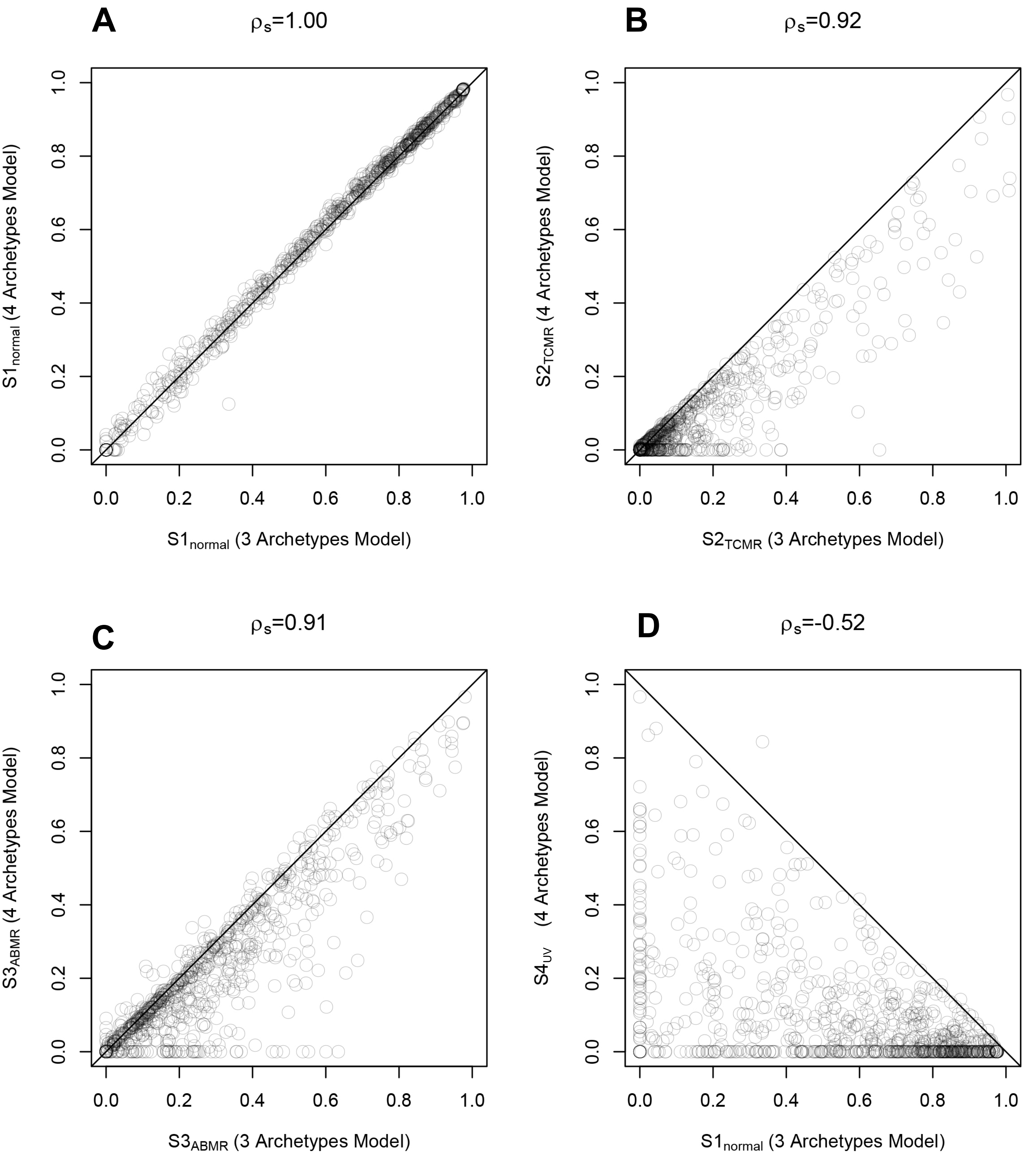
A
ρ_s=1.00
$S1_{normal}$ (4 Archetypes Model)
$S1_{normal}$ (3 Archetypes Model)
B
ρ_s=0.92
$S2_{TCMR}$ (4 Archetypes Model)
$S2_{TCMR}$ (3 Archetypes Model)
C
ρ_s=0.91
$S3_{ABMR}$ (4 Archetypes Model)
$S3_{ABMR}$ (3 Archetypes Model)
D
ρ_s=-0.52
$S4_{UV}$ (4 Archetypes Model)
$S1_{normal}$ (3 Archetypes Model)
0.0
0.2
0.4
0.6
0.8
1.0

