Table 1

Demographic data of PD-patients. Data are represented as counts or median and full range.

Parameter	**Number**
Patients	5
Diabetes mellitus	0
Previous NTX	0
Steroids	0
Patients with residual renal function (RRF)	5
Smokers	1
	Median (range)
Age (years)	56 (29 - 67)
Men/women	2/3
Weight (kg)	72 (53 - 84)
Month on dialysis	8 (4 - 18)
Albumin (g/L)	39 (36 - 43)
Hematocrit (%)	34.8 (34 – 40.8)
EPO (IU/week)	2000 (0 - 5000)
Kt/V (weekly)	2.5 (2.2 - 3.3)
RRF	1.2 (0.9 – 1.9)

Table 2
Biological processes separating IBF and GBF treated patient groups as derived on the level of PBMC differential gene expression. Categories are ranked by the p-value indicating the relevance of a particular process.

DEGs up-regulated by IBF treatment

Biological process	Gene-Symbols	p-value
Immunity and defence	CIITA, UNQ3033, SCGB1C1, CLEC1B, CTSW, CLEC4E, TNFRSF7, CLEC10A	<0.001
Natural killer cell mediated immunity	UNQ3033, CLEC1B, CTSW	<0.001
T-cell mediated immunity	CIITA, CTSW, TNFRSF7	0.001
Cell communication	UNQ3033, SCGB1C1, CLEC1B, STAT4, CLEC10A	0.008
Other neuronal activity	SP110, RASGRP2	0.009
Macrophage-mediated immunity	CLEC4E, CLEC10A	0.010
Ligand-mediated signaling	STAT4, UNQ3033, SCGB1C1	0.010
Other immune and defense	SCGB1C1, CLEC4E	0.012
Glucose hemeostasis	STAT4	0.021
Signal transduction	LST1, STAT4, UNQ3033, SCGB1C1, RASGRP2, CLEC1B, TNFRSF7, CLEC10A	0.022
MHCI-mediated immunity	CTSW	0.023
Cytokine und chemokine mediated signaling pathways	STAT4, TNFRSF7	0.029
MHCII-mediated immunity	CIITA	0.036
Glycolysis	HK3	0.048

DEGs up-regulated by GBF treatment

Biological process	Gene-Symbols	p-value
Ectoderm development	CELSR2, FOXA2, HLF, KRT80, TNFRSF21, COBLL1, NTN4, CRABP1, NLGN2, FGFR3, THSD3	<0.001
Signal transduction	FRAS1, DOC1, CELSR2, MGP, RND3,CGA, GNG4, RAB23, FOXA2, AXL, CAP2, CDH13, INPP5F, TACSTD2, TNFRST21, MFAP4, DIRAS1, CRABP1, NLGN2, SFRP2, THSD3, GPR161, FGFR3, NTN4	<0.001
Neurogenesis	CELSR2, FOXA2, HLF, TNFRSF21, COBLL1, NTN4, NLGN2, FGFR3, THSD3	<0.001
Cell communication	FRAS1, CELSR2, MGP, CGA, FOXA2, CAP2, CDH13, MFAP4, NTN4, CRABP1, NLGN2, SFRP2, THSD3	<0.001
Oncogenesis	DOC1, AXL, CDH13, MAGEA12, NTN4, MLF1, FGFR3, THSD3	<0.001
Developmental processes	DOC1, CELSR2, MGP, FOXA2, HLF, KRT80, TTK, MAGEA12, EFHD1, TNFRSF21, COBLL1, NTN4, CRABP1,	0.001

