Supplementary Table 1 – Genes tested using the NanoString assay

Gene	Accession	Targeted Region	Target Sequence
ADRB1	NM_000684.1	795-895	TGTGCATCATGGCCTTCGTGTACCTGCGGGTGTTCCGCGAGGCCCAGAAGCAGGTGAAGAAGATCGACAGCTGCGAGCGCCGTTTCCTCGGCGGCCCAGC
AIM2	NM_004833.1	607-707	ACGTGCTGCACCAAAAGTCTCTCCTCATGTTAAGCCTGAACAGAAACAGATGGTGGCCCAGCAGGAATCTATCAGAGAAGGGTTTCAGAAGCGCTGTTTG
ANKRD22	NM_144590.2	57-157	ACTGGCAGAGCAAATATGACTCAGAAACCGGCTCCTCAGGGTTGTAACATTAGATGATACAGGCTTGGGTCGTTACACATGACACCAGTGCCTTTGTTTC
ANXA1	NM_000700.1	515-615	GAAATCAGAGACATTAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGC
APOBEC3A	NM_145699.3	31-131	CAGCAGCTTCCAGGTTGCTCTGATGATATATTAAGGCTCCTGAATCCTAAGAGAATGTTGGTGAAGATCTTAACACCACGCCTTGAGCAAGTCGCAAGAG
ARNTL	NM_001178.4	140-240	GCCACGGTGGTGCTGGCTAGAGTGTATACGTTTGGACCCAAGCTTAACTTTTCCAATGTGGAATCCTGGGCCTTCATTGGTTCCGATGTCATAGGAATCT
ATF3	NM_001674.2	705-805	TTTGATATACATGCTCAACCTTCATCGGCCCACGTGTATTGTCCGGGCTCAGAATGGGAGGACTCCAGAAGATGAGAGAAACCTCTTTATCCAACAGATA
ATP10A	NM_024490.3	5095-5195	AAAAATTCACAGTTGAGTGCATCCCAGCATTCTGTTCCGGGCAGGCATTTCAGGAAGACCGCCTTGTAGGTATTACATCCCTGGTGTCGTATTTTGCCTG
BATF2	NM_138456.3	2004-2104	GGAGAGAAACCCTGGCTCTTCACCCAGGTTTCACACACATGTAAATGAAACACTATGTTAGTATCTAACACACTCCTGGATACAGAACACAAGTCTTGGC
BLZF1	NM_003666.2	1100-1200	AGCAGGGTAATGGCAGATGAGTTAACCAACTCAAGAGCAGCTTTACAGCGTCAAAACCGTGATGCACACGGGGCTATACAAGATCTCCTAAGTGAACGGG
C12orf69	NM_001013698.2	565-665	GTTGCTGTTCTTGGCCTTGGCATAGATATGATTGTCCGTGCCATCCTGGGAGCAGTGGAAAAAACACAGCTTCAAGCAGCCATCAAAAGTTATGAGAAGC
C15orf56	NM_001013717.1	451-551	TGAACAAAACCACCAGCCCTGCTCTCATGCAGCTTATAATCAAGTAGAGAGACAGACATAAATGATTAATAGATGCTCCTGTAATGGCGGTTGTGAGGTG
CARD16	NM_033292.2	575-675	ACAGGCATGACAATGCTGCTACAAAATCTGGGGTACAGCGTAGATGTGAAAAAAAATCTCACTGCTTCGGACATGACTACAGAGCTGGAGGCATTTGCAC
CCL2	NM_002982.3	0-100	GAGGAACCGAGAGGCTGAGACTAACCCAGAAACATCCAATTCTCAAACTGAAGCTCGCACTCTCGCCTCCAGCATGAAAGTCTCTGCCGCCCTTCTGTGC
CCL8	NM_005623.2	689-789	AAGGAGAGATGGGTCAGGGATTCCATGAAGCATCTGGACCAAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGACTGAGAGTCAGAGCTTGAA
CD274	NM_014143.2	684-784	TAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTCTGGCACATCCTCCAAATGAAAGGACTCACTTGGTAATTCTG
CD69	NM_001781.1	460-560	AGGACATGAACTTTCTAAAACGATACGCAGGTAGAGAGGAACACTGGGTTGGACTGAAAAAGGAACCTGGTCACCCATGGAAGTGGTCAAATGGCAAAGA
CD80	NM_005191.3	1288-1388	AAAGATCTGAAGGTCCCACCTCCATTTGCAATTGACCTCTTCTGGGAACTTCCTCAGATGGACAAGATTACCCCACCTTGCCCTTTACGTATCTGCTCTT
CFB	NM_001710.5	2029-2129	TAAGCTGAAATATGGCCAGACTATCAGGCCCATTTGTCTCCCCTGCACCGAGGGAACAACTCGAGCTTTGAGGCTTCCTCCAACTACCACTTGCCAGCAA
CLEC2B	NM_005127.2	980-1080	AGCTACATTTACCAAATCGTTTGGCATGAGAGGGAGTGAAGGATGTGCCTACCTCAGCGATGATGGTGCAGCAACAGCTAGATGTTACACCGAAAGAAAA
CMPK2	NM_207315.2	1570-1670	GCAGAAAACTGGAGACCAGGCATCTTAATTTTACTTCAGCCATCGTACCCTCTTCTGACTGATGGACCCGTCATCACAAAGGTCCCTCTCATCATGTTCC
CXCL10	NM_001565.1	40-140	GCAGAGGAACCTCCAGTCTCAGCACCATGAATCAAACTGCGATTCTGATTTGCTGCCTTATCTTTCTGACTCTAAGTGGCATTCAAGGAGTACCTCTCTC
CXCL11	NM_005409.3	590-690	CAGAATTCCACTGCCCAAAGGAGTCCAGCAATTAAATGGATTTCTAGGAAAAGCTACCTTAAGAAAGGCTGGTTACCATCGGAGTTTACAAAGTGCTTTC
DDX58	NM_014314.3	2130-2230	CTGGCATATTGACTGGACGTGGCAAAACAAATCAGAACACAGGAATGACCCTCCCGGCACAGAAGTGTATATTGGATGCATTCAAAGCCAGTGGAGATCA
DDX60	NM_017631.5	660-760	TTCGAGATGCTTATCAAAAGAGTGGGGAAGTTTCTTGGAAGAGAGTTACCCATATTTCCTGATAGTTGCAGACGAAGGCCTGAACGATCTACAAACACAG
DDX60L	NM_001012967.1	4700-4800	TCAAAGGTGATCCTTGCCGAACTCCCGGAGGATTTTAAAGCTGCTTTATATGAGTATAACCTGGCAGTAATGAAGGATTTTGCCTCCTTCCTGCTGATTG
DNMT3L	NM_013369.2	1050-1150	AGTCCGGGTGCTGTCCCTTTTTGAAGACATCAAGAAAGAGCTGACGAGTTTGGGCTTTTTGGAAAGTGGTTCTGACCCGGGACAACTGAAGCATGTGGTT
EIF2AK2	NM_002759.1	1760-1860	TGGAAAGCGAACAAGGAGTAAGGGAACTTTGCGATACATGAGCCCAGAACAGATTTCTTCGCAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGG
EPSTI1	NM_001002264.1	610-710	AGAGAAGCATTTAGAGAGCATCAGCAATACAAAACCGCTGAGTTCTTGAGCAAACTGAACACAGAATCGCCAGACAGAAGTGCCTGTCAAAGTGCTGTTT

ETV7	NM_016135.2	794-894	ATTGACGGCAGGATCGCTGACTGCCGCCTGCTGTGGGATTACGTGTATCAGCTGCTCCTTGATACCCGATATGAGCCCTACATCAAGTGGGAAGACAAGG
FAM122C	NM_001170779.1	375-475	AAGCCTTGAGAACTTATTCCTCGACCCGGACATGGCACAGGAGAAAATGAAACTAGGTTTCAAGTCGCTGCCGAGTTCCACTACCGCAGACGGCAACATT
FAM124A	NM_145019.2	1050-1150	ATGGGAACAAGATCCTCCTACAGGCACAAAGGGTGCATAAGAAGTTTCCTAAACCTGGCAGAGTACATCATGCCTCCGAGAAGAAACGTCATTCCACTCC
FAM153A	NM_173663.3	1621-1721	TTTTCAAGATGAGGTTGGAGGCTTCTGTATGTAGAGGGCACTGGCTTGGGCCAAATGCCAACAAAACAAACCCTTGAAGACATTTCAGGGCCATGCTCAC
FAM26F	NM_001010919.1	900-1000	AGGGCCAGTACTACAGCATGTTGCACAAATATGTCAACAGAAAAGAGAAGACTCACAGTATCAGGTCTACTGAAGGAGATACGGTGATTCCTGTTCTTGG
FAR2	NM_018099.3	235-335	TCTTTCAGGAGCTATAAAAGAAAGGGAGGAATCATGTCCACAATTGCAGCTTTCTATGGCGGCAAGTCCATTCTCATCACGGGGGCCACAGGCTTTCTGG
FBXO6	NM_018438.5	420-520	TAGGAACCTCCTGCGCAACCCGTGTGCTGAAGAGGATATGTTTGCATGGCAAATTGATTTCAATGGTGGGGACCGCTGGAAGGTGGAGAGCCTCCCTGGA
FCGR1A	NM_000566.3	1545-1645	CCAGGAGTGGGTAGATTTCAGGGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTACTTACAAATGACTCCTAAGGGACTGTGAGACTGAG
FCGR1B	NM_001017986.2	980-1080	ACAACACCAGAACTGTGTGTCTCATGGTATATAACTCTTAAAGCAAATAAATGAACTGACTTCAACTGGGATACATTTGGAAATGTGGTCATCAAAGATG
FRMD3	NM_174938.4	1580-1680	ACGATGAGATTGACATGCTCTTTGACTGTCCTTCTAGGCTTGAGTTGGAAAGAGAAGACACAGATTCATTTGAGGATCTGGAAGCAGATGAAAACGCCTT
FUT4	NM_002033.2	1345-1445	GGGGCAGCCGGTGCCCGAAATTGGGCTCCTGCACACAGTGGCCCGCTACAAGTTCTACCTGGCTTTCGAGAACTCGCAGCACCTGGATTATATCACCGAG
GBP1	NM_002053.1	2110-2210	CCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTTGGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCA
GBP4	NM_052941.4	5150-5250	TTCTACAAGATATGCCATGGGCCTTTTCACAGGGGACACAGGCTTCTTAAAACAACCCGGCTTCCTCACCCTATGTCCTTTATTTACAAAGCTGTGCTCC
GBP5	NM_052942.3	1955-2055	ATTACAGACTGACCAGGCTCTCACAGAGACGGAAAAAAAGAAGAAAGAGGCACAAGTGAAAGCAGAAGCTGAAAAGGCTGAAGCGCAAAGGTTGGCGGCG
GLS	NM_014905.3	3730-3830	TCTATGAGCACACTCTGCTGCTTCTAAACTTTACATGCCTGATGGCACCTTACTCCAGCAGCCTCCAGGTGCTTTCATTTTCACTTCCAGTCTAAGCCAG
GMPR	NM_006877.3	325-425	CCATGTTTACAGCAATTCATAAGCATTACTCCCTGGATGACTGGAAGCTCTTTGCCACAAATCACCCAGAATGCCTGCAGAATGTAGCCGTGAGTTCAGG
GOLGA6L4	NM_033238.2	5295-5395	CGTGTCAACTAATGGGAGCTTACTGGGTTAGAAGTCAGGACACTGAGTTTCAATCCTCACTTAGTAGTCTGTGGCCCTCTTTGGCACATTAACCTCCCTC
HEATR7B1	XM_001721240.3	2560-2660	TCATGAAGAGTGTTGTGCAGGTTACCAAGGCCATCAACAACATCAAGGACCTGGAGGACTTTCACTTTGCCCAGAAGACGACTCTTACCAGCATTATAGT
HERC5	NM_016323.2	935-1035	TGGGCTGCTGTTTACTTTCGGTGCTGGAAAACATGGGCAACTTGGTCATAATTCAACACAGAATGAGCTAAGACCCTGTTTGGTGGCTGAGCTTGTTGGG
HERC6	NM_001165136.1	2075-2175	TCCATCACCCAGATTTATACTTAGAGTCAGACGAAGTCGCCTGGTTAAAGATGCTCTGCGTCAATTAAGTCAAGCTGAAGCTACTGACTTCTGCAAAGTA
HPSE	NM_006665.3	1625-1725	GGTCTAACTCTAAAGATGGTGGATGATCAAACCTTGCCACCTTTAATGGAAAAACCTCTCCGGCCAGGAAGTTCACTGGGCTTGCCAGCTTTCTCATATA
HSH2D	NM_032855.2	1960-2060	GTGTCAGCACCAGGATTTGAAGCCAGGTGAATCCGAGCCCTTTTCCCATATCATCTGTTTGTTCTGTTGTCTAAAAGCACACTGCAAGCCGGGCTCAGTG
IDO1	NM_002164.3	50-150	CTATTATAAGATGCTCTGAAAACTCTTCAGACACTGAGGGGCACCAGAGGAGCAGACTACAAGAATGGCACACGCTATGGAAAACTCCTGGACAATCAGT
IFI16	NM_005531.1	2255-2355	ACGACTGAACACAATCAACTGTGAGGAAGGAGATAAACTGAAACTCACCAGCTTTGAATTGGCACCGAAAAGTGGGAATACCGGGGAGTTGAGATCTGTA
IFI44	NM_006417.4	750-850	TTTCCAAGGGCATGTAACGCATCAGGCTTTGGTGGGCACTAATACAACTGGGATATCTGAGAAGTATAGGACATACTCTATTAGAGACGGGAAAGATGGC
IFI44L	NM_006820.2	940-1040	ATCTCTGCCATTTATGTTGTGTGACACTATGGGGCTAGATGGGGCAGAAGGAGCAGGACTGTGCATGGATGACATTCCCCACATCTTAAAAGGTTGTATG
IFI6	NM_002038.3	180-280	GGGGTGGAGGCAGGTAAGAAAAAGTGCTCGGAGAGCTCGGACAGCGGCTCCGGGTTCTGGAAGGCCCTGACCTTCATGGCCGTCGGAGGAGGACTCGCAG
IFIH1	NM_022168.2	185-285	GCTTGGGAGAACCCTCTCCCTTCTCTGAGAAAGAAAGATGTCGAATGGGTATTCCACAGACGAGAATTTCCGCTATCTCATCTCGTGCTTCAGGGCCAGG
IFIT1	NM_001548.3	1440-1540	GAGAAAGGCATTAGATCTGGAAAGCTTGAGCCTCCTTGGGTTCGTCTACAAATTGGAAGGAAATATGAATGAAGCCCTGGAGTACTATGAGCGGGCCCTG
IFIT2	NM_001547.4	1995-2095	TGCATCCCATAGAGGTTAGTCCTGCATAGCCAGTAATGTGCTAAGTTCATCCAAAAGCTGGCGGACCAAAGTCTAAATAGGGCTCAGTATCCCCCATCGC
IFIT3	NM_001549.4	170-270	GAAGAACAAATCAGCCTGGTCACCAGCTTTTCGGAACAGCAGAGACACAGAGGGCAGTCATGAGTGAGGTCACCAAGAATTCCCTGGAGAAAATCCTTCC
IFIT5	NM_012420.2	775-875	TCACAGTGTATCGGCTGGATGATTCTGATAGAGAAGGGTCTGTAAAGAGCTTTTCTCTGGGGCCTTTGAGAAAGGCTGTTACCCTGAACCCAGATAACAG
IFITM1	NM_003641.3	482-582	CCTGTTACTGGTATTCGGCTCTGTGACAGTCTACCATATTATGTTACAGATAATACAGGAAAAACGGGGTTACTAGTAGCCGCCCATAGCCTGCAACCTT

