

Article

A *PDCD1* Role in the Genetic Predisposition to NAFLD-HCC?

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Supplementary Materials:

Table S1. Applied Biosciences Taqman Assays.

SNP ID	Assay ID
<i>MICA</i> rs2596542	C_27301153_10
<i>CD44</i> rs187115	C_779820_10
<i>PDCD1</i> rs7421861	C_26891639_10
<i>PDCD1</i> rs10204525	C_172862_10
<i>PNPLA3</i> rs738409	C_7241_10
<i>TM6SF2</i> rs2596542	C_89463510_10

Table S2. Calculations to estimate the power of our cohorts to evaluate the genetic variation on HCC risk in NAFLD.

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SNP ID	% Prevalence of HCC in NAFLD	MA Allelic F	RR	Power (for detecting effect at $p = 0.05$) with 391 cases and 594 controls	Power (for detecting effect at $p = 0.05$) with 198 cases and 416 controls
Calculations of power to detect an allelic relative risk greater than ≥ 1.3					
<i>PNPLA3</i> <i>rs738409</i>	0.5	0.41 9	1.3	0.8131	0.5774
<i>TM6SF2</i> <i>rs2596542</i>	0.5	0.11 9	1.45	0.8120	0.5843
<i>MICA</i> <i>rs2596542</i>	0.5	0.33 2	1.3	0.7876	0.5517
<i>CD44</i> <i>rs187115</i>	0.5	0.34 4	1.3	0.7930	0.5571
<i>PDCD1</i> <i>rs7421861</i>	0.5	0.33 2	1.3	0.7876	0.5517
<i>PDCD1</i> <i>rs10204525</i>	0.5	0.09 5	1.5	0.8131	0.5870
Calculations of power to detect an allelic relative risk greater than ≥ 1.4					
<i>PNPLA3</i> <i>rs738409</i>	0.5	0.41 9	1.4	0.9552	0.7900
<i>TM6SF2</i> <i>rs2596542</i>	0.5	0.11 9	1.6	0.9563	0.8023
<i>MICA</i> <i>rs2596542</i>	0.5	0.33 2	1.4	0.9446	0.7689
<i>CD44</i> <i>rs187115</i>	0.5	0.34 4	1.4	0.9470	0.7737
<i>PDCD1</i> <i>rs7421861</i>	0.5	0.33 2	1.4	0.9446	0.7689
<i>PDCD1</i> <i>rs10204525</i>	0.5	0.09 5	1.65	0.9485	0.7867
Calculations of power if HCC prevalence was in keeping with that for NAFLD-cirrhosis					
Calculations of power to detect an allelic relative risk greater than ≥ 1.3					
<i>PNPLA3</i> <i>rs738409</i>	2.6	0.41 9	1.3	0.8293	0.5957
<i>TM6SF2</i> <i>rs2596542</i>	2.6	0.11 9	1.45	0.8295	0.6043
<i>MICA</i> <i>rs2596542</i>	2.6	0.33 2	1.3	0.8049	0.5700
<i>CD44</i> <i>rs187115</i>	2.6	0.34 4	1.3	0.8100	0.5754
<i>PDCD1</i> <i>rs7421861</i>	2.6	0.33 2	1.3	0.8049	0.5700
<i>PDCD1</i> <i>rs10204525</i>	2.6	0.09 5	1.5	0.8307	0.6073
Calculations of power to detect an allelic relative risk greater than ≥ 1.4					
<i>PNPLA3</i> <i>rs738409</i>	2.6	0.41 9	1.4	0.9622	0.8070
<i>TM6SF2</i> <i>rs2596542</i>	2.6	0.11 9	1.6	0.9638	0.8207
<i>MICA</i> <i>rs2596542</i>	2.6	0.33 2	1.4	0.9529	0.7868
<i>CD44</i> <i>rs187115</i>	2.6	0.34 4	1.4	0.9550	0.7914
<i>PDCD1</i> <i>rs7421861</i>	2.6	0.33 2	1.4	0.9529	0.7868

