Figures and tables

Table 1
Demographic data of patients comparing ESA positive case and ESA negative control group. Continuous data are given as median and interquartile range. Categorical data are shown as counts or fractions. Significant p-values are given in bold.

Table 2
Multivariate logistic regression model. The discriminative power of this model is indicated by a cross-validation c-statistics of 0.93 (AUC). Given is the odds ratio (OR), the confidence interval, and the p-values.

Table 3
Discrimination of the models and optimism (3A) derived from the re-sampling procedure (50-fold cross validation). Calibration of the ESA prediction model by the Hosmer-Lemeshow goodness of fit test (3B). The expected to observed number of cases in each of the deciles of patients were not statistically different suggesting good calibration (p=0.88, Chi-square test).

Figure 1
Dendrogram derived by applying unsupervised hierarchical clustering on the basis of the expression profiles characterizing the ESA group (anaemia within the first year after transplantation, orange bar) and the non-ESA group (no anaemia within the first year after transplantation, blue bar). Red spots indicate upregulated transcripts, whereas green spots indicate downregulated transcripts relative to the reference RNA used. The 34 differentially expressed genes can be categorized according to PANTHER ontologies into their main biological processes: 1. immunity and defence, 2. endoderm development, 3. protein-lipid modification, 4. amino acid catabolism, 5. protein complex assembly, 6. carbon metabolism, 7. transport, 8. protein ADP-ribosylation, and 9. signal transduction.

Figure 2
Given is the largest protein-protein interaction subnetwork holding genes exhibiting differential expression further including protein interaction partners derived from OPHID. Blue nodes (38 features) indicate down-regulated genes and red nodes (40 features) denote up-regulated genes as found in the ESA positive group. Gray nodes represent proteins identified by the nearest neighbour expansion method.

Figure 3
ROC curves: Discrimination for ESA need within the first year after transplantation using clinical data (dotted line), expression features (dashed line), or the combination of both (solid line).

Table 1

	Nr. of drugs	ESA case group	non ESA control group	p-value
Samples		25	25	
Mean creatinine, first year after transplantation (mg/dl)		1.97 (1.10)	1.49 (0.47)	**0.006**
Mean eGFR (MDRD2), first year after transplantation (per ml/min/1.73 m^2)		37.6 (19.3)	44.7 (16.7)	**0.009**
Mean CRP, first year after transplantation (mg/dl)		0.80 (0.94)	0.57 (1.0)	0.922
Donor age (years)		53.5 (11)	42.6 (22)	**0.003**
Recipient age (years)		53.0 (27.0)	55.7 (21.4)	0.741
Recipient weight (kg)		77.0 (16.0)	71.0 (15.0)	0.234
Recipient sex (male / female)		17 / 8	19 / 6	0.529
Donor sex (male / female)		12 / 13	12 / 13	1.000
BCAR (%)		48	12	**0.006**
PRA latest		0 (2)	0 (3)	0.925
CIT (hours)		13 (12)	14.5 (7.5)	0.714
DM		5	6	0.733
Delayed graft function (no / yes)		22 / 3	25 / 0	*0.235
CMV (negative / positive)		13 / 6	13 / 5	0.800
Pyelonephritis (negative / positive)		23 / 2	20 / 5	*0.417
Hyperlipidemia (number of drugs 0 / 1)		18 / 7	12 / 13	0.083
Cholesterin	0	206 (104)	182 (48)	0.208
	1	224 (122)	186 (112)	0.812
Hypertension (number of drugs 0 / 1 / 2 / 3 / 4 / 5)		5 / 4 / 1 / 3 / 9 / 3	0 / 2 / 8 / 8 / 5 / 2	***0.008**
Mean arterial pressure	0	88 (17)	--	na
	1	97 (0)	103 (0)	0.480
	2	--	97 (3)	na
	3	107 (7)	97 (18)	0.306
	4	97 (17)	92 (8)	0.103
	5	107 (7)	98 (5)	0.149

* Fisher test

Table 2

Predictors	OR	95% CI		p-value
Donor age (per year)	1.086	1.007	1.171	**0.032**
Mean eGFR (per ml/min/1.73 m^2)	0.994	0.955	1.035	0.779
BCAR (1 vs 0)	6.491	0.733	57.496	0.093
Mean CRP (per mg/dl)	0.698	0.400	1.216	0.204
SPRR2C (AU)	0.238	0.067	0.847	**0.027**
B3GALTL (AU)	0.474	0.156	1.442	0.188
GSTT1 (AU)	2.397	1.205	4.767	**0.013**

AU: arbitrary units ($\log_2$-ratio of the amount of mRNA as found in the sample with respect to the concentration of the respective mRNA given by the universal reference mRNA used in the transcriptomics experiment).

