Supplemental Methods

Thioglycolate peritonitis and analysis of isolated macrophages

White blood cell analysis of peripheral blood was performed using a MS9V5 apparatus (MELET SCHLOESING Laboratoires, Osny, France).

For isolation of activated primary monocytes/macrophages, thioglycolate peritonitis was induced in periostin WT and KO littermates (C57BL/6) after intra-peritoneal injection of 1ml sterile 4% thioglycolate solution (Sigma Aldrich). The mice were sacrificed 72 hours after injection and the peritoneal cavities were washed twice with 5ml sterile PBS in order to collect the infiltrated monocytes/macrophages. Monocyte cell counts were performed in a Neubauer hemocytometer and expressed as total number of isolated cells.

For migration assays, $2x10^4$ peritoneal monocytes/macrophages diluted in RPMI 1640 medium were placed in the upper chambers of 48-well 5μm-pore Transwell chemotaxis supports (Corning Inc). 100ng/ml mouse recombinant monocyte chemattractant protein-1 (MCP-1) (R&D Systems) diluted in RPMI 1640 medium was added in the lower chambers. After incubation at 37^oC/5% CO_2 for 3 hours, the cells migrated in the lower chamber were fixed in 4% Parafolmadehyde (PFA) and counted under a microscope. The results were expressed as total number of cells migrated in the lower chamber.

For quantitative RT-PCR analysis, total RNA was extracted from peritoneal monocytes/macrophages using the EZ-10 Spin Column Total RNA Mini-preps Super kit (Bio Basic Inc) and transcribed to cDNA followed by Real-time PCR analysis as described in Concise Methods.

n=5-6 per group.

