Convergent architecture of the transcriptome in human cancer

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ABSTRACTS

Despite large-scale efforts to systematically map the cancer genome, little is known about how the interplay of genetic and epigenetic alternations shapes the architecture of the tumor's transcriptome. With the goal of constructing a system-level view of the deregulated pathways in cancer cells, we systematically investigated the functional organization of the transcriptomes of 10 tumor types using data sets generated by The Cancer Genome Atlas project (TCGA). Our analysis indicates that the human cancer transcriptome is organized into well-conserved modules of co-expressed genes. In particular, our analysis identified a set of conserved gene modules with distinct cancer hallmark themes involving cell cycle regulation, angiogenesis, innate and adaptive immune response, differentiation, metabolism and regulation of protein phosphorylation. We applied a network inference approach to nominate candidate drivers of these conserved gene modules. The predicted drivers have consistent cancer-relevant functions related to the specific hallmarks and are enriched with cancer consensus genes and significantly mutated genes. We showed genetic alternations of *TP53* and other cell cycle drivers have major downstream transcriptional impact on cell cycle regulation. Collectively, our analysis provided global views of convergent transcriptome architecture of human cancer. The result of our analysis can serve as a foundation to link diverse genomic alternations to common transcriptomic features in human cancer.

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INTRODUCTION

The evolutionary history of a cancer cell has documented the accumulation of random ‘passenger’ mutations along with a few rate-limiting ‘driver’ events which confer fitness benefit to the cell. The cumulative effect of acquired driver events eventually set cancerous cells into uncontrolled state of proliferation, immortality, angiogenesis, cell death, invasion and metastasis. However, how the genetic and epigenetic effects propagate through intricate gene and biochemical circuits to cause deregulated cellular states within a cancer cell is still largely unknown. A promising approach is to decompose the oncogenic state of tumor cells directly in terms of the activity of sets of conserved biological features that has been described as the hallmarks of cancers¹.

The comprehensive multi-dimensional genomic data provided by TCGA datasets across many tumor types offers an unprecedented opportunity to deepen our understanding of cancer biology and the discovery of new therapeutic and diagnostic targets. Gene expression analyses using unsupervised clustering approaches have been widely used in cancer research. Although informative, these methods analyzed gene level information and are prone to intrinsic noise caused by various biological and experimental factors. During the last decade, studies²⁻⁵ showed that gene modules consisting of co-regulated or co-expressed genes can be considered as higher-order building blocks of the global transcriptomic network and have been successfully applied to detect gene-disease association by improving the statistical power beyond the level of individual genes. Systematic data-driven approaches⁶⁻¹⁰ have also been developed to identify co-expressed gene modules in order to elucidate patterns of transcriptome organization across tissues and species.

We adopt the data-driven strategy to investigate the co-expression networks across 10 TCGA human cancer data sets including glioblastoma multiforme (GBM), ovarian carcinoma (OV), colon and rectal cancer (COADREAD), lung squamous cell carcinoma (LUSC), breast invasive carcinoma (BRCA), head and neck squamous cell carcinoma (HNSC), kidney renal

clear cell carcinoma (KIRC), bladder urothelial carcinoma (BLCA), uterine corpus endometrioid carcinoma (UCEC) (Supplementary Table 1). Our analysis pipeline has four components: 1) construction of the co-expression network for each cancer data set and decomposition of the network into Co-expressed Gene Modules (CGMs) (Figure 1a); 2) identification of 'conserved' (or overlapping) CGMs across multiple tumor types (Figure 1b); 3) extraction of the core genes of conserved CGMs and classification of CGMs by cancer hallmark themes (Figure 1c); and 4) nomination of putative drivers of CGMs based on analysis of the human protein interaction network (Figure 1d).

Overall, we identified a set of conserved cancer CGMs across multiple tissue lineages. These conserved cancer CGMs are enriched with distinct gene ontology and cancer hallmark themes. Predicted module drivers have consistent cellular functions with their corresponding hallmarks and are enriched with cancer consensus genes and significantly mutated genes.

RESULTS

Co-expression network analysis reveals conservation of gene modules

We followed a previously described method⁹ and constructed gene co-expression networks on the basis of Pearson correlation between the RNA-seq expression profiles for the 10 TCGA cancer data sets (Supplementary Methods). For each cancer data set, co-expressed gene modules (CGMs) were identified in two steps: First, we performed unsupervised hierarchical clustering of the gene expression profiles using the topological overlap^{8,11} as a pair-wise distance measure; and then applied the dynamic tree cut method¹² to decompose the dendrogram at different height and merge the clusters to form stable CGMs iteratively (Supplementary Methods). We defined 12 CGMs in GBM, 5 in OV, 10 in COADREAD, 8 in LUSC, 7 in BRCA, 9 in HNSC, 11 in BLCA, 8 in KIRC, and 9 in UCEC. In total, 79 cancer CGMs were identified by this analysis.

Next we tested whether these CGMs can be validated using data from other experimental platforms and in independent data sets. We first compared the TCGA GBM expression data (syn1446212) measured by RNA-seq and by Affymetrix microarrays. We applied the same procedures to both data sets and were able to detect the majority of the CGMs defined using Affymetrix microarray when using RNA-seq data, suggesting that CGMs are reproducible across technical platforms (Supplementary Figure 1). We performed a similar comparison using 2 independently published GBM expression data sets (GSE4271, GSE13041) and reassuringly, as above, the majority of CGMs detected in the TCGA data were also detected in the external data sets demonstrating the robustness of the CGMs (Supplementary Figure 1).

To determine whether CGMs from different cancer data sets were composed of overlapping genes, we enumerated all pair-wise CGMs ($n=2,756$) from any two different cancer data sets and identified 509 pairs of CGMs with significant mutual overlap (Bonferroni corrected hypergeometric test, $p < 0.05$, Supplementary Materials). The list of overlapping pairs of CGMs is provided in Supplementary Table 2. Surprisingly, 63 out of 79 (82%) CGMs showed significant overlap with CGMs detected in at least two different tumor types (Figures 2 and 3). Taken together, our analysis suggests that the human cancer transcriptome is organized into modules of co-expressed genes that are conserved across tumor types.

Hierarchical organization of co-expressed gene modules

To better understand their global organization, we sought to define the relationships between these CGMs through the construction of a module-module network. The resulting network has 79 nodes, each represents one CGM, and 509 edges between significantly overlapping CGMs. Many module nodes appear to be closely connected on the resulting network (Figure 3b). To visualize the multi-level relationship among the CGMs, we transformed the module-module network into a hierarchical tree (Figure 3a) based on the random walk distance¹³. We

partitioned the hierarchical tree into subtrees or module groups based on network modularity¹⁴ (modularity threshold=0.37, Supplementary Materials), a graph structure measure reflecting the enrichment of edges among nodes within a group (or cluster) relative to the nodes between the groups.

As shown in Figure 3b, our analysis revealed 11 groups of CGMs comprised of the 63 CGMs with high degree of mutual overlap (Figures 2 and 3). The 11 CGM groups have a median of 5 CGMs representing at least 3 different tumor types in each group. This implies that these CGM groups capture common or ‘conserved’ cellular processes across cancer types. The 11 CGM groups are shown as distinct subtrees on the transformed hierarchical tree of CGMs (Figure 3a). Notably, the red, turquoise, and orange CGMs fall within one branch delineated by the green square on Figure 3a which mostly involves immune response. The blue, purple, and magenta modules fall within another branch (enclosed by the blue square on Figure 3a) which primarily involves angiogenesis, epithelial-mesenchymal transformation (EMT) and muscle development. The hierarchical tree of identified gene modules suggests convergent functional organization of cellular programs of tumor independent of their tissue lineage.

To test whether genes belonging to each of the CGM groups are indeed co-expressed across their tumor types, we calculated the Pearson correlation for all gene pairs between their expression levels in the relevant tumor types. We confirmed the gene-gene correlation within the overlapping CGMs is significantly higher than expected from a random gene set of the same size (Kolmogorov-Smirnov test $p < 2.6 \times 10^{-16}$, Figure 3c).

Conserved expression modules are enriched with cancer hallmarks

To assess possible biological functions of the CGMs, we calculated gene ontology enrichment for individual CGM (Figure 4, Supplementary Materials). We also extract core module genes (Supplementary Materials) for each of the 11 CGM group and calculate its functional enrichment

using DAVID tools (<http://david.niaid.nih.gov/david/>). We classified the CGMs into 7 functional categories based on their specific enrichment of gene ontology¹⁵ and cancer hallmarks (Supplementary Table 3): (i) cell cycle ($FDR < 2.2 \times 10^{-51}$, black modules of Figure 2-4); (ii) innate immune response ($FDR < 7 \times 10^{-14}$, red modules of Figure 2-4); (iii) adaptive immune response ($FDR < 5.6 \times 10^{-109}$, turquoise and orange modules of Figure 2-4); (iv) differentiation ($FDR < 9 \times 10^{-10}$, brown modules of Figure 2-4); (v) angiogenesis/EMT ($FDR < 2 \times 10^{-7}$, blue, purple, and magenta modules of Figure 2-4); (vi) metabolism ($FDR < 0.1$ green and pink modules of Figure 2-4); (vii) phosphorylation ($FDR < 0.3$, yellow modules). We referred to these classified CGMs as “hallmark gene modules” and highlighted their core module genes below. We provide the full list of core module genes in Supplementary Table 4.

The cell cycle modules (class i, black modules of Figure 2-4) are enriched with genes involving chromosome instability (i.e. *CENPA*, *BUB3*, *NUF2*¹⁶⁻¹⁸) and DNA replication (i.e. *CDC45*, *MCM10*¹⁹). Other notable genes in this module include transcription factors *MYBL2*, *FOXM1*, *E2F2* and mitotic regulators such as *CCNB2*, *CDK1*, *AURKB*, *CDC25A* and *CDC25C*. The innate immune modules (class ii, red modules of Figure 2-4) include multiple INF-signaling and virus-response pathway genes including *IFI27*, *IFI6*, *IRF9* and several MHC class I genes including *HLA-B*, *HLA-H*, *HLA-L*. Mutations and somatic copy number alternations (SCNAs)(doi:10.7303/syn300013) in several *HLA* gene family members affect about 10% of total TCGA cancer patients (Supplementary Figure 2). The adaptive immune modules (class iii, turquoise and orange modules of Figure 2-4) are present in all 10 TCGA cancer data sets for this analysis. The core adaptive immune genes include multiple inflammatory response genes *CD163*, *CPVL*, *FPR3* and members of MHC class II genes including *HLA-DOA*, *HLA-DPA1*, *HLA-DPB1*.

The angiogenesis/EMT modules (class iv, blue modules of Figure 2-4) are present across all 10 TCGA data sets in this study. Core genes of the angiogenesis/EMT modules

include *FN1*, *MMP2*, *TWIST1*, and *WNT5A* that are involved with cell adhesion, embryonic development, angiogenesis and TGF-beta mediated signaling¹. Somatic mutations and SCNAs in members of angiogenesis and TGF-beta pathway are shown to affect 37% of human cancers (Supplementary Figure 2). The differentiation modules (class v, brown modules of Figure 2-4) appear to be specific to squamous carcinoma including LUSC, HNSC and BLCA. The core genes of the differentiation module contains multiple tissue differentiation genes, for example, *SOX2*, *TP63*, *KRT5*, *KRT16*, *HOXA10* and *WNT* signaling pathway genes *WNT4* and *WNT7B*^{20,21}. *SOX2* is reported previously as lineage-survival proto-oncogene with essential roles in the differentiation and development of normal squamous cell²². *SOX2* is located on 3q26, a frequent amplified region in HNSC and LUSC²³. The mutual exclusivity between *SOX2* and *TP63* mutations (Supplementary Figure 2) suggests a convergent mechanism driving the differentiation transcriptional programs among a subset of squamous carcinoma.

Functions of imputed module drivers reflect hallmark themes

We next sought to nominate candidate drivers of the conserved CGMs. Previous studies suggest that disease genes in close proximity on the protein interaction network (PIN) will likely be functionally related^{24,25}. We compiled a joint human PIN dataset from various resources including HPRD²⁶, NCI-PID²⁷, Cancer Cell Map from (<http://cancer.cellmap.org/cellmap/>), and REACTOME²⁸ (Supplementary Material). For each of the CGM groups, we applied a network-based driver inference algorithm (*NetSig*, Supplementary Materials) to prioritize putative module drivers based on their proximity to the core module genes on the PIN. Figure 5 shows examples of protein subnetworks comprised of the direct protein interactions between the top candidate module drivers (red node, Figure 5) and the most connected core module genes (Supplementary Materials).

Our analysis identified a total of 318 candidate module drivers (doi:10.7303/syn1960770). Many of the top candidate drivers identified by *NetSig* have

consistent oncogenic roles relevant to the functional classes of their CGMs. For example, top candidate drivers (red nodes, Figure 5a) of the cell cycle modules (black modules, Figure 5) include *TP53*, *BRCA1*, *CDKN1A*, *CDK2*, *CDC6*, *PCNA* and *BUB1A*, all of which have well-known roles in the regulation of cell cycle and genomic stability¹. Notably, non-synonymous mutations and focal SCNAs of *TP53* and other cell cycle drivers are present in 55% of the human cancers (Figure 6d). This highlights the role of DNA repair and genomic instability as the key enabling hallmarks of human cancer. Tumor patients carrying genetic alternations of *TP53* and other cell cycle drivers tend to have increased number of SCNA events (especially deletions) (Figure 6b), which is in agreement with the observation made independently by Zack et al. *Submitted*. To assess the downstream transcriptional impact of the genetic alternations to the cell cycle drivers, we defined the pathway activity of a gene set in terms of the coefficient of the first principle component of the expression matrix of the pre-defined gene set²⁹. Then we calculated the pathway activity for the cell cycle modules and the knowledge-based KEGG cell cycle pathway³⁰. The activity profile of the cell cycle modules and the KEGG cell cycle pathway (Figure 6e) are concordant with each other and both highly up-regulated among tumor patients with genetic changes of cell cycle drivers (student t-test, $p < 2.2 \times 10^{-16}$). In addition, the cell cycle module genes are expressed at much higher level than adjacent non-tumor tissues across 6 TCGA tumor types with such comparison available (Figure 6f).

The protein subnetworks of the angiogenesis/EMT modules (blue and purple modules, Figure 5) share several common candidate drivers including *CTNNB1*, *SMAD4*, *SRC*, and *ITGB1*, which have known regulatory and signaling roles in TCF-beta signaling, angiogenesis and EMT^{1,31,32}. Other notable candidate drivers in the subnetworks include *RAC1*, *EP300*, *EGFR* which have been shown to be frequently mutated in human cancer (doi:10.7303/syn1715784.2). The top predicted drivers of the closely related module group

(magenta modules, Figure 5f and Figure 3) include several muscle development genes including *DMD*, *DMN*, *SGCD* and *SRC* among others.

The top predicted drivers of the innate immune modules (red modules, Figure 5g) include *STAT2* and *RNASEL* among others. *STAT2* is reported to mediate the innate immunity and host defense mechanism via the Type I Interferon receptor³³. *RNASEL* contributes in many ways to the interferon anti-virus system³⁴. The top candidate drivers of the adaptive immune modules (turquoise and orange module, Figure 5) include *LCK*, *CD4*, *CBL*, *PTPN11* (also known as *SHP2*) with important roles in diverse immune response through the antigen recognition by the T cell receptor (TCR)³⁵. The top predicted drivers of the phosphorylation modules (yellow modules, Figure 5c) are linked to members of several major signaling pathways including *AR*, *ESR1*, *PIK3R1*, *HSP90AA1*, *JAK1*, *STAT3*, *SMAD4*¹.

The top predicted drivers of the metabolism modules (green modules, Figure 5b) include multiple members of the cohesin complex *SMC1A*, *SMC1B*, *SMC3*, *RAD21*, *STAG1* and *STAG2*. Cohesin complex are frequently mutated in acute myeloid leukemia (AML)³⁶ and defects in cohesin complex may underlie chromosomal instability of human cancers^{37,38}. Other notable candidates of the subnetwork include *H2AFX*, *HIST3H3*, *RHOA*, *MAPK8* and *MAPK14*. *H2AFX* is frequently mutated in the Pan-Cancer data by MutSig algorithm³⁹ (doi:10.7303/syn1715784.2).

We next asked whether the module drivers are enriched with cancer genes targeted by genomic alternations. We compared the predicted module drivers with the mutation drivers identified by the MutSig algorithm in the Pan-Cancer data (doi:10.7303/syn1715784.2). There are 29 out of 318 predicted modules drivers (Supplementary Table 3) overlapping with mutation drivers (hypergeometric test $p < 8 \times 10^{-26}$). There are 41 out of 318 module drivers (Supplementary Table 5) overlapping with the Cancer Consensus Genes (CCG)⁴⁰³⁸ (hypergeometric test $p < 1 \times 10^{-20}$). Overall, the result suggests that the predicted module

drivers likely capture aspects of the biology and shed new light on the functional context of the cancer drivers discovered via mutation analysis.

DISCUSSION

To our knowledge, this is the first extensive investigation of human cancer transcriptome to date. Our study defined the global transcriptome architecture of human cancer. We identified 11 groups of CGMs conserved across multiple tumor types. These conserved CGMs display distinct gene ontologies and cancer hallmark themes. The highly conserved CGMs across tumor types suggest the existence of selective force shaping the cancer transcriptome. Such conserved CGMs can be viewed as ‘building blocks’ of the cancer transcriptome and be used as surrogate for the common cellular functions of human cancer. We noticed these conserved CGMs are significantly correlated with a large collection of published gene signatures (data not shown) although they are derived directly from the data and not dependent on any prior knowledge. As an example, we showed that the activity profile of the cell cycle modules is highly concordant with the knowledge-based KEGG cell cycle pathway (Figure 6e).

As a starting point to understand the common genetic and regulatory mechanism of these conserved CGMs, we integrated cancer transcriptome and interactome to nominated drivers for the conserved CGMs. We showed the predicted module drivers recapitulate known tumor biology and have consistent cancer-relevant functions with the hallmark themes of the conserved CGMs. Our analysis support that the cell cycle regulation and chromatin maintenance are the key system hallmarks of human cancer. Genetic alternations of *TP53* and other cell cycle drivers have major downstream transcriptional impact on the cell cycle regulation from our Pan-Cancer analysis. We anticipate future studies to elucidate mechanism leading to the deregulation of the hallmark gene modules would have direct implications for the design of new drug targets and contribute to novel pathway-focused therapeutic paradigm.

