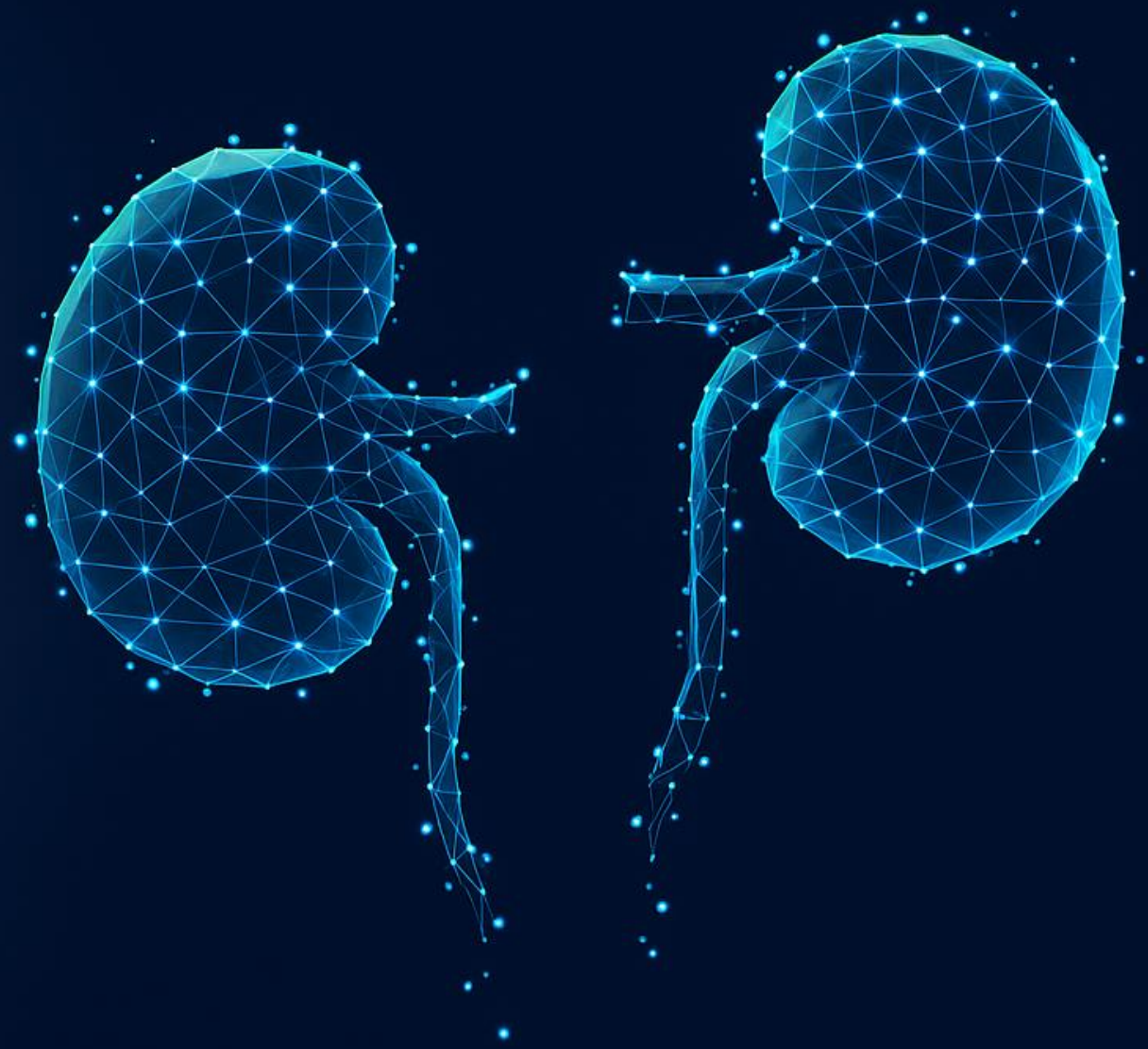
TAVI forum 14
Friday, April 17, 2026

TAVI Forum BK Project Update: Leuven/Roche



Maarten Naesens, MD, PhD

UZ/KU Leuven, Belgium

An observational cohort study of histological screening for BK polyomavirus nephropathy following viral replication in plasma

OPEN

Evert Cleenders[1,2], Priyanka Koshy[3], Elisabet Van Loon[1,4], Katrien Lagrou[5], Kurt Beuselinck[5,6], Graciela Andrei[7], Marta Crespo[8], Katrien De Vusser[1,4], Dirk Kuypers[1,4], Evelyne Lerut[3], Kris Mertens[1], Olga Mineeva-Sangwo[7], Parmjeet Randhawa[9], Aleksandar Senev[1,10], Robert Snoeck[7], Ben Sprangers[4,11], Claire Tinel[1], Amaryllis Van Craenenbroeck[1,4], Jan van den Brand[1], Marc Van Ranst[12], Geert Verbeke[2], Maarten Coemans[1,2] and Maarten Naesens[1,4]

[1]Department of Microbiology, Immunology and Transplantation, Nephrology and Renal Transplantation Research Group, KU Leuven, Leuven, Belgium; [2]Department of Public Health and Primary Care, Leuven Biostatistics and Statistical Bioinformatics Centre, KU Leuven, Leuven, Belgium; [3]Department of Imaging and Pathology, University Hospitals Leuven, Leuven, Belgium; [4]Department of Nephrology and Renal Transplantation, University Hospitals Leuven, Leuven, Belgium; [5]Department of Microbiology, Immunology and Transplantation, Laboratory of Clinical Microbiology, KU Leuven, Leuven, Belgium; [6]Department of Laboratory Medicine, University Hospitals Leuven, Leuven, Belgium; [7]Department of Microbiology, Immunology and Transplantation, Rega Institute, Laboratory of Virology and Chemotherapy, KU Leuven, Leuven, Belgium; [8]Department of Nephrology, Hospital del Mar Medical Research Institute (IMIM), Hospital del Mar, Barcelona, Spain; [9]Division of Transplantation Pathology, the Thomas E. Starzl Transplantation Institute, University of Pittsburgh Medical Center-Montefiore Hospital, University of Pittsburgh, Pittsburgh, Pennsylvania, USA; [10]Histocompatibility and Immunogenetics Laboratory, Belgian Red Cross-Flanders, Mechelen, Belgium; [11]Department of Microbiology, Immunology and Transplantation, Rega Institute, Laboratory of Molecular Immunology, KU Leuven, Leuven, Belgium; and [12]Department of Microbiology, Immunology and Transplantation, Rega Institute, Laboratory of Clinical and Epidemiological Virology, KU Leuven, Leuven, Belgium

