

Contents

Supplemental Methods	1
Supplemental Table 1: Antibodies for frozen PBMC flow panels	3
Supplemental Table 2: Immunohistochemistry reagents and procedures.....	4
Supplemental Table 3: Patient characteristics at baseline.....	5
Supplemental Table 4: Details for patients that failed IS withdrawal.....	5
Supplemental Table 5: Results of frozen, batched, flow cytometry.....	6
Supplemental Table 6: Blood probesets distinguishing participants at baseline (p<0.005)	7
Supplementary Table 7: Differential liver tissue gene expression between TOL and Non-TOL recipients at baseline	11
Supplemental Table 8: p values and n values for quantitative immunohistochemistry staining..	16

Supplemental Methods

Frozen PBMC Immunophenotyping

Frozen cells were thawed and re-suspended in R10 containing benzonase nuclease (Novagen, Madison, WI). $1.5-2 \times 10^6$ cells/well were plated in 96 well U bottom plates before being washed and re-suspended in Live/Dead Blue stain for 30 min at room temperature. After wash, non-specific receptor staining was blocked with Human TruStain FcX (Biolegend) before re-suspension in antibody cocktails (in BV Stain Buffer Plus, BD) for 30 min at room temperature in the dark. Cells were washed and permeabilized (Foxp3 Fix/Perm Buffer, eBioscience, San Diego, CA). After wash and Fc block, cells were incubated with intracellular antibody cocktails for 45 min at room temperature. Cells were washed, re-suspended in PBS + 1% FBS, stored at 2-8°C, and protected from light until analysis.

During analysis, the DIVA Application Settings feature was used to set voltages, which were then verified with Spherotech Mid-Range Beads. Compensations tubes were acquired with each run.

Liver Graft Gene Expression Profiling

A 1 cm liver biopsy core was placed in RNAlater for gene expression profiling. Liver tissue samples were homogenized in TRIzol reagent (Invitrogen) using a pestle and nuclease-free 1.5-ml reaction tubes (Ambion). Total RNA was extracted following the manufacturers guidelines, and quality was assessed with the Agilent2100 Bioanalyzer (Agilent Technologies).

The statistical significance of pre-defined sets of genes representing biological pathways on the whole transcriptional dataset, was computed employing *Gene Set Enrichment Analysis* (GSEA; <http://software.broadinstitute.org/gsea/index.jsp>), using the *Kyoto Encyclopedia of Genes and Genomes* (KEGG) and *REACTOME* pathway database, and the transplantation-related *Pathogenesis-Based Transcript* (PBT) gene sets from the Alberta Transplant Applied Genomics Centre (ATAGC; <http://atagc.med.ualberta.ca/Research/GeneLists>). For GSEA analysis the threshold of statistical significance was set at $FDR < 0.10$.

Immunohistochemical Biopsy Staining

Batched slide sets were multiplex-stained at room temperature on a Ventana Discovery ULTRA, followed by nuclear counterstaining with DAPI (Fisher, 62248), as per manufacturer's instructions. A Zeiss AxioScan Z.1 (Carl Zeiss, Jena, Germany) Whole Slide Imaging system was setup using a 20x/0.8NA objective, cooled 16-bit sCMOS camera (Hamamatsu Photonics, Hamamatsu City, Japan), and HXP-120V metal halide excitation source for creation of the multiplex WSI. Filter sets appropriately matched each fluorophore to maximize the emission spectra signal to noise ratio (Semrock, Rochester, NY; Chroma, Bellows Falls, VT). All WSIs were checked for image quality and optimized staining; suboptimal areas were discarded. Fully automated tissue-tethered cytometry was then performed using internally developed image analysis software (NearCYTE; <http://nearcyte.org>) that co-localizes multiple analytes via a defined nuclear marker and parametric segmentation.

Analyte expression patterns were defined via morphological parameters, such as staining intensity, area of nucleus covered by transcription factors, circumferential expansion of the

segmented nuclear edges to define cytoplasmic areas, and threshold of signal expression per area (nuclear versus cytoplasmic) needed to define “positive” cell labeling. Expression patterns were then applied via automated batch processing across all slides without human intervention. Classification results were then reviewed as a WSI overlay and/or via generated summary statistics.

Supplemental Table 1: Antibodies for frozen PBMC flow panels

Antibody	Fluorochrome	Clone	Vendor
CD244	PC5	C1.7	Beckman-Coulter
CD57	APC-Vio770	TB03	Miltenyi Biotec
Anti-KLRG1	FITC	REA261	Miltenyi Biotec
Anti-KLRG1	PE-Vio770	REA261	Miltenyi Biotec
BV 421 CD279(PD-1)	BV421	EH12.2H7	BioLegend
CD57	FITC	HCD57	BioLegend
CD3	BUV737	UCHT1	BD
CD45RA	BUV737	HI100	BD
CD223 (LAG-3) PE-Cy7	Pe-Cy7	3DS223H	eBioscience
CD197(CCR7)	BUV395	150503	BD
CD127 (IL-7R α)	Alexa647	A019D5	BioLegend
CD45RA	Alexa F700	HI100	BD
CD45RO	BV510	UCHL1	BioLegend
CD3	eVolve 605	OKT3	eBioscience (Discontinued)
anti-TIM-3	PE	344823	R&D Systems
CD4	BV650	OKT4	BioLegend
CD56	BV605	NCAM16.2	BD
CD45RO	APC eFluor 780	UCHL1	eBioscience
TIGIT	APC	MBSA43	eBioscience
Anti-T-bet	BV711	4B10	Biolegend
CD8a	Alexa 700	HIT8a	BioLegend
CD8a	PerCP-eFluor 710	SK1	eBioscience
Eomes	PE	WD1928	eBioscience
CD56	BUV395	NCAM16.2	BD
CD197(CCR7)	BV510	G043H7	BioLegend
CXCR5 (CD185)	BV421	RF8B2	BD
Anti-Ki-67	BV711	B56	BD
CD28	PE-CF594	CD28.2	BD
CD152(CTLA-4)	BV786	BNI3	BD
CD279 PD-1	BV650	EH12.2H7	BioLegend
FoxP3	PE-CF594	259D/C7	BD
Live/Dead Blue	UV	fixable UV live dead cell stain	Invitrogen

BV Stain Buffer Plus

Intracellular staining with Ebioscience FoxP3 staining kit

FC Block Biolegend

Supplemental Table 2: Immunohistochemistry reagents and procedures

Panel: CD4/CD8/T-bet/FOXP3								
Ventana Discovery ULTRA *OmniMap Secondary Antibody Detection Kit	Rabbit α -human CD4	Ventana SP35 #790-4423	Predilute	4 hours (@RT)	Rhodamine 6G	Predilute	8 Min	DAPI
	Mouse α -human CD8	Dako (M7103)	1:500	32 min (@37°C)	DCC	Predilute	12 min	
	Rabbit α -human T-bet	Abcam (ab154200)	1:250	32 min (@37°C)	Red610	Predilute	8 min	
	Rat α -human FoxP3	Invitrogen (14-4776-80)	1:250	32 min (@37°C)	Cy5	Predilute	12 min	

Panel: DC Panel								
Ventana Discovery ULTRA *OmniMap Secondary Antibody Detection Kit	Mouse α -human IRF4	Biorbyt (orb89631)	1:400	32 min (@37°C)	Rhodamine 6G	Predilute	8 Min	DAPI
	Rabbit α -human IRF8	Abcam (ab207418)	1:500	32 min (@37°C)	DCC	Predilute	8 Min	
	Rabbit α -human HLA-DPB1	Abcam (ab157210)	1:1000	32 min (@37°C)	Red610	Predilute	8 Min	
	Rabbit α -human ILT4	EMDMillipore (abn1023)	1:50	32 min (@37°C)	Cy5	Predilute	8 Min	
	Rabbit α -human CD11c	Abcam (ab52632)	1:250	32 min (@37°C)	FAM	Predilute	8 Min	

