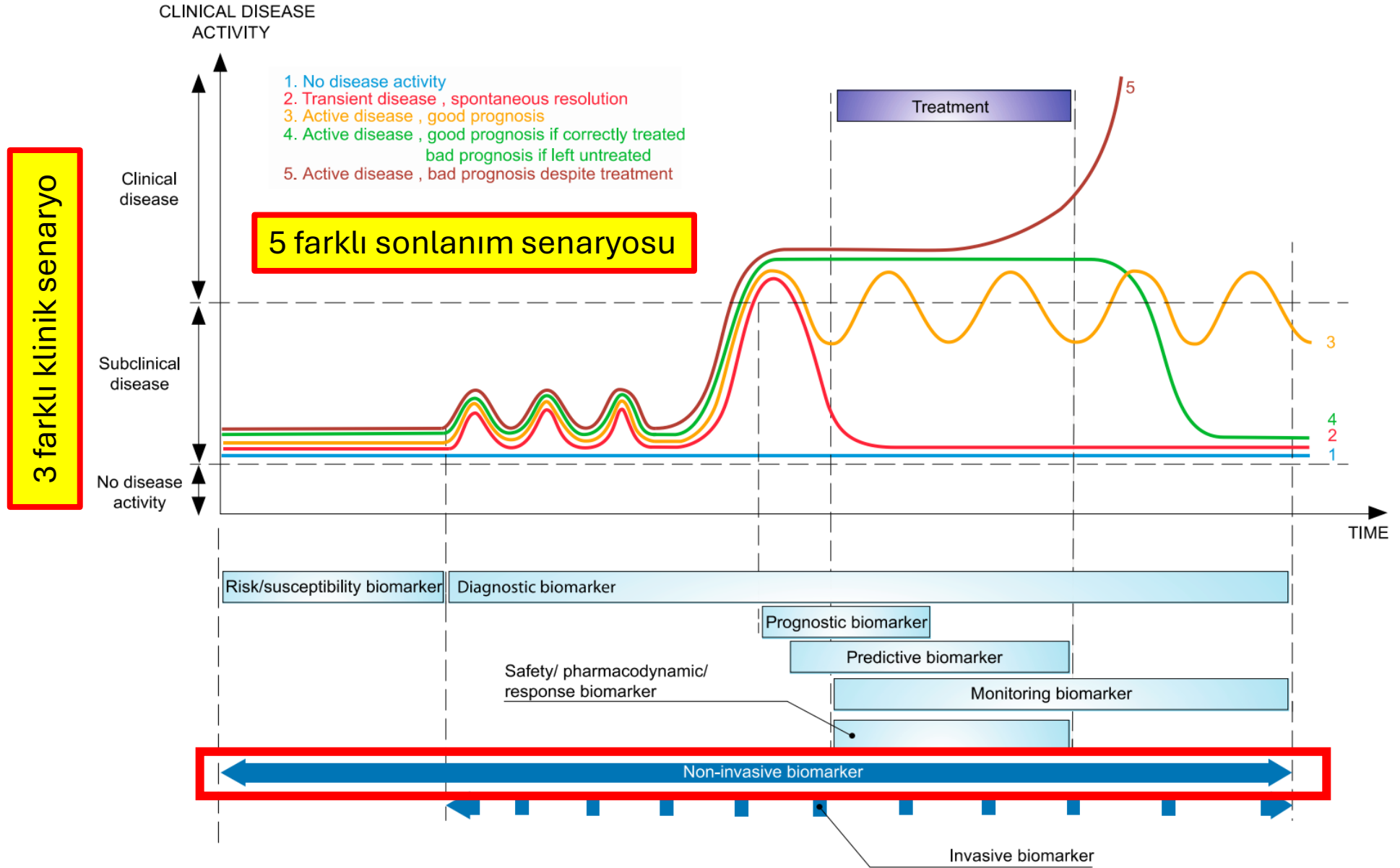


Transplantasyonda Yeni Biyobelirteçler

Dr. Özgür Akın Oto
İstanbul Tıp Fakültesi Nefroloji BD

TİGED-2024

- Risk tayini
- Tanı
- Tarama
- Prognoz
- Tedaviye yanıt



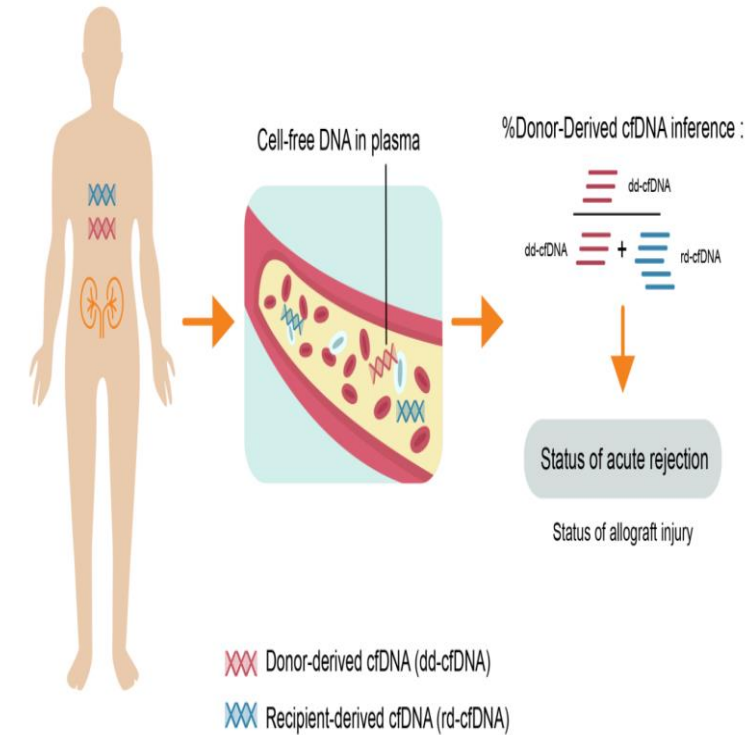
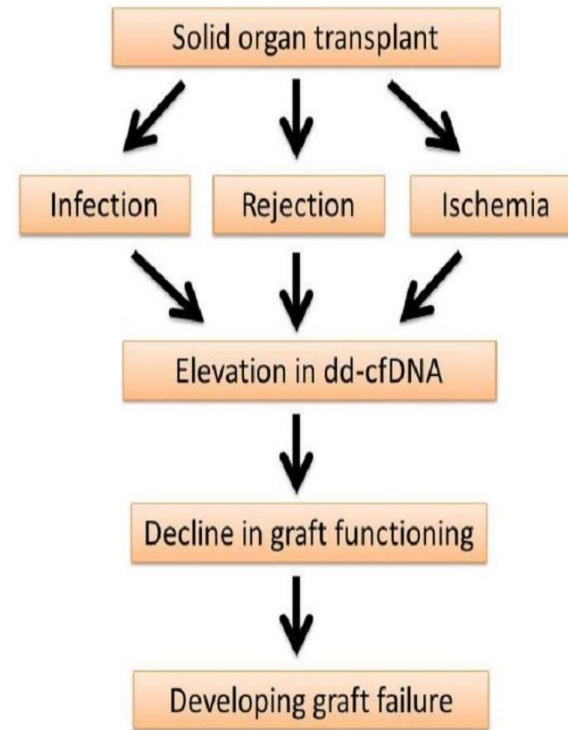
Geleneksel Tarama Yöntemleri

- **Kreatinin artışı / Proteinüri**
 - Hasarla eş zamanlı yükselmez
- **DSA**
 - Tüm DSA'lar patojenik değildir
 - Non-HLA antikorlar da rejeksiyona neden olabilir.
- **Biyopsi → Altın standart**
 - İnvaziv
 - Komplikeasyonlu
 - Pahalı
 - Örneklem ve yorumlama hataları

- İmmünolojik biyobelirteçler
 - Cell-free DNA
 - Gen ekspresyon profilleri
 - İdrar kemokinleri
 - İdrar mRNA
- Non-immünolojik biyobelirteçler
 - Graft kalitesi
 - Gecikmiş graft fonksiyonu
 - Kardiyovasküler olaylar/mortalite
 - Enfeksiyonlar
 - Malignite
 - Posttransplant DM

Allograft hasarı → dd-cfDNA artışı

- Büyük oranda endotelial hücre hasarını yansıtır
- Yarı ömrü çok kısa (<1 saat)
- Rejeksiyon, infeksiyon, ilaç toksitesi
- % → Dd-cfDNA/Total cfDNA
- 3 farklı ticari kit mevcut
 - Allosure (CareDx)
 - Prospera (Natera)
 - TRAC (Viracor Eurofins)

