Supplementary Materials for

Immunoregulatory and lipid presentation pathways are upregulated in human face transplant rejection

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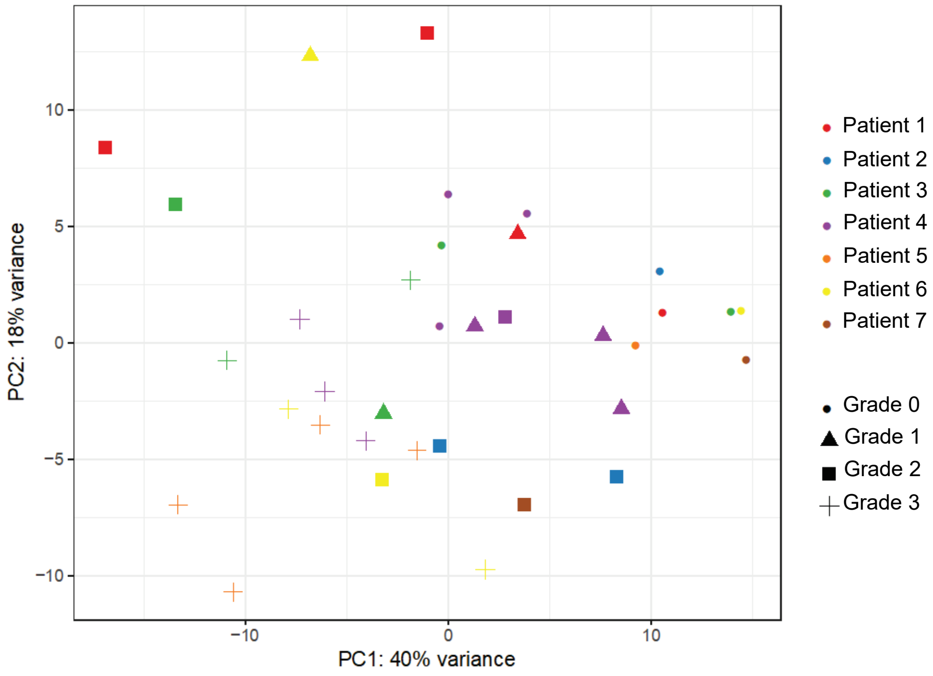
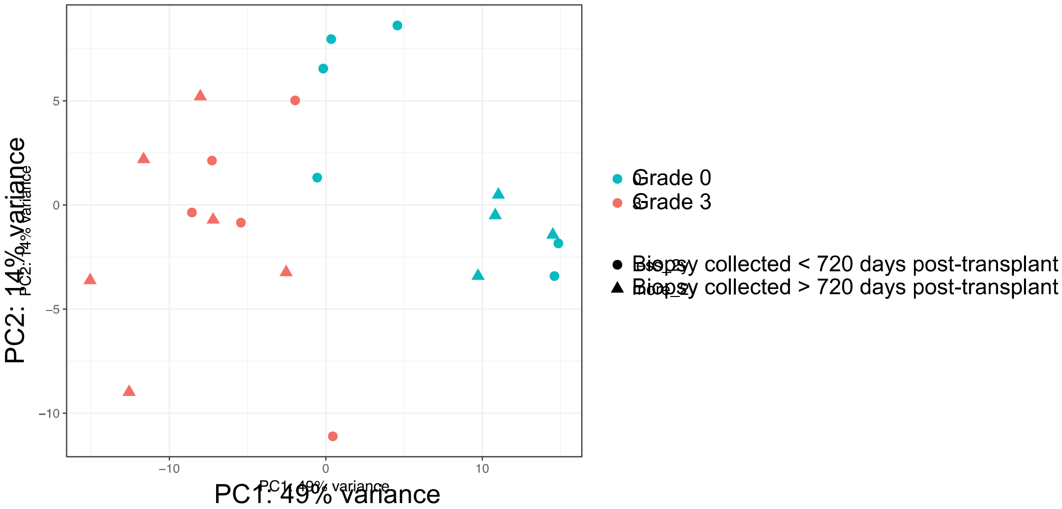
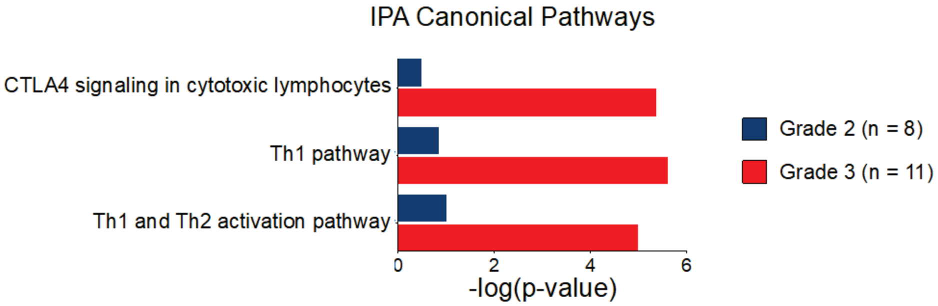


Supplementary Figure 1. Principal component analysis revealed that the samples clustered on the basis of rejection status.

Unsupervised principal component analysis of all allograft biopsies (n = 35) included in the analyses of the study revealed that the samples clustered on the basis of rejection status irrespective of the origin of the biopsies.

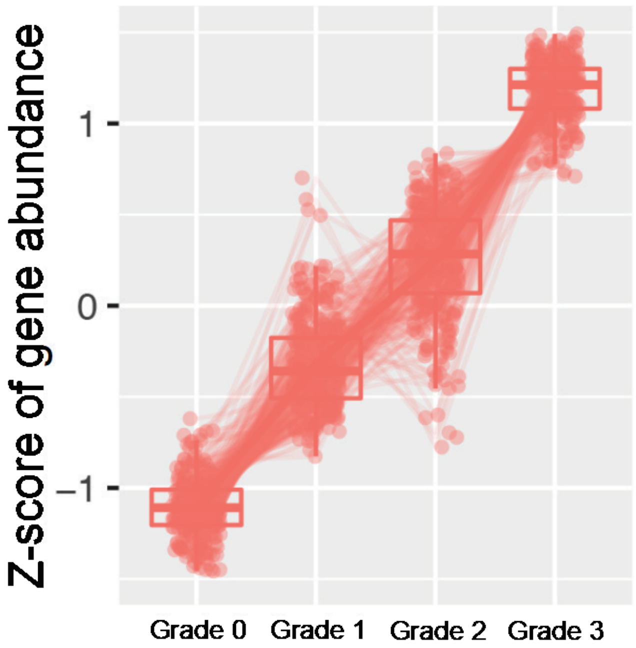


Supplementary Figure 2. Biopsies did not cluster on the basis of the time of biopsy collection. Unsupervised principal component analysis revealed that the biopsy samples (Grade 0, n = 10; Grade 3, n = 11) clustered on the basis of rejection status irrespective of the time of biopsy collection from transplantation.



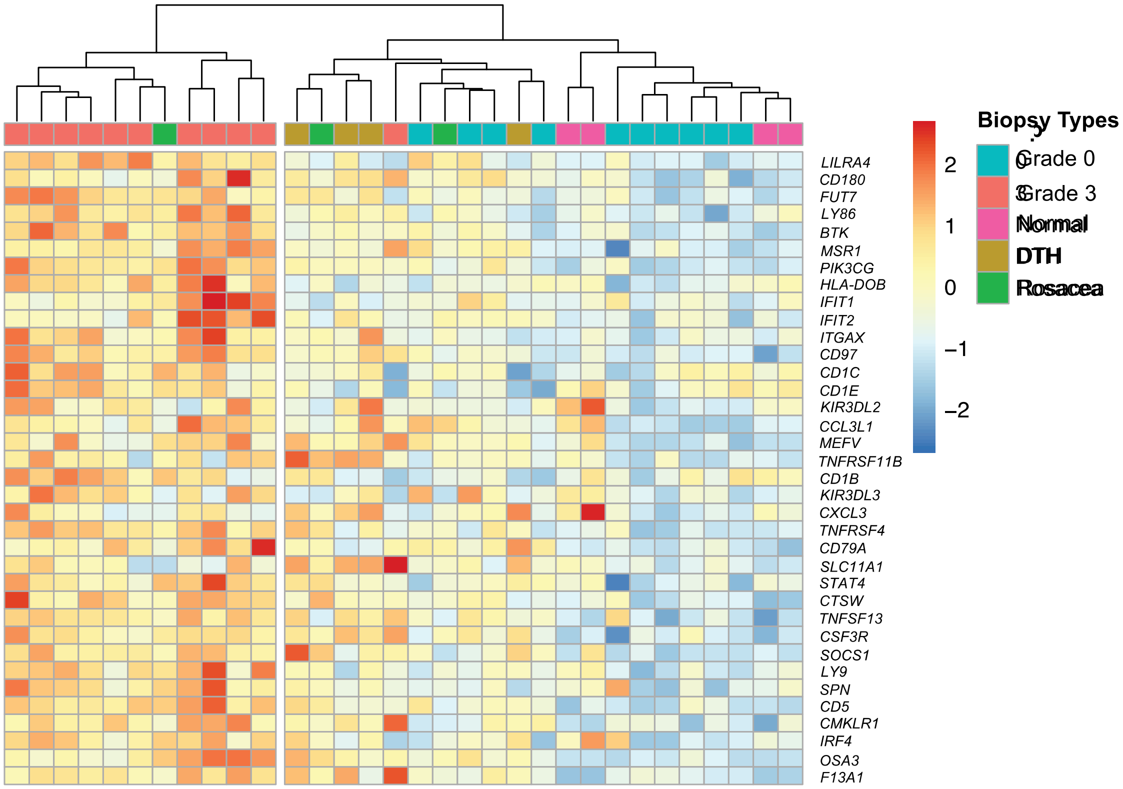
Supplementary Figure 3. Ingenuity pathway analysis identified progressive enrichment of T cell associated pathways with increasing severity of rejection.

Benjamini-Hochberg corrected Fischer’s exact test P values are shown.



Supplementary Figure 4. Pattern of increased expression correlating with rejection grade for a cluster of 273 genes, differentially expressed across rejection grades.

The x-axis represents the Banff rejection grades [Grade 0 (n = 10); Grade 1 (n = 6); Grade 2 (n = 8); Grade 3 (n = 11)] and the y-axis, the centered and scaled expression for the genes (equivalent to z-score). The complete list of 273 genes is shown in Supplementary Table 8.



Supplementary Figure 5. Heatmap of normalized expression values for thirty-six genes upregulated in face transplant rejection that have not been reported in solid organ transplant rejection.

The complete list of the thirty-six genes is detailed in Supplementary Table 13. Each column represents a biopsy sample. Gene expression row scaled. The cell color represents normalized levels from high (red) to middle (yellow) to low (blue). The degree of relatedness is represented by the dendrogram at the top of the panel (unsupervised hierarchical clustering). All except one biopsy collected from non-transplanted patients with rosacea clustered separately from rejection (Banff Grade 3) samples.

