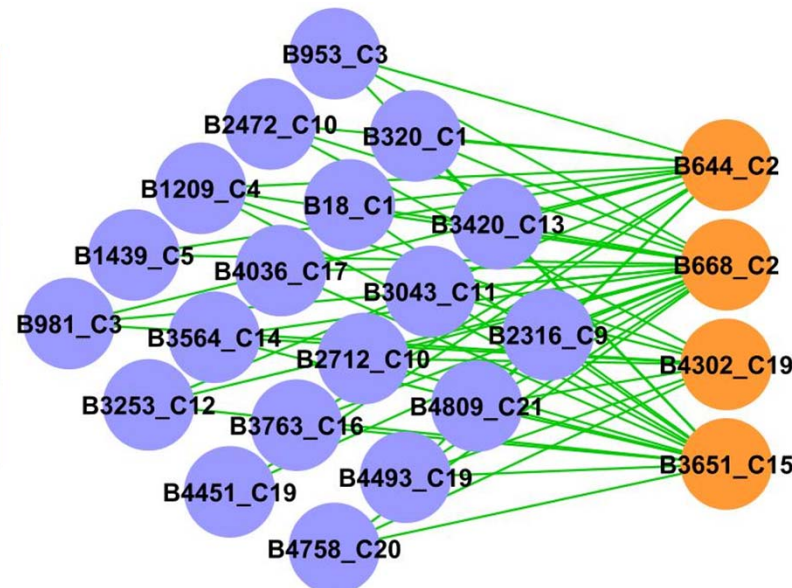


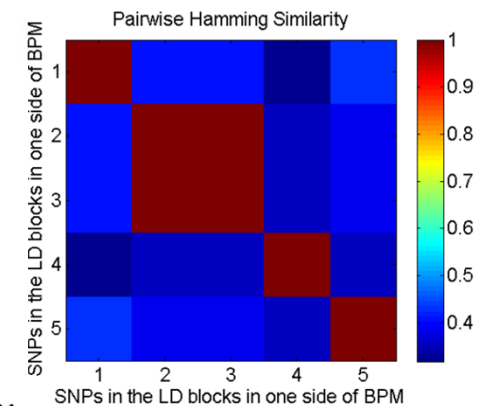
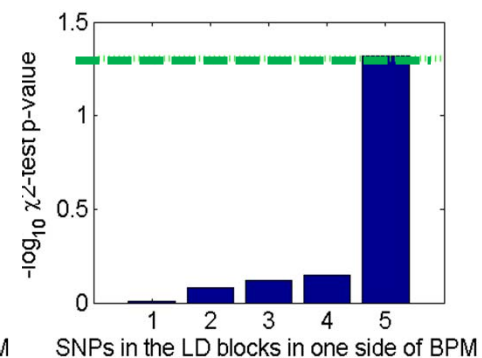
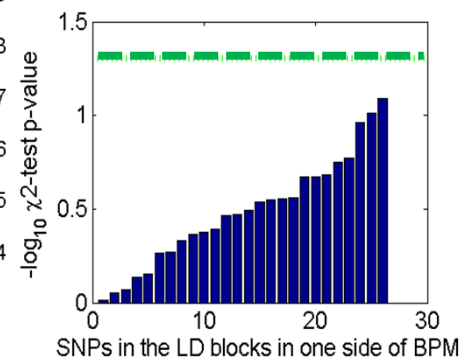
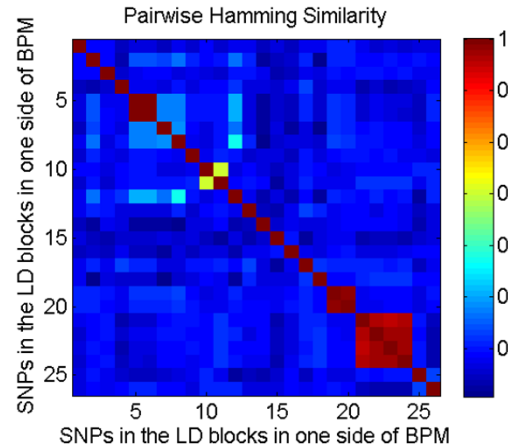
Parkinson

Name	S_Sum	S_Max	D_XY	F_XX	F_YY	F_XY
value	23	19	0.7368	0.4641	0.9886	0.7057
FDR	0.12	0.12	0	0.01	0.05	0.03