An observational cohort study of kidney function evolution following increased BK viral replication

OPEN

Evert Cleenders[1,2], Maarten Coemans[1,2], Olga Mineeva-Sangwo[3], Priyanka Koshy[4], Dirk Kuypers[1,5], Geert Verbeke[2] and Maarten Naesens[1,5]

[1]Nephrology and Renal Transplantation Research Group, Department of Microbiology, Immunology and Transplantation, KU Leuven, Leuven, Belgium; [2]Leuven Biostatistics and Statistical Bioinformatics Centre, Department of Public Health and Primary Care, KU Leuven, Leuven, Belgium; [3]Laboratory of Virology and Chemotherapy, Department of Microbiology, Immunology and Transplantation, Rega Institute, KU Leuven, Leuven, Belgium; [4]Department of Imaging and Pathology, University Hospitals Leuven, Leuven, Belgium; and [5]Department of Nephrology and Renal Transplantation, University Hospitals Leuven, Leuven, Belgium

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An observational cohort study of histological screening for BK polyomavirus nephropathy following viral replication in plasma

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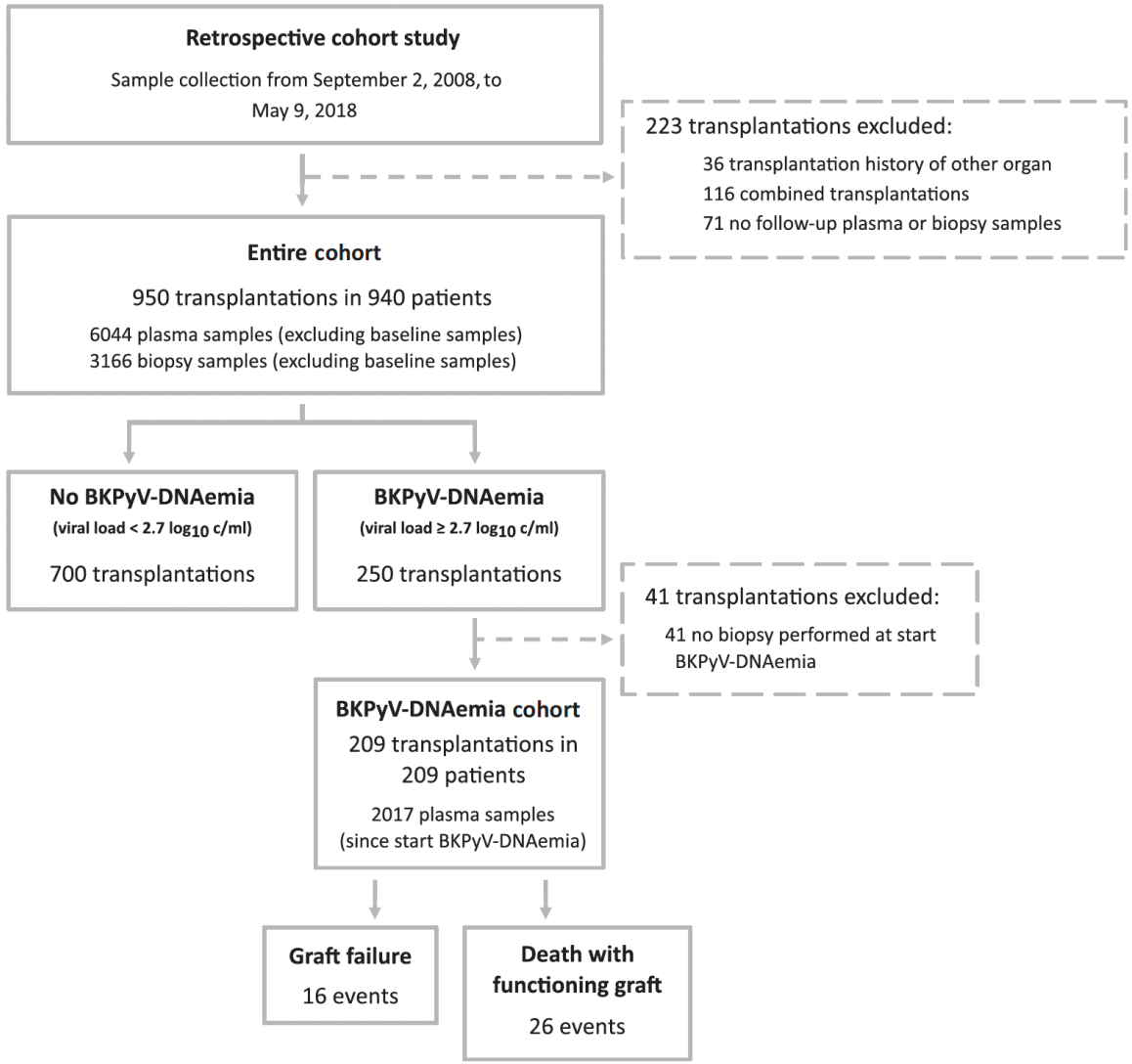
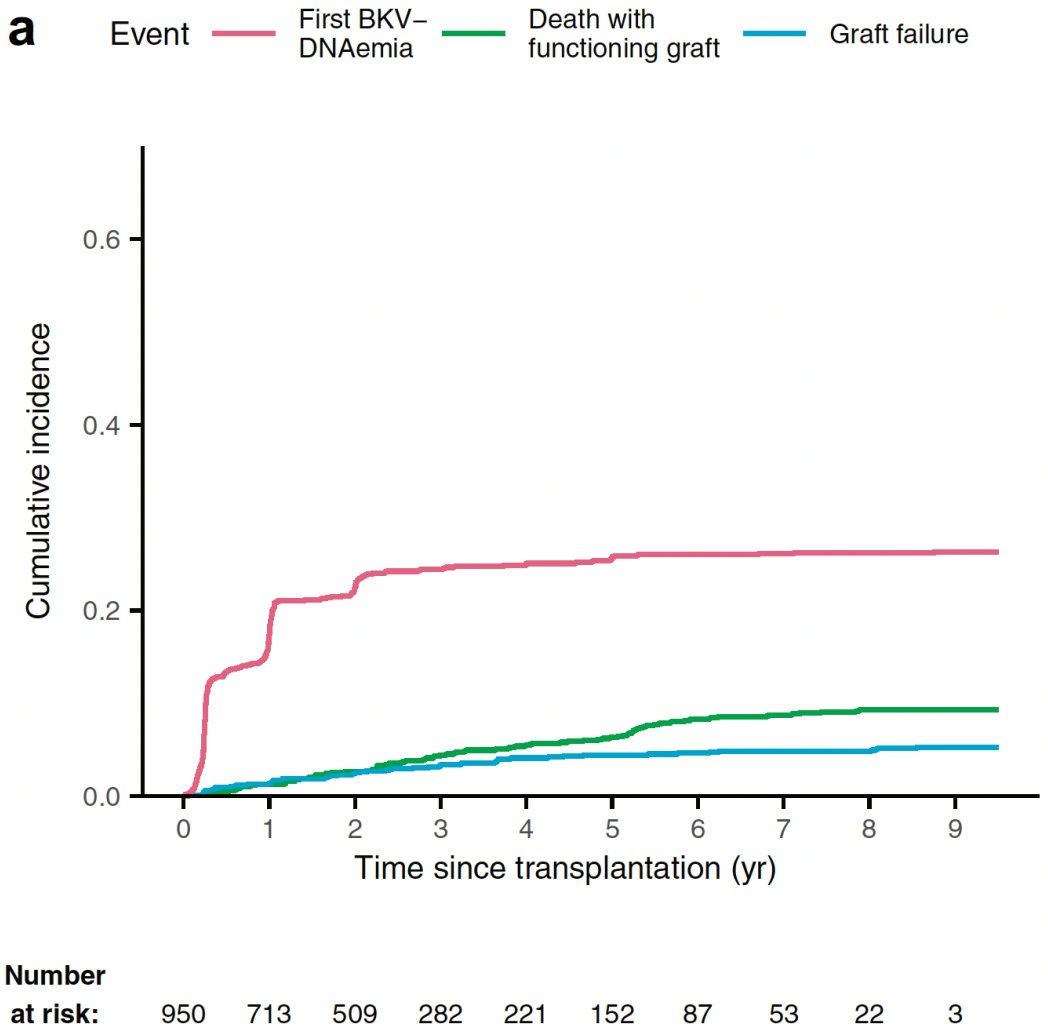
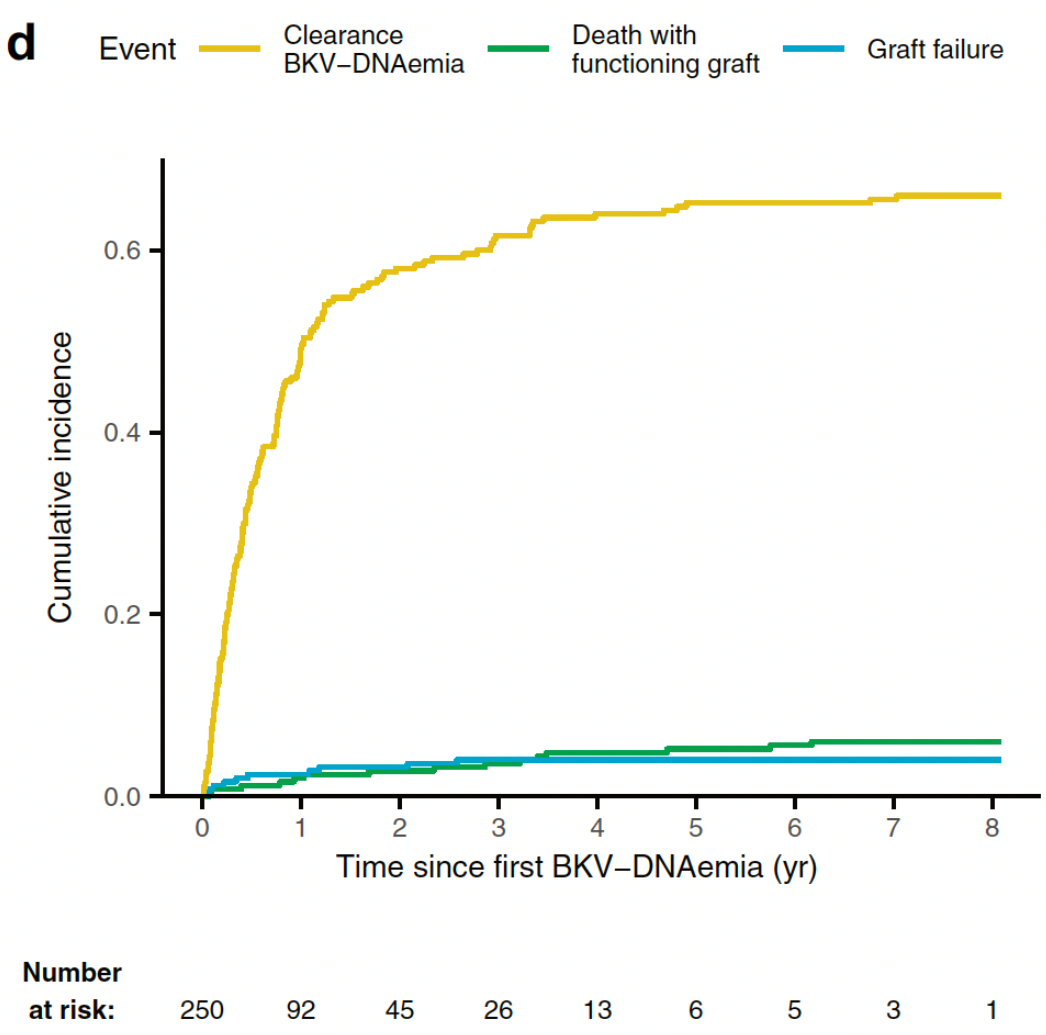


