

SUPPLEMENTAL MATERIAL

I. Statistical analysis

Microarray expression data were processed with *GeneSpring GX* v11 software. Expression data were normalized based upon quantiles (threshold 1). Baseline transformation was not performed. Data were filtered by expression level (percentile 20 lower cut-off on raw data) and flag (not detected and compromised spots were removed) when less than 75% of the values in any of both conditions had not acceptable values. Asymptotic T-Test was performed to find differentially expressed genes according to *IL28B* genotype and to treatment response. Z-ratio was also obtained for *IL28B* genotype and for treatment response comparisons [1]. Genes with a *p*-value less than 0.05 and a Z-ratio higher than 3 or lower than -3 were selected for functional analysis.

Gene annotation and functional pathways analysis was based on GeneDecks v.3 (GeneCards website <http://www.genecards.org>) and Ingenuity Pathways Analysis (<http://www.ingenuity.com>). GeneDecks v3, is an analysis tool which enables the elucidation of unsuspected putative functional paralogs, and a refined scrutiny of various gene-sets for discovering relevant biological patterns [2]. Set distiller was used to rank descriptors by their degree of sharing within the selected genes. For each descriptor, a *p*-value was calculated from the binomial distribution, testing the null hypothesis that the frequency of the descriptor in the query set was not significantly different from what was expected with a random sampling of genes, given the frequency of the descriptor in the set of all genes. Bonferroni correction was used to correct for

multiple testing and only descriptors with p -value < 0.05 were displayed. Ingenuity Pathways Analysis (IPA) is software that helps analyze and understand complex list of genes generated by high-throughput technologies. IPA was used to rank the top canonical pathways represented in the differentially expressed genes. Hierarchical clustering was conducted by average linkage and Pearson correlation using Multiexperiment Viewer v4.6 [3].

References

- [1] Cheadle C, Vawter M, Freed W, Becker K. Analysis of microarray data using Z score transformation. J Mol Diagn 2003; 5:73-81.
- [2] Stelzer G, Inger A, Olender T, Iny-Stein T, Dalah I, Harel A, et al. GeneDecks: paralog hunting and gene-set distillation with GeneCards annotation. OMICS 2009; 13:477-87.
- [3] Saeed AI, Sharov V, White J, Li J, Liang W, Bhagabati N, et al. TM4: a free, open-source system for microarray data management and analysis. Biotechniques 2003; 34:374-8.

Supplemental Table 1. Sequences of reverse and forward oligonucleotides used in RT-PCR assays

Gene	Forward oligonucleotide	Reverse oligonucleotide
ACTB	5'-CCC GCG AGT ACA ACC TTC T-3'	5'-GTC ATC CAT GGC GAA CT-3'
HPRT1	5'- GAC CAG TCA ACA GGG GAC AT -3'	5'- GTG TCA ATT ATA TCT TCC ACA ATC AAG -3'
GAPDH	5'- AGC CAC ATC GCT CAG ACA C-3'	5'- GCC CAA TAC GAC CAA ATC C-3'
IFI44L	5'- AGC CGT AGT GGG GTC TGA TA-3'	5'- CCA TCT AGC CCC ATA GTG TCA-3'
IFIT3	5'- GCA GAG ACA CAG AGG GCA GT-3'	5'- TGG CAT TTC AGC TGT GGA-3'
RSAD2	5'- TGC TTT TGC TTA AGG AAG CTG-3'	5'- AGG TAT TCT CCC CGG TCT TG-3'
PNPLA2	5'- CTC CAC CAA CAT CCA CGA G-3'	5'-CCC TGC TTG CAC ATC TCT C-3'
IL1B	5'-CTG TCC TGC GTG TTG AAA GA-3'	5'- TTG GGT AAT TTT TGG GAT CTA-3'

Supplemental Table 2.- *IL28B* genotype associated genes. Genes with a p-value < 0.05 and Z-ratio >3 ó <-3 were selected as differentially expressed. Fold Change is calculated as ratio between mean signal in CC patients and mean signal in CT patients for rs12979860. Ratios lower than 1 are expressed as -1/ratio to obtain an equivalent value to ratios higher than 1.