IFITM2	NM_006435.2	4-104	AAACTGTTGAGAAAACGGAACTACTGGGGAAAGGGAGGGCTCACTGAGAACCATCCCGGTAACCCGATCACCGCTGGTCACCATGAACCACATTGTGCAA
IFITM3	NM_021034.2	40-140	AGGGAGGGCTCACTGAGAACCATCCCAGTAACCCGACCGCCGCTGGTCTTCGCTGGACACCATGAATCACACTGTCCAAACCTTCTTCTCTCCTGTCAAC
IFNA4^{1}	NM_021068.2	725-825	ATAACCACCACGAGTTGAATCAAAATTTTCAAATGTTTTCAGCAGTGTGAAGAAGCTTGGTGTATACCTGTGCAGGCACTAGTCCTTTACAGATGACAAT
IFNA6^{2}	NM_021002.1	46-146	GCAAGTCAAGCTGCTCTCTGGACTGTGATCTGCCTCAGACCCACAGCCTGGGTCACAGGAGGACCATGATGCTCCTGGCACAAATGAGGAGAATCTCTCT
IFNB1	NM_002176.2	610-710	ACAGACTTACAGGTTACCTCCGAAACTGAAGATCTCCTAGCCTGTGCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTCAACCAGCAGATGCTGTTTA
IFNG	NM_000619.2	970-1070	ATACTATCCAGTTACTGCCGGTTTGAAAATATGCCTGCAATCTGAGCCAGTGCTTTAATGGCATGTCAGACAGAACTTGAATGTGTCAGGTGACCCTGAT
IL15RA	NM_002189.2	505-605	ACAACAGCAGCTATTGTCCCGGGCTCCCAGCTGATGCCTTCAAAATCACCTTCCACAGGAACCACAGAGATAAGCAGTCATGAGTCCTCCCACGGCACCC
IL28A-B^{3}	NM_172139.2	104-204	CAAGGGGCTGCCACATAGCCCAGTTCAAGTCCCTGTCTCCACAGGAGCTGCAGGCCTTTAAGAGGGCCAAAGATGCCTTAGAAGAGTCGCTTCTGCTGAA
IL28RA	NM_173065.1	2690-2790	TCAGTTAACCTACACCCACCTGAATATAGATGAGCGTAGCTGAGTTTTCACCCGTAGGACCGAAGTGTTTTGTGGTGGAGTATCTGAACAACCTTGGCTC
IL29	NM_172140.1	233-333	AGCTAGCGAGCTTCAAGAAGGCCAGGGACGCCTTGGAAGAGTCACTCAAGCTGAAAAACTGGAGTTGCAGCTCTCCTGTCTTCCCCGGGAATTGGGACCT
IRF1	NM_002198.1	510-610	CTGTGCGAGTGTACCGGATGCTTCCACCTCTCACCAAGAACCAGAGAAAAGAAAGAAAGTCGAAGTCCAGCCGAGATGCTAAGAGCAAGGCCAAGAGGAA
IRF2	NM_002199.2	1375-1475	CAGTACCTGGAGCTTCTCTTTAACTCAGGACTCCAGCCCATTGGTAGACGTGTGTTTCTAGAGCCTGCTGGATCTCCCAGGGCTACTCACTCAAGTTCAA
IRF7	NM_001572.3	1763-1863	CGCAGCGTGAGGGTGTGTCTTCCCTGGATAGCAGCAGCCTCAGCCTCTGCCTGTCCAGCGCCAACAGCCTCTATGACGACATCGAGTGCTTCCTTATGGA
IRF9	NM_006084.4	385-485	GCACTCAACAAGAGTTCTGAATTTAAGGAGGTTCCTGAGAGGGGCCGCATGGATGTTGCTGAGCCCTACAAGGTGTATCAGTTGCTGCCACCAGGAATCG
ISG15	NM_005101.3	305-405	CCCGGCAGCACGGTCCTGCTGGTGGTGGACAAATGCGACGAACCTCTGAGCATCCTGGTGAGGAATAACAAGGGCCGCAGCAGCACCTACGAGGTACGGC
ISG20	NM_002201.4	358-458	GAGTGGCCTGGCTCGTTGCAGCCTCGTGAACGTCCACGGTGCTGTGCTGTACGACAAGTTCATCCGGCCTGAGGGAGAGATCACCGATTACAGAACCCGG
JAK2	NM_004972.2	455-555	CTCCTCCCGCGACGGCAAATGTTCTGAAAAAGACTCTGCATGGGAATGGCCTGCCTTACGATGACAGAAATGGAGGGAACATCCACCTCTTCTATATATC
JAK3	NM_000215.2	1715-1815	GTGCTGCTGAAGGTCATGGATGCCAAGCACAAGAACTGCATGGAGTCATTCCTGGAAGCAGCGAGCTTGATGAGCCAAGTGTCGTACCGGCATCTCGTGC
JUN	NM_002228.3	140-240	ACACAGCCAGCCAGCCAGGTCGGCAGTATAGTCCGAACTGCAAATCTTATTTTCTTTTCACCTTCTCTCTAACTGCCCAGAGCTAGCGCCTGTGGCTCCC
JUNB	NM_002229.2	1155-1255	GCGCGCCTGGAGGACAAGGTGAAGACGCTCAAGGCCGAGAACGCGGGGCTGTCGAGTACCGCCGGCCTCCTCCGGGAGCAGGTGGCCCAGCTCAAACAGA
LAMP3	NM_014398.3	1400-1500	GGTCTCTGCCTTATGGGTATGGGTGTCTATAAAATCCGCCTAAGGTGTCAATCATCTGGATACCAGAGAATCTAATTGTTGCCCGGGGGGAATGAAAATA
LIPA	NM_001127605.1	406-506	GGAAGAACCATTCTGACAAAGGTCCCAAACCAGTTGTCTTCCTGCAACATGGCTTGCTGGCAGATTCTAGTAACTGGGTCACAAACCTTGCCAACAGCAG
MCOLN2	NM_153259.2	165-265	GGCGAAATGAGTCGGCCGTGAACGGTGTTTCCTGTTCCGAATCCCGAGAGCCCTGGAAAGTTTTGAAGGAGGAGGCATGGCCCGGCAGCCTTATCGTTTT
MKX	NM_173576.2	545-645	CCTCGGCTCGCAGATGACGCTAGTGCAGGTGTCAAATTGGTTTGCTAATGCAAGACGTCGGCTTAAGAATACCGTTCGACAGCCAGATTTAAGCTGGGCT
MLKL	NM_152649.1	2375-2475	CAACCAACATGGCAGCTAACACATGAATGAGGCCAATCAAGACCAGAAGAACCACTCAAGCAGATCCCAGCCCAAATTGCCCATTCACACAATCAGGAGC
MNDA	NM_002432.1	787-887	CCAACGGCAGGTGGATGCAAGAAGAAATGTTCCCCAAAACGACCCAGTGACAGTGGTGGTACTGAAAGCAACAGCGCCATTTAAATACGAGTCCCCAGAA
MX1	NM_002462.2	1485-1585	GCCTTTAATCAGGACATCACTGCTCTCATGCAAGGAGAGGAAACTGTAGGGGAGGAAGACATTCGGCTGTTTACCAGACTCCGACACGAGTTCCACAAAT
MX2	NM_002463.1	2188-2288	AATTTACCGGCTCACTCAGGCGCGACACGCACTCTGTCAATTCTCCAGCAAAGAGATCCACTGAAGGGCGGCGATGCCTGTGGTTGTTTTCTTGTGCGTA
MYD88	NM_002468.3	2145-2245	ACGTTTTTCTAGGTACAGCTCCCAGGAACAGCTAGGTGGGAAAGTCCCATCACTGAGGGAGCCTAACCATGTCCCTGAACAAAAATTGGGCACTCATCTA
MYOF	NM_013451.3	5805-5905	CTGGATGACTACTTGGGTTTCCTAGAACTTGACTTGCGTCACACGATCATTCCTGCAAAATCACCAGAGAAATGCAGATTGGACATGATTCCGGACCTCA
NCOA7	NM_181782.3	3075-3175	TCAGGATCTGGAGGTGTGGGCATTTGATTGAAATTCAGACTGCCTTAAAATATAACATTAAAAAGACTGGGTTCGATCAGCCCTCCTAAAGCTGGCTGGA
NEXN	NM_144573.3	2035-2135	GAGCTCCATGGTTCAAGAAGCCTCTTAAAAACACATCAGTTGTAGACAGTGAGCCAGTCAGATTTACGGTTAAAGTAACAGGAGAACCCAAACCAGAAAT
NMI	NM_004688.1	770-870	TTCCTGACACACTGCGTGAAGATCAAATGAGAGACAAACTAGAGCTGAGCTTTTCAAAGTTCCGAAATGGAGGCGGAGAGGTGGACCGCGTGGACTATGA

NPAS2	NM_002518.3	540-640	CACCCAGCTGATGTTGGAGGCATTAGATGGCTTCATTATCGCAGTGACAACAGACGGCAGCATCATCTATGTCTCTGACAGTATCACGCCTCTCCTTGGG
NT5C3	NM_016489.11	94-194	ATGCCAGAATTCCAGAAAAGTTCAGTTCGAATCAAGAACCCTACAAGAGTAGAAGAAATTATCTGTGGTCTTATCAAAGGAGGAGCTGCCAAACTTCAGA
OAS1	NM_016816.2	5-105	TCTGAGGAAACGAAACCAACAGCAGTCCAAGCTCAGTCAGCAGAAGAGATAAAAGCAAACAGGTCTGGGAGGCAGTTCTGTTGCCACTCTCTCTCCTGTC
OAS2	NM_016817.2	2115-2215	AAGCAAAGGAATGGTTATCCTCTCCCTGCTTCAAGGATGGGACTGGAAACCCAATACCACCTTGGAAAGTGCCGACAATGCAGACACCAGGAAGTTGTGG
OAS3	NM_006187.2	4980-5080	GAGTGCCTTAGACAGCCTGACTCTCCACAAACCACTGTTAAAACTTACCTGCTAGGAATGCTAGATTGAATGGGATGGGAAGAGCCTTCCCTCATTATTG
ODF2L	NM_020729.2	460-560	CCAGTGAAAGTCATCTCAGCTGCCTGAAGCAGGACATTCTAAATGAAAAGACTGAATTGGAAGCAACACTTAAGGAAGCGGAGTTGGTAACTCATTCTGT
PARP12	NM_022750.2	2810-2910	CCTTCTATGATAGCTGCGTGAACAGTGTGTCCGACCCCTCCATCTTTGTGATCTTTGAGAAACACCAGGTCTACCCAGAGTATGTCATCCAGTACACCAC
PARP8	NM_024615.3	1215-1315	CTATGACAGCAATTAAATCGCACAAACTTTTGAACCGTCCTTGCCCTGCAGCTGTTAAGTCAGAGGAATGCCTAACTCTAAAGTCGCATAGACTATTGAC
PARP9	NM_031458.2	2696-2796	TGGTCATGACAGTGTGGTTGACAATGTCTCCAGCCCTGAAACCTTTGTTATTTTTAGTGGCATGCAGGCTATACCTCAGTATTTGTGGACATGCACCCAG
PER3	NM_016831.1	1075-1175	GACCTGATTGGAACATCGATCCTAAGCTACCTGCACCCTGAAGATCGTTCTCTGATGGTTGCCATACACCAAAAAGTTTTGAAGTATGCAGGGCATCCTC
PITPNM3	NM_031220.3	6210-6310	AAAAGCAGACTCCTTTCATGCATTGGGATGAACGGCCCTCTTGTCTGGGTGCTGGGCTACAGCAAACAAATGTGTTTGAATCCCAGTATTCCAGAGATTC
PLEKHA4	NM_020904.1	320-420	AGTGTAAAAGGAAGAGAGAGAGAGAGAGACCGTAAGAGACAGGAGACAAAGAGACAAAAAGTGTGAGTGAGCAGGTGAGGAGAGAGATTGAGAACTATGA
PLSCR1	NM_021105.2	355-455	GGAAACAGCGGCAGCCAGAGAACTGTTTTAATCATGGACAAACAAAACTCACAGATGAATGCTTCTCACCCGGAAACAAACTTGCCAGTTGGGTATCCTC
PNPT1	NM_033109.3	1540-1640	GGATTCAGGGGTTCCAATTTCATCTGCTGTTGCAGGCGTAGCAATAGGATTGGTCACCAAAACCGATCCTGAGAAGGGTGAAATAGAAGATTATCGTTTG
PRIC285	NM_033405.3	7298-7398	TGCTTCCACCCTGGACTGAGTGTTCGGGGCAGCCTGCTCGGCTGTATGTTTCTCGCACGCTCACCCGCTTCAGTGCGGCTCTGTCCCTGCTGCCGCCTCC
RGS1	NM_002922.3	675-775	CAGGCTAATAGCCTAAAGTGACTGGTCCCTGGCTGAAGGGAATTAACAGATAGTATCAAGCGCAGAAGGAATGTGCCAGTATGGCTCCCTGGGTGAACAG
RIPK2	NM_003821.5	1695-1795	ATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTAC
RNF213	NM_020954.2	2475-2575	TTGAGCACCTGGGTCGTTTTCCTGCTCATATCCTGGACTGTCTTTCAGGGATTTACTACCGGCTTCCGGGACTTGAGCAAGTCTTGAATACGCAGGATGT
RSAD2	NM_080657.4	473-573	AGGAAGCTGGTATGGAGAAGATCAACTTTTCAGGTGGAGAGCCATTTCTTCAAGACCGGGGAGAATACCTGGGCAAGTTGGTGAGGTTCTGCAAAGTAGA
SAMD9	NM_017654.2	6525-6625	TGTGGGGGTGGTGAAAGGGAAGTAGAACCGAAACAAGATTAGTCCTGAGTTAACAATGGCTGCAAGCTGGATACATGGAATTCAGCACACTTTTCTCCCT
SAMD9L	NM_152703.2	422-522	ACACAGCAGAAAGTTGGGTCATTCCGGCTGCTTTTTTGAGAAGTCCCTGAAGAGATCAATAACAGCAAGAGGGAACCTGGCAAGGAAGCTATTCCTATAA
SERPINB9	NM_004155.3	950-1050	GTTGATGCCTTCCAACAGGGCAAGGCTGACTTGTCGGCAATGTCAGCGGAGAGAGACCTGTGTCTGTCCAAGTTCGTGCACAAGAGTTTTGTGGAGGTGA
SMCHD1	NM_015295.2	4675-4775	AACCACCTACACCAGCTGTTTCAAATGTTCGCTCAGTTGCCAGTAGGACCTTGGTCAGAGATCTACATCTTAGTATCACGGATGACTACGACAACCATAC
SOCS1	NM_003745.1	1025-1125	TTAACTGTATCTGGAGCCAGGACCTGAACTCGCACCTCCTACCTCTTCATGTTTACATATACCCAGTATCTTTGCACAAACCAGGGGTTGGGGGAGGGTC
SP100	NM_003113.3	1085-1185	TCATCATAACCAGGCATCTGACATAATAGTCATCAGCAGTGAGGACTCTGAAGGATCCACTGACGTTGATGAGCCCTTAGAAGTCTTCATCTCAGCACCG
SP110	NM_004510.3	265-365	AAGAGGCTCTTTTTCAGCACTTCATGCACCAGAAGCTGGGGATCGCCTATGCCATACACAAGCCATTTCCCTTCTTTGAAGGCCTCCTAGACAACTCCAT
SP140	NM_001005176.2	245-345	GGTTCTTCAGAGAAAACAAGGTGGAGATTGCAAGTGCAATAACAAGGCCATTTCCTTTCCTTATGGGCCTCCGAGACCGCTCCTTCATCTCCGAGCAGAT
ST3GAL5	NM_003896.2	1155-1255	CACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTTGGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
STAP1	NM_012108.2	660-760	GAACCCTTCTTTGGGAAATATGATCCTGAGGCCTGGTAGTGACAGTAGAAACTACTCCATCACTATTCGGCAGGAGATAGACATTCCAAGAATCAAGCAC
STAT1	NM_007315.2	205-305	TTTGCTGTATGCCATCCTCGAGAGCTGTCTAGGTTAACGTTCGCACTCTGTGTATATAACCTCGACAGTCTTGGCACCTAACGTGCTGTGCGTAGCTGCT
TAP2	NM_000544.3	4025-4125	TTCTTGTGCAGATTTGCCTTTCTTTCATCCTGGGGCTGACTTGCAGCTCCACACCCATCCATCTCTCAAATTTCACAGAGGGTAAAATAGGCATTTGGAG
TFEC	NM_012252.2	890-990	CTTCACTTGGCACGGTTGATTTAGGTGCTCATGTCACCAAACAGCAGAGCCATCCTGAGCAGAATTCAGTAGACTATTGCCAACAACTGACTGTGTCTCA
TLR7	NM_016562.3	4120-4220	TGTGGGCACCACACAGGTGGTTGCTGCTTCAGTGCTTCCTGCTCTTTTTCCTTGGGCCTGCTTCTGGGTTCCATAGGGAAACAGTAAGAAAGAAAGACAC

