SUPPLEMENTARY MATERIALS

SUPPLEMENTARY METHODS:

Patient groups:

All protocols were approved by the Northwestern University (NWU) and University of Louisville Institutional Review Boards. Informed written consent was obtained for all donors and recipients. For the FCRx therapy group, conditioning regimen, kidney transplantation, maintenance immunosuppression, and infusion of bioengineered FDA-regulated HSC product enriched for facilitating cells (FCRx) (IDE 13947) were reported previously (*12-14*).

For the standard immunosuppression group, induction therapy with alemtuzumab and short course of steroids was used for all except one patient, who underwent basiliximab induction. Tacrolimus (8-10 ng/mL) and MMF (1-1.25 g orally twice daily) were used as maintenance immunosuppression. Adjustments in immunosuppression dose were made for adverse events.

Renal biopsy samples:

This study utilized FFPE allograft kidney biopsy samples from KTx recipients diagnosed with acute cellular rejection (R; n = 10) and without acute rejection under standard immunosuppression (SIS; n = 10, 6 samples used for the microarray analyses and RT-qPCR reactions, and 4 for additional independent validation of genes using RT-qPCR) as well as from FCRx induced tolerant recipients (FCRx; n = 7) and paired pre-implantation donor allograft biopsy samples from FCRx (D; n = 5) and SIS (SIS_D; n = 2).

Validation of gene expression profiling from FFPE samples:

In order to assess the performance characteristics of gene expression profiling from possibly degraded specimens, such as FFPE archival samples, we run paired fresh-frozen: FFPE in triplicates of two different tissue types from archival samples (collected and banked in 2009),

on HG-U133Plus 2.0 arrays. For the fresh-frozen samples, total RNA was isolated from 10-µm thick frozen tissue sections using the MagMAX™-96 for Microarrays Total RNA Isolation Kit (Invitrogen™ Life Technologies, Carlsbad, CA), in an automated fashion using the magnetic particle processors MagMAX™ Express. For the paired FFPE samples, total RNA was isolated as described above.

Validation of array reactions using RT-qPCR reactions for top up- and down–regulated genes:

To validate the results from the microarrays, top genes (up- and down –regulated in unique and common analysis) were validated using RT-qPCR reactions as previously described (*40*). Additionally, two genes differentially expressed between FCRx and SIS samples were validated (a) using same samples (FCRx, n =7 *vs.* SIS; n = 6); and (b) using same RNA used for microarray reactions from FCRx (n =7) and an independent set of SIS samples (n= 4).

SUPPLEMENTARY RESULTS

Successful validation of FFPE samples using gene expression analysis.

As most of the studies were carried out using formalin fixed paraffin embedded (FFPE) biopsy samples in which molecular messages can be degraded, we performed quality control analyses using paired FFPE and frozen samples. Highly reproducible results were obtained between paired fresh-frozen vs. FFPE samples (**Fig. S1**). A gene signature of 241 probe sets created from FFPE samples (**Fig. S2A**) showed a near 70% overlap with a similar gene signature created from fresh-frozen samples (**Fig. S2B**). The 241 probe set signature was able to cluster together in replicates for both FFPE (r=0.991) and paired fresh-frozen (r=0.994) samples as well as to distinguish different biological phenotypes (**Fig. S3).** Thus, the analyses showed that despite a lower number of genes being captured in the FFPE samples, the overall critical top pathways

and functions were comparable, and hence FFPE samples were used for subsequent studies of differentially expressed genes (DEGs).

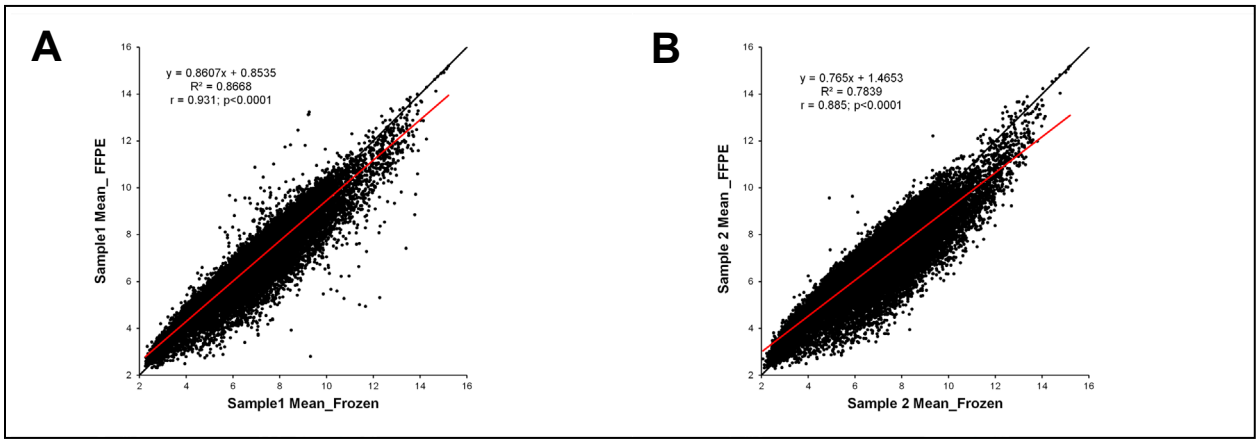

Fig. S1. ***Scatterplots of RMA-normalized probe set summary means.***

(**A**) Pearson's correlation of the mean values for the paired FFPE: fresh-frozen samples for tissue type 1 (Sample 1), and (**B**) for tissue type 2 (Sample 2). The identity line is shown in red.

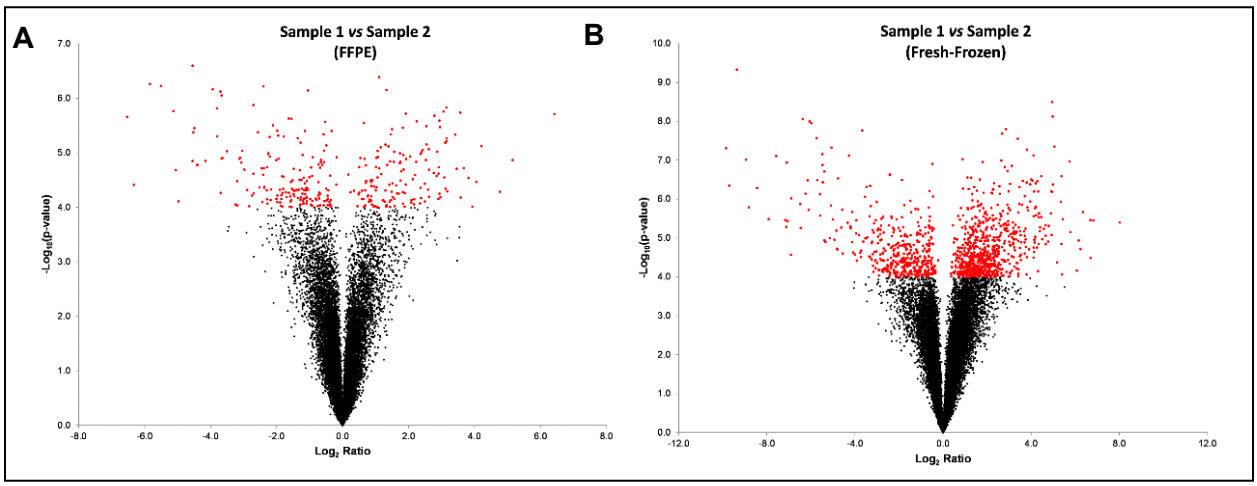

Fig. S2. ***Differentially expressed genes between biological types.*** Volcano plots for (**A**) FFPE and (**B**) fresh-frozen comparisons, where red points correspond to significantly altered probe sets for each comparison.