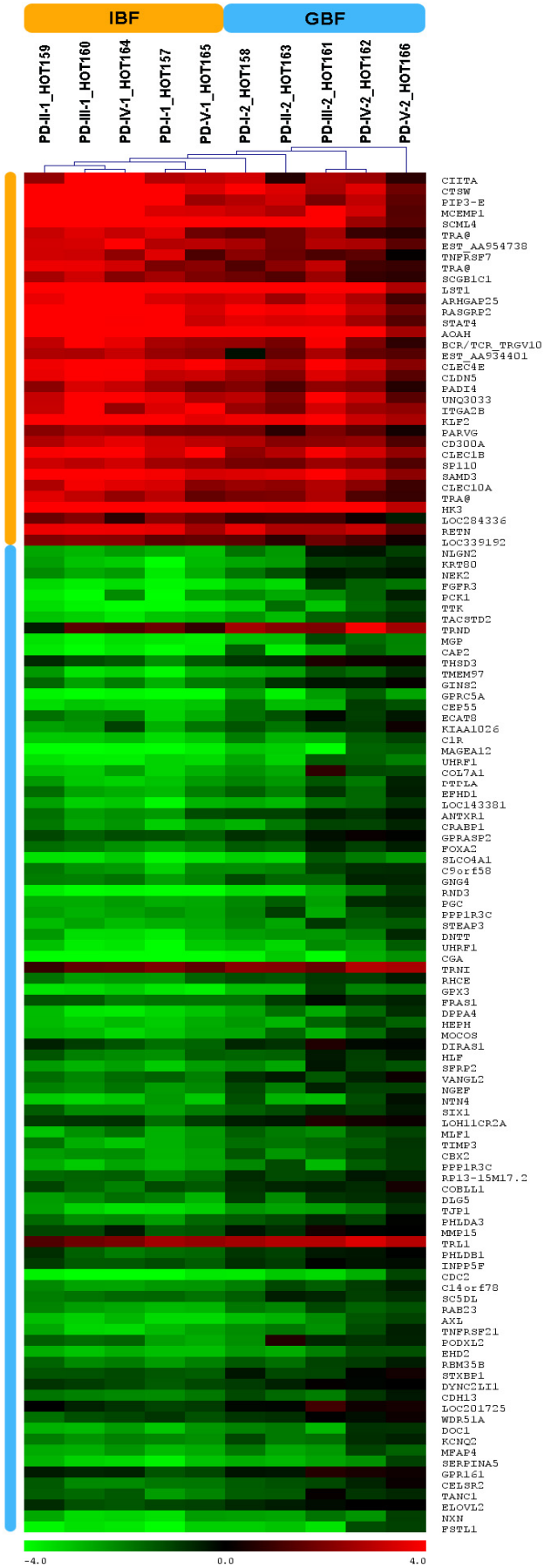
	NLGN2, FGFR3, THSD3	
Other oncogenesis	MAGEA12, FGFR3, THSD3	0.002
Cell proliferation and differentation	DOC1, FOXA2, AXL, TACSTD2, C9orf58, UHRF1, NTN4, MLF1, GINS2, FGFR3	0.002
Cell structure	DLG5, CELSR2, COL7A1, FOXA2, KRT80, PHLDB1, TJP1	0.006
Cell structure and motility	DLG5, CELSR2, COL7A1, FOXA2, KRT80, PHLDB1, TJP1, RND3, CAP2	0.011
DNA replication	DOC1, CDC2, GINS2	0.014
Homeostasis	CGA, HEPH, FSTL1	0.025
Stress response	MOCOS, C9orf58, GPX3	0.026
Other cell cycle process	UHRF1	0.028
DNA metabolism	DOC1, CDC2, DNTT, GINS2	0.028
Other receptor mediated signaling pathway	FOXA2, TACSTD2, TNFRSF21	0.030
Proteolysis	DOC1, DGC, C1R, MMP15, CAP2, SERPINA5, TIMP3	0.033
Cell surface receptor mediated signal transduction	CELSR2, RND3, GNG4, FOXA2, AXL, TACSTD2, TNFRSF21, FGFR3, THSD3, GPR161	0.035
Other steroid metabolism	SC5DL	0.041
Cell cycle	DOC1, CDC2, FOXA2, TTK, C9orf58, UHRF1, GINS2	0.042
Sex determination	TTK	0.044
Cell cycle control	DOC1, CDC2, FOXA2, C9orf58	0.045
Neurotransmitter release	STXBP1, EHD2	0.046
Cell adhesion	CELSR2, COL7A1, CDH13, MFAP4, NLGN2	0.049

Figure Legends

Figure 1
The dendrogram derived by unsupervised hierarchical clustering of differentially expressed genes comparing IBF and GBF treatment (PD: Peritoneal dialysis, I-V: patient ID, 1: IBF, 2: GBF, microarray label). The Pearson correlation and complete linkage were used as distance measure and linkage rule in the hierarchical cluster algorithm. Red spots indicate abundantly expressed transcripts, whereas green spots indicate transcripts expressed on low level when compared to the reference RNA.

