SRGAP1 controls small Rho GTPases to regulate podocyte foot process maintenance

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Supplemental Material

Supplemental Figure 1. Podocyte Rho GTPase network analysis, corresponding to Figure 1.

Supplemental Figure 2. ISH analysis of *Srgap1*/2/3 expression, corresponding to Figure 1.

Supplemental Figure 3. Analysis of SRGAP1 expression, corresponding to Figure 2.

Supplemental Figure 4. Characteristics of experimental mice, corresponding to Figure 2&3.

Supplemental Figure 5. Characteristics of experimental mice, corresponding to Figure 3.

Supplemental Figure 6. Analysis of subcellular SRGAP1 localization, corresponding to Figure 4.

Supplemental Figure 7. Analysis of *SRGAP1* KO podocytes, corresponding to Figure 5

Supplemental Figure 8. Analysis of *SRGAP1* KO podocytes, corresponding to Figure 5

Supplemental Figure 9. SRGAP1 interactome, corresponding to Figure 5.

Supplemental Figure 10. PEMP of *Srgap1* mice, corresponding to Figure 6.

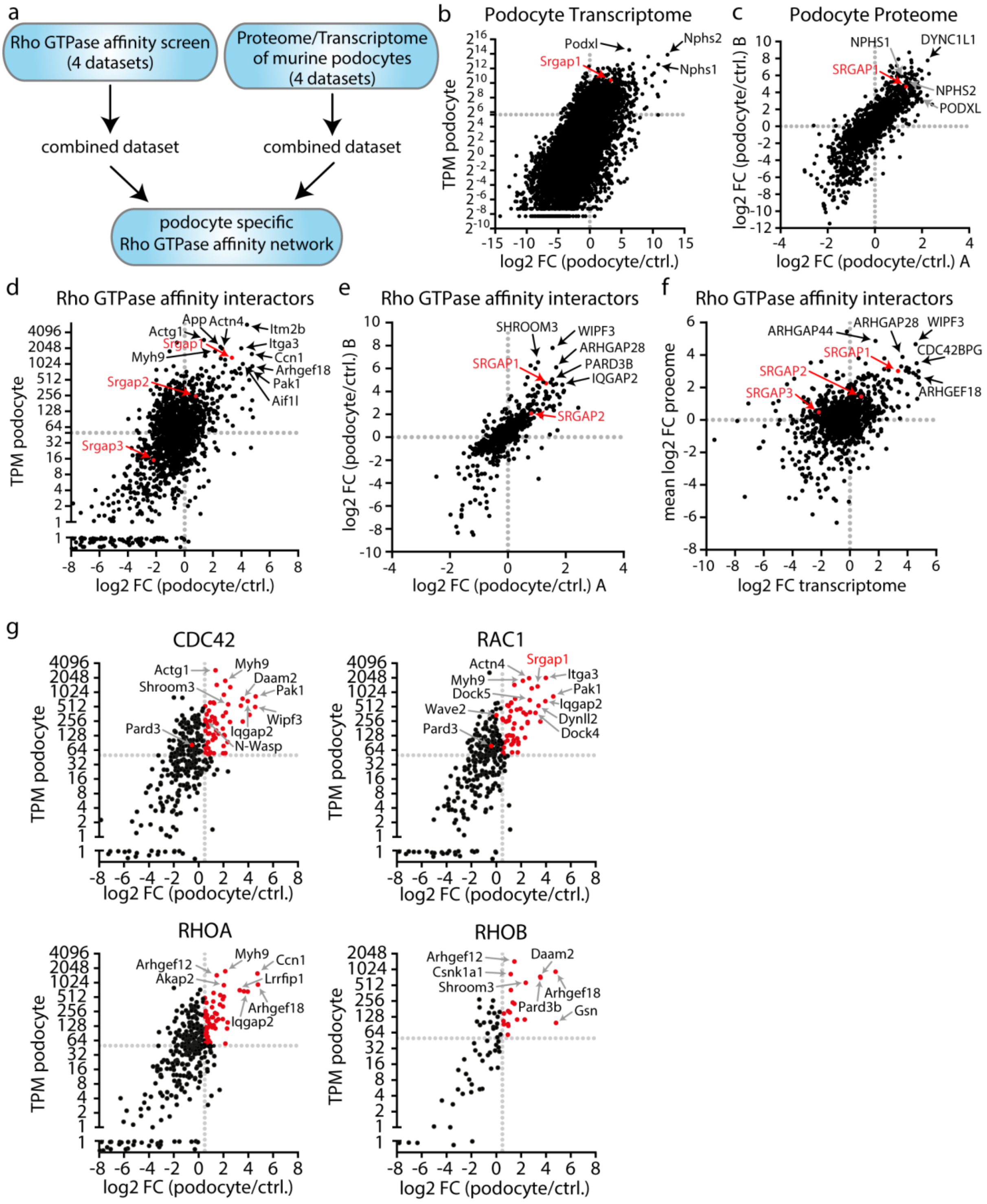
Supplementary Table 1. Antibodies.

Supplementary Table 2. In situ hybridization primer.

Supplementary Table 3. Rho GTPase expression in murine podocytes.

Supplementary Table 4. RhoGEF & RhoGAP expression in murine podocytes.

Supplemental Figure 1



Supplemental Figure 1

(a) Schematic depicting the generation of a podocyte specific Rho GTPase affinity interaction network.

(b) Volcano plot of transcriptome analysis of isolated murine podocytes analyzed and assembled from open available and published datasets[1, 2] showed highly selective enrichment in podocytes for *Podxl*, *Nphs1*, *Nphs2* and *Srgap1*.

(c) Volcano plot of proteome analysis of isolated murine podocytes analyzed and assembled from published datasets[3, 4] showed highly podocyte specific enrichment for PODXL, NPHS1, NPHS2, DYNC1L1 and SRGAP1.

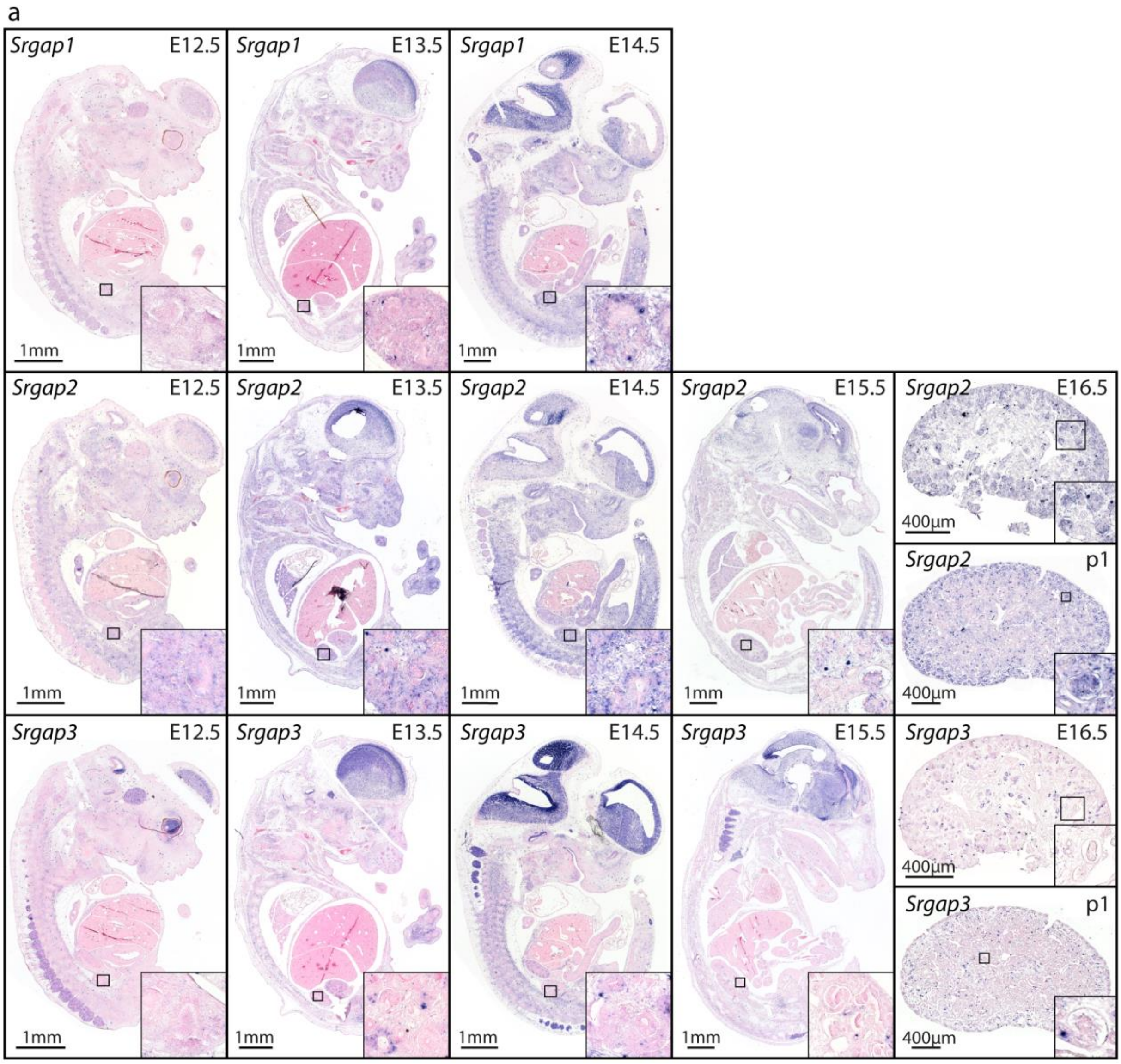
(d) Volcano plot of podocyte transcriptome data filtered for mapped Rho GTPase affinity interactions demonstrated highly specific enrichment of *Srgap1* and other known hereditary nephrosis genes like *Actn4* and *Itga3* as well as novel podocyte specific Rho GTPase interacting genes.

