# Supplementary Materials

## 1 Active score comparison

SAM and $t$-statistic are also used as observed active score metric for predicting the real active score of each gene. We first compare the correlation of different scores. All genes' active scores compose to a vector. The observed active score vector calculated by $t$-statistic, SAM and SNR are denoted as $t$-stat, SAM and SNR respectively, and the corresponding predicted underlying active score vector are denoted as $t$-stat_pre, SAM_pre and SNR_pre respectively. Then, the Pearson correlation coefficient (PCC) are used to evaluate the relationship between these score vectors (See Figure S1). High PCC value indicates high similarity between score vectors. In the both case studies, the observed score vectors ($t$-stat, SAM and SNR) are with high similarity and predicted score vectors ($t$-stat_pre, SAM_pre and SNR_pre) are also similar to each other, while the similarity between observed scores and predicted scores are low. The predicted active score using SNR metric is a little different from other predicted active score. However, in the ranking list of genes based on active scores, the disease related gene enrichment is higher than the ranking list based on other active score (See Figure S2). It is noticed that the predicted underlying active score ranking list ($t$-stat_pre, SAM_pre and SNR_pre) enrich of more disease gene than observed active score ranking list ($t$-stat, SAM and SNR).

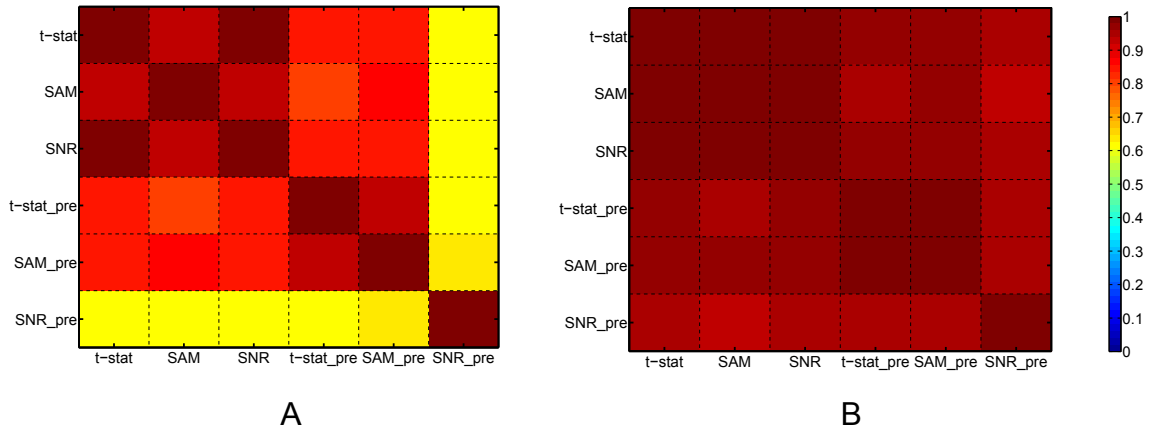


Figure S1: Correlation between different active score of genes. Subfigure A represents the results in the breast cancer metastasis dataset and subfigure B represents the results in the prostate cancer dataset.

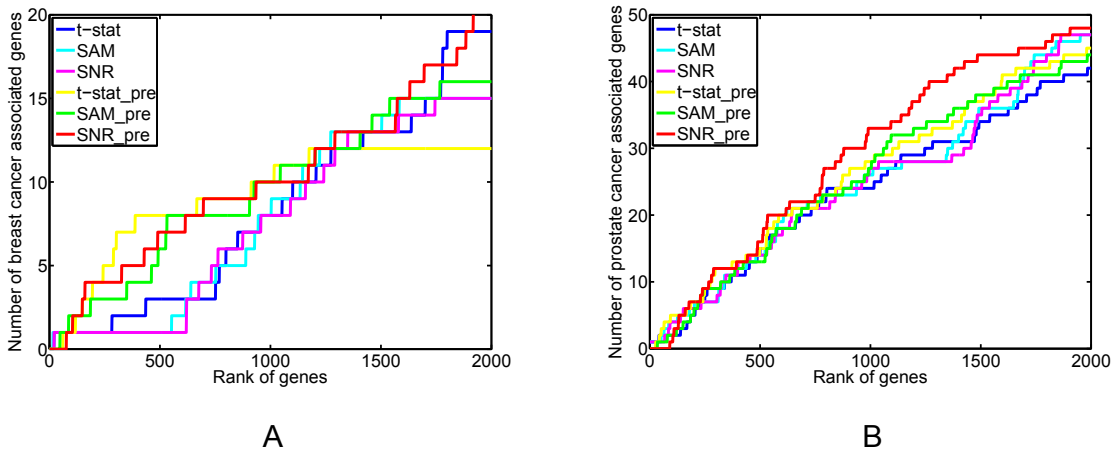


Figure S2: The distribution of disease related gene in the ranking lists based on different active score of genes. Subfigure A represents the results in the breast cancer metastasis dataset and subfigure B represents the results in the prostate cancer dataset.