Supplemental Table 3: Baseline vs. Study End Patient Characteristics

	TOL	P value	Non-TOL	P value		TOL	P value	Non-TOL	P value
Systolic blood pressure					eGFR by MDRD-4				
Baseline	138.3±19.4		135±16.8		Baseline	48.8±11.9		57.1±12.1	
Study End	131.6± 4.9		125.3± 10.1	0.14	Study End	50.3± 15.2		58.7± 20.1	
Baseline to Study End		0.34			Baseline to Study End		0.68		0.77
Diastolic blood pressure					Urine Prot/Cr Ratio				
Baseline	74.5±12.5		77±7.8		Baseline	0.57±0.69		0.16±0.15	
Study End	72±10.4		66.4±5.9	0.08	Study End	0.14± 0.12		0.08± 0.05	
Baseline to Study End		0.64			Baseline to Study End		0.07		0.19
Weight (kg)					HbA1c				
Baseline	110.4±27.9		82.8±9.7		Baseline	6.1±1.4		5.8±0.68	
Study End	108.3±27.2		85.4±9.96	0.97	Study End	6.3± 0.9		6.9± 2.7	
Baseline to Study End		0.15			Baseline to Study End		0.49		0.39
WBC					LDL				
Baseline	5.8±1.3		5.1±1.8		Baseline	98.7±36.6		99±50.9	
Study End	5.6± 1.6		4.9± 1.3	0.46	Study End	92.6± 16.5		114.1± 40.4	0.55
Baseline to Study End		0.58			Baseline to Study End		0.75		
Hemoglobin					HDL				
Baseline	12.7±1.3		13.7±1.5		Baseline	40.7±45.4		49.1±12.5	
Study End	13.1± 1.9		14± 2.3	0.68	Study End	45.4± 15.9		50.3± 21.5	
Baseline to Study End		0.45			Baseline to Study End		0.11		0.94
Platelet					TG				
Baseline	180.5±77.3		226.9±66.9		Baseline	238.8±310.5		195.3±182.5	
Study End	182± 41.6		230.6± 49.8	0.98	Study End	213.7± 301.7		160.4± 122.1	
Baseline to Study End		.95			Baseline to Study End		0.15		0.81

Supplemental Table 4: Clinical Course of Non-Tolerant Recipients

Consent to rejection (years)	SRL dose at rejection	Reason for IS therapy Resumption	Treatment of Rejection	Current Therapy
0.54	0.5mg 2x/week	Hepatoma recurrence	---	SRL 2mg/day
0.50	0.5mg 1x/week	Mild AR during weaning	Resumption of SRL + prednisone taper	SRL 1mg/day
0.41	0.5mg 1x/week	Mild AR during weaning	Tacrolimus + prednisone taper	Tacrolimus 1mg 2x/day
0.67	1mg 1x/week	Mild AR during weaning	Tacrolimus + I.V. methylprednisolone + prednisone taper	Tacrolimus 2mg 2x/day
1.45	off	Moderate AR on final biopsy	Resumption of SRL	SRL 1mg/day
1.27	off	Mild AR on final biopsy	Resumption of SRL	SRL 0.5mg/day
1.37	off	Mild AR on final biopsy	Resumption of SRL	SRL 1mg/day

Supplemental Table 5: Results of frozen, batched, flow cytometry

Cell Population	Visit	Exact P-value, Wilcoxon (Two-sided)	Trend Description
<i>CD4- CD8+ T cells Eomes+ as % of T cells CD4- CD8+</i>	<i>End of Study</i>	<i>0.000666001</i>	<i>TOL up vs. non-TOL</i>
CD3+CD56-CD4+PD-1-CD57-TIGIT+ as % of CD3+CD56-CD4+PD-1-CD57-NKT Eomes+ and Tbet+ cells as % of NKT cells CD3+ CD56+	Baseline	0.001332	TOL up vs. non-TOL
NKT Tbet+ cells as % of NKT cells CD3+ CD56+	End of Study	0.002664	TOL up vs. non-TOL
<i>CD8+ Naive CCR7+ cells as % of T cells CD4- CD8+</i>	<i>Baseline</i>	<i>0.004662</i>	<i>non-TOL up vs. TOL</i>
CD8+ TEMRA Exhausted Eomes+ and Tbet+ cells as % of CD8+ TEMRA Exhausted KLRG1+ CD57- cells	End of Study	0.004662	TOL up vs. non-TOL
CD8+ TEMRA Exhausted Tbet+ cells as % of CD8+ TEMRA Exhausted KLRG1+ CD57- cells	End of Study	0.004662	TOL up vs. non-TOL
CD3+CD56-CD4+PD-1-CD57-TIGIT+ as % of CD3+CD56-CD4+PD-1-CD57-NKT Eomes+ and Tbet+ cells as % of NKT cells CD3+ CD56+	End of Study	0.007992	TOL up vs. non-TOL
<i>CD8+ TEMRA CCR7- cells as % of T cells CD4- CD8+</i>	<i>End of Study</i>	<i>0.007992</i>	<i>TOL up vs. non-TOL</i>
<i>CD8+ Naive CCR7+ cells as % of T cells CD4- CD8+</i>	<i>End of Study</i>	<i>0.012654</i>	<i>non-TOL up vs. TOL</i>
CD8+ TEMRA Exhausted Tbet+ cells as % of CD8+ TEMRA Exhausted KLRG1+ CD57- cells	Baseline	0.012654	TOL up vs. non-TOL
<i>CD4- CD8+ T cells Eomes+ and Tbet+ as % of T cells CD4- CD8+</i>	<i>End of Study</i>	<i>0.012654</i>	<i>TOL up vs. non-TOL</i>
<i>CD4- CD8+ T cells Eomes+ as % of T cells CD4- CD8+</i>	<i>Baseline</i>	<i>0.01998</i>	<i>TOL up vs. non-TOL</i>
CD4- CD8+ T cells Tbet+ as % of T cells CD4- CD8+	End of Study	0.01998	TOL up vs. non-TOL
CD3+CD56-CD8+PD-1+CD57-KLRG-1 -CTLA-4 + as % of CD3+CD56-CD8+PD-1+CD57-KLRG-1 -	End of Study	0.026307	non-TOL up vs. TOL
CD8+ TEMRA Exhausted Eomes+ and Tbet+ cells as % of CD8+ TEMRA Exhausted KLRG1+ CD57- cells	Baseline	0.026307	TOL up vs. non-TOL
<i>CD8+ TEMRA CCR7- cells as % of T cells CD4- CD8+</i>	<i>Baseline</i>	<i>0.029304</i>	<i>TOL up vs. non-TOL</i>
T Cells CD4+ CD8- as % of Lymphocyte Singlets	Baseline	0.042624	non-TOL up vs. TOL
Non Treg Effector Memory PD-1- cells as % of T cells CD4+ CD8-	End of Study	0.042624	TOL up vs. non-TOL
CD8+ Naive PD-1+ cells as % of CD8+ Naive CCR7+ cells	End of Study	0.042624	TOL up vs. non-TOL
CD8+ TEMRA PD-1- cells as % of T cells CD4- CD8+	End of Study	0.042624	TOL up vs. non-TOL
CD4+ CD8- T cells PD-1+ as % of T cells CD4+ CD8-	End of Study	0.042624	TOL up vs. non-TOL
CD4+ CD8- T cells PD-1- as % of T cells CD4+ CD8-	End of Study	0.042624	non-TOL up vs. TOL
CD4- CD8+ T cells KLRG1+ as % of T cells CD4- CD8+	End of Study	0.042624	TOL up vs. non-TOL
CD4- CD8+ T cells KLRG1- as % of T cells CD4- CD8+	End of Study	0.042624	non-TOL up vs. TOL
CD4- CD8+ T cells Tbet+ as % of T cells CD4- CD8+	Baseline	0.042624	TOL up vs. non-TOL

Cell populations with statistical differences between TOL and non-TOL participants at either the baseline or end of study visit, as indicated. Green color indicates CD8+ cell populations, yellow color indicates CD4+ cell populations, salmon color indicates small cell populations that should be interpreted with extreme care. Population names in bold italics are described in the main body of the manuscript.