(e) Volcano plot of podocyte proteome filtered for mapped Rho GTPase affinity interactors showed highly specific enrichment of SRGAP1 and known as well as novel podocyte specific Rho GTPase interacting proteins.

(f) Volcano plot comparing podocyte transcriptome and proteome data filtered for mapped Rho GTPase affinity interactors showing podocyte enrichment of SRGAP1.

(g) Rho GTPase affinity interactome mapping confirmed RAC1, CDC42, RHOA and RHOB as central nodes for cytoskeletal signaling in podocytes. Volcano plots show transcriptome analysis of isolated murine podocytes filtered for proximity interactors of *Rac1*, *Cdc42*, *Rhoa* and *Rhob* (TPM – transcripts per million; FC – fold change).

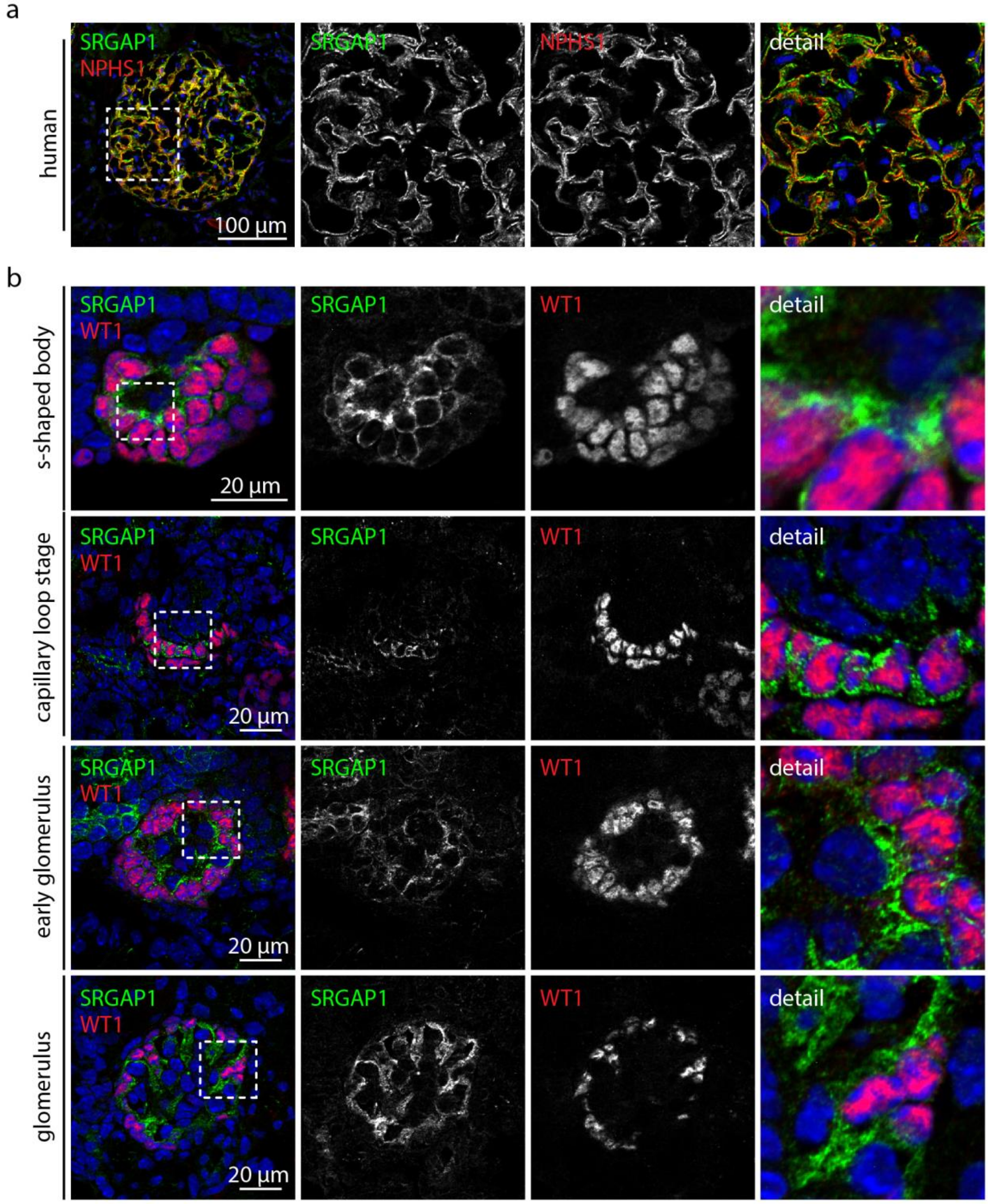
Supplemental Figure 2



Supplemental Figure 2

(a) mRNA in situ hybridization confirmed expression of *Srgap2* and no detectable expression of *Srgap3* in murine podocytes (boxes indicate magnified areas; overviews are stitched from multiple pictures). mRNA in situ hybridization of *Srgap1 at E12.5 to 14.5* (corresponding to main Figure 1),

