

Supplementary Materials

Table S1. Physiological parameters of WT and *Tlr2*^{-/-} diabetic mice

DM duration		Body weight (g)	Glucose (mg/dl)	Water intake (ml)	Urine output (ml)
1 m	WT	19.0±0.9 (15)	588±15 (15)	19.2±2.5 (12)	8.6±1.3 (12)
	<i>Tlr2</i> ^{-/-}	22.2±0.6** (13)	578±29 (13)	14.4±1.7 (12)	6.1±1.1 (12)
2 m	WT	24.7±1.9 (9)	550±71 (5)	14.7±2.0 (9)	7.6±1.2 (9)
	<i>Tlr2</i> ^{-/-}	24.0±0.8 (11)	656±71 (5)	13.5±2.0 (11)	5.0±1.0 (11)
3 m	WT	22.7±1.6 (3)	472±55 (3)	27.6±9.9 (3)	22±11.9 (3)
	<i>Tlr2</i> ^{-/-}	22.6±1.6 (5)	358±30 (5)	18.75±3.0 (5)	10±5.6 (5)

***P* < 0.01 relative to WT mice. Numbers in parentheses indicate the number of mice for each group.

Table S2. Physiological parameters of WT and *Tlr4*^{-/-} diabetic mice

DM duration		Body weight (g)	Glucose (mg/dl)	Water intake (ml)	Urine output (ml)
1 m	WT	23.1±1.0 (10)	649±11 (10)	18.0±1.6 (10)	9.4±1.2 (10)
	<i>Tlr4</i> ^{-/-}	22.2±1.2 (8)	609±34 (8)	15.3±2.0 (8)	7.0±1.5 (8)
2 m	WT	20.9±0.7 (10)	611±39 (10)	25.9±1.6 (10)	15.1±1.4 (10)
	<i>Tlr4</i> ^{-/-}	23.4±0.7* (11)	571±33 (11)	14.2±2.4*** (11)	7.2±1.5** (11)
3 m	WT	21.4± 2.5 (4)	740±33 (4)	27.0±1.1 (4)	17.3±2.1 (4)
	<i>Tlr4</i> ^{-/-}	25±1.3* (5)	644±75 (5)	17.3±7.1*(5)	8.3±4.4**(5)

P* < 0.05, *P* < 0.01, and ****P* < 0.001 relative to WT mice. Numbers in parentheses indicate the number of mice for each group.

Table S3.

Clinical data and immunohistochemical staining score of DN and non-diabetic control patients

Group	Age(y)/Sex	GLU-A.C (mg/dL)	HbA1C (%)	SCr (mg/dL)	UPCR	eGFR	Duration of diagnosed diabetes (y)	Immunohistochemical staining score (0~5)			
								TLR4	TLR2	HSP70	Cytoplasmic HMGB1
Control group (n=10)	73/F	111	N.A.	0.82	N.A.	68	N.A.	1	0	1	0
	63/M	112	N.A.	1.02	N.A.	74	N.A.	3	2	3	0
	34/M	111	N.A.	1.16	N.A.	73	N.A.	1	0	0	0
	56/F	95	N.A.	0.68	N.A.	≥90	N.A.	1	2	1	0
	64/M	110	N.A.	1.11	N.A.	67	N.A.	1	2	0	1
	45/M	79	N.A.	1.18	N.A.	67	N.A.	0	1	1	2
	54/F	111	N.A.	0.75	N.A.	81	N.A.	0	0	3	0
	59/M	102	N.A.	1.16	N.A.	65	N.A.	0	0	3	2
	57/M	106	N.A.	1.02	N.A.	75	N.A.	0	2	2	1
	58/F	95	N.A.	0.66	N.A.	≥90	N.A.	2	2	4	1
Mean±SD	56.3±10.7 F:M=4:6	103.2±10.7		0.96±0.2		71.3±5.4		0.9±1.0	1.1±1.0	1.8±1.4	0.7±0.8