Supplementary Table 1. Participating Centers

Center	Principal investigators	Number in 889 cohort
A Coruña, Spain	Dr. Maria G. Crespo-Leiro	92
Bologna, Italy	Dr. Luciano Potena	201
Los Angeles - Cedars-Sinai, USA	Dr. Jon Kobashigawa	51
Edmonton, Canada	Dr. Daniel Kim	113
France (6)	Drs. Alex Loupy, P. Bruneval, Xavier Jouven	
Bordeaux		1
Hospital Center University de Rouen		9
Hôpital Européen Georges-Pompidou		203
Nantes		11
Necker		7
Pitie		24
Sydney, Australia	Dr. Peter Macdonald	92
Los Angeles – UCLA, USA	Drs. Mario Deng, Martin Cadeiras And Eugene C. Depasquale	7
Vienna, Austria	Drs. Andreas Zuckermann, Arezu Aliabadi and Johannes Goekler	76
Virginia – VCU*, USA	Dr. Keyur B. Shah	2*
TOTAL		**889**

* 2 biopsies from Virginia were not formally part of the INTERHEART study but we included on request of the center, with patient consent.

Supplementary Table 2. The top 30 transcripts correlating with the PC3 score

Gene Symbol	Gene Name	Correlation* with PC3	Principal expression in cell panel[†]
PYGL	Phosphorylase, glycogen, liver	0.58	MC, MP, DC
LYVE1	Lymphatic vessel endothelial hyaluronan receptor 1	0.57	HUVEC
VSIG4	V-set and immunoglobulin domain containing 4	0.54	MP
VCAN	Versican	0.53	MC, MP, RPTEC
LOX	Lysyl oxidase	0.52	HUVEC, RPTEC
SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin 3	0.52	MP, RPTEC
PLBD1	Phospholipase B domain containing 1	0.51	MC, MP, DC
S100A9	S100 calcium binding protein A9	0.50	MC, MP, DC
MARCO	Macrophage receptor with collagenous structure	0.50	MP
MFAP5	Microfibrillar associated protein 5	0.50	MP
S100A8	S100 calcium binding protein A8	0.49	MC, MP
CD55	CD55 molecule, decay accelerating factor for complement	0.49	MC, MP, HUVEC
SPP1	Secreted phosphoprotein 1	0.47	MP, DC, RPTEC
LAMP2	Lysosomal-associated membrane protein 2, uncharacterized	0.47	MC, MP, DC
CEBPD	CCAAT/enhancer binding protein (C/EBP, delta	0.47	MC, MP, RPTEC
RNASE2[§]	Ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin	0.47	MC
MERTK	MER proto-oncogene, tyrosine kinase	0.47	MP
LHFPL2	Lipoma HMGIC fusion partner-like 2	0.47	MP, DC
GFPT2	Glutamine-fructose-6-phosphate transaminase 2	0.46	HUVEC
FBN1	Fibrillin 1	0.46	RPTEC
NAMPT	Nicotinamide phosphoribosyl transferase	0.46	MC, MP, RPTEC
MS4A4A	Membrane-spanning 4-domains, subfamily A, member 4A	0.46	MP
FGFR1OP2	FGFR1 oncogene partner 2	0.46	MP
ADORA3	Adenosine A3 receptor	0.46	MP, DC
CCT2	Chaperonin containing TCP1, subunit 2 (beta	0.46	MP, HUVEC
PTX3	Pentraxin 3, long	0.46	HUVEC
CD163	CD163 molecule	0.46	MC, MP
PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	0.45	MP
SH3GLB1	SH3-domain GRB2-like endophilin B1	0.45	MC, MP, DC, HUVEC
COMT	Catechol-O-methyltransferase	0.45	MC, MP, DC, HUVEC

* Spearman rank correlation coefficient

[†] The cell panel is described previously (see Methods). Note the granulocytes were not represented in this cell panel, and expression in such cells is not assessed.

