



Transcriptome Profiling And Identification Of Differentially Expressed Genes And Pathways With The Treatment Of N-Alkyl Amine-Noscapinoids In Human Breast Cancer

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ABSTRACT

Breast cancer is effectively controlled through the utilization of noscapine and its derivatives, commonly known as noscapinoids, in the management of the disease. We utilised the function RNA-seq to perform full transcriptome sequencing and compared the gene expression profiles of the untreated and treated MCF-7 human breast carcinoma cell line in order to determine the mechanism of action of noscapinoids in breast cancer. A total of 3237 differential expression genes (DEGs) were identified, including the genes BTG2, DCBLD2, MCL1, TOB2, ABHD2, TBRG1, VIM, CLOCK, MAD2L1BP, BRCC3, HUS1B, CLOCK, BC.L2L11, BCL2, CEBPB, TP63, SIN3A, FN1, CD14, MAP1LC3A, EME1, IL17D, ATG13, BRCC3, HUS1B and JTB. The top 20 pathways enriched with the most DEGs from up and down regulation, including pathways in actin cytoskeleton regulation, the PI3K-AKT pathway, and cell cycle, were determined by annotation of the function of DEGs in the KEGG database. We compared the gene expression profiles between the treatment vs control and calculated the up and down regulated genes. Annotation of DEGs on the basis of biological process, molecular function, and cellular component analyses revealed 20 regulating activities from up- and down-regulating DEGs. The co-expression of various genes from up- and down-regulated genes were analysed using a protein-protein interaction network. Based on the network analysis 50 most functional genes from each group were chosen. The down-regulated genes targeted in the analysis were further evaluated in RtPCR. These major down-regulated genes are involved in a wide variety of biological processes, including cell survival and proliferation, migration and motility, and tumour cell invasion. The interactions of these down-regulated DEGs in drug treated cell line elucidated at a functional level explain the mechanism of action of noscapinoid in breast

cancer. Our research shows that these DEGs could be exploited as therapeutic targets and potential biomarkers to create novel therapeutic approaches.

Key words: Noscainoids, breast cancer, transcriptome analysis, protein-protein network

INTRODUCTION

Noscain (an opium alkaloid, non-narcotic, orally available, safe antitussive drug for over 40 years) and its derivatives (known as Noscainoids) were discovered as a small-molecule tubulin-binding anticancer agent that arrests cancer cells in mitosis and induces apoptosis [1]. However, unlike the other microtubule-targeting drugs that either overpolymerize (taxanes) or depolymerize (vincas) microtubules and thus present various debilitating toxicities [2-3] noscainoids does not alter the steady state monomer/polymer ratio of tubulin [1, 4] and thus lacking of any obvious side effects [2, 3, 5, 6]. It has already been shown that noscainoids inhibit the progression of various cancer types in cultured cells and animal models. Surprisingly, apoptosis is much more pronounced in cancer cells than normal healthy cells [7]. In addition, noscainoids have several advantages compared to existing tubulin binding agents: (1) retain activity against paclitaxel-resistant cell lines (1A9/PTX10, 1A9/PTX22); (2) favorable pharmacokinetics (clearance in 6-10 hours) [8]; (3) a poor substrate for drug-pumps (polyglycoproteins and MDR-related proteins) [9] that comprise a significant cause of drug resistance; (4) does not show immunological [10- 11] and neurological toxicities [12], (5) bind tubulin perhaps at a site distinct from taxanes [13-14], also substantiated by enhanced taxane therapy and toxicities to taxane resistant cancer cells, (6) very much effective against a panel of breast cancer cells [14]. Mechanistically, the noscainoids were demonstrated to bind tubulin, arrest the cell cycle progression and induced apoptosis to cancer cells. Reports show that noscainoids exert anticancer properties via different mechanisms such as inducing cellular apoptosis through mitochondria-mediated pathway, inhibiting migration and metastasis, and attenuating angiogenesis [15-16]. However, the exact mechanism of induction of apoptosis is not yet deciphered. High throughput transcriptome analysis associated with bioinformatics data mining tools provides an opportunity to simultaneously analyze a large number of genes/targets and identify the mechanisms of action after treatments. RNA-seq has many advantages due to it's being free from the probe-specific hybridization, allowing the unbiased detection of both coding and noncoding novel transcripts as well as low-abundance transcripts [17]. In this work we differentiate the total functional annotation like Biological process, cellular component, molecular function and pathways studies between MCF7 (control) and Noscainoids/MCF7 (treated) cell line. We calculated the Up-regulated and Down-regulated genes and differentiate between different functions.

MATERIALS AND METHODS

Cell culture and establishment of the MCF-7 cell line:

The Institute of Life Sciences in Bhubaneswar donated the MCF-7 wild-type human ER expressing breast cancer cell line, and the cells were grown in Dulbecco's modified Eagle medium (DMEM), which contains 10% FBS and 0.1% penicillin-streptomycin. The cells were kept at 37 °C in a humidified 5% CO₂ environment. Every other day, the culture media were replaced. Dimethyl sulfoxide (DMSO) was utilized to create a stock

solution (100 mM) of the recently synthesised 9-(N-arylmethylamino) noscapinoid, that was then kept at 4 °C. For bioassays, cells at a confluence of 70–80% were subcultured using trypsin–EDTA (0.25%).

Cell viability assay:

Cell viability was determined using the MTT colorimetric assay. The MCF-7 cells were seeded in 96-well plates in culture media at a density of 1×10^4 cells/well overnight and then treated with various concentrations of 9-(N-arylmethylamino) noscapinoid between 5 μ M to 100 μ M for 72 h in a 5% CO₂ humidified incubator. Subsequently, MTT in PBS (0.1 mg) was added to each well and incubated for 4 hours at 37 °C. After 20 minutes, the optical density (OD) was measured with a microplate reader (BIO-RAD, Hercules, CA, USA) at 570 nm. The IC₅₀ value (the concentration at which 50% inhibition to the proliferation of cancer cell take place) of the noscapinoid was determined using the online tool Quest Graph™ IC₅₀ Calculator (AAT Bioquest, Inc., Sunnyvale, CA, USA, <https://www.aatbio.com/tools/ic50-calculator>).

Cell cycle progression analysis:

MCF-7 cells were maintained in DMEM at 37 °C in 5% CO₂ with 4.5 g/L glucose and L-glutamine, 10% FBS, and 1% penicillin/streptomycin. Noscapine and 9-(N-arylmethylamino) noscapinoids, diluted in 1% phosphate buffer saline (PBS), were applied to treat cells at IC₅₀ concentration for 72 hours. Cells were trypsinized, washed twice by cold PBS, and fixed in 70% cold ethanol overnight at –20 °C. After fixation, cells were washed twice by cold PBS and stained with PI/Triton X-100 staining solution (0.1% Triton X-100, 2 mg/mL PI, and 0.2 mg/mL DNase-free RNase) for 30 minutes. Samples were analyzed using flow cytometry (BD FACS Aria-III) and the progress in the cell cycle was determined.

Apoptosis assay:

The IC₅₀ concentrations of noscapine and 9-(N-arylmethylamino) noscapinoids were treated to MCF-7 cells for 72 hours. According to the manufacturer's instructions, cells were trypsinized, two times in cold PBS, and stained with Alexa Fluor® 488, Annexin V, and propidium iodide (PI) (Thermo Fisher Scientific, Rockford, IL, USA). Apoptotic cells were determined using flow cytometer with 488 nm excitation for PI and emission at 530 nm were collected. Viable cells (Annexin V⁻ / PI⁻), early apoptotic cells (Annexin V⁺ / PI⁻), late apoptotic/necrotic cells (Annexin V⁺ / PI⁺) and late necrotic cells (Annexin V⁻ / PI⁺) were identified and determined their percentage.

Cell preparation for RNA Sequencing:

The subculture of breast cancer cell line, MCF-7, was cultured in Dulbecco's modified Eagle medium (DMEM) containing 10% FBS with 0.1% penicillin-streptomycin. The cells were maintain at 37 °C in a humidified atmosphere of 5% CO₂. The culture media were replaced every other day. Stock solution (100 mM) of the newly synthesized 9-(N-arylmethylamino) noscapinoid was prepared with dimethyl sulfoxide (DMSO) and stored at 4°C. After treating MCF-7 cells with IC₅₀ concentration of 5 μ M 9-(N-arylmethylamino)

noscapinoids, for 72h, the treated cells and control cells of triplicate biological replicates were preserved in 2ml of RNAlater at 2-8 °C overnight, for the RNAlater to permeate into the tissue. Then the frozen treated as well as control samples were shifted to Clevergene Private Ltd., Bengaluru for mRNA sequencing.

mRNA Enrichment and Library Preparation:

Total RNA (250 ng) was used to enrich the mRNA using the NEBNext Poly (A) mRNA magnetic isolation module (Catalog: E7490, New England Biolabs) following the manufacturers' protocol. The enriched mRNAs were further taken for library preparation using the NEBNext® UltraTM II RNA Library Prep Kit for Illumina (Catalog: E7775S, New England Biolabs). In brief, the enriched mRNAs were primed with NEBNext random primers and chemically fragmented in a magnesium-based buffer at 94 °C for 10 minutes to get an insert of ~200 nucleotides. The fragmented mRNAs were reverse transcribed to form cDNA and the first strand cDNA reactions were converted to ds DNA. The double-stranded cDNA fragments obtained were cleaned up by using 1.8X of AMPure XP beads (Catalog: A63881, Beckman Coulter)

(<https://international.neb.com/products/e7490-nebnext-polya-mrna-magnetic-isolation-module#Product%20Information>)

The cDNA undergoes end repair wherein the mix converts the overhangs resulting from fragmentation into blunt ends. The 3' to 5' exonuclease activity of end-repair mix removes the 3' overhangs and polymerase activity fills in the 5' overhangs. To the blunt-ended fragments, adenylation was performed by adding single 'A' nucleotide to the 3' ends. To the adenylated fragments, loop adapters were ligated and cleaved with uracil-specific excision reagent (USER) enzyme. Size selection was performed using AMPure beads (Catalog: A63881, Beckman Coulter) with the manufacturer's protocol for the library size of 400-600bp.

Furthermore, the cDNA was amplified by 12 cycles of PCR with the addition of NEBNext Ultra II Q5 master mix, and "NEBNext® Multiplex Oligos for Illumina" to facilitate multiplexing while sequencing. The amplified products were then purified using 0.9X AMPure XP beads (Catalog: A63881, Beckman Coulter) and the final DNA library was eluted in 15 µl of 0.1X TE buffer (<https://international.neb.com/products/e7335-nebnext-multiplex-oligos-for-illumina-index-primers-set-1#Product%20Information>).

Library Quantification:

The library concentration was determined in a Qubit.3 Fluorometer (Catalog: Q33216, Life technologies) using the Qubit dsDNA HS (High Sensitivity) assay kit (Catalog: Q32854, ThermoFisher Scientific). The Qubit™ 1X dsDNA HS assay kit contains high sensitivity DNA reagent, buffers and two DNA standards. It is one of the most sensitive detection dyes for the accurate quantitation of DNA/library in solution, with linear fluorescence detection in the range of 10 pg/µl to 100 ng/µl of DNA. One dye and the buffers were diluted at 1:200 ratio and 1µl of the library was mixed with the dye mix and incubated at RT for 2 minutes. The readings were taken in the Qubit.3 Fluorometer (Catalog: Q33216, Life technologies). Prior to the sample's measurement, the instrument was calibrated using the two standards provided in the kit

(<https://international.neb.com/products/e7770-nebnext-ultra-ii-rna-library-prep-kit-for-illumina#Product%20Information>).

Library Validation:

The library quality assessment was done using Agilent D5000 ScreenTape System (Catalog: 5067-5588, Agilent) and Agilent D1000 ScreenTape System (Catalog: 5067- 5582, Agilent) in a 4150 Tape Station System (Catalog: G2992AA, Agilent) which is designed for analyzing DNA molecules from 100 to 5000bp. One μ l of the purified library was mixed with 10 μ l of D5000 sample buffer (Catalog: 5067-5589) and vortexed using IKA vortexer at 2000 rpm for 1 minute and spun down to collect the sample to the bottom of the strip. The strip was then loaded on the Agilent 4150 TapeStation system (<https://international.neb.com/products/e7770-nebnext-ultra-ii-rna-library-prep-kit-for-illumina#Product%20Information>).

Data quality control check (QC) and preprocessing of the raw data:

All transcriptional activity, involving genes both with and without coding functions, is characterised by transcriptome analysis. To build a functional picture of cell function, it either concentrates on a small sample of pertinent target genes and transcripts or profiles a large number simultaneously. The processing of RNA-seq data includes analysis of raw reads, adapter trimming, read alignment, gene quantification, and quality check (QC) after each analysis step. The QC of the raw reads was analyzed using FastQC (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>, Babraham Bioinformatics, UK). The reads were trimmed using Cutadapt (v2.6) [18] to remove the adapter sequence and low-quality bases to nullify the alignment biases.

Read alignment of raw data and Abundance of genes calculation:

The raw reads were mapped against the reference human genome using HISAT2 (v2.1.0) [19] to avoid the loss of unannotated regions of the genome. The aligner varied in their indexing algorithm and the mappability of the reads with different memory requirements. The expression counts reads were generated using the feature count (v2.0.0) package [20]. Gene expression of the MCF-7 cells with the treatment of noscapioid and untreated was measured using the FeatureCount for each sample. The transcript abundance was estimated using StringTie (v2.1.1), which is developed based on the optimization theory of the network flow algorithm [21].

Analysis of essential unique genes:

The completed transcriptome was mapped utilizing the clean data, and each gene's read count was determined. Differential expression analysis of samples was performed using EdgeR package (<http://www.bioconductor.org/packages/2.12/bioc/html/edgeR.html>) [21]. It uses the Poisson dispersion model to account for the biological and technical variabilities and the Bayesian empirical model for optimizing the degree of overdispersion against the transcripts. Trimmed mean of M values (TMM) normalization is employed to normalize the data to counts per million (CPM). The q-value was employed to refine the p-value, enabling adjustments for multiple comparisons. A significance threshold of $p < 0.05$ was utilized, in conjunction with \log_2

(fold change) > 1 for upregulated genes and \log_2 (fold change) < -1 for downregulated genes, to determine significantly altered expression levels.

Gene ontology profiling:

The functional annotation of identified DEGs was performed by searching the databases of Clusters of Orthologous Groups (COG), Gene Ontology (GO), and Kyoto Encyclopedia of Genes and Genomes (KEGG). The functional enrichment analysis of the DEGs was performed using the DAVID web-accessible bioinformatics program (<http://david.abcc.ncifcrf.gov/>) with a significance threshold of $p < 0.05$. After achieving GO annotation for every unigene, g:profiler (<https://biit.cs.ut.ee/gprofiler/>) was used to perform GO classification and construction of a GO tree which gives separate GO id and p-value for up- and down-regulated DEGs. The classification of the DEGs into functional pathways was performed using KEGG analysis (<https://www.genome.jp/kegg/>). The KEGG automatic annotation server was used for KEGG Orthology (KO) and KEGG pathway annotation.

Protein-protein network analysis:

Using BLASTX, the query gene sequences were compared to the subject sequences in the various databases for protein-protein interactions using an E-value cut-off of 10^{-5} (0.00001). Using physical binding, genetic, and functional links, protein-protein interaction networks investigate the downstream relationship between proteins. The STRING (<https://string-db.org/>) website was used to investigate the relationship between the specifically discovered DEGs responsible for the therapeutic efficacy of noscapinoid and functionally related genes involved in breast cancer.

Gene expression by RT-PCR :

Finally, the expressed genes identified by using of RNA-seq data were authentication provided by RT-PCR. According the manufacturer's instructions, reverse transcription of aliquots of 2 mg of mRNA was conducted using a PrimeScript™ RT reagent Kit and a gDNA Eraser Kit (TaKaRa Bio, China). ABI ViiA 7 Real-Time PCR machine was then used to conduct SYBR Green-based qPCR (Applied Biosystems, Foster City, CA, USA). All the reactions were run in triplicate, and GAPDH served as the endogenous control. The comparative cycle threshold (2CT) method was used to determine the relative level of gene expression.

RESULTS:

N-alkyl amine-noscapinoids inhibits proliferation of MCF-7 :

We investigated the 9-(N-arylmethylamino) noscapinoid's impacts on the survival of the MCF-7 breast cancer cell line. N-arylmethylamino-noscapinoid shown higher cytotoxic activity than noscapine. In Table 1.1, the IC₅₀ values for the test substances for both cell lines are compiled. For noscapine, the IC₅₀ values for MCF-7 cells were 44.3 M and 3.9 M, respectively.

Table 1.1. new 9-(N-arylmethylamino) noscapinoid IC₅₀ values using MCF-7 human breast cancer cell lines. When compared to noscapine, all of the new compounds were found to have stronger antiproliferative effects.

	IC ₅₀ (μM)	
	Noscapine	9-(N-arylmethylamino) noscapinoid
MCF-7	44.3±3.9	3.9±0.8

N-arylmethylamino-noscapinoids induced apoptosis to cancer cells:

N-alkyl amine-noscapinoid treatment of breast cancer cells caused the formation of apoptotic cell death, which was evaluated by FACS applying of fluorescent dyes, annexin V and propidium iodide (PI). Annexin V is used to label the phosphatidylserine that is translocated to the outer leaflet of the cell membrane during apoptosis. In contrast, when cells undergo apoptosis, the DNA-binding fluorescent dye propidium iodide intercalates with the DNA. Hence, the FACS analysis uses both colours to a large extent to quantify the apoptotic cells. For the treatment of noscapine and its N-alkyl amine-noscapinoid with IC₅₀ concentration for 72 hours, the percentage of early and late apoptotic cells using MCF-7 cell lines is compiled in Table 1.2. Figure 1.1 includes examples of flow cytometry analysis results. The control untreated cell culture had relatively few early (3.5%) and late (2.0%) apoptotic cells after 72 hours, which was regarded as background cell death brought on by routine damage during cell culture (Table 3.6). However, the percentage of early apoptotic cells with treatments of noscapine and its N-alkyl amine-noscapinoids, respectively, was found to be 20% and 6%, as well as late apoptotic cells with treatments of 25% and 24%. (Table 1.2).

Additionally, examination using the dyes DAPI, Acridyne Orange, and Ethidium Bromide demonstrated that MCF-7 cancer cells had undergone apoptotic cell death, which is characterised by condensed chromatin, the development of membrane blebs, and a large number of broken nuclei. (Figure 1.2).

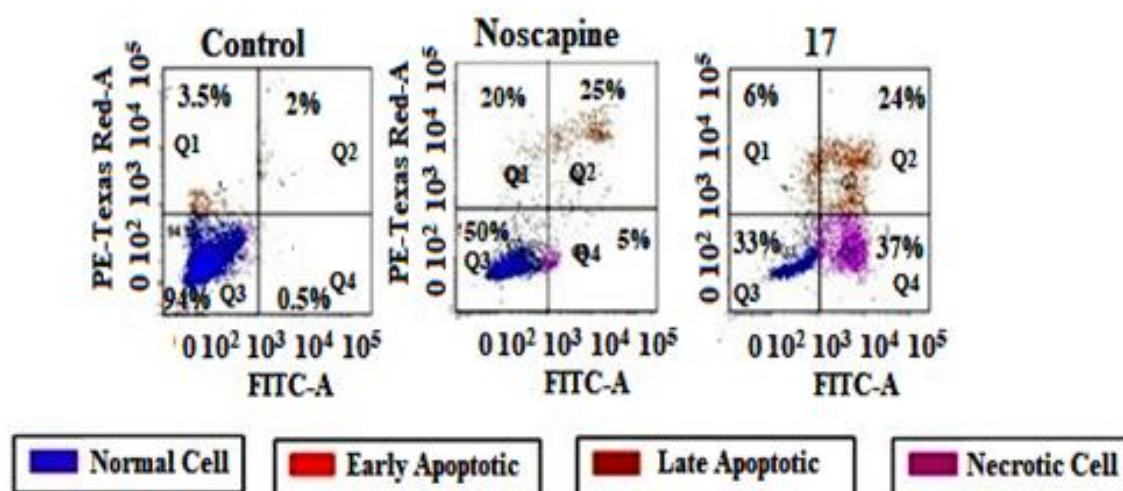
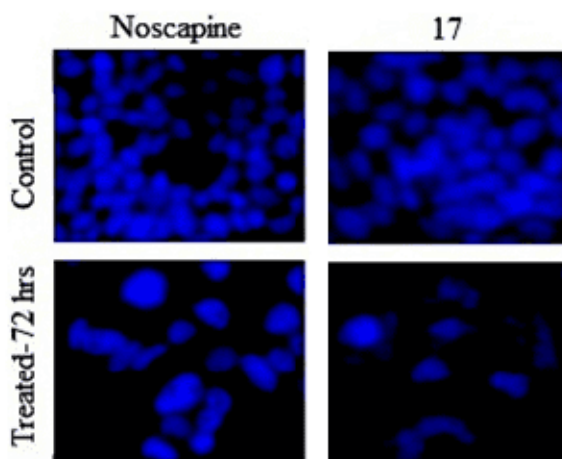


Figure 1.1. Flow cytometry analysis of induction of apoptosis in MCF-7 cells treated with noscapine and its 9-(N-arylmethylamino), 17 noscapinoid with IC₅₀ concentration for 72 hours. Cells with PI- and Alexa Fluor 488- indicate viable cells, PI- and Alexa Fluor 488+ indicate early apoptotic cells, PI+, Alexa Fluor 488+ indicate late apoptotic cells.

Table 1.2. By using flow cytometry, the percentage of cells that underwent early (Q1), late (Q2), viable (Q3), and necrotic (Q4) apoptosis after being exposed to 9-(N-arylmethylamino) noscapinoid.

Viability/Apoptotic	Control	Noscapine	9-(N-arylmethylamino)
Q1	3.5%	20%	6%
Q2	2%	25%	24%
Q3	94%	50%	32.4%
Q4	0.5%	5%	37%

**Figure 1.2.** Apoptotic cells were identified by changes in morphological characteristics as chromatin condensation, blebbing of the plasma membrane, and the formation of tiny, apoptotic entities. The panels display the morphological characteristics of cells stained with DAPI from control cells (upper panels) and cells treated for 72 hours with the IC50 doses of noscapine and 9-(N-arylmethylamino) noscapinoids, 17.

Interference in cell cycle progression by 9-(N-arylmethylamino) noscapinoids:

Figure 1.3 depicts the impact of noscapine and 9-(N-arylmethylamino) noscapinoids (25 M concentration) on the MCF-7 cell cycle progression using FACS analysis. Fluorescently coloured DNA builds up in the presence of noscapinoid, showing that the cell cycle and cell death have been disturbed. The concentration of duplicated 4N DNA suggests that the cells are in the G2 and M phases, while the presence of 2N DNA shows that the cells are in the G1 phase. The presence of DNA accumulation between the 2N and 4N peaks suggests that the cells are in the S phase. Less than 2N DNA, on the other side, indicates apoptotic cells in which the DNA has undergone varying degrees of degradation. Noscapine and 9-(N-arylmethylamino) noscapinoids (17) treatment of MCF-7 cells for 72 hours resulted in a considerable reduction of the cell cycle profile at IC50. After 72 hours of treatment with the test drugs, FACS analysis showed a significant buildup of cells in the G2/M phase (Table 1.3). A hypodiploid DNA content peak (sub-G1) was observed to rise after 72 hours after drug treatment, in contrast to G2/M block, indicating dying cells.

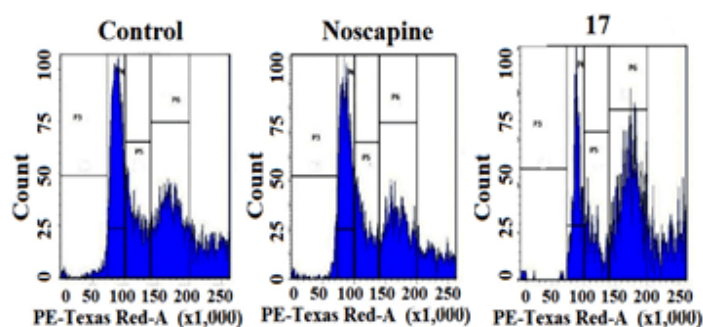


Figure 1.3 Noscapine and its 9-(N-arylmethylamino) noscapinoids, 17, interrupt the G2/M phase of the cell cycle and cause a hypodiploid (sub-G1) DNA peak to develop, which marks the process of apoptotic in the cells. Panels A through E revealed flow cytometric assessments of cell cycle progression in MCF-7 cells that had been exposed to the IC50 concentration of noscapine and its N-alkyl-amine derivatives for 72 hours.

Table 1.3. Effect of noscapine and its 9-(N-arylmethylamino) noscapinoids, 17, on cell cycle progression in MCF-7 cells when IC50 concentration was applied for 72 hours, followed by propidium iodide staining for cell cycle analysis.

	72 hours			
	Sub-G ₁	G ₀ /G ₁	S	G ₂ /M
Control	0.7	21	23.4	10.4
Noscapine	6.4	17.5	13.4	26.5
17	18.5	15.3	13.4	32.7

Analysis of transcriptome data:

After received the data of Triplicate biological control1, control2, control3 and treated1, treated2, treated3 samples, the raw transcriptome data were clean by eliminating low quality reads and obtained a data set of 29.7 GB. The statistical summary of the transcriptome data is collated in Table 1.4. Total number of reads obtained for untreated MCF-7 cell are 24689279, whereas for the MCF-7 cells treated with noscapinoids are 25478201. Human genome GRCh38 was used as reference sequence to align the reads using HISAT2 software. The percentage of readings mapped to the reference genome are 88.04% and 88.33%, respectively for the untreated MCF-7 and treated MCF-7 cells with noscapinoids. Table 1.5 include the statistical summary of the mapping results. The transcript abundances were determined using the StringTie programme. The reads were calculated using the Feature Count package and the DEGs were detected using the Edge R tool. Using the q value, the p value was changed. The cutoff for significantly altered expression was set at p value 0.05 and \log_2 (fold change) > 1 for upregulated gene and < -1 for downregulated gene. Total number of DEGs identified are 3237 from untreated and treated MCF-7 cells (Table 1.6). Out of DEGs identified, 1192 were upregulated and 2045 were downregulated DEGs. The Volcano plot examine the variations in the gene expression levels between the untreated MCF-7 and treated MCF-7 cells (Figure 1.4).

Table 1.4: Statistical summary of Quality control of transcriptome sequencing

Filename	MCF-7 cells treated 1	MCF-7 cells treated 2	MCF-7 cells treated 2	Untreated MCF-7 cells 1	Untreated MCF-7 cells 2	Untreated MCF-7 cells 3
Encoding	Sanger / Illumina 1.9	Sanger / Illumina 1.9	Sanger / Illumina 1.9	Sanger / Illumina 1.9	Sanger / Illumina 1.9	Sanger / Illumina 1.9
Total Sequences	25478201	25478201	25478201	24689279	25689375	23559229
Sequences flagged as poor quality	0	0	0	0	0	0
Sequence length	151	151	151	151	151	151
%GC	49	49	49	50	50	50
Basic Statistics	pass	pass	pass	pass	pass	pass

Table 1.5: Statistical summary of the mapping results.

SAMPLES	MCF7-1	MCF7-2	MCF7-3	Noscapinoids/ MCF7-1	Noscapinoids /MCF7-2	Noscapinoids /MCF7-3
TOTAL ALIGNED	24689279 (100.00%)	25689375 (100.00%)	23559229 (100.00%)	15478201 (100.00%)	15498281 (100.00%)	14478901 (100.00%)
ALIGNED 0 TIMES	22358611 (90.56%)	23297694 (90.69%)	21443610 (91.02%)	13672411 (88.33%)	13776421 (88.89%)	12835545 (88.33%)

Table 1.6 Summary of the prediction of up-regulated and down-regulated genes.

DEGS	Pvalue	Fold change	DEGs
All significant genes	pvalue<0.05		3237
Up Regulated genes	pvalue<0.05	>= 1	1192
Down Regulated genes	pvalue<0.05	<= -1	2045

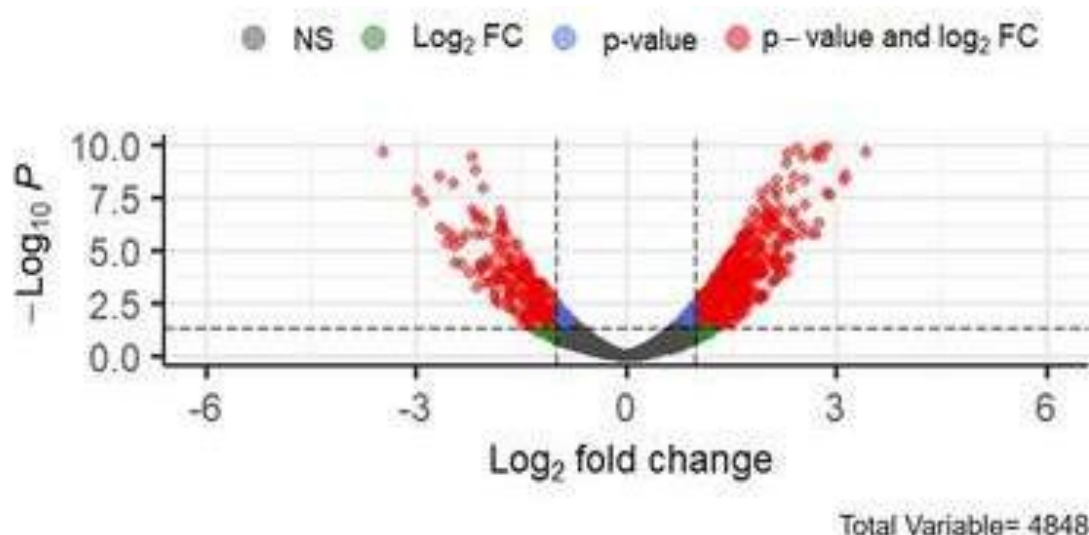


Figure 1.4: The volcano diagram representing the distribution of the differentially expressed genes. Genes are symbolised by each red, blue, and green point. Genes that are up-regulated or differentially expressed are represented by red dots on the positive line, down-regulated or differently expressed genes are represented by red dots on the negative line, and non-differentially expressed genes are represented by black dots.

The Volcano Plot is depicted in the figure to evaluate the differences in gene expression levels between two groups of samples and their statistical significance. Total number of 4848 variable was examined for the statistical analysis to calculate for up and down regulated genes.

Venn diagram:

Similarly the common and unique genes between the untreated and treated MCF-7 cells were represented in Venn diagram (Figure 1.5). As well as calculating the unique gene and common gene in between two groups, the Venn diagram also displays the amount of significant correlations between differentially expressed genes (DEGs) between two groups of up-regulated and down-regulated genes, showing in the figure 1.5.

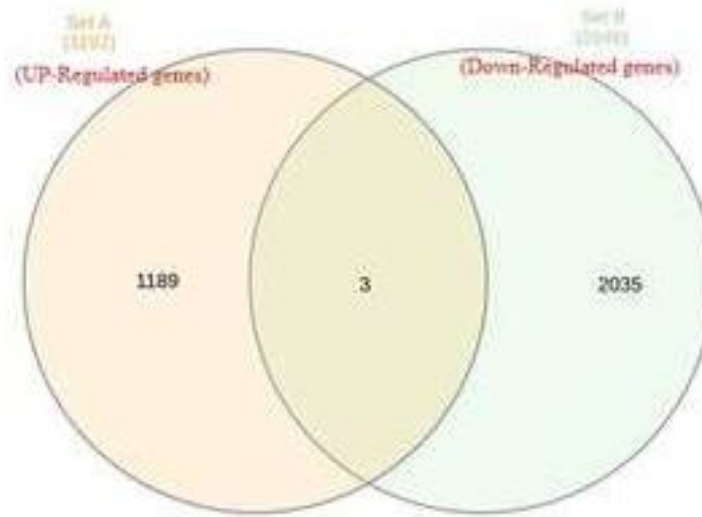
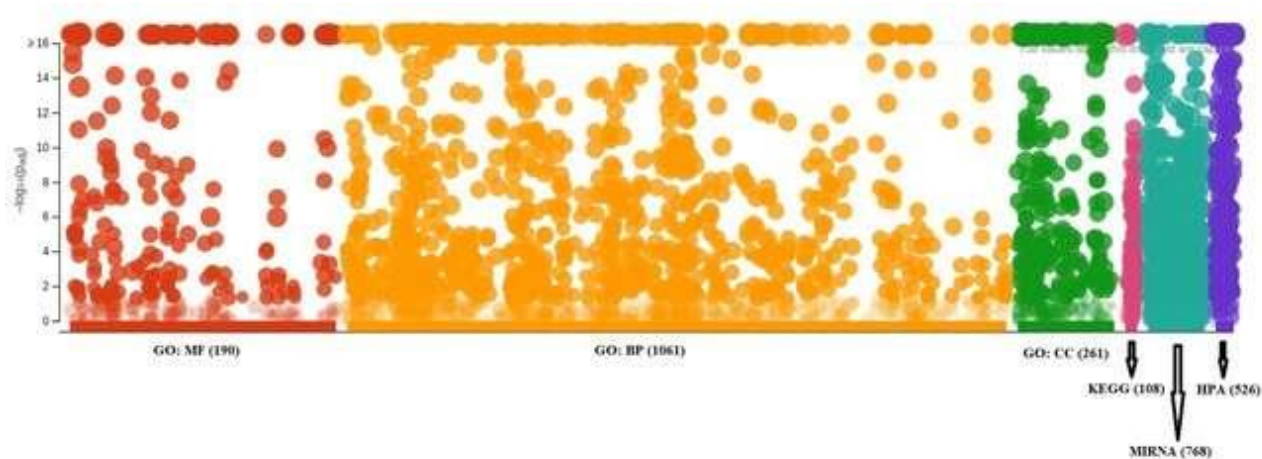


Figure 1.5 Venn diagram showing the number of significant associations between differentially expressed genes (DEGs) between two groups of Up-regulated and Down-regulated gene and calculate the unique gene and common gene in between two group. Here in Figure 1.5 Showing the Up- regulation and Down-regulation gene differentially expressed in both group. Set A represent the number of up-stream gene and Set B represent the number of down-stream genes. 1189 unigenes are identified in up-regulation genes from 1192 variables. And 2035 unigenes are identified in down-regulation genes from 2045 variables. Where 3 genes are common in both up and down-stream and 7 genes are lost to identify in the plot.

Annotation of DEG and enrichment analysis:

The DEGs were annotated using DAVID (<https://david.ncifcrf.gov/>) and g: profiler (<https://biit.cs.ut.ee/gprofiler/>) database. Out of 1189 upregulated and 2035 downregulated genes, 696 upregulated and 1301 downregulated genes were annotated using David database. The annotation was done with respect to biological process, cellular component, molecular function and KEGG pathways (Figure 1.6 A & B). Highest proportion of DEGs were distributed in the category of biological process (511 among upregulated and 1061 among downregulated DEGs). Second highest proportion of DEGs was found in the category of cellular component (146 among upregulated and 261 among downregulated DEGs) in which the DEGs were distributed in the sub-category of cell or cellular part. In the category of molecular function, 129 upregulated and 190 downregulated genes distributed in the binding sub-category. Finally 22 upregulated and 106 downregulated genes were distributed to KEGG pathways. The category of MIRNA, the proportion of DEGs was 551 up-regulated and 768 in down-regulated genes, which is useful as marker. 483 up-regulated and 526 down-regulated DEGs calculated in HPA (Human Protein Atlas).

