

### **S1. Scoring method for liver tissue sections after H&E and immunohistochemistry.**

All slides were imaged using a Leica DMR microscope (Leica Biosystems, Newcastle, UK) equipped with a Leica DFC300 FX camera (Leica Biosystems, Newcastle, UK). Five high power fields were randomly selected for each case from the lobular region and the number of MPO positive cells was counted in each field. H&E stained slides were scored using a routine system with several changes, for neutrophil clustering (0 = none; 1 = occasional, found after very scrupulous search at high magnification (400×); 2 = scattered, easily seen at 100× magnification; 3 = scattered in most lobules; 4 many neutrophil clusters in close proximity on the verge of confluence; 5 = dense confluent sheets), apoptosis or necrosis (0 = absent; 1 = 1-2 apoptotic bodies per 200× magnification field (highest number per field recorded); 3 = focal hepatocyte necrosis, 1-2 foci per 200× magnification field (highest number per field recorded); 4 = 3 or more foci per 200× magnification field (highest number per field recorded); 5 = focal confluent hepatocellular necrosis; 6 = multiple foci of confluent necrosis; 7 = areas of necrotic parenchyma more extensive than the viable parenchyma in the sample examined; 8 = a limited amount of viable parenchyma is identified), mitosis (number of mitoses in 10 HPF at 400× magnification), canalicular cholestasis (0 = none; 1 = mild; 2 = moderate; 3 = severe), ductular cholestasis (0 = none; 1 = mild; 2 = moderate; 3 = severe), and signs of cholangitis (0 = absent; 1 = present). Steatosis was assessed as large droplet steatosis (a single large steatotic vacuole pushing the hepatocyte nucleus to the periphery), and small droplet steatosis (one or more small cytoplasmic vacuoles mostly associated with a centrally placed nucleus) as two separate yet identical scores (0 = none; 1 = < 26%; 2 = 26-50%; 3 = 51-75%; 4 = > 75%). Large droplet steatosis was scored first. The small droplet steatosis was assessed afterwards, this second score representing the percentage of hepatocytes without large droplet steatosis. Stains were assessed by a Liver

Histopathology Fellow (O.P.) who was blinded to the clinical data. All counts were performed using the ImageJ software (Bethesda, Maryland, USA).

**S2:** Full list of canonical GSEA pathways, a total of 123 pathways, that were considered significantly down-regulated in NMP compared to CS in the pre-reperfusion stage, based on the cut-off value of <25% false discovery rate (FDR). NES: Normalised enrichment score.

NAME	NES	FDR q-val
REACTOME DNA REPLICATION	-2.29613	0
REACTOME MITOTIC M M G1 PHASES	-2.2940412	0
PID FOXM1PATHWAY	-2.232673	0
REACTOME MITOTIC PROMETAPHASE	-2.1544688	0
REACTOME CELL CYCLE CHECKPOINTS	-2.1525562	0