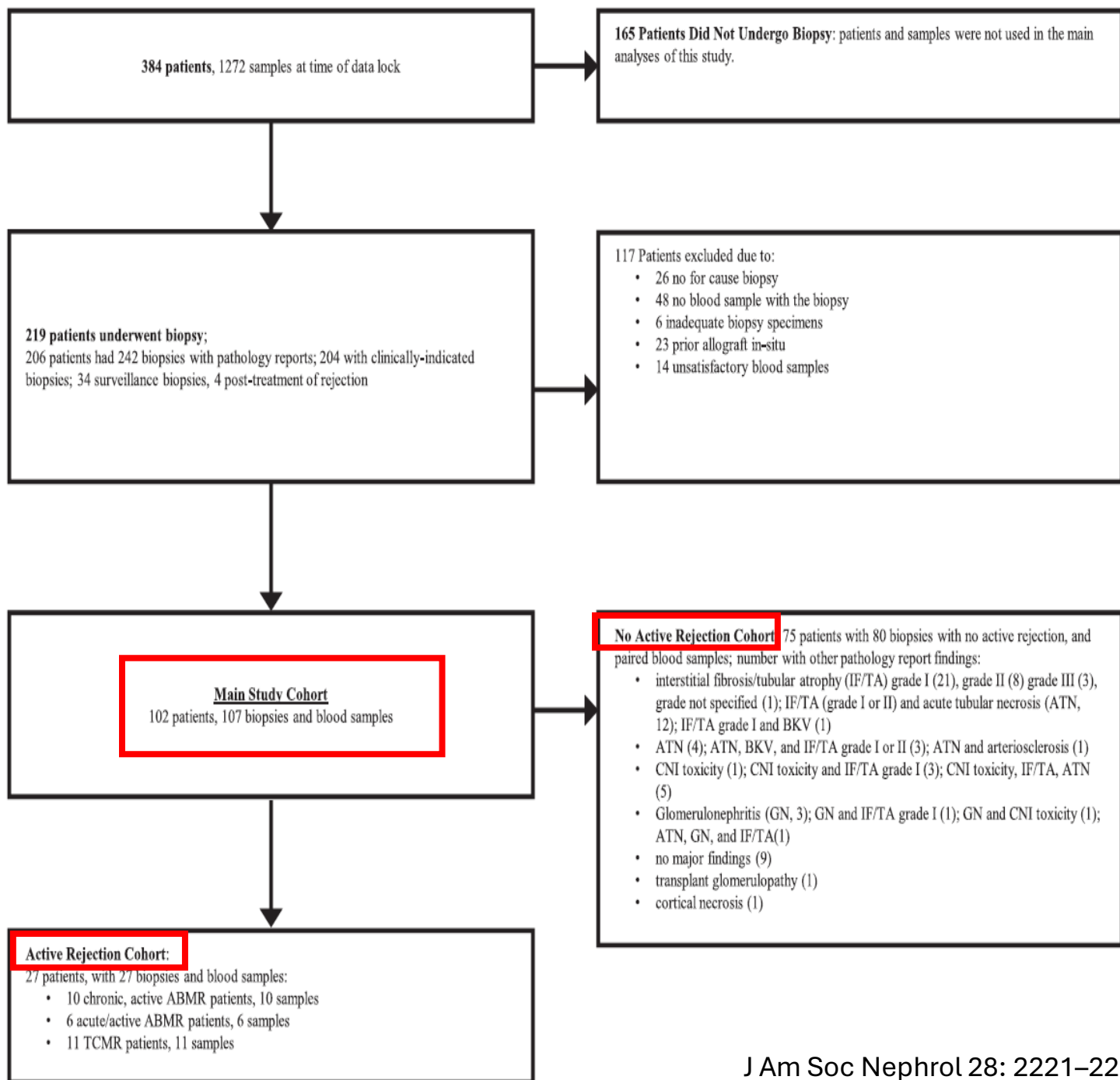


Cell-Free DNA and Active Rejection in Kidney Allografts

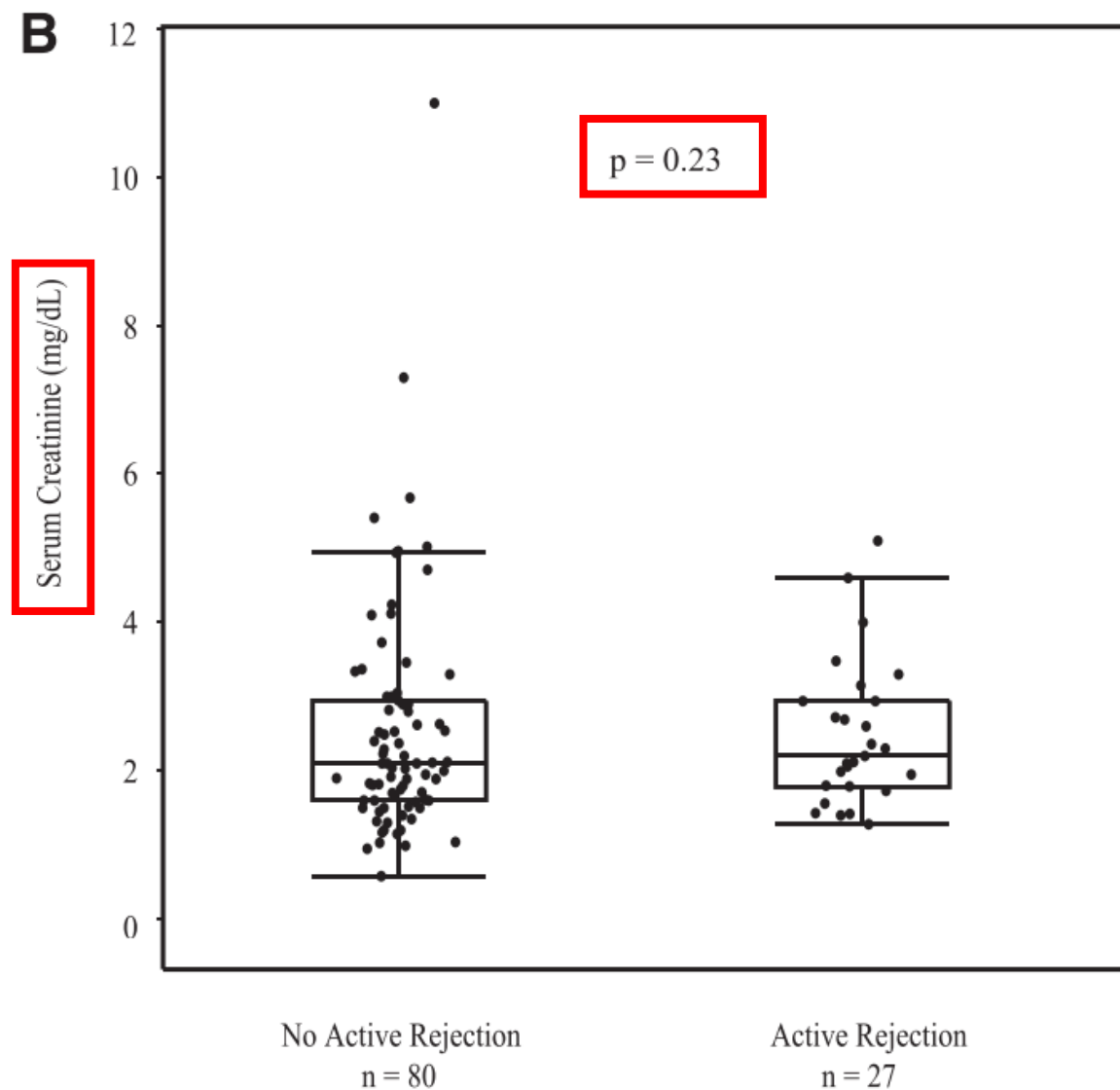
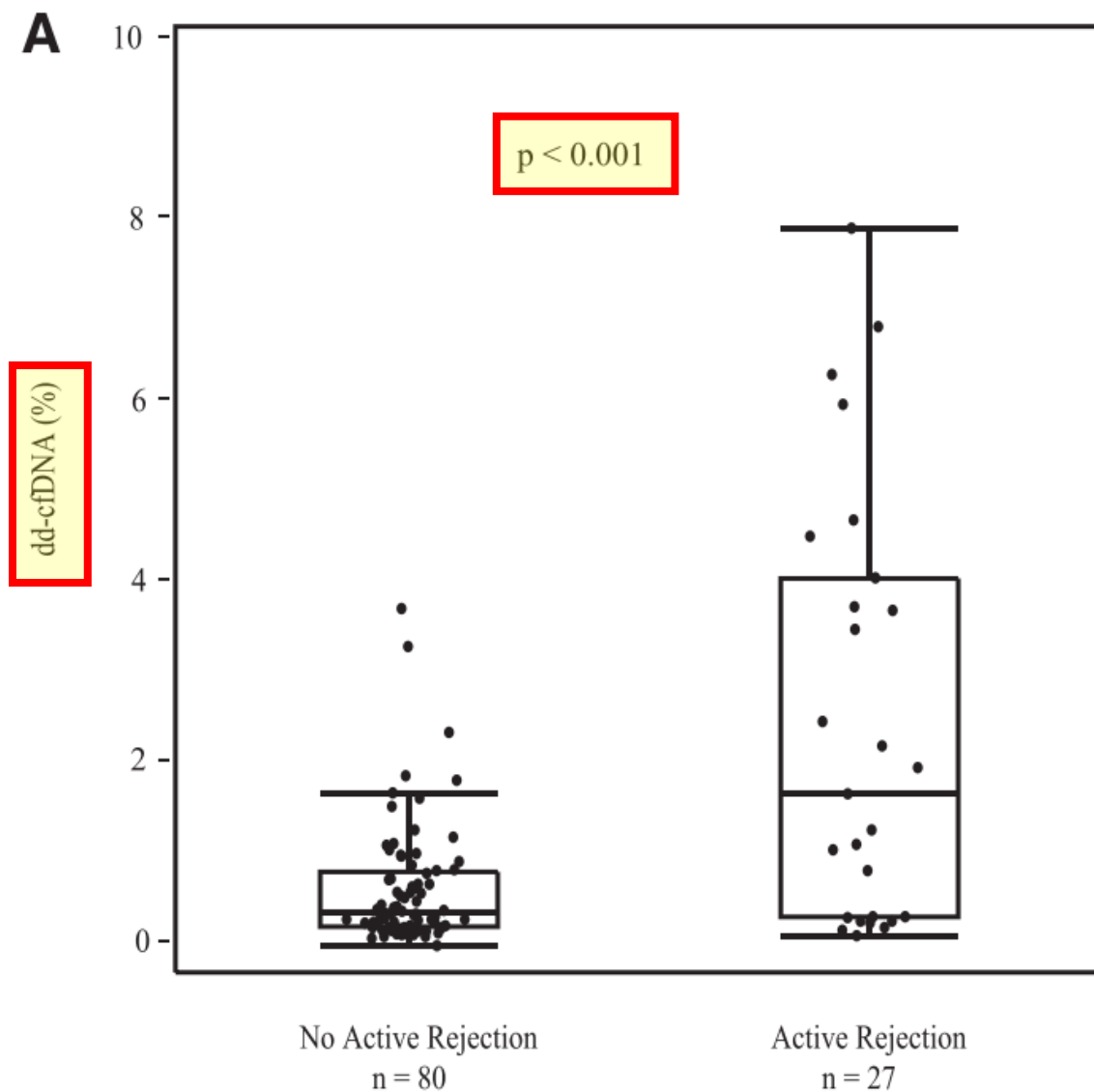
Roy D. Bloom,* Jonathan S. Bromberg,[†] Emilio D. Poggio,[‡] Suphamai Bunnapradist,[§] Anthony J. Langone,^{||} Puneet Sood,[¶] Arthur J. Matas,** Shikha Mehta,^{††} Roslyn B. Mannon,^{‡‡‡} Asif Sharfuddin,^{§§} Bernard Fischbach,^{|||} Mohanram Narayanan,^{¶¶} Stanley C. Jordan,^{§§§} David Cohen,^{†††} Matthew R. Weir,^{‡‡‡} David Hiller,^{§§§} Preethi Prasad,^{|||} Robert N. Woodward,^{¶¶¶} Marica Grskovic,^{¶¶¶} John J. Sninsky,^{¶¶¶} James P. Yee,^{|||} and Daniel C. Brennan,^{****} for the Circulating Donor-Derived Cell-Free DNA in Blood for Diagnosing Active Rejection in Kidney Transplant Recipients (DART) Study Investigators

- 14 merkez, 384 hasta
- Prospektif gözlemsel çalışma
- 2 yıl takip

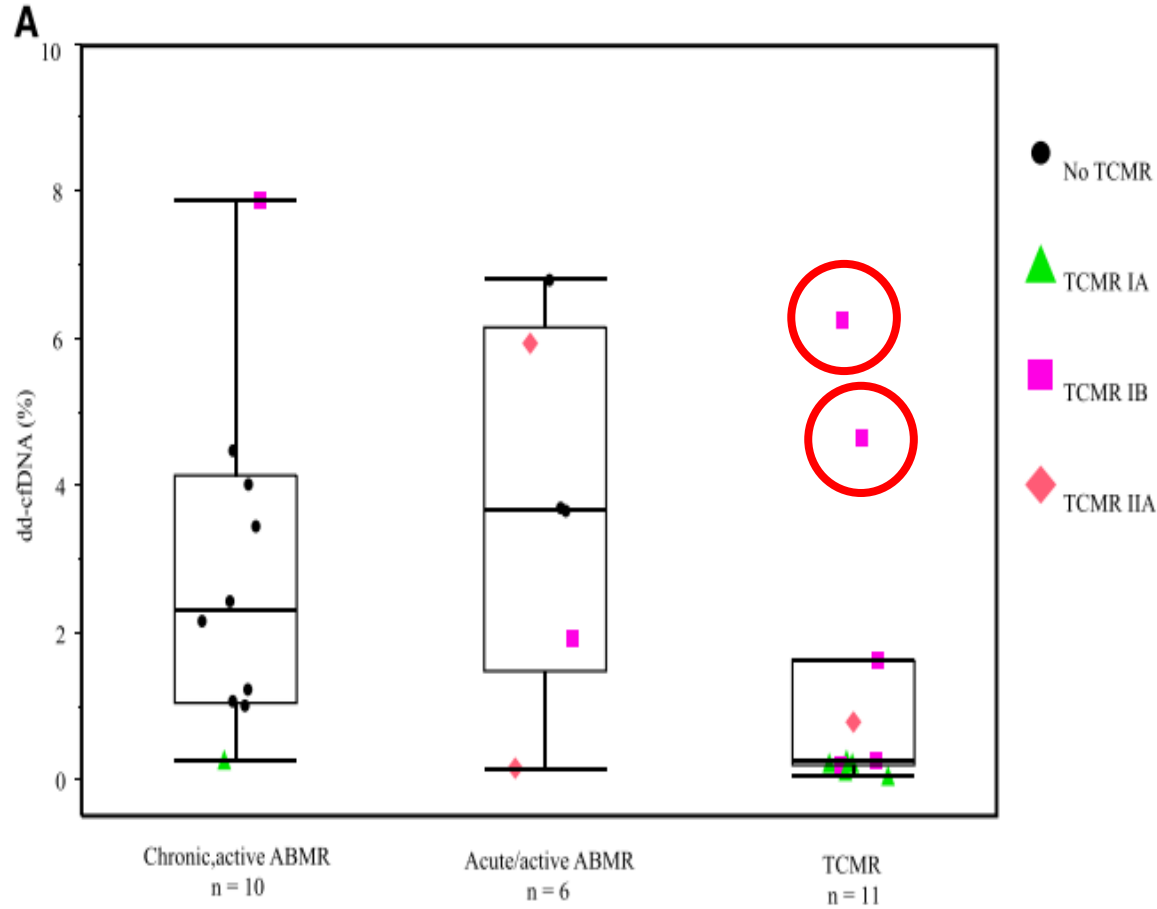
TANISAL



Dd-cfDNA rejeksiyon tanısı koymakta kreatinininden daha hassas

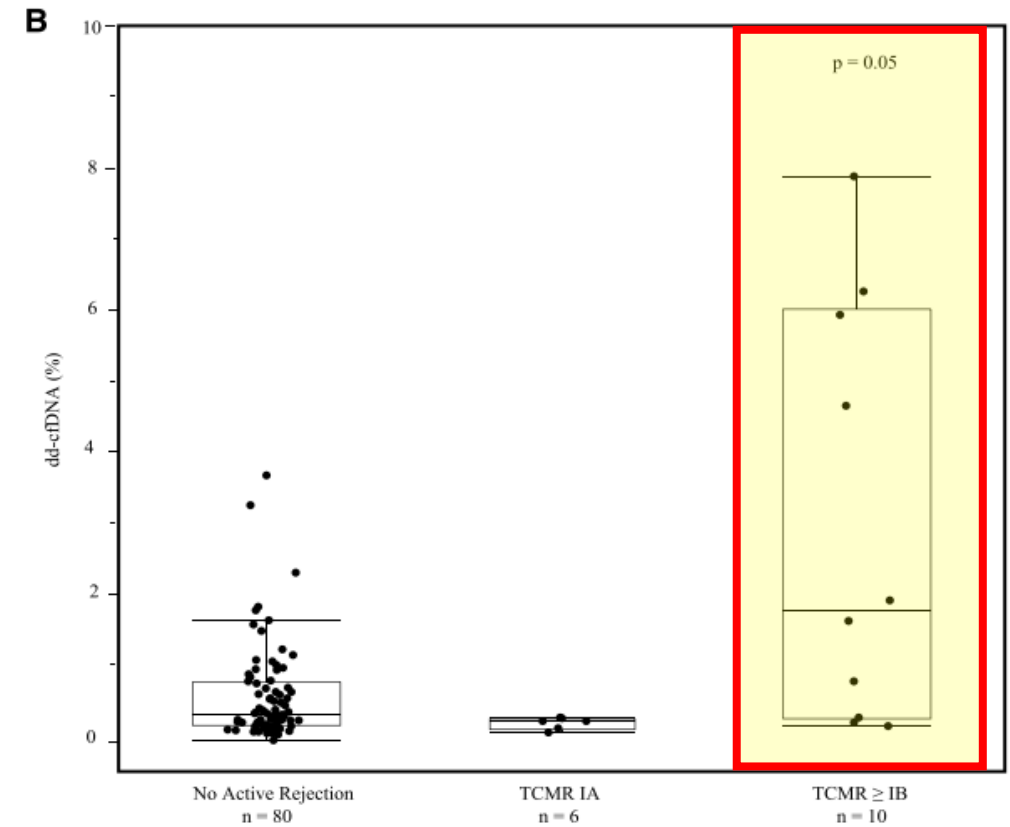


- Dd-cfDNA AMR'yi saptayabiliyor
- TCMR için aynı şey geçerli değil



Cut-off %1

TCMR >1B ise tanısal potansiyele sahip



Clinical outcomes from the Assessing Donor-derived cell-free DNA Monitoring Insights of kidney Allografts with Longitudinal surveillance (ADMIRAL) study.