(A)



(B)

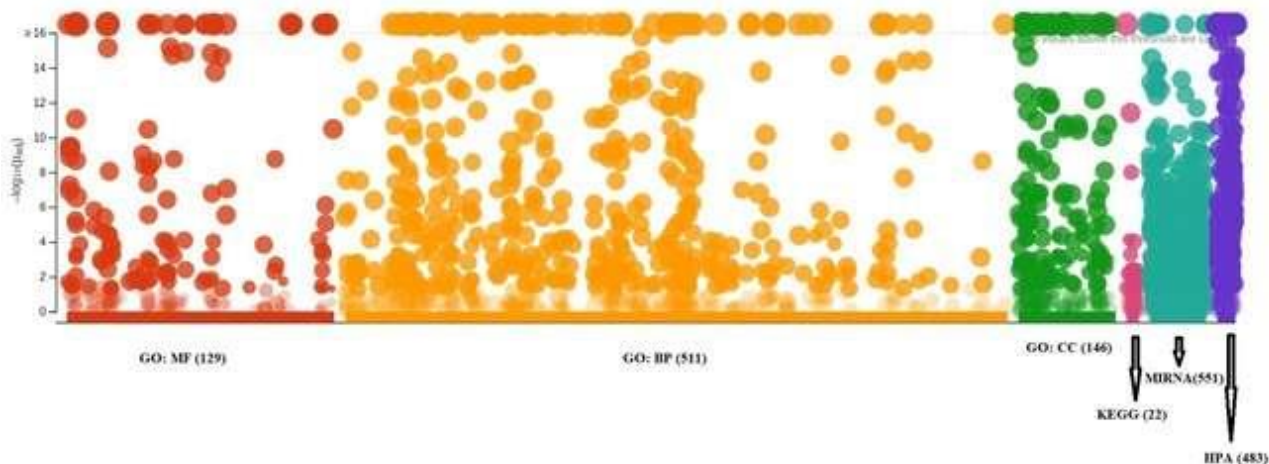
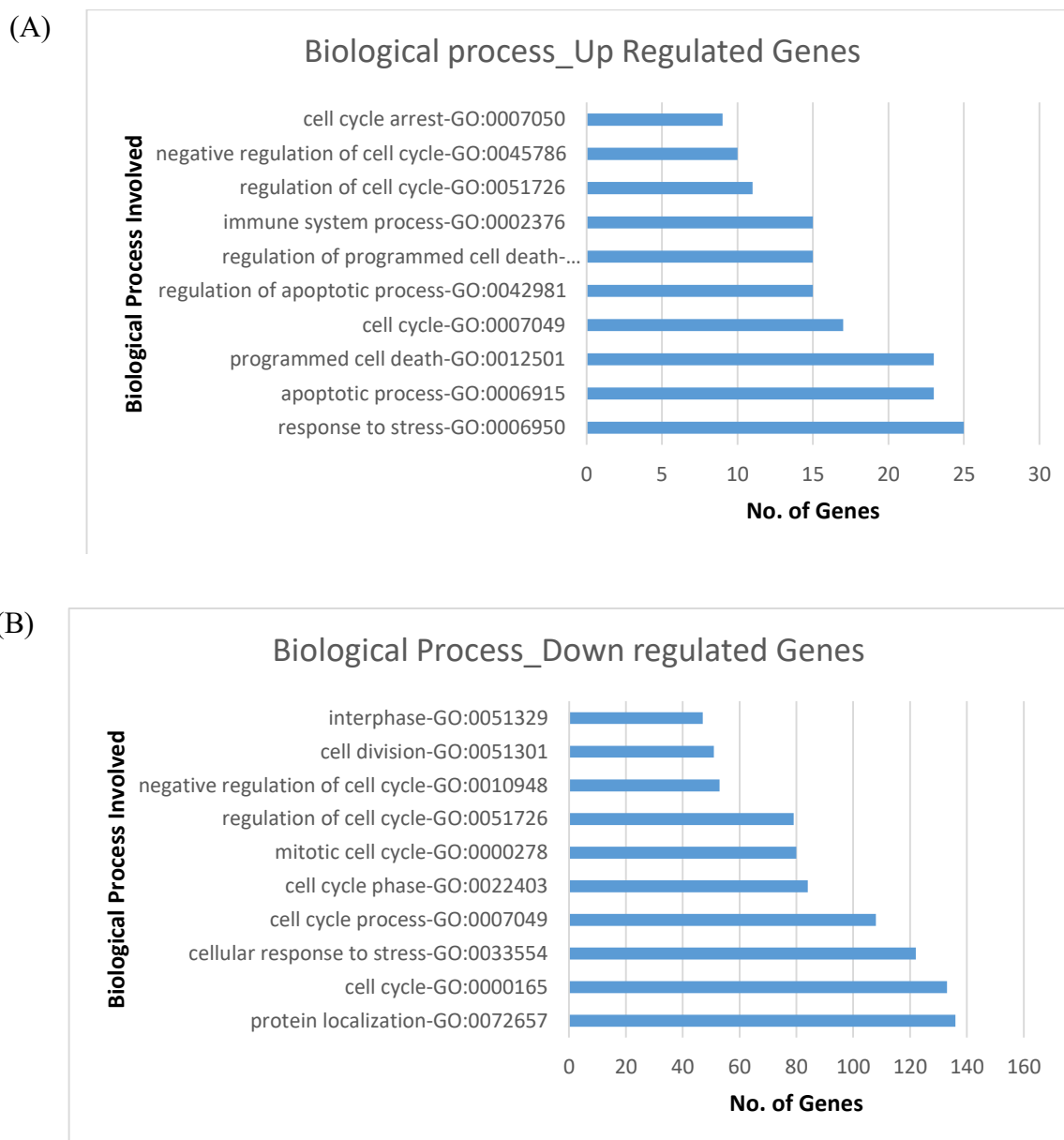


Figure 1.6: The classification of COG (Cluster of Orthologous Group of Proteins) in different function, which were annotated. Distribution of 1189 up-regulated and 2035 down-regulated DEGs into five functional groups. Gene numbers and proportions are represented on the vertical axis, which also displays the COG categories. Classification of the annotated DEGs in COG functions. The horizontal axis displays the COG categories and the vertical axis plots the gene counts and proportions.

Biological Process from differentially expressed Up and Down Regulated genes:

The top 20 differentially expressed genes from upregulated DEGs distributed in different biological process. Most of the genes were found to involved in negative regulation of cellular process, response to stress, and negative regulation to biological process. The genes are mostly involved in the process of cell proliferation, cell cycle arrest and programmed cell death, indicating valuable information in the action of the noscapinoids (Figure 1.7 (A)). (Pelengaris et. al. 2000). In the function apoptosis process and programmed cell death the family of gene like MCL1, BCL2, BCL2L11, BTG2 involved. Similarly, the differentially expressed genes from downregulated DEGs distributed in different biological process. Most of the genes were found to involve in the process of protein localization, regulation in MAPK cascade, cellular response to stress, establishment of protein localization, protein transport, cell cycle process, mitotic cell cycle, cell division and cell cycle phases (Figure 1.7 (B)). All the details of Biological Process data along with the details of expressed genes given in the Supplementary_UPFunction_Sheet1 and Supplementary_DownFunction_Sheet1.

Figure 1.7: The grap A and B showing the Up-regulated and Down-regulated Biological Process of Genes. In the figure A showing the name of



the Biological Process in horizontal axis and the no. of genes regulated by the Process. Also in the figure B the name of the Biological Process mentioned and the the horizontal axis showinf g the no. of genes regulated by the Process.

Molecular Function from differentially expressed Up and Down Regulated genes:

The top 20 upregulated DEGs distributed in the category of molecular function. Most of the DEGs were predicted to involved in the functions of DNA binding, ATP binding, enzyme binding, cytoskeletal binding, receptor binding, cytoskeletal protein binding and tubulin binding (Figure 1.8 (A)). Similarly the top 20 downregulated DEGs distributed in the category of molecular function. Most of the DEGs were predicted to involved in functions like methyltransferase activity, double-stranded RNA binding, purine ribonucleotide binding and kinase binding (Figure 1.8 (B)). All the details of Molecular Function data along with the details of expressed genes given in the Supplementary_UPFunction_Sheet2 and Supplementary_DownFunction_Sheet2.

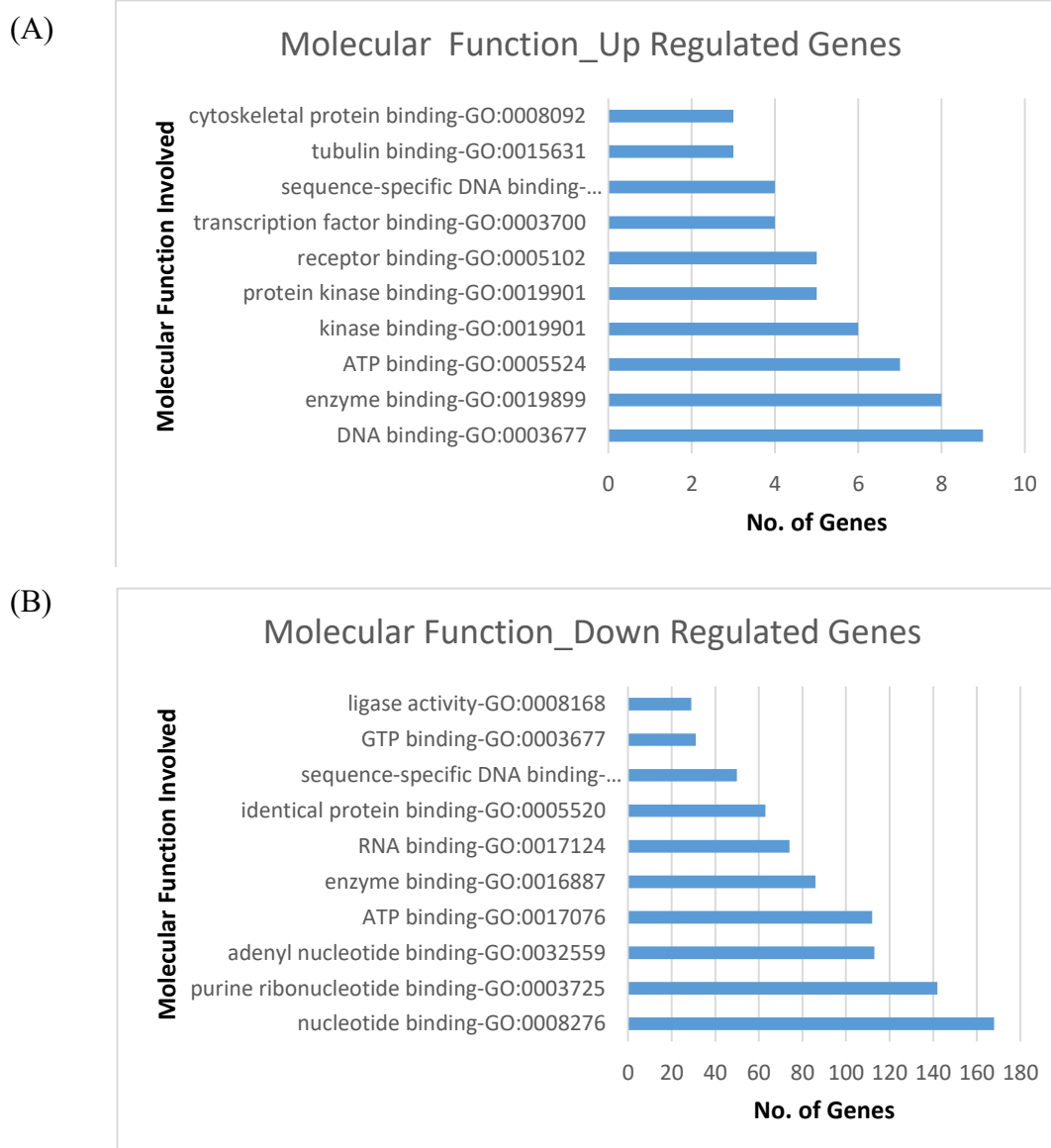


Figure 1.8: The graph A and B showing the Up- regulated and Down- regulated Molecular Function of Genes. In the figure A showing the name of the Molecular Function in the horizontal axis and the no. of genes regulated by the Function. Also in the figure B the name of the Molecular Function mentioned and the the horizontal axis showing the no. of genes regulated by the Function.

Cellular Component from differentially expressed Up and Down Regulated genes:

It was found that a good number of upregulated DEGs (33 number) were involved in the regulation of intracellular and intercellular organelle functions. In contrast, maximum number of downregulated DEGs (251 DEGs) were distributed in the cellular component of non membrane bounded organelle and intracellular non membrane bounded organelle. Further, 231 DEGs were distributed to membrane enclosed lumen. The DEGs distributed among organelle lumen, nuclear part and cytosol were 228, 217 and 201, respectively. DEGs_Supplementary: Supplementary Table 6 showed the cellular component of down regulated genes.

Some cellular component like membrane bounded organelle, intracellular non membrane bounded organelle, nuclear part, cytosol and organelle lumen are common in both up and down regulated DEGs. But cytoskeleton, microtubule cytoskeleton, cytoskeleton component are present in only upregulated DEGs. In contrast, actin cytoskeleton, cell junction, endosome, golgi membrane are some cellular component, are only present in down regulated DEGs (Figure 1.9 (A), (B)). All the details of Cellular Component data along with

the details of expressed genes given in the Supplementary_UPFunction_Sheet3 and Supplementary_DownFunction_Sheet3.

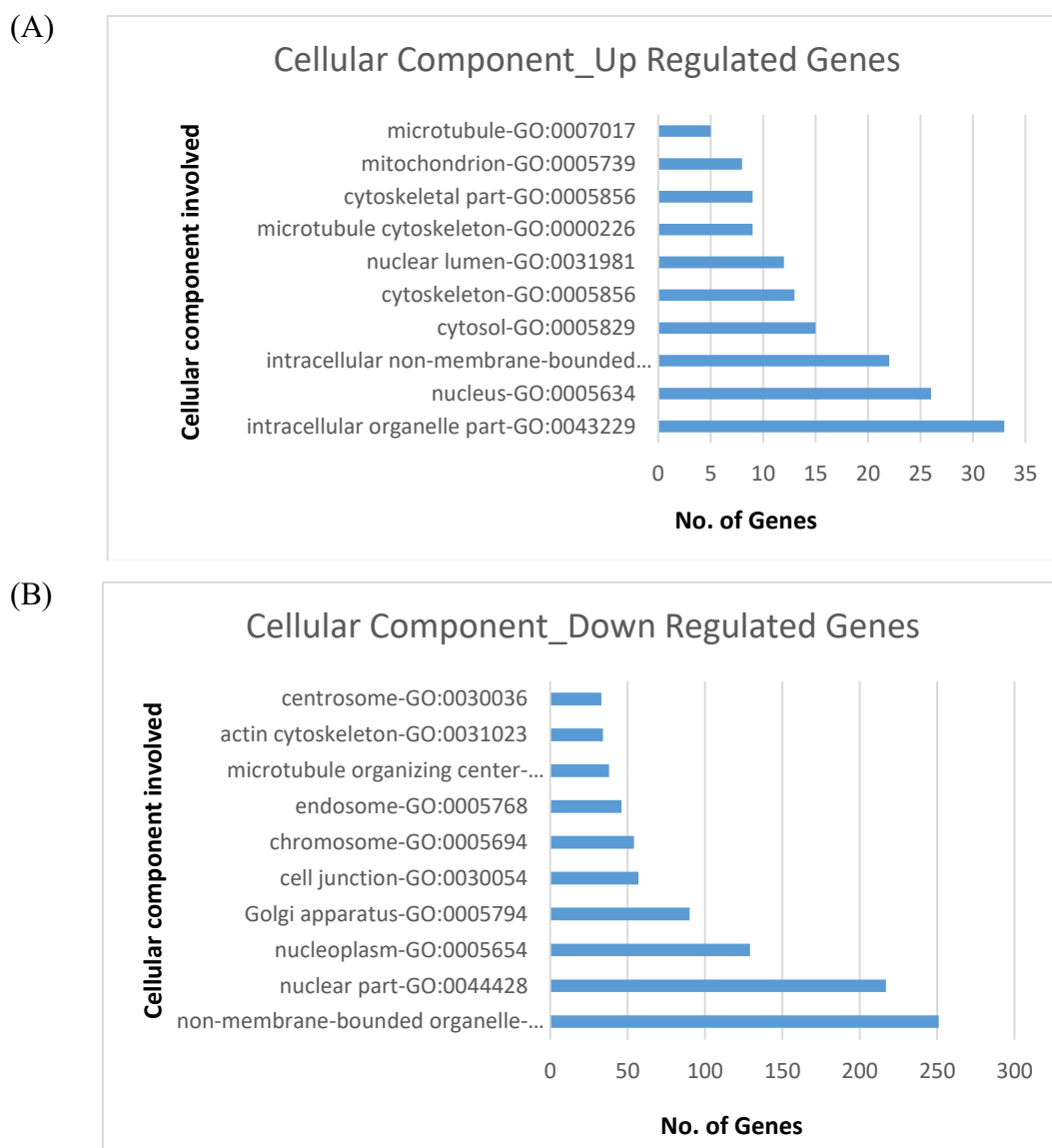


Figure 1.9: The graph A and B showing the Up- regulated and Down- regulated Cellular Component of Genes. In the figure A showing the name of the Cellular Component in the horizontal axis and the no. of genes regulated by the Function. Also in the figure B the name of the Cellular Component mentioned and the the horizontal axis showing the no. of genes regulated by the Component.

KEGG Pathway analysis in differentially expressed Up and Down Regulated genes:

The miRNet tool programme was employed in the current investigation to examine the statistical enrichment of DEGs in KEGG pathways. The KEGG database (<http://www.genome.jp/kegg/>) revealed that a total of 3237 DEGs were split up into 104 pathways. The pathways that were DEGs-enriched in cancer included those that process environmental information and control cellular activities such as focal adhesion, actin cytoskeleton regulation, and mitogen-activated protein kinase (MAPK), Rap1, PI3K-AKT, Ras, and CAM (cell adhesion molecules) signalling. Utilizing transcriptome profiling, tamoxifen resistance-related genes and pathways in human breast cancer were identified to be differentially expressed [24].

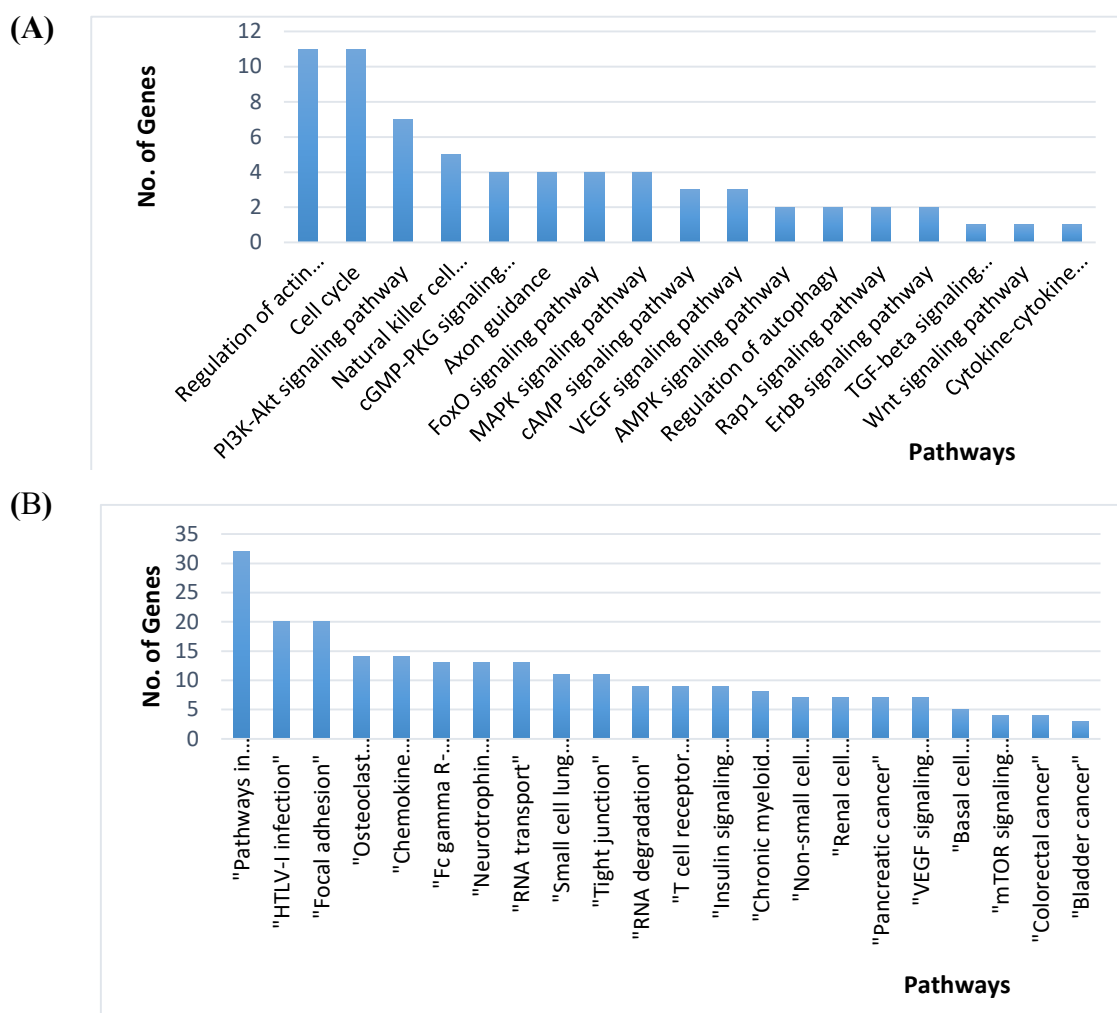


Figure 1.10: The graph A and B showing the Up-regulated and Down-regulated gene pathways. In the figure A in the left side showing the name of the pathways the vertical axis showing the no. Of genes regulated by the pathways. In the figure B the name of the pathways mentioned below and the the horizontal axis showing the no. of genes regulated by the pathways.

KEGG hierarchy and KEGG pathway enrichment analysis of the 696 upregulated DEGs and 1301 downregulated DEGs were performed. The most over-represented pathways of up and down regulated DEGs are represented in Figure 1.10 A & B. The pathway involved in the regulation of actin cytoskeleton ("CD14", "ARAF", "BRK1") is most active in the upregulated DEGs. Also more number of DEGs distributed to cell cycle pathways ("CDC6", "CCNA2", "SKP2" and "MCM4"). (Figure 1.10 A). The downregulated DEGs that involve in were expression gene, pathways in cancer have more identified gene for e.g. ("CTNNB1", "FOXO1", "NKX3-1", "PML", "STAT1", "PTGS2", "CDKN2B", "HRAS", "DAPK1") etc. HTLV-I infection is the second most pathways where many genes are regulated ("CTNNB1", "PTTG1", "CDKN2B", "CHEK1", "HRAS", "IL2RB", "WNT4", "CDK4"). Non-small cell lung cancer, Small cell lung cancer, Basal cell carcinoma, Prostate cancer are down regulated pathways shows. (Figure 1.10 B).

Protein-Protein Interaction Network Analysis:

We built a PPI network for the proteins encoded by the up- and down-regulated DEGs to understand the biological significance of the detected DEGs at the protein level. The PPI network for the upregulated DEGs include 66 nodes/43 edges, whereas for the downregulated DEGs include 46 nodes/102 edges. From the PPI network of proteins enrichment p-value for up and down regulated DEGs is 0.000211 and 3.33E-016. The average node degree and avg. local clustering coefficient for up and down regulated DEGs is 1.3, 4.43 and 0.291, 0.516 respectively. From the PPI network of upregulated DEGs 60 hub proteins were determined based on the number of interacting edges which are included in DEG_Name: Supplementary Table 1. Similarly from the PPI network of downregulated DEGs 50 hub proteins were determined and included in DEG_Name: Supplementary Table 2. The PPI network analysis of upregulated DEGs showed higher coexpression between CCNA2 and KIF18A genes. Similarly the genes CCNA2, FN1, MAP1LC3A, BCL2L11 and VIM showed coexpression with many other genes. MARK2 and MARK3 revealed the highest homology (0.964) to each other. The gene like ARAF and MARK3, KIF13B and KIF18A showed homology of 0.576 and 0.659 respectively (Figure 1.11 and PPI_Network: Supplementary Table 1). The PPI network analysis of downregulated DEGs showed the higher coexpression (0.779) and high homology value (0.85) between COL1A1 and COL5A1. The gene like COL1A1, AKT3, CTNNB1, BCAR1, CSF1R and ITGA2 showed mostly coexpression with other different genes. The gene ITGA2 and ITGAV, PPP2R5A and PPP2R5E showed the homology between each others in the PPI network (Figure 1.12 and PPI_Network: Supplementary Table 2 and Supplementary_Pro-Pro_Sheet1).

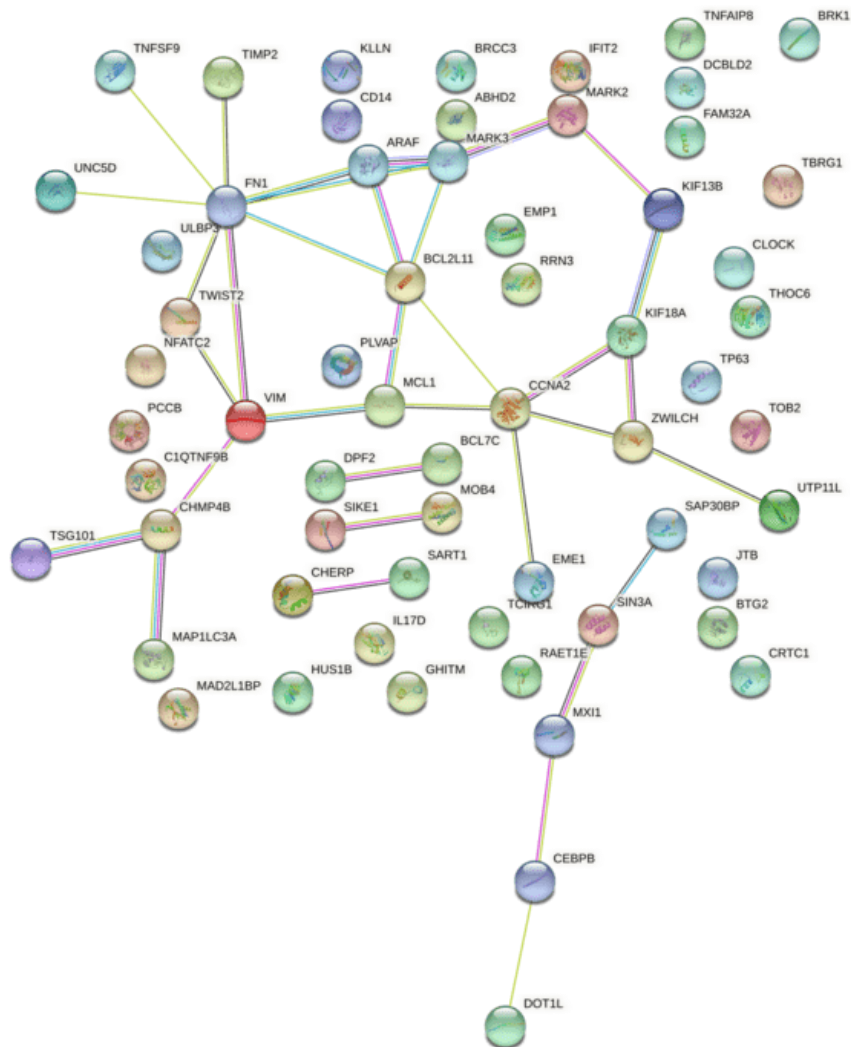


Figure 1.11: Protein-protein interaction network analysis. In order to investigate the relationship between these DEGs, certain chosen genes from the (n=696) DEGs that were utilised to build the PPI network and which are involved in various signal pathways were integrated using the STRING website. The result showed that three common DEGs including FN1, BCL2L11, MCL1 and VIM closely coexpressed to other genes.

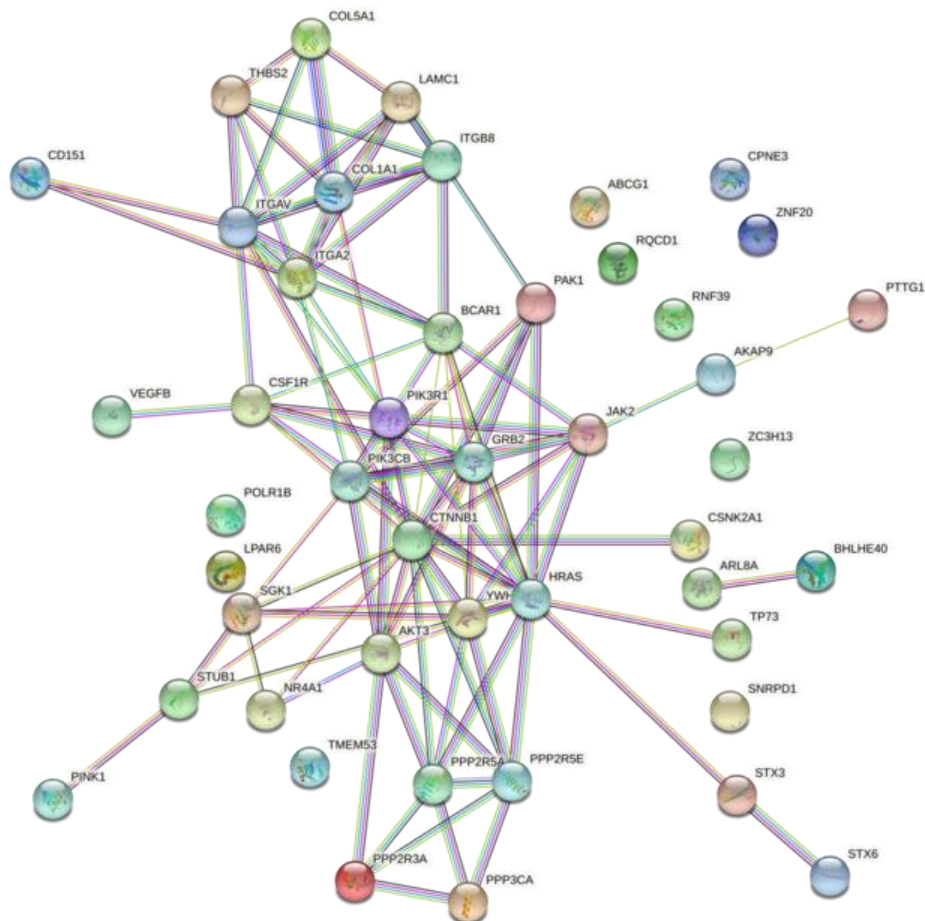


Figure 1.12: network study of protein-protein interactions. To investigate the relationship between these DEGs, certain chosen genes from (n=1301) DEGs that were utilised to build the PPI network and are involved in various signal pathways (Figure: 8B) were integrated using the STRING website. The results reveal close coexpression between three common DEGs, namely COL1A1, AKT3, CTNNB1, and PPP2R3A.

Gene Expression analysis by RT-PCR:

RT-PCR was used to confirm the expression of 15 genes from the MCF-7 cells treated with Noscapinoid at three different concentrations, 0.5 μ M, 1 μ M, and 5 μ M, in order to validate the RNA-seq data. The test was run three times, with three duplicate runs for each run (Supplementary_RT-PCR). The findings demonstrated that 15 down genes expression levels in the cell lines were comparable to those of RNA-seq and reached the same level. Following the results of the transcriptome sequencing, we used RT-PCR to examine the expression of 15 genes in Noscapinoids/MCF-7 (Treated) samples. A summary of the RT-PCR data is shown in Figure 1.13. Log₂ FC and Ct served as the relative expression's defining characteristics. Although there were differences in the relative levels of expression of 15 genes between RT-PCR and RNA-Seq, it was noteworthy that the Noscapinoids/MCF7 (Treated) cell line had lower expression levels of 15 downregulated genes identified from the DEGs data. Which are primarily controlled in several processes of cancerous cell growth, proliferation, migration, and survival.

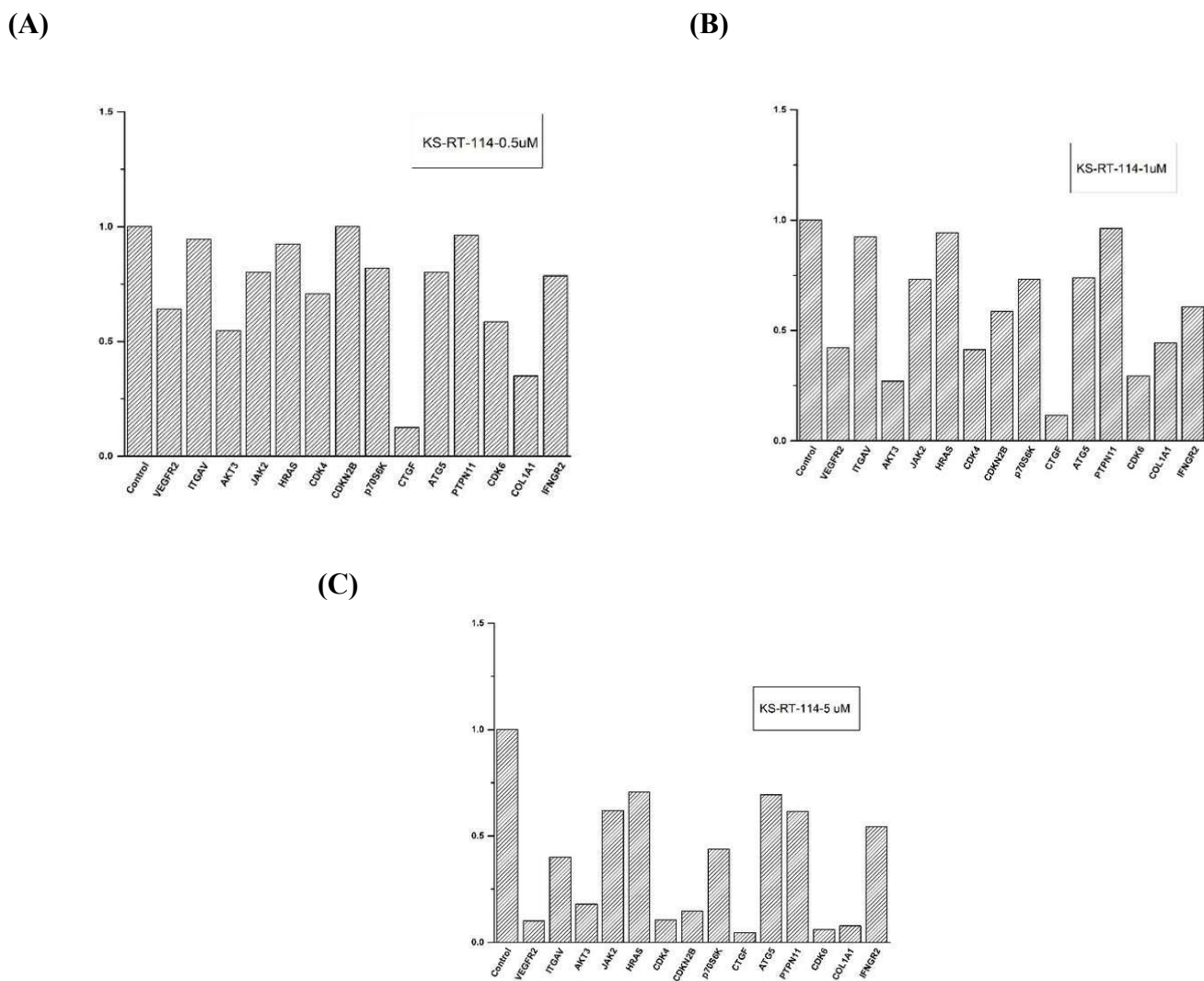


Figure 1.13. RT-PCR validated the differentially expressed genes discovered by transcriptome sequencing. For 15 genes that were downregulated when Noscapinods/MCF7 cell line was treated with various concentrations, such as 0.5 M, 1 M, and 5 M, RT-PCR was carried out. Each gene's expression level was standardised to that of the MCF7 control cell. The down-regulated gene and its expression level at different concentration are shown in figures A, B, and C. The x-axis displays the genes in the different concentration, and the y-axis displays the various expression levels.4.

DISCUSSION:

In this study the noscapinoids is major drug for survival of many cancer. Here this study 9-(N-arylmethylamino) noscapinoid plays a major role for cell survival, in the process of apoptosis, cell death, cell cycle progress, programmed cell death, regulation of apoptotic process in different function. Many different genes involved in the function for creating this molecular mechanism after treatment in MCF-7 breast cancer cell line. In this study of gene expression of this data analysis of MCF7 and Noscapinoid/ MCF7 using the next generation study (NGS) technique to screen of DEGS in treatment vs control sample.

In the gene-expression studies by the transcriptome data analysis, the primary study was around in p-value and log 2 FC of DEGs showed. From many functions and genes few of the calculated top up- or down-regulated DEGs were found in decrease and developmental processes of many types of tumor. In this comparative study of the treatment samples, the genes and the functions some common genes are up- regulated- after treatment and some down-regulated. In the case after the treatment of noscapinoid the particular and previous studies reported

that most of the genes were involved in carcinogenesis of various types of cancer such as of the breast cancer are down regulated.

We attempt to analyse the relationship between these Noscapioids treatment MCF7 cell line versus normal MCF7 cell line transcriptome data and study the Different pathway and functional annotation of different genes because we are informed that Noscapiine and its derivatives are a tubuline binding potent inhibitor used to prevent the recurrence of breast cancer [1]. The data showed in the table of up regulated function DEGs of molecular function and in Cellular component showing most of the genes functioning in the tubulin binding, cytoskeletal protein binding, DNA binding, cytosol, cytoskeleton, microtubule cytoskeleton, cytoskeletal part and microtubule.