TMEM132E	NM_207313.1	1505-1605	TGGAATGCGAGTCTGACAATGAAGACATCATCAAGGTATCCAGCAGCTGTGACTACGTGTTTGTGAGTGGAAAAGAGTCTCGAGGGTCCATGAACGCCAG
TMEM171	NM_173490.6	492-592	CCCGACCGAGCCTTCATCTGTGGAGAGAGCCGCCAGTTTGCCCAGTGCCTTATCTTTGGGTTTCTGTTCTTGACAAGCGGCATGCTCATCAGCGTCCTGG
TMEM229B	NM_182526.2	1935-2035	GTTTGGTGGGGAAAAGCCAGAGTTCTAGGTCATCTATTCCCTGCCTGGTTTATTTTCAAGCCAAAACTGAGCAGTCTAGCTTTCTATGGGATGGAGAAGC
TNFRSF10B	NM_003842.3	565-665	GCATCTCCTGCAAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACCAGGTGTGATTCAGGTGAAGTGGAGCTAAG
TNFSF13B	NM_006573.3	635-735	CAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAGTGAAACACCA
TOX2	NM_001098798.1	784-884	GAAGCCTGTGTCGGCCTACGCACTCTTCTTCAGAGACACTCAGGCCGCCATCAAGGGTCAGAACCCCAGTGCCACTTTCGGTGACGTGTCCAAAATCGTG
TRIM21	NM_003141.3	1190-1290	AGAGACTCTGTGCGCAGGAAGGGGCACTTTTTGCTTAGTTCCAAGAGTGGCTTCTGGACAATTTGGTTGTGGAACAAACAAAAATATGAGGCTGGCACCT
TRIM22	NM_006074.3	1745-1845	CCATGACTGTGTGCCCACCGAGCTCCTGAGTGTTCTCATTCCTTTACCCACTTCTGCATAGTAGCCCTTGTGCTGAGACTCAGATTCTGCACCTGAGTTC
TRIM56	NM_030961.1	2570-2670	GTGGAGGCCGAGGACATTTTCCTGAAGGGCAGGGGTTGGCAACTTTTCAACATGGAGTGCCAAACTGCTAACCCGTCTTCTAGTGTGTGAGAATAGGGAC
TRIM69	NM_080745.3	5-105	GCTATGAACCTTAAGATTAGACCACTAACTCGAATCTAAATGAGCTGCCCTTGTCTCCTACAAAAGAAAAGTTGGGCAGGTAGGGTATTCTAATGAGGGT
UBE2L6	NM_004223.3	1110-1210	TGTTTCAAAACCACTTGCCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGCCTCAGACTGTGAAGTATATATCCTCCAGCATTCAGTCCAGGGGGAGCC
USP18	NM_017414.3	1458-1558	GGAAATGCCCAAAACCTTCAGAGATTGACACGCTGTCATTTTCCATTTCCGTTCCTGGATCTACGGAGTCTTCTAAGAGATTTTGCAATGAGGAGAAGCA
WARS	NM_173701.1	2552-2652	GCAAAGCCAAATCTCAGGGAAGTCCTTGGTTGATGTATCTGGGTCTCCTCTGGAGCACTCTGCCCTCCTGTCACCCAGTAGAGTAAATAAACTTCCTTGG
XAF1	NM_199139.1	3405-3505	GTTTGCCCAAGGACTACAAATAAACCAACGGGAAAAAAGAAAGGTTCCAGTTTTGTCTGAAAATTCTGATTAAGCCTCTGGGCCCTACAGCCTGGAGAAC
House-keeping Genes			
GAPDH	NM_002046.3	35-135	TCCTCCTGTTCGACAGTCAGCCGCATCTTCTTTTGCGTCGCCAGCCGAGCCACATCGCTCAGACACCATGGGGAAGGTGAAGGTCGGAGTCAACGGATTT
HPRT1	NM_000194.1	240-340	TGTGATGAAGGAGATGGGAGGCCATCACATTGTAGCCCTCTGTGTGCTCAAGGGGGGCTATAAATTCTTTGCTGACCTGCTGGATTACATCAAAGCACTG
TBP1	NM_001328.2	425-525	GAAGTTCAAAGCCCTCCGCATCATCGTCCGGATTGGCAGTGGTTTTGACAACATCGACATCAAGTCGGCCGGGGATTTAGGCATTGCCGTCTGCAACGTG
HMBS	NM_000190.3	315-415	CATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCACTCTCTAAGATTGGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGCCCTGGAG

[1] Also detects IFNA10, IFNA16, IFNA17 and IFNA21

[2] Also detects IFNA2, IFNA1, IFNA13, IFNA14

[3] Detects both IL28A and IL28B

Supplementary Table 2 – Genes with significantly affected hepatic expression by peginteferon treatment. Results are from 2-way ANOVA on microarray results with treatment group and presence of cirrhosis as factors.

Probeset ID	**Gene Symbol**	**Gene Title**	**RefSeq Transcript ID**	**Fold-Change (IFN vs. None)**	**p-value (IFN vs. None)**
1555131_a_at	PER3	period homolog 3 (Drosophila)	NM_016831	-2.58901	1.97E-05
230076_at	PITPNM3	PITPNM family member 3	NM_001165966 /// NM_031220	-2.34598	5.35E-10
220139_at	DNMT3L	DNA (cytosine-5-)-methyltransferase 3-like	NM_013369 /// NM_175867	-2.31126	6.06E-05
229309_at	ADRB1	adrenergic, beta-1-, receptor	NM_000684	-2.11897	0.000280762
228737_at	TOX2	TOX high mobility group box family member 2	NM_001098796 /// NM_001098797 /// NM_001098798 /// NM_032883	-2.09388	6.31E-06
237226_at	---	---	---	-2.05325	0.000119247
220307_at	CD244	CD244 molecule, natural killer cell receptor 2B4	NM_001166663 /// NM_001166664 /// NM_016382	-1.98763	0.000154448
237484_at	C12orf69	chromosome 12 open reading frame 69	NM_001013698	-1.96939	0.000162124
220112_at	ANKRD55	ankyrin repeat domain 55	NM_001039935 /// NM_024669	-1.95544	4.45E-05
204482_at	CLDN5	claudin 5	NM_001130861 /// NM_003277	-1.89668	6.93E-06
221756_at	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	NM_001135911 /// NM_052880	-1.8669	0.000149497
224042_at	UPB1	ureidopropionase, beta	NM_016327	-1.8472	2.97E-05
220625_s_at	ELF5	E74-like factor 5 (ets domain transcription factor)	NM_001422 /// NM_198381	-1.82274	0.000139391
209782_s_at	DBP	D site of albumin promoter (albumin D-box) binding protein	NM_001352	-1.79787	0.00022127

220999_s_at	CYFIP2	cytoplasmic FMR1 interacting protein 2	NM_001037332 /// NM_001037333 /// NM_014376	-1.78427	0.000317255
243708_at	TMEM132E	transmembrane protein 132E	NM_207313	-1.73746	0.000111643
232270_at	C9orf3	Chromosome 9 open reading frame 3	NM_032823	-1.73668	0.000181653
214058_at	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	NM_001033081 /// NM_001033082 /// NM_005376	-1.69851	0.000155322
219452_at	DPEP2	dipeptidase 2	NM_022355	-1.69379	0.000278204
1559033_at	LOC255167	hypothetical LOC255167	NR_024423 /// NR_024424	-1.69355	0.000241934
223602_at	USP30	ubiquitin specific peptidase 30	NM_032663	-1.67493	7.93E-05
231947_at	MYCT1	myc target 1	NM_025107	-1.63305	7.84E-05
229754_at	TMEM44	transmembrane protein 44	NM_001011655	-1.63012	0.000129103
225840_at	TEF	thyrotrophic embryonic factor	NM_001145398 /// NM_003216	-1.62372	0.000106191
237419_at	---	---	---	-1.60975	4.13E-05
238628_s_at	TRAPPC2L	trafficking protein particle complex 2-like	NM_016209	-1.58259	0.000280711
207224_s_at	SIGLEC7	sialic acid binding Ig-like lectin 7	NM_014385 /// NM_016543	-1.57979	0.000325177
1556012_at	KLHDC7A	kelch domain containing 7A	NM_152375	-1.5629	0.000316468
215768_at	SOX5	SRY (sex determining region Y)-box 5	NM_152989	-1.53629	0.000288759
227596_at	LOC100288612	hypothetical protein LOC100288612	XM_002342040 /// XM_002347514	-1.52925	0.000105269
219698_s_at	METTL4	methyltransferase like 4	NM_022840	1.51848	0.000260465
233085_s_at	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	NM_001031716 /// NR_024415	1.51881	8.71E-05
219062_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	NM_017742	1.51941	5.57E-06
1552365_at	SCIN	scinderin	NM_001112706 /// NM_033128	1.52845	4.22E-05
219994_at	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting prot	NM_019043	1.5288	0.000131892

203567_s_at	TRIM38	tripartite motif-containing 38	NM_006355	1.53423	0.000162345
212569_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	NM_015295	1.53472	9.45E-07
200797_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	NM_021960 /// NM_182763	1.53799	0.00021963
221816_s_at	PHF11	PHD finger protein 11	NM_001040443 /// NM_001040444	1.53812	4.10E-06
224701_at	PARP14	poly (ADP-ribose) polymerase family, member 14	NM_017554	1.54773	1.76E-05
233072_at	NTNG2	netrin G2	NM_032536	1.55178	0.000124256
227688_at	LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	NM_020871	1.55676	9.05E-06
217518_at	MYOF	myoferlin	NM_013451 /// NM_133337	1.57131	6.66E-07
221050_s_at	GTPBP2	GTP binding protein 2	NM_019096	1.57687	0.000158291
219716_at	APOL6	apolipoprotein L, 6	NM_030641	1.5771	5.18E-05
231876_at	TRIM56	tripartite motif-containing 56	NM_030961	1.58135	7.60E-05
218928_s_at	SLC37A1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	NM_018964	1.59762	0.000179542
216202_s_at	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	NM_004863	1.61302	0.000121372
205992_s_at	IL15	interleukin 15	NM_000585 /// NM_172174	1.63316	0.000116026
224917_at	MIR21	microRNA 21	NR_029493	1.63991	0.000203125
227877_at	C5orf39	chromosome 5 open reading frame 39	NM_001014279	1.6403	1.47E-05
217497_at	TYMP	thymidine phosphorylase	NM_001113755 /// NM_001113756 /// NM_001953	1.64178	2.31E-05
1562289_at	---	---	---	1.6543	2.02E-05
233220_at	GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	NM_133445	1.65612	0.000159116
207113_s_at	TNF	tumor necrosis factor	NM_000594	1.65705	6.99E-05

203217_s_at	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_001042437 /// NM_003896	1.66133	0.00013857
240770_at	TMEM171	transmembrane protein 171	NM_001161342 /// NM_173490	1.67229	0.000258764
225557_at	CSRNP1	cysteine-serine-rich nuclear protein 1	NM_033027	1.67348	0.000208113
222146_s_at	TCF4	transcription factor 4	NM_001083962 /// NM_003199	1.68179	0.000229171
237223_at	---	---	---	1.69817	0.000133884
204211_x_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	NM_001135651 /// NM_001135652 /// NM_002759	1.70006	1.93E-07
218805_at	GIMAP5	GTPase, IMAP family member 5	NM_018384	1.70127	0.00020245
1568592_at	TRIM69	tripartite motif-containing 69	NM_080745 /// NM_182985	1.707	4.69E-05
231292_at	EID3	EP300 interacting inhibitor of differentiation 3	NM_001008394	1.71686	7.37E-05
229109_s_at	BLVRA	Biliverdin reductase A	NM_000712	1.72178	0.000288321
226773_at	---	---	---	1.72678	0.000261065
234987_at	C20orf118	chromosome 20 open reading frame 118	NM_080628	1.73253	6.60E-05
222859_s_at	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	NM_014395	1.73254	0.000190071
210705_s_at	TRIM5	tripartite motif-containing 5	NM_033034 /// NM_033092 /// NM_033093	1.73459	7.07E-05
228577_x_at	ODF2L	outer dense fiber of sperm tails 2-like	NM_001007022 /// NM_001184765 /// NM_001184766 /// NM_020729	1.73702	4.52E-05
209305_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta	NM_015675	1.73806	0.000319618
1555853_at	LOC100507463	hypothetical LOC100507463	NR_037173	1.73936	1.65E-05
218543_s_at	PARP12	poly (ADP-ribose) polymerase family, member 12	NM_022750	1.74678	5.70E-06
210785_s_at	C1orf38	chromosome 1 open reading frame 38	NM_001039477 /// NM_001105556 ///	1.74932	0.000236668

			NM_004848		
213596_at	CASP4	caspase 4, apoptosis-related cysteine peptidase	NM_001225 /// NM_033306	1.75085	7.33E-05
219734_at	SIDT1	SID1 transmembrane family, member 1	NM_017699	1.75167	0.00013273
228617_at	XAF1	XIAP associated factor 1	NM_017523 /// NM_199139	1.75313	5.45E-05
218501_at	ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	NM_001128615 /// NM_001128616 /// NM_019555	1.76164	6.32E-06
220449_at	MGC5566	hypothetical protein MGC5566	XM_926767 /// XM_938022	1.7695	2.08E-05
212641_at	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	NM_006734	1.78903	6.04E-05
221044_s_at	TRIM34 /// TRIM6-TRIM34	tripartite motif-containing 34 /// TRIM6-TRIM34 readthrough	NM_001003819 /// NM_001003827 /// NM_021616 /// NM_130389 /// NM_130390	1.78915	8.77E-06
219033_at	PARP8	poly (ADP-ribose) polymerase family, member 8	NM_001178055 /// NM_001178056 /// NM_024615	1.7942	0.000143264
225646_at	CTSC	cathepsin C	NM_001114173 /// NM_001814 /// NM_148170	1.79429	8.58E-05
225447_at	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	NM_000408 /// NM_001083112	1.797	0.000216468
209716_at	CSF1	colony stimulating factor 1 (macrophage)	NM_000757 /// NM_172210 /// NM_172211 /// NM_172212	1.80368	7.17E-05
226497_s_at	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular perme	NM_001159920 /// NM_001160030 /// NM_001160031 /// NM_002019	1.82657	9.82E-05
221841_s_at	KLF4	Kruppel-like factor 4 (gut)	NM_004235	1.83109	0.000325972
225710_at	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	NM_021629	1.84623	2.98E-07