Table S3. Continued

Group	Age(y)/Sex	GLU-A.C (mg/dL)	HbA1C (%)	SCr (mg/dL)	UPCR	eGFR	Duration of diagnosed diabetes (y)	Immunohistochemical staining score (0~5)			
								TLR4	TLR2	HSP70	Cytoplasmic HMGB1
DN group (n=11)	53/F	568	12.8	8.30	1220	5	10	5	4	5	4
	32/F	156	7.1	4.51	22693	10	3	2	3	5	1
	38/F	162	7.4	7.3	32877	6	10	5	1	5	0
	69/M	105	6.4	3.57	15296	17	14	5	5	3	4
	63/M	135	7.2	1.63	17817	43	5	4	5	5	1
	46/F	142	6.2	0.84	2174	74	4	5	5	4	0
	75/F	195	7.5	2.36	10349	20	10	5	5	5	0
	64/F	158	7.5	1.08	3504	51	7	5	4	4	5
	46/M	119	10.0	3.25	11995	21	11	5	4	5	3
	56/M	201	7.9	10.61	19247	5	4	1	3	5	5
	33/M	220	4.8	9.04	6171	7	2	4	3	5	2
Mean±SD	52.2±15.4	196.5±128.1	7.7±2.1	4.8±3.5	13031±9784	23.6±22.8	7.3±3.9	4.2±1.4	3.8±1.3	4.6±0.7	2.3±2.0
	F:M=6:5										

HbA1c, hemoglobin A1c; SCr, serum creatinine; UPCR, urinary protein/creatinine ratio; eGFR, estimated glomerular filtration rate (ml/min per 1.73 m²);

F, female; M, male; N.A., not applicable/not available. Results are shown as mean ± standard deviation.

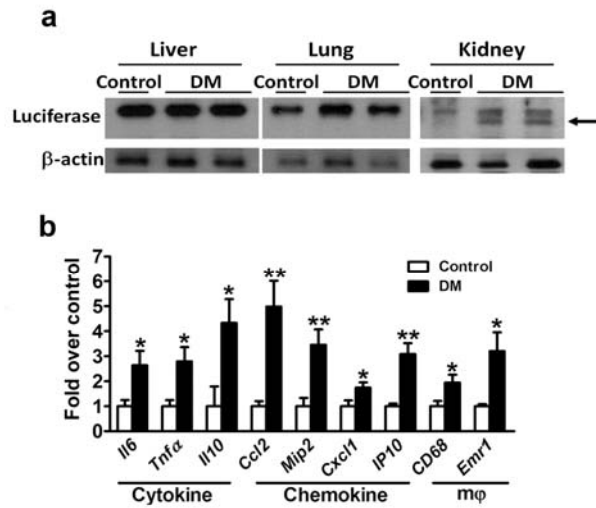


Fig. S1. Expression of inflammatory mediators in diabetic mice. (a) Immunoblot analysis on luciferase in the liver, lung, and kidney of 3-month diabetic and control NF- κ B reporter mice. (b) Expression of inflammatory genes, including cytokines, chemokines, and macrophage markers, in the kidney of 3-month diabetic ($n=6$) relative to the control ($n=5$) C57BL/6 mice. * $P<0.05$ and ** $P<0.01$.