METHODS SUMMARY

The 10 TCGA Pan-Cancer data sets used for our study are available from Sage Bionetworks (doi:10.7303/syn300013). The RNAseq molecular profiling was based on IlluminaHiSeq_RNAseqV2. The RNAseq data preprocessing was carried out using the SeqWare Pipeline project, version 0.7.0. The normalized level 3 RNAseq expression was based on RSEM⁴¹. Significantly recurrent SCNAs were identified using GISTIC 2.0^{42,43} on relative total copy-number data after correction for sample purity. Significantly mutated genes were identified using MutSig³⁹. Co-expression network analysis was based on WGCNA package⁴⁴.

FIGURE LEGENDS

Figure 1. Overview of Pan-Cancer hallmark module analysis. **a**, For RNAseq data of each cancer data set, we construct the co-expression network based on the pair-wise Pearson correlation of gene expression profile. In total, 79 CGMs were identified by dynamic tree cut algorithm¹². **b**, We enumerate all possible pairs of CGMs from any two different cancer data sets to find 11 groups of conserved CGMs across tumor types. **c**, We extract core module genes for each of the conserved CGM groups. We also classify the conserved CGMs into 7 functional categories by their enriched cancer hallmarks. **d**, We map the core module genes onto a human protein interaction network and apply NetSig to nominate module drivers (Supplementary Methods).

Figure 2. Detection of conserved co-expressed gene modules. **a-i**, Each dendrogram corresponds to the co-expression network of one of the 10 cancer data set (COAD and READ are combined into one cancer data set) produced by average linkage hierarchical clustering of genes on the basis of topological overlap¹¹. The vertical scale of the dendrogram is the measure

of distance i.e. $1 - ||d||$, where d is Pearson correlation of a pair of expression profile. CGMs in each cancer data set are assigned unique color to distinguish different modules and numbered uniquely (e.g. M1, M2 ..) within the set. The M2 module of OV (indicated by *) is at the borderline of modularity cutoff (Supplementary Materials) and is manually assigned to the pink group. We merged the M7 module of COADREAD with two close neighbors M3, M9 as indicated within the brackets. Conserved CGMs from different cancer data sets with significant gene overlap were assigned the same color as indicated by the horizontal bar beneath each dendrogram. For clarity, only CGMs conserved in at least 3 different tumor types are shown. The remaining non-conserved or poorly connected genes are colored white. The color key at the bottom shows the function categories of the conserved CGMs.

Figure 3. Hierarchical organization of conserved co-expressed gene modules. **a**, The leafs of the hierarchical tree represent a CGM. Groups of highly conserved CGMs are shown as distinct subtrees of the hierarchical tree corresponding to the module-module network shown below. The dotted line represents modularity threshold. **b**, Each node in the module-module network represents a CGM. Each edge represents the gene overlap between two CGMs of different tumor types. The color circles indicate the conserved CGM groups. The node color matches the leaf color of the tree. **c**, Each colored histogram shows the Pearson correlation of all possible gene pairs from one of the conserved module group. The overlapping grey histogram to the left shows the Pearson correlation of all genes pairs from a random gene set which has the same size of the conserved module group.

Figure 4: Gene ontology of co-expressed gene modules. The columns of the matrix are the conserved CGMs. Examples of core genes (indicated within the colored square) for each of the conserved CGMs are shown below the matrix. The color rectangulars along the diagonal

indicate the conserved CGM groups (columns) and their most significantly associated gene ontology terms (rows). The color intensity of the matrix cell represents the level of association by one-sided hypergeometric test. Columns are ordered so the modules of the same group are together. The rows are grouped so the most significantly enriched gene ontology terms for a module group are together.

Figure 5: Examples of protein subnetworks connecting conserved module genes. a-i, The red round shaped nodes in each protein subnetwork indicate top candidate drivers of one of the conserved CGM group. The red square shaped nodes represent the predicted drivers that are also SMGs according to MutSig analysis. The edges connecting two nodes represent the human protein-protein interactions. The predominate cellular functions of the predicted module drivers are indicated next to each protein subnetwork. The functional classes of the predicted module drivers are shown at the bottom.

Figure 6: Transcriptional impact of genetic alternations of cell cycle drivers. a, The color keys for different tumor types used in this study. **b,** The stacked barplot shows sample-by-sample counts of broad amplification (red) and deletion events (blue) across tumor types (horizontal axis). **c,** The heatmap shows the SCNAs in each cancer sample (horizontal axis) plotted by chromosomal locations (vertical axis). **d,** The heatmap shows the somatic mutations of key cell cycle drivers sample-by-sample across tumor types. **e,** The pathway activity profile²⁹ of the core cell cycle modules and the KEGG cell cycle pathway. The color key of somatic mutations and SCNA, the scale of pathway activity and copy number value based on GISTIC2⁴³ are shown below the activity profile from left to right. **f,** The boxplots show the comparison between the expression level (vertical axis) of the core cell cycle genes in adjacent normal tissue versus tumor tissue in 6 different TCGA data sets.

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Author Contributions

LZ conceived the study and performed the analysis and wrote the paper.

Zou_Fig.1

Zou_Fig.2

Color keys of conserved Co-expressed Gene Modules (CGMs):

i) Cell Cycle	iii) Adaptive Immune	v) Differentiation	vii) Phosphorylation
ii) Innate Immune	iv) Angiogenesis/EMT	vi) Metabolism	

Zou_Fig.3

Zou_Fig.6

Zou_Suppl_Fig.1

Zou_Suppl_Fig.2

Zou_Suppl_Fig.3

Zou_Suppl_Table_1

Cancer	SynapseID	Number of Samples	Number of Exome	Number of CNV	Number of MIR	Number of RPPA	Number of Co-expr. Modules	Gene Size of Co-expr. Network
GBM	syn1461183	154	563	112	491	214	12	3526
OV	syn1461171	262	559	582	568	332	5	3487
COADREAD	syn1461155 and syn1461175	264	575	350	551	399	10	2712
LUSC	syn1461168	220	343	226	332	195	8	3499
BRCA	syn1461151	841	866	575	868	408	7	3268
HNSC	syn1461156	303	306	310	309	212	9	3394
KIRC	syn1461159	469	493	283	480	453	11	3363
BLCA	syn1461149	96	135	138	124	54	8	3380
UCEC	syn1461180	333	492	383	485	200	9	3251

Zou_Suppl_Table_2

Module.1	Module.2	Adjusted.P-value
GBM.black	OV.green	3.60E-38
GBM.black	BRCA.turquoise	2.87E-31
GBM.black	KIRC.yellow	3.91E-54
GBM.black	UCEC.blue	1.81E-25
GBM.blue	LUSC.blue	0.001955469
GBM.blue	BRCA.blue	0.00028959
GBM.blue	HNSC.blue	8.68E-07
GBM.blue	KIRC.red	0.02992095
GBM.blue	UCEC.red	0.002824684
GBM.brown	COADREAD.turquoise	0.02830111
GBM.brown	HNSC.brown	0.00147624
GBM.brown	KIRC.brown	0.004390626
GBM.brown	BLCA.yellow	2.06E-05
GBM.green	OV.brown	1.45E-11
GBM.green	COADREAD.purple	6.96E-46
GBM.green	LUSC.black	1.09E-63
GBM.green	BRCA.turquoise	0.002820383
GBM.green	HNSC.pink	4.29E-50
GBM.green	KIRC.blue	1.23E-88
GBM.green	UCEC.black	1.13E-61
GBM.greenyellow	BRCA.red	2.40E-18
GBM.greenyellow	KIRC.purple	1.05E-29
GBM.greenyellow	UCEC.pink	9.97E-33
GBM.magenta	LUSC.green	0.0136676
GBM.magenta	BRCA.green	0.006473287
GBM.magenta	KIRC.brown	0.01165685
GBM.pink	OV.blue	3.41E-34
GBM.pink	COADREAD.brown	1.94E-08
GBM.pink	LUSC.blue	3.51E-34

GBM.pink	BRCA.blue	9.83E-31
GBM.pink	HNSC.blue	2.54E-22
GBM.pink	KIRC.red	3.92E-25
GBM.pink	BLCA.brown	3.03E-14
GBM.pink	UCEC.green	2.36E-22
GBM.purple	OV.blue	2.68E-07
GBM.purple	COADREAD.brown	8.20E-06
GBM.purple	LUSC.blue	8.82E-05
GBM.purple	BRCA.green	0.000226317
GBM.purple	HNSC.blue	0.000124524
GBM.purple	KIRC.brown	4.09E-12
GBM.purple	BLCA.yellow	0.02121653
GBM.purple	UCEC.green	5.95E-08
GBM.red	OV.turquoise	8.97E-13
GBM.red	COADREAD.green	9.66E-06
GBM.red	LUSC.turquoise	5.50E-11
GBM.red	BRCA.yellow	5.99E-14
GBM.red	HNSC.yellow	3.92E-06
GBM.red	KIRC.pink	1.10E-20
GBM.red	BLCA.turquoise	7.33E-12
GBM.red	UCEC.yellow	3.84E-13
GBM.tan	OV.yellow	2.51E-40
GBM.tan	COADREAD.yellow	9.95E-14
GBM.tan	LUSC.yellow	3.41E-31
GBM.tan	BRCA.black	5.00E-45
GBM.tan	HNSC.magenta	6.00E-49
GBM.tan	KIRC.green	2.85E-16
GBM.tan	BLCA.pink	4.51E-36
GBM.tan	UCEC.magenta	1.68E-60
GBM.turquoise	OV.turquoise	9.89E-63
GBM.turquoise	COADREAD.yellow	2.50E-22
GBM.turquoise	LUSC.turquoise	4.56E-37
GBM.turquoise	BRCA.yellow	3.25E-35
GBM.turquoise	HNSC.yellow	1.93E-51

GBM.turquoise	KIRC.pink	3.10E-26
GBM.turquoise	BLCA.turquoise	1.72E-39
GBM.turquoise	UCEC.yellow	9.09E-38
GBM.yellow	OV.brown	5.97E-48
GBM.yellow	COADREAD.magenta	0.00554752
GBM.yellow	LUSC.pink	7.30E-31
GBM.yellow	BRCA.turquoise	2.05E-05
GBM.yellow	KIRC.turquoise	6.07E-06
GBM.yellow	UCEC.turquoise	5.97E-23
OV.blue	GBM.pink	1.39E-29
OV.blue	COADREAD.brown	5.15E-24
OV.blue	LUSC.blue	8.16E-140
OV.blue	BRCA.blue	1.55E-109
OV.blue	HNSC.blue	4.75E-77
OV.blue	KIRC.red	4.62E-43
OV.blue	BLCA.brown	5.69E-73
OV.blue	UCEC.green	2.74E-90
OV.brown	GBM.yellow	2.77E-47
OV.brown	COADREAD.purple	5.77E-14
OV.brown	LUSC.pink	3.09E-62
OV.brown	BRCA.turquoise	3.08E-13
OV.brown	HNSC.pink	3.98E-19
OV.brown	KIRC.blue	4.73E-15
OV.brown	UCEC.turquoise	3.93E-49
OV.green	GBM.black	1.52E-34
OV.green	BRCA.turquoise	1.31E-14
OV.green	KIRC.yellow	3.13E-19
OV.green	BLCA.blue	0.0086865
OV.green	UCEC.blue	1.14E-24
OV.turquoise	GBM.turquoise	2.60E-71
OV.turquoise	COADREAD.yellow	1.46E-37
OV.turquoise	LUSC.turquoise	3.91E-49
OV.turquoise	BRCA.yellow	2.19E-71

OV.turquoise	HNSC.yellow	1.05E-55
OV.turquoise	KIRC.pink	1.65E-56
OV.turquoise	BLCA.turquoise	3.06E-75
OV.turquoise	UCEC.yellow	2.07E-71
OV.yellow	GBM.tan	2.51E-45
OV.yellow	COADREAD.yellow	5.45E-10
OV.yellow	LUSC.yellow	3.97E-19
OV.yellow	BRCA.black	1.53E-57
OV.yellow	HNSC.magenta	2.96E-40
OV.yellow	KIRC.green	7.32E-08
OV.yellow	BLCA.pink	2.47E-40
OV.yellow	UCEC.magenta	2.47E-43
COADREAD.black	HNSC.black	0.007794982
COADREAD.black	KIRC.blue	0.03646471
COADREAD.black	BLCA.green	0.002211642
COADREAD.blue	GBM.turquoise	0.00457559
COADREAD.blue	LUSC.brown	0.01203316
COADREAD.blue	BRCA.red	0.006733661
COADREAD.blue	HNSC.brown	0.001154678
COADREAD.blue	KIRC.purple	0.001713155
COADREAD.blue	UCEC.magenta	0.000212338
COADREAD.brown	GBM.pink	2.23E-09
COADREAD.brown	OV.blue	9.77E-31
COADREAD.brown	LUSC.blue	2.15E-30
COADREAD.brown	BRCA.blue	9.80E-20
COADREAD.brown	HNSC.blue	6.42E-26
COADREAD.brown	KIRC.red	1.69E-08
COADREAD.brown	BLCA.brown	1.77E-23
COADREAD.brown	UCEC.green	9.80E-12
COADREAD.green	GBM.turquoise	5.53E-09
COADREAD.green	OV.turquoise	3.01E-32
COADREAD.green	LUSC.yellow	2.40E-30
COADREAD.green	BRCA.brown	1.70E-40
COADREAD.green	HNSC.turquoise	3.86E-18

COADREAD.green	KIRC.green	3.98E-26
COADREAD.green	BLCA.turquoise	7.34E-30
COADREAD.green	UCEC.brown	2.15E-22
COADREAD.magenta	OV.blue	1.20E-11
COADREAD.magenta	LUSC.blue	1.61E-06
COADREAD.magenta	BRCA.blue	3.34E-08
COADREAD.magenta	HNSC.green	3.29E-11
COADREAD.magenta	KIRC.greenyellow	2.01E-17
COADREAD.magenta	BLCA.red	1.89E-33
COADREAD.magenta	UCEC.red	8.68E-26
COADREAD.pink	GBM.pink	1.12E-06
COADREAD.pink	OV.blue	3.07E-12
COADREAD.pink	LUSC.blue	2.95E-19
COADREAD.pink	BRCA.blue	4.96E-17
COADREAD.pink	HNSC.blue	3.96E-17
COADREAD.pink	KIRC.red	8.40E-14
COADREAD.pink	BLCA.brown	3.28E-12
COADREAD.pink	UCEC.green	1.84E-10
COADREAD.purple	GBM.green	1.20E-36
COADREAD.purple	OV.brown	1.16E-08
COADREAD.purple	LUSC.black	1.08E-30
COADREAD.purple	HNSC.pink	5.64E-35
COADREAD.purple	KIRC.blue	9.05E-40
COADREAD.purple	UCEC.black	2.63E-38
COADREAD.red	GBM.pink	1.57E-06
COADREAD.red	OV.blue	1.89E-13
COADREAD.red	LUSC.blue	1.36E-13
COADREAD.red	BRCA.blue	1.17E-21
COADREAD.red	HNSC.blue	5.52E-20
COADREAD.red	KIRC.red	1.31E-07
COADREAD.red	BLCA.brown	8.38E-12

COADREAD.red	UCEC.green	3.40E-11
COADREAD.turquoise	BRCA.turquoise	7.55E-08
COADREAD.turquoise	KIRC.turquoise	1.76E-06
COADREAD.turquoise	BLCA.green	0.002901911
COADREAD.turquoise	UCEC.turquoise	0.01069324
COADREAD.yellow	GBM.turquoise	1.67E-20
COADREAD.yellow	OV.turquoise	1.12E-26
COADREAD.yellow	LUSC.turquoise	1.91E-19
COADREAD.yellow	BRCA.yellow	3.15E-31
COADREAD.yellow	HNSC.yellow	1.10E-24
COADREAD.yellow	KIRC.pink	6.02E-25
COADREAD.yellow	BLCA.turquoise	4.03E-31
COADREAD.yellow	UCEC.yellow	1.08E-33
LUSC.black	GBM.green	3.12E-52
LUSC.black	OV.brown	1.19E-08
LUSC.black	COADREAD.purple	1.80E-28
LUSC.black	HNSC.pink	1.25E-42
LUSC.black	KIRC.blue	3.82E-59
LUSC.black	UCEC.black	8.91E-50
LUSC.blue	GBM.pink	2.08E-29
LUSC.blue	OV.blue	1.21E-146
LUSC.blue	COADREAD.brown	2.03E-28
LUSC.blue	BRCA.blue	4.53E-148
LUSC.blue	HNSC.blue	3.68E-159
LUSC.blue	KIRC.red	4.83E-60
LUSC.blue	BLCA.brown	2.52E-95
LUSC.blue	UCEC.green	1.76E-69
LUSC.brown	HNSC.red	1.79E-18
LUSC.brown	BLCA.green	2.14E-28
LUSC.green	KIRC.turquoise	0.004866037
LUSC.green	BLCA.black	2.00E-09
LUSC.pink	GBM.yellow	2.10E-31