kidney
NATIONAL



PREDİKTİF

Cohort

1094 patients



7 transplant centers

Single Kidney Adult Recipients



90% deceased donor

Multiorgan and pregnancy excluded



3 yrs. post transplant dd-cfDNA surveillance

Median of 6 results per patient

Methods

Post transplant events



Centralized biopsy reporting

Center Standard of Care protocols



3 years of Outcomes Surveillance



Analysis of

- De-Novo DSA
- eGFR trajectories
- Allograft rejection

Outcomes



eGFR Decline

Persistently elevated dd-cfDNA (>1 result above 0.5%) predicted a > 25% decline in eGFR over 3 years



Temporal Relationship

dd-cfDNA values $\geq 0.5\%$ were associated with a nearly 3-fold increase in the risk of development of de novo donor specific antibody (DSA)



Subclinical Rejection

Significant elevations in dd-cfDNA during rejection ahead of changes in serum creatinine

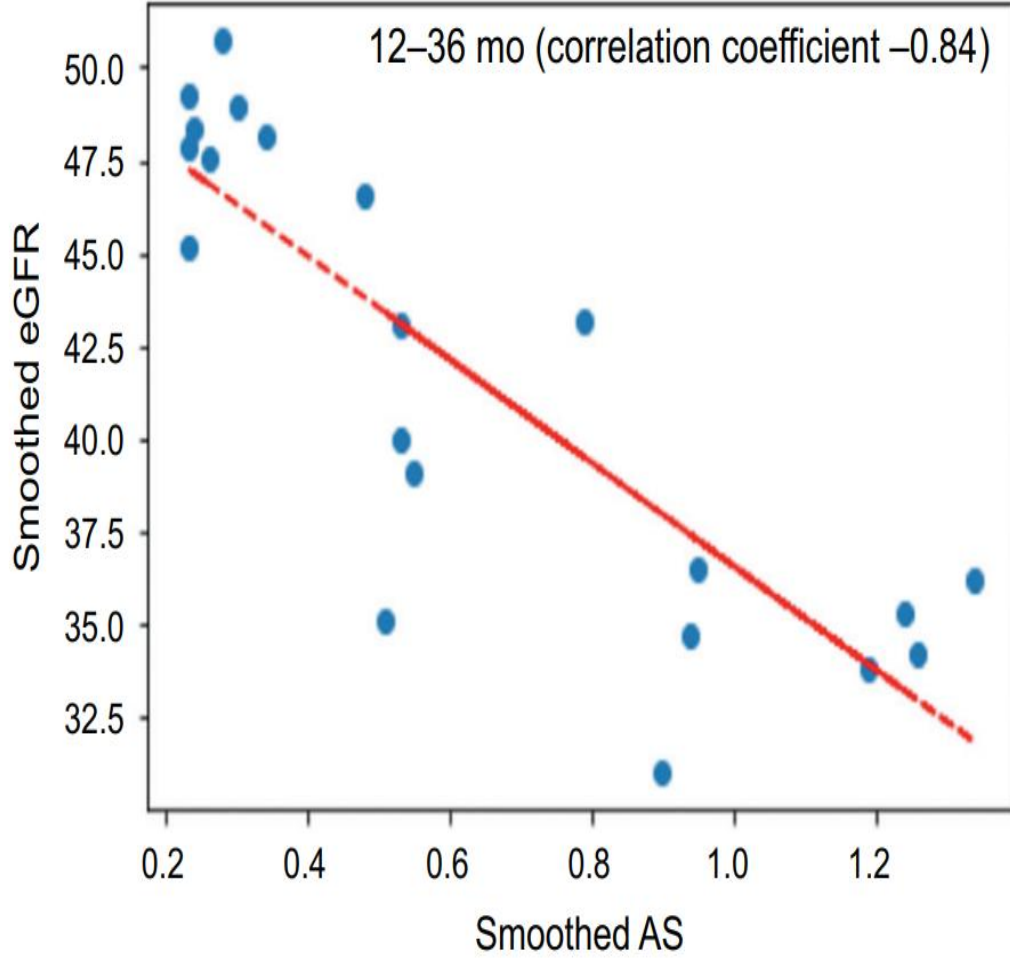
Bu et al 2021

ClinicalTrials.gov Identifier: NCT04566055

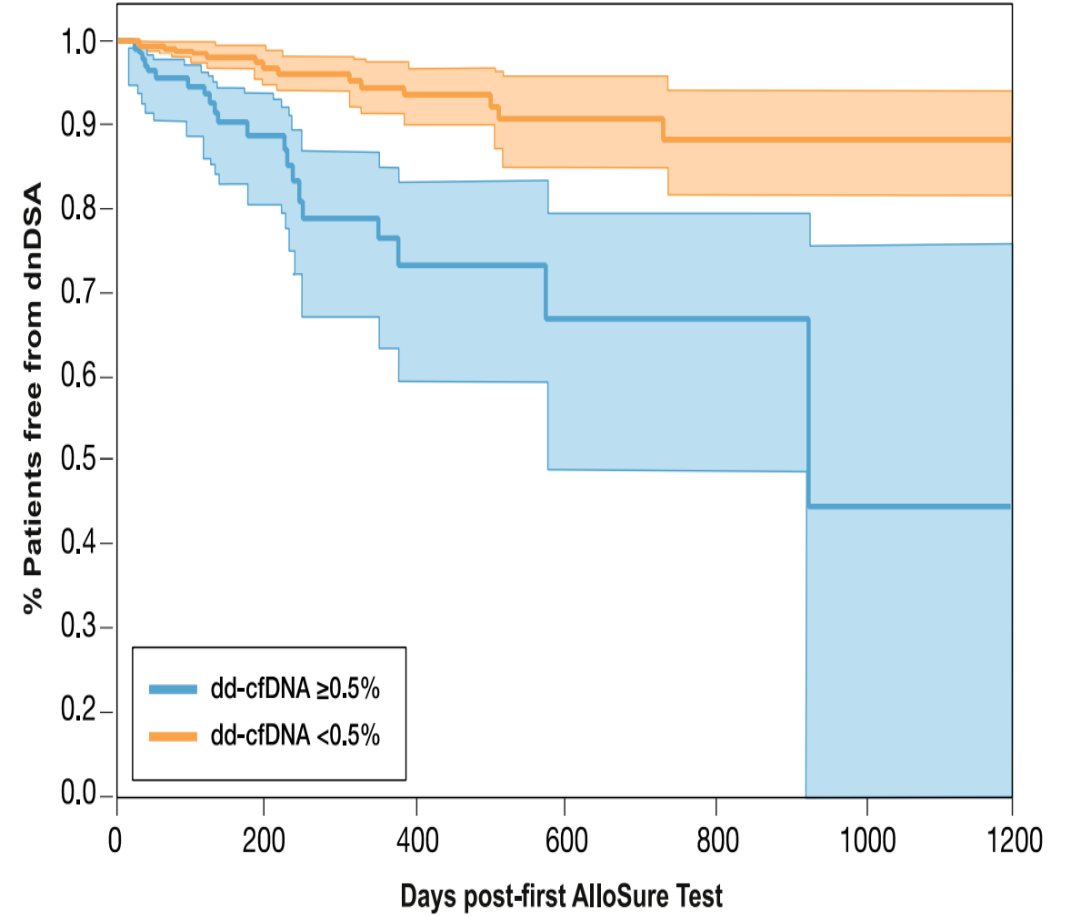


CONCLUSION: The ADMIRAL study demonstrates a broad utility of dd-cfDNA as a leading indicator ahead of clinical presentations of allograft injury, formation of dnDSA, eGFR decline and subclinical rejection.

dd-cfDNA düzeyleri arttıkça GFR düşüyor

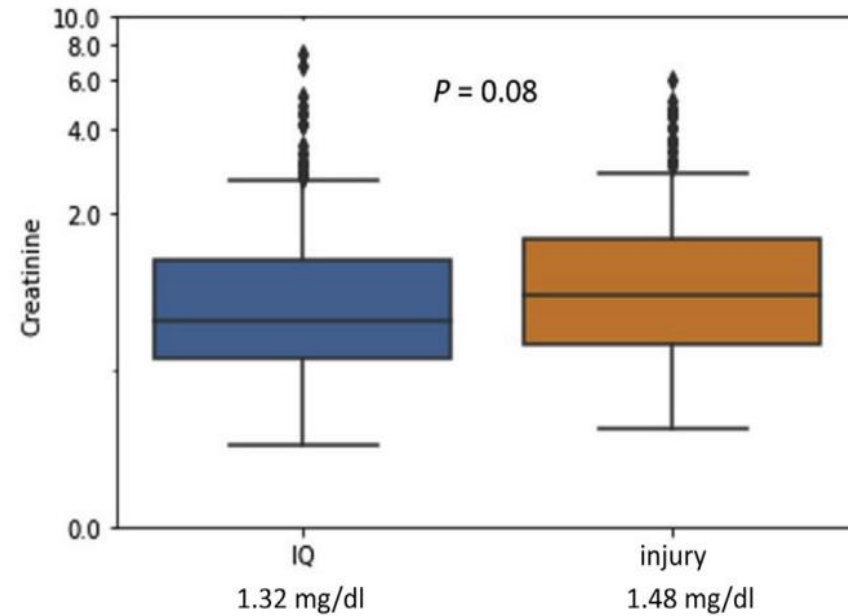
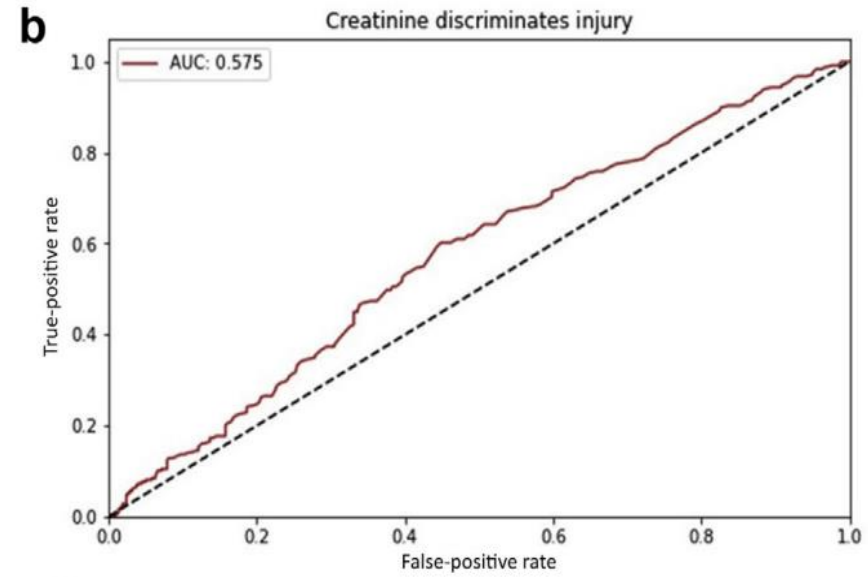
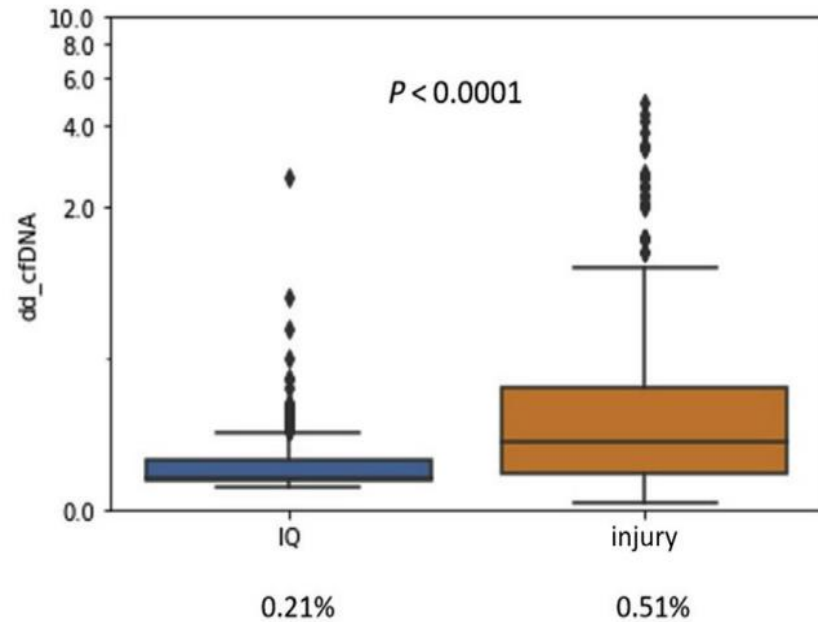
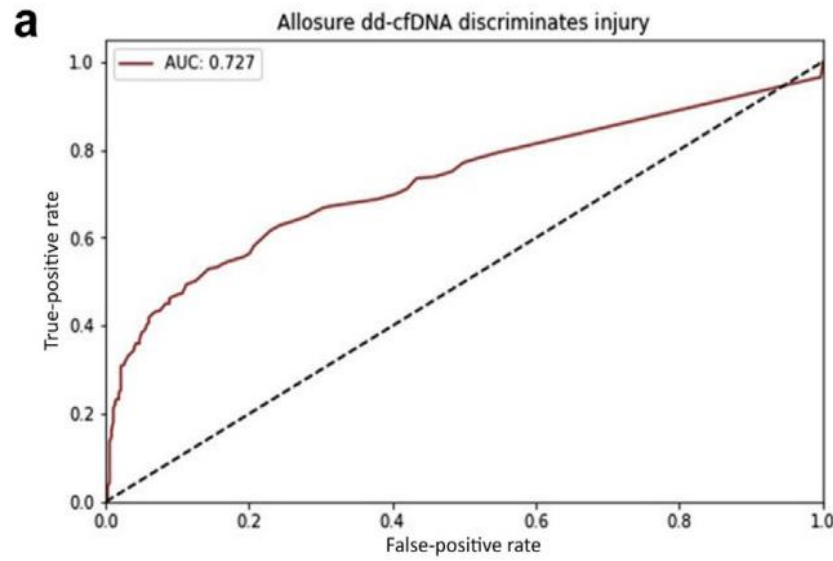


dd-cfDNA >%0.5 olanlarda DSA riski 3 kat daha fazla



Persistan dd-cfDNA yüksekliği (en az 1 ölçümü >%0.5'ten fazla) olanlarda GFR'de %25 azalma riski 2 kat daha fazla

dd-cfDNA allograft hasarını saptamada kreatinine göre daha hassas.