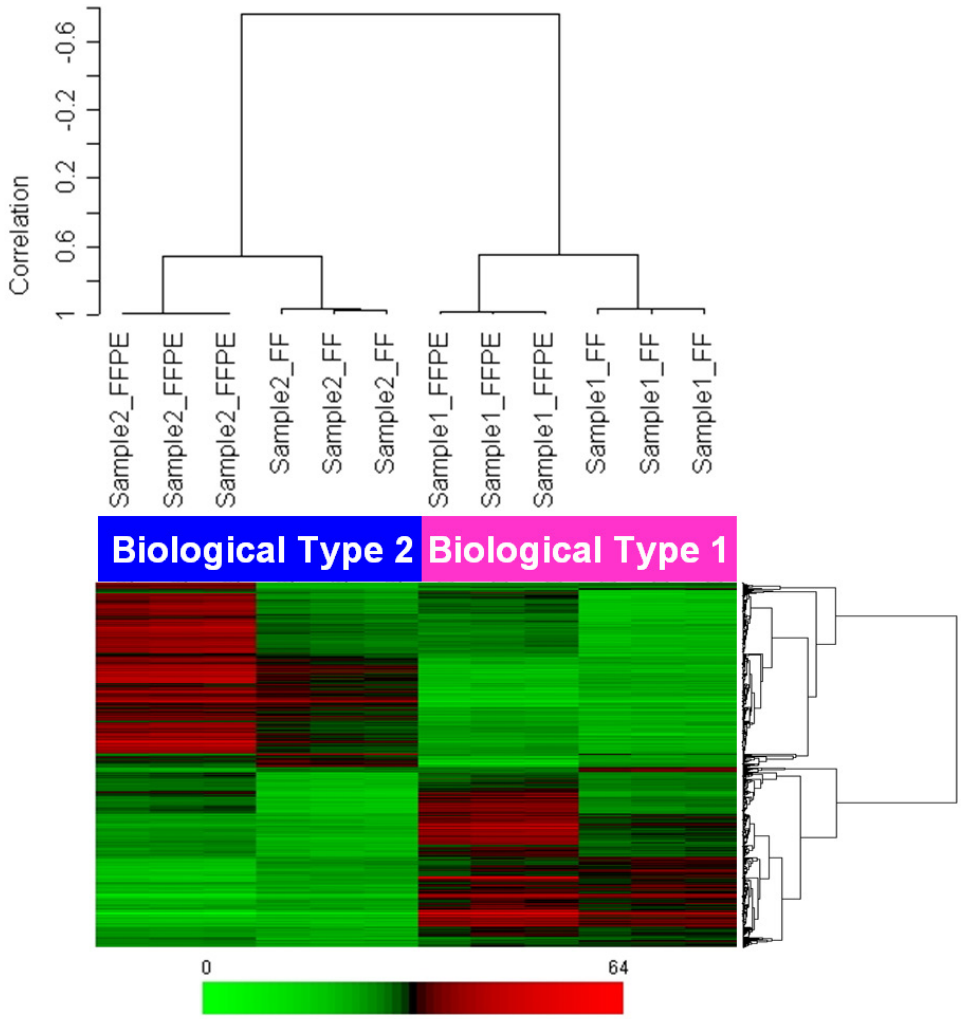

Fig. S3. ***Supervised hierarchical clustering analysis.*** The heat map and agglomerative dendrogram illustrate the correlation between triplicates of paired FFPE: fresh-frozen samples based on 241 differentially expressed probe sets between the two different biological types. The dendrogram correlation distance bar among tissue types (Biological Types) is shown. Green: down-regulation; Red: up-regulation; FFPE: formalin-fixed, paraffin-embedded; FF: fresh-frozen.

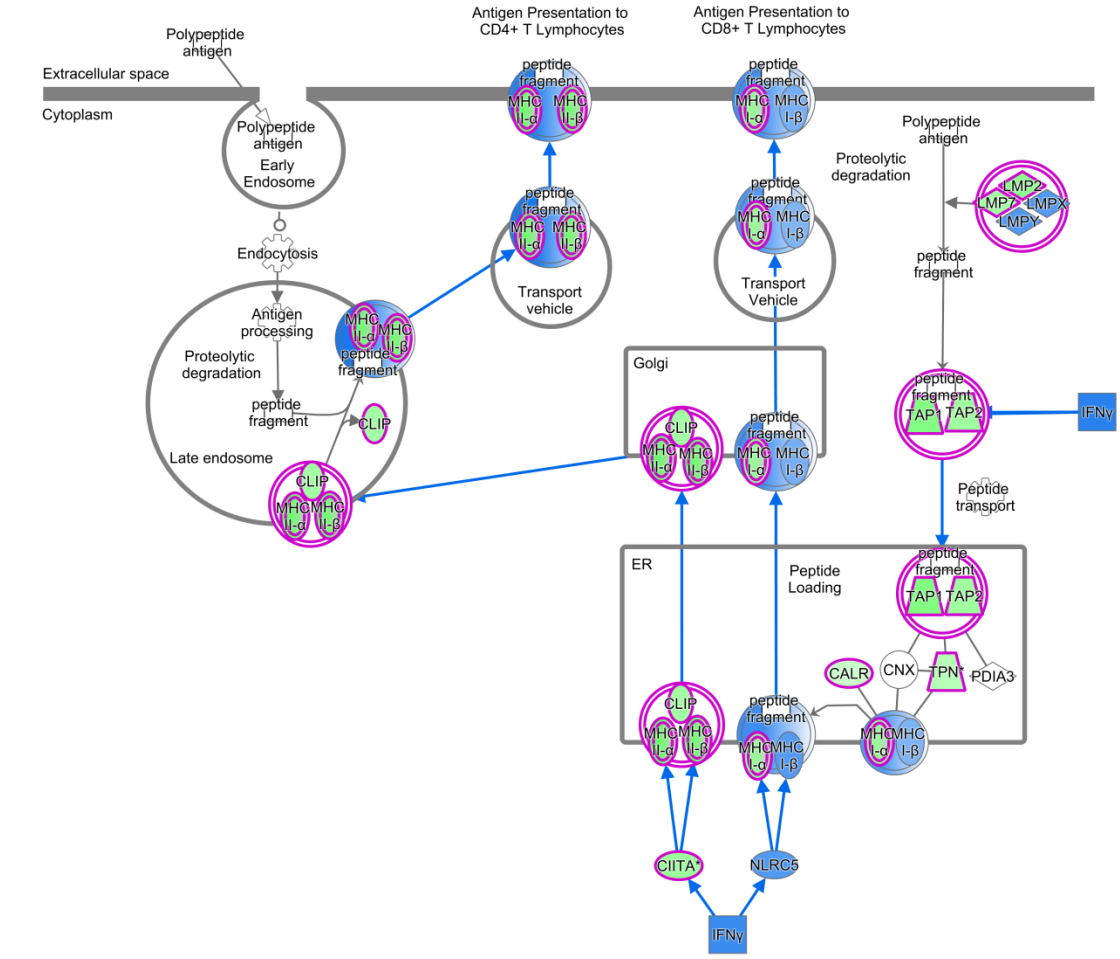

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Fig. S4A. ***Principal canonical pathways downregulated in FCRx vs. R samples.***