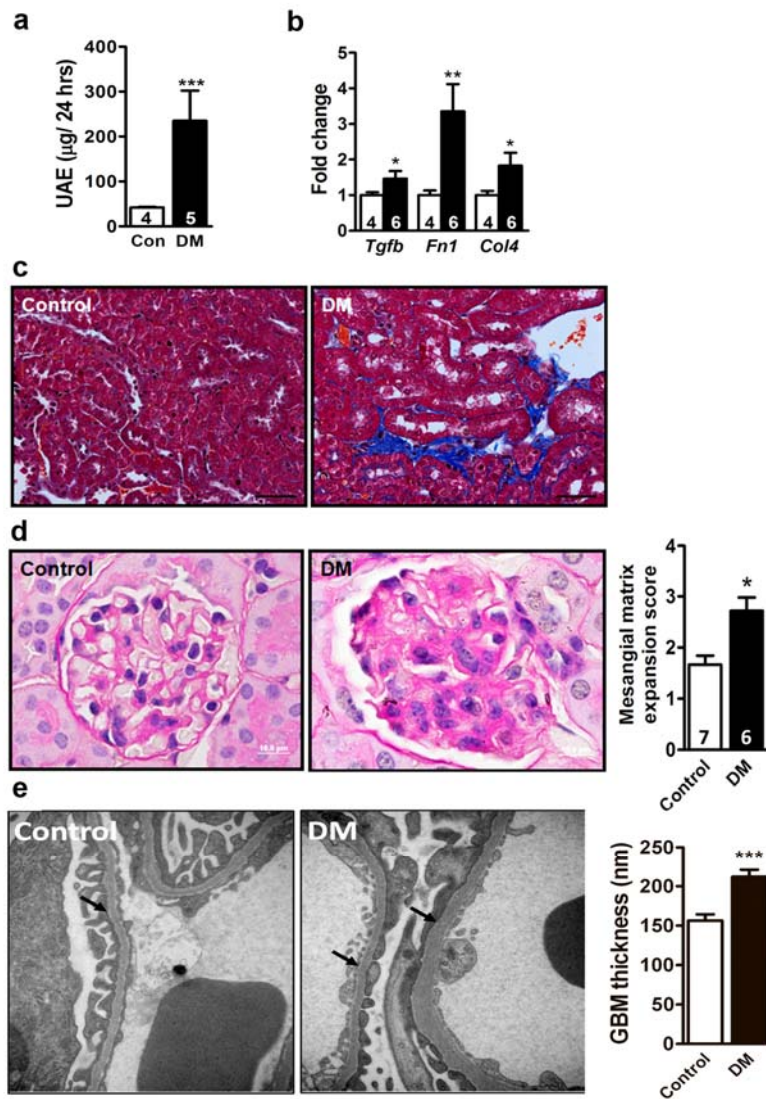


Fig. S2. Renal function and morphology in diabetic mice. (a) Daily urinary albumin excretion (UAE), (b) expression of fibrotic genes, and (c) masson trichrome stain in the kidney of 3-month diabetic and control mice. Scale bar, 50 µm. (d) Representative PAS-stained glomerular morphology and quantification of mesangial matrix expansion of 3-month diabetic and control mice. Scale bar, 30 µm. The scoring of mesangial matrix expansion was based on >30 glomeruli examined per mouse. (e) Representative image and thickness measurement of glomerular basement membrane (GBM, *arrows*) in the kidney of 3-month diabetic and control mice. Magnification, x30,000. Numbers inside bars indicate the mouse number for each group. * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$.

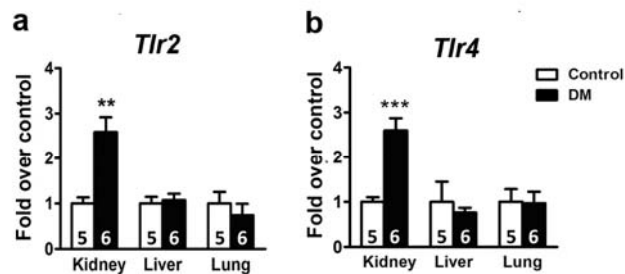


Fig. S3. Expression of TLRs in diabetic mice. Expression of (a) TLR2 and (b) TLR4 in the kidney, liver and lung of 1-month diabetic relative to control mice. Numbers inside bars indicate the mouse number for each group. ** $P < 0.01$ and *** $P < 0.001$.