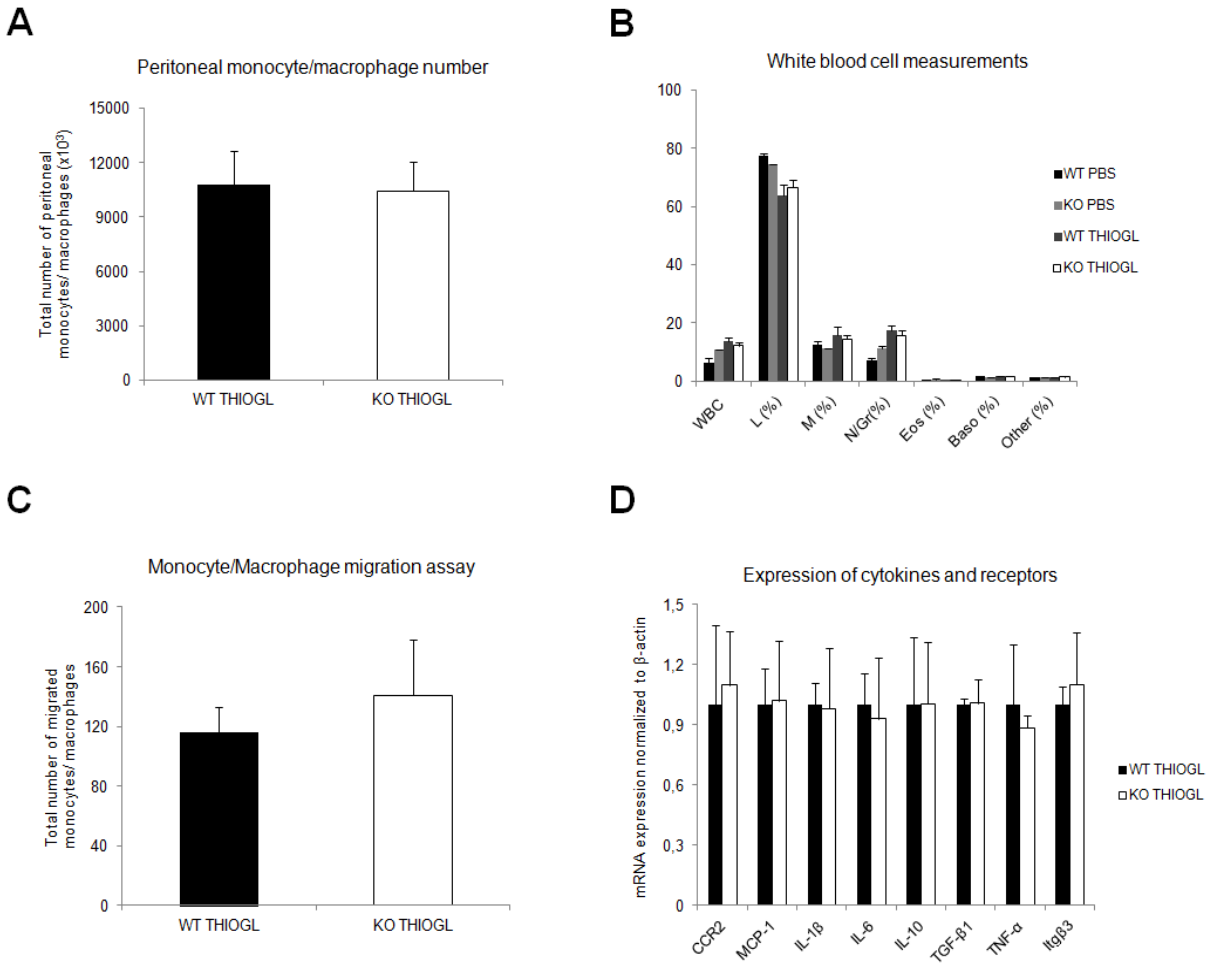
Supplemental figures and figure legends

Fold change of Itgβ3 and Postn in several nephropathies

Dataset	Reich IgA nephropathy (vs. healthy donor)	Rodwell Aging (anormal vs. normal proteinuria)	Schmid Diabetes (vs. Minimal Change Disease)	Woroniecka Diabetes (vs. healthy donor)	Berthier Lupus			Hodgin FSGS (vs. normal kidney)
Subcategory					Class II vs. Class III	Nephrotic vs. Subnephrotic	Class II vs. Class IV	
ITGB3 (Fold Change)	1,5 **	1,29 *	1,25 **	1,8 ***	1,27 **	1,97 **	1,14 *	1,31 *
POSTN (Fold Change)	1,57 **	2,03 *	2,02 *	5,23 **	2,36 *	3,87 ***	2,48 *	1,93 *

Dataset	Neusser Hypertension (Nephrosclerosis vs. Tumor nephrectomy)	Nakagawa CKD (vs. normal kidney)		Ju CKD 2					
Subcategory		Validation Set	Discovery Set	Vasculitis vs. Healthy Donor	IgA nephropathy vs. Healthy Donor	FSGS vs. Healthy Donor	Lupus Nephritis vs. Healthy Donor	Membranous Nephropathy vs. Healthy Donor	Minimal Change Disease vs. Healthy Donor
ITGB3 (Fold Change)	1,27 *	5,99 **	2,06 ***	1,44 ***	1,15 *	1,2 *	1,14 **	Not significant	Not significant
POSTN (Fold Change)	2,32 **	3,12 *	1,56 **	2,12 ***	1,31 *	1,29 *	1,59 **	Not significant	Not significant

Supplemental Figure 1. Comparison of the gene expression profiles of periostin (Postn) and integrin-β3 (Itgβ3) in different renal disease datasets as deposited in the publicly available Nephroseq platform (www.nephroseq.org). Postn and Itgβ3 are significantly up-regulated to a comparable level in several categories of renal disease patients. **P*<0.05, ***P* <0.01, ****P*<0.001 vs. respective control.