LUSC.pink	OV.brown	4.44E-56
LUSC.pink	BRCA.turquoise	2.90E-09
LUSC.pink	HNSC.pink	0.01970745
LUSC.pink	KIRC.turquoise	0.0251461
LUSC.pink	UCEC.turquoise	1.01E-31
LUSC.red	BRCA.green	0.01869355
LUSC.red	HNSC.green	0.000642402
LUSC.red	KIRC.turquoise	0.001324934
LUSC.red	BLCA.blue	0.00032609
LUSC.turquoise	GBM.turquoise	7.65E-47
LUSC.turquoise	OV.turquoise	1.66E-60
LUSC.turquoise	COADREAD.yellow	7.80E-28
LUSC.turquoise	BRCA.yellow	1.29E-76
LUSC.turquoise	HNSC.yellow	5.00E-110
LUSC.turquoise	KIRC.pink	7.22E-75
LUSC.turquoise	BLCA.turquoise	3.52E-59
LUSC.turquoise	UCEC.yellow	7.86E-59
LUSC.yellow	GBM.tan	2.28E-34
LUSC.yellow	OV.turquoise	4.28E-21
LUSC.yellow	COADREAD.green	5.21E-36
LUSC.yellow	BRCA.brown	1.74E-62
LUSC.yellow	HNSC.turquoise	9.20E-62
LUSC.yellow	KIRC.green	1.47E-112
LUSC.yellow	BLCA.turquoise	2.11E-23
LUSC.yellow	UCEC.brown	2.24E-48
BRCA.black	GBM.tan	5.95E-50
BRCA.black	OV.yellow	2.29E-56
BRCA.black	COADREAD.yellow	1.98E-09
BRCA.black	LUSC.yellow	3.27E-23
BRCA.black	HNSC.magenta	9.05E-43
BRCA.black	KIRC.green	1.28E-11
BRCA.black	BLCA.pink	1.35E-41
BRCA.black	UCEC.magenta	5.76E-55
BRCA.blue	GBM.pink	8.15E-29

BRCA.blue	OV.blue	5.32E-118
BRCA.blue	COADREAD.brown	7.69E-21
BRCA.blue	LUSC.blue	1.21E-145
BRCA.blue	HNSC.blue	4.59E-143
BRCA.blue	KIRC.red	1.05E-58
BRCA.blue	BLCA.brown	6.51E-90
BRCA.blue	UCEC.green	3.17E-60
BRCA.brown	GBM.turquoise	1.80E-16
BRCA.brown	OV.turquoise	1.35E-32
BRCA.brown	COADREAD.green	2.80E-44
BRCA.brown	LUSC.yellow	4.60E-59
BRCA.brown	HNSC.turquoise	7.13E-54
BRCA.brown	KIRC.green	1.77E-67
BRCA.brown	BLCA.turquoise	5.43E-36
BRCA.brown	UCEC.brown	3.56E-58
BRCA.green	GBM.purple	0.001997649
BRCA.green	OV.blue	2.31E-12
BRCA.green	COADREAD.brown	6.27E-06
BRCA.green	LUSC.turquoise	0.003788179
BRCA.green	HNSC.green	3.95E-20
BRCA.green	KIRC.brown	2.89E-33
BRCA.green	BLCA.yellow	9.53E-21
BRCA.green	UCEC.green	2.13E-09
BRCA.red	COADREAD.blue	1.76E-05
BRCA.red	LUSC.brown	0.01183595
BRCA.red	KIRC.purple	2.86E-42
BRCA.red	BLCA.blue	0.00402368
BRCA.red	UCEC.pink	4.11E-32
BRCA.turquoise	GBM.black	4.85E-42
BRCA.turquoise	OV.green	3.30E-15
BRCA.turquoise	COADREAD.turquoise	2.97E-05
BRCA.turquoise	HNSC.brown	3.97E-06
BRCA.turquoise	KIRC.yellow	2.36E-35

BRCA.turquoise	BLCA.blue	7.58E-16
BRCA.turquoise	UCEC.blue	1.70E-27
BRCA.yellow	GBM.turquoise	8.66E-39
BRCA.yellow	OV.turquoise	2.09E-68
BRCA.yellow	COADREAD.yellow	1.91E-38
BRCA.yellow	LUSC.turquoise	1.01E-75
BRCA.yellow	HNSC.yellow	2.95E-80
BRCA.yellow	KIRC.pink	1.02E-82
BRCA.yellow	BLCA.turquoise	3.71E-67
BRCA.yellow	UCEC.yellow	4.56E-86
HNSC.black	COADREAD.magenta	1.17E-05
HNSC.black	BRCA.green	0.004042421
HNSC.black	BLCA.red	3.14E-11
HNSC.black	UCEC.red	1.02E-08
HNSC.blue	GBM.pink	7.18E-23
HNSC.blue	OV.blue	8.20E-83
HNSC.blue	COADREAD.brown	9.67E-23
HNSC.blue	LUSC.blue	8.04E-159
HNSC.blue	BRCA.blue	1.01E-138
HNSC.blue	KIRC.red	3.21E-49
HNSC.blue	BLCA.brown	5.41E-98
HNSC.blue	UCEC.green	5.20E-58
HNSC.brown	GBM.brown	0.003436834
HNSC.brown	LUSC.brown	8.58E-20
HNSC.brown	BRCA.turquoise	0.000143654
HNSC.brown	BLCA.blue	9.45E-07
HNSC.brown	UCEC.turquoise	4.01E-06
HNSC.green	GBM.purple	0.008049011
HNSC.green	OV.blue	7.14E-11
HNSC.green	COADREAD.magenta	8.67E-16
HNSC.green	BRCA.green	2.18E-22
HNSC.green	KIRC.brown	4.54E-09
HNSC.green	BLCA.yellow	1.03E-19

HNSC.green	UCEC.green	6.80E-09
HNSC.magenta	GBM.tan	3.15E-52
HNSC.magenta	OV.yellow	6.50E-41
HNSC.magenta	COADREAD.yellow	1.19E-09
HNSC.magenta	LUSC.yellow	7.11E-17
HNSC.magenta	BRCA.black	1.22E-43
HNSC.magenta	KIRC.green	1.20E-09
HNSC.magenta	BLCA.pink	4.48E-53
HNSC.magenta	UCEC.magenta	8.20E-59
HNSC.pink	GBM.green	2.17E-47
HNSC.pink	OV.brown	2.72E-14
HNSC.pink	COADREAD.purple	5.69E-35
HNSC.pink	LUSC.black	2.45E-43
HNSC.pink	KIRC.blue	3.49E-63
HNSC.pink	BLCA.blue	0.002532541
HNSC.pink	UCEC.black	1.84E-37
HNSC.red	LUSC.brown	4.40E-22
HNSC.red	KIRC.turquoise	9.54E-05
HNSC.red	BLCA.green	3.78E-45
HNSC.turquoise	GBM.red	4.98E-12
HNSC.turquoise	OV.turquoise	8.27E-21
HNSC.turquoise	COADREAD.green	9.31E-29
HNSC.turquoise	LUSC.yellow	3.40E-61
HNSC.turquoise	BRCA.brown	4.85E-59
HNSC.turquoise	KIRC.green	4.40E-49
HNSC.turquoise	BLCA.turquoise	9.44E-24
HNSC.turquoise	UCEC.brown	6.20E-48
HNSC.yellow	GBM.turquoise	7.52E-56
HNSC.yellow	OV.turquoise	1.84E-55
HNSC.yellow	COADREAD.yellow	9.35E-36
HNSC.yellow	LUSC.turquoise	2.69E-118
HNSC.yellow	BRCA.yellow	2.02E-88
HNSC.yellow	KIRC.pink	2.43E-60
HNSC.yellow	BLCA.turquoise	4.43E-80

HNSC.yellow	UCEC.yellow	5.41E-98
KIRC.black	GBM.purple	2.98E-08
KIRC.black	OV.blue	3.65E-18
KIRC.black	COADREAD.brown	8.80E-11
KIRC.black	LUSC.blue	2.13E-17
KIRC.black	BRCA.blue	4.00E-16
KIRC.black	HNSC.blue	6.43E-18
KIRC.black	BLCA.yellow	8.16E-15
KIRC.black	UCEC.green	1.68E-18
KIRC.blue	GBM.green	1.08E-87
KIRC.blue	OV.brown	9.70E-13
KIRC.blue	COADREAD.purple	1.31E-48
KIRC.blue	LUSC.black	1.29E-68
KIRC.blue	HNSC.pink	2.36E-70
KIRC.blue	UCEC.black	1.41E-68
KIRC.brown	GBM.purple	1.16E-16
KIRC.brown	OV.blue	9.71E-14
KIRC.brown	COADREAD.red	0.002307719
KIRC.brown	LUSC.blue	2.76E-05
KIRC.brown	BRCA.green	2.07E-43
KIRC.brown	HNSC.green	1.82E-09
KIRC.brown	BLCA.yellow	2.05E-17
KIRC.brown	UCEC.green	1.06E-15
KIRC.green	GBM.turquoise	7.48E-18
KIRC.green	OV.turquoise	1.58E-24
KIRC.green	COADREAD.green	8.60E-32
KIRC.green	LUSC.yellow	1.23E-96
KIRC.green	BRCA.brown	2.13E-71
KIRC.green	HNSC.turquoise	4.31E-40
KIRC.green	BLCA.turquoise	2.29E-38
KIRC.green	UCEC.brown	1.98E-52
KIRC.greenyellow	GBM.pink	0.000250163
KIRC.greenyellow	OV.blue	1.51E-08

KIRC.greenyellow	COADREAD.magenta	3.77E-19
KIRC.greenyellow	LUSC.blue	2.03E-06
KIRC.greenyellow	BRCA.blue	1.78E-10
KIRC.greenyellow	HNSC.blue	1.42E-07
KIRC.greenyellow	BLCA.red	2.90E-14
KIRC.greenyellow	UCEC.red	3.07E-22
KIRC.magenta	GBM.turquoise	7.35E-23
KIRC.magenta	OV.turquoise	2.81E-18
KIRC.magenta	COADREAD.green	2.34E-13
KIRC.magenta	LUSC.turquoise	1.29E-14
KIRC.magenta	BRCA.yellow	2.08E-13
KIRC.magenta	HNSC.yellow	2.05E-22
KIRC.magenta	BLCA.turquoise	4.39E-16
KIRC.magenta	UCEC.yellow	3.49E-31
KIRC.pink	GBM.turquoise	3.57E-24
KIRC.pink	OV.turquoise	4.24E-55
KIRC.pink	COADREAD.yellow	1.54E-32
KIRC.pink	LUSC.turquoise	6.76E-70
KIRC.pink	BRCA.yellow	8.40E-84
KIRC.pink	HNSC.yellow	3.28E-60
KIRC.pink	BLCA.turquoise	1.74E-44
KIRC.pink	UCEC.yellow	4.22E-57
KIRC.purple	COADREAD.blue	0.005537789
KIRC.purple	BRCA.red	2.87E-37
KIRC.purple	UCEC.pink	2.18E-37
KIRC.red	GBM.pink	4.34E-24
KIRC.red	OV.blue	6.66E-43
KIRC.red	COADREAD.pink	1.04E-13
KIRC.red	LUSC.blue	1.26E-52
KIRC.red	BRCA.blue	1.66E-54
KIRC.red	HNSC.blue	3.72E-45
KIRC.red	BLCA.brown	2.47E-33
KIRC.red	UCEC.green	4.60E-29

KIRC.turquoise	GBM.yellow	5.32E-05
KIRC.turquoise	LUSC.red	0.001475322
KIRC.turquoise	BLCA.blue	0.007362857
KIRC.yellow	GBM.black	6.05E-54
KIRC.yellow	OV.green	8.70E-20
KIRC.yellow	BRCA.turquoise	1.17E-22
KIRC.yellow	BLCA.blue	0.01085711
KIRC.yellow	UCEC.blue	6.11E-20
BLCA.black	HNSC.green	0.000186086
BLCA.blue	LUSC.brown	6.56E-16
BLCA.blue	BRCA.turquoise	8.33E-09
BLCA.blue	HNSC.brown	3.84E-08
BLCA.blue	KIRC.turquoise	0.000131954
BLCA.brown	GBM.pink	6.02E-16
BLCA.brown	OV.blue	3.58E-78
BLCA.brown	COADREAD.brown	7.84E-27
BLCA.brown	LUSC.blue	3.18E-97
BLCA.brown	BRCA.blue	1.09E-95
BLCA.brown	HNSC.blue	2.46E-96
BLCA.brown	KIRC.red	1.51E-37
BLCA.brown	UCEC.green	8.65E-48
BLCA.green	LUSC.brown	4.55E-29
BLCA.green	HNSC.red	4.56E-42
BLCA.green	UCEC.turquoise	0.007472986
BLCA.pink	GBM.tan	1.43E-41
BLCA.pink	OV.yellow	2.27E-40
BLCA.pink	COADREAD.yellow	1.54E-10
BLCA.pink	LUSC.yellow	2.85E-21
BLCA.pink	BRCA.black	5.02E-43
BLCA.pink	HNSC.magenta	2.29E-51
BLCA.pink	KIRC.green	1.92E-07
BLCA.pink	UCEC.magenta	6.37E-55
BLCA.red	OV.blue	3.72E-08

BLCA.red	COADREAD.magenta	8.58E-40
BLCA.red	LUSC.blue	3.27E-14
BLCA.red	BRCA.blue	2.91E-09
BLCA.red	HNSC.black	2.36E-09
BLCA.red	KIRC.greenyellow	1.22E-14
BLCA.red	UCEC.red	3.81E-30
BLCA.turquoise	GBM.turquoise	3.23E-52
BLCA.turquoise	OV.turquoise	7.02E-88
BLCA.turquoise	COADREAD.yellow	8.47E-45
BLCA.turquoise	LUSC.turquoise	7.53E-60
BLCA.turquoise	BRCA.yellow	4.51E-73
BLCA.turquoise	HNSC.yellow	4.86E-74
BLCA.turquoise	KIRC.pink	2.37E-43
BLCA.turquoise	UCEC.yellow	7.90E-77
BLCA.yellow	GBM.brown	0.000627877
BLCA.yellow	OV.blue	0.000259226
BLCA.yellow	COADREAD.brown	0.003223737
BLCA.yellow	LUSC.blue	9.16E-05
BLCA.yellow	BRCA.green	8.26E-22
BLCA.yellow	HNSC.green	3.52E-23
BLCA.yellow	KIRC.black	9.87E-16
BLCA.yellow	UCEC.green	5.59E-10
UCEC.black	GBM.green	1.04E-57
UCEC.black	OV.brown	2.24E-08
UCEC.black	COADREAD.purple	6.97E-38
UCEC.black	LUSC.black	1.79E-53
UCEC.black	HNSC.pink	5.16E-41
UCEC.black	KIRC.blue	1.97E-65
UCEC.black	BLCA.blue	0.01510793
UCEC.blue	GBM.black	4.20E-27
UCEC.blue	OV.green	3.91E-24
UCEC.blue	BRCA.turquoise	8.61E-24
UCEC.blue	KIRC.yellow	1.37E-24

UCEC.blue	BLCA.blue	0.000279847
UCEC.brown	GBM.turquoise	1.72E-16
UCEC.brown	OV.turquoise	5.03E-53
UCEC.brown	COADREAD.green	1.49E-28
UCEC.brown	LUSC.yellow	2.79E-47
UCEC.brown	BRCA.brown	2.73E-61
UCEC.brown	HNSC.turquoise	1.87E-44
UCEC.brown	KIRC.green	1.52E-54
UCEC.brown	BLCA.turquoise	2.25E-43
UCEC.green	GBM.pink	1.08E-19
UCEC.green	OV.blue	6.98E-95
UCEC.green	COADREAD.brown	2.08E-12
UCEC.green	LUSC.blue	5.76E-69
UCEC.green	BRCA.blue	1.35E-59
UCEC.green	HNSC.blue	3.22E-55
UCEC.green	KIRC.red	5.11E-24
UCEC.green	BLCA.brown	3.21E-45
UCEC.magenta	GBM.tan	1.52E-69
UCEC.magenta	OV.yellow	4.75E-43
UCEC.magenta	COADREAD.yellow	7.11E-11
UCEC.magenta	LUSC.yellow	1.81E-29
UCEC.magenta	BRCA.black	6.93E-57
UCEC.magenta	HNSC.magenta	1.85E-58
UCEC.magenta	KIRC.green	1.85E-13
UCEC.magenta	BLCA.pink	3.92E-57
UCEC.pink	BRCA.red	9.08E-34
UCEC.pink	KIRC.purple	1.31E-38
UCEC.pink	BLCA.blue	0.007672225
UCEC.red	GBM.pink	0.000169972
UCEC.red	OV.blue	1.74E-24
UCEC.red	COADREAD.magenta	7.97E-28
UCEC.red	LUSC.blue	1.26E-32
UCEC.red	BRCA.blue	1.08E-29

UCEC.red	HNSC.blue	6.67E-22
UCEC.red	KIRC.greenyellow	5.87E-21
UCEC.red	BLCA.red	1.13E-25
UCEC.turquoise	GBM.yellow	6.82E-22
UCEC.turquoise	OV.brown	1.71E-40
UCEC.turquoise	LUSC.pink	3.89E-30
UCEC.turquoise	BRCA.turquoise	4.03E-12
UCEC.turquoise	HNSC.brown	1.79E-05
UCEC.turquoise	KIRC.turquoise	1.34E-07
UCEC.yellow	GBM.turquoise	5.63E-49
UCEC.yellow	OV.turquoise	1.21E-84
UCEC.yellow	COADREAD.yellow	8.05E-39
UCEC.yellow	LUSC.turquoise	1.85E-59
UCEC.yellow	BRCA.yellow	4.22E-88
UCEC.yellow	HNSC.yellow	1.93E-88
UCEC.yellow	KIRC.pink	4.17E-45
UCEC.yellow	BLCA.turquoise	3.73E-74

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module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
GBM.M1	238	CELL_CYCLE_GO_0007049	6.99E-22
GBM.M1	238	CELL_CYCLE_PROCESS	4.50E-21
GBM.M1	238	M_PHASE	3.78E-20
GBM.M1	238	M_PHASE_OF_MITOTIC_CELL_CYCLE	4.87E-20
GBM.M1	238	CELL_CYCLE_PHASE	5.07E-20
GBM.M1	238	MITOTIC_CELL_CYCLE	7.25E-20
GBM.M1	238	MITOSIS	6.82E-19
GBM.M1	238	REGULATION_OF_MITOSIS	4.47E-13
GBM.M1	238	REGULATION_OF_CELL_CYCLE	1.51E-11
GBM.M1	238	CHROMOSOME_SEGREGATION	1.40E-09
GBM.M2	482	NERVOUS_SYSTEM_DEVELOPMENT	1.01E-14
GBM.M2	482	SYSTEM_DEVELOPMENT	3.92E-12
GBM.M2	482	ANATOMICAL_STRUCTURE_DEVELOPMENT	7.68E-12
GBM.M2	482	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	3.13E-11
GBM.M2	482	GLUTAMATE_SIGNALING_PATHWAY	3.73E-08
GBM.M2	482	CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	8.33E-08
GBM.M2	482	NEURON_DIFFERENTIATION	9.29E-08
GBM.M2	482	GENERATION_OF_NEURONS	2.53E-07
GBM.M2	482	AXONOGENESIS	3.14E-07
GBM.M2	482	NEURON_DEVELOPMENT	7.70E-07
GBM.M3	346	TRANSMISSION_OF_NERVE_IMPULSE	2.82E-18
GBM.M3	346	SYNAPTIC_TRANSMISSION	3.86E-18
GBM.M3	346	CELL_CELL_SIGNALING	1.78E-15
GBM.M3	346	NEUROLOGICAL_SYSTEM_PROCESS	7.49E-11