Figure 2
Largest protein-protein interaction subgraph derived on the basis of differentially regulated genes with a fold change over 1.5, respectively. Blue nodes (98 DEGs) indicate up-regulated genes by GBF treatment and orange nodes (34 DEGs) up-regulated genes by IBF treatment. Gray nodes represent proteins identified by the nearest neighbour expansion method.

Figure 1


IBF
GBF
PD-II-1_HOT159
PD-III-1_HOT160
PD-IV-1_HOT164
PD-I-1_HOT157
PD-V-1_HOT165
PD-I-2_HOT158
PD-II-2_HOT163
PD-III-2_HOT161
PD-IV-2_HOT162
PD-V-2_HOT166
CIITA
CTSW
PIP3-E
MCEMP1
SCML4
TRA@
EST_AA954738
TNFRSF7
TRA@
SCGB1C1
LST1
ARHGAP25
RASGRP2
STAT4
AOAH
BCR/TCR_TRGV10
EST_AA934401
CLEC4E
CLDN5
PADI4
UNQ3033
ITGA2B
KLF2
PARVG
CD300A
CLEC1B
SP110
SAMD3
CLEC10A
TRA@
HK3
LOC284336
RETN
LOC339192
NLGN2
KRT80
NEK2
FGFR3
PCK1
TTK
TACSTD2
TRND
MGP
CAP2
THSD3
TMEM97
GINS2
GPRC5A
CEP55
ECAT8
KIAA1026
C1R
MAGEA12
UHRF1
COL7A1
TTPLA
EFHD1
LOC143381
ANTXR1
CRABP1
GPRASP2
FOXA2
SLCO4A1
C9orf58
GNG4
RND3
PGC
PPP1R3C
STEAP3
DNTT
UHRF1
CGA
TRNI
RHCE
GPX3
FRAS1
DPPA4
HEPH
MOCOS
DIRAS1
HLF
SFRP2
VANGL2
NGEF
NTN4
SIX1
LOH11CR2A
MLF1
TIMP3
CBX2
PPP1R3C
RP13-15M17.2
COBLL1
DLG5
TYP1
PHLDA3
MMP15
TRL1
PHLDB1
INPP5F
CDC2
C14orf78
SC5DL
RAB23
AXL
TNFRSF21
PODXL2
EHD2
RBM35B
STXBP1
DYNC2LI1
CDH13
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WDR51A
DOC1
KCNQ2
MFAP4
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FSTL1
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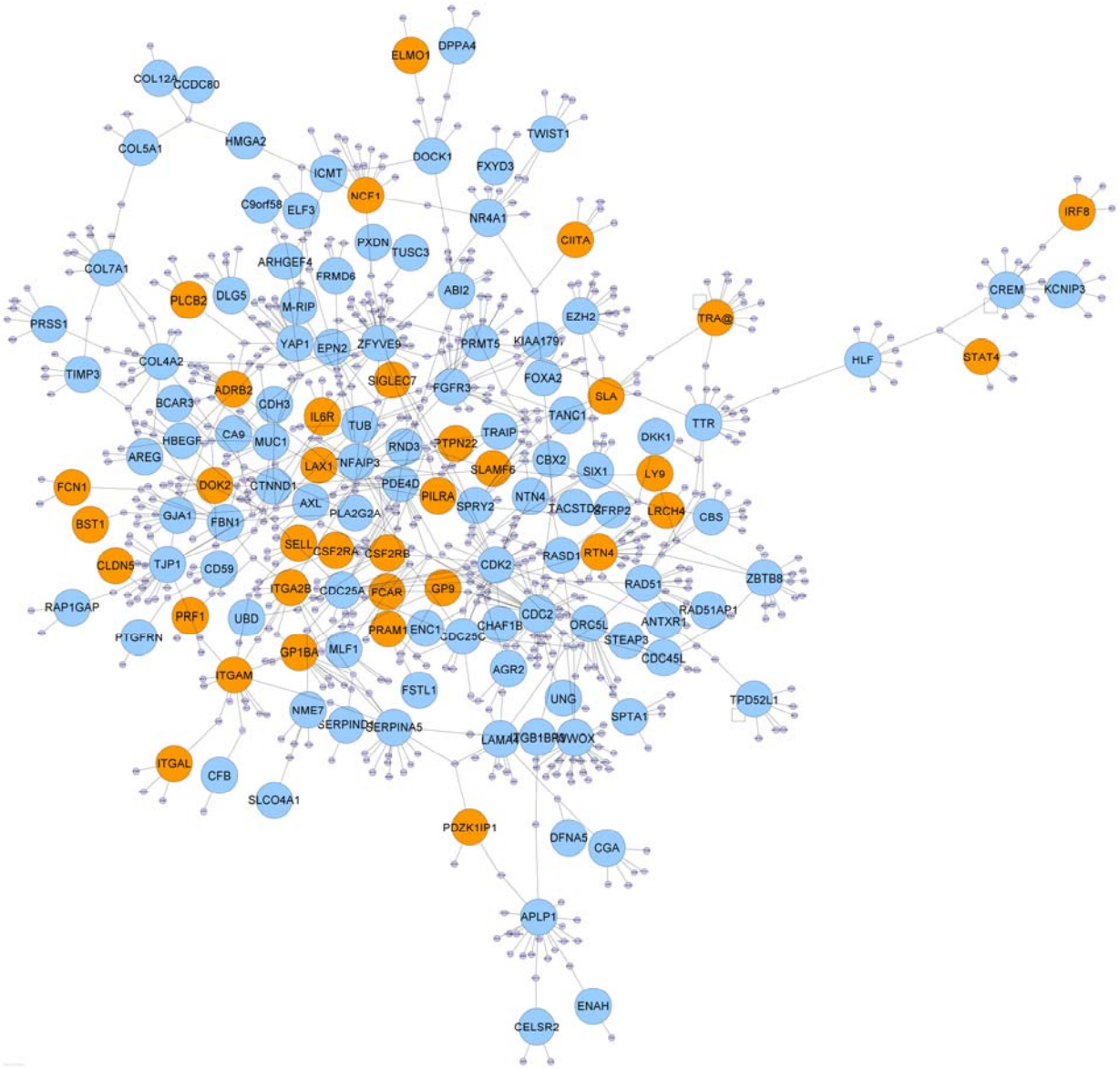
0.0
4.0