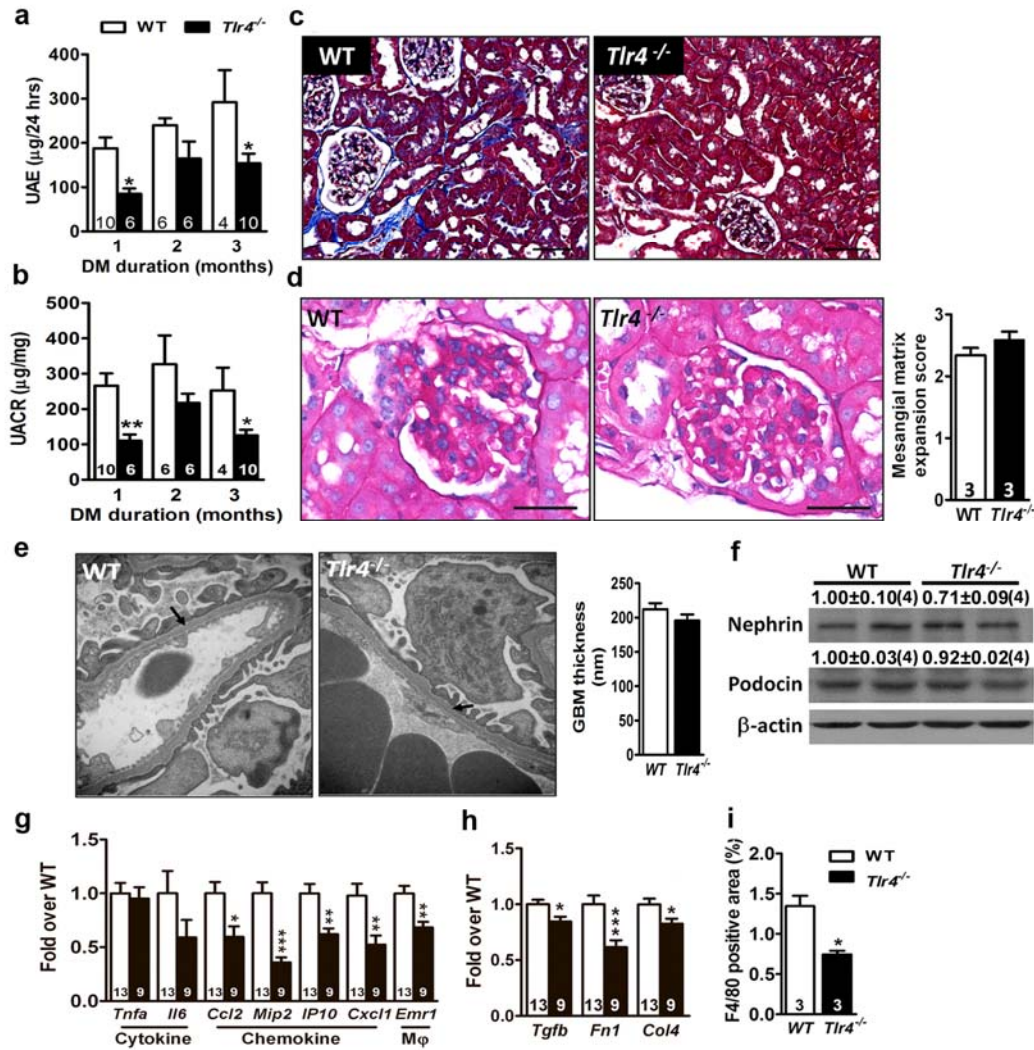


Fig. S4. Renal function, morphology, and gene expression of *Tlr4*^{-/-} diabetic mice. (a) UAE and (b) urinary albumin-creatinine ratio (UACR) of *Tlr4*^{-/-} and WT mice 1 to 3 months after induction of diabetes. (c) Masson trichrome stain in the kidney of *Tlr4*^{-/-} and WT 3-month diabetic mice. Scale bar, 50 µm. (d) Representative PAS-stained glomerular morphology and quantification of mesangial matrix expansion of *Tlr4*^{-/-} and WT 3-month diabetic mice. Scale bar, 30 µm. (e) Representative image and thickness measurement of GBM (arrows) of *Tlr4*^{-/-} and WT 3-month diabetic mice. Magnification, x30,000. (f) Immunoblot analyses on nephrin and podocin from the kidney of *Tlr4*^{-/-} and WT 1-month diabetic mice. The relative intensities of the bands by densitometric quantification to WT with the number of mice in parentheses are indicated. Expression of (g) inflammatory and (h) fibrotic genes in the kidney of *Tlr4*^{-/-} and WT 1-month diabetic mice. (i) The percentage of F4/80 positive area quantified by the immunofluorescence analysis in the kidney of *Tlr4*^{-/-} and WT 1-month diabetic mice. Numbers inside bars indicate the mouse number for each group. **P*<0.05, ***P*<0.01, and ****P*<0.001.