A. Antigen presentation pathway. Green: downregulated.

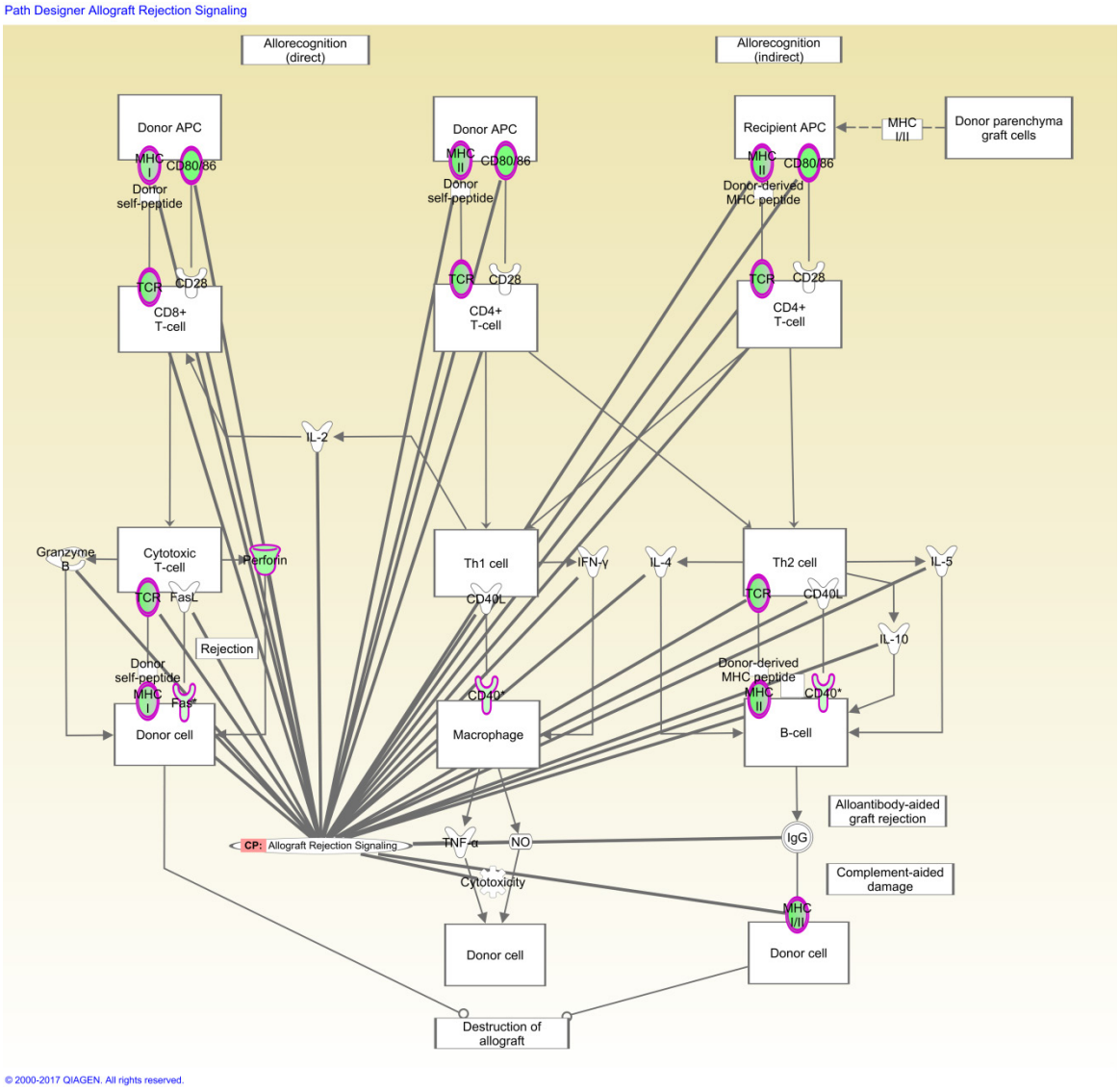

Fig. S4B. Principal canonical pathways downregulated in FCRx vs. R samples.

B. Pathway design for allograft rejection signaling in association with differentially expressed genes robustly related with absence of acute rejection in the FCRx samples.

