

SUPPLEMENTARY DATA

TABLE S1

Gene name	Direction Primer sequence (5'-3')
β5 (rat and mouse)	<i>fwd</i> : ACCTGCCAAGATGGCATATC <i>rev</i> : CACGGACACTTCAAAGGATG
GRP78 (rat)	<i>fwd</i> : CCGTAACAATCAAGGTCTACGA <i>rev</i> : AAGGTGACTTCAATCTGGGGTA
GRP78 (mouse)	<i>fwd</i> : CTGAGGCGTATTTGGGAAAG <i>rev</i> : TCATGACATTCAGTCCAGCAA
ISM1 (rat and mouse)	<i>fwd</i> : TCCAGATCTTTCCAAAGCTGAT <i>rev</i> : GCCATCAACCACCTCTATGG
IL6 (mouse)	<i>fwd</i> : CCAGGTAGCTATGGTACTCCAGAA <i>rev</i> : TGCCTTCATTATCCCTTGAA
HPRT (mouse)	<i>fwd</i> : GGAGCGGTAGCACCTCCT <i>rev</i> : CTGGTTCATCATCGCTAATCAC
HPRT (rat)	<i>fwd</i> : GACCGGTTCTGTCATGTCG <i>rev</i> : ACCTGGTTCATCATCACTAATCAC
Gusb (Mouse)	<i>fwd</i> : CTCTGGTGGCCTTACCTGAT <i>rev</i> : CAGTTGTTGTCACCTTCACCTC

Table S1. Gene-specific primer sequences used for RT-qPCR

TABLE S2

Up-regulated genes				Down-regulated genes		
Symbol	Fold Change	p-value		Symbol	Fold Change	p-value
HAVCR1	36,082	7.42E-08		Slc7a12	-9,996	1.35E-03
SERPINA3	23,150	1.28E-03		RGD1563294	-6,425	3.16E-05
FGB	18,605	1.92E-07		Akr1c12	-5,578	1.76E-03
GPNMB	8,954	7.32E-06		RGN	-5,501	7.61E-04
HMOX1	8,562	2.21E-03		Slco1a1	-5,164	1.06E-02
IGFBP1	7,673	1.06E-05		CACNG5	-5,028	5.68E-03
ALOX15	7,133	1.35E-03		HNMT	-5,010	5.81E-04
PDK4	6,936	1.05E-06		SLC7A13	-4,980	1.50E-03
ADAMTS1	6,929	1.53E-06		PRIMA1	-4,795	4.32E-03
GPX2	6,715	1.43E-03		HRG	-4,737	1.98E-03
ANGPTL4	6,471	4.85E-07		Olf136	-4,648	1.83E-02
S100A8	6,372	2.49E-02		GC	-4,339	6.88E-03
SPP1	6,313	1.48E-06		Cml1	-4,216	7.29E-04
HMGCS2	6,023	3.00E-03		Ces1e	-4,207	5.15E-04
SERPINE1	5,975	6.62E-06		Slco1a6	-3,863	5.63E-03
FGA	5,805	4.59E-05		Olr1408	-3,808	1.29E-02
TIMP1	5,453	3.26E-06		Kap	-3,754	3.25E-02
CLU	5,208	7.98E-06		CYP2C9	-3,724	2.40E-02
SLC34A2	5,155	1.61E-05		GUCY1B2	-3,631	7.38E-05
FGG	5,067	1.06E-05		CHTF18	-3,572	4.34E-03
LAMC2	4,874	4.02E-05		SPATA22	-3,511	1.25E-04
FAM129A	4,755	1.03E-08		SLCO4C1	-3,498	2.77E-04
CDKN1A	4,742	6.29E-05		AFM	-3,472	1.59E-03
RASD1	4,539	3.07E-05		MLC1	-3,426	3.18E-03
BTG2	4,533	2.45E-03		SLC22A25	-3,407	1.28E-03

Table S2: Top 25 up- and down-regulated genes in L-NAME model between W0 and CTL groups.

TABLE S3

	UAER			UPER			Albuminemia		
	CTL	model	p	CTL	model	p	CTL	model	p
<i>PAN</i>	0.00±0.000	2.42±0.15	<0.001	0.06±0.004	12.71±0.75	<0.001	14.9±0.65	4.38±0.35	<0.001
<i>DOXO</i>	0.00±0.000	3.02±0.12	<0.001	0.15±0.01	9.18±0.51	<0.001	16.47±0.57	4.25±0.16	<0.001
<i>ob/ob</i>	0.002±0.001	0,056±0.008	<0.001						
<i>LPS</i>	0.04±0.01	0.27±0.04	<0.001						

Table S3. Biochemical parameters in animal models of glomerulopathy. UAER (g/mmol), UPER (g/mmol) and albuminemia (g/L) in PAN and DOX models. UAER (g/mmol) in ob/ob model and UAER (g/g) in LPS model. . UAER: Urinary albumin excretion ratio and UPER: Urinary protein excretion ratio.