Figure 2


ELMO1
DPPA4
COL12A1
CCDC80
COL5A1
HMGA2
TWIST1
DOCK1
FXYD3
ICMT
NCF1
C9orf58
ELF3
NR4A1
IRF8
CIITA
PXDN
TUSC3
COL7A1
ARHGEF4
FRMD6
ABI2
CREM
KCNIP3
PLCB2
DLG5
M-RIP
EZH2
TRA@
PRSS1
YAP1
EPN2
ZFYVE9
PRMT5
KIAA1797
HLF
STAT4
TIMP3
COL4A2
SIGLEC7
FGFR3
FOXA2
ADRB2
SLA
BCAR3
CDH3
IL6R
TUB
TANC1
TTR
HBEGF
CA9
MUC1
RND3
PTPN22
TRAIP
DKK1
AREG
LAX1
NFAIP3
CBX2
SIX1
LY9
FCN1
DOK2
CTNND1
PDE4D
SLAMF6
PILRA
SPRY2
NTN4
TACSTD2
SFRP2
LRCH4
CBS
BST1
GJA1
FBN1
AXL
PLA2G2A
SELL
CSF2RA
CSF2RB
CDK2
RASD1
RTN4
CLDN5
TJP1
CD59
ZBTB8
ITGA2B
CDC25A
FCAR
GP9
RAD51
RAP1GAP
PRF1
UBD
CDC2
RAD51AP1
PRAM1
ENC1
CHAF1B
ORC5L
ANTXR1
PTGFRN
CDC25C
STEAP3
GP1BA
MLF1
CDC45L
ITGAM
AGR2
FSTL1
UNG
TPD52L1
NME7
SERPIND1
SERPINA5
SPTA1
LAMA4
ITGB1BP3
WOX
ITGAL
CFB
SLCO4A1
PDZK1IP1
DFNA5
CGA
APLP1
ENAH
CELSR2