## 2 Sensitivity analysis

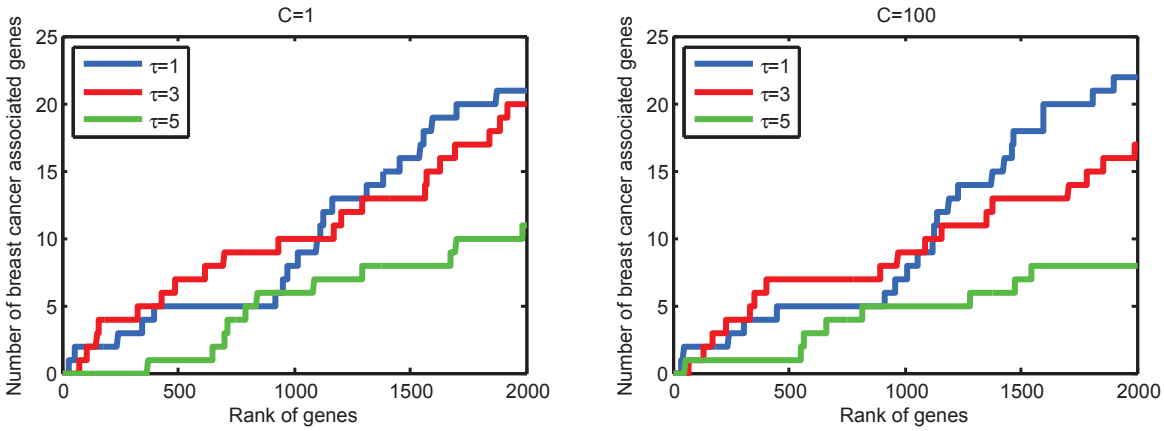


Figure S3: Parameter sensitivity analysis in breast cancer dataset. Using different combination of $C$ and $\tau$, the distribution of disease related gene in the ranking lists based on predicted active score of genes are compared.

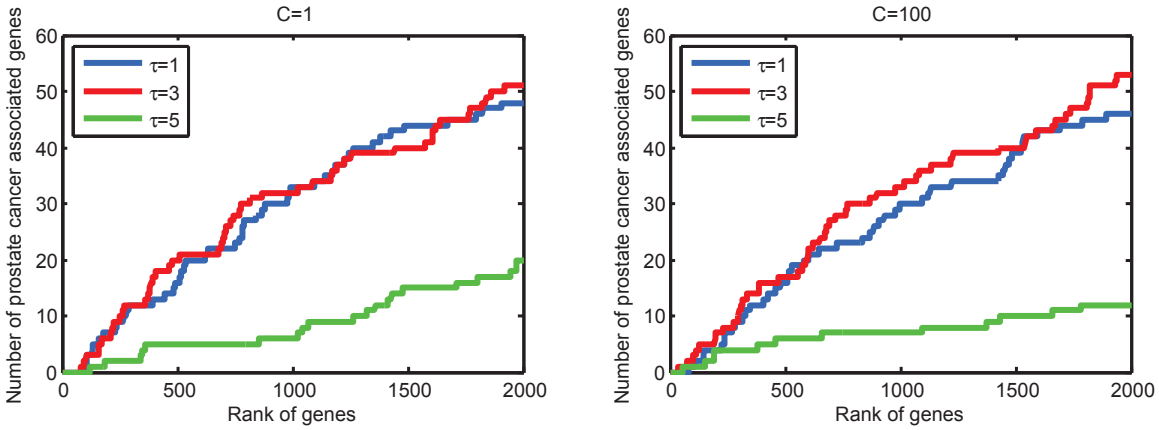


Figure S4: Parameter sensitivity analysis in prostate cancer dataset. Using different combination of $C$ and $\tau$, the distributions of disease related gene in the ranking lists based on predicted active score of genes are compared.