Supplemental Table 6: Blood probesets distinguishing participants at baseline (p<0.005)

ID	Symbol	Entrez Gene Name	p-value	Expr Fold Change
242864_PM_at	ZNF554	zinc finger protein 554	0.000006	-1.472
226032_PM_at	CASP2	caspase 2	0.000023	-1.277
40446_PM_at	PHF1	PHD finger protein 1	0.000024	-1.283
239015_PM_at	THAP7-AS1	THAP7 antisense RNA 1	0.000065	-1.371
227731_PM_at	CNBP	CCHC-type zinc finger nucleic acid binding protein	0.000085	-1.282
1553220_PM_at	FAM117B	family with sequence similarity 117 member B	0.000096	-1.721
228910_PM_at	CD82	CD82 molecule	0.000132	-1.67
205203_PM_at	PLD1	phospholipase D1	0.000171	-1.46
202928_PM_s_at	PHF1	PHD finger protein 1	0.000174	-1.488
1565829_PM_at	CEP295	centrosomal protein 295	0.000198	1.402
213340_PM_s_at	TP73-AS1	TP73 antisense RNA 1	0.000215	-1.479
237283_PM_at	-	-	0.000223	1.281
41858_PM_at	PGAP2	post-GPI attachment to proteins 2	0.000232	-1.394
244051_PM_at	-	-	0.000242	1.314
215411_PM_s_at	TRAF3IP2	TRAF3 interacting protein 2	0.000244	-1.48
1553998_PM_at	DMRTC1/DMRTC1B	DMRT like family C1	0.000265	-1.488
233401_PM_at	-	-	0.000269	-1.385
224935_PM_at	EIF2S3	eukaryotic translation initiation factor 2 subunit gamma	0.000290	-1.407
239377_PM_at	EIF1AD	eukaryotic translation initiation factor 1A domain containing	0.000329	-1.429
1556967_PM_at	ZDHHC14	zinc finger DHHC-type containing 14	0.000335	1.357
1552701_PM_a_at	CARD16	caspase recruitment domain family member 16	0.000355	1.776
210120_PM_s_at	RANBP3	RAN binding protein 3	0.000384	-1.346
219634_PM_at	CHST11	carbohydrate sulfotransferase 11	0.000394	-1.576
218402_PM_s_at	HPS4	HPS4, biogenesis of lysosomal organelles complex 3 subunit 2	0.000399	-1.711
200810_PM_s_at	CIRBP	cold inducible RNA binding protein	0.000401	-1.469
235674_PM_at	TMEM131L	transmembrane 131 like	0.000438	-1.271
212914_PM_at	CBX7	chromobox 7	0.000441	-1.391
205294_PM_at	BAIAP2	BAI1 associated protein 2	0.000445	-1.472
218955_PM_at	BRF2	BRF2, RNA polymerase III transcription initiation factor subunit	0.000461	-1.246
1555390_PM_at	NOP9	NOP9 nucleolar protein	0.000469	-1.276
227515_PM_at	STAMBP	STAM binding protein	0.000477	-1.275
241769_PM_at	-	-	0.000507	1.474
221838_PM_at	KLHL22	kelch like family member 22	0.000547	-1.382
203904_PM_x_at	CD82	CD82 molecule	0.000582	-1.583
226879_PM_at	HVCN1	hydrogen voltage gated channel 1	0.000611	-1.384
1554283_PM_at	NOCT	nocturnin	0.000628	1.52
218168_PM_s_at	COQ8A	coenzyme Q8A	0.000641	-1.461
235085_PM_at	PRAG1	PEAK1 related, kinase-activating pseudokinase 1	0.000664	-1.667
221571_PM_at	TRAF3	TNF receptor associated factor 3	0.000664	-1.34
219315_PM_s_at	TMEM204	transmembrane protein 204	0.000674	-1.79
49329_PM_at	KLHL22	kelch like family member 22	0.000703	-1.41
44146_PM_at	GMEB2	glucocorticoid modulatory element binding protein 2	0.000703	-1.344
209782_PM_s_at	DBP	D-box binding PAR bZIP transcription factor	0.000713	-1.535
220099_PM_s_at	LUC7L2	LUC7 like 2, pre-mRNA splicing factor	0.000714	-1.395
238506_PM_at	LRRRC58	leucine rich repeat containing 58	0.000768	1.339
223029_PM_s_at	TRAF7	TNF receptor associated factor 7	0.000770	-1.296
209858_PM_x_at	MPPE1	metallophosphoesterase 1	0.000799	-1.549
218273_PM_s_at	PDP1	pyruvate dehydrogenase phosphatase catalytic subunit 1	0.000800	1.558
244391_PM_at	TSEN2	tRNA splicing endonuclease subunit 2	0.000810	-1.302
222561_PM_at	LANCL2	LanC like 2	0.000826	-1.313
204027_PM_s_at	METTL1	methyltransferase like 1	0.000859	-1.333
208774_PM_at	CSNK1D	casein kinase 1 delta	0.000882	-1.505
236239_PM_at	XPNPEP1	X-prolyl aminopeptidase 1	0.000951	-1.416
235257_PM_at	ODF3B	outer dense fiber of sperm tails 3B	0.000956	-1.337
230223_PM_at	CINP	cyclin dependent kinase 2 interacting protein	0.000960	-1.3
212400_PM_at	FAM102A	family with sequence similarity 102 member A	0.000971	-1.732
218856_PM_at	TNFRSF21	TNF receptor superfamily member 21	0.000979	-1.627
225075_PM_at	PDRG1	p53 and DNA damage regulated 1	0.001010	-1.23
209828_PM_s_at	IL16	interleukin 16	0.001020	-1.492
206629_PM_at	ADAMTSL2	ADAMTS like 2	0.001030	-1.177
207598_PM_x_at	XRCC2	X-ray repair cross complementing 2	0.001030	1.364
203315_PM_at	NCK2	NCK adaptor protein 2	0.001040	-1.404
215827_PM_x_at	CROCCP3	ciliary rootlet coiled-coil, rootletin pseudogene 3	0.001040	-1.274
216508_PM_x_at	-	-	0.001050	1.461

Supplemental Table 6: Blood probesets distinguishing participants at baseline (continued)

