Supplementary Table 1: ABMR Treatment

	All patients (n= 205)		Pre-existing DSA (n= 103)		*De novo* DSA (n= 102)		P
	n		n		n		
Treatment after biopsy							
Steroids, No. (%)	205	120 (58.54)	103	81 (78.64)	102	39 (38.24)	**<0.0001**
Plamaspheresis, No. (%)	205	91 (44.39)	103	63 (61.17)	102	28 (26.92)	**<0.0001**
Anti-CD20 therapy, No. (%)	205	90 (43.90)	103	49 (47.57)	102	41 (40.20)	**0.178**
Immunoglobin IV, No. (%)	205	109 (53.17)	103	56 (54.37)	102	53 (51.96)	**0.419**
Baseline Immunosuppression at the time of ABMR	205		103		102		
Tacrolimus, No. (%)		151 (73.66)		90 (87.38)		61 (59.80)	**<0.0001**
Cyclosporine, No. (%)		45 (21.95)		9 (8.74)		36 (35.29)	**<0.0001**

Supplementary Table 2: Top 30 pre-existing DSA ABMR related transcripts with their corresponding fold change and p value (t-test) and the fold change and p value in the *de novo* DSA group

Probe Set ID	Name	GENE	Adjusted P.Value in the pre-existing DSA group	Fold change in the pre-existing DSA group	Adjusted P.Value in the *de novo* DSA group	Fold change in the *de novo* DSA group
11744128_x_at	Chemokine (C-X-C motif) ligand 2	**CXCL2**	1.31e-29	7.62	.0005019	1.92
11719218_at	Suppressor of cytokine signaling 3	**SOCS3**	3.54e-30	7.47	.0008198	1.87
11718982_s_at	Chemokine (C-C motif) ligand 4	**CCL4**	7.85e-20	6.45	2.54e-15	5.22
11732467_x_at	Chemokine (C-X-C motif) ligand 11	**CXCL11**	5.00e-14	6.13	7.05e-12	5.64
11749245_a_at	Chemokine (C-X-C motif) ligand 11	**CXCL11**	2.15e-13	5.96	1.48e-11	5.56
11718983_x_at	Chemokine (C-C motif) ligand 4	**CCL4**	1.29e-21	5.70	2.39e-16	4.60
11717345_a_at	FBJ murine osteosarcoma viral oncogene homolog B	**FOSB**	1.06e-36	5.32	.0021794	1.51
11732466_a_at	Chemokine (C-X-C motif) ligand 11	**CXCL11**	4.27e-12	5.28	1.12e-11	5.54
11723679_s_at	CD69 molecule	**CD69**	1.66e-17	4.99	8.31e-08	2.89
11746954_s_at	Chemokine (C-C motif) ligand 4	**CCL4**	1.02e-22	4.81	2.15e-16	3.79
11719943_at	Chemokine (C-X-C motif) ligand 9	**CXCL9**	6.17e-11	4.70	8.41e-10	4.52
11718396_x_at	Jun proto-oncogene	**JUN**	9.15e-39	4.42	.0000453	1.61
11718394_at	Jun proto-oncogene	**JUN**	1.86e-34	4.31	.0001103	1.62
11744127_at	Chemokine (C-X-C motif) ligand 2	**CXCL2**	1.42e-27	4.17	.0061218	1.46
11718395_s_at	Jun proto-oncogene	**JUN**	5.81e-33	4.09	.0002306	1.58
11720298_at	Chemokine (C-X-C motif) ligand 10	**CXCL10**	4.19e-11	4.05	1.42e-09	3.80
11720994_x_at	Chemokine (C-C motif) ligand 3	**CCL3**	6.25e-34	3.971	2.41e-09	1.93
11744660_s_at	Chemokine (C-C motif) ligand 4-like 1	**CCL4L1**	1.19e-20	3.96	1.45e-13	3.12
11722728_a_at	Early growth response 2	**EGR2**	5.46e-15	3.59	7.03e-07	2.35
11726316_at	Selectin E	**SELE**	1.88e-17	3.47	6.97e-08	2.25
11717861_a_at	Early growth response 1	**EGR1**	2.12e-23	3.47	.001777	1.50
11742765_at	Regulator of G-protein signaling 1	**RGS1**	2.28e-20	3.42	5.58e-06	1.92
11719344_a_at	Activating transcription factor 3	**ATF3**	2.54e-19	3.38	.0050197	1.48
11715493_a_at	Cysteine-rich, angiogenic inducer, 61	**CYR61**	8.79e-28	3.21	.0000255	1.63
11759525_at	Growth arrest and DNA-damage-inducible, beta	**GADD45B**	1.73e-27	3.12	.0073953	1.34
11725631_a_at	Nuclear receptor subfamily 4, group A, member 2	**NR4A2**	1.53e-23	3.08	.0000189	1.63
11717994_a_at	Nuclear receptor subfamily 4, group A, member 1	**NR4A1**	4.42e-21	3.03	.0020826	1.48
11757865_a_at	Growth arrest and DNA-damage-inducible, beta	**GADD45B**	4.52e-23	2.94	.0563202	1.26
11763715_a_at	Granulysin	**GNLY**	7.62e-20	2.93	3.64e-20	3.09
11743168_at	indoleamine 2,3-dioxygenase 1	**IDO1**	2.479e-09	2.90	1.333e-12	3.71