ProbeName	Gene Symbol	Description	Fold Change CC/CT	p-value
A_23_P140527	FOXB1	Homo sapiens forkhead box B1 (FOXB1). mRNA [NM_012182]	-4.030729	0.000094
A_24_P15640		Homo sapiens chromosome 19 open reading frame 31. mRNA (cDNA clone MGC:168631 IMAGE:9021008). complete cds. [BC137015]	-3.008071	0.000235
A_32_P84369	FAM153B	Homo sapiens family with sequence similarity 153. member B (FAM153B). mRNA [NM_001079529]	-2.7284489	0.019615
A_23_P211212	COL18A1	Homo sapiens collagen. type XVIII. alpha 1 (COL18A1). transcript variant 1. mRNA [NM_030582]	-2.5211244	0.002111
A_33_P3219870	PNPLA2	Homo sapiens patatin-like phospholipase domain containing 2 (PNPLA2). mRNA [NM_020376]	-2.4376597	0.000677
A_33_P3268167			-2.3137696	0.000982
A_33_P3287113		KIAA1530 [Source:HGNC Symbol;Acc:29304] [ENST00000296312]	-2.1725488	0.025847
A_33_P3456233		Sequence 1231 from Patent EP1308459. [AX747706]	-2.1424015	0.000058
A_33_P3393537	PTAFR	Homo sapiens platelet-activating factor receptor (PTAFR). transcript variant 2. mRNA [NM_001164722]	-2.0698624	0.026518
A_24_P224727	CEBPA	Homo sapiens CCAAT/enhancer binding protein (C/EBP). alpha (CEBPA). mRNA [NM_004364]	-1.9908366	0.024186
A_23_P256663	GALR3	Homo sapiens galanin receptor 3 (GALR3). mRNA [NM_003614]	-1.9719876	0.003422
A_33_P3387756	C20orf201	Homo sapiens chromosome 20 open reading frame 201 (C20orf201). mRNA [NM_001007125]	-1.9622935	0.019515
A_33_P3209581	IQSEC3	Homo sapiens IQ motif and Sec7 domain 3 (IQSEC3). transcript variant 1. mRNA [NM_001170738]	-1.9454334	0.015077
A_33_P3246010		family with sequence similarity 38. member A [Source:HGNC Symbol;Acc:28993] [ENST00000358442]	-1.9064708	0.003025
A_33_P3388588	LOC400558	cDNA FLJ27068 fis. clone SPL01475 [Source:UniProtKB/TrEMBL;Acc:Q6ZNV2] [ENST00000378340]	-1.8933753	0.005423
A_23_P36753	ALDH2	Homo sapiens aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2). nuclear gene encoding mitochondrial protein. mRNA [NM_000690]	-1.882977	0.046328
A_33_P3411388	UNCX	Homo sapiens UNC homeobox (UNCX). mRNA [NM_001080461]	-1.8672414	0.000466
A_33_P3265606	GCLM	Homo sapiens glutamate-cysteine ligase. modifier subunit (GCLM). mRNA [NM_002061]	-1.8572714	0.000012
A_23_P352435	RGS12	Homo sapiens regulator of G-protein signaling 12 (RGS12). transcript variant 2. mRNA [NM_002926]	-1.8482109	0.018843
A_23_P213832	SPINK7	Homo sapiens serine peptidase inhibitor. Kazal type 7 (putative) (SPINK7). mRNA [NM_032566]	-1.8468797	0.005333
A_33_P3274009	LOC100132966	Homo sapiens cDNA FLJ42565 fis. clone BRACE3007472. [AK124556]	-1.8438154	0.003077
A_33_P3546363	LOC400128	AGENCOURT_8883169 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6199956 5'. mRNA sequence [BQ950045]	-1.8155982	0.002572
A_24_P280497	FBRSL1	Homo sapiens fibrosin-like 1 (FBRSL1). mRNA [NM_001142641]	-1.7633984	0.018194
A_33_P3338961		Q96ID7_HUMAN (Q96ID7) E2F2 protein. partial (18%) [THC2597193]	-1.761964	0.000881
A_33_P3219720	ZNF248	Homo sapiens zinc finger protein 248. mRNA (cDNA clone IMAGE:4940056). complete cds. [BC021819]	-1.7312063	0.000522
A_33_P3883985		Homo sapiens cDNA clone IMAGE:5285809. [BC098409]	-1.7204062	0.040778
A_24_P105933	VIPR1	Homo sapiens vasoactive intestinal peptide receptor 1 (VIPR1). mRNA [NM_004624]	-1.7103155	0.023268
A_33_P3312030			-1.6671058	0.034174
A_33_P3275835	TOR2A	Homo sapiens torsin family 2. member A (TOR2A). transcript variant 3. mRNA [NM_001134430]	-1.6364704	0.007449