In the most of the function from the 60 up-regulated genes, which are mostly involved are BTG2, DCBLD2, MCL1, TOB2, ABHD2, TBRG1, VIM, CLOCK, MAD2L1BP, BRCC3, HUS1B, CLOCK, BCL2L11, BCL2, CEBPB, TP63, SIN3A, FN1, CD14, MAP1LC3A, EME1, IL17D, ATG13, BRCC3, HUS1B, JTB in different functiuon. In the function apoptosis process and programmed cell death the family of gene like MCL1, BCL2, BCL2L11 involved. Also the PPI network showed the co-expression with different other genes, which are related to this family.

The down-regulated gene, which are targeted in the the analysis calculate in RtPCR. Total 50 most functional gene are calculated and from these selected 15 genes are run in PCR to check the ragulation expression in the cell line. These analysis is showing the down regulation of the genes, which are involve in cancer cell growth, poliferation, initiation, development and migration of cancer cell.

We showed the data of functional pathways of up regulated genes, They function in the pathways that control a variety of biological activities, such as cell division, apoptosis, and survival, as well as tumour cell invasion and migration. Where all the 60 up regulated genes involved, that are identified and showing in the PPI network. 50 common genes are found in the analysis results, which are down regulated and showing the interation in PPI network. And 15 of them including VEGFR2, ITGAV, AKT3, JAK2, HRAS, CDK4, CDKN2B, p70S6K, CTGF, ATG5, PTPN11, CDK6, COL1A1, IFNGR2 are identified to be closely associated with ER related pathway including induced oncogenes and lousing of tumor suppressor genes, promote rapid proliferation and reduced of apoptosis. Some genes are showing in the involvement in Renal cell carcinoma, Pancreatic cancer, Basal cell carcinoma, Colorectal cancer and Bladder cancer pathways.

CONCLUSION:

In conclusion, deciphering the potential mechanism of Noscapiine medication and controlling disease development in breast cancer may be achieved by studying breast cancer RNA-seq data of noscapioids treatment indicating the correlations among these DEGs. We propose that these DEGs may serve as therapeutic targets for resistance in breast cancer as well as potential indicators. **ACKNOWLEDGMENTS:**

The authors would like to thank Center of excellence, Natural Products and Therapeutics, OHEPEE, World Bank, Department of Biotechnology and Bioinformatics, Sambalpur University supporting this research.

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SUPPLEMENTARY DATA

Supplementary Table 1: Showing the top 20 Biological process of up-regulated DEGs with p-value, totals genes involve and GO Id.

Biological process	pval	Genes num	GO term
negative regulation of cellular process	0.0215	25	GO:0048523
response to stress	0.0246	25	GO:0006950
negative regulation of biological process	0.0764	25	GO:0048519
positive regulation of cellular process	0.173	24	GO:0048522
apoptotic process	7.4E-06	23	GO:0006915
programmed cell death	9.2E-06	23	GO:0012501
organelle organization	0.0373	18	GO:0006996
cell cycle	0.00127	17	GO:0007049
regulation of apoptotic process	0.00136	15	GO:0042981
regulation of programmed cell death	0.00153	15	GO:0043067
cellular response to stress	0.0024	15	GO:0033554
cell proliferation	0.0105	15	GO:0008283
immune system process	0.154	15	GO:0002376
cell cycle process	0.00514	13	GO:0007049
regulation of cell proliferation	0.0143	12	GO:0042127
regulation of developmental process	0.0882	12	GO:0032502
regulation of cell cycle	0.00102	11	GO:0051726
regulation of cellular component organization	0.0505	11	GO:0051128
negative regulation of cell cycle	5.5E-05	10	GO:0045786
regulation of cell differentiation	0.0409	10	GO:0045595
positive regulation of nucleobase-containing compound metabolic process	0.0905	10	GO:0045935
multi-organism process	0.174	10	GO:0051704
cell cycle arrest	6.8E-05	9	GO:0007050

Supplementary Table 2: Showing the top 20 Biological process of down-regulated DEGs with pValue, totals genes involve and GO Id.

Biological Process	pval	Genes num	GO term
protein localization	0.0466	136	GO:0072657
cell cycle	0.0974	133	GO:0000165
cellular response to stress	0.0361	122	GO:0033554
establishment of protein localization	0.00795	116	GO:0045184
protein transport	0.0148	110	GO:0006886
cell cycle process	0.0321	108	GO:0007049
cell cycle phase	0.033	84	GO:0022403
mitotic cell cycle	0.0115	80	GO:0000278
macromolecule catabolic process	0.0866	80	GO:0044265
regulation of cell cycle	0.00178	79	GO:0051726
cellular macromolecule catabolic process	0.0253	69	GO:0044265
intracellular protein transport	0.00883	68	GO:0006886
response to DNA damage stimulus	0.0774	66	GO:0061025
viral reproduction	0.0428	64	GO:0016032
protein modification by small protein conjugation	0.0904	55	GO:0000737

negative regulation of cell cycle	0.000573	53	GO:0010948
viral reproductive process	0.0104	53	GO:0016032
protein ubiquitination	0.0523	53	GO:0016567
cell division	0.000971	51	GO:0051301
protein catabolic process	0.0709	51	GO:0030163
cellular membrane organization	0.00058	49	GO:0061024
interphase	0.000486	47	GO:0051329

Supplementary Table 3: Top 20 Molecular function of up regulated gene with Pvalue, no. Of gene and GO id.

Molecular Function	pval	Genes num	GO term
DNA binding	0.552	9	GO:0003677
enzyme binding	0.0375	8	GO:0019899
positive regulation of transcription, DNA-dependent	0.11	7	GO:0045893
ATP binding	0.204	7	GO:0005524
adenyl ribonucleotide binding	0.222	7	GO:0032559
adenyl nucleotide binding	0.224	7	GO:0030554
purine ribonucleotide binding	0.418	7	GO:0032555
purine nucleotide binding	0.422	7	GO:0017076
transcription from RNA polymerase II promoter	0.438	7	GO:0006366
kinase binding	0.0022	6	GO:0019901
protein dimerization activity	0.101	6	GO:0046983
protein kinase binding	0.0072	5	GO:0019901
enzyme regulator activity	0.311	5	GO:0030234
receptor binding	0.601	5	GO:0005102
protein heterodimerization activity	0.0327	4	GO:0046982
transcription factor binding	0.0823	4	GO:0003700
protein binding transcription factor activity	0.129	4	GO:0003700
sequence-specific DNA binding	0.213	4	GO:0043565
negative regulation of transcription, DNA-dependent	0.4	4	GO:0045892
hydrolase activity, acting on ester bonds	0.415	4	GO:0016788
tubulin binding	0.0205	3	GO:0015631
transcription cofactor activity	0.266	3	GO:0003712
protein serine/threonine kinase activity	0.284	3	GO:0004674
cytoskeletal protein binding	0.432	3	GO:0008092

Supplementary Table 4: Top 20 Molecular function of down regulated gene with Pvalue, no. Of gene and GO id.

Molecular Function	pval	Genes num	GO term
nucleotide binding	0.0837	168	GO:0008276
purine ribonucleotide binding	0.00651	142	GO:0003725
purine nucleotide binding	0.00726	142	GO:0032555
adenyl ribonucleotide binding	0.0211	113	GO:0019901
adenyl nucleotide binding	0.0226	113	GO:0032559
ATP binding	0.014	112	GO:0017076
enzyme binding	0.0758	86	GO:0016887
RNA binding	0.0361	74	GO:0017124
pyrophosphatase activity	0.114	67	GO:0005516
hydrolase activity	0.124	67	GO:0019001

nucleoside-triphosphatase activity	0.0828	65	GO:0004540
identical protein binding	0.181	63	GO:0005520
protein domain specific binding	0.000229	56	GO:0030554
structural molecule activity	0.0234	54	GO:0042826
sequence-specific DNA binding	0.242	50	GO:0016817
protein homodimerization activity	0.138	42	GO:0003735
kinase binding	0.017	37	GO:0005070
protein kinase binding	0.0402	32	GO:0016706
enzyme activator activity	0.174	32	GO:0045182
GTP binding	0.0525	31	GO:0003677
guanyl nucleotide binding	0.117	31	GO:0016705
ATPase activity	0.161	31	GO:0016706
ligase activity	0.181	29	GO:0008168

Supplementary Table 5: Top 20 cellular component pvalue, no of gene and GO id from up regulated gene.

Cellular Component	pval	Genes num	GO term
intracellular organelle part	0.301	33	GO:0043229
organelle part	0.36	33	GO:0043226
nucleus	0.643	26	GO:0005634
macromolecular complex	0.0329	24	GO:0032991
protein complex	0.00866	23	GO:0032991
non-membrane-bounded organelle	0.013	22	GO:0043228
intracellular non-membrane-bounded organelle	0.013	22	GO:0043232
cytosol	0.0414	15	GO:0005829
nuclear part	0.281	14	GO:0044428
organelle lumen	0.303	14	GO:0043233
membrane-enclosed lumen	0.327	14	GO:0031974
cytoskeleton	0.0411	13	GO:0005856
nuclear lumen	0.236	12	GO:0031981
microtubule cytoskeleton	0.0161	9	GO:0000226
cytoskeletal part	0.101	9	GO:0005856
nucleoplasm	0.316	8	GO:0005654
mitochondrion	0.445	8	GO:0005739
chromosome	0.0202	7	GO:0005694
plasma membrane part	0.729	7	GO:0005886
chromosomal part	0.0306	6	GO:0005694
extracellular region part	0.324	6	GO:0005576
cell projection	0.381	6	GO:0030030
microtubule	0.00804	5	GO:0007017

Supplementary Table 6: Top 20 cellular component pvalue, no of gene and GO id from down regulated gene.

Cellular_Component	pval	Genes num	GO term
non-membrane-bounded organelle	0.155	251	GO:0043228
intracellular non-membrane-bounded organelle	0.155	251	GO:0043232
membrane-enclosed lumen	0.0317	231	GO:0031974
organelle lumen	0.028	228	GO:0043233
nuclear part	0.0968	217	GO:0044428
cytosol	0.00025	201	GO:0005829
nuclear lumen	0.0241	185	GO:0031981
nucleoplasm	0.0271	129	GO:0005654
Golgi apparatus	0.268	90	GO:0005794
nucleoplasm part	0.0101	72	GO:0044451
membrane-bounded vesicle	0.324	70	GO:0031982
cytoplasmic membrane-bounded vesicle	0.339	65	GO:0000307
cell junction	0.204	57	GO:0030054
nucleolus	0.00453	56	GO:0005730
ribonucleoprotein complex	0.0228	54	GO:0022613
chromosome	0.165	54	GO:0005694
Golgi apparatus part	0.228	51	GO:0005794
endosome	0.231	46	GO:0005768
chromosomal part	0.24	45	GO:0044427
Golgi membrane	0.11	44	GO:0005794
perinuclear region of cytoplasm	0.00802	42	GO:0048471
microtubule organizing center	0.186	38	GO:0031023
actin cytoskeleton	0.0628	34	GO:0031023
centrosome	0.0573	33	GO:0030036

KEGG_PATHWAYS	P. Value	KEGG_ID
Regulation of actin cytoskeleton	0.00236	hsa04810
Cell cycle	0.517	hsa04110
PI3K-Akt signaling pathway	0.00776	hsa04151
Natural killer cell mediated cytotoxicity	0.218	hsa04650
cGMP-PKG signaling pathway	0.106	hsa04022
Axon guidance	0.0577	hsa04360
FoxO signaling pathway	0.323	hsa04068
MAPK signaling pathway	0.529	hsa04010
cAMP signaling pathway	0.117	hsa04024
VEGF signaling pathway	0.396	hsa04370
AMPK signaling pathway	0.323	hsa04152
Regulation of autophagy	0.137	hsa04140
Rap1 signaling pathway	0.134	hsa04015
ErbB signaling pathway	0.481	hsa04012
TGF-beta signaling pathway	0.432	hsa04350
Wnt signaling pathway	0.615	hsa04310
Cytokine-cytokine receptor interaction	0.24	hsa04060

Supplementary Table 7: Showing the pathways data of up-regulated gene with pvalue (Generate from miRNet software Tool) and KEGG id.

Supplementary Table 8: Showing the pathways data of Down-regulated gene with pvalue (Generate from miRNet software Tool) and KEGG id.

KEGG_PATHWAYS	pval	KEGG_ID
Pathways in cancer	0.0018	hsa05200
HTLV-I infection	0.0168	hsa05166
Focal adhesion	0.0177	hsa04510
Osteoclast differentiation	0.0123	hsa04380
Chemokine signaling pathway	0.256	hsa04062
Neurotrophin signaling pathway	0.0344	hsa04722
Fc gamma R-mediated phagocytosis	0.00533	hsa04666
RNA transport	0.0407	hsa03013
Tight junction	0.101	hsa04530
Small cell lung cancer	0.00831	hsa05222
RNA degradation	0.00941	hsa03013
T cell receptor signaling pathway	0.138	hsa04660
Insulin signaling pathway	0.453	hsa04910
Chronic myeloid leukemia	0.073	hsa05220
VEGF signaling pathway	0.176	hsa04370
Non-small cell lung cancer	0.036	hsa05223
Renal cell carcinoma	0.0692	hsa05211
Pancreatic cancer	0.123	hsa05212
Basal cell carcinoma	0.154	hsa05217
mTOR signaling pathway	0.29	hsa04150
Colorectal cancer	0.346	hsa05210
Bladder cancer	0.256	hsa05219

BIOLOGICAL_PROCESS_MCF7

Function	Gene
apoptotic process	"DPF2", "BTG2", "TNFSF9", "PPP2R1A", "MCL1", "VIM", "SART1", "BCL2L11", "RRN3", "CEBPB", "TP63", "KLLN", "SIN3A", "GHITM", "JTB", "IFIT2", "TNFAIP8", "BCL7C", "CD14", "ARAF", "FAM32A", "UNC5D", "SAP30BP"
programmed cell death	"DPF2", "BTG2", "TNFSF9", "PPP2R1A", "MCL1", "VIM", "SART1", "BCL2L11", "RRN3", "CEBPB", "TP63", "KLLN", "SIN3A", "GHITM", "JTB", "IFIT2", "TNFAIP8", "BCL7C", "CD14", "ARAF", "FAM32A", "UNC5D", "SAP30BP"
negative regulation of cell cycle	"CCNA2", "TBRG1", "SART1", "CLOCK", "TIMP2", "TP63", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"
cell cycle arrest	"CCNA2", "TBRG1", "SART1", "CLOCK", "TP63", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"
cell cycle checkpoint	"CCNA2", "CLOCK", "TP63", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"
DNA damage checkpoint	"CCNA2", "CLOCK", "TP63", "BRCC3", "HUS1B"
DNA integrity checkpoint	"CCNA2", "CLOCK", "TP63", "BRCC3", "HUS1B"
DNA integrity checkpoint	"CCNA2", "CLOCK", "TP63", "BRCC3", "HUS1B"
regulation of cell cycle	"CCNA2", "TBRG1", "SART1", "CLOCK", "BCL2L11", "TIMP2", "TP63", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"

cell cycle	"CCNA2", "PPP2R1A", "TBRG1", "SART1", "CLOCK", "BCL2L11", "TIMP2", "TP63", "KLLN", "SIN3A", "JTB", "FAM32A", "KIF18A", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"
regulation of apoptotic process	"DPF2", "BTG2", "PPP2R1A", "MCL1", "SART1", "BCL2L11", "RRN3", "CEBPB", "TP63", "SIN3A", "JTB", "IFIT2", "TNFAIP8", "ARAF", "SAP30BP"
regulation of programmed cell death	"DPF2", "BTG2", "PPP2R1A", "MCL1", "SART1", "BCL2L11", "RRN3", "CEBPB", "TP63", "SIN3A", "JTB", "IFIT2", "TNFAIP8", "ARAF", "SAP30BP"
negative regulation of apoptotic process	"BTG2", "MCL1", "RRN3", "CEBPB", "TP63", "SIN3A", "JTB", "TNFAIP8", "ARAF"
negative regulation of programmed cell death	"BTG2", "MCL1", "RRN3", "CEBPB", "TP63", "SIN3A", "JTB", "TNFAIP8", "ARAF"
cellular response to stress	"CCNA2", "BTG2", "MCL1", "CLOCK", "BCL2L11", "CEBPB", "TP63", "ATG4C", "SIN3A", "MAP1LC3A", "NFATC2", "EME1", "ATG13", "BRCC3", "HUS1B"
vacuole organization	"ATG4C", "MAP1LC3A", "ATG13"
mitotic cell cycle checkpoint	"CCNA2", "TP63", "MAD2L1BP", "ZWILCH"
apoptotic signaling pathway	"DPF2", "MCL1", "SART1", "BCL2L11", "TP63"
cell cycle process	"CCNA2", "PPP2R1A", "TBRG1", "SART1", "CLOCK", "TP63", "SIN3A", "JTB", "KIF18A", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"
interaction with host	"VIM", "BCL2L11", "ULBP3", "CRT1", "TCIRG1", "THOC6"
response to DNA damage stimulus	"CCNA2", "BTG2", "MCL1", "CLOCK", "TP63", "NFATC2", "EME1", "BRCC3", "HUS1B"
cell proliferation	"BTG2", "TNFSF9", "TOB2", "TBRG1", "CHERP", "MXI1", "RRN3", "TIMP2", "CEBPB", "TP63", "EMP1", "JTB", "NFATC2", "TCIRG1", "BRK1"
cell proliferation	"BTG2", "TNFSF9", "TOB2", "TBRG1", "CHERP", "MXI1", "RRN3", "TIMP2", "CEBPB", "TP63", "EMP1", "JTB", "NFATC2", "TCIRG1", "BRK1"
response to ionizing radiation	"CLOCK", "TP63", "BRCC3"
regulation of cell proliferation	"BTG2", "TNFSF9", "TOB2", "TBRG1", "CHERP", "MXI1", "TIMP2", "TP63", "JTB", "NFATC2", "TCIRG1", "BRK1"
regulation of mitotic cell cycle	"CCNA2", "TIMP2", "TP63", "MAD2L1BP", "ZWILCH"
cellular response to nutrient levels	"ATG4C", "MAP1LC3A", "ATG13"
mitotic cell cycle	"CCNA2", "PPP2R1A", "TIMP2", "TP63", "SIN3A", "JTB", "KIF18A", "MAD2L1BP", "ZWILCH"
intrinsic apoptotic signaling pathway	"SART1", "BCL2L11", "TP63"
negative regulation of cellular process	"CCNA2", "BTG2", "PPP2R1A", "DCBLD2", "MCL1", "TOB2", "ABHD2", "TBRG1", "VIM", "SART1", "CHERP", "MXI1", "CLOCK", "RRN3", "TIMP2", "CEBPB", "TP63", "SIN3A", "JTB",

	"TNFAIP8", "ARAF", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"
cellular response to extracellular stimulus	"ATG4C", "MAP1LC3A", "ATG13"]
negative regulation of cell proliferation	"BTG2", "TOB2", "TBRG1", "CHERP", "MXI1", "TIMP2"
organelle organization	"CCNA2", "VIM", "BCL2L11", "RRN3", "TP63", "DOT1L", "ATG4C", "SIN3A", "JTB", "IFIT2", "MAP1LC3A", "MARK2", "TCIRG1", "KIF18A", "ZWILCH", "ATG13", "BRCC3", "BRK1"
regulation of neurogenesis	"VIM", "TIMP2", "KIF13B", "MARK2", "FEZ1"
M phase of mitotic cell cycle	"CCNA2", "JTB", "KIF18A", "MAD2L1BP", "ZWILCH"
regulation of cell differentiation	"PPP2R1A", "TOB2", "VIM", "SART1", "TIMP2", "CEBPB", "TP63", "KIF13B", "MARK2", "FEZ1"
negative regulation of binding	"SIN3A", "IFIT2"
regulation of JAK-STAT cascade	"PPP2R1A", "DOT1L"
regulation of binding	"DOT1L", "SIN3A", "IFIT2"
apoptotic mitochondrial changes	"BCL2L11", "IFIT2"
protein tetramerization	"TP63", "CRTC1"
aging	"TIMP2", "TP63", "SIN3A"
regulation of cellular component organization	"PPP2R1A", "DCBLD2", "VIM", "BCL2L11", "RRN3", "SIN3A", "FN1", "CD14", "KIF13B", "MARK2", "FEZ1"
protein homooligomerization	"BCL2L11", "TP63", "CRTC1"
regulation of axonogenesis	"KIF13B", "MARK2"
negative regulation of biological process	"CCNA2", "BTG2", "PPP2R1A", "DCBLD2", "MCL1", "TOB2", "ABHD2", "TBRG1", "VIM", "SART1", "CHERP", "MXI1", "CLOCK", "RRN3", "TIMP2", "CEBPB", "TP63", "SIN3A", "JTB", "TNFAIP8", "ARAF", "MAD2L1BP", "ZWILCH", "BRCC3", "HUS1B"
cell cycle phase	"CCNA2", "PPP2R1A", "TP63", "SIN3A", "JTB", "KIF18A", "MAD2L1BP", "ZWILCH"
nuclear transport	"TBRG1", "CHERP", "MXI1", "THOC6"
acute inflammatory response	"CEBPB", "FN1"
regulation of developmental process	"PPP2R1A", "TOB2", "VIM", "SART1", "BCL2L11", "TIMP2", "CEBPB", "TP63", "FN1", "KIF13B", "MARK2", "FEZ1"
positive regulation of nucleobase-containing compound metabolic process	"CCNA2", "BTG2", "CLOCK", "RRN3", "TIMP2", "TP63", "SIN3A", "CRTC1", "NFATC2", "BRCC3"
positive regulation of cell differentiation	"SART1", "TIMP2", "CEBPB", "TP63", "FEZ1"
JAK-STAT cascade	"PPP2R1A", "DOT1L"

establishment of organelle localization	"KIF18A", "FEZ1"
mitosis	"CCNA2", "JTB", "KIF18A", "ZWILCH"
viral reproductive process	"VIM", "BCL2L11", "ULBP3", "CRT1C1", "THOC6"
interphase of mitotic cell cycle	"CCNA2", "PPP2R1A", "TP63", "SIN3A"
interphase	"CCNA2", "PPP2R1A", "TP63", "SIN3A"
neuron differentiation	"BTG2", "VIM", "TIMP2", "CEBPB", "KIF13B", "MARK2", "FEZ1", "UNC5D"
neuron projection development	"BTG2", "VIM", "KIF13B", "MARK2", "FEZ1", "UNC5D"
response to nutrient levels	"ATG4C", "MAP1LC3A", "ATG13"
regulation of neuron apoptotic process	"BCL2L11", "TP63"
G2/M transition of mitotic cell cycle	"CCNA2", "PPP2R1A"
gland development	"BCL2L11", "CEBPB", "TP63"
immune response	"TNFSF9", "SIKE1", "CEBPB", "ULBP3", "RAET1E", "SIN3A", "IFIT2", "CD14", "NFATC2"
cellular component disassembly	"VIM", "TIMP2", "KIF18A"
histone modification	"DOT1L", "SIN3A", "BRCC3"
cell-matrix adhesion	"BCL2L11", "FN1"
response to extracellular stimulus	"ATG4C", "MAP1LC3A", "ATG13"
covalent chromatin modification	"DOT1L", "SIN3A", "BRCC3"
immune system process	"TNFSF9", "SIKE1", "TOB2", "SART1", "BCL2L11", "CEBPB", "ULBP3", "RAET1E", "SIN3A", "FN1", "IFIT2", "CD14", "KIF13B", "NFATC2", "KIF18A"
response to virus	"BCL2L11", "SIN3A", "IFIT2"
regulation of cell morphogenesis	"FN1", "KIF13B", "MARK2"
neuron apoptotic process	"BCL2L11", "TP63"

CELLULAR_COMPONENT_MCF7

Function	Gene
microtubule	"BCL2L11", "KIF13B", "MAP1LC3A", "KIF18A", "FEZ1"
protein complex	"PPP2R1A", "MCL1", "VIM", "CLOCK", "BCL2L11", "TP63", "ULBP3", "RAET1E", "SIN3A", "JTB", "FN1", "KIF13B", "MAP1LC3A", "NFATC2", "TCIRG1", "KIF18A", "MAD2L1BP", "THOC6", "FEZ1", "ZWILCH", "ATG13", "BRCC3", "HUS1B"
non-membrane-bounded organelle	"DPF2", "PPP2R1A", "VIM", "CLOCK", "BCL2L11", "RRN3", "CEBPB", "TP63", "SIN3A", "JTB", "KIF13B", "MAP1LC3A", "NFATC2", "FAM32A", "KIF18A", "MAD2L1BP", "FEZ1", "EME1", "SAP30BP", "ZWILCH", "HUS1B", "BRK1"
nuclear chromosome part	"CEBPB", "TP63", "SIN3A", "HUS1B"
microtubule cytoskeleton	"DPF2", "PPP2R1A", "BCL2L11", "JTB", "KIF13B", "MAP1LC3A", "KIF18A", "MAD2L1BP", "FEZ1"
nuclear chromatin	"CEBPB", "TP63", "SIN3A"
chromosome	"PPP2R1A", "CLOCK", "CEBPB", "TP63", "SIN3A", "ZWILCH", "HUS1B"
transcription factor complex	"CLOCK", "TP63", "SIN3A", "NFATC2"
nuclear chromosome	"CEBPB", "TP63", "SIN3A", "HUS1B"
chromosomal part	"PPP2R1A", "CEBPB", "TP63", "SIN3A", "ZWILCH", "HUS1B"
macromolecular complex	"PPP2R1A", "MCL1", "VIM", "SART1", "CLOCK", "BCL2L11", "TP63", "ULBP3", "RAET1E", "SIN3A", "JTB", "FN1", "KIF13B", "MAP1LC3A", "NFATC2", "TCIRG1", "KIF18A", "MAD2L1BP", "THOC6", "FEZ1", "ZWILCH", "ATG13", "BRCC3", "HUS1B"
chromosome	"PPP2R1A", "SIN3A", "ZWILCH"
cytoskeleton	"DPF2", "PPP2R1A", "VIM", "BCL2L11", "JTB", "KIF13B", "MAP1LC3A", "NFATC2", "KIF18A", "MAD2L1BP", "FEZ1", "SAP30BP", "BRK1"
cytosol	"SIKE1", "PPP2R1A", "CHMP4B", "VIM", "SART1", "CLOCK", "BCL2L11", "TP63", "ATG4C", "IFIT2", "MAP1LC3A", "NFATC2", "KIF18A", "ZWILCH", "ATG13"
basement membrane	"TIMP2", "FN1"
spindle	"JTB", "KIF18A", "MAD2L1BP"
nucleolus	"RRN3", "SIN3A", "FAM32A", "EME1", "HUS1B"
mitochondrial outer membrane	"MCL1", "BCL2L11"
anchored to membrane	"ULBP3", "CD14"
kinetochore	"SIN3A", "ZWILCH"

cytoskeletal part	"DPF2", "VIM", "BCL2L11", "JTB", "KIF13B", "MAP1LC3A", "KIF18A", "MAD2L1BP", "FEZ1"
organelle outer membrane	"MCL1", "BCL2L11"
chromatin	"CEBPB", "TP63", "SIN3A"
cell surface	"DCBLD2", "TIMP2", "CD14", "UNC5D"
outer membrane	"MCL1", "BCL2L11"
microtubule organizing center	"DPF2", "JTB", "KIF18A", "FEZ1"
late endosome	"CHMP4B", "MAP1LC3A"
centrosome	"DPF2", "JTB", "FEZ1"
extracellular space	"TNFSF9", "TIMP2", "FN1", "CD14", "IL17D"
nucleoplasm part	"SART1", "CLOCK", "TP63", "SIN3A", "NFATC2"
intermediate filament cytoskeleton	"VIM", "SAP30BP"
endosome	"CHMP4B", "CD14", "MAP1LC3A", "TCIRG1"
neuron projection	"TIMP2", "TP63", "KIF13B", "FEZ1"
organelle lumen	"CCNA2", "PCCB", "MCL1", "SART1", "CLOCK", "RRN3", "CEBPB", "TP63", "SIN3A", "FN1", "NFATC2", "FAM32A", "EME1", "HUS1B"
nucleoplasm	"CCNA2", "MCL1", "SART1", "CLOCK", "RRN3", "TP63", "SIN3A", "NFATC2"
extracellular region part	"TNFSF9", "VIM", "TIMP2", "FN1", "CD14", "IL17D"
mitochondrial matrix	"PCCB", "MCL1"
membrane-enclosed lumen	"CCNA2", "PCCB", "DPF2", "PPP2R1A", "MCL1", "MOB4", "CHMP4B", "VIM", "SART1", "CHERP", "CLOCK", "BCL2L11", "RRN3", "CEBPB", "TP63", "SIN3A", "GHITM", "JTB", "FN1", "CD14", "KIF13B", "MAP1LC3A", "NFATC2", "FAM32A", "TCIRG1", "KIF18A", "MAD2L1BP", "THOC6", "FEZ1", "EME1", "ZWILCH", "BRCC3", "HUS1B"
focal adhesion	"VIM", "TIMP2", "TP63", "KIF13B", "KIF18A", "FEZ1"
spliceosomal complex	"MCL1", "BCL2L11", "GHITM"
ubiquitin ligase complex	"PCCB", "PPP2R1A", "MCL1", "BCL2L11", "GHITM", "JTB", "ARAF", "TCIRG1"
peroxisome	"MCL1", "BCL2L11", "GHITM"
endocytic vesicle	"FN1", "TCIRG1"
cell cortex	"MOB4", "CHERP"
mitochondrial part	"PCCB", "MCL1", "BCL2L11", "GHITM"
vacuole	"MAP1LC3A", "TCIRG1"
secretory granule	"VIM", "FN1", "MAP1LC3A", "TCIRG1"

nucleus	"CCNA2", "DPF2", "PPP2R1A", "MCL1", "TOB2", "TBRG1", "SART1", "MXI1", "CLOCK", "RRN3", "CEBPB", "TP63", "KLLN", "DOT1L", "SIN3A", "CRTC1", "MARK2", "NFATC2", "FAM32A", "KIF18A", "MAD2L1BP", "THOC6", "EME1", "SAP30BP", "BRCC3", "HUS1B"
plasma membrane part	"DCBLD2", "ULBP3", "RAET1E", "JTB", "FN1", "TCIRG1", "KIF18A"
membrane-bounded vesicle	"VIM", "FN1", "TCIRG1"
cytoplasmic vesicle	"FN1", "MAP1LC3A", "TCIRG1"
organelle envelope	"MCL1", "BCL2L11", "GHITM"

MOLECULAR_FUNCTION_MCF7

Function	Gene
kinase binding	"CCNA2", "MOB4", "JTB", "KIF13B", "FEZ1", "ATG13"
protein kinase binding	"CCNA2", "JTB", "KIF13B", "FEZ1", "ATG13"
ubiquitin binding	"KIF18A", "BRCC3"
tubulin binding	"BCL2L11", "KIF18A", "FEZ1"
microtubule motor activity	"KIF13B", "KIF18A"
small conjugating protein binding	"KIF18A", "BRCC3"
protein heterodimerization activity	"PPP2R1A", "MCL1", "BCL2L11", "CEBPB"
enzyme binding	"CCNA2", "MOB4", "RRN3", "UBE2K", "JTB", "KIF13B", "FEZ1", "ATG13"
microtubule binding	"BCL2L11", "KIF18A"
pattern recognition receptor activity	"KIF13B", "KIF18A"
transcription factor binding	"TOB2", "CEBPB", "DOT1L", "SIN3A"]
nuclear hormone receptor binding	"TOB2", "CEBPB"
protein dimerization activity	"PPP2R1A", "MCL1", "MXI1", "CLOCK", "BCL2L11", "CEBPB"
carboxylesterase activity	"CCNA2", "CLOCK", "RRN3", "TP63", "SIN3A", "CRTC1", "NFATC2"
hormone receptor binding	"TOB2", "CEBPB"
protein deacetylase activity	"ATG4C", "BRCC3"
protein binding transcription factor activity	"MXI1", "CLOCK", "SIN3A", "CRTC1"
cysteine-type endopeptidase regulator activity involved in apoptotic process	"TIMP2", "TNFAIP8"
transcription corepressor activity	"MXI1", "SIN3A"
histone acetyltransferase activity	"TNFSF9", "IL17D"

small conjugating protein-specific protease activity	"PCCB", "UBE2K", "KIF13B", "MARK2", "MARK3", "ARAF", "KIF18A"
RNA polymerase II transcription cofactor activity	"CLOCK", "CEBPB", "TP63", "NFATC2"
RNA polymerase II transcription cofactor activity	"CLOCK", "CEBPB", "TP63", "NFATC2"
cysteine-type endopeptidase activity	"PCCB", "UBE2K", "KIF13B", "MARK2", "MARK3", "ARAF", "KIF18A"
adenyl nucleotide binding	"PCCB", "UBE2K", "KIF13B", "MARK2", "MARK3", "ARAF", "KIF18A"
structural constituent of cytoskeleton	"MXI1", "SIN3A", "CRT1C1"
N-acyltransferase activity	"MARK2", "MARK3", "ARAF"
hydrogen ion transmembrane transporter activity	"TP63", "SIN3A"
protein complex binding	"TIMP2", "SIN3A"
receptor signaling protein activity	"PPP2R1A", "TIMP2", "FN1", "TNFAIP8", "BRCC3"
endonuclease activity	"TIMP2", "TNFAIP8"
thiolester hydrolase activity	"MXI1", "CEBPB", "TP63", "SIN3A"
protein C-terminus binding	"PPP2R1A", "ABHD2", "EME1", "BRCC3"
enzyme activator activity	"TIMP2", "FN1"
purine ribonucleotide binding	"PCCB", "UBE2K", "KIF13B", "MARK2", "MARK3", "ARAF", "KIF18A"
purine nucleotide binding	"PCCB", "UBE2K", "KIF13B", "MARK2", "MARK3", "ARAF", "KIF18A"
cytoskeletal protein binding	"BCL2L11", "KIF18A", "FEZ1"
transcription from RNA polymerase II promoter	"MXI1", "CLOCK", "CEBPB", "TP63", "SIN3A", "CRT1C1", "NFATC2"
glycosaminoglycan binding	"CD14", "MAP1LC3A", "MARK2"
nuclease activity	"MXI1", "CLOCK", "CEBPB", "TP63", "KLLN", "DOT1L", "SIN3A", "NFATC2", "EME1"
ligase activity	"PCCB", "UBE2K"
transferase activity	"VIM", "CEBPB", "TP63"
cytokine receptor binding	"TNFSF9", "TOB2", "TIMP2", "CEBPB", "IL17D"
protein kinase activity	"MARK2", "MARK3", "ARAF"
ubiquitin-protein ligase activity	"CHERP", "IFIT2", "THOC6"
transcription coactivator activity	"VIM", "FN1"
RNA splicing	"MARK2", "MARK3", "ARAF"

PATHWAYS_KEGG_MCF7

Function	Gene
Glyoxylate and dicarboxylate metabolism	"PCCB", "GRHPR", "GCSH", "GLYCTK", "SHMT2"
Regulation of actin cytoskeleton	"NRAS", "RRAS2", "CD14", "ITGA3", "MAP2K2", "PIP4K2A", "PPP1R12A", "GNA13", "CFL1", "ARPC3", "ARAF", "SSH1", "BRK1"
RNA degradation	"BTG2", "TOB2", "DHX36", "PAN2", "EXOSC3", "DCP1B"
Purine metabolism	"GUCY2C", "POLE2", "ADA", "POLD1", "PAPSS1", "POLR3B", "POLR2E", "PDE4C", "HPRT1", "GMPR2", "NME7"
Glycine, serine and threonine metabolism	"GNMT", "GRHPR", "GLYCTK", "SHMT2"
Pyruvate metabolism	"ME1", "PDHB", "ACSS2", "GRHPR"
Lysine degradation	"SETD1A", "SETD1B", "KMT5B", "DOT1L"
Bladder cancer	"NRAS", "MAP2K2", "ARAF"
Long-term potentiation	"NRAS", "RPS6KA3", "MAP2K2", "PPP1R12A", "ARAF"
Long-term depression	"NRAS", "MAP2K2", "PPP2R1A", "GNA13", "ARAF"
Axon guidance	"NRAS", "EFNB3", "CFL1", "SEMA4D", "EFNA5", "NFATC2", "UNC5D"
Lipoic acid metabolism	"NRAS", "IRAK2", "RPS6KA3", "MAP2K2", "IRS1", "RPS6KA4", "MAGED1"
ECM-receptor interaction	"FN1", "ITGA3", "COL5A2", "COL4A6", "SDC2"
Transcriptional misregulation in cancer	"SIN3A", "CD14"
Insulin signaling pathway	"NRAS", "MAP2K2", "PHKB", "IRS1", "PHKA2", "ARAF", "SORBS1"
PPAR signaling pathway	"PLTP", "ACOX1", "ME1", "SORBS1"
Propanoate metabolism	"PCCB", "ACSS2"
Endometrial cancer	"NRAS", "MAP2K2", "ARAF"
Phenylalanine, tyrosine and tryptophan biosynthesis	"UBE2D2", "ARPC3", "U2AF1"
RNA transport	"SMN1", "EIF1", "STRAP", "NMD3", "THOC6", "NXF1"
Pyrimidine metabolism	"POLE2", "POLD1", "POLR3B", "POLR2E", "NME7"
SNARE interactions in vesicular transport	"GOSR2", "STX8"
Aminoacyl-tRNA biosynthesis	"NRAS", "MAP2K2", "ARAF"
Thyroid cancer	"NRAS", "MAP2K2"
Small cell lung cancer	"FN1", "SKP2", "ITGA3", "COL4A6"

