# Supporting information

### Supporting information figures:



**Figure S1**: PTEN expression was reduced in control and PTEN KD SVF cells. (A) PTEN mRNA expression in subcutaneous PTEN KD SVF cells was downregulated  $0.3 \pm 0.01$  fold (n=3, p=0.009) compared to controls. (B) Western blots of visceral PTEN KD/control SVF cells: PTEN knockdown was stable for 7 days after siRNA transfection. (C) *PTEN* mRNA expression in visceral PTEN KD/ SVF cells was downregulated upon induction of differentiation (d0, one day after transfection) and after eight days of adipose differentiation (d8) compared to controls. Lines between individual data points indicate matched data from single experiments (control vs. respective knockdown). p-values were determined via paired t-test (\*\* p<0.001 \*\*\* p<0.001).



**Figure S2**: mRNA expression of senescence marker was reduced after PTEN KD. (A) Senescence marker qPCRs of PTEN KD/control visceral SVF cells: On the mRNA level we found a reduction of *CDKN1A* (*p21*) (to 0.6 ± 0.06 fold, n=3, p=0.031) and senescence marker *CDKN2A* (*p16*) (to 0.68 ± 0.05 fold, n=4, p=0.014). (B) Senescence marker qPCRs comparing low passage vs. high passage LipPD1 cells: On the mRNA level we found *p21* elevated 2.3 ± 0.8 fold, (n=4, p=0.27), *CDKN2B* (*p15*) reduced to 0.02 ± 0.05 fold (n=3, p=0.07) and HIPK2 elevated 3.2 ± 0.8 fold (n=4, p=0.028). (C) qPCRs to confirm results from RNA-sequencing: *p15* (to 0.23 ± 0.04 fold, n=4, p=0.017) and *HIPK2* (to 0.73 ± 0.09 fold, n=4, p=0.02) were downregulated after PTEN KD in visceral SVF cells. Lines between individual data points indicate matched data from single experiments (control vs. respective knockdown). p-values for (A) and (B) were determined via one-sample t-test of the log(fold change), p-values for (C) were determined via paired t-test.



**Figure S3**: FOXO1 and RNF144B are downregulated in PTEN KD cells. (A) qPCRs to confirm results from RNA-sequencing: *FOXO1* (to 0.75 ± 0.03 fold, n=4, p=0.018) and *RNF144B* (to 0.23 ± 0.04 fold, n=4, p=0.025) were downregulated after PTEN KD in visceral SVF cells. (B) *SREBF1* was upregulated on the mRNA level (1.6 ± 0.1 fold, n=3, p=0.013) in visceral PTEN KD cells. (C) Neither overexpression of constitutively active FOXO1 nor RNF144B in PTEN CR cells had effects on proliferation (as determined via Hoechst assay 7 days post transfection normalized to day 1 after transfection). (D) RNF144B overexpression had no influence on adipogenesis of PTEN CR cells. Lines between individual data points indicate matched data from single experiments (control vs. respective knockdown or overexpression). p-values were determined via paired t-test.

## PTEN/α-Tubulin Gel 1 Lane cell strain p

										the second se
1	SVF#10	15	17.5	control	29685.8	30858.8	1.0395	1	PTEN	50 - '
2	SVF#10	15	17.5	PTEN	25892.3	6868.3	0.2653	0.255		20 - 4
3	SVF#10	19	20.5	control	26662.7	25792.9	0.9674	1		5
4	SVF#10	19	20.5	PTEN	25048.1	14121.5	0.5638	0.583		75-5
5	SVF#10	21	21.5	control	21221.5	16851.7	0.7941	1	a-Tubulin	-
6	SVF#10	21	21.5	PTEN	24097.4	1199.8	0.0498	0.063		20-1
Gel 2 Lane	cell strain	passage	generation	siRNA	α-Tubulin	PTEN	PTEN/Tubulin	Fold		. F
1	SVF#6	20	19.5	control	28432.6	34222.4	1.2036	1	PTEN	2-
2	SVF#6	20	19.5	PTEN	28163.5	13651.6	0.4847	0.403	~	× 5
										the second se

a-Tubulin

PTEN

1307

PTEN/Tubulin

1.594

PTER

6	SVF#6	13	15	PTEN	27552.4	13760.5	0.4994	0.44
Gel 3 Lane	cell strain	passage	generation	siRNA	α-Tubulin	PTEN	PTEN/Tubulin	Fold
1	SVF#9	12	14.5	control	26326.2	34254.7	1.3012	1
2	SVF#9	12	14.5	PTEN	23683.8	18228.0	0.7696	0.592
3	SVF#9	16	19.5	control	26977.9	38985.1	1.4451	1
4	SVF#9	16	19.5	PTEN	23271.4	4514.9	0.1940	0.134
5	SVF#9	19	23	control	22783.1	25602.5	1.1237	1
6	SVF#9	19	23	PTEN	25241.9	6661.7	0.2639	0.235

