Supplementary Table S1 All significant molecular pathways between SRL *vs.* Tac groups

Number	Ingenuity Canonical Pathways	*p*-value
1	Xenobiotic Metabolism Signaling	0.0001
2	Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	0.0003
3	Synaptic Long Term Depression	0.0006
4	Estrogen Biosynthesis	0.0007
5	IL-12 Signaling and Production in Macrophages	0.0007
6	PXR/RXR Activation	0.0008
7	Antigen Presentation Pathway	0.0008
8	Endothelin-1 Signaling	0.0009
9	LXR/RXR Activation	0.0009
10	Bupropion Degradation	0.0009
11	Type I Diabetes Mellitus Signaling	0.002
12	Acetone Degradation I (to Methylglyoxal)	0.002
13	LPS/IL-1 Mediated Inhibition of RXR Function	0.003
14	OX40 Signaling Pathway	0.003
15	Factors Promoting Cardiogenesis in Vertebrates	0.004
16	Neuropathic Pain Signaling In Dorsal Horn Neurons	0.004
17	Leukocyte Extravasation Signaling	0.006
18	Acute Phase Response Signaling	0.006
19	Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	0.007
20	Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	0.007
21	Remodeling of Epithelial Adherens Junctions	0.008
22	Aldosterone Signaling in Epithelial Cells	0.009
23	Sperm Motility	0.010
24	Antioxidant Action of Vitamin C	0.011
25	Induction of Apoptosis by HIV1	0.012
26	TWEAK Signaling	0.012
27	Molecular Mechanisms of Cancer	0.013
28	Graft-versus-Host Disease Signaling	0.013
29	Atherosclerosis Signaling	0.014
30	Melatonin Signaling	0.014
31	Protein Kinase A Signaling	0.015

32	Granulocyte Adhesion and Diapedesis	0.017
33	Autoimmune Thyroid Disease Signaling	0.017
34	Eicosanoid Signaling	0.018
35	Dendritic Cell Maturation	0.019
36	Synaptic Long Term Potentiation	0.019
37	Aryl Hydrocarbon Receptor Signaling	0.020
38	Calcium-induced T Lymphocyte Apoptosis	0.021
39	Nitric Oxide Signaling in the Cardiovascular System	0.022
40	Phospholipases	0.022
41	Glutathione-mediated Detoxification	0.023
42	Tyrosine Degradation I	0.023
43	Noradrenaline and Adrenaline Degradation	0.023
44	UVB-Induced MAPK Signaling	0.023
45	Role of PKR in Interferon Induction and Antiviral Response	0.026
46	Gap Junction Signaling	0.027
47	Nicotine Degradation II	0.030
48	Wnt/β-catenin Signaling	0.030
49	IL-10 Signaling	0.032
50	IL-8 Signaling	0.032
51	Apoptosis Signaling	0.032
52	Nicotine Degradation III	0.032
53	Ethanol Degradation II	0.034
54	Growth Hormone Signaling	0.034
55	Chemokine Signaling	0.034
56	Cell Cycle: G2/M DNA Damage Checkpoint Regulation	0.037
57	Dopamine-DARPP32 Feedback in cAMP Signaling	0.037
58	UVA-Induced MAPK Signaling	0.041
59	p70S6K Signaling	0.041
60	NRF2-mediated Oxidative Stress Response	0.042
61	Cdc42 Signaling	0.044
62	RAN Signaling	0.044
63	B Cell Development	0.045
64	Hepatic Cholestasis	0.049
65	Epithelial Adherens Junction Signaling	0.049

