Supplementary Materials

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Supplementary Methods:

RNA sequencing

Total RNA was extracted from blood samples using Trizol and the RNA quality was assessed by the Bioanalyzer 2100 (Agilent Technologies). The libraries were generated by following manufactory protocol and were sequenced on Illumina HisSeq2000 sequencer: Briefly, mRNA was firstly extracted from 2ug of total RNA using oligo-dT magnetic beads and fragmented at high temperature. A cDNA library was then prepared from the fragmented mRNA by reverse transcription, second strand synthesis and ligation of specific adapters. Next generation sequencing was performed on Illumina Hiseq 4000 (Illumina Inc.) with single-ended 51 read cycles. Image analysis and bases calling was conducted in real-time by the Illumina analysis pipeline.

The raw RNAseq data was processed as follows: The clean reads with good quality were firstly aligned to several human reference databases including hg19 human genome, exon, splicing junction and contamination database including ribosome and mitochondria RNA sequences using BWA [1] alignment algorithm. After filtering the reads mapped to contamination database, the reads that are uniquely aligned to the exon and splicing-junction sites with a maximal 2 mis-matches for each transcript were then counted as the expression level for corresponding transcript and further subjected to quantile normalization cross samples after log2 transformation.

Microarray experiments

Microarray experiments using Affymetrix human Exon 1.0 ST geneChip were performed on total RNA of blood samples following standard protocols provided by the manufacturer (Affymetrix). Briefly, ENCORE amplification and labeling kit (NuGen, San Carlos, CA) was applied to blood RNA samples starting with approximately 100 ng of total RNA to generate biotin-labeled RNA fragments for hybridization to the chip. The chips were scanned by GeneChip Scanner 7G (Affymetrix Inc)

The raw intensity data of Exon geneChip experiments at gene level were extracted and summarized with RMA algorithm [2] and data quality was assessed in Affymetrix Expression Console (Affymetrix Inc). The Affymetrix control probesets or the probesets with low intensity across all samples were excluded from downstream analysis.

Correlation of microarray and RNA sequencing data were investigated on 26 patients. Top 10 percentile of genes with the most variable expression levels across the samples were selected from RNA sequencing and microarray data for Pearson correlation analysis.

Design of sequencing-based targeted expression (TREx) assay

The TREx assay for diagnosis of acute cellular rejection using peripheral blood was designed using the 17-gene set (**Figure S5**). Twelve house-keeping genes with following criteria were included: 1) minimum variation gene expression across samples and 2) expression values at the average level for all genes detected by RNA sequencing. Sixty-four PCR primers assays were designed for the 17 genes, 12 housekeeping genes and the controls from Illumina Design Studio. The assay kit was manufactured by Illumina Inc (Product No. 75629, Illumina Inc.). PCR was performed on total RNA to amplify the groups of genes using the primer sets and to generate sequencing libraries on the amplicons. After barcoding, the libraries were sequenced using MiSEQ sequencer. The short sequencing data for each sample were analyzed using the sequencing analysis pipeline after de-multiplexing mixed raw sequences.

Bioinformatics data analysis:

Identification of ACR-3 gene set using RNA sequencing

Data analysis workflow to identify a set of focus genes for the diagnosis of acute rejection post-transplant and subsequently develop a TREx assay was depicted in **Suppl. Figure 1**.

Using RNA sequencing data of 88 patients we identified genes correlated with ACR-3, based on unpaired differential LIMMA test [3] with p value < 0.05 by including clinical factors

(induction therapy and deceased donor) as confounders. Biological functional/pathways for the DEGs were determined by enrichment analysis with fisher-exact test using the databases of Gene Ontology (GO) and pathways (KEGG, Ingenuity, BIOCARTA, NABA, Panther, PID, REACTOME, Wiki-pathway). The immune cell types correlated with ACR-3 were evaluated by fisher-exact test of enrichment of immune cell specific genes amongst the DEGs. The immune cell specific genes were identified from ImmGene databases as described previously [4].

We next chose a focused geneset that was specifically associated with ACR-3 from the pre-selected ACR-3 genes using an approach of 100-times randomization analysis described previously [4]. Briefly, the whole cohort was randomly assigned to 2 groups of equal size (1:1 ratio) and LIMMA testing was performed on each group to identify DEG associated with ACR-3, and this process was repeated 100 times. Genes that occurred more than twice in the 100 iterations with a LIMMA $P<0.05$ were considered as the focused geneset. An optimal gene set with the highest AUC (area under the receiver operating characteristic (ROC) curve) for prediction of ACR-3 was then determined after fitting penalized logistic regression model on expression data of the focus geneset with 5000 time iterations[4]. The process started by randomly selecting 20 genes from the focus geneset. The expression values of the 20-gene group were fitted into the penalized regression model in logistf R package for ACR-3 diagnosis. The penalized logistic regression model used Firth's bias reduction method to reduce the bias of maximum likelihood estimates due to small sample size, which will resolve the issue of overfitting from standard logistic regression method. The genes that were significantly associated with AC-3 were identified from the regression model for the 20-gene group. These steps were repeated 5000 time and statistically significant genes ($P<0.05$) were identified from each iteration. The occurrence of significant genes from the 5000 iterations was computed. Finally, the top 40 genes ranked by the occurrences were applied back to the penalized logistic regression model for ACR-3 diagnosis. Statistically significant genes ($P<0.05$) in this model were considered as the final optimal geneset.

The probability was calculated based on the formula $P = \frac{e^{\sum \beta X}}{1+e^{\sum \beta X}}$ where β are coefficients generated from the penalized logistic regression model using the final geneset and X are expression values (normalized sequencing read count). The AUC was calculated to estimate the overall accuracy for the diagnosis of ACR-3. The final gene set was cross-validated using a leave-one-out cross-validation method to avoid over-fitting issue of self-training of the dataset. In leave one crossvalidation for a dataset (n samples), one sample was left out and the model was built on the rest of samples (n-1) and applied to the left-out one sample to generate the probability score. This step was repeated n times until all samples were tested. AUC was calculated based on the probability scores of all the samples. The gene set was validated for diagnosis of ACR-3 on microarray data for 65 GOCAR patients and 3 public blood microarray datasets for clinical acute rejection (GSE14346 [5], GSE15296 [6] and GSE50084 [7])

Supplementary Result:

Correlation of RNA sequencing and microarray data

Due to different scale of gene expression measurement by RNA sequencing and microarray technologies, we firstly subtracted the expression value of each gene by its median value across 26 samples to generate relative expression values for RNAseq and microarray, respectively. We then calculated the sample correlation between RNAseq and microarray based on the relative expression values of top 10% of the genes with the most variable expression. The average Pearson correlation was 0.83±0.06 (**Figure S2**). Our data indicated that RNA sequencing and microarray had good correlation in detecting expression changes among the samples

Development of TREx assay

We developed a molecular assay of 17 gene set from blood RNA to diagnose acute rejection using sequencing-base targeted RNA expression (TREx) analysis technology (**Figure S5**). Prior to application of blood RNA from transplant patients, the TREx assay was tested with universal human RNA (UHR) and brain RNA samples. The replicated experiments with test samples showed high reproducibility (R=0.993 for UHR samples; **Figure S6a**), and the fold change for brain RNA versus UHR samples showed concordance between standard RNA sequencing and targeted RNA sequencing (R=0.949; **Figure S6b**). The reproducibility of TREx assay on blood RNA from transplant recipients was similar to universal reference samples (R=0.998; in **Figure S6c**) and overall reproducibility by heatmap (median R =0.978 [0.840~0.998]; **Figure S6d**). The median correlation between standard RNA sequencing and targeted RNAseq data of blood RNA from 87 transplant recipients is 0.87 [0.933-0.745] (**Figure S6f**). These data on high quality reference samples and clinical blood RNA from kidney transplant recipients indicated that the TREx assay we developed is a reliable assay for clinical diagnosis.

Demographic characteristics of Belgian cohort

46 patients with 3-month allograft biopsies and simultaneous PAXgene RNA were collected from University of Leuven hospital, Belgium. The clinical epidemiologic characteristics of the Belgian cohort are compared with GoCAR cohort in **Table S1**. The Belgian cohort had similar a ACR-3 rate and follow-up as GoCAR, but differed in donor/recipient demographics given the Northern European ancestry of its population and immunosuppression protocols with no lymphocyte depleting therapy and a statistically higher number of patients on a steroid withdrawal maintenance regimen (**Table S1**).

Figure S1. Genomic data analysis workflow: The genomic data analysis workflow includes transcriptomic analysis for identification of ACR-3 diagnosis gene set and TREx assay validation. The transcriptomic analysis identified the transcriptomic signatures and pathways associated with ACR-3 in the RNAseq discovery set and further discovered a 17-gene set for ACR-3 diagnosis which was validated in GoCAR microarray and public dataset. TREx assay was developed for 17-gene set. 113 out of 127 patients in transcriptomic analysis cohort was used as training set to build a penalized logistic regression model which was validated on an independent ACR-3 testing cohort (N= 110).