PTEN 28809.4 26735.5 32007.1

6 Gel

2	SVF#10	18	27	PTEN	29801.7	17714.1	0.5944	0.747
3	SVF#9	25	29.5	control	28390.2	24607.5	0.8668	1
4	SVF#9	25	29.5	PTEN	31141.2	14283.6	0.4587	0.529
5	SVF#10	16	24.5	control	42170.0	53220.4	1.2620	1
6	SVF#10	16	24.5	PTEN	49634.0	41527.7	0.8367	0.663
7	SVF#10	19	28	control	36816.0	36749.9	0.9982	1
8	SVF#10	19	28	PTEN	33632.1	18851.5	0.5605	0.562

Lane	cell strain	passage	generation	siRNA	a-Tubulin	PTEN	PTEN/Tubulin	Fold
1	SVF#10	22	31.5	control	25567.1	26008.5	1.0173	1
2	SVF#10	22	31.5	PTEN	22026.5	14362.9	0.6521	0.641
3	SVF#8	6	11.5	control	23997.8	27608.4	1.1505	1
4	SVF#8	6	11.5	PTEN	22733.3	20224.4	0.8896	0.773
5	SVF#6	19	27.5	control	25526.2	28333.1	1.1100	1
6	SVF#6	19	27.5	PTEN	22336.8	14500.3	0.6492	0.585
7	SVF#6	10	16.5	control	32681.5	48733.2	1.4912	1
8	SVF#6	10	16.5	PTEN	31490.7	31924.4	1.0138	0.68
9	SVF#6	14	21	control	23326.8	21936.5	0.9404	1
10	SVF#6	14	21	PTEN	27925.7	10446.5	0.3741	0.398

control PTEN 839

PTEN 43

25284 3142 CONTROL PTEN

control 20953 PTEN 24168 control 36576 CONT

contro

16 PTEN 89 3752

102.2

2.711



50 - T 15 - L



---

---

pAKT/AKT Gel 1 Lan

Gel 2 La SVF#10 SVF#10

г	AKT	pAKT/AKT	Fold							
.953	24410.3	0.3439	1	pAKT (T308)	25-			-		ł
5.38	28621.7	0.7943	2.31		-					
2.92	27179.5	0.0152	1		50-		Contraction of the local division of the loc		April	ł
.749	26966.7	0.0340	2.235			75-	A CONTRACTOR OF THE OWNER	1000		
6.95	27450.6	0.0050	1	AKT						ł
.263	28802	0.0150	3.015			50-	A state of the second sec		Contraction of Contra	
.477	45455.4	0.0197	1							
.342	50902.8	0.7372	37.38							
7.38	40361.9	0.6245	1							
.664	34367.8	0.9763	1.563							
6	pAKT	pAKT/AKT	Fold							
451			-	pAKT (T308)	29-	1				
.43					20		•			
945					50-	14				
702						-				
794	191.192	0.0052	1	AKT	75-	r -		-		

50-

SVF#S SVF#S SVF#1

SVF#1 SVF#1

Gel 1	coll strain	0200200	apparation	TIPMA	a-Tubulia	320	o\$6/Tubulio	Fold					
Lane	cell strain	passage	Reveration	SIRINA	0-1000im	1501.70	pso/rubuan	Foid	all (Ser 225 (226) 23	٢			
- 1	SVF#10	15	17.5	CONTRAL	29685.765	1591.79	0.0536	10.2	ps6 (ser235/236) 57	-	-		-
- 2	50/6#10	15	17.5	FIEN	23652.236	14250.5	0.3522	10.5	2	5- 6			
3	SVF#10	19	20.5	DTEN	20002.073	36794.3	1.0693	4 094					
	SVF#10	21	20.5	control	21221 450	20784.3	1.0055	4.004	a Tubulia	22-L			
6	SVF#10	21	21.5	PTEN	24097.409	15372.4	0.6379	13.73	u-rubuin	50- L			
Gal 2													
Lane	cell strain	passage	generation	siRNA	a-Tubulin	pS6	pS6/Tubulin	Fold					
1	SVF#10	22	31.5	control	25567.078	64222.7	2.5119	1	pS6 (Ser235/236)		-	11-1-	
2	SVF#10	22	31.5	PTEN	22026.501	73514.5	3.3375	1.329	25	6	_		
3	SVF#8	6	11.5	control	23997.794	2306.21	0.0961	1		10-			
4	SVF#8	6	11.5	PTEN	22733.258	6170.49	0.2714	2.824		**-			
5	SVF#6	19	27.5	control	25526.208				a-Tubulin	50-	-		_
6	SVF#6	19	27.5	PTEN	22336.773					eccino de	and the second se	and the second division of	
7	SVF#6	10	16.5	control	32681.501	1563.01	0.0478	1					
8	SVF#6	10	16.5	PTEN	31490.723	5657.71	0.1797	3.757					
9	SVF#6	14	21	control	23326.752	239.192	0.0103	1					
10	SVF#6	14	21	PTEN	27925.693	15612.9	0.5591	54.52					
1	SVF#10	18	27	control	25150.572	471.556	0.0187	1 47.99	pS6 (Ser235/236) 37	- r			-
2	SVF#10	18	2/	PIEN	29801.744	24020.1	0.8060	42.99			-		
-	SVEHO	25	29.5	DTEN	20390.179	421.435	0.0148	4 5 2 7		r =	A		
4	SVF#9	16	29.5	PIEN	31141.229 47160.0E7	2097.5	0.0674	4.537	a Tubulia	5- 1			-
6	SVF#10	16	24.5	PTEN	42105.537	29104.5	0.1402	4 181	u-rubuin	50-			
7	SVE#10	19	28	control	36816.007	41326.6	1 1225	1					-
8	SVF#10	19	28	PTEN	33632.057	40305.2	1.1984	1.068					
pFO)	KO1/α-Tu	bulin					pFOXO1/						
Lane	cell strain	passage	generation	siRNA	α-Tubulin	pFOXO1	Tubulin	Fold		1.00			
1	SVF#6	23	25	control	23465.723	1664.86	0.0709	1	pFOXO1	75-		-	-
2	SVF#6	23	25	PTEN	25824.551	9051.15	0.3505	4.94			-	-	
3	SVF#9	16	19.5	control	19014.723	5445.25	0.2864	1		50-			
4	SVF#9	16	19.5	PTEN	21137.915	9373.2	0.4434	1.548		2			
5	SVF#10	19	28	control	18774.551	219.778	0.0117	1	α-Tubulin	75			
				and and and and and and		0.000 00	10 10 10 10 IN						

