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Supplementary Materials for

Circulating Breast Tumor Cells Exhibit Dynamic Changes in Epithelial and Mesenchymal Composition

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This PDF file includes:

- Materials and Methods
- Figs. S1 to S7
- Tables S1 to S7
- References

Other Supplementary Material for this manuscript includes the following:
(available at www.sciencemag.org/cgi/content/full/339/6119/580/DC1)

- Movie S1

Material and Methods

^{Hb}CTC-Chip Production and Blood Processing

^{Hb}CTC-Chips were manufactured on site at the MGH Cancer Center/ BioMEMS Resource Facility, and chips were functionalized using biotinylated antibodies as previously described (*10*). Chips functionalized with 50 µg of NeutrAvidin were coated with a cocktail of 10 µg/ml each of biotinylated antibodies against EpCAM, HER2, and EGFR. Antibodies were purchased from the following vendors: EpCAM (R&D Systems BAF960); HER2 (R&D Systems BAF1129); EGFR (Cetuximab, Lilly, biotinylated in-house); and control goat IgG antibody (R&D Systems BAF108).

Blood specimens for CTC analysis were obtained after informed patient consent, per IRB protocol (05-300), at the Massachusetts General Hospital (MGH). A maximum of 20 mL of blood was obtained at any given blood draw in EDTA vacutainers, and approximately 3 mL of blood was processed through the ^{Hb}CTC-Chip within 4 hours of blood draw, at a target flow rate of 1.5 mL/hr as previously described (*10*).

CTC staining and enumeration

Following blood processing, captured cells on the ^{Hb}CTC-Chip were fixed with 4% paraformaldehyde and washed with PBS. Fixed cells were then permeabilized with 1% NP40 in PBS, blocked with 3% goat serum/2% BSA, and immunostained with relevant primary antibodies. Primary antibodies for CTC analyses were rabbit wide spectrum anti-cytokeratin (1:100, Abcam ab9377), mouse IgG2a anti-CD45 (1:500, Abcam ab30470), and mouse IgG1 anti-CD61 (1:100, Abcam ab11027). Secondary immunofluorescence-tagged antibodies were used for signal amplification. The secondary antibodies were goat anti-rabbit Alexa Fluor 647 (1:500, Invitrogen A-21245), goat anti-mouse IgG2a Alexa Fluor 488 (1:500, Invitrogen A-21131), and goat anti-mouse IgG1 Alexa Fluor 488 (1:500, Invitrogen A-21121). Nuclei were then stained with DAPI and the devices were washed with PBS and stored at 4°C. The devices were imaged under 10x and followed by 40x magnification using the BioView Ltd. automated imaging system (Billerica, MA) as well as an automated upright fluorescence microscope (Eclipse 90i, Nikon, Melville, NY). Positive staining for CK, without CD45 staining, was required for scoring potential CTCs, which were then manually reviewed. Threshold and baseline signals were established using specimens from healthy human controls.

QuantiGene ViewRNA *in-situ* hybridization on ^{Hb}CTC-Chip

Following blood processing, ^{Hb}CTC-Chips were fixed with 4% paraformaldehyde, washed with PBS and dehydrated with ethanol at increasing concentrations (50%, 70%, and 100%). ^{Hb}CTC-Chips were submerged in 100% ethanol at -20° C for storage. Before further analysis, cells were rehydrated using decreasing concentrations of ethanol (70% and 50%) and washed with PBS. ISH was performed using QuantiGene ViewRNA (Affymetrix, Santa Clara, CA) protocols as previously described (*17*). Briefly, ^{Hb}CTC-Chips were permeabilized with Working Detergent Solution, and digested with Protease at 1:2000 dilution in PBS. The ^{Hb}CTC-Chips were hybridized for 3 hours at 40° C with a cocktail of custom-designed QuantiGene ViewRNA probes against epithelial (CDH1, EpCAM, KRT5, KRT7, KRT8, KRT18, KRT19; type 10 probes) and mesenchymal markers (FN1, CDH2, SERPINE1; type 6 probes) and FOXC1 (type 1 probe). Unbound probes were flushed out with Wash Buffer and ^{Hb}CTC-Chips were stored overnight at 4° C in Storage Buffer. The bound probes were amplified the following day through PreAmp hybridization for 1 hour at 40° C, followed by Amp hybridization for 1 hour at 40° C. Label Probes (LP) targeting the epithelial (LP10-cy3), mesenchymal (LP6-cy5), or FOXC1 (LP1-cy3) probe types were added for 1 hour at 40° C. ^{Hb}CTC-Chips were stained with DAPI, washed with PBS and stored at 4°C. The devices were imaged under 10x using the BioView Ltd. automated imaging system (Billerica, MA). Candidate targets were followed by 40x magnification imaging in 25 z-steps per 1 µm using BioView. Positive signals presenting as punctate speckles were quantified in each channel and cells with more than 5 speckles were considered positive. Candidate targets were manually reviewed and those with bi-lobe and multi-lobe nuclear morphology and high fluorescent diffused background were excluded from final count (leukocytes tend to have such highly fluorescent diffused background based on HD testing). Selected targets were also imaged in an automated upright fluorescence microscope (Eclipse 90i, Nikon, Melville, NY). Threshold and baseline signals were established using healthy human controls.

QuantiGene ViewRNA *in-situ* hybridization on FFPE tissue

Breast cancer TMA was purchased from US Biomax (BR1503a). Human breast cancer FFPE specimens were processed for RNA-ISH as previously described (*17*). Briefly, 5-micron sections were fixed in 10% formaldehyde (Fisher Scientific, Pittsburgh, PA), deparaffinized, boiled in pre-treatment solution (Affymetrix, Santa Clara, CA) and digested with proteinase K. Sections were hybridized for 3 hours at 40° with a cocktail of custom designed QuantiGene ViewRNA probes against epithelial (CDH1, EpCAM, KRT5, KRT7, KRT8, KRT18, KRT19; type 1 probes) and mesenchymal markers (FN1, CDH2, SERPINE1; type 6 probes), HER2, FOXC1 and TFF1 (type 1 probes) (Affymetrix, Santa Clara, CA). Bound probes were then amplified per protocol from Affymetrix using PreAmp and Amp molecules. Multiple Label Probe oligonucleotides conjugated to alkaline phosphatase (LP-AP Type 1) were then added and Fast Red Substrate was used to produce signal (red dots). For two color assays, an LP-AP type 6 probe was used with Fast Blue substrate (blue dots) followed by LP-AP type 1 probe with Fast Red Substrate (red dots) to produce a dual colorimetric signals. Slides were then counterstained with Hematoxylin. Images were taken by Aperio scanscope, a Nikon 90i scope, and an Olympus scope with color camera.

RNA isolation from the ^{Hb}CTC-Chip

RNA from CTC-enriched cell populations was isolated from the devices using a modified Qiagen RNeasy MinElute kit (Qiagen) protocol. Briefly, 350 μl of the RLT buffer with 2-mercaptoethanol was pipetted into the ^{Hb}CTC-Chip with mixing between the inlet and outlet of the device. The resulting RLT lysate was loaded onto Qiagen RNeasy MinElute column, RNA was purified per protocol and eluted in a total of ~ 10 μL RNase free water.

Single Molecule Sequencing

Purified RNA was subjected to Digital Gene Expression (DGE) sample prepping and analyzed on the HeliScope^{TM} Single Molecule Sequencer from Helicos BioSciences. For CTC samples, application of a low quantity RNA-seq method was utilized as previously described (*16*). Briefly, the purified RNA was converted to first-strand cDNA with the SuperScript III first-strand cDNA synthesis kit (Invitrogen) using random hexamers according to manufacturer's recommendation. RNA was digested and single stranded cDNA was purified using a combination of QIAquick nucleotide removal kit (Invitrogen) and ethanol precipitated with ammonium acetate and glycogen. Single stranded cDNA was denatured and then a poly-A tail was added to the 3' end using terminal transferase (New England Biolabs). Tailed cDNAs were hybridized to the sequencing flow cell followed by "Fill and Lock" and subjected to single molecule sequencing by synthesis.

DGE analysis

Helicos single molecule sequencing and digital gene expression (DGE) profiling was performed as previously described (*16*). In order to find differential transcript expression we first normalized the DGE profile by linearly transforming to transcripts per million (tpm), discarding transcripts for which the 95th percentile of tpm was less than 10 and then dividing the tpm values for each transcript by the 95th percentile of the tpm values for that transcript. We then subtracted the thus normalized expression values from each IgG chip from those from the corresponding CTC chip, forming what we call "controlled expression values." To find transcripts consistently expressed higher in class A than class B, for each transcript we computed a statistic defined as the 5th percentile of the controlled expression values from class A minus the 95th percentile of the controlled expression values from class B. We then computed FDR estimates by comparing the actual statistics to those obtained by permuting class labels as was done in SAM (*30*). We called transcripts with FDR estimate less than 15% significantly over-expressed. To help interpret each list of significantly over-expressed transcripts, we used hypergeometric tests to look for significant overlap with the gene sets in the MSigDBv3.0 collection (*31*) augmented by gene lists from three studies (*32-34*). We used the method of Benjamini and Hochberg (*35*) to convert the hypergeometric p-values to FDR estimates and considered a gene set enriched if its FDR estimate was below 25%. The enriched gene signatures were manually annotated for their functional categories (group, subgroup, and specifics in Table S3 and S5) and the top repetitively occurred ones were summarized in Figure 4.

Mouse Xenograft Tumor Assays

The animal protocol was approved by the MGH Subcommittee on Research Animal Care. Six-week old female NSG (NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ) mice (Jackson Laboratory) were anesthetized with isofluorane, 5 x 10^6 BT474 cells and 2 x 10^6 MDA-

MB-231 cells in 100ul of 1:1 PBS and Matrigel (BD) were injected into the 4th right mammary fat pad. A 90 day release 0.72mg estrogen pellet (Innovative Research of America) was implanted subcutaneously behind the neck of the mice injected with BT474. Primary tumors were sampled after 6-8 weeks.

cDNA Expression Constructs and Viral Infection

The *LBX1* open reading frame fused with ER (G525R mutation) was cloned into pBabe vector. Vesicular stomatitis virus glycoprotein-pseudotyped retroviruses were generated using the packaging cell line HEK293T as previously described (*11*). MCF-10A cells were infected with pBabe-LBX1-ER virus followed by 2 μg/ml puromycin selection for 3 days.

Flow Cytometry Analysis

Cells were collected using Accutase (eBioscience) and washed in PBS. Cells ($5x10^5$) were blocked with blocking buffer (PBS + 2% FBS + 1%BSA) on ice for 10 mins, incubated with 0.5 ug of goat anti-human EpCAM antibody (R&D Systems) and corresponding isotype control antibodies (Santa Cruz) for 30 mins on ice, then washed with blocking buffer. After incubation with donkey anti-goat secondary antibody conjugated with Alexa-488 at 1:1000 dilution for 30 mins on ice, cells were washed with blocking buffer, and EpCAM level was analyzed using a FACSCalibur flow cytometer (BD Biosciences).

Antibodies and Immunoblot Analysis

Antibodies used were EpCAM (R&D), EGFR (Cell Signaling), HER2 (Cell Signaling), and β-tubulin (Santa Cruz). Cells were lysed in RIPA buffer [20mM Tris, pH8/150mM NaCl/10mM NaF/0.1% SDS/1% Nonidet P-40/1x protease inhibitor mixture (Roche)]. Lysates were run on SDS/4-15% polyacrylamide gel (Bio-Rad) and transferred onto PVDF membranes (Invitrogen), and immunoblots were visualized with Western Lightning Plus chemiluminescence kit (PerkinElmer).

Real-time qRT-PCR

Total RNA (300 ng) was reverse transcribed using SuperscriptIII kit (Invitrogen). Real-time quantitative RT-PCR was performed using SYBR green in an ABI PRISM 7500 sequence detection system with 96-block module and automation accessory (Applied Biosystems). GAPDH was used as internal control. The primers used are shown below:

GAPDH: GGTCTCCTCTGACTTCAACA; GTGAGGGTCTCTCTCTTCCT.

CDH1: CACGGTAACCGATCAGAATG ; ACCTCCATCACAGAGGTTCC.

EpCAM: CTGCCAAATGTTTGGTGATG ; AGCCCATCATTGTTCTGGAG .

KRT5: CAAGCGTACCACTGCTGAGA ; CATCCATCAGTGCATCAACC.

KRT7: CAGGATGTGGTGGAGGACTT ; TTGCTCATGTAGGCAGCATC.

KRT8: TGGAGCAGCAGAACAAGATG ; CCGCCTAAGGTTGTTGATGT.

KRT18: CACAGTCTGCTGAGGTTGGA ; CAAGCTGGCCTTCAGATTTC.

KRT19: TGAGCAGGTCCGAGGTTACT ; TCTTCCAAGGCAGCTTTCAT.

FN1: GAAGCCGAGGTTTTAACTGC ; ACCCACTCGGTAAGTGTTCC.

CDH2: AGAAAACTCCAGGGGACCTT ; ATACCAGTTGGAGGCTGGTC.

SERPINE1: TGGCTCAGACCAACAAGTTC ; GTAGGGCAGTTCCAGGATGT.

Clinical Response Analysis

The definition for clinical response or progression was made on clinical, serological, and/or radiological criteria, as routinely used in clinic for clinical decision making. The clinician was blinded to the CTC results.

Fig. S1. Validation of E and M markers in BT474 and MDA-MB-231 breast tumor xenografts grown in mice**.**

(A) Relative expression levels of E and M markers in highly epithelial, luminal-type BT474 and the highly mesenchymal triple negative (ER-, PR-, HER2-) MDA-MB-231 breast cancer cells measured by qRT-PCR (mean ± s.d., n=3). **(B)** RNA-ISH analysis of E (red dots) and M (dark blue dots) markers in mammary tumors derived from BT474 and MDA-MB-231 cells injected orthotopically in NSG mice. Scale bar = 20 µm.

Fig. S2. Capture efficiency of breast cancer cell lines on ^{Hb}CTC-Chips functionalized with antibodies against EpCAM, HER2 and EGFR.

(A) Western blot analysis of EGFR, EpCAM and HER2 expression in breast cancer cell lines MCF7 (ER+/PR+), SKBR3 and BT474 (HER2+), and MCF10A, MDA-MB-231, BT549, HCC1937, and HS578T (ER/PR/HER2 triple negative). **(B)** Capture efficiency of three different breast cancer cell lines (MCF7, SKBR3, and MDA-MB-231) spiked into healthy donor blood and isolated using a ^{Hb}CTC-Chip coated with antibodies against EpCAM, HER2, and EGFR used either individually or as a triple cocktail. Coating the ^{Hb}CTC-Chip with all three antibodies resulted in equivalent capture (>80%) of fluorescent-tagged MCF7 (epithelial ER+/PR+), SKBR3 (HER2+), and MDA-MB-231 cells (mesenchymal, triple negative) spiked into healthy donor blood, whereas none of the individual antibodies efficiently captured all three cell types.

Fig. S3. Induction of EMT in breast epithelial MCF-10A cells using the master transcriptional regulator LBX1 (*11*) induces E to M state transition within 72 hours.

(A) Phase contrast image of MCF-10A/LBX1-ER cells, untreated (control) and treated with 4-hydroxytamoxifen (4-OHT) (LBX1 induced) for 72 hours. Scale bar = 10 µm. **(B)** Immunofluorescent staining of LBX1 (green) in parental and induced cells. Nuclei were stained with DAPI (blue). Scale bar = 20 µm. **(C)** Flow cytometry analysis of surface EpCAM expression level in parental (red) and LBX1-induced (blue) cells demonstrating downregulation of surface EpCAM in LBX1 induced cells. Isotype control is shown in green. **(D)** RNA-ISH staining for E (yellow dots) and M (red dots) markers in parental MCF-10A cells and in cells that have undergone EMT by induced expression of the master regulator LBX1, following capture on the ^{Hb}CTC-Chip. Nuclei are stained with DAPI (blue). Scale bar = 10 µm. **(E)** Quantification of EMT features in parental and LBX1-induced cells based on dot counts of E and M markers. The RNA-ISH technology (Panomics, Affymetrix Inc.,) offers the flexibility of custom designed and validated probes against multiple genes that are pooled within a single fluorescent spectral channel, as well as the ease of multiplexing with different fluors with a highly reproducible quantitative signal for each fluor, thus enabling not only dual staining, but also precise quantitation of a continuous spectrum from epithelial to mesenchymal states (E, E>M, E=M, M>E, and M) within each CTC analyzed. Compared to traditional protein-based immunofluoresecence staining, this RNA-based method provides dramatically improved signal to noise ratio, linearity of signal, and absence of false positive (dual) staining (which is common in CTC analyses using antibody staining). The RNA-ISH signal appears as specific fluorescent speckles or dots, whereas any background signal is diffuse and clearly distinct. We used automated microscopic scanning (Bioview and Nikon platforms) to scan the target in 25 z steps (1um distance in each step) to ensure reproducibility of quantitation.

Fig. S4. Longitudinal monitoring of EMT features in CTCs from an index patient.

Plot of CTC counts based on protein (CK, dotted line) and RNA (E and M markers, solid line) detection methods in a patient sampled on different days during the course of treatment. Color-coded quantitation of single CTCs (S-CTC) or clustered CTCs (C-CTC) based on RNA-ISH staining at various time points is shown above each time point. Treatment history and clinical responses are shown in the chart (P=Disease progression; R=Treatment response).

Fig. S5. M+ clusters of CTCs from two ER/PR+ patients.

(A) Representative images of M+ clusters from patient #1 stained for E (green) and M (red) markers by RNA-ISH. Different planes of focus for clusters 2 and 3 are shown. Nuclei were stained with DAPI (blue). Scale bar = 10 μm. **(B)** Examples of M+ clusters in patient #7. Scale bar = 10 μm.

Fig. S6. Expression of TFF1 (red dots) in primary tumor and lymph nodes.

Primary tumor and metastatic lymph node of patient #1 were analyzed for TFF1 expression by RNA-ISH. Nuclei were stained with hematoxylin (blue). Scale bar = 20 µm.

Fig. S7. FOXC1 expression in breast tumor samples.

(A) Tumor sections of xenografted mammary tumors generated by BT474 (negative control, left image) and MDA-MB-231 (MDA-231, positive control, middle image) cells were stained for FOXC1 (red dots). FOXC1 staining in a tumor sample from a triple negative patient is shown (right image). Scale bar = 20 µm. **(B)** Images of FOXC1 (red dots, arrow) expression in the primary tumor (left) and metastatic lymph node (middle), and FOXC1 (green dots, arrow) and M markers (red dots, arrow head) in the CTCs (right) from patient #1 as visualized by RNA-ISH. (Nuclei are stained with hematoxylin, light blue or DAPI, blue). Scale bar (left two images) = 20 µm; scale bar (right image) = 10 µm. **(C)** Images of FOXC1 (red dots, arrow) expression in primary tumor and metastatic lymph node from patient #7 analyzed by RNA-ISH. (Nuclei are stained with hematoxylin, light blue). Bottom panel: Expression of FOXC1 at the invasive edge of the tumor from patient #7. Scale bar = 20 µm.

Table S1. Expression levels of E/M, CD45, and receptor markers in WBC and SKBR3 cells analyzed by RNA sequencing.

Table S2: SNaPshot tumor genotyping analysis of patients shown in figure 2c.

Table S3. The list of 45 genes expressed in E+ CTCs at all five time points.

Table S4. The list of GSEA gene signatures enriched in the 45 genes from Table S3. The list was manually annotated for different categories as group, subgroup, and specifics.

Table S5. The list of 170 genes expressed in M+ clusters.

Table S6. The list of GSEA gene signatures enriched in the 170 genes from Table S5. The list was manually annotated for different categories as group, subgroup, and specifics.

Table S7. The list of genes that demonstrate overlap between the 170 cluster genes and the core EMT signature (*18*).

Movie S1. The movie of different z-plane images of a cluster of CTCs (from patient #1), which stained positive for M markers (red) and weakly positive for E markers (green) at time point 8. Fluorescent images were merged with DIC images. Nuclei were stained with DAPI (blue).

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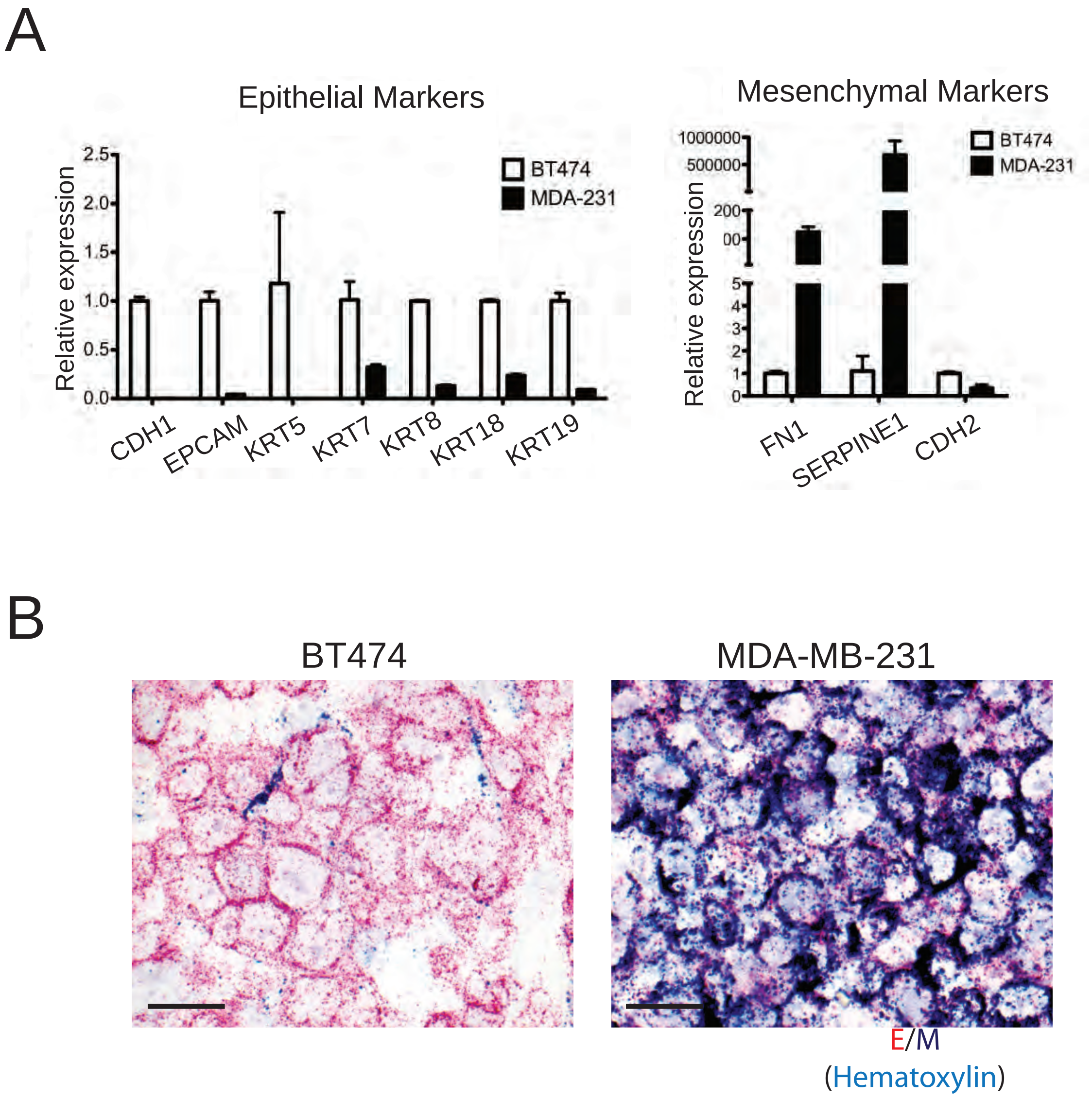
Fig. S1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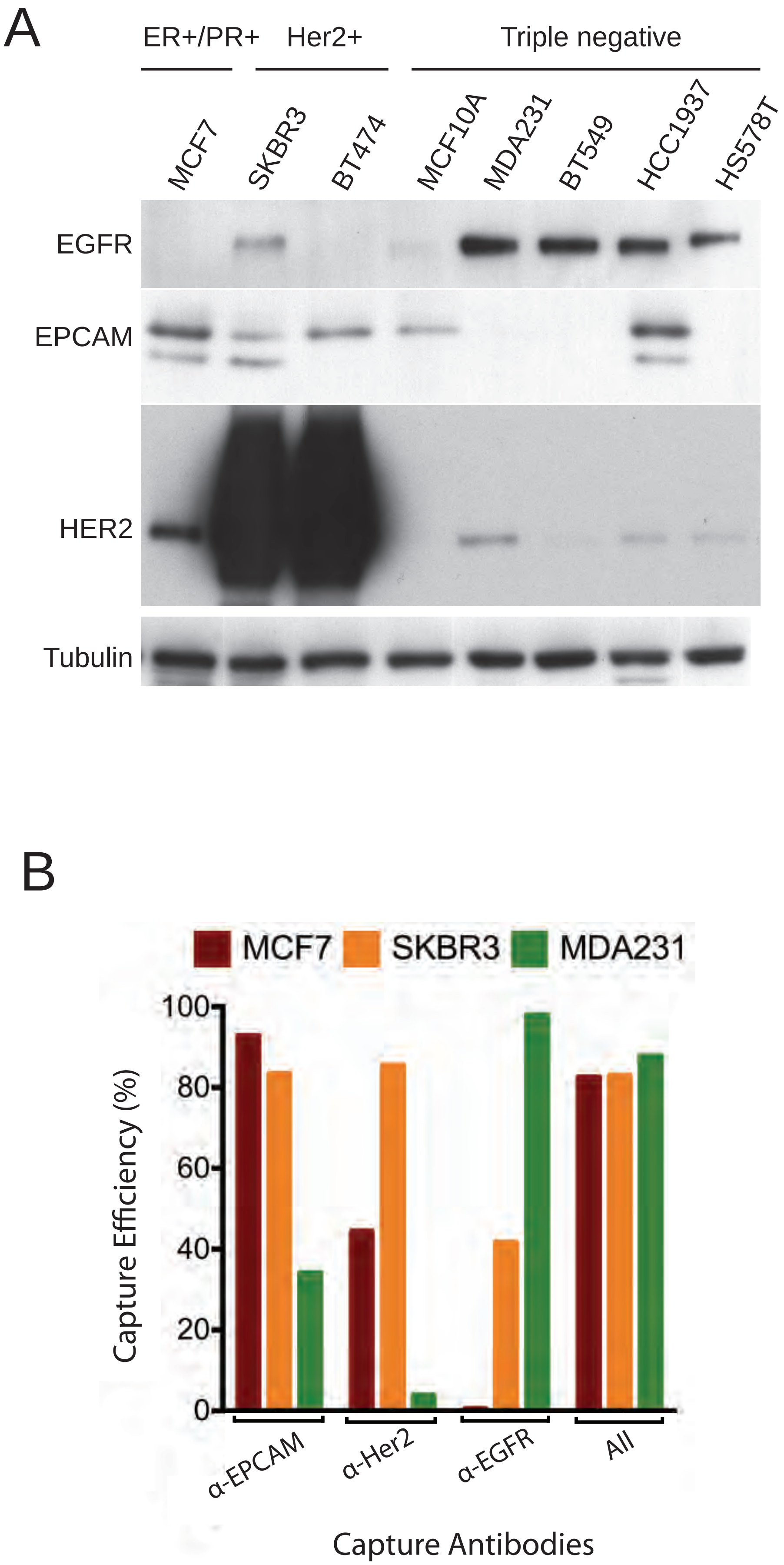
2.0
1.5
1.0
0.5
0.0
□ BT474
■ MDA-231
CDH1
EPCAM
KRT5
KRT7
KRT8
KRT18
KRT19
Mesenchymal Markers
Relative expression
1000000
500000
200
00
5
4
3
2
1
0
□ BT474
■ MDA-231
FN1
SERPINE1
CDH2
B
BT474
MDA-MB-231
E/M
(Hematoxylin)

Fig. S2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HER2
Tubulin
B
MCF7
SKBR3
MDA231
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40
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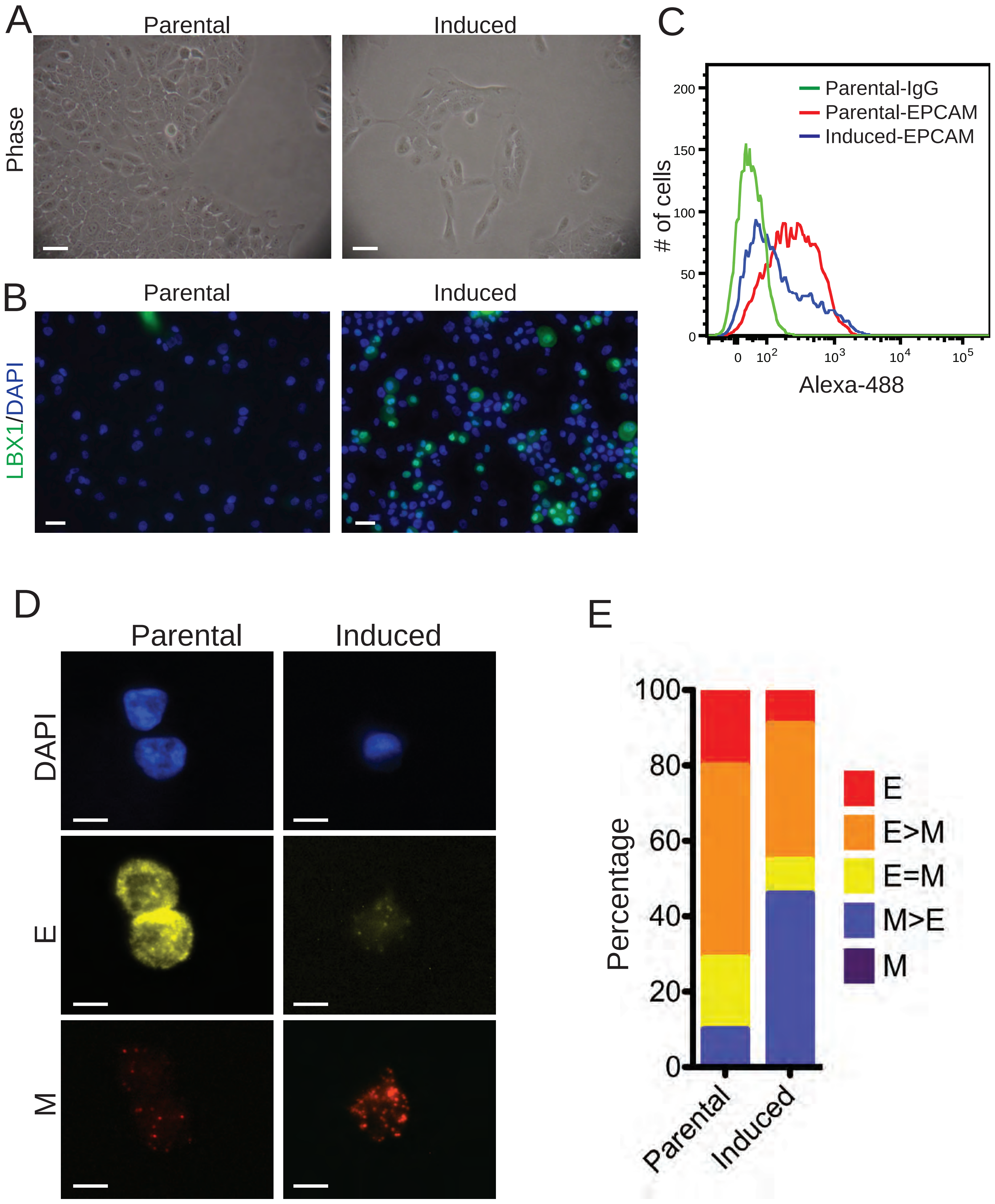
α-Her2
α-EGFR
All
Capture Antibodies

Fig. S3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Induced
Phase
B
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150
100
50
0
0
10^2
10^3
10^4
10^5
Alexa-488
D
Parental
Induced
DAPI
E
M
E
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20
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M>E
M

Fig. S4

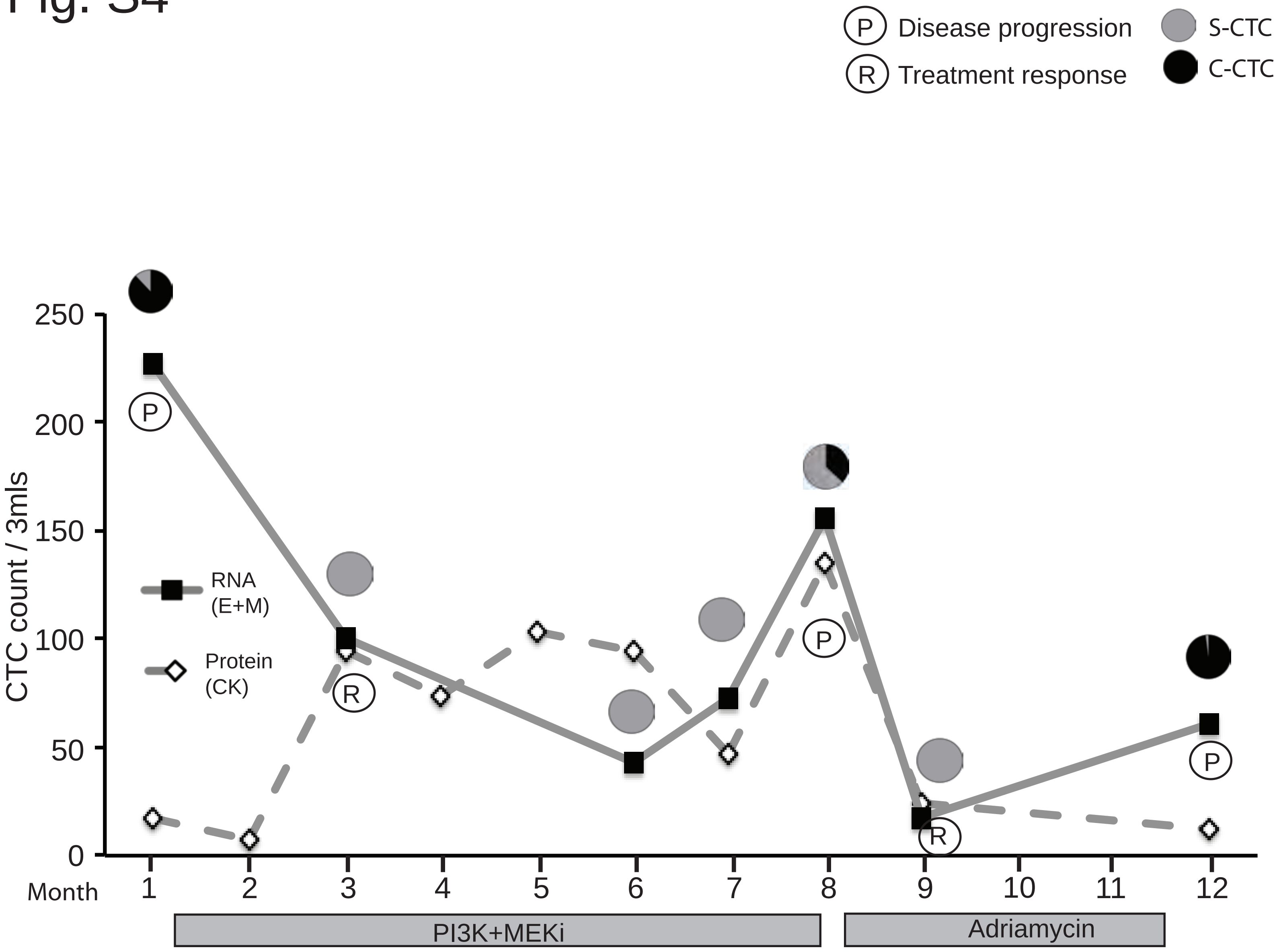
P Disease progression
R Treatment response
S-CTC
C-CTC
CTC count / 3mls
250
200
150
100
50
0
RNA (E+M)
Protein (CK)
P
R
P
R
P
Month
1
2
3
4
5
6
7
8
9
10
11
12
PI3K+MEKi
Adriamycin

Fig. S5

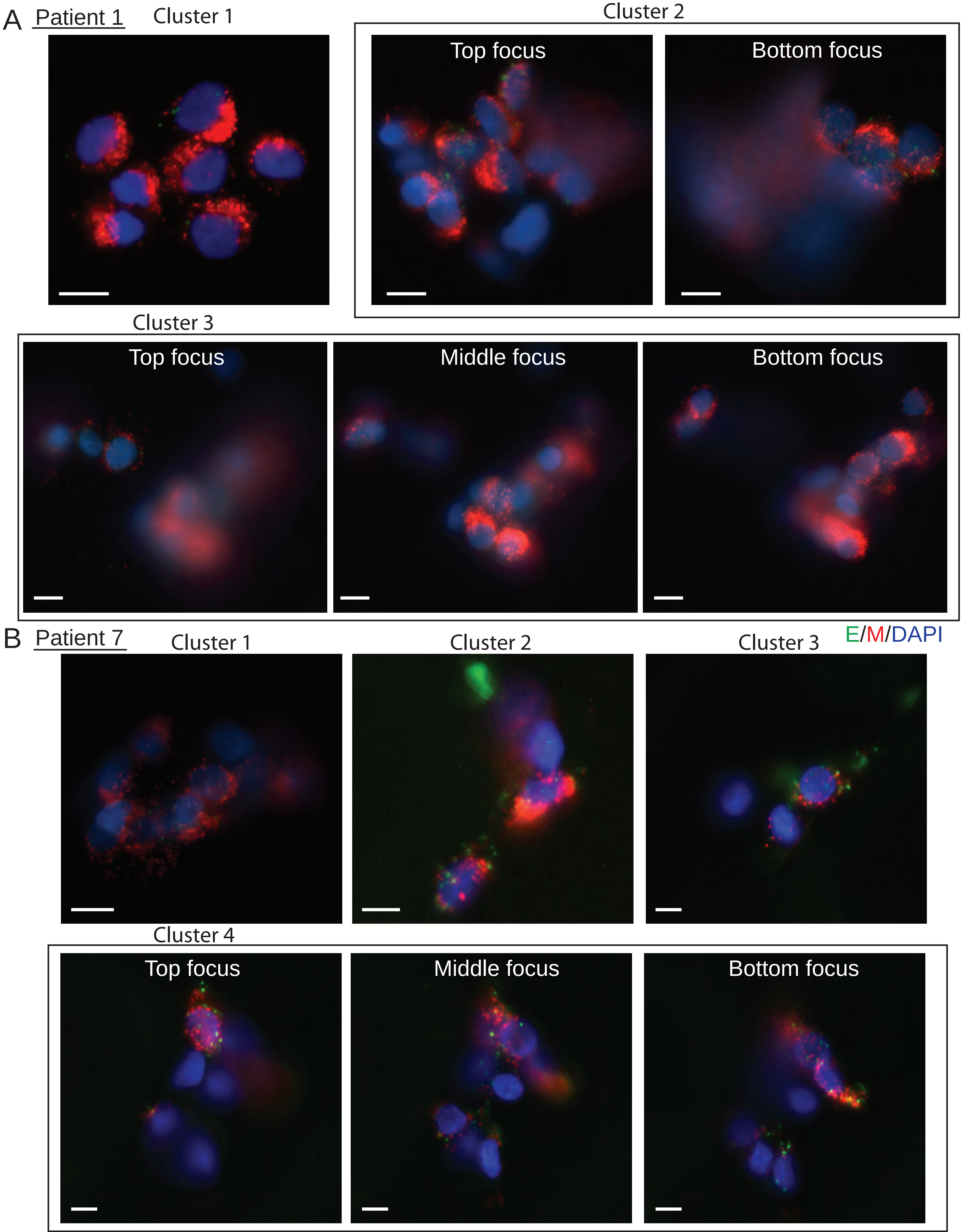
A
Patient 1
Cluster 1
Cluster 2
Top focus
Bottom focus
Cluster 3
Top focus
Middle focus
Bottom focus
B
Patient 7
Cluster 1
Cluster 2
Cluster 3
E/M/DAPI
Cluster 4
Top focus
Middle focus
Bottom focus

Fig. S6

Patient 1

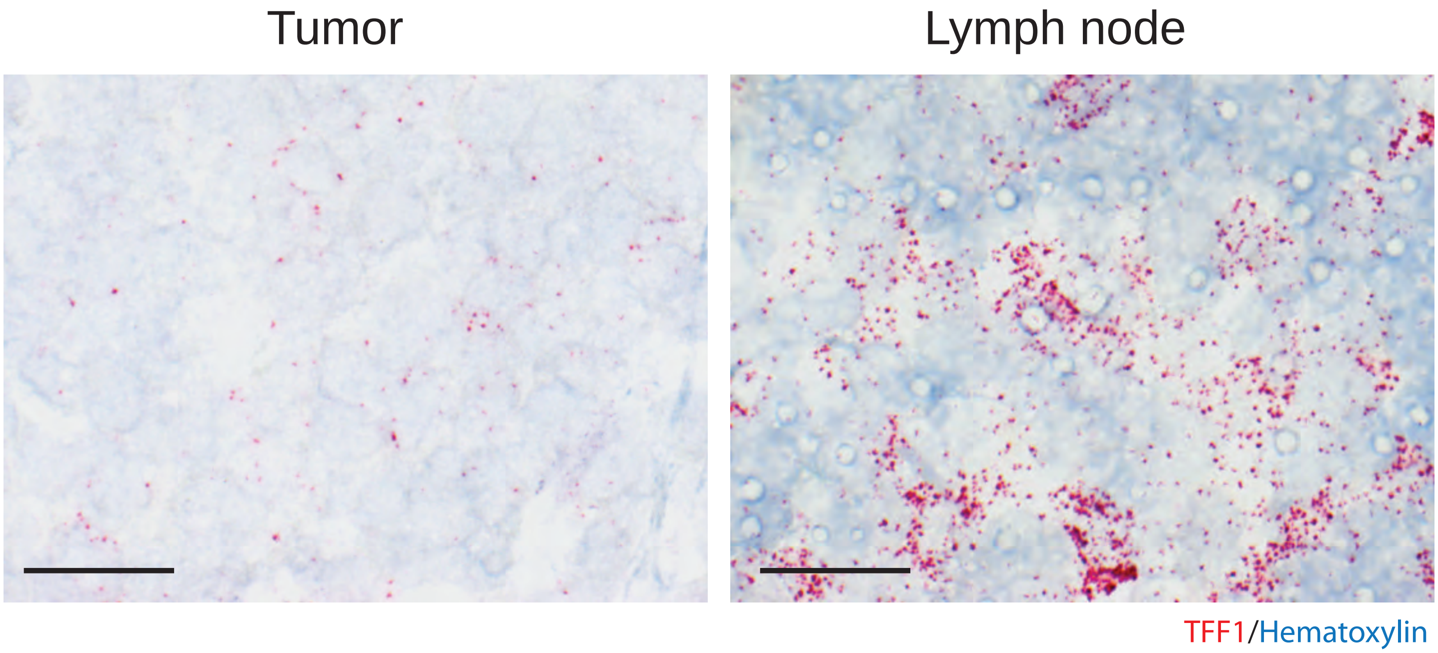

Fig. S7

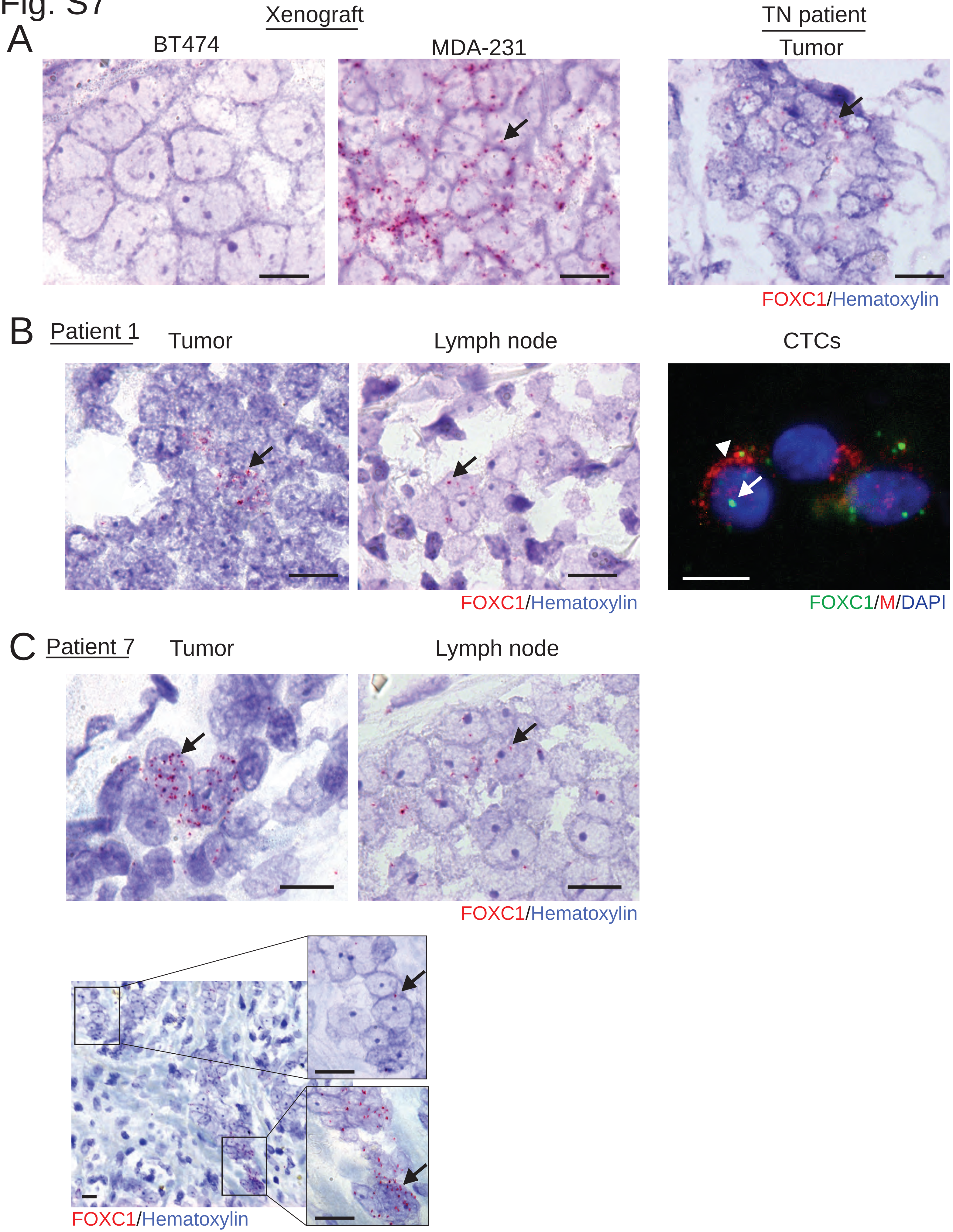
A
Xenograft
BT474
MDA-231
TN patient
Tumor
FOXC1/Hematoxylin
B
Patient 1
Tumor
Lymph node
CTCs
FOXC1/Hematoxylin
FOXC1/M/DAPI
C
Patient 7
Tumor
Lymph node
FOXC1/Hematoxylin
FOXC1/Hematoxylin

Table S1. Expression level of different genes in a female healthy donor white blood cells (WBC) and SKBR3 cells by Helicos RNA sequencing

	WBC (tpm)	SKBR3 (tpm)
WBC marker		
CD45	1036	0
Mammary origin markers		
ERBB2	0	2383
ESR1	1	0
PGR	1	0
EGFR	0	27
Epithelial markers		
CDH1	0	3
EPCAM	0	187
KRT5	0	0
KRT7	0	1811
KRT8	2	2918
KRT18	4	2056
KRT19	0	2177
Mesenchymal markers		
FN1	8	26
SERPINE1	0	13
CDH2	3	0

tpm: transcript per million

Table S2: SNaPshot tumor genotyping analysis of patients shown in figure 2c.

