

Titles and legends

Table 1

Representation of differentially expressed genes involved in a significant biological process, pathway or molecular function according to PANTHER ontologies when comparing semi-synthetic and full-synthetic membranes. The biological processes are ranked by p-value (as given by a chi-square test including Bonferroni correction when comparing the number of genes associated to the category with the total number of genes belonging to this particular pathway).

Table 2

Demographic data of HD patients. Data are represented as counts or median and interquartile range (IQR).

Figure 1

Correlation of the differential gene expression values of 299 features showing a fold change > 2 after hemodialysis derived from PBMCs harvested before HD. Given are the expression values before using semi-synthetic membranes (M1), plotted against expression values before using full-synthetic membranes (M2). Patient-specific correlation ranges in between 0.88 and 0.96.

Figure 2A

Protein-protein interaction network derived on the basis of differentially expressed genes when comparing semi- and full-synthetic membranes, additionally including interacting proteins as determined by the next neighbour expansion. Orange nodes (110 DEGs) indicate up-regulated genes afflicted with the semi-synthetic membrane, and blue nodes (49 DEGs) indicate features up-regulated in the context of full-synthetic membranes. Gray nodes represent proteins identified by the nearest neighbour expansion method on the basis of protein interactions represented in OPHID.

Figure 2B

The index of aggregation (IA; y-axis) in dependence of the number of proteins used for constructing protein interaction networks (x-axis). The IA of DEGs is significantly above the IA of randomly selected lists. The thick black line represents mean IAs of randomly selected gene lists. Dotted lines represent the double standard deviations of these distributions.

Table 1

DEGs up-regulated in the context of semi-synthetic HD membranes		
Biological Process	Gene-Symbols	p-value
Immunity and defense	ABCC5, ALOX12, CAMP, CCL2, CCR1, CD163, CLEC1B, CSF1R, CSF3R, CTSS, EPHX1, F2, FCGR1A, FCGR2B, GAB3, GBP1, GZMA, HLA-DQB1, HLA-DRB1, HLA-E, IRF7, ITGB1, KLRB1, LGALS9, LILRB3, LRRK2, LTB, MS4A2, PF4, PHCA, PPARA, PTPRC, RGS1, S100A8, SLA, TAP2, TGIF, TNFRSF8, XRCC6	<0.001
Signal transduction	ABI3, ADRBK2, ARHGAP30, CCL2, CCR1, CENTA1, CHES1, CLEC1B, CSF1R, CSF3R, DOCK10, DTX4, ERBB3, FAS, FCGR1A, FCGR2B, FLJ23834, FPR1, GAB3, GABBR1, IFT140, ITGB1, LATS2, LILRA2, LILRB3, LIMS1, LRRK2, LTB, LTBP1, MAPK8, MS4A2, MYLK, NCF1, NRTN, P2RY13, PF4, PLCB2, PPARA, PTPN7, PTPRC, RAB9A, RASSF4, RGS1, RGS18, RGS6, SLA, SOCS3, TGIF, TNFRSF8, WSB2, WWTR1	<0.001
Macrophage-mediated immunity	CD163, FCGR1A, FCGR2B, GAB3, GBP1, LTB, PF4, S100A8, TGIF	<0.001
Natural killer cell mediated immunity	CLEC1B, FCGR1A, FCGR2B, GZMA, KLRB1, LILRB3, LTB	<0.001
T-cell mediated immunity	CTSS, GAB3, GZMA, HLA-DQB1, HLA-DRB1, HLA-E, LTB, SLA, TNFRSF8	0.001
Cell motility	ABI3, CCR1, CSF1R, DOCK10, FPR1, ITGB1, LIMS1, LTBP1, PF4, S100A8, TUBB1	0.005
Cell surface receptor mediated signal transduction	ADRBK2, CCL2, CCR1, CENTA1, CHES1, CSF1R, CSF3R, DTX4, ERBB3, FAS, FPR1, GAB3, GABBR1, IFT140, LIMS1, LTB, MS4A2, P2RY13, PF4, PLCB2, RGS1, RGS18, RGS6, SLA, TGIF, TNFRSF8	0.007
Apoptosis	FAS, GZMA, LGALS9, MYBL2, NAIP, NALP1, PDCD5, PF4, RASSF4, SOCS3, STK17B, TGIF	0.009
Intracellular protein traffic	CAMP, CD163, COMT, DOCK10, ERO1L, IFT140, MX1, RAB9A, RASSF4, RIN1, RTN4, SSR2, STON2, STX5, TRAK2, TUBB1, YIPF5	0.017
Other metabolism	AKR1C3, CA2, COMT, CRSP2, DIO2, GNPAT1, MAP3K14, NEK2, PHCA, SLC27A3, SNAPC3	0.050
Pathway		
Inflammation mediated by chemokine and cytokine signaling pathway	ADRBK2, CCL2, SOCS3, PF4, ALOX12, PLCB2, RGS1, MYLK, CCR1, RGS18, FPR1, ITGB1	<0.001
Molecular Function		
Defense / immunity protein	CAMP, CLEC1B, FCGR1A, FCGR2B, HLA-DQB1, HLA-DRB1, HLA-E, KLRB1, LILRA2,	<0.001