SREBP1/ $\alpha$ -Tubulin

Lane	cell strain	passage	generation	siRNA	a-Tubulin	SREBP1	SREBP1/ Tubulin	Fold	
1	SVF#10	19	20.5	control	6903.933	9476.12	1.3726	1	SREBP1
2	SVF#10	19	20.5	PTEN	8575.296	19465.1	2.2699	1.654	250
3	SVF#6	20	19.5	control	5463.64	6880.17	1.2593	1	150
4	SVF#6	20	19.5	PTEN	5284.004	11169.2	2.1138	1.679	100
5	SVF#9	12	14.5	control	3411.983	6350.1	1.8611	1	α-Tubulin
6	SVF#9	12	14.5	PTEN	2969.569	6134.44	2.0658	1.11	75
7	SVF#8	13	22.5	control	4734.225	3256.18	0.6878	1	
8	SVF#8	13	22.5	PTEN	5846.175	6014.9	1.0289	1.496	50

Figure S4: Western blots of PTEN KD/control SVF cells: exposed films and densitometric analyses of PTEN (normalized to α-Tubulin), pAKT (T308) (normalized to total AKT), pS6 (Ser235/236) (normalized to α-Tubulin), NAMPT(normalized to α-Tubulin), p21 (normalized to α-Tubulin), pFOXO1 (normalized to α-Tubulin) and SREBP1 (normalized to α-Tubulin). Western blot images presented in Figures 1(a) and 6(b) were reused (indicated with red boxes).

PTEN	I CRISPR SV	/F						
PTEN/	α-Tubulin							-
Lane	Cells	guideRNA	α-Tubulin	PTEN	PTEN/Tubulin	Fold	PTEN 25	
1	CRISPR SVF#1	control	44983.5	35283.2	0.7844	1	-	
2	CRISPR SVF#1	PTEN #3+4	41204.8	23047.4	0.5593	0.7131	30*	
3	CRISPR SVF#3	control	39369.1	34844.8	0.8851	1		F
4	CRISPR SVF#3	PTEN #3+4	32432.8	2196.4	0.0677	0.0765	α-Tubulin	
Col 2							DTEN	°i
Lane	Cells	guideRNA	a-Tubulin	PTEN	PTEN/Tubulin	Fold	FIEN	
1	CRISPR SVF#9	control	30284.5	37275.7	1,2309	1		50
2	CRISPR SVF#9	PTEN #3+4	25771.4	40277.4	1.5629	1.2697		7-26
							α-Tubulin	
Gel 3							-	6
Lane	Cells	guideRNA	GAPDH	PTEN	PTEN/GAPDH	Fold	+	>-
1	CRISPR SVF#6	control	46613.2	25935.4	0.5564	1	PTEN	
2	CRISPR SVF#6	control	37796.5	20527.1	0.5431	0.9761	-	
3	CRISPR SVF#6	PTEN #3	48217.2	22996.5	0.4769	0.8572	GARDH	-
	CRISER SVF#0	FILM #314	50464.5	10203.0	0.3211	0.3770	GAPUN	
pAKT/ Gel 1	AKT							F
Lane	Cells	guideRNA	pAKT	AKT	pAKT/AKT	Fold	pAKT (T308)	
1	CRISPR SVF#1	control	24115.673	47316.22	0.50967032	1		
2	CRISPR SVF#1	PTEN #3+4	15713.116	42532.735	0.369435824	0.724852536	34	L
3	CRISPR SVF#3	control	16171.53	46697.271	0.346305676	1		16
4	CRISPR SVF#3	PTEN #3+4	28030.016	43814.614	0.639741252	1.847331118	AKT	
Gel 2								50-
Lane	Cells	guideRNA	DAKT	AKT	nAKT/AKT	Fold	pAKT (T308)	
1	CRISPR SVF#9	control	18924.9	45458.3	0.4163	1	p (1.000)	
2	CRISPR SVF#9	PTEN #3+4	40323.7	41352.1	0.9751	2.3423		·
						-	AKT	¥5. F
lane	Cells	quideRNA	nAKT	ΔΚΤ	DAKT/AKT	Fold		6
1	CRISDR SVE#6	control	1557.7	34414.0	0.0453	1	DAKT (T308)	; -
2	CRISPR SVF#6	control	1137.2	24325.5	0.0455	1.0329	PART (1300)	
3	CRISPR SVF#6	PTEN #3	18959.9	32016.1	0.5922	13.0837	*	
4	CRISPR SVF#6	PTEN #3+4	43735.2	37969.8	1.1518	25.4480		25
							AKT	50
pS6/α <sub>Gel 1</sub>	-Tubulin							
Lane	Cells	guideRNA	α-Tubulin	pS6	pS6/Tubulin	Fold	pS6 (Ser235/236)	
1	CRISPR SVF#1	control	19917.5	29887.6	1.5006	1		15-
2	CRISPR SVF#1	PTEN #3+4	20513.1	47436.4	2.3125	1.5411		-
3	CRISPR SVF#3	control	24033.8	20507.5	0.8533	1		75-
4	CRISPR SVF#3	PTEN #3+4	22460.1	49393.8	2.1992	2.5773	α-Tubulin	50
Gel 2								22 F
Lane	Cells	guideRNA	a-Tubulin	pS6	pS6/Tubulin	Fold	pS6 (Ser235/236)	25-
1	CRISPR SVF#9	control	30284.5	527.7	0.0174	1	pee (sector) 200)	
2	CRISPR SVF#9	PTEN #3+4	25771.4	19182.4	0.7443	42.7126		25 -
Gel 3							α-Tubulin	50
Lane	Cells	guideRNA	GAPDH	pS6	pS6/GAPDH	Fold		
1	CRISPR SVF#6	control	55297.3	8164.4	0.1476	1	pS6 (Ser235/236)	37-
2	CRISPR SVF#6	control	41454.0	3526.6	0.0851	0.5762		15-
3	CRISPR SVF#6	PTEN #3	35198.0	23966.1	0.6809	4.6117		
4	CRISPR SVF#6	PTEN #3+4	37901.3	49345.4	1.3019	8.8180	CARDIA	12-

