Table S1 - List of antibodies used for immunofluorescence, flow cytometry and western blot analysis.

Antibodies used in this study are listed along with catalogue numbers and concentration and whenever applicable, protein size expressed in kDa. IF = Immunofluorescence, WB = Western Blotting, FC = Flow Cytometry

PROTEIN	Antibody	Concentration	Band Size (Kda)
Actin Beta	GeneTex #109639	1:10000	42 kDa
CD151	Epitomics #5901-1	1:100 (IF)	
CITED1	Abcam #ab55467	5mg/ml(WB)	20 kDa
	Novus Biological #H00004435-M03	1mg/ml(FC)	
COL4A1	Shigei Research Institute #H12	1:500 (WB)	25, 50 kDa
COL4A2	Shigei Research Institute #H22	1:500 (WB)	25, 50 kDa
COL4A3	Shigei Research Institute #H31	1:500 (WB)	25, 50 kDa
COL4A4	Shigei Research Institute #RH42	1:500 (WB)	25, 50 kDa
COL4A5	Shigei Research Institute #H53	1:500 (WB)	25, 50 kDa
ILK	Abcam#ab52480	1:500 (WB)	51 Kda
Integrin alpha 1	Abcam#ab106267	0.8mg/ml (WB)	131 kDa
Integrin alpha 3	Abcam#ab251428	3.3mg/ml (WB)	131 kDa
Integrin beta 5	Abcam #ab95623	2.5mg/ml (WB)	88 kDa
Laminin alpha 5	Abbiotec#251457	2mg/ml(WB)	37kDa
Nephrin	Santa Cruz #sc-28192	1mg/ml(IF)	
	Thermo Scientific PA5-25932	1mg/ml(FC)	
P-Cadherin	Cell Signaling, #2189	1:25 (IF)	
Phalloidin	Invitrogen #R415	1:1000 (IF)	
Podocalyxin	Invitrogen #393800	1:100 (IF)	
		1mg/ml(WB)	160 kDa
	R&D #MAB1556	1mg/ml (FC mouse)	
Podocin	Abcam#ab50339	1:100 (IF)	
		1mg/ml(WB)	42 kDa
Six-2	Santa Cruz	1mg/ml(FC)	
Synaptopodin	USBio #S9500	1:100 (IF)	
Tropomyosin	Abcam #7785	8mg/ml	55 kDa
VEGF	Abcam#ab46154	1mg/ml(WB)	43 kDa
Wilms Tumor Protein	Abcam#ab52933	1:100 (IF)	
		1:500 (WB)	51kDa
	R&D AF5729	2.5mg/ml (FC)	
	Abcam #89901	1:100 (FC mouse)	
Zonal Occludens 1	Abcam#ab59720	1mg/ml(IF)	

Supplementary Tables S2-S6

Summary Tables for Ingenuity Pathway Analysis of Microarrays

A detailed list of genes compared for differential expression between undifferentiated AKPC-P and dedifferentiated hIPod and between differentiated hAKPC-P and re-differentiated hIPod. All fold variations listed are statistically significant (P<0.05).

Table S2 – Summary table reporting fold variation for podocyte and slit diaphragm markers A detailed list of podocyte and slit diaphragm genes compared for differential expression between de-differentiated hIPod and undifferentiated hAKPC-P (on the left, light grey) and between re-differentiated hIPod and differentiated hAKPC-P (on the right, dark grey). Positive values indicate a higher gene expression in the hIPod versus the hAKPC-P, while negative values indicate a higher gene expression in hAKPC-P. All fold variations listed are statistically significant (P<0.05).