209545_s_at	RIPK2	receptor-interacting serine-threonine kinase 2	NM_003821	1.84869	1.85E-05
35254_at	TRAFD1	TRAF-type zinc finger domain containing 1	NM_001143906 /// NM_006700	1.85817	5.12E-05
227262_at	HAPLN3	hyaluronan and proteoglycan link protein 3	NM_178232	1.85858	3.17E-05
203236_s_at	LGALS9	lectin, galactoside-binding, soluble, 9	NM_002308 /// NM_009587 /// NR_024043	1.85999	1.87E-05
227606_s_at	STAMBPL1	STAM binding protein-like 1	NM_020799	1.86576	2.48E-05
202307_s_at	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	NM_000593	1.86785	5.87E-06
219011_at	PLEKHA4	pleckstrin homology domain containing, family A (phosphoinositide binding specif	NM_001161354 /// NM_020904	1.87129	0.000114178
213293_s_at	TRIM22	tripartite motif-containing 22	NM_006074	1.87179	1.67E-05
210561_s_at	WSB1	WD repeat and SOCS box-containing 1	NM_015626 /// NM_134265	1.88158	9.26E-05
201631_s_at	IER3	immediate early response 3	NM_003897	1.88788	0.000247675
226474_at	NLRC5	NLR family, CARD domain containing 5	NM_032206	1.88875	0.000281632
239108_at	FAR2	Fatty acyl CoA reductase 2	NM_018099	1.89228	5.89E-05
213982_s_at	RABGAP1L	RAB GTPase activating protein 1-like	NM_001035230 /// NM_014857	1.89546	1.89E-06
230480_at	PIWIL4	piwi-like 4 (Drosophila)	NM_152431	1.91289	0.000162972
227807_at	PARP9	poly (ADP-ribose) polymerase family, member 9	NM_001146102 /// NM_001146103 /// NM_001146104 /// NM_001146105 /// NM_001146106	1.91913	5.69E-05
235457_at	MAML2	mastermind-like 2 (Drosophila)	NM_032427	1.92146	7.74E-06
218694_at	ARMCX1	armadillo repeat containing, X-linked 1	NM_016608	1.92246	0.000300344
202531_at	IRF1	interferon regulatory factor 1	NM_002198	1.92273	0.000207967

203964_at	NMI	N-myc (and STAT) interactor	NM_004688	1.92464	5.84E-05
225778_at	RBMS2	RNA binding motif, single stranded interacting protein 2	NM_002898	1.92704	3.02E-07
232155_at	RNF213	ring finger protein 213	NM_020914 /// NM_020954 /// XM_002343588	1.93287	1.28E-05
208373_s_at	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	NM_004154 /// NM_176796 /// NM_176797 /// NM_176798	1.93383	3.36E-06
213069_at	HEG1	HEG homolog 1 (zebrafish)	NM_020733	1.94495	2.84E-05
229937_x_at	LILRB1	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains),	NM_001081637 /// NM_001081638 /// NM_001081639 /// NM_006669	1.94644	4.71E-05
242814_at	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	NM_004155	1.94785	0.000300053
220066_at	NOD2	nucleotide-binding oligomerization domain containing 2	NM_022162	1.95003	0.000272543
205841_at	JAK2	Janus kinase 2	NM_004972	1.9576	9.58E-07
213337_s_at	SOCS1	suppressor of cytokine signaling 1	NM_003745	1.96539	0.000141556
227677_at	JAK3	Janus kinase 3	NM_000215	1.97588	0.000175399
203821_at	HBEGF	heparin-binding EGF-like growth factor	NM_001945	1.9765	3.37E-05
213294_at	---	---	---	1.98194	9.57E-06
242974_at	CD47	CD47 molecule	NM_001025079 /// NM_001777 /// NM_198793	2.00366	8.08E-05
205692_s_at	CD38	CD38 molecule	NM_001775	2.00546	2.65E-05
205226_at	PDGFRL	platelet-derived growth factor receptor-like	NM_006207	2.0078	9.98E-06
220302_at	MAK	male germ cell-associated kinase	NM_005906	2.0306	6.75E-05
229842_at	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	NM_001114309 /// NM_004433	2.03141	0.000264383

205505_at	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2	NM_001097633 /// NM_001097634 /// NM_001097635 /// NM_001097636 /// NM_001490	2.03674	2.97E-06
220358_at	BATF3	basic leucine zipper transcription factor, ATF-like 3	NM_018664	2.04382	0.000228799
204205_at	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	NM_021822	2.04662	8.35E-06
32088_at	BLZF1	basic leucine zipper nuclear factor 1	NM_003666	2.0629	0.000131081
202934_at	HK2	hexokinase 2	NM_000189	2.07231	5.42E-05
202430_s_at	PLSCR1	phospholipid scramblase 1	NM_021105	2.07464	3.41E-07
212810_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	NM_001135581 /// NM_003038	2.08046	0.000266998
209493_at	PDZD2	PDZ domain containing 2	NM_178140	2.08458	2.86E-05
223374_s_at	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	NM_001038628 /// NM_003781 /// NM_033167 /// NM_033168 /// NM_033169	2.08806	0.000120044
212573_at	ENDOD1	endonuclease domain containing 1	NM_015036	2.08929	5.56E-05
206011_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase	NM_001223 /// NM_033292 /// NM_033293 /// NM_033294 /// NM_033295	2.09196	0.000269084
210985_s_at	SP100	SP100 nuclear antigen	NM_001080391 /// NM_003113	2.09473	1.04E-05
236796_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	NM_001170794 /// NM_021813	2.10739	4.94E-05
204804_at	TRIM21	tripartite motif-containing 21	NM_003141	2.11044	4.90E-05
211267_at	HESX1	HESX homeobox 1	NM_003865	2.11138	3.32E-07
211434_s_at	CCRL2	chemokine (C-C motif) receptor-like 2	NM_001130910 /// NM_003965	2.12387	9.12E-05
218943_s_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	NM_014314	2.13869	1.86E-05

1570541_s_at	GBP1P1	guanylate binding protein 1, interferon-inducible pseudogene 1	NR_003133	2.14315	0.000250624
206026_s_at	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	NM_007115	2.14606	0.000197842
239582_at	PML	promyelocytic leukemia	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246	2.15443	0.000111514
204502_at	SAMHD1	SAM domain and HD domain 1	NM_015474	2.15639	9.47E-06
209417_s_at	IFI35	interferon-induced protein 35	NM_005533	2.1688	0.000246251
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	NM_000076 /// NM_001122630 /// NM_001122631	2.18304	9.82E-05
223501_at	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	NM_001145645 /// NM_006573	2.19558	3.35E-08
209732_at	CLEC2B	C-type lectin domain family 2, member B	NM_005127	2.20616	3.13E-06
227544_at	TMEM229B	transmembrane protein 229B	NM_182526	2.21676	1.37E-05
207375_s_at	IL15RA	interleukin 15 receptor, alpha	NM_002189 /// NM_172200 /// NR_033494	2.26153	3.06E-06
244796_at	---	---	---	2.26193	4.34E-06
225076_s_at	ZNFX1	zinc finger, NFX1-type containing 1	NM_021035	2.2721	6.77E-05
1564276_at	C5orf56	chromosome 5 open reading frame 56	NM_001013717	2.27742	0.000176475
235061_at	PPM1K	protein phosphatase, Mg2+/Mn2+ dependent, 1K	NM_152542	2.28503	1.77E-05
202207_at	ARL4C	ADP-ribosylation factor-like 4C	NM_005737	2.29035	4.72E-05
202869_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	NM_001032409 /// NM_002534 /// NM_016816	2.29902	9.67E-05
211012_s_at	GOLGA6L4 /// PML	golgin A6 family-like 4 /// promyelocytic leukemia	NM_002675 /// NM_033238 /// NM_033239 /// NM_033240 /// NM_033244 /// NM_033246	2.29932	6.77E-05
230130_at	---	---	---	2.31309	0.000186003

217967_s_at	FAM129A	family with sequence similarity 129, member A	NM_052966	2.32134	1.38E-05
219863_at	HERC5	hect domain and RLD 5	NM_016323	2.32937	0.000142361
237538_at	---	---	---	2.33203	9.90E-05
209959_at	NR4A3	nuclear receptor subfamily 4, group A, member 3	NM_006981 /// NM_173198 /// NM_173199 /// NM_173200	2.33457	3.88E-05
209892_at	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	NM_002033	2.33596	7.50E-06
36564_at	RNF19B	ring finger protein 19B	NM_001127361 /// NM_153341	2.35944	0.000141267
213361_at	TDRD7	tudor domain containing 7	NM_014290	2.36564	9.35E-05
203596_s_at	IFIT5	interferon-induced protein with tetratricopeptide repeats 5	NM_012420	2.3663	2.08E-07
208436_s_at	IRF7	interferon regulatory factor 7	NM_001572 /// NM_004029 /// NM_004031	2.37311	5.17E-05
225344_at	NCOA7	nuclear receptor coactivator 7	NM_001122842 /// NM_181782	2.3777	1.23E-06
229548_at	SUN2	Sad1 and UNC84 domain containing 2	NM_001199579	2.38576	1.89E-05
200628_s_at	WARS	tryptophanyl-tRNA synthetase	NM_004184 /// NM_173701 /// NM_213645 /// NM_213646	2.38713	7.86E-06
205098_at	CCR1	chemokine (C-C motif) receptor 1	NM_001295	2.39001	6.44E-07
225973_at	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	NM_000544 /// NM_018833	2.41897	7.37E-06
204187_at	GMPR	guanosine monophosphate reductase	NM_006877	2.42462	7.91E-06
202988_s_at	RGS1	regulator of G-protein signaling 1	NM_002922	2.42585	3.86E-07
221680_s_at	ETV7	ets variant 7	NM_016135	2.44152	0.000149867
221432_s_at	SLC25A28	solute carrier family 25, member 28	NM_031212	2.44769	0.000103283
202270_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	NM_002053	2.44805	1.23E-06
220146_at	TLR7	toll-like receptor 7	NM_016562	2.45272	1.11E-05

241457_at	FBXL7	F-box and leucine-rich repeat protein 7	NM_012304	2.45523	0.000179202
207777_s_at	SP140	SP140 nuclear body protein	NM_001005176 /// NM_007237	2.46555	1.52E-05
237105_at	MIR548N	microRNA 548n	NR_031666	2.49181	6.91E-07
209795_at	CD69	CD69 molecule	NM_001781 /// NR_026671 /// NR_026672	2.50037	2.82E-06
230519_at	FAM124A	family with sequence similarity 124A	NM_145019	2.53208	1.80E-07
208012_x_at	SP110	SP110 nuclear body protein	NM_004509 /// NM_004510 /// NM_080424	2.53349	1.84E-08
1552623_at	HSH2D	hematopoietic SH2 domain containing	NM_032855	2.58663	8.20E-06
222881_at	HPSE	heparanase	NM_001098540 /// NM_001166498 /// NM_006665	2.62662	1.85E-07
242713_at	---	---	---	2.64367	8.98E-06
228152_s_at	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	NM_001012967	2.65189	2.75E-08
206715_at	TFEC	transcription factor EC	NM_001018058 /// NM_012252	2.65745	4.40E-08
1568615_a_at	SRD5A3	steroid 5 alpha-reductase 3	NM_024592	2.68402	7.94E-06
228439_at	BATF2	basic leucine zipper transcription factor, ATF-like 2	NM_138456	2.73706	1.23E-06
219209_at	IFIH1	interferon induced with helicase C domain 1	NM_022168	2.76461	4.57E-07
229893_at	FRMD3	FERM domain containing 3	NM_174938	2.78557	6.43E-07
219211_at	USP18	ubiquitin specific peptidase 18	NM_017414	2.82724	0.000111634
238025_at	MLKL	mixed lineage kinase domain-like	NM_001142497 /// NM_152649	2.84196	3.41E-07
235276_at	EPSTI1	epithelial stromal interaction 1 (breast)	NM_001002264 /// NM_033255	2.86108	2.40E-05
230110_at	MCOLN2	mucolipin 2	NM_153259	2.92668	7.06E-05
220059_at	STAP1	signal transducing adaptor family member 1	NM_012108	2.93794	1.54E-05

225291_at	PNPT1	polyribonucleotide nucleotidyltransferase 1	NM_033109	2.94729	3.23E-07
219684_at	RTP4	receptor (chemosensory) transporter protein 4	NM_022147	2.95087	9.36E-05
226757_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	NM_001547	2.9748	1.31E-06
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	NM_001548	3.00582	4.18E-06
229625_at	GBP5	guanylate binding protein 5	NM_001134486 /// NM_052942	3.00697	5.02E-08
204959_at	MNDA	myeloid cell nuclear differentiation antigen	NM_002432	3.0148	2.09E-06
235175_at	GBP4	guanylate binding protein 4	NM_052941	3.03041	3.77E-07
204533_at	CXCL10	chemokine (C-X-C motif) ligand 10	NM_001565	3.07474	0.00022319
216951_at	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	NM_000566	3.11791	1.72E-06
210029_at	IDO1	indoleamine 2,3-dioxygenase 1	NM_002164	3.12432	4.78E-06
219352_at	HERC6	hect domain and RLD 6	NM_001165136 /// NM_017912	3.15105	6.06E-06
228230_at	PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	NM_001037335 /// NM_033405	3.15732	1.05E-05
202672_s_at	ATF3	activating transcription factor 3	NM_001030287 /// NM_001040619 /// NM_001674 /// NM_004024	3.15851	7.98E-07
240232_at	TIMMDC1	translocase of inner mitochondrial membrane domain containing 1	NM_016589	3.16704	3.68E-05
228531_at	SAMD9	sterile alpha motif domain containing 9	NM_017654	3.21209	9.24E-09
201798_s_at	MYOF	myoferlin	NM_013451 /// NM_133337	3.22684	1.44E-09
236156_at	LIPA	lipase A, lysosomal acid, cholesterol esterase	NM_000235 /// NM_001127605	3.23218	1.21E-06
226702_at	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	NM_207315	3.38597	1.24E-06

208965_s_at	IFI16	interferon, gamma-inducible protein 16	NM_005531	3.39401	3.39E-06
203157_s_at	GLS	glutaminase	NM_014905	3.42022	6.64E-06
204972_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	NM_001032731 /// NM_002535 /// NM_016817	3.44657	1.82E-05
228362_s_at	FAM26F	Family with sequence similarity 26, member F	NM_001010919	3.46023	3.40E-08
33304_at	ISG20	interferon stimulated exonuclease gene 20kDa	NM_002201	3.56131	1.80E-07
206513_at	AIM2	absent in melanoma 2	NM_004833	3.56837	1.43E-07
1554519_at	CD80	CD80 molecule	NM_005191	3.70194	5.17E-07
223298_s_at	NT5C3	5'-nucleotidase, cytosolic III	NM_001002009 /// NM_001002010 /// NM_001166118 /// NM_016489 /// NR_029372	3.84017	6.98E-07
232375_at	STAT1	signal transducer and activator of transcription 1	NM_007315	3.84556	2.21E-06
202086_at	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mous	NM_001144925 /// NM_001178046 /// NM_002462	3.91435	1.51E-06
210873_x_at	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	NM_145699	4.00738	2.50E-10
227458_at	CD274	CD274 molecule	NM_014143	4.12901	2.55E-06
210163_at	CXCL11	chemokine (C-X-C motif) ligand 11	NM_005409	4.15411	5.89E-05
218400_at	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	NM_006187	4.27865	1.19E-05
226603_at	SAMD9L	sterile alpha motif domain containing 9-like	NM_152703	4.29144	4.32E-12
214059_at	IFI44	Interferon-induced protein 44	NM_006417	4.32234	2.32E-05
214511_x_at	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	NM_001004340 /// NM_001017986	4.45403	1.76E-09
226103_at	NEXN	nexilin (F actin binding protein)	NM_001172309 /// NM_144573	4.47698	1.02E-07

216598_s_at	CCL2	chemokine (C-C motif) ligand 2	NM_002982	4.47878	5.98E-06
204747_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	NM_001031683 /// NM_001549	4.71567	1.28E-05
214255_at	ATP10A	ATPase, class V, type 10A	NM_024490	4.73559	1.04E-06
204439_at	IFI44L	interferon-induced protein 44-like	NM_006820	5.04895	3.78E-06
239196_at	ANKRD22	ankyrin repeat domain 22	NM_144590	6.469	2.45E-06
204994_at	MX2	myxovirus (influenza virus) resistance 2 (mouse)	NM_002463	6.79779	4.78E-14
242625_at	RSAD2	radical S-adenosyl methionine domain containing 2	NM_080657	7.09398	2.56E-08
214038_at	CCL8	chemokine (C-C motif) ligand 8	NM_005623	13.0092	1.11E-13