#### Constitutive active FOXO1 overexpression in CRISPR SVF

FOXO1 active/α-Tubulin

Gel 2

Lane 1 Cells

guideRNA

CRISPR SVF#6 p23 PTEN #3+4 control CRISPR SVF#6 p23 PTEN #3+4 FOXO1 active

Plasmid

α-Tubulin

5765.4

6649.6

Gel 1 FOXO1 (FLAG) FOXO1/Tubulin Fold Lane Cells guideRNA CRISPR SVF#6 p16 PTEN #3+4 Plasmid α-Tubulin FOXO1 (FLAG) 1 control 7418.8 476.2 0.0642 1 CRISPR SVF#6 p16 PTEN #3+4 CONtrol CRISPR SVF#6 p16 PTEN #3+4 FOXO1 active CRISPR SVF#6 p17 PTEN #3+4 control CRISPR SVF#6 p17 PTEN #3+4 FOXO1 active 23.58 9221. 13958.1 1.5136 7703.0 7416.1 0.0320 246.1 7366.7 1 31.09 α-Tubulin 4 0.9933 Gel 2 
 Cells
 guideRNA
 Plasmid

 CRISPR SVF#6 p23
 PTEN #3+4
 control

 CRISPR SVF#6 p23
 PTEN #3+4
 FOXO1 activ
 FOXO1 (FLAG) FOXO1/Tubulin Fold α-Tubulin Lane 1 5765.4 19.0 0.0033 FOXO1 (FLAG) 414.60 6649.6 9061.5 1.3627 α-Tubulin SREBP1/a-Tubulin Gel 1 Cells guideRNA CRISPR SVF#6 p16 PTEN #3+4 Plasmid SREBP1 SREBP1/Tubulin Fold Lane α-Tubulin SREBP1 1 control 7418.8 5959.8 0.8033 
 CRISPR SVF#6 p16
 PTEN #3+4
 CONTO

 CRISPR SVF#6 p16
 PTEN #3+4
 FOXO1 active

 CRISPR SVF#6 p17
 PTEN #3+4
 control

 CRISPR SVF#6 p17
 PTEN #3+4
 FOXO1 active
 0.52 9221. 7703.0 3821.9 7921.5 0.4145 1 0.71 α-Tubulin 7416.1 5395.6 0.7276

**Figure S5**: Western blots of PTEN CR/control SVF cells: exposed films and densitometric analyses of PTEN (normalized to  $\alpha$ -Tubulin), pAKT (T308) (normalized to total AKT), pS6 (Ser235/236) (normalized to  $\alpha$ -Tubulin), FOXO1 (FLAG antibody, normalized to  $\alpha$ -Tubulin) and SREBP1 (normalized to  $\alpha$ -Tubulin). Western blot images presented in Figures 1(b) and 6(d) were reused (indicated with red boxes).