Sulfur relay system	"NRAS", "MAP2K2", "ULBP3", "RAET1E", "ARAF", "NFATC2"
Ribosome biogenesis in eukaryotes	"NMD3", "MPHOSPH10", "NXF1"
mRNA surveillance pathway	"SMG7", "PPP2R1A", "NXF1", "PPP2R3B"
Acute myeloid leukemia	"NRAS", "MAP2K2", "ARAF"
Inositol phosphate metabolism	"PIP4K2A", "PLCZ1", "INPP5B"
Prostate cancer	"NRAS", "HSP90AB1", "MAP2K2", "ARAF"
Pathogenic Escherichia coli infection	"CD14", "ARPC3"
Riboflavin metabolism	"PFKFB2", "MTMR2"
Melanoma	"NRAS", "MAP2K2", "ARAF"
Glycosaminoglycan biosynthesis - chondroitin sulfate	"NRAS", "MAP2K2", "NFATC2", "TEC"
Sulfur metabolism	"NRAS", "MAP2K2", "ARAF"
Phosphatidylinositol signaling system	"PIP4K2A", "PLCZ1", "INPP5B"
B cell receptor signaling pathway	"NRAS", "MAP2K2", "NFATC2"
VEGF signaling pathway	"NRAS", "MAP2K2", "NFATC2"
Glutathione metabolism	"GSTO2", "GSTT1"
Vascular smooth muscle contraction	"MAP2K2", "PPP1R12A", "GNA13", "ARAF"
RIG-I-like receptor signaling pathway	"SIKE1", "ISG15"
alpha-Linolenic acid metabolism	"NRAS", "MAP2K2", "ARAF"
Circadian rhythm - mammal	"CNDP2", "GLS2"
Bacterial invasion of epithelial cells	"FN1", "ARPC3"
Cell cycle	"CDC6", "CCNA2", "SKP2", "MCM4"
Dopaminergic synapse	"CLOCK", "PPP2R1A", "GNB5", "PPP2R3B"
MAPK signaling pathway	"NRAS", "RRAS2", "CD14", "RPS6KA3", "MAP2K2", "NFATC2", "DUSP9", "RPS6KA4"
Hypertrophic cardiomyopathy (HCM)	"MAP2K2", "ARAF"
HTLV-I infection	"NRAS", "RRAS2", "CRTC1", "POLE2", "POLD1", "NFATC2"
Histidine metabolism	"CFL1", "ARPC3", "ASAP1"
Pentose phosphate pathway	"NRAS", "PPP2R1A", "ARAF"
Endocytosis	"TSG101", "RAB11FIP2", "CHMP4B"
Melanogenesis	"NRAS", "EDNRB", "MAP2K2"
Glycolysis / Gluconeogenesis	"PDHB", "ACSS2"

Retinol metabolism	"RETSAT", "DHRS4"
Tuberculosis	"CEBPB", "IRAK2", "CD14", "KSR1", "TCIRG1"
Citrate cycle (TCA cycle)	"GSTO2", "GSTT1"
Metabolism of xenobiotics by cytochrome P450	"RPS6KA3", "PPP2R1A", "PLCZ1"
Salmonella infection	"CD14", "ARPC3"
Aldosterone-regulated sodium reabsorption	"NRAS", "MAP2K2"
Endocrine and other factor-regulated calcium reabsorption	"ITGA3", "TPM4"
Tight junction	"NRAS", "RRAS2", "PPP2R1A"
Pathways in cancer	"FN1", "NRAS", "SKP2", "HSP90AB1", "ITGA3", "MAP2K2", "COL4A6", "ARAF"

Biological Process Down regulated genes

binding, bridging	["HSPA5", "SPRR1B", "WWC1", "GRB2", "PIK3R1", "SKAP2", "GATAD2A", "STUB1", "FSCN1", "DUSP19", "OPHN1", "ANK3", "VAV3", "KHDRBS1", "FRMD4A", "ANXA1", "BAIAP2L1", "NUFIP1", "SKAP1", "SH3RF1", "SLA", "KSR2", "BAIAP2", "PTPN11", "GAS2L1", "COL14A1"],
protein binding, bridging	["HSPA5", "SPRR1B", "WWC1", "GRB2", "PIK3R1", "SKAP2", "GATAD2A", "STUB1", "FSCN1", "OPHN1", "ANK3", "VAV3", "KHDRBS1", "FRMD4A", "ANXA1", "BAIAP2L1", "NUFIP1", "SKAP1", "SLA", "BAIAP2", "PTPN11", "GAS2L1", "COL14A1"],
protein domain specific binding	["NKX3-1", "PTTG1", "BHLHE40", "HSPA5", "JAK2", "PAX6", "ERCC1", "BCAR1", "VCP", "SQSTM1", "SOCS7", "DOCK1", "PLSCR1", "UBE2I", "LYN", "SON", "HGS", "DLC1", "SH3GLB1", "TNFAIP1", "HIF1AN", "ACVR2A", "CLCN3", "GRB2", "HOXA3", "THAP7", "CARD19", "EPB41L2", "PKD2", "FOXJ3", "ACAP2", "NDFIP1", "STUB1", "PLEKHA2", "ZXDA", "CRIPT", "TACC3", "FUT8", "PINK1", "OPHN1", "NDFIP2", "KHDRBS1", "HOMER2", "YWHAB", "FZD8", "TRIM16", "ARHGEF37", "BAIAP2L1", "FZD3", "FOXJ1", "SKAP1", "LDB2", "BAIAP2", "PTPN11", "HCLS1", "IGSF5"],
double-stranded RNA binding	["DROSHA", "DDX58", "OAS1", "SON", "ADAD2", "OAS2", "OASL", "STAU2", "DDX1"],
purine ribonucleotide binding	["MCM5", "SGK1", "HSPA5", "CHEK1", "JAK2", "EPHB2", "HRAS", "DAPK1", "TOP1", "MX1", "MAP3K5", "MCM8", "VCP", "BLM", "CDK4", "CSNK2A1", "HYOU1", "RHOB", "ASS1", "PAK1", "ABCG8", "FGFR4", "DDX58", "TAP1", "ABCG1", "CSF1R", "MFN2", "PRKCA", "ABCA3", "CDC42BPG", "ACLY", "OAS1", "UBE2I", "LYN", "MYO1E", "NDUFA10", "UCK2", "DHX16", "BAZ1B", "NME6", "WARS2", "GATB", "ACVR2A", "CLCN3", "PSMC4", "KIF23", "AKT3", "RAB40B", "RAB9B", "PRKAR1A", "TEP1", "PDXK", "MDN1", "RAB30", "DHX35", "ATL2", "ATP2B1", "CCT6A", "KIF5C", "RABEP1", "DNM1L",

	"MAP3K2", "NKIRAS1", "MTHFD1", "HIPK3", "RAB14", "DHX40", "ARL8A", "ABCD3", "RALA", "MYO10", "RABL3", "PINK1", "FRK", "PIK3CB", "SPAG1", "MAP2K6", "MAP4K4", "CARS2", "OAS2", "MYH15", "PDK3", "RRAGA", "PIP5K1A", "HSPA14", "DDX53", "GNAT2", "STK24", "OASL", "DYNC1LI1", "TUBB2B", "MMAB", "IPMK", "ATP7A", "CAMK4", "OBSCN", "TIMM44", "NTRK2", "ADCK1", "CHD6", "ARF5", "RECQL", "LIG3", "LARS2", "ATP11A", "RAB7A", "MCCC1", "PIK3C3", "DDX1", "MOK", "UBA5", "MTIF2", "RAD54L", "CDKL1", "LIG1", "DNM1", "NEK11", "STK16", "RHO", "RAB29", "RASL11A", "MOCS1", "CLPP", "CHD1L", "ITM2C", "KIF12", "CENPE", "DGKQ", "SAR1B", "EPHB1", "ORC5", "DIRAS2", "RAB24", "NPR1", "KSR2", "SUCLG2", "POMK", "FANCM", "GTF2F2", "UCKL1", "UBE2QL1", "STRADA"],
purine nucleotide binding	["MCM5", "SGK1", "HSPA5", "CHEK1", "JAK2", "EPHB2", "HRAS", "DAPK1", "TOP1", "MX1", "MAP3K5", "MCM8", "VCP", "BLM", "CDK4", "CSNK2A1", "HYOU1", "RHOB", "ASS1", "PAK1", "ABCG8", "FGFR4", "DDX58", "TAP1", "ABCG1", "CSF1R", "MFN2", "PRKCA", "ABCA3", "CDC42BPG", "ACLY", "OAS1", "UBE2I", "LYN", "MYO1E", "NDUFA10", "UCK2", "DHX16", "BAZ1B", "NME6", "WARS2", "GATB", "ACVR2A", "CLCN3", "PSMC4", "KIF23", "AKT3", "RAB40B", "RAB9B", "PRKAR1A", "TEP1", "PDXK", "MDN1", "RAB30", "DHX35", "ATL2", "ATP2B1", "CCT6A", "KIF5C", "RABEP1", "DNM1L", "MAP3K2", "NKIRAS1", "MTHFD1", "HIPK3", "RAB14", "DHX40", "ARL8A", "ABCD3", "RALA", "MYO10", "RABL3", "PINK1", "FRK", "PIK3CB", "SPAG1", "MAP2K6", "MAP4K4", "CARS2", "OAS2", "MYH15", "PDK3", "RRAGA", "PIP5K1A", "HSPA14", "DDX53", "GNAT2", "STK24", "OASL", "DYNC1LI1", "TUBB2B", "MMAB", "IPMK", "ATP7A", "CAMK4", "OBSCN", "TIMM44", "NTRK2", "ADCK1", "CHD6", "ARF5", "RECQL", "LIG3", "LARS2", "ATP11A", "RAB7A", "MCCC1", "PIK3C3", "DDX1", "MOK", "UBA5", "MTIF2", "RAD54L", "CDKL1", "LIG1", "DNM1", "NEK11", "STK16", "RHO", "RAB29", "RASL11A", "MOCS1", "CLPP", "CHD1L", "ITM2C", "KIF12", "CENPE", "DGKQ", "SAR1B", "EPHB1", "ORC5", "DIRAS2", "RAB24", "NPR1", "KSR2", "SUCLG2", "POMK", "FANCM", "GTF2F2", "UCKL1", "UBE2QL1", "STRADA"],
ATP binding	["MCM5", "SGK1", "HSPA5", "CHEK1", "JAK2", "EPHB2", "DAPK1", "TOP1", "MAP3K5", "MCM8", "VCP", "BLM", "CDK4", "CSNK2A1", "HYOU1", "ASS1", "PAK1", "ABCG8", "FGFR4", "DDX58", "TAP1", "ABCG1", "CSF1R", "PRKCA", "ABCA3", "CDC42BPG", "ACLY", "OAS1", "UBE2I", "LYN", "MYO1E", "NDUFA10", "UCK2", "DHX16", "BAZ1B", "NME6", "WARS2", "GATB", "ACVR2A", "CLCN3", "PSMC4", "KIF23", "AKT3", "TEP1", "PDXK", "MDN1", "DHX35", "ATP2B1", "CCT6A", "KIF5C", "RABEP1", "MAP3K2", "MTHFD1", "HIPK3", "DHX40", "ABCD3",

	"MYO10", "PINK1", "FRK", "PIK3CB", "MAP2K6", "MAP4K4", "CARS2", "OAS2", "MYH15", "PDK3", "PIP5K1A", "HSPA14", "DDX53", "STK24", "OASL", "DYNC1LI1", "MMAB", "IPMK", "ATP7A", "CAMK4", "OBSCN", "TIMM44", "NTRK2", "ADCK1", "CHD6", "RECQL", "LIG3", "LARS2", "ATP11A", "MCCC1", "PIK3C3", "DDX1", "MOK", "UBA5", "RAD54L", "CDKL1", "LIG1", "NEK11", "STK16", "CLPP", "CHD1L", "ITM2C", "KIF12", "CENPE", "DGKQ", "EPHB1", "ORC5", "NPR1", "KSR2", "SUCLG2", "POMK", "FANCM", "GTF2F2", "UCKL1", "UBE2QL1", "STRADA"],
structural constituent of ribosome	["MRPS33", "MRPL47", "RPS25", "MRPL1", "MRPL32", "RPS9", "RPS29", "RPL35A", "MRPL16", "RPS14", "UBA52", "MRPL49", "RPL34", "RPL35", "MRPL15", "MRPS18C", "MRPL14", "MRPS18B"],
kinase binding	["CTNNB1", "FOXO1", "FOXO4", "TP73", "ADIPOR1", "CDKN2B", "JAK2", "PAX6", "MAP3K5", "BCAR1", "CD24", "CD8A", "SQSTM1", "ITGAV", "PAK1", "TRAF6", "PRC1", "PRKAB1", "CCNY", "GRB2", "CACUL1", "MAP3K2", "STUB1", "DUSP19", "MAP2K6", "PIP5K1A", "PPP2R5A", "CNPPD1", "ARRB1", "KIZ", "PARN", "SKAP1", "DGKQ", "NPR1", "KSR2", "HCLS1", "STRADA"],
adenyl ribonucleotide binding	["MCM5", "SGK1", "HSPA5", "CHEK1", "JAK2", "EPHB2", "DAPK1", "TOP1", "MAP3K5", "MCM8", "VCP", "BLM", "CDK4", "CSNK2A1", "HYOU1", "ASS1", "PAK1", "ABCG8", "FGFR4", "DDX58", "TAP1", "ABCG1", "CSF1R", "PRKCA", "ABCA3", "CDC42BPG", "ACLY", "OAS1", "UBE2I", "LYN", "MYO1E", "NDUFA10", "UCK2", "DHX16", "BAZ1B", "NME6", "WARS2", "GATB", "ACVR2A", "CLCN3", "PSMC4", "KIF23", "AKT3", "PRKAR1A", "TEP1", "PDXK", "MDN1", "DHX35", "ATP2B1", "CCT6A", "KIF5C", "RABEP1", "MAP3K2", "MTHFD1", "HIPK3", "DHX40", "ABCD3", "MYO10", "PINK1", "FRK", "PIK3CB", "MAP2K6", "MAP4K4", "CARS2", "OAS2", "MYH15", "PDK3", "PIP5K1A", "HSPA14", "DDX53", "STK24", "OASL", "DYNC1LI1", "MMAB", "IPMK", "ATP7A", "CAMK4", "OBSCN", "TIMM44", "NTRK2", "ADCK1", "CHD6", "RECQL", "LIG3", "LARS2", "ATP11A", "MCCC1", "PIK3C3", "DDX1", "MOK", "UBA5", "RAD54L", "CDKL1", "LIG1", "NEK11", "STK16", "CLPP", "CHD1L", "ITM2C", "KIF12", "CENPE", "DGKQ", "EPHB1", "ORC5", "NPR1", "KSR2", "SUCLG2", "POMK", "FANCM", "GTF2F2", "UCKL1", "UBE2QL1", "STRADA"],
adenyl nucleotide binding	["MCM5", "SGK1", "HSPA5", "CHEK1", "JAK2", "EPHB2", "DAPK1", "TOP1", "MAP3K5", "MCM8", "VCP", "BLM", "CDK4", "CSNK2A1", "HYOU1", "ASS1", "PAK1", "ABCG8", "FGFR4", "DDX58", "TAP1", "ABCG1", "CSF1R", "PRKCA", "ABCA3", "CDC42BPG", "ACLY", "OAS1", "UBE2I", "LYN", "MYO1E", "NDUFA10", "UCK2", "DHX16", "BAZ1B", "NME6", "WARS2", "GATB", "ACVR2A", "CLCN3", "PSMC4", "KIF23", "AKT3", "PRKAR1A", "TEP1", "PDXK", "MDN1", "DHX35", "ATP2B1", "CCT6A",

	"KIF5C", "RABEP1", "MAP3K2", "MTHFD1", "HIPK3", "DHX40", "ABCD3", "MYO10", "PINK1", "FRK", "PIK3CB", "MAP2K6", "MAP4K4", "CARS2", "OAS2", "MYH15", "PDK3", "PIP5K1A", "HSPA14", "DDX53", "STK24", "OASL", "DYNC1LI1", "MMAB", "IPMK", "ATP7A", "CAMK4", "OBSCN", "TIMM44", "NTRK2", "ADCK1", "CHD6", "RECQL", "LIG3", "LARS2", "ATP11A", "MCCC1", "PIK3C3", "DDX1", "MOK", "UBA5", "RAD54L", "CDKL1", "LIG1", "NEK11", "STK16", "CLPP", "CHD1L", "ITM2C", "KIF12", "CENPE", "DGKQ", "EPHB1", "ORC5", "NPR1", "KSR2", "SUCLG2", "POMK", "FANCM", "GTF2F2", "UCKL1", "UBE2QL1", "STRADA"],
structural molecule activity	["CTNNB1", "COL1A1", "WNT4", "SPRR1B", "EPB41L4B", "ASPH", "BAZ1B", "COPG1", "MRPS33", "MRPL47", "LAMC1", "TPM2", "NUP98", "RPS25", "LAMTOR3", "EIF3A", "MRPL1", "EPB41L2", "MRPL32", "ADD3", "DUSP19", "COL5A1", "RPS9", "RPS29", "ANK3", "HOMER2", "ANXA1", "TUBB2B", "RPL35A", "NEBL", "CLTA", "MRPL16", "OBSCN", "RPS14", "UBA52", "MRPL49", "NUMA1", "COPE", "RPL34", "NUP107", "CTNNAL1", "RPL35", "MRPL15", "SH3RF1", "LAD1", "MRPS18C", "KRT6C", "KSR2", "TLN2", "MRPL14", "NEB", "COL14A1", "MRPS18B", "KRT40"],
protein transporter activity	["TNPO1", "ABCG1", "IPO11", "AP2A1", "ZFYVE16", "SNX1", "CALCR", "AP2A2", "TIMM44", "AP4S1", "KPNA4"],
GTPase activity	["HRAS", "MX1", "RHOB", "MFN2", "RAB30", "ATL2", "DNM1L", "NKIRAS1", "RAB14", "ARL8A", "RALA", "GNAT2", "TUBB2B", "ARF5", "RAB7A", "MTIF2", "NUDT1", "DNM1", "RHOU", "RAB29", "RASL11A", "SAR1B", "DIRAS2"],
SH3 domain binding	["PTTG1", "BCAR1", "SOCS7", "DOCK1", "PLSCR1", "LYN", "GRB2", "FUT8", "OPHN1", "KHDRBS1", "BAIAP2L1", "BAIAP2", "HCLS1"],
RNA binding	["DROSHA", "RBM38", "CPEB1", "ATXN2", "COPS5", "IGF2BP2", "DDX58", "PDCD4", "OAS1", "SON", "CBX6", "CHTOP", "NAF1", "TIMM50", "TRIM71", "GATB", "EIF1AX", "FECH", "RPS25", "SRP68", "TEP1", "EIF3A", "MRPL1", "ADAD2", "GTF2H3", "PAIP1", "TRUB1", "GRSF1", "PABPC4L", "PATL1", "IREB2", "SRSF11", "THOC2", "SNRNP1", "CSTF2", "AQR", "DIMIT1", "OAS2", "RPS9", "NUDT4", "CTIF", "KHDRBS1", "NUDT5", "PARK7", "DAZAP1", "DDX53", "OASL", "RPL35A", "SF3A1", "DIS3", "MRPL16", "RPS14", "STAU2", "DDX1", "NUFIP1", "MTIF2", "NUDT1", "RPL34", "EIF1B", "TRMT1L", "RPL35", "SLTM", "SNRPF", "PARN", "EIF2D", "ZC3H8", "CELF3", "HENMT1", "TYW5", "APOBEC3B", "ZNF74", "NOP9", "OOEP", "EXOSC6"],
SH3/SH2 adaptor activity	["GRB2", "SKAP2", "VAV3", "KHDRBS1", "SKAP1", "SLA", "PTPN11"],
protein kinase binding	["CTNNB1", "FOXO1", "FOXO4", "TP73", "ADIPOR1", "CDKN2B", "JAK2", "PAX6", "MAP3K5", "BCAR1", "CD24", "CD8A", "SQSTM1", "ITGAV", "PAK1", "TRAF6", "PRC1", "PRKAB1", "CCNY", "GRB2",

	"CACUL1", "MAP3K2", "DUSP19", "MAP2K6", "CNPPD1", "ARRB1", "KIZ", "PARN", "SKAP1", "NPR1", "KSR2", "HCLS1"],
mRNA binding	["RBM38", "IGF2BP2", "FECH", "GRSF1", "IREB2", "PARK7", "RPS14", "DDX1", "RPL35", "PARN", "CELF3"],
ATP-dependent helicase activity	["BLM", "DDX58", "DHX16", "DHX35", "DHX40", "DDX53", "CHD6", "RECQL", "DDX1", "CHD1L", "FANCM", "GTF2F2"],
translation regulator activity	["IGF2BP2", "PAIP1", "RPS9", "RPS14"],
GTP binding	["HRAS", "MX1", "RHOB", "MFN2", "RAB40B", "RAB9B", "RAB30", "ATL2", "DNM1L", "NKIRAS1", "RAB14", "ARL8A", "RALA", "RABL3", "SPAG1", "RRAGA", "GNAT2", "TUBB2B", "ARF5", "RAB7A", "MTIF2", "DNM1", "RHOA", "RAB29", "RASL11A", "MOCS1", "SAR1B", "DIRAS2", "RAB24", "NPR1", "SUCLG2"],
ribonucleoprotein complex binding	["HSPA5", "CD2BP2", "TIMM50", "SRP68", "NAA16", "MTIF2", "PITX2"],
beta-tubulin binding	["ARL8A", "EMD", "GABARAPL2", "FGF13"],
ATPase activity, coupled	["TOP1", "BLM", "DDX58", "TAP1", "ABCG1", "ABCA3", "MYO1E", "DHX16", "DHX35", "LONRF2", "ATP2B1", "GTF2H3", "DHX40", "ABCD3", "MYO10", "CECR2", "DDX53", "ATP7A", "CHD6", "RECQL", "ATP11A", "DDX1", "CHD1L", "ATP6V0C", "FANCM", "GTF2F2"],
enzyme binding	["CTNNB1", "FOXO1", "FOXO4", "NKX3-1", "PML", "STAT1", "TP73", "PTGS2", "ADIPOR1", "HSPA5", "CDKN2B", "JAK2", "PAX6", "MAP3K5", "BCAR1", "VCP", "CD24", "CD8A", "SQSTM1", "ITGAV", "TXNIP", "BACE1", "BID", "PAK1", "BIRC7", "CD74", "MFN2", "PRKCA", "TRAF6", "DHCR24", "PLSCR1", "PRC1", "PRKAB1", "UBE2I", "LYN", "CUL1", "BAG5", "BCOR", "OTUB1", "CCNY", "TNFAIP1", "SGSM3", "GRB2", "PIK3R1", "CACUL1", "SMAD5", "PRKAR1A", "CUL4A", "DOCK9", "PKD2", "RFXANK", "DNM1L", "MAP3K2", "BICD2", "STUB1", "ZNF326", "RANBP1", "DUSP19", "PINK1", "MAP2K6", "YWHAB", "PIP5K1A", "PPP2R5A", "UBE4B", "CNPPD1", "GLI3", "ARRB1", "FZD8", "PLCE1", "GABARAPL2", "RAB7A", "KIZ", "EHHADH", "RAB3GAP1", "PPP3CA", "PARN", "SKAP1", "DGKQ", "NPR1", "LDB2", "KSR2", "ANAPC2", "PTPN11", "HCLS1", "ATP6V0C", "STRADA"],
S-adenosylmethionine-dependent methyltransferase activity	["KMT2A", "PCMT1", "COMT", "SETD7", "KMT5C", "DIMIT1", "ASH2L", "METTL21A", "TRMT1L", "GAMT", "SETMAR", "TRMT2B"],
ribonuclease activity	["DROSHA", "RPP38", "CNOT6L", "RNASE1", "TSEN34", "XRN2", "DIS3", "PARN", "RNASE8"],
protein methyltransferase activity	["KMT2A", "SUZ12", "PCMT1", "SETD7", "KMT5C", "ASH2L", "METTL21A", "N6AMT1", "SETMAR"],
nucleoside-triphosphatase activity	["MCM5", "HSPA5", "HRAS", "TOP1", "MX1", "MCM8", "VCP", "BLM", "RHOB", "ABCG8", "DDX58", "TAP1", "ABCG1", "MFN2", "ABCA3", "MYO1E", "DHX16", "PSMC4", "KIF23", "KLC2", "MDN1", "RAB30", "DHX35", "ATL2", "LONRF2", "ATP2B1", "GTF2H3", "KIF5C", "DNM1L", "NKIRAS1", "RAB14",

	"DHX40", "ARL8A", "ABCD3", "RALA", "NAV1", "MYO10", "CECR2", "MYH15", "DDX53", "GNAT2", "DYNC1LI1", "TUBB2B", "ATP7A", "CHD6", "ARF5", "RECQL", "ATP11A", "RAB7A", "DDX1", "MTIF2", "RAD54L", "NUDT1", "DNM1", "RHOU", "RAB29", "RASL11A", "CHD1L", "KIF12", "CENPE", "SAR1B", "DIRAS2", "ATP6V0C", "FANCM", "GTF2F2"],
nucleotide binding	["MCM5", "SGK1", "HSPA5", "CHEK1", "JAK2", "EPHB2", "HRAS", "DAPK1", "TOP1", "MX1", "MAP3K5", "MCM8", "RBM38", "CPEB1", "VCP", "BLM", "CDK4", "CSNK2A1", "HYOU1", "RHOB", "ASS1", "PAK1", "IGF2BP2", "ABCG8", "FGFR4", "DDX58", "TAP1", "ABCG1", "CSF1R", "MFN2", "PRKCA", "ABCA3", "CDC42BPG", "DHCR24", "ACLY", "OAS1", "UBE2I", "LYN", "MYO1E", "NDUFA10", "QDPR", "UCK2", "DHX16", "BAZ1B", "NME6", "WARS2", "GATB", "ACVR2A", "CLCN3", "PSMC4", "KIF23", "AKT3", "RAB40B", "RAB9B", "HSDL2", "PRKAR1A", "TEP1", "PDXK", "MDN1", "RAB30", "DHX35", "ATL2", "ATP2B1", "CCT6A", "KIF5C", "RABEP1", "DNM1L", "MAP3K2", "NKIRAS1", "GRSF1", "MTHFD1", "HIPK3", "RAB14", "DHX40", "ARL8A", "PABPC4L", "ABCD3", "SRSF11", "RALA", "NAV1", "CSTF2", "MYO10", "RABL3", "PINK1", "FRK", "PIK3CB", "SPAG1", "MAP2K6", "MAP4K4", "CARS2", "OAS2", "MYH15", "PDK3", "RRAGA", "POLE", "PIP5K1A", "DAZAP1", "HSPA14", "DDX53", "GNAT2", "STK24", "OASL", "DYNC1LI1", "TUBB2B", "MMAB", "IPMK", "ATP7A", "CAMK4", "OBSCN", "TIMM44", "NTRK2", "ADCK1", "CHD6", "ARF5", "RECQL", "LIG3", "LARS2", "ATP11A", "RAB7A", "MCCC1", "PIK3C3", "DDX1", "MOK", "UBA5", "MTIF2", "RAD54L", "CDKL1", "DHRS7", "LIG1", "DNM1", "EHHADH", "NEK11", "PECR", "STK16", "RHOU", "RAB29", "RASL11A", "MOCS1", "CLPP", "CHD1L", "ITM2C", "KIF12", "SLTM", "MDH1B", "CENPE", "PARN", "DGKQ", "SAR1B", "EPHB1", "CELF3", "ORC5", "DIRAS2", "KDM1B", "DHRS13", "RAB24", "NPR1", "DCXR", "KSR2", "SUCLG2", "POMK", "FANCM", "GTF2F2", "UCKL1", "DXO", "CRYZL1", "UBE2QL1", "STRADA", "DHRS11"],
methyltransferase activity	["KMT2A", "SUZ12", "PCMT1", "COMT", "SETD7", "TYW3", "KMT5C", "DIMT1", "ASH2L", "METTL21A", "TRMT1L", "GAMT", "METTL5", "N6AMT1", "HENMT1", "TRMT10B", "METTL17", "SETMAR", "TRMT2B"],
kinase activator activity	["NKX3-1", "CD24", "DUSP19", "FGF13", "ABI1", "STRADA"],
chromatin binding	["CTNNB1", "FOXO1", "PBX2", "TP73", "TERF1", "BRD2", "TOP1", "MTA3", "TFAM", "SMARCC2", "BAZ1B", "SUZ12", "RCOR3", "PHF13", "PCGF2", "MCMBP", "POLE", "BAP1", "GLI3", "KDM5A", "CHD6", "ZIC2", "DDX1", "SSBP1", "PITX2", "ING2", "FANCM"],
protein complex binding	["CTNNB1", "MMP14", "VCP", "CDK4", "TGFB1", "TXN2", "FCGRT", "LYN", "ACVR2A", "PIK3R1",

	"ZNF326", "CRIPT", "COL5A1", "KHDRBS1", "YWHAB", "GNAT2", "MFGE8", "DNM1", "UCLH5", "MFAP2", "PDCL", "SKAP1", "DMP1", "ING2", "TLN2", "PTPN11", "HCLS1"],
calmodulin binding	["DAPK1", "GRIN1", "MYO1E", "SNTB2", "NDUF4F4", "ATP2B1", "CEP97", "ADD3", "MYO10", "CACNA1C", "MYH15", "EDF1", "CAMK4", "OBSCN", "PPP3CA"],
structure-specific DNA binding	["CTNNB1", "FOXO1", "FOXO4", "STAT1", "TP73", "TERF1", "PAX6", "ERCC1", "BLM", "DDX58", "NABP2", "FOXJ3", "FOXN2", "ZIC2", "SSBP1", "NEIL3", "FOXJ1", "SSBP3", "PITX2", "SETMAR"],
pyrophosphatase activity	["MCM5", "HSPA5", "HRAS", "TOP1", "MX1", "MCM8", "VCP", "BLM", "RHOB", "ABCG8", "DDX58", "TAP1", "ABCG1", "MFN2", "ABCA3", "MYO1E", "DHX16", "PSMC4", "KIF23", "KLC2", "MDN1", "RAB30", "DHX35", "ATL2", "LONRF2", "ATP2B1", "GTF2H3", "KIF5C", "DNM1L", "NKIRAS1", "RAB14", "DHX40", "ARL8A", "ABCD3", "RALA", "NAV1", "MYO10", "CECR2", "MYH15", "NUDT4", "NUDT5", "DDX53", "GNAT2", "DYNC1LI1", "TUBB2B", "ATP7A", "CHD6", "ARF5", "RECQL", "ATP11A", "RAB7A", "DDX1", "MTIF2", "RAD54L", "NUDT1", "DNM1", "RHOU", "RAB29", "RASL11A", "CHD1L", "KIF12", "CENPE", "SAR1B", "DIRAS2", "ATP6V0C", "FANCM", "GTF2F2"],
guanyl nucleotide binding	["HRAS", "MX1", "RHOB", "MFN2", "RAB40B", "RAB9B", "RAB30", "ATL2", "DNM1L", "NKIRAS1", "RAB14", "ARL8A", "RALA", "RABL3", "SPAG1", "RRAGA", "GNAT2", "TUBB2B", "ARF5", "RAB7A", "MTIF2", "DNM1", "RHOU", "RAB29", "RASL11A", "MOCS1", "SAR1B", "DIRAS2", "RAB24", "NPR1", "SUCLG2"],
protein C-terminus binding	["CTNNB1", "SREBF2", "JAK2", "HRAS", "ERCC1", "NPAT", "SIAH1", "ATXN2", "UBE2I", "AP2A1", "YWHAB", "DNM1", "CLIC6", "BAIAP2"],
hydrolase activity, acting on acid anhydrides	["MCM5", "HSPA5", "HRAS", "TOP1", "MX1", "MCM8", "VCP", "BLM", "RHOB", "ABCG8", "DDX58", "TAP1", "ABCG1", "MFN2", "ABCA3", "MYO1E", "DHX16", "PSMC4", "KIF23", "KLC2", "MDN1", "RAB30", "DHX35", "ATL2", "LONRF2", "ATP2B1", "GTF2H3", "KIF5C", "DNM1L", "NKIRAS1", "RAB14", "DHX40", "ARL8A", "ABCD3", "RALA", "NAV1", "MYO10", "CECR2", "MYH15", "NUDT4", "NUDT5", "DDX53", "GNAT2", "DYNC1LI1", "TUBB2B", "ATP7A", "CHD6", "ARF5", "RECQL", "ATP11A", "RAB7A", "DDX1", "MTIF2", "RAD54L", "NUDT1", "DNM1", "RHOU", "RAB29", "RASL11A", "CHD1L", "KIF12", "CENPE", "SAR1B", "DIRAS2", "ATP6V0C", "FANCM", "GTF2F2"],
helicase activity	["MCM5", "MCM8", "BLM", "DDX58", "DHX16", "DHX35", "DHX40", "DDX53", "CHD6", "RECQL", "DDX1", "RAD54L", "CHD1L", "FANCM", "GTF2F2"],
transferase activity, transferring one-carbon groups	["KMT2A", "SUZ12", "PCMT1", "COMT", "SETD7", "TYW3", "KMT5C", "DIMIT1", "ASH2L", "METTL21A", "TRMT1L", "GAMT", "METTL5", "N6AMT1",