1552664_PM_at	FLCN	folliculin	0.001070	-1.482
224638_PM_at	SPPL3	signal peptide peptidase like 3	0.001070	-1.291
218868_PM_at	ACTR3B	ARP3 actin related protein 3 homolog B	0.001100	-1.343
213499_PM_at	CLCN2	chloride voltage-gated channel 2	0.001160	1.24
244070_PM_at	SYNE1	spectrin repeat containing nuclear envelope protein 1	0.001170	1.402
212390_PM_at	PDE4DIP	phosphodiesterase 4D interacting protein	0.001180	-1.89
235451_PM_at	SMAD5	SMAD family member 5	0.001190	1.641
239217_PM_x_at	ABCC3	ATP binding cassette subfamily C member 3	0.001240	-1.688
213195_PM_at	LYRM9	LYR motif containing 9	0.001250	-1.361
224248_PM_x_at	FAM192A	family with sequence similarity 192 member A	0.001250	-1.278
206617_PM_s_at	RENBP	renin binding protein	0.001260	-1.504
204153_PM_s_at	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0.001270	-1.366
205929_PM_at	GPA33	glycoprotein A33	0.001280	-1.648
236845_PM_at	TRIM62	tripartite motif containing 62	0.001280	-1.307
1555623_PM_at	-	-	0.001290	1.3
218584_PM_at	TCTN1	tectonic family member 1	0.001330	-1.379
209811_PM_at	CASP2	caspase 2	0.001350	-1.452
1564208_PM_x_at	LINC00957	long intergenic non-protein coding RNA 957	0.001360	-1.343
228312_PM_at	PI16	peptidase inhibitor 16	0.001370	-1.375
1555454_PM_at	LITAF	lipopolysaccharide induced TNF factor	0.001370	-1.237
1561039_PM_a_at	ZNF81	zinc finger protein 81	0.001410	1.211
209678_PM_s_at	PRKCI	protein kinase C iota	0.001410	1.544
201236_PM_s_at	BTG2	BTG anti-proliferation factor 2	0.001440	-1.531
227516_PM_at	SF3A1	splicing factor 3a subunit 1	0.001470	-1.508
203831_PM_at	R3HDM2	R3H domain containing 2	0.001480	-1.381
222251_PM_s_at	GMEB2	glucocorticoid modulatory element binding protein 2	0.001490	-1.326
225596_PM_at	KLC4	kinesin light chain 4	0.001500	-1.394
232107_PM_at	SDHC	succinate dehydrogenase complex subunit C	0.001500	-1.232
1558289_PM_at	RFT1	RFT1 homolog	0.001510	-1.322
202382_PM_s_at	GNPDA1	glucosamine-6-phosphate deaminase 1	0.001520	-1.414
208776_PM_at	PSMD11	proteasome 26S subunit, non-ATPase 11	0.001540	-1.474
200811_PM_at	CIRBP	cold inducible RNA binding protein	0.001550	-1.459
226314_PM_at	CHST14	carbohydrate sulfotransferase 14	0.001550	-1.394
227305_PM_s_at	SMCR8	Smith-Magenis syndrome chromosome region, candidate 8	0.001550	-1.338
210775_PM_x_at	CASP9	caspase 9	0.001580	-1.447
205252_PM_at	ZNF174	zinc finger protein 174	0.001610	-1.307
205031_PM_at	EFNB3	ephrin B3	0.001610	1.227
1566138_PM_at	PTPRN2	protein tyrosine phosphatase, receptor type N2	0.001620	1.216
202015_PM_x_at	METAP2	methionyl aminopeptidase 2	0.001620	1.323
201706_PM_s_at	PEX19	peroxisomal biogenesis factor 19	0.001640	-1.347
212547_PM_at	BRD3	bromodomain containing 3	0.001640	-1.313
237707_PM_at	-	-	0.001650	-1.472
1555902_PM_at	ARMCX5	armadillo repeat containing X-linked 5	0.001670	1.352
243149_PM_at	-	-	0.001680	1.718
243639_PM_at	-	-	0.001690	-1.601
237114_PM_at	-	-	0.001750	1.524
201212_PM_at	LGMN	legumain	0.001760	-1.495
222995_PM_s_at	RHBDD2	rhomboid domain containing 2	0.001770	-1.538
233881_PM_s_at	TOLLIP	toll interacting protein	0.001820	-1.462
211692_PM_s_at	BBC3	BCL2 binding component 3	0.001820	-1.382
218325_PM_s_at	DIDO1	death inducer-obliterator 1	0.001910	-1.429
233209_PM_at	-	-	0.001980	-1.225
231798_PM_at	NOG	noggin	0.002050	-2.896
218916_PM_at	ZNF768	zinc finger protein 768	0.002060	-1.378
203279_PM_at	EDEM1	ER degradation enhancing alpha-mannosidase like protein 1	0.002080	-1.406
203126_PM_at	IMPA2	inositol monophosphatase 2	0.002090	-1.595
225982_PM_at	UBTF	upstream binding transcription factor	0.002090	-1.206
228856_PM_at	ZNF747	zinc finger protein 747	0.002110	-1.27
211715_PM_s_at	BDH1	3-hydroxybutyrate dehydrogenase 1	0.002150	-1.459
229247_PM_at	FBLN7	fibulin 7	0.002150	-1.361
227898_PM_s_at	ZFP41	ZFP41 zinc finger protein	0.002190	-1.253
230856_PM_at	ARSG	arylsulfatase G	0.002200	-1.43
214915_PM_at	ZNF362	zinc finger protein 362	0.002200	1.287
212825_PM_at	PAXIP1	PAX interacting protein 1	0.002210	-1.59
204487_PM_s_at	KCNQ1	potassium voltage-gated channel subfamily Q member 1	0.002210	-1.413

Supplemental Table 6: Blood probesets distinguishing participants at baseline (continued)