			PODOCIETE AND CUT DIA	DUDACAAAA	DIVERS				
PODOCYTE AND SLIT DIAPHRAGM MARKERS hAKPC-P undifferentiated versus hIPod de-differentiated hAKPC-P differentiated versus hIPod re-differentiated									
NAKPC-P (hAKPC-P undifferentiated versus hIPod de-differentiated				PC-P differentiated ver	sus nipod i	re-differentiated		
Gene	Fold Change	Gene	Fold Change	Gene	Fold Change	Gene	Fold Change		
ACTN4		LRRC7	3.51	ACTN4		LRRC7	3.51		
CD2AP	1.44	NPHS1	-1.26	CD2AP	1.44	NPHS1	-1.26		
CD36	1.02	NPHS2		CD36	1.02	NPHS2			
CDH3	-1.35	PDPN	-1.40	CDH3	-1.35	PDPN	-1.40		
CHKA	2.29	PLCE1	-1.39	CHKA	2.29	PLCE1	-1.39		
CR1	-1.13	PODXL	-4.78	CR1	-1.13	PODXL	-4.78		
CTNNB1	1.13	PTPRO	-1.08	CTNNB1	1.13	PTPRO	-1.08		
EFNB1	-2.44	SYNPO	-1.38	EFNB1	-2.44	SYNPO	-1.38		
EZR	-1.02	TJP1	1.32	EZR	-1.02	TJP1	1.32		
F Actin		TRPC6		F Actin		TRCP6			
FAT1	-1.49	WT1	1.19	FAT1	-1.49	WT1	1.19		
LMX1B	-1.11			LMX1B	-1.11				

Table S3 – Summary table reporting fold variation for markers for GBM formation A detailed list of GBM related genes compared for differential expression between de-differentiated hIPod and undifferentiated hAKPC-P (on the left, light grey) and between re-differentiated hIPod and differentiated hAKPC-P (on the right, dark grey). Positive values indicate a higher gene expression in the hIPod versus the hAKPC-P, while negative values indicate a higher gene expression in hAKPC-P. All fold variations listed are statistically significant (P<0.05).

GLOMERULAR BASEMENT MEMBRANE MARKERS								
hAKPC-P undifferentiated versus hIPod de-differentiated					hAKPC-P differentiated versus hIPod re-differentiated			
Gene	Fold Change	Gene	Fold Change	Gene	Fold Change	Gene	Fold Change	
AGRN	-1.37	ITGAV	-1.41	AGRN		ITGAV	6.28	
CDH1	-1.13	ITGB1	-1.29	CDH1	-2.37	ITGB1	3.17	
COL4A1	-1.68	ITGB3	-1.58	COL4A1	2.36	ITGB3	20.80	
COL4A2	-1.21	LAMA1	1.36	COL4A2	2.87	LAMA1		
COL4A3	-1.07	LAMA5	-2.46	COL4A3	-2.80	LAMA5	-2.67	
COL4A4	-1.14	LAMB1	-1.28	COL4A4	-2.56	LAMB1	6.84	
COL4A5	-1.80	LAMB2	-2.28	COL4A5	-1.95	LAMB2		
ELN	-1.18	LAMC1	-1.15	ELN	-2.77	LAMC1	7.18	
FN1	-1.06	MPV17	-1.49	FN1	19.65	MPV17	6.27	
HSPG2		MYO1E	-1.14	HSPG2		MYO1E	2.12	
ILK		NID1	1.50	ILK	1.33	NID1		
ITGA1	1.37	NID2	-7.26	ITGA1	9.40	NID2		
ITGA3	-1.42	WT1	1.19	ITGA3	8.16	WT1	-1.62	
ITGA5	-2.16			ITGA5	2.58			

Table S4 – **Summary table reporting fold variation for markers involved in cell cycle regulation in podocytes** A detailed list of cell cycle related genes compared for differential expression between dedifferentiated hIPod and undifferentiated hAKPC-P (on the left, light grey) and between re-differentiated hIPod and differentiated hAKPC-P (on the right, dark grey). Positive values indicate a higher gene expression in the hIPod versus the hAKPC-P, while negative values indicate a higher gene expression in hAKPC-P. All fold variations listed are statistically significant (P<0.05).