SREBP1/Tubulin Fold

0.24

0.6833

0.1648

SREBP1

α-Tubulin

150

SREBP1

3939.5

1095.8

#### PTEN KD

# NAMPT/α-Tubulin Gel 1

Lane	cell strain	passage	generation	siRNA	α-Tubulin	NAMPT	NAMPT/Tubulin	Fold
1	SVF#10	15	17.5	control	29685.8	11692.5	0.3939	1
2	SVF#10	15	17.5	PTEN	25892.3	25617.6	0.9894	2.5119
3	SVF#10	19	20.5	control	26662.7	11961.0	0.4486	1
4	SVF#10	19	20.5	PTEN	25048.1	24268.8	0.9689	2.1598
5	SVF#10	21	21.5	control	21221.5	19353.1	0.9120	1
6	S\/E#10	21	21.5	DTEN	24007.4	22921.2	0.0995	1.0940

Gel 2

Lane	cell strain	passage	generation	siRNA	α-Tubulin	NAMPT	NAMPT/Tubulin	Fold
1	SVF#10	18	27	control	25150.572	18085.338	0.7191	1
2	SVF#10	18	27	PTEN	29801.744	29915.401	1.0038	1.3960
3	SVF#9	25	29.5	control	28390.179	20071.702	0.7070	1
4	SVF#9	25	29.5	PTEN	31141.229	31966.886	1.0265	1.4519
5	SVF#10	16	24.5	control	42169.957	33930.229	0.8046	1
6	SVF#10	16	24.5	PTEN	49634.049	50054.726	1.0085	1.2534
7	SVF#10	19	28	control	36816.007	37188.907	1.0101	1
8	SVE#10	19	28	PTEN	33632.057	43514 605	1 7938	1 2809

# p21/α-Tubulin

cell strain	passage	generation	siRNA	α-Tubulin	p21	p21/Tubulin	Fold
SVF#10	18	27	control	25150.572	12232.974	0.4864	1
SVF#10	18	27	PTEN	29801.744	5668.246	0.1902	0.3910
SVF#9	25	29.5	control	28390.179	11907.723	0.4194	1
SVF#9	25	29.5	PTEN	31141.229	8778.782	0.2819	0.6721
SVF#10	16	24.5	control	42169.957	32319.451	0.7664	1
SVF#10	16	24.5	PTEN	49634.049	15655.045	0.3154	0.4115
SVF#10	19	28	control	36816.007	25134.057	0.6827	1
SVF#10	19	28	PTEN	33632.057	4063.104	0.1208	0.1770
	cell strain SVF#10 SVF#10 SVF#9 SVF#9 SVF#10 SVF#10 SVF#10 SVF#10	cell strain         passage           SVF#10         18           SVF#10         18           SVF#9         25           SVF#9         25           SVF#10         16           SVF#10         16           SVF#10         19           SVF#10         19	cell strain         passage         generation           SVF#10         18         27           SVF#10         18         27           SVF#2         25         29.5           SVF#3         25         29.5           SVF#40         16         24.5           SVF#10         16         24.5           SVF#10         16         28           SVF#10         19         28	cell strain         passage         generation         siRNA           SVF#10         18         27         control           SVF#10         18         27         PTEN           SVF#2         25         29.5         control           SVF#3         25         29.5         PTEN           SVF#10         16         24.5         control           SVF#10         16         24.5         PTEN           SVF#10         19         28         control	cell strain         passage         generation         siRNA         o-Tubulin           SVF#10         18         27         control         25150.572           SVF#10         18         27         PTEN         2980.714           SVF#2         255         control         28390.174           SVF#9         25         29.5         control         28390.179           SVF#10         16         24.5         control         42169.957           SVF#10         16         24.5         PTEN         4964.049           SVF#10         19         28         PTEN         3632.057	cell strain         passage         generation         siRNA         o-Tubulin         p21           SVF#10         18         27         control         2510.572         1232.974           SVF#10         18         27         PTEN         2980.1744         5668.246           SVF#9         25         29.5         control         2830.179         1907.723           SVF#9         25         29.5         pTEN         31141.229         8778.782           SVF#10         16         24.5         control         42169.957         32319.451           SVF#10         16         24.5         pTEN         4964.049         15655.045           SVF#10         19         28         control         3631.007         25134.057           SVF#10         19         28         PTEN         3632.007         4063.104	cell strain         passage         generation         siRNA         or-Tubulin         p21         p21/Tubulin           SVF#10         18         27         control         25150-572         12232-974         0.4864           SVF#10         18         27         PTEN         29801.744         5668.246         0.1902           SVF#9         25         29.5         PTEN         28300.179         11907.723         0.4194           SVF#9         25         29.5         PTEN         3231.917         11907.723         0.4194           SVF#9         25         29.5         PTEN         31141.229         8778.782         0.2819           SVF#10         16         24.5         control         42169.957         32319.451         0.7664           SVF#10         16         24.5         PTEN         4963.404         15655.045         0.3154           SVF#10         16         24.5         PTEN         3681.607         25134.057         0.6827           SVF#10         19         28         PTEN         3363.2057         4063.104         0.1208