204269_PM_at	PIM2	Pim-2 proto-oncogene, serine/threonine kinase	0.002210	-1.336
1558407_PM_at	PLEKHG2	pleckstrin homology and RhoGEF domain containing G2	0.002210	-1.223
207075_PM_at	NLRP3	NLR family pyrin domain containing 3	0.002230	-1.588
220349_PM_s_at	ENGASE	endo-beta-N-acetylglucosaminidase	0.002230	-1.49
215293_PM_s_at	PGAP2	post-GPI attachment to proteins 2	0.002230	-1.316
214343_PM_s_at	ATXN7L1	ataxin 7 like 1	0.002250	1.269
203580_PM_s_at	SLC7A6	solute carrier family 7 member 6	0.002320	-1.402
233568_PM_x_at	CWF19L1	CWF19 like 1, cell cycle control (S. pombe)	0.002350	-1.167
225249_PM_at	SPPL2B	signal peptide peptidase like 2B	0.002360	-1.331
243746_PM_at	IGHMBP2	immunoglobulin mu DNA binding protein 2	0.002400	-1.37
218988_PM_at	SLC35E3	solute carrier family 35 member E3	0.002500	-1.326
231193_PM_s_at	TAOK1	TAO kinase 1	0.002500	1.346
223554_PM_s_at	RANGRF	RAN guanine nucleotide release factor	0.002510	-1.263
202987_PM_at	TRAF3IP2	TRAF3 interacting protein 2	0.002520	-1.339
201365_PM_at	OAZ2	ornithine decarboxylase antizyme 2	0.002530	-1.429
202004_PM_x_at	SDHC	succinate dehydrogenase complex subunit C	0.002590	-1.289
219997_PM_s_at	COP9B	COP9 signalosome subunit 7B	0.002600	-1.36
1557680_PM_at	SAMD15	sterile alpha motif domain containing 15	0.002620	-1.285
242023_PM_at	ABHD4	abhydrolase domain containing 4	0.002670	-1.71
222790_PM_s_at	RSBN1	round spermatid basic protein 1	0.002670	1.226
213638_PM_at	PHACTR1	phosphatase and actin regulator 1	0.002680	-1.561
209947_PM_at	UBAP2L	ubiquitin associated protein 2 like	0.002690	-1.332
228615_PM_at	FBXO25	F-box protein 25	0.002700	-1.402
223322_PM_at	RASSF5	Ras association domain family member 5	0.002700	-1.332
231597_PM_x_at			0.002700	2.118
218210_PM_at	FN3KRP	fructosamine 3 kinase related protein	0.002730	-1.412
219897_PM_at	RNF122	ring finger protein 122	0.002740	-1.309
213091_PM_at	CRTC1	CREB regulated transcription coactivator 1	0.002760	-1.373
227762_PM_at			0.002770	-1.875
206453_PM_s_at	NDRG2	NDRG family member 2	0.002770	-1.346
229564_PM_at	RRP7A	ribosomal RNA processing 7 homolog A	0.002860	-1.425
218032_PM_at	SNN	stannin	0.002900	-1.358
210715_PM_s_at	SPINT2	serine peptidase inhibitor, Kunitz type 2	0.002920	-1.394
239000_PM_at	BRD4	bromodomain containing 4	0.002930	-1.352
227964_PM_at	FRMD8	FERM domain containing 8	0.002940	-1.316
209932_PM_s_at	DUT	deoxyuridine triphosphatase	0.002940	1.266
1561038_PM_at	ZNF81	zinc finger protein 81	0.002980	-1.27
236554_PM_x_at	TMC8	transmembrane channel like 8	0.003040	-1.465
207771_PM_at	SLC5A2	solute carrier family 5 member 2	0.003050	-1.248
229265_PM_at	SKI	SKI proto-oncogene	0.003070	-1.549
203395_PM_s_at	HES1	hes family bHLH transcription factor 1	0.003080	-1.462
217978_PM_s_at	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	0.003110	-1.257
201032_PM_at	BLCAP	BLCAP, apoptosis inducing factor	0.003130	-1.211
222307_PM_at	PDCD4-AS1	PDCD4 antisense RNA 1	0.003190	-1.471
225763_PM_at	RCSL1	RCSL domain containing 1	0.003210	-1.341
225357_PM_s_at	INO80	INO80 complex subunit	0.003230	-1.38
202001_PM_s_at	NDUFA6	NADH:ubiquinone oxidoreductase subunit A6	0.003230	1.447
211976_PM_at	NUDT3	nudix hydrolase 3	0.003240	-1.276
201936_PM_s_at	EIF4G3	eukaryotic translation initiation factor 4 gamma 3	0.003240	1.438
211793_PM_s_at	ABI2	abl interactor 2	0.003260	-1.282
		BRD4 interacting chromatin remodeling complex associated protein		
219445_PM_at	BICRA		0.003280	-1.323
225498_PM_at	CHMP4B	charged multivesicular body protein 4B	0.003280	-1.226
240147_PM_at	C7orf50	chromosome 7 open reading frame 50	0.003290	-1.307
219041_PM_s_at	REPIN1	replication initiator 1	0.003290	-1.241
224688_PM_at	TMEM248	transmembrane protein 248	0.003300	-1.308
242180_PM_at	TSPAN16	tetraspanin 16	0.003330	-1.238
231497_PM_at	ZBTB20-AS1	ZBTB20 antisense RNA 1	0.003360	1.306
209477_PM_at	EMD	emerin	0.003410	-1.263
213643_PM_s_at	INPP5B	inositol polyphosphate-5-phosphatase B	0.003430	-1.514
219765_PM_at	ZNF329	zinc finger protein 329	0.003480	-1.412
200851_PM_s_at	IST1	IST1, ESCRT-III associated factor	0.003480	-1.286
213913_PM_s_at	TBC1D30	TBC1 domain family member 30	0.003500	-1.272
211783_PM_s_at	MTA1	metastasis associated 1	0.003510	-1.472
221741_PM_s_at	YTHDF1	YTH N6-methyladenosine RNA binding protein 1	0.003600	-1.163

Supplemental Table 6: Blood probesets distinguishing participants at baseline (continued)

201705_PM_at	PSMD7	proteasome 26S subunit, non-ATPase 7	0.003630	-1.19
214714_PM_at	ZNF394	zinc finger protein 394	0.003660	-1.156
233439_PM_at	LETM1	leucine zipper and EF-hand containing transmembrane protein	0.003660	1.208
212917_PM_x_at	RECQL	RecQ like helicase	0.003680	1.552
210800_PM_at	TIMM8A	translocase of inner mitochondrial membrane 8A	0.003700	1.37
213727_PM_x_at	MPPE1	metallophosphoesterase 1	0.003710	-1.476
31861_PM_at	IGHMBP2	immunoglobulin mu DNA binding protein 2	0.003740	-1.314
213039_PM_at	ARHGEF18	Rho/Rac guanine nucleotide exchange factor 18	0.003740	-1.279
1555990_PM_at	C22orf42	chromosome 22 open reading frame 42	0.003740	-1.235
226935_PM_s_at	CLPTM1L	CLPTM1 like	0.003760	-1.237
1553959_PM_a_at	B3GALT6	beta-1,3-galactosyltransferase 6	0.003770	-1.366
213174_PM_at	TTC9	tetratricopeptide repeat domain 9	0.003830	-1.732
215177_PM_s_at	ITGA6	integrin subunit alpha 6	0.003840	-1.465
231844_PM_at	RBM28	RNA binding motif protein 28	0.003850	-1.418
229261_PM_at	SOS1-IT1	SOS1 intronic transcript 1	0.003860	1.453
203380_PM_x_at	SRSF5	serine and arginine rich splicing factor 5	0.003900	-1.358
223960_PM_s_at	CDIP1	cell death inducing p53 target 1	0.003910	-1.721
219131_PM_at	UBIAD1	UbiA prenyltransferase domain containing 1	0.003910	-1.421
229181_PM_s_at	HAUS2	HAUS augmin like complex subunit 2	0.003910	1.447
231865_PM_at	NCKAP5L	NCK associated protein 5 like	0.003940	-1.471
211210_PM_x_at	SH2D1A	SH2 domain containing 1A	0.003970	2.211
213530_PM_at	RAB3GAP1	RAB3 GTPase activating protein catalytic subunit 1	0.004020	-1.323
217013_PM_at	AZGP1P1	alpha-2-glycoprotein 1, zinc-binding pseudogene 1	0.004030	-1.192
223406_PM_x_at	FAM192A	family with sequence similarity 192 member A	0.004050	-1.233
235528_PM_at	GUCA1B	guanylate cyclase activator 1B	0.004090	-1.316
218937_PM_at	ZSCAN32	zinc finger and SCAN domain containing 32	0.004090	-1.221
227009_PM_at	LOC103611081	uncharacterized LOC103611081	0.004110	-1.47
229356_PM_x_at	INO80	INO80 complex subunit	0.004120	-1.297
227882_PM_at	FKRP	fukutin related protein	0.004130	-1.377
209504_PM_s_at	PLEKHB1	pleckstrin homology domain containing B1	0.004210	-1.684
224855_PM_at	PYCR2	pyrroline-5-carboxylate reductase 2	0.004220	-1.352
202617_PM_s_at	MECP2	methyl-CpG binding protein 2	0.004230	-1.306
33778_PM_at	TBC1D22A	TBC1 domain family member 22A	0.004280	-1.347
217788_PM_s_at	GALNT2	polypeptide N-acetylgalactosaminyltransferase 2	0.004280	-1.335
204686_PM_at	IRS1	insulin receptor substrate 1	0.004330	-1.223
227981_PM_at	CYB561D1	cytochrome b561 family member D1	0.004330	-1.2
228854_PM_at	-	-	0.004340	-1.786
213313_PM_at	RABGAP1	RAB GTPase activating protein 1	0.004340	-1.217
206999_PM_at	IL12RB2	interleukin 12 receptor subunit beta 2	0.004360	-1.731
239231_PM_at	ZNF101	zinc finger protein 101	0.004400	-1.394
233504_PM_at	C9orf84	chromosome 9 open reading frame 84	0.004440	1.426
235896_PM_s_at	MIEF2	mitochondrial elongation factor 2	0.004460	-1.213
200623_PM_s_at	CALM1 (includes others)	calmodulin 1	0.004470	-1.329
201003_PM_x_at	UBE2V1	ubiquitin conjugating enzyme E2 V1	0.004490	-1.624
209491_PM_s_at	AMPD3	adenosine monophosphate deaminase 3	0.004530	-1.295
236624_PM_at	LINC01128	long intergenic non-protein coding RNA 1128	0.004570	-1.193
217822_PM_at	WBP11	WW domain binding protein 11	0.004600	-1.334
217124_PM_at	IQCE	IQ motif containing E	0.004650	-1.335
240561_PM_at	RAP2C-AS1	RAP2C antisense RNA 1	0.004680	-1.314
236520_PM_at	SDCBP2-AS1	SDCBP2 antisense RNA 1	0.004700	-1.377
37152_PM_at	PPARD	peroxisome proliferator activated receptor delta	0.004720	-1.435
212766_PM_s_at	ISG20L2	interferon stimulated exonuclease gene 20 like 2	0.004720	-1.313
212082_PM_s_at	MYL6	myosin light chain 6	0.004730	1.212
217168_PM_s_at	HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1	0.004750	-1.34
209518_PM_at	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	0.004780	-1.271
218474_PM_s_at	KCTD5	potassium channel tetramerization domain containing 5	0.004790	-1.54
232845_PM_at	CDH23	cadherin related 23	0.004790	-1.414
213535_PM_s_at	UBE2I	ubiquitin conjugating enzyme E2 I	0.004790	-1.307
217024_PM_x_at	SIRPA	signal regulatory protein alpha	0.004800	-1.454
200914_PM_x_at	KTN1	kinectin 1	0.004830	1.263
224732_PM_at	CHTF8	chromosome transmission fidelity factor 8	0.004840	-1.233
219809_PM_at	WDR55	WD repeat domain 55	0.004850	-1.269
215210_PM_s_at	DLST	dihydrolipoamide S-succinyltransferase	0.004920	-1.233
212434_PM_at	GRPEL1	GrpE like 1, mitochondrial	0.004950	-1.319
205688_PM_at	TFAP4	transcription factor AP-4	0.004960	-1.204