Supplemental Figure 3

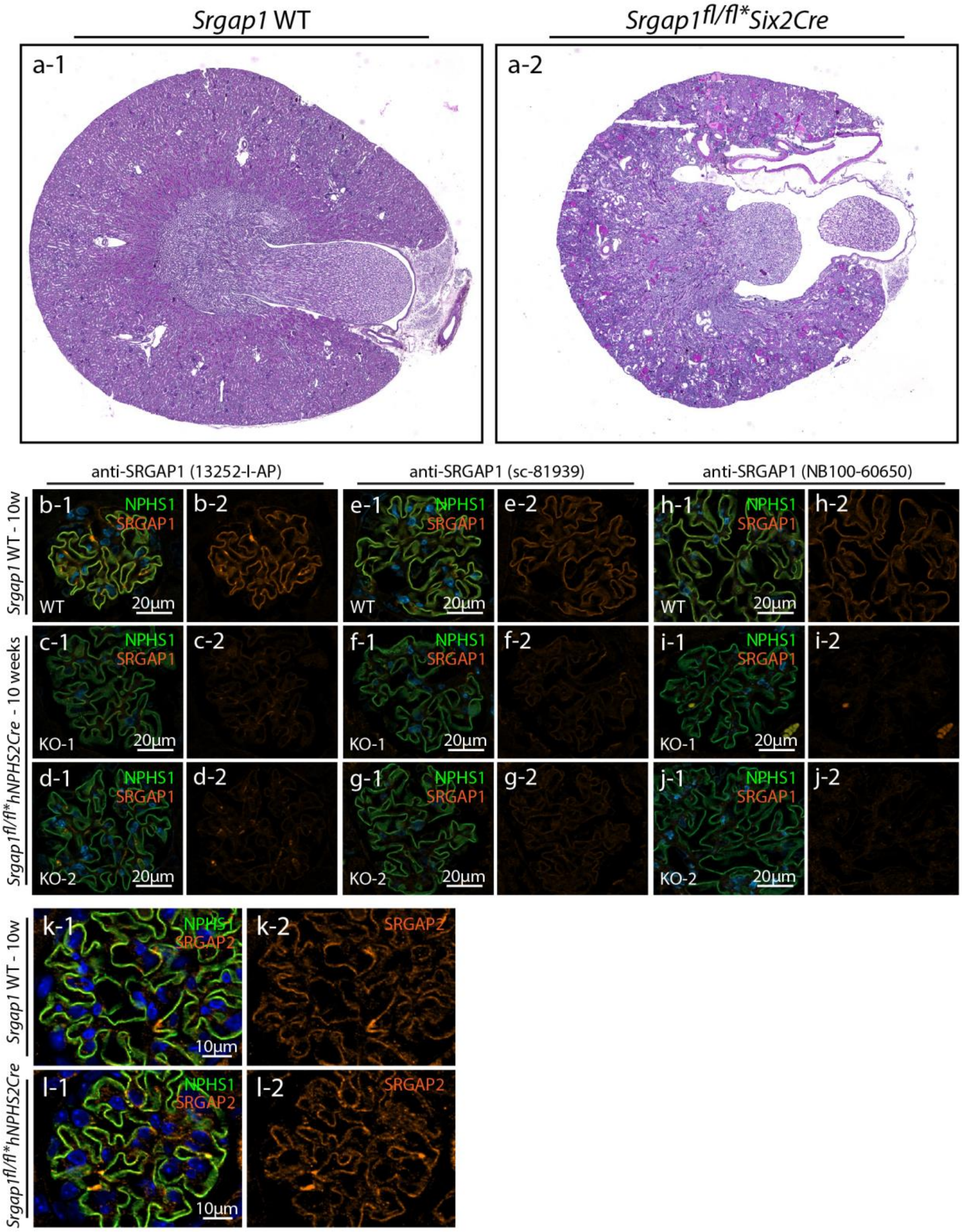


Supplemental Figure 3

(a) Immunofluorescence staining of human kidney section for SRGAP1 and the podocyte marker NPHS1 demonstrated specific localization of SRGAP1 in human podocytes *in vivo* (box indicates magnified area).

(b) Immunofluorescence staining of developing murine nephrons for SRGAP1 and the podocyte marker WT1 demonstrated specific localization of SRGAP1 in podocytes (boxes indicate magnified areas).

Supplemental Figure 4



Supplemental Figure 4

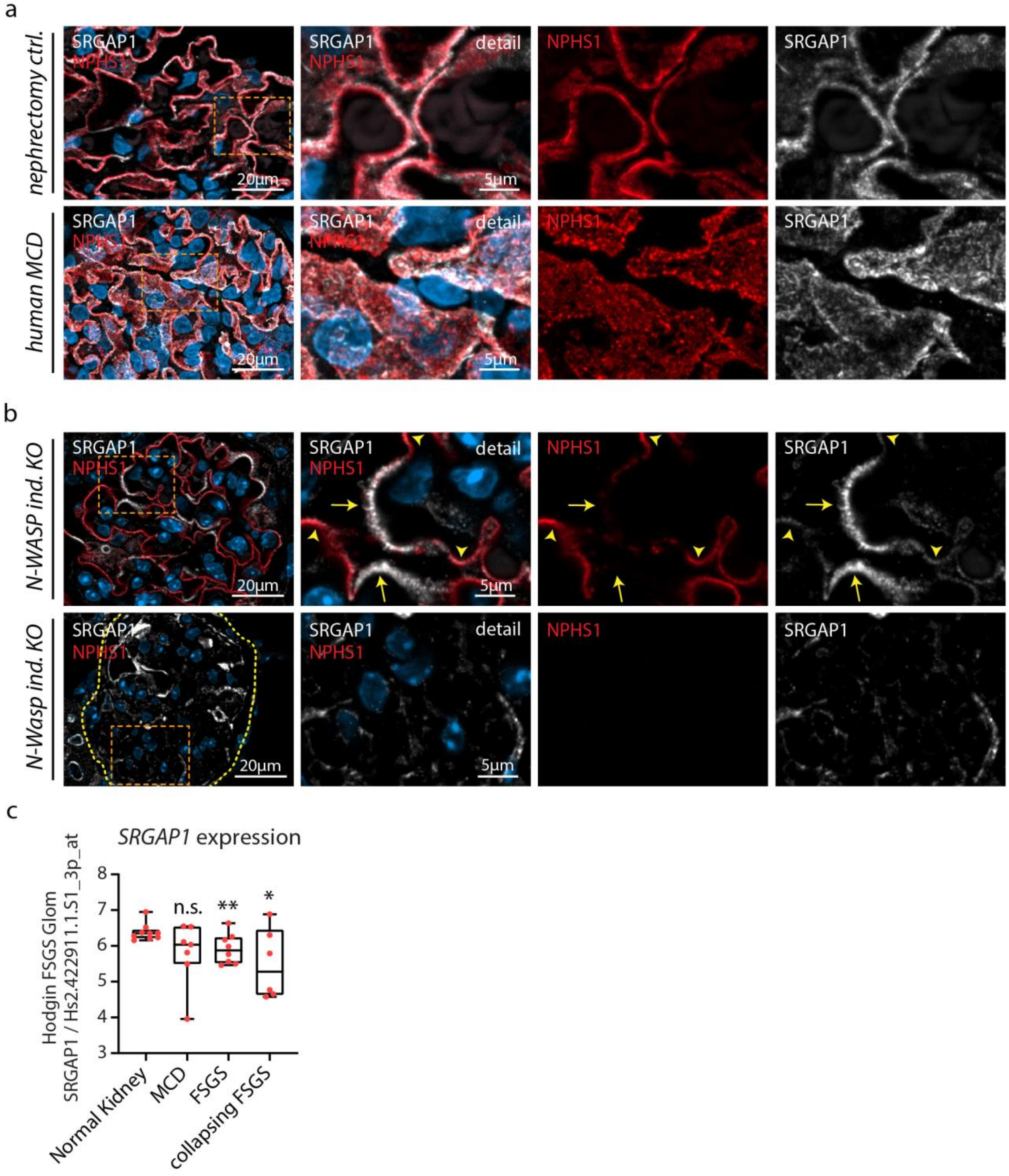
(a) Overview histology of wild type and *Srgap1*$^{fl/fl}$**Six2Cre* kidney sections demonstrated proteinaceous casts, dilated tubules, focal obliteration and sclerosis of glomeruli in kidneys of

KO mice (overview images for PAS staining presented in Figure 2f; overviews were stitched from multiple pictures).

(b-j) Immunofluorescence of murine kidney sections of *Srgap1* WT and *Srgap1*$^{fl/fl}$**hNPHS2Cre* KO mice for SRGAP1 and NPHS1 demonstrated loss of SRGAP1 signal in podocytes of KO mice by 3 independent antibodies (for details about individual antibodies see material and methods section).

(k-l) Levels ofSRGAP2 signal was not obviously altered in *Srgap1*$^{fl/fl}$**hNPHS2Cre* mice as demonstrated by immunofluorescence for SRGAP2 and NPHS1.

