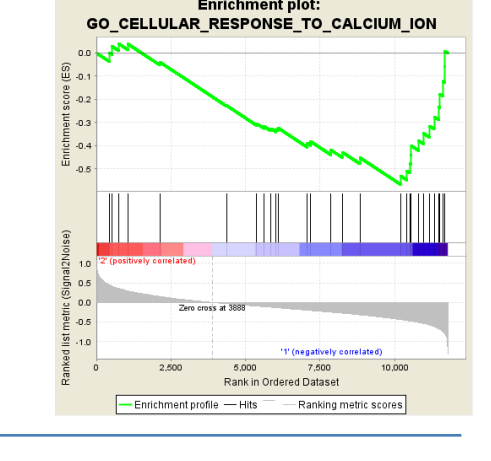
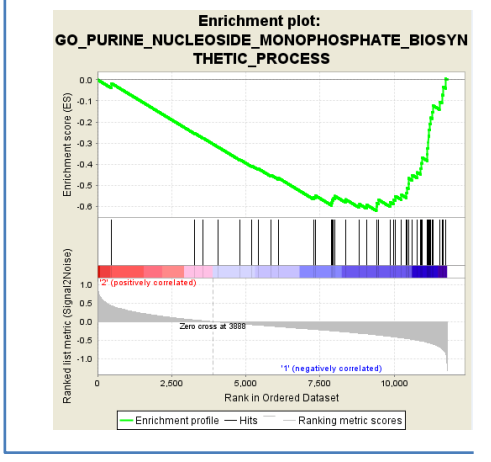
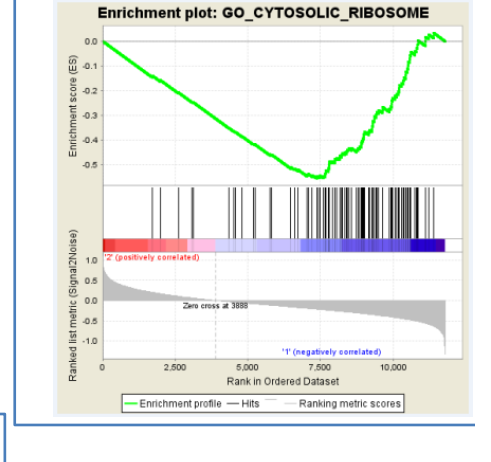
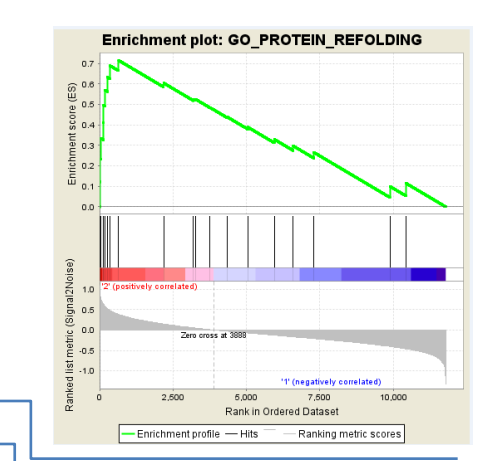
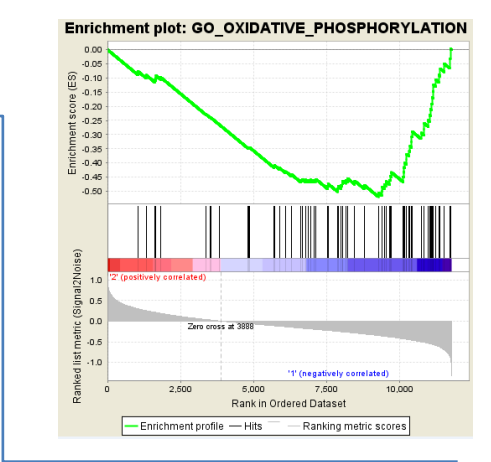
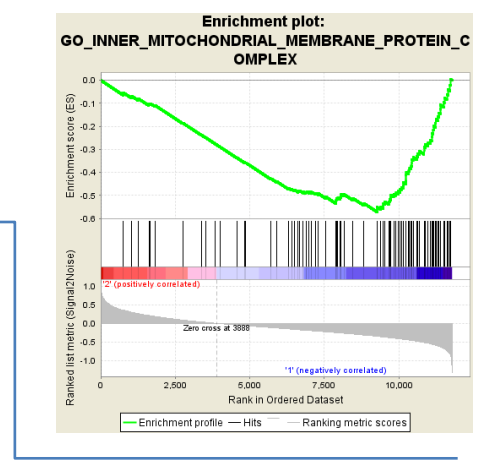