REACTOME CELL CYCLE MITOTIC	-2.1444168	6.22E-04
PID AURORA B PATHWAY	-2.1330037	7.09E-04
REACTOME G1 S TRANSITION	-2.1107106	7.70E-04
REACTOME DEFENSINS	-2.0819955	0.001085643
PID PLK1 PATHWAY	-2.0603943	0.002339838
REACTOME MITOTIC G1 G1 S PHASES	-2.047034	0.003012222
REACTOME KINESINS	-2.0140617	0.004397905
REACTOME G2 M CHECKPOINTS	-2.006888	0.004809324
REACTOME PHOSPHORYLATION OF CD3 AND TCR ZETA CHAINS	-1.9521085	0.011367376
REACTOME ADP SIGNALLING THROUGH P2RY12	-1.935871	0.014830092
REACTOME IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	-1.9245734	0.016770834
REACTOME CELL CYCLE	-1.9222678	0.016444638
REACTOME FORMATION OF FIBRIN CLOT CLOTTING CASCADE	-1.9187808	0.016228056
KEGG CELL CYCLE	-1.9104751	0.018110206
PID IL2 1PATHWAY	-1.9020989	0.020119123
REACTOME REGULATION OF MITOTIC CELL CYCLE	-1.8872261	0.023610713
BIOCARTA RANMS PATHWAY	-1.8836989	0.023892116
KEGG FATTY ACID METABOLISM	-1.880491	0.023552239
REACTOME APC CDC20 MEDIATED DEGRADATION OF NEK2A	-1.8738097	0.024071764
REACTOME TRANSLOCATION OF ZAP 70 TO IMMUNOLOGICAL SYNAPSE	-1.8733943	0.023158072
REACTOME GROWTH HORMONE RECEPTOR SIGNALING	-1.8730614	0.022313401
KEGG LEISHMANIA INFECTION	-1.8662692	0.023038197
REACTOME G1 S SPECIFIC TRANSCRIPTION	-1.8614343	0.023506477
REACTOME G BETA GAMMA SIGNALING THROUGH PI3KGAMMA	-1.8549144	0.025254514
REACTOME RESPIRATORY ELECTRON TRANSPORT	-1.8476763	0.027168
REACTOME APC C CDC20 MEDIATED DEGRADATION OF CYCLIN B	-1.824076	0.035216954
REACTOME E2F MEDIATED REGULATION OF DNA REPLICATION	-1.8183917	0.03586717
REACTOME S PHASE	-1.8183115	0.03485424
KEGG VALINE LEUCINE AND ISOLEUCINE DEGRADATION	-1.81019	0.037253827
BIOCARTA BLYMPHOCYTE PATHWAY	-1.8001733	0.041157354
REACTOME PD1 SIGNALING	-1.7944977	0.04307159
BIOCARTA AHSP PATHWAY	-1.7938621	0.042473935
REACTOME APC C CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS	-1.7888354	0.043702405
REACTOME COMMON PATHWAY	-1.7791827	0.04733705
REACTOME ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS	-1.7711408	0.050520085
PID AP1 PATHWAY	-1.7706399	0.049589064
REACTOME THROMBOXANE SIGNALING THROUGH TP RECEPTOR	-1.7698544	0.04873131
BIOCARTA EPHA4 PATHWAY	-1.7698401	0.047598023
REACTOME TANDEM PORE DOMAIN POTASSIUM CHANNELS	-1.768912	0.046885736
REACTOME SYNTHESIS OF DNA	-1.766471	0.04711265
BIOCARTA CSK PATHWAY	-1.7623891	0.048130058
REACTOME CYCLIN A B1 ASSOCIATED EVENTS DURING G2 M TRANSITION	-1.7594842	0.048666183
KEGG ALLOGRAFT REJECTION	-1.7565793	0.04969094
REACTOME APC C CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC C CDH1 TARGETED PROTEINS IN LATE MITOSIS EARLY G1	-1.7521992	0.051198844
REACTOME UNWINDING OF DNA	-1.7511548	0.050795645
PID CMYB PATHWAY	-1.7503731	0.05030583
REACTOME RESPIRATORY ELECTRON TRANSPORT ATP SYNTHESIS BY CHEMIOSMOTIC COUPLING AND HEAT PRODUCTION BY UNCOUPLING PROTEINS	-1.7482016	0.050384436