Supplementary Table 7: Differential liver tissue gene expression between TOL and Non-TOL recipients at baseline

GENE	GENE NAME	ID	p-value	FDR
AVPR1A	arginine vasopressin receptor 1A	AVPR1A	0.00003	0.18
SLC47A1	solute carrier family 47 member 1	SLC47A1	0.00003	0.18
TPPP2	tubulin polymerization promoting protein family member 2	TPPP2	0.00004	0.18
FNDC3B	fibronectin type III domain containing 3B	FNDC3B	0.00008	0.18
SLC16A4	solute carrier family 16 member 4	SLC16A4	0.00009	0.18
CLMN	calmin	CLMN	0.00010	0.18
ACBD3	acyl-CoA binding domain containing 3	ACBD3	0.00010	0.18
ETNK2	ethanolamine kinase 2	ETNK2	0.00011	0.18
ABLIM3	actin binding LIM protein family member 3	ABLIM3	0.00013	0.18
FUT6	fucosyltransferase 6	FUT6	0.00014	0.18
LOC100505985	uncharacterized LOC100505985 hexose-6-phosphate dehydrogenase/glucose 1- dehydrogenase	LOC100505985	0.00015	0.18
H6PD		H6PD	0.00017	0.18
CEMP1	cementum protein 1	CEMP1	0.00017	0.18
MACROD1	MACRO domain containing 1	MACROD1	0.00018	0.18
SUSD3	sushi domain containing 3	SUSD3	0.00018	0.18
KDELR3	KDEL endoplasmic reticulum protein retention receptor 3	KDELR3	0.00021	0.19
MREG	melanoregulin	MREG	0.00022	0.20
MGC32805	uncharacterized LOC153163	MGC32805	0.00024	0.20
CCDC126	coiled-coil domain containing 126	CCDC126	0.00029	0.20
PELI2	pellino E3 ubiquitin protein ligase family member 2	PELI2	0.00029	0.20
NUAK1	NUAK family kinase 1	NUAK1	0.00029	0.20
AADAT	aminoadipate aminotransferase	AADAT	0.00031	0.20
PLPP5	phospholipid phosphatase 5	PLPP5	0.00034	0.20
SLC2A10	solute carrier family 2 member 10	SLC2A10	0.00036	0.20
GTF2IRD1	GTF2I repeat domain containing 1	GTF2IRD1	0.00037	0.20
GLMP	glycosylated lysosomal membrane protein	GLMP	0.00037	0.20
SLC38A3	solute carrier family 38 member 3	SLC38A3	0.00038	0.20
TTY14	testis-specific transcript, Y-linked 14 (non-protein coding)	TTY14	0.00039	0.20
NELFE	negative elongation factor complex member E	NELFE	0.00041	0.20
LRG1	leucine rich alpha-2-glycoprotein 1	LRG1	0.00043	0.20
SLC25A33	solute carrier family 25 member 33	SLC25A33	0.00047	0.20
LRP5L	LDL receptor related protein 5 like	LRP5L	0.00048	0.20
ALDH7A1	aldehyde dehydrogenase 7 family member A1	ALDH7A1	0.00048	0.20
LOC100505570	uncharacterized LOC100505570	LOC100505570	0.00050	0.20
LBP	lipopolysaccharide binding protein	LBP	0.00050	0.20
LOC100130548	uncharacterized LOC100130548	LOC100130548	0.00051	0.20
LINC01093	long intergenic non-protein coding RNA 1093	LINC01093	0.00055	0.20
SLCO2B1	solute carrier organic anion transporter family member 2B1	SLCO2B1	0.00056	0.20
SEC24D	SEC24 homolog D, COPII coat complex component	SEC24D	0.00058	0.20
VNN3	vanin 3	VNN3	0.00058	0.20
DNAJB11	DnaJ heat shock protein family (Hsp40) member B11	DNAJB11	0.00059	0.20
SLC6A12	solute carrier family 6 member 12	SLC6A12	0.00059	0.20
LOC400499	vitellogenin	LOC400499	0.00060	0.20
DBH-AS1	DBH antisense RNA 1	DBH-AS1	0.00062	0.20
FMO4	flavin containing monooxygenase 4	FMO4	0.00062	0.20
DLGAP1-AS3	DLGAP1 antisense RNA 3	DLGAP1-AS3	0.00063	0.20

Supplementary Table 7: Differential liver tissue gene expression between TOL and Non-TOL recipients at baseline (continued)

