

## Supplementary Figures

**Supplementary Figure S1. Immunohistochemical analysis of the inflammatory response in IHCA.** This IHCA overexpressed SAA (a) and CRP (b) with a sharp demarcation from the non-tumoural liver (NTL). Only hepatocytes of the IHCA expressed SAA or CRP; inflammatory infiltrates are negative for these acute phase inflammation proteins (asterisk). Inflammatory infiltrates are made predominantly of lymphocytes (CD45<sup>+</sup>), localized around vascular axis inside the tumour (c); T lymphocytes (CD3<sup>+</sup>) with CD4/CD8 (d-f) ratio around 2/1 are more numerous than B lymphocytes (CD20<sup>+</sup>) (g), intermingled with CD68<sup>+</sup> histiocytes (h).

**Supplementary Figure S2. Example of somatic DNA alterations identified in exon 6 of the *IL6ST* gene.** Boundaries of the deletions are indicated by an arrow; mutated sequences are represented below the *IL6ST* wild-type sequence. **a**, Forward sequence of one representative case of mutated IHCA (T) and its matching non-tumour DNA (N) showing the somatic origin of the most frequent deletion identified; the nucleotide sequence deleted in tumour 382 is boxed. Amino acids (AA) and nucleotides (NT) are numbered according to *IL6ST* cDNA ORF. **b**, cDNA sequence analysis of two cases of mutated IHCA (T), showing expression of both the wild type and the mutant allele. **c**, Individual 770 is heterozygous for the polymorphism rs3729960 (697 G>C leading to G148R) located in exon 5 (arrow). The same ratio of allele is observed in normal and tumour sample both at the DNA and cDNA level. As this polymorphism is amplified in the same cDNA fragment than the mutated exon 6, these results show that the wild-type and the mutated allele are expressed at the same level in IHCA.

**Supplementary Figure S3. Comparison of expression profiles between gp130 mutated inflammatory HCA and gp130 non-mutated IHCA.** Comparison was carried out for the 24 genes validated by quantitative RT-PCR that were significantly differentially expressed between IHCA and non-tumour livers. Seven gp130 mutated IHCA (in black) were compared to 7 gp130 non-mutated IHCA (in grey). Results are expressed as mean  $\pm$  SD; \* difference between groups at  $P < 0.05$  (two-tailed Mann-Whitney test).

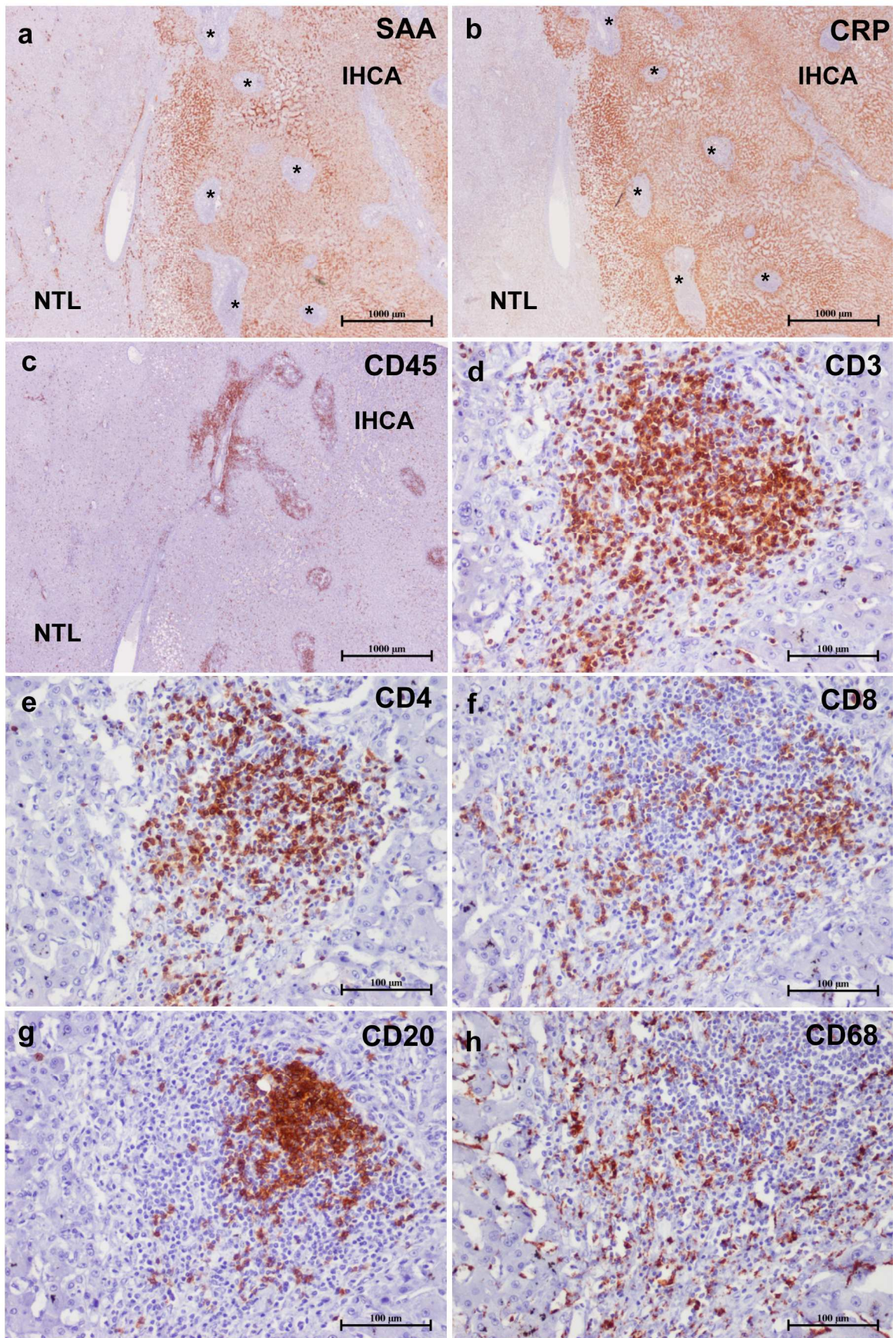
**Supplementary Figure S4. Analysis of gp130 and p-STAT3 expression in inflammatory HCA.** **a**, *IL6ST* mRNA level in 6 non-tumour livers (NTL) was compared with that of 7 gp130-mutated IHCA (M) and 7 gp130-non-mutated IHCA (NM), using qRT-PCR. Results are expressed as mean-fold difference  $\pm$  SD, relative to NTL; ns: non significant (two-tailed Mann-Whitney test). **b**, Western-blotting analysis of gp130 protein level in 3 non-tumour livers (NTL), 2 gp130-mutated IHCA and 7 gp130-non-mutated IHCA. Red ponceau staining was used as loading control. **c**, **d**, Immunohistochemical analysis of gp130 showing

overexpression of the protein in both gp130-mutated (c) and gp130-non-mutated (d) IHCA compared to their adjacent non-tumour liver parenchyma (NTL). e, f, g, Immunohistochemistry of phospho-STAT3 (tyr705) in gp130-mutated (e) and non-mutated (f) IHCA showing an intense nuclear staining in tumour cells while p-STAT3 is undetectable in non-tumour liver (NTL) (g).

**Supplementary Figure S5. mRNA expression of *IL11* and *IL11RA* in inflammatory HCA and transfected Hep3B cells.** a, *IL11* and *IL11RA* mRNA levels were assessed using qRT-PCR in 6 non-tumour livers (NTL), 7 gp130-mutated IHCA (M) and 7 gp130-non-mutated IHCA (NM). Results are expressed as mean-fold difference  $\pm$  SD, relative to NTL (mean NTL=1) \*, \*\*, difference between groups at  $P < 0.05$  and  $0.01$ , respectively (two-tailed Mann-Whitney test). b, qRT-PCR analysis of *IL11* mRNA expression in Hep3B cells transfected either with Wt gp130 or with four IHCA mutants of gp130 ( $\Delta$ ) (Y186\_Y190del (Y); K173\_D177del (K); S187\_Y190del (S) and V184\_Y186del, S187A (V)), as described in Fig3. Experiments were performed in triplicate and expressed as mean  $\pm$  SD in comparison to empty plasmid-transfected and untreated cells (mean=1). ns: non significant (two-tailed t-test).

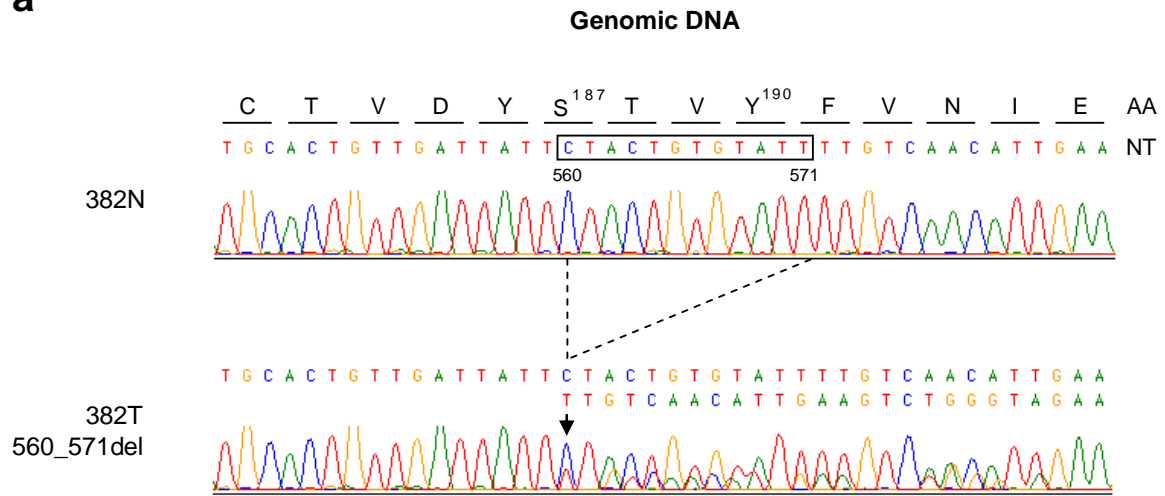
**Supplementary Figure S6. Western blotting analysis of ERK1/2 activation in inflammatory HCA and Hep3B cells.** a, Expression of the phosphorylated forms of ERK1 and ERK2 was compared between 10 IHCA (including 4 cases mutated for gp130) and 6 non-tumour livers (NTL). Red ponceau staining was used as loading control. b, Expression of phospho-ERK1/2 was compared between Hep3B cells transfected with the wild-type (Wt) or the mutant ( $\Delta$ S) gp130 (S187\_Y190del). As a control cells were transfected with empty plasmid and untreated or stimulated with 100 ng/ $\mu$ l of IL6.