			CELL CYCLE N	MARKERS			
	hAKPC-P undifferentiated versu	hAKPC-P differentiated versus hIPod re-differentiated					
Gene	Fold Change	Gene	Fold Change	Gene	Fold Change	Gene	Fold Change
ATM		Cyclin B		ATM	13.19	Cyclin B	
ATR		Cyclin D		ATR		Cyclin D	
CCNH	1.36	Cyclin E		CCNH	2.96	Cyclin E	
CDC25A	2.21	DP1-E2F-Rb		CDC25A		DP1-E2F-Rb	
CDK1	1.99	E2f		CDK1		E2f	
CDK2	1.46	GSK3B		CDK2	4.01	GSK3B	2.14
CDK4/6		Hdac		CDK4/6		Hdac	
CDK7	1.40	MYT1	-1.17	CDK7	2.70	MYT1	-3.00
CDKN1A	-2.90	PP2A		CDKN1A	6.89	PP2A	
CDKN1B	1.35	RAF1	1.18	CDKN1B	2.83	RAF1	
CDKN1C		RB1	1.14	CDKN1C	-2.68	RB1	29.82
CDKN2A	1.65	Scf		CDKN2A	6.84	Scf	
CDKN2B		TFDP1	1.41	CDKN2B		TFDP1	11.27
CDKN2C	1.42	Tgf beta		CDKN2C	-3.02	Tgf beta	
CDKN2D		TP53	1.21	CDKN2D		TP53	9.81
Cyclin A		WEE1	1.57	Cyclin A		WEE1	19.11

Table S5 – Summary table reporting fold variation for markers involved in Ca⁺⁺ signaling in podocytes A detailed list of Ca⁺⁺ signaling related genes compared for differential expression between de-differentiated hIPod and undifferentiated hAKPC-P (on the left, light grey) and between re-differentiated hIPod and differentiated hAKPC-P (on the right, dark grey). Positive values indicate a higher gene expression in the hIPod versus the hAKPC-P, while negative values indicate a higher gene expression in hAKPC-P. All fold variations listed are statistically significant (P<0.05).

Ca++/K+/Na+ SIGNALING MARKERS								
hAKPC-P undiffe	ıs hIPod de-different	hAKPC-P differentiated versus hIPod re-differentiated						
Gene	Fold Change	Gene	Fold Change	Gene	Fold Change	Gene	Fold Change	
AKAP5	1.74	KCNMA1	-3.89	AKAP5		KCNMA1	3.05	
Alpha actin		KCNQ1		Alpha actin		KCNQ1	-3.68	
ASPH		LETM1	-1.07	ASPH		LETM1		
ATP1A2	-1.11	MAGI1		ATP1A2	-3.55	MAGI1	-1.85	
ATP2A1		MCU		ATP2A1		MCU	4.48	
ATP2A2		MEF2		ATP2A2	6.78	MEF2		
ATP2C1	-1.15	MICU1		ATP2C1	6.07	MICU1	5.22	
CABIN1	-1.20	MICU1-MCU		CABIN1	-1.83	MICU1-MCU		
CACNA1C		Myosin		CACNA1C	-4.54	Myosin		
CACNA1H	-1.16	Ncx		CACNA1H	-3.09	Ncx		
CACNG1	-1.11	nAChRs		CACNG1	-3.12	nAChRs		
Calcineurin protein(s)		NMDA Receptor		Calcineurin protein(s)		NMDA Receptor		
Calmodulin		NPHS1	-1.26	Calmodulin		NPHS1	-3.66	
CALR	-1.13	Pka		CALR	3.47	Pka		
CaMK I		Pmca		CaMK I		Pmca		
CAMK2D	-1.79	Rap		CAMK2D	2.15	Rap		
CAMK4	4.00	Ryr		CAMK4	2.46	Ryr		
CaMKII		RYR1	-1.11	CaMKII		RYR1	-3.34	
Camkk		RYR2	-1.08	Camkk		RYR2	-2.67	
CASQ		RYR3	-1.15	CASQ		RYR3	-2.74	
CHP	-1.21	SCN4A	-1.21	CHP	6.07	SCN4A	-3.28	
CLCN1	-1.06	SERCA		CLCN1	-2.62	SERCA		
Creb		SLC24A6	1.09	Creb		SLC24A6		
ERK1/2		SLC5A3	-2.66	ERK1/2		SLC5A3	-1.30	
FXYD1	-1.09	Tni		FXYD1	-3.78	Tni		
GRIA		TRDN	-1.02	GRIA		TRDN	-1.70	
GRIK1		Tropomyosin		GRIK1	-2.69	Tropomyosin		
Hdac		Troponin C		Hdac		Troponin C		
HTR3A	-1.05	Troponin t		HTR3A	-3.27	Troponin t		
ITPR		TRP		ITPR		TRP		
KCNB2	1.27	TRPC3	1.29	KCNB2	-2.11	TRPC3		
KCNE2	-1.33	TRPC6		KCNE2	-3.21	TRPC6	-2.58	
KCNJ12	-1.12	VG Ca2++ channels		KCNJ12	-2.70	VG Ca2++ channels		