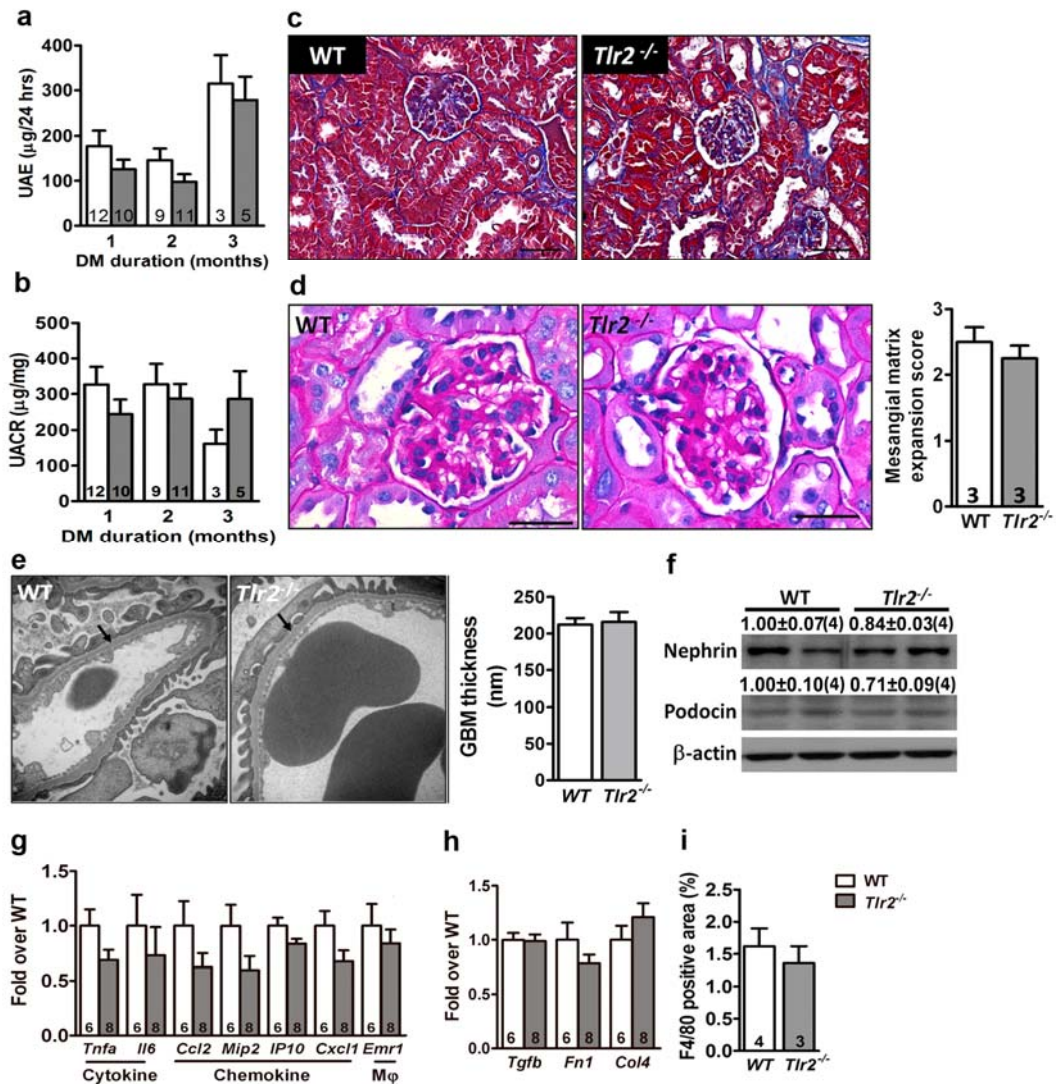


Fig. S5. Renal function, morphology, and gene expression of *Tlr2*^{-/-} diabetic mice. (a) Daily urinary albumin excretion (UAE) and (b) urinary albumin-creatinine ratio (UACR) of *Tlr2*^{-/-} and WT mice 1 to 3 months after induction of diabetes. (c) Masson trichrome stain in the kidney of 3-month *Tlr2*^{-/-} and WT diabetic mice. Scale bar, 50 µm. (d) Representative PAS-stained glomerular morphology and quantification of mesangial matrix expansion of *Tlr2*^{-/-} and WT 3-month diabetic mice. Scale bar, 30 µm. (e) Representative image and thickness measurement of GBM (arrows) of *Tlr2*^{-/-} and WT 3-month diabetic mice. Magnification, x30,000. (f) Immunoblot analyses on nephrin and podocin from the kidney of *Tlr2*^{-/-} and WT 1-month diabetic mice. The relative intensities of the bands by densitometric quantification to WT with the number of mice in parentheses are indicated. Expression of (g) inflammatory and (h) fibrotic genes in the kidney of *Tlr2*^{-/-} and WT 1-month diabetic mice. (i) The percentage of F4/80 positive area quantified by the immunofluorescence analysis in the kidney of *Tlr2*^{-/-} and WT 1-month diabetic mice. Numbers inside bars indicate the mouse number for each group.