MROH2A	maestro heat like repeat family member 2A	MROH2A	0.00063	0.20
ME2	malic enzyme 2	ME2	0.00066	0.21
C15orf39	chromosome 15 open reading frame 39	C15orf39	0.00069	0.21
CHURC1	churchill domain containing 1	CHURC1	0.00069	0.21
FOCAD	focadhesin	FOCAD	0.00073	0.21
C1orf216	chromosome 1 open reading frame 216	C1orf216	0.00078	0.23
ENO1-AS1	ENO1 antisense RNA 1	ENO1-AS1	0.00083	0.23
C16orf45	chromosome 16 open reading frame 45	C16orf45	0.00084	0.23
UROC1	urocanate hydratase 1	UROC1	0.00088	0.23
KYAT3	kynurenine aminotransferase 3	KYAT3	0.00090	0.23
USP2	ubiquitin specific peptidase 2	USP2	0.00093	0.23
HSPC102	uncharacterized HSPC102	HSPC102	0.00093	0.23
SLC22A18	solute carrier family 22 member 18	SLC22A18	0.00094	0.23
LINC00930	long intergenic non-protein coding RNA 930	LINC00930	0.00094	0.23
SLC17A1	solute carrier family 17 member 1	SLC17A1	0.00095	0.23
TKFC	triokinase and FMN cyclase	TKFC	0.00105	0.25
GCDH	glutaryl-CoA dehydrogenase	GCDH	0.00108	0.25
CYB561	cytochrome b561	CYB561	0.00111	0.25
TGFB3	transforming growth factor beta 3	TGFB3	0.00113	0.25
HEATR5A	HEAT repeat containing 5A	HEATR5A	0.00113	0.25
NOP9	NOP9 nucleolar protein	NOP9	0.00113	0.25
ACSF2	acyl-CoA synthetase family member 2	ACSF2	0.00119	0.25
PRKCZ	protein kinase C zeta	PRKCZ	0.00120	0.25
MIR7515HG	MIR7515 host gene	MIR7515HG	0.00120	0.25
MME	membrane metalloendopeptidase	MME	0.00120	0.25
SAMD4A	sterile alpha motif domain containing 4A	SAMD4A	0.00126	0.26
HLF	HLF, PAR bZIP transcription factor	HLF	0.00134	0.27
MAP2K6	mitogen-activated protein kinase kinase 6	MAP2K6	0.00138	0.28
CA14	carbonic anhydrase 14	CA14	0.00140	0.28
LOC105370002	uncharacterized LOC105370002	LOC105370002	0.00142	0.28
RNF165	ring finger protein 165	RNF165	0.00145	0.28
IYD	iodotyrosine deiodinase	IYD	0.00152	0.29
GLIS2	GLIS family zinc finger 2	GLIS2	0.00152	0.29
CADM1	cell adhesion molecule 1	CADM1	0.00155	0.29
NLGN4Y	neuroligin 4, Y-linked	NLGN4Y	0.00155	0.29
LRP2	LDL receptor related protein 2	LRP2	0.00156	0.29
PYCR2	pyrroline-5-carboxylate reductase 2	PYCR2	0.00163	0.30
CNGA1	cyclic nucleotide gated channel alpha 1	CNGA1	0.00169	0.30
ABHD4	abhydrolase domain containing 4	ABHD4	0.00171	0.30
BAMBI	BMP and activin membrane bound inhibitor	BAMBI	0.00173	0.30
KNOP1	lysine rich nucleolar protein 1	KNOP1	0.00174	0.30
CRYBA2	crystallin beta A2	CRYBA2	0.00175	0.30
DOPEY2	dopey family member 2	DOPEY2	0.00180	0.30
CCT6B	chaperonin containing TCP1 subunit 6B	CCT6B	0.00183	0.30
VWCE	von Willebrand factor C and EGF domains	VWCE	0.00188	0.30
KCND3	potassium voltage-gated channel subfamily D member 3	KCND3	0.00189	0.30
CRELD2	cysteine rich with EGF like domains 2	CRELD2	0.00190	0.30
CRP	C-reactive protein	CRP	0.00191	0.30
PNP	purine nucleoside phosphorylase	PNP	0.00192	0.30
TMEM182	transmembrane protein 182	TMEM182	0.00195	0.30
NPBWR1	neuropeptides B and W receptor 1	NPBWR1	0.00196	0.30
NTHL1	nth like DNA glycosylase 1	NTHL1	0.00198	0.30
RDH13	retinol dehydrogenase 13	RDH13	0.00199	0.30
HELB	DNA helicase B	HELB	0.00203	0.30

Supplementary Table 7: Differential liver tissue gene expression between TOL and Non-TOL recipients at baseline (continued)

ZSCAN4	zinc finger and SCAN domain containing 4	ZSCAN4	0.00203	0.30
RHBG	Rh family B glycoprotein (gene/pseudogene)	RHBG	0.00205	0.30
DPY19L1P1	DPY19L1 pseudogene 1	DPY19L1P1	0.00213	0.30
SIRPA	signal regulatory protein alpha ATP binding cassette subfamily G member 2 (Junior blood group)	SIRPA	0.00214	0.30
ABCG2		ABCG2	0.00217	0.30
ZNF653	zinc finger protein 653	ZNF653	0.00217	0.30
TPST1	tyrosylprotein sulfotransferase 1	TPST1	0.00219	0.30
FAXDC2	fatty acid hydroxylase domain containing 2	FAXDC2	0.00221	0.30
CLIC1	chloride intracellular channel 1	CLIC1	0.00221	0.30
GLYCTK	glycerate kinase	GLYCTK	0.00222	0.30
RFNG	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	RFNG	0.00227	0.30
HDAC1	histone deacetylase 1	HDAC1	0.00228	0.30
ZNF30	zinc finger protein 30	ZNF30	0.00228	0.30
RBM26-AS1	RBM26 antisense RNA 1	RBM26-AS1	0.00229	0.30
KDM6A	lysine demethylase 6A	KDM6A	0.00229	0.30
PDCD4	programmed cell death 4	PDCD4	0.00238	0.30
POLE	DNA polymerase epsilon, catalytic subunit	POLE	0.00238	0.30
SLC38A1	solute carrier family 38 member 1	SLC38A1	0.00238	0.30
SLC25A25-AS1	SLC25A25 antisense RNA 1	SLC25A25-AS1	0.00250	0.31
HNF4A-AS1	HNF4A antisense RNA 1	HNF4A-AS1	0.00251	0.31
GMEB1	glucocorticoid modulatory element binding protein 1	GMEB1	0.00254	0.31
DOLPP1	dolichyldiphosphatase 1	DOLPP1	0.00254	0.31
BDH2	3-hydroxybutyrate dehydrogenase 2	BDH2	0.00257	0.31
ELL2	elongation factor for RNA polymerase II 2	ELL2	0.00258	0.31
INMT	indolethylamine N-methyltransferase	INMT	0.00261	0.31
OTUD3	OTU deubiquitinase 3	OTUD3	0.00266	0.31
C11orf71	chromosome 11 open reading frame 71	C11orf71	0.00266	0.31
SCG2	secretogranin II	SCG2	0.00270	0.31
MORC3	MORC family CW-type zinc finger 3	MORC3	0.00270	0.31
ADRA1A	adrenoceptor alpha 1A	ADRA1A	0.00275	0.31
IL7	interleukin 7	IL7	0.00276	0.31
PAQR3	progesterin and adipoQ receptor family member 3	PAQR3	0.00280	0.31
COL18A1-AS1	COL18A1 antisense RNA 1	COL18A1-AS1	0.00280	0.31
TMEM45A	transmembrane protein 45A	TMEM45A	0.00282	0.31
CEP120	centrosomal protein 120	CEP120	0.00284	0.31
SLC2A4RG	SLC2A4 regulator	SLC2A4RG	0.00285	0.31
SLC29A1	solute carrier family 29 member 1 (Augustine blood group)	SLC29A1	0.00293	0.32
IGHV3-54	immunoglobulin heavy variable 3-54 (pseudogene)	IGHV3-54	0.00296	0.32
TCEA2	transcription elongation factor A2	TCEA2	0.00301	0.32
NDRG1	N-myc downstream regulated 1	NDRG1	0.00302	0.32
COBL	cordon-bleu WH2 repeat protein	COBL	0.00305	0.32
LOC105370997	uncharacterized LOC105370997	LOC105370997	0.00306	0.32
SLC41A1	solute carrier family 41 member 1 zinc finger CCCH-type, RNA binding motif and serine/arginine rich 2	SLC41A1	0.00307	0.32
ZRSR2		ZRSR2	0.00310	0.32
GFPT1	glutamine--fructose-6-phosphate transaminase 1	GFPT1	0.00310	0.32
FBXO4	F-box protein 4	FBXO4	0.00317	0.32
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	ENPP1	0.00319	0.32
CD70	CD70 molecule	CD70	0.00322	0.32
DUSP22	dual specificity phosphatase 22	DUSP22	0.00323	0.32
LIME1	Lck interacting transmembrane adaptor 1	LIME1	0.00324	0.32
CPOX	coproporphyrinogen oxidase	CPOX	0.00325	0.32

