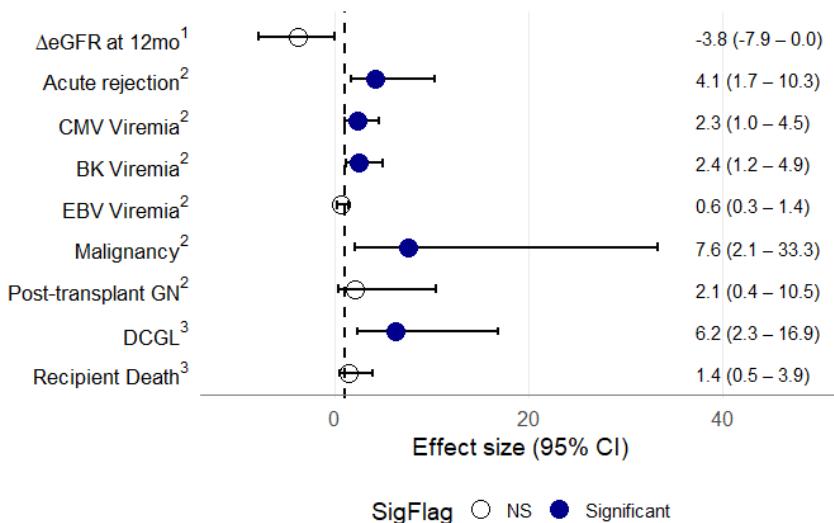


Supplementary Figure 1 Love plot showing the Covariate balance after propensity matching. It presents a love plot showing the post-matching standardized mean differences for matched covariates. The reduction in standardized mean difference (SMD) across covariates illustrates the success of the propensity score matching process in achieving balance. An SMD < 0.1 indicates adequate balance. The treatment effects along with the corresponding 95% CI.



Supplementary Figure 2 Treatment effects of Alemtuzumab induction vs basiliximab induction (full matching). The treatment effects, along with their

corresponding 95%CI, were calculated using various statistical methods depending on the nature of the outcome variable. ¹estimate by linear regression. ² Odd ratio by binary logistic regression. ³Hazard ratio by Cox proportional hazard model.

Supplementary Table 1 Variable balance assessment pre-propensity score matching using standardised mean differences, n (%)

Variables	Simulect (n = 319)	Campath (n = 117)	Total (n = 436)	SMD	P value
Age(years): Mean (SD)	52.1 (14.3)	50.1 (13.8)	51.6 (14.2)	-0.14	0.178
Sex: Female	114 (35.7)	51 (43.6)	165 (37.8)	0.06	0.134
Ethnicity					
White	239 (74.9)	111 (94.9)	350 (80.3)	0.81	< 0.001
Asian	63 (19.7)	4 (3.4)	67 (15.4)	-0.87	
Black	16 (5.0)	1 (0.9)	17 (3.9)	-0.26	
Other	1 (0.3)	1 (0.9)	2 (0.5)	0.05	
Primary renal disease					
ADPKD	57 (17.9)	16 (13.7)	73 (16.7)	-0.20	0.047
GN	81 (25.4)	31 (26.5)	112 (25.7)	-0.03	
DKD	48 (15.0)	16 (13.7)	64 (14.7)	0.01	
Reflux/CPN	33 (10.3)	17 (14.5)	50 (11.5)	0.17	
Other	63 (19.7)	33 (28.2)	96 (22.0)	-0.46	
Unknown	37 (11.6)	4 (3.4)	41 (9.4)	0.19	
Recipient diabetes	66 (20.8)	20 (17.9)	86 (20.0)	0.03	0.510
BMI (kg/M ²); Mean (SD)	27.6 (4.5)	26.8 (4.8)	27.4 (4.6)	-0.16	0.141
Pre-emptive transplant	127 (39.8)	20 (17.2)	147 (33.8)	0.58	< 0.001
Donor type					
Living donor	88 (27.6)	45 (38.5)	133 (30.5)	0.29	< 0.001
DBD	152 (47.6)	21 (17.9)	173 (39.7)	-0.83	