<i>PDCD1</i> <i>rs10204525</i>	2.6	0.09 5	1.65	0.9571	0.8060
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Legend: These power calculations were performed comparing 392 cases with 594 controls, or 199 cases with 416 controls, using GPC software (<http://zzz.bwh.harvard.edu/gpc/>) and the case control for discrete traits option. The minor allele frequencies (MAF) for the SNPs in control cases with NAFLD are as described in Supplementary Table 6. We have estimated the prevalence of HCC with a control population like ours to be 0.5%, although in cirrhotic cases this may be as high as 2.6% [1]. Calculations for the two estimates of prevalence, alongside relative risk (RR) of ≥ 1.3 or ≥ 1.4 are shown.

Table S3. Changes in association with TNM Stage.

Table S3A: The decline in BMI through different TNM stages in NAFLD-HCC patients compared to the control group (Newcastle cohort).

	TNM stage	NAFLD (n = 407)	NAFLD-HCC (n = 190)	p-Value
BMI	0	35.031±0.28		
	I		32.38± 0.67	<0.0001 ¹ <0.002 ²
	II		34.11±0.83	
	III		29.99±0.78	
	IV		29.01±1.63	

BMI—body mass index; TNM—Tumour Node Metastases; p-value estimated by Kruskal-Wallis test. In a small number of cases BMI was not available. ¹significance across all stages including controls. ²significance in cancer cases only.

Table S3B: comparison of BMI values between NAFLD and NAFLD-HCC patients according to the cirrhotic changes in their livers.

TNM stage	Non-cirrhotic NAFLD			Cirrhotic NAFLD		
	Control	HCC	Number	Control	HCC	Number
0	34.20		353	36.85		63
I		30.90***	37		32.05*	43
II		33.50	5		34.00	44
III		26.30	28		33.00	27
IV		25.00	7		32.00	8

p-values for TNM Stage I compared to controls. ***<0.0001; *p = 0.014. Mann-Whitney Test.

Table S4. Demographic characteristics of Newcastle cirrhotic and NC NAFLD-HCC cohort.

	Newcastle NAFLD-HCC	All n = 198 (%)	Cirrhosis n = 121 (%)	No-cirrhosis n = 77 (%)	p-Value
Age (years, median)		73	71	76	<0.0001
Gender	Male	157 (79.3)	92 (76.0)	65 (84.4)	0.156
	female	41 (20.7)	29 (24.0)	12 (15.6)	
BMI (median)	All	31.3	33.0	28.6	<0.0001
	TNM I	31.4	32.1	30.9	
	TNM II	34.0	34.0	33.5	
	TNM III	30.0	33.0	26.3	
	TNM IV	28.0	32.0	25.0	
T2DM	absent	60 (30.3)	29 (24.0)	31 (40.3)	0.015*
	present	138 (69.7)	92 (76.0)	46 (59.7)	
Albumin (median)		41.0	39.0	43.0	<0.0001
Bilirubin (median)		12.0	13.0	9.0	<0.0001
PT (median)		13.0	13.0	12.0	<0.0001
Ascites	absent	170 (85.9)	98 (81.0)	72 (93.5)	0.014*
	present	28 (14.1)	23 (19.0)	5 (6.5)	
Encephalopathy	absent	189 (95.5%)	112 (92.6)	77 (100.0)	0.014*