Table S1. Immune response related cellular functions of FCRx upregulated genes versus SIS			
Cellular Function	**Molecules**	**z-score**	**p-Value**
recruitment of granulocytes	ACKR1,APOA1,CAT,CD14,CXCL8,CXCL9,CYP1A2,DPP4,FASTK,GRK6,HSPA1A/HSPA1B,IKBKB,IL1RL1,IRF3,KDM6B,KITLG,MDK,PIK3CD,PRKCQ,PTN,RASGRP2,SELPLG,SMAD3,SOD2,ST3GAL4,THBS1,TRAF3IP2,VAV2	3.32	4.97E-02
proliferation of blood cells	ACLY,ADA,AHNAK,APOA1,ARIH2,BABAM1,BAX,BBC3,BCL2,BCL6,BCLAF1,BHLHE40,BMI1,BMP4,CASP8,CAT,CD14,CD24,CD27,CD58,CD79A,CD83,CDKN1B,CEBPB,CSF2RA,CTSZ,CXCL8,DGCR8,DGKA,DIAPH1,DLG1,DPP4,DRD2,EPO,EPOR,ERCC1,ETS1,ETV6,FGFR1,FUBP1,GADD45A,GADD45B,GP2,GRM5,GSTP1,HES1,HMGA1,HOXB3,HSF1,HSPA1A/HSPA1B,ID2,IFNGR1,IKBKB,IKZF2,IL1RL1,IL23A,IMPDH1,ITGB1,JUNB,JUND,KITLG,KLF9,LAT2,LPIN1,MAF,MAPK11,MAPK3,MARCH7,MDK,MED1,MICA,MSN,MYH10,NDFIP1,NFATC3,NFKBIA,NOTCH3,PBX1,PIK3CD,PKN1,PLAU,PRKAR1A,PRKCQ,PRNP,PTN,PTPN11,RARA,RHBDF2,RNF128,SLAMF1,SMAD3,SPHK2,SPN,ST3GAL2,STAT1,STAT5B,TCF12,TCF3,TG,THBS1,TNFRSF12A,TNFRSF21,TOB1,TRAF2,TRIM33,VAV2,VEGFA,ZBTB32	2.614	2.54E-02
cell viability of leukocyte cell lines	BCL2,CADM1,CD27,CSF2RA,EPO,ETV6,FGFR1,GRK6,KITLG,MCL1,MYBL2,PTPN1,YWHAZ	2.6	1.26E-02
growth of lymphoid organ	APP,BBC3,BMP4,CD79A,CDKN1B,IFNGR1,IKBKB,IMPDH1,KITLG,LFNG,MAP3K3,MAPK3,NFKBIA,PIK3CD,PRKCQ,PTGES2,RNF128,SMAD3,STAT5B,TCF12,TCF3	2.449	1.51E-02
production of hematopoietic progenitor cells	ADA,EPO,EPOR,ETS1,ID2,KITLG,NFKBIA,THRA	2.433	3.38E-03
quantity of T lymphocytes	ADA,APOA1,APP,ARID5A,ATP6AP2,BAD,BAX,BBC3,BCL2,BCLAF1,BHLHE40,CASP8,CD27,CD79A,CD83,CDKN1B,DDX58,DGKA,DIAPH1,DNMT1,DNMT3A,E2F4,EEF1D,ETS1,ETV6,FGFR1,GADD45A,GADD45B,GALNT1,GRK6,HDAC3,HELLS,HIVEP2,ID1,ID2,IFNGR1,IKBKB,IL1RL1,IL23A,IRAK1,KITLG,MAF,MAPK3,MCL1,MDK,MR1,MYBL2,NBN,NDFIP1,NFATC3,NFKBIA,NOTCH3,PBX1,PIK3CD,PRKCQ,PRNP,SELPLG,ST14,ST3GAL2,STAT1,STAT5B,TCF12,TCF3,TCF4,TG,THBS1,THRA,TNFRSF21,TOB1,TRAF2,TRAF3IP2,TRIB2,UPF1,VAV2,VEGFA,ZBTB17	2.224	2.67E-03
development of burst-forming erythroid cells	EPO,EPOR,IFNGR1,KITLG,STAT1,VEGFA	2.219	3.75E-05
survival of pro-B lymphocytes	BCL2,HLF,PML,STAT5B,TCF3	2.191	8.33E-03

cell movement	ACKR1,ADA,ADAM15,ADD2,APBA3,APOA1,APP,AQP3,BAX,BCL2,BMP4,CAT,CD14,CD200,CD207,CD58,CKLF,CREB3,CSF2RA,CTSZ,CX3CL1,CXCL8,CXCL9,CYP1A2,DAXX,DCTN2,DIAPH1,DPP4,DRD2,EGFL7,ENTPD1,EPO,EPS8,ETS1,ETV6,FASTK,FCER1A,FGFR1,FLNA,G6PC,GALNT1,GNA11,GNAS,GPSM3,GRK6,HP,HSPA1A/HSPA1B,IFNGR1,IKBKB,IL1RL1,IL23A,IRF3,ITGB1,KDM6B,KITLG,KNG1,LUM,MAPK3,MDK,MMP14,NARS,NDST1,NFE2L2,NFKBIA,NOTCH3,PA2G4,PIK3CD,PLAU,PLXND1,PRKCQ,PRNP,PTN,PTPN1,PTPN11,PVR,RALGDS,RAMP1,RAP1A,RAP1GAP,RASGRP2,RGS3,SELPLG,SLAMF1,SLAMF8,SMAD3,SOD2,SPHK2,SPN,ST3GAL4,STAT2,THBS1,TRAF3IP2,VAMP7,VASP,VAV2,VEGFA	2.055	4.1E-02
proliferation of activated T lymphocytes	BAX,BCL2,CD24,CDKN1B,EPO,HSPA1A/HSPA1B,IL23A,PRKCQ,SLAMF1,SMAD3,STAT5B	2.035	2.02E-02

Table S2A. Upstream regulators with significant predicted activation in FCRx *vs*. SIS			
Upstream Regulator (*)	**Molecule Type**	**Activation z-score**	**p-value of overlap**
EIF4E	translation regulator	2.6	0.013
CD5	transmembrane receptor	2	0.238
MYCN	transcription regulator	3.1	0.00273
IRF3	transcription regulator	2.9	0.00289
IRF7	transcription regulator	2.8	0.232
EBF1	transcription regulator	2.8	0.00054
IRF5	transcription regulator	2.6	0.0867
ETS1	transcription regulator	2.4	0.00452
POU2F2	transcription regulator	2.3	0.0114
NEUROG1	transcription regulator	2.2	0.388
KLF11	transcription regulator	2.2	0.0189
IRF8	transcription regulator	2	0.0379
IRF1	transcription regulator	2	0.432
GMNN	transcription regulator	2	1
SOX1	transcription regulator	2	0.488
SOX3	transcription regulator	2	1
STAT5B	transcription regulator	2	0.0158
TP73	transcription regulator	2	0.00113
NFATC2	transcription regulator	2	0.144
RUNX3	transcription regulator	2	0.238
PTF1A	transcription regulator	2	0.0868
FGF8	growth factor	2.8	0.22
IGF1	growth factor	2.4	3.7E-05
BMP2	growth factor	2.2	0.00798
TGFB1	growth factor	2	1.8E-17
IFNA2	cytokine	3	6.9E-05
IFNB1	cytokine	2.9	0.00125
IFNG	cytokine	2.4	6.9E-05
IFNL1	cytokine	2.2	5.5E-05
IFNA1/IFNA13	cytokine	2	0.0188
FHIT	enzyme	2.4	0.00981
MGEA5	enzyme	2.4	2.2E-07
PIN1	enzyme	2.2	0.164
IRS1	enzyme	2.2	0.00024
EHHADH	enzyme	2	0.0121
HSD17B4	enzyme	2	0.0603
Fcor	enzyme	2	0.00358
ERBB2	kinase	2.9	3.5E-08
EPHB4	kinase	2.1	0.0135
Smad	complex	2	0.018
NR5A2	ligand-dependent nuclear receptor	2.2	0.049
miR-200b-3p	mature microrna	2	0.0769
FSHR	g-protein coupled receptor	2	0.0135
Interferon alpha	group	3.2	0.00121
IFN Beta	group	2.4	0.00072

IFN type 1	group	2.3	0.00067
Insulin	group	2.1	0.00645
Akt	group	2.1	2.8E-05
Calmodulin	group	2	0.312
Ins1	other	3.4	0.00017
MAVS	other	2.4	0.164
MUC1	other	2.2	0.00018
(*) All upstream regulators are predicted as activated			