A_33_P3220152	SBNO2	Homo sapiens strawberry notch homolog 2 (Drosophila) (SBNO2). transcript variant 1. mRNA [NM_014963]	-1.6243027	0.024749
A_33_P3227731			1.5972579	0.049055
A_32_P216602		DB229023 TRACH3 Homo sapiens cDNA clone TRACH3022015 5'. mRNA sequence [DB229023]	1.6992368	0.000022
A_32_P219368	WTAP	Homo sapiens Wilms tumor 1 associated protein (WTAP). transcript variant 3. mRNA [NM_152858]	1.7007257	0.000084
A_33_P3231277	HIF1A	Homo sapiens hypoxia inducible factor 1. alpha subunit (basic helix-loop-helix transcription factor) (HIF1A). transcript variant 2. mRNA [NM_181054]	1.7570627	0.008423
A_33_P3412125			1.777858	0.000735
A_23_P79518	IL1B	Homo sapiens interleukin 1. beta (IL1B). mRNA [NM_000576]	1.7939132	0.011670
A_33_P3308115		Homo sapiens. Similar to LOC223018. clone IMAGE:4732541. mRNA. [BC029410]	1.7953843	0.006618
A_33_P3219105			1.7985915	0.026716
A_33_P3424803	HLA-C	Human MHC class I HLA-Cw1 gene. complete cds. [M26429]	1.8221884	0.009815
A_33_P3375934	NAMPT	Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT). mRNA [NM_005746]	1.8289874	0.046994
A_23_P37983	MT1B	Homo sapiens metallothionein 1B (MT1B). mRNA [NM_005947]	1.8377678	0.045383
A_24_P333106	RPL23AP71	full-length cDNA clone CS0DI028YD16 of Placenta Cot 25-normalized of Homo sapiens (human). [CR595167]	1.8417434	0.001259
A_24_P349743	RPSA	Homo sapiens ribosomal protein SA (RPSA). transcript variant 1. mRNA [NM_002295]	1.8946574	0.000879
A_33_P3369550	SFRS11	Homo sapiens splicing factor. arginine/serine-rich 11 (SFRS11). mRNA [NM_004768]	1.9219003	0.006734
A_23_P79094	LILRA3	Homo sapiens leukocyte immunoglobulin-like receptor. subfamily A (without TM domain). member 3 (LILRA3). transcript variant 1. mRNA [NM_006865]	1.9693302	0.035283
A_23_P12572	CASP7	Homo sapiens caspase 7. apoptosis-related cysteine peptidase (CASP7). transcript variant delta. mRNA [NM_033338]	1.9915092	0.035417
A_33_P3350056	MT1X	Homo sapiens metallothionein 1X (MT1X). mRNA [NM_005952]	2.049589	0.026567
A_33_P3267865		major histocompatibility complex. class I. J (pseudogene) (HLA-J). non-coding RNA [Source:RefSeq DNA;Acc:NR_024240] [ENST00000376793]	2.0965207	0.015003
A_23_P72096	IL1A	Homo sapiens interleukin 1. alpha (IL1A). mRNA [NM_000575]	2.1018004	0.044863
A_33_P3354607	CCL4	Homo sapiens chemokine (C-C motif) ligand 4 (CCL4). transcript variant 1. mRNA [NM_002984]	2.1212718	0.020578
A_33_P3382560	RPL23A	Homo sapiens ribosomal protein L23a (RPL23A). mRNA [NM_000984]	2.2807457	0.000140
A_23_P121596	PPBP	Homo sapiens pro-platelet basic protein (chemokine (C-X-C motif) ligand 7) (PPBP). mRNA [NM_002704]	2.3638093	0.038956
A_23_P55649	FPR2	Homo sapiens formyl peptide receptor 2 (FPR2). transcript variant 1. mRNA [NM_001462]	2.4725761	0.009985
A_23_P41344	EREG	Homo sapiens epiregulin (EREG). mRNA [NM_001432]	2.5473683	0.003161
A_24_P245379	SERPINB2	Homo sapiens serpin peptidase inhibitor. clade B (ovalbumin). member 2 (SERPINB2). transcript variant 2. mRNA [NM_002575]	3.7200422	0.009475
A_23_P71037	IL6	Homo sapiens interleukin 6 (interferon. beta 2) (IL6). mRNA [NM_000600]	3.9431932	0.021323

Supplemental Table 3.- Treatment outcome associated genes. Genes with a p-value < 0.05 and Z-ratio>3 ó <-3 were selected as differentially expressed. Fold Change is calculated as ratio between mean signal in SVR patients and mean signal in non-SVR patients. Ratios lower than 1 are expressed as -1/ratio to obtain an equivalent value to ratios higher than 1.