	present	9 (4.5)	9 (7.4)	0 (0.0)	
	Tumour number (med)	2.16 (1)	2.29 (2)	1.95 (1)	0.111
	Tumour size cm (med)	5.65 (4.0)	4.48 (3.5)	7.44 (6.0)	<0.0001
PVT	absent	163 (82.3)	100 (82.6)	63 (81.8)	1.00
	present	35 (17.7)	21 (17.4)	14 (18.2)	
EHD	absent	179 (90.4)	111 (91.7)	68 (88.3)	0.585
	present	19 (9.6)	10 (8.2)	9 (11.7)	
	AFP (median)	3755 (7)	3385 (7)	4340 (6)	0.532
	I	80 (40.4)	43 (35.5)	37 (48.1)	
TNM Stage	II	49 (24.7)	44 (36.4)	5 (6.5)	
	III	55 (27.8)	27 (22.3)	28 (36.4)	<0.0001
	IV	14 (7.1)	7 (5.8)	7 (9.1)	
	0+A	49 (24.7)	34 (27.1)	15 (19.5)	
BCLC Stage	B	30 (15.2)	18 (14.9)	12 (15.6)	
	C	101 (51.0)	57 (47.1)	44 (57.1)	0.522
	D	18 (9.0)	12 (9.9)	6 (7.8)	
	Well	31 (33.3)	11 (33.3)	20 (33.3)	
Histology differentiation	moderate-poor	48 (51.6)	15 (45.5)	33 (55.0)	0.470
	poor	14 (15.1)	7 (21.2)	7 (11.7)	
	Trabecular	48 (55.2)	14 (45.2)	34 (55.7)	
Histology Architecture	Solid/compact	32 (34.8)	11 (35.5)	21 (34.4)	0.562
	Pseudoglandular	5 (5.4)	2 (6.5)	3 (4.9)	
	Mixed/cholangio	7 (7.6)	4 (12.9)	3 (4.9)	
	No subtype	57 (63.3)	18 (58.1)	39 (66.1)	
	SH-HCC	23 (25.6)	11 (35.5)	12 (20.3)	
	Clear Cell	3 (3.3)	1 (3.2)	2 (3.4)	
	Macrotrabecular Massive	0	0	0	
Histology Subtype	Scirrhous	3 (3.3)	1 (3.2)	2 (3.4)	
	Chromophobe	0	0	0	
	Fibrolamellar	3 (3.3)	0	3 (5.1)	0.552
	Neutrophil rich	0	0	0	
	Lymphocyte rich	1 (1.1)	0	1 (1.7)	
	OLTx	6 (3.0)	6 (5.0)	0 (0.0)	
	Resection	12 (6.1)	2 (1.7)	10 (13.0)	
Treatment	Ablation	22 (11.1)	18 (14.9)	4 (5.2)	
	Arterial	85 (42.9)	56 (46.3)	29 (37.7)	<0.0001
	Medical	17 (8.6)	11 (9.1)	6 (7.8)	
	Supportive	56 (28.3)	28 (23.1)	28 (36.4)	

Table S5. Features associated with survival in NAFLD-HCC patients (Newcastle).

Variable	Univariate Analysis		Multivariate Analysis		
	p-Value	HR	p-Value	HR	Confidence
Age	<0.0001	1.034	0.006	1.071	1.020-1.124
Gender	0.717				
BMI	0.010		0.225		
T2DM	0.050	0.709	0.110		
Cirrhosis	0.791				
Tumour Number	<0.0001	1.159	<0.0001	1.356	1.158-1.588
Tumour Size	<0.0001	1.068	0.002	1.122	1.042-1.208
Extra hepatic disease	<0.0001	0.316	0.689		
Portal Vein Thrombus	<0.0001	0.317	0.002	0.207	0.078-0.550
Ascites	<0.0001	0.244	0.163		
Encephalopathy	0.199				
ECOG PST					
	0	<0.0001	0.030		
	1	0.001	0.250	0.051	0.115
					0.013-1.011

	2	0.022	0.395	0.063	0.121	0.013-1.118
	3 (reference)	0.266	0.626	0.319	0.320	0.034-3.007
Prothrombin Time		0.085				
Albumin		<0.0001	0.914	0.097		
Bilirubin		<0.0001	1.109	0.763		
AFP		<0.0001	1.000	0.238		
Histology differentiation	well	0.001		0.004		
	moderate	<0.0001	0.257	0.001	0.161	0.054-0.481
	poor (reference)	0.11	0.597	0.047	0.412	0.172-0.988

Table S6. Genotype frequencies of the candidate SNPs in Newcastle NAFLD and NAFLD-HCC.