Top Enriched GO Annotations or Gene-Sets	$-\log_{10}$ P-values
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	2.29
CATION_TRANSPORT	1.90
ION_CHANNEL_ACTIVITY	1.86
PROTEIN_COMPLEX_ASSEMBLY	1.84
METAL_ION_TRANSMEMBRAN E_TRANSPORTER_ACTIVITY	1.82



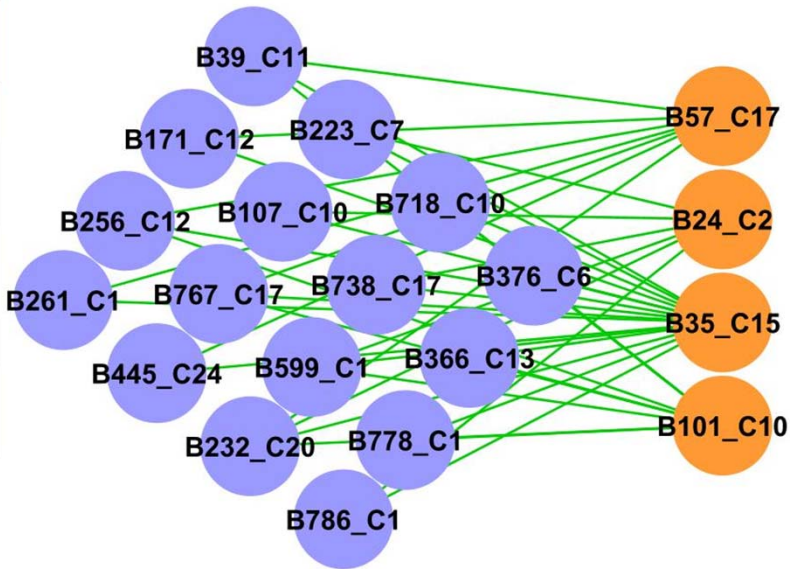
Top Enriched GO Annotations or Gene-Sets	$-\log_{10}$ p-values
PROTEIN_AMINO_ACID_PH OSPHORYLATION	3.01
PROTEIN_KINASE_ACTIVITY	3.01
PHOSPHORYLATION	2.93
PHOSPHOTRANSFERASE_AC TIVITY_ALCOHOL_GROUP_ AS_ACCEPTOR	2.84
KINASE_ACTIVITY	2.78



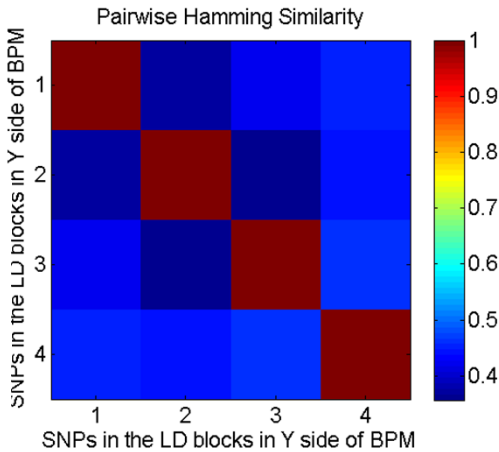
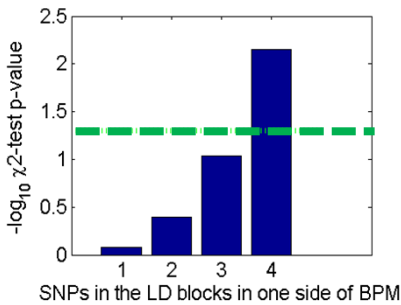
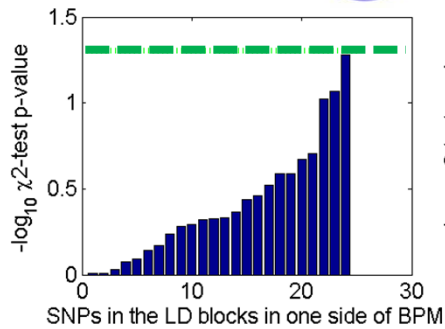
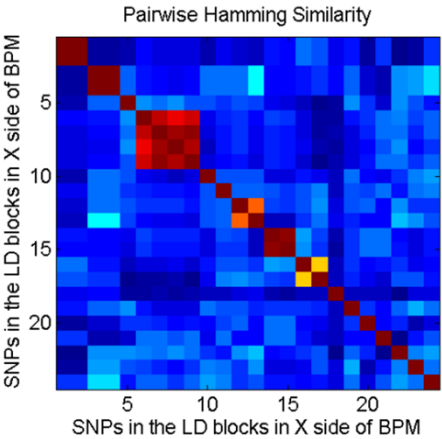
M-Survival