	"HENMT1", "TRMT10B", "METTL17", "SETMAR", "TRMT2B"],
protein homodimerization activity	["PML", "STAT1", "PTGS2", "BHLHE40", "TERF1", "MAP3K5", "MECOM", "CD8A", "SQSTM1", "VEGFB", "NR4A1", "TAP1", "ABCG1", "CSF1R", "TBX18", "KMT2A", "QDPR", "CALCOCO2", "SH3GLB1", "HIF1AN", "CLCN3", "PAFAH1B2", "PDXK", "PKD2", "RABEP1", "ABCD3", "STUB1", "MOAP1", "INHBB", "RRAGA", "OLFML2A", "HOMER2", "ANXA1", "PARK7", "NTRK2", "TIMELESS", "CLIC6", "TYW5", "PITX2", "SLC39A13", "SETMAR", "HNF1B"],
transferase activity, transferring acyl groups other than amino-acyl groups	["DLAT", "SH3GLB1", "NAA40", "NAA50", "MBOAT7", "MBOAT1", "DLST", "KANS2", "CRAT", "NAA16", "KAT7", "SOAT1", "GCAT", "PLA2G15", "CERS5", "OXSM"],
SH2 domain binding	["JAK2", "SQSTM1", "DLC1", "SKAP1"],
N-methyltransferase activity	["KMT2A", "SETD7", "KMT5C", "DIMT1", "ASH2L", "METTL21A", "TRMT1L", "SETMAR"],
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	["ASPH", "HIF1AN", "TET2", "KDM5A", "TYW5", "UTY"],
growth factor binding	["COL1A1", "IL2RB", "ITGAV", "FGFR4", "ACVR2A", "COL5A1", "IGFBP7", "NTRK2", "TRIM16", "SEC61B", "IGFBP6"],
protein phosphatase type 2A regulator activity	["PPP2R5E", "PPP2R5A", "PPP2R3A"],
damaged DNA binding	["TP73", "ERCC1", "POLK", "GTF2H3", "NEIL3"],
oxidoreductase activity, acting on peroxide as acceptor	["PTGS2", "PRDX6", "PRDX4", "PARK7", "GPX8"],
non-membrane spanning protein tyrosine kinase activity	["JAK2", "LYN", "BAZ1B", "FRK", "STK16"],
ATPase activity	["HSPA5", "TOP1", "VCP", "BLM", "ABCG8", "DDX58", "TAP1", "ABCG1", "ABCA3", "MYO1E", "DHX16", "PSMC4", "MDN1", "DHX35", "LONRF2", "ATP2B1", "GTF2H3", "DHX40", "ABCD3", "MYO10", "CECR2", "DDX53", "ATP7A", "CHD6", "RECQL", "ATP11A", "DDX1", "CHD1L", "ATP6V0C", "FANCM", "GTF2F2"],
histone methyltransferase activity	["KMT2A", "SUZ12", "SETD7", "KMT5C", "ASH2L", "SETMAR"],
enzyme activator activity	["NKX3-1", "TERF1", "MMP14", "DBF4", "MAP3K5", "CD24", "DOCK1", "DLC1", "TBC1D20", "SGSM3", "HSPB2", "RABEP1", "ACAP2", "TBC1D17", "TBC1D4", "RANBP1", "DUSP19", "OPHN1", "TBC1D10B", "GIT1", "VAV3", "AHS1", "ARRB1", "ARHGAP45", "SMAP1", "RAB3GAP1", "FGF13", "ABI1", "RAP1GDS1", "RGS3", "SGSM2", "STRADA"],
ligase activity, forming carbon-nitrogen bonds	["PAX6", "SIAH1", "ASS1", "BIRC7", "TRAF6", "UBE2I", "BCOR", "TRIM71", "GATB", "TNFAIP1", "TTLL5", "MTHFD1", "KLHL21", "PCGF2", "STUB1", "SUMO3", "RNF139", "RNF152", "ZFP91", "HERC5", "UBE4B", "UFL1", "TTLL1", "MCCC1", "FBXL15", "ANAPC11", "ANAPC2", "RNF5", "UBE2QL1"],

identical protein binding	["PML", "STAT1", "TP73", "PTGS2", "BHLHE40", "ADIPOR1", "TERF1", "DAPK1", "COL1A1", "MAP3K5", "VCP", "MECOM", "CD8A", "SQSTM1", "VEGFB", "NR4A1", "PAK1", "DDX58", "TAP1", "CD74", "ABCG1", "CSF1R", "TBX18", "KMT2A", "PRC1", "QDPR", "CALCOCO2", "SH3GLB1", "HIF1AN", "CLCN3", "GRB2", "PAFAH1B2", "SNX16", "AMOTL1", "PDXK", "ATL2", "PKD2", "RABEP1", "DNM1L", "ABCD3", "STUB1", "MOAP1", "CEP57L1", "INHBB", "RRAGA", "OLFML2A", "HOMER2", "ANXA1", "PARK7", "LZTFL1", "NTRK2", "KCTD17", "NUFIP1", "DNM1", "TIMELESS", "CLIC6", "TYW5", "PITX2", "SLC39A13", "SETMAR", "ZNF408", "BAIAP2", "HNF1B"],
structural constituent of muscle	["ASPH", "TPM2", "NEBL", "OBSCN", "NEB"],
PDZ domain binding	["ACVR2A", "CLCN3", "PLEKHA2", "CRIPT", "FZD8", "FZD3", "IGSF5"],
phosphatidylinositol binding	["MYO1E", "PIK3R1", "SNX16", "MPPE1", "FCHO2", "ZFYVE16", "PLEKHA2", "SNX1", "MYO10", "DAPP1", "HS1BP3", "AMER2", "ING2"],
translation initiation factor activity	["COPS5", "EIF1AX", "EIF3A", "MTIF2", "EIF1B", "EIF2D"],
hormone binding	["ADIPOR1", "ACE2", "PIK3R1", "CALCR", "SEC61B", "NPR1"],
DNA polymerase activity	["POLK", "TEP1", "POLE3", "POLE"],
double-stranded DNA binding	["CTNNB1", "FOXO1", "FOXO4", "STAT1", "TP73", "TERF1", "PAX6", "DDX58", "FOXJ3", "FOXN2", "NEIL3", "FOXJ1"],
histone deacetylase binding	["NKX3-1", "TRAF6", "BCOR", "RFXANK", "YWHAB", "GLI3"],
single-stranded DNA binding	["ERCC1", "BLM", "NABP2", "SSBP1", "NEIL3", "SSBP3"],
carbonate dehydratase activity	["CA9", "CA12"],
insulin-like growth factor receptor binding	["PIK3R1", "ARRB1"],
GTPase activator activity	["DOCK1", "DLC1", "TBC1D20", "SGSM3", "RABEP1", "ACAP2", "TBC1D17", "TBC1D4", "RANBP1", "OPHN1", "TBC1D10B", "GIT1", "VAV3", "ARRB1", "ARHGAP45", "SMAP1", "RAB3GAP1", "RAP1GDS1", "RGS3", "SGSM2"],
intramolecular oxidoreductase activity	["PTGES2", "GLRX2", "PDIA4", "SPATA20", "EHHADH"],
small conjugating protein ligase activity	["PAX6", "SIAH1", "BIRC7", "TRAF6", "UBE2I", "BCOR", "TRIM71", "TNFAIP1", "KLHL21", "PCGF2", "STUB1", "SUMO3", "RNF139", "RNF152", "ZFP91", "HERC5", "UBE4B", "UFL1", "FBXL15", "ANAPC11", "ANAPC2", "RNF5", "UBE2QL1"],
small conjugating protein ligase activity	["PAX6", "SIAH1", "BIRC7", "TRAF6", "UBE2I", "BCOR", "TRIM71", "TNFAIP1", "KLHL21", "PCGF2", "STUB1", "SUMO3", "RNF139", "RNF152", "ZFP91", "HERC5", "UBE4B", "UFL1", "FBXL15", "ANAPC11", "ANAPC2", "RNF5", "UBE2QL1"],
sterol binding	["ABCG1", "HSDL2", "OSBPL1A", "SOAT1"],
endoribonuclease activity	["DROSHA", "RPP38", "RNASE1", "TSEN34", "RNASE8"],
SMAD binding	["CTNNB1", "PML", "PAX6", "STUB1", "PRDM16", "SNW1"],

sequence-specific DNA binding	["FOSL1", "FOXO1", "FOXO4", "NKX3-1", "PBX2", "SREBF2", "STAT1", "TP73", "TERF1", "HOXA2", "ETV3", "PAX6", "SOX18", "MTA3", "NR4A1", "RARG", "HOXC6", "TBX18", "TBX3", "KMT2A", "FOSB", "HOXA4", "SUZ12", "HOXA3", "GATAD2A", "TSPYL2", "SMAD5", "FOXJ3", "CC2D1A", "FOXN2", "NR1D2", "PRDM16", "POLE3", "ELF5", "HOXC10", "EDF1", "LHX4", "GLI3", "POU6F1", "RORC", "HOXB2", "HOXA6", "DLX4", "FOXJ1", "CERS5", "ZC3H8", "PITX2", "ORC5", "ATF6B", "HNF1B"],
acid-amino acid ligase activity	["PAX6", "SIAH1", "BIRC7", "TRAF6", "UBE2I", "BCOR", "TRIM71", "TNFAIP1", "TTLL5", "KLHL21", "PCGF2", "STUB1", "SUMO3", "RNF139", "RNF152", "ZFP91", "HERC5", "UBE4B", "UFL1", "TTLL1", "FBXL15", "ANAPC11", "ANAPC2", "RNF5", "UBE2QL1"],
sugar transmembrane transporter activity	["SLC2A14", "SLC35A3", "SLC2A8"],
ubiquitin-protein ligase activity	["PAX6", "SIAH1", "BIRC7", "TRAF6", "UBE2I", "BCOR", "TRIM71", "TNFAIP1", "KLHL21", "PCGF2", "STUB1", "RNF139", "RNF152", "ZFP91", "HERC5", "UBE4B", "FBXL15", "ANAPC11", "ANAPC2", "RNF5", "UBE2QL1"],
hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	["AMPD2", "ADAD2", "MTHFD1", "APOBEC3B"],
single-stranded RNA binding	["DDX58", "CBX6", "PATL1", "DDX1"],
lipid transporter activity	["FABP2", "ABCG8", "ABCG1", "PLSCR1", "GLTPD2", "ATP11A", "APOL6"],
steroid hormone receptor activity	["NKX3-1", "NR4A1", "RARG", "NR1D2", "RORC"],
thyroid hormone receptor binding	["OASL", "TAF11", "GAS2L1"],
acetyltransferase activity	["DLAT", "NAA40", "NAA50", "KANSL2", "CRAT", "NAA16", "KAT7", "GCAT"],
L-amino acid transmembrane transporter activity	["SLC25A13", "SLC25A15", "SLC43A1", "SLC38A3"],
ligand-activated sequence-specific DNA binding RNA polymerase II transcription factor activity	["NKX3-1", "NR4A1", "RARG", "NR1D2", "RORC"],
peptide binding	["ACE2", "TAP1", "TNPO1", "CD74", "DHCR24", "PIK3R1", "NUP98", "SRP68", "CALCR", "CLTA", "ITM2C", "NPR1"],
protein N-terminus binding	["GAD1", "NPAT", "CSNK2A1", "TRAF6", "THAP7", "GTF2H3", "TAF11"],
DNA-directed DNA polymerase activity	["POLK", "POLE3", "POLE"],
pattern recognition receptor activity	["PGLYRP2", "PGLYRP4"],
nuclease activity	["DROSHA", "ERCC1", "RPP38", "ZC3H12C", "CNOT6L", "RNASE1", "TSEN34", "XRN2", "DIS3", "ASTE1", "DDX1", "PARN", "SETMAR", "RNASE8", "FANCM"],

endonuclease activity	["DROSHA", "ERCC1", "RPP38", "ZC3H12C", "RNASE1", "TSEN34", "DIS3", "SETMAR", "RNASE8"],
Ras GTPase activator activity	["DLC1", "TBC1D20", "SGSM3", "TBC1D17", "TBC1D4", "OPHN1", "TBC1D10B", "RAB3GAP1", "SGSM2"],
oxidoreductase activity, acting on NAD(P)H	["NDUFA10", "ND3", "NDUFS5", "NDUFB5", "NDUFB6", "ECSIT", "GMPR", "DCXR", "CRYZL1"],
cysteine-type endopeptidase regulator activity involved in apoptotic process	["NKX3-1", "TERF1", "MAP3K5", "ARRB1"],
protein phosphatase binding	["CTNNB1", "FOXO1", "MAP3K5", "VCP", "GRB2", "PIK3R1"],
fucosyltransferase activity	["FUT8", "FUT9"],
chaperone binding	["HSPA5", "BAG1", "BAG5", "AHSA1"]

Molecular Function Down regulated genes

G1/S transition of mitotic cell cycle	["MCM5", "TP73", "CDKN2B", "HRAS", "DBF4", "MCM8", "NPAT", "CDK4", "BID", "PSMD9", "CUL1", "TRIM71", "PSMD2", "PSMC4", "CACUL1", "CUL4A", "PKD2", "PSMA3", "ORC6", "POLE", "UBA52", "TJP3", "RHOU", "PSMB7", "PPP3CA", "PSMA5", "ORC5", "GPR132", "PSMB3"],
interphase	["FOXO4", "MCM5", "TP73", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "NPAT", "BLM", "CDK4", "MTA3", "BID", "PSMD9", "CUL1", "TRIM71", "CCNY", "PSMD2", "PSMC4", "CACUL1", "CUL4A", "PKD2", "AKAP9", "TUBGCP5", "PSMA3", "ORC6", "KHDRBS1", "MCMBP", "POLE", "CEP41", "UBA52", "NUMA1", "SDCCAG8", "TJP3", "LIG1", "FBXL15", "TIMELESS", "RHOU", "PSMB7", "PPP3CA", "NEDD1", "PSMA5", "ORC5", "MTBP", "GPR132", "PSMB3"],
negative regulation of cell cycle	["FOXO4", "MCM5", "NKX3-1", "PML", "TP73", "PTGS2", "GADD45A", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "RBM38", "BLM", "CSNK2A1", "RHOB", "PDCD4", "DHCR24", "BTG3", "PRKAB1", "PSMD9", "CUL1", "NME6", "INTS7", "NABP2", "MED25", "PSMD2", "SGSM3", "PSMC4", "TSPYL2", "CUL4A", "PKD2", "INTS3", "PSMA3", "ORC6", "MAP2K6", "KHDRBS1", "DYNC1L1", "UBA52", "ANAPC15", "NEK11", "PSMB7", "ANAPC11", "PSMA5", "ORC5", "SETMAR", "MTBP", "ANAPC2", "PTPN11", "GAS2L1", "STRADA", "PSMB3"],
cellular membrane organization	["BBC3", "WNT4", "CD24", "BID", "PAK1", "MFN2", "DOCK1", "DHCR24", "PLSCR1", "STX3", "HGS", "CLINT1", "COPG1", "SH3GLB1", "TIMM50", "PIK3R1", "VPS33B", "PPT1", "RABEP1", "DNM1L", "STX6", "FCHO2", "CLN8", "SERP1", "CALCR", "COL5A1", "ANK3", "VAV3", "FLOT1", "ANXA1", "PIP5K1A", "LETM1", "PPP2R5A", "VAMP7", "CLTA", "MYRF", "UBA52", "ARRB1", "MFGE8", "SEC24D", "ATP11A", "RAB7A", "COPE", "TPST2", "FGF13", "MTCH1", "SAR1B", "CHCHD6", "CHMP4C"],
interphase of mitotic cell cycle	["FOXO4", "MCM5", "TP73", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "NPAT", "BLM", "CDK4", "MTA3", "BID", "PSMD9", "CUL1", "TRIM71", "CCNY", "PSMD2", "PSMC4", "CACUL1", "CUL4A", "PKD2", "AKAP9", "TUBGCP5", "PSMA3", "ORC6", "KHDRBS1", "MCMBP", "POLE", "CEP41", "UBA52", "NUMA1", "SDCCAG8", "TJP3", "LIG1", "FBXL15", "RHOU",

	"PSMB7", "PPP3CA", "NEDD1", "PSMA5", "ORC5", "MTBP", "GPR132", "PSMB3"],
cell cycle arrest	["FOXO4", "MCM5", "NKX3-1", "PML", "TP73", "GADD45A", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "RBM38", "BLM", "CSNK2A1", "DHCR24", "PRKAB1", "PSMD9", "CUL1", "INTS7", "NABP2", "MED25", "PSMD2", "SGSM3", "PSMC4", "CUL4A", "PKD2", "INTS3", "PSMA3", "ORC6", "MAP2K6", "KHDRBS1", "UBA52", "NEK11", "PSMB7", "ANAPC11", "PSMA5", "ORC5", "SETMAR", "MTBP", "ANAPC2", "PTPN11", "GAS2L1", "STRADA", "PSMB3"],
cell division	["NKX3-1", "PTTG1", "TERF1", "TOP1", "BCAR1", "BLM", "CDK4", "VEGFB", "TXNIP", "RHOB", "PRC1", "UBE2I", "CCNF", "SON", "NCAPD2", "CKAP2", "CCNY", "KIF23", "NCAPG", "RABEP1", "HAUS8", "ARL8A", "PHF13", "KLHL21", "RALA", "PIK3CB", "SPIRE1", "CECR2", "MPLKIP", "ANK3", "MCMBP", "DYNC1LI1", "NUMA1", "CTDP1", "LIG3", "PIK3C3", "CDC14A", "NUMBL", "LIG1", "ANAPC15", "TIMELESS", "PARD3B", "DSTN", "FGF13", "CENPE", "NEDD1", "ANAPC11", "CENPC", "ING2", "ANAPC2", "DCLRE1A"],
cell cycle checkpoint	["FOXO4", "MCM5", "PML", "TP73", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "RBM38", "BLM", "CSNK2A1", "PSMD9", "INTS7", "NABP2", "PSMD2", "PSMC4", "INTS3", "PSMA3", "ORC6", "DYNC1LI1", "UBA52", "ANAPC15", "NEK11", "PSMB7", "ANAPC11", "PSMA5", "ORC5", "ANAPC2", "PTPN11", "PSMB3"],
mitotic cell cycle checkpoint	["FOXO4", "PML", "TP73", "TERF1", "CDKN2B", "HRAS", "RBM38", "CSNK2A1", "PSMD9", "PSMD2", "PSMC4", "PSMA3", "DYNC1LI1", "UBA52", "ANAPC15", "PSMB7", "ANAPC11", "PSMA5", "ANAPC2", "PSMB3"],
regulation of cell cycle	["CTNNB1", "FOSL1", "FOXO4", "MCM5", "NKX3-1", "PML", "TP73", "PTGS2", "GADD45A", "TERF1", "CDKN2B", "CHEK1", "HRAS", "GADD45G", "DBF4", "MCM8", "RBM38", "WNT4", "MECOM", "BLM", "CDK4", "MTA3", "CSNK2A1", "COPS5", "RHOB", "BID", "PDCD4", "PRKCA", "TBX3", "HDAC8", "DHCR24", "BTG3", "PRKAB1", "CCNF", "PSMD9", "SON", "CUL1", "NME6", "INTS7", "NABP2", "MED25", "CCNY", "PSMD2", "SGSM3", "PSMC4", "KIF23", "TSPYL2", "CUL4A", "PKD2", "TMEM67", "INTS3", "RANBP1", "TACC3", "PSMA3", "ORC6", "MAP2K6", "KHDRBS1", "BAP1", "DYNC1LI1", "HERC5", "CNPPD1", "UBA52", "TJP3", "TMEM8B", "ANAPC15", "TIMELESS", "NEK11", "PSMB7", "ANAPC11", "PSMA5", "ORC5", "SETMAR", "MTBP", "ANAPC2", "SH2B1", "PTPN11", "GAS2L1", "STRADA", "PSMB3"],
S phase	["MCM5", "CHEK1", "MCM8", "CDK4", "PSMD9", "CUL1", "PSMD2", "PSMC4", "CUL4A", "PSMA3", "ORC6", "MCMBP", "POLE", "UBA52", "LIG1", "TIMELESS", "PSMB7", "PSMA5", "ORC5", "PSMB3"],
response to oxidative stress	["FOSL1", "FOXO1", "PML", "PTGS2", "JAK2", "COL1A1", "MMP14", "ERCC1", "MAP3K5", "TXNIP", "RHOB", "TXN2", "DHCR24", "STX3", "PKD2", "CLN8", "PRDX6", "GLRX2", "ANXA1", "PARK7", "GPX8", "STK24", "COQ7", "STC2", "ATP7A", "ATR", "HMOX2", "LIG1", "NUDT1", "FANCC"],
S phase of mitotic cell cycle	["MCM5", "MCM8", "CDK4", "PSMD9", "CUL1", "PSMD2", "PSMC4", "CUL4A", "PSMA3", "ORC6", "MCMBP", "POLE", "UBA52", "LIG1", "PSMB7", "PSMA5", "ORC5", "PSMB3"],
epidermal growth factor receptor signaling pathway	["FOXO1", "FOXO4", "HRAS", "BCAR1", "SPRY1", "NR4A1", "PRKCA", "HGS", "GRB2", "PIK3R1", "AP2A1", "PRKAR1A",

	"AP2A2", "YWHAB", "CAMK4", "CLTA", "UBA52", "PLCE1", "RAB7A", "PTPN11"],
establishment of protein localization	["PML", "PTGS2", "JAK2", "COL1A1", "BBC3", "WNT4", "VCP", "CD24", "TXNIP", "RHOB", "BID", "DDX58", "TAP1", "TNPO1", "CD74", "ASPH", "ABCG1", "CSF1R", "TOMM34", "MFN2", "TRAF6", "LYN", "STX3", "HGS", "SEC23B", "COPG1", "PMPCA", "SH3GLB1", "IPO11", "TIMM50", "NUP35", "TMED4", "PIK3R1", "RAB40B", "TRAM1", "VPS33B", "RAB9B", "SNX16", "AP2A1", "NUP98", "PPT1", "RPS25", "SRP68", "TNPO3", "RAB30", "PKD2", "RABEP1", "DNM1L", "STX6", "BTN3A2", "RAB14", "NDFIP1", "SELENBP1", "PTPN14", "ZFYVE16", "VPS13A", "STXBP5", "SNX1", "CRIPT", "TACC3", "MCM3AP", "SERP1", "CALCR", "NDFIP2", "RPS9", "RPS29", "AP2A2", "ANK3", "ANXA1", "YWHAB", "PIP5K1A", "EMD", "PPP2R5A", "VAMP7", "RPL35A", "SFT2D3", "CAMK4", "CLTA", "CEP41", "RPS14", "TIMM44", "GLI3", "UBA52", "ARRB1", "PDIA4", "SEC24D", "TRIM16", "RGPD1", "ARF5", "GABARAPL2", "AP3M2", "RAB7A", "PIK3C3", "EXOC1", "NAGPA", "COPE", "SEC61B", "RPL34", "NUP107", "RAB29", "RPL35", "PPP3CA", "EIF2D", "SAR1B", "S100A12", "CHMP4C", "RAB24", "YIF1A", "PTPN11", "HCLS1", "UTY", "ATP6V0C", "KPNA4", "NFKBIL1", "STON1", "STRADA"],
intracellular protein transport	["PML", "PTGS2", "JAK2", "VCP", "CD24", "TXNIP", "BID", "DDX58", "TAP1", "TNPO1", "CD74", "ASPH", "TOMM34", "MFN2", "STX3", "HGS", "SEC23B", "COPG1", "PMPCA", "IPO11", "TIMM50", "PIK3R1", "TRAM1", "SNX16", "AP2A1", "NUP98", "RPS25", "SRP68", "TNPO3", "PKD2", "STX6", "PTPN14", "ZFYVE16", "SNX1", "TACC3", "MCM3AP", "RPS9", "RPS29", "AP2A2", "ANK3", "YWHAB", "PIP5K1A", "EMD", "VAMP7", "RPL35A", "CAMK4", "CLTA", "RPS14", "TIMM44", "GLI3", "UBA52", "SEC24D", "RGPD1", "AP3M2", "RAB7A", "NAGPA", "SEC61B", "RPL34", "RPL35", "PPP3CA", "EIF2D", "SAR1B", "PTPN11", "HCLS1", "KPNA4", "NFKBIL1", "STON1", "STRADA"],
mitochondrial membrane organization	["BBC3", "BID", "MFN2", "SH3GLB1", "TIMM50", "CLN8", "LETM1", "CHCHD6"],
DNA damage checkpoint	["FOXO4", "PML", "TP73", "CHEK1", "RBM38", "BLM", "PSMD9", "INTS7", "PSMD2", "PSMC4", "PSMA3", "UBA52", "NEK11", "PSMB7", "PSMA5", "PTPN11", "PSMB3"],
viral reproductive process	["PML", "STAT1", "TOP1", "MX1", "MAP3K5", "IL2RB", "ITGAV", "ACE2", "DDX58", "TAP1", "TNPO1", "IFITM3", "ITGA2", "PLSCR1", "OAS1", "UBE2I", "LYN", "CUL1", "TRMO", "TBC1D20", "GRB2", "PIK3R1", "TRAM1", "NUP98", "RPS25", "CUL4A", "ACOT8", "GTF2H3", "THOC2", "RALA", "PSMA3", "RPS9", "RPS29", "RRAGA", "POLR2K", "OASL", "DYNC1LI1", "RPL35A", "RPS14", "CXCR6", "UBA52", "MFGE8", "CTDP1", "TAF11", "SNW1", "RPL34", "CCDC86", "PSMB7", "RPL35", "ATP6V0C", "GTF2F2", "UCKL1", "PSMB3"],
regulation of mitotic cell cycle	["FOXO4", "NKX3-1", "PML", "TP73", "TERF1", "CDKN2B", "CHEK1", "HRAS", "RBM38", "MTA3", "CSNK2A1", "BID", "PRKCA", "BTG3", "PSMD9", "NME6", "PSMD2", "PSMC4", "CUL4A", "PKD2", "RANBP1", "PSMA3", "DYNC1LI1", "UBA52", "TJP3", "TMEM8B", "ANAPC15", "PSMB7", "ANAPC11", "PSMA5", "MTBP", "ANAPC2", "SH2B1", "PSMB3"],
lysosomal transport	["RHOB", "HGS", "SNX16", "ZFYVE16", "VAMP7", "RAB7A", "NAGPA"],
mitotic cell cycle	["FOXO4", "MCM5", "NKX3-1", "PML", "PTTG1", "TP73", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "NPAT", "BLM",

	"CDK4", "MTA3", "CSNK2A1", "BID", "PRKCA", "BTG3", "PRC1", "UBE2I", "CCNF", "PSMD9", "CUL1", "NCAPD2", "NME6", "TRIM71", "CCNY", "PSMD2", "CENPP", "PSMC4", "KIF23", "CACUL1", "NUP98", "CUL4A", "NCAPG", "PKD2", "HAUS8", "ARL8A", "PHF13", "KLHL21", "MPHOSPH9", "AKAP9", "TUBGCP5", "RANBP1", "PSMA3", "ORC6", "MPLKIP", "KHDRBS1", "MCMBP", "POLE", "DYNC1LI1", "CEP41", "UBA52", "NUMA1", "CTDP1", "SDCCAG8", "TJP3", "TMEM8B", "LIG1", "FBXL15", "ANAPC15", "NUP107", "TIMELESS", "RHO", "PSMB7", "CENPE", "PPP3CA", "NEDD1", "ANAPC11", "PSMA5", "CENPC", "ORC5", "MTBP", "ANAPC2", "SH2B1", "GPR132", "DCLRE1A", "PSMB3"],
Golgi vesicle transport	["VCP", "CLINT1", "SEC23B", "COPG1", "RAB9B", "AP2A1", "TRAPPC2", "STX6", "MPPE1", "RAB14", "VPS13A", "SNX1", "RNF139", "ANK3", "VAMP7", "CLTA", "ARRB1", "SEC24D", "RGPD1", "GABARAPL2", "COPE", "SAR1B"],
protein transport	["PML", "PTGS2", "JAK2", "COL1A1", "VCP", "CD24", "TXNIP", "RHOB", "BID", "DDX58", "TAP1", "TNPO1", "CD74", "ASPH", "ABCG1", "CSF1R", "TOMM34", "MFN2", "TRAF6", "LYN", "STX3", "HGS", "SEC23B", "COPG1", "PMPCA", "IPO11", "TIMM50", "NUP35", "TMED4", "PIK3R1", "RAB40B", "TRAM1", "VPS33B", "RAB9B", "SNX16", "AP2A1", "NUP98", "PPT1", "RPS25", "SRP68", "TNPO3", "RAB30", "PKD2", "RABEP1", "DNM1L", "STX6", "BTN3A2", "RAB14", "NDFIP1", "SELENBP1", "PTPN14", "ZFYVE16", "VPS13A", "STXBP5", "SNX1", "TACC3", "MCM3AP", "SERP1", "CALCR", "NDFIP2", "RPS9", "RPS29", "AP2A2", "ANK3", "ANXA1", "YWHAB", "PIP5K1A", "EMD", "VAMP7", "RPL35A", "SFT2D3", "CAMK4", "CLTA", "CEP41", "RPS14", "TIMM44", "GLI3", "UBA52", "ARRB1", "PDIA4", "SEC24D", "TRIM16", "RGPD1", "ARF5", "GABARAPL2", "AP3M2", "RAB7A", "PIK3C3", "EXOC1", "NAGPA", "COPE", "SEC61B", "RPL34", "NUP107", "RAB29", "RPL35", "PPP3CA", "EIF2D", "SAR1B", "S100A12", "CHMP4C", "RAB24", "YIF1A", "PTPN11", "HCLS1", "ATP6V0C", "KPNA4", "NFKBIL1", "STON1", "STRADA"],
apoptotic signaling pathway	["NKX3-1", "PML", "TP73", "JAK2", "HRAS", "DAPK1", "BBC3", "MAP3K5", "TNFSF10", "SIAH1", "CD24", "BID", "PRKCA", "CUL1", "DEDD", "SH3GLB1", "TIMM50", "CUL4A", "DNM1L", "PINK1", "PARK7", "STK24", "ATP7A", "SNW1", "IFI6", "SH3RF1"],
DNA integrity checkpoint	["FOXO4", "PML", "TP73", "CHEK1", "RBM38", "BLM", "PSMD9", "INTS7", "PSMD2", "PSMC4", "PSMA3", "UBA52", "NEK11", "PSMB7", "PSMA5", "PTPN11", "PSMB3"],
vacuolar transport	["RHOB", "HGS", "SNX16", "ZFYVE16", "VAMP7", "RAB7A", "NAGPA"],
regulation of JUN kinase activity	["TP73", "MAP3K5", "PAK1", "BIRC7", "PDCD4", "TRAF6", "MAP3K2", "HIPK3", "DUSP19", "FZD8"],
cellular macromolecule catabolic process	["PML", "PTTG1", "HSPA5", "DROSHA", "ERCC1", "HPSE", "SIAH1", "VCP", "BLM", "SQSTM1", "BIRC7", "UBE2I", "CCNF", "PSMD9", "CUL1", "ATE1", "USP38", "PSMD2", "TNFAIP1", "PSMC4", "CACUL1", "PPT1", "RPS25", "CUL4A", "GTF2H3", "SOCS6", "PAIP1", "TMEM67", "CNOT6L", "PATL1", "NDFIP1", "STUB1", "CLN8", "SUMO3", "PSMA3", "CECR2", "OAS2", "RPS9", "RPS29", "CTIF", "BAP1", "HERC5", "RPL35A", "UBE4B", "XRN2", "DIS3", "CNOT9", "RPS14", "UBA52", "ARRB1", "RAB7A", "DERL3", "SEC61B", "FBXL15", "RPL34", "UCHL5", "PSMB7", "RPL35", "PARN", "ANAPC11", "PSMA5", "CNOT11", "USP39", "SETMAR", "ENC1", "ANAPC2", "RNF5", "EXOSC6", "PSMB3"],

intrinsic apoptotic signaling pathway	["NKX3-1", "PML", "TP73", "JAK2", "HRAS", "BBC3", "MAP3K5", "SIAH1", "CD24", "PRKCA", "CUL1", "CUL4A", "DNM1L", "STK24", "SNW1"],
response to ionizing radiation	["PML", "TP73", "GADD45A", "ERCC1", "BLM", "RHOB", "INTS7", "NABP2", "GRB2", "INTS3", "ANXA1", "RAD54L", "TSPYL5"],
centrosome cycle	["CTNNB1", "GADD45A", "CHEK1", "CCNF", "PKD2", "TMEM67", "RANBP1"],
cellular response to extracellular stimulus	["FOSL1", "FOXO1", "HSPA5", "CDKN2B", "SQSTM1", "TXN2", "LYN", "PAFAH1B2", "GLRX2", "INHBB", "FADS1", "PIK3C3", "SNW1", "NUDT1", "NRBP2", "GAS2L1"],
activation of cysteine-type endopeptidase activity involved in apoptotic process	["NKX3-1", "PML", "TERF1", "JAK2", "BBC3", "MAP3K5", "TNFSF10", "VCP", "DLC1", "MOAP1", "MTCH1"],
regulation of JNK cascade	["TP73", "HRAS", "MAP3K5", "MECOM", "COPPS5", "PAK1", "BIRC7", "PDCD4", "TRAF6", "MAP3K2", "HIPK3", "DUSP19", "MAP4K4", "FZD8", "SH3RF1", "EPHB1"],
negative regulation of MAP kinase activity	["TP73", "DUSP4", "SPRY1", "PDCD4", "PRKCA", "LYN", "HIPK3", "DUSP19", "RGS3"],
cell cycle process	["CTNNB1", "FOXO4", "MCM5", "NKX3-1", "PML", "PTTG1", "TP73", "GADD45A", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "NPAT", "RBM38", "WNT4", "TDRD1", "BLM", "CDK4", "MTA3", "CSNK2A1", "RHOB", "BID", "HDAC8", "DHCR24", "PRC1", "PRKAB1", "UBE2I", "CCNF", "PSMD9", "CUL1", "NCAPD2", "NME6", "INTS7", "CKAP2", "NABP2", "MED25", "TRIM71", "CCNY", "PSMD2", "SGSM3", "CENPP", "PSMC4", "KIF23", "CACUL1", "NUP98", "CUL4A", "NCAPG", "PKD2", "TMEM67", "HAUS8", "ARL8A", "PHF13", "KLHL21", "MPHOSPH9", "INTS3", "AKAP9", "TUBGCP5", "RANBP1", "TACC3", "PSMA3", "ORC6", "SPIRE1", "MAP2K6", "MPLKIP", "ANK3", "KHDRBS1", "MCMBP", "POLE", "DYNC1LI1", "CEP41", "UBA52", "NUMA1", "CTDP1", "SDCCAG8", "TJP3", "LIG3", "RAD54L", "KIZ", "LIG1", "FBXL15", "ANAPC15", "NUP107", "TIMELESS", "NEK11", "RHOU", "SLC2A8", "PSMB7", "CENPE", "PPP3CA", "NEDD1", "ANAPC11", "PSMA5", "CENPC", "ORC5", "ING2", "SETMAR", "MTBP", "ANAPC2", "SH2B1", "PTPN11", "GPR132", "GAS2L1", "FANCM", "DCLRE1A", "STRADA", "PSMB3"],
cell cycle phase	["FOXO4", "MCM5", "PTTG1", "TP73", "TERF1", "CDKN2B", "CHEK1", "HRAS", "DBF4", "MCM8", "NPAT", "WNT4", "TDRD1", "BLM", "CDK4", "MTA3", "BID", "PRC1", "UBE2I", "CCNF", "PSMD9", "CUL1", "NCAPD2", "NME6", "TRIM71", "CCNY", "PSMD2", "CENPP", "PSMC4", "KIF23", "CACUL1", "NUP98", "CUL4A", "NCAPG", "PKD2", "HAUS8", "ARL8A", "PHF13", "KLHL21", "MPHOSPH9", "AKAP9", "TUBGCP5", "RANBP1", "TACC3", "PSMA3", "ORC6", "SPIRE1", "MPLKIP", "KHDRBS1", "MCMBP", "POLE", "DYNC1LI1", "CEP41", "UBA52", "NUMA1", "CTDP1", "SDCCAG8", "TJP3", "LIG3", "RAD54L", "KIZ", "LIG1", "FBXL15", "ANAPC15", "NUP107", "TIMELESS", "RHOU", "SLC2A8", "PSMB7", "CENPE", "PPP3CA", "NEDD1", "ANAPC11", "PSMA5", "CENPC", "ORC5", "ING2", "MTBP", "ANAPC2", "SH2B1", "GPR132", "FANCM", "DCLRE1A", "PSMB3"],
positive regulation of DNA binding	["JAK2", "TRAF6", "PLSCR1", "EDF1", "PITX2"],

cellular response to stress	["FOXO1", "FOXO4", "NKX3-1", "PML", "PTTG1", "SREBF2", "TP73", "CA9", "PTGS2", "SGK1", "HSPA5", "GADD45A", "CHEK1", "JAK2", "HRAS", "GADD45G", "DUSP4", "BBC3", "ERCC1", "MAP3K5", "MCM8", "RBM38", "VCP", "MECOM", "BLM", "SQSTM1", "HYOU1", "SRPX", "COPS5", "RHOB", "PAK1", "POLK", "BIRC7", "PDCD4", "CD74", "TRAF6", "PARG", "LYN", "PSMD9", "STX3", "BAZ1B", "INTS7", "SEMA4C", "OTUB1", "NABP2", "PSMD2", "HIF1AN", "GRB2", "PAFAH1B2", "PSMC4", "TSPYL2", "FECH", "CUL4A", "GTF2H3", "PKD2", "MAP3K2", "SEL1L", "HIPK3", "ATMIN", "INTS3", "FGF12", "IREB2", "STUB1", "PRDX6", "GLRX2", "DUSP19", "PSMA3", "SERP1", "MAP2K6", "MAP4K4", "PKD3", "INHBB", "VAV3", "MRPS26", "ANXA1", "POLE", "PARK7", "FADS1", "POLR2K", "STK24", "ASH2L", "COQ7", "STC2", "ATP7A", "UBE4B", "SLC52A3", "UBA52", "FZD8", "RECQL", "LIG3", "ASTE1", "XAB2", "PIK3C3", "DDX1", "RAD54L", "DERL3", "SNW1", "LIG1", "NUDT1", "NEIL3", "TIMELESS", "NEK11", "UCHL5", "CHD1L", "PSMB7", "PSMA5", "SH3RF1", "EPHB1", "FANCC", "CHCHD6", "ING2", "SETMAR", "YIF1A", "PTPN11", "NRBP2", "GAS2L1", "PARPBP", "RTN4RL1", "FANCM", "DCLRE1A", "RNF5", "PSMB3"],
signal transduction in response to DNA damage	["PML", "TP73", "GADD45A", "RBM38", "CD74", "PSMD9", "PSMD2", "GRB2", "PSMC4", "PSMA3", "UBA52", "PSMB7", "PSMA5", "PSMB3"],
female gamete generation	["CTNNB1", "FOSL1", "PTGS2", "PLAT", "ERCC1", "MCM8", "WNT4", "INHBB", "GDF9", "PAQR8", "PARN"],
morphogenesis of an epithelium	["CTNNB1", "MYCN", "NKX3-1", "PML", "STAT1", "CA9", "MMP14", "SOX18", "WNT4", "PAK1", "RARG", "CSF1R", "TBX18", "TRAF6", "TBX3", "DLC1", "SEMA4C", "CTHRC1", "TRIM71", "GRB2", "GATAD2A", "SLC12A2", "PKD2", "GRSF1", "COL5A1", "DEAF1", "COQ7", "IPMK", "GLI3", "PSPN", "GRHL3", "HOXB2", "ZIC2", "FZD3", "TIMELESS", "FOXJ1", "PITX2", "HNF1B"],
tube morphogenesis	["CTNNB1", "MYCN", "NKX3-1", "PML", "MMP14", "SOX18", "WNT4", "PAK1", "CSF1R", "TRAF6", "TBX3", "DLC1", "SEMA4C", "CTHRC1", "TRIM71", "GATAD2A", "SLC12A2", "PKD2", "DEAF1", "COQ7", "IPMK", "GLI3", "PSPN", "SDCCAG8", "GRHL3", "ZIC2", "FZD3", "TIMELESS", "FOXJ1", "PITX2", "HNF1B"],
apoptotic mitochondrial changes	["TP73", "BBC3", "TNFSF10", "BID", "SH3GLB1", "TIMM50", "DNM1L", "PINK1", "ATP7A", "IFI6"],
viral reproduction	["PML", "STAT1", "TOP1", "MX1", "MAP3K5", "IL2RB", "ITGAV", "ACE2", "DDX58", "TAP1", "TNPO1", "IFITM3", "ITGA2", "PLSCR1", "OAS1", "UBE2I", "LYN", "PSMD9", "CUL1", "CALCOCO2", "TRMO", "TBC1D20", "NUP35", "PSMD2", "GRB2", "PIK3R1", "PSMC4", "TRAM1", "AP2A1", "NUP98", "RPS25", "CUL4A", "ACOT8", "GTF2H3", "THOC2", "RALA", "RANBP1", "PSMA3", "RPS9", "RPS29", "AP2A2", "RRAGA", "POLR2K", "OASL", "DYNC1LI1", "RPL35A", "RPS14", "CXCR6", "UBA52", "MFGE8", "CTDP1", "TAF11", "ZNF213", "SNW1", "RPL34", "CCDC86", "NUP107", "PSMB7", "RPL35", "PSMA5", "ATP6V0C", "GTF2F2", "UCKL1", "PSMB3"],
ER to Golgi vesicle-mediated transport	["VCP", "SEC23B", "TRAPPC2", "MPPE1", "RNF139", "VAMP7", "SEC24D", "SAR1B"],
regulation of homeostatic process	["CTNNB1", "FOXO1", "PML", "SREBF2", "PTGS2", "TERF1", "BBC3", "ERCC1", "FGFR4", "RARG", "TG", "CD74", "ASPH", "CSF1R", "LYN", "ACVR2A", "PKD2", "KITLG", "CACNA1C",