Supplementary Table 1. Donor and recipient characteristics.

Recipient characteristic	Patient 1	Patient 2	Patient 3	Patient 4	Patient 5	Patient 6	Patient 7
Age at transplant (years)	57	25	30	44	59	38	33
Gender	Female	Male	Male	Female	Male	Male	Male
Mechanism of injury	Animal bite	Electrical burn	Electrical burn	Chemical burn	Electrical burn	Gunshot	Gunshot
Year of transplant	2011	2011	2011	2013	2009	2014	2014
Follow-up (months)	89	91	90	68	114	55	48
Facial allograft details	Full face	Full face	Full face	Full face	Partial face	Partial face	Partial face
Panel reactive antibodies (%)	0	68	0	97	0	22	32
Donor specific antibodies	Negative	Negative	Negative	Positive	Negative	Negative	Negative
HLA mismatch (A, B, C, DR, DQ, DP)	8	8	5	11	4	8	7
CMV status	Positive	Positive	Negative	Positive	Positive	Negative	Positive
EBV status	Positive	Positive	Positive	Positive	Positive	Positive	Positive
Induction therapy	ATG 1.5mg/kg/day x4; high dose steroids	ATG 1.5mg/kg/day x4; high dose steroids	ATG 1.5mg/kg/day x4; high dose steroids	ATG 1.5mg/kg/day x4; MMF 2g/day; tacrolimus 4mg/day; high dose steroids*	ATG 1.5mg/kg/day x3; high dose steroids	ATG 1.5mg/kg/day x2/0.75mg/kg/day x2; high dose steroids	ATG 1.5mg/kg/day x3; high dose steroids
Donor characteristic							
Age (years)	42	48	31	56	55	51	23
Gender	Female	Male	Male	Female	Male	Male	Male
CMV status	Positive	Positive	Positive	Negative	Positive	Positive	Negative
EBV status	Positive	Positive	Positive	Positive	Positive	Positive	Positive
Ischemia time (minutes)	120	240	120	180	150	180	90

*Patient 4 was highly sensitized and therefore, received additional immunosuppressants alongside the standard induction regimen with rabbit anti-thymocyte globulin (ATG) as previously reported (1). HLA, human leukocyte antigen; MMF, mycophenolate mofetil; CMV, cytomegalovirus; EBV, Epstein-Barr virus.

Supplementary Table 2. Histological and clinical characteristics of allograft skin biopsy samples included in the analyses of the study.

Sample No.	Patient	Banff Grade	Immunosuppressive regime at time of biopsy	Treatment of acute rejection
1	Patient 1	2	Tacrolimus, MMF	Tacrolimus dose increased
2	Patient 1	1	Tacrolimus, MMF	None
3	Patient 1	0	Tacrolimus, MMF	NA
4	Patient 1	2	Tacrolimus, MMF	None
5	Patient 2	2	Tacrolimus, MMF	Oral glucocorticoids, anti-thymocyte globulin
6	Patient 2	0	Tacrolimus, MMF	NA
7	Patient 2	2	Tacrolimus, MMF	Oral glucocorticoids
8	Patient 3	2	Tacrolimus, MMF, maintenance glucocorticoid	Glucocorticoid pulse[A], Tacrolimus dose increased
9	Patient 3	1	Tacrolimus, MMF, maintenance glucocorticoid	None
10	Patient 3	0	Tacrolimus, MMF	NA
11	Patient 3	3	Tacrolimus, MMF	Glucocorticoid pulse[A], Tacrolimus and MMF doses increased
12	Patient 3	3	Tacrolimus, MMF	Glucocorticoid pulse[A]
13	Patient 3	0	Tacrolimus, MMF	NA
14	Patient 4	0	Tacrolimus, MMF, maintenance glucocorticoid	NA
15	Patient 4	0	Tacrolimus, MMF, maintenance glucocorticoid	NA
16	Patient 4	1	Tacrolimus, MMF, maintenance glucocorticoid	None
17	Patient 4	0	Tacrolimus, MMF, maintenance glucocorticoid	NA
18	Patient 4	3	Tacrolimus, MMF, maintenance glucocorticoid	Glucocorticoid pulse[A]
19	Patient 4	3	Tacrolimus, MMF, maintenance glucocorticoid	Oral glucocorticoids
20	Patient 4	1	Tacrolimus, MMF, maintenance glucocorticoid	None
21	Patient 4	3	Tacrolimus, MMF, maintenance glucocorticoid	Oral glucocorticoids
22	Patient 4	1	Tacrolimus, MMF, maintenance glucocorticoid	None
23	Patient 4	2	Tacrolimus, MMF, maintenance glucocorticoid	None
24	Patient 5	3	Tacrolimus, MMF	Glucocorticoid pulse[A]
25	Patient 5	3	Tacrolimus, MMF, maintenance glucocorticoid	Glucocorticoid pulse[A]
26	Patient 5	3	Tacrolimus, MMF, maintenance glucocorticoid	Glucocorticoid pulse[A], topical tacrolimus
27	Patient 5	3	Tacrolimus, MMF	Glucocorticoid pulse[A]
28	Patient 5	0	Tacrolimus, MMF	NA
29	Patient 6	3	Tacrolimus, MMF	Glucocorticoid pulse[A]
30	Patient 6	1	Tacrolimus, MMF	None
31	Patient 6	2	Tacrolimus, MMF	Glucocorticoid pulse[A]
32	Patient 6	0	Tacrolimus, MMF	NA
33	Patient 6	3	Tacrolimus, MMF	Glucocorticoid pulse[A]
34	Patient 7	2	Tacrolimus, MMF, maintenance glucocorticoid	Glucocorticoid pulse[A]
35	Patient 7	0	Tacrolimus, MMF	NA

[A] Glucocorticoid pulse treatment consisted of 3 days course of intravenous methylprednisolone.

MMF, mycophenolate mofetil; NA, not applicable.

Supplementary Table 3. List of the 202 significantly differentially expressed genes in Grade 3 biopsies compared to Grade 0 biopsies.

Differentially expressed genes (log2 fold change > 1; adjusted p value < 0.05) in Grade 3 (n = 11) compared to Grade 0 (n = 10) were evaluated by the Wald test, using the *R* package DESeq2-v.1.20.0. P values were adjusted using Benjamini-Hochberg procedure.

Gene Symbol	Log2 Fold Change	Adjusted p value
GZMB	3.408399293	2.44E^{-14}
CXCL10	3.254782936	7.73E^{-09}
CXCL9	3.018622816	1.54E^{-08}
CCL18	2.492905496	1.02E^{-05}
IDO1	2.345913685	4.38E^{-09}
C1QB	2.28873685	8.12E^{-07}
CXCR3	2.257045809	1.42E^{-10}
LAG3	2.229244219	1.24E^{-10}
CXCL11	2.039479683	1.21E^{-05}
IL2RG	2.036657811	3.61E^{-11}
XCL2	2.027650828	5.73E^{-08}
FCGR3A	2.024118189	6.86E^{-08}
ISG15	2.022203685	2.99E^{-06}
CLEC4C	2.005658346	2.42E^{-05}
IRF8	1.995988235	7.12E^{-10}
HLA-DRA	1.969404649	2.23E^{-11}
CD3D	1.938555344	2.29E^{-10}
CTSS	1.894946302	4.84E^{-12}
LTB	1.889930162	3.61E^{-05}
GZMK	1.889537791	2.71E^{-08}
CD2	1.885599484	4.01E^{-08}
CD8A	1.884316831	2.71E^{-08}
GNLY	1.882614297	4.46E^{-05}
C1QA	1.861448083	1.09E^{-07}
CD163	1.857206159	2.17E^{-06}
CD53	1.829408761	1.01E^{-11}
PTPRC	1.823290478	9.13E^{-13}
CCR1	1.817694789	5.10E^{-07}
CCL4	1.799557075	2.11E^{-06}
HLA-DPB1	1.794999976	3.70E^{-14}
SELPLG	1.793854415	9.01E^{-16}
TNFRSF4	1.790937255	1.58E^{-06}
CTLA4	1.78880823	5.18E^{-06}
SH2D1A	1.775909849	3.83E^{-09}
PRF1	1.771469169	9.88E^{-09}
CD3G	1.763318844	4.01E^{-08}
HLA-DOB	1.752992601	1.96E^{-08}
GZMA	1.750937452	2.09E^{-08}
HLA-DPA1	1.749449127	1.01E^{-11}
CCL5	1.742809019	4.08E^{-07}
LY86	1.728837002	7.25E^{-10}
TNFSF13B	1.722516488	6.33E^{-08}
CYBB	1.717387747	3.12E^{-08}
LAMP3	1.716565652	5.24E^{-06}
CD27	1.71537078	1.86E^{-07}
STAT1	1.714005729	2.82E^{-07}
FCGR2A	1.698741423	1.09E^{-09}
LCP1	1.689301726	5.24E^{-11}
CD80	1.686424973	7.56E^{-04}

CCR5	1.68192851	1.98E^{-05}
CD48	1.679219002	1.69E^{-07}
CR1	1.675121323	6.60E^{-05}
HLA-DQA1	1.673744106	1.31E^{-02}
CD83	1.670818169	4.77E^{-07}
CXCR6	1.668507932	1.75E^{-06}
FCER1G	1.662460795	1.89E^{-09}
IL21R	1.66218193	3.24E^{-06}
ITGB2	1.660191473	6.22E^{-10}
IL2RA	1.659106244	1.19E^{-05}
MRC1	1.651088087	1.01E^{-07}
KLRK1	1.646248207	1.01E^{-07}
CD247	1.63887623	2.31E^{-07}
ITGAX	1.627537174	1.27E^{-06}
C3AR1	1.620167907	1.01E^{-07}
TNFRSF9	1.617281196	8.84E^{-06}
CD4	1.610947153	7.85E^{-13}
CLEC7A	1.603891284	9.56E^{-08}
CCR4	1.596704791	6.60E^{-05}
TLR8	1.592851237	2.71E^{-08}
CD209	1.580960996	1.12E^{-05}
BST2	1.576819838	2.05E^{-07}
IL7R	1.565475358	4.23E^{-05}
IFIT2	1.564689645	4.48E^{-05}
HLA-DMB	1.564191477	1.96E^{-08}
TIGIT	1.563162051	3.64E^{-06}
FUT7	1.557799451	3.42E^{-05}
LILRB1	1.553953951	5.86E^{-05}
MARCO	1.553703623	5.31E^{-04}
OAS3	1.546994494	8.30E^{-06}
HLA-DQB1	1.542804204	1.76E^{-02}
C2	1.542693492	4.30E^{-06}
IFI27	1.525854402	6.88E^{-05}
SIGLEC1	1.523424602	1.24E^{-05}
CD1B	1.522087168	5.4E^{-03}
CD3E	1.514546888	1.00E^{-06}
SELL	1.496460311	2.22E^{-05}
LY9	1.492315019	1.53E^{-07}
CCR2	1.488987159	1.94E^{-06}
TARP	1.483563718	1.69E^{-05}
CTSW	1.482246845	7.47E^{-06}
F13A1	1.472671683	9.84E^{-07}
CD96	1.471749044	4.35E^{-07}
CCL13	1.464536682	7.67E^{-04}
MX1	1.46074994	0.000953455
CCL19	1.458698343	0.000602318
ITGAL	1.450189741	2.51E^{-05}
CD38	1.449036275	0.00027041
FCGR2B	1.443028258	1.42E^{-10}
LY96	1.440162539	3.23E^{-08}
CFB	1.436060987	4.58E^{-06}
IFITM1	1.433847803	1.27E^{-06}
HAVCR2	1.429854578	3.16E^{-10}
ICOS	1.424698348	0.000513781
LCK	1.423323638	7.89E^{-08}
CD28	1.422732251	1.01E^{-05}
GZMH	1.42243173	2.22E^{-05}
CCL3L1	1.418558965	0.004708418
LTF	1.41457572	0.005932137
IL10RA	1.408137054	1.01E^{-11}
CCR7	1.407974758	0.00196475
VCAM1	1.400957189	6.67E^{-07}
FOXP3	1.386625115	0.000365591
CD68	1.38359601	4.72E^{-07}
CD5	1.383126435	1.27E^{-06}
KLRC2	1.382087803	0.000825181

