAP1	2202	1068	2.062	transporter 1, ATP binding cassette subfamily B member
TAS1R3	1146	547	2.097	taste 1 receptor member 3
TBC1D17	1233	627	1.968	TBC1 domain family member 17
TCTA	1085	364	2.985	T-cell leukemia translocation altered
TDGF1	1273	533	2.39	teratocarcinoma-derived growth factor 1
TECR	3800	1938	1.961	trans-2,3-enoyl-CoA reductase
TEF	1754	869	2.018	TEF, PAR bZIP transcription factor
TGFB11	1148	433	2.649	transforming growth factor beta 1 induced transcript 1
TIMP1	13651	5423	2.517	TIMP metalloproteinase inhibitor 1
TK1	6478	3300	1.963	thymidine kinase 1
TM7SF2	1933	620	3.116	transmembrane 7 superfamily member 2
TMEM139	1934	695	2.782	transmembrane protein 139
TMEM45B	5704	2498	2.284	transmembrane protein 45B
TNFRSF11B	2639	699	3.775	TNF receptor superfamily member 11b
TNFRSF19	6343	2411	2.631	TNF receptor superfamily member 19
TP53INP2	2468	1261	1.957	tumor protein p53 inducible nuclear protein 2
TRDC	1217	253	4.812	T cell receptor delta constant
TRIM21	1049	452	2.318	tripartite motif containing 21
TRIM29	8188	3601	2.274	tripartite motif containing 29
TRIM69	1237	609	2.032	tripartite motif containing 69
TSPAN1	1647	802	2.054	tetraspanin 1
TST	1544	787	1.963	thiosulfate sulfurtransferase
TUBA1A	3439	1321	2.604	tubulin alpha 1a
UBE2L6	1128	353	3.192	ubiquitin conjugating enzyme E2 L6
VAMP8	4193	2053	2.043	vesicle associated membrane protein 8
VDAC3	9894	4862	2.035	voltage dependent anion channel 3
VDR	7091	3213	2.207	vitamin D (1,25- dihydroxyvitamin D3) receptor
VEGFB	1822	843	2.162	vascular endothelial growth factor B
VEPH1	1033	505	2.047	ventricular zone expressed PH domain containing 1
VPS18	1463	735	1.991	VPS18, CORVET/HOPS core subunit
WBP1L	3685	1703	2.164	WW domain binding protein 1-like
WBP2	7986	4093	1.951	WW domain binding protein 2
WDR54	2873	1471	1.954	WD repeat domain 54
WNT6	1497	449	3.337	Wnt family member 6
ZBTB7C	1366	636	2.149	zinc finger and BTB domain containing 7C
ZDHC12	2123	1078	1.97	zinc finger DHHC-type containing 12
ZNF831	2565	785	3.266	zinc finger protein 831

Table S3E

Random correlation between increased mRNA recovery in CIC-TEX-treated CD44v6kd cells and higher recovery in CIC-TEX^a

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
AASDHPT	1927	1639	1.18	NAA50	4251	6623	0.64
ABCA2	1481	3392	0.44	NADK2	1161	640	1.81
ABCA3	83	1475	0.06	NAE1	3368	2976	1.13
ABCC3	3547	1023	3.47	NAMPT	1736	2289	0.76
ABCC4	608	1081	0.56	NARS	10362	4139	2.50
ABCE1	2428	2367	1.03	NARS2	2089	863	2.42
ABL2	737	1706	0.43	NBEAL2	2233	2460	0.91
ACAP2	2350	2291	1.03	NCS1	2372	509	4.66
ACBD3	3615	1362	2.65	NDC1	1065	3610	0.30
ADGRA3	1137	809	1.41	NDFIP2	1302	1330	0.98
ADGRL1	593	1235	0.48	NDUFA5	1691	892	1.90
ADSS	2969	1121	2.65	NDUFAF2	1164	455	2.56
AEBP2	718	1052	0.68	NDUFAF7	1194	909	1.31
AGO2	2056	650	3.16	NEAT1	2675	3531	0.76
AGPS	2409	3210	0.75	NEDD1	763	1460	0.52
AGTPBP1	2411	736	3.28	NEDD4	1740	1164	1.49
AHCTF1	1343	1606	0.84	NEK6	1672	462	3.62
AHNAK2	773	1124	0.69	NET1	133073	3555	37.43
AIM1	1594	275	5.80	NETO2	45	2191	0.02
AIMP1	3563	1817	1.96	NFAT5	676	4445	0.15
AK2	5595	6100	0.92	NFKB2	3224	3058	1.05
AK3	2291	2483	0.92	NFXL1	1493	782	1.91
AKAP11	871	3369	0.26	NFYB	1456	725	2.01
AKAP12	1623	2129	0.76	NGLY1	1347	790	1.71
AKAP9	1907	4754	0.40	NHLRC2	539	1604	0.34
AKNA	2190	330	6.64	NIFK	2270	1567	1.45
AMD1	3108	3245	0.96	NKTR	952	1244	0.77
ANKRD10	2840	1788	1.59	NLN	2899	1568	1.85
ANKRD11	5118	6913	0.74	NMD3	3493	3667	0.95
ANKRD12	1241	1526	0.81	NMT2	864	1174	0.74
ANO1	33	4644	0.01	NOC3L	1373	1297	1.06
AP1AR	2032	610	3.33	NOL11	5141	1736	2.96
APPL1	1630	2352	0.69	NOL4L	1041	391	2.66
ARFGEF3	3035	1364	2.22	NOL8	2922	1659	1.76
ARGLU1	1827	1471	1.24	NOL9	586	1078	0.54
ARHGAP29	4090	1386	2.95	NOLC1	13164	12943	1.02
ARL5A	1158	2702	0.43	NOP16	2817	1634	1.72
ARL5B	1352	1318	1.03	NOP58	6467	4169	1.55
ARMC10	1580	1359	1.16	NORAD	4399	10194	0.43
ARRDC4	2127	108	19.70	NPDC1	4074	1848	2.20
ASMTL	1203	352	3.42	NQO1	11304	8264	1.37
ASNS	22530	5813	3.88	NR1D1	1231	2341	0.53
ASS1	10739	2767	3.88	NRARP	1152	2203	0.52
ASUN	2652	4550	0.58	NRP1	217	1308	0.17
ATAD1	1262	2014	0.63	NSMCE4A	2030	918	2.21
ATAD3B	1246	1016	1.23	NT5C3A	1264	1581	0.80
ATE1	3486	1516	2.30	NTSR1	3440	7496	0.46
ATF3	4050	508	7.97	NUDCD1	1250	1844	0.68
ATG12	1349	2117	0.64	NUFIP2	2461	2818	0.87
ATP11A	525	3036	0.17	NUP155	1385	3519	0.39
ATP13A3	2866	5803	0.49	NUP160	2720	3407	0.80
ATR	1434	2584	0.55	NUP210	779	6451	0.12
ATXN2	1251	1309	0.96	NUP35	893	1260	0.71
BAG2	1783	1348	1.32	NUP43	704	1185	0.59
BAZ1A	1625	2091	0.78	NUP58	2723	5330	0.51
BBX	1719	2179	0.79	ODC1	34704	6478	5.36
BDP1	1316	1603	0.82	OGT	3558	4423	0.80
BET1	1564	810	1.93	OPA1	5428	5473	0.99
BMI1	1444	511	2.83	ORC2	1507	2485	0.61
BRCA2	273	1525	0.18	ORC6	1220	1518	0.80

Table S3E continued

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
BRIX1	2206	1354	1.63	OSBPL1A	1166	1234	0.94
BROX	1383	1910	0.72	OSBPL8	1684	2539	0.66
BRWD1	1430	2618	0.55	OSGIN1	1788	449	3.98
BTAF1	1656	2307	0.72	OTUD6B-AS1	1881	764	2.46
BTG3	1288	2190	0.59	PABPC1L	1298	684	1.90
C10orf2	2897	1536	1.89	PANK3	2862	3612	0.79
C11orf68	2350	1308	1.80	PAWR	2345	2382	0.98
C12orf45	1623	317	5.12	PAX8-AS1	761	2636	0.29
C1GALT1	669	1510	0.44	PAXBPA1	846	1829	0.46
C1orf52	1630	525	3.11	PCID2	2993	1518	1.97
C21orf91	226	1013	0.22	PDCD11	4006	3420	1.17
C2orf69	415	1203	0.34	PFDN2	8384	2354	3.56
C5orf24	1112	2717	0.41	PHIP	716	2421	0.30
C5orf30	461	1033	0.45	PHKA1	1302	947	1.37
C6orf48	11384	2450	4.65	PHLDA2	8933	585	15.27
CABLES1	2849	331	8.61	PIEZO1	1747	7607	0.23
CAMKK2	1931	1154	1.67	PIK3CA	1095	1354	0.81
CAMSAP1	4229	3502	1.21	PIM3	3377	1732	1.95
CAPN15	2195	2085	1.05	PIP4K2A	1088	1362	0.80
CAPRN2	4241	631	6.72	PKD1	542	1136	0.48
CASC4	2211	1774	1.25	PKN2	1309	2949	0.44
CASP8	1568	376	4.17	PLA2G12A	2355	1293	1.82
CAV2	1003	459	2.18	PLD1	593	1192	0.50
CBFB	2461	5971	0.41	PLK2	3599	468	7.69
CBS/CBSL	38	1946	0.02	PLS1	2756	3406	0.81
CBX2	815	1511	0.54	PLXNA1	918	4199	0.22
CCAR1	4686	3558	1.32	PLXND1	2162	1173	1.84
CCDC14	1045	1242	0.84	PM20D2	620	1715	0.36
CCDC57	2781	1083	2.57	PMAIP1	574	1309	0.44
CCDC58	1053	502	2.10	PMEPA1	1187	1371	0.87
CCDC59	2560	823	3.11	PNISR	1295	1610	0.80
CCDC88A	205	3077	0.07	PNN	8108	4326	1.87
CCDC91	2259	382	5.91	PNO1	1960	1561	1.26
CCNB1IP1	6624	1995	3.32	PNPT1	2390	3660	0.65
CCNC	2673	2119	1.26	PODXL	638	1310	0.49
CCND2	35	1747	0.02	POLQ	400	1073	0.37
CCNL1	2506	1820	1.38	POLR1B	1554	2919	0.53
CCNL2	1161	4122	0.28	POLR3D	1107	872	1.27
CCNT2	395	1194	0.33	POLR3E	2597	1519	1.71
CD164	2484	5261	0.47	POT1	937	1119	0.84
CD2AP	2876	2325	1.24	PPAT	1816	1805	1.01
CD55	3217	283	11.37	PPID	2571	1613	1.59
CDC25A	631	1872	0.34	PPIG	2819	3465	0.81
CDC42EP1	7020	178	39.44	PPIL4	1774	1033	1.72
CDC47	2541	3021	0.84	PPIP5K2	739	3006	0.25
CDK6	1656	3158	0.52	PPP1CB	3992	5742	0.70
CEBPB	3509	764	4.59	PPP1R15A	8353	3045	2.74
CEBPG	9321	1899	4.91	PPP1R2	1853	4203	0.44
CEBPZ	3857	2855	1.35	PPP3CA	1635	1433	1.14
CELF1	2675	4882	0.55	PPP4R2	1112	1700	0.65
CENPJ	422	1438	0.29	PPRC1	2000	2471	0.81
CENPV	1206	1014	1.19	PPTC7	1316	1068	1.23
CEP120	702	1827	0.38	PREPL	2857	2594	1.10
CEP170	400	1142	0.35	PRKAA1	2918	1966	1.48
CEP170B	2923	3044	0.96	PRKAA2	30	1925	0.02
CEP95	2496	656	3.80	PRKAB2	959	2761	0.35
CFAP97	2562	3123	0.82	PRKCI	3711	2755	1.35
CHCHD4	1326	338	3.92	PRKDC	3141	21757	0.14
CHD1	2025	4369	0.46	PRMT3	1408	1555	0.91
CHD7	2093	3361	0.62	PRPF38B	5252	2509	2.09
CHMP2B	1138	1572	0.72	PRPF40A	4576	6698	0.68
CHORDC1	1121	864	1.30	PRPF4B	1802	2462	0.73