[§] Gene belonging to rejection-associated transcripts (RATs)

Abbreviations: HUVEC – human umbilical vein endothelial cells; RPTEC – human renal proximal tubule cells; MC - monocyte; MP - macrophage; DC – dendritic cell ;

Supplementary Table 3. Top 30 unique genes correlated with S1$_{normal}$ in 889 heart transplant biopsies

Gene Symbol	Gene Name	Correlation* with S1$_{normal}$	PBT[†,‡]	Principal Expression[§]
GBP5[‡]	guanylate binding protein 5	-0.96	(GRIT)	T, NK, MP, HUVEC
PSMB8[‡]	proteasome subunit beta 8	-0.95	GRIT1	All
HLA-DRA[‡]	major histocompatibility complex, class II, DR alpha	-0.95	GRIT1	All
TAP1[‡]	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-0.95	(GRIT)	DC, MC, MP, HUVEC, RPTEC
HLA-DPB1[‡]	major histocompatibility complex, class II, DP beta 1	-0.95	(GRIT)	All
HLA-DPA1[‡]	major histocompatibility complex, class II, DP alpha 1	-0.95	(GRIT)	All
PSMB9[‡]	proteasome subunit beta 9	-0.95	GRIT1	All
NLRC5[‡]	NLR family, CARD domain containing 5	-0.94	(GRIT)	All
GBP1[‡]	guanylate binding protein 1, interferon-inducible	-0.94	(GRIT)	MC, MP, HUVEC, RPTEC
CD74[‡]	CD74 molecule, major histocompatibility complex, class II invariant chain	-0.94	GRIT1	DC, MP
HLA-DRB1[‡]	major histocompatibility complex, class II, DR beta 1	-0.94	GRIT1 DSAST	All
HLA-DMA[‡]	major histocompatibility complex, class II, DM alpha	-0.94	GRIT1	All
HLA-F[‡]	major histocompatibility complex, class I, F	-0.93	(GRIT)	All
IRF1[‡]	interferon regulatory factor 1	-0.93	(GRIT)	All
HLA-DOA[‡]	major histocompatibility complex, class II, DO alpha	-0.93	(GRIT)	B
LCP2[‡]	lymphocyte cytosolic protein 2	-0.93	-	T, NK, MC, MP
AIM1	absent in melanoma 1	-0.93	(GRIT)	DC, MC, MP
CXCL9[‡]	chemokine (C-X-C motif) ligand 9	-0.93	GRIT1	MP, HUVEC
GBP2[‡]	guanylate binding protein 2, interferon-inducible	-0.93	GRIT1	MC, MP, HUVEC, RPTEC
ITGAL[‡]	integrin alpha L	-0.93	-	T, NK, MC
CCL4	chemokine (C-C motif) ligand 4	-0.93	(GRIT)	T, NK, DC, MC, MP
HLA-DMB[‡]	major histocompatibility complex, class II, DM beta	-0.93	GRIT1	All
FAM26F[‡]	family with sequence similarity 26, member F	-0.93	-	B, MC, MP
GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	-0.93	GRIT1	MC
GZMA[‡]	granzyme A	-0.92	QCAT	T, NK
LCP1	lymphocyte cytosolic protein 1 (L-plastin)	-0.92	IRIT5	B, T, NK, DC, MC, MP
CD48	CD48 molecule	-0.92	-	B, T, NK, DC, MC, MP
CASP1	caspase 1	-0.92	(GRIT); ENDAT	MC, MP
IRF8	interferon regulatory factor 8	-0.92	(GRIT)	B, NK, DC, MC, MP
UBE2L6[‡]	ubiquitin-conjugating enzyme E2L 6	-0.92	(GRIT)	T, NK, DC, MP, HUVEC, RPTEC

* Spearman rank correlation coefficient

[†] Indicates transcripts which belong to previously annotated pathogenesis-based transcript sets. DSAST – DSA-associated transcripts; GRIT1 – IFNG-inducible transcripts; (GRIT) – not formally annotated as GRIT1 but IFNG-inducible in cell panel; ENDAT – endothelial transcripts; QCAT – cytotoxic T cell transcripts; IRIT5 – 5 day injury transcripts (mouse kidney isograft). See https://www.ualberta.ca/medicine/institutes-centres-groups/atagc/research/gene-list

[§] Principal expression in a primary human cell panel. B – B cells; DC – dendritic cells; MC – monocytes; MP – macrophages; NK – NK cells; T – T cells; HUVEC – human umbilical vein endothelial cells; RPTEC – renal proximal tubule epithelial cells.