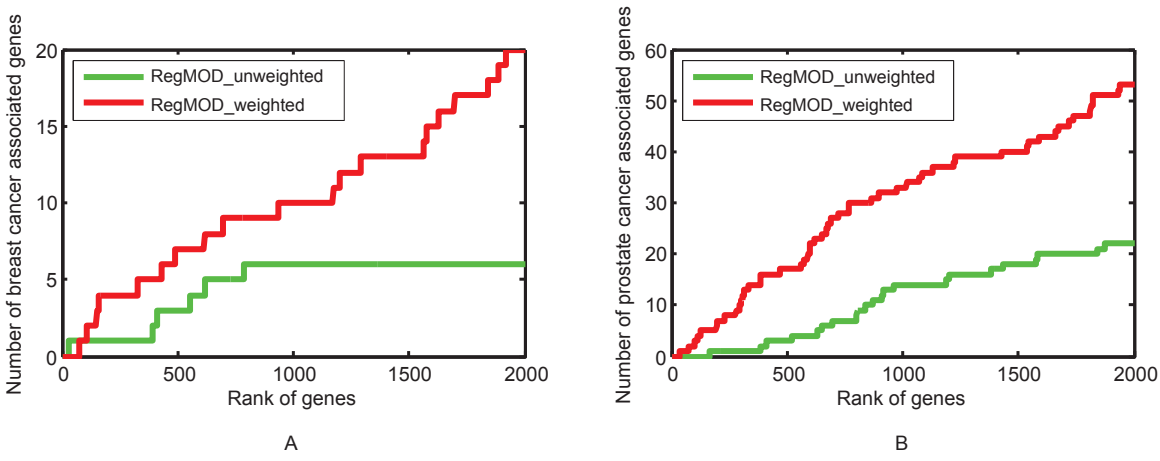


Figure S5: Comparison of RegMOD in terms of network with weighted and unweighted interaction. A is for the breast cancer dataset and B is for the prostate dataset. The parameters were all set that $C = 1$ and $\tau = 3$.

# 3 Threshold selection

The quality of the induced modules are evaluated by two quantitatively measures: cohesion $s_m$ and average activity $ac_m$ measurement. In the induced active modules including up-regulated and down-regulated genes, the cohesion which represents the within module similarity is calculated by mean value of similarity between each gene pair,

$$s_m = \frac{1}{|m|(|m|-1)} \sum_{i,j \in m, i \neq j} k_{ij},$$

where $m$ represents a module and $|m|$ is the size of the module. The high cohesion indicates the genes within the module are more likely to function coordinately and to achieve one specific biological process. Thus, we should select the threshold to reveal the modules with high cohesion. Meanwhile, the active score of the modules is defined as the average underlying active score as follows,

$$ac_m = \frac{1}{|m|} \sum_{i \in m} f_i \quad .$$

These two measures guide us to select a proper $\theta$ to have consistent cohesion and high active score for further analysis. Specifically, we select $\theta = 6$ according to Figure S6.

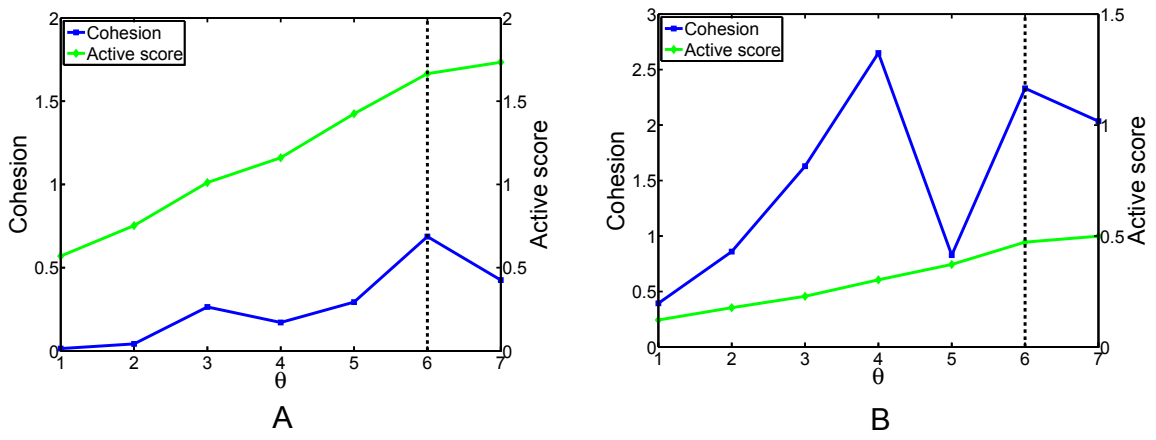


Figure S6: Quality of the active modules based on different threshold. Subfigure A represents the results in the breast cancer metastasis dataset and subfigure B represents the results in the prostate cancer dataset.

# 4 Note on the results of breast cancer dataset

The jActiveModules was used to find active subnetworks for comparison. Using the greedy search strategy of jActiveModules, we obtained 5 active subnetworks , and 3 of them contain more than 5 genes, denoted as BCjAM1, BCjAM2 and BCjAM3. But it outputted no active subnetworks when using the simulated annealing strategy. GiGA was also applied to these data by setting the parameter $m$ to 52 and 33 for finding up- and down-regulated modules, and the result is compatible with the modules by our method. The identified 4 significant active subnetworks, i.e. 2 up- and 2 down-regulated modules which are denoted as BCGUM1, BCGUM2, BCGDM1 and BCGDM2 respectively.