Table S2B. Regulator effects associated with FCRx vs. SIS gene profile

Regulators	Consistency Score	Target Molecules in Dataset	Diseases & Functions
EPHB4	6.124	BMP4,CSF2RA,KITLG,PAX3,STAT5B,TBX2	cell transformation,development of genitourinary system,organismal death,proliferation of blood cells
EIF4E,Ins1,INSR,Insulin,IRF8,MGEA5,PKD1,PPARGC1A	5.774	BCL2,CDKN1B,CEBPB,ERCC1,FGF18,MED1,NFE2L2,NFKBIA,PML,THBS1,TNFRSF12A,VEGFA	proliferation of hepatocytes
EIF4E	4.596	BAD,BCL2,CDC34,CEBPB,MCL1,NFKBIA,NOL3,PA2G4	cell death of melanoma cell lines,invasion of cells,proliferation of epithelial cells
ETS1,GFI1	3.328	BMP4,CXCL8,DIAPH1,ID2,IKBKB,JUNB,MAPK3,NFKBIA,PLAU,PML,SMAD3,STAT1,TRAF2	Growth Failure,transactivation
mir-122,miR-122-5p	2.858	MAPK11,PKM,PTPN1,RAD21,SLC7A1,TRPV6	cell viability
IRS1	2.673	BMP6,CEBPB,G6PC,ID2,LAMA4,MAPK12,MMP14,MYBL2,NR2F1,PAX3,PCK1,PDGFA,THRA,VEGFA	cell movement of endothelial cells,cell movement of tumor cell lines,cell survival,concentration of D-glucose,neonatal death,quantity of T lymphocytes,transactivation of RNA
IFNL1,IRF3,MUC1	2.593	AHNAK,BAD,CD83,CXCL8,DDX58,HERC6,IFI44,IFITM1,IKBKB,JUNB,NFKBIA,PLAU,PML,PPP2R3A,SOD2,SORL1,SP100,STAT1	cell cycle progression,neoplasia of epithelial cells,Renal Cancer and Tumors,urinary tract cancer
EBF1,POU2F2	2.5	BCL6,PIK3CD,SCD,TCF3	hypoplasia of organ
NR5A2	2.449	APOA1,BCL2,CEBPB,JUNB,LHB,TDGF1	growth of tumor,transcription of RNA
mir-133	2.236	DNMT1,FSCN1,GSTP1,HCN2,MMP14	migration of tumor cell lines,organismal death

ESR1,IFN Beta,IFNA2,IFNB1,Interferon alpha,MUC1	2.186	AHNAK,ATP2B1,BAX,BCL2,BHLHE40,CALD1,CDKN1B,CXCL8,DDX58,ENPEP,FGFR1,FLNA,G6PD,GLS,GNAS,HSP90AA1,HSPA1A/HSPA1B,IFITM1,IGFBP5,IKBKB,ITGB1,KL,MCRS1,MR1,MUC5AC,NFKBIA,NUP153,PALLD,PDE4A,PSD4,PTPRT,RAD21,RARA,RHEB,SMC3,SOD2,SULT1C2,THBS1,UBA7,VCL,VEGFA	Renal Cancer and Tumors,urinary tract cancer
EBF1	2.041	ACACB,BCL6,EIF4EBP1,INPPL1,PTPN1,STAT1	size of body
Ins1	2	CDKN1B,CEBPB,E2F4,ERCC1,G6PD,JUNB,MAPK3,PRLR,VEGFA	proliferation of fibroblast cell lines,proliferation of hepatocytes
IFNA1/IFNA13	1.732	IFITM1,STAT1,UBE2L6	invasion of tumor cell lines
IFN Beta,IFN type 1,IFNA2,Interferon alpha,MUC1	1.491	APOL2,ATF5,BAX,BCL2,BCL6,BMP4,CASP8,CD83,CDKN1B,CEBPB,CHMP5,CX3CL1,CXCL8,CYP1A2,DDX58,DPP4,E2F4,ENPEP,EPB41L3,GLS,GNAS,HERC6,HSPA1A/HSPA1B,IFI44,IFITM1,IKBKB,ITGB1,KDM5A,MCL1,MCRS1,N4BP1,NFKBIA,OGFR,PLAU,PML,PTBP1,RNF31,SOD2,SP100,STAT1,STAT2,TRANK1,TRIB2,UBA7,VEGFA	neoplasia of epithelial cells,Renal Cancer and Tumors,tumorigenesis of genital tumor,urinary tract cancer
COL18A1,mir-122,TFAM	1.429	ACADM,AUH,BAD,BCL2,CYP1A2,ETS1,F11,FGFR1,HK1,ID1,KNG1,MAP3K3,MAX,MCL1,PFKP,PKM,PLAU,PTPN1,RAD21,SPOCK1,STAT1,THBS1,TNPO2,VEGFA	epithelial-mesenchymal transition,necrosis of malignant tumor,tumorigenesis of genital tumor
ESR1,IFN Beta,IFN type 1,IFNA2,IFNB1,MUC1,PKD1	1.209	ABCA4,ACTR2,ADD3,AHNAK,ANAPC5,ATP11A,ATP2A3,ATP2B1,ATP6V1A,BAX,BAZ2A,BCL2,BCL6,BCLAF1,BHLHE40,BMP4,BRAP,CA2,CALD1,CASP8,CD14,CDKN1B,CKB,CNP,CPE,CX3CL1,CXCL8,CYFIP2,CYP1A2,CYP2C9,DAB2,DDX58,DIAPH1,DLG1,DPP4,ENPEP,EPB41L3,EZH1,FBN1,FGFR1,FLNA,FMR1,FOXC1,G6PC,G6PD,GABBR2,GATM,GLS,GNAS,GPRASP1,GULP1,HERC6,HSP90AA1,HSPA2,IDH1,IFI44,IFITM1,IFNGR1,IFRD1,IGFBP5,IKBKB,IL1RL1,IRF3,JUNB,KDM4B,KDM5A,KL,KNG1,KPNA3,KTN1,LANCL1,LHB,MADD,MAN1A1,MAPK11,MAPK8IP3,MAST2,MINK1,MR1,MUC5AC,MYH10,MYO6,N4BP1,NFIX,NFKBIA,NOTCH3,NUP153,NUP210,PAH,PALLD,PCDH9,PDCD4,PDE4A,PDZK1,PLCB1,PLCE1,PPP5C,PRKAR1A,PRLR,PSD4,PTPRT,RAD21,RAMP3,RARA,RDX,RGS3,RHEB,RRBP1,SEC23IP,SEMA4C,SH2B1,SLC25A36,SLC2A2,SLC7A1,SMC3,SOD2,STAT1,STAT2,STX6,SULT1C2,TBCD,TEAD4,TGOLN2,THBS1,THBS3,THBS4,TMF1,TNFAIP2,TNPO1,TRAF2,TRIM38,UBA7,VCL,VEGFA	genitourinary carcinoma,Renal Cancer and Tumors,tumorigenesis of genital tumor,urinary tract cancer