Supplemental Information

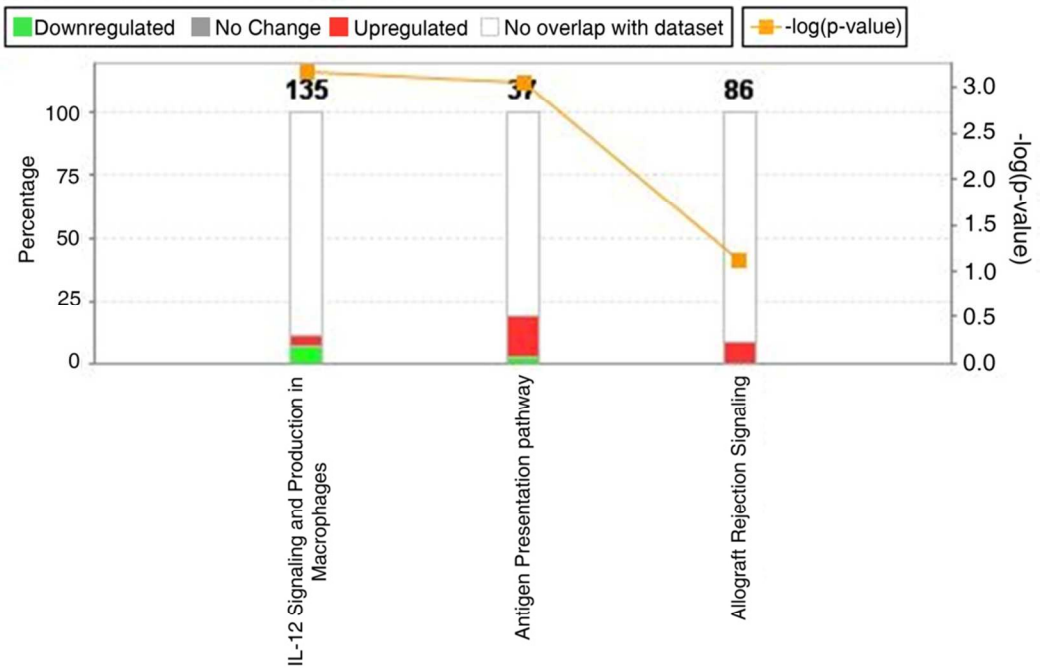
We aimed to validate some of the genes differentially expressed between groups (TAC *vs.* SRL) that were relevant in specific pathways associated with immune response. Specifically, we choose for the validation genes that were statistically differentially expressed between groups and associated with IL-12 signaling and Production in Macrophages, Antigen Presentation, and Allograft rejection. These canonical pathways were identified as relevant between groups (**Supplemental Figure 1**).

Specifically, reverse transcription quantitative real time PCR (RT-qPCR) was performed for quantifying the expression of lysozyme (LYZ) (Assay ID: Hs00426232_m1), and toll-like receptor 2 (TLR2) (Assay ID: HS01872448_s1), STAT1 (Assay ID: Hs01013996_m1), and IRF8 (Assay: Hs01128712_m1), using pre-developed TaqMan® gene expression assays (Life Technologies, Carlsbad, CA) following the manufacturer's protocol. For initial reverse transcription reactions (TaqMan Reverse Transcription Reagents Kit (Life Technologies)), RNA from the same samples and stock tubes used in the microarray analysis were evaluated. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH, ID: 4310884E) expression was used as the endogenous control for normalization. Gene expression fold changes were obtained using the delta Ct calculation model between the target gene mean cycle threshold (Ct) and GAPDH Ct as endogenous control, or ΔCt (gene) – ΔCt (GAPDH). Two tailed t test was performed to compare the mean expression between samples for the validated genes. A p-value < 0.05 were considered significant. Threshold cycle (Ct) values were used to calculate relative expression using the $\Delta\Delta$Ct method.

Validation of microarray results for 4 genes up-regulated in the SRL group when compared to TAC group using RT-qPCR reactions.

All the studied genes were differentially up-regulated in the SRL converted group and in concordance with the microarray results ($p<0.05$) (**Supplemental Figure-2**). These results validate the microarray findings by using a different reaction using the same tested total RNAs and confirm the relevance of the identified differential pathways.

Supplemental Figure 1: Canonical pathways identified as with genes differentially expressed between studied groups.



Supplemental Figure 2: Graphical representation of the average fold changes detected by RT-qPCR when comparing SRL converted samples to TAC samples. Changes in gene expression were calculated using the using the ΔΔCt method. GAPDH was used as the endogenous control. Two tailed t test was performed to compare the mean expression between samples for the validated genes. A *p*-value < 0.05 were considered significant.