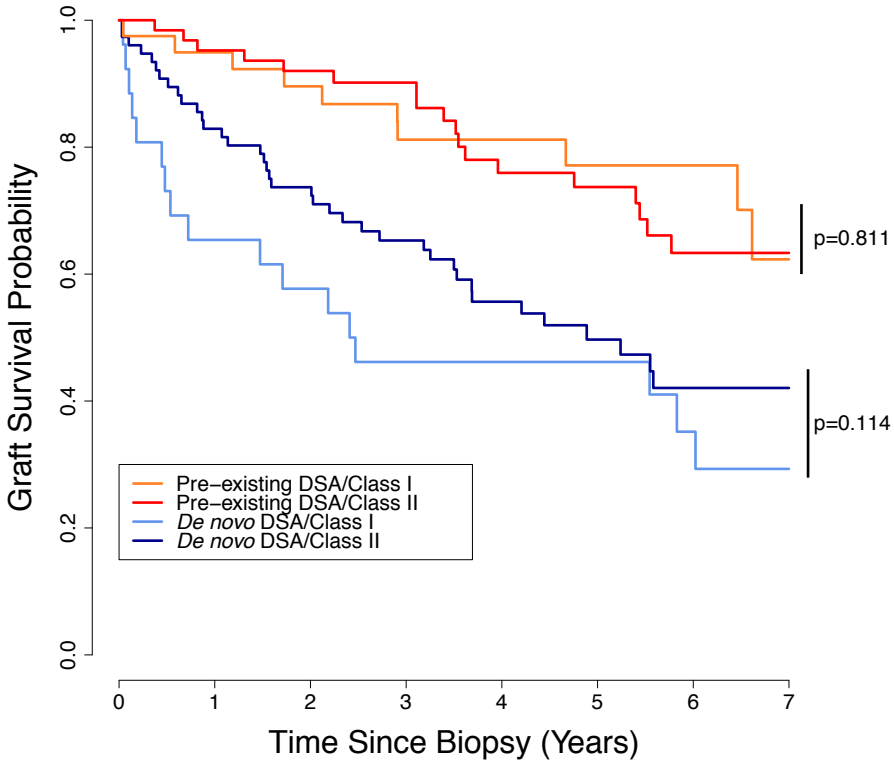
Supplementary Table 3: Factors associated with kidney allograft loss in the multivariate analysis for the ABMR during the first 6 years after transplantation

		Number of patients	Number of events	HR	95% CI	P
Proteinuria (g/g creatinine)	< 0.30	90	21	1	-	
	≥ 0.30	71	38	2.890	(1.683-4.962)	**0.0001**
DSA characteristic	Pre-existing DSA	101	28	1	-	
	De novo DSA	60	31	1.737	(1.016-2.972)	**0.0438**
Transplant glomerulopathy (cg) score	Negative	103	28	1	-	
	Positive	58	31	2.038	(1.200-3.962)	**0.0085**