Tumor	PI3K [1]	TP53 [1]	Other Mutations[2]
R1	Wild-type	Wild-type	None
R2	Mutant (E545-1633G)	Wild-type	None
R3	Wild-type	Wild-type	None
R4	Mutant (H1047-3140A)	Mutant (R248-743G)	None
R5	Mutant (H1047-3140A)	Wild-type	None
P1	Wild-type	Mutant (R273H-818G)	None
P2	Mutant (E542-1624G)	Wild-type	None
P3	Wild-type	Wild-type	None
P4	Wild-type	Wild-type	None
P5	Wild-type	Wild-type	None

Mutational status of the primary tumors is based on the SNaPshot clinical tumor genotyping assay, which detects mutations in 60 different loci from 14 cancer genes (*36*).
[1] Mutations shown represent amino acid-cDNA residue **[2]** Genes analyzed for other mutations: AKT1, APC, BRAF, CTNNB1, EGFR, ERBB2 (HER-2), IDH1, KIT, KRAS, NOTCH1, NRAS, and PTEN. Patients responding to therapy: R1- R5; Patients progressing on therapy: P1-P5

Table S3. The list of 45 genes expressed in E+ CTCs at all five time points.

Symbol	Name	Entrez GeneID	name in Helicos transcriptome
TFF1	Trefoil factor 1	7031	TFF1
KRT19	Keratin 19	3880	KRT19
SCGB2A2	Secretoglobin, family 2A, member 2	4250	SCGB2A2
TFF3	Trefoil factor 3 (intestinal)	7033	TFF3
SLC39A6	Solute carrier family 39 (zinc transporter), member 6	25800	SLC39A6
MGP	Matrix Gla protein	4256	MGP
MUCL1	Mucin-like 1	118430	SBEM
XPOT	Exportin, tRNA (nuclear export receptor for tRNAs)	11260	XPOT
MRPL9	Mitochondrial ribosomal protein L9	65005	MRPL9
ORAI2	ORAI calcium release-activated calcium modulator 2	80228	TMEM142B
SCGB2A1	Secretoglobin, family 2A, member 1	4246	SCGB2A1
SCGB1D2	Secretoglobin, family 1D, member 2	10647	SCGB1D2
CRABP2	Cellular retinoic acid binding protein 2	1382	CRABP2
MYO18A	Myosin XVIIIA	399687	MYO18A
CRNKL1	Crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	51340	CRNKL1
TRIAP1	TP53 regulated inhibitor of apoptosis 1	51499	TRIAP1
IMP3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	55272	IMP3
DERL3	Der1-like domain family, member 3	91319	DERL3
NKD2	Naked cuticle homolog 2 (Drosophila)	85409	NKD2
HYAL1	Hyaluronoglucosaminidase 1	3373	HYAL1
KRT8	Keratin 8	3856	KRT8
LOC641298 /// LOC729602	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene	641298 /// 729602	DKFZP547E087
SLC7A6	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	9057	SLC7A6
---	---	---	RP5-1126H10.1
FSD1	Fibronectin type III and SPRY domain containing 1	79187	FSD1
MYST2	MYST histone acetyltransferase 2	11143	MYST2
ZNF497	Zinc finger protein 497	162968	ZNF497
LYPLA1	Lysophospholipase I	10434	LYPLA1
GPR113	G protein-coupled receptor 113	165082	GPR113
BTG1	B-cell translocation gene 1, anti-proliferative	694	BTG1
CDC27	Cell division cycle 27 homolog (S. cerevisiae)	996	CDC27
NBPF1	Neuroblastoma breakpoint family, member 1	55672	NBPF1
SPTA1	Spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	6708	SPTA1
PIGW	Phosphatidylinositol glycan anchor biosynthesis, class W	284098	PIGW
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CLDN4	Claudin 4	1364	HCPE-R
DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	23181	DIP2A
HSPE1	Heat shock 10kDa protein 1 (chaperonin 10)	3336	HSPE1
DTX2	Deltex homolog 2 (Drosophila)	113878	DTX2
MTG1	Mitochondrial GTPase 1 homolog (S. cerevisiae)	92170	MTG1

NSUN5	NOL1/NOP2/Sun domain family, member 5	55695	NSUN5
TAF1C	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	9013	TAF1C
ZBTB48	Zinc finger and BTB domain containing 48	3104	PP9964
---	---	---	AK124927
---	---	---	AK094224
ZNF70	Zinc finger protein 70	7621	ZNF70
TNFAIP8	Tumor necrosis factor, alpha-induced protein 8	25816	TNFAIP8
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PCTP	Phosphatidylcholine transfer protein	58488	PCTP
FES	Feline sarcoma oncogene	2242	FES

Table S4. The list of GSEA gene signatures enriched in the 45 genes from Table S3.

name	group	subgroup	specifics	descr	source	num in set	num in intersection	num expected in intersection	odds ratio	p-val	FWER	FDR	intersection
SMID BREAST CANCER RELAPSE IN BONE UP	tumor	breast	metastasis	Genes up-regulated in bone relapse of breast cancer.	MSigDBv 3.0 CGP	98	6	0.2	30.6	1.32E-07	0.000859	0.00077	SCGB1D2, SCGB2A1, SCGB2A2, SLC39A6, TFF1, TFF3
LIEN BREAST CARCINOMA METAPLASTIC VS DUCTAL DN	tumor	breast	MCB vs DCB	Genes down-regulated between two breast carcinoma subtypes: metaplastic (MCB) and ductal (DCB).	MSigDBv 3.0 CGP	108	6	0.3	27.6	2.36E-07	0.00153	0.00077	KRT19, MUCL1, SCGB1D2, SCGB2A1, SCGB2A2, TFF3
SMID BREAST CANCER RELAPSE IN LUNG DN	tumor	breast	metastasis	Genes down-regulated in lung relapse of breast cancer.	MSigDBv 3.0 CGP	38	4	0.1	52.7	2.14E-06	0.0139	0.00463	SCGB1D2, SCGB2A1, SCGB2A2, TFF1
DOANE BREAST CANCER ESR1 UP	tumor	breast	ER	Genes changed in breast cancer samples according to the ESR1 [Gene ID=2099] status: ER positive vs ER negative tumors.	MSigDBv 3.0 CGP	114	5	0.3	21	8.25E-06	0.0535	0.0134	SCGB1D2, SCGB2A2, SLC39A6, TFF1, TFF3
module 139	others			Genes in module_139	MSigDBv 3.0 CM	74	4	0.2	25.5	3.13E-05	0.203	0.0406	CLDN4, CRABP2, KRT19, KRT8
LI AMPLIFIED IN LUNG CANCER	tumor	other	amplicon	Genes with increased copy number that correlates with increased expression across six different lung adenocarcinoma cell lines.	MSigDBv 3.0 CGP	164	5	0.4	14.3	4.77E-05	0.309	0.0442	CLDN4, CRABP2, HSPE1, TFF1, TFF3
SCHLOSSER MYC TARGETS REPRESSED BY SERUM	tumor	other	MYC	Cluster 7: genes up-regulated in B493-6 cells (B lymphocytes) by MYC [Gene ID=4609] and down-regulated by the combination of MYC and serum.	MSigDBv 3.0 CGP	164	5	0.4	14.3	4.77E-05	0.309	0.0442	HSPE1, LYPLA1, SLC39A6, TRIAP1, XPOT
module 342	others			Genes in module_342	MSigDBv 3.0 CM	198	5	0.5	11.8	0.000116	0.754	0.0944	CLDN4, CRABP2, HYAL1, KRT19, KRT8
module 180	others			Genes in module_180	MSigDBv 3.0 CM	112	4	0.3	16.5	0.000158	1	0.114	CLDN4, CRABP2, KRT19, KRT8
WANG CISPLATIN RESPONSE AND XPC UP	tumor	other		Genes up-regulated in fibroblasts with defective XPC [Gene ID=7508] in response to cisplatin [PubChem=2767].	MSigDBv 3.0 CGP	136	4	0.3	13.5	0.000332	1	0.215	CLDN4, KRT8, MGP, TFF1
HUPER BREAST BASAL VS LUMINAL DN	tumor	breast	basal vs luminal	Genes down-regulated in basal mammary epithelial cells compared to the luminal ones.	MSigDBv 3.0 CGP	59	3	0.1	23.4	0.000399	1	0.236	CLDN4, KRT19, KRT8
CASPASE REGULATOR ACTIVITY	signaling	apoptosis		Genes annotated by the GO term GO:0043028. Modulates the activity of a caspase, any of a group of cysteine proteases involved in apoptosis.	MSigDBv 3.0 MF	13	2	0	77.8	0.000445	1	0.241	TNFAIP8, TRIAP1

Table S5. The list of 170 genes expressed in M+ clusters.

Symbol	Name	Entrez GeneID	name in Helicos transcriptome
SERPINE1	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	5054	SERPINE1
CTGF	Connective tissue growth factor	1490	CTGF
FN1	Fibronectin 1	2335	FN1
ELN	Elastin	2006	ELN
PODXL	Podocalyxin-like	5420	PODXL
LAMB1	Laminin, beta 1	3912	LAMB1
IGFBP7	Insulin-like growth factor binding protein 7	3490	IGFBP7
HSPG2	Heparan sulfate proteoglycan 2	3339	HSPG2
POSTN	Periostin, osteoblast specific factor	10631	POSTN
ANO1	Anoctamin 1, calcium activated chloride channel	55107	TMEM16A
COL3A1	Collagen, type III, alpha 1	1281	COL3A1
CFH	Complement factor H	3075	CFH
CXCR7	Chemokine (C-X-C motif) receptor 7	57007	CXCR7
TM4SF1	Transmembrane 4 L six family member 1	4071	TM4SF1
GJA1	Gap junction protein, alpha 1, 43kDa	2697	GJA1
HEG1	HEG homolog 1 (zebrafish)	57493	HEG1
HMCN1	Hemicentin 1	83872	HMCN1
COL6A1	Collagen, type VI, alpha 1	1291	COL6A1
SLCO2A1	Solute carrier organic anion transporter family, member 2A1	6578	SLCO2A1
ENG	Endoglin	2022	ENG
AQP1	Aquaporin 1 (Colton blood group)	358	AQP1
CDH13	Cadherin 13, H-cadherin (heart)	1012	CDH13
MMP2	Matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	4313	MMP2
PLK2	Polo-like kinase 2 (Drosophila)	10769	PLK2
EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	2202	EFEMP1
CAV1	Caveolin 1, caveolae protein, 22kDa	857	CAV1
SULF1	Sulfatase 1	23213	SULF1
CDH11	Cadherin 11, type 2, OB-cadherin (osteoblast)	1009	CDH11
ANGPTL2	Angiopoietin-like 2	23452	ANGPTL2
ITGB4	Integrin, beta 4	3691	ITGB4
DPYSL3	Dihydropyrimidinase-like 3	1809	DPYSL3
LTBP4	Latent transforming growth factor beta binding protein 4	8425	LTBP4
WWTR1	WW domain containing transcription regulator 1	25937	WWTR1
FLNB	Filamin B, beta	2317	FLNB
RHOJ	Ras homolog gene family, member J	57381	RHOJ
HYAL2	Hyaluronoglucosaminidase 2	8692	HYAL2
CDH5	Cadherin 5, type 2 (vascular endothelium)	1003	CDH5
PLA2G2A	Phospholipase A2, group IIA (platelets, synovial fluid)	5320	PLA2G2A
EMP1	Epithelial membrane protein 1	2012	EMP1
ITGA9	Integrin, alpha 9	3680	ITGA9
LAMB2	Laminin, beta 2 (laminin S)	3913	LAMB2
COL1A2	Collagen, type I, alpha 2	1278	COL1A2
ECM1	Extracellular matrix protein 1	1893	ECM1
DKK3	Dickkopf homolog 3 (Xenopus laevis)	27122	DKK3
CRIP2	Cysteine-rich protein 2	1397	CRIP2
TNXB	Tenascin XB	7148	TNXB
BMPER	BMP binding endothelial regulator	168667	BMPER
SCARA3	Scavenger receptor class A, member 3	51435	SCARA3
FSTL1	Follistatin-like 1	11167	FSTL1
PTRF	Polymerase I and transcript release factor	284119	PTRF
BGN	Biglycan	633	BGN
MMRN2	Multimerin 2	79812	MMRN2
PTPRB	Protein tyrosine phosphatase, receptor type, B	5787	PTPRB
TIE1	Tyrosine kinase with immunoglobulin-like and EGF-like domains 1	7075	TIE1
NOS3	Nitric oxide synthase 3 (endothelial cell)	4846	NOS3
LRIG1	Leucine-rich repeats and immunoglobulin-like domains 1	26018	LRIG1
TPPP3	Tubulin polymerization-promoting protein family member 3	51673	CGI-38
STAB1	Stabilin 1	23166	STAB1
GPRC5B	G protein-coupled receptor, family C, group 5, member B	51704	GPRC5B

RNASE1	Ribonuclease, RNase A family, 1 (pancreatic)	6035	RNASE1
PLXND1	Plexin D1	23129	PLXND1
COL4A2	Collagen, type IV, alpha 2	1284	COL4A2
FLNC	Filamin C, gamma	2318	FLNC
CGNL1	Cingulin-like 1	84952	CGNL1
LEPR	Leptin receptor	3953	LEPR
SLC29A1	Solute carrier family 29 (nucleoside transporters), member 1	2030	ENT1
LOXL2	Lysyl oxidase-like 2	4017	LOXL2
DKK2	Dickkopf homolog 2 (Xenopus laevis)	27123	DKK2
PLTP	Phospholipid transfer protein	5360	PLTP
CCDC3	Coiled-coil domain containing 3	83643	CCDC3
EHD2	EH-domain containing 2	30846	EHD2
CD9	CD9 molecule	928	CD9
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TEK	TEK tyrosine kinase, endothelial	7010	TEK
ITGAV	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	3685	ITGAV
SERPINE2	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	5270	SERPINE2
S100A16	S100 calcium binding protein A16	140576	S100A16
APCDD1	Adenomatosis polyposis coli down-regulated 1	147495	APCDD1
LAMA4	Laminin, alpha 4	3910	LAMA4
TXNDC5	Thioredoxin domain containing 5 (endoplasmic reticulum)	81567	TXNDC5
COL6A2	Collagen, type VI, alpha 2	1292	COL6A2
GPR116	G protein-coupled receptor 116	221395	GPR116
PLXNA4	Plexin A4	91584	PLXNA4
CD34	CD34 molecule	947	CD34
PKHD1L1	Polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	93035	PKHD1L1
IL1R1	Interleukin 1 receptor, type I	3554	IL1R1
PERP	PERP, TP53 apoptosis effector	64065	PERP
BMP6	Bone morphogenetic protein 6	654	BMP6
CLEC3B	C-type lectin domain family 3, member B	7123	CLEC3B
FSCN1	Fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	6624	FSCN1
S100A10	S100 calcium binding protein A10	6281	S100A10
TNFRSF21	Tumor necrosis factor receptor superfamily, member 21	27242	TNFRSF21
DOCK6	Dedicator of cytokinesis 6	57572	DOCK6
DSTN	Destrin (actin depolymerizing factor)	11034	DSTN
ITGA6	Integrin, alpha 6	3655	ITGA6
LTBP3	Latent transforming growth factor beta binding protein 3	4054	LTBP3
COL5A2	Collagen, type V, alpha 2	1290	COL5A2
GOLM1	Golgi membrane protein 1	51280	GOLPH2
CRIM1	Cysteine rich transmembrane BMP regulator 1 (chordin-like)	51232	CRIM1
MDK	Midkine (neurite growth-promoting factor 2)	4192	MDK
CD59	CD59 molecule, complement regulatory protein	966	CD59
SLC29A1	Solute carrier family 29 (nucleoside transporters), member 1	2030	SLC29A1
RHOC	Ras homolog gene family, member C	389	RHOC
LIMS2	LIM and senescent cell antigen-like domains 2	55679	LIMS2
AGRN	Agrin	375790	AGRN
FBLN2	Fibulin 2	2199	FBLN2
BCAM	Basal cell adhesion molecule (Lutheran blood group)	4059	BCAM
ANXA2	Annexin A2	302	ANXA2
PTMS	Parathymosin	5763	PTMS
SYNPO	Synaptopodin	11346	SYNPO
IL33	Interleukin 33	90865	IL33
EPHB4	EPH receptor B4	2050	EPHB4
VCAN	Versican	1462	VCAN
ALDH1A2	Aldehyde dehydrogenase 1 family, member A2	8854	ALDH1A2
NPDC1	Neural proliferation, differentiation and control, 1	56654	NPDC1
LRRC32	Leucine rich repeat containing 32	2615	LRRC32
MRC2	Mannose receptor, C type 2	9902	MRC2
PLEC	Plectin 1, intermediate filament binding protein 500kDa	5339	PLEC1
FBXL7	F-box and leucine-rich repeat protein 7	23194	FBXL7
MEST	Mesoderm specific transcript homolog (mouse)	4232	MEST
GATA6	GATA binding protein 6	2627	GATA6
CD151	CD151 molecule (Raph blood group)	977	CD151
MYOF	Myoferlin	26509	FER1L3

FOXC1	Forkhead box C1	2296	FOXC1
ADAM15	ADAM metallopeptidase domain 15	8751	ADAM15
MUC1	Mucin 1, cell surface associated	4582	MUC1
ARHGAP23	Rho GTPase activating protein 23	57636	ARHGAP23
SCARB2	Scavenger receptor class B, member 2	950	SCARB2
CRIP1	Cysteine-rich protein 1 (intestinal)	1396	CRIP1
PTPRB	Protein tyrosine phosphatase, receptor type, B	5787	DKFZP686E2262
VIM	Vimentin	7431	VIM
SEMA3F	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	6405	SEMA3F
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	9510	ADAMTS1
FAM38A	Family with sequence similarity 38, member A	9780	FAM38A
PLS3	Plastin 3 (T isoform)	5358	PLS3
NRG1	Neuregulin 1	3084	NRG1
PVRL2	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	5819	PVRL2
SLC9A3R2	Solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	9351	SLC9A3R2
HSPB1	Heat shock 27kDa protein 1	3315	HSPB1
DCHS1	Dachsous 1 (Drosophila)	8642	DCHS1
ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	476	ATP1A1
COL5A1	Collagen, type V, alpha 1	1289	COL5A1
PTGIS	Prostaglandin I2 (prostacyclin) synthase	5740	PTGIS
ROBO4	Roundabout homolog 4, magic roundabout (Drosophila)	54538	ROBO4
TJP1	Tight junction protein 1 (zona occludens 1)	7082	TJP1
GAS6	Growth arrest-specific 6	2621	GAS6
A4GALT	Alpha 1,4-galactosyltransferase	53947	A4GALT
MYH10	Myosin, heavy chain 10, non-muscle	4628	MYH10
FBN1	Fibrillin 1	2200	FBN1
KIAA1522	KIAA1522	57648	KIAA1522
ITFG3	Integrin alpha FG-GAP repeat containing 3	83986	ITFG3
SPTAN1	Spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	6709	SPTAN1
PLVAP	Plasmalemma vesicle associated protein	83483	PLVAP
IL1RL1	Interleukin 1 receptor-like 1	9173	IL1RL1
GATA4	GATA binding protein 4	2626	GATA4
LPHN2	Latrophilin 2	23266	LPHN2
SFRP5	Secreted frizzled-related protein 5	6425	SFRP5
CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	9578	CDC42BPB
NTN1	Netrin 1	9423	NTN1
PALM	Paralemmin	5064	PALM
MAOA	Monoamine oxidase A	4128	MAOA
RBMS2	RNA binding motif, single stranded interacting protein 2	5939	RBMS2
NFE2L1	Nuclear factor (erythroid-derived 2)-like 1	4779	NFE2L1
MMP28	Matrix metallopeptidase 28	79148	MMP28
FGD5	FYVE, RhoGEF and PH domain containing 5	152273	FGD5
EPS8	Epidermal growth factor receptor pathway substrate 8	2059	EPS8
MAGED1	Melanoma antigen family D, 1	9500	MAGED1
ID1	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	3397	ID1
PPP2R5B	Protein phosphatase 2, regulatory subunit B', beta isoform	5526	PPP2R5B
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KIF1C	Kinesin family member 1C	10749	KIF1C
MARVELD1	MARVEL domain containing 1	83742	MARVELD1
IFI27 /// PSMD9 /// SSSCA1 /// DCTN6	Interferon, alpha-inducible protein 27	3429 /// 5715 /// 10534 /// 10671	P27
EDN1	Endothelin 1	1906	EDN1

Table S6. The list of GSEA gene signatures enriched in the 170 genes from Table S5.

name	group	subgroup	specifics	descr	source	num in set	num in intersection	num expected in intersection	odds ratio	p-val	FWER	FDR	intersection
module 47	ECM	component		Genes in module_47: ECM and collagens	MSigDBv3.0 CM	216	38	2	29.3	4.00E-38	2.60E-34	2.60E-34	ADAMTS1, AQP1, BGN, CD34, CDH11, CDH5, CLEC3B, COL1A2, COL3A1, COL4A2, COL5A2, COL6A1, COL6A2, CTGF, DKK3, DPYSL3, ECM1, FBLN2, FBN1, FN1, GAS6, GJA1, IGFBP7, LAMB1, LOXL2, LRRC32, MMP2, MRC2, PLTP, PLXND1, POSTN, PTGIS, SERPINE1, TEK, TIE1, VCAN, VIM, WWTR1
module 1	others			Genes in module_1: Ovary genes	MSigDBv3.0 CM	358	43	3.3	19.3	7.30E-36	4.74E-32	2.37E-32	ALDH1A2, ANGPTL2, AQP1, BCAM, CAV1, CD151, CD34, CDH11, CFH, CLEC3B, COL1A2, COL3A1, COL5A2, COL6A1, COL6A2, CRIM1, CRIP1, DPYSL3, EMP1, ENG, EPS8, FBN1, FBXL7, FN1, GJA1, HEG1, HSPG2, IFI27, IL1R1, ITGA6, LAMB1, LAMB2, MDK, PLA2G2A, PLXND1, PTGIS, PVRL2, RNASE1, SERPINE1, STAB1, TM4SF1, TNXB, WWTR1
module 2	others			Genes in module_2: DRG (dorsal root ganglia) genes	MSigDBv3.0 CM	375	37	3.4	14.8	1.15E-27	7.45E-24	2.48E-24	AQP1, CAV1, CD151, CD34, CDH5, CFH, CLEC3B, COL1A2, COL3A1, COL6A1, COL6A2, CRIM1, CRIP1, DPYSL3, EMP1, ENG, EPS8, FBLN2, FBN1, FN1, GJA1, HSPG2, IFI27, IL1R1, ITGA6, ITGB4, LAMA4, LAMB1, LAMB2, LEPR, MAOA, PLA2G2A, SLC29A1, STAB1, TM4SF1, TNXB, WWTR1
module 5	others			Genes in module_5: Lung genes	MSigDBv3.0 CM	421	38	3.9	13.5	5.49E-27	3.56E-23	8.91E-24	ANXA2, AQP1, BCAM, CAV1, CD151, CD34, CDH11, CDH5, CLEC3B, COL1A2, COL3A1, COL6A1, COL6A2, CRIM1, CRIP1, DPYSL3, ENG, FN1, GJA1, HEG1, HSPG2, ID1, IFI27, IL1R1, ITGA6, LAMB2, LRRC32, MAOA, MUC1, PLXND1, POSTN, RNASE1, STAB1, TEK, TM4SF1, TNXB, VCAN, WWTR1
SCHUETZ BREAST CANCER DUCTAL INVASIVE UP	tumor	breast	aggressive	Genes up-regulated in invasive ductal carcinoma (IDC) relative to ductal carcinoma in situ (DCIS, non-invasive).	MSigDBv3.0 CGP	353	35	3.2	14.7	3.03E-26	1.97E-22	3.94E-23	ANGPTL2, BGN, CDH11, CFH, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2, CTGF, CXCR7, DPYSL3, EMP1, FBLN2, FBN1, FN1, FSTL1, GPR116, HEG1, IGFBP7, IL1R1, LAMA4, LAMB1, LOXL2, MMP2, MRC2, PLS3, POSTN, PTRF, SERPINE2, SULF1, VCAN, WWTR1
REN ALVEOLAR RHABDOMYOSARCOMA DN	tumor	other		Genes commonly down-regulated in human alveolar rhabdomyosarcoma (ARMS) and its mouse model overexpressing PAX3-FOXO1 [Gene ID=5077, 2308] fusion.	MSigDBv3.0 CGP	411	36	3.8	12.9	4.12E-25	2.67E-21	4.46E-22	ANXA2, CAV1, CD151, COL5A1, COL5A2, COL6A1, COL6A2, CTGF, DPYSL3, ECM1, EFEMP1, EMP1, ENG, FBN1, FN1, FSTL1, GAS6, GJA1, IGFBP7, ITGAV, LAMA4, LOXL2, MMP2, MRC2, NPDC1, NRG1, PLS3, PSMD9, PTRF, RHOC, S100A10, SCARA3, SERPINE2, TM4SF1, TXNDC5, VCAN
module 38	others			Genes in module_38: Planceta genes	MSigDBv3.0 CM	454	37	4.2	11.9	1.07E-24	6.93E-21	9.90E-22	CAV1, CD151, CD34, CDH5, CLEC3B, COL1A2, COL3A1, COL5A2, COL6A1, COL6A2, CRIM1, CRIP1, ECM1, ELN, ENG, FBLN2, FN1, HEG1, HSPG2, IFI27, IL1R1, ITGB4, LAMB2, LRRC32, MAOA, MEST, MMP2, PLA2G2A, PLXND1, PVRL2, RNASE1, SEMA3F, SERPINE1, SLC29A1, STAB1, TM4SF1, TNXB
PICCALUGA ANGIOIMMUNOBLASTIC LYMPHOMA UP	tumor	other		Up-regulated genes in angioimmunoblastic lymphoma (AILT) compared to normal T lymphocytes.	MSigDBv3.0 CGP	207	27	1.9	19	1.53E-23	9.92E-20	1.24E-20	ADAMTS1, CDH11, CDH5, CFH, COL1A2, COL3A1, COL4A2, COL6A1, DPYSL3, ENG, FBN1, FN1, FSTL1, GJA1, GPR116, GPRC5B, HSPG2, IFI27, IGFBP7, IL33, ITGA9, LAMA4, LAMB1, PTRF, SULF1, TJP1, WWTR1
GNF2 CDH11	EMT	gene	CDH11	Neighborhood of CDH11	MSigDBv3.0 CGN	25	13	0.2	126.6	9.55E-21	6.19E-17	6.89E-18	CDH11, COL1A2, COL3A1, COL5A1, COL5A2, COL6A1, COL6A2, FBN1, FN1, FSTL1, LAMB1, LOXL2, SERPINE1
EXTRACELLULAR REGION PART	ECM			Genes annotated by the GO term GO:0044421. Any constituent part of the extracellular region, the space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers constituent parts of the host cell environment outside an intracellular parasite.	MSigDBv3.0 CC	332	29	3	12.2	2.89E-20	1.87E-16	1.88E-17	AGRN, ANGPTL2, CDH13, CFH, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, CTGF, DKK2, DKK3, ECM1, EDN1, EFEMP1, FBLN2, FBN1, FSTL1, LAMA4, LAMB1, LAMB2, LOXL2, LTBP4, MMP2, POSTN, SEMA3F, SFRP5, TNXB, VCAN

KEGG ECM RECEPTOR INTERACTION	ECM	receptor		ECM-receptor interaction	MSigDBv3.0 CP:KEGG	83	18	0.8	33.3	3.73E-20	2.42E-16	2.04E-17	AGRN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2, FN1, HSPG2, ITGA6, ITGA9, ITGAV, ITGB4, LAMA4, LAMB1, LAMB2, TNXB
LIU PROSTATE CANCER DN	tumor	other		Genes down-regulated in prostate cancer samples.	MSigDBv3.0 CGP	466	33	4.3	10	3.77E-20	2.45E-16	2.04E-17	ANGPTL2, ANO1, ANXA2, ARHGAP23, CAV1, COL1A2, COL4A2, COL5A1, COL6A1, CRIM1, CXCR7, DKK3, DPYSL3, EFEMP1, EHD2, FBN1, FGD5, FLNC, GAS6, GJA1, HSPB1, HSPG2, ID1, IL33, ITGA9, LAMA4, LAMB1, LAMB2, MARVELD1, MRC2, MYOF, PTRF, RHOJ
EXTRACELLULAR REGION	ECM	component		Genes annotated by the GO term GO:0005576. The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.	MSigDBv3.0 CC	439	31	4	9.8	6.41E-19	4.15E-15	3.20E-16	AGRN, ANGPTL2, CDH13, CFH, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, CTGF, DKK2, DKK3, ECM1, EDN1, EFEMP1, FBLN2, FBN1, FSTL1, LAMA4, LAMB1, LAMB2, LOXL2, LTBP4, MMP2, PLA2G2A, PLTP, POSTN, SEMA3F, SFRP5, TNXB, VCAN
ONDER CDH1 TARGETS 2 UP	EMT	gene	CDH1	Genes up-regulated in HMLE cells (immortalized nontransformed mammary epithelium) after E-cadhedrin (CDH1) [Gene ID=999] knockdown by RNAi.	MSigDBv3.0 CGP	254	25	2.3	13.6	8.04E-19	5.21E-15	3.73E-16	BGN, CDH11, CLEC3B, COL1A2, COL3A1, COL5A1, COL5A2, COL6A1, COL6A2, CRIP2, CTGF, CXCR7, DPYSL3, EPS8, FBN1, FN1, IGFBP7, LEPR, LRIG1, MAGED1, MMP2, PODXL, POSTN, SERPINE1, VCAN
PROTEINACEOUS EXTRACELLULAR MATRIX	ECM	component		Genes annotated by the GO term GO:0005578. A layer consisting mainly of proteins (especially collagen) and glycosaminoglycans (mostly as proteoglycans) that forms a sheet underlying or overlying cells such as endothelial and epithelial cells. The proteins are secreted by cells in the vicinity.	MSigDBv3.0 CC	98	18	0.9	27.1	9.14E-19	5.92E-15	3.95E-16	AGRN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, CTGF, ECM1, EFEMP1, FBLN2, FBN1, LAMA4, LAMB1, LAMB2, LTBP4, POSTN, TNXB, VCAN
CHARAFE BREAST CANCER LUMINAL VS MESENCHYMAL DN	tumor	breast	EMT-mesenchymal	Genes down-regulated in luminal-like breast cancer cell lines compared to the mesenchymal-like ones.	MSigDBv3.0 CGP	446	31	4.1	9.6	1.01E-18	6.55E-15	4.10E-16	ANXA2, ARHGAP23, CAV1, CDH11, COL4A2, COL5A1, COL6A1, COL6A2, CRIM1, DKK3, ENG, FBN1, FLNC, FOXC1, FSCN1, FSTL1, GJA1, GPRC5B, HEG1, IGFBP7, ITGAV, LAMB1, LOXL2, MARVELD1, MMP2, MRC2, PTRF, SERPINE1, SERPINE2, VIM, WWTR1
EXTRACELLULAR MATRIX	ECM	component		Genes annotated by the GO term GO:0031012. A structure lying external to one or more cells, which provides structural support for cells or tissues; may be completely external to the cell (as in animals) or be part of the cell (as in plants).	MSigDBv3.0 CC	100	18	0.9	26.4	1.34E-18	8.68E-15	5.12E-16	AGRN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, CTGF, ECM1, EFEMP1, FBLN2, FBN1, LAMA4, LAMB1, LAMB2, LTBP4, POSTN, TNXB, VCAN
module 6	others			Genes in module_6: Trachea genes	MSigDBv3.0 CM	404	29	3.7	9.8	6.28E-18	4.07E-14	2.27E-15	AQP1, CAV1, CD151, CD34, CFH, CLEC3B, COL1A2, COL6A1, COL6A2, CRIM1, CRIP1, DPYSL3, ENG, FBLN2, FN1, HSPG2, IFI27, ITGA6, ITGB4, LAMB2, MAOA, MDK, MUC1, PLA2G2A, RNASE1, STAB1, TM4SF1, TNXB, WWTR1
module 12	others			Genes in module_12: Spinal cord (neuro-development) genes	MSigDBv3.0 CM	349	27	3.2	10.6	1.46E-17	9.45E-14	4.99E-15	AQP1, CAV1, CLEC3B, COL1A2, COL3A1, COL5A2, COL6A1, COL6A2, CRIM1, DPYSL3, ELN, ENG, FBXL7, FN1, GJA1, GPRC5B, HSPG2, ITGA6, ITGB4, LAMB2, PALM, POSTN, RNASE1, SERPINE1, STAB1, VCAN, WWTR1
module 122	ECM	adhesion		Genes in module_122: Adhesion molecules	MSigDBv3.0 CM	138	19	1.3	19.3	2.75E-17	1.78E-13	8.93E-15	BGN, CD151, CDH13, CDH5, COL3A1, COL5A1, COL5A2, COL6A1, COL6A2, CTGF, ELN, FBN1, FN1, ITGAV, LAMA4, LAMB1, LAMB2, POSTN, TNXB
WU CELL MIGRATION	EMT	migration		Genes associated with migration rate of 40 human bladder cancer cells.	MSigDBv3.0 CGP	185	21	1.7	15.6	3.11E-17	2.01E-13	9.62E-15	ADAMTS1, COL4A2, COL6A2, DKK3, EFEMP1, EPS8, FN1, GJA1, IGFBP7, ITGB4, LOXL2, MAOA, MEST, PERP, PODXL, SERPINE1, TM4SF1, TNFRSF21, VCAN, VIM, WWTR1
module 88	others	metabolism		Genes in module_88: Heart, liver, Kidney and pancreas metabolic and xenobiotic response genes	MSigDBv3.0 CM	814	38	7.5	6.5	5.74E-17	3.71E-13	1.69E-14	AQP1, BCAM, CAV1, CD151, CFH, CLEC3B, COL1A2, COL3A1, COL5A2, COL6A1, COL6A2, CRIM1, ECM1, ELN, ENG, FBLN2, FBXL7, FN1, GPRC5B, HSPG2, IFI27, IL1R1, ITGA6, LAMB2, LRRC32, MAOA, MDK, MMP2, MUC1, PALM, PLA2G2A, PTGIS, PVRL2, RNASE1, SERPINE1, STAB1, TM4SF1, TNXB
module 60	others			Genes in module_60: Heart genes	MSigDBv3.0 CM	409	28	3.7	9.3	8.47E-17	5.48E-13	2.39E-14	AQP1, BCAM, CD151, CD34, CDH5, CLEC3B, COL1A2, COL6A1, COL6A2, CRIP1, ELN, ENG, FBLN2, FN1, HSPG2, IFI27, ITGB4, LAMB2, LRRC32, PLXND1, PTGIS, PVRL2, RNASE1, SEMA3F, SLC29A1, STAB1, TJP1, TNXB
GNF2 PTX3	others	genes	PTX3	Neighborhood of PTX3	MSigDBv3.0 CGN	36	12	0.3	58	2.45E-16	1.59E-12	6.63E-14	CDH11, COL1A2, COL3A1, COL5A1, COL5A2, CTGF, EFEMP1, FBN1, FSTL1, LAMB1, LOXL2, SERPINE1

