Table 3. Pathway enrichment analysis of predicted and validated miRNA targets and differentially regulated transcripts in delayed graft function and acute rejection.

Delayed graft function	predicted targets	exp. validated targets	Cleveland dataset	Cleveland dataset (ATN)
Pathways	p-value	p-value	p-value	p-value
Angiogenesis	<0.001	<0.001	0.015	0.035
Apoptosis signaling pathway	<0.001	0.008	0.014	0.011
TGF-beta signaling pathway	<0.001	<0.001	0.001	0.001
Endothelin signaling pathway	0.001	0.038	0.002	0.002
VEGF signaling pathway	0.011	<0.001	0.028	0.016
PDGF signaling pathway	<0.001	0.002	0.025	0.037

Acute rejection	predicted targets	exp. validated targets	Cleveland dataset (acute rejection)	Acute rejection transcript set (ARTS)
Pathways	p-value	p-value	p-value	p-value
EGF receptor signaling pathway	<0.001	0.014	0.001	0.012
Inflammation mediated by chemokine and cytokine signaling pathway	<0.001	<0.001	0.039	<0.001
T cell activation	0.003	0.044	<0.001	<0.001
Cytoskeletal regulation by Rho GTPase	0.001	0.011	0.005	0.047
B cell activation	0.013	0.020	0.031	0.034