

Supplementary Table S1: Relationship with Scheuer score in GSE84044

	Scheuer Score / Necroinflammatory Activity										p-value
	Grade 0		Grade 1		Grade 2		Grade 3		Grade 4		
	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%	
PCM1-D	36	40.90%	28	31.80%	19	21.60%	3	3.40%	2	2.30%	<0.001
PCM1-U	1	2.80%	5	13.90%	15	41.70%	12	33.30%	3	8.30%	

Grade 0: portal/periportal activity (PPA) none or minimal, lobular activity (LA) none; Grade 1: PPA portal inflammation, LA inflammation but no necrosis; Grade 2: PPA mild piecemeal necrosis, LA focal necrosis or acidophil bodies; Grade 3: PPA moderate piecemeal necrosis, LA severe focal cell damage; Grade 4: PPA severe piecemeal necrosis, LA damage includes bridging necrosis

	Scheuer Score / Fibrosis and Cirrhosis										p-value
	Grade 0		Grade 1		Grade 2		Grade 3		Grade 4		
	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%	
PCM1-D	42	47.70%	18	20.50%	21	23.90%	5	5.70%	2	2.30%	<0.001
PCM1-U	1	2.80%	2	5.60%	12	33.30%	13	36.10%	8	22.20%	

Grade 0: Fibrosis (F) none; Grade 1: F enlarged, fibrotic portal tracts; Grade 2: F periportal or portal-portal septa but intact architecture; Grade 3: F fibrosis with architectural distortion but no obvious cirrhosis; Grade 4: F probable or definite cirrhosis

Supplementary Table S2 Overrepresentation among 176 gene panel via PANTHER (biological process)

GO <u>Biological Process</u> Complete	GO ID	Fold Enrichment	p value
regulation of mitotic metaphase/anaphase transition	GO:0030071	13.98	0.00822
chemokine-mediated signaling pathway	GO:0070098	13.2	0.00036
neutrophil chemotaxis	GO:0030593	12.52	0.00307
mitotic spindle organization	GO:0007052	12.04	0.00413
killing of cells of other organism	GO:0031640	11.3	0.00659
mitotic sister chromatid segregation	GO:0000070	10.93	0.000361
antimicrobial humoral immune response mediated by antimicrobial peptide	GO:0061844	10.12	0.00329
cell cycle G1/S phase transition	GO:0044843	8.41	0.015
mitotic prometaphase	GO:0000236	6.81	0.0253
mitotic cell cycle phase transition	GO:0044772	5.38	0.0111
cell division	GO:0051301	4.91	2.44E-05
regulation of cell adhesion	GO:0030155	3.47	0.00794
response to bacterium	GO:0009617	3.29	0.0324
regulation of cell population proliferation	GO:0042127	2.46	0.00547
regulation of multicellular organismal development	GO:2000026	2.19	0.0212
system development	GO:0048731	1.72	0.0152
positive regulation of cellular process	GO:0048522	1.6	0.0303

Supplementary Table S3: Cibersort based immune cell fractions

Cell Type	GSE83148			GSE84044			GSE65359			RANKSUM***
	Fold Dif. (U-D)*	Adjusted p**	Rank	Fold Dif. (U-D)*	Adjusted p**	Rank	Fold Dif. (U-D)*	Adjusted p**	Rank	
Macrophages M1	0.114921	4.97E-12	1	0.104081	1.20E-11	1	0.094086	3.12E-06	1.5	3.5
T cells gamma delta	0.074287	3.27E-05	3	0.072302	2.35E-06	2	0.083591	3.12E-06	1.5	6.5
T cells regulatory (Tregs)	-0.02179	2.83E-05	2	-0.0217	2.39E-05	4	-0.02074	0.000456	3	9
Neutrophils	-0.0148	0.000224	5.5	-0.01759	1.51E-05	3	-0.01499	0.00371	4	12.5
Mast cells resting	-0.02742	7.16E-05	4	-0.02007	0.000766	5	-0.01907	0.018482	5.5	14.5
T cells CD4 naive	-0.02232	0.000224	5.5	-0.0226	0.001022	6	-0.024	0.018482	5.5	17
Mast cells activated	0.016651	0.006123	7	0.015993	0.007288	10	0.021127	0.032138	7.5	24.5
T cells CD8	0.031053	0.016941	12	0.045602	0.003301	7	0.039411	0.039486	9	28
Plasma cells	0.017459	0.014917	11	0.019663	0.007288	10	0.023444	0.032138	7.5	28.5
T cells follicular helper	0.015767	0.008299	8	0.013245	0.011093	12	0.013039	0.134801	10	30
NK cells activated	-0.01729	0.010251	10	-0.01768	0.004743	8	-0.0133	0.184301	12	30
Dendritic cells resting	0.020762	0.008722	9	0.020295	0.007288	10	0.011482	0.232201	13.5	32.5
Macrophages M0	0.013035	0.073013	13	0.014576	0.026025	13	0.014452	0.159462	11	37
Macrophages M2	0.009749	0.184636	14	0.012304	0.086664	14	0.014553	0.232201	13.5	41.5
B cells naive	-0.00111	0.423248	15	-0.00101	0.429288	15	0.000743	0.915693	15	45