ProbeName	GeneSymbol	Description	Fold change SVR/nonSVR	p-value
A_23_P112026	IDO1	Homo sapiens indoleamine 2,3-dioxygenase 1 (IDO1). mRNA [NM_002164]	-5.5233984	0.027833974
A_23_P29773	LAMP3	Homo sapiens lysosomal-associated membrane protein 3 (LAMP3). mRNA [NM_014398]	-4.2253113	0.033904858
A_23_P52266	IFIT1	Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1). transcript variant 2. mRNA [NM_001548]	-3.7085612	0.015016953
A_32_P108254	FAM20A	Homo sapiens family with sequence similarity 20. member A (FAM20A). transcript variant 1. mRNA [NM_017565]	-3.623914	0.013336637
A_33_P3283611	IFIT3	Homo sapiens interferon-induced protein with tetratricopeptide repeats 3 (IFIT3). transcript variant 1. mRNA [NM_001549]	-3.3377995	0.008421991
A_23_P45871	IFI44L	Homo sapiens interferon-induced protein 44-like (IFI44L). mRNA [NM_006820]	-2.7573175	0.023291888
A_24_P28722	RSAD2	Homo sapiens radical S-adenosyl methionine domain containing 2 (RSAD2). mRNA [NM_080657]	-2.7362208	0.026865238
A_33_P3258346	XAF1	Homo sapiens XIAP associated factor 1 (XAF1). transcript variant 1. mRNA [NM_017523]	-2.5389526	0.003222211
A_23_P500271	IRF5	Homo sapiens interferon regulatory factor 5 (IRF5). transcript variant 3. mRNA [NM_001098627]	-2.4437551	0.048883535
A_33_P3264846	SAMD9L	Homo sapiens sterile alpha motif domain containing 9-like (SAMD9L). mRNA [NM_152703]	-2.4320135	0.008996204
A_23_P351148	SH2D1B	Homo sapiens SH2 domain containing 1B (SH2D1B). mRNA [NM_053282]	-2.4244852	0.019071968
A_24_P117147	KIR3DL1	Homo sapiens killer cell immunoglobulin-like receptor. three domains. long cytoplasmic tail. 1 (KIR3DL1). mRNA [NM_013289]	-2.408801	0.005727541
A_23_P64828	OAS1	Homo sapiens 2'-5'-oligoadenylate synthetase 1. 40/46kDa (OAS1). transcript variant 2. mRNA [NM_002534]	-2.364372	0.00690191
A_24_P350622	KIR2DL4	Homo sapiens killer cell immunoglobulin-like receptor. two domains. long cytoplasmic tail. 4 (KIR2DL4). transcript variant 1. mRNA [NM_002255]	-2.348277	0.005375568
A_23_P62890	GBP1	Homo sapiens guanylate binding protein 1. interferon-inducible. 67kDa (GBP1). mRNA [NM_002053]	-2.3425112	0.005080546
A_33_P3401826	CMPK2	Homo sapiens cytidine monophosphate (UMP-CMP) kinase 2. mitochondrial (CMPK2). nuclear gene encoding mitochondrial protein. mRNA [NM_207315]	-2.2391787	0.02827096
A_23_P111132	HSPA1A	Homo sapiens heat shock 70kDa protein 1A (HSPA1A). mRNA [NM_005345]	-2.1233635	0.009430891
A_23_P69383	PARP9	Homo sapiens poly (ADP-ribose) polymerase family. member 9 (PARP9). transcript variant 1. mRNA [NM_031458]	-2.1184762	0.005155049
A_23_P17663	MX1	Homo sapiens myxovirus (influenza virus) resistance 1. interferon-inducible protein p78 (mouse) (MX1). transcript variant 2. mRNA [NM_002462]	-2.1162214	0.011462783
A_23_P50946	RAMP1	Homo sapiens receptor (G protein-coupled) activity modifying protein 1 (RAMP1). mRNA [NM_005855]	-2.099104	0.005913074
A_23_P41470	DDX60	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 (DDX60). mRNA [NM_017631]	-2.0902658	0.005535078
A_23_P24004	IFIT2	Homo sapiens interferon-induced protein with tetratricopeptide repeats 2 (IFIT2). mRNA [NM_001547]	-2.0766997	0.01489391
A_33_P3225512	OAS2	Homo sapiens 2'-5'-oligoadenylate synthetase 2. 69/71kDa (OAS2). transcript variant 2. mRNA [NM_002535]	-2.0726624	0.018963384
A_23_P132159	USP18	Homo sapiens ubiquitin specific peptidase 18 (USP18). mRNA [NM_017414]	-2.0556118	0.029526122