Name	S_Sum	S_Max	D_XY	F_XX	F_YY	F_XY
Value	20	16	0.7031	0.4381	0.993	0.7617
FDR	0.12	0.11	0.035	0.07	0	0.02

Top Enriched GO Annotations or Gene-Sets	$-\log_{10}P$ -values
DASU_IL6_SIGNALING_UP	3.40
REACTOME_Glutathione_cofactor_catabolism	3.40
SMID_BREAST_CANCER_LUMINAL_B_DN	3.23
TRAYNOR_RETT_SYNDROME_UP	2.73
RICKMAN_HEAD_AND_NECK_CANCER_E	2.69



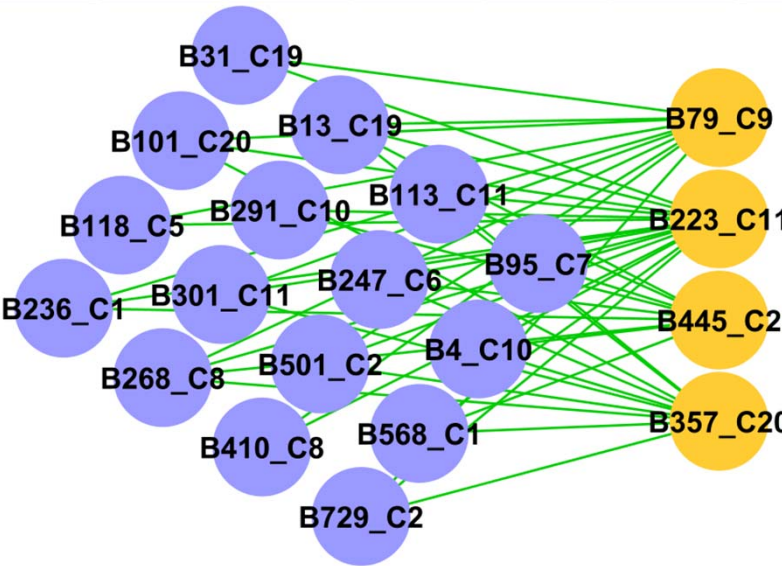
Top Enriched GO Annotations or Gene-Sets	$-\log_{10}P$ -Values
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	1.99
REACTOME_BIOLOGICAL_OXIDATIONS	1.45



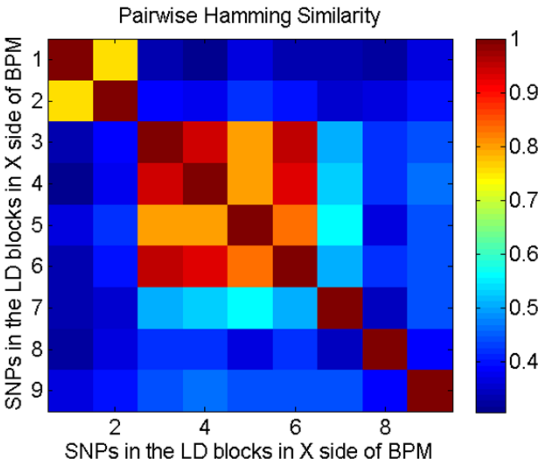
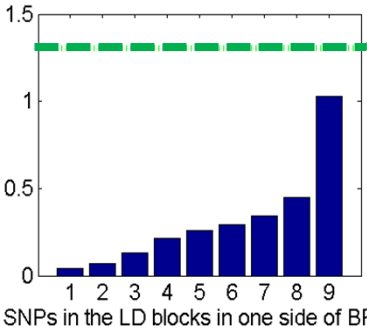
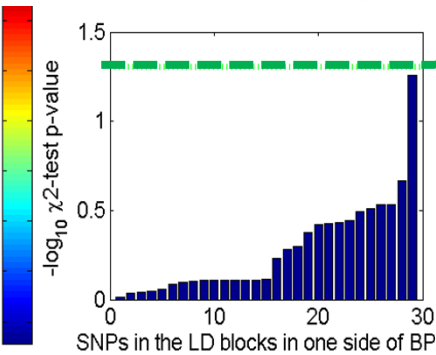
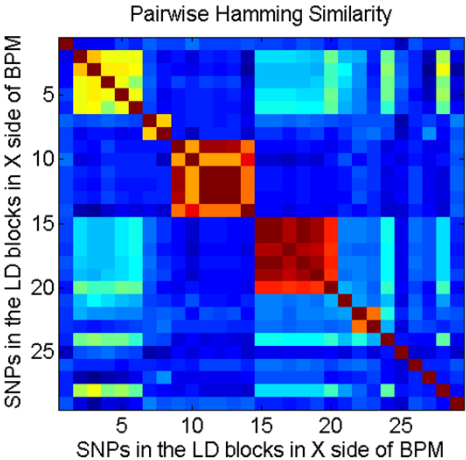
Arkansas