High levels of dd-cfDNA identify patients with TCMR 1A and borderline allograft rejection at elevated risk of graft injury

Erik Stites¹ | Dhiren Kumar²  | Oyedolamu Olaitan³ | Sidney John Swanson⁴ | Nicolae Leca⁵ | Matthew Weir⁶ | Jonathan Bromberg⁷  | Joseph Melancon⁸  | Irfan Agha⁹ | Hasan Fattah¹⁰ | Tarek Alhamad¹¹  | Yasir Qazi^{12,13} | Alexander Wiseman¹ | Gaurav Gupta² 

- 11 merkez
- 79 hasta (27 borderline, 52 TCMR 1A)
- Hastalar dd-cfDNA açısında düşük (%0.5) ve yüksek (>%0.5) olarak katmanlandırılmış

Dd-cfDNA>%0.5 ise

- GFR kaybı daha fazla
- DSA gelişim riski yüksek
- Rekürren rejeksiyon riski yüksek

TABLE 2 Summary statistics for high vs low donor-derived cell-free DNA (dd-cfDNA)

Measurement	Statistics	All patients	Low (dd-cfDNA < 0.5%)	High (dd-cfDNA ≥ 0.5%)	P value
dd-cfDNA measurements ^a (%)	N	79	37	42	-
	Mean (SD)	1.05 (1.267)	0.25 (0.087)	1.76 (1.40)	
	Median (Q1, Q3)	0.64 (0.21, 1.40)	0.21 (0.19, 0.29)	1.40 (0.87, 2.02)	
	Min, Max	0.19, 6.70	0.19, 0.49	0.52, 6.70	
Change in estimated glomerular filtration rate (eGFR; 3-6 mo)	N	79	37	42	.019 ^b
	Mean (SD)	-2.85 (7.526)	-0.74 (7.369)	-4.74 (7.247)	
	Median (Q1, Q3)	-2.00 (-5.00, 1.00)	0.00 (-3.00, 2.00)	-3.50 (-8.00, -1.00)	
	Min, Max	-29.00, 16.00	-29.00, 12.00	-20.00, 16.00	
% Change in eGFR (3-6 mo)	N	79	37	42	.004 ^b
	Mean (SD)	-4.70 (16.937)	-0.40 (18.149)	-8.54 (14.98)	
	Median (Q1, Q3)	-3.89 (-9.89, 2.33)	0.00 (-4.92, 4.76)	-8.50 (-16.22, -1.39)	
	Min, Max	-70.73, 33.33	-70.73, 33.33	-37.50, 32.65	
Presence of donor-specific antibodies (3-6 mo)	Percentage	18/79 (22.9%)	1/37 (2.7%)	17/42 (40.5%)	<.001 ^c
Recurrent rejection	Percentage	9/79 (11.4%)	0/37 (0.0%)	9/42 (21.4%)	.003 ^c

Dd-cfDNA riskli borderline rejeksiyonları ayırt edici potansiyele sahip

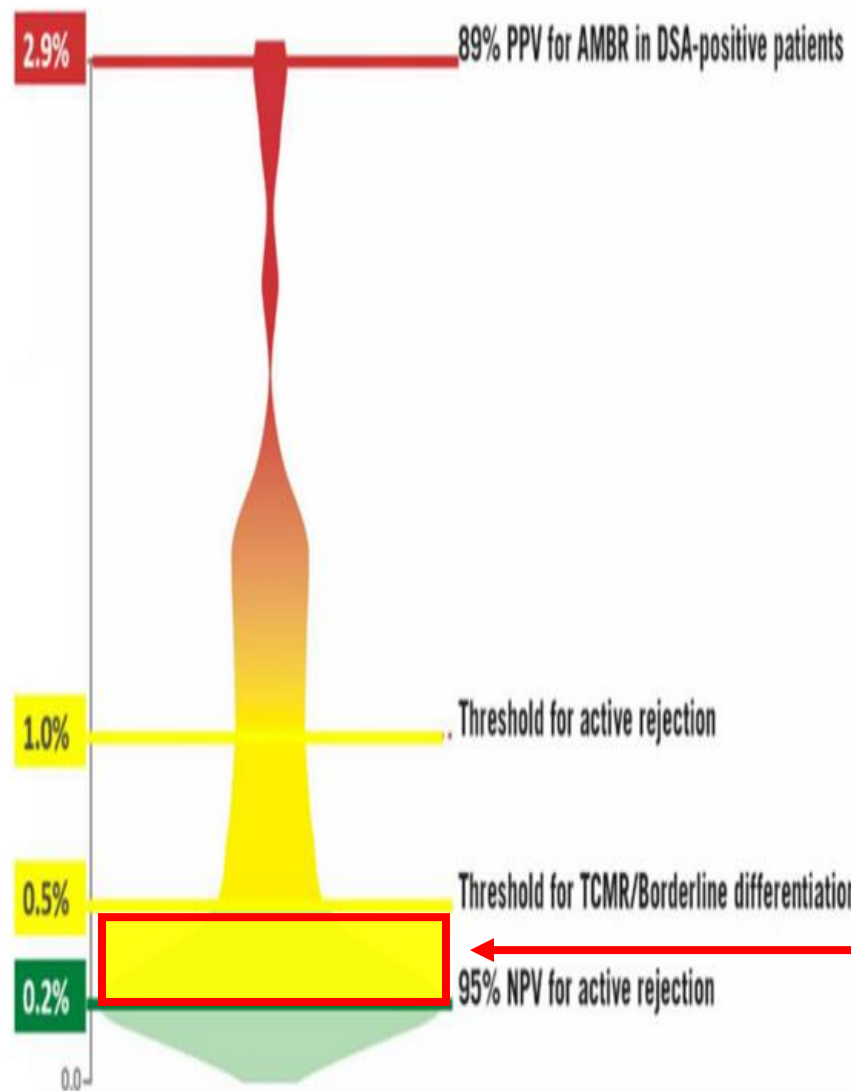


Table 2. Biological variation for dd-cfDNA, cardiac injury biomarkers, and other commonly measured analytes.

Biomarker, typical value ^a	CV _A , %	CV _I , %	CV _G , %	II	RCV, %	RCV, absolute ^a
dd-cfDNA, 1%	6.8	21	37	0.57	61	0.61%

- dd-cfDNA >%1 ise ABMR veya TCMR 1B riski yüksek
- dd-cfDNA >%0.5 <%1 ise DSA gelişme, GFR kaybı ve rejeksiyon riski riski yüksek

dd-cfDNA <%0.5 olan hastalarda seri ölçümlerde %61'den fazla olan artışlar anlamlı

Genel olarak her 3 testin de performansları benzer

	TRAC Kidney	AlloSure Kidney	Prospera
# of SNPs	>100,000 (whole genome sequencing)	405 SNPs	13,392 SNPs
Sensitivity	64%	59.3%	88.7%
Specificity	85.1%	84.7%	72.6%
PPV†	39.7%	40.9%	36.6%
NPV†	91.9%	92.1%	97.3%

Dezavantajlar:

- PPV düşük: BK nefropati, piyelonefrit vb diğer hasar nedenleri ile rejeksiyonu ayırt edemiyor
- Pahalı

J Am Soc Nephrol 2017; 28:2221.

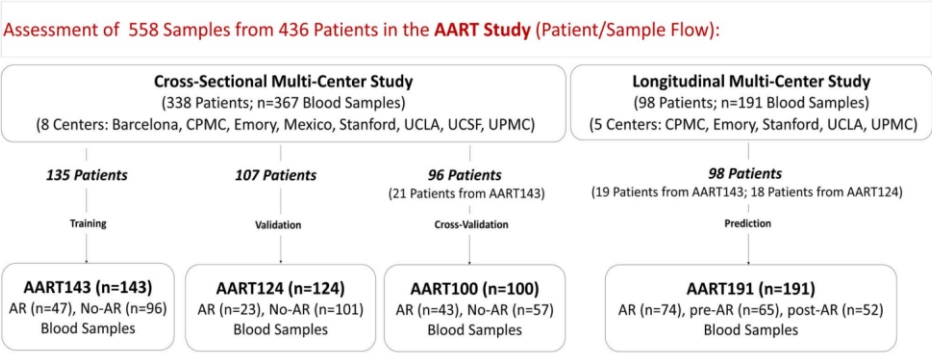
J Clin Med 2018; 8:19.

TRAC White Paper.

The kSORT Assay to Detect Renal Transplant Patients at High Risk for Acute Rejection: Results of the Multicenter AART Study

Silke Roedder^{1,3}, Tara Sigdel^{1,3}, Nathan Salomonis^{2,3}, Sue Hsieh¹, Hong Dai^{3,2a}, Oriol Bestard⁴, Diana Metes⁵, Andrea Zeevi⁵, Albin Gritsch⁶, Jennifer Cheeseman⁷, Camila Macedo⁵, Ram Peddy³, Mara Medeiros⁸, Flavio Vincenti¹, Nancy Asher¹, Oscar Salvatierra⁹, Ron Shapiro⁵, Allan Kirk^{7,2b}, Elaine Reed⁶, Minnie M. Sarwal^{1*}

KSORT akut rejeksiyonu tespit edebiliyor



AR için anlamlı 17 genin ekspresyonu için tarama (PCR)

- Apoptozis
- Lökosit trafiği
- Monosit aktivasyonu
- Hücre sağkalımı

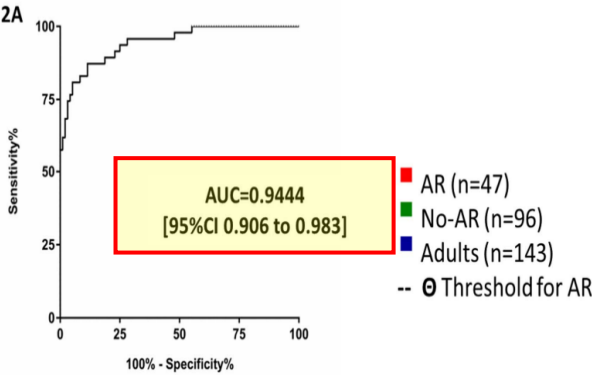
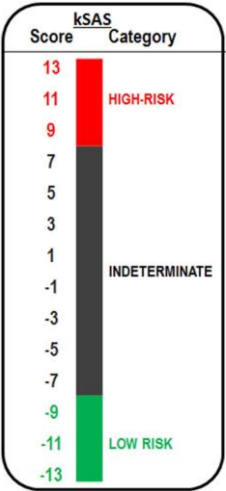


Table 2. Performance of kSORT in the AART143, AART124, and AART100 cohorts.

