Table S1. Participating Centers		
Center	**Location**	**Principal investigators**
University of Alabama Birmingham	**Birmingham, AL, USA**	Roslyn Mannon
Val d'Hebron University Hospital	**Barcelona, Spain**	Daniel Serón and Joana Sellarés
Montefiore Medical Center	**Bronx, NY, USA**	Enver Akalin
Manchester Royal Infirmary	**Manchester, UK**	Declan de Freitas and Michael Picton
University of Maryland	**Baltimore, MD, USA**	Jonathan Bromberg and Matt Weir
Charite-Medical University of Berlin	**Berlin, Germany**	Klemens Budde and Timm Heinbokel
Medical University of Hannover	**Hannover, Germany**	Gunilla Einecke
PinnacleHealth Transplant Associates	**Harrisburg, PA, USA**	Harold Yang and Seth Narins
University of Michigan	**Detroit, MI, USA**	Milagros Samaniego-Picota
Pomeranian Medical University	**Szczecin, Poland**	Marek Myslak
Warsaw Medical University	**Warsaw, Poland**	Agnieszka Perkowska-Ptasinska
Methodist Transplant and Specialty Hospital	**San Antonio, TX, USA**	Adam Bingaman
Washington University at St. Louis	**St Louis, MO, USA**	Daniel Brennan and Andrew Malone
Hennepin County Medical Center	**Minneapolis, MN, USA**	Bertram Kasiske
University of Alberta	**Edmonton, AB, CA**	Philip F Halloran
University of Minnesota	**Minneapolis, MN, USA**	Arthur Matas
University of Wisconsin	**Madison, WI, USA**	Arjang Djamali
Medical University of Vienna	**Vienna, Austria**	Georg Böhmig and Farsad Eskandary
Virginia Commonwealth University	**Richmond, VA, USA**	Gaurav Gupta

Table S2. Regression equations[a] for TCMR and AMR models 1 and 2	
Model	**Equation**
TCMR Model 1	-5.39 - 0.40*g - 0.10*ptc - 0.46*cg + 0.62*v + 0.82*i + 0.93*t + 0.22*(DSA[b]) + 0.02*(PRA) + 0.26*(C4d) + 0.91* logTxBx - 0.26*max(logTxBx-1.45,0)^3 + 0.64*max(logTxBx-2.75,0)^3 - 0.38*max(logTxBx-3.65,0)^3
TCMR Model 2 (No C4d/DSA/PRA)	-5.35 - 0.37*g - 0.05*ptc - 0.45*cg + 0.64*v + 0.80*i + 0.92*t + 0.92* logTxBx - 0.25*max(logTxBx -1.45,0)^3 + 0.62*max(logTxBx-2.75,0)^3 - 0.37*max(logTxBx-3.65,0)^3
AMR Model 1	-3.97 + 0.76*g + 0.66*ptc + 0.51*cg + 0.56*v + 0.41*i - 0.22*t + 0.47*(DSA) + 0.35*(PRA) + 0.57*(C4d) + 0.68* logTxBx - 0.09*max(logTxBx-1.45,0)^3 + 0.21*max(logTxBx-2.75,0)^3 - 0.13*max(logTxBx-3.65,0)^3
AMR Model 2 (No C4d/DSA/PRA)	-3.64 + 0.79*g + 0.78*ptc + 0.54*cg + 0.60*v + 0.32*i - 0.21*t + 0.71* logTxBx - 0.08*max(logTxBx-1.45,0)^3 + 0.20*max(logTxBx-2.75,0)^3 - 0.13*max(logTxBx-3.65,0)^3

[a] TxBx, entered as log10(days), is modeled as a spline, and has non-linear effects on the probabilities. Its evaluation depends on its location relative to the three knots in the model (1.45, 2.75, and 3.65). These equations generate linear scores, e.g. the TCMR Model 1 score for a sample with 0 for all inputs other than a TxBx of 100 days (=2 in log10 units) is: z = -5.39 + 0.91*2 - 0.26*(0.55) +0 +0 = ~ -3.71.