[‡] Gene belonging to rejection-associated transcripts (RATs)

Supplementary Table 4. Top 30 unique genes correlated with S2$_{\text{TCMR}}$ in 889 heart transplant biopsies

Gene Symbol	**Gene Name**	**Correlation* with S2$_{\text{TCMR}}$**	**PBT[†,‡]**	**Principal Expression[§]**
TRBC2	T cell receptor beta constant 2	0.78	-	T, NK
CD27[‡]	CD27 molecule	0.76	-	T
BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.76	-	T, NK
TRBC1	T cell receptor beta constant 1, T cell receptor beta variable 19	0.75	-	T, NK
CD3D[‡]	CD3d molecule, delta (CD3-TCR complex)	0.75	QCAT TCB	T
CD3G[‡]	CD3g molecule, gamma (CD3-TCR complex)	0.75	-	T
SIRPG[‡]	signal-regulatory protein gamma	0.75	-	T
IL23A[‡]	interleukin 23, alpha subunit p19	0.75	-	B, T, MP
PVRIG	poliovirus receptor related immunoglobulin domain containing, stromal antigen 3	0.74	-	T, NK
BTLA[‡]	B and T lymphocyte associated	0.74	-	B
CD2[‡]	CD2 molecule	0.74	QCAT	T, NK
TRAC	T-cell receptor alpha constant	0.74	QCAT TCB	T
LEF1	lymphoid enhancer-binding factor 1	0.74	-	T
LAT	linker for activation of T-cells	0.74	-	T, NK, MP
CD6[‡]	CD6 molecule	0.73	-	T, NK
RHOH	ras homolog family member H	0.73	-	B, T
TESPA1	thymocyte expressed, positive selection associated 1	0.73	-	T, NK
CCR7	chemokine (C-C motif) receptor 7	0.73	-	B, T, DC
GZMK[‡]	granzyme K	0.73	QCAT	T, NK
SKAP1	src kinase associated phosphoprotein 1	0.73	-	T, NK
TRAT1	T cell receptor associated transmembrane adaptor 1	0.73	-	T
LCK[‡]	LCK proto-oncogene, Src family tyrosine kinase	0.73	QCAT	T, NK
CD8A[‡]	CD8a molecule	0.73	QCAT	T, NK
NLRC3	NLR family, CARD domain containing 3	0.72	-	T, NK
GPR18	G protein-coupled receptor 18	0.72	-	B
PTPN7[‡]	protein tyrosine phosphatase, non-receptor type 7	0.72	-	T, NK, DC
CD96[‡]	CD96 molecule	0.72	-	T, NK
MCOLN2	mucolipin 2	0.72	-	DC
P2RY10	purinergic receptor P2Y, G-protein coupled, 10	0.72	-	B, T
TBC1D10C	TBC1 domain family, member 10C	0.72	-	T, NK

* Spearman rank correlation coefficient

[†] Indicates transcripts which belong to previously annotated pathogenesis-based transcript sets. QCAT – cytotoxic T cell transcripts; TCB – T cell burden transcripts. See https://www.ualberta.ca/medicine/institutes-centres-groups/atagc/research/gene-list

[§] Principal expression in a primary human cell panel. B – B cells; DC – dendritic cells; MC – monocytes; MP – macrophages; NK – NK cells; T – T cells; HUVEC – human umbilical vein endothelial cells; RPTEC – renal proximal tubule epithelial cells.

[‡] Gene belonging to rejection-associated transcripts (RATs)

Supplementary Table 5. Top 30 unique genes correlated with $S3_{ABMR}$ in 889 heart transplant biopsies