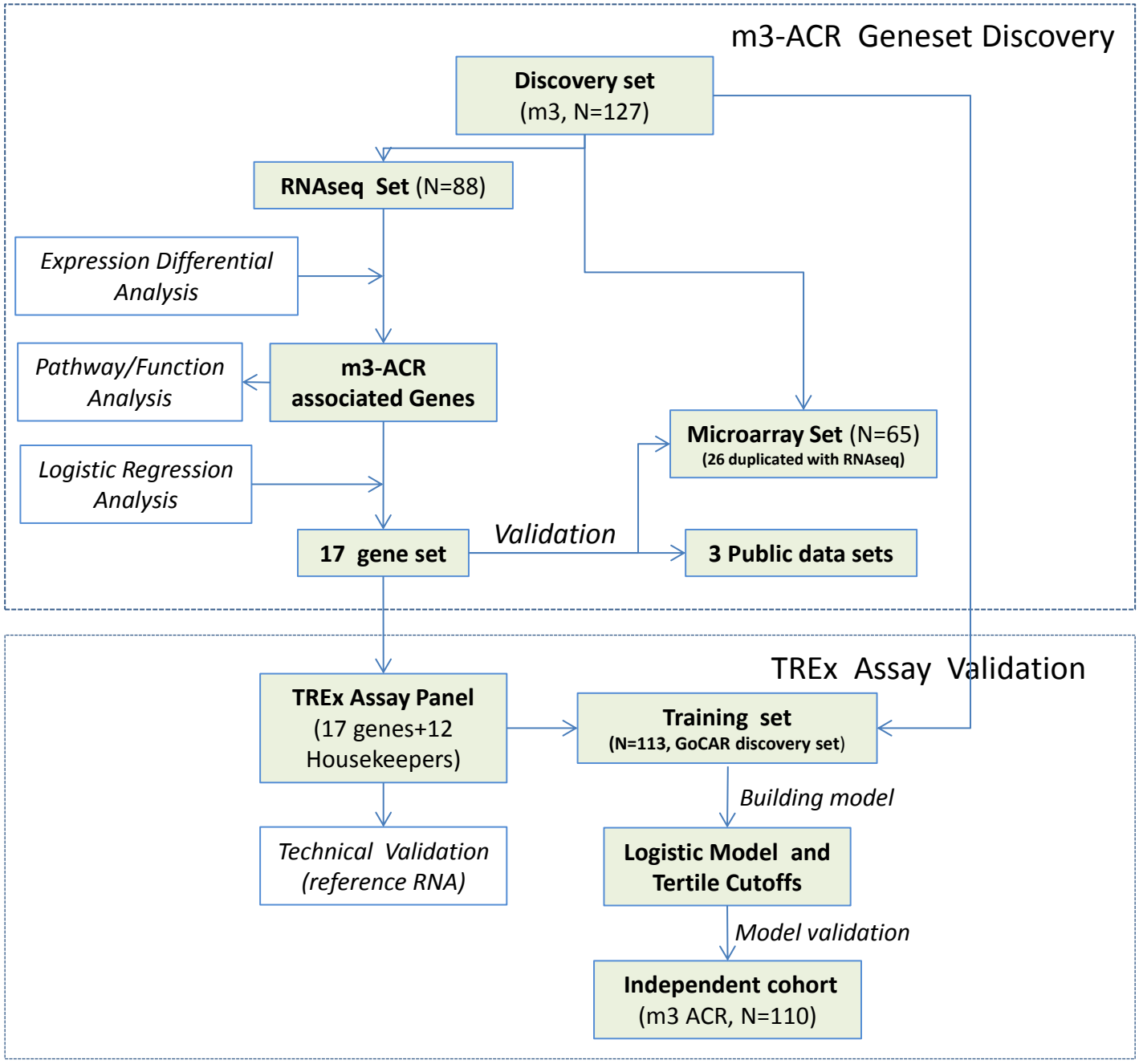


Figure S2. The heatmap of Pearson correlation matrix of RNA sequencing and Microarray data on 26 patients.

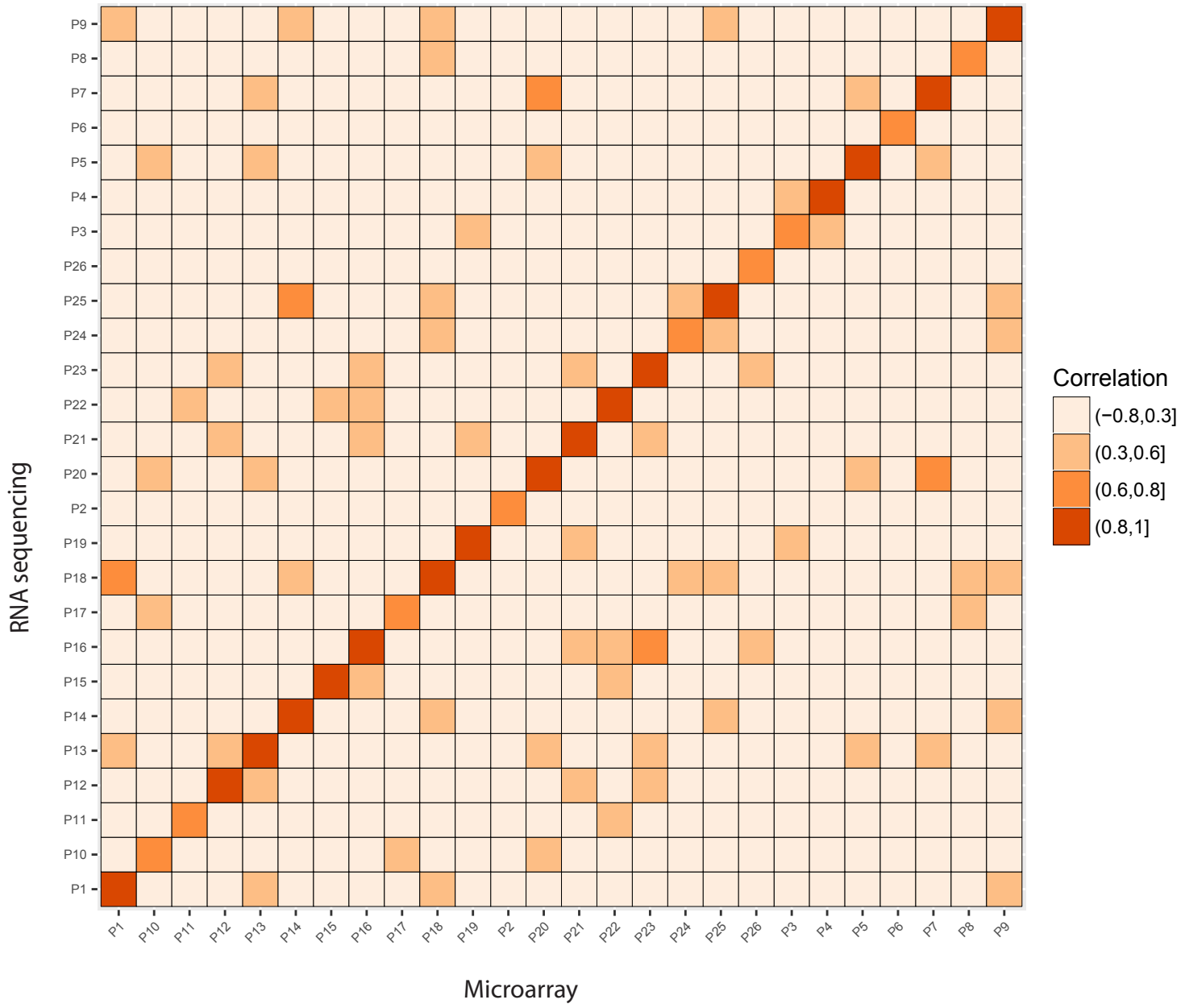


Figure 3S. Association of demographic and pathological characteristics with clinical outcomes: a) The Receiver operating characteris- tic (ROC) curve of association of donor age, induction types and 3m creatinine with ACR-3 (AUC (area under the curve) = 0.720 (black curve) and cross-validated AUC=0.672 (blue curve)); c) The bar charts compares delta eGFR (12m-6m, 12m-3m, 24m-3m or 24m-6m) between ACR-3 and NACR-3 d) Kaplan Meier curves compare all cause survival of ACR-3 (green) and NACR-3 (blue) groups in the GoCAR cohort.