Table S1: Comparison of modules' overlap of known pathways. The green cells represent pathways significantly overlapping with BCDM1, the red cells represent pathways significantly overlapping with BCDM2, and the blue cells represent pathways significantly overlapping with BCUM1.

| *RegMOD* | *GiGA* | *jActiveModules* |
|---|---|---|
| BCDM1 | BCGDM1 | |
| IL6PATHWAY | TNFR2PATHWAY | |
| TPOPATHWAY | HSA04060 CYTOKINE CYTOKINE RECEPTOR INTERACTION | |
| APOPTOSIS KEGG | IL22BPPATHWAY | |
| EGFPATHWAY | IL7PATHWAY | |
| PDGFPATHWAY | RELAPATHWAY | |
| D4GDIPATHWAY | HSA04920 ADIPOCYTOKINE SIGNALING PATHWAY | |
| IL22BPPATHWAY | IL2RBPATHWAY | |
| HSA05223 NON SMALL CELL LUNG CANCER | HSA04630 JAK STAT SIGNALING PATHWAY | |
| IL2PATHWAY | HSA04640 HEMATOPOIETIC CELL LINEAGE | |
| CASPASEPATHWAY | BIOPEPTIDESPATHWAY | |
| PYK2PATHWAY | APOPTOSIS GENMAPP | |
| PKCPATHWAY | KERATINOCYTEPATHWAY | |
| HSA04920 ADIPOCYTOKINE SIGNALING PATHWAY | IL10PATHWAY | |
| STAT3PATHWAY | APOPTOSIS KEGG | |
| AT1RPATHWAY | THELPERPATHWAY | |
| IL2RBPATHWAY | HSA05221 ACUTE MYELOID LEUKEMIA | |
| BIOPEPTIDESPATHWAY | HIVNEFPATHWAY | |
| NUCLEAR RECEPTORS | 41BBPATHWAY | |
| HSA04630 JAK STAT SIGNALING PATHWAY | CCR5PATHWAY | |
| | TIDPATHWAY | |
| BCDM2 | BCGDM2 | BCjAM2 |
| HSA04612 ANTIGEN PROCESSING AND PRESENTATION | HSA04940 TYPE I DIABETES MELLITUS | HSA04612 ANTIGEN PROCESSING AND PRESENTATION |
| HSA04940 TYPE I DIABETES MELLITUS | HSA04612 ANTIGEN PROCESSING AND PRESENTATION | HSA04940 TYPE I DIABETES MELLITUS |
| HSA04514 CELL ADHESION MOLECULES | HSA04514 CELL ADHESION MOLECULES | HSA04514 CELL ADHESION MOLECULES |
| BBCELLPATHWAY | BBCELLPATHWAY | BBCELLPATHWAY |
| EOSINOPHILSPATHWAY | EOSINOPHILSPATHWAY | EOSINOPHILSPATHWAY |
| IL5PATHWAY | IL5PATHWAY | IL5PATHWAY |
| BLYMPHOCYTEPATHWAY | BLYMPHOCYTEPATHWAY | BLYMPHOCYTEPATHWAY |
| ASBCELLPATHWAY | ASBCELLPATHWAY | ASBCELLPATHWAY |
| TCRAPATHWAY | TCRAPATHWAY | TCRAPATHWAY |
| HSA04640 HEMATOPOIETIC CELL LINEAGE | TH1TH2PATHWAY | TH1TH2PATHWAY |
| TH1TH2PATHWAY | CTLA4PATHWAY | CTLA4PATHWAY |
| CTLA4PATHWAY | MTORPATHWAY | AMIPATHWAY |
| AMIPATHWAY | AMIPATHWAY | CSKPATHWAY |
| CSKPATHWAY | CSKPATHWAY | INFLAMPATHWAY |
| INFLAMPATHWAY | EIF4PATHWAY | HSA04640 HEMATOPOIETIC CELL LINEAGE |
| | INFLAMPATHWAY | |
| | HSA04640 HEMATOPOIETIC CELL LINEAGE | |
| BCUM1 | BCGUM1 | BCjAM1 |
| HSA04110 CELL CYCLE | HSA04110 CELL CYCLE | CELL CYCLE KEGG |
| HSA05215 PROSTATE CANCER | CELL CYCLE KEGG | HSA04115 P53 SIGNALING PATHWAY |
| HSA04910 INSULIN SIGNALING PATHWAY | HSA04115 P53 SIGNALING PATHWAY | HSA04110 CELL CYCLE |
| HSA05212 PANCREATIC CANCER | DNA REPLICATION REACTOME | SA G2 AND M PHASES |
| MPRPATHWAY | CELLCYCLEPATHWAY | G2PATHWAY |
| HSA05220 CHRONIC MYELOID LEUKEMIA | G2PATHWAY | PTC1PATHWAY |
| HSA05214 GLIOMA | G1 TO S CELL CYCLE REACTOME | RBPATHWAY |
| HSA04720 LONG TERM POTENTIATION | PTC1PATHWAY | CELLCYCLEPATHWAY |
| HSA05211 RENAL CELL CARCINOMA | SRCRPTPPATHWAY | HSA05130 PATHOGENIC ESCHERICHIA COLI INFECTION EHEC |
| HSA05219 BLADDER CANCER | RBPATHWAY | HSA05131 PATHOGENIC ESCHERICHIA COLI INFECTION EPEC |
| HSA04930 TYPE II DIABETES MELLITUS | SA REG CASCADE OF CYCLIN EXPR | G1 TO S CELL CYCLE REACTOME |
| HSA04012 ERBB SIGNALING PATHWAY | P53PATHWAY | HIVNEFPATHWAY |
| RACCYCDPATHWAY | MPRPATHWAY | CDC25PATHWAY |
| HSA04350 TGF BETA SIGNALING PATHWAY | G1PATHWAY | DEATHPATHWAY |
| G2PATHWAY | HSA05215 PROSTATE CANCER | HSA05222 SMALL CELL LUNG CANCER |
| HSA05221 ACUTE MYELOID LEUKEMIA | PYRIMIDINE METABOLISM | MAPKPATHWAY |
| NFATPATHWAY | SIG PIP3 SIGNALING IN CARDIAC MYOCTES | APOPTOSIS |
| HSA05223 NON SMALL CELL LUNG CANCER | HSA04720 LONG TERM POTENTIATION | EPONFKBPATHWAY |
| | HSA05222 SMALL CELL LUNG CANCER | SRCRPTPPATHWAY |
| | HSA04350 TGF BETA SIGNALING PATHWAY | HSA05221 ACUTE MYELOID LEUKEMIA |
| BCUM2 | BCGUM2 | BCjAM3 |
| ST FAS SIGNALING PATHWAY | PROTEASOME | HSA04620 TOLL LIKE RECEPTOR SIGNALING PATHWAY |
| | PROTEASOMEPATHWAY | TOLLPATHWAY |
| | HSA03050 PROTEASOME | GLEEVECPATHWAY |
| | GLUCONEOGENESIS | NGFPATHWAY |
| | GLYCOLYSIS | FCER1PATHWAY |
| | HSA00010 GLYCOLYSIS AND GLUCONEOGENESIS | IGF1PATHWAY |
| | HIFPATHWAY | INSULINPATHWAY |
| | GLYCOLYSIS AND GLUCONEOGENESIS | HSA05211 RENAL CELL CARCINOMA |
| | | HSA04664 FC EPSILON RI SIGNALING PATHWAY |
| | | EGFPATHWAY |
| | | GSK3PATHWAY |
| | | PDGFPATHWAY |
| | | HSA04210 APOPTOSIS |
| | | HSA05215 PROSTATE CANCER |
| | | IL1RPATHWAY |
| | | HSA04910 INSULIN SIGNALING PATHWAY |
| | | AT1RPATHWAY |
| | | LONGEVITYPATHWAY |
| | | BCRPATHWAY |
| | | HSA05214 GLIOMA |