Table S3E continued

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
CHUK	1997	1298	1.54	PRPS2	777	1332	0.58
CLASP2	907	1528	0.59	PRRC2C	2621	10028	0.26
CLK1	2207	1589	1.39	PSAT1	15152	6706	2.26
CLNS1A	16000	3222	4.97	PSMD12	6630	3126	2.12
CLPX	3245	2284	1.42	PTAR1	1069	4806	0.22
CLUH	5277	4219	1.25	PTER	504	1185	0.43
CMPK1	8172	2517	3.25	PTPDC1	1660	527	3.15
CMTM4	4590	2831	1.62	PTPN11	9618	4262	2.26
CMTR2	1587	1265	1.25	PTPN2	4364	1624	2.69
CNBP	22773	12576	1.81	PTPRF	3273	3192	1.03
CNTRL	1335	496	2.69	PUM2	5138	6530	0.79
COG5	2166	2944	0.74	PUM3	2312	1473	1.57
COL16A1	1307	379	3.45	PUS1	1999	606	3.30
COL6A1	269	2575	0.10	PUS7	2056	1950	1.05
COMTD1	1343	349	3.85	PVR	1992	2873	0.69
COX11	1529	1162	1.32	QKI	115	1057	0.11
CPT1A	1361	5499	0.25	QSER1	1625	2521	0.64
CREBZF	1861	1230	1.51	R3HDM4	4444	1926	2.31
CTDSPL2	1173	1533	0.77	RAB12	1055	869	1.21
CUL4A	6975	3014	2.31	RAB14	3639	3569	1.02
CUL5	1338	1910	0.70	RAB5A	2296	1298	1.77
CYCS	4639	5780	0.80	RABEP1	4232	2669	1.59
DCAF13	4230	3006	1.41	RABGGTB	8200	2625	3.12
DCBLD2	2303	3053	0.75	RAD23B	9769	8564	1.14
DCP2	944	1784	0.53	RAD50	2146	2695	0.80
DCUN1D1	1382	1292	1.07	RAI14	5005	1169	4.28
DCUN1D4	1051	722	1.46	RAP1GAP2	1858	1277	1.45
DCUN1D5	2610	1808	1.44	RAP2A	892	1180	0.76
DDIT3	12242	634	19.31	RB1CC1	3127	3691	0.85
DDIT4	3629	1933	1.88	RBAK	433	1243	0.35
DDX10	3372	1770	1.90	RBBP8	3850	2694	1.43
DDX11	1489	784	1.90	RBM19	1455	902	1.61
DDX17	5748	11228	0.51	RBM25	7899	4560	1.73
DDX21	13974	8676	1.61	RBM26	1399	1832	0.76
DDX39B	607	1080	0.56	RBM27	1123	4717	0.24
DDX55	1373	871	1.58	RBM28	2442	2069	1.18
DEK	5136	7986	0.64	RBM39	9156	6346	1.44
DFFA	1627	3712	0.44	RCN2	2524	1717	1.47
DGKD	2478	1289	1.92	REEP3	1284	1979	0.65
DGKH	720	2233	0.32	RELB	1629	558	2.92
DHX33	1611	2732	0.59	RFC3	1118	3046	0.37
DICER1	737	2766	0.27	RFC4	2070	2163	0.96
DIMT1	1086	1306	0.83	RFK	1076	1043	1.03
DIS3	2831	2156	1.31	RHPN1	1093	654	1.67
DKC1	16468	6778	2.43	RICTOR	657	1044	0.63
DLGAP1-AS2	1326	2430	0.55	RIDA	1043	552	1.89
DMTF1	1557	1688	0.92	RIF1	872	4250	0.21
DNAJA4	1323	641	2.06	RINT1	826	1793	0.46
DNAJC10	7532	5013	1.50	RLIM	2117	3119	0.68
DNAJC2	2504	2044	1.23	RNF149	410	1423	0.29
DNTTIP2	3858	3192	1.21	RNGTT	586	1149	0.51
DOCK5	539	1415	0.38	RPAP3	1556	2341	0.66
DOCK6	1434	435	3.30	RPE	1917	2155	0.89
DOT1L	947	1179	0.80	RPF2	2249	1161	1.94
DPY19L1	415	1976	0.21	RPIA	1910	1027	1.86
DSCC1	1795	949	1.89	RPL22L1	15234	832	18.31
DST	28133	1300	21.64	RPRD1A	2146	1572	1.37
DUS1L	6740	2863	2.35	RPS6KA3	5018	2222	2.26
DUSP5	2612	3367	0.78	RPS6KB1	1229	606	2.03
DVL1	3817	4848	0.79	RRAS2	1239	428	2.90
DYNLT3	1498	714	2.10	RRP1B	2070	7058	0.29
DYRK2	1173	696	1.69	RSL1D1	15190	7869	1.93

Table S3E continued

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
EDEM3	464	1139	0.41	RSL24D1	10273	2532	4.06
EEA1	1354	485	2.79	RSRC2	4423	2127	2.08
EIF1AX	3377	1185	2.85	RSRP1	574	1096	0.52
EIF3J	8739	2929	2.98	SACS	379	3533	0.11
EIF4A2	25620	7489	3.42	SAMD8	509	1405	0.36
EIF4EBP1	5407	2180	2.48	SAT1	10687	4870	2.19
ELK4	662	2574	0.26	SATB1	1589	332	4.78
EMP1	600	1511	0.40	SATB2	249	1375	0.18
ENAH	4856	3202	1.52	SBDS	4498	3246	1.39
EP400	1726	2119	0.81	SBNO1	4150	2403	1.73
EPB41L4A-AS1	4712	692	6.81	SBNO2	1510	1276	1.18
EPB41L4B	1498	794	1.89	SCAMP1	433	1253	0.35
EPRS	15524	12744	1.22	SCFD1	2677	1802	1.49
EPS15	2889	1285	2.25	SCOC	2579	1093	2.36
EPT1	886	4951	0.18	SCRIB	4920	3495	1.41
ERGIC2	1841	1299	1.42	SDC4	1476	7053	0.21
ERN1	1032	927	1.11	SDE2	1147	1303	0.88
ERO1A	1076	5034	0.21	SDHD	1323	1061	1.25
ERRFI1	5146	3241	1.59	SEC63	1781	2538	0.70
ESCO1	1203	1315	0.91	SEH1L	5942	3852	1.54
ESF1	4163	813	5.12	SERBP1	11619	9788	1.19
ESRRA	4998	1582	3.16	SERPINE1	259	13639	0.02
EV15	1027	465	2.21	SERTAD2	1055	1548	0.68
EXOC6	1095	1687	0.65	SET	20976	15220	1.38
EXOSC7	1705	1053	1.62	SETD6	1187	566	2.10
FAM107B	6924	972	7.12	SETD7	4296	2822	1.52
FAM122B	1912	3808	0.50	SF3B6	10692	4993	2.14
FAM129A	4449	122	36.47	SFXN4	2711	927	2.92
FAM135A	1472	394	3.74	SH3BGRL2	1093	446	2.45
FAM171A1	1244	594	2.09	SH3BP2	1792	1663	1.08
FAM208A	1940	4003	0.48	SH3D19	3469	1609	2.16
FAM208B	2091	2276	0.92	SH3YL1	4208	930	4.52
FAM210A	1248	1009	1.24	SHTN1	2166	2140	1.01
FAM35A	1041	675	1.54	SHKE1	1696	1163	1.46
FAM60A	5463	2818	1.94	SIPA1L2	1552	419	3.70
FAM84B	7075	1519	4.66	SIX4	184	2026	0.09
FAM91A1	4103	1774	2.31	SKIL	1910	1775	1.08
FAR1	2355	2786	0.85	SLC12A7	1425	5885	0.24
FARP2	1399	1461	0.96	SLC16A6	23	2370	0.01
FASTKD2	1083	2081	0.52	SLC17A9	1243	1934	0.64
FBRSL1	1957	1094	1.79	SLC20A1	944	7097	0.13
FBXO41	1945	1906	1.02	SLC25A22	2988	1143	2.61
FBXO45	2023	1425	1.42	SLC25A32	1425	1074	1.33
FEM1B	1773	1414	1.25	SLC25A36	3770	2683	1.41
FEM1C	773	1311	0.59	SLC35F2	1748	1219	1.43
FERMT1	8024	2414	3.32	SLC38A1	7051	17988	0.39
FGFR1OP2	1448	1628	0.89	SLC38A2	3200	10038	0.32
FGFR4	1747	533	3.28	SLC39A10	341	1664	0.20
FIGNL1	403	1628	0.25	SLC39A4	1947	672	2.90
FKBP4	6978	7820	0.89	SLC39A6	641	2005	0.32
FLNA	15950	86124	0.19	SLC43A1	3900	994	3.92
FMNL2	1724	2008	0.86	SLC43A3	130	1308	0.10
FNBP4	2386	1982	1.20	SLC44A2	1010	816	1.24
FNDC3A	3224	3454	0.93	SLC6A6	577	2142	0.27
FOSL1	2809	1914	1.47	SLC6A8	4684	2630	1.78
FOXK1	949	4305	0.22	SLC7A1	3525	10935	0.32
FRMD5	1566	847	1.85	SLC7A11	1611	274	5.88
G2E3	365	1431	0.26	SLFN5	2287	691	3.31
GAB2	2367	292	8.11	SLIRP	3081	2662	1.16
GALT	4218	3676	1.15	SLMAP	2852	2206	1.29
GAN	408	1053	0.39	SLTM	9091	3375	2.69
GART	4847	10960	0.44	SMAD5	1505	4561	0.33

Table S3E continued

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
GAS5	33726	5263	6.41	SMARCAD1	1509	1427	1.06
GATAD2A	3309	2862	1.16	SMC3	4265	5050	0.84
GCC2	1960	1839	1.07	SMC5	1330	1620	0.82
GCLC	4086	1541	2.65	SMC6	1158	1864	0.62
GCLM	951	1261	0.75	SMCHD1	3556	3435	1.04
GDF15	6382	1592	4.01	SMG1	2324	3808	0.61
GEMIN5	846	2369	0.36	SMIM15	1707	1152	1.48
GFPT1	14575	5195	2.81	SMIM20	3683	509	7.24
GJB3	754	1537	0.49	SMS	4625	1728	2.68
GLO1	6677	6344	1.05	SNAPC4	1076	969	1.11
GMFB	1349	1772	0.76	SNHG1	11994	1852	6.48
GNB1L	3130	406	7.71	SNHG12	1194	326	3.66
GNG12	5928	3833	1.55	SNHG15	2656	1003	2.65
GNL2	5826	3606	1.62	SNHG17	1755	701	2.50
GNL3	6365	2381	2.67	SNHG19	2211	563	3.93
GOLGA4	5953	3752	1.59	SNHG8	19650	1028	19.11
GOLT1B	869	1204	0.72	SNX10	549	1773	0.31
GPD2	935	3464	0.27	SNX4	1187	1033	1.15
GPN3	1210	1046	1.16	SOCS4	605	2180	0.28
GPRC5A	3384	623	5.43	SOWAHC	730	1207	0.60
GPSM1	1333	421	3.17	SOX4	3146	1195	2.63
GRB10	4534	179	25.33	SPCS3	1175	3265	0.36
GRPEL2	1114	1377	0.81	SPIRE1	4328	1101	3.93
GSAP	619	1144	0.54	SPNS2	6695	1566	4.28
GSR	3094	3503	0.88	SPOPL	560	1405	0.40
GSTP1	35506	959	37.02	SPTBN2	1768	3017	0.59
GTF2F2	3255	2414	1.35	SQSTM1	20854	7440	2.80
GTF2H3	2259	1367	1.65	SREK1	2263	2099	1.08
GTF3C4	2004	4154	0.48	SREK1IP1	1159	700	1.66
GTPBP4	5984	2675	2.24	SRP9	3544	3781	0.94
GUF1	1931	1213	1.59	SRPK1	3313	3884	0.85
HAUS6	454	1403	0.32	SRRM1	1662	2679	0.62
HDDC2	3907	802	4.87	SRSF1	10160	9122	1.11
HEATR1	1747	3031	0.58	SRSF11	4613	4649	0.99
HGS	3174	2964	1.07	SRSF5	5285	4918	1.07
HK2	2079	1711	1.22	SSB	6276	5443	1.15
HMGA1	37164	23082	1.61	SSR1	2637	3568	0.74
HNRNPDL	8139	5444	1.50	SSX2IP	1352	1534	0.88
HOOK1	3360	2913	1.15	ST6GALNAC4	3177	1372	2.32
HPCAL1	4411	2101	2.10	STC2	19	4816	0.00
HPRT1	3003	3578	0.84	STEAP2	236	1014	0.23
HS2ST1	1253	2013	0.62	STK26	2525	2998	0.84
HSPA13	509	2612	0.19	STK32C	2252	466	4.83
HSPA1A/1B	1644	765	2.15	STRN3	567	1070	0.53
HSPA4L	1239	2094	0.59	STX1A	2025	371	5.46
HSPA9	24871	15327	1.62	STXBP3	1575	1137	1.39
HSPD1	33648	29489	1.14	SULF2	155	2160	0.07
HSPH1	8443	16435	0.51	SUN1	944	10481	0.09
IARS	24534	10051	2.44	SUPV3L1	2781	1345	2.07
IBTK	3471	2349	1.48	SVIL	1095	282	3.88
IFRD1	4998	4335	1.15	TAF13	1128	575	1.96
IFT88	1257	831	1.51	TAF1C	720	1045	0.69
IGF2BP2	3495	2120	1.65	TAF1D	9978	2204	4.53
IMPA1	612	1288	0.48	TANC2	914	1448	0.63
IMPACT	1689	1142	1.48	TATDN1	3954	455	8.69
IMPAD1	1757	3423	0.51	TAX1BP3	779	1012	0.77
INO80D	375	1131	0.33	TBC1D15	2604	864	3.01
IQCB1	1693	1109	1.53	TBC1D30	1503	442	3.40
ISCU	4418	1191	3.71	TBC1D4	1385	1825	0.76
ITGA6	2454	13205	0.19	TBK1	2089	905	2.31
ITGB1	2847	6126	0.46	TBL1XR1	5103	4826	1.06
ITGB3BP	1191	720	1.65	TC2N	1602	1176	1.36