Name	S_Sum	S_Max	D_XY	F_XX	F_YY	F_XY
Value	18	13	0.6462	0.4929	0.5481	0.5857
						15

Top Enriched GO Annotations or Gene-Sets	$-\log_{10}P$ Values
V\$HNF4_01_B	3.29
CAGCAGG,MIR-370	3.14
BROWNE_HCMV_INFECTION_4HR_UP	2.67
REGULATION_OF_MAPK_KK_CASCADE	2.67
NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION	2.67



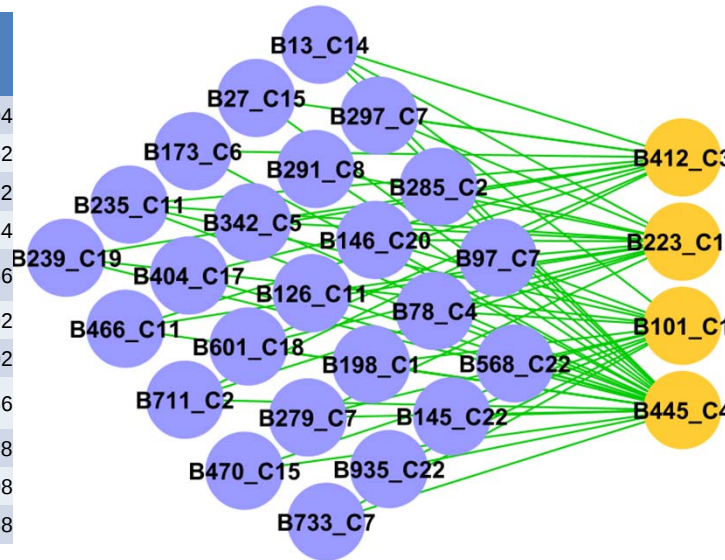
Top Enriched GO Annotations or Gene-Sets	$-\log_{10}P$ Values
REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	3.51
POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	3.51
PEPTIDYL_TYROSINE_PHOSPHORYLATION	3.12
PEPTIDYL_TYROSINE_MODIFICATION	3.12
GAGACCA,MIR-133A,MIR-133B	3.12



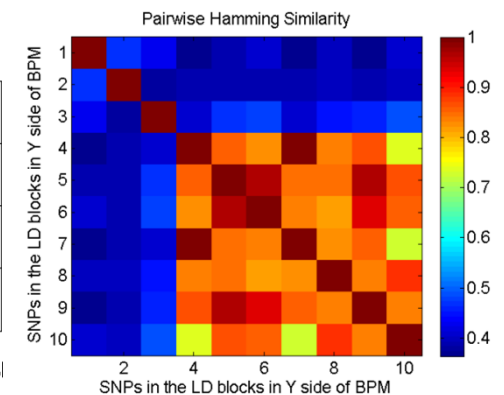
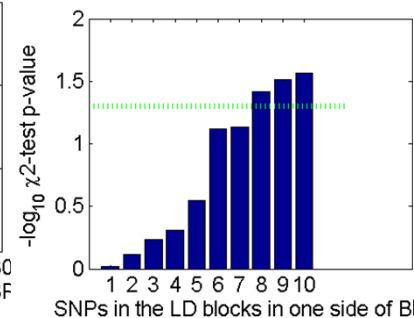
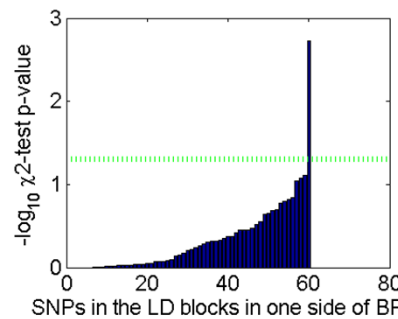
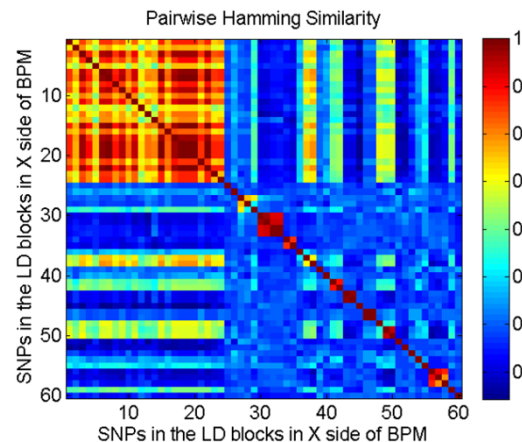
Lung