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
GBM.M3	346	NERVOUS_SYSTEM_DEVELOPMENT	5.40E-10
GBM.M3	346	SYSTEM_PROCESS	2.55E-08
GBM.M3	346	MICROTUBULE_BASED_MOVEMENT	1.02E-07
GBM.M3	346	CYTOSKELETON_DEPENDENT_INTRACELLULAR_TRANSPORT	2.56E-06
GBM.M3	346	GENERATION_OF_A_SIGNAL_INVOLVED_IN_CELL_CELL_SIGNALING	5.07E-06
GBM.M3	346	TRANSPORT	2.58E-05
GBM.M4	268	PROTEIN_HOMOOIGOMERIZATION	0.000132505
GBM.M4	268	BODY_FLUID_SECRETION	0.000201352
GBM.M4	268	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	0.000351599
GBM.M4	268	PROTEIN_OLIGOMERIZATION	0.001393972
GBM.M4	268	REGULATION_OF_PROTEIN_STABILITY	0.00149916
GBM.M4	268	MEIOSIS_I	0.00174793
GBM.M4	268	SODIUM_ION_TRANSPORT	0.002319194
GBM.M4	268	FOCAL_ADHESION_FORMATION	0.006237476
GBM.M4	268	PEPTIDE_METABOLIC_PROCESS	0.006237476
GBM.M4	268	NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	0.006237476
GBM.M5	87	PROTEIN_AMINO_ACID_PHOSPHORYLATION	1.61E-06
GBM.M5	87	PHOSPHORYLATION	4.13E-06
GBM.M5	87	PROTEIN_AMINO_ACID_AUTOPHOSPHORYLATION	6.62E-06
GBM.M5	87	PROTEIN_AUTOPROCESSING	7.54E-06
GBM.M5	87	POST_TRANSLATIONAL_PROTEIN_MODIFICATION	1.85E-05
GBM.M5	87	PROTEIN_PROCESSING	4.22E-05
GBM.M5	87	POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_ACTIVITY	0.000113847
GBM.M5	87	POSITIVE_REGULATION_OF_DNA_BINDING	0.000145412

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
GBM.M5	87	POSITIVE_REGULATION_OF_BINDING	0.000182175
GBM.M5	87	PROTEIN_MODIFICATION_PROCESS	0.000192739
GBM.M7	217	NERVOUS_SYSTEM_DEVELOPMENT	3.06E-07
GBM.M7	217	REGULATION_OF_ACTION_POTENTIAL	1.98E-05
GBM.M7	217	SYSTEM_DEVELOPMENT	4.58E-05
GBM.M7	217	ANATOMICAL_STRUCTURE_DEVELOPMENT	6.72E-05
GBM.M7	217	PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	0.000194982
GBM.M7	217	CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	0.000222563
GBM.M7	217	HEART_DEVELOPMENT	0.000471087
GBM.M7	217	ICOSANOID_METABOLIC_PROCESS	0.000581111
GBM.M7	217	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	0.000725646
GBM.M7	217	EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.001269072
GBM.M8	229	ANATOMICAL_STRUCTURE_DEVELOPMENT	7.58E-08
GBM.M8	229	SKELETAL_DEVELOPMENT	1.24E-07
GBM.M8	229	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	5.29E-07
GBM.M8	229	ORGAN_DEVELOPMENT	6.28E-07
GBM.M8	229	SYSTEM_DEVELOPMENT	1.20E-06
GBM.M8	229	NEURON_DIFFERENTIATION	0.000141844
GBM.M8	229	NEGATIVE_REGULATION_OF_PHOSPHORYLATION	0.000228472
GBM.M8	229	GENERATION_OF_NEURONS	0.00023054
GBM.M8	229	NEGATIVE_REGULATION_OF_PHOSPHATE_METABOLIC_PROCESS	0.000294735
GBM.M8	229	REGULATION_OF_HORMONE_SECRETION	0.000372241
GBM.M9	91	RESPONSE_TO_WOUNDING	9.42E-08
GBM.M9	91	REGULATION_OF_BODY_FLUID_LEVELS	1.30E-07
GBM.M9	91	BLOOD_COAGULATION	9.21E-07
GBM.M9	91	COAGULATION	1.04E-06
GBM.M9	91	HEMOSTASIS	1.61E-06

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
GBM.M9	91	WOUND_HEALING	2.92E-06
GBM.M9	91	RESPONSE_TO_EXTERNAL_STIMULUS	5.85E-06
GBM.M9	91	CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	1.10E-05
GBM.M9	91	NEGATIVE_REGULATION_OF_ANGIOGENESIS	1.90E-05
GBM.M9	91	ANATOMICAL_STRUCTURE_MORPHOGENESIS	2.58E-05
GBM.M10	241	IMMUNE_SYSTEM_PROCESS	5.31E-16
GBM.M10	241	DEFENSE_RESPONSE	3.33E-15
GBM.M10	241	IMMUNE_RESPONSE	1.65E-12
GBM.M10	241	RESPONSE_TO_EXTERNAL_STIMULUS	5.34E-12
GBM.M10	241	LOCOMOTORY_BEHAVIOR	7.54E-09
GBM.M10	241	RESPONSE_TO_OTHER_ORGANISM	2.49E-08
GBM.M10	241	RESPONSE_TO_WOUNDING	2.50E-08
GBM.M10	241	RESPONSE_TO_BIOTIC_STIMULUS	8.82E-08
GBM.M10	241	INTERFERON_GAMMA_PRODUCTION	2.80E-07
GBM.M10	241	REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	4.16E-07
GBM.M11	56	DEFENSE_RESPONSE	2.53E-08
GBM.M11	56	LOCOMOTORY_BEHAVIOR	0.000100899
GBM.M11	56	RESPONSE_TO_VIRUS	0.000281284
GBM.M11	56	IMMUNE_RESPONSE	0.000326651
GBM.M11	56	INFLAMMATORY_RESPONSE	0.000327278
GBM.M11	56	SENSORY_PERCEPTION_OF_TASTE	0.000344898
GBM.M11	56	APOPTOTIC_MITOCHONDRIAL_CHANGES	0.000344898
GBM.M11	56	DEFENSE_RESPONSE_TO_VIRUS	0.000413201
GBM.M11	56	PROTEIN_TARGETING_TO_MEMBRANE	0.000413201
GBM.M11	56	NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	0.000567857
GBM.M12	700	IMMUNE_SYSTEM_PROCESS	1.58E-26

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
GBM.M12	700	IMMUNE_RESPONSE	3.20E-25
GBM.M12	700	DEFENSE_RESPONSE	2.28E-18
GBM.M12	700	SIGNAL_TRANSDUCTION	5.56E-17
GBM.M12	700	RESPONSE_TO_EXTERNAL_STIMULUS	1.02E-16
GBM.M12	700	NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	7.91E-14
GBM.M12	700	CELL_DEVELOPMENT	1.25E-13
GBM.M12	700	PROGRAMMED_CELL_DEATH	8.16E-13
GBM.M12	700	NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	1.10E-12
GBM.M12	700	RESPONSE_TO_WOUNDING	2.47E-12
GBM.M13	302	AMINO_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	1.12E-07
GBM.M13	302	AMINO_ACID_DERIVATIVE_METABOLIC_PROCESS	6.96E-07
GBM.M13	302	REGULATION_OF_NEUROTRANSMITTER_LEVELS	1.62E-05
GBM.M13	302	AMINE_BIOSYNTHETIC_PROCESS	4.22E-05
GBM.M13	302	BIOGENIC_AMINE_METABOLIC_PROCESS	7.19E-05
GBM.M13	302	GLUCAN_METABOLIC_PROCESS	0.000286139
GBM.M13	302	SYSTEM_PROCESS	0.00031423
GBM.M13	302	DEVELOPMENTAL_GROWTH	0.000389449
GBM.M13	302	NITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	0.00041
GBM.M13	302	AROMATIC_COMPOUND_METABOLIC_PROCESS	0.000476137
OV.M1	629	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.57E-21
OV.M1	629	ANATOMICAL_STRUCTURE_DEVELOPMENT	1.12E-18
OV.M1	629	ORGAN_DEVELOPMENT	2.75E-18
OV.M1	629	SYSTEM_DEVELOPMENT	2.28E-17
OV.M1	629	SKELETAL_DEVELOPMENT	1.25E-12
OV.M1	629	ANATOMICAL_STRUCTURE_MORPHOGENESIS	1.02E-09
OV.M1	629	RESPONSE_TO_EXTERNAL_STIMULUS	1.96E-09
OV.M1	629	MUSCLE_DEVELOPMENT	3.91E-07
OV.M1	629	CELL_MATRIX_ADHESION	9.36E-07

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
OV.M1	629	CELL_SUBSTRATE_ADHESION	1.19E-06
OV.M2	186	SPERMATID_DEVELOPMENT	0.003059772
OV.M2	186	PEPTIDE_METABOLIC_PROCESS	0.003059772
OV.M2	186	REGULATION_OF_PROTEIN_POLYMERIZATION	0.003718979
OV.M2	186	SPERMATID_DIFFERENTIATION	0.003718979
OV.M2	186	MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	0.003718979
OV.M2	186	ISOPRENOID_METABOLIC_PROCESS	0.004438039
OV.M2	186	N_ACETYLGUCOSAMINE_METABOLIC_PROCESS	0.004438039
OV.M2	186	NEUROTRANSMITTER_SECRETION	0.005215905
OV.M2	186	GLUCOSAMINE_METABOLIC_PROCESS	0.005215905
OV.M2	186	STRIATED_MUSCLE_CONTRACTION_GO_0006941	0.00605154
OV.M3	51	CELL_CYCLE_CHECKPOINT_GO_0000075	4.62E-06
OV.M3	51	REGULATION_OF_MITOTIC_CELL_CYCLE	2.01E-05
OV.M3	51	MITOSIS	3.92E-05
OV.M3	51	M_PHASE_OF_MITOTIC_CELL_CYCLE	4.52E-05
OV.M3	51	REGULATION_OF_CELL_CYCLE	6.33E-05
OV.M3	51	CELL_CYCLE_GO_0007049	8.60E-05
OV.M3	51	REGULATION_OF_MITOSIS	0.000117568
OV.M3	51	REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	0.000135664
OV.M3	51	M_PHASE	0.000141626
OV.M3	51	REGULATION_OF_DNA_METABOLIC_PROCESS	0.000155481
OV.M5	1037	IMMUNE_SYSTEM_PROCESS	1.61E-35
OV.M5	1037	DEFENSE_RESPONSE	2.22E-34
OV.M5	1037	IMMUNE_RESPONSE	4.41E-33
OV.M5	1037	SIGNAL_TRANSDUCTION	5.68E-26

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
OV.M5	1037	RESPONSE_TO_EXTERNAL_STIMULUS	4.05E-18
OV.M5	1037	INFLAMMATORY_RESPONSE	1.32E-17
OV.M5	1037	RESPONSE_TO_WOUNDING	9.59E-16
OV.M5	1037	LOCOMOTORY_BEHAVIOR	1.57E-13
OV.M5	1037	INTRACELLULAR_SIGNALING_CASCADE	3.30E-13
OV.M5	1037	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	9.72E-13
OV.M6	62	RESPONSE_TO_OTHER_ORGANISM	1.25E-07
OV.M6	62	RESPONSE_TO_VIRUS	2.90E-07
OV.M6	62	RESPONSE_TO_BIOTIC_STIMULUS	1.11E-06
OV.M6	62	MULTI_ORGANISM_PROCESS	7.06E-06
OV.M6	62	IMMUNE_SYSTEM_PROCESS	0.000340928
OV.M6	62	RESPONSE_TO_TOXIN	0.000346569
OV.M6	62	EPITHELIAL_CELL_DIFFERENTIATION	0.000346569
OV.M6	62	REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	0.000422815
OV.M6	62	RESPONSE_TO_STEROID_HORMONE_STIMULUS	0.000422815
OV.M6	62	XENOBIOTIC_METABOLIC_PROCESS	0.000422815
COADREAD.M1	136	NEGATIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_ACTIVITY	9.96E-05
COADREAD.M1	136	NEGATIVE_REGULATION_OF_DNA_BINDING	0.000147466
COADREAD.M1	136	NEGATIVE_REGULATION_OF_BINDING	0.00017616
COADREAD.M1	136	RNA_3END_PROCESSING	0.001652514
COADREAD.M1	136	S_PHASE_OF_MITOTIC_CELL_CYCLE	0.001652514
COADREAD.M1	136	REGULATION_OF_TRANSCRIPTION_FACTOR_ACTIVITY	0.001931301
COADREAD.M1	136	RESPONSE_TO_STEROID_HORMONE_STIMULUS	0.002011569
COADREAD.M1	136	VESICLE_LOCALIZATION	0.002011569
COADREAD.M1	136	NOTCH_SIGNALING_PATHWAY	0.002404122
COADREAD.M1	136	REGULATION_OF_DNA_BINDING	0.00307146

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
COADREAD.M2	573	CHROMOSOME_CONDENSATION	8.44E-05
COADREAD.M2	573	GLAND_DEVELOPMENT	0.000269985
COADREAD.M2	573	TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	0.000307092
COADREAD.M2	573	CELL_PROJECTION_BIOGENESIS	0.000406198
COADREAD.M2	573	ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	0.000417593
COADREAD.M2	573	MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION_AND_BIOGENESIS	0.000645798
COADREAD.M2	573	ORGANELLE_ORGANIZATION_AND_BIOGENESIS	0.000714211
COADREAD.M2	573	ACTIN_FILAMENT_BASED_PROCESS	0.000856578
COADREAD.M2	573	LIPID_BIOSYNTHETIC_PROCESS	0.000968958
COADREAD.M2	573	ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	0.001041795
COADREAD.M3	321	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.35E-13
COADREAD.M3	321	ANATOMICAL_STRUCTURE_DEVELOPMENT	1.41E-13
COADREAD.M3	321	SYSTEM_DEVELOPMENT	1.83E-12
COADREAD.M3	321	ORGAN_DEVELOPMENT	8.79E-11
COADREAD.M3	321	MUSCLE_DEVELOPMENT	1.13E-07
COADREAD.M3	321	ANATOMICAL_STRUCTURE_MORPHOGENESIS	1.81E-07
COADREAD.M3	321	ORGAN_MORPHOGENESIS	1.41E-06
COADREAD.M3	321	ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	3.22E-06
COADREAD.M3	321	ACTIN_FILAMENT_BASED_PROCESS	7.33E-06
COADREAD.M3	321	POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	1.35E-05
COADREAD.M4	184	IMMUNE_SYSTEM_PROCESS	7.55E-14
COADREAD.M4	184	IMMUNE_RESPONSE	1.39E-09
COADREAD.M4	184	LEUKOCYTE_ACTIVATION	6.06E-09
COADREAD.M4	184	DEFENSE_RESPONSE	9.19E-09
COADREAD.M4	184	CELL_ACTIVATION	1.63E-08
COADREAD.M4	184	LYMPHOCYTE_ACTIVATION	4.15E-08
COADREAD.M4	184	T_CELL_ACTIVATION	7.53E-08
COADREAD.M4	184	REGULATION_OF_IMMUNE_SYSTEM_PROCESS	8.80E-08

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
COADREAD.M4	184	SIGNAL_TRANSDUCTION	2.21E-07
COADREAD.M4	184	RESPONSE_TO_BIOTIC_STIMULUS	7.75E-07
COADREAD.M6	75	SMOOTH_MUSCLE_CONTRACTION_GO_0006939	8.19E-06
COADREAD.M6	75	SYSTEM_PROCESS	2.07E-05
COADREAD.M6	75	MYOBLAST_DIFFERENTIATION	2.50E-05
COADREAD.M6	75	ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	2.98E-05
COADREAD.M6	75	REGULATION_OF_MUSCLE_CONTRACTION	3.55E-05
COADREAD.M6	75	ACTIN_FILAMENT_BASED_PROCESS	4.61E-05
COADREAD.M6	75	MUSCLE_CELL_DIFFERENTIATION	5.59E-05
COADREAD.M6	75	CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	7.78E-05
COADREAD.M6	75	SKELETAL_MUSCLE_DEVELOPMENT	0.000159698
COADREAD.M6	75	MUSCLE_DEVELOPMENT	0.000289133
COADREAD.M7	104	NEGATIVE_REGULATION_OF_PHOSPHORYLATION	2.27E-07
COADREAD.M7	104	NEGATIVE_REGULATION_OF_PHOSPHATE_METABOLIC_PROCESS	3.26E-07
COADREAD.M7	104	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.91E-06
COADREAD.M7	104	NEGATIVE_REGULATION_OF_CELL_CYCLE	2.03E-06
COADREAD.M7	104	CELL_CYCLE_ARREST_GO_0007050	7.38E-06
COADREAD.M7	104	ANATOMICAL_STRUCTURE_DEVELOPMENT	2.13E-05
COADREAD.M7	104	REGULATION_OF_NEUROGENESIS	3.60E-05
COADREAD.M7	104	GENERATION_OF_NEURONS	4.64E-05
COADREAD.M7	104	AXONOGENESIS	5.05E-05
COADREAD.M7	104	SYSTEM_DEVELOPMENT	5.38E-05
COADREAD.M8	58	PEPTIDE_METABOLIC_PROCESS	0.000303244
COADREAD.M8	58	FATTY_ACID_BETA_OXIDATION	0.000370003
COADREAD.M8	58	REGULATION_OF_JNK_CASCADE	0.000443252

