1 Array design description

A brief description of the array design, feature location, information on the **Human Exonic Evidence Based Oligonucleotide (HEEBO) Arrays** and the spotting protocols can be found on the producer website (http://www.microarray.org/sfgf/jsp/home.jsp).

All microarray experiment protocols can be found on the Stanford University webpage at http://cmgm.stanford.edu/pbrown/protocols/index.html.

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 PBMCs from peritoneal dialysis (PD) patients between two different PD solutions (Physioneal® 40 and Extraneal®).

2.1.3 Experiment factor

The expression of genes were investigated and compared between the two treatments Physioneal® 40 and Extraneal®.

2.1.4 Hybridizations

Ten hybridizations (five replicates Physioneal® 40 treatment, five Extraneal® treatment).

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*

2.2.2 Biomaterial manipulations, hybridization and labeling protocol

Protocols for PBMC isolation and RNA extraction can be found on our website (http://www.meduniwien.ac.at/nephrogene/). Protocols for RNA labeling, hybridization and washing of microarrays can be found on the Stanford University webpage at http://cmgm.stanford.edu/pbrown/protocols/index.html.

2.3 Hybridization procedures and parameters

Patient-No.	PD-Solution	Batch-ID	Barcode
1	Extraneal® (1)	HOT157	00058071
1	Physioneal® 40 (2)	HOT158	00058072
2	Extraneal® (1)	HOT159	00058073
2	Physioneal® 40 (2)	HOT163	00058077
3	Extraneal® (1)	HOT160	00058074
3	Physioneal® 40 (2)	HOT161	00058075
4	Extraneal® (1)	HOT164	00058078
4	Physioneal® 40 (2)	HOT162	00058076
5	Extraneal® (1)	HOT165	00058079
5	Physioneal® 40 (2)	HOT166	00058080

The hybridization protocol can be found on the Stanford University webpage at http://cmgm.stanford.edu/pbrown/protocols/index.html.

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 6.0

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

Array	Laser power		PMT Gain		Lines Averaged	Background Subtraction	Scan region
	635 nm	532 nm	635 nm	532 nm			
HOT157	3.44	3.46	500	505	1	LocalFeature	139,490,2058,6521
HOT158	3.43	3.48	530	505	1	LocalFeature	160,490,2079,6406
HOT159	3.39	3.47	545	490	1	LocalFeature	164,528,2083,6185
HOT163	3.28	3.48	500	490	1	LocalFeature	159,564,2065,6455
HOT160	3.30	3.48	520	485	1	LocalFeature	164,528,2083,6537
HOT161	3.30	3.52	500	500	1	LocalFeature	148,466,2067,6422
HOT164	3.37	3.48	515	465	1	LocalFeature	152,542,2060,6439
HOT162	3.32	3.51	495	500	1	LocalFeature	148,531,2067,6373
HOT165	3.30	3.44	535	490	1	LocalFeature	159,564,2065,6439
HOT166	3.33	3.49	520	500	1	LocalFeature	114,603,2069,6480

2.4.2 Image analysis and quantitation

Image griding and calculation of spot intensity was performed with GenePix Pro 6.0 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/Descriptions/EMV.html) 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 TIGR Multi Experiment Viewer 3.0.3 (http://www.tm4.org/mev.html).

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

Significance analysis:
No adjustment for multiple testing was performed. Genes showing a fold change of at least two and a p-value (paired t-test) smaller than 0.05 were considered differentially expressed and used for further analysis.