## **MIAME Checklist:**

## Experiment Design:

- Type of Experiment: Comparison of transplant kidneys from living and cadaveric donors
- Experiment factors: The compared kidneys belonged to 2 different donor groups and had 3 different clinical outcomes in the recipients (living donor with primary function, cadaveric donors with primary function and cadaveric donors with acute renal failure).
- 36 hybridisations with 36 kidneys with 12 kidney samples in each of the 3 groups
- Stratagene Universal Human Reference RNA was used as hybridisation reference
- Quality control was performed on 3 pairs of left and right kidney from the same donor, quality of amplification was performed on RNA from tissue culture cells.

## Samples, Extraction and Labelling:

- Demographic data of kidney donors and recipients can be found in the manuscript.
- Kidney wedge biopsies were obtained immediately before implantation of the grafts, and put into RNAlater to preserve RNA.
- Protocols for RNA extraction, RNA labelling ,hybridisation and washing of microarrays can be found on our website (<u>http://www.akh-</u><u>wien.ac.at/nephrogene</u>).
- The RNA quality was checked with the Agilent 2100 Bioanalyzer and RNA6000 LabChip® kit.

## Data measurement:

- Data files containing raw image data can be found in the data section of our site
- Arrays were scanned on an GenePix 4000B scanner (Axon Instruments, Union City, California).
- Image griding and calculation of spot intensity was performed with GenePix Pro 4.0 software.
- Software used for statistical analysis: Statistica 6 (Statsoft Inc., Tulsa, Oklahoma).
- Significance analysis performed with the Bioconductor module of the R software package (<u>http://www.bioconductor.org/</u>).
- Characterisation of the biological function of the found genes was done using GenMAPP and HAPI

A brief description of the array design, feature location, information over the cDNA collection an the spotting protocols can be found on the producer website (<u>http://www.microarray.org/sfgf/jsp/home.jsp</u>). Protocols for the post processing procedure can be found on our website

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