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
COADREAD.M8	58	MEIOTIC_RECOMBINATION	0.000905659
COADREAD.M8	58	FATTY_ACID_OXIDATION	0.001017142
COADREAD.M8	58	MEIOSIS_I	0.001258847
COADREAD.M8	58	REGULATION_OF_MAPKKK_CASCADE	0.001258847
COADREAD.M8	58	CHROMOSOME_SEGREGATION	0.003220225
COADREAD.M8	58	MEIOTIC_CELL_CYCLE	0.003843446
COADREAD.M8	58	CELLULAR_LIPID_CATABOLIC_PROCESS	0.003843446
COADREAD.M9	149	SYSTEM_DEVELOPMENT	3.81E-09
COADREAD.M9	149	ANATOMICAL_STRUCTURE_DEVELOPMENT	4.38E-09
COADREAD.M9	149	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	8.98E-09
COADREAD.M9	149	ORGAN_DEVELOPMENT	3.50E-07
COADREAD.M9	149	CELL_CELL_SIGNALING	2.06E-05
COADREAD.M9	149	BONE_REMODELING	4.21E-05
COADREAD.M9	149	TISSUE_DEVELOPMENT	4.39E-05
COADREAD.M9	149	TISSUE_REMODELING	4.83E-05
COADREAD.M9	149	VIRAL_INFECTIONOUS_CYCLE	6.27E-05
COADREAD.M9	149	REGULATION_OF_VIRAL_REPRODUCTION	6.40E-05
COADREAD.M10	665	SYNAPSE_ORGANIZATION_AND_BIOGENESIS	4.78E-10
COADREAD.M10	665	SYNAPTOGENESIS	7.61E-10
COADREAD.M10	665	EXTRACELLULAR_STRUCTURE_ORGANIZATION_AND_BIOGENESIS	2.11E-08
COADREAD.M10	665	CELL_CELL_SIGNALING	4.49E-05
COADREAD.M10	665	REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	0.000107599
COADREAD.M10	665	GENERATION_OF_A_SIGNAL_INVOLVED_IN_CELL_CELL_SIGNALING	0.000195535
COADREAD.M10	665	TRANSMISSION_OF_NERVE_IMPULSE	0.000211834
COADREAD.M10	665	SYNAPTIC_TRANSMISSION	0.000271751
COADREAD.M10	665	SYSTEM_PROCESS	0.000517515
COADREAD.M10	665	REGULATION_OF_HORMONE_SECRETION	0.000650164

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
COADREAD.M11	210	IMMUNE_SYSTEM_PROCESS	1.08E-20
COADREAD.M11	210	IMMUNE_RESPONSE	5.78E-18
COADREAD.M11	210	DEFENSE_RESPONSE	1.43E-16
COADREAD.M11	210	RESPONSE_TO_EXTERNAL_STIMULUS	2.34E-11
COADREAD.M11	210	INFLAMMATORY_RESPONSE	2.51E-11
COADREAD.M11	210	RESPONSE_TO_WOUNDING	4.57E-10
COADREAD.M11	210	RESPONSE_TO_VIRUS	9.89E-10
COADREAD.M11	210	SIGNAL_TRANSDUCTION	3.02E-09
COADREAD.M11	210	LOCOMOTORY_BEHAVIOR	2.53E-08
COADREAD.M11	210	MULTI_ORGANISM_PROCESS	6.56E-08
LUSC.M1	131	PEPTIDE_METABOLIC_PROCESS	0.001534666
LUSC.M1	131	FATTY_ACID_BETA_OXIDATION	0.001868397
LUSC.M1	131	DIGESTION	0.002286341
LUSC.M1	131	CELL_MATURATION	0.003997835
LUSC.M1	131	MEIOTIC_RECOMBINATION	0.004513281
LUSC.M1	131	POTASSIUM_ION_TRANSPORT	0.005014208
LUSC.M1	131	DEVELOPMENTAL_MATURATION	0.005057728
LUSC.M1	131	FATTY_ACID_OXIDATION	0.005057728
LUSC.M1	131	DETECTION_OF_CHEMICAL_STIMULUS	0.005057728
LUSC.M1	131	MEIOSIS_I	0.006232196
LUSC.M2	646	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.55E-23
LUSC.M2	646	ANATOMICAL_STRUCTURE_DEVELOPMENT	2.51E-22
LUSC.M2	646	SYSTEM_DEVELOPMENT	8.13E-22
LUSC.M2	646	ORGAN_DEVELOPMENT	4.13E-17
LUSC.M2	646	SKELETAL_DEVELOPMENT	2.25E-13
LUSC.M2	646	NERVOUS_SYSTEM_DEVELOPMENT	1.32E-08
LUSC.M2	646	ANATOMICAL_STRUCTURE_MORPHOGENESIS	2.52E-08
LUSC.M2	646	MUSCLE_DEVELOPMENT	5.38E-07

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
LUSC.M2	646	CELL_MATRIX_ADHESION	1.17E-06
LUSC.M2	646	CELL_SUBSTRATE_ADHESION	1.48E-06
LUSC.M3	622	ECTODERM_DEVELOPMENT	5.98E-21
LUSC.M3	622	TISSUE_DEVELOPMENT	1.96E-17
LUSC.M3	622	EPIDERMIS_DEVELOPMENT	2.01E-17
LUSC.M3	622	ANATOMICAL_STRUCTURE_DEVELOPMENT	4.59E-12
LUSC.M3	622	ORGAN_DEVELOPMENT	6.38E-11
LUSC.M3	622	SYSTEM_DEVELOPMENT	3.47E-10
LUSC.M3	622	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	4.04E-10
LUSC.M3	622	KERATINOCYTE_DIFFERENTIATION	2.01E-06
LUSC.M3	622	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	2.83E-06
LUSC.M3	622	MORPHOGENESIS_OF_AN_EPITHELIUM	3.13E-06
LUSC.M4	219	CARBOXYLIC_ACID_METABOLIC_PROCESS	1.80E-06
LUSC.M4	219	COENZYME_BIOSYNTHETIC_PROCESS	1.91E-06
LUSC.M4	219	ORGANIC_ACID_METABOLIC_PROCESS	2.00E-06
LUSC.M4	219	RESPONSE_TO_CHEMICAL_STIMULUS	3.47E-06
LUSC.M4	219	GLUCOSE_METABOLIC_PROCESS	7.61E-06
LUSC.M4	219	CARBOHYDRATE_METABOLIC_PROCESS	1.36E-05
LUSC.M4	219	RESPONSE_TO_HORMONE_STIMULUS	1.77E-05
LUSC.M4	219	MYOBLAST_DIFFERENTIATION	2.05E-05
LUSC.M4	219	MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	2.82E-05
LUSC.M4	219	COENZYME_METABOLIC_PROCESS	3.59E-05
LUSC.M6	69	NEUROTRANSMITTER_SECRETION	0.000739482
LUSC.M6	69	REGULATED_SECRETORY_PATHWAY	0.000991429
LUSC.M6	69	REGULATION_OF_NEUROTRANSMITTER_LEVELS	0.002558979

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
LUSC.M6	69	REGULATION_OF_HEART_CONTRACTION	0.002775878
LUSC.M6	69	GENERATION_OF_A_SIGNAL_INVOLVED_IN_CELL_CELL_SIGNALING	0.003726435
LUSC.M6	69	DIGESTION	0.008423994
LUSC.M6	69	SEXUAL_REPRODUCTION	0.009543131
LUSC.M6	69	REPRODUCTION	0.00964598
LUSC.M6	69	FEMALE_PREGNANCY	0.012050729
LUSC.M6	69	POTASSIUM_ION_TRANSPORT	0.014311191
LUSC.M7	136	EXCRETION	2.71E-06
LUSC.M7	136	ESTABLISHMENT_OF_LOCALIZATION	2.71E-05
LUSC.M7	136	TRANSPORT	3.34E-05
LUSC.M7	136	RESPIRATORY_GASEOUS_EXCHANGE	8.00E-05
LUSC.M7	136	ION_TRANSPORT	0.00015554
LUSC.M7	136	INORGANIC_ANION_TRANSPORT	0.00017616
LUSC.M7	136	CALCIUM_INDEPENDENT_CELL_CELL_ADHESION	0.000326495
LUSC.M7	136	RESPONSE_TO_DRUG	0.000326495
LUSC.M7	136	INNATE_IMMUNE_RESPONSE	0.000373776
LUSC.M7	136	REGULATION_OF_HEART_CONTRACTION	0.000481055
LUSC.M8	675	DEFENSE_RESPONSE	2.15E-31
LUSC.M8	675	IMMUNE_SYSTEM_PROCESS	4.32E-29
LUSC.M8	675	IMMUNE_RESPONSE	7.35E-27
LUSC.M8	675	RESPONSE_TO_EXTERNAL_STIMULUS	3.52E-26
LUSC.M8	675	RESPONSE_TO_WOUNDING	2.37E-21
LUSC.M8	675	INFLAMMATORY_RESPONSE	2.48E-18
LUSC.M8	675	SIGNAL_TRANSDUCTION	6.51E-17
LUSC.M8	675	LOCOMOTORY_BEHAVIOR	7.09E-17
LUSC.M8	675	BEHAVIOR	1.72E-13
LUSC.M8	675	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	2.14E-11

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
LUSC.M9	427	IMMUNE_SYSTEM_PROCESS	8.15E-31
LUSC.M9	427	IMMUNE_RESPONSE	5.43E-24
LUSC.M9	427	DEFENSE_RESPONSE	7.93E-21
LUSC.M9	427	LYMPHOCYTE_ACTIVATION	2.80E-14
LUSC.M9	427	SIGNAL_TRANSDUCTION	3.13E-14
LUSC.M9	427	LEUKOCYTE_ACTIVATION	2.29E-13
LUSC.M9	427	T_CELL_ACTIVATION	1.39E-12
LUSC.M9	427	CELL_ACTIVATION	1.42E-12
LUSC.M9	427	CELLULAR_DEFENSE_RESPONSE	6.61E-11
LUSC.M9	427	LOCOMOTORY_BEHAVIOR	4.38E-10
BRCA.M1	40	RESPONSE_TO_VIRUS	2.03E-06
BRCA.M1	40	IMMUNE_RESPONSE	3.95E-06
BRCA.M1	40	RESPONSE_TO_OTHER_ORGANISM	1.55E-05
BRCA.M1	40	IMMUNE_SYSTEM_PROCESS	2.81E-05
BRCA.M1	40	I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	5.41E-05
BRCA.M1	40	RESPONSE_TO_BIOTIC_STIMULUS	6.61E-05
BRCA.M1	40	DEFENSE_RESPONSE	0.000124237
BRCA.M1	40	SENSORY_PERCEPTION_OF_TASTE	0.000175453
BRCA.M1	40	APOPTOTIC_MITOCHONDRIAL_CHANGES	0.000175453
BRCA.M1	40	APOPTOTIC_PROGRAM	0.000177326
BRCA.M2	641	ANATOMICAL_STRUCTURE_DEVELOPMENT	5.38E-22
BRCA.M2	641	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.63E-21
BRCA.M2	641	SYSTEM_DEVELOPMENT	1.08E-19
BRCA.M2	641	ORGAN_DEVELOPMENT	1.19E-16
BRCA.M2	641	SKELETAL_DEVELOPMENT	1.89E-15
BRCA.M2	641	SYNAPTOGENESIS	1.68E-08
BRCA.M2	641	ANATOMICAL_STRUCTURE_MORPHOGENESIS	7.02E-08

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
BRCA.M2	641	TISSUE_DEVELOPMENT	1.13E-07
BRCA.M2	641	CELL_CELL_SIGNALING	1.15E-07
BRCA.M2	641	SYNAPSE_ORGANIZATION_AND_BIOGENESIS	1.66E-07
BRCA.M3	385	IMMUNE_SYSTEM_PROCESS	6.47E-31
BRCA.M3	385	IMMUNE_RESPONSE	4.64E-30
BRCA.M3	385	DEFENSE_RESPONSE	1.37E-17
BRCA.M3	385	LOCOMOTORY_BEHAVIOR	1.04E-10
BRCA.M3	385	INFLAMMATORY_RESPONSE	1.13E-10
BRCA.M3	385	RESPONSE_TO_WOUNDING	1.61E-10
BRCA.M3	385	CELLULAR_DEFENSE_RESPONSE	3.01E-10
BRCA.M3	385	RESPONSE_TO_EXTERNAL_STIMULUS	3.06E-10
BRCA.M3	385	SIGNAL_TRANSDUCTION	3.51E-10
BRCA.M3	385	CELLULAR_CATION_HOMEOSTASIS	4.91E-09
BRCA.M4	170	REGULATION_OF_BODY_FLUID_LEVELS	2.78E-07
BRCA.M4	170	BLOOD_COAGULATION	9.37E-07
BRCA.M4	170	COAGULATION	1.08E-06
BRCA.M4	170	HEMOSTASIS	1.83E-06
BRCA.M4	170	RESPONSE_TO_WOUNDING	2.34E-06
BRCA.M4	170	WOUND_HEALING	3.70E-06
BRCA.M4	170	RESPONSE_TO_EXTERNAL_STIMULUS	5.95E-06
BRCA.M4	170	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	2.04E-05
BRCA.M4	170	ORGAN_DEVELOPMENT	3.91E-05
BRCA.M4	170	GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	4.87E-05
BRCA.M6	128	CERAMIDE_METABOLIC_PROCESS	3.07E-05
BRCA.M6	128	GLYCOPHINGOLIPID_METABOLIC_PROCESS	4.07E-05
BRCA.M6	128	SPHINGOID_METABOLIC_PROCESS	4.07E-05

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
BRCA.M6	128	GLYCOLIPID_METABOLIC_PROCESS	0.000101926
BRCA.M6	128	REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	0.000273233
BRCA.M6	128	REGULATION_OF_INTRACELLULAR_TRANSPORT	0.000402906
BRCA.M6	128	SPHINGOLIPID_METABOLIC_PROCESS	0.000629316
BRCA.M6	128	REGULATION_OF_TRANSPORT	0.000631171
BRCA.M6	128	PROTEIN_AMINO_ACID_AUTOPHOSPHORYLATION	0.000767618
BRCA.M6	128	PROTEIN_AUTOPROCESSING	0.000843442
BRCA.M7	1173	MITOTIC_CELL_CYCLE	1.30E-16
BRCA.M7	1173	CELL_CYCLE_GO_0007049	1.44E-15
BRCA.M7	1173	CELL_CYCLE_PROCESS	1.97E-14
BRCA.M7	1173	M_PHASE_OF_MITOTIC_CELL_CYCLE	1.47E-13
BRCA.M7	1173	CELL_CYCLE_PHASE	1.67E-13
BRCA.M7	1173	M_PHASE	1.70E-13
BRCA.M7	1173	MITOSIS	4.68E-13
BRCA.M7	1173	REGULATION_OF_CELL_CYCLE	2.32E-09
BRCA.M7	1173	REGULATION_OF_MITOSIS	1.26E-08
BRCA.M7	1173	RESPONSE_TO_STEROID_HORMONE_STIMULUS	3.29E-07
BRCA.M8	320	IMMUNE_SYSTEM_PROCESS	5.08E-22
BRCA.M8	320	DEFENSE_RESPONSE	5.56E-19
BRCA.M8	320	IMMUNE_RESPONSE	1.11E-16
BRCA.M8	320	SIGNAL_TRANSDUCTION	6.27E-15
BRCA.M8	320	RESPONSE_TO_EXTERNAL_STIMULUS	3.69E-11
BRCA.M8	320	INFLAMMATORY_RESPONSE	6.69E-10
BRCA.M8	320	CYTOKINE_PRODUCTION	8.29E-09
BRCA.M8	320	RESPONSE_TO_WOUNDING	2.03E-08
BRCA.M8	320	MULTI_ORGANISM_PROCESS	1.43E-07
BRCA.M8	320	POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	1.90E-07
HNSC.M1	137	STRIATED_MUSCLE_CONTRACTION_GO_0006941	1.51E-10

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
HNSC.M1	137	MUSCLE_DEVELOPMENT	6.67E-09
HNSC.M1	137	SYSTEM_PROCESS	1.41E-08
HNSC.M1	137	ION_TRANSPORT	0.000162766
HNSC.M1	137	ANATOMICAL_STRUCTURE_DEVELOPMENT	0.000190506
HNSC.M1	137	REGULATION_OF_MUSCLE_CONTRACTION	0.000212791
HNSC.M1	137	CARBOHYDRATE_TRANSPORT	0.000212791
HNSC.M1	137	ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CELL_POLARITY	0.000212791
HNSC.M1	137	ORGAN_DEVELOPMENT	0.000243776
HNSC.M1	137	CATION_TRANSPORT	0.000321926
HNSC.M2	683	ANATOMICAL_STRUCTURE_DEVELOPMENT	1.47E-19
HNSC.M2	683	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.42E-18
HNSC.M2	683	SYSTEM_DEVELOPMENT	1.65E-17
HNSC.M2	683	ORGAN_DEVELOPMENT	3.70E-13
HNSC.M2	683	SKELETAL_DEVELOPMENT	6.85E-13
HNSC.M2	683	NERVOUS_SYSTEM_DEVELOPMENT	1.57E-08
HNSC.M2	683	MUSCLE_DEVELOPMENT	1.71E-07
HNSC.M2	683	ANATOMICAL_STRUCTURE_MORPHOGENESIS	2.92E-07
HNSC.M2	683	GENERATION_OF_A_SIGNAL_INVOLVED_IN_CELL_CELL_SIGNALING	1.99E-06
HNSC.M2	683	REGULATION_OF_HORMONE_SECRETION	2.13E-06
HNSC.M3	399	ECTODERM_DEVELOPMENT	1.69E-10
HNSC.M3	399	EPIDERMIS_DEVELOPMENT	5.24E-09
HNSC.M3	399	TISSUE_DEVELOPMENT	3.34E-08
HNSC.M3	399	ORGAN_DEVELOPMENT	2.21E-07
HNSC.M3	399	SYSTEM_DEVELOPMENT	4.53E-07
HNSC.M3	399	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	5.64E-07
HNSC.M3	399	ANATOMICAL_STRUCTURE_DEVELOPMENT	3.58E-06
HNSC.M3	399	FATTY_ACID_BIOSYNTHETIC_PROCESS	9.24E-05
HNSC.M3	399	CYTOPLASM_ORGANIZATION_AND_BIOGENESIS	0.000124158