A_24_P87746	KIR2DS4	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4 (KIR2DS4). mRNA [NM_012314]	-2.0277166	0.041217156
A_23_P23074	IFI44	Homo sapiens interferon-induced protein 44 (IFI44). mRNA [NM_006417]	-1.9618266	0.04616727
A_23_P166797	RTP4	Homo sapiens receptor (chemosensory) transporter protein 4 (RTP4). mRNA [NM_022147]	-1.957311	0.022059795
A_23_P201459	IFI6	Homo sapiens interferon, alpha-inducible protein 6 (IFI6). transcript variant 3. mRNA [NM_022873]	-1.9270054	0.028370604
A_23_P130815	KIR2DS2	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 (KIR2DS2). mRNA [NM_012312]	-1.9104661	0.046191942
A_24_P274270	STAT1	Homo sapiens signal transducer and activator of transcription 1, 91kDa (STAT1). transcript variant beta. mRNA [NM_139266]	-1.8948139	0.008881594
A_23_P819	ISG15	Homo sapiens ISG15 ubiquitin-like modifier (ISG15). mRNA [NM_005101]	-1.864327	0.029337415
A_23_P152782	IFI35	Homo sapiens interferon-induced protein 35 (IFI35). mRNA [NM_005533]	-1.8330567	0.00436053
A_33_P3315314	MT1H	Homo sapiens metallothionein 1H (MT1H). mRNA [NM_005951]	-1.7851877	0.04789922
A_33_P3411075	FSCN1	Homo sapiens fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus) (FSCN1). mRNA [NM_003088]	-1.7785951	0.006562724
A_23_P68155	IFIH1	Homo sapiens interferon induced with helicase C domain 1 (IFIH1). mRNA [NM_022168]	-1.764253	0.011714094
A_23_P38346	DHX58	Homo sapiens DEXH (Asp-Glu-X-His) box polypeptide 58 (DHX58). mRNA [NM_024119]	-1.7479421	0.027008846
A_23_P54840	MT1A	Homo sapiens metallothionein 1A (MT1A). mRNA [NM_005946]	-1.7220764	0.04461922
A_33_P3309231	HSCB	Homo sapiens HscB iron-sulfur cluster co-chaperone homolog (E. coli) (HSCB). mRNA [NM_172002]	1.4852506	0.02087879
A_33_P3381870	EPB49	Homo sapiens erythrocyte membrane protein band 4.9 (dematin) (EPB49). transcript variant 1. mRNA [NM_001978]	2.384218	0.032221053
A_23_P416581	GNAZ	Homo sapiens guanine nucleotide binding protein (G protein), alpha z polypeptide (GNAZ). mRNA [NM_002073]	2.4356751	0.03590241
A_24_P120934	GADD45G	Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G). mRNA [NM_006705]	2.4928758	0.028136263
A_23_P99693	ZBTB1	Homo sapiens zinc finger and BTB domain containing 1 (ZBTB1). transcript variant 2. mRNA [NM_014950]	2.79575	0.014746751

Supplemental Table 4. Functional analysis of differentially expressed genes by *IL28B* genotype. Differentially expressed genes in CC *versus* CT patients were used to identify over- or down-represented biological characteristics [Disorder, compound, phenotype, Gene Ontology biological process (GO_BIOL_PROC), Gene Ontology Cell Component (GO_CELL_COMP), and pathways].