CHIARADONNA NEOPLASTIC TRANSFORMATION CDC25 DN	tumor	other		Genes down-regulated in reverted NIH3T3 cells (fibroblasts transformed by activated KRAS [Gene ID=3845] which then reverted to normal cells upon stable over-expression of a dominant negative form of CDC25 [Gene ID=5923]) vs normal fibroblasts.	MSigDBv3.0 CGP	148	18	1.4	16.6	1.85E-15	1.20E-11	4.81E-13	AGRN, AQP1, CD151, CD34, CD9, CLEC3B, COL4A2, COL5A2, CTGF, ELN, FBN1, ITGB4, NFE2L1, PLTP, RBMS2, SEMA3F, SLC29A1, TNXB
ROZANOV MMP14 TARGETS SUBSET	ECM	component	MMP14-regulated	Genes linked to the ECM maintenance and angiogenesis that were changed in HT1080 cells (fibrosarcoma) over-expressing MMP14 [Gene ID=4323] compared to those with knockdown of the gene by RNAi.	MSigDBv3.0 CGP	33	11	0.3	57.7	4.49E-15	2.90E-11	1.12E-12	ANGPTL2, COL4A2, COL5A1, COL6A1, COL6A2, EFEMP1, FN1, LAMA4, LAMB1, MDK, PLXND1
module 3	others			Genes in module_3	MSigDBv3.0 CM	375	25	3.4	8.9	8.09E-15	5.23E-11	1.94E-12	ANXA2, CAV1, CD151, CRIM1, DPYSL3, EFEMP1, EMP1, ENG, FN1, FSTL1, GJA1, HSPG2, ITGA6, LAMB1, LOXL2, MDK, MEST, PLK2, PLS3, PLXND1, SERPINE1, SLC29A1, STAB1, TM4SF1, WWTR1
KEGG FOCAL ADHESION	ECM	adhesion		Focal adhesion	MSigDBv3.0 CP:KEGG	198	19	1.8	12.8	2.46E-14	1.59E-10	5.71E-12	CAV1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2, FLNB, FLNC, FN1, ITGA6, ITGA9, ITGAV, ITGB4, LAMA4, LAMB1, LAMB2, TNXB
GU PDEF TARGETS UP	signaling	integrin,VEGF, TGFB	PDEF	Integrin, VEGF, Wnt and TGF-?? signaling pathway genes up-regulated in PC-3 cells (prostate cancer) after knockdown of PDEF [Gene ID=25803] by RNAi.	MSigDBv3.0 CGP	68	13	0.6	27.6	4.10E-14	2.65E-10	9.18E-12	CDH11, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2, CTGF, DKK3, FN1, ITGA6, LAMB2, SERPINE1, VIM
HOSHIDA LIVER CANCER SUBCLASS S1	signaling	WNT		Genes from 'subtype S1' signature of hepatocellular carcinoma (HCC): aberrant activation of the WNT signaling pathway.	MSigDBv3.0 CGP	236	20	2.2	11.2	5.35E-14	3.46E-10	1.16E-11	ADAM15, AQP1, CD151, CDH11, COL1A2, COL3A1, COL4A2, COL5A2, COL6A1, COL6A2, CRIP2, CTGF, EFEMP1, FBN1, LAMB1, LTBP3, POSTN, RNASE1, S100A10, VCAN
ZHU CMV 24 HR DN	others			Down-regulated at 24 h following infection of primary human foreskin fibroblasts with CMV	MSigDBv3.0 CGP	54	12	0.5	33.1	5.83E-14	3.76E-10	1.22E-11	CD151, CDH11, COL1A2, COL3A1, COL5A2, COL6A2, EFEMP1, LAMB2, POSTN, PTGIS, SERPINE1, VCAN
module 19	others	metabolism		Genes in module_19: Adrenal gland- metabolic genes	MSigDBv3.0 CM	305	22	2.8	9.5	7.56E-14	4.88E-10	1.53E-11	CD34, CLEC3B, COL1A2, COL6A1, COL6A2, ENG, FBXL7, FSTL1, GJA1, HSPG2, IFI27, IL1R1, LAMB2, LRRC32, MAOA, PVRL2, RNASE1, SLC29A1, STAB1, TNXB, VCAN, WWTR1
module 52	tumor	other		Genes in module_52: Cell line expressed genes	MSigDBv3.0 CM	416	25	3.8	7.9	8.58E-14	5.54E-10	1.69E-11	ANXA2, CAV1, CD151, COL5A2, CRIM1, DPYSL3, EFEMP1, EMP1, ENG, EPS8, FN1, GJA1, HSPG2, IFI27, ITGA6, LAMB1, LOXL2, MDK, MEST, PLK2, RNASE1, SERPINE1, STAB1, TM4SF1, WWTR1
ZHU CMV ALL DN	others			Down-regulated at any timepoint following infection of primary human foreskin fibroblasts with CMV	MSigDBv3.0 CGP	72	13	0.7	25.7	8.98E-14	5.80E-10	1.71E-11	CD151, CDH11, COL1A2, COL3A1, COL5A2, COL6A2, EFEMP1, ENG, LAMB2, POSTN, PTGIS, SERPINE1, VCAN
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS DN	tumor	other		Genes down-regulated in transformed NIH3T3 cells (fibroblasts transformed by activated KRAS [Gene ID=3845]) vs normal cells.	MSigDBv3.0 CGP	135	16	1.2	15.9	1.09E-13	7.05E-10	2.02E-11	AQP1, CD151, CD9, COL1A2, COL4A2, COL5A1, COL5A2, CTGF, ELN, FBN1, FSTL1, LAMB2, PLTP, RBMS2, SLC29A1, TNXB
ROZANOV MMP14 TARGETS UP	EMT	MMP		Genes up-regulated in HT1080 cells (fibrosarcoma) over-expressing MMP14 [Gene ID=4323] compared to those with knockdown of the gene by RNAi.	MSigDBv3.0 CGP	261	20	2.4	10	3.58E-13	2.31E-09	6.34E-11	ANGPTL2, CGNL1, COL4A2, COL5A1, COL6A1, COL6A2, CTGF, DSTN, EFEMP1, FN1, HEG1, IGFBP7, IL1R1, LAMA4, LAMB1, LRIG1, MDK, PLK2, PLXND1, SLCO2A1
CROONQUIST STROMAL STIMULATION UP	signaling	IL6		Genes up-regulated in ANBL-6 cell line (multiple myeloma, MM) co-cultured with bone marrow stromal cells compared to those grown in the presence of IL6 [Gene ID=3569].	MSigDBv3.0 CGP	47	11	0.4	35.2	3.62E-13	2.33E-09	6.34E-11	COL1A2, COL6A1, CTGF, FSCN1, ID1, IGFBP7, LAMA4, MYOF, SERPINE1, SULF1, VCAN
module 55	others			Genes in module_55	MSigDBv3.0 CM	809	33	7.4	5.4	3.91E-13	2.52E-09	6.67E-11	AQP1, BCAM, CAV1, CFH, CLEC3B, COL1A2, COL3A1, COL5A2, COL6A1, COL6A2, CRIM1, ECM1, ELN, ENG, FBXL7, FN1, HSPG2, IFI27, IL1R1, ITGA6, LAMB2, LRRC32, MAOA, MMP2, MUC1, PALM, PLA2G2A, PVRL2, RNASE1, SERPINE1, STAB1, TM4SF1, TNXB
MANALO HYPOXIA UP	signaling	hypoxia		Genes up-regulated in response to both hypoxia and overexpression of an active form of HIF1A [Gene ID=3091].	MSigDBv3.0 CGP	207	18	1.9	11.4	6.71E-13	4.33E-09	1.12E-10	BGN, COL1A2, COL4A2, COL5A1, CXCR7, DCHS1, DKK3, EDN1, GAS6, LAMB1, LEPR, LOXL2, LRRC32, MMP2, PTGIS, PTPRB, SERPINE1, SYNPO
LINDGREN BLADDER CANCER CLUSTER 2B	tumor	other		Genes specifically up-regulated in Cluster IIb of urothelial cell carcinom (UCC) tumors.	MSigDBv3.0 CGP	379	23	3.5	7.9	7.48E-13	4.83E-09	1.20E-10	ANGPTL2, AQP1, CAV1, COL1A2, COL5A2, COL6A1, COL6A2, CRIP1, CTGF, DKK3, EFEMP1, ELN, FBLN2, GPR116, IGFBP7, LAMA4, LAMB2, LRIG1, MMP2, PODXL, POSTN, PTRF, SYNPO
TURASHVILI BREAST LOBULAR CARCINOMA VS DUCTAL NORMAL UP	tumor	breast	aggressive	Genes up-regulated in lobular carcinoma vs normal ductal breast cells.	MSigDBv3.0 CGP	66	12	0.6	25.8	7.61E-13	4.91E-09	1.20E-10	BGN, COL1A2, COL3A1, COL5A1, COL5A2, FBN1, FN1, LAMB1, POSTN, SULF1, TIE1, VCAN
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION ERYTHROCYTE UP	others			Genes up-regulated in erythroid lineage cells by RUNX1-RUNX1T1 [Gene ID=861, 862] fusion .	MSigDBv3.0 CGP	159	16	1.5	13.2	1.43E-12	9.23E-09	2.21E-10	ALDH1A2, ANXA2, COL1A2, DKK2, ECM1, EMP1, HSPB1, ID1, MYOF, PALM, PLK2, PLTP, SPTAN1, TM4SF1, TNFRSF21, VCAN

TURASHVILI BREAST LOBULAR CARCINOMA VS LOBULAR NORMAL DN	tumor	breast	aggressive	Genes down-regulated in lobular carcinoma vs normal lobular breast cells.	MSigDBv3.0 CGP	70	12	0.6	24	1.59E-12	1.03E-08	2.40E-10	BGN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, FBN1, FN1, LAMB1, MMP2, POSTN, VCAN
SMID BREAST CANCER LUMINAL B DN	tumor	breast	luminal	Genes down-regulated in the luminal B subtype of breast cancer.	MSigDBv3.0 CGP	574	27	5.3	6.1	2.71E-12	1.74E-08	3.99E-10	ADAMTS1, AQP1, CAV1, COL4A2, CTGF, EDN1, EFEMP1, ELN, FBLN2, FOXC1, FSCN1, GPR116, ID1, IL33, ITGA6, LEPR, PERP, PLA2G2A, PLTP, PTGIS, SERPINE2, TIE1, TM4SF1, TNFRSF21, TNXB, VCAN, WWTR1
KAAB HEART ATRIUM VS VENTRICLE UP	others			Genes up-regulated in the atria of healthy hearts, compared to venticles.	MSigDBv3.0 CGP	258	19	2.4	9.5	2.91E-12	1.87E-08	4.19E-10	ALDH1A2, CFH, CRIP1, CTGF, DPYSL3, EFEMP1, EPS8, FBLN2, HEG1, HSPG2, IL1R1, IL1RL1, MAGED1, MDK, PLA2G2A, PTGIS, SYNPO, VCAN, VIM
EXTRACELLULAR MATRIX PART	ECM	component		Genes annotated by the GO term GO:0044420. Any constituent part of the extracellular matrix, the structure lying external to one or more cells, which provides structural support for cells or tissues; may be completely external to the cell (as in animals) or be part of the cell (as often seen in plants).	MSigDBv3.0 CC	57	11	0.5	27.6	3.54E-12	2.28E-08	4.99E-10	AGRN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, FBN1, LAMA4, LAMB1, LAMB2, TNXB
RODWELL AGING KIDNEY NO BLOOD UP	others			Genes whose expression increases with age in normal kidney, excluding those with higher expression in blood.	MSigDBv3.0 CGP	153	15	1.4	12.8	1.08E-11	6.94E-08	1.49E-09	ANXA2, CDH11, COL1A2, COL3A1, COL5A1, DKK3, FBN1, FN1, FSCN1, MYOF, PLK2, PTRF, SERPINE2, STAB1, TXNDC5
SANA TNF SIGNALING DN	others			Genes down-regulated in five primary endothelial cell types (lung, aortic, iliac, dermal, and colon) by TNF [Gene ID=7124].	MSigDBv3.0 CGP	82	12	0.8	19.9	1.13E-11	7.27E-08	1.52E-09	ANXA2, BGN, CD34, CRIP2, CTGF, EFEMP1, ITGA6, MYOF, NOS3, POSTN, RHOJ, TXNDC5
KINSEY TARGETS OF EWSR1 FLII FUSION DN	tumor	other		Genes down-regulated in TC71 and EWS502 cells (Ewing's sarcoma) upon knockdown of the EWSR1-FLII fusion [Gene ID=2130, 2314].	MSigDBv3.0 CGP	315	20	2.9	8.2	1.15E-11	7.40E-08	1.52E-09	ANGPTL2, CD59, COL3A1, COL5A1, COL5A2, FBN1, FLNB, FN1, FOXC1, FSTL1, HMCN1, IGFBP7, LAMA4, LAMB2, LTBP3, MAGED1, POSTN, S100A10, SPTAN1, VIM
module 44	others			Genes in module_44: Thymus genes	MSigDBv3.0 CM	316	20	2.9	8.1	1.22E-11	7.84E-08	1.58E-09	AQP1, CAV1, CD34, CLEC3B, COL1A2, COL6A1, COL6A2, CRIM1, CRIP1, ENG, FN1, FSTL1, HSPG2, IFI27, IL1R1, ITGA6, MAOA, PLXND1, RNASE1, STAB1
module 24	others	metabolism		Genes in module_24: Fetal liver genes - Metabolism and xenobiotics	MSigDBv3.0 CM	444	23	4.1	6.7	1.91E-11	1.23E-07	2.41E-09	AQP1, BCAM, CFH, CLEC3B, COL1A2, COL3A1, COL5A2, COL6A1, COL6A2, ECM1, ELN, ENG, FN1, HSPG2, IL1R1, LAMB2, MAOA, PLA2G2A, PVRL2, SERPINE1, SLC29A1, STAB1, TNXB
ROY WOUND BLOOD VESSEL UP	others			Genes up-regulated in blood vessel cells from wound site.	MSigDBv3.0 CGP	49	10	0.4	29.4	1.93E-11	1.24E-07	2.41E-09	ANGPTL2, CDH5, COL3A1, COL5A2, FBXL7, HEG1, POSTN, SLCO2A1, SULF1, VCAN
VERRECCHIA EARLY RESPONSE TO TGFB1	signaling	TGFB	ECM	ECM related genes up-regulated early (within 30 min) in dermal fibroblasts after addition of TGFB1 [Gene ID=7040].	MSigDBv3.0 CGP	51	10	0.5	27.9	2.96E-11	1.90E-07	3.62E-09	CD59, COL1A2, COL3A1, COL6A1, FN1, HSPG2, LAMA4, RHOC, SERPINE1, VCAN
DOUGLAS BMI1 TARGETS UP	tumor	other		Genes up-regulated in A4573 cells (Ewing's sarcoma, ESFT) after knockdown of BMI1 [Gene ID=648] by RNAi.	MSigDBv3.0 CGP	509	24	4.7	6.1	4.74E-11	3.05E-07	5.70E-09	ADAMTS1, ANGPTL2, APCDD1, BGN, CCDC3, COL4A2, COL5A1, COL6A1, COL6A2, DCHS1, DKK2, DKK3, DOCK6, ECM1, ELN, FN1, GPRC5B, HYAL2, LOXL2, MMP2, PLTP, PODXL, S100A10, SLC29A1
GRUETZMANN PANCREATIC CANCER UP	tumor	other		Genes up-regulated in pancreatic ductal adenocarcinoma (PDAC) identified in a meta analysis across four independent studies.	MSigDBv3.0 CGP	346	20	3.2	7.4	6.23E-11	4.01E-07	7.35E-09	CAV1, CD9, COL5A2, CRIP2, DPYSL3, ECM1, EPS8, FBLN2, FBN1, FN1, ITGB4, LAMA4, LOXL2, MMP2, MYH10, PLEC, POSTN, S100A10, SERPINE1, VCAN
LI WILMS TUMOR VS FETAL KIDNEY 1 UP	tumor	other		Genes up-regulated in Wilm's tumor samples compared to fetal kidney.	MSigDBv3.0 CGP	182	15	1.7	10.5	1.30E-10	8.36E-07	1.51E-08	AGRN, ATP1A1, CDH5, COL1A2, CRIM1, DSTN, GPRC5B, IGFBP7, IL1R1, LRRC32, MYOF, PLS3, PODXL, S100A10, TEK
VERHAAK AML WITH NPM1 MUTATED DN	tumor	other		Genes down-regulated in acute myeloid leukemia (AML) patients with mutated NPM1 [Gene ID=4869].	MSigDBv3.0 CGP	255	17	2.3	8.5	2.05E-10	1.32E-06	2.34E-08	CAV1, CD34, DCHS1, EMP1, EPS8, FLNB, GJA1, HSPB1, HSPG2, IGFBP7, ITGA6, MEST, PALM, PLXND1, PTRF, SERPINE2, TNFRSF21
CROONQUIST NRAS VS STROMAL STIMULATION DN	tumor	other		Genes down-regulated in ANBL-6 cell line (multiple myeloma, MM) expressing an activated form of NRAS [Gene ID=4893] off a plasmid vector compared to those co-cultured with bone marrow stromal cells.	MSigDBv3.0 CGP	82	11	0.8	17.8	2.21E-10	1.42E-06	2.47E-08	COL1A2, CTGF, FSCN1, GJA1, ID1, IGFBP7, LAMA4, LAMB1, POSTN, SULF1, VCAN
REACTOME AXON GUIDANCE	others			Genes involved in Axon guidance	MSigDBv3.0 CP:REACTOME	159	14	1.5	11.3	2.29E-10	1.47E-06	2.51E-08	AGRN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2, DPYSL3, MYH10, PLXNA4, PLXND1, RHOC, SPTAN1
LU AGING BRAIN DN	others			Genes down-regulated in postmortem brain frontal cortex samples from old subjects compared to those from the young ones.	MSigDBv3.0 CGP	264	17	2.4	8.1	3.52E-10	2.26E-06	3.80E-08	CAV1, CFH, DPYSL3, EFEMP1, GJA1, GPRC5B, IL33, ITGAV, LRIG1, MAOA, MYOF, PODXL, RNASE1, TM4SF1, VCAN, VIM, WWTR1
PETRETTO CARDIAC HYPERTROPHY	others			Genes that correlated most highly with left ventricular mass (LVM) index.	MSigDBv3.0 CGP	34	8	0.3	34.9	6.24E-10	4.01E-06	6.63E-08	COL5A2, CRIM1, EFEMP1, FBN1, FN1, FSTL1, LTBP3, TM4SF1
LANDIS ERBB2 BREAST TUMORS 324 DN	tumor	breast	ERBB2	The 324 genes identified by two analytical methods as changed in the mammary tumors induced by transgenic expression of ERBB2 [Gene ID=2064].	MSigDBv3.0 CGP	142	13	1.3	11.7	6.34E-10	4.07E-06	6.63E-08	ANGPTL2, CD151, CD34, CLEC3B, COL3A1, COL5A1, COL6A1, CRIP1, FSTL1, GAS6, GJA1, POSTN, PTPRB

DELYS THYROID CANCER UP	tumor	other		Genes up-regulated in papillary thyroid carcinoma (PTC) compared to normal tissue.	MSigDBv3.0 CGP	398	20	3.6	6.3	7.35E-10	4.72E-06	7.57E-08	AGRN, ANXA2, CD151, COL3A1, COL5A2, DPYSL3, ECM1, EPS8, FN1, GPRC5B, ITGA9, LOXL2, MDK, MRC2, MUC1, MYH10, PLXND1, S100A10, SEMA3F, TNFRSF21
BRUECKNER TARGETS OF MIRLET7A3 DN	tumor	other		Genes down-regulated in A549 cells (lung cancer) expressing MIRLET7A3 [Gene ID=406883] microRNA off a plasmid vector.	MSigDBv3.0 CGP	75	10	0.7	17.6	1.59E-09	1.02E-05	1.61E-07	COL4A2, COL5A1, DPYSL3, EFEMP1, FLNB, FN1, GPRC5B, LOXL2, PLK2, VIM
WINTER HYPOXIA METAGENE	signaling	hypoxia		Genes regulated by hypoxia, based on literature searches.	MSigDBv3.0 CGP	218	15	2	8.7	1.62E-09	1.04E-05	1.62E-07	ANXA2, COL5A1, COL5A2, EDN1, ENG, FN1, IFI27, MMP2, MUC1, NOS3, PSMD9, SERPINE1, SSSCA1, TEK, VIM
ANATOMICAL STRUCTURE DEVELOPMENT	others			Genes annotated by the GO term GO:0048856. The biological process whose specific outcome is the progression of an anatomical structure from an initial condition to its mature state. This process begins with the formation of the structure and ends with the mature structure, whatever form that may be including its natural destruction. An anatomical structure is any biological entity that occupies space and is distinguished from its surroundings. Anatomical structures can be macroscopic such as a carpel, or microscopic such as an acrosome.	MSigDBv3.0 BP	1002	31	9.2	4	2.19E-09	1.41E-05	2.15E-07	AGRN, ANXA2, CD9, CDC42BPB, CDH13, CLEC3B, COL1A2, COL4A2, COL5A2, CRIM1, CTGF, DKK3, DPYSL3, ELN, EMP1, ENG, EPHB4, FBN1, FGD5, FOXC1, GATA4, GATA6, LAMB1, MDK, MEST, NFE2L1, POSTN, ROBO4, SFRP5, STAB1, TIE1
module 324	others			Genes in module_324: metal/Ca ion binding	MSigDBv3.0 CM	131	12	1.2	11.6	2.93E-09	1.88E-05	2.84E-07	ANXA2, CDH13, CDH5, EFEMP1, FBLN2, FBN1, FSTL1, GAS6, MMP2, PLA2G2A, PLS3, S100A10
module 84	others			Genes in module_84: Immune (humoral) and inflammatory response	MSigDBv3.0 CM	527	22	4.8	5.3	3.14E-09	2.01E-05	2.99E-07	AQP1, CAV1, CLEC3B, COL1A2, COL6A1, COL6A2, CRIM1, ENG, FN1, HSPG2, IFI27, IGFBP7, IL1R1, ITGA6, LRRC32, MDK, MUC1, PVRL2, RNASE1, SERPINE1, TNXB, VCAN
REACTOME INTEGRIN CELL SURFACE INTERACTIONS	ECM	receptor		Genes involved in Integrin cell surface interactions	MSigDBv3.0 CP:REACTOME	81	10	0.7	16.1	3.43E-09	2.20E-05	3.22E-07	COL1A2, COL4A2, FBN1, FN1, ITGA6, ITGA9, ITGAV, ITGB4, LAMB1, LAMB2
VECCHI GASTRIC CANCER ADVANCED VS EARLY UP	tumor	other	aggressive	Up-regulated genes distinguishing between two subtypes of gastric cancer: advanced (AGC) and early (EGC).	MSigDBv3.0 CGP	163	13	1.5	10.1	3.48E-09	2.23E-05	3.22E-07	BGN, CDH11, COL1A2, COL3A1, COL5A2, EFEMP1, FBN1, FN1, FSTL1, MYH10, SULF1, VCAN, WWTR1
module 118	tumor	other		Genes in module_118: Cell line expressed genes	MSigDBv3.0 CM	393	19	3.6	6.1	3.79E-09	2.44E-05	3.47E-07	CAV1, CD151, COL5A2, CRIM1, DPYSL3, EFEMP1, EMP1, ENG, FN1, GJA1, HSPG2, IFI27, ITGA6, LAMB1, LOXL2, MDK, MMP2, SERPINE1, TM4SF1
SUNG METASTASIS STROMA UP	tumor	other	metastasis	Genes up-regulated in metastatic vs non-metastatic stromal cells originated from either bone or prostate tissues.	MSigDBv3.0 CGP	107	11	1	13.2	4.01E-09	2.57E-05	3.59E-07	AGRN, CD59, COL3A1, COL5A1, COL5A2, EPS8, FBLN2, GOLM1, HSPG2, PLK2, VCAN
WANG SMARCE1 TARGETS UP	tumor	other		Genes up-regulated in BT549 cells (breast cancer) by expression of SMARCE1 [Gene ID=6605] off a retroviral vector.	MSigDBv3.0 CGP	165	13	1.5	9.9	4.03E-09	2.59E-05	3.59E-07	BCAM, CFH, COL3A1, COL5A1, DPYSL3, FN1, HEG1, IL1R1, MMP2, PLXND1, POSTN, SULF1, VCAN
REACTOME CELL JUNCTION ORGANIZATION	ECM	adhesion		Genes involved in Cell junction organization	MSigDBv3.0 CP:REACTOME	83	10	0.8	15.7	4.37E-09	2.81E-05	3.84E-07	CD151, CDH11, CDH13, CDH5, FLNC, ITGA6, ITGB4, LIMS2, PLEC, PVRL2
REACTOME NCAM1 INTERACTIONS	ECM	adhesion	NCAM1	Genes involved in NCAM1 interactions	MSigDBv3.0 CP:REACTOME	43	8	0.4	25.9	4.65E-09	2.98E-05	4.02E-07	AGRN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2
CHARAFE BREAST CANCER LUMINAL VS BASAL DN	tumor	breast	EMT-basal	Genes down-regulated in luminal-like breast cancer cell lines compared to the basal-like ones.	MSigDBv3.0 CGP	447	20	4.1	5.6	5.38E-09	3.45E-05	4.54E-07	ANXA2, ARHGAP23, ATP1A1, CAV1, CD59, CDH13, COL4A2, EMP1, FSCN1, FSTL1, IFI27, IGFBP7, ITGA6, LOXL2, PERP, PLS3, PTRF, S100A10, SERPINE2, WWTR1
SENESE HDAC1 TARGETS DN	tumor	other		Genes down-regulated in U2OS cells (osteosarcoma) upon knockdown of HDAC1 [Gene ID=3065] by RNAi.	MSigDBv3.0 CGP	238	15	2.2	7.9	5.38E-09	3.45E-05	4.54E-07	BCAM, CDH13, COL3A1, COL5A1, DKK3, EDN1, FSTL1, GOLM1, KIAA1522, LAMB2, MAGED1, MRC2, MYH10, PTRF, S100A10
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION SUSTAINDED IN ERYTHROCYTE UP	others			Genes up-regulated by RUNX1-RUNX1T1 [Gene ID=861, 862] fusion protein in normal hematopoietic progenitors; their expression was sustained in subsequently developing erythroid lineage.	MSigDBv3.0 CGP	44	8	0.4	25.2	5.64E-09	3.61E-05	4.69E-07	ALDH1A2, ANXA2, ECM1, EMP1, HSPB1, ID1, TM4SF1, VCAN
WEST ADRENOCORTICAL TUMOR DN	tumor	other		Down-regulated genes in pediatric adrenocortical tumors (ACT) compared to the normal tissue.	MSigDBv3.0 CGP	547	22	5	5	6.19E-09	3.97E-05	5.08E-07	BGN, CD34, CFH, CLEC3B, COL6A1, DKK3, IL33, LAMB2, LEPR, LRRC32, LTBP4, MMP2, PLTP, PODXL, POSTN, PTGIS, PTRF, SLCO2A1, STAB1, TEK, TM4SF1, VCAN
DANG REGULATED BY MYC DN	TF	MYC		Genes down-regulated by MYC [Gene ID=4609], according to the MYC Target Gene Database.	MSigDBv3.0 CGP	243	15	2.2	7.7	7.14E-09	4.57E-05	5.72E-07	AQP1, CAV1, CD151, COL1A2, COL3A1, COL5A1, CTGF, EDN1, FN1, FSTL1, HSPB1, PERP, PLS3, POSTN, SERPINE1
MULLIGHAN MLL SIGNATURE 1 DN	tumor	other		The 'MLL signature 1': genes down-regulated in pediatric AML (acute myeloid leukemia) with rearranged MLL [Gene ID=4297] compared to all AML cases with the intact gene.	MSigDBv3.0 CGP	243	15	2.2	7.7	7.14E-09	4.57E-05	5.72E-07	AGRN, CAV1, FSCN1, HYAL2, ITGAV, LAMB2, MDK, MMP2, MYH10, PTRF, SERPINE2, SLC9A3R2, TIE1, TM4SF1, TNFRSF21

LANDIS BREAST CANCER PROGRESSION DN	tumor	breast	aggressive	Genes down-regulated in preneoplastic mammary tissues and whose expression is maintained in tumors.	MSigDBv3.0 CGP	66	9	0.6	18	8.71E-09	5.58E-05	6.89E-07	ANGPTL2, CD34, CLEC3B, COL3A1, COL5A1, CRIP1, FSTL1, GAS6, GJA1
TURASHVILI BREAST DUCTAL CARCINOMA VS DUCTAL NORMAL UP	tumor	breast	ductal	Genes up-regulated in ductal carcinoma vs normal ductal breast cells.	MSigDBv3.0 CGP	47	8	0.4	23.2	9.77E-09	6.26E-05	7.64E-07	COL1A2, COL3A1, COL5A2, FBN1, FN1, POSTN, SULF1, VCAN
ORGAN DEVELOPMENT	others			Genes annotated by the GO term GO:0048513. Development of a tissue or tissues that work together to perform a specific function or functions. Development pertains to the process whose specific outcome is the progression of a structure over time, from its formation to the mature structure. Organs are commonly observed as visibly distinct structures, but may also exist as loosely associated clusters of cells that work together to perform a specific function or functions.	MSigDBv3.0 BP	565	22	5.2	4.9	1.11E-08	7.12E-05	8.58E-07	ANXA2, CDH13, CLEC3B, COL1A2, COL4A2, COL5A2, CTGF, ELN, EMP1, ENG, EPHB4, FBN1, FOXC1, GATA4, GATA6, LAMB1, MDK, MEST, POSTN, ROBO4, STAB1, TIE1
REACTOME NCAM SIGNALING FOR NEURITE OUT GROWTH	signaling	NCAM		Genes involved in NCAM signaling for neurite out-growth	MSigDBv3.0 CP:REACTOME	68	9	0.6	17.4	1.14E-08	7.31E-05	8.71E-07	AGRN, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2, SPTAN1
FARMER BREAST CANCER CLUSTER 5	tumor	breast	amplicon	Cluster 5: selected 17q21_23 amplicon genes clustered together across breast cancer samples.	MSigDBv3.0 CGP	19	6	0.2	51.7	1.33E-08	8.52E-05	1.00E-06	CDH11, COL1A2, COL3A1, COL5A1, COL5A2, FBN1
DAVICIONI TARGETS OF PAX FOXO1 FUSIONS UP	tumor	other		Genes up-regulated in RD cells (embryonal rhabdomyosarcoma, ERMS) by expression of PAX3- or PAX7-FOXO1 [Gene ID=5077, 5081, 2308] fusions off retroviral vectors.	MSigDBv3.0 CGP	258	15	2.4	7.2	1.60E-08	0.000102	1.19E-06	ADAMTS1, CAV1, CD9, COL5A1, COL6A2, CXCR7, DKK2, ECM1, EMP1, HEG1, LOXL2, MYOF, S100A10, SERPINE2, SULF1
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION HSC UP	others			Genes up-regulated in normal hematopoietic progenitors by RUNX1-RUNX1T1 [Gene ID=861, 862] fusion.	MSigDBv3.0 CGP	186	13	1.7	8.7	1.72E-08	0.00011	1.26E-06	ALDH1A2, ANXA2, COL3A1, ECM1, EMP1, EPS8, FSTL1, HSPB1, ID1, IL1RL1, RHOC, TM4SF1, VCAN
GAUSSMANN MLL AF4 FUSION TARGETS F UP	tumor	other		Up-regualted genes from the set F (Fig. 5a): specific signature shared by cells expressing AF4-MLL [Gene ID=4299, 4297] alone and those expressing both AF4-MLL and MLL-AF4 fusion proteins.	MSigDBv3.0 CGP	130	11	1.2	10.6	3.13E-08	0.000201	2.29E-06	BMPER, COL3A1, COL6A1, COL6A2, DKK3, ECM1, GAS6, S100A16, SCARA3, SYNPO, TEK
VART KSHV INFECTION ANGIOGENIC MARKERS DN	tumor	other		Angiogenic markers down-regulated in lymph endothelial cells upon infection with KSHV (Kaposi's sarcoma herpes virus).	MSigDBv3.0 CGP	134	11	1.2	10.3	4.30E-08	0.000275	3.10E-06	CDH5, CFH, CTGF, EPHB4, ID1, MDK, MMP2, NOS3, SFRP5, STAB1, TIE1
COLLAGEN	ECM	component		Genes annotated by the GO term GO:0005581. Any of the various assemblies in which collagen chains form a left-handed triple helix; may assemble into higher order structures.	MSigDBv3.0 CC	23	6	0.2	39.5	4.80E-08	0.000307	3.42E-06	COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, TNXB
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION MONOCYTE UP	others			Genes up-regulated in monocytes by RUNX1-RUNX1T1 [Gene ID=861, 862] fusion.	MSigDBv3.0 CGP	203	13	1.9	7.9	4.85E-08	0.00031	3.42E-06	ALDH1A2, AQP1, COL1A2, EHD2, EPS8, FLNB, HSPB1, MYOF, PLS3, PLTP, PTRF, SPTAN1, TM4SF1
NAKAMURA TUMOR ZONE PERIPHERAL VS CENTRAL UP	tumor	other		Up-regulated genes in peripheral zone of human pancreatic cancer growing in the pancreas of nude mice compared to that of the tumor from the central zone.	MSigDBv3.0 CGP	283	15	2.6	6.5	5.45E-08	0.000349	3.76E-06	ADAMTS1, ANO1, CAV1, CDH11, COL1A2, COL3A1, CRIM1, DKK3, EFEMP1, EMP1, FN1, LAMA4, MMP2, PODXL, VCAN
SENGUPTA NASOPHARYNGEAL CARCINOMA UP	tumor	other		Genes up-regulated in nsopharyngeal carcinoma relative to the normal tissue.	MSigDBv3.0 CGP	283	15	2.6	6.5	5.45E-08	0.000349	3.76E-06	CDH11, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, FBN1, FN1, GATA6, GJA1, ITGAV, LAMB1, POSTN, SULF1, VCAN
CAGGTG V$E12 Q6	TF	TCF3		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CAGGTG which matches annotation for TCF3: transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	MSigDBv3.0 TFT	1839	41	16.8	2.9	5.58E-08	0.000357	3.81E-06	A4GALT, ALDH1A2, AQP1, BMP6, CD9, CDH13, COL1A2, CRIM1, DPYSL3, DSTN, EDN1, EFEMP1, ELN, EPS8, FLNB, FLNC, GPRC5B, HYAL2, ID1, ITGA6, ITGB4, KIF1C, LAMA4, LRIG1, LTBP3, MDK, MYH10, NRG1, PALM, PODXL, PTMS, PTPRB, PVRL2, S100A16, SEMA3F, SERPINE2, SLCO2A1, SPTAN1, SULF1, TJP1, TNFRSF21
ONDER CDH1 SIGNALING VIA CTNNB1	EMT	gene	CDH1	Genes changed in HMLE cells (mmortalized nontransformed mammary epithelium) after RNAi knockdown of both CDH1 [Gene ID=999] and CTNNB1 [Gene ID=1499], compared to the knockdown of CDH1 alone.	MSigDBv3.0 CGP	83	9	0.8	13.8	6.77E-08	0.000433	4.54E-06	BGN, CDH11, COL1A2, FBN1, IGFBP7, PODXL, POSTN, SERPINE1, VCAN
MULTICELLULAR ORGANISMAL DEVELOPMENT	others			Genes annotated by the GO term GO:0007275. The biological process whose specific outcome is the progression of an organism over time from an initial condition (e.g. a zygote or a young adult) to a later condition (e.g. a multicellular animal or an aged adult).	MSigDBv3.0 BP	1035	29	9.5	3.5	6.79E-08	0.000434	4.54E-06	AGRN, ANGPTL2, ANXA2, CD9, CDH13, CLEC3B, COL1A2, COL4A2, COL5A2, CRIM1, CTGF, DPYSL3, ELN, EMP1, ENG, EPHB4, FBN1, FOXC1, GATA4, GATA6, LAMB1, LEPR, MDK, MEST, POSTN, ROBO4, STAB1, TIE1, VCAN

SYSTEM DEVELOPMENT	others			Genes annotated by the GO term GO:0048731. The process whose specific outcome is the progression of an organismal system over time, from its formation to the mature structure. A system is a regularly interacting or interdependent group of organs or tissues that work together to carry out a given biological process.	MSigDBv3.0 BP	853	26	7.8	3.8	6.90E-08	0.000441	4.57E-06	AGRN, ANXA2, CD9, CDH13, CLEC3B, COL1A2, COL4A2, COL5A2, CRIM1, CTGF, DPYSL3, ELN, EMP1, ENG, EPHB4, FBN1, FOXC1, GATA4, GATA6, LAMB1, MDK, MEST, POSTN, ROBO4, STAB1, TIE1
MAHAJAN RESPONSE TO IL1A DN	others			Genes down-regulated in corneal fibroblasts after treatment with IL1A [Gene ID=3552].	MSigDBv3.0 CGP	61	8	0.6	17.1	8.20E-08	0.000524	5.38E-06	CTGF, EPHB4, LAMA4, MYH10, PLS3, POSTN, SLC29A1, VCAN
CHIANG LIVER CANCER SUBCLASS CTNNB1 DN	tumor	other		Top 200 marker genes down-regulated in the 'CTNNB1' subclass of hepatocellular carcinoma (HCC); characterized by activated CTNNB1 [Gene ID=1499].	MSigDBv3.0 CGP	143	11	1.3	9.6	8.41E-08	0.000537	5.45E-06	ADAMTS1, BGN, COL1A2, COL3A1, COL5A1, EFEMP1, GATA6, PLTP, SERPINE1, SERPINE2, SULF1
WILCOX PRESPONSE TO ROGESTERONE DN	signaling	progesterone		Genes down-regulated in primary cultures of ovarian surface epithlium cells exposed to progesterone [PubChem=5994] for 5 days.	MSigDBv3.0 CGP	63	8	0.6	16.4	1.06E-07	0.000679	6.82E-06	COL1A2, COL5A2, COL6A1, FAM38A, FN1, LOXL2, MMP2, PLEC
PLASMA MEMBRANE	ECM	adhesion	membrane	Genes annotated by the GO term GO:0005886. The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.	MSigDBv3.0 CC	1390	34	12.7	3.1	1.14E-07	0.00073	7.27E-06	ANXA2, AQP1, ATP1A1, BCAM, CAV1, CD151, CDC42BPB, CDH13, CDH5, CTGF, ENG, EPHB4, GJA1, GOLM1, IL1R1, ITGA9, ITGB4, LAMB1, LRRC32, MUC1, PALM, PODXL, PTPRB, PTRF, PVRL2, SCARB2, SLC29A1, SLC9A3R2, SLCO2A1, STAB1, TEK, TIE1, TJP1, TM4SF1
CROMER TUMORIGENESIS UP	tumor	other		Tumorigenesis markers of head and neck squamous cell carcinoma (HNSCC): up-regulated in the 'early' tumors vs normal samples.	MSigDBv3.0 CGP	44	7	0.4	21.3	1.38E-07	0.000881	8.69E-06	COL1A2, COL3A1, COL4A2, COL5A2, FN1, POSTN, SERPINE1
RODWELL AGING KIDNEY UP	others			Genes whose expression increases with age in normal kidney.	MSigDBv3.0 CGP	349	16	3.2	5.6	1.43E-07	0.000911	8.90E-06	ANXA2, CDH11, COL1A2, COL3A1, COL5A1, CRIP1, DKK3, FBN1, FN1, FSCN1, MYOF, SERPINE2, STAB1, TXNDC5, VCAN, VIM
BROWNE HCMV INFECTION 18HR DN	others			Genes down-regulated in primary fibroblast cell culture after infection with HCMV (AD169 strain) at 18 h time point that were not down-regulated at the previous time point, 16 h.	MSigDBv3.0 CGP	186	12	1.7	7.9	1.49E-07	0.000952	9.22E-06	ANGPTL2, ANXA2, COL3A1, COL6A1, COL6A2, GAS6, ID1, LRRC32, PLXND1, PTGIS, PTRF, VCAN
DEBIASI APOPTOSIS BY REOVIRUS INFECTION DN	others			Genes down-regulated in HEK293 cells (embryonic kidney) at 6 h, 12 h or 24 h after infection with reovirus strain T3A (known as a strong inducer of apoptosis).	MSigDBv3.0 CGP	226	13	2.1	7.1	1.70E-07	0.00108	1.03E-05	AGRN, CD9, COL4A2, EPHB4, FLNC, FSCN1, ITGA6, LAMB2, PLEC, PODXL, PPP2R5B, SLC29A1, VCAN
SENESE HDAC1 AND HDAC2 TARGETS DN	tumor	other		Genes down-regulated in U2OS cells (osteosarcoma) upon knockdown of both HDAC1 and HDAC2 [Gene ID=3065, 3066] by RNAi.	MSigDBv3.0 CGP	226	13	2.1	7.1	1.70E-07	0.00108	1.03E-05	AQP1, CAV1, COL3A1, COL5A2, CXCR7, DSTN, FSTL1, IGFBP7, LAMB2, LTBP3, PLS3, SCARA3, SYNPO
module 23	others	metabolism		Genes in module_23: Liver genes - Metabolism and xenobiotics	MSigDBv3.0 CM	555	20	5.1	4.4	1.90E-07	0.00121	1.12E-05	CD151, CD34, CFH, CLEC3B, COL6A1, DCHS1, ECM1, ELN, ENG, FBXL7, FN1, HSPG2, IFI27, LAMB2, MAOA, MUC1, PVRL2, SERPINE1, STAB1, TNXB
VANHARANTA UTERINE FIBROID UP	others			Genes up-regulated in uterine fibroids vs normal myometrium samples.	MSigDBv3.0 CGP	46	7	0.4	20.2	1.90E-07	0.00121	1.12E-05	COL3A1, COL4A2, COL5A2, FN1, LOXL2, MEST, SULF1
AMUNDSON POOR SURVIVAL AFTER GAMMA RADIATION 2G	tumor	other	survival	Genes with basal expression distinguishing NCI-60 cell lines with poor survival after 2 Gy gamma irradiation.	MSigDBv3.0 CGP	155	11	1.4	8.8	1.91E-07	0.00122	1.12E-05	AGRN, ANXA2, CDC42BPB, ITGAV, KIF1C, LAMB2, PLK2, PLS3, PTMS, S100A10, WWTR1
BROWNE HCMV INFECTION 48HR DN	others			Genes down-regulated in primary fibroblast cell culture after infection with HCMV (AD169 strain) at 48 h time point that were not down-regulated at the previous time point, 24 h.	MSigDBv3.0 CGP	503	19	4.6	4.6	1.91E-07	0.00122	1.12E-05	ANXA2, CD151, CFH, COL6A1, COL6A2, EFEMP1, FN1, GJA1, HEG1, HSPG2, LAMB1, LOXL2, MUC1, POSTN, PTRF, RNASE1, SLCO2A1, SULF1, TJP1
RUIZ TNC TARGETS UP	tumor	other		Genes up-regulated in T98G cells (glioblastoma) by TNC [Gene ID=3371].	MSigDBv3.0 CGP	156	11	1.4	8.7	2.04E-07	0.0013	1.18E-05	CDH11, COL1A2, COL3A1, COL5A2, IGFBP7, IL1R1, LRIG1, LTBP3, MAGED1, PLK2, TM4SF1
LE SKI TARGETS UP	EMT	breast cells	metastasis	Selected genes implicated in metastasis and epithelial-to-mesenchymal transition (EMT) which were up-regulated in MDA-MB-231 cells (breast cancer) upon knockdown of SKI [Gene ID=6497] by RNAi.	MSigDBv3.0 CGP	16	5	0.1	50.6	2.45E-07	0.00156	1.41E-05	ADAMTS1, CDH11, ITGB4, NRG1, SERPINE2
RODRIGUES NTN1 TARGETS DN	tumor	other		Genes down-regulated in HCT8/S11 cells (colon cancer) engineered to stably express NTN1 [Gene ID=1630] off a plasmid vector.	MSigDBv3.0 CGP	159	11	1.5	8.5	2.48E-07	0.00158	1.41E-05	BCAM, FLNB, FN1, FSCN1, HSPG2, ID1, ITGB4, MYOF, PVRL2, RBMS2, TNFRSF21
URS ADIPOCYTE DIFFERENTIATION DN	others			Genes down-regulated in primary adipocytes compared to preadipocytes.	MSigDBv3.0 CGP	30	6	0.3	28	2.68E-07	0.00171	1.51E-05	COL3A1, COL4A2, COL5A1, COL6A1, FN1, MMP2
MULLIGHAN MLL SIGNATURE 2 DN	tumor	other		The 'MLL signature 2': genes down-regulated in pediatric AML (acute myeloid leukemia) with rearranged MLL [Gene ID=4297] compared to the AML cases with intact MLL and NPM1 [Gene ID=4869].	MSigDBv3.0 CGP	279	14	2.6	6.1	3.00E-07	0.00192	1.68E-05	AGRN, CD34, FSCN1, HYAL2, ITGAV, LAMB2, MDK, MMP2, PTRF, SERPINE2, SLC9A3R2, TIE1, TM4SF1, TNFRSF21
BERTUCCI MEDULLARY VS DUCTAL BREAST CANCER DN	tumor	breast	MBC vs DBD	Genes down-regulated in medullary breast cancer (MBC) relative to ductal breast cancer (DBD).	MSigDBv3.0 CGP	165	11	1.5	8.2	3.60E-07	0.00229	2.00E-05	ANO1, AQP1, BGN, CAV1, FLNC, FSTL1, HSPG2, LIMS2, MYH10, PERP, PTRF
VART KSHV INFECTION ANGIOGENIC MARKERS UP	others			Angiogenic markers up-regulated in lymph endothelial cells upon infection with KSHV (Kaposi's sarcoma herpes virus).	MSigDBv3.0 CGP	166	11	1.5	8.1	3.82E-07	0.00244	2.10E-05	ANGPTL2, COL4A2, ENG, HEG1, ITGAV, MMP2, NOS3, ROBO4, STAB1, TEK, TIE1