Table S2: Comparison of modules' enriched GO categories. The green cells represent GO categories enriched in BCDM1, the red cells represent GO categories enriched in BCDM2, and the blue cells represent GO categories enriched in BCUM1.

| *RegMOD* | *GiGA* | *jActiveModules* |
|---|---|---|
| BCDM1 | BCGDM1 | |
| INTRACELLULAR SIGNALING CASCADE | JAK STAT CASCADE | |
| LIGAND DEPENDENT NUCLEAR RECEPTOR ACTIVITY | RECEPTOR ACTIVITY | |
| CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY | PROTEIN KINASE CASCADE | |
| RESPONSE TO VIRUS | CYTOKINE BINDING | |
| STEROID HORMONE RECEPTOR ACTIVITY | PROTEIN TYROSINE KINASE ACTIVITY | |
| CYSTEINE TYPE PEPTIDASE ACTIVITY | TRANSMEMBRANE RECEPTOR ACTIVITY | |
| RECEPTOR ACTIVITY | MULTI ORGANISM PROCESS | |
| IMMUNE SYSTEM PROCESS | APOPTOSIS GO | |
| CELL SURFACE RECEPTOR LINKED SIGNAL TR TRANSDUCTION GO 0007166 | PROGRAMMED CELL DEATH | |
| SECOND MESSENGER MEDIATED SIGNALING | SIGNAL TRANSDUCTION | |
| CELL CELL SIGNALING | IMMUNE SYSTEM PROCESS | |
| RESPONSE TO OTHER ORGANISM | CELL DEVELOPMENT | |
| EXOCYTOSIS | RESPONSE TO VIRUS | |
| PROTEIN KINASE CASCADE | PROTEIN KINASE ACTIVITY | |
| RESPONSE TO WOUNDING | TRANSCRIPTION FACTOR BINDING | |
| RESPONSE TO EXTERNAL STIMULUS | INTRACELLULAR SIGNALING CASCADE | |
| JAK STAT CASCADE | RESPONSE TO EXTERNAL STIMULUS | |
| G PROTEIN SIGNALING COUPLED TO CYCLIC NUCLEOTIDE SECOND MESSENGER | PROTEIN KINASE BINDING | |
| CYCLIC NUCLEOTIDE MEDIATED SIGNALING | ENZYME BINDING | |
| | PHOSPHOTRANSFERASE ACTIVITY ALCOHOL GROUP AS ACCEPTOR | |
| BCDM2 | BCGDM2 | BCjAM2 |
| LYSOSOME | LYSOSOME | MEMBRANE |
| LYTIC VACUOLE | LYTIC VACUOLE | PLASMA MEMBRANE |
| VACUOLE | VACUOLE | |
| IMMUNE RESPONSE | INTRACELLULAR PROTEIN TRANSPORT | |
| IMMUNE SYSTEM PROCESS | PROTEIN TRANSPORT | |
| TRANSMEMBRANE RECEPTOR ACTIVITY | PROTEIN COMPLEX ASSEMBLY | |
| MEMBRANE | | |
| RECEPTOR ACTIVITY | | |
| PLASMA MEMBRANE | | |
| INTEGRAL TO MEMBRANE | | |
| INTRINSIC TO MEMBRANE | | |
| CYTOPLASMIC PART | | |
| MEMBRANE PART | | |
| CYTOPLASM | | |
| BCUM1 | BCGUM1 | BCjAM1 |
| CELL CYCLE PROCESS | SPINDLE | CELL CYCLE GO 0007049 |
| CELL CYCLE GO 0007049 | CELL CYCLE PROCESS | CELL CYCLE PROCESS |
| MITOTIC CELL CYCLE | CELL CYCLE GO 0007049 | MITOTIC CELL CYCLE |
| MITOTIC SPINDLE ORGANIZATION AND BIOGENESIS | MITOTIC CELL CYCLE | CELL CYCLE PHASE |
| SPINDLE ORGANIZATION AND BIOGENESIS | SPINDLE ORGANIZATION AND BIOGENESIS | NUCLEUS |
| CELL CYCLE PHASE | MICROTUBULE CYTOSKELETON | REGULATION OF CELL CYCLE |