qRT-PCR Validation

Method

Expression profiles of four selected genes (CIITA, TNFRSF7, CTSW, CLEC1B) were analyzed by real time PCR. Total RNA isolated from the same samples like in the microarray experiments was used for cDNA synthesis with the High Capacity cDNA Reverse Transcription Kit. Real time PCR was performed using TaqMan Gene Expression Master Mix and TaqMan Gene expression assays (Hs00172106_m1, Hs00386811_m1, Hs00175160_m1, Hs00212925_m1) on an ABI 7300 Sequence Detection System. Relative gene expression values were evaluated with the $2^{-\Delta\Delta Ct}$ method using PPIA (Hs99999904_m1, cyclophilin A) as housekeeping gene and Stratagene Universal human reference RNA (Stratagene, La Jolla, California) as reference. All instruments and real time PCR reagents were purchased by Applied Biosystems (Foster City, CA, USA).

Results

The relative expression levels of the four selected genes after the peritoneal dialysis treatment with glucose (GBF) or icodextrin (IBF) in the oligo microarray and qRT-PCR experiment are shown in table S1. For the visualization in figure S1 the median relative expression of the five PD-patients after GBF treatment in both experiments was set to zero allowing to compare the differences to the IBF treatment directly in one figure. All four genes show an up-regulation after the IBF treatment. Almost all of the patients show the same trend in the qRT-PCR and microarray experiment, although the up-regulation is less in the validation experiment

Table S1. Log_2 (relative expression) in the microarray and qRT-PCR experiment of five patients (PD-I – PD-V) after glucose based fluid (GBF) or icodextrin based fluid (IBF) peritoneal dialysis treatment.

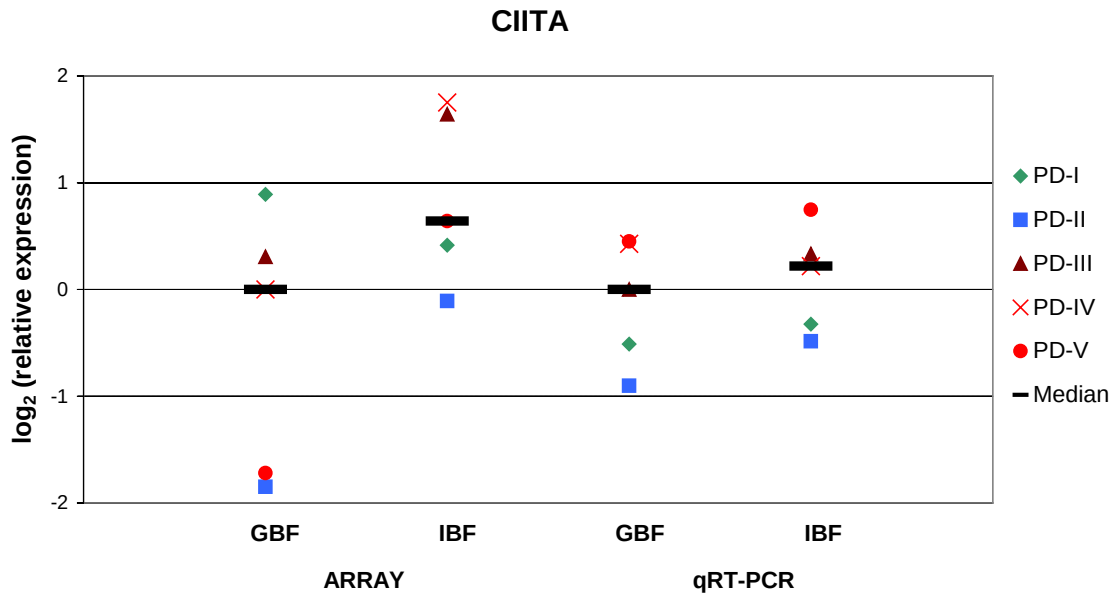
	CIITA			
	Array		**qRT-PCR**	
	GBF	IBF	GBF	IBF
PD-I	3.31	2.83	7.76	7.95
PD-II	0.57	2.31	7.37	7.79
PD-III	2.73	4.06	8.27	8.61
PD-IV	2.42	4.17	8.70	8.49
PD-V	0.70	3.06	8.72	9.02