Cell types with 0 fractions in more than %50 of the samples' were excluded

*Fold difference was calculated by subtraction of mean fraction of PCM1-D group from mean fraction of PCM1-U group

** Student's t-test based p values were adjusted using Benjamini Hochberg method.

*** "rank" indicates the rank of adjusted p value, "RANKSUM" is the sum of the ranks from three datasets

Supplementary Table S4: GSEA results of the curated liver cancer related gene sets between PCM1-U and PCM1-D groups

Enriched Geneset Name	GSE83148				GSE84044			
	ES	NES	NOM p-val	FDR q-val	ES	NES	NOM p-val	FDR q-val
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2	0.661864	1.75598	0	0.005025	0.664639	1.774459	0	0
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM1	0.534732	1.743875	0	0.003141	0.545578	1.763564	0	0.00063
BOYALT_LIVER_CANCER_SUBCLASS_G3_UP	0.637219	1.66648	0	0.009228	0.646725	1.690628	0	0.002579
LEE_LIVER_CANCER_SURVIVAL_DN	0.699302	1.657646	0.00202	0.007408	0.709841	1.67129	0	0.003189
LEE_LIVER_CANCER_E2F1_UP	0.71679	1.660932	0.002024	0.008136	0.738627	1.721376	0	0.001759
HOSHIDA_LIVER_CANCER_SUBCLASS_S1	0.741411	1.638775	0	0.006771	0.744788	1.664884	0	0.003453
MARTORIATI_MDM4_TARGETS_FETAL_LIVER_UP	0.42286	1.611421	0.004107	0.009433	0.428096	1.642822	0	0.004225
HOSHIDA_LIVER_CANCER_SURVIVAL_UP	0.776975	1.601924	0	0.009615	0.767106	1.622994	0	0.005642
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM6	0.575014	1.617768	0.005929	0.009366	0.583005	1.612019	0.003899	0.005062
VILLANUEVA_LIVER_CANCER_KRT19_UP	0.704284	1.571792	0.004016	0.013037	0.715163	1.60189	0	0.0059
HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_UP	0.731084	1.585396	0.00198	0.010807	0.741896	1.632933	0	0.004946
SERVITJA_LIVER_HNF1A_TARGETS_UP	0.637742	1.556358	0.00409	0.013685	0.652335	1.579946	0.002008	0.006629
CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN	0.75385	1.548381	0.008048	0.015115	0.751845	1.571491	0	0.007393
LEE_LIVER_CANCER_MYC_E2F1_UP	0.742595	1.54601	0.004032	0.015113	0.761261	1.595766	0	0.006476
LEE_LIVER_CANCER_DENA_UP	0.748118	1.570467	0.004016	0.012566	0.746142	1.584371	0.002004	0.006736
WOO_LIVER_CANCER_RECURRENCE_UP	0.812587	1.527697	0	0.017641	0.810137	1.546168	0	0.010427
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_U P	0.825271	1.48445	0.001996	0.025768	0.832444	1.479867	0	0.02598

Supplementary Table S5: Genes that are significantly related to overall survival in GSE14520

Gene	Probeset	HR	Cox p
NTS	206291_at	1.136602	0.000377
SULT1C2	211470_s_at	1.223927	0.00107
MAFF	36711_at	1.253452	0.001977
PHLDA2	209803_s_at	1.23706	0.002095
SPP1	209875_s_at	1.143059	0.003081
SULT1C2	205342_s_at	1.193248	0.004022
BICC1	213429_at	1.196197	0.007116
KIF11	204444_at	1.402865	0.007119
CD24	208650_s_at	1.165789	0.010313
TOP2A	201291_s_at	1.213884	0.010848
GLRB	205280_at	1.578242	0.011776
CXCR4	217028_at	1.256456	0.01545
KRT19	201650_at	1.176433	0.018503
NCAPG	218663_at	1.360636	0.018947
KIF20A	218755_at	1.286384	0.022774
CD24	266_s_at	1.154963	0.02361
DLK1	209560_s_at	1.067821	0.029951
CXCL8	202859_x_at	1.13132	0.034523
ARG2	203946_s_at	1.196763	0.035267
DLGAP5	203764_at	1.263921	0.042502
CXCL13	205242_at	0.798521	0.044972
TOP2A	201292_at	1.17908	0.048795