Supplemental Figure 5



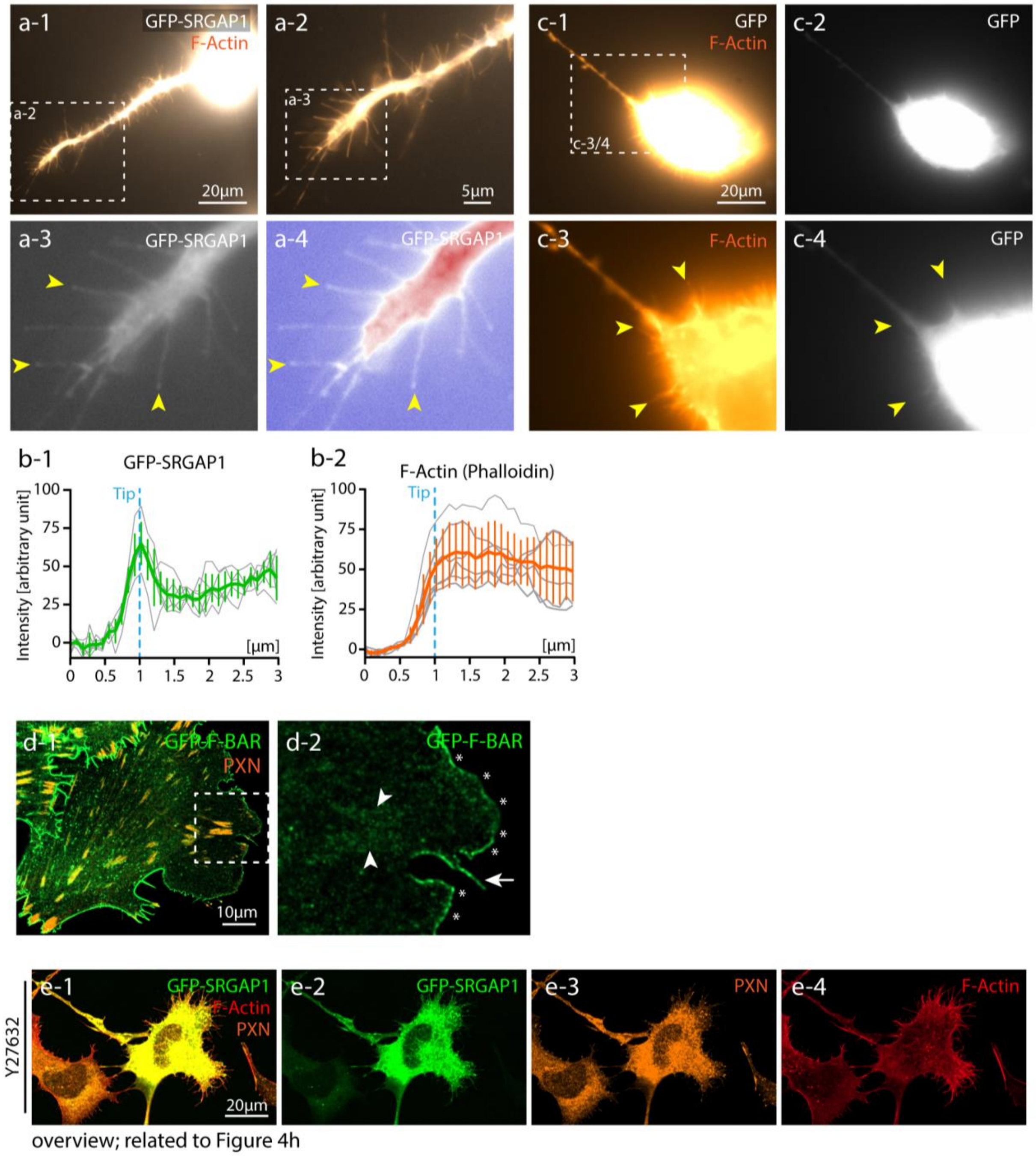
Supplemental Figure 5

(a) Immunofluorescence analysis of human nephrectomy and minimal change disease (MCD) specimens showed only slight alterations of SRGAP1 signal (SDs were co-stained by NPHS1; boxes indicate magnified areas).

(b) Immunofluorescence analysis of a genetic FSGS model demonstrated increased recruitment of SRGAP1 to glomerular regions with diminished levels of NPHS1 signal intensities (indicative of SD degradation - yellow arrows; yellow arrowheads mark regions with unaffected NPHS1 and SRGAP1 signals). Strongly diseased glomeruli show pronounced decrease in SRGAP1 signal and loss of NPHS1 signal as evaluated by immunofluorescence straining.

(c) Analysis of *SRGAP1* mRNA expression in human glomerular disease using microarrays of the “Hodgin FSGS Glom” dataset deposited in the *Nephroseq* database (scatter dots indicate individual cases; n.s. non-significant, *p<0.05, **p<0.01).

Supplemental Figure 6



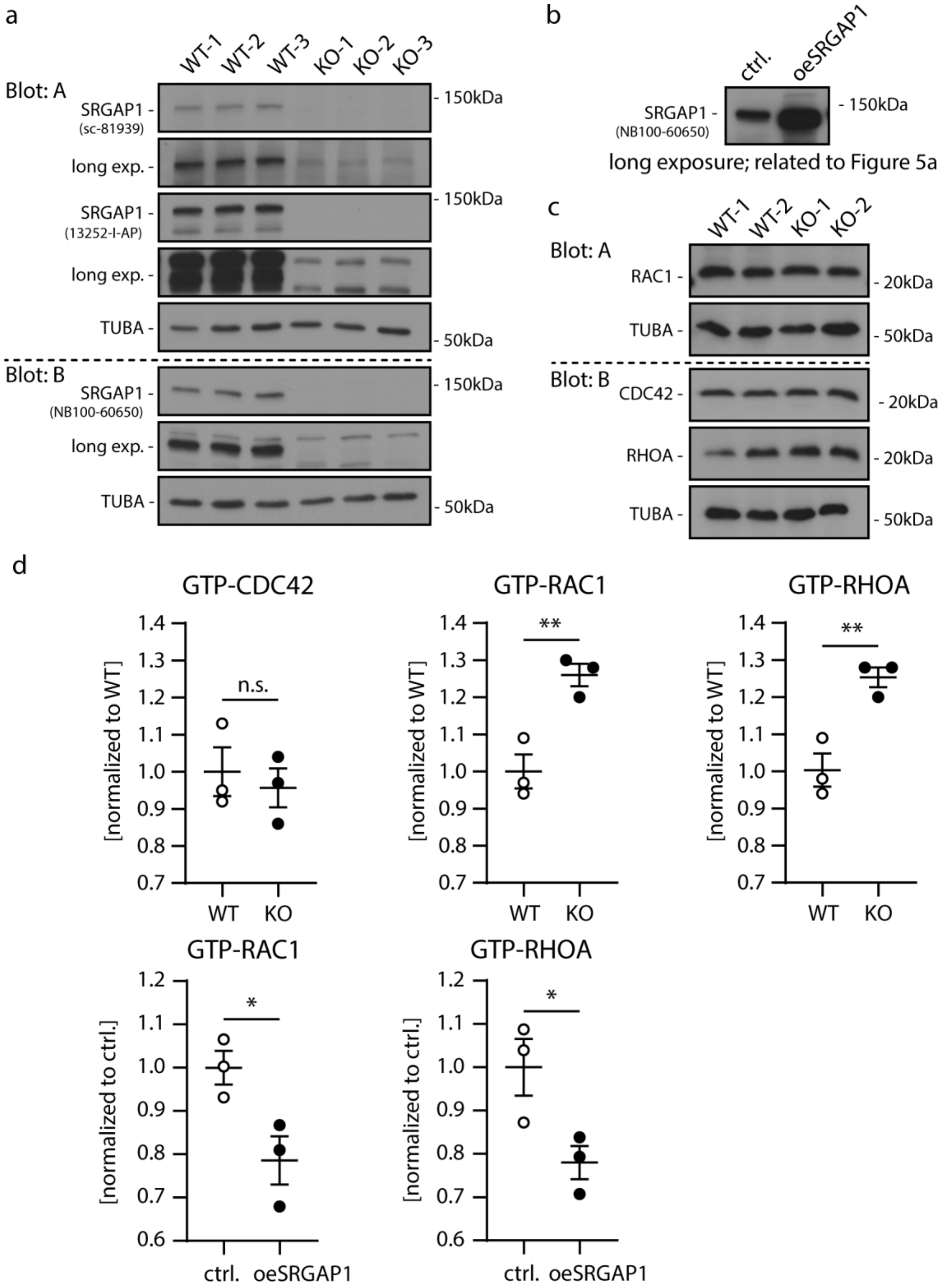
Supplemental Figure 6

(a-c) Immunofluorescence analysis demonstrated enhanced cytoplasmic localization of GFP-SRGAP1 to podocyte 3D protrusions *in vitro* (arrowheads indicate filopodial protrusions). GFP was expressed as control.

(d) Recruitment to lamellipodia and filopodia but not to IACs is probably mediated by the F-BAR domain of SRGAP1 as indicated by a SRGAP1 GFP-F-BAR domain reporter.

(e) Subcellular distribution of GFP-SRGAP1, PXN and F-Actin (Phalloidin) in Y27632 treated podocytes (overview related to Figure 4h).