Descriptor	Attribute type	Score	P Value	Genes sharing this descriptor
tumors	DISORDER	22	1,00E-16	ALDH2, CASP7, CCL4, CEBPA, COL18A1, EREG, FPR2, HIF1A, HLA-C, IL1A, IL1B, IL6, MT1X, NAMPT, PNPLA2, PPBP, PTAFR, RPL23A, RPSA, SERPINB2, SPINK7, VIPR1
necrosis	DISORDER	16	1,11E-16	ALDH2, CASP7, CCL4, CEBPA, EREG, FPR2, HIF1A, IL1A, IL1B, IL6, NAMPT, PNPLA2, PPBP, PTAFR, RPSA, SERPINB2
nitric oxide	COMPOUND	12	3,71E-14	ALDH2, CASP7, CCL4, GCLM, HIF1A, IL1A, IL1B, IL6, PPBP, PTAFR, SERPINB2, VIPR1
pge2	COMPOUND	10	8,70E-14	CASP7, CCL4, FPR2, HIF1A, IL1A, IL1B, IL6, PPBP, PTAFR, SERPINB2
dexamethasone	COMPOUND	11	3,54E-13	CASP7, CCL4, CEBPA, FPR2, HIF1A, IL1A, IL1B, IL6, NAMPT, PPBP, SERPINB2
leukemia	DISORDER	12	4,39E-13	ALDH2, CASP7, CCL4, CEBPA, HLA-C, IL1A, IL1B, IL6, NAMPT, PPBP, PTAFR, SERPINB2
rheumatoid arthritis	DISORDER	10	1,54E-12	CASP7, CCL4, FPR2, IL1A, IL1B, IL6, LILRA3, NAMPT, PPBP, SERPINB2
retinoic acid	COMPOUND	11	8,25E-12	ALDH2, CASP7, CCL4, CEBPA, HIF1A, IL1A, IL1B, IL6, PTAFR, SERPINB2, VIPR1
inflammation	DISORDER	12	8,70E-12	CASP7, CCL4, EREG, FPR2, HIF1A, IL1A, IL1B, IL6, NAMPT, PPBP, PTAFR, SERPINB2
histamine	COMPOUND	8	1,51E-11	ALDH2, CCL4, FPR2, HIF1A, IL1B, IL6, PPBP, PTAFR
groalpha	COMPOUND	5	2,79E-11	CCL4, IL1A, IL1B, IL6, PPBP
breast cancer	DISORDER	12	4,48E-11	ALDH2, CASP7, CCL4, COL18A1, EREG, HIF1A, MT1X, NAMPT, PPBP, RPSA, SERPINB2, VIPR1
leukotriene b4	COMPOUND	6	5,47E-11	FPR2, IL1A, IL1B, IL6, PPBP, PTAFR
sepsis	DISORDER	7	7,81E-11	CCL4, IL1A, IL1B, IL6, NAMPT, PTAFR, SERPINB2
cancer	DISORDER	14	1,09E-10	ALDH2, CASP7, CCL4, EREG, FPR2, HIF1A, IL6, NAMPT, PPBP, PTAFR, RPSA, SERPINB2, SPINK7, VIPR1
cytokine-mediated signaling pathway	GO_BIOL_PROC	5	1,82E-10	CEBPA, EREG, IL1A, IL1B, IL6
lipid	COMPOUND	11	1,85E-10	ALDH2, CEBPA, FPR2, IL6, NAMPT, PNPLA2, PPBP, PTAFR, RPSA, SERPINB2, VIPR1
psoriasis	DISORDER	7	2,05E-10	CCL4, HLA-C, IL1A, IL1B, IL6, PTAFR, SERPINB2
atherosclerosis	DISORDER	8	5,21E-10	CCL4, IL1A, IL1B, IL6, NAMPT, PPBP, PTAFR, SERPINB2
vegf	COMPOUND	9	6,65E-10	CASP7, CCL4, HIF1A, IL1A, IL1B, IL6, PPBP, PTAFR, SERPINB2
endotoxin	COMPOUND	6	8,68E-10	CCL4, IL1A, IL1B, IL6, PTAFR, SERPINB2
cycloheximide	COMPOUND	8	1,09E-09	CASP7, CCL4, HIF1A, IL1A, IL1B, IL6, PTAFR, SERPINB2
pdtc	COMPOUND	5	1,81E-09	GCLM, HIF1A, IL1A, IL1B, IL6
actinomycin d	COMPOUND	7	1,89E-09	HIF1A, IL1A, IL1B, IL6, PTAFR, SERPINB2, VIPR1
immune response	GO_BIOL_PROC	7	1,96E-09	CCL4, HLA-C, IL1A, IL1B, PPBP, PTAFR, VIPR1
carcinoma	DISORDER	10	2,38E-09	ALDH2, CASP7, CCL4, EREG, HIF1A, HLA-C, PTAFR, RPSA, SERPINB2, VIPR1
cell damage	DISORDER	6	2,81E-09	ALDH2, CASP7, IL1A, IL1B, IL6, PPBP
rantes	COMPOUND	6	6,41E-09	CCL4, IL1A, IL1B, IL6, PPBP, PTAFR
inflammatory response	GO_BIOL_PROC	6	6,75E-09	CCL4, FPR2, IL1A, IL1B, IL6, PTAFR
thrombocytosis	DISORDER	4	8,11E-09	IL1A, IL1B, IL6, PPBP
cancer lung	DISORDER	8	8,72E-09	ALDH2, CASP7, EREG, HIF1A, PPBP, RPSA, SERPINB2, VIPR1
osteolysis	DISORDER	4	9,05E-09	CCL4, IL1A, IL1B, IL6