Statistics	kSORT Predictions					
	AART143 (Training Set)		AART124 (Validation Set)		AART100 (Cross-Validation Set)	
	AR	No-AR	AR	No-AR	AR	No-AR
Real Results						
AR	39	8	21	2	36	3
No-AR	9	87	1	100	3	43
Sensitivity (95% CI)	82.98% (69.19%–92.35%)		91.30% (71.96%–98.93%)		92.31% (79.13%–98.38%)	
Specificity (95% CI)	90.63% (82.95%–95.62%)		99.01% (94.61%–99.97%)		93.48% (82.1%–98.63%)	
PPV (95% CI)	81.25% (68.06%–89.81%)		95.46% (78.20%–99.19%)		93.21% (79.68%–97.35%)	
NPV (95% CI)	91.58% (84.25%–95.67%)		98.04% (93.13%–99.46%)		93.48% (82.45%–97.76%)	
AUC (95% CI)	0.94 (0.91–0.98)		0.95 (0.88–1.00)		0.92* (0.86–0.98)	

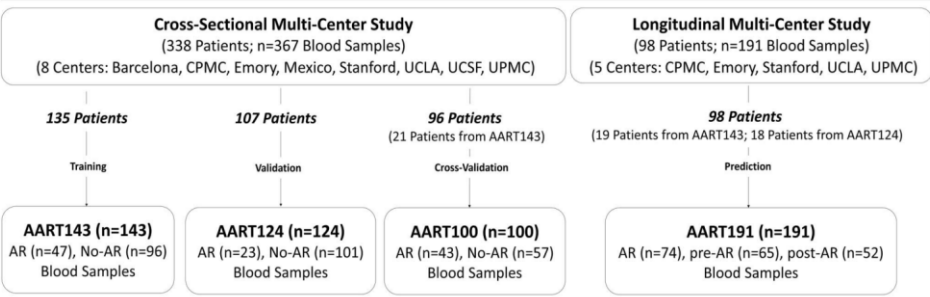
*AUC was calculated based on kSORT scores for $n = 100$ patients including high risk for AR ($n = 39$), low risk for AR ($n = 46$), and indeterminate ($n = 15$).
NPV, negative predictive value.
doi:10.1371/journal.pmed.1001759.t002

The kSORT Assay to Detect Renal Transplant Patients at High Risk for Acute Rejection: Results of the Multicenter AART Study

Silke Roedder^{1,3}, Tara Sigdel^{1,3}, Nathan Salomonis^{2,3}, Sue Hsieh¹, Hong Dai^{3,2a}, Oriol Bestard⁴, Diana Metes⁵, Andrea Zeevi⁵, Albin Gritsch⁶, Jennifer Cheeseman⁷, Camila Macedo⁵, Ram Peddy³, Mara Medeiros⁸, Flavio Vincenti¹, Nancy Asher¹, Oscar Salvatierra⁹, Ron Shapiro⁵, Allan Kirk^{7a,b}, Elaine Reed⁶, Minnie M. Sarwal^{1*}

KSORT akut rejeksiyonu tespit edebiliyor

Assessment of 558 Samples from 436 Patients in the AART Study (Patient/Sample Flow):



AR için anlamlı 17 genin ekspresyonu için tarama (PCR)

- Apoptozis
- Lökosit trafiği
- Monosit aktivasyonu
- Hücre sağkalımı

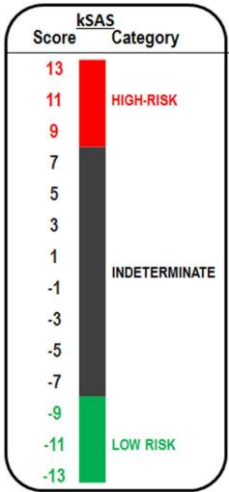
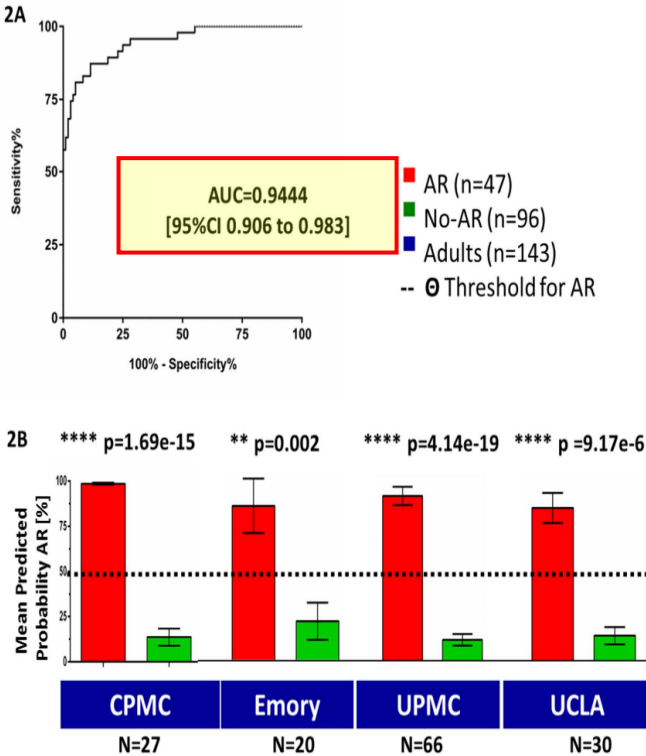


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	AR	No-AR	AR	No-AR	AR	No-AR
Real Results						
AR	39	8	21	2	36	3
No-AR	9	87	1	100	3	43
Sensitivity (95% CI)	82.98% (69.19%–92.35%)		91.30% (71.96%–98.93%)		92.31% (79.13%–98.38%)	
Specificity (95% CI)	90.63% (82.95%–95.62%)		99.01% (94.61%–99.97%)		93.48% (82.1%–98.63%)	
PPV (95% CI)	81.25% (68.06%–89.81%)		95.46% (78.20%–99.19%)		93.21% (79.68%–97.35%)	
NPV (95% CI)	91.58% (84.25%–95.67%)		98.04% (93.13%–99.46%)		93.48% (82.45%–97.76%)	
AUC (95% CI)	0.94 (0.91–0.98)		0.95 (0.88–1.00)		0.92* (0.86–0.98)	

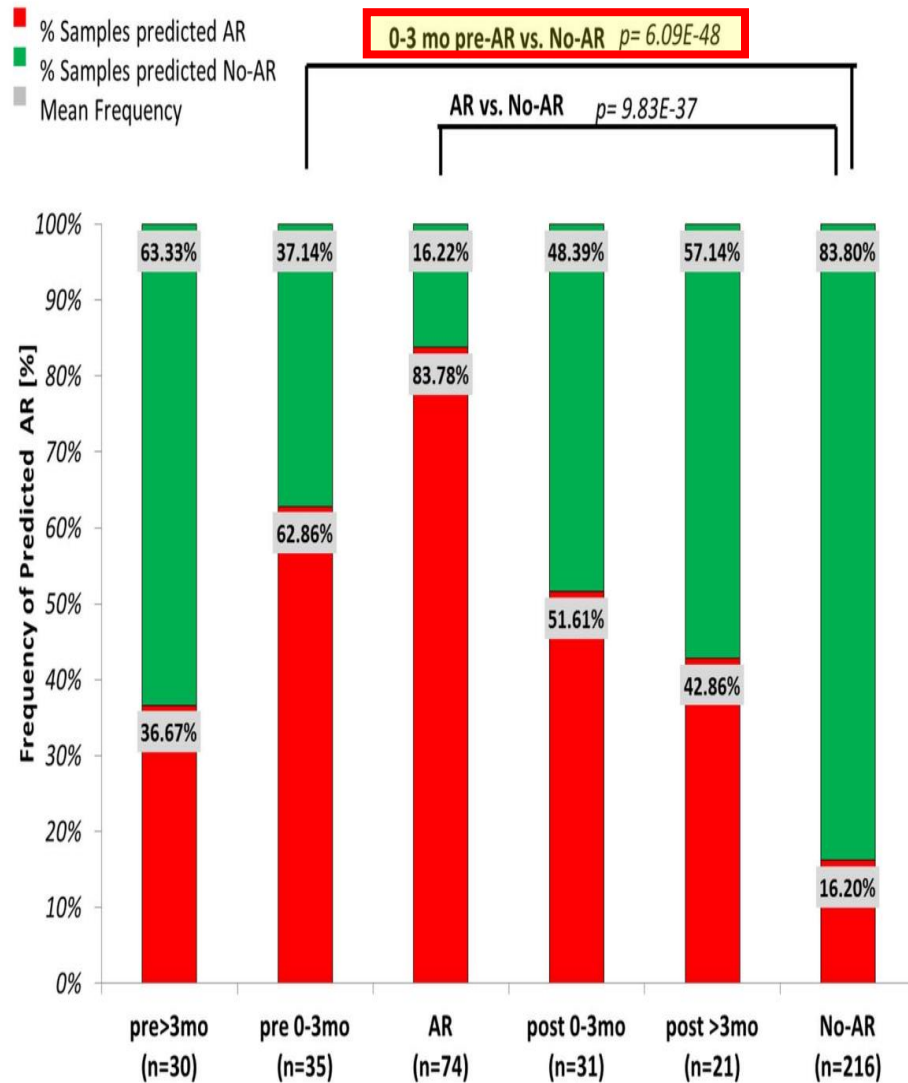
*AUC was calculated based on kSORT scores for $n = 100$ patients including high risk for AR ($n = 39$), low risk for AR ($n = 46$), and indeterminate ($n = 15$). NPV, negative predictive value.

doi:10.1371/journal.pmed.1001759.t002



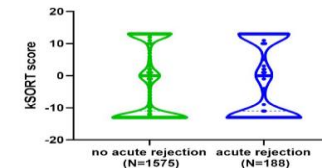
Validasyon kohortları da benzer

KSORT akut rejeksiyon gelişebileceğini 3 ay öncesinden öngörebiliyor



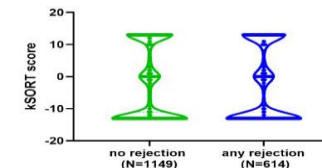
Acute rejection

kSORT score distribution



Any rejection

kSORT score distribution



Presence vs absence of acute rejection (TCMR and/or ABMR)				
Sample Characteristic	No acute rejection (N = 1575)	Acute rejection (N = 188)	Total (N = 1763)	P value
Donor-specific HLA antibodies	349/1548 (22.55%)	95/185 (51.35%)	444/1733 (25.62%)	<.0001
eGFR (mL/min/1.73m ²)*	46.0 ± 19.7	36.4 ± 21.3	45.0 ± 20.1	<.0001
Proteinuria (g/24h)*	0.17 (0.10;0.30)	0.30 (0.17;0.64)	0.18 (0.10;0.38)	.009
Biopsy timing after transplant	361 (91;370)	148.0 (30;365)	358.0 (90;370)	<.0001
Biopsy quality				
Adequate	1346/1572 (85.62%)	174/188 (92.55%)	1520/1760 (86.36%)	.01
Marginal	226/1572 (14.38%)	14/188 (7.45%)	240/1760 (13.64%)	
Type of biopsy				
Protocol biopsy	1194/1575 (75.81%)	82/188 (43.62%)	1276/1763 (72.38%)	<.0001
Indication biopsy	381/1575 (24.19%)	106/188 (56.38%)	487/1763 (27.62%)	
kSORT score	-11.0 (-13;13)	-11.0 (-13;13)	-11.0 (-13;13)	.46
kSORT Rejection Risk Category				
Low risk (LR)	803/1575 (50.98%)	95/188 (50.53%)	898/1763 (50.94%)	.53
Indeterminate risk (IND)	294/1575 (18.67%)	26/188 (13.83%)	320/1763 (18.15%)	
High risk (HR)	478/1575 (30.35%)	67/188 (35.64%)	545/1763 (30.91%)	

Application of TruGraf v1: A Novel Molecular Biomarker for Managing Kidney Transplant Recipients With Stable Renal Function

C.L. Marsh^{a,b,*}, S.M. Kurian^b, J.C. Rice^a, T.C. Whisenant^c, J. David^d, S. Rose^d, C. Schieve^d, D. Lee^d, J. Case^b, B. Barrick^b, V.R. Peddi^e, R.B. Mannon^f, R. Knight^g, D. Maluf^h, D. Mandelbrotⁱ, A. Patel^j, J.J. Friedewald^k, M.M. Abecassis^k, and M.R. First^{d,k}

^aScripps Center for Organ Transplantation, La Jolla, California, United States; ^bScripps Clinic Bio-Repository and Transplantation Research, La Jolla, California, United States; ^cUniversity of California, San Diego, School of Medicine, Center for Computational Biology and Bioinformatics, La Jolla, California, United States; ^dTransplant Genomics Inc, Mansfield, Massachusetts, United States; ^eCalifornia Pacific Medical Center, San Francisco, California, United States; ^fUniversity of Alabama School of Medicine, Birmingham, Alabama, United States; ^gHouston Methodist Hospital, Houston, Texas, United States; ^hUniversity of Virginia, Charlottesville, Virginia, United States; ⁱUniversity of Wisconsin, Madison, Wisconsin, United States; ^jHenry Ford Hospital, Detroit, Michigan, United States; and ^kComprehensive Transplant Center, Northwestern University, Chicago, Illinois, United States

- 192 hasta
- 7 merkez
- 120 farklı genin ekspresyonu
 - TX (Transplant eXcellence)
 - Not-TX (renal disfonksiyon/rejeksiyon)

Table 1A. Results of TruGraf Blood Test and Comparison With Clinical Phenotype in All 192 Kidney Transplant Recipients with Stable Renal Function

	Clinical Phenotype not-TX	Clinical Phenotype TX
TruGraf Blood Test not-TX	26	42
TruGraf Blood Test TX	8	116

Accuracy = 142/192 (74%).
Accuracy of TruGraf TX result 116/124 (94%).
NPV = 91%.
PPV = 48%.
Sensitivity = 76%.
Specificity = 73%.

Table 1B. Results of TruGraf Blood Test and Comparison With Clinical Phenotype in 99 Kidney Transplant Recipients With Stable Renal Function and Biopsy-Confirmed Phenotypes

	Clinical Phenotype Not-TX	Clinical Phenotype TX
TruGraf Blood Test not-TX	17	19
TruGraf Blood Test TX	7	56

Accuracy = 73/99 (74%).
Accuracy of TruGraf TX result 56/63 (89%).
NPV = 89%.
PPV = 48%.
Sensitivity = 71%.
Specificity = 75%.