		NAFLD Controls		NAFLD-HCC	
		Number (%)	Number (%)	Number (%)	Number (%)
<i>PNPLA3</i> rs738409	CC	170 (40.9%)	67 (33.8%)		
	CG	184 (44.2%)	85 (42.9%)		
	GG	62 (14.9%)	46 (23.2%)		
<i>TM6SF2</i> rs58542926	CC	323 (77.6%)	132 (66.7%)		
	CT	85 (20.4%)	60 (30.3%)		
	TT	8 (1.9%)	6 (3.0%)		
<i>MICA</i> rs2596542	CC	183 (44.0%)	92 (46.9%)		
	TC	190 (45.7%)	89 (45.4%)		
	TT	43 (10.3%)	15 (7.7%)		
<i>CD44</i> rs187115	TT	175 (42.1%)	79 (39.9%)		
	CT	197 (47.4%)	96 (48.5%)		
	CC	44 (10.6%)	23 (11.6%)		
<i>PDCD1</i> rs7421861	AA	180 (43.3%)	126 (63.6%)		
	GA	189 (45.4%)	53 (26.8%)		
	GG	47 (11.3%)	19 (9.6%)		
<i>PDCD1</i> rs10204525	CC	345 (82.9%)	154 (78.6%)		
	TC	66 (15.9%)	38 (19.4%)		
	TT	5 (1.2%)	4 (2.0%)		

Table S7. Dominant, recessive and genotype associations with HCC risk assessed by logistic regression in the Newcastle cohort.

Dominant Model		Identity	p Value	OR
<i>PNPLA3</i>	C>G	rs738409	0.104	1.341
<i>TM6SF2</i>	C>T	rs58542926	3.90E-03	1.737
<i>MICA</i>	T>C	rs2596542	0.535	0.898
<i>CD44</i>	C>T	rs187115	0.484	1.132
<i>PDCD1</i>	A>G	rs7421861	2.195E-06	0.430
<i>PDCD1</i>	C>T	rs10204525	0.185	1.334
Recessive Model				
<i>PNPLA3</i>	C>G	rs738409	0.01094	1.739
<i>TM6SF2</i>	C>T	rs58542926	0.3943	1.594
<i>MICA</i>	T>C	rs2596542	0.3003	0.7229
<i>CD44</i>	C>T	rs187115	0.6841	1.118
<i>PDCD1</i>	A>G	rs7421861	0.5378	0.838
<i>PDCD1</i>	C>T	rs10204525	0.422	1.721
Genotype Model				
<i>PNPLA3</i>	C>G	rs738409	0.02997	
<i>TM6SF2</i>	C>T	rs58542926	0.01546	
<i>MICA</i>	T>C	rs2596542	0.5537	
<i>CD44</i>	C>T	rs187115	0.7653	
<i>PDCD1</i>	A>G	rs7421861	7.837e-6	
<i>PDCD1</i>	C>T	rs10204525	0.3717	

Table S8. Minor Allele Frequency (MAF) for the candidate genes in the Newcastle NAFLD GWAS study, reporting any difference (p value) compared to NAFLD GWAS controls (without NAFLD).

	SNP	Chromosome	maf	p-Value	OR	se
PDCD1	rs7421861	2	0.3548	0.503259	0.9683	0.048125
MICA	rs2596542	6	0.3235	0.102425	1.054	0.032202
CD44	rs187115	11	0.3484	0.798905	1.005	0.019577
TM6SF2	rs58542926	19	0.06636	2.05E-11	1.609	0.070964
PNPLA3	rs738409	22	0.2183	1.45E-49	1.827	0.040716

Table S9. Prevalence of PDCD1rs10204525 SNP in Newcastle NAFLD versus NAFLD-HCC patients — gender comparison.