Supplementary Table 4: Baseline characteristics of the reference set population

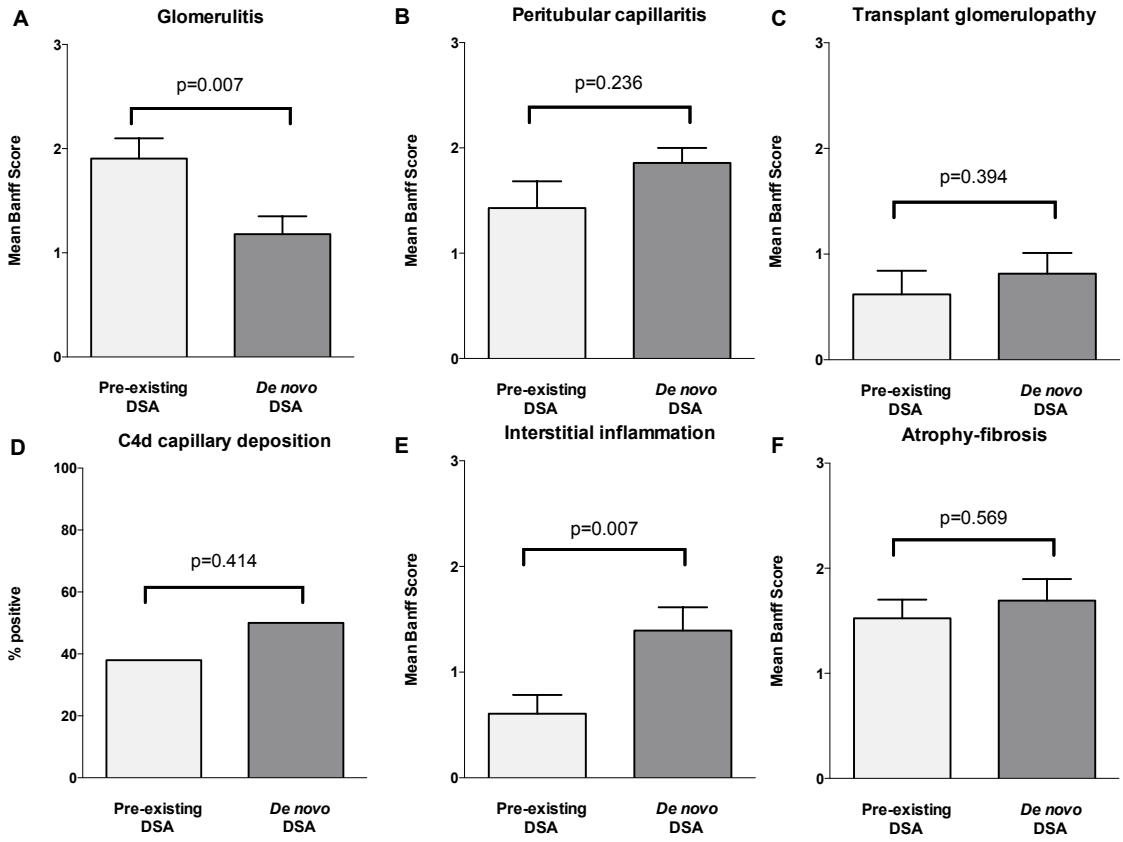
	Reference set: Kidney biopsies without ABMR (n=461)
Recipient age *(years, mean ± SD)*	48.98 ± 14.57
Recipient male sex *(n, %)*	292 (65.18%)
ESRD causes	
Glomerulonephritis, No. (%)	151 (32.75%)
Diabetes, No. (%)	82 (17.79%)
Polycystic Kidney Disease, No. (%)	44 (9.54%)
Tubulo-interstitial disease, No. (%)	47 (10.20%)
Hypertension, No. (%)	16 (3.47%)
Unknown, No. (%)	86 (18.66%)
Other, No. (%)	35 (7.59%)
Donor age *(years, mean ± SD)*	43.66 ± 14.27
Donor male sex *(n, %)*	188 (46.88%)
Donor deceased *(n, %)*	269 (61.00%)
Biopsy characteristics	
Time since transplantation *(years, mean ± SD)*	3.10 ± 4.79
GFR *(mL/min/1.73m^2, mean ± SD)*	36.71 ± 23.54
Acute kidney injury *(n, %)*	45 (9.76%)
T-cell mediated rejection *(n, %)*	56 (12.5%)
Borderline lesions *(n, %)*	79 (17.14%)
Recurrent glomerulonephritis *(n, %)*	65 (14.10%)
BK virus nephropathy *(n, %)*	17 (3.69%)
Isolated interstitial fibrosis – tubular atrophy *(n, %)*	74 (16.05%)
No major abnormalities *(n, %)*	101 (21.91%)
Other *(n, %)*	24 (5.21%)