Name	S_Sum	S_Max	D_XY	F_XX	F_YY	F_XY
value	28	24	0.6458	0.2386	0.993	0.6138
FDR	0.08	0.08	0.08	0.08	0.02	0.07

Top Enriched GO Annotations or Gene-Sets	$-\log_{10}$ P-Values
WELCSH_BRCA1_TARGETS_1_UP	2.7504
SMID_BREAST_CANCER_LUMINAL_B_UP	2.6062
GAL_LEUKEMIC_STEM_CELL_UP	2.4912
REGULATION_OF_CELL_CYCLE	2.4834
REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	2.4756
CELLULAR_LIPID_METABOLIC_PROCESS	2.3592
WANG_HCP_PROSTATE_CANCER	2.302
TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	2.2486
LEE_NEURAL_CRESCENT_STEM_CELL_UP	2.1408
PROTEIN_PROCESSING	2.1408
KINASE_ACTIVITY	2.1058



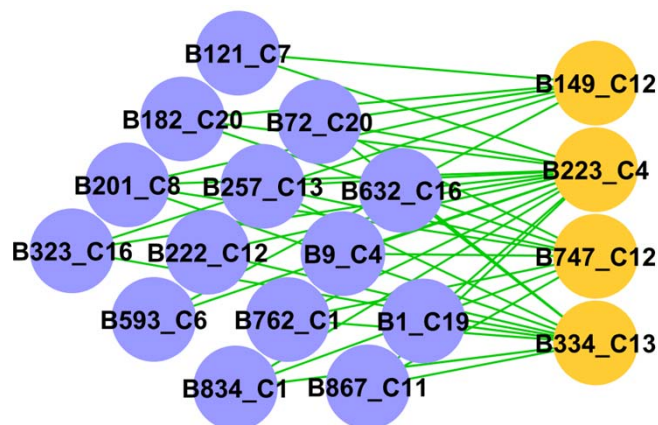
Top Enriched GO Annotations or Gene-Sets	$-\log_{10}$ p-values
WANG_CISPLATIN_RESPONSE_AND_XPC_DN	2.8256
ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN	2.2473
CAIRO_HEPATOBLASTOMA_DN	1.8337
EXTRACELLULAR_REGION	1.5362
REGULATION_OF_BIOLOGICAL_QUALITY	1.4429



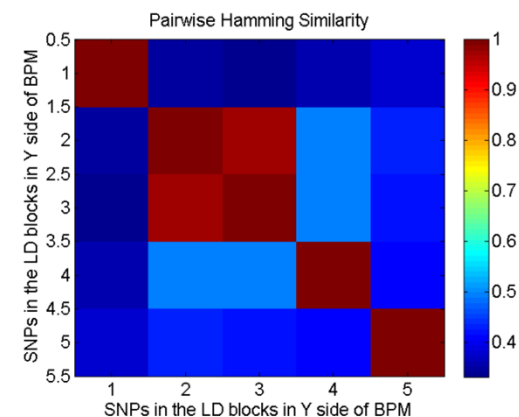
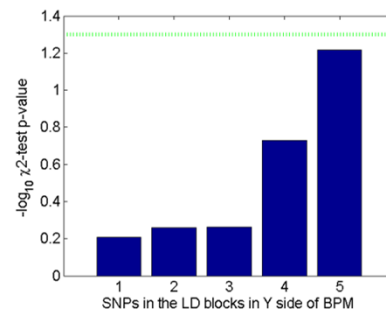
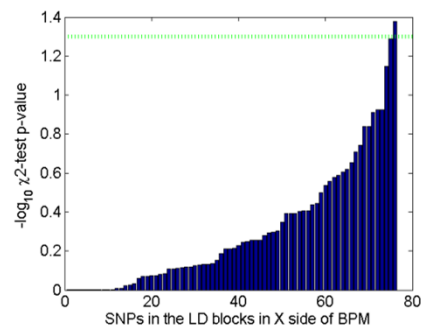
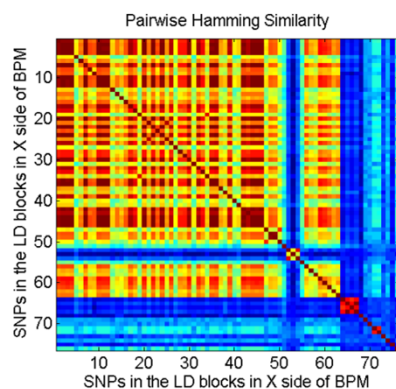
Kidney