		Male		Female	
		Control	HCC	Control	HCC
		Number (%)	Number (%)	Number (%)	Number (%)
<i>PDCD1</i> <i>rs10204525</i>	CC	191 (82.3)	128 (82.6)	154 (83.7)	26 (63.4)
	TC	39 (16.8)	24 (15.5)	27 (14.7)	14 (34.1)
	TT	2 (0.9)	3 (1.9)	3 (1.6)	1 (2.4)

Table S10. Linkage disequilibrium analysis for PDCD1 rs7421861 A>G and rs10204525 C>T.

Haplotype	Frequency	Expectation under LE
TG	0	0.030488
CG	0.304878	0.274390
TA	0.1	0.069512
CA	0.595122	0.625610

In phase alleles are TA/CG. R-sq = 0.0487329 D' = 1.

Table S11. Allelic analyses restricted to 353 NAFLD controls and 78 NAFLD-HCC cases without cirrhosis.

Gene	Identity	p Value	OR	Conditioned on PNPLA3 + TM6SF2	
				p Value	OR
PNPLA3	C>G rs738409	0.9086	1.02		
TM6SF2	C>T rs58542926	0.2607	1.34		
MICA	T>C rs2596542	0.8134	1.05	0.8239	1.04
CD44	C>T rs187115	0.2943	1.22	0.386	1.18
PDCD1	A>G rs7421861	5.214e-3	0.56	6.841e-3	0.57
PDCD1	C>T rs10204525	0.1111	1.51	0.159	1.442
Age, Sex, T2DM					
PNPLA3	C>G rs738409	0.6912	1.13		
TM6SF2	C>T rs58542926	0.1895	0.54		
MICA	T>C rs2596542	0.8175	1.08	0.6734	1.15
CD44	C>T rs187115	0.4658	1.27	0.4891	1.26
PDCD1	A>G rs7421861	0.02129	0.46	0.02487	0.47
PDCD1	C>T rs10204525	0.1524	1.83	0.1334	1.92

Table S12. Genotype frequencies of the candidate SNPs in Berne and Milan NAFLD and NAFLD-HCC cohorts.

		Berne				Milan			
		NAFLD controls		NAFLD-HCC		NAFLD controls		NAFLD-HCC	
		Number	(%)	Number	(%)	Number	(%)	Number	(%)
<i>PNPLA3</i> <i>rs738409</i>	CC	22	(28.9%)	25	(29.8%)	26	(25.5%)	23	(21.1%)
	CG	30	(39.5%)	33	(39.3%)	42	(41.2%)	48	(44.0%)
	GG	24	(31.6%)	26	(31.0%)	34	(33.3%)	38	(34.9%)
<i>TM6SF2</i>	CC	58	(76.3%)	61	(72.6%)	86	(84.3%)	91	(83.5%)

rs58542926	CT	12	(15.8%)	20	(23.8%)	16	(15.7%)	16	(14.7%)
	TT	6	(7.9%)	3	(3.6%)	0	(0.0%)	2	(1.8%)
PDCD1 rs7421861	AA	62	(81.6%)	65	(78.3%)	82	(80.4%)	94	(86.2%)
	GA	14	(18.4%)	17	(20.5%)	17	(16.7%)	15	(13.8%)
	GG	0	(0.0%)	1	(1.2%)	3	(2.9%)	0	(0.0%)
PDCD1 rs10204525	CC	36	(47.4%)	40	(47.6%)	47	(46.1%)	45	(41.3%)
	TC	34	(44.7%)	34	(40.5%)	45	(44.1%)	49	45.0%
	TT	6	(7.9%)	10	(11.9%)	10	(9.8%)	15	13.8%

Table S13. Statistical analysis of the candidate SNPs in Berne and Milan NAFLD and NAFLD-HCC cohorts.