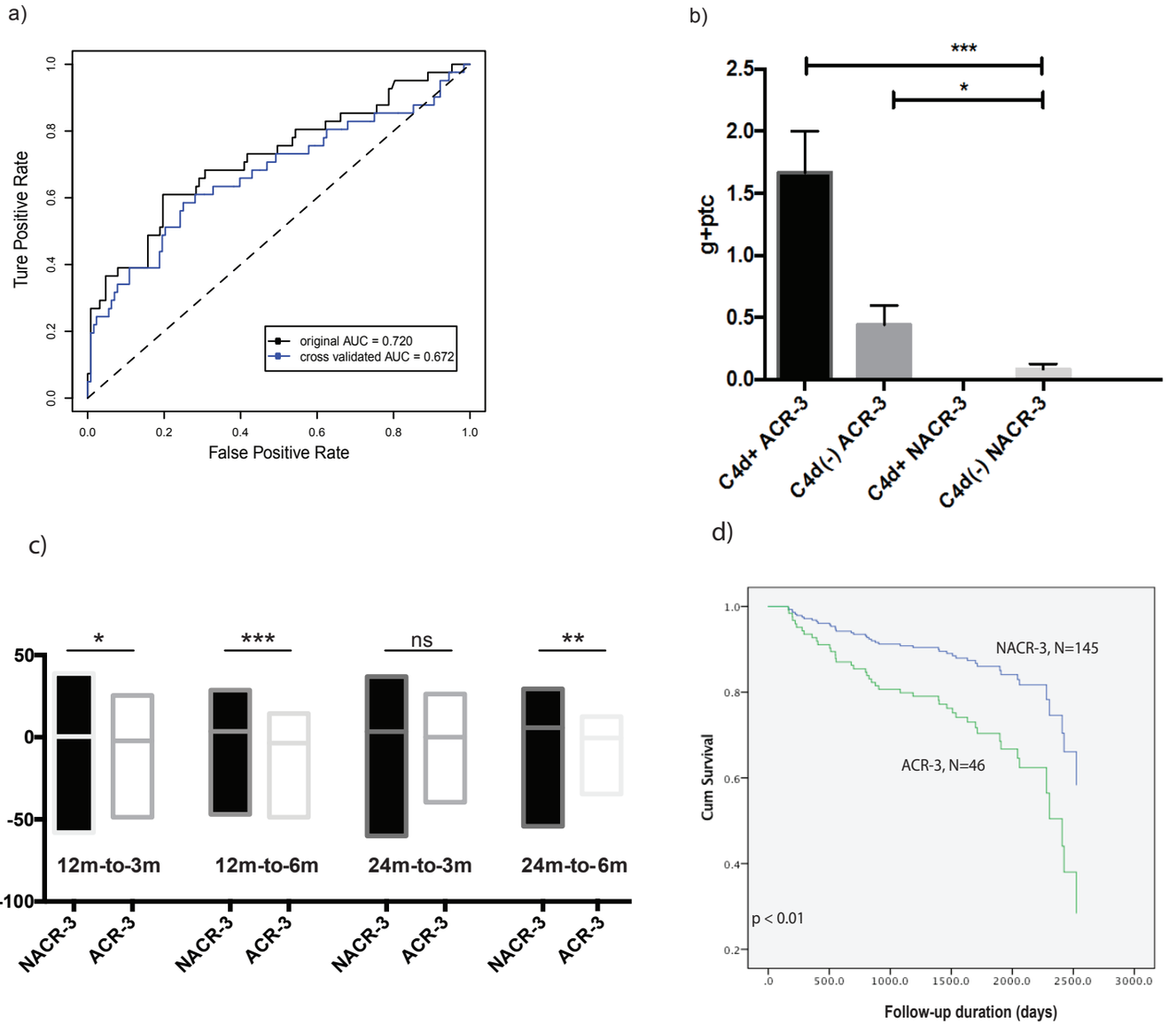


Figure S4: Pathway and Gene Ontology enrichment analysis on differentially expressed genes (DEGs): a) The barchart of enriched Canonical pathways for DEGs from multiple public pathway databases (upper panel) and Ingenuity (lower panel) . The bar represents –log10 p value of enrichment significance of gene pathways by Fisher-exact test; the lengths of red and green bars represent the percentage of up and down regulated genes, respectively; b) The barchart of enriched Gene Ontology functional terms for the top 100 upregulated (upper panel) or down-regulated (lower panel) genes.

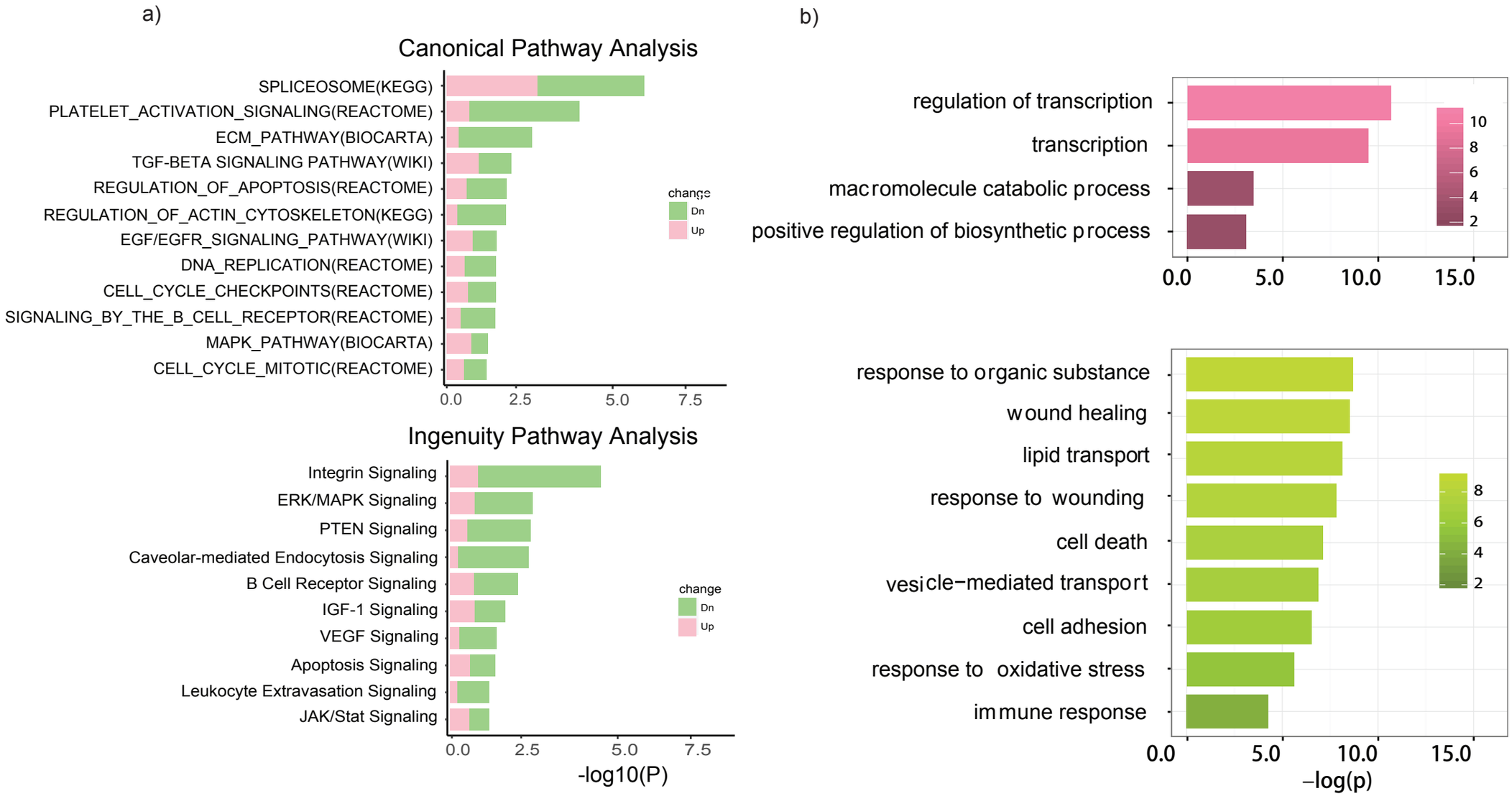


Figure S5: The procedure of development of TREx assay for 17-gene set: 12 genes that had the least expression variation and similar expression range as for 17-gene set were selected as house-keeping genes. 64-assay kit was designed for 29 genes (17-gene set and 12 house-keeping genes) with at least 2 amplicons for each gene. The sequencing library were generated on 96-well plate and sequenced by MiSEQ sequencer. The sequence read count of 17-gene set was normalized using the house keeping genes as reference.