Table S3E continued

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
ITM2C	3646	1805	2.02	TCEA1	4769	1634	2.92
IVNS1ABP	4684	3451	1.36	TCERG1	2171	4604	0.47
JAG1	322	2135	0.15	TCF3	6147	4285	1.43
JMJD1C	2604	2724	0.96	TCOF1	2548	9059	0.28
JMY	1102	979	1.13	TFAP4	1265	692	1.83
JUN	4971	1016	4.89	THAP12	2383	876	2.72
JUNB	2836	827	3.43	THAP9-AS1	2607	694	3.76
KATNB1	2701	1897	1.42	THOC1	1448	1148	1.26
KDM6B	1413	1183	1.19	THOC2	3015	5181	0.58
KDSR	687	1086	0.63	TIA1	1048	1389	0.75
KIAA0753	1305	811	1.61	TIMM17A	3485	2959	1.18
KIAA0907	1387	2543	0.55	TIMM44	4096	1353	3.03
KIAA0930	2871	1324	2.17	TINAGL1	2324	5036	0.46
KIAA1549	631	1057	0.60	TM4SF1	5370	2311	2.32
KIAA1551	2141	556	3.85	TMED5	1481	2048	0.72
KIAA1804	874	1032	0.85	TMED7	662	2066	0.32
KIAA1958	530	1308	0.41	TMEM126B	3287	1123	2.93
KIF20B	535	4265	0.13	TMEM167A	3028	1840	1.65
KIF21A	3789	913	4.15	TMEM170A	740	1275	0.58
KIF3A	452	1130	0.40	TMEM181	791	1602	0.49
KIFC3	3871	1401	2.76	TMEM209	306	1683	0.18
KLF4	2075	344	6.03	TMEM259	1406	2314	0.61
KLF5	7063	3083	2.29	TMEM263	1922	712	2.70
KLF6	2981	1730	1.72	TMEM33	1444	2036	0.71
KMT2A	2423	4883	0.50	TMEM38B	488	1442	0.34
KNTC1	542	2416	0.22	TMEM65	1046	291	3.60
KRAS	2504	4675	0.54	TMF1	1516	1323	1.15
LACTB2	1383	672	2.06	TNC	718	7020	0.10
LAMA5	1236	8158	0.15	TNFRSF10D	262	2404	0.11
LAMB3	2849	1517	1.88	TNFRSF12A	7897	4988	1.58
LAPTM4B	2287	5128	0.45	TNFRSF21	2902	648	4.48
LARP1B	3532	1013	3.49	TNKS2	3078	3287	0.94
LARP4	1933	3717	0.52	TNPO1	3692	5561	0.66
LARS	3127	10215	0.31	TNRC6A	794	1777	0.45
LBR	627	5372	0.12	TPD52	3577	3004	1.19
LCLAT1	219	1148	0.19	TPP2	2602	2733	0.95
LCOR	794	1174	0.68	TRABD	1987	1070	1.86
LENG8	973	2506	0.39	TRAP1	5847	4135	1.41
LHFPL2	541	1140	0.47	TRAPPC8	1102	752	1.47
LIF	528	1401	0.38	TRIB3	28178	2258	12.48
LIG3	3857	680	5.67	TRIM65	1027	1326	0.77
LIN7C	1298	806	1.61	TRNT1	1116	550	2.03
LMAN1	1773	4314	0.41	TROVE2	574	1375	0.42
LOC220729	1531	893	1.71	TSC22D2	1034	634	1.63
LONP1	11554	5743	2.01	TSEN15	1455	2171	0.67
LPCAT1	1236	2093	0.59	TSR1	3665	3263	1.12
LRP6	662	2011	0.33	TUBE1	1095	194	5.64
LRP8	1029	2260	0.46	TWF1	1814	1995	0.91
LRPPRC	11937	11375	1.05	TWISTNB	593	1346	0.44
LRRC58	1630	2861	0.57	TXLNG	2939	1533	1.92
LRRC8D	1076	1301	0.83	TXNRD1	11241	4802	2.34
LRRFIP1	6955	4259	1.63	U2SURP	6738	7106	0.95
LTN1	700	2549	0.27	UBA5	2277	1315	1.73
LUC7L	1872	674	2.78	UBE2B	2736	2077	1.32
LUC7L2	1067	1193	0.89	UBE2E1	3994	2171	1.84
LUC7L3	4383	2366	1.85	UBE2K	4842	3479	1.39
LYAR	2207	2046	1.08	UBE2V2	2842	2394	1.19
LYPLA1	2345	2020	1.16	UBN2	718	1448	0.50
LYRM7	441	1628	0.27	UCHL5	1698	2509	0.68
MACC1	919	4173	0.22	UFL1	989	1348	0.73
MAD2L1	2056	2887	0.71	UFM1	5774	2918	1.98
MAFF	2334	846	2.76	UHRF2	1051	1131	0.93

Table S3E continued

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
MAL2	19591	4146	4.73	UPP1	2451	596	4.11
MALAT1	3083	4201	0.73	URI1	4950	1959	2.53
MAN2A1	551	2910	0.19	USP12	1736	1759	0.99
MAP4K5	1295	1571	0.82	USP15	1237	1124	1.10
MAP7D3	1284	1544	0.83	USP25	2014	1540	1.31
MAPK6	4919	1283	3.83	USP4	780	1381	0.56
MAPK8	2875	1116	2.58	USP53	2192	807	2.72
MAPK8IP3	1208	1111	1.09	VAMP7	3563	1993	1.79
MARCH6	1220	6246	0.20	VGf	2678	1092	2.45
MARS	12686	10566	1.20	VHL	1126	1051	1.07
MAT2A	4303	5655	0.76	VMA21	3149	3278	0.96
MBNL2	1500	766	1.96	VMP1	2480	3127	0.79
MBP	1046	613	1.71	VPS13A	919	2970	0.31
MBTD1	1354	675	2.01	VPS13C	951	1649	0.58
MBTPS2	393	1207	0.33	VPS37A	652	1857	0.35
MCM10	600	1740	0.34	WARS	19987	8097	2.47
MCM8	999	1120	0.89	WASL	2670	2227	1.20
MDN1	2605	2213	1.18	WDHD1	640	1976	0.32
ME1	1547	1738	0.89	WDR12	1987	3881	0.51
ME2	2788	1575	1.77	WDR19	1058	405	2.61
MED13	3210	4592	0.70	WDR3	3982	2194	1.81
METRNL	1990	533	3.73	WDR35	725	1189	0.61
MEX3A	1051	2041	0.51	WDR36	900	2300	0.39
MFSD10	2009	1312	1.53	WDR41	1512	1268	1.19
MIB1	1528	2744	0.56	WDR43	8005	3775	2.12
MIGA1	224	1021	0.22	WDR75	2501	3060	0.82
MINA	1274	370	3.44	WSB1	1535	539	2.85
MIOS	1053	1308	0.81	XPO4	2527	3937	0.64
MITD1	1330	774	1.72	XPOT	17938	5223	3.43
MKLN1	1538	2782	0.55	YARS	15162	8848	1.71
MMS22L	389	1130	0.34	YES1	5103	4813	1.06
MORC3	775	1355	0.57	YRDC	2845	900	3.16
MOSPD1	1960	1907	1.03	YTHDC2	709	1787	0.40
MPHOSPH6	1682	1228	1.37	ZBTB21	594	1123	0.53
MPP6	772	2270	0.34	ZBTB33	1031	3088	0.33
MRPL12	2638	535	4.93	ZC3H15	6203	4103	1.51
MRPL32	1960	1596	1.23	ZCCHC7	1455	1114	1.31
MRPL42	3149	1648	1.91	ZDHHC8	4607	692	6.66
MRPL50	1910	1070	1.79	ZFAND1	5662	1422	3.98
MRPS25	1827	1049	1.74	ZFAS1	29226	4764	6.13
MTA1	3711	3059	1.21	ZFC3H1	713	2150	0.33
MTAP	1644	1169	1.41	ZFP36	1898	672	2.82
MT-CO1	11406	197061	0.06	ZFP36L1	2504	4903	0.51
MTF2	838	1202	0.70	ZHX1	2265	906	2.50
MTHFD1L	5310	2268	2.34	ZMPSTE24	650	1818	0.36
MTHFD2	18673	6552	2.85	ZNF131	2270	899	2.52
MTIF2	2817	2262	1.25	ZNF146	6597	3692	1.79
MT-ND4	16050	277843	0.06	ZNF148	1121	1709	0.66
MT-ND4L	1528	23921	0.06	ZNF195	2016	683	2.95
MT-ND5	3361	66592	0.05	ZNF292	627	1474	0.43
MT-ND6	711	19740	0.04	ZNF330	2112	1268	1.67
MT-RNR2	10765	218742	0.05	ZNF367	221	1264	0.17
MTRR	1759	1443	1.22	ZNF451	996	1284	0.78
MTURN	7265	449	16.18	ZNF473	1121	729	1.54
MXD1	1467	1571	0.93	ZNF507	845	1379	0.61
MXI1	1882	1235	1.52	ZNF598	2828	1719	1.64
MYC	7526	6589	1.14	ZNF614	2751	387	7.11
MYCBP2	2781	2402	1.16	ZNF639	1703	1045	1.63
MYRF	1446	151	9.58	ZNF644	1743	2005	0.87
MYSM1	1361	902	1.51	ZNF664	15171	6956	2.18
MZT1	1604	1588	1.01	ZNF697	238	1113	0.21
N4BP2L2	2678	3070	0.87	ZNF706	2214	1145	1.93

Table S3E continued

Symbol	CIC-TEX	CD44v6kd	TEX:v6kd	Symbol	CIC-TEX	CD44v6kd	TEX:v6kd
NAA15	2699	3251	0.83	ZNF770	1422	1128	1.26
NAA20	5589	2789	2.00	ZRANB2	2232	2235	1.00
NAA25	2063	1298	1.59	ZWILCH	1684	1736	0.97

^a The ratio of CIC-TEX : CD44v6kd cells is shown for the signal strength of either CIC-TEX or CD44v6kd cells ≥ 1000 ; ≥ 1.5 -fold higher signal strength in CIC-TEX: red, in CD44v6kd cells: green, no significant difference in the signal strength between CIC-TEX and CD44v6kd cells: black.

Table S3F

Correlation between increased mRNA recovery in CIC-TEX-treated Tspan8kd cells and recovery in CIC-TEXIncreased mRNA recovery in CIC-TEX-treated Tspan8kd cells and recovery in CIC-TEX^a

Symbol ^b	Tsp8kd cells	kd cells + holo-TEX	kd + TEX: kd cells	CIC-TEX	CIC-TEX: kd cells
ADAM19	2957	7989	2.70	693	0.23
AHNAK2	734	1928	2.63	773	1.05
AKAP12	1433	4331	3.02	1623	1.13
AKR1B10	1393	2848	2.04	3512	2.52
ANXA10	1679	3758	2.24	5529	3.29
CALB2	2954	5968	2.02	4936	1.67
CAPRIN2	2225	6480	2.91	4241	1.91
CEACAM5	321	4033	12.58	24	0.08
CEACAM6	1230	8612	7.00	28	0.02
CEMIP	4256	9726	2.29	2882	0.68
CHAC1	710	1713	2.41	2583	3.64
COL17A1	3337	8869	2.66	148	0.04
DCBLD2	3135	7757	2.47	2303	0.73
DDIT3	612	1646	2.69	12242	20.00
DDIT4	1828	4879	2.67	3629	1.98
DKK1	2518	6444	2.56	2136	0.85
DUSP5	568	1135	2.00	2612	4.60
EGR1	1742	3700	2.12	1437	0.83
EMP1	1981	5526	2.79	600	0.30
EREG	8012	16797	2.10	1225	0.15
ERRF1	4536	13557	2.99	5146	1.13
FAM129A	1730	3450	1.99	4449	2.57
FAM135A	930	1894	2.04	1472	1.58
FRMD5	621	1236	1.99	1566	2.52
H1FO	11089	33900	3.06	22262	2.01
HMGA1	32429	66203	2.04	37164	1.15
ID1	1280	3276	2.56	589	0.46
IFI27	1863	6985	3.75	301	0.16
IFI6	1105	2514	2.27	301	0.27
IGFBP6	3224	6619	2.05	1992	0.62
JAG1	1956	6030	3.08	322	0.16
KLK10	1770	3634	2.05	26	0.01
LAMA3	1699	3660	2.15	542	0.32
LAMC2	1850	4027	2.18	587	0.32
LCN2	8428	17538	2.08	7399	0.88
MAOB	543	1190	2.19	151	0.28
NDRG1	2303	6502	2.82	7592	3.30
NEBL	827	1797	2.17	4592	5.55
NR1D1	723	2202	3.05	1231	1.70
NR1D2	1248	2932	2.35	1719	1.38
NRP1	933	2345	2.51	217	0.23
NTSR1	3605	8527	2.37	3440	0.95
PER1	667	1406	2.11	739	1.11
PMEPA1	4418	9628	2.18	1187	0.27
PSD3	1879	3824	2.04	907	0.48
SCEL	714	2590	3.63	295	0.41
SERPINE2	612	1315	2.15	1177	1.92
SLCO4A1	1270	3104	2.44	478	0.38
SMOX	1392	3598	2.58	8763	6.29
UPP1	697	2110	3.03	2451	3.51

^a The ratio of CIC-TEX-treated : untreated Tsp8kd cells is shown for the signal strength of CIC-TEX-treated Tsp8kd cells ≥ 1000 ;^b ≥ 2 -fold higher signal strength in CIC-TEX and CIC-TEX-treated Tsp8kd cells compared to untreated Tsp8kd cells is indicated in bold.

Table S4

The impact of CIC-TEX treatment on miRNA recovery in CD44v6kd and Tspan8kd cells

Table S4A

Higher miRNA signal strength in CIC-TEX than CD44v6kd and/or Tspan8kd cells

miRNA	CIC-TEX	TEX:v6kd cells	TEX:Tsp8kd cells	miRNA	CIC-TEX	TEX:v6kd cells	TEX:Tsp8kd cells
let-7b-5p	17099	1.65	1.49	miR-361-5p	945	2.14	1.83
let-7c-5p	2964	2.10	2.20	miR-3656	1621	6.11	4.87
let-7d-5p	10268	2.84	1.71	miR-3679-5p	1585	6.25	12.25
miR-101-3p	1330	3.73	2.48	miR-374a-5p	2487	1.82	1.49
miR-106b-5p	14130	2.30	2.07	miR-4257	527	2.67	2.39
miR-10a-5p	12693	1.90	1.77	miR-4271	1510	7.39	3.95
miR-10b-5p	1499	4.53	4.26	miR-4281	5197	7.05	1.92
miR-1202	3211	1.54	1.69	miR-429	5931	1.54	1.85
miR-1207-5p	2892	3.03	1.57	miR-4299	1269	1.64	1.73
miR-1225-5p	2735	2.46	2.36	miR-4306	6255	12.32	2.04
miR-1246	59235	58.42	75.97	miR-4428	532	3.78	1.86
miR-125a-5p	1849	2.04	1.57	miR-4442	865	4.67	1.70
miR-1268a	5693	13.55	5.91	miR-4443	1440	4.57	9.86
miR-130b-3p	1508	1.64	1.60	miR-4505	3848	6.23	6.04
miR-148b-3p	628	3.34	2.94	miR-4507	1919	6.45	6.07
miR-151a-3p	1208	2.51	1.71	miR-4530	12265	3.72	3.18
miR-151b	2786	10.63	3.65	miR-4532	513	2.86	1.77
miR-183-5p	1169	1.65	2.71	miR-455-3p	730	1.51	1.82
miR-197-5p	1487	2.86	4.35	miR-4655-5p	798	1.96	2.75
miR-200a-3p	8550	2.83	1.72	miR-4687-3p	2116	3.46	2.29
miR-200b-3p	16703	1.62	1.49	miR-4721	1349	2.20	3.06
miR-20b-5p	2920	1.71	2.32	miR-4728-5p	1123	1.92	2.72
miR-210-3p	2231	5.08	1.69	miR-4741	1246	6.05	3.59
miR-215-5p	11754	5.23	2.03	miR-4787-5p	961	2.42	2.43
miR-224-5p	835	8.07	1.70	miR-4788	842	1.56	1.64
miR-23a-3p	10758	2.99	1.76	miR-494-3p	11645	6.29	5.21
miR-26a-5p	3055	1.71	1.69	miR-5001-5p	1391	6.63	6.03
miR-26b-5p	6160	7.45	2.33	miR-574-5p	4835	19.60	6.03
miR-2861	1969	4.46	3.88	miR-582-5p	483	4.47	1.98
miR-30b-5p	5821	1.80	1.61	miR-590-5p	1902	2.46	2.79
miR-30d-5p	1743	3.17	2.13	miR-638	2064	3.90	4.55
miR-320a	1166	2.32	3.74	miR-642a-3p	8756	5.09	8.62
miR-320c	2894	3.43	6.73	miR-98-5p	1147	1.72	1.87
miR-320d	1990	2.18	3.04	miR-99b-5p	1312	1.93	1.80
miR-320e	1231	2.21	2.83				
let-7e-5p	9113	3.96		let-7g-5p	8467		1.56
miR-135b-5p	1066	1.70		miR-196a-5p	3451		1.90
miR-141-3p	17720	1.68		miR-20a-5p	18978		1.54
miR-151a-5p	3790	4.98		miR-301a-3p	784		1.90
miR-181a-5p	1626	3.78		miR-31-3p	1842		1.50
miR-185-5p	3596	3.54		miR-320b	966		1.91
miR-1915-3p	2601	2.47		miR-92a-3p	2531		1.94
miR-192-5p	21112	3.25					
miR-194-5p	9526	3.21					
miR-200c-3p	8567	1.55					
miR-22-3p	4163	1.93					
miR-28-5p	629	3.78					
miR-29c-3p	4232	3.30					
miR-30c-5p	1507	1.85					
miR-30e-5p	1597	1.93					
miR-34a-5p	1858	3.41					
miR-374b-5p	1661	1.76					
miR-4466	1747	3.10					
miR-4485-5p	1173	2.53					
miR-4516	12953	4.68					
miR-4739	620	1.85					