Supplementary Table 3 – Genes significantly affected by biochemical response to RBV. Analysis limited to 11 patients from group C (4 biochemical responders and 7 non-responders). Significance set at p<0.0001

Probeset ID	**Gene Symbol**	**Gene Title**	**RefSeq Transcript ID**	**Fold-Change (Biochemical responder vs. Non-Responder)**	**p-value (Responder vs. Non-responder)**
221491_x_at	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133661 /// LOC100294036	major histocompatibility complex, class II, DR beta 1 /// major histocompatibili	NM_002124 /// NM_002125 /// NM_021983 /// NM_022555 /// XM_001713857 /// XM_0023	-9.66247	0.000602055
1554890_a_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	NM_022037 /// NM_022173	-2.002	0.000885062
1568720_at	ZNF506	zinc finger protein 506	NM_001099269 /// NM_001145404	-1.75141	0.000771341
230122_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	NM_001009569 /// NM_004641	-1.664	0.000758586
230132_at	---	---	---	-1.57853	0.000147288
1559534_at	---	---	---	-1.56947	0.000149082
233073_at	---	---	---	-1.4423	0.000257106
1561146_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	NM_018206	-1.42419	0.000247016
234151_at	---	---	---	-1.38873	0.000446784
214234_s_at	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	NM_000777	-1.33741	0.000551526
1557501_a_at	---	---	---	-1.32185	0.000620807
244707_at	---	---	---	-1.32052	0.000132219

239703_at	---	---	---	-1.30278	0.000529117
241254_at	---	---	---	-1.2858	0.000717329
220419_s_at	USP25	ubiquitin specific peptidase 25	NM_013396	-1.28515	0.000818128
1560918_at	---	---	---	-1.27321	0.000367402
224076_s_at	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	NM_017778 /// NM_023034	-1.24571	2.93E-05
236652_at	LOC149703	hypothetical protein LOC149703	---	-1.22909	0.000753747
224363_at	---	---	---	-1.1935	0.000431319
226261_at	ZNRF2	zinc and ring finger 2	NM_147128	-1.18777	0.000530898
1569517_at	LOC646482	hypothetical LOC646482	XR_040959 /// XR_040960 /// XR_040961	-1.17859	0.00026739
229471_s_at	---	---	---	-1.17855	0.000423279
242148_at	BCL6B	B-cell CLL/lymphoma 6, member B	NM_181844	-1.14357	0.000807418
203475_at	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	NM_000103 /// NM_031226	-1.10382	0.000700704
232519_at	NSFL1C	NSFL1 (p97) cofactor (p47)	NM_016143 /// NM_018839 /// NM_182483	1.19916	0.000477953
228358_at	SOX12	SRY (sex determining region Y)-box 12	NM_006943	1.20088	0.000773892
223842_s_at	SCARA3	scavenger receptor class A, member 3	NM_016240 /// NM_182826	1.21065	0.000600464
227826_s_at	---	---	---	1.26475	0.000186848
229134_at	VANGL1	vang-like 1 (van gogh, Drosophila)	NM_001172411 /// NM_001172412 /// NM_138959	1.28068	0.000646713
y204729_s_at	STX1A	syntaxin 1A (brain)	NM_001165903 /// NM_004603	1.32551	0.000334617
211534_x_at	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	NM_002847 /// NM_130842 /// NM_130843	1.33861	0.000760029

204792_s_at	IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	NM_014714	1.35134	0.000983623
228472_at	CCDC61	coiled-coil domain containing 61	NM_001080402	1.36459	0.000587411
218371_s_at	PSPC1	paraspeckle component 1	NM_001042414 /// NR_003272	1.36978	0.000796441
1556065_at	LOC284926	hypothetical protein LOC284926	---	1.3858	0.000801
235286_at	---	---	---	1.41273	0.000882527
228292_at	---	---	---	1.45457	0.00036622
223707_at	RPL27A	ribosomal protein L27a	NM_000990	1.54586	3.08E-05
219900_s_at	ZNF446	zinc finger protein 446	NM_017908	1.57955	0.00018267
224742_at	ABHD12	abhydrolase domain containing 12	NM_001042472 /// NM_015600	1.61192	0.000578195
1053_at	RFC2	replication factor C (activator 1) 2, 40kDa	NM_002914 /// NM_181471	1.64437	0.000445032
200897_s_at	PALLD	palladin, cytoskeletal associated protein	NM_001166108 /// NM_001166109 /// NM_001166110 /// NM_016081	1.841	0.000666866
219512_at	DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_001145315 /// NM_001145316 /// NM_001145317 /// NM_001145318 /// NM_024918	1.89845	0.000220357
219513_s_at	SH2D3A	SH2 domain containing 3A	NM_005490	1.91176	0.00046238
1557322_at	ZNF230	zinc finger protein 230	NM_006300	2.08556	0.000703733
244479_at	---	---	---	2.16315	7.16E-05
224367_at	BEX2	brain expressed X-linked 2	NM_001168399 /// NM_001168400 /// NM_001168401 ///	3.58958	0.000919075

			NM_032621		
202949_s_at	FHL2	four and a half LIM domains 2	NM_001039492 /// NM_001450 /// NM_201555 /// NM_201557	4.31229	0.000407909
221491_x_at	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133661 /// LOC100294036	major histocompatibility complex, class II, DR beta 1 /// major histocompatibili	NM_002124 /// NM_002125 /// NM_021983 /// NM_022555 /// XM_001713857 /// XM_0023	-9.66247	0.000602055
1554890_a_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	NM_022037 /// NM_022173	-2.002	0.000885062
1568720_at	ZNF506	zinc finger protein 506	NM_001099269 /// NM_001145404	-1.75141	0.000771341
230122_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	NM_001009569 /// NM_004641	-1.664	0.000758586
230132_at	---	---	---	-1.57853	0.000147288
1559534_at	---	---	---	-1.56947	0.000149082
233073_at	---	---	---	-1.4423	0.000257106
1561146_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	NM_018206	-1.42419	0.000247016
234151_at	---	---	---	-1.38873	0.000446784
214234_s_at	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	NM_000777	-1.33741	0.000551526
1557501_a_at	---	---	---	-1.32185	0.000620807
244707_at	---	---	---	-1.32052	0.000132219
239703_at	---	---	---	-1.30278	0.000529117
241254_at	---	---	---	-1.2858	0.000717329
220419_s_at	USP25	ubiquitin specific peptidase 25	NM_013396	-1.28515	0.000818128
1560918_at	---	---	---	-1.27321	0.000367402

224076_s_at	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	NM_017778 /// NM_023034	-1.24571	2.93E-05
236652_at	LOC149703	hypothetical protein LOC149703	---	-1.22909	0.000753747
224363_at	---	---	---	-1.1935	0.000431319
226261_at	ZNRF2	zinc and ring finger 2	NM_147128	-1.18777	0.000530898
1569517_at	LOC646482	hypothetical LOC646482	XR_040959 /// XR_040960 /// XR_040961	-1.17859	0.00026739
229471_s_at	---	---	---	-1.17855	0.000423279
242148_at	BCL6B	B-cell CLL/lymphoma 6, member B	NM_181844	-1.14357	0.000807418
203475_at	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	NM_000103 /// NM_031226	-1.10382	0.000700704
232519_at	NSFL1C	NSFL1 (p97) cofactor (p47)	NM_016143 /// NM_018839 /// NM_182483	1.19916	0.000477953
228358_at	SOX12	SRY (sex determining region Y)-box 12	NM_006943	1.20088	0.000773892
223842_s_at	SCARA3	scavenger receptor class A, member 3	NM_016240 /// NM_182826	1.21065	0.000600464
227826_s_at	---	---	---	1.26475	0.000186848
229134_at	VANGL1	vang-like 1 (van gogh, Drosophila)	NM_001172411 /// NM_001172412 /// NM_138959	1.28068	0.000646713
204729_s_at	STX1A	syntaxin 1A (brain)	NM_001165903 /// NM_004603	1.32551	0.000334617
211534_x_at	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	NM_002847 /// NM_130842 /// NM_130843	1.33861	0.000760029
204792_s_at	IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	NM_014714	1.35134	0.000983623

228472_at	CCDC61	coiled-coil domain containing 61	NM_001080402	1.36459	0.000587411
218371_s_at	PSPC1	paraspeckle component 1	NM_001042414 /// NR_003272	1.36978	0.000796441
1556065_at	LOC284926	hypothetical protein LOC284926	---	1.3858	0.000801
235286_at	---	---	---	1.41273	0.000882527
228292_at	---	---	---	1.45457	0.00036622
223707_at	RPL27A	ribosomal protein L27a	NM_000990	1.54586	3.08E-05
219900_s_at	ZNF446	zinc finger protein 446	NM_017908	1.57955	0.00018267
224742_at	ABHD12	abhydrolase domain containing 12	NM_001042472 /// NM_015600	1.61192	0.000578195
1053_at	RFC2	replication factor C (activator 1) 2, 40kDa	NM_002914 /// NM_181471	1.64437	0.000445032
200897_s_at	PALLD	palladin, cytoskeletal associated protein	NM_001166108 /// NM_001166109 /// NM_001166110 /// NM_016081	1.841	0.000666866
219512_at	DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_001145315 /// NM_001145316 /// NM_001145317 /// NM_001145318 /// NM_024918	1.89845	0.000220357
219513_s_at	SH2D3A	SH2 domain containing 3A	NM_005490	1.91176	0.00046238
1557322_at	ZNF230	zinc finger protein 230	NM_006300	2.08556	0.000703733
244479_at	---	---	---	2.16315	7.16E-05

224367_at	BEX2	brain expressed X-linked 2	NM_001168399 /// NM_001168400 /// NM_001168401 /// NM_032621	3.58958	0.000919075
202949_s_at	FHL2	four and a half LIM domains 2	NM_001039492 /// NM_001450 /// NM_201555 /// NM_201557	4.31229	0.000407909

Supplementary Table 4 – Effects of treatment on hepatic expression of ISGs. Results are from 2-way ANOVA on nCounter assay results with treatment group and presence of cirrhosis as factors.

Gene Symbol	PEG-IFN (Group B) vs. Controls (Group A)		RBV (Group C) vs. Controls (Group A)		PEG-IFN+RBV (Group D) vs. Controls (Group A)	
	Fold Change	p-Value	Fold Change	p-Value	Fold Change	p-Value
ADRB1	-1.32	0.444	-1.53	0.300	-1.69	0.262
AIM2	12.09	<0.001	2.04	0.661	9.42	0.002
ANKRD22	5.06	0.003	-1.53	0.797	6.29	<0.001
ANXA1	1.19	0.486	-1.31	0.416	1.04	0.892
APOBEC3A	2.09	0.715	1.85	0.787	12.78	0.001
ARNTL	1.89	0.004	1.07	0.836	2.06	0.003
ATF3	6.77	0.005	-1.38	0.895	9.45	<0.001
ATP10A	5.82	0.005	-1.43	0.860	4.92	0.040
BATF2	119.11	<0.001	3.85	0.874	162.01	<0.001
BLZF1	1.97	0.002	1.16	0.606	2.29	<0.001
C12orf69	-2.56	0.028	-4.82	0.007	-1.86	0.140
C5orf56	2.59	<0.001	-1.30	0.578	2.22	0.010
CARD16(CASP1)	2.40	<0.001	-1.15	0.706	2.69	<0.001
CCL2	3.54	<0.001	-1.19	0.789	2.52	0.020
CCL8	31.17	<0.001	-1.22	0.982	34.31	<0.001
CD274	7.13	0.001	-1.24	0.938	9.13	<0.001
CD69	3.97	0.001	-1.93	0.593	4.41	<0.001
CD80	3.86	<0.001	1.00	0.999	2.93	0.001
CFB	1.20	0.209	1.05	0.779	1.34	0.065
CLEC2B	2.86	<0.001	1.31	0.576	3.06	0.001

CMPK2	12.98	0.001	-1.05	0.991	22.02	<0.001
CXCL10	7.14	<0.001	-2.83	0.687	7.38	<0.001
CXCL11	15.28	<0.001	-1.00	0.999	15.19	0.003
DDX58	4.12	0.005	-1.72	0.819	7.51	<0.001
DDX60	4.56	0.016	-1.70	0.785	7.30	<0.001
DDX60L	6.07	0.002	-1.83	0.840	8.78	<0.001
DNMT3L	-1.07	0.891	-1.08	0.881	-1.19	0.776
EIF2AK2	4.53	0.002	1.14	0.902	6.59	<0.001
EPSTI1	7.15	0.001	-1.04	0.985	10.76	<0.001
ETV7	8.63	<0.001	-5.98	0.709	12.05	<0.001
FAM122C	2.51	0.004	-1.06	0.917	2.34	0.021
FAM124A	1.41	0.303	-1.11	0.812	-1.94	0.289
FAM153A(FAM153B)	1.44	0.475	1.08	0.896	1.59	0.407
FAM26F	28.96	<0.001	4.21	0.635	31.56	<0.001
FAR2	2.83	<0.001	-1.09	0.874	2.22	0.029
FBXO6	2.73	0.002	1.05	0.924	3.49	<0.001
FCGR1A	17.34	0.110	1.07	0.845	39.47	0.002
FCGR1B	6.70	<0.001	1.26	0.874	5.45	0.015
FRMD3	20.05	<0.001	1.90	0.875	19.18	0.005
FUT4	3.08	0.012	-1.46	0.707	2.07	0.248
GBP1	12.01	<0.001	-1.38	0.932	13.13	0.001
GBP4	12.23	<0.001	1.10	0.977	14.73	<0.001
GBP5	6.18	0.001	-1.25	0.900	6.44	0.003
GLS	-1.02	0.963	-1.27	0.614	1.01	0.979
GMPR	7.34	<0.001	-1.95	0.760	7.84	<0.001
GOLGA6L4(PML)	6.68	<0.001	-1.58	0.794	5.75	0.003
HEATR7B1	1.23	0.589	-1.08	0.874	1.33	0.494

HERC5	40.43	0.009	-1.07	0.997	76.51	<0.001
HERC6	31.99	0.002	-1.59	0.972	53.45	<0.001
HPSE	8.06	<0.001	1.12	0.934	8.72	<0.001
HSH2D	3.13	<0.001	-2.63	0.222	2.92	<0.001
IDO1	38.20	<0.001	1.52	0.811	33.26	0.004
IFI16	4.69	<0.001	-1.23	0.840	4.48	0.001
IFI44	3.84	0.001	-1.11	0.909	5.27	<0.001
IFI44L	4.45	<0.001	-2.93	0.463	4.85	<0.001
IFI6	1.37	0.146	-1.72	0.117	1.34	0.233
IFIH1	21.58	0.001	-2.54	0.924	32.37	<0.001
IFIT1	12.50	0.005	1.09	0.986	20.03	<0.001
IFIT2	3.89	0.050	-1.36	0.917	5.60	0.022
IFIT3	3.29	0.008	-1.25	0.904	6.10	<0.001
IFIT5	4.11	<0.001	-1.06	0.943	5.68	<0.001
IFITM1	2.09	0.011	-1.39	0.516	2.12	0.021
IFITM2	1.28	0.208	1.00	0.996	1.54	0.038
IFITM3	1.22	0.128	-1.13	0.435	1.09	0.575
IL15RA	2.77	<0.001	-1.13	0.800	2.56	0.003
IRF1	2.87	<0.001	-1.26	0.684	2.66	0.004
IRF2	1.58	0.019	1.10	0.701	2.05	<0.001
IRF7	6.19	<0.001	-1.63	0.713	7.06	<0.001
IRF9	1.57	0.003	-1.20	0.388	1.84	<0.001
ISG15	4.12	0.020	-3.19	0.617	6.12	0.001
ISG20	8.28	<0.001	-5.56	0.663	9.14	<0.001
JAK2	2.62	<0.001	-1.09	0.822	2.61	<0.001
JAK3	1.60	0.115	-2.20	0.174	1.01	0.990
JUN	1.92	0.005	-1.23	0.572	1.98	0.008

