

Corrigendum to “Defining Relationships Among Tests for Kidney Transplant Antibody-Mediated Rejection” [Kidney International Reports Volume 10, Issue 9, September 2025, Pages 3225-3238]



Kidney Int Rep (2026) **11**, 106407; <https://doi.org/10.1016/j.ekir.2026.106407> © 2026 International Society of Nephrology. Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Katelynn S. Madill-Thomsen¹, Luis G. Hidalgo², Zachary P. Demko³, Philippe M. Gauthier³, Adam Prewett³, Dave Lowe⁴, Jessica J. Chang¹, Martina Mackova¹, Klemens Budde⁵, Jonathan S. Bromberg⁶ and Philip F. Halloran^{1,7}; on behalf of the Trifecta-Kidney Study Group⁸

¹Alberta Transplant Applied Genomics Centre, University of Alberta, Edmonton, Alberta, Canada; ²Department of Surgery, University of Wisconsin, Madison School of Medicine and Public Health, Wisconsin, USA; ³Natera, Inc., San Carlos, California, USA; ⁴One Lambda Inc., West Hills, California, USA; ⁵Department of Nephrology, Charite-Medical University of Berlin, Berlin, Germany; ⁶Division of Transplantation, Department of Surgery, University of Maryland School of Medicine, Baltimore, Maryland, USA; and ⁷Division of Nephrology and Immunology, Department of Medicine, University of Alberta, Edmonton, Alberta, Canada

The authors regret that there were errors in Table 8 of the published article.

In the column Test type, Likelihood ratio test, upper box in the Description for Model 1 (MMDx) + model 2 (Histology) vs. model 1 alone, *P*-value, in the column In *n* = 5086 dataset (INTERCOMEX), the text should have read, “*P* = 0.047 (combined model adds value to model 1 [MMDx] alone, borderline significance).”

In the column Test type, Likelihood ratio test, bottom box in the Description should have read, “Model 1 (MMDx) + model 2 (histology) vs. model 2 alone, *P*-value.”

The corrected Table 8 is shown below.

Table 8. Comparing MMDx-based and histology-based models predicting 3-year post-biopsy graft survival using Akaike’s Information Criterion (AIC)

Test type	Description	In <i>n</i> = 717 (Trifecta-Kidney)	In <i>n</i> = 5086 dataset (INTERCOMEX)
AIC	Model 1 (MMDx)	AIC = 270.855	AIC = 2508.164
	Model 2 (histology)	AIC = 278.775	AIC = 2523.782
	ΔAIC	7.920	15.618
	Direction of difference	Model 1 (MMDx) is better	Model 1 (MMDx) is better
Likelihood ratio test	Model 1 (MMDx) + model 2 (Histology) vs. model 1 alone, <i>P</i> -value	<i>P</i> = 0.67 (combined model does not add to model 1 [MMDx] alone)	<i>P</i> = 0.047 (combined model adds value to model 1 [MMDx] alone, borderline significance)
	Model 1 (MMDx) + model 2 (histology) vs. model 2 alone, <i>P</i> -value	<i>P</i> = 0.049 (combined model adds value to model 2 [histology] alone, borderline significance)	<i>P</i> = 6.1E-5 (combined model adds significantly to model 2 [histology] alone)

AIC, Akaike Information Criterion; MMDx, Molecular Microscope Diagnostic System.

DOI of original article: <https://doi.org/10.1016/j.ekir.2025.06.017>

Correspondence: Philip F. Halloran, Alberta Transplant Applied Genomics Centre, #250 Heritage Medical Research Centre, University of Alberta, Edmonton, Alberta T6G 2S2, Canada. E-mail: phallora@ualberta.ca

⁸Members of the Trifecta-Kidney Study Group are listed in the Appendix of the original article.