Table S4B

miRNA upregulation in CIC-TEX-treated CD44v6kd and/or Tspan8kd cells^a

geneID	v6kd cells	v6kd cells+ TEX	v6kd cells+ TEX:v6kd cells	Tsp8kd cells	Tsp8kd cells+TEX	Tsp8kd c.+TEX: Tsp8kd c.
miR-1246	10149	49465	4.87	33443	82066	2.45
miR-146a-5p	133	690	5.20	216	312	1.44
miR-21-3p	427	884	2.07	1380	2266	1.64
miR-21-5p	164171	540707	3.29	838408	1345789	1.61
miR-25-5p	44	195	4.43	102	220	2.15
miR-27a-3p	6229	9490	1.52	9634	14260	1.48
miR-3196	737	1122	1.52	718	2177	3.03
miR-3656	225	399	1.77	538	1907	3.54
miR-3960	222	360	1.62	96	773	8.05
miR-4485-3p	171	493	2.89	92	258	2.80
miR-4488	234	636	2.71	106	290	2.74
miR-4492	373	742	1.99	145	871	6.01
miR-4497	2105	121021	57.49	1062	5148	4.85
miR-4508	326	513	1.57	62	187	3.01
miR-4516	452	678	1.50	304	895	2.94
miR-5585-3p	3046	15632	5.13	2203	12304	5.59
miR-6087	775	4579	5.91	474	856	1.81
miR-7704	989	2837	2.87	210	339	1.62
miR-24-3p				6008	9063	1.51
miR-3074-5p				3085	5001	1.62
miR-101-3p	3124	7199	2.30			
miR-1248	137	778	5.68			
miR-1301-3p	70	492	7.04			
miR-16-2-3p	478	737	1.54			
miR-181d-5p	111	868	7.82			
miR-19a-3p	191	562	2.94			
miR-19b-3p	655	1081	1.65			
miR-20a-5p	7797	11922	1.53			
miR-29b-3p	275	590	2.15			
miR-335-3p	992	1788	1.80			
miR-3529-3p	33977	70356	2.07			
miR-424-3p	102	505	4.95			
miR-4284	129	2012	15.60			
miR-450a-5p	335	609	1.82			
miR-450b-5p	60	534	8.90			
miR-4521	101	536	5.31			
miR-499a-5p	109	6240	57.25			
miR-499b-3p	81	6178	76.27			
miR-503-5p	36	599	16.64			
miR-514a-3p	69	680	9.86			
miR-5701	1158	5910	5.10			
miR-584-5p	51	487	9.51			
miR-7-5p	33620	69692	2.07			
miR-92b-3p	432	1122	2.60			
miR-9-5p	60	7535	125.58			
miR-96-5p	526	1437	2.73			

^a miRNA upregulated in CIC-TEX-treated A818.4-v6kd and -Tsp8kd cells: red, -Tsp8kd cells: blue, -v6kd cells: green

Table S4C

miRNA downregulation in CIC-TEX-treated CD44v6kd and/or Tspan8kd cells^a

genelD	v6kd cells	v6kd cells+TEX	v6kd cells+TEX:v6kd cells	Tsp8kd cells	Tsp8kd cells+TEX	Tsp8kd c.+TEX:Tsp8kd c.
miR-10a-3p	581	353	0.61	1096	688	0.63
miR-1273g-3p	9592	2795	0.29	3184	1216	0.38
miR-29c-3p	1608	38	0.02	127	76	0.60
miR-3195	3034	137	0.05	1783	824	0.46
miR-4454	144	85	0.59	900	435	0.48
miR-4791	3575	1395	0.39	2143	900	0.42
miR-574-3p	402	91	0.23	152	93	0.61
miR-103a-3p				41298	25800	0.62
miR-103b				41298	25800	0.62
miR-1248				5449	1023	0.19
miR-205-5p				8329	4240	0.51
miR-26a-5p				35403	22017	0.62
miR-3607-3p				1783	265	0.15
miR-4284				14594	4981	0.34
miR-744-5p				1499	748	0.50
miR-934				683	363	0.53
let-7b-5p	12169	7447	0.61			
let-7c-5p	1726	1063	0.62			
let-7d-3p	1278	572	0.45			
let-7e-5p	2514	991	0.39			
miR-10a-5p	105622	70093	0.66			
miR-125a-5p	4229	1605	0.38			
miR-126-5p	4358	45	0.01			
miR-1296-5p	1737	67	0.04			
miR-132-3p	635	94	0.15			
miR-152-3p	1264	709	0.56			
miR-181a-5p	1358	704	0.52			
miR-191-5p	12698	8219	0.65			
miR-200b-5p	742	410	0.55			
miR-200c-3p	30928	20354	0.66			
miR-23b-3p	13810	6096	0.44			
miR-28-3p	890	564	0.63			
miR-30c-5p	6406	4145	0.65			
miR-30d-5p	86505	49971	0.58			
miR-3182	244834	96766	0.40			
miR-3184-3p	1677	1113	0.66			
miR-320a	6727	4317	0.64			
miR-339-5p	1523	701	0.46			
miR-361-5p	719	314	0.44			
miR-423-5p	1677	1113	0.66			
miR-425-5p	834	485	0.58			
miR-4448	238922	19553	0.08			
miR-4532	1551	929	0.60			
miR-615-3p	533	292	0.55			
miR-629-5p	7691	1399	0.18			
miR-7641	65136	18501	0.28			
miR-95-3p	1337	635	0.48			
miR-99b-3p	616	273	0.44			
miR-99b-5p	3701	1786	0.48			

^a miRNA downregulated in CIC-TEX-treated A818.4-v6kd and -Tsp8kd cells: red, -Tsp8kd cells: blue, -v6kd cells: green

Table S5

Correlation between upregulated miRNA and downregulated mRNA

Table S5A

Reduced mRNA and increased miRNA recovery in CIC-TEX-treated CD44v6kd and Tspan8kd cells^a**Reduced mRNA in TEX-treated CD44v6kd and Tspan8kd cells**

mRNA	miRNA					
ACSS2	miR-4492					
CEACAM1	miR-29b-3p	miR-4488	miR-4516			
FUCA1	miR-9-5p	miR-503-5p	miR-1248	miR-4516		
HMGCS1	miR-29b-3p					
HOXB8	miR-27a-3p	miR-92b-3p	miR-146a-5p	miR-181d-5p	miR-3529-3p	miR-3960
IDI1	miR-499a-5p					
IFIT3	miR-146a-5p					
INSIG1	miR-24-3p	miR-29b-3p	miR-1246	miR-3656	miR-4284	
MSMO1	miR-19a-3p	miR-20a-5p	miR-424-3p			
SCD	miR-181d-5p					

Reduced mRNA in TEX-treated Tspan8kd cells

mRNA	miRNA				
ALDH1L1	miR-7704				
ARL15	miR-335-3p				
ATP6V1B1	miR-21-5p	miR-3960			
BCAS1	miR-21-3p	miR-3656	miR-4488	miR-4492	
BTG2	miR-21-5p	miR-27a-3p			
CFH	miR-21-5p	miR-146a-5p			
CLEC3A	miR-4492				
F2R	miR-3196	miR-4488			
FGD3	miR-4488	miR-4492	miR-4497	miR-6087	
GAA	miR-3960	miR-4488			
GABRP	miR-27a-3p				
GATA2	miR-27a-3p				
KLHDC7A	miR-7704				
LMO4	miR-21-3p	miR-335-3p			
MEIS2	miR-21-3p	miR-24-3p	miR-4485-3p	miR-7704	
PRICKLE4	miR-4488				
RGS2	miR-21-3p	miR-3074-5p			
RNF141	miR-27a-3p	miR-1246	miR-4488		
SHROOM1	miR-3196	miR-4516			
TACSTD2	miR-4497				
TGM2	miR-4488	miR-4492	miR-7704		
THBS1	miR-3074-5p				
WWOX	miR-24-3p	miR-146a-5p			
ZNF704	miR-21-5p				

Reduced mRNA in TEX-treated CD44v6kd cells

mRNA	miRNA						
ABHD12B	miR-21-3p	miR-27a-3p	miR-499b-3p	miR-4488	miR-4492		
ACAT2	miR-92b-3p						
ACP2	miR-4492	miR-7704					
ADAMTS8	miR-335-3p	miR-7704					
ADAMTSL2	miR-3196	miR-3960	miR-4488	miR-4492			
ADI1	miR-4521						
ALDH3A1	miR-4492						
AMOT	miR-29b-3p						
APCDD1	miR-7-5p	miR-20a-5p	miR-4492				
APOE	miR-3196	miR-7704					
ARHGAP1	miR-19a-3p	miR-20a-5p	miR-25-5p	miR-3196	miR-4488	miR-4492	miR-6087
ARHGAP18	miR-101-3p	miR-181d-5p	miR-499b-3p				
ARHGEF40	miR-4492						

Table S5A continued

Reduced mRNA in TEX-treated CD44v6kd cells

mRNA	miRNA								
ARMC7	miR-29b-3p	miR-3656	miR-4492						
ASPSCR1	miR-25-5p								
ATP6V0D1	miR-5701								
ATP6V0E2	miR-7-5p	miR-3656	miR-4492	miR-4497	miR-6087	miR-7704			
AXIN2	miR-1246	miR-3656							
BAMBI	miR-19a-3p	miR-20a-5p							
BCL2L15	miR-20a-5p								
BHLHE40	miR-181d-5p								
C12orf57	miR-5701								
C6orf223	miR-3196	miR-3960	miR-4488	miR-4497	miR-4516				
CASS4	miR-25-5p	miR-6087							
CCDC3	miR-4488	miR-7704							
CDKN1A	miR-20a-5p	miR-21-3p	miR-92b-3p	miR-499a-5p	miR-503-5p	miR-3196	miR-4488	miR-4516	
CDKN2C	miR-450b-5p								
CDX2	miR-181d-5p								
CEMIP	miR-29b-3p	miR-4488							
CHI3L1	miR-4492								
CHRNA3	miR-450b-5p	miR-4488							
CHRNB1	miR-4492								
CLU	miR-19a-3p	miR-25-5p	miR-1301-3p	miR-4488					
CPNE2	miR-181d-5p	miR-4492							
CRAT	miR-6087								
CREB3L4	miR-424-3p								
CST1	miR-4488								
CST3	miR-25-5p	miR-450b-5p	miR-4492						
DBH	miR-25-5p	miR-3196	miR-4492	miR-6087					
DHCR24	miR-96-5p	miR-503-5p	miR-4492						
DYSF	miR-25-5p								
EBP	miR-1248								
ENTPD8	miR-4488	miR-4497							
FADS2	miR-4492	miR-4516	miR-6087	miR-7704					
FAM178B	miR-3196	miR-4492	miR-4508	miR-7704					
FAM46C	miR-9-5p								
FBXO2	miR-4492								
FBXW4	miR-4492								
GALNT6	miR-4488	miR-4492	miR-4497						
GBA	miR-1248	miR-4488	miR-4492	miR-4516					
GMFG	miR-450b-5p								
GPR155	miR-450a-5p	miR-4497							
GRM8	miR-450a-5p	miR-514a-3p							
HELZ2	miR-25-5p	miR-3196	miR-3656	miR-4492					
HMGCR	miR-27a-3p	miR-29b-3p	miR-3529-3p						
HOXA11	miR-9-5p	miR-181d-5p	miR-584-5p	miR-4492	miR-6087				
HOXB7	miR-25-5p	miR-4492							
HUNK	miR-9-5p	miR-27a-3p							
HYAL2	miR-4488								
IFIT1	miR-499b-3p								
IFITM3	miR-29b-3p								
IL17RD	miR-21-3p	miR-29b-3p							
ISG15	miR-3529-3p								
KAZALD1	miR-3196	miR-4488	miR-4492						
KCNJ5	miR-96-5p	miR-3196	miR-4488	miR-4492					
KLHL25	miR-29b-3p	miR-4488	miR-4492						
LINC01124	miR-4488	miR-4516							