Supplementary Figure 1: Graft survival according to anti-HLA DSA characteristics (pre-existing anti-HLA DSA and *de novo* anti-HLA DSA) and anti-HLA DSA class at the time of ABMR. This shows the probability of graft survival, which is based on the DSA characteristics and the DSA class.

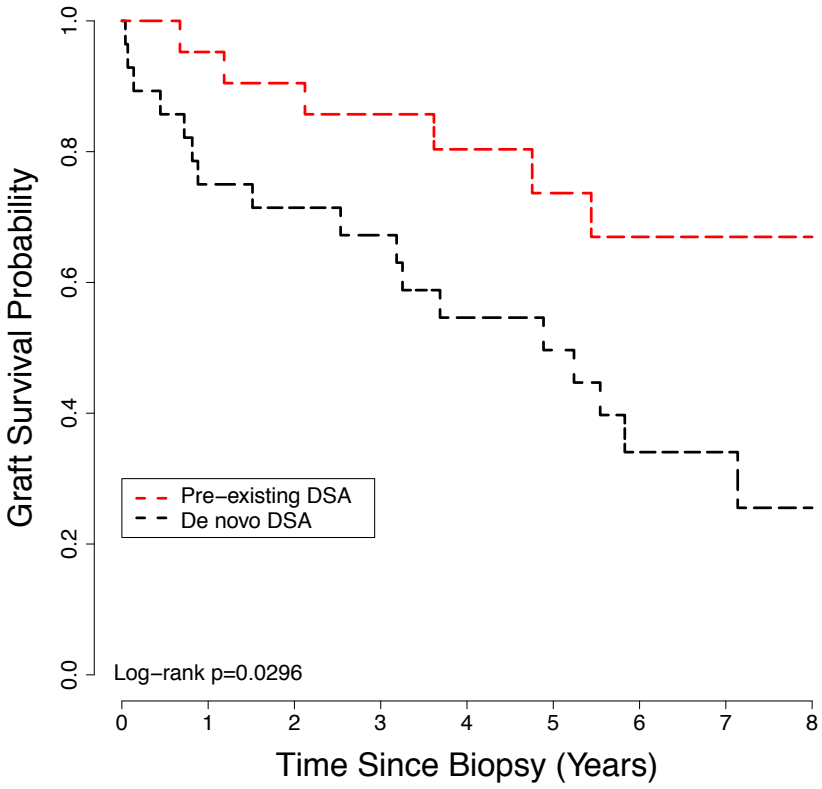


N at Risk								
De novo DSA/Class I	26	17	15	12	11	9	6	1
De novo DSA/Class II	76	63	55	44	32	22	16	9
Pre−existing DSA/Class I	40	36	32	29	25	18	14	6
Pre−existing DSA/Class II	63	59	55	45	36	31	18	11

Supplementary Figure 2: Histology according to DSA characteristics in ABMR biopsies performed between the first and the third year post-transplant. Data are based on 49 allograft biopsies performed between the first and the third year post-transplant. The T bars indicate standard errors and DSA denotes donor-specific anti-HLA antibodies.



Supplementary Figure 3: Graft survival according to anti-HLA DSA characteristics in ABMR biopsies performed between the first and the third year post-transplant. This shows the probability of graft survival, which is based on the DSA characteristics.



N at Risk									
De novo DSA	28	21	19	16	13	10	6	4	2
Pre-existing DSA	21	20	19	16	13	11	6	4	2