IFN type 1,IGF1,IL1RN, MYCN,RB1	1.134	ADA,APP,BAX,BBC3,BCL2,BCL6,CAD,CCNA2,CDKN1B,CEBPB,CXCL8,DNMT1,DNMT3A,ETV6,FBN1,ID1,ID2,IFI44,IFI6,IGFBP7,MAF,MCL1,NBN,NFKBIA,SP100,STAT1,STAT2,VEGFA	non-Hodgkin disease
TCF7L2	0.354	BMP4,CDKN1B,HSPA2,ID4,LAMP1,PTPN11,QKI,VEGFA	development of genital organ
PKD1	0.218	DDX3Y,DPEP1,EIF4EBP1,EZH1,FGFR1,GATM,GLS,GPRASP1,IDH1,KNG1,MINK1,PAH,PCDH7,PCDH9,PCK1,PRLR,RGS3,SEMA4C,SLC16A4,SLC2A2,TRAF2	tumorigenesis of epithelial neoplasm

Table S3. Cell type enrichment for differentially expressed genes between FCRx and SIS	
Cell Type	Enrichment adjusted-*P* value
Kidney	0.000176064
CD33+ Myeloid	0.005398789
CD8+ T Cells	0.007401828
BDCA4+ Dentritic Cells	0.007764024
CD4+ T Cells	0.009844623
CD19+ B cells	0.036294635

Table S4. Cell type enrichment for differentially expressed genes between FCRx and D	
Cell type	**Enrichment adjusted-*P* value**
CD56+ NK Cells	0.001628
CD14+ Monocytes	0.006796
CD19+ B cells	0.008276
CD105+ Endothelial	0.010358
CD33+ Myeloid	0.018414
CD34+	0.024458

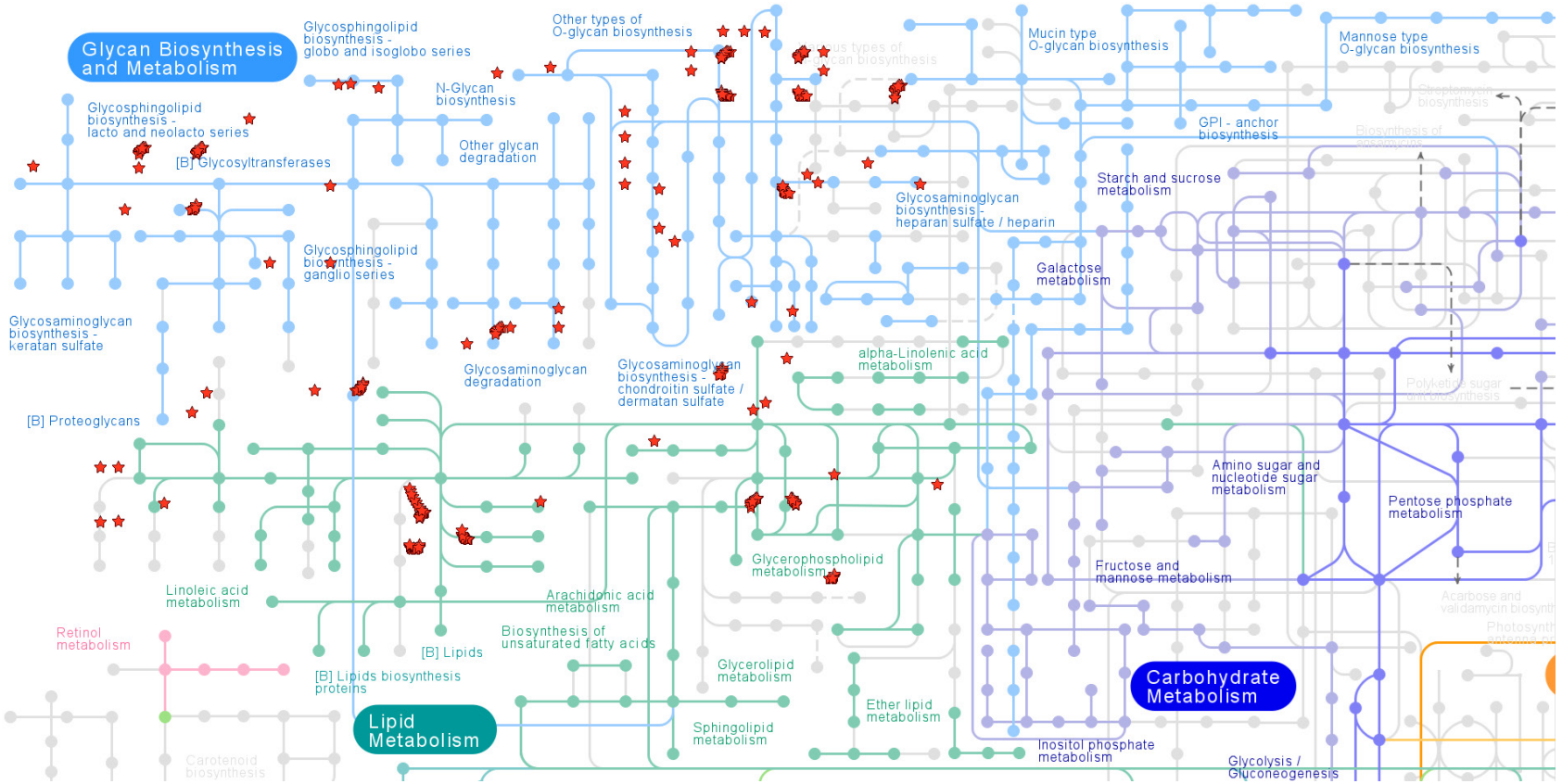

Fig. S5. ***KEGG pathway for metabolism showing involvement of listed genes in Glycan biosynthesis and metabolism*** The differentially expressed genes between FCRx and D were plotted on KEGG pathway (using DAVID)for metabolism and the genes (red stars) were found to be involved in glycan biosynthesis.

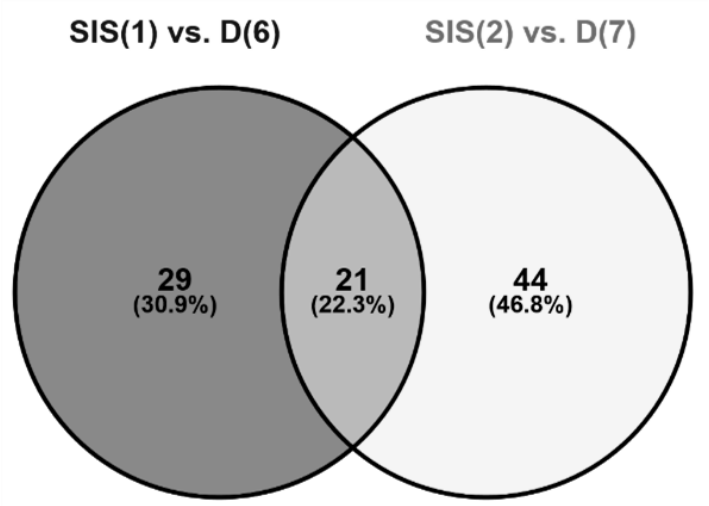

Fig. S6. ***Venn diagrams from FCRX vs. D and SIS vs. D pairwise comparisons.*** The numbers of unique and common differentially expressed genes between single SIS *vs.* D comparisons are shown.