Table S5A continued

Reduced mRNA in TEX-treated CD44v6kd cells

mRNA	miRNA							
LRRRC75A	miR-584-5p	miR-4492						
MCTP1	miR-514a-3p	miR-1301-3p						
MSRB2	miR-92b-3p							
MSRB3	miR-499b-3p	miR-4497						
MVD	miR-1301-3p							
MVK	miR-20a-5p	miR-514a-3p	miR-3196	miR-4488	miR-4497			
MX2	miR-7704							
MYCL	miR-4492							
MYH7B	miR-4488	miR-4508						
MYL6	miR-29b-3p							
MYO1D	miR-20a-5p	miR-3196	miR-4492	miR-6087				
NAT16	miR-3196	miR-4488	miR-4492	miR-5701				
NEDD9	miR-29b-3p							
NEURL1B	miR-27a-3p	miR-92b-3p	miR-503-5p	miR-4488	miR-4508			
NFATC4	miR-4492							
NFE2	miR-7-5p							
NGFR	miR-27a-3p	miR-3196	miR-4488	miR-4492				
NKD1	miR-503-5p							
NOTUM	miR-3656	miR-4492						
NUCB1	miR-3196	miR-4488	miR-4492	miR-7704				
NUDT19	miR-25-5p	miR-181d-5p	miR-6087					
OAS1	miR-1301-3p							
OAS3	miR-7-5p							
OBSL1	miR-7704							
OGDHL	miR-9-5p	miR-3196						
ORAI3	miR-6087							
PARM1	miR-181d-5p	miR-424-3p	miR-499a-5p	miR-503-5p	miR-1246	miR-3529-3p	miR-4492	
PARP10	miR-3196	miR-3960	miR-4488					
PBXIP1	miR-4492							
PCCA	miR-514a-3p							
PCSK9	miR-29b-3p							
PCYT2	miR-4488							
PDE6D	miR-27a-3p							
PHLDB2	miR-9-5p	miR-21-3p	miR-499b-3p					
PIK3R3	miR-9-5p	miR-19a-3p	miR-29b-3p	miR-92b-3p	miR-181d-5p	miR-4492		
PLEKHA4	miR-146a-5p	miR-7704						
PLIN3	miR-4284							
POLR1D	miR-25-5p	miR-29b-3p	miR-3529-3p					
PPARD	miR-4488	miR-4492	miR-4508					
PPP2R2C	miR-6087							
PRDX2	miR-4488							
PRR5L	miR-19a-3p	miR-3196						
QSOX1	miR-7704							
RAB15	miR-7-5p	miR-29b-3p	miR-101-3p	miR-1248	miR-4492	miR-4497	miR-7704	
RAB42	miR-4284							
RASL11B	miR-20a-5p							
RDH11	miR-7-5p	miR-96-5p						
REEP2	miR-3196	miR-3656	miR-4492	miR-4508				
SAMHD1	miR-4508							
SCNN1A	miR-7-5p	miR-25-5p	miR-4492					
SEC14L2	miR-96-5p							
SFN	miR-3656	miR-4488	miR-7704					
SLC12A4	miR-4492							
SLC1A4	miR-21-3p	miR-6087						

Table S5A continued

Reduced mRNA in TEX-treated CD44v6kd cells

mRNA	miRNA								
SLC25A1	miR-25-5p	miR-96-5p	miR-3196	miR-6087					
SLC2A6	miR-3196	miR-4492							
SLC4A8	miR-146a-5p	miR-181d-5p							
SLC5A1	miR-3529-3p								
SLC7A8	miR-96-5p	miR-1301-3p	miR-3196	miR-3656	miR-3960	miR-4488	miR-4492		
SORT1	miR-96-5p	miR-146a-5p							
SPRYD4	miR-92b-3p								
SPTB	miR-4492								
SQLE	miR-584-5p								
SREBF1	miR-4497								
ST5	miR-4488	miR-4492							
STARD3	miR-146a-5p	miR-499a-5p	miR-3196	miR-4508	miR-4488				
STARD4	miR-4516	miR-20a-5p	miR-181d-5p	miR-499b-3p	miR-1246	miR-4284	miR-4521	miR-5701	
STAT1	miR-19a-3p								
STAT2	miR-27a-3p	miR-4492							
SYNE1	miR-7-5p	miR-20a-5p	miR-1248						
TAP1	miR-21-3p	miR-101-3p							
TAS1R3	miR-4492	miR-7704							
TBC1D17	miR-20a-5p	miR-3960							
TCTA	miR-4284	miR-7704							
TDGF1	miR-4521	miR-5585-3p							
TECR	miR-4497								
TEF	miR-92b-3p								
TGFB111	miR-20a-5p	miR-3196	miR-4497						
TM7SF2	miR-4492								
TMEM45B	miR-19a-3p								
TNFRSF11B	miR-21-3p	miR-181d-5p							
TNFRSF19	miR-3656	miR-4485-3p							
TP53INP2	miR-29b-3p	miR-4488							
TRIM21	miR-450b-5p								
TRIM29	miR-3656	miR-4488							
TSPAN1	miR-27a-3p								
TST	miR-7704								
UBE2L6	miR-27a-3p	miR-29b-3p							
VAMP8	miR-7-5p	miR-96-5p	miR-4497	miR-4521					
VDAC3	miR-27a-3p								
VDR	miR-4492	miR-6087	miR-7704						
VEGFB	miR-27a-3p	miR-101-3p	miR-4488	miR-4492					
VEPH1	miR-450b-5p								
WBP1L	miR-19a-3p	miR-27a-3p	miR-29b-3p	miR-4485-3p	miR-4488				
WBP2	miR-19a-3p	miR-4492							
WNT6	miR-4508								
ZBTB7C	miR-101-3p	miR-4492							
ZDHC12	miR-499a-5p	miR-4492	miR-4508	miR-7704					
ZNF831	miR-19a-3p								

^a miRNA targeting the indicated mRNA are shown. miRNA increased in CIC-TEX treated CD44v6kd and Tspan8kd cells: red, miRNA increased in CIC-TEX treated Tspan8kd cells: blue, miRNA increased in CIC-TEX treated CD44v6kd cells: green

Table S5B

Increased mRNA and reduced miRNA recovery in CIC-TEX-treated CD44v6kd and Tspan8kd cells^a**Increased mRNA in TEX-treated CD44v6kd and Tspan8kd cells**

mRNA	miRNA
CAPRIN2	miR-181a-5p
DCBLD2	miR-99b-3p miR-200b-5p miR-574-3p
DDIT3	miR-934
EMP1	miR-29c-3p miR-95-3p miR-152-3p miR-1248
FAM129A	miR-99b-3p
FAM135A	let-7c-5p
HMGA1	let-7c-5p miR-26a-5p
NRP1	miR-152-3p miR-423-5p miR-1248
PMEPA1	miR-574-3p

Increased mRNA in TEX-treated Tspan8kd cells

mRNA	miRNA
ADAM19	miR-29c-3p
CALB2	miR-744-5p miR-3607-3p
CEACAM5	miR-3607-3p
CEACAM6	miR-29c-3p
CEMIP	miR-29c-3p
CHAC1	miR-26a-5p
DKK1	miR-103b
DUSP5	miR-205-5p
EREG	miR-26a-5p miR-29c-3p
ERRF1	miR-205-5p
H1FO	miR-1273g-3p miR-3607-3p
ID1	miR-29c-3p miR-103b
IFI6	miR-1273g-3p
IGFBP6	miR-744-5p
LCN2	miR-1273g-3p
NEBL	miR-205-5p

Increased mRNA in TEX-treated CD44v6kd cells

mRNA	miRNA
ABCE1	miR-29c-3p miR-629-5p
ADGRL1	miR-10a-5p miR-423-5p miR-615-3p
AKNA	let-7c-5p
AP1AR	miR-99b-5p miR-181a-5p miR-200b-5p
ARGLU1	miR-200b-5p miR-361-5p
ARL5B	miR-181a-5p
ASNS	miR-23b-3p
ATF3	miR-200b-5p miR-629-5p
ATP11A	miR-152-3p
ATP13A3	let-7c-5p
B3GNT5	let-7c-5p miR-10a-5p miR-29c-3p miR-30c-5p
B4GALNT4	miR-423-5p
BAG2	miR-181a-5p
BAZ1A	miR-320a miR-7641
BDP1	let-7c-5p miR-30c-5p miR-200b-5p miR-423-5p
BMI1	miR-629-5p miR-1273g-3p
BRWD1	miR-125a-5p miR-132-3p
BTAF1	miR-23b-3p miR-132-3p miR-152-3p
CARNMT1	let-7c-5p miR-320a
CCDC14	miR-30c-5p miR-99b-3p
CCND2	let-7c-5p miR-29c-3p miR-191-5p
CCNT2	miR-23b-3p miR-30c-5p
CDC42EP1	miR-339-5p miR-423-5p
CDK6	let-7c-5p miR-10a-5p miR-29c-3p miR-95-3p miR-125a-5p miR-152-3p miR-191-5p miR-320a

Table S5B continued

Increased mRNA in TEX-treated CD44v6kd cells

mRNA	miRNA								
CEBPG	miR-125a-5p	miR-152-3p							
CEP290	miR-99b-3p								
CFAP97	miR-152-3p	miR-200b-5p							
CHORDC1	miR-10a-3p	miR-30c-5p	miR-200b-5p						
CLK1	miR-320a								
CNTRL	let-7c-5p	miR-181a-5p							
CREBZF	miR-23b-3p	miR-181a-5p	miR-423-5p	miR-425-5p					
CSNK1A1	miR-28-3p	miR-30c-5p	miR-3182						
DCAF17	miR-339-5p	miR-3184-3p							
DCUN1D4	miR-29c-3p	miR-132-3p	miR-152-3p	miR-1273g-3p					
DGKE	miR-28-3p	miR-30c-5p	miR-423-5p						
DGKH	miR-29c-3p	miR-30c-5p	miR-126-5p						
DICER1	let-7c-5p	miR-125a-5p							
DNAH14	miR-126-5p								
DNAJB14	miR-361-5p								
DOCK6	miR-152-3p								
DPY19L3	miR-99b-5p	miR-7641							
DST	miR-126-5p	miR-3182							
DUS4L	miR-95-3p								
DVL1	miR-423-5p								
EDEM3	let-7c-5p	miR-30c-5p							
EIF1AX	miR-10a-5p	miR-200b-5p	miR-361-5p						
EIF3J	let-7c-5p	miR-29c-3p	miR-425-5p						
EIF4A2	miR-132-3p	miR-181a-5p							
ENAH	miR-181a-5p								
FAM107B	miR-125a-5p	miR-3184-3p	miR-7641						
FAM60A	miR-28-3p	miR-1273g-3p	miR-4448						
FHL1	miR-200b-5p	miR-339-5p	miR-574-3p						
FMNL2	miR-181a-5p								
FOXN2	miR-629-5p								
GAL	miR-200b-5p								
GCLC	miR-30c-5p	miR-95-3p							
GCLM	miR-28-3p	miR-425-5p							
GOLT1B	miR-152-3p	miR-425-5p							
GPD1L	miR-181a-5p								
GPRC5A	miR-152-3p								
GRB10	miR-30c-5p	miR-125a-5p	miR-629-5p						
GTF2F2	miR-629-5p	miR-3184-3p	miR-4448						
HES7	miR-99b-5p	miR-423-5p	miR-4532						
HK2	let-7c-5p	miR-125a-5p	miR-423-5p	miR-1296-5p					
JPH1	miR-423-5p								
KLHL17	miR-4532								
LCOR	let-7c-5p	miR-125a-5p	miR-30c-5p	miR-152-3p	miR-425-5p	miR-615-3p	miR-629-5p	miR-1296-5p	
LENG8	miR-152-3p								
LIN7C	miR-30c-5p								
LUC7L3	let-7c-5p								
LYPLA1	miR-23b-3p	miR-29c-3p	miR-126-5p						
MAFK	miR-423-5p	miR-4532							
MAK16	miR-23b-3p								
MAL2	miR-425-5p	miR-3182							
MAPK8IP3	miR-423-5p								
MAT2A	miR-30c-5p								
MBNL2	miR-30c-5p								
MBP	miR-574-3p	miR-1273g-3p	miR-1296-5p						

Table S5B continued

Increased mRNA in TEX-treated CD44v6kd cells

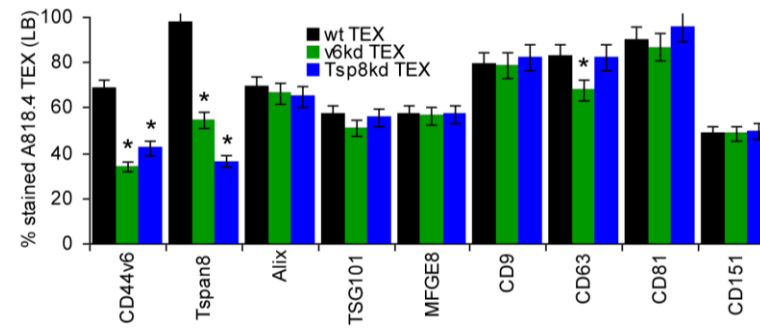
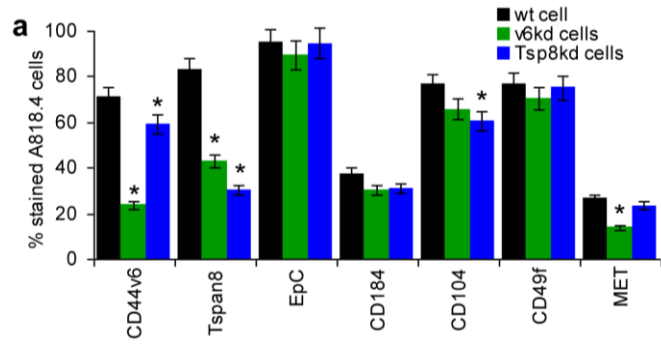
mRNA	miRNA					
MCOLN3	miR-132-3p	miR-7641				
MIB1	let-7c-5p	miR-200b-5p				
MTURN	let-7d-3p	miR-28-3p	miR-29c-3p	miR-132-3p	miR-181a-5p	miR-423-5p
MXD1	let-7c-5p	miR-152-3p				
MXI1	miR-29c-3p	miR-320a				
MYC	let-7c-5p	miR-629-5p				
NAA16	miR-23b-3p	miR-361-5p				
NAA25	miR-152-3p					
NAMPT	miR-23b-3p	miR-200b-5p				
NCS1	miR-200b-5p	miR-629-5p	miR-4532			
NEK6	miR-10a-5p	miR-23b-3p				
NKTR	miR-10a-5p	miR-1296-5p				
ODC1	miR-423-5p					
OGT	miR-339-5p					
OTUD3	miR-132-3p	miR-1273g-3p				
PABPC1L	miR-152-3p					
PAPD5	miR-10a-5p	miR-181a-5p	miR-200b-5p	miR-320a		
PAQR3	miR-200b-5p					
PARD6B	let-7c-5p	miR-23b-3p	miR-1273g-3p			
PAWR	miR-30c-5p	miR-181a-5p				
PAXBPI	miR-23b-3p					
PIM1	miR-423-5p					
PIM3	miR-423-5p	miR-574-3p	miR-7641			
PMAIP1	let-7c-5p	miR-23b-3p	miR-181a-5p	miR-200b-5p		
PNISR	miR-181a-5p					
PNN	miR-126-5p	miR-132-3p				
PODXL	miR-99b-5p	miR-125a-5p	miR-615-3p	miR-1273g-3p		
POLQ	let-7c-5p					
POLR3E	miR-1273g-3p					
POLR3G	miR-23b-3p	miR-30c-5p	miR-361-5p	miR-3184-3p		
PPP3CA	let-7c-5p	miR-30c-5p	miR-99b-5p			
PPTC7	let-7c-5p	miR-30c-5p				
PRPF39	miR-3184-3p					
PRPS2	miR-200b-5p					
PSAT1	miR-200b-5p					
PTER	miR-200b-5p	miR-3184-3p				
PUS7	miR-126-5p					
RAB12	miR-29c-3p	miR-152-3p	miR-361-5p	miR-3182		
RABGGTB	miR-132-3p					
RICTOR	let-7c-5p	miR-152-3p	miR-1273g-3p	miR-4532		
RIDA	miR-23b-3p	miR-191-5p	miR-7641			
RIMKLB	miR-200b-5p					
RPIA	miR-23b-3p					
RSRC2	miR-629-5p					
S100A2	miR-132-3p					
SASS6	miR-7641					
SCAMP1	miR-30c-5p	miR-200b-5p	miR-425-5p	miR-3184-3p		
SCML1	miR-29c-3p	miR-30c-5p				
SLC19A2	miR-181a-5p	miR-3184-3p				
SLC20A1	let-7c-5p	miR-23b-3p	miR-132-3p	miR-3182		
SLC25A36	miR-23b-3p					
SLC25A37	miR-181a-5p					
SLC35A3	miR-30c-5p					
SLC35F2	miR-425-5p					