BAELDE DIABETIC NEPHROPATHY UP	others			Top 50 up-regulated genes in glomeruli from kidneys with diabetic nephropathy (type 2 diabetes mellitus).	MSigDBv3.0 CGP	32	6	0.3	25.8	4.03E-07	0.00256	2.20E-05	AQP1, CD34, CLEC3B, GAS6, HYAL2, TEK
module 513	ECM	component		Genes in module_513: Collagen and collagen binding proteins	MSigDBv3.0 CM	8	4	0.1	110.7	4.62E-07	0.00295	2.50E-05	COL3A1, COL5A1, COL5A2, FN1
PLASMA MEMBRANE PART	ECM	adhesion	membrane	Genes annotated by the GO term GO:0044459. Any constituent part of the plasma membrane, the membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.	MSigDBv3.0 CC	1138	29	10.4	3.2	4.97E-07	0.00317	2.67E-05	AQP1, ATP1A1, BCAM, CAV1, CD151, CDC42BPB, CDH13, ENG, EPHB4, GJA1, GOLM1, IL1R1, ITGA9, ITGB4, LAMB1, LRRC32, MUC1, PALM, PODXL, PTPRB, PTRF, SCARB2, SLC29A1, SLCO2A1, STAB1, TEK, TIE1, TJP1, TM4SF1
COLIN PILOCYTIC ASTROCYTOMA VS GLIOBLASTOMA UP	tumor	other		Genes up-regulated in pilocytic astrocytoma compared to glioblastoma samples.	MSigDBv3.0 CGP	34	6	0.3	24	5.88E-07	0.00375	3.13E-05	ANGPTL2, DKK3, GPRC5B, PLA2G2A, SERPINE2, TNFRSF21
BLALOCK ALZHEIMERS DISEASE UP	others			Genes up-regulated in brain from patients with Alzheimer's disease.	MSigDBv3.0 CGP	1709	37	15.7	2.8	6.03E-07	0.00384	3.18E-05	AGRN, ALDH1A2, ANGPTL2, ANXA2, AQP1, BCAM, BGN, COL1A2, COL6A2, CXCR7, DKK3, DPYSL3, EFEMP1, EMP1, EPS8, FBN1, FBXL7, FLNC, GJA1, GPRC5B, IL1R1, ITGA6, ITGB4, LAMA4, LTBP3, MMP2, MRC2, MUC1, NFE2L1, PLEC, PTGIS, PTRF, RBMS2, SEMA3F, TNXB, VCAN, WWTR1
VERRECCHIA RESPONSE TO TGFB1 C2	signaling	TGFB	ECM	Cluster 2: ECM related genes up-regulated in dermal fibroblasts within 30 min after TGFB1 [Gene ID=7040] addition; reached a plateau after that.	MSigDBv3.0 CGP	19	5	0.2	39.8	6.38E-07	0.00406	3.34E-05	COL1A2, COL3A1, COL6A1, FN1, RHOC
HELLEBREKERS SILENCED DURING TUMOR ANGIOGENESIS	others			Genes down-regulated in tumor-conditioned vs quiescent endothelial cells and up-regulated upon treatment with decitabine and TSA [PubChem=451668, 5562].	MSigDBv3.0 CGP	56	7	0.5	16.1	7.61E-07	0.00484	3.95E-05	COL4A2, COL6A1, DKK3, FBN1, IGFBP7, SERPINE2, VCAN
BEGUM TARGETS OF PAX3 FOXO1 FUSION DN	tumor	other		Genes down-regulated in SaOS-2 cells (osteosarcoma) upon expression of PAX3-FOXO1 [Gene ID=5077, 2308] fusion protein off an adenoviral vector.	MSigDBv3.0 CGP	36	6	0.3	22.4	8.39E-07	0.00534	4.32E-05	COL5A1, DKK3, FLNB, ID1, ITGB4, SERPINE1
BASEMENT MEMBRANE	ECM	component		Genes annotated by the GO term GO:0005604. A thin layer of dense material found in various animal tissues interposed between the cells and the adjacent connective tissue. It consists of the basal lamina plus an associated layer of reticulin fibers.	MSigDBv3.0 CC	37	6	0.3	21.7	9.94E-07	0.00633	5.08E-05	AGRN, COL4A2, FBN1, LAMA4, LAMB1, LAMB2
JAATINEN HEMATOPOIETIC STEM CELL UP	others	stem cell	CD133	Genes up-regulated in CD133+ [Gene ID=8842] cells (hematopoietic stem cells, HSC) compared to the CD133- cells.	MSigDBv3.0 CGP	310	14	2.8	5.5	1.06E-06	0.00676	5.39E-05	CD34, CFH, COL5A1, CRIM1, DPYSL3, EMP1, FGD5, HSPB1, IGFBP7, ITGA9, MEST, MMP28, PLS3, TNFRSF21
TGANTCA V$AP1 C	TF	JUN		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGANTCA which matches annotation for JUN: jun oncogene	MSigDBv3.0 TFT	862	24	7.9	3.4	1.18E-06	0.00749	5.92E-05	ADAM15, CD151, CDH5, COL5A2, DSTN, ECM1, EMP1, FLNC, GJA1, HSPG2, IL1R1, ITGB4, LPHN2, LTBP3, MAGED1, MMRN2, NRG1, PERP, PTMS, PTRF, RHOC, S100A10, SYNPO, TNXB
BROWNE HCMV INFECTION 24HR DN	others			Genes down-regulated in primary fibroblast cell culture after infection with HCMV (AD169 strain) at 24 h time point that were not down-regulated at the previous time point, 20 h.	MSigDBv3.0 CGP	150	10	1.4	8.1	1.24E-06	0.0079	6.20E-05	CAV1, CD59, CDH13, COL5A2, CRIM1, FBN1, GAS6, LAMA4, MEST, S100A10
KOKKINAKIS METHIONINE DEPRIVATION 96HR UP	tumor	other		Genes up-regulated in MEWO cells (melanoma) after 96 h of methionine [PubChem=876] deprivation.	MSigDBv3.0 CGP	119	9	1.1	9.3	1.50E-06	0.00956	7.45E-05	BGN, CAV1, GJA1, HSPB1, IGFBP7, IL1R1, MMP2, PERP, SPTAN1
module 291	tumor	other		Genes in module_291: B-cell malignancies expression clusters	MSigDBv3.0 CM	62	7	0.6	14.3	1.54E-06	0.0098	7.58E-05	CDH11, COL1A2, FAM38A, FN1, IFI27, NRG1, POSTN
GGGTGGRR V$PAX4 03	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GGGTGGRR which matches annotation for PAX4: paired box gene 4	MSigDBv3.0 TFT	1005	26	9.2	3.2	1.59E-06	0.0101	7.76E-05	CRIM1, ELN, FLNC, GATA6, HSPG2, HYAL2, ITGA6, KIF1C, LAMB2, MAGED1, MMP28, NFE2L1, NOS3, NRG1, NTN1, PLS3, PPP2R5B, PTMS, PTRF, RBMS2, S100A10, S100A16, SERPINE1, SPTAN1, TNXB, VIM
REACTOME SIGNALING BY PDGF	signaling	PDGF		Genes involved in Signaling by PDGF	MSigDBv3.0 CP:REACTOME	63	7	0.6	14.1	1.72E-06	0.0109	8.31E-05	COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A1, COL6A2
SENESE HDAC2 TARGETS DN	tumor	other		Genes down-regulated in U2OS cells (osteosarcoma) upon knockdown of HDAC2 [Gene ID=3066] by RNAi.	MSigDBv3.0 CGP	121	9	1.1	9.1	1.73E-06	0.011	8.31E-05	AQP1, BCAM, CDH11, COL3A1, COL5A2, CXCR7, EDN1, IGFBP7, SCARA3

MEMBRANE	ECM	adhesion	membrane	Genes annotated by the GO term GO:0016020. Double layer of lipid molecules that encloses all cells, and, in eukaryotes, many organelles; may be a single or double lipid bilayer; also includes associated proteins.	MSigDBv3.0 CC	1939	39	17.8	2.6	1.77E-06	0.0112	8.44E-05	ANXA2, AQP1, ATP1A1, BCAM, CAV1, CD151, CDC42BPB, CDH13, CDH5, CRIM1, CTGF, EMP1, ENG, EPHB4, GJA1, GOLM1, GPR116, IL1R1, ITGA9, ITGB4, LAMB1, LPHN2, LRRC32, MUC1, PALM, PODXL, PTPRB, PTRF, PVRL2, ROBO4, SCARB2, SLC29A1, SLC9A3R2, SLCO2A1, STAB1, TEK, TIE1, TJP1, TM4SF1
module 33	others			Genes in module_33: Immune/stress response genes	MSigDBv3.0 CM	372	15	3.4	4.9	1.78E-06	0.0113	8.45E-05	CD9, COL6A1, ELN, EMP1, FBLN2, GJA1, HSPG2, IL1R1, ITGA6, MAOA, MEST, MUC1, NRG1, PTMS, STAB1
ANATOMICAL STRUCTURE MORPHOGENESIS	others			Genes annotated by the GO term GO:0009653. The process by which anatomical structures are generated and organized. Morphogenesis pertains to the creation of form.	MSigDBv3.0 BP	373	15	3.4	4.9	1.84E-06	0.0117	8.67E-05	CD9, CDC42BPB, CDH13, COL4A2, DKK3, ELN, ENG, EPHB4, FGD5, FOXC1, LAMB1, NFE2L1, ROBO4, SFRP5, STAB1
module 174	others			Genes in module_174	MSigDBv3.0 CM	91	8	0.8	10.9	1.88E-06	0.0119	8.75E-05	CDH11, COL1A2, ENG, FAM38A, FN1, IFI27, NRG1, POSTN
CASTELLANO NRAS TARGETS UP	others			Genes up-regulated in MEF cells (embryonic fibroblast) isolated from NRAS [Gene ID=4893] knockout mice.	MSigDBv3.0 CGP	65	7	0.6	13.6	2.13E-06	0.0135	9.88E-05	CFH, CRIP2, GJA1, MEST, PERP, PLTP, SERPINE2
EXTRACELLULAR SPACE	ECM	component		Genes annotated by the GO term GO:0005615. That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.	MSigDBv3.0 CC	239	12	2.2	6.1	2.16E-06	0.0137	9.93E-05	ANGPTL2, CDH13, CFH, DKK2, DKK3, EDN1, FBN1, FSTL1, LOXL2, MMP2, SEMA3F, SFRP5
YAGI AML WITH T 8 21 TRANSLOCATION	tumor	other		Genes specifically expressed in samples from patients with pediatric AML (acute myeloid leukemia) bearing t(8;21) translocation.	MSigDBv3.0 CGP	378	15	3.5	4.8	2.17E-06	0.0138	9.93E-05	AGRN, BCAM, CAV1, CD34, CXCR7, FSCN1, ITGB4, MDK, PALM, PLTP, PLXND1, RNASE1, SERPINE2, TEK, TNFRSF21
LINDGREN BLADDER CANCER HIGH RECURRENCE	tumor	other		Genes up-regulated among the high recurrence rate urothelial cell carcinoma (UCC) tumors.	MSigDBv3.0 CGP	43	6	0.4	18.1	2.49E-06	0.0158	0.000113	COL1A2, COL4A2, COL5A2, CRIP1, LAMA4, PTMS
MARCHINI TRABECTEDIN RESISTANCE DN	tumor	resistance	trabectedin	Genes down-regulated in chondrosarcoma and ovarian carcinoma cell lines which developed resistance to trabectedin [PubChem=3199].	MSigDBv3.0 CGP	45	6	0.4	17.2	3.28E-06	0.0208	0.000148	BCAM, CDH13, COL3A1, COL4A2, FSTL1, IGFBP7
module 241	tumor	other		Genes in module_241	MSigDBv3.0 CM	70	7	0.6	12.5	3.53E-06	0.0224	0.000158	CDH11, COL1A2, FAM38A, FN1, IFI27, NRG1, POSTN
module 79	others			Genes in module_79	MSigDBv3.0 CM	99	8	0.9	9.9	3.55E-06	0.0225	0.000158	CD151, CDH13, FN1, GAS6, GATA6, IL1R1, MMP2, VIM
KOKKINAKIS METHIONINE DEPRIVATION 48HR UP	tumor	other		Genes up-regulated in MEWO cells (melanoma) after 48h of methionine [PubChem=876] deprivation.	MSigDBv3.0 CGP	134	9	1.2	8.2	4.03E-06	0.0256	0.000178	BGN, CAV1, GJA1, HSPB1, IGFBP7, IL1R1, MMP2, PERP, SPTAN1
EXTRACELLULAR MATRIX STRUCTURAL CONSTITUENT	ECM	component		Genes annotated by the GO term GO:0005201. The action of a molecule that contributes to the structural integrity of the extracellular matrix.	MSigDBv3.0 MF	27	5	0.2	25.3	4.17E-06	0.0265	0.000183	COL4A2, FBLN2, FBN1, LAMA4, LAMB1
MEMBRANE PART	ECM	adhesion	membrane	Genes annotated by the GO term GO:0044425. Any constituent part of a membrane, a double layer of lipid molecules that encloses all cells, and, in eukaryotes, many organelles; may be a single or double lipid bilayer; also includes associated proteins.	MSigDBv3.0 CC	1630	34	14.9	2.6	4.33E-06	0.0275	0.000189	AQP1, ATP1A1, BCAM, CAV1, CD151, CDC42BPB, CDH13, CRIM1, EMP1, ENG, EPHB4, GJA1, GOLM1, GPR116, IL1R1, ITGA9, ITGB4, LAMB1, LPHN2, LRRC32, MUC1, PALM, PODXL, PTPRB, PTRF, ROBO4, SCARB2, SLC29A1, SLCO2A1, STAB1, TEK, TIE1, TJP1, TM4SF1
CAIRO HEPATOBLASTOMA CLASSES DN	tumor	other		Genes down-regulated in robust Cluster 2 (rC2) of hepatoblastoma samples compared to those in the robust Cluster 1 (rC1).	MSigDBv3.0 CGP	213	11	2	6.2	4.42E-06	0.028	0.000191	CD59, DKK3, ECM1, ENG, GAS6, IL1R1, LIMS2, MMRN2, PTPRB, SYNPO, TJP1
LOPEZ MBD TARGETS	tumor	other		Genes up-regulated in HeLa cells (cervical cancer) after simultaneus knockdown of all three MBD (methyl-CpG binding domain) proteins MeCP2, MBD1 and MBD2 [Gene ID=4204, 4152, 8932] by RNAi.	MSigDBv3.0 CGP	868	23	8	3.2	4.58E-06	0.029	0.000197	CDH5, COL4A2, CRIM1, DCTN6, ECM1, EHD2, ENG, EPHB4, FAM38A, FN1, HSPG2, IL1R1, ITFG3, LTBP3, MMP2, MMRN2, NPDC1, PSMD9, RHOC, S100A10, SCARB2, SERPINE1, SPTAN1
ACACTGG,MIR-199A,MIR-199B	microRNA			Targets of MicroRNA ACACTGG,MIR-199A,MIR-199B	MSigDBv3.0 MIR	137	9	1.3	8	4.84E-06	0.0307	0.000206	BCAM, CAV1, CTGF, HMCN1, NFE2L1, PLXND1, PODXL, PVRL2, SULF1
SIMBULAN UV RESPONSE IMMORTALIZED DN	others			Genes down-regulated in response to UVB radiation in HFK cells (keratinocytes) immortalized by overexpression of HPV E6 and E7 viral oncogenes.	MSigDBv3.0 CGP	28	5	0.3	24.2	5.04E-06	0.0319	0.000214	EMP1, FN1, ID1, ITGA6, PLEC
GAUSSMANN MLL AF4 FUSION TARGETS E UP	tumor	other		Up-regulated genes from the set E (Fig. 5a): specific signature shared by cells expressing either MLL-AF4 [Gene ID=4297, 4299] or AF4-MLL fusion proteins alone, and those expressing both fusion proteins.	MSigDBv3.0 CGP	74	7	0.7	11.7	5.14E-06	0.0326	0.000215	CD34, CDH11, CRIP1, NTN1, POSTN, S100A10, SULF1
TURASHVILI BREAST DUCTAL CARCINOMA VS LOBULAR NORMAL UP	tumor	breast	ductal vs normal	Genes up-regulated in ductal carcinoma vs normal lobular breast cells.	MSigDBv3.0 CGP	74	7	0.7	11.7	5.14E-06	0.0326	0.000215	COL1A2, COL3A1, COL5A2, FBN1, FN1, SULF1, VCAN

ZHANG PROLIFERATING VS QUIESCENT	others			Genes up-regulated in HDMEC cells (microvascular endothelium): proliferating vs quiescent cells.	MSigDBv3.0 CGP	49	6	0.4	15.6	5.46E-06	0.0346	0.000227	CTGF, HSPB1, ITGA6, ITGAV, TEK, TIE1
RODRIGUES THYROID CARCINOMA POORLY DIFFERENTIATED DN	tumor	other		Genes down-regulated in poorly differentiated thyroid carcinoma (PDTC) compared to normal thyroid tissue.	MSigDBv3.0 CGP	752	21	6.9	3.4	5.56E-06	0.0352	0.00023	ATP1A1, BCAM, CD59, COL3A1, COL4A2, CTGF, DPYSL3, EMP1, FBN1, FLNB, GJA1, LAMA4, LEPR, LRIG1, LTBP3, MMRN2, PODXL, PTPRB, SCARB2, SLC29A1, VIM
GGGAGGRR V$MAZ Q6	TF	MYC	MAZ:MYC	Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GGGAGGRR which matches annotation for MAZ: MYC-associated zinc finger protein (purine-binding transcription factor)	MSigDBv3.0 TFT	1729	35	15.8	2.5	5.91E-06	0.0375	0.000243	ADAM15, ADAMTS1, ALDH1A2, AQP1, ATP1A1, CD151, COL1A2, COL5A2, CTGF, DKK2, DOCK6, FBN1, FLNC, HSPB1, HSPG2, ID1, KIF1C, MAGED1, MDK, MMP2, MRC2, NPDC1, NRG1, PLS3, POSTN, PTMS, PTRF, PVRL2, RHOC, ROBO4, S100A16, SLCO2A1, STAB1, TNXB, VIM
CYTOPLASM ORGANIZATION AND BIOGENESIS	others			Genes annotated by the GO term GO:0007028. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of the cytoplasm and its components.	MSigDBv3.0 BP	14	4	0.1	44.3	6.33E-06	0.0401	0.000255	CD9, GJA1, ITGA6, TJP1
MAHADEVAN GIST MORPHOLOGICAL SWITCH	tumor	resistance	imatinib-morphological change	Genes up-regulated in the GIST (gastrointestinal stromal tumor) cell line resistant to imatinib [PubChem=5291] that may correlate with the morphological switch in these cells.	MSigDBv3.0 CGP	14	4	0.1	44.3	6.33E-06	0.0401	0.000255	CDH13, CTGF, FSCN1, MMP2
ZIRN TRETINOIN RESPONSE UP	tumor	other		Genes up-regulated in MS427 cells (Wilms tumor with normal WT1 [Gene ID=7490]) after treatment with 10 microM tretinoin (ATRA) [PubChem=5538] for 24 h.	MSigDBv3.0 CGP	14	4	0.1	44.3	6.33E-06	0.0401	0.000255	CTGF, LAMA4, PLK2, SLCO2A1
FRIDMAN SENESCENCE UP	others	senescent		Genes up-regulated in senescent cells.	MSigDBv3.0 CGP	77	7	0.7	11.2	6.72E-06	0.0425	0.000269	COL1A2, CTGF, FN1, IGFBP7, NRG1, SERPINE1, VIM
INTEGRAL TO MEMBRANE	ECM	adhesion	membrane	Genes annotated by the GO term GO:0016021. Penetrating at least one phospholipid bilayer of a membrane. May also refer to the state of being buried in the bilayer with no exposure outside the bilayer. When used to describe a protein, indicates that all or part of the peptide sequence is embedded in the membrane.	MSigDBv3.0 CC	1300	29	11.9	2.8	7.01E-06	0.0444	0.000279	AQP1, ATP1A1, BCAM, CAV1, CD151, CRIM1, EMP1, ENG, EPHB4, GJA1, GOLM1, GPR116, IL1R1, ITGA9, ITGB4, LPHN2, LRRC32, MUC1, PALM, PODXL, PTPRB, ROBO4, SCARB2, SLC29A1, SLCO2A1, STAB1, TEK, TIE1, TM4SF1
RIGGI EWING SARCOMA PROGENITOR DN	others	mesenchymal stem cells		Genes down-regulated in mesenchymal stem cells (MSC) engineered to express EWS-FLI1 [Gene ID=2130, 2321] fusion protein.	MSigDBv3.0 CGP	182	10	1.7	6.6	7.06E-06	0.0446	0.000279	COL6A2, DPYSL3, ECM1, GATA6, HEG1, IL1R1, LAMA4, PTGIS, SCARA3, VCAN
module 524	cytoskeleton			Genes in module_524: Actin cytoskeleton binding	MSigDBv3.0 CM	30	5	0.3	22.2	7.20E-06	0.0455	0.000281	DSTN, FLNB, FLNC, PLS3, SPTAN1
SIMBULAN UV RESPONSE NORMAL DN	others			Genes down-regulated in HFK cells (primary keratinocytes) in response to UVB irradiation.	MSigDBv3.0 CGP	30	5	0.3	22.2	7.20E-06	0.0455	0.000281	EMP1, ID1, ITGA6, ITGB4, PLEC
HELLER HDAC TARGETS UP	tumor	other		Genes up-regulated in at least one of three multiple myeloma (MM) cell lines by TSA [PubChem=5562].	MSigDBv3.0 CGP	269	12	2.5	5.4	7.26E-06	0.0459	0.000281	ADAM15, AGRN, CD9, CFH, CRIP2, DOCK6, FN1, FSCN1, GATA4, ITGA6, MAOA, PLK2
ORGAN MORPHOGENESIS	others			Genes annotated by the GO term GO:0009887. Morphogenesis of an organ. An organ is defined as a tissue or set of tissues that work together to perform a specific function or functions. Morphogenesis is the process by which anatomical structures are generated and organized. Organs are commonly observed as visibly distinct structures, but may also exist as loosely associated clusters of cells that work together to perform a specific function or functions.	MSigDBv3.0 BP	144	9	1.3	7.6	7.27E-06	0.0459	0.000281	CDH13, COL4A2, ELN, ENG, EPHB4, FOXC1, LAMB1, ROBO4, STAB1
INTEGRAL TO PLASMA MEMBRANE	ECM	adhesion	receptor	Genes annotated by the GO term GO:0005887. Penetrating at least one phospholipid bilayer of a plasma membrane. May also refer to the state of being buried in the bilayer with no exposure outside the bilayer.	MSigDBv3.0 CC	961	24	8.8	3.1	7.61E-06	0.0481	0.000292	AQP1, ATP1A1, BCAM, CAV1, CD151, ENG, EPHB4, GJA1, GOLM1, IL1R1, ITGA9, ITGB4, LRRC32, MUC1, PALM, PODXL, PTPRB, SCARB2, SLC29A1, SLCO2A1, STAB1, TEK, TIE1, TM4SF1
RUTELLA RESPONSE TO HGF UP	others			Genes up-regulated in peripheral blood monocytes by HGF [Gene ID=3082].	MSigDBv3.0 CGP	425	15	3.9	4.2	8.97E-06	0.0567	0.000342	ANXA2, CD59, CD9, CRIM1, EMP1, FSCN1, HSPB1, IL1R1, MAOA, MMP2, MYOF, PLTP, PVRL2, SCARB2, SERPINE1
INTRINSIC TO MEMBRANE	ECM	adhesion	membrane	Genes annotated by the GO term GO:0031224. Located in a membrane such that some covalently attached portion of the gene product, for example part of a peptide sequence or some other covalently attached moiety such as a GPI anchor, spans or is embedded in one or both leaflets of the membrane.	MSigDBv3.0 CC	1318	29	12.1	2.7	9.12E-06	0.0576	0.000346	AQP1, ATP1A1, BCAM, CAV1, CD151, CRIM1, EMP1, ENG, EPHB4, GJA1, GOLM1, GPR116, IL1R1, ITGA9, ITGB4, LPHN2, LRRC32, MUC1, PALM, PODXL, PTPRB, ROBO4, SCARB2, SLC29A1, SLCO2A1, STAB1, TEK, TIE1, TM4SF1
NUYTTEN EZH2 TARGETS UP	tumor	other	EZH2	Genes up-regulated in PC3 cells (prostate cancer) after knockdown of EZH2 [Gene ID=2146] by RNAi.	MSigDBv3.0 CGP	972	24	8.9	3	9.20E-06	0.0581	0.000347	AGRN, ANXA2, CD59, CDH11, COL5A1, COL6A1, CTGF, EDN1, EFEMP1, FN1, GAS6, GATA6, GJA1, GPRC5B, MEST, NFE2L1, PLK2, PODXL, PPP2R5B, RHOC, ROBO4, SCARB2, SERPINE1, SERPINE2

V$ETS1 B	TF	ETS1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RCAGGAAGTGNNTNS which matches annotation for ETS1: v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	MSigDBv3.0 TFT	188	10	1.7	6.4	9.39E-06	0.0593	0.000352	ADAM15, DKK2, FLNC, HYAL2, KIF1C, MAGED1, MYH10, NRG1, RBMS2, S100A10
LAIHO COLORECTAL CANCER SERRATED UP	tumor	other		Genes up-regulated in serrated vs conventional colorectal carcinoma (CRC) samples.	MSigDBv3.0 CGP	113	8	1	8.6	9.52E-06	0.0601	0.000355	ANXA2, CAV1, CTGF, EMP1, IFI27, LAMB1, POSTN, TM4SF1
INTRINSIC TO PLASMA MEMBRANE	ECM	adhesion	receptor	Genes annotated by the GO term GO:0031226. Located in the plasma membrane such that some covalently attached portion of the gene product, for example part of a peptide sequence or some other covalently attached moiety such as a GPI anchor, spans or is embedded in one or both leaflets of the membrane.	MSigDBv3.0 CC	975	24	8.9	3	9.68E-06	0.0611	0.000358	AQP1, ATP1A1, BCAM, CAV1, CD151, ENG, EPHB4, GJA1, GOLM1, IL1R1, ITGA9, ITGB4, LRRC32, MUC1, PALM, PODXL, PTPRB, SCARB2, SLC29A1, SLCO2A1, STAB1, TEK, TIE1, TM4SF1
MINN LUNG UP	tumor	breast	metastasis	minn nature 2005 up in breast cancer likely to metastasize to lung	minn nature 2005 supplementary table 2	54	6	0.5	14	9.71E-06	0.0613	0.000358	COL6A1, EMP1, FSCN1, ID1, MMP2, SERPINE2
ACTIN FILAMENT BASED PROCESS	cytoskeleton			Genes annotated by the GO term GO:0030029. Any cellular process that depends upon or alters the actin cytoskeleton, that part of the cytoskeleton comprising actin filaments and their associated proteins.	MSigDBv3.0 BP	114	8	1	8.5	1.02E-05	0.0641	0.000372	CDC42BPB, DSTN, FGD5, FLNB, FSCN1, MYH10, RHOJ, TNXB
HADDAD T LYMPHOCYTE AND NK PROGENITOR UP	others			Genes up-regulated in hematopoietic progenitor cells (HPC) of T lymphocyte and NK (natural killer) lineage.	MSigDBv3.0 CGP	83	7	0.8	10.3	1.11E-05	0.0699	0.000404	CFH, COL5A1, HSPB1, LRIG1, MDK, MYH10, PTRF
DASU IL6 SIGNALING SCAR DN	signaling	IL6		Genes down-regulated in hypertrophic scar fibroblasts in response to IL6 [Gene ID=3569].	MSigDBv3.0 CGP	16	4	0.1	36.9	1.14E-05	0.0716	0.000412	CTGF, LOXL2, SERPINE1, SULF1
module 18	others			Genes in module_18	MSigDBv3.0 CM	435	15	4	4.1	1.18E-05	0.0745	0.000426	ANXA2, ATP1A1, CAV1, CD151, CRIM1, EPS8, FN1, HEG1, ITGA6, LAMB1, PLK2, SEMA3F, SERPINE1, TM4SF1, WWTR1
KEGG SMALL CELL LUNG CANCER	tumor	other		Small cell lung cancer	MSigDBv3.0 CP:KEGG	84	7	0.8	10.2	1.20E-05	0.0756	0.00043	COL4A2, FN1, ITGA6, ITGAV, LAMA4, LAMB1, LAMB2
CERVERA SDHB TARGETS 1 UP	tumor	other		Genes turned on in Hep3B cells (hepatocellular carcinoma, HCC) upon knockdown of SDHB [Gene ID=6390] by RNAi.	MSigDBv3.0 CGP	117	8	1.1	8.3	1.23E-05	0.0776	0.000439	AQP1, ARHGAP23, CXCR7, EDN1, FSTL1, GOLM1, LOXL2, MYOF
WGGAATGY V$TEF1 Q6	TF	TEAD1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif WGGAATGY which matches annotation for TEAD1: TEA domain family member 1 (SV40 transcriptional enhancer factor)	MSigDBv3.0 TFT	284	12	2.6	5.1	1.25E-05	0.0791	0.000445	CAV1, CTGF, EDN1, FSTL1, ITGB4, KIF1C, LAMB2, MDK, NRG1, PLS3, PTMS, PTRF
AMIT SERUM RESPONSE 240 MCF10A	signaling	serum	MCF10A	Genes whose expression peaked at 240 min after stimulation of MCF10A cells with serum.	MSigDBv3.0 CGP	57	6	0.5	13.1	1.33E-05	0.0841	0.00047	EMP1, PVRL2, SERPINE1, TJP1, TM4SF1, TNFRSF21
GLYCOSAMINOGLYCAN BINDING	ECM	component		Genes annotated by the GO term GO:0005539. Interacting selectively with any glycan (polysaccharide) containing a substantial proportion of aminomonosaccharide residues.	MSigDBv3.0 MF	34	5	0.3	19.2	1.37E-05	0.0861	0.000476	FSTL1, MDK, POSTN, TNXB, VCAN
module 419	others			Genes in module_419	MSigDBv3.0 CM	34	5	0.3	19.2	1.37E-05	0.0861	0.000476	DSTN, FLNB, FLNC, PLS3, SPTAN1
module 75	others			Genes in module_75: Immune response	MSigDBv3.0 CM	390	14	3.6	4.3	1.49E-05	0.0941	0.000518	CD59, CFH, CRIP1, CTGF, EDN1, EMP1, EPS8, FN1, GAS6, IFI27, IL1R1, MDK, PTMS, TEK
RUTELLA RESPONSE TO CSF2RB AND IL4 UP	others			Genes up-regulated in peripheral blood monocytes by CSF2RB (GM-CSF) [Gene ID=1437] and IL4 [Gene ID=3565].	MSigDBv3.0 CGP	339	13	3.1	4.6	1.52E-05	0.096	0.000526	ANXA2, CD59, CD9, CRIM1, CRIP1, FSCN1, GAS6, HSPB1, IL1R1, MAOA, MMP2, PVRL2, SERPINE1
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS CDC25 UP	tumor	other		Genes up-regulated in NIH3T3 cells (fibroblasts) transformed by activated KRAS [Gene ID=3845] vs those reverted to normal cells upon over-expression of a dominant negative form of CDC25 [Gene ID=5923].	MSigDBv3.0 CGP	59	6	0.5	12.7	1.63E-05	0.103	0.00056	ANGPTL2, APCDD1, CD9, GJA1, ITGA6, WWTR1
POLYSACCHARIDE BINDING	others			Genes annotated by the GO term GO:0030247. Interacting selectively with any polysaccharide.	MSigDBv3.0 MF	36	5	0.3	17.9	1.82E-05	0.115	0.000622	FSTL1, MDK, POSTN, TNXB, VCAN
SENESE HDAC3 TARGETS DN	tumor	other		Genes down-regulated in U2OS cells (osteosarcoma) upon knockdown of HDAC3 [Gene ID=8841] by RNAi.	MSigDBv3.0 CGP	508	16	4.7	3.8	1.84E-05	0.116	0.000625	BCAM, CGNL1, COL3A1, COL5A2, CRIM1, CTGF, CXCR7, DCHS1, EDN1, HEG1, KIAA1522, MAOA, PLXND1, PTRF, SCARA3, SYNPO
AMIT EGF RESPONSE 480 HELA	signaling	EGF	Hela	Genes whose expression peaked at 480 min after stimulation of HeLa cells with EGF [Gene ID=1950].	MSigDBv3.0 CGP	162	9	1.5	6.7	1.88E-05	0.118	0.000633	AGRN, COL4A2, ITGA6, PLEC, RHOC, SERPINE1, SERPINE2, TM4SF1, TNFRSF21
DAZARD UV RESPONSE CLUSTER G24	tumor	other		Cluster G24: genes induced in NHEK (normal keratinocyte) but not in SCC12B2 cells (squamous cell carcinoma) by UV-B radiation.	MSigDBv3.0 CGP	18	4	0.2	31.6	1.88E-05	0.118	0.000633	ECM1, IFI27, IL1RL1, TM4SF1
HELLER HDAC TARGETS SILENCED BY METHYLATION UP	tumor	other		Genes up-regulated in multiple myeloma (MM) cell lines treated with both decitabine [PubChem=451668] TSA [PubChem=5562].	MSigDBv3.0 CGP	399	14	3.7	4.2	1.92E-05	0.121	0.000642	AGRN, CD9, CFH, COL6A2, CRIP2, FBN1, FLNB, FN1, FSCN1, ID1, IFI27, ITGA6, PLK2, SERPINE2

RUTELLA RESPONSE TO HGF VS CSF2RB AND IL4 DN	others			Genes down-regulated in peripheral blood mononucleocytes by HGF [Gene ID=3082] compared to those regulated by CSF2RB (GM-CSF) [Gene ID=1437] and IL4 [Gene ID=3565].	MSigDBv3.0 CGP	249	11	2.3	5.3	1.93E-05	0.121	0.000642	ANXA2, CD59, CRIP1, FSCN1, GAS6, HSPB1, IL1R1, MAOA, NRG1, PVRL2, VCAN
V$GATA C	TF	GATA1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NGATAAGNMNN which matches annotation for GATA1: GATA binding protein 1 (globin transcription factor 1)	MSigDBv3.0 TFT	207	10	1.9	5.8	2.17E-05	0.136	0.000718	BMP6, CD34, EDN1, FBXL7, GATA6, GPR116, IL1RL1, PKHD1L1, PVRL2, TEK
FLECHNER BIOPSY KIDNEY TRANSPLANT OK VS DONOR UP	others			Genes diffierentially expressed in kidney biopsies from patients with well functioning kidneys more than 1-year post transplant compared to the biopsies from normal living kidney donors.	MSigDBv3.0 CGP	580	17	5.3	3.5	2.50E-05	0.157	0.000822	CD9, CDH11, CFH, COL1A2, COL3A1, DSTN, EPS8, ID1, MAOA, MYH10, MYOF, PLS3, SERPINE2, TEK, VCAN, VIM, WWTR1
REACTOME CELL SURFACE INTERACTIONS AT THE VASCULAR WALL	ECM	adhesion	membrane interact with vascalar wall	Genes involved in Cell surface interactions at the vascular wall	MSigDBv3.0 CP:REACTOME	94	7	0.9	9	2.51E-05	0.158	0.000822	CAV1, COL1A2, FN1, GAS6, ITGA6, ITGAV, TEK
RTAAACA V$FREAC2 01	TF	FOXF2		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RTAAACA which matches annotation for FOXF2: forkhead box F2	MSigDBv3.0 TFT	709	19	6.5	3.2	2.83E-05	0.178	0.000922	ANXA2, CTGF, EDN1, EFEMP1, EMP1, FSTL1, GJA1, HSPG2, MDK, NPDC1, NRG1, NTN1, PALM, PLS3, PTGIS, PTMS, SULF1, SYNPO, TEK
MOROSETTI FACIOSCAPULOHUMERAL MUSCULAR DISTROPHY UP	others			Genes up-regulated in FSHD (facioscapulohumeral muscular dystrophy) mesoangioblasts.	MSigDBv3.0 CGP	20	4	0.2	27.7	2.94E-05	0.185	0.000953	ID1, IFI27, LPHN2, POSTN
module 128	others			Genes in module_128	MSigDBv3.0 CM	97	7	0.9	8.7	3.08E-05	0.194	0.000992	CD151, CDH13, FN1, GAS6, IL1R1, MMP2, VIM
HUANG FOXA2 TARGETS DN	tumor	other		Genes down-regulated in H358 cells (lung cancer) by inducible expression of FOXA2 [GeneID=3170] in a Tet-off system.	MSigDBv3.0 CGP	40	5	0.4	15.9	3.09E-05	0.194	0.000992	COL6A1, CRIP2, ITGB4, LEPR, LOXL2
module 121	others			Genes in module_121	MSigDBv3.0 CM	98	7	0.9	8.6	3.29E-05	0.207	0.00105	CRIP1, EDN1, EMP1, EPHB4, EPS8, GAS6, MDK
module 170	others			Genes in module_170: Immune response	MSigDBv3.0 CM	99	7	0.9	8.5	3.51E-05	0.221	0.00112	CD151, CDH13, FN1, GAS6, IL1R1, MMP2, VIM
SMID BREAST CANCER NORMAL LIKE UP	tumor	breast	normal-like	Genes up-regulated in the normal-like subtype of breast cancer.	MSigDBv3.0 CGP	478	15	4.4	3.7	3.53E-05	0.222	0.00112	AQP1, CAV1, CFH, CLEC3B, EFEMP1, GPR116, ID1, IL1R1, IL33, LAMA4, LEPR, PLA2G2A, PLTP, TIE1, TNXB
BASAL LAMINA	ECM	component		Genes annotated by the GO term GO:0005605. A thin sheet of proteoglycans and glycoproteins, especially laminin, secreted by cells as an extracellular matrix.	MSigDBv3.0 CC	21	4	0.2	26	3.60E-05	0.226	0.00113	AGRN, LAMA4, LAMB1, LAMB2
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION SUSTAINED IN MONOCYTE UP	others			Genes up-regulated by RUNX1-RUNX1T1 [Gene ID=861, 862] fusion protein in normal hematopoietic progenitors; their expression was sustained in subsequently developing monocytes.	MSigDBv3.0 CGP	21	4	0.2	26	3.60E-05	0.226	0.00113	ALDH1A2, EPS8, HSPB1, TM4SF1
KYNG DNA DAMAGE UP	others			Genes changed after DNA damage in cell lines from young donors, and that had a GO annotation.	MSigDBv3.0 CGP	100	7	0.9	8.4	3.75E-05	0.235	0.00117	COL3A1, CTGF, FBLN2, FN1, ID1, SERPINE2, VIM
CROMER TUMORIGENESIS DN	tumor	other		Tumorigenesis markers of head and neck squamous cell carcinoma (HNSCC): down-regulated in the 'early' tumors vs normal samples.	MSigDBv3.0 CGP	42	5	0.4	15	3.93E-05	0.247	0.00121	CLEC3B, ECM1, EMP1, MUC1, PLA2G2A
MCGARVEY SILENCED BY METHYLATION IN COLON CANCER	tumor	other		Genes silenced in HCT116 cells (colon cancer) by methylation of CpG islands in their promoters.	MSigDBv3.0 CGP	42	5	0.4	15	3.93E-05	0.247	0.00121	DKK3, EFEMP1, FBLN2, GATA4, SFRP5
PAPASPYRIDONOS UNSTABLE ATEROSCLEROTIC PLAQUE DN	others			Genes down-regulated in unstable aterosletotic plaques compared to the stable ones.	MSigDBv3.0 CGP	42	5	0.4	15	3.93E-05	0.247	0.00121	CRIM1, DSTN, GJA1, HSPB1, PTGIS
BOS BRAIN UP	tumor	breast	metastasis	bos nature 2009 up in breast cancer likely to metastasize to brain	bos nature 2009 supplementary table 2	141	8	1.3	6.8	4.74E-05	0.298	0.00145	COL5A1, CRIP2, FSCN1, GJA1, ITGB4, LPHN2, SERPINE2, SYNPO
ACTIN CYTOSKELETON ORGANIZATION AND BIOGENESIS	others			Genes annotated by the GO term GO:0030036. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of cytoskeletal structures comprising actin filaments and their associated proteins.	MSigDBv3.0 BP	104	7	1	8.1	4.82E-05	0.303	0.00147	CDC42BPB, DSTN, FGD5, FLNB, FSCN1, RHOJ, TNXB