Supplementary Table 7: Differential liver tissue gene expression between TOL and Non-TOL recipients at baseline (continued)

ATOH7	atonal bHLH transcription factor 7	ATOH7	0.00327	0.32
RAD54L	RAD54 like	RAD54L	0.00333	0.33
HSD17B14	hydroxysteroid 17-beta dehydrogenase 14	HSD17B14	0.00337	0.33
FAAP100	Fanconi anemia core complex associated protein 100	FAAP100	0.00348	0.34
PRG2	proteoglycan 2, pro eosinophil major basic protein	PRG2	0.00350	0.34
GPOR1	G protein-coupled estrogen receptor 1	GPOR1	0.00353	0.34
SDF2L1	stromal cell derived factor 2 like 1	SDF2L1	0.00355	0.34
GEN1	GEN1, Holliday junction 5' flap endonuclease	GEN1	0.00356	0.34
CYBA	cytochrome b-245 alpha chain	CYBA	0.00363	0.34
CALU	calumenin	CALU	0.00368	0.34
DIEXF	digestive organ expansion factor homolog (zebrafish)	DIEXF	0.00370	0.34
TP53INP2	tumor protein p53 inducible nuclear protein 2	TP53INP2	0.00375	0.34
LOC100507389	uncharacterized LOC100507389	LOC100507389	0.00375	0.34
FAM83D	family with sequence similarity 83 member D	FAM83D	0.00376	0.34
SLC20A2	solute carrier family 20 member 2	SLC20A2	0.00382	0.34
SEC14L2	SEC14 like lipid binding 2	SEC14L2	0.00384	0.34
GNAT2	G protein subunit alpha transducin 2	GNAT2	0.00385	0.34
ODC1	ornithine decarboxylase 1	ODC1	0.00389	0.34
MIR3682	microRNA 3682	MIR3682	0.00391	0.34
IDO2	indoleamine 2,3-dioxygenase 2	IDO2	0.00392	0.34
KLF11	Kruppel like factor 11	KLF11	0.00394	0.34
DNER	delta/notch like EGF repeat containing	DNER	0.00394	0.34
ZC3H12C	zinc finger CCCH-type containing 12C	ZC3H12C	0.00396	0.34
LOC105371228	uncharacterized LOC105371228	LOC105371228	0.00400	0.34
SARS2	seryl-tRNA synthetase 2, mitochondrial	SARS2	0.00405	0.34
SLC25A10	solute carrier family 25 member 10	SLC25A10	0.00410	0.34
SMIM2-AS1	SMIM2 antisense RNA 1	SMIM2-AS1	0.00411	0.34
RMI1	RecQ mediated genome instability 1	RMI1	0.00413	0.34
TMEM52	transmembrane protein 52	TMEM52	0.00414	0.34
CAPN2	calpain 2	CAPN2	0.00415	0.34
ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	ST3GAL6	0.00415	0.34
AASS	aminoadipate-semialdehyde synthase	AASS	0.00419	0.34
OAT	ornithine aminotransferase phosphatidylinositol specific phospholipase C X domain containing 1	OAT	0.00421	0.34
PLCXD1	SH3 and PX domains 2A	PLCXD1	0.00422	0.34
SH3PXD2A	CNNM3 divergent transcript	SH3PXD2A	0.00429	0.35
CNNM3-DT	RALY antisense RNA 1	CNNM3-DT	0.00430	0.35
RALY-AS1	M-phase phosphoprotein 9	RALY-AS1	0.00435	0.35
MPHOSPH9	zinc finger protein 662	MPHOSPH9	0.00437	0.35
ZNF662	zinc finger protein 431	ZNF662	0.00441	0.35
ZNF431	transmembrane p24 trafficking protein 1	ZNF431	0.00445	0.35
TMED1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	TMED1	0.00449	0.35
PAG1	ZFP30 zinc finger protein	PAG1	0.00450	0.35
ZFP30	ADP ribosylation factor GTPase activating protein 3	ZFP30	0.00454	0.35
ARFGAP3	amyloid beta precursor protein binding family B member 1 interacting protein	ARFGAP3	0.00457	0.35
APBB1IP	oxysterol binding protein	APBB1IP	0.00462	0.35
OSBP	desmoglein 1	OSBP	0.00463	0.35
DSG1	STARD7 antisense RNA 1	DSG1	0.00465	0.35
STARD7-AS1	UDP-glucose glycoprotein glucosyltransferase 1	STARD7-AS1	0.00466	0.35
UGGT1	formimidoyltransferase cyclodeaminase	UGGT1	0.00466	0.35
FTCD	annexin A5	FTCD	0.00467	0.35
ANXA5		ANXA5	0.00472	0.35

Supplementary Table 7: Differential liver tissue gene expression between TOL and Non-TOL recipients at baseline (continued)

L3MBTL4	L3MBTL4, histone methyl-lysine binding protein	L3MBTL4	0.00475	0.35
PTPRH	protein tyrosine phosphatase, receptor type H	PTPRH	0.00477	0.35
GALK1	galactokinase 1	GALK1	0.00484	0.35
TSPYL4	TSPY like 4	TSPYL4	0.00484	0.35
IFNA21	interferon alpha 21	IFNA21	0.00488	0.35
TMEM263	transmembrane protein 263	TMEM263	0.00492	0.35
ZNF408	zinc finger protein 408	ZNF408	0.00495	0.35
CYP46A1	cytochrome P450 family 46 subfamily A member 1	CYP46A1	0.00496	0.35

Supplemental Table 8: p values and n values for quantitative immunohistochemistry staining

p values	TOL vs. non-TOL at baseline	TOL vs. non-TOL at end of study	TOL baseline vs. end of study	non-TOL baseline vs. end of study
CD4+ T cells	0.042624	0.0221445	n.s.	n.s.
FoxP3+CD4+	n.s.	0.00799	n.s.	0.0151515
CD3+	n.s.	0.0021645	n.s.	0.0021645
Tbet+CD8+	n.s.	n.s.	n.s.	0.0411255
APC:Lymphocyte pairings	n.s.	0.0221445	n.s.	0.0411255
Lobular MHCII+ILT4+CD11c+ DC	n.s.	0.0081585	n.s.	0.0021645
n values	TOL at baseline	TOL at end of study	non-TOL at baseline	non-TOL at end of study
CD4+ T cells	8	8	6	6
FoxP3+CD4+	8	8	6	6
CD3+	8	8	6	6
Tbet+CD8+	8	8	6	6
APC:Lymphocyte pairings	8	7	6	6
Lobular MHCII+ILT4+CD11c+ DC	8	7	6	6