Evaluation of the occurrence and clearance of BKV





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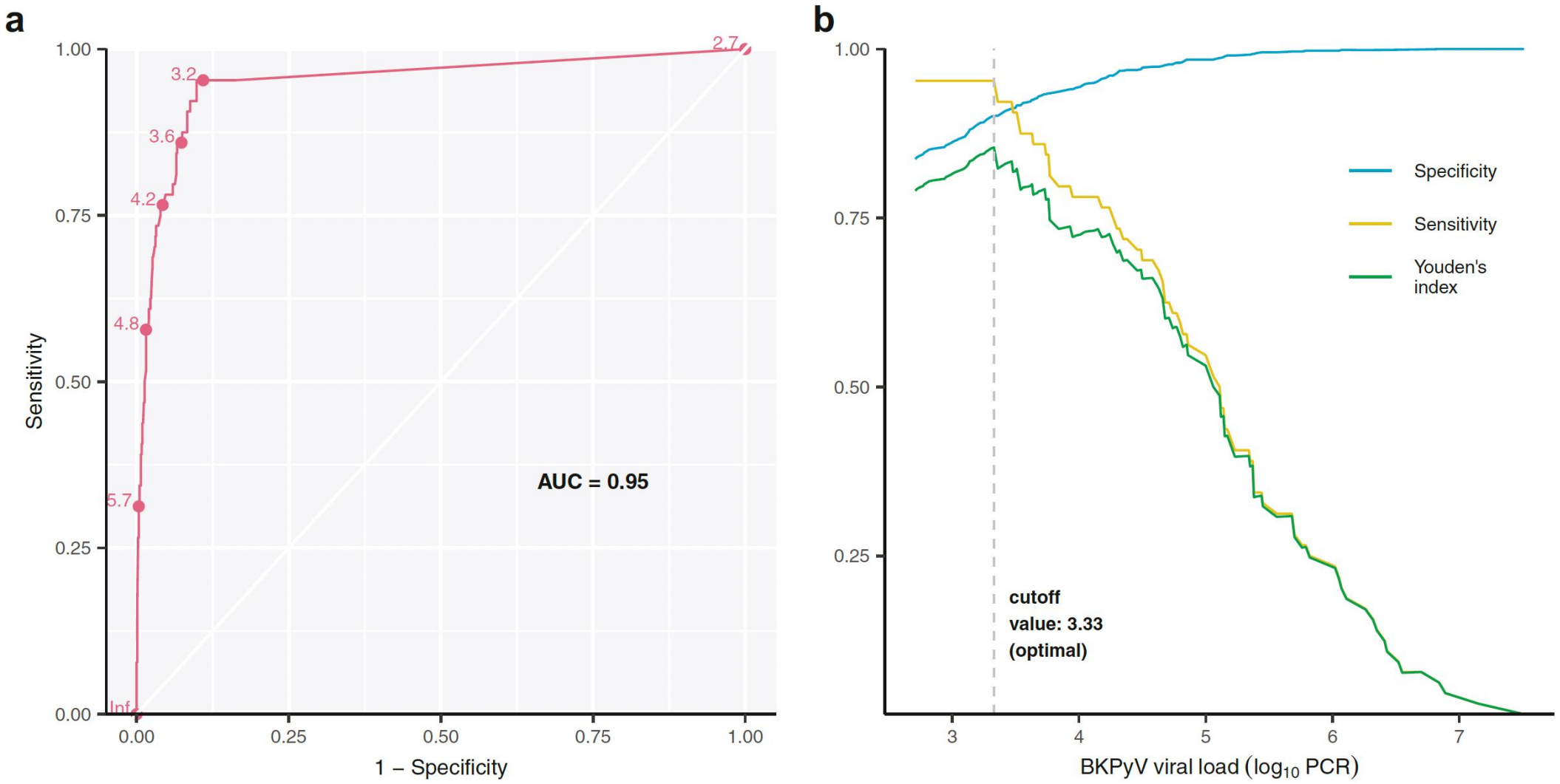
Diagnostic accuracy for BKPyV viral load for SV40 positivity (PyVAN)



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Diagnostic accuracy for BKPyV viral load for SV40 positivity (PyVAN)

Table 3 | Accuracy metrics for BKPyV viral load as a predictor for SV40 positivity

