Figure captions

Fig. 1 Cell-type specific morphology of cultured vascular smooth muscle cells. SMCs were isolated from the veins of human umbilical cords and cultivated for 24 hrs in the presence (A) and absence (B) of 30 µg /ml Fe(II)-gluconate, respectively and photographed with a phase contrast visible light microscope. Scale bar, 100 µm.

Fig. 2. Determination of effective Fe(II) concentrations. SMCs were cultured in the presence or absence of the ion concentrations indicated in mg/ml in the inserted legend. After incubation for the time periods indicated cells were collected and mitochondrial enzyme activity was determined by a WST assay. The value of the control culture at 24 hrs was set to 1.

Fig. 3. Cell growth promoting genes are down regulated in the presence of excess Fe(II). Genes that were down regulated in both cells grown for 12 h and in cells grown for 24 h in the presence of 30 µg /ml Fe(II) relative to the controls were clustered into biological processes by using the program GO surfer.

Fig. 4. The cell cycle is down regulated by Fe(II). Individual regulated genes in the cell cycle regulatory scheme were highlighted by using the program Genmapp. Genes with reduced expression are marked in grey whereas the two inhibitory cell cycle control proteins whose expression increases in the presence of Fe(II) are shown with a double frame. Expression of genes with a dotted frame was determined by hybridization to several different sequences, whereby all of the ProbsetIDs for this gene must be regulated in the same way. The Figure has been adapted from KEGG 10/02/2002 by GenMAPP.org and was simplified to show only the central part of the pathway.

Fig. 5. Membrane component biosynthetic genes and cell death related genes are up regulated in the presence of excess Fe(II). Genes that were up regulated in cells grown in the presence of Fe(II) were clustered into biological processes by using the program GO surfer.

Fig. 6. Cholesterol synthesis and lipid metabolic genes are up regulated by Fe(II). Individual up regulated genes (shaded rectangles) and genes not found (colorless rectangles) in the cholesterol biosynthesis pathway were marked using the program Genmapp with the gene database HS-std_2004 1021.gdb and the Cholesterol Biosynthesis pathway scheme from Michael Lieberman and Fred Mantei 2004, Gladstone Institutes. For additional details see legend to Figure 4.