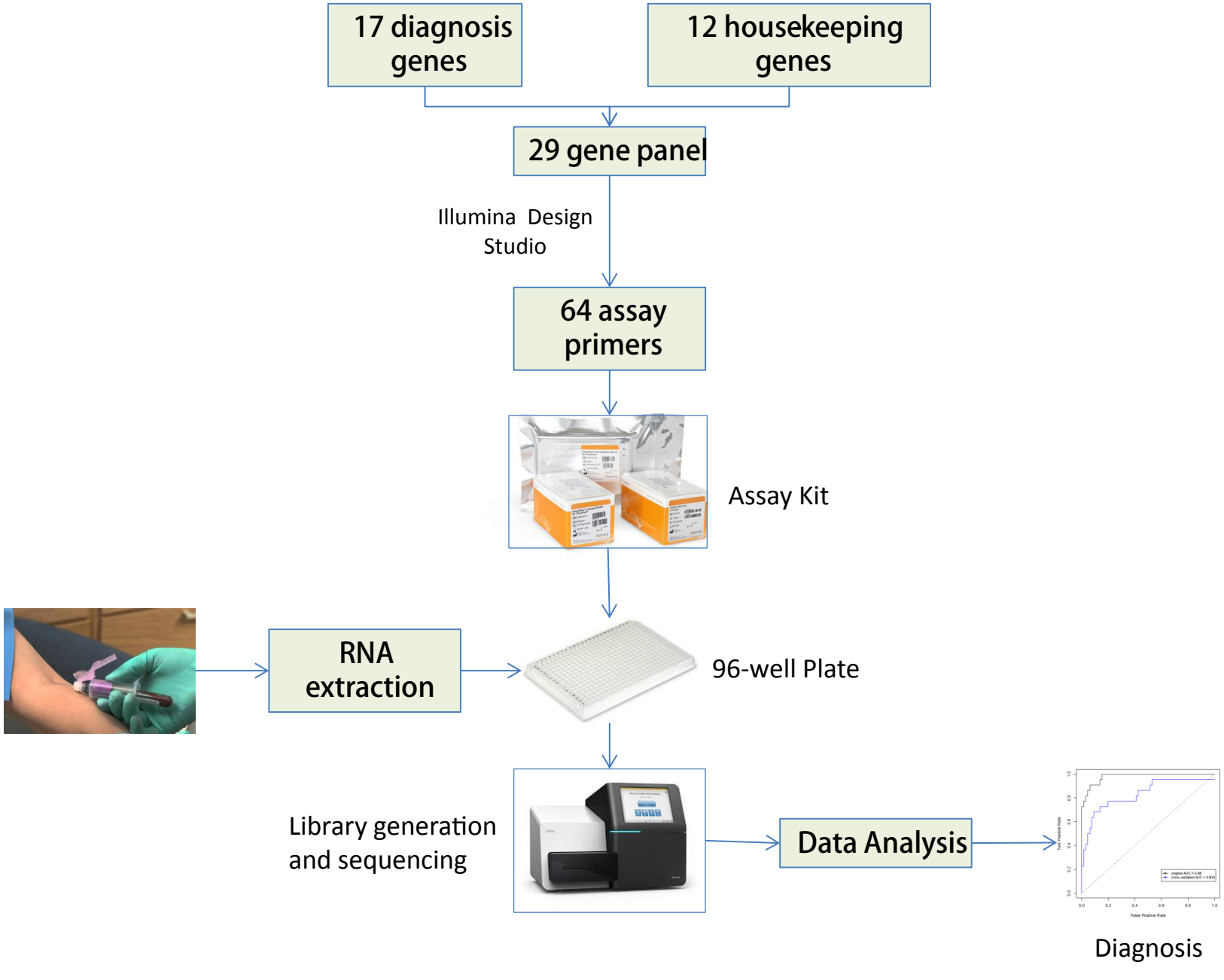
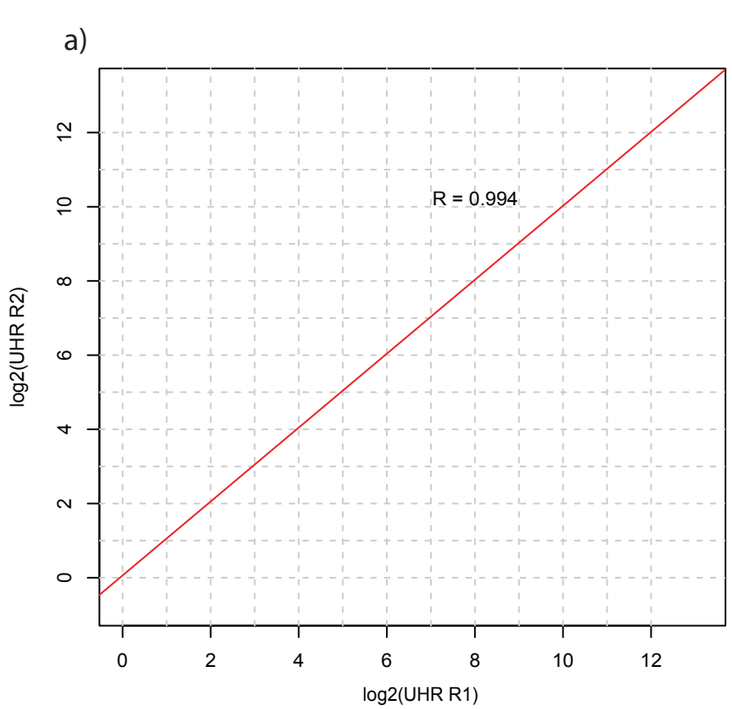
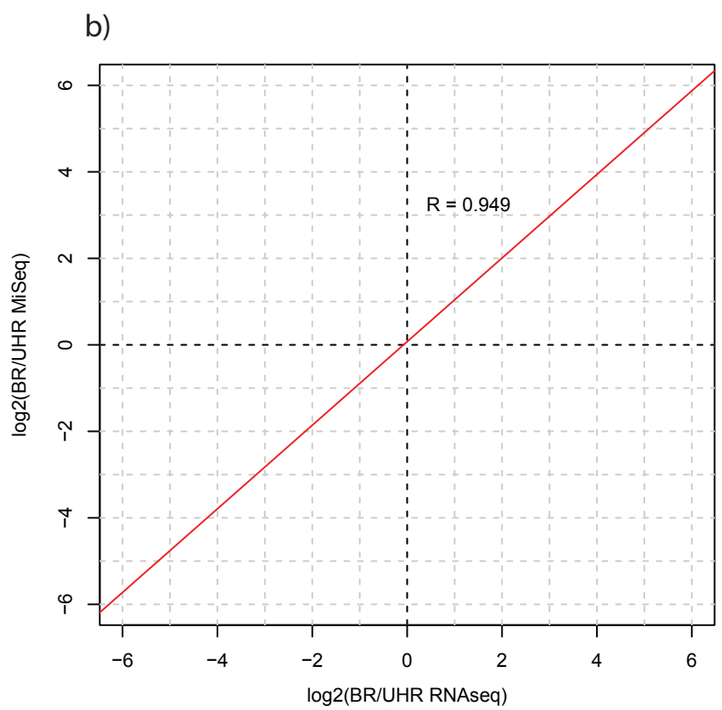
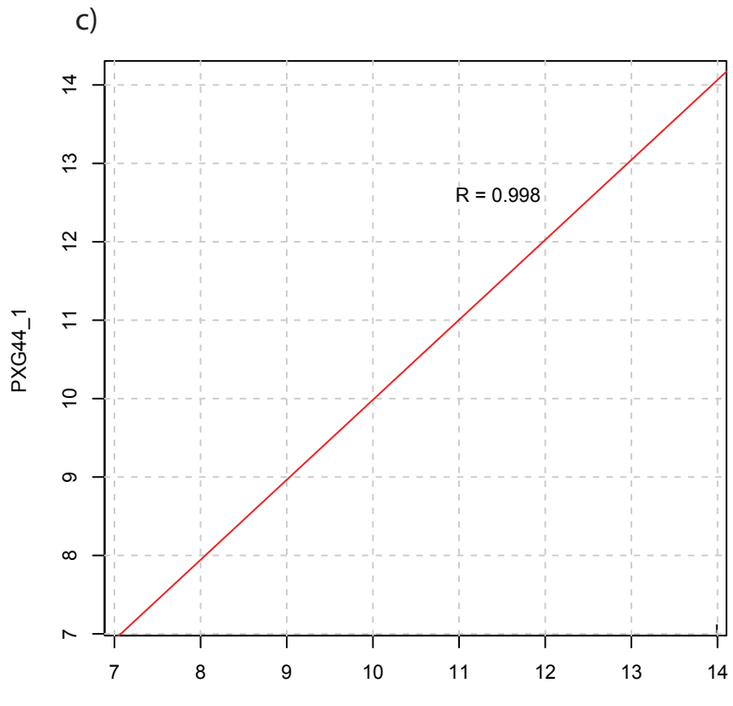
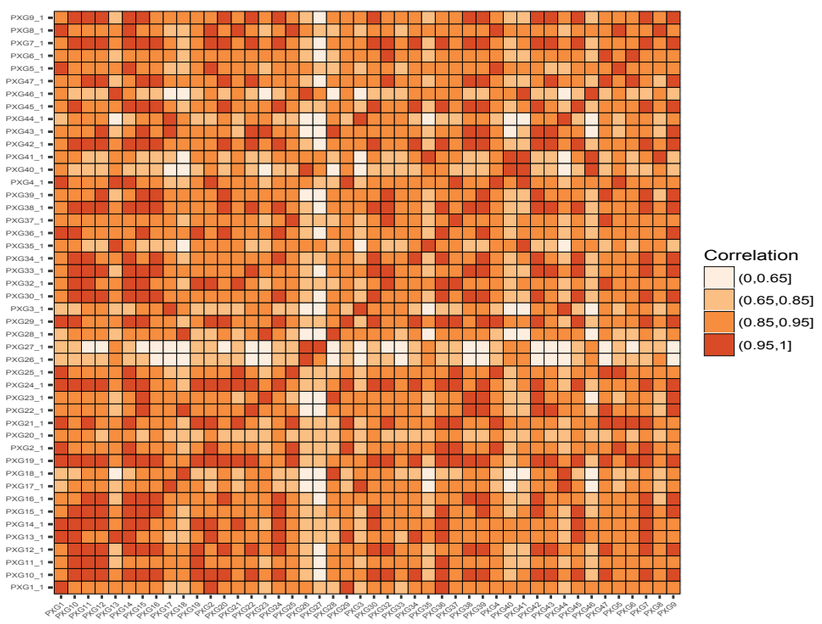


Figure S6: Development of TREx assay for 17-gene set: a) The scatterplot of log2 count of duplicated experiments using RNA sample of the Universal Human Reference (UHR) (R=0.994); b)The scatterplot of log2 ratio of the count data of brain vs UHR RNA between duplicated experiments (R=0.949); c) The scatterplot of log2 count of duplicated experiments using RNA sample of the blood of a kidney transplant (R=0.998); d) The heatmap of expression correlation of duplicated experiments for a group of transplant patients. e) The barchart of correlation of 17 gene expression from TREx assay and RNA sequencing (mean correlation coefficient=0.864, [0.745-0.933], IQR=0.049).









