



Figure S1

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(A) Quantitative RT-PCR was carried out to determine mRNA expression of nephrin, synaptopodin, Wilms tumor 1 (WT1), P-cadherin, podocalyxin and non-muscle myosin heavy chain IIA (*MYH9*) in podocytes transformed by CDK4 (CDK4-p) and mesangial cell line MES13, each of which were confluent. Data were shown relative to the CDK4-p. Expression of every gene analyzed in MES13 was significantly lower than CDK4-p.

(B) The mRNA expression of histone cluster 2, H4 (Hist2h4) and Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) in CDK4-p at various cell densities was measured by quantitative RT-PCR. The data were presented relative to that of the confluent culture. No significant difference in Hist2h4 or GAPDH expression was observed among diverse densities.

(C) The mRNA expression of nephrin, synaptopodin, WT1, P-cadherin, podocalyxin and *MYH9* in podocytes transformed by tsA58U19 (tsT podocytes) at high (H) or low (L) density was analyzed by quantitative RT-PCR. Expression of each gene was shown relative to the cells at high density. Expression level of each gene was higher in tsT-podocytes at high density than low density.

For all three panels, mRNA data were normalized to beta-actin and presented as mean \pm SD of triplicate samples. *** denotes $P < 0.001$, ** denotes $p < 0.01$ and * denotes $P < 0.05$