	LILRB3, MS4A2, PLTP	
Receptor	CCR1, CD163, CLEC1B, CRSP2, CSF1R, CSF3R, ERBB3, FAS, FCGR1A, FCGR2B, FPR1, GABBR1, ITGB1, KLRB1, LILRA2, LILRB3, MS4A2, MS4A7, P2RY13, PIM1, PPARA, PTPRC, SSR2, TNFRSF8	0.003
Select regulatory molecule	ABI3, ARHGAP30, CAMP, CDK5R1, CENTA1, DOCK10, GBP1, MX1, NAIP, PDCD5, RAB9A, RASSF4, RGS1, RGS18, RGS6, RIN1, SEPT6, SIPA1, WWTR1	0.014

DEGs up-regulated in the context of full-synthetic membranes		
Biological Process	Gene-Symbols	p-value
Cell cycle	CCNB2, CYR61, EGFR, FOXF2, HTLF, JUN, KIF11, NBR2, TTK, TUBD1, UHRF1, WEE1	0.001
Cell cycle control	CCNB2, CYR61, EGFR, FOXF2, HTLF, JUN, WEE1	0.027

Table 2

	Median (IQR)
Age (years)	51.5 (15)
Male / female	2 / 2
Weight (kg)	79 (7)
Months on dialysis	16 (10)
Albumin (g/L)	42.5 (2.5)
Hematocrit (%)	37.5 (5)
EPO (IU/week)	3000 (155000)
Kt/V (weekly)	1.2 (0.09)