HLA-G	1.378184589	7.47E^{-06}
CD74	1.369125345	2.84E^{-06}
SELE	1.358885964	0.00316245
CX3CR1	1.348772914	1.75E^{-05}
PDCD1	1.342678056	0.000779329
CD79A	1.339049379	0.00295576
IRF1	1.32916762	1.75E^{-05}
INPP5D	1.326791502	1.42E^{-10}
C3	1.319632594	2.61E^{-05}
HLA-DMA	1.312347193	3.88E^{-06}
CHIT1	1.307736078	0.022457808
LILRA4	1.307366465	0.008905254
CD86	1.306149567	0.0002268
MSR1	1.295051071	1.19E^{-05}
IL12RB1	1.28710024	0.000325291
IRF7	1.279719469	0.0002268
PDCD1LG2	1.27704318	3.65E^{-06}
CXCL1	1.271792987	0.00884873
SOCS1	1.263138008	5.02E^{-05}
CD274	1.257136507	0.000786564
PIK3CG	1.252822308	3.71E^{-06}
BTLA	1.241711508	0.000868284
LAIR2	1.241691117	0.000872268
AMICA1	1.237415871	8.14E^{-07}
CSF2	1.235232215	0.012196226
TNFSF14	1.233606776	5.77E^{-05}
LTA	1.229292537	0.001841094
JAK3	1.219381406	0.000584673
ITGA4	1.202602679	1.86E^{-05}
ICAM1	1.196994857	8.93E^{-06}
CD84	1.19436403	1.00E^{-08}
CD6	1.178264638	0.000308299
CMKLR1	1.176747021	1.63E^{-06}
LILRB3	1.175980408	0.00249483
CD180	1.174706382	0.005932137
HLA-DRB3	1.17242994	0.001982257
ITK	1.1723483	0.000500812
CD1E	1.168435387	0.017040854
TNF	1.166604013	0.000584673
HCK	1.161271846	2.68E^{-05}
CCL8	1.158072287	0.005584385
CD37	1.157267712	0.00295576
ITGAM	1.152076995	2.05E^{-06}
MICB	1.150563386	1.19E^{-05}
CFP	1.144262312	6.51E^{-05}
STAT4	1.144100101	0.000333008
KIR2DL3	1.143001731	0.006297416
CD97	1.142879019	1.96E^{-08}
TAP1	1.142052487	4.94E^{-06}
PSMB10	1.140090572	1.19E^{-05}
IFIT1	1.132404496	0.007676868
MEFV	1.131552017	0.003799779
CSF3R	1.130203545	6.02E^{-05}
ZAP70	1.126096852	0.000175359
PSMB9	1.118659707	4.48E^{-05}
TNFRSF1B	1.118003216	2.69E^{-07}
SPN	1.110504202	0.000580813
KLRD1	1.10995538	0.001220199
SLC11A1	1.109150197	0.003515892
CLEC5A	1.104395359	0.000756391
CD40	1.103274453	4.80E^{-07}
GZMM	1.102053892	0.003994252
IFIH1	1.096466865	0.000108958
HLA-B	1.093918753	5.47E^{-07}
CD1C	1.093425001	0.01278048
XCR1	1.092025771	0.000858944

BTK	1.088264529	$1.08E^{-05}$
CXCL2	1.086420393	0.040542955
ISG20	1.084887314	0.001771997
IL2RB	1.076363405	0.000175639
CD8B	1.076170759	0.001346439
CD14	1.068924112	0.001763805
NCF4	1.062393035	$6.02E^{-05}$
CCL22	1.060626053	0.022042894
CXCL3	1.058356047	0.034564049
KIR3DL2	1.054927913	0.046551827
TNFRSF11B	1.054912213	0.011076697
TAP2	1.041351946	$5.61E^{-05}$
LYN	1.041200598	0.00013837
PIK3CD	1.039168077	$1.31E^{-05}$
CD33	1.036837165	0.000108958
IRF4	1.034578728	0.001441221
TNFRSF17	1.025477513	0.042732214
HLA-C	1.014680298	$2.68E^{-05}$
KLRB1	1.01282837	0.00128477
PSMB8	1.007799043	$1.43E^{-06}$
TNFSF13	1.007161918	$6.26E^{-03}$

Supplementary Table 4. Ingenuity canonical pathways.

Top 25 Ingenuity canonical pathways overrepresented by the 202 differentially expressed genes in Grade 3 biopsies (n = 11), compared to Grade 0 (n = 10).

Ingenuity Canonical Pathways	-log(p-value)[A]	DEG/Genes Ratio[B]
iCOS-iCOSL Signalling in T Helper Cells	5.79	0.587
Th1 Pathway	5.6	0.5
Allograft Rejection Signalling	5.59	0.667
CTLA4 Signalling in Cytotoxic T Lymphocytes	5.36	0.708
Antigen Presentation Pathway	5.36	0.708
Calcium-induced T Lymphocyte Apoptosis	5.26	0.75
Nur77 Signalling in T Lymphocytes	5.26	0.75
Th1 and Th2 Activation Pathway	4.98	0.45
B Cell Development	4.78	0.737
Autoimmune Thyroid Disease Signalling	4.54	0.667
Th2 Pathway	4.31	0.467
Cdc42 Signalling	4.26	0.594
Graft-versus-Host Disease Signalling	3.91	0.615
Pathogenesis of Multiple Sclerosis	3.85	0.889
Primary Immunodeficiency Signalling	3.63	0.593
OX40 Signalling Pathway	3.54	0.543
Role of NFAT in Regulation of the Immune Response	3.37	0.466
CD28 Signalling in T Helper Cells	2.83	0.46
Crosstalk between Dendritic Cells and Natural Killer Cells	2.54	0.431
T Helper Cell Differentiation	2.42	0.429
Super pathway of Inositol phosphate compounds	2.38	0.588
Communication between Innate and adaptive immune cells	2.3	0.417
Natural killer cell signalling	2.21	0.471
Type I diabetes mellitus signalling	2.09	0.4
Cytotoxic T lymphocyte-mediated apoptosis of target cells	2.01	0.562

[A] Benjamini-Hochberg corrected Fischer’s exact test p values are shown.

[B] Ratio of the differentially expressed genes (DEG) that mapped to the pathway divided by the total number of genes that mapped to the canonical pathway.

Supplementary Table 5. Gene ontology biological process terms.

Top 20 Gene Ontology (GO) biological process terms enriched among the 202 differentially expressed genes in Grade 3 biopsies (n = 11), compared to Grade 0 (n = 10). Fisher's one-tailed test was used and p values were adjusted using Benjamini-Hochberg False Discovery Rate for multiple testing correction.

GO Biological Processes	GO ID	Benjamini's adjusted p-value
Lymphocyte co-stimulation	GO:0031294	$2.26E^{-05}$
T cell co-stimulation	GO:0031295	$2.26E^{-05}$
Immune system process	GO:0022376	$2.75E^{-05}$
Leukocyte activation	GO:0045321	$2.75E^{-05}$
Antigen processing and presentation of exogenous antigen	GO:0019884	$6.02E^{-05}$
Antigen processing and presentation	GO:0019882	$9.42E^{-05}$
T cell activation	GO:0042110	$9.42E^{-05}$
Antigen processing and presentation of peptide antigen	GO:0048002	$1.21E^{-04}$
Cell activation	GO:0001775	$1.31E^{-04}$
Antigen processing and presentation of exogenous peptide antigen	GO:0002478	$1.48E^{-04}$
Immune response	GO:0006955	$1.48E^{-04}$
Lymphocyte activation	GO:0046649	$1.50E^{-04}$
Antigen processing and presentation of exogenous peptide antigen via MHC class II	GO:0019886	$1.56E^{-04}$
Leukocyte cell-cell adhesion	GO:0007159	$1.51E^{-03}$
Antigen processing and presentation of peptide antigen via MHC class II	GO:0002495	$1.84E^{-03}$
Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	GO:0002504	$4.73E^{-03}$
Regulation of lymphocyte activation	GO:0051249	$5.03E^{-03}$
Regulation of immune system process	GO:0002682	$6.94E^{-03}$
Regulation of T cell activation	GO:0050863	$8.42E^{-03}$
Positive regulation of lymphocyte activation	GO:0051251	$8.68E^{-03}$

Supplementary Table 6. Upstream regulators.

The upstream regulators of the 202 differentially expressed genes in Grade 3 biopsies (n = 11), compared to Grade 0 (n = 10).

Cytokine Upstream Regulator	Z-score[A]	P-value of overlap[B]
IFNγ	8.416	$4.82E^{-06}$
TNF	7.701	$3.43E^{-03}$
IL2	6.52	$3.53E^{-05}$
CSF2	6.494	$7.48E^{-03}$
IL18	4.815	$1.95E^{-03}$

[A] Z-score accounts for both the total number of genes differentially expressed and direction of activation; a z-score ≥ 2 (activated) or ≤ –2 (inhibited) was considered significant.

[B] P-value of overlap represents the significance in the overlap between the identified differentially expressed genes (the known downstream targets) and all genes associated with a particular upstream regulator in the Ingenuity database.

Supplementary Table 7. List of the 153 differentially expressed genes in Grade 2 biopsies compared to Grade 0.

Differentially expressed genes (log2 fold change > 1; adjusted p value < 0.05) in Grade 2 biopsies (n = 8) compared to Grade 0 biopsies (n = 10) were evaluated using normalized gene expression counts as input and the Wald significance test. P values were adjusted using Benjamini-Hochberg procedure.