Table S6 – Summary table reporting fold variation for contractility markers in podocytes A detailed list of contractility genes compared for differential expression between de-differentiated hIPod and undifferentiated hAKPC-P (on the left, light grey) and between re-differentiated hIPod and differentiated hAKPC-P (on the right, dark grey). Positive values indicate a higher gene expression in the hIPod versus the hAKPC-P, while negative values indicate a higher gene expression in hAKPC-P. All fold variations listed are statistically significant

(P<0.05).

CONTRACTILITY MARKERS							
hA	hAKPC-P undifferentiated versus hIPod de-differentiated			hAKPC-P differentiated versus hIPod re-differentiated			
Gene	Fold Char	_	Fold Change		Fold Chang		Fold Change
ACTA1		MYH9		ACTA1	-3.30	MYH9	3.33
ACTA2	-1.63	MYL1		ACTA2	-1.42	MYL1	-2.45
ACTC1	1.10	MYL2	-1.18	ACTC1	-2.86	MYL2	
ACTG2		MYL3		ACTG2	-4.28	MYL3	-3.44
ACTN2		MYL4	-1.11	ACTN2	-2.69	MYL4	-3.10
ACTN3		MYL5	-1.20	ACTN3		MYL5	-2.76
ACTN4		MYL6	-1.18	ACTN4	1.62	MYL6	-1.79
AGT	-1.08	MYL6B		AGT		MYL6B	
ANXA6	-1.20	MYL9		ANXA6	3.13	MYL9	1.68
ARHGAP24	-1.83	MYLK		ARHGAP24	-1.45	MYLK	
ARID5B	-1.71	MYLK2		ARID5B		MYLK2	-3.30
Arp2/3		MYLPF	1.01	Arp2/3		MYLPF	-2.62
AVP		MYO10	-1.53	AVP		MYO10	2.61
C3	1.53	MYO1B	-1.15	C3	12.61	MYO1B	9.19
CALCB	-1.52	MYO1C	-1.10	CALCB	-3.08	MYO1C	3.29
CAPZA1	1.07	MYO1D	3.02	CAPZA1	1.72	MYO1D	
CAPZA2		MYO1E	-1.14	CAPZA2	-1.39	MYO1E	2.12
CAPZB	-1.09	MYO6	1.23	CAPZB	2.42	MYO6	7.23
CASQ1		MYOCD	1.01	CASQ1	-3.12	MYOCD	4.38
CAV1	-1.52	MYOF	-1.04	CAV1	33.76	MYOF	17.44
CAV3	-1.44	MYOM1	-1.04	CAV3	-3.09	MYOM1	-2.57
CD2AP	1.44	MYOM2	-1.04	CD2AP	10.04	MYOM2	-2.79
CNN1	1.95	Myosin2		CNN1		Myosin2	
COL4A3BP	-1.07	MYOT		COL4A3BP	1.77	MYOT	-3.05
CTGF	-1.14	NEB		CTGF	4.63	NEB	
CTSL2	1.36	NKX2-5	-1.11	CTSL2		NKX2-5	-2.30