Gene Symbol	Gene Name	Correlation* with $S3_{ABMR}$	PBT[†]	Principal Expression[§]
CX3CL1[‡]	chemokine (C-X3-C motif) ligand 1	0.75	-	HUVEC, RPTEC
TM4SF18[‡]	transmembrane 4 L six family member 18	0.71	DSAST	HUVEC, RPTEC
ROBO4[‡]	roundabout guidance receptor 4	0.68	DSAST	HUVEC
GBP4[‡]	guanylate binding protein 4	0.67	(GRIT)	MP, HUVEC
CX3CR1[‡]	chemokine (C-X3-C motif) receptor 1	0.65	DSAST IRIT5	MC, NK
PLA1A[‡]	phospholipase A1 member A	0.64	DSAST	HUVEC, RPTEC
CXCL11[‡]	chemokine (C-X-C motif) ligand 11	0.64	(GRIT)	HUVEC, RPTEC
GNLY[‡]	granulysin	0.64	DSAST QCAT	T, NK
MYCN[‡]	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived	0.64	-	NK
GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	0.63	GRIT1	MC
CDH5[‡]	cadherin 5, type 2 (vascular endothelium)	0.63	DSAST ENDAT	HUVEC
RAPGEF5[‡]	Rap guanine nucleotide exchange factor 5	0.62	-	HUVEC
RASIP1[‡]	Ras interacting protein 1	0.62	ENDAT	HUVEC
IDO1[‡]	indoleamine 2,3-dioxygenase 1	0.62	-	DC, MP, HUVEC, RPTEC
GBP1[‡]	guanylate binding protein 1, interferon-inducible	0.61	(GRIT)	MC, MP, HUVEC, RPTEC
TRDC[‡]	T cell receptor delta constant	0.61	-	T, NK
MALL[‡]	mal, T cell differentiation protein-like	0.61	DSAST	HUVEC
HCP5[‡]	HLA complex P5 (non-protein coding)	0.61	-	T, NK, B, DC, MC, MP,
WARS[‡]	tryptophanyl-tRNA synthetase	0.61	(GRIT)	DC, MC, MP, HUVEC,
TM4SF1[‡]	transmembrane 4 L six family member 1	0.61	-	HUVEC
MMRN2[‡]	multimerin 2	0.61	-	HUVEC
CCL4	chemokine (C-C motif) ligand 4	0.60	(GRIT)	T, NK, DC, MC, MP
APOL3[‡]	apolipoprotein L, 3	0.60	-	MP, HUVEC
PRF1[‡]	perforin 1 (pore forming protein	0.60	QCAT	T, NK
TNFAIP8L1	tumor necrosis factor, alpha induced protein 8-like 1	0.60	-	All
MEOX1	mesenchyme homeobox 1	0.60	ENDAT	DC, MP
C2CD4B[‡]	C2 calcium-dependent domain containing 4B	0.60	-	DC, MP, HUVEC
NLRC5[‡]	NLR family, CARD domain containing 5	0.59	-	All
IRF1[‡]	interferon regulatory factor 1	0.59	(GRIT)	All
CXCL9[‡]	chemokine (C-X-C motif) ligand 9	0.59	GRIT1	MP, HUVEC

* Spearman rank correlation coefficient

[†] Indicates transcripts which belong to previously annotated pathogenesis-based transcript sets. DSAST – DSA selective transcripts; ENDAT – endothelial transcripts; NKB - NK cell burden transcripts; GRIT1 – IFNG-inducible transcripts; IRIT5 – 5 day injury transcripts (mouse kidney isograft). See https://www.ualberta.ca/medicine/institutes-centres-groups/atagc/research/gene-list

[§] Principal expression in a primary human cell panel. B – B cells; DC – dendritic cells; MC – monocytes; MP – macrophages; NK – NK cells; T – T cells; HUVEC – human umbilical vein endothelial cells; RPTEC – renal proximal tubule epithelial cells.

[‡] Gene belonging to rejection-associated transcripts (RATs)

Supplementary Table 6. Top 30 unique genes correlated with PC1 in 889 heart transplant biopsies

