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.akh-wien.ac.at/nephrogene/).

2 Experiment description

2.1 Experimental design

2.1.1 Laboratory, authors, contact

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2.1.2 Type of experiment

Comparison of compartments (tubulointerstitium, glomeruli) of transplant kidneys from living and cadaveric donors.

2.1.3 Experiment factors

The investigated kidneys were derived from two different donor sources (living donor and cadaveric donor). All of them exhibited immediate graft function.

2.1.4 Hybridizations

Twenty hybridizations (5 cadaveric donor kidney biopsies, 5 living donor kidney biopsies, each micro dissected into glomeruli and tubulointerstitium).

2.1.5 Reference

Stratagene Universal Human Reference RNA was used as hybridization reference.

2.1.6 Quality control

To test for reproducibility of sample processing a cadaveric biopsy was split in three parts and processed independently from RNA isolation to array readout.

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 and on our website (http://www.akh-wien.ac.at/nephrogene/).

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.akh-wien.ac.at/nephrogene/).

2.3 Hybridization procedures and parameters

Sample	Array	Sample	Array
LIV 140 G	shdb 197	CAD 151 TI	shdl 200
LIV 140 TI	shdb 198	CAD 185 TI	shdl 201
LIV 148 G	shdl 192	CAD 187 TI	shdl 202
LIV 148 TI	shdl 193	CAD 203 TI	shdl 203
LIV 199 TI	shdl 194	CAD 151 G	shdl 204
LIV 124 TI	shdl 195	CAD 185 G	shdl 205
LIV 139 TI	shdl 196	CAD 187 G	shdl 074
LIV 124 G	shdl 197	CAD 203 G	shdl 075
LIV 139 G	shdl 198	CAD 149 G	shdl 072
LIV 199 G	shdl 199	CAD 149 T	shdl 073

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

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 images can be found in the data section of our website (http://www.akh-wien.ac.at/nephrogene/).

Array	Laser power		PMT Gain		Lines Averaged	Background Subtraction	Scan region
	635 nm	532 nm	635 nm	532 nm			
shdl 072	2.98	3.45	600	560	1	LocalFeature	91,762,2016,6494
shdl 073	3.31	3.45	630	540	1	LocalFeature	89,809,2014,6567
shdl 074	3.3	3.47	620	570	1	LocalFeature	129,721,2026,6470
shdl 075	3.23	3.39	630	530	1	LocalFeature	89,779,2050,6478
shdl 192	3.45	3.3	840	620	1	LocalFeature	89,89,2103,7053
shdl 193	3.34	3.28	810	610	1	LocalFeature	97,137,2087,7045
shdl 194	3.2	3.26	740	600	1	LocalFeature	97,324,2079,6583
shdl 195	2.93	3.44	840	570	1	LocalFeature	138,316,2079,6656
shdl 196	2.93	3.44	840	570	1	LocalFeature	138,316,2079,6656
shdl 197	2.86	3.44	650	520	1	LocalFeature	154,713,2070,6598
shdl 198	2.86	3.41	650	400	1	LocalFeature	154,770,2094,6493
shdl 199	2.89	3.45	730	590	1	LocalFeature	129,526,2086,6671
shdl 200	2.94	3.46	650	540	1	LocalFeature	165,680,2035,6356
shdl 201	2.93	3.45	650	540	1	LocalFeature	146,763,2040,6381
shdl 202	2.98	3.48	620	540	1	LocalFeature	170,721,2033,6332
shdl 203	3.2	3.45	630	525	1	LocalFeature	146,713,2038,6502
shdl 204	3.15	3.45	625	570	1	LocalFeature	133,729,2026,6470
shdl 205	2.9	3.45	625	570	1	LocalFeature	138,883,2036,6567
shdb 197	3.34	3.27	830	570	1	LocalFeature	138,470,2014,6640
shdb 198	3.44	3.27	840	610	1	LocalFeature	89,154,2111,6980

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

Normalization:
Normalization was done through the default computed normalization by SMD (see http://genome-www5.stanford.edu/help/results_normalization.shtml). For data retrieval the $\log_2$ (R/G normalized ratio [median]) was used.

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/PACKAGES.html#EMV) of the R software package (http://cran.r-project.org).

Cluster analysis:
Before cluster analysis different standard deviation filters were applied (program Cluster ©1998-9 (http://rana.lbl.gov/EisenSoftware.htm). Software used for cluster analysis was Statistica 6 (Statsoft Inc., Tulsa, Oklahoma).

Linkage rule: Complete linkage
Distance measure: 1 – Pearson r

Significance analysis:
Significance analysis was performed with the maxT algorithm, which is available in the Bioconductor module (http://www.bioconductor.org) of the R software package