superoxide	COMPOUND	7	9,80E-09	ALDH2, CCL4, FPR2, HIF1A, IL1B, PPBP, SERPINB2
osteoarthritis	DISORDER	6	9,99E-09	CCL4, IL1A, IL1B, IL6, PPBP, SERPINB2
extracellular region	GO_CELL_COMP	11	1,05E-08	COL18A1, EREG, HLA-C, IL1A, IL1B, IL6, LILRA3, PPBP, SERPINB2, SPINK7, TOR2A
positive regulation of cell division	GO_BIOL_PROC	4	1,12E-08	EREG, IL1A, IL1B, PPBP
Graft-versus-Host Disease Signaling	PATHWAY_SIGMA	4	1,36E-08	HLA-C, IL1A, IL1B, IL6
bacterial infections	DISORDER	5	1,44E-08	CCL4, FPR2, IL1A, IL1B, IL6
extracellular space	GO_CELL_COMP	8	1,60E-08	CCL4, COL18A1, EREG, IL1A, IL1B, IL6, PPBP, SERPINB2
bronchoalveolar lavage fluid	DISORDER	5	1,62E-08	CCL4, IL1B, IL6, NAMPT, PPBP
Graft-versus-host disease	PATHWAY_KEGG	4	1,65E-08	HLA-C, IL1A, IL1B, IL6
creatinine	COMPOUND	7	1,67E-08	ALDH2, CCL4, IL1A, IL6, NAMPT, PPBP, PTAFR
systemic inflammatory response syndrome	DISORDER	4	2,55E-08	IL1A, IL1B, IL6, PTAFR
negative regulation of cell proliferation	GO_BIOL_PROC	6	3,06E-08	CEBPA, COL18A1, EREG, IL1A, IL1B, IL6
adenocarcinoma	DISORDER	8	3,27E-08	ALDH2, CASP7, EREG, GCLM, HIF1A, RPSA, SERPINB2, VIPR1
Dendritic Cell Maturation	PATHWAY_SIGMA	5	3,46E-08	COL18A1, HLA-C, IL1A, IL1B, IL6
il 10	COMPOUND	4	3,78E-08	CCL4, IL1A, IL1B, IL6
cardiovascular system phenotype & the observable morphological and physiological characteristics of the mammalian heart blood ve	PHENOTYPE	10	3,82E-08	CASP7, CEBPA, COL18A1, HIF1A, IL1A, IL1B, IL6, PNPLA2, PTAFR, RPSA
immune system phenotype	PHENOTYPE	11	4,44E-08	CASP7, CEBPA, EREG, HIF1A, HLA-C, IL1A, IL1B, IL6, NAMPT, PTAFR, SERPINB2
melanoma	DISORDER	8	4,74E-08	CASP7, CCL4, HIF1A, IL1A, PPBP, PTAFR, RPSA, SERPINB2

Supplemental Table 5. Functional analysis of differentially expressed genes by sustained virological response (SVR). Differentially expressed genes in SVR *versus* non-SVR patients were used to identify over- or down-represented biological characteristics [Disorder, compound, phenotype, expression, domain, Gene Ontology biological process (GO_BIOL_PROC), Gene Ontology Cell Component (GO_CELL_COMP), and pathways].