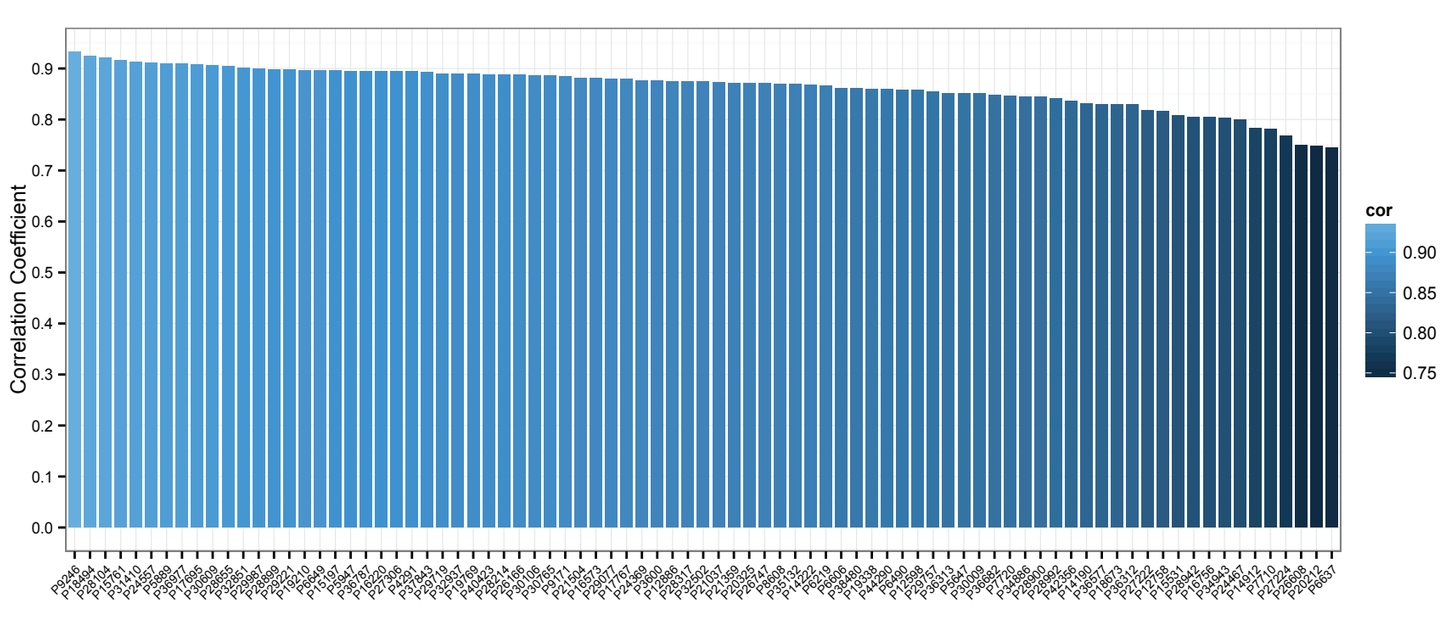


Table S1: Comparison of demographic statistics between GoCAR and Belgian dataset

Characteristics	GOCAR	Belgian	pvalue
ACR/NACR			1
N	145(75.92)	35(76.09)	
Y	46(24.08)	11(23.91)	
Follow up (days)	1637.12 ±597.78	1659.09 ±482.31	0.79
Recipient age	48.73 ±13.58	51.85 ±14.92	0.2
Recipient gender			0.39
Female	65(34.03)	19(41.3)	
Male	126(65.97)	27(58.7)	
Recipient race			<0.01
White / Caucasian	120(62.83)	46(100)	
Black or African American	33(17.28)	0(0)	
Hispanic	14(7.33)	0(0)	
Asian	14(7.33)	0(0)	
Other	10(5.24)	0(0)	
Kidney Disease			<0.01
DM	65(34.03)	4(8.69)	
GN	44(23.04)	9(19.57)	
HTN	31(16.23)	2(4.35)	
PKD	17(8.90)	8(17.39)	
OTHER	34(17.80)	23(50.00)	
Donor age	41.2 ±16.33	48 ±14.78	<0.01
Donor gender			0.74
Female	94(49.21)	21(45.65)	
Male	97(50.79)	25(54.35)	
Donor race			0.04
White / Caucasian	155(81.15)	46(100)	
Black or African American	13(6.81)	0(0)	
Hispanic	13(6.81)	0(0)	
Asian	6(3.14)	0(0)	
Other	4(2.09)	0(0)	
Donor status			<0.01
Living	78(40.84)	4(8.7)	
Deceased	113(59.16)	42(91.3)	
m3 creatinine	1.44 ±0.72	1.71 ±0.54	<0.01
Delayed graft function			0.32
N	154(80.63)	34(73.91)	
Y	37(19.37)	12(26.09)	
Anti_HLA_Ab_Class_I			0.71
N	139(72.77)	35(76.09)	
Y	52(27.23)	11(23.91)	
Anti_HLA_Ab_Class_II			0.31
N	155(81.15)	34(73.91)	
Y	36(18.85)	12(26.09)	
DSA			1
N	27(67.5)	10(71.43)	
Y	13(32.5)	4(28.57)	
Induction Type			<0.01
LND	70(36.65)	21(45.65)	
LymDep	65(34.03)	0(0)	
None	56(29.32)	25(54.35)	
Steroid			<0.01
N	12(6.28)	10(21.74)	

Y	179(93.72)	36(78.26)	
CNI			0.03
N	5(2.62)	5(10.87)	
Y	186(97.38)	41(89.13)	

Legend:

[#] ACR –Acute rejection at 3months; CNI- Calcineurin inhibitors; DSA- Donor-specific antibody; LND - non lymphocyte depletion; LymDep – lymphocyte depletion

P-value – comparison of ACR-3 with NACR-3(unpaired T test or non-parametric test), Chi-square or Fisher's exact test

*Only deceased-donor allografts included in analysis

Table S2: ACR-3 predicts CADI-12 and 24 independent of simultaneous chronic damage indices.

Covariates:	**Outcome: CADI-12**		**Outcome: CADI-24**	
	Coefficient	**P-Value**	**Coefficient**	**P-Value**
ACR-3	1.16	**0.01**	1.71	**0.02**
Ci+Ct 3m	-0.16	0.58	-0.17	0.72
CADI 3m	0.53	<0.01	0.35	0.24

Ci+Ct= Ci score + Ct score at 3 months, CADI- Chronic allograft dysfunction index score; ACR-3: Borderline or greater cellular rejection at 3 month biopsy

Table S3: Comparison of local and central biopsy reports at 3-month biopsy

		3-month Central reports			
		NACR	BACR	ACR	Total
Local diagnosis	NACR	48	13	3	64
	BACR	2	8	1	11
	ACR	5	6	4	15
Total		55	27	8	90

Table S4: Comparison of clinical characteristics between ACR-3 and NACR-3 without AMBR

	ACR-3 N=38 mean ±SD	NACR-3 N=140 mean ±SD	P-value
3 month g-score	0.32 ± 0.66	0.07 ±0.40	<0.01
3-month ptc-score	0.21 ± 0.58	0.01 ± 0.09	<0.01
3-month g+ptc score	0.54 ± 0.93	0.08 ± 0.41	<0.0001
3-month C4d Y/N	4/34	2/138	0.01
Outcomes			
CADI-12	3.36 ± 2.69	1.85 ± 2.14	<0.01
CADI-24	4.00 ± 2.44	2.24 ± 2.73	<0.01
ACR-12 Y/N	14/11	13/74	<0.0001
ACR-24 Y/N	10/3	17/36	<0.01

Table S5: Comparison of clinical outcomes post 3 month between C4d negative ACR-3 and NACR-3 groups

	C4d negative ACR-3 N=33 mean ±SD	NACR-3 N=140 mean ±SD	P value
CADI-12	3.48 ± 2.66	1.85 ± 2.14	<0.01
CADI-24	4.46 ± 2.25	2.24 ± 2.73	<0.01
ACR-12 Y/N	14/10	13/74	<0.0001
ACR-24 Y/N	9/2	17/36	<0.01

Table S6: ACR-3 independently predicts long-term allograft survival

Covariates (Reference parameter)	Outcome: Death censored allograft loss		Outcome: All-cause allograft loss	
	HR	**P-value**	**HR**	**P-value**
ACR-3	4.113	**<0.01**	2.718	**<0.01**
Donor status (LD)	2.921	0.12	1.250	0.59
Donor race (W)	NA	0.26	NA	0.07
Donor gender (F)	0.706	0.46	0.678	0.27
Donor age	1.019	0.26	1.010	0.41
Recipient race (W)	NA	0.28	NA	0.38
Recipient gender (F)	0.826	0.68	0.616	0.14
Recipient age	0.946	0.08	0.994	0.69
Recipient ESRD diagnosis (DM)	NA	0.59	NA	0.53
Induction type (none)	1.982	0.26	1.746	0.19
Anti HLA antibodies (none)	1.617	0.36	1.507	0.25

LD- Live-donor; W- White/Caucasian, F- Female, DM- Diabetic kidney disease, ACR-3: Borderline or greater cellular rejection at 3 month biopsy
Race categories– White/Caucasian, African American, Hispanic, Other; HR-Hazard ratio

Table S7: The list of 240 focus gene set

Symbol	Refseq	Name	P value	Log2Ratio
ZMAT1	NM_001282400	zinc finger, matrin-type 1	0.010685	0.744899
USP32P1	NR_003190	ubiquitin specific peptidase 32 pseudogene 1	0.003553	0.710375
ETAA1	NM_019002	Ewing tumor-associated antigen 1	0.040757	0.703351
ANKRD12	NM_001083625	ankyrin repeat domain 12	0.00716	0.66995
ZNF493	NM_001076678	zinc finger protein 493	0.001647	0.663139
ZNF292	NM_015021	zinc finger protein 292	0.004037	0.642252
CCDC82	NM_024725	coiled-coil domain containing 82	0.019098	0.622008
LINC00672	NR_038847	long intergenic non-protein coding RNA 672	0.002386	0.618656
FLJ31306	NR_029434	uncharacterized LOC379025	0.001288	0.591691
NFYB	NM_006166	nuclear transcription factor Y, beta	0.029003	0.589093
ASTN2	NM_001184734	astrotactin 2	0.001204	0.587956
SENP7	NM_001077203	SUMO1/sentrin specific peptidase 7	0.000291	0.581319
CLK1	NR_027855	CDC-like kinase 1	0.007945	0.567156
SP3	NM_003111	Sp3 transcription factor	0.004195	0.538865
OSBPL8	NM_001003712	oxysterol binding protein-like 8	0.005226	0.526053
UGDH-AS1	NR_047679	UGDH antisense RNA 1	0.00088	0.516391
TMF1	NM_007114	TATA element modulatory factor 1	0.006042	0.514646
KCNQ1OT1	NR_002728	KCNQ1 opposite strand/antisense transcript 1 (non-protein coding)	0.000984	0.513155
SENP6	NM_001100409	SUMO1/sentrin specific peptidase 6	0.005788	0.510019
NAA38	NM_032356	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	0.005145	0.503528
MAB21L3	NM_152367	mab-21-like 3 (C. elegans)	0.000991	0.478708
MALAT1	NR_002819	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	0.00558	0.474576
TBC1D15	NM_001146213	TBC1 domain family, member 15	0.001248	0.474139
PGM5P2	NR_002836	phosphoglucomutase 5 pseudogene 2	0.0017	0.470392
DCP2	NR_038352	decapping mRNA 2	0.007665	0.467892
ANKDD1A	NM_182703	ankyrin repeat and death domain containing 1A	0.005791	0.460633