	"ANK3", "ANXA1", "RNF10", "FIG4", "MYRF", "ARRB1", "SMAP1", "IFI6", "NPR1", "GAS2L1"],
cytokinesis	["RHOB", "PRC1", "SON", "CKAP2", "KIF23", "RABEP1", "KLHL21", "RALA", "SPIRE1", "CECR2", "ANK3", "PIK3C3", "DSTN"],
regulation of MAP kinase activity	["TP73", "HRAS", "DUSP4", "MAP3K5", "SPRY1", "CD24", "PAK1", "BIRC7", "PDCD4", "CD74", "PRKCA", "TRAF6", "LYN", "MAP3K2", "KITLG", "HIPK3", "DUSP19", "PIK3CB", "MAP2K6", "UBA52", "FZD8", "PLCE1", "RGS3", "S100A12", "PTPN11"],
embryo implantation	["PTGS2", "BSG", "RECK", "POLR1B", "STC2", "OOEP"],
protein localization	["CTNNB1", "PML", "PTGS2", "JAK2", "COL1A1", "BBC3", "PAX6", "WNT4", "VCP", "CD24", "SQSTM1", "TXNIP", "RHOB", "BID", "PAK1", "DDX58", "TAP1", "TNPO1", "CD74", "ASPH", "ABCG1", "CSF1R", "TOMM34", "MFN2", "TRAF6", "HDAC8", "DHCR24", "HAP1", "LYN", "STX3", "HGS", "SEC23B", "COPG1", "PMPCA", "SH3GLB1", "IPO11", "TIMM50", "NUP35", "TMED4", "VPS13D", "PIK3R1", "RAB40B", "TRAM1", "VPS33B", "RAB9B", "SNX16", "AP2A1", "NUP98", "PPT1", "RPS25", "SRP68", "LAMTOR3", "TNPO3", "RAB30", "PKD2", "RABEP1", "DNM1L", "STX6", "BTN3A2", "BICD2", "ANKRD13C", "FCHO2", "RAB14", "NDFIP1", "SELENBP1", "PTPN14", "ZFYVE16", "VPS13A", "STXBP5", "SUMO3", "SNX1", "CRIPT", "TACC3", "CEP57L1", "MCM3AP", "SERP1", "CALCR", "NDFIP2", "RPS9", "RPS29", "AP2A2", "ANK3", "RRAGA", "FLOT1", "ANXA1", "YWHAB", "PIP5K1A", "EMD", "PPP2R5A", "VAMP7", "RPL35A", "SFT2D3", "CAMK4", "CLTA", "OBSCN", "CEP41", "RPS14", "TIMM44", "GLI3", "UBA52", "ARRB1", "COLQ", "PDIA4", "SEC24D", "TRIM16", "RGPD1", "ARF5", "GABARAPL2", "AP3M2", "RAB7A", "PIK3C3", "EXOC1", "NAGPA", "COPE", "SEC61B", "RPL34", "NUP107", "RAB29", "FGF13", "RPL35", "PPP3CA", "EIF2D", "SAR1B", "S100A12", "CHMP4C", "RAB24", "TLN2", "YIF1A", "PTPN11", "HCLS1", "UTY", "ATP6V0C", "KPNA4", "NFKBIL1", "STON1", "STRADA"],
DNA-dependent DNA replication	["MCM5", "TERF1", "MCM8", "BLM", "TFAM", "CIZ1", "ORC6", "MCMBP", "POLE", "LIG3", "LIG1", "ORC5", "FANCM"],
protein targeting	["PML", "PTGS2", "JAK2", "TXNIP", "BID", "DDX58", "TNPO1", "TOMM34", "MFN2", "PMPCA", "IPO11", "TIMM50", "PIK3R1", "TRAM1", "SNX16", "NUP98", "RPS25", "SRP68", "TNPO3", "PKD2", "ZFYVE16", "TACC3", "MCM3AP", "RPS9", "RPS29", "ANK3", "YWHAB", "PIP5K1A", "EMD", "VAMP7", "RPL35A", "RPS14", "TIMM44", "GLI3", "UBA52", "RGPD1", "RAB7A", "NAGPA", "SEC61B", "RPL34", "RPL35", "PPP3CA", "HCLS1", "KPNA4", "NFKBIL1"],
cellular protein catabolic process	["PML", "PTTG1", "HSPA5", "SIAH1", "VCP", "SQSTM1", "UBE2I", "CCNF", "PSMD9", "CUL1", "ATE1", "USP38", "PSMD2", "TNFAIP1", "PSMC4", "CACUL1", "PPT1", "CUL4A", "SOCS6", "TMEM67", "NDFIP1", "STUB1", "CLN8", "SUMO3", "PSMA3", "BAP1", "HERC5", "UBE4B", "UBA52", "ARRB1", "RAB7A", "DERL3", "SEC61B", "FBXL15", "UCHL5", "PSMB7", "ANAPC11", "PSMA5", "USP39", "ENC1", "ANAPC2", "RNF5", "PSMB3"],
protein ubiquitination	["PML", "HSPA5", "PAX6", "SIAH1", "VCP", "FBXO32", "BIRC7", "SOCS7", "TRAF6", "CCNF", "PSMD9", "CUL1", "BAG5", "BCOR", "OTUB1", "TRIM71", "PSMD2", "TNFAIP1", "SUZ12", "PSMC4", "RAB40B", "DCAF17", "CUL4A", "ASB6", "SOCS6", "KLHL21", "NDFIP1", "STUB1", "SUMO3", "PSMA3", "RNF139", "PINK1", "RNF152", "ZFP91", "BTBD1", "NDFIP2", "HERC5", "UBE4B", "UFL1", "RNF19A", "UBA52", "ARRB1", "FBXL15", "SPSB2",

	"PSMB7", "ANAPC11", "PSMA5", "SH3RF1", "ENC1", "ANAPC2", "TSPYL5", "RNF5", "PSMB3"],
ribonucleoprotein complex assembly	["ATXN2", "CD2BP2", "GEMIN7", "RPS25", "EIF3A", "PATL1", "SNRPD1", "SF3A1", "RPS14", "DDX1", "NUFIP1", "SNRPF", "USP39"],
maintenance of location in cell	["CTNNB1", "PML", "CIZ1", "PKD2", "BICD2", "ANKRD13C", "TACC3", "CEP57L1", "ANK3", "YWHAB", "TLN2", "NFKBIL1"],
interaction with host	["PML", "STAT1", "TOP1", "MAP3K5", "IL2RB", "ITGAV", "ACE2", "DDX58", "TAP1", "TNPO1", "IFITM3", "ITGA2", "UBE2I", "LYN", "CUL1", "TRMO", "TBC1D20", "GRB2", "PIK3R1", "TRAM1", "NUP98", "CUL4A", "ACOT8", "THOC2", "RALA", "PSMA3", "RRAGA", "DYNC1LI1", "UBA52", "MFG8", "SNW1", "CCDC86", "PSMB7", "ATP6V0C", "UCKL1", "PSMB3"],
ectoderm development	["CTNNB1", "ELF5", "GRHL3", "AMER2"],
endosomal transport	["SQSTM1", "RHOB", "HGS", "RAB9B", "SNX16", "AP2A1", "STX6", "RAB14", "ZFYVE16", "VPS13A", "SNX1", "VAMP7", "UBA52", "RAB7A", "PIK3C3", "CHMP4C"],
negative regulation of DNA metabolic process	["PML", "TERF1", "ERCC1", "BLM", "OTUB1", "TSPYL2", "NDFIP1", "LIG3", "PARPBP"],
mitochondrion organization	["NRF1", "TP73", "BBC3", "TNFSF10", "BID", "TFAM", "TOMM34", "MFN2", "PMPCA", "SH3GLB1", "TIMM50", "NDUFS5", "GATB", "AKT3", "NDUFAF4", "DNM1L", "CLN8", "PINK1", "PARK7", "LETM1", "COQ7", "ATP7A", "TIMM44", "LIG3", "SSBP1", "IFI6", "CHCHD6"],
maintenance of protein location in cell	["CTNNB1", "PML", "PKD2", "BICD2", "ANKRD13C", "TACC3", "CEP57L1", "ANK3", "YWHAB", "TLN2", "NFKBIL1"],
regulation of translation	["PML", "DAPK1", "CPEB1", "CDK4", "ATXN2", "IGF2BP2", "TRIM71", "FECH", "PAIP1", "IREB2", "SERP1", "RNF139", "RPS9", "CTIF", "KHDRBS1", "LSM14B", "RPS14", "DDX1", "MTIF2", "EIF1B", "ENC1"],
double-strand break repair	["CHEK1", "ERCC1", "MCM8", "VCP", "BLM", "BAZ1B", "OTUB1", "NABP2", "LIG3", "DDX1", "RAD54L", "LIG1", "SETMAR", "PARPBP"],
protein polyubiquitination	["TRAF6", "PSMD9", "OTUB1", "PSMD2", "PSMC4", "STUB1", "PSMA3", "RNF152", "ZFP91", "UBE4B", "UBA52", "PSMB7", "ANAPC11", "PSMA5", "ANAPC2", "RNF5", "PSMB3"],
post-Golgi vesicle-mediated transport	["CLINT1", "RAB9B", "AP2A1", "RAB14", "VPS13A", "ANK3", "VAMP7", "CLTA", "ARRB1"],
negative regulation of cell proliferation	["CTNNB1", "FOSL1", "FOXO4", "NKX3-1", "PML", "STAT1", "PTGS2", "CDKN2B", "JAK2", "HRAS", "PAX6", "RBM38", "SPRY1", "SRPX", "PAK1", "RARG", "SERPINF1", "ASPH", "FABP6", "MFN2", "PRKCA", "DHCR24", "BTG3", "LYN", "CUL1", "HGS", "DLC1", "TMEM115", "MED25", "SKAP2", "COMT", "CUL4A", "PKD2", "NDFIP1", "PTPN14", "RNF139", "FRK", "RNF10", "BAP1", "EMD", "IGFBP7", "GLI3", "FOXJ1", "ABI1", "IGFBP6", "NPR1", "MTBP"],
cellular component disassembly	["CTNNB1", "MMP14", "MMP10", "FGFR4", "BIRC7", "CAPG", "SMARCC2", "BAZ1B", "CKAP2", "LAMC1", "PPT1", "RPS25", "MRRF", "DNM1L", "MOAP1", "CECR2", "RPS9", "RPS29", "STK24", "RPL35A", "RPS14", "UBA52", "RPL34", "DSTN", "FGF13", "RPL35", "GAS2L1"],
stress-activated protein kinase signaling cascade	["FOXO1", "TP73", "HRAS", "DUSP4", "MAP3K5", "MECOM", "COPS5", "PAK1", "BIRC7", "PDCD4", "TRAF6", "LYN", "SEMA4C",

	"MAP3K2", "HIPK3", "FGF12", "DUSP19", "MAP2K6", "MAP4K4", "UBA52", "FZD8", "SH3RF1", "EPHB1"],
insulin receptor signaling pathway	["FOXO1", "FOXO4", "HRAS", "BCAR1", "FGFR4", "SOCS7", "PRKCA", "PRKAB1", "GRB2", "PIK3R1", "PIK3CB", "YWHAB", "PIK3C3", "SLC2A8", "BAIAP2", "PTPN11", "ATP6V0C", "STRADA"],
nucleotide-excision repair	["ERCC1", "POLK", "GTF2H3", "POLE", "POLR2K", "LIG3", "XAB2", "LIG1", "NEIL3", "FANCC", "DCLRE1A"],
protein catabolic process	["PML", "PTTG1", "HSPA5", "HPSE", "SIAH1", "VCP", "SQSTM1", "ACE2", "UBE2I", "CCNF", "PSMD9", "CUL1", "HGS", "DEDD", "ATE1", "USP38", "PSMD2", "TNFAIP1", "SGSM3", "PSMC4", "CACUL1", "PPT1", "CUL4A", "SOCS6", "TMEM67", "NDFIP1", "STUB1", "CLN8", "SUMO3", "SNX1", "PSMA3", "BAP1", "HERC5", "UBE4B", "PPP2R3A", "UBA52", "ARRB1", "GABARAPL2", "RAB7A", "DERL3", "SEC61B", "FBXL15", "UCHL5", "PSMB7", "ANAPC11", "PSMA5", "USP39", "ENC1", "ANAPC2", "RNF5", "PSMB3"],
axon guidance	["EPHB2", "HRAS", "HOXA2", "COL1A1", "PAX6", "SIAH1", "CD24", "CSNK2A1", "ITGAV", "RHOB", "PAK1", "SEMA6A", "DOCK1", "ITGA2", "GRB2", "LAMC1", "AP2A1", "KIF5C", "MYO10", "CACNA1C", "COL5A1", "OPHN1", "AP2A2", "ANK3", "YWHAB", "LHX4", "CLTA", "GLI3", "PSPN", "ZIC2", "FZD3", "EPHB1", "PTPN11"],
DNA damage response, signal transduction by p53 class mediator	["PML", "TP73", "RBM38", "CD74", "PSMD9", "PSMD2", "PSMC4", "PSMA3", "UBA52", "PSMB7", "PSMA5", "PSMB3"],
tube development	["CTNNB1", "MYCN", "NKX3-1", "PML", "STAT1", "ARG2", "MMP14", "SOX18", "SPRY1", "WNT4", "CD24", "PAK1", "FGFR4", "CSF1R", "TRAF6", "TBX3", "DLC1", "SEMA4C", "CTHRC1", "TRIM71", "GATAD2A", "SMAD5", "SLC12A2", "PKD2", "HEG1", "DEAF1", "COQ7", "IPMK", "ATP7A", "GLI3", "NUMA1", "PSPN", "SDCCAG8", "GRHL3", "ZIC2", "FZD3", "TIMELESS", "FOXJ1", "GPC3", "PITX2", "HNF1B"],
membrane fusion	["MFN2", "STX3", "VPS33B", "RABEP1", "STX6", "VAV3", "ANXA1", "VAMP7", "RAB7A", "TPST2"],
response to DNA damage stimulus	["FOXO1", "FOXO4", "NKX3-1", "PML", "PTTG1", "TP73", "SGK1", "GADD45A", "CHEK1", "GADD45G", "BBC3", "ERCC1", "MCM8", "RBM38", "VCP", "BLM", "POLK", "CD74", "PARG", "LYN", "PSMD9", "BAZ1B", "INTS7", "OTUB1", "NABP2", "PSMD2", "GRB2", "PSMC4", "CUL4A", "GTF2H3", "ATMIN", "INTS3", "STUB1", "PSMA3", "MAP2K6", "VAV3", "MRPS26", "POLE", "POLR2K", "ASH2L", "UBA52", "RECQL", "LIG3", "ASTE1", "XAB2", "DDX1", "RAD54L", "SNW1", "LIG1", "NUDT1", "NEIL3", "TIMELESS", "NEK11", "UCHL5", "CHD1L", "PSMB7", "PSMA5", "FANCC", "CHCHD6", "ING2", "SETMAR", "PTPN11", "PARPBP", "FANCM", "DCLRE1A", "PSMB3"],
G1 phase of mitotic cell cycle	["FOXO4", "CDKN2B", "CDK4", "CUL1", "UBA52", "MTBP"],
centrosome organization	["CTNNB1", "GADD45A", "CHEK1", "CCNF", "PKD2", "TMEM67", "HAUS8", "RANBP1"],
regulation of myeloid cell differentiation	["CTNNB1", "PRKCA", "TRAF6", "LYN", "ACVR2A", "PIK3R1", "KITLG", "NDFIP1", "PRDM16", "CAMK4", "RBP1", "SMAP1", "HCLS1", "GAS2L1"],
positive regulation of MAP kinase activity	["TP73", "HRAS", "MAP3K5", "CD24", "PAK1", "BIRC7", "CD74", "TRAF6", "MAP3K2", "KITLG", "DUSP19", "PIK3CB", "MAP2K6", "UBA52", "FZD8", "PLCE1", "S100A12", "PTPN11"],

macromolecule catabolic process	["PML", "PTTG1", "HSPA5", "DROSHA", "ERCC1", "HPSE", "SIAH1", "VCP", "BLM", "SQSTM1", "ACE2", "BIRC7", "PGLYRP2", "UBE2I", "AGL", "CCNF", "PSMD9", "CUL1", "HGS", "DEDD", "ATE1", "USP38", "PSMD2", "TNFAIP1", "SGSM3", "PSMC4", "CACUL1", "PPT1", "RPS25", "CUL4A", "GTF2H3", "SOCS6", "PAIP1", "TMEM67", "CNOT6L", "PATL1", "NDFIP1", "STUB1", "CLN8", "SUMO3", "SNX1", "PSMA3", "CECR2", "OAS2", "RPS9", "RPS29", "CTIF", "BAP1", "HERC5", "RPL35A", "UBE4B", "XRN2", "PPP2R3A", "DIS3", "CNOT9", "RPS14", "UBA52", "ARRB1", "GABARAPL2", "RAB7A", "DERL3", "SEC61B", "FBXL15", "RPL34", "UHL5", "PSMB7", "RPL35", "PARN", "ANAPC11", "PSMA5", "GPC3", "CNOT11", "PGLYRP4", "USP39", "SETMAR", "ENC1", "ANAPC2", "RNF5", "EXOSC6", "PSMB3"],
macromolecule catabolic process	["PML", "PTTG1", "HSPA5", "DROSHA", "ERCC1", "HPSE", "SIAH1", "VCP", "BLM", "SQSTM1", "ACE2", "BIRC7", "PGLYRP2", "UBE2I", "AGL", "CCNF", "PSMD9", "CUL1", "HGS", "DEDD", "ATE1", "USP38", "PSMD2", "TNFAIP1", "SGSM3", "PSMC4", "CACUL1", "PPT1", "RPS25", "CUL4A", "GTF2H3", "SOCS6", "PAIP1", "TMEM67", "CNOT6L", "PATL1", "NDFIP1", "STUB1", "CLN8", "SUMO3", "SNX1", "PSMA3", "CECR2", "OAS2", "RPS9", "RPS29", "CTIF", "BAP1", "HERC5", "RPL35A", "UBE4B", "XRN2", "PPP2R3A", "DIS3", "CNOT9", "RPS14", "UBA52", "ARRB1", "GABARAPL2", "RAB7A", "DERL3", "SEC61B", "FBXL15", "RPL34", "UHL5", "PSMB7", "RPL35", "PARN", "ANAPC11", "PSMA5", "GPC3", "CNOT11", "PGLYRP4", "USP39", "SETMAR", "ENC1", "ANAPC2", "RNF5", "EXOSC6", "PSMB3"],
nucleocytoplasmic transport	["PML", "PTGS2", "JAK2", "TXNIP", "DDX58", "TNPO1", "IPO11", "PIK3R1", "NUP98", "NEMF", "TNPO3", "PKD2", "PTPN14", "ANP32A", "SRF11", "THOC2", "TACC3", "MCM3AP", "NUDT4", "KHDRBS1", "EMD", "CAMK4", "GLI3", "SEC61B", "NUP107", "PPP3CA", "RITA1", "PTPN11", "HCLS1", "KPNA4", "NFKBIL1", "STRADA"],
DNA catabolic process	["ERCC1", "BLM", "BIRC7", "PPT1", "GTF2H3", "CECR2", "XRN2", "SETMAR"],
protein modification by small protein conjugation	["PML", "HSPA5", "PAX6", "SIAH1", "VCP", "FBXO32", "BIRC7", "SOCS7", "TRAF6", "UBE2I", "CCNF", "PSMD9", "CUL1", "BAG5", "BCOR", "OTUB1", "TRIM71", "PSMD2", "TNFAIP1", "SUZ12", "PSMC4", "RAB40B", "DCAF17", "CUL4A", "ASB6", "SOCS6", "KLHL21", "NDFIP1", "STUB1", "SUMO3", "PSMA3", "RNF139", "PINK1", "RNF152", "ZFP91", "BTBD1", "NDFIP2", "HERC5", "UBE4B", "UFL1", "RNF19A", "UBA52", "ARRB1", "UBA5", "FBXL15", "SPSB2", "PSMB7", "ANAPC11", "PSMA5", "SH3RF1", "ENC1", "ANAPC2", "TSPYL5", "RNF5", "PSMB3"],
G1 phase	["FOXO4", "CDKN2B", "CDK4", "CUL1", "UBA52", "MTBP"],
regulation of MAPK cascade	["CTNNB1", "FOXO1", "TP73", "JAK2", "HRAS", "GADD45G", "DUSP4", "MAP3K5", "SPRY1", "MECOM", "CD24", "VEGFB", "COPS5", "PAK1", "FGFR4", "BIRC7", "PDCD4", "CD74", "CSF1R", "PRKCA", "TRAF6", "WWC1", "LYN", "SEMA4C", "GRB2", "MAP3K2", "KITLG", "HIPK3", "DUSP19", "PIK3CB", "MAP2K6", "MAP4K4", "YWHAB", "UBA52", "ARRB1", "NTRK2", "FZD8", "PLCE1", "RGS3", "SH3RF1", "EPHB1", "S100A12", "KSR2", "PTPN11"],
cell cycle	["CTNNB1", "FOSL1", "FOXO4", "MCM5", "NKX3-1", "PML", "PTTG1", "TP73", "PTGS2", "GADD45A", "TERF1", "CDKN2B", "CHEK1", "HRAS", "GADD45G", "DBF4", "MCM8", "NPAT", "RBM38", "WNT4", "SIAH1", "MECOM", "TDRD1", "BLM", "CDK4", "MTA3", "CSNK2A1", "TXNIP", "COPS5", "RHOB", "BID", "PDCD4",

	"PRKCA", "TBX3", "HDAC8", "DHCR24", "BTG3", "PRC1", "PRKAB1", "UBE2I", "WTAP", "CCNF", "PSMD9", "SON", "CUL1", "NCAPD2", "NME6", "INTS7", "CKAP2", "NABP2", "MED25", "TRIM71", "CCNY", "PSMD2", "SGSM3", "CENPP", "PSMC4", "KIF23", "TSPYL2", "CACUL1", "NUP98", "CUL4A", "NCAPG", "PKD2", "TMEM67", "HAUS8", "ARL8A", "PHF13", "KLHL21", "MPHOSPH9", "INTS3", "AKAP9", "TUBGCP5", "RALA", "RANBP1", "TACC3", "PSMA3", "ORC6", "TET2", "SPIRE1", "MAP2K6", "MPLKIP", "ANK3", "KHDRBS1", "MCMBP", "ANXA1", "POLE", "BAP1", "DYNC1LI1", "HERC5", "CNPPD1", "CEP41", "UBA52", "NUMA1", "CTDP1", "SDCCAG8", "TJP3", "TMEM8B", "LIG3", "PIK3C3", "CDC14A", "RAD54L", "KIZ", "CDKL1", "LIG1", "FBXL15", "ANAPC15", "NUP107", "TIMELESS", "NEK11", "PARD3B", "RHOU", "SLC2A8", "PSMB7", "CENPE", "PPP3CA", "NEDD1", "ANAPC11", "PSMA5", "CENPC", "ORC5", "ING2", "SETMAR", "MTBP", "ANAPC2", "SH2B1", "PTPN11", "GPR132", "GAS2L1", "FANCM", "DCLRE1A", "STRADA", "PSMB3"],
nuclear transport	["PML", "PTGS2", "JAK2", "TXNIP", "DDX58", "TNPO1", "IPO11", "PIK3R1", "NUP98", "NEMF", "TNPO3", "PKD2", "PTPN14", "ANP32A", "SRSF11", "THOC2", "TACC3", "MCM3AP", "NUDT4", "KHDRBS1", "EMD", "CAMK4", "GLI3", "SEC61B", "NUP107", "PPP3CA", "RITA1", "PTPN11", "HCLS1", "KPNA4", "NFKBIL1", "STRADA"],
protein import into nucleus	["PML", "PTGS2", "JAK2", "TXNIP", "DDX58", "TNPO1", "IPO11", "PIK3R1", "NUP98", "TNPO3", "PKD2", "TACC3", "MCM3AP", "EMD", "GLI3", "SEC61B", "PPP3CA", "HCLS1", "KPNA4", "NFKBIL1"],
myeloid cell differentiation	["CTNNB1", "PML", "CDKN2B", "JAK2", "CSF1R", "PRKCA", "TRAF6", "LYN", "ACVR2A", "PIK3R1", "FECH", "SMAD5", "KITLG", "NDFIP1", "IREB2", "TET2", "PRDM16", "CAMK4", "RPS14", "RBP1", "SMAP1", "MFAP2", "NBEAL2", "HCLS1", "GAS2L1"],
microtubule organizing center organization	["CTNNB1", "GADD45A", "CHEK1", "CCNF", "PKD2", "TMEM67", "HAUS8", "RANBP1"],
inactivation of MAPK activity	["DUSP4", "PRKCA", "DUSP19", "RGS3"],
G2/M transition of mitotic cell cycle	["FOXO4", "TERF1", "CDKN2B", "CHEK1", "MTA3", "CCNY", "AKAP9", "TUBGCP5", "KHDRBS1", "CEP41", "NUMA1", "SDCCAG8", "FBXL15", "NEDD1"],
JNK cascade	["TP73", "HRAS", "MAP3K5", "MECOM", "COPS5", "PAK1", "BIRC7", "PDCD4", "TRAF6", "MAP3K2", "HIPK3", "FGF12", "DUSP19", "MAP4K4", "UBA52", "FZD8", "SH3RF1", "EPHB1"],
positive regulation of JUN kinase activity	["MAP3K5", "PAK1", "BIRC7", "TRAF6", "MAP3K2", "DUSP19", "FZD8"],
nuclear import	["PML", "PTGS2", "JAK2", "TXNIP", "DDX58", "TNPO1", "IPO11", "PIK3R1", "NUP98", "TNPO3", "PKD2", "TACC3", "MCM3AP", "EMD", "GLI3", "SEC61B", "PPP3CA", "HCLS1", "KPNA4", "NFKBIL1"]

Cellular component Down regulated genes	
cytosol	["CTNNB1", "FOSL1", "FOXO1", "FOXO4", "PML", "PTTG1", "STAT1", "TP73", "CDKN2B", "CHEK1", "JAK2", "HRAS", "MX1", "BEST1", "BBC3", "RBM38", "BCAR1", "SPRY1", "SIAH1", "VCP", "CDK4", "CSNK2A1", "SQSTM1", "TXNIP", "RHOB", "ASS1", "BID", "PAK1", "IGF2BP2", "DDX58", "TAP1", "TNPO1", "PDCD4", "FABP6", "MFN2", "DOCK1", "PRKCA", "CAPN10", "TRAF6", "CD151", "DHCR24", "PARG", "ACLY", "PLSCR1", "OAS1", "WWC1", "PRKAB1", "AGL", "LYN", "PSMD9", "QDPR", "UCK2", "CUL1", "HGS", "CLINT1", "DLC1", "COPG1", "GEMIN7", "PTGES2", "AMPD2", "PSMD2", "HIF1AN", "CENPP", "EIF1AX", "GRB2", "PAFAH1B2", "PIK3R1", "PSMC4", "TPM2", "SKAP2", "KIF23", "KLC2", "AMOTL1", "AP2A1", "COMT", "SMAD5", "NUP98", "PPT1", "PRKAR1A", "RPS25", "SRP68", "PDXK", "EIF3A", "DOCK9", "CARD19", "CCT6A", "HSPB2", "DNM1L", "PAIP1", "COX19", "CNOT6L", "MTHFD1", "RAB14", "FBLIM1", "PATL1", "SELENBP1", "IREB2", "ABCD3", "AKAP9", "STUB1", "TUBGCP5", "FSCN1", "SNRPD1", "SNX1", "PRDX6", "MYO10", "PSMA3", "MCM3AP", "PINK1", "PIK3CB", "MAP2K6", "OPHN1", "CARS2", "OAS2", "RPS9", "RPS29", "AP2A2", "VAV3", "AHS1", "YWHAB", "PIP5K1A", "HSPA14", "STK24", "OASL", "HERC5", "PLEKHG2", "RPL35A", "ATP7A", "CAMK4", "DIS3", "CLTA", "CNOT9", "OBSCN", "CEP41", "RPS14", "GLI3", "UBA52", "ARRB1", "NTRK2", "NUMA1", "RBP1", "SEC24D", "SDCCAG8", "ARHGAP45", "PLCE1", "PKHD1L1", "CPNE3", "BAIAP2L1", "GABARAPL2", "DAPP1", "PIK3C3", "NUFIP1", "SULT2B1", "SPG21", "SMS", "COPE", "RPL34", "NUP107", "EHHADH", "RHOU", "UCHL5", "CTNNAL1", "MOCS1", "GAMT", "ABI1", "PSMB7", "RPL35", "GMPR", "GGH", "CENPE", "PPP3CA", "RGS3", "SNRPF", "NEDD1", "PARN", "ANAPC11", "PSMA5", "DGKQ", "CENPC", "ENOPH1", "SAR1B", "SH3RF1", "FANCC", "CNOT11", "S100A12", "CHMP4C", "RAB24", "KSR2", "BAIAP2", "ANAPC2", "PNPLA2", "SH2B1", "PTPN11", "NEB", "KPNA4", "NFKBIL1", "CRYZL1", "EXOSC6", "HMBS", "STRADA", "PSMB3"],
late endosome	["SQSTM1", "RHOB", "IFITM3", "PMEL", "CD74", "HGS", "CLCN3", "VPS33B", "SNX16", "LAMTOR3", "RAB14", "ARL8A", "OSBPL1A", "NDFIP2", "VAMP7", "FIG4", "ATP7A", "RAB7A", "PIK3C3", "CHMP4C"],
nucleolus	["PML", "STAT1", "CA9", "BHLHE40", "TOP1", "DROSHA", "BLM", "CDK4", "TXN2", "PLSCR1", "UBE2I", "CAPG", "DEDD", "RPP38", "POLR1B", "PAFAH1B2", "TSPYL2", "DCAF17", "RPS25", "SRP68", "EIF3A", "MDN1", "RRP15", "SELENBP1", "ZC3H15", "MYO10", "DIMIT1", "PNMA1", "TSEN34", "RPS9", "CARF", "BAP1", "FRG1", "OASL", "EDF1", "THAP2", "XRN2", "CAMK4", "RPS14", "GLI3", "KDM5A", "STAU2", "NUFIP1", "ZNF330", "CCDC86", "NEK11", "RASL11A", "ELL3", "FGF13", "RPL35", "PARN", "ZNF593", "DMP1", "DCLRE1A", "ATF6B", "EXOSC6"],
perinuclear region of cytoplasm	["CTNNB1", "HRAS", "MX1", "CDK4", "ATXN2", "COPS5", "FAT1", "PRKCA", "TRAF6", "WWC1", "LYN", "BAG5", "CLINT1", "CALCOCO2", "SEC23B", "PTGES2", "SLC30A7", "HIF1AN", "VPS33B", "TRAPPC2", "DNM1L", "STX6", "ANKRD13C", "RAB14", "NDFIP1", "ANP32A", "SPIRE1", "OAS2", "NDFIP2", "INHBB", "CTIF", "YWHAB", "VAMP7", "HERC5", "ATP7A", "LPXN", "SEC24D", "ARF5", "STK16", "ITM2C", "SH3RF1", "SLC39A13"],
ribosome	["MRPS33", "MRPL47", "RPS25", "SRP68", "MRPL1", "MRPL32", "SERP1", "RPS9", "RPS29", "MRPS26", "HSPA14", "RPL35A", "MRPL16", "MRPS34", "RPS14", "UBA52", "MRPL49", "NUFIP1",