Gene Symbol	Gene Name	Correlation* with PC1	PBT[†,‡]	Principal Expression[§]
GBP5[‡]	guanylate binding protein 5	0.96	(GRIT)	T, NK, MP, HUVEC
HLA-DRA[‡]	major histocompatibility complex, class II, DR alpha	0.96	GRIT1	All
HLA-DPA1[‡]	major histocompatibility complex, class II, DP alpha 1	0.96	(GRIT)	All
HLA-DPB1[‡]	major histocompatibility complex, class II, DP beta 1	0.96	(GRIT)	All
PSMB8[‡]	proteasome subunit beta 8	0.96	GRIT1	All
LCP2[‡]	lymphocyte cytosolic protein 2	0.95	(GRIT)	T, NK, MC, MP
HLA-DMB[‡]	major histocompatibility complex, class II, DM beta	0.95	GRIT1	All
PSMB9[‡]	proteasome subunit beta 9	0.95	GRIT1	All
FAM26F[‡]	family with sequence similarity 26, member F	0.95	(GRIT)	B, MC, MP
HLA-DMA[‡]	major histocompatibility complex, class II, DM alpha	0.95	GRIT1	All
CD48	CD48 molecule	0.95	-	B, T, NK, MC, MP
CD74[‡]	CD74 molecule, major histocompatibility complex, class II invariant chain	0.95	GRIT1	DC, MP
LCP1	lymphocyte cytosolic protein 1 (L-plastin)	0.95	IRIT5	B, T, NK, DC, MC, MP
TAP1[‡]	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.95	(GRIT)	DC, MC, MP, HUVEC, RPTEC
IRF8	interferon regulatory factor 8	0.94	(GRIT)	
HLA-DRB1[‡]	major histocompatibility complex, class II, DR beta 1	0.94	DSAST GRIT1	All
RAC2	ras-related C3 botulinum toxin substrate 2 (rho family), small GTP binding protein Rac2	0.94	-	B, T, NK, DC, MC, MP
FYB[‡]	FYN binding protein	0.94	-	MC, MP
ITGAL[‡]	integrin alpha L	0.94	-	T, NK, MC
HLA-DOA[‡]	major histocompatibility complex, class II, DO alpha	0.94	(GRIT)	B
AIM1	absent in melanoma 1	0.94	(GRIT)	DC, MC, MP
CORO1A	coronin, actin binding protein, 1A	0.94	-	B, T, NK, DC, MC, MP
GZMA[‡]	granzyme A	0.94	QCAT	T, NK
PTPRC	protein tyrosine phosphatase, receptor type, C	0.94	IRRAT	B, T, NK, DC, MC, MP
NLRC5[‡]	NLR family, CARD domain containing 5	0.94	(GRIT)	All
HLA-DQA1[‡]	major histocompatibility complex, class II, DQ alpha 1	0.93	GRIT1	B, DC, MC, MP
DOCK2	dedicator of cytokinesis 2	0.93	-	B, T, NK, DC, MC, MP
KLRC4-KLRK1	KLRC4-KLRK1 readthrough	0.93	QCAT	T, NK
HLA-F[‡]	major histocompatibility complex, class I, F	0.93	(GRIT)	All
DOCK10	dedicator of cytokinesis 10	0.93	-	DC, MP

* Spearman rank correlation coefficient

[†] Indicates transcripts which belong to previously annotated pathogenesis-based transcript sets. DSAST – DSA selective transcripts; GRIT1 – IFNG-inducible transcripts; IRRAT – injury and repair transcripts (human kidney transplant); IRIT5 – 5 day injury transcripts (mouse kidney isograft); QCAT – cytotoxic T cell transcripts. See https://www.ualberta.ca/medicine/institutes-centres-groups/atagc/research/gene-list

[§] Principal expression in a primary human cell panel. B – B cells; DC – dendritic cells; MC – monocytes; MP – macrophages; NK – NK cells; T – T cells; HUVEC – human umbilical vein endothelial cells; RPTEC – renal proximal tubule epithelial cells.

[‡] Gene belonging to rejection-associated transcripts (RATs)

Supplementary Table 7. Top 30 unique genes correlated with PC2 in 889 heart transplant biopsies