	TNFRSF7			
	Array		**qRT-PCR**	
	GBF	IBF	GBF	IBF
PD-I	2.18	3.54	10.35	10.62
PD-II	1.71	3.28	10.50	11.26
PD-III	1.22	3.20	9.61	9.91
PD-IV	1.47	2.29	9.62	9.30
PD-V	0.08	1.21	10.93	12.30

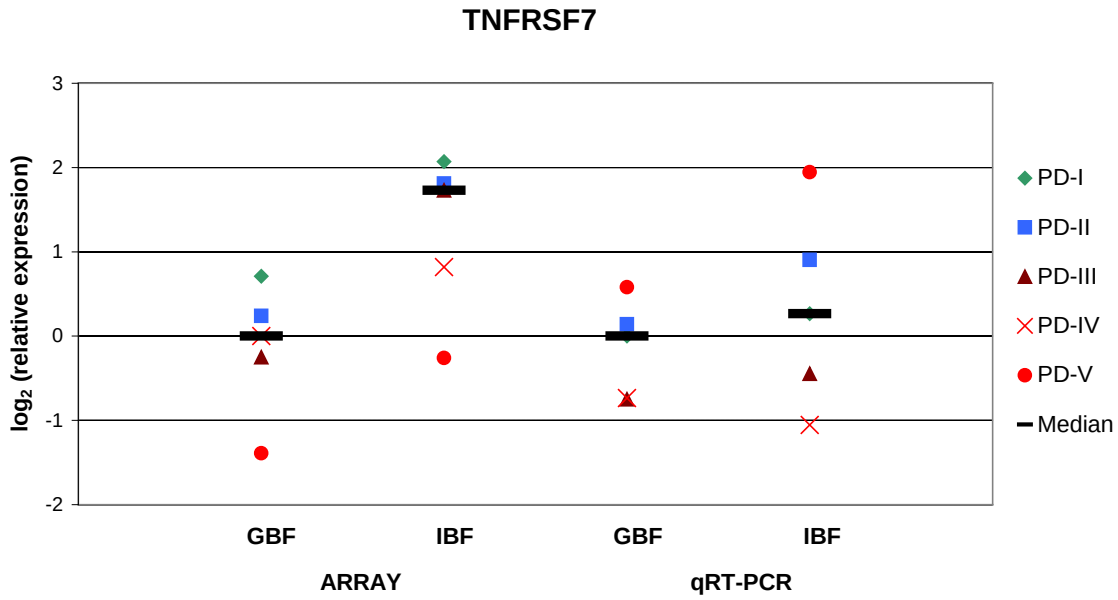
	CTSW			
	Array		**qRT-PCR**	
	GBF	IBF	GBF	IBF
PD-I	4.23	4.28	11.70	11.65
PD-II	3.47	4.98	11.88	11.81
PD-III	2.67	4.45	11.78	11.86
PD-IV	3.54	4.47	12.33	12.83
PD-V	1.75	3.46	11.69	12.12

	CLEC1B			
	Array		**PCR**	
	GBF	IBF	GBF	IBF
PD-I	2.25	3.27	13.00	13.83
PD-II	2.87	3.92	13.92	14.09
PD-III	3.91	4.67	14.76	15.15
PD-IV	3.32	4.52	15.47	15.55
PD-V	2.31	4.07	16.85	16.98

A


CIITA
log2 (relative expression)
2
1
0
-1
-2
GBF
IBF
GBF
IBF
ARRAY
qRT-PCR
PD-I
PD-II
PD-III
PD-IV
PD-V
Median

B


TNFRSF7
log2 (relative expression)
3
2
1
0
-1
-2
GBF
IBF
GBF
IBF
ARRAY
qRT-PCR
PD-I
PD-II
PD-III
PD-IV
PD-V
Median