Descriptor	Attribute type	Score	P Value	Genes sharing this descriptor
2',5'-oligoadenylate	COMPOUND	6	3,98E-13	IDO1, ISG15, MX1, OAS1, OAS2, STAT1
virus infection	DISORDER	9	2,38E-12	HSPA1A, IDO1, IFIH1, IRF5, ISG15, KIR3DL1, MX1, OAS1, STAT1
Interferon Signaling	PATHWAY_SIGMA	5	8,67E-12	IFI35, IFIT1, IFIT3, MX1, STAT1
Immune response IFN alpha/beta signaling pathway	PATHWAY_MLPR	5	2,36E-11	IFI6, IFIT2, ISG15, STAT1, USP18
tumors	DISORDER	16	1,66E-10	FSCN1, GADD45G, GBP1, HSPA1A, IDO1, IFI35, IFIH1, IRF5, ISG15, KIR2DL4, KIR2DS4, KIR3DL1, LAMP3, MX1, STAT1, XAF1
response to virus	GO_BIOL_PROC	6	1,83E-10	IFI35, IFI44, IFIH1, ISG15, MX1, STAT1
Activation of IRF by Cytosolic Pattern Recognition Receptors	PATHWAY_SIGMA	5	5,02E-10	DHX58, IFIH1, IFIT2, ISG15, STAT1
SPLEEN - 70th percentile	EXPRESSION	10	1,16E-09	CMPK2, EPB49, IFI35, IFIH1, ISG15, MX1, PARP9, SAMD9L, STAT1, XAF1
hepatitis c	DISORDER	6	1,34E-09	IDO1, IFIH1, ISG15, KIR3DL1, MX1, STAT1
immune response	GO_BIOL_PROC	7	2,34E-09	IFI35, IFI44L, IFI6, KIR2DS2, KIR3DL1, OAS1, OAS2
melanoma	DISORDER	9	2,82E-09	FSCN1, HSPA1A, IDO1, IFIH1, KIR3DL1, MT1A, MX1, STAT1, XAF1
Natural Killer Cell Signaling	PATHWAY_SIGMA	5	6,76E-09	KIR2DL4, KIR2DS2, KIR2DS4, KIR3DL1, SH2D1B
cytoplasm	GO_CELL_COMP	16	8,97E-09	DHX58, EPB49, FSCN1, IDO1, IFI44, IFI44L, IFIH1, IFIT1, ISG15, MT1A, MX1, OAS1, PARP9, RTP4, STAT1, XAF1
lupus erythematosus systemic	DISORDER	6	2,32E-08	IRF5, ISG15, LAMP3, MX1, OAS1, STAT1
cancer	DISORDER	12	2,33E-08	FSCN1, GADD45G, HSPA1A, IDO1, IFIH1, ISG15, KIR2DS4, KIR3DL1, LAMP3, MX1, STAT1, XAF1
poly(i-c)	COMPOUND	4	3,31E-08	IDO1, MX1, RSAD2, STAT1
influenza	DISORDER	5	5,60E-08	IDO1, IFIH1, ISG15, MX1, STAT1
immune system phenotype	PHENOTYPE	11	5,85E-08	DHX58, GADD45G, IDO1, IFIH1, IRF5, MT1A, RAMP1, RSAD2, SH2D1B, STAT1, USP18
inflammation	DISORDER	9	7,12E-08	FSCN1, GBP1, HSPA1A, IDO1, IFIH1, ISG15, KIR3DL1, MX1, STAT1
protein binding	GO_MOLEC_FUNC	18	1,59E-07	DHX58, FSCN1, GADD45G, IFI35, IFI6, IFIH1, IFIT1, IFIT3, IRF5, ISG15, KIR2DL4, MT1H, MX1, PARP9, RTP4, SH2D1B, STAT1, ZBTB1
Immunoglobulin	DOMAIN	4	1,94E-07	KIR2DL4, KIR2DS2, KIR2DS4, KIR3DL1
Antigen processing and presentation	PATHWAY_KEGG	4	1,94E-07	HSPA1A, KIR2DL4, KIR2DS4, KIR3DL1
vesicular stomatitis	DISORDER	3	9,03E-07	ISG15, MX1, STAT1
Hepatitis C	PATHWAY_KEGG	4	1,65E-06	IFIT1, OAS1, OAS2, STAT1
RIG-I_C-RD	DOMAIN	2	1,70E-06	DHX58, IFIH1
Natural killer cell mediated cytotoxicity	PATHWAY_KEGG	4	1,75E-06	KIR2DL4, KIR2DS4, KIR3DL1, SH2D1B
biological_process	GO_BIOL_PROC	6	2,18E-06	HSCB, IFIT1, IFIT2, IFIT3, MT1A, SH2D1B
molecular_function	GO_MOLEC_FUNC	6	2,82E-06	HSCB, IFIT1, IFIT2, IFIT3, RSAD2, SH2D1B
breast cancer	DISORDER	8	2,87E-06	FSCN1, HSPA1A, IDO1, ISG15, KIR3DL1, MT1A, MX1, STAT1
nucleotide binding	GO_MOLEC_FUNC	9	2,98E-06	CMPK2, DDX60, DHX58, GBP1, GNAZ, IFIH1, MX1, OAS1, OAS2
2-5-oligoAdlate_synth_1_dom2/C	DOMAIN	2	3,03E-06	OAS1, OAS2
2-5-oligoadenylate_synth_CS	DOMAIN	2	3,03E-06	OAS1, OAS2
2-5-oligoadenylate_synth_N	DOMAIN	2	4,73E-06	OAS1, OAS2
gtp	COMPOUND	5	4,79E-06	GBP1, GNAZ, IDO1, MX1, STAT1

hiv infections	DISORDER	4	6,10E-06	IDO1, KIR3DL1, MX1, STAT1
Restrct_endonuc_I_R/III_Res	DOMAIN	2	6,81E-06	DHX58, IFIH1
Immune response Role of DAP12 receptors in NK cells	PATHWAY_MLPR	3	9,56E-06	KIR2DL4, KIR2DS2, KIR3DL1
aids	DISORDER	4	1,01E-05	IDO1, KIR3DL1, LAMP3, STAT1
tyrosine	COMPOUND	8	1,24E-05	FSCN1, HSPA1A, IDO1, IRF5, KIR2DS4, KIR3DL1, SH2D1B, STAT1
RIG-I-like receptor signaling pathway	PATHWAY_KEGG	3	1,30E-05	DHX58, IFIH1, ISG15
cadmium	COMPOUND	3	1,41E-05	HSPA1A, MT1A, MT1H
Nucleotidyltransferase	DOMAIN	2	1,89E-05	OAS1, OAS2
cycloheximide	COMPOUND	5	1,99E-05	HSPA1A, IDO1, ISG15, MX1, STAT1
Metallothionein_vert_metal_BS	DOMAIN	2	2,28E-05	MT1A, MT1H
Crosstalk between Dendritic Cells and Natural Killer Cells	PATHWAY_SIGMA	3	2,54E-05	FSCN1, KIR2DL4, KIR3DL1
regulation of immune response	GO_BIOL_PROC	3	2,63E-05	KIR2DL4, KIR2DS2, KIR3DL1