Gene Symbol	Log2 Fold Change	Adjusted p value
FOS	2.455652707	7.71E^{-04}
CXCL9	2.209491481	7.71E^{-04}
CT45A1	2.157359485	1.63E^{-03}
CXCL2	2.102018385	6.36E^{-04}
GZMB	1.90580579	6.36E^{-04}
MARCO	1.884154274	6.36E^{-04}
CXCL3	1.812645106	1.45E^{-03}
LILRB3	1.811202713	1.84E^{-04}
IFNB1	1.785339862	5.98E^{-03}
ICAM4	1.766102906	2.37E^{-03}
C1QB	1.718422306	2.35E^{-03}
CD79A	1.710451026	1.48E^{-03}
LAIR2	1.681420935	3.94E^{-04}
GAGE1	1.664517231	1.04E^{-02}
IL1RAPL2	1.66321669	1.50E^{-03}
FCGR3A	1.66057526	6.18E^{-04}
MS4A1	1.649967192	1.04E^{-02}
CD22	1.631539768	2.03E^{-03}
CD80	1.626937579	5.61E^{-03}
POU2AF1	1.626183328	5.66E^{-03}
CXCL10	1.621822078	1.39E^{-02}
LILRB1	1.620578114	7.71E^{-04}
CCL18	1.605107499	1.49E^{-02}
TNFRSF17	1.601512981	4.17E^{-03}
IL17F	1.598183772	1.23E^{-02}
SSX1	1.591600596	1.02E^{-02}
CXCL1	1.591064335	4.3E^{-03}
MAGEC1	1.590939324	8.79E^{-03}
CD180	1.563168965	1.91E^{-03}
KIR3DL2	1.560513282	6.59E^{-03}
SPO11	1.558902886	1.02E^{-02}
ULBP2	1.558023389	4.66E^{-03}
CXCL5	1.545228313	6.57E^{-03}
CR1	1.542697541	2.37E^{-03}
IL2RA	1.532446671	1.12E^{-03}
IL5	1.529129187	1.58E^{-02}
CYBB	1.526998136	1.84E^{-04}
LILRA4	1.526535338	6.9E^{-03}
CD19	1.500245448	2.37E^{-03}
CCR1	1.496546371	8.89E^{-04}
IFNA1	1.491409698	2.72E^{-02}
CLEC4C	1.490920047	8.2E^{-03}
PRM1	1.489332107	1.43E^{-02}
CEACAM6	1.488984116	8.49E^{-03}
FUT5	1.477350316	1.56E^{-02}

IL27	1.473025646	1.24E^{-02}
CD8A	1.468830529	6.36E^{-04}
LILRA5	1.466766573	5.88E^{-03}
CD163	1.466725971	2.32E^{-03}
CCR9	1.465666559	2.55E^{-02}
TNFSF18	1.460105613	1.98E^{-02}
KLRC2	1.438121863	3.3E^{-03}
MEFV	1.431754279	1.91E^{-03}
IFNA7	1.423307163	2.46E^{-02}
IDO1	1.406481241	3.6E^{-03}
CD209	1.403930476	1.58E^{-03}
CCR3	1.403135774	2.24E^{-02}
LTB	1.401097331	1E^{-02}
TNFRSF11B	1.399140579	3.36E^{-03}
SSX4	1.394206267	3.1E^{-02}
CSF3	1.388628186	1.04E^{-02}
CD38	1.388360374	3.39E^{-03}
FCER1G	1.385139695	1.84E^{-04}
C9	1.382969686	1.5E^{-02}
TLR8	1.382075206	1.84E^{-04}
C3AR1	1.380628137	4.49E^{-04}
CXCR3	1.379340333	1.63E^{-03}
IL12RB1	1.367922752	1.63E^{-03}
CCL15	1.363102103	2.81E^{-02}
SLC11A1	1.359217792	2.37E^{-03}
CCL19	1.354572483	6.59E^{-03}
CCL4	1.34801205	3.38E^{-03}
SELL	1.346057762	1.91E^{-03}
MAGEA12	1.345155145	2.83E^{-02}
CCL26	1.334470142	1.39E^{-02}
CASP10	1.321114673	1.29E^{-02}
SIGLEC1	1.320849018	2.03E^{-03}
CCL1	1.320438647	3.55E^{-02}
IL2	1.317105257	3.31E^{-02}
C1QA	1.316340113	2.32E^{-03}
CCR5	1.304702801	5.88E^{-03}
CXCR1	1.300698461	2.25E^{-02}
CR2	1.299775085	1.48E^{-02}
MAGEA1	1.298780615	3.55E^{-02}
IFNL2	1.298016765	3.59E^{-02}
LY86	1.29698285	3.94E^{-04}
CCR7	1.295105034	1.39E^{-02}
CXCL11	1.290066485	1.95E^{-02}
FCGR1A	1.280094986	8.2E^{-03}
IL21R	1.279215804	3.3E^{-03}
PAX5	1.271600078	1.35E^{-02}
PDCD1	1.26752442	6.7E^{-03}
XCL2	1.267522086	5.12E^{-03}
CLEC7A	1.261274383	8.28E^{-04}
STAT4	1.24688113	1.45E^{-03}
ITGAX	1.24657862	2.37E^{-03}
C2	1.243272902	2.37E^{-03}
IFNA2	1.242444272	2.96E^{-02}
FPR2	1.231563626	1.95E^{-02}
FUT7	1.218619614	6.59E^{-03}
CCR4	1.218142222	1.09E^{-02}
FCGR2A	1.209587947	6.36E^{-04}
CD2	1.208090111	3.95E^{-03}
ISG15	1.204792378	1.95E^{-02}
IL7R	1.195957062	8.81E^{-03}
AMBP	1.191951549	2.7E^{-02}
LILRB2	1.188870695	2.37E^{-03}
TNFSF13	1.182566855	5.67E^{-03}
CD28	1.17434713	2.76E^{-03}
ATG12	1.167495823	1.24E^{-02}

CD8B	1.167180913	3.37E^{-03}
KLRF1	1.162898923	1.59E^{-02}
CD48	1.160687732	3.16E^{-03}
CD68	1.150476142	8.27E^{-04}
CXCR6	1.143874367	6.57E^{-03}
LAG3	1.14311045	6.44E^{-03}
CCL3	1.139613232	3.09E^{-02}
KLRC1	1.136957846	7.68E^{-03}
BLK	1.13400885	2.49E^{-02}
CD53	1.130768599	8.28E^{-04}
CD37	1.128433334	1.24E^{-02}
LTA	1.12791676	1.39E^{-02}
MSR1	1.127121404	2.02E^{-03}
CTSW	1.123315139	5.12E^{-03}
MRC1	1.120686873	3.16E^{-03}
THY1	1.116328967	1.58E^{-02}
HLA-DRB3	1.107855802	1.24E^{-02}
CTSS	1.104773928	1.22E^{-03}
GZMK	1.104413632	6.84E^{-03}
CD27	1.103585969	5.67E^{-03}
CD3D	1.097111551	3.37E^{-03}
IRF8	1.096880792	5.39E^{-03}
TLR10	1.095212797	1.52E^{-02}
ICAM1	1.09516621	1.12E^{-03}
CMKLR1	1.085314698	6.36E^{-04}
BTLA	1.070875022	1.45E^{-02}
TARP	1.062855629	1.04E^{-02}
TNFSF13B	1.059087445	5.95E^{-03}
HLA-DOB	1.056175854	5.28E^{-03}
CD79B	1.053888767	3.33E^{-02}
ITGB2	1.052404892	1.63E^{-03}
C4B	1.048068078	1.5E^{-02}
PRF1	1.04770254	5.22E^{-03}
ITGAL	1.044826263	1.15E^{-02}
F13A1	1.038407237	4.53E^{-03}
KIR2DL3	1.033529359	3.09E^{-02}
CFB	1.024228759	6.59E^{-03}
HLA-DMA	1.022231016	3.3E^{-03}
SH2D1A	1.015544078	5.67E^{-03}
JAK3	1.015065255	1.49E^{-02}
CCL23	1.009173348	3.44E^{-02}
SLAMF6	1.008554831	2.26E^{-02}
FOXJ1	-1.915769459	4.3E^{-03}

Supplementary Table 8. Pattern analysis.

The list of 273 genes that progressively over-expressed as the rejection severity increased from Grade 0 through Grade 3 acute cellular rejection according to the pattern analysis. The pattern analysis is detailed in Methods.

Gene Symbol				
A2M	*CD68*	*GZMH*	*ISG20*	*PTGS2*
ADA	*CD7*	*GZMK*	*ITGA4*	*PTPRC*
AMICA1	*CD74*	*GZMM*	*ITGA5*	*RELB*
ANXA1	*CD80*	*HAVCR2*	*ITGAL*	*RUNX3*
BAX	*CD83*	*HCK*	*ITGAM*	*S100B*
BCL10	*CD84*	*HLA-A*	*ITGAX*	*SBNO2*
BST2	*CD86*	*HLA-B*	*ITGB2*	*SELE*
BTK	*CD8A*	*HLA-C*	*ITK*	*SELL*
BTLA	*CD8B*	*HLA-DMA*	*JAK2*	*SELPLG*
C1QA	*CD96*	*HLA-DMB*	*JAK3*	*SERPING1*
C1QB	*CD97*	*HLA-DOB*	*KIR3DL3*	*SH2D1A*
C1R	*CFB*	*HLA-DPA1*	*KIR2DL3*	*SIGIRR*
C1S	*CFP*	*HLA-DPB1*	*KLRB1*	*SIGLEC1*
C2	*CHIT1*	*HLA-DQB1*	*KLRC2*	*SOCS1*
C3	*CKLF*	*HLA-DRA*	*KLRD1*	*SPN*
C3AR1	*CLEC4C*	*HLA-DRB3*	*KLRK1*	*SPP1*
CARD11	*CLEC7A*	*HLA-E*	*LAG3*	*ST6GAL1*
CASP1	*CMA1*	*HLA-G*	*LAMP3*	*STAT1*
CASP3	*CMKLR1*	*ICAM1*	*LCK*	*STAT2*
CASP8	*CR1*	*ICAM2*	*LCP1*	*STAT4*
CCL13	*CSF1R*	*ICAM3*	*LILRA4*	*SYK*
CCL18	*CSF2RB*	*ICOS*	*LRP1*	*TAP1*
CCL19	*CSF3R*	*IDO1*	*LTA*	*TAP2*
CCL2	*CTLA4*	*IFI16*	*LTB*	*TAPBP*
CCL22	*CTSL*	*IFI27*	*LY86*	*TARP*
CCL4	*CTSS*	*IFI35*	*LY9*	*TICAM2*
CCL5	*CTSW*	*IFIH1*	*LY96*	*TIGIT*
CCL8	*CX3CR1*	*IFIT1*	*LYN*	*TLR1*
CCR1	*CXCL10*	*IFIT2*	*MAP2K1*	*TLR2*
CCR2	*CXCL11*	*IFITM1*	*MFGE8*	*TLR3*
CCR4	*CXCL16*	*IFITM2*	*MICB*	*TLR7*
CCR5	*CXCL9*	*IFNGR1*	*MR1*	*TLR8*
CCR7	*CXCR3*	*IL10RA*	*MRC1*	*TNF*
CD14	*CXCR4*	*IL12RB1*	*MSR1*	*TNFAIP3*
CD163	*CXCR6*	*IL12RB2*	*MX1*	*TNFRSF14*
CD2	*CYBB*	*IL15*	*MYD88*	*TNFRSF1B*
CD209	*CYFIP2*	*IL15RA*	*NCF4*	*TNFRSF4*
CD244	*CYLD*	*IL17RA*	*NCR1*	*TNFRSF9*
CD247	*DDX58*	*IL1RL1*	*NFATC3*	*TNFSF13*
CD27	*ELK1*	*IL21R*	*NLRC5*	*TNFSF13B*
CD274	*ENG*	*IL2RA*	*OAS3*	*TNFSF14*
CD28	*ETS1*	*IL2RB*	*PDCD1*	*TNFSF4*
CD33	*F13A1*	*IL2RG*	*PDCD1LG2*	*TRAF2*
CD37	*FCER1G*	*IL3RA*	*PDGFC*	*TYK2*
CD38	*FCER2*	*IL6R*	*PECAM1*	*VCAM1*
CD3D	*FCGR2A*	*IL6ST*	*PIK3CD*	*XCL2*
CD3E	*FCGR2B*	*IL7R*	*PIK3CG*	*XCR1*
CD3G	*FCGR3A*	*INPP5D*	*PIN1*	*YTHDF2*
CD4	*FLT3*	*IRAK1*	*PLAU*	*ZAP70*
CD40	*FLT3LG*	*IRF1*	*ISG21*	*CNOT10*
CD40LG	*FOXP3*	*IRF2*	*ITGA6*	*NUBP1*