Probability = $1/(1+e^{-z})$: e is the base of the natural logarithms (=~ 2.71828): ~1/41.85 =~ 0.02.

[b] DSA, PRA, and C4d =1 if positive and 0 if negative

Abbreviations: TCMR, T cell-mediated rejection; AMR, antibody-mediated rejection; TxBx, time of biopsy post-transplant, DSA - Donor-specific HLA antibody, PRA - all HLA antibody ("panel reactive antibody"), C4d - Complement factor d.

Table S3. Relationship between diagnoses assigned by Model 1 regression equations using the default cutoff and the Banff histologic diagnoses assigned by the local center (N=1679)

		Regression diagnoses				
		AMR	**Mixed**	**No rejection**	**TCMR**	**Total**
Histology groups	**AMR**	**274**	4	55	0	333
	Mixed	38	**10**	5	3	56
	No rejection	47	3	**834**	3	887
	pAMR	42	0	42	0	84
	pTCMR (Borderline)	9	0	109	10	128
	TCMR	13	15	44	**67**	139
	BK	0	1	39	12	52
	Total	423	33	1128	95	1679

Bolding denotes concordance between Banff histology diagnoses and regression diagnoses.
Abbreviations: AMR, antibody-mediated rejection; pAMR, possible AMR; pTCMR, possible TCMR; TCMR, T cell-mediated rejection

Table S4. Mean histology lesion and molecular scores, categorized by regression categories (Model 2), within histology no rejection (BK biopsies included as no rejection) (N=939)					
		No rejection-regression (N=865)	**TCMR-regression (N=15)**	**Mixed-regression (N=4)**	**AMR-regression (N=55)**
Histology lesion scores, plus DSA and C4d					
TCMR-related	t (tubulitis)	0.15	2.79[c]	2.75[c]	0.23
	i (interstitial infiltrate)	0.25	2.43[c]	3.0[c]	0.73[c]
All rejection-related	v (vasculitis)	0.00	0.07[c]	0.33[c]	0.04[b]
AMR-related	g (glomerulitis)	0.11	0.00	0.50	1.51[c]
	ptc (capillaritis)	0.08	0.07	3.00[c]	1.04[c]
	cg (double contours)	0.05	0.00	0.00	1.02[c]
Atrophy-fibrosis-related	ci (scarring)	1.08	1.86[a]	1.67	1.51[b]
	ct (atrophy)	1.02	1.86[b]	1.67	1.27
DSA-related	DSA positivity	0.34	0.08	0.00	0.32
C4d-related	C4d positivity	0.06	0.08	0.33[a]	0.14[a]
Transcript set and molecular classifier scores					
TCMR-related classifiers	TCMR classifier ($TCMR_{Prob}$)	0.04	0.22[c]	0.33[c]	0.04[a]
All-rejection-related	Rejection classifier (Rej_{Prob})	0.16	0.41[c]	0.59[b]	0.45[c]
	IFNG-inducible (GRIT3)	0.41	1.08[c]	1.26[b]	0.65[c]
AMR-related	DSA-selective (DSAST)	0.10	0.04	0.12	0.39[c]
	NK cell burden (NKB)	0.42	0.61[b]	0.84[a]	0.87[c]
	AMR classifier ($ABMR_{Prob}$)	0.10	0.07	0.07	0.32[c]

Wilcoxon test compared with the No rejection group:

[a] *P* value <0.05

[b] *P* value <0.01

[c] *P* value <0.001

* AMR is used throughout this manuscript per journal style, however the official classifier name is provided in this table.