Gel 2

Lane	cell strain	passage	generation	siRNA	α-Tubulin	p21	p21/Tubulin	Fold
1	SVF#10	22	31.5	control	25002.208	16890.459	0.6756	1
2	SVF#10	22	31.5	PTEN	28004.329	7717.246	0.2756	0.4079
3	SVF#8	6	11.5	control	25806.501	17323.752	0.6713	1
4	SVF#8	6	11.5	PTEN	30205.886	7867.246	0.2605	0.3880
5	SVF#6	19	27.5	control	23217.016	15644.974	0.6739	1
6	SVF#6	19	27.5	PTEN	24411.501	2608.912	0.1069	0.1586
7	SVF#6	10	16.5	control	28875.522	4094.447	0.1418	1
8	SVF#6	10	16.5	PTEN	41495.463	97.778	0.0024	0.0166

#### Longterm culture

Gel 1

Lane	cell strain	passage	generation	days	α-Tubulin	PTEN	PTEN/Tubulin	NAMPT	NAMPT/Tubulin	pAkt	Akt	pAKT/AKT
1	SVF#6	4	5.5	11	21897.7	2176.0	0.0994	10473.0	0.4783	56901.7	1123.8	50.6324
2	SVF#6	8	12	24	36210.7	8694.3	0.2401	4683.2	0.1293	42782.3	28394.1	1.5067
3	SVF#6	5	8.5	17	34287.5	2348.0	0.0685	5311.5	0.1549	38720.3	27248.1	1.4210
4	SVF#6	12	17.5	35	44295.3	20148.3	0.4549	8349.9	0.1885	7610.3	41283.3	0.1843
5	SVF#6	14	19.5	39	45090.0	40007.0	0.8873	1639.7	0.0364	16317.2	38784.3	0.4207
6	SVF#6	16	21.5	43	36260.4	29828.0	0.8226	544.0	0.0150	26400.0	33258.7	0.7938
7	SVF#6	18	22.5	45	22367.2	17480.7	0.7815	408.3	0.0183	16106.4	15828.7	1.0175
8	SVF#6	19	23	46	31162.5	22429.2	0.7198	3111.9	0.0999	18106.7	34120.4	0.5307
9	SVF#6	21	26.5	53	38233.7	23050.0	0.6029	2255.5	0.0590	5655.3	32125.4	0.1760
10	SVF#6	21	27	54	36219.0	18207.8	0.5027	968.6	0.0267	4665.3	36954.7	0.1262
11	SVF#6	22	28.5	57	36973.0	27925.5	0.7553	1786.5	0.0483	404.3	45943.9	0.0088
12	SVF#6	20	40.5	81	33873.7	17538.0	0.5177	391.0	0.0115	16532.7	17372.9	0.9516

PTEN	75- 50-		PAKT	75-	
NAMPT	75. 50	2	12 AKT	25 - 50	
α-Tubulin	25-				

Gel 2

Lane	cell strain	passage	generation	ys in culti	$\alpha$ -Tubulin	PTEN	PTEN/Tubulin	NAMPT	NAMPT/Tubulin	pAkt	Akt	pAKT/AKT
1	SVF#8	2	2	4	14337.7	12774.77	0.890991582	14437	1.006936259	29543.81	3388.518	8.71879978
2	SVF#8	3	3.5	7	24164.33	52807.38	2.185344266	6341.5	0.262433885	41677.32	16287.34	2.55887825
3	SVF#8	5	8.5	17	42892.41	37488.32	0.874008245	558.92	0.013030744	56173.32	2402.326	23.3828881
4	SVF#8	11	18.5	37	84696.81	49400.24	0.583259747	198.95	0.002348967	13984.12	20216.09	0.69173218
5	SVF#8	12	21	42	69102.91	23498.9	0.340056591	777.65	0.011253477	42.536	14095.02	0.0030178
6	SVF#8	13	22.5	45	57271.12	38048.1	0.664350549	277.9	0.004852341	8259.246	11969.27	0.69003757
7	SVF#8	14	25.5	51	50289.697	68391.49	1.359950329	717.75	0.014272287	7757.368	32665.81	0.23747668