TABLE S4

(DOWNLOAD EXCEL FILE)

Table S4: Genes related to ISM1 regulation during renal regeneration. This table describes the statistics identified by the supervised Pavlidis template matching algorithm on ISM1 expression during renal regeneration. For each column of significant genes: correlation coefficient rvalues, raw p-values and False Discovery Rate adjust qvalues.

FIGURE S1

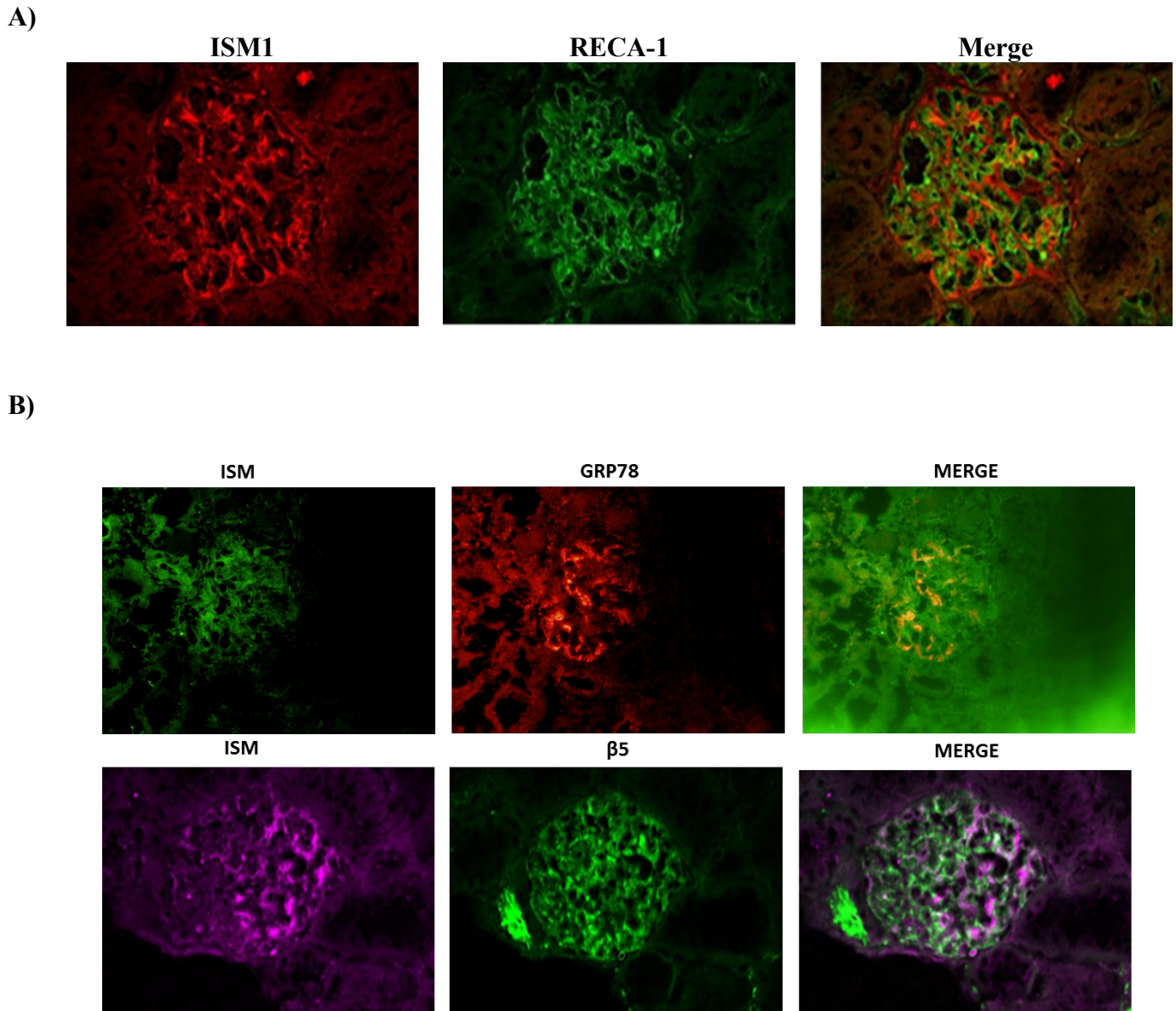


Figure S1. Immunohistochemical analysis of co-localization of ISM1: A) ISM1 does not colocalize with RECA-1, a rodent pan-endothelial cell marker. B) Co-localization of ISM1 with its receptors, GRP78 and beta5 integrin in rats.