| SPINDLE | SPINDLE MICROTUBULE | SPINDLE ORGANIZATION AND BIOGENESIS |
| MICROTUBULE CYTOSKELETON ORGANIZATION AND BIOGENESIS | CELL CYCLE PHASE | TRANSCRIPTION FACTOR BINDING |
| MICROTUBULE CYTOSKELETON | MITOTIC SPINDLE ORGANIZATION AND BIOGENESIS | SPINDLE |
| M PHASE | CYTOSKELETAL PART | TRANSCRIPTION COACTIVATOR ACTIVITY |
| MICROTUBULE BASED PROCESS | CYTOSKELETON | PHOSPHATASE REGULATOR ACTIVITY |
| M PHASE OF MITOTIC CELL CYCLE | MICROTUBULE | MITOSIS |
| INTRACELLULAR ORGANELLE PART | INTRACELLULAR NON MEMBRANE BOUND ORGANELLE | M PHASE OF MITOTIC CELL CYCLE |
| ORGANELLE PART | NON MEMBRANE BOUND ORGANELLE | SPINDLE MICROTUBULE |
| CYTOSKELETAL PART | MICROTUBULE CYTOSKELETON ORGANIZATION AND BIOGENESIS | M PHASE |
| SPINDLE MICROTUBULE | SPINDLE POLE | JAK STAT CASCADE |
| MITOSIS | M PHASE | PROTEIN COMPLEX |
| SPINDLE POLE | MICROTUBULE BASED PROCESS | TRANSCRIPTION ACTIVATOR ACTIVITY |
| CYTOSKELETON ORGANIZATION AND BIOGENESIS | REGULATION OF CELL CYCLE | MICROTUBULE CYTOSKELETON |
| INTRACELLULAR NON MEMBRANE BOUND ORGANELLE | M PHASE OF MITOTIC CELL CYCLE | REGULATION OF PROTEIN KINASE ACTIVITY |
| BCUM2 | | BCjAM3 |
| INDUCTION OF APOPTOSIS BY EXTRACELLULAR SIGNALS | | POSITIVE REGULATION OF CYTOKINE BIOSYN SYNTHETIC PROCESS |
| REGULATION OF APOPTOSIS | | POSITIVE REGULATION OF TRANSLATION |
| REGULATION OF PROGRAMMED CELL DEATH | | REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS |
| APOPTOSIS GO | | CYTOKINE BIOSYNTHETIC PROCESS |
| PROGRAMMED CELL DEATH | | POSITIVE REGULATION OF CELLULAR PROTEIN METABOLIC PROCESS |
| REGULATION OF DEVELOPMENTAL PROCESS | | CYTOKINE METABOLIC PROCESS |
| CELL DEVELOPMENT | | POSITIVE REGULATION OF PROTEIN METABOLIC PROCESS |
| POSITIVE REGULATION OF DEVELOPMENTAL PROCESS | | REGULATION OF CELLULAR PROTEIN METABOLIC PROCESS |
| IDENTICAL PROTEIN BINDING | | I KAPPAB KINASE NF KAPPAB CASCADE |
| RECEPTOR BINDING | | CYTOKINE PRODUCTION |
| INTRACELLULAR SIGNALING CASCADE | | REGULATION OF PROTEIN METABOLIC PROCESS |
| POSITIVE REGULATION OF CELLULAR PROCESS | | POSITIVE REGULATION OF CELLULAR PROCESS |
| POSITIVE REGULATION OF BIOLOGICAL PROCESS | | REGULATION OF I KAPPAB KINASE NF KAPPAB CASCADE |
| NUCLEUS | | REGULATION OF TRANSLATION |
| SIGNAL TRANSDUCTION | | POSITIVE REGULATION OF BIOLOGICAL PROCESS |
| CYTOPLASM | | PROTEIN KINASE CASCADE |
| | | POSITIVE REGULATION OF CELLULAR METABOLIC PROCESS |
| | | POSITIVE REGULATION OF METABOLIC PROCESS |
| | | MACROMOLECULE BIOSYNTHETIC PROCESS |
| | | LIPID RAFT |

