

S1: Characterisation of tetracyline induced Hek-tet-Nox4 cells (tet) and non-induced Hek-tet-Nox4 cells (ctr).

- A Analysis of Nox4 mRNA expression relative to housekeeping gene GAPDH. N=3
- **B** Representative Western blot for NOX4 expression in tetracyline induced Hek-tet-Nox4 cells (tet) and in non-induced Hek-tet-Nox4 cells (ctr).
- C ROS measurements assessed by chemiluminescence with Luminol (100µM) / HRP (1U/ml). n=3

oxidation-reduction process

reactive oxygen species metabolism

cellular oxidant detoxification

cofactor catabolism

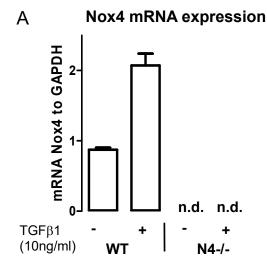
hydrogen peroxide catabolism

antibiotic catabolism

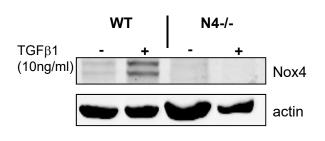
cell redox homeostasis

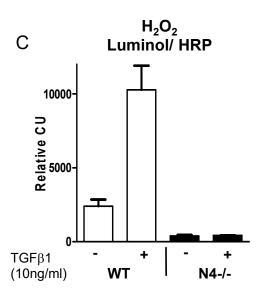
DNA replication initiation

S2: Nox5 oxidized proteins cluster in different functional processes.

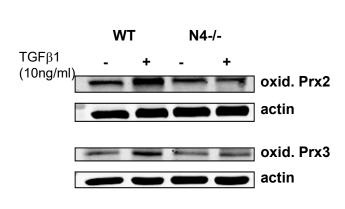


B Nox4 protein expression



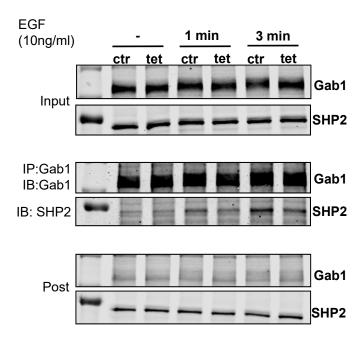


D Peroxiredoxin oxidation



S3: Characterisation and Redox-western of primary murine podocytes from WT and Nox4-/- mice treated with TGFβ1 (24h, 10ng/ml)

- A Analysis of Nox4 mRNA expression relative to housekeeping gene GAPDH. N=3
- **B** Representative Western blot for NOX4 expression in primary murine podocytes.
- C ROS measurements assessed by chemiluminescence with Luminol (100µM) / HRP (1U/ml).
- **D** Redox-Western for oxidised forms of Prx2, Prx3. Cells were blocked with NEM (100mM), washed with PBS- NEM (100mM). Cells were scraped in alkylation buffer (40mM Hepes, 50 mM NaCl, 1mM EGTA, Inhibitors, Catalase, 100mM NEM) and 1% CHAPS for solubilization.



S4: Co-IP of Gab1 and SHP2 (PTPN11) in tetracyline induced Hek-tet-Nox4 cells (tet) and non-induced Hek-tet-Nox4 cells (ctr) treated with EGF (10ng/ml).

Hek-tet-Nox4 cells were induced with tetracyline (tet) or not (ctr) and treated with EGF (10ng/ml) for the indicated time. Cells were lysed and Co-IP was performed with 800µg protein lysate.