

Table 3. Order of magnitude of mRNA expression levels of candidate genes normalized to nephrin mRNA

Gene	Kidney	Glom.	Podoc. I	Podoc. II	Control
<i>ARHGDI1B</i>	10 ³	10 ⁰	10 ⁴	10 ³	nd
<i>CDH5</i>	10 ²	10 ⁰	10 ⁴	10 ¹	positive
<i>JUNB</i>	10 ³	10 ⁰	10 ⁴	10 ³	nd
<i>RAB5C</i>	10 ⁴	10 ⁰	10 ⁶	10 ⁵	positive
<i>SEMA3A</i>	10 ¹	10 ⁻¹	10 ⁵	10 ³	positive
<i>TTN</i>	0	0	0	0	positive

The mRNA expression of the six predicted genes found by screening the human promoter library was analyzed in whole human kidney, microdissected glomeruli, two human podocyte cell lines [Podoc. I (1) and Podoc. II (2)], and control cDNA. The control cDNA derived from human microvascular endothelial cell (HUVEC) [for cadherin-5 (*CDH5*)], human brain [for Rab5c (*RAB5C*) and semaphorin 3A (*SEMA3A*)], and muscle [for titin (*TTN*)], respectively. All genes with the exception of titin were found to be expressed by podocytes. To judge the expression levels, the mRNA expression was normalized to the expression of nephrin mRNA, the “seed” gene for the computational prediction, and expressed in orders of magnitude (i.e., ratio 1–9 = 10⁰, 10–99 = 10¹, ...). The expression levels were determined by using real-time RT-PCR (3). nd, not determined.

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3. Cohen, C. D., Frach, K., Schlondorff, D. & Kretzler, M. (2002) *Kidney Int.* **61**, 133–140.