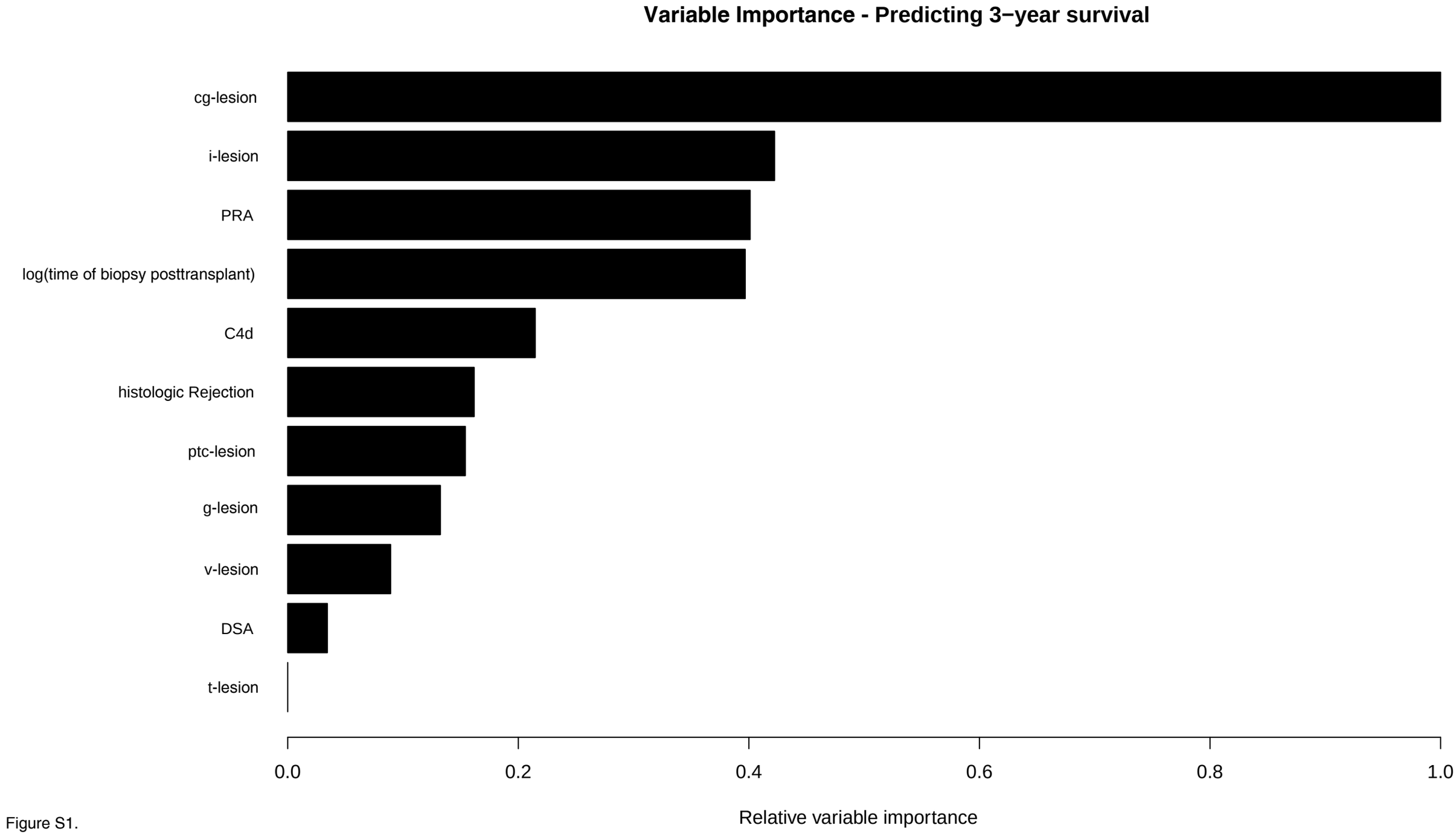
Variable Importance - Predicting 3−year survival
cg-lesion
i-lesion
PRA
log(time of biopsy posttransplant)
C4d
histologic Rejection
ptc-lesion
g-lesion
v-lesion
DSA
t-lesion
0.0
0.2
0.4
0.6
0.8
1.0
Relative variable importance

Figure S1.