Gene	Identity	Berne pvalue	OR	Milan	
				p value	OR
PNPLA3	C>G	rs738409	0.9069	0.98	1.11
TM6SF2	C>T	rs58542926	0.9449	0.98	1.18
PDCD1	A>G	rs7421861	0.7187	1.09	1.21
PDCD1	C>T	rs10204525	0.5043	1.28	0.60

Table S14. Table shows the eQTL effect size and significance for PDCD1 rs7421861 and indicated gene expression in specific tissues or cell types.

rs7421861				
Gene	Symbol	p-Value (-log10)	Effect size	Tissue/Cell type
ENSG00000154252	GAL3ST2	2.106816573	0.893287	macrophage_Salmonella
ENSG00000188011	RTP5	3.34931761	-0.593432	monocyte_R848
ENSG00000188389	PDCD1	4.672716691	-0.521107	monocyte_R848
ENSG00000204099	NEU4	3.122583154	0.58719	monocyte
ENSG00000204099	NEU4	6.98505965	-0.840789	macrophage_Listeria
ENSG00000215692	AC114730.8	1.574226201	0.551741	macrophage_Salmonella
ENSG00000224272	AC114730.3	2.768008245	-0.525108	monocyte_R848
ENSG00000224272	AC114730.3	2.441329822	-0.540187	macrophage_Listeria
ENSG00000235151	AC131097.3	1.996448999	0.567401	monocyte
ENSG00000235151	AC131097.3	1.513586525	0.520945	macrophage_Salmonella

Table S15. Table shows the eQTL effect size and significance for PDCD1 rs10204525 and indicated gene expression in specific tissues or cell types.

rs10204525				
Gene	Symbol	p-Value (-log10)	Effect Size	Tissue/Cell Type
ENSG00000235351	AC114730.4	1.773549611	-0.558197	Tfh_memory
ENSG00000224272	AC114730.3	4.994952543	2.04677	CD4_T-cell_anti-CD3-CD28
ENSG00000224272	AC114730.3	2.762056834	1.19196	CD8_T-cell_anti-CD3-CD28
ENSG00000224272	AC114730.3	6.825815129	1.11348	monocyte_Pam3CSK4
ENSG00000224272	AC114730.3	2.94709454	1.07584	Th1_memory
ENSG00000224272	AC114730.3	5.839852731	1.07347	monocyte_LPS
ENSG00000224272	AC114730.3	2.781146899	0.998949	CD8_T-cell_naive
ENSG00000224272	AC114730.3	6.697188712	0.977589	monocyte_IAV
ENSG00000224272	AC114730.3	2.732894008	0.966898	Th1-17_memory
ENSG00000224272	AC114730.3	6.180712769	0.960048	monocyte_naive
ENSG00000224272	AC114730.3	5.872186001	0.885419	monocyte_R848
ENSG00000224272	AC114730.3	2.037487186	0.861265	Tfh_memory
ENSG00000224272	AC114730.3	1.737084013	0.763997	Th2_memory
ENSG00000180902	D2HGDH	7.181600555	0.809552	monocyte_LPS
ENSG00000180902	D2HGDH	7.951499932	0.802942	monocyte_Pam3CSK4
ENSG00000180902	D2HGDH	7.659242672	0.681617	monocyte_R848
ENSG00000180902	D2HGDH	7.443067024	0.660345	monocyte_naive
ENSG00000180902	D2HGDH	7.577838757	0.63055	monocyte_IAV

