

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 ($400\times$); 2 = scattered, easily seen at $100\times$ 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 $200\times$ magnification field (highest number per field recorded); 3 = focal hepatocyte necrosis, 1-2 foci per $200\times$ magnification field (highest number per field recorded); 4 = 3 or more foci per $200\times$ 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 $400\times$ 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	-2.154688	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	0.0167770834
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_APP_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	-1.8738097	0.024071764
REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAPSE	-1.8733943	0.023158072
REACTOME_GROWTH_HORMONE_RECECTOR_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_SIGNALLING_THROUGH_PI3KGAMMA	-1.8549144	0.025254514
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	-1.8476763	0.027168
REACTOME_APP_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_APP_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	-1.7711406	0.050520085
PID_AP1_PATHWAY	-1.7706399	0.049589064
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECECTOR	-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	-1.7664771	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_APP_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APP_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	-1.7521992	0.051198844
REACTOME_UNWINDING_OF_DNA	-1.7511548	0.050795645
PID_CMV_B_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_APP_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	-1.7341126	0.0535347
REACTOME_DNA_STRAND_ELONGATION	-1.7283843	0.055606063
KEGGARGININE_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	-1.6928277	0.07237005
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRDUCTION	-1.6900392	0.073106125
KEGG_AUTOIMMUNE_THYROID_DISEASE	-1.6863005	0.07456936
REACTOME_NUCLEAR_RECEPORTRANSCRIPTION 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_APP_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_RECECTOR	-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	-1.5675628	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_SIGNALLING_BY_BMP	-1.5069265	0.21231881
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	-1.5035547	0.215813
REACTOME_CONVERSION_FROM_AP_C_CDC20_TO_AP_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	9.91E-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_RECEPATOR_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
KEGGARGININE_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	-1.62339792	0.14497954
BIOCARTA_EPH4_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_RECEPтор_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_CIRCADIAN_RHYTHM_MAMMAL	-1.5324442	0.22977114
REACTOME_AMINE_LIGAND_BINDING_RECEPtors	-1.5267936	0.23662196
BIOCARTA_VITC8_PATHWAY	-1.5212425	0.24380153
REACTOME_PD1_SIGNALING	-1.5172613	0.24816193