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
HNSC.M3	399	INTERLEUKIN_2_PRODUCTION	0.000876675
HNSC.M4	233	ANATOMICAL_STRUCTURE_DEVELOPMENT	1.04E-05
HNSC.M4	233	SYSTEM_DEVELOPMENT	1.62E-05
HNSC.M4	233	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.93E-05
HNSC.M4	233	CELL_CELL_ADHESION	3.61E-05
HNSC.M4	233	ORGAN_DEVELOPMENT	4.09E-05
HNSC.M4	233	SKELETAL_DEVELOPMENT	0.000114245
HNSC.M4	233	HETEROPHILIC_CELL_ADHESION	0.000133208
HNSC.M4	233	INTERCELLULAR_JUNCTION_ASSEMBLY	0.000181729
HNSC.M4	233	N_ACETYLGUCOSAMINE_METABOLIC_PROCESS	0.000240413
HNSC.M4	233	SMOOTH_MUSCLE_CONTRACTION_GO_0006939	0.000240413
HNSC.M6	113	RESPONSE_TO_VIRUS	2.12E-07
HNSC.M6	113	RESPONSE_TO_OTHER_ORGANISM	4.40E-06
HNSC.M6	113	DEFENSE_RESPONSE	1.09E-05
HNSC.M6	113	MULTI_ORGANISM_PROCESS	2.33E-05
HNSC.M6	113	RESPONSE_TO_BIOTIC_STIMULUS	3.65E-05
HNSC.M6	113	I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	0.000307631
HNSC.M6	113	IMMUNE_SYSTEM_PROCESS	0.000320374
HNSC.M6	113	ION_HOMEOSTASIS	0.00054269
HNSC.M6	113	REGULATION_OF_CELL_ADHESION	0.000902707
HNSC.M6	113	CELLULAR_HOMEOSTASIS	0.000978858
HNSC.M7	127	REGULATION_OF_MEMBRANE_POTENTIAL	8.13E-05
HNSC.M7	127	SPERMATID_DEVELOPMENT	0.001443428
HNSC.M7	127	PEPTIDE_METABOLIC_PROCESS	0.001443428
HNSC.M7	127	FATTY_ACID_BETA_OXIDATION	0.00175753
HNSC.M7	127	SPERMATID_DIFFERENTIATION	0.00175753

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
HNSC.M7	127	REGULATION_OF_ACTION_POTENTIAL	0.004248538
HNSC.M7	127	BASE_EXCISION_REPAIR	0.004248538
HNSC.M7	127	EMBRYONIC_DEVELOPMENT	0.004599437
HNSC.M7	127	FATTY_ACID_OXIDATION	0.004761619
HNSC.M7	127	DETECTION_OF_CHEMICAL_STIMULUS	0.004761619
HNSC.M8	212	KERATINOCYTE_DIFFERENTIATION	1.61E-17
HNSC.M8	212	EPIDERMIS_DEVELOPMENT	1.52E-13
HNSC.M8	212	ECTODERM_DEVELOPMENT	7.63E-13
HNSC.M8	212	TISSUE_DEVELOPMENT	7.13E-11
HNSC.M8	212	TISSUE_MORPHOGENESIS	7.78E-06
HNSC.M8	212	EMBRYO_IMPLANTATION	7.78E-06
HNSC.M8	212	OVULATION_CYCLE	7.78E-06
HNSC.M8	212	CYTOKINE_AND_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	6.43E-05
HNSC.M8	212	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	7.96E-05
HNSC.M8	212	EPITHELIAL_CELL_DIFFERENTIATION	0.000100716
HNSC.M9	745	IMMUNE_SYSTEM_PROCESS	7.51E-33
HNSC.M9	745	IMMUNE_RESPONSE	1.16E-28
HNSC.M9	745	DEFENSE_RESPONSE	7.06E-16
HNSC.M9	745	T_CELL_ACTIVATION	4.39E-13
HNSC.M9	745	LEUKOCYTE_ACTIVATION	8.74E-13
HNSC.M9	745	SIGNAL_TRANSDUCTION	5.42E-12
HNSC.M9	745	CELL_ACTIVATION	7.44E-12
HNSC.M9	745	LYMPHOCYTE_ACTIVATION	1.13E-11
HNSC.M9	745	RESPONSE_TO_CHEMICAL_STIMULUS	1.82E-10
HNSC.M9	745	LOCOMOTORY_BEHAVIOR	3.72E-10
HNSC.M10	392	IMMUNE_SYSTEM_PROCESS	1.64E-25
HNSC.M10	392	IMMUNE_RESPONSE	3.63E-21

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
HNSC.M10	392	DEFENSE_RESPONSE	3.26E-19
HNSC.M10	392	SIGNAL_TRANSDUCTION	7.11E-14
HNSC.M10	392	RESPONSE_TO_EXTERNAL_STIMULUS	4.46E-10
HNSC.M10	392	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	4.99E-09
HNSC.M10	392	INFLAMMATORY_RESPONSE	1.05E-08
HNSC.M10	392	HUMORAL_IMMUNE_RESPONSE	6.85E-08
HNSC.M10	392	CELLULAR_DEFENSE_RESPONSE	7.01E-08
HNSC.M10	392	RESPONSE_TO_WOUNDING	1.73E-06
KIRC.M1	214	ANATOMICAL_STRUCTURE_DEVELOPMENT	4.10E-09
KIRC.M1	214	SYSTEM_DEVELOPMENT	8.79E-08
KIRC.M1	214	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.19E-07
KIRC.M1	214	NERVOUS_SYSTEM_DEVELOPMENT	1.27E-06
KIRC.M1	214	CELLULAR_CATION_HOMEOSTASIS	9.37E-06
KIRC.M1	214	CATION_HOMEOSTASIS	1.15E-05
KIRC.M1	214	EXTRACELLULAR_STRUCTURE_ORGANIZATION_AND_BIOGENESIS	1.35E-05
KIRC.M1	214	CELLULAR_HOMEOSTASIS	1.42E-05
KIRC.M1	214	MYOBLAST_DIFFERENTIATION	1.88E-05
KIRC.M1	214	CELL_MATRIX_ADHESION	3.21E-05
KIRC.M2	451	STRIATED_MUSCLE_CONTRACTION_GO_0006941	0.002632494
KIRC.M2	451	CELL_MATURATION	0.003928635
KIRC.M2	451	MYOBLAST_DIFFERENTIATION	0.004698584
KIRC.M2	451	MEIOTIC_RECOMBINATION	0.004698584
KIRC.M2	451	DEVELOPMENTAL_MATURATION	0.005553409
KIRC.M2	451	MEIOSIS_I	0.007526941
KIRC.M2	451	MUSCLE_CELL_DIFFERENTIATION	0.009865225
KIRC.M2	451	SPERMATID_DEVELOPMENT	0.016922323

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
KIRC.M2	451	S_PHASE_OF_MITOTIC_CELL_CYCLE	0.016922323
KIRC.M2	451	AMINE_CATABOLIC_PROCESS	0.017378794
KIRC.M3	440	ANATOMICAL_STRUCTURE_DEVELOPMENT	5.45E-11
KIRC.M3	440	SIGNAL_TRANSDUCTION	6.63E-11
KIRC.M3	440	SYSTEM_DEVELOPMENT	4.99E-10
KIRC.M3	440	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	5.75E-10
KIRC.M3	440	NERVOUS_SYSTEM_DEVELOPMENT	1.14E-09
KIRC.M3	440	SYNAPSE_ORGANIZATION_AND_BIOGENESIS	9.05E-09
KIRC.M3	440	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	2.93E-08
KIRC.M3	440	G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	2.96E-08
KIRC.M3	440	SYNAPTOGENESIS	3.21E-08
KIRC.M3	440	CELL_CELL_SIGNALING	5.33E-08
KIRC.M4	291	IMMUNE_SYSTEM_PROCESS	1.77E-23
KIRC.M4	291	IMMUNE_RESPONSE	7.86E-20
KIRC.M4	291	DEFENSE_RESPONSE	3.11E-15
KIRC.M4	291	T_CELL_ACTIVATION	3.31E-13
KIRC.M4	291	LYMPHOCYTE_ACTIVATION	1.08E-12
KIRC.M4	291	SIGNAL_TRANSDUCTION	3.61E-12
KIRC.M4	291	LEUKOCYTE_ACTIVATION	5.79E-12
KIRC.M4	291	CELL_ACTIVATION	2.50E-11
KIRC.M4	291	REGULATION_OF_IMMUNE_SYSTEM_PROCESS	7.18E-11
KIRC.M4	291	REGULATION_OF_LYMPHOCYTE_ACTIVATION	5.72E-10
KIRC.M5	79	NEUROTRANSMITTER_SECRETION	1.07E-07
KIRC.M5	79	REGULATED_SECRETORY_PATHWAY	2.04E-07
KIRC.M5	79	REGULATION_OF_MUSCLE_CONTRACTION	5.73E-07
KIRC.M5	79	REGULATION_OF_NEUROTRANSMITTER_LEVELS	1.55E-06
KIRC.M5	79	GENERATION_OF_A_SIGNAL_INVOLVED_IN_CELL_CELL_SIGNALING	3.42E-06
KIRC.M5	79	SYSTEM_PROCESS	5.24E-06

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
KIRC.M5	79	REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.74E-05
KIRC.M5	79	POTASSIUM_ION_TRANSPORT	5.64E-05
KIRC.M5	79	REGULATION_OF_TRANSPORT	9.94E-05
KIRC.M5	79	SECRETORY_PATHWAY	0.000238941
KIRC.M7	213	DEFENSE_RESPONSE	9.45E-09
KIRC.M7	213	PHAGOCYTOSIS	4.57E-07
KIRC.M7	213	HUMORAL_IMMUNE_RESPONSE	5.64E-07
KIRC.M7	213	IMMUNE_SYSTEM_PROCESS	9.23E-07
KIRC.M7	213	IMMUNE_RESPONSE	3.35E-06
KIRC.M7	213	CELLULAR_DEFENSE_RESPONSE	2.04E-05
KIRC.M7	213	SIGNAL_TRANSDUCTION	4.54E-05
KIRC.M7	213	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	5.60E-05
KIRC.M7	213	POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	6.47E-05
KIRC.M7	213	G_PROTEIN_SIGNALING_COUPLED_TO_IP3_SECOND_MESSENGERPHOSPHOLIPASE_C_ACTIVATING	7.24E-05
KIRC.M8	213	DEFENSE_RESPONSE	2.61E-24
KIRC.M8	213	IMMUNE_SYSTEM_PROCESS	2.11E-18
KIRC.M8	213	RESPONSE_TO_EXTERNAL_STIMULUS	4.61E-18
KIRC.M8	213	IMMUNE_RESPONSE	1.04E-16
KIRC.M8	213	LOCOMOTORY_BEHAVIOR	2.09E-14
KIRC.M8	213	SIGNAL_TRANSDUCTION	7.08E-13
KIRC.M8	213	INFLAMMATORY_RESPONSE	2.12E-12
KIRC.M8	213	RESPONSE_TO_WOUNDING	5.13E-12
KIRC.M8	213	BEHAVIOR	2.57E-11
KIRC.M8	213	CELLULAR_DEFENSE_RESPONSE	4.46E-09
KIRC.M9	189	REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	1.47E-05
KIRC.M9	189	REGULATION_OF_PHOSPHORYLATION	6.23E-05
KIRC.M9	189	REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	7.16E-05

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
KIRC.M9	189	POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	7.16E-05
KIRC.M9	189	POSITIVE_REGULATION_OF_CELL_MIGRATION	7.16E-05
KIRC.M9	189	REGULATION_OF_TRANSFERASE_ACTIVITY	7.84E-05
KIRC.M9	189	PEPTIDYL_TYROSINE_PHOSPHORYLATION	7.93E-05
KIRC.M9	189	CELL_CELL_ADHESION	9.87E-05
KIRC.M9	189	POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	9.87E-05
KIRC.M9	189	PEPTIDYL_TYROSINE_MODIFICATION	0.000105926
KIRC.M10	221	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	2.40E-11
KIRC.M10	221	ORGAN_DEVELOPMENT	2.66E-11
KIRC.M10	221	ANATOMICAL_STRUCTURE_DEVELOPMENT	1.56E-10
KIRC.M10	221	SYSTEM_DEVELOPMENT	1.71E-10
KIRC.M10	221	SKELETAL_DEVELOPMENT	9.81E-07
KIRC.M10	221	HEART_DEVELOPMENT	3.28E-05
KIRC.M10	221	MUSCLE_DEVELOPMENT	4.28E-05
KIRC.M10	221	TISSUE_DEVELOPMENT	7.92E-05
KIRC.M10	221	EPIDERMIS_DEVELOPMENT	7.98E-05
KIRC.M10	221	EPITHELIAL_TO_MESENCHYMAL_TRANSITION	0.000113915
KIRC.M11	581	VITAMIN_TRANSPORT	4.84E-07
KIRC.M11	581	CARBOXYLIC_ACID_TRANSPORT	9.68E-07
KIRC.M11	581	ORGANIC_ACID_TRANSPORT	1.20E-06
KIRC.M11	581	MONOCARBOXYLIC_ACID_TRANSPORT	2.85E-06
KIRC.M11	581	ESTABLISHMENT_OF_LOCALIZATION	3.05E-06
KIRC.M11	581	RESPONSE_TO_DRUG	1.72E-05
KIRC.M11	581	TRANSPORT	1.76E-05
KIRC.M11	581	NITROGEN_COMPOUND_METABOLIC_PROCESS	6.55E-05
KIRC.M11	581	CARBOXYLIC_ACID_METABOLIC_PROCESS	8.06E-05
KIRC.M11	581	ORGANIC_ACID_METABOLIC_PROCESS	9.14E-05
KIRC.M12	341	CELL_CYCLE_PROCESS	3.38E-18

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
KIRC.M12	341	M_PHASE	3.91E-18
KIRC.M12	341	CELL_CYCLE_GO_0007049	4.59E-18
KIRC.M12	341	MITOTIC_CELL_CYCLE	1.75E-17
KIRC.M12	341	CELL_CYCLE_PHASE	1.82E-17
KIRC.M12	341	M_PHASE_OF_MITOTIC_CELL_CYCLE	4.22E-17
KIRC.M12	341	MITOSIS	4.06E-16
KIRC.M12	341	REGULATION_OF_MITOSIS	5.14E-10
KIRC.M12	341	REGULATION_OF_CELL_CYCLE	3.92E-09
KIRC.M12	341	CELL_CYCLE_CHECKPOINT_GO_0000075	4.58E-08
BLCA.M1	111	COENZYME_BIOSYNTHETIC_PROCESS	1.46E-05
BLCA.M1	111	COFACTOR_BIOSYNTHETIC_PROCESS	0.000155596
BLCA.M1	111	COENZYME_METABOLIC_PROCESS	0.000927251
BLCA.M1	111	RESPONSE_TO_TOXIN	0.001105661
BLCA.M1	111	NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	0.001105661
BLCA.M1	111	XENOBIOTIC_METABOLIC_PROCESS	0.001346913
BLCA.M1	111	APOPTOTIC_MITOCHONDRIAL_CHANGES	0.001346913
BLCA.M1	111	TRICARBOXYLIC_ACID_CYCLE_INTERMEDIATE_METABOLIC_PROCESS	0.001346913
BLCA.M1	111	RESPONSE_TO_XENOBIOTIC_STIMULUS	0.001610975
BLCA.M1	111	RESPONSE_TO_CARBOHYDRATE_STIMULUS	0.001610975
BLCA.M2	697	EMBRYONIC_DEVELOPMENT	1.75E-06
BLCA.M2	697	LIPID_METABOLIC_PROCESS	1.87E-06
BLCA.M2	697	CYTOPLASM_ORGANIZATION_AND_BIOGENESIS	3.88E-06
BLCA.M2	697	CELLULAR_LIPID_METABOLIC_PROCESS	7.24E-06
BLCA.M2	697	ANATOMICAL_STRUCTURE_DEVELOPMENT	1.04E-05

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
BLCA.M2	697	CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	1.24E-05
BLCA.M2	697	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	2.84E-05
BLCA.M2	697	INTERCELLULAR_JUNCTION_ASSEMBLY_AND_MAINTENANCE	3.28E-05
BLCA.M2	697	EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	4.78E-05
BLCA.M2	697	SYSTEM_DEVELOPMENT	5.92E-05
BLCA.M3	437	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.31E-14
BLCA.M3	437	ANATOMICAL_STRUCTURE_DEVELOPMENT	3.35E-14
BLCA.M3	437	SYSTEM_DEVELOPMENT	1.16E-11
BLCA.M3	437	ORGAN_DEVELOPMENT	4.29E-09
BLCA.M3	437	SKELETAL_DEVELOPMENT	1.67E-08
BLCA.M3	437	MUSCLE_DEVELOPMENT	3.16E-07
BLCA.M3	437	ANATOMICAL_STRUCTURE_MORPHOGENESIS	6.00E-07
BLCA.M3	437	NERVOUS_SYSTEM_DEVELOPMENT	3.28E-05
BLCA.M3	437	GENERATION_OF_NEURONS	3.97E-05
BLCA.M3	437	CELL_MATRIX_ADHESION	9.56E-05
BLCA.M4	256	KERATINOCYTE_DIFFERENTIATION	5.60E-07
BLCA.M4	256	EPIDERMIS_DEVELOPMENT	1.70E-06
BLCA.M4	256	ECTODERM_DEVELOPMENT	4.24E-06
BLCA.M4	256	TISSUE_DEVELOPMENT	3.53E-05
BLCA.M4	256	CALCIUM_INDEPENDENT_CELL_CELL_ADHESION	0.000111075
BLCA.M4	256	EPITHELIAL_CELL_DIFFERENTIATION	0.00017591
BLCA.M4	256	RESPONSE_TO_STEROID_HORMONE_STIMULUS	0.000239798
BLCA.M4	256	REGULATION_OF_ACTIN_FILAMENT_LENGTH	0.000408544
BLCA.M4	256	CELL_CELL_ADHESION	0.000505858
BLCA.M4	256	POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	0.000505858
BLCA.M6	89	DEFENSE_RESPONSE	1.39E-05
BLCA.M6	89	RESPONSE_TO_OTHER_ORGANISM	2.19E-05
BLCA.M6	89	RESPONSE_TO_VIRUS	5.00E-05