	BKPyV-DNAemia cutoff value (log_{10} copies/ml)	
	3.0	4.0
Diagnostic accuracy measure for SV40 positivity	(Cutoff for probable PyVAN)	(Cutoff for presumptive PyVAN)
Prevalence of SV40 positivity	0.071 (0.056–0.089)	0.079 (0.063–0.098)
Sensitivity	0.953 (0.871–0.984)	0.875 (0.779–0.933)
Specificity	0.863 (0.838–0.885)	0.938 (0.920–0.953)
Positive predictive value	0.347 (0.280–0.419)	0.548 (0.457–0.636)
Negative predictive value	0.996 (0.988–0.999)	0.989 (0.979–0.994)
Positive likelihood ratio	6.970 (5.832–8.331)	14.219 (10.774–18.764)
Negative likelihood ratio	0.054 (0.018–0.164)	0.133 (0.072–0.245)
ROC-AUC	0.950 (0.916–0.978)	0.949 (0.915–0.976)

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An in-house RT-PCR test was used for this study

An inhouse real-time polymerase chain reaction (PCR) technique, using primers that were able to detect different BKPyV genotypes. The sequences and concentrations of primers and probes, as described by Herman et al., were not changed over time. In 2015, the assay was converted to a fast real-time PCR in a total volume of 30 ml on the QuantStudio Dx thermocycler (Life Technologies) using the TaqMan Fast Virus 1-step Mastermix (Life technologies) and a fast PCR program consisting of 20 seconds at 95 C, followed by 45 cycles of 3 seconds at 95 C and 30 seconds at 60 C.

Pediatr Transplantation 2004: 8: 485–492
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Pediatric Transplantation

Polyomavirus infection in pediatric renal transplant recipients: Evaluation using a quantitative real-time PCR technique

Herman J, Van Ranst M, Snoeck R, Beuselinck K, Lerut E, Van Damme-Lombaerts R. Polyomavirus infection in pediatric renal transplant recipients: Evaluation using a quantitative real-time PCR technique.
Pediatr Transplantation 2004: 8: 485–492. © 2004 Blackwell Munksgaard

Abstract: Polyomavirus infection and related nephropathy is being increasingly recognized as an important cause of allograft dysfunction in adult renal transplant recipients. We prospectively monitored pediatric renal transplant recipients for the presence of BK and JC polyomavirus in urine and blood using a quantitative PCR assay to evaluate the prevalence and clinical relevance of polyomavirus infection in the pediatric renal transplant population. Of 46 pediatric renal recipients

Jean Herman[1], Marc Van Ranst[2,3], Robert Snoeck[3], Kurt Beuselinck[2], Evelyne Lerut[4] and Rita Van Damme-Lombaerts[1]

Departments of [1]Pediatric Transplantation, [2]Laboratory Medicine, University Hospital Gasthuisberg, University of Leuven, [3]Laboratory of Virology, Rega Institute for Medical Research, University of Leuven, Leuven, [4]Department of Pathology, University Hospital Gasthuisberg, University of Leuven, Leuven, Belgium

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Collaboration Leuven-Roche (TAVI)

- 348 plasma samples from kidney transplant patients at University Hospitals Leuven.
- Partial overlap with the *BKPyV-DNAemia cohort* from Cleenders et al.
- Roche PCR: lower quantitation limit is 21.5 IU/ml.
- In-house PCR: lower quantitation limit is 500 copies/ml.
- SV40 antigen immunohistochemistry available for some samples.
- Polyomavirus viral loads measured via whole genome cell-free DNA sequencing for another subset. Strain-specific viral loads include BK, JC, MW, LI, Merkel cell, human polyomavirus 6, and trichodysplasia spinulosa-associated polyomavirus.

NB. In-house PCR detects all polyomavirus strains; Roche PCR only BK polyomavirus.

Statistical analysis

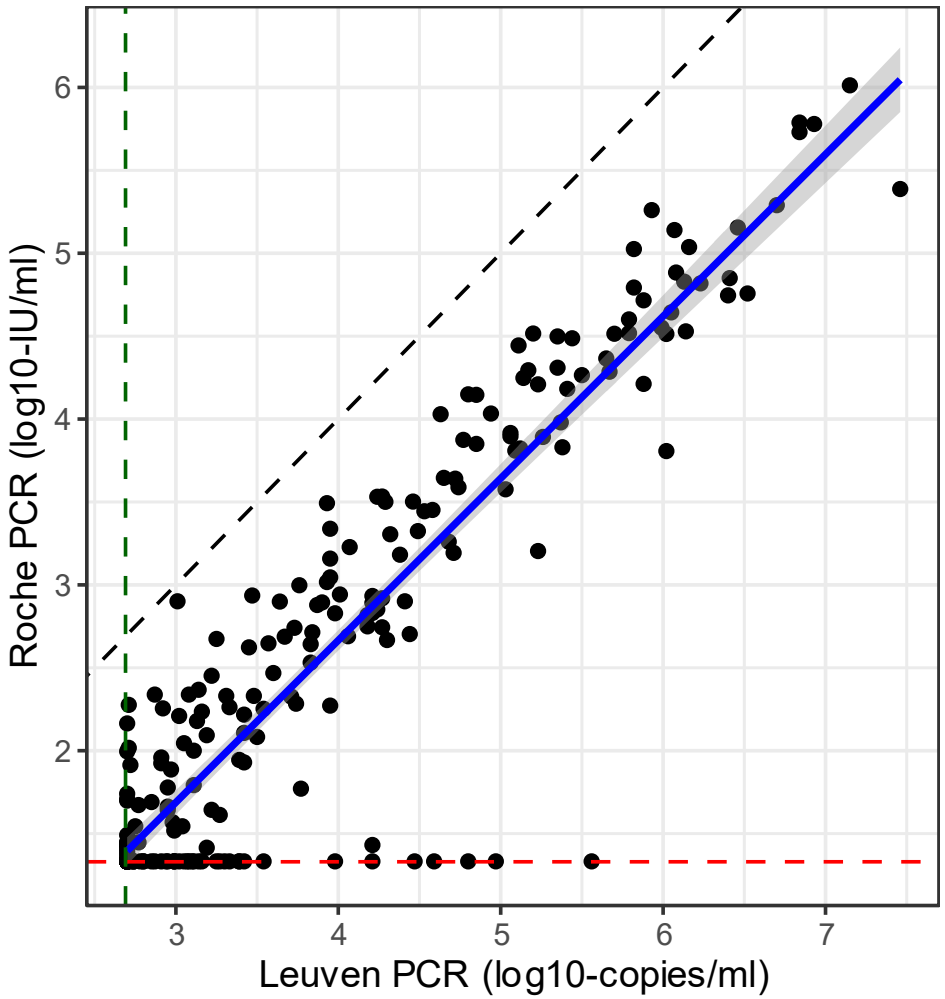
- PCR values below quantitation limit set to the limit.
- Bland-Altman plot and Pearson correlation used to compare assays after conversion.
- Associations with SV40 positivity and cell-free DNA viral load analyzed using AIC and F-tests.
- SV40 discrimination assessed by AUC.
- Linear model estimates link between non-BK polyomavirus proportion and PCR discrepancies.