V$NFAT Q6	TF	NFAT		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NANWGGAAAANN which matches annotation for NFAT
 NFATC	MSigDBv3.0 TFT	183	9	1.7	5.8	4.90E-05	0.307	0.00149	COL3A1, EDN1, EMP1, GATA4, HSPG2, MAGED1, SULF1, TEK, TNXB
CARBOHYDRATE BINDING	others			Genes annotated by the GO term GO:0030246. Interacting selectively with any carbohydrate.	MSigDBv3.0 MF	72	6	0.7	10.2	5.13E-05	0.322	0.00155	CD34, FSTL1, MDK, POSTN, TNXB, VCAN
module 220	others			Genes in module_220: Developmental processes	MSigDBv3.0 CM	328	12	3	4.3	5.15E-05	0.323	0.00155	CTGF, DPYSL3, EMP1, EPS8, FBN1, GJA1, ID1, LEPR, MDK, NRG1, PTMS, TEK
HEPARIN BINDING	ECM	component		Genes annotated by the GO term GO:0008201. Interacting selectively with heparin, any member of a group of glycosaminoglycans found mainly as an intracellular component of mast cells and which consist predominantly of alternating alpha1-4-linked D-galactose and N-acetyl-D-glucosamine-6-sulfate residues.	MSigDBv3.0 MF	23	4	0.2	23.3	5.25E-05	0.33	0.00156	FSTL1, MDK, POSTN, TNXB
JEON SMAD6 TARGETS UP	signaling	SMAD		Genes up-regulated in H1299 cells (lung cancer) upon knockdown of SMAD6 [Gene ID=4091] by RNAi.	MSigDBv3.0 CGP	23	4	0.2	23.3	5.25E-05	0.33	0.00156	DKK3, FBN1, NRG1, SERPINE1
PATTERN BINDING	ECM	component		Genes annotated by the GO term GO:0001871. Interacting selectively with a repeating or polymeric structure, such as a polysaccharide or peptidoglycan.	MSigDBv3.0 MF	45	5	0.4	13.9	5.53E-05	0.346	0.00164	FSTL1, MDK, POSTN, TNXB, VCAN
module 154	cytoskeleton			Genes in module_154: Intermediate filaments	MSigDBv3.0 CM	73	6	0.7	10	5.55E-05	0.348	0.00164	CAV1, ITGA6, ITGB4, MAOA, SERPINE1, TM4SF1
BOS BRAIN DN	tumor	breast	metastasis	bos nature 2009 down in breast cancer likely to metastasize to brain	bos nature 2009 supplementary table 2	107	7	1	7.8	5.79E-05	0.363	0.0017	ADAMTS1, CAV1, CTGF, EDN1, HSPB1, LAMA4, SERPINE1
LEE NEURAL CREST STEM CELL UP	others			Genes up-regulated in the neural crest stem cells (NCS), defined as p75+/HNK1+ [Gene ID=4804, 27087].	MSigDBv3.0 CGP	146	8	1.3	6.5	6.07E-05	0.38	0.00177	BGN, COL1A2, COL3A1, IGFBP7, LAMB1, PODXL, POSTN, S100A10
BERTUCCI INVASIVE CARCINOMA DUCTAL VS LOBULAR DN	tumor	breast	IDC vs ILC	Genes down-regulated in the invasive ductal carcinoma (IDC) compared to the invasive lobular carcinoma (ILC), the two major pathological types of breast cancer.	MSigDBv3.0 CGP	46	5	0.4	13.6	6.15E-05	0.386	0.00179	CAV1, CD34, ELN, TEK, TNXB
ZHANG ANTIVIRAL RESPONSE TO RIBAVIRIN UP	tumor	other		Genes up-regulated in A549 cells (lung carcinoma) upon infection with RSV (respiratory syncytial virus) and up-regulated by further treatment with ribavirin [PubChem=5064].	MSigDBv3.0 CGP	24	4	0.2	22.1	6.26E-05	0.392	0.00181	CFH, GJA1, IFI27, MDK
JI RESPONSE TO FSH DN	tumor	other		Down-regulated in ovarian epithelial cells (MCV152) 72 hours following FSH treatment, compared to untreated	MSigDBv3.0 CGP	47	5	0.4	13.2	6.84E-05	0.428	0.00196	EMP1, FN1, ITGA6, SERPINE1, VCAN
NUTT GBM VS AO GLIOMA UP	tumor	other		Top 50 marker genes for glioblastoma multiforme (GBM), a class of high grade glioma.	MSigDBv3.0 CGP	47	5	0.4	13.2	6.84E-05	0.428	0.00196	ANXA2, ITGB4, LAMB2, RHOC, VIM
ACEVEDO LIVER CANCER UP	tumor	other		Genes up-regulated in hepatocellular carcinoma (HCC) compared to normal liver samples.	MSigDBv3.0 CGP	962	22	8.8	2.8	7.07E-05	0.442	0.00202	ADAM15, CD9, CDH5, CLEC3B, COL1A2, COL3A1, COL4A2, FOXC1, GPR116, HSPB1, IFI27, IGFBP7, ITGAV, KIF1C, LAMB1, PLS3, PLVAP, RNASE1, S100A10, SLCO2A1, TJP1, VIM
WAMUNYOKOLI OVARIAN CANCER LMP DN	tumor	other		Genes down-regulated in mucinous ovarian carcinoma tumors of low malignant potential (LMP) compared to normal ovarian surface epithelium tissue.	MSigDBv3.0 CGP	192	9	1.8	5.6	7.10E-05	0.445	0.00202	CAV1, CRIM1, DPYSL3, EFEMP1, FBXL7, FLNC, LAMA4, MYH10, SULF1
BLALOCK ALZHEIMERS DISEASE INCIPIENT UP	others			Genes up-regulated in patients at the incipient stage of Alzheimer's disease.	MSigDBv3.0 CGP	394	13	3.6	3.9	7.20E-05	0.451	0.00204	ANGPTL2, BGN, EFEMP1, EPS8, FBN1, FLNC, GJA1, ITGA6, LAMA4, PTGIS, TNXB, VCAN, WWTR1
WANG ESOPHAGUS CANCER VS NORMAL UP	tumor	other		Genes specific to esophageal adenocarcinoma (EAC) relative to normal tissue.	MSigDBv3.0 CGP	111	7	1	7.5	7.31E-05	0.457	0.00206	CD34, COL3A1, COL5A2, FN1, GPRC5B, IGFBP7, SERPINE1
module 105	others			Genes in module_105	MSigDBv3.0 CM	194	9	1.8	5.5	7.69E-05	0.481	0.00216	COL3A1, COL4A2, COL5A2, CTGF, EMP1, GJA1, HSPB1, LAMB1, VCAN
CTTTGT V$LEF1 Q2	TF	LEF1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CTTTGT which matches annotation for LEF1: lymphoid enhancer-binding factor 1	MSigDBv3.0 TFT	1481	29	13.6	2.4	7.76E-05	0.486	0.00217	ANGPTL2, AQP1, CDH11, CDH5, COL3A1, CRIM1, CRIP2, DKK2, DPYSL3, EPS8, GJA1, GPRC5B, HYAL2, LAMA4, LPHN2, LTBP3, MDK, MMRN2, MYH10, NRG1, NTN1, PALM, PLK2, PTMS, PVRL2, ROBO4, SEMA3F, TNFRSF21, VIM
module 297	others			Genes in module_297	MSigDBv3.0 CM	78	6	0.7	9.3	8.06E-05	0.504	0.00223	CAV1, ITGA6, ITGB4, MAOA, SERPINE1, TM4SF1
module 357	cytoskeleton			Genes in module_357: Intermediate filaments and keratins	MSigDBv3.0 CM	78	6	0.7	9.3	8.06E-05	0.504	0.00223	CAV1, ITGA6, ITGB4, MAOA, SERPINE1, TM4SF1
INTERCELLULAR JUNCTION ASSEMBLY	ECM	adhesion		Genes annotated by the GO term GO:0007043. The aggregation, arrangement and bonding together of a set of components to form a junction between cells.	MSigDBv3.0 BP	10	3	0.1	47.2	8.64E-05	0.541	0.00239	CD9, GJA1, TJP1

module 72	others			Genes in module_72: Testis genes	MSigDBv3.0 CM	295	11	2.7	4.4	8.98E-05	0.562	0.00247	CAV1, CLEC3B, COL1A2, COL6A2, CRIM1, ENG, FBLN2, GJA1, GPRC5B, IFI27, ITGA6
SANA RESPONSE TO IFNG DN	others			Genes down-regulated in five primary endothelial cell types (lung, aortic, iliac, dermal, and colon) by IFNG [Gene ID=3458].	MSigDBv3.0 CGP	80	6	0.7	9.1	9.29E-05	0.581	0.00253	ANGPTL2, ANXA2, CD34, GJA1, RHOC, TXNDC5
CONCANNON APOPTOSIS BY EPOXOMICIN UP	tumor	other		Genes up-regulated in SH-SY5Y cells (neuroblastoma) after treatment with epoxomicin [PubChem=3035402], a protease inhibitor causing apoptosis.	MSigDBv3.0 CGP	246	10	2.3	4.8	9.30E-05	0.581	0.00253	ALDH1A2, ANXA2, FLNC, HEG1, HSPB1, LRIG1, MEST, PLK2, SERPINE1, WWTR1
module 100	others			Genes in module_100	MSigDBv3.0 CM	528	15	4.8	3.4	0.000108	0.675	0.00293	AQP1, CDH11, CLEC3B, COL6A2, DPYSL3, FBXL7, GJA1, GPRC5B, IFI27, ITGA6, MAOA, MDK, PALM, RNASE1, VCAN
module 137	others			Genes in module_137: CNS genes	MSigDBv3.0 CM	530	15	4.9	3.4	0.000113	0.704	0.00303	AQP1, CDH11, CLEC3B, COL6A2, DPYSL3, FBXL7, GJA1, GPRC5B, IFI27, ITGA6, MAOA, MDK, PALM, RNASE1, VCAN
TARTE PLASMA CELL VS PLASMABLAST UP	others			Genes up-regulated in mature plasma cells compared with plasmablastic B lymphocytes.	MSigDBv3.0 CGP	412	13	3.8	3.7	0.000113	0.704	0.00303	CD34, CD9, FBN1, FLNB, FSCN1, FSTL1, HSPB1, MDK, PALM, RBMS2, RNASE1, TJP1, TNXB
RUGO ENVIRONMENTAL STRESS RESPONSE UP	others			Human environmental stress response (H-ESR, ESR) signature: genes up-regulated in young donors after all of the stress types tested.	MSigDBv3.0 CGP	28	4	0.3	18.4	0.000117	0.732	0.00314	COL3A1, CTGF, FN1, VIM
CLAUS PGR POSITIVE MENINGIOMA DN	tumor	other	PGR	Genes changed in meningioma samples positive for PGR [Gene ID=5241] compared to those without the receptor.	MSigDBv3.0 CGP	11	3	0.1	41.3	0.000118	0.737	0.00315	FSTL1, HEG1, TM4SF1
V$GATA Q6	TF	GATA1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif WGATARN which matches annotation for GATA1: GATA binding protein 1 (globin transcription factor 1)	MSigDBv3.0 TFT	161	8	1.5	5.9	0.00012	0.752	0.0032	BMP6, CD34, EDN1, GATA6, GPR116, PVRL2, SFRP5, TNXB
module 66	others			Genes in module_66	MSigDBv3.0 CM	535	15	4.9	3.3	0.000125	0.78	0.00331	AQP1, CDH11, CLEC3B, COL6A2, DPYSL3, FBXL7, GJA1, GPRC5B, IFI27, ITGA6, MAOA, MDK, PALM, RNASE1, VCAN
ONDER CDH1 TARGETS 2 DN	EMT	gene	CDH1	Genes down-regulated in HMLE cells (immortalized nontransformed mammary epithelium) after E-cadhedrin (CDH1) [Gene ID=999] knockdown by RNAi.	MSigDBv3.0 CGP	476	14	4.4	3.5	0.000129	0.803	0.00339	AGRN, ANO1, CD9, EDN1, FLNB, ITGA6, ITGB4, LPHN2, MAOA, NRG1, PERP, PLK2, SEMA3F, TNFRSF21
AMUNDSON POOR SURVIVAL AFTER GAMMA RADIATION 8G	tumor	other	survival	Genes with basal expression distinguishing NCI-60 cell lines with poor survival after 8 Gy gamma irradiation.	MSigDBv3.0 CGP	85	6	0.8	8.5	0.00013	0.812	0.00342	ITGAV, LAMB2, LOXL2, NFE2L1, PLK2, WWTR1
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION GRANULOCYTE UP	others			Genes up-regulated in granulocytes by RUNX1-RUNX1T1 [Gene ID=861, 862] fusion.	MSigDBv3.0 CGP	54	5	0.5	11.3	0.000134	0.835	0.0035	FSCN1, HSPB1, ID1, TIE1, TM4SF1
LU TUMOR VASCULATURE UP	others			Genes up-regulated in endothelial cells derived from invasive ovarian cancer tissue.	MSigDBv3.0 CGP	29	4	0.3	17.7	0.000135	0.843	0.0035	MUC1, POSTN, TNFRSF21, VCAN
REACTOME ADHERENS JUNCTIONS INTERACTIONS	ECM	adhesion		Genes involved in Adherens junctions interactions	MSigDBv3.0 CP:REACTOME	29	4	0.3	17.7	0.000135	0.843	0.0035	CDH11, CDH13, CDH5, PVRL2
V$AP1 Q4 01	TF	JUN		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGAGTCAN which matches annotation for JUN: jun oncogene	MSigDBv3.0 TFT	210	9	1.9	5.1	0.000141	0.877	0.00363	ADAM15, ECM1, EMP1, FSTL1, GJA1, ITGB4, LTBP3, SYNPO, TNXB
TTGTTT V$FOXO4 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TTGTTT which matches annotation for MLLT7: myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7	MSigDBv3.0 TFT	1534	29	14.1	2.3	0.000143	0.894	0.00369	ALDH1A2, CDH11, CDH5, COL1A2, CRIM1, CRIP2, EFEMP1, EMP1, FN1, FSTL1, GATA6, HSPG2, HYAL2, ID1, ITGB4, LAMA4, LPHN2, MRC2, NOS3, NRG1, NTN1, PALM, RBMS2, ROBO4, TEK, TJP1, TM4SF1, TNFRSF21, TNXB
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS CDC25 DN	tumor	other		Genes down-regulated in NIH3T3 cells (fibroblasts) transformed by activated KRAS [Gene ID=3845] vs those reverted to normal cells upon over-expression of a dominant negative form of CDC25 [Gene ID=5923].	MSigDBv3.0 CGP	55	5	0.5	11.1	0.000146	0.911	0.00375	COL6A1, IL1R1, IL1RL1, LAMA4, MAGED1
KYNG ENVIRONMENTAL STRESS RESPONSE UP	others			All common stress response genes (Human Environmental Stress Response, H-ESR).	MSigDBv3.0 CGP	30	4	0.3	17	0.000155	0.964	0.00395	COL3A1, CTGF, FN1, VIM
CAIRO HEPATOBLASTOMA UP	tumor	other		Genes up-regulated in hepatoblastoma samples compared to normal liver tissue.	MSigDBv3.0 CGP	213	9	2	5	0.000156	0.975	0.00395	BCAM, CRIM1, GJA1, HSPB1, ITGA6, MAGED1, PLVAP, PODXL, SERPINE2
INTERCELLULAR JUNCTION ASSEMBLY AND MAINTENANCE	ECM	adhesion		Genes annotated by the GO term GO:0045216. The assembly and maintenance of junctions between cells.	MSigDBv3.0 BP	12	3	0.1	36.7	0.000156	0.975	0.00395	CD9, GJA1, TJP1

REACTOME CASPASE MEDIATED CLEAVAGE OF CYTOSKELETAL PROTEINS	signaling	apoptosis		Genes involved in Caspase-mediated cleavage of cytoskeletal proteins	MSigDBv3.0 CP:REACTOME	12	3	0.1	36.7	0.000156	0.975	0.00395	PLEC, SPTAN1, VIM
ANATOMICAL STRUCTURE FORMATION	others			Genes annotated by the GO term GO:0048646. The process pertaining to the initial formation of an anatomical structure from unspecified parts. This process begins with the specific processes that contribute to the appearance of the discrete structure and ends when the structural rudiment is recognizable. An anatomical structure is any biological entity that occupies space and is distinguished from its surroundings. Anatomical structures can be macroscopic such as a carpel, or microscopic such as an acrosome.	MSigDBv3.0 BP	56	5	0.5	10.9	0.000159	0.993	0.00401	CD9, CDH13, COL4A2, ROBO4, STAB1
SMID BREAST CANCER RELAPSE IN BONE DN	tumor	breast	metastasis	Genes down-regulated in bone relapse of breast cancer.	MSigDBv3.0 CGP	316	11	2.9	4.1	0.000164	1	0.00412	BGN, COL4A2, EDN1, ELN, FOXC1, FSCN1, ITGA6, PERP, TM4SF1, TNFRSF21, WWTR1
KANG IMMORTALIZED BY TERT UP	others			Up-regulated genes in the signature of adipose stromal cells (ADSC) immortalized by forced expression of telomerase (TERT) [Gene ID=7015].	MSigDBv3.0 CGP	89	6	0.8	8.1	0.000168	1	0.00419	BGN, COL6A2, ELN, LAMB1, LEPR, POSTN
module 129	signaling			Genes in module_129: signaling	MSigDBv3.0 CM	216	9	2	4.9	0.000174	1	0.00432	CFH, DPYSL3, EFEMP1, GPRC5B, ITGA6, LEPR, MDK, NRG1, RNASE1
DASU IL6 SIGNALING SCAR UP	signaling	IL6		Genes up-regulated in hypertrophic scar fibroblasts in response to IL6 [Gene ID=3569].	MSigDBv3.0 CGP	31	4	0.3	16.4	0.000176	1	0.00437	AGRN, CLEC3B, PLEC, TNXB
GGGYGTGNY UNKNOWN	TF	unknown		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif GGGYGTGNY. Motif does not match any known transcription factor	MSigDBv3.0 TFT	492	14	4.5	3.4	0.000181	1	0.00447	ANXA2, ATP1A1, BMP6, CAV1, CDH13, CDH5, COL1A2, FLNB, ITGB4, MDK, PALM, PERP, SSSCA1, VIM
KORKOLA TERATOMA	tumor	other		Genes predicting the teratoma (T) subtype of nonseminomatous male germ cell tumors (NSGCT).	MSigDBv3.0 CGP	32	4	0.3	15.8	2.00E-04	1	0.00492	ELN, EMP1, EPS8, TM4SF1
KEGG CELL ADHESION MOLECULES CAMS	ECM	adhesion		Cell adhesion molecules (CAMs)	MSigDBv3.0 CP:KEGG	131	7	1.2	6.3	0.000206	1	0.00503	CD34, CDH5, ITGA6, ITGA9, ITGAV, PVRL2, VCAN
RIGGINS TAMOXIFEN RESISTANCE DN	tumor	resistance	ER	Genes down-regulated SUM44/LCCTam cells (breast cancer) resistant to 4-hydroxytamoxifen [PubChem=63062] relative to the parental SUM44 cells sensitive to the drug.	MSigDBv3.0 CGP	221	9	2	4.8	0.000206	1	0.00503	COL3A1, EMP1, GJA1, IFI27, LTBP3, MUC1, MYOF, SCARB2, TM4SF1
module 46	others			Genes in module_46	MSigDBv3.0 CM	385	12	3.5	3.7	0.000232	1	0.00564	CD59, CFH, CRIP1, EDN1, EMP1, EPS8, FN1, GAS6, IFI27, IL1R1, MDK, PTMS
SMID BREAST CANCER BASAL DN	tumor	breast	basal	Genes down-regulated in basal subtype of breast cancer samles.	MSigDBv3.0 CGP	702	17	6.4	2.9	0.000255	1	0.00617	ANO1, BCAM, CLEC3B, CRIP1, CRIP2, CXCR7, ECM1, FBXL7, GJA1, HSPB1, IL33, LRIG1, MAOA, MUC1, NPDC1, TNXB, TPPP3
DASU IL6 SIGNALING UP	signaling	IL6		Genes up-regulated in normal fibroblasts in response to IL6 [Gene ID=3569].	MSigDBv3.0 CGP	62	5	0.6	9.7	0.000258	1	0.00623	AGRN, COL6A1, ENG, GAS6, PLEC
FRASOR RESPONSE TO ESTRADIOL DN	tumor	other	ER	Genes down-regulated in MCF-7 cells (breast cancer) by estradiol (E2) [PubChem=5757].	MSigDBv3.0 CGP	63	5	0.6	9.6	0.000278	1	0.00669	IL1R1, LAMB1, LAMB2, MUC1, PLK2
POOLA INVASIVE BREAST CANCER DN	tumor	breast	ADHC vs ADH	Genes down-regulated in atypical ductal hyperplastic tissues from patients with (ADHC) breast cancer vs those without the cancer (ADH).	MSigDBv3.0 CGP	138	7	1.3	6	0.000284	1	0.00677	CD151, CD59, CLEC3B, DKK3, FLNB, LTBP3, LTBP4
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 10D DN	others			Genes down-regulated in CD34+ [Gene ID=947] hematopoetic cells by expression of NUP98-HOXA9 fusion [Gene ID=4928, 3205] off a retroviral vector at 10 days after transduction.	MSigDBv3.0 CGP	138	7	1.3	6	0.000284	1	0.00677	CD59, CD9, EMP1, IL1R1, MAOA, RNASE1, STAB1
STOSSI RESPONSE TO ESTRADIOL	tumor	other	ER	Genes up-regulated by estradiol (E2) [PubChem=5757] in U2OS cells (osteosarcoma) expressing ESR1 or ESR2 [[Gene ID = 2099, 2100].	MSigDBv3.0 CGP	35	4	0.3	14.3	0.000285	1	0.00678	BMP6, CD34, GJA1, ITGA6
CHANG POU5F1 TARGETS UP	tumor	other		Genes up-regulated by POU5F1 [Gene ID=5460] in bladder cancer cell lines.	MSigDBv3.0 CGP	15	3	0.1	27.5	0.000317	1	0.00743	COL3A1, COL5A1, FN1
KARAKAS TGFB1 SIGNALING	signaling	TGFB	MCF10A	Genes up-regulated by TGFB1 [Gene ID=7040] in MCF10A cells (breast cancer): both wild-type and those lacking p21 [Gene ID=1026].	MSigDBv3.0 CGP	15	3	0.1	27.5	0.000317	1	0.00743	FN1, IGFBP7, MMP2
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION SUSTAINED IN GRANULOCYTE UP	others			Genes up-regulated by RUNX1-RUNX1T1 [Gene ID=861, 862] fusion protein in normal hematopoietic progenitors; their expression was sustained in subsequently developing granulocytes.	MSigDBv3.0 CGP	15	3	0.1	27.5	0.000317	1	0.00743	HSPB1, ID1, TM4SF1
BONOME OVARIAN CANCER SURVIVAL SUBOPTIMAL DEBULKING	tumor	other	prognosis	Genes whose expression in suboptimally debulked ovarian tumors is associated with survival prognosis.	MSigDBv3.0 CGP	520	14	4.8	3.2	0.000318	1	0.00743	ADAM15, CAV1, CDH13, DCHS1, DKK2, EFEMP1, EPS8, GPR116, ITGB4, LEPR, MAOA, MYOF, PTRF, SEMA3F
VERRECCHIA DELAYED RESPONSE TO TGFB1	signaling	TGFB	ECM	ECM related genes up-regulated later than 30 min following addition of TGFB1 [Gene ID=7040] in dermal fibroblasts.	MSigDBv3.0 CGP	36	4	0.3	13.8	0.000319	1	0.00743	EPHB4, LAMB1, MMP2, SEMA3F

ALCALAY AML BY NPM1 LOCALIZATION UP	tumor	other		Genes changed in acute myeloid leukemia (AML) with respect to cellular localization of NPM1 [Gene ID=4869]: cytoplasmic vs. nucleolar.	MSigDBv3.0 CGP	141	7	1.3	5.8	0.000323	1	0.00752	CDC42BPB, CFH, DPYSL3, FOXC1, LAMB2, LRIG1, MMP2
REACTOME SEMAPHORIN INTERACTIONS	others			Genes involved in Semaphorin interactions	MSigDBv3.0 CP:REACTOME	66	5	0.6	9.1	0.000346	1	0.00801	DPYSL3, MYH10, PLXNA4, PLXND1, RHOC
V$GATA3 01	TF	GATA3		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NNGATARNG which matches annotation for GATA3: GATA binding protein 3	MSigDBv3.0 TFT	188	8	1.7	5	0.000347	1	0.00801	BMP6, CD34, EDN1, EFEMP1, HSPG2, IL1RL1, PVRL2, TNXB
BASAKI YBX1 TARGETS UP	tumor	other		Genes up-regulated in SKOC-3 cells (ovarian cancer) after YB-1 (YBX1) [Gene ID=4904] knockdown by RNAi.	MSigDBv3.0 CGP	290	10	2.7	4	0.000351	1	0.00809	CAV1, CTGF, DKK3, DPYSL3, EHD2, FBN1, FLNB, PLK2, PTRF, TNFRSF21
REACTOME GENES INVOLVED IN APOPTOTIC CLEAVAGE OF CELLULAR PROTEINS	signaling	apoptosis		Genes involved in Apoptotic cleavage of cellular proteins	MSigDBv3.0 CP:REACTOME	37	4	0.3	13.4	0.000355	1	0.00813	PLEC, SPTAN1, TJP1, VIM
module 8	others			Genes in module_8	MSigDBv3.0 CM	405	12	3.7	3.5	0.000367	1	0.00838	CAV1, CD151, COL5A2, CRIM1, EPS8, FN1, GJA1, ITGA6, MDK, MEST, SLC29A1, TM4SF1
CHEN LVAD SUPPORT OF FAILING HEART UP	others			Up-regulated genesin the left ventricle myocardium of patients with heart failure following implantation of LVAD (left ventricular assist device).	MSigDBv3.0 CGP	103	6	0.9	6.9	0.000372	1	0.00846	CTGF, FLNC, HYAL2, LAMB1, POSTN, SERPINE1
AACTTT UNKNOWN	TF	unknown		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif AACTTT. Motif does not match any known transcription factor	MSigDBv3.0 TFT	1467	27	13.4	2.2	0.000383	1	0.00868	AQP1, CD34, CDH11, CDH13, CDH5, COL1A2, COL3A1, CRIM1, DPYSL3, GJA1, GPRC5B, HSPB1, HSPG2, ITGB4, LAMA4, LAMB2, LPHN2, MMP2, MYH10, NFE2L1, NRG1, NTN1, POSTN, PPP2R5B, SEMA3F, TNFRSF21, VIM
ONDER CDH1 TARGETS 3 UP	EMT	gene	CDH1	Genes up-regulated in HMLE cells (immortalized nontransformed mammary epithelial) cells after loss of function of E-cadhedrin (CDH1) [Gene ID=999], which was achieved either by RNAi knockdown or by expression of a dominan-negative form of CDH1.	MSigDBv3.0 CGP	16	3	0.1	25.4	0.000387	1	0.00876	CRIP2, LEPR, MAGED1
VANTVEER BREAST CANCER BRCA1 DN	tumor	other		Down-regulated genes from the optimal set of 100 markers discriminating ER(-) breast cancer tumors by BRCA1 [Gene ID=672] mutation status.	MSigDBv3.0 CGP	38	4	0.3	13	0.000393	1	0.00887	CDH11, DKK3, GOLM1, TPPP3
STRUCTURAL MOLECULE ACTIVITY	ECM	component		Genes annotated by the GO term GO:0005198. The action of a molecule that contributes to the structural integrity of a complex or assembly within or outside a cell.	MSigDBv3.0 MF	242	9	2.2	4.4	0.000402	1	0.00903	AGRN, CAV1, COL4A2, FBLN2, FBN1, LAMA4, LAMB1, SPTAN1, VIM
RUIZ TNC TARGETS DN	tumor	other		Genes down-regulated in T98G cells (glioblastoma) by TNC [Gene ID=3371].	MSigDBv3.0 CGP	147	7	1.3	5.6	0.000416	1	0.00931	CAV1, CRIM1, EFEMP1, MEST, MYOF, NRG1, SERPINE2
WOO LIVER CANCER RECURRENCE UP	tumor	other		Genes positively correlated with recurrence free survival in patients with hepatitis B-related (HBV) hepatocellular carcinoma (HCC).	MSigDBv3.0 CGP	106	6	1	6.7	0.000433	1	0.00966	COL1A2, CRIP1, CTGF, DPYSL3, LAMA4, POSTN
WANG SMARCE1 TARGETS DN	tumor	other		Genes down-regulated in BT549 cells (breast cancer) by expression of SMARCE1 [Gene ID=6605] off a retroviral vector.	MSigDBv3.0 CGP	356	11	3.3	3.6	0.000455	1	0.0101	ADAMTS1, CAV1, CD9, IFI27, LAMA4, LPHN2, NRG1, PLK2, SLC29A1, TM4SF1, TNFRSF21
HORIUCHI WTAP TARGETS UP	others			Genes up-regulated in primary endothelial cells (HUVEC) after knockdown of WTAP [Gene ID=9589] by RNAi.	MSigDBv3.0 CGP	305	10	2.8	3.8	0.000522	1	0.0116	CDH11, CDH13, CFH, COL5A1, DKK3, FBN1, HMCN1, IL1R1, LRRC32, SERPINE2
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 6HR DN	others			Genes down-rgulated in CD34+ [Gene ID=947] hematopoetic cells by expression of NUP98-HOXA9 fusion [Gene ID=4928, 3205] off a retroviral vector at 6h.	MSigDBv3.0 CGP	41	4	0.4	11.9	0.000528	1	0.0117	AQP1, SERPINE1, SPTAN1, TM4SF1
THUM SYSTOLIC HEART FAILURE UP	others			Genes up-regulated in samples with systolic heart failure compared to normal hearts.	MSigDBv3.0 CGP	424	12	3.9	3.3	0.000552	1	0.012	DKK3, EDN1, ENG, IL33, LEPR, PLK2, RNASE1, SCARA3, SCARB2, SERPINE2, TM4SF1, VCAN
HOSHIDA LIVER CANCER SURVIVAL UP	tumor	other	prognosis	Survival signature genes defined in adjacent liver tissue: genes correlated with poor survival of hepatocellular carcinoma (HCC) patients.	MSigDBv3.0 CGP	73	5	0.7	8.2	0.000553	1	0.012	FBN1, ITGA9, LOXL2, PODXL, RNASE1
SESTO RESPONSE TO UV C8	others			Cluster 8: genes changed in primary keratinocytes by UVB irradiation.	MSigDBv3.0 CGP	73	5	0.7	8.2	0.000553	1	0.012	COL5A2, FLNB, LAMB1, MYH10, SERPINE1
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS GREY UP	others			Genes from the grey module which are up-regulated in HAEC cells (primary aortic endothelium) after exposure to the oxidized 1-palmitoyl-2-arachidonyl-sn-3-glycerophosphorylcholine (oxPAPC).	MSigDBv3.0 CGP	18	3	0.2	22	0.000557	1	0.012	ADAMTS1, EMP1, KIAA1522
MAHADEVAN IMATINIB RESISTANCE DN	tumor	resistance	Imatnib	Top genes down-regulated in the GIST (gastrointestinal stromal tumor) cell line resistant to imatinib [PubChem=5291] compared to the parental cell line sensitive to the drug.	MSigDBv3.0 CGP	18	3	0.2	22	0.000557	1	0.012	ALDH1A2, LPHN2, PTGIS

VERRECCHIA RESPONSE TO TGFB1 C1	signaling	TGFB	ECM	Cluster 1: ECM related genes up-regulated in dermal fibroblasts within 30 min after TGFB1 [Gene ID=7040] addition, and which kept increasing with time.	MSigDBv3.0 CGP	18	3	0.2	22	0.000557	1	0.012	HSPG2, SERPINE1, VCAN
HATADA METHYLATED IN LUNG CANCER UP	tumor	other		Genes with hypermethylated DNA in lung cancer samples.	MSigDBv3.0 CGP	365	11	3.3	3.5	0.00056	1	0.0121	ANGPTL2, CDH13, COL1A2, COL5A1, LRIG1, MARVELD1, MMRN2, NOS3, PLTP, PTRF, TPPP3
WONG ENDMETRIUM CANCER DN	tumor	other		Genes down-regulated in cancer endometrium samples compared to the normal endometrium.	MSigDBv3.0 CGP	42	4	0.4	11.6	0.00058	1	0.0125	ALDH1A2, FBN1, GAS6, LTBP4
HUANG DASATINIB RESISTANCE UP	tumor	other	dasatinib	Genes whose expression positively correlated with sensitivity of breast cancer cell lines to dasatinib [PubChem=3062316].	MSigDBv3.0 CGP	74	5	0.7	8	0.000588	1	0.0126	CAV1, COL5A1, FSTL1, PTRF, TNFRSF21
KEGG ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY ARVC	others			Arrhythmogenic right ventricular cardiomyopathy (ARVC)	MSigDBv3.0 CP:KEGG	74	5	0.7	8	0.000588	1	0.0126	GJA1, ITGA6, ITGA9, ITGAV, ITGB4
YAGI AML WITH INV 16 TRANSLOCATION	tumor	other		Genes specifically expressed in samples from patients with pediatric acute myeloid leukemia (AML) bearing inv(16) translocation.	MSigDBv3.0 CGP	429	12	3.9	3.3	0.000612	1	0.013	BCAM, CD9, COL5A2, CRIM1, DPYSL3, EMP1, EPHB4, HSPB1, MEST, PLS3, S100A10, VIM
CYTOSKELETON ORGANIZATION AND BIOGENESIS	others			Genes annotated by the GO term GO:0007010. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of cytoskeletal structures.	MSigDBv3.0 BP	205	8	1.9	4.6	0.000616	1	0.013	CDC42BPB, DSTN, FGD5, FLNB, FSCN1, MYH10, RHOJ, TNXB
ALONSO METASTASIS UP	tumor	other	metastasis	Up-regulated genes in melanoma tumous that developed metastatic disease compared to primary melanoma that did not.	MSigDBv3.0 CGP	157	7	1.4	5.2	0.000617	1	0.013	ALDH1A2, CAV1, EMP1, IL1RL1, ITGAV, MMP2, S100A10
CHIBA RESPONSE TO TSA UP	tumor	other		Cancer related genes up-regulated in any of four hepatoma cell lines following 24 h treatment with TSA [PubChem=5562].	MSigDBv3.0 CGP	43	4	0.4	11.3	0.000635	1	0.0134	BMP6, CD9, COL1A2, CTGF
RICKMAN METASTASIS DN	tumor	other	metastasis	Genes down-regulated in metastatic vs non-metastatic HNSCC (head and neck squamous cell carcinoma) samples.	MSigDBv3.0 CGP	258	9	2.4	4.1	0.000638	1	0.0134	A4GALT, ADAM15, ITGB4, KIAA1522, MMP28, MUC1, PERP, S100A16, SEMA3F
BACOLOD RESISTANCE TO ALKYLATING AGENTS UP	tumor	resistance	carmustine, O6-BG	Genes up-regulated in D-341 MED (OBR) cells (medulloblastoma) resistant to both carmustine and O6-BG [PubChem=2578, 4578].	MSigDBv3.0 CGP	19	3	0.2	20.6	0.000657	1	0.0136	CDH11, MDK, MYOF
DUNNE TARGETS OF AML1 MTG8 FUSION DN	tumor	other		Genes down-regulated in Kasumi-1 cells (acute myeloid leukaemia (AML) with the t(8;21) translocation) after knockdown of the AML1 MTG8 fusion [Gene ID=861, 862] by RNAi.	MSigDBv3.0 CGP	19	3	0.2	20.6	0.000657	1	0.0136	CD34, ECM1, ID1
module 400	others			Genes in module_400	MSigDBv3.0 CM	19	3	0.2	20.6	0.000657	1	0.0136	COL5A1, EFEMP1, TIE1
module 545	signaling	IL1		Genes in module_545: IL-1 signaling	MSigDBv3.0 CM	19	3	0.2	20.6	0.000657	1	0.0136	CDH13, IL1R1, IL1RL1
ZHAN MULTIPLE MYELOMA SPIKED	tumor	other		'Spiked' genes: genes most highly up-regulated in multiple myeloma samples; were not differentially expressed as compared to the normal plasma cells.	MSigDBv3.0 CGP	19	3	0.2	20.6	0.000657	1	0.0136	CTGF, FBLN2, IFI27
CELL PROLIFERATION GO 0008283	others			Genes annotated by the GO term GO:0008283. The multiplication or reproduction of cells, resulting in the expansion of a cell population.	MSigDBv3.0 BP	501	13	4.6	3	0.000734	1	0.0151	ADAMTS1, CDH13, CRIP1, EDN1, ELN, EMP1, EPHB4, EPS8, FSCN1, GAS6, IGFBP7, LAMB1, MAGED1
ROSS AML WITH AML1 ETO FUSION	tumor	other		Top 100 probe sets for pediatric acute myeloid leukemia (AML) subtype t(8;21) ; has AML1 ETO fusion [Gene ID=861, 862].	MSigDBv3.0 CGP	78	5	0.7	7.6	0.000749	1	0.0154	CAV1, CD34, HYAL2, ITGB4, PALM
RGAGGAARY V$PU1 Q6	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RGAGGAARY which matches annotation for SPI1: spleen focus forming virus (SFFV) proviral integration oncogene spi1	MSigDBv3.0 TFT	379	11	3.5	3.4	0.000763	1	0.0156	ADAM15, ANGPTL2, ELN, FLNC, MAGED1, MMRN2, PLVAP, RHOJ, S100A10, STAB1, VIM
REGULATION OF SIGNAL TRANSDUCTION	signaling	signal transduction		Genes annotated by the GO term GO:0009966. Any process that modulates the frequency, rate or extent of signal transduction.	MSigDBv3.0 BP	213	8	2	4.4	0.000791	1	0.0161	CDC42BPB, CDH13, ECM1, ENG, FGD5, GJA1, PLK2, RHOC
LI AMPLIFIED IN LUNG CANCER	tumor	other	amplicon	Genes with increased copy number that correlates with increased expression across six different lung adenocarcinoma cell lines.	MSigDBv3.0 CGP	164	7	1.5	5	0.000798	1	0.0161	BGN, COL1A2, FSCN1, HSPB1, MAGED1, MDK, MUC1
MULLIGHAN NPM1 SIGNATURE 3 DN	tumor	other		The 'NPM1 signature 3': genes down-regulated in pediatric AML (acute myeloid leukemia) with mutated NPM1 [Gene ID=4869] compared to the AML cases with intact NPM1 and MLL [[Gene ID=4297].	MSigDBv3.0 CGP	164	7	1.5	5	0.000798	1	0.0161	CD34, HEG1, HSPB1, HSPG2, LTBP4, SPTAN1, TPPP3
CHIARADONNA NEOPLASTIC TRANSFORMATION CDC25 UP	tumor	other		Genes up-regulated in reverted NIH3T3 cells (fibroblasts transformed by activated KRAS [Gene ID=3845] which then reverted to normal cells upon stable over-expression of a dominant negative form of CDC25 [Gene ID=5923]) vs normal fibroblasts.	MSigDBv3.0 CGP	119	6	1.1	5.9	8.00E-04	1	0.0161	IL1R1, IL1RL1, LAMA4, MAGED1, SYNPO, VCAN
TSAI RESPONSE TO IONIZING RADIATION	others			Genes up-regulated in TK6, WTK1, and NH32 cell lines (lymphoblast) in response to ionizing radiation.	MSigDBv3.0 CGP	119	6	1.1	5.9	8.00E-04	1	0.0161	CD59, COL4A2, COL6A1, DPYSL3, FN1, NFE2L1