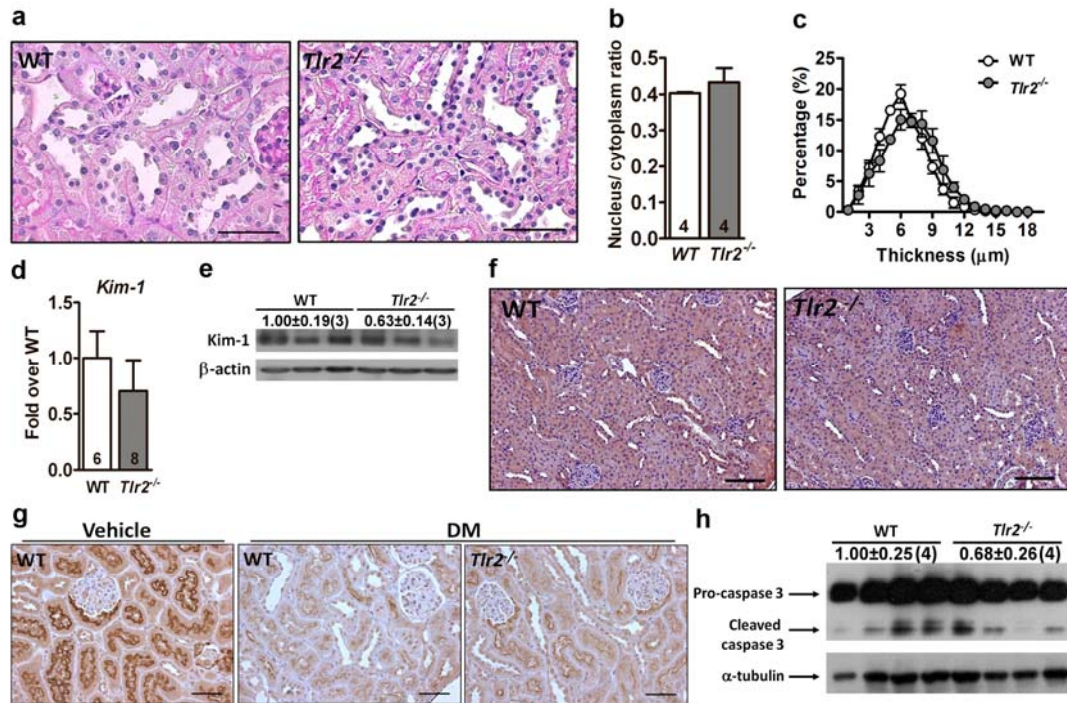


Fig. S6. Tubular injury and apoptosis in *Tlr2*^{-/-} diabetic mice. (a) Representative tubular morphology, (b) quantification of the tubular nucleus-to-cytoplasm ratio, and (c) distribution of tubular epithelial thickness in *Tlr2*^{-/-} and WT 1-month diabetic mice. Scale bar, 50 μm. (d) Expression of *Kim-1* in *Tlr2*^{-/-} and WT 1-month diabetic mice. Numbers inside bars indicate the mouse number for each group. (e) Immunoblot analyses and (f) immunohistochemical staining of *Kim-1* in the kidney of *Tlr2*^{-/-} and WT 1-month diabetic mice. Scale bar, 100 μm. (g) Immunohistochemical staining of cubilin in the kidney of WT control, and WT and *Tlr2*^{-/-} 3-month diabetic mice. Scale bar, 50 μm. (h) Immunoblot analyses of caspase 3 in the kidney of *Tlr2*^{-/-} and WT 1-month diabetic mice. The relative intensities of the bands by densitometric quantification to WT with the number of mice in parentheses are indicated.