Table S5. Genes differentially expressed in common between SIS *vs.* D

Symbol	Gene Name	Fold-change (SIS *vs.* D)
PDK4	pyruvate dehydrogenase kinase, isozyme 4	-14.1
EGR1	early growth response 1	-13.9
DUSP1	dual specificity phosphatase 1	-9.0
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-7.0
CYR61	cysteine-rich, angiogenic inducer, 61	-6.5
FOS	FBJ murine osteosarcoma viral oncogene homolog	-5.7
ZFP36	ZFP36 ring finger protein	-5.0
GADD45B	growth arrest and DNA-damage-inducible, beta	-4.3
JUN	jun proto-oncogene	-4.1
IER2	immediate early response 2	-3.9
KLF6	Kruppel-like factor 6	-3.2
RHOB	ras homolog family member B	-2.7
FOSL2	FOS-like antigen 2	-2.2
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	-2.1
KLF9	Kruppel-like factor 9	-1.8
JUND	jun D proto-oncogene	-1.4
HLA-B	major histocompatibility complex, class I, B	2.1
CYCS	cytochrome c, somatic	3.8
CD24	CD24 molecule	5.2
IGF2	insulin-like growth factor 2 (somatomedin A)	6.5
SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	10.3

Confirmation of DEGs identified by SensationPlus with RT-qPCR assays.

To further validate the global gene expression profile comparisons described above using SensationPlus assays, the relative levels of the top 3 DEGs were quantified using Taqman RT-qPCR assays. As shown in **Fig. S7**, there was concordance between the two assays with the selected genes demonstrating comparable expression trends albeit with different levels of statistical significance and dynamic ranges. Moreover, the two differentially expressed genes tested between SIS and FCRx (referred as a T in the Fig. 7), were validated for same RNA samples used for arrays (Fig. 7A) and evaluating same FCRx RNA samples with an independent set of SIS samples (Fig. 7B) [SIS samples used for second validation are described in Table-1 as labeled with (*)].

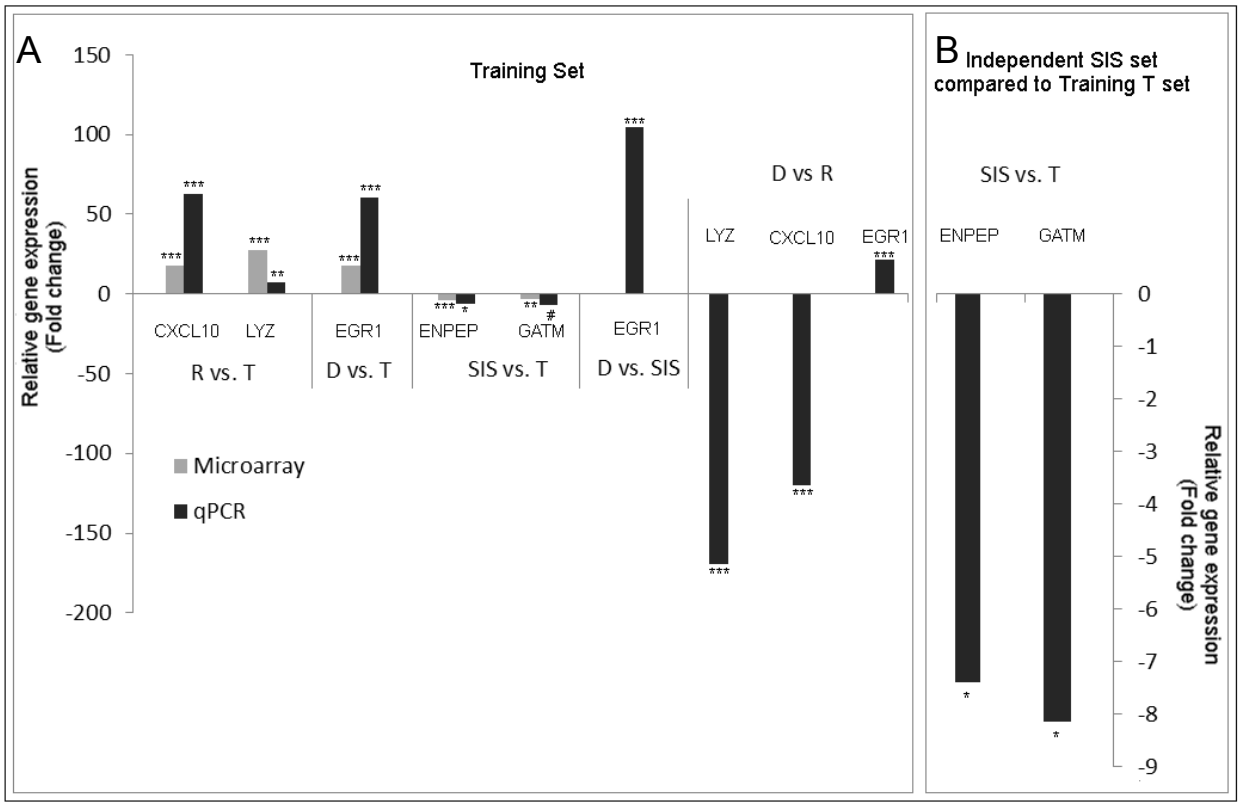

Fig. S7. ***Comparison and validation of selected genes.*** Taqman RT-qPCR assays were performed to validate the differential expression of CXCL10, LYZ, and EGR1. Expression trends observed by RT-qPCR (black bars) were compared to those obtained by microarrays (gray bars) in the comparisons mentioned in the graphic. (#) trend of significance; (*) $p < 0.05$; (**) $p < 0.01$; (***) $p < 0.001$. T refers to FCRx sample group.