Supplementary Figure S1

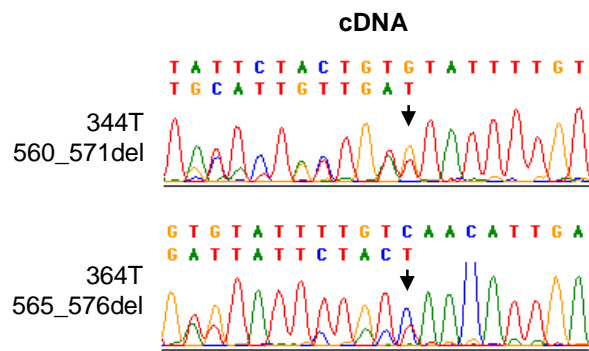


## Supplementary Figure S2

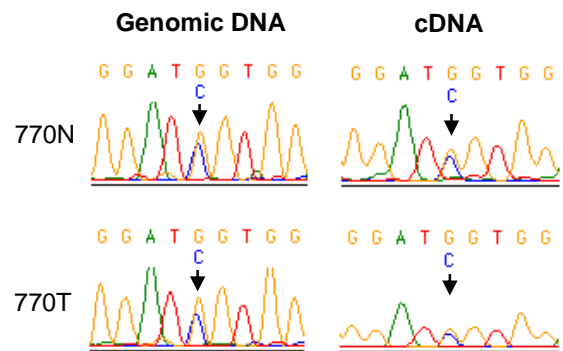
**a**



**b**

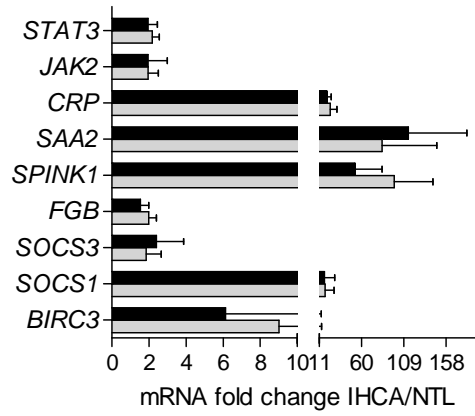


**c**

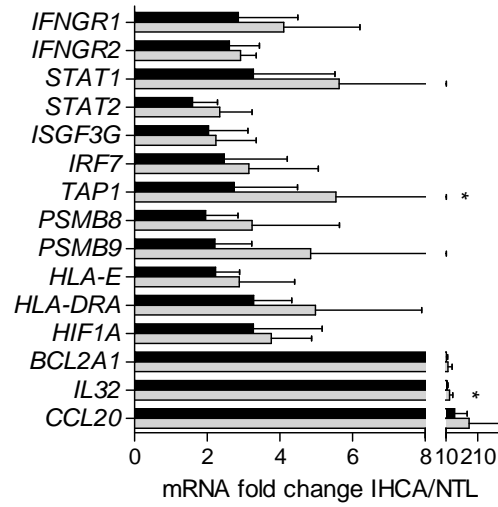


## Supplementary Figure S3

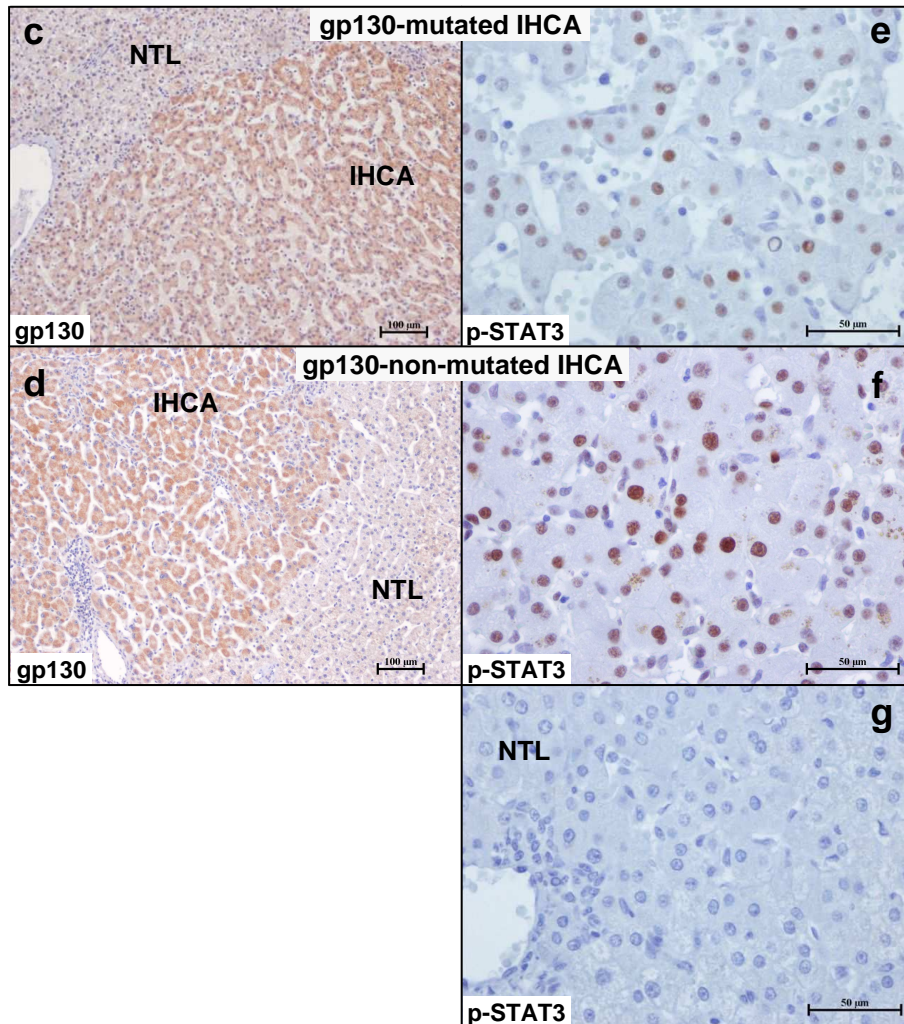
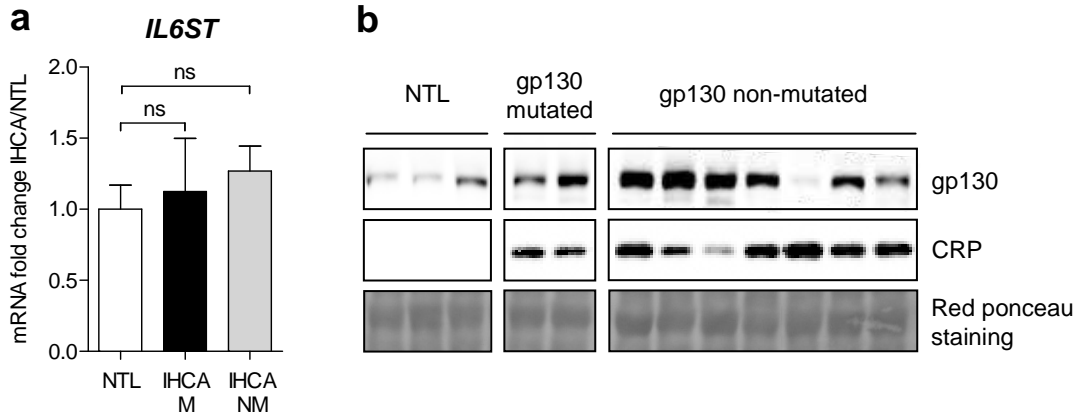
### Interleukin-6 pathway



### Interferon pathway

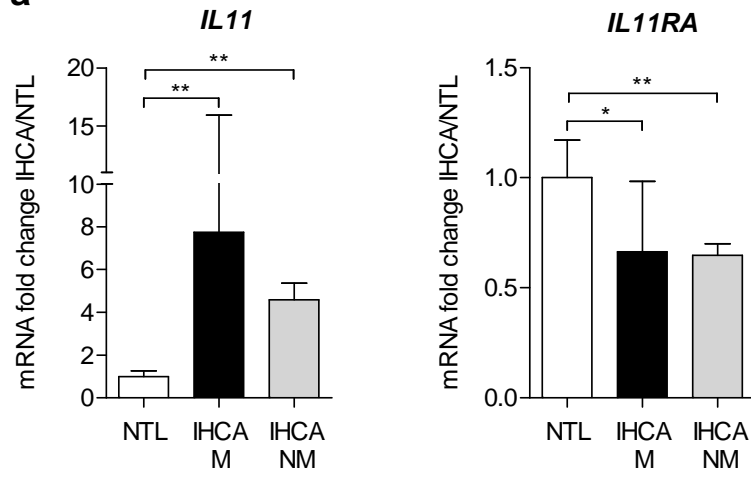


# Supplementary Figure S4

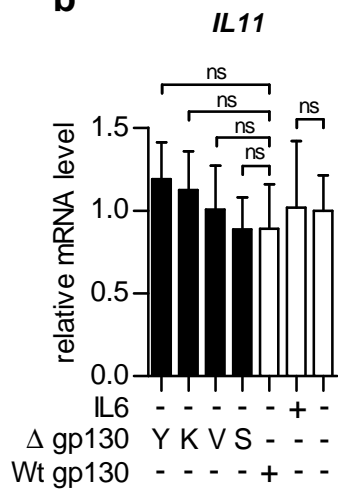


## Supplementary Figure S5

**a**

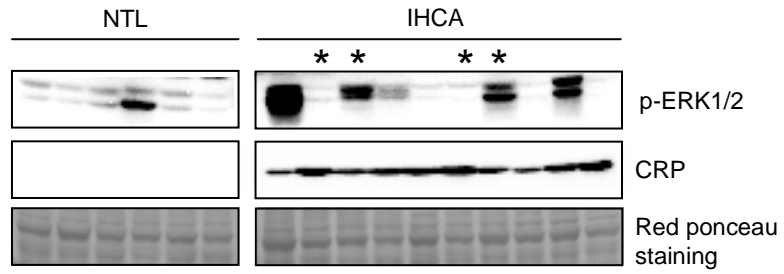


**b**



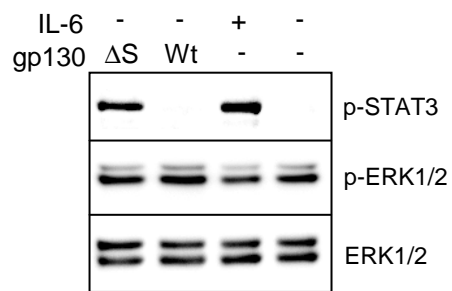
## Supplementary Figure S6

**a**



\* IHCA gp130-mutated

**b**





## Supplementary Table S1. Affymetrix microarray analysis

Expression profiles of four inflammatory HCA (IHCA) were compared to those of four non-tumour livers (NTL). Data are expressed as the mean-fold difference in gene expression in IHCA relative to NTL.