# 5 Note on the results of prostate cancer dataset

The GiGA found 373 genes involving 2 up- and 2 down-regulated modules, denoted as PCGUM1 PCGUM2, PCGDM1 and PCGDM2. The parameter m used in GiGA was set to 69 which is the size of PCDM1. The jActiveModules found an active module of 441 genes, denoted as PCjAM1.

Table S3: Comparison of modules' overlap of known pathways. The green cells represent pathways significantly overlapping with PCDM1, the red cells represent pathways significantly overlapping with PCDM2, and the blue cells represent pathways significantly overlapping with PCDM3.

| *RegMOD* | *GiGA* | *jActivModules* |
|---|---|---|
| PCDM1 | PCGDM1 | PCjAM1 |
| HSA04520_ADHERENS_JUNCTION | HSA05220_CHRONIC_MYELOID_LEUKEMIA | HSA04510_FOCAL_ADHESION |
| ERYTHPATHWAY | HSA05212_PANCREATIC_CANCER | HSA04520_ADHERENS_JUNCTION |
| TOB1PATHWAY | HSA04520_ADHERENS_JUNCTION | HSA05212_PANCREATIC_CANCER |
| HSA04510_FOCAL_ADHESION | HSA05210_COLORECTAL_CANCER | PYK2PATHWAY |
| HSA04060_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | TOB1PATHWAY | ST_INTEGRIN_SIGNALING_PATHWAY |
| HSA05220_CHRONIC_MYELOID_LEUKEMIA | HSA04510_FOCAL_ADHESION | HSA05220_CHRONIC_MYELOID_LEUKEMIA |
| METPATHWAY | BADPATHWAY | METPATHWAY |
| ALKPATHWAY | RAC1PATHWAY | CXCR4PATHWAY |
| INTEGRIN_MEDIATED_CELL_ADHESION_KEGG | TPOPATHWAY | HSA04810_REGULATION_OF_ACTIN_CYTOSKELETON |
| BIOPEPTIDESPATHWAY | HSA04060_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | HSA04012_ERBB_SIGNALING_PATHWAY |
| CARDIACEGFPATHWAY | EGFPATHWAY | MAPKPATHWAY |
| HSA04916_MELANOGENESIS | HSA04630_JAK_STAT_SIGNALING_PATHWAY | EGFPATHWAY |
| HSA05211_RENAL_CELL_CARCINOMA | IL10PATHWAY | INTEGRINPATHWAY |
| TGFBPATHWAY | IL22BPPATHWAY | RACCYCDPATHWAY |
| HSA05212_PANCREATIC_CANCER | HSA04012_ERBB_SIGNALING_PATHWAY | TPOPATHWAY |
| IL6PATHWAY | ERYTHPATHWAY | BIOPEPTIDESPATHWAY |
| HSA04630_JAK_STAT_SIGNALING_PATHWAY | HSA04010_MAPK_SIGNALING_PATHWAY | AT1RPATHWAY |
| TPOPATHWAY | HSA04810_REGULATION_OF_ACTIN_CYTOSKELETON | HSA05215_PROSTATE_CANCER |
| ST_INTEGRIN_SIGNALING_PATHWAY | METPATHWAY | INTEGRIN_MEDIATED_CELL_ADHESION_KEGG |
| | IL7PATHWAY | FMLPPATHWAY |
| PCDM2 | PCGDM2 | |
| HSA04810_REGULATION_OF_ACTIN_CYTOSKELETON | HSA04520_ADHERENS_JUNCTION | |
| HSA04010_MAPK_SIGNALING_PATHWAY | CELL2CELLPATHWAY | |
| HSA04512_ECM_RECEPTOR_INTERACTION | INTEGRINPATHWAY | |
| HSA04510_FOCAL_ADHESION | INTEGRIN_MEDIATED_CELL_ADHESION_KEGG | |
| | HSA04670_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | |
| | HSA01430_CELL_COMMUNICATION | |