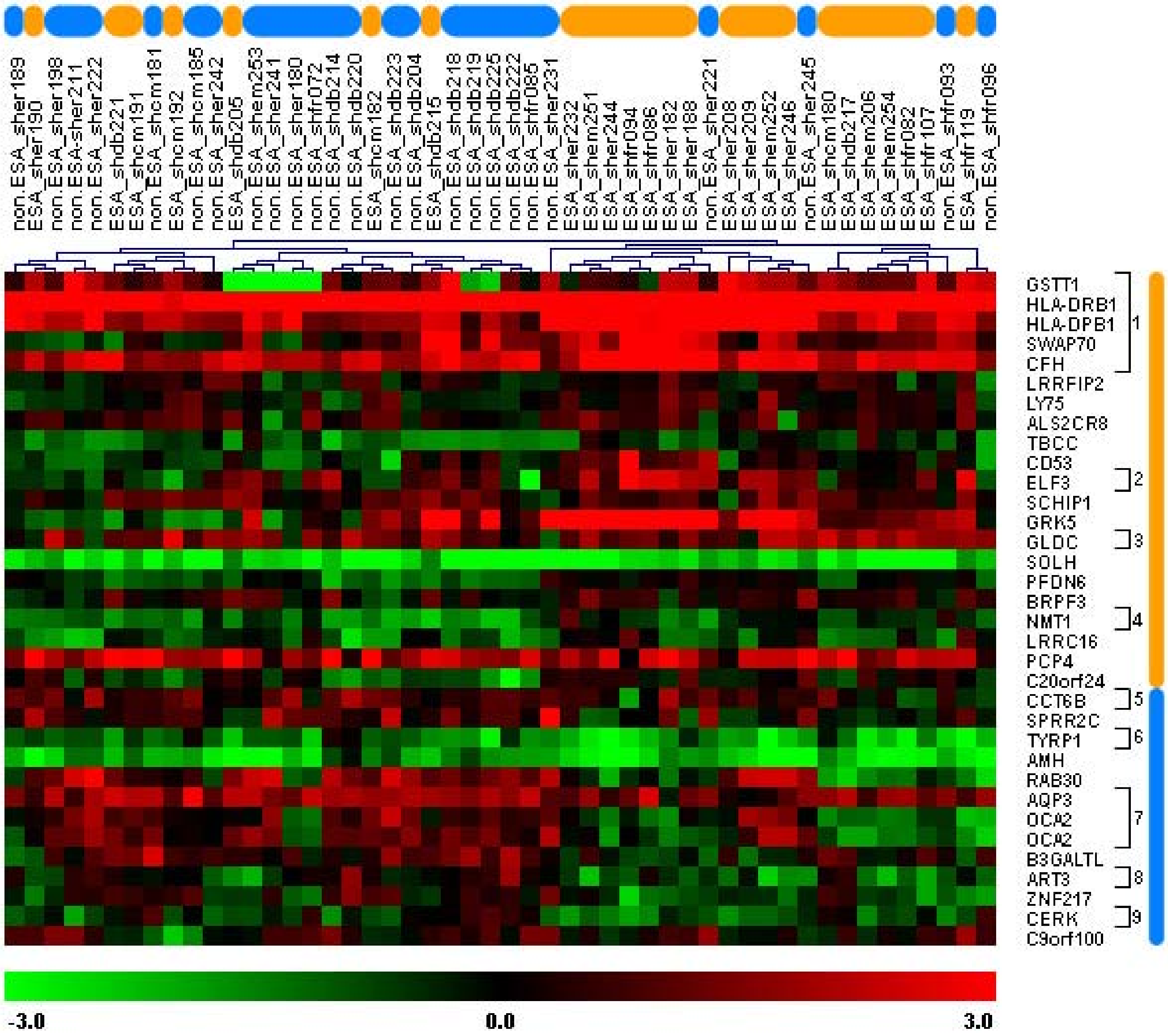
Table 3A

Model	AUC (c-statistic)	AUC (X-validation)	Optimism
Clinical predictors	0.84	0.75	0.09
Molecular predictors	0.85	0.79	0.06
Clinical and molecular predictors	0.93	0.84	0.09

Table 3B

Group	Total number of patients	ESA need		Non ESA need	
		Observed	Expected	Observed	Expected
1	5	0	0.05	5	4.95
2	5	0	0.26	5	4.74
3	5	1	0.62	4	4.38
4	5	1	0.80	4	4.20
5	5	2	1.66	3	3.34
6	5	2	3.12	3	1.88
7	5	5	4.18	0	0.82
8	5	4	4.54	1	0.46
9	5	5	4.81	0	0.19
10	5	5	4.95	0	0.05