Validation of a Blood Gene Expression Classifier to Differentiate Immune Quiescence from Rejection

Kidney360



DCAF12
MARCH8
FLT3
IL1R2
PDCD1

5 gene classifier
(Developed on
56 peripheral blood
samples)

AlloMap Kidney



PRIMARY
Validation set

Q samples 98
R samples 18
7 TCMR
10 ABMR
1 Mixed

SECONDARY
Validation set

Q samples 8
R samples 11
7 TCMR
2 ABMR
2 Mixed

Q, quiescence; R, rejection

AlloMap Kidney Classifier Scores

	PRIMARY Validation	SECONDARY Validation
 Quiescence	9.49 (7.68-11.53) <i>Median</i>	The cohorts were statistically different and the medians were similar to the primary validation set
 Rejection	13.09 (11.25-15.28) <i>Median</i> $p < 0.001$	
 AUC for discriminating rejection	0.786	0.800
0.894 AUC	The ability to discriminate rejection from quiescence was improved when AlloSure and AlloMap Kidney were used together	

Conclusions Validation of AlloMap Kidney demonstrated the ability to differentiate between rejection and immune quiescence using a range of scores. The diagnostic performance suggests that assessment of the mechanisms of immunological activity is complementary to allograft injury information derived from AlloSure dd-cfDNA.

Enver Akalin, Matthew R. Weir, Suphamai Bunnapradist, et al. *Clinical Validation of an Immune Quiescence Gene Expression Signature in Kidney Transplantation*. *Kidney360*. DOI: 10.34067/KID.0005062021
Visual Abstract by Edgar Lerma, MD, FASN

AlloMap Kidney Skor 11.5 → maksimum spesifite, sensitivite

A peripheral blood gene expression signature to diagnose subclinical acute rejection

METHODS

Discovery of 17 gene set for Acute Cellular Rejection (ACR) diagnosis

Transcriptomic Analysis
(N=127)

Discovery Cohort
(RNA-seq, N=88)

Validation Cohort
(Microarray, N=65)

Development of Targeted Expression (TREx) Assay

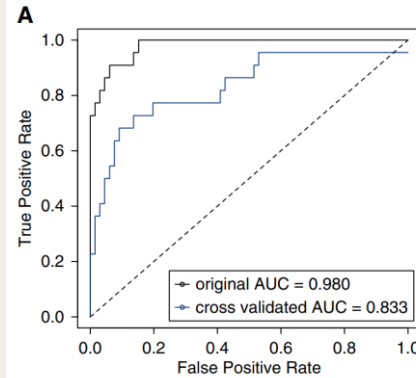
GoCAR*
Training (N=113)

Logistic
Regression Model

GoCAR Testing
(N=64)

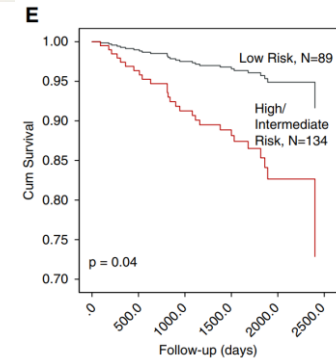
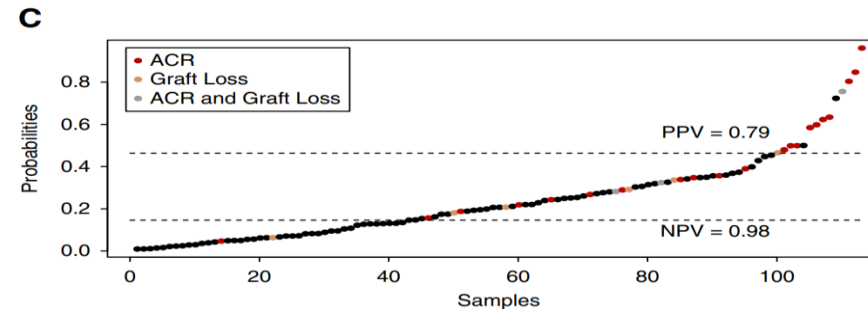
Belgian Testing
(N=46)

*GoCAR: Genomics of Chronic Allograft Rejection study



OUTCOMES

1. RNA sequencing identified a 17 gene set for accurate diagnosis of subclinical acute rejection
2. TREx assay based on the 17 gene set achieved PPV=0.79 and NPV=0.98 for subclinical ACR diagnosis
3. The patients with high or intermediate risk scores had high risk of graft loss



CONCLUSION: The TREx assay allows the noninvasive diagnosis of subclinical acute rejection in the graft and may represent a useful tool to risk-stratify kidney transplant recipients.

Can blood gene expression assays and donor-derived cellfree DNA be used to diagnose subclinical rejection?

Methods



Post hoc analysis
Clinical Trials in Organ
Transplantation 08



Surveillance biopsies
2 to 6, 12, and 24 months
post-transplant



208 subjects
428 biopsy samples



2011 – 2014

Results



Diagnosis of
Subclinical
Rejection



TruGraf

Gene Expression
Profile Assay
(95% CI)

Positive
Predictive Value

47%
(0.35-0.59)

Negative
Predictive Value

82%
(0.78-0.86)

AUROC

0.75



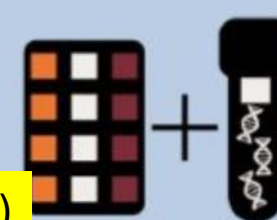
TRAC (Eurofins)

Donor Derived
cfDNA
(95% CI)

56%
(0.44-0.67)

84%
(0.80-0.88)

0.72

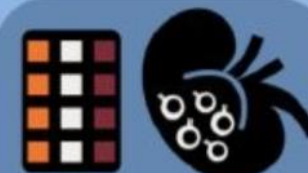


Combined
Tests
(95% CI)

81%
(0.63-0.95)

88%
(0.84-0.92)

0.81



Gene expression
profile better at
detecting cellular
rejection

AUROC 0.80 vs. 0.62,
P=0.001



Donor Derived
cfDNA better at
detecting antibody
rejection

AUROC 0.84 vs. 0.71,
P=0.003

Conclusions Donor-derived cellfree DNA and gene expression profiles provide a less invasive monitoring strategy for subclinical rejection, with different detection of antibody- and cell-mediated rejection.

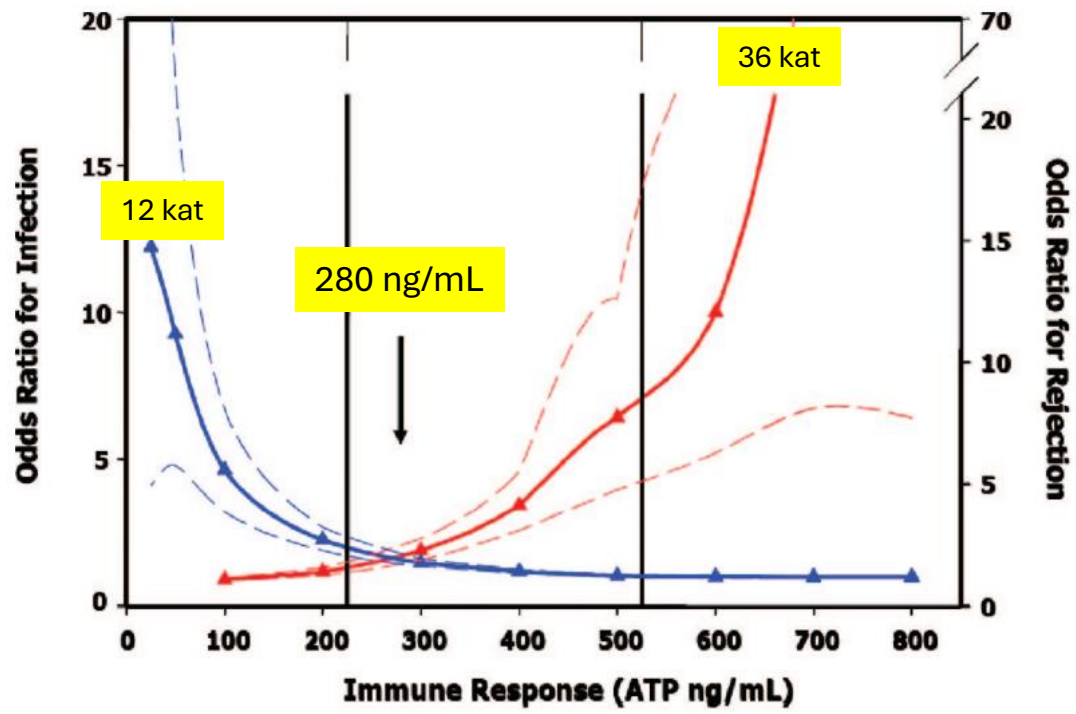
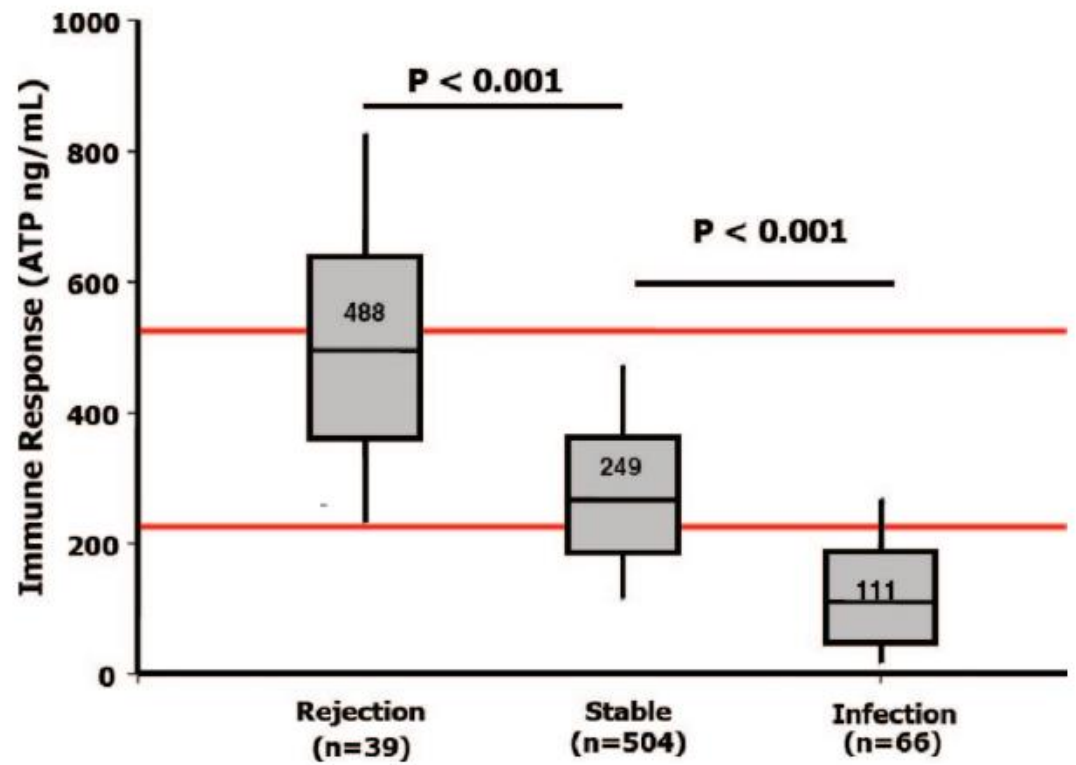
Sookhyeon Park, Kexin Guo, Raymond L. Heilman, et al. *Combining Blood Gene Expression and Cell-Free DNA to Diagnose Subclinical Rejection in Kidney Transplant Recipients*. CJASN doi: 10.2215/CJN.05530421. **Visual Abstract by Sinead Stoneman, MB BCH BAO, MRCPI**

Assessing Relative Risks of Infection and Rejection: A Meta-analysis using an Immune Function Assay

Richard J. Kowalski,^{1,11} Diane R. Post,¹ Roslyn B. Mannon,² Anthony Sebastian,³ Harlan I. Wright,³ Gary Sigle,³ James Burdick,⁴ Kareem Abu Elmagd,⁵ Adriana Zeevi,⁵ Mayra Lopez-Cepero,⁶ John A. Daller,⁷ H. Albin Gritsch,⁸ Elaine F. Reed,⁸ Johann Jonsson,⁹ Douglas Hawkins,¹⁰ and Judith A. Britz¹

ImmuKnow

- Mitogen ile stimüle edilmiş CD4+T-hücrelerini intraselüler ATPdüzeylerini ölçer
- Yüksek ise rejeksiyon, düşük ise enfeksiyon



ImmuKnow → Tanısal gücü tartışmalı

Table 4. Distribution of T cell assay (TCA, ImmuKnow) values in the setting of subsequent opportunistic infection (OI) versus controls without OI

TCA Result	OI (n = 94)	No OI (n = 94)
Low (≤ 225 ng/ml)	20 (21%)	16 (17%)
Moderate (226 to 524 ng/ml)	53 (57%)	52 (55%)
Strong (≥ 525 ng/ml)	21 (22%)	26 (28%)

The values are the percentages of tests.