Unigene ID	Ensembl Gene ID	Gene Symbol	Fold change ratio IHCA/NTL	P-value
Hs.75498	ENSG00000115009	CCL20	219.8	3.7E-04
Hs.494337	ENSG00000135052	GOLPH2	129.0	3.1E-05
Hs.382202	ENSG00000133048	CHI3L1	103.3	5.2E-04
Hs.49407	ENSG00000115386	REG1A	100.4	2.7E-04
Hs.306834	ENSG00000119782	FKBP1B	84.5	1.4E-04
Hs.368632	ENSG00000170214	ADRA1B	57.9	5.0E-06
Hs.332053	ENSG00000173432	SAA1	33.1	1.2E-04
Hs.148909	ENSG00000134121	CHL1	30.2	3.8E-04
Hs.44532	ENSG00000197402	UBD	30.2	4.0E-07
Hs.131269	ENSG00000118849	RARRES1	29.9	1.0E-03
Hs.183114	ENSG00000088756	ARHGAP28	28.3	0.0E+00
Hs.13349	ENSG00000163531	NFASC	21.0	5.7E-14
Hs.21422	ENSG00000091129	NRCAM	20.2	1.0E-07
Hs.407882	ENSG00000143450	OAZ3	20.0	1.7E-04
Hs.407856	ENSG00000164266	SPINK1	17.4	4.8E-04
Hs.943	ENSG00000008517	NK4	16.8	1.0E-04
Hs.431099	ENSG00000162366	MAP17	16.4	2.5E-06
Hs.466804	ENSG00000188257	PLA2G2A	15.2	1.0E-06
Hs.238756	ENSG00000177791	MYOZ1	12.6	0.0E+00
Hs.208600	ENSG00000160183	TMPRSS3	11.7	4.1E-04
Hs.531682	ENSG00000108602	ALDH3A1	11.0	6.7E-07
Hs.546335	ENSG00000138028	CGREF1	10.2	8.6E-06
Hs.268785	ENSG00000068366	ACSL4	10.2	7.5E-05
Hs.50640	ENSG00000185338	SOCS1	9.8	2.8E-04
Hs.14415	ENSG00000171311	EXOSC1	9.8	8.2E-09
Hs.127799	ENSG00000023445	BIRC3	9.1	2.7E-05
Hs.440848	ENSG00000110799	VWF	8.9	3.4E-04
Hs.385861	ENSG00000122550	KLHL7	8.2	1.4E-08
Hs.546468	ENSG00000179038	LOC94431	8.1	0.0E+00
Hs.513316	ENSG00000103199	ZNF500	8.0	4.0E-07
Hs.2704	ENSG00000176153	GPX2	7.9	7.5E-06
Hs.435735	ENSG00000138074	SLC5A6	7.6	5.0E-07
Hs.76452	ENSG00000132693	CRP	7.3	5.6E-04
Hs.56319	ENSG00000101441	CST4	7.2	3.6E-04
Hs.522373	ENSG00000148180	GSN	7.2	9.3E-06
Hs.350321	ENSG00000165731	RET	7.1	7.9E-06
Hs.2303	ENSG00000130427	EPO	6.8	2.1E-07
Hs.404568	ENSG00000107521	HPS1	6.7	4.7E-08
Hs.95162		KCNQ1OT1	6.7	1.2E-07
Hs.486031	ENSG00000112249	ASCC3	6.2	2.2E-05
Hs.258326	ENSG00000103528	LOC51760	6.2	4.4E-04
Hs.190043	ENSG00000130150	MOSPD2	6.1	2.0E-06
Hs.493275	ENSG00000137397	TRIM31	6.0	7.2E-07
Hs.502759	ENSG00000149541	B3GAT3	6.0	1.5E-07
Hs.227817	ENSG00000140379	BCL2A1	5.9	4.3E-04
Hs.295626	ENSG00000131355	EMR3	5.7	0.0E+00
Hs.479766	ENSG00000134851	TPARL	5.6	1.6E-04
Hs.151220	ENSG00000129116	KIAA0992	5.5	1.6E-04
Hs.250281	ENSG00000158296	SLC13A3	5.2	1.9E-06
Hs.441783	ENSG00000185567	C14orf78	5.1	1.8E-05
Hs.293130	ENSG00000112303	VNN2	4.9	1.7E-05
Hs.130989	ENSG00000111319	SCNN1A	4.8	9.5E-04
Hs.437083	ENSG00000114388	TUSC4	4.7	0.0E+00
Hs.443160	ENSG00000176920	FUT2	4.6	3.2E-04
Hs.269128	ENSG00000170145	PPP2R1B	4.6	1.9E-04
Hs.352018	ENSG00000168394	TAP1	4.6	7.3E-04
Hs.36566	ENSG00000106683	LIMK1	4.5	1.4E-05
Hs.470457	ENSG00000082438	COBL1	4.4	3.3E-04
Hs.502328	ENSG00000026508	CD44	4.4	8.9E-04
Hs.129708	ENSG00000125735	TNFSF14	4.3	5.9E-04
Hs.517033	ENSG00000198959	TGM2	4.3	2.1E-04
Hs.8261	ENSG00000171621	SSB1	4.2	9.6E-04
Hs.533446	ENSG00000164929	BAALC	4.2	4.9E-04
Hs.155048	ENSG00000187244	LU	4.2	2.0E-04
Hs.380250	ENSG00000163565	IFI16	4.2	3.2E-04
Hs.271955	ENSG00000145779	TNFAIP8	4.1	5.4E-04
Hs.515126	ENSG00000090339	ICAM1	4.0	2.0E-04
Hs.221889	ENSG00000060138	CSDA	4.0	2.1E-05
Hs.190495	ENSG00000136235	GPNMB	4.0	0.0E+00
Hs.501280	ENSG00000166033	PRSS11	3.9	3.6E-06
Hs.268887	ENSG00000164543	STK17A	3.9	8.0E-04
Hs.521973	ENSG00000101940	WDR13	3.9	5.2E-05
Hs.386567	ENSG00000162645	GBP2	3.8	1.2E-04
Hs.351327	ENSG00000140365	COMMD4	3.8	5.3E-15
Hs.487046	ENSG00000112096	SOD2	3.8	3.0E-04
Hs.370725	ENSG00000141447	OSBPL1A	3.7	5.8E-10
Hs.154078	ENSG00000129988	LBP	3.7	1.5E-04
Hs.449009	ENSG00000179403	WARP	3.6	6.0E-06
Hs.464469	ENSG00000101605	MYOM1	3.6	1.6E-04
Hs.443687	ENSG00000115641	FHL2	3.6	9.3E-04
Hs.501778	ENSG00000132274	TRIM22	3.6	3.8E-04
Hs.144496	ENSG00000112699	GMDS	3.5	1.1E-11
Hs.463045	ENSG00000108773	GCN5L2	3.5	3.2E-05
Hs.437599	ENSG00000110756	HPS5	3.4	6.4E-04
Hs.18858	ENSG00000105499	PLA2G4C	3.4	3.4E-07
Hs.491805	ENSG00000198846	TOX	3.4	9.2E-04
Hs.4205	ENSG00000074276	PC-LKC	3.3	7.3E-05
Hs.79411	ENSG00000117748	RPA2	3.3	5.0E-06
Hs.125867	ENSG00000196405	EVL	3.3	1.1E-15

Hs.187284	ENSG00000116183	PAPPA2	3.3	1.4E-07
Hs.462684	ENSG00000173012	DKFZp667M2411	3.2	3.0E-08
Hs.208544	ENSG00000135750	KCNK1	3.2	5.9E-04
Hs.2161	ENSG00000197405	C5R1	3.1	9.0E-04
Hs.94865	ENSG00000197905	TEAD4	3.1	1.7E-04
Hs.408061	ENSG00000166900	FABP5	3.1	8.0E-04
Hs.248116	ENSG00000173578	XCR1	3.0	1.4E-11
Hs.12211	ENSG00000181830	SLC35C1	3.0	9.2E-05
Hs.61635	ENSG00000164647	STEAP	3.0	1.4E-04
Hs.519884	ENSG00000111846	GCNT2	3.0	1.1E-10
Hs.77961	ENSG00000198638	HLA-B	3.0	6.3E-04
Hs.474737	ENSG00000128284	APOL3	3.0	1.5E-04
Hs.138378	ENSG00000196954	CASP4	2.9	2.9E-05
Hs.517070	ENSG00000124107	SLPI	2.9	3.5E-05
Hs.194754	ENSG00000117597	MGC29875	2.9	4.9E-04
Hs.27695	ENSG00000101871	MID1	2.9	4.3E-04
Hs.387856	ENSG00000100154	KIAA1043	2.9	9.8E-05
Hs.129944	ENSG00000164283	ESM1	2.9	9.9E-04
Hs.172684	ENSG00000168899	VAMP5	2.9	8.8E-04
Hs.513141	ENSG00000182054	IDH2	2.8	5.8E-04
Hs.347270	ENSG00000168384	HLA-DPA1	2.8	6.3E-08
Hs.512152	ENSG00000187888	HLA-G	2.8	8.9E-04
Hs.463059	ENSG00000168610	STAT3	2.8	2.8E-04
Hs.115838	ENSG00000103534	TMC5	2.8	4.0E-07
Hs.381167	ENSG0000021355	SERPINB1	2.8	7.4E-04
Hs.440168	ENSG00000172348	DSCR1L1	2.8	7.9E-08
Hs.529493	ENSG00000204657	OR2H2	2.7	6.8E-04
Hs.519972	ENSG00000137403	HLA-F	2.7	5.0E-04
Hs.304475	ENSG0000043462	LCP2	2.7	2.4E-07
Hs.50649	ENSG00000115129	TP53I3	2.7	1.8E-04
Hs.2131	ENSG00000166148	AVPR1A	2.7	2.0E-04
Hs.371021	ENSG00000162511	LAPTM5	2.7	4.5E-11
Hs.514038	ENSG00000132589	FLOT2	2.7	1.9E-04
Hs.74120	ENSG00000148671	C10orf116	2.7	5.8E-07
Hs.471783	ENSG00000132329	RAMP1	2.7	3.9E-06
Hs.459049	ENSG00000136371	MTHFS	2.7	7.3E-05
Hs.107125	ENSG00000130300	PLVAP	2.7	4.7E-04
Hs.513488	ENSG0000013364	MVP	2.6	1.1E-04
Hs.12956	ENSG00000108392	TAX1BP3	2.6	7.6E-05
Hs.352548	ENSG00000126246	FLJ22573	2.6	1.4E-04
Hs.458425	ENSG00000182782	GPR109B	2.6	5.4E-04
Hs.467101	ENSG00000130529	TRPM4	2.6	2.8E-04
Hs.534125	ENSG00000198479	HLA-C	2.6	9.4E-04
Hs.351279	ENSG00000124546	HLA-DMA	2.6	8.2E-04
Hs.482017	ENSG00000197147	TA-LRRP	2.6	6.4E-06
Hs.534392	ENSG00000100196	KDELR3	2.6	1.4E-04
Hs.67928	ENSG00000163435	ELF3	2.6	5.0E-04
Hs.520414	ENSG0000027697	IFNGR1	2.6	3.0E-04
Hs.530988	ENSG00000132950	ZNF237	2.6	1.7E-04
Hs.302963	ENSG00000159674	SPON2	2.6	3.4E-04
Hs.518055	ENSG00000144749	LRIG1	2.6	3.1E-04
Hs.123352	ENSG00000175354	PTPN2	2.6	5.8E-04
Hs.131704	ENSG00000099250	NRP1	2.5	5.5E-11
Hs.459538	ENSG00000184254	ALDH1A3	2.5	8.4E-06
Hs.474596	ENSG00000182541	LIMK2	2.5	4.2E-03
Hs.489615	ENSG00000105835	PBEF1	2.5	9.8E-04
Hs.278430	ENSG00000168482	CYP21A2	2.5	6.8E-06
Hs.409934	ENSG00000206237	HLA-DQB1	2.5	2.3E-06
Hs.520714	ENSG00000086300	SNX10	2.5	3.5E-06
Hs.444301	ENSG00000161280	FLJ10986	2.5	9.9E-04
Hs.509554	ENSG00000100644	HIF1A	2.5	6.8E-04
Hs.387255	ENSG00000140632	N-PAC	2.5	3.0E-04
Hs.511093	ENSG00000137804	NUSAP1	2.5	4.8E-04
Hs.519033	ENSG00000137462	TLR2	2.5	4.8E-04
Hs.368623	ENSG00000152229	PSTPIP2	2.5	2.7E-04
Hs.80658	ENSG00000175567	UCP2	2.5	6.0E-04
Hs.167741	ENSG00000111801	BTN3A3	2.4	3.7E-04
Hs.438419	ENSG00000198246	SLC29A3	2.4	9.4E-08
Hs.246381	ENSG00000129226	CD68	2.4	2.6E-10
Hs.491143	ENSG00000104760	FGL1	2.4	3.5E-04
Hs.301865	ENSG00000080166	DCT	2.4	7.2E-12
Hs.388297	ENSG00000156831	FLJ32440	2.4	1.9E-06
Hs.515536	ENSG00000126458	RRAS	2.4	1.9E-09
Hs.181301	ENSG00000163131	CTSS	2.4	8.1E-07
Hs.323878	ENSG00000115902	SLC1A4	2.4	8.9E-04
Hs.17466	ENSG00000133321	RARRES3	2.4	1.4E-07
Hs.512633	ENSG00000186652	PRG2	2.4	8.0E-04
Hs.525392	ENSG00000054654	SYNE2	2.4	7.8E-04
Hs.7972	ENSG00000018189	RIPX	2.4	5.9E-04
Hs.369201	ENSG00000183087	GAS6	2.4	1.2E-03
Hs.444451	ENSG00000091436	ZAK	2.3	2.8E-04
Hs.163113	ENSG00000178927	MGC4368	2.3	2.7E-04
Hs.102471	ENSG00000112419	PHACTR2	2.3	4.9E-07
Hs.28988	ENSG00000118990	GLRX	2.3	1.4E-04
Hs.400740	ENSG00000119383	PPP2R4	2.3	4.9E-04
Hs.520049	ENSG00000196126	HLA-DRB1	2.3	2.8E-06
Hs.530077	ENSG00000105854	PON2	2.3	1.0E-04
Hs.201641	ENSG00000176788	BASP1	2.3	1.7E-07
Hs.509765	ENSG00000072110	ACTN1	2.3	3.2E-04
Hs.154654	ENSG00000138061	CYP11B1	2.3	7.2E-04
Hs.301921	ENSG00000163823	CCR1	2.3	5.0E-06
Hs.434253	ENSG00000148120	C9orf3	2.3	5.6E-04
Hs.522684	ENSG00000147130	ZNF261	2.3	1.6E-08
Hs.128686	ENSG00000070081	NUCB2	2.3	9.3E-04
Hs.99528	ENSG00000168461	RAB31	2.3	2.3E-07
Hs.495219	ENSG00000148334	PTGES2	2.3	1.3E-09
Hs.309602	ENSG00000137384	TRIM15	2.3	1.0E-03
Hs.522605	ENSG00000165175	MID1IP1	2.3	1.2E-06
Hs.446079	ENSG00000108582	CPD	2.3	3.8E-04
Hs.1706	ENSG00000092098	ISGF3G	2.2	7.4E-07