Demographics

Variable	N = 348
Roche PCR in IU/ml, median (IQR)	102 (2608.5)
Roche PCR in log10-IU/ml, median (IQR)	2.009 (2.085)
Below limit of quantitation, no. (%)	91 (26.1)
Missing values, no. (%)	94 (27.0)
Leuven PCR in copies/ml, median (IQR)	4039 (54157)
Leuven PCR in log10-copies/ml, median (IQR)	3.606 (1.905)
Leuven PCR in IU/ml, median (IQR)	201.95 (2707.85)
Leuven PCR in log10-IU/ml, median (IQR)	2.305 (1.905)
Below limit of quantitation, no. (%)	66 (19.0)
Missing values, no. (%)	0 (0.0)
SV40 positivity, no. (%)	112 (32.2)
Missing values, no. (%)	43 (12.4)
Polyomavirus cell-free DNA in standardized tpm, median (IQR)	68326.2 (410938.5)
Polyomavirus cell-free DNA in log10-transformed standardized tpm, median (IQR)	4.835 (1.984)
Missing values, no. (%)	297 (85.3)

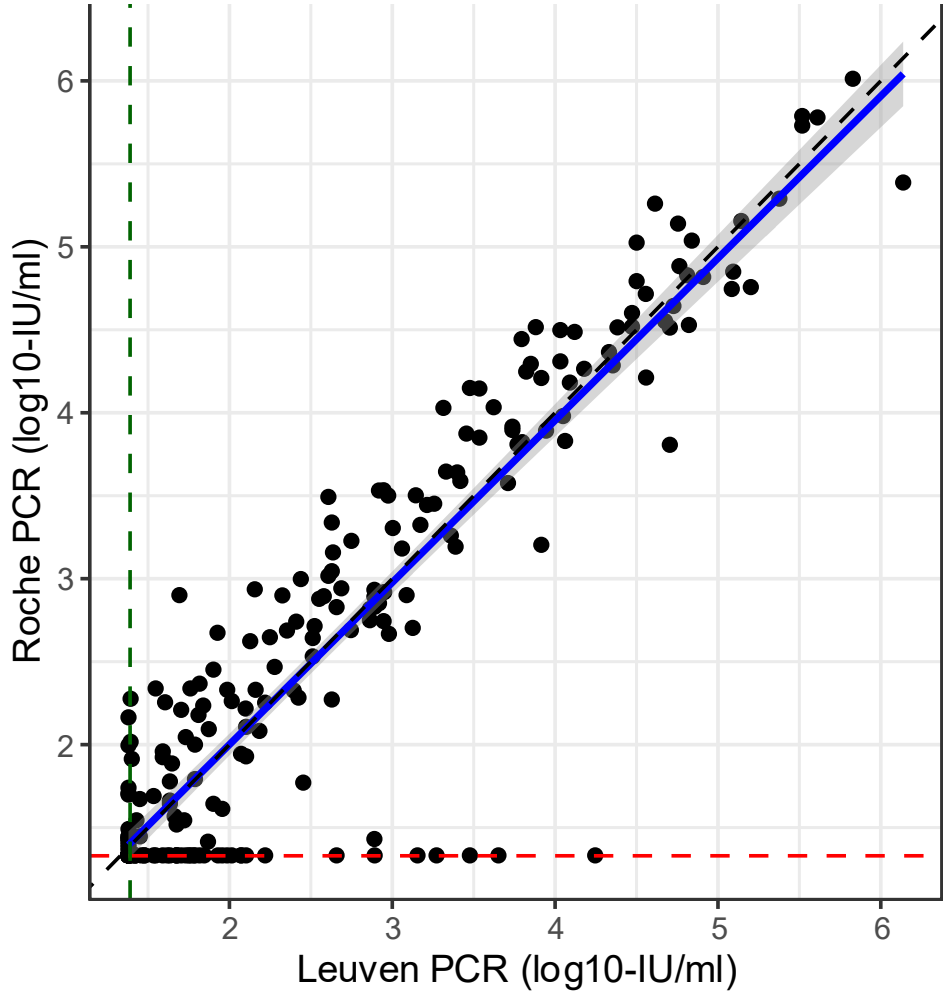
Correlation Leuven – Roche

Original Leuven results (copies/mL)