CCDC144B	NR_036647	coiled-coil domain containing 144B (pseudogene)	0.002709	0.459372
PRPF39	NM_017922	pre-mRNA processing factor 39	0.001465	0.458515
ZMYM2	NM_001190964	zinc finger, MYM-type 2	0.006753	0.439666
ZNF772	NM_001144068	zinc finger protein 772	0.003221	0.43705
ZNF681	NM_138286	zinc finger protein 681	0.001113	0.432181
LOC286437	NR_039980	uncharacterized LOC286437	0.000345	0.41494
ZNF626	NM_145297	zinc finger protein 626	0.002308	0.412885
NUFIP2	NM_020772	nuclear fragile X mental retardation protein interacting protein 2	0.002554	0.410953
SLK	NM_014720	STE20-like kinase	0.007308	0.400349
LOC100131257	NR_034022	zinc finger protein 655 pseudogene	0.000535	0.391003
TP53INP1	NM_033285	tumor protein p53 inducible nuclear protein 1	0.002797	0.39032
LOC646719	NR_046262	uncharacterized LOC646719	0.004209	0.380808
PARP8	NM_001178056	poly (ADP-ribose) polymerase family, member 8	0.002312	0.371843
TIGD7	NM_033208	tigger transposable element derived 7	0.003467	0.371245
SYCP2	NM_014258	synaptonemal complex protein 2	0.005715	0.370693
ZFX	NM_001178086	zinc finger protein, X-linked	0.004024	0.367898
LOC643406	NR_029405	uncharacterized LOC643406	0.000704	0.358162
MARCH7	NM_001282805	membrane-associated ring finger (C3HC4) 7, E3 ubiquitin protein ligase	0.003041	0.357718
TTBK2	NM_173500	tau tubulin kinase 2	0.005404	0.35577
LINC00547	NR_040244	long intergenic non-protein coding RNA 547	0.000879	0.353288
RBM33	NM_053043	RNA binding motif protein 33	0.001573	0.352226
TMEM212	NM_001164436	transmembrane protein 212	0.001346	0.348308
ARHGEF26-AS1	NR_037901	ARHGEF26 antisense RNA 1	0.000501	0.348275
N4BP2L2	NM_001278432	NEDD4 binding protein 2-like 2	0.005388	0.347375
CENPK	NM_001267038	centromere protein K	0.004712	0.345004
TVP23C	NM_001135036	trans-golgi network vesicle protein 23 homolog C (S. cerevisiae)	0.002806	0.342506
ZNF43	NM_001256649	zinc finger protein 43	0.006685	0.33965
SCRN3	NM_024583	secernin 3	0.000647	0.339225

METTL21D	#N/A	#N/A	0.006524	0.336662
SNRNP48	NM_152551	small nuclear ribonucleoprotein 48kDa (U11/U12)	0.001466	0.336015
SRFBP1	NM_152546	serum response factor binding protein 1	0.000816	0.334015
ORC4	NM_001190881	origin recognition complex, subunit 4	0.00064	0.331708
FAM73A	NM_001270384	family with sequence similarity 73, member A	0.00098	0.323062
CARD8	NR_033680	caspase recruitment domain family, member 8	0.002618	0.320462
CEP135	NM_025009	centrosomal protein 135kDa	0.008398	0.320318
ZNF148	NM_021964	zinc finger protein 148	0.001813	0.319371
LOC642236	NR_033907	FSHD region gene 1 pseudogene	0.002214	0.318163
DPY19L4	NM_181787	dpy-19-like 4 (C. elegans)	0.004208	0.312664
LOC646214	NR_027053	p21 protein (Cdc42/Rac)-activated kinase 2 pseudogene	0.00581	0.31057
STXBP3	NM_007269	syntaxin binding protein 3	0.001745	0.305446
NFE2L3	NM_004289	nuclear factor, erythroid 2-like 3	0.002168	0.305192
SEPSECS	NM_016955	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0.004177	0.29773
LOC100507032	#N/A	#N/A	0.005423	0.295099
LOC100130557	#N/A	#N/A	0.00601	0.294332
SLU7	NM_006425	SLU7 splicing factor homolog (S. cerevisiae)	0.01357	0.293447
SNTG2	NM_018968	syntrophin, gamma 2	0.000824	0.29246
C1GALT1C1	NM_001011551	C1GALT1-specific chaperone 1	0.005362	0.292181
LYRM7	NM_181705	LYR motif containing 7	0.002832	0.289061
PIK3C2A	NM_002645	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	0.003215	0.288895
ZMYM5	NM_001039649	zinc finger, MYM-type 5	0.000711	0.283367
ZFAND6	NM_001242912	zinc finger, AN1-type domain 6	0.003972	0.279163
NAA30	NM_001011713	N(alpha)-acetyltransferase 30, NatC catalytic subunit	0.002624	0.278991
ANKRD20A9P	NR_027995	ankyrin repeat domain 20 family, member A9, pseudogene	0.000544	0.278946
KIAA1456	NM_020844	KIAA1456	0.001203	0.277708
ZNF471	NM_020813	zinc finger protein 471	0.001736	0.275492
SCAI	NM_001144877	suppressor of cancer cell invasion	3.38E-05	0.274807

CDKN2B-AS1	NR_047536	CDKN2B antisense RNA 1	0.003036	0.274342
SHISA9	NM_001145204	shisa family member 9	0.001969	0.268846
THAP6	NM_144721	THAP domain containing 6	0.000966	0.262071
CUL5	NM_003478	cullin 5	0.004477	0.260938
AMY2B	NM_020978	amylase, alpha 2B (pancreatic)	0.003767	0.255726
ACADSB	NM_001609	acyl-CoA dehydrogenase, short/branched chain	0.002158	0.255625
ZNF737	NM_001159293	zinc finger protein 737	0.002296	0.253601
MGC27345	NR_046216	uncharacterized protein MGC27345	0.003909	0.251378
L2HGDH	NM_024884	L-2-hydroxyglutarate dehydrogenase	0.000377	0.251247
TAT	NM_000353	tyrosine aminotransferase	0.001832	0.250305
SAR1B	NM_001033503	secretion associated, Ras related GTPase 1B	0.001127	0.24866
ZNF793	NM_001013659	zinc finger protein 793	0.007068	0.24427
KRBOX4	NM_001129900	KRAB box domain containing 4	0.004665	0.244081
CCNL1	NM_020307	cyclin L1	0.007558	0.240872
ZFP14	NM_020917	ZFP14 zinc finger protein	0.002957	0.238291
MCTS1	NM_014060	malignant T cell amplified sequence 1	0.001188	0.236175
AKAP5	NM_004857	A kinase (PRKA) anchor protein 5	0.001768	0.231229
CCDC41	#N/A	#N/A	0.000633	0.227085
FLJ31662	NR_033966	uncharacterized LOC440594	0.00485	0.226492
SPCS3	NM_021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)	0.025128	0.221611
ACOT13	NM_001160094	acyl-CoA thioesterase 13	5.94E-06	0.220781
RSRC2	NR_036435	arginine/serine-rich coiled-coil 2	0.003263	0.219897
TBCC	NM_003192	tubulin folding cofactor C	0.000139	0.219769
FLJ43663	#N/A	#N/A	0.003319	0.218677
TMEM167B	NM_020141	transmembrane protein 167B	0.005043	0.216933
ZNF818P	NR_073396	zinc finger protein 818, pseudogene	0.004324	0.205814
LOC284581	NR_046097	uncharacterized LOC284581	0.005106	0.19901
MCFD2	NM_001171508	multiple coagulation factor deficiency 2	0.002665	0.196994

CCT6P1	NR_003110	chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1	0.001993	0.192564
PGM2L1	NM_173582	phosphoglucomutase 2-like 1	0.001637	0.192297
MFSD8	NM_152778	major facilitator superfamily domain containing 8	0.001699	0.191118
FAM184B	NM_015688	family with sequence similarity 184, member B	0.000526	0.190255
OMA1	NM_145243	OMA1 zinc metallopeptidase	0.001243	0.189318
FLJ10038	NR_026891	uncharacterized protein FLJ10038	0.002391	0.181249
ATP6V0A2	NM_012463	ATPase, H+ transporting, lysosomal V0 subunit a2	0.001804	0.179872
HEXIM1	NM_006460	hexamethylene bis-acetamide inducible 1	0.000698	0.175234
RCN2	NM_001271837	reticulocalbin 2, EF-hand calcium binding domain	0.000375	0.166166
LOC100289230	NR_036530	uncharacterized LOC100289230	0.001915	0.1631
AP1S3	NR_110905	adaptor-related protein complex 1, sigma 3 subunit	0.002637	0.162669
C6orf170	#N/A	#N/A	0.002535	0.159546
MTMR9	NM_015458	myotubularin related protein 9	0.003152	0.142602
ABCC2	NM_000392	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	0.002316	0.140493
TACO1	NM_016360	translational activator of mitochondrially encoded cytochrome c oxidase I	0.010064	0.138106
PLK1S1	#N/A	#N/A	0.00516	0.136264
NGLY1	NM_001145295	N-glycanase 1	0.001745	0.134795
TPM3	NR_103461	tropomyosin 3	0.003304	-0.06326
P4HB	NM_000918	prolyl 4-hydroxylase, beta polypeptide	0.002652	-0.07978
ACACA	NM_198837	acetyl-CoA carboxylase alpha	0.003379	-0.1034
GTF2F1	NM_002096	general transcription factor IIF, polypeptide 1, 74kDa	0.004371	-0.12437
DOCK2	NM_004946	dedicator of cytokinesis 2	0.002408	-0.12792
ILK	NM_001014794	integrin-linked kinase	0.003594	-0.12892
ECD	NM_007265	ecdysoneless homolog (Drosophila)	0.000851	-0.13423
STK24	NM_001032296	serine/threonine kinase 24	0.001692	-0.13662
ARCN1	NM_001142281	archain 1	0.003408	-0.13942
VAC14	NM_018052	Vac14 homolog (S. cerevisiae)	0.005718	-0.14201
PSMC4	NM_006503	proteasome (prosome, macropain) 26S subunit, ATPase, 4	0.004188	-0.14776