Supplemental Figure 7



Supplemental Figure 7

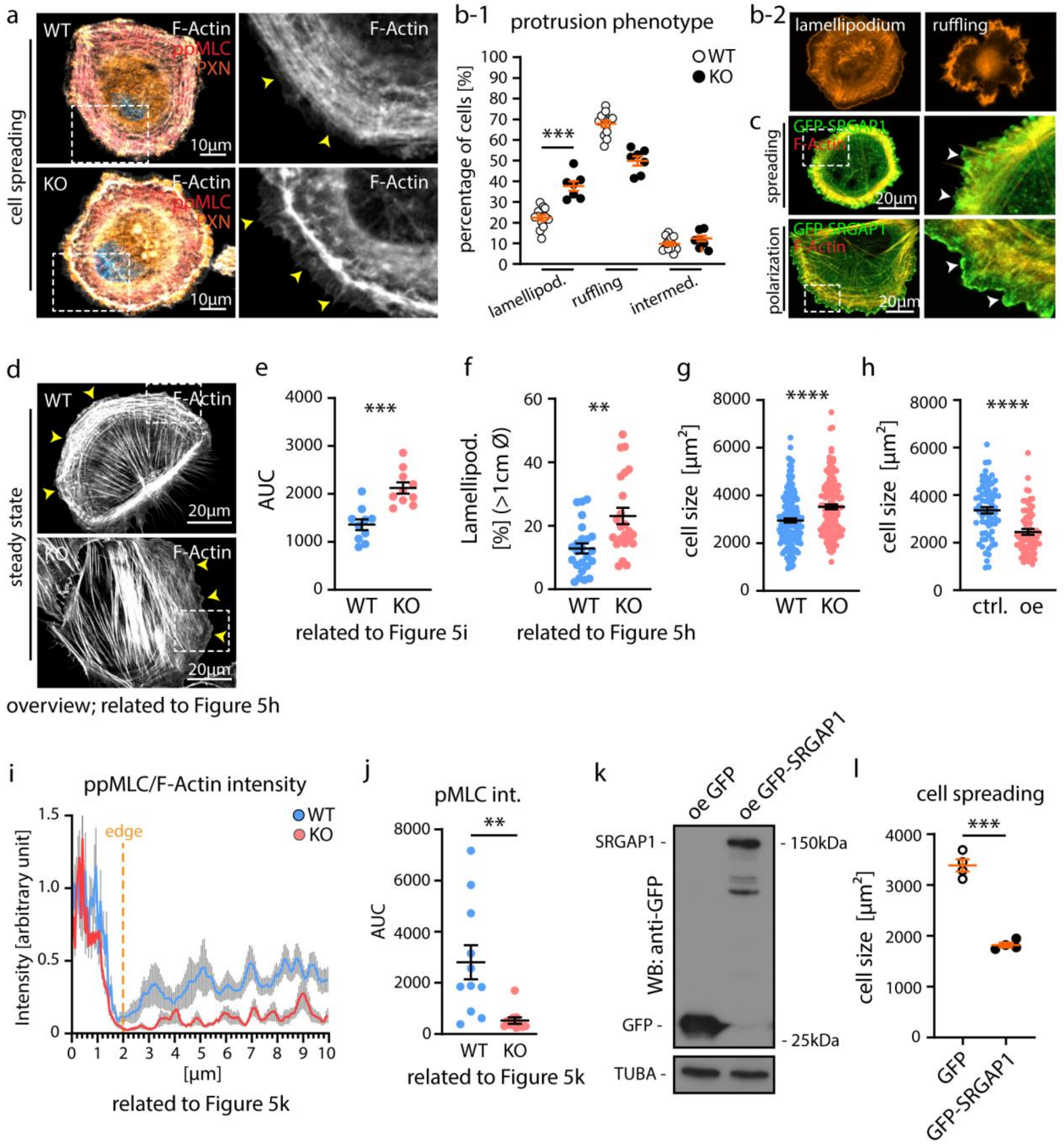
(a) Western blot analysis of CRISPR/Cas9 genome edited *SRGAP1* WT and KO podocyte clones. Loss of SRGAP1 signal was validated by 3 independent antibodies (exp. - exposure).

(b) Western blot analysis of SRGAP1 overexpression and control podocytes Long exposure immunoblot related to SRGAP1 expression analysis shown in Figure 5a.

(c) Western blot analysis of *SRGAP1* WT and KO podocyte for expression of the Rho GTPases RAC1, CDC42 and RHOA.

(d) Quantification of GTP-CDC42, GTP-RAC1 and GTP-RHOA levels in *SRGAP1* WT, *SRGAP1* KO, SRGAP1 overexpression and control podocytes (n=3 replicates; *p<0.05, **p<0.01).

Supplemental Figure 8



Supplemental Figure 8

(a) Spreading *SRGAP1* KO podocytes exhibited increased lamellipodia formation (arrowheads). Podocytes were co-stained for F-Actin and PXN (boxes indicate magnified areas).

(b) Quantification of protrusion phenotypes of spreading *SRGAP1* KO and WT podocytes (scatter dots indicate independent experiments; *** p<0.001; bi-2 shows representative images for lamellipodium and ruffling cells).

(c) GFP-SRGAP1 localized to lamellipodia (arrowhead) during spreading and subsequent polarization phase.

(d) *SRGAP1* KO podocytes showed extended and widened lamellipodia (arrowheads) and lamella at steady state (full spread) conditions (boxes indicate magnified areas shown in main Figure 5k).

(e) Corresponding to line scan analysis shown in main Figure 5i areas under the curve (AUC) were quantified for the lamellipodia region (10 cells per condition were analyzed; *** $p<0.001$).

(f) Quantification of cellular circumference covered by widened (>1 µm) lamellipodia (24 WT and 23 KO podocytes at steady state were analyzed; ** $p<0.01$).

(g-h) Podocyte cell size is modulated due to expression levels of *SRGAP1* (161 WT-1&2, 134 *SRGAP1* KO-1&2, 69 control and 66 SRGAP1 overexpression cells were analyzed; **** $p<0.0001$).

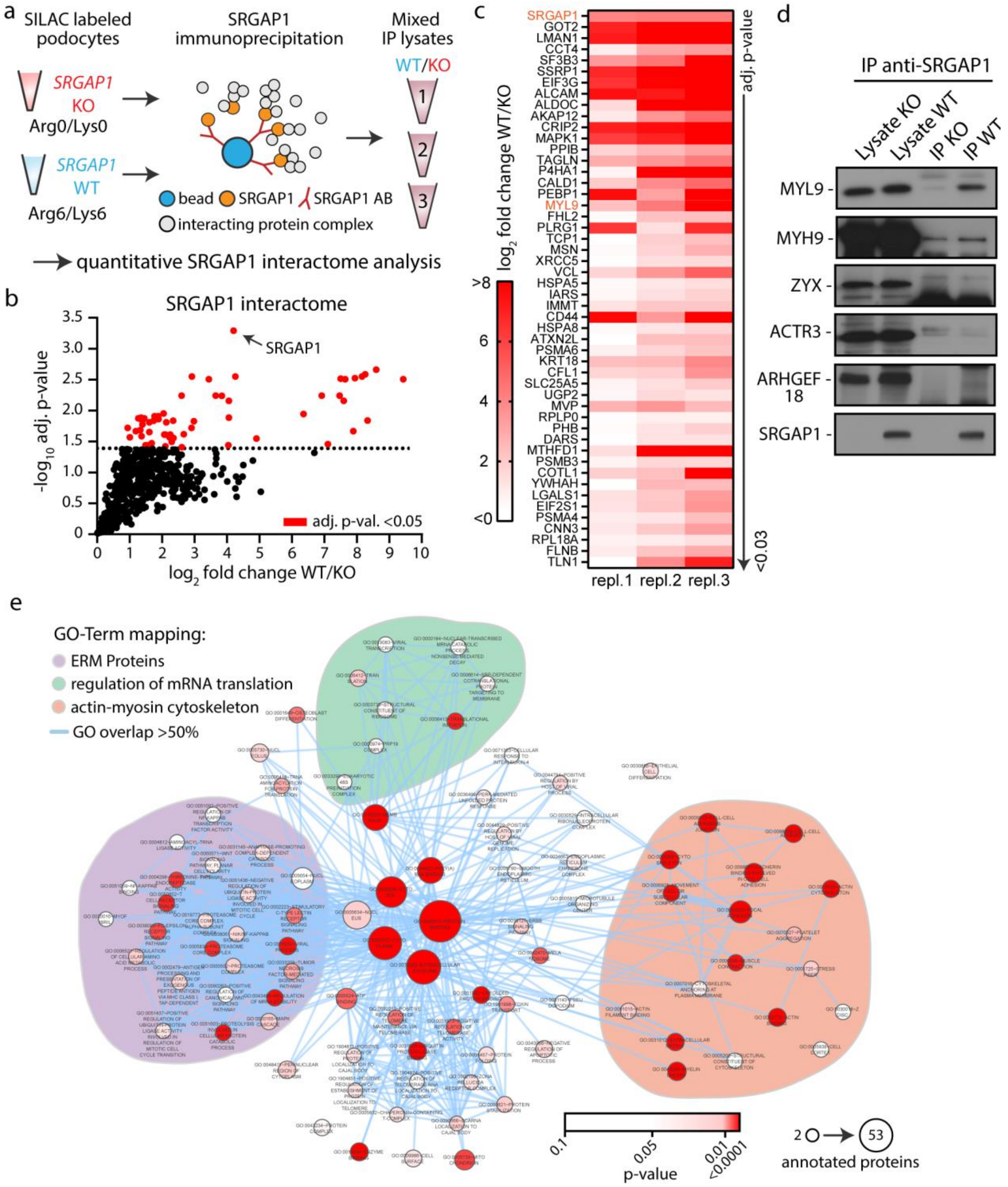
(i) Corresponding to line scan analysis shown in main Figure 5k immunofluorescence analysis of pMYL9 was correlated to F-Actin (Phalloidin) intensity (line scans were analyzed for 11 cells per genotype; lines show mean and error bars indicate SEM)

(j) Corresponding to line scan analysis shown in main Figure 5k areas under the curve (AUC) were quantified for the lamellipodia region (11 cells per condition were analyzed; ** $p<0.01$).

(k) Western blot analysis of GFP or GFP-SRGAP1 overexpression podocyte.

(l) Overexpression of GFP-SRGAP1 inhibited podocyte spreading (GFP overexpression was used as control; dots indicate independent experiments, >85 cells per experiment and genotype; *** $p<0.001$).