	75-	L	 
α-Tubulin	50-		

Gel 3												
Lane	cell strain	passage	generation	ys in culti	α-Tubulin	PTEN	PTEN/Tubulin	NAMPT	NAMPT/Tubulin	pAkt	Akt	pAKT/AKT
1	SVF#9	1	1	2	14337.7	76.778	0.005354973	61101	4.261530789	7211.966	2503.69	2.88053473
2	SVF#9	1	1.5	3	24164.33	14126.92	0.584618733	90193	3.732468063	17232.77	13080.48	1.31744171
3	SVF#9	6	8.5	17	42892.41	39505.61	0.921039643	47385	1.104740909	77.607	38965.78	0.00199167
4	SVF#9	9	13.5	27	84696.81	65594.47	0.774462108	32540	0.384194281	137.728	69093.95	0.00199334
5	SVF#9	12	14.5	29	69102.91	62116.41	0.898897167	18288	0.264652096	29267.32	64161.54	0.45615052
6	SVF#9	13	16.5	33	57271.12	20776.06	0.362766784	10323	0.180255598	9554.147	42402.8	0.22531878
7	SVF#9	18	24	48	44063.59	25981.66	0.589640109	18145	0.411791005	73.192	48147.8	0.00152015
	PTEN	7	5- 3-					pAKT	75- 60-			
	NAMPT	2	· ·	-		-	-	AKT 7	FE-			
Gel 4	α-Tubulin	3	5 - TO _	ur in cult	Tubulin	PTEN	PTEN/Tubulin	NAMPT	NAMPT /Tubulin	nåkt	Ak+	-
1	SVE#10	1	2	6	22006 10	9064 299	0 204164772	54166	2 255449446	267.021	26170 77	0.00729222
2	SVF#10	2	4.5	9	22990.19	20824.288	0.803591261	15888	0.613089748	207.021	38533 37	0.00758225
2	SVE#10	2	5.5	11	29100 14	24220 42	0.93609391201	7606.6	0.261204997	12492.07	44735 27	0.79707100
4	SVF#10	6	10	20	21255 58	29670 3	1 395882869	14390	0.677006697	36794.81	37088 32	0.99208619
5	SVF#10	9	14.5	29	40137.3	66097.88	1.646794378	2711.4	0.067553049	485.435	72107.16	0.00673213
	PTEN	25-				==,	-	pAKT	75 50-			
	NAMPT		25- 56-					AKT 5	5-			
	α-Tubulin		75-	-			-					

**Figure S6**: Western blots of four SVF cell long term cultures: exposed films and densitometric analyses of PTEN (normalized to  $\alpha$ -Tubulin), pAKT (T308) (normalized to total AKT) and pS6 (Ser235/236) (normalized to  $\alpha$ -Tubulin).



**Figure S7**: (A) Normalized read counts mapping to *PTEN* mRNA in the investigated samples. (B) PCA of samples clearly cluster according patients (upper panel), after removing the variance caused by the individual cell donors the second principal component (PC2) segregates the samples into control *vs*. PTEN (lower panel).

### Supporting information tables:

Lists of differentially expressed genes (Supporting information Tables S1-3) are available separately.

Name	Sex	Age at resection	Origin
SVF#1	female	31	visceral
SVF#3	female	30	visceral
SVF#5	female	33	visceral
SVF#6	male	27	visceral
SVF#8	male	37	visceral
SVF#9	female	32	visceral
SVF#10	female	29	visceral
SVF#11S	male	18	subcutaneous
SVF#12S	male	24	subcutaneous
SVF#14S	female	28	subcutaneous

Table S	34. SVF	cell c	ultures.
---------	---------	--------	----------

Marker	Fluorophore	Distributor	Clone	Cat. no
MSCA1	PE	Miltenyi	W8B2	130-093-587
CD34	FITC	Miltenyi	AC136	130-113-178
CD14	PeVio770	Miltenyi	Tük4	130-113-149
CD271	APC	Miltenyi	ME20.4-1-H4	130-113-418
CD8	PerCP	BD Horizon	SK1	345774
CD31	V450	BD Horizon	WM59	561653
CD45	BV510	BioLegend	HI30	304036

Table S5. Antibodies used for flow cytometry.

**Table S6.** Flow cytometry analysis of cell surface markers.

cells	passage	generation	single cells	viable cells	CD8+	CD14+	CD31+	CD34+	CD45+	CD271+	MSCA1+
LipPD1	6	8	97%	77.60%	none	none	none	none	none	4.70%	4.74%
LipPD1	28	34	93.60%	66.70%	none	6%	none	3.62%	none	3.86%	1.51%
SVF#1	6	19	95.30%	57.00%	none	2.56%	none	18.60%	none	3.67%	none
SVF#1	12	17.5	93.70%	51.90%	none	2.76%	none	22.00%	none	1.58%	3.00%
SVF#1	22	35.5	99.10%	71.20%	none	none	none	29.00%	none	none	1.63%
SVF#5	0	0	98.90%	23.00%	none	9.10%	3.04%	58.70%	6.18%	15.80%	5.96%
SVF#5	11	25.5	96.50%	79.90%	none	none	none	2%	none	none	none
SVF#6	0	1.5	99.60%	8.04%	none	2.98%	2%	none	none	19%	19%
SVF#6	16	19	96.20%	79.30%	none	none	none	12.90%	none	none	4.46%
SVF#6	23	31	97.10%	74.80%	none	none	none	38.60%	none	none	2.44%
SVF#8	0	1	99.20%	53.10%	1.59%	2.82%	3.53%	74.40%	2.67%	55.60%	7.29%
SVF#8	11	23.5	92%	65.50%	none	none	none	17%	none	none	none
SVF#9	0	1	99%	33.90%	5.30%	9.44%	2.72%	56.70%	4.50%	27.20%	5.17%
SVF#9	4	6	95.50%	74.50%	none	none	none	none	none	23.20%	11.60%
SVF#9	14	20	97.30%	82.60%	none	none	none	44.70%	none	none	1.11%
SVF#10	15	20.5	96.90%	89.20%	none	none	none	5.94%	none	2.27%	1.54%
SVF#10	15	24	94.50%	77.90%	none	none	none	15%	none	none	20.20%
SVF#10	23	27	90.40%	79%	none	none	none	none	none	none	none
SVF#11S	22	29	95.30%	65.40%	none	none	none	6.18%	none	15.60%	none
SVF#12S	18	26.5	96%	78%	none	none	none	12.80%	none	none	none
SVF#14S	8	12.5	96.40%	87%	none	none	none	9.53%	none	1.72%	none
SVF #3	0	3.5	99%	26%	none	none	none	5.14%	none	1.62%	2.75%

Table S7. crRNAs used for CRISPR/Cas9 PTEN knockout.