JUNB	2.77	<0.001	-1.04	0.937	2.38	0.007
LAMP3	9.88	0.004	-2.34	0.641	12.53	0.001
LIPA	1.25	0.101	1.42	0.011	1.34	0.059
MCOLN2	6.72	<0.001	-2.02	0.723	5.27	0.008
MKX	3.94	0.042	-1.24	0.897	1.97	0.548
MLKL	8.86	<0.001	1.16	0.934	9.97	<0.001
MNDA	4.13	<0.001	-1.08	0.897	3.59	<0.001
MX1	726.66	0.003	17.12	0.940	1046.18	<0.001
MX2	24.07	<0.001	1.21	0.965	27.40	<0.001
MYD88	2.38	0.006	1.01	0.987	3.15	<0.001
MYOF	9.52	<0.001	1.47	0.825	9.59	<0.001
NCOA7	7.24	<0.001	1.57	0.741	9.50	<0.001
NEXN	9.00	<0.001	-1.11	0.960	6.78	0.011
NMI	3.15	0.001	-1.02	0.982	4.04	<0.001
NPAS2	1.63	0.011	1.19	0.454	1.72	0.011
NT5C3	14.73	0.003	-3.12	0.804	23.09	<0.001
OAS1	2.97	<0.001	-1.17	0.801	4.18	<0.001
OAS2	6.15	0.002	-2.12	0.749	8.24	<0.001
OAS3	17.75	<0.001	-2.25	0.909	23.21	<0.001
ODF2L	2.33	<0.001	1.12	0.720	2.13	0.004
PARP12	3.47	0.003	-1.41	0.724	4.77	<0.001
PARP8	1.63	0.004	-1.00	0.993	1.57	0.021
PARP9	2.32	<0.001	-1.13	0.736	2.78	<0.001
PER3	-2.12	0.005	1.20	0.292	-1.76	0.040
PITPNM3	-1.60	0.223	-1.73	0.190	1.09	0.793
PLEKHA4	4.83	0.076	-11.33	0.626	5.80	0.053
PLSCR1	6.21	<0.001	1.13	0.924	8.37	<0.001

PNPT1	18.41	0.001	2.81	0.739	25.71	<0.001
PRIC285	5.67	0.065	1.04	0.987	8.58	0.010
RGS1	10.93	0.003	-1.46	0.925	13.42	0.001
RIPK2	2.79	0.001	1.27	0.626	3.36	<0.001
RNF213	2.92	<0.001	-1.20	0.752	3.69	<0.001
RSAD2	4.72	0.002	-1.15	0.945	7.23	<0.001
SAMD9	25.74	0.001	-2.48	0.942	41.97	<0.001
SAMD9L	10.06	<0.001	-1.29	0.897	10.24	<0.001
SERPINB9	1.79	0.002	-1.35	0.321	1.99	<0.001
SMCHD1	2.45	<0.001	1.08	0.843	3.01	<0.001
SOCS1	3.27	0.006	-1.78	0.778	5.81	<0.001
SP100	2.24	0.003	-1.17	0.723	2.93	<0.001
SP110	6.07	<0.001	1.00	0.999	7.87	<0.001
SP140	10.86	<0.001	-1.69	0.869	11.18	<0.001
ST3GAL5	1.93	<0.001	-1.09	0.709	1.76	0.003
STAP1	30.97	0.001	1.55	0.956	39.19	<0.001
STAT1	5.09	<0.001	-1.28	0.824	6.24	<0.001
TAP2	4.34	<0.001	-1.98	0.594	5.55	<0.001
TFEC	4.53	<0.001	1.36	0.569	4.54	<0.001
TLR7	7.68	0.107	-1.25	0.675	13.49	0.010
TMEM132E	-1.91	0.129	-1.99	0.130	-1.10	0.794
TMEM171	5.39	0.007	-1.34	0.878	5.15	0.025
TMEM229B	7.33	0.015	1.18	0.946	9.44	0.005
TNFRSF10B	1.15	0.291	-1.15	0.402	1.11	0.488
TNFSF13B	7.62	<0.001	1.69	0.590	8.11	<0.001
TOX2	-1.05	0.893	1.25	0.534	-1.19	0.712
TRIM21	7.29	0.003	1.21	0.919	12.02	<0.001

TRIM22	3.22	<0.001	-1.15	0.800	3.92	<0.001
TRIM56	1.66	0.013	-1.39	0.300	2.15	<0.001
TRIM69	4.54	0.014	1.44	0.763	5.19	0.011
UBE2L6	2.48	0.001	-1.09	0.847	3.01	<0.001
USP18	150.25	0.005	1.29	0.966	257.20	<0.001
WARS	4.16	<0.001	-1.24	0.819	4.18	0.001
XAF1	2.38	<0.001	-1.36	0.400	2.53	<0.001

Supplementary Table 5 – Select SNP genotypes

	Group A	Group B	Group C	Group D	p-value
rs12979860					0.84[2]
CC	10 (67%[1])	6 (43%)	8 (53%)	6 (43%)	
CT	4 (27%)	5 (36%)	4 (27%)	5 (36%)	
TT	1 (7%)	3 (21%)	3 (20%)	3 (21%)	
Unavailable	2	4	3	3	
rs7270101					0.21[2]
AA	13 (100%)	7 (70%)	8 (89%)	6 (67%)	
CA	0 (0%)	2 (20%)	1 (11%)	3 (33%)	
CC	0 (0%)	1 (10%)	0 (0%)	0 (0%)	
Unavailable	4	8	9	8	
rs1127354					0.56[2]
AA	0 (0%)	1 (10%)	0 (0%)	0 (0%)	
CA	3 (23%)	1 (10%)	4 (33%)	2 (22%)	
CC	10 (77%)	8 (80%)	8 (67%)	7 (78%)	
Unavailable	4	8	6	8	

[1] Percentage from patients with available genotype

[2] Pearson Chi-square

SUPPLEMENTARY FIGURES

Supplementary figure 1– Examples of individual patterns of virological response to RBV monotherapy. Virological responders (A) can demonstrate a pattern of early (blue), late (black) or persistent response (red). Non-responders (B) could demonstrate no response, (black) or response with relapse (red). Dashed line represents the response cut-off of 0.5 $\log_{10}$.

Supplementary figure 2 – Relative decline in serum ALT activity vs. decrease in serum HCV-RNA (A) or decrease in hemoglobin (B) after 4 weeks of ribavirin monotherapy. Data shown only for patients treated with RBV.

Supplementary Figure 3 – Microarray gene expression profiles based on response to monotherapy, limited to patients in groups A and C. (A) Clustering of samples according to the top three principal components of principal component analysis (PCA) of the expression of all 54613 transcripts. Red denotes virological non-responders to RBV and blue – responders. (B) Hierarchical clustering of patients in groups A and C based on the expression of 8 genes, identified as significantly ($p<0.001$) different between virological responders and non-responders to RBV. (C) Clustering of samples by PCA of the expression of all transcripts. Red denotes biochemical non-response to RBV and red – biochemical responders. (D) Hierarchical clustering of patients in groups A and C based on the expression of 48 genes, identified as significantly ($p<0.001$) different between biochemical responders and non-responders.

Supplementary Figure 4 – Hepatic mRNA expression of IRF9 (A), IRF7 (B) and ISG15 (C) according to treatment at time of liver biopsy. Expression measured by nCounter assay. Lines denote median values.

Supplementary Figure 5 – Relative hepatic expression level of interferon genes according to treatment at the time of liver biopsy, compared to untreated controls. Geometric mean + 95% CI. X- $p<0.1$, * - $p<0.05$, ** - $p<0.01$. Significance tested using Mann-Whitney U test.

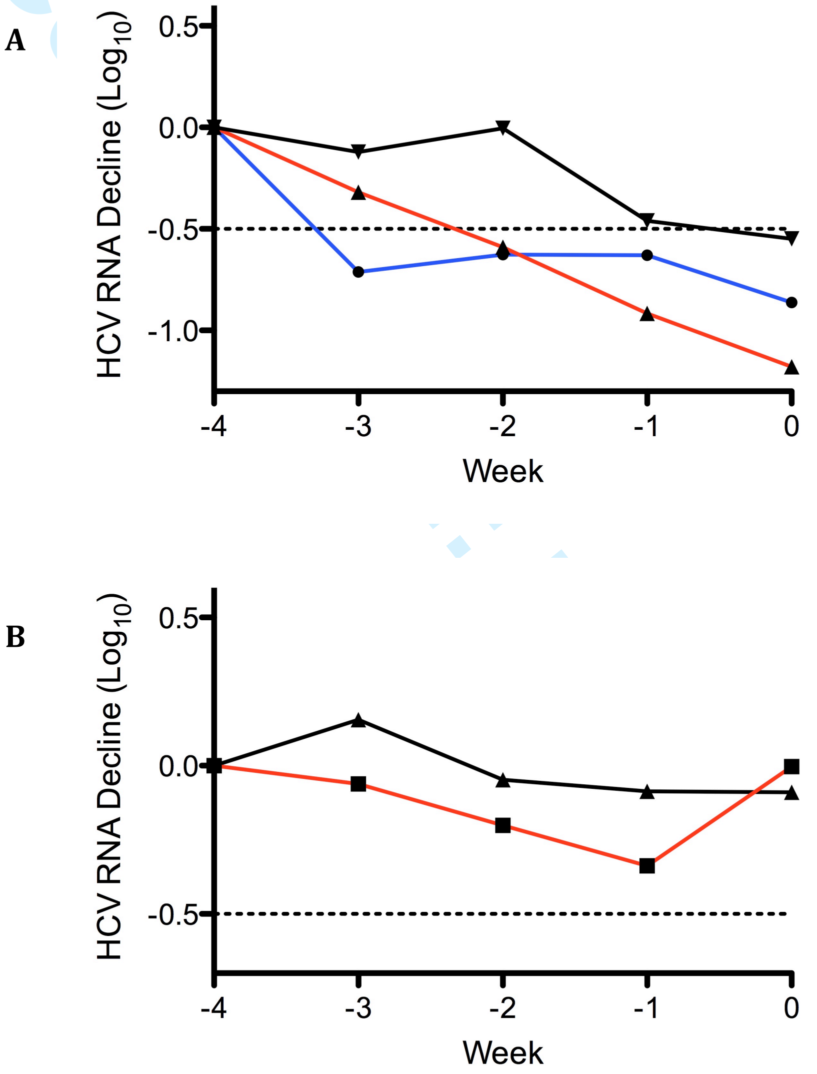
Supplementary Figure 6 - Serial median mRNA expression levels in PBMC of CD274 (A), ISG15 (B), RSAD2 (C), CXCL10 (D) and IRF7 (E) during treatment. Solid line – patients treated with RBV monotherapy on weeks -4 to 0. Dotted line – controls with no pre-treatment.

Supplementary Figure 7 – Association between serum IP-10 level decline over 4 weeks of RBV treatment and the decline in HCV-RNA (A) or ALT (B) during the same time in patients with genotype 1 treated with RBV. The association between serum

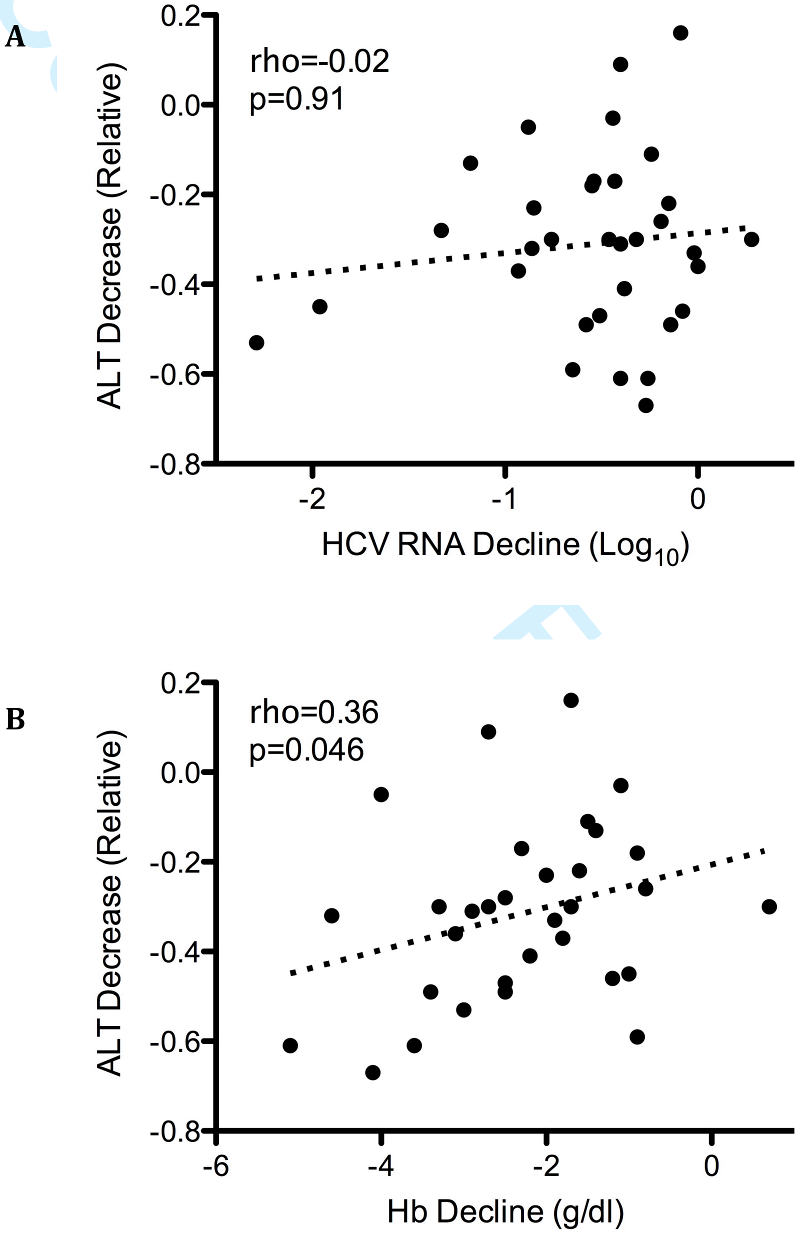
IP-10 levels and hepatic CXCL10 mRNA expression (nCounter assay) at time 0 (C) for groups A and C or at 6 hours (D) for groups B and D.

Supplementary Figure 8 – Decline in HCV-RNA during 4 weeks of ribavirin pre-treatment by IL28B genotype.