Supplemental Figure 9



Supplemental Figure 9

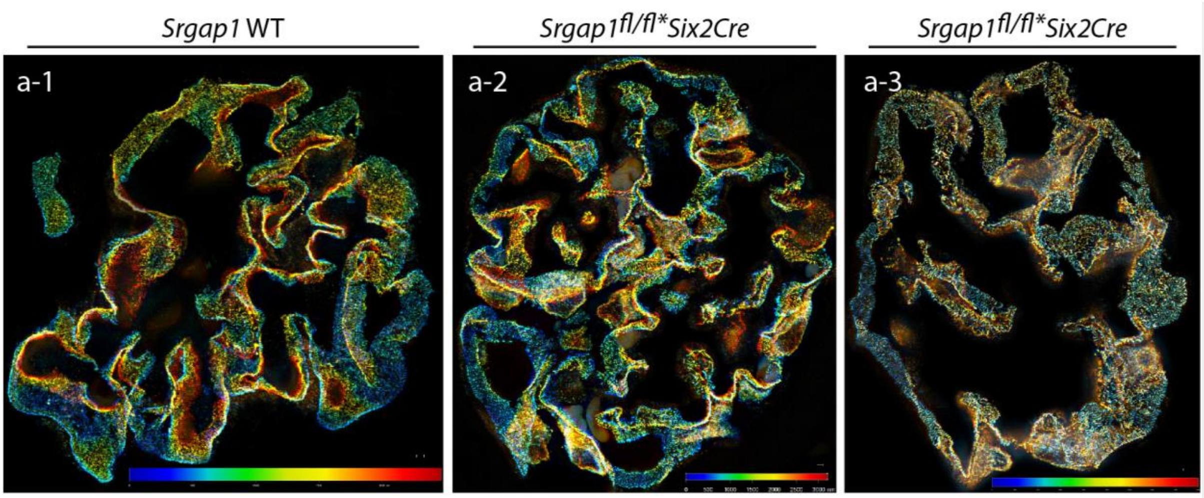
(a) Schematic depicting SILAC labeling strategy for interactome analysis of SRGAP1 via endogenous immunoprecipitation (IP).

(b-c) Analysis of SRGAP1 interactome data per volcano plot and heat map identified significant enriched affinity interactors for SRGAP1 (n=3 independent replicates).

(d) Endogenous IP experiments for SRGAP1 confirmed co-precipitation of Myosin Regulatory Light Chain 2 (MYL9).

(e) GO-Term analysis for the podocyte SRGAP1 interactome revealed enrichment of GO-Terms related to ERM protein signaling, regulation of mRNA translation and actin-myosin cytoskeleton regulation.

Supplemental Figure 10



Supplemental Figure 10

(a) Overviews of 3D SIM microscopy in respective WT and KO animals corresponding to Figure 6k.

Supplementary Table 1

Primary Antibodies

Target	Clone	Species	Manufacturer	Application
NPHS1	GP-N2	guinea pig	PROGEN	IF FFPE tissue (1:400, HIAR pH9), cryo tissue (1:300)
p-MYL9, Phospho-Myosin Light Chain 2 (Ser19)	#3671	rabbit	Cell Signaling	IF cells (1:100)
p-MYL9, Phospho-Myosin Light Chain 2 (Thr18/Ser19)	#3674	rabbit	Cell Signaling	IF cells (1:100), WB (1:1000)
PXN	610051	mouse IgG1	BD Biosciences	IF cells (1:300)
TUBA	T9026 (DM1A)	mouse IgG1	Merck KGaA	WB (1:10000)
CTTN	#3503	rabbit	Cell Signaling	IF (1:50)
WT1	05-753	mouse	Millipore	IF cryo tissue (1:100)
SRGAP1	13252-I-AP	rabbit	Proteintech	IF FFPE tissue (1:200, HIAR pH9), WB (1:1000), IP 2µg, human samples (1:200, HIAR pH9 for 15min)
SRGAP1	NB100-60650	rabbit	Novus Biologicals	IF FFPE tissue (1:300, HIAR pH9), WB (1:1000)
SRGAP1 (SQ-6)	sc-81939	mouse	Santa Cruz	IF FFPE tissue (1:50, HIAR pH9), WB (1:250)
ILK	#3862	rabbit	Cell Signaling	IF FFPE tissue (1:200, HIAR pH9)
ITGB1 (CD29)	610467	mouse IgG1	BD Biosciences	IF FFPE tissue (1:200, HIAR pH9)
NPHS2	P0372	rabbit	Sigma-Aldrich	IF FFPE tissue (1:600, HIAR pH9)
TOM20	sc-11415	rabbit	Santa Cruz	IF FFPE tissue (1:400, HIAR pH9)
MYL9, MLC (Myosin light chain)	#8505	rabbit	Cell Signaling	WB (1:1000)
MYH9, NMHC-IIA (Myosin II)	PRB-440P	rabbit	Covance	WB (1:1000)
CFL1 (Cofilin)	#3318	rabbit	Cell Signaling	WB (1:1000)
CFL1 Phospho-Cofilin (Ser3)	#3311	rabbit	Cell Signaling	WB (1:1000)
ZYX	HPA004835	rabbit	Atlas Antibodies	WB (1:1000)
ARHGEF18	HPA042689	rabbit	Atlas Antibodies	WB (1:1000)
SRGAP2	HPA028191	rabbit	Atlas Antibodies	IF FFPE tissue (1:100, HIAR pH9)
ACTR3 (ARP3)	ab151729	rabbit	Abcam	WB (1:5000)
RAC1	240106	mouse	Cell Biolabs	WB (1:1000)
RHOA	ARH03	mouse	Cytoskeleton	WB (1:500)
CDC42	#2462	rabbit	Cell Signaling	WB (1:1000)

Secondary Antibodies

Name	ID	Species	Manufacturer	Application
Alexa Fluor Phalloidin 488/555			Thermo Fisher Scientific	cells (1:200-750)
DAPI			Thermo Fisher Scientific	cells/tissue (1:1000)
Alexa Fluor 555, donkey anti-rabbit IgG	A-31572	rabbit	Thermo Fisher Scientific	cells/tissue (1:500)
Alexa Fluor 488, goat anti-guinea pig IgG	A-11073	giunea pig	Thermo Fisher Scientific	cells/tissue (1:500)
Alexa Fluor 555, goat anti-mouse IgG1	A-21127	mouse IgG1	Thermo Fisher Scientific	cells/tissue (1:500)
Alexa Fluor 488, goat anti-mouse IgG1	A-21121	mouse IgG1	Thermo Fisher Scientific	cells/tissue (1:500)
Goat anti-rabbit IgG, HRP-linked Antibody	#7074	rabbit	Cell Signaling	WB (1:5000)
Goat anti-mouse Immunglobulins/HRP	P0447	mouse	Dako	WB (1:10000)
Alexa Fluor 647, goat anti-guinea pig IgG	A-21450	giunea pig	giunea pig	tissue (1:400)

Supplementary Table 2

ISH	
Primer	**Sequence 5'-3'**
Srgap1_Exon 3_fw	AGGTTCATGGCCAAAACAAG
Srgap1_Exon 3_rv	GTGAAGCTGGAACGCAATCT
Srgap1_CDS_fw	ACAATCTGGCCATTTGCT
Srgap1_CDS_rv	TCAGTCGGGGAGTTCATG
Srgap1_fw	AGCCTGCTGTTCTTCCAAAA
Srgap1_rv	TGCTTGTTGTCGGTTGCT
Srgap2_CDS_fw	ATGTCCGCATTGAGGAGA
Srgap2_CDS_rv	GCCTCCATTGTCTTT
Srgap3_CDS_fw	GAACAAGCTCAAGTGCAC
Srgap3_CDS_rv	CTTTTGGCGATGTTGATT