Hs.488143	ENSG00000106605	BLVRA	2.2	2.7E-04
Hs.482411	ENSG00000198605	SMA4	2.2	2.6E-03
Hs.386793	ENSG00000157566	GPX3	2.2	1.8E-04
Hs.334587	ENSG00000157110	RBPMS	2.2	6.3E-08
Hs.433529	ENSG00000142534	RPS11	2.2	1.2E-04
Hs.89890	ENSG00000173599	PC	2.2	3.2E-04
Hs.173288	ENSG00000198730	SH2BP1	2.2	1.3E-05
Hs.433300	ENSG00000158869	FCER1G	2.2	2.9E-06
Hs.355264	ENSG00000008283	CYB561	2.2	4.5E-04
Hs.280987	ENSG00000113318	MSH3	2.2	7.1E-08
Hs.446574	ENSG00000034510	TMSB10	2.2	1.4E-09
Hs.458414	ENSG00000185885	IFITM1	2.2	1.1E-09
Hs.440932	ENSG00000184640	40057	2.2	1.3E-07
Hs.143703	ENSG00000103966	EHD4	2.2	5.1E-06
Hs.8904	ENSG00000155659	VSIG4	2.2	4.0E-06
Hs.489284	ENSG00000130429	ARPC1B	2.2	9.1E-04
Hs.175473	ENSG00000106992	AK1	2.2	1.3E-04
Hs.438695	ENSG00000134285	FKBP11	2.2	2.1E-07
Hs.520048	ENSG00000168423	HLA-DRA	2.2	1.4E-07
Hs.107393	ENSG00000080822	C3orf4	2.2	3.6E-04
Hs.300834	ENSG00000143641	GALNT2	2.2	3.8E-04
Hs.381081	ENSG00000112082	PSMB9	2.2	8.8E-04
Hs.508716	ENSG00000134871	COL4A2	2.2	4.8E-07
Hs.118110	ENSG00000130303	BST2	2.2	7.3E-04
Hs.180062	ENSG00000168396	PSMB8	2.2	7.2E-05
Hs.211600	ENSG00000118503	TNFALP3	2.2	6.2E-04
Hs.350899	ENSG00000162909	CAPN2	2.2	1.4E-06
Hs.513457	ENSG00000077238	IL4R	2.2	2.7E-05
Hs.73090	ENSG00000077150	NFKB2	2.2	1.0E-04
Hs.546248	ENSG00000117984	CTSD	2.1	3.2E-05
Hs.10649	ENSG00000130775	C1orf38	2.1	7.7E-06
Hs.466791	ENSG00000167601	AXL	2.1	1.0E-05
Hs.75431	ENSG00000162551	ALPL	2.1	2.4E-04
Hs.549038	ENSG00000197499	HLA-A	2.1	5.8E-04
Hs.367992	ENSG00000141401	IMPA2	2.1	9.3E-07
Hs.148178	ENSG00000076864	RAP1GA1	2.1	1.9E-04
Hs.508644	ENSG00000134884	FLJ10154	2.1	2.4E-04
Hs.511397	ENSG00000076706	MCAM	2.1	1.5E-05
Hs.81134	ENSG00000136689	IL1RN	2.1	1.8E-06
Hs.522632	ENSG00000102265	TIMP1	2.1	6.2E-07
Hs.11923	ENSG00000058799	DJ167A19.1	2.1	4.6E-04
Hs.29106	ENSG00000112679	DUSP22	2.1	4.6E-04
Hs.436873	ENSG00000138448	ITGAV	2.1	2.4E-08
Hs.76716	ENSG00000162267	ITIH3	2.1	8.6E-07
Hs.381008	ENSG00000137361	HLA-E	2.1	4.9E-06
Hs.511605	ENSG00000182718	ANXA2	2.1	4.7E-06
Hs.517543	ENSG00000100029	PES1	2.1	8.9E-04
Hs.484047	ENSG00000113645	KIBRA	2.0	4.5E-04
Hs.369397	ENSG00000120708	TGFB1	2.0	1.4E-04
Hs.186486	ENSG00000197442	MAP3K5	2.0	5.6E-08
Hs.376046	ENSG00000186470	BTN3A2	2.0	1.1E-04
Hs.467701	ENSG00000115758	ODC1	2.0	1.6E-06
Hs.50842	ENSG00000068079	IFI35	2.0	7.5E-08
Hs.13640	ENSG00000169855	ROBO1	2.0	5.3E-05
Hs.404289	ENSG00000136842	TMOD1	2.0	8.6E-04
Hs.133397	ENSG00000091409	ITGA6	2.0	1.7E-07
Hs.159430	ENSG00000075420	FNDC3B	2.0	3.0E-06
Hs.166120	ENSG00000185507	IRF7	2.0	2.3E-06
Hs.523696	ENSG00000110042	DTX4	2.0	1.2E-04
Hs.491148	ENSG00000078674	PCM1	2.0	3.2E-06
Hs.81791	ENSG00000164761	TNFRSF11B	2.0	5.8E-04
Hs.404119	ENSG00000104522	TSTA3	2.0	6.5E-04
Hs.23131	ENSG00000140859	KIFC3	2.0	2.9E-04
Hs.421194	ENSG00000169902	TPST1	2.0	4.1E-04
Hs.522412	ENSG00000171159	C9orf16	2.0	9.3E-04
Hs.523852	ENSG00000110092	CCND1	2.0	1.1E-04
Hs.517240	ENSG00000159128	IFNGR2	2.0	4.6E-04
Hs.491767	ENSG00000147507	LYN	1.9	4.8E-06
Hs.140452	ENSG00000105355	M6PRBP1	1.9	2.9E-04
Hs.535499	ENSG00000131759	RARA	1.9	5.1E-07
Hs.343522	ENSG00000058668	ATP2B4	1.9	6.5E-04
Hs.450972	ENSG00000102804	TGFB14	1.9	9.2E-04
Hs.517168	ENSG00000117063	TAGLN2	1.9	5.6E-06
Hs.14601	ENSG00000180353	HCLS1	1.9	1.1E-05
Hs.435765	ENSG00000138792	ENPEP	1.9	6.1E-06
Hs.459855	ENSG00000140650	PMM2	1.9	5.0E-04
Hs.272011	ENSG00000086062	B4GALT1	1.9	9.8E-06
Hs.289092	ENSG00000103187	COTL1	1.9	1.5E-06
Hs.489033	ENSG00000085563	ABCB1	1.9	5.0E-04
Hs.278573	ENSG00000085063	CD59	1.9	5.8E-04
Hs.282594	ENSG00000134389	CFHL5	1.9	8.0E-04
Hs.35947	ENSG00000129071	MBD4	1.9	1.3E-05
Hs.405667	ENSG00000172116	CD8B1	1.9	9.5E-06
Hs.408909	ENSG00000113384	GOLPH3	1.9	5.8E-05
Hs.123232	ENSG00000140025	C14orf143	1.9	1.0E-05
Hs.454534	ENSG00000105698	USF2	1.9	6.9E-04
Hs.517666	ENSG00000100243	DIA1	1.9	3.3E-07
Hs.149239	ENSG00000125266	EFNB2	1.9	9.6E-06
Hs.518301	ENSG00000177311	FLJ35036	1.9	8.8E-04
Hs.369762	ENSG00000176890	TYMS	1.9	4.4E-04
Hs.87752	ENSG00000147065	MSN	1.8	1.4E-07
Hs.515169	ENSG00000104907	FLJ20244	1.8	1.4E-05
Hs.146447	ENSG00000166147	FBN1	1.8	4.8E-06
Hs.473256	ENSG00000130702	LAMA5	1.8	7.8E-06
Hs.498173	ENSG00000166311	SMPD1	1.8	5.8E-05
Hs.534847	ENSG00000166308	C4A	1.7	1.1E-06
Hs.171142	ENSG00000108381	ASPA	-1.5	8.3E-06
Hs.269180	ENSG00000095203	EPB41L4B	-1.6	9.4E-06
Hs.487925	ENSG00000178104	PDE4DIP	-1.7	2.5E-07
Hs.180919	ENSG00000115738	ID2	-1.8	1.3E-06

