

Supplementary Table 7: Transplantation-related gene sets employed in quantitative set analysis for gene expression

Gene Set	Description
QCAT*	Transcripts associated with cytotoxic T lymphocytes defined in purified cell lines; associated with TCMR in renal transplants with expression levels correlating with T cell infiltration.
QCMAT*	Macrophage associated transcripts defined in purified cell lines, associated with TCMR in kidney patients.
GRIT1*	Human orthologs of IFN- γ dependent, rejection-associated transcripts defined in mice; expressed in TCMR, especially in association with AMAT1.
DSAST*	DSA-positive-specific transcripts derived from comparative analysis of DSA with or without renal biopsies; observed both in ABMR and TCMR with higher levels in ABMR.
AMAT1*	Alternative Macrophage Associated Transcript 1; human orthologs of mouse data; high GRIT1 plus AMAT1 scores correlate with TCMR.
IGT*	Immunoglobulin associated transcripts, observed both in ABMR and TCMR and associated with allograft fibrosis.
ENDAT*	Endothelial cell associated transcripts derived from purified cell lines; increased in ABMR and TCMR with higher levels in ABMR.
IRRAT*	Injury-repair response associated with transcripts, defined in early renal transplants with no rejection, derived as a model for acute kidney injury.
NKB*	Natural killer cell-specific transcripts derived from purified cells lines; identified in early TCMR and late ABMR in renal patients.
TCB*	T cell-specific transcripts based on purified cell lines.
BAT*	B cell-associated transcripts derived from purified B cells; upregulated in both ABMR and TCMR.
MCAT*	Mast cell associated transcripts, associated with scarring and poor survival in renal transplants.
IRITD3*	Injury and rejection induced transcripts upregulated 3 days after isograft transplant (humanized results from mouse model).
IRITD5*	Same as for IRITD3 but measured on day 5.
KT2.1*	Epithelial solute carriers reduced in day 21 mouse allografts.
KT1*	Kidney selective transcripts, the majority decreased after injury.
KT1.1*	Kidney selective transcripts reduced in day 21 mouse allografts
Liver TCMR	Gene signature previously described as being associated with TCMR in stable liver recipients undergoing immunosuppression withdrawal. The 13 genes in this set are: <i>CCL19, SLC1A3, HMMR, GPNMB, CXCL9, GBP2, HLA-DMA, MMP9, MMP7, TOP2A, PLA2G7, FABP5, CD74</i>

* Pathogenesis-based transcript gene sets from the Alberta Transplant Applied Genomics Centre