WDR1	NM_005112	WD repeat domain 1	0.001574	-0.15196
EXOC4	NM_001037126	exocyst complex component 4	0.002071	-0.15438
HNRNPUL2	NM_001079559	heterogeneous nuclear ribonucleoprotein U-like 2	0.005773	-0.15438
RHOA	NM_001664	ras homolog family member A	0.000474	-0.15707
PKN1	NM_002741	protein kinase N1	0.002776	-0.15887
ARL2-SNX15	NR_037650	ARL2-SNX15 readthrough (NMD candidate)	0.00745	-0.16377
UBAP2L	NM_001127320	ubiquitin associated protein 2-like	0.005124	-0.1644
PCCA	NM_000282	propionyl CoA carboxylase, alpha polypeptide	0.008922	-0.16576
PSMD1	NM_001191037	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	0.004619	-0.17145
PTPN18	NM_001142370	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	0.003853	-0.17162
TLN1	NM_006289	talin 1	0.002461	-0.17227
CSNK2A1	NM_177559	casein kinase 2, alpha 1 polypeptide	0.000724	-0.17287
GNB1	NM_002074	guanine nucleotide binding protein (G protein), beta polypeptide 1	0.002856	-0.17308
XPNPEP1	NR_030724	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.004141	-0.17539
SH3KBP1	NM_001184960	SH3-domain kinase binding protein 1	0.000984	-0.17634
ZNF79	NM_001286698	zinc finger protein 79	0.002766	-0.17698
SCAF4	NM_001145444	SR-related CTD-associated factor 4	0.001875	-0.17832
WDR60	NM_018051	WD repeat domain 60	1.99E-05	-0.18329
ZC3H18	NM_144604	zinc finger CCCH-type containing 18	0.005911	-0.18472
PSMD2	NM_002808	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	0.000867	-0.18492
TMEM214	NM_017727	transmembrane protein 214	0.00151	-0.18805
PPP1CA	NM_206873	protein phosphatase 1, catalytic subunit, alpha isozyme	0.00462	-0.18872
UBA1	NM_153280	ubiquitin-like modifier activating enzyme 1	0.004154	-0.1896
YWHAH	NM_003405	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta	0.003149	-0.19575
SEC23B	NM_001172745	Sec23 homolog B (S. cerevisiae)	0.002745	-0.19816
MSN	NM_002444	moesin	0.004451	-0.19833
DAK	NM_015533	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	0.002058	-0.19962
ACO2	NM_001098	aconitase 2, mitochondrial	0.000528	-0.20439

AIFM1	NM_004208	apoptosis-inducing factor, mitochondrion-associated, 1	0.002388	-0.20691
CSNK2A3	NM_001256686	casein kinase 2, alpha 3 polypeptide	0.007062	-0.2073
HNRNPUL2-BSCL2	NR_037946	HNRNPUL2-BSCL2 readthrough	0.001509	-0.21401
NCKAP1L	NM_005337	NCK-associated protein 1-like	0.001668	-0.21588
AACS	NM_023928	acetoacetyl-CoA synthetase	0.004333	-0.21711
POTEE	NM_001083538	POTE ankyrin domain family, member E	0.006779	-0.21804
CHMP4B	NM_176812	charged multivesicular body protein 4B	0.00394	-0.22168
MCM5	NM_006739	minichromosome maintenance complex component 5	0.007251	-0.2221
SMARCAL1	NM_014140	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	0.001475	-0.22253
NCOR2	NM_001206654	nuclear receptor corepressor 2	0.003793	-0.2232
SMG9	NM_019108	SMG9 nonsense mediated mRNA decay factor	0.002132	-0.22511
SNX15	NM_147777	sorting nexin 15	0.01338	-0.22723
DPP3	NM_130443	dipeptidyl-peptidase 3	0.004145	-0.22835
KDELR1	NM_006801	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	0.001309	-0.2297
AP1B1	NM_145730	adaptor-related protein complex 1, beta 1 subunit	0.003784	-0.23089
CDIP1	NM_013399	cell death-inducing p53 target 1	0.003277	-0.23208
VIM	NM_003380	vimentin	0.005627	-0.23276
PLOD3	NM_001084	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0.000379	-0.23603
ALDOA	NM_001243177	aldolase A, fructose-bisphosphate	0.001223	-0.23811
CAPZB	NM_001206541	capping protein (actin filament) muscle Z-line, beta	0.001198	-0.24334
IPO13	NM_014652	importin 13	0.00071	-0.24421
SCAMP2	NM_005697	secretory carrier membrane protein 2	0.004873	-0.24567
DDX19B	NM_001014451	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19B	0.002377	-0.2474
IDH3G	NM_174869	isocitrate dehydrogenase 3 (NAD+) gamma	0.0022	-0.24835
INTS9	NM_001172562	integrator complex subunit 9	0.001924	-0.24949
SH3BGRL3	NM_031286	SH3 domain binding glutamate-rich protein like 3	0.000913	-0.25377
LSP1	NM_001242932	lymphocyte-specific protein 1	0.003391	-0.25752

KLHL26	NM_018316	kelch-like family member 26	0.005511	-0.25938
EXT2	NM_001178083	exostosin glycosyltransferase 2	0.002941	-0.26011
ACTG1	NR_037688	actin, gamma 1	0.002775	-0.26136
VCL	NM_003373	vinculin	0.0048	-0.26335
LOC442459	#N/A	#N/A	0.003032	-0.26406
CAPN1	NM_005186	calpain 1, (mu/I) large subunit	0.001312	-0.26462
SF3A1	NM_005877	splicing factor 3a, subunit 1, 120kDa	0.00313	-0.26544
PIGT	NR_047693	phosphatidylinositol glycan anchor biosynthesis, class T	0.000903	-0.27039
MAP2K5	NM_002757	mitogen-activated protein kinase kinase 5	0.004707	-0.27111
UQCRC1	NM_003365	ubiquinol-cytochrome c reductase core protein I	0.003185	-0.27113
MAP1A	NM_002373	microtubule-associated protein 1A	0.008216	-0.27124
APP	NM_001204303	amyloid beta (A4) precursor protein	0.000348	-0.27241
HDLBP	NM_203346	high density lipoprotein binding protein	0.001542	-0.27329
C16orf62	NM_020314	chromosome 16 open reading frame 62	0.000326	-0.27372
ARHGDIA	NM_001185078	Rho GDP dissociation inhibitor (GDI) alpha	0.000604	-0.27471
PPP2R4	NM_178000	protein phosphatase 2A activator, regulatory subunit 4	0.005519	-0.2825
CFL1	NM_005507	cofilin 1 (non-muscle)	0.001075	-0.29047
HEATR2	NM_017802	HEAT repeat containing 2	0.003104	-0.2946
RNF40	NM_001207034	ring finger protein 40, E3 ubiquitin protein ligase	0.001848	-0.30261
OGDH	NM_001165036	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	0.000322	-0.30669
UCP2	NM_003355	uncoupling protein 2 (mitochondrial, proton carrier)	0.000854	-0.30851
CHST14	NM_130468	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	0.000634	-0.31805
PLBD2	NM_173542	phospholipase B domain containing 2	0.002506	-0.32099
TPP1	NM_000391	tripeptidyl peptidase I	0.000684	-0.32453
EHD3	NM_014600	EH-domain containing 3	0.00783	-0.32757
VRK3	NM_001025778	vaccinia related kinase 3	0.005303	-0.33009
EFTUD2	NM_001142605	elongation factor Tu GTP binding domain containing 2	0.001449	-0.33174
AP1M1	NM_032493	adaptor-related protein complex 1, mu 1 subunit	0.000161	-0.33596

MAP4	NM_030885	microtubule-associated protein 4	0.002285	-0.33685
CTNNBL1	NM_030877	catenin, beta like 1	0.000682	-0.33777
NUP93	NM_001242796	nucleoporin 93kDa	0.00098	-0.34037
SSBP3	NM_018070	single stranded DNA binding protein 3	0.002873	-0.34183
CTSA	NM_001167594	cathepsin A	0.009862	-0.34479
RNH1	NM_203385	ribonuclease/angiogenin inhibitor 1	0.006126	-0.35105
BCAS3	NM_017679	breast carcinoma amplified sequence 3	0.006131	-0.35844
TRAPPC9	NM_031466	trafficking protein particle complex 9	0.001364	-0.35975
ANXA5	NM_001154	annexin A5	0.000328	-0.36446
BCKDHA	NM_001164783	branched chain keto acid dehydrogenase E1, alpha polypeptide	0.004641	-0.36764
SND1	NM_014390	staphylococcal nuclease and tudor domain containing 1	0.000666	-0.37393
FAM127A	NM_001078171	family with sequence similarity 127, member A	0.002681	-0.38623
BRE	NM_199191	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.001421	-0.40204
CLU	NM_001831	clusterin	0.004967	-0.42146
CAPNS1	NM_001003962	calpain, small subunit 1	6.94E-05	-0.4336
CTSD	NM_001909	cathepsin D	0.004336	-0.43371
TSC22D1	NM_001243797	TSC22 domain family, member 1	0.007989	-0.44781
F13A1	NM_000129	coagulation factor XIII, A1 polypeptide	0.02124	-0.5544
TUBB1	NM_030773	tubulin, beta 1 class VI	0.032961	-0.55441

Table S8: Demographic characteristics of RNAseq and Microarray cohorts in GoCAR cohort.