GSEA HCC versus LC Gene Ontology

NAME	SIZE	NES	NOM p-val	FDR q-val
MITOCHONDRIAL DYSFUNCTION				
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	90	-2.18678	0	0
GO_MITOCHONDRIAL_MEMBRANE_PART	137	-2.01429	0	0.004719
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	115	-2.03868	0	0.004798
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	23	-1.9601	0	0.00756
GO_NADH_DEHYDROGENASE_COMPLEX	42	-1.96615	0	0.008232
GO_ATP_BIOSYNTHETIC_PROCESS	26	-1.94758	0	0.008974
GO_ELECTRON_TRANSPORT_CHAIN	79	-1.94113	0	0.009417
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN	17	-1.93893	0	0.009452
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	62	-1.92775	0	0.011359
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	48	-1.905	0	0.015069
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	17	-1.88984	0	0.016879
GO_OXIDATIVE_PHOSPHORYLATION	71	-1.89153	0	0.017096
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	46	-1.89245	0	0.017665
GO_RESPIRATORY_CHAIN	67	-1.85864	0	0.024454
GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT	19	-1.84973	0.001284	0.0257
GO_NAD_BINDING	40	-1.79873	0.001192	0.0429
GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	40	-1.78476	0.001168	0.047952
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	49	-1.78605	0	0.04835
GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT	68	-1.7771	0	0.049632
GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	18	-1.7785	0	0.049891
GO_CELLULAR_RESPIRATION	123	-1.7334	0	0.069382
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	38	-1.73439	0.001147	0.069692
GO_CAMP_METABOLIC_PROCESS	15	2.246914	0.004545	0.034514
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	63	-1.68519	0.001088	0.108061
GO_OXIDOREDUCTASE_ACTIVITY	400	-1.69481	0	0.10038
GO_GTP_METABOLIC_PROCESS	16	-1.73047	0.006477	0.070835
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	64	2.013771	0	0.077292
GO_OXIDOREDUCTASE_COMPLEX	79	-1.71882	0.001068	0.078704
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_CYCLIC_AMIDINES	26	-1.76669	0.004884	0.055173
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	44	-1.76234	0	0.056343
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX	20	-1.75673	0.001289	0.058445
GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	261	-1.71933	0	0.080813
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	91	-1.71279	0	0.084428
GO_NUCLEOCYTOPLASMIC_TRANSPORTER_ACTIVITY	22	1.986325	0	0.08588
GO_AMMONIUM_ION_BINDING	19	2.028993	0	0.094029
RIBOSOME AND PROTEIN ORGANIZATION				
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	55	-1.97672	0	0.008941
GO_PROTEIN_TARGETING_TO_MEMBRANE	132	-1.90806	0	0.015275
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	188	-1.8801	0	0.018291
GO_PROTEIN_REFOLDING	20	2.586325	0	0
GO_CYTOSOLIC_RIBOSOME	98	-2.08889	0	0.001523
GO_TRANSLATIONAL_INITIATION	136	-2.00724	0	0.004828
GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	63	-2.02115	0	0.005115
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	113	-1.97406	0	0.007482
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	39	-1.98801	0	0.007885
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	99	-1.97001	0	0.008004
GO_RIBOSOME	202	-1.83056	0	0.031554
GO_RIBOSOMAL_SUBUNIT	151	-1.82886	0	0.031651
GO_PEPTIDE_METABOLIC_PROCESS	435	-1.74206	0	0.067685
GO_LARGE_RIBOSOMAL_SUBUNIT	87	-1.73534	0.001079	0.069745
GO_MONOSACCHARIDE_CATABOLIC_PROCESS	41	-1.71921	0.001166	0.079588
NUCLEOSIDE SYNTHESIS				
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	47	-1.97595	0	0.008138
GO PURINE NUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS	47	-2.11791	0	9.11E-04
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	112	-1.85323	0	0.025229
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	67	-1.8541	0	0.025607
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	89	-1.83465	0	0.030567
GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	169	-1.81471	0	0.036301
GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	181	-1.8077	0	0.039335
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	40	-1.80487	0	0.040153
GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	121	-1.76432	0	0.055888
MOTILITY AND CELLULAR FUNCTION				
GO_CORTICAL_ACTIN_CYTOSKELETON	32	-1.88011	0	0.018986
GO_CELLULAR_RESPONSE_TO_CALCIIUM_ION	30	-1.78688	0	0.048909
GO_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	18	-1.74066	0.0013	0.06633
GO_CELL_CELL_CONTACT_ZONE	30	-1.74198	0	0.066563
GO_NECROPTOTIC_PROCESS	18	2.021373	0	0.084175
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	23	-1.69787	0.001259	0.098417



Supplementary Figure 2

GSEA (Gene Set enrichment analysis). List of enriched gene sets in NK-cells from patients with HCC and LC, identified by GSEA (MSigDB, C5 gene Ontology set), and divided in four distinct functions (Mitochondrial Dysfunction, Ribosome and protein organization, Nucleoside synthesis and motility and cellular function). Representative enrichment plots are shown on the right.