Table S5B continued

Increased mRNA in TEX-treated CD44v6kd cells

mRNA	miRNA						
SLC4A7	miR-30c-5p						
SLC7A11	miR-30c-5p						
SLC7A2	miR-10a-5p	miR-425-5p	miR-615-3p				
SMC5	miR-28-3p	miR-1273g-3p					
SOWAHC	miR-23b-3p	miR-29c-3p	miR-361-5p	miR-629-5p			
SPNS2	miR-4532						
STEAP2	let-7c-5p	miR-361-5p	miR-1273g-3p	miR-1296-5p			
STK26	miR-28-3p	miR-320a					
SVIL	miR-29c-3p						
TAF1D	miR-152-3p	miR-200b-5p					
TBC1D4	miR-181a-5p						
TCEA1	miR-7641						
TEX19	miR-95-3p	miR-125a-5p	miR-339-5p	miR-1273g-3p	miR-3182		
TIA1	miR-30c-5p						
TMED7	miR-23b-3p	miR-30c-5p	miR-152-3p				
TMEM168	miR-10a-5p	miR-125a-5p					
TRAF5	miR-29c-3p	miR-1273g-3p					
TRMT11	miR-10a-3p						
TRNT1	miR-10a-5p	miR-23b-3p	miR-425-5p				
TRUB1	miR-28-3p						
TTC14	let-7c-5p	miR-29c-3p	miR-320a				
TXNRD1	miR-23b-3p	miR-1273g-3p	miR-4532				
UHRF2	let-7c-5p						
VMP1	miR-152-3p						
WDR19	miR-152-3p	miR-320a					
WDR43	miR-1273g-3p						
WNK2	miR-423-5p						
XPOT	miR-99b-3p	miR-1273g-3p					
XRCC2	miR-200b-5p	miR-1273g-3p					
YOD1	let-7c-5p	miR-23b-3p	miR-30c-5p	miR-320a	miR-361-5p	miR-99b-3p	miR-181a-5p
YRDC	miR-29c-3p						
ZBTB10	let-7c-5p	miR-29c-3p	miR-99b-3p				
ZBTB21	miR-425-5p						
ZFAND1	miR-30c-5p	miR-361-5p					
ZNF267	miR-23b-3p	miR-200b-5p					
ZNF280C	miR-10a-5p	miR-23b-3p	miR-339-5p				
ZNF697	let-7c-5p	miR-28-3p					
ZNF92	miR-23b-3p	miR-200b-5p					
ZRANB2	miR-30c-5p	miR-320a	miR-629-5p				

^a miRNA targeting the indicated mRNA are shown. miRNA reduced in CIC-TEX treated CD44v6kd and Tspan8kd cells: red, miRNA reduced in CIC-TEX treated Tspan8kd cells: blue, miRNA reduced in CIC-TEX treated CD44v6kd cells: green



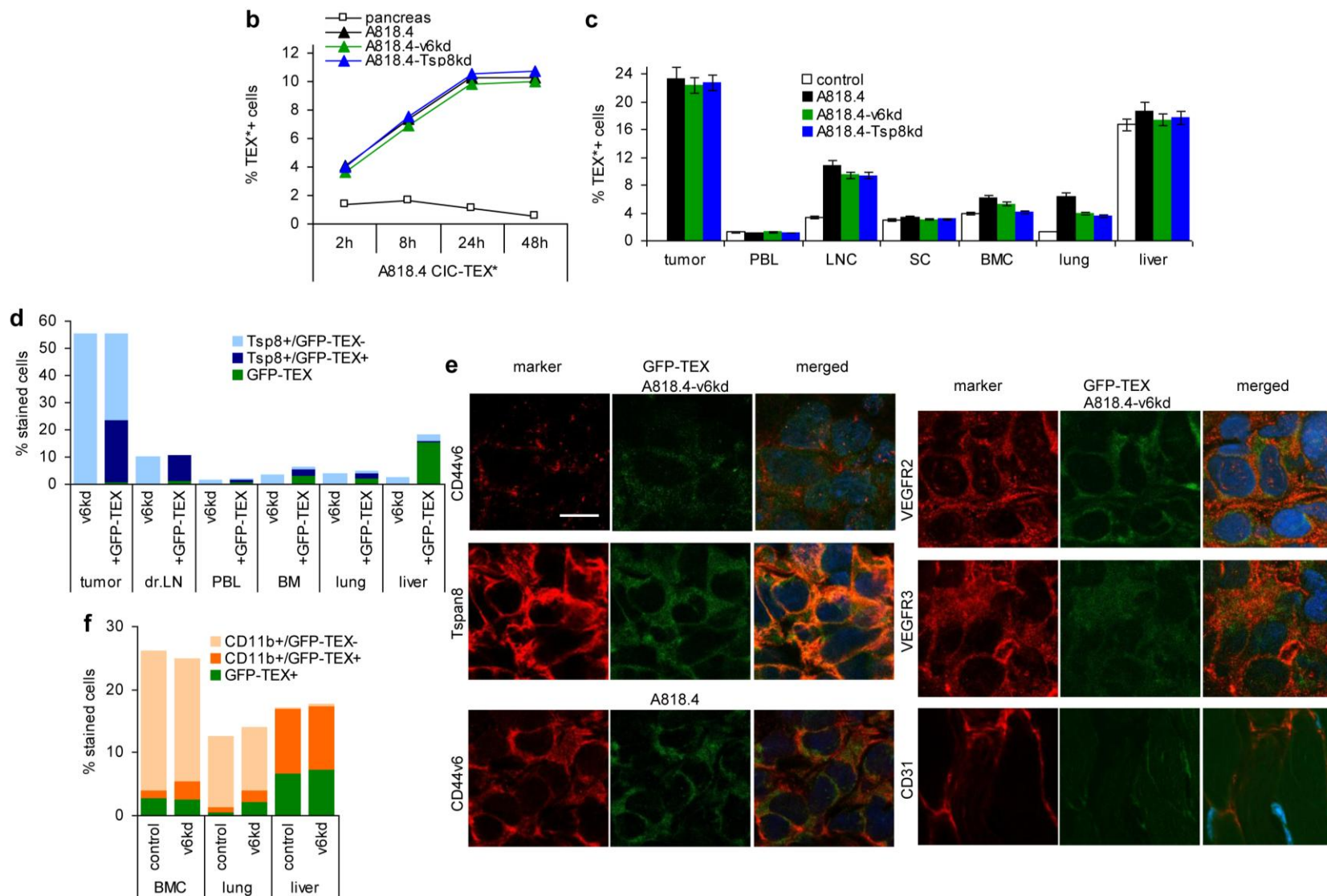
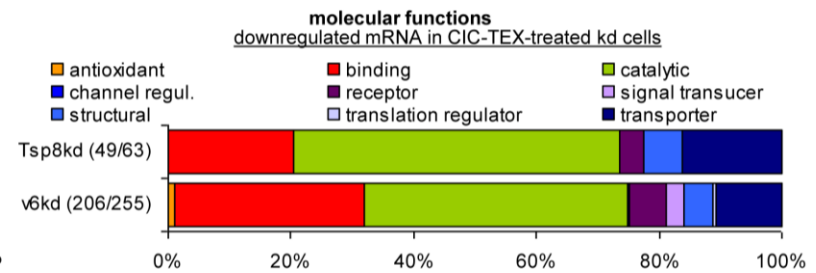
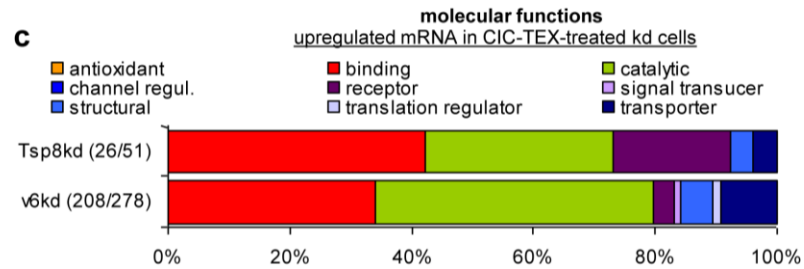
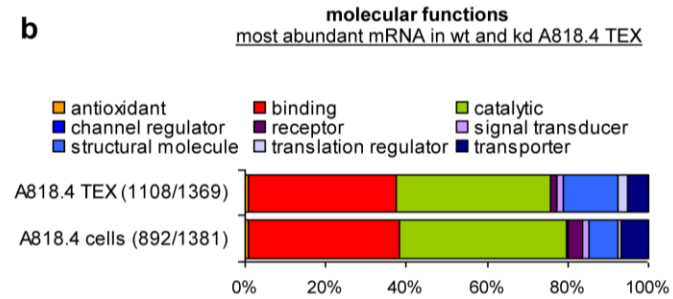
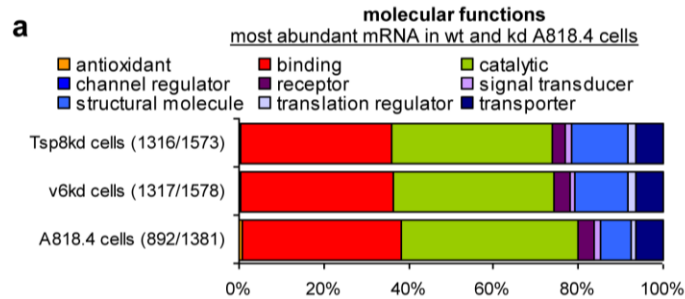


Figure S1 **TEX characterization and in vivo distribution of CIC-TEX**. (a) Flow-cytometry of A818.4, -v6kd and -Tsp8kd cells and LB-coated TEX were stained for the indicated CIC-markers and prominent Exo markers. The mean \pm SD of 3 assays are shown; significant differences between wt, v6kd and Tsp8kd cells and TEX: *. (b-e) CIC-TEX were Dio-labeled or derived from GFP-transfected A818.4 cells. (b,c) Mice bearing intrapancreatic tumors received a single iv injection of Dio labeled TEX. (b) Uptake in the pancreas, A818.4, -v6kd and Tsp8kd tumors was evaluated by flow-cytometry after 2h-48h and (c) in the indicated organs 24h after TEX application; the mean % Dio-labeled cells \pm SD (3 mice/group) is shown. (d-f) Nude mice received a sc injection of tumor cells and weekly iv injections of CIC-TEX derived from GFP-transfected A818.4 cells (GFP-TEX). Mice were sacrificed, when the tumor reached a mean diameter of 0.5cm. (d,f) Flow-cytometry analysis of dispersed cells from the tumor and metastasis-prone organs stained with anti-GFP-FITC and anti-Tsp8-APC or anti-CD11b-APC; the mean % (3 mice/group) of single and double stained cells is shown; (e) confocal microscopy of shock-frozen tumor sections counterstained with the indicated antibody and Cy3-labeled secondary antibodies and DAPI; representative examples are shown; scale bar: 10 μ m. As described, a v6kd affects Tsp8 and MET expression, a Tsp8kd has a minor impact on v6 and CD104 expression. With the exception of slightly reduced CD63 expression in v6kd TEX, the v6kd and the Tsp8kd do not affect TEX marker expression. TEX are preferentially taken up by the tumor and in the liver. In the tumor, draining LN, lung and PB mostly tumor cells take-up TEX; in the BM and most pronounced in the liver CIC-TEX are also taken-up by M \square . There was no difference in the uptake between wt and v6kd or Tsp8kd cells.