Supplementary Table 3

Rho GTPases		**Podocyte transcriptome**				**Podocyte proteome**				
Ensembl transcript	**Gene names**	**mean podocyte TPM**	**log2 FC (podocyte/non-podocyte TPM based)**	**log2(FC) DESeq2**	**Adj. p-val. DESeq2**	**-Log t-test p value (Schell et al.)**	**t-test Difference (Schell et al.)**	**-Log t-test p value (Rinschen et al.)**	**t-test Difference (Rinschen et al.)**	**mean t-test Difference**
ENSMUSG00000007815	Rhoa	400.53	-0.16	0.20	5.94E-01	2.01	0.61	2.72	1.12	0.87
ENSMUSG00000054364	Rhob	357.98	1.72	2.05	2.44E-02	0.02	0.01	0.63	0.38	0.19
ENSMUSG00000006699	Cdc42	318.35	-0.27	0.20	5.27E-01	0.75	-0.18	2.77	0.67	0.24
ENSMUSG00000001847	Rac1	317.13	-1.34	-0.94	4.52E-04	0.72	-0.20	1.93	0.34	0.07
ENSMUSG00000017144	Rnd3	54.73	-0.32	0.12	8.22E-01			1.10	1.04	1.04
ENSMUSG00000024143	Rhoq	42.05	0.05	0.54	1.03E-01					
ENSMUSG00000002233	Rhoc	33.40	0.19	0.58	4.90E-01	1.01	-0.24	0.42	-0.58	-0.41
ENSMUSG00000073982	Rhog	23.89	-1.04	-0.68	2.09E-01	2.08	-0.52	0.62	0.26	-0.13
ENSMUSG00000022075	Rhobtb2	13.59	-0.93	-0.44	1.39E-01					
ENSMUSG00000054855	Rnd1	7.59	1.03	2.69	2.65E-02					
ENSMUSG00000046768	Rhoj	5.81	-2.95	-2.56	2.95E-02			0.57	-1.82	-1.82
ENSMUSG00000029449	Rhof	4.70	1.35	0.96	1.65E-01					
ENSMUSG00000001313	Rnd2	3.52	-1.85	-0.27	6.84E-01					
ENSMUSG00000041845	Rhod	3.39	-1.97	-1.60	1.74E-02					
ENSMUSG00000019944	Rhobtb1	2.42	-3.80	-2.75	1.74E-13					
ENSMUSG00000033220	Rac2	1.68	-1.78	-0.70	5.59E-01					
ENSMUSG00000018012	Rac3	0.67	-1.99	-1.50	1.12E-02					
ENSMUSG00000039960	Rhou	0.46	-7.11	-7.61	3.39E-16					
ENSMUSG00000029204	Rhoh	0.16	-2.57	-3.76	1.72E-03					
ENSMUSG00000034226	Rhov	0.11	-2.02	-2.05	1.70E-01					

Supplementary Table 4

RhoGAPs & RhoGEFs		Podocyte transcriptome				Podocyte proteome				
Ensembl transcript	**Gene names**	**mean podocyte TPM**	**log2 FC (podocyte/non-podocyte TPM based)**	**log2(FC) DESeq2**	**adj- p-val. DESeq2**	**-Log t-test p value (Schell et al.)**	**t-test Difference (Schell et al.)**	**-Log t-test p value (Rinschen et al.)**	**t-test Difference (Rinschen et al.)**	**mean t-test Difference**
ENSMUSG00000057315	Arhgap24	1520.71	4.18	4.34	8.46E-05	4.40	1.83	0.88	1.32	1.57
ENSMUSG00000059495	Arhgef12	1452.70	1.46	1.74	5.58E-04	6.35	0.81	0.82	1.60	1.21
ENSMUSG00000020121	Srgap1	1348.14	3.34	3.73	7.10E-07	6.67	1.32	6.22	4.70	3.01
ENSMUSG00000004568	Arhgef18	928.74	4.77	5.27	5.91E-86	5.90	1.33	4.53	3.90	2.61
ENSMUSG00000024043	Arhgap28	675.60	3.65	4.10	3.27E-09	4.28	1.67	3.65	6.09	3.88
ENSMUSG00000032875	Arhgef17	564.68	1.74	2.92	1.74E-09	4.30	0.70	3.20	2.53	1.62
ENSMUSG00000031523	Dlc1	491.77	0.50	0.76	5.38E-01	2.09	-0.24	0.11	0.27	0.01
ENSMUSG00000049807	Arhgap23	464.36	1.96	2.14	2.29E-02	5.07	0.72	4.47	3.67	2.19
ENSMUSG00000017631	Abr	415.66	1.18	1.56	2.26E-04	3.37	0.31	0.03	-0.02	0.15
ENSMUSG00000029032	Arhgef16	345.20	4.10	4.39	9.36E-06	5.14	1.67	8.35	4.65	3.16
ENSMUSG00000041444	Arhgap32	315.94	1.08	1.80	9.97E-06	3.37	0.95	4.65	5.99	3.47
ENSMUSG00000026425	Srgap2	249.27	0.79	1.27	8.16E-03	6.31	0.81	4.69	2.08	1.45
ENSMUSG00000058230	Arhgap35	224.34	-0.86	-0.43	2.43E-01	3.63	0.38	3.72	1.15	0.76
ENSMUSG00000027247	Arhgap1	217.99	0.68	1.03	1.04E-02	1.12	0.11	2.36	0.92	0.51
ENSMUSG00000021990	Spata13	185.11	-0.10	0.44	5.56E-01			3.31	1.97	1.97
ENSMUSG00000039031	Arhgap18	178.49	0.97	1.32	9.59E-02	6.22	1.01	0.70	-0.52	0.24
ENSMUSG00000041417	Pik3r1	160.05	-0.55	0.56	1.66E-01	0.92	0.08	1.88	1.15	0.62
ENSMUSG00000034801	Sos2	141.83	0.81	1.06	2.03E-02	5.16	0.66	3.21	2.89	1.77
ENSMUSG00000035133	Arhgap5	128.05	0.11	0.51	3.57E-01	2.82	0.45	2.72	1.22	0.83
ENSMUSG00000041225	Arhgap12	125.60	0.86	1.27	4.81E-10	4.76	0.82	2.54	3.60	2.21
ENSMUSG00000025555	Farp1	118.31	-0.33	0.17	6.94E-01	6.45	1.03	4.03	2.35	1.69
ENSMUSG00000037552	Plekhg2	111.69	-0.08	0.41	5.35E-01					
ENSMUSG00000040964	Arhgef10l	104.70	2.19	2.63	7.66E-06			1.57	1.48	1.48
ENSMUSG00000066406	Akap13	104.41	-1.55	-0.44	3.11E-01			0.36	-0.31	-0.31
ENSMUSG00000039585	Myo9a	99.24	-0.98	-0.60	1.66E-01			3.04	-4.97	-4.97
ENSMUSG00000040940	Arhgef1	95.00	0.08	0.40	4.14E-01	1.36	-0.09	0.14	0.07	-0.01
ENSMUSG00000032714	Syde1	91.95	0.38	1.36	1.72E-03			1.45	2.81	2.81
ENSMUSG00000024096	Ralbp1	91.10	0.49	0.95	6.32E-04	1.50	0.26	1.03	0.86	0.56
ENSMUSG00000022788	Fgd4	86.92	-0.76	0.16	7.71E-01			1.30	1.73	1.73
ENSMUSG00000036591	Arhgap21	86.57	-0.55	0.00	9.92E-01	0.42	0.09	1.13	0.47	0.28
ENSMUSG00000020640	Itsn2	86.54	-0.19	0.20	7.02E-01	0.49	0.03	2.42	0.76	0.40
ENSMUSG00000033389	Arhgap44	85.06	1.78	2.27	4.40E-06			2.59	4.87	4.87
ENSMUSG00000022263	Trio	84.53	-1.56	-1.09	3.27E-06	3.86	1.71	1.13	0.60	1.16
ENSMUSG00000030766	Arhgap17	78.10	2.01	1.83	5.80E-10	2.83	0.49	0.29	0.67	0.58
ENSMUSG00000036501	Fam13b	70.52	0.56	0.96	1.29E-03					
ENSMUSG00000001173	Ocrl	70.01	-0.10	0.50	2.44E-02	5.44	0.78	2.66	2.45	1.61
ENSMUSG00000033542	Arhgef5	66.03	-1.01	-0.66	1.89E-01			0.50	-0.66	-0.66