Name	S_Sum	S_Max	D_XY	F_XX	F_YY	F_XY
value	18	14	0.6786	0.4411	0.9642	0.6749
FDR	0.445	0.37	0.17	0.17	0.34	0.2

Top Enriched GO Annotations or Gene-Sets	-log ₁₀ P-Values
KOYAMA_SEMA3B_TARGETS_UP	3.997
PARENT_MTOR_SIGNALING_UP	3.9409
DAZARD_RESPONSE_TO_UV_NHEK_UP	2.7317
FERNANDEZ_BOUND_BY_MYC	2.4163
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP	2.3949
ENK_UV_RESPONSE_KERATINOCYTE_UP	2.3561
STEIN_ESRRA_TARGETS_UP	2.1723
SHEPARD_CRUSH_AND_BURN_MUTANT_UP	2.168
NAGASHIMA_NRG1_SIGNALING_UP	2.0678
SCHLOSSER_SERUM_RESPONSE_UP	1.975
DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	1.9552



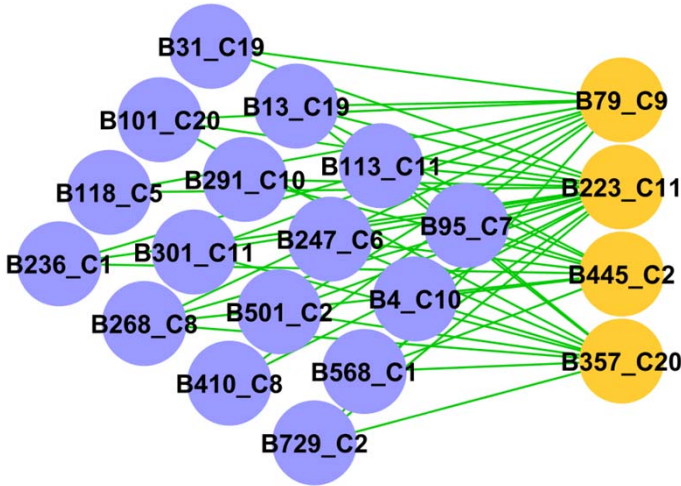
Top Enriched GO Annotations or Gene-Sets	-log ₁₀ p-values
HOSHIDA_LIVER_CANCER_SURVIVAL_DN	2.7098
KAUFFMANN_DNA_REPAIR_GENES	2.5706
TGCACTT,MIR-519C,MIR-519B,MIR-519A	2.3714
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP	1.9662
SCHLOSSER_SERUM_RESPONSE_DN	1.9246
REACTOME_DNA_REPAIR	1.8291
DNA_REPAIR	1.6376
RESPONSE_TO_DNA_DAMAGE_STIMULUS	1.5193
RESPONSE_TO_ENDOGENOUS_STIMULUS	1.4606
DNA_METABOLIC_PROCESS	1.3751
NEGATIVE_REGULATION_OF_CELLULAR_PROCESS	1.3261



EPI

Name	S_Sum	S_Max	D_XY	F_XX	F_YY	F_XY
Value	20	16	0.7031	0.4381	0.993	0.7617
FDR	0.12	0.11	0.035	0.07	0	0.02

Top Enriched GO Annotations or Gene-Sets	$-\log_{10}$ P-Values
NIKOLSKY_BREAST_CANCER_20Q12_Q13_A_MPLICON	3.1081
REACTOME_PHASE_1_FUNCTIONALIZATION	3.0453
MULLIGHAN_NPM1_SIGNATURE_3_DN	2.5913
KEGG_ARACHIDONIC_ACID_METABOLISM	2.3744
XU_HGF_TARGETS_REPRESSED_BY_AKT1_DN	2.2383
CAIRO_HEPATOBLASTOMA_CLASSES_DN	2.1985
REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUNDS	2.1206



Top Enriched GO Annotations or Gene-Sets	$-\log_{10}$ P-Values
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN	2.1356
MOOTHA_MITOCHONDRIA	2.028
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN	1.8083