CD4	79 (24.8)	51 (43.6)	130 (29.8)	0.33	
Donor CMV	133 (42.6)	61 (53.0)	194 (45.4)	0.19	0.055
Recipient CMV	126 (40.4)	59 (50.9)	185 (43.2)	0.23	0.052
Recipient EBV	9 (8.7)	3 (2.9)	12 (5.9)	-	0.077
HLA DR mismatch; Mean (SD)	0.6 (0.6)	0.7 (0.6)	0.6 (0.6)	0.08	0.588
Total HLA mismatch	Mean 2.7 (1.3)	2.7 (1.4)	2.7 (1.3)	0.01	0.919
(SD)					
Crossmatch positive	1 (0.3)	5 (4.3)	6 (1.4)	0.19	0.002
PRA; Mean (SD)	15.8 (29.8)	31.2 (38.9)	19.9 (33.2)	0.33	< 0.001
Cold ischaemia time; Median (IQR)	12.0 (5.5-17.0)	12.0 (5.0-15.0)	12.0 (5.0-16.0)	-0.19	0.417
CNI					
Tac	313 (98.4)	117 (100.0)	430 (98.9)	0.17	0.394
Cyc	4 (1.3)	0 (0.0)	4 (0.9)	-0.16	
Other	1 (0.3)	0 (0.0)	1 (0.2)	-0.07	
Antimetabolite					
MPA	295 (94.6)	112 (95.7)	407 (94.9)	0.04	0.189
Aza	14 (4.5)	2 (1.7)	16 (3.7)	-0.18	
None	3 (1.0)	3 (2.6)	6 (1.4)	0.09	
Steroid maintenance	64 (25.4)	22 (18.8)	86 (23.3)	0.25	0.163
Baseline eGFR; Median (IQR)	47.0 (35.0-59.0)	43.0 (34.0-54.0)	46.0 (35.0-58.0)	-0.33	0.059

To assess the adequacy of balance between treatment groups, standardized mean differences (SMDs) were calculated for each covariate before and after propensity score matching. SMD values < 0.1 were considered indicative of adequate balance. Values shown are pre-matching SMDs for each covariate. *P* values of covariates had the largest pre-matching imbalance are highlighted.

Supplementary Table 2 Treatment effects of alemtuzumab induction *vs* basiliximab induction 1:1 nearest neighbour matching *vs* full matching

score									
Malignancy	preemptive	transplant, 6.2	1.6	29.9	<0.013	7.6	2.1	33.3	< 0.001
		primary disease, propensity							
		scores							
Post-	preemptive	transplant, 1.4	0.3	6.3	NS	2.1	0.4	10.5	NS
transplant	primary disease, propensity								
GN	Scores								
DCGL	preemptive	transplant, 3.6	1.2	11.4	<0.05	6.2	2.3	16.9	< 0.001
	primary disease, propensity								
	score, acute rejection								
Recipient	preemptive	transplant, 0.6	0.2	1.6	NS	1.4	0.5	3.9	NS
Death	primary disease, propensity								
	score, Age, baseline eGFR								

The treatment effects along with the corresponding 95%CI for 1:1 nearest neighbour matching without caliper and full matching. The treatment effects, along with their corresponding 95%CI (adjusted for confounding factors including propensity scores, primary kidney disease and pre-emptive transplant rate), estimates were calculated using various statistical methods depending on the nature of the outcome variable. Δ eGFR at 12 months, estimated by linear regression; Acute rejection, CMV Viremia, BK Viremia, EBV Viremia, Malignancy, and Post-transplant GN were estimated using odd ratio by binary logistic regression, whereas DCGL and Recipient death were estimated using Hazard ratio by Cox proportional hazard model.

Supplementary Table 3 Characteristics of recipients of campath induction who were subsequently maintained of steroids compared to those who did not receive steroids, n (%)

Characteristic	< 6months of steroid, n =	≥ 6months of steroid, n =	P
	75 (64%)	42(35%)	value ¹
Age at transplantation	52 ±13.1	48 (14.9)	0.14
Sex (male)	40 (53)	26 (62)	0.4
Ethnicity			0.8
White	71 (95)	40 (95)	
Asian	2 (2.7)	2 (4.8)	
Black	1 (1.3)	0 (0)	
Other	1 (1.3)	0 (0)	
Primary kidney disease			0.7
ADPKD	10 (13)	6 (14)	
DKD	12 (16)	4 (9.5)	
GN	22 (29)	9 (21)	
Reflux/CPN	11 (15)	6 (14)	
Unknown	2 (2.7)	2 (4.8)	
Other	18 (24)	15 (36)	
Donor type			0.3
Living donor	28 (37)	17 (40)	
DBD	11 (15)	10 (24)	
DCD	36 (48)	15 (36)	
Cold ischemia time (hour)	12.0 (5.0-14.5)	13.5 (5.0-15.0)	0.7
Total mismatch	3(2-4)	3(1-3)	0.019
Graft loss	11 (15)	8 (19)	0.5
DSA positive	9 (12)	4 (9.5)	0.8
CMV viremia	15 (20)	20 (48)	0.002
EBV Viremia	6 (8.1)	6 (14)	0.3
Bk Viremia	14 (19)	11 (26)	0.4
Acute rejection	10 (13)	11 (26)	0.08

eGFR at 3 months	44 (34-58)	42 (34-49)	0.4
eGFR at 12 months	47 (34-61)	43 (35-50)	0.12
Cancer	7 (9.3)	6 (14)	0.5

¹Wilcoxon rank sum test; Pearson's χ^2 test; Fisher's exact test.

There was no significant difference between Campath recipients who went on to receive long term steroids due to cytopenia or infections apart from a higher incidence of CMV viremia in the recipients of steroids and number of mis-match.