	"RPL34", "RPL35", "MRPL15", "MRPS18C", "METTL17", "MRPL14", "MRPS18B"],
nucleoplasm part	["CTNNB1", "FOXO1", "FOXO4", "PBX2", "PML", "TP73", "ETV3", "NPAT", "MECOM", "BLM", "CDK4", "MTA3", "CSNK2A1", "NR4A1", "RARG", "HDAC8", "KMT2A", "UBE2I", "SMARCC2", "SON", "CD2BP2", "INTS7", "GEMIN7", "TIMM50", "SUZ12", "GATAD2A", "SMAD5", "ENY2", "THAP7", "GTF2H3", "FOXJ3", "HIPK3", "NACC1", "PATL1", "INTS3", "FOXN2", "PCGF2", "SUMO3", "CSTF2", "MAML3", "PRDM16", "MED29", "POLE3", "KANSL2", "DEAF1", "YWHAB", "PIP5K1A", "FRG1", "EDF1", "ASH2L", "INTS6", "NAA16", "KAT7", "GLI3", "ZNF473", "TRIM16", "TAF11", "DDX1", "NUFIP1", "SNW1", "ELL3", "FOXJ1", "ECSIT", "DGKQ", "FANCC", "PITX2", "ING2", "LDB2", "HCLS1", "FANCM", "GTF2F2", "HNF1B"],
vesicle coat	["SEC23B", "COPG1", "AP2A1", "AP2A2", "CLTA", "SEC24D", "COPE"],
trans-Golgi network transport vesicle	["AP2A1", "RAB14", "ATP7A", "CLTA", "SPG21"],
nuclear chromosome	["STAT1", "TERF1", "CHEK1", "TOP1", "PAX6", "ERCC1", "SOX18", "BLM", "CSNK2A1", "HDAC8", "UBE2I", "BAZ1B", "NCAPD2", "SUZ12", "PCGF2", "ADD3", "ORC6", "KMT5C", "CECR2", "POLE3", "POLE", "LIG3", "NUFIP1", "TIMELESS", "UCHL5", "CENPE", "CENPC", "ORC5", "ING2"],
ribonucleoprotein complex	["TOP1", "CPEB1", "TDRD1", "ATXN2", "SQSTM1", "CD2BP2", "RPP38", "MRPS33", "GPATCH1", "MRPL47", "GEMIN7", "NAF1", "TRIM71", "PPIL1", "RPS25", "SRP68", "TEP1", "SYF2", "DHX35", "MRPL1", "PATL1", "MRPL32", "ZNF326", "SNRPD1", "AQR", "SERP1", "BTBD1", "RPS9", "RPS29", "MRPS26", "HSPA14", "FRG1", "RPL35A", "LSM14B", "SF3A1", "CNOT9", "MRPL16", "MRPS34", "RPS14", "UBA52", "MRPL49", "XAB2", "DDX1", "NUFIP1", "SNW1", "RPL34", "RPL35", "MRPL15", "SNRPF", "HENMT1", "MRPS18C", "METTL17", "MRPL14", "MRPS18B"],
nuclear chromosome part	["STAT1", "TERF1", "TOP1", "PAX6", "ERCC1", "SOX18", "BLM", "CSNK2A1", "UBE2I", "BAZ1B", "SUZ12", "PCGF2", "ORC6", "KMT5C", "CECR2", "POLE3", "POLE", "LIG3", "NUFIP1", "TIMELESS", "UCHL5", "CENPE", "CENPC", "ORC5", "ING2"],
nuclear lumen	["CTNNB1", "FOXO1", "FOXO4", "MCM5", "PBX2", "PML", "STAT1", "TP73", "CA9", "BHLHE40", "TERF1", "CHEK1", "JAK2", "TOP1", "ETV3", "DUSP4", "PAX6", "DBF4", "DROSHA", "ERCC1", "MCM8", "NPAT", "SOX18", "MECOM", "BLM", "CDK4", "MTA3", "CSNK2A1", "SQSTM1", "NR4A1", "RARG", "PRKCA", "TXN2", "HDAC8", "KMT2A", "PLSCR1", "UBE2I", "WTAP", "CAPG", "PSMD9", "SMARCC2", "SON", "CUL1", "BAZ1B", "DEDD", "NCAPD2", "CD2BP2", "RPP38", "INTS7", "CHTOP", "GEMIN7", "MED25", "POLR1B", "TIMM50", "PSMD2", "SUZ12", "CENPP", "PAFAH1B2", "PSMC4", "KIF23", "GATAD2A", "TSPYL2", "DCAF17", "SMAD5", "NUP98", "RPS25", "SRP68", "TEP1", "EIF3A", "MDN1", "RRP15", "ENY2", "WDR18", "THAP7", "GTF2H3", "FOXJ3", "HIPK3", "NACC1", "PHF13", "PATL1", "SELENBP1", "INTS3", "FOXN2", "PCGF2", "ANP32A", "SRSF11", "ANKRD28", "ZNF326", "ADD3", "SUMO3", "SNRPD1", "ZC3H15", "CSTF2", "MYO10", "PSMA3", "ORC6", "NR1D2", "KMT5C", "DIMIT1", "MAML3", "PRDM16", "MAP2K6", "CECR2", "PNMA1", "MED29", "POLE3", "TSEN34", "RPS9", "KANSL2", "CARF", "DEAF1", "YWHAB", "POLE", "PIP5K1A", "BAP1", "FRG1", "POLR2K", "STK24", "OASL", "EDF1", "ASH2L", "INTS6", "THAP2", "SF3A1", "XRN2", "CAMK4", "DIS3", "NAA16", "RPS14", "KAT7", "GLI3", "UBA52", "ZNF473", "NUMA1", "KDM5A",

	"RORC", "CTDP1", "TRIM16", "LIG3", "STAU2", "TAF11", "TLE2", "XAB2", "DDX1", "NUFIP1", "SNW1", "LIG1", "ZNF330", "CCDC86", "NUP107", "TIMELESS", "NEK11", "UCHL5", "RASL11A", "ELL3", "FOXJ1", "FGF13", "ECSIT", "PSMB7", "RPL35", "CENPE", "SNRPF", "PARN", "ANAPC11", "ZNF593", "PSMA5", "DGKQ", "CENPC", "DMP1", "FANCC", "PITX2", "ORC5", "ING2", "LDB2", "ENC1", "ANAPC2", "HCLS1", "KPNA4", "FANCM", "GTF2F2", "DCLRE1A", "ATF6B", "EXOSC6", "HNF1B", "PSMB3"],
nucleoplasm	["CTNNB1", "FOXO1", "FOXO4", "MCM5", "PBX2", "PML", "STAT1", "TP73", "TERF1", "CHEK1", "TOP1", "ETV3", "DUSP4", "DBF4", "DROSHA", "ERCC1", "MCM8", "NPAT", "MECOM", "BLM", "CDK4", "MTA3", "CSNK2A1", "SQSTM1", "NR4A1", "RARG", "PRKCA", "HDAC8", "KMT2A", "UBE2I", "WTAP", "PSMD9", "SMARCC2", "SON", "CUL1", "CD2BP2", "INTS7", "CHTOP", "GEMIN7", "MED25", "POLR1B", "TIMM50", "PSMD2", "SUZ12", "CENPP", "PSMC4", "KIF23", "GATAD2A", "TSPYL2", "SMAD5", "NUP98", "ENY2", "WDR18", "THAP7", "GTF2H3", "FOXJ3", "HIPK3", "NACC1", "PHF13", "PATL1", "INTS3", "FOXN2", "PCGF2", "ANP32A", "SRSF11", "ANKRD28", "SUMO3", "SNRPD1", "CSTF2", "PSMA3", "ORC6", "NR1D2", "MAML3", "PRDM16", "MAP2K6", "MED29", "POLE3", "KANSL2", "CARF", "DEAF1", "YWHAB", "POLE", "PIP5K1A", "FRG1", "POLR2K", "STK24", "EDF1", "ASH2L", "INTS6", "SF3A1", "CAMK4", "DIS3", "NAA16", "KAT7", "GLI3", "UBA52", "ZNF473", "NUMA1", "RORC", "CTDP1", "TRIM16", "LIG3", "TAF11", "TLE2", "XAB2", "DDX1", "NUFIP1", "SNW1", "LIG1", "ELL3", "FOXJ1", "ECSIT", "PSMB7", "SNRPF", "ANAPC11", "PSMA5", "DGKQ", "FANCC", "PITX2", "ORC5", "ING2", "LDB2", "ANAPC2", "HCLS1", "KPNA4", "FANCM", "GTF2F2", "HNF1B", "PSMB3"],
organelle lumen	["CTNNB1", "FOXO1", "FOXO4", "MCM5", "PBX2", "PML", "STAT1", "TP73", "CA9", "PTGS2", "ARG2", "BHLHE40", "HSPA5", "TERF1", "CHEK1", "JAK2", "TOP1", "COL1A1", "ETV3", "DUSP4", "PAX6", "MMP14", "DBF4", "DROSHA", "ERCC1", "MCM8", "NPAT", "HPSE", "SOX18", "MECOM", "BLM", "CDK4", "MTA3", "CSNK2A1", "SQSTM1", "VEGFB", "HYOU1", "NR4A1", "RARG", "TFAM", "CD74", "PRKCA", "TXN2", "HDAC8", "KMT2A", "PARG", "PLSCR1", "UBE2I", "WTAP", "CAPG", "DLAT", "NDUFA10", "PSMD9", "SMARCC2", "SON", "CUL1", "BAZ1B", "DEDD", "NCAPD2", "WARS2", "CD2BP2", "RPP38", "PMPCA", "INTS7", "CHTOP", "MRPS33", "MRPL47", "GEMIN7", "MED25", "POLR1B", "TIMM50", "PSMD2", "SUZ12", "CENPP", "PAFAH1B2", "PSMC4", "KIF23", "GATAD2A", "TSPYL2", "DCAF17", "FECH", "SMAD5", "NUP98", "RPS25", "SRP68", "TEP1", "EIF3A", "ACOT8", "MDN1", "RRP15", "ENY2", "WDR18", "THAP7", "GTF2H3", "FOXJ3", "HIPK3", "NACC1", "PHF13", "PATL1", "MRPL32", "SELENBP1", "INTS3", "FOXN2", "ABCD3", "PCGF2", "ANP32A", "SRSF11", "ANKRD28", "ZNF326", "ADD3", "SUMO3", "SNRPD1", "ZC3H15", "CSTF2", "MYO10", "PSMA3", "ORC6", "NR1D2", "KMT5C", "DIMT1", "MAML3", "PRDM16", "COL5A1", "MAP2K6", "CECR2", "DLST", "PNMA1", "MED29", "CARS2", "POLE3", "TSEN34", "PDK3", "RPS9", "KANSL2", "MRPS26", "CARF", "DEAF1", "YWHAB", "POLE", "PIP5K1A", "BAP1", "FRG1", "POLR2K", "STK24", "OASL", "EDF1", "ASH2L", "INTS6", "THAP2", "NEU1", "SF3A1", "XRN2", "CAMK4", "DIS3", "CRAT", "GALC", "NAA16", "RPS14", "KAT7", "TIMM44", "GLI3", "UBA52", "ZNF473", "MRPL49", "NUMA1", "KDM5A", "RORC", "CTDP1", "PDIA4", "TRIM16", "LIG3", "LARS2", "STAU2", "TAF11", "TLE2", "XAB2", "MCCC1", "DDX1", "NUFIP1", "SNW1", "LIG1", "SSBP1", "NUDT1", "ZNF330", "CCDC86", "NUP107", "TIMELESS", "NEK11", "UCHL5",

	"RASL11A", "CLPP", "ELL3", "FOXJ1", "FGF13", "ECSIT", "PSMB7", "RPL35", "CENPE", "SNRPF", "PARN", "ANAPC11", "ZNF593", "PSMA5", "DGKQ", "CENPC", "GPC3", "DMP1", "FANCC", "MRPS18C", "PITX2", "ORC5", "ING2", "LDB2", "ENC1", "SUCLG2", "ANAPC2", "HCLS1", "KPNA4", "FANCM", "COL14A1", "GTF2F2", "CFD", "DCLRE1A", "MRPS18B", "ATF6B", "EXOSC6", "HNF1B", "PSMB3"],
membrane-enclosed lumen	["CTNNB1", "FOXO1", "FOXO4", "MCM5", "PBX2", "PML", "STAT1", "TP73", "CA9", "PTGS2", "ARG2", "BHLHE40", "HSPA5", "TERF1", "CHEK1", "JAK2", "TOP1", "COL1A1", "ETV3", "DUSP4", "PAX6", "MMP14", "DBF4", "DROSHA", "ERCC1", "MCM8", "NPAT", "HPSE", "SOX18", "MECOM", "BLM", "CDK4", "MTA3", "CSNK2A1", "SQSTM1", "VEGFB", "HYOU1", "TXNIP", "NR4A1", "RARG", "TFAM", "CD74", "PRKCA", "TXN2", "HDAC8", "KMT2A", "PARG", "PLSCR1", "UBE2I", "WTAP", "CAPG", "DLAT", "LYN", "NDUFA10", "PSMD9", "SMARCC2", "SON", "CUL1", "BAZ1B", "DEDD", "NCAPD2", "WARS2", "CD2BP2", "RPP38", "PMPCA", "INTS7", "CHTOP", "MRPS33", "MRPL47", "GEMIN7", "MED25", "POLR1B", "TIMM50", "NDUFS5", "PSMD2", "SUZ12", "CENPP", "PAFAH1B2", "PSMC4", "KIF23", "GATAD2A", "TSPYL2", "DCAF17", "FECH", "SMAD5", "NUP98", "RPS25", "SRP68", "TEP1", "EIF3A", "ACOT8", "MDN1", "RRP15", "ENY2", "WDR18", "THAP7", "GTF2H3", "FOXJ3", "HIPK3", "NACC1", "PHF13", "PATL1", "MRPL32", "SELENBP1", "INTS3", "FOXN2", "ABCD3", "PCGF2", "ANP32A", "SRSF11", "ANKRD28", "ZNF326", "ADD3", "SUMO3", "SNRPD1", "ZC3H15", "CSTF2", "MYO10", "PSMA3", "ORC6", "NR1D2", "KMT5C", "DIMT1", "MAML3", "PRDM16", "COL5A1", "MAP2K6", "CECR2", "DLST", "PNMA1", "MED29", "CARS2", "POLE3", "TSEN34", "PDK3", "RPS9", "KANSL2", "MRPS26", "CARF", "DEAF1", "YWHAB", "POLE", "PIP5K1A", "BAP1", "FRG1", "POLR2K", "STK24", "OASL", "EDF1", "ASH2L", "INTS6", "THAP2", "NEU1", "SF3A1", "XRN2", "CAMK4", "DIS3", "CRAT", "GALC", "NAA16", "RPS14", "KAT7", "TIMM44", "GLI3", "UBA52", "ZNF473", "MRPL49", "NUMA1", "KDM5A", "RORC", "CTDP1", "PDIA4", "TRIM16", "LIG3", "LARS2", "STAU2", "TAF11", "TLE2", "XAB2", "MCCC1", "DDX1", "NUFIP1", "SNW1", "LIG1", "SSBP1", "NUDT1", "ZNF330", "CCDC86", "NUP107", "TIMELESS", "NEK11", "UCHL5", "RASL11A", "CLPP", "ELL3", "FOXJ1", "FGF13", "ECSIT", "PSMB7", "RPL35", "CENPE", "SNRPF", "PARN", "ANAPC11", "ZNF593", "PSMA5", "DGKQ", "CENPC", "GPC3", "DMP1", "FANCC", "MRPS18C", "PITX2", "ORC5", "ING2", "LDB2", "ENC1", "SUCLG2", "ANAPC2", "HCLS1", "KPNA4", "FANCM", "COL14A1", "GTF2F2", "CFD", "DCLRE1A", "MRPS18B", "ATF6B", "EXOSC6", "HNF1B", "PSMB3"],
integrator complex	["INTS7", "INTS3", "INTS6"],
organellar small ribosomal subunit	["MRPS33", "MRPS26", "MRPS18C", "MRPS18B"],
mitochondrial small ribosomal subunit	["MRPS33", "MRPS26", "MRPS18C", "MRPS18B"],
cell-substrate adherens junction	["CTNNB1", "BCAR1", "PAK1", "DLC1", "ZFYVE21", "FBLIM1", "PALLD", "PNMA1", "GIT1", "AFAP1", "LPXN", "RHOU", "TLN2", "ATF6B"],
membrane coat	["SEC23B", "COPG1", "AP2A1", "AP2A2", "CLTA", "SEC24D", "AP3M2", "COPE", "DNM1", "STON1"],

coated membrane	["SEC23B", "COPG1", "AP2A1", "AP2A2", "CLTA", "SEC24D", "AP3M2", "COPE", "DNM1", "STON1"],
lysosomal membrane	["HPSE", "IFITM3", "CD74", "VPS33B", "GPR137B", "SLC48A1", "ARL8A", "OSBPL1A", "RNF152", "VAMP7", "TSPAN1", "NEU1", "ARRB1", "RAB7A", "ITM2C"],
ribosomal subunit	["MRPS33", "RPS25", "MRPL1", "MRPL32", "RPS9", "RPS29", "MRPS26", "RPL35A", "RPS14", "UBA52", "RPL34", "RPL35", "MRPL15", "MRPS18C", "MRPS18B"],
transport vesicle	["SREBF2", "HLA-E", "CD74", "SEC23B", "YIPF3", "CLCN3", "SNTB2", "AP2A1", "RAB14", "VAMP7", "ATP7A", "CLTA", "SEC24D", "SPG21", "SAR1B"],
focal adhesion	["BCAR1", "PAK1", "DLC1", "ZFYVE21", "FBLIM1", "PALLD", "PNMA1", "GIT1", "AFAP1", "LPXN", "RHO", "TLN2", "ATF6B"],
coated vesicle	["SREBF2", "GAD1", "HLA-E", "CD74", "GRIN1", "MYO1E", "CLINT1", "SEC23B", "COPG1", "SEMA4C", "AP2A1", "PPT1", "STX6", "FCHO2", "RAB14", "STXBP5", "AP2A2", "ATP7A", "CLTA", "SEC24D", "SPG21", "COPE", "SLC2A8", "SAR1B"],
centrosome	["CTNNB1", "CHEK1", "CDC42BPG", "CCNF", "CKAP2", "NAF1", "KIF23", "TTLL5", "TSPYL2", "NCAPG", "CEP97", "TMEM67", "HAUS8", "CEP350", "MPHOSPH9", "AKAP9", "TUBGCP5", "RANBP1", "TACC3", "MPLKIP", "FLOT1", "DYNC1LI1", "CEP295", "CEP41", "RNF19A", "CTDP1", "SDCCAG8", "CDC14A", "KIZ", "RAB3GAP1", "NEDD1", "RITA1", "YIF1A"],
Golgi-associated vesicle	["COPG1", "AP2A1", "RAB14", "ATP7A", "CLTA", "SPG21", "COPE", "STK16"],
cell-substrate junction	["CTNNB1", "BCAR1", "PAK1", "DLC1", "ZFYVE21", "FBLIM1", "PALLD", "PNMA1", "GIT1", "AFAP1", "LPXN", "RHO", "TLN2", "ATF6B"],
actin cytoskeleton	["DAPK1", "PAK1", "DDX58", "HAP1", "CAPG", "MYO1E", "WASF1", "TPM2", "NCAPG", "EPB41L2", "IPP", "PKD2", "FBLIM1", "PALLD", "FSCN1", "MYO10", "OPHN1", "MYH15", "INTS6", "AFAP1", "NEBL", "LPXN", "CTDP1", "CORO2B", "BAIAP2L1", "RHO", "CTNNAL1", "DSTN", "LAD1", "TLN2", "BAIAP2", "NEB", "ZNF74", "GAS2L1"],
organellar ribosome	["MRPS33", "MRPL47", "MRPL32", "MRPS26", "MRPL49", "MRPS18C", "MRPS18B"],
mitochondrial ribosome	["MRPS33", "MRPL47", "MRPL32", "MRPS26", "MRPL49", "MRPS18C", "MRPS18B"],
membrane raft	["BSG", "JAK2", "HPSE", "CD24", "ACE2", "PLSCR1", "LYN", "DLC1", "EFHD2", "PPT1", "LAMTOR3", "CACNA1C", "FLOT1", "STOM", "EPHB1", "P2RY12", "RTN4RL1"],
small ribosomal subunit	["MRPS33", "RPS25", "RPS9", "RPS29", "MRPS26", "RPS14", "MRPS18C", "MRPS18B"],
condensed nuclear chromosome	["CHEK1", "BLM", "UBE2I", "ADD3", "KMT5C", "LIG3", "CENPE", "CENPC"],
ubiquitin ligase complex	["CCNF", "CUL1", "TNFAIP1", "DCAF17", "CACUL1", "CUL4A", "KLHL21", "STUB1", "DCUN1D1", "UBE4B", "FBXL15", "ANAPC15", "ANAPC11", "ENC1", "ANAPC2"],
nuclear matrix	["PML", "JAK2", "BLM", "TEP1", "ZNF326", "NUMA1", "NUFIP1", "SNW1", "ENC1"],
replication fork	["CHEK1", "TOP1", "BLM", "BAZ1B", "POLE3", "POLE"],
nuclear body	["PML", "NPAT", "MECOM", "BLM", "UBE2I", "SON", "CD2BP2", "GEMIN7", "TIMM50", "GATAD2A", "THAP7", "HIPK3", "NACC1", "PATL1", "PCGF2", "SUMO3", "CSTF2", "MAML3", "PIP5K1A", "FRG1", "ZNF473", "TRIM16", "DDX1", "DGKQ"],
spindle pole	["CTNNB1", "PRC1", "CKAP2", "HAUS8", "KLHL21", "TUBGCP5", "DYNC1LI1", "NUMA1", "CTDP1", "RMDN2"],

nuclear replication fork	["TOP1", "BAZ1B", "POLE3", "POLE"],
nuclear part	["CTNNB1", "FOXO1", "FOXO4", "MCM5", "PBX2", "PML", "STAT1", "TP73", "CA9", "BHLHE40", "HSPA5", "TERF1", "CHEK1", "JAK2", "TOP1", "ETV3", "DUSP4", "PAX6", "DBF4", "DROSHA", "ERCC1", "MCM8", "NPAT", "SOX18", "MECOM", "BLM", "CDK4", "MTA3", "CSNK2A1", "SQSTM1", "COPS5", "NR4A1", "PAK1", "TNPO1", "RARG", "PRKCA", "TRAF6", "TXN2", "HDAC8", "KMT2A", "PLSCR1", "UBE2I", "WTAP", "CAPG", "PSMD9", "SMARCC2", "SON", "CUL1", "BAZ1B", "DEDD", "NCAPD2", "CD2BP2", "RPP38", "CBX6", "INTS7", "CHTOP", "IPO11", "BCOR", "PARP16", "GPATCH1", "NABP2", "GEMIN7", "MED25", "POLR1B", "TIMM50", "NUP35", "PSMD2", "SUZ12", "CENPP", "GRB2", "PAFAH1B2", "PSMC4", "KIF23", "PPIL1", "GATAD2A", "TSPYL2", "DCAF17", "AMOTL1", "SMAD5", "NUP98", "RPS25", "SRP68", "TEP1", "EIF3A", "MDN1", "SYF2", "RRP15", "ENY2", "WDR18", "DHX35", "COPS7B", "THAP7", "EPB41L2", "GTF2H3", "FOXJ3", "HIPK3", "NACC1", "PHF13", "PATL1", "SELENBP1", "TMEM97", "INTS3", "FOXN2", "PCGF2", "ANP32A", "SRSF11", "STUB1", "ANKRD28", "THOC2", "ZNF326", "ADD3", "RANBP1", "SUMO3", "SNRPD1", "ZC3H15", "CSTF2", "MYO10", "PSMA3", "AQR", "ORC6", "NR1D2", "KMT5C", "DIMT1", "MAML3", "PRDM16", "MAP2K6", "CECR2", "PNMA1", "MED29", "POLE3", "TSEN34", "RPS9", "KANSL2", "CARF", "DEAF1", "DPF1", "FLOT1", "HOXC10", "YWHAB", "POLE", "PIP5K1A", "BAP1", "EMD", "FRG1", "POLR2K", "STK24", "OASL", "EDF1", "ASH2L", "INTS6", "THAP2", "SF3A1", "XRN2", "CAMK4", "DIS3", "NAA16", "RPS14", "KAT7", "GLI3", "UBA52", "ZNF473", "NUMA1", "POU6F1", "KDM5A", "RORC", "CTDP1", "TRIM16", "LIG3", "STAU2", "TAF11", "TLE2", "XAB2", "DDX1", "NUFIP1", "SNW1", "LIG1", "ZNF330", "CCDC86", "ANAPC15", "NUP107", "TIMELESS", "NEK11", "UCHL5", "RASL11A", "ELL3", "FOXJ1", "FGF13", "ECSIT", "PSMB7", "RPL35", "CENPE", "SNRPF", "CERS5", "PARN", "ANAPC11", "ZNF593", "PSMA5", "DGKQ", "CENPC", "DMP1", "FANCC", "PITX2", "ORC5", "GHDC", "ING2", "LDB2", "ENC1", "ANAPC2", "HCLS1", "KPNA4", "FANCM", "GTF2F2", "DCLRE1A", "ATF6B", "EXOSC6", "HNF1B", "PSMB3"],
histone deacetylase complex	["MECOM", "MTA3", "CSNK2A1", "HDAC8", "GATAD2A", "ING2"],
integral to endoplasmic reticulum membrane	["SREBF2", "HSPA5", "HLA-E", "TAP1", "CD74", "ASPH", "PKD2", "SAMD8", "SLC35D1", "DERL3", "DPM3"],
endocytic vesicle	["ITGAV", "HLA-E", "CD74", "MYO1E", "RAB9B", "AP2A1", "RABEP1", "RAB14", "RALA", "AP2A2", "VAMP7", "CLTA", "UBA52", "RAB7A", "NOSTRIN", "ATP6V0C"],
transcription factor complex	["CTNNB1", "FOXO1", "FOXO4", "PBX2", "TP73", "CDK4", "NR4A1", "RARG", "SMAD5", "GTF2H3", "FOXJ3", "FOXN2", "DEAF1", "EDF1", "NAA16", "TAF11", "FOXJ1", "ECSIT", "PITX2", "ING2", "LDB2", "HCLS1", "GTF2F2", "HNF1B"],
Golgi membrane	["SREBF2", "BSG", "HRAS", "GLCE", "HLA-E", "CD74", "ABCG1", "DHCR24", "POMGNT1", "SEC23B", "COPG1", "SH3GLB1", "PTGES2", "SLC30A7", "CLCN3", "AP2A1", "MGAT4A", "STX6", "RAB14", "MPHOSPH9", "NDFIP1", "DSE", "FUT8", "SLC35C1", "NDFIP2", "EXT2", "FIG4", "CLTA", "ARRB1", "SEC24D", "FUT9", "GALNT5", "PLCE1", "IL17RD", "GABARAPL2", "NAGPA", "COPE", "RHO", "SLC35A3", "TPST2", "SAR1B", "SLC39A13", "MGAT2", "YIF1A"],

intrinsic to endoplasmic reticulum membrane	["SREBF2", "HSPA5", "HLA-E", "TAP1", "CD74", "ASPH", "PKD2", "SAMD8", "SLC35D1", "EXT2", "DERL3", "DPM3"],
vacuolar membrane	["HPSE", "IFITM3", "CD74", "VPS33B", "GPR137B", "SLC48A1", "ARL8A", "OSBPL1A", "RNF152", "VAMP7", "TSPAN1", "NEU1", "ARRB1", "GABARAPL2", "RAB7A", "ITM2C", "ATP6V0C"],
microtubule	["PRC1", "CKAP2", "SNTB2", "KIF23", "KLC2", "CCT6A", "KIF5C", "DNM1L", "HAUS8", "KLHL21", "TUBGCP5", "NAV1", "CEP57L1", "EMD", "DYNC1LI1", "TUBB2B", "NUMA1", "TTLL1", "SARM1", "STAU2", "WDR47", "DNM1", "RMDN2", "FGF13", "KIF12", "CENPE", "GAS2L1"],
integrin complex	["ITGB8", "ITGAV", "ITGA2", "LYN"],
vesicle membrane	["SREBF2", "BSG", "GAD1", "BACE1", "HLA-E", "CD74", "ABCA3", "SEC23B", "COPG1", "SEMA4C", "CLCN3", "GRB2", "SNTB2", "RAB9B", "AP2A1", "TMEM67", "RAB14", "STXBP5", "SPIRE1", "AP2A2", "VAMP7", "CLTA", "UBA52", "ARRB1", "SEC24D", "RAB7A", "COPE", "SLC2A8", "SAR1B", "NOSTRIN", "ATP6V0C"],
intercalated disc	["CTNNB1", "PAK1", "ANK3", "FGF13", "TLN2"],
cytoplasmic vesicle membrane	["SREBF2", "BSG", "GAD1", "BACE1", "HLA-E", "CD74", "ABCA3", "SEC23B", "COPG1", "SEMA4C", "CLCN3", "SNTB2", "RAB9B", "AP2A1", "TMEM67", "RAB14", "STXBP5", "SPIRE1", "AP2A2", "VAMP7", "CLTA", "UBA52", "ARRB1", "SEC24D", "RAB7A", "COPE", "SLC2A8", "SAR1B", "NOSTRIN", "ATP6V0C"],
mitochondrial matrix	["ARG2", "TFAM", "PARG", "DLAT", "NDUFA10", "WARS2", "PMPCA", "MRPS33", "MRPL47", "FECH", "MRPL32", "DLST", "CARS2", "PDK3", "MRPS26", "TIMM44", "MRPL49", "LARS2", "MCCC1", "SSBP1", "NUDT1", "CLPP", "MRPS18C", "SUCLG2", "MRPS18B"],
mitochondrial matrix	["ARG2", "TFAM", "PARG", "DLAT", "NDUFA10", "WARS2", "PMPCA", "MRPS33", "MRPL47", "FECH", "MRPL32", "DLST", "CARS2", "PDK3", "MRPS26", "TIMM44", "MRPL49", "LARS2", "MCCC1", "SSBP1", "NUDT1", "CLPP", "MRPS18C", "SUCLG2", "MRPS18B"],
lamellipodium	["CTNNB1", "SPRY1", "FAT1", "WASF1", "AMOTL1", "PKD2", "PALLD", "MYO10", "PIP5K1A", "ABI1", "SH3RF1"],
non-membrane-bounded organelle	["CTNNB1", "MYCN", "PML", "STAT1", "TP73", "CA9", "BHLHE40", "TERF1", "CHEK1", "JAK2", "DAPK1", "TOP1", "PAX6", "DROSHA", "ERCC1", "CPEB1", "SOX18", "SPRR1B", "VCP", "EPB41L4B", "TDRD1", "BLM", "CDK4", "MTA3", "ATXN2", "CSNK2A1", "SQSTM1", "PAK1", "IGF2BP2", "DDX58", "TFAM", "GRIN1", "MFN2", "TXN2", "HDAC8", "CDC42BPG", "DHCR24", "NSFL1C", "HAP1", "PLSCR1", "PRC1", "UBE2I", "CAPG", "CCNF", "LYN", "MYO1E", "WASF1", "BAZ1B", "DEDD", "NCAPD2", "CALCOCO2", "RPP38", "CBX6", "INTS7", "CKAP2", "MRPS33", "SEMA4C", "MRPL47", "POLR1B", "NAF1", "NUP35", "TRIM71", "SUZ12", "CENPP", "PAFAH1B2", "SNTB2", "TPM2", "KIF23", "TTLL5", "TSPYL2", "KLC2", "DCAF17", "NUP98", "RPS25", "SRP68", "TEP1", "EIF3A", "MDN1", "RRP15", "PPP4R3B", "NCAPG", "MRPL1", "THAP7", "CCT6A", "EPB41L2", "IPP", "KIF5C", "PKD2", "DNM1L", "BICD2", "CEP97", "TMEM67", "HAUS8", "KITLG", "CEP350", "FBLIM1", "CC2D1A", "ARL8A", "PATL1", "KLHL21", "MPHOSPH9", "PALLD", "MRPL32", "SELENBP1", "PTPN14", "PCGF2", "AKAP9", "TUBGCP5", "ADD3", "RANBP1", "SUMO3", "FSCN1", "CRIPT", "TACC3", "ZC3H15", "SETD7", "NAV1", "CEP57L1", "MYO10", "ORC6", "SERP1", "CACNA1C", "KMT5C", "DIMIT1", "SPIRE1", "MAP2K6", "CECR2", "OPHN1", "PNMA1", "BTBD1", "MYH15", "POLE3", "TSEN34",

	<p>"MPLKIP", "RPS9", "RPS29", "ANK3", "FRMD4A", "MRPS26", "CARF", "HOMER2", "FLOT1", "ANXA1", "POLE", "HSPA14", "BAP1", "EMD", "FRG1", "PPP2R5A", "OASL", "EDF1", "INTS6", "DYNC1LI1", "AFAP1", "THAP2", "CEP295", "TUBB2B", "RPL35A", "NEBL", "LPXN", "XRN2", "CAMK4", "CNOT9", "MRPL16", "MRPS34", "OBSCN", "CEP41", "RPS14", "RNF19A", "GLI3", "UBA52", "ARRB1", "MRPL49", "NTRK2", "NUMA1", "KDM5A", "CTDP1", "CORO2B", "SDCCAG8", "TTLL1", "SARM1", "RECQL", "LIG3", "BAIAP2L1", "STAU2", "CDC14A", "DDX1", "NUFIP1", "WDR47", "KIZ", "SNW1", "TRIP4", "LIG1", "SSBP1", "DNM1", "ZNF330", "RPL34", "CCDC86", "NUP107", "TIMELESS", "NEK11", "RAB3GAP1", "RMDN2", "RHOU", "UCHL5", "CTNNAL1", "RASL11A", "DSTN", "ELL3", "FGF13", "ABI1", "KIF12", "RPL35", "MRPL15", "CENPE", "PPP3CA", "NEDD1", "RITA1", "PARN", "ZNF593", "DGKQ", "CENPC", "STOM", "DMP1", "LAD1", "HENMT1", "NOSTRIN", "S100A12", "MRPS18C", "ORC5", "METTL17", "ING2", "SETMAR", "KRT6C", "DLGAP1", "ENC1", "TLN2", "YIF1A", "BAIAP2", "MRPL14", "RELL1", "NEB", "ZNF74", "GAS2L1", "PARPBP", "GTF2F2", "DCLRE1A", "MRPS18B", "KRT40", "ATF6B", "EXOSC6"],</p>
intracellular non-membrane-bounded organelle	<p>["CTNNB1", "MYCN", "PML", "STAT1", "TP73", "CA9", "BHLHE40", "TERF1", "CHEK1", "JAK2", "DAPK1", "TOP1", "PAX6", "DROSHA", "ERCC1", "CPEB1", "SOX18", "SPRR1B", "VCP", "EPB41L4B", "TDRD1", "BLM", "CDK4", "MTA3", "ATXN2", "CSNK2A1", "SQSTM1", "PAK1", "IGF2BP2", "DDX58", "TFAM", "GRIN1", "MFN2", "TXN2", "HDAC8", "CDC42BPG", "DHCR24", "NSFL1C", "HAP1", "PLSCR1", "PRC1", "UBE2I", "CAPG", "CCNF", "LYN", "MYO1E", "WASF1", "BAZ1B", "DEDD", "NCAPD2", "CALCOCO2", "RPP38", "CBX6", "INTS7", "CKAP2", "MRPS33", "SEMA4C", "MRPL47", "POLR1B", "NAF1", "NUP35", "TRIM71", "SUZ12", "CENPP", "PAFAH1B2", "SNTB2", "TPM2", "KIF23", "TTLL5", "TSPYL2", "KLC2", "DCAF17", "NUP98", "RPS25", "SRP68", "TEP1", "EIF3A", "MDN1", "RRP15", "PPP4R3B", "NCAPG", "MRPL1", "THAP7", "CCT6A", "EPB41L2", "IPP", "KIF5C", "PKD2", "DNM1L", "BICD2", "CEP97", "TMEM67", "HAUS8", "KITLG", "CEP350", "FBLIM1", "CC2D1A", "ARL8A", "PATL1", "KLHL21", "MPHOSPH9", "PALLD", "MRPL32", "SELENBP1", "PTPN14", "PCGF2", "AKAP9", "TUBGCP5", "ADD3", "RANBP1", "SUMO3", "FSCN1", "CRIPT", "TACC3", "ZC3H15", "SETD7", "NAV1", "CEP57L1", "MYO10", "ORC6", "SERP1", "CACNA1C", "KMT5C", "DIMIT1", "SPIRE1", "MAP2K6", "CECR2", "OPHN1", "PNMA1", "BTBD1", "MYH15", "POLE3", "TSEN34", "MPLKIP", "RPS9", "RPS29", "ANK3", "FRMD4A", "MRPS26", "CARF", "HOMER2", "FLOT1", "ANXA1", "POLE", "HSPA14", "BAP1", "EMD", "FRG1", "PPP2R5A", "OASL", "EDF1", "INTS6", "DYNC1LI1", "AFAP1", "THAP2", "CEP295", "TUBB2B", "RPL35A", "NEBL", "LPXN", "XRN2", "CAMK4", "CNOT9", "MRPL16", "MRPS34", "OBSCN", "CEP41", "RPS14", "RNF19A", "GLI3", "UBA52", "ARRB1", "MRPL49", "NTRK2", "NUMA1", "KDM5A", "CTDP1", "CORO2B", "SDCCAG8", "TTLL1", "SARM1", "RECQL", "LIG3", "BAIAP2L1", "STAU2", "CDC14A", "DDX1", "NUFIP1", "WDR47", "KIZ", "SNW1", "TRIP4", "LIG1", "SSBP1", "DNM1", "ZNF330", "RPL34", "CCDC86", "NUP107", "TIMELESS", "NEK11", "RAB3GAP1", "RMDN2", "RHOU", "UCHL5", "CTNNAL1", "RASL11A", "DSTN", "ELL3", "FGF13", "ABI1", "KIF12", "RPL35", "MRPL15", "CENPE", "PPP3CA", "NEDD1", "RITA1", "PARN", "ZNF593", "DGKQ", "CENPC", "STOM", "DMP1", "LAD1", "HENMT1", "NOSTRIN", "S100A12", "MRPS18C", "ORC5", "METTL17", "ING2", "SETMAR", "KRT6C", "DLGAP1", "ENC1", "TLN2", "YIF1A", "BAIAP2", "MRPL14", "RELL1", "NEB", "ZNF74",</p>