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
BLCA.M6	89	I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	0.000100388
BLCA.M6	89	RESPONSE_TO_BIOTIC_STIMULUS	0.000127869
BLCA.M6	89	EPIDERMIS_DEVELOPMENT	0.0001977
BLCA.M6	89	ECTODERM_DEVELOPMENT	0.000313021
BLCA.M6	89	IMMUNE_SYSTEM_PROCESS	0.000399913
BLCA.M6	89	LEUKOCYTE_DIFFERENTIATION	0.000487311
BLCA.M6	89	MULTI_ORGANISM_PROCESS	0.000557908
BLCA.M7	183	MUSCLE_DEVELOPMENT	3.29E-10
BLCA.M7	183	SKELETAL_MUSCLE_DEVELOPMENT	1.89E-07
BLCA.M7	183	MYOBLAST_DIFFERENTIATION	2.15E-07
BLCA.M7	183	ORGAN_DEVELOPMENT	3.21E-07
BLCA.M7	183	MUSCLE_CELL_DIFFERENTIATION	8.85E-07
BLCA.M7	183	STRIATED_MUSCLE_DEVELOPMENT	9.26E-07
BLCA.M7	183	REGULATION_OF_HEART_CONTRACTION	1.75E-06
BLCA.M7	183	SYSTEM_DEVELOPMENT	1.05E-05
BLCA.M7	183	SYSTEM_PROCESS	2.06E-05
BLCA.M7	183	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	2.15E-05
BLCA.M8	916	IMMUNE_SYSTEM_PROCESS	6.01E-56
BLCA.M8	916	IMMUNE_RESPONSE	1.35E-45
BLCA.M8	916	SIGNAL_TRANSDUCTION	2.56E-36
BLCA.M8	916	DEFENSE_RESPONSE	1.51E-30
BLCA.M8	916	RESPONSE_TO_EXTERNAL_STIMULUS	1.37E-23
BLCA.M8	916	LOCOMOTORY_BEHAVIOR	7.57E-20
BLCA.M8	916	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	3.36E-19
BLCA.M8	916	RESPONSE_TO_WOUNDING	1.40E-17
BLCA.M8	916	LEUKOCYTE_ACTIVATION	1.61E-17

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
BLCA.M8	916	INFLAMMATORY_RESPONSE	1.63E-16
BLCA.M9	309	EXTRACELLULAR_STRUCTURE_ORGANIZATION_AND_BIOGENESIS	4.87E-06
BLCA.M9	309	SYSTEM_PROCESS	5.22E-05
BLCA.M9	309	SYNAPTOGENESIS	1.00E-04
BLCA.M9	309	NERVOUS_SYSTEM_DEVELOPMENT	0.000120749
BLCA.M9	309	POSITIVE_REGULATION_OF_SECRETION	0.000154822
BLCA.M9	309	SYNAPTIC_TRANSMISSION	0.000183308
BLCA.M9	309	SYSTEM_DEVELOPMENT	0.000222238
BLCA.M9	309	RESPONSE_TO_DRUG	0.000228631
BLCA.M9	309	ESTABLISHMENT_OF_LOCALIZATION	0.00026093
BLCA.M9	309	SYNAPSE_ORGANIZATION_AND_BIOGENESIS	0.000273718
UCEC.M1	155	PEPTIDE_METABOLIC_PROCESS	0.002138568
UCEC.M1	155	FATTY_ACID_BETA_OXIDATION	0.002601739
UCEC.M1	155	TRICARBOXYLIC_ACID_CYCLE_INTERMEDIATE_METABOLIC_PROCESS	0.002601739
UCEC.M1	155	VITAMIN_TRANSPORT	0.00365578
UCEC.M1	155	PROTEIN_TETRAMERIZATION	0.004245421
UCEC.M1	155	NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	0.004245421
UCEC.M1	155	NEUROPEPTIDE_SIGNALING_PATHWAY	0.004245421
UCEC.M1	155	STRIATED_MUSCLE_CONTRACTION_GO_0006941	0.004245421
UCEC.M1	155	AEROBIC_RESPIRATION	0.004875999
UCEC.M1	155	LIPID_HOMEOSTASIS	0.005546917
UCEC.M2	429	MITOTIC_CELL_CYCLE	2.84E-13
UCEC.M2	429	CELL_CYCLE_PHASE	2.52E-12
UCEC.M2	429	CELL_CYCLE_PROCESS	4.55E-12
UCEC.M2	429	M_PHASE_OF_MITOTIC_CELL_CYCLE	7.61E-12
UCEC.M2	429	MITOSIS	5.32E-11
UCEC.M2	429	CELL_CYCLE_GO_0007049	7.24E-10

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
UCEC.M2	429	M_PHASE	7.45E-10
UCEC.M2	429	REGULATION_OF_MITOSIS	1.06E-06
UCEC.M2	429	CHROMOSOME_SEGREGATION	2.25E-06
UCEC.M2	429	INTERPHASE_OF_MITOTIC_CELL_CYCLE	3.05E-06
UCEC.M3	349	IMMUNE_SYSTEM_PROCESS	1.03E-20
UCEC.M3	349	IMMUNE_RESPONSE	1.15E-17
UCEC.M3	349	SIGNAL_TRANSDUCTION	1.37E-15
UCEC.M3	349	T_CELL_ACTIVATION	2.81E-12
UCEC.M3	349	DEFENSE_RESPONSE	1.08E-11
UCEC.M3	349	LEUKOCYTE_ACTIVATION	5.60E-11
UCEC.M3	349	LYMPHOCYTE_ACTIVATION	1.83E-10
UCEC.M3	349	CELL_ACTIVATION	2.38E-10
UCEC.M3	349	REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.93E-08
UCEC.M3	349	CELLULAR_DEFENSE_RESPONSE	2.36E-08
UCEC.M4	300	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1.04E-18
UCEC.M4	300	ANATOMICAL_STRUCTURE_DEVELOPMENT	5.11E-18
UCEC.M4	300	SYSTEM_DEVELOPMENT	8.12E-17
UCEC.M4	300	ORGAN_DEVELOPMENT	1.16E-13
UCEC.M4	300	BLOOD_COAGULATION	2.47E-10
UCEC.M4	300	COAGULATION	3.15E-10
UCEC.M4	300	HEMOSTASIS	7.92E-10
UCEC.M4	300	SKELETAL_DEVELOPMENT	1.55E-09
UCEC.M4	300	WOUND_HEALING	2.70E-09
UCEC.M4	300	REGULATION_OF_BODY_FLUID_LEVELS	4.69E-09
UCEC.M6	97	RESPONSE_TO_VIRUS	2.72E-06
UCEC.M6	97	DEFENSE_RESPONSE	3.08E-06
UCEC.M6	97	IMMUNE_RESPONSE	9.60E-06
UCEC.M6	97	I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	1.14E-05

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
UCEC.M6	97	APOPTOTIC_MITOCHONDRIAL_CHANGES	1.34E-05
UCEC.M6	97	IMMUNE_SYSTEM_PROCESS	1.62E-05
UCEC.M6	97	RESPONSE_TO_OTHER_ORGANISM	3.32E-05
UCEC.M6	97	POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	4.17E-05
UCEC.M6	97	PROTEIN_KINASE_CASCADE	4.66E-05
UCEC.M6	97	REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	5.74E-05
UCEC.M7	123	REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	6.30E-06
UCEC.M7	123	REGULATION_OF_INTRACELLULAR_TRANSPORT	1.07E-05
UCEC.M7	123	ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	1.40E-05
UCEC.M7	123	SPHINGOLIPID_BIOSYNTHETIC_PROCESS	1.99E-05
UCEC.M7	123	PROTEIN_EXPORT_FROM_NUCLEUS	3.62E-05
UCEC.M7	123	PHOSPHORYLATION	6.78E-05
UCEC.M7	123	TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	0.000103166
UCEC.M7	123	PROTEIN_AMINO_ACID_PHOSPHORYLATION	0.000177072
UCEC.M7	123	EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.000242999
UCEC.M7	123	PEPTIDYL_AMINO_ACID_MODIFICATION	0.000429533
UCEC.M8	167	CELL_MATRIX_ADHESION	3.95E-07
UCEC.M8	167	CELL_SUBSTRATE_ADHESION	4.64E-07
UCEC.M8	167	SKELETAL_DEVELOPMENT	1.20E-06
UCEC.M8	167	REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	2.37E-06
UCEC.M8	167	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	4.69E-06
UCEC.M8	167	SYSTEM_PROCESS	6.47E-06
UCEC.M8	167	ANATOMICAL_STRUCTURE_DEVELOPMENT	8.94E-06
UCEC.M8	167	SYSTEM_DEVELOPMENT	8.97E-06
UCEC.M8	167	REGULATION_OF_MUSCLE_CONTRACTION	1.14E-05
UCEC.M8	167	ORGAN_DEVELOPMENT	3.18E-05

module name	module size	MSigDB.c5.bp (v3.1, Top10 is shown)	hypergeometric p-value
UCEC.M9	607	PROTEIN_AMINO_ACID_O_LINKED_GLYCOSYLATION	1.00E-04
UCEC.M9	607	SEXUAL_REPRODUCTION	0.000482434
UCEC.M9	607	GAMETE_GENERATION	0.001236102
UCEC.M9	607	DIGESTION	0.001245424
UCEC.M9	607	BODY_FLUID_SECRETION	0.002169668
UCEC.M9	607	CALCIUM_INDEPENDENT_CELL_CELL_ADHESION	0.002825644
UCEC.M9	607	COFACTOR_TRANSPORT	0.002922453
UCEC.M9	607	N_ACETYGLUCOSAMINE_METABOLIC_PROCESS	0.00381725
UCEC.M9	607	SECRETION	0.003992735
UCEC.M9	607	G2_M_TRANSITION_OF_MITOTIC_CELL_CYCLE	0.004861511
UCEC.M10	324	IMMUNE_SYSTEM_PROCESS	6.86E-27
UCEC.M10	324	IMMUNE_RESPONSE	1.12E-21
UCEC.M10	324	DEFENSE_RESPONSE	7.55E-18
UCEC.M10	324	RESPONSE_TO_EXTERNAL_STIMULUS	3.25E-15
UCEC.M10	324	INFLAMMATORY_RESPONSE	5.50E-14
UCEC.M10	324	RESPONSE_TO_WOUNDING	7.33E-12
UCEC.M10	324	HUMORAL_IMMUNE_RESPONSE	1.57E-08
UCEC.M10	324	SIGNAL_TRANSDUCTION	2.70E-07
UCEC.M10	324	CDC42_PROTEIN_SIGNAL_TRANSDUCTION	4.89E-07
UCEC.M10	324	LOCOMOTORY_BEHAVIOR	1.40E-06

Zou_Suppl_Table_4

Core module genes of the conserved CGMs
<p># 1:black modules # function class: cell cycle # core genes are present in at least three different cancer types</p>
<p>BIRC5 BRIP1 CENPA CLSPN DEPDC1 DEPDC1B E2F7 HMMR MCM10 MYBL2 PBK APOBEC3B ASPM AURKB BRCA2 BUB1 CASC5 CCNE1 CCNE2 CDC25C CDC45 CDCA2 CENPE CENPF CKAP2L DIAPH3 DLGAP5 E2F8 ESCO2 ESPL1 EXO1 FAM111B FAM64A FAM83D FOXM1 GGH GSG2 IQGAP3 KIF14 KIF15 LDHD MELK NCAPG NDC80 NEIL3 NUF2 PIF1 POLQ RRM2 SGOL1 SKA1 TOP2A TROAP TTK UBE2C VASH2 WDR62 ANLN APLP1 ARHGAP11B ARHGEF37 ASF1B ATP8B3 BUB1B C15orf42 C17orf96 C19orf57 C9orf140 CCDC150 CCNB2 CDC20 CDC25A CDCA7 CDK1 CDKN3 CDT1 CENPI CENPK CENPM CENPV CENPW CEP55 DTL E2F2 ERCC6L FAM54A FAM72D FANCA FBXO43 GPRIN1 GTSE1 HJURP IGF2BP3 KIAA0101 KIF18A KIF18B KIF20A KIF23 KIF2C KIF4A KIFC1 LRP8 MFSD4 MKI67 MLLT11 MND1 MYBL1 NCAPH NEK2 OIP5 ORC1L PLK1 PTTG1 RAD54L RECQL4 RPL39L RTKN2 SKA3 SLC7A5 SPC24 SPC25 STEAP3 TK1 TMEM38B TMSB15B TPX2 UHRF1 XRCC2 ZNF695</p>
<p># 2:turquoise modules # function class: adaptive immune # core genes are present in at least 8 different cancer types</p>
<p>ALOX5AP CD163 CD53 CPVL FCGR3A FGL2 FPR3 HLA-DOA HLA-DPA1 HLA-DPB1 HLA-DQA1 HLA-DRA SIGLEC10 SLAMF8 VSIG4 APOC1 BTK C1QA C1QB C1QC C3AR1 CD300A CD86 CLEC7A CMKLR1 CTSS CYBB FCGR2B FPR1 GPR183 HLA-DMB HLA-DRB1 HLA-DRB5 IL10RA LAIR1 LILRB4 LYZ MPEG1 MS4A4A MSR1 NCKAP1L PLEK SDS SRGN</p>
<p># 3:orange modules # function class: adaptive immune # core genes are present in at least 4 different cancer types</p>
<p>ACAP1 ADAM6 CD27 CD3E CD6 DERL3 IGJ IL12RB1 IL2RB ITGAL JAK3 LAG3 LCK LOC96610 MAP4K1 NKG7 PSTPIP1 PTPN7 RASAL3 TBC1D10C TMC8 AGAP2 APOBEC3D APOBEC3G ARHGAP9 BATF BIRC3 CCL5 CCR5 CCR7 CD2 CD247 CD3D CD5 CD52 CD79B CD96 CIITA CORO1A CST7 CTSW CXCL9 CXCR6 CYTIP ERAP2 FAIM3 FOXP3 GBP4 GPR132 HCST IDO1 IL2RG IPCEF1 ITGB7 KIF21B LAT LRMP LSP1 MMP25 MYO1G P2RY8 PPP1R16B PRF1 PTPRCAP RAB37 RAC2 SEPT1 SLAMF7 SP140 SPN SPOCK2 TRAF3IP3 UBD ACSL5 ANKRD22 APOL4 ASB2 BATF3 BIN2 C16orf54 C4A CD37 CD48 CD69 CD7 CD79A CD8A CPNE5 CXCL10 ETV7 FAM113B FAM46C FAM65B GBP5 GIMAP1 GIMAP7 GJD3 GNG7 GRAP2 GZMA GZMB IKZF1 IL15 IL34 ISG20 KLHDC7B LOC606724 LTB MCOLN2 MEI1 MGAT3 POU2F2 PTGDS RASGRP1 RASGRP2 RUNX3 SARDH SASH3 SELL SLA2 SOCS1 ST8SIA1 TCF7 TLR9 TMEM156 TNFAIP2 TNFRSF4 TRIM69 TYMP WAS ZAP70</p>
<p># 4:red modules # function class: innate immune # core genes are present in at least 3 different cancer types</p>
<p>BST2 CMPK2 HERC5 HERC6 IFI27 IFI44L IFI6 IFIH1 IFIT1 IFIT3 IFITM1 ISG15 MX1 MX2 OAS1 OAS2 OASL RSAD2 XAF1 DDX60 EPSTI1 IFI35 IFI44 IFIT2 IRF7 LY6E OAS3 RTP4 SAMD9 SAMD9L BATF2 DDX60L HCG26 HCP5 HLA-F HSH2D LAMP3 PSMB9 STAT1 TRIM22 USP18 APOL1 APOL6 DDX58 GBP1 HLA-B HLA-H HLA-L IFI16 TAP1 TNFSF10</p>
<p># 5::blue modules # function class: EMT # core genes are present in at least 5 cancer types</p>

