**Supplementary Table 1.** Transcripts with mRNA expression correlation to *FRMD3* in DN. Co-regulated transcripts listed by descending person correlation. Top 10 transcripts are concordantly regulated in DN. For 5 of the 10 transcripts or close variants an association with diabetes, cardiovascular pathophysiology or inflammatory diseases has been published, summarized in columns 4 and 5.

| Gene Name | Gene ID | R with FRMD3 | Relevance for diabetes, cardiovascular/inflammational disease | PMID |
|-----------|---------|--------------|-------------------------------------------------------------|-------|
| ADD3      | 120     | 0.93         | interaction of ADD1 and ADD3 gene variants in humans is statistically associated with variation in blood pressure | 15716695 |
| DNAJB14   | 79982   | 0.93         |                                                             |       |
| DACH1     | 1602    | 0.9          | differentially regulated in diabetic mouse model, candidate gene identified by Diabetes Genetics Initiative and Wellcome Trust Case Control Consortium genome-wide scans for T2D | 19902174 |
| ZYG11B    | 79699   | 0.9          |                                                             |       |
| FKBP14    | 55033   | 0.89         | FKBP12.6-knockout mice display hyperinsulinemia and resistance to high-fat diet-induced hyperglycemia | 19805579 |
| FAM126B   | 285172  | 0.88         |                                                             |       |
| KIF5B     | 3799    | 0.88         | essential for cardiac potassium channels, candidate gene for the response of cardiac stroke volume | 19675065, 18984674 |
| LOC153222 | 153222  | 0.88         |                                                             |       |
| LYRM7     | 90624   | 0.88         |                                                             |       |
| RSBN1     | 54665   | 0.88         | genetic variant in RSBN1 locus associated with juvenile idiopathic arthritis | 20722033 |
Supplementary Table 2. Clinical characteristics of 22 Pima Indians with T2D diabetic nephropathy.
Age at the time of biopsy, gender, iothalamate clearance (iGFR) at the time of biopsy, ACR at the time of biopsy, delta GFR (mL/min/year), delta ACR/year, fractional mesangial area (%), observation time (defined as time of enrollment until latest available clinical data point) and FRMD3 steady state mRNA levels are shown as mean group values±standard deviation (SDEV) where suitable for both main clusters. Subjects are sorted by affiliation to one of the main clusters displayed in Fig. 1. *P<0.05 and **P<0.01 between cluster 1 and cluster 2.

| Cluster | Age  | Gender | GFR (mL/min) | ACR  | HbA1c (%) | delta GFR/year (mL/min) | delta ACR/year | Fractional mesangial area (%) | Observation t in yrs. | glom. FRMD3 expression |
|---------|------|--------|--------------|------|-----------|-------------------------|----------------|-------------------------------|----------------------|----------------------|
| 1       | 44±15| 4xF    | 148±37       | 584±932 | 10.5±1.8  | -3±7                    | 212±228*       | 30±14*                        | 9.0±2.2              | 8.3±0.5**             |
| 2       | 46±10| 14xF   | 132±42       | 48±53  | 8.6±2.2   | 6±24                    | 4±9*           | 17±7*                         | 9.5±0.9              | 9.7±0.4**             |