CD48	*FUT7*	*IRF4*	*ITGA7*	*TMUB2*
CD5	*GNLY*	*IRF7*	*ITGAL*	*USP39*
CD53	*GZMA*	*IRF8*	*ITGAM*	
CD6	*GZMB*	*ISG15*	*ITGAX*	

Supplementary Table 9. Top 20 Gene Ontology (GO) biological process terms.

Top 20 Gene Ontology (GO) biological process terms enriched among the 273 genes that progressively over-expressed as the rejection severity increased from Grade 0 through Grade 3 acute cellular rejection. The complete list of 273 genes is shown in Supplementary Table 8. P values were obtained using Fisher's one-tailed test and adjusted using Benjamini-Hochberg False Discovery Rate for multiple testing correction.

GO Biological Processes	GO ID	Benjamini's adjusted p-value
T cell costimulation	GO:0031295	$2.69E^{-06}$
Lymphocyte costimulation	GO:0031294	$1.73E^{-05}$
Immune system process	GO:0002376	$5.59E^{-04}$
Positive regulation of leukocyte cell-cell adhesion	GO:1903039	$6.43E^{-04}$
Leukocyte cell-cell adhesion	GO:0007159	$1.63E^{-03}$
Positive regulation of T cell activation	GO:0050870	$1.95E^{-03}$
Positive regulation of cell-cell adhesion	GO:0022409	$2.55E^{-03}$
Regulation of leukocyte cell-cell adhesion	GO:1903037	$5.42E^{-03}$
Regulation of T cell activation	GO:0050863	$6.15E^{-03}$
Antigen processing and presentation of exogenous peptide antigen	GO:0002478	$6.15E^{-03}$
Antigen processing and presentation of peptide antigen	GO:0048002	$6.37E^{-03}$
Immune response	GO:0006955	$9.07E^{-03}$
Positive regulation of lymphocyte activation	GO:0051251	$9.07E^{-03}$
T cell activation	GO:0042110	$1.58E^{-02}$
Positive regulation of cell activation	GO:0050867	$1.58E^{-02}$
Positive regulation of leukocyte activation	GO:0002696	$1.66E^{-02}$
Cellular response to type I interferon	GO:0071357	$1.67E^{-02}$
Type I interferon signalling pathway	GO: 0060337	$1.67E^{-02}$
Cell-cell adhesion	GO:0098609	$2.13E^{-02}$
Regulation of lymphocyte activation	GO:0051249	$2.13E^{-02}$

Supplementary Table 10. List of 107 genes that were exclusively differentially expressed in Grade 3 biopsies.

List of 107 genes that were exclusively differentially expressed in Grade 3 biopsies (n = 11) but not in Grade 2 (n = 8), when compared to Grade 0 (n = 10).

Gene Symbol
AMICA1
BST2
BTK
C3
CCL13
CCL22
CCL3L1
CCL5
CCL8
CCR2
CD14
CD1B
CD1C
CD1E
CD247
CD274
CD33
CD3E
CD3G
CD4
CD40
CD5
CD6
CD74
CD83
CD84
CD86
CD96
CD97
CFP
CHIT1
CLEC5A
CSF2
CSF3R
CTLA4
CX3CR1
FCGR2B
FOXP3
GNLY
GZMA
GZMH
GZMM
HAVCR2
HCK
HLA-B
HLA-C
HLA-DMB
HLA-DPA1
HLA-DPB1
HLA-DQA1
HLA-DQB1
HLA-DRA
HLA-G
ICOS
IFI27
IFIH1
IFIT1
IFIT2
IFITM1
IL10RA
IL2RB
IL2RG
INPP5D
IRF1
IRF4
IRF7
ISG20
ITGA4
ITGAM
ITK
KLRB1
KLRD1
KLRK1
LAMP3
LCK
LCP1
LTF
LY9
LY96
LYN
MICB
MX1
NCF4
OAS3
PDCD1LG2
PIK3CD
PIK3CG
PSMB10
PSMB8
PSMB9
PTPRC
SELE
SELPLG
SOCS1
SPN
STAT1
TAP1
TAP2
TIGIT
TNF
TNFRSF1B
TNFRSF4
TNFRSF9
TNFSF14
VCAM1
XCR1
ZAP70

Supplementary Table 11. Literature searches for the scoping review.

Details of the literature searches run and imported to Endnote for the scoping review.

Database	Search Terms	Results
PubMed	((("Gene Expression"[Mesh] OR (gene[tiab] AND expression[tiab]) OR biomarkers[MeSH] OR biomarker*[tiab] OR (overexpress*[tiab] AND gene*[tiab]) OR molecular marker*[tiab] OR gene*[tiab] OR signature gene*[tiab]) AND ("Organ Transplantation"[Mesh] OR organ transplant*[tiab] OR allotransplantation[tiab] OR allograft*[tiab] OR intragraft[tiab] OR “solid organ transplant”[tiab]) AND ("Graft Rejection"[Mesh])) AND (rejection[ti] OR (gene*[ti] AND expression[ti]) OR allo*[ti])) AND "Humans"[Mesh]	2340
Web of Science Indexes=SCI-EXPANDED, SSCI, A&HCI, CPCI-S, CPCI-SSH, BKCI-S, BKCI-SSH, ESCI, CCR-EXPANDED, IC Timespan=All years	TS = (“gene expression” OR “biomarker” OR “molecular marker” OR “signature gene” OR “overexpression”) AND TS = (“organ transplantation” OR “organ transplant” OR “allotransplantation” OR allograft* OR intragraft* OR “solid organ transplant”) AND TS = (“Graft rejection” OR “rejection”)	2526
Embase	('gene expression':ti,ab,kw OR 'biological marker':ti,ab,kw OR 'gene overexpression':ti,ab,kw OR 'molecular marker':ti,ab,kw OR 'signature gene':ti,ab,kw) AND ('organ transplantation':ti,ab,kw OR 'allograft':ti,ab,kw OR 'allotransplantation':ti,ab,kw OR 'intragraft':ti,ab,kw OR 'solid organ transplantation':ti,ab,kw OR 'solid organ transplant':ti,ab,kw) AND ('graft rejection':ti,ab,kw OR 'rejection':ti,ab,kw) AND 'human':ti,ab,kw	315
Countway Discovery Medicine-EBSCO	AB (“gene expression” OR “biomarker” OR “molecular marker” OR “signature gene” OR “overexpression”) AND AB (“organ transplantation” OR “organ transplant” OR “allotransplantation” OR allograft* OR intragraft* OR “solid organ transplant”) AND AB (“Graft rejection” OR “rejection”)	1124

Supplementary Table 12. Genes shared with solid organ transplant rejection.

166/202 genes upregulated in face transplant severe Grade 3 acute rejection (when compared to non-rejection biopsies) were shared with genes previously reported to be increased in solid organ transplants (kidney, liver, heart) during acute rejection. Details of the 202 differentially expressed genes are listed in Supplementary Table 3. P values were obtained using the Wald test and adjusted using Benjamini-Hochberg procedure.

