

S6 Table. The linkage disequilibrium results for *HLA-G* 3'-UTR and *MICA* in each group (Ct, CKD, KTN and KTR).

Ct (n = 75)				CKD (n = 94)				
<i>p</i>	<i>r</i> ²	D'	UTR	<i>HLA-G</i> alleles	UTR	D'	<i>r</i> ²	<i>p</i>
0.036	0.029	+0.790	UTR-4	<i>HLA-G*01:01</i>	---	---	---	---
<0.001	0.282	+0.583	UTR-5		UTR-5	+0.377	0.142	<0.001
<0.001	0.161	+1.000	UTR-13	<i>HLA-G*01:03</i>	UTR-13	+0.225	0.033	0.012
0.008	0.046	+0.306	UTR-8		---	---	---	---
<0.001	0.194	+0.440	UTR-3		UTR-3	+0.375	0.134	<0.001
0.003	0.056	+1.000	UTR-15	<i>HLA-G*01:04</i>	---	---	---	---
0.01	0.044	+0.731	UTR-1		---	---	---	---
0.009	0.045	+0.533	UTR-2	<i>HLA-G*01:06</i>	UTR-10	+0.225	0.033	0.012
KTN (n = 36)				KTR (n = 28)				
<i>p</i>	<i>r</i> ²	D'	UTR	<i>HLA-G</i> alleles	UTR	D'	<i>r</i> ²	<i>p</i>
0.04	0.058	+0.760	UTR-1	<i>HLA-G*01:01</i>	---	---	---	---
<0.001	0.422	+0.731	UTR-5		UTR-5	+1.000	0.491	<0.001
<0.001	0.189	+1.000	UTR-13	<i>HLA-G*01:03</i>	---	---	---	---
<0.001	0.480	+0.813	UTR-3	<i>HLA-G*01:04</i>	---	---	---	---
0.032	0.064	+0.294	UTR-10	<i>HLA-G*01:06</i>	---	---	---	---

The inferences of *HLA-G* haplotype through ELB algorithm of *HLA-G* alleles with determined UTRs. Analysis performed in Arlequin. The significant linkage disequilibrium had a $p < 0.05$. Ct: Control group. CKD: Patients with chronic kidney disease. KTN: Kidney-transplant patients with no rejection. KTR: Kidney-transplant patients who developed episodes of rejection.