Table S4: Comparison of modules' enriched GO categories. The green cells represent GO categories enriched in PCDM1, the red cells represent GO categories enriched in PCDM2, and the blue cells represent GO categories enriched in PCDM3.

| *RegMOD* | *GiGA* | *jActivModules* |
|---|---|---|
| PCDM1 | PCGDM1 | PCjAM1 |
| CELL_MATRIX_JUNCTION | SIGNAL_TRANSDUCTION | CYTOSKELETON |
| BASOLATERAL_PLASMA_MEMBRANE | TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY | ACTIN_FILAMENT_BASED_PROCESS |
| CELL_JUNCTION | POSITIVE_REGULATION_OF_CELLULAR_PROCESS | POSITIVE_REGULATION_OF_CELLULAR_PROCESS |
| CELL_SUBSTRATE_ADHERENS_JUNCTION | POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS | BLOOD_COAGULATION |
| ADHERENS_JUNCTION | RECEPTOR_COMPLEX | CYTOSKELETAL_PROTEIN_BINDING |
| FOCAL_ADHESION_FORMATION | POSITIVE_REGULATION_OF_CELL_PROLIFERATION | INTRINSIC_TO_MEMBRANE |
| SIGNAL_TRANSDUCTION | INTRACELLULAR_SIGNALING_CASCADE | CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS |
| FOCAL_ADHESION | PROTEIN_KINASE_ACTIVITY | COAGULATION |
| POSITIVE_REGULATION_OF_CELLULAR_PROCESS | PROTEIN_TYROSINE_KINASE_ACTIVITY | REGULATION_OF_CELL_MIGRATION |
| CELL_MATRIX_ADHESION | JAK_STAT_CASCADE | WOUND_HEALING |
| CELL_SUBSTRATE_ADHESION | TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY | MEMBRANE_PART |
| REGULATION_OF_PROTEIN_IMPORT_INTO_NUCLEUS | PHOSPHOTRANSFERASE_ACTIVITY__ALCOHOL_GROUP_AS_ACCEPTOR | POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS |
| POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS | RECEPTOR_SIGNALING_PROTEIN_ACTIVITY | INTEGRAL_TO_MEMBRANE |
| PROTEIN_IMPORT_INTO_NUCLEUS | SMAD_BINDING | ACTIN_CYTOSKELETON |
| NUCLEAR_IMPORT | ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY | CELL_SUBSTRATE_ADHERENS_JUNCTION |
| REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT | TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY | SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY |
| RECEPTOR_COMPLEX | G_PROTEIN_SIGNALING__COUPLED_TO_IP3_SECOND_MESSENGER__PHOSPHOLIPASE_C_ACTIVATING | HEMOSTASIS |
| REGULATION_OF_INTRACELLULAR_TRANSPORT | PHOSPHOLIPASE_C_ACTIVATION | CYTOSKELETAL_PART |
| REGULATION_OF_CELL_MIGRATION | TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY | NEGATIVE_REGULATION_OF_METABOLIC_PROCESS |
| RESPONSE_TO_HYPOXIA | KINASE_ACTIVITY | INTRACELLULAR_NON_MEMBRANE_BOUND_ORGANELLE |
| PCDM2 | PCGDM2 | |
| RECEPTOR_BINDING | CELL_MATRIX_JUNCTION | |
| | CELL_JUNCTION | |
| | BASOLATERAL_PLASMA_MEMBRANE | |
| PCDM3 | CELL_SUBSTRATE_ADHERENS_JUNCTION | |
| REGULATION_OF_APOPTOSIS | ADHERENS_JUNCTION | |
| REGULATION_OF_PROGRAMMED_CELL_DEATH | FOCAL_ADHESION | |
| NERVOUS_SYSTEM_DEVELOPMENT | CYTOSKELETAL_PROTEIN_BINDING | |
| APOPTOSIS_GO | CELL_MATRIX_ADHESION | |
| PROGRAMMED_CELL_DEATH | CELL_SUBSTRATE_ADHESION | |
| REGULATION_OF_DEVELOPMENTAL_PROCESS | PROTEIN_COMPLEX_BINDING | |
| EXTRACELLULAR_REGION | FOCAL_ADHESION_FORMATION | |
| CELL_DEVELOPMENT | INTERCELLULAR_JUNCTION | |
| STRUCTURAL_MOLECULE_ACTIVITY | ACTIN_BINDING | |
| SYSTEM_DEVELOPMENT | CYTOSKELETAL_PART | |
| EXTRACELLULAR_REGION_PART | MYOFIBRIL | |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | CONTRACTILE_FIBER_PART | |
| MULTICELLULAR_ORGANISMAL_DEVELOPMENT | CONTRACTILE_FIBER | |
| PROTEIN_METABOLIC_PROCESS | REGULATION_OF_CELL_MIGRATION | |
| | ACTIN_CYTOSKELETON | |
| | INTEGRIN_BINDING | |