1 Array design description

A brief description of the array design, feature location, information on the cDNA collection and the spotting protocols can be found on the producer website (http://www.microarray.org/sfgf/jsp/home.jsp).

Protocols for the post processing procedure can be found on our website (http://www.meduniwien.ac.at/nephrogene/).

2 Experiment description

2.1 Experimental design

2.1.1 Laboratory, authors, contact

Paul Perco[1,2,3]	paul.perco@meduniwien.ac.at
Alexander Kainz[1,2]	alexander.kainz@meduniwien.ac.at
Julia Wilflingseder[1,2]	julia.wilflingseder@elisabethinen.or.at
Afschin Soleiman[4]	afschin.soleiman@meduniwien.ac.at
Bernd Mayer[3]	bernd.mayer@emergentec.com
Rainer Oberbauer[1,2,5]	rainer.oberbauer@elisabethinen.or.at

[1] Krankenhaus der Elisabethinen, Linz, AUSTRIA
[2] Department of Nephrology, Medical University of Vienna, AUSTRIA
[3] emergentec biodevelopment, Vienna, AUSTRIA
[4] Department of Pathology, Medical University of Vienna, AUSTRIA
[5] Austrian Dialysis and Transplant Registry, AUSTRIA

2.1.2 Type of experiment

Comparison of histological parameters based on the Chronic Allograft Damage Index (CADI) in zero hour renal transplant biopsies.

2.1.3 Experiment factors

The expression levels of genes were investigated and compared between kidneys showing no or only mild damage versus kidneys with severe tissue damage based on the CADI.

2.1.4 Hybridizations

82 microarrays were analyzed.
52 with CADI < 2
21 with CADI 2 - <4
9 with CADI ≥ 4

2.1.5 Reference

Universal Human reference RNA (Stratagene®) was used as hybridization reference.

2.1.6 Quality control

To test for reproducibility of sample processing, RNA of three specimen was reprocessed twice.

2.2 Samples used, extract preparation and labeling

2.2.1 Bio-source properties

Organism: *Homo sapiens*
Demographic data of kidney donors can be found in the manuscript.

2.2.2 Biomaterial manipulations, hybridization and labeling protocol

Kidney wedge biopsies were obtained immediately before implantation of the grafts and submerged into RNAlater™ to preserve RNA.

Protocols for RNA extraction, RNA labeling, hybridization and washing of microarrays can be found on our website (http://www.meduniwien.ac.at/nephrogene/).

2.3 Hybridization procedures and parameters

The hybridization protocol can be found on our website (http://www.meduniwien.ac.at/nephrogene/).

82 samples were processed and the grouping according to the Chronic Allograft Damage Index (CADI) is given in the table below.

Slide Name	CADI group	CADI	ta	ii	if	as	gs	ati
sher182	3	12.5	2.5	2.5	2.5	3	2	2.5
sher188	3	9.5	2	1.5	2	2	2	2.5
sher210	3	7.5	1.5	1	2	1	2	2
shcm190	3	4	1	0	1	1	1	3
shdb224	3	4	1	1	1	1	0	2
shfr86	3	4	1	0	1	2	0	2
shcm186	3	4	0	1	1	0	2	2
sheo190	3	9	2	1	2	2	2	2
sheo168	3	7	1.5	1	1.5	1	2	2
shdb216	2	3	1	0	1	1	0	2
shem252	2	3	1	1	0	0	1	2
sher238	2	3	1	0	1	0	1	1
sher244	2	3	1	0	1	0	1	2.5
shfr082	2	3	1	0	1	0	1	3
shfr094	2	3	1	0	1	1	0	2
shdb219	2	3	0	0	1	2	0	2
shem253	2	3	0	0	1	1	1	2
sher221	2	3	0	0	0	2	1	2
shfr085	2	2.5	0	0	0	1.5	1	2
sheo22_A	2	2	1	0	1	0	0	1
sher246	2	2	1	0	1	0	0	1
shfr092	2	2	1	0	1	0	0	2
shcm182	2	2	0	0	0	2	0	2
shcm229	2	2	0	0	1	1	0	2.5
shdb208	2	2	0	0	0	1	1	2