ENSG00000234793	AC114730.2	1.655509481	0.590658	CD4_T-cell_anti-CD3-CD28
ENSG00000234793	AC114730.2	3.890819823	0.514726	monocyte_R848
ENSG00000154252	GAL3ST2	6.26525936	1.22017	monocyte_Pam3CSK4
ENSG00000154252	GAL3ST2	4.815183692	1.14643	monocyte_LPS
ENSG00000154252	GAL3ST2	3.441375417	1.13322	CD8_T-cell_anti-CD3-CD28
ENSG00000154252	GAL3ST2	5.18360225	0.978941	monocyte_R848
ENSG00000154252	GAL3ST2	4.402815081	0.898332	monocyte_IAV
ENSG00000154252	GAL3ST2	5.088239593	0.884157	monocyte_naive
ENSG00000154252	GAL3ST2	1.53802752	0.54554	Tfh_memory
ENSG00000215023	AC131097.1	6.281411959	1.09421	monocyte_R848
ENSG00000215023	AC131097.1	6.676743774	0.963099	monocyte_Pam3CSK4
ENSG00000215023	AC131097.1	5.262106371	0.899721	monocyte_LPS
ENSG00000215023	AC131097.1	4.248800216	0.767043	monocyte_IAV
ENSG00000215023	AC131097.1	4.802168307	0.503798	monocyte_naive
ENSG00000204099	NEU4	4.327127571	1.71814	CD4_T-cell_anti-CD3-CD28
ENSG00000204099	NEU4	3.486851679	1.42685	CD8_T-cell_anti-CD3-CD28
ENSG00000204099	NEU4	4.891194895	1.2448	Th2_memory
ENSG00000204099	NEU4	3.951900173	1.22149	Tfh_memory
ENSG00000204099	NEU4	2.57289707	1.10052	monocyte_CD16_naive
ENSG00000204099	NEU4	4.452547752	1.0358	Th17_memory
ENSG00000204099	NEU4	5.76352824	0.942486	monocyte_Pam3CSK4
ENSG00000204099	NEU4	5.6025345	0.88854	monocyte_naive
ENSG00000204099	NEU4	4.47954398	0.846016	monocyte_LPS
ENSG00000204099	NEU4	5.110591838	0.772023	monocyte_IAV
ENSG00000204099	NEU4	2.110257502	0.756715	Th1_memory
ENSG00000204099	NEU4	4.958398114	0.684009	monocyte_R848
ENSG00000204099	NEU4	2.096251471	0.585624	Th1-17_memory
ENSG00000235151	AC131097.3	2.774155935	0.975154	CD4_T-cell_anti-CD3-CD28
ENSG00000235151	AC131097.3	5.655419114	0.837051	monocyte_naive
ENSG00000235151	AC131097.3	4.160501213	0.717407	monocyte_LPS
ENSG00000235151	AC131097.3	2.772578677	0.709116	monocyte_CD16_naive
ENSG00000235151	AC131097.3	4.503774923	0.706194	monocyte_Pam3CSK4
ENSG00000235151	AC131097.3	2.185641181	0.558619	Th17_memory
ENSG00000188389	PDCD1	8.853481275	0.964331	monocyte_Pam3CSK4
ENSG00000188389	PDCD1	8.408514665	0.96187	monocyte_LPS
ENSG00000188389	PDCD1	9.498040203	0.944919	monocyte_naive
ENSG00000188389	PDCD1	2.345629946	0.916861	monocyte_CD16_naive
ENSG00000188389	PDCD1	5.26611451	0.738328	CD4_T-cell_anti-CD3-CD28
ENSG00000188389	PDCD1	7.349027457	0.735695	monocyte_R848
ENSG00000188389	PDCD1	4.761554931	0.591227	CD8_T-cell_anti-CD3-CD28
ENSG00000188389	PDCD1	6.33987668	0.581108	monocyte_IAV
ENSG00000188011	RTP5	11.53507548	1.25191	monocyte_R848
ENSG00000188011	RTP5	11.47059916	1.15669	monocyte_Pam3CSK4
ENSG00000188011	RTP5	9.398728969	1.10802	monocyte_LPS
ENSG00000188011	RTP5	2.879666313	1.03183	CD8_T-cell_anti-CD3-CD28
ENSG00000188011	RTP5	8.25559435	0.908154	monocyte_IAV
ENSG00000188011	RTP5	8.655446615	0.632605	monocyte_naive
ENSG00000261186	LINC01238	1.646953613	-0.511456	Th1-17_memory

Reference

1. Ascha, M.S.; Hanouneh, I.A.; Lopez, R.; Tamimi, T.A.; Feldstein, A.F.; Zein, N.N. The incidence and risk factors of hepatocellular carcinoma in patients with nonalcoholic steatohepatitis. *Hepatology* **2010**, *51*, 1972-1978.