

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
In biological process				
protein kinase cascade	13	5.5	2.36	3E-03
JAK-STAT cascade	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
negative regulation of protein metabolism	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
organismal physiological process	61	35.54	1.72	6E-06
immune system process	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
response to stimulus	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
carbohydrate biosynthesis	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
developmental maturation	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

anatomical structure development	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
cell adhesion	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
cell motility	14	4.79	2.92	3E-04
cell migration	7	2.07	3.38	5E-03
locomotion	14	4.79	2.92	3E-04
cell proliferation	20	11.22	1.78	8E-03
phospholipid catabolism	2	0.15	13.33	8E-03
localization of cell	14	4.79	2.92	3E-04
<i>In molecular function</i>				
interferon binding	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
obsolete molecular function	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
enzyme inhibitor activity	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
glutathione peroxidase activity	2	0.09	22.22	3E-03
erythropoietin receptor binding	2	0.07	28.57	2E-03
selenium binding	2	0.12	16.67	5E-03
aldehyde dehydrogenase [NAD(P)+] activity	2	0.14	14.29	8E-03