Supplemental Figure 2. Comparative phenotypic analysis of activated monocytes isolated after thioglycolate-induced peritonitis did not reveal any differences between WT and KO mice. (A) The total number of infiltrated peritoneal monocytes/macrophages was similar in WT and KO mice. (B) White blood cell analysis of peripheral blood before and after thioglycolate treatment did not reveal any variations in the leukocyte subtypes between WT and KO mice. (C) Isolated peritoneal monocytes/macrophages from WT and KO mice were left to migrate towards chemoattractant protein MCP-1 in Transwell chambers for 3hr at 37^{o}C, before measurement of the total number of migrated cells in the lower chamber. Macrophages from both WT and KO mice showed the same migratory capacities. (D) Quantitative RT-PCR analysis of various cytokines/receptors in isolated peritoneal

monocytes/macrophages from WT and KO mice did not show any differences between groups. Total monocyte/macrophage number is in millions (x 10^3) (A). Total WBC number is in thousands/mm^3 (x $10^3/mm^3$), while subtypes are in percentage of total cells (%). L=lymphocytes, M=monocytes, N/Gr=neutrophils, Eos=eosinophils, Baso=basophiles (B). *n*=5-6 per group.

Supplemental Tables

ODN	Sequence
AS1	G*A*G*AGGAACCATCTTCAGCCCTGAGCT*C*C*G
AS2	G*T*C*TCTCCTGTTTCTCC*A*C*C
SCR1	C*T*C*TCCGGAGAGCCACCGAGATCTGAG*T*C*A
SCR2	G*C*T*ATCCTTCCCGCTCT*C*T*T

Supplemental Table 1. SCR and AS ODN sequences used for *in vivo* administration in mice. *Residues modified with phosphorothioates to inhibit degradation.

Target mRNA	Forward	Reverse
COL1	GCAGGTTCACCTACTCTGTCCT	CTTGCCCCATTCATTTGTCT
COL3	TGGTTTCTTCTCACCCTTCTTC	TGCATCCCAATTCATCTACGT
TGF-β1	TGGAGCAACATGTGGAACTC	GTCAGCAGCCGGTTACCA
MCP-1	CATCCACGTGTTGGCTCA	GATCATCTTGCTGGTGAATGAGT
RANTES	CTACTCCCACTCCGGTCCT	GATTTCTTGGGTTTCGTGGTC
VCAM-1	TGGTGAAATGGAATCTGAACC	CCCAGATGGTGGTTTCCTT
CSF-1	CAGCTGCTTCACCAAGGACT	TCATGGAAAGTTCGGACACA
ITGβ3	GTGGGAGGGCAGTCCTCTA	CAGGATATCAGGACCCTTGG
mPOSTN	CGGGAAGAACGAATCATTACA	ACCTTGGAGACCTCTTTTTGC
hPOSTN	GAACCAAAAATTAAAGTGATTGAAGG	TGACTTTTGTTAGTGTGGGTCCT

Supplemental Table 2. Primer sequences used in quantitative real-time PCR analysis to detect target mRNA expression.

Position on periostin promoter	Forward primer	Reverse primer
-2100-2000	AAACTGCCTTCCTTTTCTCAGC	GAGAAACAGAGGCCAGGTCAGA
-1450-1300	CACAAGTGCCCTGGAAGGAA	ACACAGCCAAACAACACAGT
-1100-950	TGCCTTGTCAGTGGGAAAACA	GCAAGGAATGGAAACAGCCAT
-950-800	CCATTCCTTGCCAACTGAAGC	CTCAGCATTCTTAGCTGAGGGA
-750-650	CTCTTGGCAGCAACCCTGTT	ACACACACACTGCATACTCTGAT
-500-300	GTTGAAAAGACATGGCCCCAG	ATCACTCCACAGCAGAACACG
-250-100	GTGCAATCAGATCAAACCAGGA	TTCAATCATGGTGAGCCCGTTT
-50+100	CCACAGCCCAGAGCTATATAAAC	TAACTGTTGGCATTTGCAGGG

Supplemental Table 3. Primer sequences used in quantitative real-time PCR analysis to detect enrichment of mouse periostin promoter fragments in ChIP assays.