REACTOME REGULATION OF IFNG SIGNALING	-1.7468873	0.050391123
REACTOME M G1 TRANSITION	-1.7387816	0.053739294
REACTOME ACTIVATION OF THE PRE REPLICATIVE COMPLEX	-1.7358578	0.05448803
PID IL12 2PATHWAY	-1.7344279	0.0543796
REACTOME INHIBITION OF THE PROTEOLYTIC ACTIVITY OF APC C REQUIRED FOR THE ONSET OF ANAPHASE BY MITOTIC SPINDLE CHECKPOINT COMPONENTS	-1.7341126	0.0535347
REACTOME DNA STRAND ELONGATION	-1.7283843	0.055606063
KEGG ARGININE AND PROLINE METABOLISM	-1.71155	0.065332614
KEGG TRYPTOPHAN METABOLISM	-1.710929	0.06466091
REACTOME G PROTEIN ACTIVATION	-1.7078817	0.066033095
REACTOME SIGNAL AMPLIFICATION	-1.7034291	0.06820412
BIOCARTA TCRA PATHWAY	-1.7010832	0.068743795
KEGG RENIN ANGIOTENSIN SYSTEM	-1.7005799	0.06790059
SA REG CASCADE OF CYCLIN EXPR	-1.6982277	0.07237005
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	-1.6900392	0.073106125
KEGG AUTOIMMUNE THYROID DISEASE	-1.6863005	0.07456936
REACTOME NUCLEAR RECEPTOR TRANSCRIPTION PATHWAY	-1.6851524	0.074398845
REACTOME ASSEMBLY OF THE PRE REPLICATIVE COMPLEX	-1.6846893	0.07359138
REACTOME MHC CLASS II ANTIGEN PRESENTATION	-1.6709789	0.08317746
PID IL12_STAT4PATHWAY	-1.6657766	0.08641996
KEGG HEMATOPOIETIC CELL LINEAGE	-1.6650457	0.085831605
BIOCARTA NKT PATHWAY	-1.6497651	0.09844879
REACTOME PHOSPHORYLATION OF THE APC C	-1.6422149	0.10361172

NAME	NES	FDR q-val
BIOCARTA IL2RB PATHWAY	-1.6386422	0.10557376
BIOCARTA CCR5 PATHWAY	-1.6384279	0.10431379
SA MMP CYTOKINE CONNECTION	-1.6374986	0.10384191
KEGG DRUG METABOLISM CYTOCHROME P450	-1.6199338	0.1207039
KEGG GLUTATHIONE METABOLISM	-1.6129658	0.12652901
REACTOME INITIAL TRIGGERING OF COMPLEMENT	-1.6110873	0.12733056
REACTOME COMPLEMENT CASCADE	-1.6110547	0.1257892
REACTOME MITOCHONDRIAL FATTY ACID BETA OXIDATION	-1.6085422	0.12702975
BIOCARTA MCM PATHWAY	-1.6032194	0.13148572
BIOCARTA RB PATHWAY	-1.5924413	0.14217252
KEGG COMPLEMENT AND COAGULATION CASCADES	-1.5915059	0.1416344
BIOCARTA MONOCYTE PATHWAY	-1.5796223	0.15480086
REACTOME PROSTACYCLIN SIGNALLING THROUGH PROSTACYCLIN RECEPTOR	-1.578742	0.15403664
REACTOME ORC1 REMOVAL FROM CHROMATIN	-1.5750569	0.15706544
PID E2F PATHWAY	-1.5708511	0.16088429
BIOCARTA COMP PATHWAY	-1.5702333	0.15993011
REACTOME RECYCLING OF BILE ACIDS AND SALTS	-1.5696535	0.158868
KEGG ASTHMA	-1.5675828	0.1598575
BIOCARTA TH1TH2 PATHWAY	-1.5598512	0.16877984
PID ATR PATHWAY	-1.559401	0.16752253
BIOCARTA DC PATHWAY	-1.5591149	0.16618778
REACTOME GLUTATHIONE CONJUGATION	-1.5457652	0.18218002
REACTOME METABOLISM OF NUCLEOTIDES	-1.5434095	0.18329805
BIOCARTA ASBCELL PATHWAY	-1.5407579	0.18496957
KEGG GRAFT VERSUS HOST DISEASE	-1.5391943	0.185307
REACTOME DEGRADATION OF THE EXTRACELLULAR MATRIX	-1.5382034	0.18494456
PID NFAT TFPATHWAY	-1.5374179	0.1840864