Characteristics	Microarray Cohort (n=65)	RNAseq Cohort (n=88)	pvalue
Age	49.51 ±13.87	48.33 ±12.41	0.5878
Gender			0.5011
F	22(33.85)	35(39.77)	
M	43(66.15)	53(60.23)	
Race			0.0087
Black or African American	13(20)	11(12.5)	
Others	22(33.85)	15(17.05)	
White / Caucasian	30(46.15)	62(70.45)	
CMV_Status_R			0.1058
No	9(13.85)	22(25)	
Yes	56(86.15)	66(75)	
CMV_Status_D			0.2539
No	32(49.23)	35(39.77)	
Yes	33(50.77)	53(60.23)	
Days_to_first_Dialysis	1516.25 ±1576.52	1213.44 ±1625.49	0.2484
Anti_HLA_Ab_Class_I			0.0434
No	53(81.54)	58(65.91)	
Yes	12(18.46)	30(34.09)	
Anti_HLA_Ab_Class_II			0.1622
No	59(90.77)	72(81.82)	
Yes	6(9.23)	16(18.18)	
Anti_HLA_Ab_Class			0.0434
No	53(81.54)	58(65.91)	
Yes	12(18.46)	30(34.09)	
Induction_Type			0.1582
LND	20(30.77)	40(45.45)	
LymDep	21(32.31)	25(28.41)	
None	24(36.92)	23(26.14)	
KD			0.9838
DM	22(33.85)	26(29.55)	
GN	15(23.08)	23(26.14)	
HTN	9(13.85)	14(15.91)	
PKD	6(9.23)	9(10.23)	
REFLUX DISEASE	4(6.15)	6(6.82)	
OTHER	9(13.85)	10(11.36)	
Donor_Age	39.63 ±17.87	40.74 ±16.28	0.6945
Donor_Gender			0.3276
F	25(38.46)	41(46.59)	
M	40(61.54)	47(53.41)	
Donor_Race			0.1928
Black or African American	8(12.31)	5(5.68)	
Others	11(16.92)	10(11.36)	
White / Caucasian	46(70.77)	73(82.95)	
Deceased_Donor			0.4962
No	21(32.31)	34(38.64)	
Yes	44(67.69)	54(61.36)	
CIT_min	671.17 ±503.15	562.55 ±457.96	0.1728
DGF			0.2918
NO	51(78.46)	75(85.23)	
Yes	14(21.54)	13(14.77)	
Baseline DSA			1
No	58(93.55)	77(92.77)	
Yes	4(6.45)	6(7.23)	

Table S9: Frequency of anytime Rejection episodes in TREx risk groups:

Group	12-month SCR* (ACR/BACR)	24-month SCR** (ACR/BACR)	Any time ACR (1A or greater)	Anytime ACR/BACR	ABMR[1]	DDSA[2] Y	C4d>0[3] (3-months)	g+ptc ≥2 (3-months)
Low risk (70)	6 (13.61%)	9 (32.14%)	4 (6.06%)	20 (28.57%)	4 (5.72%)	3(13.61%)	3 (5.89%)	1 (1.96%)
Intermediate risk (85)	13 (23.61%)	14 (46.67%)	14 (16.47%)	39 (45.88%)	5 (5.88%	7(24.14%)	3 (4.28%)	7 (9.33%)
High Risk (22)	9 (64.28%)	7 (77.78%)	8 (36.3%)	20 (90.90%)	1 (4.54%)	1 (9.09%)	2 (10.0%)	3 (15.0%)

*A total of 44, 55 & 14 surveillance biopsies were performed in Low, Intermediate and High risk groups at 12-months, respectively.

** A total of 28, 30 & 9 surveillance biopsies were performed in Low, Intermediate and High risk groups at 24-months, respectively.

[1] ABMR- Acute Antibody-mediated rejection < 24 months. 10/11 of ABMR cases had TREx assay performed.

[2] DDSA- Denovo DSA; Only 22, 29 and 11 patients in low-, intermediate, and high-risk groups had serum reported for DDSA within 24-months

[3]C4d- by immunohistochemistry method.

Table S10: Summary of clinical events of TREx cohorts post kidney transplant

By training/testing set

	Training (N=113)	Testing (N=110)
ACR/BACR/NACR	7/17/89	6/23/81
Death Censored Graft Loss (DCGS)	9	13
All Cause Graft Loss (ACGS)	23	23

By study cohort

	GOCAR (N=177)	Belgian (N=46)
ACR/BACR/NACR	10/32/135	3/8/35
Death Censored Graft Loss (DCGS)	20	2
All Cause Graft Loss (ACGS)	39	7

Table S11: TREX-risk group status impact allograft survival (GoCAR+Belgian cohorts, n=223)[1]

Covariates	Death Censored graft Survival				
	HR	P-Value		HR	P-Value
TREx Risk group status High/Intermediate (Ref – Low risk)	**3.740**	**0.04**	TREx Risk group status High Intermediate (Ref – Low risk)	3.758 **3.723**	0.12 0.11 **0.04**
Induction therapy (Ref – None)	2.178	0.24	Induction therapy (Ref – None)	2.172	0.24
Donor Age	1.010	0.56	Donor Age	1.009	0.56
Recipient Age	0.980	0.34	Recipient Age	0.981	0.35
Donor Status (Ref-Live)	0.422	0.18	Donor Status (Ref-Live)	0.420	0.18
Anti-HLA antibody (Ref-none)	1.638	0.34	Anti-HLA antibody (Ref-none)	1.626	0.36
Donor Race (ref: Caucasian) African American Hispanic Other	 0.747 1.364 1.904	0.90 0.74 0.70 0.64	Donor Race (ref: Caucasian) African American Hispanic Other	 0.738 1.344 1.928	0.91 0.74 0.73 0.89
Recipient Race (ref: Caucasian) African American Hispanic Other	 4.410 0.820 1.093	0.08 **0.01** 0.87 0.93	Recipient Race (ref: Caucasian) African American Hispanic Other	 4.414 0.826 1.091	0.08 **0.01** 0.87 0.93
[#]**Parsimonious covariate models**					
TREx Risk group status High/Intermediate (Ref – Low risk)	4.149	**0.02**	TREx Risk group status High Intermediate (Ref – Low risk)	5.300 4.122	0.05 **0.03** **0.02**
Induction therapy (Ref – None)	3.258	0.05	Recipient Race (ref: Caucasian) African American Hispanic Other	 4.003 0.852 1.255	**0.02** <**0.01** 0.88 0.77

*HR = Hazard ratio

[1]There were 22 death-censored graft loss events in this group

[#]Parsimonious models were generated using backward stepwise conditional predictor selection. Final models are displayed here.

Table S12: Comparison of Banff scores between Intermediate- and Low-risk NACR-3 groups

3-month Banff Scores	**Low risk NACR-3 Mean ±SD (n=67)**	**Intermediate NACR-3 Mean ±SD (n=63)**	P-value
i-score	0.02 ±0.123	0.00 ±0.000	0.34
t-score	0.02 ±0.123	0.00 ±0.000	0.34
ti-score	0.06 ±0.240	0.05 ±0.218	0.78
Ci-score	0.24 ±0.498	0.18 ±0.466	0.47
Ct-score	0.36 ±0.485	0.42 ±0.529	0.54
Cv-score	0.35 ±0.803	0.39 ±0.671	0.78
Cg-score	0.02 ±0.124	0.03 ±0.181	0.52
g-score	0.03 ±0.248	0.13 ±0.536	0.16
mm-score	0.02 ±0.124	0.22 ±0.715	**0.03**
Ci+Ct-score	0.59 ±0.871	0.59 ±0.835	0.95
CADI-score	1.23 ±1.497	1.45 ±1.565	0.41
12-month Banff scores	**(n=42)**	**(n=42)**	
mm-score	0.00 ±0.000	0.28 ±0.793	**0.03**
Ci+Ct-score	0.90 ±1.225	1.33 ±1.603	0.17
CADI-score	1.48 ±1.742	2.29 ±2.361	0.07
24-month Banff scores	**(n=26)**	**(n=29)**	
mm-score	0.12 ±0.588	0.24 ±0.723	0.50
Ci+Ct-score	0.65 ±1.017	2.10 ±2.350	**<0.01**
CADI-score	1.15 ±1.592	2.89 ±3.075	**0.01**

Table S13: High/Intermediate risk NACR-3 impacts allograft survival

Covariates	Death Censored graft Survival				
	HR	P-Value		HR	P-Value
TREx NACR-3 Risk group I-H NACR-3 (Ref – L-NACR-3)	**6.305**	**0.02**	TREx NACR-3 Risk group Intermediate NACR-3 (Ref – L-NACR-3)	**5.265**	**0.03**
Induction therapy (Ref – None)	4.654	0.16	Induction therapy (Ref – None)	3.907	0.20
Donor Age	0.990	0.59	Donor Age	0.994	0.76
Recipient Age	0.962	0.16	Recipient Age	0.979	0.46
Donor Status (Ref-Live)	1.882	0.36	Donor Status (Ref-Live)	1.700	0.45
Anti-HLA antibody (Ref-none)	0.973	0.97	Anti-HLA antibody (Ref-none)	1.128	0.87

I-H NACR-3=High/Intermediate TREX risk group NACR-3; L-NACR-3= Low risk TREx risk group NACR-3
HR= Hazard ratio. There were 12 death censored graft loss events in this cohort.
Other models including Donor and Recipient race showed similar results.

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