Figure 1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non.ESA_shcm185
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non.ESA_sher241
non.ESA_sher180
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ESA_shdb217
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ESA_shfr107
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HLA-DRB1
HLA-DPB1
SWAP70
CFH
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LY75
ALS2CR8
TBCC
CD53
ELF3
2
SCHIP1
GRK5
GLDC
3
SOLH
PFDN6
BRPF3
NMT1
4
LRRC16
PCP4
C20orf24
CCT6B
5
SPRR2C
TYRP1
6
AMH
RAB30
AQP3
OCA2
OCA2
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9
C9orf100
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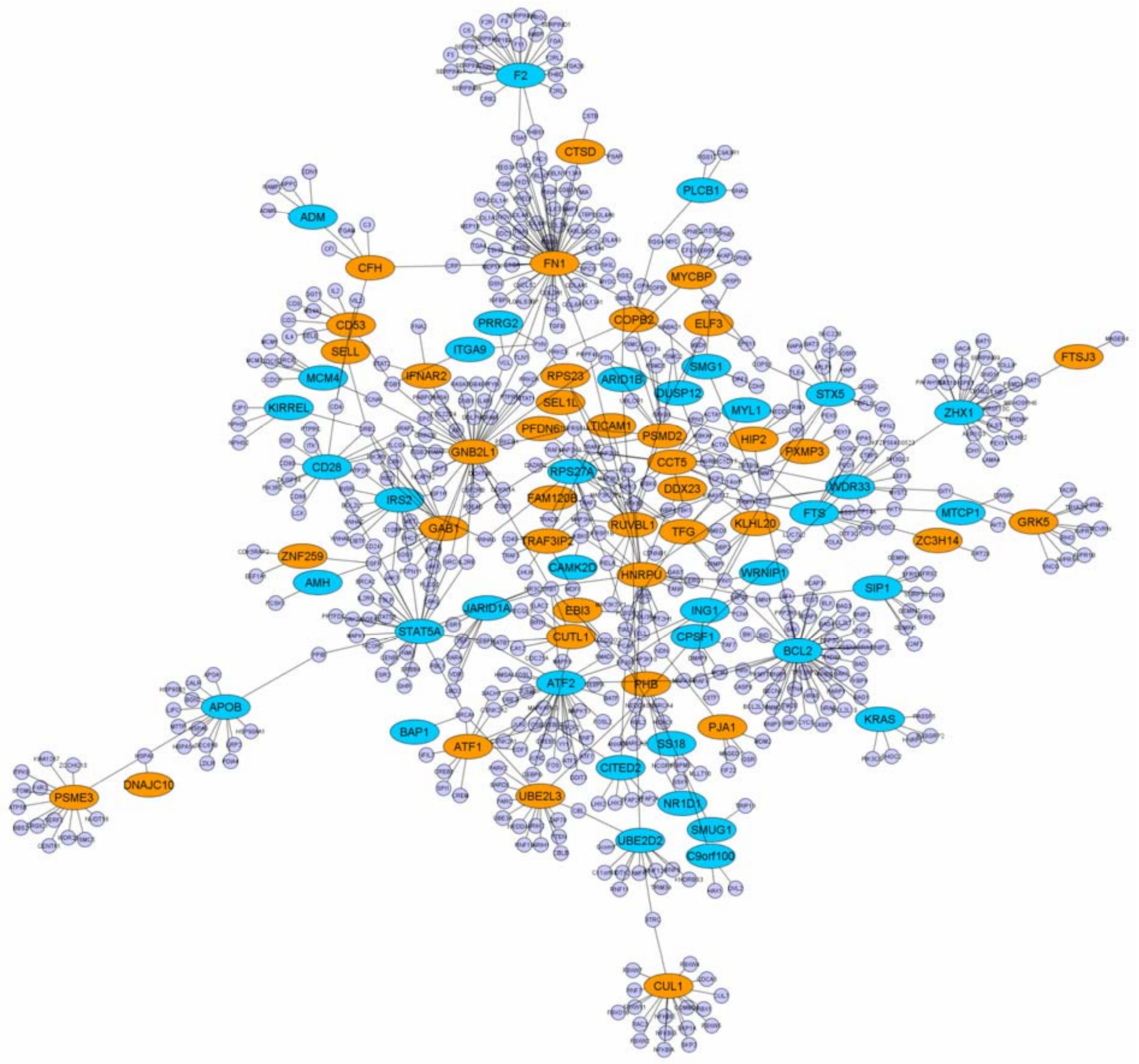
0.0
3.0