Core module genes of the conserved CGMs
<p>COL12A1 COL1A1 COL1A2 COL3A1 COL5A1 COL5A2 COL6A1 COL6A2 COL6A3 CTSK DCN EMILIN1 FBN1 FN1 ISLR LUM MMP11 MMP2 OLFML2B PCOLCE POSTN ADAM12 ADAMTS12 ADAMTS2 ADAMTS4 ADAMTS7 CDH11 COL5A3 CRISPLD2 CTGF DACT1 EDNRA FAM26E FBLN2 GLT8D2 HTRA3 ITGA11 KIF26B LEPREL2 MXRA5 NDN OLFML1 PRRX1 PXDN RCN3 SERPINE1 SGIP1 SPON2 SSC5D THBS2 VCAN WISP1 ZNF469 ADAMTS14 AEBP1 AG2 ALDH1A3 ASPN BGN C13orf33 C1QTNF1 CACNA1C CCDC80 CD248 CHSY3 COL8A1 CPZ CYR61 ECM1 ECM2 FAP FBLN1 FNDC1 FNDC4 GAS1 HEPH INHBA KCNE4 LOXL2 LTBP2 MRC2 P4HA3 PDGFRA PID1 PMEPA1 PRICKLE1 SERPINF1 SFRP4 SPOCK1 SRPX2 SULF1 SVEP1 TGFβ3 THBS1 TMEM200B TNC TWIST1 AKAP12 AKT3 APCDD1 ASAM C10orf72 CACNA1H COL16A1 COLEC12 COX7A1 CPXM1 CSPG4 CTHRC1 DDR2 DIO2 DNM1 DPYSL3 DSEL EGFLAM ETV1 FGF1 FLRT2 GPC6 HHIPL1 HMCN1 IGDCC4 ISM1 LAMA2 MEX3B MFAP2 MSRB3 MXRA8 NID2 NOX4 NRP2 NTM OLFM2 PAMR1 PCDH18 PDGFRL PDPN PDZRN3 PODNL1 RARRES2 RBMS3 SCARF2 SDC2 SLC24A3 SNAI2 SPARC SRPX THY1 TMEM119 TMEM158 TMEM200A TSHZ3 VGLL3 WNT5A ABCC9 ACAN ACTA2 ACTG2 ADAMTS10 ANGPTL2 ATP10A BASP1 BEND6 BNC2 C12orf68 CCDC8 CDC42EP5 CDH23 CHRDL CLEC11A CNN1 COL14A1 COL8A2 CPE CREB3L1 CSMD2 DAAM2 DENND2A EDIL3 EFEMP1 EGR2 EPHA3 FAM19A5 FAT4 FBLN7 FILIP1L FLNC FMOD FOXL1 GALNTL2 GEM GGT5 GJA5 GLI3 HIC1 HTRA1 IGF2 ITGB3 ITGBL1 KDELR3 LOC399959 LOX LOXL1 LRCH2 LRRC17 LTBP1 LZTS1 MAP1B MATN3 MDGA1 MEG3 MEIS3 MMP23B MOXD1 MRV1 MSC NACAD NAV3 NKD2 OLFML3 PAPP1 PCDH7 PCDHGB7 PDGFRB PLA1 PMP22 PNMAL2 PODN PPAPDC3 PROS1 PRR16 PTGIS RASD2 RASGRF2 RGS4 ROR2 RPLP0P2 RUNX2 SH3RF3 SLIT3 SNED1 STC1 STMN3 SULF2 TAGLN TGFβ1 TIMP3 TPM2 TRPC1 TSPAN11 WTIP XYLT1 ZFH4 ZFPM2 ZNF521</p>
<p># 6::purple modules # function class: angiogenesis # core genes are present in at least two different cancer types</p>
<p>APLN CLEC3B EDNRB EMCN HSPA12B JAM2 NPR1 PDE7B RASD1 SOX17 SPARCL1 ST6GALNAC3 TAL1 TEK ABCG2 ADAMTS9 AVPR1A CACHD1 CETP CLDN11 CLDN5 COL15A1 EBF1 EBF3 ECSCR F2RL3 FAM124B FGD5 GJA5 ITIH5 LHX6 LPL NR5A2 PCDH17 PDE1A PDE2A PDE8B PDGFD PDK4 PGM5 PTPRB RASL11A RBP7 RGS5 RUNDC3B SEMA3G SHE SLC02A1 TMTC1 TRPC6 A2M ABCB1 ADAMTS5 ADCY1 ADCY4 AGT ALPL ANK2 ANO2 AOC3 APOD APOLD1 AQP1 ARHGAP28 ATOH8 ATP1B2 BEND7 BMP6 BTNL9 C14orf49 C17orf72 C2CD4C CABLES1 CADM1 CALCRL CCDC85A CD36 CDH6 CDKN1C CFD CLEC1A CLIC5 COL14A1 CXCL12 CYR1 DACH1 DCHS1 DENND2A DUSP1 EGR1 EGR3 EMID1 ENPP2 ESR1 FAM107A FAM13C FAM155A FAM171A1 FAM38B FILIP1 FLT4 FOLH1 FOS FOSB FOXF1 GABRD GATA2 GJA4 GNA14 GNG7 GPC3 GPR85 GPRASP1 GPRC5B GPX3 GRRP1 GYG2 HIGD1B HOXD9 ID1 ID4 IGF1 INHBB ITGA10 ITGA9 ITM2A JPH4 KBTBD11 KCNAB1 KDR KIAA0754 KIF26A KL KLF2 KLF4 LIPE LOC100190938 LOC158376 LOC339524 LXN LYVE1 MPPED2 MYH11 MYOM1 NGFR NLGN4X NOSTRIN NR4A1 NRXN2 NYNRIN OR51E1 PALMD PAMR1 PARK2 PARM1 PCDH19 PCDHB15 PCDHB3 PCDHB4 PDE1B PDE5A PEAR1 PKD1L1 PLAC9 PLCB1 PLCB4 QPRT RARB RASGRF2 RASIP1 RASL12 RGAG4 S1PR1 SAMD5 SCN4B SDPR SEMA6B SEMA6D SEPP1 SERPINI1 SH3BGL2 SHROOM4 SLC35F1 SNED1 SOCS2 SORBS2 SOX18 SPRY1 SPTBN4 TFPI TGFβR3 TM4SF18 TMEM150C TMEM88 TNXB USHBP1 VWF WSCD1 ZFP36 ZNF423 ZNF521 ZNF788</p>
<p># 7:magenta modules # function class: muscle development # core genes are present in at least two different cancer types</p>
<p>FHL1 HSPB6 JPH2 PDLIM3 SYNM SYNPO2 ACTA2 ACTG2 AOC3 CNN1 DES ELN FBLN5 FLNC FXYD6 HSPB7 INMT ITGA7 KCNMB1 LIMS2 LMOD1 MFAP4 MRGPRF MYH11 MYL9 MYLK NCAM1 PODN PRELP RASL12 SORBS1 TAGLN TPM2 ACACB AKAP6 ATOH8 BOC C5orf4 CLIP3 CPXM2 CRYAB DACT3 DTNA EBF4 EFHD1 FAM134B FBXL22 FBXO32 FOXF1 FRZB HSPB8 HSPB9 IGF2 IGFBP5 LOC728264 LOXL1 MGP MYH3 MYOM1 NEXN PGM5 PHYHIP PKNOX2 PLA2G16 POPDC2 PPAPDC3 PPP1R14A PSD RAI2 REEP1 RERG SLC2A4 SMOC2 SRL STON1 SYN1 SYNC TIMP3 TNS1 TSPAN18 TSPAN2 WFDC1</p>
<p># 8:brown modules # function class: differentiation # core genes are present in at least two different cancer types</p>

Core module genes of the conserved CGMs

ACPP AIM1L ALDH3B2 ALS2CL BNIPL C1orf170 CSTA EHF EPHA1 EPHB3 EPS8L1 EVPL FGFR2 FUT2 GJB2 GJB6 GRHL1 GRHL3 IFFO2 IL1RN KCNJ15 KCNS3 KLF8 KRT13 KRT17 KRT80 LYPD3 MALL NCCRP1 NIPAL1 NIPAL4 OCLN P2RY2 PLAC2 PPL PROM2 PRSS27 PTK6 RAET1G RAPGEFL1 RHOV SDCBP2 SERINC2 SLC2A9 SLC37A2 TMEM154 TMEM184A TMEM45B TNS4 TTC22 TTC39A ZNF185 ZNF750 A4GALT ABCA12 ACBD7 ACSS1 ADAMTS17 ADAMTSL5 AHNK2 ALOX12 ANKLE1 ANKRD22 ANKRD35 ANXA1 ANXA8 AQP3 ARHGEF37 ARHGEF4 ATP10B B4GALT6 BCL11A BNC1 BSPRY BTBD11 C12orf34 C15orf62 C16orf74 C17orf104 C19orf33 C1orf106 C1orf116 C20orf54 C3orf58 C6orf114 C6orf132 C7orf13 C8orf73 CA12 CABYR CARD14 CAV1 CBS CCDC64B CD24 CDH26 CDH3 CDHR1 CEACAM19 CEACAM6 CGN CHST7 CITED4 CLDN1 CLDN4 CLDN7 CLIC3 CNFN COCH COL17A1 CRABP2 CTS2L CXADR CXCL14 CXCR2 DHRS3 DHRS9 DMKN DSC2 DSG3 DSP DUOX1 DUOX2 DUOX1 E2F5 EMP1 EPB49 EPCAM EPN3 EPPK1 EXPH5 F2RL1 F3 FABP5 FAM43A FAM53A FAM81A FAM83A GBP6 GJA1 GJB3 GKAP1 GLB1L2 GPR109A GPR109B GPR157 HBEGF HES2 HLF HOMER2 HOOK1 HOPX HOXA10 HSPB1 HTR7 IL17RB IL1A IL1B IL20RB IL22RA1 ILDR1 INPP4B ITGA6 ITGB4 ITGB6 KCNK1 KIAA1543 KLF4 KLF5 KLK10 KRT15 KRT16 KRT19 KRT5 KRT6A KRT6B KRT6C LAD1 LAMA3 LCN2 LMTK3 LTB4R LTB4R2 LY6D MACC1 MAL2 MDK MICALL MNS1 MPP7 MPZL2 MYO5B NEBL NELL2 NRCAM NTRK2 OVOL1 P2RY1 PARD6A PHLDA2 PI3 PKP1 PLA2G4F PLCD3 PLCH2 PLEKHG6 PLEKH1 PODXL2 POU2F3 PPM1E PPP1R14C PRKX PRRG4 PRSS22 PRSS8 PSCA PTCH1 PTGES PVRL1 PVRL4 RAB11FIP1 RAB25 RAB38 RASL10B RASSF9 RHBDL2 RHOD RNF165 RNF39 RNFT2 S100A14 S100A8 S100A9 S100P S1PR5 SCEL SDC1 SEC14L2 SERPINB2 SERPINB5 SFN SGPP2 SH3TC2 SLPI SOX15 SOX2 SPINK5 SPRR1A ST6GALNAC1 ST6GALNAC2 STAR STARD5 STEAP1 STOX1 STOX2 SULT2B1 SUS4 SV2A SYCP2 SYT8 TACSTD2 TFAP2C TG TGM1 THBD THRB THSD1 TMC4 TMEM40 TMEM79 TMPRSS4 TP63 TPRG1 TRIM2 TRIM29 TRPV4 TSPAN1 TTC9 ULBP2 WNT4 WNT7B XDH ZNF117 ZNF239

9::green modules

function class: metabolism

core genes are present in at least two different cancer types

ATHL1 CPT1B GOLGA2B GOLGA8A HSF4 MST1 NCRNA00105 NEAT1 PABPC1L RNF207 SEC31B ADAMTS13 AHS2 C9orf45 CELF6 CHKB-CPT1B KCNQ1OT1 L3MBTL LOC100190986 LOC100272228 LOC162632 MST1P2 MYO15B PRICKLE4 SEC16B WDR52 AGAP8 AGER AOC2 ARHGAP33 AVIL CAPN3 CEACAM19 DNAH1 DNHD1 FAM13AOS FLJ42627 GABBR1 GABRE GOLGA6L9 GOLGA8B GSDMB HERC2P2 KIAA1683 LOC100132247 LOC100132287 LOC220594 LOC221442 LOC338799 LOC400931 LOC91316 LRP5L MALAT1 MAMDC4 MTMR9L NCRNA00201 NPIPL3 OVGP1 PAQR6 PILRB PLGLB2 PPIEL SLC25A27 SPTBN5 TNFRSF25 TLL3 ? ADHFE1 AMT AMY2B ATAD3C BZRAP1 C1orf104 C6orf26 C7orf53 CAPN12 CG030 COL27A1 COLQ CRYGS DFNB59 EGFL8 FER1L4 FLJ45445 FOXD4 KCNIP2 KLRA1 LENG8 LOC100131434 LOC100133161 LOC100133331 LOC100270804 LOC388692 LOC613037 LRRC56 MST1P9 NCRNA00174 NCRNA00176 NEIL1 NSUN5P1 NSUN5P2 PCSK4 PI4KAP2 PNPLA7 PRR22 PRRT2 QRICH2 REC8 RPL36A SLC6A16 SLC9A5 UNC5CL ZMAT1 ZNF177 ZNF404 ZNF662 ABCA7 ACCS ACRC AGAP11 AGAP7 ALS2CL ANKRD24 ANKRD36 ANKRD36B ANO9 AURKAPS1 C14orf181 C16orf79 C1orf126 C1orf175 C1orf213 C20orf46 C2orf63 C6orf164 C9orf68 CACNB1 CAPS CARD14 CCDC150 CDHR3 CDK3 CHRNA10 CNTD1 CROCCL2 CTRL CYP2D7P1 DNAH17 DNASE1L2 DNM1P35 DPY19L2P2 FAM95B1 FLJ13197 FLJ45244 FLJ45340 GNB3 GOLGA6L10 GOLGA6L5 GPC2 HCG27 HIST4H4 HSD17B7P2 INE1 ITIH4 KCNAB3 KCP KIAA1529 KIFC2 KLHL3 LCAT LOC100128288 LOC100128842 LOC100272146 LOC100272217 LOC100302650 LOC143666 LOC202181 LOC253039 LOC283314 LOC283663 LOC286367 LOC349114 LOC728264 LPIN3 LRRC37A2 LTB4R LY6G5B MAPK8IP3 MC1R MEGF6 MGC16121 MIR17HG MPP3 MSH5 MSTO2P MYH3 NBPFF16 NCRNA00085 NPFF NPIP NTN5 OBSCN OXER1 PBX4 PDXDC2 PI4KAP1 PLEKHG4 PLEKHH2 PLIN4 PMS2L11 PPFIA4 PRSS53 PTK6 PVT1 RGL3 RHPN1 RRN3P1 RRP7B SCNN1D SGK494 SLFNL1 SNHG12 SNHG4 SPDY6 SPIRE2 SYCP2 TBC1D3B TCTE3 TFAP2E TRPV1 TSSK6 TTC18 TTC21A TTN UCKL1AS WDR27 WDR90 YJEFN3 ZNF135 ZNF233 ZNF37B ZNF577 ZNF833

10::pink modules

function class: metabolism

core genes are present in at least two different cancer types

Note: OV.M2 added to the groups after manual examination.

Core module genes of the conserved CGMs

BAIAP3 C17orf72 C19orf51 C6orf97 C9orf98 CAPS CCDC11 CCDC40 DNALI1 FHAD1 KIAA1377 LOC646851 LRRC34 LRRC46 PPIL6 RSPH1 TPPP3 TTC18 TTC25 WDR78 ZMYND12 AK7 C10orf79 C11orf63 C11orf66 C14orf174 C16orf71 C1orf192 C1orf228 C1orf88 C2orf77 C6orf27 C7orf63 C9orf117 C9orf24 CASC1 CCDC103 CCDC114 CCDC146 CCDC153 CCDC19 CCDC39 CCDC65 CCDC74B CCDC81 DNAH3 DNAH7 EFCAB10 FAM164C FAM47E FANK1 FBXO15 FOXJ1 HYDIN KCNRG LRP2BP LRRC48 LRRC6 MAP6 MDH1B NHLRC4 PIH1D2 RAB36 RIBC1 SPA17 SPAG8 SPATA17 SPEF1 UBXN10 WDR66 ZMYND10 ? AGBL2 ANKRD35 ANKRD45 ATG9B BCO2 BEST4 C10orf95 C11orf70 C2orf88 C3orf15 C6orf154 C6orf165 C6orf217 C9orf116 CADPS2 CAPS2 CCDC113 CCDC17 CCDC74A CCDC78 CCDC89 CCDC96 CCNO CDHR3 CERKL CHST5 CHST6 CTXN1 DLEC1 DNAH9 DPY19L2P2 DYX1C1 DZIP1L EFHC2 ENKUR EPHX2 F3 FAM167A FAM179A FAM189A2 GALNT3 GATM GLIS3 GPR135 GPR162 HAGHL IGF2BP2 INHBB IQCD KIF17 LRRC10B LRRC56 MAK MAOB MAPK15 MNS1 MORN3 MUC5B MYB NME5 NUDT7 PCSK4 PLCH1 PRRT2 RFX2 RSPH4A SERINC2 SH3BGR SLC15A2 SPAG1 SPATA18 SPEF2 STK33 STOX1 TCF7 TCTEX1D1 TFF3 TMEM220 TPPP TSNAXIP1 TSPAN1 TTC16 TTC21A TTLL9 TXNDC6 UCKL1AS WDR93 ZNF204P ZNF214

11:yellow modules

function class: phosphorylation/signaling

core genes are present in at least three different cancer types

CCNT1 CDYL2 IL6ST IPMK MGAT5 UHMK1 ZNF704 AMIGO1 ANKRD36BP1 DDI2 DKFZp686O24166 ERN1 FRRS1 KIAA0754 KIAA1161 KIAA1244 KIRREL KLHL11 LCOR LOC150381 MAN2A1 MAP3K13 MAST4 N4BP2 NCOA2 NOS1AP PPM1L RAD54L2 RALGAPA2 ROR1 RUNDC2A SERINC5 SGK196 SLC9A7 SOCS7 TAOK1 ZDHHC20 ZNF221 ACER2 ASXL2 ATP11A C6orf204 C9orf129 CBX6 CITED4 CXADR DENND1B DGKH EGFR ETV3 EXOC6B FAM160A1 GLI4 GSR GTF2A1 HIST1H4J IL6R ITGB3 KIAA1958 KLHL23 LMTK2 LNPEP LOC202181 LOC387646 LOC650623 LONRF3 MBNL3 MFHAS1 NACC2 NBEAL1 NBPF10 NIPAL2 NUPR1 OSMR PARD3B PDE3A POTEF PRKAR2A PTPLB REL RNF152 RPL13AP3 RPL22L1 RPPH1 SERTAD4 SESN3 SGPP2 SLC12A2 SMAD9 SNHG9 SPATA13 STOX2 THSD7A TSPAN5 UGCG WDR31 ZC3HAV1L ZNF462 ZNF486

Zou_Suppl_Table_5

	predicted module drivers
overlap with significantly mutated genes (MutSig)	TP53 BRCA1 BUB1B CDKN1A RB1 PTPN11 PIK3R1 JAK2 PIK3CA EGFR CTNNB1 RAC1 RASA1 AKT1 HRAS EP300 B2M HLA-A CCND1 SMAD4 CDH1 SMAD2 NCOA3 DMD MYH9 ERBB2 STAG2 FGFR3 ERCC2
overlap with cancer consensus genes	TP53 BRCA1 BUB1B XPO1 MYC RB1 CD74 LCK PTPN11 CBL JAK1 ITK CD79B CD79A PIK3R1 JAK2 IL2 PIK3CA JUN EGFR SYK CTNNB1 AKT1 HRAS EP300 CREBBP CYLD CCND1 ELN KDR TCF3 CDH1 NCOA1 PDGFRB MYH9 ERBB2 MET FGFR3 JAK3 ERCC2 ERCC3