Hs.499674	ENSG00000165471	MBL2	-1.8	3.0E-06
Hs.552573	ENSG00000164850	GPR30	-1.8	2.5E-04
Hs.235390	ENSG00000121413	FLJ12895	-1.9	9.4E-04
Hs.300863	ENSG00000185513	L3MBTL	-1.9	9.8E-03
Hs.318894	ENSG00000112414	GPR126	-1.9	4.8E-04
Hs.368243	ENSG00000023839	ABCC2	-1.9	7.8E-04
Hs.343911	ENSG00000149547	EI24	-1.9	3.3E-08
Hs.164226	ENSG00000137801	THBS1	-1.9	1.6E-08
Hs.250	ENSG00000158125	XDH	-1.9	7.9E-05
Hs.271264	ENSG00000001084	GCLC	-1.9	8.5E-04
Hs.546303	ENSG00000100380	ST13	-1.9	1.0E-08
Hs.233220	ENSG00000197114	FLJ20406	-1.9	7.6E-06
Hs.287749	ENSG00000109929	SC5DL	-2.0	1.3E-06
Hs.520710	ENSG00000128607	KIAA0265	-2.0	2.6E-04
Hs.11900	ENSG00000197114	ZGPAT	-2.0	9.4E-06
Hs.184507	ENSG00000198338	ZG16	-2.0	9.1E-04
Hs.448520	ENSG00000003989	SLC7A2	-2.0	5.6E-04
Hs.471508	ENSG00000169047	IRS1	-2.0	7.0E-06
Hs.251415	ENSG00000181150	DIO1	-2.0	5.7E-04
Hs.427202	ENSG00000118271	TTR	-2.0	1.2E-04
Hs.161220	ENSG00000139597	CG018	-2.0	6.9E-04
Hs.149252	ENSG00000021826	CPS1	-2.0	9.5E-04
Hs.169378	ENSG00000107186	MPDZ	-2.0	1.4E-05
Hs.77293	ENSG00000179833	SERTAD2	-2.0	7.8E-04
Hs.94896	ENSG00000096092	TMEM14A	-2.1	1.9E-06
Hs.5243	ENSG00000114023	E2IG5	-2.1	8.8E-04
Hs.408790	ENSG00000185808	DSCR5	-2.1	1.4E-05
Hs.132225	ENSG00000145675	PIK3R1	-2.1	8.6E-04
Hs.335139	ENSG00000136636	KCTD3	-2.1	5.2E-06
Hs.496459	ENSG00000143337	LAP1B	-2.1	5.4E-06
Hs.223858	ENSG00000123454	DBH	-2.1	2.4E-07
Hs.495912	ENSG00000198947	DMD	-2.1	5.4E-06
Hs.107003	ENSG00000100814	CCNB1IP1	-2.1	7.9E-04
Hs.144795	ENSG00000156113	KCNMA1	-2.1	1.5E-05
Hs.7303	ENSG00000144852	NR1I2	-2.1	1.1E-05
Hs.552	ENSG00000145545	SRD5A1	-2.1	2.9E-12
Hs.502176	ENSG00000205213	LGR4	-2.1	1.0E-05
Hs.12393	ENSG00000088451	TGDS	-2.1	6.7E-04
Hs.546304	ENSG00000197165	SULT1A2	-2.1	5.7E-04
Hs.460587	ENSG00000132207	SULT1A3	-2.1	1.3E-08
Hs.102308	ENSG00000121361	KCNJ8	-2.1	1.2E-05
Hs.325404	ENSG00000171759	PAH	-2.2	7.0E-05
Hs.150557	ENSG00000119138	KLF9	-2.2	9.5E-04
Hs.371763	ENSG00000176201	GBA3	-2.2	3.4E-05
Hs.80409	ENSG00000116717	GADD45A	-2.2	6.0E-11
Hs.268700	ENSG00000172828	FLJ21736	-2.2	3.7E-06
Hs.145442	ENSG00000169032	MAP2K1	-2.2	7.4E-04
Hs.156540	ENSG00000166922	SGNE1	-2.2	4.8E-04
Hs.145384	ENSG00000149124	GLYAT	-2.3	6.5E-05
Hs.409368	ENSG00000147654	EBAG9	-2.3	1.5E-04
Hs.407190	ENSG00000096060	FKBP5	-2.3	5.2E-06
Hs.142	ENSG00000196502	SULT1A1	-2.3	1.2E-04
Hs.525205	ENSG00000165795	NDRG2	-2.3	1.9E-04
Hs.326035	ENSG00000120738	EGR1	-2.3	4.7E-11
Hs.500761	ENSG00000141526	SLC16A3	-2.3	1.4E-08
Hs.83190	ENSG00000169710	FASN	-2.3	1.1E-11
Hs.232054	ENSG00000142494	FLJ10847	-2.3	2.6E-04
Hs.478673	ENSG00000196083	IL1RAP	-2.3	2.7E-06
Hs.118681	ENSG00000065361	ERBB3	-2.3	1.2E-06
Hs.160786	ENSG00000130707	ASS	-2.4	7.2E-04
Hs.465337	ENSG00000081913	PLEKHE1	-2.4	5.9E-05
Hs.7921		LOC221362	-2.4	2.9E-04
Hs.160562	ENSG00000017427	IGF1	-2.4	8.7E-04
Hs.136885	ENSG00000127870	RNF6	-2.4	7.1E-08
Hs.80756	ENSG00000145692	BHMT	-2.4	6.6E-04
Hs.327179	ENSG00000124564	SLC17A3	-2.4	6.1E-04
Hs.8361	ENSG00000182704	TSK	-2.4	2.8E-08
Hs.483067	ENSG00000134986	C5orf13	-2.5	5.3E-08
Hs.75231	ENSG00000155380	SLC16A1	-2.5	3.4E-04
Hs.444488	ENSG00000072080	SPP2	-2.5	1.5E-07
Hs.487296	ENSG00000092621	PHGDH	-2.5	4.6E-04
Hs.97270	ENSG00000138640	FAM13A1	-2.6	6.3E-04
Hs.144879	ENSG00000130829	DUSP9	-2.6	1.4E-04
Hs.209128	ENSG00000002822	MAD1L1	-2.6	3.1E-06
Hs.510334	ENSG00000188488	SERPINA5	-2.6	8.2E-04
Hs.149032	ENSG00000196455	PIK3R4	-2.6	5.9E-04
Hs.480218	ENSG00000118777	ABCG2	-2.6	1.8E-04
Hs.25155	ENSG00000173848	NET1	-2.6	2.4E-06
Hs.443874	ENSG00000157103	SLC6A1	-2.7	6.1E-04
Hs.91747	ENSG00000070087	PFN2	-2.7	8.3E-05
Hs.126906	ENSG00000049883	PTCD2	-2.7	9.4E-04
Hs.111944	ENSG00000160870	CYP3A7	-2.7	8.2E-04
Hs.159628	ENSG00000100665	SERPINA4	-2.8	6.2E-04
Hs.143261	ENSG00000092529	CAPN3	-2.8	9.4E-07
Hs.501624	ENSG00000185187	SIGIRR	-2.8	8.7E-04
Hs.155097	ENSG00000104267	CA2	-2.8	5.2E-05
Hs.284712	ENSG00000136881	BAAT	-2.9	2.2E-04
Hs.282624	ENSG00000138109	CYP2C9	-2.9	3.0E-12
Hs.25647	ENSG00000170345	FOS	-2.9	6.3E-12
Hs.528295	ENSG00000008311	AASS	-2.9	1.3E-08
Hs.407966	ENSG00000108479	GALK1	-3.0	7.7E-12
Hs.494261	ENSG00000135069	PSAT1	-3.0	6.0E-04
Hs.8944	ENSG00000163710	PCOLCE2	-3.0	5.9E-04
Hs.302742	ENSG00000198743	MRPS6	-3.1	4.6E-05
Hs.205816	ENSG00000124568	SLC17A1	-3.1	6.2E-04
Hs.444870	ENSG00000115942	ORC2L	-3.1	2.0E-04
Hs.306220	ENSG00000021461	CYP3A43	-3.2	9.8E-04
Hs.212606	ENSG00000135423	GLS2	-3.3	9.1E-15
Hs.197043	ENSG00000117643	MAN1C1	-3.4	1.5E-10
Hs.160976	ENSG00000005187	SAH	-3.4	6.4E-15

Hs.30246	ENSG00000117479	SLC19A2	-3.4	4.8E-04
Hs.524085	ENSG00000036672	USP2	-3.5	6.6E-06
Hs.203717	ENSG00000115414	FN1	-3.5	9.4E-04
Hs.144845	ENSG00000129151	BBOX1	-3.5	1.0E-11
Hs.479898	ENSG00000109193	SULT1E1	-3.5	5.9E-04
Hs.439056	ENSG00000198470	CYP2A6	-3.9	0.0E+00
Hs.485572	ENSG00000120833	SOCS2	-4.3	1.9E-12
Hs.463375	ENSG00000198740	ZNF652	-4.4	3.5E-06
Hs.839	ENSG00000099769	IGFALS	-4.4	2.9E-04
Hs.124112	ENSG00000167165	UGT1A6	-4.4	2.5E-03
Hs.505662	ENSG00000135447	PPP1R1A	-4.5	0.0E+00
Hs.72912	ENSG00000140465	CYP1A1	-4.7	2.6E-14
Hs.87889	ENSG00000100697	DICER1	-4.9	1.9E-03
Hs.127648	ENSG00000173930	SLCO4C1	-5.0	8.9E-04
Hs.144914	ENSG00000124713	GNMT	-5.3	6.3E-04
Hs.169948	ENSG00000177272	KCNA3	-5.4	2.0E-14
Hs.418167	ENSG00000163631	ALB	-5.7	3.0E-11
Hs.150595	ENSG00000095596	CYP26A1	-5.7	1.2E-05
Hs.75678	ENSG00000125740	FOSB	-5.9	3.6E-14
Hs.127826	ENSG00000187266	EPOR	-5.9	2.2E-06
Hs.224171	ENSG00000108515	ENO3	-6.1	0.0E+00
Hs.534364	ENSG00000127831	VIL1	-6.6	4.4E-16
Hs.523332	ENSG00000065154	OAT	-6.8	2.7E-04
Hs.272499	ENSG00000100867	DHRS2	-7.0	1.6E-11
Hs.107474	ENSG00000138386	NAB1	-8.5	1.6E-04
Hs.489786	ENSG00000001626	CFTR	-9.2	8.6E-06
Hs.98280	ENSG00000080709	KCNN2	-11.3	5.7E-05
Hs.351306	ENSG00000168679	SLC16A4	-14.9	1.6E-04
Hs.724	ENSG00000126351	THRA	-17.3	1.0E-07
Hs.234775	ENSG00000171119	NRTN	-19.4	6.7E-10
Hs.307734	ENSG00000196549	MME	-20.4	3.3E-05
Hs.282409	ENSG00000165841	CYP2C19	-21.6	1.8E-05

## Supplementary Table S2. Gene Ontology (GO) analysis

Liste of GO terms significantly enriched in genes over-expressed in inflammatory HCA, obtained using the web-based tool GOTree Machine and the hypergeometric test. GO terms related to inflammation and immune response are indicated in red.

**O:** Observed gene number in the GO category (referred to genes over-expressed in inflammatory HCA compared to non-tumour livers)

**E:** Expected gene number in the GO category (referred to the whole content of the HG-U133A Affymetrix array)

**R:** Ratio of enrichment for the GO category (O/E)

**P-value:** Significance of enrichment for the GO category

GO categories were considered significantly enriched when the *P*-value was less than 0.01