DACOSTA UV RESPONSE VIA ERCC3 DN	others			Genes down-regulated in fibroblasts expressing mutant forms of ERCC3 [Gene ID=2071] after UV irradiation.	MSigDBv3.0 CGP	849	18	7.8	2.5	0.000811	1	0.0163	COL1A2, COL5A2, CRIM1, CTGF, EPS8, FBXL7, FLNB, GJA1, HEG1, ID1, IL1R1, ITGA6, LRIG1, MYOF, NRG1, PODXL, SERPINE1, WWTR1
COLLER MYC TARGETS DN	TF	MYC		Genes regulated by forced expression of MYC [Gene ID=4609] in 293T (transformed fetal renal cell).	MSigDBv3.0 CGP	5	2	0	73	0.000819	1	0.0164	COL3A1, CTGF
VERNELL RETINOBLASTOMA PATHWAY DN	TF	RB, CDNK2A, E2F		Cluster 2: genes down-regulated by RB1 [Gene ID=5925], CDNK2A [Gene ID=1029], and one of the E2Fs (E2F1, E2F2, or E2F3 [Gene ID=1869, 1870, 1871]).	MSigDBv3.0 CGP	5	2	0	73	0.000819	1	0.0164	CTGF, SERPINE1
TGTTTGY V$HNF3 Q6	TF	FOXA		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGTTTGY which matches annotation for FOXA1: forkhead box A1	MSigDBv3.0 TFT	573	14	5.2	2.9	0.000828	1	0.0165	ADAM15, ALDH1A2, CTGF, FSTL1, GATA6, LPHN2, MMRN2, NOS3, NRG1, NTN1, ROBO4, SLC29A1, SLCO2A1, TJP1
CTGCAGY UNKNOWN	TF	unknown		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif CTGCAGY. Motif does not match any known transcription factor	MSigDBv3.0 TFT	577	14	5.3	2.8	0.000886	1	0.0176	ANGPTL2, CD151, CDH13, CRIM1, CRIP2, DPYSL3, DSTN, GATA6, MAGED1, NRG1, PPP2R5B, SERPINE1, SLCO2A1, TNXB
MAHADEVAN IMATINIB RESISTANCE UP	tumor	resistance	imatinib	Top genes up-regulated in the GIST (gastrointestinal stromal tumor) cell line resistant to imatinib [PubChem=5291] compared to the parental cell line sensitive to the drug.	MSigDBv3.0 CGP	21	3	0.2	18.3	0.00089	1	0.0176	CRIM1, DKK3, SERPINE2
KIM WT1 TARGETS 8HR UP	tumor	other		Genes up-regulated in UB27 cells (osteosarcoma) at 8 hr after inducing the expression of a mutant form of WT1 [Gene ID=7490].	MSigDBv3.0 CGP	168	7	1.5	4.9	0.00092	1	0.0181	EMP1, PLEC, PLXND1, PODXL, SERPINE1, TM4SF1, WWTR1
BUYTAERT PHOTODYNAMIC THERAPY STRESS DN	tumor	other		Genes down-regulated in T24 (bladder cancer) cells in response to the photodynamic therapy (PDT) stress.	MSigDBv3.0 CGP	647	15	5.9	2.7	0.000922	1	0.0181	COL4A2, CRIM1, CTGF, EDN1, EFEMP1, FBN1, FN1, HYAL2, ID1, LOXL2, PLK2, SERPINE1, SSSCA1, SYNPO, VCAN
ROSS ACUTE MYELOID LEUKEMIA CBF	tumor	other		Top 100 probe sets for core-binding factor (CBF) acute myeloid leukemia (AML): contains CBFB MYH11 [Gene ID=865, 4629] or AML1 ETO [Gene ID=861, 862] fusions.	MSigDBv3.0 CGP	82	5	0.8	7.2	0.00094	1	0.0184	CAV1, CD34, CRIP2, HYAL2, ITGB4
ZHOU INFLAMMATORY RESPONSE FIMA UP	others			Genes up-regulated in macrophages by P.gingivalis FimA pathogen.	MSigDBv3.0 CGP	516	13	4.7	2.9	0.000962	1	0.0187	COL3A1, COL5A1, CXCR7, DPYSL3, EDN1, EFEMP1, FSCN1, IL1R1, ITGA9, LTBP4, POSTN, RHOJ, SERPINE1
ANGIOGENESIS	others			Genes annotated by the GO term GO:0001525. Blood vessel formation when new vessels emerge from the proliferation of pre-existing blood vessels.	MSigDBv3.0 BP	48	4	0.4	10	0.000966	1	0.0187	CDH13, COL4A2, ROBO4, STAB1
HENDRICKS SMARCA4 TARGETS UP	tumor	other		Genes up-regulated in ALAB cells (breast cancer) upon reintroduction of SMARCA4 [Gene ID=6597] expressed off adenoviral vector.	MSigDBv3.0 CGP	48	4	0.4	10	0.000966	1	0.0187	FLNB, LOXL2, PERP, SERPINE2
REACTOME APOPTOTIC EXECUTION PHASE	signaling	apoptosis		Genes involved in Apoptotic execution phase	MSigDBv3.0 CP:REACTOME	48	4	0.4	10	0.000966	1	0.0187	PLEC, SPTAN1, TJP1, VIM
REACTOME HEMOSTASIS	others			Genes involved in Hemostasis	MSigDBv3.0 CP:REACTOME	274	9	2.5	3.8	0.000977	1	0.0189	CAV1, CD9, COL1A2, FN1, GAS6, ITGA6, ITGAV, SERPINE1, TEK
module 426	others			Genes in module_426	MSigDBv3.0 CM	83	5	0.8	7.1	0.000993	1	0.0191	CD151, CDH5, FSCN1, GAS6, ITGB4
KIM WT1 TARGETS 12HR UP	tumor	other		Genes up-regulated in UB27 cells (osteosarcoma) at 12 hr after inducing the expression of a mutated form of WT1 [Gene ID=7490].	MSigDBv3.0 CGP	171	7	1.6	4.8	0.00102	1	0.0195	AQP1, EPS8, HEG1, MYOF, PODXL, SERPINE1, TM4SF1
LU TUMOR ENDOTHELIAL MARKERS UP	tumor	other		Genes specifically up-regulated in tumor endothelium.	MSigDBv3.0 CGP	22	3	0.2	17.4	0.00102	1	0.0195	POSTN, TNFRSF21, VCAN
MEMBRANE FRACTION	ECM	adhesion	membrane	Genes annotated by the GO term GO:0005624. That fraction of cells, prepared by disruptive biochemical methods, that includes the plasma and other membranes.	MSigDBv3.0 CC	333	10	3.1	3.5	0.00102	1	0.0195	A4GALT, ATP1A1, CD151, CD59, CDH5, EMP1, SCARB2, SLC29A1, SLCO2A1, SPTAN1
JAEGER METASTASIS UP	tumor	other	metastasis	Genes up-regulated in metastases from malignant melanoma compared to the primary tumors.	MSigDBv3.0 CGP	49	4	0.4	9.8	0.00104	1	0.0199	BGN, EPS8, FN1, SULF1
KESHELAVA MULTIPLE DRUG RESISTANCE	tumor	resistance	multiple drug	Genes up-regulated in multiple drug resistant neuroblastoma cell lines.	MSigDBv3.0 CGP	84	5	0.8	7	0.00105	1	0.0199	ADAM15, CD151, CRIP2, FN1, HSPB1
ELVIDGE HYPOXIA UP	signaling	hypoxia	breast cells	Genes up-regulated in MCF7 cells (breast cancer) under hypoxia conditions.	MSigDBv3.0 CGP	173	7	1.6	4.7	0.00109	1	0.0206	CAV1, CD59, FLNB, GJA1, LOXL2, PTRF, SERPINE1
BASSO HAIRY CELL LEUKEMIA DN	tumor	other		Genes down-regulated in hairy cell leukemia (HCL) compared with normal and other neoplastic B cell populations.	MSigDBv3.0 CGP	85	5	0.8	6.9	0.00111	1	0.0208	EMP1, ENG, IL1R1, MYOF, WWTR1

NAKAYAMA SOFT TISSUE TUMORS PCA1 UP	tumor	other		Top 100 probe sets contrubuting to the positive side of the 1st principal component; predominantly associated with spindle cell and pleomorphic sarcoma samples.	MSigDBv3.0 CGP	85	5	0.8	6.9	0.00111	1	0.0208	CFH, ECM1, EFEMP1, PLTP, SERPINE1
SMID BREAST CANCER BASAL UP	tumor	breast	basal	Genes up-regulated in basal subtype of breast cancer samles.	MSigDBv3.0 CGP	659	15	6	2.7	0.00111	1	0.0208	CD59, COL4A2, CTGF, EDN1, ELN, FOXC1, FSCN1, GATA6, GPRC5B, ITGA6, PERP, S100A10, TM4SF1, TNFRSF21, WWTR1
module 11	others			Genes in module_11	MSigDBv3.0 CM	525	13	4.8	2.9	0.00112	1	0.021	AQP1, CDH11, CLEC3B, DPYSL3, FBXL7, GJA1, GPRC5B, IFI27, ITGA6, MAOA, PALM, RNASE1, VCAN
MULLIGHAN NPM1 MUTATED SIGNATURE 1 DN	tumor	other		The 'NPM1-mutated signature 1': genes down-regulated in pediatric AML (acute myeloid leukemia) samples with mutated NPM1 [Gene ID=4869] compared to all AML cases with the intact gene.	MSigDBv3.0 CGP	127	6	1.2	5.5	0.00112	1	0.021	CD34, HEG1, HSPB1, LTBP4, SPTAN1, TPPP3
REACTOME SIGNALING IN IMMUNE SYSTEM	others			Genes involved in Signaling in Immune system	MSigDBv3.0 CP:REACTOME	338	10	3.1	3.4	0.00114	1	0.0213	CAV1, CD34, COL1A2, FN1, GAS6, ITGA6, ITGAV, PPP2R5B, PVRL2, TEK
COULOUARN TEMPORAL TGFB1 SIGNATURE UP	signaling	TGFB		'Late-TGFB1 signature': genes overexpressed in primary hepatocytes at a late phase of TGFB1 [Gene ID=7040] treatment; is associated with a more invasive phenotype.	MSigDBv3.0 CGP	86	5	0.8	6.8	0.00116	1	0.0215	CTGF, ITGA6, SERPINE1, SLC29A1, VIM
KEGG HEMATOPOIETIC CELL LINEAGE	others			Hematopoietic cell lineage	MSigDBv3.0 CP:KEGG	86	5	0.8	6.8	0.00116	1	0.0215	CD34, CD59, CD9, IL1R1, ITGA6
ACEVEDO LIVER CANCER WITH H3K27ME3 UP	tumor	other	H3K27me3	Genes whose promoters display higher levels of histone H3 trimethylation mark at K27 (H3K27me3) in hepatocellular carcinoma (HCC) compared to normal liver.	MSigDBv3.0 CGP	282	9	2.6	3.7	0.00119	1	0.022	COL1A2, COL3A1, GPR116, IL1RL1, MAGED1, PKHD1L1, PLA2G2A, RNASE1, SULF1
module 85	others			Genes in module_85	MSigDBv3.0 CM	51	4	0.5	9.4	0.00121	1	0.0222	EPHB4, LEPR, TEK, TIE1
DACOSTA LOW DOSE UV RESPONSE VIA ERCC3 XPCS DN	others			Genes down-regulated in fibroblasts expressing the XP/CS mutant form of ERCC3 [Gene ID=2071], after low dose UVC irradiation.	MSigDBv3.0 CGP	6	2	0.1	54.7	0.00122	1	0.0222	ID1, SERPINE1
module 496	others			Genes in module_496	MSigDBv3.0 CM	6	2	0.1	54.7	0.00122	1	0.0222	IL1R1, IL1RL1
SMID BREAST CANCER RELAPSE IN PLEURA UP	tumor	breast	metastasis	Genes up-regulated in pleura relapse of breast cancer.	MSigDBv3.0 CGP	6	2	0.1	54.7	0.00122	1	0.0222	GJA1, TPPP3
WALLACE PROSTATE CANCER DN	tumor	other		Genes down-regulated in prostate tumor vs normal tissue samples.	MSigDBv3.0 CGP	6	2	0.1	54.7	0.00122	1	0.0222	GJA1, LAMA4
HOOI ST7 TARGETS UP	tumor	other		Genes up-regulated in PC-3 cells (prostate cancer) stably expressing ST7 [Gene ID=7982] off a plasmid vector.	MSigDBv3.0 CGP	87	5	0.8	6.8	0.00123	1	0.0222	CDH11, FLNC, MEST, PODXL, SERPINE1
V$AREB6 03	TF	TCF8		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif VNRCACCTGKNC which matches annotation for TCF8: transcription factor 8 (represses interleukin 2 expression)	MSigDBv3.0 TFT	177	7	1.6	4.6	0.00125	1	0.0225	DSTN, FLNB, ITGA6, ITGB4, KIF1C, MYH10, SEMA3F
SCHLESINGER METHYLATED DE NOVO IN CANCER	tumor	other	H3K27me3, SUZ12/EED	Genes bearing H3K27me3 mark or whose promoters are bound by the polycomb proteins SUZ12 or EED [Gene ID=23512, 8726]; their DNA is methylated de novo in cancer.	MSigDBv3.0 CGP	88	5	0.8	6.7	0.00129	1	0.0233	CDH13, CRIP1, FBN1, GATA4, SFRP5
OSADA ASCL1 TARGETS DN	tumor	other		Genes down-regulated in A549 cells (lung cancer) upon expression of ASCL1 [Gene ID=429] off a viral vector.	MSigDBv3.0 CGP	24	3	0.2	15.7	0.00133	1	0.0238	CRIM1, DKK3, NRG1
VALK AML WITH EVI1	tumor	other		Genes that best predicted acute myeloid leukemia (AML) with the up-regulated expression of EVI1 [Gene ID=2122].	MSigDBv3.0 CGP	24	3	0.2	15.7	0.00133	1	0.0238	CD34, CRIM1, NPDC1
BECKER TAMOXIFEN RESISTANCE DN	tumor	resistance	ER	Genes down-regulated in a breast cancer cell line resistant to tamoxifen [PubChem ID=5376] compared to the parental line sensitive to the drug.	MSigDBv3.0 CGP	53	4	0.5	9	0.0014	1	0.025	EMP1, GJA1, IL1R1, TM4SF1
module 234	others	bone		Genes in module_234: Bone remodeling	MSigDBv3.0 CM	53	4	0.5	9	0.0014	1	0.025	CLEC3B, FBN1, POSTN, TIE1
LU TUMOR ANGIOGENESIS UP	tumor	other		Up-regulated genes of putative pathways stimulated in tumor endothelial cells by papillary serous ovarian epithelial tumor cells.	MSigDBv3.0 CGP	25	3	0.2	15	0.0015	1	0.0266	EDN1, ITGAV, VCAN
WATANABE RECTAL CANCER RADIOTHERAPY RESPONSIVE DN	tumor	resistance		Genes down-regulated in rectal cancer patients resistant to radiotherapy (non-responders) relative to the sensitive ones (responders).	MSigDBv3.0 CGP	91	5	0.8	6.4	0.0015	1	0.0266	AGRN, COL1A2, COL3A1, COL5A2, ITGAV

NAKAMURA TUMOR ZONE PERIPHERAL VS CENTRAL DN	tumor	other		Down-regulated genes in peripheral zone of human pancreatic cancer growing in the pancreas of nude mice compared to that of the tumor from the central zone.	MSigDBv3.0 CGP	611	14	5.6	2.7	0.00152	1	0.0269	AGRN, APCDD1, CFH, COL6A1, CXCR7, FOXC1, IL1R1, IL1RL1, IL33, ITFG3, LOXL2, LRIG1, MAOA, MUC1
CELLULAR COMPONENT ASSEMBLY	others			Genes annotated by the GO term GO:0022607. A cellular process that results in the assembly of a part of the cell.	MSigDBv3.0 BP	293	9	2.7	3.6	0.00155	1	0.0274	AGRN, CD9, GJA1, HSPB1, ITGA6, PTRF, SLC9A3R2, TJP1, TNXB
HUPER BREAST BASAL VS LUMINAL UP	tumor	breast	basal vs luminal	Genes up-regulated in basal mammary epithelial cells compared to the luminal ones.	MSigDBv3.0 CGP	55	4	0.5	8.7	0.00161	1	0.0282	GJA1, ITGA6, POSTN, SERPINE2
V$FOXO4 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RWAAACAANNN which matches annotation for MLLT7: myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7	MSigDBv3.0 TFT	185	7	1.7	4.4	0.00161	1	0.0282	ALDH1A2, FSTL1, GATA6, LPHN2, NRG1, PALM, TJP1
VASCULATURE DEVELOPMENT	others			Genes annotated by the GO term GO:0001944. The process whose specific outcome is the progression of the vasculature over time, from its formation to the mature structure.	MSigDBv3.0 BP	55	4	0.5	8.7	0.00161	1	0.0282	CDH13, COL4A2, ROBO4, STAB1
DASU IL6 SIGNALING DN	signaling	IL6		Genes down-regulated in normal fibroblasts in response to IL6 [Gene ID=3569].	MSigDBv3.0 CGP	7	2	0.1	43.8	0.0017	1	0.0296	SERPINE1, SULF1
HOQUE METHYLATED IN CANCER	tumor	other		Genes whose DNA was methylated both in primary tumors and across a panel of cancer cell lines.	MSigDBv3.0 CGP	56	4	0.5	8.5	0.00172	1	0.03	CDH13, GATA4, SFRP5, VCAN
CELL FRACTION	others			Genes annotated by the GO term GO:0000267. A generic term for parts of cells prepared by disruptive biochemical techniques.	MSigDBv3.0 CC	485	12	4.4	2.9	0.00175	1	0.0303	A4GALT, ANXA2, ATP1A1, CD151, CD59, CDH5, EDN1, EMP1, SCARB2, SLC29A1, SLCO2A1, SPTAN1
module 223	others			Genes in module_223: Immune (defense) response	MSigDBv3.0 CM	140	6	1.3	5	0.00185	1	0.032	CRIP1, EDN1, EMP1, EPS8, GAS6, MDK
SENESE HDAC3 TARGETS UP	tumor	other		Genes up-regulated in U2OS cells (osteosarcoma) upon knockdown of HDAC3 [Gene ID=8841] by RNAi.	MSigDBv3.0 CGP	489	12	4.5	2.8	0.00187	1	0.032	DPYSL3, EMP1, FN1, FOXC1, ITGA6, LEPR, PTPRB, RHOC, ROBO4, SCARB2, SERPINE2, TM4SF1
GUENTHER GROWTH SPHERICAL VS ADHERENT DN	tumor	other		Genes down-regulated in glioblastoma cell lines displaying spherical growth (cluster-1) compared to those displaying semiadherent or adherent growth phenotype (cluster-2).	MSigDBv3.0 CGP	27	3	0.2	13.7	0.00188	1	0.032	CAV1, CD59, FN1
HAHTOLA MYCOSIS FUNGOIDES SKIN DN	others			Genes down-regulated in lesional skin biopsies from mycosis fundoides patients compared to the normal skin samples.	MSigDBv3.0 CGP	27	3	0.2	13.7	0.00188	1	0.032	DSTN, ECM1, ITGA6
module 265	signaling	IL	receptor	Genes in module_265: IL receptors	MSigDBv3.0 CM	27	3	0.2	13.7	0.00188	1	0.032	IL1R1, IL1RL1, LEPR
NAKAMURA CANCER MICROENVIRONMENT UP	tumor	other		Genes up-regulated in pancreatic cancer cells grown in orthotopic xenograft tumors compared to those grown in vitro.	MSigDBv3.0 CGP	27	3	0.2	13.7	0.00188	1	0.032	COL1A2, COL3A1, POSTN
SAKAI TUMOR INFILTRATING MONOCYTES UP	others			Selected genes up-regulated in inflammatory monocytes infiltrating hepatocellular carcinoma (HCC).	MSigDBv3.0 CGP	27	3	0.2	13.7	0.00188	1	0.032	FLNB, ITGA9, NRG1
HELLER SILENCED BY METHYLATION UP	tumor	other		Genes up-regulated in at least one of three multiple myeloma (MM) cell lines treated with the DNA hypomethylating agent decitabine (5-aza-2'-deoxycytidine) [PubChem=451668].	MSigDBv3.0 CGP	245	8	2.2	3.8	0.00193	1	0.0326	AGRN, CDH11, FBN1, FSCN1, ID1, IFI27, MUC1, SYNPO
UDAYAKUMAR MED1 TARGETS DN	tumor	other		Genes down-regulated in HeLa cells after knockdown of MED1 [Gene ID=5469] by RNAi.	MSigDBv3.0 CGP	245	8	2.2	3.8	0.00193	1	0.0326	ADAMTS1, BMP6, CXCR7, EPHB4, NFE2L1, PLK2, RHOC, SPTAN1
V$E12 Q6	TF	TCF3		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RRCAGGTGNCV which matches annotation for TCF3: transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	MSigDBv3.0 TFT	191	7	1.7	4.2	0.00193	1	0.0326	ALDH1A2, BMP6, CDH5, ITGA6, ITGB4, SEMA3F, TNFRSF21
AMIT SERUM RESPONSE 60 MCF10A	signaling	serum	MCF10A	Genes whose expression peaked at 60 min after stimulation of MCF10A cells with serum.	MSigDBv3.0 CGP	58	4	0.5	8.2	0.00196	1	0.033	CTGF, FN1, PLK2, TM4SF1
REACTOME CELL CELL ADHESION SYSTEMS	ECM	adhesion		Genes involved in Cell-cell adhesion systems	MSigDBv3.0 CP:REACTOME	58	4	0.5	8.2	0.00196	1	0.033	CDH11, CDH13, CDH5, PVRL2
FLECHNER BIOPSY KIDNEY TRANSPLANT REJECTED VS OK DN	others			Genes differentially expressed in kidney biopsies from patients with acute transplant rejection compared to the biopsies from patients with well functioning kidneys more than 1-year post transplant.	MSigDBv3.0 CGP	560	13	5.1	2.7	0.00199	1	0.0334	AQP1, CD9, DSTN, EPS8, GPR116, HSPB1, ITGA6, MAOA, MYH10, PLS3, PODXL, TEK, WWTR1
V$LMO2COM 02	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NMGATANSG which matches annotation for LMO2: LIM domain only 2 (rhombotin-like 1)	MSigDBv3.0 TFT	193	7	1.8	4.2	0.00204	1	0.0342	BMP6, CD34, CDH5, GATA6, MYH10, PVRL2, SFRP5

GRADE COLON VS RECTAL CANCER UP	tumor	other		Genes up-regulated in rectal but down-regulated in colon carcinoma compared to normal mucosa samples.	MSigDBv3.0 CGP	28	3	0.3	13.2	0.00209	1	0.0348	CD34, FSTL1, GPR116
module 385	others			Genes in module_385: Heparin binding	MSigDBv3.0 CM	28	3	0.3	13.2	0.00209	1	0.0348	FN1, FSTL1, MDK
RHEIN ALL GLUCOCORTICOID THERAPY DN	tumor	other		Genes down-regulated in ALL (acute lymphoblastic leukemia) blasts after 1 week of treatment with glucocorticoids.	MSigDBv3.0 CGP	367	10	3.4	3.2	0.0021	1	0.0348	CD34, CD9, EMP1, HSPB1, IGFBP7, LRIG1, MAGED1, MEST, MYH10, SERPINE1
V$FOXO1 01	TF	FOXO1A		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NRWAAACAAN which matches annotation for FOXO1A: forkhead box O1A (rhabdomyosarcoma)	MSigDBv3.0 TFT	194	7	1.8	4.2	0.0021	1	0.0348	EFEMP1, EMP1, FSTL1, GATA6, LPHN2, NRG1, PALM
YAGI AML FAB MARKERS	tumor	other		Genes specifically expressed in FAB subtypes M2, M4, M5 and M7 of pediatric AML (acute myeloid leukemia).	MSigDBv3.0 CGP	195	7	1.8	4.2	0.00216	1	0.0357	ANXA2, CAV1, CFH, ITGA6, MYH10, S100A10, SERPINE2
GAUTSCHI SRC SIGNALING	tumor	other	AZD0530	Genes down-regulated in A549 cells (lung cancer) after treatment with AZD0530 [PubChem=10302451], a SRC [Gene ID=6714] kinase inhibitor.	MSigDBv3.0 CGP	8	2	0.1	36.5	0.00225	1	0.0371	ID1, SERPINE1
KAAB FAILED HEART ATRIUM DN	others			Genes down-regulated in atria of failing hearts (DCM and ICM) compared to healthy controls.	MSigDBv3.0 CGP	146	6	1.3	4.8	0.00228	1	0.0375	CD59, LRRC32, MYH10, PODXL, PSMD9, PTPRB
GAUSSMANN MLL AF4 FUSION TARGETS D UP	others			Up-regulated genes from the set D (Fig. 5a): specific signature shared by cells expressing MLL-AF4 [Gene ID=4297, 4299] alone and those expressing both MLL-AF4 and AF4-MLL fusion proteins.	MSigDBv3.0 CGP	29	3	0.3	12.7	0.00232	1	0.038	LOXL2, PERP, SERPINE2
ONKEN UVEAL MELANOMA UP	tumor	other		Genes up-regulated in uveal melanoma: class 2 vs class 1 tumors.	MSigDBv3.0 CGP	785	16	7.2	2.4	0.00236	1	0.0385	CDC42BPB, COL1A2, COL6A1, CXCR7, EMP1, FBXL7, FLNC, GOLM1, IGFBP7, ITGA6, MMP2, MYOF, PLTP, SPTAN1, SYNPO, WWTR1
SKELETAL DEVELOPMENT	others			Genes annotated by the GO term GO:0001501. The process whose specific outcome is the progression of the skeleton over time, from its formation to the mature structure. The skeleton is the bony framework of the body in vertebrates (endoskeleton) or the hard outer envelope of insects (exoskeleton or dermoskeleton).	MSigDBv3.0 BP	101	5	0.9	5.8	0.00237	1	0.0387	ANXA2, CLEC3B, COL1A2, FBN1, POSTN
module 64	ECM	adhesion	receptor	Genes in module_64: Membranal receptors	MSigDBv3.0 CM	506	12	4.6	2.7	0.00248	1	0.0402	AQP1, CAV1, CD9, GJA1, GPRC5B, IL1R1, LEPR, LRRC32, MUC1, NRG1, TEK, TNFRSF21
TGACCTY V$ERR1 Q2	TF	ESRRA	ER	Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGACCTY which matches annotation for ESRRA: estrogen-related receptor alpha	MSigDBv3.0 TFT	789	16	7.2	2.4	0.00248	1	0.0402	ADAM15, CDH13, FAM38A, FSTL1, KIF1C, LAMB2, LTBP3, NFE2L1, NRG1, PLXND1, SEMA3F, SLCO2A1, SPTAN1, SYNPO, TEK, TNXB
HAN SATB1 TARGETS UP	tumor	other		Genes up-regulated in MDA-MB-231 cells (breast cancer) after knockdown of SATB1 [Gene ID=6304] by RNAi.	MSigDBv3.0 CGP	315	9	2.9	3.3	0.00254	1	0.0411	ADAM15, ADAMTS1, CDH11, COL6A2, CTGF, FN1, GATA6, IGFBP7, NRG1
ALONSO METASTASIS EMT UP	EMT	tumor	metastasis	EMT (epithelial-mesenchymal transition) genes up-regulated genes in melanoma tumous that developed metastatic disease compared to primary melanoma that did not.	MSigDBv3.0 CGP	30	3	0.3	12.2	0.00256	1	0.0411	EMP1, ITGAV, MMP2
GILDEA METASTASIS	tumor	other		Top genes down-regulated in metastatic (T24T) vs non-metastatic (T24) bladder cancer cell lines.	MSigDBv3.0 CGP	30	3	0.3	12.2	0.00256	1	0.0411	COL5A2, FN1, IFI27
VALK AML CLUSTER 13	tumor	other		Top 40 genes from cluster 13 of acute myeloid leukemia (AML) expression profile; 91% of the samples are FAB M2 subtype, all bear the t(8;21) translocation producing the AML1-ETO fusion [Gene ID=861, 862]; indicate good survival.	MSigDBv3.0 CGP	30	3	0.3	12.2	0.00256	1	0.0411	CAV1, HSPG2, ITGB4
ELVIDGE HIF1A AND HIF2A TARGETS DN	tumor	other	hypoxia	Genes down-regulated in MCF7 cells (breast cancer) after knockdown of both HIF1A and HIF2A [Gene ID=3091, 2034] by RNAi.	MSigDBv3.0 CGP	104	5	1	5.6	0.0027	1	0.0432	CAV1, GJA1, LOXL2, PTRF, SERPINE1
TGGAAA V$NFAT Q4 01	TF	NFAT		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGGAAA which matches annotation for NFAT
 NFATC	MSigDBv3.0 TFT	1426	24	13.1	2	0.00276	1	0.044	ANGPTL2, BMP6, CCDC3, CDH5, COL1A2, CTGF, DKK2, DSTN, EMP1, FLNC, FN1, FSTL1, GATA6, HSPG2, HYAL2, IGFBP7, MRC2, NRG1, PTRF, RBMS2, S100A10, SULF1, TNXB, VIM
TATAAA V$TATA 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TATAAA which matches annotation for TAF
 TATA	MSigDBv3.0 TFT	1026	19	9.4	2.2	0.00277	1	0.0442	ADAMTS1, ALDH1A2, AQP1, CCDC3, COL1A2, CTGF, DKK2, DSTN, ECM1, EDN1, EFEMP1, FN1, ID1, PLTP, POSTN, SERPINE1, SLCO2A1, SPTAN1, SULF1
ST WNT BETA CATENIN PATHWAY	signaling	WNT		Wnt/beta-catenin Pathway	MSigDBv3.0 CP	31	3	0.3	11.8	0.00281	1	0.0447	DKK2, DKK3, FSTL1
WAMUNYOKOLI OVARIAN CANCER GRADES 1 2 DN	tumor	other		Genes down-regulated in mucinous ovarian carcinoma tumors of grades 1 and 2 compared to the normal ovarian survace epithelium tissue.	MSigDBv3.0 CGP	64	4	0.6	7.4	0.00282	1	0.0447	CAV1, IL1R1, PODXL, SULF1
V$CACCCBINDINGFACTOR Q6	TF	unknown		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif CANCCNNWGGGTGDGG. Motif does not match any known transcription factor	MSigDBv3.0 TFT	205	7	1.9	3.9	0.00286	1	0.0453	FLNC, ITGB4, NRG1, PLS3, PLTP, SERPINE1, SULF1

TSUNODA CISPLATIN RESISTANCE UP	tumor	resistance	cisplatin	Genes up-regulated in bladder cancer cells resistant to cisplatin [PubChem=2767] compared to the parental cells sensitive to the drug.	MSigDBv3.0 CGP	9	2	0.1	31.3	0.00288	1	0.0454	CTGF, EFEMP1
V$ZIC3 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NGGGKGGTC which matches annotation for ZIC3: Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)	MSigDBv3.0 TFT	206	7	1.9	3.9	0.00294	1	0.0463	ADAMTS1, ANGPTL2, DOCK6, FSTL1, NRG1, NTN1, SULF1
CROMER METASTASIS DN	tumor	other	metastasis	Metastatic propensity markers of head and neck squamous cell carcinoma (HNSCC): down-regulated in metastatic vs non-metastatic tumors.	MSigDBv3.0 CGP	65	4	0.6	7.2	0.00298	1	0.0467	CAV1, FLNB, ITGB4, PLEC
KANG BONE DN	tumor	breast	metastasis	kang cancerCell 2003 down in breast cancer likely to metastasize to bone	kang cancerCell 2003 mmc8.xls	65	4	0.6	7.2	0.00298	1	0.0467	COL5A1, FN1, ITGB4, LAMB1
ENK UV RESPONSE EPIDERMIS DN	others			Genes down-regulated in epidermis after to UVB irradiation.	MSigDBv3.0 CGP	519	12	4.8	2.7	0.00305	1	0.0477	ADAMTS1, CRIP1, DKK3, EMP1, FSCN1, GAS6, HSPB1, ITGAV, POSTN, PVRL2, SPTAN1, TPPP3
EXTRACELLULAR STRUCTURE ORGANIZATION AND BIOGENESIS	others			Genes annotated by the GO term GO:0043062. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of structures in the space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane, and also covers the host cell environment outside an intracellular parasite.	MSigDBv3.0 BP	32	3	0.3	11.4	0.00308	1	0.0478	AGRN, COL5A2, TNXB
GNF2 MMP1	EMT	gene	MMP	Neighborhood of MMP1	MSigDBv3.0 CGN	32	3	0.3	11.4	0.00308	1	0.0478	FBN1, LOXL2, SERPINE1
VALK AML CLUSTER 10	tumor	other		Top 40 genes from cluster 10 of acute myeloid leukemia (AML) expression profile; 41% of the samples are FAB M1 subtype, 45% have up-regulated EVI1 [Gene ID=2122] expression; indicate poor survival.	MSigDBv3.0 CGP	32	3	0.3	11.4	0.00308	1	0.0478	CRIM1, FLNB, NPDC1
SHAFFER IRF4 TARGETS IN PLASMA CELL VS MATURE B LYMPHOCYTE	others			IRF4 [Gene ID=3662] target genes up-regulated in plasma cells compared to mature B lymphocytes.	MSigDBv3.0 CGP	66	4	0.6	7.1	0.00315	1	0.0488	BMP6, CAV1, HSPB1, TXNDC5
module 63	others			Genes in module_63: Porins/transporters	MSigDBv3.0 CM	210	7	1.9	3.8	0.00327	1	0.0505	GJA1, GPRC5B, HYAL2, ITGA9, TEK, TIE1, TNFRSF21
FRIDMAN IMMORTALIZATION DN	others			Genes down-regulated in immortalized cell lines.	MSigDBv3.0 CGP	33	3	0.3	11	0.00337	1	0.0519	CTGF, IGFBP7, SERPINE1
GOZGIT ESR1 TARGETS DN	tumor	other	ER	Genes down-regulated in TMX2-28 cells (breast cancer) which do not express ESR1 [Gene ID=2099]) compared to the parental MCF7 cells which do.	MSigDBv3.0 CGP	741	15	6.8	2.4	0.00343	1	0.0527	COL3A1, CXCR7, EDN1, EFEMP1, GATA6, HMCN1, IFI27, ITGA6, MAGED1, MAOA, PLK2, PVRL2, RBMS2, RNASE1, SULF1
ACEVEDO METHYLATED IN LIVER CANCER UP	tumor	other		Genes whose DNA is hypo-methylated in hepatocellular carcinoma (HCC) compared to normal liver.	MSigDBv3.0 CGP	2227	33	20.4	1.8	0.00349	1	0.0536	A4GALT, ANO1, ANXA2, ARHGAP23, CD34, CDC42BPB, CGNL1, COL1A2, COL3A1, COL4A2, COL6A2, DSTN, FAM38A, FBN1, FGD5, FN1, GAS6, GPRC5B, HEG1, HMCN1, ITFG3, KIF1C, LAMB1, LTBP3, LTBP4, PKHD1L1, PLEC, PLS3, PLXND1, SERPINE2, SFRP5, SLC29A1, SPTAN1
CORRE MULTIPLE MYELOMA UP	tumor	other		Genes up-regulated in multiple myeloma (MM) bone marrow mesenchymal stem cells.	MSigDBv3.0 CGP	68	4	0.6	6.9	0.00351	1	0.0537	GATA6, PTGIS, RHOJ, SERPINE1
CERVERA SDHB TARGETS 2	tumor	other		Genes present but differentially expressed between Hep3B cells (hepatocellular carcinoma, HCC) with RNAi knockdown of SDHB [Gene ID=6390] and control cells.	MSigDBv3.0 CGP	111	5	1	5.2	0.00357	1	0.0544	GJA1, GPRC5B, IGFBP7, LEPR, SERPINE2
MCCOLLUM GELDANAMYCIN RESISTANCE UP	tumor	resistance	geldanamycin, 17-AAG	Genes up-regulated in A549GARS cells (lung cancer) resistant to the geldanamycin and 17-AAG [PubChem=5476289, 6440175].	MSigDBv3.0 CGP	10	2	0.1	27.3	0.00358	1	0.0544	CDH11, SEMA3F
POSITIVE REGULATION OF CELL MIGRATION	EMT	migration		Genes annotated by the GO term GO:0030335. Any process that activates or increases the frequency, rate or extent of cell migration.	MSigDBv3.0 BP	10	2	0.1	27.3	0.00358	1	0.0544	CDH13, LAMB1
DOANE BREAST CANCER CLASSES DN	tumor	breast	ER	Genes down-regulated in ER(-) / PR(-) breast tumors (do not express ESR1 and PGR [Gene ID=2099, 5241]) with molecular similarity to ER(+) (class A) relative to the rest of the ER(-) / PR(-) samples (class B).	MSigDBv3.0 CGP	34	3	0.3	10.6	0.00367	1	0.0555	FOXC1, FSCN1, WWTR1
LI CISPLATIN RESISTANCE DN	tumor	resistance	cisplatin	Genes consistently down-regulated in ACRP cells (ovarian cancer, resistant to cisplatin [PubChem=2767]) compared to the parental sensitive A2780 cells, regardless of cisplatin exposure.	MSigDBv3.0 CGP	34	3	0.3	10.6	0.00367	1	0.0555	CFH, LAMA4, MEST
module 69	others			Genes in module_69	MSigDBv3.0 CM	464	11	4.2	2.7	0.00373	1	0.0564	CD9, CDH13, CDH5, EDN1, GJA1, HYAL2, IFI27, IL1RL1, KIAA1522, PLA2G2A, SCARA3

V$AP1 Q2	TF	JUN		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RSTGACTNANW which matches annotation for JUN: jun oncogene	MSigDBv3.0 TFT	216	7	2	3.7	0.00382	1	0.0575	DKK2, DSTN, FLNC, ID1, LTBP3, MAGED1, VIM
CTACCTC,LET-7A,LET-7B,LET-7C,LET-7D,LET-7E,LET-7F,MIR-98,LET-7G,LET-7I	microRNA			Targets of MicroRNA CTACCTC,LET-7A,LET-7B,LET-7C,LET-7D,LET-7E,LET-7F,MIR-98,LET-7G,LET-7I	MSigDBv3.0 MIR	337	9	3.1	3.1	0.00396	1	0.0595	ADAM15, CGNL1, COL1A2, COL3A1, COL5A2, DKK3, LRIG1, PLXND1, SEMA3F
SIG REGULATION OF THE ACTIN CYTOSKELETON BY RHO GTPASES	cytoskeleton			Genes related to regulation of the actin cytoskeleton	MSigDBv3.0 CP	35	3	0.3	10.3	0.00399	1	0.0596	ANGPTL2, FLNC, FSCN1
VALK AML CLUSTER 6	tumor	other		Top 40 genes from cluster 6 of acute myeloid leukemia (AML) expression profile; all samples are FAB M1 or M2 subtypes and all samples have internal tundem duplication of FLT3 [Gene ID=2322].	MSigDBv3.0 CGP	35	3	0.3	10.3	0.00399	1	0.0596	CFH, DPYSL3, FOXC1
SMIRNOV CIRCULATING ENDOTHELIOCYTES IN CANCER UP	tumor	other		Genes up-regulated in circulating endothelial cells (CEC) from cancer patients compared to those from healthy donors.	MSigDBv3.0 CGP	164	6	1.5	4.2	0.00406	1	0.0605	CD9, DKK3, ENG, NRG1, PERP, TIE1
NEWMAN ERCC6 TARGETS DN	others			Genes down-regulated in Cockayne syndrome fibroblasts rescued by expression of ERCC6 [Gene ID=2074] off a plasmid vector.	MSigDBv3.0 CGP	36	3	0.3	10	0.00432	1	0.0643	ADAMTS1, PODXL, SERPINE1
HOEGERKORP CD44 TARGETS DIRECT DN	others			Genes directly down-regulated by CD44 [Gene ID=960] stimulation of B lymphocytes.	MSigDBv3.0 CGP	11	2	0.1	24.3	0.00435	1	0.0645	BCAM, PALM
KIM WT1 TARGETS 12HR DN	tumor	other		Genes down-regulated in UB27 cells (osteosarcoma) at 12 hr after inducing the expression of a mutated form of WT1 [Gene ID=7490].	MSigDBv3.0 CGP	222	7	2	3.6	0.00443	1	0.0657	CRIM1, CTGF, CXCR7, IGFBP7, LAMB1, NRG1, PLK2
TRANSMEMBRANE RECEPTOR ACTIVITY	ECM	adhesion	receptor	Genes annotated by the GO term GO:0004888. Combining with an extracellular or intracellular messenger to initiate a change in cell activity, and spanning to the membrane of either the cell or an organelle.	MSigDBv3.0 MF	409	10	3.7	2.8	0.00454	1	0.067	BCAM, CRIM1, GPR116, IL1R1, LPHN2, PTPRB, SCARA3, STAB1, TEK, TIE1
VANTVEER BREAST CANCER ESR1 DN	tumor	breast	ER	Down-regulated genes from the optimal set of 550 markers discriminating breast cancer samples by ESR1 [Gene ID=2099] expression: ER(+) vs ER(-) tumors.	MSigDBv3.0 CGP	223	7	2	3.6	0.00454	1	0.067	FOXC1, FSCN1, GPRC5B, PLTP, S100A10, TM4SF1, TNFRSF21
AAAGACA,MIR-511	microRNA			Targets of MicroRNA AAAGACA,MIR-511	MSigDBv3.0 MIR	168	6	1.5	4.1	0.00456	1	0.0671	CRIM1, FN1, GJA1, GPR116, RHOJ, SEMA3F
module 27	others			Genes in module_27	MSigDBv3.0 CM	345	9	3.2	3	0.00461	1	0.0677	GPRC5B, HYAL2, IL1R1, ITGA9, LEPR, LPHN2, TEK, TIE1, TNFRSF21
chr7q32	others			Genes in cytogenetic band chr7q32	MSigDBv3.0	37	3	0.3	9.7	0.00467	1	0.0682	FLNC, MEST, PODXL
CONRAD STEM CELL	others			Supplementary Table 2. Genelist comparing microarray expression profiles of spermatogonial cells, haGSCs and hES (H1) cells. Examples of expression rates of different hES cell enriched and germ cell specific genes, surface markers for germ cell selection and signal transduction in all three cell types (spermatogonial cells = SC).	MSigDBv3.0 CGP	37	3	0.3	9.7	0.00467	1	0.0682	CD9, DKK3, GJA1
V$FOX Q2	TF	FOXF2		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif KATTGTTTRTTTW which matches annotation for FOXF2: forkhead box F2	MSigDBv3.0 TFT	169	6	1.5	4.1	0.00469	1	0.0684	CRIM1, EFEMP1, FSTL1, GATA6, NRG1, NTN1
POSITIVE REGULATION OF SIGNAL TRANSDUCTION	signaling	signal transduction		Genes annotated by the GO term GO:0009967. Any process that activates or increases the frequency, rate or extent of signal transduction.	MSigDBv3.0 BP	119	5	1.1	4.9	0.0048	1	0.0698	CDH13, ECM1, GJA1, PLK2, RHOC
GTGCCTT,MIR-506	microRNA			Targets of MicroRNA GTGCCTT,MIR-506	MSigDBv3.0 MIR	623	13	5.7	2.4	0.00493	1	0.0715	ATP1A1, CAV1, CD151, COL5A1, EPS8, GATA6, LRIG1, MARVELD1, MDK, MYH10, SFRP5, SLC29A1, VIM
CELL SURFACE	ECM	adhesion	membrane	Genes annotated by the GO term GO:0009986. The external part of the cell wall and/or plasma membrane.	MSigDBv3.0 CC	75	4	0.7	6.2	0.00499	1	0.072	BCAM, EPHB4, HSPB1, SULF1
FERRANDO T ALL WITH MLL ENL FUSION UP	tumor	other		Top 100 genes positively (UP) and negatively (DN) associated with T-cell acute lymphoblastic leukemia MLL T-ALL) expressing MLL-ENL fusion [Gene ID=4297, 4298].	MSigDBv3.0 CGP	75	4	0.7	6.2	0.00499	1	0.072	CD34, DSTN, PLEC, VIM
LIAO HAVE SOX4 BINDING SITES	tumor	other	metastasis	Genes up-regulated in the samples with intrahepatic metastatic hepatocellular carcinoma (HCC) vs primary HCC that also have putative binding sites for SOX4 [Gene ID=6659].	MSigDBv3.0 CGP	38	3	0.3	9.4	0.00503	1	0.0726	GPRC5B, LAMB1, SERPINE2
module 37	others			Genes in module_37	MSigDBv3.0 CM	416	10	3.8	2.8	0.0051	1	0.0734	CD9, CDH13, CDH5, EDN1, GJA1, HYAL2, IFI27, IL1RL1, KIAA1522, SCARA3