Gene Symbol	Gene Name	Correlation* with PC2	PBT[†,‡]	Principal Expression[§]
CX3CL1[‡]	chemokine (C-X3-C motif) ligand 1	0.63	-	HUVEC, RPTEC
TM4SF1[‡]	transmembrane 4 L six family member 1	0.60	-	HUVEC
RASIP1[‡]	Ras interacting protein 1	0.60	ENDAT	HUVEC
MMRN2[‡]	multimerin 2	0.59	-	HUVEC
ROBO4[‡]	roundabout guidance receptor 4	0.59	DSAST	HUVEC
CDH5[‡]	cadherin 5, type 2 (vascular endothelium)	0.57	DSAST ENDAT	HUVEC
BCL6B[‡]	B-cell CLL/lymphoma 6, member B	0.56	-	HUVEC
KIAA1462	KIAA1462	0.54	-	HUVEC
TM4SF18[‡]	transmembrane 4 L six family member 18	0.54	DSAST	HUVEC, RPTEC
RAPGEF5[‡]	Rap guanine nucleotide exchange factor 5	0.54	-	HUVEC
ERG	v-ets avian erythroblastosis virus E26 oncogene homolog	0.53	-	HUVEC
MCAM	melanoma cell adhesion molecule	0.52	ENDAT	HUVEC
CCND1	cyclin D1	0.52	-	MP, HUVEC
MALL	mal, T-cell differentiation protein-like	0.52	DSAST	HUVEC
ATP8B1	ATPase, aminophospholipid transporter, class I, type 8B, member 1	0.52	-	HUVEC
ARHGAP29	Rho GTPase activating protein 29	0.51	-	HUVEC, RPTEC
ADGRL4[‡]	adhesion G protein-coupled receptor L4	0.50	KT1	HUVEC, RPTEC
SMAD1	SMAD family member 1	0.49	IRIT5	DC, HUVEC
TEK[‡]	TEK tyrosine kinase, endothelial	0.49	DSAST ENDAT KT1	HUVEC
PLS3	plastin 3	0.49	-	HUVEC, RPTEC
C2CD4B[‡]	C2 calcium-dependent domain containing 4B	0.48	-	DC, MP, HUVEC
DOCK4	dedicator of cytokinesis 4	0.48	-	DC, MP, HUVEC, RPTEC
MEOX1	mesenchyme homeobox 1	0.48	ENDAT	DC, MP
PODXL	podocalyxin-like	0.48	ENDAT	HUVEC
SOX18	SRY box 18	0.47	ENDAT	HUVEC
JAG1	jagged 1	0.47	-	DC, MP, HUVEC, RPTEC
KCTD15	potassium channel tetramerization domain containing 15	0.47	-	MC, HUVEC
IGF2	insulin-like growth factor 2	0.46	-	HUVEC
DLC1	DLC1 Rho GTPase activating protein	0.46	ENDAT	HUVEC
CLEC14A	C-type lectin domain family 14, member A	0.46	-	HUVEC

* Spearman rank correlation coefficient

[†] Indicates transcripts which belong to previously annotated pathogenesis-based transcript sets. DSAST – DSA selective transcripts; ENDAT – endothelial transcripts; IRIT5 – 5 day injury transcripts (mouse kidney isograft); KT1 – kidney parenchymal transcripts. See https://www.ualberta.ca/medicine/institutes-centres-groups/atagc/research/gene-list

[§] Principal expression in a primary human cell panel. DC – dendritic cells; MC – monocytes; MP – macrophages; HUVEC – human umbilical vein endothelial cells; RPTEC – renal proximal tubule epithelial cells.

[‡] Gene belonging to rejection-associated transcripts (RATs)

Supplementary Table 8. Pathways associated with top 100 transcripts associated with principal components PC1, PC2, and PC3.*

Pathways associated with PC1		Pathways associated with PC2		Pathways associated with PC3	
Description	**Adjusted p-value**	**Description**	**Adjusted p-value**	**Description**	**Adjusted p-value**
T cell activation	4.E-21	angiogenesis	1.E-14	neutrophil activation	1.E-10
cellular response to interferon-gamma	1.E-19	regulation of vasculature development	5.E-09	neutrophil mediated immunity	1.E-10
immune response-activating signal transduction	1.E-18	regulation of angiogenesis	9.E-09	granulocyte activation	1.E-10
response to interferon-gamma	1.E-18	endothelial cell proliferation	7.E-08	neutrophil degranulation	4.E-10
leukocyte cell-cell adhesion	1.E-18	vasculogenesis	2.E-07	neutrophil activation involved in immune response	4.E-10
antigen receptor-mediated signaling pathway	1.E-18	endothelium development	5.E-07	acute inflammatory response	1.E-05
T cell receptor signaling pathway	3.E-18	negative regulation of vasculature development	1.E-06	platelet degranulation	3.E-04
interferon-gamma-mediated signaling pathway	1.E-17	regulation of endothelial cell migration	1.E-06	humoral immune response	3.E-04
immune response-activating cell surface receptor signaling pathway	3.E-17	endothelial cell migration	1.E-06	response to molecule of bacterial origin	7.E-03
immune response-regulating cell surface receptor signaling pathway	3.E-16	regulation of endothelial cell proliferation	2.E-06	immune response-activating signal transduction	7.E-03

*****The 10 most significant gene ontology biological processes (BP) associated with each of the first 3 PCs of a RAT-based heart transplant biopsy principal component analysis (based on the top 100 unique transcripts)