CTTN	-1.18	NMU	-1.23	CTTN	4.01	NMU	-2.33
CXCR4	-1.02	NOS1	-1.05	CXCR4	-2.00	NOS1	-2.72
DES		NPHS1	-1.26	DES	-3.06	NPHS1	-3.66
DTNA		NPHS2		DTNA		NPHS2	-2.81
EDN1	-2.00	PAR3-PAR6-aPK	C	EDN1	9.06	PAR3-PAR6-aPKC	
EDN2	-1.57	PLCE1	-1.39	EDN2	-2.78	PLCE1	4.61
EGF	1.58	PXN	-1.60	EGF	-1.90	PXN	
ELANE	-1.00	RHOA	1.03	ELANE	-3.39	RHOA	1.63
EZR	-1.02	ROCK1	1.73	EZR	4.15	ROCK1	10.32
F Actin		ROCK2	1.10	F Actin		ROCK2	3.01
FKBP1A	-1.31	RRAD	1.10	FKBP1A	5.14	RRAD	1.54
FLT1	-1.21	SGCA	-1.11	FLT1	-2.22	SGCA	-3.30
GJA1	-2.54	SLN	1.62	GJA1	10.16	SLN	
GJC1		SMAD5	1.05	GJC1		SMAD5	7.26
HOMER1		SMPX		HOMER1		SMPX	
HSBP1	1.62	SMTN	-1.49	HSBP1	4.04	SMTN	1.52
ID1	-1.68	SNTA1	1.05	ID1		SNTA1	-2.14
ID2	-1.72	SNTB1	1.10	ID2		SNTB1	2.06
ID3	-1.36	SPHK1	1.40	ID3		SPHK1	1.65
IGF1	-1.26	SRF		IGF1	-3.87	SRF	-2.23
ILK		SRI	-1.08	ILK	1.33	SRI	15.44
INF2		SRSF1	1.13	INF2		SRSF1	-1.64
ITGA2	-1.22	SYNPO	-1.38	ITGA2	12.32	SYNPO	-1.99
JSRP1	-1.12	TAC3	-1.11	JSRP1	-3.18	TAC3	-2.77
KNG1		Talin		KNG1		Talin	
MAP2K1	-1.32	TNNC1	-1.10	MAP2K1	3.34	TNNC1	-3.74
MAP2K3		TNNC2	-1.15	MAP2K3	-1.34	TNNC2	-3.64
MAP2K6	-1.29	TNNI1	-1.14	MAP2K6	-3.94	TNNI1	-3.40
MBNL1	1.27	TNNI2	-1.10	MBNL1	-1.37	TNNI2	-3.68
MMP1	-10.88	TNNI3	-1.03	MMP1	-1.33	TNNI3	-2.67
MYBPC1		TNNT1	-1.37	MYBPC1		TNNT1	-1.71
MYBPC2	-1.16	TNNT2	-1.26	MYBPC2	-2.88	TNNT2	-4.69
MYBPC3	-1.02	TNNT3	-1.08	MYBPC3	-3.06	TNNT3	-3.61
МҮВРН	-1.09	TPM1		МҮВРН	-3.78	TPM1	
MYH1	-1.06	TPM2	-1.73	MYH1		TPM2	1.55
MYH10		Tpm4		MYH10	1.72	Tpm4	
MYH11		TRPV1	-1.13	MYH11		TRPV1	
MYH13	-1.12	TTN	-1.09	MYH13	-3.04	TTN	-2.84
MYH14	-1.06	UCN	-1.19	MYH14	-3.71	UCN	-3.23
MYH2	-1.26	UTRN	-1.02	MYH2	-2.43	UTRN	5.28
MYH4	-1.21	UTS2		MYH4	-2.87	UTS2	
MYH6	-1.08	VCL	-1.10	МҮН6	-3.14	VCL	3.39
MYH7	-1.00	VEGFB	-1.10	MYH7	-2.37	VEGFB	
		* EGI B			-2.3/	720,0	