POOLA INVASIVE BREAST CANCER UP	tumor	breast	ADHC vs ADH	Genes up-regulated in atypical ductal hyperplastic tissues from patients with (ADHC) breast cancer vs those without the cancer (ADH).	MSigDBv3.0 CGP	288	8	2.6	3.2	0.00515	1	0.0738	CDH11, COL5A1, COL5A2, ECM1, FN1, SERPINE1, SULF1, VCAN
FRIDMAN SENESCENCE DN	signaling	senescent		Genes down-regulated in senescent cells.	MSigDBv3.0 CGP	12	2	0.1	21.9	0.00518	1	0.0738	COL3A1, ID1
LOPEZ MESOTHELIOMA SURVIVAL DN	tumor	other	prognosis	Top genes associated with unfavorable survival after surgery of patients with epithelioid mesothelioma.	MSigDBv3.0 CGP	12	2	0.1	21.9	0.00518	1	0.0738	COL5A1, VCAN
LOW DENSITY LIPOPROTEIN BINDING	others			Genes annotated by the GO term GO:0030169. Interacting selectively with low-density lipoprotein, one of the classes of lipoproteins found in blood plasma in many animals (data normally relate to humans).	MSigDBv3.0 MF	12	2	0.1	21.9	0.00518	1	0.0738	CDH13, STAB1
module 190	signaling	IGFBP		Genes in module_190: IGFBPs	MSigDBv3.0 CM	12	2	0.1	21.9	0.00518	1	0.0738	CTGF, IGFBP7
SENESE HDAC1 AND HDAC2 TARGETS UP	tumor	other		Genes up-regulated in U2OS cells (osteosarcoma) upon knockdown of both HDAC1 and HDAC2 [Gene ID=3065, 3066] by RNAi.	MSigDBv3.0 CGP	229	7	2.1	3.5	0.00524	1	0.0744	DKK2, FN1, ITGA6, MAOA, PLEC, ROBO4, TIE1
AMIT EGF RESPONSE 60 MCF10A	signaling	EGF	MCF10A	Genes whose expression peaked at 60 min after stimulation of MCF10A cells with EGF [Gene ID=1950].	MSigDBv3.0 CGP	39	3	0.4	9.2	0.00542	1	0.0763	CTGF, ID1, PLK2
KERLEY RESPONSE TO CISPLATIN UP	tumor	resistance	cisplatin	Genes genes up-regulated in NT2/D1 cells (embryonal carcinoma) in response to treatment with cisplatin [PubChem=2767].	MSigDBv3.0 CGP	39	3	0.4	9.2	0.00542	1	0.0763	CAV1, PLK2, SERPINE1
KRASNOSELSKAYA ILF3 TARGETS DN	tumor	other		Down-regulated in GHOST(3)CXCR4 cells (osteosarcoma) upon ectopic expression of ILF3 [Gene ID=3609].	MSigDBv3.0 CGP	39	3	0.4	9.2	0.00542	1	0.0763	CDH11, CXCR7, TEK
TOMLINS PROSTATE CANCER DN	tumor	other		Genes down-regulated in prostate cancer vs benign prostate tissue, based on a meta-analysis of five gene expression profiling studies.	MSigDBv3.0 CGP	39	3	0.4	9.2	0.00542	1	0.0763	ITGB4, LAMA4, PTRF
LEE NEURAL CREST STEM CELL DN	others			Genes down-regulated in the neural crest stem cells (NCS), defined as p75+/HNK1+ [Gene ID=4804, 27087].	MSigDBv3.0 CGP	123	5	1.1	4.7	0.00551	1	0.0775	CD9, CXCR7, EFEMP1, GAS6, PLK2
YAGI AML WITH 11Q23 REARRANGED	tumor	other		Genes specifically expressed in samples from patients with pediatric acute myeloid leukemia (AML) bearing 11q23 rearrangements.	MSigDBv3.0 CGP	355	9	3.3	2.9	0.00554	1	0.0776	ADAM15, COL6A2, CTGF, FOXC1, FSCN1, HSPG2, ITGAV, LRIG1, S100A10
V$FOXO1 02	TF	FOXO1A		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GNNTTGTTTACNTT which matches annotation for FOXO1A: forkhead box O1A (rhabdomyosarcoma)	MSigDBv3.0 TFT	175	6	1.6	3.9	0.00555	1	0.0776	FSTL1, MDK, NRG1, NTN1, PTMS, TEK
CREIGHTON ENDOCRINE THERAPY RESISTANCE 4	tumor	resistance	ER	The 'group 4 set' of genes associated with acquired endocrine therapy resistance in breast tumors expressing ESR1 but not ERBB2 [Gene ID=2099, 2064].	MSigDBv3.0 CGP	293	8	2.7	3.1	0.00569	1	0.0795	BMPER, COL5A1, FLNB, LRIG1, MRC2, SEMA3F, SULF1, VCAN
ST INTEGRIN SIGNALING PATHWAY	signaling	integrin		Integrin Signaling Pathway	MSigDBv3.0 CP	78	4	0.7	6	0.00573	1	0.0798	ANGPTL2, CAV1, ITGA6, ITGA9
VALK AML CLUSTER 11	tumor	other		Top 40 genes from cluster 11 of acute myeloid leukemia (AML) expression profile; 67% of the samples are FAB M4 or M5.	MSigDBv3.0 CGP	40	3	0.4	8.9	0.00582	1	0.0808	CD34, ITGA6, PALM
HARRIS HYPOXIA	signaling	hypoxia		Genes known to be induced by hypoxia	MSigDBv3.0 CGP	79	4	0.7	5.9	0.00599	1	0.0829	COL5A1, EDN1, TEK, VIM
WANG HCP PROSTATE CANCER	tumor	other		Genes with the high-CpG-density promoters (HCP) that were up-regulated in 1542-CP3TX cells (prostate cancer) compared to 1542-NPTX (normal prostate).	MSigDBv3.0 CGP	79	4	0.7	5.9	0.00599	1	0.0829	CRIP1, FLNC, FN1, SPTAN1
GATAAGR V$GATA C	TF	unknown		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif GATAAGR. Motif does not match any known transcription factor	MSigDBv3.0 TFT	235	7	2.2	3.4	0.00602	1	0.0831	BMP6, CD34, EDN1, MYH10, PKHD1L1, PVRL2, TNXB
NEGATIVE REGULATION OF ANGIOGENESIS	others	angiogenesis		Genes annotated by the GO term GO:0016525. Any process that stops, prevents or reduces the frequency, rate or extent of angiogenesis.	MSigDBv3.0 BP	13	2	0.1	19.9	0.00609	1	0.0835	COL4A2, STAB1
REACTOME METABOLISM OF NITRIC OXIDE	others			Genes involved in Metabolism of nitric oxide	MSigDBv3.0 CP:REACTOME	13	2	0.1	19.9	0.00609	1	0.0835	CAV1, NOS3
SABATES COLORECTAL ADENOMA SIZE DN	tumor	other		A selection of genes whose expression displayed significant negative correlation with size of colorectal adenoma.	MSigDBv3.0 CGP	13	2	0.1	19.9	0.00609	1	0.0835	MAOA, MMP28
HAMAI APOPTOSIS VIA TRAIL DN	tumor	resistance	TRAIL	Genes down-regulated in T1 cells (primary melanoma, sensitive to TRAIL [Gene ID=8743]) compared to G1 cells (metastatic melanoma, resistant to TRAIL).	MSigDBv3.0 CGP	126	5	1.2	4.6	0.0061	1	0.0835	COL6A1, MAOA, MDK, PLTP, SLC29A1
DAVICIONI MOLECULAR ARMS VS ERMS DN	tumor	other		Genes down-regulated in mARMS (molecular ARMS) compared to the mERMS (molecular ERMS) class of rhabdomyosarcoma tumors.	MSigDBv3.0 CGP	179	6	1.6	3.9	0.00618	1	0.0843	COL5A2, EPHB4, LTBP4, MMP2, PLK2, SCARA3

V$PU1 Q6	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif WGAGGAAG which matches annotation for SPI1: spleen focus forming virus (SFFV) proviral integration oncogene spi1	MSigDBv3.0 TFT	179	6	1.6	3.9	0.00618	1	0.0843	ADAM15, ADAMTS1, ELN, FAM38A, PSMD9, PTMS
LIU TARGETS OF VMYB VS CMYB DN	others			Gene in the opposite directions by v-MYB (DN) and c-MYB (UP) variants of CMYB [Gene ID=4602] overexpressed in primary monocyte cultures off adenoviral vectors.	MSigDBv3.0 CGP	41	3	0.4	8.7	0.00624	1	0.0848	COL4A2, TM4SF1, VCAN
POSITIVE REGULATION OF I KAPPAB KINASE NF KAPPAB CASCADE	signaling	NF-KB		Genes annotated by the GO term GO:0043123. Any process that activates or increases the frequency, rate or extent of an I-kappaB kinase/NF-kappaB induced cascade.	MSigDBv3.0 BP	80	4	0.7	5.8	0.00626	1	0.0848	ECM1, GJA1, PLK2, RHOC
ROSS AML WITH PML RARA FUSION	tumor	other		Top 100 probe sets for pediatric acute myeloid leukemia (AML) subtype t(15;17): has PML RARA fusion [Gene ID=5371, 5914].	MSigDBv3.0 CGP	80	4	0.7	5.8	0.00626	1	0.0848	AGRN, MMP2, MRC2, STAB1
ACTIN CYTOSKELETON	others			Genes annotated by the GO term GO:0015629. The part of the cytoskeleton (the internal framework of a cell) composed of actin and associated proteins. Includes actin cytoskeleton-associated complexes.	MSigDBv3.0 CC	127	5	1.2	4.5	0.0063	1	0.0852	FLNB, FSCN1, MYH10, SPTAN1, SYNPO
RECEPTOR ACTIVITY	others			Genes annotated by the GO term GO:0004872. Combining with an extracellular or intracellular messenger to initiate a change in cell activity.	MSigDBv3.0 MF	570	12	5.2	2.4	0.00637	1	0.0859	BCAM, CRIM1, GPR116, IL1R1, LPHN2, PTPRB, PVRL2, ROBO4, SCARA3, STAB1, TEK, TIE1
module 20	others			Genes in module_20	MSigDBv3.0 CM	81	4	0.7	5.7	0.00654	1	0.0881	ADAM15, CD34, HYAL2, PALM
CHEN LVAD SUPPORT OF FAILING HEART DN	others			Down-regulated genesin the left ventricle myocardium of patients with heart failure following implantation of LVAD (left ventricular assist device).	MSigDBv3.0 CGP	42	3	0.4	8.5	0.00667	1	0.0896	GJA1, PTGIS, TM4SF1
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS UP	tumor	other		Genes up-regulated in transformed NIH3T3 cells (fibroblasts transformed by activated KRAS [Gene ID=3845]) vs normal cells.	MSigDBv3.0 CGP	129	5	1.2	4.5	0.00673	1	0.0896	ANGPTL2, APCDD1, GJA1, IL1RL1, ITGA6
KAN RESPONSE TO ARSENIC TRIOXIDE	tumor	other		Genes changed in U373-MG cells (malignant glioma) upon treatment with arsenic trioxide [PubChem=14888], a chemical that can cause autophagic cell death.	MSigDBv3.0 CGP	129	5	1.2	4.5	0.00673	1	0.0896	DPYSL3, PLK2, PODXL, SERPINE1, VCAN
KIM WT1 TARGETS 8HR DN	tumor	other		Genes down-regulated in UB27 cells (osteosarcoma) at 8 hr after inducing the expression of a mutant form of WT1 [Gene ID=7490].	MSigDBv3.0 CGP	129	5	1.2	4.5	0.00673	1	0.0896	CTGF, CXCR7, ID1, NRG1, PLK2
REACTOME APOPTOSIS	signaling	apoptosis		Genes involved in Apoptosis	MSigDBv3.0 CP:REACTOME	129	5	1.2	4.5	0.00673	1	0.0896	PLEC, PSMD9, SPTAN1, TJP1, VIM
CREIGHTON ENDOCRINE THERAPY RESISTANCE 1	tumor	resistance	ER	The 'group 1 set' of genes associated with acquired endocrine therapy resistance in breast tumors expressing ESR1 and ERBB2 [Gene ID=2099, 2064].	MSigDBv3.0 CGP	503	11	4.6	2.5	0.00676	1	0.0899	BMPER, CAV1, COL5A1, FLNB, HMCN1, HSPB1, MARVELD1, MEST, MYOF, SLC29A1, SULF1
ACAWYAAAG UNKNOWN	others			Genes with promoter regions [-2kb,2kb] around transcription start site containing motif ACAWYAAAG. Motif does not match any known transcription factor	MSigDBv3.0 TFT	82	4	0.8	5.7	0.00683	1	0.0904	ALDH1A2, FN1, MMRN2, MYH10
TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE SIGNALING PATHWAY	signaling	RTK		Genes annotated by the GO term GO:0007169. The series of molecular signals generated as a consequence of a transmembrane receptor tyrosine kinase binding to its physiological ligand.	MSigDBv3.0 BP	82	4	0.8	5.7	0.00683	1	0.0904	AGRN, CDH13, EPS8, TEK
AMIT EGF RESPONSE 20 MCF10A	signaling	EGF	MCF10A	Genes whose expression peaked at 20 min after stimulation of MCF10A cells with EGF [Gene ID=1950].	MSigDBv3.0 CGP	14	2	0.1	18.2	0.00706	1	0.0926	SCARB2, SEMA3F
BIOCARTA PLATELETAPP PATHWAY	others			Platelet Amyloid Precursor Protein Pathway	MSigDBv3.0 CP:BIOCARTA	14	2	0.1	18.2	0.00706	1	0.0926	COL4A2, SERPINE1
module 470	others			Genes in module_470	MSigDBv3.0 CM	14	2	0.1	18.2	0.00706	1	0.0926	LPHN2, MAOA
VERRECCHIA RESPONSE TO TGFB1 C3	signaling	TGFB	ECM	Cluster 3: ECM related genes up-regulated in dermal fibroblasts within 30 min after TGFB1 [Gene ID=7040] addition; returned rapidly to basal level after that.	MSigDBv3.0 CGP	14	2	0.1	18.2	0.00706	1	0.0926	CD59, LAMA4
WANG RESPONSE TO PACLITAXEL VIA MAPK8 UP	signaling	JNK		Genes specifically up-regulated via JNK (MAPK8) [Gene ID=5599] signaling pathway activated by paclitaxel [PubChem=4666] in BR cells (ovarian cancer).	MSigDBv3.0 CGP	14	2	0.1	18.2	0.00706	1	0.0926	EMP1, PLK2

KEGG HYPERTROPHIC CARDIOMYOPATHY HCM	others			Hypertrophic cardiomyopathy (HCM)	MSigDBv3.0 CP:KEGG	83	4	0.8	5.6	0.00712	1	0.093	ITGA6, ITGA9, ITGAV, ITGB4
TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE ACTIVITY	others			Genes annotated by the GO term GO:0004714. Catalysis of the reaction: ATP + a protein-L-tyrosine = ADP + a protein-L-tyrosine phosphate, to initiate a change in cell activity.	MSigDBv3.0 MF	43	3	0.4	8.2	0.00712	1	0.093	CRIM1, TEK, TIE1
ELVIDGE HYPOXIA BY DMOG UP	tumor	other	hypoxia	Genes up-regulated in MCF7 cells (breast cancer) treated with hypoxia mimetic DMOG [PubChem=3080614].	MSigDBv3.0 CGP	132	5	1.2	4.4	0.0074	1	0.0964	CAV1, CD59, GJA1, LOXL2, SERPINE1
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 10D UP	others			Genes up-regulated in CD34+ [Gene ID=947] hematopoetic cells by expression of NUP98-HOXA9 fusion [Gene ID=4928, 3205] off a retroviral vector at 10 days after transduction.	MSigDBv3.0 CGP	186	6	1.7	3.7	0.00741	1	0.0964	CAV1, FLNB, FN1, IFI27, SERPINE2, TM4SF1
SCHUETZ BREAST CANCER DUCTAL INVASIVE DN	tumor	breast	IDC vs DCIS	Genes down-regulated in invasive ductal carcinoma (IDC) relative to ductal carcinoma in situ (DCIS, non-invasive).	MSigDBv3.0 CGP	84	4	0.8	5.5	0.00743	1	0.0964	MDK, PERP, PLK2, TM4SF1
JIANG TIP30 TARGETS UP	tumor	other		Up-regulated genes in HepG2 cells (liver cancer) overexpressing an oncogenic variant of tumor suppressor TIP30 [Gene ID=10553] compared to its wild type form.	MSigDBv3.0 CGP	44	3	0.4	8	0.00759	1	0.0984	ANXA2, ITGA6, LAMB1
MEMBRANE ORGANIZATION AND BIOGENESIS	others			Genes annotated by the GO term GO:0016044. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of membranes inside and surrounding the cell.	MSigDBv3.0 BP	133	5	1.2	4.3	0.00763	1	0.0986	A4GALT, AGRN, CD9, CDH13, STAB1
CELL CELL ADHESION	ECM	adhesion		Genes annotated by the GO term GO:0016337. The attachment of one cell to another cell via adhesion molecules.	MSigDBv3.0 BP	85	4	0.8	5.4	0.00774	1	0.0997	CD34, CDH13, CDH5, PVRL2
SMID BREAST CANCER LUMINAL A UP	tumor	breast	luminal A	Genes up-regulated in the luminal A subtype of breast cancer.	MSigDBv3.0 CGP	85	4	0.8	5.4	0.00774	1	0.0997	LEPR, MAOA, SPTAN1, TNXB
MOREAUX MULTIPLE MYELOMA BY TACI UP	tumor	other		Genes distinguishing in multiple myeloma (MM) samples with higher expression of TACI [Gene ID=23495].	MSigDBv3.0 CGP	375	9	3.4	2.8	0.00782	1	0.101	EPHB4, LTBP4, MMRN2, MRC2, NRG1, PVRL2, RNASE1, ROBO4, SEMA3F
NAKAYAMA SOFT TISSUE TUMORS PCA2 DN	others			Top 100 probe sets contrubuting to the negative side of the 2nd principal component; associated with adipocytic differentiation.	MSigDBv3.0 CGP	86	4	0.8	5.4	0.00806	1	0.103	CLEC3B, MAOA, MEST, PLA2G2A
REACTOME PLATELET DEGRANULATION	others			Genes involved in Platelet degranulation	MSigDBv3.0 CP:REACTOME	86	4	0.8	5.4	0.00806	1	0.103	CD9, FN1, GAS6, SERPINE1
REGULATION OF I KAPPAB KINASE NF KAPPAB CASCADE	signaling	NF-KB		Genes annotated by the GO term GO:0043122. Any process that modulates an I-kappaB kinase/NF-kappaB induced cascade.	MSigDBv3.0 BP	86	4	0.8	5.4	0.00806	1	0.103	ECM1, GJA1, PLK2, RHOC
BIOCARTA HIF PATHWAY	signaling	hypoxia		Hypoxia-Inducible Factor in the Cardiovascular System	MSigDBv3.0 CP:BIOCARTA	15	2	0.1	16.8	0.0081	1	0.103	EDN1, NOS3
LOPEZ MESOTHELIOMA SURVIVAL OVERALL DN	tumor	other	prognosis	Top genes associated with unfavorable overall survival of mesothelioma patients after surgery.	MSigDBv3.0 CGP	15	2	0.1	16.8	0.0081	1	0.103	COL5A1, FLNB
module 431	others			Genes in module_431: Eicosanoid metabolism	MSigDBv3.0 CM	15	2	0.1	16.8	0.0081	1	0.103	PLA2G2A, PTGIS
REACTOME PHASE 1 FUNCTIONALIZATION	others			Genes involved in Phase 1 functionalization	MSigDBv3.0 CP:REACTOME	15	2	0.1	16.8	0.0081	1	0.103	MAOA, PTGIS
RYTTCCTG V$ETS2 B	TF	ETS2		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RYTTCCTG which matches annotation for ETS2: v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	MSigDBv3.0 TFT	816	15	7.5	2.1	0.00816	1	0.103	ADAM15, CDH5, DKK2, ECM1, FLNB, FSTL1, GATA4, HYAL2, LTBP3, MYH10, RBMS2, RHOJ, ROBO4, SEMA3F, SPTAN1
CAGCTG V$AP4 Q5	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CAGCTG which matches annotation for REPIN1: replication initiator 1	MSigDBv3.0 TFT	1138	19	10.4	1.9	0.00829	1	0.105	ANGPTL2, BMP6, CD9, CDH13, CRIP2, DOCK6, ELN, FLNC, HYAL2, ID1, ITGA6, LAMB2, MAGED1, MDK, MMRN2, PLS3, ROBO4, SERPINE1, SPTAN1

TISSUE DEVELOPMENT	others			Genes annotated by the GO term GO:0009888. The process whose specific outcome is the progression of a tissue over time, from its formation to the mature structure.	MSigDBv3.0 BP	136	5	1.2	4.2	0.00836	1	0.105	COL5A2, CTGF, EMP1, MEST, TIE1
AMIT EGF RESPONSE 60 HELA	signaling	EGF	Hela	Genes whose expression peaked at 60 min after stimulation of HeLa cells with EGF [Gene ID=1950].	MSigDBv3.0 CGP	46	3	0.4	7.7	0.00859	1	0.107	CTGF, FOXC1, SERPINE1
LUI THYROID CANCER PAX8 PPARG UP	tumor	other		Top genes distinguishing between follicular thyroid carcinoma (FTC) samples by the presence or absence of the PAX8-PPARG [Gene ID=7849, 5468] fusion protein.	MSigDBv3.0 CGP	46	3	0.4	7.7	0.00859	1	0.107	FBN1, FSCN1, IL1R1
module 259	signaling	RTK		Genes in module_259: RTK signaling	MSigDBv3.0 CM	46	3	0.4	7.7	0.00859	1	0.107	LEPR, TEK, TIE1
ALCALAY AML BY NPM1 LOCALIZATION DN	tumor	other		Genes changed in acute myeloid leukemia (AML) with respect to cellular localization of NPM1 [Gene ID=4869]: cytoplasmic vs. nucleolar.	MSigDBv3.0 CGP	192	6	1.8	3.6	0.0086	1	0.107	CD34, EPS8, IGFBP7, ITGA9, PLXND1, TNXB
V$ATF4 Q2	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CVTGACGYMABG which matches annotation for ATF4: activating transcription factor 4 (tax-responsive enhancer element B67)	MSigDBv3.0 TFT	192	6	1.8	3.6	0.0086	1	0.107	ECM1, FLNC, ID1, MAOA, PPP2R5B, TNXB
V$FOXO4 02	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NNGTTGTTTACNTN which matches annotation for MLLT7: myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7	MSigDBv3.0 TFT	192	6	1.8	3.6	0.0086	1	0.107	EMP1, FLNC, NRG1, NTN1, PALM, TEK
HOEBEKE LYMPHOID STEM CELL DN	others			Genes down-regulated in the common lymphoid progenitor (CLP, defined as CD34+CD38-CD7+ [Gene ID=947, 952, 924]) compared to a multipotent cord blood cell (defined as CD34+CD38+CD7-).	MSigDBv3.0 CGP	88	4	0.8	5.2	0.00873	1	0.108	CFH, HSPB1, PLS3, SERPINE2
ZHANG TARGETS OF EWSR1 FLI1 FUSION	tumor	other		Genes up-regulated in RD-EF cells (rhabdomyosarcoma) engineered to express EWSR1-FLI1 fusion [Gene ID=2130, 2313] and which are also highly expressed in Ewing's famliy tumors.	MSigDBv3.0 CGP	88	4	0.8	5.2	0.00873	1	0.108	ATP1A1, CAV1, CDH11, CRIP2
V$GATA6 01	TF	GATA6		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NNNGATWANN which matches annotation for GATA6: GATA binding protein 6	MSigDBv3.0 TFT	193	6	1.8	3.6	0.00881	1	0.109	AQP1, BMP6, GATA6, LEPR, PVRL2, SFRP5
V$HNF4 DR1 Q3	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGAMCTTTGNCCN which matches annotation for HNF4A: hepatocyte nuclear factor 4, alpha	MSigDBv3.0 TFT	194	6	1.8	3.5	0.00902	1	0.11	EFEMP1, GATA4, GPRC5B, ID1, MYH10, PTMS
V$NRF2 Q4	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NTGCTGAGTCAKN which matches annotation for NFE2L2: nuclear factor (erythroid-derived 2)-like 2	MSigDBv3.0 TFT	194	6	1.8	3.5	0.00902	1	0.11	ADAM15, FLNC, HSPG2, MMRN2, SYNPO, TNXB
V$P53 02	TF	TP53		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NGRCWTGYCY which matches annotation for TP53: tumor protein p53 (Li-Fraumeni syndrome)	MSigDBv3.0 TFT	194	6	1.8	3.5	0.00902	1	0.11	GATA4, MDK, MMP28, MRC2, NRG1, PPP2R5B
module 486	others			Genes in module_486	MSigDBv3.0 CM	89	4	0.8	5.2	0.00908	1	0.11	ARHGAP23, ENG, PLXND1, SLC9A3R2
HUANG FOXA2 TARGETS UP	tumor	other		Genes up-regulated in H358 cells (lung cancer) by inducible expression of FOXA2 [GeneID=3170] in a Tet-off system.	MSigDBv3.0 CGP	47	3	0.4	7.5	0.00911	1	0.11	CXCR7, FN1, NRG1
ENZYME LINKED RECEPTOR PROTEIN SIGNALING PATHWAY	signaling			Genes annotated by the GO term GO:0007167. Any series of molecular signals initiated by the binding of an extracellular ligand to a receptor on the surface of the target cell, where the receptor possesses catalytic activity or is closely associated with an enzyme such as a protein kinase.	MSigDBv3.0 BP	139	5	1.3	4.1	0.00914	1	0.11	AGRN, CDH13, ENG, EPS8, TEK
ALONSO METASTASIS NEURAL UP	tumor	other	metastasis	Neural-related genes up-regulated in melanoma tumors that developed metastases compared to primary melanoma that did not.	MSigDBv3.0 CGP	16	2	0.1	15.6	0.0092	1	0.11	EMP1, S100A10
HOMOPHILIC CELL ADHESION	ECM	adhesion		Genes annotated by the GO term GO:0007156. The attachment of an adhesion molecule in one cell to an identical molecule in an adjacent cell.	MSigDBv3.0 BP	16	2	0.1	15.6	0.0092	1	0.11	CDH5, PVRL2
KANG FLUOROURACIL RESISTANCE DN	tumor	resistance	5-fluorouracil	Genes down-regulated in gastric cancer cell lines resistant to 5-fluorouracil [PubChem=3385].	MSigDBv3.0 CGP	16	2	0.1	15.6	0.0092	1	0.11	FLNB, ITGB4
KORKOLA TERATOMA UP	tumor	other		Genes from the 12p region that up-regulated in teratoma cells compared to normal testis.	MSigDBv3.0 CGP	16	2	0.1	15.6	0.0092	1	0.11	EMP1, PTMS
MACLACHLAN BRCA1 TARGETS DN	tumor	other		Genes down-regulated in SW480 cells (colon cancer with mutated p53 [Gene ID=7157]) upon expression of BRCA1 [Gene ID=672] off an adenovirus vector.	MSigDBv3.0 CGP	16	2	0.1	15.6	0.0092	1	0.11	CD59, CD9
module 275	others			Genes in module_275	MSigDBv3.0 CM	16	2	0.1	15.6	0.0092	1	0.11	ITGA9, ITGAV

module 474	others			Genes in module_474	MSigDBv3.0 CM	16	2	0.1	15.6	0.0092	1	0.11	CTGF, IGFBP7
MURATA VIRULENCE OF H PILORI	others			Selected genes up-regulated in WT-A10 cells (gastric epithelium) expressing the H. pilori virulence gene CagA.	MSigDBv3.0 CGP	16	2	0.1	15.6	0.0092	1	0.11	COL6A2, GAS6
NIKOLSKY BREAST CANCER 21Q22 AMPLICON	tumor	breast	amplicon	Genes within amplicon 21q22 identified in a copy alterations study of 191 breast tumor samples.	MSigDBv3.0 CGP	16	2	0.1	15.6	0.0092	1	0.11	COL6A1, COL6A2
REACTOME CELLEXTRACELLULAR MATRIX INTERACTIONS	ECM	ECM interaction		Genes involved in Cell-extracellular matrix interactions	MSigDBv3.0 CP:REACTOME	16	2	0.1	15.6	0.0092	1	0.11	FLNC, LIMS2
REACTOME CRMPS IN SEMA3A SIGNALING	others			Genes involved in CRMPs in Sema3A signaling	MSigDBv3.0 CP:REACTOME	16	2	0.1	15.6	0.0092	1	0.11	DPYSL3, PLXNA4
REACTOME OTHER SEMAPHORIN INTERACTIONS	others			Genes involved in Other semaphorin interactions	MSigDBv3.0 CP:REACTOME	16	2	0.1	15.6	0.0092	1	0.11	PLXNA4, PLXND1
SCHAVOLT TARGETS OF TP53 AND TP63	TF	TF53		Genes up-regulated by TP53 [Gene ID=7157] and down-regulated by an isoform of TP63 [Gene ID=8626] in primary HEK cells (epidermal keratinocytes).	MSigDBv3.0 CGP	16	2	0.1	15.6	0.0092	1	0.11	PODXL, VCAN
GOZGIT ESR1 TARGETS UP	tumor	other	ER	Genes up-regulated in TMX2-28 cells (breast cancer) which do not express ESR1 [Gene ID=2099]) compared to the parental MCF7 cells which do.	MSigDBv3.0 CGP	140	5	1.3	4.1	0.00941	1	0.112	ECM1, LAMB1, MMRN2, PALM, SERPINE1
KEGG DILATED CARDIOMYOPATHY	others			Dilated cardiomyopathy	MSigDBv3.0 CP:KEGG	90	4	0.8	5.1	0.00943	1	0.112	ITGA6, ITGA9, ITGAV, ITGB4
ZHONG RESPONSE TO AZACITIDINE AND TSA UP	tumor	resistance	azacitidine	Genes up-regulated in 3 out of 4 NSCLC cell lines (non-small cell lung cancer) after treatment with azacitidine [PubChem=9444] and TSA [PubChem=5562].	MSigDBv3.0 CGP	196	6	1.8	3.5	0.00946	1	0.112	CD9, COL1A2, ECM1, FLNC, MMP2, PTRF
CTTTGA V$LEF1 Q2	TF	LEF1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CTTTGA which matches annotation for LEF1: lymphoid enhancer-binding factor 1	MSigDBv3.0 TFT	910	16	8.3	2	0.00954	1	0.113	BGN, CDC42BPB, CDH13, COL5A1, EMP1, IL1RL1, LAMB2, LPHN2, NFE2L1, NRG1, PKHD1L1, PLXND1, ROBO4, SPTAN1, SULF1, TNXB
module 112	others			Genes in module_112	MSigDBv3.0 CM	257	7	2.4	3.1	0.00961	1	0.114	CAV1, COL3A1, COL4A2, COL5A2, DPYSL3, LRRC32, NRG1
KONDO EZH2 TARGETS	tumor	other	EZH2	Genes up-regulated in PC3 cells (prostate cancer) after EZH2 [Gene ID=2146] knockdown by RNAi.	MSigDBv3.0 CGP	141	5	1.3	4.1	0.00968	1	0.114	ANO1, CTGF, EMP1, GJA1, ITGA6
ELVIDGE HIF1A TARGETS DN	signaling	hypoxia	breast cells	Genes down-regulated in MCF7 cells (breast cancer) after knockdown of HIF1A [Gene ID=3091] by RNAi.	MSigDBv3.0 CGP	91	4	0.8	5.1	0.0098	1	0.115	CAV1, GJA1, LOXL2, PTRF
SEIDEN ONCOGENESIS BY MET	tumor	other		Genes changed in xenograft tumors formed by DLD-1 or DKO-4 cells (colon cancer) overexpressing MET [Gene ID=4233].	MSigDBv3.0 CGP	91	4	0.8	5.1	0.0098	1	0.115	EPS8, ITGA6, LAMB1, PLS3
V$HNF4 Q6	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif AARGTCCAN which matches annotation for HNF4A: hepatocyte nuclear factor 4, alpha	MSigDBv3.0 TFT	198	6	1.8	3.5	0.00992	1	0.117	CTGF, EMP1, GATA4, KIF1C, MAGED1, PTMS
ONDER CDH1 TARGETS 1 UP	EMT	gene	CDH1	Genes up-regulated in HMLE cells (mmortalized nontransformed mammary epithelial) by expression of a dominant-negative form of E-cadhedrin (CDH1) [Gene ID=999].	MSigDBv3.0 CGP	142	5	1.3	4	0.00996	1	0.117	CRIP2, LEPR, MAGED1, MMP28, SEMA3F
ONKEN UVEAL MELANOMA DN	tumor	other		Genes down-regulated in uveal melanoma: class 2 vs class 1 tumors.	MSigDBv3.0 CGP	532	11	4.9	2.4	0.0101	1	0.118	CAV1, DSTN, HYAL2, LAMA4, LAMB2, MEST, NFE2L1, POSTN, SCARB2, TJP1, TXNDC5
BROWNE HCMV INFECTION 2HR DN	others			Genes down-regulated in primary fibroblast cell culture point after infection with HCMV (AD169 strain) at 2 h time point that were not down-regulated at the previous time point, 1 h.	MSigDBv3.0 CGP	49	3	0.4	7.2	0.0102	1	0.119	ANXA2, ITGA6, SERPINE1
LENAOUR DENDRITIC CELL MATURATION UP	others			Genes up-regulated during in vitro maturation of CD14+ [Gene ID=929] monocytes (day 0) into immature (day 7) and mature dendritic cells (day 14).	MSigDBv3.0 CGP	92	4	0.8	5	0.0102	1	0.119	ECM1, GAS6, MAOA, SPTAN1
NATSUME RESPONSE TO INTERFERON BETA DN	tumor	other		Genes down-regulated in T98 cells (glioma) 48 h after treatment with interferon beta.	MSigDBv3.0 CGP	49	3	0.4	7.2	0.0102	1	0.119	ANXA2, GAS6, MMP2
CAGTATT,MIR-200B,MIR-200C,MIR-429	microRNA			Targets of MicroRNA CAGTATT,MIR-200B,MIR-200C,MIR-429	MSigDBv3.0 MIR	392	9	3.6	2.6	0.0103	1	0.119	CDH11, EPS8, FN1, GATA4, LEPR, PLK2, PLS3, SEMA3F, SULF1

KEGG PATHWAYS IN CANCER	tumor	other		Pathways in cancer	MSigDBv3.0 CP:KEGG	325	8	3	2.8	0.0103	1	0.12	COL4A2, FN1, ITGA6, ITGAV, LAMA4, LAMB1, LAMB2, MMP2
GOUYER TATI TARGETS DN	tumor	other		Genes down-regulated in constitutively invasive HT-29 5M21 cells (colon cancer) vs those expressing functionally inactive TATI [Gene ID=6690].	MSigDBv3.0 CGP	17	2	0.2	14.6	0.0104	1	0.12	A4GALT, FN1
NELSON RESPONSE TO ANDROGEN DN	tumor	other		Genes down-regulated in LNCaP cells (prostate cancer) in response to synthetic androgen R1881 [PubChem=13766].	MSigDBv3.0 CGP	17	2	0.2	14.6	0.0104	1	0.12	FN1, SLC29A1
V$PXR Q2	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RRGGTYANTRNM which matches annotation for NR1H4: nuclear receptor subfamily 1, group H, member 4	MSigDBv3.0 TFT	200	6	1.8	3.4	0.0104	1	0.12	ADAM15, ALDH1A2, CTGF, FSTL1, GATA4, NRG1
ION BINDING	others			Genes annotated by the GO term GO:0043167. Interacting selectively with ions, charged atoms or groups of atoms.	MSigDBv3.0 MF	263	7	2.4	3	0.0108	1	0.125	CDC42BPB, CRIP1, CRIP2, FBLN2, FBN1, LTBP4, MMP2
chr3q21	others			Genes in cytogenetic band chr3q21	MSigDBv3.0	95	4	0.9	4.8	0.0113	1	0.131	HEG1, PLXND1, SLCO2A1, TM4SF1
CHARAFE BREAST CANCER BASAL VS MESENCHYMAL DN	tumor	breast	basal vs mesenchymal	Genes down-regulated in basal-like breast cancer cell lines as compared to the mesenchymal-like ones.	MSigDBv3.0 CGP	51	3	0.5	6.9	0.0114	1	0.131	COL6A2, FLNC, LOXL2
TRANSMEMBRANE RECEPTOR PROTEIN KINASE ACTIVITY	others			Genes annotated by the GO term GO:0019199.	MSigDBv3.0 MF	51	3	0.5	6.9	0.0114	1	0.131	CRIM1, TEK, TIE1
KYNG DNA DAMAGE BY 4NQO	tumor	other		Genes specifically responding to 4NQO treatment of primary fibroblasts.	MSigDBv3.0 CGP	18	2	0.2	13.7	0.0116	1	0.132	FBLN2, ID1
LIPOPROTEIN BINDING	others			Genes annotated by the GO term GO:0008034. Interacting selectively with any conjugated, water-soluble protein in which the nonprotein moiety consists of a lipid or lipids.	MSigDBv3.0 MF	18	2	0.2	13.7	0.0116	1	0.132	CDH13, STAB1
module 156	others			Genes in module_156	MSigDBv3.0 CM	18	2	0.2	13.7	0.0116	1	0.132	COL6A1, PTGIS
RUGO RESPONSE TO 4NQO	tumor	other		Subset C (Fig 2c): genes changed upon exposure to the carcinogen 4-nitroquinoline-1-oxide (4NQO) [PubChem=5955].	MSigDBv3.0 CGP	18	2	0.2	13.7	0.0116	1	0.132	FBLN2, ID1
WATANABE ULCERATIVE COLITIS WITH CANCER UP	tumor	other		Genes up-regulated in non-neoplastic rectal mucosa samples from patients having cancer associated with ulcerative collitis, compared to those who did not have the cancer.	MSigDBv3.0 CGP	18	2	0.2	13.7	0.0116	1	0.132	ANGPTL2, FBN1
HAMAI APOPTOSIS VIA TRAIL UP	tumor	other		Genes up-regulated in T1 cells (primary melanoma, sensitive to TRAIL [Gene ID=8743]) compared to G1 cells (metastatic melanoma, resistant to TRAIL).	MSigDBv3.0 CGP	333	8	3.1	2.7	0.0118	1	0.134	EMP1, FSTL1, ITGA6, ITGAV, MYH10, NPDC1, PLS3, PODXL
SHAFFER IRF4 TARGETS IN MYELOMA VS MATURE B LYMPHOCYTE	tumor	other		IRF4 [Gene ID=3662] target genes up-regulated in primary myeloma vs. mature B lymphocytes.	MSigDBv3.0 CGP	96	4	0.9	4.8	0.0118	1	0.133	BMP6, CAV1, HSPB1, TXNDC5
RNCTGNYNRNCTGNY UNKNOWN	TF	unknown		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif RNCTGNYNRNCTGNY. Motif does not match any known transcription factor	MSigDBv3.0 TFT	52	3	0.5	6.7	0.012	1	0.136	BMP6, ID1, NOS3
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 8D UP	others			Genes up-regulated in CD34+ [Gene ID=947] hematopoetic cells by expression of NUP98-HOXA9 fusion [Gene ID=4928, 3205] off a retroviral vector at 8 days after transduction.	MSigDBv3.0 CGP	149	5	1.4	3.8	0.0121	1	0.136	FOXC1, GJA1, IFI27, LTBP3, MYH10
ARGGGTTAA UNKNOWN	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif ARGGGTTAA. Motif does not match any known transcription factor	MSigDBv3.0 TFT	97	4	0.9	4.7	0.0122	1	0.137	CDH5, DSTN, FLNC, PVRL2
V$NF1 Q6 01	TF	NF1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NTGGNNNNNNGCCAANN which matches annotation for NF1: neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)	MSigDBv3.0 TFT	207	6	1.9	3.3	0.0122	1	0.137	BMP6, LAMB2, POSTN, RHOJ, SLCO2A1, TEK
CATION BINDING	others			Genes annotated by the GO term GO:0043169. Interacting selectively with cations, charged atoms or groups of atoms with a net positive charge.	MSigDBv3.0 MF	208	6	1.9	3.3	0.0124	1	0.139	CRIP1, CRIP2, FBLN2, FBN1, LTBP4, MMP2
module 111	others			Genes in module_111	MSigDBv3.0 CM	151	5	1.4	3.8	0.0127	1	0.143	BGN, CD34, CDH5, SEMA3F, SLC9A3R2
TGASTMAGC V$NFE2 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGASTMAGC which matches annotation for NFE2: nuclear factor (erythroid-derived 2), 45kDa	MSigDBv3.0 TFT	151	5	1.4	3.8	0.0127	1	0.143	ADAM15, MMRN2, PLS3, SYNPO, TNXB