Figure 1

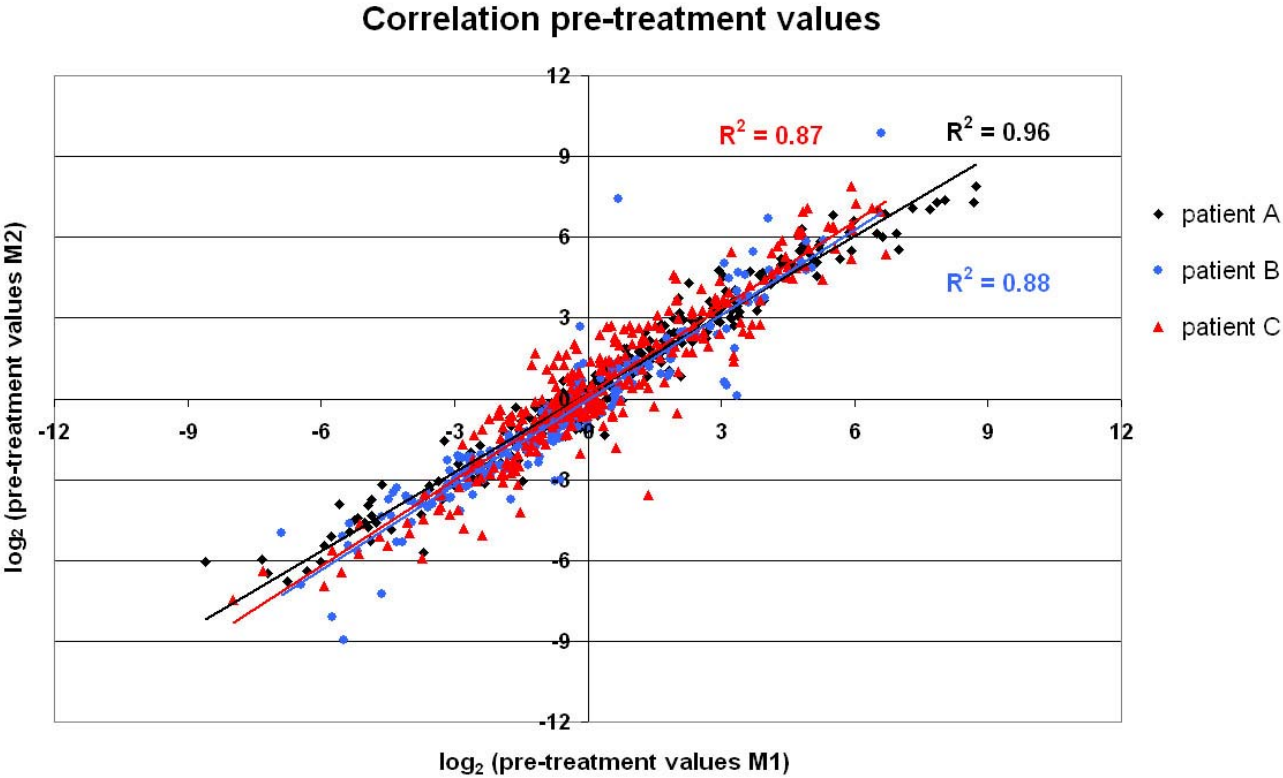


Figure 2A

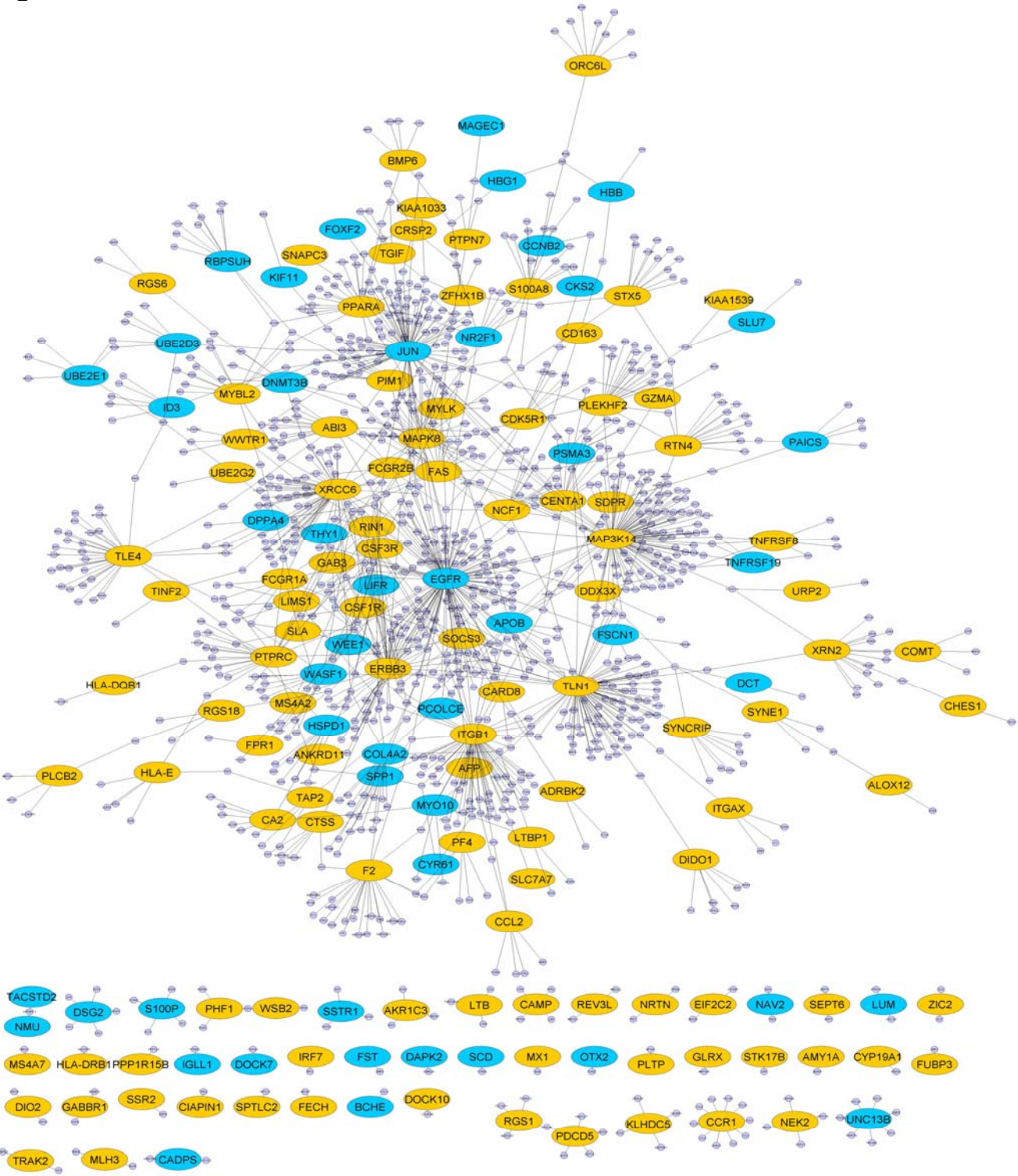


Figure 2B

Network complexity