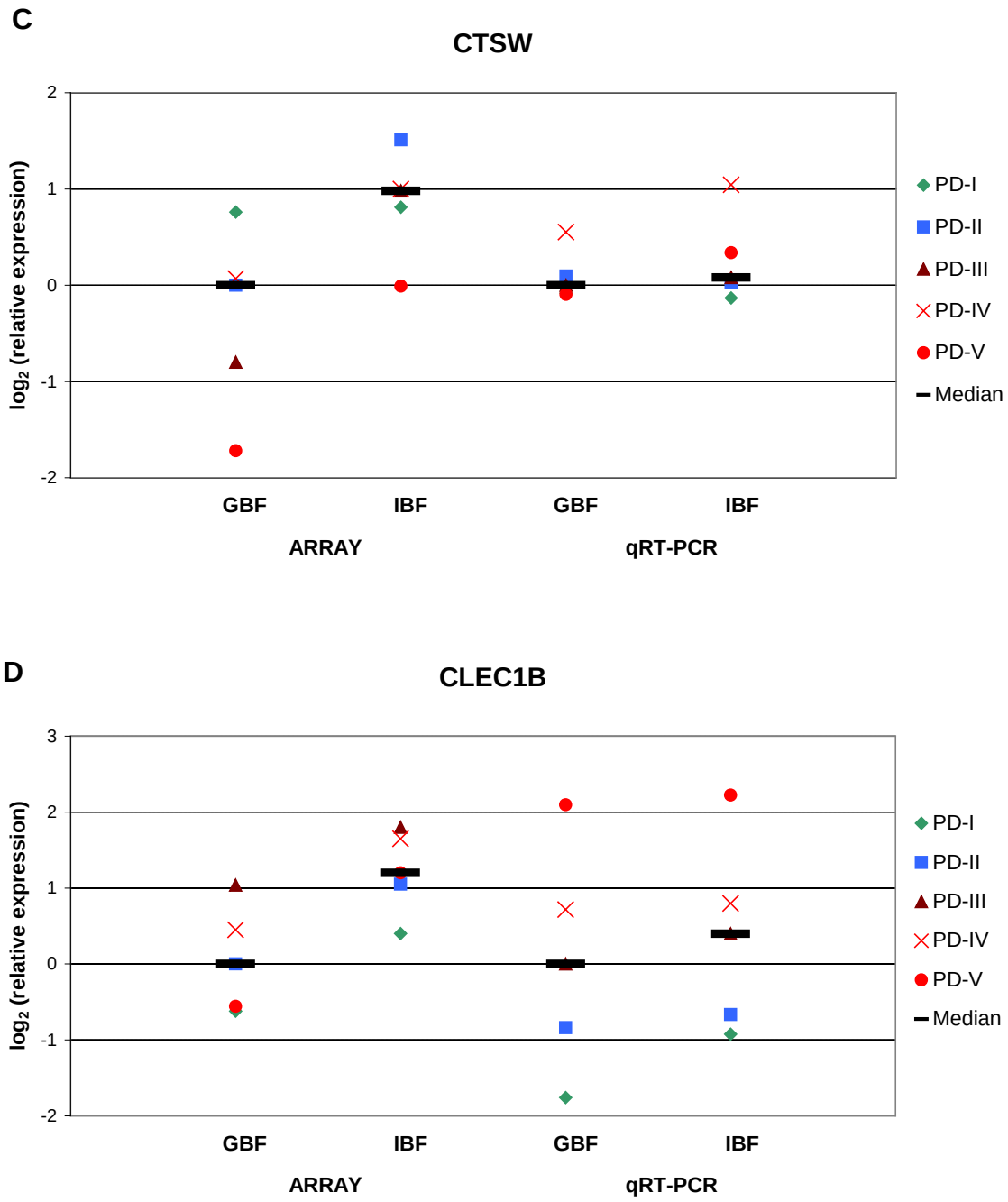


Figure S1. qRT-PCR validation of four selected genes (CIITA, TNFRSF7, CTSW, CLEC1B): The $\log_2$ (relative expression) measured in the microarray and in the realtime RT-PCR (TaqMan assays) experiment of five PD patient (PD-I – PD-V) and their median is shown. Median $\log_2$ (relative expression) after the glucose based fluid (GBF) peritoneal dialysis treatment in the microarray and qRT-PCR experiment was set to zero allowing to compare the relative differences to the icodextrin based fluid

(IBF) treatment in both experiments in one figure. All genes (A-D) are up-regulated by IBF in both methods although the up-regulation is less in the validation experiment.