	O	E	R	P-value
<b>In biological process</b>				
<b>protein kinase cascade</b>	13	5.5	2.36	3E-03
<b>JAK-STAT cascade</b>	5	0.66	7.58	4E-04
regulation of JAK-STAT cascade	4	0.17	23.53	1E-05
negative regulation of JAK-STAT cascade	2	0.1	20	3E-03
negative regulation of tyrosine phosphorylation of STAT protein	2	0.1	20	3E-03
negative regulation of tyrosine phosphorylation of Stat3 protein	2	0.1	20	3E-03
positive regulation of JAK-STAT cascade	2	0.07	28.57	2E-03
positive regulation of tyrosine phosphorylation of STAT protein	2	0.07	28.57	2E-03
regulation of tyrosine phosphorylation of STAT protein	4	0.17	23.53	1E-05
regulation of tyrosine phosphorylation of Stat3 protein	2	0.12	16.67	6E-03
tyrosine phosphorylation of STAT protein	4	0.24	16.67	6E-05
tyrosine phosphorylation of Stat3 protein	2	0.12	16.67	6E-03
<b>negative regulation of protein metabolism</b>	6	1.36	4.41	2E-03
regulation of phosphorus metabolism	4	0.68	5.88	4E-03
regulation of amino acid metabolism	4	0.41	9.76	6E-04
negative regulation of amino acid metabolism	2	0.1	20	3E-03
negative regulation of protein amino acid phosphorylation	2	0.1	20	3E-03
regulation of phosphate metabolism	4	0.68	5.88	4E-03
negative regulation of phosphate metabolism	2	0.15	13.33	8E-03
negative regulation of phosphorylation	2	0.15	13.33	8E-03
negative regulation of peptidyl-tyrosine phosphorylation	2	0.1	20	3E-03
regulation of phosphorylation	4	0.61	6.56	3E-03
peptidyl-amino acid modification	5	1.19	4.2	6E-03
peptidyl-tyrosine modification	5	0.51	9.8	1E-04
peptidyl-tyrosine phosphorylation	4	0.46	8.7	1E-03
regulation of protein amino acid phosphorylation	4	0.39	10.26	5E-04
regulation of peptidyl-tyrosine phosphorylation	4	0.36	11.11	4E-04
<b>organismal physiological process</b>	61	35.54	1.72	6E-06
<b>immune system process</b>	38	12.02	3.16	1E-10
antigen processing and presentation	11	0.88	12.5	5E-10
antigen processing and presentation of endogenous antigen	6	0.41	14.63	2E-06
antigen processing and presentation of endogenous peptide antigen	6	0.36	16.67	8E-07
antigen processing and presentation of endogenous peptide antigen via MHC class I	6	0.36	16.67	8E-07
antigen processing and presentation of exogenous antigen	5	0.27	18.52	3E-06
antigen processing and presentation of exogenous peptide antigen	5	0.27	18.52	3E-06
antigen processing and presentation of exogenous peptide antigen via MHC class II	5	0.27	18.52	3E-06
antigen processing and presentation of peptide antigen	11	0.68	16.18	2E-11
antigen processing and presentation of peptide antigen via MHC class I	6	0.36	16.67	8E-07
antigen processing and presentation of peptide antigen via MHC class II	5	0.27	18.52	3E-06
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	5	0.27	18.52	3E-06
immune response	27	9.59	2.82	9E-07
<b>response to stimulus</b>	49	28.25	1.73	6E-05
response to external stimulus	20	9.49	2.11	1E-03
response to stress	31	15.4	2.01	1E-04
response to wounding	19	7.06	2.69	8E-05
physiological response to stimulus	47	22.38	2.1	5E-07
physiological response to wounding	19	6.81	2.79	5E-05
physiological defense response	16	7.18	2.23	2E-03
inflammatory response	15	5.04	2.98	2E-04
acute-phase response	4	0.58	6.9	2E-03
response to biotic stimulus	13	4.96	2.62	1E-03
response to other organism	12	4.01	2.99	7E-04
response to virus	7	1.41	4.96	5E-04
platelet activation	3	0.32	9.38	3E-03
<b>carbohydrate biosynthesis</b>	7	1.65	4.24	1E-03
alcohol biosynthesis	4	0.51	7.84	1E-03
monosaccharide biosynthesis	4	0.51	7.84	1E-03
hexose biosynthesis	4	0.51	7.84	1E-03
fucose biosynthesis	2	0.05	40	6E-04
L-fucose biosynthesis	2	0.05	40	6E-04
GDP-L-fucose biosynthesis	2	0.05	40	6E-04
de novo' GDP-L-fucose biosynthesis	2	0.05	40	6E-04
fucose metabolism	3	0.29	10.34	3E-03
L-fucose metabolism	3	0.24	12.5	2E-03
nucleotide-sugar biosynthesis	3	0.07	42.86	1E-05
nucleotide-sugar metabolism	3	0.24	12.5	2E-03
GDP-L-fucose metabolism	2	0.05	40	6E-04
GDP-mannose metabolism	2	0.05	40	6E-04
<b>developmental maturation</b>	4	0.46	8.7	1E-03
cell maturation	2	0.07	28.57	2E-03
myeloid cell differentiation	5	0.83	6.02	1E-03
erythrocyte differentiation	4	0.32	12.5	2E-04
erythrocyte development	2	0.07	28.57	2E-03
erythrocyte maturation	4	0.46	8.7	1E-03

<b>anatomical structure development</b>	39	26.1	1.49	6E-03
cell development	8	2.51	3.19	4E-03
cellular morphogenesis during differentiation	5	1.05	4.76	4E-03
cell projection morphogenesis	5	0.97	5.15	3E-03
neuron development	5	1.24	4.03	8E-03
neuron morphogenesis during differentiation	5	0.97	5.15	3E-03
neurite development	5	1.07	4.67	4E-03
neurite morphogenesis	5	0.97	5.15	3E-03
axonogenesis	5	0.92	5.43	2E-03
<b>cell adhesion</b>	24	11.22	2.14	3E-04
regulation of cell adhesion	5	0.78	6.41	1E-03
positive regulation of cell adhesion	2	0.1	20	3E-03
<b>cell motility</b>	14	4.79	2.92	3E-04
cell migration	7	2.07	3.38	5E-03
<b>locomotion</b>	14	4.79	2.92	3E-04
<b>cell proliferation</b>	20	11.22	1.78	8E-03
<b>phospholipid catabolism</b>	2	0.15	13.33	8E-03
<b>localization of cell</b>	14	4.79	2.92	3E-04
<b><i>In molecular function</i></b>				
<b>interferon binding</b>	2	0.09	22.22	3E-03
interferon receptor activity	2	0.09	22.22	3E-03
interferon-gamma receptor activity	2	0.05	40	6E-04
interferon-gamma binding	2	0.05	40	6E-04
<b>obsolete molecular function</b>	11	0.61	18.03	5E-12
MHC class I receptor activity	6	0.38	15.79	1E-06
MHC class II receptor activity	6	0.26	23.08	7E-08
<b>enzyme inhibitor activity</b>	12	4.21	2.85	1E-03
protease inhibitor activity	7	2.26	3.1	7E-03
endopeptidase inhibitor activity	7	2.23	3.14	7E-03
<b>glutathione peroxidase activity</b>	2	0.09	22.22	3E-03
<b>erythropoietin receptor binding</b>	2	0.07	28.57	2E-03
<b>selenium binding</b>	2	0.12	16.67	5E-03
<b>aldehyde dehydrogenase [NAD(P)+] activity</b>	2	0.14	14.29	8E-03

**Supplementary Table S3. Classification of the main genes related to inflammation that are differentially expressed between inflammatory HCA and non-tumour livers.**

Data are expressed as the mean-fold difference in gene expression in inflammatory HCA (IHCA) relative to non-tumour livers (NTL). \*, \*\*, \*\*\* difference between groups at  $P < 0.05$ ; 0.01 and 0.001 respectively. Abbreviations: ns: not significant; nd: not done; na: not analysed.

Gene Symbol	Gene Name	Microarray data		qRT-PCR validation	
		Fold change ratio IHCA (n=4)/NTL (n=4)	P-value	Fold change ratio IHCA (n=14)/NTL (n=6)	P-value
<b>Acute phase proteins</b>					
SAA1	Serum amyloid A1	33.1	1.20E-04	nd	
SAA2	Serum amyloid A2	na	na	99.0	***
SPINK1	Serine protease inhibitor, Kazal type 1	17.4	4.80E-04	75.2	***
PLA2G2A	Phospholipase A2, group IIA (platelets, synovial fluid)	15.2	1.00E-06	nd	
VWF	Von Willebrand factor	8.9	3.40E-04	nd	
CRP	C-reactive protein, pentraxin-related	7.3	5.60E-04	21.6	***
LBP	Lipopolysaccharide binding protein	3.7	1.50E-04	nd	
SLPI	Secretory leukocyte protease inhibitor (antileukoproteinase)	2.9	3.50E-05	nd	
GLRX	Glutaredoxin (thioltransferase)	2.3	1.40E-04	nd	
IL1RN	Interleukin 1 receptor antagonist	2.1	1.80E-06	nd	
FGB	Fibrinogen, B beta polypeptide	1.1	ns	1.8	**
C4A	Complement component 4B, telomeric	1.6	1.10E-06	nd	
TTR	Transthyretin (prealbumin, amyloidosis type I)	-2.0	1.20E-04	nd	
IGF1	Insulin-like growth factor 1 (somatomedin C)	-2.4	8.70E-04	nd	
ALB	Albumin	-5.7	3.00E-11	nd	
<b>MHC class I</b>					
HLA-A	Major histocompatibility complex, class I, A	2.1	5.8E-04	nd	
HLA-B	Major histocompatibility complex, class I, B	3.0	6.3E-04	nd	
HLA-C	Major histocompatibility complex, class I, C	2.6	9.4E-04	nd	
HLA-E	Major histocompatibility complex, class I, E	2.1	4.9E-06	2.6	***
HLA-F	Major histocompatibility complex, class I, F	2.7	5.0E-04	nd	
HLA-G	HLA-G histocompatibility antigen, class I, G	2.8	8.9E-04	nd	
<b>MHC class II</b>					
HLA-DMA	Major histocompatibility complex, class II, DM alpha	2.6	8.2E-04	nd	
HLA-DPA1	Major histocompatibility complex, class II, DP alpha 1	2.8	6.3E-08	nd	
HLA-DQB1	Major histocompatibility complex, class II, DQ beta 1	2.5	2.3E-06	nd	
HLA-DRA	Major histocompatibility complex, class II, DR alpha	2.2	1.4E-07	4.1	***
HLA-DRB1	Major histocompatibility complex, class II, DR beta 4	2.3	2.8E-06	nd	
<b>Antigen processing</b>					
TAP1	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	4.6	7.3E-04	4.1	**
PSMB8	Proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)	2.2	7.2E-05	2.6	**
PSMB9	Proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	2.2	8.8E-04	3.5	**
CTSS	Cathepsin S	2.4	8.1E-07	nd	
<b>Cytokine and chemokines</b>					
CCL20	Chemokine (C-C motif) ligand 20	219.8	3.7E-04	nd	
NK4	Interleukin 32	16.8	1.0E-04	nd	
EPO	Erythropoietin	6.8	2.1E-07	nd	
TNFSF14	Tumor necrosis factor (ligand) superfamily, member 14	4.3	5.9E-04	nd	
PBEF1	Pre-B-cell colony enhancing factor 1	2.5	9.8E-04	nd	
<b>Chemokine and toll-like receptors</b>					
XCR1	Chemokine (C motif) receptor 1	3.0	1.4E-11	nd	
TLR2	Toll-like receptor 2	2.5	4.8E-04	nd	
CCR1	Chemokine (C-C motif) receptor 1	2.3	5.0E-06	nd	
<b>Cytokine receptors</b>					
IFNGR1	Interferon gamma receptor 1	2.6	3.0E-04	3.5	***
IFNGR2	Interferon gamma receptor 2 (interferon gamma transducer 1)	1.9	4.6E-04	2.8	***
IL4R	Interleukin 4 receptor	2.1	2.7E-05	nd	
TNFRSF11B	Tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	2.0	5.8E-04	nd	
IL1RAP	Interleukin 1 receptor accessory protein	-2.3	2.7E-06	nd	
SIGIRR	Single Ig IL-1R-related molecule	-2.8	8.7E-04	nd	
EPOR	Erythropoietin receptor	-5.9	2.2E-06	nd	
<b>Transcription factors related to inflammation</b>					
IFI16	Interferon, gamma-inducible protein 16	4.2	3.2E-04	nd	
STAT1	Signal transducer and activator of transcription 1, 91kDa	2.1	ns	4.5	***
STAT2	Signal transducer and activator of transcription 2, 113kDa	1.2	ns	2.0	*
STAT3	Signal transducer and activator of transcription 3 (acute-phase response factor)	2.8	2.8E-04	2.1	***
HIF1A	Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	2.5	6.8E-04	3.5	***
ISGF3G	Interferon-stimulated transcription factor 3, gamma 48kDa	2.2	7.4E-07	2.1	**
NFKB2	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	2.1	1.0E-04	2.2	**
IRF7	Interferon regulatory factor 7	2.0	2.3E-06	2.8	**
HCLS1	Hematopoietic cell-specific Lyn substrate 1	1.9	1.1E-05	nd	
<b>Other proteins involved in signal transduction related to inflammation</b>					
JAK2	Janus kinase 2 (a protein tyrosine kinase)	1.1	ns	2.0	**
GOLPH2	Golgi phosphoprotein 2	129.0	3.1E-05	nd	
SOCS1	Suppressor of cytokine signaling 1	9.8	2.8E-04	17.4	***
SOCS3	Suppressor of cytokine signaling 3	1.5	ns	2.1	*
BIRC3	Baculoviral IAP repeat-containing 3	9.1	2.7E-05	7.6	***
BCL2A1	BCL2-related protein A1	5.9	4.3E-04	17.2	***
TNFAIP8	Tumor necrosis factor, alpha-induced protein 8	4.1	5.4E-04	nd	
GBP2	Guanylate binding protein 2, interferon-inducible	3.8	1.2E-04	nd	
PLA2G4C	Phospholipase A2, group IVC (cytosolic, calcium-independent)	3.4	3.4E-07	nd	
C5R1	Complement component 5 receptor 1 (C5a ligand)	3.1	9.0E-04	nd	
PTGES2	Prostaglandin E synthase 2	2.3	1.3E-09	nd	
IFITM1	Interferon induced transmembrane protein 1 (9-27)	2.2	1.1E-09	nd	
TNFAIP3	Tumor necrosis factor, alpha-induced protein 3	2.2	6.2E-04	nd	
IFI35	Interferon-induced protein 35	-2.0	7.5E-08	nd	
SOCS2	Suppressor of cytokine signaling 2	-4.3	1.9E-12	nd	