Table 8. Sensitivity, specificity of a TCA ≥ 525 , and acute rejection

	Versus Controls	Versus All Samples
Sensitivity	23.4	25.0
Specificity	80.9	77.5
Odds ratio	1.87	1.15
95% confidence interval	0.47 to 8.38	0.61 to 2.19

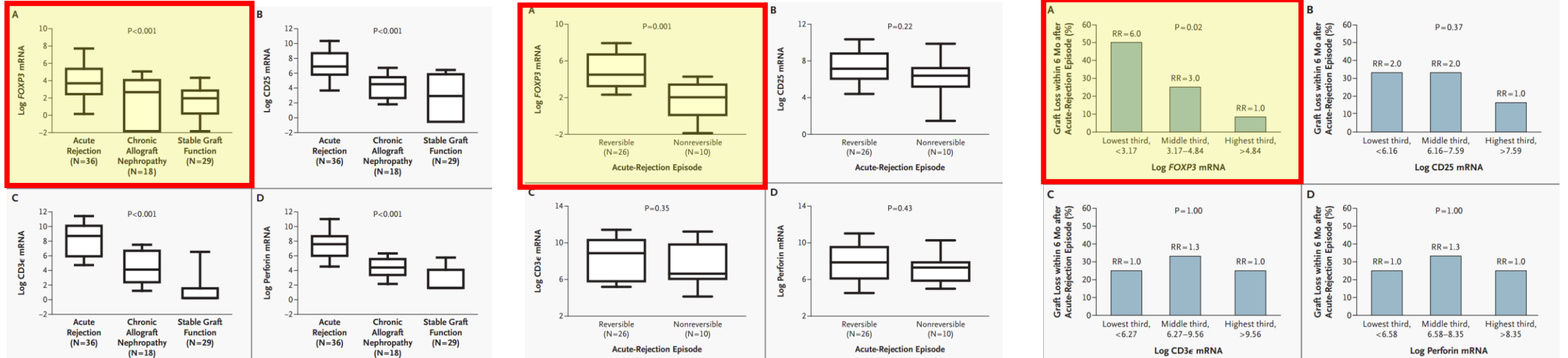
Performance of the ImmuKnow Assay in Differentiating Infection and Acute Rejection After Kidney Transplantation: A Meta-Analysis

Z. Wang^a, X. Liu^a, P. Lu^a, Z. Han^a, J. Tao^a, J. Wang^b, K. Liu^c, B. Wu^a, C. Yin^a, R. Tan^a, and M. Gu^{a,*}

^aDepartment of Urology, the First Affiliated Hospital of Nanjing Medical University, Nanjing, China; ^bDepartment of Urology, Nanjing Children's Hospital, Nanjing, China; and ^cDepartment of Urology, Huai'an First People's Hospital, Huai'an, China

Conclusions. Our analysis did not support the use of the ImmuKnow assay to predict or monitor the risks of infection and acute rejection in renal transplant recipients. Further studies are needed to confirm the relationships between the ImmuKnow assay and infection and acute rejection in kidney transplantation.

Treg markeri → FOXP3 (üriner mRNA düzeyleri)



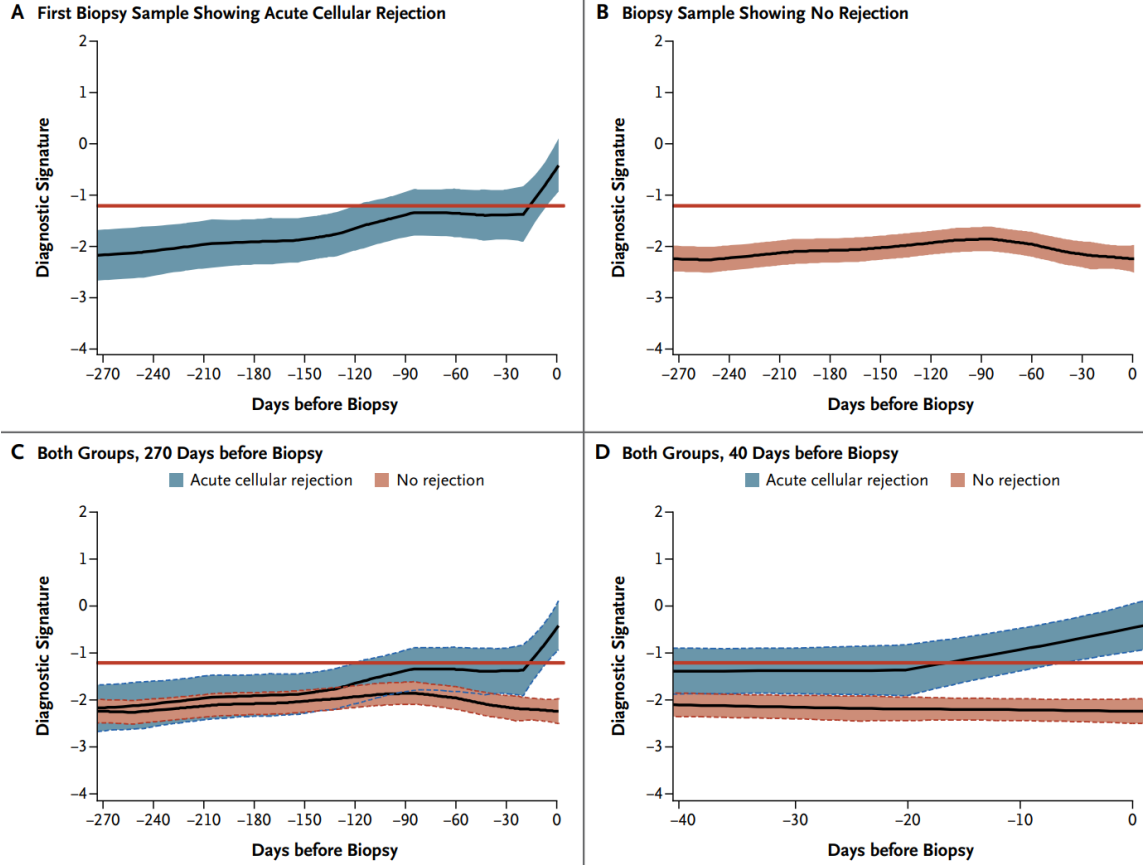
Tanısal

Tedavi yanıtını ön gördürücü

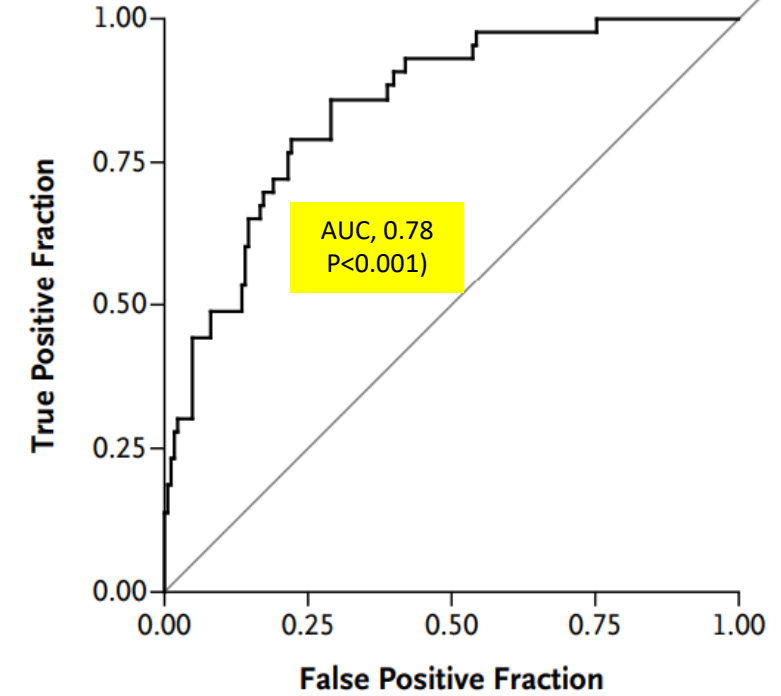
Prognostik

Urinary-Cell mRNA Profile and Acute Cellular Rejection in Kidney Allografts

- 485 hasta
4300 idrar örneği
3 gen imzası
- CD3ε mRNA
 - İnterferon-inducible protein 10
 - 18S rRNA



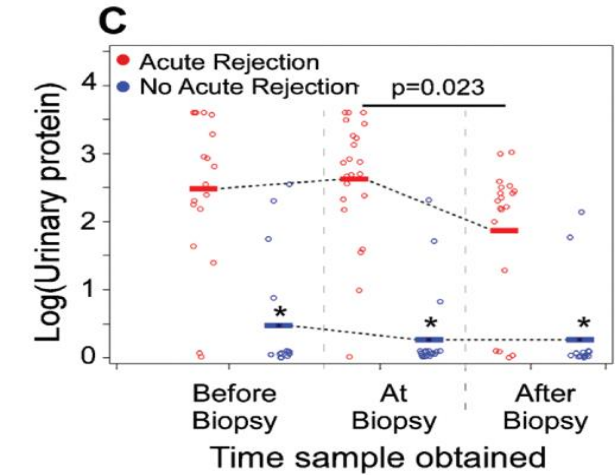
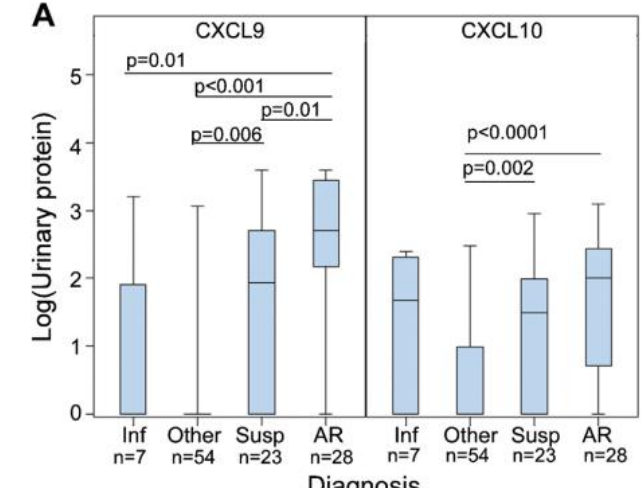
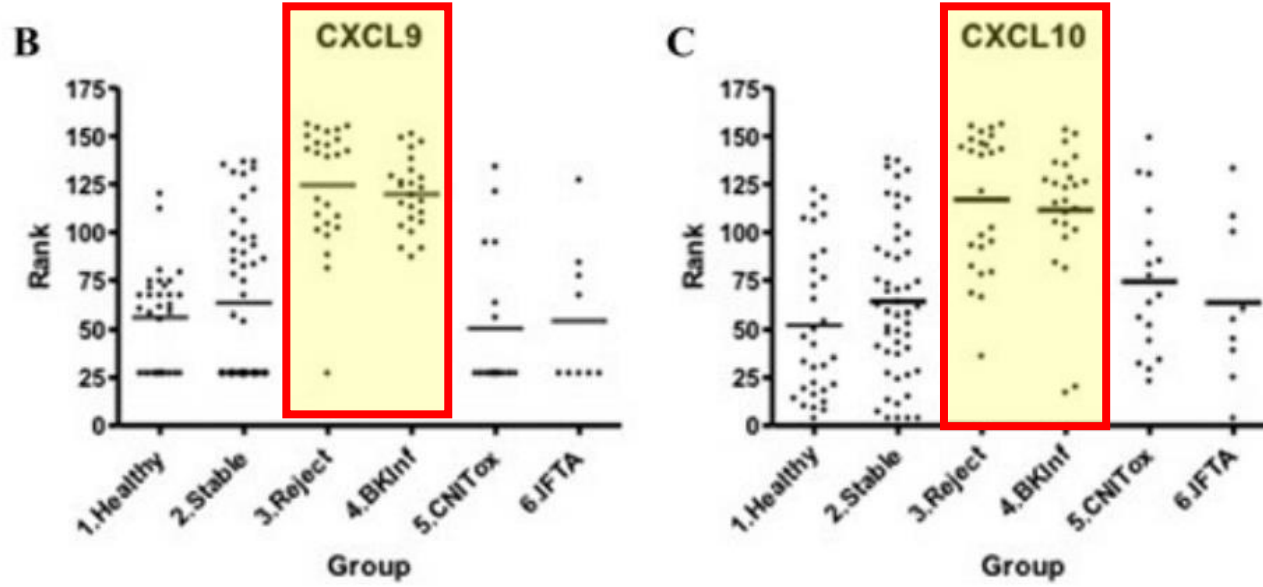
A Acute Cellular Rejection vs. No Rejection



Rejeksiyondan önce m-RNA düzeyleri yükseliyor

İdrar kemokinleri CXCL9-CXCL10

İlk çalışmalarda BK ile rejeksiyonda artıyor
Ancak ikisini birbirinden ayıramıyor



Randomized Trial to Assess the Clinical Utility of Renal Allograft Monitoring by Urine CXCL10 Chemokine

CXCL10 monitörizasyonu sonuçlarını değiştiriyor

METHODS

**Intervention arm
(n=120)**



Urine CXCL10
at month 1, 3, 6



If elevated



biopsy and
treatment of rejection



at 1-year



- death-censored graft loss
- clinical rejection second month to 1-year
- rejection in 1-year surveillance biopsy
- de novo DSA
- estimated GFR<25ml/min

**Control arm
(n=121)**



Results
concealed



OUTCOME

1 Intention-to-treat analysis (n=241)

Combined endpoint at 1-year 51%

Individual endpoints at 1-year

- death-censored graft loss
- clinical rejection second month to 1-year
- rejection in 1-year surveillance biopsy
- de novo DSA
- estimated GFR<25ml/min