d

reduced mRNA recovery in TEX-treated Tspan8kd and CD44v6kd cells

transcription/ translation

BTG2
GATA2
GATA2-AS1
HOXB8
LMO4
MEIS2
WVVOX
ZNF704
ARID5A
BHLHE40
CCDC69
CDK5
CDKN1A
CDKN2C
CDX2
CREB3L4
HOXA11
HOXB7
HOXB8
INTS5
MYCL
NFATC4
NFE2
PARP10
PARP9
PBXIP1
POLR1D
SP5
SREBF1
SRFEB2
STAT1
STAT2
TDGF1
TEF
TGFB1/1
TP53INP2
TRIM29
VDR
WBP2
ZBTB7C
ZNF831

transport/drug transport

ABCG2
AQP3
ATP6V1B1
AZGP1
CACNA1D
GABRP
NOX1
SLC35D1
SLC38A11
SLC40A1
SLC4A4
ANXA6
APOE
ARHGAP18
ATP6V0D1
ATP6V0E2
CALHM3
CDK5
CDX2
CHRNA3
CHRNB1
CPNE2
CRAT
CTSZ
DBH
DBI
DYSF
EBP
FXVD6
GJB1
GLUL
GPR155
GRM8
KCNJ5
MCTP1
MX1
MX2
MYO1D
NEURL1B
NGFR
NPC2
ORAI3
PCSK9
PLIN3
PSMB9
RAB15
REEP2
SCNN1A
SEC14L2
SLC12A4
SLC1A4
SLC25A1
SLC2A6
SLC4A8
SLC5A1
SLC7A8
SORT1
STARD3
STARD4
SV2A
TAP1
TBC1D17
VAM8
VDAC3
VDR
VPS18

oncogenesis

BCAS1
PARM1
ST5

angiogenesis

CEACAM1
GATA2
TGM2
THBS1
AMOT
CEACAM1
CHI3L1
CXCR4
SYK

apoptosis

HPGD
IFIT2
IFIT3
RARRES1
THBS1
WVVOX
ANXA6
AXIN2
BCL2L15
CDKN1A
CHI3L1
CST3
DDAH2
DHCR24
DNASE1
HYAL2
IFI6
IFIT3
NGFR
PCSK9
PIK3R3
PLSCR1
PPARD
PRDX2
SFN
STAT1
TNFRSF19
TRIM69

structure/ECM/proteolysis

CEACAM1
CLEC3A
ERMP1
FGG3
LMO4
PRCKLE4
PRSS23
RHBDL2
SHROOM1
ACP2
ADAMTS8
ADAMTSL2
APOE
ARHGAP18
BTBD6
CCDC69
CDK5
CST1
CST3
CTSZ
FBOX2
GMFG
KAZALD1
MYHB7
MYL6
NEDD9
OBSL1
PRKCBDBP
SPTB
SYNE1
TIMP1
TNFRSF11B
TUBA1A1

signaling/EMT signaling

ARL15
ATP6V1B1
CACNA1D
DDX60
F2R
FGD3
GATA2
GBP2
HPGD
IFIT2
IFIT3
NOX1
OASL
RASL11A
RGS2
TGM2
WVVOX
AMOT
APCDD1
APOE
ARHGAP1
ARHGAP18
ARHGEF40
ATP6V0D1
ATP6V0E2
AXIN2
BAMBI
BST2
CCDC3
CDK5
CDKN1A
CDKN2C
CEACAM1
CHI3L1
CXCR4
DDAH2
DDX58
DDX60
DKK4
FBXW4
GPA
GPR155
GRM8
HMGCR
HUNK
IFI6
IFIH1
IFIT1
IFIT3
IFITM3
IL17RD
ISG15
KLK1
LSS
MVK
MX1
MX2
MYL6
NEDD9
NEURL1B
NGFR
NKD1
NOTUM
OAS1
OAS2
OAS3
PARP10
PARP9
PIK3R3
PRKCDBP
PRRL5
PSMB9
RAB15
RAB42
RASL11B
S100A13
SAMHD1
SFN
SPTB
ST5
STARD13
STAT1
STAT2
SYK
TAS1R3
TBC1D17
TDGF1
TGFB1/1
TNFRSF11b
TNFRSF19
TRDC
TRIM21
TRIM29
TUBA1A1
UBE2L6
VDR
VEGFB
WBP2
WNT6

blue: Tsp8kd cells, violet: v6kd cells
red: function according to heading
underlined: repeatedly presented

List of synonyms: Table S1

e

increased mRNA recovery in TEX-treated Tspan8kd and CD44v6kd cells

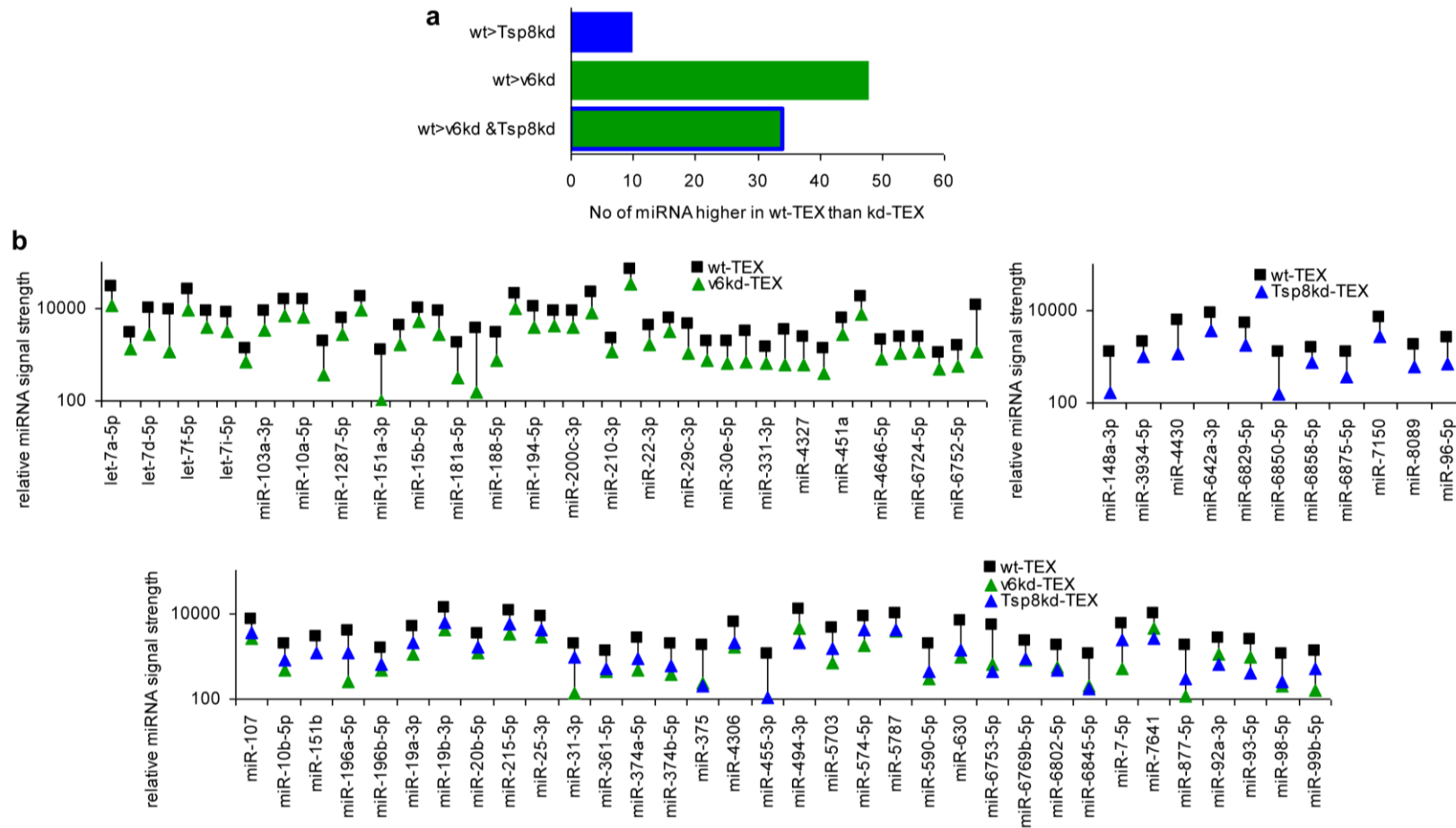
transcription/ translation/splicing			transport/drug transport	oncogenesis	angiogenesis	apoptosis	structure/ECM/proteolysis	signaling/EMT signaling
<u>Caprin2</u>	<u>ABCE1</u>	PABPC1L	<u>LCN2</u>	ABCA3	EMP1	<u>CHAC1</u>	ADAM19	AKAP12
<u>DDIT3</u>	AKNA	PAPD5	SLCO4A1	ABCC3	<u>DDIT3</u>	<u>DDIT4</u>	CEACAM6	<u>CAPRIN2</u>
<u>FAM129A</u>	BAZ1A	PAXBP1		ABCC4	<u>EREG</u>	<u>EGR1</u>	COL17A1	<u>CHAC1</u>
<u>HMGA1</u>	BDP1	PNN		<u>ABCE1</u>	<u>ID1</u>	<u>H1F0</u>	COL17A1	<u>DCBLD2</u>
<u>ID1</u>	BMI1	POLR3E		ANO1	<u>JAG1</u>	<u>ID1</u>	LAMA3	<u>DDIT3</u>
<u>NDRG1</u>	BTAF1	POLR3G		ATP11A	<u>NRP1</u>	<u>IFI27</u>	LAMC2	<u>DDIT4</u>
<u>PER1</u>	C6orf48	PRPF39		ATP13A3		<u>IFI6</u>	NEBL	<u>DKK1</u>
	<u>CAPRIN2</u>	PUM3		CEP290		<u>JAG1</u>	AGTPBP1	<u>DUSP5</u>
	<u>CCNL1</u>	PUS7		CHML		<u>LCN2</u>	AP1AR	<u>EGR1</u>
	<u>CCNT2</u>	RBM26		FHL1		<u>NTR1</u>	BRWD1	<u>EREG</u>
	<u>CEBPG</u>	<u>RBM39</u>		<u>GAL</u>			<u>CDC42EP1</u>	<u>ERRF1</u>
	<u>CLK1</u>	RIDA		<u>GOLT1B</u>			<u>CSNK1A1</u>	<u>ID1</u>
	CREBZF	RIF1		DUS4L		ATF3	DNAH14	<u>IFI27</u>
	<u>DDIT3</u>	RPL32P3		FHL1		CEACAM5	<u>DST</u>	<u>IFI6</u>
	<u>DDX21</u>	SCML1		<u>GAL</u>		CLDND1	<u>DVL1</u>	<u>IFI6</u>
	<u>DICER1</u>	TAF1D		<u>GOLT1B</u>		<u>DICER1</u>	<u>FMNL2</u>	<u>IGFBP6</u>
	EIF1AX	TCEA1		GPD1L		<u>GAL</u>	<u>HSPA1A/1B</u>	<u>JAG1</u>
	EIF3J	TFAP4		<u>HMGA1</u>		GCLM	KLHL17	<u>NRP1</u>
	<u>EIF4A2</u>	<u>TRMT11</u>		JPH1		INHBE	LAMB3	<u>NTR1</u>
	ESF1	TRNT1		LIN7C		NEA1	MAL2	<u>PER1</u>
	<u>FAM129A</u>	TRUB1		LYPLA1		NEK6	MBP	<u>PMEPA1</u>
	FOXN2	<u>U2SURP</u>		MAPK8IP3		OGT	PARD6B	<u>PSD3</u>
	GAS5	WDR36		MCOLN3		PAWR	PKD1	<u>SCEL</u>
	<u>GEMIN5</u>	WDR43		MT-ND5		PHLDA2	PLAUR	
	<u>GTF2F2</u>	ZBTB10		NCS1		PIM1	PVR	
	HES7	ZBTB21		<u>PPP3CA</u>		PIM3	RICTOR	
	<u>HMGA1</u>	ZFAS1		SAT1		<u>PMAIP1</u>	SASS6	
	KCNQ1OT1	ZMYM1		SCAMP1		RABGGT8	SVIL	
	LCOR	ZNF121		SLC19A2		<u>STK26</u>	VMP1	
	<u>LUC7L3</u>	ZNF146		SLC20A1		<u>TIA1</u>		
	MAFK	ZNF267		SLC25A36		<u>TRAF5</u>		
	MAK16	ZNF280C		SCL25A37				
	MALAT1	ZNF518A		SLC35A3				
	<u>MBNL2</u>	ZNF697		SLC35F2				
	MDN1	ZNF770		SLC4A7				
	MRPL12	TNF92		SLC7A11				
	MXD1	ZRANB2		SCL7A2				
	MXI1			SPNS2				
	NFXL1			STEAP2				
	NMD3			TBC1D4				
	NOP58			TMED7				
	<u>NR1D1</u>			TXRND1				
	OGT			VPS13A				
				WNK2				
				XPOT				
				YRDC				

Legend:
 blue: Tsp8kd cells, violet: v6kd cells
 red: function according to heading
 underlined: repeatedly presented

List of synonyms: Table S1

Figure S2 Differences in the mRNA profile of A818.4, -CD44v6kd and -Tspan8kd cells and TEX and the impact of CIC-TEX on CD44v6kd and Tspan8kd cells. (a-c) mRNA of A818.4, -v6kd and -Tsp8kd cells and TEX and of CIC-TEX-treated (72h) v6kd and Tsp8kd cells were analyzed by DS. After normalization data were evaluated (a,b) for molecular functions of most abundant (signal strength ≥ 5000) mRNA in wt versus kd cells and wt cells versus TEX, (c) mRNA (signal strength ≥ 1000) ≥ 2 -fold up- or downregulated by CIC-TEX coculture of kd cells. (d,e) Combined Panther pathway and Reactome analysis of mRNA (signal strength ≥ 1000) that differed ≥ 2 -fold between kd cells and CIC-TEX-treated kd cells according to the indicated groups (differences in Tsp8kd cells: blue, in v6kd cells: violet; genes that are repeatedly mentioned in distinct groups are underlined) (List of synonyms: Table S1).

TEX coculture-induced differences in the mRNA profile are more frequent in v6kd than Tsp8kd cells; genes engaged in transcription/translation, transport and signaling are most abundantly affected.