	"GAS2L1", "PARPBP", "GTF2F2", "DCLRE1A", "MRPS18B", "KRT40", "ATF6B", "EXOSC6"],
protein serine/threonine phosphatase complex	["PPP2R5E", "PPP4R3B", "PPP2R5A", "PPP2R3A", "PPP3CA"],
chromosome	["MYCN", "STAT1", "TP73", "TERF1", "CHEK1", "TOP1", "PAX6", "ERCC1", "SOX18", "VCP", "BLM", "CDK4", "MTA3", "CSNK2A1", "HDAC8", "NSFL1C", "UBE2I", "BAZ1B", "NCAPD2", "CBX6", "INTS7", "SUZ12", "CENPP", "NUP98", "TEP1", "NCAPG", "THAP7", "PCGF2", "ADD3", "SUMO3", "SETD7", "ORC6", "KMT5C", "CECR2", "POLE3", "POLE", "PPP2R5A", "DYNC1LI1", "ARRB1", "NUMA1", "LIG3", "NUFIP1", "SNW1", "LIG1", "ZNF330", "NUP107", "TIMELESS", "UCHL5", "CENPE", "CENPC", "ORC5", "ING2", "SETMAR", "PARPBP"],
spliceosomal complex	["GPATCH1", "GEMIN7", "PPIL1", "SYF2", "DHX35", "ZNF326", "SNRPD1", "AQR", "FRG1", "SF3A1", "XAB2", "SNW1", "SNRPF"],
kinesin complex	["KIF23", "KLC2", "KIF5C"],
lytic vacuole	["HPSE", "SQSTM1", "IFITM3", "CD74", "STX3", "VPS33B", "SNX16", "PPT1", "GPR137B", "RAB14", "SLC48A1", "ARL8A", "TMEM97", "OSBPL1A", "PRDX6", "RNF152", "ANK3", "RRAGA", "VAMP7", "TSPAN1", "NEU1", "GALC", "ARRB1", "RAB7A", "PLA2G15", "ITM2C", "PRCP", "GGH", "GPC3"],
lysosome	["HPSE", "SQSTM1", "IFITM3", "CD74", "STX3", "VPS33B", "SNX16", "PPT1", "GPR137B", "RAB14", "SLC48A1", "ARL8A", "TMEM97", "OSBPL1A", "PRDX6", "RNF152", "ANK3", "RRAGA", "VAMP7", "TSPAN1", "NEU1", "GALC", "ARRB1", "RAB7A", "PLA2G15", "ITM2C", "PRCP", "GGH", "GPC3"],
coated vesicle membrane	["SREBF2", "GAD1", "HLA-E", "CD74", "SEC23B", "COPG1", "SEMA4C", "AP2A1", "AP2A2", "CLTA", "SEC24D", "COPE", "SAR1B"],
tight junction	["CDK4", "DDX58", "AMOTL1", "ANK3", "FRMD4A", "TJP3", "PARD3B", "MARVELD2", "IGSF5"],
microtubule organizing center	["CTNNB1", "CHEK1", "CDC42BPG", "CCNF", "CKAP2", "NAF1", "KIF23", "TTLL5", "TSPYL2", "PPP4R3B", "NCAPG", "PKD2", "CEP97", "TMEM67", "HAUS8", "CEP350", "CC2D1A", "MPHOSPH9", "AKAP9", "TUBGCP5", "RANBP1", "TACC3", "CEP57L1", "MPLKIP", "FLOT1", "DYNC1LI1", "CEP295", "CEP41", "RNF19A", "CTDP1", "SDCCAG8", "CDC14A", "KIZ", "TRIP4", "RAB3GAP1", "NEDD1", "RITA1", "YIF1A"],
clathrin-coated vesicle	["GAD1", "CD74", "GRIN1", "MYO1E", "CLINT1", "SEMA4C", "AP2A1", "PPT1", "STX6", "FCHO2", "RAB14", "STXBP5", "AP2A2", "ATP7A", "CLTA", "SPG21", "SLC2A8"],
cell-cell junction	["CTNNB1", "CDK4", "PAK1", "FGFR4", "FAT1", "DDX58", "PKP3", "MYO1E", "STX3", "SGSM3", "AMOTL1", "PKD2", "HEG1", "ADD3", "ANK3", "FRMD4A", "SDCCAG8", "TJP3", "PARD3B", "FGF13", "MARVELD2", "PANX3", "STEAP1", "TLN2", "IGSF5"],
nuclear ubiquitin ligase complex	["ANAPC15", "ANAPC11", "ANAPC2"],
cell junction	["CTNNB1", "CPEB1", "BCAR1", "CDK4", "PAK1", "FGFR4", "FAT1", "DDX58", "GRIN1", "PKP3", "MYO1E", "STX3", "DLC1", "SEMA4C", "NAF1", "SGSM3", "SNTB2", "AMOTL1", "EPB41L2", "PKD2", "ZFYVE21", "FBLIM1", "PALLD", "HEG1", "STXBP5", "ADD3", "FSCN1", "CRIPT", "OPHN1", "PNMA1", "GIT1", "ANK3", "FRMD4A", "HOMER2", "VAMP7", "AFAP1", "NEU1", "LPXN", "GABRP", "COLQ", "SDCCAG8", "TJP3", "SARM1", "BAIAP2L1", "PARD3B", "RHOU",

	"FGF13", "ABI1", "CBLN3", "MARVELD2", "PANX3", "STEAP1", "DLGAP1", "TLN2", "BAIAP2", "IGSF5", "ATF6B"],
apical junction complex	["CTNNB1", "CDK4", "DDX58", "AMOTL1", "ANK3", "FRMD4A", "TJP3", "PARD3B", "MARVELD2", "IGSF5"],
cytoplasmic vesicle part	["SREBF2", "BSG", "GAD1", "VEGFB", "BACE1", "HLA-E", "CD74", "ABCA3", "SEC23B", "COPG1", "SEMA4C", "CLCN3", "SNTB2", "RAB9B", "AP2A1", "TMEM67", "RAB14", "STXBP5", "SPIRE1", "AP2A2", "VAMP7", "CLTA", "UBA52", "ARRB1", "SEC24D", "RAB7A", "COPE", "SLC2A8", "SAR1B", "NOSTRIN", "ATP6V0C", "CFD"],
Golgi apparatus part	["SREBF2", "BSG", "HRAS", "GLCE", "MMP14", "HLA-E", "CD74", "ABCG1", "DHCR24", "NSFL1C", "POMGNT1", "SEC23B", "COPG1", "SH3GLB1", "PTGES2", "SLC30A7", "CLCN3", "AP2A1", "MGAT4A", "RAB30", "STX6", "RAB14", "MPHOSPH9", "NDFIP1", "DSE", "FUT8", "SLC35C1", "NDFIP2", "EXT2", "FIG4", "ATP7A", "CLTA", "ARRB1", "SEC24D", "FUT9", "GALNT5", "PLCE1", "IL17RD", "GABARAPL2", "SPG21", "NAGPA", "COPE", "STK16", "RHO", "SLC35A3", "TPST2", "GPC3", "SAR1B", "SLC39A13", "MGAT2", "YIF1A"],
endosome	["PML", "JAK2", "SIAH1", "SQSTM1", "BACE1", "RHOB", "HLA-E", "FGFR4", "IFITM3", "PMEL", "CD74", "ABCG1", "TRAF6", "HGS", "TNFAIP1", "CLCN3", "GRB2", "VPS33B", "SNX16", "LAMTOR3", "RABEP1", "STX6", "OCIAD1", "RAB14", "SLC48A1", "ARL8A", "NDFIP1", "ZFYVE16", "OSBPL1A", "SNX1", "NDFIP2", "FLOT1", "VAMP7", "FIG4", "ATP7A", "UBA52", "NTRK2", "ATP11A", "RAB7A", "PIK3C3", "SPG21", "EPHB1", "SLA", "STEAP1", "CHMP4C", "ATP6V0C"],
chromosomal part	["MYCN", "STAT1", "TP73", "TERF1", "CHEK1", "TOP1", "PAX6", "ERCC1", "SOX18", "VCP", "BLM", "CDK4", "MTA3", "CSNK2A1", "UBE2I", "BAZ1B", "NCAPD2", "CBX6", "SUZ12", "CENPP", "NUP98", "TEP1", "NCAPG", "PCGF2", "SUMO3", "ORC6", "KMT5C", "CECR2", "POLE3", "POLE", "PPP2R5A", "DYNC1LI1", "ARRB1", "LIG3", "NUFIP1", "SNW1", "ZNF330", "NUP107", "TIMELESS", "UCHL5", "CENPE", "CENPC", "ORC5", "ING2", "PARPBP"],
dendrite	["CTNNB1", "STAT1", "EPHB2", "CPEB1", "PAK1", "GRIN1", "PRKCA", "TXN2", "UBE2I", "LYN", "SEMA4C", "PPT1", "CRIPT", "CACNA1C", "OPHN1", "HOMER2", "NTRK2", "SARM1", "PALMD", "FZD3", "FGF13", "NPF", "EPHB1", "DLGAP1"],
vacuole	["HPSE", "SQSTM1", "SRPX", "IFITM3", "CD74", "STX3", "VPS33B", "SNX16", "PPT1", "GPR137B", "RAB14", "SLC48A1", "ARL8A", "TMEM97", "OSBPL1A", "PRDX6", "RNF152", "ANK3", "RRAGA", "VAMP7", "TSPAN1", "NEU1", "GALC", "ARRB1", "GABARAPL2", "RAB7A", "PLA2G15", "ITM2C", "PRCP", "GGH", "GPC3", "RAB24", "ATP6V0C"],
axon	["STAT1", "EPHB2", "BACE1", "PAK1", "NMU", "SEMA6A", "GRIN1", "KCNC4", "PPT1", "OPHN1", "ANK3", "NCAM2", "NTRK2", "SARM1", "FZD3", "FGF13", "NPF", "EPHB1", "AMIGO1"],
Golgi apparatus	["KLF5", "SREBF2", "BSG", "BHLHE40", "HRAS", "GLCE", "MMP14", "WNT4", "ATXN2", "BACE1", "HLA-E", "PAK1", "BIRC7", "PMEL", "CD74", "ABCG1", "FABP6", "DHCR24", "NSFL1C", "PLSCR1", "WWC1", "POMGNT1", "LYN", "CLINT1", "CALCOCO2", "SEC23B", "TMEM115", "COPG1", "YIPF3", "SH3GLB1", "PTGES2", "SLC30A7", "CLCN3", "GRB2", "AKT3", "AP2A1", "PPT1", "MGAT4A", "RAB30", "TRAPPC2", "DNM1L", "STX6", "BICD2", "MPPE1", "RAB14", "MPHOSPH9", "NDFIP1", "AKAP9", "FAM3C", "DSE", "SNX1", "FUT8", "SLC35C1", "NDFIP2", "EXT2", "RRAGA", "VAMP7", "FIG4", "STC2", "ATP7A", "CLTA", "ARRB1", "NTSR1", "FZD8", "SEC24D", "FUT9", "GALNT5", "PLCE1", "IL17RD", "ARF5", "GABARAPL2", "AP3M2", "RAB7A", "SPG21", "AP4S1", "NAGPA", "COPE", "STK16", "RHO",

	"SLC35A3", "TPST2", "ITM2C", "GPC3", "SAR1B", "SH3RF1", "BEND5", "SLC39A13", "IGFBP6", "MGAT2", "YIF1A"],
nucleolar part	["UBE2I", "RPP38", "POLR1B"],
basolateral plasma membrane	["CTNNB1", "BEST1", "SLCO4C1", "AP2A1", "SLC12A2", "PKD2", "SLC16A10", "ANK3", "ANXA1", "ATP7A", "SLC34A1", "P2RY12"],
proteasome complex	["VCP", "PSMD9", "PSMD2", "PSMC4", "PSMA3", "UCHL5", "PSMB7", "PSMA5", "PSMB3"],
eukaryotic translation initiation factor 3 complex	["COPS5", "EIF3A"],
condensed chromosome	["CHEK1", "BLM", "MTA3", "UBE2I", "BAZ1B", "NCAPD2", "NCAPG", "ADD3", "KMT5C", "DYNC1LI1", "LIG3", "NUP107", "CENPE", "CENPC"],
cell cortex	["CTNNB1", "FABP2", "ASPH", "TRAF6", "EPB41L2", "PKD2", "FBLIM1", "NDFIP1", "ADD3", "MYO10", "SPIRE1", "EXOC1", "DSTN", "OOEP"],
adherens junction	["CTNNB1", "BCAR1", "PAK1", "MYO1E", "DLC1", "ZFYVE21", "FBLIM1", "PALLD", "PNMA1", "GIT1", "AFAP1", "LPXN", "RHO", "TLN2", "ATF6B"],
DNA-directed RNA polymerase complex	["INTS7", "POLR1B", "GTF2H3", "INTS3", "EDF1", "INTS6", "TAF11", "GTF2F2"],
nuclear DNA-directed RNA polymerase complex	["INTS7", "POLR1B", "GTF2H3", "INTS3", "EDF1", "INTS6", "TAF11", "GTF2F2"],
RNA polymerase complex	["INTS7", "POLR1B", "GTF2H3", "INTS3", "EDF1", "INTS6", "TAF11", "GTF2F2"],
nuclear speck	["MECOM", "SON", "CD2BP2", "TIMM50", "GATAD2A", "THAP7", "PATL1", "MAML3", "PIP5K1A", "FRG1", "DGKQ"],
PML body	["PML", "BLM", "UBE2I", "HIPK3", "PATL1", "TRIM16"],
vacuolar part	["HPSE", "IFITM3", "CD74", "VPS33B", "GPR137B", "SLC48A1", "ARL8A", "OSBPL1A", "RNF152", "VAMP7", "TSPAN1", "NEU1", "GALC", "ARRB1", "GABARAPL2", "RAB7A", "ITM2C", "GPC3", "ATP6V0C"],
membrane-bounded vesicle	["SREBF2", "BSG", "GAD1", "PLAT", "HSPA5", "MMP14", "ITGAV", "VEGFB", "BACE1", "HLA-E", "PMEL", "SERPINF1", "CD74", "GRIN1", "TGFB1", "ABCA3", "HAP1", "CAPG", "MYO1E", "STX3", "HGS", "CLINT1", "SEC23B", "COPG1", "YIPF3", "SEMA4C", "SLC30A7", "CLCN3", "GRB2", "LAMC1", "SNTB2", "VPS33B", "RAB9B", "AP2A1", "PPT1", "RABEP1", "STX6", "ZFYVE21", "TMEM67", "FCHO2", "RAB14", "FAM3C", "STXBP5", "RALA", "PRDX6", "SPIRE1", "AP2A2", "FLOT1", "ANXA1", "YWHAB", "VAMP7", "NEU1", "ATP7A", "CLTA", "UBA52", "ARRB1", "MFGE8", "PDIA4", "SEC24D", "RAB7A", "SPG21", "COPE", "STK16", "SLC2A8", "GGH", "STOM", "SAR1B", "NOSTRIN", "ATP6V0C", "CFD"],
DNA-directed RNA polymerase II, holoenzyme	["INTS7", "GTF2H3", "INTS3", "EDF1", "INTS6", "TAF11", "GTF2F2"],
cytoplasmic membrane-bounded vesicle	["SREBF2", "BSG", "GAD1", "PLAT", "HSPA5", "MMP14", "ITGAV", "VEGFB", "BACE1", "HLA-E", "PMEL", "SERPINF1", "CD74", "GRIN1", "ABCA3", "HAP1", "CAPG", "MYO1E", "STX3", "HGS", "CLINT1", "SEC23B", "COPG1", "YIPF3", "SEMA4C", "SLC30A7", "CLCN3", "SNTB2", "VPS33B", "RAB9B", "AP2A1", "PPT1", "RABEP1", "STX6", "ZFYVE21", "TMEM67", "FCHO2", "RAB14", "FAM3C",

	"STXBP5", "RALA", "PRDX6", "SPIRE1", "AP2A2", "FLOT1", "YWHAB", "VAMP7", "NEU1", "ATP7A", "CLTA", "UBA52", "ARRB1", "PDIA4", "SEC24D", "RAB7A", "SPG21", "COPE", "STK16", "SLC2A8", "GGH", "STOM", "SAR1B", "NOSTRIN", "ATP6V0C", "CFD"],
cell leading edge	["CTNNB1", "BCAR1", "SPRY1", "PAK1", "FAT1", "DDX58", "CDC42BPG", "WWC1", "WASF1", "AMOTL1", "PKD2", "PALLD", "MYO10", "PIP5K1A", "FZD3", "ABI1", "SH3RF1", "TLN2", "BAIAP2"],
nuclear chromatin	["STAT1", "PAX6", "SOX18", "CSNK2A1", "SUZ12", "PCGF2", "CECR2", "NUFIP1", "TIMELESS", "UCHL5", "ING2"],
transcription factor TFIID complex	["EDF1", "TAF11"]

Supplementary Table 1: Protein-protein interaction network analysis table, which is showing the interaction, Coexpression and homology genes of up-regulated genes from n=696 DEGS.

Node1	Node2	Homology	Coexpression	Combined_score
CCNA2	KIF18A	0	0.787	0.562
CCNA2	ZWILCH	0	0.752	0.622
SAP30BP	SIN3A	0	0.358	0.918
CCNA2	EME1	0	0.296	0.93
KIF18A	ZWILCH	0	0.27	0.711
BRCC3	UBE2K	0	0.144	0.976
CHERP	SART1	0	0.142	0.983
FN1	TIMP2	0	0.139	0.457
FN1	VIM	0	0.129	0.734
ATG4C	MAP1LC3A	0	0.122	0.999
MARK2	MARK3	0.964	0.113	0.603
MOB4	PPP2R1A	0	0.104	0.955
CHMP4B	MAP1LC3A	0	0.086	0.406
ATG13	MAP1LC3A	0	0.083	0.852
BCL7C	DPF2	0	0.076	0.441
UTP11L	ZWILCH	0	0.076	0.505
ARAF	MARK3	0.576	0.069	0.522
ARAF	PPP2R1A	0	0.065	0.769
HDAC11	SIN3A	0	0.065	0.795
CCNA2	HDAC11	0	0.064	0.401
MOB4	SIKE1	0	0.064	0.433
MXI1	SIN3A	0	0.063	0.684
ARAF	FN1	0	0.062	0.518
ATG13	ATG4C	0	0.062	0.917
CCNA2	PPP2R1A	0	0.062	0.415
MCL1	VIM	0	0.062	0.775
KIF13B	KIF18A	0.659	0.056	0.711
CCNA2	MCL1	0	0.049	0.441
MARK3	PPP2R1A	0	0.046	0.535

Supplementary Table 13: Protein-protein interaction network analysis table, which is showing the interaction, Coexpression and homology genes of down-regulated genes from n=1301 DEGS.

Node1	Node2	Homology	Coexpression	Combined_score
COL1A1	COL5A1	0.85	0.779	0.955
COL1A1	THBS2	0	0.31	0.659
COL5A1	THBS2	0	0.307	0.658

COL5A1	LAMC1	0	0.226	0.665
COL1A1	LAMC1	0	0.21	0.626
HRAS	STUB1	0	0.17	0.407
ITGAV	LAMC1	0	0.159	0.95
PPP2R5E	YWHAB	0	0.118	0.921
COL5A1	ITGAV	0	0.109	0.935
ITGA2	LAMC1	0	0.103	0.939
COL1A1	ITGAV	0	0.098	0.943
GRB2	YWHAB	0	0.096	0.537
GRB2	HRAS	0	0.089	0.994
BCAR1	ITGAV	0	0.087	0.951
CSNK2A1	CTNNB1	0	0.087	0.903
ITGAV	THBS2	0	0.087	0.72
AKT3	GRB2	0	0.083	0.586
AKT3	PPP2R3A	0	0.083	0.652
AKT3	CTNNB1	0	0.083	0.713
ITGA2	ITGAV	0.598	0.079	0.931
PPP2R3A	PPP2R5A	0	0.079	0.941
PPP2R3A	PPP2R5E	0	0.079	0.876
CTNNB1	SGK1	0	0.078	0.446
BCAR1	HRAS	0	0.076	0.43

#node	node2	node1_string_id	node2_string_id	neighborhood_on_chromosome	gene_usage	phylogenetic_cooccurrence	homology	coexpression	experimentally_determined_interaction	database_annotated	automated_textmining	combined_score
COL1A1	COL5A1	9606.ENSPP000000225964	9606.ENSPP000000360882	0	0	0.42	0.85	0.779	0.192	0.72	0.82	0.955
COL1A1	COL5A1	9606.ENSPP000000225964	9606.ENSPP000000355751	0	0	0	0	0.31	0.057	0	0.518	0.659
COL5A1	COL1A1	9606.ENSPP000000360882	9606.ENSPP000000355751	0	0	0	0	0.307	0.057	0	0.519	0.658
COL5A1	COL1A1	9606.ENSPP000000360882	9606.ENSPP000000258341	0	0	0	0	0.226	0.13	0	0.543	0.665
COL1A1	COL5A1	9606.ENSPP000000225964	9606.ENSPP000000258341	0	0	0	0	0.21	0.13	0	0.499	0.626
HRAS	STUB1	9606.ENSPP000000407586	9606.ENSPP000000219548	0	0	0	0	0.17	0	0	0.315	0.407
ITGAV	LAMC1	9606.ENSPP000000261023	9606.ENSPP000000258341	0	0	0	0	0.159	0.153	0.9	0.383	0.95
PPP2R5E	YWHAB	9606.ENSPP000000000000	9606.ENSPP000000000000	0	0	0	0	0.118	0.101	0.9	0.124	0.921

R5 E	H A B	000337 641	000361 930									
C OL 5A 1	IT G AV	9606.E NSP00 000360 882	9606.E NSP00 000261 023	0	0	0	0	0.1 09	0	0.9	0.338	0.93 5
IT G A2	L A M C1	9606.E NSP00 000296 585	9606.E NSP00 000258 341	0	0	0	0	0.1 03	0.153	0.9	0.299	0.93 9
C OL 1A 1	IT G AV	9606.E NSP00 000225 964	9606.E NSP00 000261 023	0	0	0	0	0.0 98	0	0.9	0.428	0.94 3
G RB 2	Y W H A B	9606.E NSP00 000376 345	9606.E NSP00 000361 930	0	0	0	0	0.0 96	0.41	0	0.202	0.53 7
G RB 2	H R AS	9606.E NSP00 000376 345	9606.E NSP00 000407 586	0	0	0	0	0.0 89	0.5	0.9	0.901	0.99 4
BC A R1	IT G AV	9606.E NSP00 000391 669	9606.E NSP00 000261 023	0	0	0	0	0.0 87	0.27	0.9	0.354	0.95 1
CS N K2 A1	CT N N B1	9606.E NSP00 000217 244	9606.E NSP00 000344 456	0	0	0	0	0.0 87	0.213	0.8	0.407	0.90 3
IT G AV	T H BS 2	9606.E NSP00 000261 023	9606.E NSP00 000355 751	0	0	0	0	0.0 87	0.108	0.6	0.243	0.72
A KT 3	G R B2	9606.E NSP00 000263 826	9606.E NSP00 000376 345	0	0	0	0	0.0 83	0.156	0	0.508	0.58 6
A KT 3	PP P2 R3 A	9606.E NSP00 000263 826	9606.E NSP00 000264 977	0	0	0	0	0.0 83	0.07	0.6	0.101	0.65 2
A KT 3	CT N N B1	9606.E NSP00 000263 826	9606.E NSP00 000344 456	0	0	0	0	0.0 83	0.142	0	0.665	0.71 3
IT G A2	IT G AV	9606.E NSP00 000296 585	9606.E NSP00 000261 023	0	0	0	0. 59 8	0.0 79	0	0.9	0.713	0.93 1
PP P2 R3 A	PP P2 R5 A	9606.E NSP00 000264 977	9606.E NSP00 000261 461	0	0	0	0	0.0 79	0	0.72	0.792	0.94 1

PP P2 R3 A	PP P2 R5 E	9606.E NSP00 000264 977	9606.E NSP00 000337 641	0	0	0	0	0.0 79	0	0.54	0.732	0.87 6
CT N N B1	SG K1	9606.E NSP00 000344 456	9606.E NSP00 000356 832	0	0	0	0	0.0 78	0	0	0.424	0.44 6
BC A R1	H R AS	9606.E NSP00 000391 669	9606.E NSP00 000407 586	0	0	0	0	0.0 76	0	0	0.409	0.43
CS F1 R	PI K3 R1	9606.E NSP00 000286 301	9606.E NSP00 000428 056	0	0	0	0	0.0 76	0.84	0	0.721	0.95 5
JA K2	PI K3 R1	9606.E NSP00 000371 067	9606.E NSP00 000428 056	0	0	0	0	0.0 73	0.752	0.9	0.416	0.98 4
N R4 A1	SG K1	9606.E NSP00 000440 864	9606.E NSP00 000356 832	0	0	0	0	0.0 73	0	0	0.414	0.43 4
BC A R1	IT G A2	9606.E NSP00 000391 669	9606.E NSP00 000296 585	0	0	0	0	0.0 69	0	0.6	0.229	0.68 7
C D1 51	IT G A2	9606.E NSP00 000380 565	9606.E NSP00 000296 585	0	0	0	0	0.0 69	0.058	0	0.391	0.41 9
C OL 1A 1	IT G A2	9606.E NSP00 000225 964	9606.E NSP00 000296 585	0	0	0	0	0.0 69	0.463	0.9	0.402	0.96 6
CT N N B1	IT G AV	9606.E NSP00 000344 456	9606.E NSP00 000261 023	0	0	0	0	0.0 69	0.119	0	0.387	0.45 3
PP P2 R5 E	PP P3 R5 A	9606.E NSP00 000337 641	9606.E NSP00 000378 323	0	0	0	0	0.0 69	0.246	0.54	0.252	0.72 6
CT N N B1	Y W H A B	9606.E NSP00 000344 456	9606.E NSP00 000361 930	0	0	0	0	0.0 68	0.058	0.9	0.281	0.92 8
CT N N B1	JA K2	9606.E NSP00 000344 456	9606.E NSP00 000371 067	0	0	0	0	0.0 66	0.142	0	0.586	0.63 9
H R AS	PP P2 R5 A	9606.E NSP00 000407 586	9606.E NSP00 000261 461	0	0	0	0	0.0 66	0.101	0.9	0.155	0.91 9

H R AS	PP P2 R5 E	9606.E NSP00 000407 586	9606.E NSP00 000337 641	0	0	0	0	0.0 66	0.101	0.9	0.118	0.91 6
SG K1	Y W H A B	9606.E NSP00 000356 832	9606.E NSP00 000361 930	0	0	0	0	0.0 66	0.109	0	0.602	0.64 1
CT N N B1	PP P2 R5 A	9606.E NSP00 000344 456	9606.E NSP00 000261 461	0	0	0	0	0.0 65	0	0.9	0.641	0.96 3
CT N N B1	PA K1	9606.E NSP00 000344 456	9606.E NSP00 000278 568	0	0	0	0	0.0 65	0.078	0.9	0.567	0.95 7
CT N N B1	PP P2 R5 E	9606.E NSP00 000344 456	9606.E NSP00 000337 641	0	0	0	0	0.0 65	0	0.6	0.215	0.68
CT N N B1	G R B2	9606.E NSP00 000344 456	9606.E NSP00 000376 345	0	0	0	0	0.0 65	0.077	0	0.551	0.57 9
ST X3	ST X6	9606.E NSP00 000338 562	9606.E NSP00 000258 301	0	0	0	0	0.0 65	0.759	0.54	0.821	0.97 9
A KT 3	PP P2 R5 A	9606.E NSP00 000263 826	9606.E NSP00 000261 461	0	0	0	0	0.0 64	0.347	0.9	0.194	0.94 4
A KT 3	PI K3 C B	9606.E NSP00 000263 826	9606.E NSP00 000289 153	0	0	0	0	0.0 64	0.204	0.6	0.699	0.89 8
A KT 3	PP P2 R5 E	9606.E NSP00 000263 826	9606.E NSP00 000337 641	0	0	0	0	0.0 64	0.347	0.9	0.139	0.94
PI K3 CB	PI K3 R1	9606.E NSP00 000289 153	9606.E NSP00 000428 056	0	0	0	0	0.0 64	0.946	0.9	0.988	0.99 9
IT G A2	IT G B8	9606.E NSP00 000296 585	9606.E NSP00 000222 573	0	0	0	0	0.0 63	0.19	0.9	0.527	0.95 9
IT G AV	IT G B8	9606.E NSP00 000261 023	9606.E NSP00 000222 573	0	0	0	0	0.0 63	0.964	0.9	0.847	0.99 9
PA K1	PI K3 C B	9606.E NSP00 000278 568	9606.E NSP00 000289 153	0	0	0	0	0.0 63	0.318	0	0.153	0.41 2

PP P2 R3 A	PP P3 C A	9606.E NSP00 000264 977	9606.E NSP00 000378 323	0	0	0	0	0.0 63	0.139	0.72	0.225	0.80 1
A KT 3	PI K3 R1	9606.E NSP00 000263 826	9606.E NSP00 000428 056	0	0	0	0	0.0 62	0.102	0.65	0.702	0.9
A RL 8A	B H L H E4 0	9606.E NSP00 000272 217	9606.E NSP00 000256 495	0	0	0	0	0.0 62	0.065	0	0.551	0.57 1
CS F1 R	G R B2	9606.E NSP00 000286 301	9606.E NSP00 000376 345	0	0	0	0	0.0 62	0.883	0.6	0.951	0.99 7
CT N N B1	H R AS	9606.E NSP00 000344 456	9606.E NSP00 000407 586	0	0	0	0	0.0 62	0.183	0	0.824	0.85 4
G RB 2	PA K1	9606.E NSP00 000376 345	9606.E NSP00 000278 568	0	0	0	0	0.0 62	0.27	0.6	0.549	0.86
H R AS	PI K3 C B	9606.E NSP00 000407 586	9606.E NSP00 000289 153	0	0	0	0	0.0 62	0.38	0.9	0.565	0.97 1
H R AS	ST X3	9606.E NSP00 000407 586	9606.E NSP00 000338 562	0	0	0	0	0.0 62	0.451	0	0.065	0.47 6
H R AS	Y W H A B	9606.E NSP00 000407 586	9606.E NSP00 000361 930	0	0	0	0	0.0 62	0.251	0.9	0.267	0.94 1
IT G B8	T H BS 2	9606.E NSP00 000222 573	9606.E NSP00 000355 751	0	0	0	0	0.0 62	0	0.6	0.194	0.67 1
IT G B8	L A M C1	9606.E NSP00 000222 573	9606.E NSP00 000258 341	0	0	0	0	0.0 62	0.13	0.6	0.151	0.68 6
JA K2	PI K3 C B	9606.E NSP00 000371 067	9606.E NSP00 000289 153	0	0	0	0	0.0 62	0.104	0.9	0.319	0.93 5
LA M C1	PA K1	9606.E NSP00 000258 341	9606.E NSP00 000278 568	0	0	0	0	0.0 62	0	0.9	0	0.90 2
PP P2	PP P2	9606.E NSP00	9606.E NSP00	0	0	0	0.	0.0 98 62	0	0.54	0.824	0.55 7

R5 A	R5 E	000261 461	000337 641									
PP P2 R5 A	PP P3 C A	9606.E NSP00 000261 461	9606.E NSP00 000378 323	0	0	0	0	0.0 62	0.246	0.9	0.269	0.94 1
SG K1	ST U B1	9606.E NSP00 000356 832	9606.E NSP00 000219 548	0	0	0	0	0.0 62	0.486	0	0.557	0.76 8
H R AS	PA K1	9606.E NSP00 000407 586	9606.E NSP00 000278 568	0	0	0	0	0.0 59	0.18	0.9	0.39	0.94 6
PI N K1	ST U B1	9606.E NSP00 000364 204	9606.E NSP00 000219 548	0	0	0	0	0.0 58	0.151	0	0.325	0.41 3
H R AS	JA K2	9606.E NSP00 000407 586	9606.E NSP00 000371 067	0	0	0	0	0.0 56	0.14	0.9	0.698	0.97 2
C D1 51	IT G AV	9606.E NSP00 000380 565	9606.E NSP00 000261 023	0	0	0	0	0.0 53	0.058	0	0.427	0.44 4
G RB 2	PI K3 C B	9606.E NSP00 000376 345	9606.E NSP00 000289 153	0	0	0	0	0.0 52	0.452	0.9	0.445	0.96 7
BC A R1	IT G B8	9606.E NSP00 000391 669	9606.E NSP00 000222 573	0	0	0	0	0.0 49	0.102	0.6	0.251	0.71
C OL 1A 1	IT G B8	9606.E NSP00 000225 964	9606.E NSP00 000222 573	0	0	0	0	0.0 49	0.061	0.6	0.228	0.68 7
H R AS	TP 73	9606.E NSP00 000407 586	9606.E NSP00 000367 545	0	0	0	0	0.0 49	0.284	0	0.332	0.50 6
A K AP 9	PT T G1	9606.E NSP00 000348 573	9606.E NSP00 000377 536	0	0	0	0	0	0	0	0.49	0.49
A K AP 9	JA K2	9606.E NSP00 000348 573	9606.E NSP00 000371 067	0	0	0	0	0	0	0.9	0.057	0.90 1
A KT 3	H R AS	9606.E NSP00 000263 826	9606.E NSP00 000407 586	0	0	0	0	0	0.14	0	0.629	0.66 7
A KT 3	N R4 A1	9606.E NSP00	9606.E NSP00	0	0	0	0	0	0.057	0.9	0	0.90 1

		000263 826	000440 864									
BC A R1	CS F1 R	9606.E NSP00 000391 669	9606.E NSP00 000286 301	0	0	0	0	0	0	0.9	0.135	0.90 9
BC A R1	CT N N B1	9606.E NSP00 000391 669	9606.E NSP00 000344 456	0	0	0	0	0	0	0	0.446	0.44 6
BC A R1	Y W H A B	9606.E NSP00 000391 669	9606.E NSP00 000361 930	0	0	0	0	0	0	0	0.44	0.44
BC A R1	JA K2	9606.E NSP00 000391 669	9606.E NSP00 000371 067	0	0	0	0	0	0.057	0.9	0.195	0.91 7
BC A R1	G R B2	9606.E NSP00 000391 669	9606.E NSP00 000376 345	0	0	0	0	0	0.865	0	0.941	0.99 1
BC A R1	PI K3 R1	9606.E NSP00 000391 669	9606.E NSP00 000428 056	0	0	0	0	0	0.334	0.9	0.247	0.94 5
C OL 1A 1	CT N N B1	9606.E NSP00 000225 964	9606.E NSP00 000344 456	0	0	0	0	0	0.056	0	0.599	0.60 5
CS F1 R	IT G AV	9606.E NSP00 000286 301	9606.E NSP00 000261 023	0	0	0	0	0	0.27	0.9	0.291	0.94 3
CS F1 R	CT N N B1	9606.E NSP00 000286 301	9606.E NSP00 000344 456	0	0	0	0	0	0.056	0	0.455	0.46 3
CS F1 R	V E GF B	9606.E NSP00 000286 301	9606.E NSP00 000311 127	0	0	0	0	0	0.059	0.6	0.382	0.74 7
CS F1 R	H R AS	9606.E NSP00 000286 301	9606.E NSP00 000407 586	0	0	0	0	0	0.102	0.9	0.519	0.95 3
CT N N B1	ST U B1	9606.E NSP00 000344 456	9606.E NSP00 000219 548	0	0	0	0	0	0.311	0	0.537	0.66 8
CT N N B1	N R4 A1	9606.E NSP00 000344 456	9606.E NSP00 000440 864	0	0	0	0	0	0.486	0	0.425	0.69 2

CT N N B1	PI K3 R1	9606.E NSP00 000344 456	9606.E NSP00 000428 056	0	0	0	0	0	0.761	0.9	0.74	0.99 3
G RB 2	JA K2	9606.E NSP00 000376 345	9606.E NSP00 000371 067	0	0	0	0	0	0.728	0.9	0.982	0.99 9
G RB 2	PI K3 R1	9606.E NSP00 000376 345	9606.E NSP00 000428 056	0	0	0	0	0	0.907	0.9	0.934	0.99 9
H R AS	SG K1	9606.E NSP00 000407 586	9606.E NSP00 000356 832	0	0	0	0	0	0.305	0	0.391	0.55 9
H R AS	PI K3 R1	9606.E NSP00 000407 586	9606.E NSP00 000428 056	0	0	0	0	0	0.789	0.9	0.778	0.99 4
IT G A2	PI K3 C B	9606.E NSP00 000296 585	9606.E NSP00 000289 153	0	0	0	0	0	0	0.6	0.143	0.64 2
IT G A2	PI K3 R1	9606.E NSP00 000296 585	9606.E NSP00 000428 056	0	0	0	0	0	0	0.6	0.15	0.64 5
IT G A2	T H BS 2	9606.E NSP00 000296 585	9606.E NSP00 000355 751	0	0	0	0	0	0.067	0.6	0.246	0.69 4
IT G AV	PI K3 R1	9606.E NSP00 000261 023	9606.E NSP00 000428 056	0	0	0	0	0	0	0.9	0.155	0.91 1
JA K2	Y W H A B	9606.E NSP00 000371 067	9606.E NSP00 000361 930	0	0	0	0	0	0.165	0.9	0.076	0.91 6
PI K3 CB	SG K1	9606.E NSP00 000289 153	9606.E NSP00 000356 832	0	0	0	0	0	0.213	0	0.481	0.57 4
PP P2 R5 A A B	Y W H A B	9606.E NSP00 000261 461	9606.E NSP00 000361 930	0	0	0	0	0	0.101	0.9	0.118	0.91 3