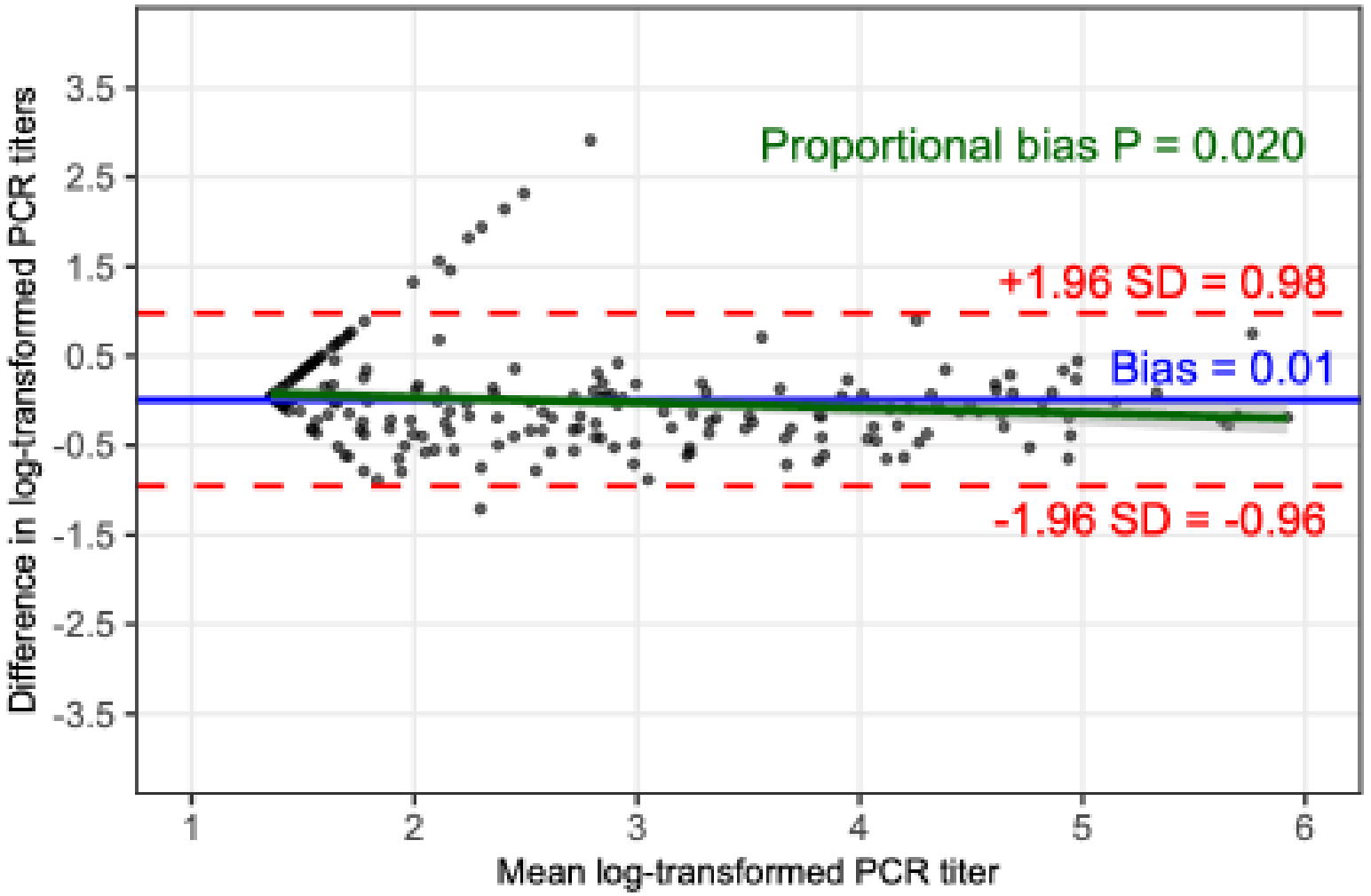


Reference lines
1:1 line
Leuven threshold
Linear fit
Roche threshold

Transformation (IU/mL) (*0.049)