REACTOME BRANCHED CHAIN AMINO ACID CATABOLISM	-1.534096	0.18681887
KEGG ARACHIDONIC ACID METABOLISM	-1.5339826	0.18522206
PID IL6 7PATHWAY	-1.5328293	0.18510984
KEGG TYPE I DIABETES MELLITUS	-1.5271368	0.19147868
KEGG DNA REPLICATION	-1.5227566	0.19635348
REACTOME ADP SIGNALLING THROUGH P2RY1	-1.5199224	0.1986063
PID ALK2PATHWAY	-1.5163498	0.20207061
REACTOME REPAIR SYNTHESIS FOR GAP FILLING BY DNA POL IN TC NER	-1.5118651	0.20685416
REACTOME SIGNALING BY BMP	-1.5069265	0.21231881
REACTOME INWARDLY RECTIFYING K CHANNELS	-1.5035547	0.215813
REACTOME CONVERSION FROM APC C CDC20 TO APC C CDH1 IN LATE ANAPHASE	-1.5016005	0.21638788
REACTOME GENERATION OF SECOND MESSENGER MOLECULES	-1.4938353	0.22652157
BIOCARTA ETC PATHWAY	-1.4856122	0.23820293
REACTOME G PROTEIN BETA GAMMA SIGNALLING	-1.4853015	0.23656961
BIOCARTA AKAP95 PATHWAY	-1.4848385	0.23536421
REACTOME METABOLISM OF AMINO ACIDS AND DERIVATIVES	-1.4846997	0.23358503
KEGG INTESTINAL IMMUNE NETWORK FOR IGA PRODUCTION	-1.4831004	0.23422723
REACTOME POTASSIUM CHANNELS	-1.4808972	0.23546265
REACTOME TCA CYCLE AND RESPIRATORY ELECTRON TRANSPORT	-1.4729375	0.2474483
REACTOME G ALPHA I SIGNALLING EVENTS	-1.4723016	0.24654138
PID TCRCALCIUMPATHWAY	-1.4710652	0.24660696
REACTOME CYCLIN E ASSOCIATED EVENTS DURING G1 S TRANSITION	-1.4666383	0.24999736

**S3:** Full list of canonical GSEA pathways, a total of 74 pathways, that were considered significantly down-regulated in NMP compared to CS in the post-reperfusion stage, based on the cut-off value of <25% false discovery rate (FDR). NES: Normalised enrichment score

NAME	NES	FDR q-val
PID_PLK1_PATHWAY	-2.1062422	991E-04
REACTOME_DEFENSINS	-2.0898297	0.001933677
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	-2.0372832	0.00414583
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	-2.0353913	0.003109372
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	-1.9885366	0.007984079
PID_AURORA_B_PATHWAY	-1.9449568	0.016328156
REACTOME_GLUTATHIONE_CONJUGATION	-1.905502	0.0318719
REACTOME_PHASE_II_CONJUGATION	-1.9022944	0.029057624
BIOCARTA_STEM_PATHWAY	-1.8958164	0.028671328
REACTOME_KINESINS	-1.8827841	0.03202401
BIOCARTA_IL17_PATHWAY	-1.882609	0.029112738
KEGG_GLUTATHIONE_METABOLISM	-1.8817769	0.027239444
BIOCARTA_ERYTH_PATHWAY	-1.87452	0.028037656
PID_FOXM1PATHWAY	-1.8614515	0.031779926
BIOCARTA_NKT_PATHWAY	-1.859673	0.030679483
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	-1.8226315	0.050665352
KEGG_HEMATOPOIETIC_CELL_LINEAGE	-1.8017666	0.061762292
REACTOME_MITOTIC_PROMETAPHASE	-1.798228	0.06086322
REACTOME_COMMON_PATHWAY	-1.7979599	0.057711057
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	-1.790865	0.06081692
BIOCARTA_MCM_PATHWAY	-1.7816662	0.06542463
KEGG_CELL_CYCLE	-1.7813783	0.06266661
REACTOME_G2_M_CHECKPOINTS	-1.7719921	0.06750453