ENSMUSG00000022957	Itsn1	65.14	-0.65	-0.17	7.03E-01	3.59	0.34	2.38	1.13	0.74
ENSMUSG00000021215	Net1	64.77	-0.91	-0.43	4.50E-01					
ENSMUSG00000031511	Arhgef7	62.62	-0.82	-0.46	4.01E-01	2.99	-0.36	0.32	0.39	0.01
ENSMUSG00000071176	Arhgef10	62.05	0.06	0.57	3.24E-01			1.33	0.68	0.68
ENSMUSG00000039713	Plekhg5	58.17	0.93	1.29	7.81E-03					
ENSMUSG00000028894	Inpp5b	57.66	-0.33	0.30	6.66E-01	5.19	-0.89	2.93	-2.13	-1.51
ENSMUSG00000024241	Sos1	53.40	-1.11	-0.62	2.71E-02	4.51	0.37	0.60	1.49	0.93
ENSMUSG00000004677	Myo9b	50.11	-0.56	0.08	8.12E-01			0.33	-1.44	-1.44
ENSMUSG00000021662	Arhgef28	45.58	-0.19	0.27	7.70E-01			0.17	-0.41	-0.41
ENSMUSG00000009681	Bcr	44.76	-0.73	-0.24	5.58E-01			0.21	-0.58	-0.58
ENSMUSG00000039831	Arhgap29	39.21	0.95	0.37	6.86E-01	0.78	0.12	0.18	-0.19	-0.04
ENSMUSG00000048960	Prex2	38.84	-2.22	-1.53	1.68E-01			1.59	-3.60	-3.60
ENSMUSG00000037999	Arap2	32.55	-0.93	0.85	3.55E-01			4.39	-6.33	-6.33
ENSMUSG00000052609	Plekhg3	32.50	-0.48	-0.05	9.44E-01			0.05	0.14	0.14
ENSMUSG00000026024	Als2	30.47	-0.45	0.09	8.28E-01			1.28	-2.22	-2.22
ENSMUSG00000034037	Fgd5	30.42	-2.14	-1.66	2.29E-01	4.77	-1.98	3.13	-6.76	-4.37
ENSMUSG00000004562	Arhgef40	28.15	-1.66	-1.33	3.14E-05	2.96	-0.49	1.37	-1.76	-1.12
ENSMUSG00000032812	Arap1	27.05	-0.25	0.17	8.01E-01	2.70	-0.70	0.89	0.79	0.05
ENSMUSG00000052921	Arhgef15	25.02	-2.79	-1.71	2.37E-01	5.79	-1.13	2.05	-5.49	-3.31
ENSMUSG00000022799	Arhgap31	24.58	-2.54	-2.07	1.13E-01	6.13	-1.30	1.36	-0.85	-1.08
ENSMUSG00000034066	Farp2	22.74	-0.21	0.64	1.73E-01	4.16	0.82	2.52	3.01	1.91
ENSMUSG00000009621	Vav2	20.17	-0.92	-0.16	8.34E-01					
ENSMUSG00000036246	Gmip	19.81	0.15	0.70	1.64E-01			1.18	-0.87	-0.87
ENSMUSG00000036882	Arhgap33	19.67	-0.82	0.01	9.87E-01					
ENSMUSG00000031834	Pik3r2	19.44	0.96	1.54	1.52E-03			0.02	0.09	0.09
ENSMUSG00000033697	Arhgap39	18.90	-1.43	-0.92	2.88E-02					
ENSMUSG00000031216	Stard8	18.63	-2.02	-1.06	3.79E-01			1.31	-2.65	-2.65
ENSMUSG00000036452	Arhgap26	16.50	-2.25	-1.60	7.40E-02	5.38	-1.59	2.80	-6.34	-3.96
ENSMUSG00000020021	Fgd6	15.69	-2.38	-1.90	1.07E-02			0.13	-0.09	-0.09
ENSMUSG00000021895	Arhgef3	15.66	-1.99	-1.65	1.04E-01			0.59	-0.52	-0.52
ENSMUSG00000030257	Srgap3	15.10	-2.19	-1.57	1.98E-01			0.16	0.39	0.39
ENSMUSG00000024451	Arap3	13.31	-3.07	-2.53	4.18E-02	2.40	-0.73	3.36	-6.20	-3.46
ENSMUSG00000028059	Arhgef2	12.40	-3.06	-2.49	1.11E-10	2.29	-0.48	2.18	-4.59	-2.54
ENSMUSG00000025154	Arhgap19	11.41	-3.05	-2.51	6.16E-04					
ENSMUSG00000061751	Kalrn	11.03	-2.79	-2.32	7.33E-04			0.47	0.53	0.53
ENSMUSG00000056486	Chn1	10.70	-1.51	-0.91	6.53E-02					
ENSMUSG00000053199	Arhgap20	10.10	-0.28	0.39	8.01E-01					
ENSMUSG00000037148	Arhgap10	7.34	-1.74	-1.60	5.75E-04					
ENSMUSG00000031214	Ophn1	7.25	-1.59	-1.02	1.75E-02			0.07	0.11	0.11
ENSMUSG00000039621	Prex1	6.52	-3.08	-2.59	1.20E-02			1.29	-3.81	-3.81
ENSMUSG00000025656	Arhgef9	6.09	-2.13	-2.69	3.95E-05					
ENSMUSG00000023015	Racgap1	6.06	-3.83	-4.17	4.61E-10					
ENSMUSG00000002489	Tiam1	5.55	-3.38	-2.98	1.47E-03			0.32	-0.80	-0.80
ENSMUSG00000016128	Stard13	5.39	-2.53	-1.74	2.24E-02					

ENSMUSG00000031133	Arhgef6	5.35	-1.70	0.73	NA			2.96	-3.57	-3.57
ENSMUSG00000025265	Fgd1	5.11	-3.05	-2.93	4.15E-12					
ENSMUSG00000031442	Mcf2l	4.52	-2.91	-3.20	7.04E-05	3.75	-1.30	2.62	-3.36	-2.33
ENSMUSG00000033450	Tagap	4.51	1.03	0.05	8.31E-01					
ENSMUSG00000031355	Arhgap6	4.40	-1.81	-1.44	1.12E-01			0.79	-1.63	-1.63
ENSMUSG00000078954	Arhgap8	3.99	-2.53	-1.74	1.30E-01					
ENSMUSG00000034255	Arhgap27	3.63	-3.81	-3.30	1.21E-03	5.52	-1.15	3.71	-4.39	-2.77
ENSMUSG00000022436	Sh3bp1	3.51	-3.30	-1.87	4.79E-04			3.15	-2.97	-2.97
ENSMUSG00000023800	Tiam2	3.32	-0.87	-0.32	6.02E-01					
ENSMUSG00000027699	Ect2	3.25	-4.37	-3.82	5.73E-08					
ENSMUSG00000035697	Arhgap45	3.24	-1.66	-0.12	NA	0.15	0.02	3.96	-3.58	-1.78
ENSMUSG00000044037	Als2cl	3.17	-2.44	-1.07	3.22E-01			0.92	-0.74	-0.74
ENSMUSG00000037709	Fam13a	3.00	-2.64	-1.18	9.85E-02					
ENSMUSG00000037509	Arhgef4	2.95	-1.76	-0.92	3.11E-01					
ENSMUSG00000019467	Arhgef25	2.67	-2.90	-2.34	4.61E-02					
ENSMUSG00000050730	Arhgap42	2.28	-5.03	-4.65	8.54E-12					
ENSMUSG00000004633	Chn2	2.25	-3.25	-3.31	1.39E-05					
ENSMUSG00000041219	Arhgap11a	2.23	-5.80	-5.03	3.09E-15					
ENSMUSG00000021708	Rasgrf2	1.41	-3.02	-2.42	1.07E-01			1.95	-3.48	-3.48
ENSMUSG00000032356	Rasgrf1	1.33	-1.69	-5.51	1.62E-03			0.17	0.27	0.27
ENSMUSG00000061462	Obscn	1.22	0.45	0.10	9.38E-01					
ENSMUSG00000024013	Fgd2	1.01	-2.31	-1.51	1.05E-01					
ENSMUSG00000033721	Vav3	0.82	-5.17	-4.03	4.02E-06			0.22	0.56	0.56
ENSMUSG00000045094	Arhgef37	0.78	-1.07	-0.46	6.84E-01			2.01	-1.20	-1.20
ENSMUSG00000048865	Arhgap30	0.73	-1.55	-1.20	3.50E-01					
ENSMUSG00000030047	Arhgap25	0.70	-4.20	-3.53	6.44E-03			1.99	-3.67	-3.67
ENSMUSG00000038167	Plekhg6	0.67	-3.04	-2.52	8.03E-04					
ENSMUSG00000034116	Vav1	0.50	-0.05	-0.36	7.99E-01					
ENSMUSG00000037946	Fgd3	0.48	-2.68	-1.32	2.56E-01					
ENSMUSG00000049744	Arhgap15	0.42	-1.77	0.22	NA					
ENSMUSG00000051517	Arhgef39	0.34	-4.27	-3.60	1.05E-10					
ENSMUSG00000026259	Ngef	0.24	-3.30	-0.07	9.65E-01					
ENSMUSG00000040969	Arhgef38	0.24	-5.93	-4.84	2.33E-03					
ENSMUSG00000054901	Arhgef33	0.16	-0.94	-2.36	1.42E-01					
ENSMUSG00000028919	Arhgef19	0.14	-6.37	-6.04	2.16E-07					
ENSMUSG00000063506	Arhgap22	0.10	-3.29	-2.57	9.23E-02					
ENSMUSG00000021697	Depdc1b	0.07	-7.35	-6.89	6.13E-18					
ENSMUSG00000074625	Arhgap40	0.06	-3.98	-1.55	4.56E-01					
ENSMUSG00000036198	Arhgap36	0.05	-3.58	-3.13	3.54E-02					
ENSMUSG00000025195	Dnmbp	0.00	-	-0.65	1.40E-01			0.13	-0.46	-0.46

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