Gene Symbol	Log2 fold change (Grade 0 vs. 3 in face transplants)	Adjusted p value (Grade 0 vs. 3 in face transplants)	Literature in Solid Organ Transplant Studies*
GZMB	3.408399293	2.44E^{-14}	Kidney(2-11), Heart(12-15), Liver(16, 17)
CXCL10	3.254782936	7.73E^{-09}	Kidney(10, 18, 19), Heart(15, 20), Liver(21)
CXCL9	3.018622816	1.54E^{-08}	Kidney(10, 19), Kidney and Heart(22),Heart(15, 20), Liver(17, 21)
CCL18	2.492905496	1.02E^{-05}	Kidney and Heart(22), Heart(14)
IDO1	2.345913685	4.38E^{-09}	Kidney(19), Heart(15)
C1QB	2.28873685	8.12E^{-07}	Kidney(23), Heart(15)
CXCR3	2.257045809	1.42E^{-10}	Heart(20)
LAG3	2.229244219	1.24E^{-10}	Kidney(24, 25), Heart(14)
CXCL11	2.039479683	1.21E^{-05}	Kidney(10, 19), Heart(15, 20)
IL2RG	2.036657811	3.61E^{-11}	Heart(15), Liver(26)
XCL2	2.027650828	5.73E^{-08}	Kidney(10)
FCGR3A	2.024118189	6.86E^{-08}	Kidney(23), Heart(15)
ISG15	2.022203685	2.99E^{-06}	Heart(14)
CLEC4C	2.005658346	2.42E^{-05}	Heart(14)
IRF8	1.995988235	7.12E^{-10}	Heart(27)
HLA-DRA	1.969404649	2.23E^{-11}	Kidney and Heart(22), Liver(17, 21)
CD3D	1.938555344	2.29E^{-10}	Kidney(23, 25), Heart(15), Liver(17)
CTSS	1.894946302	4.84E^{-12}	Kidney and Heart(22), Heart(15)
LTB	1.889930162	3.61E^{-05}	Kidney and Heart(22), Heart(14), Liver(17)
GZMK	1.889537791	2.71E^{-08}	Kidney and Heart(22), Heart(14)
CD2	1.885599484	4.01E^{-08}	Kidney(23), Kidney and Heart(22), Heart(14), Liver(17, 21)
CD8A	1.884316831	2.71E^{-08}	Kidney(10, 19, 23-25), Heart(14, 15), Liver(17)
GNLY	1.882614297	4.46E^{-05}	Kidney(28)
C1QA	1.861448083	1.09E^{-07}	Kidney and Heart(22)
CD163	1.857206159	2.17E^{-06}	Kidney(23)
CD53	1.829408761	1.01E^{-11}	Kidney(23), Kidney and Heart(22), Heart(15)
PTPRC	1.823290478	9.13E^{-13}	Kidney and Heart(22), Heart(15)
CCR1	1.817694789	5.10E^{-07}	Kidney(29, 30)
CCL4	1.799557075	2.11E^{-06}	Kidney(10)
HLA-DPB1	1.794999976	3.70E^{-14}	Kidney(10), Heart(14)
SELPLG	1.793854415	9.01E^{-16}	Kidney and Heart(22)
CTLA4	1.78880823	5.18E^{-06}	Kidney(3, 8, 25, 31), Heart(13)
SH2D1A	1.775909849	3.83E^{-09}	Kidney(25)
PRF1	1.771469169	9.88E^{-09}	Kidney(2-4, 7, 9-11, 19), Heart(12, 32)
CD3G	1.763318844	4.01E^{-08}	Liver(17)
GZMA	1.750937452	2.09E^{-08}	Kidney(10, 23), Heart(32, 33), Liver(26)
HLA-DPA1	1.749449127	1.01E^{-11}	Kidney(10), Heart(14)
CCL5	1.742809019	4.08E^{-07}	Kidney(10, 19, 23, 29, 34, 35), Kidney and Heart(22), Heart(15, 20)
TNFSF13B	1.722516488	6.33E^{-08}	Kidney and Heart(22)
CYBB	1.717387747	3.12E^{-08}	Kidney(23)
LAMP3	1.716565652	5.24E^{-06}	Kidney(30), Heart(14)

CD27	1.71537078	1.86E^{-07}	Kidney(23), Heart(14, 36), Liver(17)
STAT1	1.714005729	2.82E^{-07}	Kidney and Heart(22), Heart(15)
FCGR2A	1.698741423	1.09E^{-09}	Kidney(23)
LCP1	1.689301726	5.24E^{-11}	Kidney(23), Kidney and Heart(22), Heart(14, 15)
CD80	1.686424973	0.000756391	Kidney(31), Heart(37)
CCR5	1.68192851	1.98E^{-05}	Kidney(18), Heart(14, 20)
CD48	1.679219002	1.69E^{-07}	Kidney(23), Liver(17)
CR1	1.675121323	6.60E^{-05}	Kidney(25)
HLA-DQA1	1.673744106	0.013162812	Kidney and Heart(22), Heart(14)
CD83	1.670818169	4.77E^{-07}	Liver(21)
CXCR6	1.668507932	1.75E^{-06}	Kidney(25)
FCER1G	1.662460795	1.89E^{-09}	Kidney(23), Kidney and Heart(22), Heart(15), Liver(17)
IL21R	1.66218193	3.24E^{-06}	Kidney(24, 25), Heart(38), Liver(17)
ITGB2	1.660191473	6.22E^{-10}	Kidney(23), Kidney and Heart(22), Heart(15, 27)
IL2RA	1.659106244	1.19E^{-05}	Kidney(8)
MRC1	1.651088087	1.01E^{-07}	Kidney(23)
KLRK1	1.646248207	1.01E^{-07}	Kidney(10, 39)
CD247	1.63887623	2.31E^{-07}	Kidney and Heart(22)
C3AR1	1.620167907	1.01E^{-07}	Heart(15)
TNFRSF9	1.617281196	8.84E^{-06}	Kidney(19)
CD4	1.610947153	7.85E^{-13}	Heart(14)
CLEC7A	1.603891284	9.56E^{-08}	Kidney(19)
CCR4	1.596704791	6.60E^{-05}	Kidney(23)
TLR8	1.592851237	2.71E^{-08}	Kidney(40, 41)
CD209	1.580960996	1.12E^{-05}	Kidney(30)
BST2	1.576819838	2.05E^{-07}	Kidney and Heart(22)
IL7R	1.565475358	4.23E^{-05}	Kidney(23)
HLA-DMB	1.564191477	1.96E^{-08}	Kidney(19), Kidney and Heart(22)
TIGIT	1.563162051	3.64E^{-06}	Kidney(19, 24, 25)
LILRB1	1.553953951	5.86E^{-05}	Kidney(10)
MARCO	1.553703623	0.00053121	Kidney(42)
HLA-DQB1	1.542804204	0.017649896	Kidney(10), Kidney and Heart(22), Liver(21)
C2	1.542693492	4.30E^{-06}	Kidney(41)
IFI27	1.525854402	6.88E^{-05}	Heart(14)
SIGLEC1	1.523424602	1.24E^{-05}	Kidney(43)
CD3E	1.514546888	1.00E^{-06}	Kidney(23)
SELL	1.496460311	2.22E^{-05}	Kidney and Heart(22), Liver(26)
CCR2	1.488987159	1.94E^{-06}	Liver(17)
TARP	1.483563718	1.69E^{-05}	Heart(44)
CD96	1.471749044	4.35E^{-07}	Kidney(24, 25)
CCL13	1.464536682	0.000766965	Heart(14)
MX1	1.46074994	0.000953455	Kidney and Heart(22)
CCL19	1.458698343	0.000602318	Kidney(19), Kidney and Heart(22), Liver(17)
ITGAL	1.450189741	2.51E^{-05}	Heart(44)
CD38	1.449036275	0.00027041	Heart(14), Liver(21)
FCGR2B	1.443028258	1.42E^{-10}	Heart(14)
LY96	1.440162539	3.23E^{-08}	Kidney(23), Kidney and Heart(22)
CFB	1.436060987	4.58E^{-06}	Heart(45)
IFITM1	1.433847803	1.27E^{-06}	Kidney(23)
HAVCR2	1.429854578	3.16E^{-10}	Kidney(46)
ICOS	1.424698348	0.000513781	Kidney(25, 31)
LCK	1.423323638	7.89E^{-08}	Kidney(23), Kidney and Heart(22), Liver(17)
CD28	1.422732251	1.01E^{-05}	Kidney(24, 25, 31)
GZMH	1.42243173	2.22E^{-05}	Heart(14)
LTF	1.41457572	0.005932137	Kidney(23)
IL10RA	1.408137054	1.01E^{-11}	Heart(14)
CCR7	1.407974758	0.00196475	Heart(14)
VCAM1	1.400957189	6.67E^{-07}	Heart(47), Liver(26)
FOXP3	1.386625115	0.000365591	Kidney(8, 9, 30, 48-50), Heart(51)
CD68	1.38359601	4.72E^{-07}	Heart(15)
KLRC2	1.382087803	0.000825181	Heart(44)
HLA-G	1.378184589	7.47E^{-06}	Kidney and Heart(22)
CD74	1.369125345	2.84E^{-06}	Kidney and Heart(22), Heart(14, 15)

SELE	1.358885964	0.00316245	Liver(26)
CX3CR1	1.348772914	1.75E^{-05}	Kidney(52)
PDCD1	1.342678056	0.000779329	Kidney(31)
IRF1	1.32916762	1.75E^{-05}	Kidney(10, 19), Kidney and Heart(22)
INPP5D	1.326791502	1.42E^{-10}	Kidney and Heart(22), Heart(14)
C3	1.319632594	2.61E^{-05}	Kidney(30, 31, 53, 54), Heart(45)
HLA-DMA	1.312347193	3.88E^{-06}	Kidney and Heart(22), Liver(21)
CHIT1	1.307736078	0.022457808	Kidney(42)
CD86	1.306149567	0.0002268	Kidney(25, 31), Heart(37)
IL12RB1	1.28710024	0.000325291	Kidney(24, 25)
IRF7	1.279719469	0.0002268	Kidney and Heart(22), Liver(55)
PDCD1LG2	1.27704318	3.65E^{-06}	Kidney(25), Heart(44)
CXCL1	1.271792987	0.00884873	Kidney(56)
CD274	1.257136507	0.000786564	Kidney(25)
BTLA	1.241711508	0.000868284	Kidney(24, 25)
LAIR2	1.241691117	0.000872268	Heart(44)
AMICA1	1.237415871	8.14E^{-07}	Liver(17)
CSF2	1.235232215	0.012196226	Kidney(30)
TNFSF14	1.233606776	5.77E^{-05}	Heart(14)
LTA	1.229292537	0.001841094	Kidney(30)
JAK3	1.219381406	0.000584673	Kidney(43)
ITGA4	1.202602679	1.86E^{-05}	Liver(26)
ICAM1	1.196994857	8.93E^{-06}	Kidney(18), Heart(14, 47)
CD84	1.19436403	1.00E^{-08}	Kidney(25)
CD6	1.178264638	0.000308299	Kidney and Heart(22), Heart(44)
LILRB3	1.175980408	0.00249483	Heart(14)
HLA-DRB3	1.17242994	0.001982257	Kidney and Heart(22)
ITK	1.1723483	0.000500812	Kidney(25), Heart(44)
TNF	1.166604013	0.000584673	Kidney(18, 57, 58), Heart(13)
HCK	1.161271846	2.68E^{-05}	Kidney(43)
CCL8	1.158072287	0.005584385	Heart(27)
CD37	1.157267712	0.00295576	Kidney(23)
ITGAM	1.152076995	2.05E^{-06}	Heart(14)
MICB	1.150563386	1.19E^{-05}	Kidney(23)
CFP	1.144262312	6.51E^{-05}	Kidney and Heart(22)
TAP1	1.142052487	4.94E^{-06}	Kidney(10, 19, 25), Kidney and Heart(22), Heart(14, 15), Liver(21)
PSMB10	1.140090572	1.19E^{-05}	Kidney and Heart(22), Heart(44)
ZAP70	1.126096852	0.000175359	Kidney and Heart(22), Heart(14)
PSMB9	1.118659707	4.48E^{-05}	Kidney(10, 19), Kidney and Heart(22)
TNFRSF1B	1.118003216	2.69E^{-07}	Kidney(23)
KLRD1	1.10995538	0.001220199	Kidney(10)
CLEC5A	1.104395359	0.000756391	Kidney and Heart(22)
CD40	1.103274453	4.80E^{-07}	Kidney(31), Heart(14, 37)
GZMM	1.102053892	0.003994252	Heart(14)
IFIH1	1.096466865	0.000108958	Heart(14)
HLA-B	1.093918753	5.47E^{-07}	Kidney and Heart(22), Heart(14)
XCR1	1.092025771	0.000858944	Kidney and Heart(22)
CXCL2	1.086420393	0.040542955	Kidney(59)
ISG20	1.084887314	0.001771997	Kidney(10), Kidney and Heart(22)
IL2RB	1.076363405	0.000175639	Kidney and Heart(22), Heart(15), Liver(26)
CD8B	1.076170759	0.001346439	Kidney(25), Heart(14), Liver(17)
CD14	1.068924112	0.001763805	Kidney(23), Kidney and Heart(22), Heart(15)
NCF4	1.062393035	6.02E^{-05}	Kidney(42)
CCL22	1.060626053	0.022042894	Kidney(60)
TAP2	1.041351946	5.61E^{-05}	Kidney(10)
LYN	1.041200598	0.00013837	Heart(15)
PIK3CD	1.039168077	1.31E^{-05}	Kidney and Heart(22)
CD33	1.036837165	0.000108958	Heart(14)
TNFRSF17	1.025477513	0.042732214	Kidney(42), Heart(14)
HLA-C	1.014680298	2.68E^{-05}	Heart(14)
KLRB1	1.01282837	0.00128477	Kidney(43)
PSMB8	1.007799043	1.43E^{-06}	Kidney(19), Heart(15)

*For each gene, the table provides the literature references where the gene is shown to be upregulated in human solid organ transplant biopsies during acute rejection compared to the biopsies collected during non-rejection.