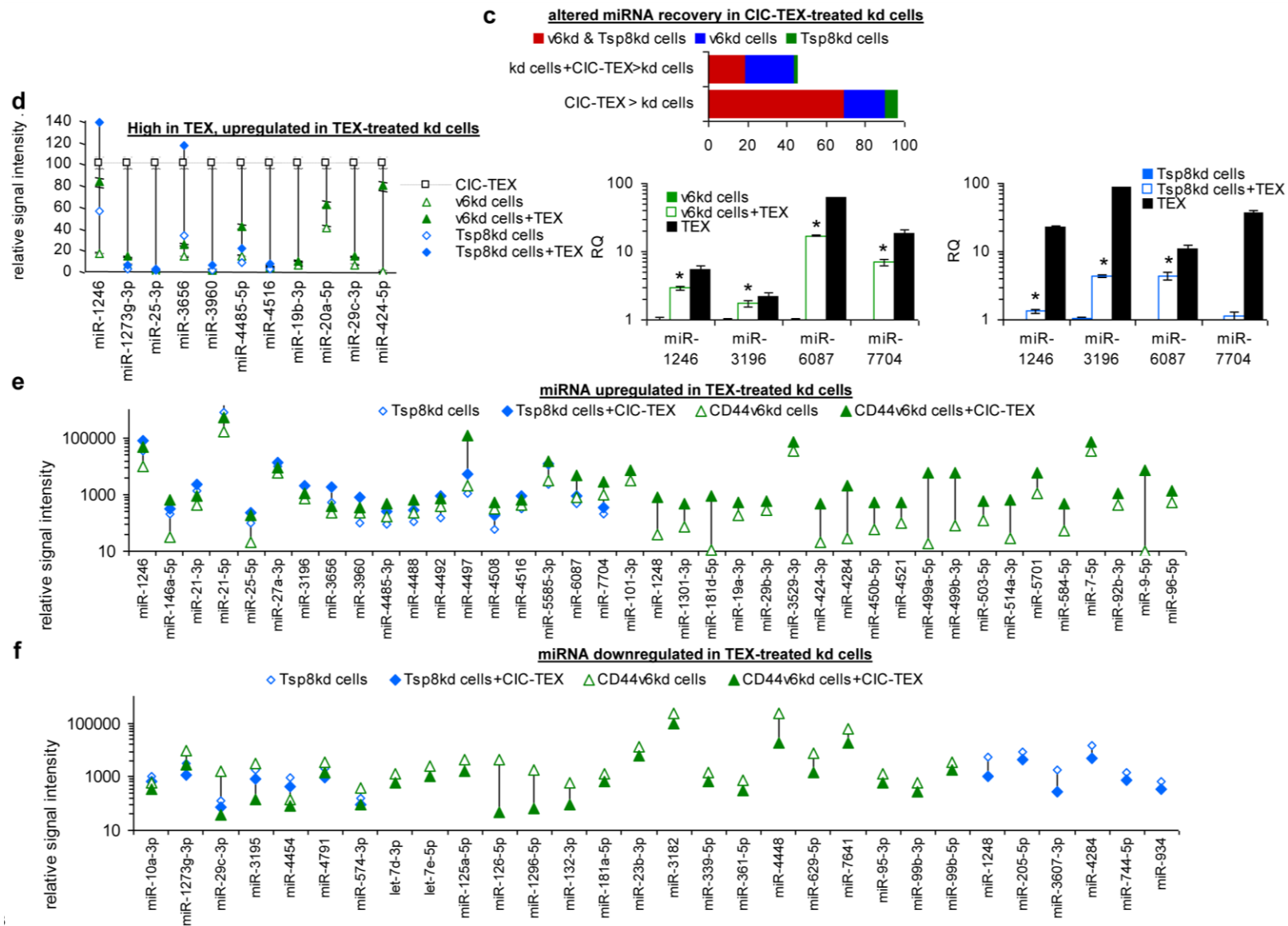


Figure S3 Distinct miRNA recovery in wt-TEX versus CD44v6kd and Tspan8kd TEX and in kd cells cocultured with CIC-TEX. (a,b) Recovery of miRNA (signal strength in wt TEX ≥ 1000) that expression is ≥ 2 -fold reduced in v6kd and/or Tsp8kd TEX. (c-f) miRNA of CIC-TEX, v6kd and Tsp8kd cells and kd cells cocultured with CIC-TEX was evaluated by DS. After normalization miRNA with a signal strength ≥ 500 were analyzed for (c) significant differences (≥ 1.5 -fold) in the signal strength between CIC-TEX and kd cells and between kd cells versus CIC-TEX-treated kd cells; (d) miRNA recovered at an ≥ 1.5 -fold lower level in kd cells than CIC-TEX (values normalized to 100) and being ≥ 1.5 -fold increased after coculture with CIC-TEX, which was confirmed by qRT-PCR for selected examples, showing RQ values for kd cells, CIC-TEX-treated kd cells and CIC-TEX; RQ values \pm SD (triplicates) are shown, significant increase in kd cells by coculture with CIC-TEX: *; (e,f) ≥ 1.5 -fold increased or decreased miRNA recovery in CIC-TEX-treated v6kd and/or Tsp8kd cells compared to untreated kd cells (independent of the signal strength in CIC-TEX).

The miRNA profile of wt TEX differs from that of kd, particularly v6kd TEX, most prominent being the loss in let7 miRNA in v6kd TEX. CIC-TEX miRNA also strongly differs from that of kd cells. Coculture with CIC-TEX alters the miRNA profile of the kd, mostly v6kd cells. However, despite recovery of CIC-TEX miRNA in kd cells, coculture-induced changes rarely are related to the CIC-TEX miRNA content.

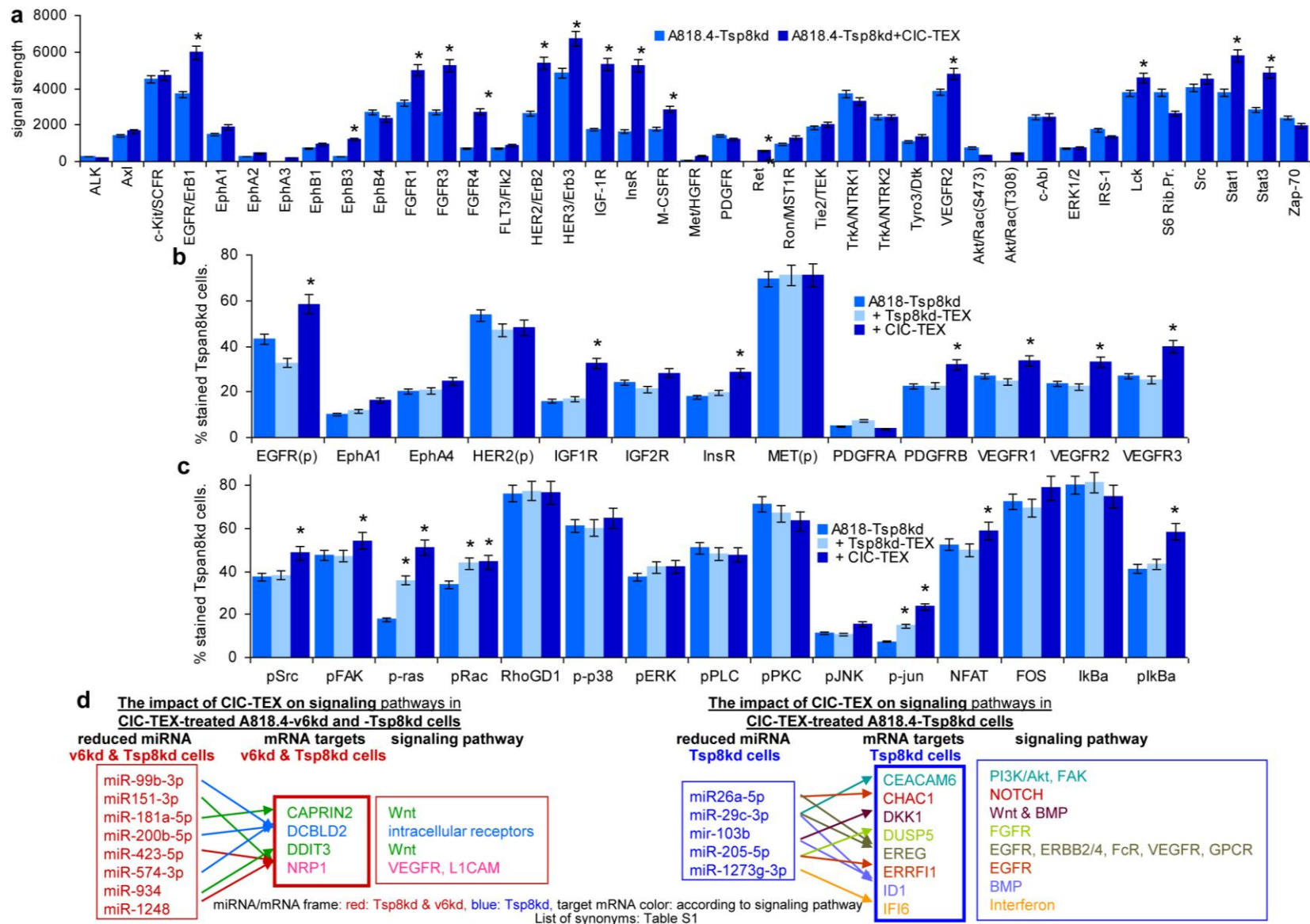


Figure S4 **CIC-TEX-initiated changes in RTK and downstream signaling molecules in Tspan8kd cells and mRNA release from repression by reduced miRNA expression in CD44v6kd and/or Tsp8kd cells.** (a) Signaling array of A818.4-Tsp8kd cells cultured for 72h with/without CIC-TEX. The relative signal strength was evaluated by ImageJ; significant differences by coculture with CIC-TEX: *. Flow-cytometry of (b) RTK expression and (c) major pathway-engaged cytosolic signaling molecules in Tsp8kd cells and Tsp8kd-TEX- or CIC-TEX-treated Tsp8kd cells; (b,c) mean % stained cells \pm SD (3 assays), significant differences by coculture with TEX: *; (d) IPA-based STRING analysis after predicted target mRNA selection by microrna.org and targetscan.org for ≥ 2 -fold reduced miRNA in CIC-TEX-treated compared to untreated v6kd and/or Tsp8kd cells and of ≥ 2 -fold upregulated predicted mRNA targets, that are engaged in signal transduction. (List of synonyms: Table S1). The signaling array and flow-cytometry analysis of TEX-treated Tsp8ko cells confirms the striking impact of CIC-TEX on promoting signaling cascade activation. The analysis of inversely correlating miRNA and predicted mRNA in CIC-TEX-treated v6kd and/or Tsp8kd cells backs the potential engagement of regulated miRNA expression on mRNA recovery.

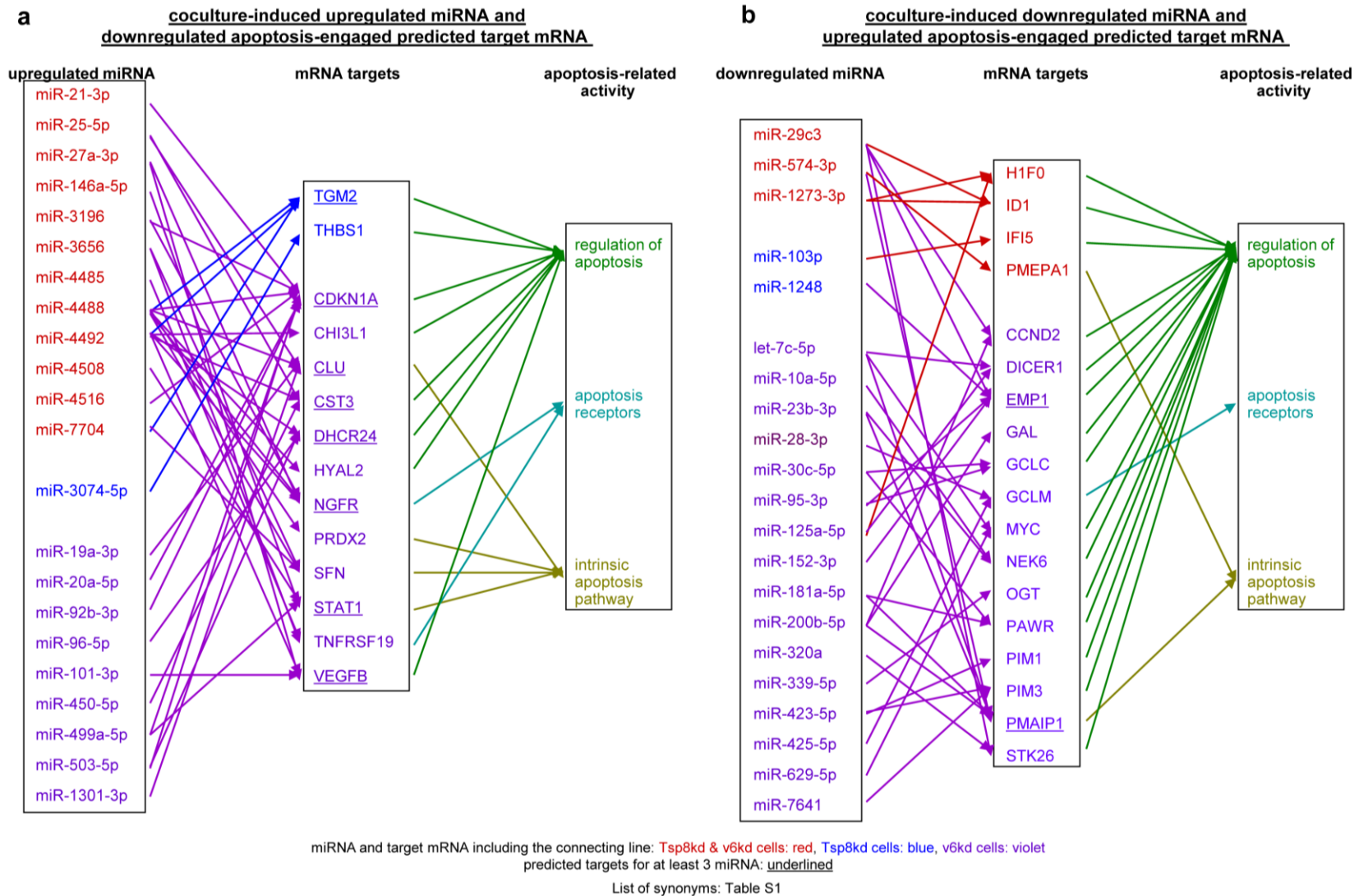


Figure S5 **CIC-TEX-promoted changed miRNA recovery and predicted target mRNA engaged in apoptosis**. List of miRNA that expression was expression was ≥ 2 -fold higher (a) or lower (b) in CIC-TEX treated than untreated v6kd and/or Tspan8kd cells (v6kd and Tsp8kd cells: red, Tsp8kd cells: blue, v6kd cells: violet). After selection of predicted target mRNA by microrna.org and targetscan.org that expression was inversely to miRNA ≥ 2 -fold altered after CIC-TEX coculture, mRNA engagement in apoptosis-related processes was evaluated by IPA-based STRING analysis. (List of synonyms: Table S1). CIC-TEX coculture-promoted changes in apoptosis-related miRNA are most pronounced in v6kd cells. This also accounts for predicted target mRNA that expression inversely correlated with miRNA up- or downregulation. Predicted target mRNA mostly is engaged in regulation of apoptosis. In addition, several predicted mRNA are only targets for 1 or 2 miRNA.