Figure 2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CFH
FN1
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CD53
SELL
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ITGA9
COPB2
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RPS23
ARID1B
SMG1
STX5
FTSJ3
KIRREL
SEL1L
DUSP12
MYL1
ZHX1
PFDN6
TICAM1
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HIP2
PXMP3
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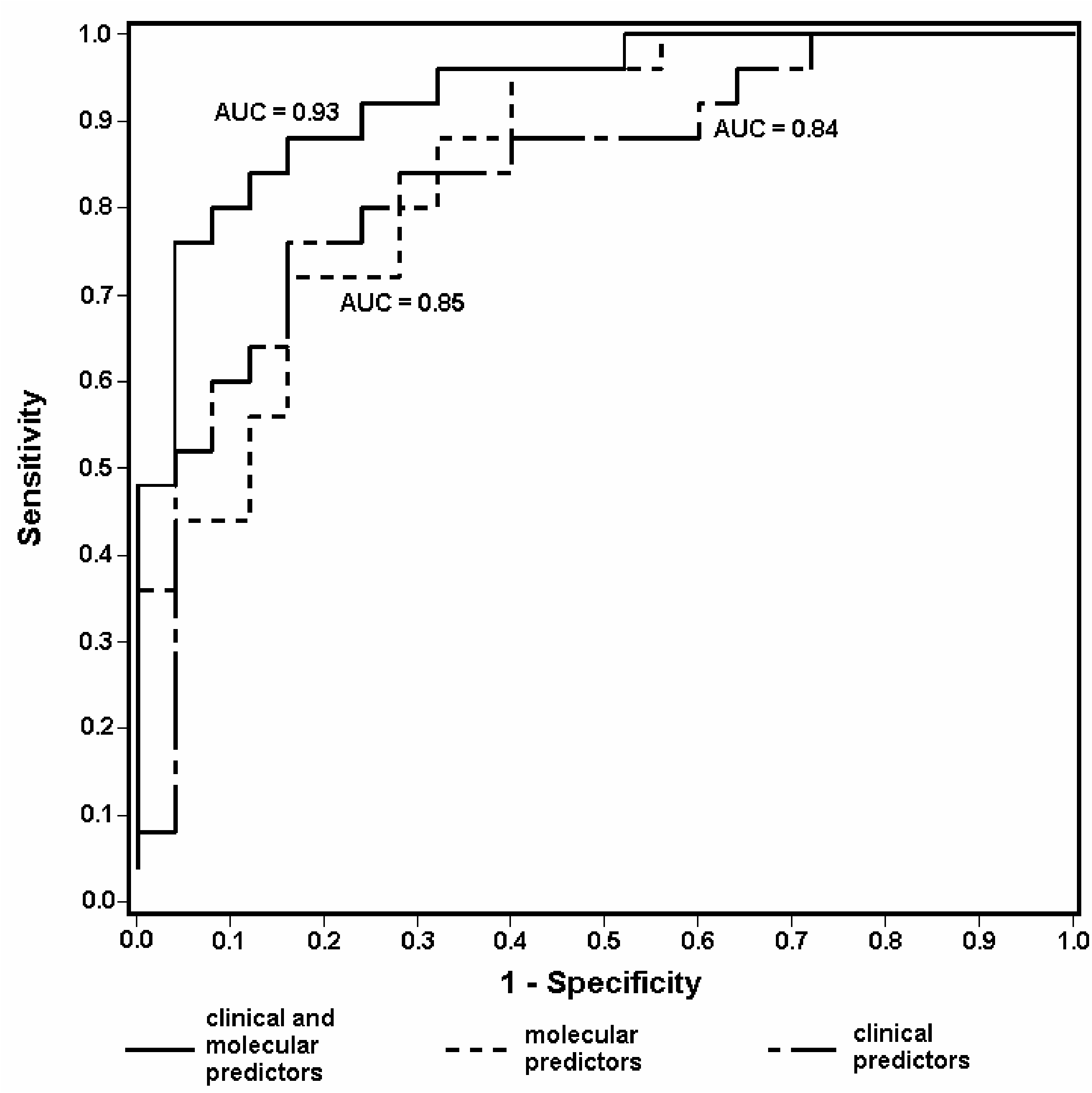
CUL1

Figure 3



Sensitivity
1 - Specificity
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
AUC = 0.93
AUC = 0.85
AUC = 0.84
clinical and molecular predictors
molecular predictors
clinical predictors