#	Design ID	crRNA Sequence	PAM	Strand
1	Hs.Cas9.PTEN.1.AC	TTATCCAAACATTATTGCTA	TGG	+
2	Hs.Cas9.PTEN.1.AF	TATCCAAACATTATTGCTAT	GGG	+
3	CD.Cas9.VCTN3398.AH	ATATCTGAGTACTTTAGTTA	AGG	-
4	CD.Cas9.VCTN3398.BE	TTTCCTGCAGAAAGACTTGA	AGG	+

Primary antibody	Dilution	Distributor	Cat. no
PTEN ( 138G6) Rabbit map	1:1000 TBS-T 5%BSA (Wb)	CST	#9559
AKT antibody Rabbit polyclonal Ab	1:1000 TBS-T 5%BSA (Wb)	CST	#9272
Phospho-AKT (Thr308) (224F9) Rabbit mAb	1:1000 TBS-T 5%BSA (Wb)	CST	#4056
Phospho-S6 Ribosomal protein (Ser235/236)	1:1000 TBS-T 5%BSA (Wb)	CST	#4858
(D57.2.2E) XP® Rabbit mAb			
mAb anti -NAMPT Antibody	1:1000 TBS-T 5%BSA (Wb)	Novus	#NBP1-
		Biologicals	96585
P21 Waf 1/Cip1 D(S60)	1:1000 TBS-T 5%BSA (Wb)	CST	#2496
alpha Tublin (11H10) Rabbit mAb	1:2000 TBS-T 5%BSA (Wb)	CST	#2125
Phospho-FoxO1 (Ser256) Antibody	1:1000 TBS-T 5%BSA (Wb)	CST	#9461
SREBP-1 polyclonal antibody	1:1000 TBS-T 5% milk (Wb)	Santa Cruz	sc-8984
ANTI-FLAG Rabbit antibody	1:1000 TBS-T 5%BSA (Wb)	Sigma	F7425
KI-67 (MIB-1) Mouse mAb	1:200 IF-buffer (IF)	Dako	P0447
Secondary antibody	Dilution	Supplier	Cat. no
Polyclonal goat anti-rabbit immunoglobulin/HRP	1:2000 TBS-T 5% milk (Wb)	Dako	P0447
Polyclonal goat anti-mouse immunoglobulin/HRP	1:2000 TBS-T 5% milk (Wb)	Dako	P0448
Alexa Fluor 488 goat anti-mouse IgG H+L	1:1000 IF-buffer (IF)	Invitrogen	A11001

# Table S8. Antibodies used for Western blot (Wb) and immunofluorescence staining (IF).

Gene	Forward	Reverse	Probe
HPRT	GGCAGTATAATCCAAAGATGGT	GTCTGGCTTATATCCAACACTT	CAAGCTTGCTGGTGAAAAGGA
	CAA	CGT	CCCC
TBP	TTGTAAACTTGACCTAAAGACC	TTCGTGGCTCTCTTATCCTCAT	AACGCCGAATATAATCCCAAGC
	ATTGC	G	GGTTTG
PTEN	TGTAAAGCTGGAAAGGGACGA	GGAATAGTTACTCCCTTTTTGT	
		CTC	
ADIPOQ	GGCCGTGATGGCAGAGAT	CCTTCAGCCCCGGGTACT	CGATGTCTCCCTTAGGACCAAT
			AAGACCTGG
FABP4	GCTTTTGTAGGTACCTGGAAAC	ACACTGATGATCATGTTAGGTT	CCTGGTGGCAAAGCCCACTCC
	TTG	TGG	TCAT
FASN	GGCAAATTCGACCTTTCTCAGA	GGACCCCGTGGAATGTCA	CACCCGCTCGGCATGGCTATC
			TT
CDKN1A	CGAAGTCAGTTCCTTGTGGAG	CATGGGTTCTGACGGACAT	
(p21)			
CDKN2A	CTTCGGCTGACTGGCTGG	TCATCATGACCTGGATCGGC	
(p16)			
CDKN2B	AGGCGCGCGATCCAG	GGTGAGAGTGGCAGGGTCT	
(p15)			
HIPK2	GCTCAAGATGGCAGATTCCG	ACTTGCACATGTGAGGCCATA	
FOXO1	CCTACGCCGACCTCATCAC	AATTGAATTCTTCCAGCCCGC	
RNF144B	TGCCTGAAACAGTACATGCAG	ACCAAACAGGCAATCTCAGC	
SREBF-1	ACCGACATCGAAGGTGAAGT	CAGGGAAGTCACTGTCTTGGT	

## Table S9. Primers used for RT-qPCR.