Intervention
arm

Control
arm

49%

=

1%

2%

=

13%

14%

=

45%

38%

=

5%

3%

=

1%

3%

=

2 Per-protocol analysis (n=175)

Combined endpoint at 1-year 55%

Individual endpoints at 1-year

49%

=

=

Conclusion

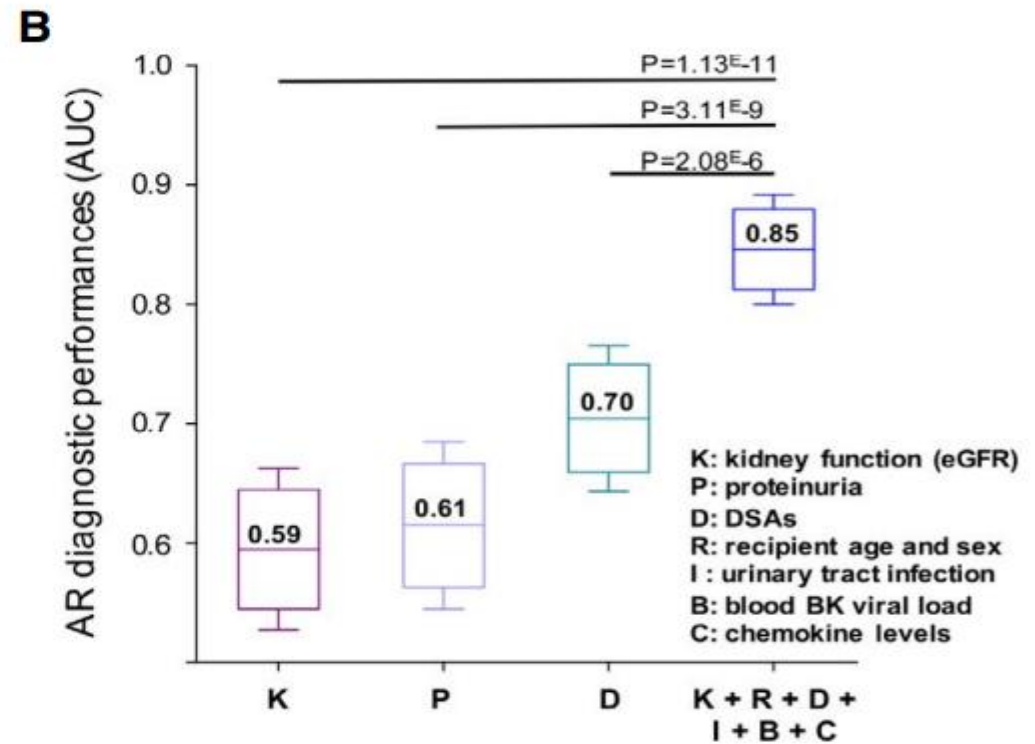
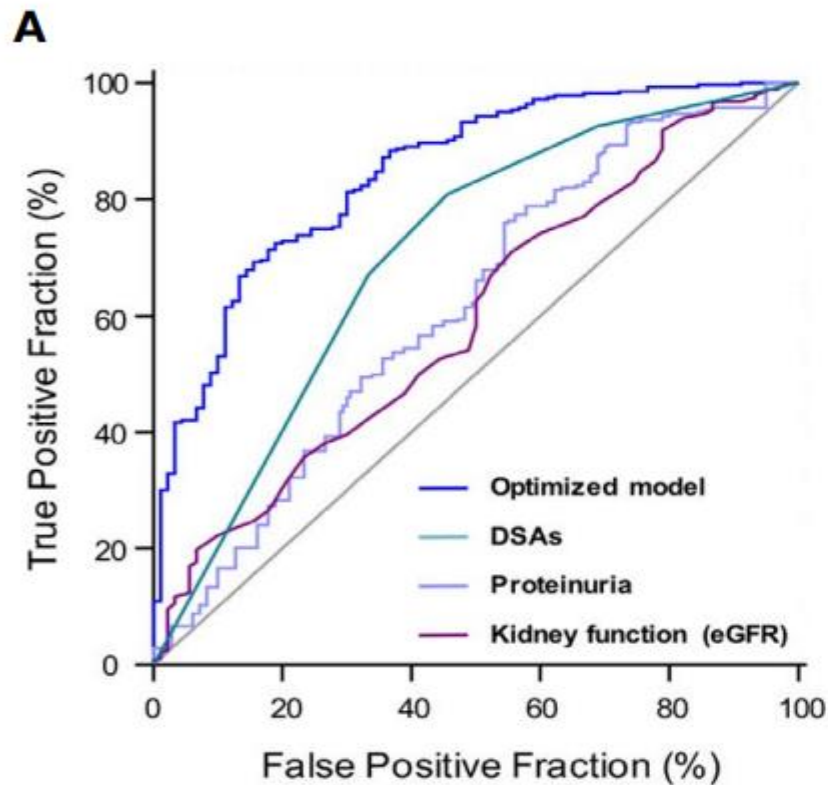
This study could not demonstrate a beneficial effect of urine CXCL10 monitoring on 1-year outcomes

J Am Soc Nephrol. 2023 Aug 1;34(8):1456-1469.

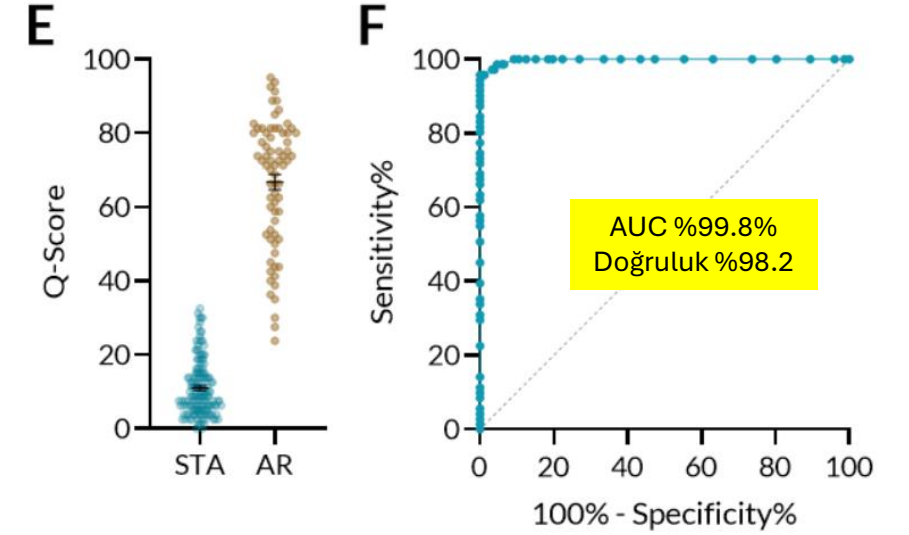
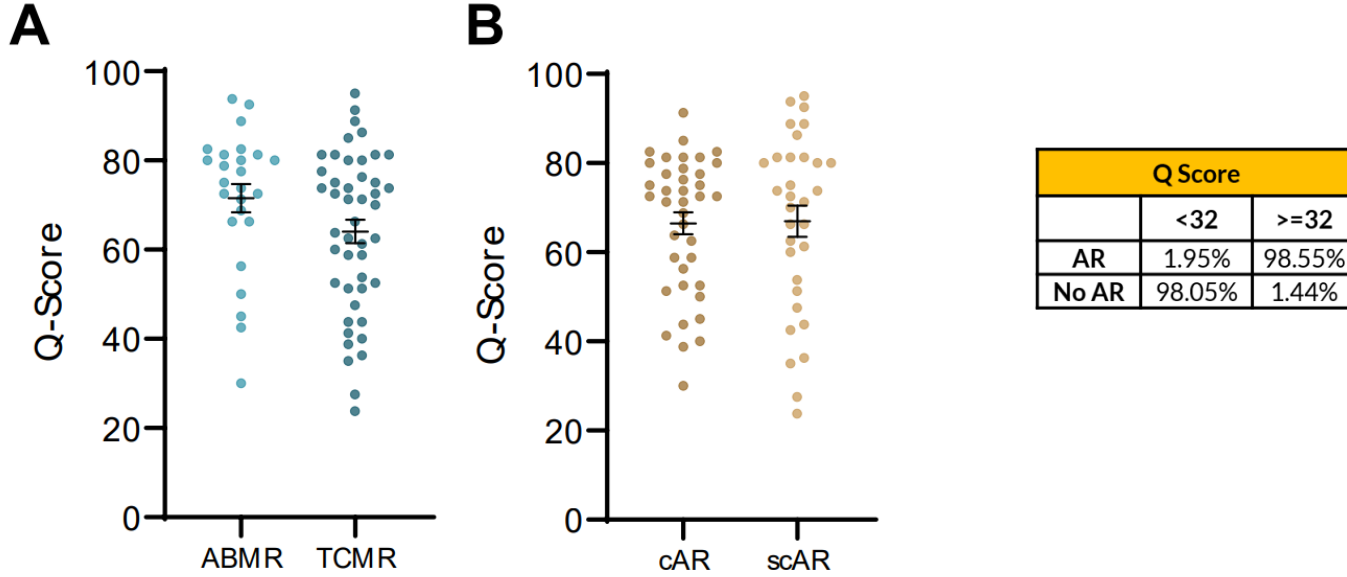
Development and validation of an optimized integrative model using urinary chemokines for noninvasive diagnosis of acute allograft rejection

Claire Tinel^{1,2,3,4}  | Arnaud Devresse^{1,5,6} | Agathe Vermorel¹ | Virginia Sauvaget² | David Marx⁷  | Véronique Avettand-Fenoel^{4,8} | Lucile Amrouche^{1,2,4} | Marc-Olivier Timsit^{4,9} | Renaud Snanoudj¹⁰  | Sophie Caillard⁷ | Bruno Moulin⁷ | Jérôme Ollagne⁷ | Marie Essig^{11,12} | Wilfried Gwinner¹³ | Maarten Naesens^{14,15} | Pierre Marquet¹² | Christophe Legendre^{1,2,3,4}  | Fabiola Terzi² | Marion Rabant^{2,4,16}  | Dany Anglicheau^{1,2,3,4} 

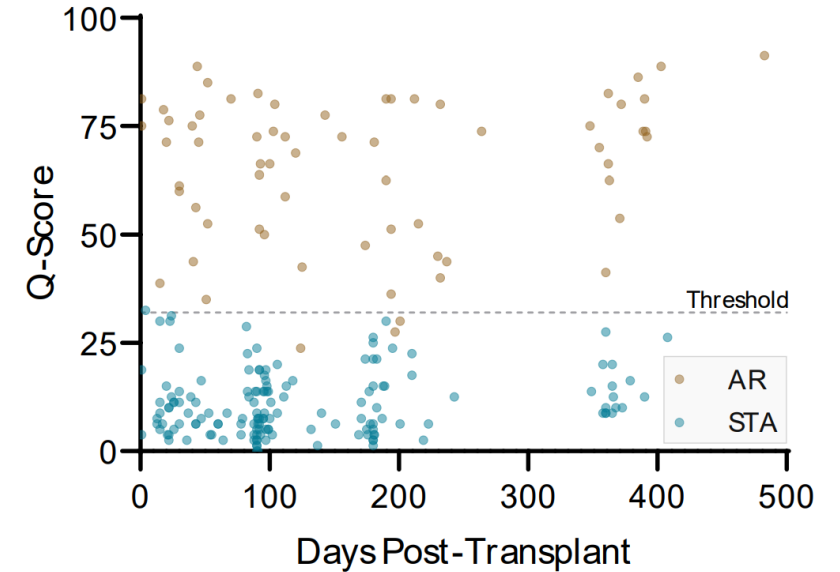
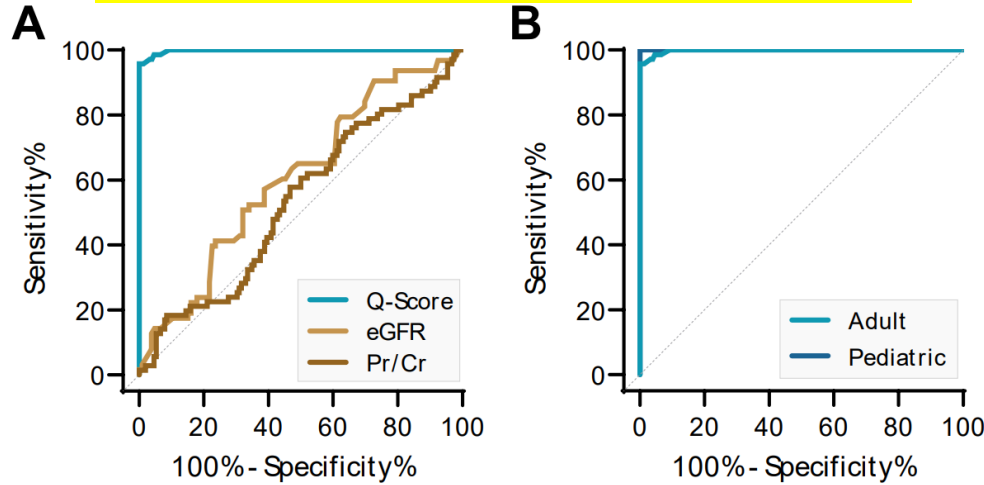
Kemokinler ile diğer değişkenlerin kombinasyonunun tanısal gücü daha yüksek



Qsant test: cell-free DNA, methylated-cell-free DNA, clusterin, CXCL10, kreatinin, proteinüri



Klinik/subklinik rejeksiyonları ayırt edebiliyor



Tüm yaş gruplarında konvansiyonel belirteçlerden daha üstün