CHIBA RESPONSE TO TSA DN	tumor	other		Cancer related genes down-regulated in any of four hepatoma cell lines following 24 h treatment with TSA [PubChem=5562].	MSigDBv3.0 CGP	19	2	0.2	12.9	0.0129	1	0.143	ITGAV, LAMB1
ESTABLISHMENT AND OR MAINTENANCE OF CELL POLARITY	others			Genes annotated by the GO term GO:0007163. The specification, formation and maintenance of anisotropic intracellular organization or cell growth patterns.	MSigDBv3.0 BP	19	2	0.2	12.9	0.0129	1	0.143	CDC42BPB, SFRP5
INTEGRIN COMPLEX	ECM	adhesion	receptor	Genes annotated by the GO term GO:0008305. Any member of a family of heterodimeric transmembrane receptors for cell-adhesion molecules. The alpha and beta subunits are noncovalently bonded.	MSigDBv3.0 CC	19	2	0.2	12.9	0.0129	1	0.143	ITGA9, ITGB4
KANG DOXORUBICIN RESISTANCE DN	tumor	resistance	doxorubicin	Genes differentialy expressed in gastric cancer cell lines: doxorubicin [PubChem=31703] resistant vs sensitive.	MSigDBv3.0 CGP	19	2	0.2	12.9	0.0129	1	0.143	CRIM1, TJP1
MASRI RESISTANCE TO TAMOXIFEN AND AROMATASE INHIBITORS UP	tumor	resistance	ER	Genes up-regulated in derivatives of MCF-7aro cells (breast cancer) that developed resistance to tamoxifen [PubChem=5376] or inhibitors of aromatase (CYP19A1) [Gene ID=1588].	MSigDBv3.0 CGP	19	2	0.2	12.9	0.0129	1	0.143	GJA1, SULF1
V$IK2 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif NNNTGGGAWNNC. Motif does not match any known transcription factor	MSigDBv3.0 TFT	210	6	1.9	3.3	0.013	1	0.143	CDH5, CTGF, MAGED1, RBMS2, SEMA3F, TNFRSF21
V$NFKB C	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif NGGGACTTTCCA. Motif does not match any known transcription factor	MSigDBv3.0 TFT	210	6	1.9	3.3	0.013	1	0.143	CDH5, CTGF, GATA4, ITGB4, PTMS, S100A10
FLOTHO PEDIATRIC ALL THERAPY RESPONSE UP	tumor	other		Up-regulated genes significantly associated with positive minimal residual disease (MRD) on day 46 after chemotherapy treatment of children with acute lymphoblastic leukemia (ALL).	MSigDBv3.0 CGP	54	3	0.5	6.5	0.0133	1	0.146	CD34, EMP1, ITGA6
JI RESPONSE TO FSH UP	tumor	other		Genes up-regulated in MCV152 cells (ovarian cancer) treated with follicle stimulating hormone (FSH).	MSigDBv3.0 CGP	54	3	0.5	6.5	0.0133	1	0.146	COL3A1, DPYSL3, LAMA4
RRCCGTTA UNKNOWN	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif RRCCGTTA. Motif does not match any known transcription factor	MSigDBv3.0 TFT	54	3	0.5	6.5	0.0133	1	0.146	ID1, MYH10, VIM
MACROMOLECULAR COMPLEX ASSEMBLY	others			Genes annotated by the GO term GO:0065003. The aggregation, arrangement and bonding together of a set of macromolecules to form a complex.	MSigDBv3.0 BP	275	7	2.5	2.9	0.0136	1	0.149	AGRN, CD9, GJA1, HSPB1, PTRF, SLC9A3R2, TJP1
BLUM RESPONSE TO SALIRASIB DN	tumor	other	salirasib	Selected genes down-regulated in response to the Ras inhibitor salirasib [PubChem=5469318] in a panel of cancer cell lines with constantly active HRAS [Gene ID=3265].	MSigDBv3.0 CGP	342	8	3.1	2.7	0.0137	1	0.15	CRIP2, DPYSL3, HSPB1, ID1, LTBP3, MEST, PLS3, WWTR1
KEGG REGULATION OF ACTIN CYTOSKELETON	cytoskeleton	related		Regulation of actin cytoskeleton	MSigDBv3.0 CP:KEGG	213	6	2	3.2	0.0138	1	0.151	FN1, ITGA6, ITGA9, ITGAV, ITGB4, MYH10
MASSARWEH TAMOXIFEN RESISTANCE UP	tumor	resistance	ER	Genes up-regulated in breast cancer tumors (formed by MCF-7 xenografts) resistant to tamoxifen [PubChem=5376].	MSigDBv3.0 CGP	557	11	5.1	2.3	0.0138	1	0.151	BCAM, CDH11, COL1A2, COL5A2, CXCR7, EDN1, EMP1, IL1R1, MUC1, SCARA3, TXNDC5
V$AP1 Q4	TF	JUN		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RGTGACTMANN which matches annotation for JUN: jun oncogene	MSigDBv3.0 TFT	213	6	2	3.2	0.0138	1	0.151	CD151, DSTN, EDN1, LTBP3, SYNPO, VIM
V$LXR Q3	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGGGGTYACTNNCGGTCA which matches annotation for NR1H3: nuclear receptor subfamily 1, group H, member 3	MSigDBv3.0 TFT	55	3	0.5	6.3	0.014	1	0.152	NRG1, PTMS, SULF1
GTCAACC,MIR-380-5P	microRNA			Targets of MicroRNA GTCAACC,MIR-380-5P	MSigDBv3.0 MIR	20	2	0.2	12.1	0.0142	1	0.154	COL1A2, ITGA9
LIANG SILENCED BY METHYLATION UP	others			Genes up-regulated in LD419 cells (fibroblast) after treatment with decitabine (5-aza-2'-deoxycytidine) [PubChem=451668].	MSigDBv3.0 CGP	20	2	0.2	12.1	0.0142	1	0.154	AQP1, IFI27
MASRI RESISTANCE TO TAMOXIFEN AND AROMATASE INHIBITORS DN	tumor	resistance	ER	Genes down-regulated in derivatives of MCF-7aro cells (breast cancer) that developed resistance to tamoxifen [PubChem=5376] or inhibitors of aromatase (CYP19A1) [Gene ID=1588].	MSigDBv3.0 CGP	20	2	0.2	12.1	0.0142	1	0.154	CTGF, EFEMP1
NEURON PROJECTION	others			Genes annotated by the GO term GO:0043005. A prolongation or process extending from a nerve cell, e.g. an axon or dendrite.	MSigDBv3.0 CC	20	2	0.2	12.1	0.0142	1	0.154	CDH13, SYNPO
VERRECCHIA RESPONSE TO TGFB1 C5	signaling	TGFB	ECM	Cluster 5: ECM related genes up-regulated in dermal fibroblasts later than 30 min after TGFB1 [Gene ID=7040] addition; decreased slowly after the peak at 120 min time point.	MSigDBv3.0 CGP	20	2	0.2	12.1	0.0142	1	0.154	MMP2, SEMA3F

KOBAYASHI EGFR SIGNALING 24HR UP	tumor	resistance	CL-387785/EGFRi	Genes up-regulated in H1975 cells (non-small cell lung cancer, NSCLC) resistant to gefitinib [PubChem=123631] after treatment with EGFR inhibitor CL-387785 [PubChem=2776] for 24h.	MSigDBv3.0 CGP	102	4	0.9	4.5	0.0144	1	0.155	BCAM, HEG1, MAOA, MUC1
CHIANG LIVER CANCER SUBCLASS UNANNOTATED DN	tumor	other		Marker genes down-regulated in the 'unannotated' subclass of hepatocellular carcinoma (HCC) samples.	MSigDBv3.0 CGP	156	5	1.4	3.7	0.0145	1	0.156	ATP1A1, GJA1, MAGED1, S100A10, SLC29A1
V$CEBP C	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NGWVTKNKGYAAKNSAYA which matches annotation for CEBPA: CCAAT/enhancer binding protein (C/EBP), alpha	MSigDBv3.0 TFT	156	5	1.4	3.7	0.0145	1	0.156	CRIM1, CTGF, FSTL1, GATA4, ROBO4
CATTGTYY V$SOX9 B1	TF	Sox9		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CATTGTYY which matches annotation for SOX9: SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	MSigDBv3.0 TFT	279	7	2.6	2.9	0.0146	1	0.156	ADAM15, CD151, EDN1, GPR116, HSPG2, HYAL2, KIF1C
BROWNE HCMV INFECTION 30MIN UP	others			Genes up-regulated in primary fibroblast cell culture at 30 min time point after infection with HCMV (AD169 strain).	MSigDBv3.0 CGP	56	3	0.5	6.2	0.0147	1	0.157	COL6A1, COL6A2, IFI27
CCACACA,MIR-147	microRNA			Targets of MicroRNA CCACACA,MIR-147	MSigDBv3.0 MIR	56	3	0.5	6.2	0.0147	1	0.157	ATP1A1, GPRC5B, SEMA3F
PEREZ TP53 TARGETS	TF	TP53	breast cells	Genes up-regulated in the HMEC cells (primary mammary epithelium) upon expression of TP53 [Gene ID=7157] off adenoviral vector.	MSigDBv3.0 CGP	1123	18	10.3	1.9	0.0148	1	0.158	APCDD1, ARHGAP23, CCDC3, CGNL1, COL5A2, COL6A1, CRIP1, CRIP2, CXCR7, FGD5, FLNC, FOXC1, HEG1, ITGA9, LTBP3, MMP28, NTN1, VCAN
RUTELLA RESPONSE TO HGF VS CSF2RB AND IL4 UP	others			Genes up-regulated in peripheral blood mononucleocytes by HGF [Gene ID=3082] compared to those regulated by CSF2RB (GM-CSF) [Gene ID=1437] and IL4 [Gene ID=3565].	MSigDBv3.0 CGP	417	9	3.8	2.5	0.0149	1	0.159	CD9, CRIM1, EMP1, IGFBP7, MMP2, MYOF, PLTP, SCARB2, SERPINE1
module 199	others			Genes in module_199	MSigDBv3.0 CM	57	3	0.5	6.1	0.0154	1	0.163	LEPR, TEK, TIE1
STRUCTURAL CONSTITUENT OF CYTOSKELETON	cytoskeleton	related		Genes annotated by the GO term GO:0005200. The action of a molecule that contributes to the structural integrity of a cytoskeletal structure.	MSigDBv3.0 MF	57	3	0.5	6.1	0.0154	1	0.163	AGRN, SPTAN1, VIM
FOURNIER ACINAR DEVELOPMENT EARLY UP	signaling	breast cells	acinar development	Genes up-regulated early in HMEC cells (mammary epithelium) during acinar development in vitro.	MSigDBv3.0 CGP	21	2	0.2	11.5	0.0156	1	0.165	EFEMP1, LEPR
LANDIS ERBB2 BREAST TUMORS 65 UP	tumor	breast	ERBB2	The 65 most significantly changed (p<0.01) genes out of the 324 genes identified by two analytical methods in the mammary tumors induced by transgenic expression of ERBB2 [Gene ID=2064].	MSigDBv3.0 CGP	21	2	0.2	11.5	0.0156	1	0.165	CD9, PERP
module 73	others			Genes in module_73	MSigDBv3.0 CM	21	2	0.2	11.5	0.0156	1	0.165	IL1R1, IL1RL1
NGUYEN NOTCH1 TARGETS UP	others			Genes up-regulated in primary keratinocytes by expression of constantly active NOTCH1 [Gene ID=4851].	MSigDBv3.0 CGP	21	2	0.2	11.5	0.0156	1	0.165	ITGAV, LAMB2
TIAN TNF SIGNALING VIA NFKB	signaling	NF-KB		Genes modulated in HeLa cells (cervical carcinoma) by TNF [Gene ID=7124] via NFKB pathway.	MSigDBv3.0 CGP	21	2	0.2	11.5	0.0156	1	0.165	CTGF, PLK2
NAGASHIMA EGF SIGNALING UP	signaling	EGF	MCF7	Genes up-regulated in MCF7 cells (breast cancer) after stimulation with EGF [Gene ID=1950].	MSigDBv3.0 CGP	58	3	0.5	6	0.0161	1	0.17	CTGF, EDN1, ID1
KIM WT1 TARGETS UP	tumor	other		Genes up-regulated in UB27 cells (osteosarcoma) at any time point after inducing the expression of a mutant form of WT1 [Gene ID=7490].	MSigDBv3.0 CGP	221	6	2	3.1	0.0163	1	0.171	FLNC, FOXC1, MYH10, SERPINE1, TM4SF1, WWTR1
V$AP1 Q2 01	TF	JUN		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGACTCANNSKN which matches annotation for JUN: jun oncogene	MSigDBv3.0 TFT	221	6	2	3.1	0.0163	1	0.171	ADAM15, COL1A2, FLNC, LTBP3, PERP, TNXB
V$AP1FJ Q2	TF	JUN		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif RSTGACTNMNW which matches annotation for JUN: jun oncogene	MSigDBv3.0 TFT	222	6	2	3.1	0.0166	1	0.174	DSTN, FLNC, ID1, LTBP3, SYNPO, VIM
DAVICIONI PAX FOXO1 SIGNATURE IN ARMS UP	tumor	other		'PAX-FKHR signature': genes up-regulated by PAX3- or PAX7-FOXO1 [Gene ID=5081, 5077, 2308] fusion in primary alveolar rhabdomyosarcoma(ARMS) tumors.	MSigDBv3.0 CGP	59	3	0.5	5.9	0.0169	1	0.176	CD9, CXCR7, SULF1
I KAPPAB KINASE NF KAPPAB CASCADE	signaling	NF-KB		Genes annotated by the GO term GO:0007249. A series of reactions initiated by the activation of the transcription factor NF-kappaB. NF-kappaB is sequestered by the inhibitor I-kappaB, and is released when I-kappaB is phosphorylated by activated I-kappaB kinase.	MSigDBv3.0 BP	107	4	1	4.3	0.0169	1	0.176	ECM1, GJA1, PLK2, RHOC
SAMOLS TARGETS OF KHSV MIRNAS DN	tumor	other		Genes down-regulated in 293 cells (embryonic kidney) upon expression of KHSV (Kaposi sarcoma???associated herpesvirus) microRNAs.	MSigDBv3.0 CGP	59	3	0.5	5.9	0.0169	1	0.176	DKK3, FN1, MAOA

EPIDERMAL GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	signaling			Genes annotated by the GO term GO:0007173. The series of molecular signals generated as a consequence of an epidermal growth factor receptor binding to one of its physiological ligands.	MSigDBv3.0 BP	22	2	0.2	10.9	0.0171	1	0.177	CDH13, EPS8
MESODERM DEVELOPMENT	others			Genes annotated by the GO term GO:0007498. The process whose specific outcome is the progression of the mesoderm over time, from its formation to the mature structure. The mesoderm is the middle germ layer that develops into muscle, bone, cartilage, blood and connective tissue.	MSigDBv3.0 BP	22	2	0.2	10.9	0.0171	1	0.177	MEST, TIE1
MISHRA CARCINOMA ASSOCIATED FIBROBLAST UP	tumor	other		Top genes up-regulated in mesenchyme stem cells (MSC) grown in a tumor conditioned medium, which leads to carcinoma-associated fibroblast phenotype.	MSigDBv3.0 CGP	22	2	0.2	10.9	0.0171	1	0.177	COL6A1, COL6A2
REGULATION OF SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	signaling			Genes annotated by the GO term GO:0051056. Any process that modulates the frequency, rate or extent of small GTPase mediated signal transduction.	MSigDBv3.0 BP	22	2	0.2	10.9	0.0171	1	0.177	CDC42BPB, FGD5
RODRIGUES THYROID CARCINOMA ANAPLASTIC DN	tumor	other		Genes down-regulated in anaplastic thyroid carcinoma (ATC) compared to normal thyroid tissue.	MSigDBv3.0 CGP	500	10	4.6	2.3	0.0171	1	0.177	BCAM, CFH, ID1, IGFBP7, LPHN2, LRIG1, MMRN2, PODXL, PTPRB, SCARA3
BENPORATH OCT4 TARGETS	TF		4-Oct	Set 'Oct4 targets': genes upregulated and identified by ChIP on chip as OCT4 [Gene ID=5460] transcription factor targets in human embryonic stem cells.	MSigDBv3.0 CGP	289	7	2.6	2.8	0.0173	1	0.179	CTGF, DPYSL3, GATA6, GJA1, LAMA4, MMP2, SULF1
V$AP1 C	TF	JUN		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif NTGASTCAG which matches annotation for JUN: jun oncogene	MSigDBv3.0 TFT	224	6	2.1	3	0.0173	1	0.179	ADAM15, EMP1, FLNC, FSTL1, GJA1, LTBP3
module 136	others			Genes in module_136	MSigDBv3.0 CM	430	9	3.9	2.4	0.0178	1	0.183	CD9, CDH5, EDN1, GJA1, HYAL2, IFI27, IL1RL1, KIAA1522, SCARA3
NEGATIVE REGULATION OF BIOLOGICAL PROCESS	others			Genes annotated by the GO term GO:0048519. Any process that stops, prevents or reduces the frequency, rate or extent of a biological process. Biological processes are regulated by many means; examples include the control of gene expression, protein modification or interaction with a protein or substrate molecule.	MSigDBv3.0 BP	657	12	6	2.1	0.018	1	0.185	ADAMTS1, CDH13, COL4A2, FOXC1, HSPB1, ID1, IGFBP7, MAGED1, NRG1, SERPINE1, STAB1, TXNDC5
V$HFH4 01	TF	FOXJ1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif AWKTGTTTGTTTA which matches annotation for FOXJ1: forkhead box J1	MSigDBv3.0 TFT	165	5	1.5	3.5	0.0181	1	0.185	CRIM1, FSTL1, ID1, NRG1, NTN1
CYTOSKELETON	cytoskeleto n			Genes annotated by the GO term GO:0005856. Any of the various filamentous elements that form the internal framework of cells, and typically remain after treatment of the cells with mild detergent to remove membrane constituents and soluble components of the cytoplasm. The term embraces intermediate filaments, microfilaments, microtubules, the microtrabecular lattice, and other structures characterized by a polymeric filamentous nature and long-range order within the cell. The various elements of the cytoskeleton not only serve in the maintenance of cellular shape but also have roles in other cellular functions, including cellular movement, cell division, endocytosis, and movement of organelles.	MSigDBv3.0 CC	361	8	3.3	2.5	0.0184	1	0.188	CDC42BPB, FLNB, FSCN1, HSPB1, MYH10, SPTAN1, SYNPO, VIM
MASSARWEH RESPONSE TO ESTRADIOL	tumor	other	ER	Genes rapidly up-regulated in breast cancer cell cultures by estradiol [PubChem=5757].	MSigDBv3.0 CGP	61	3	0.6	5.7	0.0184	1	0.188	FLNB, LRIG1, MYOF
module 176	signaling			Genes in module_176: signaling	MSigDBv3.0 CM	227	6	2.1	3	0.0184	1	0.188	CAV1, COL3A1, COL5A2, DPYSL3, LRRC32, NRG1
PROTEIN COMPLEX ASSEMBLY	others			Genes annotated by the GO term GO:0006461. The aggregation, arrangement and bonding together of a set of components to form a protein complex.	MSigDBv3.0 BP	166	5	1.5	3.4	0.0185	1	0.188	AGRN, CD9, GJA1, SLC9A3R2, TJP1
chr6p24	others			Genes in cytogenetic band chr6p24	MSigDBv3.0	23	2	0.2	10.4	0.0186	1	0.188	BMP6, TXNDC5
DACOSTA ERCC3 ALLELE XPCS VS TTD UP	others			Genes up-regulated in fibroblasts expressing different mutant forms of ERCC3 [Gene ID=2071]: XP/CS (xeroderma pigmentosum (XP) and Cockraine's syndrome (CS)) vs TTD (trichothiodystrophy).	MSigDBv3.0 CGP	23	2	0.2	10.4	0.0186	1	0.188	MDK, MEST
KEGG PROXIMAL TUBULE BICARBONATE RECLAMATION	others			Proximal tubule bicarbonate reclamation	MSigDBv3.0 CP:KEGG	23	2	0.2	10.4	0.0186	1	0.188	AQP1, ATP1A1

TAVOR CEBPA TARGETS DN	tumor	other		Genes down-regulated in KCL22 cells (chronic myelogenous leukemia, CML, with BCR-ABL1 [GeneID=613, 25] fusion) by expression of CEBPA [GeneID=1050].	MSigDBv3.0 CGP	23	2	0.2	10.4	0.0186	1	0.188	GJA1, IFI27
ZHAN LATE DIFFERENTIATION GENES UP	others			B lymphocyte late differentiation genes (LDG): top genes up-regulated in plasma cells from tonsils (TPC) compared to those from bone marrow (BPC).	MSigDBv3.0 CGP	23	2	0.2	10.4	0.0186	1	0.188	BMP6, CAV1
REACTOME PLATELET ACTIVATION	others			Genes involved in Platelet Activation	MSigDBv3.0 CP:REACTOME	167	5	1.5	3.4	0.0189	1	0.191	CD9, COL1A2, FN1, GAS6, SERPINE1
BRUECKNER TARGETS OF MIRLET7A3 UP	tumor	other		Genes up-regulated in A549 cells (lung cancer) expressing MIRLET7A3 [Gene ID=406883] microRNA off a plasmid vector.	MSigDBv3.0 CGP	111	4	1	4.1	0.0191	1	0.192	FOXC1, GJA1, PERP, VCAN
HOOI ST7 TARGETS DN	tumor	other		Genes down-regulated in PC-3 cells (prostate cancer) stably expressing ST7 [Gene ID=7982] off a plasmid vector.	MSigDBv3.0 CGP	111	4	1	4.1	0.0191	1	0.192	CRIP1, FN1, TM4SF1, VIM
module 493	others			Genes in module_493	MSigDBv3.0 CM	62	3	0.6	5.6	0.0192	1	0.193	GJA1, LAMA4, LAMB1
module 94	signaling			Genes in module_94: Signaling	MSigDBv3.0 CM	364	8	3.3	2.5	0.0192	1	0.193	CAV1, CDH5, COL5A2, ELN, EPS8, GPRC5B, IL1R1, ITGB4
module 180	others			Genes in module_180	MSigDBv3.0 CM	112	4	1	4.1	0.0197	1	0.197	BCAM, CD9, MDK, MUC1
DODD NASOPHARYNGEAL CARCINOMA DN	tumor	other		Genes down-regulated in nasopharyngeal carcinoma (NPC) compared to the normal tissue.	MSigDBv3.0 CGP	1332	20	12.2	1.7	0.0199	1	0.199	BGN, CAV1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, EPHB4, FBN1, FN1, FSCN1, GATA6, GJA1, ITGAV, LAMA4, LAMB1, POSTN, SERPINE1, SULF1, VCAN
BROWNE HCMV INFECTION 14HR DN	others			Genes down-regulated in primary fibroblast cell culture after infection with HCMV (AD169 strain) at 14 h time point that were not down-regulated at the previous time point, 12 h.	MSigDBv3.0 CGP	298	7	2.7	2.7	0.0201	1	0.2	ANXA2, CDH13, CXCR7, LPHN2, PLEC, SERPINE1, TJP1
INTERCELLULAR JUNCTION	ECM	adhesion		Genes annotated by the GO term GO:0005911. A specialized region of connection between two cells including but not limited to gap junctions, desmosomes, and tight junctions, but excluding direct cytoplasmic junctions such as ring canals.	MSigDBv3.0 CC	63	3	0.6	5.5	0.0201	1	0.2	CDC42BPB, GJA1, TJP1
PROTEIN TYROSINE KINASE ACTIVITY	others			Genes annotated by the GO term GO:0004713. Catalysis of the reaction: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.	MSigDBv3.0 MF	63	3	0.6	5.5	0.0201	1	0.2	CRIM1, TEK, TIE1
KORKOLA EMBRYONIC CARCINOMA VS SEMINOMA UP	tumor	other		Top 25 most highly expressed genes in embryonic carcinoma relative to seminoma tumors.	MSigDBv3.0 CGP	24	2	0.2	9.9	0.0202	1	0.2	GJA1, VCAN
REACTOME SEMA4D INDUCED CELL MIGRATION AND GROWTH CONE COLLAPSE	EMT	migration		Genes involved in Sema4D induced cell migration and growth-cone collapse	MSigDBv3.0 CP:REACTOME	24	2	0.2	9.9	0.0202	1	0.2	MYH10, RHOC
V$FREAC4 01	TF	FOXD1		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CTWAWGTAAACANWGN which matches annotation for FOXD1: forkhead box D1	MSigDBv3.0 TFT	113	4	1	4	0.0202	1	0.2	ALDH1A2, EMP1, HSPG2, PLS3
WATTEL AUTONOMOUS THYROID ADENOMA DN	tumor	other		Down-regulated genes characteristic for autonomous thyroid adenoma.	MSigDBv3.0 CGP	24	2	0.2	9.9	0.0202	1	0.2	CAV1, IL1RL1
ZUCCHI METASTASIS UP	tumor	breast	metastasis	The 50 most up-regulated genes in primary invasive breast dutcal carcinoma (IDC) or lymph node metastases, compared to normal mammary epithelium.	MSigDBv3.0 CGP	24	2	0.2	9.9	0.0202	1	0.2	CTGF, FSCN1
chr14q32	others			Genes in cytogenetic band chr14q32	MSigDBv3.0	114	4	1	4	0.0208	1	0.205	CDC42BPB, CRIP1, CRIP2, IFI27
module 397	others			Genes in module_397	MSigDBv3.0 CM	114	4	1	4	0.0208	1	0.205	EPHB4, LAMB1, SEMA3F, TJP1
DEURIG T CELL PROLYMPHOCYTIC LEUKEMIA UP	tumor	other		Genes up-regulated in T-PLL cells (T-cell prolymphocytic leukemia) bearing the inv(14)/t(14:14) chromosomal aberration.	MSigDBv3.0 CGP	370	8	3.4	2.5	0.0209	1	0.206	ANGPTL2, COL6A2, EPHB4, FAM38A, FN1, IGFBP7, LAMB2, MEST
CELL PROJECTION BIOGENESIS	others			Genes annotated by the GO term GO:0030031. Formation of a prolongation or process extending from a cell, e.g. a flagellum or axon.	MSigDBv3.0 BP	25	2	0.2	9.5	0.0218	1	0.213	CDH13, FGD5

REACTOME BASIGIN INTERACTIONS	others			Genes involved in Basigin interactions	MSigDBv3.0 CP:REACTOME	25	2	0.2	9.5	0.0218	1	0.213	CAV1, ITGA6
RICKMAN TUMOR DIFFERENTIATED WELL VS POORLY DN	tumor	other	aggressive	Down-regulated genes that vary between HNSCC (head and neck squamous cell carcinoma) groups formed on the basis of their level of pathological differentiation: well vs poorly differentiated tumors.	MSigDBv3.0 CGP	373	8	3.4	2.4	0.0218	1	0.213	DOCK6, EHD2, NRG1, PERP, PLS3, PPP2R5B, PTRF, SYNPO
WANG BARRETTS ESOPHAGUS AND ESOPHAGUS CANCER UP	tumor	other		Genes up-regulated in esophageal adenocarcinoma (EAC) and Barret's esophagus (BE) relative to normal esophagi.	MSigDBv3.0 CGP	25	2	0.2	9.5	0.0218	1	0.213	COL4A2, CRIP1
WEINMANN ADAPTATION TO HYPOXIA UP	signaling	hypoxia		Genes most up-regulated in hypoxia tolerant NCI H460 cells (lung cancer).	MSigDBv3.0 CGP	25	2	0.2	9.5	0.0218	1	0.213	IGFBP7, MEST
DITTMER PTHLH TARGETS UP	tumor	other		Genes up-regulated in MDA-MB-231 cells (breast cancer) after knockdown of PTHLH [Gene ID=5744] by RNAi.	MSigDBv3.0 CGP	116	4	1.1	3.9	0.022	1	0.214	ATP1A1, COL4A2, COL6A1, ECM1
V$PAX5 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif BCNNNRNGCANBGNTGNRTAGCSGCHNB which matches annotation for PAX5: paired box gene 5 (B-cell lineage specific activator)	MSigDBv3.0 TFT	116	4	1.1	3.9	0.022	1	0.214	ANGPTL2, FLNC, MYH10, NRG1
LIAO METASTASIS	tumor	other	metastasis	Genes up-regulated in the samples with intrahepatic metastatic hepatocellular carcinoma (HCC) vs primary HCC.	MSigDBv3.0 CGP	522	10	4.8	2.2	0.0223	1	0.216	AGRN, ANXA2, COL1A2, EHD2, GPRC5B, KIAA1522, LAMB1, SEMA3F, SERPINE2, VCAN
FERNANDEZ BOUND BY MYC	TF	MYC	CHIP	Genes identified by ChIP within the high-affinity group of MYC [Gene ID=4609] targets.	MSigDBv3.0 CGP	175	5	1.6	3.2	0.0226	1	0.218	COL4A2, ITGA6, MUC1, SERPINE1, SLC9A3R2
GCANCTGNY V$MYOD Q6	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GCANCTGNY which matches annotation for MYOD1: myogenic differentiation 1	MSigDBv3.0 TFT	679	12	6.2	2	0.0226	1	0.218	BMP6, CDH13, CRIP2, HYAL2, ID1, ITGB4, MAGED1, MYH10, NRG1, PPP2R5B, TJP1, TNFRSF21
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 16D UP	others			Genes up-regulated in CD34+ [Gene ID=947] hematopoetic cells by expression of NUP98-HOXA9 fusion [Gene ID=4928, 3205] off a retroviral vector at 16 days after transduction.	MSigDBv3.0 CGP	175	5	1.6	3.2	0.0226	1	0.218	APCDD1, FLNB, FN1, IFI27, NRG1
chr2q31	others			Genes in cytogenetic band chr2q31	MSigDBv3.0	66	3	0.6	5.2	0.0227	1	0.218	COL3A1, ITGA6, ITGAV
FALVELLA SMOKERS WITH LUNG CANCER	tumor	other		Genes that distinguish normal from cancer (lung adenocarcinoma) samples and smokers from non-smoking subjects.	MSigDBv3.0 CGP	66	3	0.6	5.2	0.0227	1	0.218	ADAMTS1, ENG, SERPINE1
HINATA NFKB TARGETS FIBROBLAST UP	signaling	NF-KB		Genes up-regulated in primary fibroblast cells by expression of p50 (NFKB1) and p65 (RELA) [Gene ID=4790, 5970] components of NFKB.	MSigDBv3.0 CGP	66	3	0.6	5.2	0.0227	1	0.218	CD9, FN1, VIM
V$SMAD4 Q6	TF	SMAD4		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GKSRKKCAGMCANCY which matches annotation for SMAD4: SMAD, mothers against DPP homolog 4 (Drosophila)	MSigDBv3.0 TFT	176	5	1.6	3.2	0.0231	1	0.222	CDH13, COL1A2, FAM38A, HYAL2, SULF1
TGATTTRY V$GFI1 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGATTTRY which matches annotation for GFI1: growth factor independent 1	MSigDBv3.0 TFT	240	6	2.2	2.8	0.0234	1	0.223	ALDH1A2, ANXA2, CDH13, CRIM1, FN1, SLCO2A1
CHIANG LIVER CANCER SUBCLASS INTERFERON UP	tumor	other		All marker genes up-regulated in the 'interferon' subclass of hepatocellular carcinoma (HCC).	MSigDBv3.0 CGP	26	2	0.2	9.1	0.0235	1	0.223	IFI27, PLA2G2A
LI CISPLATIN RESISTANCE UP	tumor	resistance	cisplatin	Genes consistently up-regulated in ACRP cells (ovarian cancer, resistant to cisplatin [PubChem=2767]) compared to the parental sensitive A2780 cells, regardless of cisplatin exposure.	MSigDBv3.0 CGP	26	2	0.2	9.1	0.0235	1	0.223	GJA1, LPHN2
REGULATION OF ANGIOGENESIS	others			Genes annotated by the GO term GO:0045765. Any process that modulates the frequency, rate or extent of angiogenesis.	MSigDBv3.0 BP	26	2	0.2	9.1	0.0235	1	0.223	COL4A2, STAB1
AKL HTLV1 INFECTION DN	others			Genes down-regulated in WE17/10 cells (CD4+ [Gene ID=920] T lymphocytes) infected by HTLV1 (and thus displaying low CD7 [Gene ID=924]) compared to the uninfected (i.e., CD7+) cells.	MSigDBv3.0 CGP	67	3	0.6	5.1	0.0236	1	0.223	IGFBP7, LPHN2, MAOA
GGARNTKYCCA UNKNOWN	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing motif GGARNTKYCCA. Motif does not match any known transcription factor	MSigDBv3.0 TFT	67	3	0.6	5.1	0.0236	1	0.223	COL1A2, HSPG2, NPDC1
NAGASHIMA NRG1 SIGNALING UP	tumor	other	ERBB2	Genes up-regulated in MCF7 cells (breast cancer) after stimulation with NRG1 [Gene ID=3084].	MSigDBv3.0 CGP	177	5	1.6	3.2	0.0236	1	0.223	CTGF, EDN1, GATA6, ID1, TNFRSF21

RIGGINS TAMOXIFEN RESISTANCE UP	tumor	resistance	ER	Genes up-regulated SUM44/LCCTam cells (breast cancer) resistant to 4-hydroxytamoxifen [PubChem=63062] relative to the parental SUM44 cells sensitive to the drug.	MSigDBv3.0 CGP	67	3	0.6	5.1	0.0236	1	0.223	GATA4, LAMA4, SLCO2A1
V$CIZ 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif SAAAAANNN which matches annotation for ZNF384: zinc finger protein 384	MSigDBv3.0 TFT	177	5	1.6	3.2	0.0236	1	0.223	COL3A1, MMP2, SEMA3F, SSSCA1, TXNDC5
V$FOXJ2 02	TF	FOXJ2		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif AYMATAATATTTKN which matches annotation for FOXJ2: forkhead box J2	MSigDBv3.0 TFT	177	5	1.6	3.2	0.0236	1	0.223	CRIM1, EDN1, EFEMP1, ID1, IGFBP7
V$SMAD3 Q6	TF	SMAD3		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGTCTGTCT which matches annotation for SMAD3: SMAD, mothers against DPP homolog 3 (Drosophila)	MSigDBv3.0 TFT	177	5	1.6	3.2	0.0236	1	0.223	EDN1, MRC2, NOS3, S100A16, SYNPO
VANHARANTA UTERINE FIBROID DN	others			Genes down-regulated in uterine fibroids vs normal myometrium samples.	MSigDBv3.0 CGP	67	3	0.6	5.1	0.0236	1	0.223	CXCR7, LEPR, TNXB
BENPORATH ES WITH H3K27ME3	others		H3K27me3	Set 'H3K27 bound': genes posessing the trimethylated H3K27 (H3K27me3) mark in their promoters in human embryonic stem cells, as identified by ChIP on chip.	MSigDBv3.0 CGP	1097	17	10	1.8	0.0237	1	0.223	ADAM15, BMP6, CD34, CRIP1, DKK2, FBN1, FOXC1, GATA4, GATA6, LAMB1, MMP2, NRG1, NTN1, PLEC, SFRP5, SLCO2A1, TPPP3
GGGCGGR V$SP1 Q6	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GGGCGGR which matches annotation for SP1: Sp1 transcription factor	MSigDBv3.0 TFT	2171	29	19.9	1.6	0.0237	1	0.223	CD9, COL1A2, CRIP1, DKK2, ELN, GATA6, HSPB1, HYAL2, IGFBP7, ITGA6, KIF1C, LEPR, MAOA, MUC1, MYH10, NFE2L1, NPDC1, NTN1, PKHD1L1, PLK2, PLS3, PLTP, PTMS, PTRF, PVRL2, SPTAN1, TJP1, TNFRSF21, VIM
BENPORATH NOS TARGETS	TF	NANAG, OCT4, SOX2	CHIP	Set 'NOS targets': genes upregulated and identified by ChIP on chip as targets of the transcription factors NANOG [Gene ID=79923], OCT4[Gene ID=5460], and Sox2 [Gene ID=6657] (NOS) in human embryonic stem cells.	MSigDBv3.0 CGP	178	5	1.6	3.2	0.0241	1	0.227	CTGF, DPYSL3, GJA1, LAMA4, SULF1
HAHTOLA MYCOSIS FUNGOIDES SKIN UP	others			Genes up-regulated in lesional skin biopsies from mycosis fundoides patients compared to the normal skin samples.	MSigDBv3.0 CGP	178	5	1.6	3.2	0.0241	1	0.227	CFH, CRIM1, SPTAN1, TM4SF1, TXNDC5
KEGG COMPLEMENT AND COAGULATION CASCADES	others			Complement and coagulation cascades	MSigDBv3.0 CP:KEGG	68	3	0.6	5.1	0.0245	1	0.23	CD59, CFH, SERPINE1
BENPORATH SUZ12 TARGETS	signaling	SUZ12	CHIP	Set 'Suz12 targets': genes identified by ChIP on chip as targets of the Polycomb protein SUZ12 [Gene ID=23512] in human embryonic stem cells.	MSigDBv3.0 CGP	1017	16	9.3	1.8	0.0246	1	0.231	CD34, CDH11, CDH13, CRIP1, DKK2, EPS8, FBN1, GATA4, GATA6, NRG1, NTN1, PLEC, PLS3, SFRP5, SLCO2A1, TPPP3
AMUNDSON RESPONSE TO ARSENITE	others			Genes discriminating responses to sodium arsenite [PubChem ID=26435] from other stresses.	MSigDBv3.0 CGP	180	5	1.6	3.2	0.0252	1	0.234	HYAL2, LEPR, NFE2L1, PLTP, PTPRB
METALLOENDOPEPTIDASE ACTIVITY	others			Genes annotated by the GO term GO:0004222. Catalysis of the hydrolysis of nonterminal peptide linkages in oligopeptides or polypeptides. Enzymes of this class contain a chelated metal ion essential to their catalytic activity at their active sites.	MSigDBv3.0 MF	27	2	0.2	8.7	0.0252	1	0.234	MMP2, MMP28
module 200	others			Genes in module_200	MSigDBv3.0 CM	27	2	0.2	8.7	0.0252	1	0.234	NRG1, TEK
OHM METHYLATED IN ADULT CANCERS	tumor	other		Genes showing frequent DNA methylation and which are silenced in adult cancers but remain unmethylated in embryonic carcinoma and embryonic stem (ES) cells.	MSigDBv3.0 CGP	27	2	0.2	8.7	0.0252	1	0.234	GATA4, SFRP5
OLSSON E2F3 TARGETS DN	tumor	other		Genes down-regulated in the 5637 cell line (bladder cancer) after knockdown of E2F3 [Gene ID=1871] by RNAi.	MSigDBv3.0 CGP	27	2	0.2	8.7	0.0252	1	0.234	EDN1, VIM
REGULATION OF CELL MIGRATION	EMT	migration		Genes annotated by the GO term GO:0030334. Any process that modulates the frequency, rate or extent of cell migration.	MSigDBv3.0 BP	27	2	0.2	8.7	0.0252	1	0.234	CDH13, LAMB1
XU GH1 AUTOCRINE TARGETS DN	tumor	other		Genes down-regulated in MFCF-7 cells (breast cancer) upon stable autocrine expression of HG1 [Gene ID=2688].	MSigDBv3.0 CGP	121	4	1.1	3.8	0.0253	1	0.234	PLK2, PODXL, SULF1, TJP1
chr8p21	others			Genes in cytogenetic band chr8p21	MSigDBv3.0	69	3	0.6	5	0.0255	1	0.235	LOXL2, NRG1, SCARA3
ENGELMANN CANCER PROGENITORS DN	tumor	other	cancer stem cells	Down-regulated genes in the cancer progenitor (stem) cells corresponding to side population (SP) MCF7 cells (breast cancer) positive for MUC1 [Gene ID=4582].	MSigDBv3.0 CGP	69	3	0.6	5	0.0255	1	0.235	CTGF, FN1, ID1
V$SP1 01	TF	others		Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GGGGCGGGGT which matches annotation for SP1: Sp1 transcription factor	MSigDBv3.0 TFT	182	5	1.7	3.1	0.0262	1	0.242	HYAL2, KIF1C, MAGED1, MUC1, NFE2L1

EPIDERMIS DEVELOPMENT	others		Genes annotated by the GO term GO:0008544. The process whose specific outcome is the progression of the epidermis over time, from its formation to the mature structure. The epidermis is the outer epithelial layer of a plant or animal, it may be a single layer that produces an extracellular material (e.g. the cuticle of arthropods) or a complex stratified squamous epithelium, as in the case of many vertebrate species.	MSigDBv3.0 BP	70	3	0.6	4.9	0.0264	1	0.244	COL5A2, CTGF, EMP1
COLIN PILOCYTIC ASTROCYTOMA VS GLIOBLASTOMA DN	tumor	other	Genes down-regulated in pilocytic astrocytoma compared to glioblastoma samples.	MSigDBv3.0 CGP	28	2	0.3	8.4	0.027	1	0.246	ANXA2, FN1
DACOSTA ERCC3 ALLELE XPCS VS TTD DN	others		Genes down-regulated in fibroblasts expressing different mutant forms of ERCC3 [Gene ID=2071]: XP/CS (xeroderma pigmentosum (XP) and Cockraine's syndrome (CS)) vs TTD (trichothiodystrophy).	MSigDBv3.0 CGP	28	2	0.3	8.4	0.027	1	0.246	COL1A2, VCAN
LI PROSTATE CANCER EPIGENETIC	tumor	other	Genes affected by epigenetic aberrations in prostate cancer.	MSigDBv3.0 CGP	28	2	0.3	8.4	0.027	1	0.246	CAV1, CDH13
LIPID TRANSPORT	ECM	adhesion	Genes annotated by the GO term GO:0006869. The directed movement of lipids into, out of, within or between cells. Lipids are compounds soluble in an organic solvent but not, or sparingly, in an aqueous solvent.	MSigDBv3.0 BP	28	2	0.3	8.4	0.027	1	0.246	CAV1, SLCO2A1
module 202	others		Genes in module_202	MSigDBv3.0 CM	28	2	0.3	8.4	0.027	1	0.246	DSTN, FLNB
module 210	others		Genes in module_210	MSigDBv3.0 CM	28	2	0.3	8.4	0.027	1	0.246	ADAM15, MMP2
module 330	others		Genes in module_330	MSigDBv3.0 CM	28	2	0.3	8.4	0.027	1	0.246	DSTN, GJA1
TING SILENCED BY DICER	tumor	other	Epigenetically silenced genes up-regulated in HCT116 cells (colon cancer) hypomorphic for DICER1 [Gene ID=23405].	MSigDBv3.0 CGP	28	2	0.3	8.4	0.027	1	0.246	TM4SF1, VIM
RESPONSE TO WOUNDING	others	damage response	Genes annotated by the GO term GO:0009611. A change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a stimulus indicating damage to the organism.	MSigDBv3.0 BP	184	5	1.7	3.1	0.0273	1	0.248	CD59, CTGF, MDK, NFE2L1, SERPINE1
V$ARP1 01	TF	others	Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGARCCYTTGAMCCCW which matches annotation for PITX2: paired-like homeodomain transcription factor 2	MSigDBv3.0 TFT	124	4	1.1	3.7	0.0273	1	0.248	CTGF, EMP1, LTBP3, MMP28
V$MYOD Q6 01	TF	others	Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CNGNRNCAGGTGNNGNAN which matches annotation for MYOD1: myogenic differentiation 1	MSigDBv3.0 TFT	184	5	1.7	3.1	0.0273	1	0.248	DOCK6, HYAL2, ITGA6, SEMA3F, SPTAN1
HINATA NFKB TARGETS KERATINOCYTE UP	signaling	NF-KB	Genes up-regulated in primary keratinocytes by expression of p50 (NFKB1) and p65 (RELA) [Gene ID=4790, 5970] components of NFKB.	MSigDBv3.0 CGP	71	3	0.7	4.8	0.0274	1	0.248	CD9, FN1, VIM
RODRIGUES THYROID CARCINOMA DN	tumor	other	Genes down-regulated in poorly differentiated thyroid carcinoma (PDTC) compared to anaplastic thyroid carcinoma (ATC).	MSigDBv3.0 CGP	71	3	0.7	4.8	0.0274	1	0.248	FN1, PLEC, S100A10

Table S7. The list of genes that demonstrate overlap between the 170 genes and the core EMT signature (17).

symbol	Entrez GeneID	descr
CTGF	1490	Connective tissue growth factor
COL3A1	1281	Collagen, type III, alpha 1
POSTN	10631	Periostin, osteoblast specific factor
COL1A2	1278	Collagen, type I, alpha 2
MMP2	4313	Matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
CDH11	1009	Cadherin 11, type 2, OB-cadherin (osteoblast)
FSTL1	11167	Follistatin-like 1
ECM1	1893	Extracellular matrix protein 1
BGN	633	Biglycan
COL5A2	1290	Collagen, type V, alpha 2
VIM	7431	Vimentin

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