## Supplementary Table S4. *IL6ST*, *HNF1A* and *CTNNB1* gene mutations

Abbreviations: del: deletion; fs: frameshift; ins: insertion; nm: non-mutated; IHCA: inflammatory hepatocellular adenoma; HCA: hepatocellular adenoma; HCC: hepatocellular carcinoma

#469T: HCC associated with an IHCA (470T)

\* Previously described in Zucman-Rossi *et al.* 2006; \*\* and the remaining 111 HCC were previously described in Boyault *et al.* 2007

N° ID	Sexe	Age	Diagnosis	<i>IL6ST</i> mutations	<i>HNF1A</i> mutations		<i>CTNNB1</i> mutations
					Allele 1	Allele 2	
344T	F	38	IHCA	560_571del; S187_Y190del	nm	nm	nm
362T	F	54	IHCA	560_571del; S187_Y190del	nm	nm	nm
364T	F	35	IHCA	565_576del; V189_V192del	nm	nm	nm
377T	F	42	IHCA	565_576del; V189_V192del	nm	nm	nm
382T	F	40	IHCA	560_571del; S187_Y190del	nm	nm	nm
390T	M	50	IHCA	557_574del; Y186_F191del, V192F	nm	nm	nm
455T	F	27	IHCA	565_576del; V189_V192del	nm	nm	nm
466T	F	50	IHCA	560_571del; S187_Y190del	nm	nm	nm
552T	F	55	IHCA	563_574del; T188_F191del, V192I	nm	nm	nm
555T	F	40	IHCA	503_580del; K168_N192del	nm	nm	nm
560T	F	49	IHCA	557_571del; Y186_Y190del	nm	nm	nm
670T	F	37	IHCA	560_571del; S187_Y190del	nm	nm	nm
691T	F	35	IHCA	518_532del; K173_D177del	nm	nm	nm
770T	F	34	IHCA	559_573del; S187_F191del	nm	nm	nm
771T	F	33	IHCA	564_575del; T188_F191del, V192T	nm	nm	nm
867T	F	38	IHCA	583-588del; E195_V196del	nm	nm	nm
1020T	F	40	IHCA	557_571del; Y186_Y190del	nm	nm	nm
1121T	F	25	IHCA	557_571del; Y186_Y190del	nm	nm	nm
1232T	F	36	IHCA	563_574del; T188_F191del, V192I	nm	nm	nm
1238T	F	41	IHCA	573T>G, 574_582del; F191L, V192_I194del	nm	nm	nm
470T	F	32	IHCA	557_571del; Y186_Y190del	nm	nm	*100G>A; G34R
711T	F	26	IHCA	643_645del; D215del	nm	nm	121A>G; T41A
786T	M	59	IHCA	551_559del; V184_Y186del, S187A	nm	nm	IVS2+9_399del; A5_K133del
819T	F	46	IHCA	560_571del; S187_Y190del	nm	nm	116C>G; A39G
1023T	M	35	IHCA	614_646dup; K206_P216dup, G205R	nm	nm	121A>G; T41A
1124T	M	50	IHCA	575_583del; V192_I194del	nm	nm	121A>G; T41A
343T	F	45	IHCA	nm	nm	nm	134C>A; S45Y
1234T	F	21	IHCA	nm	nm	nm	133T>C; S45P
222T	M	29	IHCA	nm	nm	nm	nm
341T	M	43	IHCA	nm	nm	nm	nm
346T	F	38	IHCA	nm	nm	nm	nm
353T	F	27	IHCA	nm	nm	nm	nm
375T	F	46	IHCA	nm	nm	nm	nm
378T	F	51	IHCA	nm	nm	nm	nm
379T	F	46	IHCA	nm	nm	nm	nm
458T	F	25	IHCA	nm	nm	nm	nm
471T	F	31	IHCA	nm	nm	nm	nm
574T	M	55	IHCA	nm	nm	nm	nm
622T	F	31	IHCA	nm	nm	nm	nm
781T	F	39	IHCA	nm	nm	nm	nm
873T	M	33	IHCA	nm	nm	nm	nm
1123T	F	46	IHCA	nm	nm	nm	nm
1215T	F	33	IHCA	nm	nm	nm	nm
372T	F	37	HCA	nm	nm	nm	*101G>A; G34E
376T	M	14	HCA	nm	nm	nm	*98C>T; S33Y
517T	F	28	HCA	nm	nm	nm	*133T>C; S45P
361T	F	67	HCA	nm	nm	nm	*7_378del; T3_A126del
1214T	F	32	HCA	nm	IVS3-85_753del	1894del13bp + dup11bp	nm
357T	F	28	HCA	nm	*IVS2+1G>A	*618G>T; W206C	nm
358T	F	46	HCA	nm	*617G>T; W206L	*872_884del; P291fs	nm
368T	F	49	HCA	nm	*710A>G; N237S	*LOH	nm
369T	F	41	HCA	nm	*436_437delC; Q146fs	*LOH	nm
370T	F	49	HCA	nm	*872_873insC; P291fs	*803T>G; F268C	nm
371T	F	37	HCA	nm	*617G>T; W206L	*730A>G; R244G	nm
373T	F	35	HCA	nm	*82C>T; Q28X	*LOH	nm
380T	F	27	HCA	nm	*196G>T; E66X	*779C>T; T260M	nm
383T	F	30	HCA	nm	*493T>A; W165R	*1340C>T; P447L	nm
385T	F	38	HCA	nm	*817A>G; K273E	*LOH	nm
387T	F	51	HCA	nm	1326G>A; Q442Q	LOH	nm
461T	F	41	HCA	nm	*872_873insC; P291fs	*872_873delC; P291fs	nm
462T	F	34	HCA	nm	*632A>C; Q211P	*617G>T; W206L	nm
464T	F	51	HCA	nm	*71_82del; A25_Q28del	*747_764del; Q250_G255del	nm
516T	M	67	HCA	nm	*185_194del; N62fs	*788G>A; R263H	nm
575T	F	33	HCA	nm	*IVS2+1del13	*956_957delG; G319fs	nm
687T	F	24	HCA	nm	*814C>A; R272S	*LOH	nm
694T	F	45	HCA	nm	*682G>T; E228X	*IVS2_2 A>G	nm
759T	F	56	HCA	nm	IVS2+1 G>A	608G>T; R203L	nm
766T	F	26	HCA	nm	IVS2+1 G>A	872_873insC; P291fs	nm
817T	F	42	HCA	nm	196G>T; E66X	711T>A; N237K	nm
342T	F	34	HCA	nm	nm	nm	nm
452T	M	18	HCA	nm	nm	nm	nm
459T	F	41	HCA	nm	nm	nm	nm
573T	F	28	HCA	nm	nm	nm	nm
603T	F	48	HCA	nm	nm	nm	nm
674T	F	24	HCA	nm	nm	nm	nm
706T	M	52	HCA	nm	nm	nm	nm
469T#	F	32	HCC	557_571del; Y186_Y190del	nm	nm	*100G>A; G34R
059T	M	40	HCC	577_579del, 580A>T; N193del, I194F	nm	nm	**121A>G; T41A
199T	M	75	HCC	569_577del, 578A>C; Y190_V192del, N193S	nm	nm	**101G>T; G34V

**Supplementary Table S5. TaqMan® pre-designed gene expression assays used for quantitative RT-PCR analyses**

Assay ID	Gene Symbol	Gene Name
Hs99999901_s1	18S	Eukaryotic 18S rRNA
Hs00187845_m1	BCL2A1	BCL2-related protein A1
Hs00154109_m1	BIRC3	baculoviral IAP repeat-containing 3
Hs00355476_m1	CCL20	chemokine (C-C motif) ligand 20
Hs00265044_m1	CRP	C-reactive protein, pentraxin-related
Hs00170586_m1	FGB	fibrinogen beta chain
Hs00153153_m1	HIF1A	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
Hs00219575_m1	HLA-DRA	major histocompatibility complex, class II, DR alpha
Hs00428366_m1	HLA-E	major histocompatibility complex, class I, E
Hs00166223_m1	IFNGR1	interferon gamma receptor 1
Hs00194264_m1	IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)
Hs00174148_m1	IL11	interleukin 11
Hs00234415_m1	IL11RA	interleukin 11 receptor, alpha
Hs00992441_m1	IL32	interleukin 32
Hs00174360_m1	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)
Hs00185375_m1	IRF7	interferon regulatory factor 7
Hs00196051_m1	ISGF3G	interferon-stimulated transcription factor 3, gamma 48kDa
Hs00234567_m1	JAK2	Janus kinase 2 (a protein tyrosine kinase)
Hs00544758_m1	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
Hs00544762_m1	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)
Hs01667582_m1	SAA2	serum amyloid A2
Hs00705164_s1	SOCS1	suppressor of cytokine signaling 1
Hs00269575_s1	SOCS3	suppressor of cytokine signaling 3
Hs00162154_m1	SPINK1	serine peptidase inhibitor, Kazal type 1
Hs00234829_m1	STAT1	signal transducer and activator of transcription 1, 91kDa
Hs00237139_m1	STAT2	signal transducer and activator of transcription 2, 113kDa
Hs00374280_m1	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)
Hs00388682_m1	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)