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	-1.75483	0.07948689
SA_REG_CASCADE_OF_CYCLIN_EXPR	-1.7482476	0.08262195
PID_AMB2_NEUTROPHILS_PATHWAY	-1.743144	0.08422391
REACTOME_MITOTIC_M_M_G1_PHASES	-1.738372	0.085475355
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	-1.7379984	0.082798846
REACTOME_DNA_REPLICATION	-1.7327751	0.08415706
BIOCARTA_FIBRINOLYSIS_PATHWAY	-1.7312906	0.08270144
REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	-1.7256606	0.08513527
BIOCARTA_INFLAM_PATHWAY	-1.7252083	0.08291531
SA_MMP_CYTOKINE_CONNECTION	-1.716011	0.08895741
KEGG_ARACHIDONIC_ACID_METABOLISM	-1.6985717	0.10409312
KEGG_FATTY_ACID_METABOLISM	-1.6965761	0.10303425
REACTOME_CELL_CYCLE_MITOTIC	-1.6954285	0.101377405
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	-1.6948214	0.099227265
REACTOME_BIOLOGICAL_OXIDATIONS	-1.68678	0.10534956
PID_RXR_VDR_PATHWAY	-1.6805995	0.110053495
REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYNTHESIS	-1.6780992	0.10997198
PID_FRA_PATHWAY	-1.6770531	0.1086859
PID_INTEGRIN2_PATHWAY	-1.6763628	0.10690503
KEGG_ARGININE_AND_PROLINE_METABOLISM	-1.6655043	0.11578747
REACTOME_G1_S_TRANSITION	-1.6572543	0.12253033
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	-1.6445711	0.13540506
REACTOME_UNWINDING_OF_DNA	-1.6433128	0.13390453
REACTOME_G0_AND_EARLY_G1	-1.641419	0.13322043
REACTOME_MITOTIC_G1_G1_S_PHASES	-1.6371974	0.13563676
REACTOME_MUSCLE_CONTRACTION	-1.6324629	0.13896687
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	-1.6296283	0.14001699
REACTOME_CELL_CYCLE_CHECKPOINTS	-1.6239792	0.14497954
BIOCARTA_EPHA4_PATHWAY	-1.6231822	0.14326264
BIOCARTA_AMI_PATHWAY	-1.6167133	0.14914909
REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT	-1.6062521	0.16094962
KEGG_ASTHMA	-1.6022092	0.16442026
KEGG_P53_SIGNALING_PATHWAY	-1.588828	0.18201679
PID_E2F_PATHWAY	-1.5859764	0.18307793
REACTOME_CELL_CYCLE	-1.5824031	0.18574578
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	-1.5801599	0.18633376
BIOCARTA_BCR_PATHWAY	-1.5767827	0.18911791
BIOCARTA_GLYCOLYSIS_PATHWAY	-1.571081	0.19538577
REACTOME_HYALURONAN_METABOLISM	-1.5710039	0.19232422
PID_AP1_PATHWAY	-1.570901	0.18934637
BIOCARTA_RANMS_PATHWAY	-1.5604287	0.20364311
KEGG_RENIN_ANGIOTENSIN_SYSTEM	-1.5535103	0.21219708
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	-1.5528599	0.21012536
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	-1.547661	0.21647425
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	-1.5465118	0.21547873
BIOCARTA GRANULOCYTES_PATHWAY	-1.5385084	0.22589356
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	-1.5327946	0.2324858
KEGG_CIRCADIEN_RHYTHM_MAMMAL	-1.5324442	0.22977114
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	-1.5267936	0.23662196
BIOCARTA_VITCB_PATHWAY	-1.5212425	0.24380153
REACTOME_PD1_SIGNALING	-1.5172613	0.24816193