Supplementary Table 13. Genes unique to face transplant rejection.

36/202 genes upregulated in face transplant severe Grade 3 rejection (n = 11) (compared to non-rejection biopsies, Grade 0; n=10) were unique to face transplant rejection. Details of the 202 differentially expressed genes are listed in Supplementary Table 3. P values were obtained using the Wald test and adjusted using Benjamini-Hochberg procedure.

Gene Symbol	Log2 fold change (Grade 0 vs. 3 in face transplants)	Adjusted p value (Grade 0 vs. 3 in face transplants)	Functional Annotation
FUT7	1.557799451	$3.42E^{-05}$	Skin homing
HLA-DOB	1.752992601	$1.96E^{-08}$	Immunoregulation
LY9	1.492315019	$1.53E^{-07}$	Immunoregulation
LILRA4	1.307366465	$8.9E^{-03}$	Immunoregulation
MEFV	1.131552017	$3.8E^{-03}$	Immunoregulation
SOCS1	1.263138008	$5.02E^{-05}$	Immunoregulation
TNFRSF11B	1.054912213	$1.1E^{-02}$	Immunoregulation
LY86	1.728837002	$7.25E^{-10}$	Immunoregulation
CD180	1.174706382	$5.93E^{-03}$	Immunoregulation
KIR3DL2	1.054927913	$4.66E^{-02}$	Immunoregulation
KIR2DL3	1.143001731	$6.3E^{-03}$	Immunoregulation
MSR1	1.295051071	$1.19E^{-05}$	APC and innate cell adhesion
ITGAX	1.627537174	$1.27E^{-06}$	APC and innate cell adhesion
CD97	1.142879019	$1.96E^{-08}$	APC and innate cell adhesion
F13A1	1.472671683	$9.84E^{-07}$	APC and innate cell adhesion
IRF4	1.034578728	$1.44E^{-03}$	Type I interferon signaling
OAS3	1.546994494	$8.30E^{-06}$	Type I interferon signaling
IFIT1	1.132404496	$7.68E^{-03}$	Type I interferon signaling
IFIT2	1.564689645	$4.48E^{-05}$	Type I interferon signaling
CD5	1.383126435	$1.27E^{-06}$	Co-stimulation
TNFRSF4	1.790937255	$1.58E^{-06}$	Co-stimulation
SPN	1.110504202	$5.8E^{-04}$	Co-stimulation
CD1B	1.522087168	$5.4E^{-03}$	Lipid presentation
CD1E	1.168435387	$1.7E^{-02}$	Lipid presentation
CD1C	1.093425001	$1.28E^{-02}$	Lipid presentation
CD79A	1.339049379	$2.96E^{-03}$	B cell related
TNFSF13	1.007161918	$6.26E^{-03}$	B cell related
BTK	1.088264529	$1.08E^{-05}$	B cell related
CXCL3	1.058356047	$3.46E^{-02}$	Chemokines and receptors
CCL3L1	1.418558965	$4.7E^{-03}$	Chemokines and receptors
CMKLR1	1.176747021	$1.63E^{-06}$	Chemokines and receptors
PIK3CG	1.252822308	$3.71E^{-06}$	Other
CSF3R	1.130203545	$6.02E^{-05}$	Other
SLC11A1	1.109150197	$3.51E^{-03}$	Other
STAT4	1.144100101	$3.33E^{-04}$	Other
CTSW	1.482246845	$7.47E^{-06}$	Other

Supplementary Table 14. CDR3 sequences predicted to bind CD1b or CD1c by the GLIPH algorithm.

CD1b-associated sequences			CD1c-associated sequences
CASSRSSDRANNQPQHF	CASSVLDSLHNEQFF	CASKRRGVRKTYGYTF	CASSLVPTGELFF
CASSQDNTGGASYEQYF	CASSRRSHFVLDEQYF	CASIRNLPGKTYGYTF	CASSLGGGPTGELFF
CASSFTSGRLLNTGELFF	CASSRKFVLDEQYF	CASGSTRAARLVGDSRKTYGYTF	CASSAPTGETQYF
CASRDGLAGGFKQETQYF	CASSQHCVLDEQYF	CASAPIYPRKTYGYTF	CASSPKTGRVIIPEAFF
CSVSQGLAYKSRANVLTF	CASSQGPLNTGELFF	CSVSQGLAYKSRANVLTF	CASSAGSLPHQPQHF
CSASKITSGVQETQYF	CASSQGPFKAYNSPLHF	CSASKITSGVQETQYF	CSAREHTGHQPQHF
CSARLLEREQFF	CASSQESASGNLNTGELFF	CSARLLEREQFF	CASSSAGHQPQHF
CSARLLDFEAFF	CASSQDRLLAQHSPLHF	CSARLLDFEAFF	CASSQERKETYEQYF
CGRQRKITQSRANVLTF	CASSFVLDEQYF	CGRQRKITQSRANVLTF	CASSQSRGWADTQYF
CAWSVLDREAEQYF	CASRNRVLHVLDEQYF	CAWSVLDREAEQYF	CASRTIARKRYEQYF
CATSRKGYNSPLHF	CASIKGGLNTGELFF	CAVRNTGGFKTIF	CASKSRLENTEAFF
CASSYRFIPYYGYTF	CASSSAGHQPQHF	CATSRKGYNSPLHF	CTSSEHCLCTSRANVLTF
CASSVNVATVMQDTQYF	CASSQERKETYEQYF	CASSYRFIPYYGYTF	CTSRLCSCAQSRANVLTF
CASSVLDSLHNEQFF	CASSQSRGWADTQYF	CASSVNVATVMQDTQYF	CTSRIRGLCTSRANVLTF
CASSVDLTRKTYGYTF	CASRTIARKRYEQYF	CASSVLDSLHNEQFF	CSVQGQLAYKGRANVLTF
CASSSKRSRKTYGYTF	CASKSRLENTEAFF	CASSVDLTRKTYGYTF	CSAHHGGNTIYF
CASSSAGTGGFMNTEAFF	CTSSEHCLCTSRANVLTF	CASSSKRSRKTYGYTF	CGNYFKITQSRANVLTF
CASSRYDSASQSRANVLTF	CTSRQVCLRKTYGYTF	CASSSAGTGGFMNTEAFF	CAWSLQCYRKTYGYTF
CASSRTGGGGYTF	CTSRLLRLWRKTYGYTF	CASSRYDSASQSRANVLTF	CAWLSRVIQSRANVLTF
CASSRSRYHDKGRANVLTF	CTSRLCSCAQSRANVLTF	CASSRTGGGGYTF	CATSSNIGCGKTYGYTF
CASSRRSPFVMQDTQYF	CTSRIRGLCTSRANVLTF	CASSRSSDRANNQPQHF	CATSGRNSQSRANVLTF
CASSRRSHFVLDEQYF	CSVQGQLAYKGRANVLTF	CASSRSRYHDKGRANVLTF	CASSYIIPICMQDTQYF
CASSRRLATWHHQPQHF	CGSALRIRKTYGYTF	CASSRRSPFVMQDTQYF	CASSYFWHHQPQHF
CASSRRGPFVMQDTQYF	CGNYFKITQSRANVLTF	CASSRRSHFVLDEQYF	CASSVIMRKTYGYTF
CASSRQPPICKRKNIQYF	CAWSLQCYRKTYGYTF	CASSRRGPFVMQDTQYF	CASSVGNPIFMQDTQYF
CASSRNVPILQRKNIQYF	CAWLSRVIQSRANVLTF	CASSRQPPICKRKNIQYF	CASSVDTGRKTQYF
CASSRKFVLDEQYF	CATSSNIGCGKTYGYTF	CASSRNVPILQRKNIQYF	CASSVCAPFIHHNSPLHF
CASSQKIATHARNTIYF	CATSGRNSQSRANVLTF	CASSRKFVLDEQYF	CASSTWVISQSRANVLTF
CASSQHCVLDEQYF	CATSDFRGYNEQFF	CASSQKIATHARNTIYF	CASSTPLPFVMQDTQYF
CASSQGPLNTGELFF	CATSDFLAGDTGELFF	CASSQHCVLDEQYF	CASSTKGPIFDHQPQHF
CASSQGPFKAYNSPLHF	CASSYIIPICMQDTQYF	CASSQGPLNTGELFF	CASSTHAWHRQSRANVLTF
CASSQGIALRKTYGYTF	CASSYGRPHGKTYGYTF	CASSQGPFKAYNSPLHF	CASSSVIPHGKTYGYTF
CASSQGGGTYEQYF	CASSVIMRKTYGYTF	CASSQGIALRKTYGYTF	CASSSSFPIFWHHQPQHF
CASSQESASGNLNTGELFF	CASSVGVGFKRGSDNEKLFF	CASSQGGGTYEQYF	CASSSRVTGRQSRANVLTF
CASSQDRLLAQHSPLHF	CASSVGNPIFMQDTQYF	CASSQESASGNLNTGELFF	CASSSPAKCHKSGQRPDF
CASSQAGVFIHEQFF	CASSVFFPICMQDTQYF	CASSQDRLLAQHSPLHF	CASSSNITRKTYGYTF
CASSPYCYRIQSRANVLTF	CASSVDTGRKTQYF	CASSQDNTGGASYEQYF	CASSSMLQNRKTYGYTF
CASSPLAPIQRKNIQYF	CASSTWVISQSRANVLTF	CASSQAGVFIHEQFF	CASSSFLLHWHHQPQHF
CASSPFLLHHSDNEQFF	CASSTVCPIVMQDTQYF	CASSPYCYRIQSRANVLTF	CASSRRGKTYGYTF
CASSNTGGWGYTF	CASSTPLPFVMQDTQYF	CASSPLAPIQRKNIQYF	CASSRQSPIVMQDTQYF