## Supplementary Table S6. List of primers used in PCR and sequencing

F: forward primer; R: reverse primer

Exon	Sequence primer 5'->3'	Primer Name
<b>IL6ST genomic DNA amplification and sequencing</b>		
3	CACAGCTACAGCATGGAAACA	3F-IL6ST
	GCATGTAAGATGACTGTTACAACCTCAA	3R-IL6ST
4	TGACGGTTGAGGGACTCTACA	4F-IL6ST
	GCAGTTCAATAGTCATGACAAAGTC	4R-IL6ST
5	CGCAAATGCCTTGGGTAGTA	5F-IL6ST
	AAAAATTCCAGCAAAAATGACT	5R-IL6ST
6	TAGTGACCAGCAGTTATATTGCAA	6F-IL6ST
	CGACTACAGTGTCAAATAAACTCTCA	6R-IL6ST
7	TTGGAAAACATAATAAACCTTAGGA	7F-IL6ST
	GGGTTGAAAGAAGGACTATTTGA	7R-IL6ST
8	TGTTTGGTTTGCTTTGTTTCA	8F-IL6ST
	TCACAAACTAAGAAGCAATGAGG	8R-IL6ST
9	GCAATTGGAGGGCAAGAGTA	9F-IL6ST
	AATGGAGCGAGACTCGGTTT	9R-IL6ST
10	AGAGATTTGACATAATGGCATG	10F-IL6ST
	GTGTTTTTATGGGAGCCCTG	10R-IL6ST
11	TCACATGTTTTGGAAATGACTG	11F-IL6ST
	AGTCGTTTCAACGGACCAAA	11R-IL6ST
12-13	TGCAGTTTTAAAAGAAAATTAAGTGG	12/13F-IL6ST
	GGTGTCCTCGAGGCCAATA	12/13R-IL6ST
14	CAATGCCAAATATAGGCCAAA	14F-IL6ST
	CCACCAACCAAGCCAGATA	14R-IL6ST
15	CAGTAAGTCTGGTTGGGAAGTTG	15F-IL6ST
	TTGGGCTGAGAAGAAGACAGA	15R-IL6ST
16	TGGTTTGGTTTGTAAAGAGCTTTG	16F-IL6ST
	TTCAGCTTGAATATCTTATCTTT	16R-IL6ST
17	CTGGGAAGTTTCAGAGATGC	17F-IL6ST
	CTTGCCGTACAGTCTGTGGT	17R-IL6ST
<b>IL6ST cDNA amplification and sequencing</b>		
3-7	ACCCAATGGAAAAAGCATGA	3F.RT-IL6ST
	TGCTGTGTCTTCAGGAGGAA	7R.RT-IL6ST
7-11	AGAAGCAGAGAATGCCCTTG	7F.RT-IL6ST
	CCTCTTAAATAGGTGCGATGC	11R.RT-IL6ST
11-15	TCACAAGATGGAATCACAT	11F.RT-IL6ST
	TGACCACTGGGCAATATGAC	15R.RT-IL6ST
16-17	TTCTGCTTAAATAAGCGAGACC	16F.RT-IL6ST
	GGGCAATGATCATCTTCAGAG	17R.RT-IL6ST
<b>IL6ST cDNA sequencing</b>		
3-7	GAACAGCATCCAGTGTCC	3FintRT-IL6ST
	GTTTTGCTTTGCAATCA	7RintRT-IL6ST
7-11	GCTGTATGAAGGAAGATG	7FintRT-IL6ST
	TCAGTTTTGTGGCATTAACTGTG	11RintRT-IL6ST
11-15	AGACTGGCAACAAGAAGA	11FintRT-IL6ST
	CTGTGTATGCTGCCATT	15RintRT-IL6ST
16-17	GACCTGTTCAAAAAGGAAA	16FintRT-IL6ST
	ATCAGTCGCAGCCTCCAT	17RintRT-IL6ST
<b>IL6R cDNA amplification and sequencing</b>		
1-5	GGCTCCTGCGGATGGGGCC	5'UTRF.RT-IL6R
	GGGTCTTGCCAGGTGACAC	703R.RT-IL6R
4-10	CCAGTAGTGTCGGGAGCAA	583F.RT-IL6R
	CATCTTTTGTGAGCCCGT	3'UTRR.RT-IL6R
<b>IL6R cDNA sequencing</b>		
1-5	GAGGAGCCCCAGCTCTCC	342F-IL6R
1-3	CTCACCAAGAGCACAGCC	434R-IL6R
9-10	CGACAAGCCTCCAGTGC	1051F-IL6R
5-10	AGTACGGCGGATGCATGC	1207R-IL6R
<b>LIFR cDNA amplification and sequencing</b>		
1-6	AAGGTGAGCCTTCAGAACAATC	5'UTRF.RT-LIFR
	GCAGTTTGTATGGCCAATCAGT	6R.RT-LIFR
6-10	AGGTTTTTCTCAAGATAAAGTGA	6F.RT-LIFR
	CTTTGAAGGACTGGCTTCTG	10R.RT-LIFR
10-15	TTTCGGATTCTGTTGTCTACTGA	10F.RT-LIFR
	TTCTTAACTTTTATGTCAGAACGACCT	15R.RT-LIFR
15-19	GGGAAGACATTCCTGTGGA	15F.RT-LIFR
	CCCCTCCTACAGGGTCATTT	19R.RT-LIFR
19	GGGACTGCACAGGTTATTTACA	19F.RT-LIFR
	CACATGAGAAAACCACAAACA	3'UTRR.RT-LIFR

<b>LIFR cDNA sequencing</b>		
1-6	AAAACAGGTCCCGTTCTTGTATCA	5'UTRintFRT-LIFR
	GTCTGAGCCTACAAGTATCAC	6RintRT-LIFR
6-10	TCTTGGCATTACCAGGCAACT	6FintRT-LIFR
	TCCTCATCTGATGAACACGAT	10RintRT-LIFR
10-15	CGCTCCATGATTGGATATATAG	10FintRT-LIFR
	GGTTTTCAGGCTCTGCATCAGA	15RintRT-LIFR
19	TTACAGACCTCAGGCCAATG	19FintRT-LIFR
<b>OSMR cDNA amplification and sequencing</b>		
1-4	TGGATACAGGGAAGGAGAA	3'UTRF.RT-OSMR
	GTCCTCAAGTACTTTTGAGACAA	4R.RT-OSMR
4-10	GGAAGGGAACAGATTCATG	4F.RT-OSMR
	TGGATGGTTTGTCTAGGTTTT	10R.RT-OSMR
8-14	TGGAGTGAATGGAGTGGTCA	8F.RT-OSMR
	TGAATCAGCATCGAGGAGT	14R.RT-OSMR
14-17	CAAATTGACAACCCGGAAG	14F.RT-OSMR
	GTGCCAGCTCTGCTTCTT	5'UTRR.RT-OSMR
<b>SOCS3 genomic DNA amplification and sequencing</b>		
2	AGGGTTCGGGCACTCAA	2F-SOCS3
	TTCTTGTGCTTGCCATGT	2R-SOCS3
<b>JAK1 genomic DNA amplification and sequencing</b>		
11	CAGCAGACGTTGGCTGTC	11F-JAK1
	CCCCAAGCTGCTCCATC	11R-JAK1
12	ATTGAGGACCCATTCCCAG	12F-JAK1
	GTTCCACTGGCTCCAGAAAC	12R-JAK1
13	CTGGCTTCCCTCAACAG	13F-JAK1
	ACAGCACCAAGTCCC	13R-JAK1
14	CTGTCGTAAGGGGATGAAGG	14F-JAK1
	TCCCAGGACACTCTGGTTTC	14R-JAK1
15	GGGACCAGGTTGGAATAG	15F-JAK1
	CAGCCCTTCTCTGCTGAC	15R-JAK1
16	TCACTGTTCTGGCTGCAGTG	16F-JAK1
	ACAACCTCTGGGAAGCCC	16R-JAK1
17-18	GGGGCTGAGAAGTTGTAGG	17/18F-JAK1
	TACGTGCAGAGAGTGGCG	17/18R-JAK1
19	GACTTCTGTGTGTTCCGTGG	19F-JAK1
	TTGCACTGGCCTTATGACC	19R-JAK1
20	CTTGCTCTCCCATGGTTC	20F-JAK1
	CAAACCAATTACCCAGGACAG	20R-JAK1
21	TCTGCATTATTTAGATGAAAAGTTAGC	21F-JAK1
	TCAGGCCAGAGGAATGAGAC	21R-JAK1
22	TCCTGTAATGTCGGATGGAG	22F-JAK1
	TTAACCAAGCAGAGGGATGG	22R-JAK1
23	ATTTACCTTAATCTGTTTGGC	23F-JAK1
	CAACTCAAGCTGCGAAAAC	23R-JAK1
24	TGAACTAGAGTTGTATCCCATTTTC	24F-JAK1
	ACTTGGGCATTTGTTGCAG	24R-JAK1
<b>JAK2 genomic DNA amplification and sequencing</b>		
12	CAAAGTTCAATGAGTTGACCCC	12F-JAK2
	TGCTAACATCTAACACAAGGTTGG	12R-JAK2
13	TGTATTTTCTTGTTCCTACTTCGTTTC	13F-JAK2
	TTACAATTTTAAAAGCTGCAC	13R-JAK2
14	GAGAAAGTGCATCTTTATTATGGC	14F-JAK2
	CTGACACCTAGCTGTGATCCTG	14R-JAK2
15	TGTTTAGACTCCTACTCTTGCTGTTG	15F-JAK2
	CACAGACTATTTTACATGAATTGGC	15R-JAK2
16	TTCTTCTTAAATCTGTTTGGGG	16F-JAK2
	CCTTTACACCACTGCCCAAG	16R-JAK2
17-18	CCCCTCCAAAATAAAGAAAATAGG	17/18F-JAK2
	AGGGCCCAAATGACATCAAG	17/18R-JAK2
19	GACCAGTGTGGTGCGGG	19R-JAK2
	GAAGGCCTGTCAGATTATGGG	19F-JAK2
20	TTTATTTGTAATTTGCCTTGAAAAC	20F-JAK2
	TTACACAGGATGCCAAACAC	20R-JAK2
21-22	CCCACGTGGACTATAACCATGAC	21/22R-JAK2
	CTGAAACGCAAATAGTTTCAAAGC	21/22F-JAK2
23	GTAGATGTCAGCATAAACCGTATTG	23F-JAK2
	GCCATTGGTGGAGTAGATGC	23R-JAK2
24-25	CCATTGACTGGAGGAAATTGAG	24/25F-JAK2
	TCCACAGCAATGTGAAATATAAAAC	24/25R-JAK2

<b>TYK2 genomic DNA amplification and sequencing</b>		
12-13	GTGGGATGTGGCATCTCTCC	12/13F-TYK2
	CCACAGACACACCCCTCC	12/13R-TYK2
14	GTGTCCGTGGAGGAGGTG	14F-TYK2
	GGAGTGGGTATAAGTCAGGGG	14R-TYK2
15	ACATGCCAAGTCCCTCCC	15F-TYK2
	TCTCGAACTCCTGGGCTCC	15R-TYK2
16-17	GAGCTCTGATTCTGTCCTCTGG	17R-TYK2
	GTTGTCCTTTTCACATTGGCTG	16F-TYK2
18	CTGCCTCTTGGGGAACG	18F-TYK2
	GCTATAGGCATACAGCAGGG	18R-TYK2
19	TTTGTGACTCCCAAGTGTGG	19F-TYK2
	CCAAACTCCTTCCCGACC	19R-TYK2
20	GAGTGGTGCAGGGATTGG	20F-TYK2
	CACAAGGCCACACCCAC	20R-TYK2
21	CTCTGCTGGGCTCAAGGTAG	21F-TYK2
	CAGCCCAAGCTGAAGAGG	21R-TYK2
22	GCTGCTCAGGTCCTGCC	22F-TYK2
	CTACTCCACCCTGCCTGTTC	22R-TYK2
23	GTCTCAGGTGAGGGCTTCAG	23F-TYK2
	TCTCTCCGTCTGTCCTGTC	23R-TYK2
24-25	CGTGCCTGCCTTTCATTG	24/25F-TYK2
	TTGGTTTCATCCTGGAGCAG	24/25R-TYK2
<b>TYK2 genomic DNA sequencing</b>		
22	CGAACCCCGCCCCACTGA	22F-TYK2
	CCAAGTGACCCACGACC	22R-TYK2