shem251	2	2	0	0	0	1	1	1
sher209	2	2	0	0	1	0	1	1
shfr093	2	2	0	0	1	0	1	2
sheo142	2	3	0	0	1	1	1	2
sheo139	2	3.5	0	0	0	2.5	1	1
shem205	1	1.5	0	0	0	1.5	0	2
shfr083	1	1.5	0	0	0	1.5	0	2
shcm181	1	1	0	0	1	0	0	2
shcm228	1	1	0	0	1	0	0	2.5
shdb211	1	1	0	0	0	0	1	2
shdb212	1	1	0	0	1	0	0	1.5
shdb218	1	1	0	0	0	0	1	1
sheo42_A	1	1	0	0	0	0	1	1
sher180	1	1	0	0	0	1	0	1
sher190	1	1	0	0	0	0	1	2
sher208	1	1	0	0	0	0	1	2
shfr072	1	1	0	0	0	1	0	2
shfr084	1	1	0	0	0	0	1	1
shfr117	1	1	0	0	1	0	0	2
shfr119	1	1	0	0	1	0	0	2
shcm180	1	0	0	0	0	0	0	2
shcm185	1	0	0	0	0	0	0	1
shcm191	1	0	0	0	0	0	0	2
shcm192	1	0	0	0	0	0	0	1
shcm193	1	0	0	0	0	0	0	2
shdb204	1	0	0	0	0	0	0	2
shdb214	1	0	0	0	0	0	0	2
shdb215	1	0	0	0	0	0	0	1.5
shdb217	1	0	0	0	0	0	0	2
shdb221	1	0	0	0	0	0	0	2
shem206	1	0	0	0	0	0	0	2
shem254	1	0	0	0	0	0	0	1
sheo41_A	1	0	0	0	0	0	0	2
sher189	1	0	0	0	0	0	0	2
sher198	1	0	0	0	0	0	0	2
sher211	1	0	0	0	0	0	0	2
sher222	1	0	0	0	0	0	0	1
sher228	1	0	0	0	0	0	0	2
sher230	1	0	0	0	0	0	0	1
sher231	1	0	0	0	0	0	0	2
sher232	1	0	0	0	0	0	0	2
sher239	1	0	0	0	0	0	0	3
sher240	1	0	0	0	0	0	0	1
sher241	1	0	0	0	0	0	0	2
sher242	1	0	0	0	0	0	0	1
sher245	1	0	0	0	0	0	0	2
shfr073	1	0	0	0	0	0	0	2
shfr075	1	0	0	0	0	0	0	2
shfr076	1	0	0	0	0	0	0	2
shfr095	1	0	0	0	0	0	0	2
shfr106	1	0	0	0	0	0	0	2
shfr107	1	0	0	0	0	0	0	2
shfr118	1	0	0	0	0	0	0	2
sheo65_A	1	1	0	0	0	0	1	2
sheo141	1	0	0	0	0	0	0	2
sheo64_A	1	0	0	0	0	0	0	2
sheo67_A	1	0	0	0	0	0	0	2

2.4 Measurement data and specification of data processing

2.4.1 Raw data description

Scan hardware: GenePix Personal 4100 A
Scan software: GenePix Pro 4.1

Raw data can be found in the data section of our website (http://www.meduniwien.ac.at/nephrogene.at)

2.4.2 Image analysis and quantitation

Image griding and calculation of spot intensity was performed with GenePix Pro 4.1 software.

2.4.3 Normalized and summarized data

Preprocessing and Normalization:
For data retrieval the $\log_2$ (R/G normalized ratio [median]) values were used.
Quantile quantile normalization was applied to the dataset using the Bioconductor affy package.

Computation of missing values:
Missing values were obtained through computation of k-nearest-neighbor (k=10) with the EMV module (http://cran.at.r-project.org/src/contrib/Descriptions/EMV.html) of the R software package (http://cran.r-project.org).

Significance analysis:
The Statistical Analysis of Microarrays (SAM) method was used to identify differentially expressed genes (DEGs). The False Discovery Rate (FDR) was used to correct for multiple testing and was set to 5%.