CASSNTGGGGYTF
CASSNTGGADYGYTF
CASSNIPPIVMQDTQYF
CASSNALRTGKTYGYTF
CASSMQGINGELFF
CASSLPVPMQDTQYF
CASSLGSRSRKIYGYTF
CASSLFRTLRKIYGYTF
CASSLEDPFVMQDTQYF
CASSLDRANTIYF
CASSLAVSGFKNIQYF
CASSKYCPMQRKNIQYF
CASSKRSHEGKIYGYTF
CASSKRPGSRKTYGYTF
CASSKMRPFVMQDTQYF
CASSKCVPICMQDTQYF
CASSIWLQQSRANVLTF
CASSHNHHRQSRANVLTF
CASSHCDPARKTYGYTF
CASSGVLPFVMQDTQYF
CASSGSSKLQSRANVLTF
CASSGSKANRKTYGYTF
CASSGRNHFIHHNSPLHF
CASSFWVRIGKTYGYTF
CASSFVLDEQYF
CASSFSVPMQDTQYF
CASSFKGASGANVLTF
CASSFIIPFVMQDTQYF
CASSFIFFRVFSGNTIYF
CASSEINPIIHHNSPLHF
CASSEFKGTVSNQPQHF
CASSDMFPWHHQPQHF
CASSCTGDIYQSRANVLTF
CASSASQASRKTYGYTF
CASSALLVMQDTQYF
CASRVQIATIHHNSPLHF
CASRTLWQHNSPLHF
CASRTGLATHTHNSPLHF
CASRNRVLHVLDEQYF
CASRLFIATRCNEKLFF
CASRKSGAPRKTYGYTF
CASRIDLAQSRANVLTF
CASRFTSRTGKTYGYTF
CASRAPLATQRKNIQYF
CASSTKGPIFDHQPQHF
CASSTHAWHRQSRANVLTF
CASSSVIPHGKTYGYTF
CASSSRVTGRQSRANVLTF
CASSSPAKCHKSGQRPDF
CASSSNITRKTYGYTF
CASSSMLQNRKTYGYTF
CASSSFAQNRKTYGYTF
CASSRRVPMRKTYGYTF
CASSRRLATWHHQPQHF
CASSRRGKTYGYTF
CASSRQSPIVMQDTQYF
CASSRLVRSRKIYGYTF
CASSRHISRKTYGYTF
CASSQHHQPQHF
CASSPGFKGKTYGYTF
CASSPFNPMRKTYGYTF
CASSPCATVMQDTQYF
CASSNRVATPIRTEAFF
CASSNMSIVRKTYGYTF
CASSLRFSMRKAYGYTF
CASSLIDPICMQDTQYF
CASSLHSPFVMQDTQYF
CASSLGVQNRKTYGYTF
CASSLERTQQSRANVLTF
CASSLCNESRKTYGYTF
CASSLCKRSHKSRANVLTF
CASSKTGFKNIQYF
CASSKMIHFHSDNEQFF
CASSGPLRSHKSRANVLTF
CASSGGGPICHEDTQYF
CASSGFISRQSRANVLTF
CASSGEVPIKNIQYF
CASSGCSPISIHTEAFF
CASSGCEGSRKTYGYTF
CASSFKLTLRKAYGYTF
CASSEYLYPQSRANVLTF
CASSEHPQSRANVLTF
CASSEGSPIYARNTIYF
CASSDVGPISSDNEQFF
CASSDRQANRKTYGYTF
CASSDFGGSSYEQYF
CASSATDPIVMQDTQYF
CASSAPATSNKSRANVLTF
CASSPFLLHHSDNEQFF
CASSNTGGWGYTF
CASSNTGGGGYTF
CASSNTGGADYGYTF
CASSNIPPIVMQDTQYF
CASSNALRTGKTYGYTF
CASSMQGINGELFF
CASSLPVPMQDTQYF
CASSLGSRSRKIYGYTF
CASSLFRTLRKIYGYTF
CASSLEDPFVMQDTQYF
CASSLDRANTIYF
CASSLAVSGFKNIQYF
CASSKYCPMQRKNIQYF
CASSKRSHEGKIYGYTF
CASSKRPGSRKTYGYTF
CASSKMRPFVMQDTQYF
CASSKCVPICMQDTQYF
CASSIWLQQSRANVLTF
CASSHNHHRQSRANVLTF
CASSHCDPARKTYGYTF
CASSGVLPFVMQDTQYF
CASSGSSKLQSRANVLTF
CASSGSKANRKTYGYTF
CASSGRNHFIHHNSPLHF
CASSFWVRIGKTYGYTF
CASSFVLDEQYF
CASSFTSGRLLNTGELFF
CASSFSVPMQDTQYF
CASSFKGASGANVLTF
CASSFIIPFVMQDTQYF
CASSFIFFRVFSGNTIYF
CASSEINPIIHHNSPLHF
CASSEFKGTVSNQPQHF
CASSDMFPWHHQPQHF
CASSCTGDIYQSRANVLTF
CASSASQASRKTYGYTF
CASSALLVMQDTQYF
CASRVQIATIHHNSPLHF
CASRTLWQHNSPLHF
CASRTGLATHTHNSPLHF
CASRNRVLHVLDEQYF
CASRLFIATRCNEKLFF
CASRKSGAPRKTYGYTF
CASSRLVRSRKIYGYTF
CASSRHISRKTYGYTF
CASSQHHQPQHF
CASSPFNPMRKTYGYTF
CASSPCATVMQDTQYF
CASSNRVATPIRTEAFF
CASSNMSIVRKTYGYTF
CASSLRFSMRKAYGYTF
CASSLIDPICMQDTQYF
CASSLERTQQSRANVLTF
CASSLCNESRKTYGYTF
CASSLCKRSHKSRANVLTF
CASSKMIHFHSDNEQFF
CASSKLHHSDNEQFF
CASSGVRPIFGNHQPQHF
CASSGPLRSHKSRANVLTF
CASSGGGPICHEDTQYF
CASSGFISRQSRANVLTF
CASSGEVPIKNIQYF
CASSGCSPISIHTEAFF
CASSGCEGSRKTYGYTF
CASSFKLTLRKAYGYTF
CASSFCSPIFWHHQPQHF
CASSEYLYPQSRANVLTF
CASSESHRHHQPQHF
CASSEHPQSRANVLTF
CASSEGSPIYARNTIYF
CASSDVGPISSDNEQFF
CASSDRQANRKTYGYTF
CASSATDPIVMQDTQYF
CASSAPATSNKSRANVLTF
CASRVCVTTQSRANVLTF
CASRTRLATHSDNEQFF
CASRLKVATWHHQPQHF
CASRIHGVQSRANVLTF
CASRGVLATLAHQPQHF
CASRGSVLHHSDNEQFF
CASRFRVATLHHQPQHF
CASRAPRKTYGYTF
CASPSHVSRKIYGYTF
CASKVRKTYGYTF
CASKRRGVRKTYGYTF
CASIRNLPGKTYGYTF
CASGSTRAARLVGDSRKTYGYTF

CASKGNGEYTSRANVLTF
CASIKGGLNTGELFF
CASGGLAAGQSRANVLTF
CASFGRHSRKTYGYTF
CASALFIPGKTYGYTF
CARQSPMVRKTYGYTF
CAIVMQDTQYF
CASSFTSGRLLNTGELFF
CSARLLEREQFF
CSARLLDFEAFF
CAWSVLDREAEQYF
CASSAFSPFVMQDTQYF
CASRVCVTTQSRANVLTF
CASRTRLATHSDNEQFF
CASRNKLATVMQDTQYF
CASRLKVATWHHQPQHF
CASRIHGVQSRANVLTF
CASRGVLATLAHQPQHF
CASRGSVLHHSDNEQFF
CASRAPRKTYGYTF
CASPSHVSRKIYGYTF
CASKVRKTYGYTF
CASRIDLAQSRANVLTF
CASRFTSRTGKTYGYTF
CASRDGLAGGFKQETQYF
CASRAPLATQRKNIQYF
CASKGNGEYTSRANVLTF
CASIKGGLNTGELFF
CASGGLAAGQSRANVLTF
CASFGRHSRKTYGYTF
CASALFIPGKTYGYTF
CARQSPMVRKTYGYTF
CAIVMQDTQYF
CASAPIYPRKTYGYTF
CASSLVPTGELFF
CASSLGGGPTGELFF
CASSAPTGETQYF

Supplementary Table 15: Antibodies used for immunostaining.

Target	Isotype	Clone	Manufacturer (Cat #)	Concentration
CD3	mIgG2b	C3e/1308	Novus (NBP2-53387)	1:100
CD3	rbIgG	polyclonal	Dako (A0452),	1:150
Ki-67	rbIgG	sp6	Abcam (ab16667)	1:1000
Granzyme	ratIgG2a	496B	ThermoFisher (14-8889-82)	1:200
Granzyme	rbIgG	polyclonal	Abcam (ab53097)	1:300
Perforin	mIgG1	5B10	ThermoFisher (MA5-12469)	1:100
CD107a	mIgG1	H4A3	BioLegend (328602)	1:100
CD107a	rbIgG	D2D11	Cell Signaling (9091)	1:200
CD40L	rbIgG	D5J9Y	Cell Signaling (54535),	1:50
CD56	mIgG1	BC56C04	Biocare Medical (CM164A)	1:100
Caspase8/p43/p18	mIgG2b	2B9H8	ThermoFisher (66093-1-IG)	1:100
FOXP3	mIgG1	206D	Biolegend (320102)	1:100
Mouse IgG2a	Goat IgG	polyclonal	Invitrogen (A21135)	1:1000
Mouse IgG2a	Goat IgG	polyclonal	Invitrogen (A21241)	1:1000
Mouse IgG2b	Goat IgG	polyclonal	Invitrogen (A21147)	1:1000
Mouse IgG1	Goat IgG	polyclonal	Invitrogen (A21121)	1:1000
Rabbit IgG	Goat IgG	polyclonal	Invitrogen (A32731)	1:1000
Rabbit IgG	Goat IgG	polyclonal	Invitrogen (A21429)	1:1000
Rabbit IgG	Goat IgG	polyclonal	Invitrogen (A32733)	1:1000
Rabbit IgG	Goat IgG	polyclonal	Invitrogen (B2770)	1:1000
Biotin	Streptavidin	n/a	ThermoFisher (S21381)	1:1000

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