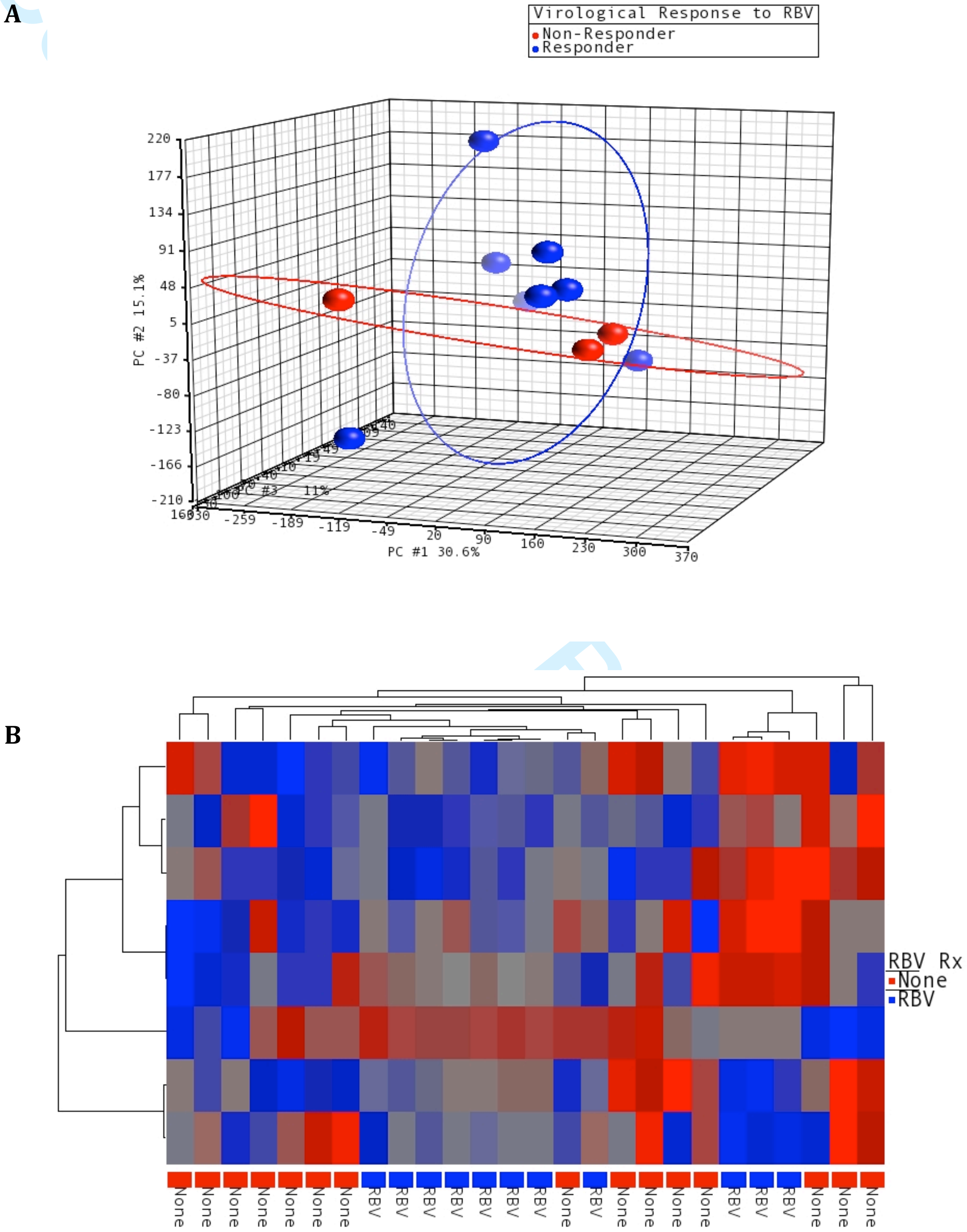
Supplementary Figure 1



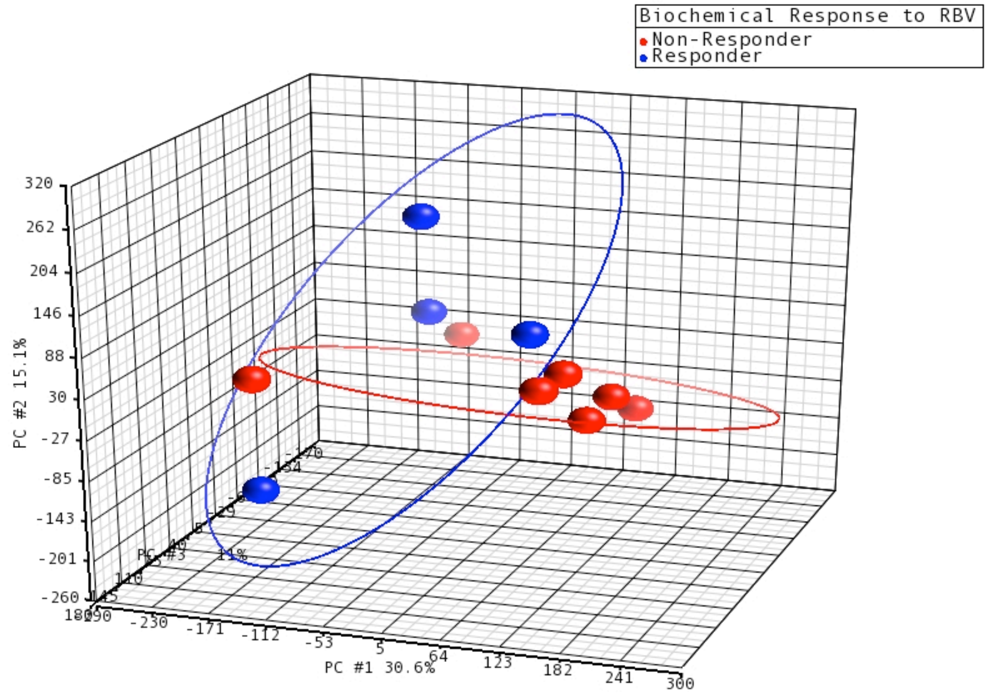
Supplementary Figure 2



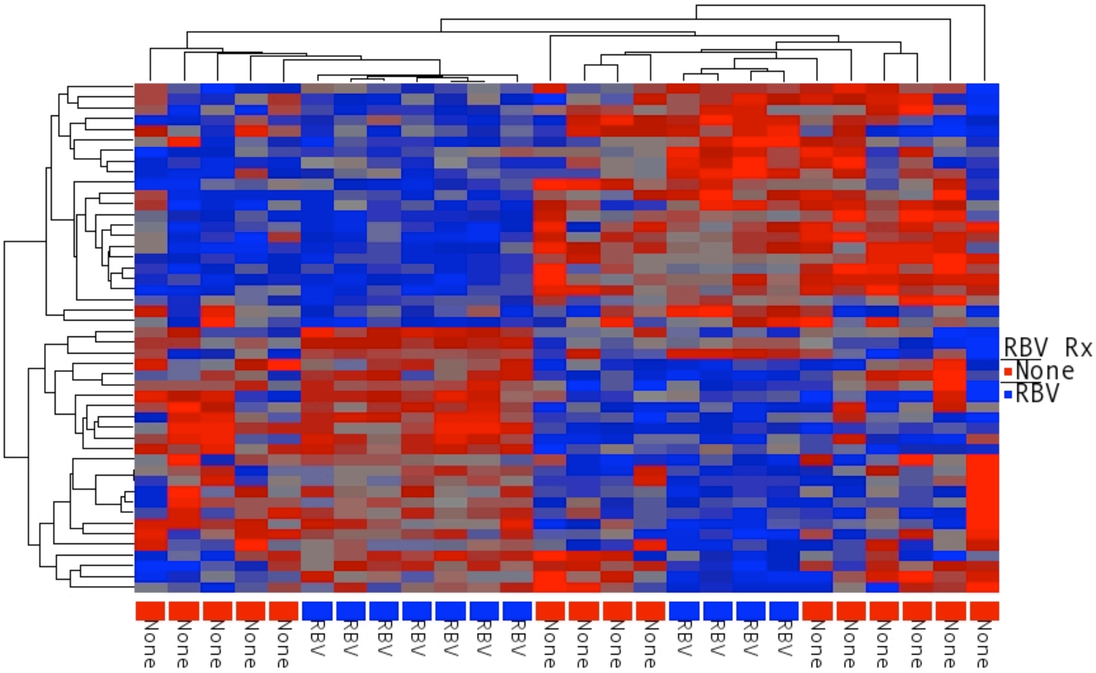
Supplementary Figure 3



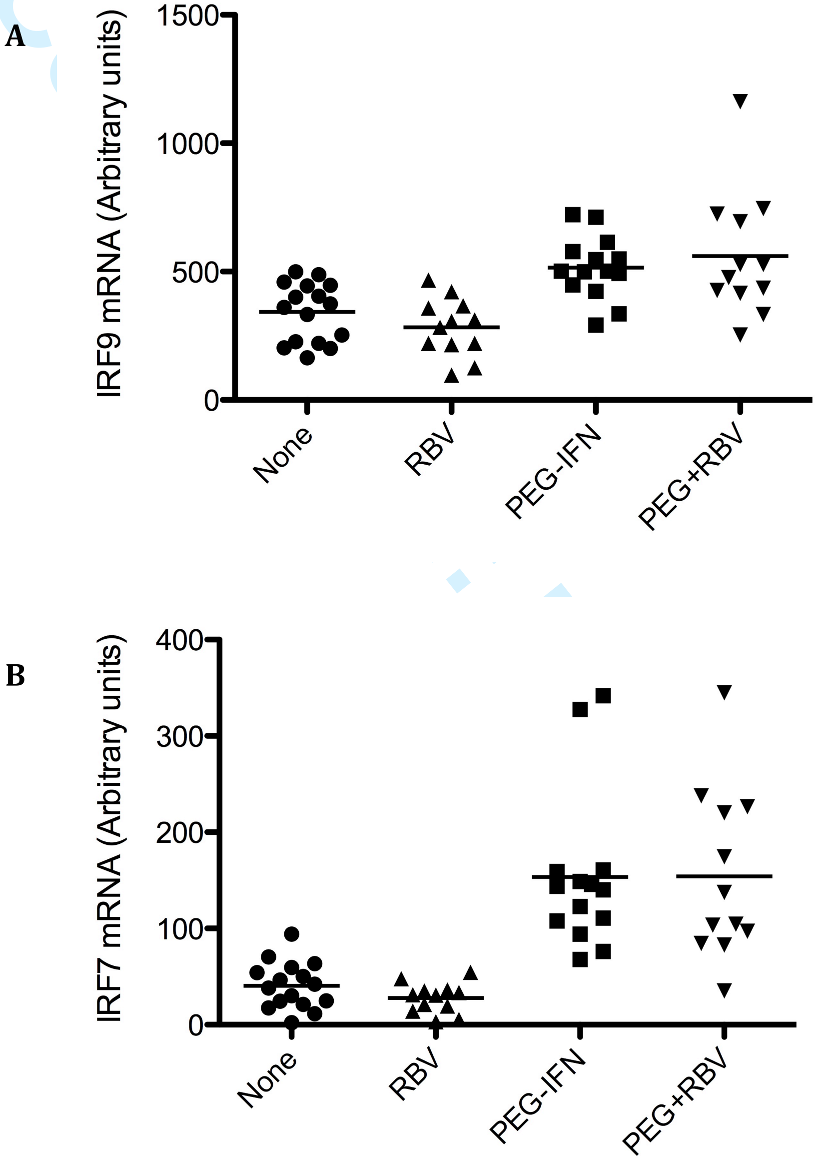
C


Biochemical Response to RBV
Non-Responder
Responder
PC #2 15.1%
320
262
204
146
88
30
-27
-85
-143
-201
-260
PC #1 30.6%
-290
-230
-171
-112
-53
5
64
123
182
241
300
PC #3 11%

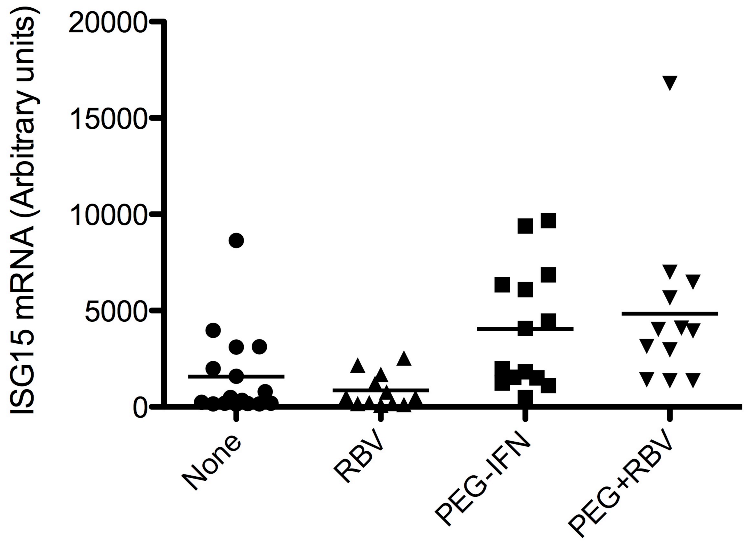
D


RBV Rx
None
RBV
None
None
None
None
None
RBV
RBV
RBV
RBV
RBV
RBV
RBV
None
None
None
None
RBV
RBV
RBV
RBV
None
None
None
None
None
None