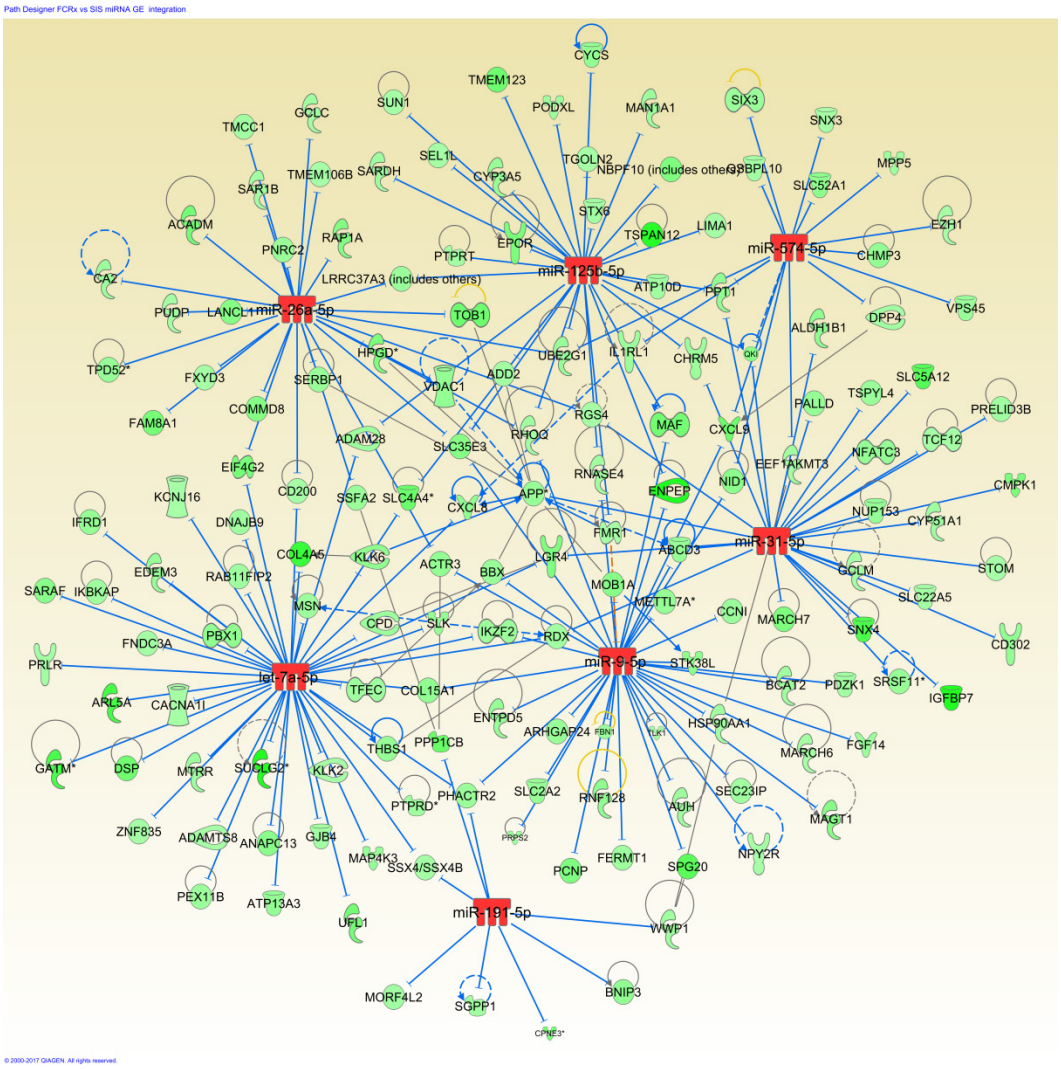

Fig. S8. ***Integrative networks showing miRNA differentially expressed from FCRx vs. SIS and their targets***. The 7 significantly upregulated miRNA in FCRx target 198 genes to be differentially down regulated as shown in the network generated by the miRNA target profiler using Ingenuity pathway analysis software. The color codes are represented in the legend present in the figure.

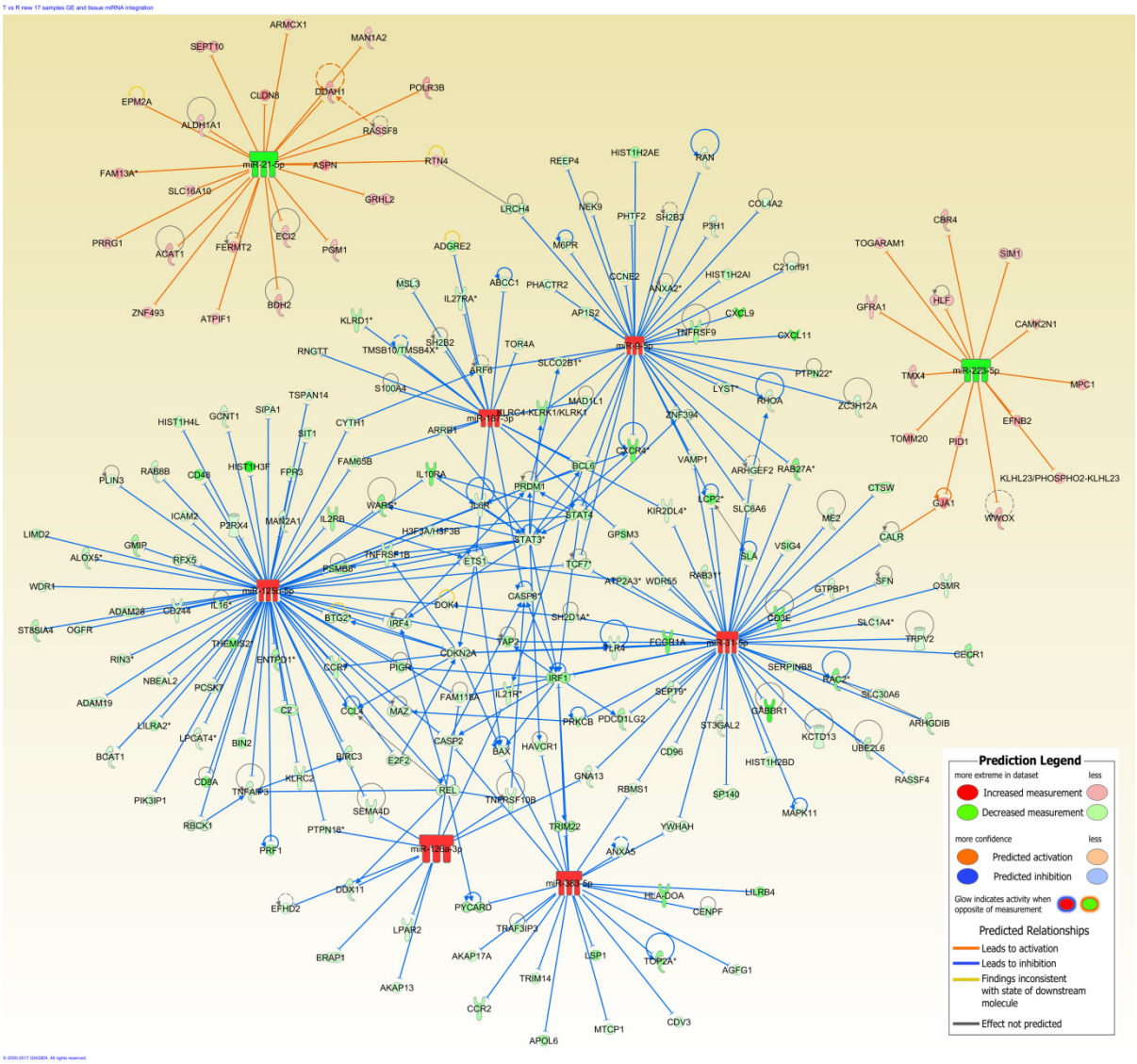

Fig. S9. ***Integrative networks showing miRNA differentially expressed from FCRx vs. R and their targets.*** Seven of the 10 significantly upregulated miRNA in FCRx target 75 differentially down regulated genes as shown in the network generated by the miRNA target profiler using Ingenuity pathway analysis software. The color codes are represented in the legend present in the figure.