Bland-Altman Leuven – Roche



Accuracy metrics for SV40 positivity

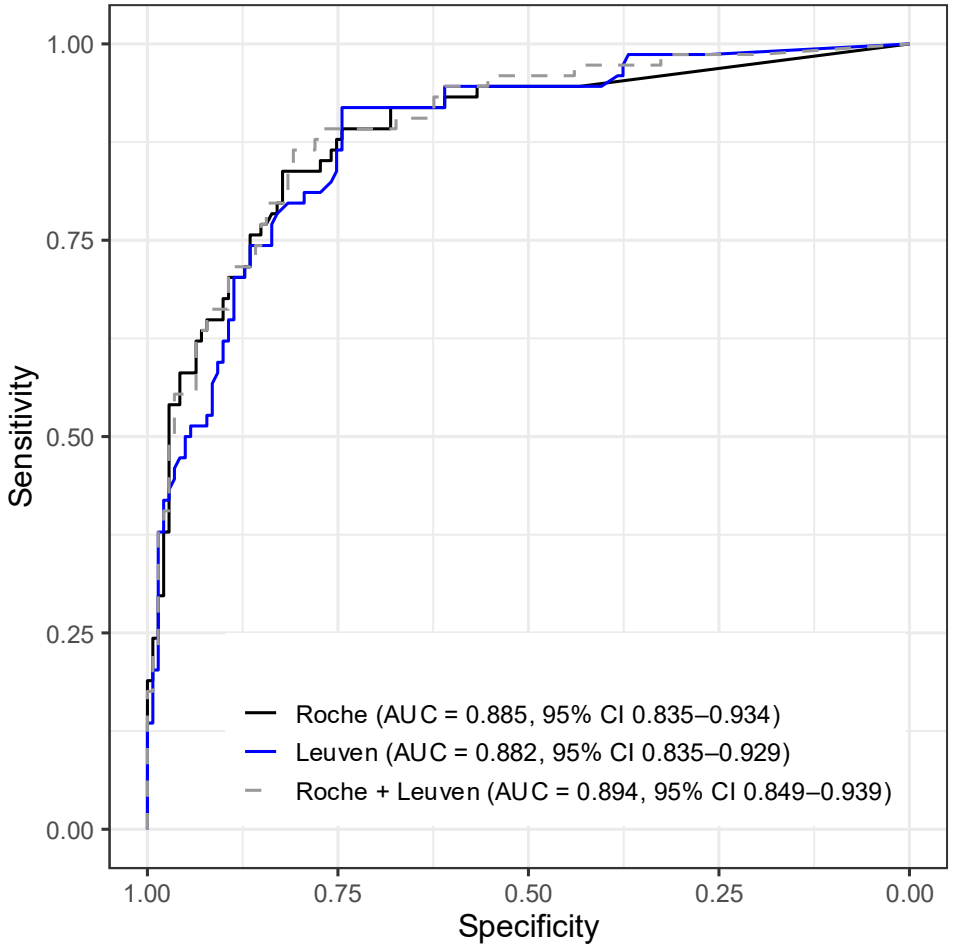
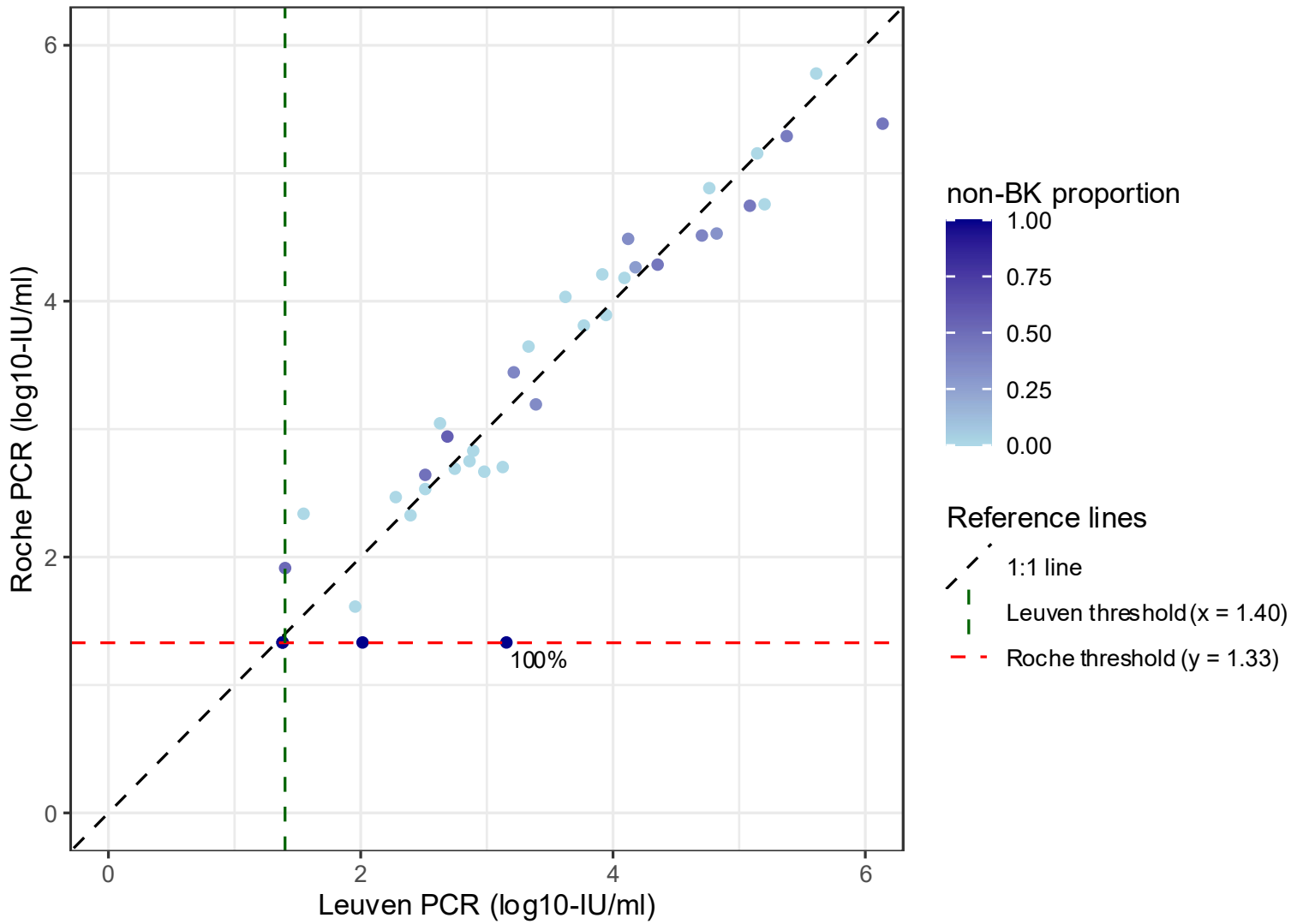


Table 2. Evaluation metrics for logistic regression models for SV40 positivity, comparing Leuven PCR and Roche PCR as predictors.

Model	AIC (lower is better)	AUC (95% CI)
Roche PCR	171.52	0.885 (0.835-0.934)
Leuven PCR	178.25	0.882 (0.835-0.929)
Combination of both	171.32	0.894 (0.849-0.939)

Abbreviations: AIC, Akaike Information Criterion; AUC, area under the receiver-operating characteristic curve; PCR, polymerase chain reaction.

Discrepancies and non-BK polyomavirus strains



Conclusion

- A scale transformation is required to compare Leuven in-house PCR values with Roche PCR values.
- Multiplying by 0.049 or subtracting 1.31 from log10-copies/ml achieves the conversion to IU/ml.
- The Leuven in-house assay strongly agrees with the Roche industry standard.
- Both assays have highly correlated log-transformed titers and similar predictive performance.
- Discrepancies are due to broader polyomavirus strain sensitivity in the in-house assay compared to the BK-specific Roche assay.

Thank you!

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maarten.naesens@kuleuven.be