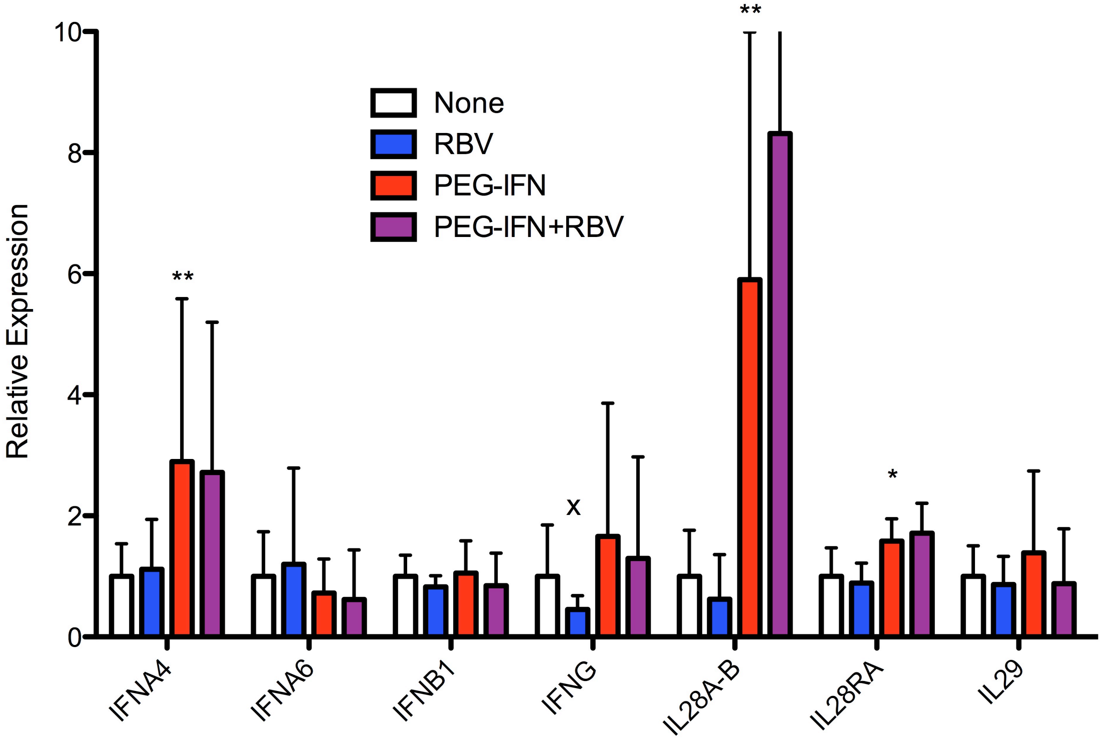
Supplementary Figure 4



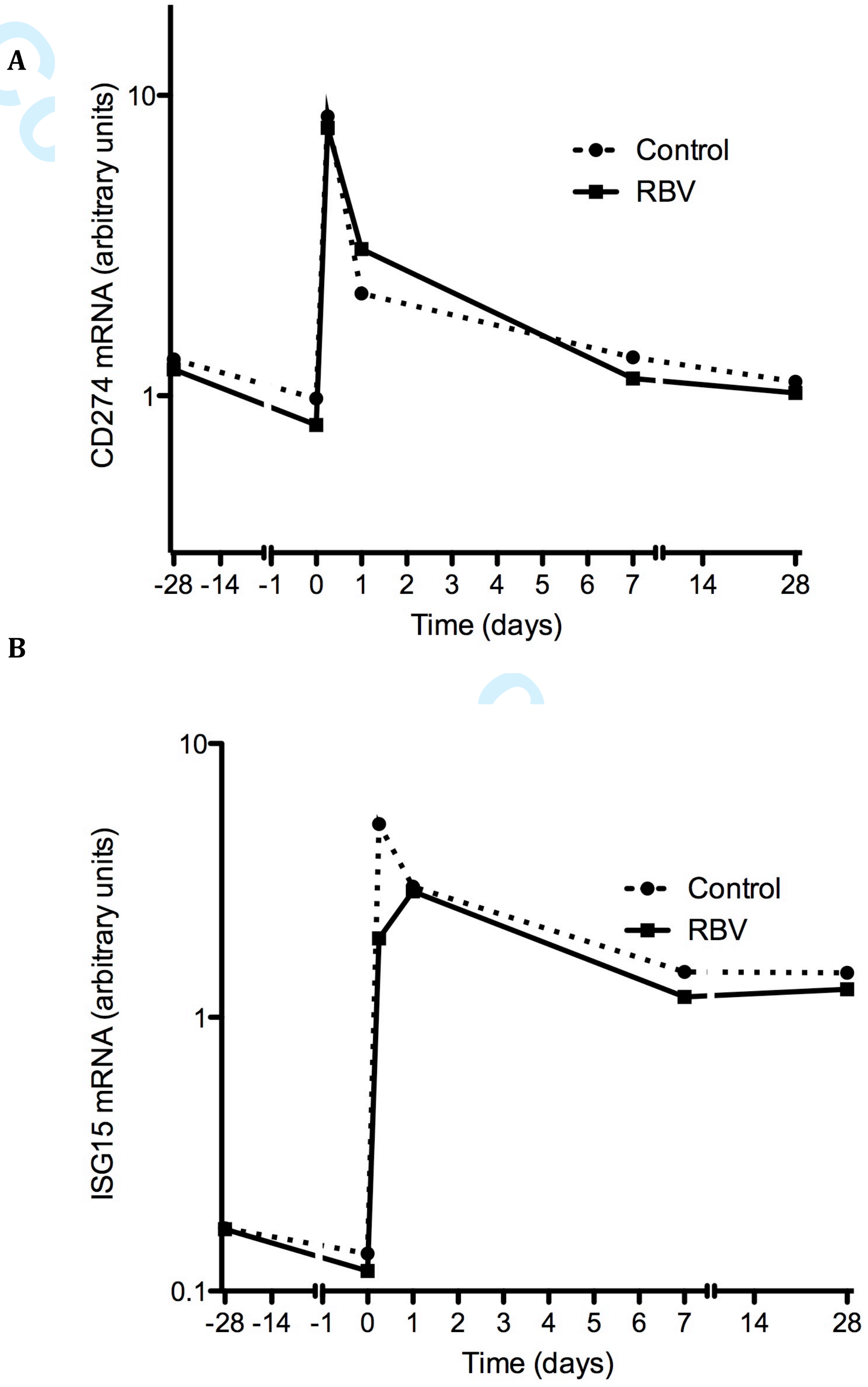
C


ISG15 mRNA (Arbitrary units)
20000
15000
10000
5000
0
None
RBV
PEG-IFN
PEG+RBV

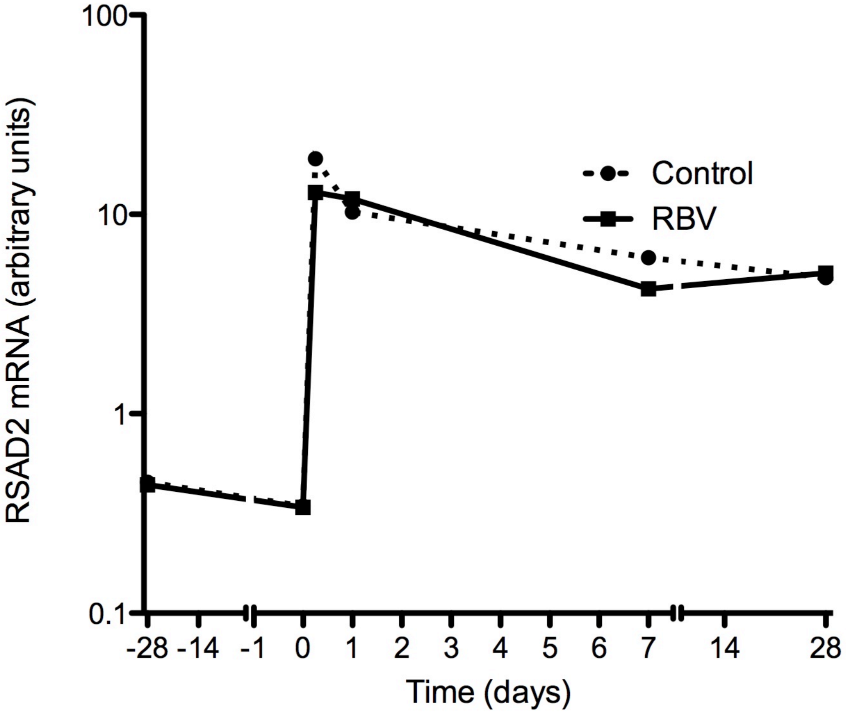
Supplementary Figure 5



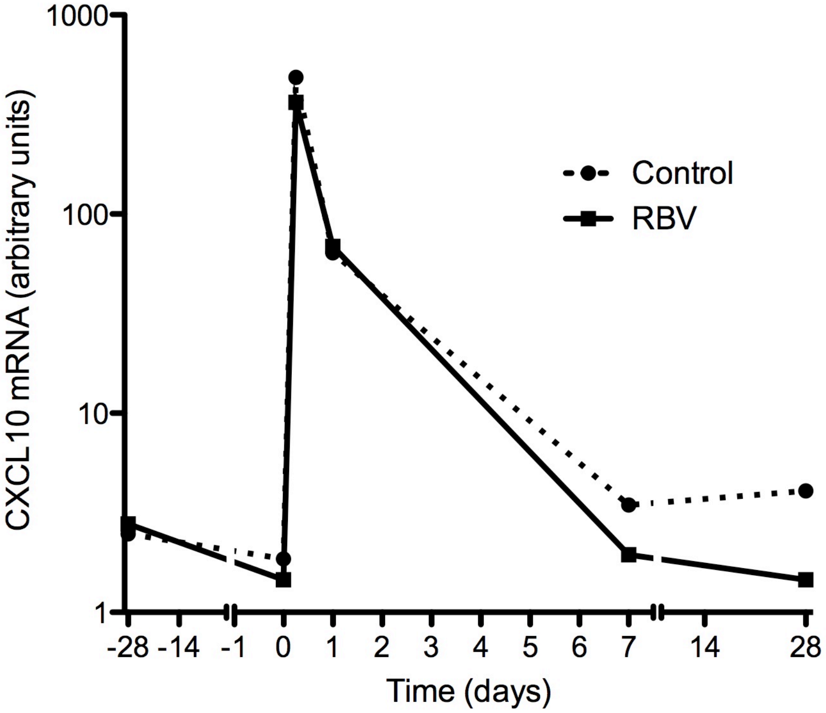
Supplementary Figure 6



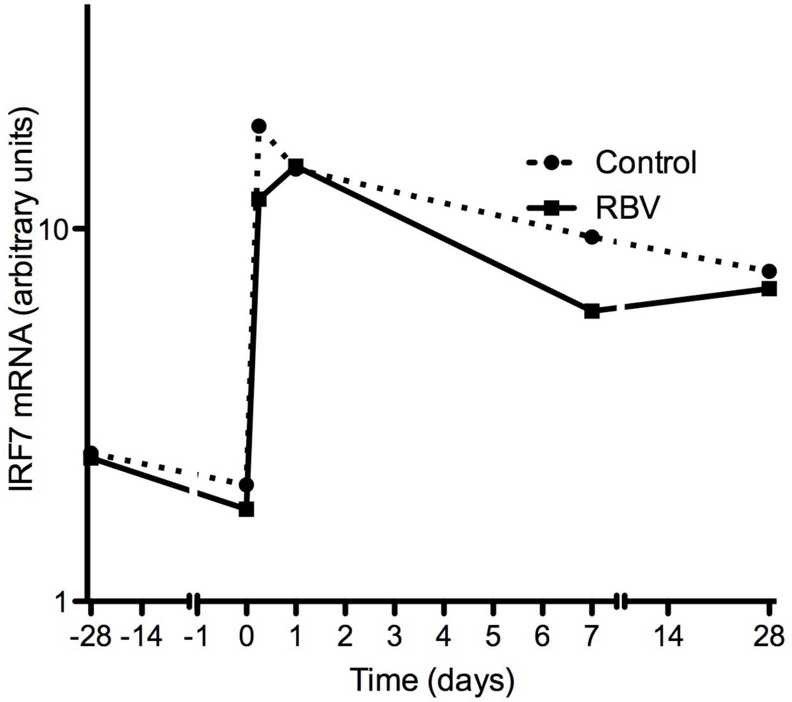
C


100
10
1
0.1
RSAD2 mRNA (arbitrary units)
Control
RBV
-28
-14
-1
0
1
2
3
4
5
6
7
14
28
Time (days)

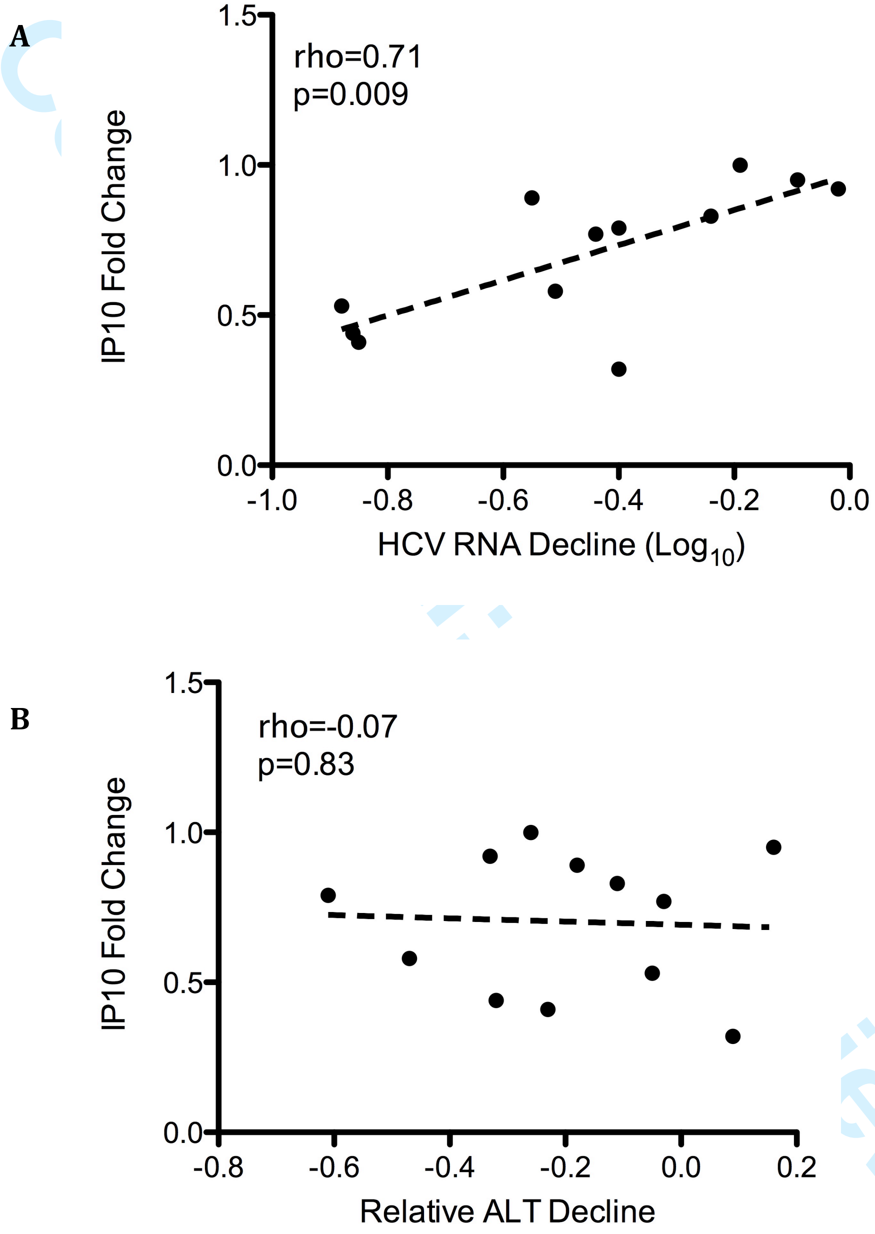
D


1000
100
10
1
CXCL10 mRNA (arbitrary units)
Control
RBV
-28
-14
-1
0
1
2
3
4
5
6
7
14
28
Time (days)

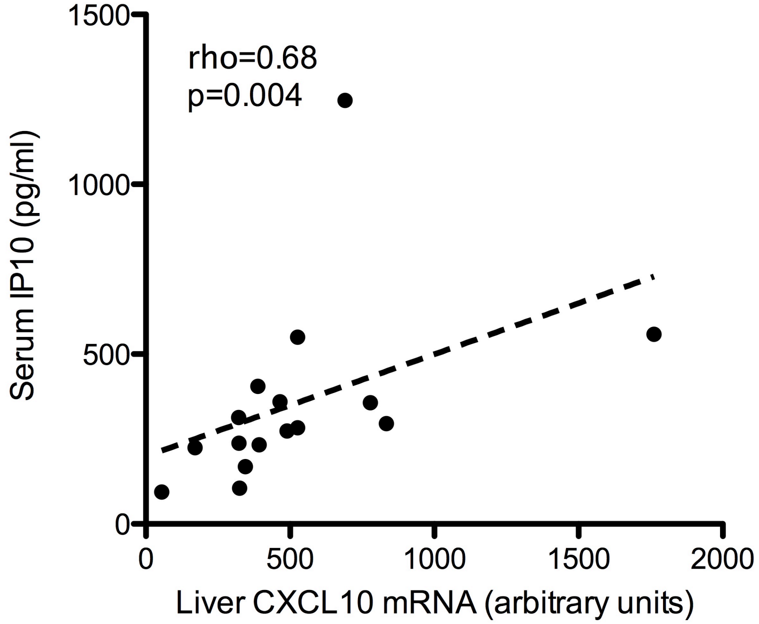
E


IRF7 mRNA (arbitrary units)
10
1
Control
RBV
-28
-14
-1
0
1
2
3
4
5
6
7
14
28
Time (days)

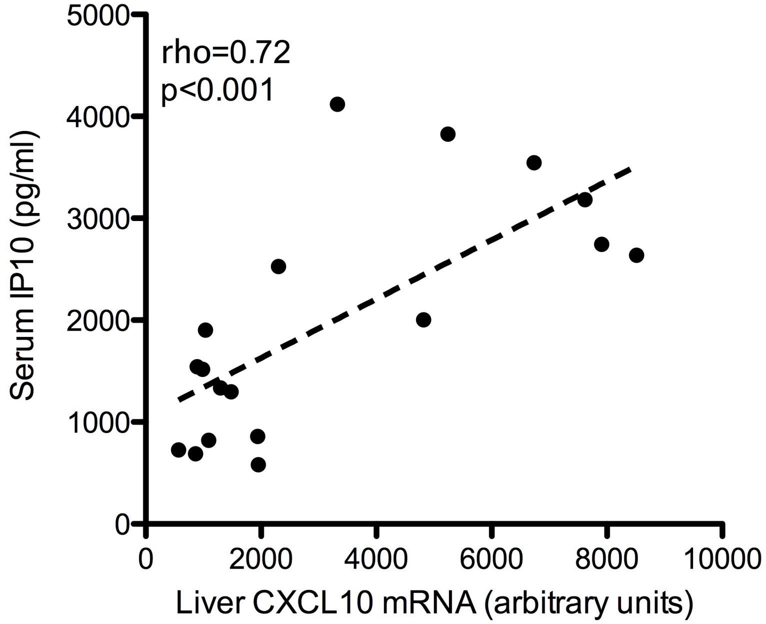
Supplementary Figure 7



C


rho=0.68
p=0.004
Serum IP10 (pg/ml)
1500
1000
500
0
0
500
1000
1500
2000
Liver CXCL10 mRNA (arbitrary units)

D


rho=0.72
p<0.001
Serum IP10 (pg/ml)
5000
4000
3000
2000
1000
0
0
2000
4000
6000
8000
10000
Liver CXCL10 mRNA (arbitrary units)

Supplementary Figure 8